Late-life fitness gains and reproductive death in *Cardiocondyla obscurior* ants

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Suppementary files 1 A-I

**Supplementary File 1A. Estimates calculated for 10, 20 and 30 workers using a glmmTMB model with Gaussian distribution and ‘setup date’, ‘experimental box’, ‘box’ and ‘nest of origin’ as random factors for (Queen\*c) / [(Queen\*c) + Worker].** The coefficient c as the dry average weight measurements of queen over workers to the power conversion factor of 0.6-1 (see text). All comparisons between 10 and 20 workers treatments are statistically significant (p<0.001), but not between 20 and 30 workers.

|  |  |  |  |
| --- | --- | --- | --- |
| Power conversion | Estimates | | |
|  | 10 workers | 20 workers | 30 workers |
| 0.6 | 0.091 | 0.092 | 0.083 |
| 0.7 | 0.095 | 0.095 | 0.086 |
| 0.8 | 0.099 | 0.098 | 0.088 |
| 0.9 | 0.103 | 0.101 | 0.091 |
| 1 | 0.107 | 0.104 | 0.094 |

**Supplementary File 1B.** **The 15 most significant enriched GO-terms per type in DEGs enriched in middle-aged queens in the head-thorax tissue.** BP = Biological processes, CC = Cellular component, and MF = Molecular functions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Type | GO.ID | Term | Annotated | Significant | Expected | Fisher |
| BF | GO:0006412 | translation | 200 | 78 | 21,65 | < 1e-30 |
| BF | GO:0006099 | tricarboxylic acid cycle | 17 | 6 | 1,84 | 0,0001 |
| BF | GO:0006816 | calcium ion transport | 15 | 7 | 1,62 | 0,00011 |
| BF | GO:0006614 | SRP-dependent cotranslational protein ta... | 8 | 4 | 0,87 | 0,00034 |
| BF | GO:1902600 | proton transmembrane transport | 26 | 12 | 2,81 | 0,00036 |
| BF | GO:0006414 | translational elongation | 14 | 5 | 1,52 | 0,00058 |
| BF | GO:0006357 | regulation of transcription by RNA polym... | 28 | 8 | 3,03 | 0,00065 |
| BF | GO:0030150 | protein import into mitochondrial matrix | 5 | 3 | 0,54 | 0,00108 |
| BF | GO:0006511 | ubiquitin-dependent protein catabolic pr... | 50 | 10 | 5,41 | 0,00113 |
| BF | GO:0007186 | G protein-coupled receptor signaling pat... | 115 | 15 | 12,45 | 0,00128 |
| BF | GO:0006470 | protein dephosphorylation | 35 | 7 | 3,79 | 0,00131 |
| BF | GO:0007154 | cell communication | 396 | 49 | 42,87 | 0,00211 |
| BF | GO:0042773 | ATP synthesis coupled electron transport | 10 | 5 | 1,08 | 0,00236 |
