

Population- and sex-biased gene expression in the excretion organs of *Drosophila*

melanogaster

Ann Kathrin Huylmans and John Parsch*

Department of Biology II, University of Munich (LMU), 82152 Planegg, Germany

*Corresponding author: LMU Biocenter, Grosshaderner Str. 2, 82152 Planegg, Germany, E-mail: parsch@bio.lmu.de

DOI: 10.1534/g3.114.013417

File S1

Tab-delimited text file containing gene ID, mapped read count, RPKM, *P*-value, and FDR for each gene compared between sexes and populations. Populations are abbreviated as "A" (Africa) or "E" (Europe). Sexes are abbreviated as "F" (female) or "M" (male).

Available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013417/-/DC1>

File S2

Excel spreadsheet containing transcript ID, gene ID, mapped read count, RPKM, *P*-value, and FDR for transcript isoforms showing a significant expression difference between sexes (worksheet 1) or populations (worksheet 2). Populations are abbreviated as "A" (Africa) or "E" (Europe). Sexes are abbreviated as "F" (female) or "M" (male).

Available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013417/-/DC1>

Table S1 Number of genes meeting various read-count thresholds

| Reads | Genes | Sex-biased (female, male) | Population-biased (Africa, Europe) |
|-------|--------|---------------------------|------------------------------------|
| 12 | 12,547 | 2,308 (905, 1,403) | 2,474 (1,230, 1,244) |
| 20 | 12,001 | 2,272 (898, 1,374) | 2,459 (1,222, 1,237) |
| 50 | 10,793 | 2,098 (858, 1,240) | 2,436 (1,206, 1,230) |
| 100 | 9,785 | 1,871 (798, 1,073) | 2,382 (1,182, 1,200) |
| 150 | 9,272 | 1,785 (772, 1,013) | 2,340 (1,164, 1,176) |

Shown is the total number of genes meeting each read-count threshold, as well as the number of significant sex- and population-biased genes at a FDR of 5%.

Table S2 Number of significant genes detected by different methods

| Bias | DESeq2 | edgeR (overlap ^a) | baySeq (overlap ^a) |
|------------|--------|-------------------------------|--------------------------------|
| Sex | 2,308 | 1,249 (85.6%) | 557 (98.4%) |
| Female | 905 | 251 (91.2%) | 88 (98.9%) |
| Male | 1,403 | 998 (84.2%) | 469 (98.3%) |
| Population | 2,474 | 1,015 (87.9%) | 496 (97.2%) |
| Africa | 1,230 | 465 (88.2%) | 200 (95.5%) |
| Europe | 1,244 | 550 (87.6%) | 296 (98.3%) |

^a Percent overlap with the significant genes detected by DESeq2.

Table S3 Over-represented GO terms among female-biased genes.

| Ontology | GO Term | Genes | Adj. <i>P</i> |
|--------------------|---|-------|---------------|
| Molecular function | structural constituent of ribosome | 54 | 1.8e-12 |
| Molecular function | proton-transporting ATPase activity, rotational mechanism | 15 | 1.1e-08 |
| Molecular function | ATP binding | 70 | 9.6e-05 |
| Molecular function | mRNA binding | 29 | 0.001 |
| Molecular function | proton-transporting ATP synthase activity, rotational mechanism | 7 | 0.001 |
| Molecular function | structural constituent of chorion | 6 | 0.001 |
| Molecular function | ATP-dependent RNA helicase activity | 11 | 0.003 |
| Molecular function | hydrogen-exporting ATPase activity, phosphorylative mechanism | 8 | 0.005 |
| Molecular function | actin binding | 19 | 0.01 |
| Molecular function | microtubule binding | 14 | 0.02 |
| Molecular function | aminoacyl-tRNA editing activity | 4 | 0.02 |
| Molecular function | L-amino acid transmembrane transporter activity | 5 | 0.03 |
| Molecular function | symporter activity | 14 | 0.03 |
| Molecular function | protein serine/threonine kinase activity | 25 | 0.03 |
| Molecular function | inorganic anion transmembrane transporter activity | 11 | 0.04 |
| Molecular function | acid phosphatase activity | 5 | 0.04 |
| Cellular component | cytosolic large ribosomal subunit | 22 | 6.0e-10 |
| Cellular component | cytosolic small ribosomal subunit | 19 | 6.0e-10 |
| Cellular component | plasma membrane proton-transporting V-type ATPase complex | 10 | 1.6e-07 |
| Cellular component | microtubule associated complex | 50 | 6.8e-06 |
| Cellular component | lipid particle | 34 | 1.8e-05 |
| Cellular component | vacuolar proton-transporting V-type ATPase, V1 domain | 7 | 0.001 |
| Cellular component | chorion | 11 | 0.001 |
| Cellular component | spindle midzone | 6 | 0.002 |
| Cellular component | nucleolus | 21 | 0.003 |
| Cellular component | mitochondrial matrix | 23 | 0.006 |
| Cellular component | mitochondrial proton-transporting ATP synthase complex, catalytic core F(1) | 5 | 0.01 |
| Cellular component | small-subunit processome | 4 | 0.02 |
| Cellular component | euchromatin | 6 | 0.03 |
| Cellular component | centrosome | 14 | 0.03 |
| Biological process | mitotic spindle elongation | 24 | 5.8e-09 |
| Biological process | ATP hydrolysis coupled proton transport | 15 | 4.7e-07 |
| Biological process | rRNA processing | 14 | 1.3e-05 |
| Biological process | centrosome duplication | 20 | 1.3e-05 |
| Biological process | germ cell development | 44 | 0.0002 |
| Biological process | protein localization | 49 | 0.002 |
| Biological process | asymmetric neuroblast division | 11 | 0.002 |
| Biological process | regulation of cell shape | 19 | 0.004 |

