Table S1. *RAG1/2-like* copies in *P. flava* genomes.

🟧 Orange color = complete RAG-like protein

🟨 Yellow color = RAG1/2-like in the same scaffold

RAG1x – RAG2x : Not phylogenetically assigned

Genomics

Species	Genomics	RAG ID	scaffold ID
P. flava		RAG1A-like	**BCFJ01043787.1**
P. flava		RAG1A-like	**BCFJ01026384.1**
P. flava		RAG1A-like	BCFJ01053939.1
P. flava		RAG1A-like	BCFJ01053937.1
P. flava		RAG1A-like	BCFJ01050366.1
P. flava		RAG1B1-like – RAG2B1-like	BCFJ01017854_/BCFJ01152714.1_BCFJ01052781.1
P. flava		RAG1B1-like – RAG2B1-like	BCFJ01094280.1
P. flava		RAG1B1-like	**BCFJ01096996.1**
P. flava		RAG2Bb-like	**BCFJ01034179.1**
P. flava		RAG2Bc-like	**BCFJ01293284.1**
P. flava		RAG2Bc-like	BCFJ01291212.1
P. flava		RAG1Bd-like – RAG2Bd-like	**BCFJ01059137.1**
P. flava		RAG1Bd-like	**BCFJ01067914.1**
P. flava		RAG1Bd-like	**BCFJ01059136.1**
P. flava		RAG1Bd-like	**BCFJ01281385.1**
P. flava		RAG1x-like – RAG2x-like	BCFJ01006354.1
P. flava		RAG1B-like	**BCFJ01097859.1**
P. flava		RAG1B-like	**BCFJ01065830.1**
P. flava		RAG1B-like	**BCFJ01171729.1**
P. flava		RAG2B-like	**BCFJ01142432.1**
P. flava		RAG1C-like – RAG2C-like	**BCFJ01036631.1**
P. flava		RAG1C-like	**BCFJ01041895.1**
P. flava		RAG1C-like	BCFJ01047137.1

P. flava		RAG1C-like	BCFJ01088492.1
P. flava		RAG1C-like	BCFJ01263664.1
P. flava		RAG1C-like	**BCFJ01236165.1**
P. flava		RAG1C-like	**BCFJ01236166.1**

Species	**Transcript**	**RAG ID**	scaffold ID
P. flava	TRANSCRIPT	RAG1A -like	
P. flava	TRANSCRIPT	RAG1B-like (allele)	**gb|GDGM01438088.1**|
P. flava	TRANSCRIPT	RAG2B-like (allele)*	gb|GDGM01245220.1|
P. flava		RAG2B-like (allele)*	gb|GDGM01047156.1|
P. flava	TRANSCRIPT	RAG2Bc-like	
P. flava	TRANSCRIPT	RAG1C-like (allele)*	**gb|GDGM01025609.1**|
P. flava	TRANSCRIPT	RAG2C-like (allele)*	gb|GDGM01097917.1|
P. flava	TRANSCRIPT	RAG2E-like	gb|GDGM01150449.1|

Another RAG2-like transcript not analyzed with a 96% of Ident to BCFJ01127436.1 is **GDGM01229808.1**.

RAG1-like		RAG2-like	
Start	**End**	**Start**	**End**
6511	7692		
8838	11546		
588	2285		
155	415		
1104	1367		
*		2256	4186
11811	10838	8625	10516
1529	3333		
		9714	10894
		2	562
		2	220
3484	5013	5496	7684
9267	7317		
9896	9976		
941	3		
6381	4010	3854	3016
2644	4283		
27741	26621		
1474	200		
888	10209	11187	14650
5629	7445		
43	237		

224	601
1296	994
340	5
340	5

RAG1		RAG2	
Start	**End**	**Start**	**End**
87	3011		
		325	2
		205	20
2	1876		
		25	739
		3	476

Structure
TSD-5TIR-RAG1-RAG2-3TIR-TSD
TSD-5TIR-RAG1-RAG2-3TIR-TSD
TSD-5TIR-RAG1-RAG2-3TIR-TSD
TSD-5TIR-RAG1

TSD Sequence
>Pfl_B1_BCFJ01017854_BCFJ01052781 ccgCTGCGtgc >Pfl_B1_BCFJ01094280 gccCAATGtgc
>Pfl_C_BCFJ01036631_5 CacCATCCgtg >Pfl_C_BCFJ01036631_3 gtgCATCCgta
>Pfl_C_BCFJ01047137 gtgCATTG---

TIR sequence
>Pfl_B1_BCFJ01052781_3_71_bp CAC----ATATCAATTACCGGTAACCGATAG----CGAATCGTAAAAAATCAACATGGCCGCCT >Pfl_B_BCFJ01017854_5_71_bp CACTTATAGAGCAGCTANGAGCGCCATCTTG----CTAATTATAAATTATAATGACTGTATGAT >Pfl_B1_BCFJ01094280_3_71_bp CACCTATATATCAATTACATGTAACCGATAG----CAAATCGTAAAAAATCAAAATGGCCGC >Pfl_B1_BCFJ01094280_5_71_bp CACTTTGCGAGCAGCTANGAACGCCATGTTG----CTAATTATAAATAATTAAAATTATATTGA
>Pfl_C_BCFJ01036631_3_71_bp CACATCGCATTGTACCTGATTAAACCATTAGAA— ATATGCTTTGTTTAGTTGCGG--GCAAAT >Pfl_C_BCFJ01036631_5_71_bp CACATCGCATTCTCTTTTAGAAATTTGCTTG----TTCAATTACGCGC
>Pfl_C_BCFJ01047137_5_71_bp TACATCGCATTCTCTTTTAGAAATTTGCTTG----TTCAATTACGCGCGCATGCGCCAACATTC

