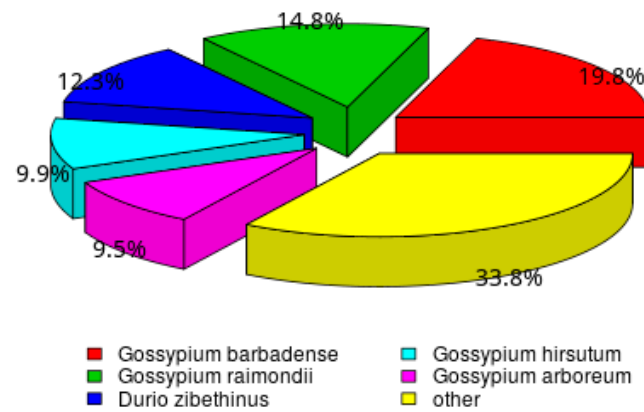**Figure. S1** Veen

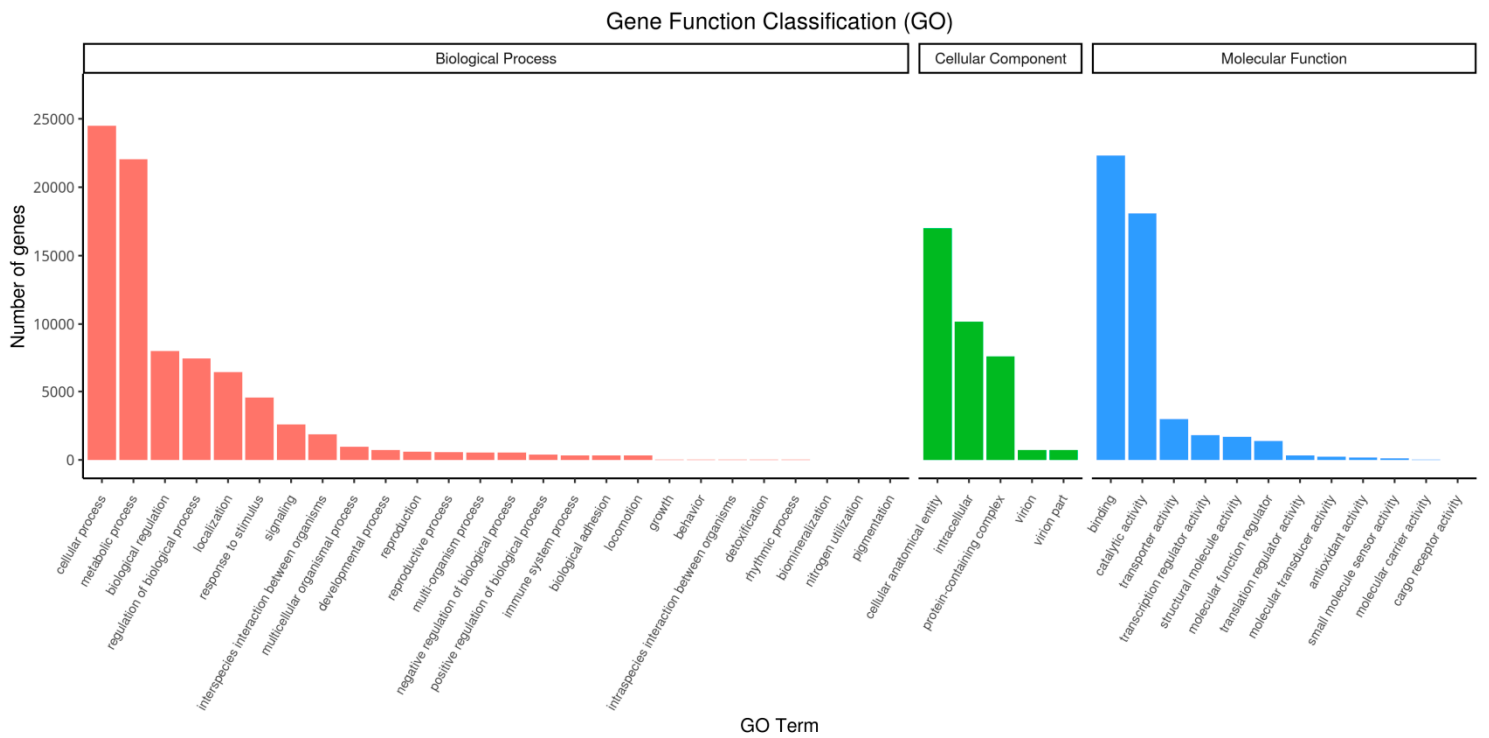**Figure. S2** Species distribution map of NR library ratio pairs of okra Unigene sequence

