

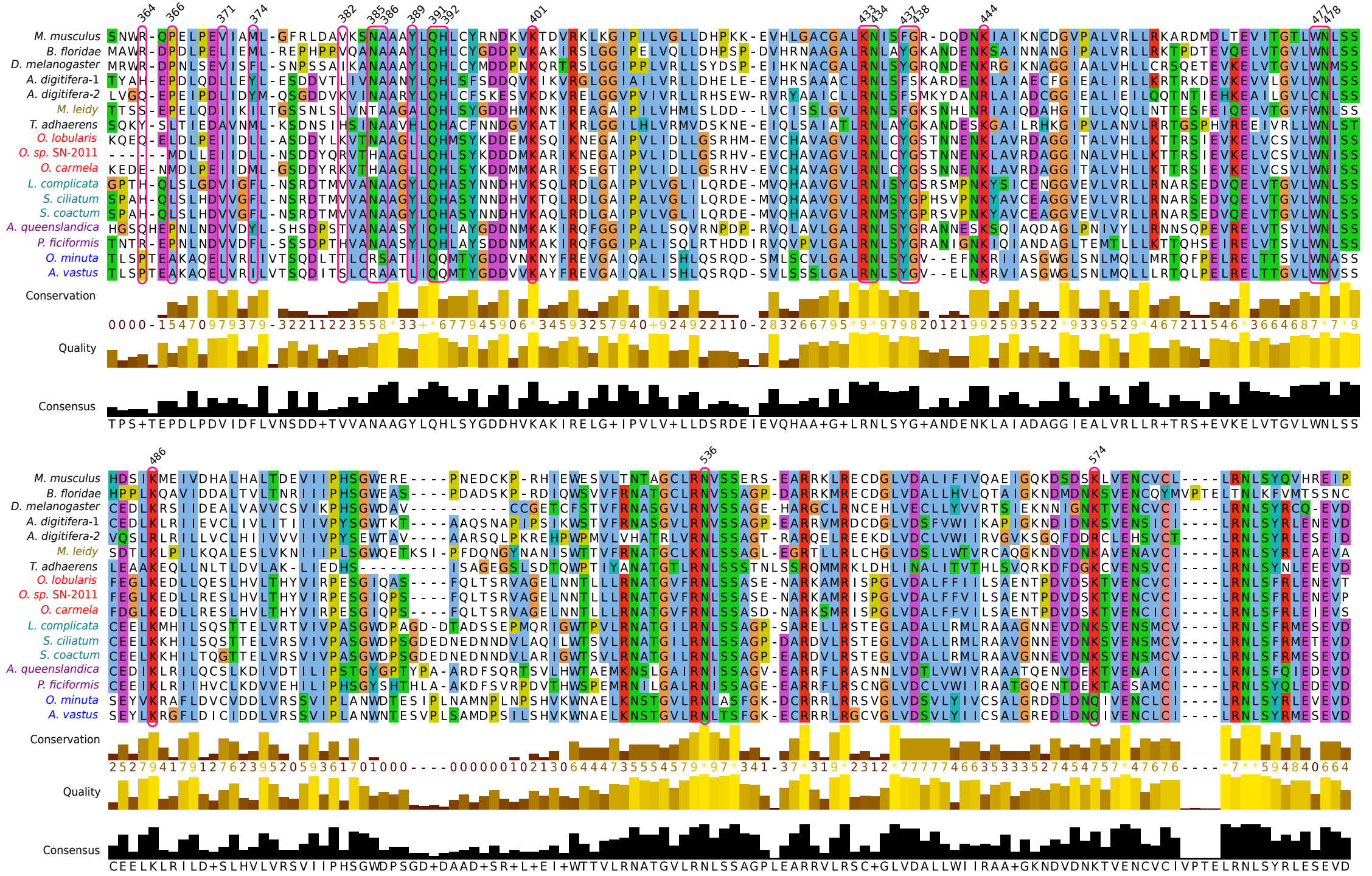
Figure S1A. Comparison of p120 sequences. Residues involved in interaction with E-cadherin are boxed in red. Most of them are conserved.

Figure S1B. Comparison of β -catenin sequences. A single β -catenin gene copy was identified in every studied species except for calcareous sponges that exhibit a duplication. All residues essential for E-cadherin interaction are boxed in pink and are highly conserved except for the R386 and N387 residues (replaced by L and T, respectively) in two hexactinellids and a more anecdotal change from A656 to S in placozoans. Residues boxed in blue are involved in α -catenin binding and in orange for the DTDL PDZ binding motif.

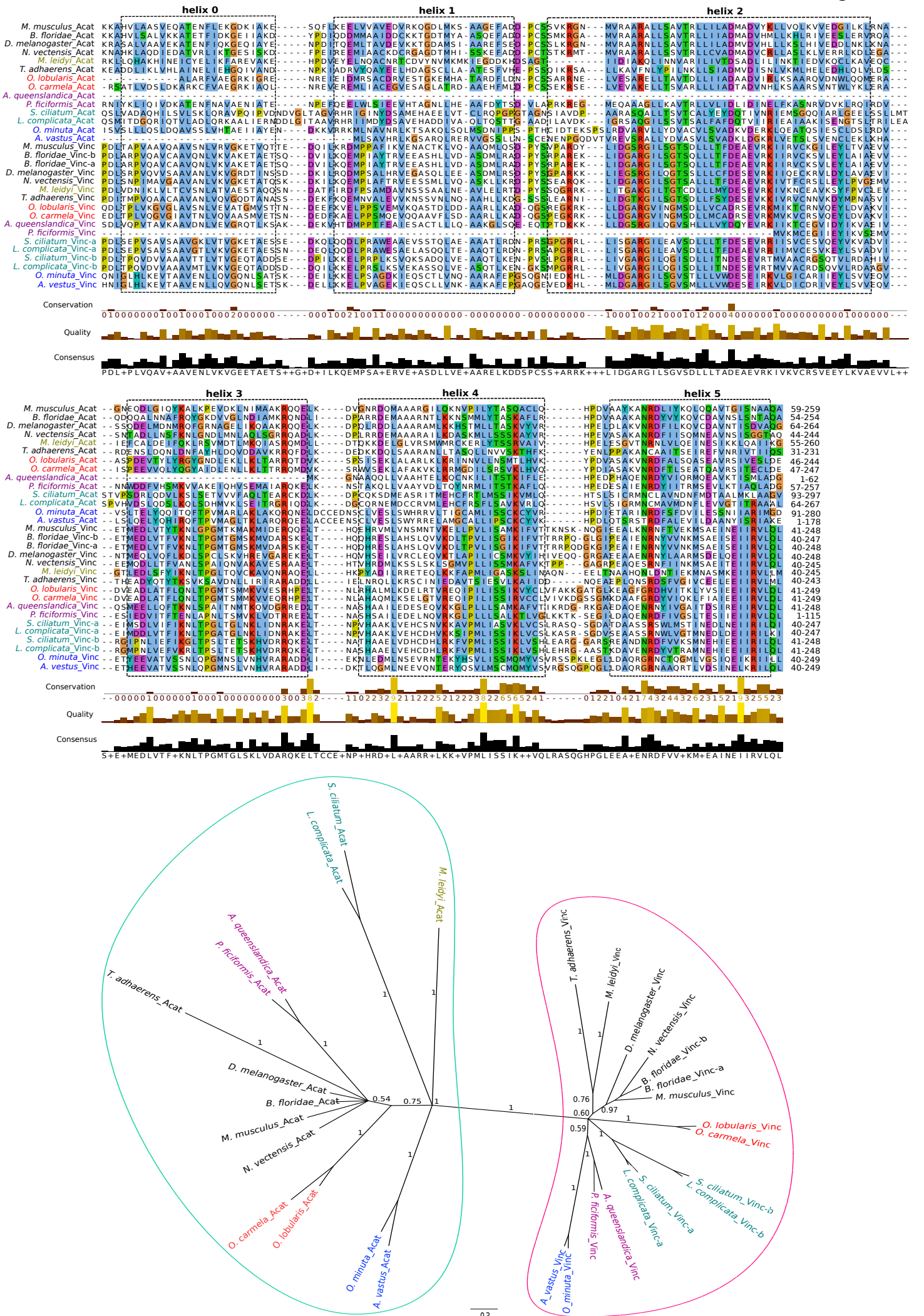
Figure S1C. Analyses of α -catenins and vinculins sequences. Sequences of α -catenins and vinculins were aligned based on the structural domains helix0 to helix5 in *Mus musculus* α -catenin and vinculin. Helices are boxed and the numbers at the end of each sequence indicate the range encompassed in the alignment. Secondary structure prediction by JNet (Jalview option) identified six helices in all sponge α -catenin sequences except for *A. queenslandica* (missing the 4 first helices) and *A. vastus* (missing helix0). All species analyzed in this study have one copy of α -catenin and one copy of vinculin well-separated in Bayesian tree with high support (pp=1) (bottom).

