

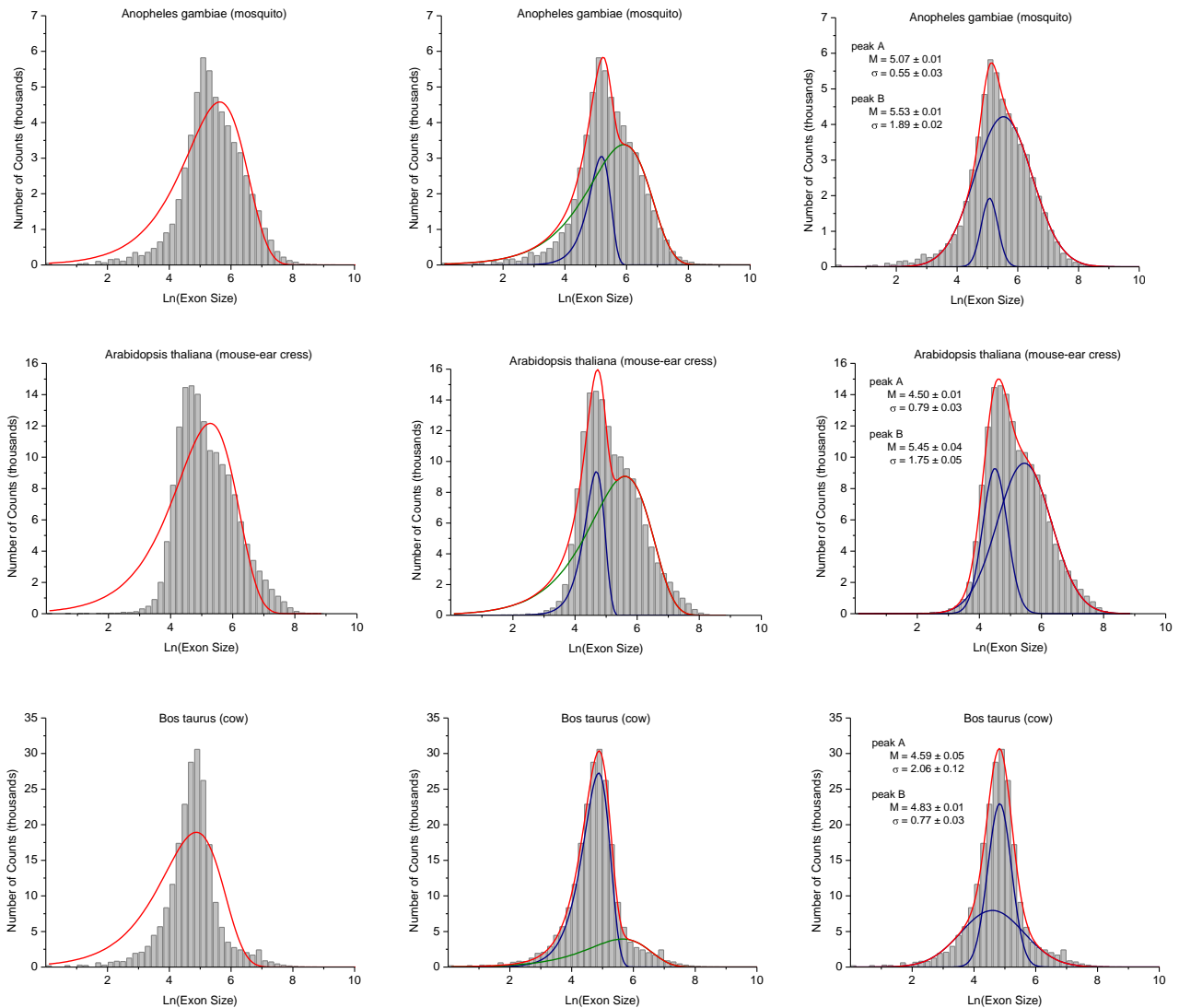
# Supplementary data

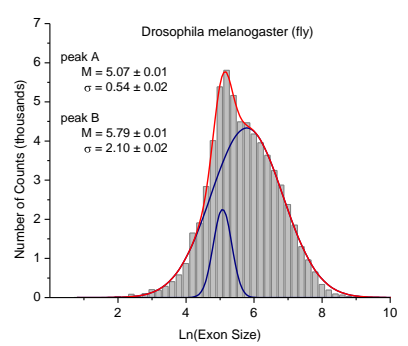
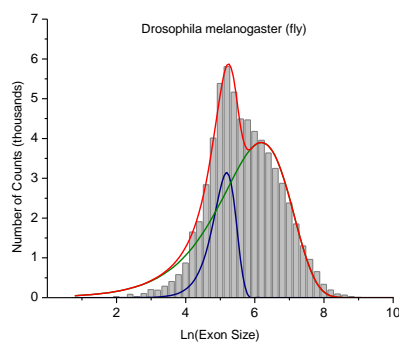
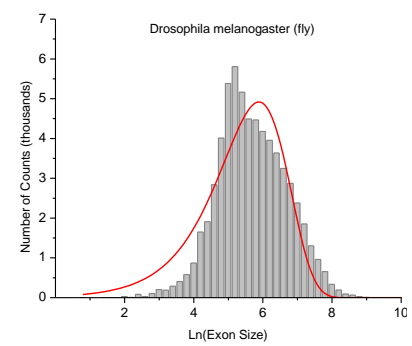
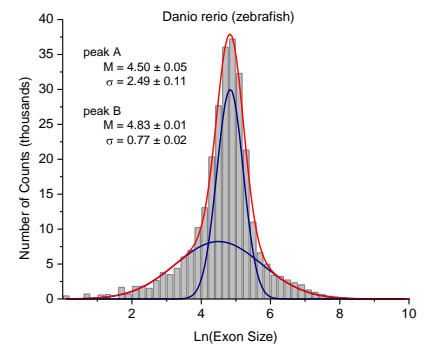
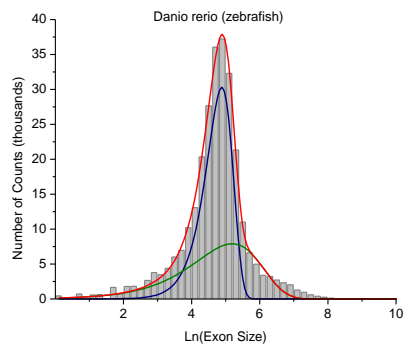
