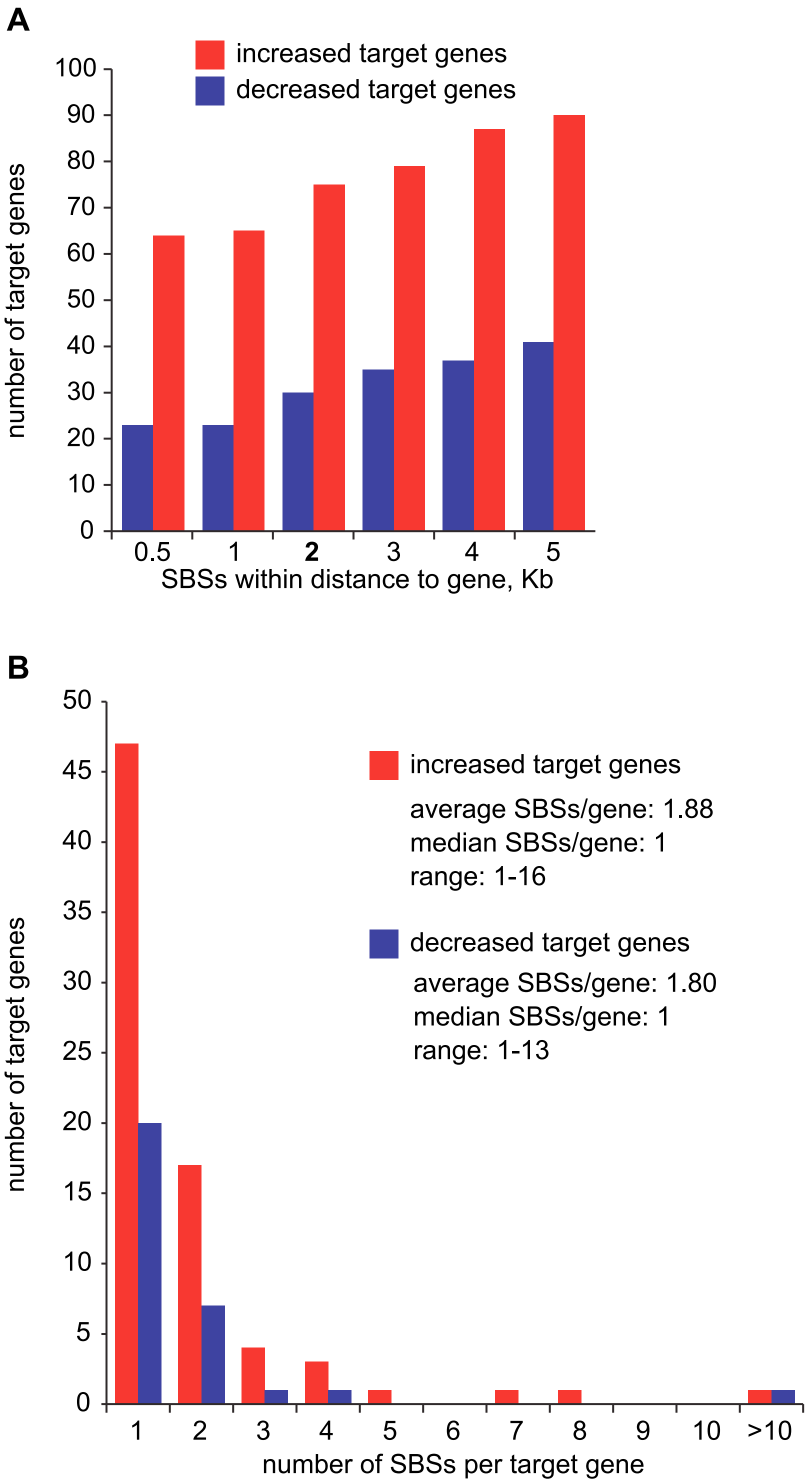

Fig. S1. Distribution of SBSs relative to the genes identified in microarray analyses. (**A**) Numbers of genes classified as direct targets, considering the presence of an SBS at different distance cutoffs of regulatory DNA flanking the mis-regulated gene (0.5 to 5 Kb). Activated and repressed genes are shown in red and blue, respectively. (**B**) Numbers of SBSs per target gene, with average, median and range indicated for activated (red) and repressed (blue) genes.

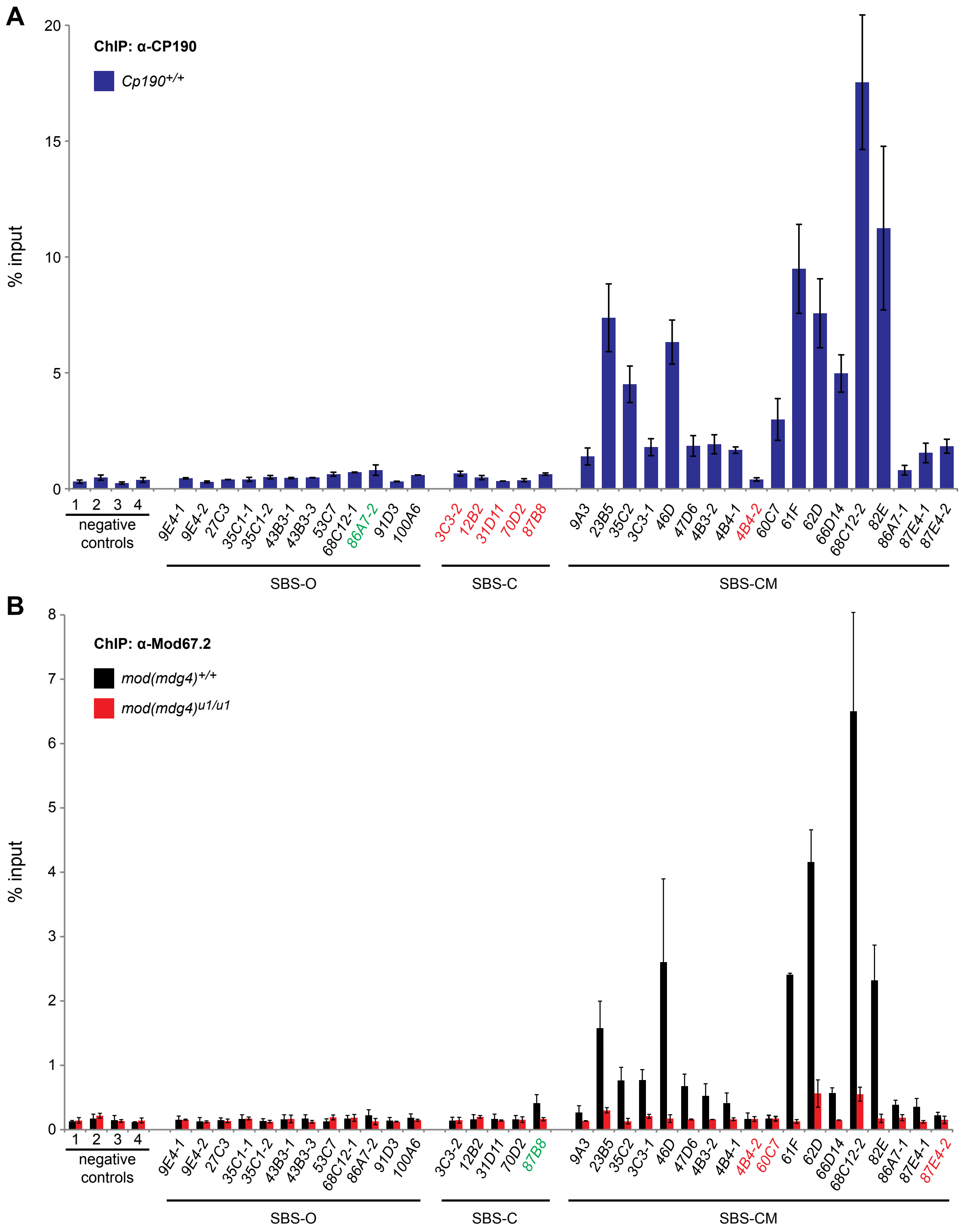

Fig. S2. CP190 and Mod67.2 association at SBSs in the ovary. (**A**,**B**) ChIP-qPCR analyses of ovary CP190 (A) and Mod67.2 (B) distribution. Negative controls: genomic regions with no SBS and no reported CP190 and Mod67.2 association. Sites are arranged into classes based on ModEncode results [SBS-O, SBS-C and SBS-CM (Negre et al., 2010, Soshnev et al., 2012)] and are labeled based on cytological location. Red indicates a loss of protein occupancy in the ovary relative to embryos; green indicates gain of occupancy in the ovary relative to embryos. In B, *mod(mdg4)*^{u1} null mutant background is shown as an additional negative control (black bars). In total, 28/35 (80%) sites demonstrate expected CP190 occupancy and 31/35 (89%) sites demonstrate expected Mod67.2 occupancy. Error bars indicate s.d. of two independent biological replicates.

