Supplemental Table S12. Non-coding RNA annotation statistics of Brachymystax lenok tsinlingensis genome.

Type	Number	Average Length(bp)	Total Length(bp)	Base Ratio(%)
28S rRNA	260	2,211	575,081	0.0283
18S rRNA	168	1,341	225,380	0.0111
5.8S rRNA	56	153	8,607	0.0004
5S rRNA	38,887	116	4,511,868	0.2220
tRNA	46,231	73	3,417,846	0.1681
miRNA	1,618	86	139,620	0.0069
snoRNA	881	130	114,548	0.0056
catalytic RNA	106	303	32,176	0.0016
spliceosomal RNA	3,240	129	420,847	0.0207
other snRNA	131	54	7,130	0.0004
lncRNA	13	213	2,769	0.0001
cis regulator	4,848	53	259,010	0.0127
other ncRNA	175	283	49,641	0.0024