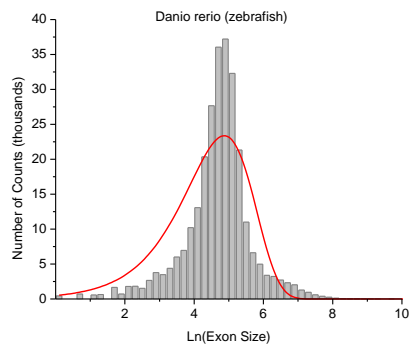
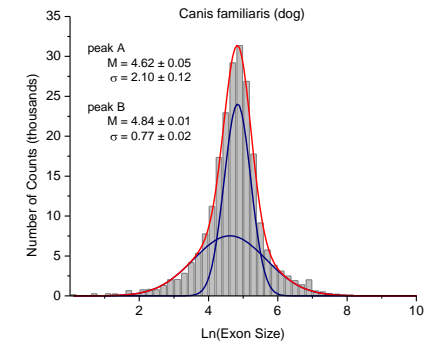
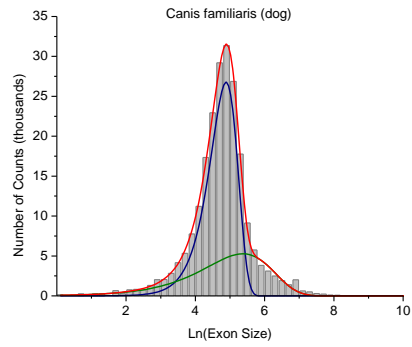
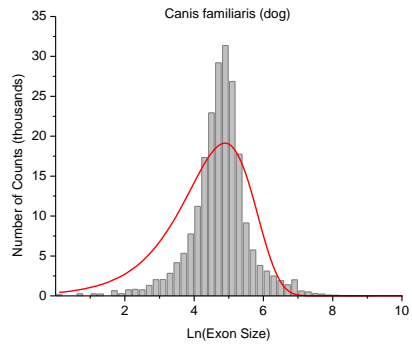
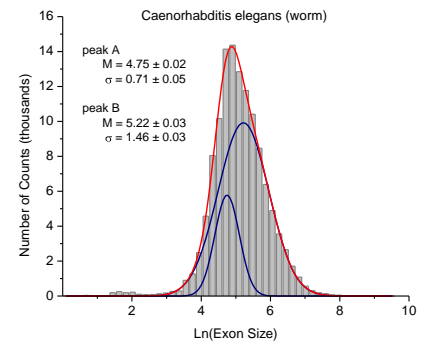
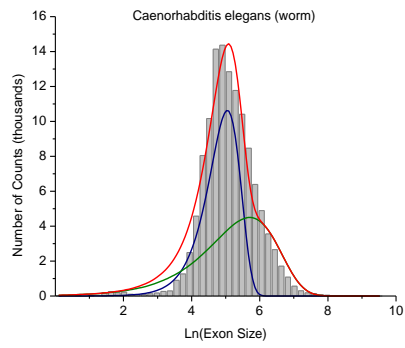
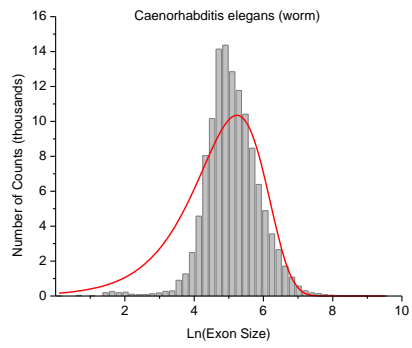
*for the paper*

