

# Structural and molecular characterization of paraventricular thalamic glucokinase-expressing neuronal circuits in the mouse

Sevasti Gaspari | Simon Quenneville | Ana Rodriguez Sanchez-Archipidona |

Bernard Thorens | Sophie Croizier 

Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland

#### Correspondence

Sophie Croizier, Center for Integrative Genomics, University of Lausanne, Genopode building, 1015 Lausanne, Switzerland.  
Email: [sophie.croizier@unil.ch](mailto:sophie.croizier@unil.ch)

Bernard Thorens and Sophie Croizier are co-last authors.

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## Abstract

The thalamic paraventricular nucleus (PVT) is a structure highly interconnected with several nuclei ranging from forebrain to hypothalamus and brainstem. Numerous rodent studies have examined afferent and efferent connections of the PVT and their contribution to behavior, revealing its important role in the integration of arousal cues. However, the majority of these studies used a region-oriented approach, without considering the neuronal subtype diversity of the nucleus. In the present study, we provide the anatomical and transcriptomic characterization of a subpopulation of PVT neurons molecularly defined by the expression of glucokinase (Gck). Combining a genetically modified mouse model with viral tracing approaches, we mapped both the anterograde and the retrograde projections of Gck-positive neurons of the anterior PVT ( $Gck^{aPVT}$ ). Our results demonstrated that  $Gck^{aPVT}$  neurons innervate several nuclei throughout the brain axis. The strongest connections are with forebrain areas associated with reward and stress and with hypothalamic structures involved in energy balance and feeding regulation. Furthermore, transcriptomic analysis of the Gck-expressing neurons revealed that they are enriched in receptors for hypothalamic-derived neuropeptides, adhesion molecules, and obesity and diabetes susceptibility transcription factors. Using retrograde labeling combined with immunohistochemistry and *in situ* hybridization, we identify that  $Gck^{aPVT}$  neurons receive direct inputs from well-defined hypothalamic populations, including arginine-vasopressin-, melanin-concentrating hormone-, orexin-, and proopiomelanocortin-expressing neurons. This detailed anatomical and transcriptomic characterization of  $Gck^{aPVT}$  neurons provides a basis for functional studies of the integration of homeostatic and hedonic aspects of energy homeostasis, and for deciphering the potential role of these neurons in obesity and diabetes development.

**Abbreviations:** AAV, adeno-associated virus; AD, anterodorsal nucleus; AHN, anterior hypothalamic nucleus; aPVT, anterior paraventricular nucleus of the thalamus; ARH, arcuate nucleus of the hypothalamus; AVP, arginine-vasopressin; BLA, basolateral amygdaloid nucleus, anterior part; BNST, bed nucleus of the stria terminalis; ceA, central amygdaloid nucleus; CeL, central amygdaloid nucleus, lateral division; Cg, cingulate cortex; CM, centromedial nucleus; CRH, corticotropin-releasing hormone; DMH, dorsomedial nucleus of the hypothalamus; DTT, dorsal tenia tecta; Ect, ectorhinal cortex; Gck, glucokinase; IL, infralimbic cortex; LHA, lateral hypothalamic area; MCH, melanin-concentrating hormone; MPO, medial preoptic nucleus; NAC, nucleus accumbens; ORX, orexin; PAG, periaqueductal gray; PBS, phosphate-buffered saline; PFA, paraformaldehyde; POMC, proopiomelanocortin; PrL, prelimbic cortex; PT, paratenial thalamic nucleus; PVH, paraventricular nucleus of the hypothalamus; PVT, paraventricular nucleus of the thalamus; SST, somatostatin; TH, tyrosine hydroxylase; TRH, thyrotropin-releasing hormone; VMH, ventromedial nucleus of the hypothalamus

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**KEY WORDS**

anterograde and retrograde tract tracing, glucokinase-expressing neurons, hypothalamic nuclei, neurohormones, neuropeptides, neurotransmitters, paraventricular nucleus of the thalamus, TRAP

## 1 | INTRODUCTION

The paraventricular nucleus of the thalamus (PVT) belongs to a complex neuronal network that involves a large number of brain sites implicated in a broad range of functions from rewarding to aversive behaviors (Choi et al., 2019; Millan et al., 2017; Zhou & Zhu, 2019). While the afferent and efferent projections of the anterior PVT (aPVT) have been described in great detail in rats (Kirouac, 2015; Li & Kirouac, 2008, 2012), similar studies in mice or based on specific subpopulations of aPVT neurons are less developed.

The aPVT is well connected to brain areas controlling goal-oriented and decision-making behaviors such as the prefrontal cortex, the nucleus accumbens (NAc), and the lateral hypothalamic area (LHA) (Li & Kirouac, 2008; Li & Kirouac, 2012). In line with these anatomical properties, functional studies showed a preponderant role of the aPVT neurons in cue-motivated behaviors (Millan et al., 2017). Indeed, several studies reported a role of aPVT neurons in drug- and food-seeking behaviors (Choi & McNally, 2017; Choi et al., 2019; Millan et al., 2017; Otis et al., 2019). Moreover, recent work from our laboratory showed a role for Glut2 neurons of the aPVT, which are activated by hypoglycemia and that project to the NAc in regulating sucrose-seeking behavior (Labouébe et al., 2016). More recently, we identified another neuronal population of the aPVT, which expresses the glycolytic enzyme glucokinase (Gck). The Gck-expressing neurons of the aPVT ( $Gck^{aPVT}$ ) are activated by hyperglycemia and negatively control sucrose-seeking behavior through their projections to the NAc (Kessler et al., 2021). The precise description of the overall networks formed by the glucose responsive neurons of the aPVT and the molecular characterization of their upstream and downstream neuronal populations are still unknown.

In this study, we used viral anterograde and retrograde tracing methods combined with transcriptomic analysis, immunohistochemistry, and *in situ* hybridization, to describe the  $Gck^{aPVT}$  neuronal network. We focused our study on forebrain structures involved in motivated behavior, in particular, the NAc, the amygdala, and the bed nucleus of the stria terminalis (BNST), and on hypothalamic nuclei involved in energy and glucose homeostasis such as the paraventricular (PVH), the dorsomedial (DMH), the ventromedial (VMH), the arcuate nuclei (ARH), and the LHA (Christoffel et al., 2021; Ruud et al., 2017; Smith et al., 2019; Stuber & Wise, 2016; Timper & Brüning, 2017). Our transcriptomic characterization revealed that  $Gck^{aPVT}$  neurons are enriched in mRNAs encoding for a subset of neuroactive receptors, axon guidance molecules, and obesity- and diabetes-related genes. Based on these hints for neurotransmitter responsiveness, we showed that presynaptic neurons to  $GCK^{aPVT}$  neurons express

arginine-vasopressin (AVP), melanin-concentrating hormone (MCH), orexin (ORX), and pro-opiomelanocortin (POMC) and were GABAergic or glutamatergic.

## 2 | RESULTS

### 2.1 | $GCK^{aPVT}$ neuronal outputs

#### 2.1.1 | Viral targeting of the aPVT

For viral-based tracing experiments, we used  $Gck^{Cre/+}$  mice, which express the Cre recombinase in all Gck neurons (Kessler et al., 2021).

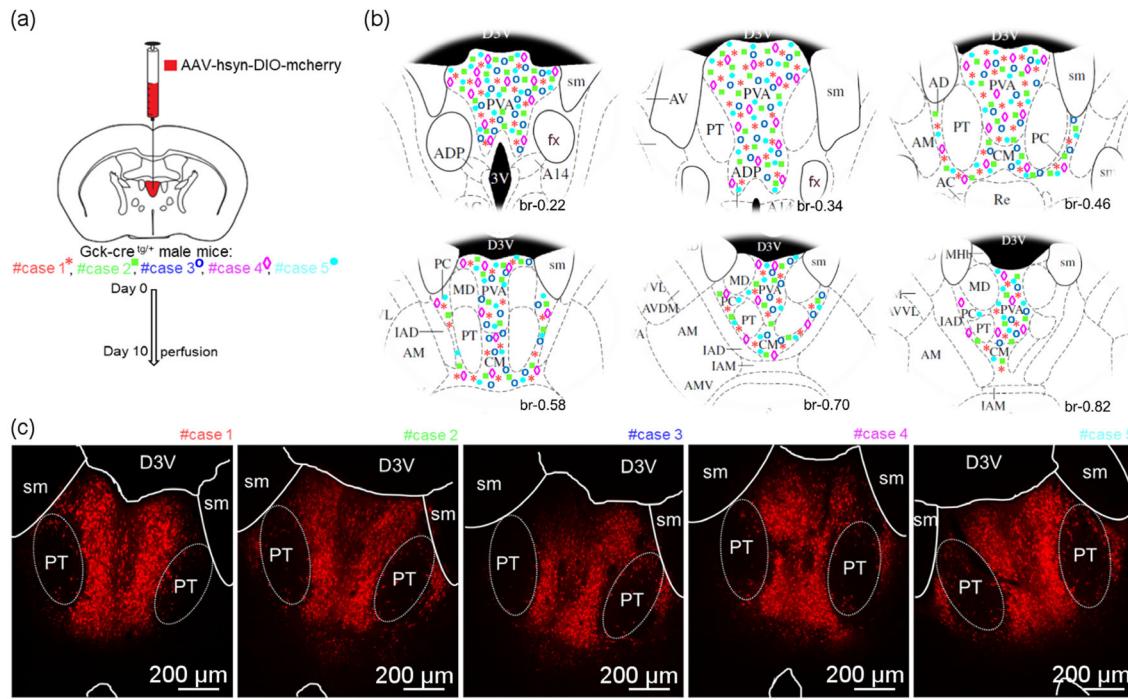
Five  $Gck^{Cre/+}$  male mice were used for anterograde tracing analysis. Mice were injected in the aPVT with an adeno-associated virus (AAV) allowing for the Cre-dependent expression of mCherry (AAV-hSyn-DIO-mCherry) (Figure 1a). Ten days later, the mice were perfused fixed and their brain collected for injection site verification and projection tracing. In all five cases, viral targeting was mainly localized in aPVT with some spreading observed in anterodorsal nucleus (AD) and centromedial thalamus (CM) (Figure 1b). Representative pictures of the infected areas for the five mice are presented in Figure 1c.

#### 2.1.2 | Anterograde projections of the $GCK^{aPVT}$ neurons

Our analysis was focused on brain sections extending from the anterior cortex to the midbrain. The majority of the  $GCK^{aPVT}$  fibers were observed in forebrain areas and the hypothalamus, with very few labeled fibers identified at the midbrain level. An overview of the output projection areas for  $GCK^{aPVT}$  neurons from mouse #1 is presented in Figures 2 and 19.

#### Forebrain

The  $GCK^{aPVT}$  neurons provide inputs to several forebrain areas (Figures 2a-o and 3; Table 1). Numerous projections were observed in cortical areas, with the strongest ones appearing in prelimbic (PrL) and infralimbic cortex (IL) (Figures 2a-d and 3a,b; Table 1) and some localized at the level of cingulate cortex (Cg) (predominantly Cg, area 2 [Cg2]) (Figure 3c). A small but consistent number of mCherry-labeled fibers were also observed at the ectorhinal cortex (Ect) (Figure 3d; Table 1), and the septum along the lateral ventricle (Figure 2e-f; Table 1). Lastly, fewer fibers, but consistent over all the



**FIGURE 1** (a) Experimental approach. AAV-hSyn-DIO-mCherry was injected into the aPVT of 16–20-week-old Gck<sup>Cre/+</sup> male mice that were sacrificed 10 days later. Schematic representation of the viral distribution across the anteroposterior axis of the PVT (b) and representative images of the injection site at bregma –0.4 (c) in all five cases used (#1 to #5). A14, dopaminergic group A14; AC, anterior commissural nucleus; ADP, anterodorsal preoptic nucleus; AM, anteromedial nucleus; AV, anteroventral nucleus; AVDM, anteroventral nucleus, dorsomedial part; D3V, dorsal 3rd ventricle; fx, fornix; IAD, interanterodorsal thalamic nucleus; IAM, interanteromedial thalamic nucleus; MD, medial dorsal nucleus; PC, paracentral thalamic nucleus; PT, paratenial thalamic nucleus; PVA, paraventricular thalamic nucleus, anterior part; Re, reunions thalamic nucleus; sm, stria medullaris

five cases reported, were observed in the subiculum of the hippocampus (Figures 2o and 3e). The densest projection sites appeared to be the NAc and the BNST (Figures 2c–h and 3f–i; Table 1). In all cases, Gck<sup>aPVT</sup> fibers were observed throughout the anteroposterior axis with emphasis in the accumbens shell (Figures 2d–f and 3f,g; Table 1) and the dorsomedial and dorsolateral divisions of the anterior part of the BNST (Figures 2g and 3h,i; Table 1). Another important output target of Gck<sup>aPVT</sup> neurons was the amygdala, with strong projections observed in both central (CeL) and basolateral (BL) amygdala, extended until its very posterior division (Figures 2k–n and 3j–m; Table 1).

#### Hypothalamus

In the hypothalamus, sparse projections were present in the anterior nucleus of hypothalamus (AHN), the LHA, the PVH, and the ARH (Figures 2j–m and 4). The nuclei that received the densest projections were the dorsomedial divisions of the DMH (Figure 4b,c) and the dorsomedial division of the VMH (Figure 4b,c).

#### Olfactory structures and midbrain

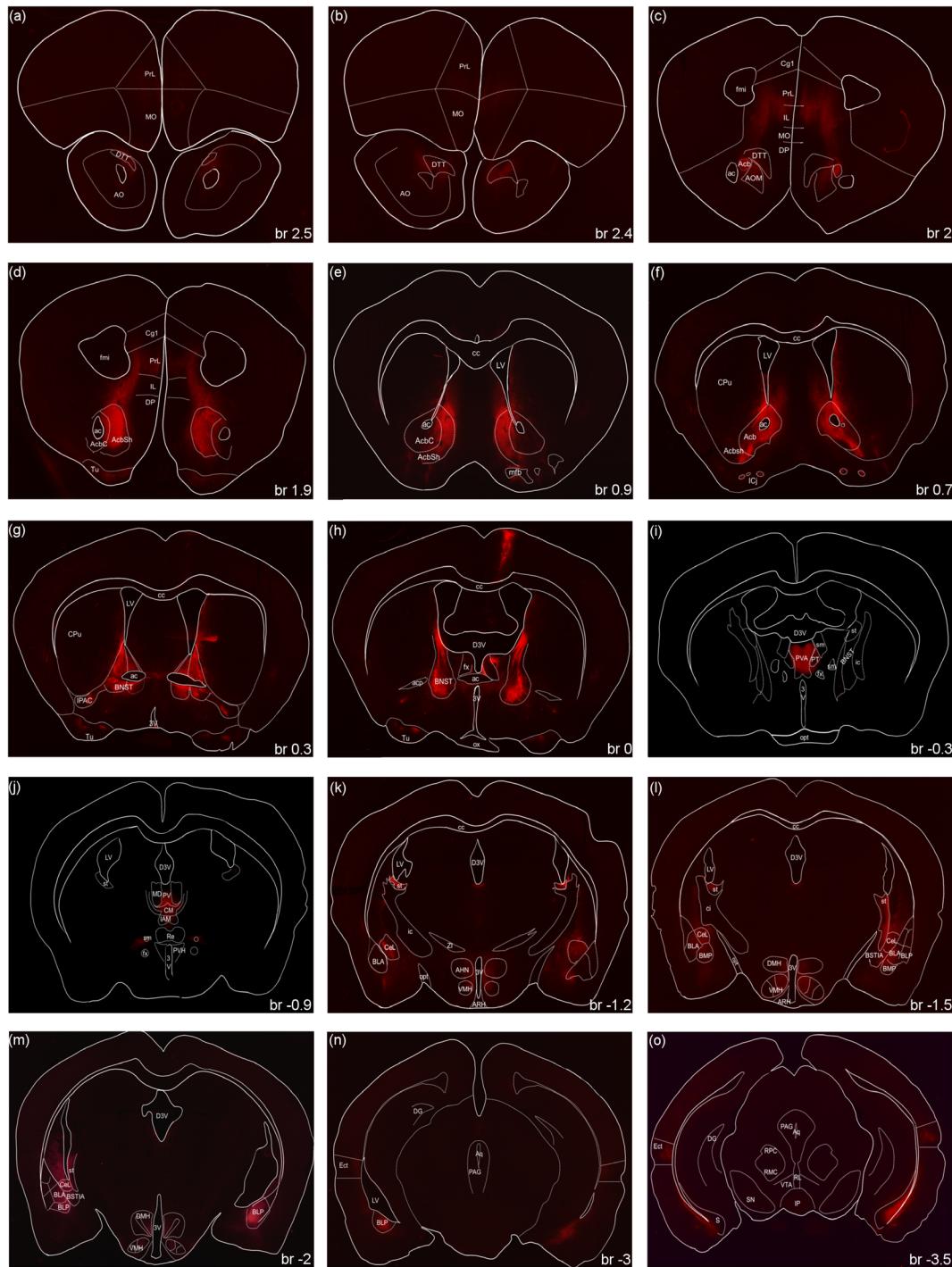
Sparse fibers were detected in the dorsal tenia tecta (DTT) (Figure 5a; Table 1). The inputs from GCK<sup>aPVT</sup> neurons were minimal in the midbrain, including the superior colliculus and the periaqueductal gray (PAG; Figure 5b).

## 2.2 | GCK<sup>aPVT</sup> neuronal inputs

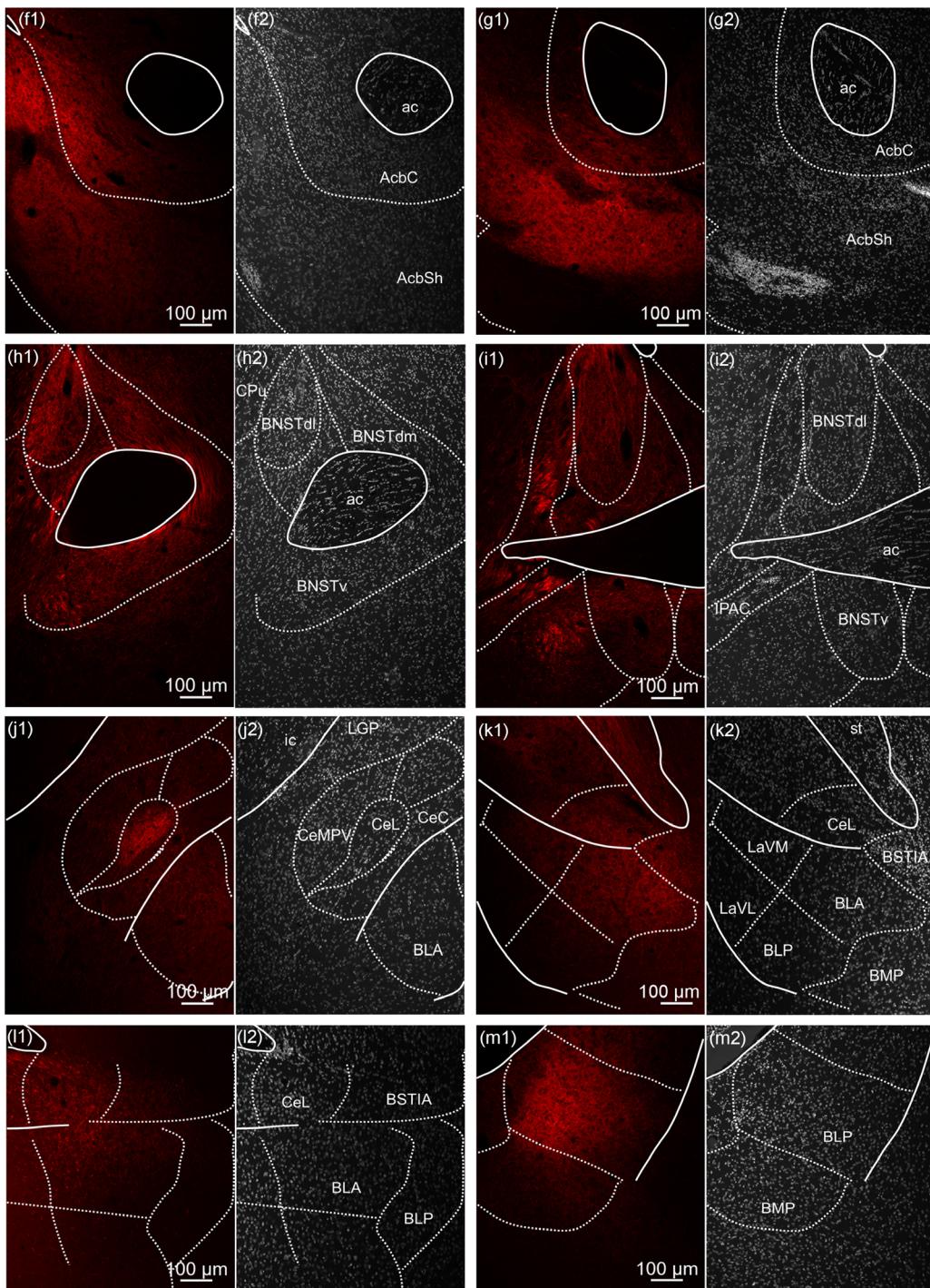
### 2.2.1 | Virus injection sites into the aPVT

For monosynaptic retrograde tracing of Gck<sup>aPVT</sup> neuronal inputs, eight Gck<sup>Cre/+</sup> mice were injected first with an AAV directing the expression of the avian tumor virus receptor A (TVA) for the avian sarcoma leucosis virus glycoprotein (EnvA; AAV-TREtight-mTagBFP2-B19G) and an AAV allowing for the Cre-dependent expression of the rabies envelop glycoprotein (RG; AAV-syn-FLEX-splitTVA-EGFP-tTA) followed a week later by the injection of an EnvA-G-deleted-mCherry pseudotyped rabies virus (Figure 6a). A week later, mice were perfusion fixed and their brain prepared to assess the distribution of the mCherry-positive signal on brain sections from the anterior cortex to the midbrain. No mCherry-positive neurons were observed in Gck<sup>Cre/+</sup> mice that were injected only with the pseudotyped rabies virus, nor in control Gck<sup>+/+</sup> littermates injected with the helper virus and the pseudotyped rabies virus.

Out of the eight mice studied, two (#1092 and #84290; Figure 6b) had injection sites exclusively restricted to the aPVT (Bregma –0.22 to –0.82 of the Franklin and Paxinos Mouse Atlas, 2001). In five mice (#1077, #1091, #1076, #783, and #4; Figure 6b,c), the injections were centered in the aPVT (Bregma –0.22 to –0.58) but also involved part



**FIGURE 2** (a–o) Stereomicroscope images showing the overall distribution of mCherry-positive projections arising from GCK $\alpha$ PVT from Bregma 2.5 to –3.5 (case #1). 3V, 3rd ventricle; ac, anterior commissure; Acb, accumbens nucleus; AcbC, accumbens nucleus core; AcbSh, accumbens nucleus shell; acp, posterior part of anterior commissure; AHN, anterior hypothalamic nucleus; AO, anterior olfactory; AOM, anterior olfactory area, medial part; aq, aqueduct; ARH, arcuate nucleus of the hypothalamus; BLA, basolateral amygdaloid nucleus, anterior part; BLP, basolateral amygdaloid nucleus, posterior part; BMP, basolateral amygdaloid nucleus, posterior part; BNST, bed nucleus of the stria terminalis; BSTIA, nucleus of stria terminalis; cc, corpus callosum; CeL, central amygdaloid nucleus, lateral part; Cg1, cingulate cortex, area 1; CM, central medial nucleus; CPu, caudate putamen; D3V, diencephalic 3rd ventricle; DG, dentate gyrus; DMH, dorsomedial nucleus of the hypothalamus; DP, dorsal penduncular cortex; DTT, dorsal tenia tecta; Ect, ectorhinal cortex; fmi, forceps minor of the corpus callosum; fx, fornix; IAM, interanteromedial thalamic nucleus; ic, internal capsule; ICj, islands of Calleja; IL, infralimbic cortex; IP, interpeduncular nucleus; IPAC, interstitial nucleus of posterior limb of anterior commissure; LV, lateral ventricle; MD, medial dorsal nucleus; mfb, medial forebrain bundle; MO, medial orbital cortex; opt, optic tract; ox, optic chiasm; PAG, periaqueductal gray; PrL, prelimbic cortex; PT, paratenial nucleus; PVH, paraventricular nucleus of the hypothalamus; Re, reunions thalamic nucleus; RL, rostral linear nucleus of the raphe; RMC, red nucleus, magnocellular part; RPC, red nucleus parvocellular part; S, subiculum; sm, stria medullaris; SN, substantia nigra; st, stria terminalis; Tu, olfactory tubercle; VMH, ventromedial nucleus of the hypothalamus; VTA, ventral tegmental area; ZI, zona incerta



**FIGURE 3** Fluorescent photomicrographs illustrating the distribution of mCherry-positive axons from GCK<sup>aPVT</sup> neurons in the prefrontal (a1, b1), cingulate (Cg, c1), and ectorhinal (Ect, d1) cortex, in the subiculum (e1), the NAc (f1, g1), the BNST (h1, i1), and in the amygdala (j1–m1). The latest receive both light (BLA) and more intense (CeL and BLP) innervation from the GCK<sup>aPVT</sup> neurons. The case #1 is illustrated. (a2–m2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Scale bars are shown in the figure. ac, anterior commissure; AcbC, accumbens nucleus core; AcbSh, accumbens nucleus shell; AHiPM, amygdalohippocampal area, posteromedial part; APiR, amygdalopiriform transition area; BLA, basolateral amygdaloid nucleus, anterior part; BLP, basolateral amygdaloid nucleus, posterior part; BMP, basomedial amygdaloid nucleus, posterior part; BNSTdl, bed nucleus of the stria terminalis, dorsolateral part; BNSTdm, bed nucleus of the stria terminalis, dorsomedial part; BNSTv, bed nucleus of the stria terminalis, ventral part; BNSTIA, nucleus of the stria terminalis; CA1, field CA1 of the hippocampus; CeC, central amygdaloid nucleus, capsular part; CeL, central amygdaloid nucleus, lateral division; CeMPV, central amygdaloid nucleus, medial posteroventral part; Cg1, cingulate cortex, area 1; Cg2, cingulate cortex, area 2; CPu, caudate putamen; DP, dorsal penduncular cortex; ec, external capsule; Ect, ectorhinal cortex; ggc, genu of the corpus callosum; ic, internal capsule; IL, infralimbic cortex; IPAC, interstitial nucleus of the posterior limb of anterior commissure; LaVL, lateral amygdaloid nucleus, ventrolateral part; LaVM, lateral amygdaloid nucleus, ventromedial part; LGP, lateral globus pallidus; LV, lateral ventricle; MO, medial orbital cortex; PrL, prelimbic cortex; S, subiculum; st, stria terminalis; TeA, temporal association cortex

**TABLE 1** Quantification of Gck<sup>aPVT</sup> fiber density in each target area

Gck <sup>aPVT</sup>	Gck <sup>aPVT</sup>
Projection areas	Fiber intensity
DTT	++
PrL	+++
IL	+++
LS	++
NAc	+++++
BNST	++++
ZI	+++
DMH	++
VMH	++
ceA	+++
BLA	+++
Ect	+
S	++

Note: Projection intensity equivalence: +++++, very dense; +++, dense; ++, moderate; +, light; +, very light. BLA, basolateral amygdaloid nucleus, anterior part; BNST, bed nucleus of the stria terminalis; ceA, central amygdaloid nucleus; DMH, dorsomedial nucleus of the hypothalamus; DTT, dorsal tenia tecta; Ect, ectorhinal cortex; IL, infralimbic cortex; LS, lateral septal nucleus; NAc, nucleus accumbens; PrL, prelimbic cortex; S, subiculum; VMH, ventromedial nucleus of the hypothalamus; ZI, zona incerta

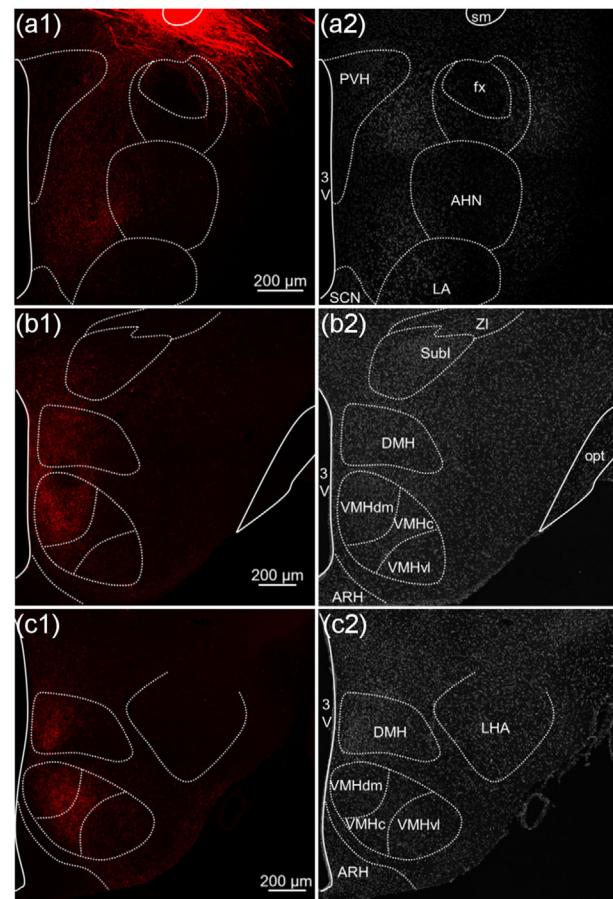
of the paratenial thalamic nucleus (PT, Bregma  $-0.34$  to  $-0.58$ ) and the AD (Bregma  $-0.46$ ). The last injection site involved the aPVT (Bregma  $-0.34$  to  $-0.82$ , #1088; Figure 6b) and a part of the CM.

## 2.2.2 | General input pattern of the Gck<sup>aPVT</sup> neurons

In *Gck*<sup>Cre/+</sup> animals injected with the three viruses, mCherry-labeled presynaptic neurons were observed in telencephalic, hypothalamic, and mesencephalic structures (Figure 19). No major labeling was found in most of the cortical areas nor in the thalamus. The four brains used for the quantification displayed viral contamination outside the aPVT, notably in the PT, and this was considered in our analyses. On average, Gck<sup>aPVT</sup> neurons received projections from  $831 \pm 144$  neurons (mean  $\pm$  SEM) from the studied areas ( $n = 4$  brains; Figure 7). Quantification of the number of presynaptic neurons from each nucleus and division of the brain was then performed and normalized to the total number of presynaptic inputs received by Gck<sup>aPVT</sup> neurons (Figure 7).

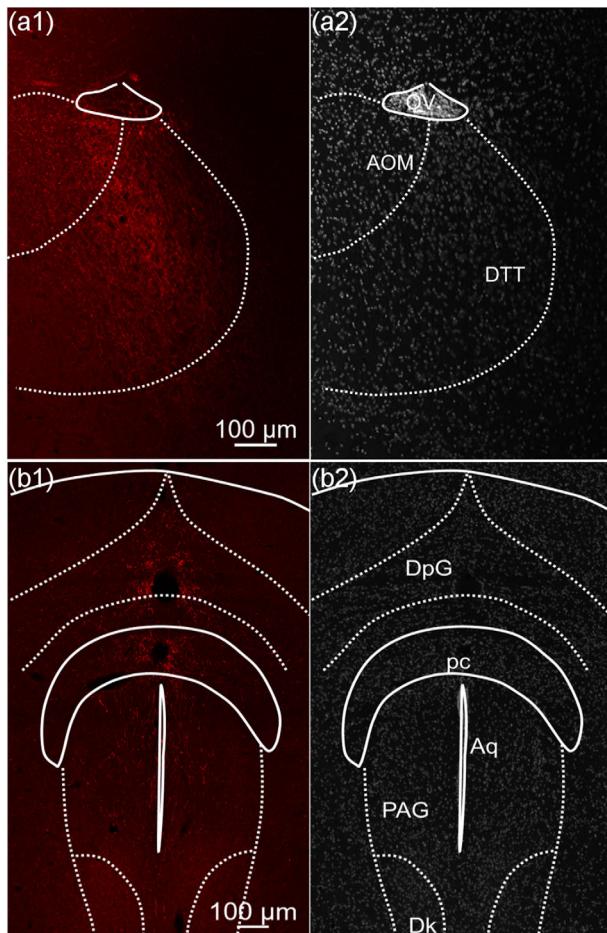
### Forebrain

The Gck<sup>aPVT</sup> neurons received inputs from numerous telencephalic areas (Figure 8). The largest number of monosynaptic inputs was found in the medial prefrontal cortex (PrL and IL, 2.2 and 1.5%, respectively; Figures 7 and 8a). To a lesser extent, labeled neurons were found in other cortical areas, including the cingulate, insular, peduncular, and



**FIGURE 4** Fluorescent photomicrographs illustrating the distribution of mCherry-positive axons from Gck<sup>aPVT</sup> neurons in the anterior division of the hypothalamus and notably in the PVH and AHN (a1), and in the tuberal division of the hypothalamus, mostly in the VMHdm (b1) and in the LHA (c1). The case #1 is illustrated. (a2–c2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Scale bars are shown in the figure. 3V, 3rd ventricle; AHN, anterior hypothalamic nucleus; ARH, arcuate nucleus of the hypothalamus; DMH, dorsomedial nucleus of the hypothalamus; fx, fornix; LA, lateroanterior hypothalamic nucleus; LHA, lateral hypothalamic area; opt, optic tract; PVH, paraventricular nucleus of the hypothalamus; SCN, suprachiasmatic nucleus of the hypothalamus; sm, stria medullaris; Subl, subincertal nucleus; VMHdm, ventromedial hypothalamic nucleus, central part; VMHc, ventromedial hypothalamic nucleus, dorsomedial part; VMHvl, ventromedial hypothalamic nucleus, ventrolateral part; ZI, zona incerta

motor cortex (Figure 8). Labeled neurons were consistently seen in the intermediate and the ventral parts of the septum (0.8% and 0.7%, respectively; Figures 7, 8b–d, and 9a). A larger proportion of presynaptic neurons was observed in the shell of the NAc when compared to the core (2.8% vs. 0.8%; Figures 7 and 8b), and in several divisions of the amygdala including the CeL, and the anterior and the posterior parts of the BL (1.5% in total; Figures 7 and 9d,e). A number of presynaptic neurons was observed in the dorsal divisions of the anterior BNST (2.5%) and to a lesser extent in the ventral divisions (0.3%) and in the posterior part (1.5%) (Figures 7, 8c,d, and 9a,b).



**FIGURE 5** Fluorescent photomicrographs illustrating the distribution of mCherry-positive axons from  $GCK^{aPVT}$  neurons in the tectum (a1, a2) and in the PAG (b1, b2). These areas receive light (PAG) to moderate (tectum) innervation from the  $GCK^{aPVT}$  neurons. The case #1 is illustrated. (a2, b2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Scale bars are shown in the figure. AOM, anterior olfactory area, medial part; aq, aqueduct; Dk, nucleus of Darkschewitsch; DpG, deep gray layer of the superior colliculus; DTT, dorsal tenia tecta; OV, olfactory part of lateral ventricle; PAG, periaqueductal gray; pc, posterior commissure

#### Hypothalamus

The  $GCK^{aPVT}$  neurons received most of their inputs from hypothalamic areas (72.3%; Figures 7 and 9), including the PVH (14.4%; Figures 7 and 9c), the AHN (11.7%; Figures 7 and 9c-e), the LHA, the perifornical area (10%; Figures 7 and 9c-g), and the medial preoptic nucleus (8.3%; Figures 7 and 9a,b). A smaller number of labeled neurons was found in the periventricular nucleus (3.3%; Figures 7 and 9c,d), the ARH (4.3%; Figures 7 and 9f-h), the DMH (3.1%; Figures 7 and 9f,g), the VMH (3.2%; Figures 7 and 9e-g), the tuberal nucleus (4.1%; Figures 7 and 9e-g), and the mammillary bodies (4%; Figures 7 and 9j). Other nuclei of the hypothalamus, such as the retrochiasmatic area (1.7%), the supraoptic (0.7%), the suprachiasmatic (2.5%), the parasubthalamic (0.3%), the posterior hypothalamic (3.2%), and the dorsal and ventral parts of the premammillary nuclei (0.5% and 1.3%, respectively), contained sparsely distributed labeled neurons (Figure 9).

#### Thalamus

Abundant retrogradely labeled neurons were consistently found in the reticular nucleus of the thalamus (6%; Figures 7 and 9c) and in a smaller proportion in the zona incerta (3.1%; Figures 7 and 9d,e). We did not observe any additional accumulation of mCherry-labeled neurons in the other thalamic nuclei.

#### Midbrain

The density of mCherry-positive neurons in the midbrain was low (Figure 10) with 0.8% and 0.2% of the total number of presynaptic neurons localized in the substantia nigra and the ventral tegmental area, respectively (Figures 7 and 10a). mCherry-positive neurons were also found in the roof of the midbrain in the superior colliculus (0.4%; Figures 7 and 9a,b). In the very posterior part of the midbrain, presynaptic neurons were detected in several divisions of the PAG, including the dorsolateral (0.2%), the ventrolateral (0.2%), and the lateral (0.07%) areas (Figures 7 and 9a-d).

#### 2.2.3 | Transcript profiling of $GCK^{aPVT}$ neurons

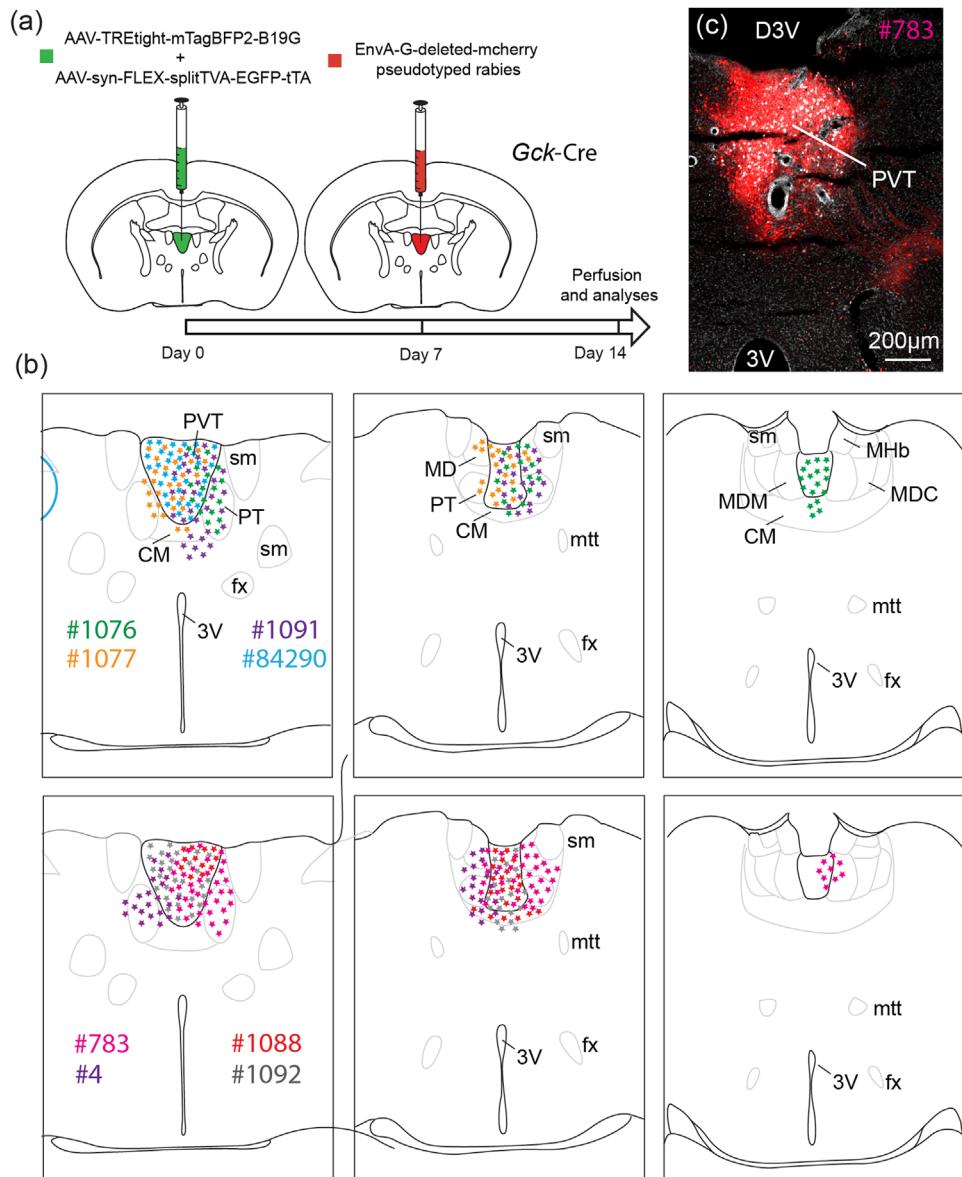
##### General information and control

To determine the transcriptome of  $GCK^{aPVT}$  neurons, we used a Transcribing Ribosome Affinity Purification (TRAP) approach (Figure 11).  $GCK^{Cre/+}$  mice were injected in the aPVT with an AAV-DIO-L10-GFP encoding an L10 ribosomal protein-GFP fusion protein that integrates in ribosomes. Ten days later, after an overnight fast, aPVT was dissected, lysed, and the ribosomes were immunoprecipitated with an anti-GFP antibody. RNA sequencing (RNA-seq) was then performed on the immunoprecipitated ribosomal fraction (output) and on the non-immunoprecipitated (input) material. RNA-seq data were analyzed and for each mRNA, we measured their enrichment in the immunoprecipitated fraction (ratio of output vs. input). Out of 14,646 detected genes, 3121 were significantly enriched in  $GCK^{aPVT}$  neurons and 3245 were significantly depleted (adjusted  $p$ -value  $\leq .05$ ; Appendix Table A1). The volcano plot of Figure 11a shows the distribution of the mRNAs enriched in (red dots) and depleted from (blue dots) the immunoprecipitated fraction. The heat map of Figure 11b shows that, as expected, the immunoprecipitated ribosomes are enriched in ribosomal L10 (*Rpl10a*) and  $GCK$  mRNAs, as well as in the mRNA encoding the vesicular glutamate transporter (*Slc17a6*). It also shows that the output fraction was depleted in the key markers of oligodendrocytes, astrocytes, microglia, and endothelial cells.

##### Identification of mRNAs expressed by $GCK^{aPVT}$ neurons

KEGG pathway analysis of the mRNAs enriched in the  $GCK^{aPVT}$  neurons (Figure 11c) shows that they encoded for essential components of neurotransmitter-based synapses, neuroactive ligand-receptor interaction, axon guidance, and cell-to-cell communication proteins.

**Neurotransmitter receptors.** They were, in particular, enriched in serotonin receptors (*Htr5b*, *Htr7*, *Htr1d*, *Htr1b*), glycine receptors (*Gla1*,



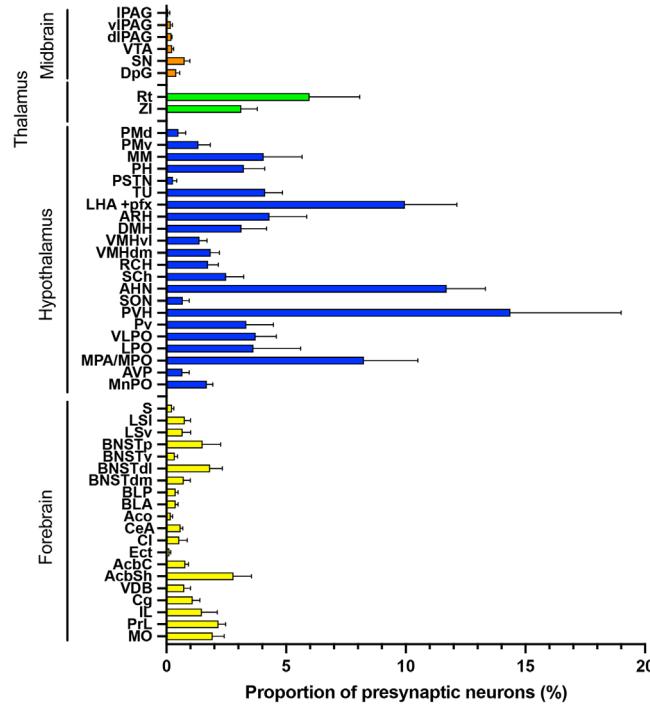
**FIGURE 6** (a) Experimental approach. A mix of AAV-TREtight-mTagBFP2-B19G and AAV-syn-FLEX-splitTVA-EGFP-tTA was injected at day 0 in the anterior PVT of 13- to 20-week-old *Gck*<sup>Cre/+</sup> male mice. Seven days later, mice received injection of EnvA-G-deleted-mCherry pseudotyped rabies. Drawings (b) and photomicrograph (c) illustrating the injection sites of viruses in the anterior PVT in experiments #1076 (green stars), #1077 (orange stars), #84290 (blue stars), #1088 (red stars), #1091 (purple stars upper panel), #1092 (gray stars), #4 (purple stars, lower panel), and #783 (pink stars) (c). Scale bar is shown in the figure. 3V, 3rd ventricle; CM, central medial nucleus; D3V, dorsal 3rd ventricle; fx, fornix; MDC, medial dorsal nucleus, central part; MDM, medial dorsal nucleus, medial part; MHb, medial habenular nucleus; mtt, mammillothalamic tract; PT, paratenial nucleus; PVT, paraventricular nucleus of the thalamus; sm, stria medullaris

*Glia3*), ionotropic glutamate and GABA receptors (NMDA, AMPA, Kainate, GABA<sub>A</sub>), and metabotropic glutamate and GABA<sub>B</sub> receptors (Figure 11d).

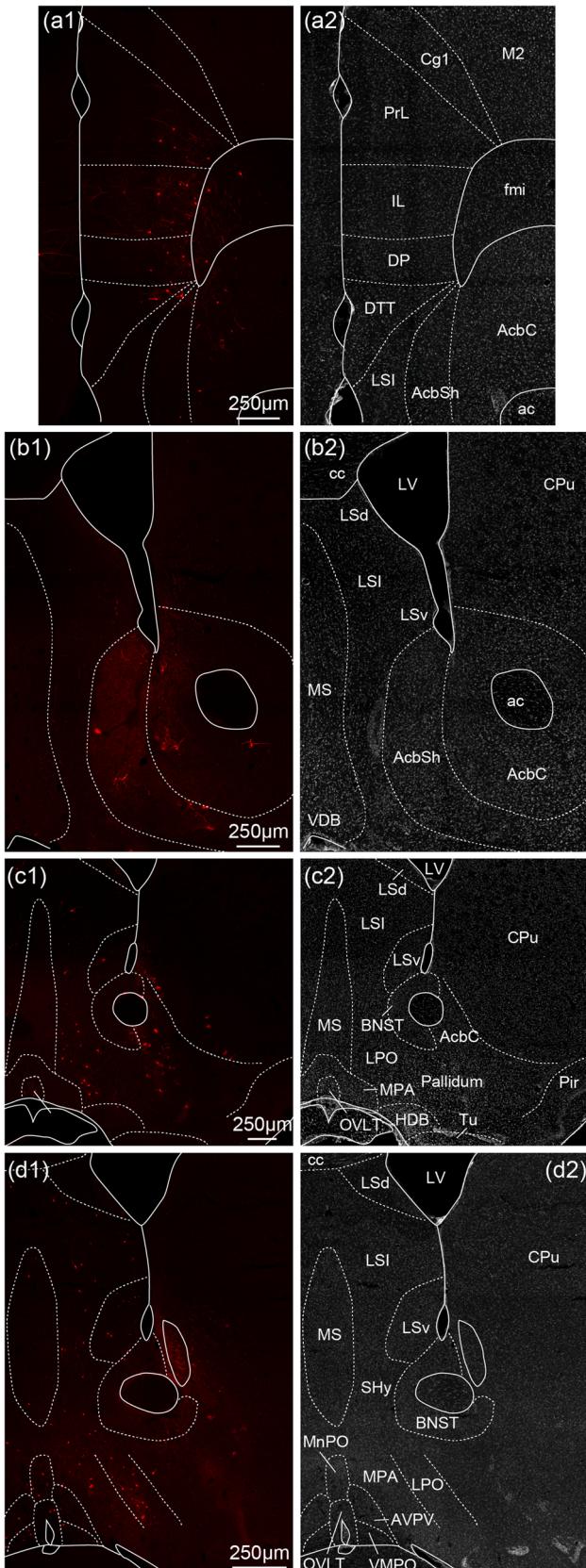
**Neuropeptide/neurohormone receptors.** They also included the neuropeptide/neurohormone receptors for oxytocin (*Oxtr*), galanin (*Galr1*), melanocortin (*Mc3r*), neuropeptide Y (*Npy2r*), tachykinin (*Tacr3*), melanin-concentrating hormone (*Mchr1*), hypocretin/orexin (*Hcrtr2*), dopamine (*Drd2*), neurotensin (*Ntsr1*), and opioids (*Oprk1*, *Oprm1*).

**Axon guidance and synaptic plasticity.** Axon guidance mRNAs were found to encode the four major guidance protein families, Semaphorin (*Sema3a*, *Sema3f*, *Sema4f*, *Sema4g*, *Sema5a*, *Sema6b*), Ephrin (*Efna5*, *Efnb2*, *Epha4*, *Epha5*, *Epha6*), Slit (*Slit1*, *Slit3*), and Netrin G1 (*Ntnng1*). Of note, these Semaphorin and Ephrin family members, in addition to their role in axon guidance, are also involved in synaptic plasticity (Hruska & Dalva, 2012; Koropouli & Kolodkin, 2014).

**Glucose-sensing-, diabetes-, and obesity-related genes.** Differential gene expression analysis showed an enrichment of mRNAs involved in



**FIGURE 7** Quantification of presynaptic inputs of GCK<sup>a</sup>PVT neurons performed on four independent experiments (#1077, #1076, #1091, and #783). Most of presynaptic neurons are found in hypothalamic areas (blue). Quantification in the telencephalon is shown in yellow, the thalamus in green, and the midbrain in orange. AcbC, accumbens nucleus core; AcbSh, accumbens nucleus shell; Aco, anterior cortical nucleus of amygdala; AHN, anterior hypothalamic nucleus; ARH, arcuate nucleus of the hypothalamus; AVP, anteroventral periventricular nucleus; BLA, basolateral amygdaloid nucleus, anterior part; BLP, basolateral amygdaloid nucleus, posterior part; BNSTdl, bed nucleus of the stria terminalis, dorsolateral part; BNSTdm, bed nucleus of the stria terminalis, dorsomedial part; BNSTv, bed nucleus of the stria terminalis, ventral part; ceA, central amygdaloid nucleus; Cg, cingulate cortex; Cl, clostrum; dIPAG, periaqueductal gray, dorsolateral part; DMH, dorsomedial nucleus of the hypothalamus; DpG, deep gray layer of the superior colliculus; Ect, ectorhinal cortex; IL, infralimbic cortex; LHA, lateral hypothalamic area; IPAG, periaqueductal gray, lateral part; LPO, lateral preoptic area; LSI, lateral septal nucleus, intermediate part; LSv, lateral septal nucleus, ventral part; MM, medial mammillary nucleus; MnPO, median preoptic nucleus; MO, medial orbital cortex; MPA/MPO, medial preoptic area/medial preoptic nucleus; pfx, perifornical area; PH, posterior hypothalamic nucleus; PMd, premammillary nucleus, dorsal part; PMv, premammillary nucleus, ventral part; PrL, prelimbic cortex; PSTN, parasubthalamic nucleus; Pv, periventricular nucleus of the hypothalamus; PVH, paraventricular nucleus of the hypothalamus; RCH, retrochiasmatic area; Rt, reticular thalamic nucleus; S, subiculum; Sch, suprachiasmatic nucleus; SN, substantia nigra; SON, supraoptic nucleus; TU, tuberal nucleus; VDB, nucleus of the verticle limb of the diagonal band; vIPAG, periaqueductal gray, ventrolateral part; VLPO, ventrolateral preoptic nucleus; VMHdm, ventromedial hypothalamic nucleus, dorsomedial part; VMHvl, ventromedial hypothalamic nucleus, ventrolateral part; VTA, ventral tegmental area; ZI, zona incerta



**FIGURE 8** Confocal photomicrographs illustrating direct inputs to GCK<sup>a</sup>PVT neurons in the telencephalon (a1-d1, Case #783) and in preoptic hypothalamic areas (c1, d1). (a2-d2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Important number of presynaptic inputs is observed in the prefrontal

obesity and diabetes physiopathology (Figure 11b; Appendix Table A1) such as the fat mass and obesity gene *Fto*, as well as the type 2 diabetes susceptibility gene *Tcf7l2*, the neuropeptide B/W receptor 1 (*Npbwr1*), the insulin receptor substrates 1 and 2 (*Irs1*, *Irs2*), and the MAP kinases *Mpak1*, *Mpak9*, and *Mpak10*.

#### *Identification of the neuronal inputs to Gck<sup>aPVT</sup> neurons*

To identify the neuronal source of neurotransmitters and neuropeptides targeting Gck<sup>aPVT</sup> neurons, we prepared brains from Gck<sup>Cre/+</sup> mice previously injected with the pseudorabies virus retrograde labeling system described above and searched for mCherry-positive neurons co-labeled by *in situ* hybridization or immunohistochemistry for neurotransmitter markers (tyrosine hydroxylase, TH, *Gad1*) or selected neuropeptides.

**Forebrain.** We identified extrahypothalamic sources of GABAergic inputs onto Gck<sup>aPVT</sup> neurons, by performing *in situ* hybridization detection of the mRNAs for *Gad1* (*Gad67*) and for *Slc17a6* (Figure 12). We found mCherry-expressing GABAergic neurons but no glutamatergic neurons in the BNST (Figure 12a).

**Anterior hypothalamic nuclei.** Several nuclei of the anterior hypothalamus displayed exclusively glutamatergic neurons such as the PVH or both glutamatergic and GABAergic neurons, such as the preoptic area. By using *in situ* hybridization approach, we found mCherry-expressing GABAergic neurons in the medial preoptic area (Figure 12c), and mCherry-expressing glutamatergic neurons in the PVH (Figure 13a) and in the medial preoptic nucleus (Figure 13b).

The neuroendocrine PVH is composed of magnocellular (AVP, OXT) and parvocellular (corticotropin-releasing hormone, CRH; thyrotropin-releasing hormone, TRH; Somatostatin, SST; TH) neurons (Biag et al., 2012). Despite a significant enrichment of *Oxtr* mRNA in the Gck<sup>aPVT</sup> neurons (Figure 11d; Table 2), we only detected one OXT and mCherry-double-positive neuron in the most rostral part of the PVH out of

cortex (a1), and in the preoptic areas (c1, d1). Scale bars are shown in the figure. (c–e) Microphotographs illustrating the distribution of neurons projecting onto MCH neurons of the DMH and the capsule of the VMH (tRFP, red), at several levels of the anterior bed nucleus of the stria terminalis (BNST). tRFP-positive cells are observed in the dorsomedial and lateral division of the BNST as well as in the ventral division. Scale bars are shown in the figure. ac, anterior commissure; AcbC, accumbens nucleus core; AcbSh, accumbens nucleus shell; AVPV, anteroventral periventricular nucleus, ventral part; BNST, bed nucleus of the stria terminalis; cc, corpus callosum; Cg1, cingulate cortex, area 1; CPU, caudate putamen; DP, dorsal peduncular cortex; DTT, dorsal tenia tecta; fmi, forceps minor of the corpus callosum; IL, infralimbic cortex; LPO, lateral preoptic area; LSd, lateral septal nucleus, dorsal part; LSI, lateral septal nucleus, intermediate part; LSv, lateral septal nucleus, ventral part; LV, lateral ventricle; M2, secondary motor cortex; MPA, medial preoptic area; MS, medial septum; OVLT, organum vasculosum of the lamina terminalis; Pir, piriform cortex; PrL, prelimbic cortex; StHy, striohypothalamic nucleus; Tu, tubercle; VDB, nucleus of the verticle limb of the diagonal band; VMPO, ventromedial preoptic nucleus

all five studied animals (Figure 14a–c). We found numerous AVP and mCherry-positive neurons in the neuroendocrine part of the PVH (Figure 14d), and one in the supraoptic nucleus. In this structure, no mCherry-positive neurons were found to express OXT. By *in situ* hybridization, we observed numerous mCherry-positive neurons that were also positive for either *Crh* or *Galanin* (Figure 14e). Thus, in the PVH, retrogradely labeled neurons are mostly parvocellular.

#### *Posterior hypothalamic nuclei*

The posterior hypothalamus is composed of several nuclei such as the DMH, the VMH, the ARH, and the LHA. In addition to the anterior hypothalamic nuclei, we found mCherry-expressing GABAergic neurons also in the LHA (Figure 12b), the ARH (Figure 12d), the DMH (Figure 12e), and the tuberal nucleus (not shown). mCherry-expressing glutamatergic neurons were seen in the VMH (Figure 13c,d) and the retrochiasmatic area and ARH (Figure 15b,c).

mCherry-positive neurons positive for TH were found in the ARH (group A12; Figure 15a) but not in the DMH nor in the zona incerta (group A13; Figure 16e). As the melanocortin receptor *Mc3r* was enriched in Gck<sup>aPVT</sup> neurons, we assessed whether mCherry was found in POMC or AgRP (labeled with NPY) neurons of the ARH. POMC, but not AgRP/NPY, neurons were found to express mCherry (Figure 15b–d). In addition, although we immunodetected NPY-expressing neurons in the DMH, none of them was in contact with Gck<sup>aPVT</sup> neurons. *Leprb* mRNA was also found to be expressed by Gck<sup>aPVT</sup> presynaptic neurons in the ARH (Figure 15d2).

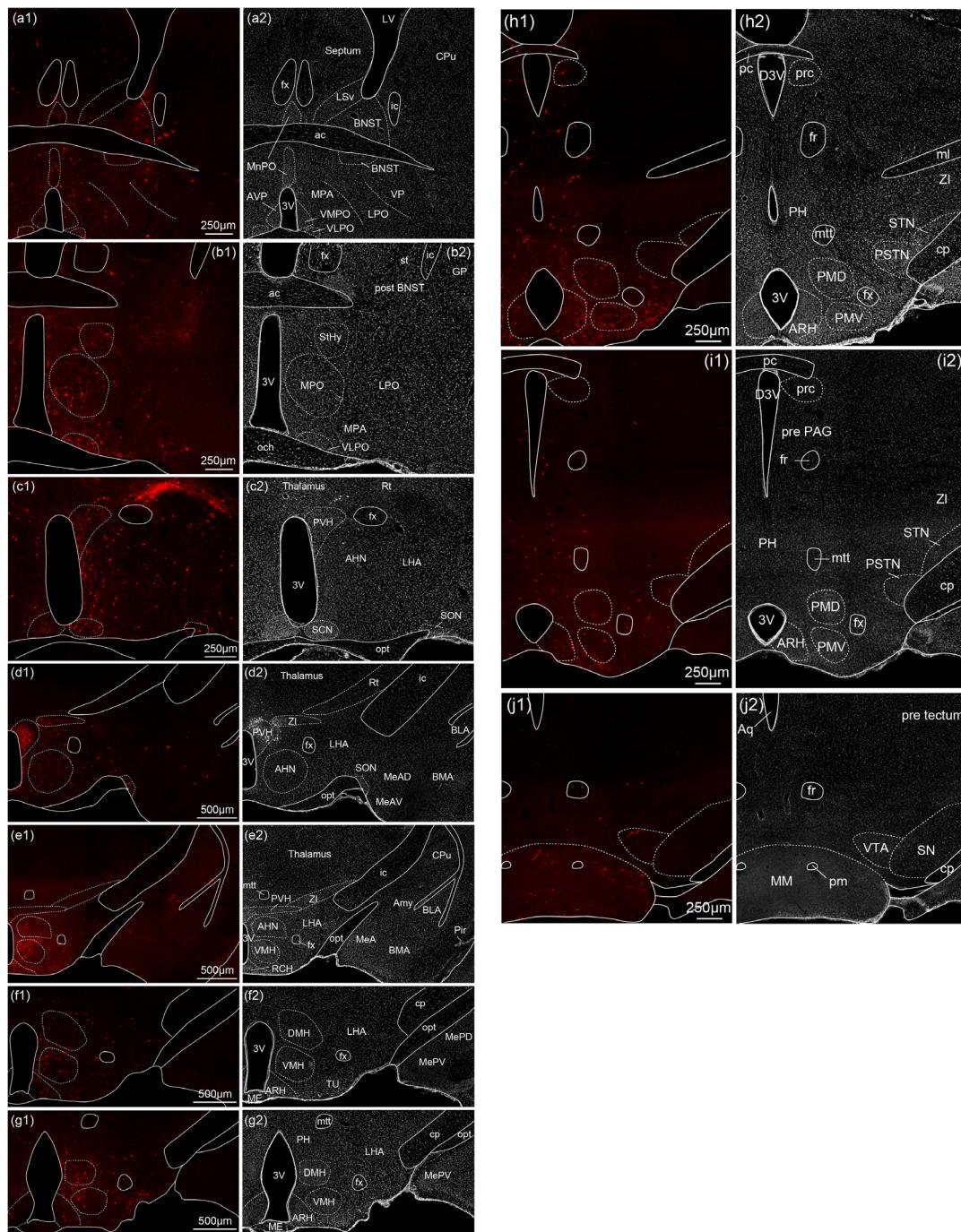
The dorsomedial division of the VMH was enriched for mCherry-positive cells when compared to the ventrolateral part (Figure 9e–g). This division is known to include leptin receptor b (*Leprb*)- and estrogen receptor alpha (ER $\alpha$ )-expressing neurons. We revealed by *in situ* hybridization that VMH presynaptic neurons expressed both receptors (Figure 17).

Then, we immunodetected orexin (ORX) and MCH in the LHA and found that both neuropeptide-expressing neurons have direct inputs to Gck<sup>aPVT</sup> neurons (Figure 16a–c). However, no mCherry-positive neurons were found to express MCH in the capsule of the VMH (Figure 16d).

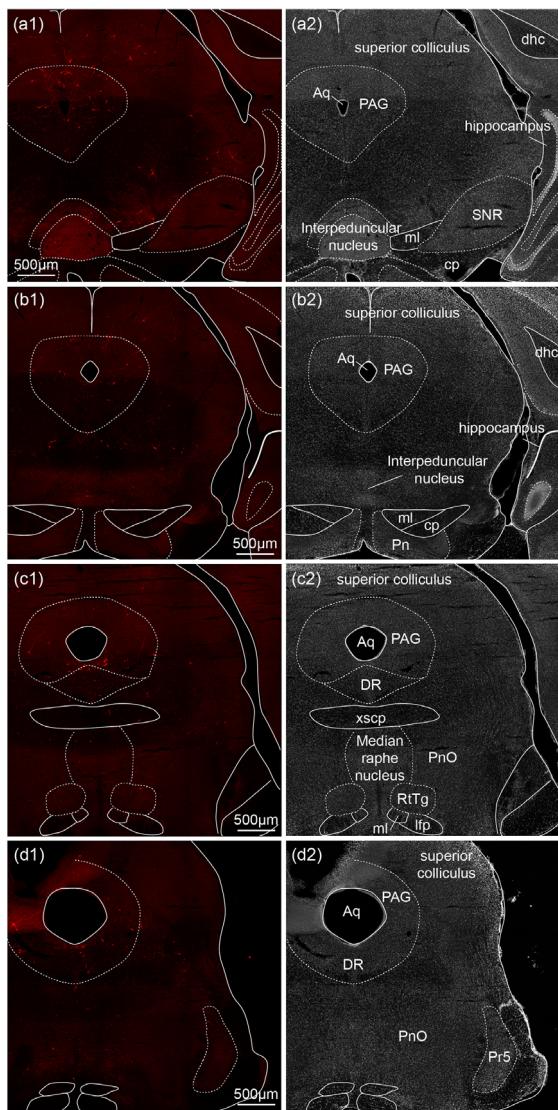
Finally, we identified, by immunofluorescence microscopy, the terminals/fibers in the aPVT that expressed TH, OXT, AVP, ORX, MCH, POMC, and AgRP. Figure 18 illustrates that there is a high density of TH fibers in the aPVT (Figure 18a). AgRP and POMC fibers showed a more lateral, symmetric distribution (Figure 18b,c); MCH and ORX fibers were sparse (Figure 18d,e). OXT fibers showed a striking localization close to the ventricle (Figure 18f), and AVP fibers were present bilaterally in relatively narrow regions of the PVT (Figure 18g).

## 3 | DISCUSSION

The PVT is generally considered a hub for integration of signals from diverse neuronal circuits. Its afferent and efferent connections have been thoroughly characterized in rat (Kirovac, 2015; Vertes et al., 2015), and functional studies have highlighted its important role in



**FIGURE 9** Confocal photomicrographs illustrating direct inputs to GCK<sup>aPVT</sup> neurons in the hypothalamus (a1–j1, Case #783). (a2–j2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Important number of presynaptic inputs is observed in preoptic areas (a1, b1), in the PVH (c1–e1), in the VMHdm (e1), in the DMH (f1, g1), and in the premammillary nuclei and mammillary bodies (h1–j1). Scale bars are shown in the figure. 3V, 3rd ventricle; ac, anterior commissure; AHN, anterior hypothalamic nucleus; Amy, amygdaloid nucleus; ARH, arcuate nucleus of the hypothalamus; AVP, anteroventral periventricular nucleus; BLA, basolateral amygdaloid nucleus, anterior part; BMA, accessory basal amygdaloid nucleus; BNST, bed nucleus of the stria terminalis; CPu, caudate putamen; D3V, dorsal 3rd ventricle; DMH, dorsomedial nucleus of the hypothalamus; fr, fasciculus retroflexus; fx, fornix; GP, globus pallidus; LHA, lateral hypothalamic area; LPO, lateral preoptic area; LSv, lateral septal nucleus, ventral part; ME, median eminence; MeAD, medial amygdaloid nucleus, anterodorsal part; MeAV, medial amygdaloid nucleus, anteroventral part; MePD, medial amygdaloid nucleus, posterodorsal part; MePV, medial amygdaloid nucleus, posteroventral part; ml, medial lemniscus; MM, medial mammillary nucleus; MPA, medial preoptic area; MPO, medial preoptic nucleus; mtt, mammillothalamic tract; och, optic chiasm; opt, optic tract; PAG, periaqueductal gray; pc, posterior commissure; PH, posterior hypothalamic nucleus; Pir, piriform cortex; pm, principal mammillary tract; PMD, premammillary nucleus, dorsal part; PMV, premammillary nucleus, ventral part; prc, precommissural nucleus; PSTN, parasubthalamic nucleus; PVH, paraventricular nucleus of the hypothalamus; RCH, retrochiasmatic area; Rt, reticular thalamic nucleus; sm, stria medullaris; SN, substantia nigra; SON, supraoptic nucleus; StHy, striohypothalamic nucleus; TU, tuberal nucleus; VLPO, ventrolateral preoptic area; VMH, ventromedial nucleus of the hypothalamus; VMPO, ventromedial preoptic nucleus; VTA, ventral tegmental area; ZI, zona incerta



**FIGURE 10** Confocal photomicrographs illustrating direct inputs to GCK<sup>aPVT</sup> neurons in the midbrain (Case #783). (a2–d2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Abundant presynaptic inputs are observed in the PAG (a1–d1). Scale bars are shown in the figure. Aq, aqueduct; cp, cerebral peduncle; dhc, dorsal hippocampal commissure; Ifp, longitudinal fasciculus of the pons; ml, medial lemniscus; PAG, periaqueductal gray; Pn, pontine nuclei; PnO, pontine reticular nucleus, oral part; Pr5, principal sensory trigeminal nucleus; RtTg, reticulotegmental nucleus of the pons; SNR, substantia nigra, reticular part; xscp, decussation of the superior cerebellar peduncle

the integration of arousal cues, including rewarding and aversive stimuli (Choi et al., 2019; Millan et al., 2017; Petrovich, 2021). The majority of these studies examined PVT as a unit, using a region-oriented approach. Only recently studies have started to dissect individual subpopulations with distinct expression markers and functional outputs (Clark et al., 2017; Hua et al., 2018; Kessler et al., 2021; Labouèbe et al., 2016; Luo et al., 2018). Given the multifactorial implication of the region in behavioral outcomes, focusing on particular neuronal subpopulations is essential for untangling the underlying neuronal net-

works. Toward this direction, we examined the aPVT neurons that are characterized by the expression of Gck. In the current study, we provide a detailed anatomical description of the neuronal network formed by Gck<sup>aPVT</sup> neurons using viral anterograde and retrograde tracing experiments, and we define the transcriptomic profile of these neurons by using TRAP RNAseq analysis combined with histological approaches.

### 3.1 | Methodological considerations

The viral-mediated tracing approaches we used are well established (Nectow & Nestler, 2020). Nevertheless, methodological limitations must be considered. One of the main challenges is the accuracy of the injection sites and the viral spread. In the present study, the sites of injection in the different animals displayed very low variability leading to consistent anterograde or retrograde tracing results. However, the viral spread in the areas surrounding the PVT (including CM, PT, and AD) should be considered during result interpretation. In particular, the consistent contamination from CM Gck-expressing neurons in the animals used for anterograde tracing (Figure 1b,c) is contributing to the list of identified target areas. PrL, IL, central amygdaloid nucleus (ceA), basolateral amygdaloid nucleus, anterior part (BLA), NAc, and Ect have all been identified as output areas of CM-residing neurons in rat (Vertes et al., 2012). Thus, some of the fibers detected could be due to the contribution of projections from CM Gck-expressing neurons.

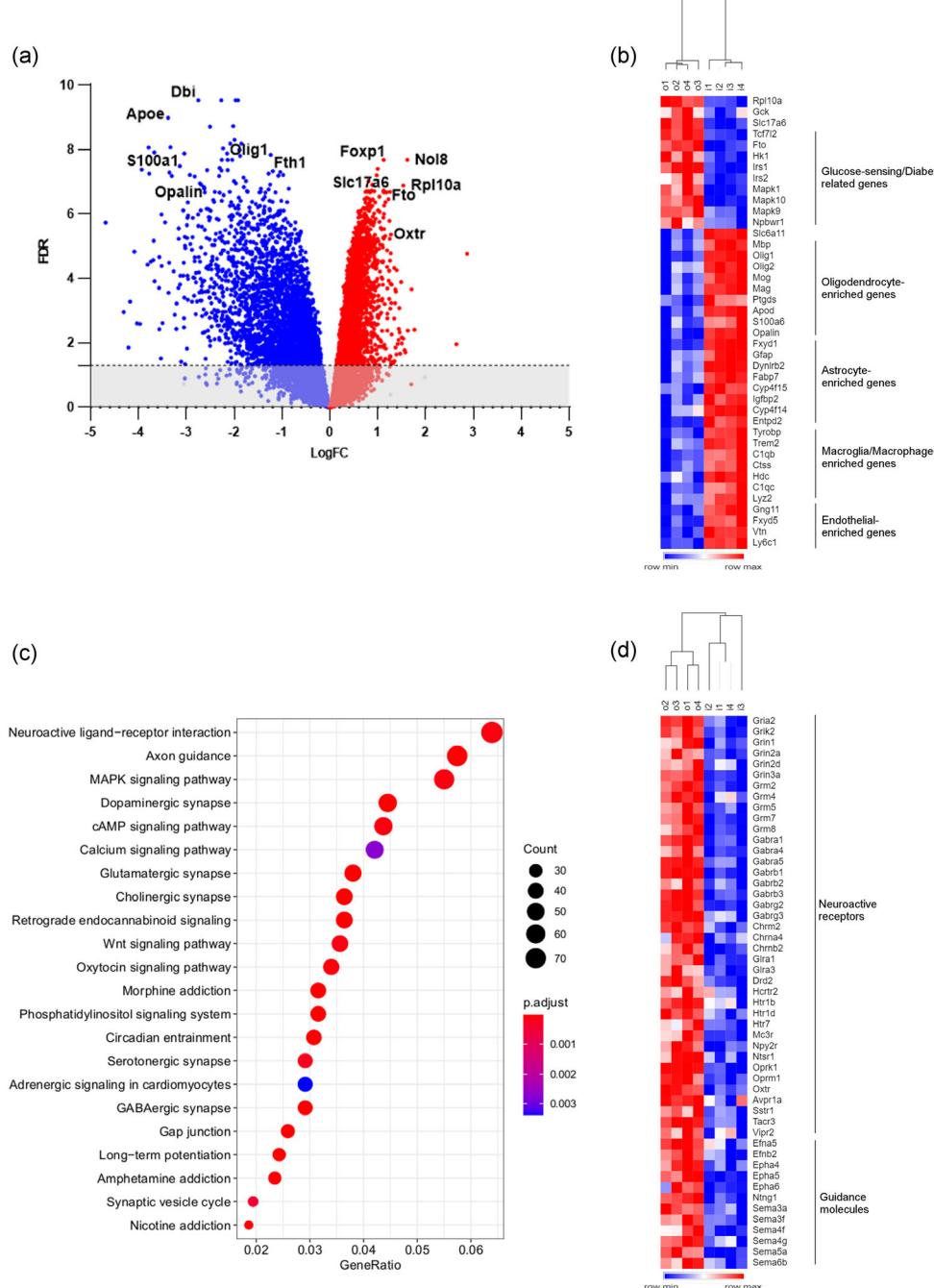
For retrograde studies, we also observed a viral spread in the PT that could explain the detection of mCherry-positive presynaptic neurons in the NAc. Indeed, such projections have been already described in the literature (Williams et al., 1977).

A second point of consideration is the limited capacity for long-range diffusion of the B19 rabies strain used (Reardon et al., 2016). Thus, for instance, the high density of retrogradely labeled neurons in hypothalamic areas may reflect their close location to the aPVT injection sites, and more distant sites may not be as efficiently labeled.

### 3.2 | Gck<sup>Cre/+</sup> mice to characterize the Gck<sup>aPVT</sup> neuronal network and functional interpretation

A collective view of both anterograde and retrograde results suggests that Gck<sup>aPVT</sup> neurons are part of a highly interconnected network consisting of reciprocal projections that may form feedback loops as described for thalamocortical circuits (Bannister, 2005; Briggs & Usrey, 2008; Kirouac, 2015).

Indeed, this study provides an exhaustive description of Gck<sup>aPVT</sup> neuronal outputs and inputs throughout the brain from the PrL to midbrain areas. The intensity of Gck<sup>aPVT</sup> neuronal projections ranges from low to high. The strongest innervation is in telencephalic structures such as the NAc, amygdala, and the BNST, and in hypothalamic nuclei such as the VMH. Weaker projections are observed in the



**FIGURE 11** (a) Volcano plot showing the differential gene expression in output (Gck expressing cells of the aPVT) versus input (non-Gck expressing cells of the aPVT). Dashed line represents the significance cutoff of False Discovery Rate (FDR) > 1.3. (b) Heat map representation of the differentially expressed genes between input and output. Each sample is represented by a single column and hierarchical clustering verifies the clear separation of the two distinct transcriptional profiles. (c) KEGG pathway analysis for the Gck<sup>aPVT</sup>-enriched genes. Only pathways with an adjusted *p*-value lower than .01 are shown. (d) Heat map representation of the Gck<sup>aPVT</sup>-enriched neuroactive receptors and guidance molecules

telencephalic subiculum and in the hypothalamic DMH. The projection areas identified for Gck<sup>aPVT</sup> neurons are in line with data previously reported from rodent studies (Kessler et al., 2021; Kirouac, 2015; Labouèbe et al., 2016; Otis et al., 2019; Ren et al., 2018; Vertes & Hoover, 2008; Zhu et al., 2016).

On the other hand, our monosynaptic retrograde tracing approach revealed terminals deriving from a wide spectrum of areas, including

telencephalic (BNST, cortical areas), hypothalamic (LHA, DMH), and midbrain (PAG) regions. Most areas innervated by Gck<sup>aPVT</sup> projections also send reciprocal projections. While we cannot quantify the level of reciprocity with the techniques we used, the prefrontal cortex, the NAc, the BNST, and the dorsomedial part of the VMH and the DMH appear as major sites of reciprocal projections with Gck<sup>aPVT</sup> neurons, while the PVH does not seem to be a major actor of this reciprocal

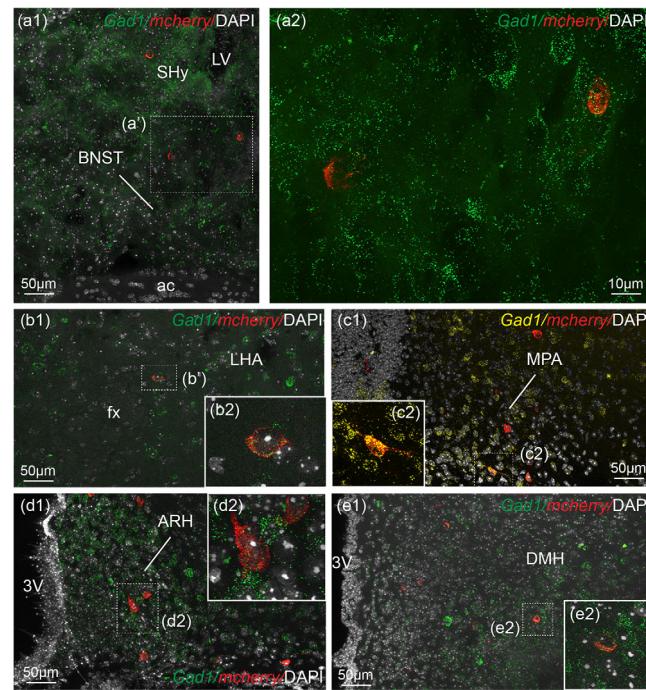
network. This observation is in line with previous reports of reciprocal projections from the PVT in rats (Kirouac, 2015) and mice (Clark et al., 2017).

Collective research effort over the years has established PVT as an integrator that modulates motivated behaviors based on the interoceptive signals received (Millan et al., 2017). Interoceptive signals are transmitted through afferent connections from the brainstem and hypothalamus and modulation is a result of efferent signals on cortical and limbic areas (Kirouac, 2015). Through these various afferent and efferent projections, PVT has been linked with a plethora of motivated behaviors, including cue-dependent reward learning (Choi & McNally, 2017; Kessler et al., 2021; Labouèbe et al., 2016; Otis et al., 2019), addiction (Hamlin et al., 2009; Kuhn et al., 2018; Matzeu et al., 2017; Zhu et al., 2016), and feeding (Christoffel et al., 2021; Luo et al., 2018; Zhang & van den Pol, 2017). The fact that *Gck<sup>a</sup>PVT* neurons present a connectome pattern highly similar to that obtained through whole PVT tracing approaches implies their involvement in several aspects of the PVT-regulated behaviors. We have so far confirmed their contribution to sucrose seeking behavior through their projections to the NAc (Kessler et al., 2021). Further functional studies are required in order to untangle the complex involvement of PVT neuronal subpopulations in behavioral responses and the detailed characterization of *Gck<sup>a</sup>PVT* neurons provided with the current study is setting the basis for exploration of additional circuits involved.

### 3.3 | Transcriptomic characterization of *Gck<sup>a</sup>PVT* neurons and functional interpretation

Our transcriptomic analysis of *Gck<sup>a</sup>PVT* neurons revealed that they are enriched in mRNAs involved in neurotransmitter-based synapses, neuroactive ligand–receptor interaction, axon guidance, cell-to-cell communication, and obesity and diabetes physiopathology.

This provides important information notably regarding neurotransmitter and neuropeptide responsiveness. Indeed, TRAP data analysis revealed that *Gck<sup>a</sup>PVT* neurons express receptors for GABA, glutamate, serotonin, and glycine neurotransmitters, but also for various neuropeptides and neuromodulators known to control goal-oriented behavior including feeding and water intake such as NPY, POMC, MCH, AVP, neuropeptidin, galanin, among others (Crawley, 1999; Diniz & Bittencourt, 2017; Pei et al., 2014; Schroeder & Leininger, 2018; Timper & Brüning, 2017). Using *in situ* hybridization and immunohistochemistry approaches to detect neurotransmitters and neuropeptides in retrogradely labeled neurons, we confirmed the existence of direct inputs from several forebrain and hypothalamic subpopulations, notably POMC-, CRH-, ORX-, and MCH-expressing neurons. On the contrary, while OXT receptor was highly enriched in *Gck<sup>a</sup>PVT* neurons, we were not able to observe evident colocalization of OXT in mCherry-positive presynaptic neurons in the PVH and supraoptic nucleus of the hypothalamus. Interestingly, significant OXT-positive fibers were observed close to the surface of the dorsal part of the third ventri-

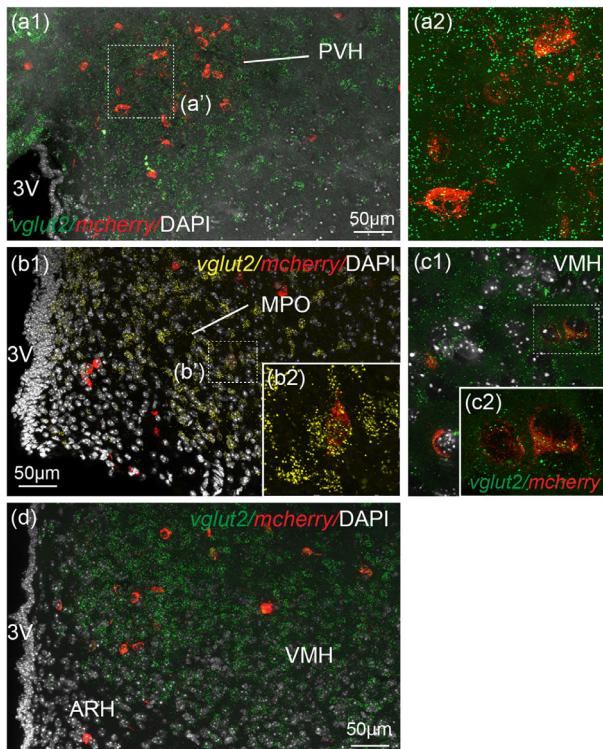


**FIGURE 12** Microscope images illustrating the expression of *Gad1* mRNA in *GCK<sup>a</sup>PVT* presynaptic neurons labeled with mCherry (red, case #1092) in the BNST (a1, a2), in the LHA (b1, b2), in the MPA (c1, c2), in the ARH (d1, d2), and in the DMH (e1, e2). DAPI-stained nuclei allow illustration of cytoarchitectonic purposes. Scale bars are shown in the figure. 3V, 3rd ventricle; ac, anterior commissure; ARH, arcuate nucleus of the hypothalamus; BNST, bed nucleus of the stria terminalis; DMH, dorsomedial nucleus of the hypothalamus; LHA, lateral hypothalamic area; LV, lateral ventricle; MPA, medial preoptic area; SHy, septohypothalamic nucleus

cle, suggesting it may be released in the cerebrospinal fluid. Furthermore, OXT is also released in the bloodstream by the posterior pituitary (Samson & Schell, 1995). Therefore, an explanation for the high enrichment of *Oxtr* in *Gck<sup>a</sup>PVT* neurons could be that they are responsive to circulating OXT.

Our transcriptomic data show that genes controlling axon guidance and synaptic plasticity are expressed at a relatively high level in *Gck<sup>a</sup>PVT* neurons. Because this analysis was performed using overnight food-deprived mice, this may suggest that synaptic remodeling is activated in the fasted state. This would be compatible with these neurons being glucose responsive (Kessler et al., 2021) and with the observation that synaptic remodeling is activated by fasting in hypothalamic neurons involved in feeding control (Kong et al., 2016; Liu et al., 2012).

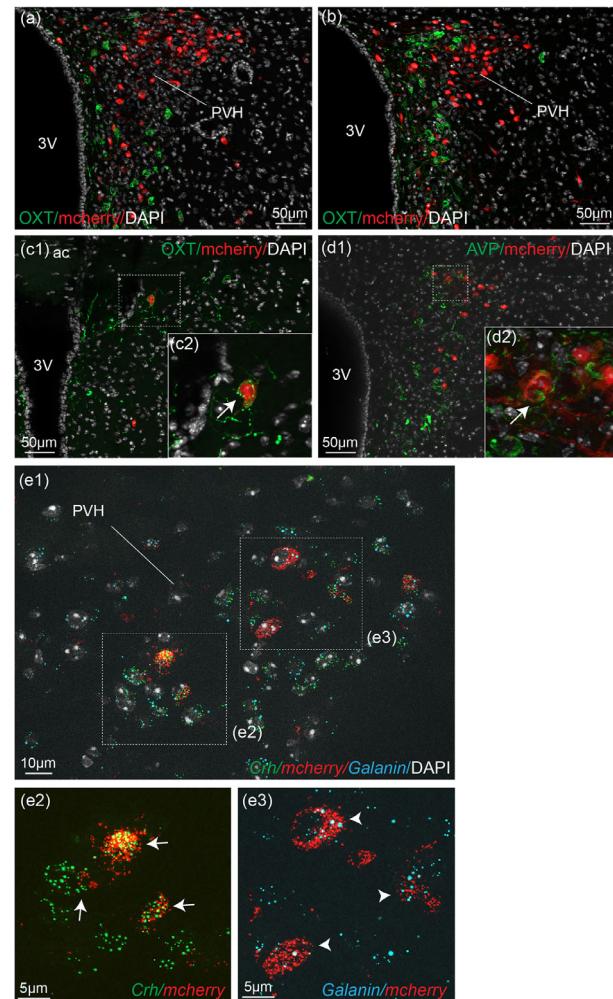
In line with the indication that *Gck<sup>a</sup>PVT* neurons play an important role in linking the animal energy status with goal-oriented behavior is the observation that these neurons are enriched in *Fto* and *Npbwr1* genes, both involved in feeding-related behavior (Chottova Dvorakova, 2018; Fawcett & Barroso, 2010). Furthermore, they express *Tcf7l2*, identified in human genome-wide association studies as a type 2 diabetes susceptibility gene (Grant et al., 2006) suggesting that the central expression of *Tcf7l2* plays a role in glucoregulation. Of note, the major



**FIGURE 13** Microscope images illustrating the expression of *vglut2* (*Slc17a6*) mRNA in  $GCK^{\alpha PVT}$  presynaptic neurons positive for mCherry (red, case #84290) in the PVH (a1, a2), in the MPO (b1, b2), and in the VMH (c1, c2, d). DAPI-stained nuclei allow illustration of cytoarchitectonic purposes. Scale bars are shown in the figure. ARH, arcuate nucleus of the hypothalamus; MPO, medial preoptic nucleus; PVH, paraventricular nucleus of the hypothalamus; VMH, ventromedial nucleus of the hypothalamus

site of expression of *Tcf7l2* within the brain is the thalamus that encompasses the PVT (Allen brain mouse atlas) (Lein et al., 2007).

Collectively, the  $Gck^{Cre/+}$  mouse line used here proved to be an excellent model to define the precise projection sites of the  $Gck^{\alpha PVT}$  neurons as well as to support the identification of their neuronal inputs. Analysis of the inputs into  $Gck^{\alpha PVT}$  neurons shows that they receive rich information coming, in large part, from distinct hypothalamic nuclei and using a diversity of neurotransmitters/neuropeptides. Mapping of these inputs in the PVT shows some neuropeptide-based regional selectivity. Our transcriptomic analysis further indicate that the  $Gck^{\alpha PVT}$  neurons express a large number of neurotransmitter/neuropeptide receptors. This suggests that subpopulations of  $Gck^{\alpha PVT}$  neurons may exist that are characterized by the expression of various combinations of these receptors. It may be hypothesized that such subpopulations may also display some functional specificities. Thus, our study provides more detailed information about the topographic and functional connectivity of  $Gck^{\alpha PVT}$  neurons and their molecular make-up. This information will help further untangle how the PVT participates in the control of behavioral responses and to explore additional circuits involved in goal-oriented behaviors.



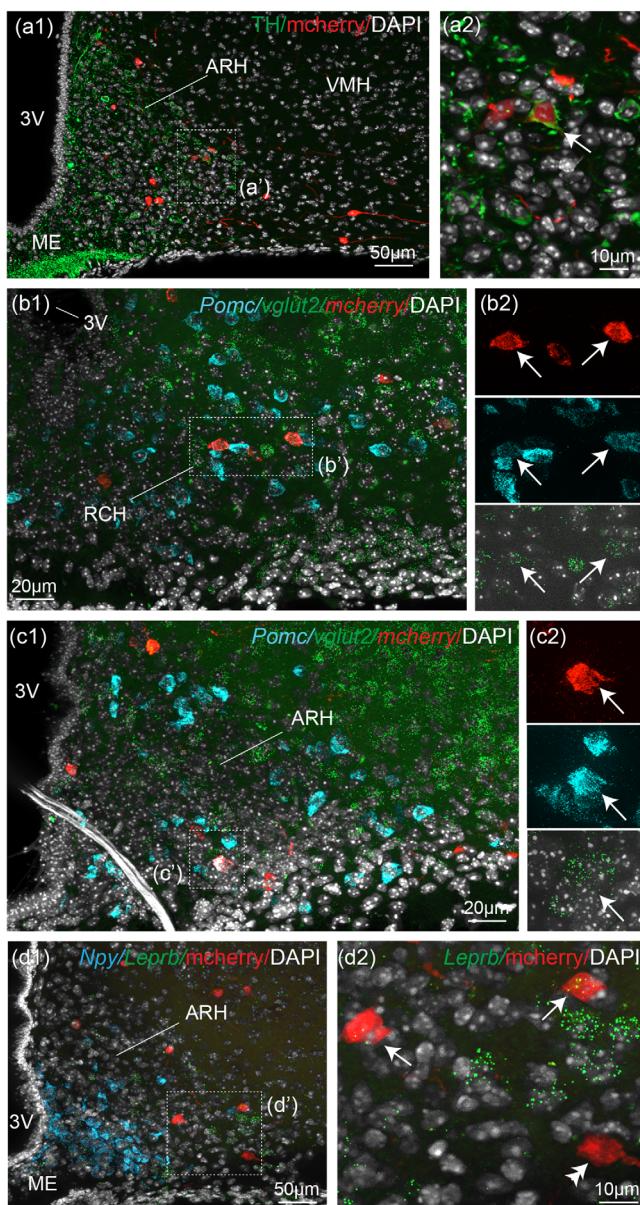
**FIGURE 14** Photomicrographs showing immunodetection of OXT (a-c1, cases #1088 and #1091) and AVP (d1, Case #1088) in mCherry-positive  $GCK\alpha PVT$  presynaptic neurons in the PVH. (e1) Photomicrographs illustrating detection of Crh (green, case #84290) and galanin (blue, case #84290) mRNA colocalized in mCherry-positive  $GCK\alpha PVT$  presynaptic neurons in the PVH. Nuclei are stained with DAPI (white). (e2 and e3) High magnifications of the insets shown in panel e1. Scale bars are shown in the figure. 3V, 3rd ventricle; PVH, paraventricular nucleus of the hypothalamus

## 4 | METHODS

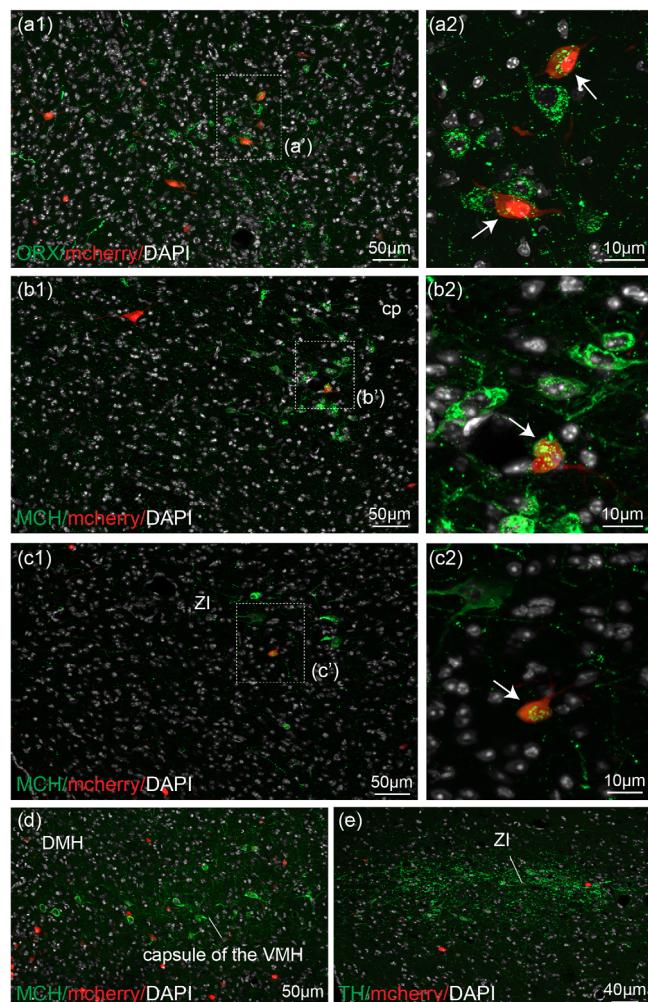
### 4.1 | Animals

#### 4.1.1 | Ethics statement

All procedures were conducted in accordance with the Swiss National Institutional Guidelines of Animal Experimentation (OExA; 455.163) with license approval (VD3184, VD3340) issued by the Cantonal Veterinary Authorities (Vaud, Switzerland). Mice were group housed in individual cages and maintained in a temperature-controlled room with a 12-h light/dark cycle and provided ad libitum access to water and standard laboratory chow (Kliba Nafag).



**FIGURE 15** Photomicrographs showing immunodetection of TH (a1, case #1077) in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the ARH. (a2) High magnification of the inset shown in panel a1. Photomicrographs illustrating detection of vglut2 (*Slc17a6*, green, case #84290) and POMC mRNA (blue, case #84290) colocalized in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the retrochiasmatic area (RCH) (b1, b2) and in the ARH (c1). (b2) High magnifications of the insets shown in panel b1. (b2) Arrows show mCherry-positive GCK $\alpha$ PVT presynaptic neurons expressing *Leprb* mRNA. (c2) High magnifications of the insets shown in panel c1. (c2) Arrows show mCherry-positive GCK $\alpha$ PVT presynaptic neurons expressing both POMC and vglut2 mRNA in the ARH. (d1) Photomicrographs illustrating detection of *Leprb* mRNA (green, case #1092) and *Npy* mRNA (blue, case #1092) colocalized in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the ARH. (d2) High magnifications of the insets shown in panel d1. Double arrowhead shows mCherry-positive GCK $\alpha$ PVT presynaptic neurons that do not express *Leprb* mRNA. Nuclei are stained with DAPI (white). Scale bars are shown in the figure. ARH, arcuate nucleus of the hypothalamus; ME, median eminence; RCH, retrochiasmatic area; VMH, ventromedial nucleus of the hypothalamus



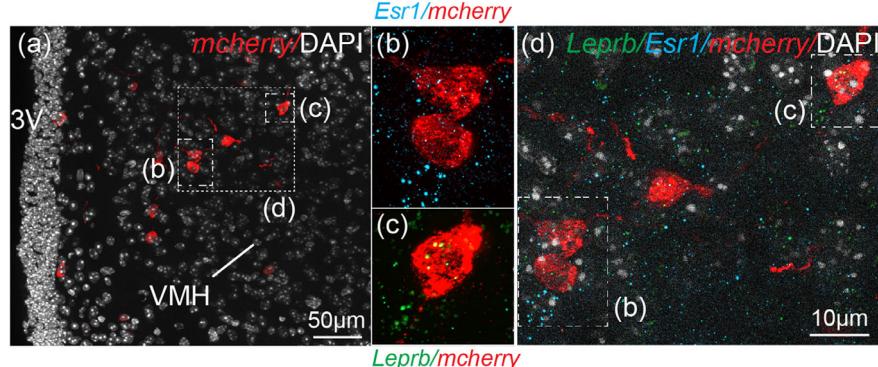
**FIGURE 16** (a1) Photomicrographs showing immunodetection of ORX (green, case #1092) in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the lateral hypothalamic area (LHA). (a2) High magnification of the inset shown in panel a1. Photomicrographs showing immunodetection of MCH (green, case #1091) in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the LHA (b1) and in the ZI (c1). (b1) High magnification of the inset shown in panel b1. (c2) High magnification of the inset shown in panel c1. (d) Photomicrographs showing immunodetection of MCH (green, case #1091) in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the capsule of the VMH. No colocalization has been observed in our material. (e) Photomicrographs showing immunodetection of TH (green, case #1091) in mCherry-positive GCK $\alpha$ PVT presynaptic neurons in the ZI. No colocalization has been observed in our material. Nuclei are stained with DAPI (white). Scale bars are shown in the figure. DMH, dorsomedial nucleus of the hypothalamus; VMH, ventromedial nucleus of the hypothalamus; ZI, zona incerta

## 4.2 | Surgery

### 4.2.1 | Anterograde tracing

16 to 20 weeks old male *Gck*<sup>Cre/+</sup> mice were used for the anterograde tracing experiments. A total of 300 nl of AAV2-hsyn-DIO-mCherry (titer 9 × 10<sup>11</sup> VG/ml) was injected in aPVT (from Bregma,

**FIGURE 17** Microscope images illustrating the expression of Esr1 (blue, a, b) and Leprb (green, c, d) mRNA in GCK<sup>aPVT</sup> presynaptic neurons positive for mCherry (a–d, red, case #4) in the VMH. DAPI-stained nuclei allow illustration of cytoarchitectonic purposes. Scale bars are shown in the figure. VMH, ventromedial nucleus of the hypothalamus



anteroposterior (AP): –0.4 mm, mediolateral (ML): +0.7 mm, dorsoventral (DV): –3.5 mm, with an angle of 10°). Ten days after injection, mice were transcardially perfused with phosphate-buffered saline (PBS) followed by 4% paraformaldehyde (PFA; Electron Microscopy Sciences, Hatfield, US). Brains were postfixed O/N in 4% PFA at 4°C and then cryopreserved in 30% sucrose (Sigma, Merck, Darmstadt, Germany) solution in PBS for at least 24 h at 4°C (until completely sunk to the bottom of the container). Cryopreserved brains were frozen using powdered dry-ice and sliced in 25-μm thick sections.

#### 4.2.2 | Monosynaptic retrograde tracing

##### Virus

pAAV-syn-FLEX-splitTVA-EGFP-tTA (Addgene viral prep # 100798-AAV1; <http://n2t.net/addgene:100798>; RRID: Addgene\_100798) and pAAV-TREtight-mTagBFP2-B19G were a gift from Ian Wickersham (Addgene viral prep # 100799-AAV1; <http://n2t.net/addgene:100799>; RRID: Addgene\_100799).

##### Surgery

Monosynaptic retrograde tracing using rabies virus was performed as follow: 13- to 20-week-old adult male *Gck*<sup>Cre/+</sup> mice were anesthetized with a mix of xylazine ketamine. Viruses were injected with a Nanofil microsyringe (World Precision, Sarasota, FL, USA, 35G) and microinjection pump (World Precision, Sarasota, FL, USA, rate at 100 nl/min). Mice receive 300 nl of mixed AAV1-Syn-FLEX-splitTVA-eGFP-tTA and AAV1-TREtight-BFP2-B19G in the aPVT (from Bregma, AP: –0.4 mm; ML: +0.65 mm; DV: –3.4 mm, 10°). After 7 days, the same mice received a second injection of 300 nl of pseudotyped rabies virus EnvA-SADdG-mCherry (Salk Institute, La Jolla, CA, USA) using the same coordinates. Control mice were injected with EnvA-SADdG-mCherry alone. One week later, mice were anesthetized and transcardially perfused with 0.9% NaCl followed by 4% PFA (Applichem, Darmstadt, Germany). Brains were postfixed 4 h in 4% PFA/20% sucrose at 4°C and then cryopreserved in 20% sucrose solution in PBS overnight at 4°C. Thirty-micrometer-thick brain cryosections were processed for immunofluorescence and *in situ* hybridization using standard procedures.

### 4.3 | Immunohistochemistry

#### 4.3.1 | Characterization of the primary antisera

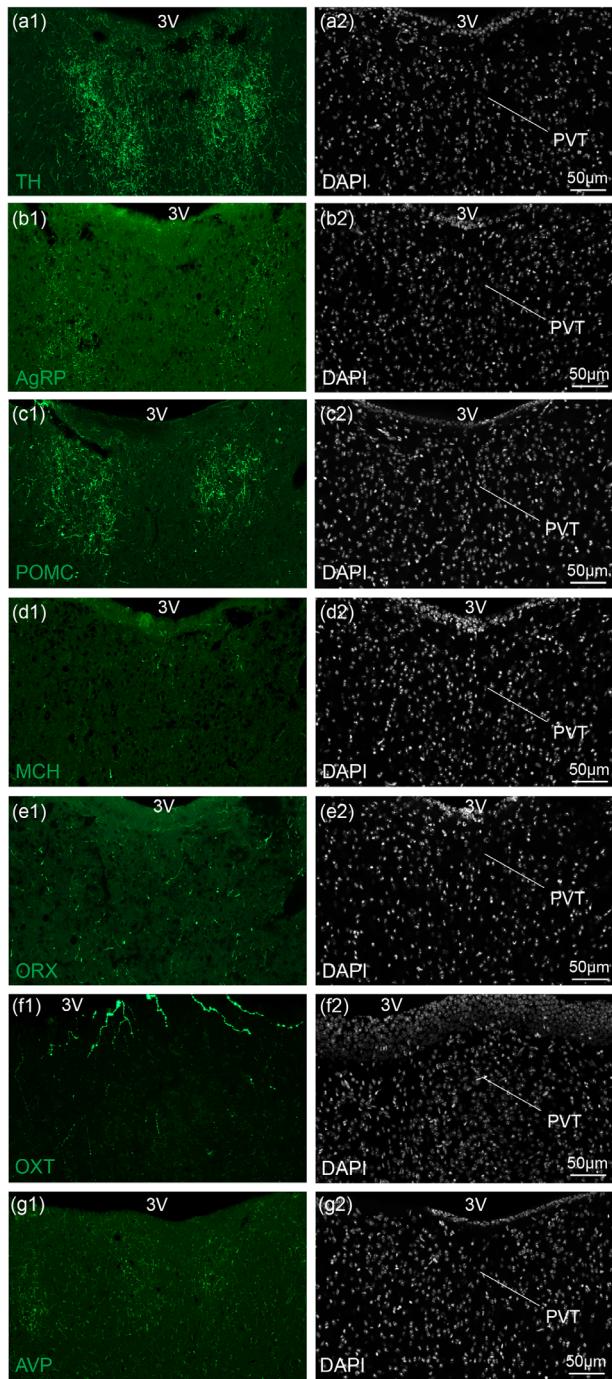
Table 2 lists the antigen, immunogen, manufacturer, catalog number, species in which the antibodies were raised, and working dilution for each of the primary antibodies. Information about the specificity of the antibodies in the following paragraphs is from the manufacturers and/or the cited references.

The rabbit polyclonal TH antibody (Merck Millipore, Darmstadt, Germany, AB152, RRID: AB\_390204) has been produced against denatured tyrosine hydroxylase from rat pheochromocytoma and targets catecholamine neurons. Sections of liver have been used as negative control and brain sections (corpus striatum) and adrenal glands as positive control and produced a pattern of staining similar to that reported elsewhere in the literature (Goff et al., 2015).