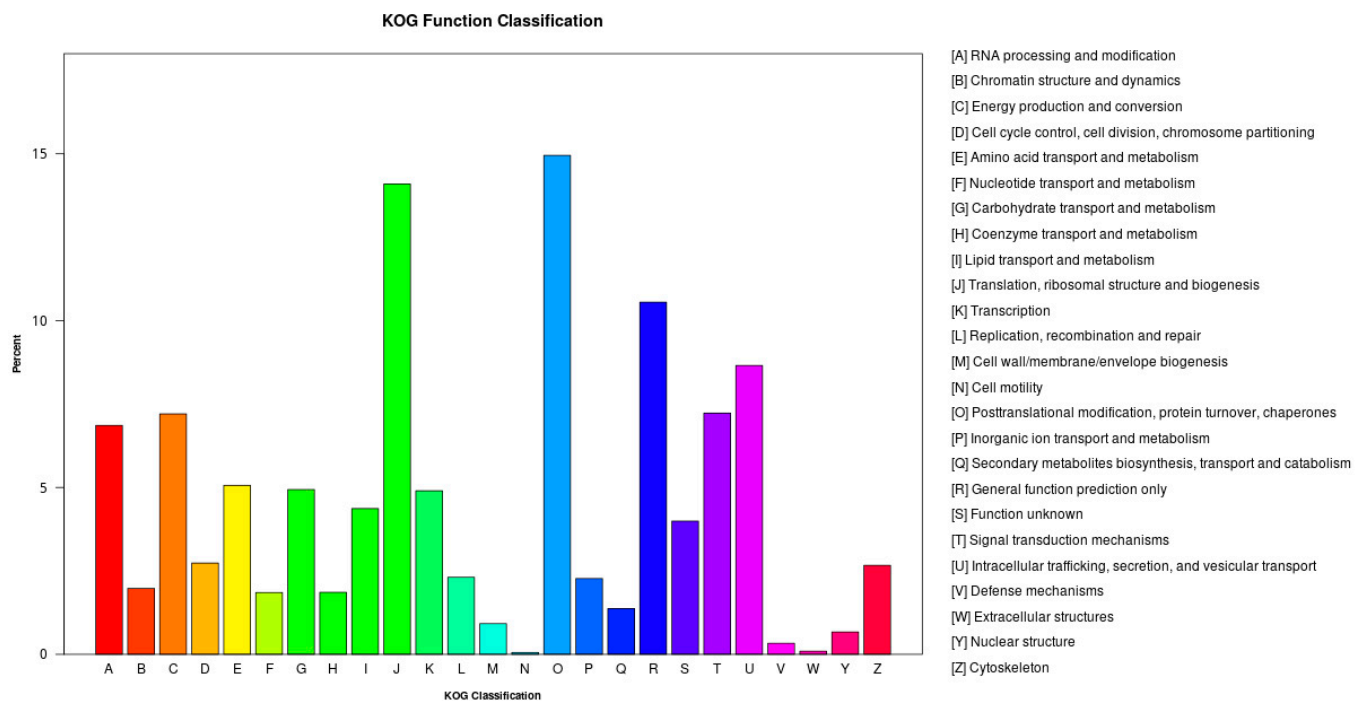**Figure. S3** GO annotation classification statistics of okra Unigene sequence

