Supplemental Table S8. Hi-C assembly results of Brachymystax lenok tsinlingensis genome.

Pseudomolecule	Contig Num	Length(bp)	Percent(%)
chr01	82	112,269,073	5.52
chr02	101	97,116,746	4.78
chr03	51	80,620,550	3.97
chr04	31	60,489,296	2.98
chr05	52	59,751,755	2.94
chr06	38	59,437,483	2.92
chr07	30	58,324,833	2.87
chr08	33	56,744,124	2.79
chr09	43	56,702,824	2.79
chr10	33	53,280,834	2.62
chr11	38	51,773,359	2.55
chr12	52	51,749,971	2.55
chr13	39	50,420,684	2.48
chr14	48	49,749,905	2.45
chr15	39	49,239,683	2.42
chr16	37	48,200,182	2.37
chr17	47	48,171,172	2.37
chr18	56	48,065,492	2.36
chr19	70	46,267,247	2.28
chr20	59	45,494,848	2.24
chr21	53	45,254,300	2.23
chr22	91	44,999,662	2.21
chr23	83	44,992,799	2.21

Pseudomolecule	**Contig Num**	**Length(bp)**	**Percent(%)**
chr24	37	44,736,387	2.2
chr25	57	44,175,905	2.17
chr26	58	43,859,280	2.16
chr27	46	43,524,281	2.14
chr28	34	43,163,597	2.12
chr29	45	42,996,185	2.12
chr30	30	42,243,236	2.08
chr31	32	42,143,523	2.07
chr32	56	41,728,143	2.05
chr33	48	40,292,826	1.98
chr34	34	39,526,706	1.94
chr35	53	39,448,624	1.94
chr36	50	38,032,780	1.87
chr37	15	37,497,716	1.84
chr38	63	33,494,297	1.65
chr39	52	29,237,078	1.44
chr40	54	28,608,702	1.41
Total anchored	1,970	1,993,826,088	98.09
Unanchored	105	38,847,319	1.91
Total	2,075	2,032,673,407	100