S12 Table. Prediction of the gene structure in the Yap hadal snailfish genome.

Gene set		Number	Average transcript length (bp)	Average CDS length (bp)	Average exons per gene	Average intron length (bp)
De novo	Augustus	36,404	7,416.78	1,182.51	6.50	1,132.99
	GlimmerHMM	121,413	6,046.06	618.52	3.66	2,039.36
	SNAP	70,320	8,325.18	806.70	4.98	1,888.45
	Geneid	61,556	7,947.94	933.00	4.41	2,058.36
	Genscan	40,464	14,225.07	1,452.56	7.80	1,878.54
Homolog	*Dre*	28,362	7,570.47	1,402.73	6.64	1,094.15
	Gac	41,014	5,621.77	1,017.79	5.28	1,076.64
	Hsa	21,915	8,614.11	1,381.58	7.16	1,173.46
	Lcr	33,542	7,487.63	1,354.76	6.50	1,116.06
	Mmu	22,232	8,488.07	1,360.13	7.08	1,172.85
	Oni	38,860	6,180.03	1,223.68	5.59	1,079.56
	Tni	25,602	8,143.45	1,339.64	7.22	1,093.05
	Tru	32,858	6,659.68	1,264.91	5.98	1,083.81
RNAseq	PASA	96,601	6,658.02	1,045.17	6.70	984.93
	Cufflinks	57,534	12,016.39	2,920.45	8.37	1,233.84
EVM		30,938	9,449.83	1,300.12	7.59	1,237.26
Pasa-update		30,282	9,858.55	1,348.63	7.82	1,247.13
Final set		24,329	10,675.78	1,420.88	8.41	1,249.54

Abbreviation: *Danio rerio* (*Dre*), *Gasterosteus aculeatus* (*Gac*), *Homo sapiens* (*Hsa*), *Ictalurus punctatus* (*Ipu*), *Lepisosteus oculatus* (*Loc*), *Oreochromis niloticus* (*Oni*), *Takifugu rubripes* (*Tru*), *Tetraodon nigroviridis* (*Tni*), *Larimichthys crocea* (*Lcr*), *Mus musculus (Mmu).*