| BF | GO:0031032 | actomyosin structure organization | 2 | 2 | 0,22 | 0,00239 |
| BF | GO:0008615 | pyridoxine biosynthetic process | 2 | 2 | 0,22 | 0,00239 |
| CC | GO:0005840 | ribosome | 126 | 67 | 14,23 | < 1e-30 |
| CC | GO:0019773 | proteasome core complex, alpha-subunit c... | 7 | 4 | 0,79 | 0,00025 |
| CC | GO:0005737 | cytoplasm | 378 | 83 | 42,69 | 0,00025 |
| CC | GO:0015934 | large ribosomal subunit | 13 | 7 | 1,47 | 0,00046 |
| CC | GO:0005874 | microtubule | 9 | 4 | 1,02 | 0,00082 |
| CC | GO:0000276 | mitochondrial proton-transporting ATP sy... | 5 | 3 | 0,56 | 0,00141 |
| CC | GO:0042025 | host cell nucleus | 73 | 11 | 8,24 | 0,00158 |
| CC | GO:0005839 | proteasome core complex | 14 | 8 | 1,58 | 0,00259 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 2 | 2 | 0,23 | 0,00286 |
| CC | GO:0046658 | anchored component of plasma membrane | 2 | 2 | 0,23 | 0,00286 |
| CC | GO:0016593 | Cdc73/Paf1 complex | 2 | 2 | 0,23 | 0,00286 |
| CC | GO:0000814 | ESCRT II complex | 2 | 2 | 0,23 | 0,00286 |
| CC | GO:0016020 | membrane | 1234 | 142 | 139,36 | 0,00414 |
| CC | GO:0005739 | mitochondrion | 87 | 28 | 9,83 | 0,00725 |
| CC | GO:0005787 | signal peptidase complex | 3 | 2 | 0,34 | 0,00828 |
| MF | GO:0003735 | structural constituent of ribosome | 126 | 68 | 14,68 | < 1e-30 |
| MF | GO:0005515 | protein binding | 1576 | 206 | 183,57 | < 1e-30 |
| MF | GO:0005509 | calcium ion binding | 146 | 19 | 17,01 | 0,00012 |
| MF | GO:0004784 | superoxide dismutase activity | 3 | 3 | 0,35 | 0,00012 |
| MF | GO:0005524 | ATP binding | 593 | 50 | 69,07 | 0,00019 |
| MF | GO:0003924 | GTPase activity | 104 | 15 | 12,11 | 0,00019 |
| MF | GO:0003676 | nucleic acid binding | 955 | 129 | 111,23 | 0,00024 |
| MF | GO:0005200 | structural constituent of cytoskeleton | 8 | 4 | 0,93 | 0,00036 |
| MF | GO:0004672 | protein kinase activity | 216 | 21 | 25,16 | 0,00067 |
| MF | GO:0046982 | protein heterodimerization activity | 33 | 7 | 3,84 | 0,00101 |
| MF | GO:0042302 | structural constituent of cuticle | 43 | 8 | 5,01 | 0,00112 |
| MF | GO:0003824 | catalytic activity | 2228 | 279 | 259,51 | 0,00132 |
| MF | GO:0009055 | electron transfer activity | 43 | 18 | 5,01 | 0,00141 |
| MF | GO:0016757 | glycosyltransferase activity | 84 | 15 | 9,78 | 0,00145 |
| MF | GO:0051539 | 4 iron, 4 sulfur cluster binding | 11 | 4 | 1,28 | 0,00152 |