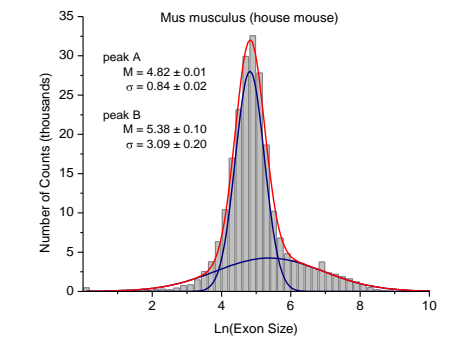
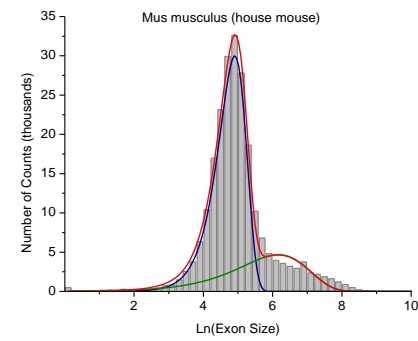
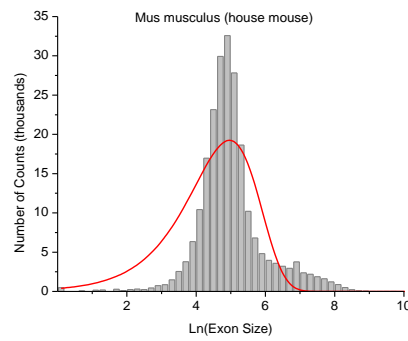
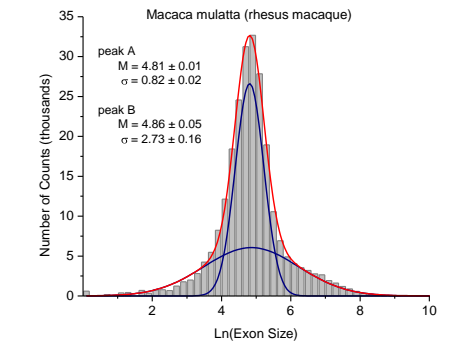
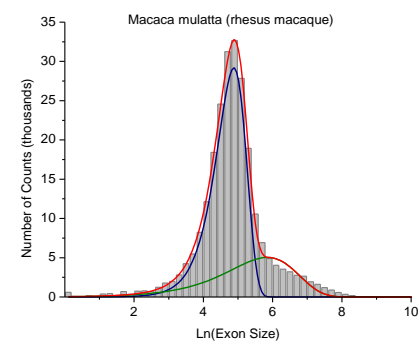
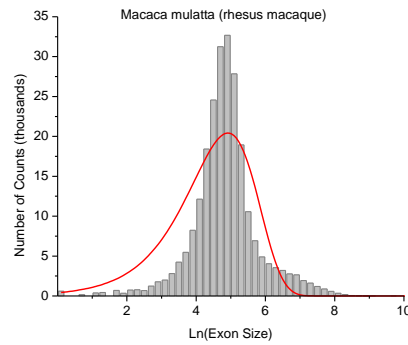
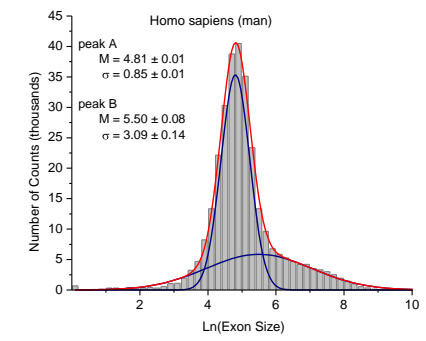