Figure S2. Structure of Par3 proteins in metazoans. Par3 exhibits a conserved N-terminal domain (CR1), three central PDZ domains, and a C-terminal region containing multiple protein binding sites including the aPKC-binding motif.

Figure S5. Domain composition of PatJ (*D. melanogaster*), INADL and MUPP1 (*M. musculus*) and Multiple PDZ containing protein (MPDZ) (*O. lobularis*, *S. ciliatum*, *A. queenslandica* and *O. minuta*). Note that only *O. lobularis* exhibits an MPDZ with a well-detected L27 domain (Evalue=8.5 10^{-4}) as bilaterians. *A. queenslandica* and *S. ciliatum* MPDZ have a low-scoring L27 domain (shaded in grey) according to the HMM profile search. There is no recognizable similarity to the L27 domain in the N-terminal region of *O. minuta* MPDZ.

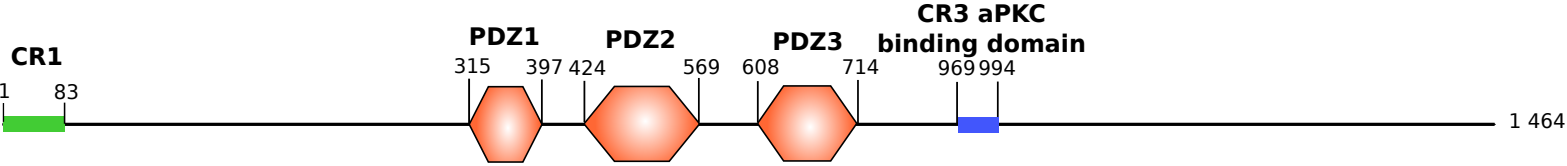






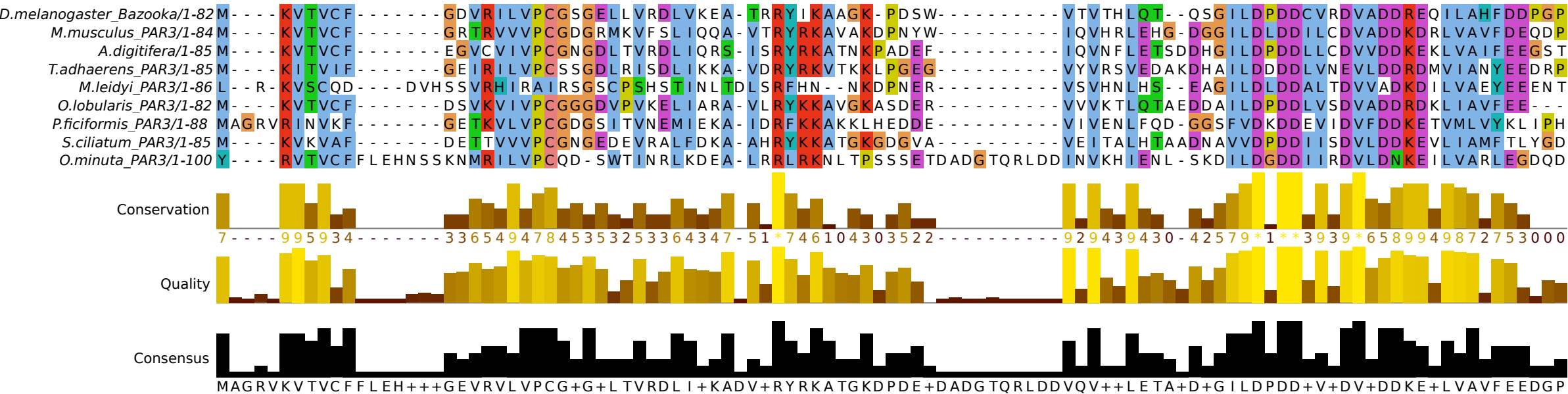
A

D. melanogaster Bazooka (PAR3) (O96782)

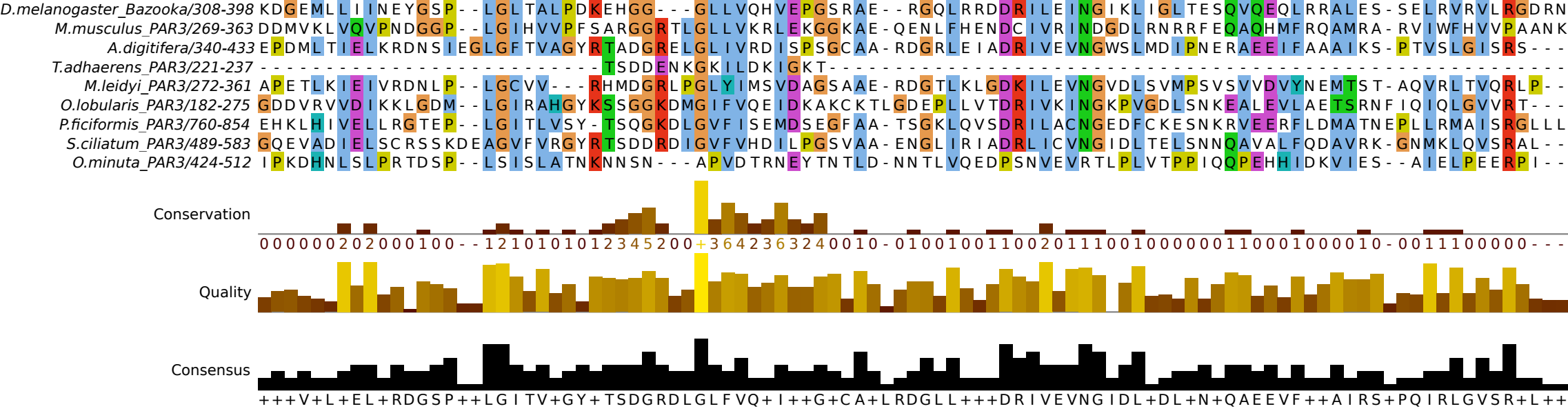


B

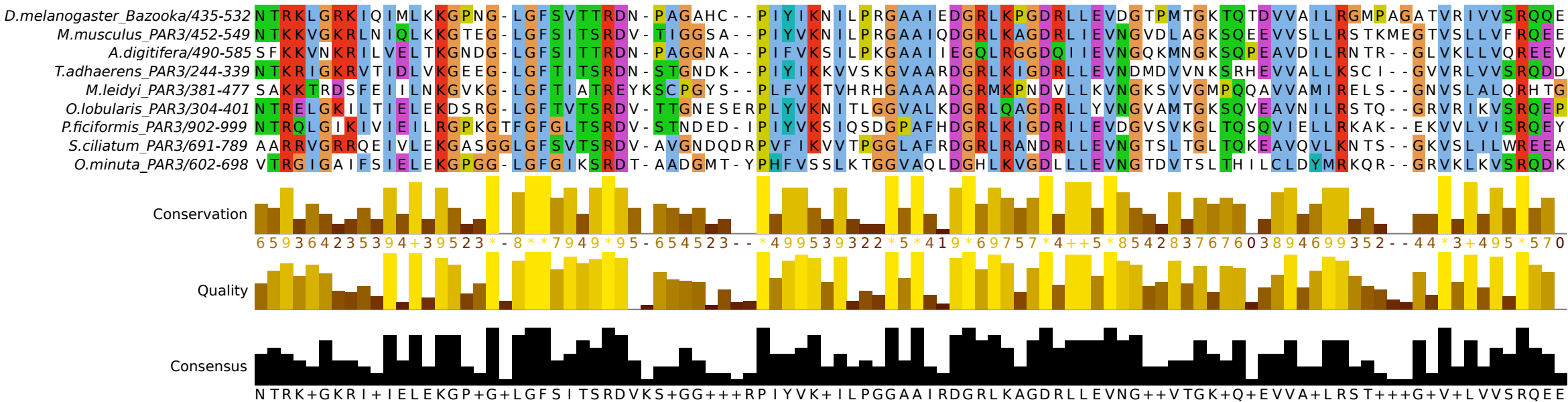
CR1 domain



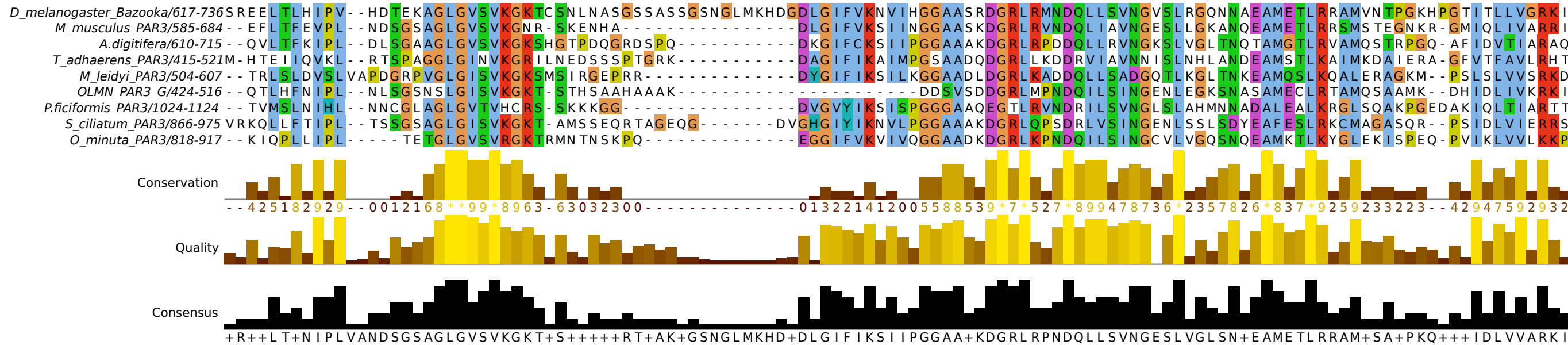
PDZ1 domain



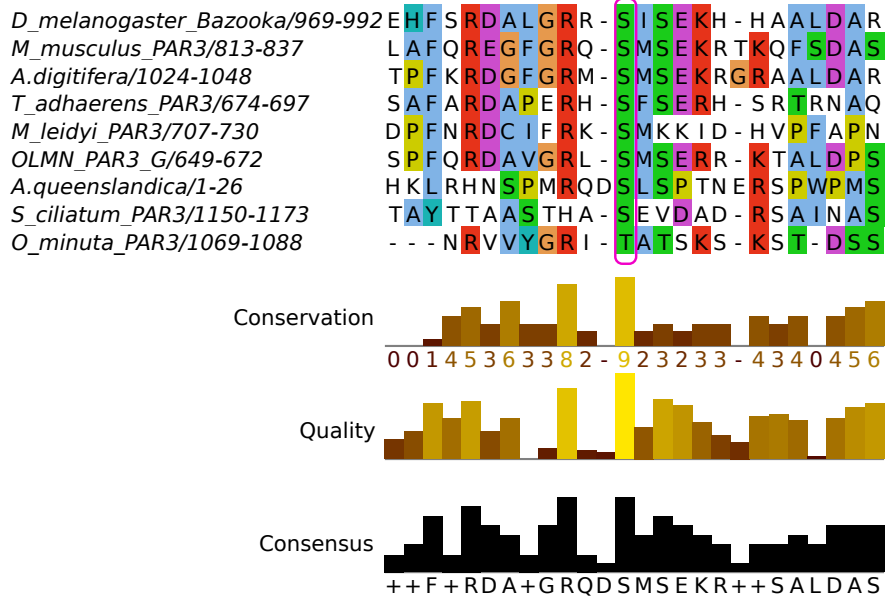
PDZ2 domain



PDZ3 domain



CR3 aPKC binding site



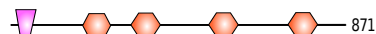
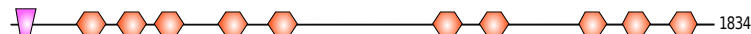
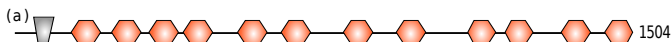
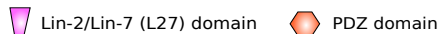
D. melanogaster* PATJ**M. musculus* INADL*****M. musculus* MUPP*****T. adhaerens* MPDZ*****O. lobularis* MPDZ*****A. queenslandica* MPDZ*****S. ciliatum* MPDZ*****O. minuta* MPDZ**

