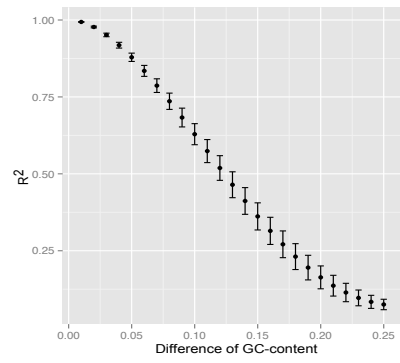
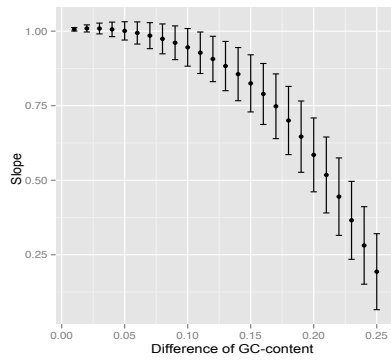


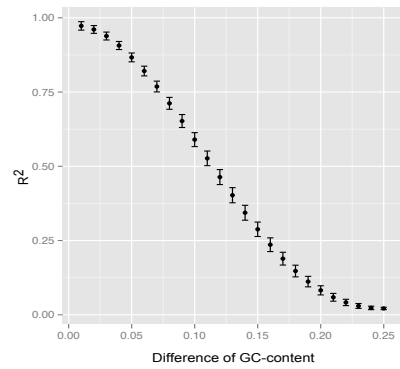
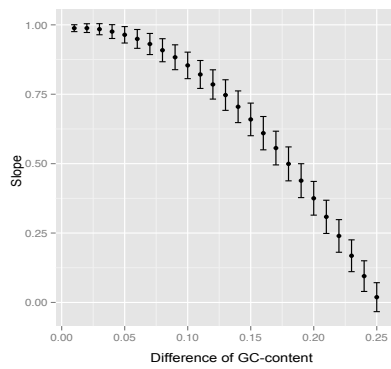
a

prokaryotes



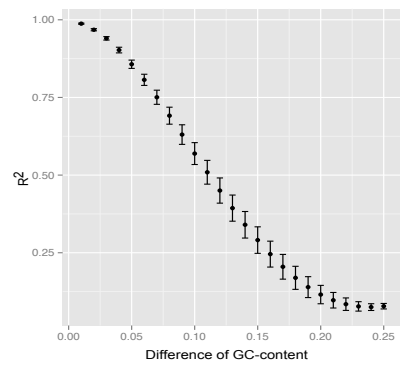
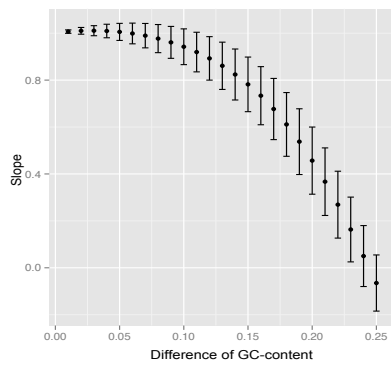
b

mammals



c

plants



d

other eukaryotes

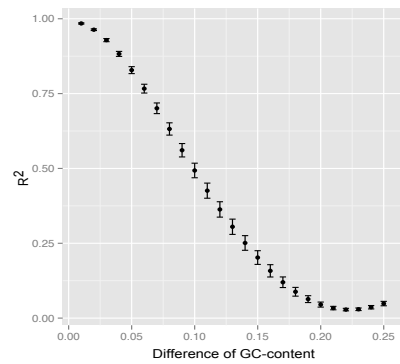
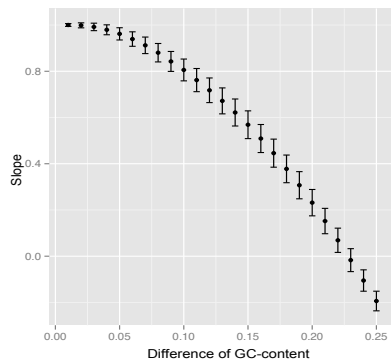


Figure S3. The patterns of the correlation slope (left column) and the coefficient of determination R^2 values (right column) for codon usages between different GC-groups. We performed regression analysis by separating the 65 organisms into (a) prokaryotes, (b) mammals, (c) plants and (d) other eukaryotes.