

Table S1. The results of sequencing and quality control

Sample Name	Clean Reads	HQ Clean Reads	Adapter	Low Quality	N	HQ Clean Reads	Adapter	Low Quality	N
C1	22087871	21806203	214550	193003	40	98.72%	0.97%	0.87%	0%
C2	31529978	31145791	290092	254251	51	98.78%	0.92%	0.81%	0%
M1	25289482	24962850	293912	230461	42	98.71%	1.16%	0.91%	0%
M2	22278390	21997619	217421	194131	38	98.74%	0.98%	0.87%	0%
JP1	21708720	21439919	250108	189484	42	98.76%	1.15%	0.87%	0%
JP2	22987086	22719729	237738	179801	39	98.84%	1.03%	0.78%	0%

Table S2. The statistical results of sample assembly

Sample Name	Contigs Num	Total length	Average length	Max length	N50	N90
C1	223208	357121986	1599.95	298512	2228	645
C2	284391	477264588	1678.20	374103	2509	653
M1	273113	368778102	1350.28	352303	1589	608
M2	261526	359477785	1374.54	251869	1648	618
JP1	196438	272379756	1386.59	322285	1631	608
JP2	232354	331859144	1428.25	344326	1741	620