Table S1. Domain structures of the Lethal giant larvae (LGL) proteins in various metazoans

SMART domain diagram of *M. musculus* LGL1 (Q80Y17) canonical domain structure, and number of protein domains WD40, LLGL: Lethal giant larvae homologue 2 (Interpro domain IPR013577) and Lgl_C: Lethal giant larvae(Lgl) like, C-terminal (Pfam PF08596) for *M. musculus* (M. m); *Drosophila melanogaster* (D. m); *Nematostella vectensis* (N. v); *Oscarella lobularis* (O. l); *Oopsacas minuta* (O. m); *Sycon ciliatum* (S. c); *Amphimedon queenslandica* (A. q); *Trichoplax adhaerens* (T. a) and *Mnemiopsis leidyi* (M. l)



	M. m	D. m	N. v	O. l	O. m	S. c	A. q		T. a	M. l
	5	4	5	6	5	6	5	4	6	4
	1	1	1	1	1	1	1	1	1	1
	1	1	1	1	1	1	1	1	1	1
Length in aa	1, 036	1, 161	920	1, 117	1, 032	1, 241	1169	1130	1093	1170

Table S2. Domain structures of the Scribble (Src) proteins in various metazoans

SMART domain diagram of *M. musculus* Scribble (Q80U72) canonical domain structure, and number of protein domains LRR (leucine rich repeats), LRR TYP (leucine rich repeats, typical) and PDZ for *M. musculus* (M. m); *Drosophila melanogaster* (D. m); *Nematostella vectensis* (N. v); *Oscarella lobularis* (O. l); *Opsacas minuta* (O. m); *Sycon ciliatum* (S. c); *Amphimedon queenslandica* (A. q); *Trichoplax adhaerens* (T. a) and *Mnemiopsis leidyi* (M. l).

