SUPPLEMENTARY MATERIALS
to the article by A.A. Yushkova, A.A. Ogienko, E.N. Andreyeva, A.V. Pindyurin, A.E. Letiagina, E.S. Omelina "The effects of *Non3* mutations on chromatin organization in *Drosophila melanogaster*"

Table S1. Crossover classes analyzed for meiotic recombination frequency using the strain #306

Strain #306	Number of flies	
F2 phenotype	*Non3*^{ex}	*Non3*$^{\Delta 600}$
+ + + + +	467	415
ru + + + +	228	244
+ + *Diap1 st cu*	49	52
ru + *Diap1 st cu*	1	1
ru hry + + +	0	1
ru hry Diap1 st +	0	13
ru + *Diap1 st* +	9	16
+ + + + *cu*	1	6
ru + *Diap1* + +	0	0
ru hry Diap1 st cu	349	311
+ *hry Diap1 st cu*	52	93
ru hry + *st cu*	1	0
ru hry + + *cu*	17	10
ru + *Diap1* + *cu*	2	1
+ + *Diap1* + +	0	0
+ + *Diap1 st* +	6	5
ru hry Diap1 + +	0	0
+ *hry* + + *cu*	4	5
+ *hry Diap1 st* +	2	8
ru hry Diap1 + *cu*	1	4
+ *hry* + + +	1	0
ru + + *st* +	0	2
+ + + *st cu*	0	0
+ + *Diap1* + *cu*	0	2
+ *hry* + *st cu*	0	1
Total	1,190	1,190

Table S2. Crossover classes analyzed for meiotic recombination frequency using the strain #620

BDSC Strain #620	Number of flies	
F2 phenotype	*Non3*^{ex}	*Non3*$^{\Delta 600}$
Diap1 st cp in kni p	623	548
+ + + + + +	1,161	655
+ + + + + *p*	17	21
Diap1 st cp in kni +	6	9
Diap1 + + + + *p*	1	0
+ + + + *kni p*	1	1
+ + *cp in kni p*	7	3
Diap1 st + + + *p*	1	2
Diap1 st + + + +	3	2
Diap1 st cp in + *p*	1	0
Diap1 + + + + +	1	0
+ *st cp in kni p*	2	1
+ + *cp in kni* +	1	0
Diap1 + *cp in kni p*	2	4
Diap1 + + + + *p*	0	2
+ *st* + + + +	0	1
Diap1 st cp in + +	0	1
Diap1 + *cp in kni* +	0	2
Total	1,827	1,252

