

**Supplementary Table S1** Reads quality statistics

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
Ctrl	75.2	70.8	7.08	97.53	89.62	94.15
Ctrl	77.7	72.83	7.28	97.56	89.75	93.73
Ctrl	72.33	67.85	6.79	97.56	89.75	93.81
OA1	70.18	65.93	6.59	97.53	89.66	93.93
OA2	75.2	70.66	7.07	97.54	89.6	93.97
OA3	72.69	68.39	6.84	97.58	89.75	94.09

**Supplementary Table S2** Reference genome alignment statistics

Sample	Total Clean Reads (M)	Total Mapping (%)	Uniquely Mapping (%)
Ctrl	70.8	89.96	67.82
Ctrl	72.83	89.84	67.97
Ctrl	67.85	89.6	67.81
OA1	65.93	89.27	67.17
OA2	70.66	90.16	68.03
OA3	68.39	89.5	67.5

**Figure Legends**

**Supplementary Figure 1** Classification map of GO annotation after OA treatment.

**Supplementary Figure 2** Differential gene KEGG Pathway classification after exposed to OA.

**Supplementary Figure 3** Correlation between different biological replicates.

Figure S1

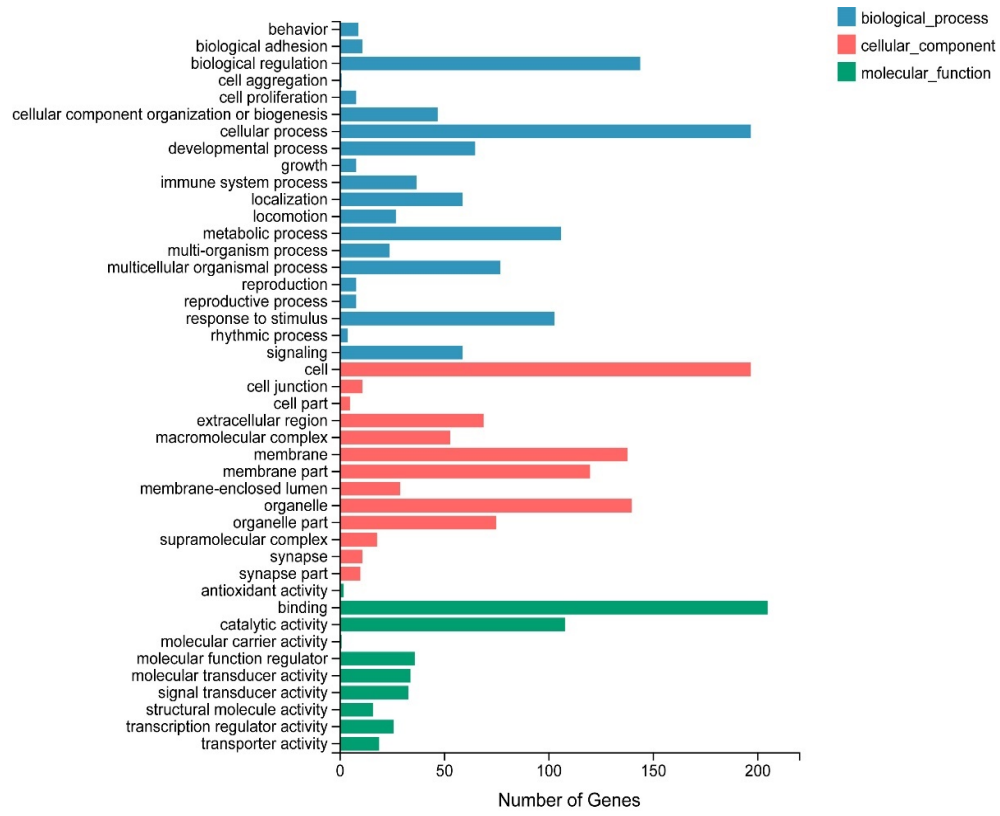


Figure S2

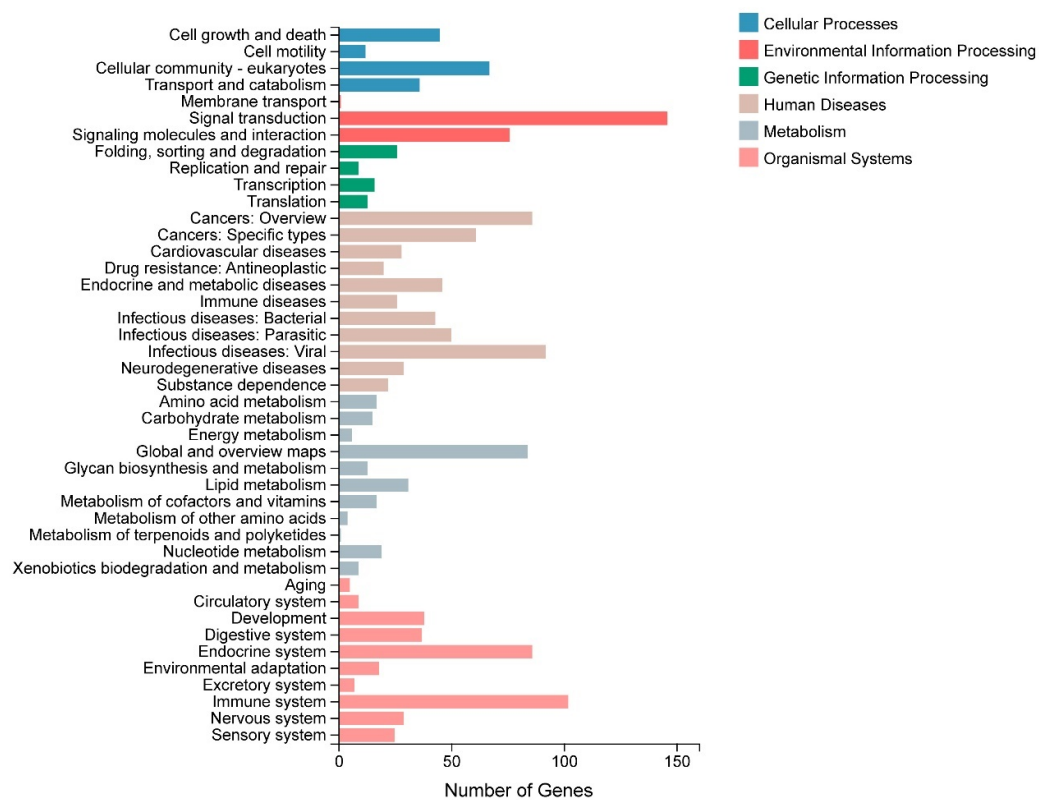


Figure S3

