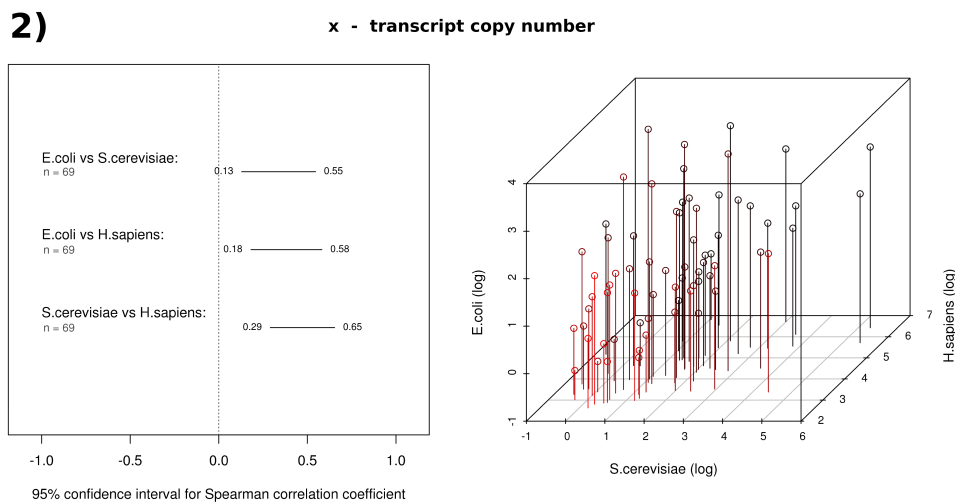
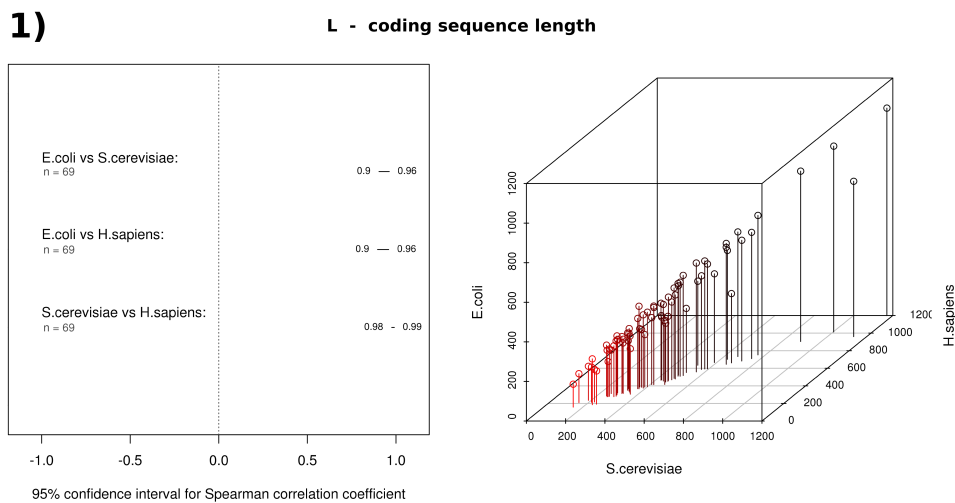
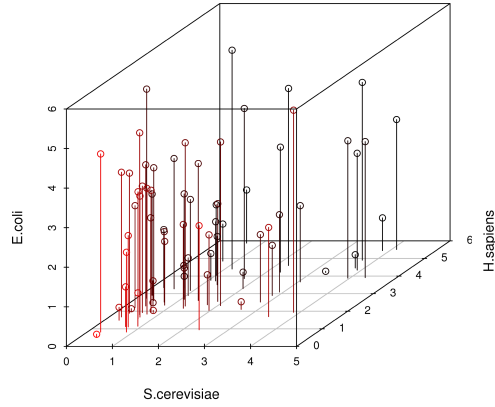
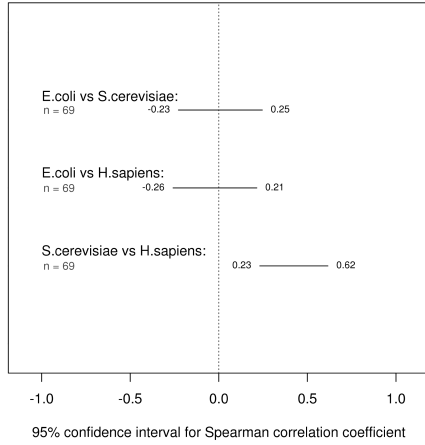


**Figure S2:** Correlations of translational parameters values of orthologous genes common for three analyzed species (plots 1-7 and 9-10), and correlations of mean elongation times of 61 sense codons calculated for three analyzed species (plot 8). All pairwise comparisons between species are presented. Left panels: 95% confidence intervals for Spearman correlation coefficients are plotted as horizontal lines, n stands for sample size. Right panels: three-dimensional scatter plots of compared parameters' values; if necessary, the values are logged.



