Table S1: Raw data and quality analysis

Samples	Read Number	Base Number	GC Content	Q30
CK1	21,635,277	6,472,224,836	49.96%	87.38%
CK2	27,442,858	8,219,515,664	49.80%	87.14%
CK3	28,500,163	8,523,530,860	49.95%	86.94%
T1	24,109,625	7,214,171,494	49.02%	93.45%
T2	24,869,729	7,434,822,846	48.79%	93.63%
T3	23,856,426	7,149,200,002	49.82%	87.23%

Table S2: Length range of the unigenes

Length Range	Unigene
200-300	23,992(42.91%)
300-500	13,939(24.93%)
500-1000	9,217(16.49%)
1000-2000	5,136(9.19%)
2000+	3,622(6.48%)
Total Number	55906
Total Length	37227738
N50 Length	1130

Mean Length	665.9

Table S3:   Annotation of the unigenes

Anno_Database	Annotated_Number	300<=length<1000	length>=1000
COG_Annotation	11240	4612	3562
GO_Annotation	24611	10781	4415
KEGG_Annotation	10843	4400	3675
KOG_Annotation	22067	9446	5294
Pfam_Annotation	22222	9565	6656
Swissprot_Annotation	13471	5140	5388
eggNOG_Annotation	35362	15306	7191
nr_Annotation	36964	15850	7296
All_Annotated	37302	15948	7380

Nr(NCBI nonredundant protein databases); COG (Clusters of Orthologous Groups); KOG (euKaryotic Orthologous Groups);

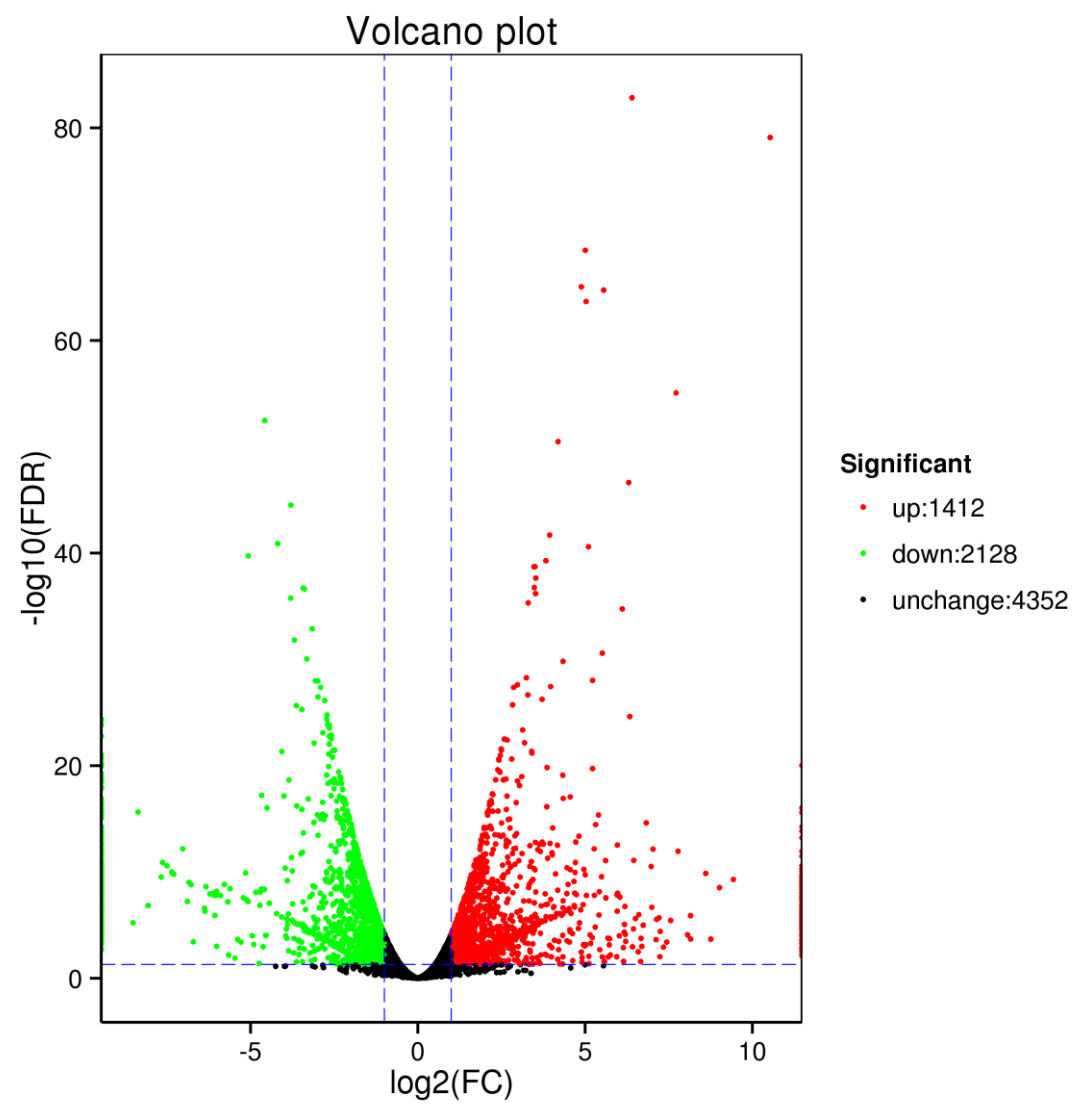GO(Gene Ontology); KEGG (Kyoto Encyclopedia of Genes and Genomes); Pfam (Protein family).

