

Table S5. Table of sequence alignment results between sample sequencing data and selected reference genome of RG and ‘Yanli’.

Samples	Clean reads	Clean bases	GC Content	%≥Q30
RG-G1	24,733,913	7,420,173,900	46.23%	91.38%
RG-G2	28,473,088	8,541,926,400	46.17%	91.91%
RG-G3	22,146,970	6,644,091,000	46.21%	91.51%
RG-W1	21,993,820	6,598,146,000	45.95%	91.63%
RG-W2	17,358,383	5,207,514,900	46.16%	92.82%
RG-W3	25,745,827	7,723,748,100	46.07%	91.25%
RG-T1	29,358,857	8,807,657,100	45.87%	90.65%
RG-T2	25,023,893	7,507,167,900	45.96%	91.52%
RG-T3	27,905,265	8,371,579,500	45.83%	93.88%
RG-R1	26,136,097	7,840,829,100	45.77%	94.07%
RG-R2	25,242,685	7,572,805,500	45.76%	94.55%
RG-R3	23,143,225	6,942,967,500	45.78%	94.82%
YL-G1	19,595,453	5,824,388,348	47.40%	93.51%
YL-G2	23,047,235	6,869,479,498	47.19%	93.85%
YL-G3	19,933,915	5,930,619,676	47.40%	93.51%
YL-W1	26,768,461	7,945,821,092	47.11%	93.70%
YL-W2	19,892,894	5,899,253,654	47.04%	93.81%
YL-W3	25,043,100	7,420,102,756	47.07%	94.00%
YL-T1	19,763,372	5,868,108,812	47.22%	92.96%
YL-T2	21,112,039	6,282,416,972	47.04%	92.93%
YL-T3	21,179,752	6,300,545,796	46.94%	93.69%
YL-R1	20,043,554	5,954,566,396	46.92%	93.45%
YL-R2	23,359,549	6,932,307,974	47.19%	93.12%
YL-R3	20,528,355	6,078,806,470	46.87%	93.46%