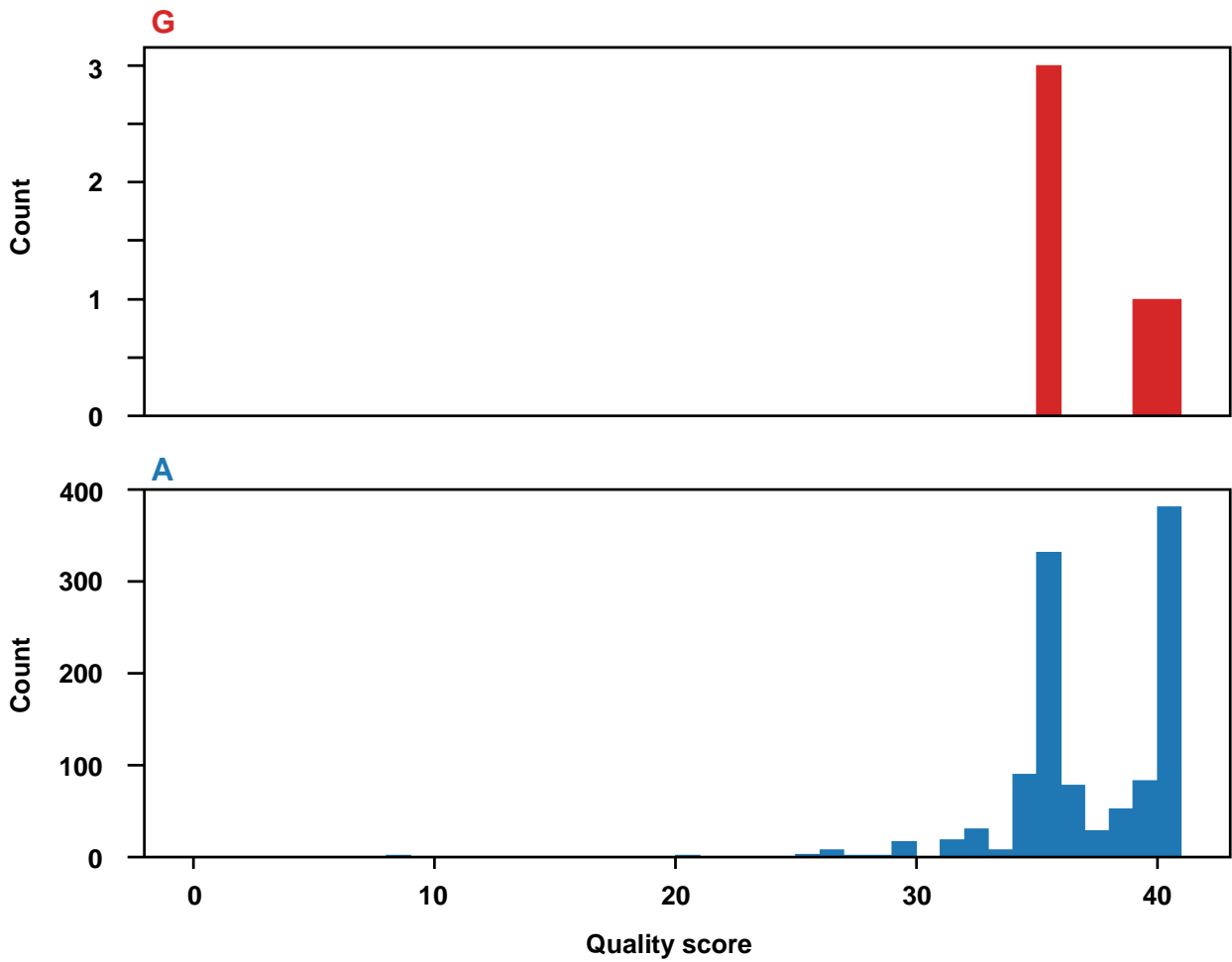


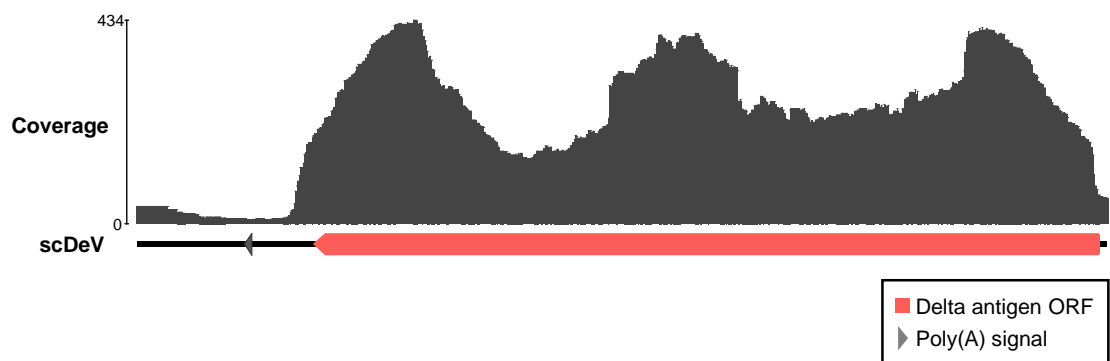
Supplementary Figure 1. Self-dotplot analyses for deltavirus-like contigs.

Deltavirus-like contigs were analyzed by YASS web server. The analyzed virus names are shown above and left-side of the dotplot. Numbers