

Table S10 GO term and functional classification enrichment analysis using DAVID for gene families that are contracted in the *Drosophila suzukii* genome as compared to 14 *Drosophila* species analyzed in this study.

| CATEGORY | TERM | COUNT | P VALUE | GENE FAMILIES: REPRESENTATIVE GENE SYMBOLS |
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| Annotation Cluster 1 | Enrichment Score: 3.023489574033364 | | | |
| GOTERM CC | GO:0000786 nucleosome | 5 | 8.14E-06 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| SWISSPROT PIR | acetylation | 5 | 2.48E-05 | His2Av, Adh, Cam, His4r, His3.3A |
| SWISSPROT PIR | nucleosome core | 4 | 2.71E-05 | His2B:CG33882, His2Av, His4r, His3.3A |
| INTERPRO | IPR007125:Histone core | 4 | 8.38E-05 | His2B:CG33882, His2Av, His4r, His3.3A |
| GOTERM BP | GO:0006334 nucleosome assembly | 5 | 9.51E-05 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM BP | GO:0031497 chromatin assembly | 5 | 3.55E-04 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| SWISSPROT PIR | chromosomal protein | 5 | 7.88E-04 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM BP | GO:0006323 DNA packaging | 6 | 8.32E-04 | eIF-4E, His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM BP | GO:0065004 protein-DNA complex assembly | 5 | 9.25E-04 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM CC | GO:0032993 protein-DNA complex | 5 | 9.82E-04 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM BP | GO:0034728 nucleosome organization | 5 | 1.06E-03 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM BP | GO:0006333 chromatin assembly or disassembly | 5 | 2.96E-03 | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| INTERPRO | IPR009072:Histone-fold | 4 | 3.47E-03 | His2B:CG33882, His2Av, His4r, His3.3A |
| GOTERM BP | GO:0034621 cellular macromolecular | 7 | 2.60E-02 | His2B:CG33882, His2Av, His1:CG33834, gammaTub23C, Cam, His4r, |

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| | complex subunit organization | | | | His3.3A |
| GOTERM BP | GO:0034622 cellular macromolecular complex assembly | 6 | 3.27E-02 | | His2B:CG33882, His2Av, His1:CG33834, gammaTub23C, His4r, His3.3A |
| GOTERM BP | GO:0006325 chromatin organization | 6 | 6.55E-02 | | eIF-4E, His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| GOTERM CC | GO:0000785 chromatin | 5 | 7.12E-02 | | His2B:CG33882, His2Av, His1:CG33834, His4r, His3.3A |
| Annotation Cluster 2 | Enrichment Score: 2.5911442503164333 | | | | |
| SWISSPROT PIR | hydrolase | 26 | 4.48E-06 | | CG1637, CG31821, S-Lap7, CG9449, Ace, CG30049, CG5731, Ance, PGRP-SA, CG14022, CG9391, ApepP, primo-2, CG14034, SPE, cathD, kraken, mag, CG2680, CG42264, CG31272, gd, LysC, Mdr49, CG6465, sda |
| GOTERM MF | GO:0008238 exopeptidase activity | 6 | 3.74E-04 | | CG31821, ApepP, CG42264, S-Lap7, Ance, sda |
| GOTERM MF | GO:0008233 peptidase activity | 12 | 2.21E-03 | | CG31821, CG30049, ApepP, CG42264, S-Lap7, gd, SPE, CG6465, cathD, Ance, sda, PGRP-SA |
| GOTERM BP | GO:0006508 proteolysis | 11 | 1.06E-02 | | CG31821, CG30049, CG42264, Nedd8, S-Lap7, gd, SPE, CG6465, cathD, Ance, sda |
| GOTERM MF | GO:0070011 peptidase activity, acting on L-amino acid peptides | 10 | 1.47E-02 | | CG31821, ApepP, CG42264, S-Lap7, gd, SPE, CG6465, cathD, Ance, sda |
| GOTERM MF | GO:0008237 metallopeptidase activity | 5 | 3.28E-02 | | CG42264, S-Lap7, CG6465, Ance, sda |
| SWISSPROT PIR | Protease | 5 | 3.85E-02 | | gd, SPE, cathD, Ance, PGRP-SA |