M. leidyi possesses multiple proteins containing LRR domains but since none PDZ domain is associated, these proteins were not taken into account.



	M. m	D. m	N. v	O. l	O. m	S. c	A. q	T. a
	10	14	12	12	11	13	10	12
	2	0	0	0	2	0	0	0
	4	4	4	3	3	3	3	4
Length in aa	1, 612	1, 756	1, 030	1, 460	978	1, 011	1, 561	1, 145

Table S3 :characteristics of the new private databases used in this study

	Taxa	species	Dataset	raw reads	corrected/selected reads	mapped reads	depth
Porifera	Hexactinellida		Pacbio	751 460	124 793	112 130	
		Leucopsacidae	PE ¹	395 851 746	335 361 472	234 150 237	380
			MP ² _3-5kb	245 157 912	92 657 868	24 712 816	54
		<i>Oopsacas minuta</i>	MP_5-8kb	274 964 868	116 755 522	25 643 839	56
			MP_8-11kb	191 742 544	79 280 536	15 423 954	34
			Transcriptome	421 126 244		207 529 788	1 443
	Homoscleromorpha		PE	307 384 094	112 751 740	51 225 276	97
		Oscarellidae	MP_3-5kb	254 563 152	106 866 702	20 327 965	51
		<i>Oscarella lobularis</i>	MP_5-8kb	251 314 628	106 866 702	18 165 914	45
			MP_8-11kb	295 517 160	114 050 246	13 598 285	34
			Transcriptome	380 096 086		231 475 388	710

1: Paired end

2: Mate Pair

Table S4: public databases used in this study : nature (genome/transcriptome) and link for accession

Taxa	Species	Database name	Sequence Type	URL
Demospongiae	<i>Amphimedon queenslandica</i>	Amphimedon_queenslandica.Aqu1.30.dna.genome.fa	Genome	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/amphimedon_queenslandica/dna/
		Aqu2_Genes_proteins.fasta	Prediction 1	
		Aqu2.1_Genes_proteins.fasta	Prediction 2	http://amphimedon.qcloud.qcif.edu.au/downloads.html
		Aqu2.1_Genes_mRNA.fasta	Transcriptome	
	<i>Petrosia ficiformis</i>	Petrosia_ficiformis_CLC.fasta	Transcriptome	https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/24737
Hexactinellida	<i>Aphrocallistes vastus</i>	Aphrocallistes_transcriptome-alberta.fasta	Transcriptome	https://era.library.ualberta.ca/files/bvd66w001v#.WEbM_tFVKIM
Porifera	Calcareia	SCIL_WGA_130802	Genome	
		SCIL_P-CDS_130802	Prediction	http://www.compagen.org/datasets.html
		SCIL_T-CDS_130802	Transcriptome 1	
		Sycon_coactum	Transcriptome 2	https://era.library.ualberta.ca/files/bjh343s467
	<i>Leucosolenia complicata</i>	LCOM_T-CDS_130802	Transcriptome	http://www.compagen.org/datasets.html
	Homoscleromorpha	Oscarella_sp.	Transcriptome	
		Oscar_WGA_120614.fas	Genome	http://www.compagen.org/datasets.html
		Oscar_T-CDS_130911	Transcriptome	
Cnidaria	Anthozoa	Corticium_candelabrum	Transcriptome	https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/24737
		Nematostella_vectensis.GCA_000209225.1.30.dna.genome.fa	Genome	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/nematostella_vectensis/dna/
		Nematostella_vectensis.GCA_000209225.1.30.pep.genome.fa	Prediction	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/nematostella_vectensis/pep/
		GCA_000222465.1_Adig_1.0_genomic.fna	Genome	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/222/465/GCA_000222465.1_Adig_1.0/
Placozoa	<i>Trichoplax adhaerens</i>	adi_transcriptome_assembly.v1.fa	Transcriptome	http://marinegenomics.oist.jp/coral/viewer/download?project_id=3
		Trichoplax_adhaerens.ASM15027v1.30.dna.genome.fa	Genome	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/trichoplax_adhaerens/dna/
Ctenophora	Lobata	Trichoplax_adhaerens.ASM15027v1.30.pep.all.fa	Prediction	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/trichoplax_adhaerens/pep/
		Mnemiopsis_leidy.GCA_000226015.1.30.dna.genome.fa	Genome	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-30/fasta/mnemiopsis_leidy/dna/
		Mnemiopsis_leidy.GCA_000226015.1.dna.nonchromosomal.fa	Genome	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-33/fasta/mnemiopsis_leidy/dna/
		Mnemiopsis_leidy.GCA_000226015.1.30.pep.all.fa	Prediction	ftp://ftp.ensemblgenomes.org/pub/metazoa/release-33/fasta/mnemiopsis_leidy/pep/
		ML_Trinity_transcripts.fa	Transcriptome 1	https://kona.nhgri.nih.gov/mnemiopsis/download/download.cgi?dl=transcript
	Pleurobrachiidae	Mnemiopsis_leidy_Illumina_RNA-seq	Transcriptome 2	http://neurobase.rc.ufl.edu/pleurobrachia/download
		GCA_000695325.1_P.bachei_draft_genome_v.1.1_genomic.fna	Genome 1	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/695/325/GCA_000695325.1_P.bachei_draft_genome_v.1.1/
		genome.v1b.fa	Genome 2	http://rogaevlab.ru/pleurobrachia/data/genome.v1b.fa
	Beroidea	Pleurobrachia_bachei_transcriptome_assembly.fasta	Transcriptome	http://rogaevlab.ru/pleurobrachia/data/Pleurobrachia_bachei_transcriptome_assembly.fasta.gz
		Beroe_abyssicola_Illumina_RNA-seq	Transcriptome	
Mollusca	Gastropoda	Beroe_sp_pink_Illumina_RNA-seq	Transcriptome	http://neurobase.rc.ufl.edu/pleurobrachia/download
		Aplysia_californica	Genome	ftp://ftp.ncbi.nlm.nih.gov/genomes/Aplysia_californica/CHR_Un/
Chordata	Cephalochordata	Branchiostoma_floridae_v2.0.assembly.fasta	Genome	
		transcripts.Braf1.fasta (assembly 1.0)	Transcriptome	http://genome.jgi.doe.gov/Braf11/Braf11.home.html

Table S5: Cadherin-Catenin Complex (CCC) sequence retrieval: Accession numbers or contig/scaffold references where candidate genes In bold accession numbers of sequences annotated from our two new transcriptomic and genomic sponge datasets.