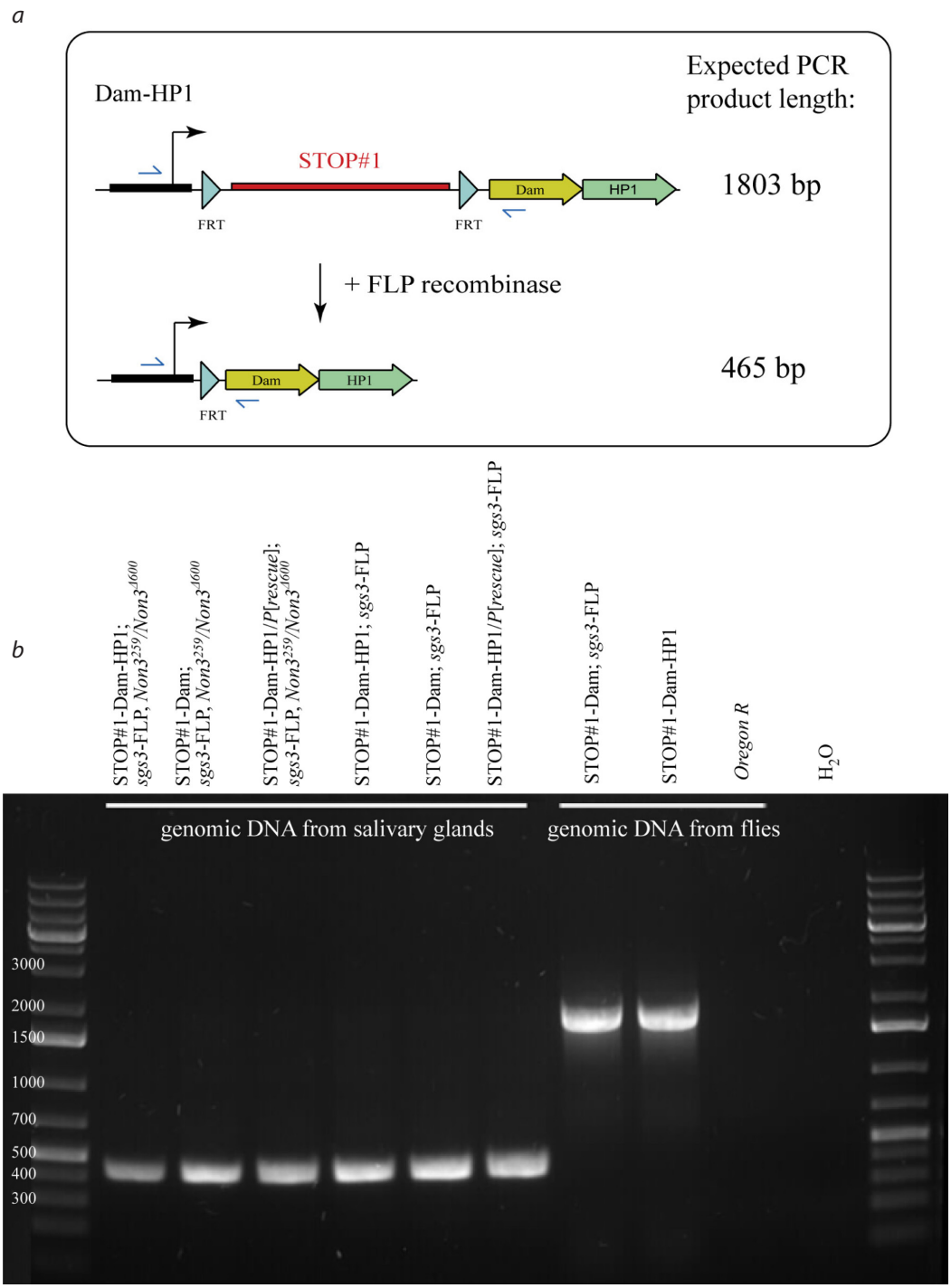

Fig. S1. The presence of the *sgs3*-FLP transgene allows to specifically remove FRT-flanked transcriptional terminator STOP#1 from Dam-encoding transgenes only in larval salivary gland cells.

a – Schematic representation of the min.hsp70P-FRT-STOP#1-FRT-Dam(-HP1) transgenes and removal of the STOP#1 cassette placed between the minimal *hsp70* promoter and Dam(-HP1) coding sequence in the presence of FLP recombinase. PCR products of different lengths are expected from the intact and FLP-recombined transgenes. *b* – PCR products obtained from genomic DNA isolated from dissected larval salivary glands and whole adult flies. The presence of the *sgs3*-FLP transgene leads to specific removal of the STOP#1 cassette in larval salivary glands but not in adult flies' tissues.