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| Annotation Cluster 3 | | Enrichment Score: 2.535780529609017 | | |
| SWISSPROT PIR | disulfide bond | 9 | 1.56E-03 | crq, Adk2, gd, LysC, C1GalTA, Ace, CG5210, Ance, PGRP-SA |
| SWISSPROT PIR | glycoprotein | 12 | 2.31E-03 | PGRP-LE, crq, Orct2, Gr64a, pip, gd, Mdr49, C1GalTA, ninaG, Ace, CG5210, Ance |
| UP_SEQ_FEATURE | glycosylation site:N-linked (GlcNAc...) | 12 | 6.87E-03 | PGRP-LE, crq, Orct2, Gr64a, pip, gd, Mdr49, C1GalTA, ninaG, Ace, CG5210, Ance |
| Annotation Cluster 4 | | Enrichment Score: 2.302060885904615 | | |
| GOTERM MF | GO:0008238 exopeptidase activity | 6 | 3.74E-04 | CG31821, ApepP, CG42264, S-Lap7, Ance, sda |
| SWISSPROT PIR | carboxypeptidase | 3 | 1.40E-02 | CG31821, CG42264, Ance |
| GOTERM MF | GO:0004180 carboxypeptidase activity | 3 | 2.37E-02 | CG31821, CG42264, Ance |
| Annotation Cluster 5 | | Enrichment Score: 2.2415486548709147 | | |
| GOTERM MF | GO:0008238 exopeptidase activity | 6 | 3.74E-04 | CG31821, ApepP, CG42264, S-Lap7, Ance, sda |
| SWISSPROT PIR | Aminopeptidase | 3 | 1.62E-02 | ApepP, S-Lap7, sda |
| GOTERM MF | GO:0004177 aminopeptidase activity | 3 | 3.11E-02 | ApepP, S-Lap7, sda |
| Annotation Cluster 6 | | Enrichment Score: 2.0347426002055675 | | |
| SWISSPROT PIR | disulfide bond | 9 | 1.56E-03 | crq, Adk2, gd, LysC, C1GalTA, Ace, CG5210, Ance, PGRP-SA |

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| SWISSPROT PIR | signal | 11 | 4.87E-03 | Acp1, Cpr47Eg, Acp53Ea, gd, LysC, ninaG, rumi, Ace, CG5210, Ance, PGRP-SA |
| SWISSPROT PIR | Secreted | 7 | 1.17E-02 | PGRP-LE, Acp53Ea, gd, ninaG, CG5210, Ance, PGRP-SA |
| UP_SEQ_FEATURE | disulfide bond | 8 | 1.55E-02 | crq, Adk2, gd, LysC, Ace, CG5210, Ance, PGRP-SA |
| UP_SEQ_FEATURE | signal peptide | 11 | 1.60E-02 | Acp1, Cpr47Eg, Acp53Ea, gd, LysC, ninaG, rumi, Ace, CG5210, Ance, PGRP-SA |
| GOTERM CC | GO:0005576 extracellular region | 12 | 2.79E-02 | PGRP-LE, Cpr47Eg, obst-A, Acp53Ea, CG6933, gd, ninaG, CG5210, Ance, PGRP-SA, Spn27A, CG17739 |
| Annotation Cluster 7 | Enrichment Score: 1.8301156780099452 | | | |
| GOTERM BP | GO:0008063 Toll signaling pathway | 5 | 5.04E-04 | pip, gd, SPE, PGRP-SA, Spn27A |
| GOTERM BP | GO:0016485 protein processing | 3 | 7.78E-02 | pip, gd, SPE |
| GOTERM BP | GO:0051604 protein maturation | 3 | 8.25E-02 | pip, gd, SPE |
| Annotation Cluster 8 | Enrichment Score: 1.5505648241814785 | | | |
| GOTERM BP | GO:0006026 aminoglycan catabolic process | 3 | 1.50E-02 | PGRP-LE, CG5210, PGRP-SA |
| GOTERM BP | GO:0000272 polysaccharide catabolic process | 3 | 1.76E-02 | PGRP-LE, CG5210, PGRP-SA |
| GOTERM BP | GO:0006022 aminoglycan metabolic process | 5 | 4.30E-02 | PGRP-LE, obst-A, CG6933, CG5210, PGRP-SA |

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| GOTERM BP | GO:0005976 polysaccharide metabolic process | 5 | 5.51E-02 | PGRP-LE, obst-A, CG6933, CG5210, PGRP-SA |
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Annotation Cluster 9 Enrichment Score: 1.5454649543144068

