



FIGURE S2.—Proportion of genomes with $o/e > 1.0$ for different number of mononucleotide runs in sense:sense codon pair junction (among 13 eukaryotic, 53 bacterial and 68 archaeal genomes). Under the null hypothesis of no bias (observation counts = expected counts), the proportion should be around 50%, whereas the downward bias is obvious for codon pairs with long mononucleotide runs (5N or 6N) in these organisms.