**Supplementary File 1C.** **The 15 most significant enriched GO-terms per type in DEGs enriched in *prope mortem* queens in the head-thorax tissue.** BP = Biological processes, CC = Cellular component., and MF = Molecular functions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Type | GO.ID | Term | Annotated | Significant | Expected | Fisher |
| BF | GO:0003735 | structural constituent of ribosome | 126 | 68 | 14,68 | < 1e-30 |
| BF | GO:0005515 | protein binding | 1576 | 206 | 183,57 | < 1e-30 |
| BF | GO:0005509 | calcium ion binding | 146 | 19 | 17,01 | 0,00012 |
| BF | GO:0004784 | superoxide dismutase activity | 3 | 3 | 0,35 | 0,00012 |
| BF | GO:0005524 | ATP binding | 593 | 50 | 69,07 | 0,00019 |
| BF | GO:0003924 | GTPase activity | 104 | 15 | 12,11 | 0,00019 |
| BF | GO:0003676 | nucleic acid binding | 955 | 129 | 111,23 | 0,00024 |
| BF | GO:0005200 | structural constituent of cytoskeleton | 8 | 4 | 0,93 | 0,00036 |
| BF | GO:0004672 | protein kinase activity | 216 | 21 | 25,16 | 0,00067 |
| BF | GO:0046982 | protein heterodimerization activity | 33 | 7 | 3,84 | 0,00101 |
| BF | GO:0042302 | structural constituent of cuticle | 43 | 8 | 5,01 | 0,00112 |
| BF | GO:0003824 | catalytic activity | 2228 | 279 | 259,51 | 0,00132 |
| BF | GO:0009055 | electron transfer activity | 43 | 18 | 5,01 | 0,00141 |
| BF | GO:0016757 | glycosyltransferase activity | 84 | 15 | 9,78 | 0,00145 |
| BF | GO:0051539 | 4 iron, 4 sulfur cluster binding | 11 | 4 | 1,28 | 0,00152 |
| CC | GO:0030117 | membrane coat | 21 | 5 | 2,69 | 0,00051 |
| CC | GO:0005737 | cytoplasm | 378 | 43 | 48,34 | 0,00057 |
| CC | GO:0005643 | nuclear pore | 6 | 3 | 0,77 | 0,00102 |
| CC | GO:0000124 | SAGA complex | 2 | 2 | 0,26 | 0,00146 |
| CC | GO:0008290 | F-actin capping protein complex | 2 | 2 | 0,26 | 0,00146 |
| CC | GO:0032040 | small-subunit processome | 7 | 3 | 0,9 | 0,00173 |
| CC | GO:0005615 | extracellular space | 9 | 3 | 1,15 | 0,00392 |
| CC | GO:0016459 | myosin complex | 18 | 4 | 2,3 | 0,0042 |
| CC | GO:0005685 | U1 snRNP | 3 | 2 | 0,38 | 0,00427 |
| CC | GO:0000813 | ESCRT I complex | 3 | 2 | 0,38 | 0,00427 |
| CC | GO:0016592 | mediator complex | 21 | 4 | 2,69 | 0,0075 |
| CC | GO:0005885 | Arp2/3 protein complex | 5 | 2 | 0,64 | 0,01352 |
| CC | GO:0005667 | transcription regulator complex | 30 | 7 | 3,84 | 0,01724 |
| CC | GO:0005815 | microtubule organizing center | 6 | 2 | 0,77 | 0,01978 |
| CC | GO:0005680 | anaphase-promoting complex | 7 | 2 | 0,9 | 0,02699 |
| MF | GO:0005515 | protein binding | 1576 | 216 | 195,1 | < 1e-30 |
| MF | GO:0004842 | ubiquitin-protein transferase activity | 38 | 8 | 4,7 | 0,00011 |
| MF | GO:0003682 | chromatin binding | 8 | 4 | 0,99 | 0,00016 |
| MF | GO:0003824 | catalytic activity | 2228 | 222 | 275,81 | 0,00021 |
| MF | GO:0035091 | phosphatidylinositol binding | 27 | 6 | 3,34 | 0,0006 |
| MF | GO:0004675 | transmembrane receptor protein serine/th... | 5 | 3 | 0,62 | 0,00061 |
| MF | GO:0003700 | DNA-binding transcription factor activit... | 119 | 13 | 14,73 | 0,001 |
| MF | GO:0008017 | microtubule binding | 30 | 6 | 3,71 | 0,00108 |
| MF | GO:0051015 | actin filament binding | 13 | 4 | 1,61 | 0,00139 |
| MF | GO:0004715 | non-membrane spanning protein tyrosine k... | 2 | 2 | 0,25 | 0,00162 |
| MF | GO:0004832 | valine-tRNA ligase activity | 2 | 2 | 0,25 | 0,00162 |
| MF | GO:0000049 | tRNA binding | 8 | 3 | 0,99 | 0,00313 |
| MF | GO:0004714 | transmembrane receptor protein tyrosine ... | 9 | 3 | 1,11 | 0,00455 |
| MF | GO:0018024 | histone-lysine N-methyltransferase activ... | 9 | 3 | 1,11 | 0,00455 |
| MF | GO:0004000 | adenosine deaminase activity | 3 | 2 | 0,37 | 0,00473 |

