

Supplementary Materials for

The histone code reader PHD finger protein 7 controls sex-linked disparities in gene expression and malignancy in *Drosophila*

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Table S4. Sex-dependent dysregulation of MBTS genes in *l(3)mbt^{ts1}* tumors versus wild-type and in *Phf7^{ΔN2}; l(3)mbt^{ts1}* versus *l(3)mbt^{ts1}*.

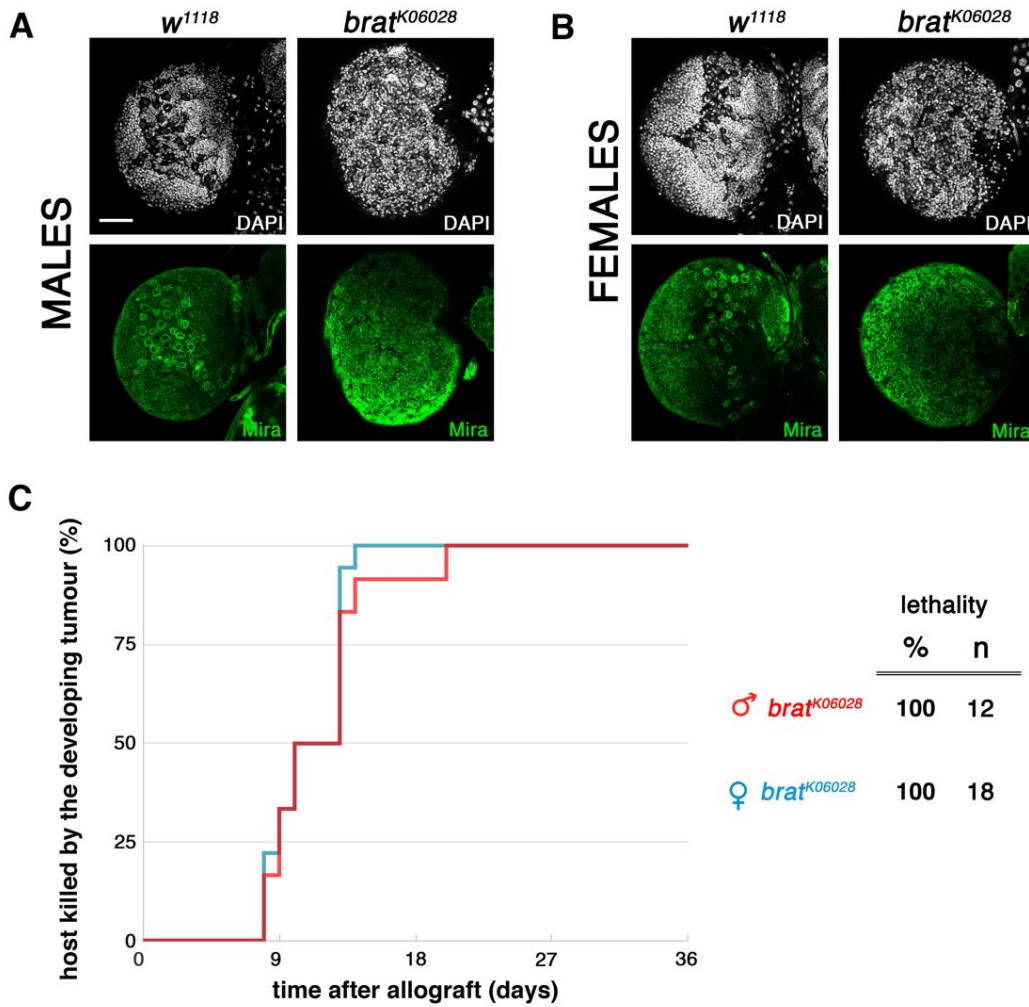


Fig. S1. *brat* tumors do not present sex-dependent dimorphism. (A-B) Dorsal views of larval brain lobes from male (A) and female (B) control (*w¹¹¹⁸*) and *brat* mutant (*brat^{K06028}*) larvae, stained with DAPI (grey) and anti-Miranda (green). The extent of tumours spreading over the brain lobe is indistinguishable between male and female larvae. Scale bar = 50 μ m. (C) Tumour growth rate and host lethality caused by allografted *brat^{K06028}* male (red) and female (blue) brain lobes, shown as the fraction of allografted hosts that are killed by the developing tumour as a function of time after allograft. Male and female implants kill hosts at same rate and time.

