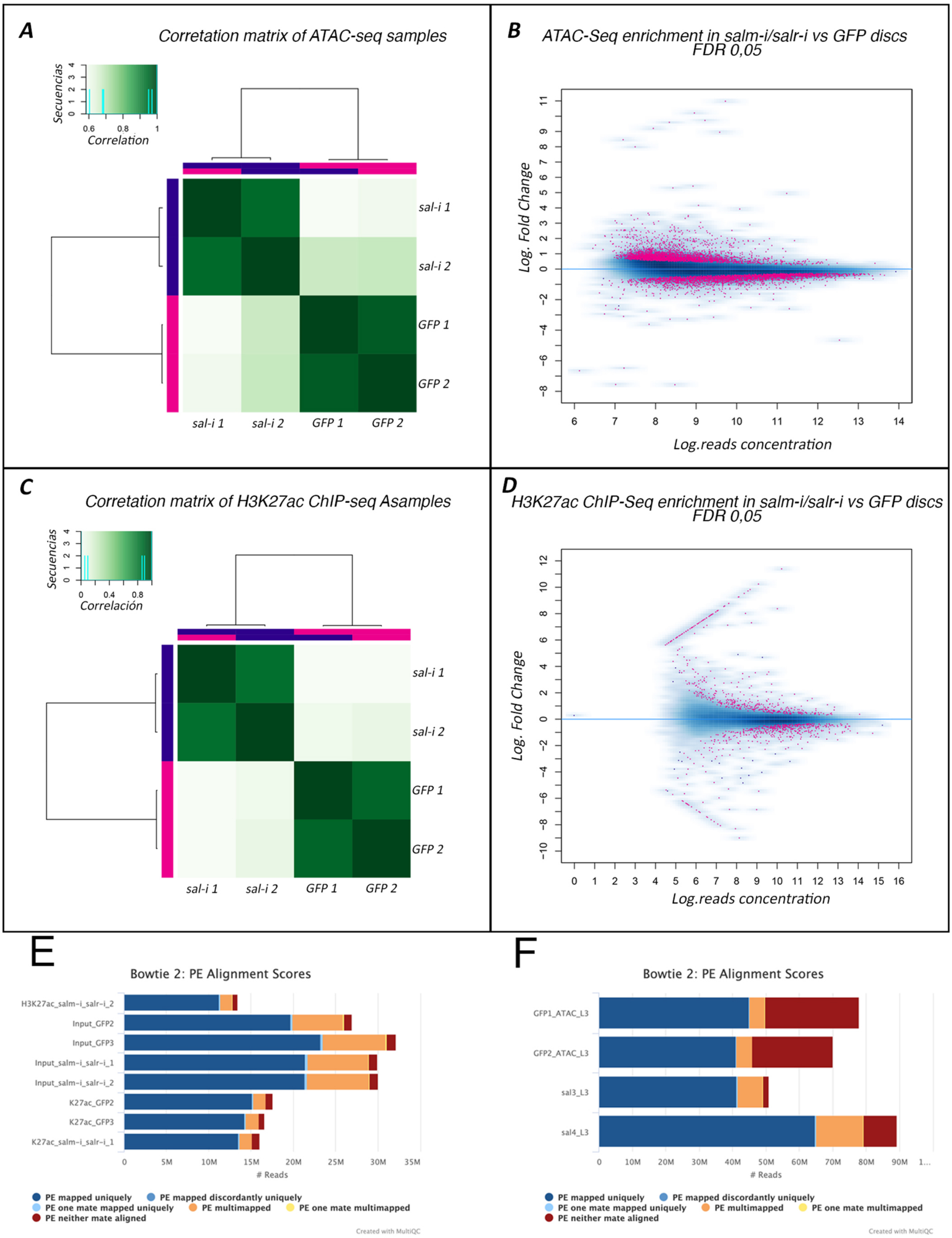
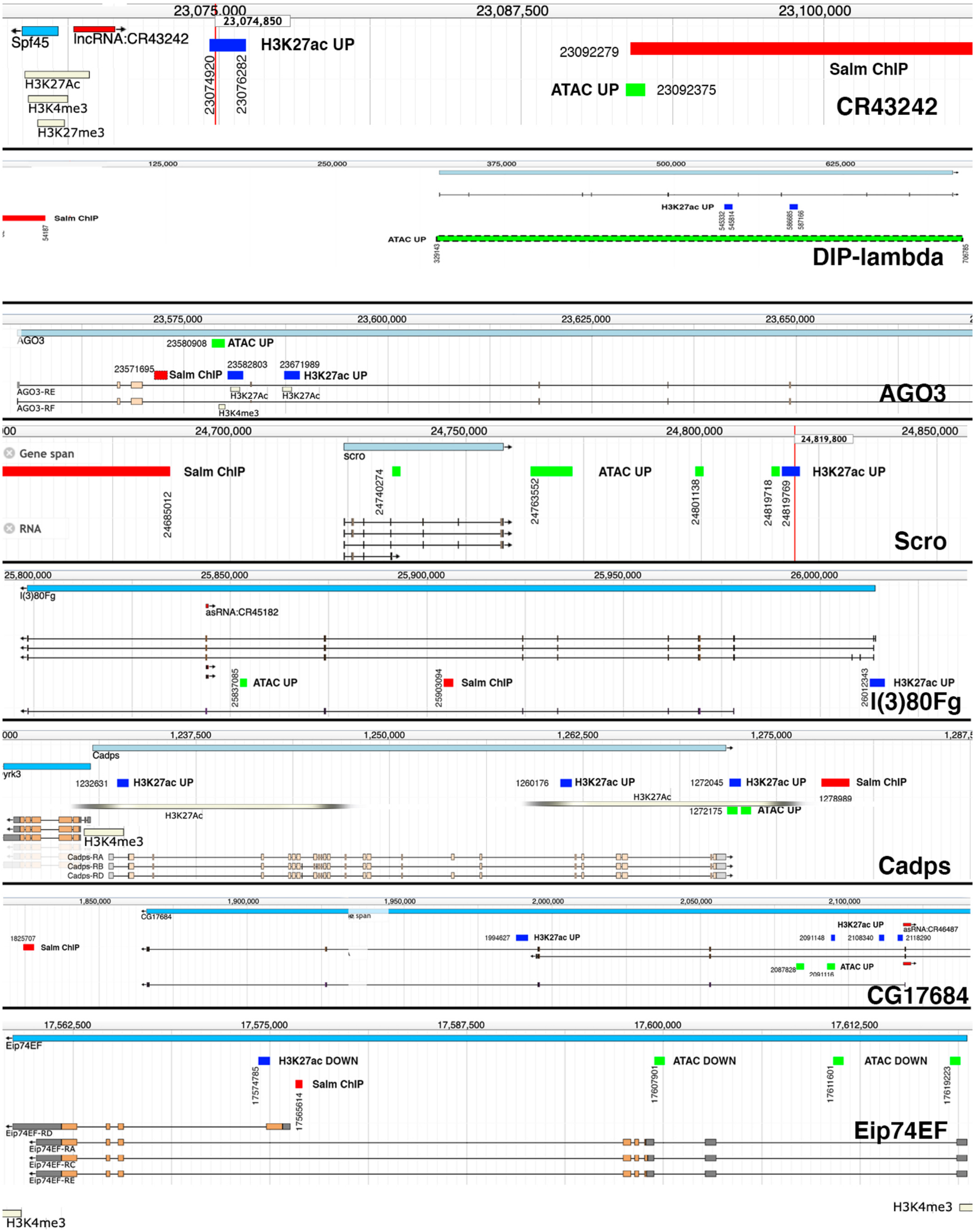