Notes	
Pseudogene (stop codon)	
Pseudogene (stop codon)	
Pseudogene (stop at the beggining of the contig)	
Pseudogene (stop codon)	
***Note: RAG1B 1575-139 (BCFJ01152714.1) + 3-1918 (BCFJ01052781.1)** Pseudogene (stop codon)	
Pseudogene (stop codon)	
Short Scaffold. Length: 697	*P. flava*
Short Scaffold. Length: 221	*P. flava*
Pseudogene (stop codon)	Intron
Pseudogene (stop codon)	
*Probably from RAG1H family (Query 100% & Ident 75%)	
Pseudogene (stop codon)	
Pseudogene (stop codon)	
Pseudogene (stop codon)	
Pseudogene (stop codon)	
Intron vs Exon: With Spidey (DNA vs mRNA) we observe a single exon (Genomic coordinates 8334-102	
Pseudogene (stop codon).	
Pseudogene (stop codon).	

Pseudogene (stop codon).

Notes

****************** Contig 2 *******************
gb|GDGM01238538.1|+ Length 996
gb|GDGM01177394.1|+ is in gb|GDGM01238538.1|+
gb|GDGM01469753.1|+ is in gb|GDGM01238538.1|+
gb|GDGM01063948.1|+ is in gb|GDGM01469753.1|+
gb|GDGM01085983.1|+ is in gb|GDGM01238538.1|+

Intron vs Exon: E

Other transcripts:
gb|GDGM01014902.1|
gb|**GDGM01481817.1**|

Frame 3

*RAG2B potential transcript. Length: 327

*RAG2B potential transcript. Length: 205

****************** Contig 1 *******************
gb|GDGM01081107.1|+
gb|GDGM01504835.1|+ is in gb|GDGM01081107.1|+

*RAG1C potential transcript. Length: 1937

*RAG2C potential transcript. Length: 1641

Length: 528

71 and mRNA coordinates 1-1937) with a length of 1937bases and a 99.2% of Ident; blastx 2 sequences: We find 3 introns (Query 1 / Sbjct 888__

xpasy Frame 2. Traduction: Positions 503-1499; blastx 2 sequecences: (Query 1 / Sbjct 4712 - Query 996 / Sbjct 7692) jct1532 - INTRON - Query 216 / Sbjct 6621__Query292 / Sbjct6848 - INTRON - Query293 / Sbjct 7552__Query348 / Sbjct 7716 -

INTRON - Query349 / Sbjct8164__Query1030 / Sbjct10209)

Table S2. *RAG1/2-like* copies in *Saccoglossus kowalevskii* genomes.

Genomics

We do not find significant results (NS)

Transcripts

We do not find any TSA project

Table S3. *RAG1/2-like* copies in *Anneissia japonica* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

A. japonica

Table S4. *RAG1/2-like* copies in *Psathyrometra fragilis* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

P. fragilis

Table S5. *RAG1/2-like* copies in *Abyssocucumis albatrossi* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

A. albatrossi

Table S6. *RAG1/2-like* copies in *Sclerodactyla briareus* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

S. briareus

Table S7. *RAG1/2-like* copies in *Apostichopus japonicus* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

A. japonicus

Table S8. *RAG1/2-like* copies in *Parastichopus parvimensis* genomes.

Genomics

We do not find significant results (NS)

Transcripts

We do not find any TSA project

P. parvimensis

Table S9. *RAG1/2-like* copies in *Parastichopus californicus* genomes.

Genomics

We do not find WGS project

Transcripts

We do not find significant transcript results.

P. californicus

Table S10. *RAG1/2-like* copies in *Echinarachnius parma* genomes.

Genomics

We do not find WGS project

Transcripts

				RAG1-like		RAG2-like	
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
E. parma	TRANSCRIPT	RAG1B1-like	Contig1				
E. parma	TRANSCRIPT	RAG1B1-like	GAVF01032929.1	1	789		
E. parma	TRANSCRIPT	RAG1B1-like	GAVF01009690.1	5	607		
E. parma	TRANSCRIPT	RAG2B1-like	Contig2				
E. parma	TRANSCRIPT	RAG2B1-like	Contig1				
E. parma	TRANSCRIPT	RAG2B1-like	GAVF01015158.1			15	875

Transcript fragments for **RAG1-like** (**GAVF01077322.1** & **GAVF01077325.1**)

RAG2-like transcript fragments (**GAVF01052863.1** & **GAVF01015159.1**).

*RAG1-like of E. parma are different from each other and they are part of the RAG1B1-like family.

