Supplement

The following figure is a supplement to:
Lynch, M. and Conery, J.S. The evolutionary fate and consequences of duplicate genes. 

The relationship between the number of substitutions per silent site (S) and the number of nucleotides separating the two members of a duplicate pair on the same chromosome. The data for Arabidopsis thaliana (At) are derived from the complete sequences of chromosomes 2 and 4; those for Caenorhabditis elegans (Ce) are derived from the complete genomic sequence; and those for Drosophila melanogaster (Dm) are pairs of duplicates contained within the same scaffolds. Least-squares regression involve the natural logarithm of physical distance. For At, slope = 0.111 (0.003), r² = 0.115, n = 811; for Ce, slope = 0.091 (0.003), r² = 0.028, n = 1027; for Dm, slope = 0.183 (0.009), r² = 0.031, n = 250. All regressions are significant at the P = 0.01 level, although the proportion of the variance explained by the model (r²) is very low in all cases. In no case is the intercept significantly different from zero.