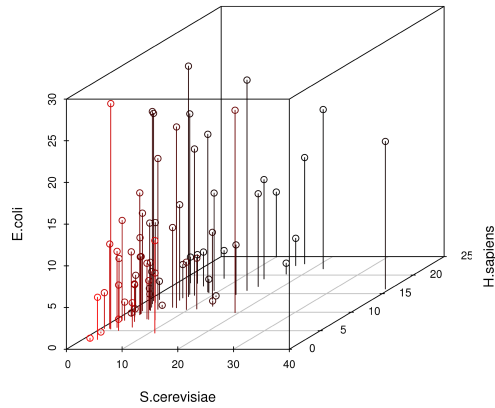
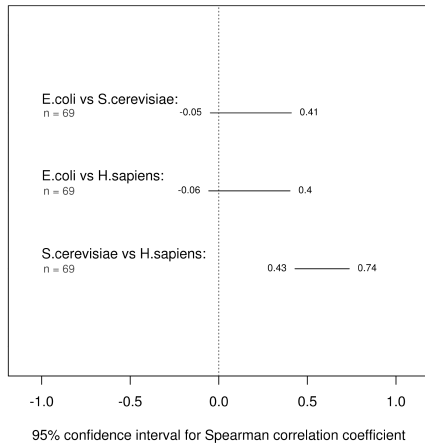
3)

**g - ribosome density**



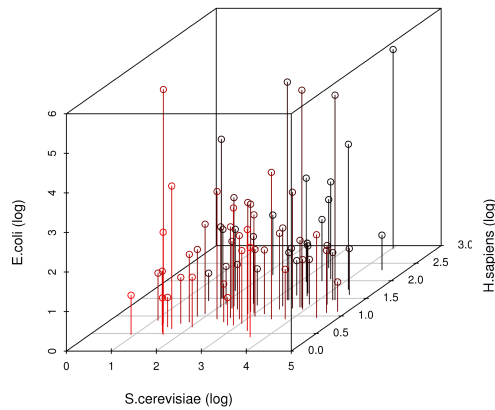
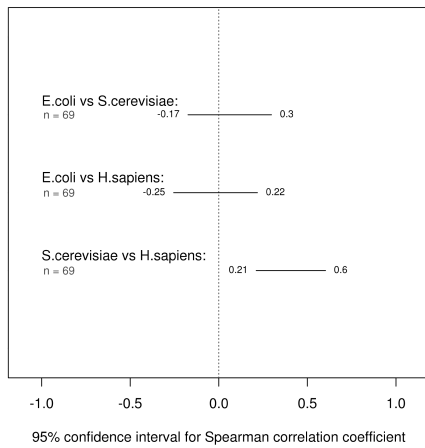
4)

**w - number of ribosomes per transcript**



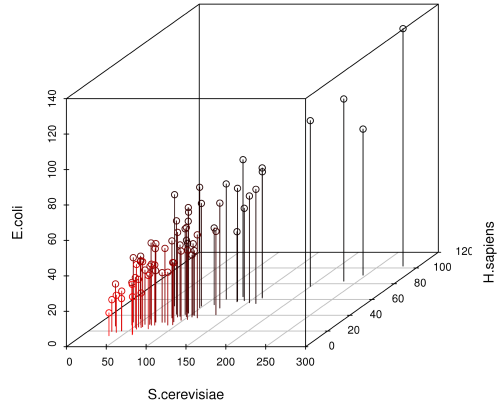
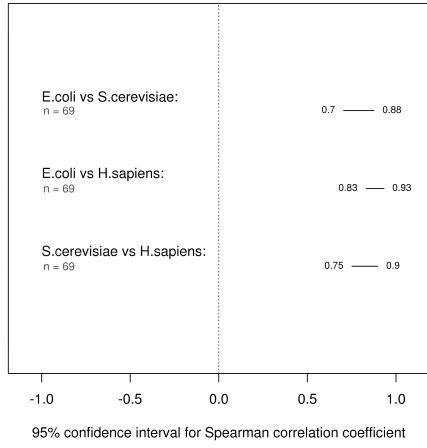
5)