**Supplementary File 1D**. The 15 most significant enriched GO-terms per type in DEGs enriched *in prope mortem* queens in the gaster tissue. BP = Biological processes, CC = Cellular component., and MF = Molecular functions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Type | GO.ID | Term | Annotated | Significant | Expected | Fisher |
| BF | GO:0043248 | proteasome assembly | 6 | 4 | 1,14 | 0,00028 |
| BF | GO:0042147 | retrograde transport, endosome to Golgi | 3 | 3 | 0,57 | 0,00031 |
| BF | GO:0007186 | G protein-coupled receptor signaling pat... | 115 | 19 | 21,86 | 0,00039 |
| BF | GO:0006367 | transcription initiation from RNA polyme... | 12 | 5 | 2,28 | 0,00075 |
| BF | GO:0007264 | small GTPase mediated signal transductio... | 36 | 8 | 6,84 | 0,00086 |
| BF | GO:0007018 | microtubule-based movement | 39 | 9 | 7,41 | 0,00096 |
| BF | GO:0006869 | lipid transport | 37 | 12 | 7,03 | 0,00115 |
| BF | GO:0015914 | phospholipid transport | 10 | 5 | 1,9 | 0,00117 |
| BF | GO:0006904 | vesicle docking involved in exocytosis | 8 | 4 | 1,52 | 0,00117 |
| BF | GO:0000077 | DNA damage checkpoint signaling | 4 | 3 | 0,76 | 0,00118 |
| BF | GO:0000723 | telomere maintenance | 4 | 3 | 0,76 | 0,00118 |
| BF | GO:0009058 | biosynthetic process | 873 | 132 | 165,93 | 0,00244 |
| BF | GO:0006355 | regulation of transcription, DNA-templat... | 297 | 33 | 56,45 | 0,00282 |
| BF | GO:0006364 | rRNA processing | 22 | 9 | 4,18 | 0,0032 |
| BF | GO:0006470 | protein dephosphorylation | 35 | 9 | 6,65 | 0,00323 |
| CC | GO:0008305 | integrin complex | 3 | 3 | 0,6 | 0,0003 |
| CC | GO:0030127 | COPII vesicle coat | 3 | 3 | 0,6 | 0,0003 |
| CC | GO:0005615 | extracellular space | 9 | 4 | 1,81 | 0,002 |
| CC | GO:0005783 | endoplasmic reticulum | 47 | 11 | 9,46 | 0,0022 |
| CC | GO:0030117 | membrane coat | 21 | 9 | 4,23 | 0,0027 |
| CC | GO:0000775 | chromosome, centromeric region | 7 | 3 | 1,41 | 0,0045 |
| CC | GO:0005672 | transcription factor TFIIA complex | 2 | 2 | 0,4 | 0,0045 |
| CC | GO:0072669 | tRNA-splicing ligase complex | 2 | 2 | 0,4 | 0,0045 |
| CC | GO:0005694 | chromosome | 54 | 15 | 10,87 | 0,0051 |
| CC | GO:0042025 | host cell nucleus | 73 | 10 | 14,69 | 0,0236 |
| CC | GO:0000808 | origin recognition complex | 4 | 2 | 0,81 | 0,0248 |
| CC | GO:0030286 | dynein complex | 18 | 4 | 3,62 | 0,0292 |
| CC | GO:0005840 | ribosome | 126 | 15 | 25,36 | 0,0305 |
| MF | GO:0005515 | protein binding | 1576 | 283 | 289,43 | < 1e-30 |
| MF | GO:0005524 | ATP binding | 593 | 127 | 108,91 | < 1e-30 |
| MF | GO:0003723 | RNA binding | 202 | 33 | 37,1 | 0,00012 |
| MF | GO:0035091 | phosphatidylinositol binding | 27 | 8 | 4,96 | 0,0002 |
| MF | GO:0003777 | microtubule motor activity | 35 | 9 | 6,43 | 0,00027 |
| MF | GO:0008289 | lipid binding | 56 | 17 | 10,28 | 0,00084 |
| MF | GO:0051015 | actin filament binding | 13 | 5 | 2,39 | 0,00088 |
| MF | GO:0004252 | serine-type endopeptidase activity | 95 | 15 | 17,45 | 0,00097 |
| MF | GO:0019901 | protein kinase binding | 4 | 3 | 0,73 | 0,00099 |
| MF | GO:0042626 | ATPase-coupled transmembrane transporter... | 31 | 8 | 5,69 | 0,00157 |
| MF | GO:0004721 | phosphoprotein phosphatase activity | 42 | 11 | 7,71 | 0,00232 |
| MF | GO:0004435 | phosphatidylinositol phospholipase C act... | 5 | 3 | 0,92 | 0,00236 |
| MF | GO:0004930 | G protein-coupled receptor activity | 96 | 15 | 17,63 | 0,00332 |
| MF | GO:0004386 | helicase activity | 34 | 10 | 6,24 | 0,00335 |
| MF | GO:0032217 | riboflavin transmembrane transporter act... | 2 | 2 | 0,37 | 0,00408 |