| | | | |
|--------------------|--|----|-------|
| Biological process | regulation of growth | 28 | 0.005 |
| Biological process | ribosomal small subunit biogenesis | 5 | 0.005 |
| Biological process | protein phosphorylation | 33 | 0.006 |
| Biological process | negative regulation of cellular process | 78 | 0.007 |
| Biological process | actin cytoskeleton organization | 27 | 0.007 |
| Biological process | female germ-line sex determination | 4 | 0.008 |
| Biological process | translational elongation | 8 | 0.008 |
| Biological process | regulation of cellular component size | 17 | 0.01 |
| Biological process | chorion-containing eggshell formation | 20 | 0.01 |
| Biological process | cellular macromolecule localization | 39 | 0.01 |
| Biological process | long-term memory | 12 | 0.01 |
| Biological process | ATP synthesis coupled proton transport | 7 | 0.01 |
| Biological process | ommochrome biosynthetic process | 7 | 0.01 |
| Biological process | regulation of cell differentiation | 35 | 0.01 |
| Biological process | regulation of cellular component biogenesis | 22 | 0.02 |
| Biological process | regulation of cytoskeleton organization | 15 | 0.02 |
| Biological process | L-amino acid transport | 4 | 0.02 |
| Biological process | mitotic cell cycle phase transition | 7 | 0.02 |
| Biological process | establishment of localization in cell | 53 | 0.02 |
| Biological process | pupariation | 5 | 0.03 |
| Biological process | regulation of DNA replication | 6 | 0.03 |
| Biological process | cellular component assembly involved in morphogenesis | 23 | 0.03 |
| Biological process | amino acid transmembrane transport | 8 | 0.03 |
| Biological process | positive regulation of cellular component organization | 16 | 0.03 |

Table S4 Over-represented GO terms among male-biased genes.

| Ontology | GO Term | Genes | Adj. <i>P</i> |
|--------------------|---|-------|---------------|
| Molecular function | electron carrier activity | 42 | 5.2e-10 |
| Molecular function | manganese ion binding | 12 | 4.1e-06 |
| Molecular function | iron ion binding | 37 | 5.4e-06 |
| Molecular function | glutathione transferase activity | 17 | 7.3e-06 |
| Molecular function | acyl-CoA dehydrogenase activity | 10 | 2.2e-05 |
| Molecular function | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 37 | 4.6e-05 |
| Molecular function | flavin adenine dinucleotide binding | 19 | 5.4e-05 |
| Molecular function | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 23 | 7.5e-05 |
| Molecular function | NAD binding | 13 | 0.003 |
| Molecular function | aminopeptidase activity | 13 | 0.01 |
| Molecular function | carbohydrate kinase activity | 8 | 0.01 |
| Molecular function | hydro-lyase activity | 13 | 0.02 |
| Molecular function | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | 11 | 0.02 |
| Molecular function | long-chain fatty acid transporter activity | 5 | 0.03 |
| Molecular function | disulfide oxidoreductase activity | 10 | 0.03 |
| Cellular component | lipid particle | 44 | 5.9e-06 |
| Cellular component | mitochondrial matrix | 35 | 2.6e-05 |
| Cellular component | endoplasmic reticulum part | 23 | 0.02 |
| Cellular component | coated vesicle membrane | 9 | 0.03 |
| Cellular component | peroxisome | 12 | 0.03 |
| Cellular component | Golgi membrane | 11 | 0.04 |
| Biological process | fatty acid beta-oxidation | 10 | 4.6e-06 |
| Biological process | glutathione metabolic process | 18 | 5.8e-06 |
| Biological process | protein folding | 27 | 3.8e-05 |
| Biological process | glycolysis | 12 | 0.0002 |
| Biological process | dicarboxylic acid metabolic process | 10 | 0.02 |
| Biological process | branched-chain amino acid metabolic process | 5 | 0.03 |
| Biological process | glycerol ether metabolic process | 7 | 0.03 |

Table S5 Over-represented GO terms among Africa-biased genes.

