

Table S8. Rapidly evolving pathways in BSF genome

ID	KEGG pathway	#Genes	H-M ^a	H-D	M-D
ko00190	Oxidative phosphorylation	28	0.027	0.025	0.020
ko00260	Glycine, serine and threonine metabolism	4	0.026	0.026	0.017
ko00310	Lysine degradation	4	0.033	0.022	0.014
ko00340	Histidine metabolism	3	0.045	0.029	0.023
ko00350	Tyrosine metabolism	5	0.024	0.026	0.018
ko00564	Glycerophospholipid metabolism	3	0.042	0.028	0.013
ko00625	Chloroalkane and chloroalkene degradation	3	0.028	0.026	0.018
ko00910	Nitrogen metabolism	5	0.026	0.021	0.010
ko00982	Drug metabolism - cytochrome P450	3	0.028	0.026	0.018
ko04012	ErbB signaling pathway	11	0.029	0.027	0.020
ko04080	Neuroactive ligand-receptor interaction	10	0.039	0.021	0.020
ko04130	SNARE interactions in vesicular transport	5	0.044	0.039	0.019
ko04150	mTOR signaling pathway	7	0.030	0.030	0.018
ko04260	Cardiac muscle contraction	7	0.032	0.034	0.021
ko04612	Antigen processing and presentation	4	0.027	0.022	0.014
ko04621	NOD-like receptor signaling pathway	6	0.035	0.020	0.015

^a Median dN/dS ratio of all mapped genes in the corresponding pathway between: H-M, *H. illucens* and *M. domestica*; H-D, *H. illucens* and *D. melanogaster*; M-D, *M. domestica* and *D. melanogaster*. Pathways in green indicate related to amino acid metabolism and those in red indicate related to immune systems.