Ribo-seq enlightens Codon Usage Bias

Supplementary material

A.

	Shrap	This study
C. elegans	178	181
C. albicans	28	113

B.

Organism	Sample	Experiment
M. musculus	SAMN03098049	SRR1605293
H. sapiens	SAMN00990790	SRR493747
D. melanogaster	SAMN02264622	SRR942868
H. capsulatum	SAMN03649616	SRR2015214
P. falciparum	SAMN02850772	SRR1378560
R. norvegicus	SAMN03008628	SRR1557705
C. elegans	SAMN01090422	SRR522871 SRR522872
S. pombe	SAMEA2292866	ERR392085
C. albicans	SAMN02400884	SRR1027795
S. cerevisiae	SAMN00002142	SRR014378

Table 1.

A. Number of genes used in highly expressed genes in Sharp and this study.

B. Species and Ribo-seq samples used in this study.

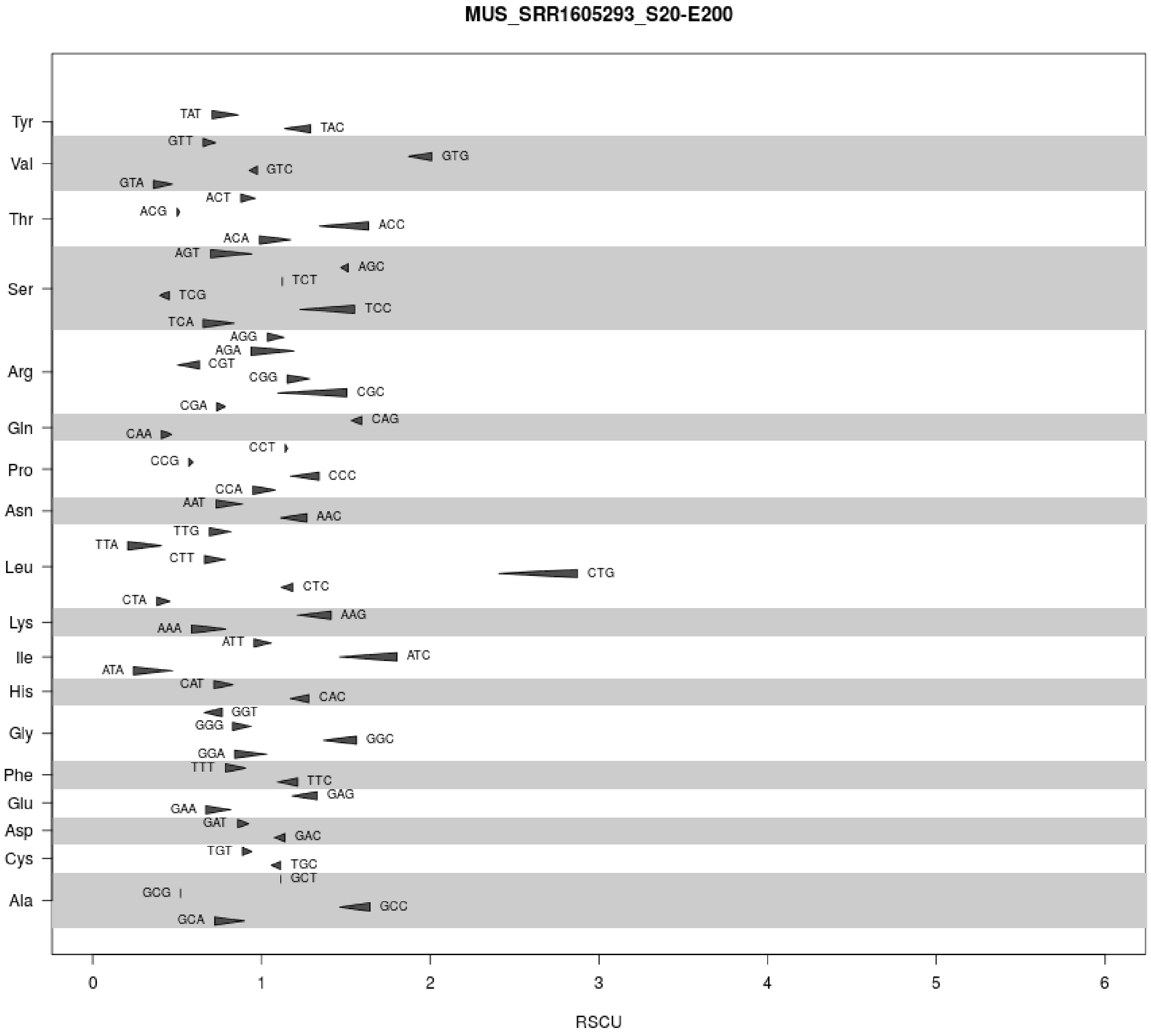

Figure 1. RSCU$_{RS}$ in *M. musculus*. Large borders of triangles represent RSCU$_{RS}$ in highly expressed genes, and peaks represent RSCU$_{RS}$ in lowly expressed genes.

