

Epigenetic mechanisms of insect polyphenisms: Appendices

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Appendix A

ASE supplementary information

TABLE A.1: Nineteen genes showing both monoallelic methylation and monoallelic expression. Blast results and genomic coordinates of the reads from the RNA-seq, MRE-seq and MeDip-seq libraries.

Contig	mRNA start	mRNA end	mRNA length	min read cov	hemi-meth (start : end)	medip (start : end)	mre (start : end)	CpG islands (start : end)	snps (expressed allele— mRNA info— medip info— mre info)	Blast hit	Hit description	Score	e value
AELG01000543.1	2414	4660	2246	3	2318: 2460,2472: 2589, 2598: 2696, 2819: 3251, 3753: 3907, 3937: 4009, 4232: 4237,4256:4313	2318: 2460, 2472: 2589, 2598: 2696, 2819:3251, 3753: 3907, 3937:4009, 4232: 4237, 4256: 4313	2107: 4397, 4405: 4558, 4562: 4618		mre— 3143— 1/1:99:18:255,54,0— 0/0:NA— 1/1:33:6:149,18,0	XR411076.1	PREDICTED: <i>Apis mellifera</i> ecdysone receptor (Ecr), transcript variant X2, misc RNA	438	1.00E-118
AELG01000544.1	153356	154477	1121	3	153593: 153717, 154091: 154151, 154161: 154181	153586: 153776, 154037: 154151, 154161: 154432	153593: 153717, 154091: 154181		medip— 153622— 0/0:NA— 0/0:NA— 1/1:4:13:42,2,0	XM003399876.1	PREDICTED: <i>Bombus terrestris</i> methionine aminopeptidase 1-like	494	3.00E-135
AELG01000620.1	45487	46965	1478	3	45841: 45927, 45988: 46145, 46178: 46410	45841: 45927, 45988: 46145, 46178: 46410	43353: 46644, 46677: 46686, 46924: 48590	46043: 46323	medip— 45850— 0/0:NA— 0/0:NA— 1/1:45:8:213,24,0	XM003398265.1	PREDICTED: <i>Bombus ter-</i> <i>restris</i> hypo- thetical protein LOC100651168	1175	0
AELG01000623.1	2	3526	3524	3	2044: 2099, 2219: 2318, 2321: 2362, 2364: 2544, 2547: 2656, 2948: 3136, 3138: 3461, 3477: 3596	1208: 1435, 1441: 1685, 1754: 1765, 2044: 2099, 2219: 2318, 2321: 2362, 2364: 2544, 2547: 2656, 2948: 3136, 3138: 3461, 3477: 3596	1997: 8031	1425: 1787, 1870: 2101, 2410: 2922, 3155: 3479	medip— 2544— 1/1:99:28:255,84,0— 1/1:45:8:213,24,0— 0/0:NA	XM003398378.1	<i>Bombus terrestris</i> slit homolog 2 protein-like	3007	0

TABLE A.1: (continued)

Contig	mRNA start	mRNA end	mRNA length	min read cov	hemi-meth (start : end)	medip (start : end)	mre (start : end)	CpG islands (start : end)	snps (expressed allele— mRNA info— medip info— mre info)	Blast hit	Hit description	Score	e value
AELG01000829.1	2651	4107	1456	3	2413: 2934, 3095: 3449, 3485: 4038, 4061: 4062	2413: 2934, 3095: 4038, 4061: 4062	1065: 3449, 3485: 4221	3635: 3835, 3981: 4320	mre— 3176— 1/1:69:12:255,36,0— 0/0:NA— 1/1:45:8:197,24,0	XM003396390.1	PREDICTED: <i>Bombus terrestris</i> potassium voltage-gated channel protein Shaker-like, transcript variant 2	1243	0
AELG01000969.1	141301	142147	846	3	141394: 141633, 141652: 141669, 141676: 141825, 141839: 141935	141306: 141633, 141652: 141669, 141676: 141825, 141839: 141935	141394: 142147	141807: 142006	mre— 141694— 1/1:51:9:244,27,0— 0/0:NA— 1/1:51:9:219,27,0	XM003395308.1	PREDICTED: <i>Bombus terrestris</i> excitatory amino acid transporter 4-like	424	4.00E-114
AELG01000977.1	210957	213434	2477	3	210834: 210964, 211460: 211492, 211644: 211743, 211782: 212114, 212117: 212216, 212393: 212397, 212400: 212506, 212512: 212611, 212665: 212764, 212813: 212911, 212943: 213231, 213234: 213951	210834: 210964, 211460: 211492, 211644: 211743, 211782: 212114, 212117: 212216, 212393: 212397, 212400: 212506, 212512: 212611, 212665: 212764, 212813: 212911, 212943: 213231, 213234: 213951	207996: 215483	210405: 211046, 212156: 212355	medip— 211476— 1/1: 99: 32: 255, 96, 0— 1/1: 97: 75: 255, 50, 0— 0/0:NA	XM006567669.1	<i>Apis mellifera</i> centrosomal and chromosomal factor-like	625	1.00E-174
AELG01001021.1	2595	3944	1349	3	2879: 3095, 3222: 3244, 3336: 3389, 3434: 3435, 3516: 3533, 3600: 3718, 3737: 3836	2879: 3095, 3222: 3244, 3336: 3389, 3434: 3435, 3516: 3533, 3600: 3718, 3737: 3836	2336: 3217, 3220: 5596	-	medip—3434—1/1: 1/1:39:7:214,21,0— 0/0:NA	XM003514024.1	PREDICTED: <i>Apis dorsata</i> protein yippee-like 1-like	311	3.00E-80
AELG01001796.1	10244	11803	1559	3	10496: 10946, 11446: 12186	10496: 10946, 11446: 12186	10451: 15319, 7927: 10418	10665: 10891, 11697: 11956	medip— 10938— 1/1:45:21:255,24,0— 1/1:99:46:255,138,0— 0/0:NA	No Hits	-	-	-

TABLE A.1: (continued)

Contig	mRNA start	mRNA end	mRNA length	min read cov	hemi-meth (start : end)	medip (start : end)	mre (start : end)	CpG islands (start : end)	snps (expressed allele— mRNA info— medip info— mre info)	Blast hit	Hit description	Score	e value
AELG01002224.1	26170	28244	2074	3	26883: 26982, 27019: 27020, 27049: 27080, 27116: 27215, 27404: 27678, 27712: 27834, 28116: 28394	26883: 26982, 27019: 27020, 27049: 27080, 27116: 27215, 27404: 27678, 27712: 27834, 28116: 28394	25274: 31026	27647: 27900, 28202: 28401	medip— 27215— 1/ 1: 99: 33: 255, 99, 0— 1/1:69: 12: 255, 36, 0— 0/ 0: NA	XR131831.1	PREDICTED: <i>Bombus terrestris</i> hypothetical LOC100650069	3823	0.00E+00
AELG01002224.1	30371	30980	609	3	30455: 30803, 30811: 30836	30455: 30803, 30811: 30836	25274: 31026	-	medip— 30824— 1/1: 99: 50: 255, 151, 0— 1/1: 57: 10: 255, 30, 0— 0/0:NA	XR131831.1	PREDICTED: <i>Bombus terrestris</i> hypothetical LOC100650069 (LOC100650069)	1040	0.00E+00
AELG01002621.1	84719	85551	832	3	84789: 84888, 85001: 85134	84789: 84888, 85001: 85134, 85142: 85234	84189: 85141, 85401: 85989	-	mre— 85071— 1/1:39:7:154,21,0— 0/0:NA— 1/1:93:16:255,48,0	No Hits	-	-	
AELG01003249.1	27	770	743	3	547: 573, 606: 745	510: 573, 606: 745	23:489, 547: 3804	-	medip— 647— 1/1:45:8:208,24,0— 1/1:12:7:148,7,0— 0/0:NA	XM003402116.1	PREDICTED: <i>Bombus terrestris</i> hypothetical protein LOC100648919	235	2.00E-57
AELG01003672.1	34174	36205	2031	3	34068: 34314, 34361: 34432, 34443: 34460, 34465: 34564, 34942: 34962, 34991: 35090, 35093: 35949, 35993: 36110	34068: 34314, 34361: 34432, 34443: 34460, 34465: 34564, 34942: 34962, 34991: 35090, 35093: 35949, 35993: 36110	34068: 37895	34514: 34999, 35215: 35414, 35606: 36223	mre— 34537— 1/1:33:6:185,18,0— 0/0:NA— 1/1:45:8:227,24,0	XM003395223.1	PREDICTED: <i>Bombus terrestris</i> calmodulin-lysine N-methyltransferase-like	2771	0.00E+00

TABLE A.1: (continued)

Contig	mRNA start	mRNA end	mRNA length	min read cov	hemi-meth (start : end)	medip (start : end)	mre (start : end)	CpG islands (start : end)	snps (expressed allele— mRNA info— medip info— mre info)	Blast hit	Hit description	Score	e value
AELG01004342.1	151574	152335	761	3	151570: 151859, 152028: 152131, 152139: 152142	151513: 151859, 152028: 152131, 152139: 152142	151570: 152157, 152183: 152282	-	medip— 152075— 0/0:NA— 0/0:NA— 1/1:32:6:59,18,0	No Hit	-	-	-
AELG01004467.1	2976	7852	4876	3	3338: 3421	2928: 3057, 3338: 3455, 3571: 3572, 3651: 3670, 3688: 3740, 4148: 4252, 4256: 4268, 4272: 4348, 4833: 4932, 5003: 5200, 5208: 5249, 5254: 5366, 5457: 5539, 5942: 6125, 7593: 7680	3319: 3421, 4014: 4073	-	medip— 3372— 0/0:NA— 0/0:NA— 1/1:9:18:183,5,0	XM003402652.1	PREDICTED: <i>Bombus terrestris</i> elongation of very long chain fatty acids protein 6-like, transcript variant 2	676	0.00E+00
AELG01004618.1	50434	51141	707	3	50596: 50957, 51045: 51046	50409: 50442, 50480: 50957, 51045: 51046	50596: 52827	50539: 50928	medip— 50955— 1/1:99:30:255,90,0— 1/1:93:16:255,48,0— 0/0:NA	XM006568398.1	PREDICTED: <i>Apis mellifera</i> ras GTPase-activating protein nGAP-like	405	1.00E-108
AELG01005399.1	62869	63510	641	3	62569: 63150, 63313: 63325, 63345: 63407, 63410: 63444	62569: 63150, 63313: 63325, 63345: 63407, 63410: 63444	61502: 63526	63152: 63409	medip— 63410— 1/1:45:8:212,24,0— 1/1:39:7:190,21,0— 0/0:NA	XM003393820.1	PREDICTED: <i>Bombus terrestris</i> bicaudal D-related protein homolog	985	0.00E+00
AELG01006475.1	1	1769	1768	3	1420: 1576, 1668: 1769, 757: 758, 851: 852	1420: 1576, 1668: 1769, 757: 758, 851: 852	1.3125	-	medip— 1492— 0/0:NA— 0/0:NA— 1/1:39:7:195,21,0	No Hit	-	-	-

TABLE A.2: Confirmation of single allele expression of nineteen monoallelically expressed genes in twenty-nine previously published transcriptomes. For each of the 19 contigs are the previously published RNA-seq libraries with associated read counts.

Contig	SNPs pressed allele, mRNA info, medip info, mre info)	(ex- Present in the 30 libraries)
AELG01000543.1	mre— 3143—gi—313881757—gb—AELG01000543.1— 3143 . C T 94.5 . DP=4; VDB=7.064840e-02; AF1=1; AC1=2; DP4=0,0,2,2; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:99:18:255,54,0— 1/1:127, 12, 0:4:21 0/0:NA— 1/1:33:6:149,18,0	gi—313881757—gb—AELG01000543.1— 3143 . C T 76 . DP=8; VDB=8.228788e-02; RPB=6.486824e-01; AF1=0.5; AC1=1; DP4=2,1,3,1; MQ=37; FQ=57; PV4=1,0.081,1,0.41 GT:PL:DP:GQ 0/1:106,0,84:7:87 gi—313881757—gb—AELG01000543.1— 3143 . C T 222 . DP=43; VDB=2.788887e-01; AF1=1; AC1=2; DP4=0,0,14,28; MQ=60; FQ=-153 GT:PL:DP:GQ 1/1:255,126,0:42:99
AELG01000544.1	medip— 153622— 0/0:NA— 0/0:NA— 1/1:4:13:42,2,0	
AELG01000620.1	medip— 45850—gi—313881680—gb—AELG01000620.1— 45850 . C G 119 . DP=20; VDB=1.701483e-02; RPB=1.118699e+00; AF1=0.5; AC1=1; DP4=2,10,5,3; MQ=36; 0/0:NA— 0/0:NA—FQ=122; PV4=0.062,0.099,0.39,1 GT:PL:DP:GQ 0/1:149,0,206:20:99 1/1:45:8:213,24,0	gi—313881680—gb—AELG01000620.1— 45850 . C G 119 . DP=28; VDB=2.899710e-02; RPB=2.038931e-01; AF1=0.5; AC1=1; DP4=6,11,4,4; MQ=36; FQ=122; PV4=0.67,0.22,0.29,0.46 GT:PL:DP:GQ 0/1:149,0,255:25:99 gi—313881680—gb—AELG01000620.1— 45850 . C G 41 . DP=20; VDB=2.444842e-02; RPB=1.539883e+00; AF1=0.5; AC1=1; DP4=7,7,1,3; MQ=36; FQ=44; PV4=0.59,0.32,1,1 GT:PL:DP:GQ 0/1:71,0,255:18:74 gi—313881680—gb—AELG01000620.1— 45850 . C G 77 . DP=26; VDB=9.052525e-02; RPB=2.450490e-01; AF1=0.5; AC1=1; DP4=7,10,4,2; MQ=37; FQ=80; PV4=0.37,0.034,1,1 GT:PL:DP:GQ 0/1:107,0,255:23:99 gi—313881680—gb—AELG01000620.1— 45850 . C G 141 . DP=27; VDB=5.388302e-02; RPB=3.772776e-01; AF1=0.5; AC1=1; DP4=8,9,4,5; MQ=37; FQ=144; PV4=1,0.081,1,1 GT:PL:DP:GQ 0/1:171,0,255:26:99 gi—313881680—gb—AELG01000620.1— 45850 . C G 95 . DP=24; VDB=1.896654e-02; RPB=1.460747e+00; AF1=0.5; AC1=1; DP4=9,8,2,5; MQ=36; FQ=98; PV4=0.39,0.47,0.26,1 GT:PL:DP:GQ 0/1:125,0,255:24:99 gi—313881680—gb—AELG01000620.1— 45850 . C G 143 . DP=23; VDB=1.112095e-02; RPB=6.677806e-02; AF1=0.5; AC1=1; DP4=5,8,4,5; MQ=37; FQ=146; PV4=1,0.12,1,0.47 GT:PL:GQ 0/1:173,0,249:99 gi—313881680—gb—AELG01000620.1— 45850 . C G 172 . DP=25; VDB=8.484775e-03; RPB=-1.760447e-01; AF1=0.5; AC1=1; DP4=4,6,4,7; MQ=36; FQ=169; PV4=1,0.26,1,0.17 GT:PL:GQ 0/1:202,0,197:99

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	gi-313881680-gb-AELG01000620.1- 45850 . C G 159 . DP=27 VDB=9.441084e-03 RPB=-6.255175e-01 AF1=0.5 AC1=1 DP4=6,7,7,5 MQ=37 FQ=162 PV4=0.7,0.0046,1,0.072 GT:PL:GQ 0/1:189,0,244:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 81 . DP=26; VDB=1.034012e-01; RPB=3.026138e-02; AF1=0.5; AC1=1;DP4=8,10,4,3; MQ=37; FQ=84; PV4=0.67,0.0088,1,1 GT:PL:GQ 0/1:111,0,255:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 126 . DP=22; VDB=1.289334e-02; RPB=3.983138e-01; AF1=0.5; AC1=1;DP4=6,7,4,4; MQ=36; FQ=129; PV4=1,0.18,0.37,1 GT:PL:GQ 0/1:156,0,252:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 72 . DP=26; VDB=2.979435e-02; RPB=1.142675e+00; AF1=0.5; AC1=1; DP4=7,9,3,3; MQ=36;FQ=75; PV4=1,0.16,0.41,1 GT:PL:GQ 0/1:102,0,255:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 117 . DP=26; VDB=7.125761e-02; RPB=6.429911e-01; AF1=0.5; AC1=1; DP4=7,9,4,4; MQ=37; FQ=120; PV4=1,0.067,1,1 GT:PL:DP:GQ 0/1:147,0,255:24:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 222 . DP=25; VDB=3.478231e-02; AF1=1; AC1=2; DP4=0,0,9,12; MQ=36; FQ=-90 GT:PL:GQ 1/1:255,63,0:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 222 . DP=93; VDB=7.718160e-13; AF1=1; AC1=2; DP4=0,0,22,46; MQ=36; FQ=-232 GT:PL:DP:GQ 1/1:255,205,0:68:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 222 . DP=26; VDB=7.327349e-04; AF1=1; AC1=2; DP4=0,0,9,9; MQ=36; FQ=-81 GT:PL:DP:GQ 1/1:255,54,0:18:99
	gi-313881680-gb-AELG01000620.1- 45850 . C G 222 . DP=92; VDB=2.645789e-12; AF1=1; AC1=2; DP4=0,0,23,48; MQ=36; FQ=-241 GT:PL:DP:GQ 1/1:255,214,0:71:99
AELG01000623.1	medip- 2544-/monometh-monoexp/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 222 . DP=73; VDB=3.311361e-01; AF1=1; AC1=2; DP4=0,0,34,26; 1/1:99:28:255,84,0- MQ=60; FQ=-208 GT:PL:DP:GQ 1/1:255,181,0:60:99 1/1:45:8:213,24,0- 0/0:NA
	/Mark010/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 98.5 . DP=5; VDB=7.268232e-02; AF1=1; AC1=2; DP4=0,0,2,2; MQ=37;FQ=-39 GT:PL:DP:GQ 1/1:131,12,0:4:21
	/MarkNRW8/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 94.3 . DP=6; VDB=5.992068e-02; AF1=1;AC1=2; DP4=0,0,5,0; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:127,15,0:5:27
	/MarkNRW9/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 48 . DP=3; VDB=5.624503e-02; AF1=1; AC1=2; DP4=0,0,1,2; MQ=37; FQ=-36 GT:PL:DP:GQ 1/1:80,9,0:3:16
	/MarkNRW11/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 77.5 . DP=5; VDB=4.829127e-02; AF1=1; AC1=2; DP4=0,0,4,0; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:110,12,0:4:21
	/bee1.1/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 31.8 . DP=2; VDB=7.520000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:63,6,0:2:10
	/bee1.3/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 42.8 . DP=3; VDB=5.920000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:74,6,0:2:10

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	/bee1.4/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 40.8 . DP=3; VDB=4.960000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:72,6,0:2:10
	/bee1.6/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 70 . DP=3; VDB=6.089532e-02; AF1=1; AC1=2; DP4=0,0,2,1; MQ=37; FQ=-36 GT:PL:DP:GQ 1/1:102,9,0:3:16
	/bee1.7/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 42.8 . DP=3; VDB=7.360000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:GQ 1/1:74,6,0:10
	/bee1.11/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 64 . DP=4; VDB=5.361253e-02; AF1=1; AC1=2; DP4=0,0,1,2; MQ=37; FQ=-36 GT:PL:GQ 1/1:96,9,0:16
	/bee2.2/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 29 . DP=3; VDB=7.680000e-02; RPB=8.745357e-01; AF1=0.5004; AC1=1; DP4=1,0,2,0; MQ=37; FQ=3.55; PV4=1,0.33,1,0.029 GT:PL:DP:GQ 0/1:59,0,28:3:31
	/bee2.3/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 32.8 . DP=2; VDB=4.640000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:GQ 1/1:64,6,0:10
	/bee2.9/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 222 . DP=26; VDB=1.574179e-01; AF1=1; AC1=2; DP4=0,0,13,9; MQ=37; FQ=-93 GT:PL:DP:GQ 1/1:255,66,0:22:99
	/bee1.11/test.raw.vcf:gi-313881677-gb-AELG01000623.1- 2544 . A G 64 . DP=4; VDB=5.361253e-02; AF1=1; AC1=2; DP4=0,0,1,2; MQ=37; FQ=-36 GT:PL:GQ 1/1:96,9,0:16
AELG01000829.1	mre- 3176-/monometh.monoexp/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 222 . DP=29; VDB=1.992445e-01; AF1=1; AC1=2; DP4=0,0,8,21; 1/1:69:12:255,36,0- MQ=60;FQ=-114 GT:PL:DP:GQ 1/1:255,87,0:29:99 0/0:NA- 1/1:45:8:197,24,0
	/Mark010/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 105 . DP=5; VDB=9.444086e-02; AF1=1; AC1=2; DP4=0,0,4,1; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:138,15,0:5:27
	/Mark011/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 105 . DP=5; VDB=9.444087e-02; AF1=1; AC1=2; DP4=0,0,3,2; MQ=35; FQ=-42 GT:PL:DP:GQ 1/1:138,15,0:5:27
	/MarkNRW8/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 47 . DP=7; VDB=6.278483e-02; RPB=5.460172e-01; AF1=0.5; AC1=1; DP4=2,1,1,2;MQ=37;FQ=49.6;PV4=1,0.15,1,0.28 GT:PL:DP:GQ 0/1:77,0,87:6:80
	/MarkNRW11/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 29 . DP=3; VDB=5.440000e-02; RPB=-8.745357e-01; AF1=0.5004; AC1=1; DP4=0,1,2,0; MQ=37; FQ=3.55; PV4=0.33,0.33,1,0.27 GT:PL:DP:GQ 0/1:59,0,28:3:31
	/bee1.4/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 71 . DP=3; VDB=6.442004e-02; AF1=1; AC1=2; DP4=0,0,2,1; MQ=37;FQ=-36 GT:PL:DP:GQ 1/1:103,9,0:3:16
	/bee1.6/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 74.5 . DP=6; VDB=6.845168e-02; AF1=1; AC1=2; DP4=0,0,1,3; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:107,12,0:4:21
	/bee1.7/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 97.5 . DP=4; VDB=8.051522e-02; AF1=1; AC1=2; DP4=0,0,1,3; MQ=37; FQ=-39 GT:PL:GQ 1/1:130,12,0:21

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	/bee1.11/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 73 . DP=4; VDB=5.227153e-02; AF1=1; AC1=2; DP4=0,0,1,2; MQ=37; FQ=-38 GT:PL:GQ 1/1:105,9,0:16
	/bee2.2/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 36.8 . DP=3;VDB=6.880000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:68,6,0:2:10
	/bee1.11/test.raw.vcf:gi-313881471-gb-AELG01000829.1- 3176 . C T 73 . DP=4;VDB=5.227153e-02;AF1=1;AC1=2;DP4=0,0,1,2;MQ=37;FQ=-36 GT:PL:GQ 1/1:105,9,0:16
AELG01000969.1	mre- 141694-/monometh.monoexp/test.raw.vcf:gi-313881324-gb-AELG01000969.1- 141694 . A G 222 . DP=15; VDB=1.072004e-01; AF1=1; AC1=2; DP4=0,0,9,5; 1/1:51:9:244,27,0- MQ=60; FQ=-69 GT:PL:DP:GQ 1/1:255,42,0:14:81 0/0:NA-1/1:51:9:219,27,0
	/bee1.11/test.raw.vcf:gi-313881324-gb-AELG01000969.1- 141694 . A G 21.8 . DP=2; VDB=6.240000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:GQ 1/1:53,6,0:10
	/bee2.9/test.raw.vcf:gi-313881324-gb-AELG01000969.1- 141694 . A G 32.8 . DP=2;VDB=4.320000e-02;AF1=1;AC1=2;DP4=0,0,1,1;MQ=37;FQ=-33 GT:PL:DP:GQ 1/1:64,6,0:2:10
	/bee1.11/test.raw.vcf:gi-313881324-gb-AELG01000969.1- 141694 . A G 21.8 . DP=2;VDB=6.240000e-02;AF1=1;AC1=2;DP4=0,0,1,1;MQ=37;FQ=-33 GT:PL:GQ 1/1:53,6,0:10
AELG01000977.1	medip- 211476-- 1/1:99:32:255,96,0- 1/1:97:75:255,50,0- 0/0:NA
AELG01001021.1	medip- 3434-/monometh.monoexp/test.raw.vcf:gi-313881245-gb-AELG01001021.1- 3434 . T C 222 . DP=31;VDB=2.744060e-01; AF1=1; AC1=2; DP4=0,0,25,4; 1/1:81:14:255,42,0- MQ=60;FQ=-114 GT:PL:DP:GQ 1/1:255,87,0:29:99 1/1:39:7:214,21,0- 0/0:NA
	/Mark011/test.raw.vcf:gi-313881245-gb-AELG01001021.1- 3434 . T C 35.8 . DP=2;VDB=4.320000e-02; AF1=1; AC1=2; DP4=0,0,2,0;MQ=37;FQ=-33 GT:PL:DP:GQ 1/1:67,6,0:2:10
	/MarkNRW8/test.raw.vcf:gi-313881245-gb-AELG01001021.1- 3434 . T C 48 . DP=5; VDB=2.570870e-02; RPB=-5.314005e-01; AF1=0.5; AC1=1; DP4=2,0,3,0; MQ=37; FQ=26; PV4=1,0,13,1,1 GT:PL:DP:GQ 0/1:78,0,53:5:56
	/bee2.9/test.raw.vcf:gi-313881245-gb-AELG01001021.1- 3434 . T C 14.2 . DP=10;VDB=6.560000e-02;RPB=6.527912e-01;AF1=0.5;AC1=1;DP4=6,2,1,1;MQ=37; FQ=17.1; PV4=1,1,1,1 GT:PL:DP:GQ 0/1:44,0,182:10:47
AELG01001796.1	medip- 10938-/monometh.monoexp/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 222 . DP=53; VDB=9.236236e-04; RPB=1.316622e+00; AF1=1; 1/1:45:21:255,24,0- AC1=2; DP4=0,1,11,38; MQ=60; FQ=-139; PV4=1,0,4,1,0.24 GT:PL:DP:GQ 1/1:255,112,0:50:99 1/1:99:46:255,138,0- 0/0:NA

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	/Mark011/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 70 . DP=5; VDB=8.327157e-02; RPB=-8.293682e-01; AF1=0.5016; AC1=1; DP4=1,0,4,0; MQ=37; FQ=-6.18; PV4=1,1,1,1 GT:PL:DP:GQ 0/1:100,0,22:5:25
	/MarkNRW8/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 120 . DP=12; VDB=4.793958e-02; RPB=9.104187e-01; AF1=0.5; AC1=1; DP4=2,4,3,3; MQ=37; FQ=120; PV4=1,0.41,1,1 GT:PL:DP:GQ 0/1:150,0,150:12:99
	/MarkNRW11/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 172 . DP=9; VDB=1.111813e-01; AF1=1; AC1=2; DP4=0,0,4,3; MQ=37; FQ=-48 GT:PL:DP:GQ 1/1:205,21,0:7:39
	/bee1.2/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 41.8 . DP=2; VDB=2.560000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37;FQ=-33 GT:PL:DP:GQ 1/1:73,6,0:2:10
	/bee1.3/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 35.8 . DP=2; VDB=5.280000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:67,6,0:2:10
	/bee1.4/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 55 . DP=3; VDB=5.498856e-02; AF1=1; AC1=2; DP4=0,0,0,3; MQ=37; FQ=-36 GT:PL:DP:GQ 1/1:87,9,0:3:16
	/bee1.8/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 35.8 . DP=2; VDB=5.600000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:GQ 1/1:67,6,0:10
	/bee1.11/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 35.8 . DP=2; VDB=6.240000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:GQ 1/1:67,6,0:10
	/bee1.12/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 35.8 . DP=2; VDB=5.440000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37;FQ=-33 GT:PL:GQ 1/1:67,6,0:10
	/bee2.1/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 72 . DP=3; VDB=3.127017e-02; AF1=1; AC1=2; DP4=0,0,2,1; MQ=37; FQ=-36 GT:PL:GQ 1/1:104,9,0:16
	/bee2.3/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 32 . DP=3; VDB=4.000000e-02; RPB=-8.745357e-01; AF1=0.5004; AC1=1; DP4=0,1,1,1; MQ=37; FQ=3.55; PV4=1,0.41,1,1 GT:PL:GQ 0/1:62,0,28:31
	/bee1.11/test.raw.vcf:gi-313880457-gb-AELG01001796.1- 10938 . G A 35.8 . DP=2;VDB=6.240000e-02;AF1=1;AC1=2;DP4=0,0,0,2;MQ=37;FQ=-33 GT:PL:GQ 1/1:67,6,0:10
AELG01002224.1	medip- 27215-/monometh_monoexp/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 222 . DP=71; VDB=1.699102e-03; AF1=1; AC1=2; DP4=0,0,45,24; 1/1:99:33:255,99,0- MQ=60; FQ=-235 GT:PL:DP:GQ 1/1:255,208,0:69:99 1/1:69:12:255,36,0- 0/0:NA
	/Mark010/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 74 . DP=8; VDB=5.619835e-02; RPB=-9.980746e-01; AF1=0.5; AC1=1; DP4=2,1,2,2; MQ=37; FQ=52; PV4=1,0.42,1,0.099 GT:PL:DP:GQ 0/1:104,0,79:7:82
	/MarkRW7/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 140 . DP=11; VDB=1.037214e-01; RPB=7.343199e-01; AF1=0.5; AC1=1; DP4=3,1,5,2; MQ=37; FQ=72; PV4=1,1,1,1 GT:PL:DP:GQ 0/1:170,0,99:11:99
	/MarkNRW8/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 47 . DP=7; VDB=5.983360e-02; RPB=1.053122e+00; AF1=0.5; AC1=1; DP4=3,0,3,0; MQ=37; FQ=47; PV4=1,1,1,1 GT:PL:DP:GQ 0/1:77,0,77:6:77