*RAG2-like of E. parma are different from each other and they are likely to be part of the RAG2B-like fam

<table>
<tr><th>Notes</th><th></th></tr>
<tr><td><i>gi|638076396|gb|GAVF01032928.1|+
gi|638076394|gb|GAVF01032930.1|+</i></td><td>*</td></tr>
<tr><td><i>Length: 840</i></td><td>*</td></tr>
<tr><td><i>Length: 690</i></td><td>*</td></tr>
<tr><td><i>gi|638056455|gb|GAVF01052869.1|+
gi|638056452|gb|GAVF01052872.1|+ is in gi|638056455|gb|GAVF01052869.1|+
gi|638056454|gb|GAVF01052870.1|+ is in gi|638056455|gb|GAVF01052869.1|+ Length: 1255</i></td><td>*</td></tr>
<tr><td><i>gi|638056450|gb|GAVF01052874.1|+
gi|638056457|gb|GAVF01052867.1|+
gi|638056453|gb|GAVF01052871.1|+</i></td><td>*</td></tr>
<tr><td><i>Length: 1195</i></td><td></td></tr>
</table>

ily.

Table S11. ***RAG1/2-like*** copies in ***Evechinus chloroticus*** genomes.

🟧 Orange color = complete RAG-like protein

Genomics

There is no WGS project

Transcripts

				RAG1-like		RAG2-like	
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
E. chloroticus	TRANSCRIPT	RAG1B2-like	🟧 GAPB01003278.1	596	2638		
E. chloroticus	TRANSCRIPT	RAG1B2-like	GAPB01008000.1	324	1931		
E. chloroticus	TRANSCRIPT	RAG1B2-like	GAPB01020750.1	45	1340		
E. chloroticus	TRANSCRIPT	RAG1B2-like	GAPB01045749.1				
E. chloroticus	TRANSCRIPT	RAG1B2-like	GAPB01022367.1				
E. chloroticus	TRANSCRIPT	RAG2B2-like	🟧 Contig 1				
E. chloroticus	TRANSCRIPT	RAG2B2-like	GAPB01063365.1			3293	2442

*RAG1-like of Evechinus chloroticus are different from each other and they are likely to be part of the RAG1

*RAG2-like of Evechinus chloroticus are different from each other and they are likely to be part of the RAG2

Notes	
Length: 3050 Frame 2. Traduction positions 156-2637*	
*Length: 2875**	
*Length: 1340**	
gi|559439143|gb|GAPB01022632.1|+ gi|559439142|gb|GAPB01022633.1|+ RAG2 potential transcript of NM_001033012.2	*
RAG2 potential transcriptn of NM_001033012.2. Length: 3383	*

B2-like family.

B2-like family.

Table S12. *RAG1/2-like* copies in *Strongylocentrotus purpur*

RAG2x : Not phylogenetically assigned

Genomics

Species
There are not included those with a Query cover <15% and a Ident <58%
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus
S. purpuratus

Transcripts

- **RAG2-like** paralog, with 80% identity (**JT103600.1** – Transcript of AAGJ05108197.1 [RAG2B

- A more divergent paralog with several stop codons (pseudogene) called RAG2B1-like (GAVU01

- Very close transcript sequences (**JT106157.1** & **GAVU01023365.1** – Transcripts of AAGJ05119

- Some fragments named (Contig1_Rag2, GAVU01022021.1 – Both transcript fragment of AAGJ

- **RAG1-like** close paralog (**Contig1_RAG1**),

- Divergent paralog named RAG1B2-like (GAVU01011698.1 – Partial transcript of AAGJ050523

- Fragments named (GAVU01024843.1 –Partial transcript of AAGJ05107091.1 (Query 85% & Id

GAVU01036260.1 – Partial transcript of AAGJ05119967.1 (Query 25% & Ident 100%)

GAVU01022227.1 – Partial transcript of AAGJ05116911.1 (Query 100% & Ident 100%) & **Conti**

Notes:

Contig1_RAG2-like= gi|374748692|gb|JT099428.1|-gb|GAVU01042378.1|+ is in gi|374748692|gb|JT099428.1|-

Contig1_RAG1-like= gi|374755421|gb|JT106157.1|-gb|GAVU01015377.1|+ is in gi|374755421|gb|JT106157.1|-

S. purpuratus

Contig2_RAG1-like= gb|GAVU01041231.1|+
gi|374767377|gb|JT118113.1|+
Gb|GAVU01028205.1|+ is in gi|374767377|gb|JT118113.1|+

S. purpuratus

tus genomes.

Orange color = complete RAG-like protein

Yellow color = RAG1/2-like in the same scaffold

		RAG1-like		RAG
RAG ID	**scaffold ID**	**Start**	**End**	**Start**
RAG1B1-like - RAG2B1-like	AAGJ05119967.1	11126	6070	2882
RAG1B1-like	AAGJ05093368.1	2157	2628	
RAG1B1-like	AAGJ05091685.1	19332	18460	
RAG1B1-like	AAGJ05093365.1	22467	24496	
RAG1B1-like	AAGJ05093366.1	6734	7481	
RAG1B1-like	AAGJ05107091.1	2414	1759	
RAG1B2-like	AAGJ05052375.1 (3 Identical copies)	665	9702	
RAG1B2-like	AAGJ05052374.1 (3 Identical copies)	1336	2049	
RAG1B2-like	AAGJ05052370.1	12342	18191	
RAG1B2-like	AAGJ05086369.1	8733	10078	
RAG2B1-like	AAGJ05119965.1			18311
RAG2B1-like	AAGJ05096689.1			387
RAG2B1-like	AAGJ05108197.1			16407
RAG2B1-like	AAGJ05074252.1			38623
RAG2B-like	AAGJ05085999.1			7488
RAG2x-like	AAGJ05080929.1			1003

] in WGS databse).