Table S1. Alleles and genotypes used in the study

su(Hw) mutant alleles

Allele	Genotype	Stock	Lesion	Reference
su(Hw)^{2}	*y*^{2} *w*^{67c23} *ct*^{6} *f*^{1}*; su(Hw)*^{2}*/TM6B Tb*	n/a	*jockey* insertion in first intron of *su(Hw)* gene	Harrison et al., 1993
su(Hw)^{v}	*y*^{2} *ct*^{6} *f*^{1}*; su(Hw)*^{v}*/TM6B Tb*	n/a	deletion encompassing *su(Hw)* TSS and *RpII 15* gene	Harrison et al., 1992
su(Hw)^{Pb}	*y*^{2} *w*^{67c23} *ct*^{6} *f*^{1}*; su(Hw)*^{e04061}*/TM6B Tb*	n/a	*piggyBac* insertion in first intron of *su(Hw)* gene	Baxley et al., 2011
su(Hw)^{f}	*y*^{2} *w*^{67c23} *ct*^{6} *f*^{1}*; su(Hw)*^{f} *Ubx*$^{+}$*/su(Hw)*^{v}	n/a	C525Y mutation disrupting Su(Hw) ZF10 backbone	Harrison et al., 1993
su(Hw)^{A2663}	*y*^{2} *w*^{67c23} *ct*^{6} *f*^{1}*; su(Hw)*^{A2663}*/TM6B Tb*	n/a	EMS-generated deletion encompassing +3534 to +4633 bp relative to the TSS	n/a

Reference wild-type alleles

Allele	Genotype	Stock	Lesion	Reference
Canton S	*Canton-S*	BL 1	n/a	
BL15598	*y*^{1} *w*^{67c23}*; P{w*$^{+mC}$ *y*$^{+mDint2}$*=EPgy2} CG6499*^{EY02782}	BL 15598	n/a	

gypsy insulator partners

Allele	Genotype	Stock	Lesion	Reference
Cp190$^{H4\text{-}1}$	*y*^{2} *w ct*^{6} *omb*$^{P1\text{-}D11}$*; Cp190*$^{H4\text{-}1}$*/TM6B*		truncation of the 331 amino acids at the C-terminus of CP190	Pai et al., 2004
Cp190^{P11}	*y*^{2} *w ct*^{6}*; Cp190*^{P11}*/TM6B*		deficiency encompassing *Set, Oscp, Cp190* and *Mrg15* genes	Pai et al., 2004
mod(mdg4)^{u1}	*y*^{2} *ct*^{6}*; mod(mdg4)*^{u1}*/mod(mdg4)*^{u1}		*Stalker* insertion causing Mod67.2 truncation by 145 amino acids at the C-terminus	Gause et al., 2001

Target gene alleles and deficiency lines

Allele	Genotype	Stock	Lesion	Reference
Rbp9^{P2690}	w*; P{w^{+mC}lacW}Rbp9^{P2690}/CyO	BL 25778	P-element insertion within the coding sequence of *Rbp9* gene	Kim-Ha et al., 1999
Rbp9^{P2775}	w*; P{w^{+mC}lacW}Rbp9^{P2775}/CyO	BL 25777	P-element insertion within the coding sequence of *Rbp9* gene	Kim-Ha et al., 1999
Df(2L)ED206	*w*^{1118}*; Df(2L)ED206, P{w*$^{+mW.Scer\backslash FRT.hs3}$*3'.RS5+3.3'}ED206/SM6a*	BL 8038	deficiency	
Df(2L)ED270	*w*^{1118}*; Df(2L)ED270, P{w*$^{+mW.Scer\backslash FRT.hs3}$*3'.RS5+3.3'}ED270/SM6a*	BL 8039	deficiency	
Df(2L)ED4651	*w*^{1118}*; Df(2L)ED4651, P{w*$^{+mW.Scer\backslash FRT.hs3}$*3'.RS5+3.3'}ED4651/SM6a*	BL 8904	deficiency	
Df(2R)Exel6284	*w*^{1118}*; Df(2R)Exel6284, P{w*$^{+mC}$*XP-U}Exel6284/CyO*	BL 7749	deficiency	
Df(2R)BSC858	*w*^{1118}*; Df(2R)BSC858, P+PBac{w*$^{+mC}$*XP3.WH3}BSC858/SM6a*	BL 27928	deficiency	
Df(2R)ED1735	*w*^{1118}*; Df(2R)ED1735, P{w*$^{+mW.Scer\backslash FRT.hs3}$*3'.RS5+3.3'}ED1735/SM6a*	BL 9275	deficiency	
Df(2R)ED3683	*w*^{1118}*; Df(2R)ED3683, P{w*$^{+mW.Scer\backslash FRT.hs3}$*3'.RS5+3.3'}ED3683/SM6a*	BL 8918	deficiency	
Df(2R)50C-38	*Df(2R)50C-38, al*^{1} *b*^{1} *cn*^{1} *P{w*$^{+mC}$*CaSpeR}Cp1*$^{50C\text{-}38}$*/CyO, amos*$^{Roi\text{-}1}$ *bw*^{1}	BL 8114	deficiency	

