Supplemental Table S14. Statistics information of protein-coding BUSCOs assessment for Brachymystax lenok tsinlingensis genome.

Type	**Number**	**Percent (%)**
Complete BUSCOs (C)	3,416	93.85
Complete and single-copy BUSCOs (S)	2,263	62.17
Complete and duplicated BUSCOs (D)	1,153	31.68
Fragmented BUSCOs (F)	92	2.53
Missing BUSCOs (M)	132	3.63
Total BUSCO groups searched	3,640	100.00

Note:

Complete BUSCOs(C): sequences completely align to BUSCO;

Complete and single-copy BUSCOs (S): one BUSCO aligns to one gene;

Complete and duplicated BUSCOs (D): one BUSCO aligns to more than one gene;

Fragmented BUSCOs(F): part of sequence align to BUSCO;

Missing BUSCOs(M): none of sequnces align to BUSCO.