006082.1– Transcript of AAGJ05119967.1 [Query 97% & Ident 40%])

967.1 [Query 81% & Ident 95%] & [Query 100% & Ident 99%] respectivetly)

05074252.1 [Query 100% & Ident 82%])

75.1. Intron vs exon: We can not predict the exon-intron structure because the genomic sequence it is not complete. Bad predic

ent 87%);

ig2_RAG1-like)

Transcript fragment of AAGJ05119967.1 (Query 81% & Ident 95%)

Transcripts of AAGJ05119967.1 (Query 100% & Ident 87%)

Transcript fragment of AAGJ05119967.1 (Query 100% & Ident 99%)

S. purpuratus

2-like

End	Notes
1120	Pseudogene (stop codon at the end of RAG1-like). It correspond to RAG1/2-like published. Frame -3. I
	Pseudogene (stop codon)
	Pseudogene (stop codon)
	Pseudogene (stop codon)
	Pseudogene (stop codon)
	Pseudogene (stop codon).
	Pseudogene (stop codon)
18631	
139	
15486	Pseudogene (stop codon).
43035	
10283	Cis-duplication
596	Pseudogene (stop codon). 4Th locus (Partial locus very damaged)

tion.

S. purpuratus

ntron vs exon (see published article)

S. purpuratus

Table S13. *RAG1/2-like* copies in *Paracentro*

RAG1x : Not phylogenetically assigned

Genomics

There is no WGS project

🟧 Orange color = complete RAG-like protein

🟨 Yellow color = RAG1/2-like in the same scaffold

Transcripts fragments

Species	Transcript	RAG ID
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B2-like
P. lividus	TRANSCRIPT	RAG1B2-like
P. lividus	TRANSCRIPT	RAG1B2-like_RAG2B2-like
P. lividus	TRANSCRIPT	RAG1B2-like_RAG2B2-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1B1-like
P. lividus	TRANSCRIPT	RAG1-like

P. lividus

P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1B2-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like

P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1x-like
P. lividus	TRANSCRIPT	RAG1B2-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like

P. lividus

P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1x-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG1-like
P. lividus	TRANSCRIPT	RAG2B1-like
P. lividus	TRANSCRIPT	RAG2B2-like

*RAG1-like of P. lividus are different from each other and they are likely

*RAG2-like of P. lividus seems to have suffer a duplication (RAG2B1-li

P. lividus

tus *lividus* genomes.

scaffold ID	Notes
Contig1*	gb|GCZS01172032.1|- gb|GCZS01074202.1|+ is in gb|GCZS01172032.1|-
Contig2*	gb|GCZS01118857.1|+ gb|GCZS01118856.1|+ is in gb|GCZS01118857.1|+
Contig3*	gb|GCZS01118856.1|+ is in gb|GCZS01118857.1|+
RAG1-like – RAG2-like (GCZS01045777.1)*	
RAG1-like – RAG2-like (GCZS01045775.1_RAG2Contig1-like)*	gb|GCZS01045775.1|+ gb|GCZS01045776.1|+ is in gb|GCZS01045775.1|+
Contig16*	gb|GCZS01055975.1|- gb|GCZS01009528.1|+
GCZS01132703.1*	
GCZS01053115.1*	
Contig4*	gb|GCZS01085025.1|+ gb|GCZS01085026.1|+ is in gb|GCZS01085025.1|+
GCZS01158909.1*	
GCZS01150983.1*	
Contig5_**FRAGMENT**	*gb|GCZS01064032.1|+* *gb|GCZS01035764.1|+ is in gb|GCZS01064032.1|+* *gb|GCZS01064029.1|+ is in gb|GCZS01064032.1|+* *gb|GCZS01064037.1|+* *gb|GCZS01078431.1|-*

P. lividus

GCZS01064034.1_**FRAGMENT**	
Contig18_**FRAGMENT**	gb|GCZS01185123.1|+ gb|GCZS01096617.1|+ gb|GCZS01184645.1|- is in gb|GCZS01096617.1|+ gb|GCZS01096621.1|+
GCZS01118862.1_**FRAGMENT**	
GCZS01051899.1_**FRAGMENT**	
GCZS01112634.1_**FRAGMENT**	
GCZS01112632.1_**FRAGMENT**	
GCZS01087284.1_**FRAGMENT**	
GCZS01030082.1_**FRAGMENT**	
GCZS01042568.1_**FRAGMENT**	
GCZS01021545.1_**FRAGMENT**	
Contig6_**FRAGMENT**	*gb|GCZS01006895.1|+* *gb|GCZS01032509.1|+*
GCZS01044111.1_**FRAGMENT**	
Contig17_**FRAGMENT**	gb|GCZS01087285.1|+ gb|GCZS01087291.1|+ is in gb|GCZS01087285.1|+
Contig7_**FRAGMENT**	*gb|GCZS01132331.1|+* *gb|GCZS01132329.1|+*
GCZS01097940.1_**FRAGMENT**	
GCZS01089541.1_**FRAGMENT**	
GCZS01014750.1_**FRAGMENT**	
GCZS01055973.1_**FRAGMENT**	
GCZS01096624.1_**FRAGMENT**	
GCZS01078430.1_**FRAGMENT**	
Contig8_**FRAGMENT**	*gb|GCZS01049902.1|+* *gb|GCZS01049901.1|+ is in* *gb|GCZS01049902.1|+* *gb|GCZS01049900.1|+*
GCZS01031833.1_**FRAGMENT**	