indicate nucleotide positions in the contigs. Green lines indicate alignable sequence stretches. Contig ends consisting of identical sequences are highlighted by light pink boxes.



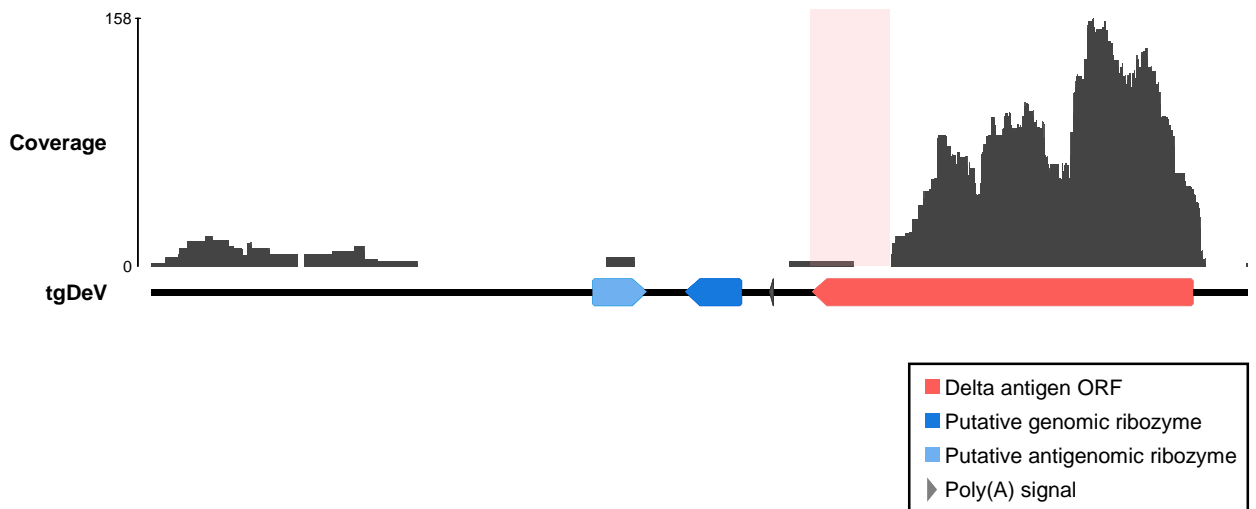
Supplementary Figure 2. Quality scores at possible RNA-editing site in ovDeV.