Table S2. Primers used in qPCR analyses

Gene expression analyses		
Target	**Forward**	**Reverse**
GAPDH2	CACTCGTCGGTGTTCGATGCCAAG	TCGATGACGCGGTTGGAGTAGC
Ras64B	AGGAAGTGCTGCCTGATGTAGAAG	TTATATGTTGGCTCCTGCTTCCGC
bTub56D	AGTTCACCGCTATGTTCA	CGCAAAACATTGATCGAG
su(Hw)	ATACCCTGCGACGGCACATACG	TTCACGCACCACAACGCCATTC
CG6293	TGCCATCATTAACATTATCATCGCCC	ATCGGTGCTACTGGGCACTACAATTCTC
CG1468	ATAGGAGCCACGGGTTTCTTCACT	ATTTGTGCGCAGACGCATATCACC
L(1)G0148	CAACTGGCGCAGATGGATCAAACA	AGACAGTTGAGGCAAACTGAGGGA
CG7582	TCCGTTTCCACATCCATCAG	GAACGCAACCACCAAACTTAG
CG9416	GCGAGCACAGTGAGTCATAA	AGCTCCGAGTCACAATCAATAC
Oct-TyrR	CGCTGGGCTCCTTCTTTATT	GCGATCGTGTTAAGCTTGTTG
neuroligin	TCGTGTTCGGGGAGTATAGCTGCTAC	GCAGTTCCACCAGCAGCTTCTCTTC
Rph	AACAACTCCGGCAACTCACAAACG	AGGCCTCACGATAGCTAATGGCAA
CG12071	TGCCACATTGGAGGAACTGATCTG	AACAACAACAACAACAGCCAGAACAATG
CG14298	AATTTCAACTGCTATGTGGGCCGC	GATTGCGATTGCCGTTGCATCCTT
dpr19	TATGACGCAACAGCATCAATCCGC	AACATGCACTGTAATGCTGGCAGG
Syn2	AATGCCAAGTCCTGCAAAGTCTGCTG	TATATCATTTTGAGTGTGAGTCCATGCG
CG15760	GCAACTCGTCCACGATTCACAAAG	GCAACTCGTCCACGATTCACAAAG
mAcR-60C	CTGCTTGGGTATGACCTTGGCGTTG	TTCAGCCTGCCACTCGGACGG
CG15270	TTCACAGCACCAGCAGCAAATAGTG	ATGAACCAGATGAAGAGTTTGATAATGCG
Rbp9	GCAGAGCAACAAGTGCAAGGGC	AGCTGACCTGAAGCACTCGGTTGC
CG3104	TGTGGATAGCAGCCCAGATGGGAC	TGTGGATAGCAGCCCAGATGGGAC
Mob2	AAATCCGAAGCATAAATCTGGTTATCTCC	CCAACACAACCACAAATCGCACC
Rbp9-TSS1	CGCAAATTCCAGGGGTATTAACAGG	TTGATGGTCATATCCTCCTCGCTGG
Rbp9-TSS2	GTGGAATCCGAATCAGTATCGAAATC	CATACAACACCGATTTTCCCAACTC
Rbp9-TSS3	CTTCCGTTTGTCTCGCCTTATGTTTTG	ACTGGTTGCTAATCAGTAGATTCCTACG
ChIP-QPCR		
Target	**Forward**	**Reverse**
chip neg 1	GTATATCCACATCACCAGACCTCAGG	ACATCCTCGAATCACTATGCAAGTCG
chip neg 2	CACTCGTCGGTGTTCGATGCCAAG	TCGATGACGCGGTTGGAGTAGC
chip neg 3	CTTCGACTTGATGTGATACTTCTGCT	AACGGATTGGAGATCGCATCAGC
chip neg 4	ACATCGGAGCCAGTGCGTCG	TATCCGACACCGTGGTAGTAGTCTGC
Rbp9 SBS1	ATACTTGTAGGCAGCGGGATGGG	AGAGAGAGCAAGGCAGGAGCGTAGG
Rbp9 SBS2	AAGAACATTTTCCAGTCCCAGTTCCAG	TTCTCTGTTCGCTTACATTTATTCGCCAG
Rbp9 SBS3	TAAGCTCGCTCTCTGGCTCCCATTC	AGATAGAGCGGGAGAGACAGTGAGAGC
9E4-1	TGCGGAGCGTTTGCGAATCGGTTG	ATAACGGTAAACGCCAGCCTGTTTG
9E4-2	AACCTTCAACTCCCCACCGCACCAC	TTCCAGAACCAACGACTATATCCCCAAC
27C3	ACAAATGCTTGTTCGCTTTCCGCC	GTTGGCTTCGCGTACACGGAATTT
35C1-1	ACACAAACACTGAGAGCGCCGATA	TTCTATGCCAGGATCCGTTGGTGA
35C1-2	TGCAAGCCCGACAATATCAGACCT	GCGCACTTAAGCGCCATGAAGTAT
4B3-1	CAGTGGAGAAGCGAGACAATC	CGGACTGACTGACAAGTACATAAA
4B3-3	TACGCCCAGTGTGCACCATAACTA	AGCGTTCAGTTCAGCTCATACCCA
53C7	TCCGCTAGCGAAGTGTTTATAACG	TTGCCCACTTCAGGCCAAATGTAC
68C12-1	AGGCGAAGCATGTGGTATAGTGGT	ATGCGCCCTGATGTAGGCTATGAA
86A7-2	TGCCAGCGGCTATTACAACACCTA	TCGTTCGATGGTCGTATGGACGAA
91D3	ATTGTTGCTCTCGGTGCCTGTTTG	GTTTGCGTACTTTCTGTGGCAGCA
100A6	CGTTGCATATCTCAAGGCGTCCAAAC	GCCATAACCACTGTGCGTGACCAG
3C3-2	AGCATCTAAACGAAAGCCACCGGA	AATCACACAGGGCGACGTCATCTA
12B2	GCAGCACTCAGTTAGCAACAAATTCTCTC	TCCGTTATTTGTACCACATGCTGTTGTTGC
31D11	CTCATAAACTGAAGTTCGTTGCAGGAGG	AGTAGCAAAAAACATGATAAATGCAAGTG
70D2	GCACAGATAAGACCGCCAACTTGT	AATTAGCGGCCACGTTTGTTTCGC
87B8	TTTGGGCAACACTAGAACATCTGGGAC	AGCAGGGAACCAAATTTACTTCAGGAC
9A3	AGCTCGAGGCAATTATGTTTGCGG	AAGAATTGGCGAAGAACGCACCAG
23B5	AACCGATTGCTTCCAAAGTTGGCG	TAGGCGTCGCTCACTCAATGAACT
35C2	ATAGATGCACCCAAACACAACGGC	ACACCCAACTGACCATCCAGTCAA
3C3-1	ACCGCTACTTCACCATACCATAGC	CGTGTCGCAACATTCCATTTCCCA
46D	AGCAGTTATTGTAGGGACAGGTTGATGG	AAGTGGCAACGCTAAAGGAAAGAGTG
47D6	ATCTGGAGCTCCTGCTATTGGCAT	AGCAGCGAAGAGAGTTCGCTAAGA

4B3-2	AGTTCCATCTGCAGTATCGCTCCA	AGCTGATTTGAATGCGGCTGTGTC
4B4-1	ATGCCACGACTCAATGGGCAAATC	ATGCGTGTGTGTGCCAGTATCTGT
4B4-2	TGCACTTGTGGATGTCTCTGTGGA	AATCCTCCAGCACTACAGCACCTT
60C7	TGTAACGGTGACATCGCTGCTGTT	AGAGGCAGCATCTCTTAGCCCAAA
61F	CAGACCAATGTCTACAGCTCAATAGGCG	AGGTACACATAAGTATGAAAGAATGACCG
62D	GAATCGCCGCAAATTGGTCGG	CGGGCAAAACGTATTTAAATTTCAGCC
66D14	GAGCGCCGCCAATACATTCACATT	AGCTGCTGATCCTCGCTTTCCATA
68C12-2	TCGGTGCGATTTGTGGTTGTGTTG	CCAGCCTGAAAGTATGCACCGAAA
82E	TAAGACCAATAATGAATGAGTCAAGCACAG	TTAAGCATGTGAAACAGTAGTGTGAAACTG
86A7-1	AAACTAATTGGGCTAACGCACGGG	TTCGATAGAAAGATCACGCCATTGAG
87E4-1	TCCAGGGTGTTCTTGAAGTTTCCC	GCAGCAGATGGGCATAACCACAAA
87E4-2	TACGACCAGTGCTTGGGTTCAAGT	ACATCCTGCTCGGACTTTGCCTAT

Table S3. Results of gene expression microarray analyses and identification of direct target genes

