

Supplementary Fig S1

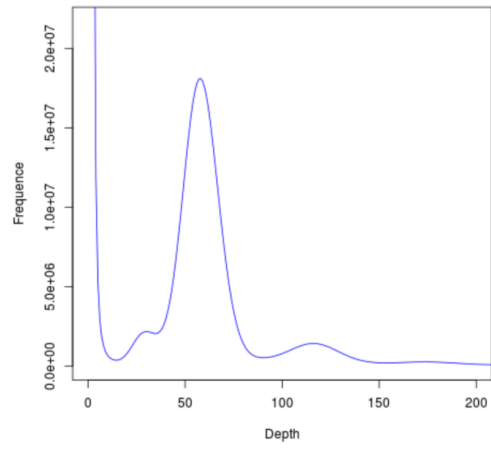


Fig. S1. 17-mer survey for genome size estimation

Supplementary table S1 Genome assembly comparison of *Sebastes schlegelii* with other public teleost genomes.

Species	Name	Contig N50(Kb)	Scaffold N50(Mb)	Genome size(Mb)
Chinese clearhead icefish	<i>Protosalanx hyalocranius</i>	17.2	1.163	536
channel catfish	<i>Ictalurus punctatus</i>	48.5	7.2	845.4
ocean sunfish	<i>Mola mola</i>	20	9	642
seahorse	<i>Hippocampus erectus</i>	14.57	1.97	458
Monopterus albus	<i>Monopterus albus</i>	22.2	2.1	689.5
yellow catfish	<i>Pelteobagrus fulvidraco</i>	1100	25.8	732.8
Siamese fighting fish	<i>Betta splendens</i>	19.01	0.949	465.24
spotted sea bass	<i>Lateolabrax maculatus</i>	31	1.04	620
Japanese flounder	<i>Paralichthys olivaceus</i>	30.5	3.9	546
Stickleback	<i>Gasterosteus aculeatus</i>	83.2	10.8	463
Asian seabass	<i>Lates calcarifer</i>	1060	25.8	700
Fugu	<i>Takifugu rubripes</i>	52.5	0.9	332.5
Green spotted puffer	<i>Tetraodon nigroviridis</i>	16	0.98	342
Platyfish	<i>Xiphophorus maculatus</i>	22	1.1	669
Zebrafish	<i>Danio rerio</i>	25	1.5	1412
Atlantic Cod	<i>Gadus morhua</i>	2.8	0.68	753
Nile tilapia	<i>Oreochromis niloticus</i>	3300	38.839	-
Medaka	<i>Oryzias latipes</i>	3516	32.853	-
black rockfish	<i>Sebastes schlegelii</i>	2960	35.63	848.31

Supplementary table S2 General statistics of predicted protein-coding genes of *S. schlegelii*.

	Gene Set	Number	Mean transcript length (bp)	Mean CDS length(bp)	Mean exons per gene	Mean exon length (bp)	Mean intron length (bp)
De novo	Augustus	33,088	10,539.75	1,261.75	7.16	176.25	1,506.47
	GlimmerH	88,475	8,460.80	626.82	4.22	148.53	2,432.82
Homolog	MM						
	SNAP	53,379	17,025.75	965.18	6.64	145.37	2,847.81
	Geneid	30,008	17,396.42	1,270.06	8.21	154.64	2,235.67
	Cse	25,368	11,492.08	1,475.24	7.89	187.08	1,454.74
	Dre	24,236	10,802.68	1,418.97	7.52	188.79	1,440.07
	Hco	24,910	11,149.68	1,483.02	7.80	190.19	1,422.11
	Mal	24,538	12,009.32	1,511.54	8.31	181.88	1,435.92
	Ola	28,713	8,431.19	1,195.74	6.39	187.07	1,341.93
	Omy	27,655	9,484.41	1,270.32	6.62	191.83	1,461.06
	Oni	27,688	10,007.18	1,334.92	7.26	183.88	1,385.40
	Pol	26,310	10,912.77	1,428.24	7.79	183.41	1,397.42
	Tru	24,076	10,651.52	1,373.31	7.60	180.66	1405.44
	Xma	27,932	9,358.03	1,314.11	7.03	187.01	1,334.63
RNAseq	PASA	111,844	11,440.67	1,180.06	7.21	163.72	1,652.83
	Clufflinks	73,010	21,892.11	3,749.42	9.81	382.34	2,060.12
	EVM	33,429	11,983.27	1,276.30	7.46	171.16	1,658.27
	Pasa-update	33,014	12,416.65	1,301.86	7.55	172.45	1,697.16
	Final set	26,979	14,159.49	1,452.03	8.63	168.32	1,666.16

Supplementary table S3 Comparison of gene structure of the *S. schlegelii* with other closely related teleost fish species.

Species	Number	Mean transcript length (bp)	Mean CDS length (bp)	Mean exons per gene	Mean exon length (bp)	Mean intron length (bp)
Cse	21,384	11,361.13	1,788.94	10.57	169.31	1,000.66
Dre	32,717	26,276.99	1,703.07	9.45	180.30	2,909.61
Hco	21,175	12,202.42	1,760.28	10.48	167.96	1,101.43
Mal	21,343	15,854.92	1,777.40	10.60	167.67	1,466.34
Ola	19,699	12,145.38	1,515.82	10.25	147.83	1,148.65
Omy	42,767	19,611.54	1,578.13	8.77	179.84	2,319.42
Oni	21,437	14,892.56	1,714.22	10.90	157.24	1,330.90
Pol	23,113	12,205.37	1,656.58	9.79	169.25	1,200.40
SSc	26,979	14,159.49	1,452.03	8.63	168.32	1,666.16
Tru	18,523	7,489.66	1,693.53	11.10	152.59	573.97
Xma	20,379	13,751.46	1,643.24	10.69	153.77	1,250.07