Histograms of the quality scores at the possible RNA editing site (the second nucleotide position of stop codon) in ovDeV DAg gene of mapped reads. Red and blue histograms indicate the quality scores of G and A nucleotide at the position.



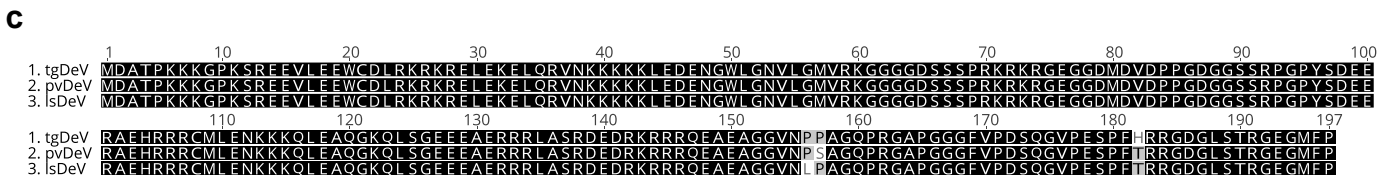
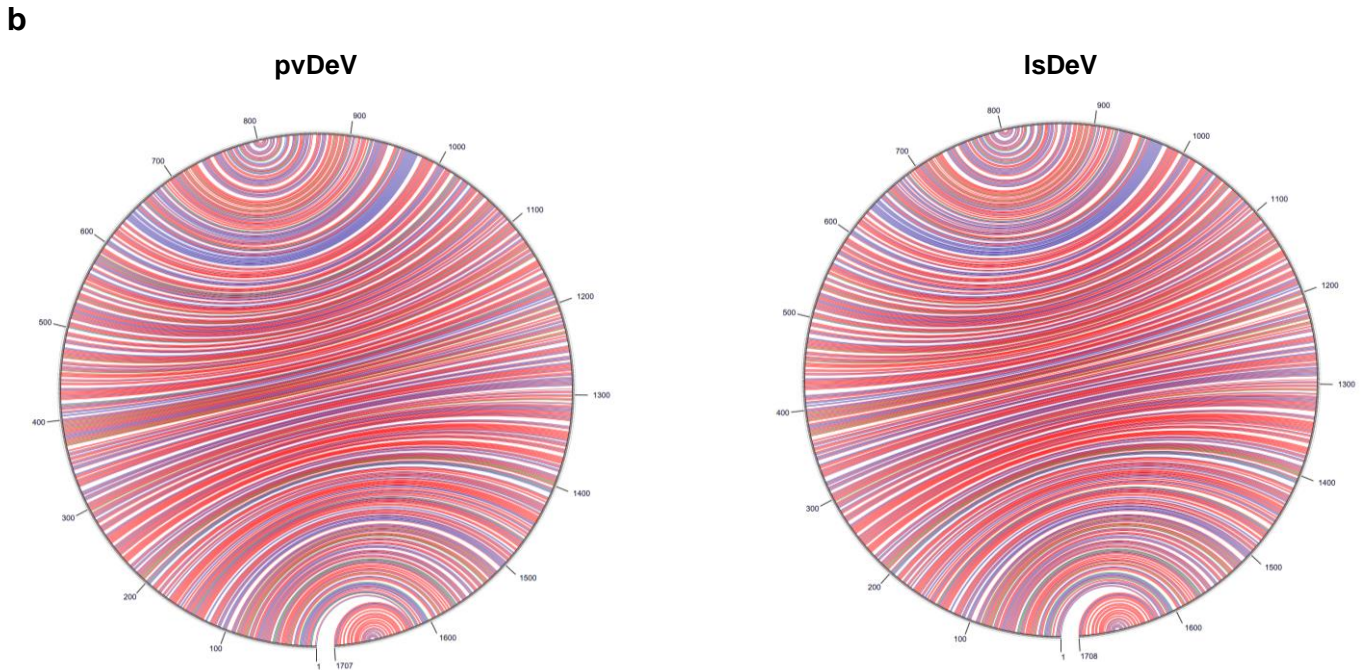
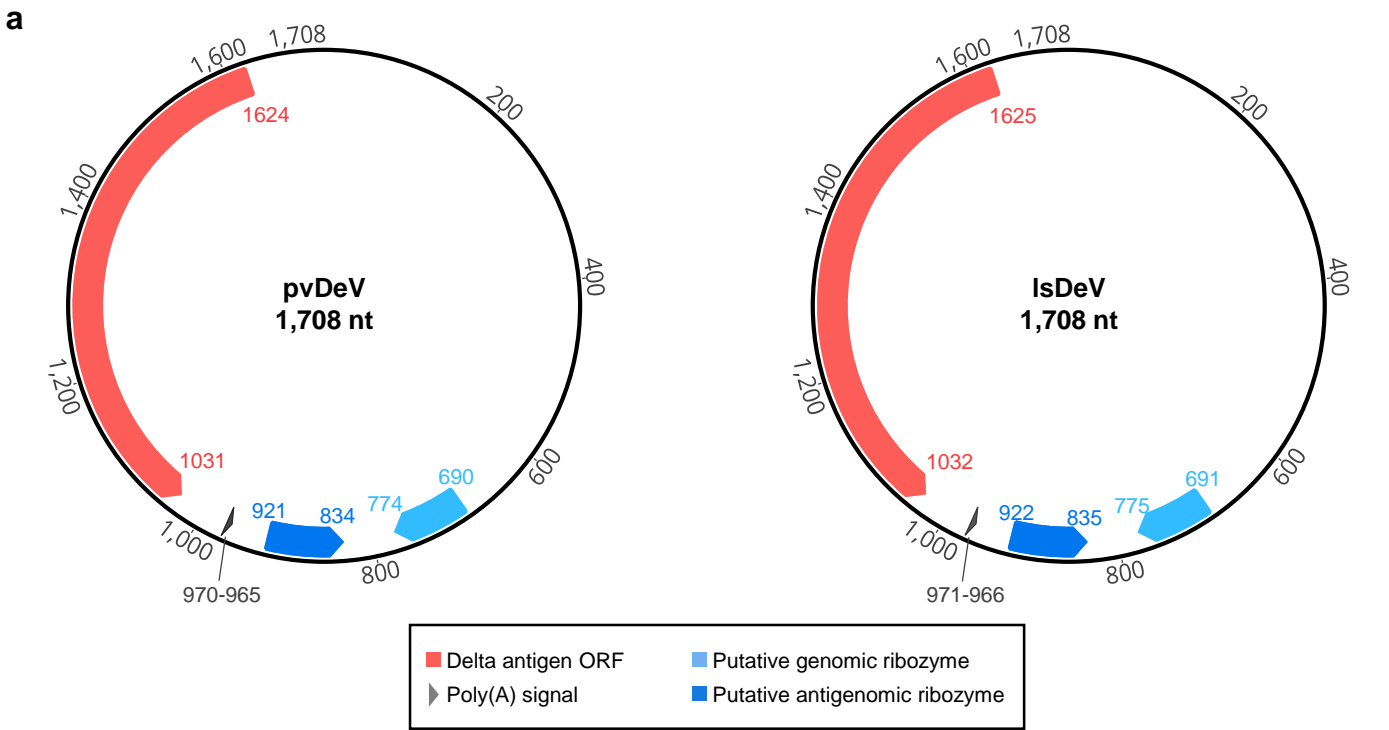
Supplementary Figure 3. Active transcription of *Serinus canaria*-associated deltavirus.

