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

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

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

COUNT



novel genes was generally much greater than the genes that are in the same corresponding gene in S. typhi. The level of sequence divergence in the

^{* 50} position. But we have demonusual codon bias or base comstrated that many of the novel or deleted). genes of unusual divergence genes we have identified do genes (red), many greater ferred (others are rearranged have been horizontally transthan 0.5 distant. The novel generally less than 0.5 distant. the same location (green) are the two species. Genes in distance of proteins between not match the genes of un-The inset shows the novel The graph shows the genetic

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