

**Table S1.** GO terms (Level 3, *Drosophila melanogaster*) of differentially-expressed genes (<http://genecodis.dacya.ucm.es/analysis/>) associated with *D. melanogaster* orthologs of *Apis mellifera* genes. Only the Level 3 terms with  $P < 0.05$  are shown. Letters in the first column (“cluster”) refer to the Venn diagram sectors in Figure 2. Cluster "c+e+f+g" represents genes that were differentially expressed with bee development (house bees → forager bees); cluster "a+e" represents genes that were differentially expressed in house bees in response to *M. anisopliae* infection but not in forager bees. BP = biological process. MF = molecular function. CC = cellular component.

| cluster   | GO ID (category) | description                                         | p-value  |
|-----------|------------------|-----------------------------------------------------|----------|
| "c+e+f+g" | GO:6091 (BP)     | generation of precursor metabolites and energy      | 3.16E-33 |
| "c+e+f+g" | GO:8151 (BP)     | cellular process                                    | 1.49E-24 |
| "c+e+f+g" | GO:6119 (BP)     | oxidative phosphorylation                           | 1.49E-24 |
| "c+e+f+g" | GO:22900 (BP)    | electron transport chain                            | 1.51E-22 |
| "c+e+f+g" | GO:55114 (BP)    | oxidation reduction                                 | 2.64E-22 |
| "c+e+f+g" | GO:22904 (BP)    | respiratory electron transport chain                | 6.05E-22 |
| "c+e+f+g" | GO:42773 (BP)    | ATP synthesis coupled electron transport            | 5.03E-20 |
| "c+e+f+g" | GO:42775 (BP)    | organelle ATP synthesis coupled electron transport  | 8.48E-18 |
| "c+e+f+g" | GO:44237 (BP)    | cellular metabolic process                          | 2.41E-17 |
| "c+e+f+g" | GO:6333 (BP)     | chromatin assembly or disassembly                   | 4.20E-16 |
| "c+e+f+g" | GO:8152 (BP)     | metabolic process                                   | 6.55E-16 |
| "c+e+f+g" | GO:6325 (BP)     | establishment/maintenance of chromatin architecture | 3.46E-14 |
| "c+e+f+g" | GO:6120 (BP)     | mitochondrial NADH to ubiquinone                    | 4.52E-11 |
| "c+e+f+g" | GO:7001 (BP)     | chromosome organization and biogenesis              | 2.08E-10 |
| "c+e+f+g" | GO:6796 (BP)     | phosphate metabolic process                         | 4.92E-09 |
| "c+e+f+g" | GO:6793 (BP)     | phosphorus metabolic process                        | 4.92E-09 |
| "c+e+f+g" | GO:16310 (BP)    | phosphorylation                                     | 7.79E-09 |
| "c+e+f+g" | GO:6996 (BP)     | organelle organization and biogenesis               | 7.51E-08 |
| "c+e+f+g" | GO:44238 (BP)    | primary metabolic process                           | 2.92E-07 |
| "c+e+f+g" | GO:15980 (BP)    | energy derivation by oxidation of organic compounds | 1.04E-06 |
| "c+e+f+g" | GO:51186 (BP)    | cofactor metabolic process                          | 1.54E-06 |
| "c+e+f+g" | GO:16043 (BP)    | cellular component organization and biogenesis      | 1.64E-06 |
| "c+e+f+g" | GO:16651 (MF)    | oxidoreductase activity, acting on NADH or NADPH    | 3.14E-14 |
| "c+e+f+g" | GO:3954 (MF)     | NADH dehydrogenase activity                         | 3.14E-14 |
| "c+e+f+g" | GO:50136 (MF)    | NADH dehydrogenase (quinone) activity               | 2.24E-11 |
| "c+e+f+g" | GO:8137 (MF)     | NADH dehydrogenase (ubiquinone) activity            | 2.24E-11 |
| "c+e+f+g" | GO:16655 (MF)    | oxidoreductase activity                             | 2.24E-11 |
| "c+e+f+g" | GO:3824 (MF)     | catalytic activity                                  | 3.58E-11 |
| "c+e+f+g" | GO:16491 (MF)    | oxidoreductase activity                             | 1.48E-08 |
| "c+e+f+g" | GO:3740 (MF)     | structural constituent of ribosome                  | 2.77E-08 |
| "c+e+f+g" | GO:15078 (MF)    | hydrogen ion transmembrane transporter activity     | 4.36E-07 |
| "c+e+f+g" | GO:15077 (MF)    | inorganic cation transmembrane transporter          | 6.67E-07 |
| "c+e+f+g" | GO:22890 (MF)    | inorganic cation transmembrane transporter          | 7.57E-06 |
| "c+e+f+g" | GO:32991 (CC)    | macromolecular complex                              | 1.59E-39 |

