SUPPLEMENTAL INFORMATION

SUPPLEMENTAL DATA

SUPPLEMENTAL FIGURES

Supplementary Figure S1 Oh et al

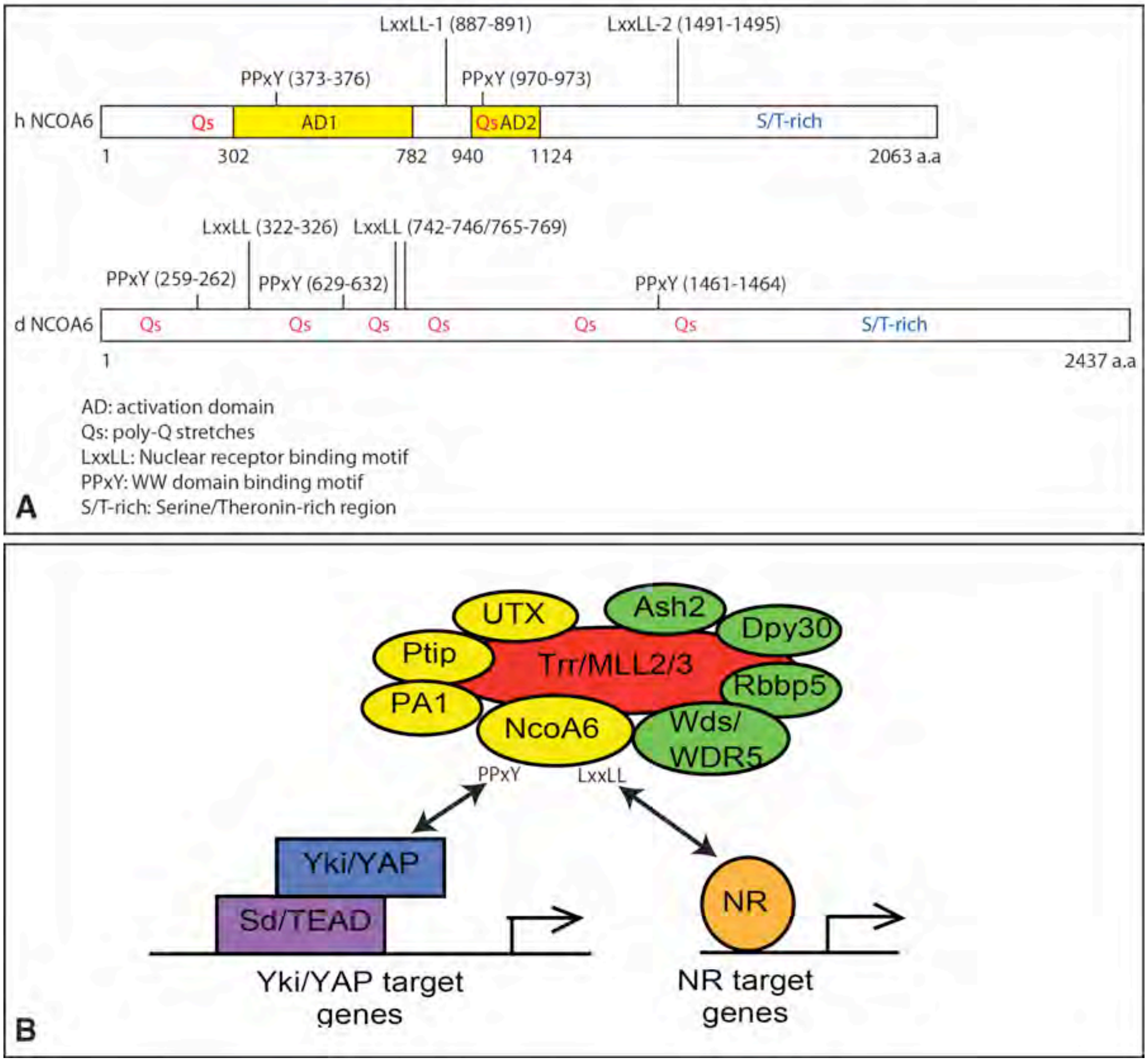

Figure S1, related to Fig. 1 A) Linear schematics of human and *Drosophila* NcoA6, depicting location of key structural motifs. The diagram for hNCOA6 is adapted and modified from (Mahajan and Samuels, 2008). B) Schematic showing subunits of the Trr HMT complex, which can interact either with YAP through PPxY motifs, or with nuclear hormone receptors (NR) through LxxLL motifs.

Supplementary Figure S2 Oh et al

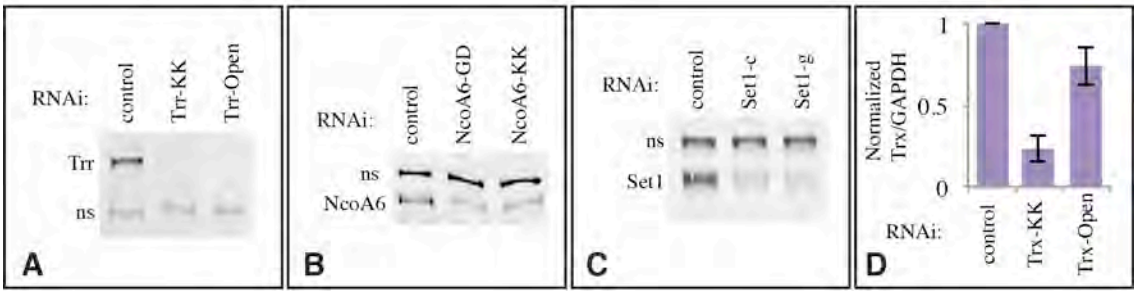

Figure S2, related to Figure 2. Western blots on lysates of S2 cells to show effectiveness of RNAi constructs. A) Trr, B) NcoA6, C) Set1. Each of these antibodies also detected a non-specific band (ns) that serves as a loading control.