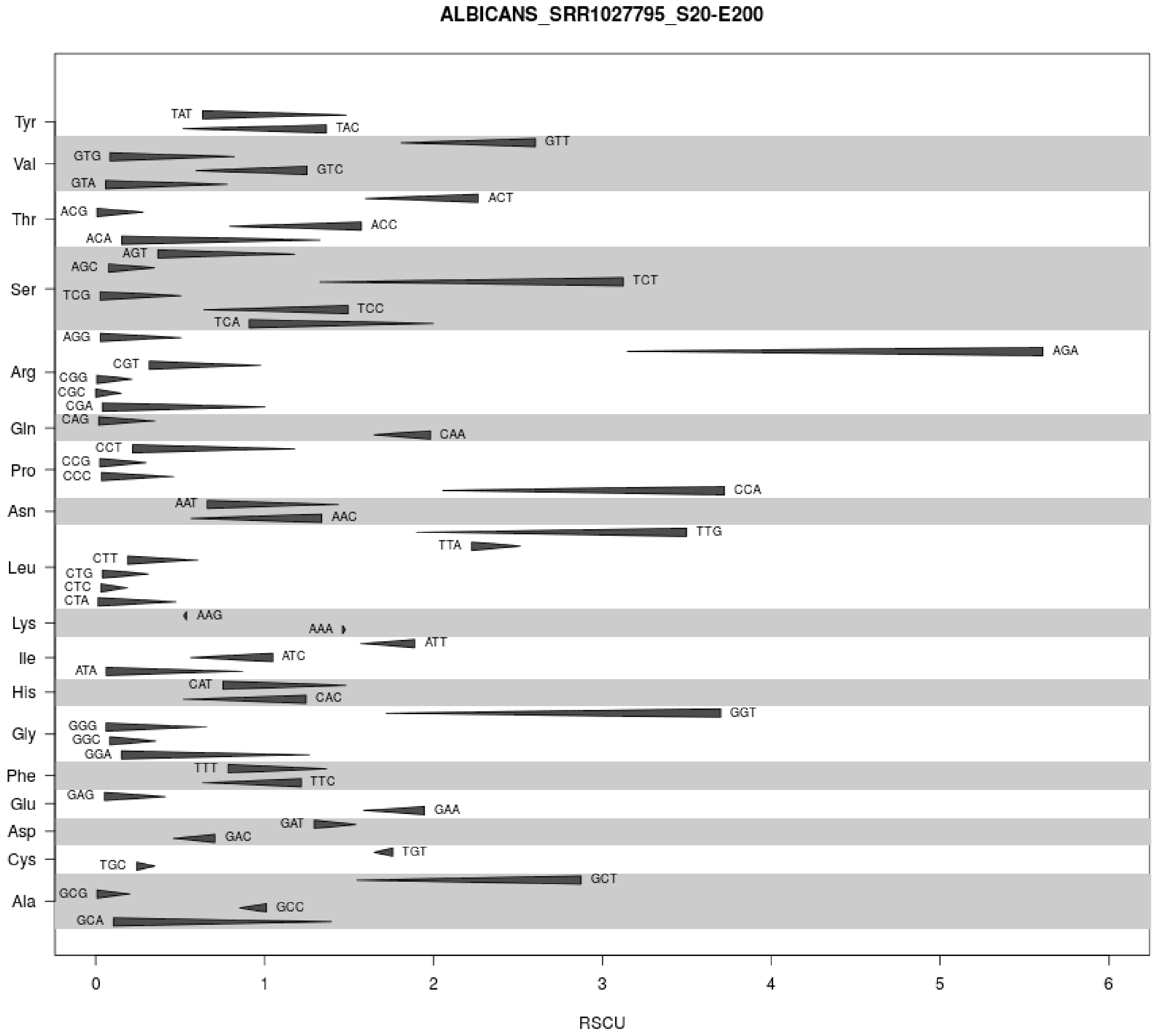

Figure 2. RSCU$_{RS}$ in *C. albicans*. Large borders of triangles represent RSCU$_{RS}$ in highly expressed genes, and peaks represent RSCU$_{RS}$ in lowly expressed genes.