Figure S1: Volcano plot analyses of differentially expressed genes in *G. citri-aurantii* underlying the treatment of cytosporone B

COG Function Classification of Consensus Sequenc

A: RNA processing and modification [14~0.8%]
B: Chromatin structure and dynamics [6~0.34%]
C: Energy production and conversion [101~5.76%]
D: Cell cycle control, cell division, chromosome partitioning [20~1.14%]
E: Amino acid transport and metabolism [158~9.02%]
F: Nucleotide transport and metabolism [39~2.23%]
G: Carbohydrate transport and metabolism [134~7.65%]
H: Coenzyme transport and metabolism [48~2.74%]
I: Lipid transport and metabolism [50~2.85%]
J: Translation, ribosomal structure and biogenesis [123~7.02%]
K: Transcription [120~6.85%]
L: Replication, recombination and repair [110~6.28%]
M: Cell wall/membrane/envelope biogenesis [44~2.51%]
N: Cell motility [2~0.11%]
O: Posttranslational modification, protein turnover, chaperones [115~6.56%]
P: Inorganic ion transport and metabolism [98~5.59%]
Q: Secondary metabolites biosynthesis, transport and catabolism [43~2.45%]
R: General function prediction only [345~19.69%]
S: Function unknown [24~1.37%]
T: Signal transduction mechanisms [105~5.99%]
U: Intracellular trafficking, secretion, and vesicular transport [17~0.97%]
V: Defense mechanisms [17~0.97%]
W: Extracellular structures [0~0%]
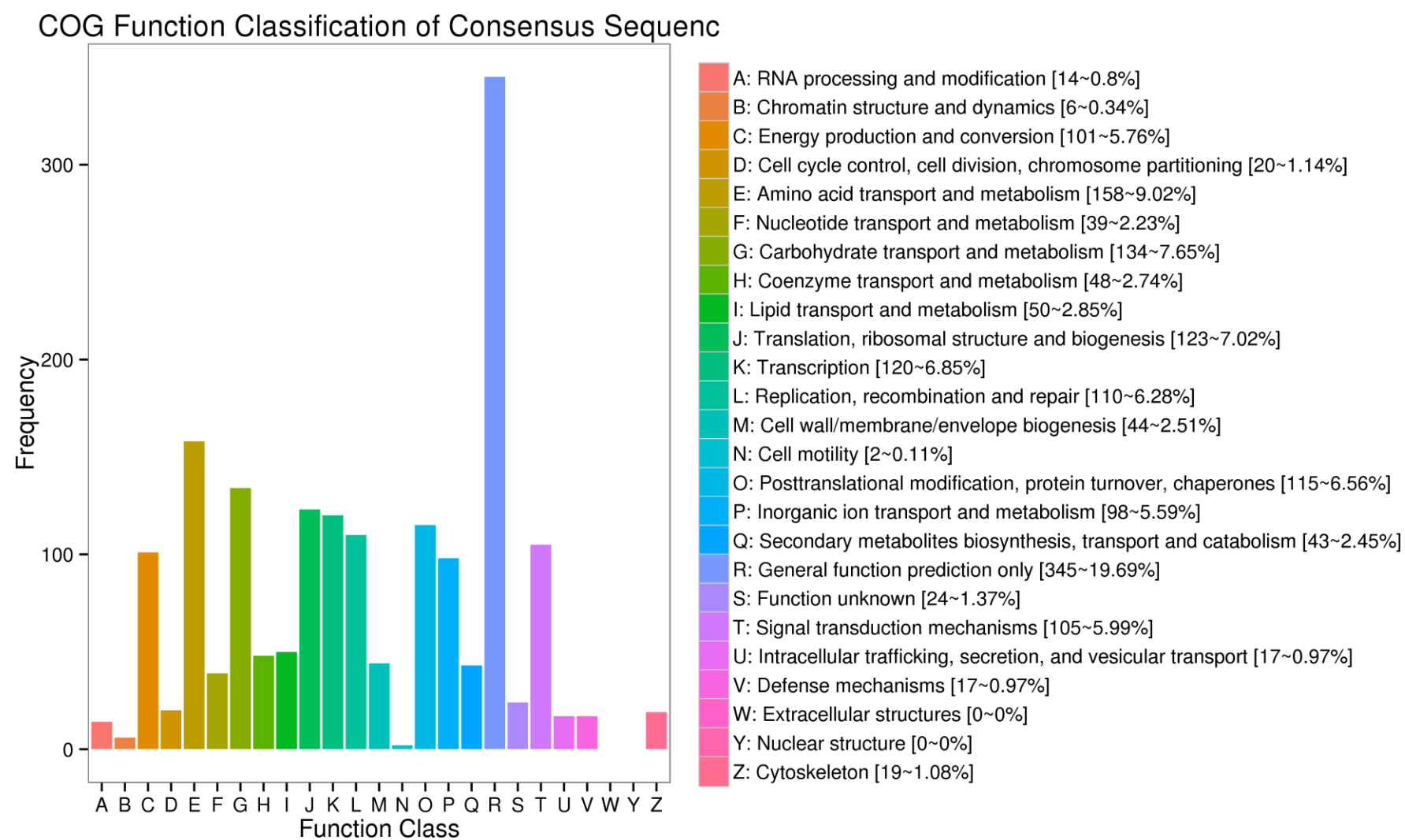Y: Nuclear structure [0~0%]
Z: Cytoskeleton [19~1.08%]