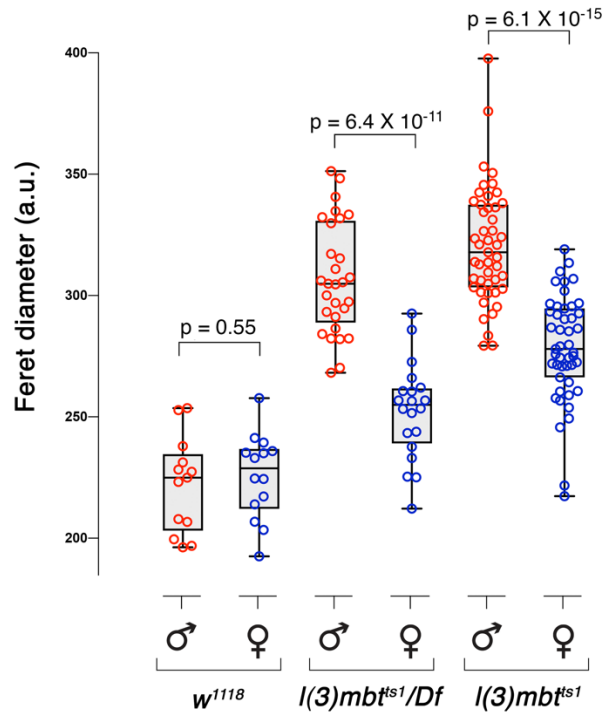


Fig. S2. mbt tumor size is sex dependent. Box-plot of maximum brain Feret diameters in male (red) and female (blue), control (*w¹¹¹⁸*) and mbt mutant (*l(3)mbt^{ts1}/Df*, and *l(3)mbt^{ts1}*) larvae. Maximum Feret diameters are significantly greater in male than in female tumour samples.

