

Figure S10: A. Histogram of distribution of 267 COG groups between *Rickettsiales* and *Caulobacter crescentus* CB15 from COG database. J, Translation; A, RNA processing and modification; K, Transcription; L, Replication, recombination and repair; B, Chromatin structure and dynamics; D, Cell cycle control, mitosis and meiosis; Y, Nuclear structure; V, Defense mechanisms; T, Signal transduction mechanisms; M, Cell wall/membrane biogenesis; N, Cell motility; Z, Cytoskeleton; W, Extracellular structures; U, Intracellular trafficking and secretion; O, Posttranslational modification, protein turnover, chaperones; C, Energy production and conversion; G, Carbohydrate transport and metabolism; E, Amino acid transport and metabolism; F, Nucleotide transport and metabolism; H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis, transport and catabolism; R, General function prediction only; S, Function unknown; na, Not in COGs

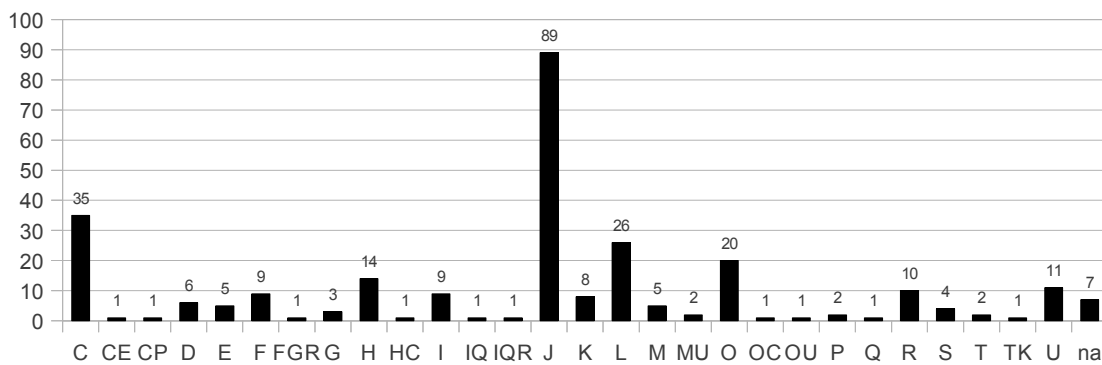


Figure S10: B. Histogram of distribution of 267 COG groups among *Rickettsia*, *Orientia*, *Wolbachia*, *Anaplasma*, *Ehrlichia*, *Neorickettsia* and *Candidatus Pelagibacter ubique* from COG database. The letters signification were indicated in the figure legend above.

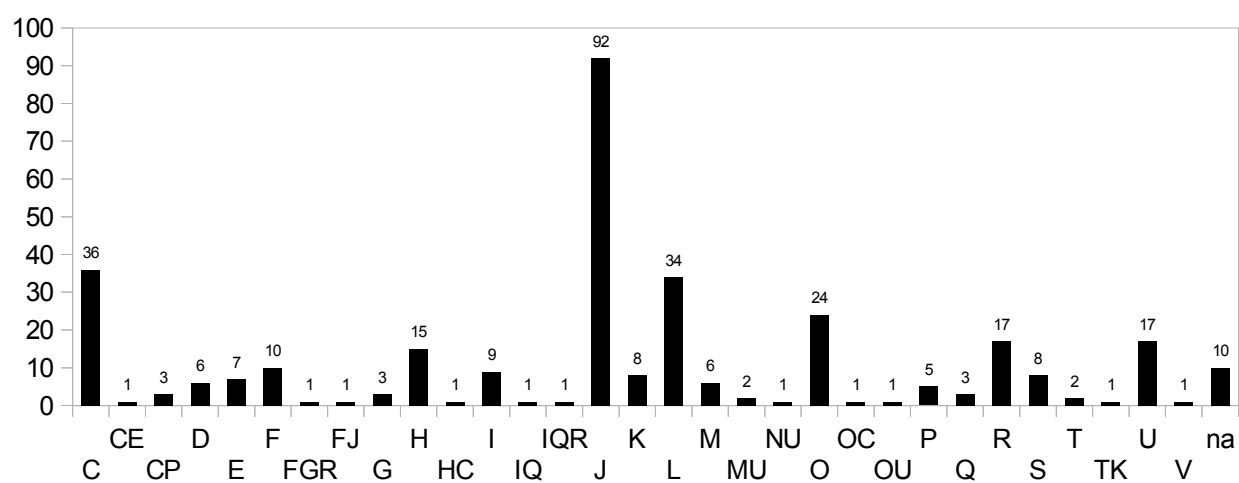


Figure S10: C. Histogram of distribution of 328 COG groups among *Rickettsia*, *Orientia*, *Wolbachia*, *Anaplasma*, *Ehrlichia* and *Neorickettsia* from COG database. The letters signification were indicated in the figure legend above.

