

Figure S1: Gene Ontology (GO) Classification of DGs in J1 vs J2.

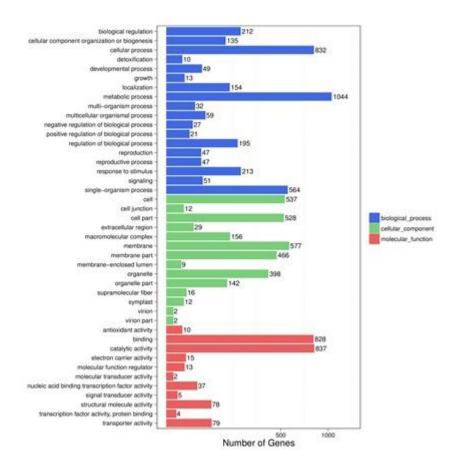
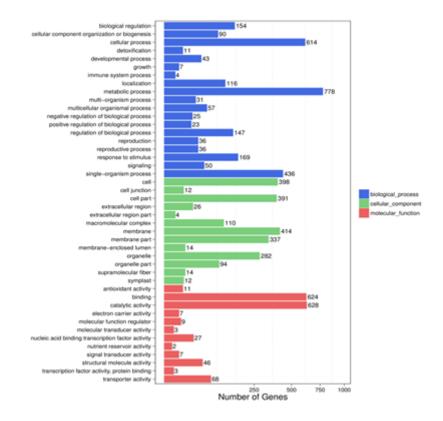
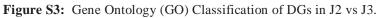


Figure S2: Gene Ontology (GO) Classification of DGs in J1 vs J3.





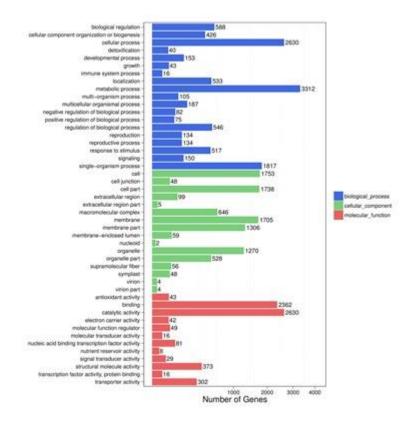


Figure S4: Gene Ontology (GO) Classification of DGs in Y1 vs Y2.

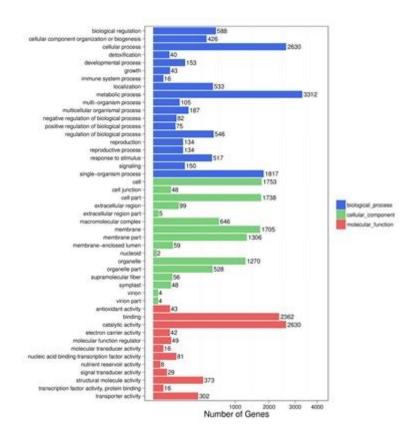


Figure S5: Gene Ontology (GO) Classification of DGs in Y1 vs Y3.

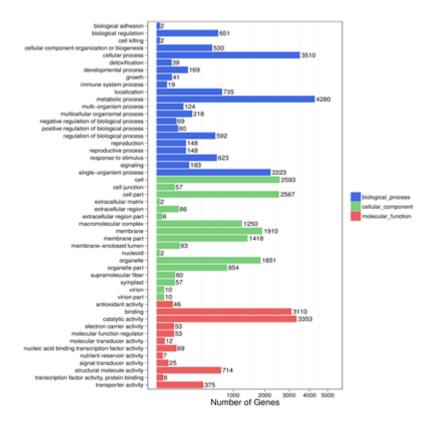


Figure S6: Gene Ontology (GO) Classification of DGs in Y2 vs Y3.

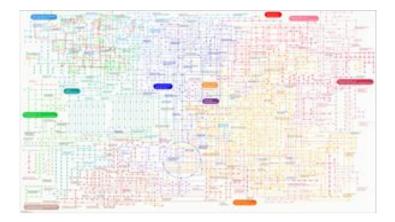


Figure S7: Metabolic pathways pathway in J1 vs J2.

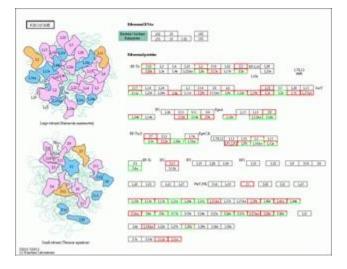


Figure S8: Biosynthesis of secondary metabolites in J1 vs J2.

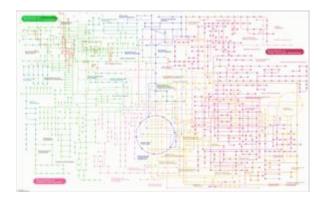


Figure S9: Ribosome in J1 vs J2.

Sample	Raw Data	Clean Data	Clean Data Ratio(%)	Clean Data Q20(%)	Clean Data Q30 (%)	GC Content (%)
J1	51963050	51963050	100	98.1	93.74	47.51
J2	53073410	53073410	100	97.8	92.91	47.95
J3	52209620	52209620	100	97.91	93.25	48.36
Y1	50899656	50899656	100	93.34	84.66	51.22
Y2	49831422	49831422	100	98	93.5	49.27
Y3	51535514	51535514	100	98.03	93.56	48.28

Table S1: The statistics of filtrated reads.