

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

Dark blue color = complete RAG-like protein  
 Aqua color = RAG1/2-like in the same scaffold

RAG1x – RAG2x: Not phylogenetically assigned

Genomics			RAG1-like		RAG2-like							
Species	Genomics	RAG ID	scaffold ID	Start	End	Start	End	Structure	TSD Sequence	TIR sequence	Notes	
<i>P. flava</i>		RAG1A-like	BCFJ01043787.1	6511	7692						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1A-like	BCFJ01026384.1	8838	11546						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1A-like	BCFJ01053939.1	588	2285						Pseudogene (stop at the beginning of the contig)	
<i>P. flava</i>		RAG1A-like	BCFJ01053937.1	155	415						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1A-like	BCFJ01050366.1	1104	1367						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1B1-like – RAG2B1-	BCFJ01017854_/BCFJ01152714.1_BCFJ01052781.1*	2256	4186			TSD-5TIR-RAG1-RAG2-3TIR-TSD	>Pfl_B1_BCFJ01017854_BCFJ01052781 ccgCTGCGtg	>Pfl_B1_BCFJ01052781_3_71_bp CAC---ATATCAATTACCGGTAACCGATAG---- CGAATCGTAAAAAATCAACATGGCCGCT >Pfl_B_BCFJ01017854_5_71_bp CACTTATAGAGCAGCTANGAGCGCCATTTG---- CTAATTATAAATTATAATGACTGTATGAT >Pfl_B1_BCFJ01094280_3_71_bp CACTTATATATCAATTACATGTAACCGATAG---- CAAATCGTAAAAAATCAAAATGGCCG >Pfl_B1_BCFJ01094280_5_71_bp CACCTTGGCAGCAGTANGAACCCATGTTG---- CTAATTATAAATAATTAATTAATTGA	*Note: RAG1B 1575-139 (BCFJ01152714.1) + 3-1918 (BCFJ01052781.1)	
<i>P. flava</i>		RAG1B1-like – RAG2B1-	BCFJ01094280.1	11811	10838			TSD-5TIR-RAG1-RAG2-3TIR-TSD	>Pfl_B1_BCFJ01094280 gccCAATGtg		Pseudogene (stop codon)	
<i>P. flava</i>		RAG1B1-like	BCFJ01096996.1	1529	3333						Pseudogene (stop codon)	
<i>P. flava</i>		RAG2Bb-like	BCFJ01034179.1			9714	10894					
<i>P. flava</i>		RAG2Bc-like	BCFJ01293284.1			2	562				Short Scaffold. Length: 697	
<i>P. flava</i>		RAG2Bc-like	BCFJ01291212.1			2	220				Short Scaffold. Length: 221	
<i>P. flava</i>		RAG1Bd-like – RAG2Bd-	BCFJ01059137.1	3484	5013	5496	7684				Pseudogene (stop codon)	
<i>P. flava</i>		RAG1Bd-like	BCFJ01067914.1	9267	7317						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1Bd-like	BCFJ01059136.1	9896	9976							
<i>P. flava</i>		RAG1Bd-like	BCFJ01281385.1	941	3						*Probably from RAG1H family (Query 100% & Ident 75%)	
<i>P. flava</i>		RAG1x-like – RAG2x-like	BCFJ01006354.1	6381	4010	3854	3016				Pseudogene (stop codon)	
<i>P. flava</i>		RAG1B-like	BCFJ01097859.1	2644	4283						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1B-like	BCFJ01065830.1	27741	26621						Pseudogene (stop codon)	
<i>P. flava</i>		RAG1B-like	BCFJ01171729.1	1474	200						Pseudogene (stop codon)	
<i>P. flava</i>		RAG2B-like	BCFJ01142432.1									
<i>P. flava</i>		RAG1C-like – RAG2C-like	BCFJ01036631.1	888	10209	11187	14650	TSD-5TIR-RAG1-RAG2-3TIR-TSD	>Pfl_C_BCFJ01036631 cacCATCCga	>Pfl_C_BCFJ01036631_3_71_bp CACATCGCATTGTACCTGATTAAACCATAGAA---ATATGCT TTGTTTAGTTGCGG--GCAAAAT >Pfl_C_BCFJ01036631_5_71_bp CACATCGCATTCTCTTTAGAAAATTGGCTTG---- TTCAATTACGCCG	Intron vs Exon: With Spidey (DNA vs mRNA) we observe a single exon (Genomic coordinates 8334-10271 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_ Query 215 / Sbjct 1532 - INTRON - Query 216 / Sbjct 6621_ Query 292 / Sbjct 6848 - INTRON - Query 293 / Sbjct 7552_ Query 348 / Sbjct 7716 - INTRON - Query 349 / Sbjct 8164_ Ouerv 1030 / Sbjct 10209) Pseudogene (stop codon).	
<i>P. flava</i>		RAG1C-like	BCFJ01041895.1	5629	7445						Pseudogene (stop codon).	
<i>P. flava</i>		RAG1C-like	BCFJ01047137.1	43	237			TSD-5TIR-RAG1	>Pfl_C_BCFJ01047137 gtgCATTG---	>Pfl_C_BCFJ01047137_5_71_bp TACATCGCATTCTCTTTAGAAAATTGCTTG---- TTCAATTACGCCGCGCATGCCCAACATTC	Pseudogene (stop codon).	
<i>P. flava</i>		RAG1C-like	BCFJ01088492.1	224	601							
<i>P. flava</i>		RAG1C-like	BCFJ01263664.1	1296	994						Pseudogene (stop codon).	
<i>P. flava</i>		RAG1C-like	BCFJ01236165.1	340	5							
<i>P. flava</i>		RAG1C-like	BCFJ01236166.1	340	5							