The rabbit polyclonal salmon MCH (sMCH) antibody (Risold Laboratory, RRID: AB\_2616562) recognized the synthetic sMCH (full 17-amino-acid sequence: DTMRKMVGRVYRPCWEV). The specificity of the sMCH antisera was tested by blotting (Risold et al., 1992). The sMCH antibody has been tested on hypothalamic sections from several species (Chometton et al., 2014; Croizier et al., 2013). Its specificity has been verified by liquid-phase inhibition, dot blot, and affinity column analyses (Fellmann et al., 1987; Risold et al., 1992). The labeling was observed exclusively in MCH-GFP cells in the lateral hypothalamus of mice (Croizier et al., 2011). Moreover, double labeling experiments detecting the prepro-MCH mRNA by *in situ* hybridization and MCH peptides by indirect immunofluorescence were performed in pigs and highlighted the same cell bodies in the posterior LHA (Chometton et al., 2014).

The mouse monoclonal ORX antibody (Angio-Proteomie, Boston, MA, USA, Cat# hAP-0500, ABIN1983384) was produced from a hybridoma (mouse myeloma fused with spleen cells from a mouse immunized with a peptide, aa 35–65, O43612) from human Orexin-A protein. The immunohistochemistry produced a pattern of staining similar to that described elsewhere in the literature (Barbier et al., 2018).

The rabbit polyclonal AVP antibody (Peninsula Lab International, San Carlos, CA, USA, T-4563, RRID: AB\_518673) was made against



**FIGURE 18** Photomicrographs illustrating TH (a1), AgRP (b1), POMC (c1), MCH (d1), ORX (e1), OXT (f1), and AVP (g1)-positive fibers in the anterior PVT. (a2–g2) Photomicrographs showing DAPI-stained nuclei to illustrate cytoarchitectonic purposes. Scale bars are shown in the figure. 3V, 3rd ventricle; PVT, paraventricular nucleus of the thalamus

synthetic human (Arg8)-vasopressin peptide. The immunohistochemistry highlights immunoreactive cells in the PVH and the supraoptic nucleus, similar to that described elsewhere in the literature (Castillo-Ruiz et al., 2018).

The rabbit polyclonal POMC antibody (Phoenix Pharmaceuticals, Mannheim, Germany, H-029-30, RRID:AB\_2307442) made against the porcine POMC precursor (amino acids 27–52) was further confirmed by immunofluorescence of POMC neurons in tau-topaz GFP mice. As expected, the POMC neurons labeled with this antiserum colocalized with GFP-expressing POMC neurons (Pinto et al., 2004).

The rabbit polyclonal AgRP antibody (Phoenix Pharmaceutical, Mannheim, Germany, H-003-53, RRID:AB\_2313908) was made against the human Agouti-Related Protein (83–132) amide. Preabsorption with the immunizing peptide AgRP (83–132) blocks the staining reaction (Haskell-Luevano et al., 1999).

The rabbit monoclonal OXT antibody (Abcam, Cambridge, UK, ab\_212193) was made against the recombinant fragment of Human Oxytocin aa 1 to the C-terminus. This antibody recognizes oxytocin protein by western blotting performed with mouse and rat pituitary tissue lysates. Oxytocin is immunodetected in the paraventricular nucleus of the hypothalamus (PVH) of rats and mice (Zhou et al., 2020).

#### 4.3.2 | Immunofluorescent staining

After rinsing in PBS, sections were incubated with primary antibodies (Table 2) dissolved in working solution (PBS, 2% goat serum, 0.3% Triton) for 48 h at 4°C. Tissues were washed three times with PBS (5 min each) and incubated for 1 h with appropriate secondary antibodies (Table 3) diluted in the working solution at room temperature. Finally, sections were washed with PBS, mounted using DAPI-fluoromount (SouthernBiotech®, Birmingham, AL, USA) solution.

#### 4.4 | In situ hybridization (RNAscope)

On 30-µm-thick brain coronal cryosections, in situ hybridization for *Pomc* (Cat# 314081), *Npy* (Cat# 313321), *Leprb* (Cat# 402731), *Crh* (Cat# 316091), *Slc17a6* (*vglut2*, Cat# 319171), *Gad1* (Cat# 400951), *Galanin* (Cat# 400961), *mcherry* (Cat# 431201), and *Esr1* (Cat# 478201) was processed using RNAscope probes and RNAscope Fluorescent Multiplex Detection Reagents (Advanced Cell Diagnostics, Newark, CA, USA) following manufacturer's instructions. As negative control, we used the negative control probe-DapB (Cat #310043).

#### 4.5 | Translating ribosomes affinity purification

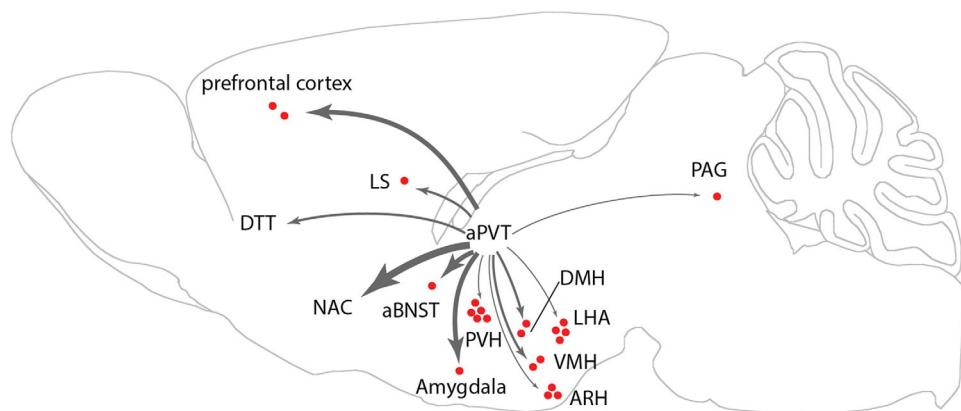
TRAP was performed as described (Heiman et al., 2008; Heiman et al., 2014) with minor modifications. Briefly, *Gck*<sup>Cre/+</sup> mice were injected in the PVT twice with 200 nl of AAV8-DIO-L10-eGFP (Nectow et al., 2017) (AP: -0.4, DV: -3.5, and ML: ±0.7, 10° angle). Ten days later, mice were fasted overnight, and killed by decapitation, and the PVT were microdissected under binoculars in ice-cold PBS, directly frozen in liquid nitrogen and stored at -150°C. TRAP extractions were

**TABLE 2** List of primary antibodies used in the study

Antibody	Immunogen	Source	Dilution
Anti-TH	Denatured tyrosine hydroxylase from rat pheochromocytoma	Rabbit, polyclonal, Merck Millipore, AB152, RRID:AB_390204	1:500
Anti-MCH	Synthetic salmon MCH; full 17-amino-acid sequence: DTMRKMVGRVYRPCWEV	Rabbit, polyclonal, Risold et al. (1992), RRID:AB_2616562	1:1000
Anti-Orexin A (Hcrt)	Human Orexin A, immunogen AA 35–65, clone MM0500-8G22	Mouse, monoclonal IgG1, Angio-Proteomie, Cat# hAP-0500, ABIN1983384	1:1000
Anti-AVP	Human (Arg8)-Vasopressin	Rabbit, polyclonal, T-4563, Peninsula Lab International, RRID:AB_518673	1:500
Anti-POMC	Porcine POMC precursor (amino acids 27–52)	Rabbit, polyclonal, Phoenix Pharmaceuticals, H-029-30, RRID:AB_2307442	1:2000
Anti-AgRP	Human Agouti-Related Protein (83–132) amide	Rabbit, polyclonal, Phoenix Pharmaceuticals, H-003-53, RRID:AB_2313908	1:2000
Anti-OXT	Recombinant fragment of Human Oxytocin aa 1 to the C-terminus	Rabbit, monoclonal, Abcam, ab_212193	1:500

**TABLE 3** List of secondary antibodies used in the study

Secondary antibodies	Conjugated	Manufacturer	Cat Number	RRID	Dilution
Goat anti-mouse IgG (H+L) cross-adsorbed secondary antibody	Alexa Fluor 488	Thermo Fisher	A11001	AB_2534069	1:500
Goat anti-rabbit IgG (H+L) cross-adsorbed secondary antibody	Alexa Fluor 488	Thermo Fisher	A11008	AB_143165	1:500

**FIGURE 19** Sagittal view of a brain showing general organization of the inputs and outputs to GCK-expressing neurons in the anterior PVT (aPVT). The relative strength of each pathway is proportional to the thickness of the gray lines. Projections from the aPVT innervate the prefrontal cortex, the dorsal tegmena tecta (DTT), the nucleus accumbens (NAC), the lateral septum (LS), the anterior part of the BNST (aBNST), the amygdala, and hypothalamic nuclei including the paraventricular (PVH), the dorsomedial (DMH), the ventromedial (VMH), the arcuate (ARH), the lateral hypothalamic area (LHA), and the periaqueductal gray (PAG). They also receive reciprocal projections from the prefrontal cortex, the LS, aBNST, the amygdala, the PVH, DMH, VMH, ARH, LHA, and PAG. The relative number of red dots is proportional to the abundance of presynaptic neurons

performed on four pools of five PVTs, lysed in 500  $\mu$ l of ice-cold lysis buffer (20 mM Hepes pH 7.3, 150 mM KCl, 10 mM MgCl<sub>2</sub>, 1% NP40, cycloheximide 100  $\mu$ g/ml, 0.5 mM DTT, Superasin [ThermoFischer, Waltham, MA, USA] and RNasin [Promega, Madison, WI, USA]) using a Potter and insoluble material was cleared by centrifugation (10 min at 10,000  $\times$  g). The supernatants were saved, 5.6  $\mu$ g of anti-GFP antibody (Sigma Aldrich, Merck, Darmstadt, Germany) was added, and the tubes were kept for 4 h of at 4°C with constant rotation. This mixture

was coupled with 200  $\mu$ l of magnetic bead suspension (ThermoFischer, Waltham, MA, USA) as 30  $\mu$ l sample of this suspension was kept as control (input). Magnetic beads were then separated using a magnet and washed once in lysis buffer and three times with lysis buffer containing 350 mM KCl. RNAs attached to beads or present in the control input fractions were purified using the Nucleospin RNA mini kit (Macherey-Nagel, Allentown, PA, USA). RNAs were then subjected to fragment analysis and amplified by single primer isothermal amplification with

the Ovation RNA-Amplification System V2 (NuGEN), providing DNA libraries for RNA sequencing. The number of reads were between 50 and 65 million per library.

#### 4.6 | RNA-sequencing analysis

Reads were aligned against *Mus musculus* GRCm38.82 genome using STAR (v. 2.4.2a [Dobin et al., 2013]). The number of read counts per gene locus was summarized with htseq-count (v. 0.6.1 [Anders et al., 2015]) using *Mus musculus* GRCm38.82 gene annotation. Quality of the RNA-sequencing (RNA-seq) data alignment was assessed using RSeQC (v. 2.3.7 [Wang et al., 2012]). Genes with less than 1 count per million (CPM) across samples were removed. Library sizes were scaled using TMM normalization (EdgeR package version 3.16.3 [Robinson et al., 2010]) and log-transformed with Limma voom function (Limma package version 3.30.4 [Law et al., 2014]). Differential expression analysis was performed for the immunoprecipitated output samples versus the remaining PVT input samples; *p*-values were adjusted for multiple comparisons using the Benjamini Hochberg procedure (Hochberg & Benjamini, 1990) and those genes with an expression that differ with an adjusted *p*-value  $\leq .05$  were considered as differentially expressed. Heatmaps were generated using Morpheus online software (<https://software.broadinstitute.org/orpheus>). KEGG pathway analysis was performed with the “clusterProfiler” R package (Yu et al., 2012) and those pathways with an adjusted *p*-value  $\leq .05$  were overrepresented. RNA-seq data are available in a public repository (GEO). Accession # GSE185964.

#### 4.7 | Image acquisition and processing

Images for the anterograde and retrograde tracing study were acquired on a confocal LSM 710 (Zeiss, Germany) equipped with lasers for excitation of Alexa 488 (488 nm), Alexa 568 (561 nm), Alexa 647 (633 nm), and DAPI (405 nm) and Plan Apochromat 10  $\times$  0.45 DIC and Plan Apochromat 20  $\times$  0.8 DIC. Images were obtained by using the Zen black 2012 software. Immunofluorescent sections were acquired on a ZEISS Axio Imager.M2 microscope, equipped with ApoTome.2 and a Camera Axiocam 702 mono (Zeiss, Germany). Specific filter sets were used for the visualization of green (Filter set 38 HE eGFP shift free [E] EX BP 470/40, BS FT 495, EM BP 525/50), red (Filter set 43 HE Cy 3 shift free [E] EX BP 550/25, BS FT 570, EM BP 605/70), blue (Filter set 49 DAPI shift free [E] EX G 365, BS FT 395, EM BP 445/50) and far red (Filter set 50 Cy 5 shift free [E] EX BP 640/30, BS FT 660, EM BP 690/50) fluorescence. Different magnifications were selected using a Zeiss  $\times 20$  objective (Objective Plan-Apochromat 20 $\times$ 0.8 M27, FWD = 0.55 mm) and a  $\times 40$  oil-immersion objective (Objective C Plan-Apochromat  $\times$  40/1.4 Oil DIC M27 [Free working distance, FWD = 0.13 mm]).

The overall distribution of mCherry-positive projections arising from GCK<sup>aPVT</sup> from Bregma 2.5 to –3.5 (case #1) has been imaged with

a stereomicroscope (Nikon SMZ-25 equipped with Plan-Apochromat 1X SHR WD 60 mm).

Neither additional treatment was made, except to enhance fluorescent intensity. We based our nomenclature and nuclear parcellation on Mouse Brain Atlas from Franklin and Paxinos (Paxinos & Franklin, 2001), on Rat Brain Atlas from Swanson (Swanson, 2004) and on the work of Barbier and colleagues (Barbier et al., 2021).

#### 4.8 | Quantification

##### 4.8.1 | Anterograde tracing

The density of Gck<sup>aPVT</sup> fibers in each target area was quantified approximately based on a 5-point scale adopted from Li and Kirouac (2008). The equivalence for projection intensity was as follows: +++++, very dense; ++++, dense; +++, moderate; ++, light; +, very light. The data presented in Table 1 are deriving from collective quantification of all five anterograde tracing cases.

##### 4.8.2 | Monosynaptic retrograde tracing

The total number of mCherry-positive neurons were quantified on the four brains (cases #1076, #1077, #1091, and #783) from confocal microscope images of sections including the IL to sections including the PAG. We did not analyze more anterior and posterior sections. We then quantified the number of mCherry-positive neurons in every brain area where cells have been observed. We expressed the results as percentage of total mCherry-positive cells.

#### 4.9 | Statistics

All values were represented as the mean  $\pm$  SEM (standard error of the mean). Numbers for every experiment are found in the relevant part of Section 4. Statistical analyses were conducted using GraphPad Prism (v. 8); *p*  $\leq .05$  was considered statistically significant.

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All the authors contributed to perform the experiments. SG, SQ, BT, and SC designed the experiments. SG, SQ, ARSA, and SC analyzed the data. SG and SC wrote the paper. SG, SQ, ARSA, BT, and SC edited the manuscript. This work was supported by an Advanced Grant from the European Research Council (INTEGRATE, No. 694798) and a grant from the Swiss National Science Foundation (grant # 310030-182496) to BT and grants from the Swiss National Science Foundation (PZ00P3\_167934/1) and the Novartis Foundation for medical-biological research (19B145) to SC.

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#### CONFLICT OF INTEREST

The authors declare no conflict of interest.

## DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

## PEER REVIEW

The peer review history for this article is available at <https://publons.com/publon/10.1002/cne.25312>.

## ORCID

Sophie Croizier  <https://orcid.org/0000-0002-0076-1008>

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## APPENDIX

**TABLE A1** List of differentially expressed genes in GCK<sup>aPVT</sup> neurons compared to aPVT cells not expressing Gck. All differentially expressed genes with an adjusted *p*-value  $\leq .05$  are included. A total of 3121 genes were enriched in GCKaPVT neurons and 3245 were depleted