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	/MarkNRW11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 96.3 . DP=5; VDB=7.760359e-02; AF1=1; AC1=2; DP4=0,0,5,0; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:129,15,0:5:27
	/bee1.2/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 52 . DP=3; VDB=6.695797e-02; AF1=1;AC1=2; DP4=0,0,3,0; MQ=33; FQ=-36 GT:PL:DP:GQ 1/1:84,9,0:3:16
	/bee1.3/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 58 . DP=7; VDB=4.829127e-02; RPB=-6.486824e-01; AF1=0.5; AC1=1; DP4=2,1,3,1; MQ=37; FQ=54.8; PV4=1,0,2,1,1 GT:PL:DP:GQ 0/1:88,0,83:7:85
	/bee1.4/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 20 . DP=6; VDB=5.920000e-02; RPB=8.071455e-01; AF1=0.5; AC1=1; DP4=3,1,2,0; MQ=37; FQ=23; PV4=1,1,1,1 GT:PL:DP:GQ 0/1:50,0,113:6:53
	/bee1.11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 188 . DP=9; VDB=8.554666e-02; AF1=1; AC1=2; DP4=0,0,5,3; MQ=37; FQ=-51 GT:PL:GQ 1/1:221,24,0:45
	/bee2.3/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 140 . DP=6; VDB=9.321602e-02; AF1=1; AC1=2; DP4=0,0,3,3; MQ=37; FQ=-45 GT:PL:GQ 1/1:173,18,0:33
	/bee2.9/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 182 . DP=22; VDB=2.965213e-02; RPB=1.373149e+00; AF1=0.5; AC1=1; DP4=8,3,5,5; MQ=37; FQ=176; PV4=0.39,1,1,0.42 GT:PL:DP:GQ 0/1:212,0,203:21:99
	/Users/zoe/Desktop/bee1.11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 27215 . A G 188 . DP=9; VDB=8.554666e-02; AF1=1; AC1=2; DP4=0,0,5,3; MQ=37; FQ=-51 GT:PL:GQ 1/1:221,24,0:45
AELG01002224.1	medip- 30824- /Mark010/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 222 . DP=18; VDB=1.831351e-01; AF1=1; AC1=2; DP4=0,0,8,9; MQ=37; 1/1:99:50:255,151,0- FQ=-78 GT:PL:DP:GQ 1/1:255,51,0:17:99 1/1:57:10:255,30,0- 0/0:NA
	/MarkNRW8/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 125 . DP=6;VDB=9.071144e-02; AF1=1; AC1=2; DP4=0,0,3,2; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:158,15,0:5:27
	/MarkNRW11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 47 . DP=8; VDB=6.570053e-02; RPB=5.460172e-01; AF1=0.5; AC1=1; DP4=0,3,3,0; MQ=37; FQ=43; PV4=0.1,1,1,1 GT:PL:DP:GQ 0/1:77,0,71:6:73
	/bee1.1/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 35.8 . DP=2;VDB=7.200000e-02;AF1=1;AC1=2;DP4=0,0,0,2;MQ=37;FQ=-33 GT:PL:DP:GQ 1/1:67,6,0:2:10
	/bee1.2/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 176 . DP=9; VDB=4.670117e-02; AF1=1; AC1=2; DP4=0,0,2,6; MQ=37; FQ=-51 GT:PL:DP:GQ 1/1:209,24,0:8:45
	/bee1.3/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 177 . DP=11; VDB=8.944587e-02; RPB=1.392621e+00; AF1=1; AC1=2; DP4=0,1,6,3; MQ=37; FQ=-33; PV4=0.4,1,1,1 GT:PL:DP:GQ 1/1:208,6,0:10:10
	/bee1.5/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 35.8 . DP=4;VDB=3.040000e-02;AF1=1;AC1=2;DP4=0,0,0,2;MQ=37;FQ=-33 GT:PL:DP:GQ 1/1:67,6,0:2:10
	/bee1.6/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 208 . DP=10; VDB=9.806732e-02;AF1=1;AC1=2;DP4=0,0,4,5;MQ=37;FQ=-54 GT:PL:DP:GQ 1/1:241,27,0:9:51

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	<p>/bee1.7/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 35.8 . DP=4; VDB=4.320000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:GQ 1/1:67,6,0:10</p> <p>/bee1.8/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 103 . DP=4; VDB=7.635114e-02; AF1=1; AC1=2; DP4=0,0,2,2; MQ=37; FQ=-39 GT:PL:GQ 1/1:135,12,0:21</p> <p>/bee1.11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 128 . DP=5; VDB=8.616185e-02; AF1=1; AC1=2; DP4=0,0,2,3; MQ=37; FQ=-42 GT:PL:GQ 1/1:161,15,0:27</p> <p>/bee1.12/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 128 . DP=5; VDB=9.505586e-02; AF1=1; AC1=2; DP4=0,0,2,3; MQ=37; FQ=-42 GT:PL:GQ 1/1:161,15,0:27</p> <p>/bee2.9/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 203 . DP=25; VDB=1.385411e-01; RPB=1.822160e+00; AF1=0.5; AC1=1; DP4=5,7,7,6; MQ=37; FQ=198; PV4=0.7,0.19,1,0.19 GT:PL:DP:GQ 0/1:233,0,226:25:99</p> <p>/bee1.11/test.raw.vcf:gi-313880010-gb-AELG01002224.1- 30824 . A G 128 . DP=5; VDB=8.616185e-02; AF1=1; AC1=2; DP4=0,0,2,3; MQ=37; FQ=-42 GT:PL:GQ 1/1:161,15,0:27</p>
AELG01002621.1	<p>mre- 85071-/Users/zoe/Desktop/monometh_monoexp/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 222 . DP=17;VDB=1.768967e- 1/1:39:7:154,21,0- 01;AF1=1;AC1=2;DP4=0,0,3,13;MQ=60;FQ=-75 GT:PL:DP:GQ 1/1:255,48,0:16:93 0/0:NA- 1/1:93:16:255,48,0</p> <p>/MarkRW7/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 42.8 . DP=2; VDB=7.840000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:74,6,0:2:10</p> <p>/MarkNRW8/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 103 . DP=5;VDB=6.522045e-02; AF1=1; AC1=2; DP4=0,0,1,4; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:136,15,0:5:27</p> <p>/bee1.3/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 42.8 . DP=2; VDB=4.320000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:74,6,0:2:10</p> <p>/bee1.7/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 35.8 . DP=2; VDB=6.400000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:GQ 1/1:67,6,0:10</p> <p>/bee2.9/test.raw.vcf:gi-313879594-gb-AELG01002621.1- 85071 . C T 175 . DP=9; VDB=1.091397e-02; AF1=1; AC1=2; DP4=0,0,2,6; MQ=37; FQ=-51 GT:PL:DP:GQ 1/1:208,24,0:8:45</p>
AELG01003249.1	<p>medip- 647-/monometh_monoexp/test.raw.vcf:gi-313878951-gb-AELG01003249.1- 520 . A T 156 . DP=34; VDB=2.248647e-01; AF1=1; AC1=2; DP4=0,0,23,10; 1/1:45:8:208,24,0- MQ=59;FQ=-112 GT:PL:DP:GQ 1/1:255,151,66:33:99 1/1:12:7:148,7,0- 0/0:NA</p> <p>/monometh_monoexp/test.raw.vcf:gi-313878951-gb-AELG01003249.1- 647 . C T 222 . DP=56; VDB=2.833189e-04; RPB=-9.666787e-01; AF1=1; AC1=2; DP4=0,2,17,36; MQ=39; FQ=-118; PV4=1,0.17,0.35,0.068 GT:PL:DP:GQ 1/1:255,91,0:55:99</p>

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
AELG01003672.1	<p>mre— 34537—/monometh_monoexp/test.raw.vcf:gi—313878519—gb—AELG01003672.1— 34537 . T C 222 . DP=18; VDB=3.293828e-02; AF1=1; AC1=2; DP4=0,0,7,11; 1/1:33:6:185,18,0— MQ=60; FQ=-81 GT:PL:DP:GQ 1/1:255,54,0:18:99 0/0:NA— 1/1:45:8:227,24,0</p> <p>/Mark010/test.raw.vcf:gi—313878519—gb—AELG01003672.1— 34537 . T C 42.8 . DP=2;VDB=5.120000e-02;AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:74,6,0:2:10</p> <p>/Mark011/test.raw.vcf:gi—313878519—gb—AELG01003672.1— 34537 . T C 42.8 . DP=2; VDB=6.560000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:74,6,0:2:10</p> <p>/MarkNRW8/test.raw.vcf:gi—313878519—gb—AELG01003672.1— 34537 . T C 73 . DP=3; VDB=6.086650e-02; AF1=1; AC1=2; DP4=0,0,1,2; MQ=37; FQ=-36 GT:PL:DP:GQ 1/1:105,9,0:3:16</p> <p>/bee2.9/test.raw.vcf:gi—313878519—gb—AELG01003672.1— 34537 . T C 97.5 . DP=4; VDB=5.619835e-02; AF1=1; AC1=2; DP4=0,0,2,2; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:130,12,0:4:21</p>
AELG01004342.1	<p>medip— 152075— 0/0:NA— 0/0:NA— 1/1:32:6:59,18,0</p>
AELG01004467.1	<p>medip— 3372— 0/0:NA— 0/0:NA— 1/1:9:18:183,5,0</p>
AELG01004618.1	<p>medip— 50955—/monometh_monoexp/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 222 . DP=66;VDB=2.193528e-02;AF1=1;AC1=2;DP4=0,0,28,37;MQ=60;FQ=-223 GT:PL:DP:GQ 1/1:255,196,0:65:99 1/1:93:16:255,48,0— 0/0:NA</p> <p>/Mark010/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 120 . DP=5; VDB=9.266921e-02; AF1=1; AC1=2; DP4=0,0,3,2; MQ=37; FQ=-42 GT:PL:DP:GQ 1/1:153,15,0:5:27</p> <p>/Mark011/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 97.5 . DP=4; VDB=7.864627e-02; AF1=1; AC1=2; DP4=0,0,1,3; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:130,12,0:4:21</p> <p>/MarkRW7/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 147 . DP=7; VDB=5.105456e-02; AF1=1; AC1=2; DP4=0,0,1,6; MQ=37; FQ=-48 GT:PL:DP:GQ 1/1:180,21,0:7:39</p> <p>/MarkNRW8/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 40.8 . DP=3; VDB=3.200000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:72,6,0:2:10</p> <p>/MarkNRW9/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 34.8 . DP=2; VDB=7.680000e-02;AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:66,6,0:2:10</p> <p>/bee1.2/test.raw.vcf:gi—313877043—gb—AELG01004618.1— 50955 . T C 62 . DP=4; VDB=5.085621e-02;AF1=1; AC1=2; DP4=0,0,2,1; MQ=33; FQ=-36 GT:PL:DP:GQ 1/1:94,9,0:3:16</p>

TABLE A.2: (continued)

Contig	SNPs (expressed Present in the 30 libraries allele, mRNA info, medip info, mre info)
	/bee1.3/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 103 . DP=4; VDB=8.050644e-02; AF1=1; AC1=2; DP4=0,0,2,2; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:135,12,0:4:21
	/bee1.4/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 35.8 . DP=3; VDB=7.360000e-02; AF1=1; AC1=2; DP4=0,0,0,2; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:67,6,0:2:10
	/bee1.6/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 97.5 . DP=4; VDB=7.549815e-02; AF1=1; AC1=2; DP4=0,0,1,3; MQ=37; FQ=-39 GT:PL:DP:GQ 1/1:130,12,0:4:21
	/bee1.7/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 42.8 . DP=2; VDB=7.360000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:GQ 1/1:74,6,0:10
	/bee1.11/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 31.8 . DP=2; VDB=5.280000e-02; AF1=1; AC1=2; DP4=0,0,2,0; MQ=37; FQ=-33 GT:PL:GQ 1/1:63,6,0:10
	/bee2.9/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 165 . DP=9; VDB=1.147958e-01; AF1=1; AC1=2; DP4=0,0,2,6; MQ=37; FQ=-51 GT:PL:DP:GQ 1/1:198,24,0:8:45
	/bee1.11/test.raw.vcf:gi-313877043-gb-AELG01004618.1- 50955 . T C 31.8 . DP=2; VDB=5.280000e-02; AF1=1; AC1=2; DP4=0,0,2,0; MQ=37; FQ=-33 GT:PL:GQ 1/1:63,6,0:10
AELG01005399.1	medip- 63410-/monometh_monoexp/test.raw.vcf:gi-313876243-gb-AELG01005399.1- 63410 . C A 222 . DP=14; VDB=1.454940e-01; AF1=1; AC1=2; DP4=0,0,5,8; 1/1:45:8:212,24,0- MQ=60; FQ=-66 GT:PL:DP:GQ 1/1:255,39,0:13:75 1/1:39:7:190,21,0- 0/0:NA /MarkNRW8/test.raw.vcf:gi-313876243-gb-AELG01005399.1- 63410 . C A 40.8 . DP=2; VDB=3.680000e-02; AF1=1; AC1=2; DP4=0,0,1,1; MQ=37; FQ=-33 GT:PL:DP:GQ 1/1:72,6,0:2:10
AELG01006475.1	medip- 1492-/MarkNRW8/test.raw.vcf:gi-313875158-gb-AELG01006475.1- 1492 . A G 73 . DP=21; VDB=6.102519e-02; RPB=-5.367199e-01; AF1=0.5; AC1=1; 0/0:NA- 0/0:NA-DP4=10,6,2,3; MQ=37; FQ=76; PV4=0.61,0.25,1,0.17 GT:PL:DP:GQ 0/1:103,0,255:21:99 1/1:39:7:195,21,0

TABLE A.3: 555 genes showing allele specific expression in at least three of the 29 previously published RNA-seq libraries. This table details the blast results from both the bumblebee and drosophila genomes and the GO terms associated with the drosophila hits.

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313870964-gb-AELG01010669.1-1056	—NA—	NA		—NA—	NA		
gi-313870964-gb-AELG01010669.1-446	—NA—	NA		—NA—	NA		
gi-313870964-gb-AELG01010669.1-473	—NA—	NA		—NA—	NA		
gi-313870964-gb-AELG01010669.1-677	—NA—	NA		—NA—	NA		
gi-313870964-gb-AELG01010669.1-718	—NA—	NA		—NA—	NA		
gi-313870964-gb-AELG01010669.1-753	—NA—	NA		—NA—	NA		
gi-313871004-gb-AELG01010629.1-123	—NA—	NA		—NA—	NA		
gi-313871004-gb-AELG01010629.1-249	—NA—	NA		—NA—	NA		
gi-313871004-gb-AELG01010629.1-289	—NA—	NA		—NA—	NA		
gi-313871046-gb-AELG01010587.1-833	—NA—	NA		—NA—	NA		
gi-313871062-gb-AELG01010571.1-137	—NA—	NA		—NA—	NA		
gi-313871062-gb-AELG01010571.1-160	—NA—	NA		—NA—	NA		
gi-313871153-gb-AELG01010480.1-351	—NA—	NA		GAGXEDROME ame: Full=Nucleic- acid-binding from transposon X-element	7.20E-21		
gi-313871265-gb-AELG01010368.1-1168	—NA—	NA		isoform A	5.50E-05		
gi-313871265-gb-AELG01010368.1-1197	—NA—	NA		isoform A	5.50E-05		
gi-313871265-gb-AELG01010368.1-1202	—NA—	NA		isoform A	5.50E-05		
gi-313871265-gb-AELG01010368.1-318	—NA—	NA		isoform A	5.50E-05		
gi-313871270-gb-AELG01010363.1-239	—NA—	NA		—NA—	NA		
gi-313871270-gb-AELG01010363.1-244	—NA—	NA		—NA—	NA		
gi-313871270-gb-AELG01010363.1-274	—NA—	NA		—NA—	NA		
gi-313871270-gb-AELG01010363.1-312	—NA—	NA		—NA—	NA		
gi-313871304-gb-AELG01010329.1-674	—NA—	NA		—NA—	NA		
gi-313871346-gb-AELG01010287.1-42	—NA—	NA		—NA—	NA		
gi-313871346-gb-AELG01010287.1-62	—NA—	NA		—NA—	NA		
gi-313871346-gb-AELG01010287.1-92	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313871359-gb-AELG01010274.1-1062	—NA—	NA		CG10206	1.00E-50		
gi-313871359-gb-AELG01010274.1-659	—NA—	NA		CG10206	1.00E-50		
gi-313871362-gb-AELG01010271.1-132	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-140	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-152	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-161	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-183	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-328	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-356	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-381	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-383	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-414	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-430	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-458	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-459	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-462	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-466	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-482	—NA—	NA		RE03814p	8.30E-11		
gi-313871362-gb-AELG01010271.1-487	—NA—	NA		RE03814p	8.30E-11		
gi-313871372-gb-AELG01010261.1-523	—NA—	NA		RTXEDROME	3.30E-42		
				ame:			
				Full=Probable			
				RNA-directed			
				DNA polymerase			
				from transposon			
				X-element ame:			
				Full=Reverse			
				transcriptase			
gi-313871432-gb-AELG01010201.1-825	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-204	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-224	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-268	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-299	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-318	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-324	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313871444-gb-AELG01010189.1-338	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-68	—NA—	NA		—NA—	NA		
gi-313871444-gb-AELG01010189.1-69	—NA—	NA		—NA—	NA		
gi-313871543-gb-AELG01010090.1-304	—NA—	NA		CG8132- partial	3.20E-19	CG8132	nitrilase activity nitrogen compound metabolic process
gi-313871543-gb-AELG01010090.1-314	—NA—	NA		CG8132- partial	3.20E-19	CG8132	nitrilase activity nitrogen compound metabolic process
gi-313871543-gb-AELG01010090.1-686	—NA—	NA		CG8132- partial	3.20E-19	CG8132	nitrilase activity nitrogen compound metabolic process
gi-313871543-gb-AELG01010090.1-708	—NA—	NA		CG8132- partial	3.20E-19	CG8132	nitrilase activity nitrogen compound metabolic process
gi-313871567-gb-AELG01010066.1-165	—NA—	NA		—NA—	NA		
gi-313871567-gb-AELG01010066.1-437	—NA—	NA		—NA—	NA		
gi-313871567-gb-AELG01010066.1-99	—NA—	NA		—NA—	NA		
gi-313871662-gb-AELG01009971.1-135	—NA—	NA		RE03814p	3.70E-10		
gi-313871675-gb-AELG01009958.1-117	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-160	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-177	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-182	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-323	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-344	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-362	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-365	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-412	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-425	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-434	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-444	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-59	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-65	—NA—	NA		—NA—	NA		
gi-313871675-gb-AELG01009958.1-90	—NA—	NA		—NA—	NA		
gi-313871683-gb-AELG01009950.1-492	—NA—	NA		CG32069- partial	1.60E-05	DsecGM24783 DyakGE20246 CG32069	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313871683-gb-AELG01009950.1-494	—NA—	NA		CG32069- partial	1.60E-05	DsecGM24783 DyakGE20246	
gi-313871683-gb-AELG01009950.1-682	—NA—	NA		CG32069- partial	1.60E-05	CG32069 DsecGM24783 DyakGE20246	
gi-313871800-gb-AELG01009833.1-126	—NA—	NA		6-phosphofructo-2- isoform A	9.20E-16	Pfrx	carbohydrate metabolic process phosphate-containing compound metabolic process
gi-313871800-gb-AELG01009833.1-143	—NA—	NA		6-phosphofructo-2- isoform A	9.20E-16	Pfrx	imaginal disc-derived wing morphogenesis carbohydrate metabolic process phosphate-containing compound metabolic process
gi-313871800-gb-AELG01009833.1-190	—NA—	NA		6-phosphofructo-2- isoform A	9.20E-16	Pfrx	imaginal disc-derived wing morphogenesis carbohydrate metabolic process phosphate-containing compound metabolic process
gi-313871800-gb-AELG01009833.1-265	—NA—	NA		6-phosphofructo-2- isoform A	9.20E-16	Pfrx	imaginal disc-derived wing morphogenesis carbohydrate metabolic process phosphate-containing compound metabolic process
gi-313871800-gb-AELG01009833.1-417	—NA—	NA		6-phosphofructo-2- isoform A	9.20E-16	Pfrx	imaginal disc-derived wing morphogenesis carbohydrate metabolic process phosphate-containing compound metabolic process
gi-313871804-gb-AELG01009829.1-270	—NA—	NA		—NA—	NA		
gi-313871866-gb-AELG01009767.1-53	—NA—	NA		GH20809p	4.00E-06		
gi-313871866-gb-AELG01009767.1-99	—NA—	NA		GH20809p	4.00E-06		
gi-313871870-gb-AELG01009763.1-360	—NA—	NA		—NA—	NA		
gi-313871870-gb-AELG01009763.1-433	—NA—	NA		—NA—	NA		
gi-313871955-gb-AELG01009678.1-564	—NA—	NA		—NA—	NA		
gi-313871994-gb-AELG01009639.1-516	—NA—	NA		—NA—	NA		
gi-313871994-gb-AELG01009639.1-628	—NA—	NA		—NA—	NA		
gi-313872199-gb-AELG01009434.1-418	—NA—	NA		—NA—	NA		
gi-313872212-gb-AELG01009421.1-1379	—NA—	NA		—NA—	NA		
gi-313872277-gb-AELG01009356.1-227	—NA—	NA		RE37382p	7.00E-08		
gi-313872277-gb-AELG01009356.1-230	—NA—	NA		RE37382p	7.00E-08		
gi-313872277-gb-AELG01009356.1-250	—NA—	NA		RE37382p	7.00E-08		
gi-313872277-gb-AELG01009356.1-312	—NA—	NA		RE37382p	7.00E-08		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313872277-gb-AELG01009356.1-313	—NA—	NA		RE37382p	7.00E-08		
gi-313872277-gb-AELG01009356.1-370	—NA—	NA		RE37382p	7.00E-08		
gi-313872281-gb-AELG01009352.1-1210	—NA—	NA		—NA—	NA		
gi-313872281-gb-AELG01009352.1-1215	—NA—	NA		—NA—	NA		
gi-313872281-gb-AELG01009352.1-929	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-237	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-332	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-355	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-378	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-380	—NA—	NA		—NA—	NA		
gi-313872296-gb-AELG01009337.1-430	—NA—	NA		—NA—	NA		
gi-313872375-gb-AELG01009258.1-134	—NA—	NA		—NA—	NA		
gi-313872375-gb-AELG01009258.1-69	—NA—	NA		—NA—	NA		
gi-313872427-gb-AELG01009206.1-292	—NA—	NA		—NA—	NA		
gi-313872427-gb-AELG01009206.1-317	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-198	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-229	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-233	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-487	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-53	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-61	—NA—	NA		—NA—	NA		
gi-313872443-gb-AELG01009190.1-87	—NA—	NA		—NA—	NA		
gi-313872523-gb-AELG01009110.1-282	—NA—	NA		isoform A	7.50E-16	CG3609	
gi-313872532-gb-AELG01009101.1-398	—NA—	NA		—NA—	NA		
gi-313872746-gb-AELG01008887.1-369	—NA—	NA		CG30069	1.80E-119	CG30069	wing disc development
gi-313872746-gb-AELG01008887.1-384	—NA—	NA		CG30069	1.80E-119	CG30069	wing disc development
gi-313872756-gb-AELG01008877.1-280	—NA—	NA		—NA—	NA		
gi-313872756-gb-AELG01008877.1-389	—NA—	NA		—NA—	NA		
gi-313872756-gb-AELG01008877.1-556	—NA—	NA		—NA—	NA		
gi-313872764-gb-AELG01008869.1-271	—NA—	NA		ORF	2.00E-06		
gi-313872764-gb-AELG01008869.1-54	—NA—	NA		ORF	2.00E-06		
gi-313872821-gb-AELG01008812.1-662	—NA—	NA		—NA—	NA		
gi-313872821-gb-AELG01008812.1-664	—NA—	NA		—NA—	NA		
gi-313872821-gb-AELG01008812.1-703	—NA—	NA		—NA—	NA		
gi-313872821-gb-AELG01008812.1-704	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313872821-gb-AELG01008812.1-724	—NA—	NA		—NA—	NA		
gi-313872830-gb-AELG01008803.1-614	—NA—	NA		—NA—	NA		
gi-313872833-gb-AELG01008800.1-178	—NA—	NA		—NA—	NA		
gi-313872833-gb-AELG01008800.1-188	—NA—	NA		—NA—	NA		
gi-313872965-gb-AELG01008668.1-400	—NA—	NA		—NA—	NA		
gi-313872965-gb-AELG01008668.1-463	—NA—	NA		—NA—	NA		
gi-313872965-gb-AELG01008668.1-659	—NA—	NA		—NA—	NA		
gi-313872965-gb-AELG01008668.1-674	—NA—	NA		—NA—	NA		
gi-313872965-gb-AELG01008668.1-707	—NA—	NA		—NA—	NA		
gi-313873064-gb-AELG01008569.1-1006	—NA—	NA		—NA—	NA		
gi-313873122-gb-AELG01008511.1-483	—NA—	NA		—NA—	NA		
gi-313873153-gb-AELG01008480.1-174	—NA—	NA		isoform A	0.00067		
gi-313873153-gb-AELG01008480.1-281	—NA—	NA		isoform A	0.00067		
gi-313873153-gb-AELG01008480.1-461	—NA—	NA		isoform A	0.00067		
gi-313873153-gb-AELG01008480.1-463	—NA—	NA		isoform A	0.00067		
gi-313873153-gb-AELG01008480.1-50	—NA—	NA		isoform A	0.00067		
gi-313873153-gb-AELG01008480.1-582	—NA—	NA		isoform A	0.00067		
gi-313873243-gb-AELG01008390.1-512	—NA—	NA		cytochrome c oxidase subunit I	5.60E-35		
gi-313873268-gb-AELG01008365.1-275	—NA—	NA		SD06427p	8.70E-114		
gi-313873268-gb-AELG01008365.1-378	—NA—	NA		SD06427p	8.70E-114		
gi-313873298-gb-AELG01008335.1-1001	—NA—	NA		—NA—	NA		
gi-313873298-gb-AELG01008335.1-659	—NA—	NA		—NA—	NA		
gi-313873307-gb-AELG01008326.1-65	—NA—	NA		—NA—	NA		
gi-313873342-gb-AELG01008291.1-477	—NA—	NA		—NA—	NA		
gi-313873425-gb-AELG01008208.1-456	—NA—	NA		—NA—	NA		
gi-313873426-gb-AELG01008207.1-375	—NA—	NA		RE17942p	6.50E-09		
gi-313873426-gb-AELG01008207.1-437	—NA—	NA		RE17942p	6.50E-09		
gi-313873426-gb-AELG01008207.1-450	—NA—	NA		RE17942p	6.50E-09		
gi-313873426-gb-AELG01008207.1-465	—NA—	NA		RE17942p	6.50E-09		
gi-313873470-gb-AELG01008163.1-161	—NA—	NA		—NA—	NA		
gi-313873470-gb-AELG01008163.1-171	—NA—	NA		—NA—	NA		
gi-313873532-gb-AELG01008101.1-65	—NA—	NA		—NA—	NA		
gi-313873532-gb-AELG01008101.1-68	—NA—	NA		—NA—	NA		
gi-313873534-gb-AELG01008099.1-114	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313873534-gb-AELG01008099.1-136	—NA—	NA		—NA—	NA		
gi-313873534-gb-AELG01008099.1-365	—NA—	NA		—NA—	NA		
gi-313873599-gb-AELG01008034.1-131	—NA—	NA		S685261pol poly	4.50E-05		
gi-313873681-gb-AELG01007952.1-779	—NA—	NA		—NA—	NA		
gi-313873693-gb-AELG01007940.1-247	—NA—	NA		GM07634p	3.50E-14		
gi-313873693-gb-AELG01007940.1-324	—NA—	NA		GM07634p	3.50E-14		
gi-313873693-gb-AELG01007940.1-347	—NA—	NA		GM07634p	3.50E-14		
gi-313873697-gb-AELG01007936.1-178	—NA—	NA		—NA—	NA		
gi-313873697-gb-AELG01007936.1-258	—NA—	NA		—NA—	NA		
gi-313873751-gb-AELG01007882.1-254	—NA—	NA		—NA—	NA		
gi-313873785-gb-AELG01007848.1-123	—NA—	NA		isoform A	1.30E-18		
gi-313873785-gb-AELG01007848.1-176	—NA—	NA		isoform A	1.30E-18		
gi-313873785-gb-AELG01007848.1-288	—NA—	NA		isoform A	1.30E-18		
gi-313873790-gb-AELG01007843.1-247	—NA—	NA		—NA—	NA		
gi-313873813-gb-AELG01007820.1-1307	—NA—	NA		ribosomal S6	4.60E-52	RpS6	cytosolic small ribosomal subunit structural constituent of ribosome mitotic spindle elongation rRNA processing translation immune response ribosomal small subunit biogenesis centrosome duplication
gi-313873813-gb-AELG01007820.1-1369	—NA—	NA		ribosomal S6	1.80E-51	RpS6	cytosolic small ribosomal subunit structural constituent of ribosome mitotic spindle elongation rRNA processing translation immune response ribosomal small subunit biogenesis centrosome duplication
gi-313873987-gb-AELG01007646.1-265	—NA—	NA		—NA—	NA		
gi-313873987-gb-AELG01007646.1-291	—NA—	NA		—NA—	NA		
gi-313873987-gb-AELG01007646.1-294	—NA—	NA		—NA—	NA		
gi-313874243-gb-AELG01007390.1-168	—NA—	NA		—NA—	NA		
gi-313874243-gb-AELG01007390.1-188	—NA—	NA		—NA—	NA		
gi-313874243-gb-AELG01007390.1-457	—NA—	NA		—NA—	NA		
gi-313874739-gb-AELG01006894.1-427	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313874834-gb-AELG01006799.1-236	—NA—	NA		coat (coatomer) isoform A	4.80E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874834-gb-AELG01006799.1-259	—NA—	NA		coat (coatomer) isoform A	4.80E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874834-gb-AELG01006799.1-263	—NA—	NA		coat (coatomer) isoform A	4.80E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874834-gb-AELG01006799.1-307	—NA—	NA		coat (coatomer) isoform A	3.20E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874834-gb-AELG01006799.1-381	—NA—	NA		coat (coatomer) isoform A	3.20E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313874834-gb-AELG01006799.1-462	—NA—	NA		coat (coatomer) isoform A	3.20E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874834-gb-AELG01006799.1-467	—NA—	NA		coat (coatomer) isoform A	3.20E-180	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874835-gb-AELG01006798.1-686	—NA—	NA		coat (coatomer) isoform A	1.10E-124	alphaCOP	COPI vesicle coat structural molecule activity intracellular protein transport retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi-313874970-gb-AELG01006663.1-308	Bombus terrestris WD repeat-containing 36-like (LOC105667016) partial mRNA	3.70E-20	XM012320063	SD06427p	1.60E-26		
gi-313875037-gb-AELG01006596.1-171	—NA—	NA		—NA—	NA		
gi-313875037-gb-AELG01006596.1-242	Bombus terrestris uncharacterized LOC105667086 (LOC105667086) partial mRNA	3.70E-20	XM012320152	—NA—	NA		
gi-313875037-gb-AELG01006596.1-284	—NA—	NA		—NA—	NA		
gi-313875037-gb-AELG01006596.1-447	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313875048-gb-AELG01006585.1-606	--NA--	NA		POL4DROME ame: Full=Retrovirus-related Pol poly from transposon 412 In- cludes: ame: Full=Protease Includes: ame: Full=Reverse transcriptase Includes: ame: Full=Endonuclease	1.30E-08		
gi-313875048-gb-AELG01006585.1-647	--NA--	NA		POL4DROME ame: Full=Retrovirus-related Pol poly from transposon 412 In- cludes: ame: Full=Protease Includes: ame: Full=Reverse transcriptase Includes: ame: Full=Endonuclease	1.30E-08		
gi-313875174-gb-AELG01006459.1-1238	--NA--	NA		blastopia poly	4.30E-08		
gi-313875220-gb-AELG01006413.1-132	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-137	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-24	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-301	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-358	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-371	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-390	--NA--	NA		--NA--	NA		
gi-313875220-gb-AELG01006413.1-490	--NA--	NA		--NA--	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			Sequence Description	De-	blastx (<i>Drosophila melanogaster</i>)		
	e Value	Accession Number	e Value			Gene Name	GO Names	
gi-313875220-gb-AELG01006413.1-506	—NA—	NA		—NA—	NA			
gi-313875220-gb-AELG01006413.1-510	—NA—	NA		—NA—	NA			
gi-313875220-gb-AELG01006413.1-52	—NA—	NA		—NA—	NA			
gi-313875220-gb-AELG01006413.1-70	—NA—	NA		—NA—	NA			
gi-313875286-gb-AELG01006347.1-1092	—NA—	NA		—NA—	NA			
gi-313875286-gb-AELG01006347.1-1216	—NA—	NA		—NA—	NA			
gi-313875286-gb-AELG01006347.1-382	—NA—	NA		—NA—	NA			
gi-313875286-gb-AELG01006347.1-793	—NA—	NA		—NA—	NA			
gi-313875286-gb-AELG01006347.1-863	Bombus terrestris uncharacterized LOC100648349 (LOC100648349) ncRNA	2.20E-12	XR001099695	—NA—	NA			
gi-313875358-gb-AELG01006275.1-1541	—NA—	NA		—NA—	NA			
gi-313875358-gb-AELG01006275.1-1566	—NA—	NA		—NA—	NA			
gi-313875358-gb-AELG01006275.1-1680	—NA—	NA		—NA—	NA			
gi-313875358-gb-AELG01006275.1-1810	—NA—	NA		—NA—	NA			
gi-313875358-gb-AELG01006275.1-1870	—NA—	NA		—NA—	NA			
gi-313875358-gb-AELG01006275.1-1936	—NA—	NA		—NA—	NA			
gi-313875379-gb-AELG01006254.1-88191	Bombus terrestris uncharacterized LOC100645500 (LOC100645500) mRNA	3.70E-20	XM003400232	—NA—	NA			
gi-313875379-gb-AELG01006254.1-88251	Bombus terrestris uncharacterized LOC100645500 (LOC100645500) mRNA	3.70E-20	XM003400232	—NA—	NA			
gi-313875379-gb-AELG01006254.1-92029	Bombus terrestris uncharacterized LOC100645500 (LOC100645500) mRNA	3.70E-20	XM003400232	isoform B	1.90E-23	CG43896		
gi-313875395-gb-AELG01006238.1-70589	Bombus terrestris histidine triad nucleotide-binding 1 (LOC105666409) mRNA	3.70E-20	XM012315624	isoform A	1.80E-42	DsimGD23182 CG2862 DsecGM18366	nucleotidase activity metabolic process	
gi-313875419-gb-AELG01006214.1-14657	—NA—	NA		—NA—	NA			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313875441—gb—AELG01006192.1—60050	—NA—	NA		C6A21DROME ame: Full=Probable cytochrome P450 6a21 ame: Full=CYPVIA21	9.80E-33	Cyp6a21	
gi—313875441—gb—AELG01006192.1—62086	Bombus terrestris uncharacterized LOC100647549 (LOC100647549) mRNA	3.70E-20	XM003400081	C6A21DROME ame: Full=Probable cytochrome P450 6a21 ame: Full=CYPVIA21	9.80E-33	Cyp6a21	
gi—313875441—gb—AELG01006192.1—65443	Bombus terrestris cytochrome P450 6a2-like (LOC100647785) transcript variant mRNA	3.70E-20	XM012315470	C6A13DROME ame: Full=Probable cytochrome P450 6a13 ame: Full=CYPVIA13	1.30E-48	Cyp6a13	
gi—313875441—gb—AELG01006192.1—65462	Bombus terrestris cytochrome P450 6a2-like (LOC100647785) transcript variant mRNA	3.70E-20	XM012315470	C6A13DROME ame: Full=Probable cytochrome P450 6a13 ame: Full=CYPVIA13	1.30E-48	Cyp6a13	
gi—313875446—gb—AELG01006187.1—49672	—NA—	NA		microsomal triacylglycerol transfer	1.50E-84	Mtp	cell part anatomical structure morphogenesis primary metabolic process neuron development organic substance metabolic process
gi—313875749—gb—AELG01005885.1—174056	Bombus terrestris transmembrane protease serine 9-like (LOC100644694) mRNA	3.70E-20	XM003400059	CG3108	7.20E-30	CG3108	metallocarboxypeptidase activity
gi—313875780—gb—AELG01005854.1—59809	Bombus terrestris probable chitinase 2 (LOC100649426) mRNA	1.70E-13	XM003400589	chitinase isoform A	6.80E-77	Cht2	chitinase activity cuticle chitin catabolic process