**Supplementary File 1E.** The 15 most significant enriched GO-terms per type in DEGs enriched in middle-aged queens in the gaster tissue. BP = Biological processes, CC = Cellular component, and MF = Molecular functions.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Type | GO.ID | Term | Annotated | Significant | Expected | Fisher |
| BF | GO:0006886 | intracellular protein transport | 86 | 23 | 19,64 | 0,00023 |
| BF | GO:0015986 | ATP synthesis coupled proton transport | 12 | 6 | 2,74 | 0,00025 |
| BF | GO:0016192 | vesicle-mediated transport | 91 | 22 | 20,78 | 0,00036 |
| BF | GO:0009166 | nucleotide catabolic process | 5 | 4 | 1,14 | 0,00065 |
| BF | GO:0007166 | cell surface receptor signaling pathway | 57 | 23 | 13,01 | 0,00082 |
| BF | GO:0006270 | DNA replication initiation | 10 | 5 | 2,28 | 0,00086 |
| BF | GO:0045454 | cell redox homeostasis | 15 | 6 | 3,42 | 0,00107 |
| BF | GO:0006096 | glycolytic process | 11 | 5 | 2,51 | 0,00146 |
| BF | GO:0005975 | carbohydrate metabolic process | 127 | 36 | 29 | 0,00189 |
| BF | GO:0006486 | protein glycosylation | 26 | 8 | 5,94 | 0,00226 |
| BF | GO:0009116 | nucleoside metabolic process | 16 | 8 | 3,65 | 0,00229 |
| BF | GO:0006470 | protein dephosphorylation | 35 | 9 | 7,99 | 0,00243 |
| BF | GO:0005978 | glycogen biosynthetic process | 4 | 3 | 0,91 | 0,00245 |
| BF | GO:0007219 | Notch signaling pathway | 4 | 3 | 0,91 | 0,00245 |
| BF | GO:0042176 | regulation of protein catabolic process | 4 | 3 | 0,91 | 0,00245 |
| CC | GO:0005886 | plasma membrane | 53 | 14 | 10,39 | 0,00012 |
| CC | GO:0016592 | mediator complex | 21 | 8 | 4,11 | 0,00014 |
| CC | GO:0005667 | transcription regulator complex | 30 | 13 | 5,88 | 0,00027 |
| CC | GO:0015935 | small ribosomal subunit | 13 | 6 | 2,55 | 0,00028 |
| CC | GO:0000502 | proteasome complex | 21 | 15 | 4,11 | 0,00185 |
| CC | GO:0000439 | transcription factor TFIIH core complex | 4 | 3 | 0,78 | 0,00197 |
| CC | GO:0015934 | large ribosomal subunit | 13 | 7 | 2,55 | 0,00222 |
| CC | GO:0045261 | proton-transporting ATP synthase complex... | 5 | 3 | 0,98 | 0,00463 |
| CC | GO:0031982 | vesicle | 25 | 10 | 4,9 | 0,00635 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 2 | 2 | 0,39 | 0,00651 |
| CC | GO:0046658 | anchored component of plasma membrane | 2 | 2 | 0,39 | 0,00651 |
| CC | GO:0005853 | eukaryotic translation elongation factor... | 2 | 2 | 0,39 | 0,00651 |
| CC | GO:0032039 | integrator complex | 2 | 2 | 0,39 | 0,00651 |
| CC | GO:0005581 | collagen trimer | 2 | 2 | 0,39 | 0,00651 |
| CC | GO:0016593 | Cdc73/Paf1 complex | 2 | 2 | 0,39 | 0,00651 |
| MF | GO:0005515 | protein binding | 1576 | 475 | 375,85 | < 1e-30 |
| MF | GO:0005524 | ATP binding | 593 | 158 | 141,42 | < 1e-30 |
| MF | GO:0005096 | GTPase activator activity | 53 | 17 | 12,64 | 0,0002 |
| MF | GO:0003924 | GTPase activity | 104 | 21 | 24,8 | 0,00035 |
| MF | GO:0016757 | glycosyltransferase activity | 84 | 24 | 20,03 | 0,0006 |
| MF | GO:0004713 | protein tyrosine kinase activity | 32 | 13 | 7,63 | 0,00061 |
| MF | GO:0050660 | flavin adenine dinucleotide binding | 51 | 14 | 12,16 | 0,00061 |
| MF | GO:0009055 | electron transfer activity | 43 | 15 | 10,25 | 0,00061 |
| MF | GO:0004784 | superoxide dismutase activity | 3 | 3 | 0,72 | 0,00074 |
| MF | GO:0004017 | adenylate kinase activity | 3 | 3 | 0,72 | 0,00074 |
| MF | GO:0004449 | isocitrate dehydrogenase (NAD+) activity | 3 | 3 | 0,72 | 0,00074 |
| MF | GO:0004674 | protein serine/threonine kinase activity | 55 | 18 | 13,12 | 0,00075 |
| MF | GO:0004177 | aminopeptidase activity | 9 | 6 | 2,15 | 0,00185 |
| MF | GO:0005085 | guanyl-nucleotide exchange factor activi... | 33 | 9 | 7,87 | 0,00204 |
| MF | GO:0016491 | oxidoreductase activity | 377 | 88 | 89,91 | 0,00209 |