Species	Transcript	RAG ID	scaffold ID	RAG1		RAG2		Notes
				Start	End	Start	End	
								Contig 2 gb GDGM01238338.1 + 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 + Other transcripts: gb GDGM01014902.1  gb GDGM01481817.1
<i>P. flava</i>	TRANSCRIP' RAG1A-like							
<i>P. flava</i>	TRANSCRIP' RAG1B-like (allele)	gb GDGM01438088.1		87	3011			
<i>P. flava</i>	TRANSCRIP' RAG2B-like (allele)*	gb GDGM01245220.1			325	2		*RAG2B potential transcript. Length: 327
<i>P. flava</i>	TRANSCRIP' RAG2B-like (allele)*	gb GDGM01047156.1			205	20		*RAG2B potential transcript. Length: 205
								Contig 1 gb GDGM01081107.1 + gb GDGM01504835.1 + is in gb GDGM01081107.1 +
<i>P. flava</i>	TRANSCRIP' RAG2Bc-like							
<i>P. flava</i>	TRANSCRIP' RAG1C-like (allele)*	gb GDGM01025609.1		2	1876			*RAG1C potential transcript. Length: 1937
<i>P. flava</i>	TRANSCRIP' RAG2C-like (allele)*	gb GDGM01097917.1			25	739		*RAG2C potential transcript. Length: 1641
<i>P. flava</i>	TRANSCRIP' RAG2E-like	gb GDGM01150449.1			3	476		Length: 528

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

**Table S2. RAG1/2-like copies in *Echinarachnius parma* genomes.**

**Genomics**

We do not find WGS project

<b>Transcripts</b>				RAG1-like		RAG2-like		
<b>Species</b>	<b>Transcript</b>	<b>RAG ID</b>	<b>scaffold ID</b>	<b>Start</b>	<b>End</b>	<b>Start</b>	<b>End</b>	<b>Notes</b>
<i>E. parma</i>	TRANSCRIP	RAG1B1-like	Contig1					<i>gi/638076396/gb/GAVF01032928.1/+</i> <i>gi/638076394/gb/GAVF01032930.1/+</i> *
<i>E. parma</i>	TRANSCRIP	RAG1B1-like	GAVF01032929.1	1	789			<i>Length: 840</i> *
<i>E. parma</i>	TRANSCRIP	RAG1B1-like	GAVF01009690.1	5	607			<i>Length: 690</i> *
<i>E. parma</i>	TRANSCRIP	RAG2B1-like	Contig2					<i>gi/638056455/gb/GAVF01052869.1/+</i> <i>gi/638056452/gb/GAVF01052872.1/+ is in</i> * <i>gi/638056455/gb/GAVF01052869.1/+</i> <i>gi/638056454/gb/GAVF01052870.1/+ is in</i> <i>gi/638056455/gb/GAVF01052869.1/+</i> <i>Length: 1255</i>
<i>E. parma</i>	TRANSCRIP	RAG2B1-like	Contig1					<i>gi/638056450/gb/GAVF01052874.1/+ gi/638056457/gb/GAVF01052867.1/+ gi/638056453/gb/GAVF01052871.1/+</i> *
<i>E. parma</i>	TRANSCRIP	RAG2B1-like	GAVF01015158.1		15	875		<i>Length: 1195</i>

