

Supplementary Table S4 RNA-seq sample sequencing data evaluation and statistics

Sample	Raw Reads	Clean Reads	Clean Base (G)	Error Rate (%)	Q20 (%)	Q30 (%)	GC Content (%)
T2DAP0-1	54325778	51460332	7.72	0.02	98.42	94.93	45.11
T2DAP0-2	46486790	41787968	6.27	0.02	98.45	95.04	44.48
T2DAP0-3	45044866	42712112	6.41	0.03	97.52	93	45.43
T2DAP15-1	45900454	43192054	6.48	0.02	98.49	95.09	45.37
T2DAP15-2	48929108	45574870	6.84	0.02	98.39	94.89	45.39
T2DAP15-3	48187088	44840110	6.73	0.02	98.34	94.78	45.42
T2DAP30-1	45945150	40068468	6.01	0.02	98.32	94.9	41.67
T2DAP30-2	48680902	43696324	6.55	0.02	98.32	94.77	42.74
T2DAP30-3	45523838	41450860	6.22	0.02	98.45	95.05	43.15
T9DAP0-1	50255852	47083454	7.06	0.02	98.19	94.35	44.78
T9DAP0-2	62887430	59161786	8.87	0.02	98.42	94.87	44.72
T9DAP0-3	43842838	40890096	6.13	0.02	98.34	94.72	44.71
T9DAP15-1	45718858	40291006	6.04	0.02	98.47	95.11	44.09
T9DAP15-2	51612886	46647338	7	0.02	98.45	95.05	43.81
T9DAP15-3	46775820	42345972	6.35	0.02	98.44	95.04	44.7
T9DAP30-1	48693316	45424392	6.81	0.02	98.3	94.71	44.73
T9DAP30-2	52076720	52641688	7.9	0.03	97.85	93.82	44.72
T9DAP30-3	47645092	65654204	9.85	0.02	98.57	95.45	44.6

Note: Cycle Q20%: Percentage of the cycle whose average quality score is greater than or equal to 20; Cycle Q30%: Percentage of the cycle whose average quality score is greater than or equal to 30. T2 represents the red peel line '2013-12', and T9 represents the gray peel line '9-6'.