

Supplementary Table S5 Reads and reference genome mapped data of RNA-seq samples

Sample	Total Reads	Mapped reads	Mapped rate (%)	Unique mapped	Unique mapped rate (%)	Multi mapped	Multi mapped rate (%)
T2DAP0-1	51460332	49186563	95.58%	47977674	93.23%	1770878	2.35%
T2DAP0-2	41787968	40401062	96.68%	39439256	94.38%	1397211	2.30%
T2DAP0-3	42712112	41125963	96.29%	40126116	93.95%	1417998	2.34%
T2DAP15-1	43192054	42058562	97.38%	40720895	94.28%	1956451	3.10%
T2DAP15-2	45574870	44466760	97.57%	43061490	94.49%	2077126	3.08%
T2DAP15-3	44840110	43666517	97.38%	42282914	94.30%	2094523	3.09%
T2DAP30-1	40068468	37250853	92.97%	36451958	90.97%	1312705	1.99%
T2DAP30-2	43696324	42263468	96.72%	41220321	94.33%	1668023	2.39%
T2DAP30-3	41450860	40245034	97.09%	39095644	94.32%	1739756	2.77%
T9DAP0-1	47083454	45534968	96.71%	44613506	94.75%	1246800	1.96%
T9DAP0-2	59161786	56637944	95.73%	55436543	93.70%	1643730	2.03%
T9DAP0-3	40890096	39959800	97.72%	39169184	95.79%	1057628	1.93%
T9DAP15-1	40291006	37551227	93.20%	36505555	90.60%	1529106	2.60%
T9DAP15-2	46647338	44788249	96.01%	43626200	93.52%	1653436	2.49%
T9DAP15-3	42345972	41274387	97.47%	40122144	94.75%	1645356	2.72%
T9DAP30-1	45424392	42992125	94.65%	41795162	92.01%	1683451	2.64%
T9DAP30-2	52641688	50059452	95.09%	48627117	92.37%	1940989	2.72%
T9DAP30-3	65654204	62353522	94.97%	60575873	92.27%	2428867	2.71%

Note: T2 represents the red peel line '2013-12', and T9 represents the gray peel line '9-6'.