1: see table S4 for the links to corresponding data sources; 2: Prediction of the protein sequence and/or the function

Complex	Gene	Taxa	Species	Sequence ID	Data sources ¹ for prediction ²
E-cadherin	Chordata		<i>Mus musculus</i>	P09803	
			<i>Gallus gallus</i>	P08641	
			<i>Ciona intest</i>	XP_009859529.1	
	Arthropoda		<i>Drosophila</i>	rQ24298	
	Cnidaria		<i>Nematostella</i>	XP_001631293.1	
	Placozoa		<i>Trichoplax adhaerens</i>		Scaffold_4 (Genome)
	Porifera		Oscarella	kMF780952	
			<i>Oscarella</i>	sx.G4W9D8	comp20092_c0_seq1
			<i>Amphimedon queenslandica</i>		Aqu2.16910_001 (Transcriptome 1)
			<i>Petrosia ficiformis</i>		SpoMult2_CAGATC_L001_R1_001_contig_5633
			<i>Sycon ciliatum</i>		scpid4789 (prediction)
			<i>Sycon coactum</i>		Contig_12142 (Transcriptome)
			<i>Leucosolenia complicata</i>		lctid26665 (Transcriptome)
			Oopsacas	rMF959449	
			<i>Aphrocallites vastus</i>		comp20072_c0_seq1 (Transcriptome)
	Ctenophora		<i>Mnemiopsis leidyi</i>		ML00359a-PA (prediction)
Beta-catenin	Chordata		<i>Mus musculus</i>	Q02248	
			<i>Branchiostoma</i>	Q4U478	
	Arthropoda		<i>Drosophila</i>	rP18824	
	Cnidaria		<i>Nematostella vectensis</i>		NEMVEscaffold_183 (Genome)
	Placozoa		<i>Trichoplax adhaerens</i>		TriadP22780 (prediction)
	Porifera		<i>Corticium candelabrum</i>		Contig_16639 (Transcriptome)
			Oscarella	kMF780953	
			<i>Oscarella carmela</i>		comp41806_c0_seq1 (Transcriptome)
			<i>Oscarella</i>	sx.G4W9D9	comp3163_c0_seq1 (Transcriptome)
			<i>Sycon ciliatum</i>	A0A077SQP5 and A0A077SQX3	
	Ctenophora		<i>Sycon coactum</i>		Contig_5031 (transcriptme) and Contig_19 (Transcriptome)
			<i>Leucosolenia complicata</i>		lctid45409 and lctid54960
			<i>Amphimedon</i>	NP_001266234.1/E2IJA6	Aqu2.23648 (Transcriptome 2)
			Oopsacas	rMF959459	
			<i>Aphrocallites vastus</i>		comp17679_c0_seq1 (Transcriptome)
	Ctenophora		<i>Mnemiopsis</i>	E3UKC7_MNELE	ML073715a-RA (prediction)
Gamma-catenin/P	Chordata		<i>Mus musculus</i>	P30999	
			<i>Branchiostoma floridae</i>		Bf_V2_15 (Transcriptome 1)
	Arthropoda		<i>Drosophila</i>	rQ7PLI0	
	Cnidaria		<i>Acropora</i>	diç	adi_EST_assem_414 (Transcriptome) adi_EST_assem_2325 (Transcriptome)
	Placozoa		<i>Trichoplax adhaerens</i>		Scaffold_11 (Genome)
	Porifera		Oscarella	kMF780954	
			<i>Oscarella</i>	sp. SN-2011	comp5428_c1_seq1 (Transcriptome)
			<i>Oscarella carmela</i>		comp43311_c0_seq1 (Transcriptome)
			Oopsacas	rMF959460	
			<i>Leucosolenia complicata</i>		lctid32410 (Transcriptome)
			<i>Sycon ciliatum</i>		sctid48573 (Transcriptome)
			<i>Sycon coactum</i>		Contig_12039 (Transcriptome)
	Ctenophora		<i>Mnemiopsis leidyi</i>		ML002622a-PA (prediction)
Alpha-catenin	Chordata		<i>Mus musculus</i>	P26231	
			<i>Branchiostoma</i>	C3Y5U8	
	Arthropoda		<i>Drosophila</i>	rP35220	
	Cnidaria		<i>Nematostella vectensis</i>		EDO48695 (prediction)
	Placozoa		<i>Trichoplax</i>	aB3S2X1	TriadP28149 (prediction)
	Porifera		Oscarella	kMF780955	
			<i>Oscarella carmela</i>		comp32633_c0_seq8 (prediction)
			<i>Amphimedon queenslandica</i>		Aqu2.37246_001 (Transcriptome)
			<i>Petrosia ficiformis</i>		Contig_18097 + contig_10589
			<i>Sycon ciliatum</i>		sctid49136 (Transcriptome)
			<i>Leucosolenia complicata</i>		lctid42595 (Transcriptome)
			Oopsacas	rMF959461	
			<i>Aphrocallites vastus</i>		comp19808_c1_seq1+comp20080_c0_seq3 (Transcriptome)
	Ctenophora		<i>Mnemiopsis leidyi</i>		ML02753a (prediction)
Vinculin	Chordata		<i>Mus musculus</i>	Q64727	
			<i>Branchiostoma floridae</i>		280829 (Transcriptome 2) and 80007 (Transcriptome 2)
	Arthropoda		<i>Drosophila</i>	rO46037	
	Cnidaria		<i>Nematostella vectensis</i>		EDO35762 (prediction)
	Placozoa		<i>Trichoplax adhaerens</i>		TriadP52110 (prediction)
	Porifera		Oscarella	kMG003328	c12786_g1_i1 (Transcriptome trinity)
			<i>Oscarella carmela</i>		comp41876_c0_seq1 (Transcriptome)
			<i>Amphimedon queenslandica</i>		Aqu2.1.44113_001 (Transcriptome)
			<i>Petrosia ficiformis</i>		contig_687 (Transcriptome)
			<i>Sycon ciliatum</i>		stpid41737 (Transcriptome) and stpid35434 (Transcriptome)
			<i>Leucosolenia complicata</i>		lctid48881 (Transcriptome) and lctid7225 (Transcriptome)
			Oopsacas	rMF959462	
			<i>Aphrocallites vastus</i>		comp21341_c0_seq8 (Transcriptome)
	Ctenophora		<i>Mnemiopsis leidyi</i>		ML148910a (prediction)

Table S6: Polarity complex sequence retrieval: Accession numbers or contig/scaffold references where candidate genes were identified. Sequences from our new genomic and transcriptomic datasets are in bold. 1: links to corresponding data sources are provided in table S4; 2: Prediction of the protein sequence and/or the function; 3: names used in figure