NULL vs WT 1% FDR				FLYATLAS				dm3 coordinates			Su(Hw) targets			
Probeset ID	**Gene Symbol**	**Fold**	***P*-value**	**Brain**	**TAG**	**L CNS**	**Ovary**	**chr**	**start**	**end**	**Su(Hw)**	**Su(Hw)-F**	**CP190**	**Mod67.2**
1631004_s_at	**su(Hw)**	-130.4	1.58E-20	0.50	0.40	1.45	2.70	chr3R	10130177	10134309	■	■	■	■
1637063_at	CG33099	-9.06	3.41E-04	0.00	0.10	0.20	0.40	chr3R	18354642	18356294	■	■	■	■
1636954_at	NetB	-7.72	2.00E-06	20.30	19.00	25.29	0.30	chrX	14580071	14643409	■	■	■	■
1624580_at	GstZ1	-7.68	8.64E-14	0.30	0.40	0.28	1.30	chr3R	5281239	5282268	■	■	■	■
1640327_at	CG6023	-5.94	2.12E-11	1.00	0.90	0.39	1.70	chrX	18208156	18215198	■	■	■	■
1637281_at	trol	-4.50	2.84E-05	1.60	0.80	2.96	0.50	chrX	2364493	2438795	■	■	■	■
1625688_at	CG6293	-4.25	6.54E-09	0.30	0.30	0.65	2.00	chr3R	6133528	6137335	■	■	■	■
1641327_at	CG9416	-4.00	4.56E-07	0.10	0.30	0.28	0.20	chr2R	15254753	15261207	■	■	■	■
1630886_at	SelR	-3.66	3.47E-05	4.10	2.90	0.63	0.80	chr3R	6689077	6694364	■	■	■	■
1639411_at	l(1)G0148	-3.00	5.54E-13	0.50	0.30	0.56	1.60	chrX	6548649	6553742	■	■	■	■
1636099_s_at	mbl	-2.88	7.82E-06	20.80	15.20	5.18	0.40	chr2R	13104054	13266881	■	■	■	■
1629897_a_at	CG6044	-2.74	1.45E-04	26.50	32.70	2.84	0.10	chr2R	18291678	18295880	■	■	■	■
1632932_a_at	mp	-2.68	1.29E-06	22.90	15.00	8.26	0.80	chr3L	6991943	7046528	■	■	■	■
1625780_a_at	CG9812	-2.15	1.56E-04	0.20	0.10	0.14	0.00	chr2R	19299859	19307207	■	■	■	■
1637590_at	CG42329	-7.30	1.70E-04	0.10	0.00	0.09	0.10	chr2L	1219293	1229802	■	■	■	
1627441_at	Oct-TyrR	-3.98	4.94E-05	27.90	26.80	16.30	0.70	chr3L	22028103	22058379	■	■		
1629072_at	CG42259 / su(w[a])	-2.11	3.52E-04	0.30	0.30	0.53	1.40	chrX	906812	941042	■	■		
1639733_s_at	CG14275	-6.74	4.13E-06	0.10	0.20	0.25	0.20	chr2L	8327456	8332911	■	■	■	■
1632021_at	Cyp6a20	-16.78	6.62E-20	1.10	2.20	0.14	0.10	chr2R	10769625	10771551	■		■	■
1633427_at	CG7582	-12.36	4.29E-12	22.00	21.40	2.69	0.20	chr3R	25505963	25508000	■		■	■
1638996_at	CG11727	-5.19	3.88E-08	3.50	2.30	2.21	1.50	chrX	11324556	11348371	■		■	■
1636119_at	CG1468	-4.95	1.13E-08	0.30	0.50	0.05	0.00	chrX	9772455	9773312	■		■	■
1623949_s_at	CG32816	-2.83	1.70E-05	0.30	0.10	0.37	1.60	chrX	210609	364670	■		■	■
1631326_at	Zasp66	-2.70	2.74E-04	0.10	0.30	0.19	0.00	chr3L	8617471	8631773	■		■	■
1635742_s_at	Cad74A	-2.53	1.09E-04	0.00	0.00	0.74	2.10	chr3L	17360853	17372630	■		■	■
1626028_at	CG4783	-2.33	9.24E-05	0.00	0.00	0.00	0.00	chr3R	15774192	15774629	■		■	■
1634440_s_at	Eip74EF	-2.14	1.97E-04	3.20	1.90	0.24	0.60	chr3L	17551772	17612425	■		■	■
1641042_at	CG16820	-8.68	4.12E-07	0.20	0.00	0.07	0.00	chr2L	13246232	13250189	■		■	
1637670_s_at	CHES-1-like	-3.99	1.86E-06	1.70	1.40	0.72	2.50	chrX	7576371	7603418	■			
1628859_at	shi	-2.21	1.74E-05	14.10	14.60	5.74	0.70	chrX	15786149	15800725	■			
1630026_s_at	dpp	-2.01	8.39E-05	0.70	0.90	1.98	0.40	chr2L	2428372	2459823	■			
1633645_at	CG42565	-39.31	1.04E-08	0.00	0.10	0.06	1.40	chr2R	18547988	18548894				
1636485_at	CTCF	-17.52	1.45E-04	2.00	3.50	0.66	1.50	chr3L	7346678	7349813				
1637180_at	CG17977	-11.15	9.61E-15	3.70	3.10	3.11	1.60	chr2R	3953779	3955160				
1640681_at	CG4950	-10.35	1.85E-05	2.10	0.80	0.03	0.10	chr3L	16258897	16261256				
1636826_at	CG14072	-10.26	6.43E-09	0.00	0.10	0.04	0.10	chr2L	10936662	10937931				
1637366_at	nimC4	-8.62	9.43E-07	0.20	0.20	0.16	0.10	chr2L	14047582	14048863				
1631803_at	Lsp1alpha	-8.46	9.00E-09	1.60	1.30	5.62	0.50	chrX	12384416	12386933				
1628918_at	CG17478	-8.40	2.73E-04	0.10	0.20	0.10	4.20	chr2R	508621	510016				
1625063_a_at	CG31606	-8.40	3.38E-06	0.50	0.70	0.15	0.40	chr2L	8147626	8148356				
1628896_a_at	CG4210	-8.38	1.04E-04	0.00	0.10	0.01	0.70	chr3R	11039696	11040567				
1630256_at	lectin-24Db	-8.07	1.76E-06	1.90	0.90	0.05	0.10	chr2L	4188123	4189284				
1631555_at	CG10062	-8.01	2.53E-11	0.20	0.20	0.03	0.10	chr2R	15262818	15267679				
1628882_at	CG7378	-6.96	1.25E-07	1.20	1.00	0.23	0.10	chrX	18794443	18803330				
1640386_at	wbl	-6.62	1.00E-04	0.00	0.00	0.01	0.40	chr2R	15137266	15138419				
1629310_at	Trf4-1	-6.52	4.76E-09	0.60	0.40	0.21	2.40	chrX	8454662	8464192				
1628258_at	CG14526	-6.36	1.24E-04	0.20	0.20	0.05	0.10	chr3R	24709415	24711737				
1639502_at	nimC1	-5.91	1.19E-07	1.70	1.10	0.42	0.20	chr2L	13974119	13976753				
1624101_at	Cyp6a23	-5.35	1.23E-07	0.10	0.10	0.03	0.10	chr2R	10763338	10765159				
1629572_a_at	fat-spondin	-5.11	3.30E-05	1.40	2.90	0.21	0.00	chr2R	12941508	12946810				
1641477_at	CG32447	-4.89	1.61E-06	0.70	0.30	3.73	0.40	chr3L	21683712	21699465				

