

Table S1. Genome sequencing statistics

Library size (bp)	Sequencing mode	Read length (bp)	Total reads (M)	Total length (Gb)	Coverage (X)
250	Paired-end	150	271.73	40.76	36.98
450	Paired-end	250	343.38	85.85	77.89
800	Paired-end	150	130.28	19.54	17.73
~3000	Mate-pair	150	237.67	35.65	32.35
~5000	Mate-pair	150	289.93	43.49	39.46
~8000	Mate-pair	150	277.07	41.56	37.71
~13,000	Mate-pair	150	316.60	47.49	43.09
Total			1866.66	314.34	>300X