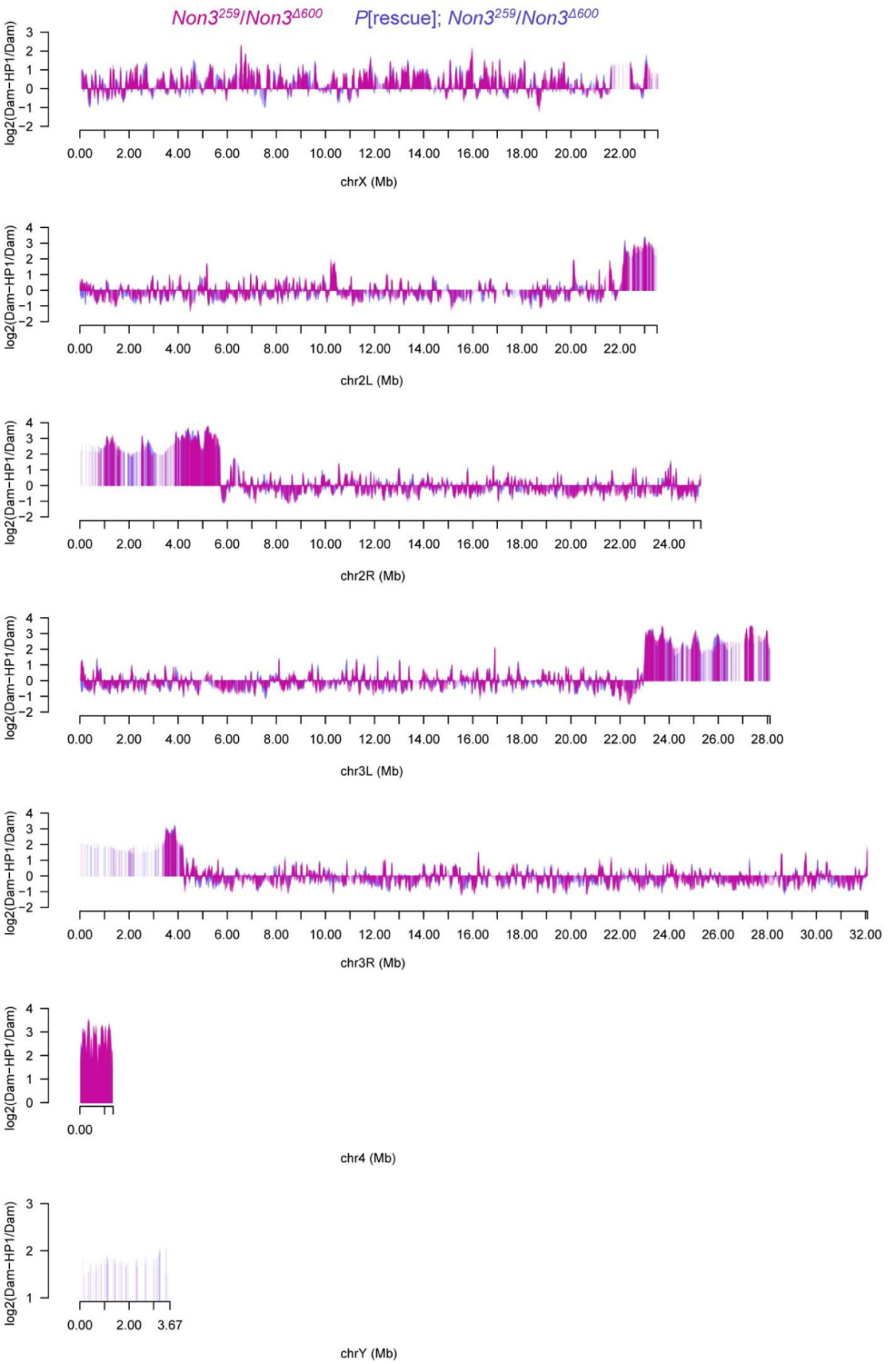

Fig. S2. Comparison of HP1 binding profiles in salivary glands of the *Non3* and *P*[*rescue*]; *Non3* mutants.

Chromosomes X, 2L, 2R, 3L, 3R, 4 and Y are shown. A running mean algorithm (a sliding window of 50 GATC fragments, one fragment per step) was applied to the HP1 binding data.