Mapped read graph of scDeV is shown. Line, arrow pentagon, and arrow heads indicate viral genome, DAg ORF, and poly(A) signal, respectively.



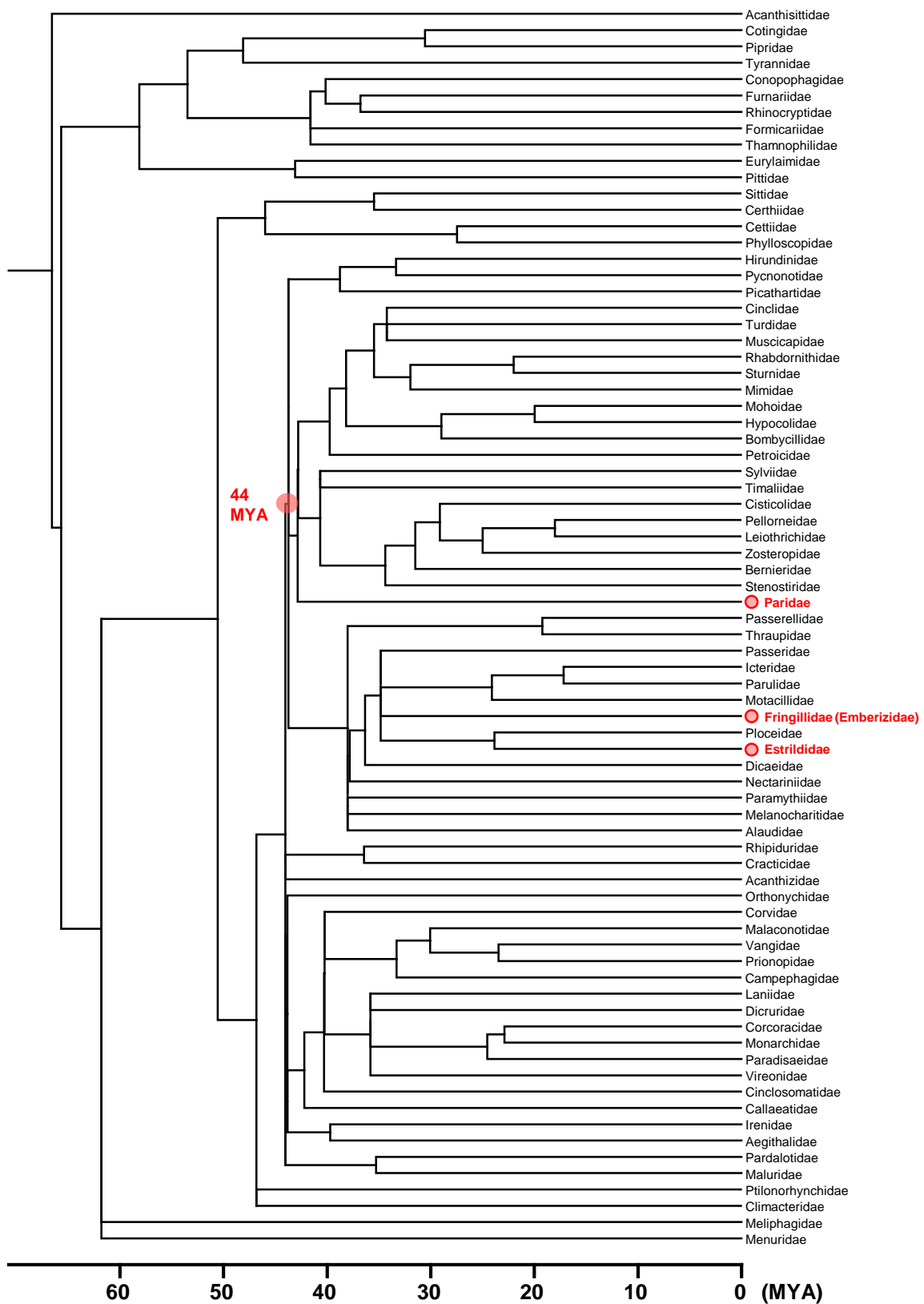
Supplementary Figure 4. Mapping coverage of *Taeniopygia guttata*-associated deltavirus.