|           |               |                                                                |          |
|-----------|---------------|----------------------------------------------------------------|----------|
| "c+e+f+g" | GO:786 (CC)   | nucleosome                                                     | 7.28E-39 |
| "c+e+f+g" | GO:44446 (CC) | intracellular organelle part                                   | 6.80E-37 |
| "c+e+f+g" | GO:44422 (CC) | organelle part                                                 | 7.67E-37 |
| "c+e+f+g" | GO:44424 (CC) | intracellular part                                             | 9.09E-35 |
| "c+e+f+g" | GO:32993 (CC) | protein-DNA complex                                            | 1.12E-34 |
| "c+e+f+g" | GO:5622 (CC)  | intracellular                                                  | 8.33E-34 |
| "c+e+f+g" | GO:5623 (CC)  | cell                                                           | 1.68E-32 |
| "c+e+f+g" | GO:44464 (CC) | cell part                                                      | 1.68E-32 |
| "c+e+f+g" | GO:43229 (CC) | intracellular organelle                                        | 1.59E-28 |
| "c+e+f+g" | GO:43226 (CC) | organelle                                                      | 1.74E-28 |
| "c+e+f+g" | GO:5717 (CC)  | chromatin                                                      | 7.67E-28 |
| "c+e+f+g" | GO:44444 (CC) | cytoplasmic part                                               | 1.12E-27 |
| "c+e+f+g" | GO:5737 (CC)  | cytoplasm                                                      | 5.75E-27 |
| "c+e+f+g" | GO:44455 (CC) | mitochondrial membrane part                                    | 5.75E-26 |
| "c+e+f+g" | GO:44429 (CC) | mitochondrial part                                             | 7.17E-25 |
| "c+e+f+g" | GO:5740 (CC)  | mitochondrial envelope                                         | 4.15E-23 |
| "c+e+f+g" | GO:31966 (CC) | mitochondrial membrane                                         | 3.61E-22 |
| "c+e+f+g" | GO:5746 (CC)  | mitochondrial respiratory chain                                | 5.68E-22 |
| "c+e+f+g" | GO:5739 (CC)  | mitochondrion                                                  | 8.28E-22 |
| "c+e+f+g" | GO:5743 (CC)  | mitochondrial inner membrane                                   | 8.30E-22 |
| "c+e+f+g" | GO:31967 (CC) | organelle envelope                                             | 1.59E-21 |
| "c+e+f+g" | GO:31975 (CC) | envelope                                                       | 1.98E-21 |
| "c+e+f+g" | GO:19866 (CC) | organelle inner membrane                                       | 8.70E-21 |
| "c+e+f+g" | GO:31090 (CC) | organelle membrane                                             | 1.31E-19 |
| "c+e+f+g" | GO:44427 (CC) | chromosomal part                                               | 3.25E-19 |
| "c+e+f+g" | GO:5694 (CC)  | chromosome                                                     | 6.01E-19 |
| "c+e+f+g" | GO:5811 (CC)  | lipid particle                                                 | 1.15E-17 |
| "c+e+f+g" | GO:43232 (CC) | intracellular non-membrane-bounded organelle                   | 9.24E-16 |
| "c+e+f+g" | GO:43228 (CC) | non-membrane-bounded organelle                                 | 9.24E-16 |
| "c+e+f+g" | GO:5747 (CC)  | mitochondrial respiratory chain complex I                      | 5.48E-15 |
| "c+e+f+g" | GO:45271 (CC) | respiratory chain complex I                                    | 5.48E-15 |
| "c+e+f+g" | GO:30964 (CC) | NADH dehydrogenase complex                                     | 5.48E-15 |
| "c+e+f+g" | GO:43234 (CC) | protein complex                                                | 1.64E-12 |
| "c+e+f+g" | GO:43231 (CC) | intracellular membrane-bounded organelle                       | 1.93E-09 |
| "c+e+f+g" | GO:43227 (CC) | membrane-bounded organelle                                     | 2.21E-09 |
| "c+e+f+g" | GO:5840 (CC)  | ribosome                                                       | 2.36E-09 |
| "c+e+f+g" | GO:5830 (CC)  | cytosolic ribosome                                             | 1.05E-08 |
| "c+e+f+g" | GO:33279 (CC) | ribosomal subunit                                              | 2.15E-08 |
| "c+e+f+g" | GO:44445 (CC) | cytosolic part                                                 | 3.30E-07 |
| "c+e+f+g" | GO:45259 (CC) | proton-transporting ATP synthase complex                       | 3.25E-06 |
| "c+e+f+g" | GO:5753 (CC)  | mitochondrial H <sup>+</sup> transporting ATP synthase complex | 3.25E-06 |
| "c+e+f+g" | GO:30529 (CC) | ribonucleoprotein complex                                      | 5.10E-06 |
| "a+e"     | GO:16043 (BP) | cellular component organization and biogenesis                 | 6.54E-06 |
| "a+e"     | GO:65007 (BP) | biological regulation                                          | 6.54E-06 |
| "a+e"     | GO:6996 (BP)  | organelle organization and biogenesis                          | 6.54E-06 |
| "a+e"     | GO:50791 (BP) | regulation of biological process                               | 6.54E-06 |
| "a+e"     | GO:5488 (MF)  | binding                                                        | 5.64E-10 |
| "a+e"     | GO:3676 (MF)  | nucleic acid binding                                           | 1.13E-06 |
| "a+e"     | GO:5623 (CC)  | cell                                                           | 3.02E-17 |
| "a+e"     | GO:44464 (CC) | cell part                                                      | 3.02E-17 |
| "a+e"     | GO:5622 (CC)  | intracellular                                                  | 4.90E-15 |
| "a+e"     | GO:44424 (CC) | intracellular part                                             | 2.83E-12 |
| "a+e"     | GO:5830 (CC)  | cytosolic ribosome                                             | 5.99E-12 |

