Supplementary Figure 1: For each class of gene, the proportion of adjacent pairs that are on the same strand. Each gene is adjacent to two other genes, and in the absence of operons, on average, one of these other genes will be on the same strand, giving a proportion of 0.5. For genes in long operons, the average proportion will be near 1.0. For each class, the solid bar shows this proportion and the error bar shows the 90% confidence interval from the binomial test. If two error bars do not overlap, then the corresponding classes have significantly different probabilities of same-strand pairs ($p < 0.05$).