1638376_at	Osi15	-4.51	1.36E-04	0.00	0.10	0.13	0.00	chr3R	2127526	2129375				
1631710_at	KaiRIA	-4.26	1.63E-04	0.40	0.40	0.37	0.30	chr3R	16474317	16478172				
1634427_at	CG15461	-4.14	2.78E-09	0.10	0.10	0.08	0.10	chrX	20357207	20357615				
1641455_at	CG6762	-4.03	4.61E-07	2.20	1.50	0.74	0.60	chrX	17751007	17752643				
1623025_at	CG3457	-4.02	2.73E-04	0.10	0.10	0.08	1.80	chrX	2081853	2082743				
1624816_at	CG30283	-3.83	6.70E-07	1.50	1.60	2.47	1.40	chr2R	17427089	17428078				
1633152_at	mod(mdg4)	-3.82	8.89E-05	3.00	2.50	0.89	3.20	chr3R	17177331	17203121				
1624663_a_at	vis	-3.75	2.38E-10	0.10	0.10	0.10	0.10	chr2R	8395396	8398311				
1640957_at	Hexo2	-3.72	6.55E-05	3.90	4.50	1.64	0.60	chrX	8603685	8606513				
1623327_at	CG43103	-3.58	6.15E-07	0.20	0.20	0.01	0.10	chr2R	13026956	13027430				
1626534_at	tko	-3.55	3.37E-12	0.80	1.00	0.98	1.30	chrX	2336346	2338009				
1629430_s_at	regucalcin	-3.46	3.66E-04	1.60	0.40	0.05	0.00	chrX	11906467	11911091				
1632656_at	CG12112	-3.33	7.77E-13	0.30	0.40	0.64	2.10	chrX	8452912	8454225				
1625901_s_at	CG34172	-3.33	1.35E-04	0.00	0.10	0.00	0.00	chr2L	2192525	2197912				
1639476_at	Vago	-3.30	1.96E-07	0.10	0.10	0.07	0.00	chrX	10983323	10984138				
1628425_at	CG31898	-3.29	1.13E-05	0.50	0.60	0.89	3.40	chr2L	8400457	8401477				
1629106_at	CG2233	-3.28	3.06E-05	0.30	0.30	0.01	0.00	chrX	7929774	7931550				
1634191_at	CG6398	-3.22	2.19E-20	0.10	0.10	0.40	1.90	chrX	17724873	17735628				
1623555_at	CG10131	-3.07	9.14E-05	1.20	0.80	0.12	0.10	chr2R	10517418	10518526				
1637315_at	larp	-3.06	5.65E-05	0.80	1.00	0.75	1.30	chr3R	24143884	24162162				
1633329_at	yellow-h	-3.06	1.02E-05	1.20	1.10	0.44	0.10	chr4	248548	251054				
1635125_a_at	LM408	-3.04	2.64E-04	0.80	1.00	0.31	0.10	chr2L	10457656	10462475				
1627324_at	lola	-2.98	2.15E-04	5.30	3.60	15.11	1.20	chr2R	6369712	6430794				
1624599_at	CG34331	-2.98	4.97E-07	0.30	0.20	0.03	0.00	chrX	20016486	20017094				
1639737_at	CG34330	-2.98	2.17E-04	0.00	0.00	0.01	0.00	chrX	18962306	18962925				
1632650_at	CG5867	-2.83	1.67E-05	0.20	0.10	0.37	0.10	chr2L	13236494	13239297				
1637421_at	Cht2	-2.83	1.48E-05	0.50	0.40	1.50	2.00	chr3L	1752328	1755934				
1624836_at	CG13795	-2.73	2.91E-05	0.20	0.40	0.11	0.00	chr2L	7723310	7726298				
1632200_s_at	Edem1	-2.71	4.83E-05	0.70	0.80	1.32	1.30	chrX	1797735	1802860				
1638127_s_at	Dlic	-2.71	1.45E-10	1.80	2.10	1.27	1.70	chrX	11048434	11057245				
1630170_at	Cyp12b2	-2.63	7.81E-07	3.40	5.10	0.71	0.10	chr2R	14642500	14644588				
1625140_at	NtR	-2.63	9.95E-08	1.60	0.90	0.14	0.10	chr2R	18015314	18017689				
1631165_at	GstE14	-2.61	1.99E-05	0.10	0.00	1.05	0.70	chr2R	9127233	9128523				
1632591_at	Phk-3	-2.56	3.08E-04	0.10	0.10	0.20	0.10	chr2R	20858366	20859365				
1637066_at	CG8239	-2.55	6.61E-06	0.40	0.20	0.93	2.60	chrX	15643210	15645255				
1629395_at	CG9743	-2.55	9.13E-06	0.80	1.60	0.77	0.10	chr3R	26022082	26028715				
1633880_s_at	Ir76a	-2.54	2.89E-04	6.60	4.80	1.62	1.50	chr3L	19792378	19796527				
1625023_a_at	nAcRbeta-21C	-2.51	1.69E-04	1.40	0.60	0.14	0.00	chr2L	545129	547096				
1637144_a_at	Map205	-2.49	5.63E-06	1.00	1.10	2.81	2.20	chr3R	27881001	27894163				
1623486_at	CG7900	-2.48	1.07E-04	0.10	0.10	0.39	0.30	chr3R	3919846	3930805				
1638567_at	CG1092	-2.47	1.09E-04	1.30	0.50	0.13	0.10	chr3R	92492	94038				
1639059_s_at	exu	-2.43	2.84E-04	0.00	0.00	0.00	1.70	chr2R	16554924	16558379				
1637135_at	nej	-2.41	7.23E-05	5.10	3.10	2.69	3.50	chrX	9559475	9581099				
1628344_at	CkIIbeta	-2.38	3.43E-04	2.20	1.30	13.79	3.30	chrX	11686566	11695620				
1638481_at	CG2736	-2.38	1.04E-04	0.20	0.20	0.03	0.00	chr2R	20860954	20862894				
1628345_at	Cyp6a9	-2.38	1.59E-04	0.60	0.60	0.25	0.80	chr2R	10766861	10768877				
1623804_a_at	hep	-2.36	5.62E-05	4.10	1.90	1.46	1.90	chrX	12973240	12984466				
1630034_at	CG12119	-2.36	5.10E-05	0.00	0.10	0.06	0.10	chrX	9100153	9104580				
1636112_s_at	CG33521	-2.35	2.97E-04	0.10	0.10	0.06	0.10	chr4	1206394	1213482				
1629857_at	CG10359	-2.33	3.31E-04	0.80	1.90	7.43	0.10	chr3L	3612192	3615244				
1625705_s_at	E(Pc)	-2.31	6.26E-05	0.90	0.90	0.82	1.80	chr2R	7339548	7352775				
1630707_at	edl	-2.26	1.21E-05	0.30	0.90	3.50	0.40	chr2R	14555026	14561037				
1630640_at	CG4594	-2.26	1.02E-05	0.10	0.20	0.38	1.80	chr2L	9920160	9921459				
1629851_at	CG31998	-2.26	1.58E-05	1.10	0.80	1.33	2.50	chr4	217301	226571				
1633254_at	CG7787	-2.23	2.04E-08	0.70	0.60	0.71	1.80	chr2L	8320328	8321285				
1626694_at	CG1674	-2.21	3.27E-04	0.10	0.10	0.07	0.00	chr4	251356	266529				
1636296_at	CG12945	-2.21	3.09E-04	0.60	0.30	0.37	1.70	chr3R	5614574	5616943				