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313875780—gb—AELG01005854.1—61684	—NA—	NA		chitinase isoform A	6.80E-77	Cht2	chitinase activity cuticle chitin catabolic process
gi—313875780—gb—AELG01005854.1—61687	Bombus terrestris probable chitinase 2 (LOC100649426) mRNA	2.90E-11	XM003400589	chitinase isoform A	6.80E-77	Cht2	chitinase activity cuticle chitin catabolic process
gi—313875837—gb—AELG01005798.1—43628	—NA—	NA		cytochrome b isoform K	9.40E-21		
gi—313875864—gb—AELG01005771.1—62391	—NA—	NA			8.00E-42	Moe	nucleus actin filament adherens junction cell cortex apical plasma membrane extrinsic component of membrane cleavage furrow subapical complex fusome mitotic spindle midzone actin binding phosphatidylinositol-4,5-bisphosphate binding establishment of mitotic spindle orientation assembly of actomyosin apparatus involved in cytokinesis mitotic spindle organization metaphase/anaphase transition of mitotic cell cycle pole plasm protein localization determination of left/right symmetry positive regulation of cell proliferation regulation of membrane potential in photoreceptor cell establishment or maintenance of polarity of larval imaginal disc epithelium cortical actin cytoskeleton organization regulation of actin cytoskeleton organization lumen formation, open tracheal system olfactory behavior establishment or maintenance of epithelial cell apical/basal polarity rhabdomere membrane biogenesis male courtship behavior, veined wing generated song production positive regulation of endocytosis photoreceptor cell axon guidance
gi—313875889—gb—AELG01005747.1—11235	—NA—	NA		IP21982p	2.10E-24		
gi—313875889—gb—AELG01005747.1—11467	—NA—	NA		IP21982p	2.10E-24		
gi—313875889—gb—AELG01005747.1—11953	—NA—	NA		IP21982p	2.10E-24		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313875889—gb—AELG01005747.1—9399	Bombus terrestris antichymotrypsin-2-like (LOC100648602) mRNA	3.70E-20	XM003399139	IP21982p	2.10E-24			
gi—313875889—gb—AELG01005747.1—9525	Bombus terrestris antichymotrypsin-2-like (LOC100648602) mRNA	3.70E-20	XM003399139	IP21982p	2.10E-24			
gi—313875889—gb—AELG01005747.1—9979	Bombus terrestris antichymotrypsin-2-like (LOC100648602) mRNA	2.20E-12	XM003399139	IP21982p	2.10E-24			
gi—313875890—gb—AELG01005746.1—117654	—NA—	NA		serpin isoform F	7.00E-26	Spn42Da	negative regulation of proteolysis	
gi—313875890—gb—AELG01005746.1—117695	—NA—	NA		serpin isoform F	7.00E-26	Spn42Da	negative regulation of proteolysis	
gi—313875937—gb—AELG01005699.1—19592	Bombus terrestris glyoxylate reductase hydroxypyruvate reductase (LOC100647868) mRNA	3.70E-20	XM003398972	CG1236- partial	1.10E-86	CG1236		
gi—313875946—gb—AELG01005690.1—55843	—NA—	NA		blastopia poly	0.00016			
gi—313876055—gb—AELG01005582.1—941	—NA—	NA		AF2455151 Ran binding 11	1.50E-15	Ranbp11		
gi—313876055—gb—AELG01005582.1—978	—NA—	NA		AF2455151 Ran binding 11	1.60E-15	Ranbp11		
gi—313876056—gb—AELG01005581.1—1162	Bombus terrestris 40S ribosomal S6-like (LOC100646070) mRNA	3.70E-20	XM003399038	ribosomal S6	3.80E-31	RpS6	cytosolic small ribosomal subunit structural constituent of ribosome mitotic spindle elongation rRNA processing translation immune response ribosomal small subunit biogenesis centrosome duplication	
gi—313876082—gb—AELG01005556.1—1187	Bombus terrestris mediator of RNA polymerase II transcription subunit 9 (LOC100649043) mRNA	3.70E-20	XM003403195	ribosomal isoform C	7.90E-115	RpL10	cytosolic large ribosomal subunit neuronal cell body structural constituent of ribosome mitotic spindle elongation translation sensory perception of pain centrosome duplication	
gi—313876082—gb—AELG01005556.1—3642	Bombus terrestris 60S ribosomal L10 (LOC100649244) mRNA	3.70E-20	XM012319839	ribosomal isoform C	1.70E-116	RpL10	cytosolic large ribosomal subunit neuronal cell body structural constituent of ribosome mitotic spindle elongation translation sensory perception of pain centrosome duplication	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313876127—gb—AELG01005512.1—419	—NA—	NA		AT25468p	3.90E-07		
gi—313876178—gb—AELG01005462.1—194	—NA—	NA		CG10206	5.30E-13		
gi—313876178—gb—AELG01005462.1—228	—NA—	NA		CG10206	5.30E-13		
gi—313876178—gb—AELG01005462.1—69	—NA—	NA		CG10206	5.30E-13		
gi—313876203—gb—AELG01005438.1—1283	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi—313876203—gb—AELG01005438.1—1335	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi—313876203—gb—AELG01005438.1—1338	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi—313876203—gb—AELG01005438.1—1440	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi—313876203—gb—AELG01005438.1—1457	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis
gi—313876203—gb—AELG01005438.1—1532	Bombus terrestris coatamer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatamer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313876203—gb—AELG01005438.1—201	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—355	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—363	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—433	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—477	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—540	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—720	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313876203—gb—AELG01005438.1—846	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876203—gb—AELG01005438.1—987	Bombus terrestris coatomer subunit alpha-like (LOC100648009) partial mRNA	3.70E-20	XM003393962	coat (coatomer) isoform A	0	alphaCOP	COPI vesicle coat retrograde vesicle-mediated transport, Golgi to ER phagocytosis male meiosis cytokinesis regulation of lipid storage neuron projection morphogenesis	
gi—313876208—gb—AELG01005433.1—48729	Bombus terrestris plastin-2 (LOC100649047) transcript variant mRNA	3.70E-20	XM003393891	isoform C	1.80E-22	Fim	cytosol apical cortex contractile ring actin binding calcium ion binding female meiosis chromosome segregation	
gi—313876208—gb—AELG01005433.1—48734	Bombus terrestris plastin-2 (LOC100649047) transcript variant mRNA	3.70E-20	XM003393891	isoform C	1.80E-22	Fim	cytosol apical cortex contractile ring actin binding calcium ion binding female meiosis chromosome segregation	
gi—313876211—gb—AELG01005430.1—69270	Bombus terrestris FAM98B (LOC100647606) mRNA	6.20E-18	XM012320234	CG5913	2.10E-16	CG5913		
gi—313876215—gb—AELG01005426.1—24722	Bombus terrestris lethal(2)essential for life-like (LOC105667090) mRNA	3.70E-20	XM012320215	GM22862p	5.10E-17			
gi—313876244—gb—AELG01005398.1—45480	Bombus terrestris cytochrome P450 9e2-like (LOC100649760) mRNA	3.70E-20	XM003393817	C28D1DROME ame: Full=Probable cytochrome P450 28d1 ame: Full=CYPXXVIII D1	4.40E-72	Cyp28d1		
gi—313876244—gb—AELG01005398.1—45515	Bombus terrestris cytochrome P450 9e2-like (LOC100649760) mRNA	3.70E-20	XM003393817	C28D1DROME ame: Full=Probable cytochrome P450 28d1 ame: Full=CYPXXVIII D1	4.40E-72	Cyp28d1		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313876244—gb—AELG01005398.1—45948	Bombus terrestris cytochrome P450 9e2-like (LOC100649760) mRNA	3.70E-20	XM003393817	C28D1DROME ame: Full=Probable cytochrome P450 28d1 ame: Full=CYPXXVIII D1	4.40E-72	Cyp28d1	
gi—313876244—gb—AELG01005398.1—45990	Bombus terrestris cytochrome P450 9e2-like (LOC100649760) mRNA	3.70E-20	XM003393817	C28D1DROME ame: Full=Probable cytochrome P450 28d1 ame: Full=CYPXXVIII D1	4.40E-72	Cyp28d1	
gi—313876273—gb—AELG01005370.1—682	—NA—	NA		—NA—	NA		
gi—313876329—gb—AELG01005316.1—38854	Bombus terrestris TAR DNA-binding 43 (LOC100646812) transcript variant mRNA	3.70E-20	XM012319677	TAR DNA-binding isoform A	3.20E-42	TBPH	nucleus H zone perinuclear region of cytoplasm nucleotide binding single-stranded DNA binding mRNA binding GU repeat RNA binding neuromuscular synaptic transmission synapse assembly central nervous system development neuromuscular junction development adult walking behavior larval locomotory behavior regulation of glucose metabolic process negative regulation of RNA splicing regulation of intracellular steroid hormone receptor signaling pathway negative regulation of neuron apoptotic process negative regulation of synaptic growth at neuromuscular junction neuron projection morphogenesis regulation of microtubule cytoskeleton organization terminal button organization positive regulation of dendrite development regulation of terminal button organization

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313876452-gb-AELG01005195.1-55	PREDICTED: Bombus terrestris uncharacterized protein DDBG0271670-like (LOC100643897), transcript variant X2, mRNA	3.70E-20	XM012312314	—NA—	NA			
gi-313876453-gb-AELG01005194.1-101991	PREDICTED: Bombus terrestris uncharacterized protein DDBG0271670-like (LOC100643897), transcript variant X2, mRNA	3.70E-20	XM012312314	—NA—	NA			
gi-313876453-gb-AELG01005194.1-41432	Bombus terrestris beta-glucuronidase-like (LOC100649299) transcript variant mRNA	3.70E-20	XM012312311	—NA—	NA			
gi-313876456-gb-AELG01005191.1-9233	—NA—	NA		RE27528p	5.40E-127			
gi-313876464-gb-AELG01005183.1-38721	Bombus terrestris paternally-expressed gene 3-like (LOC100648252) mRNA	3.70E-20	XM012312274	CG6209	4.10E-08	CG6209	spliceosomal complex	
gi-313876477-gb-AELG01005171.1-15662	—NA—	NA		adaptor complex mu subunit	0	DanaGF16536 DsecGM26246 DyakGE24766 AP-1mu DereGG17361 DsimGD20786	synaptic vesicle AP-1 adaptor complex AP1 complex protein transporter activity clathrin binding intracellular protein transport neurotransmitter secretion synaptic vesicle coating sensory perception of pain secretory granule organization negative regulation of Notch signaling pathway compound eye development negative regulation of endocytic recycling	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313876502—gb—AELG01005146.1—50332	Bombus terrestris cytochrome b5-like (LOC100648100) mRNA	3.70E-20	XM003397757	Cyt-b5-PB	2.40E-22	Cyt-b5	lipid particle endomembrane system membrane intracellular membrane-bounded organelle electron carrier activity instar larval development regulation of hemocyte proliferation regulation of hemocyte differentiation regulation of cell cycle	
gi—313876508—gb—AELG01005141.1—1449	Bombus terrestris beta-hexosaminidase subunit beta-like (LOC100649144) mRNA	3.70E-20	XM003397767	hexosaminidase isoform D	1.30E-28	Hexo1	beta-N-acetylhexosaminidase activity cellular protein modification process cellular biosynthetic process single-organism metabolic process single-organism cellular process	
gi—313876546—gb—AELG01005104.1—17531	Bombus terrestris uncharacterized LOC105666664 (LOC105666664) ncRNA	1.70E-18	XR001099483	—NA—	NA			
gi—313876677—gb—AELG01004975.1—40184	Bombus terrestris 23 kDa integral membrane (LOC100651241) transcript variant mRNA	3.70E-20	XM012321065	tetraspanin isoform A	5.60E-21	Tsp2A	integral component of membrane	
gi—313876688—gb—AELG01004965.1—40087	—NA—	NA		isoform A	1.80E-58	CG11665		
gi—313876795—gb—AELG01004861.1—18645	—NA—	NA		casein kinase I	6.40E-64			
gi—313876800—gb—AELG01004856.1—8110	Bombus terrestris uncharacterized LOC100646603 (LOC100646603) transcript variant mRNA	3.70E-20	XM003400974	—NA—	NA			
gi—313876804—gb—AELG01004852.1—79106	—NA—	NA		IP22030p	6.70E-12			
gi—313876879—gb—AELG01004779.1—22270	Bombus terrestris 28S ribosomal mitochondrial (LOC100646266) mRNA	3.70E-20	XM003398561	FI17103p1	3.20E-26			
gi—313876950—gb—AELG01004710.1—7697	—NA—	NA		endonuclease reverse transcriptase	8.80E-28			
gi—313876950—gb—AELG01004710.1—7911	—NA—	NA		endonuclease reverse transcriptase	2.50E-11			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313876950—gb—AELG01004710.1—7990	—NA—	NA		endonuclease	2.50E-11		
gi—313876950—gb—AELG01004710.1—8086	—NA—	NA		reverse transcriptase POLRDROME ame: Full=Retrovirus-related Pol poly from type-2 retrotransposable element R2DM ame: Full=Retrovirus-related Pol poly from type II retrotransposable element R2DM Includes: ame: Full=Protease Includes: ame: Full=Reverse transcriptase Includes: ame: Full=Endonuclease	4.20E-24		
gi—313876962—gb—AELG01004698.1—2132	—NA—	NA		—NA—	NA		
gi—313876962—gb—AELG01004698.1—3154	—NA—	NA		—NA—	NA		
gi—313876972—gb—AELG01004688.1—117833	Bombus terrestris mesh-like (LOC100644963) transcript variant mRNA	3.70E-20	XM012309299	isoform A	2.40E-43	mesh	smooth septate junction smooth septate junction assembly
gi—313876977—gb—AELG01004683.1—60735	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	IP13189p	4.60E-11		
gi—313876977—gb—AELG01004683.1—60836	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	IP13189p	4.60E-11		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313876977—gb—AELG01004683.1—60885	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	IP13189p	4.60E-11			
gi—313876977—gb—AELG01004683.1—66070	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	maltase isoform A	2.40E-23	Mal-B2	alpha-1,4-glucosidase activity	
gi—313876977—gb—AELG01004683.1—66072	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	maltase isoform A	2.40E-23	Mal-B2	alpha-1,4-glucosidase activity	
gi—313876977—gb—AELG01004683.1—66082	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	maltase isoform A	2.40E-23	Mal-B2	alpha-1,4-glucosidase activity	
gi—313876977—gb—AELG01004683.1—69420	Bombus terrestris maltase 1-like (LOC100643731) mRNA	3.70E-20	XM003395866	—NA—	NA			
gi—313877008—gb—AELG01004652.1—27079	Bombus terrestris uncharacterized LOC105665828 (LOC105665828) mRNA	3.70E-20	XM012309330	pol protein	2.00E-77			
gi—313877044—gb—AELG01004617.1—69648	—NA—	NA		RH65810p	4.20E-117			
gi—313877174—gb—AELG01004493.1—554	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	9.80E-06	CG4096		
gi—313877174—gb—AELG01004493.1—585	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	9.90E-06	CG4096		
gi—313877174—gb—AELG01004493.1—586	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	9.90E-06	CG4096		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313877174-gb-AELG01004493.1-589	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	9.90E-06	CG4096		
gi-313877174-gb-AELG01004493.1-596	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	9.90E-06	CG4096		
gi-313877174-gb-AELG01004493.1-608	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	1.00E-05	CG4096		
gi-313877174-gb-AELG01004493.1-635	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	1.00E-05	CG4096		
gi-313877174-gb-AELG01004493.1-685	Bombus terrestris A disintegrin and metalloase with thrombospondin motifs 14-like (LOC100642399) mRNA	3.70E-20	XM012320873	isoform C	1.00E-05	CG4096		
gi-313877174-gb-AELG01004493.1-725	—NA—	NA		isoform C	1.00E-05	CG4096		
gi-313877345-gb-AELG01004380.1-25064	Bombus terrestris uncharacterized LOC100647282 (LOC100647282) transcript variant mRNA	3.70E-20	XM012319462	—NA—	NA			
gi-313877374-gb-AELG01004351.1-258120	Bombus terrestris quinone oxidoreductase (LOC100648892) transcript variant mRNA	3.70E-20	XM003393265	CG1600-PA	5.00E-53			
gi-313877399-gb-AELG01004329.1-68002	—NA—	NA		CG10725	3.90E-06	CG10725		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313877399—gb—AELG01004329.1—85149	Bombus terrestris peritrophin-1-like (LOC100642795) mRNA	3.70E-20	XM003393292	chitin deacetylase-like isoform H	0.00049	Cda5		
gi—313877404—gb—AELG01004324.1—2267	Bombus terrestris polyubiquitin-like (LOC100643517) mRNA	3.70E-20	XM003393298	ubiquitin	1.40E-86			
gi—313877404—gb—AELG01004324.1—2271	Bombus terrestris polyubiquitin-like (LOC100643517) mRNA	3.70E-20	XM003393298	ubiquitin	1.40E-86			
gi—313877404—gb—AELG01004324.1—2272	Bombus terrestris polyubiquitin-like (LOC100643517) mRNA	3.70E-20	XM003393298	ubiquitin	1.40E-86			
gi—313877404—gb—AELG01004324.1—2321	Bombus terrestris polyubiquitin-like (LOC100643517) mRNA	3.70E-20	XM003393298	ubiquitin	1.40E-86			
gi—313877404—gb—AELG01004324.1—2495	Bombus terrestris ubiquitin-like (LOC105667029) mRNA	3.70E-20	XM012320078	ubiquitin	1.50E-86			
gi—313877476—gb—AELG01004268.1—396	—NA—	NA		—NA—	NA			
gi—313877481—gb—AELG01004263.1—1636	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC105666889) mRNA	3.70E-20	XM012319453	UMP synthase r-l gene product	1.90E-48			
gi—313877481—gb—AELG01004263.1—1826	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC105666889) mRNA	3.70E-20	XM012319453	UMP synthase r-l gene product	1.90E-48			
gi—313877481—gb—AELG01004263.1—2291	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC105666889) mRNA	3.70E-20	XM012319453	UMP synthase r-l gene product	1.90E-48			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313877481-gb-AELG01004263.1-2313	Bombus terrestris uridine 5-monophosphate synthase-like (LOC105666889) mRNA	3.70E-20	XM012319453	UMP synthase r-l gene product	1.90E-48		
gi-313877517-gb-AELG01004237.1-128	—NA—	NA		—NA—	NA		
gi-313877517-gb-AELG01004237.1-142	—NA—	NA		—NA—	NA		
gi-313877517-gb-AELG01004237.1-146	—NA—	NA		—NA—	NA		
gi-313877519-gb-AELG01004235.1-3628	—NA—	NA		cytochrome c oxidase subunit partial (mitochondrion)	1.10E-34		
gi-313877519-gb-AELG01004235.1-3649	—NA—	NA		cytochrome c oxidase subunit partial (mitochondrion)	1.10E-34		
gi-313877522-gb-AELG01004232.1-85	—NA—	NA		gag-pol poly precursor	1.00E-19		
gi-313877523-gb-AELG01004231.1-68397	Bombus terrestris uncharacterized LOC105667159 (LOC105667159) ncRNA	3.70E-20	XR001099774	GH20809p	6.10E-05		
gi-313877523-gb-AELG01004231.1-68410	Bombus terrestris uncharacterized LOC105667159 (LOC105667159) ncRNA	4.80E-14	XR001099774	GH20809p	6.00E-05		
gi-313877530-gb-AELG01004224.1-366	—NA—	NA		unnamed protein product	3.90E-69		
gi-313877537-gb-AELG01004217.1-26928	Bombus terrestris uncharacterized LOC100647524 (LOC100647524) mRNA	3.70E-20	XM003402873	CG6475	1.20E-29	CG6475	
gi-313877561-gb-AELG01004195.1-10831	Bombus terrestris heat shock beta-1 (LOC100644627) transcript variant mRNA	3.70E-20	XM012319358	isoform C	3.00E-29	CG14207	nucleoplasm cytosol Z disc protein lipidation regulation of autophagy regulation of translational initiation by eIF2 alpha phosphorylation
gi-313877579-gb-AELG01004177.1-1334	—NA—	NA		—NA—	NA		
gi-313877579-gb-AELG01004177.1-1513	—NA—	NA		—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313877579-gb-AELG01004177.1-1558	—NA—	NA		—NA—	NA		
gi-313877581-gb-AELG01004175.1-12919	—NA—	NA		POL5DROME	5.50E-51		
				ame: Full=Retrovirus-related Pol poly from transposon opus Includes: ame: Full=Protease Includes: ame: Full=Reverse transcriptase Includes: ame: Full=Endonuclease			
gi-313877585-gb-AELG01004171.1-766	—NA—	NA		SD02026p	5.00E-55		
gi-313877613-gb-AELG01004149.1-114040	—NA—	NA		lethal (3) 72Dp	3.10E-55	1(3)72Dp	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313878101-gb-AELG01004076.1-14530	Bombus terrestris actin-5C (LOC100646910) transcript variant mRNA	3.70E-20	XM003396942	actin-5C	0	DgriGH24372 DereGG18797 D0PTT4 AAEL011197 L79806755 X77703096 Q201U9 CpipJCPIJ009886 DperGL14888 ACT5CANOGA actA3b ACTB2 A4 G5I04156 KGM13185 DwilGK20124 DsimGD16764 Q5XUC4 E3UKI0 I4DLZ5 ACT1 I4DIX7 Act5C EAG04690 DvirGJ14747 S5M4E2 TcasGA2TC006296 D8WKR5 Dmo- jGI15312 EAI13843 Act DyakAct57B DsecGM12447 Act57B DpseGA17886	cytoplasm lipid particle microtubule associated complex actin filament Ino80 complex brahma complex structural constituent of cytoskeleton ATP binding mitotic cytokinesis inter-male aggressive behavior chromatin remodeling phagocytosis cytoskeleton organization sperm individualization mushroom body development maintenance of protein localization in cell tube formation