Figure. S4 KOG annotation classification statistical map of okra Unigene sequence
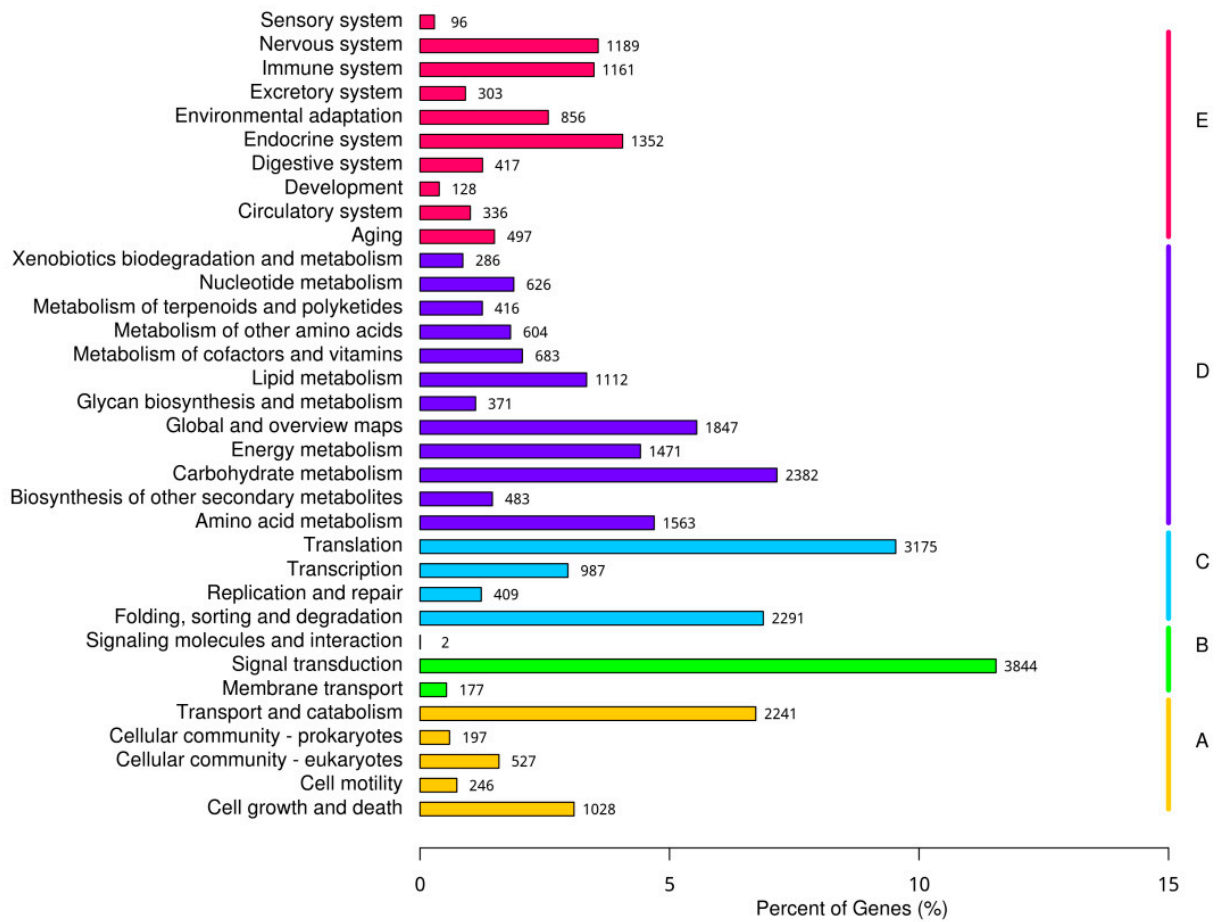
KEGG Classification

Category	Count
Sensory system	96
Nervous system	1189
Immune system	1161
Excretory system	303
Environmental adaptation	856
Endocrine system	1352
Digestive system	417
Development	128
Circulatory system	336
Aging	497
Xenobiotics biodegradation and metabolism	286
Nucleotide metabolism	626
Metabolism of terpenoids and polyketides	416
Metabolism of other amino acids	604
Metabolism of cofactors and vitamins	683
Lipid metabolism	1112
Glycan biosynthesis and metabolism	371
Global and overview maps	1847
Energy metabolism	1471
Carbohydrate metabolism	2382
Biosynthesis of other secondary metabolites	483
Amino acid metabolism	1563
Translation	3175
Transcription	987
Replication and repair	409
Folding, sorting and degradation	2291
Signaling molecules and interaction	2
Signal transduction	3844
Membrane transport	177
Transport and catabolism	2241
Cellular community - prokaryotes	197
Cellular community - eukaryotes	527
Cell motility	246
Cell growth and death	1028

Percent of Genes (%)

Figure. S5 KEGG metabolic pathway classification statistics of okra Unigene sequence

Table. S1 Summary of sequencing quality

Sample	Clean-reads	Clean-bases	Error rate	Q20	Q30	GC（%）
Control 1	19,271,851	5.8	0.03	97.65	93.25	43.82
Control 2	23,018,404	6.9	0.02	98.27	94.62	45
Control 3	20,932,939	6.3	0.03	97.47	92.9	44.31
OTEO 1	21,061,634	6.3	0.03	97.59	93.09	44.19
OTEO 2	20,252,807	6.1	0.03	97.46	92.83	44.3
OTEO 3	21,322,456	6.4	0.03	97.64	93.24	44.61

Table. S2 gene annotation results

Database Type	Unigenes	Proportion（%）
NR	67,765	70.24
NT	62,250	64.52
PFAM	42,365	43.91
GO	42,362	43.91
KOG	15,977	16.56