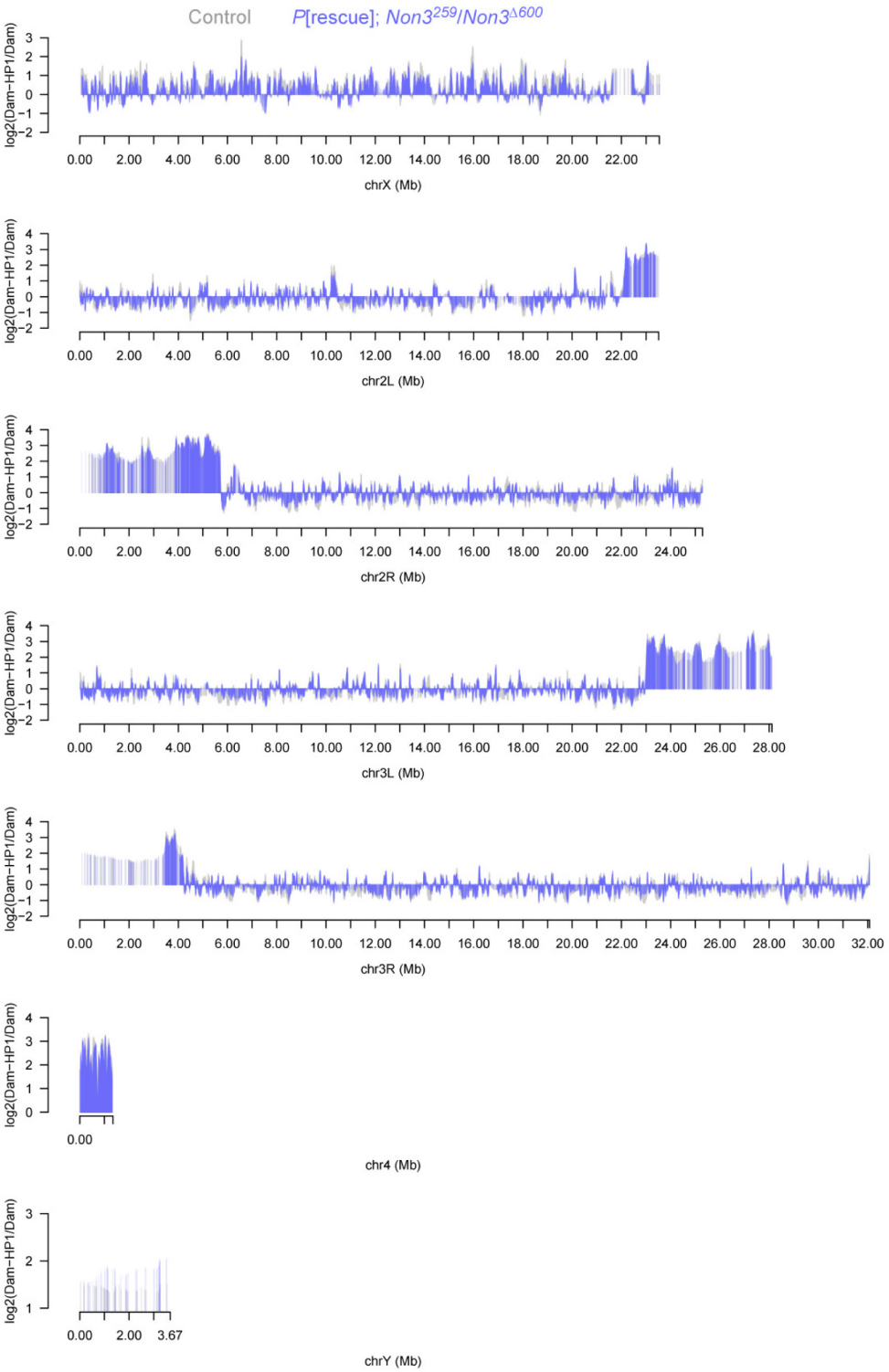

Fig. S3. Comparison of HP1 binding profiles in salivary glands of the control third instar larvae and *P*[*rescue*]; *Non3* mutants.

Chromosomes X, 2L, 2R, 3L, 3R, 4 and Y are shown. A running mean algorithm (a sliding window of 50 GATC fragments, one fragment per step) was applied to the HP1 binding data.