**Figure S1** The distribution of reads number in different average fragments depth
**Figure S2** The distribution of Top-hits species based on Gene Ontology (GO) result
Figure S3 The sequence distribution with different Evidence Codes
Figure S4 COG classification assigned sequences to top orthologous groups. The x-axis represents the abbreviation of COG Categories, and the full name of COG Categories were on the right. The y-axis denotes the sequence number.
Figure S5 The sequence distribution in different pathway detecting from KEGG database