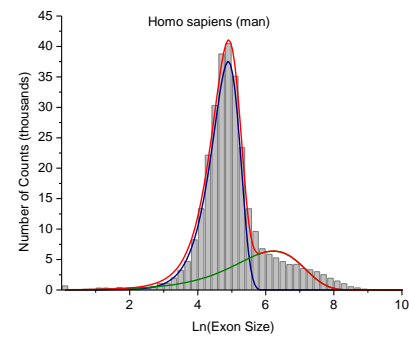
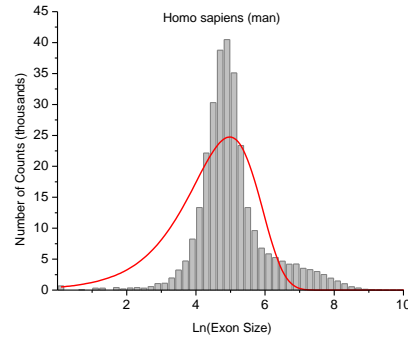
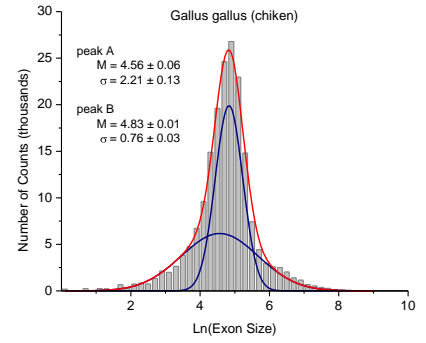
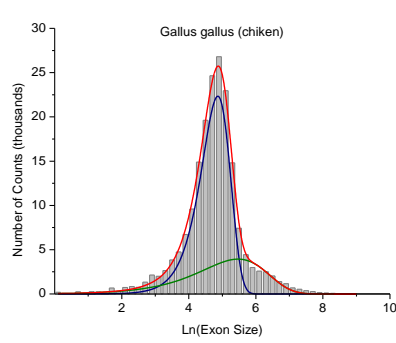
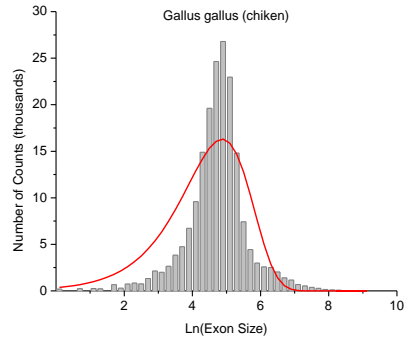
## Spontaneous Symmetry Breaking in Genome Evolution