Phf7^{ΔN2}; *l(3)mbt*^{ts1} vs *l(3)mbt*^{ts1}

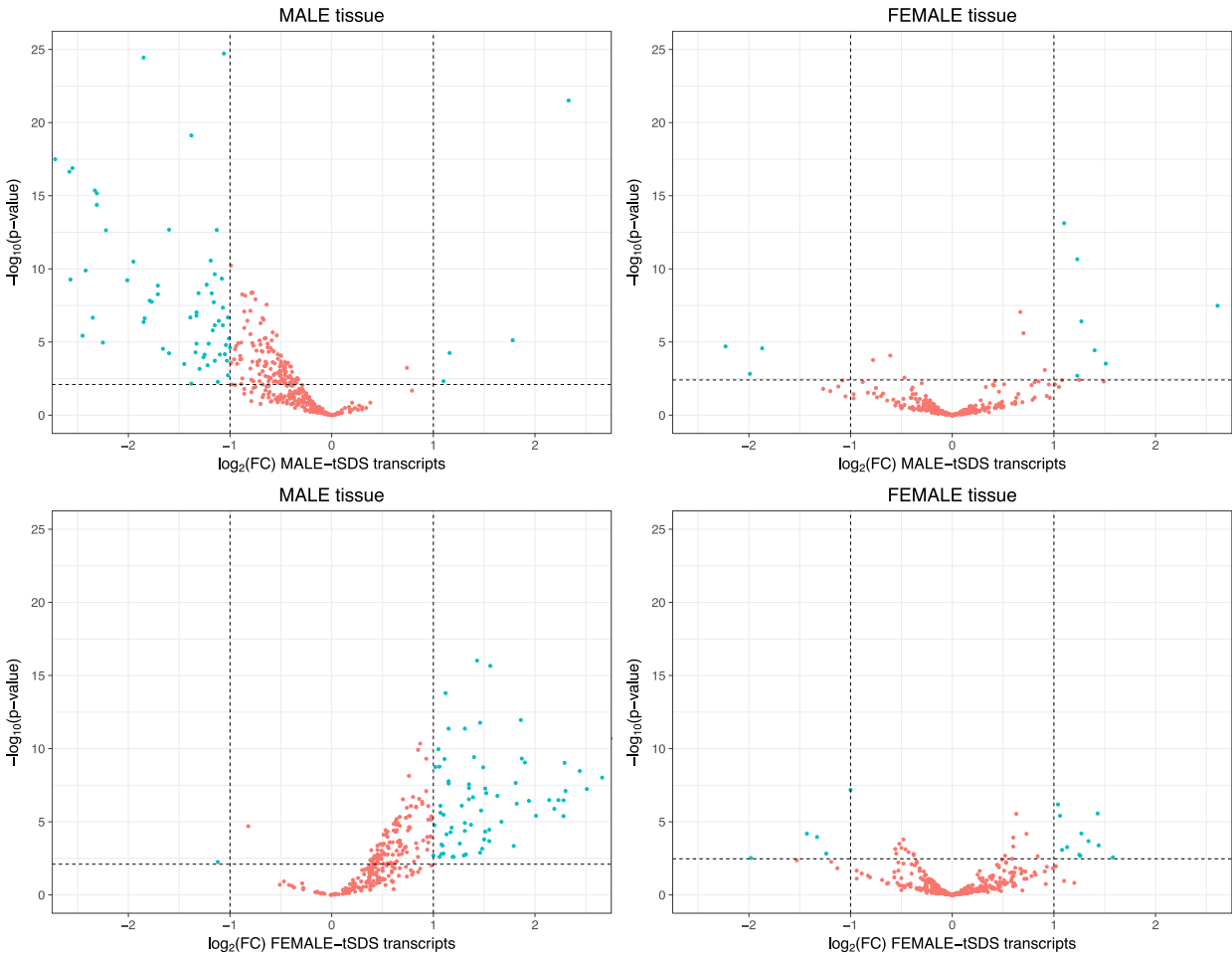


Fig. S3. Loss of *Phf7* reduces the expression of mbt M-tSDS genes and increases the expression of mbt F-tSDS genes in male tissue. Volcano plots showing the significance of the fold change in expression level of M- and F-tSDS genes between *Phf7*^{ΔN2}; *l(3)mbt*^{ts1} and *l(3)mbt*^{ts1} in male and female samples. The horizontal dotted line corresponds to negative log10 of the p-value associated to the significance threshold (FDR=0.05). Points above this line and with log2(FC) values greater than 1 and smaller than -1 are significantly upregulated and downregulated respectively in *Phf7*^{ΔN2}; *l(3)mbt*^{ts1} compared to *l(3)mbt*^{ts1} (blue). Genes whose differential expression is not significant are coloured in red. Genes presenting extreme FC values are not included in the plots to help visualisation (<15% of the total tSDS genes). In male tissue, most M-tSDS and F-tSDS genes are downregulated and upregulated respectively, while in female tissues the extend of dysregulation is very low.

Table S1. Proteomic sex-linked dimorphic signatures.