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| GOTERM BP | GO:0006952 defense response | 7 | 3.29E-03 | PGRP-LE, crq, Tak1, LysC, SPE, PGRP-SA, Spn27A |
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| GOTERM BP | GO:0006955 immune response | 7 | 3.66E-03 | PGRP-LE, crq, Tak1, LysC, SPE, PGRP-SA, Spn27A |
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| GOTERM BP | GO:0045087 innate immune response | 5 | 9.80E-03 | PGRP-LE, Tak1, SPE, PGRP-SA, Spn27A |
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| GOTERM BP | GO:0050830 defense response to Gram-positive bacterium | 3 | 1.76E-02 | PGRP-LE, SPE, PGRP-SA |
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| GOTERM BP | GO:0042742 defense response to bacterium | 4 | 2.55E-02 | PGRP-LE, LysC, SPE, PGRP-SA |
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| GOTERM BP | GO:0002786 regulation of antibacterial peptide production | 3 | 2.62E-02 | Tak1, SPE, PGRP-SA |
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| GOTERM BP | GO:0002808 regulation of antibacterial peptide biosynthetic process | 3 | 2.62E-02 | Tak1, SPE, PGRP-SA |
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| GOTERM BP | GO:0006963 positive regulation of antibacterial peptide biosynthetic process | 3 | 2.62E-02 | Tak1, SPE, PGRP-SA |
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| GOTERM BP | GO:0002697 regulation of immune | 3 | 3.99E-02 | Tak1, SPE, PGRP-SA |
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| | effector process | | | | |
| GOTERM BP | GO:0002700 regulation of production of molecular mediator of immune response | 3 | 3.99E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0002784 regulation of antimicrobial peptide production | 3 | 3.99E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0002805 regulation of antimicrobial peptide biosynthetic process | 3 | 3.99E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0002807 positive regulation of antimicrobial peptide biosynthetic process | 3 | 3.99E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0009617 response to bacterium | 4 | 4.07E-02 | PGRP-LE, LysC, SPE, PGRP-SA | |
| GOTERM BP | GO:0002759 regulation of antimicrobial humoral response | 3 | 5.15E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0043900 regulation of multi- organism process | 3 | 5.15E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0002831 regulation of response to biotic stimulus | 3 | 5.15E-02 | Tak1, SPE, PGRP-SA | |
| GOTERM BP | GO:0002920 regulation of humoral immune response | 3 | 5.15E-02 | Tak1, SPE, PGRP-SA | |

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| SWISSPROT PIR | innate immunity | 3 | 6.30E-02 | PGRP-LE, Tak1, PGRP-SA |
| SWISSPROT PIR | immune response | 3 | 7.08E-02 | PGRP-LE, Tak1, PGRP-SA |
| Annotation Cluster 10 | Enrichment Score: 1.3185781035185091 | | | |
| SWISSPROT PIR | membrane | 16 | 3.33E-02 | C1GalTA, eca, Ace, rost, Cyp6g1, crq, Orct2, Tret1-1, Gr64a, Gr93c, pip, Drip, Mdr49, ppk19, GluRIIA, Tsp42Ee |
| SWISSPROT PIR | transmembrane | 15 | 3.61E-02 | C1GalTA, eca, rost, crq, Orct2, Tret1-1, Gr64a, Gr93c, pip, Drip, Mdr49, ppk19, GluRIIA, Tsp42Ee, CG32053 |
| GOTERM CC | GO:0031224 intrinsic to membrane | 21 | 9.22E-02 | PGRP-LE, CG13078, C1GalTA, eca, CG11601, Ace, rost, crq, Orct2, Tret1-1, Gr64a, Gr93c, pip, Drip, Mdr49, PGRP-SA, Elo68alpha, ppk19, CG32053, Tsp42Ee, GluRIIA |
| Annotation Cluster 11 | Enrichment Score: 1.2323161117351618 | | | |
| SWISSPROT PIR | synapse | 3 | 4.14E-02 | Snap25, Ace, GluRIIA |
| GOTERM CC | GO:0045202 synapse | 5 | 6.14E-02 | eIF-4E, Snap25, CG31272, Ace, GluRIIA |
| SWISSPROT PIR | cell junction | 3 | 7.90E-02 | Snap25, Ace, GluRIIA |