P. lividus

<table>
<tr><th></th><th></th></tr>
<tr><td>Contig20_**FRAGMENT**</td><td>*gb|GCZS01091464.1|+*
gb|GCZS01091461.1|+ is in gb|GCZS01091464.1|+
gb|GCZS01091466.1|+
gb|GCZS01091463.1|+ is in gb|GCZS01091466.1|+</td></tr>
<tr><td>Contig15_**FRAGMENT**</td><td>gb|GCZS01019540.1|+
gb|GCZS01019539.1|+</td></tr>
<tr><td>Contig10_**FRAGMENT**</td><td>*gb|GCZS01091460.1|+*
gb|GCZS01091465.1|+</td></tr>
<tr><td>GCZS01077077.1_**FRAGMENT**</td><td></td></tr>
<tr><td>Contig9_**FRAGMENT**</td><td>*gb|GCZS01077078.1|+*
gb|GCZS01077076.1|+ is in gb|GCZS01077078.1|+</td></tr>
<tr><td>GCZS01132704.1*</td><td></td></tr>
<tr><td>Contig12*</td><td>*gb|GCZS01013198.1|+*
gb|GCZS01013199.1|+</td></tr>
<tr><td>Contig11_**FRAGMENT**</td><td>*gb|GCZS01033997.1|-*
gb|GCZS01152001.1|+ is in gb|GCZS01033997.1|-</td></tr>
<tr><td>Contig13_**FRAGMENT**</td><td>gb|GCZS01064627.1|+
gb|GCZS01064628.1|+
gb|GCZS01064630.1|+ is in gb|GCZS01064628.1|+</td></tr>
<tr><td>Contig14_**FRAGMENT**</td><td>gb|GCZS01149128.1|+
gb|GCZS01019259.1|+</td></tr>
<tr><td>GCZS01007361.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01170336.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01055974.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01052670.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01039677.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01026987.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01122106.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01087287.1_**FRAGMENT**</td><td></td></tr>
<tr><td>GCZS01033022.1_**FRAGMENT**</td><td></td></tr>
</table>

P. lividus

<table>
<tr><td>GCZS01057007.1_FRAGMENT</td><td></td></tr>
<tr><td>GCZS01027952.1_FRAGMENT</td><td></td></tr>
<tr><td>GCZS01174585.1_FRAGMENT</td><td></td></tr>
<tr><td>Contig19*</td><td>gb|GCZS01072522.1|+
gb|GCZS01072519.1|+</td></tr>
<tr><td>GCZS01057812.1_FRAGMENT</td><td></td></tr>
<tr><td>GCZS01156562.1_FRAGMENT</td><td></td></tr>
<tr><td>GCZS01182744.1*</td><td></td></tr>
<tr><td>Contig2*</td><td>gb|GCZS01031274.1|+
gb|GCZS01031273.1|+ is in
gb|GCZS01031274.1|+</td></tr>
</table>

to be part of the RAG1B1-like & RAGB2-like families.

ke & RAG2B2-like).

Table S14. *RAG1/2-like* copies in *Sphaerechinus granularis* genom

RAG1x – RAG2x : Not phylogenetically assigned

Genomics

There is no WGS project

Transcripts

				RAG1-like		RAG2-like	
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
S. granularis	TRANSCRIPT	RAG2x-like	GAVR01037695.1			1597	755

Transcript fragments for **RAG1-like** (**GAVP01036659.1**, **GAVR01070653.1**, **GAVR01070662.1**, **GAVR01**

Transcript fragment for **RAG2-like** (**GAVR01004062.1**).

ıes.

Notes
RAG2 potential transcript of NM_001033012.2. Length: 1668

*

070656.1, **GAVR01070663.1**, **GAVR01023727.1, GAVR01049989.1, GAVR01049990.1, GAVR01090577.1**)

Table S15. *RAG1/2-like* copies in *Lytechinus variegatus* genomes.

RAG2x : Not phylogenetically assigned

Genomics

			RAG1-like		RAG2-like		
Species	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**	**Notes**
There are included those with a Query cover >13%. Smallest Ident; 33%							
L. variegatus	RAG1B1-like	AGCV02054232.1	6377	9006			Pseudogene (stop codon).
L. variegatus	RAG1B1-like	AGCV02411413.1	30469	23113			Pseudogene (stop codon).
L. variegatus	RAG1B1-like	AGCV02253428.1	684	159			Pseudogene (stop codon)
L. variegatus	RAG1B-like	AGCV02377058.1	2793	4091			Pseudogene (stop codon)
L. variegatus	RAG1B-like	AGCV02060696.1	13096	11036			
L. variegatus	RAG1B1-like	AGCV02009112.1	2792	3622			Pseudogene (stop codon)
L. variegatus	RAG1B-like	AGCV02405259.1	1761	20426			Pseudogene (stop codon)
L. variegatus	RAG1B-like	AGCV02139577.1	337	837			*Similar to RAG1F family*
L. variegatus	RAG1B1-like	AGCV02280906.1	495	1			Pseudogene (stop codon)
L. variegatus	RAG1B-like	AGCV02064217.1	4585	5202			Pseudogene (stop codon)
L. variegatus	RAG1??-like	AGCV02077315.1	455	11			Pseudogene (stop codon)
L. variegatus	RAG1??-like	AGCV02050095.1	50	491			Pseudogene (stop codon)
L. variegatus	RAG2x-like	AGCV02054233.1			2797	1952	
L. variegatus	RAG2x-like	AGCV02250166.1			734	1834	

Transcripts

We can find very short **RAG1-like** transcripts (**GAUR01031317.1** – Partial transcript of AGCV02009112.1)

Table S16. *RAG1/2-like* copies in *Arbacia punctulata* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant transcript results.