66 M-pSDS		61 F-pSDS	
FBgn0033749	<i>achi</i>	FBgn0004552	<i>Akh</i>
FBgn0000047	<i>Act88F</i>	FBgn0032076	<i>Argl</i>
FBgn0036622	<i>Agpat4</i>	FBgn0039007	<i>CCAP</i>
FBgn0250816	<i>AGO3</i>	FBgn0034443	<i>cer</i>
FBgn0016762	<i>angel</i>	FBgn0032805	<i>CG10337</i>
FBgn0029094	<i>asf1</i>	FBgn0030292	<i>CG11752</i>
FBgn0000147	<i>aurA</i>	FBgn0036599	<i>CG13044</i>
FBgn0014127	<i>barr</i>	FBgn0026879	<i>CG13364</i>
FBgn0045863	<i>blood\ORF</i>	FBgn0040660	<i>CG13551</i>
FBgn0030501	<i>BthD</i>	FBgn0036835	<i>CG14075</i>
FBgn0004107	<i>Cdk2</i>	FBgn0038421	<i>CG17931</i>
FBgn0010620	<i>CG10939</i>	FBgn0029608	<i>CG3091</i>
FBgn0039733	<i>CG11504</i>	FBgn0051051	<i>CG31051</i>
FBgn0029754	<i>CG15930</i>	FBgn0085446	<i>CG34417</i>
FBgn0034931	<i>CG2812</i>	FBgn0029708	<i>CG3556</i>
FBgn0051365	<i>CG31365</i>	FBgn0262858	<i>CG43222</i>
FBgn0051373	<i>CG31373</i>	FBgn0263994	<i>CG43737</i>
FBgn0052856	<i>CG32856</i>	FBgn0031306	<i>CG4577</i>
FBgn0027521	<i>CG3679</i>	FBgn0030575	<i>CG5321</i>
FBgn0263776	<i>CG43693</i>	FBgn0031913	<i>CG5958</i>
FBgn0036522	<i>CG7372</i>	FBgn0038407	<i>CG6126</i>
FBgn0040477	<i>cid</i>	FBgn0032287	<i>CG6415</i>
FBgn0038612	<i>cona</i>	FBgn0038641	<i>CG7708</i>
FBgn0020496	<i>CtBP</i>	FBgn0033717	<i>CG8839</i>
FBgn0000392	<i>cup</i>	FBgn0026084	<i>cib</i>
FBgn0026085	<i>dgt4</i>	FBgn0000377	<i>crn</i>
FBgn0005696	<i>DNApol-alpha73</i>	FBgn0261808	<i>cu</i>
FBgn0015929	<i>dpa</i>	FBgn0034136	<i>DAT</i>
FBgn0000928	<i>fs(1)Yb</i>	FBgn0033159	<i>Dscaml</i>
FBgn0001086	<i>fzy</i>	FBgn0000564	<i>Eh</i>
FBgn0036850	<i>Gem2</i>	FBgn0000715	<i>FMRFa</i>
FBgn0053852	<i>His1:CG33852</i>	FBgn0259108	<i>futsch</i>
FBgn0001198	<i>His2B</i>	FBgn0035160	<i>hng3</i>
FBgn0001199	<i>His3</i>	FBgn0001224	<i>Hsp23</i>
FBgn0001200	<i>His4</i>	FBgn0001227	<i>Hsp67Ba</i>
FBgn0030994	<i>HP1D3csd</i>	FBgn0031294	<i>IA-2</i>
FBgn0283521	<i>lola</i>	FBgn0029994	<i>Ldsdh1</i>
FBgn0033845	<i>mars</i>	FBgn0039114	<i>Lsd-1</i>
FBgn0260986	<i>mei-38</i>	FBgn0030608	<i>Lsd-2</i>
FBgn0264695	<i>Mhc</i>	FBgn0015766	<i>Msr-110</i>
FBgn0021776	<i>mira</i>	FBgn0002868	<i>MtnA</i>
FBgn0002772	<i>Mlc1</i>	FBgn0035092	<i>Nplp1</i>

FBgn0002773	<i>Mlc2</i>	FBgn0004959	<i>phm</i>
FBgn0013717	<i>not</i>	FBgn0005626	<i>ple</i>
FBgn0032651	Oli	FBgn0003137	<i>Ppn</i>
FBgn0286788	<i>Orc1</i>	FBgn0030208	<i>PPP4R2r</i>
FBgn0015270	<i>Orc2</i>	FBgn0045038	<i>Proc</i>
FBgn0003041	<i>pbl</i>	FBgn0011828	<i>Pxn</i>
FBgn0051453	<i>pch2</i>	FBgn0016715	<i>Reg-2</i>
FBgn0005655	<i>PCNA</i>	FBgn0015521	<i>RpS21</i>
FBgn0267727	<i>Pen</i>	FBgn0003312	<i>sad</i>
FBgn0031091	<i>Phf7</i>	FBgn0030966	<i>shop</i>
FBgn0030318	<i>rho-4</i>	FBgn0025625	<i>Sik2</i>
FBgn0038853	RhoGAP93B	FBgn0039296	<i>Sil1</i>
FBgn0011704	<i>RnrS</i>	FBgn0051163	<i>SKIP</i>
FBgn0066304	<i>Rpp20</i>	FBgn0086917	<i>spok</i>
FBgn0015295	<i>Shark</i>	FBgn0035028	<i>Start1</i>
FBgn0265523	<i>Smr</i>	FBgn0004575	<i>Syn</i>
FBgn0265045	<i>Strn-Mlck</i>	FBgn0028671	<i>Vha100-1</i>
FBgn0004117	<i>Tm2</i>	FBgn0029906	xit
FBgn0033027	<i>TpnC4</i>	FBgn0265767	<i>zyd</i>
FBgn0029752	<i>TrxT</i>		
FBgn0283442	<i>vas</i>		
FBgn0001983	<i>wor</i>		
FBgn0042693	<i>wrd</i>		
FBgn0030805	<i>wus</i>		