Gene name	LogFC	Adjusted <i>p</i> -value	Average expression (AveExpr)	Gene full name
Gtf2i	2.87	$1.74 \times 10^{-5}$	9.108413	General transcription factor II I (Gtf2i)
Tfap2d	2.65	.011292057	0.410732	Transcription factor AP-2, delta (Tfap2d)
Grhl3	1.77	.004006759	0.14564	Grainyhead-like 3 (Grhl3)
Ddias	1.71	.000218273	1.865183	DNA damage-induced apoptosis suppressor (Ddias)
Acpp	1.63	.004126485	0.427175	Acid phosphatase, prostate (Acpp)
Nol8	1.62	$2.08 \times 10^{-8}$	6.491834	Nucleolar protein 8 (Nol8)
Tead4	1.58	.019985699	0.103252	TEA domain family member 4 (Tead4)
Chrdl2	1.56	.016825785	0.006153	Chordin-like 2 (Chrdl2)
Rpl10a	1.54	$1.30 \times 10^{-7}$	7.235633	Ribosomal protein L10A (Rpl10a)
Met	1.54	.00732905	0.605268	Met proto-oncogene (Met)
Gm16565	1.50	.006784345	1.023606	Predicted gene 16565 (Gm16565)
Plscr5	1.50	.010521615	0.059025	Phospholipid scramblase family, member 5 (Plscr5)
Slc10a4	1.49	.000129292	2.572029	Solute carrier family 10 (sodium/bile acid cotransporter family), member 4 (Slc10a4)
Gm14057	1.47	.021899313	-0.05272	Ppp1r14c pseudogene (Gm14057)
Ppef1	1.46	.004659662	1.42743	Protein phosphatase with EF hand calcium-binding domain 1 (Ppef1)
Fosb	1.45	.000841378	2.561443	FBJ osteosarcoma oncogene B (Fosb)
Avpr1a	1.44	.003681061	1.422	Arginine vasopressin receptor 1A (Avpr1a)
Gtse1	1.44	.008213577	1.094765	G two S phase expressed protein 1 (Gtse1)
Gm37356	1.42	.01089818	0.305063	Predicted gene 37356 (Gm37356)
Csrnp1	1.40	$5.63 \times 10^{-5}$	2.561621	Cysteine-serine-rich nuclear protein 1 (Csrnp1)
Grpr	1.39	.022676509	1.534775	Gastrin releasing peptide receptor (Grpr)
Zfp975	1.38	.000259201	2.349293	Zinc finger protein 975 (Zfp975)
Slc35d3	1.38	.014007594	0.795903	Solute carrier family 35, member D3 (Slc35d3)
Cdh24	1.37	.000216578	2.569775	Cadherin-like 24 (Cdh24)
Slco4c1	1.36	.000582403	2.365296	Solute carrier organic anion transporter family, member 4C1 (Slco4c1)
Adamts8	1.35	.037037781	-0.13248	A disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 8 (Adamts8)
Apc2	1.35	$4.82 \times 10^{-5}$	7.192544	Adenomatosis polyposis coli 2 (Apc2)
Sp9	1.34	.001796092	2.973311	Trans-acting transcription factor 9 (Sp9)
Kbtbd6	1.32	.040299298	0.283291	Kelch repeat and BTB (POZ) domain containing 6 (Kbtbd6)
Gm20518	1.32	.043972042	-0.0947	Predicted gene 20518 (Gm20518)
Rbm46	1.31	.039406932	0.193756	RNA binding motif protein 46 (Rbm46)
Prr15	1.29	.005489492	1.034567	Proline rich 15 (Prr15)
Xkrx	1.29	.000159027	2.973101	X-linked Kx blood group related, X-linked (Xkrx)
Drd3	1.29	.000570654	1.793582	Dopamine receptor D3 (Drd3)
Oxtr	1.28	$4.36 \times 10^{-6}$	4.642701	Oxytocin receptor (Oxtr)
4930426D05Rik	1.28	.043430898	-0.02356	RIKEN cDNA 4930426D05 gene (4930426D05Rik)
Ext2	1.28	$1.66 \times 10^{-5}$	6.427251	Exostoses (multiple) 2 (Ext2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
St14	1.27	.000143473	3.055597	Suppression of tumorigenicity 14 (colon carcinoma) (St14)
Gm5466	1.26	.025877944	-0.05832	Poly(A) binding protein, cytoplasmic 4 pseudogene (Gm5466)
Al606181	1.26	.000869949	2.822355	Expressed sequence Al606181 (Al606181)
Bmp3	1.26	$2.81 \times 10^{-5}$	3.508207	Bone morphogenetic protein 3 (Bmp3)
Gm17096	1.26	.027777784	-0.0146	Predicted gene 17096 (Gm17096)
Oprk1	1.26	$2.05 \times 10^{-7}$	5.706194	Opioid receptor, kappa 1 (Oprk1)
Slc38a4	1.26	.028154112	0.619424	Solute carrier family 38, member 4 (Slc38a4)
Tacr3	1.25	$5.88 \times 10^{-6}$	4.388588	Tachykinin receptor 3 (Tacr3)
Zfp92	1.25	$1.63 \times 10^{-6}$	4.735225	Zinc finger protein 92 (Zfp92)
Acot3	1.24	.033222174	0.027654	Acyl-CoA thioesterase 3 (Acot3)
Nrap	1.24	.000435793	2.108514	Nebulin-related anchoring protein (Nrap)
Mycn	1.24	$5.69 \times 10^{-5}$	3.42305	V-myc avian myelocytomatisis viral related oncogene, neuroblastoma derived (Mycn)
Dchs2	1.23	.000118811	3.378319	Dachsous 2 (Dchs2)
Prickle1	1.22	$3.50 \times 10^{-7}$	6.095453	Prickle planar cell polarity protein 1 (Prickle1)
Pthlh	1.21	.004157208	1.467854	Parathyroid hormone-like peptide (Pthlh)
Uts2r	1.20	.001720957	1.837421	Urotensin 2 receptor (Uts2r)
Ube4a	1.20	.000206451	6.754708	Ubiquitination factor E4A (Ube4a)
Gm45623	1.20	.001246157	2.353854	Predicted gene 45623 (Gm45623)
Gpr176	1.20	$4.45 \times 10^{-5}$	4.360506	G protein-coupled receptor 176 (Gpr176)
Tmem132a	1.19	$1.34 \times 10^{-5}$	4.390167	Transmembrane protein 132A (Tmem132a)
Rab3b	1.18	$2.12 \times 10^{-7}$	7.439507	RAB3B, member RAS oncogene family (Rab3b)
Gm15379	1.17	.015294905	0.679995	Zinc finger and SCAN domain containing 12 pseudogene (Gm15379)
Tox3	1.16	$4.28 \times 10^{-7}$	6.661831	TOX high-mobility group box family member 3 (Tox3)
Atp8b3	1.16	.031885543	0.422582	ATPase, class I, type 8B, member 3 (Atp8b3)
Nudt12	1.16	$4.88 \times 10^{-6}$	4.365229	Nudix (nucleoside diphosphate linked moiety X)-type motif 12 (Nudt12)
Sema3f	1.15	.000629233	2.910066	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (Sema3f)
Doc2a	1.14	.011497985	1.268657	Double C2, alpha (Doc2a)
Fto	1.14	$2.12 \times 10^{-7}$	7.342707	Fat mass and obesity associated (Fto)
Trpc5	1.13	$5.46 \times 10^{-7}$	6.407225	Transient receptor potential cation channel, subfamily C, member 5 (Trpc5)
Pter	1.13	$1.00 \times 10^{-6}$	7.327025	Phosphotriesterase related (Pter)
Dlgap2	1.13	$2.90 \times 10^{-6}$	4.60807	Discs, large homolog-associated protein 2 (Dlgap2)
Foxp2	1.13	$1.87 \times 10^{-7}$	8.115582	Forkhead box P2 (Foxp2)
Zfp442	1.13	.03719428	1.664221	Zinc finger protein 442 (Zfp442)
Pcsk5	1.13	$5.74 \times 10^{-6}$	4.997306	Proprotein convertase subtilisin/kexin type 5 (Pcsk5)
P2rx3	1.13	.013162914	0.790749	Purinergic receptor P2X, ligand-gated ion channel, 3 (P2rx3)
C1ql3	1.12	$2.05 \times 10^{-7}$	6.023888	C1q-like 3 (C1ql3)
Foxp1	1.12	$2.08 \times 10^{-8}$	7.821432	Forkhead box P1 (Foxp1)
Gprin3	1.12	$1.28 \times 10^{-6}$	5.961733	GPRIN family member 3 (Gprin3)
Dgkg	1.12	$5.36 \times 10^{-6}$	5.054086	Diacylglycerol kinase, gamma (Dgkg)
Bdnf	1.11	$2.89 \times 10^{-5}$	4.795036	Brain-derived neurotrophic factor (Bdnf)
Lancl3	1.11	.013321046	2.039189	LanC lantibiotic synthetase component C-like 3 (bacterial) (Lancl3)
Dlk1	1.11	$3.14 \times 10^{-5}$	5.72567	Delta-like 1 homolog (Dlk1)
Pdzrn3	1.11	.000158774	4.509556	PDZ domain containing RING finger 3 (Pdzrn3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Fam199x	1.11	$1.10 \times 10^{-5}$	4.484698	Family with sequence similarity 199, X-linked (Fam199x)
Pcdh18	1.10	$9.18 \times 10^{-6}$	5.579679	Protocadherin 18 (Pcdh18)
Nkd2	1.10	.000431903	3.670481	Naked cuticle 2 homolog (Nkd2)
Htr1d	1.10	.000101607	3.706647	5-Hydroxytryptamine (serotonin) receptor 1D (Htr1d)
Pdyn	1.09	.000504797	3.255823	Prodynorphin (Pdyn)
Esr1	1.09	.00422765	1.990281	Estrogen receptor 1 (alpha) (Esr1)
Zfp74	1.09	$2.93 \times 10^{-6}$	5.54294	Zinc finger protein 74 (Zfp74)
Gm14403	1.08	$9.06 \times 10^{-5}$	3.723878	Predicted gene 14403 (Gm14403)
Snx9	1.08	$3.04 \times 10^{-5}$	4.241231	Sorting nexin 9 (Snx9)
Zdhhc23	1.08	.009262626	1.622974	Zinc finger, DHHC domain containing 23 (Zdhhc23)
Epha1	1.08	.001150661	2.04453	Eph receptor A1 (Epha1)
5033406O09Rik	1.07	.013174575	1.43022	RIKEN cDNA 5033406O09 gene (5033406O09Rik)
Cpne6	1.06	$2.70 \times 10^{-6}$	6.673036	Copine VI (Cpne6)
A730046J19Rik	1.06	.030412458	1.892526	RIKEN cDNA A730046J19 gene (A730046J19Rik)
Efcc1	1.06	.008304718	2.074031	EF hand and coiled-coil domain containing 1 (Efcc1)
Doc2b	1.05	$8.93 \times 10^{-6}$	6.451608	Double C2, beta (Doc2b)
Sfrp2	1.05	$6.18 \times 10^{-5}$	3.713566	Secreted frizzled-related protein 2 (Sfrp2)
Gm26805	1.04	.00130816	2.269391	Predicted gene
Gabra5	1.04	$8.58 \times 10^{-7}$	7.085249	Gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5 (Gabra5)
AW551984	1.04	$1.77 \times 10^{-6}$	6.006546	Expressed sequence AW551984 (AW551984)
Ldb2	1.04	$2.88 \times 10^{-7}$	7.114963	LIM domain binding 2 (Ldb2)
Pom121	1.03	$1.20 \times 10^{-5}$	7.190722	Nuclear pore membrane protein 121 (Pom121)
Aloxe3	1.03	.000479377	2.991306	Arachidonate lipoxygenase 3 (Aloxe3)
Etl4	1.03	.000163311	6.360278	Enhancer trap locus 4 (Etl4)
Fos	1.03	.000738545	4.517408	FBJ osteosarcoma oncogene (Fos)
Dact2	1.02	.013209915	1.070964	Dishevelled-binding antagonist of beta-catenin 2 (Dact2)
Gm15672	1.02	.032203827	0.58211	Predicted gene 15672 (Gm15672)
Prlr	1.02	$7.09 \times 10^{-6}$	5.164952	Prolactin receptor (Prlr)
Rpp25	1.01	.007425239	1.888958	Ribonuclease P/MRP 25 subunit (Rpp25)
Magel2	1.01	.001656002	2.737994	Melanoma antigen, family L, 2 (Magel2)
Tmem132e	1.01	.0003504	3.082943	Transmembrane protein 132E (Tmem132e)
Cdh6	1.01	$7.75 \times 10^{-7}$	6.197736	Cadherin 6 (Cdh6)
Nts	1.01	.001374874	3.234018	Neurotensin (Nts)
Mybl1	1.00	$2.80 \times 10^{-5}$	5.13412	Myeloblastosis oncogene-like 1 (Mybl1)
Mc3r	1.00	.000502705	3.693045	Melanocortin 3 receptor (Mc3r)
Klf5	1.00	.002627598	3.086911	Kruppel-like factor 5 (Klf5)
Ogfod1	1.00	$3.99 \times 10^{-8}$	8.192083	2-Oxoglutarate and iron-dependent oxygenase domain containing 1 (Ogfod1)
Drd2	1.00	$3.37 \times 10^{-5}$	4.922051	Dopamine receptor D2 (Drd2)
N4bp2l2	1.00	$5.84 \times 10^{-6}$	6.027103	NEDD4 binding protein 2-like 2 (N4bp2l2)
Arhgap6	1.00	.001545653	2.653602	Rho GTPase activating protein 6 (Arhgap6)
Zfp983	0.99	.000102509	3.549722	Zinc finger protein 983 (Zfp983)
Crtac1	0.99	.000791988	4.090499	Cartilage acidic protein 1 (Crtac1)
Fam159b	0.99	.006360216	1.887299	Family with sequence similarity 159, member B (Fam159b)
Exph5	0.99	$1.30 \times 10^{-5}$	5.47877	Exophilin 5 (Exph5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gm6981	0.98	.022449139	1.179357	Glyceraldehyde-3-phosphate dehydrogenase pseudogene (Gm6981)
Nrsn2	0.98	$6.37 \times 10^{-8}$	9.589449	Neurensin 2 (Nrsn2)
Plcd3	0.98	$4.91 \times 10^{-5}$	4.856254	Phosphatidylinositol-specific phospholipase C, X domain containing 3 (Plcd3)
Pcdha11	0.97	.03706643	0.884052	Protocadherin alpha 11 (Pcdha11)
Zik1	0.97	.000123278	3.449682	Zinc finger protein interacting with K protein 1 (Zik1)
Bmp2	0.97	.000192173	3.842189	Bone morphogenetic protein 2 (Bmp2)
Galr1	0.97	.00089192	4.604638	Galanin receptor 1 (Galr1)
Gm20735	0.97	.01634046	0.873205	Predicted gene, 20735 (Gm20735)
Rtl5	0.97	$4.02 \times 10^{-5}$	5.228496	Retrotransposon Gag Like 5 (Rtl5)
Vil1	0.97	.016368768	3.340394	Villin 1 (Vil1)
C130083M11Rik	0.96	.002849927	3.632053	RIKEN cDNA C130083M11 gene (C130083M11Rik)
Ak5	0.96	$4.97 \times 10^{-5}$	5.18943	Adenylate kinase 5 (Ak5)
Gprasp2	0.96	$1.41 \times 10^{-6}$	7.914679	G protein-coupled receptor-associated sorting protein 2 (Gprasp2)
Glra2	0.96	$1.53 \times 10^{-5}$	5.922126	Glycine receptor, alpha 2 subunit (Glra2)
Slc30a3	0.96	$1.13 \times 10^{-5}$	4.964123	Solute carrier family 30 (zinc transporter), member 3 (Slc30a3)
Map3k20	0.95	$8.11 \times 10^{-6}$	5.852169	Mitogen-activated protein kinase kinase 20
Ripk4	0.95	.005677703	2.860979	Receptor-interacting serine-threonine kinase 4 (Ripk4)
Slitrk6	0.95	$4.33 \times 10^{-7}$	8.084594	SLIT and NTRK-like family, member 6 (Slitrk6)
Aldh3b2	0.95	.000238358	4.015348	Aldehyde dehydrogenase 3 family, member B2 (Aldh3b2)
Ptger3	0.95	$1.49 \times 10^{-5}$	4.512245	Prostaglandin E receptor 3 (subtype EP3) (Ptger3)
Hcrtr1	0.94	.011599886	1.687169	Hypocretin (orexin) receptor 1 (Hcrtr1)
Nptxr	0.94	$7.14 \times 10^{-6}$	10.66128	Neuronal pentraxin receptor (Nptxr)
Zfp788	0.94	$4.44 \times 10^{-6}$	6.20602	Zinc finger protein 788 (Zfp788)
Pkmyt1	0.94	.044531571	0.38337	Protein kinase, membrane-associated tyrosine/threonine 1 (Pkmyt1)
Cdh18	0.94	$2.44 \times 10^{-5}$	5.541691	Cadherin 18 (Cdh18)
4930513N10Rik	0.94	.036164296	0.782688	RIKEN cDNA 4930513N10 gene (4930513N10Rik)
Gm37811	0.94	.045603114	1.339915	Predicted gene
Ankrd55	0.94	.000176486	3.59533	Ankyrin repeat domain 55 (Ankrd55)
Pdzrn4	0.94	.000350378	3.212135	PDZ domain containing RING finger 4 (Pdzrn4)
Ankrd34b	0.94	$2.98 \times 10^{-5}$	6.500705	Ankyrin repeat domain 34B (Ankrd34b)
Zfp970	0.93	.002380137	3.53278	Zinc finger protein 970 (Zfp970)
Chl1	0.93	$1.98 \times 10^{-7}$	8.415267	Cell adhesion molecule L1-like (Chl1)
Tmem255a	0.93	$3.24 \times 10^{-5}$	7.727587	Transmembrane protein 255A (Tmem255a)
Zfr2	0.93	.000535846	5.118793	Zinc finger RNA binding protein 2 (Zfr2)
Klh14	0.93	.003699522	2.298974	Kelch-like 14 (Klh14)
Zfp804b	0.93	.000201806	4.383883	Zinc finger protein 804B (Zfp804b)
Car8	0.93	$3.14 \times 10^{-5}$	5.972933	Carbonic anhydrase 8 (Car8)
Pdxk	0.93	$1.74 \times 10^{-6}$	5.946843	Pyridoxal (pyridoxine, vitamin B6) kinase (Pdxk)
Fam210b	0.92	$9.66 \times 10^{-7}$	7.894178	Family with sequence similarity 210, member B (Fam210b)
Syt10	0.92	$2.05 \times 10^{-5}$	5.996295	Synaptotagmin X (Syt10)
Hcn1	0.92	$1.84 \times 10^{-6}$	6.215878	Hyperpolarization-activated, cyclic nucleotide-gated K+ 1 (Hcn1)
Pcdha7	0.92	.033047577	0.96439	Protocadherin alpha 7 (Pcdha7)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lhx2	0.92	$6.06 \times 10^{-6}$	6.181249	LIM homeobox protein 2 (Lhx2)
Vgf	0.92	$4.47 \times 10^{-5}$	5.867988	VGF nerve growth factor inducible (Vgf)
Cntnap3	0.92	.000132337	5.556513	Contactin-associated protein-like 3 (Cntnap3)
Jade3	0.92	.000148791	4.0821	Jade family PHD finger 3 (Jade3)
Penk	0.92	.000989107	3.714957	Preproenkephalin (Penk)
Dusp4	0.91	.005419347	2.69197	Dual-specificity phosphatase 4 (Dusp4)
Npbwr1	0.91	.004871065	2.716596	Neuropeptides B/W receptor 1 (Npbwr1)
Prrg4	0.91	$1.72 \times 10^{-5}$	5.446763	Proline-rich Gla (G-carboxyglutamic acid) 4 (transmembrane) (Prrg4)
Fhod3	0.91	$9.18 \times 10^{-6}$	6.486289	Formin homology 2 domain containing 3 (Fhod3)
Kcna4	0.91	$2.24 \times 10^{-6}$	6.267314	Potassium voltage-gated channel, shaker-related subfamily, member 4 (Kcna4)
Marchf1	0.91	$8.04 \times 10^{-6}$	5.537262	Membrane-associated ring-CH-type finger 1 (Marchf1)
Fam196b	0.91	$5.36 \times 10^{-6}$	5.962515	Family with sequence similarity 196, member B (Fam196b)
C230021G24Rik	0.91	.038954561	1.753545	RIKEN cDNA C230021G24 gene (C230021G24Rik)
Pcdha9	0.90	.00640222	1.861305	Protocadherin alpha 9 (Pcdha9)
Dclk3	0.90	$4.45 \times 10^{-5}$	4.603524	Doublecortin-like kinase 3 (Dclk3)
Ntng1	0.90	$3.54 \times 10^{-7}$	10.20391	Netrin G1 (Ntng1)
Fosl2	0.90	.000183049	4.611854	Fos-like antigen 2 (Fosl2)
Kcnh7	0.90	$1.22 \times 10^{-7}$	7.520495	Potassium voltage-gated channel, subfamily H (eag-related), member 7 (Kcnh7)
Prr7	0.90	.028793942	0.846388	Proline rich 7 (synaptic) (Prr7)
Prokr2	0.90	$9.48 \times 10^{-6}$	7.126944	Prokineticin receptor 2 (Prokr2)
AI504432	0.90	$1.21 \times 10^{-6}$	6.970405	Expressed sequence AI504432 (AI504432)
Pcdh8	0.90	.000769077	3.123033	Protocadherin 8 (Pcdh8)
Sik2	0.89	$8.60 \times 10^{-6}$	5.817372	Salt inducible kinase 2 (Sik2)
Gm18194	0.89	.016904859	1.371147	Zinc finger protein 329 pseudogene (Gm18194)
Slc7a14	0.89	$1.88 \times 10^{-6}$	7.360957	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 14 (Slc7a14)
Lypd6	0.89	$3.61 \times 10^{-5}$	6.141801	LY6/PLAUR domain containing 6 (Lypd6)
Pgm2l1	0.89	$1.25 \times 10^{-7}$	10.00328	Phosphoglucomutase 2-like 1 (Pgm2l1)
Kcnq5	0.89	$1.49 \times 10^{-5}$	5.553086	Potassium voltage-gated channel, subfamily Q, member 5 (Kcnq5)
Pcdha6	0.89	.036091936	0.834258	Protocadherin alpha 6 (Pcdha6)
Rtl9	0.89	.005562011	2.380772	Retrotransposon Gag Like 9 (Rtl9)
Glra3	0.89	.000324033	4.641539	Glycine receptor, alpha 3 subunit (Glra3)
Gm14305	0.89	.00040773	3.648955	Predicted gene 14305 (Gm14305)
Htr1b	0.89	.002771705	2.7422	5-Hydroxytryptamine (serotonin) receptor 1B (Htr1b)
Bhlhe22	0.89	.000380202	3.82147	Basic helix-loop-helix family, member e22 (Bhlhe22)
Npy2r	0.89	.000165258	4.276263	Neuropeptide Y receptor Y2 (Npy2r)
Srrm1	0.89	$5.62 \times 10^{-7}$	7.296156	Serine/arginine repetitive matrix 1 (Srrm1)
Kcna3	0.88	$4.25 \times 10^{-5}$	4.279568	Potassium voltage-gated channel, shaker-related subfamily, member 3 (Kcna3)
Klhl34	0.88	.001632556	2.741492	Kelch-like 34 (Klhl34)
Sema3a	0.88	.000212314	3.869159	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (Sema3a)
Chrm2	0.88	$1.21 \times 10^{-5}$	5.716374	Cholinergic receptor, muscarinic 2, cardiac (Chrm2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Zfp948	0.88	.003123444	3.131175	Zinc finger protein 948 (Zfp948)
Tcerg1l	0.88	.000195902	3.835645	Transcription elongation regulator 1-like (Tcerg1l)
Dsel	0.87	$6.95 \times 10^{-6}$	5.896692	Dermatan sulfate epimerase-like (Dsel)
Slc29a4	0.87	.000195766	3.820495	Solute carrier family 29 (nucleoside transporters), member 4 (Slc29a4)
Ass1	0.87	$7.70 \times 10^{-6}$	5.960647	Argininosuccinate synthetase 1 (Ass1)
Prickle2	0.87	$1.88 \times 10^{-7}$	8.116082	Prickle planar cell polarity protein 2 (Prickle2)
Neu3	0.87	.004756242	2.382245	Neuraminidase 3 (Neu3)
Sstr1	0.87	.005966396	2.295697	Somatostatin receptor 1 (Sstr1)
Gm4430	0.87	.0190868	1.380589	Predicted gene 4430 (Gm4430)
Stk26	0.87	.013647122	2.033307	Serine/threonine kinase 26 (Stk26)
Efnb2	0.87	.000136603	4.793325	Ephrin B2 (Efnb2)
Sulf1	0.87	$8.60 \times 10^{-6}$	6.34694	Sulfatase 1 (Sulf1)
Grm8	0.87	.000134227	4.655248	Glutamate receptor, metabotropic 8 (Grm8)
Ntsr1	0.86	.001773132	3.267929	Neurotensin receptor 1 (Ntsr1)
Tfcp2l1	0.86	.026439114	1.583365	Transcription factor CP2-like 1 (Tfcp2l1)
Slit3	0.86	.000766163	4.877223	Slit homolog 3 (Slit3)
Ufsp1	0.86	.000541743	3.542221	UFM1-specific peptidase 1 (Ufsp1)
C130013H08Rik	0.86	.0023674	2.754867	RIKEN cDNA C130013H08 gene (C130013H08Rik)
Mycl	0.86	.001375265	3.458158	V-myc avian myelocytomatisis viral oncogene lung carcinoma derived (Mycl)
Cntnap5a	0.86	$1.04 \times 10^{-5}$	5.614878	Contactin-associated protein-like 5A (Cntnap5a)
9330118I20Rik	0.86	.009896459	2.098238	RIKEN cDNA 9330118I20 gene (9330118I20Rik)
Zfp184	0.86	.008381585	1.82656	Zinc finger protein 184 (Kruppel-like) (Zfp184)
Rerg	0.86	.000792803	3.421739	RAS-like, estrogen-regulated, growth-inhibitor (Rerg)
Fam126b	0.86	$6.29 \times 10^{-7}$	8.394283	Family with sequence similarity 126, member B (Fam126b)
St8sia3	0.86	$1.98 \times 10^{-7}$	8.845072	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 3 (St8sia3)
Gpx3	0.85	$8.36 \times 10^{-6}$	6.926573	Glutathione peroxidase 3 (Gpx3)
Dnajc6	0.85	$3.93 \times 10^{-7}$	9.422685	DnaJ heat shock protein family (Hsp40) member C6 (Dnajc6)
Serac1	0.85	.000208784	4.925157	Serine active site containing 1 (Serac1)
Ripor2	0.85	$1.60 \times 10^{-6}$	7.444225	RHO Family Interacting Cell Polarization Regulator 2 (Ripor2)
Hap1	0.85	$8.19 \times 10^{-6}$	6.913632	Huntingtin-associated protein 1 (Hap1)
Gm14412	0.85	.029890659	1.191549	Predicted gene 14412 (Gm14412)
Gbx2	0.85	.000308797	6.131154	Gastrulation brain homeobox 2 (Gbx2)
Tubb3	0.85	$2.03 \times 10^{-6}$	8.200261	Tubulin, beta 3 class III (Tubb3)
Pcdhb4	0.85	.002688834	2.931132	Protocadherin beta 4 (Pcdhb4)
Syn2	0.85	$7.66 \times 10^{-6}$	9.391139	Synapsin II (Syn2)
Cblil	0.85	$1.34 \times 10^{-5}$	5.396486	Casitas B-lineage lymphoma-like 1 (Cblil)
Tuba8	0.85	.002405336	3.520265	Tubulin, alpha 8 (Tuba8)
Palm2	0.84	$1.56 \times 10^{-5}$	5.63211	Paralemmin 2 (Palm2)
Aff3	0.84	$2.93 \times 10^{-6}$	7.21474	AF4/FMR2 family, member 3 (Aff3)
Adar	0.84	$4.98 \times 10^{-6}$	6.384341	Adenosine deaminase, RNA specific (Adar)
Wscd2	0.84	.001197488	3.217625	WSC domain containing 2 (Wscd2)
Gpr22	0.84	$2.01 \times 10^{-5}$	4.951858	G protein-coupled receptor 22 (Gpr22)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lmtk3	0.84	.000283311	5.247359	Lemur tyrosine kinase 3 (Lmtk3)
Rusc2	0.84	$3.93 \times 10^{-7}$	7.77667	RUN and SH3 domain containing 2 (Rusc2)
Unc5d	0.84	$2.19 \times 10^{-5}$	5.78479	Unc-5 netrin receptor D (Unc5d)
Coro2a	0.84	$1.29 \times 10^{-5}$	5.591802	Coronin, actin binding protein 2A (Coro2a)
Neto1	0.84	$1.21 \times 10^{-5}$	5.643227	Neuropilin (NRP) and tolloid (TLL)-like 1 (Neto1)
Igf2bp3	0.84	.000658733	3.49969	Insulin-like growth factor 2 mRNA binding protein 3 (Igf2bp3)
Pcsk2	0.84	$2.12 \times 10^{-7}$	9.042811	Proprotein convertase subtilisin/kexin type 2 (Pcsk2)
Hsf4	0.84	.019194704	3.032579	Heat shock transcription factor 4 (Hsf4)
Ptpnu	0.84	.000363762	4.750676	Protein tyrosine phosphatase, receptor type, U (Ptpnu)
Caln1	0.83	$1.83 \times 10^{-5}$	5.270753	Calneuron 1 (Caln1)
Capn2	0.83	$1.77 \times 10^{-5}$	6.523454	Calpain 2 (Capn2)
Nkrf	0.83	$7.79 \times 10^{-6}$	6.406208	NF-kappaB repressing factor (Nkrf)
Syt5	0.83	$6.00 \times 10^{-6}$	6.971576	Synaptotagmin V (Syt5)
Gm12592	0.83	.049266826	1.224875	Predicted gene 12592 (Gm12592)
Add2	0.82	$3.37 \times 10^{-7}$	7.7095	Adducin 2 (beta) (Add2)
Cnr1	0.82	$1.52 \times 10^{-6}$	7.277001	Cannabinoid receptor 1 (brain) (Cnr1)
Zfp709	0.82	.000223098	4.253372	Zinc finger protein 709 (Zfp709)
Zfp597	0.82	.000180711	4.65163	Zinc finger protein 597 (Zfp597)
Gaa	0.82	$5.51 \times 10^{-7}$	8.894274	Glucosidase, alpha, acid (Gaa)
Nxph1	0.82	$7.97 \times 10^{-7}$	8.18269	Neurexophilin 1 (Nxph1)
Flrt3	0.82	$2.85 \times 10^{-5}$	4.785715	Fibronectin leucine-rich transmembrane protein 3 (Flrt3)
Rasgrf2	0.82	$4.40 \times 10^{-6}$	7.62645	RAS protein-specific guanine nucleotide-releasing factor 2 (Rasgrf2)
Tdrd1	0.82	.002425254	2.983741	Tudor domain containing 1 (Tdrd1)
Cdh7	0.82	$1.77 \times 10^{-6}$	6.570878	Cadherin 7, type 2 (Cdh7)
Xkr4	0.82	$4.43 \times 10^{-6}$	7.686759	X-linked Kx blood group related 4 (Xkr4)
Nkain3	0.82	.000116269	4.180711	Na+/K+ transporting ATPase interacting 3 (Nkain3)
Dzank1	0.82	$4.73 \times 10^{-7}$	9.77219	Double zinc ribbon and ankyrin repeat domains 1 (Dzank1)
Bag4	0.82	$5.64 \times 10^{-6}$	6.016898	BCL2-associated athanogene 4 (Bag4)
Vwc2l	0.81	$1.95 \times 10^{-5}$	5.876002	Von Willebrand factor C domain-containing protein 2-like (Vwc2l)
Fstl5	0.81	$1.99 \times 10^{-5}$	6.035747	Follistatin-like 5 (Fstl5)
Cntn4	0.81	$9.41 \times 10^{-6}$	7.365417	Contactin 4 (Cntn4)
Calr	0.81	$2.05 \times 10^{-7}$	7.696007	Calreticulin (Calr)
Sidt1	0.81	.00017668	5.414384	SID1 transmembrane family, member 1 (Sidt1)
Pcdh17	0.81	$1.63 \times 10^{-6}$	8.163728	Protocadherin 17 (Pcdh17)
Gabrb1	0.81	$9.51 \times 10^{-8}$	9.545682	Gamma-aminobutyric acid (GABA) A receptor, subunit beta 1 (Gabrb1)
Grp	0.81	.048479912	0.910113	Gastrin releasing peptide (Grp)
Gpr68	0.81	.000126347	4.690113	G protein-coupled receptor 68 (Gpr68)
Ccdc92	0.81	$5.51 \times 10^{-7}$	7.863169	Coiled-coil domain containing 92 (Ccdc92)
Phyhip	0.81	$1.28 \times 10^{-5}$	7.124608	Phytanoyl-CoA hydroxylase interacting protein (Phyhip)
Tmem114	0.81	.009119772	3.017253	Transmembrane protein 114 (Tmem114)
Ahi1	0.81	$7.58 \times 10^{-7}$	8.706869	Abelson helper integration site 1 (Ahi1)
Tmem26	0.80	.008976874	3.244882	Transmembrane protein 26 (Tmem26)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Wnt10a	0.80	.048886099	1.569495	Wingless-type MMTV integration site family, member 10A (Wnt10a)
A830018L16Rik	0.80	$3.32 \times 10^{-6}$	6.367862	RIKEN cDNA A830018L16 gene (A830018L16Rik)
Arl15	0.80	$4.55 \times 10^{-5}$	5.68925	ADP-ribosylation factor-like 15 (Arl15)
Cpne5	0.80	.001902752	4.470284	Copine V (Cpne5)
Egr1	0.80	$4.22 \times 10^{-5}$	6.638808	Early growth response 1 (Egr1)
Trim41	0.80	.000291431	4.596958	Tripartite motif-containing 41 (Trim41)
Gm26794	0.80	.035044154	1.009837	Predicted gene
Scn3b	0.80	$5.51 \times 10^{-7}$	8.35461	Sodium channel, voltage-gated, type III, beta (Scn3b)
Prag1	0.80	$9.40 \times 10^{-5}$	5.814942	PEAK1-related, kinase-activating pseudokinase 1 (Prag1)
Gm2824	0.80	.001833285	3.02034	Predicted gene 2824 (Gm2824)
Rab11fip3	0.80	$4.16 \times 10^{-6}$	6.705717	RAB11 family interacting protein 3 (class II) (Rab11fip3)
Rab9b	0.80	$1.34 \times 10^{-5}$	7.077013	RAB9B, member RAS oncogene family (Rab9b)
Lrfn2	0.79	.002700511	3.494055	Leucine-rich repeat and fibronectin type III domain containing 2 (Lrfn2)
A930024N18Rik	0.79	.005188067	3.387857	RIKEN cDNA A930024N18 gene (A930024N18Rik)
Smyd2	0.79	.000455514	3.994763	SET and MYND domain containing 2 (Smyd2)
Tbc1d8	0.79	$1.96 \times 10^{-5}$	4.923096	TBC1 domain family, member 8 (Tbc1d8)
Unc5a	0.79	.000103447	5.017059	Unc-5 netrin receptor A (Unc5a)
Gm30400	0.79	.00925654	2.715838	Predicted gene, 30400 (Gm30400)
Gm22771	0.79	.037361988	2.514284	Predicted gene 22771 (Gm22771)
Atf6	0.79	$1.70 \times 10^{-6}$	6.61476	Activating transcription factor 6 (Atf6)
Zfp850	0.79	.000585926	3.427017	Zinc finger protein 850 (Zfp850)
Trerf1	0.79	.00068304	4.955618	Transcriptional regulating factor 1 (Trerf1)
Cngb1	0.79	.009659964	2.063689	Cyclic nucleotide gated channel beta 1 (Cngb1)
Gse1	0.79	.00017046	4.886704	Genetic suppressor element 1, coiled-coil protein (Gse1)
Slc17a6	0.79	$1.94 \times 10^{-7}$	10.27893	Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (Slc17a6)
Gal	0.79	.019488819	3.280992	Galatin (Gal)
Csrnp3	0.79	$2.63 \times 10^{-6}$	7.934411	Cysteine-serine-rich nuclear protein 3 (Csrnp3)
Serpini1	0.79	$1.65 \times 10^{-6}$	6.742263	Serine (or cysteine) peptidase inhibitor, clade I, member 1 (Serpini1)
Slc39a6	0.78	$1.17 \times 10^{-5}$	6.204157	Solute carrier family 39 (metal ion transporter), member 6 (Slc39a6)
Maob	0.78	$3.67 \times 10^{-6}$	7.688161	Monoamine oxidase B (Maob)
Slitrk4	0.78	$2.69 \times 10^{-6}$	6.155861	SLIT and NTRK-like family, member 4 (Slitrk4)
Fbln1	0.78	.000456249	5.953307	Fibulin 1 (Fbln1)
Bace2	0.78	.013390273	3.168904	Beta-site APP-cleaving enzyme 2 (Bace2)
A430033K04Rik	0.78	$5.14 \times 10^{-5}$	5.277219	RIKEN cDNA A430033K04 gene (A430033K04Rik)
4921507P07Rik	0.78	.016036425	1.809603	RIKEN cDNA 4921507P07 gene (4921507P07Rik)
Nav3	0.78	$3.77 \times 10^{-6}$	7.27041	Neuron navigator 3 (Nav3)
Jazf1	0.78	$2.58 \times 10^{-5}$	5.545079	JAZF zinc finger 1 (Jazf1)
Nexmif	0.78	$1.31 \times 10^{-6}$	6.951173	Neurite extension and migration factor (Nexmif)
Exoc3l	0.78	.010623906	2.005843	Exocyst complex component 3-like (Exoc3l)
Ttc4	0.78	.000240505	4.946025	Tetratricopeptide repeat domain 4 (Ttc4)
Fndc3b	0.78	.000466302	4.763828	Fibronectin type III domain containing 3B (Fndc3b)
Wasf1	0.78	$1.95 \times 10^{-5}$	7.027768	WAS protein family, member 1 (Wasf1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Chn2	0.78	$1.06 \times 10^{-5}$	6.845428	Chimerin 2 (Chn2)
Syt17	0.78	$7.03 \times 10^{-6}$	7.287321	Synaptotagmin XVII (Syt17)
Susd2	0.78	.000161226	4.965493	Sushi domain containing 2 (Susd2)
Dcaf12l1	0.78	$7.58 \times 10^{-6}$	5.863629	DDB1 and CUL4-associated factor 12-like 1 (Dcaf12l1)
Lrrtm3	0.78	$3.73 \times 10^{-6}$	6.343442	Leucine-rich repeat transmembrane neuronal 3 (Lrrtm3)
Gm14399	0.77	.005702486	2.497228	Predicted gene 14399 (Gm14399)
Zfp28	0.77	.002058658	3.278972	Zinc finger protein 28 (Zfp28)
Ythdf2	0.77	$6.57 \times 10^{-5}$	4.819728	YTH domain family 2 (Ythdf2)
Lonrf2	0.77	$3.12 \times 10^{-7}$	9.289771	LON peptidase N-terminal domain and ring finger 2 (Lonrf2)
Gng4	0.77	.000120235	5.057658	Guanine nucleotide binding protein (G protein), gamma 4 (Gng4)
Best1	0.77	.007631204	2.500206	Bestrophin 1 (Best1)
Glra1	0.77	.000249468	4.105361	Glycine receptor, alpha 1 subunit (Glra1)
Fam189a1	0.77	$2.45 \times 10^{-5}$	6.576458	Family with sequence similarity 189, member A1 (Fam189a1)
Smarcc2	0.77	$5.04 \times 10^{-6}$	8.515464	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily c, member 2 (Smarcc2)
Syndig1	0.77	.00118697	3.83913	Synapse differentiation inducing 1 (Syndig1)
Lingo2	0.77	$5.51 \times 10^{-6}$	5.805379	Leucine-rich repeat and Ig domain containing 2 (Lingo2)
Fam196a	0.77	.002200659	3.821054	Family with sequence similarity 196, member A (Fam196a)
Dpysl3	0.77	$5.78 \times 10^{-6}$	7.251192	Dihydropyrimidinase-like 3 (Dpysl3)
Setd2	0.77	$5.10 \times 10^{-5}$	7.360029	SET domain containing 2 (Setd2)
Slc22a3	0.77	.007545927	2.541069	Solute carrier family 22 (organic cation transporter), member 3 (Slc22a3)
Lrrc7	0.76	$1.84 \times 10^{-6}$	8.294683	Leucine-rich repeat containing 7 (Lrrc7)
Astn2	0.76	.000115921	5.417058	Astrotactin 2 (Astn2)
Rnf220	0.76	$6.53 \times 10^{-7}$	8.714815	Ring finger protein 220 (Rnf220)
Cherp	0.76	$3.37 \times 10^{-5}$	5.505594	Calcium homeostasis endoplasmic reticulum protein (Cherp)
Cdh12	0.76	$2.17 \times 10^{-5}$	5.856131	Cadherin 12 (Cdh12)
Zfp873	0.76	.00448633	3.244932	Zinc finger protein 873 (Zfp873)
Lrrc32	0.76	.000945488	3.82761	Leucine-rich repeat containing 32 (Lrrc32)
Zfp518a	0.76	.000484519	5.211478	Zinc finger protein 518A (Zfp518a)
Pxdn	0.76	.000389255	3.740633	Peroxidasin (Pxdn)
Rtl4	0.76	.008432487	3.120882	Retrotransposon Gag Like 4 (Rtl4)
Pcdhb3	0.76	.010270502	2.449302	Protocadherin beta 3 (Pcdhb3)
Slit1	0.76	.000318988	5.361473	Slit homolog 1 (Slit1)
Zfp40	0.76	.001792056	4.01039	Zinc finger protein 40 (Zfp40)
Zfp248	0.76	$3.02 \times 10^{-5}$	4.789605	Zinc finger protein 248 (Zfp248)
Dpysl5	0.76	$6.69 \times 10^{-6}$	7.828146	Dihydropyrimidinase-like 5 (Dpysl5)
Baiap3	0.76	.000101312	5.293981	BAI1-associated protein 3 (Baiap3)
Camk1g	0.76	.001624859	3.641922	Calcium/calmodulin-dependent protein kinase I gamma (Camk1g)
Zfp160	0.76	.00086458	3.969734	Zinc finger protein 160 (Zfp160)
Pnma2	0.76	$1.11 \times 10^{-6}$	6.936649	Paraneoplastic antigen MA2 (Pnma2)
Rarb	0.76	.008900815	2.784143	Retinoic acid receptor, beta (Rarb)
Mllt3	0.76	$3.82 \times 10^{-6}$	7.136245	Myeloid/lymphoid or mixed-lineage leukemia; translocated to, 3 (Mllt3)
Slc5a5	0.75	$1.77 \times 10^{-5}$	5.516773	Solute carrier family 5 (sodium iodide symporter), member 5 (Slc5a5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Arhgap20	0.75	$7.33 \times 10^{-6}$	6.437691	Rho GTPase activating protein 20 (Arhgap20)
Hdac9	0.75	$1.60 \times 10^{-6}$	7.610087	Histone deacetylase 9 (Hdac9)
AC156802.1	0.75	.007375812	2.683187	Neuritin 1 (Nrn1)
Hcn3	0.75	$2.43 \times 10^{-5}$	5.116666	Hyperpolarization-activated, cyclic nucleotide-gated K+ 3 (Hcn3)
Tcf7l2	0.75	$2.05 \times 10^{-7}$	10.61683	Transcription factor 7 like 2, T cell-specific, HMG box (Tcf7l2)
Ldah	0.75	$6.96 \times 10^{-5}$	5.556648	Lipid droplet-associated hydrolase (Ldah)
Zfp300	0.75	.017296158	2.493119	Zinc finger protein 300 (Zfp300)
Acvr2a	0.75	$7.09 \times 10^{-6}$	6.074906	Activin receptor IIA (Acvr2a)
Ptprm	0.75	$8.01 \times 10^{-6}$	7.144231	Protein tyrosine phosphatase, receptor type, M (Ptprm)
Prox1	0.75	$4.48 \times 10^{-7}$	8.506191	Prospero homeobox 1 (Prox1)
Cacng3	0.75	.000149502	7.019381	Calcium channel, voltage-dependent, gamma subunit 3 (Cacng3)
Pi4k2a	0.75	$3.48 \times 10^{-6}$	6.571447	Phosphatidylinositol 4-kinase type 2 alpha (Pi4k2a)
Cntn6	0.75	$5.07 \times 10^{-5}$	5.577599	Contactin 6 (Cntn6)
Zfp638	0.75	.000242589	7.655059	Zinc finger protein 638 (Zfp638)
Ets2	0.75	$3.18 \times 10^{-5}$	5.814854	E26 avian leukemia oncogene 2, 3' domain (Ets2)
Kcnb2	0.75	$1.87 \times 10^{-5}$	6.159632	Potassium voltage-gated channel, Shab-related subfamily, member 2 (Kcnb2)
Epb41l4a	0.74	$8.89 \times 10^{-6}$	5.794072	Erythrocyte membrane protein band 4.1 like 4a (Epb41l4a)
Lgr5	0.74	.005372489	3.044548	Leucine-rich repeat containing G protein coupled receptor 5 (Lgr5)
Atg7	0.74	$2.81 \times 10^{-5}$	5.710862	Autophagy-related 7 (Atg7)
Ndst3	0.74	$1.08 \times 10^{-5}$	5.609031	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (Ndst3)
Adamts2	0.74	.000317285	4.072643	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2 (Adamts2)
Tox	0.74	$2.69 \times 10^{-5}$	7.915995	Thymocyte selection-associated high-mobility group box (Tox)
Pak3	0.74	$3.19 \times 10^{-6}$	8.064688	p21 protein (Cdc42/Rac)-activated kinase 3 (Pak3)
Gprasp1	0.74	$6.85 \times 10^{-7}$	10.20803	G protein-coupled receptor-associated sorting protein 1 (Gprasp1)
Pcdhg4	0.74	.000589095	4.525818	Protocadherin gamma subfamily C, 4 (Pcdhg4)
Ptprt	0.74	$2.03 \times 10^{-6}$	7.295216	Protein tyrosine phosphatase, receptor type, T (Ptprt)
Atp6v1a	0.74	$3.54 \times 10^{-7}$	9.471663	ATPase, H+ transporting, lysosomal V1 subunit A (Atp6v1a)
Perp	0.74	.002407655	3.907358	PERP, TP53 apoptosis effector (Perp)
Lrp8os2	0.74	.006688024	2.716208	Low-density lipoprotein receptor-related protein 8, apolipoprotein e receptor, opposite strand 2 (Lrp8os2)
Fndc1	0.74	.010432832	2.481106	Fibronectin type III domain containing 1 (Fndc1)
Nell2	0.74	$1.61 \times 10^{-5}$	8.514992	NEL-like 2 (Nell2)
Creg2	0.74	$7.14 \times 10^{-6}$	6.611656	Cellular repressor of E1A-stimulated genes 2 (Creg2)
Tubg2	0.74	$7.30 \times 10^{-5}$	5.338106	Tubulin, gamma 2 (Tubg2)
Syt4	0.74	$1.37 \times 10^{-6}$	9.039083	Synaptotagmin IV (Syt4)
Drd5	0.73	.006425118	2.714526	Dopamine receptor D5 (Drd5)
Slco5a1	0.73	.009407404	2.480001	Solute carrier organic anion transporter family, member 5A1 (Slco5a1)
Tspyl5	0.73	$1.32 \times 10^{-5}$	6.165507	Testis-specific protein, Y-encoded-like 5 (Tspyl5)
Pcdhb16	0.73	.000382616	4.775287	Protocadherin beta 16 (Pcdhb16)
Rcan3	0.73	$1.01 \times 10^{-5}$	7.296392	Regulator of calcineurin 3 (Rcan3)
Fam102b	0.73	$2.79 \times 10^{-6}$	7.731735	Family with sequence similarity 102, member B (Fam102b)
Zfp455	0.73	.038564227	1.739184	Zinc finger protein 455 (Zfp455)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Nedd4	0.73	$3.37 \times 10^{-7}$	9.79824	Neural precursor cell expressed, developmentally downregulated 4 (Nedd4)
Ptpro	0.73	$9.88 \times 10^{-6}$	5.498865	Protein tyrosine phosphatase, receptor type, O (Ptpro)
Tenm1	0.73	$1.91 \times 10^{-6}$	8.677358	Teneurin transmembrane protein 1 (Tenm1)
Sdk1	0.73	.003488016	3.764472	Sidekick cell adhesion molecule 1 (Sdk1)
Sdk2	0.73	$2.69 \times 10^{-5}$	6.235304	Sidekick cell adhesion molecule 2 (Sdk2)
Syt16	0.73	$5.73 \times 10^{-5}$	6.023805	Synaptotagmin XVI (Syt16)
Pja2	0.73	$9.40 \times 10^{-7}$	9.256879	Praja 2, RING-H2 motif containing (Pja2)
Satb2	0.73	.033744533	3.52513	Special AT-rich sequence binding protein 2 (Satb2)
Irs4	0.73	.007758385	2.876162	Insulin receptor substrate 4 (Irs4)
D430019H16Rik	0.73	$8.35 \times 10^{-6}$	8.001078	RIKEN cDNA D430019H16 gene (D430019H16Rik)
Gpr101	0.73	.005584713	3.578388	G protein-coupled receptor 101 (Gpr101)
Rab27b	0.73	$1.16 \times 10^{-5}$	5.669068	RAB27B, member RAS oncogene family (Rab27b)
Nell1	0.73	$7.87 \times 10^{-5}$	6.828975	NEL-like 1 (Nell1)
Zfp712	0.73	.00613382	3.000179	Zinc finger protein 712 (Zfp712)
Nyap2	0.73	$9.88 \times 10^{-6}$	6.247907	Neuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 2 (Nyap2)
Zfp971	0.73	.000684523	3.625595	Zinc finger protein 971 (Zfp971)
Kcnh1	0.73	.002814285	3.55106	Potassium voltage-gated channel, subfamily H (eag-related), member 1 (Kcnh1)
Ptpn20	0.73	.029241536	2.221325	Protein tyrosine phosphatase, nonreceptor type 20 (Ptpn20)
Ar	0.72	$8.81 \times 10^{-6}$	6.271874	Androgen receptor (Ar)
Pja1	0.72	$1.21 \times 10^{-6}$	7.784125	Praja ring finger 1, E3 ubiquitin protein ligase (Pja1)
Plppr2	0.72	$6.20 \times 10^{-6}$	6.547971	Phospholipid phosphatase related 2 (Plppr2)
Dcc	0.72	$4.71 \times 10^{-5}$	5.209965	Deleted in colorectal carcinoma (Dcc)
Sema5a	0.72	$2.91 \times 10^{-6}$	8.406449	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM), and short cytoplasmic domain, (semaphorin) 5A (Sema5a)
Taf5l	0.72	.00048829	4.214711	TATA-box binding protein-associated factor 5 like (Taf5l)
Zfp958	0.72	.012627234	3.242134	Zinc finger protein 958 (Zfp958)
Ccdc87	0.72	.009634176	2.748689	Coiled-coil domain containing 87 (Ccdc87)
Rit1	0.72	.000119843	4.659273	Ras-like without CAAX 1 (Rit1)
Cd55	0.72	.000598025	3.933316	CD55 molecule, decay accelerating factor for complement (Cd55)
Grm2	0.72	$5.63 \times 10^{-6}$	6.84357	Glutamate receptor, metabotropic 2 (Grm2)
Foxred2	0.72	.000336364	4.584256	FAD-dependent oxidoreductase domain containing 2 (Foxred2)
Rundc3b	0.72	$5.48 \times 10^{-5}$	5.567494	RUN domain containing 3B (Rundc3b)
Tmem132c	0.72	.002533602	4.719406	Transmembrane protein 132C (Tmem132c)
Pgr	0.72	$6.29 \times 10^{-5}$	5.235948	Progesterone receptor (Pgr)
D3Ert2d254e	0.72	$6.29 \times 10^{-5}$	6.041762	DNA segment, Chr 3, ERATO Doi 254, expressed (D3Ert2d254e)
Amph	0.72	$1.65 \times 10^{-6}$	8.207338	Amphiphysin (Amph)
Rgs17	0.72	$1.05 \times 10^{-6}$	8.693556	Regulator of G-protein signaling 17 (Rgs17)
Hps6	0.71	.019824798	2.486721	Hermansky-Pudlak syndrome 6 (Hps6)
Ythdf3	0.71	$1.20 \times 10^{-5}$	6.418722	YTH domain family 3 (Ythdf3)
Zbtb33	0.71	.000355134	5.272728	Zinc finger and BTB domain containing 33 (Zbtb33)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tspy12	0.71	$8.01 \times 10^{-6}$	7.85734	TSPY-like 2 (Tspy12)
Auts2	0.71	$2.79 \times 10^{-6}$	7.513667	Autism susceptibility candidate 2 (Auts2)
Slc8a2	0.71	.000248828	5.228934	Solute carrier family 8 (sodium/calcium exchanger), member 2 (Slc8a2)
Cbln4	0.71	.001215332	7.097208	Cerebellin 4 precursor protein (Cbln4)
Alkbh8	0.71	$1.13 \times 10^{-5}$	6.749302	AlkB homolog 8, tRNA methyltransferase (Alkbh8)
Btbd3	0.71	$8.18 \times 10^{-6}$	8.978045	BTB (POZ) domain containing 3 (Btbd3)
L3mbtl2	0.71	$4.93 \times 10^{-5}$	4.712922	I(3)mbt-like 2 (L3mbtl2)
Lrrtm2	0.71	$6.85 \times 10^{-7}$	8.042463	Leucine-rich repeat transmembrane neuronal 2 (Lrrtm2)
Slc16a6	0.71	.000729261	3.806251	Solute carrier family 16 (monocarboxylic acid transporters), member 6 (Slc16a6)
Rasal1	0.71	.004866842	3.826241	RAS protein activator like 1 (GAP1 like) (Rasal1)
Rorb	0.71	$3.07 \times 10^{-6}$	8.644884	RAR-related orphan receptor beta (Rorb)
St6gal2	0.71	.000196586	5.900034	Beta galactoside alpha 2,6 sialyltransferase 2 (St6gal2)
Efhc2	0.70	.004644489	2.89958	EF-hand domain (C-terminal) containing 2 (Efhc2)
Zfp758	0.70	.001170498	3.161529	Zinc finger protein 758 (Zfp758)
Ksr2	0.70	$1.55 \times 10^{-5}$	7.123772	Kinase suppressor of ras 2 (Ksr2)
Hmgcs1	0.70	$2.75 \times 10^{-6}$	8.209323	3-Hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (Hmgcs1)
Wnt9a	0.70	.000399912	4.720925	Wingless-type MMTV integration site family, member 9A (Wnt9a)
Oxr1	0.70	$6.44 \times 10^{-7}$	9.301846	Oxidation resistance 1 (Oxr1)
1700001L05Rik	0.70	.011682413	2.684811	RIKEN cDNA 1700001L05 gene (1700001L05Rik)
Foxp4	0.70	$4.22 \times 10^{-5}$	5.913491	Forkhead box P4 (Foxp4)
Oprm1	0.70	$8.04 \times 10^{-6}$	7.474937	Opioid receptor, mu 1 (Oprm1)
B3gat2	0.70	.000129323	5.463953	Beta-1,3-glucuronidyltransferase 2 (glucuronosyltransferase S) (B3gat2)
Unc5c	0.70	$2.44 \times 10^{-5}$	7.477314	Unc-5 netrin receptor C (Unc5c)
Kcnq3	0.70	$1.36 \times 10^{-5}$	9.780823	Potassium voltage-gated channel, subfamily Q, member 3 (Kcnq3)
Gnaz	0.70	$8.67 \times 10^{-6}$	6.95241	Guanine nucleotide binding protein, alpha z subunit (Gnaz)
Pgbd5	0.70	$8.74 \times 10^{-5}$	7.534544	PiggyBac transposable element derived 5 (Pgbd5)
Nmbr	0.70	.000178865	5.107571	Neuromedin B receptor (Nmbr)
Plxna2	0.70	$8.91 \times 10^{-6}$	6.966121	Plexin A2 (Plxna2)
Brinp1	0.70	$4.45 \times 10^{-5}$	7.448675	Bone morphogenic protein/retinoic acid inducible neural specific 1 (Brinp1)
Sec16a	0.70	.000788978	6.995678	SEC16 homolog A, endoplasmic reticulum export factor (Sec16a)
Fam13c	0.70	$4.82 \times 10^{-5}$	5.354801	Family with sequence similarity 13, member C (Fam13c)
Epha5	0.69	$5.64 \times 10^{-6}$	7.26791	Eph receptor A5 (Epha5)
Slc7a8	0.69	$9.18 \times 10^{-6}$	7.620459	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (Slc7a8)
Vgll3	0.69	.043363172	1.593746	Vestigial like family member 3 (Vgll3)
Nanos1	0.69	$1.10 \times 10^{-5}$	5.745121	Nanos homolog 1 (Nanos1)
Gabra1	0.69	$1.74 \times 10^{-6}$	8.626545	Gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1 (Gabra1)
Nhs	0.69	.00571752	3.295677	Nance–Horan syndrome (human) (Nhs)
Gabrg3	0.69	$2.79 \times 10^{-5}$	7.200887	Gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3 (Gabrg3)
Tubb5	0.69	$2.63 \times 10^{-5}$	8.990945	Tubulin, beta 5 class I (Tubb5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Hrh3	0.69	$7.81 \times 10^{-5}$	6.940781	Histamine receptor H3 (Hrh3)
Slitrk5	0.69	$8.21 \times 10^{-5}$	5.995581	SLIT and NTRK-like family, member 5 (Slitrk5)
Evpl	0.69	.00781795	3.359515	Envoplakin (Evpl)
Pak6	0.69	.000694143	5.414874	p21 protein (Cdc42/Rac)-activated kinase 6 (Pak6)
Gm340	0.69	.013158512	3.642348	Predicted gene 340 (Gm340)
Fam171a2	0.69	.00928351	3.749679	Family with sequence similarity 171, member A2 (Fam171a2)
Grm7	0.69	$2.53 \times 10^{-5}$	5.89921	Glutamate receptor, metabotropic 7 (Grm7)
Pcdh1	0.69	$9.57 \times 10^{-6}$	8.114862	Protocadherin 1 (Pcdh1)
Igfbp3	0.69	.012277511	3.676685	Insulin-like growth factor binding protein 3 (Igfbp3)
Gda	0.69	.042943058	5.020327	Guanine deaminase (Gda)
Gm14410	0.69	.029285353	2.557606	Predicted gene 14410 (Gm14410)
Fut9	0.69	$3.22 \times 10^{-5}$	7.372647	Fucosyltransferase 9 (Fut9)
Ackr1	0.69	.00127376	4.87562	Atypical chemokine receptor 1 (Duffy blood group) (Ackr1)
Glt1d1	0.69	.010933903	3.240601	Glycosyltransferase 1 domain containing 1 (Glt1d1)
Rlim	0.69	$2.39 \times 10^{-6}$	7.93932	Ring finger protein, LIM domain interacting (Rlim)
Sh3rf1	0.69	.004119142	4.228434	SH3 domain containing ring finger 1 (Sh3rf1)
Wnt4	0.69	.006318783	4.184562	Wingless-type MMTV integration site family, member 4 (Wnt4)
Igsf8	0.69	.000305057	6.640093	Immunoglobulin superfamily, member 8 (Igsf8)
Zfp804a	0.69	$2.69 \times 10^{-5}$	7.346291	Zinc finger protein 804A (Zfp804a)
Necab1	0.68	$2.85 \times 10^{-5}$	10.05045	N-terminal EF-hand calcium binding protein 1 (Necab1)
Lingo3	0.68	.000307701	4.196679	Leucine-rich repeat and Ig domain containing 3 (Lingo3)
Myt1l	0.68	$1.73 \times 10^{-6}$	8.471961	Myelin transcription factor 1-like (Myt1l)
Ttpal	0.68	$1.70 \times 10^{-5}$	6.151854	Tocopherol (alpha) transfer protein-like (Ttpal)
Sorcs3	0.68	.000215834	4.819786	Sortilin-related VPS10 domain containing receptor 3 (Sorcs3)
Slx4ip	0.68	.000868438	4.263561	SLX4 interacting protein (Slx4ip)
Pcdhb10	0.68	.005864134	3.159176	Protocadherin beta 10 (Pcdhb10)
Slc39a10	0.68	$6.77 \times 10^{-6}$	8.084488	Solute carrier family 39 (zinc transporter), member 10 (Slc39a10)
Cd200	0.68	$5.80 \times 10^{-5}$	7.964093	CD200 antigen (Cd200)
Nppc	0.68	.011216946	3.785836	Natriuretic peptide type C (Nppc)
Zfp354c	0.68	$4.89 \times 10^{-5}$	6.403903	Zinc finger protein 354C (Zfp354c)
Lingo1	0.68	$2.87 \times 10^{-5}$	8.272062	Leucine-rich repeat and Ig domain containing 1 (Lingo1)
Slc16a7	0.68	$1.09 \times 10^{-5}$	6.243917	Solute carrier family 16 (monocarboxylic acid transporters), member 7 (Slc16a7)
Wdr6	0.68	$1.47 \times 10^{-5}$	6.573184	WD repeat domain 6 (Wdr6)
Rxrg	0.68	.045115431	1.690986	Retinoid X receptor gamma (Rxrg)
Gabrg2	0.68	$2.91 \times 10^{-6}$	7.063949	Gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2 (Gabrg2)
AC118639.1	0.68	.04062694	1.947444	Predicted gene (Gm48956)
Flrt1	0.68	$9.04 \times 10^{-5}$	6.882979	Fibronectin leucine-rich transmembrane protein 1 (Flrt1)
Gabra3	0.68	$6.76 \times 10^{-6}$	7.241671	Gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3 (Gabra3)
Ankfn1	0.67	.002541825	4.130064	Ankyrin-repeat and fibronectin type III domain containing 1 (Ankfn1)
Kcnj5	0.67	.000596952	6.457383	Potassium inwardly-rectifying channel, subfamily J, member 5 (Kcnj5)
Zfp458	0.67	.009941695	4.083015	Zinc finger protein 458 (Zfp458)
Fam131c	0.67	.025588008	2.917946	Family with sequence similarity 131, member C (Fam131c)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rtn4rl1	0.67	$5.68 \times 10^{-6}$	8.455866	Reticulon 4 receptor-like 1 (Rtn4rl1)
Slitrk1	0.67	$3.15 \times 10^{-5}$	6.92584	SLIT and NTRK-like family, member 1 (Slitrk1)
Gpr83	0.67	.010787571	3.46233	G protein-coupled receptor 83 (Gpr83)
Pcdhac2	0.67	.000464785	5.425964	Protocadherin alpha subfamily C, 2 (Pcdhac2)
Pip5k1b	0.67	.000770792	4.331728	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta (Pip5k1b)
Zfp292	0.67	$3.61 \times 10^{-6}$	7.456565	Zinc finger protein 292 (Zfp292)
Irs1	0.67	$4.10 \times 10^{-5}$	5.28191	Insulin receptor substrate 1 (Irs1)
Edaradd	0.67	.000153222	4.592007	EDAR (ectodysplasin-A receptor)-associated death domain (Edaradd)
Nudt17	0.67	.029205333	2.296977	Nudix (nucleoside diphosphate linked moiety X)-type motif 17 (Nudt17)
Clcn5	0.67	.000128435	5.712055	Chloride channel, voltage-sensitive 5 (Clcn5)
Gnb4	0.67	$5.27 \times 10^{-5}$	5.705785	Guanine nucleotide binding protein (G protein), beta 4 (Gnb4)
Dhcr24	0.66	$3.26 \times 10^{-5}$	6.245905	24-Dehydrocholesterol reductase (Dhcr24)
Pacs1	0.66	$1.77 \times 10^{-5}$	6.956356	Phosphofuran acidic cluster sorting protein 1 (Pacs1)
Kctd16	0.66	.031485849	2.596755	Potassium channel tetramerisation domain containing 16 (Kctd16)
Rcn1	0.66	.000118658	6.101657	Reticulocalbin 1 (Rcn1)
Cdh13	0.66	$6.28 \times 10^{-5}$	6.8159	Cadherin 13 (Cdh13)
Naaladl2	0.66	.03685715	2.410721	N-acetylated alpha-linked acidic dipeptidase-like 2 (Naaladl2)
Zfp9	0.66	$4.14 \times 10^{-5}$	6.1228	Zinc finger protein 9 (Zfp9)
Micu3	0.66	$2.78 \times 10^{-6}$	7.961959	Mitochondrial calcium uptake family, member 3 (Micu3)
St8sia6	0.66	.000974263	3.896571	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 6 (St8sia6)
P4ha2	0.66	.001261355	4.292084	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (P4ha2)
B3galt1	0.66	$1.47 \times 10^{-5}$	6.602279	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3galt1)
Lsm12	0.66	$6.74 \times 10^{-6}$	6.63163	LSM12 homolog (Lsm12)
Epb41l4b	0.66	$5.78 \times 10^{-6}$	7.025423	Erythrocyte membrane protein band 4.1 like 4b (Epb41l4b)
Pcdhgc5	0.66	.002865607	4.463242	Protocadherin gamma subfamily C, 5 (Pcdhgc5)
Tubb2a	0.66	.000169512	8.653741	Tubulin, beta 2A class IIA (Tubb2a)
Cnnm1	0.66	$7.11 \times 10^{-6}$	7.342593	Cyclin M1 (Cnnm1)
Tubb6	0.66	.012627234	2.864865	Tubulin, beta 6 class V (Tubb6)
Rnf169	0.66	$1.94 \times 10^{-5}$	6.788594	Ring finger protein 169 (Rnf169)
Cxadr	0.66	.001717986	4.539335	Coxsackie virus and adenovirus receptor (Cxadr)
Zc3h12c	0.66	$1.70 \times 10^{-5}$	6.673134	Zinc finger CCCH type containing 12C (Zc3h12c)
Stac2	0.66	.009323545	3.823554	SH3 and cysteine-rich domain 2 (Stac2)
Pcdh7	0.66	$3.95 \times 10^{-5}$	6.546222	Protocadherin 7 (Pcdh7)
D430041D05Rik	0.66	$4.67 \times 10^{-5}$	8.003882	RIKEN cDNA D430041D05 gene (D430041D05Rik)
Sertad4	0.66	.000174129	5.221712	SERTA domain containing 4 (Sertad4)
Pten	0.65	$7.14 \times 10^{-6}$	8.316894	Phosphatase and tensin homolog (Pten)
Shisa9	0.65	$1.15 \times 10^{-5}$	8.321552	Shisa family member 9 (Shisa9)
Acap3	0.65	.00029248	5.159862	ArfGAP with coiled-coil, ankyrin repeat, and PH domains 3 (Acap3)
Tenm4	0.65	$1.09 \times 10^{-5}$	7.405197	Teneurin transmembrane protein 4 (Tenm4)
Sfmbt2	0.65	.003016668	4.232257	Scm-like with four mbt domains 2 (Sfmbt2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Zfp605	0.65	.001673274	4.621752	Zinc finger protein 605 (Zfp605)
Tox2	0.65	.000161226	7.262289	TOX high-mobility group box family member 2 (Tox2)
Gpr63	0.65	.000788978	3.825422	G protein-coupled receptor 63 (Gpr63)
Ythdf1	0.65	$1.95 \times 10^{-5}$	6.328597	YTH domain family 1 (Ythdf1)
Slc25a22	0.65	$7.93 \times 10^{-5}$	7.237398	Solute carrier family 25 (mitochondrial carrier, glutamate), member 22 (Slc25a22)
Pik3cb	0.65	.000240897	6.360441	Phosphatidylinositol 3-kinase, catalytic, beta polypeptide (Pik3cb)
Rwdd2a	0.65	.000322361	4.960711	RWD domain containing 2A (Rwdd2a)
Adgrg2	0.65	.006265713	4.091805	Adhesion G protein-coupled receptor G2 (Adgrg2)
Cers6	0.65	$1.22 \times 10^{-5}$	6.809188	Ceramide synthase 6 (Cers6)
L1cam	0.65	$8.11 \times 10^{-6}$	9.2205	L1 cell adhesion molecule (L1cam)
Mef2d	0.65	$1.21 \times 10^{-6}$	8.413944	Myocyte enhancer factor 2D (Mef2d)
Runx1t1	0.65	$2.17 \times 10^{-6}$	7.447176	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related) (Runx1t1)
Ap1s3	0.65	.015481813	3.015614	Adaptor-related protein complex AP-1, sigma 3 (Ap1s3)
Stk32b	0.65	.030728504	2.727759	Serine/threonine kinase 32B (Stk32b)
Srrm4	0.65	$6.21 \times 10^{-6}$	7.058903	Serine/arginine repetitive matrix 4 (Srrm4)
Gmps	0.65	$1.86 \times 10^{-6}$	8.156985	Guanine monophosphate synthetase (Gmps)
Dgkk	0.65	.000390208	6.132485	Diacylglycerol kinase kappa (Dgkk)
Dnm3	0.65	$2.05 \times 10^{-6}$	9.291565	Dynamin 3 (Dnm3)
EII	0.65	.000916584	4.196548	Elongation factor RNA polymerase II (EII)
Ankrd6	0.65	$1.10 \times 10^{-5}$	6.681168	Ankyrin repeat domain 6 (Ankrd6)
Nhsl2	0.65	$7.86 \times 10^{-7}$	8.22565	NHS-like 2 (Nhsl2)
Ddah1	0.65	$3.04 \times 10^{-5}$	9.206221	Dimethylarginine dimethylaminohydrolase 1 (Ddah1)
Taf6	0.65	.002815125	4.257428	TATA-box binding protein-associated factor 6 (Taf6)
Rph3al	0.65	.006897646	2.809707	Rabphilin 3A-like (without C2 domains) (Rph3al)
Mpp3	0.65	.00289915	3.412033	Membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (Mpp3)
Hpcal4	0.64	$5.74 \times 10^{-6}$	9.36387	Hippocalcin-like 4 (Hpcal4)
Adgra1	0.64	$5.43 \times 10^{-5}$	8.661554	Adhesion G protein-coupled receptor A1 (Adgra1)
Rnf208	0.64	$9.49 \times 10^{-5}$	6.292206	Ring finger protein 208 (Rnf208)
Pde10a	0.64	$2.68 \times 10^{-5}$	6.603144	Phosphodiesterase 10A (Pde10a)
Adamtsl1	0.64	.001644552	3.848228	ADAMTS-like 1 (Adamtsl1)
Rab6a	0.64	$1.13 \times 10^{-6}$	9.27939	RAB6A, member RAS oncogene family (Rab6a)
Stim2	0.64	$1.77 \times 10^{-5}$	5.843636	Stromal interaction molecule 2 (Stim2)
Sema3c	0.64	.007511667	3.534536	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (Sema3c)
Clstrn3	0.64	$1.66 \times 10^{-5}$	6.738189	Calsyntenin 3 (Clstrn3)
Rab39b	0.64	$2.44 \times 10^{-5}$	6.625339	RAB39B, member RAS oncogene family (Rab39b)
Fam163b	0.64	.000351859	5.568675	Family with sequence similarity 163, member B (Fam163b)
Gpr12	0.64	$2.93 \times 10^{-5}$	6.274946	G-protein coupled receptor 12 (Gpr12)
Pcdhb21	0.64	.02296658	2.770716	Protocadherin beta 21 (Pcdhb21)
Rin1	0.64	.049756401	2.189064	Ras and Rab interactor 1 (Rin1)
Urod	0.64	.000644079	5.302676	Uroporphyrinogen decarboxylase (Urod)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rap1gap2	0.64	$1.10 \times 10^{-5}$	7.542295	RAP1 GTPase activating protein 2 (Rap1gap2)
Gabrb3	0.64	$1.11 \times 10^{-6}$	9.440774	Gamma-aminobutyric acid (GABA) A receptor, subunit beta 3 (Gabrb3)
Gal3st3	0.64	.002849927	5.084091	Galactose-3-O-sulfotransferase 3 (Gal3st3)
Sept9	0.63	.000567766	4.964166	Septin 9 (Sept9)
Cep170	0.63	$8.91 \times 10^{-6}$	7.529605	Centrosomal protein 170 (Cep170)
Fam171b	0.63	$8.30 \times 10^{-7}$	9.147819	Family with sequence similarity 171, member B (Fam171b)
Negr1	0.63	$1.59 \times 10^{-5}$	8.822066	Neuronal growth regulator 1 (Negr1)
1700037H04Rik	0.63	$6.87 \times 10^{-5}$	5.809181	RIKEN cDNA 1700037H04 gene (1700037H04Rik)
Gabrq	0.63	.003992505	3.923309	Gamma-aminobutyric acid (GABA) A receptor, subunit theta (Gabrq)
Slc1a6	0.63	.010175739	2.922441	Solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (Slc1a6)
Ptpn	0.63	$1.06 \times 10^{-5}$	8.644638	Protein tyrosine phosphatase, receptor type, N (Ptpn)
Cntnap2	0.63	$6.76 \times 10^{-5}$	8.762565	Contactin-associated protein-like 2 (Cntnap2)
Rapgef1	0.63	.000178239	6.652976	Rap guanine nucleotide exchange factor (GEF)-like 1 (Rapgef1)
Asic2	0.63	$4.03 \times 10^{-5}$	5.650784	Acid-sensing (proton-gated) ion channel 2 (Asic2)
Pamr1	0.63	.002137442	4.829015	Peptidase domain containing associated with muscle regeneration 1 (Pamr1)
Ehd4	0.63	.000154388	5.014108	EH-domain containing 4 (Ehd4)
Psd	0.63	$6.87 \times 10^{-5}$	6.002483	Pleckstrin and Sec7 domain containing (Psd)
Rnf150	0.63	$3.27 \times 10^{-6}$	7.782335	Ring finger protein 150 (Rnf150)
Frat1	0.63	.030170221	2.646394	Frequently rearranged in advanced T cell lymphomas (Frat1)
Agap1	0.63	$3.36 \times 10^{-6}$	8.638516	ArfGAP with GTPase domain, ankyrin repeat, and PH domain 1 (Agap1)
Kcnh6	0.63	.023715746	2.725244	Potassium voltage-gated channel, subfamily H (eag-related), member 6 (Kcnh6)
Tmem196	0.63	$5.73 \times 10^{-5}$	5.932298	Transmembrane protein 196 (Tmem196)
Lin7a	0.63	.000159816	6.286876	Lin-7 homolog A (C. elegans) (Lin7a)
Dclk1	0.63	$1.21 \times 10^{-6}$	10.10786	Doublecortin-like kinase 1 (Dclk1)
Mal2	0.63	$3.49 \times 10^{-5}$	6.901157	Mal, T cell differentiation protein 2 (Mal2)
Tmem150c	0.63	.000312079	6.803565	Transmembrane protein 150C (Tmem150c)
2610021A01Rik	0.63	.000383143	5.077477	RIKEN cDNA 2610021A01 gene (2610021A01Rik)
Per1	0.62	$6.96 \times 10^{-5}$	6.382323	Period circadian clock 1 (Per1)
Fn1	0.62	.005166726	4.220289	Fibronectin 1 (Fn1)
Pde4b	0.62	$4.49 \times 10^{-6}$	8.249465	Phosphodiesterase 4B, cAMP specific (Pde4b)
Rasd2	0.62	.000134438	6.564986	RASD family, member 2 (Rasd2)
Lrrn2	0.62	$6.19 \times 10^{-5}$	7.567448	Leucine-rich repeat protein 2, neuronal (Lrrn2)
Mkl2	0.62	$6.51 \times 10^{-6}$	7.863098	MKL/myocardin-like 2 (Mkl2)
Smad9	0.62	.000633508	5.027931	SMAD family member 9 (Smad9)
Zfp955a	0.62	.019154935	2.964034	Zinc finger protein 955A (Zfp955a)
Pkd2l2	0.62	.008590702	3.111851	Polycystic kidney disease 2-like 2 (Pkd2l2)
Ccnt1	0.62	$1.35 \times 10^{-5}$	7.105512	Cyclin T1 (Ccnt1)
Zfp182	0.62	.020443942	3.871968	Zinc finger protein 182 (Zfp182)
Prr36	0.62	.000141143	5.95632	Proline rich 36 (Prr36)
Ecel1	0.62	.005734719	4.139147	Endothelin converting enzyme-like 1 (Ecel1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Apaf1	0.62	.004392997	3.772911	Apoptotic peptidase activating factor 1 (Apaf1)
Gdpgp1	0.62	.006070659	3.944582	GDP-D-glucose phosphorylase 1 (Gdpgp1)
Kmt2a	0.62	4.42 × 10 <sup>-5</sup>	8.633229	Lysine (K)-specific methyltransferase 2A (Kmt2a)
Plxna4	0.62	7.75 × 10 <sup>-6</sup>	7.663438	Plexin A4 (Plxna4)
Cpsf7	0.62	1.70 × 10 <sup>-5</sup>	6.368945	Cleavage and polyadenylation-specific factor 7 (Cpsf7)
Lrfn1	0.62	.000693674	4.332964	Leucine-rich repeat and fibronectin type III domain containing 1 (Lrfn1)
Rnd1	0.62	.009599513	2.96585	Rho family GTPase 1 (Rnd1)
Lrp3	0.62	.000518239	5.517911	Low-density lipoprotein receptor-related protein 3 (Lrp3)
Nyap1	0.62	.000124978	5.196396	Neuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1 (Nyap1)
Amz1	0.62	.023995602	3.208148	Archaelysin family metallopeptidase 1 (Amz1)
Astn1	0.62	9.97 × 10 <sup>-7</sup>	9.056476	Astrotactin 1 (Astn1)
Enc1	0.62	5.67 × 10 <sup>-6</sup>	7.995232	Ectodermal-neural cortex 1 (Enc1)
Parp8	0.62	.000965887	5.06552	Poly(ADP-ribose) polymerase family, member 8 (Parp8)
Ylpm1	0.62	5.49 × 10 <sup>-5</sup>	7.977073	YLP motif containing 1 (Ylpm1)
Ppfia2	0.62	1.15 × 10 <sup>-5</sup>	7.677043	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (Ppfia2)
Tmem178b	0.62	3.10 × 10 <sup>-6</sup>	8.725296	Transmembrane protein 178B (Tmem178b)
Rnf165	0.62	4.46 × 10 <sup>-5</sup>	6.906986	Ring finger protein 165 (Rnf165)
Lrfn3	0.62	.000791988	5.029696	Leucine-rich repeat and fibronectin type III domain containing 3 (Lrfn3)
Prep	0.62	.000100766	5.613128	Prolyl endopeptidase (Prep)
Zfp933	0.62	.01016329	4.072213	Zinc finger protein 933 (Zfp933)
Prkacb	0.62	2.23 × 10 <sup>-6</sup>	9.614677	Protein kinase, cAMP dependent, catalytic, beta (Prkacb)
Pcdha5	0.61	.044014232	2.616261	Protocadherin alpha 5 (Pcdha5)
Fbxl21	0.61	.000879683	4.800861	F-box and leucine-rich repeat protein 21 (Fbxl21)
Unc13a	0.61	2.67 × 10 <sup>-5</sup>	7.336045	Unc-13 homolog A (C. elegans) (Unc13a)
Sema4f	0.61	.001125939	5.459212	Sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain (Sema4f)
Fam13b	0.61	9.26 × 10 <sup>-5</sup>	7.348579	Family with sequence similarity 13, member B (Fam13b)
Ola1	0.61	8.60 × 10 <sup>-6</sup>	7.168847	Obg-like ATPase 1 (Ola1)
Neto2	0.61	.000743316	6.070033	Neuropilin (NRP) and toll-like 2 (Neto2)
Map2k4	0.61	3.79 × 10 <sup>-6</sup>	8.51202	Mitogen-activated protein kinase kinase 4 (Map2k4)
Habp4	0.61	1.34 × 10 <sup>-5</sup>	7.444208	Hyaluronic acid binding protein 4 (Habp4)
Rab3c	0.61	1.85 × 10 <sup>-6</sup>	11.49458	RAB3C, member RAS oncogene family (Rab3c)
D130043K22Rik	0.61	.000122038	5.356186	RIKEN cDNA D130043K22 gene (D130043K22Rik)
Ipcef1	0.61	.008010838	3.646607	Interaction protein for cytohesin exchange factors 1 (Ipcef1)
Sez6	0.61	.000143923	6.272899	Seizure-related gene 6 (Sez6)
Crim1	0.61	3.31 × 10 <sup>-5</sup>	6.659933	Cysteine-rich transmembrane BMP regulator 1 (chordin like) (Crim1)
Snx31	0.61	.003095396	4.438511	Sorting nexin 31 (Snx31)
Csmd2	0.61	.000257199	5.417954	CUB and Sushi multiple domains 2 (Csmd2)
Etnk1	0.61	9.15 × 10 <sup>-6</sup>	8.80845	Ethanolamine kinase 1 (Etnk1)
Mettl22	0.61	.001804152	4.00693	Methyltransferase like 22 (Mettl22)
Sfmbt1	0.61	7.54 × 10 <sup>-5</sup>	6.214588	Scm-like with four mbt domains 1 (Sfmbt1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Zfp39	0.61	.001604211	3.761073	Zinc finger protein 39 (Zfp39)
Alms1	0.61	.011824028	5.337672	Alstrom syndrome 1 (Alms1)
Rev3l	0.61	$8.33 \times 10^{-5}$	7.200502	REV3 like, DNA directed polymerase zeta catalytic subunit (Rev3l)
Stox1	0.61	.007672367	3.153065	Storkhead box 1 (Stox1)
Tro	0.61	$4.34 \times 10^{-5}$	6.489582	Trophinin (Tro)
Cdyl2	0.61	.015791444	2.722594	Chromodomain protein, Y chromosome-like 2 (Cdyl2)
Arl10	0.61	.000629233	4.317593	ADP-ribosylation factor-like 10 (Arl10)
Grik2	0.61	$2.03 \times 10^{-5}$	6.880724	Glutamate receptor, ionotropic, kainate 2 (beta 2) (Grik2)
Frmpd4	0.61	$2.23 \times 10^{-5}$	7.56353	FERM and PDZ domain containing 4 (Frmpd4)
Zfhx4	0.61	.000885694	7.534311	Zinc finger homeodomain 4 (Zfhx4)
Zfp846	0.61	.000916584	5.698572	Zinc finger protein 846 (Zfp846)
Zfpm2	0.60	.006631642	3.799049	Zinc finger protein, multitype 2 (Zfpm2)
Stc1	0.60	.010682162	3.040314	Stanniocalcin 1 (Stc1)
Cpeb4	0.60	$1.70 \times 10^{-5}$	7.892134	Cytoplasmic polyadenylation element binding protein 4 (Cpeb4)
Lmo7	0.60	.000253332	5.132992	LIM domain only 7 (Lmo7)
Plppr4	0.60	$6.87 \times 10^{-6}$	7.081929	Phospholipid phosphatase related 4 (Plppr4)
Hcrtr2	0.60	.032252429	2.965022	Hypocretin (orexin) receptor 2 (Hcrtr2)
Camsap2	0.60	$1.84 \times 10^{-6}$	8.686414	Calmodulin-regulated spectrin-associated protein family, member 2 (Camsap2)
Tug1	0.60	$3.20 \times 10^{-6}$	8.239366	Taurine upregulated gene 1 (Tug1)
Pcdh19	0.60	$1.72 \times 10^{-5}$	6.881403	Protocadherin 19 (Pcdh19)
Camk4	0.60	$7.59 \times 10^{-5}$	7.62866	Calcium/calmodulin-dependent protein kinase IV (Camk4)
Camta1	0.60	$8.26 \times 10^{-7}$	9.965754	Calmodulin binding transcription activator 1 (Camta1)
Itga3	0.60	.000541361	5.825568	Integrin alpha 3 (Itga3)
Lpin2	0.60	$2.06 \times 10^{-5}$	7.493564	Lipin 2 (Lpin2)
Cc2d1a	0.60	.000916584	4.540942	Coiled-coil and C2 domain containing 1A (Cc2d1a)
Nsf	0.60	$1.34 \times 10^{-5}$	10.22529	N-ethylmaleimide sensitive fusion protein (Nsf)
Ctif	0.60	$3.98 \times 10^{-6}$	8.786572	CBP80/20-dependent translation initiation factor (Ctif)
Zfp617	0.60	.005078156	4.004125	Zinc finger protein 617 (Zfp617)
Cachd1	0.60	$2.81 \times 10^{-5}$	6.127114	Cache domain containing 1 (Cachd1)
Zfp128	0.60	.003436977	3.456041	Zinc finger protein 128 (Zfp128)
Kbtbd4	0.60	.004194916	3.494852	Kelch repeat and BTB (POZ) domain containing 4 (Kbtbd4)
5330417C22Rik	0.60	$2.86 \times 10^{-5}$	6.264218	RIKEN cDNA 5330417C22 gene (5330417C22Rik)
Tubb4b	0.60	$2.41 \times 10^{-5}$	7.428256	Tubulin, beta 4B class IVB (Tubb4b)
C2cd2l	0.60	$2.18 \times 10^{-5}$	7.218547	C2 calcium-dependent domain containing 2-like (C2cd2l)
Fndc3a	0.60	$1.06 \times 10^{-5}$	6.92535	Fibronectin type III domain containing 3A (Fndc3a)
Zc3h6	0.60	.001676411	5.076014	Zinc finger CCCH type containing 6 (Zc3h6)
Psd3	0.60	$8.58 \times 10^{-7}$	9.862563	Pleckstrin and Sec7 domain containing 3 (Psd3)
Ppp1r26	0.60	.000187821	5.470116	Protein phosphatase 1, regulatory subunit 26 (Ppp1r26)
Atp6v1b2	0.60	$3.92 \times 10^{-6}$	9.335858	ATPase, H <sup>+</sup> transporting, lysosomal V1 subunit B2 (Atp6v1b2)
Rps6ka2	0.60	.00058054	5.598592	Ribosomal protein S6 kinase, polypeptide 2 (Rps6ka2)
Zbtb38	0.60	$1.15 \times 10^{-5}$	7.695768	Zinc finger and BTB domain containing 38 (Zbtb38)
Magee1	0.60	.0001143	7.550312	Melanoma antigen, family E, 1 (Magee1)
Tmem203	0.60	.029664061	2.42976	Transmembrane protein 203 (Tmem203)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tenm3	0.60	$3.69 \times 10^{-5}$	8.237684	Teneurin transmembrane protein 3 (Tenm3)
Synj1	0.60	$1.28 \times 10^{-6}$	9.775183	Synaptojanin 1 (Synj1)
Zfp942	0.60	.010897597	3.612969	Zinc finger protein 942 (Zfp942)
Gdap1	0.60	$2.49 \times 10^{-6}$	7.781211	Ganglioside-induced differentiation-associated-protein 1 (Gdap1)
2810474O19Rik	0.60	.00080519	5.381683	RIKEN cDNA 2810474O19 gene (2810474O19Rik)
Irgq	0.59	.000361722	7.373309	Immunity-related GTPase family, Q (Irgq)
Rapgef2	0.59	$5.07 \times 10^{-5}$	7.559592	Rap guanine nucleotide exchange factor (GEF) 2 (Rapgef2)
Ndufs1	0.59	$5.07 \times 10^{-5}$	7.073996	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (Ndufs1)
Fam43b	0.59	.011012004	3.244153	Family with sequence similarity 43, member B (Fam43b)
Cdk17	0.59	$2.95 \times 10^{-5}$	6.678857	Cyclin-dependent kinase 17 (Cdk17)
Plppr3	0.59	.000118658	5.514628	Phospholipid phosphatase related 3 (Plppr3)
Zfp382	0.59	.00348391	3.924429	Zinc finger protein 382 (Zfp382)
Ubxn2b	0.59	$9.19 \times 10^{-5}$	6.507692	UBX domain protein 2B (Ubxn2b)
Zic2	0.59	$8.34 \times 10^{-5}$	6.279457	Zinc finger protein of the cerebellum 2 (Zic2)
Zfp53	0.59	.009664109	3.361709	Zinc finger protein 53 (Zfp53)
Mgat5b	0.59	.000300779	6.04869	Mannoside acetylglucosaminyltransferase 5, isoenzyme B (Mgat5b)
Dyrk3	0.59	.021927192	2.90972	Dual-specificity tyrosine- (Y)-phosphorylation-regulated kinase 3 (Dyrk3)
AI593442	0.59	.000199344	9.144877	Expressed sequence AI593442 (AI593442)
Trim26	0.59	.000482957	5.369423	Tripartite motif-containing 26 (Trim26)
Vat1	0.59	.000319818	6.589551	Vesicle amine transport 1 (Vat1)
Nol6	0.59	$4.01 \times 10^{-5}$	6.699401	Nucleolar protein family 6 (RNA-associated) (Nol6)
B4galnt1	0.59	$7.44 \times 10^{-5}$	5.598742	Beta-1,4-N-acetyl-galactosaminyl transferase 1 (B4galnt1)
Klf16	0.59	.040219783	2.781972	Kruppel-like factor 16 (Klf16)
Slc30a4	0.59	.000135712	6.218263	Solute carrier family 30 (zinc transporter), member 4 (Slc30a4)
Arhgap5	0.59	$2.50 \times 10^{-5}$	8.516669	Rho GTPase activating protein 5 (Arhgap5)
Hs6st1	0.59	.000350378	5.921587	Heparan sulfate 6-O-sulfotransferase 1 (Hs6st1)
Rnf44	0.59	$3.28 \times 10^{-5}$	7.443965	Ring finger protein 44 (Rnf44)
Adgrl2	0.59	.000197296	6.426477	Adhesion G protein-coupled receptor L2 (Adgrl2)
Kcnn3	0.59	$1.07 \times 10^{-5}$	7.473398	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (Kcnn3)
Cdh10	0.59	.000695798	5.911244	Cadherin 10 (Cdh10)
Htr7	0.59	.001626569	5.795722	5-Hydroxytryptamine (serotonin) receptor 7 (Htr7)
Igf1	0.59	.000201734	5.825477	Insulin-like growth factor 1 (Igf1)
Rab11fip5	0.59	.005168133	6.465298	RAB11 family interacting protein 5 (class I) (Rab11fip5)
Mctp1	0.59	.001002466	5.192876	Multiple C2 domains, transmembrane 1 (Mctp1)
Prkaca	0.59	$1.36 \times 10^{-5}$	7.847747	Protein kinase, cAMP dependent, catalytic, alpha (Prkaca)
Igsf10	0.59	.002916521	4.900188	Immunoglobulin superfamily, member 10 (Igsf10)
Mcf2	0.59	.000668846	5.106316	Mcf.2 transforming sequence (Mcf2)
Dock11	0.59	.000670272	5.216213	Dedicator of cytokinesis 11 (Dock11)
Il1rapl2	0.59	.030764754	2.893582	Interleukin 1 receptor accessory protein-like 2 (Il1rapl2)
Lypd1	0.59	.001733506	5.956347	Ly6/Plaur domain containing 1 (Lypd1)
Smcr8	0.59	$5.43 \times 10^{-5}$	6.434943	Smith–Magenis syndrome chromosome region, candidate 8 homolog (human) (Smcr8)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pik3r3	0.59	.000299725	6.590621	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55) (Pik3r3)
Zc3h12b	0.59	.000174509	5.956576	Zinc finger CCCH-type containing 12B (Zc3h12b)
Dnajc5	0.59	$3.26 \times 10^{-6}$	9.121564	DnaJ heat shock protein family (Hsp40) member C5 (Dnajc5)
Zbtb7c	0.59	.041150396	2.716289	Zinc finger and BTB domain containing 7C (Zbtb7c)
Tspsy13	0.59	.000132522	5.241771	TSPY-like 3 (Tspsy13)
Peg3	0.59	$2.79 \times 10^{-6}$	10.19909	Paternally expressed 3 (Peg3)
Amigo1	0.59	$5.74 \times 10^{-5}$	6.913431	Adhesion molecule with Ig like domain 1 (Amigo1)
Zim1	0.59	.00248065	4.320476	Zinc finger, imprinted 1 (Zim1)
Bicral	0.59	$1.27 \times 10^{-5}$	6.88053	BRD4-interacting chromatin-remodeling complex-associated protein like (Bicral)
Sgpp2	0.59	.00012281	6.155436	Sphingosine-1-phosphate phosphotase 2 (Sgpp2)
2900055J20Rik	0.59	.041526403	2.484005	RIKEN cDNA 2900055J20 gene (2900055J20Rik)
Stox2	0.59	$3.49 \times 10^{-5}$	8.625542	Storkhead box 2 (Stox2)
Syt14	0.59	.000555712	6.17153	Synaptotagmin XIV (Syt14)
Pde3a	0.58	.010660414	3.686455	Phosphodiesterase 3A, cGMP inhibited (Pde3a)
Hspa12b	0.58	.025496287	2.749703	Heat shock protein 12B (Hspa12b)
Mthfd1l	0.58	.00809865	4.22552	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (Mthfd1l)
Zfp27	0.58	.000888982	4.604323	Zinc finger protein 27 (Zfp27)
Scg2	0.58	$1.66 \times 10^{-5}$	8.969157	Secretogranin II (Scg2)
Gm14322	0.58	.043935869	1.995857	Predicted gene 14322 (Gm14322)
Rasgef1a	0.58	.001357801	5.949674	RasGEF domain family, member 1A (Rasgef1a)
Cacng2	0.58	$1.10 \times 10^{-5}$	7.113562	Calcium channel, voltage-dependent, gamma subunit 2 (CACNG2)
Enpp5	0.58	$8.82 \times 10^{-6}$	8.378714	Ectonucleotide pyrophosphatase/phosphodiesterase 5 (Enpp5)
Cmip	0.58	$4.09 \times 10^{-5}$	7.555249	c-Maf inducing protein (Cmip)
Prkaa2	0.58	.00017267	7.263639	Protein kinase, AMP-activated, alpha 2 catalytic subunit (Prkaa2)
Ncoa7	0.58	.000181509	6.625896	Nuclear receptor coactivator 7 (Ncoa7)
Zyg11b	0.58	$5.51 \times 10^{-6}$	9.174217	zyg-II family member B, cell cycle regulator (Zyg11b)
Syn1	0.58	$1.74 \times 10^{-5}$	9.347181	Synapsin I (Syn1)
Fgf12	0.58	.000146824	7.89683	Fibroblast growth factor 12 (Fgf12)
Lrfn5	0.58	.000108876	7.313435	Leucine-rich repeat and fibronectin type III domain containing 5 (Lrfn5)
Sept5	0.58	$9.17 \times 10^{-5}$	7.099096	Septin 5 (Sept5)
Atg9b	0.58	.004834737	3.310422	Autophagy-related 9B (Atg9b)
Frem3	0.58	.003038398	4.220175	Fras1-related extracellular matrix protein 3 (Frem3)
Pcdhb17	0.58	.001945942	4.935722	Protocadherin beta 17 (Pcdhb17)
Asxl3	0.58	.000206366	5.327033	Additional sex combs like 3 (Asxl3)
Rimbp2	0.58	$3.56 \times 10^{-5}$	6.631099	RIMS binding protein 2 (Rimbp2)
Kcns2	0.58	.000273706	6.508744	K+ voltage-gated channel, subfamily S, 2 (Kcns2)
Arsj	0.58	.032056865	2.937889	Arylsulfatase J (Arsj)
Id4	0.58	$1.34 \times 10^{-5}$	8.265509	Inhibitor of DNA binding 4 (Id4)
Syn3	0.58	.007041793	3.967593	Synapsin III (Syn3)
Arhgap26	0.58	$4.37 \times 10^{-5}$	7.225588	Rho GTPase activating protein 26 (Arhgap26)
Stxbp1	0.58	$2.68 \times 10^{-6}$	10.03776	Syntaxin binding protein 1 (Stxbp1)
Robo2	0.58	.000357931	5.710455	Roundabout guidance receptor 2 (Robo2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ptpn4	0.58	$9.12 \times 10^{-6}$	9.854663	Protein tyrosine phosphatase, non-receptor type 4 (Ptpn4)
Kbtbd7	0.58	.000478267	5.581395	Kelch repeat and BTB (POZ) domain containing 7 (Kbtbd7)
D630045J12Rik	0.58	.001519816	7.188121	RIKEN cDNA D630045J12 gene (D630045J12Rik)
Sh2d3c	0.58	.000186998	5.3224	SH2 domain containing 3C (Sh2d3c)
Tmed8	0.58	$6.41 \times 10^{-5}$	6.631109	Transmembrane p24 trafficking protein 8 (Tmed8)
Gria2	0.58	$8.89 \times 10^{-6}$	8.948521	Glutamate receptor, ionotropic, AMPA2 (alpha 2) (Gria2)
Grwd1	0.58	.033490279	2.881446	Glutamate-rich WD repeat containing 1 (Grwd1)
Zkscan16	0.58	.000134227	6.431637	Zinc finger with KRAB and SCAN domains 16 (Zkscan16)
Grin3a	0.58	$5.32 \times 10^{-6}$	8.211914	Glutamate receptor ionotropic, NMDA3A (Grin3a)
Zfp65	0.58	.013627975	4.152468	Zinc finger protein 65 (Zfp65)
Senp8	0.57	.003319607	5.035098	SUMO/sentrin-specific peptidase 8 (Senp8)
Lypd6b	0.57	.016997013	4.532064	LY6/PLAUR domain containing 6B (Lypd6b)
Magee2	0.57	.007913771	5.146624	Melanoma antigen, family E, 2 (Magee2)
Togaram1	0.57	$2.87 \times 10^{-5}$	6.294807	TOG array regulator of axonemal microtubules 1 (Togaram1)
Kdm4b	0.57	.000555947	4.326892	Lysine (K)-specific demethylase 4B (Kdm4b)
Gm21955	0.57	.012835155	2.90302	Predicted gene (Gm21955)
Plekhg5	0.57	.0031454	3.747886	Pleckstrin homology domain containing, family G (with RhoGef domain) member 5 (Plekhg5)
Sntg1	0.57	.004400767	4.757658	Syntrophin, gamma 1 (Sntg1)
Acvr1b	0.57	$2.75 \times 10^{-5}$	6.950102	Activin A receptor, type 1B (Acvr1b)
Fam135b	0.57	.000500821	6.047804	Family with sequence similarity 135, member B (Fam135b)
Cdk7	0.57	.001303294	4.516558	Cyclin-dependent kinase 7 (Cdk7)
Rnf126	0.57	.001954802	4.729489	Ring finger protein 126 (Rnf126)
Atl1	0.57	.000244195	6.901975	Atlastin GTPase 1 (Atl1)
Grem2	0.57	.000419938	5.878845	Gremlin 2, DAN family BMP antagonist (Grem2)
Pianp	0.57	$3.09 \times 10^{-5}$	7.562343	PILR alpha-associated neural protein (Pianp)
Mkx	0.57	.011239814	3.45046	Mohawk homeobox (Mkx)
Smim10l2a	0.57	.002230325	4.82406	Small integral membrane protein 10 like 2A (Smim10l2a)
Xk	0.57	.000558255	5.504815	X-linked Kx blood group (Xk)
Pcdhb8	0.57	.02212438	2.743586	Protocadherin beta 8 (Pcdhb8)
Pde4a	0.57	$1.80 \times 10^{-5}$	7.187419	Phosphodiesterase 4A, cAMP specific (Pde4a)
Zbtb11	0.57	.000135264	6.273462	Zinc finger and BTB domain containing 11 (Zbtb11)
Gm26781	0.57	.049273774	2.736648	Predicted gene (Gm26781)
Gck	0.57	.040056873	2.611892	Glucokinase (Gck)
Klhl29	0.57	.000135149	6.006096	Kelch-like 29 (Klhl29)
Trpc7	0.57	.003795209	4.46806	Transient receptor potential cation channel, subfamily C, member 7 (Trpc7)
Zfp944	0.57	.024248549	3.227111	Zinc finger protein 944 (Zfp944)
Sdc2	0.57	.000131379	7.067678	Syndecan 2 (Sdc2)
Plcxd2	0.57	.000831387	7.86351	Phosphatidylinositol-specific phospholipase C, X domain containing 2 (Plcxd2)
Vstm2a	0.57	.000159285	6.66332	V-set and transmembrane domain containing 2A (Vstm2a)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mmp16	0.57	.016005066	5.412923	Matrix metallopeptidase 16 (Mmp16)
Ptchd1	0.57	.024341637	4.307233	Patched domain containing 1 (Ptchd1)
Rph3a	0.57	.000169033	9.039468	Rabphilin 3A (Rph3a)
Endod1	0.57	$1.77 \times 10^{-5}$	6.952131	Endonuclease domain containing 1 (Endod1)
Rad18	0.57	.024392455	3.274372	RAD18 E3 ubiquitin protein ligase (Rad18)
Avl9	0.56	.000159892	6.883059	AVL9 homolog (S. cerevisiae) (Avl9)
Rims4	0.56	.007159208	4.906962	Regulating synaptic membrane exocytosis 4 (Rims4)
Plxna1	0.56	$5.39 \times 10^{-5}$	7.016219	Plexin A1 (Plxna1)
Srsf12	0.56	.000333777	5.638118	Serine/arginine-rich splicing factor 12 (Srsf12)
Chgb	0.56	.000790225	8.799665	Chromogranin B (Chgb)
Cpeb3	0.56	.000100123	7.40079	Cytoplasmic polyadenylation element binding protein 3 (Cpeb3)
Sacs	0.56	$2.75 \times 10^{-5}$	8.199574	Sacsin (Sacs)
Brinp3	0.56	.000291693	5.871998	Bone morphogenetic protein/retinoic acid inducible neural specific 3 (Brinp3)
Tubgcp6	0.56	.001513104	4.63922	Tubulin, gamma complex-associated protein 6 (Tubgcp6)
2900026A02Rik	0.56	.000168046	5.772118	RIKEN cDNA 2900026A02 gene (2900026A02Rik)
Fzd3	0.56	$1.57 \times 10^{-5}$	8.835044	Frizzled class receptor 3 (Fzd3)
Tmem130	0.56	$6.76 \times 10^{-6}$	8.003941	Transmembrane protein 130 (Tmem130)
Gas7	0.56	.000600524	7.353036	Growth arrest specific 7 (Gas7)
Carm1	0.56	.000240505	6.13094	Coactivator-associated arginine methyltransferase 1 (Carm1)
Ifitm10	0.56	.003550056	4.237582	Interferon-induced transmembrane protein 10 (Ifitm10)
Clmp	0.56	.001145146	4.78608	CXADR-like membrane protein (Clmp)
Cbarp	0.56	$8.69 \times 10^{-6}$	8.450234	Calcium channel, voltage-dependent, beta subunit-associated regulatory protein (Cbarp)
Arhgef18	0.56	.000166667	5.582821	Rho/rac guanine nucleotide exchange factor (GEF) 18 (Arhgef18)
Opcml	0.56	$8.47 \times 10^{-6}$	8.347491	Opioid binding protein/cell adhesion molecule-like (Opcml)
Aak1	0.56	$3.18 \times 10^{-6}$	9.413373	AP2-associated kinase 1 (Aak1)
Cpne7	0.56	.000399365	6.400972	Copine VII (Cpne7)
Gpr165	0.56	.002022066	5.139856	G protein-coupled receptor 165 (Gpr165)
Cdk18	0.56	.001311192	5.987593	Cyclin-dependent kinase 18 (Cdk18)
Tvp23a	0.56	.000996895	4.637598	Trans-golgi network vesicle protein 23A (Tvp23a)
Sesn3	0.56	$5.91 \times 10^{-6}$	8.859351	Sestrin 3 (Sesn3)
Tmx4	0.56	$3.95 \times 10^{-6}$	9.799199	Thioredoxin-related transmembrane protein 4 (Tmx4)
Epha4	0.56	$6.00 \times 10^{-5}$	7.806104	Eph receptor A4 (Epha4)
Diras2	0.56	$7.99 \times 10^{-5}$	8.840377	DIRAS family, GTP-binding RAS-like 2 (Diras2)
Tbl1x	0.56	$3.95 \times 10^{-6}$	8.246198	Transducin (beta)-like 1 X-linked (Tbl1x)
Zfp72	0.56	.016654776	3.245965	Zinc finger protein 72 (Zfp72)
Kirrel3	0.56	.000821094	6.01781	Kin of IRRE like 3 (Kirrel3)
Larp4b	0.56	$1.34 \times 10^{-5}$	7.797157	La ribonucleoprotein domain family, member 4B (Larp4b)
Kif3c	0.56	.000130869	7.301565	Kinesin family member 3C (Kif3c)
Cd47	0.56	$7.97 \times 10^{-5}$	9.660572	CD47 antigen (Rh-related antigen, integrin-associated signal transducer) (Cd47)
Tenm2	0.56	$5.85 \times 10^{-5}$	7.675638	Teneurin transmembrane protein 2 (Tenm2)
Glg1	0.56	$3.96 \times 10^{-6}$	8.589533	Golgi apparatus protein 1 (Glg1)
Ppm1h	0.56	$4.42 \times 10^{-5}$	7.320371	Protein phosphatase 1H (PP2C domain containing) (Ppm1h)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Plcb1	0.56	.000261834	6.716171	Phospholipase C, beta 1 (Plcb1)
Zfp575	0.56	.031612138	3.116308	Zinc finger protein 575 (Zfp575)
Rnf217	0.56	.0007287	5.603589	Ring finger protein 217 (Rnf217)
Zfp85os	0.56	.037989591	2.373383	Zinc finger protein 85, opposite strand (Zfp85os)
Adcy3	0.56	.001016702	4.14201	Adenylate cyclase 3 (Adcy3)
Morc4	0.56	.038866642	2.384992	Microrchidia 4 (Morc4)
Lta4h	0.56	.00221034	4.314422	Leukotriene A4 hydrolase (Lta4h)
Zkscan1	0.56	$1.37 \times 10^{-5}$	7.38472	Zinc finger with KRAB and SCAN domains 1 (Zkscan1)
Mbd5	0.56	$2.23 \times 10^{-5}$	7.611572	Methyl-CpG binding domain protein 5 (Mbd5)
Flrt2	0.56	.000347683	6.384407	Fibronectin leucine-rich transmembrane protein 2 (Flrt2)
Thrb	0.56	.000221264	6.042861	Thyroid hormone receptor beta (Thrb)
Tcaf1	0.55	$4.97 \times 10^{-6}$	8.526619	TRPM8 channel-associated factor 1 (Tcaf1)
Kcnk10	0.55	.002003369	4.42852	Potassium channel, subfamily K, member 10 (Kcnk10)
Olfm1	0.55	$2.65 \times 10^{-5}$	9.568817	Olfactomedin 1 (Olfm1)
Ache	0.55	.000229445	6.154809	Acetylcholinesterase (Ache)
Pithd1	0.55	.000216578	6.269957	PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1 (Pithd1)
Usp13	0.55	.000330497	6.049492	Ubiquitin-specific peptidase 13 (isopeptidase T-3) (Usp13)
Sgsm1	0.55	.000326776	6.372506	Small G protein signaling modulator 1 (Sgsm1)
Stk32c	0.55	.02947797	3.410197	Serine/threonine kinase 32C (Stk32c)
Stxbp6	0.55	.000141739	7.953688	Syntaxin binding protein 6 (amisyn) (Stxbp6)
Ksr2	0.55	$1.96 \times 10^{-5}$	7.43066	Kinase suppressor of ras 2 (Ksr2)
Schip1	0.55	.026929022	3.090026	Schwannomin interacting protein 1 (Schip1)
Ppp2r2b	0.55	.000353493	6.897876	Protein phosphatase 2, regulatory subunit B, beta (Ppp2r2b)
Fnbp1l	0.55	.000334109	7.121316	Formin binding protein 1-like (Fnbp1l)
Hspa4	0.55	$5.51 \times 10^{-6}$	8.425166	Heat shock protein 4 (Hspa4)
Zfp955b	0.55	.002551954	4.366794	Zinc finger protein 955B (Zfp955b)
Arhgap35	0.55	$4.40 \times 10^{-6}$	9.52948	Rho GTPase activating protein 35 (Arhgap35)
Zfp93	0.55	.005947679	3.426354	Zinc finger protein 93 (Zfp93)
Scn2a	0.55	$1.50 \times 10^{-5}$	9.067337	Sodium channel, voltage-gated, type II, alpha (Scn2a)
Pnmal2	0.55	$1.34 \times 10^{-5}$	8.092527	PNMA-like 2 (Pnmal2)
Mef2c	0.55	$2.63 \times 10^{-5}$	7.660528	Myocyte enhancer factor 2C (Mef2c)
D130058E05Rik	0.55	.021943429	4.149882	RIKEN cDNA D130058E05 gene (D130058E05Rik)
Map3k9	0.55	.00155214	5.195465	Mitogen-activated protein kinase kinase kinase 9 (Map3k9)
Fign	0.55	.002106176	6.601853	Fidgetin (Fign)
Xpnpep3	0.55	.002850378	5.043502	X-prolyl aminopeptidase 3, mitochondrial (Xpnpep3)
Ubxn7	0.55	.000432114	7.504606	UBX domain protein 7 (Ubxn7)
Tmtc1	0.55	$4.99 \times 10^{-5}$	7.415042	Transmembrane and tetratricopeptide repeat containing 1 (Tmtc1)
Limk1	0.55	.002094901	3.881785	LIM-domain containing, protein kinase (Limk1)
Zfp68	0.55	.000204585	5.470606	Zinc finger protein 68 (Zfp68)
Gabra4	0.55	$3.51 \times 10^{-5}$	8.136459	Gamma-aminobutyric acid (GABA) A receptor, subunit alpha 4 (Gabra4)
Rai2	0.55	.011037004	3.168896	Retinoic acid-induced 2 (Rai2)
Dab1	0.55	.00107831	5.843548	Disabled 1 (Dab1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Plekhm3	0.55	.000378325	6.4861	Pleckstrin homology domain containing, family M, member 3 (Plekhm3)
Lrrc3	0.55	$3.65 \times 10^{-5}$	6.21028	Leucine-rich repeat containing 3 (Lrrc3)
Spata9	0.55	.007219654	3.639556	Spermatogenesis associated 9 (Spata9)
Wdr47	0.55	$3.31 \times 10^{-5}$	7.223816	WD repeat domain 47 (Wdr47)
Jade1	0.55	$8.76 \times 10^{-5}$	6.607031	Jade family PHD finger 1 (Jade1)
Stk25	0.55	$3.15 \times 10^{-5}$	7.618308	Serine/threonine kinase 25 (yeast) (Stk25)
Cd83	0.55	.000946394	5.726646	CD83 antigen (Cd83)
Pcdhb15	0.55	.04757055	3.28304	Protocadherin beta 15 (Pcdhb15)
Nmnat2	0.55	$2.69 \times 10^{-5}$	8.371272	Nicotinamide nucleotide adenylyltransferase 2 (Nmnat2)
Hrk	0.55	.002767959	4.712484	Harakiri, BCL2 interacting protein (contains only BH3 domain) (Hrk)
Dnajc30	0.55	.001945933	4.420577	DnaJ heat shock protein family (Hsp40) member C30 (Dnajc30)
Kcnc4	0.55	.000448204	5.16509	Potassium voltage gated channel, Shaw-related subfamily, member 4 (Kcnc4)
Cdh2	0.55	$3.29 \times 10^{-5}$	7.543057	Cadherin 2 (Cdh2)
Lig4	0.54	.001586914	4.500516	Ligase IV, DNA, ATP-dependent (Lig4)
Atmin	0.54	$1.77 \times 10^{-5}$	7.037499	ATM interactor (Atmin)
Mtcl1	0.54	.000201853	5.335778	Microtubule crosslinking factor 1 (Mtcl1)
Cobl	0.54	.000697017	6.772351	Cordon-bleu WH2 repeat (Cobl)
Ajap1	0.54	.000399735	5.562731	Adherens junction-associated protein 1 (Ajap1)
1700025G04Rik	0.54	.000192273	7.012242	RIKEN cDNA 1700025G04 gene (1700025G04Rik)
Usp11	0.54	$3.46 \times 10^{-5}$	7.690648	Ubiquitin-specific peptidase 11 (Usp11)
Socs5	0.54	$2.69 \times 10^{-5}$	6.890292	Suppressor of cytokine signaling 5 (Socs5)
Alg2	0.54	$1.20 \times 10^{-5}$	8.65765	Asparagine-linked glycosylation 2 (alpha-1,3-mannosyltransferase) (Alg2)
Zfp7	0.54	.012596979	3.323643	Zinc finger protein 7 (Zfp7)
Frrs1l	0.54	$1.57 \times 10^{-5}$	9.090344	Ferric-chelate reductase 1 like (Frrs1l)
Grb10	0.54	$4.81 \times 10^{-5}$	7.448536	Growth factor receptor bound protein 10 (Grb10)
Mid2	0.54	.000105858	6.504257	Midline 2 (Mid2)
Gm47163	0.54	.005939431	3.80993	Predicted gene (Gm47163)
Irf2bpl	0.54	.002536116	4.754384	Interferon regulatory factor 2 binding protein-like (Irf2bpl)
Raph1	0.54	$1.10 \times 10^{-5}$	7.274408	Ras-association (RalGDS/AF-6) and pleckstrin homology domains 1 (Raph1)
Jph1	0.54	.005199946	3.629205	Junctophilin 1 (Jph1)
Zfp174	0.54	.028821766	3.57378	Zinc finger protein 174 (Zfp174)
Mtmr4	0.54	$3.93 \times 10^{-5}$	6.790946	Myotubularin-related protein 4 (Mtmr4)
Cntn3	0.54	.000678736	5.592309	Contactin 3 (Cntn3)
Adgrl3	0.54	$7.96 \times 10^{-6}$	8.18777	Adhesion G protein-coupled receptor L3 (Adgrl3)
Zfp563	0.54	.002670409	3.98977	Zinc finger protein 563 (Zfp563)
Dennd1a	0.54	.000124742	6.430652	DENN/MADD domain containing 1A (Dennd1a)
Pdpx	0.54	.000285692	6.483275	Pyridoxal (pyridoxine, vitamin B6) phosphatase (Pdpx)
Spast	0.54	.00012459	7.067728	Spastin (Spast)
Arid5b	0.54	$1.53 \times 10^{-5}$	7.200132	AT-rich interactive domain 5B (MRF1-like) (Arid5b)
Rab15	0.54	$6.50 \times 10^{-5}$	6.567412	RAB15, member RAS oncogene family (Rab15)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Nlgn1	0.54	$6.28 \times 10^{-5}$	6.782622	Neuroligin 1 (Nlgn1)
Uhmk1	0.54	$1.31 \times 10^{-5}$	10.11173	U2AF homology motif (UHM) kinase 1 (Uhmk1)
Camsap3	0.54	.000831387	4.390712	Calmodulin-regulated spectrin-associated protein family, member 3 (Camsap3)
Mpped1	0.54	.022948124	3.966913	Metallophosphoesterase domain containing 1 (Mpped1)
Prkce	0.54	$1.77 \times 10^{-5}$	8.471382	Protein kinase C, epsilon (Prkce)
Gm42741	0.54	.014831292	3.804253	Predicted gene (Gm42741)
Aaas	0.54	.006740755	3.786443	Achalasia, adrenocortical insufficiency, alacrimia (Aaas)
Zbtb41	0.54	.000353493	6.520061	Zinc finger and BTB domain containing 41 (Zbtb41)
Carmil2	0.54	.007291969	3.258867	Capping protein regulator and myosin 1 linker 2 (Carmil2)
Tada2b	0.54	.001487578	4.989134	Transcriptional adaptor 2B (Tada2b)
Ralgps1	0.54	$8.95 \times 10^{-5}$	6.612721	Ral GEF with PH domain and SH3 binding motif 1 (Ralgps1)
Lin9	0.54	.028503249	3.360965	Lin-9 homolog (C. elegans) (Lin9)
Shh	0.54	.014755638	3.493053	Sonic hedgehog (Shh)
Rbfox1	0.54	.000176575	7.668406	RNA binding protein, fox-1 homolog (C. elegans) 1 (Rbfox1)
Zfp81	0.54	.000322361	5.630062	Zinc finger protein 81 (Zfp81)
Tmem145	0.54	.02156513	3.644266	Transmembrane protein 145 (Tmem145)
Erc2	0.54	$1.08 \times 10^{-5}$	7.524581	ELKS/RAB6-interacting/CAST family member 2 (Erc2)
Pcyox1l	0.54	.014023312	3.676339	Prenylcysteine oxidase 1 like (Pcyox1l)
Crmp1	0.54	$7.69 \times 10^{-5}$	7.205904	Collapsin response mediator protein 1 (Crmp1)
Pcbp3	0.54	.000108867	6.558212	Poly(rC) binding protein 3 (Pcbp3)
Zfp748	0.54	.001010941	4.663876	Zinc finger protein 748 (Zfp748)
Nav1	0.54	$1.32 \times 10^{-5}$	7.804273	Neuron navigator 1 (Nav1)
Elac1	0.54	.001726003	5.558953	elaC ribonuclease Z 1 (Elac1)
Gng2	0.53	$2.52 \times 10^{-5}$	8.601891	Guanine nucleotide binding protein (G protein), gamma 2 (Gng2)
Pcgf5	0.53	.000909697	5.797881	Polycomb group ring finger 5 (Pcgf5)
Celf2	0.53	$2.69 \times 10^{-6}$	9.3419	CUGBP, Elav-like family member 2 (Celf2)
Gan	0.53	.00013664	6.100883	Giant axonal neuropathy (Gan)
Rit2	0.53	$3.63 \times 10^{-5}$	8.540407	Ras-like without CAAX 2 (Rit2)
Bend4	0.53	.000558255	5.522201	BEN domain containing 4 (Bend4)
Sphkap	0.53	$1.68 \times 10^{-5}$	8.120433	SPHK1 interactor, AKAP domain containing (Sphkap)
Podxl2	0.53	.000656732	5.217602	Podocalyxin-like 2 (Podxl2)
Zfp418	0.53	.045862511	3.769525	Zinc finger protein 418 (Zfp418)
Ccser2	0.53	$1.55 \times 10^{-5}$	8.361199	Coiled-coil serine rich 2 (Ccser2)
Ankrd34c	0.53	.000416776	6.411261	Ankyrin repeat domain 34C (Ankrd34c)
Blm	0.53	.021733851	3.020316	Bloom syndrome, RecQ helicase-like (Blm)
Akap8	0.53	.00066474	5.341209	A kinase (PRKA) anchor protein 8 (Akap8)
Ago2	0.53	$2.03 \times 10^{-5}$	8.517953	Argonaute RISC catalytic subunit 2 (Ago2)
Gm42732	0.53	.025744992	5.192111	Predicted gene (Gm42732)
Crtc1	0.53	.000157484	6.794349	CREB-regulated transcription coactivator 1 (Crtc1)
Nap1l5	0.53	$6.14 \times 10^{-6}$	9.338491	Nucleosome assembly protein 1-like 5 (Nap1l5)
Tmem30a	0.53	$2.25 \times 10^{-5}$	8.630783	Transmembrane protein 30A (Tmem30a)
Ypel2	0.53	$1.66 \times 10^{-5}$	7.331298	Yippee-like 2 (Ypel2)
Chml	0.53	.00068304	5.485425	Choroideremia-like (Chml)
AU040320	0.53	.000166667	6.428786	Expressed sequence AU040320 (AU040320)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Asxl1	0.53	.00036855	5.703834	Additional sex combs like 1 (Asxl1)
Klhdc8a	0.53	.0059834	4.017285	Kelch domain containing 8A (Klhdc8a)
Cacul1	0.53	4.00 × 10 <sup>-5</sup>	7.109679	CDK2-associated, cullin domain 1 (Cacul1)
Actr1a	0.53	2.86 × 10 <sup>-5</sup>	7.654551	ARP1 actin-related protein 1A, centractin alpha (Actr1a)
Parm1	0.53	.00256652	6.121518	Prostate androgen-regulated mucin-like protein 1 (Parm1)
Arfgef3	0.53	1.77 × 10 <sup>-5</sup>	8.355611	ARFGEF family member 3 (Arfgef3)
Kitl	0.53	8.66 × 10 <sup>-5</sup>	7.734027	Kit ligand (Kitl)
Zfp235	0.53	.005677225	3.914763	Zinc finger protein 235 (Zfp235)
Ttc7b	0.53	4.18 × 10 <sup>-5</sup>	7.374514	Tetratricopeptide repeat domain 7B (Ttc7b)
Slc35f1	0.53	3.19 × 10 <sup>-5</sup>	7.29093	Solute carrier family 35, member F1 (Slc35f1)
Garem1	0.53	.001115218	5.221918	GRB2-associated regulator of MAPK1 subtype 1 (Garem1)
Uba6	0.53	.000247675	6.404118	Ubiquitin-like modifier activating enzyme 6 (Uba6)
Tlnrd1	0.53	.000706332	5.180478	Talin rod domain containing 1 (Tlnrd1)
Cdkl5	0.53	3.96 × 10 <sup>-5</sup>	9.129261	Cyclin-dependent kinase-like 5 (Cdkl5)
Pde12	0.53	.001139352	4.561145	Phosphodiesterase 12 (Pde12)
Usp32	0.53	1.25 × 10 <sup>-5</sup>	8.398708	Ubiquitin-specific peptidase 32 (Usp32)
Zfp869	0.53	.016678993	4.23269	Zinc finger protein 869 (Zfp869)
Ldlrad4	0.53	.003284405	4.103629	Low-density lipoprotein receptor class A domain containing 4 (Ldlrad4)
Sv2a	0.53	1.70 × 10 <sup>-5</sup>	9.120266	Synaptic vesicle glycoprotein 2 a (Sv2a)
Ncam2	0.53	.000188512	7.689167	Neural cell adhesion molecule 2 (Ncam2)
Ambra1	0.53	.000319742	5.909214	Autophagy/beclin 1 regulator 1 (Ambra1)
Fgf13	0.53	2.20 × 10 <sup>-5</sup>	7.20541	Fibroblast growth factor 13 (Fgf13)
Reep1	0.53	5.01 × 10 <sup>-5</sup>	8.438474	Receptor accessory protein 1 (Reep1)
Map9	0.53	2.87 × 10 <sup>-5</sup>	7.868156	Microtubule-associated protein 9 (Map9)
Pnma3	0.53	.000890423	5.264541	Paraneoplastic antigen MA3 (Pnma3)
Adra2b	0.53	.001544389	4.531226	Adrenergic receptor, alpha 2b (Adra2b)
Sgip1	0.53	1.04 × 10 <sup>-5</sup>	9.198767	SH3-domain GRB2-like (endophilin) interacting protein 1 (Sgip1)
Klf11	0.53	.020104078	3.577183	Kruppel-like factor 11 (Klf11)
Sik1	0.53	.001831427	5.128565	Salt inducible kinase 1 (Sik1)
Hspa4l	0.52	6.20 × 10 <sup>-6</sup>	9.067492	Heat shock protein 4 like (Hspa4l)
Bloc1s6	0.52	.000859819	5.114625	Biogenesis of lysosomal organelles complex-1, subunit 6, pallidin (Bloc1s6)
Cop1	0.52	5.80 × 10 <sup>-5</sup>	6.068655	COP1 E3 Ubiquitin Ligase (Cop1)
Grm4	0.52	.000526071	7.151452	Glutamate receptor, metabotropic 4 (Grm4)
Ankrd29	0.52	.000372424	5.465121	Ankyrin repeat domain 29 (Ankrd29)
9230114K14Rik	0.52	.033335482	3.428748	RIKEN cDNA 9230114K14 gene (9230114K14Rik)
C2cd4c	0.52	.026485615	3.770998	C2 calcium-dependent domain containing 4C (C2cd4c)
Atp6v0a1	0.52	1.45 × 10 <sup>-5</sup>	8.937292	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit A1 (Atp6v0a1)
Mef2a	0.52	1.74 × 10 <sup>-5</sup>	8.810571	Myocyte enhancer factor 2A (Mef2a)
B230334C09Rik	0.52	.000132522	7.596078	RIKEN cDNA B230334C09 gene (B230334C09Rik)
Scaf1	0.52	8.40 × 10 <sup>-5</sup>	5.905375	SR-related CTD-associated factor 1 (Scaf1)
Kpna6	0.52	3.49 × 10 <sup>-5</sup>	7.373171	Karyopherin (importin) alpha 6 (Kpna6)
Shox2	0.52	.000199352	7.315399	Short stature homeobox 2 (Shox2)
Samd12	0.52	.00032414	7.274502	Sterile alpha motif domain containing 12 (Samd12)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pak1	0.52	.000148143	9.293641	p21 protein (Cdc42/Rac)-activated kinase 1 (Pak1)
Gne	0.52	.000197296	5.808799	Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (Gne)
Zfp770	0.52	.000319742	5.679438	Zinc finger protein 770 (Zfp770)
Mrpl37	0.52	.013258903	5.228043	Mitochondrial ribosomal protein L37 (Mrpl37)
Ttl1	0.52	.000246398	6.64415	Tubulin tyrosine ligase-like 1 (Ttl1)
Il13ra1	0.52	.014237722	3.895478	Interleukin 13 receptor, alpha 1 (Il13ra1)
B4galnt4	0.52	.002650302	5.774207	Beta-1,4-N-acetyl-galactosaminyl transferase 4 (B4galnt4)
Cpne2	0.52	.000385	6.028711	Copine II (Cpne2)
Nup54	0.52	.00940916	3.909517	Nucleoporin 54 (Nup54)
Ccdc50	0.52	$2.65 \times 10^{-5}$	7.084979	Coiled-coil domain containing 50 (Ccdc50)
Atp8a2	0.52	$8.31 \times 10^{-5}$	7.100838	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2 (Atp8a2)
Baiap2	0.52	.009169931	3.787107	Brain-specific angiogenesis inhibitor 1-associated protein 2 (Baiap2)
Bean1	0.52	.006998773	4.057834	Brain expressed, associated with Nedd4, 1 (Bean1)
Dnajc28	0.52	.004360612	3.941868	DnaJ heat shock protein family (Hsp40) member C28 (Dnajc28)
Thbs2	0.52	.034121813	4.473553	Thrombospondin 2 (Thbs2)
D230025D16Rik	0.52	.000569011	5.864713	RIKEN cDNA D230025D16 gene (D230025D16Rik)
Cdhr1	0.52	.022329126	3.059596	Cadherin-related family member 1 (Cdhr1)
Dcaf7	0.52	$7.66 \times 10^{-6}$	8.216057	DDB1 and CUL4-associated factor 7 (Dcaf7)
Ssx2ip	0.52	.000223098	6.506209	Synovial sarcoma, X breakpoint 2 interacting protein (Ssx2ip)
Chpf2	0.52	.012084483	3.439515	Chondroitin polymerizing factor 2 (Chpf2)
Dip2c	0.52	.000109064	6.500142	Disco interacting protein 2 homolog C (Dip2c)
Fam134b	0.52	$3.01 \times 10^{-5}$	7.485044	Family with sequence similarity 134, member B (Fam134b)
Pkp4	0.52	$2.18 \times 10^{-5}$	8.881393	Plakophilin 4 (Pkp4)
Slc9a7	0.52	.000154302	6.365061	Solute carrier family 9 (sodium/hydrogen exchanger), member 7 (Slc9a7)
Zfp800	0.52	.001379238	4.987724	Zinc finger protein 800 (Zfp800)
Xxylt1	0.52	.000523987	4.925927	Xyloside xylosyltransferase 1 (Xxylt1)
Adam22	0.52	$6.47 \times 10^{-6}$	8.723296	A disintegrin and metallopeptidase domain 22 (Adam22)
Wipf3	0.52	.003285454	5.169738	WAS/WASL interacting protein family, member 3 (Wipf3)
Rap2a	0.52	$1.71 \times 10^{-5}$	7.961109	RAS-related protein 2a (Rap2a)
Slc7a3	0.52	.012309113	4.478607	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (Slc7a3)
Gm43597	0.52	.003729114	4.091525	Predicted gene (Gm43597)
Prkcg	0.52	.000576592	8.69884	Protein kinase C, gamma (Prkcg)
Zfp507	0.52	.002814285	4.769872	Zinc finger protein 507 (Zfp507)
Nxpe3	0.52	.001362517	4.892595	Neurexophilin and PC-esterase domain family, member 3 (Nxpe3)
Zdhhc15	0.52	.01955455	3.589362	Zinc finger, DHHC domain containing 15 (Zdhhc15)
Rgs12	0.52	.004453035	3.702477	Regulator of G-protein signaling 12 (Rgs12)
1700019D03Rik	0.52	.000239287	6.142601	RIKEN cDNA 1700019D03 gene (1700019D03Rik)
Vcip1	0.51	$3.15 \times 10^{-5}$	7.6758	Valosin containing protein (p97)/p47 complex interacting protein 1 (Vcip1)
Fbxo11	0.51	$2.47 \times 10^{-5}$	7.756129	F-box protein 11 (Fbxo11)
Mgat4a	0.51	.000192529	6.721662	Mannoside acetylglucosaminyltransferase 4, isoenzyme A (Mgat4a)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ankrd34a	0.51	.000196935	6.423928	Ankyrin repeat domain 34A (Ankrd34a)
Gls2	0.51	.022248496	2.833004	Glutaminase 2 (liver, mitochondrial) (Gls2)
Usp29	0.51	.000126022	7.235744	Ubiquitin-specific peptidase 29 (Usp29)
Hnrnph2	0.51	.000166655	6.670412	Heterogeneous nuclear ribonucleoprotein H2 (Hnrnph2)
Rala	0.51	.000190641	6.495384	V-ral simian leukemia viral oncogene A (ras related) (Rala)
Tsr1	0.51	.006186201	4.941772	TSR1 20S rRNA accumulation (Tsr1)
Zfp30	0.51	.022005703	3.827388	Zinc finger protein 30 (Zfp30)
Ptpn2	0.51	$7.34 \times 10^{-5}$	7.979503	Protein tyrosine phosphatase, receptor type, N polypeptide 2 (Ptpn2)
Asxl2	0.51	.001555751	6.198126	Additional sex combs like 2 (Asxl2)
Fads3	0.51	.001012111	5.19859	Fatty acid desaturase 3 (Fads3)
Zmiz1	0.51	$1.20 \times 10^{-5}$	8.069944	Zinc finger, MIZ-type containing 1 (Zmiz1)
Apba2	0.51	$9.79 \times 10^{-5}$	6.748047	Amyloid beta (A4) precursor protein-binding, family A, member 2 (Apba2)
Zswim3	0.51	.018761832	3.741888	Zinc finger SWIM-type containing 3 (Zswim3)
Zfp239	0.51	.001774577	5.400692	Zinc finger protein 239 (Zfp239)
Sgsh	0.51	.019341721	3.475588	N-sulfoglucosamine sulfohydrolase (sulfamidase) (Sgsh)
Dgat2	0.51	.000608385	6.235325	Diacylglycerol O-acyltransferase 2 (Dgat2)
Csmd3	0.51	.000625418	6.203445	CUB and Sushi multiple domains 3 (Csmd3)
Tmem132b	0.51	$2.78 \times 10^{-5}$	7.323678	Transmembrane protein 132B (Tmem132b)
Timp2	0.51	$4.33 \times 10^{-5}$	9.999863	Tissue inhibitor of metalloproteinase 2 (Timp2)
Zfp365	0.51	$9.83 \times 10^{-5}$	8.796883	Zinc finger protein 365 (Zfp365)
Vipas39	0.51	.000516594	5.736626	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog (Vipas39)
Kif3b	0.51	.000200157	6.335414	Kinesin family member 3B (Kif3b)
Rnf31	0.51	.040984338	4.278394	Ring finger protein 31 (Rnf31)
Gm14325	0.51	.02836186	2.765817	Predicted gene 14325 (Gm14325)
Hs3st5	0.51	.037133655	2.99095	Heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (Hs3st5)
1700017B05Rik	0.51	.003441896	4.646979	RIKEN cDNA 1700017B05 gene (1700017B05Rik)
Rhof	0.51	.015257988	4.340154	Ras homolog family member F (in filopodia) (Rhof)
Kcnab1	0.51	.014319962	5.415699	Potassium voltage-gated channel, shaker-related subfamily, beta member 1 (Kcnab1)
Fam168a	0.51	$1.99 \times 10^{-5}$	8.661639	Family with sequence similarity 168, member A (Fam168a)
Thsd4	0.51	.020348849	4.091881	Thrombospondin, type I, domain containing 4 (Thsd4)
Sesn2	0.51	.01139073	3.700217	Sestrin 2 (Sesn2)
Syndig1l	0.51	.000243532	5.385757	Synapse differentiation inducing 1 like (Syndig1l)
Wdr7	0.51	$1.66 \times 10^{-5}$	8.170967	WD repeat domain 7 (Wdr7)
Slc36a4	0.51	.000197692	7.233313	Solute carrier family 36 (proton/amino acid symporter), member 4 (Slc36a4)
Sntb2	0.51	.006064657	4.149545	Syntrophin, basic 2 (Sntb2)
Whrn	0.51	.008615789	3.552818	Whirlin (Whrn)
Alg11	0.51	.000132337	7.325538	Asparagine-linked glycosylation 11 (alpha-1,2-mannosyltransferase) (Alg11)
Gabrb2	0.51	.000416776	7.784328	Gamma-aminobutyric acid (GABA) A receptor, subunit beta 2 (Gabrb2)
Grin2d	0.51	.004582498	5.300155	Glutamate receptor, ionotropic, NMDA2D (epsilon 4) (Grin2d)
Gatsl2	0.51	.000427987	8.095224	GATS protein-like 2 (Gatsl2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mturn	0.51	$3.42 \times 10^{-5}$	8.311278	Maturin, neural progenitor differentiation regulator homolog (Xenopus) (Mturn)
Rhbdd2	0.51	$5.43 \times 10^{-5}$	6.409278	Rhomboid domain containing 2 (Rhbdd2)
G3bp2	0.51	$4.91 \times 10^{-5}$	7.595844	GTPase activating protein (SH3 domain) binding protein 2 (G3bp2)
Gm43682	0.51	.006833857	4.2924	Predicted gene (Gm43682)
Tab3	0.50	.000799751	5.287331	TGF-beta-activated kinase 1/MAP3K7 binding protein 3 (Tab3)
Mecp2	0.50	$8.89 \times 10^{-6}$	9.016983	Methyl CpG binding protein 2 (Mecp2)
Klf12	0.50	.000380867	7.578726	Kruppel-like factor 12 (Klf12)
Prrc2b	0.50	$3.73 \times 10^{-6}$	9.320837	Proline-rich coiled-coil 2B (Prrc2b)
Igfbp5	0.50	$8.80 \times 10^{-5}$	8.736287	Insulin-like growth factor binding protein 5 (Igfbp5)
Gnaq	0.50	$6.76 \times 10^{-6}$	8.155164	Guanine nucleotide binding protein, alpha q polypeptide (Gnaq)
Zfp655	0.50	.001488064	5.611433	Zinc finger protein 655 (Zfp655)
Pafah1b1	0.50	$6.04 \times 10^{-6}$	9.205319	Platelet-activating factor acetylhydrolase, isoform 1b, subunit 1 (Pafah1b1)
Polk	0.50	.001495063	4.969408	Polymerase (DNA directed), kappa (Polk)
Lrsam1	0.50	.003584629	4.441391	Leucine-rich repeat and sterile alpha motif containing 1 (Lrsam1)
Ndst4	0.50	.024977903	4.943704	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4 (Ndst4)
Dpp9	0.50	.000504451	5.508586	Dipeptidylpeptidase 9 (Dpp9)
Far2	0.50	.000233834	6.117339	Fatty acyl CoA reductase 2 (Far2)
Rnf10	0.50	.000586147	6.302902	Ring finger protein 10 (Rnf10)
Pura	0.50	.000569585	7.795406	Purine-rich element binding protein A (Pura)
Usp22	0.50	$4.25 \times 10^{-5}$	8.212736	Ubiquitin-specific peptidase 22 (Usp22)
Nol10	0.50	.004126718	4.021982	Nucleolar protein 10 (Nol10)
Fam120b	0.50	$4.91 \times 10^{-5}$	6.882702	Family with sequence similarity 120, member B (Fam120b)
Iqsec1	0.50	$2.25 \times 10^{-5}$	8.691885	IQ motif and Sec7 domain 1 (Iqsec1)
Pdik1l	0.50	.001182316	4.9045	PDLIM1 interacting kinase 1 like (Pdik1l)
Arhgef5	0.50	.030090444	4.214326	Rho guanine nucleotide exchange factor (GEF) 5 (Arhgef5)
Ocrl	0.50	$3.69 \times 10^{-5}$	7.343288	Oculocerebrorenal syndrome of Lowe (Ocrl)
Zfp599	0.50	.048811796	3.457343	Zinc finger protein 599 (Zfp599)
Gpr61	0.50	.010436237	3.50339	G protein-coupled receptor 61 (Gpr61)
Yme1l1	0.50	.000567106	6.54129	YME1-like 1 ( <i>S. cerevisiae</i> ) (Yme1l1)
Gnl3l	0.50	$2.90 \times 10^{-5}$	8.615794	Guanine nucleotide binding protein-like 3 (nucleolar)-like (Gnl3l)
Map6	0.50	.000271237	7.150213	Microtubule-associated protein 6 (Map6)
Pank3	0.50	.000312897	7.328627	Pantothenate kinase 3 (Pank3)
Slitrk3	0.50	$6.90 \times 10^{-5}$	7.435944	SLIT and NTRK-like family, member 3 (Slitrk3)
Arhgap27	0.50	.003255011	4.640164	Rho GTPase activating protein 27 (Arhgap27)
Eri3	0.50	.000201853	6.117831	Exoribonuclease 3 (Eri3)
Kpna3	0.50	$2.94 \times 10^{-5}$	7.022576	Karyopherin (importin) alpha 3 (Kpna3)
Zcchc2	0.50	.001371504	5.550055	Zinc finger, CCHC domain containing 2 (Zcchc2)
Dlc1	0.50	.000141082	7.254099	Deleted in liver cancer 1 (Dlc1)
Armcx2	0.50	$8.77 \times 10^{-5}$	6.827135	Armadillo repeat containing, X-linked 2 (Armcx2)
Lrrc4b	0.50	$2.81 \times 10^{-5}$	7.593234	Leucine-rich repeat containing 4B (Lrrc4b)
Fam212b	0.50	.001669081	5.301549	Family with sequence similarity 212, member B (Fam212b)
Cabyr	0.50	.040331797	3.176974	Calcium-binding tyrosine- (Y)-phosphorylation regulated (fibrous heathin 2) (Cabyr)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Sntb1	0.50	.002781292	6.301121	Syntrophin, basic 1 (Sntb1)
Tshz3	0.49	.014499583	4.271713	Teashirt zinc finger family member 3 (Tshz3)
Fam110a	0.49	.0142136	3.890638	Family with sequence similarity 110, member A (Fam110a)
Hs2st1	0.49	.000114447	7.061872	Heparan sulfate 2-O-sulfotransferase 1 (Hs2st1)
Gm16485	0.49	.003623173	4.132776	Predicted gene 16485 (Gm16485)
Abl2	0.49	.001709309	6.284897	V-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) (Abl2)
Stx1a	0.49	.010820006	5.648423	Syntaxin 1A (brain) (Stx1a)
A830082N09Rik	0.49	.014671102	5.604842	RIKEN cDNA A830082N09 gene (A830082N09Rik)
Bcl2	0.49	.000326502	6.598642	B cell leukemia/lymphoma 2 (Bcl2)
Zfp825	0.49	.043789614	2.964103	Zinc finger protein 825 (Zfp825)
Scoc	0.49	$4.09 \times 10^{-5}$	7.38511	Short coiled-coil protein (Scoc)
Aldh18a1	0.49	.016067384	4.137853	Aldehyde dehydrogenase 18 family, member A1 (Aldh18a1)
Tanc2	0.49	$5.78 \times 10^{-6}$	8.781747	Tetratricopeptide repeat, ankyrin repeat, and coiled-coil containing 2 (Tanc2)
Cdk14	0.49	$3.37 \times 10^{-5}$	8.641801	Cyclin-dependent kinase 14 (Cdk14)
Fam131b	0.49	.006674993	6.259977	Family with sequence similarity 131, member B (Fam131b)
St8sia4	0.49	.013647351	4.278556	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 4 (St8sia4)
Gpd1l	0.49	.000143473	7.304194	Glycerol-3-phosphate dehydrogenase 1-like (Gpd1l)
Sema6b	0.49	.001929587	5.742435	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b)
Skiv2l2	0.49	.000519092	6.593657	Superkiller viralicidic activity 2-like 2 ( <i>S. cerevisiae</i> ) (Skiv2l2)
Ntm	0.49	.000107235	7.887382	Neurotrimin (Ntm)
Fem1b	0.49	$6.90 \times 10^{-5}$	8.808714	Feminization 1 homolog b ( <i>C. elegans</i> ) (Fem1b)
Adam19	0.49	.002402103	5.173784	A disintegrin and metallopeptidase domain 19 (meltrin beta) (Adam19)
Senp7	0.49	.000178207	6.558744	SUMO1/sentrin-specific peptidase 7 (Senp7)
Hyou1	0.49	$5.64 \times 10^{-5}$	6.869923	Hypoxia up-regulated 1 (Hyou1)
Dcbld1	0.49	.029925528	3.206455	Discoidin, CUB, and LCCL domain containing 1 (Dcbld1)
Zfp12	0.49	.002405035	4.460931	Zinc finger protein 12 (Zfp12)
Zfp319	0.49	.001809463	4.39925	Zinc finger protein 319 (Zfp319)
Tfip11	0.49	.002376766	4.530287	Tuftelin interacting protein 11 (Tfip11)
Grin1	0.49	.000492141	7.458673	Glutamate receptor, ionotropic, NMDA1 (zeta 1) (Grin1)
Elavl2	0.49	.000118871	7.679044	ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i> )-like 2 (Hu antigen B) (Elavl2)
Papolg	0.49	.002755685	4.983342	Poly(A) polymerase gamma (Papolg)
Map3k12	0.49	$9.61 \times 10^{-5}$	6.161915	Mitogen-activated protein kinase kinase kinase 12 (Map3k12)
Galns	0.49	.048967797	2.741527	Galactosamine (N-acetyl)-6-sulfate sulfatase (Galns)
Cacnb4	0.49	.000315675	8.456173	Calcium channel, voltage-dependent, beta 4 subunit (Cacnb4)
Mmp15	0.49	.002134924	4.807218	Matrix metallopeptidase 15 (Mmp15)
Lancl2	0.49	$4.83 \times 10^{-5}$	7.484846	LanC (bacterial lantibiotic synthetase component C)-like 2 (Lancl2)
Akap17b	0.49	.000756082	5.363899	A kinase (PRKA) anchor protein 17B (Akap17b)
Tet1	0.49	.004673112	6.654421	Tet methylcytosine dioxygenase 1 (Tet1)
Akap8l	0.49	.00582108	4.125275	A kinase (PRKA) anchor protein 8-like (Akap8l)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Zfp658	0.49	.03325665	2.654369	Zinc finger protein 658 (Zfp658)
Pip4k2b	0.49	$6.41 \times 10^{-5}$	7.180139	Phosphatidylinositol-5-phosphate 4-kinase, type II, beta (Pip4k2b)
Efna5	0.49	.001508783	5.372957	Ephrin A5 (Efna5)
Impact	0.49	$4.41 \times 10^{-5}$	9.298585	Impact, RWD domain protein (Impact)
Ckmt1	0.49	.002072442	7.072179	Creatine kinase, mitochondrial 1, ubiquitous (Ckmt1)
Etaa1	0.49	.019446411	4.2819	Ewing tumor-associated antigen 1 (Etaa1)
Pptc7	0.49	.000453199	6.393041	PTC7 protein phosphatase homolog (Pptc7)
Aff2	0.49	.004242701	6.154302	AF4/FMR2 family, member 2 (Aff2)
Robo1	0.49	.000176426	7.564692	Roundabout guidance receptor 1 (Robo1)
Rnf157	0.49	$4.83 \times 10^{-5}$	7.930201	Ring finger protein 157 (Rnf157)
Fnip2	0.49	.000488931	4.974987	Folliculin interacting protein 2 (Fnip2)