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313878101-gb-AELG01004076.1-14551	Bombus terrestris actin-5C (LOC100646910) transcript variant mRNA	3.70E-20	XM003396942	actin-5C	0	DgriGH24372 DereGG18797 D0PTT4 AAEL011197 L79806755 X77703096 Q201U9 CpipJCPIJ009886 DperGL14888 ACT5CANOGA actA3b ACTB2 A4 G5I04156 KGM13185 DwilGK20124 DsimGD16764 Q5XUC4 E3UKI0 I4DLZ5 ACT1 I4DIX7 Act5C EAG04690 DvirGJ14747 S5M4E2 TcasGA2TC006296 D8WKR5 Dmo- jGI15312 EAI13843 Act DyakAct57B DsecGM12447 Act57B DpseGA17886	cytoplasm lipid particle microtubule associated complex actin filament Ino80 complex brahma complex structural constituent of cytoskeleton ATP binding mitotic cytokinesis inter-male aggressive behavior chromatin remodeling phagocytosis cytoskeleton organization sperm individualization mushroom body development maintenance of protein localization in cell tube formation	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313878147-gb-AELG01004031.1-2577	—NA—	NA		Cht8	1.40E-105	Cht8	
gi-313878234-gb-AELG01003947.1-382	Bombus terrestris G12-like (LOC100646525) mRNA	8.00E-17	XM003402944	—NA—	NA		
gi-313878236-gb-AELG01003945.1-101936	Bombus terrestris Krueppel-like factor 6 (LOC100650325) transcript variant mRNA	3.70E-20	XM012310504	isoform B	1.40E-31	luna	nucleus transcription factor activity, sequence-specific DNA binding sequence-specific DNA binding metal ion binding mitotic sister chromatid segregation regulation of transcription, DNA-templated preblastoderm mitotic cell cycle
gi-313878284-gb-AELG01003900.1-124954	Bombus terrestris CCR4-NOT transcription complex subunit 1 (LOC100642693) transcript variant mRNA	3.70E-20	XM012310292	isoform E	0	Not1	cytoplasm CCR4-NOT complex poly(A)-specific ribonuclease activity protein binding nuclear-transcribed mRNA poly(A) tail shortening mitotic G2 DNA damage checkpoint muscle organ development negative regulation of translation ovarian follicle cell development dendrite morphogenesis
gi-313878351-gb-AELG01003835.1-1600	—NA—	NA		—NA—	NA		
gi-313878390-gb-AELG01003797.1-53577	—NA—	NA		AChain Crystal Structure Of Drice	4.90E-42		
gi-313878390-gb-AELG01003797.1-53582	—NA—	NA		AChain Crystal Structure Of Drice	4.90E-42		
gi-313878402-gb-AELG01003785.1-24622	—NA—	NA		glutathione transferase-related	6.90E-08		
gi-313878426-gb-AELG01003762.1-37	Bombus terrestris RNA polymerase-associated CTR9 homolog (LOC100643523) partial mRNA	3.70E-20	XM012308334	isoform B	8.70E-83	CG2469	transcriptionally active chromatin SH2 domain binding ventral cord development positive regulation of transcription from RNA polymerase II promoter

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313878426—gb—AELG01003762.1—57	Bombus terrestris RNA polymerase-associated CTR9 homolog (LOC100643523) partial mRNA	3.70E-20	XM012308334	isoform B	1.20E-85	CG2469	transcriptionally active chromatin SH2 domain binding ventral cord development positive regulation of transcription from RNA polymerase II promoter	
gi—313878427—gb—AELG01003761.1—31364	Bombus terrestris another transcription unit -like (LOC105665680) mRNA	3.70E-20	XM012308130	—NA—	NA			
gi—313878427—gb—AELG01003761.1—31410	Bombus terrestris another transcription unit -like (LOC105665680) mRNA	3.70E-20	XM012308130	—NA—	NA			
gi—313878436—gb—AELG01003752.1—45007	Bombus terrestris venom protease (LOC100652036) transcript variant mRNA	3.70E-20	XM012308123	isoform B	4.50E-16	CG1299		
gi—313878470—gb—AELG01003720.1—79934	Bombus terrestris ankyrin-3-like (LOC100642686) transcript variant miscRNA	3.70E-20	XR001098660	—NA—	NA			
gi—313878518—gb—AELG01003673.1—16142	—NA—	NA		—NA—	NA			
gi—313878527—gb—AELG01003664.1—212671	Bombus terrestris peptidylglycine alpha-hydroxylating monooxygenase (LOC100644842) mRNA	3.70E-20	XM003394976	Peptidylglycine-alpha-hydroxylating isoform A	8.40E-107			
gi—313878638—gb—AELG01003556.1—255	—NA—	NA		—NA—	NA			
gi—313878638—gb—AELG01003556.1—271	—NA—	NA		—NA—	NA			
gi—313878638—gb—AELG01003556.1—277	—NA—	NA		—NA—	NA			
gi—313878649—gb—AELG01003545.1—15557	Bombus terrestris nucleolar 58-like (LOC100645575) mRNA	3.70E-20	XM003400883	IP10959p	4.10E-17			
gi—313878676—gb—AELG01003518.1—723	—NA—	NA		CCHamide-2 isoform B	1.80E-14	CCHa2-R	integral component of membrane neuropeptide receptor activity neuropeptide signaling pathway	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313878701-gb-AELG01003494.1-33108	Bombus terrestris filamin-A (LOC100645301) transcript variant mRNA	3.70E-20	XM012315951	isoform B	0	cher	nucleus cytosol actin filament female germline ring canal outer rim female germline ring canal inner rim apical cortex perinuclear region of cytoplasm contractile ring actin filament binding mitotic nuclear division motor neuron axon guidance protein localization female germline ring canal formation, actin assembly determination of adult lifespan olfactory learning germarium-derived female germ-line cyst encapsulation negative regulation of lamellocyte differentiation behavioral response to ethanol
gi-313878701-gb-AELG01003494.1-61528	Bombus terrestris filamin-A (LOC100645301) transcript variant mRNA	3.70E-20	XM003400474	isoform N	9.90E-72	cher	nucleus cytosol actin filament female germline ring canal outer rim female germline ring canal inner rim apical cortex perinuclear region of cytoplasm contractile ring actin filament binding mitotic nuclear division motor neuron axon guidance protein localization female germline ring canal formation, actin assembly determination of adult lifespan olfactory learning germarium-derived female germ-line cyst encapsulation negative regulation of lamellocyte differentiation behavioral response to ethanol
gi-313878750-gb-AELG01003446.1-160495	Bombus terrestris chymotrypsin-2-like (LOC105665851) mRNA	3.70E-20	XM012309549	MIP24375p	4.50E-08		
gi-313878781-gb-AELG01003416.1-3571	Bombus terrestris torso (LOC100649534) transcript variant mRNA	3.70E-20	XM012309481	torso- isoform A	7.60E-56	tsl	extracellular region terminal region determination torso signaling pathway positive regulation of multicellular organism growth

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313878837-gb-AELG01003360.1-18216	Bombus terrestris transmembrane 131 (LOC100647499) transcript variant mRNA	3.70E-20	XM012309384	isoform A	1.10E-21	CG8370	endomembrane system
gi-313878855-gb-AELG01003342.1-9337	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-40	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-52	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-796	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-833	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-879	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-906	—NA—	NA		—NA—	NA		
gi-313878916-gb-AELG01003282.1-983	—NA—	NA		—NA—	NA		
gi-313878937-gb-AELG01003262.1-3560	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3660	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3751	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3769	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3806	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3840	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		
gi-313878937-gb-AELG01003262.1-3869	Bombus terrestris integumentary mucin -like (LOC105666821) mRNA	3.70E-20	XM012319029	—NA—	NA		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			Sequence Description	e Value	Accession Number	Sequence Description	blastx (<i>Drosophila melanogaster</i>)	
	Sequence Description	e Value	Accession Number					e Value	Gene Name
gi-313879012-gb-AELG01003189.1-26381	Bombus terrestris transcription initiation factor TFIID subunit 6-like (LOC100643662) transcript variant mRNA	3.70E-20	XM012314379	TBP-associated factor isoform B	1.20E-154	Taf6	transcription factor TFIID complex transcription factor activity, RNA polymerase II core promoter sequence-specific binding involved in preinitiation complex assembly transcription from RNA polymerase II promoter positive regulation of transcription of Notch receptor target neurogenesis		
gi-313879014-gb-AELG01003187.1-5090	Bombus terrestris hornerin-like (LOC100648951) mRNA	3.70E-20	XM012314335	—NA—	NA				
gi-313879014-gb-AELG01003187.1-5115	Bombus terrestris hornerin-like (LOC100648951) mRNA	3.70E-20	XM012314335	—NA—	NA				
gi-313879014-gb-AELG01003187.1-5166	Bombus terrestris hornerin-like (LOC100648951) mRNA	3.70E-20	XM012314335	—NA—	NA				
gi-313879015-gb-AELG01003186.1-34654	Bombus terrestris glycine-rich cell wall structural 1-like (LOC100651094) transcript variant mRNA	3.70E-20	XM012314339	—NA—	NA				
gi-313879015-gb-AELG01003186.1-34721	Bombus terrestris glycine-rich cell wall structural 1-like (LOC100651094) transcript variant mRNA	3.70E-20	XM012314339	—NA—	NA				
gi-313879015-gb-AELG01003186.1-34737	Bombus terrestris glycine-rich cell wall structural 1-like (LOC100651094) transcript variant mRNA	3.70E-20	XM012314339	—NA—	NA				
gi-313879015-gb-AELG01003186.1-34745	Bombus terrestris glycine-rich cell wall structural 1-like (LOC100651094) transcript variant mRNA	3.70E-20	XM012314339	—NA—	NA				

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313879135—gb—AELG01003067.1—19619	Bombus terrestris very-long-chain (3R)-3-hydroxyacyl-dehydratase (LOC100642777) transcript variant mRNA	3.70E-20	XM012316640	CG9267	7.90E-84	CG9267	endoplasmic reticulum enzyme binding fatty acid elongation	
gi—313879157—gb—AELG01003045.1—8313	Bombus terrestris transcription factor AP-1 (LOC100645950) mRNA	3.70E-20	XM003397824	Jun-related isoform A	2.40E-09	Jra	nucleus transcription factor complex cytoplasm RNA polymerase II transcription factor activity, sequence-specific DNA binding transcription factor binding sequence-specific DNA binding protein heterodimerization activity phagocytosis JNK cascade dorsal closure R3/R4 cell fate commitment R7 cell fate commitment negative regulation of antimicrobial humoral response multicellular organism aging wound healing positive regulation of heart contraction positive regulation of transcription from RNA polymerase II promoter imaginal disc fusion, thorax closure dorsal appendage formation micropyle formation synaptic growth at neuromuscular junction	
gi—313879163—gb—AELG01003039.1—7487	Bombus terrestris probable beta-hexosaminidase fdl (LOC100645012) transcript variant mRNA	3.70E-20	XM012312159	HL07462p	8.20E-76			
gi—313879234—gb—AELG01002970.1—235	—NA—	NA		—NA—	NA			
gi—313879286—gb—AELG01002918.1—9434	Bombus terrestris DNA-directed RNA polymerase III subunit RPC7-like (LOC100646568) mRNA	3.70E-20	XM003402562	GAGXEDROME ame: Full=Nucleic-acid-binding from transposon X-element	1.30E-29			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313879286—gb—AELG01002918.1—9459	Bombus terrestris DNA-directed RNA polymerase III subunit RPC7-like (LOC100646568) mRNA	3.70E-20	XM003402562	GAGXEDROME ame: Full=Nucleic-acid-binding from transposon X-element	1.30E-29		
gi—313879286—gb—AELG01002918.1—9782	Bombus terrestris DNA-directed RNA polymerase III subunit RPC7-like (LOC100646568) mRNA	3.70E-20	XM003402562	GAGXEDROME ame: Full=Nucleic-acid-binding from transposon X-element	1.30E-28		
gi—313879333—gb—AELG01002873.1—2763	—NA—	NA		Y2R2DROME ame: Full= 115 kDa in type-1 retrotransposable element R1DM ame: Full=ORF 2 ame: Full= 115 kDa in type I retrotransposable element R1DM	4.90E-30		
gi—313879333—gb—AELG01002873.1—2784	—NA—	NA		Y2R2DROME ame: Full= 115 kDa in type-1 retrotransposable element R1DM ame: Full=ORF 2 ame: Full= 115 kDa in type I retrotransposable element R1DM	4.90E-30		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313879430—gb—AELG01002779.1—30540	Bombus terrestris large neutral amino acids transporter small subunit 2 (LOC100645983) transcript variant mRNA	3.70E-20	XM012307729	isoform A	3.60E-15	CG4502		
gi—313879468—gb—AELG01002742.1—1310	Bombus terrestris uncharacterized LOC100650678 (LOC100650678) mRNA	3.70E-20	XM003394776	Ras association family member	2.20E-55	Rassf	protein binding negative regulation of signal transduction response to gamma radiation regulation of multicellular organism growth	
gi—313879468—gb—AELG01002742.1—2028	Bombus terrestris uncharacterized LOC100650678 (LOC100650678) mRNA	3.70E-20	XM003394776	Ras association family member	2.90E-55	Rassf	protein binding negative regulation of signal transduction response to gamma radiation regulation of multicellular organism growth	
gi—313879468—gb—AELG01002742.1—2552	Bombus terrestris uncharacterized LOC100650678 (LOC100650678) mRNA	3.70E-20	XM003394776	Ras association family member	3.50E-55	Rassf	protein binding negative regulation of signal transduction response to gamma radiation regulation of multicellular organism growth	
gi—313879590—gb—AELG01002624.1—121254	Bombus terrestris uncharacterized LOC100643810 (LOC100643810) ncRNA	3.70E-20	XR001098911	—NA—	NA			
gi—313879590—gb—AELG01002624.1—121290	Bombus terrestris uncharacterized LOC100643810 (LOC100643810) ncRNA	3.70E-20	XR001098911	—NA—	NA			
gi—313879642—gb—AELG01002575.1—1876	Bombus terrestris apoptosis 1 inhibitor-like (LOC100647488) transcript variant mRNA	3.70E-20	XM012308143	isoform A	9.90E-48	Diap1	intracellular part protease binding cysteine-type endopeptidase inhibitor activity ubiquitin-like protein conjugating enzyme binding ubiquitin-like protein ligase activity protein polyubiquitination germ cell development spermatogenesis sensory organ development organ morphogenesis cell migration negative regulation of cysteine-type endopeptidase activity involved in apoptotic process positive regulation of cellular process epithelium development inhibition of cysteine-type endopeptidase activity	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313879642—gb—AELG01002575.1—1882	Bombus terrestris apoptosis 1 inhibitor-like (LOC100647488) transcript variant mRNA	3.70E-20	XM012308143	isoform A	9.90E-48	Diap1	intracellular part protease binding cysteine-type endopeptidase inhibitor activity ubiquitin-like protein conjugating enzyme binding ubiquitin-like protein ligase activity protein polyubiquitination germ cell development spermatogenesis sensory organ development organ morphogenesis cell migration negative regulation of cysteine-type endopeptidase activity involved in apoptotic process positive regulation of cellular process epithelium development inhibition of cysteine-type endopeptidase activity	
gi—313879642—gb—AELG01002575.1—1907	Bombus terrestris apoptosis 1 inhibitor-like (LOC100647488) transcript variant mRNA	3.70E-20	XM012308143	isoform A	1.00E-47	Diap1	intracellular part protease binding cysteine-type endopeptidase inhibitor activity ubiquitin-like protein conjugating enzyme binding ubiquitin-like protein ligase activity protein polyubiquitination germ cell development spermatogenesis sensory organ development organ morphogenesis cell migration negative regulation of cysteine-type endopeptidase activity involved in apoptotic process positive regulation of cellular process epithelium development inhibition of cysteine-type endopeptidase activity	
gi—313879653—gb—AELG01002564.1—32506	Bombus terrestris facilitated trehalose transporter Tret1-like (LOC100643557) transcript variant mRNA	3.70E-20	XM012321342	trehalose transporter 1- isoform A	4.10E-105	Tret1-1	integral component of membrane glucose transmembrane transporter activity trehalose transport transmembrane transport	
gi—313879653—gb—AELG01002564.1—33943	Bombus terrestris facilitated trehalose transporter Tret1-like (LOC100643557) transcript variant mRNA	3.70E-20	XM012321342	trehalose transporter 1-1A	8.70E-105			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313879725-gb-AELG01002494.1-1153	Bombus terrestris serine protease inhibitor 3 4-like (LOC100652301) partial mRNA	3.70E-20	XM003402528	serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-1295	Bombus terrestris serine protease inhibitor 3 4-like (LOC100652301) partial mRNA	3.70E-20	XM003402528	serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-1345	Bombus terrestris serine protease inhibitor 3 4-like (LOC100652301) partial mRNA	3.70E-20	XM003402528	serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2237	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2301	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2319	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2322	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2342	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879725-gb-AELG01002494.1-2360	—NA—	NA		serpin isoform B	3.70E-26	Spn42Da	negative regulation of proteolysis
gi-313879741-gb-AELG01002479.1-74104	—NA—	NA		ferritin 2 light chain homolog	1.70E-37		
gi-313879741-gb-AELG01002479.1-78151	—NA—	NA		ferritin 1 heavy chain isoform F	8.80E-42	Fer1HCH	extracellular region Golgi apparatus microtubule associated complex intracellular ferritin complex fusome ferrous iron binding ferric iron binding cellular iron ion homeostasis cell proliferation response to fungus post-embryonic development iron ion import into cell detoxification of iron ion
gi-313879745-gb-AELG01002475.1-3299	Bombus terrestris cytochrome P450 9e2-like (LOC100647368) mRNA	3.70E-20	XM003393329	CP9F2DROME ame: Full=Probable cytochrome P450 9f2 ame: Full=CYP1XF2	9.50E-89	Cyp9f2	wing disc development

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313879745—gb—AELG01002475.1—4631	Bombus terrestris cytochrome P450 9e2-like (LOC100647368) mRNA	3.70E-20	XM003393329	CP9F2DROME ame: Full=Probable cytochrome P450 9f2 ame: Full=CYP1XF2	9.50E-89	Cyp9f2	wing disc development
gi—313879745—gb—AELG01002475.1—5200	Bombus terrestris cytochrome P450 9e2-like (LOC100647251) mRNA	3.70E-20	XM003393328	CP9F2DROME ame: Full=Probable cytochrome P450 9f2 ame: Full=CYP1XF2	9.50E-89	Cyp9f2	wing disc development
gi—313879774—gb—AELG01002448.1—41	—NA—	NA		reverse transcriptase	2.50E-171		
gi—313879849—gb—AELG01002379.1—41854	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—41907	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—41909	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—42442	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—42447	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—42463	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—42479	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm- Leucylaminopeptidase 2	5.20E-88	S-Lap2	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi—313879849—gb—AELG01002379.1—42510	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm-Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879849—gb—AELG01002379.1—42522	Bombus terrestris cytosol aminopeptidase-like (LOC100643745) mRNA	3.70E-20	XM003401273	Sperm-Leucylaminopeptidase 2	5.20E-88	S-Lap2	
gi—313879870—gb—AELG01002359.1—31145	Bombus terrestris dihydropteridine reductase (LOC100642707) transcript variant miscRNA	3.70E-20	XR001099375	dihydropteridine isoform A	3.90E-49	Dhpr	6,7-dihydropteridine reductase activity metabolic process
gi—313879935—gb—AELG01002296.1—148762	Bombus terrestris mucin-19-like (LOC100649746) mRNA	3.70E-20	XM012316529	—NA—	NA		
gi—313879978—gb—AELG01002255.1—90221	Bombus terrestris uncharacterized LOC100646926 (LOC100646926) transcript variant mRNA	3.70E-20	XM012316244	—NA—	NA		
gi—313879981—gb—AELG01002252.1—85587	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	3.70E-20	XM012316239	UMP synthase r-l gene product	1.00E-108		
gi—313879981—gb—AELG01002252.1—85948	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	3.70E-20	XM012316239	UMP synthase r-l gene product	1.00E-108		
gi—313879981—gb—AELG01002252.1—86008	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	3.70E-20	XM012316239	UMP synthase r-l gene product	1.00E-108		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313879981-gb-AELG01002252.1-86013	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	3.70E-20	XM012316239	UMP synthase r-l gene product	1.00E-108			
gi-313879981-gb-AELG01002252.1-86222	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	8.00E-17	XM012316239	UMP synthase r-l gene product	1.00E-108			
gi-313879981-gb-AELG01002252.1-86352	Bombus terrestris uridine 5'-monophosphate synthase-like (LOC100651419) mRNA	3.70E-20	XM012316239	UMP synthase r-l gene product	1.00E-108			
gi-313880022-gb-AELG01002213.1-140478	—NA—	NA		isoform B	1.30E-64	CG6910		
gi-313880142-gb-AELG01002097.1-3004	—NA—	NA		transposase	8.80E-23			
gi-313880307-gb-AELG01001938.1-81876	Bombus terrestris keratin-associated 19-2-like (LOC105666039) mRNA	3.70E-20	XM012311662	—NA—	NA			
gi-313880307-gb-AELG01001938.1-81902	Bombus terrestris keratin-associated 19-2-like (LOC105666039) mRNA	3.70E-20	XM012311662	—NA—	NA			
gi-313880322-gb-AELG01001924.1-7576	Bombus terrestris uncharacterized LOC100650668 (LOC100650668) transcript variant mRNA	3.70E-20	XM012317875	—NA—	NA			
gi-313880345-gb-AELG01001903.1-4793	—NA—	NA		isoform E	6.30E-144	UGP	cytosol UTP:glucose-1-phosphate uridylyltransferase activity UDP-glucose metabolic process	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313880354-gb-AELG01001894.1-71277	Bombus terrestris E3 ubiquitin-ligase AMFR-like (LOC100647877) transcript variant mRNA	3.70E-20	XM003401710	lethal (2) k12914	2.00E-18	l(2)k12914	plasma membrane oligosaccharyltransferase complex integral component of membrane	
gi-313880357-gb-AELG01001891.1-65299	—NA—	NA		—NA—	NA	DereGG23447	dolichyl-diphosphooligosaccharide-protein	
gi-313880357-gb-AELG01001891.1-65332	—NA—	NA		—NA—	NA	DsimGD22410	glycotransferase activity protein glycosylation negative regulation of apoptotic process	
gi-313880374-gb-AELG01001875.1-33881	Bombus terrestris uncharacterized LOC100649397 (LOC100649397) transcript variant mRNA	3.70E-20	XM012317657	—NA—	NA	DyakGE11027		
gi-313880495-gb-AELG01001760.1-27036	Bombus terrestris cytochrome P450 6k1-like (LOC100642936) mRNA	3.70E-20	XM012314843	C6A13DROME ame: Full=Probable cytochrome P450 6a13 ame: Full=CYPVIA13	7.00E-23	Cyp6a13	defense response to bacterium	
gi-313880495-gb-AELG01001760.1-27812	Bombus terrestris cytochrome P450 6k1-like (LOC100642936) mRNA	3.70E-20	XM012314843	C6A23DROME ame: Full=Probable cytochrome P450 6a23 ame: Full=CYPVIA23	1.30E-27	Cyp6a23		
gi-313880506-gb-AELG01001749.1-27348	Bombus terrestris neprilysin-like (LOC100650573) transcript variant mRNA	3.70E-20	XM012314808	neprilysin isoform A	3.10E-14	Nep1	integral component of membrane metalloendopeptidase activity proteolysis	
gi-313880506-gb-AELG01001749.1-5182	PREDICTED: Bombus terrestris uncharacterized protein C05D11.1-like (LOC100649893), mRNA	3.70E-20	XM003399624	isoform A	5.70E-11	CG3107		
gi-313880511-gb-AELG01001745.1-6829	Bombus terrestris collagen alpha-1(IV) chain (LOC100649188) mRNA	3.70E-20	XM003399617	alpha-1 type IV collagen	2.20E-18			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313880548-gb-AELG01001708.1-19794	—NA—	NA		—NA—	NA		
gi-313880587-gb-AELG01001670.1-103965	Bombus terrestris alpha-glucosidase-like (LOC100650530) mRNA	3.70E-20	XM012311227	FI06514p	1.70E-173		
gi-313880652-gb-AELG01001605.1-6601	Bombus terrestris uncharacterized LOC105666222 (LOC105666222) ncRNA	3.70E-20	XR001099116	—NA—	NA		
gi-313880673-gb-AELG01001584.1-11366	—NA—	NA		cytochrome oxidase subunit partial (mitochondrion)	2.20E-57		
gi-313880677-gb-AELG01001580.1-738	—NA—	NA		—NA—	NA		
gi-313880710-gb-AELG01001547.1-38194	Bombus terrestris chymotrypsin-1-like (LOC100648122) mRNA	1.70E-13	XM003393487	isoform A	3.50E-12	CG17571	serine-type endopeptidase activity proteolysis
gi-313880710-gb-AELG01001547.1-38284	Bombus terrestris chymotrypsin-1-like (LOC100648122) mRNA	3.70E-20	XM003393487	isoform A	3.40E-12	CG17571	serine-type endopeptidase activity proteolysis
gi-313880720-gb-AELG01001537.1-16552	Bombus terrestris laminin subunit beta-1 (LOC100642555) transcript variant mRNA	3.70E-20	XM012314799	isoform A	2.00E-132	LanB1	basal lamina endomembrane system embryonic heart tube morphogenesis gonad development cell migration cell adhesion mediated by integrin substrate adhesion-dependent cell spreading positive regulation of innate immune response defense response to Gram-negative bacterium cardiac muscle cell development basement membrane assembly
gi-313880733-gb-AELG01001524.1-48128	Bombus terrestris zinc finger matrin-type 5 (LOC100644088) transcript variant mRNA	3.70E-20	XM012314407	IP04495p	1.20E-05		
gi-313880925-gb-AELG01001333.1-175	—NA—	NA		RE08130p, partial	4.00E-24		
gi-313880925-gb-AELG01001333.1-196	—NA—	NA		RE08130p, partial	1.40E-24		