**l - mean initiation time**



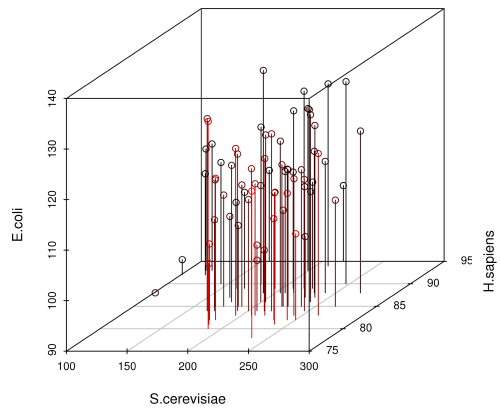
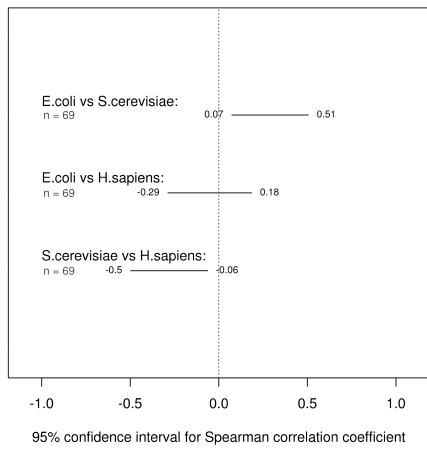
6)

**E - total elongation time**



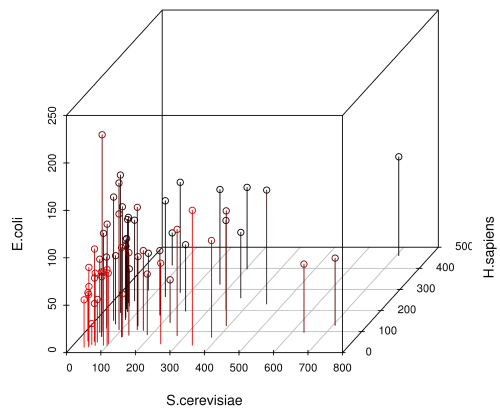
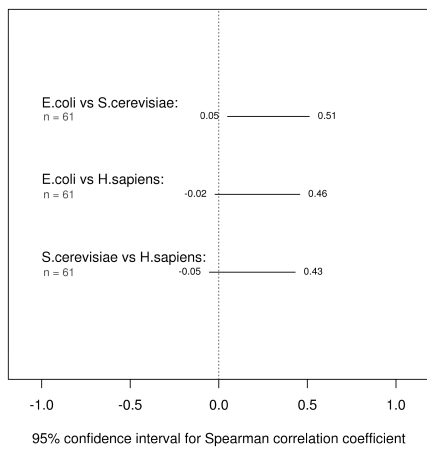
7)

**$\bar{e}$  - transcript mean elongation time of one codon**



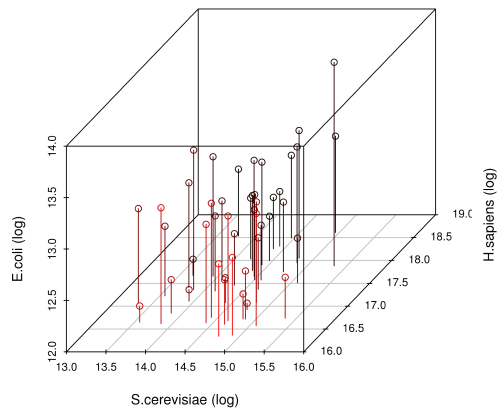
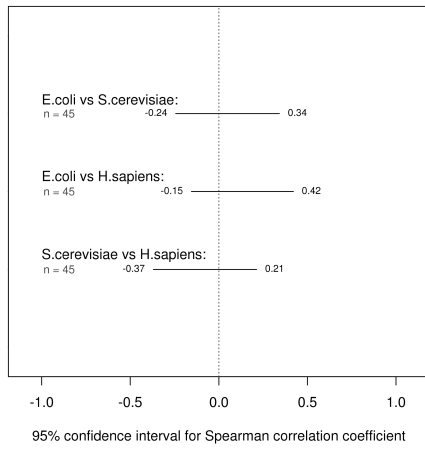
8)

**mean elongation times of 61 sense codons**



9)

m - transcript mean lifetime



10)

b - number of proteins produced from one transcript

