

Supplementary file from

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Effect of genetic drift on determinants of protein evolution

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Table S1. Ratio of nonsynonymous-to-synonymous diversities and the determinants of protein evolution (using non-overlapping genes)

Determinant	No. of genes	<i>M.m.castaneus</i>		<i>M.m.musculus</i>	
		π_N/π_S	π_N/π	π_N/π_S	π_N/π
<i>Gene expression level</i>					
High (Log mean >6.5)	602	0.083 (0.007)	0.128 (0.010)	0.141 (0.019)	0.207 (0.027)
Low (Log mean <4.1)	683	0.186 (0.010)	0.260 (0.014)	0.219 (0.019)	0.265 (0.022)
<i>Tissue specificity</i>					
Broad ($\tau < 0.11$)	641	104 (0.006)	0.145 (0.008)	0.185 (0.016)	0.221 (0.018)
Narrow ($t > 0.45$)	675	213 (0.012)	0.303 (0.017)	0.242 (0.024)	0.304 (0.029)
<i>Gene Essentiality</i>					
Essential (Lethal)	191	0.094 (0.009)	0.147 (0.014)	0.178 (0.025)	0.220 (0.030)
Non-essential (Viable)	595	0.124 (0.007)	0.179 (0.010)	0.181 (0.014)	0.231 (0.017)
<i>Protein Interactions</i>					
High (>53 interactions)*	505	0.090 (0.006)	0.130 (0.008)	0.166 (0.018)	0.211 (0.021)
Low (<3 interactions)	626	0.130 (0.008)	0.186 (0.011)	0.202 (0.021)	0.259 (0.026)

* - Since the distribution of the number of protein-protein interactions is discrete

the numbers of the genes in tails slightly differ