Osbpl6	0.49	$6.04 \times 10^{-5}$	6.705655	Oxysterol binding protein-like 6 (Osbpl6)
Atxn3	0.49	.006142459	4.733381	Ataxin 3 (Atxn3)
Gpr173	0.49	.004109817	5.094155	G-protein coupled receptor 173 (Gpr173)
Cpsf2	0.49	.000361722	6.309555	Cleavage and polyadenylation-specific factor 2 (Cpsf2)
Pcdhga2	0.49	.032948298	3.101961	Protocadherin gamma subfamily A, 2 (Pcdhga2)
Rpl10a-ps1	0.49	.034736681	3.379423	Ribosomal protein L10A, pseudogene 1 (Rpl10a-ps1)
Nceh1	0.49	.000361531	7.871803	Neutral cholesterol ester hydrolase 1 (Nceh1)
Cntnap5c	0.49	.005822095	3.972982	Contactin-associated protein-like 5C (Cntnap5c)
2900011O08Rik	0.49	.000101885	8.731101	RIKEN cDNA 2900011O08 gene (2900011O08Rik)
Chst10	0.49	.001380989	6.689756	Carbohydrate sulfotransferase 10 (Chst10)
Rsbn1	0.48	.000661433	5.599134	Rosbin, round spermatid basic protein 1 (Rsbn1)
Flot1	0.48	.000852881	6.474218	Flotillin 1 (Flot1)
Elov16	0.48	$8.18 \times 10^{-5}$	7.546458	ELOVL family member 6, elongation of long chain fatty acids (yeast) (Elov16)
Zcchc12	0.48	.000119843	7.771415	Zinc finger, CCHC domain containing 12 (Zcchc12)
Cadps	0.48	$3.41 \times 10^{-5}$	8.604124	Ca2+-dependent secretion activator (Cadps)
Ulk1	0.48	$6.83 \times 10^{-5}$	7.028295	Unc-51 like kinase 1 (Ulk1)
Kif3a	0.48	$2.98 \times 10^{-5}$	7.318835	Kinesin family member 3A (Kif3a)
Sh3pxd2a	0.48	.002622684	4.975016	SH3 and PX domains 2A (Sh3pxd2a)
Pde4d	0.48	.000129589	6.069565	Phosphodiesterase 4D, cAMP specific (Pde4d)
Ddx20	0.48	.019362505	4.159312	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 (Ddx20)
Trim46	0.48	.000598524	5.472668	Tripartite motif-containing 46 (Trim46)
Phactr2	0.48	$3.14 \times 10^{-5}$	7.605588	Phosphatase and actin regulator 2 (Phactr2)
3300002P13Rik	0.48	.03039879	3.45894	RIKEN cDNA 3300002P13 gene (3300002P13Rik)
Ube3a	0.48	$9.28 \times 10^{-5}$	6.456628	Ubiquitin protein ligase E3A (Ube3a)
Gnai1	0.48	$6.65 \times 10^{-5}$	8.536932	Guanine nucleotide binding protein (G protein), alpha inhibiting 1 (Gnai1)
Arl5a	0.48	$7.41 \times 10^{-5}$	7.538916	ADP-ribosylation factor-like 5A (Arl5a)
Ssh1	0.48	.001551125	5.940402	Slingshot homolog 1 (Ssh1)
Fam210a	0.48	$5.89 \times 10^{-5}$	6.604052	Family with sequence similarity 210, member A (Fam210a)
Galnt14	0.48	.004066876	4.713444	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (Galnt14)
Nkd1	0.48	.001683621	5.621471	Naked cuticle 1 homolog (Nkd1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ppp4r4	0.48	.001022316	5.898266	Protein phosphatase 4, regulatory subunit 4 (Ppp4r4)
2610008E11Rik	0.48	.007626304	5.003287	RIKEN cDNA 2610008E11 gene (2610008E11Rik)
Taok1	0.48	9.34 × 10 <sup>-5</sup>	9.594352	TAO kinase 1 (Taok1)
Lsamp	0.48	1.01 × 10 <sup>-5</sup>	10.0604	Limbic system-associated membrane protein (Lsamp)
Ppm1l	0.48	4.60 × 10 <sup>-5</sup>	8.075955	Protein phosphatase 1 (formerly 2C)-like (Ppm1l)
5730455P16Rik	0.48	.000138602	7.223576	RIKEN cDNA 5730455P16 gene (5730455P16Rik)
Dcun1d4	0.48	4.42 × 10 <sup>-5</sup>	7.299505	DCN1, defective in cullin neddylation 1, domain containing 4 ( <i>S. cerevisiae</i> ) (Dcun1d4)
Snx10	0.48	.000238358	7.786748	Sorting nexin 10 (Snx10)
Wdr82	0.48	.000361722	7.122292	WD repeat domain containing 82 (Wdr82)
Drp2	0.48	.000448438	6.122819	Dystrophin-related protein 2 (Drp2)
Bcr	0.48	.000353493	6.740512	Breakpoint cluster region (Bcr)
Asb18	0.48	.014242348	3.901873	Ankyrin repeat and SOCS box-containing 18 (Asb18)
Ccdc85c	0.48	.000347683	6.074509	Coiled-coil domain containing 85C (Ccdc85c)
Marchf9	0.48	.012442623	3.491126	Membrane-associated ring-CH-type finger 9 (Marchf9)
Setd5	0.48	.000123441	8.079494	SET domain containing 5 (Setd5)
Fam110b	0.48	.002813096	4.964441	Family with sequence similarity 110, member B (Fam110b)
St8sia1	0.48	.002536116	7.55041	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 1 (St8sia1)
Acsl4	0.48	6.61 × 10 <sup>-5</sup>	7.018562	Acyl-CoA synthetase long-chain family member 4 (Acsl4)
Zdhhc2	0.48	.000150122	6.447595	Zinc finger, DHHC domain containing 2 (Zdhhc2)
Plk4	0.48	.015921625	3.559392	Polo-like kinase 4 (Plk4)
Kif21a	0.48	3.15 × 10 <sup>-5</sup>	8.756079	Kinesin family member 21A (Kif21a)
Capn5	0.48	.000245613	6.53773	Calpain 5 (Capn5)
Syngr3	0.48	.000457092	7.845531	Synaptogyrin 3 (Syngr3)
Ppp3ca	0.48	2.48 × 10 <sup>-5</sup>	8.194396	Protein phosphatase 3, catalytic subunit, alpha isoform (Ppp3ca)
Rab30	0.48	.00045447	6.274733	RAB30, member RAS oncogene family (Rab30)
Pold3	0.48	.00162611	4.537717	Polymerase (DNA-directed), delta 3, accessory subunit (Pold3)
Peg10	0.48	.045165099	6.32874	Paternally expressed 10 (Peg10)
Nhlrc1	0.48	.011364489	4.664779	NHL repeat containing 1 (Nhlrc1)
Panx1	0.48	.009188406	4.124741	Pannexin 1 (Panx1)
Paqr3	0.48	.020457072	3.302473	Progesterone and adipoQ receptor family member III (Paqr3)
Nrxn1	0.48	7.21 × 10 <sup>-6</sup>	10.09364	Neurexin I (Nrxn1)
Myadm	0.48	.000225905	7.180534	Myeloid-associated differentiation marker (Myadm)
Atg9a	0.47	.001371444	5.680156	Autophagy-related 9A (Atg9a)
Rapgef6	0.47	.000758396	6.696876	Rap guanine nucleotide exchange factor (GEF) 6 (Rapgef6)
Ildr2	0.47	5.23 × 10 <sup>-5</sup>	9.271105	Immunoglobulin-like domain containing receptor 2 (Ildr2)
Pim2	0.47	.002380137	4.793028	Proviral integration site 2 (Pim2)
Cbfa2t2	0.47	.000431868	6.165581	Core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human) (Cbfa2t2)
Morc3	0.47	.00729517	4.860046	Microrchidia 3 (Morc3)
Pdp1	0.47	.000418113	8.646689	Pyruvate dehydrogenase phosphatase catalytic subunit 1 (Pdp1)
Stard9	0.47	.015474813	4.451757	START domain containing 9 (Stard9)
Ppp1r12b	0.47	.000426478	6.31093	Protein phosphatase 1, regulatory (inhibitor) subunit 12B (Ppp1r12b)
Cacnb1	0.47	.000922069	5.247032	Calcium channel, voltage-dependent, beta 1 subunit (Cacnb1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tubb4a	0.47	$7.10 \times 10^{-5}$	10.66785	Tubulin, beta 4A class IVA (Tubb4a)
Foxj3	0.47	.000246304	7.336126	Forkhead box J3 (Foxj3)
Cadm3	0.47	$3.22 \times 10^{-5}$	8.49621	Cell adhesion molecule 3 (Cadm3)
Smarca5	0.47	.000373709	6.516099	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily a, member 5 (Smarca5)
Tlk1	0.47	.000115631	7.259236	Tousled-like kinase 1 (Tlk1)
Bahd1	0.47	.029630347	3.804144	Bromo adjacent homology domain containing 1 (Bahd1)
Zfp874b	0.47	.022261006	3.870412	Zinc finger protein 874b (Zfp874b)
Hspa13	0.47	.002637907	5.6085	Heat shock protein 70 family, member 13 (Hspa13)
Dbpht2	0.47	.000816609	7.519871	DNA binding protein with his-thr domain (Dbpht2)
Ccsap	0.47	.029852464	3.287806	Centriole, cilia, and spindle-associated protein (Ccsap)
Pkp2	0.47	.017749935	3.86237	Plakophilin 2 (Pkp2)
Camta2	0.47	$9.57 \times 10^{-5}$	7.698291	Calmodulin binding transcription activator 2 (Camta2)
Gm10010	0.47	.025167712	3.552928	Predicted gene 10010 (Gm10010)
Got1	0.47	$1.71 \times 10^{-5}$	8.76152	Glutamic-oxaloacetic transaminase 1, soluble (Got1)
Dhx9	0.47	$7.25 \times 10^{-5}$	6.752181	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Dhx9)
Vipr2	0.47	.014772082	4.962402	Vasoactive intestinal peptide receptor 2 (Vipr2)
Arrb1	0.47	$7.68 \times 10^{-5}$	8.359226	Arrestin, beta 1 (Arrb1)
Usp5	0.47	.001334561	6.362961	Ubiquitin-specific peptidase 5 (isopeptidase T) (Usp5)
Epha3	0.47	.03702333	3.274886	Eph receptor A3 (Epha3)
Lclat1	0.47	.000375366	6.384792	Lysocardiolipin acyltransferase 1 (Lclat1)
Nectin1	0.47	.006772183	4.613636	Nectin cell adhesion molecule 1 (Nectin1)
Nlgn2	0.47	$4.32 \times 10^{-5}$	7.497194	Neuroligin 2 (Nlgn2)
Ptprf	0.47	.000994875	6.206784	Protein tyrosine phosphatase, receptor type, F (Ptprf)
Slc5a3	0.47	.002759123	7.089417	Solute carrier family 5 (inositol transporters), member 3 (Slc5a3)
Hmgcr	0.47	.000321323	6.999178	3-Hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr)
Man1a2	0.47	$3.10 \times 10^{-5}$	8.005426	Mannosidase, alpha, class 1A, member 2 (Man1a2)
Spata2	0.47	.00017551	6.18663	Spermatogenesis associated 2 (Spata2)
Siae	0.47	.003832065	4.787912	Sialic acid acetyltransferase (Siae)
Mtss1	0.47	$2.69 \times 10^{-5}$	7.502453	Metastasis suppressor 1 (Mtss1)
Begain	0.47	.001796092	6.177032	Brain-enriched guanylate kinase-associated (Begain)
A830073O21Rik	0.47	.036602063	3.155212	RIKEN cDNA A830073O21 gene (A830073O21Rik)
Nrg3	0.47	.000506278	6.329965	Neuregulin 3 (Nrg3)
Arhgap1	0.47	.000328088	6.414455	Rho GTPase activating protein 1 (Arhgap1)
Sobp	0.47	.000597382	6.54442	Sine oculis-binding protein homolog (Sobp)
Slc9a1	0.47	.000294425	6.621043	Solute carrier family 9 (sodium/hydrogen exchanger), member 1 (Slc9a1)
Mrap2	0.47	.01937184	4.517835	Melanocortin 2 receptor accessory protein 2 (Mrap2)
Prrg3	0.47	.000763509	7.106886	Proline-rich Gla (G-carboxyglutamic acid) 3 (transmembrane) (Prrg3)
Slc41a2	0.47	.001113675	6.106604	Solute carrier family 41, member 2 (Slc41a2)
Pcdh10	0.47	$2.14 \times 10^{-5}$	8.439189	Protocadherin 10 (Pcdh10)
Thoc3	0.47	.004992511	4.945442	THO complex 3 (Thoc3)
Mapk1	0.47	$4.34 \times 10^{-5}$	8.247123	Mitogen-activated protein kinase 1 (Mapk1)
Ctc1	0.47	.001413903	4.81425	CTS telomere maintenance complex component 1 (Ctc1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gpr137c	0.47	.000105527	7.007863	G protein-coupled receptor 137C (Gpr137c)
Jmy	0.47	.000518855	6.857806	Junction-mediating and regulatory protein (Jmy)
Disp2	0.47	$6.53 \times 10^{-5}$	9.524808	Dispatched homolog 2 (Disp2)
Trim32	0.47	$8.40 \times 10^{-5}$	8.054434	Tripartite motif-containing 32 (Trim32)
Rab6b	0.46	$1.63 \times 10^{-5}$	10.9938	RAB6B, member RAS oncogene family (Rab6b)
Pak7	0.46	.002322536	4.612248	p21 protein (Cdc42/Rac)-activated kinase 7 (Pak7)
Wdr4	0.46	.034842102	3.876873	WD repeat domain 4 (Wdr4)
Paqr9	0.46	$7.00 \times 10^{-5}$	6.747874	Progestin and adipoQ receptor family member IX (Paqr9)
Jakmip3	0.46	.003666263	5.01624	Janus kinase and microtubule interacting protein 3 (Jakmip3)
Ptcd3	0.46	.001035567	5.049192	Pentatricopeptide repeat domain 3 (Ptcd3)
Slc9a5	0.46	.015216513	3.480971	Solute carrier family 9 (sodium/hydrogen exchanger), member 5 (Slc9a5)
Peli3	0.46	.031733638	3.351909	Pellino 3 (Peli3)
Coro1c	0.46	.00145067	6.223458	Coronin, actin binding protein 1C (Coro1c)
A230056P14Rik	0.46	.007990944	4.062623	RIKEN cDNA A230056P14 gene (A230056P14Rik)
Paf1	0.46	.001197514	5.107284	Paf1, RNA polymerase II complex component (Paf1)
Top1	0.46	.000319818	6.206782	Topoisomerase (DNA) I (Top1)
Vps33a	0.46	.000274867	6.674283	VPS33A CORVET/HOPS core subunit (Vps33a)
Braf	0.46	$3.61 \times 10^{-5}$	8.555082	Braf transforming gene (Braf)
Tpgs2	0.46	.000257427	6.716296	Tubulin polyglutamylase complex subunit 2 (Tpgs2)
Tmem158	0.46	.040591569	4.232921	Transmembrane protein 158 (Tmem158)
Smg8	0.46	.007075088	4.782751	Smg-8 homolog, nonsense mediated mRNA decay factor ( <i>C. elegans</i> ) (Smg8)
Ero1l	0.46	.000314173	6.606825	ERO1-like ( <i>S. cerevisiae</i> ) (Ero1l)
Taf1	0.46	.000118896	7.125911	TATA-box binding protein-associated factor 1 (Taf1)
Nup43	0.46	.025642564	3.367705	Nucleoporin 43 (Nup43)
Ube2o	0.46	.000224403	6.088197	Ubiquitin-conjugating enzyme E2O (Ube2o)
Prepl	0.46	.000108867	8.42021	Prolyl endopeptidase-like (Prepl)
Arhgef9	0.46	$1.95 \times 10^{-5}$	9.060455	CDC42 guanine nucleotide exchange factor (GEF) 9 (Arhgef9)
Sult4a1	0.46	.000171289	8.20612	Sulfotransferase family 4A, member 1 (Sult4a1)
Skil	0.46	.001375994	6.342489	SKI-like (Skil)
AC125351.1	0.46	.003332304	4.913767	Predicted gene (Gm49654)
Supt5	0.46	.000137379	6.312683	Suppressor of Ty 5 (Supt5)
Reep6	0.46	.005572999	4.256648	Receptor accessory protein 6 (Reep6)
Dusp1	0.46	.014428159	5.495226	Dual-specificity phosphatase 1 (Dusp1)
Galnt9	0.46	.012384396	5.670193	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (Galnt9)
Zfp266	0.46	.000378676	6.804585	Zinc finger protein 266 (Zfp266)
Slc36a1	0.46	.000809945	6.298076	Solute carrier family 36 (proton/amino acid symporter), member 1 (Slc36a1)
Csnk1g3	0.46	.000327953	6.915622	Casein kinase 1, gamma 3 (Csnk1g3)
Arhgef11	0.46	.000267473	6.849974	Rho guanine nucleotide exchange factor (GEF) 11 (Arhgef11)
Wnk3	0.46	$9.08 \times 10^{-5}$	7.629332	WNK lysine-deficient protein kinase 3 (Wnk3)
Tuba4a	0.46	$5.89 \times 10^{-5}$	7.871474	Tubulin, alpha 4A (Tuba4a)
Klhl11	0.46	.000214376	6.310354	Kelch-like 11 (Klhl11)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Amer2	0.46	.000699764	7.917886	APC membrane recruitment 2 (Amer2)
Lrtm2	0.46	.000510564	8.186492	Leucine-rich repeats and transmembrane domains 2 (Lrtm2)
Capn1	0.46	.020549481	3.954359	Calpain 1 (Capn1)
Fbxw7	0.46	.000114281	7.130542	F-box and WD-40 domain protein 7 (Fbxw7)
Grid2ip	0.46	.00139493	5.517545	Glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1 (Grid2ip)
Cx3cl1	0.46	.001182316	8.722243	Chemokine (C-X3-C motif) ligand 1 (Cx3cl1)
Pip5k1c	0.46	.000232317	6.554507	Phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c)
Pcdhb20	0.46	.037450276	3.72872	Protocadherin beta 20 (Pcdhb20)
Rps6ka4	0.46	.015589952	3.449031	Ribosomal protein S6 kinase, polypeptide 4 (Rps6ka4)
Btbd9	0.46	.00014267	6.425872	BTB (POZ) domain containing 9 (Btbd9)
Alcam	0.46	.002022066	7.790447	Activated leukocyte cell adhesion molecule (Alcam)
Orai2	0.46	.000609841	5.680543	ORAI calcium release-activated calcium modulator 2 (Orai2)
Gpr158	0.46	.000118591	8.246984	G protein-coupled receptor 158 (Gpr158)
Supt6	0.46	$9.34 \times 10^{-5}$	7.659551	Suppressor of Ty 6 (Supt6)
Zfp704	0.46	.000932051	6.557274	Zinc finger protein 704 (Zfp704)
Jag2	0.46	.01578007	4.308178	Jagged 2 (Jag2)
Mpped2	0.46	.002299506	5.342379	Metallophosphoesterase domain containing 2 (Mpped2)
Tram1l1	0.46	.001395869	6.330943	Translocation-associated membrane protein 1-like 1 (Tram1l1)
Aplp2	0.45	$4.42 \times 10^{-5}$	9.326656	Amyloid beta (A4) precursor-like protein 2 (Aplp2)
Ergic1	0.45	.000604031	6.743439	Endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (Ergic1)
Tmem131	0.45	.000186284	7.811875	Transmembrane protein 131 (Tmem131)
Slc2a3	0.45	.000223704	6.820721	Solute carrier family 2 (facilitated glucose transporter), member 3 (Slc2a3)
Zbtb43	0.45	.005423168	4.635901	Zinc finger and BTB domain containing 43 (Zbtb43)
Pcbp1	0.45	.001299413	6.732799	Poly(rC) binding protein 1 (Pcbp1)
Rapgef5	0.45	.00107492	5.677724	Rap guanine nucleotide exchange factor (GEF) 5 (Rapgef5)
Asf1a	0.45	.021448062	4.578955	Anti-silencing function 1A histone chaperone (Asf1a)
Tmem198	0.45	.015827317	3.279203	Transmembrane protein 198 (Tmem198)
Prkar1b	0.45	.000163613	8.538815	Protein kinase, cAMP dependent regulatory, type I beta (Prkar1b)
Prkg1	0.45	.003907831	4.216822	Protein kinase, cGMP-dependent, type I (Prkg1)
Erlin1	0.45	.007319519	4.626003	ER lipid raft associated 1 (Erlin1)
Klh32	0.45	.007578091	4.462452	Kelch-like 32 (Klh32)
Amer1	0.45	.015053408	4.04839	APC membrane recruitment 1 (Amer1)
Tmod2	0.45	$1.57 \times 10^{-5}$	10.47214	Tropomodulin 2 (Tmod2)
Susd4	0.45	$9.50 \times 10^{-5}$	7.444392	Sushi domain containing 4 (Susd4)
Argap44	0.45	.000133152	7.961015	Rho GTPase activating protein 44 (Argap44)
Adam23	0.45	.000124023	7.615026	A disintegrin and metalloproteinase domain 23 (Adam23)
Sik3	0.45	.000114447	8.250367	SIK family kinase 3 (Sik3)
Apc	0.45	.000316176	9.360161	Adenomatous polyposis coli (Apc)
Zmat1	0.45	.003894461	4.896193	Zinc finger, matrin type 1 (Zmat1)
Gm42433	0.45	.014755638	3.359426	Predicted gene (Gm42433)
Fbxo42	0.45	.00064226	5.424557	F-box protein 42 (Fbxo42)
Tmem63c	0.45	.003672551	5.203675	Transmembrane protein 63c (Tmem63c)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gdap2	0.45	.003726249	4.981501	Ganglioside-induced differentiation-associated-protein 2 (Gdap2)
Cep295	0.45	.003604952	4.679063	Centrosomal protein 295 (Cep295)
Clic5	0.45	.009159755	4.251669	Chloride intracellular channel 5 (Clic5)
Fbxo10	0.45	.000997786	5.814775	F-box protein 10 (Fbxo10)
Gnptab	0.45	.000353493	7.163864	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits (Gnptab)
Map3k13	0.45	.002666968	5.541207	Mitogen-activated protein kinase kinase kinase 13 (Map3k13)
Vldlr	0.45	.000800046	7.07396	Very-low-density lipoprotein receptor (Vldlr)
Cep170b	0.45	.000160426	8.478236	Centrosomal protein 170B (Cep170b)
Dhx57	0.45	.000569554	5.807644	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 (Dhx57)
Sos1	0.45	.000275022	7.407906	Son of sevenless homolog 1 (Sos1)
Srm	0.45	.001780703	5.413557	Spermidine synthase (Srm)
Grik3	0.45	.002200659	6.288374	Glutamate receptor, ionotropic, kainate 3 (Grik3)
Vwc2	0.45	.007734216	5.115704	Von Willebrand factor C domain containing 2 (Vwc2)
Gm9938	0.45	.02189059	4.053592	Predicted gene 9938 (Gm9938)
Gng7	0.45	.001929587	5.662525	Guanine nucleotide binding protein (G protein), gamma 7 (Gng7)
Spock3	0.45	.00104562	7.361705	Sparc/osteonectin, cwcv, and kazal-like domains proteoglycan 3 (Spock3)
Clec16a	0.45	.000333446	6.771369	C-type lectin domain family 16, member A (Clec16a)
Atf2	0.45	.000399684	9.359601	Activating transcription factor 2 (Atf2)
6430548M08Rik	0.45	$8.66 \times 10^{-5}$	8.081681	RIKEN cDNA 6430548M08 gene (6430548M08Rik)
Prmt7	0.45	.005243557	4.707293	Protein arginine N-methyltransferase 7 (Prmt7)
Rufy3	0.45	$3.63 \times 10^{-5}$	9.147298	RUN and FYVE domain containing 3 (Rufy3)
Vash2	0.45	.008494097	4.328322	Vasohibin 2 (Vash2)
Atcay	0.45	.000128435	6.992892	Ataxia, cerebellar, Cayman type (Atcay)
Ube2ql1	0.45	.001150661	6.564043	Ubiquitin-conjugating enzyme E2Q family-like 1 (Ube2ql1)
Btbd11	0.45	.000353493	6.84126	BTB (POZ) domain containing 11 (Btbd11)
Pitpnm3	0.45	.000213184	7.121084	PITPNM family member 3 (Pitpnm3)
Mcub	0.45	.023564862	3.78699	Mitochondrial calcium uniporter dominant negative subunit beta (Mcub)
Sqle	0.45	.000146824	7.297657	Squalene epoxidase (Sqle)
Cnot4	0.45	.002098121	6.369317	CCR4-NOT transcription complex, subunit 4 (Cnot4)
Ube4b	0.45	$6.29 \times 10^{-5}$	7.659399	Ubiquitination factor E4B (Ube4b)
Spock2	0.45	$1.27 \times 10^{-5}$	10.63308	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 (Spock2)
Fzr1	0.45	.006425957	5.099393	Fizzy/cell division cycle 20 related 1 (Fzr1)
Ppm1a	0.45	$2.50 \times 10^{-5}$	8.508332	Protein phosphatase 1A, magnesium dependent, alpha isoform (Ppm1a)
Smad2	0.45	.000757973	6.061977	SMAD family member 2 (Smad2)
Anks1b	0.45	$4.78 \times 10^{-5}$	9.21956	Ankyrin repeat and sterile alpha motif domain containing 1B (Anks1b)
Zfp35	0.45	.025050269	4.45114	Zinc finger protein 35 (Zfp35)
Wipf2	0.45	.000189599	7.834029	WAS/WASL interacting protein family, member 2 (Wipf2)
Cbln2	0.44	.02947797	6.97697	Cerebellin 2 precursor protein (Cbln2)
Fstl4	0.44	.009962535	4.4189	Follistatin-like 4 (Fstl4)
Pomk	0.44	.002730156	5.190687	Protein-O-mannose kinase (Pomk)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Dzip3	0.44	.000130869	7.149074	DAZ interacting protein 3, zinc finger (Dzip3)
Spin1	0.44	$6.28 \times 10^{-5}$	8.539658	Spindlin 1 (Spin1)
Pygo2	0.44	.016061634	4.497364	Pygopus 2 (Pygo2)
Kras	0.44	.000261877	7.447538	Kirsten rat sarcoma viral oncogene homolog (Kras)
Zfp386	0.44	.003123444	5.167368	Zinc finger protein 386 (Kruppel-like) (Zfp386)
Sv2b	0.44	$1.28 \times 10^{-5}$	8.943629	Synaptic vesicle glycoprotein 2 b (Sv2b)
Osbpl8	0.44	$9.91 \times 10^{-5}$	7.217165	Oxysterol binding protein-like 8 (Osbpl8)
Tsc22d2	0.44	.001066802	6.475675	TSC22 domain family, member 2 (Tsc22d2)
Pygo1	0.44	.003285454	6.348431	Pygopus 1 (Pygo1)
Zfp280d	0.44	.001082328	5.872884	Zinc finger protein 280D (Zfp280d)
Maged1	0.44	.000157484	9.503322	Melanoma antigen, family D, 1 (Maged1)
Coq5	0.44	.003719834	5.931892	Coenzyme Q5 methyltransferase (Coq5)
Klf9	0.44	.00130816	6.591094	Kruppel-like factor 9 (Klf9)
Mak16	0.44	.012430955	3.824748	MAK16 homolog (Mak16)
Dlgap1	0.44	$8.51 \times 10^{-5}$	8.487934	Discs, large homolog-associated protein 1 (Dlgap1)
Adam15	0.44	.000926517	5.886278	A disintegrin and metalloproteinase domain 15 (metarginidin) (Adam15)
Tomm70a	0.44	.000339184	7.42258	Translocase of outer mitochondrial membrane 70 homolog A (yeast) (Tomm70a)
Ttc27	0.44	.005612815	4.373225	Tetratricopeptide repeat domain 27 (Ttc27)
Fam155a	0.44	.000170379	7.298223	Family with sequence similarity 155, member A (Fam155a)
Por	0.44	.000418113	6.368509	P450 (cytochrome) oxidoreductase (Por)
Rgs7	0.44	.001389948	7.32774	Regulator of G protein signaling 7 (Rgs7)
Vkorc1l1	0.44	.000315675	6.741713	Vitamin K epoxide reductase complex, subunit 1-like 1 (Vkorc1l1)
Ppat	0.44	.003285454	4.541544	Phosphoribosyl pyrophosphate amidotransferase (Ppat)
Gpr135	0.44	.008329523	4.65335	G protein-coupled receptor 135 (Gpr135)
Zdbf2	0.44	$8.19 \times 10^{-5}$	7.808305	Zinc finger, DBF-type containing 2 (Zdbf2)
Clvs2	0.44	.00194191	4.928738	Clavesin 2 (Clvs2)
BC005561	0.44	.01465253	3.86681	cDNA sequence BC005561 (BC005561)
Zfp444	0.44	.005068922	4.490709	Zinc finger protein 444 (Zfp444)
Nol4l	0.44	.00114897	6.799403	Nucleolar protein 4-like (Nol4l)
Nipal3	0.44	.000119643	7.088298	NIPA-like domain containing 3 (Nipal3)
Fam43a	0.44	.012147442	4.163479	Family with sequence similarity 43, member A (Fam43a)
Apbb1	0.44	$7.67 \times 10^{-5}$	7.128024	Amyloid beta (A4) precursor protein-binding, family B, member 1 (Apbb1)
Klh18	0.44	.003477372	5.200045	Kelch-like 18 (Klh18)
Lgi1	0.44	.000353493	6.981183	Leucine-rich repeat LGI family, member 1 (Lgi1)
Syt13	0.44	$8.76 \times 10^{-5}$	8.860435	Synaptotagmin XIII (Syt13)
Zfp141	0.44	.012480857	3.921562	Zinc finger protein 141 (Zfp141)
Fgd4	0.44	.000864431	6.619991	FYVE, RhoGEF, and PH domain containing 4 (Fgd4)
B3galt2	0.44	.00142528	6.288489	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 (B3galt2)
Camkmt	0.44	.029828927	3.294356	Calmodulin-lysine N-methyltransferase (Camkmt)
Dock9	0.44	.000750569	7.175141	Dedicator of cytokinesis 9 (Dock9)
Matr3	0.44	.000122525	7.984909	Matrin 3 (Matr3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Prkch	0.44	.00483422	6.154338	Protein kinase C, eta (Prkch)
Rps6ka5	0.44	.002532045	5.156039	Ribosomal protein S6 kinase, polypeptide 5 (Rps6ka5)
Nr4a3	0.44	.025918873	5.377708	Nuclear receptor subfamily 4, group A, member 3 (Nr4a3)
Csdc2	0.44	.000463921	8.042956	Cold shock domain containing C2, RNA binding (Csdc2)
Dlgap4	0.44	.000210513	7.970795	Discs, large homolog-associated protein 4 (Dlgap4)
Immt	0.44	.000101532	7.176855	Inner membrane protein, mitochondrial (Immt)
Marf1	0.44	$7.22 \times 10^{-5}$	8.936939	Meiosis arrest female 1 (Marf1)
Arsa	0.44	.012152036	4.043013	Arylsulfatase A (Arsa)
Fxyd6	0.44	.000169887	6.671847	FXYD domain-containing ion transport regulator 6 (Fxyd6)
Nomo1	0.44	.000988982	6.660549	Nodal modulator 1 (Nomo1)
Map3k2	0.44	.008630197	5.528723	Mitogen-activated protein kinase kinase kinase 2 (Map3k2)
Timm17a	0.44	$6.83 \times 10^{-5}$	7.376256	Translocase of inner mitochondrial membrane 17a (Timm17a)
Ddn	0.44	.007381789	4.874246	Dendrin (Ddn)
Ccdc71	0.44	.013183398	4.801451	Coiled-coil domain containing 71 (Ccdc71)
Celf6	0.44	.00130816	5.286741	CUGBP, Elav-like family member 6 (Celf6)
Dnm1	0.43	.000201118	9.021393	Dynamin 1 (Dnm1)
Rcan2	0.43	$8.21 \times 10^{-5}$	8.868202	Regulator of calcineurin 2 (Rcan2)
Tmed5	0.43	.004158745	5.814851	Transmembrane p24 trafficking protein 5 (Tmed5)
Yae1d1	0.43	.004906307	6.118438	Yae1 domain containing 1 (Yae1d1)
Rc3h1	0.43	.000583495	8.025294	RING CCCH (C3H) domains 1 (Rc3h1)
Mapk9	0.43	$7.36 \times 10^{-5}$	8.610604	Mitogen-activated protein kinase 9 (Mapk9)
Pex1	0.43	.011075063	5.068015	Peroxisomal biogenesis factor 1 (Pex1)
Papd5	0.43	.000188077	6.346729	PAP-associated domain containing 5 (Papd5)
Chrnb2	0.43	.000292433	6.787899	Cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) (Chrnb2)
Lrif1	0.43	.027486813	4.383491	Ligand dependent nuclear receptor interacting factor 1 (Lrif1)
Exoc8	0.43	.003792173	4.986242	Exocyst complex component 8 (Exoc8)
Ttc13	0.43	.006235333	4.333293	Tetratricopeptide repeat domain 13 (Ttc13)
Snap91	0.43	.000369437	9.139188	Synaptosomal-associated protein 91 (Snap91)
Scn2b	0.43	.000382616	8.373498	Sodium channel, voltage-gated, type II, beta (Scn2b)
Camsap1	0.43	$7.23 \times 10^{-5}$	7.025738	Calmodulin-regulated spectrin-associated protein 1 (Camsap1)
Cdkl1	0.43	.012360932	3.551885	Cyclin-dependent kinase-like 1 (CDC2-related kinase) (Cdkl1)
Ldb1	0.43	.001685832	5.424585	LIM domain binding 1 (Ldb1)
Fam46a	0.43	.046809332	3.57504	Family with sequence similarity 46, member A (Fam46a)
Cntnap4	0.43	.006225374	5.416949	Contactin-associated protein-like 4 (Cntnap4)
Fam124a	0.43	.0039276	5.284341	Family with sequence similarity 124, member A (Fam124a)
Ccdc92b	0.43	.001955352	5.225566	Coiled-coil domain containing 92B (Ccdc92b)
Cblb	0.43	.001530817	6.279503	Casitas B-lineage lymphoma b (Cblb)
Hecw1	0.43	.000196935	7.01028	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1 (Hecw1)
Gpc1	0.43	.012526707	5.628209	Glypican 1 (Gpc1)
Snx2	0.43	.008599471	6.306734	Sorting nexin 2 (Snx2)
Sh2d5	0.43	.003692731	4.910603	SH2 domain containing 5 (Sh2d5)
Smpd1	0.43	.000104861	6.8518	Sphingomyelin phosphodiesterase 1, acid lysosomal (Smpd1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Nln	0.43	.004642324	5.075862	Neurolysin (metallopeptidase M3 family) (Nln)
Lmln	0.43	.012967738	4.160177	Leishmanolysin-like (metallopeptidase M8 family) (Lmln)
Nr2c2	0.43	.000515894	7.388217	Nuclear receptor subfamily 2, group C, member 2 (Nr2c2)
Cops7b	0.43	.031726709	3.940877	COP9 signalosome subunit 7B (Cops7b)
Pde1b	0.43	.005769041	6.845212	Phosphodiesterase 1B, Ca2+-calmodulin dependent (Pde1b)
Map1s	0.43	.003935793	5.429615	Microtubule-associated protein 1S (Map1s)
Kcnip4	0.43	$6.99 \times 10^{-5}$	7.745294	Kv channel interacting protein 4 (Kcnip4)
Scai	0.43	.000150079	7.447409	Suppressor of cancer cell invasion (Scai)
Entpd6	0.43	.004872538	4.974699	Ectonucleoside triphosphate diphosphohydrolase 6 (Entpd6)
Ephb2	0.43	.017895843	3.981996	Eph receptor B2 (Ephb2)
Cacnb2	0.43	.000264641	7.794138	Calcium channel, voltage-dependent, beta 2 subunit (CACNB2)
Nfe2l3	0.43	.00765485	4.456725	Nuclear factor, erythroid derived 2, like 3 (NFE2L3)
Uevld	0.43	.005045879	4.64237	UEV and lactate/malate dehydrogenase domains (Uevld)
Asns	0.43	.000210513	6.676927	Asparagine synthetase (Asns)
Calm1	0.43	$1.77 \times 10^{-5}$	11.75562	Calmodulin 1 (Calm1)
Jade2	0.43	.00194776	5.578605	Jade family PHD finger 2 (Jade2)
Secisbp2	0.43	.022687498	3.828273	SECIS binding protein 2 (Secisbp2)
Rabgap1l	0.43	.000909733	7.916433	RAB GTPase activating protein 1-like (Rabgap1l)
Tbc1d30	0.43	.004821913	6.02772	TBC1 domain family, member 30 (Tbc1d30)
Ezh1	0.43	.000265751	6.336819	Enhancer of zeste 1 polycomb repressive complex 2 subunit (Ezh1)
B4galt6	0.43	$3.80 \times 10^{-5}$	7.86362	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 (B4galt6)
Reps2	0.43	.000120466	9.4364	RALBP1-associated Eps domain containing protein 2 (Reps2)
Cep120	0.43	.001407815	6.037168	Centrosomal protein 120 (Cep120)
Spata2l	0.43	.005347344	4.482877	Spermatogenesis associated 2-like (Spata2l)
Map4k3	0.43	.00124002	6.234116	Mitogen-activated protein kinase kinase kinase kinase 3 (Map4k3)
Wars	0.43	.000848083	6.517416	Tryptophanyl-tRNA synthetase (Wars)
Jph4	0.43	.000567763	7.64848	Junctophilin 4 (Jph4)
Trim23	0.43	.000320941	6.782246	Tripartite motif-containing 23 (Trim23)
Pld3	0.42	.000189164	8.21538	Phospholipase D family, member 3 (Pld3)
Nap1l3	0.42	.003180073	5.883284	Nucleosome assembly protein 1-like 3 (Nap1l3)
Zfp949	0.42	.010130044	4.534784	Zinc finger protein 949 (Zfp949)
Usf3	0.42	.002454392	7.349885	Upstream transcription factor family member 3 (Usf3)
Nmt2	0.42	.000179903	7.75941	N-myristoyltransferase 2 (Nmt2)
Dctn4	0.42	$8.07 \times 10^{-5}$	7.680103	Dynactin 4 (Dctn4)
Cdh11	0.42	.002539964	6.508878	Cadherin 11 (Cdh11)
Camkk2	0.42	.003976126	4.645568	Calcium/calmodulin-dependent protein kinase kinase 2, beta (Camkk2)
Zfr	0.42	$4.60 \times 10^{-5}$	8.485964	Zinc finger RNA binding protein (Zfr)
Grid2	0.42	.005274743	5.182087	Glutamate receptor, ionotropic, delta 2 (Grid2)
Tmem59l	0.42	.001058251	7.158039	Transmembrane protein 59-like (Tmem59l)
Atxn2	0.42	$3.84 \times 10^{-5}$	7.751776	Ataxin 2 (Atxn2)
Gpr45	0.42	.041670715	3.873933	G protein-coupled receptor 45 (Gpr45)
Fbxo30	0.42	.037518357	4.915909	F-box protein 30 (Fbxo30)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Cep126	0.42	.002151061	5.481591	Centrosomal protein 126 (Cep126)
Ywhab	0.42	$4.18 \times 10^{-5}$	9.901608	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (Ywhab)
Elk1	0.42	.006475162	5.246195	ELK1, member of ETS oncogene family (Elk1)
Phf20	0.42	.000244925	6.74512	PHD finger protein 20 (Phf20)
Sipa1l3	0.42	.000791988	6.117184	Signal-induced proliferation-associated 1 like 3 (Sipa1l3)
Atxn1	0.42	$5.07 \times 10^{-5}$	8.765492	Ataxin 1 (Atxn1)
Zfp280b	0.42	.002834919	5.290124	Zinc finger protein 280B (Zfp280b)
Actr1b	0.42	$5.45 \times 10^{-5}$	8.470857	ARP1 actin-related protein 1B, centractin beta (Actr1b)
Ube2d3	0.42	$9.23 \times 10^{-5}$	8.120334	Ubiquitin-conjugating enzyme E2D 3 (Ube2d3)
B3galnt1	0.42	.000945488	6.296487	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1 (B3galnt1)
Armcx1	0.42	.000922069	6.298535	Armadillo repeat containing, X-linked 1 (Armcx1)
Spred2	0.42	.001901057	6.580296	Sprouty-related, EVH1 domain containing 2 (Spred2)
Mdga2	0.42	.000688805	7.284115	MAM domain containing glycosylphosphatidylinositol anchor 2 (Mdga2)
Cntnap5b	0.42	.00738221	5.156516	Contactin-associated protein-like 5B (Cntnap5b)
Ppp3cb	0.42	.000290574	8.718173	Protein phosphatase 3, catalytic subunit, beta isoform (Ppp3cb)
Herc3	0.42	.000967774	6.778989	Hect domain and RLD 3 (Herc3)
Nos1	0.42	.00222539	5.591106	Nitric oxide synthase 1, neuronal (Nos1)
Mtpn	0.42	$2.77 \times 10^{-5}$	9.067882	Myotrophin (Mtpn)
Peg13	0.42	.000100509	8.381342	Paternally expressed 13 (Peg13)
Ube2f	0.42	.005636848	5.580955	Ubiquitin-conjugating enzyme E2F (putative) (Ube2f)
Sorl1	0.42	$3.15 \times 10^{-5}$	8.494836	Sortilin-related receptor, LDLR class A repeats-containing (Sorl1)
Zfp760	0.42	.01226005	4.300275	Zinc finger protein 760 (Zfp760)
Zfp157	0.42	.001096691	5.199262	Zinc finger protein 157 (Zfp157)
Magi1	0.42	.000303517	6.631189	Membrane-associated guanylate kinase, WW and PDZ domain containing 1 (Magi1)
Rnf112	0.42	.001085536	6.691979	Ring finger protein 112 (Rnf112)
Pcsk4	0.42	.025762705	3.350632	Proprotein convertase subtilisin/kexin type 4 (Pcsk4)
Csnk1g1	0.42	.000740466	6.240842	Casein kinase 1, gamma 1 (Csnk1g1)
Nrxn2	0.42	.000633508	7.256182	Neurexin II (Nrxn2)
Nt5dc3	0.42	.000407855	7.357036	5'-nucleotidase domain containing 3 (Nt5dc3)
Ina	0.42	$8.30 \times 10^{-5}$	8.627539	Internexin neuronal intermediate filament protein, alpha (Ina)
Irf2bp1	0.42	.01302126	4.320516	Interferon regulatory factor 2 binding protein 1 (Irf2bp1)
Tmem248	0.42	.000752914	6.402601	Transmembrane protein 248 (Tmem248)
Tub	0.42	.002313842	7.774356	Tubby candidate gene (Tub)
Dclk2	0.42	.001508783	5.746545	Doublecortin-like kinase 2 (Dclk2)
Rbm15b	0.42	.003847455	5.596457	RNA binding motif protein 15B (Rbm15b)
Ldha	0.42	.000974263	7.614148	Lactate dehydrogenase A (Ldha)
Glb1	0.42	.045702512	4.501572	Galactosidase, beta 1 (Glb1)
6330403K07Rik	0.42	.000127815	8.840355	RIKEN cDNA 6330403K07 gene (6330403K07Rik)
Prmt2	0.42	.000317567	6.740401	Protein arginine N-methyltransferase 2 (Prmt2)
Soga3	0.42	.000239929	6.974049	SOGA family member 3 (Soga3)
Larp1	0.42	.000125131	7.865978	La ribonucleoprotein domain family, member 1 (Larp1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Kpna1	0.42	.000351351	7.297605	Karyopherin (importin) alpha 1 (Kpna1)
Os9	0.42	.000341985	6.488189	Amplified in osteosarcoma (Os9)
Spryd3	0.42	.001462413	5.536067	SPRY domain containing 3 (Spryd3)
Sec23a	0.42	.000460253	6.979861	SEC23 homolog A, COPII coat complex component (Sec23a)
Evl	0.42	.012360533	5.781625	Ena-vasodilator stimulated phosphoprotein (Evl)
Rybp	0.42	.020074269	4.730474	RING1 and YY1 binding protein (Rybp)
Ttll11	0.42	.005061781	4.322861	Tubulin tyrosine ligase-like family, member 11 (Ttll11)
Zfp810	0.42	.00893466	4.605542	Zinc finger protein 810 (Zfp810)
Crb1	0.42	.018350619	4.967249	Crumbs family member 1, photoreceptor morphogenesis associated (Crb1)
Satb1	0.41	.008004366	6.437933	Special AT-rich sequence binding protein 1 (Satb1)
Rab11b	0.41	.000246082	7.271167	RAB11B, member RAS oncogene family (Rab11b)
Zfp260	0.41	.00348391	6.159883	Zinc finger protein 260 (Zfp260)
Vamp2	0.41	.000110793	10.63948	Vesicle-associated membrane protein 2 (Vamp2)
E2f3	0.41	.003402187	5.297308	E2F transcription factor 3 (E2f3)
Garnl3	0.41	.000610895	5.835878	GTPase activating RANGAP domain-like 3 (Garnl3)
Rusc1	0.41	.006977418	5.719132	RUN and SH3 domain containing 1 (Rusc1)
Tnfaip1	0.41	.000583495	6.050021	Tumor necrosis factor, alpha-induced protein 1 (endothelial) (Tnfaip1)
Htr2c	0.41	.000189599	7.479748	5-Hydroxytryptamine (serotonin) receptor 2C (Htr2c)
Trim66	0.41	.000209083	6.952454	Tripartite motif-containing 66 (Trim66)
3110043O21Rik	0.41	.017013884	4.526678	RIKEN cDNA 3110043O21 gene (3110043O21Rik)
Faxc	0.41	.006103042	7.381361	Failed axon connections homolog (Faxc)
Myo9a	0.41	.000970233	8.107909	Myosin IXa (Myo9a)
Ogdh	0.41	$6.23 \times 10^{-5}$	8.262061	Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) (Ogdh)
Nos1ap	0.41	.045906963	4.441692	Nitric oxide synthase 1 (neuronal) adaptor protein (Nos1ap)
Ube2i	0.41	.003953601	5.233666	Ubiquitin-conjugating enzyme E2I (Ube2i)
Eipr1	0.41	.015977461	4.440447	EARP complex and GARP complex interacting protein 1 (Eipr1)
Ap2m1	0.41	.000743671	7.135462	Adaptor-related protein complex 2, mu 1 subunit (Ap2m1)
Slc45a4	0.41	.003111388	5.556437	Solute carrier family 45, member 4 (Slc45a4)
Cadm1	0.41	.002292781	7.227528	Cell adhesion molecule 1 (Cadm1)
Chm	0.41	.000164147	7.020188	Choroideremia (RAB escort protein 1) (Chm)
Ap3m2	0.41	.000299954	7.43152	Adaptor-related protein complex 3, mu 2 subunit (Ap3m2)
Nudt21	0.41	.001834782	5.497201	Nudix (nucleoside diphosphate linked moiety X)-type motif 21 (Nudt21)
Nus1	0.41	.000251771	7.650265	NUS1 dehydrololichyl diphosphate synthase subunit (Nus1)
Pcnx4	0.41	.00064264	6.146426	Pecanex homolog 4 (Pcnx4)
Slc35e4	0.41	.035189543	3.70476	Solute carrier family 35, member E4 (Slc35e4)
Hipk3	0.41	.000201734	7.426973	Homeodomain interacting protein kinase 3 (Hipk3)
Nr1d2	0.41	.000320933	6.891923	Nuclear receptor subfamily 1, group D, member 2 (Nr1d2)
Ifngr2	0.41	.003320395	5.708341	Interferon gamma receptor 2 (Ifngr2)
Lcor	0.41	.014232243	5.1884	Ligand-dependent nuclear receptor corepressor (Lcor)
Ythdc2	0.41	.007274336	5.311801	YTH domain containing 2 (Ythdc2)
Ddx3x	0.41	$6.82 \times 10^{-5}$	8.291241	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked (Ddx3x)
Usp45	0.41	.003910116	6.15416	Ubiquitin-specific peptidase 45 (Usp45)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Sel1l	0.41	$7.15 \times 10^{-5}$	8.219756	Sel-1 suppressor of lin-12-like ( <i>C. elegans</i> ) (Sel1l)
Ptcd2	0.41	.005060581	5.04595	Pentatricopeptide repeat domain 2 (Ptcd2)
Kcnj12	0.41	.005726545	5.539139	Potassium inwardly-rectifying channel, subfamily J, member 12 (Kcnj12)
4833422C13Rik	0.41	.026490141	3.260002	RIKEN cDNA 4833422C13 gene (4833422C13Rik)
Celf4	0.41	.000246082	10.36565	CUGBP, Elav-like family member 4 (Celf4)
Usp46	0.41	.00064538	6.695928	Ubiquitin-specific peptidase 46 (Usp46)
Fem1c	0.41	.000161732	6.763606	Fem-1 homolog c ( <i>C.elegans</i> ) (Fem1c)
Skiv2l	0.41	.00294054	5.253537	Superkiller viralicidic activity 2-like ( <i>S. cerevisiae</i> ) (Skiv2l)
Mapk1ip1l	0.41	.00113131	6.190469	Mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip1l)
Mboat7	0.41	.000322398	7.298973	Membrane bound O-acyltransferase domain containing 7 (Mboat7)
Mtmr7	0.41	.001246157	5.647186	Myotubularin-related protein 7 (Mtmr7)
Cnot6l	0.41	.00130488	6.551036	CCR4-NOT transcription complex, subunit 6-like (Cnot6l)
Arhgap39	0.41	.002670998	5.737399	Rho GTPase activating protein 39 (Arhgap39)
Cptp	0.41	.011616227	4.827148	Ceramide-1-phosphate transfer protein (Cptp)
Uba1	0.41	$4.18 \times 10^{-5}$	8.57995	Ubiquitin-like modifier activating enzyme 1 (Uba1)
Larp4	0.41	.000437718	6.640701	La ribonucleoprotein domain family, member 4 (Larp4)
Ankrd13b	0.41	.009562188	4.910464	Ankyrin repeat domain 13b (Ankrd13b)
Sh3rf3	0.41	.028409871	3.870381	SH3 domain containing ring finger 3 (Sh3rf3)
Kcnc1	0.41	.000354443	7.625379	Potassium voltage-gated channel, Shaw-related subfamily, member 1 (Kcnc1)
Tgs1	0.41	.003840463	5.979315	Trimethylguanosine synthase 1 (Tgs1)
Psmd5	0.41	.000276441	6.78018	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (Psmd5)
Snx13	0.41	.000832183	7.408004	Sorting nexin 13 (Snx13)
Ube2d2a	0.41	.000340555	7.084271	Ubiquitin-conjugating enzyme E2D 2A (Ube2d2a)
Lmtk2	0.41	.000914788	7.69932	Lemur tyrosine kinase 2 (Lmtk2)
Basp1	0.41	.002566908	7.88251	Brain abundant, membrane-attached signal protein 1 (Basp1)
Mettl16	0.41	.001037059	6.530504	Methyltransferase like 16 (Mettl16)
Stmn2	0.41	.000266989	9.088422	Stathmin-like 2 (Stmn2)
Epm2a	0.41	.011952121	4.678135	Epilepsy, progressive myoclonic epilepsy, type 2 gene alpha (Epm2a)
Dpysl2	0.41	.000357931	10.1531	Dihydropyrimidinase-like 2 (Dpysl2)
Dgke	0.41	.000753062	6.65971	Diacylglycerol kinase, epsilon (Dgke)
Ncald	0.41	.000140278	8.235053	Neurocalcin delta (Ncald)
Wac	0.41	$9.68 \times 10^{-5}$	7.818489	WW domain containing adaptor with coiled-coil (Wac)
Rgs7bp	0.41	.000818636	8.625809	Regulator of G-protein signalling 7 binding protein (Rgs7bp)
Noct	0.41	.007008639	5.847895	Nocturnin (Noct)
Ap3s2	0.41	.00080526	6.7904	Adaptor-related protein complex 3, sigma 2 subunit (Ap3s2)
Pgap1	0.41	.000437718	7.50112	Post-GPI attachment to proteins 1 (Pgap1)
Sept3	0.41	.000163613	9.840756	Septin 3 (Sept3)
Grm5	0.41	.000361531	7.230056	Glutamate receptor, metabotropic 5 (Grm5)
Spock1	0.41	.000340555	9.134854	Sparc/osteonectin, cwcv, and kazal-like domains proteoglycan 1 (Spock1)
Zfp763	0.41	.018932095	4.359049	Zinc finger protein 763 (Zfp763)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Otub1	0.41	.002861436	7.101114	OTU domain, ubiquitin aldehyde binding 1 (Otub1)
Ptpn5	0.41	.000637681	7.590373	Protein tyrosine phosphatase, non-receptor type 5 (Ptpn5)
Frmd3	0.41	.028269613	3.344021	FERM domain containing 3 (Frmd3)
Adam10	0.41	.00277358	5.974151	A disintegrin and metalloproteinase domain 10 (Adam10)
Cxxc4	0.41	.000647762	6.915197	CXXC finger 4 (Cxxc4)
Fam169a	0.41	.000441285	6.842918	family with sequence similarity 169, member A (Fam169a)
Sike1	0.41	.000781423	7.039712	Suppressor of IKBKE 1 (Sike1)
Bcor	0.41	.007257251	4.828124	BCL6 interacting corepressor (Bcor)
Ccdc186	0.41	.000307701	7.0388	Coiled-coil domain containing 186 (Ccdc186)
Hs6st3	0.41	.045700226	3.270171	Heparan sulfate 6-O-sulfotransferase 3 (Hs6st3)
Lpgat1	0.41	$4.91 \times 10^{-5}$	8.205279	Lysophosphatidylglycerol acyltransferase 1 (Lpgat1)
Ube2g2	0.41	.005002434	4.920817	Ubiquitin-conjugating enzyme E2G 2 (Ube2g2)
Dab2ip	0.40	.000429372	7.198355	Disabled 2 interacting protein (Dab2ip)
Dnm1l	0.40	$2.85 \times 10^{-5}$	8.630402	Dynamin 1-like (Dnm1l)
Hspf1	0.40	.000197296	9.169802	Heat shock 105kDa/110kDa protein 1 (Hspf1)
Madd	0.40	$5.27 \times 10^{-5}$	8.183483	MAP-kinase activating death domain (Madd)
Trpv2	0.40	.044463496	4.366328	Transient receptor potential cation channel, subfamily V, member 2 (Trpv2)
Slc6a17	0.40	.00048829	9.454072	Solute carrier family 6 (neurotransmitter transporter), member 17 (Slc6a17)
Ppargc1a	0.40	.003548535	6.91468	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha (Ppargc1a)
Usp10	0.40	.002730156	5.868576	Ubiquitin-specific peptidase 10 (Usp10)
2610002M06Rik	0.40	.000234481	7.464064	RIKEN cDNA 2610002M06 gene (2610002M06Rik)
Vat1l	0.40	.001244935	7.700007	Vesicle amine transport protein 1 like (Vat1l)
Camk1d	0.40	.000600906	7.52445	Calcium/calmodulin-dependent protein kinase ID (Camk1d)
Zfp398	0.40	.003061616	5.797577	Zinc finger protein 398 (Zfp398)
Trp53	0.40	.032436189	4.699861	Transformation-related protein 53 (Trp53)
Ripor1	0.40	.004169398	6.606152	RHO family interacting cell polarization regulator 1 (Ripor1)
Mrs2	0.40	.000399735	6.762866	MRS2 magnesium transporter (Mrs2)
Klf7	0.40	.001150661	6.427431	Kruppel-like factor 7 (ubiquitous) (Klf7)
Tmtc4	0.40	.034545704	4.031828	Transmembrane and tetratricopeptide repeat containing 4 (Tmtc4)
Cul3	0.40	.000191831	8.552255	Cullin 3 (Cul3)
Agtpbp1	0.40	.000135161	8.786645	ATP/GTP binding protein 1 (Agtpbp1)
Arhgap33	0.40	.010617797	6.305063	Rho GTPase activating protein 33 (Arhgap33)
Tgfbr3	0.40	.016050198	3.84926	Transforming growth factor, beta receptor III (Tgfbr3)
Bclaf3	0.40	.034152331	3.483499	BCLAF1 And THRAP3 Family Member 3 (Bclaf3)
Slc4a8	0.40	.000353493	7.572343	Solute carrier family 4 (anion exchanger), member 8 (Slc4a8)
Msl3	0.40	.04826703	3.754659	Male-specific lethal 3 homolog (Msl3)
Trove2	0.40	.013171265	7.298462	TROVE domain family, member 2 (Trove2)
Pik3c3	0.40	.001935342	6.166008	Phosphoinositide-3-kinase, class 3 (Pik3c3)
Cited2	0.40	.001552945	6.203174	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2)
Zmat3	0.40	.000284543	8.922481	Zinc finger matrin type 3 (Zmat3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Zfp1	0.40	.023373455	4.180946	Zinc finger protein 1 (Zfp1)
Plppr1	0.40	.022523673	4.129302	Phospholipid phosphatase related 1 (Plppr1)
Mast1	0.40	.006070659	6.259003	Microtubule-associated serine/threonine kinase 1 (Mast1)
Rps6ka6	0.40	.03900665	4.08833	Ribosomal protein S6 kinase polypeptide 6 (Rps6ka6)
Syngr1	0.40	.000206246	7.983049	Synthopyrin 1 (Syngr1)
Rnf152	0.40	.004220257	6.75536	Ring finger protein 152 (Rnf152)
Fam208b	0.40	.001720872	6.147619	Family with sequence similarity 208, member B (Fam208b)
Slc2a13	0.40	.000624082	8.124894	Solute carrier family 2 (facilitated glucose transporter), member 13 (Slc2a13)
Pwp2	0.40	.033241896	3.754613	PWP2 periodic tryptophan protein homolog (yeast) (Pwp2)
Ap2a1	0.40	.00195702	6.022989	Adaptor-related protein complex 2, alpha 1 subunit (Ap2a1)
Wdr1	0.40	.001959813	6.738987	WD repeat domain 1 (Wdr1)
Bmpr2	0.40	.000206246	9.707483	Bone morphogenetic protein receptor, type II (serine/threonine kinase) (Bmpr2)
B4galt3	0.40	.021448062	3.857196	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 (B4galt3)
Fnip1	0.40	.006699296	5.508866	Folliculin interacting protein 1 (Fnip1)
Homer1	0.40	.004965641	5.483874	Homer scaffolding protein 1 (Homer1)
Dcp2	0.40	.000508478	8.00343	Decapping mRNA 2 (Dcp2)
Atxn7l1	0.40	.001271538	5.766965	Ataxin 7-like 1 (Atxn7l1)
Gfod1	0.40	.002669903	6.539738	Glucose-fructose oxidoreductase domain containing 1 (Gfod1)
Cmtm4	0.40	.000371635	7.60407	CKLF-like MARVEL transmembrane domain containing 4 (Cmtm4)
Magi3	0.40	.000824068	6.774429	Membrane-associated guanylate kinase, WW and PDZ domain containing 3 (Magi3)
Acot7	0.40	.002910472	8.590637	Acyl-CoA thioesterase 7 (Acot7)
Ralgps2	0.40	.010757334	6.614903	Ral GEF with PH domain and SH3 binding motif 2 (Ralgps2)
Rab22a	0.40	.00065807	6.528343	RAB22A, member RAS oncogene family (Rab22a)
Ablim3	0.40	.000602178	6.180118	Actin binding LIM protein family, member 3 (Ablim3)
Wars2	0.40	.037196124	3.951539	Tryptophanyl tRNA synthetase 2 (mitochondrial) (Wars2)
Scn9a	0.40	.015339166	5.230321	Sodium channel, voltage-gated, type IX, alpha (Scn9a)
Nprl2	0.40	.023773621	4.527652	Nitrogen permease regulator-like 2 (Nprl2)
Prr12	0.40	.000778073	6.371128	Proline rich 12 (Prr12)
Elmsan1	0.40	.007672367	5.096321	ELM2 and Myb/SANT-like domain containing 1 (Elmsan1)
Hdgfl3	0.40	.001019541	7.465852	HDGF Like 3 (Hdgfl3)
Zic1	0.40	$7.09 \times 10^{-5}$	9.325685	Zinc finger protein of the cerebellum 1 (Zic1)
Asb7	0.40	.007337365	5.629812	Ankyrin repeat and SOCS box-containing 7 (Azb7)
Dgkh	0.40	.000511567	7.007993	Diacylglycerol kinase, eta (Dgkh)
Tomm20	0.40	.000138669	8.772307	Translocase of outer mitochondrial membrane 20 homolog (yeast) (Tomm20)
Zdhhc8	0.40	.002248331	6.109384	Zinc finger, DHHC domain containing 8 (Zdhhc8)
Egfem1	0.40	.014384793	4.018775	EGF-like and EMI domain containing 1 (Egfem1)
Syp	0.40	.000381879	9.840388	Synaptophysin (Syp)
Myrip	0.40	.000455215	6.467419	Myosin VIIA and Rab interacting protein (Myrip)
Pcdhb22	0.40	.01159523	4.261345	Protocadherin beta 22 (Pcdhb22)
Klh126	0.40	.025929274	4.273419	Kelch-like 26 (Klh126)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ctnna2	0.40	.000411788	6.621573	Catenin (cadherin-associated protein), alpha 2 (Ctnna2)
Ube2q2	0.40	.002387793	6.473931	Ubiquitin-conjugating enzyme E2Q family member 2 (Ube2q2)
Arl5b	0.39	.041338926	5.501197	ADP-ribosylation factor-like 5B (Arl5b)
Abca3	0.39	.003260808	6.006602	ATP-binding cassette, sub-family A (ABC1), member 3 (Abca3)
Kdm6a	0.39	.003623173	5.852303	Lysine (K)-specific demethylase 6A (Kdm6a)
Ccdc25	0.39	.033584168	5.451267	Coiled-coil domain containing 25 (Ccdc25)
L2hgdh	0.39	.010270502	6.220135	L-2-hydroxyglutarate dehydrogenase (L2hgdh)
Ociad1	0.39	.000205316	8.188277	OCIA domain containing 1 (Ociad1)
Gpr161	0.39	.030363759	4.351626	G protein-coupled receptor 161 (Gpr161)
Samd8	0.39	.001485232	6.430399	Sterile alpha motif domain containing 8 (Samd8)
Sez6l	0.39	.000969632	7.90195	Seizure-related 6 homolog like (Sez6l)
Rac1	0.39	$5.88 \times 10^{-5}$	9.511204	RAS-related C3 botulinum substrate 1 (Rac1)
Spryd7	0.39	.002555745	6.47831	SPRY domain containing 7 (Spryd7)
Frs2	0.39	.001650842	7.108316	Fibroblast growth factor receptor substrate 2 (Frs2)
Tmem167	0.39	.005639071	6.600933	Transmembrane protein 167 (Tmem167)
Pogz	0.39	.000558255	7.295534	Pogo transposable element with ZNF domain (Pogz)
Rab3a	0.39	.000617378	8.68367	RAB3A, member RAS oncogene family (Rab3a)
Tmem87b	0.39	.000513786	6.33683	Transmembrane protein 87B (Tmem87b)
Pias1	0.39	.000598025	6.669742	Protein inhibitor of activated STAT 1 (Pias1)
Gstm7	0.39	.00820685	6.579326	Glutathione S-transferase, mu 7 (Gstm7)
Prune1	0.39	.016286848	4.91235	Prune exopolyphosphatase (Prune1)
Trmt6	0.39	.013314284	4.681655	tRNA methyltransferase 6 (Trmt6)
Arl4c	0.39	.000399735	7.287712	ADP-ribosylation factor-like 4C (Arl4c)
Rab5a	0.39	.002062208	6.359248	RAB5A, member RAS oncogene family (Rab5a)
Pgrmc1	0.39	.000522071	7.896982	Progesterone receptor membrane component 1 (Pgrmc1)
Deptor	0.39	.006565451	6.809982	DEP domain containing MTOR-interacting protein (Deptor)
Ranbp6	0.39	.001352556	6.756168	RAN binding protein 6 (Ranbp6)
Tmem206	0.39	.005728789	4.420408	Transmembrane protein 206 (Tmem206)
Usp27x	0.39	.013039787	5.188612	Ubiquitin-specific peptidase 27, X chromosome (Usp27x)
Gm1043	0.39	.026998457	4.064295	Predicted gene 1043 (Gm1043)
Erc1	0.39	.005570031	6.867958	ELKS/RAB6-interacting/CAST family member 1 (Erc1)
Pde8b	0.39	.00924387	4.681265	Phosphodiesterase 8B (Pde8b)
Kif1a	0.39	$1.46 \times 10^{-5}$	10.94517	Kinesin family member 1A (Kif1a)
Cul9	0.39	.013630894	5.197991	Cullin 9 (Cul9)
Adss	0.39	.000676472	6.782127	Adenylosuccinate synthetase, non muscle (Adss)
Stard4	0.39	.001278463	6.245919	StAR-related lipid transfer (START) domain containing 4 (Stard4)
Kctd20	0.39	.002627598	5.571934	potassium channel tetramerisation domain containing 20 (Kctd20)
Atp8a1	0.39	.000271237	7.442854	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (Atp8a1)
Lrrtm1	0.39	.001418482	7.231168	Leucine-rich repeat transmembrane neuronal 1 (Lrrtm1)
Bach2	0.39	.033903378	4.7012	BTB and CNC homology, basic leucine zipper transcription factor 2 (Bach2)
Cers1	0.39	.023529659	4.859025	Ceramide synthase 1 (Cers1)
Mier3	0.39	.005004174	5.057826	MIER family member 3 (Mier3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Klhdc10	0.39	.000960391	7.471712	Kelch domain containing 10 (Klhdc10)
Napb	0.39	$2.43 \times 10^{-5}$	9.946545	N-ethylmaleimide sensitive fusion protein attachment protein beta (Napb)
Ash1l	0.39	.000815174	8.584471	Ash1 (absent, small, or homeotic)-like (Ash1l)
Tigar	0.39	.040550101	4.333218	Trp53-induced glycolysis regulatory phosphatase (Tigar)
Ahr	0.39	.041824553	3.57323	Aryl-hydrocarbon receptor (Ahr)
Sec31a	0.39	.000447698	7.026089	Sec31 homolog A ( <i>S. cerevisiae</i> ) (Sec31a)
Ube2q1	0.39	.000589745	6.80179	Ubiquitin-conjugating enzyme E2Q family member 1 (Ube2q1)
Snap47	0.39	.000214927	8.118025	Synaptosomal-associated protein, 47 (Snap47)
Itpr1	0.39	.000581338	8.756343	Inositol 1,4,5-trisphosphate receptor 1 (Itpr1)
Kcnj6	0.39	.00924387	4.959728	Potassium inwardly-rectifying channel, subfamily J, member 6 (Kcnj6)
Daam1	0.39	.000781236	6.576575	Dishevelled-associated activator of morphogenesis 1 (Daam1)
Pcmt1	0.39	.001120233	7.793165	Protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pcmt1)
Zmym3	0.39	.000406553	6.59546	Zinc finger, MYM-type 3 (Zmym3)
Rasgrf1	0.39	.000120925	9.154793	RAS protein-specific guanine nucleotide-releasing factor 1 (Rasgrf1)
Scyl2	0.39	.002970504	5.780771	SCY1-like 2 ( <i>S. cerevisiae</i> ) (Scyl2)
Hrh1	0.39	.017296158	4.299951	Histamine receptor H1 (Hrh1)
Lnx1	0.39	.041288677	3.583226	Ligand of numb-protein X 1 (Lnx1)
Rfx3	0.39	.004066876	6.646315	Regulatory factor X, 3 (influences HLA class II expression) (Rfx3)
Dnajc21	0.39	.006972324	4.964601	DnaJ heat shock protein family (Hsp40) member C21 (Dnajc21)
Gripap1	0.39	.008322044	5.18345	GRIP1-associated protein 1 (Gripap1)
Zfand2a	0.39	.002246428	7.22935	Zinc finger, AN1-type domain 2A (Zfand2a)
Plk2	0.39	.002029562	5.633857	Polo-like kinase 2 (Plk2)
Marchf6	0.39	.006722751	9.227888	Membrane-associated ring-CH-type finger 6 (Marchf6)
Akap11	0.39	.000511567	9.066586	A kinase (PRKA) anchor protein 11 (Akap11)
Pex26	0.39	.045196493	4.573043	Peroxisomal biogenesis factor 26 (Pex26)
Iqsec2	0.39	.001319795	5.521739	IQ motif and Sec7 domain 2 (Iqsec2)
Dmwd	0.39	.003452337	6.659372	Dystrophia myotonica-containing WD repeat motif (Dmwd)
Ccar2	0.39	.00588487	5.306415	Cell cycle activator and apoptosis regulator 2 (Ccar2)
Plxdc2	0.39	.001018189	7.064167	Plexin domain containing 2 (Plxdc2)
Plppr5	0.38	.037482567	4.558783	Phospholipid phosphatase related 5 (Plppr5)
Srgap1	0.38	.001343411	7.439655	SLIT-ROBO Rho GTPase activating protein 1 (Srgap1)
Zfp868	0.38	.024817473	4.811467	Zinc finger protein 868 (Zfp868)
Wdr77	0.38	.013442886	5.356346	WD repeat domain 77 (Wdr77)
Fam49a	0.38	.000918182	7.801208	Family with sequence similarity 49, member A (Fam49a)
Rad17	0.38	.034179821	3.500613	RAD17 checkpoint clamp loader component (Rad17)
Dusp3	0.38	.000778073	6.928349	Dual-specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) (Dusp3)
Pdgfa	0.38	.001508783	5.888216	Platelet-derived growth factor, alpha (Pdgfa)
Exoc4	0.38	.001431219	6.120506	Exocyst complex component 4 (Exoc4)
Ssr1	0.38	.000140202	8.046873	Signal sequence receptor, alpha (Ssr1)
Ntrk3	0.38	.000550893	7.933633	Neurotrophic tyrosine kinase, receptor, type 3 (Ntrk3)
Ap1g1	0.38	.000356252	7.161984	Adaptor protein complex AP-1, gamma 1 subunit (Ap1g1)
Zfp827	0.38	.000460576	7.181611	Zinc finger protein 827 (Zfp827)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Suv39h1	0.38	.026738436	4.941476	Suppressor of variegation 3-9 homolog 1 (Suv39h1)
Ap2a2	0.38	.000909697	8.616947	Adaptor-related protein complex 2, alpha 2 subunit (Ap2a2)
Nr3c1	0.38	.000965144	7.316474	Nuclear receptor subfamily 3, group C, member 1 (Nr3c1)
Wasl	0.38	.000551795	7.691481	Wiskott–Aldrich syndrome-like (human) (Wasl)
Pnmal1	0.38	.001109304	7.918768	PNMA-like 1 (Pnmal1)
Zfp426	0.38	.008614762	6.01399	Zinc finger protein 426 (Zfp426)
Akap6	0.38	$8.49 \times 10^{-5}$	8.679331	A kinase (PRKA) anchor protein 6 (Akap6)
Gclc	0.38	.002332824	6.248144	Glutamate-cysteine ligase, catalytic subunit (Gclc)
Wdr17	0.38	.0098259	5.00254	WD repeat domain 17 (Wdr17)
Zer1	0.38	.004130319	6.659646	Zyg-11 related, cell cycle regulator (Zer1)
Oxct1	0.38	.000526278	8.446575	3-Oxoacid CoA transferase 1 (Oxct1)
Nek6	0.38	.003478068	5.609307	NIMA (never in mitosis gene a)-related expressed kinase 6 (Nek6)
Rnf14	0.38	$5.13 \times 10^{-5}$	8.896845	Ring finger protein 14 (Rnf14)
Hivep2	0.38	.000113642	7.792137	Human immunodeficiency virus type I enhancer binding protein 2 (Hivep2)
Zfp420	0.38	.019654656	4.499588	Zinc finger protein 420 (Zfp420)
Tbc1d22b	0.38	.003393207	5.706938	TBC1 domain family, member 22B (Tbc1d22b)
Cask	0.38	.000231785	7.799764	Calcium/calmodulin-dependent serine protein kinase (MAGUK family) (Cask)
Nacc1	0.38	.001657218	7.005599	Nucleus accumbens-associated 1, BEN and BTB (POZ) domain containing (Nacc1)
Cdh4	0.38	.044048868	5.35753	Cadherin 4 (Cdh4)
Agpat1	0.38	.001405493	7.094615	1-Acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (Agpat1)
Zfp865	0.38	.014715837	5.290492	yzinc finger protein 865 (Zfp865)
Tti2	0.38	.008852765	4.790209	TELO2 interacting protein 2 (Tti2)
Klhl24	0.38	.002238044	7.552421	Kyelch-like 24 (Klhl24)
Mrpl46	0.38	.011970613	4.525147	Mitochondrial ribosomal protein L46 (Mrpl46)
Spata5	0.38	.011247545	4.496077	Spermatogenesis associated 5 (Spata5)
Socs7	0.38	.001267838	6.229826	Suppressor of cytokine signaling 7 (Socs7)
Afg3l2	0.38	.001354681	6.658424	AFG3-like AAA ATPase 2 (Afg3l2)
Sfxn1	0.38	.00062286	7.07671	Sideroflexin 1 (Sfxn1)
Gspt2	0.38	.01139073	4.885882	G1 to S phase transition 2 (Gspt2)
Dusp8	0.38	.000490167	6.780799	Dual-specificity phosphatase 8 (Dusp8)
Kif2a	0.38	.000386344	7.482954	Kinesin family member 2A (Kif2a)
Rab3gap1	0.38	.002165084	5.807806	RAB3 GTPase activating protein subunit 1 (Rab3gap1)
Kif26b	0.38	.004282258	5.826603	Kinesin family member 26B (Kif26b)
Fpgt	0.38	.008073829	5.066639	Fucose-1-phosphate guanylyltransferase (Fpgt)
Fbxl2	0.38	.001893443	5.605073	F-box and leucine-rich repeat protein 2 (Fbxl2)
Galnt16	0.38	.00142622	6.880426	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 16 (Galnt16)
Cdr2	0.38	.031032057	4.638756	Cerebellar degeneration-related 2 (Cdr2)
Carmil3	0.38	.015385824	4.540358	Capping protein regulator and myosin 1 linker 3 (Carmil3)
Cib2	0.38	.042871766	5.011568	Calcium and integrin binding family member 2 (Cib2)
Ppp2r5b	0.38	.001669081	5.849584	Protein phosphatase 2, regulatory subunit B', beta (Ppp2r5b)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Vps26b	0.38	.000466302	7.15158	VPS26 retromer complex component B (Vps26b)
Dctd	0.38	.02220035	4.356909	dCMP deaminase (Dctd)
Smyd5	0.38	.041878616	4.120509	SET and MYND domain containing 5 (Smyd5)
Gyg	0.38	.004078923	5.467725	Glycogenin (Gyg)
Mapk10	0.38	4.12 × 10 <sup>-5</sup>	9.614797	Mitogen-activated protein kinase 10 (Mapk10)
Hk1	0.38	.000610531	7.307773	Hexokinase 1 (Hk1)
Got2	0.38	.000354889	7.489109	Glutamatic-oxaloacetic transaminase 2, mitochondrial (Got2)
Arhgap24	0.38	.004226451	6.295242	Rho GTPase activating protein 24 (Arhgap24)
Rbbp5	0.38	.007852118	6.166738	Retinoblastoma binding protein 5 (Rbbp5)
Lhx9	0.38	.00028176	7.483671	LIM homeobox protein 9 (Lhx9)
Dmtn	0.38	.002856573	7.274989	Dematin actin binding protein (Dmtn)
Clock	0.38	.001963162	7.820407	Circadian locomotor output cycles kaput (Clock)
Zfp109	0.38	.030357657	3.611124	Zinc finger protein 109 (Zfp109)
Tmem170b	0.38	.002222102	8.175563	Transmembrane protein 170B (Tmem170b)
Rangap1	0.38	.002197729	7.567514	RAN GTPase activating protein 1 (Rangap1)
Tm9sf4	0.38	.002605991	6.197603	Transmembrane 9 superfamily protein member 4 (Tm9sf4)
Cln	0.38	.017619173	4.643581	Calmegin (Cln)
Prmt6	0.38	.011239814	4.57337	Protein arginine N-methyltransferase 6 (Prmt6)
Ctps2	0.38	.009659835	6.147911	Cytidine 5'-triphosphate synthase 2 (Ctps2)
Naa60	0.38	.002785319	5.275267	N(alpha)-acetyltransferase 60, NatF catalytic subunit (Naa60)
Champ1	0.38	.003714132	5.522917	Chromosome alignment maintaining phosphoprotein 1 (Champ1)
Kcnk3	0.38	.01641655	5.688003	Potassium channel, subfamily K, member 3 (Kcnk3)
Purg	0.37	.017095265	5.384766	Purine-rich element binding protein G (Purg)
Clpb	0.37	.006435035	5.644833	ClpB caseinolytic peptidase B (Clpb)
Hlf	0.37	.000844806	8.947513	Hepatic leukemia factor (Hlf)
Smim13	0.37	.000295715	8.416634	Small integral membrane protein 13 (Smim13)
Pgam1	0.37	.015322053	4.47991	Phosphoglycerate mutase 1 (Pgam1)
Fam20a	0.37	.007275208	4.83608	Family with sequence similarity 20, member A (Fam20a)
Rbbp7	0.37	.000619461	6.459454	Retinoblastoma binding protein 7 (Rbbp7)
Cops2	0.37	.000177307	7.480547	COP9 signalosome subunit 2 (Cops2)
Ndrg3	0.37	.000150313	8.932865	N-myc downstream-regulated gene 3 (Ndrg3)
Ccny	0.37	.001709309	6.825673	Cyclin Y (Ccny)
Usp31	0.37	.000519326	8.100655	Ubiquitin-specific peptidase 31 (Usp31)
Gm5113	0.37	.015710461	5.261749	Predicted gene 5113 (Gm5113)
Sncb	0.37	.011230492	6.455265	Synuclein, beta (Sncb)
Celf5	0.37	.000784094	7.329359	CUGBP, Elav-like family member 5 (Celf5)
Klhl9	0.37	.002972648	7.226019	Kelch-like 9 (Klhl9)
Stum	0.37	.000186276	9.800934	Mechanosensory transduction mediator (Stum)
Slc4a10	0.37	.000637681	7.913263	Solute carrier family 4, sodium bicarbonate cotransporter-like, member 10 (Slc4a10)
Nefl	0.37	.000108876	8.424022	Neurofilament, light polypeptide (Nefl)
Atp1a3	0.37	.000129197	11.54334	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 3 polypeptide (Atp1a3)
Ppp1r7	0.37	.000212799	7.593926	Protein phosphatase 1, regulatory (inhibitor) subunit 7 (Ppp1r7)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Dis3l2	0.37	.038658881	4.286777	DIS3 like 3'-5' exoribonuclease 2 (Dis3l2)
Faim2	0.37	.000526975	9.308829	Fas apoptotic inhibitory molecule 2 (Faim2)
2700062C07Rik	0.37	.018226696	4.197054	RIKEN cDNA 2700062C07 gene (2700062C07Rik)
Uqcrc1	0.37	.026044985	6.872075	Ubiquinol-cytochrome c reductase core protein 1 (Uqcrc1)
Rptor	0.37	.005245347	6.093816	Regulatory-associated protein of MTOR, complex 1 (Rptor)
Mgat5	0.37	.000198745	7.631562	Mannoside acetylglucosaminyltransferase 5 (Mgat5)
Ddx3y	0.37	.005570031	6.266427	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked (Ddx3y)
Steap2	0.37	.002939966	5.887588	Six transmembrane epithelial antigen of prostate 2 (Steap2)
Sorcs1	0.37	.013039048	4.67083	Sortilin-related VPS10 domain containing receptor 1 (Sorcs1)
Clstn2	0.37	.003492165	6.971484	Calsyntenin 2 (Clstn2)
Chst12	0.37	.042970443	3.689379	Carbohydrate sulfotransferase 12 (Chst12)
Gpr85	0.37	.00467955	5.307286	G protein-coupled receptor 85 (Gpr85)
Brsk2	0.37	.00245959	6.419603	BR serine/threonine kinase 2 (Brsk2)
Abhd8	0.37	.000467941	7.402932	Abhydrolase domain containing 8 (Abhd8)
Osbpl2	0.37	.000666754	6.593087	Oxysterol binding protein-like 2 (Osbpl2)
Parp11	0.37	.039739777	4.58598	Poly(ADP-ribose) polymerase family, member 11 (Parp11)
Ahdc1	0.37	.011583164	5.721648	AT hook, DNA binding motif, containing 1 (Ahdc1)
Eif5a2	0.37	.001051251	6.930435	Eukaryotic translation initiation factor 5A2 (Eif5a2)
Vdac1	0.37	.000183049	8.321191	Voltage-dependent anion channel 1 (Vdac1)
Ywhah	0.37	.008124275	9.471084	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah)
Fam8a1	0.37	.000330962	8.143484	Family with sequence similarity 8, member A1 (Fam8a1)
Rnf24	0.37	.002093535	6.28988	Ring finger protein 24 (Rnf24)
Ica1l	0.37	.002067599	6.191748	Islet cell autoantigen 1-like (Ica1l)
Smim10l1	0.37	.008963428	7.368187	Small integral membrane protein 10 like 1 (Smim10l1)
Ywhag	0.37	.000165368	10.64164	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (Ywhag)
Ids	0.37	.000197296	10.11878	Iduronate 2-sulfatase (Ids)
Ddhd2	0.37	.002750408	6.097995	DDHD domain containing 2 (Ddhd2)
Ppp2r2a	0.37	.000322361	7.217106	Protein phosphatase 2, regulatory subunit B, alpha (Ppp2r2a)
Mmab	0.37	.005781317	5.425931	Methylmalonic aciduria (cobalamin deficiency) cbfB type homolog (human) (Mmab)
Mga	0.37	.005957175	7.557385	MAX gene associated (Mga)
Epm2aip1	0.37	.000309174	8.509031	EPM2A (laforin) interacting protein 1 (Epm2aip1)
Wdtc1	0.37	.005453244	6.403556	WD and tetratricopeptide repeats 1 (Wdtc1)
Pik3r4	0.37	.006779461	5.083617	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150 (Pik3r4)
Rraga	0.37	.004618014	6.479664	Ras-related GTP binding A (Rraga)
Cry2	0.37	.000495163	7.474626	Cryptochrome 2 (photolyase-like) (Cry2)
Crkl	0.37	.000739731	6.409162	V-crk avian sarcoma virus CT10 oncogene homolog-like (Crkl)
Rbbp4	0.37	.002858818	5.332119	Retinoblastoma binding protein 4 (Rbbp4)
H2-T24	0.37	.03030658	4.232162	Histocompatibility 2, T region locus 24 (H2-T24)
Rae1	0.37	.028603764	4.660956	Ribonucleic acid export 1 (Rae1)
Dr1	0.37	.00455895	5.340356	Downregulator of transcription 1 (Dr1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Eid1	0.37	.000606027	7.906883	EP300 interacting inhibitor of differentiation 1 (Eid1)
GlcE	0.37	.004670094	7.095472	Glucuronyl C5-epimerase (GlcE)
Dcx	0.37	.025600204	5.942022	Doublecortin (Dcx)
Pum2	0.37	.002551954	8.358474	Pumilio RNA-binding family member 2 (Pum2)
Exosc9	0.37	.018073043	4.136168	Exosome component 9 (Exosc9)
Klh23	0.37	.011993127	5.15791	Kelch-like 23 (Klh23)
Chpf	0.37	.008550744	5.334079	Chondroitin polymerizing factor (Chpf)
Elavl4	0.37	.001681934	7.315395	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) (Elavl4)
Ak4	0.37	.004799863	5.128456	Adenylate kinase 4 (Ak4)
Tmem245	0.37	.001133361	7.548487	Transmembrane protein 245 (Tmem245)
Sema4g	0.37	.002817336	5.974901	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (Sema4g)
Sprn	0.37	.000699007	6.782088	Shadow of prion protein (Sprn)
Ip6k1	0.37	.002202281	6.88511	Inositol hexaphosphate kinase 1 (Ip6k1)
Tmem127	0.37	.000607923	7.665402	Transmembrane protein 127 (Tmem127)
Nlgn3	0.37	.001563872	7.317001	Neuroligin 3 (Nlgn3)
Tacc2	0.37	.014831292	6.090831	Transforming, acidic coiled-coil containing protein 2 (Tacc2)
Ogfr1	0.37	.000303058	8.901961	Opioid growth factor receptor-like 1 (Ogfr1)
Usp37	0.37	.01135863	5.641885	Ubiquitin-specific peptidase 37 (Usp37)
Elmo1	0.37	.000629586	8.313981	Engulfment and cell motility 1 (Elmo1)
Kcnd2	0.37	.001016395	8.067926	Potassium voltage-gated channel, Shal-related family, member 2 (Kcnd2)
Men1	0.37	.006743078	5.461226	Multiple endocrine neoplasia 1 (Men1)
Dync1li1	0.37	.011800881	6.866456	Dynein cytoplasmic 1 light intermediate chain 1 (Dync1li1)
Stx1b	0.36	.000209778	8.846847	Syntaxin 1B (Stx1b)
Usp12	0.36	.004189515	5.433712	Ubiquitin-specific peptidase 12 (Usp12)
Rab16	0.36	.002516156	6.791307	RAB, member RAS oncogene family-like 6 (Rab16)
Mllt11	0.36	.000637693	8.503762	Myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11 (Mllt11)
Atg5	0.36	.012345737	4.68906	Autophagy related 5 (Atg5)
Lrrc49	0.36	.006761116	5.269223	Leucine-rich repeat containing 49 (Lrrc49)
Pcm1	0.36	.000878934	8.166669	Pericentriolar material 1 (Pcm1)
Fbxo25	0.36	.020892819	5.46722	F-box protein 25 (Fbxo25)
Cnot11	0.36	.01402629	4.632022	CCR4-NOT transcription complex, subunit 11 (Cnot11)
Stau1	0.36	.00169732	6.405388	Stau1 (RNA binding protein) homolog 1 (Stau1)
Pdk3	0.36	.009445138	4.820113	Pyruvate dehydrogenase kinase, isoenzyme 3 (Pdk3)
Sfxn3	0.36	.003272337	7.142365	Sideroflexin 3 (Sfxn3)
Fam222b	0.36	.002547353	7.046005	Family with sequence similarity 222, member B (Fam222b)
App	0.36	$7.56 \times 10^{-5}$	10.24304	Amyloid beta (A4) precursor protein (App)
Megf9	0.36	.000969837	8.415736	Multiple EGF-like-domains 9 (Megf9)
Fam69a	0.36	.015534765	4.997594	Family with sequence similarity 69, member A (Fam69a)
Ate1	0.36	.003536161	6.666896	Arginyltransferase 1 (Ate1)
Gga3	0.36	.007685283	5.417507	Golgi-associated, gamma adaptin ear containing, ARF binding protein 3 (Gga3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Kcn3	0.36	.004115371	7.710207	Potassium voltage-gated channel, Shal-related family, member 3 (Kcn3)
Dnajb14	0.36	.001520373	8.084609	DnaJ heat shock protein family (Hsp40) member B14 (Dnajb14)
Crbn	0.36	.003478127	5.701735	Cereblon (Crbn)
Appbp2	0.36	.001689861	7.608243	Amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (Appbp2)
Vps36	0.36	.02901795	4.81758	Vacuolar protein sorting 36 (Vps36)
Ubald1	0.36	.008735797	5.582003	UBA-like domain containing 1 (Ubald1)
Iffo2	0.36	.029431927	4.598901	Intermediate filament family orphan 2 (Iffo2)
Otud5	0.36	.002405336	6.291592	OTU domain containing 5 (Otud5)
Neurl1b	0.36	.006704587	5.27958	Neuralized E3 ubiquitin protein ligase 1B (Neurl1b)
Wdr18	0.36	.005753898	5.167957	WD repeat domain 18 (Wdr18)
Lrrc61	0.36	.006704746	5.612023	Leucine-rich repeat containing 61 (Lrrc61)
Chrm3	0.36	.028420636	4.549551	Cholinergic receptor, muscarinic 3, cardiac (Chrm3)
Zic5	0.36	.00348391	6.362145	Zinc finger protein of the cerebellum 5 (Zic5)
Rab14	0.36	.000361613	8.314045	RAB14, member RAS oncogene family (Rab14)
Ppa1	0.36	.035547244	5.940441	Pyrophosphatase (inorganic) 1 (Ppa1)
Pdkp1	0.36	.004301064	8.241213	3-Phosphoinositide dependent protein kinase 1 (Pdkp1)
Deaf1	0.36	.001209867	6.969719	Deformed epidermal autoregulatory factor 1 (Deaf1)
Glrb	0.36	.00294086	7.400061	Glycine receptor, beta subunit (Glrb)
Klf6	0.36	.00064147	7.025194	Kruppel-like factor 6 (Klf6)
Sssc1	0.36	.029796566	4.26011	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human) (Sssc1)
Lrp11	0.36	.000530053	6.986426	Low-density lipoprotein receptor-related protein 11 (Lrp11)
Pptrs	0.36	.000325877	8.438693	Protein tyrosine phosphatase, receptor type, S (Pptrs)
Rab40b	0.36	.046849681	3.788966	Rab40B, member RAS oncogene family (Rab40b)
Fig4	0.36	.009168298	4.493732	FIG4 phosphoinositide 5-phosphatase (Fig4)
Mpp2	0.36	.003387279	6.627087	Membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) (Mpp2)
Dcun1d1	0.36	.004030992	5.655104	DCN1, defective in cullin neddylation 1, domain containing 1 ( <i>S. cerevisiae</i> ) (Dcun1d1)
Hectd1	0.36	.001603387	7.408835	HECT domain containing 1 (Hectd1)
Dnajc16	0.36	.002681468	5.506702	DnaJ heat shock protein family (Hsp40) member C16 (Dnajc16)
Caprin1	0.36	.000383762	8.711232	Cell cycle-associated protein 1 (Caprin1)
Lsm11	0.36	.007768519	5.490697	U7 snRNP-specific Sm-like protein LSM11 (Lsm11)
Abi2	0.36	.001154546	8.384549	abl-interactor 2 (Abi2)
Slc25a12	0.36	.000233834	7.943166	Solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (Slc25a12)
Dennd5b	0.36	.001489016	6.665903	DENN/MADD domain containing 5B (Dennd5b)
Kbtbd2	0.36	.001555751	6.334365	Kelch repeat and BTB (POZ) domain containing 2 (Kbtbd2)
Gpr26	0.36	.049187748	7.76117	G protein-coupled receptor 26 (Gpr26)
Gsk3b	0.36	.000100955	9.72979	Glycogen synthase kinase 3 beta (Gsk3b)
Adra1b	0.36	.036121091	5.146998	Adrenergic receptor, alpha 1b (Adra1b)
Oprl1	0.36	.016613076	5.607268	Opioid receptor-like 1 (Oprl1)
Dcaf6	0.36	.001209176	6.229638	DDB1 and CUL4-associated factor 6 (Dcaf6)
Sbno1	0.36	.000634172	8.159213	Strawberry notch homolog 1 (Sbno1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Dkk3	0.36	.013442886	5.382548	Dickkopf WNT signaling pathway inhibitor 3 (Dkk3)
Ppp3r1	0.36	.000352905	8.261941	Protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I) (Ppp3r1)
Gpr75	0.36	.033163217	4.898318	G protein-coupled receptor 75 (Gpr75)
Fam53c	0.36	.000627708	7.305789	Family with sequence similarity 53, member C (Fam53c)
Rtn4r	0.36	.012506108	5.100161	Reticulon 4 receptor (Rtn4r)
2810021J22Rik	0.36	.047201391	4.040623	RIKEN cDNA 2810021J22 gene (2810021J22Rik)
Efr3b	0.36	.000464102	7.62011	EFR3 homolog B (Efr3b)
Polr3a	0.36	.014991223	4.489951	Polymerase (RNA) III (DNA directed) polypeptide A (Polr3a)
Noa1	0.36	.017237481	5.179052	Nitric oxide associated 1 (Noa1)
Dync1i1	0.36	.014327052	5.348554	Dynein cytoplasmic 1 intermediate chain 1 (Dync1i1)
Acp2	0.36	.001855749	7.02571	Acid phosphatase 2, lysosomal (Acp2)
Zfp281	0.36	.004640413	5.699421	Zinc finger protein 281 (Zfp281)
Rasa1	0.35	.002174483	6.21255	RAS p21 protein activator 1 (Rasa1)
Irs2	0.35	.001560274	7.023199	Insulin receptor substrate 2 (Irs2)
Csde1	0.35	.000138602	9.267221	Cold shock domain containing E1, RNA binding (Csde1)
BC037034	0.35	.014464768	5.150164	cDNA sequence BC037034 (BC037034)
Mink1	0.35	.004799863	5.554809	Missshapen-like kinase 1 (zebrafish) (Mink1)
Orc3	0.35	.00064538	6.705536	Origin recognition complex, subunit 3 (Orc3)
Mrgpre	0.35	.008130724	5.256879	MAS-related GPR, member E (Mrgpre)
Mmachc	0.35	.020957117	5.100531	Methylmalonic aciduria cblC type, with homocystinuria (Mmachc)
Igf2r	0.35	.007072378	5.608049	Insulin-like growth factor 2 receptor (Igf2r)
AW554918	0.35	.012739351	5.357931	Expressed sequence AW554918 (AW554918)
Vsnl1	0.35	.003786951	10.69616	Visinin-like 1 (Vsnl1)
Slc12a5	0.35	.000367124	8.967207	Solute carrier family 12, member 5 (Slc12a5)
Gm14295	0.35	.022261006	4.4088	Predicted gene 14295 (Gm14295)
Scyl1	0.35	.010993944	5.035249	SCY1-like 1 ( <i>S. cerevisiae</i> ) (Scyl1)
Kif5c	0.35	$5.71 \times 10^{-5}$	9.497055	Kinesin family member 5C (Kif5c)
Cyp46a1	0.35	.00624965	7.009203	Cytochrome P450, family 46, subfamily a, polypeptide 1 (Cyp46a1)
Nedd4l	0.35	.000390244	8.108562	Neural precursor cell expressed, developmentally down-regulated gene 4-like (Nedd4l)
Snx30	0.35	.005884773	6.228242	Sorting nexin family member 30 (Snx30)
Upst	0.35	.033051412	5.006643	Uracil phosphoribosyltransferase (Upst)
Eif1ax	0.35	.000445992	8.322756	Eukaryotic translation initiation factor 1A, X-linked (Eif1ax)
Grin2a	0.35	.000535846	8.14468	Glutamate receptor, ionotropic, NMDA2A (epsilon 1) (Grin2a)
Napepld	0.35	.015381659	6.692038	N-acyl phosphatidylethanolamine phospholipase D (Napepld)
Peak1	0.35	.004526907	6.859878	Pseudopodium-enriched atypical kinase 1 (Peak1)
B630019K06Rik	0.35	.00830029	5.255739	Novel protein similar to F-box and leucine-rich repeat protein 17 (Fbxl17) (B630019K06Rik)
Cul7	0.35	.027246122	4.327029	Cullin 7 (Cul7)
Armcx5	0.35	.025997015	4.702874	Armadillo repeat containing, X-linked 5 (Armcx5)
Rims3	0.35	.00125375	8.297773	Regulating synaptic membrane exocytosis 3 (Rims3)
Purb	0.35	.002165084	9.947348	Purine-rich element binding protein B (Purb)
Gad2	0.35	.026477297	7.019773	Glutamic acid decarboxylase 2 (Gad2)
Zfp866	0.35	.017206437	4.774467	Zinc finger protein 866 (Zfp866)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tmem8	0.35	.038871651	3.854879	Transmembrane protein 8 (five membrane-spanning domains) (Tmem8)
Mtrr	0.35	.037465993	3.728381	5-Methyltetrahydrofolate-homocysteine methyltransferase reductase (Mtrr)
Mast2	0.35	.001456677	7.084286	Microtubule-associated serine/threonine kinase 2 (Mast2)
Ppip5k1	0.35	.002067599	6.439583	Diphosphoinositol pentakisphosphate kinase 1 (Ppip5k1)
Gm26782	0.35	.022005703	4.916513	Predicted gene, 26782 (Gm26782)
Mgat3	0.35	.000448907	7.131476	Mannoside acetylglucosaminyltransferase 3 (Mgat3)
Mest	0.35	.002516156	6.321029	Mesoderm-specific transcript (Mest)
Fam117b	0.35	.002091306	6.894619	Family with sequence similarity 117, member B (Fam117b)
Slmap	0.35	.000350171	7.494475	Sarcolemma-associated protein (Slmap)
Srp72	0.35	.001234869	7.367705	Signal recognition particle 72 (Srp72)
Dgki	0.35	.004879997	5.554104	Diacylglycerol kinase, iota (Dgki)
Ranbp2	0.35	.003706567	7.174896	RAN binding protein 2 (Ranbp2)
Nr1d1	0.35	.00269514	7.264514	Nuclear receptor subfamily 1, group D, member 1 (Nr1d1)
Bace1	0.35	.001931456	6.638903	Beta-site APP cleaving enzyme 1 (Bace1)
Tef	0.35	.001531814	6.964537	Thyrotroph embryonic factor (Tef)
Pcdh11x	0.35	.037129423	5.622228	Protocadherin 11 X-linked (Pcdh11x)
Mpp5	0.35	.004526907	7.03449	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) (Mpp5)
Zfp790	0.35	.019962109	4.442604	Zinc finger protein 790 (Zfp790)
Meaf6	0.35	.001584324	7.044282	MYST/Esa1-associated factor 6 (Meaf6)
Uxs1	0.35	.04098874	3.926531	UDP-glucuronate decarboxylase 1 (Uxs1)
Zfp451	0.35	.010223951	7.301546	Zinc finger protein 451 (Zfp451)
Zfp780b	0.35	.010759339	4.865991	Zinc finger protein 780B (Zfp780b)
Nup88	0.35	.001495063	6.336652	Nucleoporin 88 (Nup88)
Osbp2	0.35	.006245947	5.503138	Oxysterol binding protein 2 (Osbp2)
Sybu	0.35	.002090998	6.064859	Syntabulin (syntaxin-interacting) (Sybu)
Chst11	0.35	.003452337	6.710195	Carbohydrate sulfotransferase 11 (Chst11)
Usp15	0.35	.000743316	7.027629	Ubiquitin-specific peptidase 15 (Usp15)
Phf24	0.35	.003557218	7.746974	PHD finger protein 24 (Phf24)
Ap1s2	0.35	.011651497	5.580224	Adaptor-related protein complex 1, sigma 2 subunit (Ap1s2)
Zfp644	0.35	.008016303	8.429209	Zinc finger protein 644 (Zfp644)
Eif4b	0.35	.000404679	8.088581	Eukaryotic translation initiation factor 4B (Eif4b)
6030458C11Rik	0.35	.02307615	5.189214	RIKEN cDNA 6030458C11 gene (6030458C11Rik)
Klhl42	0.35	.03248473	5.526105	Kelch-like 42 (Klhl42)
Opa1	0.35	.000247428	7.97903	Optic atrophy 1 (Opa1)
Samm50	0.35	.003726249	6.378779	SAMM50 sorting and assembly machinery component (Samm50)
Kcnt2	0.35	.013875706	5.158658	Potassium channel, subfamily T, member 2 (Kcnt2)
Fip1l1	0.35	.004182573	6.405926	FIP1 like 1 ( <i>S. cerevisiae</i> ) (Fip1l1)
Lnpk	0.35	.00367203	5.511197	Lunapark, ER Junction Formation Factor (Lnpk)
Med16	0.35	.011660604	5.33717	Mediator complex subunit 16 (Med16)
Camk2a	0.35	.00066288	9.476952	Calcium/calmodulin-dependent protein kinase II alpha (Camk2a)
Usp14	0.35	.001235525	7.172434	Ubiquitin-specific peptidase 14 (Usp14)
Fbxo31	0.35	.007276141	5.362865	F-box protein 31 (Fbxo31)
Ccdc71l	0.35	.049471758	4.300721	Coiled-coil domain containing 71 like (Ccdc71l)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rnf41	0.35	.005056229	5.803367	Ring finger protein 41 (Rnf41)
Hnrnpul1	0.35	.001545653	7.162949	Heterogeneous nuclear ribonucleoprotein U-like 1 (Hnrnpul1)
Prrc1	0.35	.017996957	4.97921	Proline-rich coiled-coil 1 (Prrc1)
Gpbp1	0.35	.000567921	7.093257	GC-rich promoter binding protein 1 (Gpbp1)
Dnajc10	0.35	.004662883	6.829364	DnaJ heat shock protein family (Hsp40) member C10 (Dnajc10)
Ss18l1	0.35	.000826034	6.998793	Synovial sarcoma translocation gene on chromosome 18-like 1 (Ss18l1)
Zfp60	0.35	.012140696	6.131928	Zinc finger protein 60 (Zfp60)
Ttc9	0.35	.003342827	6.508368	Tetratricopeptide repeat domain 9 (Ttc9)
Mbtps2	0.35	.015921625	5.1381	Membrane-bound transcription factor peptidase, site 2 (Mbtps2)
Rgs20	0.35	.026738436	5.053718	Regulator of G-protein signaling 20 (Rgs20)
Zfp629	0.35	.015385824	4.769682	Zinc finger protein 629 (Zfp629)
Slc30a9	0.35	.000345572	7.962516	Solute carrier family 30 (zinc transporter), member 9 (Slc30a9)
Phlpp2	0.35	.005273465	5.998871	PH domain and leucine-rich repeat protein phosphatase 2 (Phlpp2)
Pigk	0.34	.003739687	6.748365	Phosphatidylinositol glycan anchor biosynthesis, class K (Pigk)
Prkci	0.34	.006364795	6.450559	Protein kinase C, iota (Prkci)
Smarcal1	0.34	.002670409	6.052173	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily a-like 1 (Smarcal1)
Ptprg	0.34	.004228954	7.032648	Protein tyrosine phosphatase, receptor type, G (Ptprg)
Map2k1	0.34	.000533592	7.49615	Mitogen-activated protein kinase kinase 1 (Map2k1)
Ddi2	0.34	.02296658	5.655336	DNA-damage inducible protein 2 (Ddi2)
Dnaja3	0.34	.004754794	5.775977	DnaJ heat shock protein family (Hsp40) member A3 (Dnaja3)
Fam120c	0.34	.001400225	6.373015	Family with sequence similarity 120, member C (Fam120c)
Lrrc20	0.34	.005683854	5.101476	Leucine-rich repeat containing 20 (Lrrc20)
Igfsf21	0.34	.007778585	5.395362	Immunoglobulin superfamily, member 21 (Igfsf21)
Arvcf	0.34	.013129488	4.826695	Armadillo repeat gene deleted in velo-cardio-facial syndrome (Arvcf)
Erlec1	0.34	.007731433	5.539583	Endoplasmic reticulum lectin 1 (Erlec1)
Epha6	0.34	.008720223	5.627232	Eph receptor A6 (Epha6)
Carf	0.34	.023411535	5.042398	Calcium response factor (Carf)
Npas2	0.34	.017708814	5.393393	Neuronal PAS domain protein 2 (Npas2)
Kdm4a	0.34	.045685535	3.874372	Lysine (K)-specific demethylase 4A (Kdm4a)
Wwp1	0.34	.007362769	7.188323	WW domain containing E3 ubiquitin protein ligase 1 (Wwp1)
Dpp10	0.34	.000475613	8.008104	Dipeptidylpeptidase 10 (Dpp10)
Medag	0.34	.047961055	4.563169	Mesenteric estrogen dependent adipogenesis (Medag)
Stat5b	0.34	.015701214	4.762782	Signal transducer and activator of transcription 5B (Stat5b)
Dyrk1a	0.34	.001646502	7.123454	Dual-specificity tyrosine-(Y)-phosphorylation-regulated kinase 1a (Dyrk1a)
Arhgef3	0.34	.020470938	5.142464	Rho guanine nucleotide exchange factor (GEF) 3 (Arhgef3)
Ap3d1	0.34	.004866842	7.302974	Adaptor-related protein complex 3, delta 1 subunit (Ap3d1)
Jmjd4	0.34	.012709877	5.085019	Jumonji domain containing 4 (Jmjd4)
Prr14l	0.34	.003288547	7.568868	Proline rich 14-like (Prr14l)
Lrrn3	0.34	.001717986	7.112464	Leucine-rich repeat protein 3, neuronal (Lrrn3)
Epc2	0.34	.006250277	6.016396	Enhancer of polycomb homolog 2 (Epc2)
Hectd3	0.34	.025050269	5.213093	HECT domain containing 3 (Hectd3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lemd3	0.34	.010790798	5.150001	LEM domain containing 3 (Lemd3)
F8a	0.34	.048159565	3.890194	Factor 8-associated gene A (F8a)
Zfp667	0.34	.028936172	4.993482	Zinc finger protein 667 (Zfp667)
Ncam1	0.34	.000282765	8.827575	Neural cell adhesion molecule 1 (Ncam1)
C2cd2	0.34	.02152809	4.716592	C2 calcium-dependent domain containing 2 (C2cd2)
Zfp84	0.34	.03480973	4.893699	Zinc finger protein 84 (Zfp84)
Rai1	0.34	.004202566	6.289163	Retinoic acid induced 1 (Rai1)
Bcl2l13	0.34	.015332036	5.388948	BCL2-like 13 (apoptosis facilitator) (Bcl2l13)
Man2a1	0.34	.020476299	5.009561	Mannosidase 2, alpha 1 (Man2a1)
Farsb	0.34	.01056694	6.614422	Phenylalanyl-tRNA synthetase, beta subunit (Farsb)
Rasal2	0.34	.004753754	7.636933	RAS protein activator like 2 (Rasal2)
Slx4	0.34	.01565113	5.064388	SLX4 structure-specific endonuclease subunit homolog ( <i>S. cerevisiae</i> ) (Slx4)
Prkcz	0.34	.001586312	6.727901	Protein kinase C, zeta (Prkcz)
Haus2	0.34	.034814818	5.653202	HAUS augmin-like complex, subunit 2 (Haus2)
Lrp12	0.34	.014794905	5.024759	Low-density lipoprotein-related protein 12 (Lrp12)
Fam81a	0.34	.018482899	6.73415	Family with sequence similarity 81, member A (Fam81a)
Nrxn3	0.34	.004473838	7.946289	Neurexin III (Nrxn3)
Rbfox2	0.34	.005031819	7.904836	RNA binding protein, fox-1 homolog ( <i>C. elegans</i> ) 2 (Rbfox2)
Stambpl1	0.34	.044931661	4.372332	STAM binding protein like 1 (Stambpl1)
Fytd1	0.34	.000726232	7.175533	Forty-two-three domain containing 1 (Fytd1)
Rab11fip2	0.34	.002596521	6.519804	RAB11 family interacting protein 2 (class I) (Rab11fip2)
Tpp2	0.34	.002555745	6.299213	Tripeptidyl peptidase II (Tpp2)
Ap5m1	0.34	.036991553	4.659891	Adaptor-related protein complex 5, mu 1 subunit (Ap5m1)
Erlin2	0.34	.011668467	6.576248	ER lipid raft associated 2 (Erlin2)
Frmd5	0.34	.001487578	6.185836	FERM domain containing 5 (Frmd5)
Atxn1l	0.34	.026490141	5.92882	Ataxin 1-like (Atxn1l)
Miga1	0.34	.000987507	7.157113	Mitoguardin 1 (Miga1)
Asb8	0.34	.001524515	6.515174	Ankyrin repeat and SOCS box-containing 8 (Azb8)
Inpp4b	0.34	.004101439	6.219087	Inositol polyphosphate-4-phosphatase, type II (Inpp4b)
Spty2d1	0.34	.017044137	4.820448	SPT2, suppressor of Ty, domain containing 1 ( <i>S. cerevisiae</i> ) (Spty2d1)
Tm9sf2	0.34	.001639272	7.045575	Transmembrane 9 superfamily member 2 (Tm9sf2)
Zfp654	0.34	.018785801	5.767026	Zinc finger protein 654 (Zfp654)
Fam160a2	0.34	.001704302	6.573145	Family with sequence similarity 160, member A2 (Fam160a2)
Gm42372	0.34	.000591057	8.531127	Predicted gene, 42372 (Gm42372)
Chrna4	0.34	.00563968	7.652275	Cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4)
Sord	0.34	.029577563	4.088055	Sorbitol dehydrogenase (Sord)
Ugcg	0.34	.005934095	7.607998	UDP-glucose ceramide glucosyltransferase (Ugcg)
Rab10	0.34	.00353918	8.154457	RAB10, member RAS oncogene family (Rab10)
Mamld1	0.34	.013147262	5.604974	Mastermind-like domain containing 1 (Mamld1)
Nop58	0.34	.00233082	6.121293	NOP58 ribonucleoprotein (Nop58)
Med14	0.33	.00112575	7.147221	Mediator complex subunit 14 (Med14)
Cbx4	0.33	.011660119	5.369991	Chromobox 4 (Cbx4)
Kctd6	0.33	.023496131	4.900962	Potassium channel tetramerisation domain containing 6 (Kctd6)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Cntn1	0.33	.00017015	9.192182	Contactin 1 (Cntn1)
Fam193a	0.33	.004910651	6.678828	Family with sequence similarity 193, member A (Fam193a)
Lrrc4	0.33	.025019331	5.037492	Leucine-rich repeat containing 4 (Lrrc4)
Hlrf	0.33	.01045281	5.725832	Helicase-like transcription factor (Hlrf)
Wipi2	0.33	.005595738	6.447216	WD repeat domain, phosphoinositide interacting 2 (Wipi2)
Ddx6	0.33	.000322361	7.896737	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (Ddx6)
Trnt1	0.33	.003830189	5.825732	tRNA nucleotidyl transferase, CCA-adding, 1 (Trnt1)
Prkar2b	0.33	.00483422	6.623862	Protein kinase, cAMP dependent regulatory, type II beta (Prkar2b)
Zfp87	0.33	.026828586	4.838732	Zinc finger protein 87 (Zfp87)
Hsp90aa1	0.33	.000156221	9.275057	Heat shock protein 90, alpha (cytosolic), class A member 1 (Hsp90aa1)
Prmt1	0.33	.016243093	6.019318	Protein arginine N-methyltransferase 1 (Prmt1)
Grina	0.33	.008200963	8.245842	Glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding) (Grina)
Coro7	0.33	.00348391	5.690426	Coronin 7 (Coro7)
Galnt17	0.33	.01578007	6.610709	Polypeptide N-Acetylgalactosaminyltransferase 17 (Galnt17)
Sec23b	0.33	.019353076	5.280737	SEC23 homolog B, COPII coat complex component (Sec23b)
Myl12b	0.33	.001676411	9.04496	Myosin, light chain 12B, regulatory (Myl12b)
Flii	0.33	.006552514	6.030941	Flightless I actin binding protein (Flii)
Kdm2a	0.33	.004985644	7.330772	Lysine (K)-specific demethylase 2A (Kdm2a)
PcdhgC3	0.33	.015642118	5.179142	Protocadherin gamma subfamily C, 3 (PcdhgC3)
Brinp2	0.33	.024170506	5.977563	Bone morphogenic protein/retinoic acid inducible neural-specific 2 (Brinp2)
Rtn1	0.33	.00026507	10.98937	Reticulon 1 (Rtn1)
Mfsd6	0.33	.000439239	8.081668	Major facilitator superfamily domain containing 6 (Mfsd6)
Tspyl4	0.33	.010235626	8.733701	TSPY-like 4 (Tspyl4)
Ehd3	0.33	.006728709	6.840027	EH-domain containing 3 (Ehd3)
Esf1	0.33	.007630661	6.057988	ESF1 nucleolar pre-rRNA processing protein homolog (Esf1)
Socs6	0.33	.014278487	5.36968	Suppressor of cytokine signaling 6 (Socs6)
Snrnd3	0.33	.006661183	5.515214	Small nuclear ribonucleoprotein D3 (Snrnd3)
Uspl1	0.33	.006212613	5.611587	Ubiquitin-specific peptidase like 1 (Uspl1)
Sucla2	0.33	.004765486	6.942959	Succinate-Coenzyme A ligase, ADP-forming, beta subunit (Sucla2)
Epc1	0.33	.015648949	6.171797	Enhancer of polycomb homolog 1 (Epc1)
Zfp518b	0.33	.031580102	5.032912	Zinc finger protein 518B (Zfp518b)
Epn1	0.33	.008889292	6.13718	Epsin 1 (Epn1)
Kcnq2	0.33	.000741401	8.180647	Potassium voltage-gated channel, subfamily Q, member 2 (Kcnq2)
Pde4dip	0.33	.000587231	7.709251	Phosphodiesterase 4D interacting protein (myomegalin) (Pde4dip)
Nemf	0.33	.000566443	7.084243	Nuclear export mediator factor (Nemf)
Rfesd	0.33	.02365158	4.431779	Rieske (Fe-S) domain containing (Rfesd)
Ctr9	0.33	.016267212	5.360286	CTR9 homolog, Paf1/RNA polymerase II complex component (Ctr9)
Erich3	0.33	.010059756	6.186032	Glutamate rich 3 (Erich3)
Nol11	0.33	.039601095	4.470355	Nucleolar protein 11 (Nol11)
Luc7l	0.33	.003598651	6.611896	Luc7-like (Luc7l)
Ikbkap	0.33	.008137022	5.910105	Inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated protein (Ikbkap)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pomgnt2	0.33	.008701524	5.764593	Protein O-linked mannose beta 1,4-N-acetylglucosaminyltransferase 2 (Pomgnt2)
Ttll7	0.33	.000351859	8.940802	Tubulin tyrosine ligase-like family, member 7 (Ttll7)
Bhlhb9	0.33	.009885437	5.921434	Basic helix-loop-helix domain containing, class B9 (Bhlhb9)
Hdac11	0.33	.001738021	6.903218	Histone deacetylase 11 (Hdac11)
Timp3	0.33	.001733317	8.771546	Tissue inhibitor of metalloproteinase 3 (Timp3)
Arf1	0.33	.000802733	9.032354	ADP-ribosylation factor 1 (Arf1)
Zdhhc5	0.33	.005988349	6.36382	Zinc finger, DHHC domain containing 5 (Zdhhc5)
Gm12258	0.33	.033098326	4.746801	Predicted gene 12258 (Gm12258)
Shroom2	0.33	.008807928	5.608925	Shroom family member 2 (Shroom2)
Dnajb4	0.33	.001375265	7.110212	DnaJ heat shock protein family (Hsp40) member B4 (Dnajb4)
Foxo3	0.33	.002351931	7.01565	Forkhead box O3 (Foxo3)
Calb1	0.33	.042574984	7.81752	Calbindin 1 (Calb1)
Arl6ip5	0.33	.035189543	4.611752	ADP-ribosylation factor-like 6 interacting protein 5 (Arl6ip5)
Rnf6	0.33	.001796092	6.469322	Ring finger protein (C3H2C3 type) 6 (Rnf6)
Phf10	0.33	.006902625	6.114015	PHD finger protein 10 (Phf10)
Cggbp1	0.33	.003998385	6.59638	CGG triplet repeat binding protein 1 (Cggbp1)
Ilf3	0.33	.001568776	6.371511	Interleukin enhancer binding factor 3 (Ilf3)
Rspry1	0.33	.016708794	5.278227	Ring finger and SPRY domain containing 1 (Rspry1)
Supt16	0.33	.006758474	6.546343	Suppressor of Ty 16 (Supt16)
Smarcd1	0.33	.014907092	6.704273	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily d, member 1 (Smarcd1)
Pnck	0.33	.023023329	6.194498	Pregnancy upregulated nonubiquitously expressed CaM kinase (Pnck)
Dgcr2	0.33	.01946328	5.476247	DiGeorge syndrome critical region gene 2 (Dgcr2)
Dgcr14	0.33	.037421706	4.155779	DiGeorge syndrome critical region gene 14 (Dgcr14)
Jmjdc1c	0.33	.002622684	7.624735	Jumonji domain containing 1C (Jmjdc1c)
Mgrn1	0.33	.00354282	7.099806	Mahogunin, ring finger 1 (Mgrn1)
Ndrg4	0.33	.000922193	11.09989	N-myc downstream-regulated gene 4 (Ndrg4)
Cfap97	0.33	.026998457	6.056315	Cilia and flagella-associated protein 97 (Cfap97)
Mapre2	0.33	.00020497	9.287042	Microtubule-associated protein, RP/EB family, member 2 (Mapre2)
Tubb2b	0.33	.022470818	4.424611	Tubulin, beta 2B class IIB (Tubb2b)
Trappc11	0.33	.006032777	6.164346	Trafficking protein particle complex 11 (Trappc11)
Agfg1	0.33	.00108783	7.991137	ArfGAP with FG repeats 1 (Agfg1)
Sdha	0.33	.000377936	8.865626	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (Sdha)
Inpp5a	0.33	.034494563	6.081011	Inositol polyphosphate-5-phosphatase A (Inpp5a)
Ppp2r2c	0.33	.000385061	8.515515	Protein phosphatase 2, regulatory subunit B, gamma (Ppp2r2c)
Polr2m	0.33	.001098437	8.137719	Polymerase (RNA) II (DNA directed) polypeptide M (Polr2m)
Phf12	0.33	.008427111	6.221092	PHD finger protein 12 (Phf12)
Rfx7	0.33	.00738221	7.382932	regulatory factor X, 7 (Rfx7)
Lmbrd2	0.32	.00130007	7.685183	LMBR1 domain containing 2 (Lmbrd2)
Hivep1	0.32	.000941412	8.252872	Human immunodeficiency virus type I enhancer binding protein 1 (Hivep1)
Mcpf1	0.32	.018497358	5.327229	Microcephaly, primary autosomal recessive 1 (Mcpf1)
Ice1	0.32	.001811992	6.869076	Interactor of little elongation complex ELL subunit 1 (Ice1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pum1	0.32	.001006636	7.046814	Pumilio RNA-binding family member 1 (Pum1)
Plaa	0.32	.008016303	6.449628	Phospholipase A2, activating protein (Plaa)
Zbtb7a	0.32	.007137521	7.55393	Zinc finger and BTB domain containing 7a (Zbtb7a)
Kifap3	0.32	.00460339	8.275121	Kinesin-associated protein 3 (Kifap3)
Ddost	0.32	.035061841	5.636319	Dolichyl-di-phosphooligosaccharide-protein glycotransferase (Ddost)
Trim37	0.32	.000268967	8.749207	Tripartite motif-containing 37 (Trim37)
Tmtc3	0.32	.012432278	5.414971	Transmembrane and tetratricopeptide repeat containing 3 (Tmtc3)
Slc6a15	0.32	.019962109	5.215938	Solute carrier family 6 (neurotransmitter transporter), member 15 (Slc6a15)
Fh1	0.32	.007892335	5.960936	Fumarate hydratase 1 (Fh1)
Ap3b2	0.32	.003747685	6.379705	Adaptor-related protein complex 3, beta 2 subunit (Ap3b2)
Rab2a	0.32	.000220801	8.692405	RAB2A, member RAS oncogene family (Rab2a)
Zmym2	0.32	.000781794	7.389059	Zinc finger, MYM-type 2 (Zmym2)
Mettl6	0.32	.028282045	4.397911	Methyltransferase like 6 (Mettl6)
Cyld	0.32	.002588103	8.136469	CYLD lysine 63 deubiquitinase (Cyld)
Vps39	0.32	.006070659	6.397156	VPS39 HOPS complex subunit (Vps39)
Lemt1	0.32	.002099845	6.313361	Leucine zipper-EF-hand containing transmembrane protein 1 (Lemt1)
Vps41	0.32	.002305515	7.47014	VPS41 HOPS complex subunit (Vps41)
Syt1	0.32	.000233037	10.46581	Synaptotagmin I (Syt1)
Helz	0.32	.002424083	7.806308	Helicase with zinc finger domain (Helz)
Grik1	0.32	.039635346	4.347494	Glutamate receptor, ionotropic, kainate 1 (Grik1)
Calb2	0.32	.020979514	7.711593	Calbindin 2 (Calb2)
Mob4	0.32	.005884773	6.920589	MOB family member 4, phocean (Mob4)
Kat2a	0.32	.005806285	6.168165	K (lysine) acetyltransferase 2A (Kat2a)
Abraxas2	0.32	.028772191	4.868722	Abraxas 2, BRISC Complex Subunit (Abraxas2)
Wdr37	0.32	.003271495	7.170859	WD repeat domain 37 (Wdr37)
Cacna1c	0.32	.002438264	7.566329	Calcium channel, voltage-dependent, L type, alpha 1C subunit (CACNA1C)
Gorasp2	0.32	.008345638	6.585518	Golgi reassembly stacking protein 2 (Gorasp2)
Gm9899	0.32	.026732262	4.246155	Predicted gene 9899 (Gm9899)
Slc25a46	0.32	.002309226	7.633286	Solute carrier family 25, member 46 (Slc25a46)
Kcnk9	0.32	.032213555	5.7127	Potassium channel, subfamily K, member 9 (Kcnk9)
Zfp938	0.32	.02409866	4.562629	Zinc finger protein 938 (Zfp938)
B230219D22Rik	0.32	.00264211	7.500595	RIKEN cDNA B230219D22 gene (B230219D22Rik)
Prps1	0.32	.00613382	5.595308	Phosphoribosyl pyrophosphate synthetase 1 (Prps1)
Msl2	0.32	.004074863	6.103681	Male-specific lethal 2 homolog (Msl2)
Ccdc6	0.32	.005849225	6.834713	Coiled-coil domain containing 6 (Ccdc6)
Pigt	0.32	.003713324	6.847849	Phosphatidylinositol glycan anchor biosynthesis, class T (Pigt)
Mios	0.32	.016126436	4.817988	Missing oocyte, meiosis regulator, homolog (Mios)
Cdk5r1	0.32	.004189595	7.388953	Cyclin-dependent kinase 5, regulatory subunit 1 (p35) (Cdk5r1)
Phf1	0.32	.012419462	4.92529	PHD finger protein 1 (Phf1)
Kdm5a	0.32	.007484069	6.878055	Lysine (K)-specific demethylase 5A (Kdm5a)
Ano5	0.32	.031568417	5.225598	Anoctamin 5 (Ano5)
Tbc1d9	0.32	.004961467	6.083663	TBC1 domain family, member 9 (Tbc1d9)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Polr2a	0.32	.001285887	6.858149	Polymerase (RNA) II (DNA directed) polypeptide A (Polr2a)
Mtch1	0.32	.010792878	8.129323	Mitochondrial carrier 1 (Mtch1)
Stxbp5	0.32	.005598656	7.089531	Syntaxin binding protein 5 (tomasyn) (Stxbp5)
Mta1	0.32	.016658619	5.626356	Metastasis associated 1 (Mta1)
Fscn1	0.32	.008412892	6.441701	Fascin actin-bundling protein 1 (Fscn1)
Tmem185a	0.32	.013916409	5.548671	Transmembrane protein 185A (Tmem185a)
Lonp2	0.32	.002585912	6.490415	Lon peptidase 2, peroxisomal (Lonp2)
Spats2l	0.32	.023373455	4.698351	Spermatogenesis-associated, serine-rich 2-like (Spats2l)
Gm45884	0.32	.035687983	5.585962	Predicted gene (Gm45884)
Ints6	0.32	.02216801	5.225252	Integrator complex subunit 6 (Ints6)
Marchf5	0.32	.026796231	6.037629	Membrane-associated ring-CH-type finger 5 (Marchf5)
Cdc42se2	0.32	.003343593	6.869074	CDC42 small effector 2 (Cdc42se2)
Marchf7	0.32	.016904859	5.28631	Membrane-associated ring-CH-type finger 7 (Marchf7)
Zbtb4	0.32	.001664041	7.762387	Zinc finger and BTB domain containing 4 (Zbtb4)
Ppil4	0.32	.03994192	5.416502	Peptidylprolyl isomerase (cyclophilin)-like 4 (Ppil4)
Tcaim	0.32	.012509584	4.844963	T cell activation inhibitor, mitochondrial (Tcaim)
Zfp715	0.32	.035189543	4.903394	Zinc finger protein 715 (Zfp715)
Slc45a1	0.31	.029481696	5.392839	Solute carrier family 45, member 1 (Slc45a1)
Ctdspl2	0.31	.011236249	5.344075	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2 (Ctdspl2)
Morc2a	0.31	.004531884	5.964352	Microrchidia 2A (Morc2a)
Mtmr6	0.31	.002432771	6.86766	Myotubularin-related protein 6 (Mtmr6)
Fchsd2	0.31	.002446513	6.85829	FCH and double SH3 domains 2 (Fchsd2)
Gm10123	0.31	.040252636	4.665038	Peptidylprolyl isomerase A-like pseudogene (Gm10123)
Atg13	0.31	.005861533	6.686367	Autophagy related 13 (Atg13)
Camk2b	0.31	.00186315	8.900206	Calcium/calmodulin-dependent protein kinase II, beta (Camk2b)
Nsd3	0.31	.001306022	7.320374	Nuclear receptor binding SET domain protein 3 (Nsd3)
Terf2	0.31	.006573428	6.239424	Telomeric repeat binding factor 2 (Terf2)
Hs6st2	0.31	.018068654	5.488195	Heparan sulfate 6-O-sulfotransferase 2 (Hs6st2)
Zdhhc21	0.31	.004754794	6.810664	Zinc finger, DHHC domain containing 21 (Zdhhc21)
Azin1	0.31	.004681029	7.443452	Antizyme inhibitor 1 (Azin1)
Fat4	0.31	.042577732	4.108048	FAT atypical cadherin 4 (Fat4)
Hif1a	0.31	.003614196	6.506064	Hypoxia inducible factor 1, alpha subunit (Hif1a)
Edc4	0.31	.037971866	4.261783	Enhancer of mRNA decapping 4 (Edc4)
Xpot	0.31	.002550603	6.820754	Exportin, tRNA (nuclear export receptor for tRNAs) (Xpot)
Hspa12a	0.31	.001556569	8.314541	Heat shock protein 12A (Hspa12a)
Stk24	0.31	.002369586	6.349516	Serine/threonine kinase 24 (Stk24)
Zcchc14	0.31	.002366772	6.450568	Zinc finger, CCHC domain containing 14 (Zcchc14)
Rps6kb1	0.31	.009813086	5.978873	Ribosomal protein S6 kinase, polypeptide 1 (Rps6kb1)
Fbxo41	0.31	.011963025	5.644764	F-box protein 41 (Fbxo41)
Arcn1	0.31	.002195116	7.214013	Archain 1 (Arcn1)
Lztf1	0.31	.011037004	6.176956	Leucine zipper transcription factor-like 1 (Lztf1)
Cldn12	0.31	.010436237	6.715942	Claudin 12 (Cldn12)
Inpp5f	0.31	.011583164	8.00787	Inositol polyphosphate-5-phosphatase F (Inpp5f)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Syng	0.31	.002562882	7.223523	Synergin, gamma (Syng)
Tcf25	0.31	.000678736	9.466142	Transcription factor 25 (basic helix-loop-helix) (Tcf25)
Prdm11	0.31	.036363721	4.723243	PR domain containing 11 (Prdm11)
Senp6	0.31	.011496571	7.598651	SUMO/sentrin-specific peptidase 6 (Senp6)
Lpcat4	0.31	.033139201	6.572768	Lysophosphatidylcholine acyltransferase 4 (Lpcat4)
Slc23a2	0.31	.003391522	7.655895	Solute carrier family 23 (nucleobase transporters), member 2 (Slc23a2)
Jph3	0.31	.009833735	6.364034	Junctophilin 3 (Jph3)
Inpp4a	0.31	.001409669	7.790521	Inositol polyphosphate-4-phosphatase, type I (Inpp4a)
Foxk2	0.31	.002411011	6.765432	Forkhead box K2 (Foxk2)
Tunar	0.31	.009725869	7.166781	Tcl1 upstream neural differentiation-associated RNA (Tunar)
Ncdn	0.31	.019977453	9.538642	Neurochondrin (Ncdn)
Emd	0.31	.018784525	5.281802	Emerin (Emd)
Ttbk1	0.31	.017973161	7.24211	Tau tubulin kinase 1 (Ttbk1)
Zfp871	0.31	.031316414	7.774765	Zinc finger protein 871 (Zfp871)
Slc38a1	0.31	.001581298	8.903581	Solute carrier family 38, member 1 (Slc38a1)
Syt7	0.31	.000890892	8.877422	Synaptotagmin VII (Syt7)
Trak2	0.31	.003664544	6.994409	Trafficking protein, kinesin binding 2 (Trak2)
Cdc42bpa	0.31	.001672607	9.017793	CDC42 binding protein kinase alpha (Cdc42bpa)
Mbnl1	0.31	.004624647	7.850625	Muscleblind-like 1 (Mbnl1)
Syt11	0.31	.000170212	9.412666	Synaptotagmin XI (Syt11)
Zbtb44	0.31	.025748885	6.892859	Zinc finger and BTB domain containing 44 (Zbtb44)
Ppm1f	0.31	.041730143	5.221291	Protein phosphatase 1F (PP2C domain containing) (Ppm1f)
Rnf11	0.31	.002107953	7.184519	Ring finger protein 11 (Rnf11)
Slc22a17	0.31	.004355691	8.133587	Solute carrier family 22 (organic cation transporter), member 17 (Slc22a17)
Cacna1b	0.31	.016569902	7.298883	Calcium channel, voltage-dependent, N type, alpha 1B subunit (CACNA1B)
Asic1	0.31	.005347344	6.074872	Acid-sensing (proton-gated) ion channel 1 (Asic1)
Mapre3	0.31	.007698901	7.908402	Microtubule-associated protein, RP/EB family, member 3 (Mapre3)
Fam84a	0.31	.049871193	4.380544	Family with sequence similarity 84, member A (Fam84a)
Plxnc1	0.31	.001670639	8.075548	Plexin C1 (Plxnc1)
Trim44	0.31	.000508478	10.18059	Tripartite motif-containing 44 (Trim44)
Rabgap1	0.31	.002426589	7.429103	RAB GTPase activating protein 1 (Rabgap1)
Nsd1	0.31	.001824674	8.416994	Nuclear receptor-binding SET-domain protein 1 (Nsd1)
Rragb	0.31	.012607818	5.65292	Ras-related GTP binding B (Rragb)
Eli2	0.31	.005283976	5.624983	Elongation factor RNA polymerase II 2 (Eli2)
Hecw2	0.31	.004895996	6.438744	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 (Hecw2)
Senp2	0.31	.002516156	6.799879	SUMO/sentrin-specific peptidase 2 (Senp2)
Bmt2	0.31	.011472492	6.291756	Base methyltransferase of 25S rRNA 2 (Bmt2)
Bcas3	0.31	.02311958	5.103432	Breast carcinoma amplified sequence 3 (Bcas3)
Ddx24	0.31	.00176941	6.905864	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 (Ddx24)
Zfp462	0.31	.003803185	7.10365	Zinc finger protein 462 (Zfp462)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tbck	0.31	.00495254	6.056224	TBC1 domain containing kinase (Tbck)
Nap1l2	0.31	.004138323	6.668799	Nucleosome assembly protein 1-like 2 (Nap1l2)
Tollip	0.31	.001140999	7.410743	Toll interacting protein (Tollip)
Gpm6a	0.31	.000242589	9.699009	Glycoprotein m6a (Gpm6a)
B4galt5	0.31	.020679041	6.482451	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 (B4galt5)
Sec23ip	0.31	.014707099	5.2833	Sec23 interacting protein (Sec23ip)
Srcin1	0.31	.006815255	6.975277	SRC kinase signaling inhibitor 1 (Srcin1)
Slc43a2	0.31	.014711343	6.225303	Solute carrier family 43, member 2 (Slc43a2)
Arl8a	0.31	.001622761	7.814492	ADP-ribosylation factor-like 8A (Arl8a)
Hmbox1	0.31	.014774937	6.413729	Homeobox containing 1 (Hmbox1)
Kcna6	0.30	.006704587	5.959028	Potassium voltage-gated channel, shaker-related, subfamily, member 6 (Kcna6)
Srxn1	0.30	.007364826	6.458998	Sulfiredoxin 1 homolog ( <i>S. cerevisiae</i> ) (Srxn1)
Rbm12	0.30	.046175209	4.23747	RNA binding motif protein 12 (Rbm12)
9930021J03Rik	0.30	.004976948	8.048787	RIKEN cDNA 9930021J03 gene (9930021J03Rik)
Slc9a6	0.30	.004555812	7.140333	Solute carrier family 9 (sodium/hydrogen exchanger), member 6 (Slc9a6)
Cbl	0.30	.002555745	7.456415	Casitas B-lineage lymphoma (Cbl)
B230354K17Rik	0.30	.037538198	4.651618	RIKEN cDNA B230354K17 gene (B230354K17Rik)
Abhd13	0.30	.006840464	5.843592	Abhydrolase domain containing 13 (Abhd13)
Rb1cc1	0.30	.002032666	7.423043	RB1-inducible coiled-coil 1 (Rb1cc1)
Zfp275	0.30	.012557752	5.703578	Zinc finger protein 275 (Zfp275)
Csnk1a1	0.30	.000800046	8.160204	Casein kinase 1, alpha 1 (Csnk1a1)
Rlf	0.30	.012967738	5.919536	Rearranged L-myc fusion sequence (Rlf)
Cnot2	0.30	.010401047	6.065388	CCR4-NOT transcription complex, subunit 2 (Cnot2)
2310057M21Rik	0.30	.031437245	5.396433	RIKEN cDNA 2310057M21 gene (2310057M21Rik)
Ppm1k	0.30	.002070587	6.915927	Protein phosphatase 1K (PP2C domain containing) (Ppm1k)
Parp6	0.30	.002183471	6.808903	Poly(ADP-ribose) polymerase family, member 6 (Parp6)
Zmynd19	0.30	.037665414	4.002888	Zinc finger, MYND domain containing 19 (Zmynd19)
Sept11	0.30	.004866842	7.063208	Septin 11 (Sept11)
Tiprl	0.30	.002856573	6.284998	TIP41, TOR signalling pathway regulator-like ( <i>S. cerevisiae</i> ) (Tiprl)
Mon1b	0.30	.015563128	6.049116	MON1 homolog B, secretory trafficking associated (Mon1b)
Ciapin1	0.30	.028354648	5.027411	Cytokine-induced apoptosis inhibitor 1 (Ciapin1)
Depdc5	0.30	.007008639	6.158592	DEP domain containing 5 (Depdc5)
Timm29	0.30	.033594309	6.179825	Translocase Of Inner Mitochondrial Membrane 29 (Timm29)
Mfap3l	0.30	.005401632	6.21341	Microfibrillar-associated protein 3-like (Mfap3l)
Cenpc1	0.30	.022975836	5.59561	Centromere protein C1 (Cenpc1)
Gap43	0.30	.006425957	8.655053	Growth-associated protein 43 (Gap43)
Ptpn3	0.30	.007698901	7.506339	Protein tyrosine phosphatase, non-receptor type 3 (Ptpn3)
Nipal2	0.30	.048324369	4.657557	NIPA-like domain containing 2 (Nipal2)
Exoc2	0.30	.003992505	6.161269	Exocyst complex component 2 (Exoc2)
Ttbk2	0.30	.00924387	8.011298	Tau tubulin kinase 2 (Ttbk2)
H13	0.30	.008621433	6.027599	Histocompatibility 13 (H13)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Dubr	0.30	.036010297	4.368191	Dppa2 upstream binding RNA (Dubr)
Ankrd52	0.30	.007140692	6.294721	Ankyrin repeat domain 52 (Ankrd52)
Pdp2	0.30	.031930563	4.991922	Pyruvate dehydrogenase phosphatase catalytic subunit 2 (Pdp2)
Snrpn	0.30	.001274061	9.023082	Small nuclear ribonucleoprotein N (Snrpn)
Gnao1	0.30	.000272909	10.26961	Guanine nucleotide binding protein, alpha O (Gnao1)
Csmd1	0.30	.018773501	5.460553	CUB and Sushi multiple domains 1 (Csmd1)
Bicd1	0.30	.009227363	6.949075	Bicaudal D homolog 1 (Bicd1)
Tdrkh	0.30	.014135912	5.772278	Tudor and KH domain containing protein (Tdrkh)
Ppip5k2	0.30	.037485705	5.025493	Diphosphoinositol pentakisphosphate kinase 2 (Ppip5k2)
Dnajc27	0.30	.001237432	7.203911	DnaJ heat shock protein family (Hsp40) member C27 (Dnajc27)
Nampt	0.30	.01608854	6.729077	Nicotinamide phosphoribosyltransferase (Nampt)
Dscam	0.30	.002131015	7.088152	Down syndrome cell adhesion molecule (Dscam)
Sf3b3	0.30	.014655424	5.654957	Splicing factor 3b, subunit 3 (Sf3b3)
Pdzd4	0.30	.027677806	5.061484	PDZ domain containing 4 (Pdzd4)
Snap25	0.30	.001140235	12.44855	Synaptosomal-associated protein 25 (Snap25)
Pde7a	0.30	.044604394	4.308021	Phosphodiesterase 7A (Pde7a)
Pign	0.30	.035687983	5.112911	Phosphatidylinositol glycan anchor biosynthesis, class N (Pign)
Mtmr9	0.30	.011559559	6.230916	Myotubularin-related protein 9 (Mtmr9)
Eno2	0.30	.002253804	8.87194	Enolase 2, gamma neuronal (Eno2)