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 family.

**Table S3. RAG1/2-like copies in *Evechinus chloroticus* genomes.**

Dark blue color = complete RAG-like protein

**Genomics**

There is no WGS project

**Transcripts**

Species	Transcript	RAG ID	scaffold ID	RAG1-like		RAG2-like		Notes
				Start	End	Start	End	
<i>E. chloroticus</i>	TRANSCRIP	RAG1B2-like	GAPB01003278.1	596	2638			<i>Length: 3050* Frame 2. Traduction positions 156-2637</i>
<i>E. chloroticus</i>	TRANSCRIP	RAG1B2-like	GAPB01008000.1	324	1931			<i>Length: 2875*</i>
<i>E. chloroticus</i>	TRANSCRIP	RAG1B2-like	GAPB01020750.1	45	1340			<i>Length: 1340*</i>
<i>E. chloroticus</i>	TRANSCRIP	RAG1B2-like	GAPB01045749.1					
<i>E. chloroticus</i>	TRANSCRIP	RAG1B2-like	GAPB01022367.1					
<i>E. chloroticus</i>	TRANSCRIP	RAG2B2-like	Contig 1					<i>gi/559439143/gb/GAPB01022632.1/+ * gi/559439142/gb/GAPB01022633.1/+ *</i>
<i>E. chloroticus</i>	TRANSCRIP	RAG2B2-like	GAPB01063365.1			3293	2442	<i>RAG2 potential transcriptn of NM_001033012.2. Length: 3383 *</i>

\*RAG1-like of *Evechinus chloroticus* are different from each other and they are likely to be part of the RAG1B2-like family.

\*RAG2-like of *Evechinus chloroticus* are different from each other and they are likely to be part of the RAG2B2-like family.

**Table S4. RAG1/2-like copies in *Strongylocentrotus purpuratus* genomes.**

Dark blue color = complete RAG-like protein  
 Aqua color = RAG1/2-like in the same scaffold

There are not included those with a Query cover <15% and a Ident <58%

RAG2x : Not phylogenetically assigned

Genomics	RAG ID	scaffold ID	RAG1-like		RAG2-like		End Notes
			Start	End	Start	End	
<b>Species</b>							
<i>S. purpuratus</i>	RAG1B1-like - RAG2B1-like	AAGJ05119967.1	11126	6070	2882	1120	Pseudogene (stop codon at the end of RAG1-like). It correspond to RAG1/2-like published. Frame -3. Intron vs exon (see published article)Pseudogene (stop codon at the end of RAG1-like). It correspond to RAG1/2-like published. Frame -3. Intron vs exon (see published article)
<i>S. purpuratus</i>	RAG1B1-like	AAGJ05093368.1	2157	2628			Pseudogene (stop codon)
<i>S. purpuratus</i>	RAG1B1-like	AAGJ05091685.1	19332	18460			
<i>S. purpuratus</i>	RAG1B1-like	AAGJ05093365.1	22467	24496			Pseudogene (stop codon)
<i>S. purpuratus</i>	RAG1B1-like	AAGJ05093366.1	6734	7481			
<i>S. purpuratus</i>	RAG1B1-like	AAGJ05107091.1	2414	1759			
<i>S. purpuratus</i>	RAG1B2-like	AAGJ05052375.1 (3 Identical copie:	665	9702			Pseudogene (stop codon)
<i>S. purpuratus</i>	RAG1B2-like	AAGJ05052374.1 (3 Identical copie:	1336	2049			Pseudogene (stop codon)
<i>S. purpuratus</i>	RAG1B2-like	AAGJ05052370.1	12342	18191			Pseudogene (stop codon).
<i>S. purpuratus</i>	RAG1B2-like	AAGJ05086369.1	8733	10078			Pseudogene (stop codon)
<i>S. purpuratus</i>	RAG2B1-like	AAGJ05119965.1			18311	18631	
<i>S. purpuratus</i>	RAG2B1-like	AAGJ05096689.1			387	139	
<i>S. purpuratus</i>	RAG2B1-like	AAGJ05108197.1			16407	15486	Pseudogene (stop codon).
<i>S. purpuratus</i>	RAG2B1-like	AAGJ05074252.1			38623	43035	
<i>S. purpuratus</i>	RAG2B-like	AAGJ05085999.1			7488	10283	Cis-duplication
<i>S. purpuratus</i>	RAG2x-like	AAGJ05080929.1			1003	596	Pseudogene (stop codon). 4Th locus (Partial locus very damaged)

