

Table S13. Enrichment analysis of highly expressed genes in BSF midgut fed with organic waste

ID	Pathway	#Genes	<i>P</i>	FDR <i>P</i>
ko03010	Ribosome	71	7.18E-77	1.08E-74
ko00190	Oxidative phosphorylation	21	5.18E-10	3.91E-08
ko04972	Pancreatic secretion	26	1.09E-06	4.63E-05
ko05110	Vibrio cholerae infection	12	1.23E-06	4.63E-05
ko04974	Protein digestion and absorption	24	5.46E-06	1.49E-04
ko04966	Collecting duct acid secretion	7	5.90E-06	1.49E-04
ko05012	Parkinson's disease	15	1.41E-05	3.04E-04
ko05120	Epithelial cell signaling in Helicobacter pylori infection	10	1.68E-05	3.17E-04
ko04721	Synaptic vesicle cycle	9	2.75E-05	4.61E-04
ko05323	Rheumatoid arthritis	10	8.00E-05	0.00012
ko05164	Influenza A	18	0.00071	0.00098
ko04145	Phagosome	17	0.00111	0.01391
ko05152	Tuberculosis	9	0.00422	0.04905
ko00120	Primary bile acid biosynthesis	4	0.00529	0.05705
ko04080	Neuroactive ligand-receptor interaction	16	0.00882	0.08881
ko05016	Huntington's disease	13	0.01733	0.16344
ko05010	Alzheimer's disease	12	0.02114	0.18779
ko04260	Cardiac muscle contraction	4	0.03091	0.25927