|       |               |                                              |          |
|-------|---------------|----------------------------------------------|----------|
| "a+e" | GO:44445 (CC) | cytosolic part                               | 6.39E-10 |
| "a+e" | GO:43229 (CC) | intracellular organelle                      | 7.08E-10 |
| "a+e" | GO:43226 (CC) | organelle                                    | 7.08E-10 |
| "a+e" | GO:43232 (CC) | intracellular non-membrane-bounded organelle | 9.39E-10 |
| "a+e" | GO:43228 (CC) | non-membrane-bounded organelle               | 9.39E-10 |
| "a+e" | GO:786 (CC)   | nucleosome                                   | 2.68E-08 |
| "a+e" | GO:32993 (CC) | protein-DNA complex                          | 3.79E-08 |
| "a+e" | GO:30873 (CC) | cytosolic small ribosomal subunit            | 1.53E-06 |
| "a+e" | GO:5634 (CC)  | nucleus                                      | 1.53E-06 |
| "a+e" | GO:33279 (CC) | ribosomal subunit                            | 3.11E-06 |
| "a+e" | GO:5717 (CC)  | chromatin                                    | 3.75E-06 |
| "a+e" | GO:30498 (CC) | cytosolic large ribosomal subunit            | 5.47E-06 |
| "a+e" | GO:44446 (CC) | intracellular organelle part                 | 8.78E-06 |
| "a+e" | GO:44422 (CC) | organelle part                               | 9.23E-06 |

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