Atp6ap2	0.30	.004964581	7.064367	ATPase, H <sup>+</sup> transporting, lysosomal accessory protein 2 (Atp6ap2)
Mbnl2	0.30	.001175527	8.403007	Muscleblind-like 2 (Mbnl2)
Ywhaz	0.30	.00080519	11.54371	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz)
Impad1	0.30	.002866568	8.228553	Inositol monophosphatase domain containing 1 (Impad1)
Plcb4	0.30	.00100186	8.829629	Phospholipase C, beta 4 (Plcb4)
Sema4a	0.30	.016926657	4.932598	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (Sema4a)
Rnf111	0.30	.010674757	6.29004	Ring finger 111 (Rnf111)
Efh2	0.30	.01199216	7.294006	EF hand domain containing 2 (Efhd2)
Hdac2	0.30	.006932158	6.413361	Histone deacetylase 2 (Hdac2)
Aprt	0.30	.044457841	4.733443	Adenine phosphoribosyl transferase (Aprt)
Ube2j1	0.30	.001482053	7.436077	Ubiquitin-conjugating enzyme E2J 1 (Ube2j1)
Mlec	0.30	.00489464	7.529491	Malectin (Mlec)
Btrc	0.30	.007178446	6.243904	Beta-transducin repeat containing protein (Btrc)
Vamp4	0.30	.022789834	6.587331	Vesicle-associated membrane protein 4 (Vamp4)
Tnrc6a	0.30	.007183707	6.627867	Trinucleotide repeat containing 6a (Tnrc6a)
Svop	0.30	.010886261	5.77462	SV2-related protein (Svop)
Cdc42bpb	0.30	.001254789	7.182722	CDC42 binding protein kinase beta (Cdc42bpb)
Lnpep	0.30	.00472261	7.61621	Leucyl/cysteinyl aminopeptidase (Lnpep)
Sh3kbp1	0.30	.001401147	7.520692	SH3-domain kinase binding protein 1 (Sh3kbp1)
Srr	0.30	.035191952	6.007721	Serine racemase (Srr)
Pacsin1	0.30	.005465658	8.034317	Protein kinase C and casein kinase substrate in neurons 1 (Pacsin1)
Cacna2d1	0.30	.003035618	7.269986	Calcium channel, voltage-dependent, alpha2/delta subunit 1 (Cacna2d1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ago3	0.29	.027804757	7.051293	Argonaute RISC catalytic subunit 3 (Ago3)
Tmem50b	0.29	.002601527	7.71822	Transmembrane protein 50B (Tmem50b)
Pcgf3	0.29	.040366427	5.931799	Polycomb group ring finger 3 (Pcgf3)
Chchd4	0.29	.011136689	5.802158	Coiled-coil-helix-coiled-coil-helix domain containing 4 (Chchd4)
Snx4	0.29	.018159619	5.737659	Sorting nexin 4 (Snx4)
Cluh	0.29	.009056085	6.187234	Clustered mitochondria (cluA/CLU1) homolog (Cluh)
Zcchc18	0.29	.002477076	7.833199	Zinc finger, CCHC domain containing 18 (Zcchc18)
Ranbp9	0.29	.004659662	6.987642	RAN binding protein 9 (Ranbp9)
Wdcp	0.29	.045109819	4.119301	WD repeat and coiled coil containing (Wdcp)
Phf8	0.29	.027197609	5.560488	PHD finger protein 8 (Phf8)
Copg1	0.29	.002176579	7.741808	Coatomer protein complex, subunit gamma 1 (Copg1)
Sptlc2	0.29	.004897516	6.453922	Serine palmitoyltransferase, long chain base subunit 2 (Sptlc2)
Ddx25	0.29	.003456314	6.374034	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (Ddx25)
Phka2	0.29	.019507754	4.86431	Phosphorylase kinase alpha 2 (Phka2)
Gabrg1	0.29	.033632826	6.434823	Gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1 (Gabrg1)
BC030336	0.29	.012863723	6.643517	cDNA sequence BC030336 (BC030336)
Dpp6	0.29	.001364163	8.174877	Dipeptidylpeptidase 6 (Dpp6)
Diras1	0.29	.013137268	7.198799	DIRAS family, GTP-binding RAS-like 1 (Diras1)
Atg2b	0.29	.020091326	5.916504	Autophagy related 2B (Atg2b)
Cd99l2	0.29	.00521277	7.38619	CD99 antigen-like 2 (Cd99l2)
B230209E15Rik	0.29	.043080673	5.304688	RIKEN cDNA B230209E15 gene (B230209E15Rik)
Itfg1	0.29	.001418482	8.433981	Integrin alpha FG-GAP repeat containing 1 (Itfg1)
Nin	0.29	.019438147	6.252582	Ninein (Nin)
Plpp6	0.29	.008997858	6.339292	Phospholipid phosphatase 6 (Plpp6)
Gtf3c4	0.29	.010004425	5.78943	General transcription factor IIIC, polypeptide 4 (Gtf3c4)
Prpf6	0.29	.048835482	5.689386	Pre-mRNA splicing factor 6 (Prpf6)
Nufip2	0.29	.005168133	6.832126	Nuclear fragile X mental retardation protein interacting protein 2 (Nufip2)
Gak	0.29	.003825128	6.969948	Cyclin G-associated kinase (Gak)
Tmem181a	0.29	.022725455	5.066094	Transmembrane protein 181A (Tmem181a)
Clstn1	0.29	.0009845	9.278522	Calsyntenin 1 (Clstn1)
Cit	0.29	.004411582	9.7881	Citron (Cit)
Nefh	0.29	.013158873	5.713411	Neurofilament, heavy polypeptide (Nefh)
Dennd1b	0.29	.032048904	5.275373	DENN/MADD domain containing 1B (Dennd1b)
Ppp1r15b	0.29	.012340264	6.278374	Protein phosphatase 1, regulatory (inhibitor) subunit 15b (Ppp1r15b)
Odf2	0.29	.030685551	5.194938	Outer dense fiber of sperm tails 2 (Odf2)
Napg	0.29	.004756242	7.560103	N-ethylmaleimide sensitive fusion protein attachment protein gamma (Napg)
Poldip3	0.29	.018616322	6.535524	Polymerase (DNA-directed), delta interacting protein 3 (Poldip3)
Hprt	0.29	.003719834	7.502317	Hypoxanthine guanine phosphoribosyl transferase (Hprt)
Eps8	0.29	.007026658	6.681189	Epidermal growth factor receptor pathway substrate 8 (Eps8)
Arhgef28	0.29	.039602496	5.022086	Rho guanine nucleotide exchange factor (GEF) 28 (Arhgef28)
Tnrc6b	0.29	.004467218	8.094193	Trinucleotide repeat containing 6b (Tnrc6b)
Rhobtb2	0.29	.019058437	5.808716	Rho-related BTB domain containing 2 (Rhobtb2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mysm1	0.29	.016318799	6.244191	Myb-like, SWIRM and MPN domains 1 (Mysm1)
Rexo1	0.29	.026714238	5.369836	REX1, RNA exonuclease 1 (Rexo1)
Kcna2	0.29	.005584173	9.231444	Potassium voltage-gated channel, shaker-related subfamily, member 2 (Kcna2)
Gpatch11	0.29	.04012435	5.248353	G patch domain containing 11 (Gpatch11)
Ppp1r13b	0.29	.017206437	6.757528	Protein phosphatase 1, regulatory (inhibitor) subunit 13B (Ppp1r13b)
Xiap	0.29	.02947797	7.793085	X-linked inhibitor of apoptosis (Xiap)
Zfp62	0.29	.01508435	5.769161	Zinc finger protein 62 (Zfp62)
Rsl1d1	0.29	.007148906	6.562097	Ribosomal L1 domain containing 1 (Rsl1d1)
Scrt2	0.29	.043168071	4.507479	Scratch family zinc finger 2 (Scrt2)
Ino80d	0.29	.029832798	6.976664	INO80 complex subunit D (Ino80d)
Tnik	0.29	.003821315	7.287748	TRAF2 and NCK interacting kinase (Tnik)
Ugg1	0.29	.013058982	6.256806	UDP-glucose glycoprotein glucosyltransferase 1 (Ugg1)
Tmem43	0.29	.038260321	5.090363	Transmembrane protein 43 (Tmem43)
Trappc9	0.29	.011276503	5.753603	Trafficking protein particle complex 9 (Trappc9)
Dmxl1	0.29	.008601807	7.464723	Dmx-like 1 (Dmxl1)
Prpf19	0.29	.024329128	5.757284	Pre-mRNA processing factor 19 (Prpf19)
Apbb2	0.29	.001590425	7.721342	Amyloid beta (A4) precursor protein-binding, family B, member 2 (Apbb2)
Caly	0.29	.016466035	7.1097	Calcyon neuron-specific vesicular protein (Caly)
Txnrd1	0.29	.041416102	5.712579	Thioredoxin reductase 1 (Txnrd1)
Casc4	0.29	.002536134	8.701304	Cancer susceptibility candidate 4 (Casc4)
Ncs1	0.29	.004006759	8.041783	Neuronal calcium sensor 1 (Ncs1)
Fut8	0.29	.007012116	5.877394	Fucosyltransferase 8 (Fut8)
Senp5	0.29	.026675912	5.008522	SUMO/sentrin-specific peptidase 5 (Senp5)
1700020I14Rik	0.29	.004103231	9.731026	RIKEN cDNA 1700020I14 gene (1700020I14Rik)
Rnmt	0.29	.004993153	6.670023	RNA (guanine-7-) methyltransferase (Rnmt)
Ap2b1	0.29	.00127953	8.255721	Adaptor-related protein complex 2, beta 1 subunit (Ap2b1)
Capn7	0.29	.006186201	6.036135	Calpain 7 (Capn7)
Dhx30	0.29	.037016584	5.802387	DEAH (Asp-Glu-Ala-His) box polypeptide 30 (Dhx30)
Nup133	0.29	.043363172	4.879493	Nucleoporin 133 (Nup133)
Neb1	0.28	.003407224	7.049783	Nebulette (Neb1)
Tomm40	0.28	.018773501	5.150366	Translocase of outer mitochondrial membrane 40 homolog (yeast) (Tomm40)
Dld	0.28	.004661051	7.426299	Dihydrolipoamide dehydrogenase (Dld)
Upf1	0.28	.037918718	4.705645	UPF1 regulator of nonsense transcripts homolog (yeast) (Upf1)
Slc25a44	0.28	.004840969	6.649834	Solute carrier family 25, member 44 (Slc25a44)
Slc38a9	0.28	.036184439	5.200136	Solute carrier family 38, member 9 (Slc38a9)
Ttc3	0.28	.000182452	10.81009	Tetratricopeptide repeat domain 3 (Ttc3)
Srrt	0.28	.011195774	6.233719	Serrate RNA effector molecule homolog (Arabidopsis) (Srrt)
Zfp346	0.28	.029600607	4.88929	Zinc finger protein 346 (Zfp346)
Vdac3	0.28	.011265071	6.001346	Voltage-dependent anion channel 3 (Vdac3)
Zdhhc3	0.28	.016672002	6.248905	Zinc finger, DHHC domain containing 3 (Zdhhc3)
Gpcpd1	0.28	.013346028	6.609606	Glycerophosphocholine phosphodiesterase 1 (Gpcpd1)
Ciz1	0.28	.047239578	4.980273	CDKN1A interacting zinc finger protein 1 (Ciz1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Arel1	0.28	.010993944	6.356425	Apoptosis resistant E3 ubiquitin protein ligase 1 (Arel1)
Fbrs	0.28	.027103371	5.895547	Fibrosin (Fbrs)
Zfp329	0.28	.029964756	6.195842	Zinc finger protein 329 (Zfp329)
Mapk6	0.28	.018635944	6.656309	Mitogen-activated protein kinase 6 (Mapk6)
Rnf123	0.28	.03201848	4.687283	Ring finger protein 123 (Rnf123)
Acbd3	0.28	.020120246	6.303122	Acyl-Coenzyme A binding domain containing 3 (Acbd3)
Sacm1l	0.28	.039883798	4.754358	SAC1 suppressor of actin mutations 1-like (yeast) (Sacm1l)
Tmie	0.28	.020824676	5.415788	Transmembrane inner ear (Tmie)
Thns1l	0.28	.03144677	4.666539	Threonine synthase-like 1 (bacterial) (Thns1l)
Fam171a1	0.28	.041528396	5.761059	Family with sequence similarity 171, member A1 (Fam171a1)
Wrb	0.28	.002276371	7.091132	Tryptophan-rich basic protein (Wrb)
Rbbp6	0.28	.006620727	7.487087	Retinoblastoma binding protein 6 (Rbbp6)
Nova2	0.28	.002644938	6.921313	Neuro-oncological ventral antigen 2 (Nova2)
Nek7	0.28	.000975552	8.64502	NIMA (never in mitosis gene a)-related expressed kinase 7 (Nek7)
Camk2d	0.28	.006988592	8.021251	Calcium/calmodulin-dependent protein kinase II, delta (Camk2d)
Kidins220	0.28	.003853323	9.211366	Kinase D-interacting substrate 220 (Kidins220)
Wdr48	0.28	.022705971	5.532367	WD repeat domain 48 (Wdr48)
Rps6kc1	0.28	.013666321	5.541928	Ribosomal protein S6 kinase polypeptide 1 (Rps6kc1)
Mfsd14a	0.28	.019919356	6.128688	Major facilitator superfamily domain containing 14A (Mfsd14a)
Smarcc1	0.28	.011118138	6.548027	SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily c, member 1 (Smarcc1)
Scrn1	0.28	.009647234	8.416075	Secernin 1 (Scrn1)
Nub1	0.28	.029506175	5.291981	Negative regulator of ubiquitin-like proteins 1 (Nub1)
Dixdc1	0.28	.003557218	7.61096	DIX domain containing 1 (Dixdc1)
Gramd1b	0.28	.003199855	7.980444	GRAM domain containing 1B (Gramd1b)
Sarm1	0.28	.022871278	5.131807	Sterile alpha and HEAT/Armadillo motif containing 1 (Sarm1)
Chd5	0.28	.007324446	7.410324	Chromodomain helicase DNA binding protein 5 (Chd5)
Lrrc40	0.28	.048006728	4.828818	Leucine-rich repeat containing 40 (Lrrc40)
Dhx32	0.28	.025081808	4.859393	DEAH (Asp-Glu-Ala-His) box polypeptide 32 (Dhx32)
Zfp106	0.28	.002549789	8.823319	Zinc finger protein 106 (Zfp106)
Slc30a1	0.28	.037752699	5.657351	Solute carrier family 30 (zinc transporter), member 1 (Slc30a1)
Dner	0.28	.002333045	7.730689	Delta/notch-like EGF repeat containing (Dner)
Plekhm1	0.28	.011171292	5.608369	Pleckstrin homology domain containing, family M (with RUN domain) member 1 (Plekhm1)
Snapc1	0.28	.037630179	6.092211	Small nuclear RNA activating complex, polypeptide 1 (Snapc1)
Zfp148	0.28	.006249724	7.467128	Zinc finger protein 148 (Zfp148)
Nipsnap2	0.28	.014666795	6.397607	Nipsnap Homolog 2 (Nipsnap2)
Foxk1	0.28	.005503706	6.319636	Forkhead box K1 (Foxk1)
Vti1a	0.28	.008711502	7.112551	Vesicle transport through interaction with t-SNAREs 1A (Vti1a)
Rnf180	0.28	.036278612	4.7386	Ring finger protein 180 (Rnf180)
Vps26a	0.28	.013177194	6.988825	VPS26 retromer complex component A (Vps26a)
Rhot1	0.28	.007332104	6.283881	Ras homolog family member T1 (Rhot1)
Tmem263	0.28	.019306982	6.830252	Transmembrane protein 263 (Tmem263)
Atp9a	0.28	.027112538	7.151991	ATPase, class II, type 9A (Atp9a)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Aco2	0.28	.001371504	8.424316	Aconitase 2, mitochondrial (Aco2)
Ctnnb1	0.28	.002475998	8.407129	Catenin (cadherin-associated protein), beta 1 (Ctnnb1)
Brd4	0.28	.002418826	7.597624	Bromodomain containing 4 (Brd4)
Stradb	0.28	.018876847	5.171677	STE20-related kinase adaptor beta (Stradb)
Bri3bp	0.28	.006370693	7.355458	Bri3 binding protein (Bri3bp)
Necap1	0.28	.008035154	7.592931	NECAP endocytosis associated 1 (Necap1)
Kdm5c	0.28	.015474813	5.466005	Lysine(K)-specific demethylase 5C (Kdm5c)
Ttc17	0.28	.014313741	5.752314	Tetratricopeptide repeat domain 17 (Ttc17)
Nisch	0.28	.001290161	8.869673	Nischarin (Nisch)
Gng3	0.28	.003011943	9.34266	Guanine nucleotide binding protein (G protein), gamma 3 (Gng3)
Jak1	0.28	.005117976	7.24925	Janus kinase 1 (Jak1)
Gdi1	0.28	.003366733	10.20332	Guanosine diphosphate (GDP) dissociation inhibitor 1 (Gdi1)
Dgkb	0.28	.01143571	7.002562	Diacylglycerol kinase, beta (Dgkb)
Nfasc	0.28	.005105436	8.639035	Neurofascin (Nfasc)
Polr1a	0.28	.02947797	5.228718	Polymerase (RNA) I polypeptide A (Polr1a)
Chst1	0.28	.006620727	7.197954	Carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (Chst1)
Dhdds	0.28	.018663017	5.476029	Dehydrodolichyl diphosphate synthase (Dhdds)
Ankrd13c	0.28	.004119142	6.810589	Ankyrin repeat domain 13c (Ankrd13c)
Gls	0.28	.000852943	8.905604	Glutaminase (Gls)
Slc27a4	0.28	.033848056	5.475829	Solute carrier family 27 (fatty acid transporter), member 4 (Slc27a4)
Zfp941	0.28	.027431768	5.622759	Zinc finger protein 941 (Zfp941)
Rfn	0.28	.035189543	5.3683	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase (Rfn)
Pnpla8	0.28	.012800934	7.205701	Patatin-like phospholipase domain containing 8 (Pnpla8)
Mfn2	0.28	.003935793	7.304283	Mitofusin 2 (Mfn2)
Ccng1	0.28	.042915129	8.044842	Cyclin G1 (Ccng1)
Gria3	0.28	.010401047	6.999915	Glutamate receptor, ionotropic, AMPA3 (alpha 3) (Gria3)
Sec24b	0.28	.006998773	6.660531	Sec24-related gene family, member B ( <i>S. cerevisiae</i> ) (Sec24b)
Synm	0.27	.038916137	5.060104	Synemin, intermediate filament protein (Synm)
Mapk8	0.27	.011892902	7.565035	Mitogen-activated protein kinase 8 (Mapk8)
Cramp1l	0.27	.017619173	5.807321	Crm, cramped-like (Cramp1l)
Dennd4b	0.27	.040255746	5.204414	DENN/MADD domain containing 4B (Dennd4b)
Ssh2	0.27	.006699296	6.563733	Slingshot homolog 2 (Ssh2)
Ric8b	0.27	.014623263	6.24985	RIC8 guanine nucleotide exchange factor B (Ric8b)
Fam217b	0.27	.005273757	6.720992	Family with sequence similarity 217, member B (Fam217b)
Tiam1	0.27	.032296766	6.579118	T cell lymphoma invasion and metastasis 1 (Tiam1)
Efr3a	0.27	.008518349	7.147258	EFR3 homolog A (Efr3a)
Adgrb3	0.27	.005606181	6.921635	Adhesion G protein-coupled receptor B3 (Adgrb3)
Btbd8	0.27	.00597139	7.686081	BTB (POZ) domain containing 8 (Btbd8)
Elfn2	0.27	.00793369	7.291967	Leucine-rich repeat and fibronectin type III, extracellular 2 (Elfn2)
Sppl3	0.27	.048952288	5.325795	Signal peptide peptidase 3 (Sppl3)
Mast4	0.27	.002536136	7.549238	Microtubule-associated serine/threonine kinase family member 4 (Mast4)
Atxn7l3b	0.27	.002479883	7.940815	Ataxin 7-like 3B (Atxn7l3b)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mrps2	0.27	.028434323	5.432287	Mitochondrial ribosomal protein S2 (Mrps2)
Sez6l2	0.27	.004104083	7.926525	Seizure-related 6 homolog like 2 (Sez6l2)
Ppp2r5e	0.27	.008597578	6.871027	Protein phosphatase 2, regulatory subunit B', epsilon (Ppp2r5e)
Gspt1	0.27	.006958315	6.415081	G1 to S phase transition 1 (Gspt1)
Wasf3	0.27	.012615294	7.879823	WAS protein family, member 3 (Wasf3)
Extl3	0.27	.002807727	7.803068	Exostoses (multiple)-like 3 (Extl3)
Wbp4	0.27	.017248951	6.166412	WW domain binding protein 4 (Wbp4)
Fbxl20	0.27	.014066408	6.449564	F-box and leucine-rich repeat protein 20 (Fbxl20)
Cacna1a	0.27	.014964932	5.999306	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (Cacna1a)
Synj2	0.27	.014696318	6.22205	Synaptjanin 2 (Synj2)
Zfp322a	0.27	.009275571	5.927877	Zinc finger protein 322A (Zfp322a)
Tmem246	0.27	.034308347	5.491578	Transmembrane protein 246 (Tmem246)
Utp3	0.27	.017040002	5.980936	UTP3 small subunit processome component (Utp3)
Dcp1a	0.27	.042143098	5.341226	Decapping mRNA 1A (Dcp1a)
Dmxl2	0.27	.002023891	8.337735	Dmx-like 2 (Dmxl2)
Gdap1l1	0.27	.015980695	6.207562	Ganglioside-induced differentiation-associated protein 1-like 1 (Gdap1l1)
Zfp809	0.27	.045630469	4.969866	Zinc finger protein 809 (Zfp809)
Smyd3	0.27	.020026873	6.126087	SET and MYND domain containing 3 (Smyd3)
Efna3	0.27	.043486496	4.472326	Ephrin A3 (Efna3)
Ncor1	0.27	.000937444	8.557155	Nuclear receptor co-repressor 1 (Ncor1)
Plekhb2	0.27	.009016154	7.831677	Pleckstrin homology domain containing, family B (ejectins) member 2 (Plekhb2)
Klhdc2	0.27	.002585912	7.935284	Kelch domain containing 2 (Klhdc2)
Akt1	0.27	.009816851	6.078466	Thymoma viral proto-oncogene 1 (Akt1)
Nrd1	0.27	.005056229	7.807282	Nardilysin, N-arginine dibasic convertase, NRD convertase 1 (Nrd1)
Kdm5b	0.27	.024457348	5.933054	Lysine (K)-specific demethylase 5B (Kdm5b)
Tmx3	0.27	.013086607	5.879169	Thioredoxin-related transmembrane protein 3 (Tmx3)
Chst8	0.27	.044309093	5.16268	Carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 8 (Chst8)
Rab18	0.27	.005271689	6.598716	RAB18, member RAS oncogene family (Rab18)
Ctbp1	0.27	.042934367	6.443711	C-terminal binding protein 1 (Ctbp1)
N4bp1	0.27	.00753234	7.831815	NEDD4 binding protein 1 (N4bp1)
Grm1	0.27	.023914227	8.04685	Glutamate receptor, metabotropic 1 (Grm1)
Morf4l2	0.27	.015797858	7.60517	Mortality factor 4 like 2 (Morf4l2)
Gclm	0.27	.016928308	6.543524	Glutamate-cysteine ligase, modifier subunit (Gclm)
Cstf2t	0.27	.01048809	6.178532	Cleavage stimulation factor, 3' pre-RNA subunit 2, tau (Cstf2t)
Grid1	0.27	.031517996	5.569667	Glutamate receptor, ionotropic, delta 1 (Grid1)
Ik	0.27	.00420581	7.944608	IK cytokine (Ik)
Ago1	0.27	.021029319	6.039978	Argonaute RISC catalytic subunit 1 (Ago1)
Kdm7a	0.27	.03994192	6.245133	Lysine (K)-specific demethylase 7A (Kdm7a)
Rab3gap2	0.27	.022344908	5.827958	RAB3 GTPase activating protein subunit 2 (Rab3gap2)
U2surp	0.27	.007276141	6.895448	U2 snRNP-associated SURP domain containing (U2surp)
Agap2	0.27	.011698584	7.129894	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2 (Agap2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Kcnc2	0.27	.015859249	7.885483	potassium voltage gated channel, Shaw-related subfamily, member 2 (Kcnc2)
Galnt11	0.27	.030566665	5.115867	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (Galnt11)
Eno1	0.27	.018002481	8.527112	Enolase 1, alpha non-neuron (Eno1)
Fastk	0.27	.041943112	5.355419	Fas-activated serine/threonine kinase (Fastk)
Cmas	0.27	.005169528	7.395057	Cytidine monophospho-N-acetylneuraminc acid synthetase (Cmas)
Slc35b4	0.27	.009757436	6.319573	Solute carrier family 35, member B4 (Slc35b4)
Elavl1	0.27	.038686965	6.716569	ELAV (embryonic lethal, abnormal vision)-like 1 (Hu antigen R) (Elavl1)
Mlf2	0.26	.006634018	7.99617	Myeloid leukemia factor 2 (Mlf2)
Cds1	0.26	.008725194	6.551476	CDP-diacylglycerol synthase 1 (Cds1)
Mkl1	0.26	.041286439	5.037545	MKL (megakaryoblastic leukemia)/myocardin-like 1 (Mkl1)
Eif1a	0.26	.02596658	6.90807	Eukaryotic translation initiation factor 1A (Eif1a)
Mtmmr1	0.26	.023347531	5.282048	Myotubularin-related protein 1 (Mtmmr1)
Adgrl1	0.26	.002118505	8.506811	Adhesion G protein-coupled receptor L1 (Adgrl1)
Rragc	0.26	.021937357	6.374251	Ras-related GTP binding C (Rragc)
Slc35e3	0.26	.035687983	4.904488	Solute carrier family 35, member E3 (Slc35e3)
Mapt	0.26	.008483427	8.376632	Microtubule-associated protein tau (Mapt)
Med1	0.26	.02601574	6.868114	Mediator complex subunit 1 (Med1)
Gtpbp4	0.26	.008981087	6.112213	GTP binding protein 4 (Gtpbp4)
Etf1	0.26	.008784142	6.753486	Eukaryotic translation termination factor 1 (Etf1)
Cdk5r2	0.26	.008588632	7.214605	Cyclin-dependent kinase 5, regulatory subunit 2 (p39) (Cdk5r2)
Rab1	0.26	.003398289	9.100399	RAB1, Member RAS Oncogene Family (Rab1)
Wapl	0.26	.0041259	7.151871	WAPL cohesin release factor (Wapl)
Gfm1	0.26	.037538198	5.687408	G elongation factor, mitochondrial 1 (Gfm1)
Abcg4	0.26	.043531672	6.313969	ATP-binding cassette, sub-family G (WHITE), member 4 (Abcg4)
Tmcc1	0.26	.00943859	7.39022	Transmembrane and coiled coil domains 1 (Tmcc1)
Gmfb	0.26	.011970613	7.982291	Glia maturation factor, beta (Gmfb)
Ubqln2	0.26	.013183398	7.841759	Ubiquilin 2 (Ubqln2)
Zdhhc17	0.26	.010144508	7.018991	Zinc finger, DHHC domain containing 17 (Zdhhc17)
Ganab	0.26	.012449667	6.432821	Alpha glucosidase 2 alpha neutral subunit (Ganab)
Arih1	0.26	.00188698	7.688688	Ariadne RBR E3 ubiquitin protein ligase 1 (Arih1)
Fuca2	0.26	.013600704	6.545753	Fucosidase, alpha-L- 2, plasma (Fuca2)
Bcat1	0.26	.032071688	6.799144	Branched chain aminotransferase 1, cytosolic (Bcat1)
Rogdi	0.26	.02220035	6.717655	Rogdi homolog (Rogdi)
Ttc19	0.26	.006780863	7.304505	Tetratricopeptide repeat domain 19 (Ttc19)
Dynlt3	0.26	.001355949	8.348117	Dynein light chain Tctex-type 3 (Dynlt3)
Ccar1	0.26	.013183398	6.05194	Cell division cycle and apoptosis regulator 1 (Ccar1)
Mdm4	0.26	.019120111	7.352569	Transformed mouse 3T3 cell double minute 4 (Mdm4)
Zhx1	0.26	.004233749	7.310457	Zinc fingers and homeoboxes 1 (Zhx1)
Rbm25	0.26	.020549481	6.2242	RNA binding motif protein 25 (Rbm25)
Plch1	0.26	.037273334	5.536838	Phospholipase C, eta 1 (Plch1)
Mfsd4a	0.26	.036567968	5.358221	Major facilitator superfamily domain containing 4A (Mfsd4a)
Atp1b1	0.26	.003221607	10.12033	ATPase, Na+/K+ transporting, beta 1 polypeptide (Atp1b1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Nrip1	0.26	.030121409	6.015453	Nuclear receptor interacting protein 1 (Nrip1)
Tmem183a	0.26	.01664335	6.649414	Transmembrane protein 183A (Tmem183a)
Fgf14	0.26	.037539866	6.365664	Fibroblast growth factor 14 (Fgf14)
Eif4g1	0.26	.006613234	6.999683	Eukaryotic translation initiation factor 4, gamma 1 (Eif4g1)
Ube2h	0.26	.012775352	6.954516	Ubiquitin-conjugating enzyme E2H (Ube2h)
Usp2	0.26	.025090416	6.143011	Ubiquitin-specific peptidase 2 (Usp2)
Ndn	0.26	.037538198	7.181255	Necdin (Ndn)
Zmiz2	0.26	.006425957	7.458939	Zinc finger, MIZ-type containing 2 (Zmiz2)
Clmn	0.26	.003550056	8.458508	Calmin (Clmn)
Prkar1a	0.26	.002426589	9.697189	Protein kinase, cAMP dependent regulatory, type I, alpha (Prkar1a)
Zbtb21	0.26	.037989591	4.890952	Zinc finger and BTB domain containing 21 (Zbtb21)
Car10	0.26	.026732262	7.754017	Carbonic anhydrase 10 (Car10)
Prdm2	0.26	.027429947	6.460729	PR domain containing 2, with ZNF domain (Prdm2)
Dnajb6	0.26	.019446411	5.582239	DnaJ heat shock protein family (Hsp40) member B6 (Dnajb6)
Nptn	0.26	.024777285	8.511305	Neuroplastin (Nptn)
Armc1	0.26	.017384127	7.070633	Armadillo repeat containing 1 (Armc1)
Trim2	0.26	.002547353	8.710248	Tripartite motif-containing 2 (Trim2)
Mkln1	0.26	.006115011	7.385871	Muskelin 1, intracellular mediator containing kelch motifs (Mkln1)
Cyfip2	0.25	.006556626	9.65834	Cytoplasmic FMR1 interacting protein 2 (Cyfip2)
Ctxn1	0.25	.015502855	7.145987	Cortexin 1 (Ctxn1)
Cpeb1	0.25	.033383797	5.328657	Cytoplasmic polyadenylation element binding protein 1 (Cpeb1)
Arhgap32	0.25	.004303565	8.77535	Rho GTPase activating protein 32 (Arhgap32)
Brd3	0.25	.021115842	6.494486	Bromodomain containing 3 (Brd3)
Prkcb	0.25	.010674757	7.377941	Protein kinase C, beta (Prkcb)
Cbx6	0.25	.010913863	7.099465	Chromobox 6 (Cbx6)
Eif4enif1	0.25	.049424979	6.381699	Eukaryotic translation initiation factor 4E nuclear import factor 1 (Eif4enif1)
Rab8b	0.25	.023591412	6.281451	RAB8B, member RAS oncogene family (Rab8b)
Grk2	0.25	.011121976	6.817634	G protein-coupled receptor kinase 2 (Grk2)
Mafg	0.25	.019987601	5.761778	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian) (Mafg)
Pxk	0.25	.049871193	5.32972	PX domain containing serine/threonine kinase (Pxk)
Ahctf1	0.25	.032339039	5.974468	AT hook containing transcription factor 1 (Ahctf1)
Zswim8	0.25	.041207114	6.520703	Zinc finger SWIM-type containing 8 (Zswim8)
Gsk3a	0.25	.044531571	6.568453	Glycogen synthase kinase 3 alpha (Gsk3a)
Polr2b	0.25	.008765324	6.861404	Polymerase (RNA) II (DNA directed) polypeptide B (Polr2b)
Gatad2b	0.25	.00225318	8.306623	GATA zinc finger domain containing 2B (Gatad2b)
Tle3	0.25	.034709348	5.256824	Transducin-like enhancer of split 3 (Tle3)
Ppa2	0.25	.038742784	5.481607	Pyrophosphatase (inorganic) 2 (Ppa2)
Zrsr1	0.25	.040252636	5.358349	Zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1 (Zrsr1)
Gnl2	0.25	.048542635	5.229231	Guanine nucleotide binding protein-like 2 (nucleolar) (Gnl2)
Dlg2	0.25	.010085425	8.510236	Discs, large homolog 2 (Dlg2)
Gpi1	0.25	.012981106	8.550952	Glucose phosphate isomerase 1 (Gpi1)
Tppp	0.25	.001217446	9.084994	Tubulin polymerization promoting protein (Tppp)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Eif4g3	0.25	.002213452	8.309797	Eukaryotic translation initiation factor 4 gamma, 3 (Eif4g3)
Snx25	0.25	.02296658	6.373403	Sorting nexin 25 (Snx25)
Bcl2l1	0.25	.024494742	5.808804	BCL2-like 1 (Bcl2l1)
Hsd17b7	0.25	.019391095	6.15484	Hydroxysteroid (17-beta) dehydrogenase 7 (Hsd17b7)
Dpy19l3	0.25	.014550835	6.745629	dpy-19-like 3 (C. elegans) (Dpy19l3)
Zc3h4	0.25	.025588008	5.885946	Zinc finger CCCH-type containing 4 (Zc3h4)
Tox4	0.25	.018784525	6.172471	TOX high-mobility group box family member 4 (Tox4)
Rtn3	0.25	.005263697	10.68972	Reticulon 3 (Rtn3)
Zfp318	0.25	.028186533	6.253536	Zinc finger protein 318 (Zfp318)
Ric3	0.25	.008419765	7.159328	RIC3 acetylcholine receptor chaperone (Ric3)
Hars	0.25	.04679661	6.033038	Histidyl-tRNA synthetase (Hars)
Rictor	0.25	.009896459	6.606077	RPTOR independent companion of MTOR, complex 2 (Rictor)
Kcnab2	0.25	.034951024	6.646441	Potassium voltage-gated channel, shaker-related subfamily, beta member 2 (Kcnab2)
Kif1b	0.25	.000918952	10.2399	Kinesin family member 1B (Kif1b)
Dnmt1	0.25	.045603846	5.362349	DNA methyltransferase (cytosine-5) 1 (Dnmt1)
Dkc1	0.25	.030357657	5.517805	Dyskeratosis congenita 1, dyskerin (Dkc1)
Tnfrsf21	0.25	.017335584	6.787653	Tumor necrosis factor receptor superfamily, member 21 (Tnfrsf21)
Tcf20	0.25	.006554422	8.850207	Transcription factor 20 (Tcf20)
Tuba1b	0.25	.017513457	8.113302	Tubulin, alpha 1B (Tuba1b)
Add1	0.25	.006551052	7.73364	Adducin 1 (alpha) (Add1)
Mapk8ip3	0.25	.002650302	7.907594	Mitogen-activated protein kinase 8 interacting protein 3 (Mapk8ip3)
Chn1	0.25	.007728443	8.016187	Chimerin 1 (Chn1)
Srk2	0.25	.002131015	8.320705	Serine/arginine-rich protein-specific kinase 2 (Srpk2)
Fam32a	0.25	.030225363	6.452244	Family with sequence similarity 32, member A (Fam32a)
Me2	0.25	.046883031	5.564346	Malic enzyme 2, NAD (+)-dependent, mitochondrial (Me2)
Nudcd3	0.25	.024792245	6.990762	NudC domain containing 3 (Nudcd3)
Sept8	0.25	.017778556	7.230033	Septin 8 (Sept8)
Scaper	0.25	.018412516	6.805533	S phase cyclin A-associated protein in the ER (Scaper)
Gopc	0.25	.020478126	5.897352	Golgi-associated PDZ and coiled-coil motif containing (Gopc)
Uhrf2	0.25	.0270711	5.70033	Ubiquitin-like, containing PHD and RING finger domains 2 (Uhrf2)
Abr	0.25	.005105436	9.073203	Active BCR-related gene (Abr)
Nsg2	0.25	.004056965	9.753347	Neuron-specific gene family member 2 (Nsg2)
Dcaf5	0.25	.006972324	7.446307	DDB1 and CUL4-associated factor 5 (Dcaf5)
Tnrc6c	0.25	.033517407	6.518989	Trinucleotide repeat containing 6C (Tnrc6c)
Suz12	0.25	.029100629	6.147761	Suppressor of zeste 12 homolog (Suz12)
Chd6	0.25	.007012116	7.179272	Chromodomain helicase DNA binding protein 6 (Chd6)
Kantr	0.25	.027476306	7.107519	Kdm5c adjacent non-coding transcript (Kantr)
Tnpo3	0.25	.039248562	6.161886	Transportin 3 (Tnpo3)
Gnal	0.25	.020292867	9.496616	Guanine nucleotide binding protein, alpha stimulating, olfactory type (Gnal)
Bscl2	0.25	.03535563	5.854313	Berardinelli-Seip congenital lipodystrophy 2 (seipin) (Bscl2)
Pcyt1b	0.24	.036428621	5.69344	Phosphate cytidylyltransferase 1, choline, beta isoform (Pcyt1b)
Kpna4	0.24	.008599471	7.319111	Karyopherin (importin) alpha 4 (Kpna4)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tmem151a	0.24	.046172933	6.720247	Transmembrane protein 151A (Tmem151a)
Crk	0.24	.006545879	7.405028	V-crk avian sarcoma virus CT10 oncogene homolog (Crk)
Plekha6	0.24	.03236134	7.295051	Pleckstrin homology domain containing, family A member 6 (Plekha6)
Dnal1	0.24	.007758999	7.330454	Dynein, axonemal, light chain 1 (Dnal1)
Btbd10	0.24	.042727863	5.313358	BTB (POZ) domain containing 10 (Btbd10)
Fdft1	0.24	.014112988	7.343004	Farnesyl diphosphate farnesyl transferase 1 (Fdft1)
Ank	0.24	.023195254	7.008378	Progressive ankylosis (Ank)
Dhx15	0.24	.041329746	6.463917	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Dhx15)
Rnft2	0.24	.045862511	5.862266	Ring finger protein, transmembrane 2 (Rnft2)
Tmem63b	0.24	.028507804	6.652321	Transmembrane protein 63b (Tmem63b)
Cdkl2	0.24	.017382173	5.902465	Cyclin-dependent kinase-like 2 (CDC2-related kinase) (Cdkl2)
Zfp334	0.24	.039055913	5.637022	Zinc finger protein 334 (Zfp334)
Hsp90b1	0.24	.010059756	9.137121	Heat shock protein 90, beta (Grp94), member 1 (Hsp90b1)
Strip1	0.24	.030883398	5.861158	Striatin interacting protein 1 (Strip1)
Pkia	0.24	.04706864	7.844332	Protein kinase inhibitor, alpha (Pkia)
Creb1	0.24	.036999146	6.575222	cAMP responsive element binding protein 1 (Creb1)
Stk4	0.24	.030123955	6.091511	Serine/threonine kinase 4 (Stk4)
Rc3h2	0.24	.012241839	7.502372	Ring finger and CCCH-type zinc finger domains 2 (Rc3h2)
Kndc1	0.24	.045987994	7.643667	Kinase noncatalytic C-lobe domain (KIND) containing 1 (Kndc1)
Adcy5	0.24	.016467427	6.945322	Adenylate cyclase 5 (Adcy5)
Bptf	0.24	.019950533	7.853825	Bromodomain PHD finger transcription factor (Bptf)
Cul5	0.24	.018047502	6.614429	Cullin 5 (Cul5)
Rab11a	0.24	.01229741	6.536686	RAB11A, member RAS oncogene family (Rab11a)
Gdi2	0.24	.003074155	8.372964	Guanosine diphosphate (GDP) dissociation inhibitor 2 (Gdi2)
Abca5	0.24	.033073279	6.202761	ATP-binding cassette, sub-family A (ABC1), member 5 (Abca5)
Vapb	0.24	.013580507	7.092663	Vesicle-associated membrane protein, associated protein B and C (Vapb)
Tao2	0.24	.015190111	6.465679	TAO kinase 2 (Tao2)
Mbtps1	0.24	.032437521	5.979646	Membrane-bound transcription factor peptidase, site 1 (Mbtps1)
Rrn3	0.24	.041142492	6.603308	RRN3 RNA polymerase I transcription factor homolog (yeast) (Rrn3)
Arid4b	0.24	.02296604	6.188233	AT-rich interactive domain 4B (RBP1-like) (Arid4b)
Prmt5	0.24	.045645557	5.838054	Protein arginine N-methyltransferase 5 (Prmt5)
Prpf8	0.24	.005595738	8.014264	Pre-mRNA processing factor 8 (Prpf8)
Sgtb	0.24	.010199583	7.17704	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta (Sgtb)
Manea	0.24	.01810091	5.86709	Mannosidase, endo-alpha (Manea)
Ulk2	0.24	.012607818	7.322568	Unc-51 like kinase 2 (Ulk2)
Mrpl39	0.24	.040743171	5.060474	Mitochondrial ribosomal protein L39 (Mrpl39)
Rcc2	0.24	.014323411	6.670595	Regulator of chromosome condensation 2 (Rcc2)
Setbp1	0.24	.040056873	5.508508	SET binding protein 1 (Setbp1)
Macrod2	0.24	.042931647	6.329326	MACRO domain containing 2 (Macrod2)
Taf2	0.24	.033036522	6.274409	TATA-box binding protein-associated factor 2 (Taf2)
Ppp4r2	0.24	.020994392	6.406066	Protein phosphatase 4, regulatory subunit 2 (Ppp4r2)
Pdcd6ip	0.24	.026812881	6.862055	Programmed cell death 6 interacting protein (Pdcd6ip)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Clptm1	0.24	.010674757	7.477241	Cleft lip and palate-associated transmembrane protein 1 (Clptm1)
Trps1	0.24	.030443375	6.827773	Trichorhinophalangeal syndrome I (human) (Trps1)
Khdrbs1	0.24	.021576939	6.671807	KH domain containing, RNA binding, signal transduction associated 1 (Khdrbs1)
Elp2	0.24	.038766709	5.968091	Elongator acetyltransferase complex subunit 2 (Elp2)
Adgrb2	0.24	.038173009	6.594675	Adhesion G protein-coupled receptor B2 (Adgrb2)
Tbc1d24	0.24	.024814573	6.406851	TBC1 domain family, member 24 (Tbc1d24)
Xpr1	0.24	.017591619	9.187294	Xenotropic and polytropic retrovirus receptor 1 (Xpr1)
Ascc3	0.24	.020486611	5.894079	Activating signal cointegrator 1 complex subunit 3 (Ascc3)
Synj2bp	0.24	.041075165	6.285633	Synaptojanin 2 binding protein (Synj2bp)
B930095G15Rik	0.23	.022829429	6.251638	RIKEN cDNA B930095G15 gene (B930095G15Rik)
Cdc27	0.23	.012137354	7.095631	Cell division cycle 27 (Cdc27)
Synpo2	0.23	.037056061	7.898035	Synaptopodin 2 (Synpo2)
Casd1	0.23	.017970109	7.021037	CAS1 domain containing 1 (Casd1)
Prrt1	0.23	.045898899	6.588541	Proline-rich transmembrane protein 1 (Prrt1)
Afap1	0.23	.034479972	5.701328	Actin filament-associated protein 1 (Afap1)
Fasn	0.23	.010781429	7.875931	Fatty acid synthase (Fasn)
Thoc1	0.23	.037213395	5.629454	THO complex 1 (Thoc1)
Clcn3	0.23	.019386897	7.808005	Chloride channel, voltage-sensitive 3 (Clcn3)
Ppp2r5d	0.23	.030906742	6.600648	Protein phosphatase 2, regulatory subunit B', delta (Ppp2r5d)
Thra	0.23	.010197793	7.778314	Thyroid hormone receptor alpha (Thra)
Lgals1	0.23	.024771474	6.288153	Lectin, galactoside binding-like (Lgals1)
Lrch1	0.23	.048954948	5.236242	Leucine-rich repeats and calponin homology (CH) domain containing 1 (Lrch1)
G6pc3	0.23	.020958841	6.090829	Glucose 6 phosphatase, catalytic, 3 (G6pc3)
Tmem184c	0.23	.036194616	6.366835	Transmembrane protein 184C (Tmem184c)
Iars	0.23	.027119805	6.374181	Isoleucine-tRNA synthetase (Iars)
Pitpna	0.23	.004117539	9.032461	Phosphatidylinositol transfer protein, alpha (Pitpna)
Pik3ca	0.23	.016904859	6.874957	Phosphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca)
Pcsk1n	0.23	.01533009	8.013988	Proprotein convertase subtilisin/kexin type 1 inhibitor (Pcsk1n)
Chd3os	0.23	.008933403	7.316628	Chromodomain helicase DNA binding protein 3, opposite strand (Chd3os)
Drosha	0.23	.0102172	6.867096	Drosha, ribonuclease type III (Drosha)
Jakmip2	0.23	.042148973	6.768761	Janus kinase and microtubule interacting protein 2 (Jakmip2)
Grin2b	0.23	.004690257	9.977914	Glutamate receptor, ionotropic, NMDA2B (epsilon 2) (Grin2b)
Cpeb2	0.23	.024537408	6.907478	Cytoplasmic polyadenylation element binding protein 2 (Cpeb2)
Edem3	0.23	.01936051	6.610494	ER degradation enhancer, mannosidase alpha-like 3 (Edem3)
Atrx	0.23	.00357055	8.255195	Alpha thalassemia/mental retardation syndrome X-linked (Atrx)
Tom1l2	0.23	.005639071	8.678078	Target of myb1-like 2 (chicken) (Tom1l2)
Cbx5	0.23	.00417953	9.319247	Chromobox 5 (Cbx5)
Copb2	0.23	.013314006	6.888134	Coatomer protein complex, subunit beta 2 (beta prime) (Copb2)
Aldoa	0.23	.02921891	9.780481	Aldolase A, fructose-bisphosphate (Aldoa)
Arhgdia	0.23	.011112733	8.369957	Rho GDP dissociation inhibitor (GDI) alpha (Arhgdia)
Rock2	0.23	.004247972	8.580233	Rho-associated coiled-coil containing protein kinase 2 (Rock2)
Sept6	0.23	.017555223	6.535214	Septin 6 (Sept6)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Kazn	0.23	.024202783	6.908172	Kazrin, periplakin interacting protein (Kazn)
Stau2	0.23	.005383984	8.255218	Staufen (RNA binding protein) homolog 2 (Stau2)
Pds5b	0.23	.008679751	7.998538	PDS5 cohesin-associated factor B (Pds5b)
Vps37a	0.23	.012411112	7.512598	Vacuolar protein sorting 37A (Vps37a)
Dctn1	0.23	.045685692	6.927864	Dynactin 1 (Dctn1)
Dnajc18	0.23	.009088717	7.62907	DnaJ heat shock protein family (Hsp40) member C18 (Dnajc18)
Fam91a1	0.23	.014242206	6.905897	Family with sequence similarity 91, member A1 (Fam91a1)
Terf2ip	0.23	.015523404	6.368839	Telomeric repeat binding factor 2, interacting protein (Terf2ip)
Dek	0.23	.048577372	6.400542	DEK oncogene (DNA binding) (Dek)
Cdc37l1	0.23	.017116236	7.603095	Cell division cycle 37-like 1 (Cdc37l1)
Clcn6	0.23	.019893244	7.532963	Chloride channel, voltage-sensitive 6 (Clcn6)
Usp47	0.23	.009725869	7.14803	Ubiquitin-specific peptidase 47 (Usp47)
Tbl1xr1	0.23	.022264941	7.167374	Transducin (beta)-like 1X-linked receptor 1 (Tbl1xr1)
Eif3i	0.23	.029478024	7.064884	Eukaryotic translation initiation factor 3, subunit I (Eif3i)
Bcl7a	0.22	.038742784	5.845352	B cell CLL/lymphoma 7A (Bcl7a)
Hspa8	0.22	.018106183	9.218006	Heat shock protein 8 (Hspa8)
Azi2	0.22	.033580361	6.503647	5-Azacytidine-induced gene 2 (Azi2)
Pitpnc1	0.22	.03256127	7.709743	Phosphatidylinositol transfer protein, cytoplasmic 1 (Pitpnc1)
Csnk2a2	0.22	.038403562	6.086306	Casein kinase 2, alpha prime polypeptide (Csnk2a2)
Asap1	0.22	.0241556	7.280941	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 (Asap1)
Selenoi	0.22	.044206887	6.186981	Selenoprotein I (Selenoi)
Srpk1	0.22	.031541489	6.425031	Serine/arginine-rich protein-specific kinase 1 (Srpk1)
Crebrf	0.22	.034005247	7.967018	CREB3 regulatory factor (Crebrf)
Tmem57	0.22	.029741268	6.263453	Transmembrane protein 57 (Tmem57)
Iqsec3	0.22	.018168344	8.050706	IQ motif and Sec7 domain 3 (Iqsec3)
Large1	0.22	.039883798	5.948991	LARGE xylosyl- and glucuronyltransferase 1 (Large1)
Rabif	0.22	.029431927	5.902428	RAB interacting factor (Rabif)
Ubap2l	0.22	.006784378	7.770741	Ubiquitin-associated protein 2-like (Ubap2l)
Mcfd2	0.22	.023310887	6.360756	Multiple coagulation factor deficiency 2 (Mcfd2)
Vps53	0.22	.033260188	6.270787	VPS53 GARP complex subunit (Vps53)
Phc3	0.22	.040459768	7.704432	Polyhomeotic-like 3 (Phc3)
Suco	0.22	.026858117	7.15394	SUN domain containing ossification factor (Suco)
Errfi1	0.22	.038742784	5.789123	ERBB receptor feedback inhibitor 1 (Errfi1)
Eif4g2	0.22	.002685008	10.42965	Eukaryotic translation initiation factor 4, gamma 2 (Eif4g2)
Omg	0.22	.010711707	8.141917	Oligodendrocyte myelin glycoprotein (Omg)
Acox1	0.22	.012543035	7.605381	Acyl-Coenzyme A oxidase 1, palmitoyl (Acox1)
Dido1	0.22	.038708577	6.714423	Death inducer-obliterator 1 (Dido1)
Rad21	0.22	.018168344	7.502774	RAD21 cohesin complex component (Rad21)
Ndfip1	0.22	.009717673	8.867982	Nedd4 family interacting protein 1 (Ndfip1)
Cap2	0.22	.017738926	7.765202	CAP, adenylate cyclase-associated protein, 2 (yeast) (Cap2)
Abce1	0.22	.036399601	6.590981	ATP-binding cassette, sub-family E (OABP), member 1 (Abce1)
Atrn	0.22	.010061854	8.392604	Attractin (Atrn)
Zfp369	0.22	.048683336	5.752277	Zinc finger protein 369 (Zfp369)
Leprotl1	0.22	.037366063	6.712683	Leptin receptor overlapping transcript-like 1 (Leprotl1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
D5Ert579e	0.21	.021282694	7.421499	DNA segment, Chr 5, ERATO Doi 579, expressed (D5Ert579e)
Arl8b	0.21	.006886961	8.191092	ADP-ribosylation factor-like 8B (Arl8b)
Prrc2c	0.21	.005078156	8.985612	Proline-rich coiled-coil 2C (Prrc2c)
Map7d2	0.21	.026275616	7.251992	MAP7 domain containing 2 (Map7d2)
Txnl1	0.21	.017907964	6.938467	Thioredoxin-like 1 (Txnl1)
Fkrp	0.21	.044699789	5.979782	Fukutin-related protein (Fkrp)
Phrf1	0.21	.044693678	5.464877	PHD and ring finger domains 1 (Phrf1)
Trappc10	0.21	.033011839	6.408274	Trafficking protein particle complex 10 (Trappc10)
R3hdm1	0.21	.012152036	7.863841	R3H domain containing 1 (R3hdm1)
Mta3	0.21	.036169268	6.149123	Metastasis associated 3 (Mta3)
Syngap1	0.21	.023560786	7.569885	Synaptic Ras GTPase activating protein 1 homolog (rat) (Syngap1)
Dtd1	0.21	.034044459	7.077657	D-tyrosyl-tRNA deacylase 1 (Dtd1)
Ube2n	0.21	.025866771	7.243544	Ubiquitin-conjugating enzyme E2N (Ube2n)
Unc80	0.21	.004056965	9.577441	Unc-80, NALCN activator (Unc80)
Nat8l	0.21	.016352893	7.033942	N-acetyltransferase 8-like (Nat8l)
Spag9	0.21	.011143937	9.07335	Sperm-associated antigen 9 (Spag9)
Gtf3c1	0.21	.022270126	6.500793	General transcription factor III C 1 (Gtf3c1)
Mgea5	0.21	.006469373	8.392484	Meningioma expressed antigen 5 (hyaluronidase) (Mgea5)
Uqcrc2	0.21	.028720561	7.035127	Ubiquinol cytochrome c reductase core protein 2 (Uqcrc2)
Trim3	0.21	.03186925	6.065105	Tripartite motif-containing 3 (Trim3)
Nup50	0.21	.032541327	6.253364	Nucleoporin 50 (Nup50)
Snrk	0.21	.048207709	6.811954	SNF-related kinase (Snrk)
Strap	0.21	.014694164	7.290549	Serine/threonine kinase receptor-associated protein (Strap)
Clip1	0.21	.039060407	7.444099	CAP-GLY domain containing linker protein 1 (Clip1)
Fat1	0.21	.016156971	7.702461	FAT atypical cadherin 1 (Fat1)
Fam102a	0.21	.025954131	7.139414	Family with sequence similarity 102, member A (Fam102a)
Glyr1	0.21	.032942506	6.343444	Glyoxylate reductase 1 homolog (Arabidopsis) (Glyr1)
Atp6v0d1	0.21	.045685535	7.900166	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit D1 (Atp6v0d1)
Arhgef17	0.21	.019362505	7.500893	Rho guanine nucleotide exchange factor (GEF) 17 (Arhgef17)
Npm1	0.21	.013058982	7.651072	Nucleophosmin 1 (Npm1)
Ndst1	0.21	.023872569	7.527521	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 (Ndst1)
Fyn	0.21	.035282357	6.954519	Fyn proto-oncogene (Fyn)
Ppid	0.21	.047036448	6.592722	Peptidylprolyl isomerase D (cyclophilin D) (Ppid)
Smap2	0.21	.021282694	7.021789	Small ArfGAP 2 (Smap2)
Rbm27	0.21	.019447739	6.737948	RNA binding motif protein 27 (Rbm27)
Megf11	0.21	.031688737	6.920557	Multiple EGF-like-domains 11 (Megf11)
Bbs1	0.21	.034308347	6.075153	Bardet-Biedl syndrome 1 (human) (Bbs1)
Ankrd17	0.20	.005272877	8.604074	Ankyrin repeat domain 17 (Ankrd17)
Psip1	0.20	.016926657	7.887736	PC4 and SFRS1 interacting protein 1 (Psip1)
Hspd1	0.20	.022972473	7.851378	Heat shock protein 1 (chaperonin) (Hspd1)
Msantd4	0.20	.032313642	6.870624	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils (Msantd4)
Ncoa2	0.20	.010774339	7.639831	Nuclear receptor coactivator 2 (Ncoa2)
Pfkp	0.20	.03169816	6.784532	Phosphofructokinase, platelet (Pfkp)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Armc8	0.20	.038206676	6.974349	Armadillo repeat containing 8 (Armc8)
Capzb	0.20	.026590519	7.682041	Capping protein (actin filament) muscle Z-line, beta (Capzb)
Pfn2	0.20	.012650969	7.980521	Profilin 2 (Pfn2)
Sub1	0.20	.024511176	8.617964	SUB1 homolog ( <i>S. cerevisiae</i> ) (Sub1)
Zwint	0.20	.009821897	9.575665	ZW10 interactor (Zwint)
Eif2s1	0.20	.048683336	6.205005	Eukaryotic translation initiation factor 2, subunit 1 alpha (Eif2s1)
Usp7	0.20	.030298047	7.371317	Ubiquitin-specific peptidase 7 (Usp7)
Exoc6b	0.20	.014237722	7.298128	Exocyst complex component 6B (Exoc6b)
Tspsyl1	0.20	.036037976	7.667227	Testis-specific protein, Y-encoded-like 1 (Tspsyl1)
Cdip1	0.20	.049496716	7.380801	Cell death inducing Trp53 target 1 (Cdip1)
1500004A13Rik	0.20	.02035408	6.813499	RIKEN cDNA 1500004A13 gene (1500004A13Rik)
Slc35e1	0.20	.04543885	5.77335	Solute carrier family 35, member E1 (Slc35e1)
Spire1	0.20	.039883798	8.14859	Spire homolog 1 (Spire1)
Aida	0.20	.037918718	6.387968	Axin interactor, dorsalization associated (Aida)
Zfhx3	0.20	.033140031	8.904693	Zinc finger homeobox 3 (Zfhx3)
Scamp5	0.20	.021862153	8.218513	Secretory carrier membrane protein 5 (Scamp5)
Zfp423	0.20	.047493724	7.796412	Zinc finger protein 423 (Zfp423)
Bub3	0.20	.036051448	6.142762	BUB3 mitotic checkpoint protein (Bub3)
2310035C23Rik	0.20	.032288886	6.45985	RIKEN cDNA 2310035C23 gene (2310035C23Rik)
Trak1	0.19	.019118752	7.711733	Trafficking protein, kinesin binding 1 (Trak1)
Ccdc85a	0.19	.037916588	6.256121	Coiled-coil domain containing 85A (Ccdc85a)
Sept7	0.19	.021556437	7.534803	Septin 7 (Sept7)
Otud6b	0.19	.04543885	6.286238	OTU domain containing 6B (Otud6b)
Kpnrb1	0.19	.026285895	7.662213	Karyopherin (importin) beta 1 (Kpnrb1)
Ipmk	0.19	.039022702	6.445374	Inositol polyphosphate multikinase (Ipmk)
Smc1a	0.19	.032573303	6.696561	Structural maintenance of chromosomes 1A (Smc1a)
Spred1	0.19	.049261866	7.451375	Sprouty protein with EVH-1 domain 1, related sequence (Spred1)
Snrnp200	0.19	.028914258	6.980469	Small nuclear ribonucleoprotein 200 (U5) (Snrnp200)
Sort1	0.19	.028743818	7.937391	Sortilin 1 (Sort1)
Map4	0.19	.005612815	9.895507	Microtubule-associated protein 4 (Map4)
Gbf1	0.19	.040257526	6.992578	Golgi-specific brefeldin A-resistance factor 1 (Gbf1)
Hnrrnpk	0.19	.02218019	7.911042	Heterogeneous nuclear ribonucleoprotein K (Hnrrnpk)
Sestd1	0.19	.048334791	6.538606	SEC14 and spectrin domains 1 (Sestd1)
Eif3c	0.19	.041234666	7.586635	Eukaryotic translation initiation factor 3, subunit C (Eif3c)
Atxn10	0.19	.049619707	7.843968	Ataxin 10 (Atxn10)
Celf1	0.19	.02794052	7.598323	CUGBP, Elav-like family member 1 (Celf1)
Ubr3	0.19	.021180627	8.054207	Ubiquitin protein ligase E3 component n-recognin 3 (Ubr3)
Itsn1	0.19	.029614858	8.73734	Intersectin 1 (SH3 domain protein 1A) (Itsn1)
Celsr2	0.19	.033744533	7.667407	Cadherin, EGF LAG seven-pass G-type receptor 2 (Celsr2)
Bnip3l	0.19	.014327052	7.815339	BCL2/adenovirus E1B interacting protein 3-like (Bnip3l)
Copa	0.18	.025336187	7.963883	Coatomer protein complex subunit alpha (Copa)
Sms	0.18	.049266826	6.607688	Spermine synthase (Sms)
Ankrd11	0.18	.024248549	7.591252	Ankyrin repeat domain 11 (Ankrd11)
Zfyve9	0.18	.048277082	6.584251	Zinc finger, FYVE domain containing 9 (Zfyve9)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Atp6v1g2	0.18	.022623953	8.952172	ATPase, H+ transporting, lysosomal V1 subunit G2 (Atp6v1g2)
Smg7	0.18	.031688737	7.673229	Smg-7 homolog, nonsense mediated mRNA decay factor ( <i>C. elegans</i> ) (Smg7)
Trip12	0.17	.023634137	8.276152	Thyroid hormone receptor interactor 12 (Trip12)
Top2b	0.17	.048638299	7.07136	Topoisomerase (DNA) II beta (Top2b)
Cend1	0.17	.031032057	9.045587	Cell cycle exit and neuronal differentiation 1 (Cend1)
Appl1	0.17	.038916137	6.92413	Adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 (Appl1)
Ggnbp2	0.17	.041155115	7.23954	Gametogenitin binding protein 2 (Ggnbp2)
Srgap3	0.17	.034807889	8.609683	SLIT-ROBO Rho GTPase activating protein 3 (Srgap3)
Bclaf1	0.16	.046461052	7.931701	BCL2-associated transcription factor 1 (Bclaf1)
Aff4	0.16	.044118355	8.509122	AF4/FMR2 family, member 4 (Aff4)
Clasp2	0.16	.025284743	8.918275	CLIP associating protein 2 (Clasp2)
Tgoln1	0.16	.037254426	8.093881	Trans-golgi network protein (Tgoln1)
Ralgapb	0.16	.038812289	7.786821	Ral GTPase activating protein, beta subunit (non-catalytic) (Ralgapb)
Rabep1	0.16	.045426572	7.691113	Rabaptin, RAB GTPase binding effector protein 1 (Rabep1)
Ube2b	0.15	.037492468	7.726242	Ubiquitin-conjugating enzyme E2B (Ube2b)
Cyb5b	0.15	.047404683	7.678542	Cytochrome b5 type B (Cyb5b)
Hsp90ab1	0.15	.032185692	10.72416	Heat shock protein 90 alpha (cytosolic), class B member 1 (Hsp90ab1)
Serbp1	0.14	.042604347	8.528189	Serpine1 mRNA binding protein 1 (Serbp1)
Reep5	0.14	.035818368	9.583036	Receptor accessory protein 5 (Reep5)
Mat2a	-0.18	.029404518	7.582335	Methionine adenosyltransferase II, alpha (Mat2a)
Phyhipl	-0.19	.022680986	7.433778	Phytanoyl-CoA hydroxylase interacting protein-like (Phyhipl)
Calm3	-0.19	.028420636	8.65292	Calmodulin 3 (Calm3)
Psme3	-0.20	.029511489	6.679222	Proteaseome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) (Psme3)
9530068E07Rik	-0.20	.027380706	6.96003	RIKEN cDNA 9530068E07 gene (9530068E07Rik)
Ckap5	-0.20	.02474113	7.681142	Cytoskeleton-associated protein 5 (Ckap5)
Dtna	-0.20	.048540176	7.608819	Dystrobrevin alpha (Dtna)
Tnks2	-0.20	.038960893	7.368871	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 (Tnks2)
Dag1	-0.20	.019824798	7.131407	Dystroglycan 1 (Dag1)
Chtop	-0.20	.015123266	7.463196	Chromatin target of PRMT1 (Chtop)
Map2	-0.20	.004795535	9.983491	Microtubule-associated protein 2 (Map2)
Capns1	-0.21	.021141437	7.702451	Calpain, small subunit 1 (Capns1)
Ewsr1	-0.21	.034904516	6.072625	EWING sarcoma breakpoint region 1 (Ewsr1)
Wnk2	-0.21	.029084936	7.039452	WNK lysine deficient protein kinase 2 (Wnk2)
Ppm1b	-0.21	.032876379	7.139224	Protein phosphatase 1B, magnesium dependent, beta isoform (Ppm1b)
Mark3	-0.21	.047725201	5.69677	MAP/microtubule affinity regulating kinase 3 (Mark3)
Pacs2	-0.21	.049261866	7.922781	Phosphofuran acid cluster sorting protein 2 (Pacs2)
Lamp2	-0.22	.020902731	7.129216	Lysosomal-associated membrane protein 2 (Lamp2)
Eef1a1	-0.22	.002386636	10.01755	Eukaryotic translation elongation factor 1 alpha 1 (Eef1a1)
Tagln3	-0.22	.045645557	7.037695	Transgelin 3 (Tagln3)
Tjp1	-0.22	.037366063	7.078721	Tight junction protein 1 (Tjp1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Fez1	-0.22	.019133946	6.586395	Fasciculation and elongation protein zeta 1 (zygin I) (Fez1)
Zfyve27	-0.22	.04840043	5.356501	Zinc finger, FYVE domain containing 27 (Zfyve27)
Usp24	-0.22	.015743725	6.845824	Ubiquitin-specific peptidase 24 (Usp24)
Sptbn1	-0.22	.033918619	9.649821	Spectrin beta, non-erythrocytic 1 (Sptbn1)
Higd1a	-0.22	.048098188	6.351253	HIG1 domain family, member 1A (Higd1a)
Fundc1	-0.22	.033222174	6.078343	FUN14 domain containing 1 (Fundc1)
Dnajc8	-0.22	.048026004	5.994237	DnaJ heat shock protein family (Hsp40) member C8 (Dnajc8)
Cpped1	-0.22	.04315154	5.674905	Calcineurin-like phosphoesterase domain containing 1 (Cpped1)
Hnrnpa2b1	-0.23	.032288886	8.339669	Heterogeneous nuclear ribonucleoprotein A2/B1 (Hnrnpa2b1)
Ipo11	-0.23	.02794052	5.869566	Importin 11 (Ipo11)
Tmcc2	-0.23	.042701165	6.955315	Transmembrane and coiled-coil domains 2 (Tmcc2)
Ccni	-0.23	.031624232	8.073274	Cyclin I (Ccni)
St13	-0.23	.024270826	6.637612	Suppression of tumorigenicity 13 (St13)
Fam103a1	-0.23	.044699789	6.13996	Family with sequence similarity 103, member A1 (Fam103a1)
Edf1	-0.23	.047602141	7.219681	Endothelial differentiation-related factor 1 (Edf1)
Sall2	-0.23	.021380885	6.406947	Sal-like 2 (Sall2)
Slc25a4	-0.23	.014205371	9.314009	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4 (Slc25a4)
Serinc3	-0.23	.010268109	8.211402	Serine incorporator 3 (Serinc3)
Chmp2b	-0.23	.031387276	5.341422	Charged multivesicular body protein 2B (Chmp2b)
Pls3	-0.23	.018779257	6.951053	Plastin 3 (T-isoform) (Pls3)
Odc1	-0.23	.034180961	5.955828	Ornithine decarboxylase, structural 1 (Odc1)
Ugp2	-0.23	.019094095	6.421912	UDP-glucose pyrophosphorylase 2 (Ugp2)
Stt3b	-0.24	.037953708	6.384695	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae) (Stt3b)
Nf1	-0.24	.003894461	8.325326	Neurofibromatosis 1 (Nf1)
Nbr1	-0.24	.016135328	6.657396	Neighbor of Brca1 gene 1 (Nbr1)
Sod2	-0.24	.020239088	7.314313	Superoxide dismutase 2, mitochondrial (Sod2)
Epn2	-0.24	.019401615	6.345149	Epsin 2 (Epn2)
Zfp330	-0.24	.042604347	4.865023	Zinc finger protein 330 (Zfp330)
Hdgf	-0.24	.034308347	6.773475	Hepatoma-derived growth factor (Hdgf)
Atf7ip	-0.24	.007354928	6.895615	Activating transcription factor 7 interacting protein (Atf7ip)
Cat	-0.24	.022261006	6.349767	Catalase (Cat)
Fbxo18	-0.24	.029856638	5.325475	F-box protein 18 (Fbxo18)
Rbmx	-0.24	.031316414	5.785527	RNA binding motif protein, X chromosome (Rbmx)
Dynll2	-0.24	.008739203	7.108816	Dynein light chain LC8-type 2 (Dynll2)
Amfr	-0.24	.011650588	7.325955	Autocrine motility factor receptor (Amfr)
Acbd5	-0.24	.026300658	7.227923	Acyl-Coenzyme A binding domain containing 5 (Acbd5)
Dnttip2	-0.24	.037893608	5.073691	Deoxynucleotidyltransferase, terminal, interacting protein 2 (Dnttip2)
Calcoco1	-0.24	.021656056	5.499136	Calcium binding and coiled coil domain 1 (Calcoco1)
Pex19	-0.24	.040565049	5.906631	Peroxisomal biogenesis factor 19 (Pex19)
Sgpp1	-0.25	.022383684	6.333106	Sphingosine-1-phosphate phosphatase 1 (Sgpp1)
Smim7	-0.25	.029856638	6.244041	Small integral membrane protein 7 (Smim7)
Osbpl9	-0.25	.022861183	5.891799	Oxysterol binding protein-like 9 (Osbpl9)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Slc25a23	-0.25	.027621271	8.756569	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 (Slc25a23)
Kcnk1	-0.25	.037129423	6.110503	Potassium channel, subfamily K, member 1 (Kcnk1)
Rasgef1b	-0.25	.022676509	5.982417	RasGEF domain family, member 1B (Rasgef1b)
Bbip1	-0.25	.048703145	5.34488	BBSome interacting protein 1 (Bbip1)
Phactr3	-0.25	.030123955	6.30021	Phosphatase and actin regulator 3 (Phactr3)
Oxsr1	-0.25	.027664989	5.572511	Oxidative-stress responsive 1 (Oxsr1)
Kat6a	-0.25	.033139201	6.610582	K (lysine) acetyltransferase 6A (Kat6a)
Hnrnpm	-0.25	.043869314	5.443259	Heterogeneous nuclear ribonucleoprotein M (Hnrnpm)
2810403A07Rik	-0.25	.018929779	5.636397	RIKEN cDNA 2810403A07 gene (2810403A07Rik)
Arid1b	-0.25	.03932386	5.455294	AT-rich interactive domain 1B (SWI-like) (Arid1b)
Rpl4	-0.25	.001129865	9.115343	Ribosomal protein L4 (Rpl4)
Cog3	-0.25	.043869775	4.982244	Component of oligomeric golgi complex 3 (Cog3)
Btaf1	-0.25	.048980131	5.230846	B-TFIID TATA-box binding protein-associated factor 1 (Btaf1)
Fus	-0.25	.026567644	6.534785	Fused in sarcoma (Fus)
Slc3a2	-0.26	.03138491	6.435586	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (Slc3a2)
Tspan13	-0.26	.044048868	8.569765	Tetraspanin 13 (Tspan13)
Gnai3	-0.26	.042090453	5.639429	Guanine nucleotide binding protein (G protein), alpha inhibiting 3 (Gnai3)
Arxes2	-0.26	.037646782	4.983505	Adipocyte-related X-chromosome expressed sequence 2 (Arxes2)
Phlpp1	-0.26	.006308037	6.748707	PH domain and leucine-rich repeat protein phosphatase 1 (Phlpp1)
Ankhd1	-0.26	.015576916	6.296844	Ankyrin repeat and KH domain containing 1 (Ankhd1)
Psme4	-0.26	.042061361	5.440159	Proteasome (prosome, macropain) activator subunit 4 (Psme4)
Snn	-0.26	.023955501	6.117338	Stannin (Snn)
BC005624	-0.26	.010994407	6.164256	cDNA sequence BC005624 (BC005624)
Mapre1	-0.26	.0077379	6.934596	Microtubule-associated protein, RP/EB family, member 1 (Mapre1)
Rnh1	-0.26	.049266826	5.053477	Ribonuclease/angiogenin inhibitor 1 (Rnh1)
Necab2	-0.26	.013488601	7.788454	N-terminal EF-hand calcium binding protein 2 (Necab2)
Mterf3	-0.26	.046031584	4.501799	Mitochondrial transcription termination factor 3 (Mterf3)
Phc1	-0.26	.02813615	5.631294	Polyhomeotic-like 1 (Phc1)
Fam98a	-0.26	.049227284	4.88658	Family with sequence similarity 98, member A (Fam98a)
Rgma	-0.26	.0115973	6.693934	Repulsive guidance molecule family member A (Rgma)
Pdzd11	-0.26	.01508435	5.766269	PDZ domain containing 11 (Pdzd11)
Eps15l1	-0.26	.024649476	6.087765	Epidermal growth factor receptor pathway substrate 15-like 1 (Eps15l1)
Sltm	-0.26	.0296414	5.923339	SAFB-like, transcription modulator (Sltm)
Akap13	-0.26	.049198755	6.012378	A kinase (PRKA) anchor protein 13 (Akap13)
Snx3	-0.26	.021127669	6.289998	Sorting nexin 3 (Snx3)
Arl3	-0.27	.017852891	6.135617	ADP-ribosylation factor-like 3 (Arl3)
Nudt9	-0.27	.032750747	5.122026	Nudix (nucleoside diphosphate linked moiety X)-type motif 9 (Nudt9)
Sri	-0.27	.031541549	5.671224	Sorcin (Sri)
Sin3a	-0.27	.029170877	5.394434	Transcriptional regulator, SIN3A (yeast) (Sin3a)
Add3	-0.27	.00359095	6.715724	Adducin 3 (gamma) (Add3)
Lrba	-0.27	.019058437	6.005154	LPS-responsive beige-like anchor (Lrba)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Agpat3	-0.27	.011822831	7.742568	1-Acylglycerol-3-phosphate O-acyltransferase 3 (Agpat3)
Bod1l	-0.27	.01103335	7.14806	Biorientation of chromosomes in cell division 1-like (Bod1l)
Ddx50	-0.27	.014794905	5.628299	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50 (Ddx50)
Gabpa	-0.27	.038408411	5.396862	GA repeat binding protein, alpha (Gabpa)
Tspan9	-0.27	.045818635	5.035527	Tetraspanin 9 (Tspan9)
Shisa4	-0.27	.021282694	6.101481	Shisa family member 4 (Shisa4)
Ndufaf1	-0.27	.045685535	4.531153	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (Ndufaf1)
Bcas2	-0.27	.048334791	5.403565	Breast carcinoma amplified sequence 2 (Bcas2)
Hnrnph3	-0.27	.029169184	5.359504	Heterogeneous nuclear ribonucleoprotein H3 (Hnrnph3)
Anp32b	-0.27	.021943429	6.302753	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (Anp32b)
Stx6	-0.28	.025574347	4.776296	Syntaxin 6 (Stx6)
Pcyt1a	-0.28	.023347531	5.685035	Phosphate cytidylyltransferase 1, choline, alpha isoform (Pcyt1a)
Psma4	-0.28	.02794052	5.420277	Proteasome (prosome, macropain) subunit, alpha type 4 (Psma4)
Vti1b	-0.28	.01425755	6.755367	Vesicle transport through interaction with t-SNAREs 1B (Vti1b)
Myo10	-0.28	.02455505	5.713401	Myosin X (Myo10)
Dpy19l1	-0.28	.006968579	6.225319	Dpy-19-like 1 ( <i>C. elegans</i> ) (Dpy19l1)
Prdx5	-0.28	.048902398	6.832908	Peroxiredoxin 5 (Prdx5)
Rnf130	-0.28	.008599471	5.934991	Ring finger protein 130 (Rnf130)
Tm7sf3	-0.28	.014849369	5.751446	Transmembrane 7 superfamily member 3 (Tm7sf3)
Map4k2	-0.28	.019324903	5.559858	Mitogen-activated protein kinase kinase kinase kinase 2 (Map4k2)
Mrpl42	-0.28	.026998457	5.232647	Mitochondrial ribosomal protein L42 (Mrpl42)
Sfr1	-0.28	.017749768	6.518097	SWI5 dependent recombination repair 1 (Sfr1)
Ptpra	-0.28	.004076185	6.506519	Protein tyrosine phosphatase, receptor type, A (Ptpra)
Dst	-0.29	.033073279	9.041516	Dystonin (Dst)
Coq2	-0.29	.038847529	5.300119	Coenzyme Q2 4-hydroxybenzoate polyprenyltransferase (Coq2)
Phtf2	-0.29	.034892025	4.6744	Putative homeodomain transcription factor 2 (Phtf2)
0610009B22Rik	-0.29	.020551259	5.592015	RIKEN cDNA 0610009B22 gene (0610009B22Rik)
Btf3l4	-0.29	.025161849	4.874957	Basic transcription factor 3-like 4 (Btf3l4)
Sdh	-0.29	.012079109	6.47757	Succinate dehydrogenase complex, subunit D, integral membrane protein (Sdh)
Acsl6	-0.29	.003485907	7.3734	Acyl-CoA synthetase long-chain family member 6 (Acsl6)
Mrps15	-0.29	.024643437	4.82709	Mitochondrial ribosomal protein S15 (Mrps15)
Srp19	-0.29	.031184791	5.450445	Signal recognition particle 19 (Srp19)
Gpx1	-0.29	.007027757	6.226432	Glutathione peroxidase 1 (Gpx1)
Cyb5r3	-0.29	.008963428	6.817103	Cytochrome b5 reductase 3 (Cyb5r3)
Rtl8c	-0.29	.00336804	6.884815	Retrotransposon Gag Like 8C (Rtl8c)
Bod1	-0.29	.029856638	5.79444	Biorientation of chromosomes in cell division 1 (Bod1)
Hmgn2	-0.29	.036545246	4.46665	High-mobility group nucleosomal binding domain 2 (Hmgn2)
Mrpl34	-0.29	.019086888	4.915868	Mitochondrial ribosomal protein L34 (Mrpl34)
Tmem229a	-0.29	.037129093	7.89179	Transmembrane protein 229A (Tmem229a)
Eea1	-0.29	.005423168	6.426653	Early endosome antigen 1 (Eea1)
Herc2	-0.30	.008304718	7.716338	HECT and RLD domain containing E3 ubiquitin protein ligase 2 (Herc2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rdh14	-0.30	.033011839	4.511187	Retinol dehydrogenase 14 (all-trans and 9-cis) (Rdh14)
Smim19	-0.30	.035402795	4.66994	Small integral membrane protein 19 (Smim19)
Igfbp1	-0.30	.044827788	5.314464	Immunoglobulin (CD79A) binding protein 1 (Igfbp1)
Sympk	-0.30	.01226005	5.58604	Symplekin (Sympk)
Suds3	-0.30	.038158638	5.614964	Suppressor of defective silencing 3 homolog (S. cerevisiae) (Suds3)
Gnai2	-0.30	.003963796	7.476246	Guanine nucleotide binding protein (G protein), alpha inhibiting 2 (Gnai2)
Soat1	-0.30	.027828131	5.723837	Sterol O-acyltransferase 1 (Soat1)
Efcab14	-0.30	.011960822	7.110829	EF-hand calcium binding domain 14 (Efcab14)
Rps15a	-0.30	.001348066	7.714283	Ribosomal protein S15A (Rps15a)
Dtnbp1	-0.30	.04757055	5.344555	Dystrobrevin binding protein 1 (Dtnbp1)
Pdia4	-0.30	.028502651	5.26666	Protein disulfide isomerase associated 4 (Pdia4)
Eef1g	-0.30	.00213617	6.942786	Eukaryotic translation elongation factor 1 gamma (Eef1g)
Pnrc2	-0.30	.020227553	5.847061	Proline-rich nuclear receptor coactivator 2 (Pnrc2)
Ndufb5	-0.30	.045540796	6.505275	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (Ndufb5)
Ctsl	-0.30	.004323134	6.861777	Cathepsin L (Ctsl)
Itm2b	-0.30	.002436013	8.858788	Integral membrane protein 2B (Itm2b)
Dnajc19	-0.30	.033260188	4.55625	DnaJ heat shock protein family (Hsp40) member C19 (Dnajc19)
Porcn	-0.30	.043835047	5.01051	Porcupine homolog (Porcn)
Mpp6	-0.30	.02185883	7.652036	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (Mpp6)
Snx1	-0.30	.007757178	5.87988	Sorting nexin 1 (Snx1)
Chmp5	-0.30	.014984772	5.940911	Charged multivesicular body protein 5 (Chmp5)
B230118H07Rik	-0.30	.027788875	5.032722	RIKEN cDNA B230118H07 gene (B230118H07Rik)
Rgs2	-0.31	.034857114	5.694138	Regulator of G-protein signaling 2 (Rgs2)
Nek9	-0.31	.020366297	5.409532	NIMA (never in mitosis gene a)-related expressed kinase 9 (Nek9)
Zfand5	-0.31	.001632556	7.427132	Zinc finger, AN1-type domain 5 (Zfand5)
Slc1a4	-0.31	.004323047	5.890215	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (Slc1a4)
Ndrg1	-0.31	.008394268	5.878064	N-myc downstream-regulated gene 1 (Ndrg1)
Tex261	-0.31	.014849369	4.9824	Testis expressed gene 261 (Tex261)
Mia3	-0.31	.003317225	6.39833	Melanoma inhibitory activity 3 (Mia3)
Gm14597	-0.31	.017907964	5.520588	Predicted gene (Gm14597)
Atad2b	-0.31	.048579946	5.161203	ATPase family, AAA domain containing 2B (Atad2b)
Rpl6	-0.31	.006857215	6.385921	Ribosomal protein L6 (Rpl6)
Hnrnpa1	-0.31	.008494552	5.65413	Heterogeneous nuclear ribonucleoprotein A1 (Hnrnpa1)
Coro1b	-0.31	.018424083	5.050853	Coronin, actin binding protein 1B (Coro1b)
Map1lc3b	-0.31	.004922193	7.269997	Microtubule-associated protein 1 light chain 3 beta (Map1lc3b)
Cript	-0.31	.002137321	6.904906	Cysteine-rich PDZ-binding protein (Cript)
Hsd17b12	-0.31	.021305324	5.441834	Hydroxysteroid (17-beta) dehydrogenase 12 (Hsd17b12)
Arhgef10l	-0.31	.044110955	3.913622	Rho guanine nucleotide exchange factor (GEF) 10-like (Arhgef10l)
Psmd7	-0.31	.007008639	6.292132	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Psmd7)
Lamtor1	-0.31	.030117081	5.270539	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 (Lamtor1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tmem14c	-0.31	.040243883	4.806698	Transmembrane protein 14C (Tmem14c)
Med23	-0.31	.040901862	4.163135	Mediator complex subunit 23 (Med23)
Plxnb2	-0.31	.01013132	5.776563	Plexin B2 (Plxnb2)
5031439G07Rik	-0.32	.028092203	6.825154	RIKEN cDNA 5031439G07 gene (5031439G07Rik)
Mrps16	-0.32	.0413193	3.987191	Mitochondrial ribosomal protein S16 (Mrps16)
Pcnt	-0.32	.023529659	4.885882	Pericentrin (kendrin) (Pcnt)
Gpr108	-0.32	.016056938	4.902229	G protein-coupled receptor 108 (Gpr108)
Gcsh	-0.32	.003495536	6.435538	Glycine cleavage system protein H (aminomethyl carrier) (Gcsh)
Usf2	-0.32	.02836186	4.557085	Upstream transcription factor 2 (Usf2)
Sec61a1	-0.32	.042966543	4.465689	Sec61 alpha 1 subunit (S. cerevisiae) (Sec61a1)
Prdx1	-0.32	.017646208	7.110693	Peroxiredoxin 1 (Prdx1)
Spg11	-0.32	.024534225	4.480576	Spastic paraplegia 11 (Spg11)
Atp5c1	-0.32	.026615422	7.849047	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, gamma polypeptide 1 (Atp5c1)
Fbxo8	-0.32	.029667625	4.38742	F-box protein 8 (Fbxo8)
Cyth1	-0.32	.043127425	4.084181	Cytohesin 1 (Cyth1)
Fnta	-0.32	.014070832	6.002893	Farnesyltransferase, CAAX box, alpha (Fnta)
Gabbr1	-0.32	.000947021	10.13781	Gamma-aminobutyric acid (GABA) B receptor, 1 (Gabbr1)
Unc50	-0.32	.027261907	5.516906	Unc-50 homolog (C. elegans) (Unc50)
Srsf11	-0.32	.002452406	6.377959	Serine/arginine-rich splicing factor 11 (Srsf11)
1110004F10Rik	-0.32	.007162596	6.628161	RIKEN cDNA 1110004F10 gene (1110004F10Rik)
Ppp4r1	-0.32	.023664878	4.316199	Protein phosphatase 4, regulatory subunit 1 (Ppp4r1)
Cacng5	-0.32	.002994166	6.237949	Calcium channel, voltage-dependent, gamma subunit 5 (CACNG5)
Mpdz	-0.32	.005031819	5.725429	Multiple PDZ domain protein (Mpdz)
St6galnac4	-0.32	.020675368	4.314121	ST6(alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4 (St6galnac4)
Ndufb10	-0.32	.039714871	6.002438	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (Ndufb10)
Unc79	-0.32	.002761284	6.302647	Unc-79 homolog (C. elegans) (Unc79)
Rsu1	-0.32	.013584672	4.998013	Ras suppressor protein 1 (Rsu1)
Skp1a	-0.32	.010054031	7.672254	S-phase kinase-associated protein 1A (Skp1a)
Ptpn23	-0.33	.007698901	5.441743	Protein tyrosine phosphatase, non-receptor type 23 (Ptpn23)
Eif4a3	-0.33	.027247753	5.173418	Eukaryotic translation initiation factor 4A3 (Eif4a3)
Fbxw2	-0.33	.021265545	5.093464	F-box and WD-40 domain protein 2 (Fbxw2)
Btf3	-0.33	.02161036	5.421679	Basic transcription factor 3 (Btf3)
Rbm17	-0.33	.041302514	5.327054	RNA binding motif protein 17 (Rbm17)
Utp20	-0.33	.028592899	4.178725	UTP20 small subunit processome component (Utp20)
Tra2b	-0.33	.025845262	5.094612	Transformer 2 beta homolog (Tra2b)
Adamts20	-0.33	.045333472	3.498477	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20 (Adamts20)
Bicdl1	-0.33	.039090601	4.598759	BICD Family Like Cargo Adaptor 1 (Bicdl1)
Tspan6	-0.33	.031437245	5.12991	Tetraspanin 6 (Tspan6)
Sod1	-0.33	.011599886	8.686631	Superoxide dismutase 1, soluble (Sod1)
Eif3k	-0.33	.041166308	6.415439	Eukaryotic translation initiation factor 3, subunit K (Eif3k)
Vps13d	-0.33	.010629564	7.310236	Vacuolar protein sorting 13D (Vps13d)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Trappc6b	-0.33	.009971872	6.711676	Trafficking protein particle complex 6B (Trappc6b)
Siah1a	-0.33	.023276584	4.635733	Seven in absentia 1A (Siah1a)
Gtf2h5	-0.33	.015576268	5.463452	General transcription factor IIH, polypeptide 5 (Gtf2h5)
Chmp3	-0.33	.002485981	6.156804	Charged multivesicular body protein 3 (Chmp3)
Slc25a37	-0.33	.039256318	5.250203	Solute carrier family 25, member 37 (Slc25a37)
Surf4	-0.33	.013746434	5.581993	Surfeit gene 4 (Surf4)
Bcar1	-0.33	.02601574	4.546247	Breast cancer anti-estrogen resistance 1 (Bcar1)
Dhrs1	-0.33	.002406327	6.293994	Dehydrogenase/reductase (SDR family) member 1 (Dhrs1)
Cirbp	-0.33	.030826326	4.672219	Cold inducible RNA binding protein (Cirbp)
Otud7b	-0.33	.013955006	6.636387	OTU domain containing 7B (Otud7b)
Knop1	-0.33	.020947676	4.540222	Lysine-rich nucleolar protein 1 (Knop1)
Timm44	-0.33	.028703373	4.245006	Translocase of inner mitochondrial membrane 44 (Timm44)
Cdc42se1	-0.33	.02047175	5.071714	CDC42 small effector 1 (Cdc42se1)
Dars	-0.33	.010476027	5.114956	Aspartyl-tRNA synthetase (Dars)
Slc6a8	-0.33	.028112304	6.419921	Solute carrier family 6 (neurotransmitter transporter, creatine), member 8 (Slc6a8)
Strn3	-0.33	.006649473	6.810383	Striatin, calmodulin binding protein 3 (Strn3)
Actr3b	-0.33	.048109505	4.928606	ARP3 actin-related protein 3B (Actr3b)
Adipor2	-0.34	.009671181	5.088752	Adiponectin receptor 2 (Adipor2)
Ep400	-0.34	.004524504	6.607341	E1A binding protein p400 (Ep400)
Pdcl3	-0.34	.022289688	4.628409	phosducin-like 3 (Pdcl3)
Gle1	-0.34	.030829968	4.408031	GLE1 RNA export mediator (yeast) (Gle1)
Papss1	-0.34	.00348391	5.640647	3'-Phosphoadenosine 5'-phosphosulfate synthase 1 (Papss1)
Suclg1	-0.34	.027205934	5.889638	Succinate-CoA ligase, GDP-forming, alpha subunit (Suclg1)
Marchf8	-0.34	.029564941	5.818224	Membrane-associated ring-CH-type finger 8 (Marchf8)
Stard10	-0.34	.021265545	4.156027	START domain containing 10 (Stard10)
Trp53bp1	-0.34	.003914961	6.612606	Transformation-related protein 53 binding protein 1 (Trp53bp1)
Cers5	-0.34	.010811946	5.109968	Ceramide synthase 5 (Cers5)
Sft2d2	-0.34	.027788875	5.164481	SFT2 domain containing 2 (Sft2d2)
Fam104a	-0.34	.042574984	3.963271	Family with sequence similarity 104, member A (Fam104a)
Gcc2	-0.34	.000848083	7.047509	GRIP and coiled-coil domain containing 2 (Gcc2)
P4hb	-0.34	.00186315	6.262339	Prolyl 4-hydroxylase, beta polypeptide (P4hb)
Sorbs1	-0.34	.008775483	6.360295	Sorbin and SH3 domain containing 1 (Sorbs1)
1600012H06Rik	-0.34	.028531277	4.001906	RIKEN cDNA 1600012H06 gene (1600012H06Rik)
Med9	-0.34	.041270088	5.259304	Mediator complex subunit 9 (Med9)
Ei24	-0.34	.002896849	5.94467	Etoposide-induced 2.4 mRNA (Ei24)
Rap1a	-0.34	.02794052	5.66673	RAS-related protein-1a (Rap1a)
Luc7l2	-0.34	.00414404	6.313962	LUC7-like 2 ( <i>S. cerevisiae</i> ) (Luc7l2)
Banf1	-0.34	.039212306	4.775062	Barrier to autointegration factor 1 (Banf1)
Tead1	-0.34	.032054003	5.666116	TEA domain family member 1 (Tead1)
Map1a	-0.34	.000874691	10.06103	Microtubule-associated protein 1A (Map1a)
4933434E20Rik	-0.35	.00187235	6.501247	RIKEN cDNA 4933434E20 gene (4933434E20Rik)
Bicd2	-0.35	.007362769	5.950658	Bicaudal D homolog 2 (Bicd2)
Crcp	-0.35	.024649476	4.497548	Calcitonin gene-related peptide-receptor component protein (Crcp)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pigg	-0.35	.029404518	4.357308	Phosphatidylinositol glycan anchor biosynthesis, class P (Pigg)
Atp5g3	-0.35	.019406446	7.887496	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9) (Atp5g3)
Ccdc43	-0.35	.041439052	4.209402	Coiled-coil domain containing 43 (Ccdc43)
Gpr155	-0.35	.012676302	5.385064	G protein-coupled receptor 155 (Gpr155)
Nop53	-0.35	.01419492	5.421592	NOP53 Ribosome Biogenesis Factor (Nop53)
Tmem108	-0.35	.044600709	4.697958	Transmembrane protein 108 (Tmem108)
Ccl27a	-0.35	.011230986	4.586288	Chemokine (C-C motif) ligand 27A (Ccl27a)
Ttc21b	-0.35	.035896904	4.059452	Tetratricopeptide repeat domain 21B (Ttc21b)
Sdf2	-0.35	.031989287	5.105139	Stromal cell derived factor 2 (Sdf2)
Manf	-0.35	.0294448594	4.526091	Mesencephalic astrocyte-derived neurotrophic factor (Manf)
Cnppd1	-0.35	.045987994	4.040715	Cyclin Pas1/PHO80 domain containing 1 (Cnppd1)
Fryl	-0.35	.000519009	6.990492	FRY like transcription coactivator (Fryl)
Notch2	-0.35	.030400738	4.670483	Notch 2 (Notch2)
Golga1	-0.35	.005095247	5.307623	Golgi autoantigen, golgin subfamily a, 1 (Golga1)
Ier3ip1	-0.35	.014319962	5.238897	Immediate early response 3 interacting protein 1 (Ier3ip1)
1110032A03Rik	-0.35	.014712542	5.609509	RIKEN cDNA 1110032A03 gene (1110032A03Rik)
A830082K12Rik	-0.35	.011783889	4.938299	RIKEN cDNA A830082K12 gene (A830082K12Rik)
Rnf181	-0.35	.005731889	5.71086	Ring finger protein 181 (Rnf181)
Trib2	-0.35	.04588652	5.220302	Tribbles pseudokinase 2 (Trib2)
Mocs2	-0.35	.004316871	6.203041	Molybdenum cofactor synthesis 2 (Mocs2)
Fgfr1	-0.35	.029600607	5.016118	Fibroblast growth factor receptor 1 (Fgfr1)
Ahcyl2	-0.35	.003566774	7.338844	S-adenosylhomocysteine hydrolase-like 2 (Ahcyl2)
Pomt2	-0.35	.039883798	4.419317	Protein-O-mannosyltransferase 2 (Pomt2)
Thap11	-0.35	.027150003	3.701867	THAP domain containing 11 (Thap11)
Tspan12	-0.35	.024777285	5.337946	Tetraspanin 12 (Tspan12)
Cnbp	-0.35	.000456916	8.561758	Cellular nucleic acid binding protein (Cnbp)
Atg3	-0.36	.003322881	5.691353	Autophagy related 3 (Atg3)
Blvra	-0.36	.049187748	3.422634	Biliverdin reductase A (Blvra)
Smad3	-0.36	.015444153	4.343757	SMAD family member 3 (Smad3)
Arhgap42	-0.36	.015376064	4.531345	Rho GTPase activating protein 42 (Arhgap42)
Ppdpf	-0.36	.007540637	5.164225	Pancreatic progenitor cell differentiation and proliferation factor (Ppdpf)
Rpl19	-0.36	.021865615	5.538451	Ribosomal protein L19 (Rpl19)
Prelid3b	-0.36	.005584173	6.077624	PRELI Domain Containing 3B (Prelid3b)
Smndc1	-0.36	.021033398	4.699628	Survival motor neuron domain containing 1 (Smndc1)
Ccm2	-0.36	.012746058	5.692786	Cerebral cavernous malformation 2 (Ccm2)
Txn1	-0.36	.023338067	6.687713	Thioredoxin 1 (Txn1)
Adam11	-0.36	.002352264	6.116481	A disintegrin and metalloproteinase domain 11 (Adam11)
Rasa3	-0.36	.026272451	4.940832	RAS p21 protein activator 3 (Rasa3)
Asah1	-0.36	.006031062	5.248269	N-acylsphingosine amidohydrolase 1 (Asah1)
Tnpo1	-0.36	.02660083	6.104989	Transportin 1 (Tnpo1)
Gpt2	-0.36	.023872569	4.980208	Glutamic pyruvate transaminase (alanine aminotransferase) 2 (Gpt2)
Rps7	-0.36	.020962203	4.349939	Ribosomal protein S7 (Rps7)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
1500009C09Rik	-0.36	.007306183	6.161677	RIKEN cDNA 1500009C09 gene (1500009C09Rik)
Sirt3	-0.36	.019216825	3.894719	Sirtuin 3 (Sirt3)
Gemin7	-0.36	.034317847	4.179991	Gem (nuclear organelle)-associated protein 7 (Gemin7)
Isca2	-0.36	.020709771	5.730503	Iron-sulfur cluster assembly 2 (Isca2)
Slc35a1	-0.36	.016755359	4.649356	Solute carrier family 35 (CMP-sialic acid transporter), member 1 (Slc35a1)
Rer1	-0.36	.006545879	5.915649	Retention in endoplasmic reticulum sorting receptor 1 (Rer1)
Fmn2	-0.36	.002314967	7.301916	Formin 2 (Fmn2)
Map6d1	-0.36	.003061616	5.466221	MAP6 domain containing 1 (Map6d1)
Zfp950	-0.36	.017907964	4.392611	Zinc finger protein 950 (Zfp950)
Fam133b	-0.36	.019326279	4.280278	Family with sequence similarity 133, member B (Fam133b)
Sf3b6	-0.36	.027718749	4.791618	Splicing factor 3B, subunit 6 (Sf3b6)
Zswim6	-0.36	.031902171	4.891964	Zinc finger SWIM-type containing 6 (Zswim6)
Pnn	-0.36	.010199583	5.524106	Pinin (Pnn)
Sptb	-0.36	.015088367	6.027025	Spectrin beta, erythrocytic (Sptb)
Selenom	-0.36	.013686345	6.145625	Selenoprotein M (Selenom)
Cyb561d1	-0.37	.030800714	3.894296	Cytochrome b-561 domain containing 1 (Cyb561d1)
Commd4	-0.37	.015896224	4.730431	COMM domain containing 4 (Commd4)
Klh121	-0.37	.017918086	4.541181	Kelch-like 21 (Klh121)
Cetn2	-0.37	.036974195	5.102604	Centrin 2 (Cetn2)
Chfr	-0.37	.04773477	3.847429	Checkpoint with forkhead and ring finger domains (Chfr)
Dph7	-0.37	.023338067	4.090044	Diphthamine biosynthesis 7 (Dph7)
Ss18l2	-0.37	.028202678	5.279502	SS18 Like 2 (Ss18l2)
Emc2	-0.37	.001926553	5.769606	ER membrane protein complex subunit 2 (Emc2)
Yes1	-0.37	.017564034	4.592648	YES proto-oncogene 1, Src family tyrosine kinase (Yes1)
Trim39	-0.37	.010335023	4.280451	Tripartite motif-containing 39 (Trim39)
Hdac1	-0.37	.020824676	4.174361	Histone deacetylase 1 (Hdac1)
Spcs2	-0.37	.012536351	6.099474	Signal peptidase complex subunit 2 homolog (S. cerevisiae) (Spcs2)
Rnf13	-0.37	.000576592	7.201238	Ring finger protein 13 (Rnf13)
Hnrnpdl	-0.37	.002817175	6.956162	Heterogeneous nuclear ribonucleoprotein D-like (Hnrnpdl)
Mpnd	-0.37	.027319849	5.6926	MPN domain containing (Mpnd)
Golph3l	-0.37	.003043264	5.147593	Golgi phosphoprotein 3-like (Golph3l)
Sp1	-0.37	.043696803	5.635839	Trans-acting transcription factor 1 (Sp1)
Pdlim5	-0.37	.002406327	5.82551	PDZ and LIM domain 5 (Pdlim5)
Ndufab1	-0.37	.023149087	5.072944	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 (Ndufab1)
Farp1	-0.37	.015701214	5.51445	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived) (Farp1)
Rbl2	-0.37	.007688337	5.946285	Retinoblastoma-like 2 (Rbl2)
Parvb	-0.37	.002022362	5.643923	Parvin, beta (Parvb)
Upf3a	-0.37	.029143626	4.115451	UPF3 regulator of nonsense transcripts homolog A (yeast) (Upf3a)
Mllt6	-0.37	.007909745	6.434454	Myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6 (Mllt6)
Sec14l1	-0.37	.003637939	6.308805	SEC14-like lipid binding 1 (Sec14l1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Leng8	-0.37	.02471236	4.96617	Leukocyte receptor cluster (LRC) member 8 (Leng8)
Ppp1r9a	-0.37	.004867721	7.55654	Protein phosphatase 1, regulatory (inhibitor) subunit 9A (Ppp1r9a)
Bzw2	-0.37	.038158638	3.741907	Basic leucine zipper and W2 domains 2 (Bzw2)
Nubp2	-0.37	.045315976	3.735065	Nucleotide binding protein 2 (Nubp2)
Pcna	-0.37	.024826104	4.433702	Proliferating cell nuclear antigen (Pcna)
Gnptg	-0.37	.003393207	5.492882	N-acetylglucosamine-1-phosphotransferase, gamma subunit (Gnptg)
Rilpl1	-0.37	.014625427	4.427741	Rab interacting lysosomal protein-like 1 (Rilpl1)
Pdcl	-0.37	.032589349	3.845604	Phosducin-like (Pdcl)
Akap9	-0.37	.021631681	8.247787	A kinase (PRKA) anchor protein (yotiao) 9 (Akap9)
Camk2g	-0.37	.000912075	6.569967	Calcium/calmodulin-dependent protein kinase II gamma (Camk2g)
Map4k4	-0.37	.00742593	6.484895	Mitogen-activated protein kinase kinase kinase kinase 4 (Map4k4)
Elof1	-0.37	.005734008	5.705256	ELF1 homolog, elongation factor 1 (Elof1)
Uhrf1bp1	-0.38	.02699407	4.750968	UHRF1 (ICBP90) binding protein 1 (Uhrf1bp1)
Mtus1	-0.38	.017206437	6.197123	Mitochondrial tumor suppressor 1 (Mtus1)
Txndc9	-0.38	.01226005	5.376709	Thioredoxin domain containing 9 (Txndc9)
Focad	-0.38	.017646946	4.681616	Focadhesin (Focad)
Paxx	-0.38	.010098291	5.193032	PAXX Non-Homologous End Joining Factor (Paxx)
Macf1	-0.38	.019796206	8.720209	Microtubule-actin crosslinking factor 1 (Macf1)
Fopnl	-0.38	.004455196	5.122131	Fgfr1op N-terminal like (Fopnl)
Ehmt1	-0.38	.016199251	4.206255	Euchromatic histone methyltransferase 1 (Ehmt1)
Sppl2a	-0.38	.010389925	5.665058	Signal peptide peptidase like 2A (Sppl2a)
Ndufv3	-0.38	.01096809	5.983784	NADH dehydrogenase (ubiquinone) flavoprotein 3 (Ndufv3)
Coq10a	-0.38	.011470903	4.96198	Coenzyme Q10A (Coq10a)
Ddit4	-0.38	.035389075	3.676984	DNA-damage-inducible transcript 4 (Ddit4)
Lrrc1	-0.38	.021326175	3.734517	Leucine-rich repeat containing 1 (Lrrc1)
Stx8	-0.38	.016904859	4.336883	Syntaxin 8 (Stx8)
Sec61b	-0.38	.02210521	4.163164	Sec61 beta subunit (Sec61b)
Sema6a	-0.38	.002203446	6.792381	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (Sema6a)
Sun2	-0.38	.029143626	4.407153	Sad1 and UNC84 domain containing 2 (Sun2)
Cyb5d2	-0.38	.023023329	4.077094	Cytochrome b5 domain containing 2 (Cyb5d2)
Rpl7	-0.38	.01061723	6.632378	Ribosomal protein L7 (Rpl7)
Desi1	-0.38	.002960631	6.469185	Desumoylating isopeptidase 1 (Desi1)
Txndc12	-0.38	.043938488	4.646076	Thioredoxin domain containing 12 (endoplasmic reticulum) (Txndc12)
Mcrs1	-0.38	.041730143	3.713408	Microspherule protein 1 (Mcrs1)
Tpm4	-0.38	.015279601	5.239195	Tropomyosin 4 (Tpm4)
Slc20a1	-0.38	.002536116	5.443567	Solute carrier family 20, member 1 (Slc20a1)
Mrpl32	-0.38	.016430801	3.932454	Mitochondrial ribosomal protein L32 (Mrpl32)
Pcd6	-0.38	.008930446	5.432322	Programmed cell death 6 (Pcd6)
Rexo4	-0.38	.013084293	4.657192	REX4, 3'-5' exonuclease (Rexo4)
Cnih4	-0.38	.007750305	5.473925	Cornichon family AMPA receptor auxiliary protein 4 (Cnih4)
Zdhhc1	-0.38	.022523673	4.048519	Zinc finger, DHHC domain containing 1 (Zdhhc1)
Ndufb11	-0.39	.003485907	5.957946	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11 (Ndufb11)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ctsa	-0.39	.002812314	6.46464	Cathepsin A (Ctsa)
Camk1	-0.39	.026463697	4.039013	Calcium/calmodulin-dependent protein kinase I (Camk1)
Jam2	-0.39	.001109752	6.643172	Junction adhesion molecule 2 (Jam2)
Ankrd40	-0.39	.000293487	7.263537	Ankyrin repeat domain 40 (Ankrd40)
Specc1l	-0.39	.032381058	5.767666	Sperm antigen with calponin homology and coiled-coil domains 1-like (Specc1l)
Mrpl18	-0.39	.00405561	5.318986	Mitochondrial ribosomal protein L18 (Mrpl18)
Hey1	-0.39	.0143615	5.927487	Hairy/enhancer-of-split related with YRPW motif 1 (Hey1)
Degs1	-0.39	.000941595	6.436363	Delta (4)-desaturase, sphingolipid 1 (Degs1)
Zdhhc24	-0.39	.005734008	5.616937	Zinc finger, DHHC domain containing 24 (Zdhhc24)
Rpl28	-0.39	.01937184	4.185653	Ribosomal protein L28 (Rpl28)
Msmo1	-0.39	.003532042	6.385531	Methylsterol monooxygenase 1 (Msmo1)
Tpp1	-0.39	.001142609	6.754548	Tripeptidyl peptidase I (Tpp1)
Orai3	-0.39	.015583382	4.541553	ORAI calcium release-activated calcium modulator 3 (Orai3)
Apip	-0.39	.031612138	3.894771	APAF1 interacting protein (Apip)
Cep83	-0.39	.012458118	4.868491	Centrosomal protein 83 (Cep83)
Ssfa2	-0.39	.005465658	5.274424	Sperm-specific antigen 2 (Ssfa2)
Snrbp2	-0.39	.041485457	4.544808	U2 small nuclear ribonucleoprotein B (Snrbp2)
Qars	-0.39	.01013132	4.70361	Glutaminyl-tRNA synthetase (Qars)
Pdcld10	-0.39	.002093131	5.296319	Programmed cell death 10 (Pdcld10)
Rabac1	-0.39	.003095396	6.618743	Rab acceptor 1 (prenylated) (Rabac1)
Pcsk6	-0.39	.013501345	4.184831	Proprotein convertase subtilisin/kexin type 6 (Pcsk6)
Phf23	-0.39	.016924453	4.464982	PHD finger protein 23 (Phf23)
Cox6b1	-0.39	.009766661	6.620112	Cytochrome c oxidase, subunit VIIb polypeptide 1 (Cox6b1)
Pdk2	-0.39	.000970233	6.572492	Pyruvate dehydrogenase kinase, isoenzyme 2 (Pdk2)
Smm15	-0.39	.030278518	4.724098	Small integral membrane protein 15 (Smm15)
Aldh9a1	-0.39	.002459873	5.179273	Aldehyde dehydrogenase 9, subfamily A1 (Aldh9a1)
St6gal1	-0.39	.012453171	4.509486	Beta galactoside alpha 2,6 sialyltransferase 1 (St6gal1)
Tmeff2	-0.40	.003482828	6.858251	Transmembrane protein with EGF-like and two follistatin-like domains 2 (Tmeff2)
Rdx	-0.40	.002382967	6.442893	Radixin (Rdx)
Naa16	-0.40	.035375302	3.629829	N (alpha)-acetyltransferase 16, NatA auxiliary subunit (Naa16)
Chchd5	-0.40	.015678367	3.626452	Coiled-coil-helix-coiled-coil-helix domain containing 5 (Chchd5)
Slc25a33	-0.40	.01533009	4.168083	Solute carrier family 25, member 33 (Slc25a33)
Rcbtb2	-0.40	.011769985	4.214699	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 (Rcbtb2)
Tbcel	-0.40	.008250138	5.427753	Tubulin folding cofactor E-like (Tbcel)
Gdpd5	-0.40	.007686435	5.576238	Glycerophosphodiester phosphodiesterase domain containing 5 (Gdpd5)
Nsa2	-0.40	.029322323	3.584271	NSA2 ribosome biogenesis homolog (Nsa2)
Rcsd1	-0.40	.038866642	3.352806	RCSD domain containing 1 (Rcsd1)
Zc3h7a	-0.40	.025997015	4.485623	Zinc finger CCCH type containing 7 A (Zc3h7a)
Unc119b	-0.40	.033579875	4.044553	Unc-119 lipid binding chaperone B (Unc119b)
Ufc1	-0.40	.012572791	5.182179	Ubiquitin-fold modifier conjugating enzyme 1 (Ufc1)
Efcab2	-0.40	.006639468	5.597234	EF-hand calcium binding domain 2 (Efcab2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mcur1	-0.40	.01508435	4.4308	Mitochondrial calcium uniporter regulator 1 (Mcur1)
Adcy2	-0.40	.006257954	5.062578	Adenylate cyclase 2 (Adcy2)
Pex5l	-0.40	.015319252	6.100358	Peroxisomal biogenesis factor 5-like (Pex5l)
Acin1	-0.40	.001931456	5.489797	Apoptotic chromatin condensation inducer 1 (Acin1)
Sypl	-0.40	.012300838	5.513002	Synaptophysin-like protein (Sypl)
Cplx2	-0.40	.027804757	6.816912	Complexin 2 (Cplx2)
Cox7a2	-0.40	.019194704	6.955438	Cytochrome c oxidase subunit VIIa 2 (Cox7a2)
Fmn1	-0.40	.040583036	4.752557	Formin 1 (Fmn1)
Psmc3	-0.40	.008609779	5.667568	Proteasome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3)
1700021F05Rik	-0.40	.018956485	4.041475	RIKEN cDNA 1700021F05 gene (1700021F05Rik)
Ccdc117	-0.40	.007193457	4.626625	Coiled-coil domain containing 117 (Ccdc117)
Zfp516	-0.40	.024977903	4.518407	Zinc finger protein 516 (Zfp516)
H1f0	-0.40	.000860327	6.050358	H1 histone family, member 0 (H1f0)
Ak3	-0.41	.001318461	6.309927	Adenylate kinase 3 (Ak3)
Med8	-0.41	.027247753	3.755468	Mediator complex subunit 8 (Med8)
Nacc2	-0.41	.00158207	7.198835	Nucleus accumbens-associated 2, BEN and BTB (POZ) domain containing (Nacc2)
Tppp3	-0.41	.002860213	6.019368	Tubulin polymerization-promoting protein family member 3 (Tppp3)
Fbln5	-0.41	.019162381	4.248527	Fibulin 5 (Fbln5)
Chka	-0.41	.009767034	5.14187	Choline kinase alpha (Chka)
Faim	-0.41	.03490335	5.148838	Fas apoptotic inhibitory molecule (Faim)
Acot13	-0.41	.007021954	6.051956	Acyl-CoA thioesterase 13 (Acot13)
Gtf2e2	-0.41	.026864152	3.908014	General transcription factor II E, polypeptide 2 (beta subunit) (Gtf2e2)
Myo7a	-0.41	.02365158	3.611898	Myosin VIIA (Myo7a)
Dynll1	-0.41	.004126485	7.122626	Dynein light chain LC8-type 1 (Dynll1)
Cdyl	-0.41	.014454136	3.679257	Chromodomain protein, Y chromosome-like (Cdyl)
Rplp0	-0.41	.000828213	6.08716	Ribosomal protein, large, P0 (Rplp0)
Atp6v1g1	-0.41	.002850508	5.860596	ATPase, H+ transporting, lysosomal V1 subunit G1 (Atp6v1g1)
B4galt4	-0.41	.008337123	4.220181	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4galt4)
Rnf114	-0.41	.005503396	6.42017	Ring finger protein 114 (Rnf114)
Nxt2	-0.41	.002572666	6.028015	Nuclear transport factor 2-like export factor 2 (Nxt2)
Rtf2	-0.41	.003672551	5.246635	Replication Termination Factor 2 (Rtf2)
Prpsap1	-0.41	.020104078	4.786538	Phosphoribosyl pyrophosphate synthetase-associated protein 1 (Prpsap1)
Bad	-0.41	.011915112	4.270577	BCL2-associated agonist of cell death (Bad)
Gabarap	-0.41	.000583159	6.537115	Gamma-aminobutyric acid receptor-associated protein (Gabarap)
Trim11	-0.41	.030357657	3.466939	Tripartite motif-containing 11 (Trim11)
Parl	-0.41	.02541718	4.982809	Presenilin-associated, rhomboid-like (Parl)
Rpl22l1	-0.41	.048542635	4.250184	Ribosomal protein L22 like 1 (Rpl22l1)
Tcof1	-0.41	.023373455	3.80479	Treacle ribosome biogenesis factor 1 (Tcof1)
Mdp1	-0.41	.009073335	3.906135	Magnesium-dependent phosphatase 1 (Mdp1)
Cox7b	-0.41	.003354847	7.233903	Cytochrome c oxidase subunit VIIb (Cox7b)
Ndufa8	-0.41	.004610134	5.261944	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (Ndufa8)
Grb14	-0.41	.008500124	4.769801	Growth factor receptor bound protein 14 (Grb14)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Vta1	-0.41	.00359095	5.088706	Vesicle (multivesicular body) trafficking 1 (Vta1)
Mia2	-0.41	.001632556	5.951979	Melanoma inhibitory activity 2 (Mia2)
Trpm3	-0.41	.007375649	6.892197	Transient receptor potential cation channel, subfamily M, member 3 (Trpm3)
Tmem161a	-0.41	.03325665	3.620343	Transmembrane protein 161A (Tmem161a)
Ctdsp2	-0.41	.000605447	5.823337	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (Ctdsp2)
Zfp740	-0.41	.004772053	4.822581	Zinc finger protein 740 (Zfp740)
Lsm4	-0.42	.018412516	3.881901	LSM4 homolog, U6 small nuclear RNA and mRNA degradation-associated (Lsm4)
Ndufs4	-0.42	.008910629	5.857538	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Ndufs4)
Cadps2	-0.42	.007112601	7.096508	Ca2+-dependent activator protein for secretion 2 (Cadps2)
Cacfd1	-0.42	.015159819	5.886646	Calcium channel flower domain containing 1 (CACFD1)
Mrps33	-0.42	.010820006	4.578723	Mitochondrial ribosomal protein S33 (Mrps33)
Slc20a2	-0.42	.003131139	6.206066	Solute carrier family 20, member 2 (Slc20a2)
Fam204a	-0.42	.019874699	3.804719	Family with sequence similarity 204, member A (Fam204a)
Adi1	-0.42	.002061103	6.321408	Acireductone dioxygenase 1 (Adi1)
Safb2	-0.42	.003301053	5.003817	Scaffold attachment factor B2 (Safb2)
Itpkb	-0.42	.001865287	6.32844	Inositol 1,4,5-trisphosphate 3-kinase B (Itpkb)
Tmco1	-0.42	.009031661	5.093259	Transmembrane and coiled-coil domains 1 (Tmco1)
Minos1	-0.42	.002982715	6.250402	Mitochondrial inner membrane organizing system 1 (Minos1)
Dand5	-0.42	.029966511	3.423705	DAN domain family member 5, BMP antagonist (Dand5)
Lrrc8a	-0.42	.001430721	5.684724	Leucine-rich repeat containing 8A (Lrrc8a)
Dctn6	-0.42	.021020224	5.622318	Dynactin 6 (Dctn6)
Ccdc90b	-0.42	.009223793	4.205238	Coiled-coil domain containing 90B (Ccdc90b)
Oaz1	-0.42	.001758502	6.464603	Ornithine decarboxylase antizyme 1 (Oaz1)
Ccdc30	-0.42	.030732249	3.595489	Coiled-coil domain containing 30 (Ccdc30)
Mrps28	-0.42	.046867769	3.88398	Mitochondrial ribosomal protein S28 (Mrps28)
Cep135	-0.42	.039883798	3.362123	Centrosomal protein 135 (Cep135)
Trappc3	-0.42	.000815174	6.671699	Trafficking protein particle complex 3 (Trappc3)
Mpc2	-0.42	.017476286	6.52468	Mitochondrial pyruvate carrier 2 (Mpc2)
Ubl5	-0.42	.007558033	6.137327	Ubiquitin-like 5 (Ubl5)
Kmt2d	-0.42	.001184058	7.741809	Lysine (K)-specific methyltransferase 2D (Kmt2d)
2410015M20Rik	-0.42	.013105516	4.64786	RIKEN cDNA 2410015M20 gene (2410015M20Rik)
Cox6a1	-0.42	.007686435	8.185404	Cytochrome c oxidase subunit VIa polypeptide 1 (Cox6a1)
Ccdc157	-0.42	.036722293	4.231007	Coiled-coil domain containing 157 (Ccdc157)
Bcap31	-0.42	.002951731	5.766616	B cell receptor-associated protein 31 (Bcap31)
Cadm4	-0.42	.004868494	5.572911	Cell adhesion molecule 4 (Cadm4)
H2afz	-0.42	.022217564	4.34632	H2A histone family, member Z (H2afz)
Lamtor3	-0.42	.004684401	4.982196	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 (Lamtor3)
Mettl3	-0.42	.026667285	3.228261	Methyltransferase like 3 (Mettl3)
CT010467.1	-0.42	.027220301	3.79783	18s RNA, related sequence 5 (Rn18s-rs5)
Hmgn3	-0.42	.032589349	3.559541	High-mobility group nucleosomal binding domain 3 (Hmgn3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rack1	-0.43	.000660096	6.920318	Receptor for activated C kinase 1 (Rack1)
Pitpnb	-0.43	.001904998	5.630274	Phosphatidylinositol transfer protein, beta (Pitpnb)
Emc3	-0.43	.001099459	6.195085	ER membrane protein complex subunit 3 (Emc3)
Timm9	-0.43	.002994166	4.980975	Translocase of inner mitochondrial membrane 9 (Timm9)
Chmp1b	-0.43	.010432832	4.187301	Charged multivesicular body protein 1B (Chmp1b)
Zmpste24	-0.43	.004002513	5.2161	Zinc metallopeptidase, STE24 (Zmpste24)
Hist1h1e	-0.43	.015743725	4.151375	Histone cluster 1, H1e (Hist1h1e)
Etfdh	-0.43	.003981479	4.709052	Electron transferring flavoprotein, dehydrogenase (Etfdh)
Cmss1	-0.43	.045634291	3.56466	Cms small ribosomal subunit 1 (Cmss1)
Hint1	-0.43	.00578877	6.687905	Histidine triad nucleotide binding protein 1 (Hint1)
Rara	-0.43	.048084305	3.556643	Retinoic acid receptor, alpha (Rara)
Paqr4	-0.43	.00367203	4.919297	Progestin and adipoQ receptor family member IV (Paqr4)
Scg5	-0.43	.000569585	6.698831	Secretogranin V (Scg5)
Parp2	-0.43	.006114634	4.472915	Poly(ADP-ribose) polymerase family, member 2 (Parp2)
Man2b1	-0.43	.002971651	5.518745	Mannosidase 2, alpha B1 (Man2b1)
Txlna	-0.43	.032944447	4.639165	Taxilin alpha (Txlna)
Anapc16	-0.43	.000486801	5.703237	Anaphase promoting complex subunit 16 (Anapc16)
Dpm2	-0.43	.004207634	5.097606	Dolichol-phosphate (beta-D) mannosyltransferase 2 (Dpm2)
Snta1	-0.43	.04598509	3.066313	Syntrophin, acidic 1 (Snta1)
Mars	-0.43	.002418826	4.991893	Methionine-tRNA synthetase (Mars)
Trmt10b	-0.43	.00765485	4.205443	tRNA methyltransferase 10B (Trmt10b)
Coprs	-0.43	.04677459	5.242261	Coordinator of PRMT5, differentiation stimulator (Coprs)
Eif2b2	-0.43	.005779452	4.644576	Eukaryotic translation initiation factor 2B, subunit 2 beta (Eif2b2)
Ahcyl1	-0.43	.000143414	9.011066	S-adenosylhomocysteine hydrolase-like 1 (Ahcyl1)
Cox5b	-0.43	.021115842	6.176991	Cytochrome c oxidase subunit Vb (Cox5b)
3110082I17Rik	-0.44	.035540624	2.940827	RIKEN cDNA 3110082I17 gene (3110082I17Rik)
Gtf2b	-0.44	.00455525	4.85966	General transcription factor IIB (Gtf2b)
Elmod3	-0.44	.018047502	3.964494	ELMO/CED-12 domain containing 3 (Elmod3)
Eif2s3y	-0.44	.015076188	4.305951	Eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked (Eif2s3y)
Sdf2l1	-0.44	.044993679	2.922869	Stromal cell-derived factor 2-like 1 (Sdf2l1)
Plec	-0.44	.001520434	5.521983	Plectin (Plec)
Ift20	-0.44	.000280195	6.380937	Intraflagellar transport 20 (Ift20)
Fau	-0.44	.011750251	5.281708	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) (Fau)
Hist3h2a	-0.44	.019003802	4.514681	Histone cluster 3, H2a (Hist3h2a)
Tmf1	-0.44	.000161929	6.442435	TATA element modulatory factor 1 (Tmf1)
Commd6	-0.44	.000699718	6.032527	COMM domain containing 6 (Commd6)
Pigv	-0.44	.033359548	2.776678	Phosphatidylinositol glycan anchor biosynthesis, class V (Pigv)
Cnnm2	-0.44	.015159819	5.845062	Cyclin M2 (Cnnm2)
Tti1	-0.44	.007918353	3.76309	TELO2 interacting protein 1 (Tti1)
1110004E09Rik	-0.44	.003792173	5.334904	RIKEN cDNA 1110004E09 gene (1110004E09Rik)
Kat2b	-0.44	.005571812	4.578222	K (lysine) acetyltransferase 2B (Kat2b)
Gtf2a2	-0.44	.001814296	5.085631	General transcription factor II A, 2 (Gtf2a2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ap4s1	-0.44	.005383984	5.072882	Adaptor-related protein complex AP-4, sigma 1 (Ap4s1)
Ncan	-0.44	.000139914	7.899611	Neurocan (Ncan)
Elmo2	-0.44	.002712291	6.22453	Engulfment and cell motility 2 (Elmo2)
Ift80	-0.44	.017169007	4.868394	Intraflagellar transport 80 (IFT80)
Psmd9	-0.44	.024341637	3.935734	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (Psmd9)
Acyp2	-0.44	.003482272	5.429165	Acylphosphatase 2, muscle type (Acyp2)
Ap3b1	-0.44	.014769482	5.337996	Adaptor-related protein complex 3, beta 1 subunit (Ap3b1)
Tmc7	-0.44	.006603736	5.350307	Transmembrane channel-like gene family 7 (Tmc7)
Emc6	-0.44	.009221934	4.730617	ER membrane protein complex subunit 6 (Emc6)
Kyat1	-0.44	.043835047	2.698969	Kynurenone aminotransferase 1 (Kyat1)
Taf4	-0.44	.010617797	3.936144	TATA-box binding protein-associated factor 4 (Taf4)
Il1rap	-0.44	.015980695	4.681825	Interleukin 1 receptor accessory protein (IL1rap)
Nadk2	-0.44	.033892951	5.120271	NAD kinase 2, mitochondrial (Nadk2)
Dio2	-0.44	.005398225	4.803148	Deiodinase, iodothyronine, type II (Dio2)
Abtb1	-0.44	.048409154	3.283191	Ankyrin repeat and BTB (POZ) domain containing 1 (Abtb1)
Xpa	-0.44	.031545058	3.270251	Xeroderma pigmentosum, complementation group A (Xpa)
Atr	-0.44	.045404494	3.963495	Ataxia telangiectasia and Rad3 related (Atr)
Cd151	-0.44	.036084322	3.934619	CD151 antigen (Cd151)
Ints13	-0.44	.026490141	3.992241	Integrator Complex Subunit 13 (Ints13)
Serf2	-0.44	.022953895	3.184858	Small EDRK-rich factor 2 (Serf2)
Gria1	-0.44	.000273778	8.497389	Glutamate receptor, ionotropic, AMPA1 (alpha 1) (Gria1)
Marchf2	-0.45	.003856333	5.44614	Membrane-associated ring-CH-type finger 2 (Marchf2)
Lamtor4	-0.45	.008386012	4.427357	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 4 (Lamtor4)
Tbca	-0.45	.007290095	6.105938	Tubulin cofactor A (Tbca)
Dad1	-0.45	.000729261	5.775609	Defender against cell death 1 (Dad1)
Smim26	-0.45	.008056938	4.383132	Small Integral Membrane Protein 26 (Smim26)
Rpl29	-0.45	.012125738	4.474077	Ribosomal protein L29 (Rpl29)
Cpne9	-0.45	.001197943	6.911288	Copine family member IX (Cpne9)
Eif1ad	-0.45	.032966326	4.051912	Eukaryotic translation initiation factor 1A domain containing (Eif1ad)
Mrpl54	-0.45	.047097802	3.169198	Mitochondrial ribosomal protein L54 (Mrpl54)
Uqcrb	-0.45	.022239401	4.310601	Ubiquinol-cytochrome c reductase binding protein (Uqcrb)
Nudt19	-0.45	.005078156	4.786934	Nudix (nucleoside diphosphate linked moiety X)-type motif 19 (Nudt19)
0610030E20Rik	-0.45	.014964932	3.933243	RIKEN cDNA 0610030E20 gene (0610030E20Rik)
Tmem242	-0.45	.00877788	4.092959	Transmembrane protein 242 (Tmem242)
Ptpdc1	-0.45	.014624429	5.754945	Protein tyrosine phosphatase domain containing 1 (Ptpdc1)
Clcc1	-0.45	.019253209	4.429356	Chloride channel CLIC-like 1 (Clcc1)
P4ha1	-0.45	.006350481	4.266142	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide (P4ha1)
Fam50a	-0.45	.049871193	3.475657	Family with sequence similarity 50, member A (Fam50a)
Tmem216	-0.45	.048109505	3.228648	Transmembrane protein 216 (Tmem216)
Hspe1	-0.45	.005033126	6.226898	Heat shock protein 1 (chaperonin 10) (Hspe1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ryr3	-0.45	.013032013	5.277667	Ryanodine receptor 3 (Ryr3)
Nudc	-0.45	.003789289	5.192679	nudC nuclear distribution protein (Nudc)
Golga4	-0.45	.002304271	6.946693	Golgi autoantigen, golgin subfamily a, 4 (Golga4)
Snf8	-0.45	.011952121	4.954754	SNF8, ESCRT-II complex subunit, homolog ( <i>S. cerevisiae</i> ) (Snf8)
Ndufa6	-0.45	.018209114	5.053535	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14) (Ndufa6)
Zfp408	-0.45	.004396876	3.891377	Zinc finger protein 408 (Zfp408)
Atp5j2	-0.45	.031852455	4.997522	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 (Atp5j2)
R3hdm4	-0.45	.000655883	5.586559	R3H domain containing 4 (R3hdm4)
Gpr4	-0.45	.006149778	4.388827	G protein-coupled receptor 4 (Gpr4)
Snrpd2	-0.45	.010643184	5.043409	Small nuclear ribonucleoprotein D2 (Snrpd2)
Dip2a	-0.45	.000830682	5.714678	Disco interacting protein 2 homolog A (Dip2a)
Rassf2	-0.45	.012360533	6.240017	Ras association (RalGDS/AF-6) domain family member 2 (Rassf2)
Ryk	-0.45	.023328894	4.165696	Receptor-like tyrosine kinase (Ryk)
Rela	-0.45	.030881255	3.337454	V-rel reticuloendotheliosis viral oncogene homolog A (avian) (Rela)
Ndufc1	-0.45	.006620727	5.766976	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (Ndufc1)
Abcd2	-0.45	.002573216	5.010059	ATP-binding cassette, sub-family D (ALD), member 2 (Abcd2)
Zfp651	-0.45	.006250277	4.546392	Zinc finger protein 651 (Zfp651)
Eef1akmt2	-0.45	.011428984	4.280509	EEF1A Lysine Methyltransferase 2 (Eef1akmt2)
Acad11	-0.45	.012526707	3.872331	Acyl-Coenzyme A dehydrogenase family, member 11 (Acad11)
Cobll1	-0.45	.011495141	3.936041	Cobl-like 1 (Cobll1)
Ldhb	-0.45	$6.78 \times 10^{-5}$	8.562448	Lactate dehydrogenase B (Ldhb)
Ppp1r16b	-0.45	.035612447	6.195026	Protein phosphatase 1, regulatory (inhibitor) subunit 16B (Ppp1r16b)
Nrsn1	-0.46	.000194968	8.20317	Neurensin 1 (Nrsn1)
Gng12	-0.46	.00102596	6.425015	Guanine nucleotide binding protein (G protein), gamma 12 (Gng12)
0610037L13Rik	-0.46	.000508478	5.338903	RIKEN cDNA 0610037L13 gene (0610037L13Rik)
Rock1	-0.46	.006609834	4.781342	Rho-associated coiled-coil containing protein kinase 1 (Rock1)
Ptpmt1	-0.46	.0225033	3.466663	Protein tyrosine phosphatase, mitochondrial 1 (Ptpmt1)
Vamp1	-0.46	.00785917	6.087557	Vesicle-associated membrane protein 1 (Vamp1)
Fam19a4	-0.46	.028703373	3.545306	Family with sequence similarity 19, member A4 (Fam19a4)
Tbc1d10a	-0.46	.026440925	3.093425	TBC1 domain family, member 10a (Tbc1d10a)
Prdx4	-0.46	.020566146	3.945309	Peroxiredoxin 4 (Prdx4)
Szrd1	-0.46	.003898525	4.60083	SUZ RNA binding domain containing 1 (Szrd1)
Sdhc	-0.46	.000441905	6.350884	Succinate dehydrogenase complex, subunit C, integral membrane protein (Sdhc)
Abca2	-0.46	.00024636	7.630009	ATP-binding cassette, sub-family A (ABC1), member 2 (Abca2)
Rpap1	-0.46	.022530216	3.289161	RNA polymerase II-associated protein 1 (Rpap1)
Wnk1	-0.46	.00026372	8.986791	WNK lysine deficient protein kinase 1 (Wnk1)
Abhd14a	-0.46	.017242956	3.307686	Abhydrolase domain containing 14A (Abhd14a)
Nrgn	-0.46	.00500445	5.458358	Neurogranin (Nrgn)
Timm13	-0.46	.035345668	4.617238	Translocase of inner mitochondrial membrane 13 (Timm13)
Slc30a10	-0.46	.013253751	5.137112	Solute carrier family 30, member 10 (Slc30a10)
Krtcap2	-0.46	.005030185	4.820873	Keratinocyte-associated protein 2 (Krtcap2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Scrt1	-0.46	.002694103	6.558491	Scratch family zinc finger 1 (Scrt1)
Pde1a	-0.46	.011495141	6.734232	Phosphodiesterase 1A, calmodulin-dependent (Pde1a)
Iqgap1	-0.46	.022356736	3.678007	IQ motif containing GTPase activating protein 1 (Iqgap1)
Fam173a	-0.46	.004464385	4.798495	Family with sequence similarity 173, member A (Fam173a)
Pigc	-0.46	.035322628	3.882049	Phosphatidylinositol glycan anchor biosynthesis, class C (Pigc)
Sac3d1	-0.47	.026796231	3.16932	SAC3 domain containing 1 (Sac3d1)
Hadhb	-0.47	.003830629	4.304094	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (Hadhb)
Tom1l1	-0.47	.009720775	4.9057	Target of myb1-like 1 (chicken) (Tom1l1)
Map7	-0.47	.002501728	4.362957	Microtubule-associated protein 7 (Map7)
Mindy1	-0.47	.012012463	3.528454	MINDY Lysine 48 Deubiquitinase 1 (Mindy1)
Zfand1	-0.47	.023966523	3.992524	Zinc finger, AN1-type domain 1 (Zfand1)
Diaph2	-0.47	.000756176	5.132277	Diaphanous-related formin 2 (Diaph2)
Kif16b	-0.47	.038699906	3.448732	Kinesin family member 16B (Kif16b)
Cntln	-0.47	.002298286	4.778481	Centlein, centrosomal protein (Cntln)
Lrrc10b	-0.47	.007450764	4.829905	Leucine-rich repeat containing 10B (Lrrc10b)
Tra2a	-0.47	.002222194	5.447715	Transformer 2 alpha homolog (Tra2a)
Rbm28	-0.47	.004618014	4.729767	RNA binding motif protein 28 (Rbm28)
Gcdh	-0.47	.0305352	3.741276	Glutaryl-Coenzyme A dehydrogenase (Gcdh)
Gstz1	-0.47	.001088356	4.791127	Glutathione transferase zeta 1 (maleylacetoacetate isomerase) (Gstz1)
Tmem189	-0.47	.00521277	4.165724	Transmembrane protein 189 (Tmem189)
Cep63	-0.47	.00432711	4.581367	Centrosomal protein 63 (Cep63)
Gpr137b-ps	-0.47	.034308347	3.113276	G protein-coupled receptor 137B, pseudogene (Gpr137b-ps)
Cyccs	-0.47	.028802536	3.194359	Cytochrome c, somatic (Cyccs)
Arap2	-0.47	.004315947	6.3222	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 (Arap2)
Dlg1	-0.47	.00061393	6.286192	Discs, large homolog 1 (Dlg1)
Oat	-0.47	.000538534	5.650633	Ornithine aminotransferase (Oat)
Prkdc	-0.47	.00432711	5.157711	Protein kinase, DNA activated, catalytic polypeptide (Prkdc)
Trim62	-0.47	.048780331	4.538335	Tripartite motif-containing 62 (Trim62)
Zfp839	-0.47	.006453177	4.258793	Zinc finger protein 839 (Zfp839)
Ubr4	-0.47	.000706477	7.820195	Ubiquitin protein ligase E3 component n-recognition 4 (Ubr4)
Cacnb3	-0.47	.008030563	8.035226	Calcium channel, voltage-dependent, beta 3 subunit (Cacnb3)
Zfp362	-0.47	.003831909	4.519507	Zinc finger protein 362 (Zfp362)
Cald1	-0.47	.011730843	5.178264	Caldesmon 1 (Cald1)
Tpd52l2	-0.47	.001879225	5.669304	Tumor protein D52-like 2 (Tpd52l2)
Timm10	-0.47	.012371974	4.066029	Translocase of inner mitochondrial membrane 10 (Timm10)
Tspan3	-0.47	5.01 × 10 <sup>-5</sup>	8.179475	Tetraspanin 3 (Tspan3)
Amt	-0.47	.005496422	4.281956	Aminomethyltransferase (Amt)
Ank2	-0.48	.001585343	8.968535	Ankyrin 2, brain (Ank2)
Gemin8	-0.48	.028793942	2.9229	Gem (nuclear organelle)-associated protein 8 (Gemin8)
Oma1	-0.48	.038158638	3.391501	OMA1 zinc metallopeptidase (Oma1)
2810001G20Rik	-0.48	.010468306	4.199036	RIKEN cDNA 2810001G20 gene (2810001G20Rik)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mdc1	-0.48	.01508435	4.233727	Mediator of DNA damage checkpoint 1 (Mdc1)
Lhfp	-0.48	.004507432	4.194927	Lipoma HMGIC fusion partner (Lhfp)
Ranbp17	-0.48	.027188626	3.808555	RAN binding protein 17 (Ranbp17)
Itga9	-0.48	.022651024	3.908348	Integrin alpha 9 (Itga9)
Hyi	-0.48	.013627975	3.258372	Hydroxypyruvate isomerase (putative) (Hyi)
Elk3	-0.48	.040882725	2.934018	ELK3, member of ETS oncogene family (Elk3)
Tmem168	-0.48	.018785478	3.340635	Transmembrane protein 168 (Tmem168)
Aimp1	-0.48	.001944648	5.070269	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 (Aimp1)
Plekjh1	-0.48	.047440422	3.000487	Pleckstrin homology domain containing, family J member 1 (Plekjh1)
Gkap1	-0.48	.011171292	3.549386	G kinase anchoring protein 1 (Gkap1)
Tmbim6	-0.48	.000150079	8.13391	Transmembrane BAX inhibitor motif containing 6 (Tmbim6)
AC121965.1	-0.48	.022360633	4.498964	Predicted gene (Gm2695)
Nck2	-0.48	.005781317	3.892291	Noncatalytic region of tyrosine kinase adaptor protein 2 (Nck2)
Ska2	-0.48	.01207791	3.635161	Spindle and kinetochore-associated complex subunit 2 (Ska2)
Sbds	-0.48	.000888982	5.551983	Shwachman–Bodian–Diamond syndrome homolog (human) (Sbds)
Dnajb2	-0.48	.002100534	5.365543	DnaJ heat shock protein family (Hsp40) member B2 (Dnajb2)
P2rx4	-0.48	.005734719	3.71719	Purinergic receptor P2X, ligand-gated ion channel 4 (P2rx4)
Hsdl2	-0.48	.00237989	5.619354	Hydroxysteroid dehydrogenase like 2 (Hsdl2)
