

**Supplemental Table S9. Statistics information of BUSCOs for *Brachymystax lenok tsinlingensis* genome.**

Type	Length(bp)	Number
Complete BUSCOs (C)	3,514	96.54
Complete and single-copy BUSCOs (S)	2,319	63.71
Complete and duplicated BUSCOs (D)	1,195	32.83
Fragmented BUSCOs (F)	53	1.46
Missing BUSCOs (M)	73	2.01
Total BUSCO groups searched	3,640	100

**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 sequences align to BUSCO.