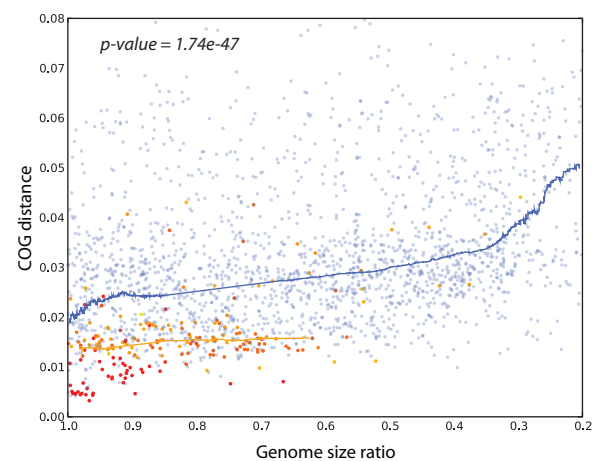
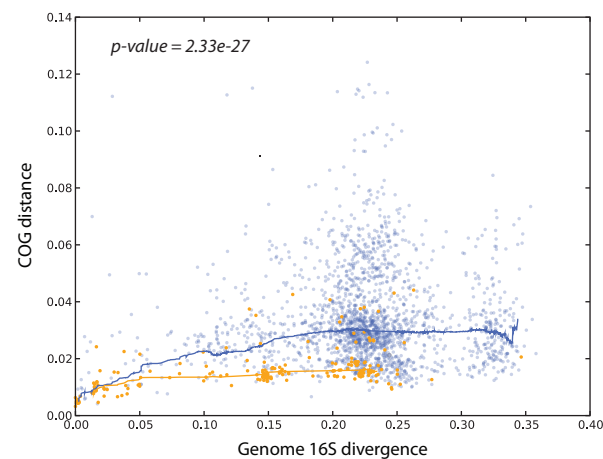
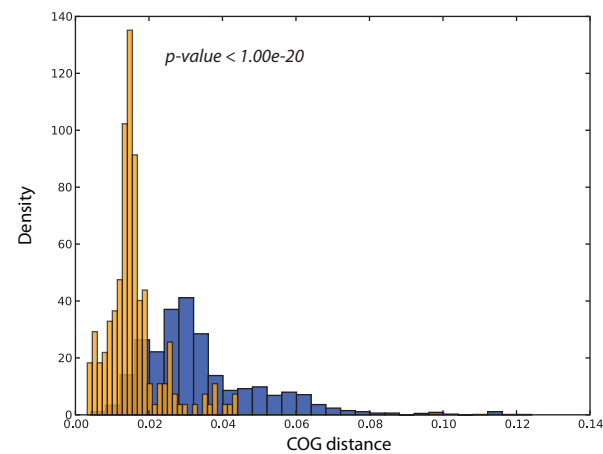
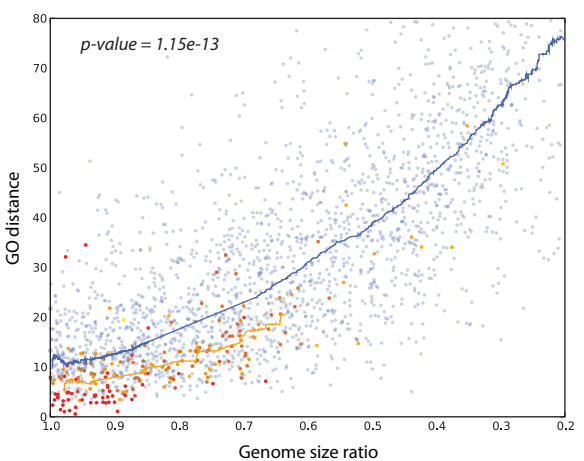
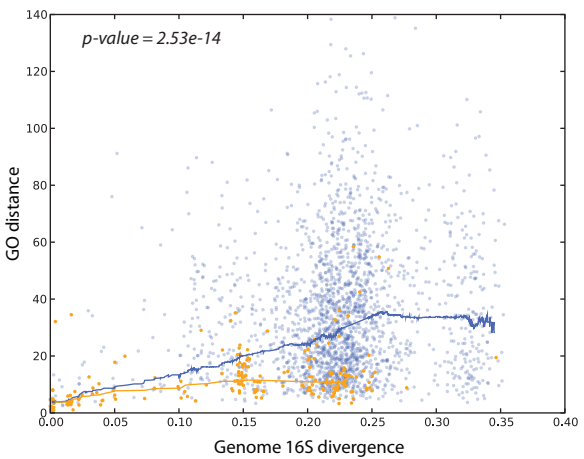
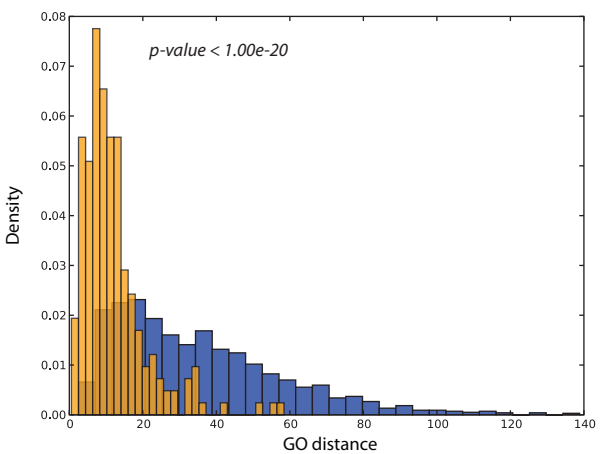




Alternative A:
using the COG database ('clusters of orthologous genes') to assess functional similarity of genomes



Alternative B:
using Gene Ontology annotation ('GO Slim') to assess functional similarity of genomes