Complex	Gene	Taxa	Species	copy name ¹	Sequence ID	Data sources ¹ for prediction ²	NCBI links for new sequences
S C R	LGL	Chordata	<i>Mus musculus</i>		Q80Y17		
		Arthropoda	<i>Drosophila melanogaster</i>		P08111		
		Cnidaria	<i>Nematostella vectensis</i>			EDO48036 (protein translation)	
		Placozoa	<i>Trichoplax adhaerens</i>			Scaffold_16 (genome) and TriadP31093 (prediction)	
			<i>Oscarella lobularis</i>	MF780964			https://www.ncbi.nlm.nih.gov/huccore/MF780964
			<i>Oscarella carmela</i>		comp39237_c0_seq14		
			<i>Oopsacas minuta</i>	MF959464			https://www.ncbi.nlm.nih.gov/huccore/MF959464
		Porifera	<i>Aphrocallites vastus</i>		comp6849_c0_seq1		
			<i>Sycon ciliatum</i>		scitd17182		
			<i>Leucosolenia complicata</i>		lctid21810		
			<i>Amphimedon queenslandica</i>		Aqu2.1.23963_001 (LGL1; transcriptome) and Aqu2.1.35936_001 (LGL2; transcriptome)		
			<i>Petrosia ficiformis</i>		Contig_4228 (LGL1; transcriptome) and Contig_10319 (LGL2; transcriptome)		
		Ctenophora	<i>Mnemiopsis leidyi</i>		ML24811a-PA (prediction)		
	Scribble	Chordata	<i>Mus musculus</i>		Q80U72		
		Arthropoda	<i>Drosophila melanogaster</i>		AAF26357.2		
		Cnidaria	<i>Nematostella vectensis</i>		A7SS78	EDO33432 (protein translation)	
		Placozoa	<i>Trichoplax adhaerens</i>			scaffold_9 (genome)	
			<i>Oscarella lobularis</i>	MF780962			https://www.ncbi.nlm.nih.gov/huccore/MF780962
			<i>Oscarella carmela</i>		comp42638_c0_seq1 (transcriptome)		
			<i>Oopsacas minuta</i>	MF959465			https://www.ncbi.nlm.nih.gov/huccore/MF959465
		Porifera	<i>Aphrocallites vastus</i>		comp22172_c0_seq3 (transcriptome)		
			<i>Sycon ciliatum</i>		Scitd30593 (transcriptome)		
			<i>Amphimedon queenslandica</i>	XP_019852372.1	Aqu2.1.31180_001 (transcriptome 2)		
			<i>Petrosia ficiformis</i>		Contig_3969		
DLG		Chordata	<i>Homo sapiens</i>	H.sapiens_DLGI	Q12959		
			<i>Mus musculus</i>	M.musculus_DLGI	Q811D0		
			<i>Branchiostoma floridae</i>	B.floridae_DLGI		Bf_V2_147 (genome)	
		Arthropoda	<i>Drosophila melanogaster</i>	D.melanogaster_DLGI	P31007		
		Cnidaria	<i>Nematostella vectensis</i>	N.vectensis_DLGI	A7SFE0	EDO37538 (protein translation)	
		Placozoa	<i>Trichoplax adhaerens</i>	T.adhaerens_DLGI	B3RLX1	TriadP63520 (prediction)	
			<i>Amphimedon queenslandica</i>	A.queenslandica_DLGI		Aqu2.1.42154_001+Aqu2.1.05916_001 (transcriptome)	
			<i>Oscarella lobularis</i>	O.lobularis_DLGI	MF780963		https://www.ncbi.nlm.nih.gov/huccore/MF780963
			<i>Oscarella carmela</i>	O.carmela_DLGI		comp41736_c0_seq1 (transcriptome)	
			<i>Oopsacas minuta</i>	O.minuta_DLGI	MF959455		https://www.ncbi.nlm.nih.gov/huccore/MF959455
		Porifera	<i>Aphrocalistes vastus</i>	A.vastus_DLGI		comp20644_c0_seq1 (transcriptome)	
			<i>Sycon ciliatum</i>	S.ciliatum_DLGIa		scpid36247 (prediction)	
				S.ciliatum_DLGIb		scpid32996 (prediction)	
			<i>Leusosolenia complicata</i>	L.complicata_DLGIa		lctid29073 (transcriptome)	
				L.complicata_DLGIb		lctid25548 (transcriptome)	
		Ctenophora	<i>Mnemiopsis leidyi</i>	M.leidyi_DLGI		comp19374_c0_seq2 (transcriptome 1)	

Crumbs	Chordata	Homo sapiens	Human_CRUM1	NP_001180569.1		
			Human_CRUM2	NP_775960.4		
			Human_CRUM3	NP_631900.1		
		Pan troglodytes	Chimpanzee_Crb1	XP_009438564.1		
			Chimpanzee_Crb2	XP_528426.3		
		Macaca mulatta	Macaca_Crb1	H9FS33		
			Macaca_Crb2	H9F357		
			Macaca_Crb3	H8EY01		
		Mus musculus	Mouse_CRUM1	NP_573502.2		
			Mouse_CRUM2	NP_001157038.1		
			Mouse_CRUM3	NP_808306.1		
		Bos taurus	Caw_Crb1	DAA21022.1		
			Caw_Crb2	XP_003586718.1		
		Canis lupus familiaris	Dog_Crb1	XP_005622350.1		
		Monodelphis domestica	Opossum_Crb1	XP_007481075.1		
			Opossum_Crb2	XP_007474690.1		
		Takifugu rubripes	Takifugu_Crb1	XP_003974391.1		
			Takifugu_Crb2	XP_011617710.1		
		Danio rerio	Danio_Crb1	NP_001038408.1		
			Danio_Crb2	NP_001038764.1		
			Danio_Crb3	NP_001038787.1		
		Gallus gallus	Gallus_Crb1_iso1	XP_003641718.2		
			Gallus_Crb2_iso1	XP_004946066.1		
		Xenopus (Silurana) tropicalis	Xenopus_Crb1	XP_002932223.2		
			Xenopus_Crb2	XP_004918981.1		
			Xenopus_Crb3	NP_001012706.1		
		Saccoglossus kowalevskii	Saccoglossus_CrbL	XP_006817326.1		
	Echinodermata	Strongylocentrotus purpuratus	Urchin_Crb1_iso2	XP_001188090.2		
	Arthropoda	Anopheles darlingi	Anopheles_Crb	ETN63846.1		
		Apis cerana	Apis_Crb_iso1	XP_016917411.1		
		Drosophila melanogaster	Fruitfly_CrbB	NP_001036751.1		
		Tribolium castaneum		XP_970640.2		
		Nasonia vitripennis	Nasonia_Crb-iso1	XP_016838844.1		
	Nematoda	Daphnia magna	Daphnia_Crb	JAM66283.1		
		Caenorhabditis elegans	C.elegans_CRB1	NP_510822.1		
			C.elegans_CRB3	NP_001041224.1		
C R U M B S	Cnidaria	Nematostella vectensis	Nematostella_CrbA		NEMVEscaffold_237 (genome)	
			Nematostella_CrbB		NEMVEscaffold_217 (genome)	
		Trichoplax adhaerens	Trichoplax_CrbA		Scaffold_2 (genome)	
	Porifera	Amphimedon queenslandica		I1FTA5 (uncharacterized)	Aqu2.28529_001 or Aqu2.1.31775_001 (transcriptome)	
		Sycon ciliatum			scis1578 (genome)	
		Oscarella lobularis		MF780959		https://www.ncbi.nlm.nih.gov/huicore/MF780959
		Oopsacas minuta		MF959458		https://www.ncbi.nlm.nih.gov/huicore/MF959458
		Aphrocallistes vastus			comp20814_c0_seq1 (transcriptome)	
	Chordata	Homo sapiens	CSKP_H.sapiens	AAB88198.1		
			MPP2_H.sapiens	NP_001265299.1		
			MPP3_H.sapiens	AAH56865.1		
			MPP4_H.sapiens	NP_149055.1		
			MPP5_H.sapiens	XP_011535389.1		
			MPP6_H.sapiens	AAH23638.1		
			MPP7_H.sapiens	AAH38105.1		
		Mus musculus	CSKP_M.musculus	NP_001271432.1		
			MPP2_M.musculus	NP_057904.1		
			MPP3_M.musculus	NP_031889.2		
	Branchiostoma floridae		MPP4_M.musculus	NP_001158154.1		
			MPP5_M.musculus	NP_062525.1		
			MPP6_M.musculus	AAI45365.1		
			MPP7_M.musculus	AAI18059.1		
			CSKP_B.floridae	C3YTR3 (uncharacterized)	jgi Brafl1 119718 estExt_genesh2_pg.C_330113 (transcriptome)	
	Arthropoda	Drosophila melanogaster	MPP2-6_B.floridae	C3Z0H4 (uncharacterized)	jgi Brafl1 265353 estExt_GenewiseH_1.C_880038 (transcriptome)	
			MPP3-4-7_B.floridae	C3Z0H2 (uncharacterized)	jgi Brafl1 79765 fgenesh2_pg.scaffold_88000029 (transcriptome)	
			MPP5_B.floridae	C3Y0J3 (uncharacterized)	jgi Brafl1 60486 fgenesh2_pm.scaffold_231000005 (transcriptome)	
			CSKP_D.melanogaster	NP_732661.1		
			Mena3_D.melanogaster	NP_610642.2		
	Cnidaria	Stardust_D.melanogaster		NP_996375.1		
		Nematostella vectensis	CSKP_N.vectensis	A7SAA1	EDO39364 (protein translation)	
			MPP2-6_N.vectensis	A7SFE0 (incomplete sequence)	NEMVEscaffold_138 (complete sequence from genome)	
			MPP5_N.vectensis		NEMVEscaffold_261 (genome)	
			MPP_N.vectensis	A7RMI8	EDO47352 (Prediction)	
	Placozoa	Acropora digitifera	MPP2-6_A.digitifera		adi_EST_assem_5910 (transcriptome)	
			MPP5_A.digitifera		adi_EST_assem_1774 (transcriptome)	
		Trichoplax adhaerens	CSKP_T.adhaerens		TriadP55243 (prediction)	
			CSKP_T.adhaerens		TriadP63748 (prediction)	
			MPP_T.adhaerens		TriadP54413 (prediction)	
MPP5/Pals1/Stardust	Oscarella lobularis		MPP5_T.adhaerens		TriadP52734 (prediction)	
		Oscarella lobularis	MP2-6_O.lobularis	MF780968		https://www.ncbi.nlm.nih.gov/huicore/MF780968
			MPP_O.lobularis	MF780969		https://www.ncbi.nlm.nih.gov/huicore/MF780969
			MPP5_O.lobularis	MF780960		https://www.ncbi.nlm.nih.gov/huicore/MF780960
		Oscarella camela	MPP2-6_O.camela		comp42953_c0_seq1 (transcriptome)	
	Oscarella camela		MPP_O.camela		comp14312_c0_seq1 (transcriptome)	
			MPP5_O.camela		comp2196_c0_seq1 (transcriptome)	