1632744_a_at	if	-2.19	2.27E-05	0.60	0.90	1.12	0.20	chrX	16646222	16677467				
1640845_at	CG10581	-2.17	1.72E-06	1.80	1.90	2.13	0.40	chr3L	21026654	21027303				
1638687_at	CG40298	-2.11	2.16E-05	0.30	0.20	0.26	0.40	chr3L	23719929	23721089				
1631331_a_at	Pxt	-2.09	4.86E-09	0.00	0.00	0.01	1.70	chr3R	13545176	13548677				
1634685_at	RpL3	-2.07	3.49E-05	1.10	0.80	1.11	1.10	chr3R	7047616	7050895				
1641117_a_at	CG17600	-2.07	3.52E-06	2.10	1.50	1.87	1.90	chrX	21917033	21943860				
1636900_at	CG5390	-2.05	2.68E-05	0.80	0.90	1.11	0.10	chr2L	10304067	10306594				
1626908_at	CG8066	-2.03	6.30E-06	1.30	2.50	1.75	0.70	chr3R	10393333	10394569				
1637873_at	scpr-C	-2.03	2.64E-04	0.00	0.00	0.02	0.10	chr3R	7051242	7052204				
1629181_at	CG33494	-2.03	1.36E-06	0.30	0.20	0.24	0.00	chr3R	21319203	21320883				
1638782_at	CG8195	-2.02	5.40E-06	3.20	3.70	1.66	2.20	chr2R	11450201	11453291				
1630129_at	CG43078	-2.02	1.07E-04	1.00	0.40	0.14	0.00	chr3L	8571842	8592717				
1636835_at	CG16700	-2.02	2.48E-04	1.50	1.90	0.85	1.40	chrX	16985887	16992520				
1624851_at	Tango13	-2.02	4.15E-05	1.50	1.00	0.63	1.30	chrX	13457856	13487257				
1640857_at	CG10208	-2.00	1.77E-06	1.10	1.40	0.79	0.70	chr3R	19598720	19599849				
1638809_at	CG34284	8.06	1.55E-04	0.00	0.00	0.01	0.00	chr3R	14728060	14728655	■	■	■	
1633646_at	inaF-B / inaF-D	2.08	3.37E-04	0.40	0.10	0.02	0.00	chrX	11618701	11626803	■	■	■	■
1636409_at	CG11034	2.19	2.50E-07	0.10	0.10	0.06	0.40	chr2L	5805395	5808858	■	■	■	■
1638198_at	CG12768	2.36	4.69E-06	13.80	13.50	20.52	0.40	chr3L	22903591	22916632	■	■	■	■
1639106_at	Grip	2.41	6.98E-05	0.70	1.40	1.28	0.70	chrX	5860314	5880729	■	■	■	■
1628009_at	fas	2.55	5.09E-05	35.90	41.50	41.39	0.10	chr2R	9510593	9636872	■	■	■	■
1625265_at	CG9119	2.59	1.39E-04	0.20	0.30	0.09	0.10	chr3L	1203316	1204795	■	■	■	■
1623173_at	CG10013	2.93	1.76E-07	0.30	0.50	0.34	0.40	chr3R	8149243	8150932	■	■	■	■
1637957_s_at	Rbp9	3.08	1.92E-18	1.00	0.60	0.06	0.10	chr2L	2954762	2968434	■	■	■	■
1627961_a_at	CG18507	3.11	2.79E-04	0.10	0.10	0.13	0.20	chr2L	13665525	13672967	■	■	■	■
1627436_s_at	Pdp1	3.34	1.58E-04	7.70	8.20	1.01	0.20	chr3L	7805015	7860472	■	■	■	■
1628083_at	CG5036	3.43	7.91E-10	8.50	7.50	4.48	1.30	chr2R	13680387	13685633	■	■	■	■
1640097_at	Pxn	3.49	2.89E-04	8.10	6.70	0.62	0.40	chr3L	2601455	2630072	■	■	■	■
1629205_at	CG32032	4.09	6.41E-06	9.80	10.80	9.82	0.10	chr3L	9086153	9087956	■	■	■	■
1637294_at	nwk	4.50	1.81E-06	21.60	19.00	5.17	0.10	chr3L	9130960	9138793	■	■	■	■
1629269_at	CG32204	4.70	1.50E-04	42.90	14.90	18.01	0.10	chr3L	18915519	18939138	■	■	■	■
1626457_s_at	SKIP	5.27	2.22E-06	15.20	9.80	22.24	1.00	chr3R	17959552	18121848	■	■	■	■
1641339_at	CG10137	5.36	1.59E-07	15.20	12.70	5.11	0.40	chr2L	19526686	19532992	■	■	■	■
1639110_at	Slc45-1	5.97	3.14E-06	2.90	4.10	2.29	0.30	chr3L	9196165	9201953	■	■	■	■
1640914_at	CG8838	6.40	8.65E-09	0.00	0.00	0.01	0.00	chr2L	3357646	3358618	■	■	■	■
1638381_s_at	CG1695 / CG32506	7.78	3.04E-08	18.00	7.80	4.14	0.10	chrX	20304977	20315623	■	■	■	■
1627297_at	CG15270	7.90	8.39E-06	22.30	21.00	8.98	0.00	chr2L	15074776	15096915	■	■	■	■
1626262_s_at	CG3104	8.02	1.19E-14	20.60	11.50	3.91	1.40	chr2L	2848989	2855778	■	■	■	■
1624577_at	Ace	8.56	9.14E-07	7.00	15.10	6.13	0.10	chr3R	9048673	9085239	■	■	■	■
1640729_s_at	nrv3	20.93	6.37E-10	9.40	11.30	4.77	0.00	chr2L	21380000	21393319	■	■	■	■
1625951_at	CG17778	21.59	1.93E-13	18.40	9.60	3.71	0.10	chrX	388933	390402	■	■	■	■
1634016_at	CG2781	22.52	9.84E-05	0.00	0.00	0.05	0.30	chr3R	3807539	3821574	■	■	■	■
1640774_a_at	Mob2	40.93	2.99E-17	8.70	10.20	3.39	0.00	chr3L	11515857	11555333	■	■	■	■
1638016_at	CG2993	41.30	1.44E-20	20.00	11.00	4.54	0.80	chr3R	3630387	3635736	■	■	■	■
1624833_a_at	mAcR-60C	47.66	6.00E-19	40.40	24.70	13.46	0.10	chr2R	20266159	20277235	■	■	■	■
1634855_s_at	CG9813	52.38	1.66E-18	14.40	13.90	1.52	0.00	chr3R	9198826	9205497	■	■	■	■
1633582_at	Ih	2.03	4.56E-06	12.80	14.10	3.56	0.40	chr2R	10163809	10187349	■	■	■	
1640976_at	Ykt6	2.08	3.58E-04	2.50	3.00	3.30	1.30	chrX	7814442	7815999	■	■	■	
1637853_a_at	Hk	6.74	6.45E-13	28.30	34.10	2.55	0.20	chrX	10128791	10157518	■	■	■	
1641390_at	dpr19	6.95	5.70E-14	28.70	26.30	16.21	0.10	chr2L	10376168	10379907	■	■	■	
1625911_at	CG15760	7.55	2.23E-06	10.40	6.50	2.75	0.20	chrX	13563732	13570265	■	■	■	
1635398_at	Scp2	15.21	1.39E-05	7.40	15.80	0.73	0.00	chr3R	12400265	12409385	■	■	■	
1639743_s_at	Syn2	23.07	5.56E-17	14.70	18.10	3.24	0.10	chr2R	12439765	12445991	■	■	■	
1626200_s_at	tipE	79.25	3.20E-19	15.00	22.00	8.54	0.20	chr3L	4188499	4193788	■	■	■	
1624098_s_at	CG18675 / tipE	110.7	1.29E-21	3.40	4.10	0.85	0.00	chr3L	4173884	4192968	■	■	■	
1631038_at	CG32773	3.39	1.48E-06	0.20	0.30	0.38	2.40	chrX	4281829	4505418	■	■		■
1638280_at	CG43102	2.79	7.52E-05	8.40	2.70	2.22	0.30	chr3R	13594157	13620296	■	■		