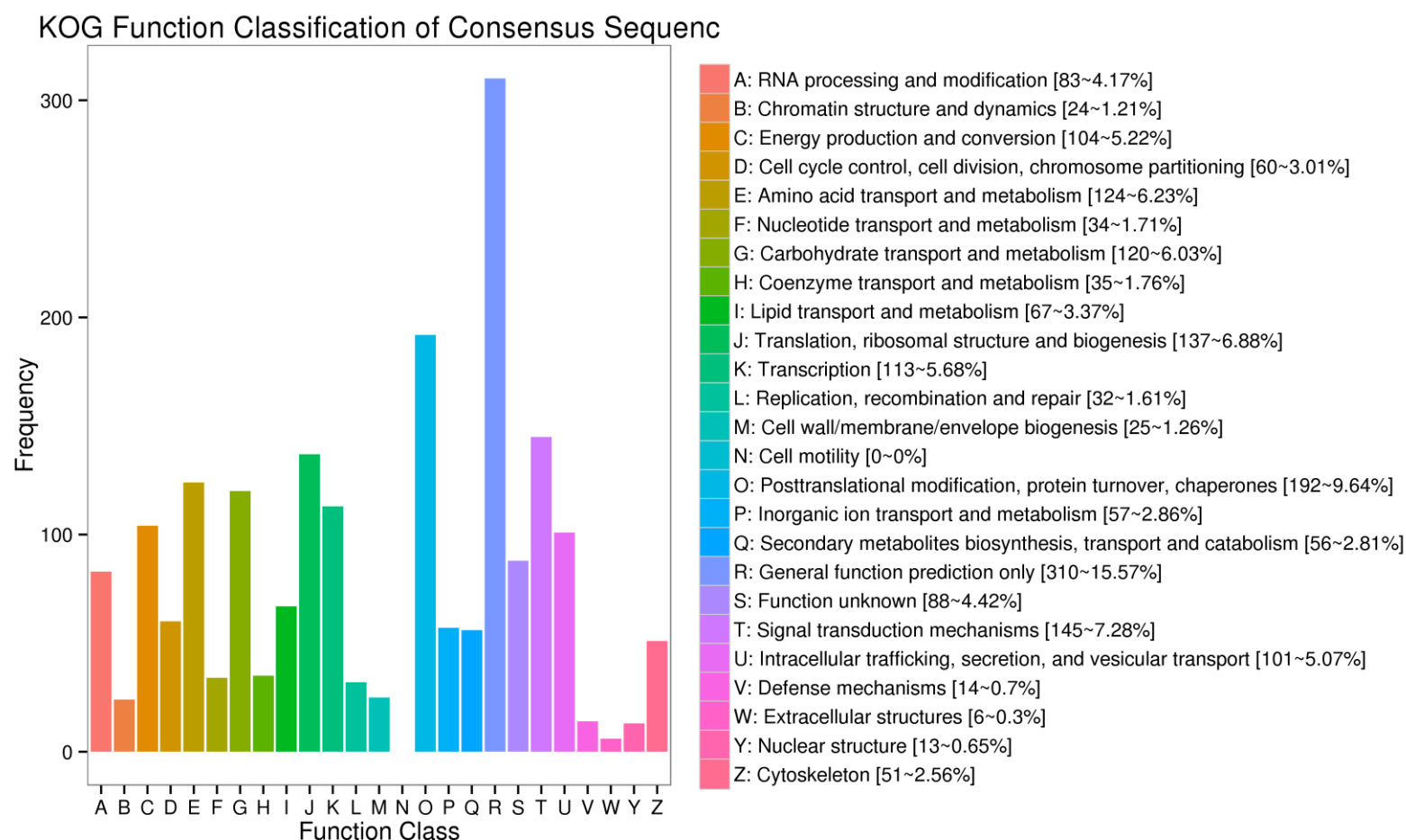Figure S2:   COG functional classification of unigenes
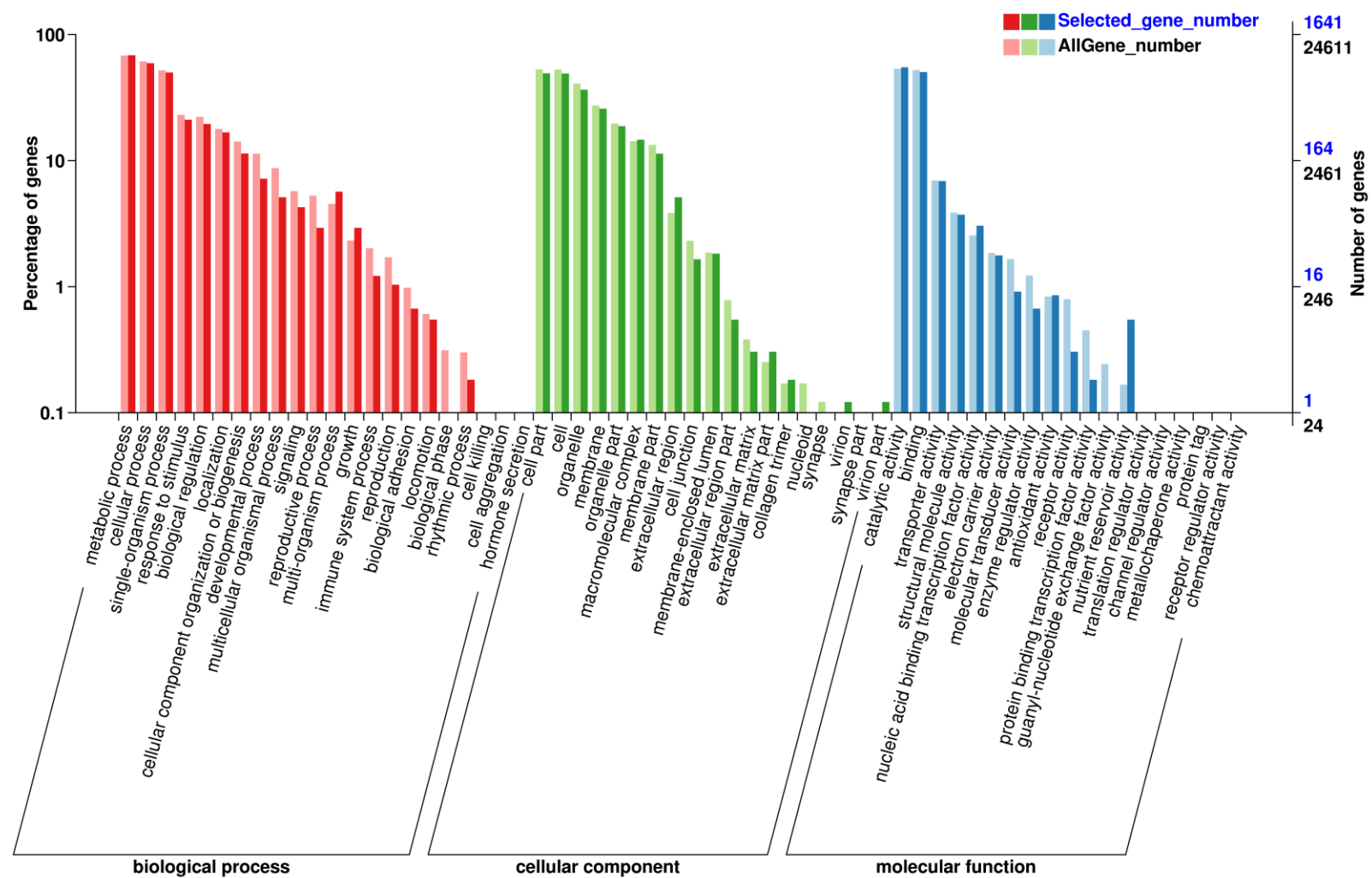
Figure S3: KOG functional classification of unigenes

Figure S4: GO functional classification of unigenes