**Fig. S1.** (A, C) Correlation between replicates of ATAC-seq (A) and H3K27ac CHIP (C) in control (GFP 1 and GFP 2; genotype *sal$^{EPv}$-Gal4 UAS-GFP/+*) and *sal* mutant (sal-i 1 and sal-i 2; genotype *sal$^{EPv}$-Gal4 UAS-GFP/UAS-salm-RNAi; UAS-salr-RNAi/+*) samples. (B, D) MA graphics representing the correlation between the magnitudes log Fold Change and log number of reads in the genotype *sal$^{EPv}$-Gal4 UAS-GFP/UAS-salm-RNAi; UAS-salr-RNAi/+* compared to controls *sal$^{EPv}$-Gal4 UAS-GFP/+*. Blue and pink dots represent non- significant (blue) and significant (pink) changes. (E-F) Alignment scores for all H3K27ac seq (E) and ATAC-seq (F) experimental samples.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23,087,500
23,100,000
Spf45
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23076282
H3K27Ac
H3K4me3
H3K27me3
23092279
Salm ChIP
ATAC UP
23092375
CR43242
125,000
250,000
375,000
500,000
625,000
Salm ChIP
54187
H3K27ac UP
543332
545814
586685
587166
ATAC UP
329143
706785
DIP-lambda
23,575,000
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23,625,000
23,650,000
AGO3
23580908
ATAC UP
23571695
Salm ChIP
23582803
23671989
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AGO3-RE
AGO3-RF
H3K27Ac
H3K27Ac
H3K4me3
AGO3
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24,819,800
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Gene span
scro
Salm ChIP
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24763552
ATAC UP
24801138
24819718
24819769
H3K27ac UP
RNA
Scro
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25,900,000
25,950,000
26,000,000
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ATAC UP
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Salm ChIP
26012343
H3K27ac UP
l(3)80Fg
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1,262,500
1,275,000
1,287,5
Cadps
yrk3
1232631
H3K27ac UP
1260176
H3K27ac UP
1272045
H3K27ac UP
Salm ChIP
1278989
H3K27Ac
H3K27Ac
1272175
ATAC UP
H3K4me3
Cadps-RA
Cadps-RB
Cadps-RD
Cadps
1,850,000
1,900,000
1,950,000
2,000,000
2,050,000
2,100,000
CG17684
1825707
Salm ChIP
1994627
H3K27ac UP
H3K27ac UP
asRNA:CR46487
2091148
2108340
2118290
2087828
2091116
ATAC UP
CG17684
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17,600,000
17,612,500
Eip74EF
H3K27ac DOWN
17574785
Salm ChIP
17565614
ATAC DOWN
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ATAC DOWN
17611601
17619223
Eip74EF
Eip74EF-RD
Eip74EF-RA
Eip74EF-RC
Eip74EF-RE
H3K4me3
H3K4me3