## Transcripts

- **RAG2-like** paralog, with 80% identity (**JT103600.1** – Transcript of **AAGJ05108197.1** [RAG2B] in WGS database).
- A more divergent paralog with several stop codons (pseudogene) called RAG2B1-like (GAVU01006082.1– Transcript of **AAGJ05119967.1** [Query 97% & Ident 40%])
- Very close transcript sequences (**JT106157.1** & **GAVU01023365.1** – Transcripts of **AAGJ05119967.1** [Query 81% & Ident 95%] & [Query 100% & Ident 99%] respectively)
- Some fragments named (Contig1\_Rag2, GAVU01022021.1 – Both transcript fragment of **AAGJ05074252.1** [Query 100% & Ident 82%])

- **RAG1-like** close paralog (**Contig1\_RAG1**),

Divergent paralog named RAG1B2-like  
(GAVU01011698.1 – Partial transcript of  
AAGJ05052375.1. Intron vs exon: We can not predict  
the exon-intron structure because the genomic  
sequence it is not complete. Bad prediction.

- Fragments named (GAVU01024843.1 –Partial transcript of **AAGJ05107091.1** (Query 85% & Ident 87%);  
**GAVU01036260.1** – Partial transcript of **AAGJ05119967.1** (Query 25% & Ident 100%)  
**GAVU01022227.1** – Partial transcript of **AAGJ05116911.1** (Query 100% & Ident 100%) & **Contig2\_RAG1-like**)

### Notes:

Contig1\_RAG2-like= gi|374748692|gb|JT099428.1|-  
gb|GAVU01042378.1|+ is in Transcript fragment of **AAGJ05119967.1** (Query 81% & Ident 95%)  
gi|374748692|gb|JT099428.1|-

Contig1\_RAG1-like= gi|374755421|gb|JT106157.1|-  
gb|GAVU01015377.1|+ is in Transcripts of **AAGJ05119967.1** (Query 100% & Ident 87%)  
gi|374755421|gb|JT106157.1|-

Contig2\_RAG1-like= gb|GAVU01041231.1|+  
gi|374767377|gb|JT118113.1|+ Transcript fragment of **AAGJ05119967.1** (Query 100% & Ident 99%)  
Gb|GAVU01028205.1|+ is  
in gi|374767377|gb|JT118113.1|+

**Table S5. RAG1/2-like copies in *Paracentrotus lividus* genomes.**

RAG1x : Not phylogenetically assigned

**Genomics**

There is no WGS project

- Dark blue color = complete RAG-like protein
- Aqua color = RAG1/2-like in the same scaffold

**Transcripts fragments**

Species	Transcript	RAG ID	scaffold ID	Notes
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		Contig1*	gb GCZS01172032.1 -
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like		Contig2*	gb GCZS01074202.1 + is in gb GCZS01172032.1 - gb GCZS01118857.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like		Contig3*	gb GCZS01118856.1 + is in gb GCZS01118857.1 + gb GCZS01118856.1 + is in gb GCZS01118857.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like_RAG2B2-li	RAG1-like – RAG2-like (GCZS01045777.1)*		gb GCZS01045775.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like_RAG2B2-li	RAG1-like – RAG2-like (GCZS01045775.1_RAG2	Contig1-	gb GCZS01045776.1 + is in gb GCZS01045775.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		Contig16*	gb GCZS01055975.1 - gb GCZS01009528.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		GCZS01132703.1*	
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		GCZS01053115.1*	
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		Contig4*	gb GCZS01085025.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		GCZS01158909.1*	gb GCZS01085026.1 + is in
<i>P. lividus</i>	TRANSCRIP' RAG1B1-like		GCZS01150983.1*	gb GCZS01085025.1 +