**Supplementary File 1F. Shared enriched GO-terms for both tissues (head-thorax and gaster) enriched in *prope mortem* queens.**

|  |  |  |
| --- | --- | --- |
| Type | GO.ID | Term |
| BF | GO:0007186 | G protein-coupled receptor signaling pat... |
| BF | GO:0007264 | small GTPase mediated signal transductio... |
| BF | GO:0007018 | microtubule-based movement |
| BF | GO:0006364 | rRNA processing |
| BF | GO:0016579 | protein deubiquitination |
| BF | GO:0006506 | GPI anchor biosynthetic process |
| BF | GO:0042157 | lipoprotein metabolic process |
| BF | GO:0007178 | transmembrane receptor protein serine/th... |
| BF | GO:0006438 | valyl-tRNA aminoacylation |
| BF | GO:0001522 | pseudouridine synthesis |
| BF | GO:0006303 | double-strand break repair via nonhomolo... |
| BF | GO:0006432 | phenylalanyl-tRNA aminoacylation |
| BF | GO:0006511 | ubiquitin-dependent protein catabolic pr... |
| BF | GO:1901642 | nucleoside transmembrane transport |
| BF | GO:0006265 | DNA topological change |
| BF | GO:0034968 | histone lysine methylation |
| BF | GO:0006406 | mRNA export from nucleus |
| BF | GO:0006397 | mRNA processing |
| CC | GO:0005615 | extracellular space |
| CC | GO:0030117 | membrane coat |
| CC | GO:0030286 | dynein complex |
| MF | GO:0005515 | protein binding |
| MF | GO:0035091 | phosphatidylinositol binding |
| MF | GO:0008289 | lipid binding |
| MF | GO:0051015 | actin filament binding |
| MF | GO:0019901 | protein kinase binding |
| MF | GO:0042626 | ATPase-coupled transmembrane transporter... |
| MF | GO:0004435 | phosphatidylinositol phospholipase C act... |
| MF | GO:0004930 | G protein-coupled receptor activity |
| MF | GO:0004832 | valine-tRNA ligase activity |
| MF | GO:0008017 | microtubule binding |
| MF | GO:0003682 | chromatin binding |
| MF | GO:0004402 | histone acetyltransferase activity |
| MF | GO:0004725 | protein tyrosine phosphatase activity |
| MF | GO:0003755 | peptidyl-prolyl cis-trans isomerase acti... |
| MF | GO:0003700 | DNA-binding transcription factor activit... |
| MF | GO:0016817 | hydrolase activity, acting on acid anhyd... |
| MF | GO:0005337 | nucleoside transmembrane transporter act... |
| MF | GO:0004826 | phenylalanine-tRNA ligase activity |
| MF | GO:0009982 | pseudouridine synthase activity |
| MF | GO:0004970 | ionotropic glutamate receptor activity |
| MF | GO:0002161 | aminoacyl-tRNA editing activity |
| MF | GO:0004675 | transmembrane receptor protein serine/th... |
| MF | GO:0003950 | NAD+ ADP-ribosyltransferase activity |

**Supplementary File 1G. Shared enriched GO-terms for both tissues (head-thorax and gaster) enriched in middle-aged queens.**