Spg20	-0.48	.001055265	5.070014	Spastic paraplegia 20, spartin (Troyer syndrome) homolog (human) (Spg20)
Abca7	-0.48	.025155748	3.178336	ATP-binding cassette, sub-family A (ABC1), member 7 (Abca7)
Pip4k2a	-0.48	.004220257	7.473879	Phosphatidylinositol-5-phosphate 4-kinase, type II, alpha (Pip4k2a)
Kctd18	-0.48	.046743784	3.834231	Potassium channel tetramerisation domain containing 18 (Kctd18)
Atf4	-0.48	.000799215	6.910545	Activating transcription factor 4 (Atf4)
Ly6e	-0.48	.037464203	7.105477	Lymphocyte antigen 6 complex, locus E (Ly6e)
Ggcx	-0.48	.041104788	2.873299	Gamma-glutamyl carboxylase (Ggcx)
Tgfbr1	-0.48	.0021464	5.027863	Transforming growth factor, beta receptor I (Tgfbr1)
Shmt2	-0.49	.027363574	3.458721	Serine hydroxymethyltransferase 2 (mitochondrial) (Shmt2)
Nudt16l1	-0.49	.023200975	4.154098	Nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 (Nudt16l1)
Lrwd1	-0.49	.046870412	2.246506	Leucine-rich repeats and WD repeat domain containing 1 (Lrwd1)
Wdr83	-0.49	.033493545	2.580416	WD repeat domain containing 83 (Wdr83)
Rpl3	-0.49	.000604982	6.106839	Ribosomal protein L3 (Rpl3)
Slc48a1	-0.49	.000148066	6.391251	Solute carrier family 48 (heme transporter), member 1 (Slc48a1)
Zfp219	-0.49	.033710186	2.841035	Zinc finger protein 219 (Zfp219)
Ctsd	-0.49	.000511823	7.041001	Cathepsin D (Ctsd)
Mfsd1	-0.49	.004169398	5.26991	Major facilitator superfamily domain containing 1 (Mfsd1)
9930104L06Rik	-0.49	.027278437	3.662379	RIKEN cDNA 9930104L06 gene (9930104L06Rik)
Dguok	-0.49	.044907598	2.910376	Deoxyguanosine kinase (Dguok)
Dtymk	-0.49	.021380885	3.978147	Deoxythymidylate kinase (Dtymk)
Mterf4	-0.49	.039687564	3.18262	Mitochondrial transcription termination factor 4 (Mterf4)
Irf2	-0.49	.011352328	4.269511	Interferon regulatory factor 2 (Irf2)
Vrk3	-0.49	.008636137	3.441625	Vaccinia-related kinase 3 (Vrk3)
Pgpep1	-0.49	.013757923	3.398452	Pyroglutamyl-peptidase I (Pgpep1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lamp1	-0.49	$2.83 \times 10^{-5}$	8.3874	Lysosomal-associated membrane protein 1 (Lamp1)
Nup93	-0.49	.009887858	3.656256	Nucleoporin 93 (Nup93)
Trrap	-0.49	.000244925	6.748986	Transformation/transcription domain-associated protein (Trrap)
Galk1	-0.49	.049088262	2.533341	Galactokinase 1 (Galk1)
Zbtb8os	-0.49	.019278772	3.003606	Zinc finger and BTB domain containing 8 opposite strand (Zbtb8os)
Tmem218	-0.49	.022106398	3.413889	Transmembrane protein 218 (Tmem218)
Emg1	-0.49	.019824921	4.40964	EMG1 N1-specific pseudouridine methyltransferase (Emg1)
Maml2	-0.49	.003986814	4.524363	Mastermind like 2 (Maml2)
Mipol1	-0.49	.035061841	3.08693	Mirror-image polydactyl 1 (Mipol1)
Naga	-0.49	.006793904	4.312178	N-acetyl galactosaminidase, alpha (Naga)
Dpp3	-0.49	.007092454	4.15024	Dipeptidylpeptidase 3 (Dpp3)
Heg1	-0.49	.001245768	5.732508	Heart development protein with EGF-like domains 1 (Heg1)
Lrp4	-0.49	.010416343	4.662759	Low-density lipoprotein receptor-related protein 4 (Lrp4)
Lrrc8c	-0.49	.006592016	4.904482	Leucine-rich repeat containing 8 family, member C (Lrrc8c)
Rpl7a	-0.49	.000109047	6.832328	Ribosomal protein L7A (Rpl7a)
2700097O09Rik	-0.50	.030695066	3.017129	RIKEN cDNA 2700097O09 gene (2700097O09Rik)
Tspan14	-0.50	.008250138	4.205027	Tetraspanin 14 (Tspan14)
Fbxl5	-0.50	.000901523	5.514143	F-box and leucine-rich repeat protein 5 (Fbxl5)
Atp1b3	-0.50	$8.74 \times 10^{-5}$	7.012412	ATPase, Na+/K+ transporting, beta 3 polypeptide (Atp1b3)
Ccdc59	-0.50	.002860462	4.180228	Coiled-coil domain containing 59 (Ccdc59)
Zscan21	-0.50	.01642792	3.611398	Zinc finger and SCAN domain containing 21 (Zscan21)
Lrp1	-0.50	.000286586	7.914638	Low density lipoprotein receptor-related protein 1 (Lrp1)
Zfp438	-0.50	.028639296	3.226506	Zinc finger protein 438 (Zfp438)
Idh2	-0.50	.005839545	4.603244	Isocitrate dehydrogenase 2 (NADP+), mitochondrial (Idh2)
Prpf38b	-0.50	.000752914	5.335866	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B (Prpf38b)
Akt2	-0.50	.03244257	4.507185	Thymoma viral proto-oncogene 2 (Akt2)
Tysnd1	-0.50	.026675912	2.757061	Trypsin domain containing 1 (Tysnd1)
Agbl3	-0.50	.010518187	3.133018	ATP/GTP binding protein-like 3 (Agbl3)
Ddx39	-0.50	.026732262	3.007384	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 (Ddx39)
Traf7	-0.50	.017180772	3.732924	TNF receptor-associated factor 7 (Traf7)
Sbf2	-0.50	.001135483	5.882387	SET binding factor 2 (Sbf2)
Cfap74	-0.50	.007153697	3.523	Cilia and flagella-associated protein 74 (Cfap74)
Arhgef40	-0.50	.01439739	3.840156	Rho guanine nucleotide exchange factor (GEF) 40 (Arhgef40)
Faat20	-0.50	.018896934	4.216039	Fanconi anemia core complex-associated protein 20 (Faat20)
Tsta3	-0.50	.031032057	2.746685	Tissue-specific transplantation antigen P35B (Tsta3)
Myl6	-0.50	.002378098	6.092635	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (Myl6)
Nmral1	-0.50	.012996689	3.40016	Nmral1-like family domain containing 1 (Nmral1)
Flvcr1	-0.50	.01498988	3.629885	FLVCR Heme Transporter 1 (Flvcr1)
Rab10os	-0.50	.033047577	3.645877	RAB10, member RAS oncogene family, opposite strand (Rab10os)
Vegfb	-0.50	.002539964	5.395321	Vascular endothelial growth factor B (Vegfb)
Adsl	-0.50	.023504725	3.020195	Adenylosuccinate lyase (Adsl)
Slc39a1	-0.50	.004566718	4.48284	Solute carrier family 39 (zinc transporter), member 1 (Slc39a1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Caml	-0.51	.016424095	3.678952	Calcium modulating ligand (Caml)
Mydgf	-0.51	.00614242	4.898177	Myeloid derived growth factor (Mydgf)
Cox4i1	-0.51	.002104514	8.13906	Cytochrome c oxidase subunit IV isoform 1 (Cox4i1)
Sem1	-0.51	.020734559	4.41879	SEM1 26S Proteasome Subunit (Sem1)
Ipp	-0.51	.01819853	2.821681	IAP promoted placental gene (Ipp)
Scg3	-0.51	$1.56 \times 10^{-5}$	7.739821	Secretogranin III (Scg3)
Dnah7a	-0.51	.030336419	3.630869	Dynein, axonemal, heavy chain 7A (Dnah7a)
Crtc2	-0.51	.005851189	3.700006	CREB-regulated transcription coactivator 2 (Crtc2)
Pno1	-0.51	.016744673	3.707357	Partner of NOB1 homolog (Pno1)
Npc1	-0.51	.000223604	6.448484	Niemann-Pick type C1 (Npc1)
Rfc2	-0.51	.016012892	3.739075	Replication factor C (activator 1) 2 (Rfc2)
Rhobtb3	-0.51	.003622651	5.322215	Rho-related BTB domain containing 3 (Rhobtb3)
Anks1	-0.51	.009912262	3.970306	Ankyrin repeat and SAM domain containing 1 (Anks1)
Bcl10	-0.51	.00467955	3.586532	B cell leukemia/lymphoma 10 (Bcl10)
Arglu1	-0.51	.003995261	5.984937	Arginine and glutamate rich 1 (Arglu1)
Nme5	-0.51	.006032777	4.354851	NME/NM23 family member 5 (Nme5)
Pskh1	-0.51	.023882343	2.96767	Protein serine kinase H1 (Pskh1)
Ube2d-ps	-0.51	.005660147	4.065762	Ubiquitin-conjugating enzyme E2D, pseudogene (Ube2d-ps)
Gm17018	-0.51	.001877449	5.003502	Predicted gene (Gm17018)
Pcp4l1	-0.51	.000774269	7.288132	PURKINJE cell protein 4-like 1 (Pcp4l1)
Rpl18	-0.51	.002225846	5.538417	Ribosomal protein L18 (Rpl18)
Bphl	-0.51	.001709309	4.239973	Biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen) (Bphl)
Acss2	-0.51	.003284931	4.745502	Acyl-CoA synthetase short-chain family member 2 (Acss2)
Agpat4	-0.51	.005728789	4.636549	1-Acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) (Agpat4)
Tspan2	-0.51	.000518239	8.10443	Tetraspanin 2 (Tspan2)
Arhgef26	-0.51	.001884219	4.801547	Rho guanine nucleotide exchange factor (GEF) 26 (Arhgef26)
Zfp775	-0.52	.036572551	2.979028	Zinc finger protein 775 (Zfp775)
Mphosph6	-0.52	.01943874	3.623721	M phase phosphoprotein 6 (Mphosph6)
Prpf31	-0.52	.003042744	4.652804	Pre-mRNA processing factor 31 (Prpf31)
Ndufa3	-0.52	.009049555	5.522135	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (Ndufa3)
Psd2	-0.52	$9.26 \times 10^{-5}$	6.733639	Pleckstrin and Sec7 domain containing 2 (Psd2)
9330151L19Rik	-0.52	.004302431	4.080096	RIKEN cDNA 9330151L19 gene (9330151L19Rik)
Ccdc107	-0.52	.009896459	3.67451	Coiled-coil domain containing 107 (Ccdc107)
Mypop	-0.52	.036456992	2.488579	Myb-related transcription factor, partner of profilin (Mypop)
Cluap1	-0.52	.013571034	3.870673	Clusterin-associated protein 1 (Cluap1)
Eci2	-0.52	.001530817	4.750868	Enoyl-Coenzyme A delta isomerase 2 (Eci2)
Tomm5	-0.52	.001856778	5.058181	Translocase of outer mitochondrial membrane 5 homolog (yeast) (Tomm5)
Wls	-0.52	.000960391	5.466917	Wntless homolog (Wls)
Ano6	-0.52	.014715837	4.698516	Anoactamin 6 (Ano6)
Tipin	-0.52	.026187218	3.20156	Timeless interacting protein (Tipin)
Ndufa7	-0.52	.001935342	5.577888	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (Ndufa7)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
4931406C07Rik	-0.52	.001209419	4.751471	RIKEN cDNA 4931406C07 gene (4931406C07Rik)
Fuom	-0.52	.005423168	4.077103	Fucose mutarotase (Fuom)
Creld2	-0.52	.047995695	3.622911	Cysteine-rich with EGF-like domains 2 (Creld2)
Cd320	-0.52	.004563875	3.708609	CD320 antigen (Cd320)
Dbn1	-0.52	.00082779	4.981159	Drebrin 1 (Dbn1)
Fam174a	-0.52	.001164473	5.141668	Family with sequence similarity 174, member A (Fam174a)
Nol7	-0.52	.000276441	4.985802	Nucleolar protein 7 (Nol7)
Ppt2	-0.52	.024451232	2.814197	Palmitoyl-protein thioesterase 2 (Ppt2)
Bicra	-0.52	.002622684	4.758494	BRD4 interacting chromatin remodeling complex-associated protein (Bicra)
Nmnat1	-0.52	.045603846	2.42555	Nicotinamide nucleotide adenylyltransferase 1 (Nmnat1)
Dnaja4	-0.52	.027344088	2.91643	DnaJ heat shock protein family (Hsp40) member A4 (Dnaja4)
Tctex1d2	-0.52	.005380427	4.257158	Tctex1 domain containing 2 (Tctex1d2)
Kif9	-0.52	.025308866	2.998886	Kinesin family member 9 (Kif9)
1810058I24Rik	-0.52	.008562762	3.953452	RIKEN cDNA 1810058I24 gene (1810058I24Rik)
Uqcr10	-0.53	.000947358	6.713035	Ubiquinol-cytochrome c reductase, complex III subunit X (Uqcr10)
Npr2	-0.53	.006032777	4.231798	Natriuretic peptide receptor 2 (Npr2)
Bri3	-0.53	.031457872	2.765699	Brain protein I3 (Bri3)
Lzts2	-0.53	.01938535	3.430145	Leucine zipper, putative tumor suppressor 2 (Lzts2)
Nphp1	-0.53	.004225136	3.975885	Nephronophthisis 1 (juvenile) homolog (human) (Nphp1)
Zdhhc18	-0.53	.000331812	6.075579	Zinc finger, DHHC domain containing 18 (Zdhhc18)
Idua	-0.53	.003003186	3.998116	Iduronidase, alpha-L- (Idua)
Sclt1	-0.53	.009740423	3.427917	Sodium channel and clathrin linker 1 (Sclt1)
Fmn1l2	-0.53	.002070685	6.297394	Formin-like 2 (Fmn1l2)
Naxd	-0.53	.008588632	4.177942	NAD (P)HX dehydratase (Naxd)
Gm3693	-0.53	.03244257	3.054183	Predicted gene 3693 (Gm3693)
Med12	-0.53	.014622213	3.965326	Mediator complex subunit 12 (Med12)
Raver2	-0.53	.006407767	3.888472	Ribonucleoprotein, PTB-binding 2 (Raver2)
Decr1	-0.53	.001472216	4.15866	2,4-Dienoyl CoA reductase 1, mitochondrial (Decr1)
Zfand3	-0.53	.000224403	5.549279	Zinc finger, AN1-type domain 3 (Zfand3)
Gtf2h3	-0.53	.017609553	2.894053	General transcription factor IIH, polypeptide 3 (Gtf2h3)
Polr2f	-0.53	.031624232	3.669594	Polymerase (RNA) II (DNA directed) polypeptide F (Polr2f)
Chchd2	-0.53	.001899198	7.0977	Coiled-coil-helix-coiled-coil-helix domain containing 2 (Chchd2)
Bak1	-0.53	.018003087	3.175554	BCL2-antagonist/killer 1 (Bak1)
Igdcc4	-0.53	.000155178	5.298658	Immunoglobulin superfamily, DCC subclass, member 4 (Igdcc4)
Kmt5a	-0.53	.006182374	5.665997	Lysine methyltransferase 5A (Kmt5a)
Slc25a5	-0.54	.000101514	7.214417	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (Slc25a5)
Patj	-0.54	.000387429	5.942844	PATJ, crumbs cell polarity complex component (Patj)
Tmem208	-0.54	.021380885	4.37907	Transmembrane protein 208 (Tmem208)
Fabp5	-0.54	.003001558	5.054629	Fatty acid binding protein 5, epidermal (Fabp5)
Uqcrq	-0.54	.003894461	6.419031	Ubiquinol-cytochrome c reductase, complex III subunit VII (Uqcrq)
Pop4	-0.54	.018688446	4.229356	Processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) (Pop4)
Washc2	-0.54	.00026507	5.33914	WASH Complex Subunit 2C (Washc2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lamtor5	-0.54	.002457495	4.542659	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 5 (Lamtor5)
Ttc5	-0.54	.002099845	4.54102	Tetratricopeptide repeat domain 5 (Ttc5)
Cln3	-0.54	.019353076	3.343761	Ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (Cln3)
Tac1	-0.54	.002203446	5.172512	Tachykinin 1 (Tac1)
Rps23	-0.54	.004189595	4.28015	Ribosomal protein S23 (Rps23)
Gas8	-0.54	.007758927	3.823829	Growth arrest specific 8 (Gas8)
Slain1	-0.54	.00034433	5.758278	SLAIN motif family, member 1 (Slain1)
Adrb1	-0.54	.021743299	3.465158	Adrenergic receptor, beta 1 (Adrb1)
Rps5	-0.54	.00012459	7.473633	Ribosomal protein S5 (Rps5)
Uqcr11	-0.54	.010674757	6.136805	Ubiquinol-cytochrome c reductase, complex III subunit XI (Uqcr11)
Bmp6	-0.54	.037538198	2.903527	Bone morphogenetic protein 6 (Bmp6)
2510002D24Rik	-0.54	.018896934	2.797231	RIKEN cDNA 2510002D24 gene (2510002D24Rik)
Gcnt1	-0.54	.026836993	2.878342	Glucosaminyl (N-acetyl) transferase 1, core 2 (Gcnt1)
Chchd3	-0.54	.001105372	5.078891	Coiled-coil-helix-coiled-coil-helix domain containing 3 (Chchd3)
Mboat2	-0.54	.000650437	6.333473	Membrane bound O-acyltransferase domain containing 2 (Mboat2)
Phf5a	-0.54	.009412668	4.822311	PHD finger protein 5A (Phf5a)
Hsd17b4	-0.54	.000269626	5.371034	Hydroxysteroid (17-beta) dehydrogenase 4 (Hsd17b4)
Pgls	-0.54	.003794321	3.494269	6-Phosphogluconolactonase (Pgls)
Nasp	-0.54	.006122743	3.872067	Nuclear autoantigenic sperm protein (histone-binding) (Nasp)
Yif1a	-0.54	.010302806	3.310781	Yip1 interacting factor homolog A ( <i>S. cerevisiae</i> ) (Yif1a)
Usmg5	-0.54	.012739351	4.130213	Upregulated during skeletal muscle growth 5 (Usmg5)
Lmo3	-0.54	.03519008	5.743879	LIM domain only 3 (Lmo3)
Cpne3	-0.54	.000646891	5.195198	Copine III (Cpne3)
Pfdn2	-0.54	5.43 × 10 <sup>-5</sup>	5.725978	Prefoldin 2 (Pfdn2)
Trabd	-0.54	.017791333	3.194985	TraB domain containing (Trabd)
Mtor	-0.55	2.36 × 10 <sup>-5</sup>	6.730726	Mechanistic target of rapamycin (serine/threonine kinase) (Mtor)
Cfaf54	-0.55	.003368354	4.544157	Cilia and flagella-associated protein 54 (Cfaf54)
Gins4	-0.55	.00187235	4.13463	GINS complex subunit 4 (Sld5 homolog) (Gins4)
Cwc15	-0.55	.000423654	5.839721	CWC15 spliceosome-associated protein (Cwc15)
Slc44a2	-0.55	.001361155	4.737299	Solute carrier family 44, member 2 (Slc44a2)
Tor1aip1	-0.55	.002601527	5.994064	Torsin A interacting protein 1 (Tor1aip1)
Odf2l	-0.55	.01013132	3.408248	Outer dense fiber of sperm tails 2-like (Odf2l)
Hexa	-0.55	.000947358	4.824397	Hexosaminidase A (Hexa)
Irak2	-0.55	.006676307	3.512588	Interleukin-1 receptor-associated kinase 2 (Irak2)
Hspb11	-0.55	.044895395	2.857482	Heat shock protein family B (small), member 11 (Hspb11)
Rpl8	-0.55	.000441285	7.049748	Ribosomal protein L8 (Rpl8)
Hscb	-0.55	.01824737	3.635238	HscB iron-sulfur cluster co-chaperone (Hscb)
Thoc7	-0.55	.000620506	4.608745	THO complex 7 (Thoc7)
Mapkapk2	-0.55	.004813324	4.301589	MAP kinase-activated protein kinase 2 (Mapkapk2)
Tedc2	-0.55	.042310303	2.678162	Tubulin Epsilon And Delta Complex 2 (Tedc2)
5930412G12Rik	-0.55	.024624252	2.585928	RIKEN cDNA 5930412G12 gene (5930412G12Rik)
Mir9-3hg	-0.55	.02388003	2.598739	Mir9-3 host gene (Mir9-3hg)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pnp	-0.55	.032203827	4.084198	Purine-nucleoside phosphorylase (Pnp)
Slc9a3r2	-0.56	.000826189	4.773769	Solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2 (Slc9a3r2)
Tcea2	-0.56	.016437857	3.442116	Transcription elongation factor A (SII), 2 (Tcea2)
2610306M01Rik	-0.56	.027298452	2.504893	RIKEN cDNA 2610306M01 gene (2610306M01Rik)
Lsm10	-0.56	.033594878	2.761455	U7 snRNP-specific Sm-like protein LSM10 (Lsm10)
Gm6483	-0.56	.018932095	2.621391	Cadherin 11 pseudogene (Gm6483)
Atp5k	-0.56	.004720456	5.587479	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E (Atp5k)
Cdk2ap1	-0.56	.003007248	3.31918	CDK2 (cyclin-dependent kinase 2)-associated protein 1 (Cdk2ap1)
Cpne8	-0.56	.010793472	3.334861	Copine VIII (Cpne8)
Ntrk2	-0.56	2.38 × 10 <sup>-5</sup>	9.939266	Neurotrophic tyrosine kinase, receptor, type 2 (Ntrk2)
Slc16a1	-0.56	.008910629	4.41073	Solute carrier family 16 (monocarboxylic acid transporters), member 1 (Slc16a1)
Polr2i	-0.56	.003920074	3.751273	Polymerase (RNA) II (DNA directed) polypeptide I (Polr2i)
Snapin	-0.56	.000442261	6.728626	SNAP-associated protein (Snapin)
Fam162a	-0.56	.005580394	4.342906	Family with sequence similarity 162, member A (Fam162a)
Atf5	-0.56	.027708733	2.894045	Activating transcription factor 5 (Atf5)
Ccnyl1	-0.56	.010539556	3.042705	Cyclin Y-like 1 (Ccnyl1)
Btg1	-0.56	.006249326	3.982653	B cell translocation gene 1, anti-proliferative (Btg1)
Atp6v0a2	-0.56	.0003803	5.676502	ATPase, H+ transporting, lysosomal V0 subunit A2 (Atp6v0a2)
Rps11	-0.56	.000728873	5.485933	Ribosomal protein S11 (Rps11)
Prkab1	-0.56	.0116519	3.605022	Protein kinase, AMP-activated, beta 1 non-catalytic subunit (Prkab1)
Lamtor2	-0.56	.01647194	4.898764	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 2 (Lamtor2)
Natd1	-0.56	.00197176	4.920486	N-acetyltransferase domain containing 1 (Natd1)
Uqcrh	-0.56	.000504797	7.424672	Ubiquinol-cytochrome c reductase hinge protein (Uqcrh)
Lair1	-0.56	.018831068	3.912171	Leukocyte-associated Ig-like receptor 1 (Lair1)
Psmg1	-0.56	.028335252	3.801052	Proteasome (prosome, macropain) assembly chaperone 1 (Psmg1)
Retsat	-0.56	.013171265	3.157733	Retinol saturase (all trans retinol 13,14 reductase) (Retsat)
Cox7a2l	-0.57	7.54 × 10 <sup>-5</sup>	6.118126	Cytochrome c oxidase subunit VIIa polypeptide 2-like (Cox7a2l)
Traf4	-0.57	.036535714	2.202446	TNF receptor-associated factor 4 (Traf4)
Hars2	-0.57	.01757566	3.790111	Histidyl-tRNA synthetase 2 (Hars2)
Cyb5a	-0.57	.000859819	5.213275	Cytochrome b5 type A (microsomal) (Cyb5a)
Washc3	-0.57	.00432711	4.239677	WASH Complex Subunit 3 (Washc3)
Syt9	-0.57	.019362505	8.004679	Synaptotagmin IX (Syt9)
Nup188	-0.57	.006768763	3.773964	Nucleoporin 188 (Nup188)
Bag3	-0.57	.01682695	3.2843	BCL2-associated athanogene 3 (Bag3)
Mvb12a	-0.57	.042781575	3.035934	Multivesicular body subunit 12A (Mvb12a)
Dbndd2	-0.57	.00019206	5.313127	Dysbindin (dystrobrevin binding protein 1) domain containing 2 (Dbndd2)
Fank1	-0.57	.045826652	2.227904	Fibronectin type 3 and ankyrin repeat domains 1 (Fank1)
Cnih1	-0.57	.000266989	5.308213	Cornichon family AMPA receptor auxiliary protein 1 (Cnih1)
Mbd3	-0.57	.003087065	4.820509	Methyl-CpG binding domain protein 3 (Mbd3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Lhpp	-0.57	.005862289	3.730477	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase (Lhpp)
Plch2	-0.57	.002152467	5.80422	Phospholipase C, eta 2 (Plch2)
Tdp1	-0.57	.010464107	3.242318	Tyrosyl-DNA phosphodiesterase 1 (Tdp1)
Sat2	-0.57	.015703885	3.096439	Spermidine/spermine N1-acetyl transferase 2 (Sat2)
Fnbp1	-0.57	$2.90 \times 10^{-5}$	7.049361	Formin binding protein 1 (Fnbp1)
Ccnd1	-0.57	.012256727	3.775621	Cyclin D1 (Ccnd1)
Cygb	-0.57	.014499583	6.166839	Cytoglobin (Cygb)
Saxo2	-0.57	.045469338	2.761986	Stablizer of axonemal microtubules 2 (Saxo2)
Mlip	-0.58	$9.08 \times 10^{-5}$	5.979582	Muscular LMNA-interacting protein (Mlip)
Ndufb3	-0.58	.001142609	5.299792	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 (Ndufb3)
Sec11a	-0.58	.00085491	4.364588	SEC11 homolog A, signal peptidase complex subunit (Sec11a)
Wasf2	-0.58	.013174575	4.575831	WAS protein family, member 2 (Wasf2)
Hspa2	-0.58	.003910116	4.225001	Heat shock protein 2 (Hspa2)
Mettl9	-0.58	.000348155	5.156757	Methyltransferase like 9 (Mettl9)
Rhbdd3	-0.58	.038932386	2.259323	Rhomboid domain containing 3 (Rhbdd3)
Atraid	-0.58	.005185826	5.203488	All-trans retinoic acid-induced differentiation factor (Atraid)
Tcta	-0.58	.000295715	4.566442	T cell leukemia translocation altered gene (Tcta)
Ddt	-0.58	.017732069	3.437489	D-dopachrome tautomerase (Ddt)
Gpr62	-0.58	.019711536	2.97008	G protein-coupled receptor 62 (Gpr62)
Cc2d2a	-0.58	.011907533	4.430492	Coiled-coil and C2 domain containing 2A (Cc2d2a)
Nexn	-0.58	.014155293	3.334773	Nexilin (Nexn)
Hnmt	-0.58	.003995261	4.006748	Histamine N-methyltransferase (Hnmt)
Fdx1	-0.58	.011196831	3.490623	Ferrodoxin 1 (Fdx1)
Bcl7b	-0.58	.000561752	4.401215	B cell CLL/lymphoma 7B (Bcl7b)
Mrps24	-0.58	.011299528	3.330482	Mitochondrial ribosomal protein S24 (Mrps24)
Naca	-0.58	.000183049	6.122107	Nascent polypeptide-associated complex alpha polypeptide (Naca)
Gt (ROSA)26Sor	-0.58	.02526197	2.487516	Gene trap ROSA 26, Philippe Soriano (Gt (ROSA)26Sor)
Abcd3	-0.58	.000111228	5.957834	ATP-binding cassette, sub-family D (ALD), member 3 (Abcd3)
Bpgm	-0.58	$4.91 \times 10^{-5}$	6.115788	2,3-Bisphosphoglycerate mutase (Bpgm)
Tifa	-0.58	.023914227	2.881693	TRAF-interacting protein with forkhead-associated domain (Tifa)
Mad2l2	-0.58	.004134027	3.289126	MAD2 mitotic arrest deficient-like 2 (Mad2l2)
Rgs6	-0.58	.00713061	5.436332	Regulator of G-protein signaling 6 (Rgs6)
Rex1bd	-0.58	.001979919	4.47241	Required For Excision 1-B Domain Containing (Rex1bd)
Taz	-0.58	.005869825	4.248677	Tafazzin (Taz)
Ech1	-0.58	.00124239	4.49546	Enoyl coenzyme A hydratase 1, peroxisomal (Ech1)
Polb	-0.58	.023020417	4.28136	Polymerase (DNA directed), beta (Polb)
Tssc4	-0.58	.005892229	3.851934	Tumor-suppressing subchromosomal transferable fragment 4 (Tssc4)
Cdh20	-0.59	.006903285	5.085429	Cadherin 20 (Cdh20)
Net1	-0.59	.003222646	3.58252	Neuroepithelial cell transforming gene 1 (Net1)
Ercc1	-0.59	.030650385	2.941334	Excision repair cross-complementing rodent repair deficiency, complementation group 1 (Ercc1)
Cldnd1	-0.59	.001559853	6.012929	Claudin domain containing 1 (Cldnd1)
Crlf3	-0.59	.011121976	2.792021	Cytokine receptor-like factor 3 (Crlf3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Snx5	-0.59	1.36 × 10 <sup>-5</sup>	6.84492	Sorting nexin 5 (Snx5)
Kiz	-0.59	.002831529	4.425713	Kizuna centrosomal protein (Kiz)
Fgf1	-0.59	.017180772	7.714394	Fibroblast growth factor 1 (Fgf1)
Scnm1	-0.59	.007750305	3.751657	Sodium channel modifier 1 (Scnm1)
Iqcg	-0.59	.004392997	3.717438	IQ motif containing G (Iqcg)
Msantd2	-0.59	.042363111	2.836545	Myb/SANT-like DNA-binding domain containing 2 (Msantd2)
Cspp1	-0.59	.005247622	4.041482	Centrosome and spindle pole-associated protein 1 (Cspp1)
Ndufa13	-0.59	.000216584	7.296876	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 (Ndufa13)
Eef1d	-0.59	.002180198	5.32275	Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (Eef1d)
Adh5	-0.59	.000120594	5.044918	Alcohol dehydrogenase 5 (class III), chi polypeptide (Adh5)
Rps26	-0.59	.000414656	5.768732	Ribosomal protein S26 (Rps26)
Efcab5	-0.59	.03623292	2.193047	EF-hand calcium binding domain 5 (Efcab5)
Taf6l	-0.59	.008905361	3.457957	TATA-box binding protein-associated factor 6 like (Taf6l)
Chd1l	-0.59	.024649476	2.372125	Chromodomain helicase DNA binding protein 1-like (Chd1l)
4732491K20Rik	-0.59	.03459078	2.757013	RIKEN cDNA 4732491K20 gene (4732491K20Rik)
Nt5c3b	-0.59	.012276984	3.832221	5'-Nucleotidase, cytosolic IIIB (Nt5c3b)
Pigh	-0.59	.030371322	2.316364	Phosphatidylinositol glycan anchor biosynthesis, class H (Pigh)
Map4k5	-0.59	.00358462	4.386346	Mitogen-activated protein kinase kinase kinase 5 (Map4k5)
Cdk10	-0.59	.004053265	4.160992	Cyclin-dependent kinase 10 (Cdk10)
Hs3st1	-0.60	.002448758	4.003497	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (Hs3st1)
D8Ertd738e	-0.60	.007193457	4.5806	DNA segment, Chr 8, ERATO Doi 738, expressed (D8Ertd738e)
Cdc42ep2	-0.60	.025845262	3.503264	CDC42 effector protein (Rho GTPase binding) 2 (Cdc42ep2)
Dhx34	-0.60	.028879506	2.285649	DEAH (Asp-Glu-Ala-His) box polypeptide 34 (Dhx34)
Slc41a1	-0.60	4.30 × 10 <sup>-5</sup>	6.34502	Solute carrier family 41, member 1 (Slc41a1)
Gm16701	-0.60	.003719834	4.053003	Predicted gene, 16701 (Gm16701)
Xylb	-0.60	.016007569	3.21511	Xylulokinase homolog (H. influenzae) (Xylb)
Taldo1	-0.60	.001518428	4.935919	Transaldolase 1 (Taldo1)
Atp5h	-0.60	.000595023	6.864817	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit D (Atp5h)
Gm13889	-0.60	.010571268	3.456098	Predicted gene 13889 (Gm13889)
Cnpy4	-0.60	.001931456	3.519628	Canopy FGF signaling regulator 4 (Cnpy4)
Adk	-0.60	.000688589	4.276751	Adenosine kinase (Adk)
Cdk4	-0.60	.00018605	4.570517	Cyclin-dependent kinase 4 (Cdk4)
Ehd2	-0.60	.049786123	2.198543	EH-domain containing 2 (Ehd2)
S100a10	-0.60	.007896907	3.529441	S100 calcium binding protein A10 (calpastatin) (S100a10)
Ldlrad3	-0.60	.002538556	4.168246	Low-density lipoprotein receptor class A domain containing 3 (Ldlrad3)
Rpl10	-0.60	.000118896	5.325176	Ribosomal protein L10 (Rpl10)
E2f1	-0.60	.028518037	2.601794	E2F transcription factor 1 (E2f1)
GalC	-0.60	.003394541	4.384328	Galactosylceramidase (GalC)
Egfr	-0.60	.001261944	4.448216	Epidermal growth factor receptor (Egfr)
Ndufa5	-0.60	.01425755	4.674703	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (Ndufa5)
Ndufa1	-0.60	.005401632	4.763444	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (Ndufa1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Chmp2a	-0.60	.000304313	4.902212	Charged multivesicular body protein 2A (Chmp2a)
Hist1h4d	-0.60	.003634809	3.828203	Histone cluster 1, H4d (Hist1h4d)
Casz1	-0.60	.025471005	3.610645	Castor zinc finger 1 (Casz1)
Rnf7	-0.60	7.00 × 10 <sup>-5</sup>	6.255796	Ring finger protein 7 (Rnf7)
Rita1	-0.60	.004283383	3.231795	RBPJ interacting and tubulin associated 1 (Rita1)
Ppard	-0.61	.0071564	4.857274	Peroxisome proliferator activator receptor delta (Ppard)
Slc35d1	-0.61	.003604952	4.499334	Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (Slc35d1)
Rest	-0.61	.004240178	3.972448	RE1-silencing transcription factor (Rest)
D330023K18Rik	-0.61	.01985075	2.190993	RIKEN cDNA D330023K18 gene (D330023K18Rik)
Myh9	-0.61	.000681594	4.222169	Myosin, heavy polypeptide 9, non-muscle (Myh9)
Usp16	-0.61	.000529106	5.157597	Ubiquitin-specific peptidase 16 (Usp16)
Ctns	-0.61	.005864587	2.934692	Cystinosis, nephropathic (Ctns)
Mrto4	-0.61	.005551783	3.333951	mRNA turnover 4, ribosome maturation factor (Mrto4)
Mrps6	-0.61	.000946959	4.012046	Mitochondrial ribosomal protein S6 (Mrps6)
Aasdh	-0.61	.012203041	2.791253	Aminoadipate-semialdehyde dehydrogenase (Aasdh)
Agtrap	-0.61	.018963115	3.350529	Angiotensin II, type I receptor-associated protein (Agtrap)
Mthfd2l	-0.61	.036775109	3.016261	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like (Mthfd2l)
Cdkl4	-0.61	.037732591	2.156503	Cyclin-dependent kinase-like 4 (Cdkl4)
Rpl27a	-0.61	5.95 × 10 <sup>-5</sup>	5.516825	Ribosomal protein L27A (Rpl27a)
Pygb	-0.61	7.72 × 10 <sup>-5</sup>	6.783398	Brain glycogen phosphorylase (Pygb)
Msi1	-0.61	.001863748	4.938594	Musashi RNA-binding protein 1 (Msi1)
Ndufs6	-0.61	.011444352	5.580973	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (Ndufs6)
Ptn	-0.61	3.44 × 10 <sup>-6</sup>	7.985841	Pleiotrophin (Ptn)
Sorbs3	-0.61	.002960631	5.452567	Sorbin and SH3 domain containing 3 (Sorbs3)
Ak6	-0.61	.011763857	2.875372	Adenylate kinase 6 (Ak6)
Reep3	-0.61	.002533143	5.670771	Receptor accessory protein 3 (Reep3)
Rnls	-0.61	.031169002	1.816941	Renalase, FAD-dependent amine oxidase (Rnls)
Atox1	-0.61	.00190298	4.43523	Antioxidant 1 copper chaperone (Atox1)
Pkd2	-0.61	.000520794	5.111793	Polycystic kidney disease 2 (Pk2)
Sft2d3	-0.61	.015297926	2.902532	SFT2 domain containing 3 (Sft2d3)
Paqr8	-0.61	.001051922	8.326806	Progestin and adipoQ receptor family member VIII (Paqr8)
Uckl1	-0.61	.002712291	3.393746	Uridine-cytidine kinase 1-like 1 (Uckl1)
Speg	-0.61	.000756471	4.317412	SPEG complex locus (Speg)
Mprip	-0.61	1.04 × 10 <sup>-5</sup>	7.840381	Myosin phosphatase Rho interacting protein (Mprip)
Neurod1	-0.61	.015768263	3.991788	Neurogenic differentiation 1 (Neurod1)
Usp3	-0.61	.000684523	4.241772	Ubiquitin-specific peptidase 3 (Usp3)
Kif26a	-0.62	.036141721	1.890234	Kinesin family member 26A (Kif26a)
Ktn1	-0.62	1.43 × 10 <sup>-5</sup>	6.635628	Kinetin 1 (Ktn1)
Fam129b	-0.62	.011251923	2.866118	Family with sequence similarity 129, member B (Fam129b)
H3f3b	-0.62	1.83 × 10 <sup>-5</sup>	6.641063	H3 histone, family 3B (H3f3b)
Dazap2	-0.62	5.27 × 10 <sup>-5</sup>	7.624097	DAZ-associated protein 2 (Dazap2)
Scd2	-0.62	3.96 × 10 <sup>-6</sup>	10.35496	Stearoyl-Coenzyme A desaturase 2 (Scd2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tmem86a	-0.62	.012708036	3.494719	Transmembrane protein 86A (Tmem86a)
Osgep	-0.62	.004104083	3.637412	O-sialoglycoprotein endopeptidase (Osgep)
Cox8a	-0.62	.000120305	7.147469	Cytochrome c oxidase subunit VIIa (Cox8a)
Zw10	-0.62	.036792516	2.832055	zw10 kinetochore protein (Zw10)
Nfkbia	-0.62	.042310303	2.099284	Nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha (Nfkbia)
Slc18b1	-0.62	.001586914	4.046394	Solute carrier family 18, subfamily B, member 1 (Slc18b1)
Ndufc2	-0.62	.000823742	6.281541	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (Ndufc2)
Sptssa	-0.62	.005186413	3.591965	Serine palmitoyltransferase, small subunit A (Sptssa)
Serp1	-0.62	.000212536	5.550364	Stress-associated endoplasmic reticulum protein 1 (Serp1)
Dgat1	-0.62	.007122829	3.063424	Diacylglycerol O-acyltransferase 1 (Dgat1)
Rnd2	-0.62	$2.81 \times 10^{-5}$	6.508868	Rho family GTPase 2 (Rnd2)
Selenos	-0.62	.000190462	4.810874	Selenoprotein S (Selenos)
BC031181	-0.62	$4.50 \times 10^{-5}$	6.691533	cDNA sequence BC031181 (BC031181)
B9d1	-0.62	.008436695	3.3404	B9 protein domain 1 (B9d1)
Grtp1	-0.62	.012627234	2.552823	GH-regulated TBC protein 1 (Grtp1)
Mcee	-0.62	.00124002	4.152572	Methylmalonyl CoA epimerase (Mcee)
Rbm3	-0.62	.000495879	4.278432	RNA binding motif protein 3 (Rbm3)
Polr3g	-0.63	.043149729	2.228887	Polymerase (RNA) III (DNA directed) polypeptide G (Polr3g)
Ppp1r15a	-0.63	.012587058	2.77325	Protein phosphatase 1, regulatory (inhibitor) subunit 15A (Ppp1r15a)
Elfn1	-0.63	.047008119	6.243181	Leucine-rich repeat and fibronectin type III, extracellular 1 (Elfn1)
Elov17	-0.63	.014218724	4.497898	ELOVL family member 7, elongation of long chain fatty acids (yeast) (Elov17)
Col18a1	-0.63	.015558377	2.671624	Collagen, type XVIII, alpha 1 (Col18a1)
Rnpepl1	-0.63	.015179962	3.928203	Arginyl aminopeptidase (aminopeptidase B)-like 1 (Rnpepl1)
Cytip	-0.63	.044874908	2.92107	Cytohesin 1 interacting protein (Cytip)
Gm13375	-0.63	.007227594	2.878242	Predicted gene 13375 (Gm13375)
Rps27a	-0.63	.002669903	4.794661	Ribosomal protein S27A (Rps27a)
Capn3	-0.63	.014715837	2.96471	Calpain 3 (Capn3)
Trmu	-0.63	.00930154	2.604666	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase (Trmu)
Rnpc3	-0.63	.003257939	3.294593	RNA-binding region (RNP1, RRM) containing 3 (Rnpc3)
Lrp10	-0.63	.000127616	4.824147	Low-density lipoprotein receptor-related protein 10 (Lrp10)
Dusp15	-0.63	.018350619	2.656935	Dual-specificity phosphatase-like 15 (Dusp15)
Kcnn2	-0.63	.004315947	4.390654	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (Kcnn2)
Ifngr1	-0.63	.002839606	3.767764	Interferon gamma receptor 1 (Ifngr1)
Sbk1	-0.63	.004922193	4.250637	SH3-binding kinase 1 (Sbk1)
Llg1	-0.63	.001453455	4.256972	Lethal giant larvae homolog 1 (Llg1)
Rpl22	-0.63	.000266171	6.339041	Ribosomal protein L22 (Rpl22)
Cep128	-0.63	.029655474	3.280109	Centrosomal protein 128 (Cep128)
Ddr1	-0.63	.000126347	5.132665	Discoidin domain receptor family, member 1 (Ddr1)
Atp1b2	-0.63	$4.81 \times 10^{-6}$	9.836582	ATPase, Na+/K+ transporting, beta 2 polypeptide (Atp1b2)
Fkbp2	-0.63	.001701475	5.330724	FK506 binding protein 2 (Fkbp2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rfxank	-0.63	.020904931	2.346	Regulatory factor X-associated ankyrin-containing protein (Rfxank)
Sar1b	-0.64	$5.89 \times 10^{-5}$	5.687738	Secretion-associated Ras-related GTPase 1B (Sar1b)
Bola1	-0.64	.007431416	2.764271	bola-like 1 ( <i>E. coli</i> ) (Bola1)
Slc25a28	-0.64	.001548544	3.844212	Solute carrier family 25, member 28 (Slc25a28)
Cox14	-0.64	.000466782	5.08454	Cytochrome c oxidase assembly protein 14 (Cox14)
Tmem141	-0.64	.010659455	3.032708	Transmembrane protein 141 (Tmem141)
Slc15a4	-0.64	.00277358	3.627289	Solute carrier family 15, member 4 (Slc15a4)
Pet100	-0.64	.049424979	2.133192	PET100 homolog (Pet100)
Lsm8	-0.64	.002195693	3.655856	LSM8 homolog, U6 small nuclear RNA associated (Lsm8)
Gfra1	-0.64	.022286212	6.543331	Glial cell line derived neurotrophic factor family receptor alpha 1 (Gfra1)
Il15ra	-0.64	.045862511	1.591228	Interleukin 15 receptor, alpha chain (Il15ra)
Sall1	-0.64	.000514043	4.329751	Sal-like 1 (Sall1)
Grm3	-0.64	.001364121	5.488486	Glutamate receptor, metabotropic 3 (Grm3)
Utp11	-0.64	.000969843	4.492416	UTP11 Small Subunit Processome Component (Utp11)
Btd	-0.64	.002308912	3.226788	Biotinidase (Btd)
Tgfa	-0.64	.009637513	4.944005	Transforming growth factor alpha (Tgfa)
1700003M07Rik	-0.64	.015710461	3.243855	RIKEN cDNA 1700003M07 gene (1700003M07Rik)
Ehhadh	-0.64	.033684125	1.968019	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (Ehhadh)
Acbd4	-0.64	.006119006	3.129769	Acyl-Coenzyme A binding domain containing 4 (Acbd4)
Arsk	-0.64	.002622684	3.404615	Arylsulfatase K (Arsk)
Rpl11	-0.64	.000238358	4.496203	Ribosomal protein L11 (Rpl11)
Nlrp5-ps	-0.64	.013823016	3.716091	NLR family, pyrin domain containing 5, pseudogene (Nlrp5-ps)
Adgrg1	-0.64	.000892557	6.519775	Adhesion G protein-coupled receptor G1 (Adgrg1)
Crybg3	-0.65	.017365805	2.062718	Beta-gamma crystallin domain containing 3 (Crybg3)
Prkcd	-0.65	.000464785	7.360998	Protein kinase C, delta (Prkcd)
Mpv17l2	-0.65	.016512284	3.821126	MPV17 mitochondrial membrane protein-like 2 (Mpv17l2)
Dusp11	-0.65	.000666953	5.234913	Dual-specificity phosphatase 11 (RNA/RNP complex 1-interacting) (Dusp11)
Zfp787	-0.65	.020880402	2.552673	Zinc finger protein 787 (Zfp787)
Immp1l	-0.65	.001626569	3.859403	IMP1 inner mitochondrial membrane peptidase-like ( <i>S. cerevisiae</i> ) (Immp1l)
Malt1	-0.65	.042163663	2.235643	MALT1 paracaspase (Malt1)
Eepd1	-0.65	.040366284	1.902663	Endonuclease/exonuclease/phosphatase family domain containing 1 (Eepd1)
Gm16432	-0.65	.026675912	2.68436	Predicted gene 16432 (Gm16432)
Slc31a2	-0.65	.015995906	3.86975	Solute carrier family 31, member 2 (Slc31a2)
Rspn4a	-0.65	.003358959	4.554405	Radial spoke head 4 homolog A ( <i>Chlamydomonas</i> ) (Rspn4a)
Egfl7	-0.65	.019386897	2.434919	EGF-like domain 7 (Egfl7)
Rpsa	-0.65	$5.78 \times 10^{-6}$	6.800309	Ribosomal protein SA (Rpsa)
Etfa	-0.65	.000320883	5.461131	Electron transferring flavoprotein, alpha polypeptide (Etfa)
Stk33	-0.65	.032509218	2.852379	Serine/threonine kinase 33 (Stk33)
Aqp4	-0.65	.014701608	8.35426	Aquaporin 4 (Aqp4)
Rnf5	-0.65	.002841706	5.430422	Ring finger protein 5 (Rnf5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rpl17	-0.65	$4.41 \times 10^{-5}$	5.393224	Ribosomal protein L17 (Rpl17)
Rpl14	-0.65	$3.04 \times 10^{-5}$	5.558006	Ribosomal protein L14 (Rpl14)
Rin2	-0.65	.000854386	4.806051	RAS and Rab interactor 2 (Rin2)
Mrpl33	-0.65	.006243377	3.273027	Mitochondrial ribosomal protein L33 (Mrpl33)
Atp5j	-0.65	.000348155	6.996285	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit F (Atp5j)
Hsd17b10	-0.65	.000504797	4.244624	Hydroxysteroid (17-beta) dehydrogenase 10 (Hsd17b10)
Tceal8	-0.65	.000244377	5.502409	Transcription elongation factor A (SII)-like 8 (Tceal8)
Selenof	-0.65	$6.66 \times 10^{-6}$	7.142503	Selenoprotein F (Selenof)
Gpx4	-0.66	.00127953	3.755899	Glutathione peroxidase 4 (Gpx4)
Kif6	-0.66	.039925457	1.990967	Kinesin family member 6 (Kif6)
Fzd4	-0.66	.020981595	2.946199	Frizzled class receptor 4 (Fzd4)
Tex9	-0.66	.003031257	3.811824	Testis expressed gene 9 (Tex9)
Ntn1	-0.66	.008818444	2.831446	Netrin 1 (Ntn1)
Dhrs7	-0.66	.006646127	3.782121	Dehydrogenase/reductase (SDR family) member 7 (Dhrs7)
Otulin	-0.66	.00490459	3.18073	OTU deubiquitinase with linear linkage specificity (Otulin)
Snhg17	-0.66	.020339082	1.816337	Small nucleolar RNA host gene 17 (Snhg17)
Etv5	-0.66	.000257266	4.821753	ets variant 5 (Etv5)
Ilkap	-0.66	.000523549	4.755555	Integrin-linked kinase-associated serine/threonine phosphatase 2C (Ilkap)
Gm45605	-0.66	.024729319	2.041045	Predicted gene (Gm45605)
Zfand2b	-0.66	.045138748	2.287668	Zinc finger, AN1 type domain 2B (Zfand2b)
Arhgap29	-0.66	.007354928	3.819825	Rho GTPase activating protein 29 (Arhgap29)
Mtmr10	-0.66	.005330084	4.437537	Myotubularin-related protein 10 (Mtmr10)
Bax	-0.66	.005598384	3.481316	BCL2-associated X protein (Bax)
Mien1	-0.66	.001652512	4.175419	Migration and invasion enhancer 1 (Mien1)
1500011K16Rik	-0.66	.000515894	4.76452	RIKEN cDNA 1500011K16 gene (1500011K16Rik)
Ctu2	-0.66	.016681558	2.277446	Cytosolic thiouridylase subunit 2 (Ctu2)
2310009A05Rik	-0.66	.011850319	2.717225	RIKEN cDNA 2310009A05 gene (2310009A05Rik)
3110056K07Rik	-0.66	.018426073	2.592994	RIKEN cDNA 3110056K07 gene (3110056K07Rik)
Rps6ka1	-0.66	.001105372	3.474464	Ribosomal protein S6 kinase polypeptide 1 (Rps6ka1)
Hip1r	-0.66	.000699718	4.082384	Huntingtin interacting protein 1-related (Hip1r)
Adgra3	-0.66	.000924156	3.69905	Adhesion G protein-coupled receptor A3 (Adgra3)
Ssbp1	-0.66	.001338799	4.263046	Single-stranded DNA binding protein 1 (Ssbp1)
Pxylp1	-0.66	.024977903	3.214745	2-Phosphoxylose phosphatase 1 (Pxylp1)
Card19	-0.66	.005128564	2.937447	Caspase recruitment domain family, member 19 (Card19)
Cgnl1	-0.66	.043059615	2.109093	Cingulin-like 1 (Cgnl1)
Ccdc58	-0.66	.016655958	2.458506	Coiled-coil domain containing 58 (Ccdc58)
Caprin2	-0.66	.012736767	2.554031	Caprin family member 2 (Caprin2)
Fcf1	-0.67	.003140864	3.610489	FCF1 rRNA processing protein (Fcf1)
Chd7	-0.67	.016146763	5.134733	Chromodomain helicase DNA binding protein 7 (Chd7)
Rpl32	-0.67	.000111999	7.617208	Ribosomal protein L32 (Rpl32)
Cmc4	-0.67	.031919077	1.727233	C-x (9)-C motif containing 4 (Cmc4)
Fyco1	-0.67	.00080519	5.588259	FYVE and coiled-coil domain containing 1 (Fyco1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Fgd6	-0.67	.000855313	5.114489	FYVE, RhoGEF and PH domain containing 6 (Fgd6)
Spsb1	-0.67	.009475074	3.438327	splA/ryanodine receptor domain and SOCS box containing 1 (Spsb1)
Snrpc	-0.67	.045805901	1.785356	U1 small nuclear ribonucleoprotein C (Snrpc)
Pard3b	-0.67	.030278518	2.978152	Par-3 family cell polarity regulator beta (Pard3b)
Synpr	-0.67	.01226005	6.371494	Synaptoporin (Synpr)
Flywch2	-0.67	.035937283	2.678039	FLYWCH family member 2 (Flywch2)
Sulf2	-0.67	.001357801	6.516621	Sulfatase 2 (Sulf2)
Slc16a2	-0.67	.00132835	3.771513	Solute carrier family 16 (monocarboxylic acid transporters), member 2 (Slc16a2)
Mcc	-0.67	.000591057	5.755009	Mutated in colorectal cancers (Mcc)
Bmp1	-0.67	.026285895	2.074876	Bone morphogenetic protein 1 (Bmp1)
Tmod3	-0.67	.000729819	4.55708	Tropomodulin 3 (Tmod3)
1110046J04Rik	-0.67	.018412516	2.18246	RIKEN cDNA 1110046J04 gene (1110046J04Rik)
Zc3h8	-0.67	.013505748	2.405338	Zinc finger CCCH type containing 8 (Zc3h8)
Rpp38	-0.67	.022072384	2.678805	Ribonuclease P/MRP 38 subunit (Rpp38)
Zfand6	-0.67	.001856778	4.71923	Zinc finger, AN1-type domain 6 (Zfand6)
Plcl1	-0.67	.003419757	5.456141	Phospholipase C-like 1 (Plcl1)
Ctnnbl1	-0.67	.002505762	3.10508	Catenin, beta like 1 (Ctnnbl1)
Nptx1	-0.67	.047700502	5.83422	Neuronal pentraxin 1 (Nptx1)
Fstl1	-0.67	.000672644	5.158487	Follistatin-like 1 (Fstl1)
Zeb2	-0.67	.002400684	6.775996	Zinc finger E-box binding homeobox 2 (Zeb2)
Smim20	-0.67	.000500932	4.365446	Small integral membrane protein 20 (Smim20)
Pld5	-0.67	.042041569	5.676102	Phospholipase D family, member 5 (Pld5)
Rps16	-0.67	.00041712	5.122946	Ribosomal protein S16 (Rps16)
Rps25	-0.67	$3.42 \times 10^{-5}$	7.237472	Ribosomal protein S25 (Rps25)
Pnpla2	-0.67	.001945325	4.256841	Patatin-like phospholipase domain containing 2 (Pnpla2)
Alkbh3	-0.67	.021161885	2.213075	alkB homolog 3, alpha-ketoglutarate-dependent dioxygenase (Alkbh3)
Cavin3	-0.67	.004002513	3.314798	Caveolae-associated protein 3 (Cavin3)
Cdpf1	-0.67	.002096016	3.519073	Cysteine-rich, DPF motif domain containing 1 (Cdpf1)
Rps8	-0.68	.000168046	4.665951	Ribosomal protein S8 (Rps8)
Pwwp2a	-0.68	.001334561	4.986938	PWWP domain containing 2A (Pwwp2a)
Sema7a	-0.68	$8.71 \times 10^{-5}$	4.646144	Sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A (Sema7a)
Sys1	-0.68	.000224073	4.063646	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae) (Sys1)
Gm16794	-0.68	.039631738	1.505798	Predicted gene, 16794 (Gm16794)
Slc35b2	-0.68	.004134027	3.596397	Solute carrier family 35, member B2 (Slc35b2)
Josd2	-0.68	.004778098	3.581197	Josephin domain containing 2 (Josd2)
Snrrpa1	-0.68	.002645101	3.643475	Small nuclear ribonucleoprotein polypeptide A' (Snrrpa1)
Smdt1	-0.68	.001109435	5.621242	Single-pass membrane protein with aspartate-rich tail 1 (Smdt1)
Eno4	-0.68	.029498843	2.06391	Enolase 4 (Eno4)
Tmem144	-0.68	.002354346	3.729227	Transmembrane protein 144 (Tmem144)
Enpp6	-0.68	.027304739	4.202956	Ectonucleotide pyrophosphatase/phosphodiesterase 6 (Enpp6)
Shc4	-0.68	.007069555	2.825835	SHC (Src homology 2 domain containing) family, member 4 (Shc4)
Iqck	-0.68	.003003186	3.349128	IQ motif containing K (Iqck)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Wdr60	-0.68	.00676544	3.126138	WD repeat domain 60 (Wdr60)
Kif1c	-0.68	.002055791	5.648548	Kinesin family member 1C (Kif1c)
1110038F14Rik	-0.68	.011435696	3.003711	RIKEN cDNA 1110038F14 gene (1110038F14Rik)
Gm1976	-0.68	.014236399	2.637521	Predicted gene 1976 (Gm1976)
Ttyh1	-0.68	$4.13 \times 10^{-6}$	8.696656	Tweety family member 1 (Ttyh1)
Lix1l	-0.68	.00091824	4.927738	Lix1-like (Lix1l)
Tmem39a	-0.68	.006533561	3.336655	Transmembrane protein 39a (Tmem39a)
Anxa5	-0.68	.001119261	5.575959	Annexin A5 (Anxa5)
Dgcr6	-0.68	.001246157	3.791271	DiGeorge syndrome critical region gene 6 (Dgcr6)
Slc4a2	-0.68	.000513786	4.040131	Solute carrier family 4 (anion exchanger), member 2 (Slc4a2)
Nudt1	-0.68	.039631738	1.841279	Nudix (nucleoside diphosphate linked moiety X)-type motif 1 (Nudt1)
Tmem232	-0.68	.012241839	2.697146	Transmembrane protein 232 (Tmem232)
Ccpg1os	-0.68	.003899723	3.293575	Cell cycle progression 1, opposite strand (Ccpg1os)
Itgb1	-0.68	.000240911	5.494356	Integrin beta 1 (fibronectin receptor beta) (Itgb1)
Ptbp1	-0.68	.0001962	4.54997	Polypyrimidine tract binding protein 1 (Ptbp1)
Ccdc88c	-0.69	.005480721	3.612535	Coiled-coil domain containing 88C (Ccdc88c)
Fadd	-0.69	.026789876	2.190976	Fas (TNFRSF6)-associated via death domain (Fadd)
Akr1b10	-0.69	.000825749	3.429434	aldo-keto reductase family 1, member B10 (aldose reductase) (Akr1b10)
Bola3	-0.69	.016566769	2.510886	bolaA-like 3 ( <i>E. coli</i> ) (Bola3)
Mri1	-0.69	.009075324	2.442271	Methylthioribose-1-phosphate isomerase 1 (Mri1)
Pts	-0.69	.000119713	5.000387	6-Pyruvoyl-tetrahydropterin synthase (Pts)
2010320M18Rik	-0.69	.017646208	2.039388	RIKEN cDNA 2010320M18 gene (2010320M18Rik)
2310011J03Rik	-0.69	.004330184	3.172291	RIKEN cDNA 2310011J03 gene (2310011J03Rik)
Gpm6b	-0.69	.000127369	8.864788	Glycoprotein m6b (Gpm6b)
Zkscan3	-0.69	.007410085	3.569379	Zinc finger with KRAB and SCAN domains 3 (Zkscan3)
Echdc1	-0.69	.035913115	1.626138	Enoyl Coenzyme A hydratase domain containing 1 (Echdc1)
Helq	-0.69	.018672717	2.427183	Helicase, POLQ-like (Helq)
Sox1ot	-0.69	.000353493	4.772023	SOX1 Overlapping Transcript (Sox1ot)
Susd5	-0.69	.016801987	2.902972	Sushi domain containing 5 (Susd5)
Dnaaf5	-0.69	.012583825	3.203969	Dynein, axonemal assembly factor 5 (Dnaaf5)
Ndufa2	-0.69	.004637548	5.281471	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (Ndufa2)
Mrpl52	-0.69	.001177158	4.191429	Mitochondrial ribosomal protein L52 (Mrpl52)
Pls1	-0.69	.005067183	3.651407	Plastin 1 (I-isoform) (Pls1)
Cystm1	-0.69	.000742407	3.757867	Cysteine-rich transmembrane module containing 1 (Cystm1)
Commd10	-0.69	.008678584	3.445984	COMM domain containing 10 (Commd10)
Zfp703	-0.69	.008458822	2.840441	Zinc finger protein 703 (Zfp703)
Spop	-0.69	$3.14 \times 10^{-5}$	8.405848	Speckle-type POZ protein (Spop)
Nfam1	-0.70	.013209915	4.778527	Nfat activating molecule with ITAM motif 1 (Nfam1)
Rreb1	-0.70	.000371674	5.42952	Ras responsive element binding protein 1 (Rreb1)
Pkig	-0.70	.004593673	2.82839	Protein kinase inhibitor, gamma (Pkig)
Rps6	-0.70	.044704187	1.109345	Ribosomal protein S6 (Rps6)
Itm2c	-0.70	$6.00 \times 10^{-6}$	7.903863	Integral membrane protein 2C (Itm2c)
Hacd2	-0.70	$4.12 \times 10^{-5}$	5.504852	3-Hydroxyacyl-CoA dehydratase 2 (Hacd2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tsc22d3	-0.70	.00101211	4.957683	TSC22 domain family, member 3 (Tsc22d3)
Ptma	-0.70	.003125493	3.293406	Prothymosin alpha (Ptma)
Pum3	-0.70	.001533596	4.586104	Pumilio RNA-binding family member 3 (Pum3)
Crocc	-0.70	.019870615	2.150926	Ciliary rootlet coiled-coil, rootletin (Crocc)
Mrps21	-0.70	.000678875	4.456485	Mitochondrial ribosomal protein S21 (Mrps21)
Tmem38b	-0.70	.013158873	2.782299	Transmembrane protein 38B (Tmem38b)
Tyro3	-0.70	.000256536	3.947445	TYRO3 protein tyrosine kinase 3 (Tyro3)
Snrpg	-0.70	.005532843	3.323614	Small nuclear ribonucleoprotein polypeptide G (Snrpg)
Itgav	-0.70	.000115082	5.833847	Integrin alpha V (Itgav)
H3f3a	-0.70	.00017438	4.244121	H3 histone, family 3A (H3f3a)
Pqlc2	-0.70	.02307615	2.403743	PQ loop repeat containing 2 (Pqlc2)
Ttc39aos1	-0.70	.005292505	3.666678	Ttc39a opposite strand RNA 1 (Ttc39aos1)
Rad9b	-0.70	.040901862	1.684189	RAD9 checkpoint clamp component B (Rad9b)
Selenok	-0.71	.000464785	5.925493	Selenoprotein K (Selenok)
Lsm6	-0.71	$6.24 \times 10^{-5}$	5.204966	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated (Lsm6)
S100a11	-0.71	.045483238	1.481447	S100 calcium binding protein A11 (S100a11)
Fmn13	-0.71	.005394472	2.936182	Formin-like 3 (Fmn13)
Gab1	-0.71	.000623531	6.031924	Growth factor receptor bound protein 2-associated protein 1 (Gab1)
Ndufb9	-0.71	.000111734	5.914792	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (Ndufb9)
Fam107b	-0.71	.008016303	3.864478	Family with sequence similarity 107, member B (Fam107b)
Coq8b	-0.71	.031118406	1.82094	Coenzyme Q8B (Coq8b)
Zdhhc4	-0.71	.00068304	3.762525	Zinc finger, DHHC domain containing 4 (Zdhhc4)
Apbb1ip	-0.71	.014794905	2.159698	Amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (Apbb1ip)
Tmem134	-0.71	.00158207	3.188746	Transmembrane protein 134 (Tmem134)
Aamdc	-0.71	.000311646	3.594922	Adipogenesis-associated Mth938 domain containing (Aamdc)
Mir670hg	-0.71	.031688737	1.484986	MIR670 host gene (non-protein coding) (Mir670hg)
Nsmce1	-0.71	.017677103	2.709915	NSE1 homolog, SMC5-SMC6 complex component (Nsmce1)
Pfdn5	-0.71	$2.05 \times 10^{-5}$	7.099518	Prefoldin 5 (Pfdn5)
Elovl2	-0.71	.001863981	4.434404	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (Elovl2)
P3h4	-0.71	.004922131	3.401554	Prolyl 3-hydroxylase family member 4 (non-enzymatic) (P3h4)
Thap3	-0.71	.006032777	2.90214	THAP domain containing, apoptosis-associated protein 3 (Thap3)
Cox6c	-0.71	.00040773	6.063557	Cytochrome c oxidase subunit VIc (Cox6c)
Usp40	-0.71	.001119261	4.185605	Ubiquitin-specific peptidase 40 (Usp40)
Elovl5	-0.71	$7.75 \times 10^{-6}$	6.674783	ELOVL family member 5, elongation of long chain fatty acids (yeast) (Elovl5)
Tomm7	-0.71	.002559336	4.401669	Translocase of outer mitochondrial membrane 7 homolog (yeast) (Tomm7)
Ctbs	-0.71	.001511183	3.238649	Chitobiase, di-N-acetyl- (Ctbs)
Zfp488	-0.71	.012811148	2.955644	Zinc finger protein 488 (Zfp488)
Zswim7	-0.71	.03051504	1.961373	Zinc finger SWIM-type containing 7 (Zswim7)
Tprkb	-0.72	$3.22 \times 10^{-5}$	6.654363	Tp53rk binding protein (Tprkb)
Rps16-ps2	-0.72	.038877403	1.495869	Ribosomal protein S16, pseudogene 2 (Rps16-ps2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Naaa	-0.72	.002516188	3.484266	N-acylethanolamine acid amidase (Naaa)
Abca8b	-0.72	.027804757	2.559968	ATP-binding cassette, sub-family A (ABC1), member 8b (Abca8b)
Arhgef1	-0.72	.001327334	3.638156	Rho guanine nucleotide exchange factor (GEF) 1 (Arhgef1)
Shank3	-0.72	$5.89 \times 10^{-5}$	7.002377	SH3/ankyrin domain gene 3 (Shank3)
Sirt2	-0.72	$6.14 \times 10^{-6}$	7.504511	Sirtuin 2 (Sirt2)
Cep152	-0.72	.049687686	1.136366	Centrosomal protein 152 (Cep152)
Actl6a	-0.72	.045645557	1.627291	Actin-like 6A (Actl6a)
Slc7a2	-0.72	.00091401	4.507206	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (Slc7a2)
Nwd2	-0.72	.027783112	8.134979	NACHT and WD repeat domain containing 2 (Nwd2)
Ccdc190	-0.72	.012360533	2.304146	Coiled-coil domain containing 190 (Ccdc190)
Ebp	-0.72	.004872538	2.793891	Phenylalkylamine Ca2+ antagonist (emopamil) binding protein (Ebp)
Rpl18a	-0.72	$1.82 \times 10^{-6}$	6.885522	Ribosomal protein L18A (Rpl18a)
Smim1	-0.72	.022261006	1.740654	Small integral membrane protein 1 (Smim1)
Ptch1	-0.72	.000111085	7.990192	Patched 1 (Ptch1)
Gna12	-0.72	.001573558	5.741384	Guanine nucleotide binding protein, alpha 12 (Gna12)
Atp5e	-0.72	.002539964	6.076804	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e)
Rian	-0.72	.000565417	7.549145	RNA imprinted and accumulated in nucleus (Rian)
Myo1d	-0.72	.002783266	4.026959	Myosin ID (Myo1d)
Fam229b	-0.73	.001669081	3.229115	Family with sequence similarity 229, member B (Fam229b)
4930570G19Rik	-0.73	.005721739	2.968658	RIKEN cDNA 4930570G19 gene (4930570G19Rik)
Esy1	-0.73	.036722293	2.175348	Extended synaptotagmin-like protein 1 (Esy1)
St5	-0.73	.002261836	4.469716	Suppression of tumorigenicity 5 (St5)
Il17rd	-0.73	.003019827	3.121452	Interleukin 17 receptor D (Il17rd)
Map3k19	-0.73	.022210779	3.079196	Mitogen-activated protein kinase kinase kinase 19 (Map3k19)
Kctd12b	-0.73	.037964848	4.245385	Potassium channel tetramerisation domain containing 12b (Kctd12b)
Dnm2	-0.73	.000171211	4.595825	Dynamin 2 (Dnm2)
Cftr	-0.73	.035891523	2.585149	Cystic fibrosis transmembrane conductance regulator (Cftr)
Hemk1	-0.73	.005660147	2.474465	HemK methyltransferase family member 1 (Hemk1)
2010107E04Rik	-0.73	.001053757	6.258876	RIKEN cDNA 2010107E04 gene (2010107E04Rik)
Abcg2	-0.73	.001207838	3.145087	ATP-binding cassette, sub-family G (WHITE), member 2 (Abcg2)
Podxl	-0.73	.002302996	3.454779	Podocalyxin-like (Podxl)
Pax6	-0.73	.025595829	2.689857	Paired box 6 (Pax6)
Fam213b	-0.73	.000573279	4.798306	Family with sequence similarity 213, member B (Fam213b)
Rpl21	-0.73	$2.93 \times 10^{-6}$	6.467392	Ribosomal protein L21 (Rpl21)
Ndufaf2	-0.73	.001967122	3.280904	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2 (Ndufaf2)
Hpgds	-0.73	.025015837	2.021919	Hematopoietic prostaglandin D synthase (Hpgds)
Arhgap18	-0.73	.001154156	3.403752	Rho GTPase activating protein 18 (Arhgap18)
Gpr37	-0.73	.000343901	5.703181	G protein-coupled receptor 37 (Gpr37)
Gal3st1	-0.73	.007688337	2.195836	Galactose-3-O-sulfotransferase 1 (Gal3st1)
Pcbd2	-0.73	.012896208	2.323069	Pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2 (Pcbd2)
Phf21b	-0.73	.019049477	2.253954	PHD finger protein 21B (Phf21b)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Bet1	-0.73	.00269514	3.74725	Bet1 golgi vesicular membrane trafficking protein (Bet1)
Garem2	-0.74	.003693994	3.697976	GRB2-associated regulator of MAPK1 subtype 2 (Garem2)
Ccdc96	-0.74	.00738221	2.817301	Coiled-coil domain containing 96 (Ccdc96)
Bmf	-0.74	.043236941	1.924173	BCL2 modifying factor (Bmf)
Gm9385	-0.74	.019351633	1.825544	Predicted pseudogene 9385 (Gm9385)
Gm43843	-0.74	.02947797	1.945163	Predicted gene (Gm9385)
Drc3	-0.74	.001849439	3.17162	Dynein Regulatory Complex Subunit 3 (Drc3)
1300002E11Rik	-0.74	.002502714	3.636221	RIKEN cDNA 1300002E11 gene (1300002E11Rik)
A230057D06Rik	-0.74	.040035138	2.127123	RIKEN cDNA A230057D06 gene (A230057D06Rik)
Sarnp	-0.74	.001803852	3.005652	SAP domain containing ribonucleoprotein (Sarnp)
Sft2d1	-0.74	.006551052	2.667601	SFT2 domain containing 1 (Sft2d1)
Trnau1ap	-0.74	.025860482	2.436853	tRNA selenocysteine 1-associated protein 1 (Trnau1ap)
Haus1	-0.74	.002061146	3.471392	HAUS augmin-like complex, subunit 1 (Haus1)
Trp53bp2	-0.74	$7.59 \times 10^{-5}$	5.636781	Transformation-related protein 53 binding protein 2 (Trp53bp2)
Cfp44	-0.74	.004100844	3.34182	Cilia and flagella-associated protein 44 (Cfp44)
Enho	-0.74	.001514895	4.922877	Energy homeostasis associated (Enho)
Pou3f3	-0.74	.007892013	4.81611	POU domain, class 3, transcription factor 3 (Pou3f3)
Rnft1	-0.74	.0043798	3.259997	Ring finger protein, transmembrane 1 (Rnft1)
Fam160b2	-0.74	.000699718	3.779263	Family with sequence similarity 160, member B2 (Fam160b2)
Sostdc1	-0.74	.041158603	3.352082	Sclerostin domain containing 1 (Sostdc1)
Gm2000	-0.75	.038801677	1.011046	Ribosomal protein L35 pseudogene (Gm2000)
Plin2	-0.75	.008099173	2.894854	Perilipin 2 (Plin2)
Pfkfb4	-0.75	.0273616	1.605476	6-Phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4)
Gm15417	-0.75	.014155293	2.080683	Predicted gene 15417 (Gm15417)
Entpd1	-0.75	.003319018	3.579577	Ectonucleoside triphosphate diphosphohydrolase 1 (Entpd1)
Rps3	-0.75	$1.68 \times 10^{-5}$	6.857745	Ribosomal protein S3 (Rps3)
Bok	-0.75	.000201806	5.339799	BCL2-related ovarian killer (Bok)
Qtrt2	-0.75	.031707255	2.436997	Queuine tRNA-Ribosyltransferase Accessory Subunit 2 (Qtrt2)
Rab13	-0.75	.00933314	2.028074	RAB13, member RAS oncogene family (Rab13)
Itga6	-0.75	.000984101	4.856695	Integrin alpha 6 (Itga6)
Ccdc74a	-0.75	.001724166	3.396714	Coiled-coil domain containing 74A (Ccdc74a)
Ikzf1	-0.75	.032655229	2.661964	IKAROS family zinc finger 1 (Ikzf1)
Cables1	-0.75	.000231785	4.437089	CDK5 and Abl enzyme substrate 1 (Cables1)
Cecr6	-0.75	.045702512	2.321249	Cat eye syndrome chromosome region, candidate 6 (Cecr6)
Hacd1	-0.75	.011616227	1.952287	3-Hydroxyacyl-CoA dehydratase 1 (Hacd1)
Asb2	-0.75	.019800604	2.797241	Ankyrin repeat and SOCS box-containing 2 (Azb2)
Dnah12	-0.75	.011575722	2.917351	Dynein, axonemal, heavy chain 12 (Dnah12)
Spata18	-0.75	.011439076	2.799041	Spermatogenesis associated 18 (Spata18)
Rps13	-0.75	.000171227	5.204694	Ribosomal protein S13 (Rps13)
Tmem178	-0.75	.006218273	2.564378	Transmembrane protein 178 (Tmem178)
Magt1	-0.75	.003249929	4.835108	Magnesium transporter 1 (Magt1)
Taf13	-0.75	$3.22 \times 10^{-5}$	5.571771	TATA-box binding protein-associated factor 13 (Taf13)
Ephb1	-0.75	.009031661	4.405649	Eph receptor B1 (Ephb1)
Myo9b	-0.75	.000815215	3.964934	Myosin IXb (Myo9b)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Sec14l5	-0.75	.036791623	2.81168	SEC14-like lipid binding 5 (Sec14l5)
Ttc34	-0.75	.046870412	1.341178	Tetratricopeptide repeat domain 34 (Ttc34)
Rpl31-ps8	-0.76	.016067384	1.835762	Ribosomal protein L31, pseudogene 8 (Rpl31-ps8)
Rps19	-0.76	$3.14 \times 10^{-5}$	4.721972	Ribosomal protein S19 (Rps19)
Rfx1	-0.76	.012360533	2.876197	Regulatory factor X, 1 (influences HLA class II expression) (Rfx1)
Rps9	-0.76	$1.84 \times 10^{-5}$	6.347229	Ribosomal protein S9 (Rps9)
Ccdc171	-0.76	.041366209	2.385024	Coiled-coil domain containing 171 (Ccdc171)
Snapc5	-0.76	.000749397	3.585373	Small nuclear RNA activating complex, polypeptide 5 (Snapc5)
Heatr5a	-0.76	.000801375	3.922107	HEAT repeat containing 5A (Heatr5a)
Col4a1	-0.76	.006340613	2.628715	Collagen, type IV, alpha 1 (Col4a1)
Drap1	-0.76	$4.26 \times 10^{-5}$	4.995156	Dr1-associated protein 1 (negative cofactor 2 alpha) (Drap1)
1500015A07Rik	-0.76	.019527927	2.026303	RIKEN cDNA 1500015A07 gene (1500015A07Rik)
Sstr2	-0.76	.013209915	4.011479	Somatostatin receptor 2 (Sstr2)
Elf1	-0.76	.007401504	2.934874	E74-like factor 1 (Elf1)
Prex2	-0.76	.000266989	6.795311	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 (Prex2)
Zc3hav1	-0.76	.017464486	3.50779	Zinc finger CCCH type, antiviral 1 (Zc3hav1)
Selenoh	-0.76	.000329398	3.880633	Selenoprotein H (Selenoh)
Fmo1	-0.76	.014738407	2.841318	Flavin containing monooxygenase 1 (Fmo1)
Dnajc1	-0.76	.001036855	3.99184	DnaJ heat shock protein family (Hsp40) member C1 (Dnajc1)
Plgrkt	-0.76	.000958584	3.325198	Plasminogen receptor, C-terminal lysine transmembrane protein (Plgrkt)
Sash1	-0.76	$1.67 \times 10^{-5}$	6.883325	SAM and SH3 domain containing 1 (Sash1)
Laptm4b	-0.76	$3.83 \times 10^{-5}$	4.941842	Lysosomal-associated protein transmembrane 4B (Laptm4b)
Rpl35	-0.76	.001169567	4.276143	Ribosomal protein L35 (Rpl35)
Syt6	-0.76	.03919844	7.26392	Synaptotagmin VI (Syt6)
Eef2kmt	-0.76	.031172433	1.929338	Eukaryotic elongation factor 2 lysine methyltransferase (Eef2kmt)
Ginm1	-0.76	.000184611	4.567676	Glycoprotein integral membrane 1 (Ginm1)
Numa1	-0.76	$1.21 \times 10^{-5}$	5.255655	Nuclear mitotic apparatus protein 1 (Numa1)
Grin2c	-0.76	.000879683	3.107485	Glutamate receptor, ionotropic, NMDA2C (epsilon 3) (Grin2c)
Grcc10	-0.76	.010387319	2.261392	Gene-rich cluster, C10 gene (Grcc10)
Sox2ot	-0.76	.000374036	5.455071	SOX2 overlapping transcript (non-protein coding) (Sox2ot)
Acaa1a	-0.76	.000266989	3.563541	Acetyl-Coenzyme A acyltransferase 1A (Acaa1a)
Rpl13	-0.76	$5.43 \times 10^{-5}$	5.208199	Ribosomal protein L13 (Rpl13)
Abcd4	-0.77	.009569385	2.292422	ATP-binding cassette, sub-family D (ALD), member 4 (Abcd4)
Rell1	-0.77	.000855313	3.451694	RELT-like 1 (Rell1)
St18	-0.77	.001624083	3.602387	Suppression of tumorigenicity 18 (St18)
Tmed1	-0.77	.012079109	2.718479	Transmembrane p24 trafficking protein 1 (Tmed1)
Bnip2	-0.77	.000262604	4.650029	BCL2/adenovirus E1B interacting protein 2 (Bnip2)
Gm32699	-0.77	.026440925	1.572241	Predicted gene, 32699 (Gm32699)
Tprn	-0.77	.001606425	3.370969	Taperin (Tprn)
Rab31	-0.77	$4.21 \times 10^{-5}$	6.125961	RAB31, member RAS oncogene family (Rab31)
Wnt7b	-0.77	.007698901	2.977884	Wingless-type MMTV integration site family, member 7B (Wnt7b)
Pola1	-0.77	.046345738	2.203394	Polymerase (DNA directed), alpha 1 (Pola1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Mccc1	-0.77	.002861667	3.02085	Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (Mccc1)
Rps10	-0.77	.000172234	5.520483	Ribosomal protein S10 (Rps10)
Nphp3	-0.77	.011439076	1.923862	Nephronophthisis 3 (adolescent) (Nphp3)
Slc22a4	-0.77	.004103231	2.69211	Solute carrier family 22 (organic cation transporter), member 4 (Slc22a4)
Antxr1	-0.77	.000474338	4.553788	Anthrax toxin receptor 1 (Antxr1)
Ngf	-0.77	.036714265	1.07354	Nerve growth factor (Ngf)
Mid1ip1	-0.77	4.20 × 10 <sup>-5</sup>	5.857974	Mid1 interacting protein 1 (gastrulation-specific G12-like (zebrafish)) (Mid1ip1)
9530059O14Rik	-0.78	.043149729	1.629187	RIKEN cDNA 9530059O14 gene (9530059O14Rik)
Adam17	-0.78	.002514103	3.977304	A disintegrin and metallopeptidase domain 17 (Adam17)
3110035E14Rik	-0.78	.001548895	3.369268	RIKEN cDNA 3110035E14 gene (3110035E14Rik)
Ubxn1	-0.78	.000245498	4.723982	UBX domain protein 1 (Ubxn1)
Fam96b	-0.78	.000378492	4.421252	Family with sequence similarity 96, member B (Fam96b)
Cdk5rap2	-0.78	.002405035	4.351515	CDK5 regulatory subunit-associated protein 2 (Cdk5rap2)
Sppl2b	-0.78	.006704587	2.843513	Signal peptide peptidase like 2B (Sppl2b)
Uimc1	-0.78	.001245615	3.380125	Ubiquitin interaction motif containing 1 (Uimc1)
Cox17	-0.78	.017924356	2.285259	Cytochrome c oxidase assembly protein 17 (Cox17)
Snhg18	-0.78	.035969357	1.730083	Small nucleolar RNA host gene 18 (Snhg18)
B4galt1	-0.78	.015710461	2.461907	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 (B4galt1)
Zfp691	-0.78	.006225374	2.179373	Zinc finger protein 691 (Zfp691)
Cenpx	-0.78	.001565671	2.711687	Centromere Protein X (Cenpx)
Efcab10	-0.78	.017169007	2.644979	EF-hand calcium binding domain 10 (Efcab10)
2610203C20Rik	-0.78	.006665097	3.283851	RIKEN cDNA 2610203C20Rik gene (2610203C20Rik)
Irf3	-0.78	.002062208	2.765632	Interferon regulatory factor 3 (Irf3)
Lipe	-0.78	.007300472	2.210418	Lipase, hormone sensitive (Lipe)
Rps4x	-0.78	4.16 × 10 <sup>-6</sup>	7.647839	Ribosomal protein S4, X-linked (Rps4x)
Jtb	-0.78	.000280269	3.932704	Jumping translocation breakpoint (Jtb)
Ccdc187	-0.78	.029741268	2.703059	Coiled-coil domain containing 187 (Ccdc187)
Adgrf5	-0.78	.001744018	4.669262	Adhesion G protein-coupled receptor F5 (Adgrf5)
Col9a2	-0.79	.049688389	0.661908	Collagen, type IX, alpha 2 (Col9a2)
2310015A10Rik	-0.79	.001365476	2.908139	RIKEN cDNA 2310015A10 gene (2310015A10Rik)
Mknk1	-0.79	.001088356	2.950945	MAP kinase-interacting serine/threonine kinase 1 (Mknk1)
Fmc1	-0.79	.000362864	4.425565	Formation of mitochondrial complex V assembly factor 1 (Fmc1)
3632451O06Rik	-0.79	.001113333	5.910194	RIKEN cDNA 3632451O06 gene (3632451O06Rik)
Rps17	-0.79	4.37 × 10 <sup>-5</sup>	5.763021	Ribosomal protein S17 (Rps17)
Zcrb1	-0.79	5.26 × 10 <sup>-5</sup>	5.202176	Zinc finger CCHC-type and RNA binding motif 1 (Zcrb1)
S1pr3	-0.79	.010098291	2.641788	Sphingosine-1-phosphate receptor 3 (S1pr3)
Gar1	-0.79	.001244955	2.981348	GAR1 ribonucleoprotein (Gar1)
Snrpe	-0.79	.004181674	3.658523	Small nuclear ribonucleoprotein E (Snrpe)
Stx4a	-0.79	1.77 × 10 <sup>-5</sup>	5.940899	Syntaxin 4A (placental) (Stx4a)
Cox6b2	-0.79	.024206628	1.52685	Cytochrome c oxidase subunit VIb polypeptide 2 (Cox6b2)
Marveld1	-0.79	.005002434	2.150035	MARVEL (membrane-associating) domain containing 1 (Marveld1)
Dchs1	-0.79	.000535846	3.976417	Dachsous 1 (Dchs1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ccdc57	-0.79	.042781575	1.50558	Coiled-coil domain containing 57 (Ccdc57)
Cyp7b1	-0.79	.001189468	3.079682	Cytochrome P450, family 7, subfamily b, polypeptide 1 (Cyp7b1)
Smim4	-0.79	.007688337	2.307316	Small integral membrane protein 4 (Smim4)
Ptprb	-0.79	.00012349	4.950459	Protein tyrosine phosphatase, receptor type, B (Ptprb)
6230400D17Rik	-0.79	.019405595	1.94552	RIKEN cDNA 6230400D17 gene (6230400D17Rik)
Golga7	-0.79	$3.25 \times 10^{-5}$	6.529813	Golgi autoantigen, golgin subfamily a, 7 (Golga7)
Sgk3	-0.79	.00429636	3.084093	Serum/glucocorticoid-regulated kinase 3 (Sgk3)
Aldh7a1	-0.79	$6.08 \times 10^{-5}$	5.000689	Aldehyde dehydrogenase family 7, member A1 (Aldh7a1)
Tnfrsf19	-0.80	.000546262	4.820842	Tumor necrosis factor receptor superfamily, member 19 (Tnfrsf19)
Vcan	-0.80	.003614196	4.294649	Versican (Vcan)
Mmgt2	-0.80	.000777717	3.032753	Membrane magnesium transporter 2 (Mmgt2)
Slco2a1	-0.80	.02947797	1.982608	Solute carrier organic anion transporter family, member 2a1 (Slco2a1)
Ccdc173	-0.80	.033047577	1.217093	Coiled-coil domain containing 173 (Ccdc173)
Abhd14b	-0.80	.026201164	2.369062	Abhydrolase domain containing 14b (Abhd14b)
Edem2	-0.80	.003672551	2.465962	ER degradation enhancer, mannosidase alpha-like 2 (Edem2)
Scn4b	-0.80	.001559853	3.00474	Sodium channel, type IV, beta (Scn4b)
Slc25a1	-0.80	.000136976	4.282414	Solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1 (Slc25a1)
1110038B12Rik	-0.80	.003003186	2.749611	RIKEN cDNA 1110038B12 gene (1110038B12Rik)
Hint2	-0.80	.003679484	3.749721	Histidine triad nucleotide binding protein 2 (Hint2)
Akain1	-0.80	.014040644	3.484438	A kinase (PRKA) anchor inhibitor 1 (Akain1)
1700008J07Rik	-0.80	.021044519	2.082983	RIKEN cDNA 1700008J07 gene (1700008J07Rik)
Nadsyn1	-0.80	.023523029	1.379723	NAD synthetase 1 (Nadsyn1)
Lrp5	-0.80	.004602407	2.702982	Low-density lipoprotein receptor-related protein 5 (Lrp5)
Wbp1	-0.80	$5.27 \times 10^{-5}$	5.084007	WW domain binding protein 1 (Wbp1)
Rplp2	-0.80	$8.21 \times 10^{-5}$	6.624557	Ribosomal protein, large P2 (Rplp2)
Pigyl	-0.80	.002588355	3.758849	Phosphatidylinositol glycan anchor biosynthesis, class Y-like (Pigyl)
Rpp25l	-0.80	.003224801	3.158995	Ribonuclease P/MRP 25 subunit-like (Rpp25l)
Osmr	-0.80	.024206628	2.196056	Oncostatin M receptor (Osmr)
Rps2	-0.80	.000122038	5.336532	Ribosomal protein S2 (Rps2)
Slc4a4	-0.80	$4.97 \times 10^{-5}$	8.737147	Solute carrier family 4 (anion exchanger), member 4 (Slc4a4)
Tpmt	-0.81	.005924864	2.958091	Thiopurine methyltransferase (Tpmt)
Cotl1	-0.81	.003452337	3.476215	Coactosin-like 1 (Dictyostelium) (Cotl1)
Cd248	-0.81	.046504656	1.019186	CD248 antigen, endosialin (Cd248)
Ackr3	-0.81	.023223447	2.230249	Atypical chemokine receptor 3 (Ackr3)
Tatdn3	-0.81	.000823742	3.487695	TatD DNase domain containing 3 (Tatdn3)
Gpr146	-0.81	.000384483	4.018847	G protein-coupled receptor 146 (Gpr146)
Ogfod3	-0.81	.001769063	2.649005	2-Oxoglutarate and iron-dependent oxygenase domain containing 3 (Ogfod3)
Pld2	-0.81	.009816926	2.573401	Phospholipase D2 (Pld2)
Cacng7	-0.81	$5.88 \times 10^{-5}$	6.738999	Calcium channel, voltage-dependent, gamma subunit 7 (Cacng7)
Plpp3	-0.81	$3.57 \times 10^{-5}$	7.484772	Phospholipid phosphatase 3 (Plpp3)
Cmbl	-0.81	.005465412	3.350448	Carboxymethylenebutenolidase-like (Pseudomonas) (Cmbl)
Adamts4	-0.81	.00448815	4.370519	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4 (Adamts4)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Dnajc25	-0.81	.016446335	1.945793	DnaJ heat shock protein family (Hsp40) member C25 (Dnajc25)
Pttg1	-0.81	$8.21 \times 10^{-5}$	4.558176	Pituitary tumor-transforming gene 1 (Pttg1)
Cyfip1	-0.81	.000113642	5.152916	Cytoplasmic FMR1 interacting protein 1 (Cyfip1)
Rps20	-0.81	$3.00 \times 10^{-5}$	5.894894	Ribosomal protein S20 (Rps20)
Wwtr1	-0.81	.000391252	4.071175	WW domain containing transcription regulator 1 (Wwtr1)
Snrnp70	-0.81	.00040773	4.877771	Small nuclear ribonucleoprotein 70 (U1) (Snrnp70)
Tia1	-0.81	.005284204	4.668968	Cytotoxic granule-associated RNA binding protein 1 (Tia1)
Lgr6	-0.81	$7.17 \times 10^{-5}$	4.305998	Leucine-rich repeat-containing G protein-coupled receptor 6 (Lgr6)
Gm14586	-0.81	.036003893	0.640953	Predicted gene 14586 (Gm14586)
Pxmp4	-0.81	.000353493	4.221599	Peroxisomal membrane protein 4 (Pxmp4)
Mfn1	-0.81	$3.22 \times 10^{-5}$	5.820155	Mitofusin 1 (Mfn1)
Tmem258	-0.81	.002885699	2.9699	Transmembrane protein 258 (Tmem258)
Rab37	-0.81	.000123895	4.435012	RAB37, member RAS oncogene family (Rab37)
Eef1b2	-0.82	$5.78 \times 10^{-6}$	6.648046	Eukaryotic translation elongation factor 1 beta 2 (Eef1b2)
Ttc21a	-0.82	.017335584	1.819283	Tetratricopeptide repeat domain 21A (Ttc21a)
C78859	-0.82	.043347921	2.544428	Expressed sequence C78859 (C78859)
Plod2	-0.82	.011107237	2.861977	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2 (Plod2)
Epas1	-0.82	.000106707	7.64891	Endothelial PAS domain protein 1 (Epas1)
Heyl	-0.82	.001647973	4.102298	Hairy/enhancer-of-split related with YRPW motif-like (Heyl)
Pou3f4	-0.82	.0293272	2.682454	POU domain, class 3, transcription factor 4 (Pou3f4)
Lix1	-0.82	.006932158	4.052236	Limb and CNS expressed 1 (Lix1)
Notch1	-0.82	.000626123	4.190655	Notch 1 (Notch1)
Hbegf	-0.82	.006235333	2.416888	Heparin-binding EGF-like growth factor (Hbegf)
Ost4	-0.82	$7.00 \times 10^{-5}$	3.966531	Oligosaccharyltransferase complex subunit 4 (non-catalytic) (Ost4)
Gm15500	-0.82	.007630386	1.786832	Ribosomal protein L5 pseudogene (Gm15500)
Pmm2	-0.82	.004532551	2.707303	Phosphomannomutase 2 (Pmm2)
Kctd5	-0.82	.00105832	3.145356	Potassium channel tetramerisation domain containing 5 (Kctd5)
Stx2	-0.82	.005052072	2.463495	Syntaxin 2 (Stx2)
Casp6	-0.82	.029866889	1.118286	Caspase 6 (Casp6)
Bmpr1b	-0.82	.0002187	4.907829	Bone morphogenetic protein receptor, type 1B (Bmpr1b)
Rpl9	-0.82	$2.23 \times 10^{-6}$	6.586888	Ribosomal protein L9 (Rpl9)
Reck	-0.82	.002791214	3.059455	Reversion-inducing-cysteine-rich protein with kazal motifs (Reck)
Megf10	-0.82	.001574308	4.96861	Multiple EGF-like-domains 10 (Megf10)
Rps3a1	-0.82	$7.21 \times 10^{-6}$	7.460305	Ribosomal protein S3A1 (Rps3a1)
Oard1	-0.82	.000660544	3.78778	O-acyl-ADP-ribose deacylase 1 (Oard1)
Chchd7	-0.82	.00139219	3.255894	Coiled-coil-helix-coiled-coil-helix domain containing 7 (Chchd7)
Smim8	-0.82	.000518855	2.889099	Small integral membrane protein 8 (Smim8)
Ddo	-0.82	.000699718	4.254757	D-aspartate oxidase (Ddo)
Trim12a	-0.82	.013328605	2.065856	Tripartite motif-containing 12A (Trim12a)
Piezo2	-0.82	.040560227	2.071866	Piezo-type mechanosensitive ion channel component 2 (Piezo2)
Mbd6	-0.82	.000341614	3.445955	Methyl-CpG binding domain protein 6 (Mbd6)
Gpr182	-0.83	.041440401	1.421411	G protein-coupled receptor 182 (Gpr182)
Serinc5	-0.83	.000711556	5.740015	Serine incorporator 5 (Serinc5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Cdc14a	-0.83	.00663037	3.635522	CDC14 cell division cycle 14A (Cdc14a)
Acot11	-0.83	.0007287	4.715474	Acyl-CoA thioesterase 11 (Acot11)
Gstt1	-0.83	.005104163	3.310823	Glutathione S-transferase, theta 1 (Gstt1)
Gm7429	-0.83	.037163002	0.670379	Predicted pseudogene 7429 (Gm7429)
Cetn3	-0.83	$2.10 \times 10^{-5}$	5.319196	Centrin 3 (Cetn3)
Gm11966	-0.83	.049097186	0.660266	Predicted gene (Gm11966)
Nfix	-0.83	.00012102	6.402135	Nuclear factor I/X (Nfix)
Tns1	-0.83	.002496348	4.891983	Tensin 1 (Tns1)
Cstb	-0.83	.000136201	4.969699	Cystatin B (Cstb)
Hmgm1	-0.83	$2.59 \times 10^{-5}$	5.620666	High-mobility group nucleosomal binding domain 1 (Hmgm1)
Rps15	-0.83	$4.23 \times 10^{-6}$	7.671732	Ribosomal protein S15 (Rps15)
Prkd3	-0.83	.001053757	4.492791	Protein kinase D3 (Prkd3)
Sat1	-0.83	$5.64 \times 10^{-5}$	4.606973	Spermidine/spermine N1-acetyl transferase 1 (Sat1)
Ttc30b	-0.83	.003477372	3.001648	Tetratricopeptide repeat domain 30B (Ttc30b)
Pak4	-0.83	.003849133	3.168903	p21 protein (Cdc42/Rac)-activated kinase 4 (Pak4)
Mtarc2	-0.83	.000535846	4.051263	Mitochondrial amidoxime reducing component 2 (Mtarc2)
Ttc12	-0.84	.012444578	2.493621	Tetratricopeptide repeat domain 12 (Ttc12)
Bola2	-0.84	.005492777	3.543962	bolA-like 2 ( <i>E. coli</i> ) (Bola2)
Cdh19	-0.84	.005056229	2.971989	Cadherin 19, type 2 (Cdh19)
Scube1	-0.84	.014300374	7.330372	Signal peptide, CUB domain, EGF-like 1 (Scube1)
Shank1	-0.84	$2.08 \times 10^{-5}$	9.296366	SH3/ankyrin domain gene 1 (Shank1)
Col4a2	-0.84	.001369036	3.249733	Collagen, type IV, alpha 2 (Col4a2)
Laptm4a	-0.84	$9.02 \times 10^{-6}$	6.348179	Lysosomal-associated protein transmembrane 4A (Laptm4a)
Slc12a2	-0.84	$5.90 \times 10^{-5}$	6.00735	Solute carrier family 12, member 2 (Slc12a2)
Rpl36	-0.84	.000187289	5.755248	Ribosomal protein L36 (Rpl36)
Dlec1	-0.84	.025095211	1.121147	Deleted in lung and esophageal cancer 1 (Dlec1)
Ybx3	-0.84	.000481987	4.316367	Y box protein 3 (Ybx3)
Fam96a	-0.84	.000103342	4.56326	Family with sequence similarity 96, member A (Fam96a)
Tcf3	-0.84	.00186405	3.426863	Transcription factor 3 (Tcf3)
Tns2	-0.84	.002062208	2.897174	Tensin 2 (Tns2)
Rpl36a	-0.84	.000515683	3.59509	Ribosomal protein L36A (Rpl36a)
Cenpb	-0.84	.000180848	4.952051	Centromere protein B (Cenpb)
Cox7c	-0.84	.001320437	2.840237	Cytochrome c oxidase subunit VIIc (Cox7c)
Ak2	-0.84	.000125541	3.973568	Adenylate kinase 2 (Ak2)
Ube2cbp	-0.85	.029534889	1.339345	Ubiquitin-conjugating enzyme E2C binding protein (Ube2cbp)
Nelfe	-0.85	.000488423	3.267102	Negative elongation factor complex member E, Rdbp (Nelfe)
Snhg6	-0.85	.034539983	0.788071	Small nucleolar RNA host gene 6 (Snhg6)
Itpr1l1	-0.85	.029829246	1.266547	Inositol 1,4,5-triphosphate receptor interacting protein-like 1 (Itpr1l1)
Rhbdd1	-0.85	.000409208	3.765076	Rhomboid domain containing 1 (Rhbdd1)
Irx2	-0.85	.024777285	4.63275	Iroquois-related homeobox 2 (Irx2)
Sox21	-0.85	.011626798	2.041729	SRY (sex determining region Y)-box 21 (Sox21)
Epb41l2	-0.85	$3.86 \times 10^{-5}$	6.012639	Erythrocyte membrane protein band 4.1 like 2 (Epb41l2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Slc17a7	-0.85	.004311803	6.565319	Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (Slc17a7)
Prrg1	-0.85	.00146253	2.565835	Proline-rich Gla (G-carboxyglutamic acid) 1 (Prrg1)
Acyp1	-0.85	$3.51 \times 10^{-5}$	4.894596	Acylphosphatase 1, erythrocyte (common) type (Acyp1)
Akip1	-0.85	.043222547	0.97787	A kinase (PRKA) interacting protein 1 (Akip1)
Pigz	-0.85	.001453455	3.180712	Phosphatidylinositol glycan anchor biosynthesis, class Z (Pigz)
Ctnna1	-0.85	$7.98 \times 10^{-6}$	5.750588	Catenin (cadherin-associated protein), alpha 1 (Ctnna1)
Ints6l	-0.85	.000974465	3.95998	Integrator complex subunit 6 like (Ints6l)
Saysd1	-0.85	.004496161	2.426683	SAYSVFN motif domain containing 1 (Saysd1)
Lrrc2	-0.85	.04593376	3.035478	Leucine-rich repeat containing 2 (Lrrc2)
Cpe	-0.86	$1.61 \times 10^{-7}$	10.55444	Carboxypeptidase E (Cpe)
Al413582	-0.86	.000441199	3.900899	Expressed sequence Al413582 (Al413582)
Zcchc24	-0.86	$2.06 \times 10^{-5}$	6.520137	Zinc finger, CCHC domain containing 24 (Zcchc24)
Carmil1	-0.86	.000336364	4.884337	Capping protein regulator and myosin 1 linker 1 (Carmil1)
Pecam1	-0.86	.00348391	2.957813	Platelet/endothelial cell adhesion molecule 1 (Pecam1)
Rab29	-0.86	.042915129	1.375417	RAB29, member RAS oncogene family (Rab29)
Fancc	-0.86	.006087716	2.462592	Fanconi anemia, complementation group C (Fancc)
Syf2	-0.86	.000181464	4.881794	SYF2 homolog, RNA splicing factor ( <i>S. cerevisiae</i> ) (Syf2)
Gm19461	-0.86	.031387276	1.001853	Predicted gene, 19461 (Gm19461)
Cth	-0.86	.03868898	1.12676	Cystathionase (cystathione gamma-lyase) (Cth)
Scube3	-0.86	.001674524	4.36148	Signal peptide, CUB domain, EGF-like 3 (Scube3)
Rasgrp3	-0.86	.000391252	4.593859	RAS, guanyl releasing protein 3 (Rasgrp3)
Otx1	-0.86	.002572666	3.452916	Orthodenticle homeobox 1 (Otx1)
Hspg2	-0.86	.007543628	1.826743	Perlecan (heparan sulfate proteoglycan 2) (Hspg2)
Kcnab3	-0.86	.008207798	2.700308	Potassium voltage-gated channel, shaker-related subfamily, beta member 3 (Kcnab3)
Rpl39	-0.86	$7.59 \times 10^{-5}$	5.844992	Ribosomal protein L39 (Rpl39)
Ddit3	-0.86	.000868541	2.693326	DNA-damage inducible transcript 3 (Ddit3)
Ccdc12	-0.86	.004625503	3.565958	Coiled-coil domain containing 12 (Ccdc12)
Atf7	-0.86	$2.45 \times 10^{-5}$	5.657754	Activating transcription factor 7 (Atf7)
Fam193b	-0.86	.000466302	3.814972	Family with sequence similarity 193, member B (Fam193b)
Plce1	-0.86	.001624083	4.95537	Phospholipase C, epsilon 1 (Plce1)
Col15a1	-0.87	.033288695	0.578448	Collagen, type XV, alpha 1 (Col15a1)
Galm	-0.87	.02914928	1.952762	Galactose mutarotase (Galm)
Hdhd5	-0.87	.005853752	2.120375	Haloacid Dehalogenase Like Hydrolase Domain Containing 5 (Hdhd5)
Gm34583	-0.87	.02090924	1.231197	Predicted gene, 34583 (Gm34583)
Dnajc24	-0.87	.001545747	2.945447	DnaJ heat shock protein family (Hsp40) member C24 (Dnajc24)
Tyk2	-0.87	.038699906	2.130587	Tyrosine kinase 2 (Tyk2)
Klh15	-0.87	.000317428	5.282945	Kelch-like 5 (Klh15)
Aldh6a1	-0.87	$7.54 \times 10^{-6}$	5.285687	Aldehyde dehydrogenase family 6, subfamily A1 (Aldh6a1)
Gprc5b	-0.87	$5.27 \times 10^{-5}$	6.473193	G protein-coupled receptor, family C, group 5, member B (Gprc5b)
Ppp1r14b	-0.87	.001407815	2.558379	Protein phosphatase 1, regulatory (inhibitor) subunit 14B (Ppp1r14b)
Matn2	-0.87	.028111721	1.788787	Matrilin 2 (Matn2)
Rpl38-ps2	-0.87	.027510951	0.847332	Ribosomal protein L38, pseudogene 2 (Rpl38-ps2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gm42549	-0.87	.046883031	0.943836	Predicted gene (Gm42549)
Stard8	-0.87	.010410972	2.54415	START domain containing 8 (Stard8)
Sptan1	-0.87	$1.83 \times 10^{-6}$	8.269392	Spectrin alpha, non-erythrocytic 1 (Sptan1)
Gstt2	-0.87	.014642207	1.415209	Glutathione S-transferase, theta 2 (Gstt2)
Leprot	-0.87	$9.20 \times 10^{-5}$	4.174056	Leptin receptor overlapping transcript (Leprot)
Use1	-0.87	$3.37 \times 10^{-5}$	5.027971	Unconventional SNARE in the ER 1 homolog ( <i>S. cerevisiae</i> ) (Use1)
Slc50a1	-0.87	.00243646	3.363631	Solute carrier family 50 (sugar transporter), member 1 (Slc50a1)
Plekhh1	-0.88	.000546007	4.864274	Pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (Plekhh1)
Hspb6	-0.88	.001584324	4.471351	Heat shock protein, alpha-crystallin-related, B6 (Hspb6)
Ppp2r5a	-0.88	$8.71 \times 10^{-5}$	4.894486	Protein phosphatase 2, regulatory subunit B', alpha (Ppp2r5a)
Rps18	-0.88	$1.96 \times 10^{-5}$	5.251159	Ribosomal protein S18 (Rps18)
Spag6	-0.88	.002084127	3.152525	Sperm-associated antigen 6 (Spag6)
Scd1	-0.88	$4.95 \times 10^{-6}$	8.35724	Stearoyl-Coenzyme A desaturase 1 (Scd1)
6030443J06Rik	-0.88	.046883031	0.882499	RIKEN cDNA 6030443J06 gene (6030443J06Rik)
Phka1	-0.88	$1.24 \times 10^{-5}$	4.650416	Phosphorylase kinase alpha 1 (Phka1)
Gm10516	-0.88	.004006469	2.536555	Predicted gene 10516 (Gm10516)
Fbxo4	-0.88	.018358096	1.634842	F-box protein 4 (Fbxo4)
Clic4	-0.88	$1.04 \times 10^{-5}$	6.905322	Chloride intracellular channel 4 (mitochondrial) (Clic4)
Flnb	-0.88	.000275022	4.880671	Filamin, beta (Flnb)
Sp3os	-0.88	.033768276	0.698985	Trans-acting transcription factor 3, opposite strand (Sp3os)
Sdhaf1	-0.88	.015746895	1.400524	Succinate dehydrogenase complex assembly factor 1 (Sdhaf1)
4930523C07Rik	-0.88	.033241896	0.8275	RIKEN cDNA 4930523C07 gene (4930523C07Rik)
Cpsf4	-0.88	.002424083	2.640389	Cleavage and polyadenylation-specific factor 4 (Cpsf4)
Gjc1	-0.88	.004460761	2.882686	Gap junction protein, gamma 1 (Gjc1)
Rilpl2	-0.89	.011225384	2.333193	Rab interacting lysosomal protein-like 2 (Rilpl2)
Pycard	-0.89	.009558675	2.369973	PYD and CARD domain containing (Pycard)
Gm17251	-0.89	.03838928	0.940431	Predicted gene, 17251 (Gm17251)
Arhgap17	-0.89	.000666827	3.325606	Rho GTPase activating protein 17 (Arhgap17)
Dhx16	-0.89	.011863812	3.045479	DEAH (Asp-Glu-Ala-His) box polypeptide 16 (Dhx16)
Ccdc191	-0.89	.004189595	2.283631	Coiled-coil domain containing 191 (Ccdc191)
Wipf1	-0.89	.002686226	3.700005	WAS/WASL interacting protein family, member 1 (Wipf1)
Gamt	-0.89	.006670722	2.273565	Guanydinoacetate methyltransferase (Gamt)
Tlr2	-0.89	.020550025	1.482156	Toll-like receptor 2 (Tlr2)
Cfap221	-0.89	.007104882	1.988202	Cilia and flagella-associated protein 221 (Cfap221)
Arsg	-0.89	.000720589	3.974855	Arylsulfatase G (Arsg)
Gas1	-0.89	.010889392	1.758437	Growth arrest specific 1 (Gas1)
Rps27l	-0.89	.001545653	3.466398	Ribosomal protein S27-like (Rps27l)
Snhg20	-0.89	.017742239	1.495503	Small nucleolar RNA host gene 20 (Snhg20)
Gm3355	-0.89	.048967797	0.349209	Predicted gene 3355 (Gm3355)
Abcc4	-0.89	.007335508	2.474674	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (Abcc4)
Sh3bp2	-0.89	.048098188	0.896831	SH3-domain binding protein 2 (Sh3bp2)
Rps27	-0.89	.000356221	3.553654	Ribosomal protein S27 (Rps27)
D130020L05Rik	-0.89	.008720223	2.009334	RIKEN cDNA D130020L05 gene (D130020L05Rik)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gm10736	-0.89	.000531272	3.450477	Predicted gene 10736 (Gm10736)
Gpr151	-0.89	.002401108	6.869296	G protein-coupled receptor 151 (Gpr151)
Eml3	-0.89	.009622699	2.205678	Echinoderm microtubule-associated protein like 3 (Eml3)
Fam213a	-0.89	$4.23 \times 10^{-7}$	7.969016	Family with sequence similarity 213, member A (Fam213a)
Tsen15	-0.90	.000299452	3.383719	tRNA splicing endonuclease subunit 15 (Tsen15)
Leng1	-0.90	.005328268	2.742513	Leukocyte receptor cluster (LRC) member 1 (Leng1)
Rgs5	-0.90	.000959283	5.920073	Regulator of G-protein signaling 5 (Rgs5)
Fkbp9	-0.90	$2.19 \times 10^{-5}$	4.816369	FK506 binding protein 9 (Fkbp9)
Frmd4b	-0.90	.000246074	3.968158	FERM domain containing 4B (Frmd4b)
Lpar6	-0.90	.015048245	1.600827	Lysophosphatidic acid receptor 6 (Lpar6)
Mtm1	-0.90	.004185043	2.220156	X-linked myotubular myopathy gene 1 (Mtm1)
Rab11fip1	-0.90	.018616322	1.785404	RAB11 family interacting protein 1 (class I) (Rab11fip1)
Slc12a9	-0.90	.000614688	3.261885	Solute carrier family 12 (potassium/chloride transporters), member 9 (Slc12a9)
Hps5	-0.90	.003784621	2.709618	Hermansky-Pudlak syndrome 5 (Hps5)
Rdh12	-0.90	.043249947	1.136116	Retinol dehydrogenase 12 (Rdh12)
Ccdc28b	-0.91	.000699718	2.848931	Coiled coil domain containing 28B (Ccdc28b)
Cdc42ep4	-0.91	.000163613	5.090688	CDC42 effector protein (Rho GTPase binding) 4 (Cdc42ep4)
Ocln	-0.91	.002410333	2.670958	Occludin (Ocln)
Gm42067	-0.91	.004308805	2.204556	Predicted gene, 42067 (Gm42067)
Smpd2	-0.91	.000346704	3.167267	Sphingomyelin phosphodiesterase 2, neutral (Smpd2)
Fis1	-0.91	$4.26 \times 10^{-5}$	5.78885	Fission, mitochondrial 1 (Fis1)
Abca1	-0.91	$5.45 \times 10^{-5}$	5.293057	ATP-binding cassette, sub-family A (ABC1), member 1 (Abca1)
Ctdsp1	-0.91	.000373022	3.668514	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 (Ctdsp1)
Sspn	-0.91	.000661433	3.26683	Sarcospan (Sspn)
Miip	-0.91	.017861809	1.351737	Migration and invasion inhibitory protein (Miip)
Cyp20a1	-0.91	.000224403	3.379148	Cytochrome P450, family 20, subfamily a, polypeptide 1 (Cyp20a1)
Ebf4	-0.91	.008495499	2.327185	Early B cell factor 4 (Ebf4)
Stxbp2	-0.91	.021819153	2.370636	Syntaxin binding protein 2 (Stxbp2)
Vcl	-0.91	.000311074	3.095304	Vinculin (Vcl)
Ccnd3	-0.91	.001298386	3.102406	Cyclin D3 (Ccnd3)
Cntrl	-0.91	.002280926	3.520487	Centriolin (Cntrl)
Colgalt2	-0.91	.009135578	2.953097	Collagen beta (1-O)galactosyltransferase 2 (Colgalt2)
Rpl31	-0.91	.000514043	2.60902	Ribosomal protein L31 (Rpl31)
Rpl34	-0.91	$2.23 \times 10^{-5}$	4.878733	Ribosomal protein L34 (Rpl34)
Dleu2	-0.91	.007135169	1.853385	Deleted in lymphocytic leukemia, 2 (Dleu2)
Il10rb	-0.91	.021264452	1.11441	Interleukin 10 receptor, beta (Il10rb)
Thbs3	-0.91	.017669152	1.163103	Thrombospondin 3 (Thbs3)
Nwd1	-0.91	.000101885	6.529115	NACHT and WD repeat domain containing 1 (Nwd1)
Jag1	-0.91	.030958631	2.197259	Jagged 1 (Jag1)
Mycbpap	-0.91	.017852891	2.283751	MYCBP-associated protein (Mycbpap)
Pgf	-0.92	.011012004	1.551239	Placental growth factor (Pgf)
Kdm1b	-0.92	.002555125	2.43241	Lysine (K)-specific demethylase 1B (Kdm1b)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gpam	-0.92	$7.56 \times 10^{-5}$	4.013024	Glycerol-3-phosphate acyltransferase, mitochondrial (Gpam)
Tldc1	-0.92	.011393152	1.740521	TBC/LysM-associated domain containing 1 (Tldc1)
Ccdc113	-0.92	.006802264	1.880966	Coiled-coil domain containing 113 (Ccdc113)
Ftx	-0.92	.006202262	2.551892	Ftx transcript, Xist regulator (non-protein coding) (Ftx)
Gm16499	-0.92	.015671334	1.612639	Predicted gene 16499 (Gm16499)
Smpd13a	-0.92	$4.45 \times 10^{-5}$	4.298341	Sphingomyelin phosphodiesterase, acid-like 3A (Smpd13a)
Frmpd1	-0.92	.000108867	3.996831	FERM and PDZ domain containing 1 (Frmpd1)
Etfb	-0.92	.011602428	1.685077	Electron transferring flavoprotein, beta polypeptide (Etfb)
Rpl23	-0.92	$3.95 \times 10^{-6}$	6.309536	Ribosomal protein L23 (Rpl23)
Gdpd2	-0.92	.007375649	2.101511	Glycerophosphodiester phosphodiesterase domain containing 2 (Gdpd2)
Tmem238	-0.92	.034857114	0.95475	Transmembrane protein 238 (Tmem238)
Nid1	-0.92	.009183618	3.470011	Nidogen 1 (Nid1)
Gm7854	-0.92	.025157365	0.888233	Predicted gene 7854 (Gm7854)
D7Ert443e	-0.93	.009341476	1.861897	DNA segment, Chr 7, ERATO Doi 443, expressed (D7Ert443e)
Rrbp1	-0.93	$1.40 \times 10^{-6}$	5.589034	Ribosome binding protein 1 (Rrbp1)
H2afv	-0.93	$3.63 \times 10^{-5}$	4.65479	H2A histone family, member V (H2afv)
Tpbgl	-0.93	.008735517	2.947913	Trophoblast glycoprotein-like (Tpbgl)
Fam181b	-0.93	.001500162	2.744614	Family with sequence similarity 181, member B (Fam181b)
Hspb1	-0.93	.013183398	1.73901	Heat shock protein 1 (Hspb1)
Dpm3	-0.93	.000848083	2.943445	Dolichyl-phosphate mannosyltransferase polypeptide 3 (Dpm3)
Tram2	-0.93	.030371322	1.687303	Translocating chain-associating membrane protein 2 (Tram2)
Tmem123	-0.93	.000135734	4.328127	Transmembrane protein 123 (Tmem123)
2900093K20Rik	-0.93	.030360006	0.815139	RIKEN cDNA 2900093K20 gene (2900093K20Rik)
Rgs22	-0.93	.004673112	2.830308	Regulator of G-protein signalling 22 (Rgs22)
Rorc	-0.93	.021240871	1.243383	RAR-related orphan receptor gamma (Rorc)
Rpl13a	-0.93	.000576649	2.933243	Ribosomal protein L13A (Rpl13a)
Rpl30	-0.93	$2.82 \times 10^{-6}$	5.709143	Ribosomal protein L30 (Rpl30)
Nrarp	-0.93	.049434346	0.327919	Notch-regulated ankyrin repeat protein (Nrarp)
Ttc16	-0.93	.040459768	0.512763	Tetratricopeptide repeat domain 16 (Ttc16)
Gm11696	-0.93	.014327052	1.51839	Predicted gene 11696 (Gm11696)
Pbib	-0.93	.00359095	3.401022	Peptidylprolyl isomerase B (Pbib)
Ccdc141	-0.93	.000373628	5.143556	Coiled-coil domain containing 141 (Ccdc141)
Apcdd1	-0.93	.002813298	2.713266	Adenomatosis polyposis coli down-regulated 1 (Apcdd1)
Lca5l	-0.94	.002937886	1.985161	Leber congenital amaurosis 5-like (Lca5l)
Hpgd	-0.94	.011682413	2.23781	Hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd)
Zfp36l2	-0.94	.000382039	3.314321	Zinc finger protein 36, C3H type-like 2 (Zfp36l2)
Lrrc56	-0.94	.010335023	1.537141	Leucine-rich repeat containing 56 (Lrrc56)
Gprc5c	-0.94	.044118023	1.236449	G protein-coupled receptor, family C, group 5, member C (Gprc5c)
Rpl26	-0.94	$1.21 \times 10^{-5}$	6.036162	Ribosomal protein L26 (Rpl26)
Carhsp1	-0.94	$2.57 \times 10^{-5}$	4.973809	Calcium-regulated heat-stable protein 1 (Carhsp1)
Prom2	-0.94	.049631771	0.873394	Prominin 2 (Prom2)
Dock8	-0.94	.007377613	2.290841	Dedicator of cytokinesis 8 (Dock8)
Fam46c	-0.94	.004659662	2.441896	Family with sequence similarity 46, member C (Fam46c)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tacc3	-0.94	.020742982	1.320972	Transforming, acidic coiled-coil containing protein 3 (Tacc3)
Gpld1	-0.94	$1.95 \times 10^{-5}$	4.654528	Glycosylphosphatidylinositol-specific phospholipase D1 (Gpld1)
Igsf11	-0.94	.000136152	5.815958	Immunoglobulin superfamily, member 11 (Igsf11)
Sec11c	-0.94	.000170788	4.856154	SEC11 homolog C, signal peptidase complex subunit (Sec11c)
Srsf9	-0.94	.000732723	3.560618	Serine/arginine-rich splicing factor 9 (Srsf9)
Hmcn1	-0.95	.018996948	1.489871	Hemicentin 1 (Hmcn1)
Kcnip3	-0.95	$6.14 \times 10^{-6}$	7.092064	Kv channel interacting protein 3, calsenilin (Kcnip3)
Nectin2	-0.95	.020457072	2.791576	Nectin cell adhesion molecule 2 (Nectin2)
Bbox1	-0.95	.006987628	3.224529	Butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase) (Bbox1)
Zbbx	-0.95	.015712901	1.141362	Zinc finger, B-box domain containing (Zbbx)
Tmem243	-0.95	.000617691	3.712374	Transmembrane protein 243, mitochondrial (Tmem243)
Slc1a5	-0.95	.047344403	0.075399	Solute carrier family 1 (neutral amino acid transporter), member 5 (Slc1a5)
Gm9843	-0.95	.006131418	1.723602	Predicted gene 9843 (Gm9843)
Rpa3	-0.95	.004956771	2.377453	Replication protein A3 (Rpa3)
Lrrc34	-0.95	.039925457	1.469465	Leucine-rich repeat containing 34 (Lrrc34)
Dnph1	-0.95	.013754677	1.460417	2'-Deoxyribonucleoside 5'-phosphate N-hydrolase 1 (Dnph1)
Apln	-0.95	.00060515	4.238171	Apelin (Apln)
Ndufaf8	-0.95	.000851916	2.598805	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 8 (Ndufaf8)
Nat8f4	-0.95	.000757973	2.762291	N-acetyltransferase 8 (GCN5-related) family member 4 (Nat8f4)
AA465934	-0.95	.016904859	1.070392	Expressed sequence AA465934 (AA465934)
Fzd6	-0.95	.002299405	2.735509	Frizzled class receptor 6 (Fzd6)
Zfp36l1	-0.95	$6.29 \times 10^{-5}$	5.448167	Zinc finger protein 36, C3H type-like 1 (Zfp36l1)
1810059H22Rik	-0.95	.040890765	0.932584	RIKEN cDNA 1810059H22 gene (1810059H22Rik)
Tor3a	-0.95	.001414651	3.323664	Torsin family 3, member A (Tor3a)
Edn3	-0.95	.011512885	1.560349	Endothelin 3 (Edn3)
Acy1	-0.95	.022974663	1.012129	Aminoacylase 1 (Acy1)
Atg4a	-0.95	.011925428	1.574637	Autophagy-related 4A, cysteine peptidase (Atg4a)
Gm37090	-0.96	.039022702	1.896429	Predicted gene (Gm37090)
Galnt10	-0.96	.000448204	3.283323	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (Galnt10)
Gm17597	-0.96	.033779628	0.403378	Predicted gene, 17597 (Gm17597)
Ush1g	-0.96	.023835431	0.791154	Usher syndrome 1G (Ush1g)
Gm45250	-0.96	.001958274	3.182017	Predicted gene (Gm45250)
Gm6145	-0.96	.000472827	3.517427	Predicted gene 6145 (Gm6145)
Dennd2a	-0.96	.002713051	3.883716	DENN/MADD domain containing 2A (Dennd2a)
Trim12c	-0.96	.020742982	1.230752	Tripartite motif-containing 12C (Trim12c)
Ddc	-0.96	.005756481	2.604593	Dopa decarboxylase (Ddc)
Cfh	-0.96	.001055265	3.750533	Complement component factor h (Cfh)
A830036E02Rik	-0.96	.002559986	2.067928	RIKEN cDNA A830036E02 gene (A830036E02Rik)
Itih5	-0.96	$2.03 \times 10^{-5}$	4.875766	Inter-alpha (globulin) inhibitor H5 (Itih5)
Gm9794	-0.96	.006636564	1.667364	Predicted pseudogene 9794 (Gm9794)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Rpl35a	-0.96	$1.60 \times 10^{-6}$	5.466421	Ribosomal protein L35A (Rpl35a)
Pik3cg	-0.96	.041779457	1.7165	Phosphoinositide-3-kinase, catalytic, gamma polypeptide (Pik3cg)
Spag1	-0.96	.003061616	2.993456	Sperm-associated antigen 1 (Spag1)
Ogg1	-0.96	.030681695	1.455673	8-Oxoguanine DNA-glycosylase 1 (Ogg1)
Rhpn2	-0.96	.000971098	2.792279	Rhophilin, Rho GTPase binding protein 2 (Rhpn2)
Gm10762	-0.96	.041657709	1.080895	Predicted gene (Gm10762)
Hif3a	-0.96	.014233758	2.049942	Hypoxia inducible factor 3, alpha subunit (Hif3a)
Golgb1	-0.97	$7.86 \times 10^{-7}$	7.077972	Golgi autoantigen, golgin subfamily b, macrogolgin 1 (Golgb1)
Slc29a3	-0.97	$6.29 \times 10^{-5}$	5.346097	Solute carrier family 29 (nucleoside transporters), member 3 (Slc29a3)
Pgm1	-0.97	.019974478	1.807861	Phosphoglucomutase 1 (Pgm1)
Cdca7l	-0.97	.044463496	1.071982	Cell division cycle-associated 7 like (Cdca7l)
Foxo4	-0.97	.016588753	1.653677	Forkhead box O4 (Foxo4)
Akna	-0.97	.001133361	3.092456	AT-hook transcription factor (Akna)
Ptpn13	-0.97	.000139503	4.199572	Protein tyrosine phosphatase, non-receptor type 13 (Ptpn13)
Ubxn11	-0.97	.001702614	2.717686	UBX domain protein 11 (Ubxn11)
Plekhf2	-0.97	.000299954	2.879884	Pleckstrin homology domain containing, family F (with FYVE domain) member 2 (Plekhf2)
Car4	-0.97	.001689054	3.198022	Carbonic anhydrase 4 (Car4)
Tulp3	-0.97	$4.12 \times 10^{-5}$	3.769663	Tubby-like protein 3 (Tulp3)
Pold4	-0.97	.000296703	3.325193	Polymerase (DNA-directed), delta 4 (Pold4)
Map3k6	-0.97	.013871901	3.325042	Mitogen-activated protein kinase kinase kinase 6 (Map3k6)
Ccl25	-0.97	.007669672	2.260765	Chemokine (C-C motif) ligand 25 (Ccl25)
Cplx1	-0.98	$1.31 \times 10^{-5}$	7.957424	Complexin 1 (Cplx1)
Itpr2	-0.98	.000909931	4.365185	Inositol 1,4,5-triphosphate receptor 2 (Itpr2)
Cd81	-0.98	$6.12 \times 10^{-8}$	8.964185	CD81 antigen (Cd81)
Mks1	-0.98	.017215924	0.899816	Meckel syndrome, type 1 (Mks1)
Sox12	-0.98	.001949677	3.111846	SRY (sex determining region Y)-box 12 (Sox12)
Gm26721	-0.98	.030364024	0.817416	Predicted gene, 26721 (Gm26721)
Ddrgk1	-0.98	$5.45 \times 10^{-5}$	4.389542	DDRGK domain containing 1 (Ddrgk1)
Plekhg2	-0.98	.040668023	1.241028	Pleckstrin homology domain containing, family G (with RhoGef domain) member 2 (Plekhg2)
Gpc5	-0.98	$1.57 \times 10^{-5}$	4.388827	Glycan 5 (Gpc5)
Ccdc103	-0.98	.048683336	0.12984	Coiled-coil domain containing 103 (Ccdc103)
Rpl41	-0.98	$1.41 \times 10^{-5}$	7.607891	Ribosomal protein L41 (Rpl41)
Fzd7	-0.98	.001502261	4.015327	Frizzled class receptor 7 (Fzd7)
Trim56	-0.98	.00126785	3.780847	Tripartite motif-containing 56 (Trim56)
Rpl12	-0.98	$1.10 \times 10^{-5}$	5.298674	Ribosomal protein L12 (Rpl12)
Myo19	-0.98	.017245303	1.644958	Myosin XIX (Myo19)
Lama5	-0.98	.021108805	1.091282	Laminin, alpha 5 (Lama5)
Tesk2	-0.98	.007133786	1.49454	Testis-specific kinase 2 (Tesk2)
Chuk	-0.98	.000188021	4.177061	Conserved helix-loop-helix ubiquitous kinase (Chuk)
Fam189a2	-0.98	.00458852	2.567309	Family with sequence similarity 189, member A2 (Fam189a2)
Tmem44	-0.99	.001294124	2.879033	Transmembrane protein 44 (Tmem44)
Hip1	-0.99	$3.57 \times 10^{-5}$	4.443614	Huntingtin interacting protein 1 (Hip1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Wtip	-0.99	.040246967	0.423633	WT1-interacting protein (Wtip)
Gm29595	-0.99	.039723343	0.655604	Predicted gene 29595 (Gm29595)
Hyal1	-0.99	.037291672	0.554396	Hyaluronoglucosaminidase 1 (Hyal1)
Itga7	-0.99	.018773501	0.99965	Integrin alpha 7 (Itga7)
4932443I19Rik	-0.99	.018226696	1.024815	RIKEN cDNA 4932443I19 gene (4932443I19Rik)
Katna1	-0.99	.000643438	2.635619	Katanin p60 (ATPase-containing) subunit A1 (Katna1)
Tmem150a	-0.99	.009542327	1.629905	Transmembrane protein 150A (Tmem150a)
Cwh43	-0.99	.03455745	0.741204	Cell wall biogenesis 43 C-terminal homolog (Cwh43)
Cubn	-0.99	.007688337	2.388458	Cubilin (intrinsic factor-cobalamin receptor) (Cubn)
Rhbdf1	-0.99	.039986994	0.501294	Rhomboid 5 homolog 1 (Rhbdf1)
Ednrb	-0.99	.000111734	5.853344	Endothelin receptor type B (Ednrb)
Hspb8	-0.99	.000282765	3.232952	Heat shock protein 8 (Hspb8)
Rps15a-ps6	-0.99	.022639486	1.147411	Ribosomal protein S15A, pseudogene 6 (Rps15a-ps6)
Adamts19	-0.99	.032966326	0.315111	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19 (Adamts19)
Nrm	-0.99	.049871193	0.597828	Nurim (nuclear envelope membrane protein) (Nrm)
Gm13111	-0.99	.000785148	2.539682	Predicted gene 13111 (Gm13111)
Lpar1	-0.99	.000785135	4.952834	Lysophosphatidic acid receptor 1 (Lpar1)
Pmp22	-0.99	4.37 × 10 <sup>-5</sup>	5.523078	Peripheral myelin protein 22 (Pmp22)
Phactr4	-0.99	.000212867	4.330217	Phosphatase and actin regulator 4 (Phactr4)
Klf4	-0.99	.008233751	1.425383	Kruppel-like factor 4 (gut) (Klf4)
Ucp3	-0.99	.015279601	1.455499	Uncoupling protein 3 (mitochondrial, proton carrier) (Ucp3)
St6galnac2	-0.99	.026969346	0.831719	ST6(alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 (St6galnac2)
Kcnj10	-1.00	2.49 × 10 <sup>-6</sup>	9.696994	Potassium inwardly-rectifying channel, subfamily J, member 10 (Kcnj10)
Syde1	-1.00	.003935793	3.020643	Synapse defective 1, Rho GTPase, homolog 1 ( <i>C. elegans</i> ) (Syde1)
Chaf1a	-1.00	.040056873	1.141897	Chromatin assembly factor 1, subunit A (p150) (Chaf1a)
Prkcq	-1.00	.016701369	6.078658	Protein kinase C, theta (Prkcq)
Tspan18	-1.00	.007462928	6.202997	Tetraspanin 18 (Tspan18)
Pde11a	-1.00	.025977553	1.224132	Phosphodiesterase 11A (Pde11a)
Kcng4	-1.00	.001235299	5.539409	Potassium voltage-gated channel, subfamily G, member 4 (Kcng4)
Rrp15	-1.00	.020868149	1.509673	Ribosomal RNA processing 15 homolog ( <i>S. cerevisiae</i> ) (Rrp15)
Ss18	-1.00	.000139609	3.793651	Synovial sarcoma translocation, Chromosome 18 (Ss18)
K230010J24Rik	-1.00	.025158345	0.614887	RIKEN cDNA K230010J24 gene (K230010J24Rik)
Vps37b	-1.00	.031541489	0.446809	Vacuolar protein sorting 37B (Vps37b)
Prr18	-1.00	.000153842	4.63153	Proline rich 18 (Prr18)
Gm17396	-1.00	.014605219	3.210163	Predicted gene_17396 (Gm17396)
Trim68	-1.00	.031978552	0.719003	Tripartite motif-containing 68 (Trim68)
Tmod1	-1.00	.002505183	2.789531	Tropomodulin 1 (Tmod1)
Cybrd1	-1.01	.008028386	2.190312	Cytochrome b reductase 1 (Cybrd1)
2310009B15Rik	-1.01	2.67 × 10 <sup>-5</sup>	3.527399	RIKEN cDNA 2310009B15 gene (2310009B15Rik)
Fermt2	-1.01	3.99 × 10 <sup>-6</sup>	5.742724	Fermitin family member 2 (Fermt2)
Eno3	-1.01	.001265523	3.286181	Enolase 3, beta muscle (Eno3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
1110034G24Rik	-1.01	.011323396	1.363119	RIKEN cDNA 1110034G24 gene (1110034G24Rik)
Vwa3a	-1.01	.002302996	2.673957	Von Willebrand factor A domain containing 3A (Vwa3a)
AC174678.1	-1.01	.01937184	1.413821	Novel transcript, antisense to Tm9sf1
Hey2	-1.01	.006794571	1.974444	Hairy/enhancer-of-split related with YRPW motif 2 (Hey2)
P3h3	-1.01	.045645557	0.771302	Prolyl 3-hydroxylase 3 (P3h3)
Prdm5	-1.01	.002093131	1.834587	PR domain containing 5 (Prdm5)
Ezh2	-1.01	.001322749	2.406659	Enhancer of zeste 2 polycomb repressive complex 2 subunit (Ezh2)
Btbd17	-1.01	.016636591	1.86766	BTB (POZ) domain containing 17 (Btbd17)
Morn2	-1.01	.002442363	2.914989	MORN repeat containing 2 (Morn2)
Plod1	-1.01	$5.99 \times 10^{-5}$	3.741833	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 (Plod1)
Dhrs4	-1.01	.000161515	2.875716	Dehydrogenase/reductase (SDR family) member 4 (Dhrs4)
Ppp1r18	-1.01	.006459495	1.83672	Protein phosphatase 1, regulatory subunit 18 (Ppp1r18)
Tesc	-1.01	$7.07 \times 10^{-5}$	4.079589	Tescalcin (Tesc)
Jam3	-1.01	$4.82 \times 10^{-5}$	4.193844	Junction adhesion molecule 3 (Jam3)
Sept4	-1.01	$3.93 \times 10^{-7}$	6.72624	Septin 4 (Sept4)
Sox1	-1.01	.000563108	4.868068	SRY (sex determining region Y)-box 1 (Sox1)
4930481A15Rik	-1.01	.011230492	1.435105	RIKEN cDNA 4930481A15 gene (4930481A15Rik)
Tmem176a	-1.02	$1.25 \times 10^{-5}$	4.751907	Transmembrane protein 176A (Tmem176a)
Rhoj	-1.02	.026691941	1.992444	Ras homolog family member J (Rhoj)
Vav2	-1.02	.015279601	3.956667	Vav 2 oncogene (Vav2)
Ttc32	-1.02	.018106183	1.241441	Tetratricopeptide repeat domain 32 (Ttc32)
Gsta4	-1.02	$1.82 \times 10^{-5}$	4.584553	Glutathione S-transferase, alpha 4 (Gsta4)
Gm2a	-1.02	$2.79 \times 10^{-6}$	6.003268	GM2 ganglioside activator protein (Gm2a)
Snhg12	-1.02	.00013334	4.335032	Small nucleolar RNA host gene 12 (Snhg12)
Ddx59	-1.02	.006128507	2.069652	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59 (Ddx59)
Rpl38	-1.02	$6.26 \times 10^{-5}$	4.87255	Ribosomal protein L38 (Rpl38)
Mapkapk3	-1.02	.00993712	1.812349	Mitogen-activated protein kinase-activated protein kinase 3 (Mapkapk3)
Mtss1l	-1.03	$7.86 \times 10^{-7}$	8.37211	Metastasis suppressor 1-like (Mtss1l)
Plekhhg3	-1.03	.003007248	2.721827	Pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (Plekhhg3)
Mr1	-1.03	$1.74 \times 10^{-5}$	4.043897	Major histocompatibility complex, class I-related (Mr1)
Otx2	-1.03	.000484519	4.454805	Orthodenticle homeobox 2 (Otx2)
Anxa4	-1.03	.010856796	1.744356	Annexin A4 (Anxa4)
Dap	-1.03	.000545422	3.778962	Death-associated protein (Dap)
Mns1	-1.03	.002165084	2.210108	Meiosis-specific nuclear structural protein 1 (Mns1)
Pdpn	-1.03	.00208589	2.586479	Podoplanin (Pdpn)
Gm10073	-1.03	.004260752	1.640832	Ribosomal protein, large, P1 pseudogene (Gm10073)
Rom1	-1.03	.006288902	1.26705	Rod outer segment membrane protein 1 (Rom1)
Prob1	-1.03	.005675655	2.684955	Proline-rich basic protein 1 (Prob1)
Six5	-1.03	.04143023	0.247005	sine oculis-related homeobox 5 (Six5)
Vit	-1.03	.000155643	3.209151	Vitrin (Vit)
Ctnnal1	-1.03	$6.92 \times 10^{-5}$	3.476178	Catenin (cadherin-associated protein), alpha-like 1 (Ctnnal1)
Gm21781	-1.03	.000314173	3.841796	Predicted gene (Gm21781)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Syt15	-1.03	.008005735	4.609842	Synaptotagmin XV (Syt15)
Spata24	-1.03	.004221449	1.612839	Spermatogenesis-associated 24 (Spata24)
Gm10076	-1.03	$8.48 \times 10^{-5}$	4.244379	Ribosomal protein L41 pseudogene (Gm10076)
E230016M11Rik	-1.03	.044048868	0.675591	RIKEN cDNA E230016M11 gene (E230016M11Rik)
Cdc42ep1	-1.03	.000483412	3.568535	CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1)
6330418K02Rik	-1.03	.022896091	0.270596	RIKEN cDNA 6330418K02 gene (6330418K02Rik)
Timm21	-1.03	.000238358	2.855592	Translocase of inner mitochondrial membrane 21 (Timm21)
Catsper2	-1.03	.016029415	1.183808	Cation channel, sperm associated 2 (Catsper2)
Slc2a10	-1.04	.042427394	0.144964	Solute carrier family 2 (facilitated glucose transporter), member 10 (Slc2a10)
Sfxn5	-1.04	$5.06 \times 10^{-8}$	7.359857	Sideroflexin 5 (Sfxn5)
Nfkbie	-1.04	.047008119	0.617041	Nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon (Nfkbie)
1110019D14Rik	-1.04	.029832798	0.915383	RIKEN cDNA 1110019D14 gene (1110019D14Rik)
Cd180	-1.04	.036997623	3.750463	CD180 antigen (Cd180)
Catip	-1.04	.031184791	0.880728	Ciliogenesis-associated TTC17 interacting protein (Catip)
Cfap45	-1.04	.005076222	2.274819	Cilia and flagella-associated protein 45 (Cfap45)
Chrm1	-1.04	.008189079	1.823646	Cholinergic receptor, muscarinic 1, CNS (Chrm1)
Cops9	-1.04	.000213184	4.397896	COP9 Signalosome Subunit 9 (Cops9)
Bmp7	-1.04	.001133361	4.810091	Bone morphogenetic protein 7 (Bmp7)
Gm19196	-1.04	.005137957	1.610969	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, B pseudogene (Gm19196)
Irx1	-1.04	.00856864	3.412898	Iroquois-related homeobox 1 (Irx1)
Glul	-1.04	$3.78 \times 10^{-6}$	9.010339	Glutamate-ammonia ligase (glutamine synthetase) (Glul)
Mpzl1	-1.04	$5.01 \times 10^{-5}$	3.963352	Myelin protein zero-like 1 (Mpzl1)
Sox9	-1.04	$1.74 \times 10^{-5}$	5.498845	SRY (sex determining region Y)-box 9 (Sox9)
Lgi4	-1.04	.003914519	1.875343	Leucine-rich repeat LGI family, member 4 (Lgi4)
Slc6a9	-1.05	$5.64 \times 10^{-6}$	4.649541	Solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (Slc6a9)
Ccdc62	-1.05	.036998497	0.57538	Coiled-coil domain containing 62 (Ccdc62)
Slc2a1	-1.05	$9.66 \times 10^{-7}$	6.024924	Solute carrier family 2 (facilitated glucose transporter), member 1 (Slc2a1)
Asrgl1	-1.05	$9.78 \times 10^{-7}$	7.456191	Asparaginase like 1 (Asrgl1)
Cd302	-1.05	.000247182	2.765785	CD302 antigen (Cd302)
Hist1h2be	-1.05	.00124002	2.551123	Histone cluster 1, H2be (Hist1h2be)
Ttpa	-1.05	.004573104	1.845821	Tocopherol (alpha) transfer protein (Ttpa)
Arhgap31	-1.05	$1.70 \times 10^{-5}$	4.007033	Rho GTPase activating protein 31 (Arhgap31)
Rspo3	-1.05	.000373022	4.188401	R-spondin 3 (Rspo3)
Pou3f1	-1.05	.006601117	2.102268	POU domain, class 3, transcription factor 1 (Pou3f1)
Tspan15	-1.05	$8.19 \times 10^{-5}$	3.667246	Tetraspanin 15 (Tspan15)
Krcc1	-1.05	$4.82 \times 10^{-5}$	3.881183	Lysine-rich coiled-coil 1 (Krcc1)
Fubp3	-1.05	$1.91 \times 10^{-5}$	4.189816	Far upstream element (FUSE) binding protein 3 (Fubp3)
Pi4k2b	-1.05	.042409274	1.144028	Phosphatidylinositol 4-kinase type 2 beta (Pi4k2b)
Dnah3	-1.05	.018234003	1.919365	Dynein, axonemal, heavy chain 3 (Dnah3)
