Supplementary Information: Draft genome of a porcupinefish, *Diodon Holocanthus*

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Platform	Metric	Value
stLFR co-barcoded reads	Insert Size	250
	Read length (bp)	100
	Total data (Gb)	154.3
	Sequence coverage (×)	219.8
MinION long reads	# of Reads	655,108
	Average length (bp)	17,378
	Total data (Gb)	11.4
	Sequence coverage (×)	15.9

Table S1. Descriptive metrics of the input sequence data for the *de novo* genome assembly.

Kmer	Kmer Depth	Kmer Number	Estimated genome size (Mb)	Heterozygous Rate (%)	Repeat Rate (%)
17	110	78,590,182,272	701.96	0.76	36.35

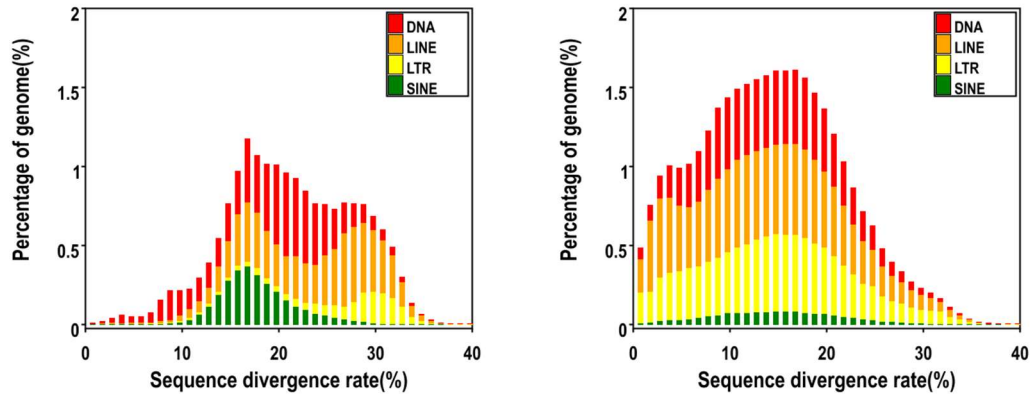**Table S2. Estimation of the genome size, heterozygous and repeat rate using K-mer analysis.**

Figure S1. Statistics of repeat elements in the *Diodon Holocanthus* genome.
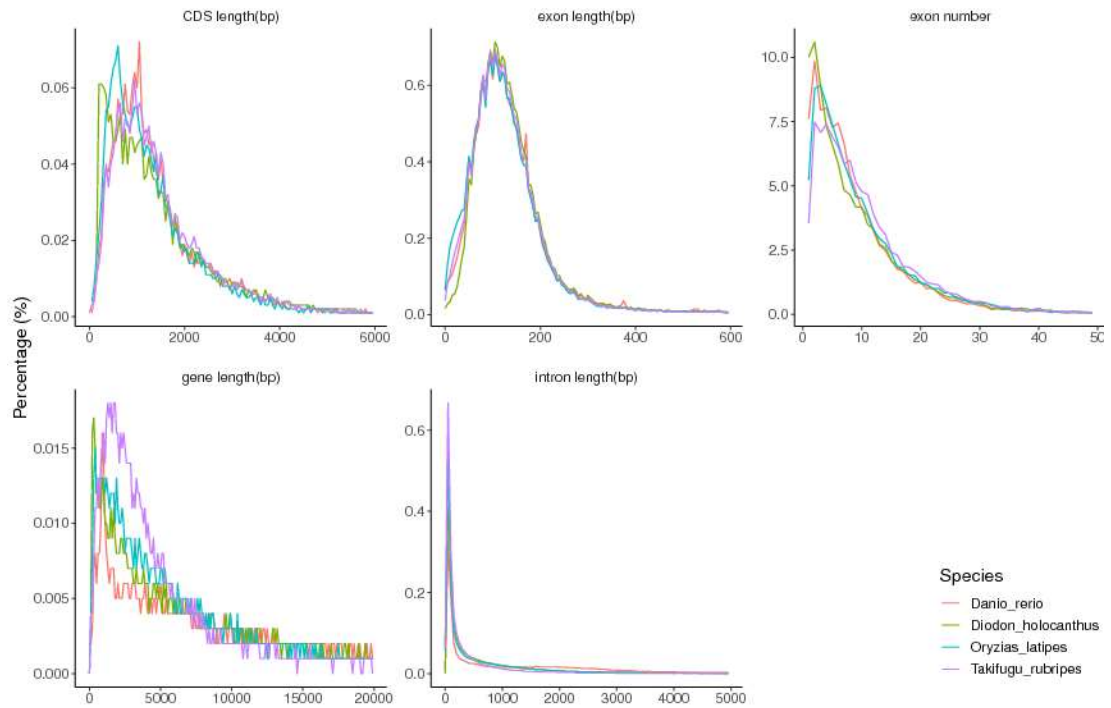

Figure S2. Length distribution comparison on total gene, CDS, exon, and intron of annotated gene models of the *Diodon Holocanthus* with other species. Length distribution of total genes (A), CDS (B), exon (C), and intron (D) were compared to those of *Danio rerio, Oryzias latipes and Takifugu rubripes*.

Values	Total	Swissprot-Annotated	TrEMBL-Annotated	Interpro-Annotated	Overall
Number	20,840	17,015	18,214	4,812	18,281
Percentage	100%	81.65%	87.40%	23.09%	87.72%

Table S3. The number of genes with homology or functional classification for *Diodon Holocanthus*.