

Supplemental Table S1. Summary of Illumina HiSeq4000 transcriptome sequencing and de novo assembly results

Samples	CK-1	CK2	CK3	Dark-1	Dark2	Dark3	L1	L2	L3
Before Trimming									
Number of raw reads	48817260	7239548	51753350	73818268	67944906	54548164	58076350	66576074	81571672
Number of clean reads	48726878	72260904	51668206	73668546	67815002	54425488	57945996	66442168	81427428
	(99.81%)	(99.81%)	(99.84%)	(99.80%)	(99.81%)	(99.78%)	(99.78%)	(99.80%)	(99.82%)
GC content (%)	51.49	51.42	51.56	51.56	51.16	51.23	51.10	50.55	51.07
Q30 percentage (%)	93.32	92.66	93.25	93.32	93.49	92.86	92.55	93.47	93.41
Clean base (bp)	7270597723	10772650770	771304730	109932279	101284763	813307924	862003762	993070975	121384532
			2	17	98	3	4	1	72
After Assembly									
Total assembled bases (bp)	72145391								
Total unigene numbers	95579								
GC percentage (%)	43.90								
N50 number	1260								
Average length (bp)	754								