A. punctulata

Table S17. *RAG1/2-like* copies in *Eucidaris tribuloides* genomes.

Genomics				RAG1-like		RAG
Species	**Genomics**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**
🟧	Orange color = complete RAG-like protein					
🟨	Yellow color = RAG1/2-like in the same scaffold					
RAG1B2a-like = 2nd duplication in RAG2B-locus in echinoderms						
RAG2x-like : Not phylogenetically assigned						
There are not included those with a Query cover <20% and a Ident <30%						
E. tribuloides		RAG1B1-like – RAG2B1-like	JZLH010201023.1	14471	10246	2995
E. tribuloides		RAG1B1-like	JZLH010588349.1	14331	12831	
E. tribuloides		RAG1B1-like	JZLH010926899.1	4294	8170	
E. tribuloides		RAG1B2-like – RAG2B2-like	JZLH010192588.1	13937	9563	3258
E. tribuloides		RAG1B2-like	JZLH010924454.1	5745	3014	
E. tribuloides		RAG1B2-like	JZLH010604796.1	992	10	
E. tribuloides		RAG1B2-like	JZLH010204041.1	1134	3739	
E. tribuloides		RAG1B-like	JZLH010029400.1	2894	927	
E. tribuloides		RAG1B-like	JZLH010807551.1	9475	8027	
E. tribuloides		RAG1B-like	JZLH010603647.1	21368	19904	
E. tribuloides		RAG1B2a-like	JZLH010134053.1	10199	8415	
E. tribuloides		RAG1B2a-like	JZLH010598024.1	7158	4750	
E. tribuloides		RAG1B2a-like	JZLH010877503.1	13693	15641	
E. tribuloides		RAG1B2a-like	JZLH010598025.1	2004	207	
E. tribuloides		RAG1B2a-like	JZLH010996576.1	4563	2869	
E. tribuloides		RAG1B2-like	JZLH010706307.1	7403	6484	
E. tribuloides		RAG1B2-like	JZLH010196803.1	21037	15964	
E. tribuloides		RAG1B2-like	JZLH010208141.1	607	1495	
E. tribuloides		RAG1B2a-like	JZLH010672642.1	700	62	
E. tribuloides		RAG1B2a-like	JZLH010402919.1	4850	3862	
E. tribuloides		RAG1B2a-like	JZLH010570475.1	11038	11899	
E. tribuloides		RAG1B2a-like	JZLH010221689.1	3230	108	
E. tribuloides		RAG1B2-like	JZLH010196804.1	7424	3632	
E. tribuloides		Fragment	JZLH010939303.1	3589	8274	
E. tribuloides		RAG1B2-like	JZLH010095137.1	11504	10225	
E. tribuloides		Fragment	JZLH011004596.1	10667	11554	
E. tribuloides		Fragment	JZLH010900583.1	5058	4335	
E. tribuloides		Fragment	JZLH010294192.1	10561	11422	
E. tribuloides		Fragment	JZLH010900582.1	4994	4288	
E. tribuloides		Fragment	JZLH010098881.1	31285	29711	
E. tribuloides		RAG1-like_Fragment – RAG2-like	JZLH010790248.1	5310	3950	1049
E. tribuloides		Fragment	JZLH010015240.1	7447	6926	
E. tribuloides		RAG2B2-like	JZLH010009838.1			12398
E. tribuloides		RAG2B2-like	JZLH010087786.1			25040

E. tribuloides

E. tribuloides	RAG2B2-like	JZLH010464424.1	3701
E. tribuloides	RAG2x-like	JZLH010029397.1	6567
E. tribuloides	Fragment	JZLH010089547.1	4092
E. tribuloides	Fragment	JZLH010921857.1	1601
E. tribuloides	Fragment	JZLH010078708.1	12883
E. tribuloides	Fragment	JZLH010941783.1	1120

Transcripts

We find only one transcript for RAG2-like (GAZP01042598.1)

				RAG1-like		RAG
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**
E. tribuloides	TRANSCRIPT	RAG2-like	GAZP01042598.1			810

2-like
End
7018
6615
837
11550
19648

E. tribuloides

7589

9709

3472

1063

13301

110

2-like

End

4

Notes
RAG1-like blastx 2 sequences: Query1 / Subjct14486__Query62 / Subjct 14301 - INTRON - Query63 / Subjct13279__Query241/Subjct12743 - IN
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon)
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon)
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon).
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon).
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon)
Pseudogene (stop codon).
Pseudogene (stop codon).