			<i>gb</i>  GCZS01064032.1 +
			<i>gb</i>  GCZS01035764.1 + is in <i>gb</i>  GCZS01064032.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig5_ <b>FRAGMENT</b>	
			<i>gb</i>  GCZS01064029.1 + is in <i>gb</i>  GCZS01064032.1 + <i>gb</i>  GCZS01064037.1 + <i>gb</i>  GCZS01078431.1 -
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01064034.1_ <b>FRAGMENT</b>	
			<i>gb</i>  GCZS01185123.1 + <i>gb</i>  GCZS01096617.1 + <i>gb</i>  GCZS01184645.1 - is in <i>gb</i>  GCZS01096617.1 + <i>gb</i>  GCZS01096621.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like	Contig18_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01118862.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01051899.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01112634.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01112632.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01087284.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01030082.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01042568.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01021545.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig6_ <b>FRAGMENT</b>	<i>gb</i>  GCZS01006895.1 + <i>gb</i>  GCZS01032509.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01044111.1_ <b>FRAGMENT</b>	
			<i>gb</i>  GCZS01087285.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig17_ <b>FRAGMENT</b>	<i>gb</i>  GCZS01087291.1 + is in <i>gb</i>  GCZS01087285.1 + <i>gb</i>  GCZS01132331.1 + <i>gb</i>  GCZS01132329.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig7_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01097940.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01089541.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01014750.1_ <b>FRAGMENT</b>	



<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01055973.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01096624.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01078430.1_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01049902.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig8_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01049901.1/+ is in <i>gb</i> /GCZS01049902.1/+ <i>gb</i> /GCZS01049900.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01031833.1_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01091464.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig20_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01091461.1/+ is in <i>gb</i> /GCZS01091464.1/+ <i>gb</i> /GCZS01091466.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig15_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01091463.1/+ is in <i>gb</i> /GCZS01091466.1/+ <i>gb</i> /GCZS01019540.1/+ <i>gb</i> /GCZS01019539.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig10_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01091460.1/+ <i>gb</i> /GCZS01091465.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01077077.1_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01077078.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig9_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01077076.1/+ is in <i>gb</i> /GCZS01077078.1/+
<i>P. lividus</i>	TRANSCRIP' RAG1x-like	GCZS01132704.1*	
<i>P. lividus</i>	TRANSCRIP' RAG1B2-like	Contig12*	<i>gb</i> /GCZS01013198.1/+ <i>gb</i> /GCZS01013199.1/+ <i>gb</i> /GCZS01033997.1/-
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig11_ <b>FRAGMENT</b>	<i>gb</i> /GCZS01152001.1/+ is in <i>gb</i> /GCZS01033997.1/-

<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig13_ <b>FRAGMENT</b>	gb GCZS01064627.1 + gb GCZS01064628.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	Contig14_ <b>FRAGMENT</b>	gb GCZS01064630.1 + is in gb GCZS01064628.1 + gb GCZS01149128.1 + gb GCZS01019259.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01007361.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01170336.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01055974.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01052670.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01039677.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01026987.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01122106.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01087287.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01033022.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01057007.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01027952.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01174585.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1x-like	Contig19*	gb GCZS01072522.1 + gb GCZS01072519.1 +
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01057812.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG1-like	GCZS01156562.1_ <b>FRAGMENT</b>	
<i>P. lividus</i>	TRANSCRIP' RAG2B1-like	GCZS01182744.1*	
<i>P. lividus</i>	TRANSCRIP' RAG2B2-like	Contig2*	gb GCZS01031274.1 + gb GCZS01031273.1 + is in gb GCZS01031274.1 +

\*RAG1-like of *P. lividus* are different from each other and they are likely to be part of the RAG1B1-like & RAG2B2-like families.