Porifera	<i>Amphimedon queenslandica</i>	MPP-CASK_A.queenslandica MPP_A.queenslandica MPP5_A.queenslandica	UPI00021A50C0	Aqu2.23933_001 (transcriptome (1)) Aqu2.23934_001 (transcriptome (1)) Aqu2.33970_001 (transcriptome (1))	
	<i>Petrosia ficiformis</i>	MPP-CASK_P.ficiformis MPP5_P.ficiformis		Contig_400 (Transcriptome) Contig_945 (Transcriptome)	
	<i>Oopsacas minuta</i>	MPP2-6-CSKP_O.minuta MPP5/Stardust.O.minuta	MG003331 MG003330	c18256_g1_i3 (transcriptome) c19478_g1_i1 (transcriptome)	https://www.ncbi.nlm.nih.gov/huicore/MG003331 https://www.ncbi.nlm.nih.gov/huicore/MG003330
	<i>Aphrocallites vastus</i>	MPP2-6_A.vastus MPP_A.vastus		comp30003_c0_seq1 (transcriptome) comp17674_c0_seq1 (transcriptome)	
	<i>Sycon ciliatum</i>	MPP2-6_S.ciliatum-65043 MPP2-6_S.ciliatum-51990 MPP_S.ciliatum		scitid65043 (transcriptome) scitid51990 (transcriptome) scitid31293 (transcriptome)	
	<i>Leucosolenia complicata</i>	MPP5_S.ciliatum MPP2-6_L.complicata MPP_L.complicata MPP5_L.complicata		scitid19242 (transcriptome) lctid72183 (transcriptome) lctid53457 (transcriptome) lctid20340 (transcriptome)	
	<i>Mnemiopsis leidyi</i>	MPP_2-6_M.leidyi-120734 MPP_2-6_M.leidyi-35887 MPPa_M.leidyi-096814 MPPb_M.leidyi-305528		ML120734a-PA (prediction) ML35887a-PA (prediction) ML096814a-PA (prediction) ML305528a-PA (prediction)	
PATJ/MPDZ	<i>Homo sapiens</i>	H.sapiens_INADL H.sapiens_MPDZ	NP_795352.2 NP_001248335.1		
	<i>Mus musculus</i>	M.musculus_INADL M.musculus_MPDZ	NP_001005784.1 NP_001292213.1		
	<i>Drosophila melanogaster</i>	D.melanogaster_INAD	NP_726260.1		
	<i>Nematostella vectensis</i>	N.vectensis_PATJ	A7SRG3_NEMVE	EDO33706 (prediction)	
	<i>Trichoplax adhaerens</i>	T.adhaerens_PATJ	B351C8	TriadP27973 (prediction)	
	<i>Amphimedon queenslandica</i>	A.queenslandica_MUPP-PATJ	1FDE9	Aqu2.1.24128_001	
	<i>Petrosia ficiformis</i>	P.ficiformis_MUPP-PATJ		contig_23858 + contig_6749 (transcriptome)	
	<i>Oscarella lobularis</i>	O.lobularis_MUPP-PATJ	MF780961		https://www.ncbi.nlm.nih.gov/huicore/MF780961
	<i>Oopsacas minuta</i>	O.minuta_MPDZ	MF959457		https://www.ncbi.nlm.nih.gov/huicore/MF959457
	<i>Aphrocallites vastus</i>	A.vastus_MPDZ		comp26018_c0_seq1 (transcriptome)	
	<i>Sycon ciliatum</i>	S.ciliatum_MPDZ-a S.ciliatum_MPDZ-b		scitid12690 (transcriptome) scitid4360 (transcriptome)	
	<i>Leucosolenia complicata</i>	L.complicata_MPDZ-a L.complicata_MPDZ-b		lctid18737 (transcriptome) lctid8806 (transcriptome)	
LIN	<i>Homo sapiens</i>	H.sapiens_LIN7A H.sapiens_LIN7B H.sapiens_LIN7C	O14910 O8HAP6 Q9NUP9		
	<i>Mus musculus</i>	M.musculus_LIN7A M.musculus_LIN7B M.musculus_LIN7C	Q8JZS0 O88951 O88952		
	<i>Branchiostoma floridae</i>	B.floridae_LIN		jgllBraff1 288594 estExt_gwp.C.6290018 (transcriptome)	
	<i>Nematostella vectensis</i>	N.vectensis_LIN	XP_001639785.1 (predicted protein)	EDO47722 (prediction)	
	<i>Trichoplax adhaerens</i>	T.adhaerens_LIN	XP_002117602.1 (hypothetical protein)	TriadP61629 (prediction)	
	<i>Amphimedon queenslandica</i>	A.queenslandica_LIN	XP_019856715.1	Aqu2.19247_001 (transcriptome)	
	<i>Oscarella lobularis</i>	O.lobularis_LIN	MG003329	c12448_g1_i1 (transcriptome Trinity) comp25532_c0_seq1 (transcriptome)	https://www.ncbi.nlm.nih.gov/huicore/MG003329
	<i>Oscarella carmela</i>	O.carmela_LIN			
	<i>Oopsacas minuta</i>	O.minuta_LIN	MF959456		https://www.ncbi.nlm.nih.gov/huicore/MF959456
	<i>Aphrocallites vastus</i>	A.vastus_LIN		comp25879_c0_seq1 (transcriptome)	
	<i>Sycon ciliatum</i>	S.ciliatum_LIN		lctid35214 (transcriptome)	
	<i>Leucosolenia complicata</i>	L.complicata_LIN		lctid40490 (transcriptome)	
	<i>Mnemiopsis leidyi</i>	M.leidyi_LIN		ML05292a-PA (prediction)	