Pseudogene (stop codon)

Pseudogene (stop codon)

Pseudogene (stop codon)

Pseudogene (stop codon)

Notes

Length: 914

Partial transcript of JZLH010941783.1 (Query 97% & Ident 70%)

E. tribuloides

E. tribuloides

Table S18. *RAG1/2-like* copies in *Ophiothrix spiculata* genomes.

Genomics

Species	RAG ID	scaffold ID	RAG1-like Start	RAG1-like End	RAG2-like Start	RAG2-like End
RAG1x : Not phylogenetically assigned						
There are included those with a Query cover >14%. Smallest Ident; 30%						
O. spiculata	RAG1B-like (1) – RAG2B-like (1)	JXSR01321259.1	6431	8453	8640	9326
O. spiculata	RAG1B-like (1)	JXSR01137909.1	3884	2097		
O. spiculata	RAG1B-like (1)	JXSR01509747.1	1802	2543		
O. spiculata	RAG1B-like (1)	JXSR01424580.1	1074	2029		
O. spiculata	RAG1B-like (1)	JXSR01174233.1	12379	7877		
O. spiculata	RAG1x2-like	JXSR01257084.1	3067	4401		
O. spiculata	RAG1x1-like	JXSR01326072.1	112	1260		
O. spiculata	RAG1x1-like	JXSR01313620.1	9747	11432		
O. spiculata	RAG1x3-like	JXSR01590818.1	7864	8317		
O. spiculata	RAG1B-like (2)	JXSR01445370.1	2127	2672		

Transcripts

We do not find any TSA project

Notes
Pseudogene (stop codon)
Pseudogene (stop codon).
Pseudogene (stop codon)

Table S19. *RAG1/2-like* copies in *Ophiocoma echinata* genomes.

Genomics

There is no WGS project

Transcripts

Transcript fragments in RAG2-like (**GAUQ01068411.1**)

Transcript fragments for RAG1-like (**GAUQ01034189.1*, GAUQ01007173.1*** & **Contig1**)

* There are to small to be classify. Both RAG1-like are the same.

Contig 1	GAUQ01058697.1|+ gi|637410679| gb|

O. echinata

Table S20. *RAG1/2-like* copies in *Henricia sp. AR-2014* genomes.

RAG2x-like : Not phylogenetically assigned

Genomics

There is no WGS project

Transcripts

				RAG1-like		RAG2-like	
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
Henricia sp.	TRANSCRIPT	RAG1B-like	GAVP01020485.1	26	1450		
Henricia sp.	TRANSCRIPT	RAG2x-like	GAVP01027111.1			194	1009

Transcript fragments for RAG1-like (**GAVP01020484.1***, **GAVP01036659.1**, GAVP01036658.1 & **GAVP0**

*RAG1-like of Henricia sp. are similar to each other (no CAP)

*RAG2-like of Henricia sp. can not be classify easily in a family.

Henricia sp. AR-2014

Notes	
Length: 1460	*
Length: 1023	*

1083962.1*)

Table S21. *RAG1/2-like* copies in *Echinaster spinulosus* genomes.

RAG1x-RAG2x like : Not phylogenetically assigned

Genomics

There is no WGS project

Transcripts

We find a significant transcript result for **RAG2x**-like (**Contig1***) and a small fragment (**GAVE01094595.1***).

Also we find some transcript fragments for **RAG1x**-like (**GAVE01108867.1**, GAVE01016803.1, **GAVE01014984.1*** & **GAVE01**

<table>
<tr><th>Species</th><th>Transcript</th><th>RAG ID</th><th>scaffold ID</th><th>Notes</th></tr>
<tr><td><i>E. spinolusus</i></td><td>TRANSCRIPT</td><td>RAG2-like</td><td></td><td><i>Other transcripts:
Contig1_RAG2 : gi|637915705|gb|GAVE01094586.1|+
gi|637915714|gb|GAVE01094577.1|+
is in gi|637915705|gb|GAVE01094586.1|+
gi|637915708|gb|GAVE01094583.1|+
gi|637915709|gb|GAVE01094582.1|+
gi|637915718|gb|GAVE01094573.1|+
is in gi|637915709|gb|GAVE01094582.1|+
gi|637915712|gb|GAVE01094579.1|+
is in gi|637915718|gb|GAVE01094573.1|+
gi|637915719|gb|GAVE01094572.1|+
is in gi|637915709|gb|GAVE01094582.1|+
gi|637915710|gb|GAVE01094581.1|+</i></td></tr>
</table>

*RAG2-like of E. spinolusus are similar from each other (no CAP)

*RAG1-like of E. spinolusus. can not be classify easily in a family.

E. spinulosus

04389.1)

Table S22. *RAG1/2-like* copies in *Peribolaster folliculatus* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant transcript results.

P. folliculatus

Table S23. *RAG1/2-like* copies in *Leptasterias sp. AR-2014* genomes.

RAG1x : Not phylogenetically assigned

Genomics

There is no WGS project

Transcripts

We find significant transcript results for **RAG2B2**-like (**GAVC01001406.1**)

Transcript fragments for **RAG1x**-like (**Contig1**)

*RAG2-like of Leptasterias sp. is likely to be part of the RAG2B2-like family.

Contig1	GAVC01066306.1|+ gi|638922403|gb|

Leptasterias sp.

