

Supplementary Table S1. Quality statistics of transcriptome.

Sample	Raw reads	Clean reads	Clean bases	Error rate	Q20	Q30	GCpct
the control _1	45919430	45224954	6.78G	0.02	98.07	94.27	42.39
the control _2	45749502	45051114	6.76G	0.03	97.99	94.08	41.61
the control _3	47928220	47106620	7.07G	0.02	98.38	94.98	42.05
ETH_1	45413156	44594122	6.69G	0.02	98.09	94.29	42.06
ETH_2	46001162	44523656	6.68G	0.02	98.23	94.69	41.5
ETH_3	47556332	45532650	6.83G	0.02	98.19	94.62	41.2