

Table S3. Statistics of sequencing data of raw read and genome coverage of trimmed read after equalizing.

DNA samples	No. of F ₂ plants in bulk	No. of reads	Average length(bp)	Total length(bp)	Q30(%) ^z	Coverage ^y	Coverage ^y after equalizing
SIT55616RN	-	23,238,593	151	3,509,027,543	93.57	≈16.51X	
		23,238,593		3,509,027,543			
FD061129	-	22,901,520	151	3,458,129,520	93.28	≈16.27X	
		22,901,520		3,458,129,520			
DG-bulk	40	64,221,090	151	9,697,384,590	94.83	≈45.63X	≈34.54X
		64,221,090		9,697,384,590			
LG-bulk	9	62,602,038	151	9,452,907,738	94.73	≈44.48X	≈34.54X
		62,602,038		9,452,907,738			
B-bulk	40	62,733,048	151	9,472,690,248	94.35	≈44.85X	≈33.86X
		62,733,048		9,472,690,248			
Bl-bulk	40	63,529,167	151	9,592,904,217	94.5	≈45.14X	≈33.86X
		63,529,167		9,592,904,217			

^z Ratio of bases that have quality score of over 30.

^y Total raw read length of each sample divided by estimated genome size (425 Mb).