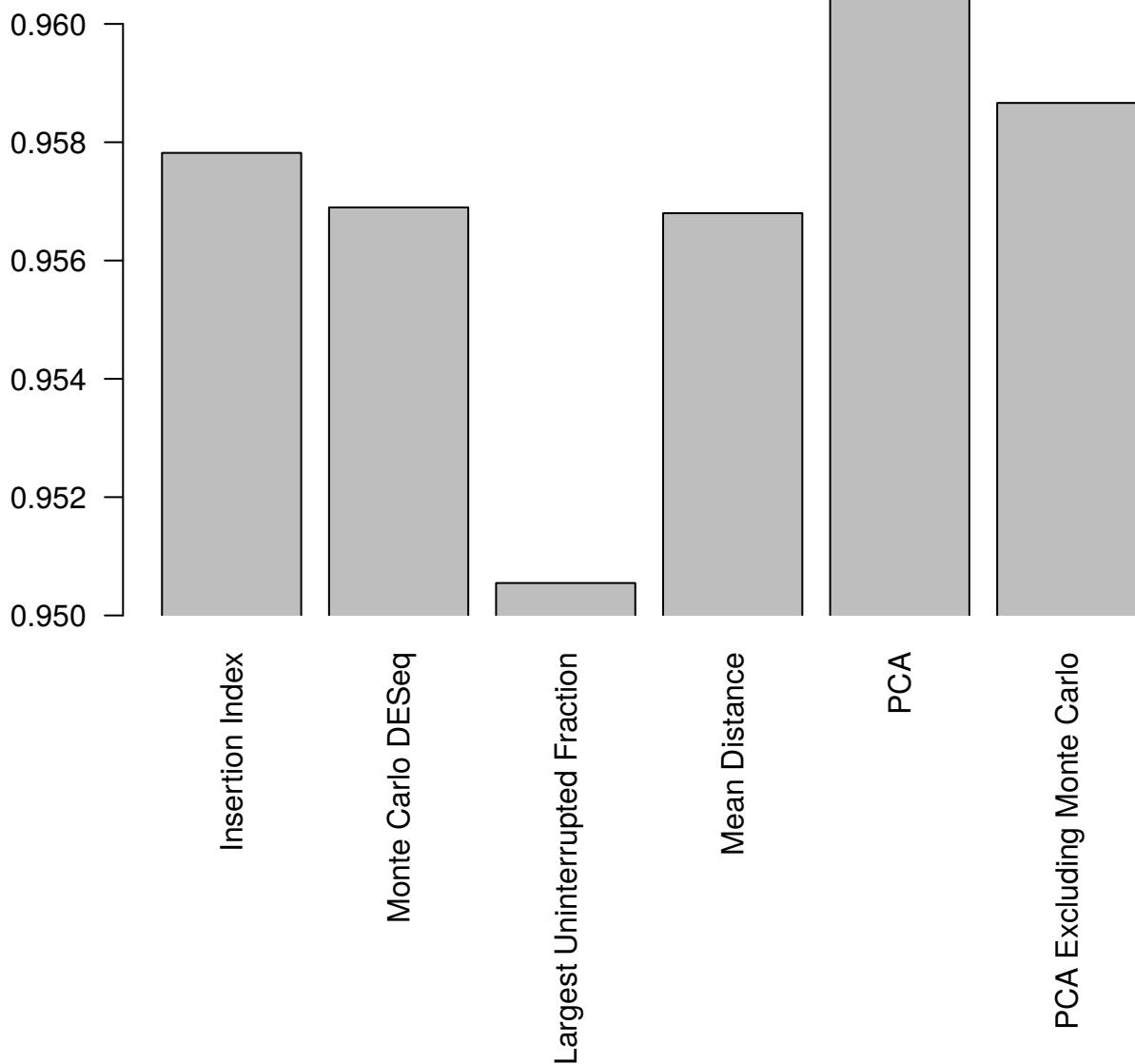**Figure S2.** Average AUC over all 13 genomes used in this study for calculating the accuracy of 6 different methods. In order to calculate AUCs, we considered true positives as genes that are predicted as essential and whose orthologs are essential in ecogene database of essential genes for E. coliK-12 and false positives as genes that arepredicted as essential, but are classed as non-essential in EcoGene.