FlybaseID and Symbol of the proteins up-regulated in male versus female (M-pSDS) and in female versus male (F-pSDS) mbt tumours. All of these proteins, except those in blue, were detected by 2 or more unique peptides.

Table S2. GO terms enriched in the M-pSDS and the F-pSDS.

M-pSDS	
<i>GO term - Biological Process</i>	<i>p-value</i>
mitotic spindle organization	2.23E-07
DNA replication initiation	1.90E-04
nucleosome assembly	5.10E-04
flight	1.69E-03
DNA replication	2.31E-03
DNA-dependent DNA replication	3.02E-03
mitotic chromosome condensation	6.23E-03
intracellular mRNA localization	6.77E-03
neurogenesis	8.26E-03
kinetochore assembly	2.06E-02
muscle thin filament assembly	2.57E-02
chromatin assembly or disassembly	2.97E-02
muscle contraction	3.57E-02
chromosome organization	4.09E-02

F-pSDS	
<i>GO term - Biological Process</i>	<i>p-value</i>
ecdysone biosynthetic process	1.47E-03
oxidation-reduction process	2.17E-03
lipid transport	4.64E-03
positive regulation of heart rate	8.89E-03
adult locomotory behavior	2.74E-02
response to heat	3.68E-02

Gene Ontology terms that are significantly enriched in the M-pSDS and the F-pSDS signatures (p values < 0.05).

Table S3. Relative expression levels of L(3)mbt and other components of the LINT and Myb/Muv/Dream complexes between male and female wild-type brain lobes.

Complex	Flybase ID	Gene Symbol	Wild-type brain lobes male versus female			
			FC	log2(FC)	pval	Adj pval
	FBgn0002441	<i>l(3)mbt</i>	1.023	0.033	0.672	0.762
LINT	FBgn0261573	<i>CoRest</i>	1.032	0.045	0.051	0.101
LINT	FBgn0030274	<i>Lint-1</i>	1.418	0.504	0.204	0.309
dREAM	FBgn0263979	<i>Caf1-55</i>	1.354	0.437	2X10 ⁻⁴	0.001
dREAM	FBgn0263979	<i>Caf1-55</i>	1.378	0.462	0.001	0.003
dREAM	FBgn0011763	<i>Dp</i>	1.003	0.005	0.932	0.954
dREAM	FBgn0011766	<i>E2f1</i>	0.947	-0.078	0.461	0.578
dREAM	FBgn0024371	<i>E2f2</i>	1.035	0.050	0.555	0.663
dREAM	FBgn0029800	<i>lin-52</i>	1.145	0.196	0.201	0.305
dREAM	FBgn0033846	<i>mip120</i>	1.063	0.088	0.010	0.028
dREAM	FBgn0023509	<i>mip130</i>	0.929	-0.106	0.280	0.395
dREAM	FBgn0023509	<i>mip130</i>	1.120	0.164	0.134	0.221
dREAM	FBgn0034430	<i>mip40</i>	1.092	0.127	0.048	0.098
dREAM	FBgn0002914	<i>Myb</i>	1.081	0.113	0.321	0.438
dREAM	FBgn0015799	<i>Rbf</i>	0.928	-0.108	0.183	0.284
dREAM	FBgn0038390	<i>Rbf2</i>	1.046	0.065	0.564	0.671
others	FBgn0003334	<i>Scm</i>	1.002	0.003	0.960	0.974
others	FBgn0004837	<i>Su(H)</i>	0.995	-0.007	0.896	0.929

None of these proteins is expressed at a significant different rate in male versus female samples using an adjusted p-value cut off of 0.05 and a FC <0.67 (down) or FC >1.5 (up).