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313880946-gb-AELG01001312.1-1440	Bombus terrestris chromatin-remodeling complex ATPase chain Iswi-like (LOC100643266) mRNA	3.70E-20	XM012318820	imitation isoform A	0	Iswi	nuclear chromatin transcription factor complex polytene chromosome CHRAC NURF complex ACF complex RSF complex brahma complex DNA binding DNA helicase activity ATP binding DNA-dependent ATPase activity transcription factor binding nucleosome binding nucleosome-dependent ATPase activity nucleosome assembly transcription, DNA-templated muscle organ development nucleosome positioning sensory perception of pain nuclear speck organization ecdysone receptor-mediated signaling pathway regulation of circadian rhythm nucleosome mobilization ATP-dependent chromatin remodeling negative regulation of transcription, DNA-templated positive regulation of transcription from RNA polymerase II promoter dendrite morphogenesis	

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313880946-gb-AELG01001312.1-2786	Bombus terrestris chromatin-remodeling complex ATPase chain Iswi-like (LOC100643266) mRNA	3.70E-20	XM012318820	imitation isoform A	0	Iswi	nuclear chromatin transcription factor complex polytene chromosome CHRAC NURF complex ACF complex RSF complex brahma complex DNA binding DNA helicase activity ATP binding DNA-dependent ATPase activity transcription factor binding nucleosome binding nucleosome-dependent ATPase activity nucleosome assembly transcription, DNA-templated muscle organ development nucleosome positioning sensory perception of pain nuclear speck organization ecdysone receptor-mediated signaling pathway regulation of circadian rhythm nucleosome mobilization ATP-dependent chromatin remodeling negative regulation of transcription, DNA-templated positive regulation of transcription from RNA polymerase II promoter dendrite morphogenesis

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313880946-gb-AELG01001312.1-375	Bombus terrestris chromatin-remodeling complex ATPase chain Iswi-like (LOC100643266) mRNA	3.70E-20	XM012318820	imitation isoform A	0	Iswi	nuclear chromatin transcription factor complex polytene chromosome CHRAC NURF complex ACF complex RSF complex brahma complex DNA binding DNA helicase activity ATP binding DNA-dependent ATPase activity transcription factor binding nucleosome binding nucleosome-dependent ATPase activity nucleosome assembly transcription, DNA-templated muscle organ development nucleosome positioning sensory perception of pain nuclear speck organization ecdysone receptor-mediated signaling pathway regulation of circadian rhythm nucleosome mobilization ATP-dependent chromatin remodeling negative regulation of transcription, DNA-templated positive regulation of transcription from RNA polymerase II promoter dendrite morphogenesis

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)				
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313880946-gb-AELG01001312.1-453	Bombus terrestris chromatin-remodeling complex ATPase chain Iswi-like (LOC100643266) mRNA	3.70E-20	XM012318820	imitation isoform A	0	Iswi	nuclear chromatin transcription factor complex polytene chromosome CHRAC NURF complex ACF complex RSF complex brahma complex DNA binding DNA helicase activity ATP binding DNA-dependent ATPase activity transcription factor binding nucleosome binding nucleosome-dependent ATPase activity nucleosome assembly transcription, DNA-templated muscle organ development nucleosome positioning sensory perception of pain nuclear speck organization ecdysone receptor-mediated signaling pathway regulation of circadian rhythm nucleosome mobilization ATP-dependent chromatin remodeling negative regulation of transcription, DNA-templated positive regulation of transcription from RNA polymerase II promoter dendrite morphogenesis	
gi-313880952-gb-AELG01001307.1-81373	Bombus terrestris uncharacterized LOC105665953 (LOC105665953) mRNA	3.70E-20	XM012310697	—NA—	NA			
gi-313880952-gb-AELG01001307.1-81374	Bombus terrestris uncharacterized LOC105665953 (LOC105665953) mRNA	3.70E-20	XM012310697	—NA—	NA			
gi-313880971-gb-AELG01001289.1-33628	Bombus terrestris uncharacterized LOC100643149 (LOC100643149) mRNA	3.70E-20	XM003393218	—NA—	NA			
gi-313880971-gb-AELG01001289.1-34609	Bombus terrestris uncharacterized LOC100643149 (LOC100643149) mRNA	3.70E-20	XM003393218	—NA—	NA			
gi-313880971-gb-AELG01001289.1-42793	Bombus terrestris uncharacterized LOC100643108 (LOC100643108) mRNA	3.70E-20	XM003393138	—NA—	NA			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313880973—gb—AELG01001287.1—7361	Bombus terrestris BMP-binding endothelial regulator -like (LOC100652150) mRNA	3.70E-20	XM003393208	—NA—	NA			
gi—313881187—gb—AELG01001076.1—6678	Bombus terrestris uncharacterized LOC100644365 (LOC100644365) mRNA	3.70E-20	XM012309129	charged multi-vesicular body isoform A	1.30E-35	DereGG15729 Chmp1	ESCRT III complex late endosome apical part of cell endosome transport via multi-vesicular body sorting pathway negative regulation of epidermal growth factor receptor signaling pathway	
gi—313881187—gb—AELG01001076.1—7455	Bombus terrestris uncharacterized LOC100644365 (LOC100644365) mRNA	3.70E-20	XM012309129	charged multi-vesicular body isoform A	1.30E-35	DereGG15729 Chmp1	ESCRT III complex late endosome apical part of cell endosome transport via multi-vesicular body sorting pathway negative regulation of epidermal growth factor receptor signaling pathway	
gi—313881235—gb—AELG01001031.1—374177	—NA—	NA		—NA—	NA			
gi—313881246—gb—AELG01001020.1—57215	Bombus terrestris voltage-dependent calcium channel subunit alpha-2 delta-3 (LOC100651196) mRNA	3.70E-20	XM012308865	CG5705- partial	1.70E-77	CG5705	mitochondrion translation release factor activity, codon specific translational termination	
gi—313881269—gb—AELG01000998.1—10150	—NA—	NA		COG4DROME ame: Full=Conserved oligomeric Golgi complex subunit 4 Short=COG complex subunit 4 ame: Full=Component of oligomeric Golgi complex 4 isoform A	3.60E-111	CG7456		
gi—313881275—gb—AELG01000992.1—15918	Bombus terrestris N-acetyltransferase 6 (LOC100646501) mRNA	1.70E-18	XM003395559	isoform A	1.70E-30	CG9471	NADPH dehydrogenase activity biliverdin reductase activity multicellular organism reproduction	
gi—313881280—gb—AELG01000987.1—1111	—NA—	NA		—NA—	NA			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			Sequence Description	De-	blastx (<i>Drosophila melanogaster</i>)		
	Sequence Description	e Value	Accession Number			e Value	Gene Name	GO Names
gi—313881323—gb—AELG01000970.1—13750	Bombus terrestris uncharacterized MFS-type transporter -like (LOC100642804) transcript variant mRNA	3.70E-20	XM003395446	isoform A	6.10E-24	CG1358		
gi—313881447—gb—AELG01000853.1—52524	Bombus terrestris uncharacterized LOC100649576 (LOC100649576) transcript variant mRNA	3.70E-20	XM012309857	Nahoda protein	2.50E-62			
gi—313881514—gb—AELG01000786.1—55539	Bombus terrestris DNA-directed RNA polymerase II subunit RPB1-like (LOC100649338) mRNA	3.70E-20	XM003398008	—NA—	NA			
gi—313881535—gb—AELG01000765.1—1194	—NA—	NA		Z band alternatively spliced PDZ-motif isoform H	1.00E-13	Zasp66	Z disc protein phosphatase 1 binding muscle alpha-actinin binding mesoderm development myofibril assembly	
gi—313881547—gb—AELG01000753.1—14606	—NA—	NA		RIO kinase isoform A	4.50E-130	RIOK1	nucleus cytoplasm protein kinase activity protein phosphorylation cellular response to starvation positive regulation of multicellular organism growth positive regulation of glial cell proliferation positive regulation of peptide hormone secretion	
gi—313881547—gb—AELG01000753.1—14658	—NA—	NA		RIO kinase isoform A	4.50E-130	RIOK1	nucleus cytoplasm protein kinase activity protein phosphorylation cellular response to starvation positive regulation of multicellular organism growth positive regulation of glial cell proliferation positive regulation of peptide hormone secretion	
gi—313881625—gb—AELG01000675.1—18319	Bombus terrestris poly(U)-specific endoribonuclease homolog (LOC100644333) mRNA	3.70E-20	XM012313044	GH21533p	1.40E-39			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi—313881671—gb—AELG01000629.1—12900	Bombus terrestris hypoxia up-regulated 1 (LOC100642850) mRNA	3.70E-20	XM003398119	isoform A	6.10E-31	CG2918	extracellular space lipid particle endomembrane system multicellular organism reproduction	
gi—313881671—gb—AELG01000629.1—12909	Bombus terrestris hypoxia up-regulated 1 (LOC100642850) mRNA	3.70E-20	XM003398119	isoform A	6.10E-31	CG2918	extracellular space lipid particle endomembrane system multicellular organism reproduction	
gi—313881671—gb—AELG01000629.1—12985	Bombus terrestris hypoxia up-regulated 1 (LOC100642850) mRNA	3.70E-20	XM003398119	isoform A	6.10E-31	CG2918	extracellular space lipid particle endomembrane system multicellular organism reproduction	
gi—313881671—gb—AELG01000629.1—13224	Bombus terrestris hypoxia up-regulated 1 (LOC100642850) mRNA	3.70E-20	XM003398119	isoform A	6.10E-31	CG2918	extracellular space lipid particle endomembrane system multicellular organism reproduction	
gi—313881671—gb—AELG01000629.1—13264	Bombus terrestris hypoxia up-regulated 1 (LOC100642850) mRNA	3.70E-20	XM003398119	isoform A	6.10E-31	CG2918	extracellular space lipid particle endomembrane system multicellular organism reproduction	
gi—313881797—gb—AELG01000503.1—37954	Bombus terrestris uncharacterized LOC100644923 (LOC100644923) transcript variant mRNA	3.70E-20	XM012307760	—NA—	NA			
gi—313881797—gb—AELG01000503.1—43129	Bombus terrestris uncharacterized LOC100644923 (LOC100644923) transcript variant mRNA	3.70E-20	XM012307761	SD02860p	2.80E-17			
gi—313881799—gb—AELG01000501.1—1129	—NA—	NA		CG9799- partial	2.10E-112	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—1138	—NA—	NA		CG9799- partial	2.10E-112	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—1158	—NA—	NA		CG9799- partial	2.10E-112	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—1365	—NA—	NA		CG9799- partial	6.30E-113	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—1405	—NA—	NA		CG9799- partial	6.30E-113	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—1870	—NA—	NA		CG9799- partial	6.30E-113	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—625	—NA—	NA		CG9799- partial	6.30E-113	CG9799	cellular response to starvation	
gi—313881799—gb—AELG01000501.1—804	—NA—	NA		CG9799- partial	6.30E-113	CG9799	cellular response to starvation	
gi—313881938—gb—AELG01000362.1—25745	—NA—	NA		CG10206-PA	0			
gi—313881938—gb—AELG01000362.1—27573	—NA—	NA		CG10206-PA	0			
gi—313881938—gb—AELG01000362.1—27590	—NA—	NA		CG10206-PA	0			
gi—313881938—gb—AELG01000362.1—27606	—NA—	NA		CG10206-PA	0			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)				blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names	
gi-313881986-gb-AELG01000314.1-36544	Bombus terrestris uncharacterized LOC100647826 (LOC100647826) transcript variant ncRNA	3.70E-20	XR001099538	—NA—	NA			
gi-313882001-gb-AELG01000299.1-10801	—NA—	NA		isoform A	3.80E-12	mrj	unfolded protein binding protein folding	
gi-313882015-gb-AELG01000285.1-31829	Bombus terrestris homeobox Hox-A3-like (LOC100650346) transcript variant mRNA	3.70E-20	XM012318240	—NA—	NA			
gi-313882060-gb-AELG01000240.1-39989	Bombus terrestris polyubiquitin-B (LOC100648000) mRNA	3.70E-20	XM003402262	ubiquitin	5.10E-140			
gi-313882060-gb-AELG01000240.1-40055	Bombus terrestris polyubiquitin-B (LOC100648000) mRNA	3.70E-20	XM003402262	ubiquitin	5.10E-140			
gi-313882060-gb-AELG01000240.1-40100	Bombus terrestris polyubiquitin-B (LOC100648000) mRNA	3.70E-20	XM003402262	ubiquitin	5.10E-140			
gi-313882060-gb-AELG01000240.1-40148	Bombus terrestris polyubiquitin-B (LOC100648000) mRNA	3.70E-20	XM003402262	ubiquitin	5.10E-140			
gi-313882060-gb-AELG01000240.1-40331	Bombus terrestris polyubiquitin-B (LOC100648000) mRNA	3.70E-20	XM003402262	ubiquitin	5.10E-140			
gi-313882080-gb-AELG01000220.1-5278	Bombus terrestris aminopeptidase N-like (LOC105666734) mRNA	3.70E-20	XM012318455	isoform A	2.10E-18	CG11951	peptidase activity, acting on L-amino acid peptides	
gi-313882110-gb-AELG01000190.1-6125	Bombus terrestris uncharacterized LOC105666179 (LOC105666179) transcript variant miscRNA	3.70E-20	XR001099071	wishful isoform B	1.00E-06	wit		
gi-313882118-gb-AELG01000182.1-3223	—NA—	NA		—NA—	NA			

TABLE A.3: (continued)

SNP	blastn (<i>Bombus terrestris</i>)			blastx (<i>Drosophila melanogaster</i>)			
	Sequence Description	e Value	Accession Number	Sequence Description	e Value	Gene Name	GO Names
gi-313882123-gb-AELG01000177.1-25203	—NA—	NA		amom partial	5.80E-19	amom	extracellular region peptidase activity instar larval or pupal development peptide hormone processing carbohydrate homeostasis larval wandering behavior hatching behavior
gi-313882123-gb-AELG01000177.1-25218	—NA—	NA		AF0331171prohormone and neuropeptide processing protease	1.00E-19		
gi-313882123-gb-AELG01000177.1-25236	—NA—	NA		AF0331171prohormone and neuropeptide processing protease	1.00E-18		
gi-313882149-gb-AELG01000151.1-112181	—NA—	NA		isoform C	3.80E-94	CG10237	intracellular transporter activity vitamin E binding retinal binding transport
gi-313882152-gb-AELG01000148.1-19326	—NA—	NA		GM13209p	5.10E-18		
gi-313882207-gb-AELG01000093.1-180	—NA—	NA		—NA—	NA		
gi-313882207-gb-AELG01000093.1-379	—NA—	NA		—NA—	NA		
gi-313882208-gb-AELG01000092.1-17302	—NA—	NA		CYP-1	1.80E-63		
gi-313882243-gb-AELG01000057.1-8974	—NA—	NA		isoform A	2.90E-45	CG9914	

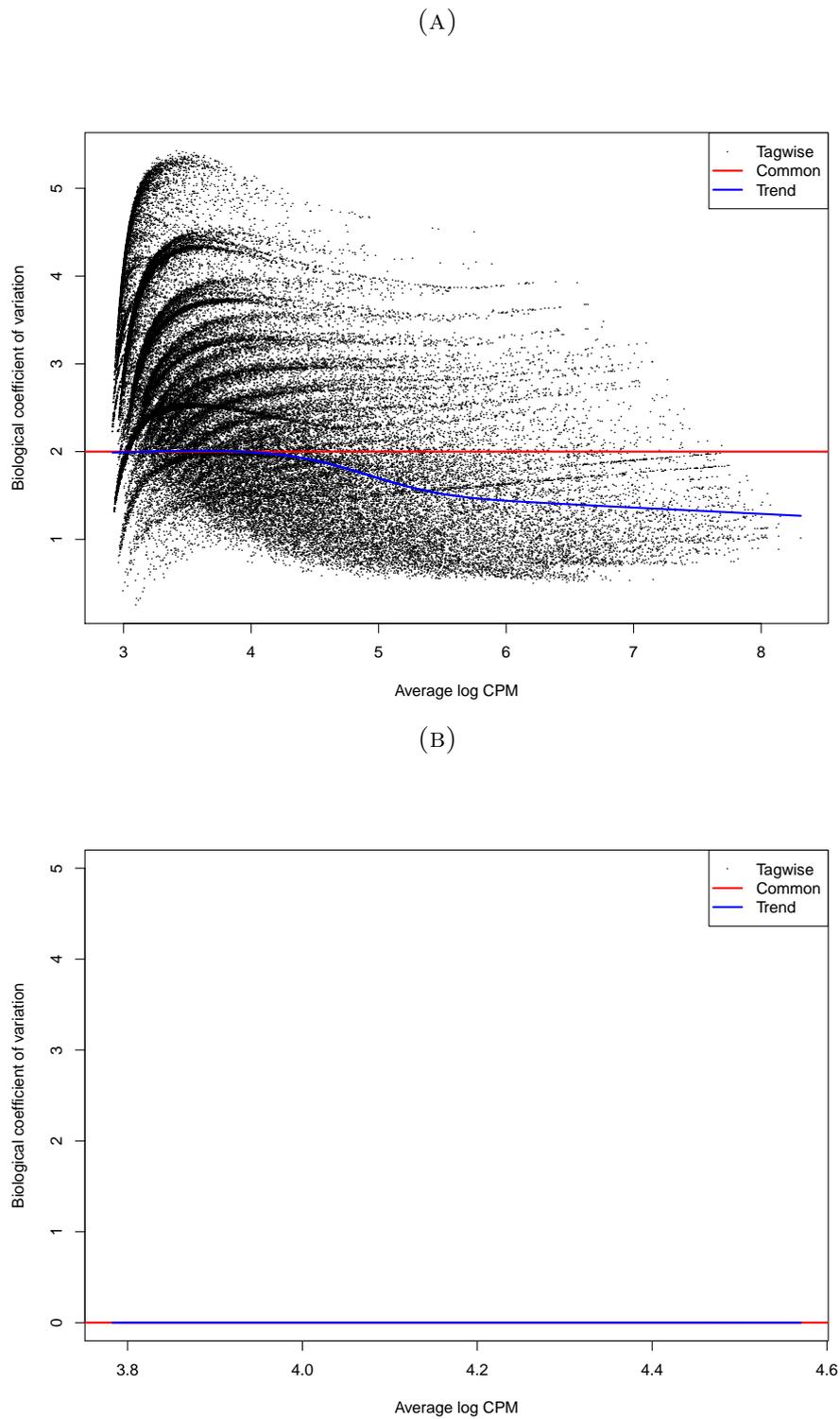


FIGURE A.1: Biological coefficient of variation (BCV) of A) raw data, and B) SVA-adjusted data for the 29 RNA-seq *Bombus terrestris* libraries

Appendix B

Significantly overlapping known genes with differential expression, methylation, and alternative splicing

TABLE B.1: Significantly overlapping known genes (LOC IDs) with differential expression (hypergeometric test, $p < 0.001$).

LOC ID	Gene name
LOC100643007	uncharacterized
LOC105666278	uncharacterized
LOC105665841	uncharacterized
LOC105665894	uncharacterized
LOC100648579	uncharacterized
LOC100649977	uncharacterized
LOC100645530	uncharacterized
LOC100646989	uncharacterized
LOC100644880	uncharacterized
LOC100643355	uncharacterized
LOC105667095	uncharacterized

Gene expression up regulated in reproductive workers compared to non-reproductive workers.

Gene expression down regulated in reproductive workers compared to non-reproductive workers.

Appendix C

Overlapping enriched Gene
Ontology terms with differential
expression, methylation, and
alternative splicing

TABLE C.1: Significantly overlapping enriched Gene Ontology (GO) terms with up regulation and down regulation in reproductive workers compared to non-reproductive workers (hypergeometric test, $p < 0.001$).

GO ID	GO term
GO:0000281	mitotic cytokinesis
GO:0000974	generation of catalytic spliceosome: first transesterification step
GO:0003012	muscle system process
GO:0005245	voltage-gated calcium channel activity
GO:0005891	voltage-gated calcium channel complex
GO:0006805	xenobiotic metabolic process
GO:0006937	regulation: muscle contraction
GO:0007051	spindle organization
GO:0007293	germarium-derived egg chamber formation
GO:0007301	female germline ring canal formation
GO:0007312	oocyte nucleus migration: oocyte dorsal/ventral axis specification
GO:0007406	negative regulation: neuroblast proliferation
GO:0008179	adenylate cyclase binding
GO:0008194	UDP-glycosyltransferase activity
GO:0008345	larval locomotory behavior
GO:0008431	vitamin E binding
GO:0009744	response to sucrose
GO:0010906	regulation of glucose metabolic process
GO:0016027	inaD signaling complex
GO:0016327	apicolateral plasma membrane
GO:0016918	retinal binding
GO:0019233	sensory perception of pain
GO:0032543	mitochondrial translation
GO:0042332	gravitaxis
GO:0042759	long-chain fatty acid biosynthetic process
GO:0045089	positive regulation: innate immune response
GO:0045313	rhabdomere membrane biogenesis
GO:0045861	negative regulation of proteolysis
GO:0046579	positive regulation: Ras protein signal transduction
GO:0046959	habituation
GO:0047497	mitochondrion transport along microtubule
GO:0048311	mitochondrion distribution
GO:0048678	response to axon injury
GO:0051647	nucleus localization
GO:0070374	positive regulation: ERK1 and ERK2 cascade
GO:0070938	contractile ring

TABLE C.2: Significantly overlapping enriched Gene Ontology (GO) terms with down regulation in reproductive workers (compared to non-reproductive workers) and alternative splicing of isoforms (hypergeometric test, $p < 0.001$).

GO ID	GO term
GO:0009922	fatty acid elongation
GO:0030497	fatty acid elongation
GO:0071689	muscle thin filament assembly
GO:0097352	muscle thin filament assembly

TABLE C.3: Significantly overlapping enriched Gene Ontology (GO) terms with alternative splicing of isoforms and hypermethylation in reproductive workers (hypergeometric test, $p < 0.001$).

GO ID	GO term
GO:0046579	positive regulation: Ras protein signal transduction
GO:0048488	synaptic vesicle endocytosis
GO:0070374	positive regulation: ERK1 and ERK2 cascade
GO:2000274	regulation of epithelial cell migration open tracheal system

Appendix D

Significantly overlapping genes with allele-specific expression and allele-specific methylation

TABLE D.10: Significantly overlapping known genes with allele-specific methylation in reproductive and non-reproductive workers (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	GENE NAME
LOC100642214	uncharacterized
LOC100642366	uncharacterized
LOC100642437	uncharacterized
LOC100642705	YEATS domain-containing protein 2
LOC100642720	basic salivary proline-rich protein 2
LOC100642736	ski oncogene
LOC100643256	broad-complex core protein isoforms 1/2/3/4/5
LOC100643495	uncharacterized
LOC100643531	WW domain-binding protein 11
LOC100643807	protein Jumonji
LOC100643910	uncharacterized
LOC100644004	dentin sialophosphoprotein

TABLE D.10: (continued)

LOC ID	GENE NAME
LOC100644059	uncharacterized
LOC100644135	MOG interacting and ectopic P-granules protein 1
LOC100644222	uncharacterized
LOC100644364	uncharacterized
LOC100644504	uncharacterized
LOC100644581	uncharacterized
LOC100644735	male-specific lethal 1 homolog
LOC100644895	uncharacterized
LOC100644972	glycine-rich protein DOT1-like
LOC100645288	uncharacterized
LOC100645332	Golgi resident protein GCP60
LOC100645468	uncharacterized
LOC100645740	uncharacterized
LOC100646064	MATH and LRR domain-containing protein PFE0570w-like
LOC100646154	uncharacterized
LOC100646419	uncharacterized
LOC100646719	uncharacterized
LOC100647323	uncharacterized
LOC100647479	uncharacterized protein DDB_G0287625-like
LOC100647656	uncharacterized
LOC100647702	uncharacterized
LOC100647708	zinc finger protein DZIP1L
LOC100647771	uncharacterized
LOC100647790	uncharacterized
LOC100647791	uncharacterized
LOC100647811	uncharacterized
LOC100648637	uncharacterized
LOC100648640	uncharacterized
LOC100648707	uncharacterized
LOC100648727	uncharacterized
LOC100648967	uncharacterized
LOC100649269	disks large-associated protein 5-like
LOC100649332	uncharacterized

TABLE D.10: (continued)

LOC ID	GENE NAME
LOC100649502	uncharacterized
LOC100649624	uncharacterized
LOC100649651	uncharacterized
LOC100649724	uncharacterized
LOC100649798	serine/arginine repetitive matrix protein 2-like
LOC100649868	uncharacterized
LOC100650027	uncharacterized
LOC100650461	uncharacterized protein KIAA2026-like
LOC100650553	glutamic acid-rich protein
LOC100650776	proline-, glutamic acid- and leucine-rich protein 1-like
LOC100651119	uncharacterized protein C17orf85 homolog
LOC100651357	uncharacterized protein C17orf104-like
LOC100651475	uncharacterized
LOC100651634	uncharacterized
LOC100651892	trithorax group protein osa
LOC100651956	uncharacterized
LOC100652055	uncharacterized
LOC100652191	uncharacterized
LOC100652264	uncharacterized
LOC100743964	transformer-2 protein homolog beta
LOC100744799	zinc finger and BTB domain-containing protein 12-like
LOC100748611	maternal B9.15 protein-like
LOC105665828	uncharacterized
LOC105665993	uncharacterized
LOC105666031	uncharacterized
LOC105666051	uncharacterized
LOC105666144	uncharacterized
LOC105666257	uncharacterized
LOC105666536	uncharacterized
LOC105666994	uncharacterized
LOC105667203	uncharacterized

TABLE D.1: Significantly overlapping known genes with allele-specific expression in reproductive and non-reproductive workers (hypergeometric test, $p < 0.05$).

LOC ID	Gene name
LOC100643007	uncharacterized
LOC100643409	uncharacterized
LOC100644154	uncharacterized
LOC100644365	uncharacterized
LOC100644869	uncharacterized
LOC100645530	uncharacterized
LOC100646149	uncharacterized
LOC100646878	uncharacterized
LOC100647524	uncharacterized
LOC100647549	uncharacterized
LOC100647684	uncharacterized
LOC100647751	uncharacterized
LOC100647906	junctophilin-1
LOC100648338	uncharacterized
LOC100648816	protein Tob1-like
LOC100649397	uncharacterized
LOC100649977	uncharacterized
LOC100650186	uncharacterized
LOC100650602	uncharacterized
LOC100650678	uncharacterized
LOC100651786	uncharacterized
LOC105666144	uncharacterized
LOC105666270	uncharacterized
LOC105666278	uncharacterized
LOC105666484	uncharacterized
LOC105666722	uncharacterized
LOC105666827	uncharacterized
LOC105666922	uncharacterized
LOC105666997	uncharacterized
LOC105667033	uncharacterized
LOC105667086	uncharacterized

TABLE D.2: Significantly overlapping known genes with allele-specific expression in reproductive workers and allele-specific methylation in reproductive workers (hypergeometric test, $p < 0.05$).

