

Supplementary Table S4
Throughput and quality of RNA-seq of samples.

Sample	Raw Reads(M)	Raw Bases(G)	Clean Reads	Clean Bases(G)	Valid Bases(%)	GC(%)	Total Mapped Reads	Multiple Mapped	Uniquely Mapped	Gene Num
P1-9d-1	47.52	7.07	47107598	7.01	99.13	44.15	46487902(98.68%)	1752128(3.72%)	44735774(94.97%)	19538
P1-9d-2	47.51	7.08	47171372	7.03	99.29	44.16	46620086(98.83%)	1793562(3.80%)	44826524(95.03%)	19595
P1-9d-3	47.14	7.01	46715676	6.95	99.1	44.34	46133655(98.75%)	1739803(3.72%)	44393852(95.03%)	19609
P2-3d-1	46.77	6.95	46315150	6.88	99.03	44.35	45764114(98.81%)	1728772(3.73%)	44035342(95.08%)	19768
P2-3d-2	47.39	7.05	46992980	6.99	99.17	44.3	46430852(98.80%)	1804515(3.84%)	44626337(94.96%)	19804
P2-3d-3	47.63	7.08	47186718	7.01	99.06	44.39	46586185(98.73%)	1802510(3.82%)	44783675(94.91%)	19908
P2-9d-1	47.49	7.06	47077238	7	99.13	44.17	46416984(98.60%)	1687923(3.59%)	44729061(95.01%)	19612
P2-9d-2	47.57	7.08	47184406	7.02	99.19	44.19	46371220(98.28%)	1679013(3.56%)	44692207(94.72%)	19450
P2-9d-3	47.69	7.1	47285688	7.04	99.15	44.26	46466743(98.27%)	1695948(3.59%)	44770795(94.68%)	19632