

Table S4. Summary of Illumina sequencing of parental lines and extremely pools

Sample	Total Data	High-Quality Reads	Mapping (%)	GC (%)	Q30 (%)	Average Depth (×)	Properly paired read	Properly paired ratio
B1-2	26,187,821,640	861,497,710	97.45	35.2	91.54	48.779	766,690,540	89.00%
D50	26,207,429,520	861,251,680	98.24	35.28	91.46	48.765	771,839,948	89.62%
EG-pool	26,687,380,200	871,859,126	98.58	35.4	91.52	49.365	784,390,422	89.97%
ED-pool	21,319,884,900	832,814,516	98.43	35.42	91.49	47.155	746,836,926	89.68%