

Table S3. Summary of the transcripts and the assembly results for *P. japonicus*

Item	No. of Sequences
Clean reads (M)	366.6572
Clean bases (G)	54.9985
No. of contig > 500bp	777,642
Total unigenes	119,882
Total length (bp)	126,146,371
Average contig size (bp)	1,052
N50 contig size (bp)	1,691
GC (%)	41.28