Mapped read graph of tgDeV is shown. Short reads in SRR2545943, which were not mapped to the genome of *Taeniopygia guttata*, were mapped to tgDeV genome. Line, arrow pentagons, and arrow heads indicate viral genome, ribozymes and DAg ORF, and poly(A) signal, respectively. Light pink box shows low-coverage region in the ORF.



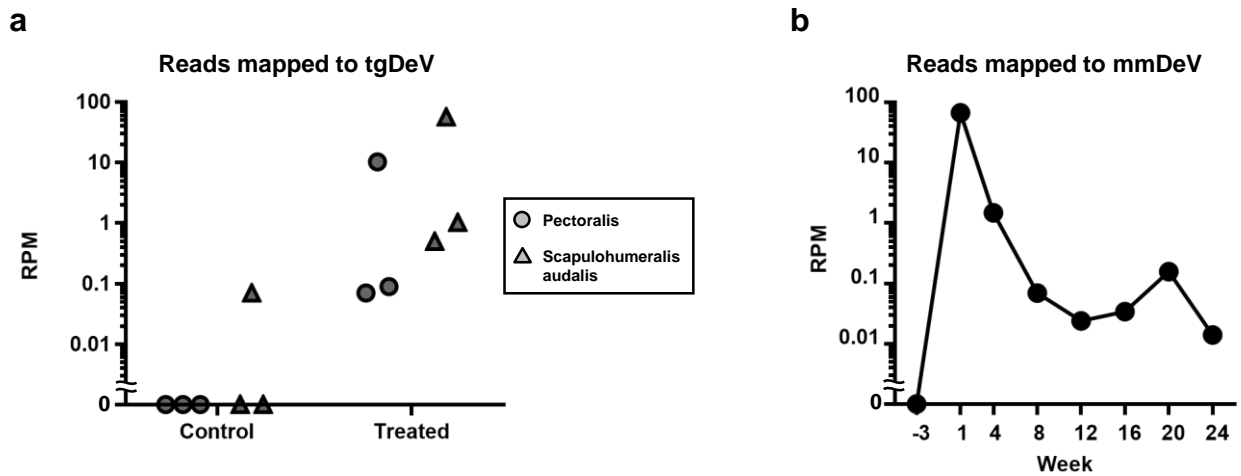
Supplementary Figure 5. Characterization of pvDeV and IsDeV.

(a) Schematic figure of the genome organizations of pvDeV and IsDeV. Annotations are shown by colored arrow pentagons. (b) Self-complementarity of pvDeV and IsDeV genomes. Circular structure plot of pvDeV, which was made by mfold web server, is shown. Red, blue, and green arcs indicate G-C, A-U, and G-U pairs, respectively. (c) Pairwise amino acid sequence alignment of DAg proteins of tgDeV, pvDeV, and IsDeV. The black boxes with white letters indicate identical amino acid residues. The numbers on the alignment show the positions.



Supplementary Figure 6. Divergent times of the order Passeriformes.

A phylogenetic tree of the genera in the order Passeriformes is shown. The time scale is shown under the phylogenetic tree. The tree information is downloaded from TimeTree. The families in which deltaviruses were detected in this study are shown by pink circles. The divergent time of those families is estimated to be 44 million years ago (MYA), which is shown by the pink circle. Note that the family Emberizidae is regarded as the subfamily Emberizinae of the family Fringillidae in TimeTree.



Supplementary Figure 7. Newly identified deltaviruses might be susceptible to the host immune responses.

(a) Possible effect of testosterone treatment for tgDeV replication and/or transcription. Mapped reads to tgDeV genome in SRR2545941-SRR2545952 are shown as read per million (RPM). The detailed data is available in Supplementary Table 5. (e) Time-course transition of mmDeV-mapped reads in a woodchuck (SRR2136906-SRR2136918). The detailed data is available in Supplementary Table 6.