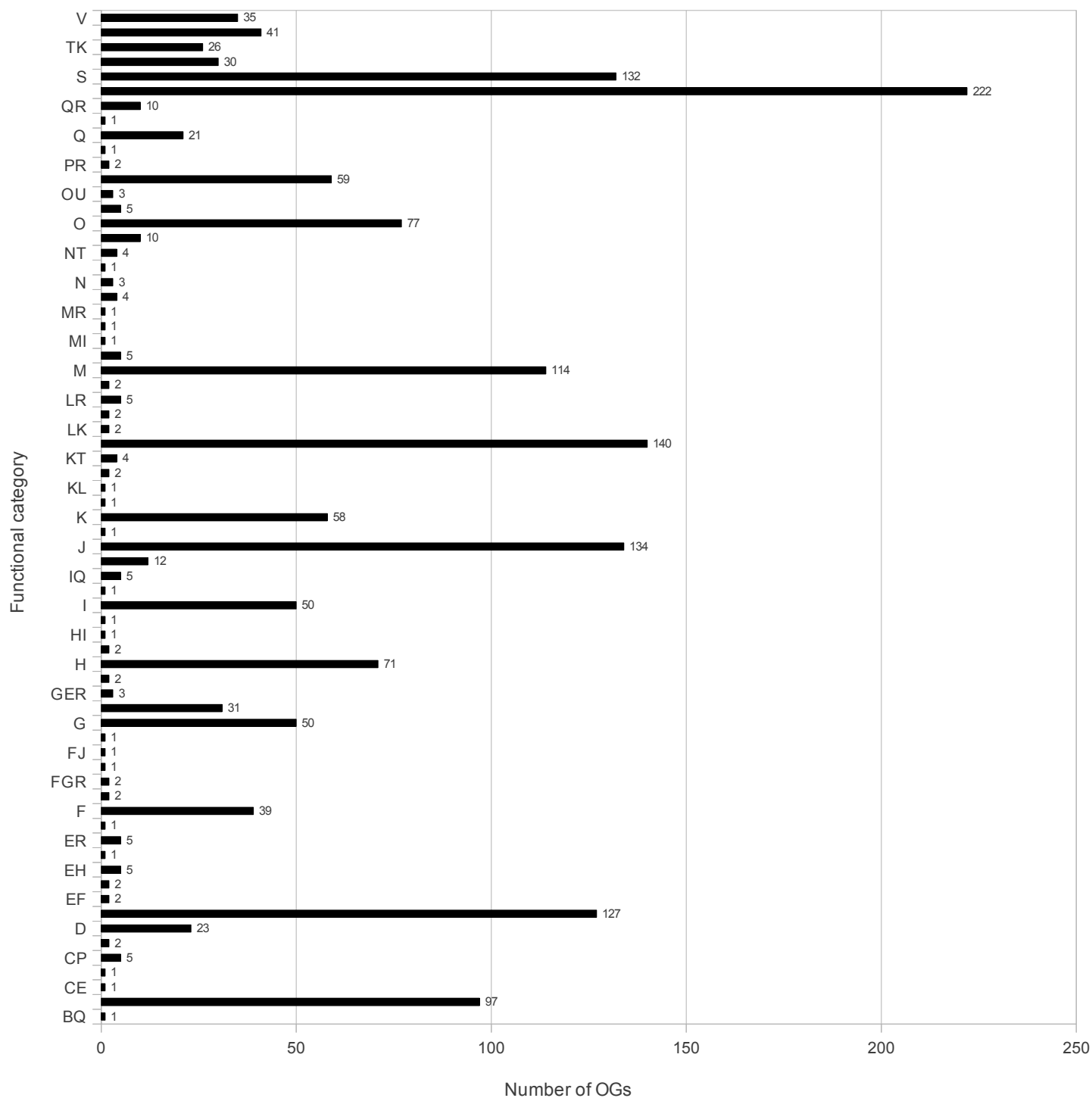


Figure S10: D. histogram of distribution of 1,709 COG groups based on COG database. The letters signification were indicated in figure legend above.