\*RAG2-like of *P. lividus* seems to have suffer a duplication (RAG2B1-like & RAG2B2-like).

**Table S6. 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%						
<i>L. variegatus</i>	RAG1B1-like	AGCV02054232.1	6377	9006		Pseudogene (stop codon).
<i>L. variegatus</i>	RAG1B1-like	AGCV02411413.1	30469	23113		Pseudogene (stop codon).
<i>L. variegatus</i>	RAG1B1-like	AGCV02253428.1	684	159		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1B-like	AGCV02377058.1	2793	4091		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1B-like	AGCV02060696.1	13096	11036		
<i>L. variegatus</i>	RAG1B1-like	AGCV02009112.1	2792	3622		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1B-like	AGCV02405259.1	1761	20426		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1B-like	AGCV02139577.1	337	837		Similar to RAG1F family
<i>L. variegatus</i>	RAG1B1-like	AGCV02280906.1	495	1		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1B-like	AGCV02064217.1	4585	5202		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1??-like	AGCV02077315.1	455	11		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG1??-like	AGCV02050095.1	50	491		Pseudogene (stop codon)
<i>L. variegatus</i>	RAG2x-like	AGCV02054233.1			2797	1952
<i>L. variegatus</i>	RAG2x-like	AGCV02250166.1			734	1834

### Transcripts

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

**Table S7. RAG1/2-like copies in *Eucidaris tribuloides* genomes.**

Genomics		RAG1-like	RAG2-like					
Species	Genomics	RAG ID	scaffold ID	Start	End	Start	End	Notes
	Dark blue color = complete RAG-like protein							
	Aqua color = RAG1/2-like in the same scaffold							
RAG1B2a-like = 2 <sup>nd</sup> 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%								
<i>E. tribuloides</i>	RAG1B1-like – RAG2B1-like	JZLH010201023.1	14471	10246	2995	7018		RAG1-like blastx 2 sequences: Query1 / Subjct14486__Query62 / Subjct 14301 - INTRON - Query63 / Subjct13279__Query241/Subjct12743 - INTRON - Query242 / Subjct12039__Query840/Subjct10243 - RAG2-like:Pseudogene
<i>E. tribuloides</i>	RAG1B1-like	JZLH010588349.1	14331	12831				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B1-like	JZLH010926899.1	4294	8170				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2-like – RAG2B2-like	JZLH010192588.1	13937	9563	3258	6615		Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2-like	JZLH010924454.1	5745	3014				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2-like	JZLH010604796.1	992	10				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2-like	JZLH010204041.1	1134	3739				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B-like	JZLH010029400.1	2894	927				
<i>E. tribuloides</i>	RAG1B-like	JZLH010807551.1	9475	8027				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B-like	JZLH010603647.1	21368	19904				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010134053.1	10199	8415				
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010598024.1	7158	4750				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010877503.1	13693	15641				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010598025.1	2004	207				Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010996576.1	4563	2869				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2-like	JZLH010706307.1	7403	6484				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2-like	JZLH010196803.1	21037	15964				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2-like	JZLH010208141.1	607	1495				Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010672642.1	700	62				
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010402919.1	4850	3862				

<i>E. tribuloides</i>	RAG1B2a-like	JZLH010570475.1	11038	11899			
<i>E. tribuloides</i>	RAG1B2a-like	JZLH010221689.1	3230	108			Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG1B2-like	JZLH010196804.1	7424	3632			
<i>E. tribuloides</i>	Fragment	JZLH010939303.1	3589	8274			Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1B2-like	JZLH010095137.1	11504	10225			
<i>E. tribuloides</i>	Fragment	JZLH011004596.1	10667	11554			
<i>E. tribuloides</i>	Fragment	JZLH010900583.1	5058	4335			Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010294192.1	10561	11422			Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010900582.1	4994	4288			Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010098881.1	31285	29711			Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG1-like_Fragment – RAG2-li	JZLH010790248.1	5310	3950	1049	837	Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010015240.1	7447	6926			Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG2B2-like	JZLH010009838.1			12398	11550	
<i>E. tribuloides</i>	RAG2B2-like	JZLH010087786.1			25040	19648	Pseudogene (stop codon).
<i>E. tribuloides</i>	RAG2B2-like	JZLH010464424.1			3701	7589	Pseudogene (stop codon)
<i>E. tribuloides</i>	RAG2x-like	JZLH010029397.1			6567	9709	
<i>E. tribuloides</i>	Fragment	JZLH010089547.1			4092	3472	Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010921857.1			1601	1063	
<i>E. tribuloides</i>	Fragment	JZLH010078708.1			12883	13301	Pseudogene (stop codon)
<i>E. tribuloides</i>	Fragment	JZLH010941783.1			1120	110	Pseudogene (stop codon)