LOC ID	Gene name
LOC100647771	uncharacterized
LOC105666144	uncharacterized
LOC105666784	uncharacterized

TABLE D.14: Annotations of genes with allele-specific expression and allele-specific methylation in reproductive and non-reproductive workers according to the custom trinotate pipeline (Section 4.2.4).

LOC ID	GO ID	NUMBER OF OVERLAP-GO TERM PING GENE LISTS
LOC100642556	-	1 Grip domain

TABLE D.14: (continued)

LOC ID	GO ID	OVERLAPPING LISTS	GO TERM
LOC100644154	GO:0003674,GO:0005488,GO:0005515,GO:0005575,GO:2001141, GO:0005634,GO:0005654,GO:0006139,GO:0006325,GO:0006333, GO:0006334,GO:0006336,GO:0006338,GO:0006352,GO:0006355, GO:0006461,GO:0006725,GO:0006807,GO:0008150,GO:0008152, GO:0009058,GO:0009059,GO:0009889,GO:0009890,GO:0009891, GO:0009892,GO:0009893,GO:0009987,GO:0010468,GO:0010556, GO:0010557,GO:0010558,GO:0010604,GO:0010605,GO:0010628, GO:0010629,GO:0016043,GO:0016070,GO:0016568,GO:0016569, GO:0016584,GO:0018130,GO:0019219,GO:0019222,GO:0019438, GO:0022607,GO:0031010,GO:0031055,GO:0031213,GO:0031323, GO:0031324,GO:0031325,GO:0031326,GO:0031327,GO:0031328, GO:0031497,GO:0032774,GO:0032991,GO:0034080,GO:0034622, GO:0034641,GO:0034654,GO:0034724,GO:0034728,GO:0042393, GO:0043044,GO:0043167,GO:0043169,GO:0043170,GO:0043226, GO:0043227,GO:0043229,GO:0043231,GO:0043234,GO:0043392, GO:0043486,GO:0043900,GO:0043902,GO:0043903,GO:0043933, GO:0044092,GO:0044237,GO:0044238,GO:0044249,GO:0044260, GO:0044271,GO:0044422,GO:0044424,GO:0044428,GO:0044446, GO:0044464,GO:0045892,GO:0045893,GO:0045934,GO:0045935, GO:0046483,GO:0046782,GO:0046872,GO:0048518,GO:0048519, GO:0048522,GO:0048523,GO:0048524,GO:0050434,GO:0050789, GO:0050792,GO:0050794,GO:0051098,GO:0051100,GO:0051101, GO:0051171,GO:0051172,GO:0051173,GO:0051252,GO:0051253, GO:0051254,GO:0060255,GO:0065003,GO:0065004,GO:0065007, GO:0065009,GO:0070603,GO:0071704,GO:0071822,GO:0071824, GO:0071840,GO:0080090,GO:0090304,GO:1901360,GO:1901362, GO:1901576,GO:1902679,GO:1902680,GO:1903506,GO:1903507, GO:1903508,GO:2000112,GO:2000113	2	chromatin modification, regulation of DNA binding
LOC100646154	GO:0000166,GO:0001882,GO:0001883,GO:0003674,GO:0003824, GO:0004672,GO:0004674,GO:0005488,GO:0005524,GO:0005575, GO:0005737,GO:0005819,GO:0006464,GO:0006468,GO:0006793, GO:0006796,GO:0008150,GO:0008152,GO:0009987,GO:0016301, GO:0016310,GO:0016740,GO:0016772,GO:0016773,GO:0017076, GO:0019538,GO:0030554,GO:0032549,GO:0032550,GO:0032553, GO:0032555,GO:0032559,GO:0035639,GO:0036094,GO:0036211, GO:0043167,GO:0043168,GO:0043170,GO:0043226,GO:0043228, GO:0043229,GO:0043232,GO:0043412,GO:0044237,GO:0044238, GO:0044260,GO:0044267,GO:0044422,GO:0044424,GO:0044430, GO:0044446,GO:0044464,GO:0071704,GO:0097159,GO:0097367, GO:1901265,GO:1901363	2	protein phosphorylation
LOC105666144	GO:0003674,GO:0003676,GO:0005488,GO:0006139,GO:0006259, GO:0006725,GO:0006807,GO:0008150,GO:0008152,GO:0008270, GO:0009987,GO:0015074,GO:0034641,GO:0043167,GO:0043169, GO:0043170,GO:0044237,GO:0044238,GO:0044260,GO:0046483, GO:0046872,GO:0046914,GO:0071704,GO:0090304,GO:0097159, GO:1901360,GO:1901363	4	nucleic acid binding
LOC100647771	GO:0000975,GO:0000976,GO:0000977,GO:0000981,GO:0001012, GO:0001047,GO:0001067,GO:0001071,GO:0001085,GO:0001101, GO:0001158,GO:0001525,GO:0001889,GO:0001935,GO:0002070, GO:0002237,GO:0002637,GO:0002639,GO:0002682,GO:0002684, GO:0002694,GO:0002696,GO:0002697,GO:0002699,GO:0002700, GO:0002702,GO:0003674,GO:0003676,GO:0003677,GO:0003682, GO:0003700,GO:0005488,GO:0005515,GO:0005575,GO:0005634, GO:0005737,GO:0005783,GO:0005789,GO:0006139,GO:0006351, GO:0006355,GO:0006357,GO:0006366,GO:0006508,GO:0006511, GO:0006725,GO:0006807,GO:0006950,GO:0006990,GO:0007154, GO:0007165,GO:0007517,GO:0008134,GO:0008150,GO:0008152, GO:0008283,GO:0008284,GO:0009056,GO:0009057,GO:0009058,	2	transcription factor

TABLE D.14: (continued)

LOC ID	GO ID	OVERLAPPING LISTS	GO TERM
	GO:0009059,GO:0009267,GO:0009605,GO:0009607,GO:0009719, GO:0009725,GO:0009888,GO:0009889,GO:0009891,GO:0009893, GO:0009894,GO:0009896,GO:0009966,GO:0009967,GO:0009968, GO:0009987,GO:0009991,GO:0010033,GO:0010243,GO:0010468, GO:0010506,GO:0010556,GO:0010557,GO:0010604,GO:0010608, GO:0010628,GO:0010646,GO:0010647,GO:0010648,GO:0010941, GO:0016020,GO:0016021,GO:0016070,GO:0018130,GO:0019219, GO:0019222,GO:0019438,GO:0019538,GO:0019725,GO:0019941, GO:0021700,GO:0022407,GO:0022409,GO:0022603,GO:0023051, GO:0023056,GO:0023057,GO:0030155,GO:0030162,GO:0030334, GO:0030335,GO:0031017,GO:0031090,GO:0031224,GO:0031323, GO:0031325,GO:0031326,GO:0031328,GO:0031329,GO:0031331, GO:0031490,GO:0031647,GO:0031648,GO:0031667,GO:0031668, GO:0031669,GO:0032268,GO:0032270,GO:0032496,GO:0032502, GO:0032774,GO:0032870,GO:0032879,GO:0033500,GO:0033554, GO:0033993,GO:0034097,GO:0034110,GO:0034112,GO:0034405, GO:0034616,GO:0034641,GO:0034645,GO:0034654,GO:0034976, GO:0035326,GO:0035356,GO:0035470,GO:0035556,GO:0040012, GO:0040017,GO:0042127,GO:0042149,GO:0042176,GO:0042221, GO:0042592,GO:0042593,GO:0042594,GO:0042632,GO:0042981, GO:0043066,GO:0043067,GO:0043069,GO:0043170,GO:0043200, GO:0043207,GO:0043226,GO:0043227,GO:0043229,GO:0043231, GO:0043434,GO:0043565,GO:0043566,GO:0043632,GO:0044212, GO:0044237,GO:0044238,GO:0044248,GO:0044249,GO:0044260, GO:0044265,GO:0044271,GO:0044422,GO:0044424,GO:0044425, GO:0044432,GO:0044444,GO:0044446,GO:0044464,GO:0044699, GO:0044763,GO:0044767,GO:0044877,GO:0045346,GO:0045348, GO:0045577,GO:0045579,GO:0045580,GO:0045582,GO:0045595, GO:0045597,GO:0045598,GO:0045600,GO:0045619,GO:0045621, GO:0045732,GO:0045765,GO:0045766,GO:0045785,GO:0045862, GO:0045893,GO:0045935,GO:0045944,GO:0046483,GO:0046982, GO:0046983,GO:0048469,GO:0048513,GO:0048518,GO:0048519, GO:0048522,GO:0048523,GO:0048583,GO:0048584,GO:0048585, GO:0048646,GO:0048732,GO:0048856,GO:0048869,GO:0048878, GO:0050673,GO:0050678,GO:0050679,GO:0050776,GO:0050778, GO:0050789,GO:0050793,GO:0050794,GO:0050801,GO:0050863, GO:0050864,GO:0050865,GO:0050867,GO:0050870,GO:0050871, GO:0050896,GO:0051046,GO:0051047,GO:0051049,GO:0051050, GO:0051094,GO:0051171,GO:0051173,GO:0051239,GO:0051240, GO:0051246,GO:0051247,GO:0051249,GO:0051251,GO:0051252, GO:0051254,GO:0051270,GO:0051272,GO:0051603,GO:0051716, GO:0055081,GO:0055082,GO:0055088,GO:0055089,GO:0055090, GO:0055092,GO:0060255,GO:0060548,GO:0060612,GO:0060691, GO:0061041,GO:0061043,GO:0061061,GO:0061136,GO:0061448, GO:0065007,GO:0065008,GO:0070059,GO:0070328,GO:0070670, GO:0070887,GO:0071216,GO:0071219,GO:0071222,GO:0071229, GO:0071230,GO:0071310,GO:0071345,GO:0071353,GO:0071375, GO:0071396,GO:0071417,GO:0071495,GO:0071496,GO:0071498, GO:0071499,GO:0071704,GO:0080090,GO:0080134,GO:0080135, GO:0090303,GO:0090304,GO:0097159,GO:0097190,GO:0097193, GO:0097659,GO:0098588,GO:0098589,GO:1900098,GO:1900100, GO:1900101,GO:1900103,GO:1901342,GO:1901360,GO:1901362, GO:1901363,GO:1901522,GO:1901575,GO:1901576,GO:1901652, GO:1901653,GO:1901698,GO:1901699,GO:1901700,GO:1901701, GO:1901800,GO:1902105,GO:1902107,GO:1902235,GO:1902236, GO:1902531,GO:1902532,GO:1902680,GO:1903034,GO:1903036, GO:1903037,GO:1903039,GO:1903050,GO:1903052,GO:1903362, GO:1903364,GO:1903487,GO:1903489,GO:1903506,GO:1903508,		

TABLE D.14: (continued)

LOC ID	GO ID	OVERLAPPING LISTS	GO TERM
	GO:1903573,GO:1903706,GO:1903708,GO:1990418,GO:2000026, GO:2000027,GO:2000112,GO:2000145,GO:2000147,GO:2000241, GO:2000243,GO:2000345,GO:2000347,GO:2001141,GO:2001233, GO:2001234,GO:2001242,GO:2001243		
LOC105666784	-	1	Transposase

TABLE D.3: Significantly overlapping known genes with allele-specific expression in reproductive workers and allele-specific methylation in non-reproductive workers (hypergeometric test, $p < 0.05$).

LOC ID	Gene name
LOC100644154	uncharacterized
LOC100647771	uncharacterized
LOC105666144	uncharacterized

TABLE D.4: Significantly overlapping known genes with allele-specific expression in reproductive workers and up regulated expression (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100643007	uncharacterized
LOC100643073	uncharacterized
LOC100645530	uncharacterized
LOC100646878	uncharacterized
LOC100647524	uncharacterized
LOC100647751	uncharacterized
LOC100647906	junctophilin-1
LOC100649397	uncharacterized
LOC100649977	uncharacterized
LOC100650186	uncharacterized
LOC100650602	uncharacterized
LOC100650678	uncharacterized
LOC105665670	uncharacterized
LOC105665841	uncharacterized
LOC105666270	uncharacterized
LOC105666278	uncharacterized
LOC105666922	uncharacterized
LOC105666997	uncharacterized

TABLE D.5: Significantly overlapping known genes with allele-specific expression in reproductive workers and down regulated expression (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100643007	uncharacterized
LOC100645530	uncharacterized
LOC100647771	uncharacterized
LOC100649977	uncharacterized
LOC105665841	uncharacterized
LOC105666278	uncharacterized

TABLE D.6: Overlapping known genes with allele-specific expression in non-reproductive workers and allele-specific methylation in reproductive workers (hypergeometric test, $p=0.14$).

LOC ID	Gene name
LOC100646154	uncharacterized
LOC105666144	uncharacterized

TABLE D.7: Significantly overlapping known genes with allele-specific expression in non-reproductive workers and allele-specific methylation in non-reproductive workers (hypergeometric test, $p<0.05$).

LOC ID	Gene name
LOC100642556	uncharacterized
LOC100644154	uncharacterized
LOC100646154	uncharacterized
LOC105666144	uncharacterized

TABLE D.8: Significantly overlapping known genes with allele-specific expression in non-reproductive workers and up regulated expression (hypergeometric test, $p<0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100643007	uncharacterized
LOC100645530	uncharacterized
LOC100646016	HIRA-interacting protein 3
LOC100646878	uncharacterized
LOC100647524	uncharacterized
LOC100647751	uncharacterized
LOC100647906	junctophilin-1
LOC100649397	uncharacterized
LOC100649977	uncharacterized
LOC100650186	uncharacterized
LOC100650602	uncharacterized
LOC100650678	uncharacterized
LOC105665827	uncharacterized
LOC105666270	uncharacterized
LOC105666278	uncharacterized
LOC105666922	uncharacterized
LOC105666997	uncharacterized

TABLE D.9: Significantly overlapping known genes with allele-specific expression in non-reproductive workers and down regulated expression (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100643007	uncharacterized
LOC100645530	uncharacterized
LOC100645889	uncharacterized
LOC100649977	uncharacterized
LOC105666278	uncharacterized
LOC105667054	uncharacterized

TABLE D.11: Significantly overlapping known genes with allele-specific methylation in reproductive workers and up regulated expression (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100642190	uncharacterized
LOC100645332	Golgi resident protein GCP60
LOC100647702	uncharacterized
LOC100649868	uncharacterized
LOC105666458	uncharacterized

TABLE D.12: Significantly overlapping known genes with allele-specific methylation in reproductive workers and hypomethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100642467	atrophin-1-like
LOC100643807	protein Jumonji
LOC100644328	uncharacterized
LOC100644972	glycine-rich protein DOT1-like
LOC100646025	uncharacterized
LOC100651475	uncharacterized
LOC100651572	uncharacterized

TABLE D.13: Significantly overlapping known genes with allele-specific methylation in non-reproductive workers and up regulated expression (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

LOC ID	Gene name
LOC100644688	interferon-inducible double-stranded RNA-dependent protein kinase activator A homolog
LOC100645247	chromobox protein homolog 5-like
LOC100645332	Golgi resident protein GCP60
LOC100647702	uncharacterized
LOC100649868	uncharacterized

Appendix E

Significantly overlapping gene ontology terms with allele-specific expression and allele-specific methylation

TABLE E.1: Significantly overlapping gene ontology terms with allele-specific expression in reproductive and non-reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO TERM
GO:0000281	mitotic cytokinesis
GO:0000710	meiotic mismatch repair
GO:0001752	compound eye photoreceptor fate commitment
GO:0002181	cytoplasmic translation
GO:0006163	purine nucleotide metabolic process
GO:0006301	postreplication repair
GO:0006438	valyl-tRNA aminoacylation
GO:0006520	cellular amino acid metabolic process
GO:0006796	phosphate-containing compound metabolic process
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER

TABLE E.1: (continued)

GO ID	GO TERM
GO:0006909	phagocytosis
GO:0007192	adenylate cyclase-activating serotonin receptor signaling pathway
GO:0007406	negative regulation of neuroblast proliferation
GO:0007465	R7 cell fate commitment
GO:0007562	eclosion
GO:0007615	anesthesia-resistant memory
GO:0007638	mechanosensory behavior
GO:0008348	negative regulation of antimicrobial humoral response
GO:0009968	negative regulation of signal transduction
GO:0010259	multicellular organism aging
GO:0010332	response to gamma radiation
GO:0010906	regulation of glucose metabolic process
GO:0016079	synaptic vesicle exocytosis
GO:0016543	male courtship behavior
GO:0016545	male courtship behavior
GO:0016546	male courtship behavior
GO:0016584	nucleosome positioning
GO:0019226	transmission of nerve impulse
GO:0019233	sensory perception of pain
GO:0022600	digestive system process
GO:0030421	defecation
GO:0032482	Rab protein signal transduction
GO:0032504	multicellular organism reproduction
GO:0032507	maintenance of protein location in cell
GO:0032509	endosome transport via multivesicular body sorting pathway
GO:0032940	secretion by cell
GO:0033363	secretory granule organization
GO:0034620	cellular response to unfolded protein
GO:0034976	response to endoplasmic reticulum stress
GO:0035041	sperm chromatin decondensation
GO:0035063	nuclear speck organization
GO:0035076	ecdysone receptor-mediated signaling pathway
GO:0035092	sperm chromatin condensation

TABLE E.1: (continued)

GO ID	GO TERM
GO:0035148	tube formation
GO:0035172	hemocyte proliferation
GO:0035249	synaptic transmission, glutamatergic
GO:0035329	hippo signaling
GO:0035626	juvenile hormone mediated signaling pathway
GO:0036335	intestinal stem cell homeostasis
GO:0042326	negative regulation: phosphorylation
GO:0042331	phototaxis
GO:0042766	nucleosome mobilization
GO:0043044	ATP-dependent chromatin remodeling
GO:0043069	negative regulation: programmed cell death
GO:0043154	negative regulation: cysteine-type endopeptidase activity (apoptotic process)
GO:0043974	histone H3-K27 acetylation
GO:0044711	single-organism biosynthetic process
GO:0045088	regulation of innate immune response
GO:0045742	positive regulation: epidermal growth factor receptor signaling pathway
GO:0045823	positive regulation: heart contraction
GO:0045956	positive regulation: calcium ion-dependent exocytosis
GO:0046579	positive regulation: Ras protein signal transduction
GO:0046844	micropyle formation
GO:0048096	chromatin-mediated maintenance of transcription
GO:0048812	neuron projection morphogenesis
GO:0050770	regulation of axonogenesis
GO:0050975	sensory perception of touch
GO:0055086	nucleobase-containing small molecule metabolic process
GO:0060180	female mating behavior
GO:0060429	epithelium development
GO:0071108	protein K48-linked deubiquitination
GO:0072375	medium-term memory
GO:0072528	pyrimidine-containing compound biosynthetic process
GO:0090277	positive regulation of peptide hormone secretion
GO:0097340	inhibition of cysteine-type endopeptidase activity
GO:1990504	dense core granule exocytosis

TABLE E.1: (continued)

GO ID	GO TERM
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle
GO:2000648	positive regulation of stem cell proliferation
GO:2001136	negative regulation of endocytic recycling
GO:0000026	alpha-1,2-mannosyltransferase activity
GO:0000257	nitrilase activity
GO:0000790	nuclear chromatin
GO:0000815	ESCRT III complex
GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding
GO:0004588	orotate phosphoribosyltransferase activity
GO:0004590	orotidine-5'-phosphate decarboxylase activity
GO:0004832	valine-tRNA ligase activity
GO:0004843	thiol-dependent ubiquitin-specific protease activity
GO:0004869	cysteine-type endopeptidase inhibitor activity
GO:0004880	juvenile hormone receptor activity
GO:0004952	dopamine neurotransmitter receptor activity
GO:0004972	NMDA glutamate receptor activity
GO:0004993	G-protein coupled serotonin receptor activity
GO:0005070	SH3/SH2 adaptor activity
GO:0005088	Ras guanyl-nucleotide exchange factor activity
GO:0005500	juvenile hormone binding
GO:0005770	late endosome
GO:0005778	peroxisomal membrane
GO:0008188	neuropeptide receptor activity
GO:0008261	allatostatin receptor activity
GO:0008328	ionotropic glutamate receptor complex
GO:0008623	CHRAC
GO:0012505	endomembrane system
GO:0015026	coreceptor activity
GO:0015379	potassium:chloride symporter activity
GO:0016528	sarcoplasm
GO:0016589	NURF complex
GO:0016590	ACF complex
GO:0030121	AP-1 adaptor complex

TABLE E.1: (continued)

GO ID	GO TERM
GO:0030276	clathrin binding
GO:0031213	RSF complex
GO:0031491	nucleosome binding
GO:0031982	vesicle
GO:0035060	brahma complex
GO:0035976	transcription factor AP-1 complex
GO:0042393	histone binding
GO:0042500	aspartic endopeptidase activity, intramembrane cleaving
GO:0042826	histone deacetylase binding
GO:0044390	ubiquitin-like protein conjugating enzyme binding
GO:0061659	ubiquitin-like protein ligase activity
GO:0070604	PBAF complex
GO:0070615	nucleosome-dependent ATPase activity
GO:0071683	sensory dendrite

TABLE E.2: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and allele-specific methylation in reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0008542	visual learning
GO:0010906	regulation of glucose metabolic process
GO:0016079	synaptic vesicle exocytosis
GO:2000169	regulation of peptidyl-cysteine S-nitrosylation
GO:0042326	negative regulation of phosphorylation
GO:0045860	positive regulation of protein kinase activity
GO:0046579	positive regulation of Ras protein signal transduction
GO:0045887	positive regulation of synaptic growth at neuromuscular junction
GO:0000790	nuclear chromatin
GO:0000794	condensed nuclear chromosome
GO:0005705	polytene chromosome interband

TABLE E.14: Significantly overlapping gene ontology terms with allele-specific methylation in reproductive and non-reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO TERM
GO:0008186	RNA-dependent ATPase activity

TABLE E.14: (continued)

GO ID	GO TERM
GO:0015321	sodium-dependent phosphate transmembrane transporter activity
GO:0003724	RNA helicase activity
GO:0042623	ATPase activity, coupled
GO:0070035	purine NTP-dependent helicase activity
GO:0006277	DNA amplification
GO:0044341	sodium-dependent phosphate transport
GO:0007274	neuromuscular synaptic transmission
GO:0007392	initiation of dorsal closure
GO:0030004	cellular monovalent inorganic cation homeostasis
GO:0051298	centrosome duplication
GO:0007098	centrosome cycle
GO:0090160	Golgi to lysosome transport
GO:0010906	regulation of glucose metabolic process
GO:0006354	DNA-templated transcription, elongation
GO:0002181	cytoplasmic translation
GO:0060968	regulation of gene silencing
GO:0031123	RNA 3'-end processing
GO:0010498	proteasomal protein catabolic process
GO:0018212	peptidyl-tyrosine modification
GO:0038127	ERBB signaling pathway
GO:0006368	transcription elongation from RNA polymerase II promoter
GO:0032784	regulation: DNA-templated transcription, elongation
GO:0000725	recombinational repair
GO:0061647	histone H3-K9 modification
GO:0046578	regulation of Ras protein signal transduction
GO:0046777	protein autophosphorylation
GO:0035167	larval lymph gland hemopoiesis
GO:0035168	larval lymph gland hemocyte differentiation
GO:0035171	lamellocyte differentiation
GO:0042065	glial cell growth
GO:0006366	transcription from RNA polymerase II promoter
GO:0042455	ribonucleoside biosynthetic process
GO:0032543	mitochondrial translation

TABLE E.14: (continued)

GO ID	GO TERM
GO:0098728	germline stem cell asymmetric division
GO:0000380	alternative mRNA splicing, via spliceosome
GO:0052548	regulation of endopeptidase activity
GO:0000076	DNA replication checkpoint
GO:0070646	protein modification by small protein removal
GO:0045047	protein targeting to ER
GO:0045055	regulated exocytosis
GO:0007469	antennal development
GO:0008038	neuron recognition
GO:0048592	eye morphogenesis
GO:0023014	signal transduction by protein phosphorylation
GO:0080009	mRNA methylation
GO:0008595	anterior/posterior axis specification, embryo
GO:0007354	zygotic determination of anterior/posterior axis, embryo
GO:0007351	tripartite regional subdivision
GO:0007315	pole plasm assembly
GO:0008358	maternal determination of anterior/posterior axis, embryo
GO:0008380	RNA splicing
GO:0016556	mRNA modification
GO:0008582	regulation of synaptic growth at neuromuscular junction
GO:0045887	positive regulation: synaptic growth at neuromuscular junction
GO:0051965	positive regulation: synapse assembly
GO:0030239	myofibril assembly
GO:1905269	positive regulation of chromatin organization
GO:0051306	mitotic sister chromatid separation
GO:0044784	metaphase/anaphase transition of cell cycle
GO:0010965	regulation: mitotic sister chromatid separation
GO:0033047	regulation: mitotic sister chromatid segregation
GO:0007091	metaphase/anaphase transition of mitotic cell cycle
GO:0000165	MAPK cascade
GO:0044786	cell cycle DNA replication
GO:1900073	regulation of neuromuscular synaptic transmission
GO:1903508	positive regulation: nucleic acid-templated transcription

TABLE E.14: (continued)

GO ID	GO TERM
GO:1902680	positive regulation: RNA biosynthetic process
GO:0051254	positive regulation: RNA metabolic process
GO:0070371	ERK1 and ERK2 cascade
GO:0006351	transcription, DNA-templated
GO:0018022	peptidyl-lysine methylation
GO:0042551	neuron maturation
GO:0050708	regulation of protein secretion
GO:1903532	positive regulation of secretion by cell
GO:0046530	photoreceptor cell differentiation
GO:0043484	regulation of RNA splicing
GO:2001234	negative regulation: apoptotic signaling pathway
GO:0014009	glial cell proliferation
GO:0043549	regulation of kinase activity
GO:0001934	positive regulation: protein phosphorylation
GO:0045860	positive regulation: protein kinase activity
GO:0001932	regulation of protein phosphorylation
GO:0045859	regulation of protein kinase activity
GO:0071900	regulation of protein serine/threonine kinase activity
GO:0042327	positive regulation: phosphorylation
GO:0033674	positive regulation: kinase activity
GO:0099500	vesicle fusion to plasma membrane
GO:1904894	positive regulation: STAT cascade
GO:0030703	eggshell formation
GO:0035309	wing and notum subfield formation
GO:0010389	regulation of G2/M transition of mitotic cell cycle
GO:0044818	mitotic G2/M transition checkpoint
GO:1902750	negative regulation: cell cycle G2/M phase transition
GO:0010972	negative regulation: G2/M transition of mitotic cell cycle
GO:0006397	mRNA processing
GO:0018205	peptidyl-lysine modification
GO:0051567	histone H3-K9 methylation
GO:0009161	ribonucleoside monophosphate metabolic process
GO:0009124	nucleoside monophosphate biosynthetic process

TABLE E.14: (continued)

GO ID	GO TERM
GO:0009156	ribonucleoside monophosphate biosynthetic process
GO:0046528	imaginal disc fusion
GO:0035096	larval midgut cell programmed cell death
GO:0045892	negative regulation: transcription, DNA-templated
GO:1902679	negative regulation: RNA biosynthetic process
GO:0051253	negative regulation: RNA metabolic process
GO:1903507	negative regulation: nucleic acid-templated transcription
GO:0045736	negative regulation: cyclin-dependent protein serine/threonine kinase activity
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process
GO:0070304	positive regulation: stress-activated protein kinase signaling cascade
GO:0046330	positive regulation: JNK cascade
GO:0046328	regulation of JNK cascade
GO:0032874	positive regulation: stress-activated MAPK cascade
GO:0032872	regulation of stress-activated MAPK cascade
GO:0007254	JNK cascade
GO:0051403	stress-activated MAPK cascade
GO:0050684	regulation: mRNA processing
GO:0048024	regulation: mRNA splicing, via spliceosome
GO:0000381	regulation: alternative mRNA splicing, via spliceosome
GO:0006357	regulation: transcription from RNA polymerase II promoter
GO:0099531	presynaptic process involved in chemical synaptic transmission
GO:0007307	eggshell chorion gene amplification
GO:0001510	RNA methylation
GO:1903311	regulation: mRNA metabolic process
GO:0090092	regulation: transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0060251	regulation: glial cell proliferation
GO:0060253	negative regulation of glial cell proliferation
GO:0035166	post-embryonic hemopoiesis
GO:0031400	negative regulation: protein modification process
GO:0006613	cotranslational protein targeting to membrane
GO:1904030	negative regulation: cyclin-dependent protein kinase activity