Robo4	-1.05	.029832798	0.894701	Roundabout guidance receptor 4 (Robo4)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Kctd11	-1.05	.038613499	1.14862	Potassium channel tetramerisation domain containing 11 (Kctd11)
Layn	-1.05	.024475939	1.264241	Laylin (Layn)
Hps1	-1.06	.037482567	0.701494	Hermansky-Pudlak syndrome 1 (Hps1)
A330023F24Rik	-1.06	.005171393	2.900362	RIKEN cDNA A330023F24 gene (A330023F24Rik)
Lxn	-1.06	.000247675	3.809813	Latexin (Lxn)
Efs	-1.06	.005779452	1.702913	Embryonal Fyn-associated substrate (Efs)
Syt1	-1.06	.048334791	-0.09553	Synaptotagmin-like 1 (Syt1)
Stk38	-1.06	$4.66 \times 10^{-5}$	3.649656	Serine/threonine kinase 38 (Stk38)
Ephx2	-1.06	.005030185	2.098436	Epoxide hydrolase 2, cytoplasmic (Ephx2)
Dapp1	-1.06	.011620722	2.056056	Dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (Dapp1)
Lpcat3	-1.06	.000202558	3.466025	Lysophosphatidylcholine acyltransferase 3 (Lpcat3)
Ankrd16	-1.06	.000168046	3.182764	Ankyrin repeat domain 16 (Ankrd16)
Dock2	-1.06	.013914945	2.173776	Dedicator of cyto-kinesis 2 (Dock2)
Pou4f1	-1.06	.012746058	5.399256	POU domain, class 4, transcription factor 1 (Pou4f1)
Lama4	-1.06	.021320228	1.326939	Laminin, alpha 4 (Lama4)
Lpar4	-1.07	.018672471	0.984859	Lysophosphatidic acid receptor 4 (Lpar4)
9930014A18Rik	-1.07	.018981597	1.076936	RIKEN cDNA 9930014A18 gene (9930014A18Rik)
Fam228b	-1.07	.020208202	0.799233	Family with sequence similarity 228, member B (Fam228b)
Sds1	-1.07	.026926928	0.44355	Serine dehydratase-like (Sds1)
Acot1	-1.07	.000142607	3.21134	Acyl-CoA thioesterase 1 (Acot1)
Kank2	-1.07	$4.55 \times 10^{-5}$	3.066684	KN motif and ankyrin repeat domains 2 (Kank2)
Fmo5	-1.07	.002194178	2.207253	Flavin containing monooxygenase 5 (Fmo5)
Anapc13	-1.07	$8.20 \times 10^{-5}$	3.722231	Anaphase promoting complex subunit 13 (Anapc13)
Selenow	-1.07	$8.06 \times 10^{-7}$	7.626596	Selenoprotein W (Selenow)
Cmtm3	-1.07	.001931456	2.566073	CKLF-like MARVEL transmembrane domain containing 3 (Cmtm3)
Nfe2l2	-1.07	.000413421	4.230263	Nuclear factor, erythroid derived 2, like 2 (Nfe2l2)
5031425E22Rik	-1.07	.000497612	2.984237	RIKEN cDNA 5031425E22 gene (5031425E22Rik)
Snap23	-1.07	$2.99 \times 10^{-5}$	3.640914	Synaptosomal-associated protein 23 (Snap23)
Slc27a1	-1.07	$3.18 \times 10^{-6}$	5.486464	Solute carrier family 27 (fatty acid transporter), member 1 (Slc27a1)
Fam120aos	-1.07	.003238703	2.35456	Family with sequence similarity 120A, opposite strand (Fam120aos)
Vamp3	-1.07	$3.19 \times 10^{-5}$	5.185294	Vesicle-associated membrane protein 3 (Vamp3)
P4ha3	-1.07	.000140484	3.429348	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III (P4ha3)
Stpg1	-1.07	.004866842	2.198324	Sperm tail PG-rich repeat containing 1 (Stpg1)
Trac	-1.07	.005138686	1.840936	T cell receptor alpha constant (Trac)
Rftn2	-1.07	$8.22 \times 10^{-5}$	5.051637	Raftlin family member 2 (Rftn2)
Myh14	-1.07	$2.98 \times 10^{-5}$	3.293594	Myosin, heavy polypeptide 14 (Myh14)
Fads1	-1.07	$6.49 \times 10^{-8}$	8.074893	Fatty acid desaturase 1 (Fads1)
Tmem80	-1.08	$8.79 \times 10^{-5}$	3.061762	Transmembrane protein 80 (Tmem80)
Boc	-1.08	.002448758	2.086176	Biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdron) binding protein (Boc)
Vwa1	-1.08	.00348391	3.169003	Von Willebrand factor A domain containing 1 (Vwa1)
Efemp1	-1.08	.009371592	2.003588	Epidermal growth factor-containing fibulin-like extracellular matrix protein 1 (Efemp1)
Col8a2	-1.08	.017803646	1.016824	Collagen, type VIII, alpha 2 (Col8a2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Fbxl8	-1.08	.017353641	0.584954	F-box and leucine-rich repeat protein 8 (Fbxl8)
1810026B05Rik	-1.08	.023198428	2.467091	RIKEN cDNA 1810026B05 gene (1810026B05Rik)
Lyn	-1.08	.001900465	2.790056	LYN proto-oncogene, Src family tyrosine kinase (Lyn)
Sept10	-1.08	.00348391	1.724381	Septin 10 (Sept10)
Hk2	-1.08	.017206437	1.245931	Hexokinase 2 (Hk2)
Rplp1	-1.09	$1.10 \times 10^{-6}$	7.566551	Ribosomal protein, large, P1 (Rplp1)
Necab3	-1.09	.000122038	7.209698	N-terminal EF-hand calcium binding protein 3 (Necab3)
Fbxo36	-1.09	.002193605	2.495713	F-box protein 36 (Fbxo36)
Ugt8a	-1.09	.000353493	6.19542	UDP galactosyltransferase 8A (Ugt8a)
Aldh1a2	-1.09	.035582118	1.952453	Aldehyde dehydrogenase family 1, subfamily A2 (Aldh1a2)
Gm33680	-1.09	.037023513	0.025029	Predicted gene, 33680 (Gm33680)
Tpcn1	-1.09	$4.97 \times 10^{-6}$	5.512309	Two pore channel 1 (Tpcn1)
Tlr3	-1.09	.000535578	4.03953	Toll-like receptor 3 (Tlr3)
Lrig3	-1.09	.009401514	1.359981	Leucine-rich repeats and immunoglobulin-like domains 3 (Lrig3)
Acaa2	-1.09	$3.41 \times 10^{-5}$	3.241949	Acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2)
She	-1.09	.021396078	0.978163	Src homology 2 domain-containing transforming protein E (She)
Cep112	-1.09	$2.69 \times 10^{-5}$	3.848475	Centrosomal protein 112 (Cep112)
Daam2	-1.09	$2.93 \times 10^{-6}$	5.212464	Dishevelled-associated activator of morphogenesis 2 (Daam2)
Rpl10-ps6	-1.09	.012543218	1.30449	Ribosomal protein L10, pseudogene 6 (Rpl10-ps6)
Bloc1s1	-1.09	.002250829	1.684672	Biogenesis of lysosomal organelles complex-1, subunit 1 (Bloc1s1)
Rps24	-1.09	$9.73 \times 10^{-7}$	6.991988	Ribosomal protein S24 (Rps24)
Prelp	-1.09	.000973217	4.831111	Proline arginine-rich end leucine-rich repeat (Prelp)
Nxt1	-1.09	.004636224	1.974019	NTF2-related export protein 1 (Nxt1)
Kif13b	-1.10	$5.57 \times 10^{-5}$	4.468318	Kinesin family member 13B (Kif13b)
Gm45708	-1.10	.030906742	-0.08747	Predicted gene (Gm45708)
Mb21d1	-1.10	.048028786	0.750674	Mab-21 domain containing 1 (Mb21d1)
Dynlt1f	-1.10	.016146763	0.325965	Dynein light chain Tctex-type 1F (Dynlt1f)
Ubxn10	-1.10	.003025684	2.92694	UBX domain protein 10 (Ubxn10)
Gm37238	-1.10	.01983704	1.209398	Predicted gene (Gm37238)
Gpsm1	-1.10	$4.93 \times 10^{-5}$	3.671139	G-protein signalling modulator 1 (AGS3-like, C. elegans) (Gpsm1)
Chrnb3	-1.10	.001344315	5.48669	Cholinergic receptor, nicotinic, beta polypeptide 3 (Chrnb3)
Thsd1	-1.10	.014279993	0.773359	Thrombospondin, type I, domain 1 (Thsd1)
Irx5	-1.10	.026477297	2.272937	IROQUOIS-related homeobox 5 (Irx5)
P2ry14	-1.10	.012953398	1.325854	Purinergic receptor P2Y, G-protein coupled, 14 (P2ry14)
Exosc3	-1.10	.001270369	3.004655	Exosome component 3 (Exosc3)
Hmox1	-1.10	.001503166	2.084193	Heme oxygenase 1 (Hmox1)
Slfn5	-1.10	.018234003	2.196344	Schlafen 5 (Slfn5)
Ctsc	-1.10	.029022449	3.178739	Cathepsin C (Ctsc)
Ifrd1	-1.10	$5.52 \times 10^{-5}$	4.217696	Interferon-related developmental regulator 1 (Ifrd1)
Il18	-1.10	$7.15 \times 10^{-5}$	2.862566	Interleukin 18 (Il18)
Lima1	-1.10	$6.18 \times 10^{-5}$	3.454519	LIM domain and actin binding 1 (Lima1)
Pde8a	-1.10	.000270051	3.769577	Phosphodiesterase 8A (Pde8a)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pon3	-1.10	.024573321	0.705249	Paraoxonase 3 (Pon3)
Mpeg1	-1.11	.004205821	4.793875	Macrophage expressed gene 1 (Mpeg1)
Rps14	-1.11	$7.58 \times 10^{-6}$	5.221231	Ribosomal protein S14 (Rps14)
Aifm3	-1.11	.000108463	4.597911	Apoptosis-inducing factor, mitochondrion-associated 3 (Aifm3)
Ccdc114	-1.11	.020938965	0.849293	Coiled-coil domain containing 114 (Ccdc114)
Lbr	-1.11	.000824747	2.060907	Lamin B receptor (Lbr)
Aga	-1.11	.000295207	2.480546	Aspartylglucosaminidase (Aga)
Smim3	-1.11	.00887688	1.048962	Small integral membrane protein 3 (Smim3)
Kcnmb1	-1.11	.004551291	2.8786	Potassium large conductance calcium-activated channel, subfamily M, beta member 1 (Kcnmb1)
Smo	-1.11	$6.61 \times 10^{-5}$	4.100241	Smoothed, frizzled class receptor (Smo)
Rbm38	-1.11	.02175209	0.485657	RNA binding motif protein 38 (Rbm38)
Alox5ap	-1.11	.029515857	0.767398	Arachidonate 5-lipoxygenase activating protein (Alox5ap)
Pacrg	-1.11	.000159027	3.898794	PARK2 co-regulated (Pacrg)
St3gal6	-1.11	.000149436	3.680103	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 (St3gal6)
Nfkbiz	-1.11	.005044978	1.604071	Nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta (Nfkbiz)
Aox1	-1.11	.020117724	0.525351	Aldehyde oxidase 1 (Aox1)
Rpl37a	-1.11	$3.18 \times 10^{-6}$	6.393297	Ribosomal protein L37a (Rpl37a)
Nos3	-1.11	.039925457	0.342762	Nitric oxide synthase 3, endothelial cell (Nos3)
4932438H23Rik	-1.11	.036194616	1.079526	RIKEN cDNA 4932438H23 gene (4932438H23Rik)
4732416N19Rik	-1.12	.003664544	1.2333	RIKEN cDNA 4732416N19 gene (4732416N19Rik)
1810037I17Rik	-1.12	$4.34 \times 10^{-5}$	4.438177	RIKEN cDNA 1810037I17 gene (1810037I17Rik)
Abracl	-1.12	.005156073	1.681769	ABRA C-terminal like (Abracl)
Cd24a	-1.12	.000172134	5.272342	CD24a antigen (Cd24a)
Rps12	-1.12	.00020497	3.107199	Ribosomal protein S12 (Rps12)
Padi2	-1.12	.000533592	4.173653	Peptidyl arginine deiminase, type II (Padi2)
S1pr2	-1.12	.038801677	0.349446	Sphingosine-1-phosphate receptor 2 (S1pr2)
Plat	-1.12	.001071094	4.032358	Plasminogen activator, tissue (Plat)
Nat8f1	-1.12	.005229145	1.402616	N-acetyltransferase 8 (GCN5-related) family member 1 (Nat8f1)
Tfpi	-1.12	.007088739	1.775694	Tissue factor pathway inhibitor (Tfpi)
Gm20342	-1.12	.034164838	2.015582	Predicted gene, 20342 (Gm20342)
Nes	-1.13	.008073829	0.898532	Nestin (Nes)
Snhg1	-1.13	$1.74 \times 10^{-5}$	4.158464	Small nucleolar RNA host gene 1 (Snhg1)
Wnk4	-1.13	.041357409	-0.02167	WNK lysine deficient protein kinase 4 (Wnk4)
Pla2r1	-1.13	.047097802	0.35419	Phospholipase A2 receptor 1 (Pla2r1)
Emp2	-1.13	.00021166	3.355918	Epithelial membrane protein 2 (Emp2)
1500035N22Rik	-1.13	.023338067	0.997441	RIKEN cDNA 1500035N22 gene (1500035N22Rik)
Parp9	-1.13	.044531516	1.66239	Poly(ADP-ribose) polymerase family, member 9 (Parp9)
Cmtm6	-1.13	$7.22 \times 10^{-6}$	4.016724	CKLF-like MARVEL transmembrane domain containing 6 (Cmtm6)
Smim11	-1.13	.000257199	2.465743	Small integral membrane protein 11 (Smim11)
Plxnb1	-1.13	$2.03 \times 10^{-6}$	5.289573	Plexin B1 (Plxnb1)
Gatm	-1.13	$1.91 \times 10^{-5}$	6.478355	Glycine amidinotransferase (L-arginine:glycine amidinotransferase) (Gatm)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Obscn	-1.13	.043393264	0.750041	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (Obscn)
4930447F24Rik	-1.13	.024325218	0.747207	RIKEN cDNA 4930447F24 gene (4930447F24Rik)
Gm27003	-1.13	.025155748	-0.08161	Predicted gene, 27003 (Gm27003)
Myo6	-1.13	$1.61 \times 10^{-5}$	6.275704	Myosin VI (Myo6)
Tns3	-1.13	$1.34 \times 10^{-5}$	6.000206	Tensin 3 (Tns3)
Tril	-1.13	$3.36 \times 10^{-6}$	5.531253	TLR4 interactor with leucine-rich repeats (Tril)
Rfx4	-1.14	.000113285	4.725023	Regulatory factor X, 4 (influences HLA class II expression) (Rfx4)
Prr5l	-1.14	.000952419	3.47516	Proline rich 5 like (Prr5l)
Pros1	-1.14	.000102301	3.426973	Protein S (alpha) (Pros1)
Lrrc51	-1.14	.00472261	2.065139	Leucine-rich repeat containing 51 (Lrrc51)
Ptprz1	-1.14	$2.12 \times 10^{-7}$	8.015394	Protein tyrosine phosphatase, receptor type Z, polypeptide 1 (Ptprz1)
C3ar1	-1.14	.004754794	2.260126	Complement component 3a receptor 1 (C3ar1)
Slc5a11	-1.14	.028695831	0.207292	Solute carrier family 5 (sodium/glucose cotransporter), member 11 (Slc5a11)
Myb	-1.14	.006117957	1.51947	Myeloblastosis oncogene (Myb)
Fsip1	-1.14	.036567968	-0.06486	Fibrous sheath-interacting protein 1 (Fsip1)
Mettl23	-1.14	.000419938	2.211524	Methyltransferase like 23 (Mettl23)
Rpl37	-1.14	$2.93 \times 10^{-6}$	6.017693	Ribosomal protein L37 (Rpl37)
4930431P19Rik	-1.15	.003429155	2.10157	RIKEN cDNA 4930431P19 gene (4930431P19Rik)
C030037D09Rik	-1.15	.000750569	2.993472	RIKEN cDNA C030037D09 gene (C030037D09Rik)
Npc2	-1.15	$2.24 \times 10^{-6}$	5.42618	Niemann-Pick type C2 (Npc2)
Atp7b	-1.15	.003894268	1.349234	ATPase, Cu++ transporting, beta polypeptide (Atp7b)
Nt5dc2	-1.15	.003522517	1.26268	5'-Nucleotidase domain containing 2 (Nt5dc2)
Fam129a	-1.15	.023338067	0.376994	Family with sequence similarity 129, member A (Fam129a)
Scp2	-1.15	$2.94 \times 10^{-6}$	4.53868	Sterol carrier protein 2, liver (Scp2)
Ifrd2	-1.15	.016218299	1.393107	Interferon-related developmental regulator 2 (Ifrd2)
Adgrl4	-1.15	.000691243	3.165261	Adhesion G protein-coupled receptor L4 (Adgrl4)
Uxt	-1.15	.008590702	0.662938	Ubiquitously expressed transcript (Uxt)
Cd33	-1.15	.000920938	2.949039	CD33 antigen (Cd33)
Slc44a1	-1.15	$1.12 \times 10^{-6}$	6.422691	Solute carrier family 44, member 1 (Slc44a1)
Yap1	-1.15	.000140484	3.139538	Yes-associated protein 1 (Yap1)
Notch3	-1.15	.001059508	3.001284	Notch 3 (Notch3)
Tmsb4x	-1.15	$1.34 \times 10^{-5}$	7.408202	Thymosin, beta 4, X chromosome (Tmsb4x)
E2f5	-1.16	.000731656	2.698102	E2F transcription factor 5 (E2f5)
Als2cl	-1.16	.025765291	1.110174	ALS2 C-terminal like (Als2cl)
4933413G19Rik	-1.16	.040027641	0.240535	RIKEN cDNA 4933413G19 gene (4933413G19Rik)
Klhdc7a	-1.16	.002337753	2.892523	Kelch domain containing 7A (Klhdc7a)
Nr2e1	-1.16	.001709309	2.717297	Nuclear receptor subfamily 2, group E, member 1 (Nr2e1)
Rabep2	-1.16	.000513935	1.96385	Rabaptin, RAB GTPase binding effector protein 2 (Rabep2)
Il11ra1	-1.16	.002425254	2.141388	Interleukin 11 receptor, alpha chain 1 (Il11ra1)
Tmem35b	-1.16	.002536116	1.980574	Transmembrane protein 35B (Tmem35b)
Crybg2	-1.16	.028793942	0.675262	Crystallin Beta-Gamma Domain Containing 2 (Crybg2)
2700046A07Rik	-1.16	.029826632	0.029924	RIKEN cDNA 2700046A07 gene (2700046A07Rik)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Ccna2	-1.16	.049561915	0.320962	Cyclin A2 (Ccna2)
Ggh	-1.16	.000157484	2.861872	Gamma-glutamyl hydrolase (Ggh)
Trim25	-1.16	.000140232	3.304243	Tripartite motif-containing 25 (Trim25)
Kmt5c	-1.17	.002681468	1.589277	Lysine methyltransferase 5C (Kmt5c)
Fam117a	-1.17	.001833285	1.40422	Family with sequence similarity 117, member A (Fam117a)
Wfikkn2	-1.17	.0004311	3.030509	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (Wfikkn2)
3110070M22Rik	-1.17	.009711278	0.78267	RIKEN cDNA 3110070M22 gene (3110070M22Rik)
Fgfr2	-1.17	$4.97 \times 10^{-5}$	5.631052	Fibroblast growth factor receptor 2 (Fgfr2)
Bgn	-1.17	.008073829	2.87013	Biglycan (Bgn)
Ulk4	-1.17	.008784142	1.81416	Unc-51-like kinase 4 (Ulk4)
Hes1	-1.17	.001945942	1.313793	Hairy and enhancer of split 1 (Hes1)
Papss2	-1.17	.000981542	3.096375	3'-Phosphoadenosine 5'-phosphosulfate synthase 2 (Papss2)
Gltp	-1.18	$6.99 \times 10^{-5}$	4.899758	Glycolipid transfer protein (Gltp)
Itgb3	-1.18	.009444664	1.366371	Integrin beta 3 (Itgb3)
BC030343	-1.18	.002847448	1.656515	cDNA sequence BC030343 (BC030343)
1700120C14Rik	-1.18	.049261866	0.175745	RIKEN cDNA 1700120C14 gene (1700120C14Rik)
Rnase4	-1.18	$4.56 \times 10^{-5}$	3.59023	Ribonuclease, RNase A family 4 (Rnase4)
Rps28	-1.18	$8.53 \times 10^{-5}$	3.417645	Ribosomal protein S28 (Rps28)
0610043K17Rik	-1.18	.008294123	1.079591	RIKEN cDNA 0610043K17 gene (0610043K17Rik)
Chrnb4	-1.18	.002127168	6.848111	Cholinergic receptor, nicotinic, beta polypeptide 4 (Chrnb4)
Qdpr	-1.18	$1.25 \times 10^{-6}$	5.30414	Quinoid dihydropteridine reductase (Qdpr)
Scnn1a	-1.18	.017169007	1.972245	Sodium channel, nonvoltage-gated 1 alpha (Scnn1a)
2900052N01Rik	-1.18	$8.86 \times 10^{-5}$	4.057103	RIKEN cDNA 2900052N01 gene (2900052N01Rik)
Tnfrsf1b	-1.18	.045782065	1.11812	Tumor necrosis factor receptor superfamily, member 1b (Tnfrsf1b)
Neu4	-1.18	.000275022	2.692901	Sialidase 4 (Neu4)
Gm10561	-1.18	.002801426	1.544058	Predicted gene 10561 (Gm10561)
Evc2	-1.18	.032066734	0.558719	Ellis van Creveld syndrome 2 (Evc2)
H2-D1	-1.18	.027298452	5.445131	Histocompatibility 2, D region locus 1 (H2-D1)
Ascl4	-1.18	.00582942	1.854344	Achaete-scute family bHLH transcription factor 4 (Ascl4)
Ccdc84	-1.18	.014232243	0.941049	Coiled-coil domain containing 84 (Ccdc84)
Hexb	-1.18	$2.79 \times 10^{-6}$	4.717284	Hexosaminidase B (Hexb)
Rps21	-1.18	$1.10 \times 10^{-5}$	5.19166	Ribosomal protein S21 (Rps21)
Acss3	-1.18	.014289176	1.072955	Acyl-CoA synthetase short-chain family member 3 (Acss3)
Pxdc1	-1.18	.015098246	1.672496	PX domain containing 1 (Pxdc1)
Prcd	-1.19	.022344908	0.513325	Photoreceptor Disc Component (Prcd)
Lrrk1	-1.19	.012371974	0.836502	Leucine-rich repeat kinase 1 (Lrrk1)
Nod1	-1.19	.007070722	1.788212	Nucleotide-binding oligomerization domain containing 1 (Nod1)
B230323A14Rik	-1.19	.000909697	1.806089	RIKEN cDNA B230323A14 gene (B230323A14Rik)
Zfp474	-1.19	.003224519	1.10621	Zinc finger protein 474 (Zfp474)
1700028P14Rik	-1.19	.019667026	1.021961	RIKEN cDNA 1700028P14 gene (1700028P14Rik)
Tnnt1	-1.19	.000348091	4.245126	Troponin T1, skeletal, slow (Tnnt1)
Fam107a	-1.19	$5.36 \times 10^{-6}$	8.044484	Family with sequence similarity 107, member A (Fam107a)
Fth1	-1.19	$4.73 \times 10^{-8}$	9.706873	Ferritin heavy polypeptide 1 (Fth1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Vmac	-1.19	.000968787	2.56346	Vimentin-type intermediate filament-associated coiled-coil protein (Vmac)
Atp2a3	-1.19	.014202937	0.994436	ATPase, Ca++ transporting, ubiquitous (Atp2a3)
Cebpa	-1.20	.042604347	0.186336	CCAAT/enhancer binding protein (C/EBP), alpha (Cebpa)
Colec12	-1.20	$9.38 \times 10^{-5}$	2.879462	Collectin sub-family member 12 (Colec12)
Hsd17b11	-1.20	$2.18 \times 10^{-5}$	3.59739	Hydroxysteroid (17-beta) dehydrogenase 11 (Hsd17b11)
Ano1	-1.20	.001339309	4.054515	Anoctamin 1, calcium activated chloride channel (Ano1)
Gm15893	-1.20	.021141437	0.073855	Predicted gene (Gm15893)
Gm27032	-1.20	.001687297	1.306945	Predicted gene (Gm27032)
Ybx1	-1.20	$4.14 \times 10^{-7}$	5.865673	Y box protein 1 (Ybx1)
Tmem181b-ps	-1.20	$1.99 \times 10^{-5}$	3.713917	Transmembrane protein 181B, pseudogene (Tmem181b-ps)
Ctnna3	-1.20	.021380885	1.194521	Catenin (cadherin-associated protein), alpha 3 (Ctnna3)
Spf2	-1.20	.00174136	2.163183	Sperm flagellar 2 (Spf2)
Sqor	-1.20	.000929719	2.494005	Sulfide Quinone Oxidoreductase (Sqor)
Plekho2	-1.20	$1.25 \times 10^{-5}$	3.730697	pleckstrin homology domain containing, family O member 2 (Plekho2)
Kank1	-1.20	.000113408	4.21666	KN motif and ankyrin repeat domains 1 (Kank1)
Sall3	-1.20	.001150534	2.707474	Sal-like 3 (Sall3)
Pdgfd	-1.20	.01425755	1.066187	Platelet-derived growth factor, D polypeptide (Pdgfd)
Pik3r5	-1.20	.031874957	1.350876	Phosphoinositide-3-kinase, regulatory subunit 5, p101 (Pik3r5)
Snhg5	-1.20	.000413421	2.155522	Small nucleolar RNA host gene 5 (Snhg5)
Cpq	-1.20	.000307293	2.745175	Carboxypeptidase Q (Cpq)
Mafb	-1.20	.006958315	2.401036	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian) (Mafb)
Ttll3	-1.20	.000111734	2.924717	Tubulin tyrosine ligase-like family, member 3 (Ttll3)
Gramd3	-1.21	$2.87 \times 10^{-5}$	3.536419	GRAM domain containing 3 (Gramd3)
Rspo4	-1.21	.01261748	1.466589	R-spondin 4 (Rspo4)
Zfp524	-1.21	.014499583	0.231873	Zinc finger protein 524 (Zfp524)
Limch1	-1.21	$2.23 \times 10^{-5}$	5.113421	LIM and calponin homology domains 1 (Limch1)
Stom	-1.21	.000175375	2.649156	Stomatin (Stom)
Nr2c2ap	-1.21	.015534765	0.193693	Nuclear receptor 2C2-associated protein (Nr2c2ap)
Pdk4	-1.21	.000273645	2.288155	Pyruvate dehydrogenase kinase, isoenzyme 4 (Pdk4)
Cped1	-1.21	.033579098	1.404764	Cadherin-like and PC-esterase domain containing 1 (Cped1)
Tmem176b	-1.21	$1.59 \times 10^{-5}$	5.682541	Transmembrane protein 176B (Tmem176b)
Fam234a	-1.21	$7.58 \times 10^{-5}$	2.625972	Family with sequence similarity 234, member A (Fam234a)
Frmd8	-1.21	.000274702	3.280708	FERM domain containing 8 (Frmd8)
Abtb2	-1.21	.000113285	3.061535	Ankyrin repeat and BTB (POZ) domain containing 2 (Abtb2)
Plscr4	-1.21	.004704001	1.059285	Phospholipid scramblase 4 (Plscr4)
Rtn4rl2	-1.21	.022857561	1.009697	Reticulon 4 receptor-like 2 (Rtn4rl2)
2810459M11Rik	-1.21	.000298204	2.443126	RIKEN cDNA 2810459M11 gene (2810459M11Rik)
Lamc3	-1.21	.016767275	1.651479	Laminin gamma 3 (Lamc3)
Trp73	-1.21	.019278772	1.088466	Transformation-related protein 73 (Trp73)
Abca9	-1.21	$9.92 \times 10^{-5}$	2.792147	ATP-binding cassette, sub-family A (ABC1), member 9 (Abca9)
Tor4a	-1.21	.037421706	0.328779	Torsin family 4, member A (Tor4a)
Tnfsf12	-1.21	.006533561	0.580528	Tumor necrosis factor (ligand) superfamily, member 12 (Tnfsf12)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tgfb2	-1.21	$6.20 \times 10^{-5}$	4.201933	Transforming growth factor, beta receptor II (Tgfb2)
Galnt4	-1.22	.001453455	1.957865	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (Galnt4)
Tsc22d4	-1.22	$2.23 \times 10^{-6}$	4.326679	TSC22 domain family, member 4 (Tsc22d4)
Vsig10	-1.22	.022971426	0.391938	V-set and immunoglobulin domain containing 10 (Vsig10)
Mettl7a1	-1.22	$3.96 \times 10^{-6}$	4.402014	Methyltransferase like 7A1 (Mettl7a1)
Ang	-1.22	.026732262	0.760579	Angiogenin, ribonuclease, RNase A family, 5 (Ang)
Il17ra	-1.22	.000161732	3.116952	Interleukin 17 receptor A (Il17ra)
Erg	-1.22	.015159819	1.58783	Avian erythroblastosis virus E-26 (v-ets) oncogene related (Erg)
4930519K11Rik	-1.22	.007956524	0.795241	RIKEN cDNA 4930519K11 gene (4930519K11Rik)
Rpl9-ps6	-1.22	.002457495	1.235462	Ribosomal protein L9, pseudogene 6 (Rpl9-ps6)
Cpt1a	-1.22	$2.75 \times 10^{-5}$	3.794592	Carnitine palmitoyltransferase 1a, liver (Cpt1a)
Gm12940	-1.22	.012084874	1.362936	Predicted gene (Gm12940)
Vcam1	-1.22	.000351859	4.600288	Vascular cell adhesion molecule 1 (Vcam1)
C230072F16Rik	-1.22	.007074567	1.988352	RIKEN cDNA C230072F16 gene (C230072F16Rik)
Amy1	-1.23	.003125048	3.124295	Amylase 1, salivary (Amy1)
Spag17	-1.23	.010228757	1.073302	Sperm-associated antigen 17 (Spag17)
Syt14	-1.23	.03201848	1.760065	Synaptotagmin-like 4 (Syt14)
Slc16a4	-1.23	.011411404	0.693355	Solute carrier family 16 (monocarboxylic acid transporters), member 4 (Slc16a4)
Msn	-1.23	.000334057	4.791074	Moesin (Msn)
Lsm5	-1.23	.025330932	1.178313	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated (Lsm5)
Msrb2	-1.23	.000646891	1.840277	Methionine sulfoxide reductase B2 (Msrb2)
Scamp2	-1.23	.000149502	2.97905	Secretory carrier membrane protein 2 (Scamp2)
Tfeb	-1.23	.005222906	1.694663	Transcription factor EB (Tfeb)
Mvp	-1.23	.001599223	2.0596	Major vault protein (Mvp)
Gm973	-1.23	.000106457	3.078131	Predicted gene 973 (Gm973)
Cdh3	-1.23	.004556736	2.374557	Cadherin 3 (Cdh3)
Gsap	-1.23	.025748885	1.650245	Gamma-secretase activating protein (Gsap)
Cbs	-1.23	$1.71 \times 10^{-5}$	3.741092	Cystathione beta-synthase (Cbs)
Gm44250	-1.23	.005309158	1.243933	Predicted gene (Gm44250)
C1ql1	-1.23	.001369036	1.903386	Complement component 1, q subcomponent-like 1 (C1ql1)
Mertk	-1.24	$1.59 \times 10^{-5}$	4.173314	C-mer proto-oncogene tyrosine kinase (Mertk)
Arhgef19	-1.24	.002302996	1.80534	Rho guanine nucleotide exchange factor (GEF) 19 (Arhgef19)
Serpine2	-1.24	$1.44 \times 10^{-8}$	7.699841	Serine (or cysteine) peptidase inhibitor, clade E, member 2 (Serpine2)
Arpc1b	-1.24	.000361722	3.536518	Actin-related protein 2/3 complex, subunit 1B (Arpc1b)
5430402O13Rik	-1.24	.010061854	0.149713	RIKEN cDNA 5430402O13 gene (5430402O13Rik)
Dab2	-1.24	$1.18 \times 10^{-6}$	4.299648	Disabled 2, mitogen-responsive phosphoprotein (Dab2)
Il12rb2	-1.24	.00781795	1.076085	Interleukin 12 receptor, beta 2 (Il12rb2)
Gpr17	-1.24	$4.43 \times 10^{-6}$	5.345105	G protein-coupled receptor 17 (Gpr17)
Kyat3	-1.24	.00248065	1.326724	Kynurenone aminotransferase 3 (Kyat3)
Golim4	-1.25	$1.66 \times 10^{-5}$	4.141702	Golgi integral membrane protein 4 (Golim4)
Slc13a4	-1.25	.032869475	1.871927	Solute carrier family 13 (sodium/sulfate symporters), member 4 (Slc13a4)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Prom1	-1.25	.000478356	2.236378	Prominin 1 (Prom1)
Blvrb	-1.25	.000246074	2.336584	Biliverdin reductase B (flavin reductase (NADPH)) (Blvrb)
Fli1	-1.25	.002176919	1.691115	Friend leukemia integration 1 (Fli1)
Chrna3	-1.25	.001565671	6.702268	Cholinergic receptor, nicotinic, alpha polypeptide 3 (Chrna3)
Ddah2	-1.25	.000240897	2.218008	Dimethylarginine dimethylaminohydrolase 2 (Ddah2)
Fuz	-1.25	.016335254	0.851709	Fuzzy planar cell polarity protein (Fuz)
Cfap57	-1.25	.007012116	1.237086	Cilia and flagella-associated protein 57 (Cfap57)
Fads2	-1.25	$1.22 \times 10^{-7}$	6.141946	Fatty acid desaturase 2 (Fads2)
Mmel1	-1.25	.020973542	0.166616	Membrane metallo-endopeptidase-like 1 (Mmel1)
Aass	-1.25	.007541978	0.920775	Aminoadipate-semialdehyde synthase (Aass)
Cers2	-1.25	$7.84 \times 10^{-7}$	5.357083	Ceramide synthase 2 (Cers2)
Cabp1	-1.25	.00161309	2.020935	Calcium binding protein 1 (Cabd1)
Tlr7	-1.25	.014564453	1.703322	Toll-like receptor 7 (Tlr7)
Gm42692	-1.25	.029964932	0.095187	Predicted gene (Gm42692)
Rspn10b	-1.26	.006744795	1.692022	Radial spoke head 10 homolog B (Chlamydomonas) (Rspn10b)
Slc6a1	-1.26	$3.93 \times 10^{-7}$	7.697146	Solute carrier family 6 (neurotransmitter transporter, GABA), member 1 (Slc6a1)
Gm26703	-1.26	.004350776	1.697319	Predicted gene, 26703 (Gm26703)
C030029H02Rik	-1.26	.00267094	1.906417	RIKEN cDNA C030029H02 gene (C030029H02Rik)
Chst3	-1.26	.008250138	1.844138	Carbohydrate (chondroitin 6/keratan) sulfotransferase 3 (Chst3)
Tln1	-1.26	$6.92 \times 10^{-7}$	4.484675	Talin 1 (Tln1)
Tec	-1.26	.004303565	0.761994	Tec protein tyrosine kinase (Tec)
Flt1	-1.26	$4.06 \times 10^{-5}$	4.772082	FMS-like tyrosine kinase 1 (Flt1)
Ephx1	-1.27	.001008685	2.789296	Epoxide hydrolase 1, microsomal (Ephx1)
Tbx18	-1.27	.023523029	-0.13114	T-box18 (Tbx18)
Slc13a3	-1.27	$1.62 \times 10^{-5}$	3.996678	Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (Slc13a3)
2410006H16Rik	-1.27	$1.74 \times 10^{-5}$	4.074663	RIKEN cDNA 2410006H16 gene (2410006H16Rik)
Ctso	-1.27	$2.62 \times 10^{-6}$	5.036704	Cathepsin O (Ctso)
G0s2	-1.27	.002195116	1.168191	G0/G1 switch gene 2 (G0s2)
Slc40a1	-1.27	.004191592	1.637292	Solute carrier family 40 (iron-regulated transporter), member 1 (Slc40a1)
Pxn	-1.27	.000104976	3.752536	Paxillin (Pxn)
Ermn	-1.27	.000150079	6.275225	Ermin, ERM-like protein (Ermn)
Tgm2	-1.27	.032610588	1.591611	Transglutaminase 2, C polypeptide (Tgm2)
Arhgef10	-1.27	$4.18 \times 10^{-5}$	5.14484	Rho guanine nucleotide exchange factor (GEF) 10 (Arhgef10)
Pdgfra	-1.27	$6.36 \times 10^{-6}$	5.295795	Platelet derived growth factor receptor, alpha polypeptide (Pdgfra)
Gm16365	-1.27	.013177697	1.190078	Predicted gene 16365 (Gm16365)
Rdm1	-1.27	.001288605	1.466372	RAD52 motif 1 (Rdm1)
Tmem107	-1.27	.000234253	3.224221	Transmembrane protein 107 (Tmem107)
Fam81b	-1.28	.008901412	0.796243	Family with sequence similarity 81, member B (Fam81b)
Al464131	-1.28	$4.05 \times 10^{-5}$	3.953476	Expressed sequence Al464131 (Al464131)
Plcb3	-1.28	.000176486	2.557937	Phospholipase C, beta 3 (Plcb3)
Lag3	-1.28	.002892783	0.945963	Lymphocyte-activation gene 3 (Lag3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
1110018N20Rik	-1.28	.033748296	-0.03408	RIKEN cDNA 1110018N20 gene (1110018N20Rik)
Agmo	-1.28	.005066877	1.574874	Alkylglycerol monooxygenase (Agmo)
Cdh23	-1.28	.007688337	0.342461	Cadherin 23 (otocadherin) (Cdh23)
Slc9a9	-1.28	.000309926	2.600591	Solute carrier family 9 (sodium/hydrogen exchanger), member 9 (Slc9a9)
Aldh1a1	-1.28	$2.60 \times 10^{-6}$	6.018856	Aldehyde dehydrogenase family 1, subfamily A1 (Aldh1a1)
Prdx6	-1.28	$1.75 \times 10^{-7}$	6.777654	Peroxiredoxin 6 (Prdx6)
Pcp4	-1.28	$5.63 \times 10^{-8}$	6.545404	Purkinje cell protein 4 (Pcp4)
Gm45716	-1.28	.01697989	0.125651	Predicted gene (Gm45716)
S1pr5	-1.28	.002953969	2.776386	Sphingosine-1-phosphate receptor 5 (S1pr5)
Nckap1l	-1.28	.000749397	2.466474	NCK-associated protein 1 like (Nckap1l)
1700113A16Rik	-1.28	.045449888	-0.23194	RIKEN cDNA 1700113A16 gene (1700113A16Rik)
Pnpla7	-1.29	.004522025	2.263436	Patatin-like phospholipase domain containing 7 (Pnpla7)
Gm20257	-1.29	.003278337	1.187467	Caspase 8 pseudogene (Gm20257)
A930005H10Rik	-1.29	.000741401	2.10605	RIKEN cDNA A930005H10 gene (A930005H10Rik)
Fam72a	-1.29	.011173289	0.068406	Family with sequence similarity 72, member A (Fam72a)
Ccdc162	-1.29	.000303517	2.167377	Coiled-coil domain containing 162 (Ccdc162)
Mill2	-1.29	.04411911	0.672528	MHC I like leukocyte 2 (Mill2)
Kcnj16	-1.29	$1.28 \times 10^{-6}$	5.619336	Potassium inwardly-rectifying channel, subfamily J, member 16 (Kcnj16)
Stamos	-1.29	.016703382	0.486983	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 1, opposite strand (Stamos)
As3mt	-1.29	.000143123	2.647238	Arsenic (+3 oxidation state) methyltransferase (As3mt)
Gm2238	-1.29	.028416049	0.13995	Predicted gene 2238 (Gm2238)
Lsm7	-1.29	.026105371	0.416061	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated (Lsm7)
BC065397	-1.29	.024815617	-0.00065	cDNA sequence BC065397 (BC065397)
Tcf7	-1.29	.001125414	2.679247	Transcription factor 7, T cell specific (Tcf7)
Gm37069	-1.29	.009061486	0.33677	Predicted gene (Gm37069)
Nqo1	-1.29	.001624859	1.127912	NAD (P)H dehydrogenase, quinone 1 (Nqo1)
Pcolce	-1.30	.01544803	0.779588	Procollagen C-endopeptidase enhancer protein (Pcolce)
Metap1d	-1.30	.000532269	2.72722	Methionyl aminopeptidase type 1D (mitochondrial) (Metap1d)
Cavin2	-1.30	.000659238	2.303618	Caveolae-associated protein 2 (Cavin2)
Stk10	-1.30	.001356037	2.367117	Serine/threonine kinase 10 (Stk10)
Mcm3	-1.30	.028752989	-0.15957	Minichromosome maintenance complex component 3 (Mcm3)
Gm29508	-1.30	.000104414	3.027245	Predicted gene 29508 (Gm29508)
Stab1	-1.30	.00735235	1.391579	Stabilin 1 (Stab1)
Cxcl11	-1.30	.049149593	0.243646	Chemokine (C-X-C motif) ligand 11 (Cxcl11)
Ptprc	-1.30	.012321532	1.962355	Protein tyrosine phosphatase, receptor type, C (Ptprc)
F11r	-1.30	.000727234	3.060361	F11 receptor (F11r)
Adgre5	-1.30	.003995261	2.345504	Adhesion G protein-coupled receptor E5 (Adgre5)
Spaca6	-1.30	.000345572	2.847876	Sperm acrosome associated 6 (Spaca6)
1700007K13Rik	-1.30	.000769424	2.498656	RIKEN cDNA 1700007K13 gene (1700007K13Rik)
Tmem88b	-1.31	$2.71 \times 10^{-5}$	6.491674	Transmembrane protein 88B (Tmem88b)
Phldb1	-1.31	$4.48 \times 10^{-5}$	4.518581	Pleckstrin homology like domain, family B, member 1 (Phldb1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Slc25a34	-1.31	.009527422	0.589197	Solute carrier family 25, member 34 (Slc25a34)
Nrrros	-1.31	.017677103	1.397366	Negative regulator of reactive oxygen species (Nrrros)
Evc	-1.31	.018500934	0.901212	Ellis van Creveld gene syndrome (Evc)
Map2k3os	-1.31	.045630469	0.485121	Mitogen-activated protein kinase kinase 3, opposite strand (Map2k3os)
Ppp1r3c	-1.31	$1.70 \times 10^{-5}$	5.094986	Protein phosphatase 1, regulatory (inhibitor) subunit 3C (Ppp1r3c)
Tmem256	-1.31	$4.25 \times 10^{-5}$	3.239443	Transmembrane protein 256 (Tmem256)
Ppil6	-1.31	.000802708	1.994358	Peptidylprolyl isomerase (cyclophilin)-like 6 (Ppil6)
A730094K22Rik	-1.31	.037664816	0.442847	RIKEN cDNA A730094K22 gene (A730094K22Rik)
Ezr	-1.31	$2.04 \times 10^{-5}$	3.89966	Ezrin (Ezr)
Ednra	-1.31	.001197488	2.12313	Endothelin receptor type A (Ednra)
Cyp27a1	-1.31	.01103335	0.971878	Cytochrome P450, family 27, subfamily a, polypeptide 1 (Cyp27a1)
4732440D04Rik	-1.31	.001093325	1.865407	RIKEN cDNA 4732440D04 gene (4732440D04Rik)
Etnppl	-1.31	$1.63 \times 10^{-6}$	6.121327	Ethanolamine phosphate phospholipase (Etnppl)
Rnf135	-1.31	.00348391	0.874615	Ring finger protein 135 (Rnf135)
Cd84	-1.31	.00373572	1.375136	CD84 antigen (Cd84)
Slco1a4	-1.31	$7.74 \times 10^{-6}$	3.906069	Solute carrier organic anion transporter family, member 1a4 (Slco1a4)
Gadd45g	-1.32	$5.75 \times 10^{-5}$	3.240926	Growth arrest and DNA-damage-inducible 45 gamma (Gadd45g)
Olfml1	-1.32	.00011805	3.400022	Olfactomedin-like 1 (Olfml1)
4930579K19Rik	-1.32	.033735273	-0.06073	RIKEN cDNA 4930579K19 gene (4930579K19Rik)
P2ry13	-1.32	.000181543	2.924089	Purinergic receptor P2Y, G-protein coupled 13 (P2ry13)
Fam92b	-1.32	.026796231	-0.08404	Family with sequence similarity 92, member B (Fam92b)
Myrf	-1.32	$8.01 \times 10^{-5}$	5.526492	Myelin regulatory factor (Myrf)
Malat1	-1.32	$1.25 \times 10^{-5}$	11.27975	Metastasis-associated lung adenocarcinoma transcript 1 (non-coding RNA) (Malat1)
Fyb	-1.33	.00064147	2.625658	FYN binding protein (Fyb)
Palmd	-1.33	.000459606	1.57698	Palmdelphin (Palmd)
Cnp	-1.33	$1.06 \times 10^{-5}$	7.288601	2',3'-Cyclic nucleotide 3' phosphodiesterase (Cnp)
Golm1	-1.33	.000187498	2.18171	Golgi membrane protein 1 (Golm1)
Ptgs1	-1.33	.000282475	2.614793	Prostaglandin-endoperoxide synthase 1 (Ptgs1)
Efemp2	-1.33	.000766188	2.238571	Epidermal growth factor-containing fibulin-like extracellular matrix protein 2 (Efemp2)
Ccdc155	-1.33	.003436977	1.880302	Coiled-coil domain containing 155 (Ccdc155)
Necap2	-1.33	$5.78 \times 10^{-5}$	3.463441	NECAP endocytosis associated 2 (Necap2)
4930447C04Rik	-1.33	$3.50 \times 10^{-5}$	3.386535	RIKEN cDNA 4930447C04 gene (4930447C04Rik)
Gm2990	-1.33	.009741717	1.185481	Predicted gene 2990 (Gm2990)
Ankub1	-1.33	.000281243	2.029349	Ankrin repeat and ubiquitin domain containing 1 (Ankub1)
Hmgn5	-1.33	.000458147	2.084144	High-mobility group nucleosome binding domain 5 (Hmgn5)
Rab32	-1.34	.024617533	0.646476	RAB32, member RAS oncogene family (Rab32)
Siglech	-1.34	.001310629	2.794549	Sialic acid binding Ig-like lectin H (Siglech)
Acss1	-1.34	$8.62 \times 10^{-6}$	4.531243	Acyl-CoA synthetase short-chain family member 1 (Acss1)
Gpnmb	-1.34	.001119119	2.765881	Glycoprotein (transmembrane) nmb (Gpnmb)
Dusp23	-1.34	.003714873	1.481088	Dual-specificity phosphatase 23 (Dusp23)
Stxbp3	-1.34	$1.19 \times 10^{-5}$	3.584292	Syntaxin binding protein 3 (Stxbp3)
Arhgef37	-1.34	.003398746	0.827707	Rho guanine nucleotide exchange factor (GEF) 37 (Arhgef37)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Stat6	-1.34	.00222539	1.887735	Signal transducer and activator of transcription 6 (Stat6)
Folh1	-1.34	.000439546	3.072827	Folate hydrolase 1 (Folh1)
Tcf7l1	-1.34	.001688666	1.71563	Transcription factor 7 like 1 (T cell-specific, HMG box) (Tcf7l1)
Lage3	-1.34	$3.19 \times 10^{-5}$	3.314088	L antigen family, member 3 (Lage3)
Ldlrap1	-1.34	.017206437	0.650118	Low-density lipoprotein receptor adaptor protein 1 (Ldlrap1)
Dapk2	-1.34	.027812722	0.653834	Death-associated protein kinase 2 (Dapk2)
Ptafr	-1.35	.00742593	1.02125	Platelet-activating factor receptor (Ptafr)
Mif4gd	-1.35	.000264674	2.247288	MIF4G domain containing (Mif4gd)
Dnajb13	-1.35	.00438234	0.987655	DnaJ heat shock protein family (Hsp40) member B13 (Dnajb13)
Abhd4	-1.35	$1.70 \times 10^{-6}$	5.322264	Abhydrolase domain containing 4 (Abhd4)
Prex1	-1.35	$2.19 \times 10^{-7}$	5.62714	Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1 (Prex1)
Tgfb1	-1.35	.018990524	0.444288	Transforming growth factor, beta 1 (Tgfb1)
Meig1	-1.35	.005503396	1.204329	Meiosis expressed gene 1 (Meig1)
Ttf2	-1.35	.012513063	0.747548	Transcription termination factor, RNA polymerase II (Ttf2)
Mmp2	-1.35	.004303565	1.38306	Matrix metallopeptidase 2 (Mmp2)
Gm28941	-1.35	.018680283	0.020033	Predicted gene (Gm28941)
Zfas1	-1.35	$1.55 \times 10^{-6}$	4.210731	Zinc finger, NFX1-type containing 1, antisense RNA 1 (Zfas1)
Acsf2	-1.35	.000296909	2.716402	Acyl-CoA synthetase family member 2 (Acsf2)
Sgpl1	-1.35	$4.91 \times 10^{-6}$	3.770929	Sphingosine phosphate lyase 1 (Sgpl1)
Pdgfrb	-1.36	.000101885	2.91282	Platelet derived growth factor receptor, beta polypeptide (Pdgfrb)
Anln	-1.36	.000146383	5.033587	Anillin, actin binding protein (Anln)
Lmtd1	-1.36	.043964816	-0.25349	Lamin tail domain containing 1 (Lmtd1)
Slc43a3	-1.36	.000518855	2.398469	Solute carrier family 43, member 3 (Slc43a3)
Pld1	-1.36	.000148712	3.057431	Phospholipase D1 (Pld1)
Casp8	-1.36	.044874908	1.248788	Caspase 8 (Casp8)
Cib1	-1.36	$9.08 \times 10^{-5}$	2.583014	Calcium and integrin binding 1 (calmyrin) (Cib1)
Rhog	-1.36	$7.09 \times 10^{-6}$	4.314896	Ras homolog family member G (Rhog)
Lhfpl1	-1.36	.008005735	1.836067	Lipoma HMGIC fusion partner-like 1 (Lhfpl1)
2310022B05Rik	-1.36	$2.94 \times 10^{-7}$	6.71281	RIKEN cDNA 2310022B05 gene (2310022B05Rik)
Lgals9	-1.36	.015972351	2.072865	Lectin, galactose binding, soluble 9 (Lgals9)
Acadl	-1.37	$6.80 \times 10^{-6}$	3.771726	Acyl-Coenzyme A dehydrogenase, long-chain (Acadl)
Pttg1ip	-1.37	$5.83 \times 10^{-7}$	5.348897	Pituitary tumor-transforming 1 interacting protein (Pttg1ip)
Sod3	-1.37	.001591042	2.556318	Superoxide dismutase 3, extracellular (Sod3)
Ift43	-1.37	$3.28 \times 10^{-5}$	2.83452	Intraflagellar transport 43 (Ift43)
Gstm1	-1.37	$8.73 \times 10^{-7}$	7.554045	Glutathione S-transferase, mu 1 (Gstm1)
P2rx7	-1.37	.000143643	2.562472	Purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7)
Ncf1	-1.37	.00483422	1.600633	Neutrophil cytosolic factor 1 (Ncf1)
Gjc3	-1.37	$3.15 \times 10^{-5}$	6.305602	Gap junction protein, gamma 3 (Gjc3)
Trim34a	-1.37	.013292882	0.479568	Tripartite motif-containing 34A (Trim34a)
Il10ra	-1.37	.03519008	1.175011	Interleukin 10 receptor, alpha (Il10ra)
Parp4	-1.37	$7.23 \times 10^{-5}$	2.944981	Poly(ADP-ribose) polymerase family, member 4 (Parp4)
Gm45552	-1.38	.006932158	0.367417	Predicted gene (Gm45552)
Lap3	-1.38	$7.58 \times 10^{-7}$	4.888293	Leucine aminopeptidase 3 (Lap3)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tjp2	-1.38	$2.09 \times 10^{-6}$	3.967861	Tight junction protein 2 (Tjp2)
Chil1	-1.38	$5.22 \times 10^{-5}$	2.650764	Chitinase-like 1 (Chil1)
Galnt6	-1.38	.000413421	3.597886	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (Galnt6)
Gm40578	-1.38	.011685617	0.368828	Predicted gene, 40578 (Gm40578)
Lrig1	-1.38	$9.28 \times 10^{-7}$	5.086225	Leucine-rich repeats and immunoglobulin-like domains 1 (Lrig1)
Dhrs3	-1.39	$5.79 \times 10^{-5}$	3.43863	Dehydrogenase/reductase (SDR family) member 3 (Dhrs3)
Tinagl1	-1.39	.023592968	-0.22512	Tubulointerstitial nephritis antigen-like 1 (Tinagl1)
Eci1	-1.39	$9.54 \times 10^{-6}$	3.02314	Enoyl-Coenzyme A delta isomerase 1 (Eci1)
Hmg20b	-1.39	.000800046	1.438421	High-mobility group 20B (Hmg20b)
Smyd1	-1.39	.000848083	1.999803	SET and MYND domain containing 1 (Smyd1)
Eya4	-1.39	.034545704	0.267291	EYA transcriptional coactivator and phosphatase 4 (Eya4)
Prkd1	-1.39	.000103447	2.702669	Protein kinase D1 (Prkd1)
Scml2	-1.39	.039883798	0.311357	Sex comb on midleg-like 2 (Scml2)
Slc7a7	-1.39	.005829219	1.13158	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7 (Slc7a7)
Pbxip1	-1.39	$9.39 \times 10^{-6}$	5.012332	Pre B cell leukemia transcription factor interacting protein 1 (Pbxip1)
Gm30238	-1.39	.000766422	1.581527	Predicted gene, 30238 (Gm30238)
Dock5	-1.39	.000262604	3.805104	Dedicator of cytokinesis 5 (Dock5)
Tst	-1.39	$1.97 \times 10^{-5}$	4.636992	Thiosulfate sulfurtransferase, mitochondrial (Tst)
Gm8451	-1.40	.006768763	0.024791	Predicted gene 8451 (Gm8451)
Tek	-1.40	.000183049	2.423851	Endothelial-specific receptor tyrosine kinase (Tek)
Axl	-1.40	$3.54 \times 10^{-7}$	4.789533	AXL receptor tyrosine kinase (Axl)
Adhfe1	-1.40	$2.14 \times 10^{-5}$	3.83685	Alcohol dehydrogenase, iron containing, 1 (Adhfe1)
Slc9a3r1	-1.40	$6.69 \times 10^{-6}$	4.518047	Solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 (Slc9a3r1)
F3	-1.40	$1.53 \times 10^{-6}$	4.066322	Coagulation factor III (F3)
Riiad1	-1.40	.000135596	1.995268	Regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1 (Riiad1)
Capn6	-1.40	.001693978	1.009957	Calpain 6 (Capn6)
Mro	-1.40	$6.64 \times 10^{-6}$	3.809738	Maestro (Mro)
Skap2	-1.40	$1.77 \times 10^{-5}$	3.077299	Src family-associated phosphoprotein 2 (Skap2)
Fermt3	-1.41	.01561507	0.444051	Fermitin family member 3 (Fermt3)
Abhd12b	-1.41	.007500187	1.464549	Abhydrolase domain containing 12B (Abhd12b)
Dnaic1	-1.41	$4.91 \times 10^{-5}$	2.688396	Dynein, axonemal, intermediate chain 1 (Dnaic1)
Adgb	-1.41	.002308912	1.323123	Androglobin (Adgb)
Enpp2	-1.41	$6.69 \times 10^{-6}$	6.989574	Ectonucleotide pyrophosphatase/phosphodiesterase 2 (Enpp2)
Tlr4	-1.41	.021115842	0.256607	Toll-like receptor 4 (Tlr4)
Ccdc60	-1.41	.014696318	0.778206	Coiled-coil domain containing 60 (Ccdc60)
Lama2	-1.42	.000281864	3.290524	Laminin, alpha 2 (Lama2)
Gm38534	-1.42	.004199058	1.966138	Predicted gene, 38534 (Gm38534)
Mlf1	-1.42	.002741921	1.647759	Myeloid leukemia factor 1 (Mlf1)
Swap70	-1.42	.003712311	1.387202	SWA-70 protein (Swap70)
Pla2g16	-1.42	$7.38 \times 10^{-6}$	5.53983	Phospholipase A2, group XVI (Pla2g16)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Cyth4	-1.42	.000541966	1.59539	Cytohesin 4 (Cyth4)
Mcrip2	-1.43	.002761074	1.147967	MAPK-regulated corepressor interacting protein 2 (Mcrip2)
Ccdc180	-1.43	.002939966	1.113061	Coiled-coil domain containing 180 (Ccdc180)
Cmklr1	-1.43	.018672717	1.355092	Chemokine-like receptor 1 (Cmklr1)
Fam114a1	-1.43	$9.26 \times 10^{-5}$	2.463574	Family with sequence similarity 114, member A1 (Fam114a1)
Nipal4	-1.43	.003540995	1.366539	NIPA-like domain containing 4 (Nipal4)
Gm28729	-1.43	.014409252	1.034236	Predicted gene 28729 (Gm28729)
9330160F10Rik	-1.43	.035457326	-0.20198	RIKEN cDNA 9330160F10 gene (9330160F10Rik)
Xdh	-1.43	.037256005	-0.01444	Xanthine dehydrogenase (Xdh)
Ctsz	-1.43	.00130488	3.409261	Cathepsin Z (Ctsz)
AC160637.1	-1.44	.013258903	-0.01741	-
Pacsin3	-1.44	$3.10 \times 10^{-5}$	2.700949	Protein kinase C and casein kinase substrate in neurons 3 (Pacsin3)
Ncf2	-1.44	.008270476	0.382622	Neutrophil cytosolic factor 2 (Ncf2)
Mmd2	-1.44	$1.64 \times 10^{-7}$	6.160072	Monocyte to macrophage differentiation-associated 2 (Mmd2)
2810468N07Rik	-1.44	$2.03 \times 10^{-6}$	3.780046	RIKEN cDNA 2810468N07 gene (2810468N07Rik)
Aif1l	-1.44	.000908224	2.379813	Allograft inflammatory factor 1-like (Aif1l)
Hepacam	-1.44	$1.60 \times 10^{-6}$	6.158098	Hepatocyte cell adhesion molecule (Hepacam)
Spa17	-1.44	.000161219	1.906076	Sperm autoantigenic protein 17 (Spa17)
Clec7a	-1.44	.039950816	0.419504	C-type lectin domain family 7, member a (Clec7a)
Selenbp1	-1.44	.000353493	1.833442	Selenium binding protein 1 (Selenbp1)
Uaca	-1.44	.000163926	2.797253	Uveal autoantigen with coiled-coil domains and ankyrin repeats (Uaca)
P3h2	-1.44	.001408207	0.972894	Prolyl 3-hydroxylase 2 (P3h2)
Drc7	-1.44	.000190641	1.894718	Dynein regulatory complex subunit 7 (Drc7)
Id2	-1.44	$2.05 \times 10^{-7}$	5.299077	Inhibitor of DNA binding 2 (Id2)
Gm5617	-1.44	$4.91 \times 10^{-5}$	2.539737	Predicted gene 5617 (Gm5617)
Smox	-1.45	$2.25 \times 10^{-5}$	4.147057	Spermine oxidase (Smox)
Cyp4f16	-1.45	.00643057	1.269148	Cytochrome P450, family 4, subfamily f, polypeptide 16 (Cyp4f16)
Bin2	-1.45	.023336107	1.211277	Bridging integrator 2 (Bin2)
4930593C16Rik	-1.45	.01926779	0.165292	RIKEN cDNA 4930593C16 gene (4930593C16Rik)
Pspn	-1.45	$1.51 \times 10^{-5}$	3.164797	Phosphoserine phosphatase (Pspn)
Lcp1	-1.46	.000396982	3.090569	Lymphocyte cytosolic protein 1 (Lcp1)
AC121997.2	-1.46	.041082914	0.981212	-
Fbxo2	-1.46	$5.68 \times 10^{-7}$	4.527276	F-box protein 2 (Fbxo2)
Gm20501	-1.46	.006565451	0.345826	Predicted gene 20501 (Gm20501)
Dnah6	-1.46	.000739731	3.382093	Dynein, axonemal, heavy chain 6 (Dnah6)
Nuf2	-1.46	$9.64 \times 10^{-5}$	1.992284	NUF2, NDC80 kinetochore complex component (Nuf2)
Firre	-1.46	.000145092	2.997797	Functional intergenic repeating RNA element (Firre)
Mmp14	-1.46	.000110599	3.390641	Matrix metallopeptidase 14 (membrane-inserted) (Mmp14)
Rps27rt	-1.46	.00907303	0.051268	Ribosomal protein S27, retrogene (Rps27rt)
Ly96	-1.46	.036867611	0.498798	Lymphocyte antigen 96 (Ly96)
Adgre1	-1.46	.000754786	1.51594	Adhesion G protein-coupled receptor E1 (Adgre1)
Gjb2	-1.47	.000538534	2.920153	Gap junction protein, beta 2 (Gjb2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tcn2	-1.47	$1.43 \times 10^{-5}$	3.350372	Transcobalamin 2 (Tcn2)
Rida	-1.47	$1.68 \times 10^{-5}$	4.438917	Reactive intermediate imine deaminase A homolog (Rida)
Rsrp1	-1.47	$2.12 \times 10^{-7}$	6.302967	Arginine-serine-rich protein 1 (Rsrp1)
Gm30731	-1.47	.006575911	0.863418	Predicted gene_30731 (Gm30731)
Ak7	-1.47	$9.08 \times 10^{-5}$	3.55344	Adenylate kinase 7 (Ak7)
Gm11478	-1.47	.002118505	0.607903	60S ribosomal protein L13a-like (Gm11478)
Lrrc23	-1.47	$4.82 \times 10^{-5}$	3.345398	Leucine-rich repeat containing 23 (Lrrc23)
Ccnb2	-1.48	.04218358	-0.35428	Cyclin B2 (Ccnb2)
Myl12a	-1.48	$4.56 \times 10^{-6}$	3.549985	Myosin, light chain 12A, regulatory, non-sarcomeric (Myl12a)
Gjb6	-1.48	$1.10 \times 10^{-6}$	6.184784	Gap junction protein, beta 6 (Gjb6)
Hadh	-1.48	$4.65 \times 10^{-5}$	3.373386	Hydroxyacyl-Coenzyme A dehydrogenase (Had)
C4b	-1.48	.009637513	3.441925	Complement component 4B (Chido blood group) (C4b)
Cyp4v3	-1.48	.000429552	2.421433	Cytochrome P450, family 4, subfamily v, polypeptide 3 (Cyp4v3)
Col27a1	-1.48	.019800604	0.611019	Collagen, type XXVII, alpha 1 (Col27a1)
Vav1	-1.48	.021295143	0.363808	Vav 1 oncogene (Vav1)
Slc14a1	-1.48	$1.25 \times 10^{-5}$	4.781116	Solute carrier family 14 (urea transporter), member 1 (Slc14a1)
Pm20d1	-1.48	.005280728	1.133294	Peptidase M20 domain containing 1 (Pm20d1)
Il33	-1.48	$3.15 \times 10^{-5}$	5.093789	Interleukin 33 (Il33)
Htr5b	-1.48	.002680017	5.118576	5-Hydroxytryptamine (serotonin) receptor 5B (Htr5b)
Gm10941	-1.48	.017669152	-0.23422	Predicted gene 10941 (Gm10941)
1700063D05Rik	-1.49	.015269086	0.136951	RIKEN cDNA 1700063D05 gene (1700063D05Rik)
Fkbp7	-1.49	.018724562	0.303922	FK506 binding protein 7 (Fkbp7)
H2-DMb1	-1.49	.036779758	0.011736	Histocompatibility 2, class II, locus Mb1 (H2-DMb1)
Tnfaip6	-1.49	.000266171	2.757342	Tumor necrosis factor alpha-induced protein 6 (Tnfaip6)
Ccdc146	-1.49	$7.72 \times 10^{-5}$	2.65406	Coiled-coil domain containing 146 (Ccdc146)
Jchain	-1.49	.034266137	0.009426	Immunoglobulin joining chain (Jchain)
Sla	-1.49	.001063084	0.848306	Src-like adaptor (Sla)
Hist2h2be	-1.49	$1.46 \times 10^{-5}$	3.652584	Histone cluster 2, H2be (Hist2h2be)
Rtl1	-1.49	.001371626	1.778547	Retrotransposon-like 1 (Rtl1)
Cdh5	-1.50	.000228378	2.532748	Cadherin 5 (Cdh5)
Col9a3	-1.50	.000684523	1.563886	Collagen, type IX, alpha 3 (Col9a3)
4930563E22Rik	-1.50	.006857215	0.775329	RIKEN cDNA 4930563E22 gene (4930563E22Rik)
Rras	-1.50	.000273634	2.064715	Related RAS viral (r-ras) oncogene (Rras)
Gadd45b	-1.50	.001543526	1.911254	Growth arrest and DNA-damage-inducible 45 beta (Gadd45b)
Vstm4	-1.50	.000506278	1.573794	V-set and transmembrane domain containing 4 (Vstm4)
Srebf1	-1.50	$6.21 \times 10^{-7}$	4.959446	Sterol regulatory element binding transcription factor 1 (Srebf1)
Tnfrsf18	-1.50	.001380989	1.290474	Tumor necrosis factor receptor superfamily, member 18 (Tnfrsf18)
Snhg15	-1.50	.007065505	0.287088	Small nucleolar RNA host gene 15 (Snhg15)
Ccdc189	-1.50	.003557218	1.157862	Coiled-coil domain containing 189 (Ccdc189)
Appl2	-1.50	$2.72 \times 10^{-6}$	4.828377	Adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2 (Appl2)
Cp	-1.50	$2.92 \times 10^{-6}$	3.336484	Ceruloplasmin (Cp)
Rab34	-1.51	.000246073	1.769783	RAB34, member RAS oncogene family (Rab34)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Calhm2	-1.51	.008016303	0.67204	Calcium homeostasis modulator 2 (Calhm2)
Slco2b1	-1.51	$7.68 \times 10^{-5}$	3.081781	Solute carrier organic anion transporter family, member 2b1 (Slco2b1)
Steap3	-1.51	.001016838	1.433418	STEAP family member 3 (Steap3)
Gja1	-1.51	$2.07 \times 10^{-6}$	6.701451	Gap junction protein, alpha 1 (Gja1)
Mobp	-1.51	$1.27 \times 10^{-5}$	7.956908	Myelin-associated oligodendrocytic basic protein (Mobp)
Ak9	-1.51	.002642234	1.029734	Adenylate kinase 9 (Ak9)
Lrrc18	-1.51	.013868542	0.589247	Leucine-rich repeat containing 18 (Lrrc18)
Rxfp2	-1.51	.007483776	0.479428	Relaxin/insulin-like family peptide receptor 2 (Rxfp2)
Ccdc78	-1.51	.009417996	0.619623	Coiled-coil domain containing 78 (Ccdc78)
Gm27202	-1.52	.017429344	0.624421	Predicted gene (Gm27202)
Cdh26	-1.52	.021141437	0.875714	Cadherin-like 26 (Cdh26)
Hapln2	-1.52	.000393804	2.235915	Hyaluronan and proteoglycan link protein 2 (Hapln2)
Spag5	-1.52	.000732723	1.308572	Sperm-associated antigen 5 (Spag5)
Parp12	-1.52	.006785903	2.428606	Poly(ADP-ribose) polymerase family, member 12 (Parp12)
Foxj1	-1.52	$8.61 \times 10^{-5}$	3.972678	Forkhead box J1 (Foxj1)
Pygm	-1.52	$3.07 \times 10^{-6}$	4.166787	Muscle glycogen phosphorylase (Pygm)
Mcam	-1.52	.001579887	2.427458	Melanoma cell adhesion molecule (Mcam)
1700055D18Rik	-1.52	.023297901	0.135207	RIKEN cDNA 1700055D18 gene (1700055D18Rik)
Atp13a5	-1.52	.000455215	1.918432	ATPase type 13A5 (Atp13a5)
Tmem220	-1.52	.014696318	0.238238	Transmembrane protein 220 (Tmem220)
Tnfaip2	-1.52	.000333777	1.775152	Tumor necrosis factor, alpha-induced protein 2 (Tnfaip2)
Fam183b	-1.52	.000196935	2.47199	Family with sequence similarity 183, member B (Fam183b)
Enpp1	-1.52	.000302481	2.539444	Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Enpp1)
Slc15a2	-1.53	.000165258	3.091365	Solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2 (Slc15a2)
Snhg11	-1.53	.000353493	7.8282	Small nucleolar RNA host gene 11 (Snhg11)
Emp3	-1.53	.006676307	0.442789	Epithelial membrane protein 3 (Emp3)
Dock1	-1.53	$1.17 \times 10^{-5}$	4.448128	Dedicator of cytokinesis 1 (Dock1)
Gatsl3	-1.53	.026781494	-0.22813	GATS protein-like 3 (Gatsl3)
Tlr13	-1.53	.014915092	1.236129	Toll-like receptor 13 (Tlr13)
Dhx58	-1.53	.04016627	-0.18403	DEXH (Asp-Glu-X-His) box polypeptide 58 (Dhx58)
Tlcd1	-1.54	$8.35 \times 10^{-6}$	3.587868	TLC domain containing 1 (Tlcd1)
Gli1	-1.54	.000661433	1.69155	GLI-Kruppel family member GLI1 (Gli1)
Erbb3	-1.54	$6.57 \times 10^{-5}$	2.959266	Erb-b2 receptor tyrosine kinase 3 (Erbb3)
Tekt1	-1.54	.00029787	1.572178	Tekton 1 (Tekt1)
Gm28424	-1.54	.002783625	2.035219	Predicted gene (Gm28424)
Foxb1	-1.54	.000756176	1.255901	Forkhead box B1 (Foxyb1)
Fblim1	-1.54	.013013877	1.070207	Filamin binding LIM protein 1 (Fblim1)
1810032O08Rik	-1.54	.005931612	-0.17641	RIKEN cDNA 1810032O08 gene (1810032O08Rik)
Cav1	-1.54	$1.20 \times 10^{-5}$	2.878065	Caveolin 1, caveolae protein (Cav1)
AI480526	-1.54	.008241829	0.230991	Expressed sequence AI480526 (AI480526)
Robo3	-1.54	$5.01 \times 10^{-5}$	2.90627	Roundabout guidance receptor 3 (Robo3)
Sardh	-1.55	.000353493	1.632956	Sarcosine dehydrogenase (Sardh)
Bcas1	-1.55	$2.26 \times 10^{-5}$	5.957158	Breast carcinoma amplified sequence 1 (Bcas1)
Cyp2j6	-1.55	$4.89 \times 10^{-7}$	4.183969	Cytochrome P450, family 2, subfamily j, polypeptide 6 (Cyp2j6)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Car5b	-1.55	.012860151	0.544803	Carbonic anhydrase 5b, mitochondrial (Car5b)
Mrc1	-1.55	.000932051	1.307069	Mannose receptor, C type 1 (Mrc1)
Kdr	-1.55	.00017657	2.326149	Kinase insert domain protein receptor (Kdr)
Ppp1r32	-1.55	.000115088	1.928675	Protein phosphatase 1, regulatory subunit 32 (Ppp1r32)
Armc4	-1.55	.021394404	0.445196	Armadillo repeat containing 4 (Armc4)
Arap3	-1.55	.005868129	0.288531	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 (Arap3)
Wsb1	-1.55	$2.91 \times 10^{-6}$	4.048311	WD repeat and SOCS box-containing 1 (Wsb1)
Gpr55	-1.55	.048280254	0.003131	G protein-coupled receptor 55 (Gpr55)
Car14	-1.56	.00124336	1.928691	Carbonic anhydrase 14 (Car14)
Gm35618	-1.56	.009758625	0.103519	Predicted gene, 35618 (Gm35618)
Cfp	-1.56	.005423168	0.544829	Complement factor properdin (Cfp)
Rbpms2	-1.56	.00053975	1.624301	RNA binding protein with multiple splicing 2 (Rbpms2)
Cfap52	-1.57	.000433349	1.431713	Cilia and flagella-associated protein 52 (Cfap52)
Gm26588	-1.57	.001364163	1.344046	Predicted gene, 26588 (Gm26588)
Itgb4	-1.57	.000504797	2.50243	Integrin beta 4 (Itgb4)
Naip2	-1.57	.044273397	0.327049	NLR family, apoptosis inhibitory protein 2 (Naip2)
A930004J17Rik	-1.57	.045820918	0.790915	RIKEN cDNA A930004J17 gene (A930004J17Rik)
Crnde	-1.57	.011444163	1.311599	Colorectal neoplasia differentially expressed (non-protein coding) (Crnde)
6820408C15Rik	-1.57	.008910629	0.799644	RIKEN cDNA 6820408C15 gene (6820408C15Rik)
Csf3r	-1.57	.000833749	1.972606	Colony stimulating factor 3 receptor (granulocyte) (Csf3r)
Suclg2	-1.57	$2.85 \times 10^{-5}$	3.309374	Succinate-Coenzyme A ligase, GDP-forming, beta subunit (Suclg2)
Arhgap25	-1.58	.0183383	0.265037	Rho GTPase activating protein 25 (Arhgap25)
Dnaic2	-1.58	.000813886	1.595223	Dynein, axonemal, intermediate chain 2 (Dnaic2)
Scara3	-1.58	.000314173	2.084317	Scavenger receptor class A, member 3 (Scara3)
Cfap65	-1.58	.000935174	2.714349	Cilia and flagella-associated protein 65 (Cfap65)
Adam32	-1.58	.01013132	-0.08731	A disintegrin and metalloproteinase domain 32 (Adam32)
Cfap161	-1.58	$2.83 \times 10^{-5}$	3.557184	Cilia and flagella-associated protein 161 (Cfap161)
Gm20554	-1.58	.007914675	0.614431	Predicted gene, 20554 (Gm20554)
Npepl1	-1.58	.000188244	2.413656	Aminopeptidase-like 1 (Npepl1)
9830144P21Rik	-1.58	.00768963	0.34146	RIKEN cDNA 9830144P21 gene (9830144P21Rik)
Rpl37rt	-1.59	.000870602	0.777031	Ribosomal protein L37, retrotransposed (Rpl37rt)
Cnn3	-1.59	$1.33 \times 10^{-6}$	4.502764	Calponin 3, acidic (Cnn3)
Gm13293	-1.59	.012691403	0.975319	Predicted gene 13293 (Gm13293)
Ccdc80	-1.59	.011978622	1.045757	Coiled-coil domain containing 80 (Ccdc80)
Mbp	-1.59	$2.79 \times 10^{-6}$	9.470224	Myelin basic protein (Mbp)
Nkx2-2	-1.59	.000508478	1.700561	NK2 homeobox 2 (Nkx2-2)
Tie1	-1.59	.008756877	0.385531	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (Tie1)
Rac2	-1.59	.030298047	1.067113	RAS-related C3 botulinum substrate 2 (Rac2)
Gm42664	-1.59	.020486611	0.186614	Predicted gene (Gm42664)
Prodh	-1.59	.000212799	2.218763	Proline dehydrogenase (Prodh)
Ly75	-1.59	.027258788	1.009157	Lymphocyte antigen 75 (Ly75)
Scrg1	-1.59	.00073809	2.814208	Scrapie responsive gene 1 (Scrg1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Fcor	-1.60	.001787266	0.642191	Foxo1 corepressor (Fcor)
Dthd1	-1.60	.005901502	1.94602	Death domain containing 1 (Dthd1)
Timp4	-1.60	$7.39 \times 10^{-6}$	4.384132	Tissue inhibitor of metalloproteinase 4 (Timp4)
Gm16861	-1.60	.007698901	0.173874	Predicted gene, 16861 (Gm16861)
Cd86	-1.60	.015676676	0.80163	CD86 antigen (Cd86)
Inppl1	-1.60	.000150122	3.15293	Inositol polyphosphate phosphatase-like 1 (Inppl1)
Gng8	-1.60	$3.01 \times 10^{-6}$	4.802463	Guanine nucleotide binding protein (G protein), gamma 8 (Gng8)
Heph	-1.60	.000188077	2.5001	Hephaestin (Heph)
Gm44800	-1.61	.046712854	-0.05125	Predicted gene (Gm44800)
Rhoc	-1.61	.000547863	1.422704	Ras homolog family member C (Rhoc)
Arap1	-1.61	$2.68 \times 10^{-5}$	2.467002	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 (Arap1)
A930017K11Rik	-1.61	.028359066	-0.18249	RIKEN cDNA A930017K11 gene (A930017K11Rik)
Serpind1	-1.61	.006060872	0.460962	Serine (or cysteine) peptidase inhibitor, clade D, member 1 (Serpind1)
Isoc2a	-1.61	.003740326	0.639465	Isochorismatase domain containing 2a (Isoc2a)
Aqp6	-1.61	.00296832	1.02764	Aquaporin 6 (Aqp6)
Emcn	-1.61	.000493717	1.295156	Endomucin (Emcn)
Lacc1	-1.61	.003513053	1.531364	Laccase (multicopper oxidoreductase) domain containing 1 (Lacc1)
1600020E01Rik	-1.61	.000441905	0.934824	RIKEN cDNA 1600020E01 gene (1600020E01Rik)
Pomc	-1.61	.007688337	-0.06049	Pro-opiomelanocortin-alpha (Pomc)
Flna	-1.61	$4.46 \times 10^{-5}$	2.518728	Filamin, alpha (Flna)
AC154683.1	-1.62	.000573743	2.202428	-
Efcab12	-1.62	.000693756	1.018516	EF-hand calcium binding domain 12 (Efcab12)
Ecm2	-1.62	$6.12 \times 10^{-5}$	2.388481	Extracellular matrix protein 2, female organ and adipocyte specific (Ecm2)
Aebp1	-1.62	$7.66 \times 10^{-5}$	3.253992	AE binding protein 1 (Aebp1)
Nxn	-1.62	$2.69 \times 10^{-5}$	2.530431	Nucleoredoxin (Nxn)
Meg3	-1.62	$3.61 \times 10^{-5}$	8.232292	Maternally expressed 3 (Meg3)
Tnfrsf13b	-1.62	.010962329	0.295921	Tumor necrosis factor receptor superfamily, member 13b (Tnfrsf13b)
Zfyve21	-1.62	$1.53 \times 10^{-5}$	2.533566	Zinc finger, FYVE domain containing 21 (Zfyve21)
Wnt11	-1.62	.012384396	0.074183	Wingless-type MMTV integration site family, member 11 (Wnt11)
Gm10421	-1.62	.000336151	2.356391	Predicted gene 10421 (Gm10421)
Enkur	-1.62	$7.44 \times 10^{-5}$	2.337315	Enkurin, TRPC channel interacting protein (Enkur)
Mir124a-1hg	-1.62	$5.34 \times 10^{-5}$	5.188186	Mir124-1 host gene (non-protein coding) (Mir124a-1hg)
Copz2	-1.63	.00040773	2.246581	Coatomer protein complex, subunit zeta 2 (Copz2)
Psat1	-1.63	$4.18 \times 10^{-7}$	5.681399	Phosphoserine aminotransferase 1 (Psat1)
Hp	-1.63	.047425746	-0.14851	Haptoglobin (Hp)
Adamtsl4	-1.63	$1.77 \times 10^{-5}$	2.229865	ADAMTS-like 4 (Adamtsl4)
Miat	-1.63	$1.70 \times 10^{-5}$	4.315439	Myocardial infarction-associated transcript (non-protein coding) (Miat)
Gm36908	-1.63	.012195178	1.58531	Predicted gene, 36908 (Gm36908)
Car2	-1.63	$9.40 \times 10^{-7}$	6.557535	Carbonic anhydrase 2 (Car2)
Rlbp1	-1.63	.002885699	1.462093	Retinaldehyde binding protein 1 (Rlbp1)
Serpingle1	-1.63	.023764968	2.609958	Serine (or cysteine) peptidase inhibitor, clade G, member 1 (Serpingle1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Sypl2	-1.64	.014910313	-0.25976	Synaptophysin-like 2 (Sypl2)
Tpm2	-1.64	.000426979	1.506816	Tropomyosin 2, beta (Tpm2)
Ccr5	-1.64	.000192636	2.068851	Chemokine (C-C motif) receptor 5 (Ccr5)
Csrp2	-1.64	.002029242	1.01531	Cysteine and glycine-rich protein 2 (Csrp2)
Gm47260	-1.64	.014794905	-0.24866	Predicted gene (Gm47260)
Zfp36	-1.64	.000758739	1.828875	Zinc finger protein 36 (Zfp36)
Mag	-1.64	$2.68 \times 10^{-6}$	5.049395	Myelin-associated glycoprotein (Mag)
Gpt	-1.64	.000361722	1.018836	Glutamic pyruvic transaminase, soluble (Gpt)
Caskin2	-1.65	$4.76 \times 10^{-5}$	2.871049	CASK-interacting protein 2 (Caskin2)
Nr1h3	-1.65	.002709218	0.279177	Nuclear receptor subfamily 1, group H, member 3 (Nr1h3)
Rd3	-1.65	.029832798	0.700243	Retinal degeneration 3 (Rd3)
Gm9958	-1.65	.000879683	0.803511	Predicted gene 9958 (Gm9958)
Art3	-1.65	.0008613	0.756292	ADP-ribosyltransferase 3 (Art3)
Mapk15	-1.65	.009966245	0.170722	Mitogen-activated protein kinase 15 (Mapk15)
Cxcr4	-1.65	.01091675	0.172224	Chemokine (C-X-C motif) receptor 4 (Cxcr4)
Ppfibp2	-1.65	$6.41 \times 10^{-5}$	2.426437	PTPRF interacting protein, binding protein 2 (liprin beta 2) (Ppfibp2)
Itgam	-1.66	$8.37 \times 10^{-5}$	3.32242	Integrin alpha M (Itgam)
B2m	-1.66	.006362253	7.486583	Beta-2 microglobulin (B2m)
Blnk	-1.66	.005754685	0.503826	B cell linker (Blnk)
Tnfaip8	-1.66	$7.21 \times 10^{-6}$	2.7278	Tumor necrosis factor, alpha-induced protein 8 (Tnfaip8)
Nek8	-1.66	.016071684	-0.13259	NIMA (never in mitosis gene a)-related expressed kinase 8 (Nek8)
Inpp5d	-1.66	.001783142	1.900644	Inositol polyphosphate-5-phosphatase D (Inpp5d)
Tifab	-1.66	.0077379	0.442907	TRAF-interacting protein with forkhead-associated domain, family member B (Tifab)
Gm43980	-1.67	.046743784	-0.23207	Predicted gene (Gm43980)
Plxnb3	-1.67	$1.72 \times 10^{-5}$	3.195993	Plexin B3 (Plxnb3)
A330076C08Rik	-1.67	.004129757	1.714381	RIKEN cDNA A330076C08 gene (A330076C08Rik)
Psmc3ip	-1.67	.001053204	0.810739	Proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein (Psmc3ip)
Fgfr3	-1.67	$8.50 \times 10^{-7}$	5.165772	Fibroblast growth factor receptor 3 (Fgfr3)
Traf1	-1.67	.002814285	0.786171	TNF receptor-associated factor 1 (Traf1)
Efhb	-1.67	.006250277	0.290435	EF hand domain family, member B (Efhb)
Gldc	-1.67	.004684401	1.149229	Glycine decarboxylase (Gldc)
Lsp1	-1.67	.000353493	1.743835	Lymphocyte specific 1 (Lsp1)
Snx22	-1.68	.00521794	0.925216	Sorting nexin 22 (Snx22)
Gm37829	-1.68	.001147291	0.381735	Predicted gene (Gm37829)
Gm20045	-1.68	.001427513	1.871184	Predicted gene, 20045 (Gm20045)
Nme9	-1.68	.004360612	0.126143	NME/NM23 family member 9 (Nme9)
Gpd1	-1.68	$9.10 \times 10^{-5}$	4.515189	Glycerol-3-phosphate dehydrogenase 1 (soluble) (Gpd1)
Spag8	-1.68	.00171823	0.742979	Sperm-associated antigen 8 (Spag8)
Ttyh2	-1.68	$6.30 \times 10^{-7}$	5.205867	Tweety family member 2 (Ttyh2)
Gm16487	-1.68	.006396682	-0.08828	Predicted gene 16487 (Gm16487)
Dnali1	-1.69	$1.48 \times 10^{-5}$	2.699567	Dynein, axonemal, light intermediate polypeptide 1 (Dnali1)
Dusp10	-1.69	.000361722	1.912183	Dual-specificity phosphatase 10 (Dusp10)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Avil	-1.69	.009816926	0.484871	Advillin (Avil)
Pdzph1	-1.69	.001033535	0.957542	PDZ and pleckstrin homology domains 1 (Pdzph1)
1700016K19Rik	-1.69	.000169557	2.742134	RIKEN cDNA 1700016K19 gene (1700016K19Rik)
AC154640.4	-1.69	.003869026	0.2316	-
Inf2	-1.69	$4.33 \times 10^{-5}$	3.371086	Inverted formin, FH2 and WH2 domain containing (Inf2)
Lamb2	-1.69	.000231785	2.610556	Laminin, beta 2 (Lamb2)
Col11a2	-1.69	.013508814	-0.27006	Collagen, type XI, alpha 2 (Col11a2)
Serinc2	-1.69	.001369036	0.303092	Serine incorporator 2 (Serinc2)
Pih1d2	-1.69	.001355794	0.801559	PIH1 domain containing 2 (Pih1d2)
Itgb5	-1.70	$4.01 \times 10^{-6}$	3.679778	Integrin beta 5 (Itgb5)
Gpr34	-1.70	.002759123	0.942269	G protein-coupled receptor 34 (Gpr34)
Ucp2	-1.70	$1.86 \times 10^{-6}$	5.177163	Uncoupling protein 2 (mitochondrial, proton carrier) (Ucp2)
Hist1h2ac	-1.70	.006863392	-0.07226	Histone cluster 1, H2ac (Hist1h2ac)
Csf2rb	-1.70	.049261866	0.890797	Colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (Csf2rb)
Efcab11	-1.70	.007689731	-0.09218	EF-hand calcium binding domain 11 (Efcab11)
Fcrls	-1.70	$2.26 \times 10^{-6}$	3.045985	Fc receptor-like S, scavenger receptor (Fcrls)
Tmem51	-1.70	.0010881	0.956865	Transmembrane protein 51 (Tmem51)
Spidr	-1.70	.002343991	0.63471	Scaffolding protein involved in DNA repair (Spidr)
Fcgr2b	-1.70	.001929587	2.363301	Fc receptor, IgG, low affinity IIb (Fcgr2b)
Marchf10	-1.71	.021759875	-0.38729	Membrane-associated ring-CH-type finger 10 (Marchf10)
Rin3	-1.71	.006113228	0.153509	Ras and Rab interactor 3 (Rin3)
Itga11	-1.71	.006520867	0.032602	Integrin alpha 11 (Itga11)
0610040J01Rik	-1.71	.015385824	-0.22102	RIKEN cDNA 0610040J01 gene (0610040J01Rik)
Ephb4	-1.71	.030357657	0.258712	Eph receptor B4 (Ephb4)
Fgfrl1	-1.72	$3.93 \times 10^{-5}$	2.519421	Fibroblast growth factor receptor-like 1 (Fgfrl1)
S1pr1	-1.72	$2.06 \times 10^{-7}$	5.542674	Sphingosine-1-phosphate receptor 1 (S1pr1)
Best3	-1.72	.000848545	0.879045	Bestrophin 3 (Best3)
Ccdc170	-1.72	.002151061	1.853048	Coiled-coil domain containing 170 (Ccdc170)
Baz1a	-1.72	.032046772	0.594979	Bromodomain adjacent to zinc finger domain 1A (Baz1a)
Hist1h1c	-1.72	$4.01 \times 10^{-5}$	2.941175	Histone cluster 1, H1c (Hist1h1c)
Gpc4	-1.72	.004221097	0.655829	Glycan 4 (Gpc4)
Tcp11	-1.72	.037789522	-0.09929	T-complex protein 11 (Tcp11)
AW047730	-1.73	$4.80 \times 10^{-5}$	1.636783	Expressed sequence AW047730 (AW047730)
Cyr61	-1.73	.014417094	0.51186	Cysteine-rich protein 61 (Cyr61)
Slc6a20a	-1.73	.001367435	0.90829	Solute carrier family 6 (neurotransmitter transporter), member 20A (Slc6a20a)
Hfe	-1.73	.000622189	1.552588	Hemochromatosis (Hfe)
Cfap43	-1.73	$8.51 \times 10^{-5}$	2.525039	Cilia and flagella-associated protein 43 (Cfap43)
Slc6a11	-1.73	$1.94 \times 10^{-7}$	8.876865	Solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (Slc6a11)
Gimap1	-1.73	.012104473	-0.16657	GTPase, IMAP family member 1 (Gimap1)
Abcb1a	-1.73	$1.57 \times 10^{-5}$	2.586089	ATP-binding cassette, sub-family B (MDR/TAP), member 1A (Abcb1a)
Slc39a8	-1.73	$8.76 \times 10^{-5}$	1.506431	Solute carrier family 39 (metal ion transporter), member 8 (Slc39a8)
Gjc2	-1.73	.000176584	2.009373	Gap junction protein, gamma 2 (Gjc2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tyrp1	-1.74	.000888982	2.277092	Tyrosinase-related protein 1 (Tyrp1)
Olfr287	-1.74	.000196935	1.77929	Olfactory receptor 287 (Olfr287)
Sult1a1	-1.74	.009095038	0.662955	Sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1)
Sox8	-1.74	$2.19 \times 10^{-6}$	4.643643	SRY (sex determining region Y)-box 8 (Sox8)
Metrn	-1.74	.002547353	0.106074	Meteorin, glial cell differentiation regulator (Metrn)
Slc18a3	-1.74	.000437718	3.357415	Solute carrier family 18 (vesicular monoamine), member 3 (Slc18a3)
Hc	-1.74	.000295715	1.212564	Hemolytic complement (Hc)
Ccdc13	-1.74	.000922193	0.975706	Coiled-coil domain containing 13 (Ccdc13)
Mal	-1.74	$1.91 \times 10^{-6}$	7.246285	Myelin and lymphocyte protein, T cell differentiation protein (Mal)
2810405F17Rik	-1.74	$3.28 \times 10^{-5}$	1.966444	RIKEN cDNA 2810405F17 gene (2810405F17Rik)
Islr	-1.74	.00633143	1.093069	Immunoglobulin superfamily containing leucine-rich repeat (Islr)
Abhd11os	-1.74	.003944624	0.222163	Abhydrolase domain containing 11, opposite strand (Abhd11os)
Dbx2	-1.74	$1.17 \times 10^{-5}$	2.894525	Developing brain homeobox 2 (Dbx2)
Tmbim1	-1.75	$1.09 \times 10^{-6}$	5.214548	Transmembrane BAX inhibitor motif containing 1 (Tmbim1)
5330413P13Rik	-1.75	.000757667	0.786697	RIKEN cDNA 5330413P13 gene (5330413P13Rik)
Rspn1	-1.75	$7.14 \times 10^{-6}$	3.911349	Radial spoke head 1 homolog (Chlamydomonas) (Rspn1)
I830077J02Rik	-1.75	.007273724	0.547545	RIKEN cDNA I830077J02 gene (I830077J02Rik)
Cavin1	-1.75	.000101856	2.037385	Caveolae-associated protein 1 (Calvin1)
Fcgtr	-1.75	.000676472	1.513949	Fc receptor, IgG, alpha chain transporter (Fcgrt)
Slc1a3	-1.75	$9.51 \times 10^{-8}$	7.783251	Solute carrier family 1 (glial high affinity glutamate transporter), member 3 (Slc1a3)
Cd164l2	-1.75	.000920406	1.404084	CD164 sialomucin-like 2 (Cd164l2)
Hmgcs2	-1.76	.002252377	1.157443	3-Hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2)
Htra3	-1.76	.001513104	0.706217	HtrA serine peptidase 3 (Htra3)
Col16a1	-1.76	.021949716	-0.19597	Collagen, type XVI, alpha 1 (Col16a1)
Cfap206	-1.76	.000554563	1.613459	Cilia and flagella-associated protein 206 (Cfap206)
Smim5	-1.76	.003935037	0.149767	Small integral membrane protein 5 (Smim5)
Fa2h	-1.76	$8.53 \times 10^{-6}$	5.714753	Fatty acid 2-hydroxylase (Fa2h)
Wdr49	-1.76	.006494042	0.503643	WD repeat domain 49 (Wdr49)
Dmpk	-1.76	.004478339	0.473583	Dystrophia myotonica-protein kinase (Dmpk)
Rpl30-ps1	-1.76	.007290272	-0.29296	Ribosomal protein L30, pseudogene 1 (Rpl30-ps1)
Pyroxd2	-1.77	.005641798	0.129902	Pyridine nucleotide-disulphide oxidoreductase domain 2 (Pyroxd2)
Uox	-1.77	.000308983	1.238275	Urate oxidase (Uox)
Cyp2d22	-1.77	$1.32 \times 10^{-5}$	3.472993	Cytochrome P450, family 2, subfamily d, polypeptide 22 (Cyp2d22)
Havcr2	-1.77	.000109206	2.138031	Hepatitis A virus cellular receptor 2 (Havcr2)
Gm11992	-1.77	.000282767	1.510296	Predicted gene 11992 (Gm11992)
Cryzl2	-1.77	.000520635	1.941624	Crystallin Zeta Like 2, Pseudogene (Cryzl2)
Mfge8	-1.78	$2.79 \times 10^{-6}$	3.622042	Milk fat globule-EGF factor 8 protein (Mfge8)
Eng	-1.78	.000109385	2.408912	Endoglin (Eng)
Naprt	-1.78	.002541825	0.329836	Nicotinate phosphoribosyltransferase (Naprt)
Eva1a	-1.78	.00017897	1.923803	Eva-1 homolog A ( <i>C. elegans</i> ) (Eva1a)
Glipr2	-1.78	$7.23 \times 10^{-5}$	1.807791	GLI pathogenesis-related 2 (Glipr2)
Cyp4f13	-1.78	.00012238	1.466176	cytochrome P450, family 4, subfamily f, polypeptide 13 (Cyp4f13)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Pabpn1	-1.79	.006450368	-0.20154	Poly(A) binding protein, nuclear 1 (Pabpn1)
Sfrp5	-1.79	.000274845	1.467786	Secreted frizzled-related sequence protein 5 (Sfrp5)
Bcan	-1.79	$1.33 \times 10^{-6}$	5.233517	Brevican (Bcan)
Atp6v0e	-1.79	$9.14 \times 10^{-6}$	3.095946	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit E (Atp6v0e)
Lims2	-1.80	$4.40 \times 10^{-6}$	2.9375	LIM and senescent cell antigen like domains 2 (Lims2)
Pantr1	-1.80	.0003803	1.382462	POU domain, class 3, transcription factor 3 adjacent noncoding transcript 1 (Pantr1)
Selenop	-1.80	$1.45 \times 10^{-7}$	7.517814	Selenoprotein P (Selenop)
2410004P03Rik	-1.80	$7.44 \times 10^{-5}$	3.756506	RIKEN cDNA 2410004P03 gene (2410004P03Rik)
Vim	-1.80	$5.25 \times 10^{-6}$	4.320862	Vimentin (Vim)
Lrrc74b	-1.80	.000168578	2.256361	Leucine-rich repeat containing 74B (Lrrc74b)
Nnat	-1.80	$7.40 \times 10^{-8}$	8.493392	Neuronatin (Nnat)
Fkbp10	-1.80	.000802855	1.544891	FK506 binding protein 10 (Fkbp10)
Rdh5	-1.80	.000163613	1.447545	Retinol dehydrogenase 5 (Rdh5)
Cd14	-1.81	.003285454	0.515404	CD14 antigen (Cd14)
Txnip	-1.81	$3.63 \times 10^{-5}$	2.771196	Thioredoxin interacting protein (Txnip)
Slc8b1	-1.81	.002736414	0.868784	Solute carrier family 8 (sodium/lithium/calcium exchanger), member B1 (Slc8b1)
4833427G06Rik	-1.81	.018679935	-0.15925	RIKEN cDNA 4833427G06 gene (4833427G06Rik)
Ceacam1	-1.82	.004846565	0.885231	Carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1)
1110017D15Rik	-1.82	$2.30 \times 10^{-5}$	1.98939	RIKEN cDNA 1110017D15 gene (1110017D15Rik)
Prss23	-1.83	.025260259	-0.14147	Protease, serine 23 (Prss23)
Syngt2	-1.83	$6.18 \times 10^{-5}$	1.995379	Synaptogyrin 2 (Syngt2)
Tmem119	-1.83	.000138809	3.284763	Transmembrane protein 119 (Tmem119)
Spag16	-1.83	.000107991	1.90364	Sperm-associated antigen 16 (Spag16)
Ttc25	-1.83	.004053896	0.244375	Tetratricopeptide repeat domain 25 (Ttc25)
Serpina3n	-1.83	.000184233	5.081741	Serine (or cysteine) peptidase inhibitor, clade A, member 3N (Serpina3n)
Gm14303	-1.83	$1.21 \times 10^{-5}$	2.459829	Ribosomal protein S29 pseudogene (Gm14303)
Cfap126	-1.83	$6.87 \times 10^{-5}$	2.570458	Cilia and flagella-associated protein 126 (Cfap126)
Cldn19	-1.84	.0001508	1.622941	Claudin 19 (Cldn19)
mt-Co1	-1.84	$1.78 \times 10^{-6}$	14.19352	Mitochondrially encoded cytochrome C oxidase I (mt-Co1)
6720427I07Rik	-1.84	.00037591	1.559681	RIKEN cDNA 6720427I07 gene (6720427I07Rik)
Cd53	-1.84	$6.73 \times 10^{-5}$	2.986068	CD53 antigen (Cd53)
Cd68	-1.84	$5.32 \times 10^{-6}$	2.865541	CD68 antigen (Cd68)
Vsir	-1.84	$6.14 \times 10^{-6}$	2.701666	V-set immunoregulatory receptor (Vsir)
Slc22a8	-1.84	$3.32 \times 10^{-5}$	2.789401	Solute carrier family 22 (organic anion transporter), member 8 (Slc22a8)
Rgcc	-1.85	.000532111	1.713011	Regulator of cell cycle (Rgcc)
C130023A14Rik	-1.85	.006264438	0.686219	RIKEN cDNA C130023A14 gene (C130023A14Rik)
Tmem204	-1.85	.000330226	1.219531	Transmembrane protein 204 (Tmem204)
Ptpn6	-1.85	.004104083	0.409271	Protein tyrosine phosphatase, non-receptor type 6 (Ptpn6)
Plp1	-1.85	$2.69 \times 10^{-6}$	9.24293	Proteolipid protein (myelin) 1 (Plp1)
Togaram2	-1.85	.007998548	0.342621	TOG Array Regulator Of Axonemal Microtubules 2 (Togaram2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Aldoc	-1.85	$6.46 \times 10^{-9}$	8.630132	Aldolase C, fructose-bisphosphate (Aldoc)
Ltbr	-1.85	.000634378	1.093577	Lymphotoxin B receptor (Ltbr)
Cnmd	-1.85	.002779435	1.634655	Chondromodulin (Cnmd)
Mog	-1.85	$3.82 \times 10^{-6}$	4.4984	Myelin oligodendrocyte glycoprotein (Mog)
Ms4a6b	-1.86	.049045741	-0.27241	Membrane-spanning 4-domains, subfamily A, member 6B (Ms4a6b)
Paqr5	-1.86	.000322361	1.164568	Progestin and adipoQ receptor family member V (Paqr5)
P2ry12	-1.86	$3.93 \times 10^{-7}$	3.672857	Purinergic receptor P2Y, G-protein coupled 12 (P2ry12)
Csf1r	-1.87	$1.75 \times 10^{-6}$	4.836905	Colony stimulating factor 1 receptor (Csf1r)
Sgk2	-1.87	.008773744	-0.12086	Serum/glucocorticoid-regulated kinase 2 (Sgk2)
Ect2l	-1.87	.006279018	-0.16173	Epithelial cell transforming sequence 2 oncogene-like (Ect2l)
Apobec3	-1.87	.021264452	1.088735	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 (Apobec3)
Esam	-1.87	.00067822	1.238903	Endothelial cell-specific adhesion molecule (Esam)
4930506C21Rik	-1.87	.002771411	-0.11277	RIKEN cDNA 4930506C21 gene (4930506C21Rik)
Fam166b	-1.87	.001027956	0.856944	Family with sequence similarity 166, member B (Fam166b)
A2m	-1.88	$1.06 \times 10^{-6}$	3.769972	Alpha-2-macroglobulin (A2m)
Olig2	-1.88	$8.18 \times 10^{-6}$	3.891852	Oligodendrocyte transcription factor 2 (Olig2)
Bst2	-1.88	.048542635	1.903151	Bone marrow stromal cell antigen 2 (Bst2)
Abhd3	-1.88	$1.59 \times 10^{-8}$	5.079703	Abhydrolase domain containing 3 (Abhd3)
A230009B12Rik	-1.88	.004302431	-0.03696	RIKEN cDNA A230009B12 gene (A230009B12Rik)
Npl	-1.88	.000219923	1.250911	N-acetylneuraminate pyruvate lyase (Npl)
Col11a1	-1.88	.012607818	-0.11904	Collagen, type XI, alpha 1 (Col11a1)
Odf3b	-1.88	$6.76 \times 10^{-6}$	2.20151	Outer dense fiber of sperm tails 3B (Odf3b)
Wdr63	-1.89	.000383762	0.900809	WD repeat domain 63 (Wdr63)
D730003I15Rik	-1.89	.000929322	1.277536	RIKEN cDNA D730003I15 gene (D730003I15Rik)
Car13	-1.89	.00098461	-0.05841	Carbonic anhydrase 13 (Car13)
Atp1a2	-1.89	$1.03 \times 10^{-8}$	8.944492	ATPase, Na+/K+ transporting, alpha 2 polypeptide (Atp1a2)
Myo1f	-1.90	.001315762	0.935222	Myosin IF (Myo1f)
Hhatl	-1.90	.000100835	1.532608	Hedgehog acyltransferase-like (Hhatl)
Parvg	-1.90	.000433349	0.729999	Parvin, gamma (Parvg)
Msx1	-1.90	.001273663	0.602755	Msh homeobox 1 (Msx1)
5730559C18Rik	-1.90	.016787428	0.779935	RIKEN cDNA 5730559C18 gene (5730559C18Rik)
Plekhb1	-1.90	$3.12 \times 10^{-7}$	7.428643	Pleckstrin homology domain containing, family B (ejectins) member 1 (Plekhb1)
Slc13a5	-1.90	$1.33 \times 10^{-5}$	2.883403	Solute carrier family 13 (sodium-dependent citrate transporter), member 5 (Slc13a5)
Cd300a	-1.91	.002391643	0.038774	CD300A molecule (Cd300a)
Slc25a18	-1.91	$5.39 \times 10^{-7}$	5.092737	Solute carrier family 25 (mitochondrial carrier), member 18 (Slc25a18)
Pltp	-1.91	$2.03 \times 10^{-6}$	4.574219	Phospholipid transfer protein (Pltp)
Cxcl14	-1.91	$6.92 \times 10^{-7}$	3.402367	Chemokine (C-X-C motif) ligand 14 (Cxcl14)
Stra6	-1.91	.005130027	0.562037	Stimulated by retinoic acid gene 6 (Stra6)
Car9	-1.91	.001145146	0.769785	Carbonic anhydrase 9 (Car9)
2010001K21Rik	-1.92	.00046524	0.91636	RIKEN cDNA 2010001K21 gene (2010001K21Rik)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Arhgap30	-1.92	.013220354	0.616513	Rho GTPase activating protein 30 (Arhgap30)
Lfng	-1.92	$3.16 \times 10^{-5}$	2.541206	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase (Lfng)
Ndrg2	-1.92	$2.93 \times 10^{-10}$	9.398886	N-myc downstream-regulated gene 2 (Ndrg2)
Chat	-1.92	.000127616	2.727393	Choline acetyltransferase (Chat)
Neat1	-1.92	$6.44 \times 10^{-7}$	5.320716	Nuclear paraspeckle assembly transcript 1 (non-protein coding) (Neat1)
Litaf	-1.92	$1.36 \times 10^{-5}$	3.726957	LPS-induced TN factor (Litaf)
Gm17750	-1.92	.00044139	0.567423	Predicted gene, 17750 (Gm17750)
A330041J22Rik	-1.92	.015558377	-0.02695	RIKEN cDNA A330041J22 gene (A330041J22Rik)
4930550C14Rik	-1.93	.006660268	-0.04719	RIKEN cDNA 4930550C14 gene (4930550C14Rik)
Cx3cr1	-1.93	$9.66 \times 10^{-7}$	3.649944	Chemokine (C-X3-C motif) receptor 1 (Cx3cr1)
Sox10	-1.93	$7.14 \times 10^{-6}$	4.213018	SRY (sex determining region Y)-box 10 (Sox10)
Sncg	-1.93	$8.71 \times 10^{-5}$	3.151988	Synuclein, gamma (Sncg)
Aspa	-1.94	$3.85 \times 10^{-6}$	4.440446	Aspartoacylase (Aspa)
Gm44430	-1.94	.006070659	-0.27533	Predicted gene (Gm44430)
Cabcoco1	-1.94	.000163008	1.009936	Ciliary-associated calcium binding coiled-coil 1 (Cabcoco1)
Dnase1l1	-1.94	.005675655	0.370842	Deoxyribonuclease 1-like 1 (Dnase1l1)
H2-Aa	-1.95	.040196696	3.5945	Histocompatibility 2, class II antigen A, alpha (H2-Aa)
Pvalb	-1.95	.000175375	1.430208	Parvalbumin (Pvalb)
Clic6	-1.95	$4.29 \times 10^{-5}$	2.641829	Chloride intracellular channel 6 (Clic6)
Ppp1r1b	-1.95	$3.20 \times 10^{-5}$	3.882371	Protein phosphatase 1, regulatory (inhibitor) subunit 1B (Ppp1r1b)
Itgb2	-1.95	.000300134	1.618245	Integrin beta 2 (Itgb2)
H2-K1	-1.95	.021173316	4.5691	Histocompatibility 2, K1, K region (H2-K1)
Celsr1	-1.96	.001189468	1.400365	Cadherin, EGF LAG seven-pass G-type receptor 1 (Celsr1)
Afaf1l2	-1.96	$5.99 \times 10^{-5}$	2.072917	Actin filament-associated protein 1-like 2 (Afaf1l2)
Itih3	-1.96	$1.11 \times 10^{-7}$	5.731097	Inter-alpha trypsin inhibitor, heavy chain 3 (Itih3)
Ttll8	-1.96	.004838896	-0.3194	Tubulin tyrosine ligase-like family, member 8 (Ttll8)
4930519F16Rik	-1.96	.007795216	-0.29348	RIKEN cDNA 4930519F16 gene (4930519F16Rik)
Slc35f2	-1.96	.007477728	0.390166	Solute carrier family 35, member F2 (Slc35f2)
Cd38	-1.97	$6.83 \times 10^{-5}$	2.686635	CD38 antigen (Cd38)
Sparcl1	-1.97	$2.93 \times 10^{-10}$	9.580819	SPARC-like 1 (Sparcl1)
Laptm5	-1.97	$3.07 \times 10^{-6}$	4.657288	Lysosomal-associated protein transmembrane 5 (Laptm5)
1700029J07Rik	-1.97	.002680338	1.465959	RIKEN cDNA 1700029J07 gene (1700029J07Rik)
Tmem100	-1.97	$1.24 \times 10^{-5}$	2.279007	Transmembrane protein 100 (Tmem100)
Lpcat2	-1.97	.000270658	2.731381	Lysophosphatidylcholine acyltransferase 2 (Lpcat2)
Cyp2j12	-1.97	.000797947	0.426562	Cytochrome P450, family 2, subfamily j, polypeptide 12 (Cyp2j12)
Slc39a12	-1.98	$6.57 \times 10^{-7}$	4.353183	Solute carrier family 39 (zinc transporter), member 12 (Slc39a12)
Zmynd12	-1.98	.041288677	-0.49462	Zinc finger, MYND domain containing 12 (Zmynd12)
Gm3764	-1.98	$1.28 \times 10^{-5}$	3.120007	Predicted gene 3764 (Gm3764)
Myoc	-1.98	.000358244	1.254251	Myocilin (Myoc)
Tekt4	-1.98	.008219937	0.613013	Tektin 4 (Tekt4)
Ccdc121	-1.98	.001179527	1.261191	Coiled-coil domain containing 121 (Ccdc121)
Atoh8	-1.98	.011654393	-0.40334	Atonal bHLH transcription factor 8 (Atoh8)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Atp13a4	-1.98	$9.18 \times 10^{-6}$	3.282583	ATPase type 13A4 (Atp13a4)
Elovl1	-1.98	.000153918	2.487994	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (Elovl1)
Tagln2	-1.99	.000131066	3.785068	Transgelin 2 (Tagln2)
Clu	-1.99	$5.05 \times 10^{-9}$	8.148085	Clusterin (Clu)
Wnt7a	-1.99	$5.13 \times 10^{-6}$	2.387486	Wingless-type MMTV integration site family, member 7A (Wnt7a)
Dcn	-1.99	.000201425	2.766588	Decorin (Dcn)
Mt2	-1.99	.000107512	1.376331	Metallothionein 2 (Mt2)
Efhd1	-2.01	$9.51 \times 10^{-8}$	4.464602	EF hand domain containing 1 (Efhd1)
Plekhf1	-2.01	.006786698	0.655115	Pleckstrin homology domain containing, family F (with FYVE domain) member 1 (Plekhf1)
Tnfrsf1a	-2.01	$3.37 \times 10^{-5}$	2.704296	Tumor necrosis factor receptor superfamily, member 1a (Tnfrsf1a)
Sugct	-2.01	$3.10 \times 10^{-5}$	2.199478	Succinyl-CoA glutarate-CoA transferase (Sugct)
4933407L21Rik	-2.01	$4.08 \times 10^{-5}$	1.532556	RIKEN cDNA 4933407L21 gene (4933407L21Rik)
Gm2830	-2.01	$3.67 \times 10^{-5}$	1.700907	Predicted gene 2830 (Gm2830)
Ramp2	-2.01	.000547863	1.379686	Receptor (calcitonin) activity modifying protein 2 (Ramp2)
Crybg3	-2.01	.006177271	-0.22485	Beta-gamma crystallin domain containing 3 (Crybg3)
Cyp2j9	-2.02	$5.37 \times 10^{-7}$	4.392277	Cytochrome P450, family 2, subfamily j, polypeptide 9 (Cyp2j9)
Vwf	-2.02	.003961198	1.276605	Von Willebrand factor (Vwf)
Evi2a	-2.02	$2.14 \times 10^{-5}$	3.517947	Ecotropic viral integration site 2a (Evi2a)
Sparc	-2.02	$1.85 \times 10^{-9}$	9.612044	Secreted acidic cysteine-rich glycoprotein (Sparc)
Nkain4	-2.02	$1.18 \times 10^{-6}$	3.663312	Na+/K+ transporting ATPase interacting 4 (Nkain4)
Nek5	-2.03	.002536116	-0.06157	NIMA (never in mitosis gene a)-related expressed kinase 5 (Nek5)
Gpsm2	-2.03	.000129292	1.406032	G-protein signalling modulator 2 (AGS3-like, C. elegans) (Gpsm2)
Stoml3	-2.03	$2.74 \times 10^{-5}$	2.954767	Stomatin (Epb7.2)-like 3 (Stoml3)
Cdhr3	-2.03	$2.45 \times 10^{-5}$	2.934715	Cadherin-related family member 3 (Cdhr3)
Gm19439	-2.03	.001246759	1.032023	Predicted gene, 19439 (Gm19439)
Abcc3	-2.03	.004859573	-0.23008	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Abcc3)
Aldh1l1	-2.03	$1.10 \times 10^{-6}$	3.334472	Aldehyde dehydrogenase 1 family, member L1 (Aldh1l1)
Bmp4	-2.04	.004713383	1.370513	Bone morphogenetic protein 4 (Bmp4)
Mt1	-2.04	$2.08 \times 10^{-8}$	4.843165	Metallothionein 1 (Mt1)
Pglyrp1	-2.05	.000229161	1.360246	Peptidoglycan recognition protein 1 (Pglyrp1)
Phkg1	-2.05	$2.87 \times 10^{-5}$	1.555353	Phosphorylase kinase gamma 1 (Phkg1)
Gm11423	-2.05	.002029242	0.375497	Predicted gene 11423 (Gm11423)
Gm11266	-2.05	.002457495	-0.26048	Predicted gene 11266 (Gm11266)
4933406C10Rik	-2.05	.04411911	-0.35264	RIKEN cDNA 4933406C10 gene (4933406C10Rik)
Gjb1	-2.05	$1.25 \times 10^{-5}$	3.002231	Gap junction protein, beta 1 (Gjb1)
Tmem63a	-2.06	$1.51 \times 10^{-6}$	3.782223	Transmembrane protein 63a (Tmem63a)
Fhl3	-2.06	.009994296	-0.12466	Four and a half LIM domains 3 (Fhl3)
Igfsf1	-2.06	$1.10 \times 10^{-6}$	3.786173	Immunoglobulin superfamily, member 1 (Igfsf1)
Cd300c2	-2.06	.000221469	1.232229	CD300C molecule 2 (Cd300c2)
Acsbg1	-2.06	$4.23 \times 10^{-7}$	5.185581	Acyl-CoA synthetase bubblegum family member 1 (Acsbg1)
Gm47794	-2.06	.0287879	-0.35252	Predicted gene (Gm47794)
Slco1c1	-2.06	$2.39 \times 10^{-6}$	3.103453	Solute carrier organic anion transporter family, member 1c1 (Slco1c1)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
C130074G19Rik	-2.07	$7.93 \times 10^{-5}$	1.551419	RIKEN cDNA C130074G19 gene (C130074G19Rik)
Casq2	-2.07	.00077846	1.124322	Calsequestrin 2 (Casq2)
Sntn	-2.07	.000320214	1.183331	Sentan, cilia apical structure protein (Sntn)
Wdr66	-2.07	$7.25 \times 10^{-5}$	1.731774	WD repeat domain 66 (Wdr66)
Nkx6-2	-2.07	$2.36 \times 10^{-5}$	1.707178	NK6 homeobox 2 (Nkx6-2)
Tmem253	-2.07	.017619173	-0.27098	Transmembrane protein 253 (Tmem253)
Cd34	-2.08	$7.54 \times 10^{-5}$	1.783674	CD34 antigen (Cd34)
Csrp1	-2.08	$6.46 \times 10^{-9}$	6.466519	Cysteine and glycine-rich protein 1 (Csrp1)
Abca6	-2.08	.002475828	0.298072	ATP-binding cassette, sub-family A (ABC1), member 6 (Abca6)
Morn5	-2.08	.003316556	0.077987	MORN repeat containing 5 (Morn5)
Iqca	-2.09	.001088356	1.126013	IQ motif containing with AAA domain (Iqca)
Itm2a	-2.09	$5.62 \times 10^{-7}$	3.031832	Integral membrane protein 2A (Itm2a)
C1qtnf1	-2.09	.000912075	0.993324	C1q and tumor necrosis factor-related protein 1 (C1qtnf1)
Pla2g7	-2.09	$2.05 \times 10^{-7}$	5.65692	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) (Pla2g7)
Phgdh	-2.10	$1.21 \times 10^{-6}$	3.112993	3-Phosphoglycerate dehydrogenase (Phgdh)
Fbln7	-2.10	.000927369	1.181143	Fibulin 7 (Fbln7)
Irak4	-2.10	.002601527	0.345948	Interleukin-1 receptor-associated kinase 4 (Irak4)
Olfml3	-2.10	$3.95 \times 10^{-6}$	2.987583	Olfactomedin-like 3 (Olfml3)
Clec18a	-2.11	$2.53 \times 10^{-5}$	1.713095	C-type lectin domain family 18, member A (Clec18a)
Tmem125	-2.11	$2.13 \times 10^{-5}$	2.014312	Transmembrane protein 125 (Tmem125)
Snhg8	-2.11	$2.43 \times 10^{-5}$	1.741734	Small nucleolar RNA host gene 8 (Snhg8)
Ifi27	-2.11	$5.61 \times 10^{-5}$	2.559219	Interferon, alpha-inducible protein 27 (Ifi27)
Slc6a13	-2.11	.001784309	0.541982	Solute carrier family 6 (neurotransmitter transporter, GABA), member 13 (Slc6a13)
3300002A11Rik	-2.11	.002076296	0.550618	RIKEN cDNA 3300002A11 gene (3300002A11Rik)
Fgd2	-2.12	.007222668	0.253991	FYVE, RhoGEF and PH domain containing 2 (Fgd2)
Dmp1	-2.12	.00995495	-0.39557	Dentin matrix protein 1 (Dmp1)
Adora2b	-2.12	.000120466	1.324014	Adenosine A2b receptor (Adora2b)
Slc7a10	-2.13	$1.57 \times 10^{-5}$	2.230329	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 10 (Slc7a10)
Hhex	-2.13	.010209566	-0.13954	Hematopoietically expressed homeobox (Hhex)
Pllp	-2.13	$7.66 \times 10^{-6}$	2.48025	Plasma membrane proteolipid (Pllp)
Pon2	-2.13	$2.08 \times 10^{-8}$	4.850478	Paraoxonase 2 (Pon2)
Sdc4	-2.14	$4.40 \times 10^{-8}$	5.928974	Syndecan 4 (Sdc4)
Icam1	-2.14	.03944603	-0.43555	Intercellular adhesion molecule 1 (Icam1)
Fzd2	-2.14	.003930125	0.105722	Frizzled class receptor 2 (Fzd2)
Abca8a	-2.14	.003161027	0.751855	ATP-binding cassette, sub-family A (ABC1), member 8a (Abca8a)
Ly86	-2.14	.00021166	3.754637	Lymphocyte antigen 86 (Ly86)
Olig1	-2.15	$1.31 \times 10^{-8}$	5.974647	Oligodendrocyte transcription factor 1 (Olig1)
Epb41l4aos	-2.15	.001542855	0.393748	Erythrocyte membrane protein band 4.1 like 4a, opposite strand (Epb41l4aos)
Casc1	-2.15	.002171616	0.950031	Cancer susceptibility candidate 1 (Casc1)
Wdfy4	-2.15	.002746533	0.161471	WD repeat and FYVE domain containing 4 (Wdfy4)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Gstt3	-2.17	$6.47 \times 10^{-5}$	1.709241	Glutathione S-transferase, theta 3 (Gstt3)
Pld4	-2.17	$8.66 \times 10^{-5}$	1.857009	Phospholipase D family, member 4 (Pld4)
AC152827.1	-2.17	.001866268	0.239561	-
Armc3	-2.17	.006786698	-0.13561	Armadillo repeat containing 3 (Armc3)
Parp3	-2.17	.00528782	1.026615	Poly(ADP-ribose) polymerase family, member 3 (Parp3)
Sox18	-2.17	.000117213	0.857294	SRY (sex determining region Y)-box 18 (Sox18)
Ppp1r36	-2.18	.001096483	1.456112	Protein phosphatase 1, regulatory subunit 36 (Ppp1r36)
Aoah	-2.18	.005533253	0.418155	Acyloxyacyl hydrolase (Aoah)
Fcgr1	-2.18	.010496936	1.214554	Fc receptor, IgG, high affinity I (Fcgr1)
Lbp	-2.19	$3.13 \times 10^{-6}$	2.798288	Lipopolysaccharide binding protein (Lbp)
Tmem98	-2.19	$8.03 \times 10^{-6}$	2.644016	Transmembrane protein 98 (Tmem98)
Col1a1	-2.20	.00069679	0.969096	Collagen, type I, alpha 1 (Col1a1)
Chp2	-2.20	.002746189	0.093954	Calcineurin-like EF hand protein 2 (Chp2)
Insc	-2.20	$8.17 \times 10^{-5}$	1.232903	Inscuteable homolog (Insc)
B230311B06Rik	-2.21	.000695798	0.253428	RIKEN cDNA B230311B06 gene (B230311B06Rik)
Loxl3	-2.21	.003095396	0.709268	Lysyl oxidase-like 3 (Loxl3)
Mfsd2a	-2.22	$1.36 \times 10^{-5}$	2.429199	Major facilitator superfamily domain containing 2A (Mfsd2a)
Cmtm5	-2.22	$2.56 \times 10^{-7}$	4.64494	CKLF-like MARVEL transmembrane domain containing 5 (Cmtm5)
Lppos	-2.22	.00060225	-0.17136	LIM domain containing preferred translocation partner in lipoma, opposite strand (Lppos)
Mlc1	-2.23	$9.11 \times 10^{-9}$	5.751964	Megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human) (Mlc1)
Tgif1	-2.23	.000361722	0.987667	TGFB-induced factor homeobox 1 (Tgif1)
Unc93b1	-2.23	.000255566	1.996307	Unc-93 homolog B1 ( <i>C. elegans</i> ) (Unc93b1)
Serpincb1a	-2.23	$1.36 \times 10^{-5}$	2.315338	Serine (or cysteine) peptidase inhibitor, clade B, member 1a (Serpincb1a)
Pifo	-2.24	$5.24 \times 10^{-5}$	1.932162	Primary cilia formation (Pifo)
Gm16845	-2.24	.001105372	-0.27274	Predicted gene, 16845 (Gm16845)
Cdhr4	-2.24	.001407815	0.340489	Cadherin-related family member 4 (Cdhr4)
Gm43267	-2.25	.000280269	0.990718	Predicted gene (Gm43267)
Tm4sf1	-2.25	$4.94 \times 10^{-6}$	3.40215	Transmembrane 4 superfamily member 1 (Tm4sf1)
Gm266	-2.25	.000111678	0.51183	Predicted gene 266 (Gm266)
Lrrc36	-2.25	$5.89 \times 10^{-5}$	1.762477	Leucine-rich repeat containing 36 (Lrrc36)
Serpinh1	-2.25	.000201734	2.474281	Serine (or cysteine) peptidase inhibitor, clade H, member 1 (Serpinh1)
Nde1	-2.25	$6.76 \times 10^{-6}$	2.341013	nudE neurodevelopment protein 1 (Nde1)
Gm26881	-2.26	.001818518	-0.31595	Predicted gene, 26881 (Gm26881)
Itih2	-2.26	.001708089	-0.22004	Inter-alpha trypsin inhibitor, heavy chain 2 (Itih2)
Ntsr2	-2.26	$2.08 \times 10^{-8}$	6.007592	Neurotensin receptor 2 (Ntsr2)
Mlxipl	-2.26	.002042396	0.017298	MLX interacting protein-like (Mlxipl)
Cldn11	-2.26	$3.93 \times 10^{-7}$	5.016633	Claudin 11 (Cldn11)
Lcat	-2.26	$4.48 \times 10^{-8}$	4.45636	Lecithin cholesterol acyltransferase (Lcat)
Slc15a3	-2.26	.004258089	-0.15162	Solute carrier family 15, member 3 (Slc15a3)
Cfap77	-2.27	.000172653	0.956349	Cilia and flagella-associated protein 77 (Cfap77)
Cst3	-2.27	$2.93 \times 10^{-10}$	9.000216	Cystatin C (Cst3)
Gm13340	-2.27	$1.72 \times 10^{-5}$	1.846743	Predicted gene (Gm13340)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Slc14a2	-2.28	$1.66 \times 10^{-5}$	1.757931	Solute carrier family 14 (urea transporter), member 2 (Slc14a2)
Gm38414	-2.29	.004129518	-0.13771	Predicted gene, 38414 (Gm38414)
Gfap	-2.29	$3.72 \times 10^{-6}$	5.579701	Glial fibrillary acidic protein (Gfap)
Selpig	-2.30	$5.68 \times 10^{-6}$	3.011718	Selectin, platelet (p-selectin) ligand (Selpig)
P2ry6	-2.30	.000517932	0.685384	Pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2ry6)
Tmem173	-2.30	.008082068	0.563428	Transmembrane protein 173 (Tmem173)
Gas5	-2.31	$3.68 \times 10^{-8}$	5.095377	Growth arrest specific 5 (Gas5)
Angptl4	-2.31	.000189638	1.228769	Angiopoietin-like 4 (Angptl4)
Agt	-2.31	$2.19 \times 10^{-7}$	5.673454	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8) (Agt)
Pdlim4	-2.31	$5.59 \times 10^{-6}$	1.981126	PDZ and LIM domain 4 (Pdlim4)
Ifitm2	-2.31	.000480185	0.04934	Interferon-induced transmembrane protein 2 (Ifitm2)
Gpx8	-2.31	$9.08 \times 10^{-5}$	1.606885	Glutathione peroxidase 8 (putative) (Gpx8)
S100b	-2.31	$6.66 \times 10^{-8}$	6.211467	S100 protein, beta polypeptide, neural (S100b)
Gm16160	-2.31	.002899795	-0.02699	Predicted gene 16160 (Gm16160)
Cd48	-2.32	.007101319	-0.58943	CD48 antigen (Cd48)
Gm38190	-2.33	.001066802	1.363964	Predicted gene (Gm38190)
Slc38a3	-2.33	$1.51 \times 10^{-6}$	3.563537	Solute carrier family 38, member 3 (Slc38a3)
Alpl	-2.33	$5.20 \times 10^{-5}$	1.556545	Alkaline phosphatase, liver/bone/kidney (Alpl)
Proca1	-2.33	$5.99 \times 10^{-5}$	1.303081	Protein interacting with cyclin A1 (Proca1)
Col1a2	-2.34	$4.18 \times 10^{-5}$	2.122734	Collagen, type I, alpha 2 (Col1a2)
Gm20515	-2.35	.002916822	0.109405	Predicted gene (Gm20515)
Arhgap45	-2.35	.001001352	0.133302	Rho GTPase Activating Protein 45 (Arhgap45)
F5	-2.36	.001113673	-0.14645	Coagulation factor V (F5)
Myl9	-2.36	$7.59 \times 10^{-5}$	1.585387	Myosin, light polypeptide 9, regulatory (Myl9)
Kcne1l	-2.36	$2.48 \times 10^{-5}$	1.525034	Potassium voltage-gated channel, Isk-related family, member 1-like, pseudogene (Kcne1l)
Hsd11b1	-2.36	$1.40 \times 10^{-6}$	2.456478	Hydroxysteroid 11-beta dehydrogenase 1 (Hsd11b1)
6430503K07Rik	-2.36	.001537478	-0.14294	RIKEN cDNA 6430503K07 gene (6430503K07Rik)
BC064078	-2.37	.002037062	0.845363	cDNA sequence BC064078 (BC064078)
Lmcd1	-2.37	.000158317	0.406117	LIM and cysteine-rich domains 1 (Lmcd1)
Slc12a4	-2.37	$4.99 \times 10^{-5}$	1.944246	Solute carrier family 12, member 4 (Slc12a4)
Dnah14	-2.37	.000411774	0.176602	Dynein, axonemal, heavy chain 14 (Dnah14)
1700012B09Rik	-2.38	$3.74 \times 10^{-5}$	1.56264	RIKEN cDNA 1700012B09 gene (1700012B09Rik)
Gstk1	-2.38	$4.08 \times 10^{-6}$	2.324627	Glutathione S-transferase kappa 1 (Gstk1)
Aldh3b1	-2.40	.001407815	-0.2842	Aldehyde dehydrogenase 3 family, member B1 (Aldh3b1)
C1qa	-2.40	$6.44 \times 10^{-6}$	3.293363	Complement component 1, q subcomponent, alpha polypeptide (C1qa)
Cryab	-2.40	$2.05 \times 10^{-7}$	5.885784	Crystallin, alpha B (Cryab)
Cst7	-2.41	.007688337	0.168082	Cystatin F (leukocystatin) (Cst7)
Crybb1	-2.41	.000304516	-0.04279	Crystallin, beta B1 (Crybb1)
Tspo	-2.41	.001685832	-0.003	Translocator protein (Tspo)
Bfsp2	-2.42	.000947121	-0.3145	Beaded filament structural protein 2, phakinin (Bfsp2)
E130114P18Rik	-2.42	.000132558	1.697918	RIKEN cDNA E130114P18 gene (E130114P18Rik)
Hes5	-2.42	$9.02 \times 10^{-6}$	1.266088	Hairy and enhancer of split 5 (Hes5)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
S100a16	-2.42	$4.18 \times 10^{-7}$	3.969094	S100 calcium binding protein A16 (S100a16)
Paqr6	-2.42	.000188921	0.897268	Progesterin and adipoQ receptor family member VI (Paqr6)
Echdc2	-2.43	.000293797	0.770259	Enoyl Coenzyme A hydratase domain containing 2 (Echdc2)
Cldn10	-2.44	$3.59 \times 10^{-7}$	3.556722	Claudin 10 (Cldn10)
Id1	-2.45	$2.14 \times 10^{-5}$	1.551946	Inhibitor of DNA binding 1 (Id1)
Wfdc1	-2.45	$2.78 \times 10^{-5}$	1.450255	WAP four-disulfide core domain 1 (Wfdc1)
C1qc	-2.46	$9.02 \times 10^{-6}$	4.120528	Complement component 1, q subcomponent, C chain (C1qc)
Spata17	-2.46	.001150661	-0.08735	Spermatogenesis associated 17 (Spata17)
Fcgr3	-2.47	$5.20 \times 10^{-5}$	2.150881	Fc receptor, IgG, low affinity III (Fcgr3)
Gm16201	-2.47	.003163212	-0.24507	Predicted gene 16201 (Gm16201)
Sept1	-2.47	.000592268	-0.25843	Septin 1 (Sept1)
Anxa3	-2.47	.000101668	0.84268	Annexin A3 (Anxa3)
Cldn5	-2.48	$2.87 \times 10^{-5}$	2.326624	Claudin 5 (Cldn5)
Gm19935	-2.48	$3.79 \times 10^{-5}$	2.436985	Predicted gene, 19935 (Gm19935)
Gng5	-2.49	$7.97 \times 10^{-7}$	2.953626	Guanine nucleotide binding protein (G protein), gamma 5 (Gng5)
Daw1	-2.49	.008807928	-0.29478	Dynein assembly factor with WDR repeat domains 1 (Daw1)
Gpr37l1	-2.50	$1.97 \times 10^{-9}$	6.201916	G protein-coupled receptor 37-like 1 (Gpr37l1)
Rbp1	-2.50	$1.28 \times 10^{-6}$	2.492214	Retinol binding protein 1, cellular (Rbp1)
Arhgdib	-2.50	.000182452	0.848466	Rho, GDP dissociation inhibitor (GDI) beta (Arhgdib)
Cpn1	-2.51	.012654915	-0.4999	Carboxypeptidase N, polypeptide 1 (Cpn1)
Vamp8	-2.51	$3.95 \times 10^{-5}$	1.416741	Vesicle-associated membrane protein 8 (Vamp8)
1700007G11Rik	-2.51	.001654961	0.440218	RIKEN cDNA 1700007G11 gene (1700007G11Rik)
Trim47	-2.51	.000399912	-0.25107	Tripartite motif-containing 47 (Trim47)
Anpep	-2.51	.000398563	1.15475	Alanyl (membrane) aminopeptidase (Anpep)
Lyz2	-2.51	$6.15 \times 10^{-6}$	5.20813	Lysozyme 2 (Lyz2)
Gsn	-2.52	$1.60 \times 10^{-6}$	2.937683	Gelsolin (Gsn)
Xaf1	-2.53	.006616552	1.614131	XIAP-associated factor 1 (Xaf1)
Id3	-2.53	$1.26 \times 10^{-6}$	3.316696	Inhibitor of DNA binding 3 (Id3)
BC028528	-2.54	.006631642	-0.48747	cDNA sequence BC028528 (BC028528)
Cd82	-2.54	$5.08 \times 10^{-5}$	1.188462	CD82 antigen (Cd82)
Ccdc153	-2.54	$7.13 \times 10^{-7}$	3.028542	Coiled-coil domain containing 153 (Ccdc153)
Ttll6	-2.54	.000259286	1.132604	Tubulin tyrosine ligase-like family, member 6 (Ttll6)
Nat8	-2.55	.004188428	-0.30007	N-acetyltransferase 8 (GCN5-related) (Nat8)
Rcn3	-2.55	.000245184	-0.12209	Reticulocalbin 3, EF-hand calcium binding domain (Rcn3)
Ramp1	-2.56	$4.38 \times 10^{-8}$	3.708342	Receptor (calcitonin) activity modifying protein 1 (Ramp1)
Clic1	-2.56	$4.38 \times 10^{-5}$	1.528673	Chloride intracellular channel 1 (Clic1)
Cyp4f15	-2.57	$5.64 \times 10^{-6}$	2.236492	Cytochrome P450, family 4, subfamily f, polypeptide 15 (Cyp4f15)
Thrsp	-2.58	$6.92 \times 10^{-7}$	2.685035	Thyroid hormone responsive (Thrsp)
Fbxl13	-2.58	.001204844	-0.51251	F-box and leucine-rich repeat protein 13 (Fbxl13)
Dnaaf1	-2.58	$4.78 \times 10^{-5}$	0.457686	Dynein, axonemal assembly factor 1 (Dnaaf1)
Ifi207	-2.60	.031485849	-0.09011	Interferon activated gene 207 (Ifi207)
Cnn2	-2.60	.001294124	0.489047	Calponin 2 (Cnn2)
1700047M11Rik	-2.60	.000257172	1.356029	RIKEN cDNA 1700047M11 gene (1700047M11Rik)
Tac2	-2.60	$1.74 \times 10^{-5}$	6.663872	Tachykinin 2 (Tac2)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Got1l1	-2.61	.004622814	-0.67916	Glutamic-oxaloacetic transaminase 1-like 1 (Got1l1)
Opalin	-2.61	$2.12 \times 10^{-7}$	3.570829	Oligodendrocytic myelin paranodal and inner loop protein (Opalin)
Rarres2	-2.61	$3.12 \times 10^{-6}$	2.458739	Retinoic acid receptor responder (tazarotene induced) 2 (Rarres2)
S100a6	-2.62	.000118658	2.196294	S100 calcium binding protein A6 (calcyclin) (S100a6)
Cdr1	-2.63	$1.62 \times 10^{-7}$	5.308522	Cerebellar degeneration-related antigen 1 (Cdr1)
Vtn	-2.63	$1.45 \times 10^{-7}$	3.695122	Vitronectin (Vtn)
Acta2	-2.63	.000922069	0.181487	Actin, alpha 2, smooth muscle, aorta (Acta2)
Nppa	-2.65	.004866842	-0.66823	Natriuretic peptide type A (Nppa)
1700001C02Rik	-2.66	.000132254	0.475533	RIKEN cDNA 1700001C02 gene (1700001C02Rik)
Kcnj8	-2.66	.000266171	0.596436	Potassium inwardly rectifying channel, subfamily J, member 8 (Kcnj8)
Ccl9	-2.67	.001472797	-0.10814	Chemokine (C-C motif) ligand 9 (Ccl9)
Tnni1	-2.67	.000174129	0.596632	Troponin I, skeletal, slow 1 (Tnni1)
Entpd2	-2.68	$2.50 \times 10^{-6}$	2.138821	Ectonucleoside triphosphate diphosphohydrolase 2 (Entpd2)
Cd37	-2.68	.00048829	0.695952	CD37 antigen (Cd37)
Ankrd66	-2.68	.00023528	0.434094	Ankyrin repeat domain 66 (Ankrd66)
Cd63	-2.69	$1.22 \times 10^{-7}$	4.833184	CD63 antigen (Cd63)
Trf	-2.69	$1.09 \times 10^{-5}$	1.932546	Transferrin (Trf)
Htra1	-2.70	$7.84 \times 10^{-7}$	3.859458	HtrA serine peptidase 1 (Htra1)
Tsnaxip1	-2.70	.000101547	0.374081	Translin-associated factor X (Tsnax) interacting protein 1 (Tsnaxip1)
Erich2	-2.71	.000488344	0.0994	Glutamate rich 2 (Erich2)
Hist1h2bc	-2.71	$1.11 \times 10^{-7}$	3.094263	Histone cluster 1, H2bc (Hist1h2bc)
Fcer1g	-2.71	$3.03 \times 10^{-5}$	3.558796	Fc receptor, IgE, high affinity I, gamma polypeptide (Fcer1g)
Renbp	-2.73	.000274029	0.001057	Renin binding protein (Renbp)
Pdlim2	-2.73	$6.41 \times 10^{-5}$	1.187617	PDZ and LIM domain 2 (Pdlim2)
Ttr	-2.74	$2.21 \times 10^{-5}$	4.510489	Transthyretin (Ttr)
Ctss	-2.74	$2.33 \times 10^{-6}$	5.114436	Cathepsin S (Ctss)
Dbi	-2.75	$2.93 \times 10^{-10}$	7.573272	Diazepam binding inhibitor (Dbi)
Cd9	-2.75	$1.03 \times 10^{-6}$	3.598137	CD9 antigen (Cd9)
Hba-a2	-2.78	.000508037	-0.63245	Hemoglobin alpha, adult chain 2 (Hba-a2)
Ly6a	-2.79	$6.77 \times 10^{-5}$	3.424054	Lymphocyte antigen 6 complex, locus A (Ly6a)
Pdlim1	-2.80	.000131379	0.293776	PDZ and LIM domain 1 (elfin) (Pdlim1)
Pkd2l1	-2.80	.00130007	-0.45888	Polycystic kidney disease 2-like 1 (Pkd2l1)
Apod	-2.82	$6.97 \times 10^{-8}$	6.35764	Apolipoprotein D (Apod)
Cyp4f14	-2.83	$2.23 \times 10^{-5}$	2.021949	Cytochrome P450, family 4, subfamily f, polypeptide 14 (Cyp4f14)
Ctsh	-2.83	$2.87 \times 10^{-5}$	2.986981	Cathepsin H (Ctsh)
Klk6	-2.83	$9.71 \times 10^{-5}$	1.19974	Kallikrein-related peptidase 6 (Klk6)
Degs2	-2.84	.000349994	-0.63263	Delta(4)-desaturase, sphingolipid 2 (Degs2)
Hba-a1	-2.85	$9.28 \times 10^{-5}$	-0.34694	Hemoglobin alpha, adult chain 1 (Hba-a1)
Ly6c1	-2.87	$1.33 \times 10^{-6}$	2.157419	Lymphocyte antigen 6 complex, locus C1 (Ly6c1)
Ptgds	-2.87	$5.25 \times 10^{-6}$	7.923294	Prostaglandin D2 synthase (brain) (Ptgds)
Pantr2	-2.88	.000529487	0.122094	POU domain, class 3, transcription factor 3 adjacent noncoding transcript 2 (Pantr2)
Igfbp2	-2.88	$1.28 \times 10^{-5}$	1.792515	Insulin-like growth factor binding protein 2 (Igfbp2)
Hdc	-2.91	$8.57 \times 10^{-6}$	1.980861	Histidine decarboxylase (Hdc)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
mt-Nd5	-2.92	$6.14 \times 10^{-8}$	11.71883	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 5 (mt-Nd5)
Emid1	-2.96	.000101196	0.237697	EMI domain containing 1 (Emid1)
Mdk	-2.96	$1.11 \times 10^{-6}$	2.248316	Midkine (Mdk)
Tbxas1	-2.97	.00045447	-0.61678	Thromboxane A synthase 1, platelet (Tbxas1)
Mgst1	-2.97	$4.33 \times 10^{-7}$	3.207941	Microsomal glutathione S-transferase 1 (Mgst1)
Tmem212	-2.97	$1.33 \times 10^{-6}$	2.830554	Transmembrane protein 212 (Tmem212)
1700024G13Rik	-2.98	$8.07 \times 10^{-5}$	1.778458	RIKEN cDNA 1700024G13 gene (1700024G13Rik)
Gm5741	-2.98	$5.59 \times 10^{-6}$	4.110074	Predicted gene 5741 (Gm5741)
C1qb	-2.99	$2.26 \times 10^{-6}$	4.422786	Complement component 1, q subcomponent, beta polypeptide (C1qb)
Slfn2	-2.99	.015188017	-0.79462	Schlafen 2 (Slfn2)
Calml4	-3.02	$1.14 \times 10^{-5}$	1.445258	Calmodulin-like 4 (Calml4)
AW112010	-3.03	.045530751	-0.34903	Expressed sequence AW112010 (AW112010)
Fxyd5	-3.03	$9.47 \times 10^{-6}$	1.694469	FXYD domain-containing ion transport regulator 5 (Fxyd5)
1500015O10Rik	-3.03	$5.13 \times 10^{-6}$	2.855535	RIKEN cDNA 1500015O10 gene (1500015O10Rik)
Lrrc71	-3.04	.000402096	-0.58253	Leucine-rich repeat containing 71 (Lrrc71)
mt-Nd1	-3.04	$1.31 \times 10^{-8}$	11.60777	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 1 (mt-Nd1)
Clec2d	-3.05	.001746984	0.07291	C-type lectin domain family 2, member d (Clec2d)
Slc39a4	-3.05	.003283469	-0.77095	Solute carrier family 39 (zinc transporter), member 4 (Slc39a4)
Plin3	-3.05	$3.22 \times 10^{-5}$	0.797856	Perilipin 3 (Plin3)
Fabp7	-3.06	$7.75 \times 10^{-7}$	5.082211	Fatty acid binding protein 7, brain (Fabp7)
Capsl	-3.06	$8.17 \times 10^{-5}$	1.08282	Calcyphosine-like (Capsl)
Ifi27l2a	-3.11	.039116732	-1.36053	Interferon, alpha-inducible protein 27 like 2A (Ifi27l2a)
Lcn2	-3.13	$8.21 \times 10^{-5}$	0.12928	Lipocalin 2 (Lcn2)
Ifitm3	-3.13	.000153918	3.445999	Interferon-induced transmembrane protein 3 (Ifitm3)
Fxyd1	-3.13	$3.23 \times 10^{-8}$	3.407838	FXYD domain-containing ion transport regulator 1 (Fxyd1)
Trem2	-3.16	$5.85 \times 10^{-6}$	1.680444	Triggering receptor expressed on myeloid cells 2 (Trem2)
mt-Rnr1	-3.16	$2.79 \times 10^{-6}$	1.726454	Mitochondrially encoded 12S rRNA (mt-Rnr1)
Ninj2	-3.17	.000197296	0.426492	Ninjurin 2 (Ninj2)
Gm10714	-3.20	.000608097	-0.65802	Predicted gene 10714 (Gm10714)
Gm12326	-3.21	.003736674	-0.91246	Predicted gene 12326 (Gm12326)
Slc11a1	-3.24	.001355949	-0.57597	Solute carrier family 11 ((proton-coupled divalent metal ion transporters), member 1 (Slc11a1))
Dmkn	-3.26	$5.99 \times 10^{-5}$	0.427697	Dermokine (Dmkn)
mt-Tp	-3.30	$6.66 \times 10^{-8}$	4.35983	Mitochondrially encoded tRNA-Pro (CCN) (mt-Tp)
mt-Nd4	-3.33	$8.43 \times 10^{-9}$	10.46327	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 4 (mt-Nd4)
S100a1	-3.35	$5.11 \times 10^{-8}$	3.8086	S100 calcium binding protein A1 (S100a1)
S100a13	-3.36	$3.22 \times 10^{-5}$	1.523038	S100 calcium binding protein A13 (S100a13)
Aif1	-3.37	.000281666	0.708752	Allograft inflammatory factor 1 (Aif1)
Apoe	-3.38	$1.02 \times 10^{-9}$	7.923024	Apolipoprotein E (Apoe)
Dynlrb2	-3.44	$1.84 \times 10^{-6}$	1.787046	Dynein light chain roadblock-type 2 (Dynlrb2)
Cd52	-3.50	.002433684	0.43572	CD52 antigen (Cd52)
Hbb-bs	-3.51	$4.10 \times 10^{-5}$	-0.03216	Hemoglobin, beta adult s chain (Hbb-bs)