## Transcripts

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

RAG1-like RAG2-like

Species	Transcript	RAG ID	scaffold ID	Start	End	Start	End	Notes
<i>E. tribuloides</i>	TRANSCRIP	RAG2-like	GAZP01042598.1			810	4	Length: 914 Partial transcript of <i>JZLH010941783.1</i> (Query 97% & Ident 70%)

**Table S8. RAG1/2-like copies in *Ophiothrix spiculata* genomes.**

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

**Genomics**

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

**Transcripts**

We do not find any TSA project

### Table S9. 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	Notes
<i>Henricia</i> sp.	TRANSCRIP	RAG1B-like	GAVP01020485.1	26	1450			<i>Length: 1460</i> *
<i>Henricia</i> sp.	TRANSCRIP	RAG2x-like	GAVP01027111.1			194	1009	<i>Length: 1023</i> *

Transcript fragments for RAG1-like (**GAVP01020484.1\***, **GAVP01036659.1**, GAVP01036658.1 & **GAVP01083962.1\***)

\*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.

## Table S10. *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\* & GAVE01004389.1)**

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

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

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



**Table S11. RAG1/2-like copies in *Asterias forbesi* genomes.**

Dark blue color = complete RAG-like protein

**Genomics**

There is no WGS project

**Transcripts**

Species	Transcript	RAG ID	scaffold ID	RAG1-like		RAG2-like		Notes
				Start	End	Start	End	
<i>A. forbesi</i>	TRANSCRIPT RAG1B2-like*		GAUS01036390.1	2643	115			<i>Length: 2943</i>
<i>A. forbesi</i>	TRANSCRIPT RAG1B2-like*		GAUS01036391.1	2040	118			<i>Length: 5072</i>
<i>A. forbesi</i>	TRANSCRIPT RAG2B2-like		GAUS01036395.1			1072	230	<i>Length: 1755</i>

*mRNA  
Traduction  
Reverse  
frame 1.  
Position:  
300-2832*

\*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.

**Table S12. RAG1/2-like copies in *Patiria miniata* genomes.**

Genomics		RAG1-like		RAG2-like		Structure	TSD Sequence	TIR Sequence	Notes
Species	RAG ID	scaffold ID	Start	End	Start				
There are included those with a Query cover >20%. Smallest Ident. 34%									
<i>P. miniata</i>	RAG1B2-like	JH771625.1	459	2171			TSD-5TIR-RAG1-3TIR-TSD	>Pmi_JH771625_5_71_bp CACAGCGAAAAATGCCTTACAT GAATTGACA---- CGGAGCGGCCTTGAGAGGGCG GCACAGCT >Pmi_JH771625_3_71_bp ---TTCAGcaa CACAGCGAAAAATCCCCATTG GTAGTGTA---- CACGGATGGAACAGTGCCGTG GGCAGACA	Alternative name AKZP01053172.1 in the NCBI database.
<i>P. miniata</i>	RAG1B2-like	JH769343.1	3828	5535			TSD-5TIR-RAG1	>Pmi_JH769343_5_71_bp CACAGTGAAAAATGCCTTANAT AAATTGGCA---- gagTTTAG--- CGGAGCGGCCGGTAGAGGGC GGCACAGCC	Alternative name AKZP01019636.1 in the NCBI database. Pseudogene (stop codon)
<i>P. miniata</i>	RAG1B2-like	AKZP01053171.1	3445	4824					Alternative name JH771625.1 in Echinobase. Pseudogene (stop codon).
<i>P. miniata</i>	RAG1B2-like	JH769405.1	5927	4209					Alternative name AKZP01020859.1 in the NCBI database. Pseudogene (stop codon)
<i>P. miniata</i>	RAG1B2-like	JH780581.1	4440	3176					Alternative name AKZP01114579.1 in the NCBI database.
<i>P. miniata</i>	RAG1-like	JH775991.1	1186	839			RAG1-3TIR	>Pmi_AKZP01172991_3_71_bp CACAGCGAAAAATCCCCATTG GCCGTGTAA---- CACGGATGGGAATGGGGCGT GGCGGACA	Alternative name AKZP01090827.1 in the NCBI database

