SUPPLEMENTAL FIGURE LEGEND
Fig. S1 GAF depletion is as efficient as reported and reduced the focal contact between promoter of hid and an intergenic region, related to Fig. 1. sfGFP signal of *sfGFP-GAF(N)* (A) and *GAF*^{deGradFP} (B); (C)Quantification of the signal for *sfGFP-GAF(N)* (n=12) and *GAF*^{deGradFP} (n=13); (D) The focal contact between promoter of *hid* and a distant 5' intergenic region is lost comparing GAF depletion embryos to the control embryos. The scale bar in B is 50µm. Boxplot in C are represented as mean ± SD.

Fig. S2 Insulation is changed at altered toperon anchors and the protein profile at different anchors are different, related to Fig. 2 and Fig. 3. Insulation score around anchor center of changed or unchanged toperon anchors (A) and toperon or non-toperon anchors (B); Protein binding profile around contact anchors different types of contacts (C) and changed or unchanged anchors (D).

Fig. S3. Cooperative binding at the tethering elements is lost in ΔPOZ at WT CUT&Tag peaks of Halo-GAF in 3rd instar larval wing discs, related to Fig. 3. (A) Histogram of number of GAGAG elements in CUT&Tag peaks. (B) Violin plots of normalized read counts at *WT* peaks, plotted by the number of non-overlapping GAGAG elements between the start and end coordinates of each peak identified with HOMER (left panel of A). Red dashed lines mark the median read counts of peaks containing 1 or ≥7 GAGAG elements. (C) log10 values of median read counts in B show correlation of GAF enrichment and number of GAGAG elements, with *ΔPOZ* showing slower increase of enrichment over number of GAGAG elements indicated by a smaller slope of linear regression. (D) Mean GAF CUT&Tag enrichment for all genes ±1kb centered around transcription start sites (TSS). Example Micro-C maps of decreased contacts with GAF CUT&Tag tracks at smal and Ddr (E) and tsh and tio (F).

Fig. S4 The loss of ΔPOZ proteins at the loop anchors, the changes of loops and the expression level in ΔPOZ mutants, related to Fig. 3 and Fig.4. Linear regression of fold change of GAF protein binding and fold change of loop strength in *ΔPOZ* (A) and *ΔQ* (B). (C) Volcano plot for the differentially expressed genes (DEGs) in *ΔPOZ* m utants. (D) Profile of the WT or ΔPOZ GAF near the DEGs transcription start sites. (E) Fraction of changed or unchanged non-toperon c ontacts in *ΔPOZ* m utant. (F) The numbers of non-overlapping GAGAG elements in changed and unchanged anchors have no significant difference (p = 0.13, two sided, unpaired t test). Note: the sizes of the anchors are designated to be 3201bp, which are most of the time wilder than GAF enriched regions (G) Average distances of neighboring non-overlapping GAGAG elements are significantly smaller in changed than in unchanged anchors (p = 0.017, two sided, unpaired t test).

