

Supplementary Information:

ChIP-mass spectrometry captures protein interactions and modified histones associated with dosage compensation in *Drosophila*

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Gene	Unique	Total
CG11198	71	144
CG1516	37	79
Hsc70-5	9	21
Aldh	6	9
ATPsyn	5	7
Hsp60	5	6
Hsc70-4	5	5
Ef1alpha48D	4	7
Nc73EF	4	4
EFTuM	4	4
blw	4	4
wal	3	6
sesB	3	3
Sucb	3	3
SmB	2	4
betaTub56D	2	3
Act5C	2	2
CG11963	2	2
His4	2	2
CG3902	2	2
I(1)G0156	2	2
mod	2	2
Sod2	1	3
snRNP69D	1	2
Hsc70-1	1	2
Hsp83	1	2
Scs	1	2
CG17896	1	2
scu	1	2
His2B	1	2
CG4389	1	2
CG7362	1	2
Nop60B	1	1
CG1673	1	1
His2A	1	1
CG7834	1	1
CG11876	1	1
Gapdh1	1	1
nop5	1	1
eIF-4a	1	1
Rm62	1	1
Acon	1	1
ERp60	1	1
mRpL12	1	1
mtacp1	1	1
I(2)37Cc	1	1
CG15093	1	1
Hel25E	1	1
bor	1	1
Hsp23	1	1
Roe1	1	1
CG7145	1	1
Fib	1	1

sni	1	1
Ef2b	1	1
Cyp1	1	1
CG1640	1	1
RpL31	1	1
CG1416	1	1
CG16935	1	1
CG12558	1	1
SRm160	1	1
Scsalpha	1	1

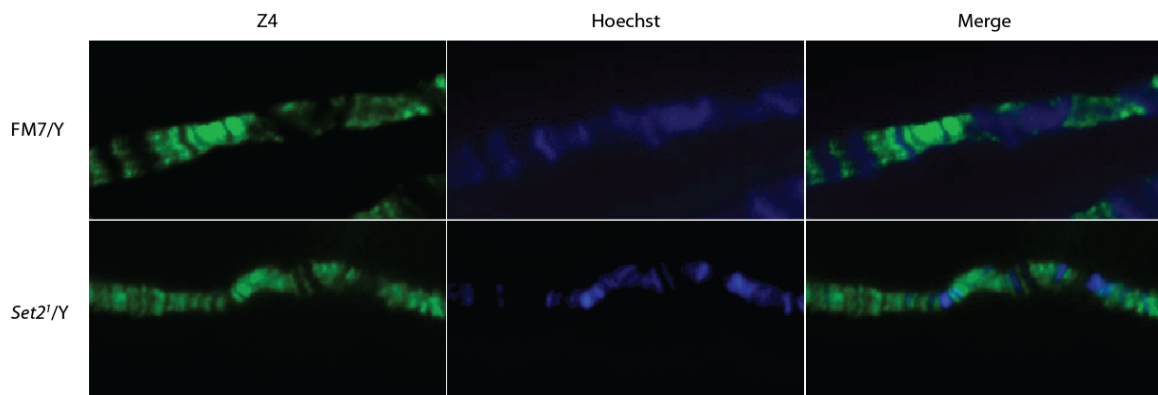
Supplementary Table 1.

List of proteins recovered with streptavidin-biotin purification of non-HTB tagged cells from one representative experiment. Unique: unique peptides; Total: total peptides.

PTM	P	Input	P/IN
Histone H3			
H3K4un	75.28%	83.02%	0.91
H3K4me1	24.63%	13.69%	1.80
H3K4me2	0.05%	2.18%	0.02
H3K4me3	0.04%	1.11%	0.03
H3K9un	45.44%	46.08%	0.99
H3K9me1	15.62%	19.05%	0.82
H3K9me2	28.22%	26.53%	1.06
H3K9me3	8.23%	6.71%	1.23
H3K9ac	2.50%	1.62%	1.54
H3K14un	80.54%	80.63%	1.00
H3K14ac	19.46%	19.37%	1.00
H3K18un	95.53%	94.77%	1.01
H3K18me1	0.03%	0.47%	0.07
H3K18ac	4.44%	4.76%	0.93
H3K23un	53.57%	57.43%	0.93
H3K23me1	0.61%	0.90%	0.68
H3K23ac	45.82%	41.67%	1.10
H3K27un	16.18%	16.56%	0.98
H3K27me1	10.53%	18.38%	0.57
H3K27me2	52.76%	39.16%	1.35
H3K27me3	20.13%	25.21%	0.80
H3K27ac	0.40%	0.69%	0.58
H3K36un	58.17%	77.38%	0.75
H3K36me1	28.05%	16.06%	1.75
H3K36me2	9.92%	4.95%	2.01
H3K36me3	3.85%	1.61%	2.39
H3K79un	50.27%	66.08%	0.76
H3K79me1	36.52%	27.21%	1.34
H3K79me2	13.21%	6.70%	1.97
Histone H4			
H4K5un	96.15%	94.13%	1.02
H4K5ac	3.85%	5.87%	0.65
H4K8un	89.14%	87.69%	1.02
H4K8ac	10.86%	12.31%	0.88
H4K12un	92.34%	94.78%	0.97
H4K12ac	7.66%	5.22%	1.47
H4K16un	68.72%	91.86%	0.75
H4K16ac	31.28%	8.14%	3.84
H4K20un	8.94%	14.40%	0.62
H4K20me1	11.87%	23.32%	0.51
H4K20me2	79.20%	62.28%	1.27

Supplementary Table 2.

Histone PTM mass spectrometry results from single-step IgG purification of MSL-TAP chromatin. Approximate percent abundance at each modified residue is shown for input (IN) and MSL3-TAP pulldown (P) experiments.



Supplementary Figure 1. *Set2*¹ mutant shows wild-type interband staining pattern when immunostained with anti Z4 antibody.

Immunostaining of larval salivary gland polytene chromosomes of *Set2*¹ mutant with an antibody to active chromatin protein Z4 (green) showed similar robust interband localization when compared to wild-type animals. Hoechst staining of DNA is shown in blue.