TABLE E.14: (continued)

GO ID	GO TERM
GO:0061564	axon development
GO:0031124	mRNA 3'-end processing
GO:0035194	posttranscriptional gene silencing by RNA
GO:0016246	RNA interference
GO:0017156	calcium ion regulated exocytosis
GO:0042706	eye photoreceptor cell fate commitment
GO:0048515	spermatid differentiation
GO:0048167	regulation: synaptic plasticity
GO:0046532	regulation: photoreceptor cell differentiation
GO:0031937	positive regulation of chromatin silencing
GO:0070372	regulation of ERK1 and ERK2 cascade
GO:0070374	positive regulation of ERK1 and ERK2 cascade
GO:0031572	G2 DNA damage checkpoint
GO:0099643	signal release from synapse
GO:0046552	photoreceptor cell fate commitment
GO:0016441	posttranscriptional gene silencing
GO:0046579	positive regulation of Ras protein signal transduction
GO:0034243	regulation of transcription elongation from RNA polymerase II promoter
GO:0021782	glial cell development
GO:0009259	ribonucleotide metabolic process
GO:0051057	positive regulation: small GTPase mediated signal transduction
GO:0032786	positive regulation: DNA-templated transcription, elongation
GO:0050804	modulation of synaptic transmission
GO:0048599	oocyte development
GO:0007308	oocyte construction
GO:0016571	histone methylation
GO:0031401	positive regulation of protein modification process
GO:0031047	gene silencing by RNA
GO:0006348	chromatin silencing at telomere
GO:0006342	chromatin silencing
GO:0046666	retinal cell programmed cell death
GO:0018393	internal peptidyl-lysine acetylation
GO:0018394	peptidyl-lysine acetylation

TABLE E.14: (continued)

GO ID	GO TERM
GO:0006473	protein acetylation
GO:0006475	internal protein amino acid acetylation
GO:0045664	regulation of neuron differentiation
GO:0050769	positive regulation of neurogenesis
GO:0050768	negative regulation of neurogenesis
GO:0050767	regulation of neurogenesis
GO:0032446	protein modification by small protein conjugation
GO:0007476	imaginal disc-derived wing morphogenesis
GO:0007560	imaginal disc morphogenesis
GO:0007472	wing disc morphogenesis
GO:1904029	regulation: cyclin-dependent protein kinase activity
GO:0042326	negative regulation: phosphorylation
GO:0001933	negative regulation: protein phosphorylation
GO:0071901	negative regulation: protein serine/threonine kinase activity
GO:0033673	negative regulation: kinase activity
GO:0010952	positive regulation: peptidase activity
GO:0090101	negative regulation: transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0045862	positive regulation: proteolysis
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity
GO:1901991	negative regulation: mitotic cell cycle phase transition
GO:0031629	synaptic vesicle fusion to presynaptic active zone membrane
GO:0032147	activation of protein kinase activity
GO:2000116	regulation: cysteine-type endopeptidase activity
GO:0014013	regulation: gliogenesis
GO:0097485	neuron projection guidance
GO:0006511	ubiquitin-dependent protein catabolic process
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
GO:0019941	modification-dependent protein catabolic process
GO:0000398	mRNA splicing, via spliceosome
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000375	RNA splicing, via transesterification reactions

TABLE E.14: (continued)

GO ID	GO TERM
GO:0006355	regulation: transcription, DNA-templated
GO:0009994	oocyte differentiation
GO:0014014	negative regulation of gliogenesis
GO:0030707	ovarian follicle cell development
GO:2001056	positive regulation: cysteine-type endopeptidase activity
GO:0010950	positive regulation: endopeptidase activity
GO:0043408	regulation of MAPK cascade
GO:0032968	positive regulation: transcription elongation from RNA polymerase II promoter
GO:0044773	mitotic DNA damage checkpoint
GO:0097659	nucleic acid-templated transcription
GO:0030509	BMP signaling pathway
GO:0030510	regulation of BMP signaling pathway
GO:0043405	regulation of MAP kinase activity
GO:0043410	positive regulation of MAPK cascade
GO:0001754	eye photoreceptor cell differentiation
GO:0001751	compound eye photoreceptor cell differentiation
GO:0009260	ribonucleotide biosynthetic process
GO:0030641	regulation of cellular pH
GO:0007304	chorion-containing eggshell formation
GO:0007297	ovarian follicle cell migration
GO:0007306	eggshell chorion assembly
GO:0048667	cell morphogenesis involved in neuron differentiation
GO:0030182	neuron differentiation
GO:0031175	neuron projection development
GO:0048666	neuron development
GO:2001141	regulation: RNA biosynthetic process
GO:0044774	mitotic DNA integrity checkpoint
GO:1903506	regulation: nucleic acid-templated transcription
GO:0007269	neurotransmitter secretion
GO:0016079	synaptic vesicle exocytosis
GO:0005938	cell cortex
GO:0005700	polytene chromosome
GO:0008541	proteasome regulatory particle, lid subcomplex

TABLE E.14: (continued)

GO ID	GO TERM
GO:0005685	U1 snRNP
GO:0015629	actin cytoskeleton
GO:0000313	organellar ribosome
GO:0005726	perichromatin fibrils
GO:0000315	organellar large ribosomal subunit
GO:0008023	transcription elongation factor complex
GO:0005681	spliceosomal complex
GO:0000793	condensed chromosome
GO:0000775	chromosome, centromeric region
GO:0016604	nuclear body
GO:0005654	nucleoplasm
GO:0015935	small ribosomal subunit
GO:0005875	microtubule associated complex
GO:0000785	chromatin
GO:0000228	nuclear chromosome
GO:0000790	nuclear chromatin
GO:0015630	microtubule cytoskeleton
GO:0019866	organelle inner membrane
GO:0022626	cytosolic ribosome
GO:0030133	transport vesicle
GO:0030016	myofibril
GO:0061174	type I terminal bouton
GO:0044445	cytosolic part
GO:0035101	FACT complex
GO:0051233	spindle midzone
GO:0036379	myofilament
GO:0030017	sarcomere
GO:0044449	contractile fiber part
GO:0031674	I band
GO:0099503	secretory vesicle
GO:0044448	cell cortex part
GO:0098687	chromosomal region
GO:0071011	precatalytic spliceosome

TABLE E.14: (continued)

GO ID	GO TERM
GO:0044429	mitochondrial part
GO:0097525	spliceosomal snRNP complex
GO:0044391	ribosomal subunit
GO:0030532	small nuclear ribonucleoprotein complex
GO:0044428	nuclear part
GO:0044451	nucleoplasm part
GO:0044430	cytoskeletal part
GO:0070382	exocytic vesicle
GO:0071013	catalytic step 2 spliceosome
GO:0061177	type Is terminal bouton
GO:0061176	type Ib terminal bouton
GO:0044427	chromosomal part
GO:0031981	nuclear lumen
GO:0044454	nuclear chromosome part
GO:0099513	polymeric cytoskeletal fiber
GO:0030864	cortical actin cytoskeleton

TABLE E.17: Significantly overlapping gene ontology terms with allele-specific methylation in reproductive workers and hypermethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO TERM
GO:0002784	regulation: antimicrobial peptide production
GO:0007098	centrosome cycle
GO:0045047	protein targeting to ER
GO:0006354	DNA-templated transcription, elongation
GO:0046528	imaginal disc fusion
GO:0010906	regulation of glucose metabolic process
GO:0002181	cytoplasmic translation
GO:0038127	ERBB signaling pathway
GO:0060968	regulation of gene silencing
GO:0031123	RNA 3'-end processing
GO:0010498	proteasomal protein catabolic process

TABLE E.17: (continued)

GO ID	GO TERM
GO:0009161	ribonucleoside monophosphate metabolic process
GO:0006368	transcription elongation from RNA polymerase II promoter
GO:0098728	germline stem cell asymmetric division
GO:0043549	regulation of kinase activity
GO:0001934	positive regulation of protein phosphorylation
GO:0001932	regulation: protein phosphorylation
GO:0045859	regulation: protein kinase activity
GO:0042327	positive regulation of phosphorylation
GO:0071900	regulation: protein serine/threonine kinase activity
GO:0033674	positive regulation: kinase activity
GO:0006366	transcription from RNA polymerase II promoter
GO:0008595	anterior/posterior axis specification, embryo
GO:0007351	tripartite regional subdivision
GO:0007315	pole plasm assembly
GO:0008358	maternal determination: anterior/posterior axis, embryo
GO:1904894	positive regulation: STAT cascade
GO:0043484	regulation of RNA splicing
GO:0070646	protein modification by small protein removal
GO:0023014	signal transduction by protein phosphorylation
GO:0045862	positive regulation: proteolysis
GO:0008038	neuron recognition
GO:0050708	regulation of protein secretion
GO:1903532	positive regulation: secretion by cell
GO:0008380	RNA splicing
GO:0046532	regulation of photoreceptor cell differentiation
GO:0000165	MAPK cascade
GO:0070371	ERK1 and ERK2 cascade
GO:0006351	transcription, DNA-templated
GO:0006397	mRNA processing
GO:0048592	eye morphogenesis
GO:0042551	neuron maturation
GO:0046530	photoreceptor cell differentiation
GO:1903507	negative regulation: nucleic acid-templated transcription

TABLE E.17: (continued)

GO ID	GO TERM
GO:1902679	negative regulation: RNA biosynthetic process
GO:0051253	negative regulation: RNA metabolic process
GO:0046578	regulation of Ras protein signal transduction
GO:0000380	alternative mRNA splicing, via spliceosome
GO:0070304	positive regulation: stress-activated protein kinase signaling cascade
GO:0046328	regulation of JNK cascade
GO:0032874	positive regulation: stress-activated MAPK cascade
GO:0032872	regulation: stress-activated MAPK cascade
GO:0007254	JNK cascade
GO:0051403	stress-activated MAPK cascade
GO:0048515	spermatid differentiation
GO:0050684	regulation: mRNA processing
GO:0048024	regulation: mRNA splicing, via spliceosome
GO:0000381	regulation: alternative mRNA splicing, via spliceosome
GO:1903311	regulation: mRNA metabolic process
GO:0031400	negative regulation: protein modification process
GO:0006613	cotranslational protein targeting to membrane
GO:0061564	axon development
GO:0007304	chorion-containing eggshell formation
GO:0007306	eggshell chorion assembly
GO:0030703	eggshell formation
GO:0070372	regulation of ERK1 and ERK2 cascade
GO:0070374	positive regulation of ERK1 and ERK2 cascade
GO:0046579	positive regulation of Ras protein signal transduction
GO:0009259	ribonucleotide metabolic process
GO:0051057	positive regulation: small GTPase mediated signal transduction
GO:0048599	oocyte development
GO:0007308	oocyte construction
GO:0007472	wing disc morphogenesis
GO:0007560	imaginal disc morphogenesis
GO:0031047	gene silencing by RNA
GO:0031401	positive regulation: protein modification process
GO:0045664	regulation of neuron differentiation

TABLE E.17: (continued)

GO ID	GO TERM
GO:0050769	positive regulation of neurogenesis
GO:0050767	regulation of neurogenesis
GO:0032446	protein modification by small protein conjugation
GO:0042326	negative regulation: phosphorylation
GO:0001933	negative regulation: protein phosphorylation
GO:0071901	negative regulation: protein serine/threonine kinase activity
GO:0033673	negative regulation: kinase activity
GO:0032147	activation of protein kinase activity
GO:0097485	neuron projection guidance
GO:0006511	ubiquitin-dependent protein catabolic process
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
GO:0019941	modification-dependent protein catabolic process
GO:0000398	mRNA splicing, via spliceosome
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000375	RNA splicing, via transesterification reactions
GO:1903506	regulation of nucleic acid-templated transcription
GO:0043406	positive regulation of MAP kinase activity
GO:0009994	oocyte differentiation
GO:0043408	regulation of MAPK cascade
GO:0097659	nucleic acid-templated transcription
GO:0043405	regulation of MAP kinase activity
GO:0043410	positive regulation of MAPK cascade
GO:0001754	eye photoreceptor cell differentiation
GO:0001751	compound eye photoreceptor cell differentiation
GO:0048667	cell morphogenesis involved in neuron differentiation
GO:0030182	neuron differentiation
GO:0031175	neuron projection development
GO:0048666	neuron development
GO:2001141	regulation of RNA biosynthetic process
GO:0044448	cell cortex part
GO:0015630	microtubule cytoskeleton
GO:0044430	cytoskeletal part

TABLE E.17: (continued)

GO ID	GO TERM
GO:0099503	secretory vesicle
GO:0019866	organelle inner membrane
GO:0044445	cytosolic part
GO:0005681	spliceosomal complex
GO:0098687	chromosomal region
GO:0044429	mitochondrial part
GO:0044391	ribosomal subunit
GO:0044428	nuclear part
GO:0022626	cytosolic ribosome
GO:0044451	nucleoplasm part
GO:0070382	exocytic vesicle
GO:0005875	microtubule associated complex
GO:0044427	chromosomal part
GO:0099513	polymeric cytoskeletal fiber
GO:0031981	nuclear lumen
GO:0044454	nuclear chromosome part
GO:0000228	nuclear chromosome
GO:0005654	nucleoplasm

TABLE E.18: Significantly overlapping gene ontology terms with allele-specific methylation in reproductive workers and hypomethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO TERM
GO:0070035	purine NTP-dependent helicase activity
GO:0042623	ATPase activity, coupled
GO:0045055	regulated exocytosis
GO:0010498	proteasomal protein catabolic process
GO:0008595	anterior/posterior axis specification, embryo
GO:0007351	tripartite regional subdivision
GO:0007315	pole plasm assembly
GO:0008358	maternal determination of anterior/posterior axis, embryo
GO:0010906	regulation of glucose metabolic process

TABLE E.18: (continued)

GO ID	GO TERM
GO:0006354	DNA-templated transcription, elongation
GO:0007098	centrosome cycle
GO:0099531	presynaptic process involved in chemical synaptic transmission
GO:0000725	recombinational repair
GO:0035194	posttranscriptional gene silencing by RNA
GO:0031123	RNA 3'-end processing
GO:0002181	cytoplasmic translation
GO:0009161	ribonucleoside monophosphate metabolic process
GO:0018205	peptidyl-lysine modification
GO:0006368	transcription elongation from RNA polymerase II promoter
GO:1904894	positive regulation of STAT cascade
GO:0038127	ERBB signaling pathway
GO:0043549	regulation of kinase activity
GO:0001932	regulation of protein phosphorylation
GO:0071900	regulation of protein serine/threonine kinase activity
GO:0032147	activation of protein kinase activity
GO:0033674	positive regulation of kinase activity
GO:0006366	transcription from RNA polymerase II promoter
GO:0007483	genital disc morphogenesis
GO:0048805	imaginal disc-derived genitalia morphogenesis
GO:0007485	imaginal disc-derived male genitalia development
GO:0007484	imaginal disc-derived genitalia development
GO:0030539	male genitalia development
GO:0035112	genitalia morphogenesis
GO:0042551	neuron maturation
GO:0043484	regulation of RNA splicing
GO:0070646	protein modification by small protein removal
GO:0023014	signal transduction by protein phosphorylation
GO:0031572	G2 DNA damage checkpoint
GO:0008380	RNA splicing
GO:0098728	germline stem cell asymmetric division
GO:1903508	positive regulation of nucleic acid-templated transcription
GO:1902680	positive regulation of RNA biosynthetic process

TABLE E.18: (continued)

GO ID	GO TERM
GO:0051254	positive regulation of RNA metabolic process
GO:0046532	regulation of photoreceptor cell differentiation
GO:0000165	MAPK cascade
GO:0051306	mitotic sister chromatid separation
GO:0010965	regulation of mitotic sister chromatid separation
GO:0033047	regulation of mitotic sister chromatid segregation
GO:0007091	metaphase/anaphase transition of mitotic cell cycle
GO:0044784	metaphase/anaphase transition of cell cycle
GO:0006351	transcription, DNA-templated
GO:0006397	mRNA processing
GO:0048592	eye morphogenesis
GO:0008582	regulation of synaptic growth at neuromuscular junction
GO:0051965	positive regulation of synapse assembly
GO:0045887	positive regulation of synaptic growth at neuromuscular junction
GO:0046530	photoreceptor cell differentiation
GO:1903507	negative regulation of nucleic acid-templated transcription
GO:1902679	negative regulation of RNA biosynthetic process
GO:0051253	negative regulation of RNA metabolic process
GO:0018022	peptidyl-lysine methylation
GO:0030703	eggshell formation
GO:0010389	regulation of G2/M transition of mitotic cell cycle
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle
GO:0044818	mitotic G2/M transition checkpoint
GO:1902750	negative regulation of cell cycle G2/M phase transition
GO:0000380	alternative mRNA splicing, via spliceosome
GO:0050684	regulation of mRNA processing
GO:0048024	regulation of mRNA splicing, via spliceosome
GO:0000381	regulation of alternative mRNA splicing, via spliceosome
GO:0006357	regulation of transcription from RNA polymerase II promoter
GO:1903311	regulation of mRNA metabolic process
GO:0061564	axon development
GO:0007306	eggshell chorion assembly
GO:0017156	calcium ion regulated exocytosis

TABLE E.18: (continued)

GO ID	GO TERM
GO:0048515	spermatid differentiation
GO:0032872	regulation of stress-activated MAPK cascade
GO:0099643	signal release from synapse
GO:0016441	posttranscriptional gene silencing
GO:0043406	positive regulation of MAP kinase activity
GO:0009259	ribonucleotide metabolic process
GO:0031401	positive regulation of protein modification process
GO:0048599	oocyte development
GO:0007308	oocyte construction
GO:0007476	imaginal disc-derived wing morphogenesis
GO:0007560	imaginal disc morphogenesis
GO:0007472	wing disc morphogenesis
GO:0016571	histone methylation
GO:0031400	negative regulation of protein modification process
GO:0031047	gene silencing by RNA
GO:0018393	internal peptidyl-lysine acetylation
GO:0006473	protein acetylation
GO:0006475	internal protein amino acid acetylation
GO:0018394	peptidyl-lysine acetylation
GO:0045664	regulation of neuron differentiation
GO:0050769	positive regulation of neurogenesis
GO:0050767	regulation of neurogenesis
GO:0032446	protein modification by small protein conjugation
GO:0042326	negative regulation of phosphorylation
GO:0001933	negative regulation of protein phosphorylation
GO:0044773	mitotic DNA damage checkpoint
GO:0000398	mRNA splicing, via spliceosome
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000375	RNA splicing, via transesterification reactions
GO:1903506	regulation of nucleic acid-templated transcription
GO:0009994	oocyte differentiation
GO:0030707	ovarian follicle cell development

TABLE E.18: (continued)

GO ID	GO TERM
GO:0048808	male genitalia morphogenesis
GO:0035126	post-embryonic genitalia morphogenesis
GO:0043408	regulation of MAPK cascade
GO:0019941	modification-dependent protein catabolic process
GO:1901991	negative regulation of mitotic cell cycle phase transition
GO:0097659	nucleic acid-templated transcription
GO:0043405	regulation of MAP kinase activity
GO:0043410	positive regulation of MAPK cascade
GO:0001754	eye photoreceptor cell differentiation
GO:0001751	compound eye photoreceptor cell differentiation
GO:0007297	ovarian follicle cell migration
GO:0048667	cell morphogenesis involved in neuron differentiation
GO:0030182	neuron differentiation
GO:0031175	neuron projection development
GO:0048666	neuron development
GO:0044774	mitotic DNA integrity checkpoint
GO:2001141	regulation of RNA biosynthetic process
GO:0044445	cytosolic part
GO:0005700	polytene chromosome
GO:0019866	organelle inner membrane
GO:0099503	secretory vesicle
GO:0015630	microtubule cytoskeleton
GO:0044430	cytoskeletal part
GO:0097525	spliceosomal snRNP complex
GO:0044429	mitochondrial part
GO:0044391	ribosomal subunit
GO:0016604	nuclear body
GO:0005681	spliceosomal complex
GO:0044428	nuclear part
GO:0098687	chromosomal region
GO:0022626	cytosolic ribosome
GO:0070382	exocytic vesicle
GO:0030133	transport vesicle

TABLE E.18: (continued)

GO ID	GO TERM
GO:0000790	nuclear chromatin
GO:0044454	nuclear chromosome part
GO:0005875	microtubule associated complex
GO:0044451	nucleoplasm part
GO:0000785	chromatin
GO:0031981	nuclear lumen
GO:0044427	chromosomal part
GO:0000228	nuclear chromosome
GO:0005654	nucleoplasm

TABLE E.21: Significantly overlapping gene ontology terms with allele-specific methylation in non-reproductive workers and hypermethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO TERM
GO:0042625	ATPase coupled ion transmembrane transporter activity
GO:0036442	hydrogen-exporting ATPase activity
GO:0043492	ATPase activity, coupled to movement of substances
GO:0044769	ATPase activity, coupled to transmembrane movement of ions, rotational mechanism
GO:0016073	snRNA metabolic process
GO:0099132	ATP hydrolysis coupled cation transmembrane transport
GO:0007098	centrosome cycle
GO:0008101	decapentaplegic signaling pathway
GO:0060446	branching involved in open tracheal system development
GO:0010498	proteasomal protein catabolic process
GO:0006101	citrate metabolic process
GO:0060968	regulation of gene silencing
GO:0006354	DNA-templated transcription, elongation
GO:0031123	RNA 3'-end processing
GO:0010906	regulation of glucose metabolic process
GO:0002181	cytoplasmic translation
GO:0045047	protein targeting to ER

TABLE E.21: (continued)

GO ID	GO TERM
GO:0046425	regulation of JAK-STAT cascade
GO:0046427	positive regulation of JAK-STAT cascade
GO:1904894	positive regulation of STAT cascade
GO:0006368	transcription elongation from RNA polymerase II promoter
GO:0098728	germline stem cell asymmetric division
GO:0046128	purine ribonucleoside metabolic process
GO:0009259	ribonucleotide metabolic process
GO:0006163	purine nucleotide metabolic process
GO:0009150	purine ribonucleotide metabolic process
GO:0006366	transcription from RNA polymerase II promoter
GO:0023014	signal transduction by protein phosphorylation
GO:0061355	Wnt protein secretion
GO:0045862	positive regulation of proteolysis
GO:0006413	translational initiation
GO:0048749	compound eye development
GO:0043484	regulation of RNA splicing
GO:0070646	protein modification by small protein removal
GO:0043628	ncRNA 3'-end processing
GO:0010160	formation of animal organ boundary
GO:0048488	synaptic vesicle endocytosis
GO:0008038	neuron recognition
GO:0008380	RNA splicing
GO:0050708	regulation of protein secretion
GO:1903532	positive regulation of secretion by cell
GO:0046532	regulation of photoreceptor cell differentiation
GO:0006399	tRNA metabolic process
GO:0000165	MAPK cascade
GO:0006405	RNA export from nucleus
GO:0070371	ERK1 and ERK2 cascade
GO:0038127	ERBB signaling pathway
GO:0006351	transcription, DNA-templated
GO:0051058	negative regulation: small GTPase mediated signal transduction
GO:0006397	mRNA processing

TABLE E.21: (continued)

GO ID	GO TERM
GO:0046528	imaginal disc fusion
GO:0042551	neuron maturation
GO:0046530	photoreceptor cell differentiation
GO:1903507	negative regulation: nucleic acid-templated transcription
GO:1902679	negative regulation: RNA biosynthetic process
GO:0051253	negative regulation: RNA metabolic process
GO:0033674	positive regulation: kinase activity
GO:0001934	positive regulation: protein phosphorylation
GO:0042327	positive regulation: phosphorylation
GO:0032147	activation of protein kinase activity
GO:0008595	anterior/posterior axis specification, embryo
GO:0007351	tripartite regional subdivision
GO:0008358	maternal determination of anterior/posterior axis, embryo
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0007304	chorion-containing eggshell formation
GO:0007306	eggshell chorion assembly
GO:0006417	regulation: translation
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient
GO:0000380	alternative mRNA splicing, via spliceosome
GO:0061357	positive regulation of Wnt protein secretion
GO:0061356	regulation: Wnt protein secretion
GO:0046579	positive regulation of Ras protein signal transduction
GO:0051057	positive regulation of small GTPase mediated signal transduction
GO:0045570	regulation: imaginal disc growth
GO:0016358	dendrite development
GO:0060966	regulation of gene silencing by RNA
GO:0009167	purine ribonucleoside monophosphate metabolic process
GO:0009205	purine ribonucleoside triphosphate metabolic process
GO:0009126	purine nucleoside monophosphate metabolic process
GO:0009144	purine nucleoside triphosphate metabolic process
GO:0009161	ribonucleoside monophosphate metabolic process
GO:0046034	ATP metabolic process

TABLE E.21: (continued)

GO ID	GO TERM
GO:0009199	ribonucleoside triphosphate metabolic process
GO:0050684	regulation: mRNA processing
GO:0048024	regulation: mRNA splicing, via spliceosome
GO:0000381	regulation: alternative mRNA splicing, via spliceosome
GO:0016198	axon choice point recognition
GO:1903311	regulation: mRNA metabolic process
GO:0070303	negative regulation: stress-activated protein kinase signaling cascade
GO:0045676	regulation: R7 cell differentiation
GO:0031400	negative regulation of protein modification process
GO:0006613	cotranslational protein targeting to membrane
GO:0051663	oocyte nucleus localization: oocyte dorsal/ventral axis specification
GO:0042773	ATP synthesis coupled electron transport
GO:0038066	p38MAPK cascade
GO:0070372	regulation of ERK1 and ERK2 cascade
GO:0070373	negative regulation: ERK1 and ERK2 cascade
GO:0070374	positive regulation: ERK1 and ERK2 cascade
GO:0045664	regulation of neuron differentiation
GO:0010975	regulation of neuron projection development
GO:0045666	positive regulation: neuron differentiation
GO:0050769	positive regulation: neurogenesis
GO:0050767	regulation of neurogenesis
GO:0030703	eggshell formation
GO:0046831	regulation: RNA export from nucleus
GO:1900744	regulation: p38MAPK cascade
GO:0007286	spermatid development
GO:0034472	snRNA 3'-end processing
GO:0001933	negative regulation: protein phosphorylation
GO:0042326	negative regulation: phosphorylation
GO:0071901	negative regulation: protein serine/threonine kinase activity
GO:0043409	negative regulation: MAPK cascade
GO:0006469	negative regulation: protein kinase activity
GO:0033673	negative regulation: kinase activity
GO:1902600	hydrogen ion transmembrane transport

TABLE E.21: (continued)

GO ID	GO TERM
GO:0046578	regulation of Ras protein signal transduction
GO:0046824	positive regulation: nucleocytoplasmic transport
GO:0007472	wing disc morphogenesis
GO:0007560	imaginal disc morphogenesis
GO:0032873	negative regulation of stress-activated MAPK cascade
GO:0031047	gene silencing by RNA
GO:0031401	positive regulation of protein modification process
GO:0045859	regulation of protein kinase activity
GO:0001932	regulation of protein phosphorylation
GO:0043549	regulation of kinase activity
GO:0048599	oocyte development
GO:0007308	oocyte construction
GO:0007309	oocyte axis specification
GO:0007316	pole plasm RNA localization
GO:0007315	pole plasm assembly
GO:0007314	oocyte anterior/posterior axis specification
GO:0036465	synaptic vesicle recycling
GO:0032446	protein modification by small protein conjugation
GO:0048592	eye morphogenesis
GO:0061564	axon development
GO:0043408	regulation of MAPK cascade
GO:0050773	regulation of dendrite development
GO:0046833	positive regulation of RNA export from nucleus
GO:0034470	ncRNA processing
GO:0007432	salivary gland boundary specification
GO:0001745	compound eye morphogenesis
GO:0001751	compound eye photoreceptor cell differentiation
GO:0097485	neuron projection guidance
GO:0006511	ubiquitin-dependent protein catabolic process
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
GO:0019941	modification-dependent protein catabolic process
GO:0000398	mRNA splicing, via spliceosome

