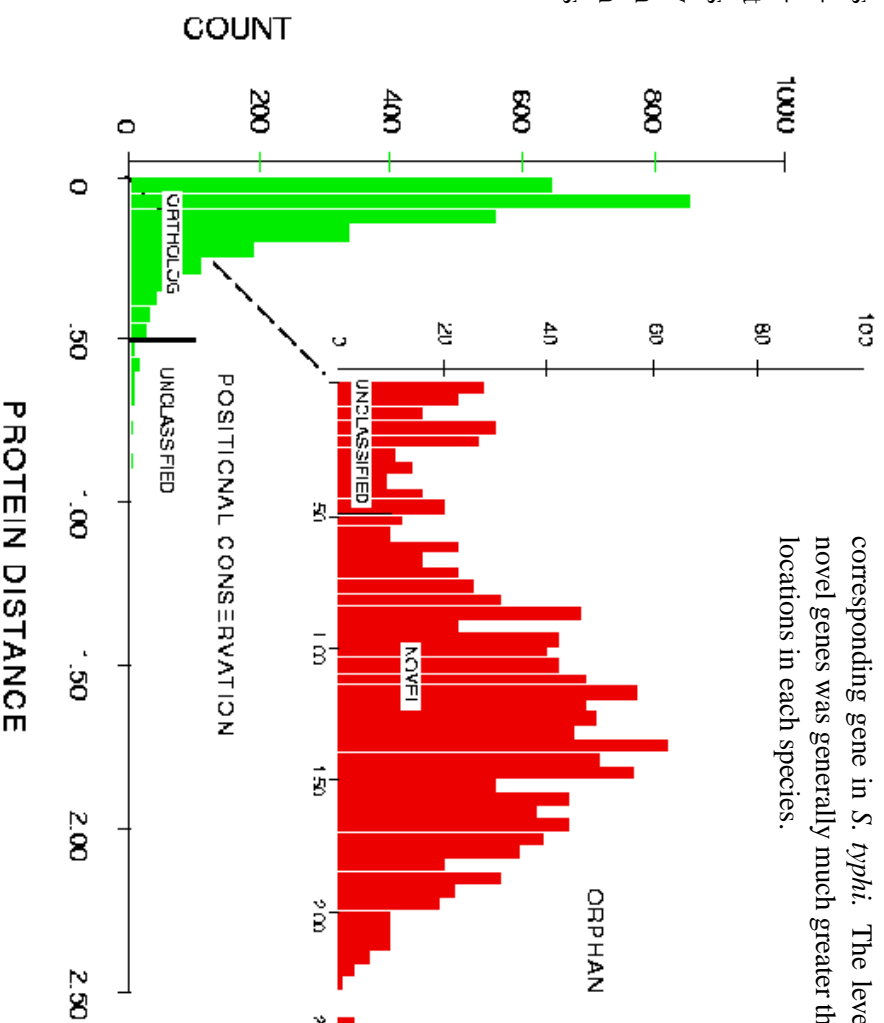


Codon Bias and Base Composition Are Poor Indicators of Horizontally Transferred Genes

Horizontal gene transfer is now recognized as an important mechanism of evolution. Several ways to detect horizontally transferred genes have been suggested. Many of these methods are based on either nucleotide composition or unusual usage of codons within proteins.

We compared the genes in *Escherichia coli* and *Salmonella typhi* (diverged 100 mya) to identify genes that are in the same location in both species. We found 2728 genes in the same location in each species and 1144 novel genes in *E. coli* without a



The graph shows the genetic distance of proteins between the two species. Genes in the same location (green) are generally less than 0.5 distant. The inset shows the novel genes (red), many greater than 0.5 distant. The novel genes we have identified do not match the genes of unusual codon bias or base composition. But we have demonstrated that many of the novel genes of unusual divergence have been horizontally transferred (others are rearranged or deleted).

Lisa B. Koski, Richard A. Morton, and G. Brian Golding,
2001, *Mol. Biol. Evol.* 18(3):404-412.