

Additional file 5 — Table of paralog-to-contig assignments of latrophilins in cod

Performance of Scipio and the EMS-pipeline in prediction of latrophilin genes in cod. The cod genome *gad6/or1* (Ensembl) was queried with zebrafish protein sequences (Ensembl *GPRC210*). Scipio was run with "cross-species default options" (min.identity=60, max.move.exon=6, blat.score=15, blat.identity=54, multiple.results, region.size=10000, exhaust.align.size=15000). Scipio occasionally returned several hits; these are indicated by a number in brackets in the paralog-column. The EMS-pipeline was run in "custom-mode" with exonerate as spliced alignment tool. The TCE-numbering refers to the homologous TCE-groups. Hits were considered even if they were partial only. Abbreviations: c – contig, fp – false positive, GS – GeneScaffold, s – scaffold.

Scipio				EMS-pipeline			
paralog	contig	score	TCEs identified	contig assignment	TCEs included by the ExonMatchSolver	TCEs included after post-processing (exonerate)	
ADGRL1a	GS_3732	0.005	1 (fp)	GS_2428	2, 5-7, 9-23, 25	2, 5-9, 11-23, 25	
	GS_2428	0.681	2, 5-7, 9, 11-23, 25	c445060	3	3	
ADGRL1a(1)	GS_1780	0.354	2-7, 9, 11, 12, 14-20, 22, 23, 25				
ADGRL1b	GS_2428	0.411	2, 5-7, 9-12, 14-18, 20, 22, 23, 25	GS_3850	2, 3, 5-20, 22, 23	2, 3, 5-12, 14-23, 25	
ADGRL1b(1)	GS_3850	0.309	2-12, 14, 15, 17, 22				
ADGRL2a	GS_1780	0.643	2-23, 25	GS_1780	2, 3, 5-23, 25	2, 3, 5-23, 25	
ADGRL2a(1)	GS_2759	0.425	2-7, 11-17, 19-20, 22, 23, 25				
	GS_1138	0.005	25				
ADGRL2a(2)	GS_871	0.005	1				
	GS_2428	0.316	2, 5-7, 9-12, 14-18, 20-23, 25				
ADGRL2b	GS_1780	0.527	1-23, 25	GS_2759	1 (fp), 2-3, 5-7, 11-17, 19-23, 25	2, 3, 5-7, 11-17, 19-23, 25	
ADGRL2b(1)	GS_2759	0.513	2-7, 11-17, 19-23, 25	s10419	18	18	
ADGRL2b(2)	GS_3429	0.009	1	c348339	10	10	
	GS_2428	0.300	2, 5-7, 9-18, 20, 22, 25				
ADGRL3a	GS_2409	0.007	1 (fp)	GS_4007	2, 3, 5-7, 9-12, 15, 16, 19, 21-23, 25	1-3, 5-7, 9-12, 15, 16, 19, 21-23, 25	
	GS_3151	0.463	2, 3, 5-14, 16, 17, 19, 23-25	GS_4123	8 (fp), 17, 18 (fp)	17 (fp, belongs to CELSR1b)	
ADGRL3a(1)	GS_4007	0.453	1-7, 9-12, 15, 16, 19, 21-25	c408339	13	13	
				c136327	14	14	
ADGRL3b	GS_3151	0.533	2, 3, 5-7, 9, 10, 13, 14, 16, 17, 19, 23-25	GS_3151	2, 3, 5-12, 15-17, 19, 23, 25	2, 3, 5-10, 13-17, 19, 23-25	
ADGRL3b(1)	GS_4007	0.402	2-7, 9, 10, 15, 16, 19, 21-23, 25	c12548	21, 22	21, 22	
				c493181	18	18	