

Table 3 Potato transcriptome sequencing data and alignment results

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q30 (%)	Total Mapping(%)	Uniquely Mapping(%)
CK_F_1	43.82	42.21	6.33	91.19	74.63	72.62
CK_F_2	43.82	42.4	6.36	90.65	73.53	71.62
CK_F_3	43.82	42.29	6.34	90.68	73.52	71.53
CK_qing9_1	43.82	42.03	6.31	93.34	80.33	78.05
CK_qing9_2	43.82	42.73	6.41	93.22	79.74	77.61
CK_qing9_3	43.82	42.45	6.37	93.22	79.98	77.82
PG10h_F_1	45.57	42.66	6.4	92.28	75.94	73.9
PG10h_F_2	43.82	42.35	6.35	92.41	76.14	74.02
PG10h_F_3	43.82	42.8	6.42	91.97	75.23	73.17
PG10h_qing9_1	43.82	42.49	6.37	93.55	78.74	76.53
PG10h_qing9_2	43.82	42.42	6.36	93.23	79.63	77.24
PG10h_qing9_3	43.82	42.73	6.41	93.52	79.29	76.98
PG24h_F_1	43.82	42.39	6.36	92.54	75.48	73.42
PG24h_F_2	43.82	42.87	6.43	92.32	75.11	73.1
PG24h_F_3	45.57	42.63	6.39	92.7	75.79	73.68
PG24h_qing9_1	43.82	42.85	6.43	93.53	80.15	77.7
PG24h_qing9_2	43.82	42.4	6.36	93.72	76.2	74.07
PG24h_qing9_3	43.82	42.68	6.4	93.44	78.34	76.14
PG2h_F_1	45.57	43.61	6.54	90.8	70.48	68.75
PG2h_F_2	43.82	42.04	6.31	90.65	71.11	69.36
PG2h_F_3	43.82	42.09	6.31	90.48	70.35	68.46
PG2h_qing9_1	43.82	42.45	6.37	93.31	79.47	76.93
PG2h_qing9_2	43.82	42.56	6.38	93.19	79.14	76.89
PG2h_qing9_3	43.82	42.69	6.4	92.97	79.06	76.87
PG48h_F_1	45.57	44.33	6.65	92.71	75.19	72.93
PG48h_F_2	45.57	44.68	6.7	92.12	75.3	73.2
PG48h_F_3	45.57	44.68	6.7	92.31	72.89	70.58
PG48h_qing9_1	43.82	42.68	6.4	93.45	79.25	76.92
PG48h_qing9_2	43.82	42.62	6.39	93.72	78.02	75.37
PG48h_qing9_3	43.82	42.44	6.37	93.66	79.46	76.97
PG6h_F_1	43.82	42.16	6.32	90.91	72.17	70.16
PG6h_F_2	43.82	42.3	6.35	91.07	72.09	70.12
PG6h_F_3	43.82	41.98	6.3	90.84	71.38	69.55
PG6h_qing9_1	43.82	42.64	6.4	93.44	77.99	75.78
PG6h_qing9_2	43.82	42.66	6.4	93.48	78.99	76.68
PG6h_qing9_3	43.82	42.54	6.38	93.34	78.58	76.45