Table S4. Sex-dependent dysregulation of MBTS genes in *l(3)mbt^{ts1}* tumors versus wild-type and in *Phf7^{ΔN2}*; *l(3)mbt^{ts1}* versus *l(3)mbt^{ts1}*.

		Up-regulated in ts1 compared to wt		Down-regulated in Phf7_ts1 compared to ts1	
100 MBTS		MALES	FEMALES	MALES	FEMALES
Germline genes*					
FBgn0000146	<i>aub</i>	yes	yes	no	no
FBgn0004581	<i>bgn</i>	yes	yes	no	no
FBgn0029754	<i>CG15930</i>	yes	yes	no	no
FBgn0052313	<i>CG32313</i>	yes	yes	no	no
FBgn0038191	<i>CG9925</i>	yes	yes	no	no
FBgn0038612	<i>cona</i>	yes	yes	no	no
FBgn0011761	<i>dhd</i>	yes	yes	no	no
FBgn0000928	<i>fs(1)Yb</i>	yes	yes	no	no
FBgn0023441	<i>fus</i>	no	no	no	no
FBgn0010097	<i>gammaTub37C</i>	yes	yes	no	no
FBgn0001120	<i>gnu</i>	yes	yes	no	no
FBgn0029977	<i>hdm</i>	yes	yes	no	no
FBgn0034098	<i>krimp</i>	yes	yes	no	no
FBgn0014342	<i>mia</i>	yes	yes	no	no
FBgn0262598	<i>mtsh</i>	yes	yes	no	no
FBgn0002962	<i>nos</i>	yes	yes	no	no
FBgn0004872	<i>piwi</i>	yes	yes	no	no
FBgn0261987	<i>Pxt</i>	yes	yes	no	no
FBgn0051755	<i>SoYb</i>	yes	yes	no	no
FBgn0003527	<i>stil</i>	yes	yes	no	no
FBgn0052088	<i>sun</i>	yes	yes	no	no
FBgn0003655	<i>swa</i>	yes	yes	no	no
FBgn0033921	<i>tej</i>	yes	yes	no	no
FBgn0037751	<i>topi</i>	yes	yes	no	no
FBgn0029752	<i>TrxT</i>	yes	yes	no	no
FBgn0283442	<i>vas</i>	yes	yes	no	no
FBgn0283545	<i>vilya</i>	yes	yes	no	no
FBgn0024177	<i>zpg</i>	yes	yes	no	no