PAR6

Chordata	Mus musculus		O9Z101		
	Homo sapiens		O9JK83		
			O9NPB6		
Arthropoda	Drosophila melanogaster		NP_573238.1		
Cnidaria	Nematostella vectensis			Scaffold_196 (Genome)	
Placozoa	Trichoplax adhaerens			ML3517 (Genome)	
Ctenophora	Mnemiopsis leidyi			Scaffold_1 (Genome)	
	Oscarella lobularis		MF780956		https://www.ncbi.nlm.nih.gov/nuccore/MF780956
	Oscarella camela			comp11890_c0_seq1 (transcriptome)	
	Oopsacas minuta		MF959450		https://www.ncbi.nlm.nih.gov/nuccore/MF959450
Porifera	Aphrocallites vastus			comp4505_c0_seq1 (transcriptome)	
	Sycon ciliatum			scld75477 (transcriptome)	
	Leucosolenia complicata			lcld87073 (transcriptome)	
	Amphimedon queenslandica			Aqu2_34456_001 (transcriptome 1)	
	Petrosia ficiformis			Contig_11878 (transcriptome)	

PAR3

Chordata	Mus musculus		O99NH2		
Arthropoda	Drosophila melanogaster		O96782		
Cnidaria	Nematostella vectensis			scaffold_26 (Genome)	
Placozoa	Trichoplax adhaerens			TriadP55106 (prediction)	
Ctenophora	Mnemiopsis leidyi			ML006311a-PA (prediction)	
	Oscarella lobularis		MF780957		https://www.ncbi.nlm.nih.gov/nuccore/MF780957
	Amphimedon queenslandica			contig13508 (Genome)	
Porifera	Petrosia ficiformis			contig_4639 (transcriptome)	
	Sycon ciliatum			scpid12913 (prediction)	
	Oopsacas minuta		MF959463		https://www.ncbi.nlm.nih.gov/nuccore/MF959463

aPKC

Chordata	Mus musculus	zeta	Q02956		
	Danio rerio		Q4JG04		
	Mus musculus	iota	Q62074		
	Danio rerio		Q6DI53		
	Mus musculus	lambda	BAA32499.1		
	Danio rerio		AAK91291.1		
Arthropoda	Drosophila melanogaster		A129X0		
Cnidaria	Nematostella vectensis		A7RU22	EDO44938 (prediction)	
Placozoa	Trichoplax adhaerens		B3RZX4	TriadP57608 (prediction)	
Ctenophora	Mnemiopsis leidyi			ML008317a-PA (prediction)	
	Petrosia ficiformis			contig_14294 (transcriptome)	
	Amphimedon queenslandica			Aqu2.1.41475_001 (Prediction 2)	
	Oopsacas minuta		MF959451		https://www.ncbi.nlm.nih.gov/nuccore/MF959451
Porifera	Aphrocallites vastus			comp18698_c0_seq1 (transcriptome)	
	Sycon ciliatum			scpid56290 (prediction)	
	Leucosolenia complicata			lcpid18427 (prediction)	
	Oscarella lobularis		MF780958		https://www.ncbi.nlm.nih.gov/nuccore/MF780958
	Oscarella camela			comp29069_c0_seq1 (transcriptome)	

PKC

Chordata	Mus musculus	gamma	P63318		
		alpha	P20444		
		beta	P68404		
	Danio rerio		Q7SY24		
Cnidaria	Nematostella vectensis		A7RUL8	EDO44925 (prediction)	
Placozoa	Trichoplax adhaerens		B3RQ26	TriadP20496 (prediction)	
Ctenophora	Mnemiopsis leidyi			ML13931a-PA (prediction)	
	Leucosolenia complicata			lcpid31219 (prediction)	
	Sycon raphanus		O61224		
	Oscarella lobularis		MF780965		https://www.ncbi.nlm.nih.gov/nuccore/MF780965
	Oscarella camela			comp37413_c0_seq29 (transcriptome)	
Porifera	Amphimedon queenslandica			Aqu2.1.43329_001 (Prediction 2)	
	Petrosia ficiformis			contig_3863 (transcriptome)	
	Suberites domuncula		O62567		
	Geodia cydonium		O96997		
	Oopsacas minuta		MF959452		https://www.ncbi.nlm.nih.gov/nuccore/MF959452
	Aphrocallites vastus			comp28256_c0_seq1 (transcriptome)	

PKC δ

Chordata	Mus musculus		P28867		
	Danio rerio		Q7ZUC5		
	Leucosolenia complicata			lcpid5946 (prediction)	
	Sycon ciliatum			lcpid32739 (prediction)	
	Sycon raphanus		O61225	scpid34149 (prediction)	
	Oscarella camela			comp42357_c0_seq1 (transcriptome)	
Porifera	Oscarella lobularis		MF780966		https://www.ncbi.nlm.nih.gov/nuccore/MF780966
	Suberites domuncula		O62569		
	Petrosia ficiformis			contig_2862 (transcriptome)	
	Amphimedon queenslandica		I1G4K3_AMPOE	Aqu2.1.37442_001 (Prediction 2)	
	Oopsacas minuta		MF959454		https://www.ncbi.nlm.nih.gov/nuccore/MF959454
	Aphrocallites vastus			comp24409_c0_seq1 (transcriptome)	

PKC ε

Chordata	Mus musculus		P16054		
Arthropoda	Drosophila melanogaster		KPC3		
Cnidaria	Nematostella vectensis		A7SL27	EDO35585 (prediction)	
Placozoa	Trichoplax adhaerens		B3S6K6	TriadP30067 (prediction)	
	Oscarella lobularis		MF780967		https://www.ncbi.nlm.nih.gov/nuccore/MF780967
	Oscarella camela			comp17286_c0_seq1 (transcriptome)	
	Sycon ciliatum			scpid30652 (prediction)	

Porifera	<i>Leucosolenia complicata</i>		lcpid37553 (prediction)	
	<i>Amphimedon queenslandica</i>	I1FUR1_AMPQE	Aqu2.1.32509_001	
	<i>Petrosia ficiformis</i>		contig_3767 (transcriptome)	
	<i>Oopsacas minuta</i>	MF959453		https://www.ncbi.nlm.nih.gov/huccore/MF959453
	<i>Aphrocallistes vastus</i>		comp15198_c0_seq1 (transcriptome)	