1625065_s_at	SK	3.16	1.71E-04	20.60	19.90	6.76	0.10	chrX	5234269	5298760	🟦	🟦		
1628666_at	CG3328	3.68	5.50E-09	5.40	6.80	1.85	0.10	chr2R	20050013	20061139	🟦	🟦		
1637820_at	X11Lbeta	3.91	2.86E-05	27.70	21.30	16.40	0.20	chrX	10521770	10604900	🟦	🟦		
1630285_at	RhoGAP100F	4.75	5.13E-05	51.90	36.10	42.99	0.20	chr3R	27638331	27670966	🟦	🟦		
1631417_s_at	CG6282	5.38	1.06E-07	20.80	17.80	5.02	0.10	chr3L	8597757	8610174	🟦	🟦		
1631327_at	mspo	6.52	9.62E-10	21.90	14.60	10.31	0.10	chr2R	10559458	10601127	🟦	🟦		
1624143_a_at	CG12071	7.22	9.56E-07	27.20	17.20	18.65	0.10	chr3R	26702806	26706597	🟦	🟦		
1626537_at	CG17321	12.40	8.17E-15	25.20	16.40	12.33	0.10	chr2L	18845184	18855118	🟦	🟦		
1639237_at	CG32814	13.59	1.27E-15	0.60	2.00	0.86	1.90	chrX	913828	920733	🟦	🟦		
1628147_at	neuroligin	15.87	4.20E-15	37.40	27.00	15.91	0.20	chr2L	6874900	6906658	🟦	🟦		
1637913_at	CG11638	17.19	3.28E-11	20.90	29.20	11.63	0.30	chrX	908017	920736	🟦	🟦		
1629228_at	Hs3st-A	18.96	1.47E-14	21.50	15.10	3.93	0.00	chr2R	14605634	14642026	🟦	🟦		
1637150_at	CG13928	55.98	3.88E-20	21.40	24.40	20.50	0.00	chr3L	1625791	1628377	🟦	🟦		
1639837_at	Rph	171.4	5.11E-18	28.00	13.90	16.82	0.20	chrX	10643108	10651699	🟦	🟦		
1633533_at	CG6329	2.36	1.88E-04	15.30	20.80	10.20	0.00	chr2R	9713880	9720419	🟦		🟦	🟦
1625249_at	fend	2.59	3.25E-04	6.80	7.70	2.78	2.80	chrX	9016006	9029073	🟦		🟦	🟦
1632313_at	CG1998	2.61	5.43E-07	7.80	9.20	2.70	0.20	chrX	13303402	13307107	🟦		🟦	🟦
1626675_at	XRCC1	2.78	4.40E-05	0.60	0.50	1.41	2.40	chrX	5223944	5226468	🟦		🟦	🟦
1638225_a_at	inx7	2.85	3.16E-05	0.20	0.10	0.04	0.20	chrX	6885645	6903902	🟦		🟦	🟦
1636846_at	lap	3.11	1.08E-08	25.60	26.30	12.59	0.10	chr3R	3012716	3026663	🟦		🟦	🟦
1634794_at	CG10924	3.22	1.74E-05	0.00	0.00	0.03	0.00	chr2R	14414937	14423263	🟦		🟦	🟦
1625840_at	CG12001	4.44	1.73E-05	1.50	1.70	0.75	1.10	chr3R	480522	483707	🟦		🟦	🟦
1627835_a_at	Cda5	4.80	3.05E-05	4.10	4.00	1.92	0.30	chr2L	25402	65404	🟦		🟦	🟦
1635196_at	CG6836	4.89	1.51E-07	3.00	1.00	0.06	0.30	chr3L	18943729	18948506	🟦		🟦	🟦
1641146_at	st	5.10	1.71E-13	0.10	0.00	0.07	0.00	chr3L	16490751	16493562	🟦		🟦	🟦
1623166_at	CG6071	6.64	3.19E-07	0.20	0.30	0.32	0.10	chr3L	11636006	11639133	🟦		🟦	🟦
1625621_s_at	f	23.72	6.08E-15	0.60	0.70	1.56	0.80	chrX	17126975	17174997	🟦		🟦	🟦
1641460_at	CanB	100.8	6.77E-22	19.70	20.50	12.30	0.00	chrX	5226532	5228482	🟦		🟦	🟦
1638334_at	CG13168	3.75	9.08E-07	0.20	0.10	0.06	0.00	chr2R	8141497	8143197	🟦		🟦	
1637105_at	rgr	2.72	1.45E-04	2.50	1.20	4.31	0.90	chr2R	4487938	4498743	🟦			
1629667_at	CG14298	3.52	3.90E-05	0.20	0.00	0.26	0.10	chr3R	14701250	14702926	🟦			
1634134_at	sff	4.61	8.28E-09	37.00	40.00	30.06	0.30	chr3L	15893256	15917961	🟦			
1634093_at	CG32017	39.26	5.03E-15	20.20	19.80	10.81	0.00	chr4	1158456	1167155	🟦			
1638654_at	CG14645	2.00	2.14E-04	0.00	0.00	0.00	0.00	chr3R	160820	161228				
1634742_at	Sodh-2	2.05	5.66E-05	1.80	2.90	0.65	1.10	chr3R	6702106	6703979				
1637610_at	Chrac-16	2.06	5.92E-05	0.30	0.20	2.04	2.30	chrX	11911307	11911989				
1634736_at	hts	2.07	4.10E-13	0.00	0.00	0.01	2.70	chr2R	15284537	15312454				
1634113_at	gk	2.07	2.36E-05	0.10	0.10	0.08	0.20	chr3L	18132502	18138518				
1625652_s_at	CG12428	2.11	4.94E-10	0.40	0.40	0.49	1.00	chr3R	23529101	23532468				
1637517_s_at	KrT95D	2.13	2.18E-05	1.10	1.00	0.48	0.90	chr3R	19824162	19857532				
1625083_at	rhi	2.13	8.24E-06	0.00	0.00	0.05	2.70	chr2R	13515994	13521018				
1634145_s_at	CG14968	2.15	2.30E-04	0.20	0.20	0.52	0.10	chr3L	3299336	3303112				
1623566_at	CG13957	2.19	1.25E-06	1.20	1.20	1.87	1.70	chrX	16207742	16211783				
1624995_at	CG12355	2.23	2.40E-09	5.70	9.80	1.40	0.20	chr3L	15486064	15488649				
1634630_at	CG5707	2.28	1.23E-05	0.20	0.20	0.16	0.90	chr3L	2189160	2192221				
1627302_at	Fmo-2	2.37	1.71E-05	0.10	0.20	0.07	0.20	chr2R	2529923	2532603				
1630038_at	pyd3	2.41	2.35E-12	1.50	2.20	0.97	0.50	chr3R	3573635	3575798				
1625945_a_at	CG1233	2.41	1.81E-04	1.00	0.70	0.96	1.80	chr3L	361472	365681				
1640344_at	CG18480	2.42	3.43E-04	0.00	0.10	0.07	0.10	chr2L	15630084	15632618				
1635807_at	CG17739	2.42	2.35E-05	2.20	4.20	1.18	0.00	chr2R	8194029	8197917				
1638810_at	Faa	2.45	3.88E-04	0.30	0.50	0.35	0.10	chr3L	4072032	4073954				
1633946_at	CG31955	2.48	3.82E-04	0.50	0.50	0.67	0.70	chr2L	3712154	3712866				
1630244_s_at	CG31809	2.51	2.56E-04	0.10	0.60	0.13	0.00	chr2L	16849018	16858714				
1624435_at	Tsp42Ej	2.52	3.47E-04	6.40	8.50	1.36	0.00	chr2R	2927641	2930267				
1639313_at	CG17650	2.53	8.30E-06	0.20	0.20	0.18	0.20	chr2L	1758286	1759093				
1638199_s_at	RhoGAPp190	2.58	6.96E-07	15.70	12.40	14.46	0.50	chrX	17533180	17546595				
1634019_at	CG2064	2.67	7.98E-09	0.60	0.90	0.41	0.10	chr2R	3553333	3554848				