Others

FBgn0034075	<i>Asph</i>	yes	yes	no	no
FBgn0036622	<i>Agpat4</i>	yes	yes	no	no
FBgn0031255	<i>BBS8</i>	yes	yes	no	no
FBgn0040487	<i>BobA</i>	yes	no	yes	no
FBgn0261053	<i>Cad86C</i>	no	no	no	no
FBgn0036369	<i>CG10089</i>	yes	yes	no	no
FBgn0038431	<i>CG10405</i>	yes	yes	no	no
FBgn0032520	<i>CG10859</i>	yes	yes	no	no
FBgn0033174	<i>CG11125</i>	yes	yes	no	no
FBgn0031232	<i>CG11617</i>	yes	yes	no	no
FBgn0030551	<i>CG11674</i>	yes	yes	no	no
FBgn0030721	<i>CG12698</i>	yes	yes	no	no
FBgn0037078	<i>CG12971</i>	yes	yes	no	no
FBgn0034966	<i>CG13563</i>	yes	yes	no	no
FBgn0031254	<i>CG13692</i>	yes	yes	no	no
FBgn0033374	<i>CG13741</i>	yes	yes	no	no
FBgn0031844	<i>CG13771</i>	yes	yes	no	no
FBgn0031677	<i>CG14036</i>	yes	yes	no	no
FBgn0036331	<i>CG14117</i>	yes	yes	no	no
FBgn0033274	<i>CG14757</i>	yes	yes	no	no
FBgn0038311	<i>CG14864</i>	yes	yes	no	no
FBgn0035431	<i>CG14968</i>	yes	no	yes	no
FBgn0038051	<i>CG17207</i>	yes	yes	no	no
FBgn0014931	<i>CG2678</i>	yes	no	no	yes
FBgn0050380	<i>CG30380</i>	yes	yes	no	no
FBgn0051205	<i>CG31205</i>	yes	yes	no	no
FBgn0051373	<i>CG31373</i>	yes	yes	no	no
FBgn0023525	<i>CG3191</i>	yes	yes	no	no
FBgn0051997	<i>CG31997</i>	no	yes	no	no
FBgn0052006	<i>CG32006</i>	yes	yes	no	no
FBgn0052436	<i>CG32436</i>	yes	yes	no	no
FBgn0052437	<i>CG32437</i>	yes	yes	no	no
FBgn0052440	<i>CG32440</i>	yes	yes	no	no
FBgn0052483	<i>CG32483</i>	yes	yes	no	no
FBgn0052625	<i>CG32625</i>	yes	yes	no	no
FBgn0053978	<i>CG33978</i>	yes	yes	no	no
FBgn0259140	<i>CG42255</i>	yes	no	no	no

FBgn0263256	<i>CG43394</i>	yes	no	yes	no
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FBgn0038290	<i>CG6912</i>	no	no	no	no
FBgn0038575	<i>CG7208</i>	yes	yes	no	no
FBgn0033373	<i>CG8080</i>	no	no	no	no
FBgn0037721	<i>CG9427</i>	yes	yes	no	no
FBgn0034850	<i>CG9875</i>	yes	yes	no	no
FBgn0031451	<i>CG9961</i>	yes	yes	no	no
FBgn0052582	<i>CR32582</i>	yes	yes	no	no
FBgn0010317	<i>CycJ</i>	yes	yes	no	no
FBgn0030607	<i>dob</i>	yes	yes	no	no
FBgn0039622	<i>eIF4E-6</i>	yes	yes	no	no
FBgn0000658	<i>fj</i>	yes	no	no	no
FBgn0004652	<i>fru</i>	no	no	no	no
FBgn0040323	<i>GNBP1</i>	yes	yes	no	no
FBgn0040321	<i>GNBP3</i>	no	no	no	no
FBgn0030994	<i>HP1D3csd</i>	yes	yes	no	no
FBgn0260874	<i>Ir76a</i>	yes	yes	no	no
FBgn0010482	<i>l(2)01289</i>	yes	yes	yes	no
FBgn0025578	<i>Lcp9</i>	yes	yes	yes	no
FBgn0011653	<i>mas</i>	yes	no	no	no
FBgn0052580	<i>Muc14A</i>	yes	yes	no	no
FBgn0034797	<i>nahoda</i>	no	no	no	no
FBgn0039564	<i>Nep7</i>	yes	yes	no	no
FBgn0040296	<i>Ocho</i>	yes	no	yes	no
FBgn0031829	<i>Osm6</i>	yes	yes	no	no
FBgn0034965	<i>ppk29</i>	yes	yes	no	no
FBgn0003250	<i>Rh4</i>	yes	yes	no	no
FBgn0026176	<i>SkpB</i>	yes	yes	no	no
FBgn0039251	<i>Trf4-2</i>	yes	yes	no	no
FBgn0037225	<i>TwlG</i>	yes	yes	no	no
FBgn0039896	<i>yellow-h</i>	yes	yes	no	no

Differential expression analysis of the MBTS genes.

*Germline genes as referred in (24).

wt = w^{1118} ; ts1 = $l(3)mbt^{ts1}$; Phf7_ts1 = $Phf7^{AN2}$; $l(3)mbt^{ts1}$