TABLE E.21: (continued)

GO ID	GO TERM
GO:0000377	RNA splicing: transesterification reactions with bulged adenosine as nucleophile
GO:0000375	RNA splicing: transesterification reactions
GO:1903506	regulation of nucleic acid-templated transcription
GO:0009994	oocyte differentiation
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade
GO:0046328	regulation of JNK cascade
GO:0032874	positive regulation of stress-activated MAPK cascade
GO:0032872	regulation of stress-activated MAPK cascade
GO:0007254	JNK cascade
GO:0051403	stress-activated MAPK cascade
GO:0046534	positive regulation of photoreceptor cell differentiation
GO:0060811	intracellular mRNA localization: anterior/posterior axis specification
GO:0019094	pole plasm mRNA localization
GO:0045451	pole plasm oskar mRNA localization
GO:0045450	bicoid mRNA localization
GO:0048515	spermatid differentiation
GO:0030722	establishment of oocyte nucleus localization: oocyte dorsal/ventral axis specification
GO:0097659	nucleic acid-templated transcription
GO:0045678	positive regulation of R7 cell differentiation
GO:0045466	R7 cell differentiation
GO:0043405	regulation of MAP kinase activity
GO:0043410	positive regulation of MAPK cascade
GO:0001754	eye photoreceptor cell differentiation
GO:0042775	mitochondrial ATP synthesis coupled electron transport
GO:0071900	regulation: protein serine/threonine kinase activity
GO:0048667	cell morphogenesis: neuron differentiation
GO:0007409	axonogenesis
GO:0048812	neuron projection morphogenesis
GO:0030182	neuron differentiation
GO:0031175	neuron projection development
GO:0048666	neuron development

TABLE E.21: (continued)

GO ID	GO TERM
GO:2001141	regulation of RNA biosynthetic process
GO:0044448	cell cortex part
GO:0015630	microtubule cytoskeleton
GO:0044430	cytoskeletal part
GO:0089701	U2AF
GO:0099503	secretory vesicle
GO:0044445	cytosolic part
GO:0044437	vacuolar part
GO:0005774	vacuolar membrane
GO:0098798	mitochondrial protein complex
GO:0090544	BAF-type complex
GO:0044432	endoplasmic reticulum part
GO:0098687	chromosomal region
GO:0019866	organelle inner membrane
GO:0070603	SWI/SNF superfamily-type complex
GO:0090575	RNA polymerase II transcription factor complex
GO:0044798	nuclear transcription factor complex
GO:0044428	nuclear part
GO:0055029	nuclear DNA-directed RNA polymerase complex
GO:0044391	ribosomal subunit
GO:0005681	spliceosomal complex
GO:0022626	cytosolic ribosome
GO:0015934	large ribosomal subunit
GO:0044451	nucleoplasm part
GO:0070382	exocytic vesicle
GO:0005746	mitochondrial respiratory chain
GO:0044429	mitochondrial part
GO:0005875	microtubule associated complex
GO:0005768	endosome
GO:0016471	vacuolar proton-transporting V-type ATPase complex
GO:0022625	cytosolic large ribosomal subunit
GO:0044427	chromosomal part
GO:0099513	polymeric cytoskeletal fiber

TABLE E.21: (continued)

GO ID	GO TERM
GO:0044455	mitochondrial membrane part
GO:0031981	nuclear lumen
GO:0099738	cell cortex region
GO:0044454	nuclear chromosome part
GO:0000228	nuclear chromosome
GO:0098800	inner mitochondrial membrane protein complex
GO:0005654	nucleoplasm
GO:0031966	mitochondrial membrane
GO:0005740	mitochondrial envelope

TABLE E.22: Significantly overlapping gene ontology terms with allele-specific methylation in non-reproductive workers and hypomethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO TERM
GO:0070035	purine NTP-dependent helicase activity
GO:0043492	ATPase activity, coupled to movement of substances
GO:0042623	ATPase activity, coupled
GO:0042625	ATPase coupled ion transmembrane transporter activity
GO:0019430	removal of superoxide radicals
GO:0048488	synaptic vesicle endocytosis
GO:0016335	morphogenesis of larval imaginal disc epithelium
GO:0010498	proteasomal protein catabolic process
GO:0006101	citrate metabolic process
GO:0090030	regulation of steroid hormone biosynthetic process
GO:0016073	snRNA metabolic process
GO:0007098	centrosome cycle
GO:0046605	regulation of centrosome cycle
GO:0001174	transcriptional start site selection at RNA polymerase II promoter
GO:0001178	regulation: transcriptional start site selection at RNA polymerase II promoter
GO:0035194	posttranscriptional gene silencing by RNA
GO:0006734	NADH metabolic process
GO:0008101	decapentaplegic signaling pathway

TABLE E.22: (continued)

GO ID	GO TERM
GO:0032482	Rab protein signal transduction
GO:0010906	regulation of glucose metabolic process
GO:0006354	DNA-templated transcription, elongation
GO:0002181	cytoplasmic translation
GO:0018209	peptidyl-serine modification
GO:0099531	presynaptic process involved in chemical synaptic transmission
GO:0043549	regulation of kinase activity
GO:0001932	regulation of protein phosphorylation
GO:0071900	regulation of protein serine/threonine kinase activity
GO:0032147	activation of protein kinase activity
GO:0033674	positive regulation of kinase activity
GO:1904894	positive regulation of STAT cascade
GO:0031056	regulation of histone modification
GO:0031060	regulation of histone methylation
GO:0006479	protein methylation
GO:0016571	histone methylation
GO:0018022	peptidyl-lysine methylation
GO:0060811	intracellular mRNA localization: anterior/posterior axis specification
GO:0045451	pole plasm oskar mRNA localization
GO:0045450	bicoid mRNA localization
GO:0019094	pole plasm mRNA localization
GO:0006366	transcription from RNA polymerase II promoter
GO:0006875	cellular metal ion homeostasis
GO:0016180	snRNA processing
GO:0034472	snRNA 3'-end processing
GO:0016319	mushroom body development
GO:0046128	purine ribonucleoside metabolic process
GO:0009150	purine ribonucleotide metabolic process
GO:0009259	ribonucleotide metabolic process
GO:0006413	translational initiation
GO:0031123	RNA 3'-end processing
GO:0043484	regulation of RNA splicing
GO:0070646	protein modification by small protein removal

TABLE E.22: (continued)

GO ID	GO TERM
GO:0031572	G2 DNA damage checkpoint
GO:0060911	cardiac cell fate commitment
GO:0023014	signal transduction by protein phosphorylation
GO:0043628	ncRNA 3'-end processing
GO:0001173	DNA-templated transcriptional start site selection
GO:1903146	regulation of mitophagy
GO:0006368	transcription elongation from RNA polymerase II promoter
GO:1901605	alpha-amino acid metabolic process
GO:0048749	compound eye development
GO:0000725	recombinational repair
GO:0045055	regulated exocytosis
GO:0045746	negative regulation of Notch signaling pathway
GO:2000142	regulation of DNA-templated transcription, initiation
GO:0008380	RNA splicing
GO:0046530	photoreceptor cell differentiation
GO:0008585	female gonad development
GO:0006116	NADH oxidation
GO:1903508	positive regulation of nucleic acid-templated transcription
GO:1902680	positive regulation of RNA biosynthetic process
GO:0051254	positive regulation of RNA metabolic process
GO:0031050	dsRNA fragmentation
GO:0070918	production of small RNA involved in gene silencing by RNA
GO:0098728	germline stem cell asymmetric division
GO:0000165	MAPK cascade
GO:0051306	mitotic sister chromatid separation
GO:0007173	epidermal growth factor receptor signaling pathway
GO:0042058	regulation: epidermal growth factor receptor signaling pathway
GO:1901184	regulation: ERBB signaling pathway
GO:1901185	negative regulation of ERBB signaling pathway
GO:0006351	transcription, DNA-templated
GO:0006397	mRNA processing
GO:0070303	negative regulation: stress-activated protein kinase signaling cascade
GO:0047497	mitochondrion transport along microtubule

TABLE E.22: (continued)

GO ID	GO TERM
GO:0042551	neuron maturation
GO:0018205	peptidyl-lysine modification
GO:0042461	photoreceptor cell development
GO:0001754	eye photoreceptor cell differentiation
GO:0018393	internal peptidyl-lysine acetylation
GO:0018394	peptidyl-lysine acetylation
GO:0006473	protein acetylation
GO:0006475	internal protein amino acid acetylation
GO:0007293	germarium-derived egg chamber formation
GO:0046496	nicotinamide nucleotide metabolic process
GO:0019362	pyridine nucleotide metabolic process
GO:0010389	regulation of G2/M transition of mitotic cell cycle
GO:0044818	mitotic G2/M transition checkpoint
GO:1902750	negative regulation of cell cycle G2/M phase transition
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle
GO:0009205	purine ribonucleoside triphosphate metabolic process
GO:0009144	purine nucleoside triphosphate metabolic process
GO:0009199	ribonucleoside triphosphate metabolic process
GO:0009064	glutamine family amino acid metabolic process
GO:0000380	alternative mRNA splicing, via spliceosome
GO:1990138	neuron projection extension
GO:0008587	imaginal disc-derived wing margin morphogenesis
GO:0008582	regulation of synaptic growth at neuromuscular junction
GO:0045887	positive regulation: synaptic growth at neuromuscular junction
GO:0051965	positive regulation: synapse assembly
GO:0030706	germarium-derived oocyte differentiation
GO:0031400	negative regulation: protein modification process
GO:0050684	regulation: mRNA processing
GO:0048024	regulation: mRNA splicing, via spliceosome
GO:0000381	regulation: alternative mRNA splicing, via spliceosome
GO:0006357	regulation: transcription from RNA polymerase II promoter
GO:0070734	histone H3-K27 methylation
GO:0009167	purine ribonucleoside monophosphate metabolic process

TABLE E.22: (continued)

GO ID	GO TERM
GO:0009126	purine nucleoside monophosphate metabolic process
GO:0009161	ribonucleoside monophosphate metabolic process
GO:0034470	ncRNA processing
GO:1903311	regulation: mRNA metabolic process
GO:0051663	oocyte nucleus localization: oocyte dorsal/ventral axis specification
GO:0006417	regulation: translation
GO:0060260	regulation: transcription initiation from RNA polymerase II promoter
GO:1903507	negative regulation: nucleic acid-templated transcription
GO:1902679	negative regulation: RNA biosynthetic process
GO:0051253	negative regulation: RNA metabolic process
GO:0060912	cardiac cell fate specification
GO:0007306	eggshell chorion assembly
GO:0038127	ERBB signaling pathway
GO:0098930	axonal transport
GO:0008090	retrograde axonal transport
GO:0016358	dendrite development
GO:0017156	calcium ion regulated exocytosis
GO:0030703	eggshell formation
GO:0045664	regulation: neuron differentiation
GO:0050769	positive regulation of neurogenesis
GO:0050767	regulation of neurogenesis
GO:0045666	positive regulation: neuron differentiation
GO:0035070	salivary gland histolysis
GO:0045314	regulation of compound eye photoreceptor development
GO:0007286	spermatid development
GO:0016322	neuron remodeling
GO:0042773	ATP synthesis coupled electron transport
GO:0099643	signal release from synapse
GO:0016441	posttranscriptional gene silencing
GO:0032873	negative regulation of stress-activated MAPK cascade
GO:0007480	imaginal disc-derived leg morphogenesis
GO:0007560	imaginal disc morphogenesis
GO:0007478	leg disc morphogenesis

TABLE E.22: (continued)

GO ID	GO TERM
GO:0007476	imaginal disc-derived wing morphogenesis
GO:0007472	wing disc morphogenesis
GO:0031401	positive regulation: protein modification process
GO:0031047	gene silencing by RNA
GO:0036465	synaptic vesicle recycling
GO:0032446	protein modification by small protein conjugation
GO:0001933	negative regulation of protein phosphorylation
GO:0042326	negative regulation of phosphorylation
GO:0043409	negative regulation of MAPK cascade
GO:0048592	eye morphogenesis
GO:0061564	axon development
GO:0042478	regulation of eye photoreceptor cell development
GO:0010893	positive regulation: steroid biosynthetic process
GO:0090031	positive regulation: steroid hormone biosynthetic process
GO:0044773	mitotic DNA damage checkpoint
GO:0048599	oocyte development
GO:0007308	oocyte construction
GO:0007309	oocyte axis specification
GO:0007316	pole plasm RNA localization
GO:0007315	pole plasm assembly
GO:0007314	oocyte anterior/posterior axis specification
GO:0045998	positive regulation: ecdysteroid biosynthetic process
GO:0045966	positive regulation: ecdysteroid metabolic process
GO:0007554	regulation: ecdysteroid biosynthetic process
GO:0031440	regulation: mRNA 3'-end processing
GO:0046532	regulation: photoreceptor cell differentiation
GO:0001745	compound eye morphogenesis
GO:0001751	compound eye photoreceptor cell differentiation
GO:0000398	mRNA splicing: spliceosome
GO:0000377	RNA splicing: transesterification reactions with bulged adenosine as nucleophile
GO:0000375	RNA splicing: transesterification reactions
GO:0045676	regulation of R7 cell differentiation

TABLE E.22: (continued)

GO ID	GO TERM
GO:1903506	regulation of nucleic acid-templated transcription
GO:0009994	oocyte differentiation
GO:0030707	ovarian follicle cell development
GO:0043408	regulation of MAPK cascade
GO:0019941	modification-dependent protein catabolic process
GO:0008595	anterior/posterior axis specification, embryo
GO:0007351	tripartite regional subdivision
GO:0008358	maternal determination of anterior/posterior axis, embryo
GO:0048515	spermatid differentiation
GO:0030722	establishment of oocyte nucleus localization: oocyte dorsal/ventral axis specification
GO:0007312	oocyte nucleus migration: oocyte dorsal/ventral axis specification
GO:1901991	negative regulation of mitotic cell cycle phase transition
GO:0044784	metaphase/anaphase transition of cell cycle
GO:1902099	regulation of metaphase/anaphase transition of cell cycle
GO:0010965	regulation of mitotic sister chromatid separation
GO:0033047	regulation of mitotic sister chromatid segregation
GO:0007091	metaphase/anaphase transition of mitotic cell cycle
GO:0097659	nucleic acid-templated transcription
GO:0045466	R7 cell differentiation
GO:0043405	regulation of MAP kinase activity
GO:0043410	positive regulation of MAPK cascade
GO:0007289	spermatid nucleus differentiation
GO:0007298	border follicle cell migration
GO:0007297	ovarian follicle cell migration
GO:0042775	mitochondrial ATP synthesis coupled electron transport
GO:0048667	cell morphogenesis involved in neuron differentiation
GO:0048812	neuron projection morphogenesis
GO:0030182	neuron differentiation
GO:0031175	neuron projection development
GO:0048666	neuron development
GO:0044774	mitotic DNA integrity checkpoint
GO:2001141	regulation of RNA biosynthetic process

TABLE E.22: (continued)

GO ID	GO TERM
GO:0032872	regulation of stress-activated MAPK cascade
GO:0044445	cytosolic part
GO:0005700	polytene chromosome
GO:0090545	CHD-type complex
GO:0099503	secretory vesicle
GO:0098791	Golgi subcompartment
GO:0015630	microtubule cytoskeleton
GO:0044430	cytoskeletal part
GO:0035098	ESC/E(Z) complex
GO:0019866	organelle inner membrane
GO:0098798	mitochondrial protein complex
GO:0034399	nuclear periphery
GO:0000791	euchromatin
GO:0070603	SWI/SNF superfamily-type complex
GO:0097525	spliceosomal snRNP complex
GO:0044391	ribosomal subunit
GO:0090568	nuclear transcriptional repressor complex
GO:0005681	spliceosomal complex
GO:0044428	nuclear part
GO:0043189	H4/H2A histone acetyltransferase complex
GO:0098687	chromosomal region
GO:0022626	cytosolic ribosome
GO:0016604	nuclear body
GO:0070382	exocytic vesicle
GO:0031981	nuclear lumen
GO:0005746	mitochondrial respiratory chain
GO:0044429	mitochondrial part
GO:0030133	transport vesicle
GO:0000790	nuclear chromatin
GO:0044454	nuclear chromosome part
GO:0016591	DNA-directed RNA polymerase II, holoenzyme
GO:0055029	nuclear DNA-directed RNA polymerase complex
GO:0005759	mitochondrial matrix

TABLE E.22: (continued)

GO ID	GO TERM
GO:0005875	microtubule associated complex
GO:0090544	BAF-type complex
GO:0000785	chromatin
GO:0044431	Golgi apparatus part
GO:0035097	histone methyltransferase complex
GO:0005768	endosome
GO:0044455	mitochondrial membrane part
GO:0044451	nucleoplasm part
GO:0044427	chromosomal part
GO:0000228	nuclear chromosome
GO:0098800	inner mitochondrial membrane protein complex
GO:1902562	H4 histone acetyltransferase complex
GO:0031985	Golgi cisterna
GO:0005654	nucleoplasm

TABLE E.3: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and allele-specific methylation in non-reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0000790	nuclear chromatin
GO:0000815	ESCRT III complex
GO:0001677	formation of translation initiation ternary complex
GO:0002181	cytoplasmic translation
GO:0005770	late endosome
GO:0005778	peroxisomal membrane
GO:0006163	purine nucleotide metabolic process
GO:0007406	negative regulation of neuroblast proliferation
GO:0007465	R7 cell fate commitment
GO:0007480	imaginal disc-derived leg morphogenesis
GO:0010906	regulation of glucose metabolic process
GO:0016079	synaptic vesicle exocytosis
GO:0030121	AP-1 adaptor complex
GO:0032482	Rab protein signal transduction
GO:0035041	sperm chromatin decondensation
GO:0035976	transcription factor AP-1 complex
GO:0042326	negative regulation of phosphorylation
GO:0045860	positive regulation of protein kinase activity
GO:0045887	positive regulation of synaptic growth at neuromuscular junction
GO:0045956	positive regulation of calcium ion-dependent exocytosis
GO:0046529	imaginal disc fusion, thorax closure
GO:0046579	positive regulation of Ras protein signal transduction
GO:0048675	axon extension
GO:0048812	neuron projection morphogenesis
GO:0050770	regulation of axonogenesis
GO:0061327	anterior Malpighian tubule development
GO:0072499	photoreceptor cell axon guidance
GO:2000370	positive regulation of clathrin-dependent endocytosis

TABLE E.4: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and alternative splicing of isoforms (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0005770	late endosome
GO:0005778	peroxisomal membrane
GO:0006909	phagocytosis
GO:0012505	endomembrane system
GO:0019233	sensory perception of pain
GO:0030431	sleep
GO:0032504	multicellular organism reproduction
GO:0034976	response to endoplasmic reticulum stress
GO:0043227	membrane-bounded organelle
GO:0046579	positive regulation of Ras protein signal transduction

TABLE E.5: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and down regulation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0032482	Rab protein signal transduction
GO:0036335	intestinal stem cell homeostasis
GO:0044390	ubiquitin-like protein conjugating enzyme binding
GO:0061659	ubiquitin-like protein ligase activity
GO:0070604	PBAF complex
GO:0090277	positive regulation: peptide hormone secretion
GO:0097340	inhibition of cysteine-type endopeptidase activity
GO:2000134	negative regulation: G1/S transition of mitotic cell cycle
GO:2000648	positive regulation: stem cell proliferation

TABLE E.6: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and hypermethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0048812	neuron projection morphogenesis
GO:0002181	cytoplasmic translation
GO:0046579	positive regulation: Ras protein signal transduction
GO:0010906	regulation: glucose metabolic process
GO:0042326	negative regulation: phosphorylation
GO:0006163	purine nucleotide metabolic process
GO:0004843	thiol-dependent ubiquitin-specific protease activity

TABLE E.7: Significantly overlapping gene ontology terms with allele-specific expression in reproductive workers and hypomethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0007480	imaginal disc-derived leg morphogenesis
GO:0042326	negative regulation of phosphorylation
GO:0032482	Rab protein signal transduction
GO:0010906	regulation of glucose metabolic process
GO:0048812	neuron projection morphogenesis
GO:0016601	Rac protein signal transduction
GO:0045887	positive regulation of synaptic growth at neuromuscular junction
GO:0000790	nuclear chromatin

TABLE E.8: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and allele-specific methylation in reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0035167	larval lymph gland hemopoiesis
GO:0042326	negative regulation: phosphorylation
GO:0046579	positive regulation: Ras protein signal transduction
GO:0010906	regulation of glucose metabolic process
GO:0016079	synaptic vesicle exocytosis
GO:0045464	R8 cell fate specification
GO:1900073	regulation: neuromuscular synaptic transmission
GO:0000790	nuclear chromatin
GO:0008541	proteasome regulatory particle, lid subcomplex
GO:0016604	nuclear body
GO:0044427	chromosomal part

TABLE E.9: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and allele-specific methylation in non-reproductive workers (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0035041	sperm chromatin decondensation
GO:0010906	regulation: glucose metabolic process
GO:0061031	endodermal digestive tract morphogenesis
GO:0032482	Rab protein signal transduction
GO:0045956	positive regulation: calcium ion-dependent exocytosis
GO:1900073	regulation: neuromuscular synaptic transmission
GO:0006163	purine nucleotide metabolic process
GO:0042326	negative regulation: phosphorylation
GO:0035167	larval lymph gland hemopoiesis
GO:0051491	positive regulation: filopodium assembly
GO:0016330	second mitotic wave involved in compound eye morphogenesis
GO:0007406	negative regulation: neuroblast proliferation
GO:1900242	regulation: synaptic vesicle endocytosis
GO:0046579	positive regulation of Ras protein signal transduction
GO:0048812	neuron projection morphogenesis
GO:0007465	R7 cell fate commitment
GO:0016079	synaptic vesicle exocytosis
GO:0050770	regulation: axonogenesis
GO:0008541	proteasome regulatory particle, lid subcomplex
GO:0005778	peroxisomal membrane
GO:0030139	endocytic vesicle
GO:0035976	transcription factor AP-1 complex
GO:0031519	PcG protein complex
GO:0044427	chromosomal part
GO:0016604	nuclear body
GO:0030121	AP-1 adaptor complex
GO:0005770	late endosome
GO:0000815	ESCRT III complex
GO:0030135	coated vesicle
GO:0000790	nuclear chromatin

TABLE E.10: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and alternative splicing of isoforms (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0006909	phagocytosis
GO:0032504	multicellular organism reproduction
GO:0034976	response to endoplasmic reticulum stress
GO:0046579	positive regulation: Ras protein signal transduction
GO:0019233	sensory perception of pain
GO:0012505	endomembrane system
GO:0005770	late endosome
GO:0005778	peroxisomal membrane

TABLE E.11: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and down regulation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0070604	PBAF complex
GO:0006011	UDP-glucose metabolic process
GO:0031000	response to caffeine
GO:0036335	intestinal stem cell homeostasis
GO:0061101	neuroendocrine cell differentiation
GO:0035180	larval wandering behavior
GO:0002181	cytoplasmic translation
GO:2000648	positive regulation: stem cell proliferation
GO:0032482	Rab protein signal transduction
GO:0097340	inhibition of cysteine-type endopeptidase activity
GO:0060024	rhythmic synaptic transmission
GO:0001582	detection of chemical stimulus: sensory perception of sweet taste
GO:0045464	R8 cell fate specification
GO:2000134	negative regulation: G1/S transition of mitotic cell cycle
GO:0031340	positive regulation: vesicle fusion
GO:0035187	hatching behavior
GO:0048791	calcium ion-regulated exocytosis of neurotransmitter
GO:0016486	peptide hormone processing
GO:1900073	regulation of neuromuscular synaptic transmission
GO:0016330	second mitotic wave involved in compound eye morphogenesis
GO:0090277	positive regulation of peptide hormone secretion
GO:0001786	phosphatidylserine binding
GO:0061659	ubiquitin-like protein ligase activity
GO:0031208	POZ domain binding
GO:0000149	SNARE binding
GO:0051019	mitogen-activated protein kinase binding
GO:0044390	ubiquitin-like protein conjugating enzyme binding

TABLE E.12: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and hypermethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0004843	thiol-dependent ubiquitin-specific protease activity
GO:0044427	chromosomal part
GO:0048812	neuron projection morphogenesis
GO:0002181	cytoplasmic translation
GO:0046579	positive regulation: Ras protein signal transduction
GO:0010906	regulation: glucose metabolic process
GO:0042326	negative regulation: phosphorylation
GO:0006163	purine nucleotide metabolic process

TABLE E.13: Significantly overlapping gene ontology terms with allele-specific expression in non-reproductive workers and hypomethylation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0002181	cytoplasmic translation
GO:0048812	neuron projection morphogenesis
GO:0032482	Rab protein signal transduction
GO:0042326	negative regulation: phosphorylation
GO:0010906	regulation: glucose metabolic process
GO:0000790	nuclear chromatin
GO:0016604	nuclear body
GO:0044427	chromosomal part

TABLE E.15: Significantly overlapping gene ontology terms with allele-specific methylation in reproductive workers and alternative splicing of isoforms (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0005703	polytene chromosome puff
GO:0030016	myofibril
GO:0046579	positive regulation: Ras protein signal transduction
GO:0030239	myofibril assembly
GO:0070374	positive regulation: ERK1 and ERK2 cascade
GO:0071689	muscle thin filament assembly

TABLE E.16: Significantly overlapping gene ontology terms with allele-specific methylation in reproductive workers and down regulation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0000788	nuclear nucleosome
GO:0002181	cytoplasmic translation
GO:1900073	regulation: neuromuscular synaptic transmission
GO:0045464	R8 cell fate specification
GO:0071689	muscle thin filament assembly

TABLE E.19: Significantly overlapping gene ontology terms with allele-specific methylation in non-reproductive workers and alternative splicing of isoforms (hypergeometric test, $p < 0.05$).

GO ID	GO term
GO:0009047	dosage compensation by hyperactivation of X chromosome
GO:0048488	synaptic vesicle endocytosis
GO:0042759	long-chain fatty acid biosynthetic process
GO:0035071	salivary gland cell autophagic cell death
GO:0046579	positive regulation: Ras protein signal transduction
GO:0031060	regulation: histone methylation
GO:0045886	negative regulation: synaptic growth at neuromuscular junction
GO:0030497	fatty acid elongation
GO:0030514	negative regulation: BMP signaling pathway
GO:0030239	myofibril assembly
GO:0070374	positive regulation: ERK1 and ERK2 cascade
GO:0030016	myofibril
GO:0005770	late endosome
GO:0005778	peroxisomal membrane

TABLE E.20: Significantly overlapping gene ontology terms with allele-specific methylation in non-reproductive workers and down regulation (hypergeometric test, $p < 0.05$). Genes are referred to as up/down regulated in the reproductive workers, compared to the non-reproductive workers.

GO ID	GO term
GO:0089701	U2AF
GO:0044665	MLL1/2 complex
GO:0044666	MLL3/4 complex
GO:0018023	peptidyl-lysine trimethylation
GO:0046833	positive regulation: RNA export from nucleus
GO:0030497	fatty acid elongation
GO:0016330	second mitotic wave involved in compound eye morphogenesis
GO:0032482	Rab protein signal transduction
GO:0002181	cytoplasmic translation
GO:1900073	regulation: neuromuscular synaptic transmission
GO:0032933	SREBP signaling pathway
GO:0044719	regulation: imaginal disc-derived wing size

Appendix F

Eusocial alternative splicing supplementary information

TABLE F.1: Image references for alternative splicing phylogeny-boxplots

Species	Image Reference
<i>Monomorium pharaonis</i>	Alex Wild, http://www.alexanderwild.com/keyword/Monomorium%20pharaonis/
<i>Pogonomyrmex barbatus</i>	Elizabeth Cash, https://www.flickr.com/photos/elizabeth-cash/with/7004802437/
<i>Harpegnathos saltator</i>	https://asunow.asu.edu/content/asu-scientists-among-first-sequence-ant-genomes
<i>Bombus terrestris</i>	http://trzmiele.pl/gatunki-trzmieli/trzmiel-ziemny
<i>Apis mellifera</i>	Getty Images, DigitalVision, Don Farrall, https://www.thoughtco.com/honey-bee-apis-mellifera-1968092
<i>Cephus cinctus</i>	Peter Cameron, British Phytophagous Hymenoptera