

Table 1 RNA-seq data statistics

Samples	Number		Total Reads	Mapped Reads (percentage)	GC Content (%)	≥Q30 (%)	Samples
	Clean reads	Clean bases					
Juvenile stem	21,260,012	6,357,478,046	42,520,024	37,747,560 (88.78%)	44.83	94.81	Juvenile stem
Apex T01-T03	21,492,957	6,424,620,892	42,985,914	38,249,203 (88.98%)	44.86	94.59	Apex T01-T03
	21,441,156	6,405,708,414	42,882,312	38,676,555 (90.19%)	44.69	94.68	
One year's flowering stem	21,285,080	6,352,022,540	42,570,160	38,062,526 (89.41%)	44.89	94.65	One year's flowering stem
	21,372,065	6,386,940,100	42,744,130	36,606,834 (85.64%)	44.95	95.11	
apex T04-T06	22,665,601	6,777,488,624	45,331,202	40,660,557 (89.70%)	44.88	95.12	apex T04-T06
Stem end of perennial f	21,395,341	6,394,514,808	42,790,682	37,703,333 (88.11%)	44.61	94.94	Stem end of perennial flower
lowerT07-T09	21,008,039	6,278,849,030	42,016,078	37,790,151 (89.94%)	44.60	95.02	T07-T09
	20,298,126	6,069,357,696	40,596,252	35,752,244 (88.07%)	44.60	95.18	

Note: ≥ Q30 means percentage of quality values of bases involved clean reads is equal or greater than 30