---

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 *JH771625.1* (Query 100% & Ident 96%) or AKZP01019636.1 [Query 100% & Ident 80%]).

## **Table S13. *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|+

**Table S14. *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 S15. *RAG1/2-like* copies in *Anneissia japonica* genomes.**

**Genomics**

We do not find WGS project

**Transcripts**

We do not find significant transcript results.

**Table S16. *RAG1/2-like* copies in *Psathyrometra fragilis* genomes.**

**Genomics**

We do not find WGS project

**Transcripts**

We do not find significant transcript results.

**Table S17. *RAG1/2-like* copies in *Abyssocucumis albatrossi* genomes.**

**Genomics**

We do not find WGS project

**Transcripts**

We do not find significant transcript results.

**Table S18. *RAG1/2-like* copies in *Sclerodactyla briareus* genomes.**

**Genomics**

We do not find WGS project

**Transcripts**

We do not find significant transcript results.

### **Table S19. *RAG1/2-like* copies in *Apostichopus japonicus* genomes.**

#### **Genomics**

We do not find WGS project

#### **Transcripts**

We do not find significant transcript results.

### **Table S20. *RAG1/2-like* copies in *Parastichopus parvimensis* genomes.**

#### **Genomics**

We do not find significant results (NS)

#### **Transcripts**

We do not find any TSA project

### **Table S21. *RAG1/2-like* copies in *Parastichopus californicus* genomes.**

#### **Genomics**

We do not find WGS project

#### **Transcripts**

We do not find significant transcript results.

### **Table S22. *RAG1/2-like* copies in *Sphaerechinus granularis* genomes.**

RAG1x – RAG2x : Not phylogenetically assigned

#### **Genomics**

There is no WGS project

#### **Transcripts**

Species	Transcript	RAG ID	scaffold ID	RAG1-like		RAG2-like		End Notes
				Start	End	Start	End	
<i>S. granularis</i>	TRANSCRIP	RAG2x-like	GAVR01037695.1		1597	755	Length: 1668	

Transcript fragments for **RAG1-like** (GAVP01036659.1, GAVR01070653.1, GAVR01070662.1, GAVR01070656.1, GAVR01070663.1, GAVR01023727.1, GAVR01049989.1, GAVR01049990.1, GAVR01090577.1)

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

**Table S23. *RAG1/2-like* copies in *Arbacia punctulata* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

We do not find significant transcript results.

**Table S24. *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 too small to be classified. Both RAG1-like are the same.

Contig 1  
gi|637410677|  
gb|GAUQ01  
058697.1|+  
gi|637410679|  
gb|GAUQ01  
058696.1|+

**Table S25. *RAG1/2-like* copies in *Peribolaster folliculatus* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

We do not find significant transcript results.

**Table S26. *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**)

Contig1

gi|638922399|  
gb|GAVC01  
066306.1|+  
gi|638922403|  
gb|GAVC01  
066303.1|+

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

**Table S27. *RAG1/2-like* copies in *Pisaster ochraceus* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

*We do not find significant results (NS)*

**Table S28. *RAG1/2-like* copies in *Marthasterias glacialis* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

*We do not find significant results (NS)*

**Table S29. *RAG1/2-like* copies in *Asterias rubens* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

*We do not find significant results (NS)*

**Table S30. *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[NS])**

**Table S31. *RAG1/2-like* copies in *Luidia clathrata* genomes.**

**Genomics**

There is no WGS project

**Transcripts**

*We do not find significant results (NS)*



**Table S32. *RAG1/2-like* copies in *Acanthaster planci* genomes.**

**Genomics**

*We do not find significant results (NS)*

**Transcripts**

*We do not find significant results (NS)*