|  |  |  |
| --- | --- | --- |
| Type | GO.ID | Term |
| BF | GO:0045454 | cell redox homeostasis |
| BF | GO:0006096 | glycolytic process |
| BF | GO:0005975 | carbohydrate metabolic process |
| BF | GO:0006470 | protein dephosphorylation |
| BF | GO:0009966 | regulation of signal transduction |
| BF | GO:0006614 | SRP-dependent cotranslational protein ta... |
| BF | GO:0045944 | positive regulation of transcription by ... |
| BF | GO:0016570 | histone modification |
| BF | GO:0071985 | multivesicular body sorting pathway |
| BF | GO:0120009 | intermembrane lipid transfer |
| BF | GO:0042256 | mature ribosome assembly |
| BF | GO:0006368 | transcription elongation from RNA polyme... |
| BF | GO:0043161 | proteasome-mediated ubiquitin-dependent ... |
| BF | GO:0006415 | translational termination |
| BF | GO:0007186 | G protein-coupled receptor signaling pat... |
| BF | GO:0051603 | proteolysis involved in cellular protein... |
| BF | GO:0009435 | NAD biosynthetic process |
| BF | GO:0006879 | cellular iron ion homeostasis |
| BF | GO:0007179 | transforming growth factor beta receptor... |
| BF | GO:0006633 | fatty acid biosynthetic process |
| BF | GO:0006413 | translational initiation |
| BF | GO:0008299 | isoprenoid biosynthetic process |
| CC | GO:0016592 | mediator complex |
| CC | GO:0015934 | large ribosomal subunit |
| CC | GO:0045261 | proton-transporting ATP synthase complex... |
| CC | GO:0062023 | collagen-containing extracellular matrix |
| CC | GO:0046658 | anchored component of plasma membrane |
| CC | GO:0016593 | Cdc73/Paf1 complex |
| CC | GO:0000814 | ESCRT II complex |
| CC | GO:0005839 | proteasome core complex |
| CC | GO:0022625 | cytosolic large ribosomal subunit |
| CC | GO:0048500 | signal recognition particle |
| CC | GO:0005779 | integral component of peroxisomal membra... |
| CC | GO:0005739 | mitochondrion |
| MF | GO:0005515 | protein binding |
| MF | GO:0005524 | ATP binding |
| MF | GO:0003924 | GTPase activity |
| MF | GO:0016757 | glycosyltransferase activity |
| MF | GO:0009055 | electron transfer activity |
| MF | GO:0004784 | superoxide dismutase activity |
| MF | GO:0004017 | adenylate kinase activity |
| MF | GO:0004449 | isocitrate dehydrogenase (NAD+) activity |
| MF | GO:0004177 | aminopeptidase activity |
| MF | GO:0003714 | transcription corepressor activity |
| MF | GO:0003747 | translation release factor activity |
| MF | GO:0004089 | carbonate dehydratase activity |
| MF | GO:0048038 | quinone binding |
| MF | GO:0004719 | protein-L-isoaspartate (D-aspartate) O-m... |
| MF | GO:0120013 | lipid transfer activity |
| MF | GO:0004421 | hydroxymethylglutaryl-CoA synthase activ... |
| MF | GO:0008312 | 7S RNA binding |
| MF | GO:0046933 | proton-transporting ATP synthase activit... |
| MF | GO:0051539 | 4 iron, 4 sulfur cluster binding |
| MF | GO:0030246 | carbohydrate binding |
| MF | GO:0008235 | metalloexopeptidase activity |
| MF | GO:0004930 | G protein-coupled receptor activity |
| MF | GO:0008138 | protein tyrosine/serine/threonine phosph... |
| MF | GO:0016409 | palmitoyltransferase activity |
| MF | GO:0004114 | 3',5'-cyclic-nucleotide phosphodiesteras... |
| MF | GO:0008199 | ferric iron binding |

**Supplementary File 1H. Deviance Information Criterion of three tested models (logistic, Gompertz and Weibull) for the age-specific mortality of ant queens.** Using the function multibasta of the R package BaSTA (Survival Bayesian Trajectory Analysis, v. 1.9.5). The model with the lowest DIC value is assumed to provide the best fit.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Model | Shape | DIC average | DIC mode | pD | k | DIC | Difference in DIC | Rank |
| Gompertz | simple | 1596 | 1454 | 71.0 | 3 | 1667 | 0 | 1 |
| Logistic | simple | 1592 | 1438 | 77.1 | 4 | 1669 | 2.26 | 2 |
| Weibull | simple | 1616 | -20798 | 11207.1 | 3 | 12823 | 11156.68 | 3 |

**Supplementary File 1I. Estimated coefficients of age-specific mortality of ant queens.** Using a logistic model and the R package BaSTA (Survival Bayesian Trajectory Analysis, v. 1.9.5).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Parameter | Estimate | Standard Error | Lower 95% confidence interval | Upper 95% confidence interval | Se Auto cor | Update Rate | Pot Scale Reduc |
| b0 | -7.37 | 0.23 | -7.85 | -6.96 | 0.61 | 0.25 | 1 |
| b1 | 0.02 | 1.1\*10-3 | 0.01 | 0.02 | 0.60 | 0.25 | 1 |
| pi.1 | 0.15 | 2.2\*10-3 | 0.14 | 0.15 | 0.01 | 1 | 1 |