

Additional file 1. Features of the unique RefSeq genes used for analysis.

Species	Chromosomes (Mb)	Genes ¹ (Mb)	Gene Density ²	CDSs ¹ (Mb)	Introns (Mb)	Intron per Gene (%)	UTRs ¹ (Mb)	UTR per Gene (%)
<i>Hs</i>	3950.0	978.6	24.8	840.6	931.1	95.1	138.0	14.1
<i>Mm</i>	3165.0	684.7	21.6	569.0	645.5	94.3	115.7	16.9
<i>Dr</i>	1589.3	131.2	8.3	110.2	120.7	92.0	20.9	15.9
<i>Dm</i>	129.3	66.7	51.6	48.5	40.1	60.1	18.1	27.1
<i>Ce</i>	100.3	48.7	48.6	47.1	25.8	53.0	1.5	3.1

¹The length does not correspond to the length of the corresponding transcript but to the length of the genomic sequence including introns.

²The gene density is calculated as geneLength/chrLength.

Abbreviations: *Hs*, Homo sapiens; *Mm*, Mus musculus; *Dr*, Danio rerio; *Dm*, Drosophila melanogaster; *Ce*, Caenorhabditis elegans.