Table S24. *RAG1/2-like* copies in *Pisaster ochraceus* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant results (NS)

P. ochraceus

Table S25. *RAG1/2-like* copies in *Marthasterias glacialis* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant results (NS)

M. glacialis

Table S26. *RAG1/2-like* copies in *Asterias rubens* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant results (NS)

A. rubens

Table S27. *RAG1/2-like* copies in *Asterias forbesi* genomes.

🟧 Orange color = complete RAG-like protein

Genomics

There is no WGS project

Transcripts

				RAG1-like		RAG2-like	
Species	**Transcript**	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
A. forbesi	TRANSCRIPT	RAG1B2-like*	GAUS01036390.1	2643	115		
A. forbesi	TRANSCRIPT	RAG1B2-like*	GAUS01036391.1	2040	118		
A. forbesi	TRANSCRIPT	RAG2B2-like	GAUS01036395.1			1072	230

*RAG1-like of A. forbesi.is likely to be part of the RAG1B2-like family.

*RAG2-like of A. forbesi.is likely to be part of the RAG2B2-like family.

Notes	
Length: 2943	*mRNA Traduction Reverse frame 1. Position: 300-2832*
Length: 5072	
Length: 1755	

Table S28. *RAG1/2-like* copies in *Asterias amurensis* genomes.

Genomics

There is no WGS project

Transcripts

We find transcript fragments in **RAG2B2**-like (**GAVL01057092.1**) and **RAG1**-like (**GAVL01012549.1_not significant [**

A. amurensis

NS])

Table S29. *RAG1/2-like* copies in *Luidia clathrata* genomes.

Genomics

There is no WGS project

Transcripts

We do not find significant results (NS)

L. clathrata

Table S30. *RAG1/2-like* copies in *Acanthaster planci* genomes.

Genomics

We do not find significant results (NS)

Transcripts

We do not find significant results (NS)

A. planci

Table S31. *RAG1/2-like* copies in *Patiria miniata* genomes.

🟧 Orange color = complete RAG-like protein

Genomics

			RAG1-like		RAG2-like	
Species	**RAG ID**	**scaffold ID**	**Start**	**End**	**Start**	**End**
There are included those with a Query cover >20%. Smallest Ident. 34%						
P. miniata	RAG1B2-like	JH771625.1	459	2171		
P. miniata	RAG1B2-like	JH769343.1	3828	5535		
P. miniata	RAG1B2-like	AKZP01053171.1	3445	4824		
P. miniata	RAG1B2-like	JH769405.1	5927	4209		
P. miniata	RAG1B2-like	JH780581.1	4440	3176		
P. miniata	RAG1-like	JH775991.1	1186	839		
There are included those with a Query cover >20%.						
P. miniata	RAG2B2-like	JH772703.1			1031	3195

Transcripts - NR database

We can find a short **RAG1-like** transcripts (**GAWB01010448.1** – partial and short transcript of *J*

P. miniata

Structure	TSD Sequence
TSD-5TIR-RAG1-3TIR-TSD	>Pmi_JH771625 ---TTCAGcaa
TSD-5TIR-RAG1	>Pmi_JH769343 gagTTTAG---
RAG1-3TIR	

771625.1 [Query 100% & Ident 96%] or AKZP01019636.1 [Query 100% & Ident 80%]).

P. miniata

TIR Sequence	Notes
CACAGCGAAAAATGCCTTACATGAATTGACA---- CGGAGCGGCCTTGAGAGGGCGGCACAGCT >Pmi_JH771625_3_71_bp CACAGCGAAAAATTCCCCATTGGTAGTGTAA---- >Pmi_JH769343_5_71_bp	Alternative name AKZP01053172.1 in the NCBI databs
CACAGTGAAAAATGCCTTANATAAATTGGCA---- CGGAGCGGCCGGTAGAGGGCGGCACAGCC	Alternative name AKZP01019636.1 in the NCBI databa
	Alternative name JH771625.1 in Echinobase. Pseudoge
	Alternative name AKZP01020859.1 in the NCBI databs
	Alternative name AKZP01114579.1 in the NCBI databs
>Pmi_AKZP01172991_3_71_bp CACAGCGAAAAATTCCCCATTGGCCGTGTAA---- CACGGATGGGAATGGGGGCGTGGGCGACA	Alternative name AKZP01090827.1 in the NCBI databs

P. miniata

se.

ase. Pseudogene (stop codon)

ne (stop codon).

se. Pseudogene (stop codon)

se.

se

P. pectinifera

Table S10. *RAG1/2* copies in *Ophiocoma echinata* genomes.

We find transcript fragments in RAG2-like (GAUQ01068411.1) and RAG1-like (GAUQ01034189.1, GAUQ01007173.1, GAUQ0

Table S32. *RAG1/2-like* copies in *Patiria pectinifera* genomes.

Genomics

There is no WGS project

Transcripts

We find transcript fragments in **RAG1B1**-like (**GAVT01102981.1***) and **RAG2B2**-like (**Contig2** & **Contig1**)

*RAG1-like of P. pectinifera.is part of the RAG1B1-like family.

Note:

Contig1_RAG2-like= gb|GAVT01098600.1|-
gi|638542668|gb|GAVK01108580.1|+ is in gb|GAVT01098600.1|-

Contig2_RAG2-like= gb|GAVT01012421.1|+
gi|638541702|gb|GAVK01109546.1|+

P. pectinifera

1058697.1 & GAUQ01058696.1)

P. pectinifera