| Ontology | GO Term | Genes | Adj. <i>P</i> |
|--------------------|---|-------|---------------|
| Molecular function | proton-transporting ATPase activity, rotational mechanism | 15 | 1.7e-06 |
| Molecular function | heme binding | 30 | 7.3e-05 |
| Molecular function | iron ion binding | 30 | 0.002 |
| Molecular function | anion binding | 117 | 0.002 |
| Molecular function | cofactor binding | 30 | 0.01 |
| Molecular function | nucleotide binding | 122 | 0.02 |
| Molecular function | protein kinase activity | 40 | 0.04 |
| Molecular function | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 17 | 0.04 |
| Molecular function | glutathione transferase activity | 11 | 0.04 |
| Cellular component | vacuolar proton-transporting V-type ATPase, V1 domain | 9 | 8.9e-05 |
| Biological process | ATP hydrolysis coupled proton transport | 16 | 7.5e-06 |
| Biological process | carbohydrate metabolic process | 48 | 0.0001 |
| Biological process | male courtship behavior, veined wing generated song production | 10 | 0.001 |
| Biological process | chemical homeostasis | 25 | 0.001 |
| Biological process | negative regulation of signal transduction | 35 | 0.001 |
| Biological process | neuron development | 83 | 0.001 |
| Biological process | regulation of organ morphogenesis | 19 | 0.004 |
| Biological process | glutathione metabolic process | 13 | 0.007 |
| Biological process | regulation of neurogenesis | 24 | 0.01 |
| Biological process | visual perception | 11 | 0.02 |
| Biological process | taxis | 43 | 0.02 |
| Biological process | regulation of transport | 24 | 0.02 |
| Biological process | dorsal/ventral pattern formation | 28 | 0.02 |
| Biological process | detection of visible light | 9 | 0.02 |
| Biological process | regulation of cell morphogenesis | 27 | 0.02 |
| Biological process | cellular response to endogenous stimulus | 20 | 0.02 |
| Biological process | regulation of immune system process | 23 | 0.02 |
| Biological process | regulation of response to external stimulus | 10 | 0.02 |
| Biological process | glycerophospholipid metabolic process | 16 | 0.02 |
| Biological process | cell morphogenesis | 78 | 0.03 |
| Biological process | cellular response to growth factor stimulus | 11 | 0.03 |
| Biological process | cell fate commitment | 60 | 0.03 |
| Biological process | regulation of organ growth | 12 | 0.03 |
| Biological process | pyridine-containing compound metabolic process | 8 | 0.03 |
| Biological process | regulation of G-protein coupled receptor protein signaling pathway | 9 | 0.04 |
| Biological process | cellular biogenic amine metabolic process | 9 | 0.04 |
| Biological process | salivary gland histolysis | 17 | 0.04 |
| Biological process | phototransduction | 12 | 0.04 |

| | | | |
|--------------------|--|----|------|
| Biological process | imaginal disc-derived wing morphogenesis | 48 | 0.04 |
| Biological process | enzyme linked receptor protein signaling pathway | 28 | 0.04 |
| Biological process | negative regulation of cell differentiation | 22 | 0.04 |
| Biological process | regulation of BMP signaling pathway | 8 | 0.04 |
| Biological process | fatty acid beta-oxidation | 6 | 0.04 |
| Biological process | protein phosphorylation | 38 | 0.05 |
| Biological process | renal system development | 16 | 0.05 |
| Biological process | morphogenesis of a polarized epithelium | 19 | 0.05 |

Table S6 Over-represented GO terms among Europe-biased genes.

| Ontology | GO Term | Genes | Adj. <i>P</i> |
|--------------------|---|-------|---------------|
| Molecular function | electron carrier activity | 32 | 0.0001 |
| Molecular function | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 31 | 0.01 |
| Molecular function | cofactor binding | 31 | 0.01 |
| Molecular function | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 19 | 0.01 |
| Molecular function | ATP binding | 79 | 0.02 |
| Molecular function | iron ion binding | 28 | 0.02 |
| Molecular function | transporter activity | 99 | 0.03 |
| Molecular function | disulfide oxidoreductase activity | 10 | 0.03 |
| Cellular component | membrane part | 173 | 0.02 |
| Cellular component | mitochondrial envelope | 38 | 0.02 |
| Cellular component | cytoskeletal part | 69 | 0.03 |
| Cellular component | lipid particle | 33 | 0.04 |
| Biological process | oxidation-reduction process | 87 | 4.6e-08 |
| Biological process | organonitrogen compound metabolic process | 84 | 0.001 |
| Biological process | carboxylic acid metabolic process | 49 | 0.001 |
| Biological process | carbohydrate derivative metabolic process | 59 | 0.01 |
| Biological process | cellular response to stress | 56 | 0.02 |
| Biological process | single-organism transport | 138 | 0.02 |
| Biological process | cellular localization | 81 | 0.03 |
| Biological process | centrosome organization | 23 | 0.03 |
| Biological process | organic substance catabolic process | 61 | 0.04 |
| Biological process | cell redox homeostasis | 13 | 0.04 |