Fig. S1 GAF depletion is as efficient as reported and reduced the focal contact between promoter of *hid* and an intergenic region, related to Fig. 1.
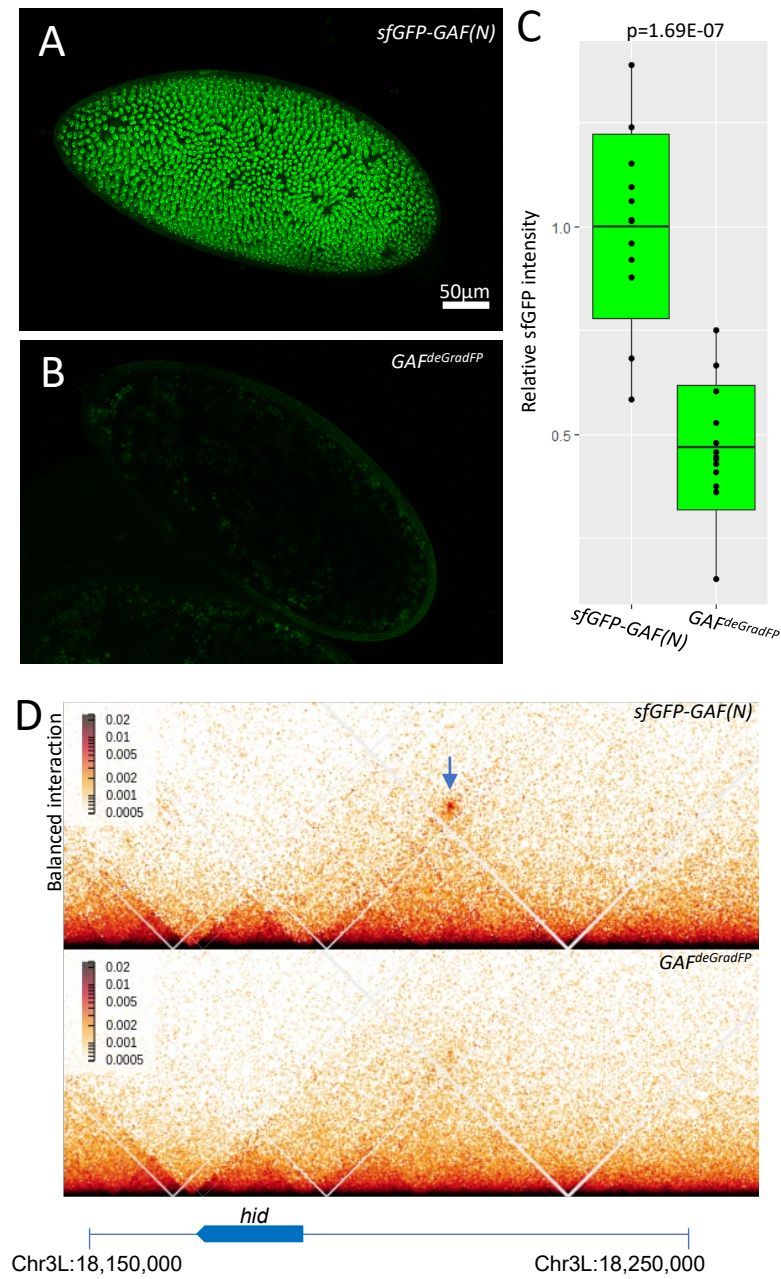
Fig. S2 Insulation is changed at altered toperon anchors and the protein profile at different anchors are different, related to Fig. 2 and Fig. 3.
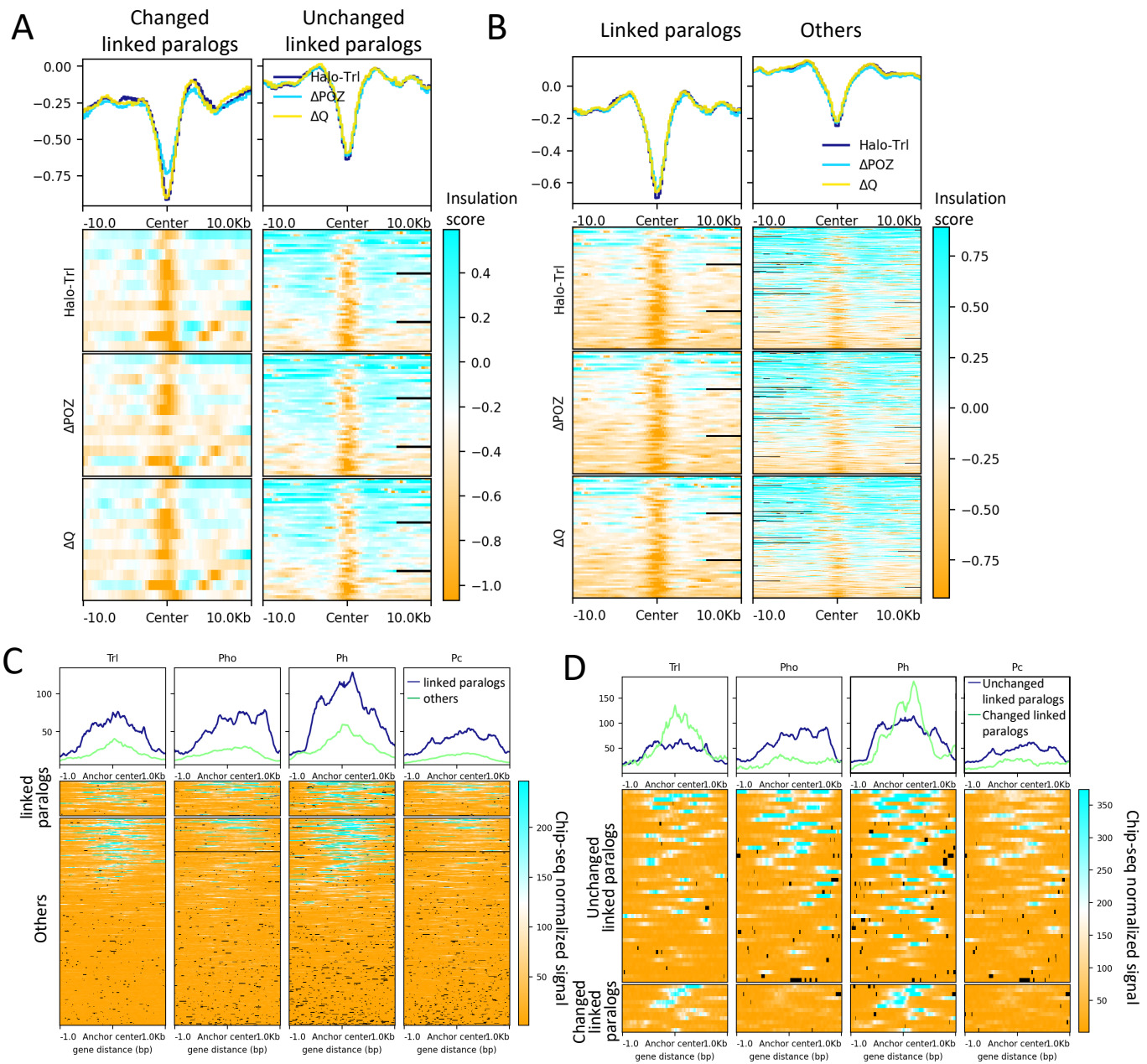
Fig. S3. Cooperative binding at the tethering elements is lost in *ΔPOZ* at *WT* CUT&Tag peaks of Halo-GAF in 3rd instar larval wing discs, related to Fig. 3.
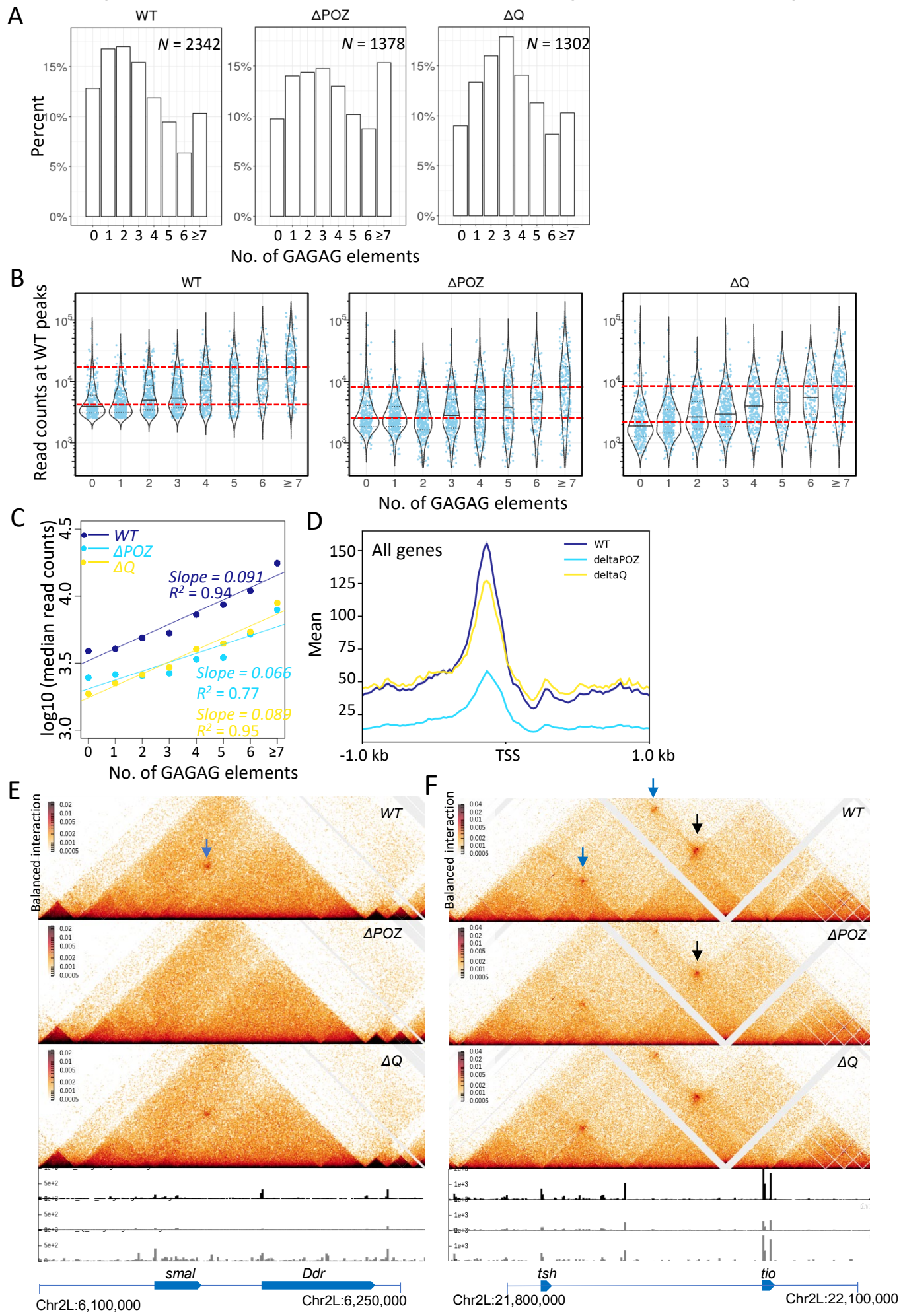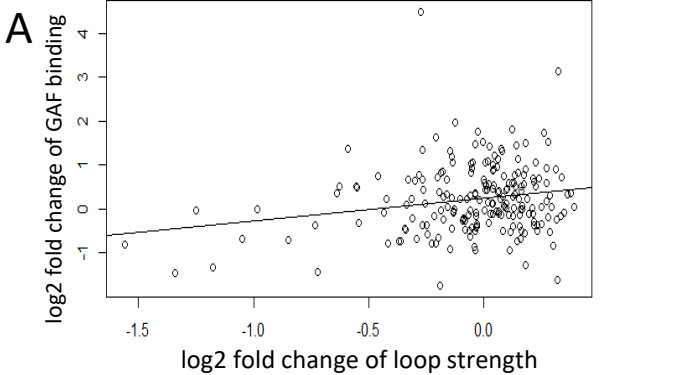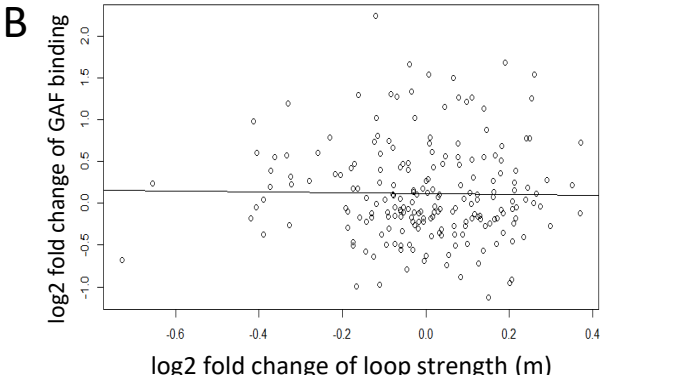
Fig. S4 The loss of ΔPOZ proteins at the loop anchors, the changes of loops and the expression level in *ΔPOZ* mutants, related to Fig. 3 and Fig.4.

A

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
Intercept	0.24205	0.05371	4.507	1.10E-05
log2 fold change of loop strength	0.52363	0.17291	3.028	0.00277

Multiple R-squared: 0.04262, Adjusted R-squared: 0.03797

F-statistic: 9.171 on 1 and 206 DF
p-value: 0.002774

B

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
Intercept	0.11736	0.03946	2.974	0.00329
log2 fold change of loop strength	-0.05613	0.22235	-0252	0.80096

Multiple R-squared: 0.0003092, Adjusted R-squared: -0.04544

F-statistic: 0.06372 on 1 and 206 DF
p-value: 0.801

C

D

E

F

G