## Update of the analysis of Muto & Osawa (PNAS, 87): regression using the 102 complete genomes

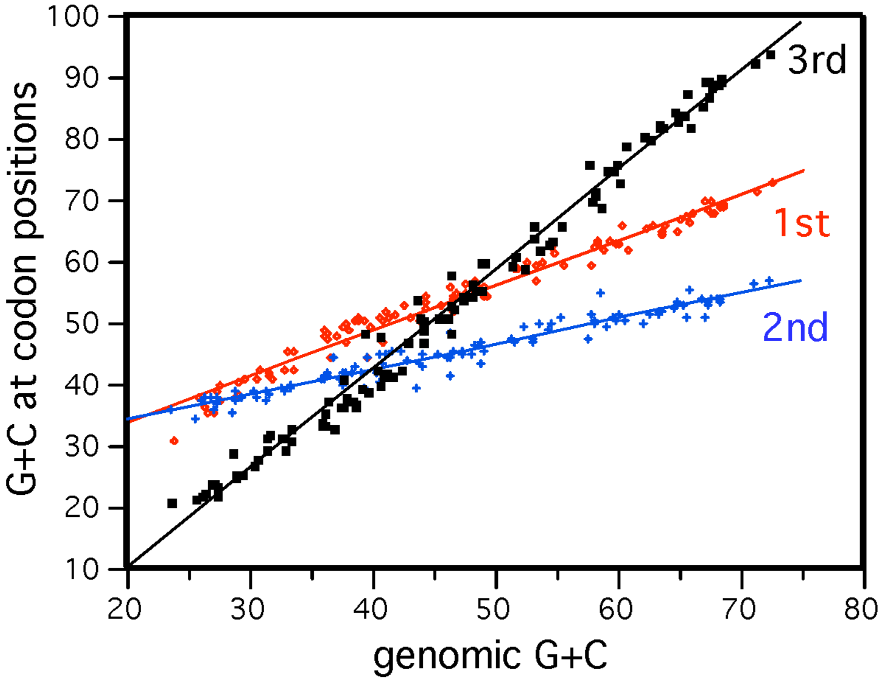

Figure A1- Regression of codon position G+C on genomic G+C for each of the three codon positions. The regression equations are ($R^2 > 0.90$, $P < 0.001$, for all cases):

$\%G+C_1 = 19,20 + 0,743\ \%G+C$

$\%G+C_2 = 17,22 + 0,459\ \%G+C$

$\%G+C_3 = -36,42 + 1,798\ \%G+C$