**TABLE A1** Continued

Gene name	LogFC	Adjusted p-value	AveExpr	Gene full name
Tyrobp	-3.52	$1.03 \times 10^{-6}$	2.750794	TYRO protein tyrosine kinase binding protein (Tyrobp)
Ccl12	-3.53	.030906742	0.333625	Chemokine (C-C motif) ligand 12 (Ccl12)
Srgn	-3.56	$2.21 \times 10^{-5}$	0.662524	Serglycin (Srgn)
Capg	-3.57	.003792173	-0.718	Capping protein (actin filament), gelsolin-like (Capg)
Cyba	-3.57	.000197296	-0.15772	Cytochrome b-245, alpha polypeptide (Cyba)
Apoc1	-3.66	.00012238	0.40079	Apolipoprotein C-I (Apoc1)
mt-Cytb	-3.67	$1.22 \times 10^{-8}$	11.63159	Mitochondrially encoded cytochrome b (mt-Cytb)
Gng11	-3.68	$6.76 \times 10^{-6}$	1.804819	Guanine nucleotide binding protein (G protein), gamma 11 (Gng11)
Crip1	-3.69	$2.69 \times 10^{-5}$	0.658334	Cysteine-rich protein 1 (intestinal) (Crip1)
Ppp1r14a	-3.74	$3.00 \times 10^{-5}$	-0.18616	Protein phosphatase 1, regulatory (inhibitor) subunit 14A (Ppp1r14a)
mt-Nd2	-3.77	$5.60 \times 10^{-8}$	8.255642	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 2 (mt-Nd2)
mt-Rnr2	-3.78	$8.79 \times 10^{-9}$	4.324646	Mitochondrially encoded 16S rRNA (mt-Rnr2)
mt-Nd3	-3.81	$3.74 \times 10^{-5}$	-0.42245	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 3 (mt-Nd3)
mt-Nd6	-3.93	$4.21 \times 10^{-8}$	6.055903	Mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 6 (mt-Nd6)
Mgp	-3.97	.002551098	-0.00964	Matrix Gla protein (Mgp)
Samsn1	-4.03	.002536116	-1.39578	SAM domain, SH3 domain, and nuclear localization signals, 1 (Samsn1)
Ccdc33	-4.08	$1.48 \times 10^{-5}$	-0.14491	Coiled-coil domain containing 33 (Ccdc33)
Tctex1d4	-4.18	.000519009	-1.00281	Tctex1 domain containing 4 (Tctex1d4)
Avp	-4.21	.014279993	-0.33205	Arginine vasopressin (Avp)
Hcls1	-4.31	.00113449	-1.15454	Hematopoietic cell-specific Lyn substrate 1 (Hcls1)
Rn7sk	-4.69	$1.85 \times 10^{-6}$	0.297819	RNA, 7SK, nuclear (Rn7sk)