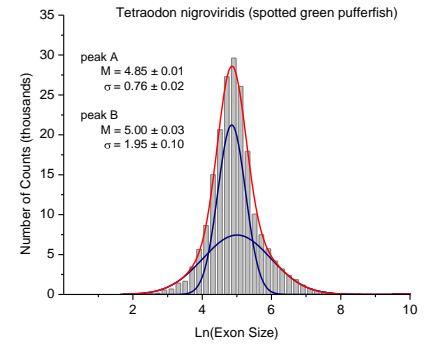
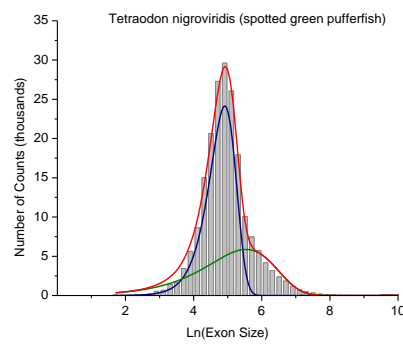
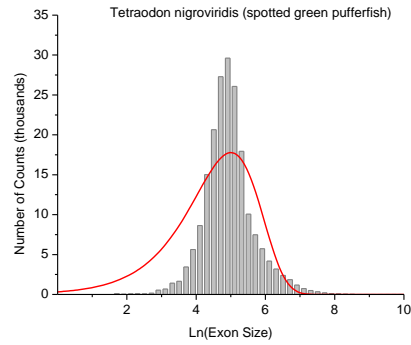
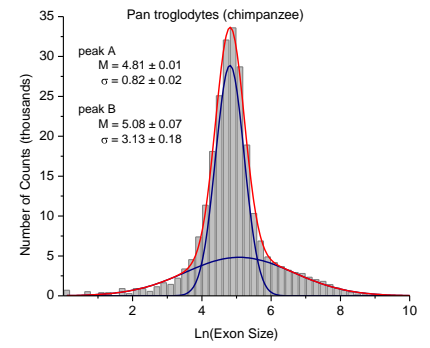
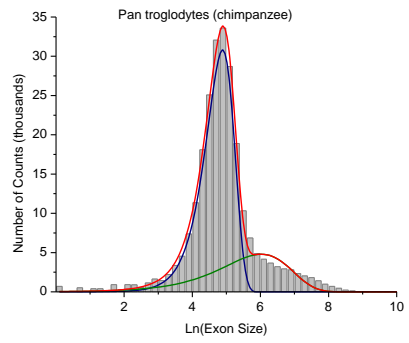
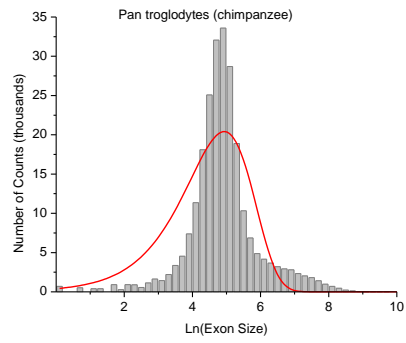
*by Yaroslav Ryabov and Michael Gribskov*

Distributions of exon sizes for genomes used in this work were fitted by exponential distribution (left panels); the combination of Weibull (blue line) distribution and exponential (olive line) distribution (middle panels); and the combination of two lognormal peaks (right panels).











## Part II. alternatively spliced exons.

Species names	<i>Mus musculus</i>	<i>Homo sapiens</i>
Exponential model vs. Lognormal model		
$\chi_1^2/\chi_{II}^2$	44.66	55.66
$F_{0.05}$	1.95	1.80
$\sigma_{II} < \sigma_I$	A	A
Weibull model vs. Lognormal model		
$\chi_1^2/\chi_{II}^2$	1.38	2.30
$F_{0.05}$	1.96	1.79
$\sigma_{II} < \sigma_I$	D	A
Exponential model vs. Weibull model		
$\chi_1^2/\chi_{II}^2$	32.34	24.22
$F_{0.05}$	1.95	1.80
$\sigma_{II} < \sigma_I$	A	A

Auxiliary figure capturing the main idea of the paper.

## Evolutionary Ladder

