FIG. S1.— Fraction of genes not matching the average and modal codon usages, at varying chi-square P-values, for simulated genomes. Simulated genomes were generated by matching the *E. coli* K-12 gene lengths and amino acid compositions, and drawing each codon randomly from the *E. coli* K-12 average codon usage for the given amino acid. The average and modal codon usages were determined for each simulated genome, and the fraction of simulated genes not matching was determined for each *P*-value. Plot symbols show the mean of 100 replicates, while the flanking lines encompass 80% of the simulations. Circles, fraction not matching average; squares, fraction not matching mode.