**Fig. S2.** (A) Examples of the 8 genes associated to binding of Salm (red bars) in wild type wing imaginal discs, and to changes in ATAC (green bars) and H3K27ac binding (blue bars) comparing *sal$^{EPv}$-Gal4 UAS-GFP/+* controls and *sal$^{EPv}$-Gal4 UAS-GFP/UAS-salm-RNAi; UAS-salr-RNAi/+* wing imaginal discs. The genomic maps were obtained from the flybase genomic browser.

**Table S1. Genomic regions and genes iden-fied in gene expression analyses**

Sal 24-48 tab: all genes showing significant change in expression levels; Organista et al., 2015)

sal 24-48 lgFC tab: all genes showing significant change in expression levels and logFC > 0.5; Organista et al., 2015).

ATAC_UP tab: all genomic regions identified as over-represented in the ATAC experiments (FDR<0.001).

ATAC_UP genes: all genes associated to at least one ATAC_UP sequence.

ATAC_DOWN tab: all genomic regions identified as under-represented in the ATAC experiments (FDR<0.001).

ATAC_DOWN genes: all genes associated to at least one ATAC_DOWN sequence.

H3K27ac_UP tab: all genomic regions identified as over-represented in the H3K27ac chromatin immunoprecipitation experiments (FDR<0.05).

H3K27ac_UP genes: all genes associated to at least one H3K27ac_UP sequence.

H3K27ac-DOWN tab: all genomic regions identified as under-represented in the H3K27ac chromatin immunoprecipitation experiments (FDR<0.05).

H3K27ac-DOWN genes tab: all genes associated to at least one H3K27ac_DOWN sequence (FDR<0.05).

salm ChIP tab: all genomic regions identified in the Salm chromatin immunoprecipitati on experiments Ostalé et al., 2024).

salm ChIP genes tab: all genes associated to at least one salm ChIP sequence.

Other symbols are:

Chr: Chromosomic arm

TSS (kb): Distance in bp to the nearest transcription start site

Gen: More proximal gene

Exp: Gene expression in the third instar disc positive (Y), negative (N) or not evaluated (NC) following RNA-seq data (Flegel et al. 2016; reads from run SRR3478156) and microarray data (GeneChip™ Drosophila Genome 2.0 Array; Affymetrix) obtained from mRNA extracted from dissected third instar wing imaginal discs (Organista et al. 2015). ATAC: Genes identified in the ATAC experiments as underrepresented (DOWN) or unrepresented (UP). HP1a and H3K9me3: Overlap for the chromosomal marks HP1a and H3K9me3.

**Table S2. Overlap between sequences and peaks identified in our ATAC and H3K27ac ChIP experiments and pericentromeric heterochromatin, HP1 binding and H3K9me3 modifications.**

Peaks: number of peaks identified for each experiment

Bp: Total number of bp

Pericentromeric peaks: number of peaks located in pericentromeric heterochromatin

Bp pericentromeric: Total number of bp located in pericentromeric heterochromatin

The comparisons between different values was made by squared Chi test.

# Table S3. Overlap between genes identified in sal RNAseq and irradiation in the wing disc Data from Organista et al., 2015 and van Bergeijk et al., 2012

SAL_UP and SAL_DOWN tabs: List of genes whose expression changes in salm/salr knockdown discs compared to normal discs. We considered changes of expression detected 24 h (SAL_UP 24) and 48 hours (SAL_UP 48) after the transfer to 29ºC of controls (tub-Gal80$^{ts}$/+; sal$^{EPV}$-Gal4 UAS-GFP/UAS-GFP) and salm/salr knockdown (tub-Gal80$^{ts}$/+; sal$^{EPv}$-Gal4 UAS-GFP/UAS-salm-RNAi; UAS-salr-RNAi/+). Genes which expression increases or decreases in salm/salr knockdown discs compared to normal discs are in the tabs SAL_UP and SAL_DOWN, respectively. These data are from Organista et al., 2015.

RX_UP and RX_DOWN tabs: List of genes which expression increases (RX_UP) or decreases (RX_DOWN) in the wing disc as a consequence of DNA damage induced after irradiation (van Bergeijk et al., 2012). Columns B and C are changes 2h after irradiation and columns D and E 18 h after irradiation. Data taken from van Bergeijk et al., 2012 and provided to us by Dr Tin Tin Su.

RX P53 (van Bergeijk et al., 2012) tab: List of genes which expression changes in irradiated wild type wing disc after 2 h (RX 2) and 18 h (RX 18), and in irradiated *p53* mutant wing discs (p53 RX 2 and p53 RX 18). Expression changes are expressed in LOG(2)FC values, and significant changes ($p<0.005$, +/-1.5 LOG(2)FC) are indicated by asterisks.

## References

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