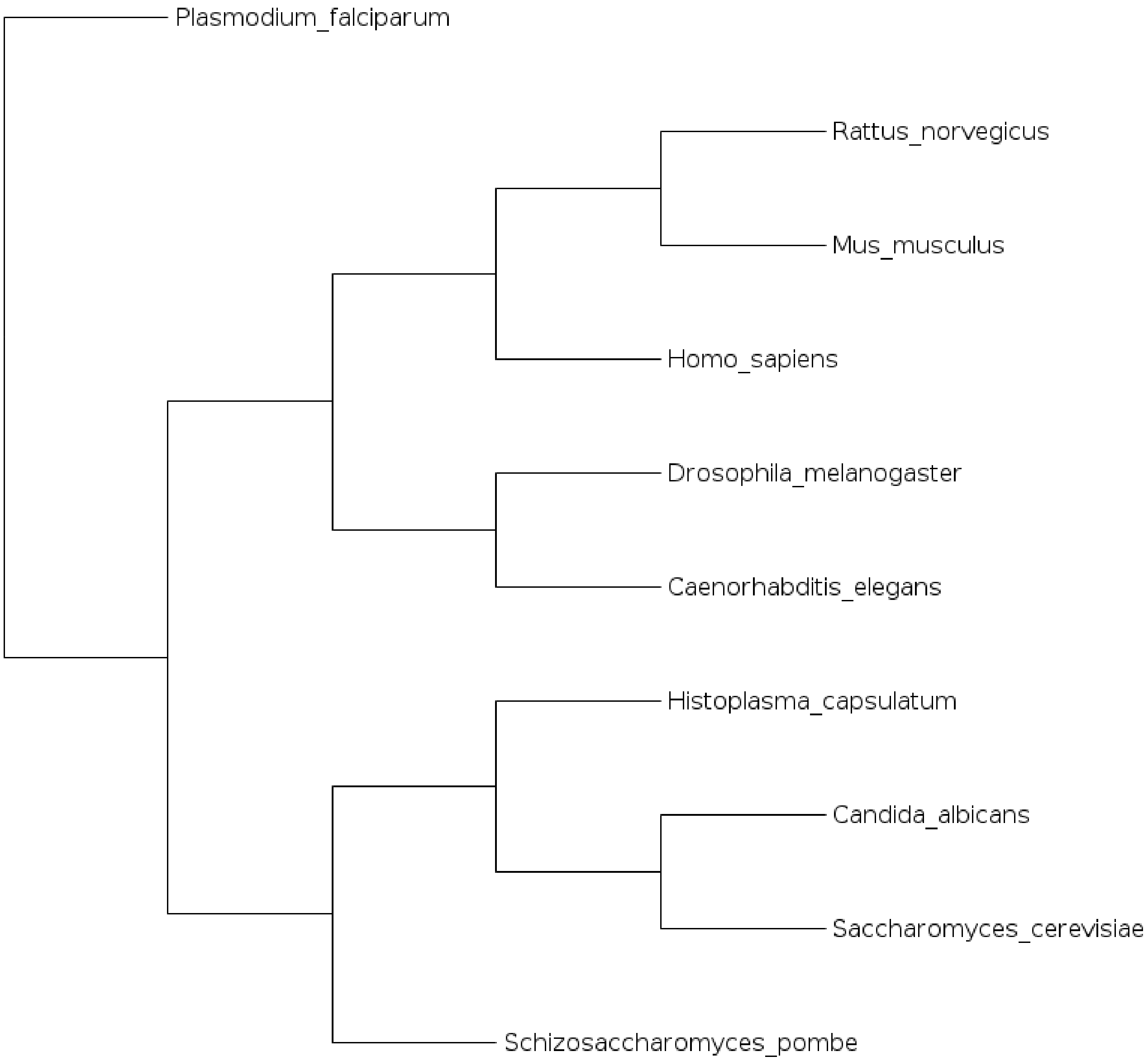

Figure 3. Species tree taken from the NCBI taxonomy.