1626384_at	CG12182	2.69	2.86E-06	2.20	1.90	3.51	1.80	chr3L	2596967	2599579				
1624381_at	CG17658	2.74	3.27E-06	0.00	0.10	0.21	3.00	chr2R	19782601	19784520				
1640884_at	CG15784	2.75	7.85E-05	0.10	0.10	0.21	0.10	chrX	5324713	5326494				
1640489_at	CG18522	2.82	8.14E-05	0.30	0.60	0.27	0.10	chr3R	11357859	11363014				
1632087_at	CG9928	2.86	9.65E-05	0.10	0.10	0.00	0.00	chr2L	13142494	13142903				
1623963_at	CG32115	2.91	2.08E-04	0.40	0.30	1.03	0.00	chr3L	12905127	12906746				
1637821_at	CG32023	2.92	1.67E-04	0.00	0.10	0.05	0.10	chr3L	8796702	8797282				
1627854_at	CG9914	2.96	1.71E-08	0.10	0.10	0.27	0.20	chrX	16200945	16202426				
1635020_s_at	phr6-4	3.07	9.51E-05	0.20	0.40	0.94	1.20	chr2L	20643351	20645791				
1634351_at	CG7860	3.07	1.86E-06	0.50	0.30	1.43	0.60	chrX	15463026	15464474				
1639712_at	CG17261	3.19	2.95E-07	0.00	0.00	0.03	0.00	chr2L	3042551	3043593				
1623903_at	CG18473	3.20	6.45E-05	0.10	0.10	0.20	0.00	chr3R	5189027	5190560				
1637476_at	CG15579	3.22	1.47E-05	0.40	0.40	0.47	0.10	chrX	4205397	4205832				
1634195_at	CORL	3.24	1.86E-05	5.40	3.20	7.80	1.90	chr4	982967	999048				
1630147_at	Hex-C	3.28	3.07E-04	0.10	0.30	0.01	0.00	chr2R	11106342	11107917				
1635376_at	CG9086	3.33	2.78E-07	1.70	1.00	0.86	2.40	chrX	16850978	16862682				
1623281_s_at	His2B	3.38	1.01E-05	0.10	0.10	0.44	2.30	n/a						
1633949_at	CG15152	3.47	5.89E-06	0.00	0.00	0.03	0.00	chr2L	18114547	18115220				
1627188_at	phm	3.49	3.20E-04	0.10	0.20	2.53	0.70	chrX	18579802	18582257				
1629418_s_at	sei	3.53	1.67E-07	9.90	10.20	3.14	1.30	chr2R	19936728	19940560				
1640488_a_at	CG9510	3.57	2.24E-10	0.10	0.10	0.05	0.00	chr2L	8939780	8943264				
1628701_a_at	CG14798	3.58	3.71E-05	1.50	2.00	1.56	1.50	chrX	1586857	1587876				
1635370_at	Tsp42El	3.59	1.44E-08	0.20	0.40	0.90	0.10	chr2R	2933274	2936043				
1623126_at	CG13912	3.60	9.35E-09	0.10	0.20	0.02	0.20	chr3L	1189590	1190472				
1631072_at	CG9512	3.64	3.79E-05	0.80	0.20	0.06	0.00	chrX	14795985	14799574				
1628690_at	CG1503	3.74	1.66E-06	0.20	0.30	0.23	0.80	chrX	20975890	20977394				
1632100_s_at	sina	3.82	4.29E-09	3.10	3.60	5.12	1.00	chr3L	16846851	16851812				
1634959_at	TfIIA-S-2	3.90	2.55E-09	0.20	0.30	0.39	0.20	chrX	905134	905676				
1630696_at	ebd2	3.93	1.02E-07	0.90	0.30	1.08	2.20	chr3L	21337868	21342388				
1624862_at	CG43117	3.98	2.54E-04	2.30	2.90	4.34	0.70	chr3R	22280516	22280834				
1625046_at	Rbm13	3.99	5.79E-07	0.30	0.30	1.08	2.10	chrX	8795724	8797497				
1623609_at	CG15172	4.17	1.17E-07	0.00	0.00	0.03	0.00	chr2L	19022417	19023646				
1632775_at	CG42254	4.20	4.97E-06	1.30	0.90	0.82	1.10	chr2R	10657104	10658804				
1629434_at	CG9380	4.29	1.94E-04	0.00	0.00	0.02	0.00	chr2R	21071151	21142841				
1627096_s_at	CG16778	4.35	7.80E-05	22.20	13.80	32.35	0.40	chr2R	20973303	20986711				
1627862_at	dao	4.38	1.09E-07	8.20	11.40	3.14	1.60	chr2L	15248879	15254715				
1628696_at	CG12643	4.47	8.14E-07	0.40	0.50	12.22	0.20	chrX	10158266	10159296				
1628611_at	CG11241	4.48	1.16E-04	1.20	0.70	0.32	1.00	chr3L	22726252	22731520				
1629853_at	CG3699	4.49	5.39E-08	0.00	0.10	0.00	0.00	chrX	840687	841517				
1627613_at	Mtk	4.65	6.02E-05	0.30	0.10	0.01	0.00	chr2R	11296351	11296618				
1637146_at	CG42694	4.70	3.97E-10	0.50	0.60	0.69	1.70	chr2R	18829772	18832670				
1630600_at	Fst / Scm	5.04	5.44E-05	0.00	0.10	0.04	0.00	chr3R	5459081	5471872				
1630829_at	PIP5K59B	5.20	5.23E-11	31.90	27.20	11.49	0.30	chr2R	18762294	18768959				
1633599_a_at	Pepck	5.32	1.82E-09	0.00	0.10	0.04	0.00	chr2R	14424272	14426924				
1637275_a_at	CG42807	5.37	1.21E-04	0.10	0.00	0.01	0.00	chr2R	9459029	9460045				
1630334_at	CG15406	5.42	4.67E-05	0.00	0.00	0.02	0.00	chr2L	3309222	3311682				
1637282_at	CG6171	5.93	1.36E-04	1.30	1.40	1.04	2.10	chr3R	11188518	11189579				
1635321_at	CG14688	6.18	1.21E-06	1.10	1.80	0.20	0.80	chr3R	6503459	6506647				
1633401_s_at	Cyp12d1	6.28	2.71E-08	0.10	0.10	0.01	1.10	chr2R	7011163	7013152				
1632677_a_at	GM130	6.28	2.95E-04	1.20	1.50	0.90	1.70	chr2R	18012072	18015002				
1625644_at	CG2641	6.50	4.86E-05	0.60	1.50	1.18	1.40	chr3R	3619931	3622321				
1629473_at	cdi	6.93	2.74E-11	4.80	4.40	6.52	0.10	chr3R	14870604	14920076				
1636431_at	CG8768	7.23	3.83E-04	2.40	3.00	0.51	0.30	chr2R	8578813	8580193				
1641722_at	Reg-2	8.03	5.18E-10	0.10	0.10	0.03	0.20	chr3L	605165	606569				
1634064_at	CG13311	8.13	6.33E-05	0.00	0.00	0.03	0.00	chr3L	8794640	8795264				
1634514_at	CG33258	8.42	2.84E-04	0.00	0.00	0.01	0.00	chr3L	16075651	16076738				
1627741_at	CG13086	10.09	5.30E-14	0.10	0.00	0.01	0.00	chr2L	19364375	19365470				

1624377_s_at	be	10.15	3.53E-13	3.20	2.80	7.49	0.70	chrX	14918467	14936093				
1639118_a_at	Hrb87F	11.58	1.85E-04	0.80	0.90	3.18	2.10	chr3R	9482568	9486253				
1624505_at	Lip4	11.66	4.22E-05	0.20	0.20	1.00	0.30	chr2L	10527572	10531777				
1630085_s_at	Peritrophin-A	12.21	3.92E-16	0.20	0.30	0.96	0.70	chrX	20115727	20119277				
1623491_at	CG15155	12.72	2.92E-05	0.00	0.00	0.02	0.00	chr2L	18154864	18155942				
1637224_at	CG13905	13.12	1.01E-06	0.00	0.20	0.32	0.10	chr3L	902898	903810				
1640881_at	CG16762	15.67	7.02E-06	0.00	0.00	0.01	0.00	chr3L	2474667	2475614				
1633959_s_at	CG30345	17.43	3.26E-10	0.60	0.30	0.17	0.00	chr2R	5036190	5039397				
1626098_at	CG11453	17.72	1.51E-09	0.10	0.10	0.14	0.20	chr3R	15609244	15611241				
1629125_at	gp210	18.75	2.67E-14	1.30	1.70	19.34	1.10	chr2R	1648367	1661829				
1637691_at	CG4570	19.71	2.42E-04	0.00	0.00	1.17	2.30	chr3R	6682529	6683788				
1635306_at	CG4650	24.84	2.08E-08	1.10	1.00	2.00	0.80	chr2L	14773812	14774981				
1628052_at	Cyp6a17	25.61	1.13E-14	2.10	1.40	0.14	0.10	chr2R	10761459	10763063				
1627736_at	Actbeta	26.91	1.46E-18	13.80	17.50	11.40	0.10	chr4	1097957	1105422				
1627551_s_at	AttA / AttB	27.02	3.80E-08	0.20	0.00	0.02	0.50	chr2R	10636728	10637670				
1625436_at	Uro	27.90	3.97E-06	0.00	0.00	0.03	0.00	chr2L	7780085	7781415				
1625124_at	AttA	39.24	4.01E-09	0.50	0.20	0.08	0.60	chr2R	10634876	10635698				
1625246_at	Her	52.93	9.94E-11	0.10	0.10	0.03	1.20	chrX	18098436	18099177				
1623477_at	CG42857	73.28	4.41E-15	0.10	0.10	0.02	0.50	chr3R	5646236	5646913				

Table S4. Tissue-specific expression of Su(Hw) target genes using anatomical expression data (FlyAtlas)

	FlyAtlas		**Su(Hw) target genes**					
	(*n*=12856)		**Repressed (*n*=75)**			**Activated (*n*=30)**		
	#	**%**	**#**	**%**	***P***	**#**	**%**	***P***
CNS	**3654**	28	**56**	75	5.3E-19	**12**	40	0.159
Ovary	**2070**	16	**4**	5	0.011	**3**	10	0.363
Ovary & CNS	**703**	5	**2**	3	0.289	**0**	0	0.187
Testis	**2778**	22	**6**	8	0.004	**3**	10	0.124
Hindgut	**1890**	15	**14**	19	0.332	**12**	40	4.8E-05
Tubule	**1788**	14	**10**	13	0.889	**5**	17	0.660
Salivary gland	**2853**	22	**11**	15	0.119	**8**	27	0.555
Fat body	**1925**	15	**9**	12	0.472	**2**	7	0.204
Midgut	**1946**	15	**6**	8	0.085	**5**	17	0.810