Supplementary Figure S3 Oh et al

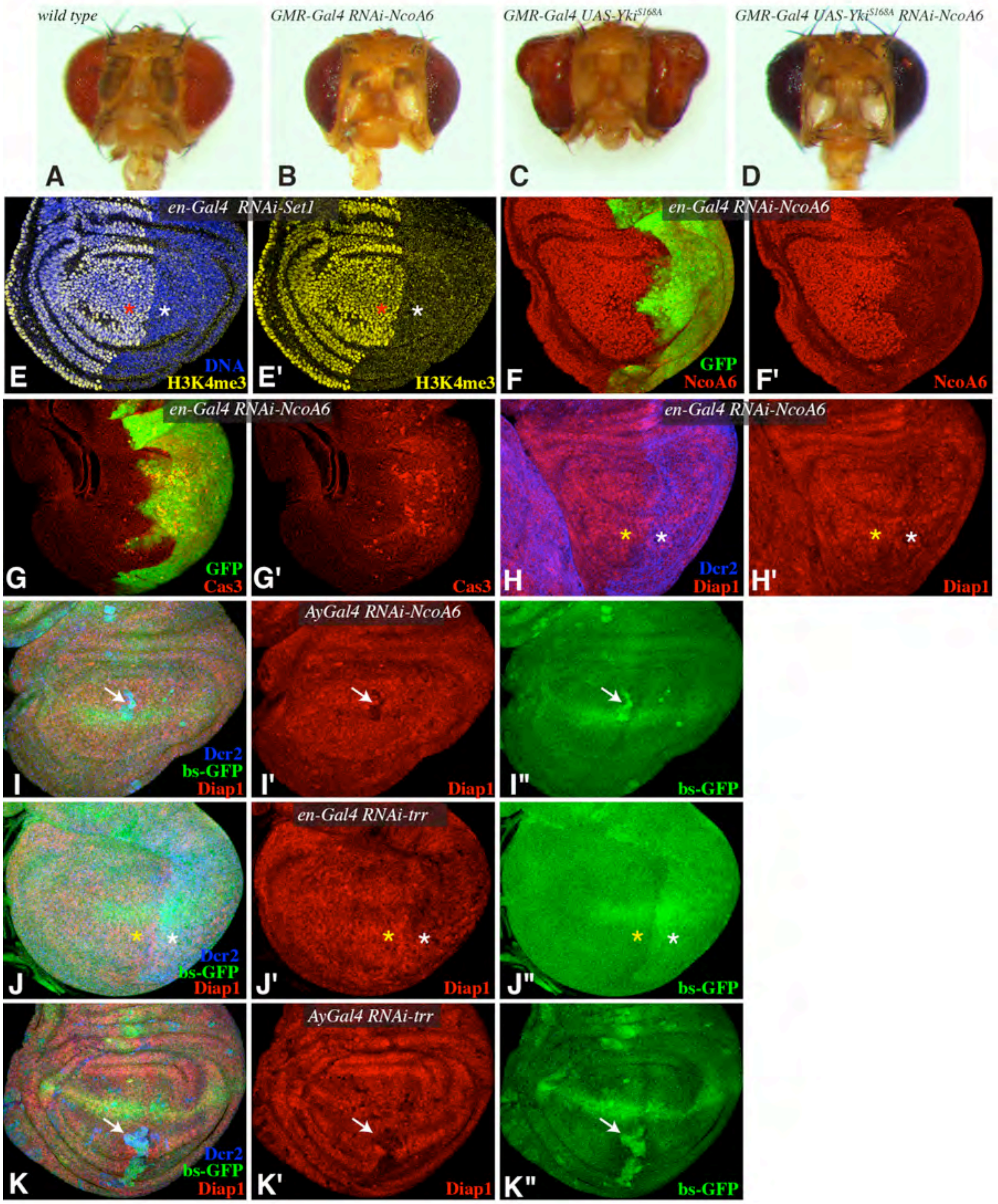

Figure S3, related to Figure 3. Characterization of the Influence of Trr HMT complex on Growth, Apoptosis, and Gene Expression. (A-D) Adult eyes from (A) *GMR-Gal4;UAS-Dcr2* (control), (B) *GMR-Gal4; UAS-RNAi-NcoA6 [*TRiP.HMS00664; *Bloomington 34964]UAS-Dcr2,* (C) *GMR-Gal4; UAS-YkiS168A:GFP*, (D) *GMR-*

*Gal4; UAS-YkiS168A:GFP; UAS-RNAi-NcoA6 [*TRiP.HMS00664; *Bloomington 34964].* (E-K) Projections through five confocal sections of wing discs; panels marked by prime symbols show separated channels. RED/Yellow asterisks identify regions with normal gene expression, and white asterisks identify regions with expression of RNAi lines and altered target gene expression. In I,K arrows point to examples of clones with altered gene expression. (E) *en-Gal4 UAS-RNAi-Set1 [*TRiP.HMS00581; *Bloomington 33704]* showing H3K4Me3 staining (yellow), in which anterior region is marked by red asterisks and posterior region is marked by white asterisks. (F-H) *en-Gal4, UAS-GFP; UAS-Dcr2* with *UAS-RNAi-NcoA6 [*TRiP.HMS00664; Bloomington 34964*]* showing expression of NcoA6 (red in F) and cleaved Caspase (red in G), in which posterior cells were marked by GFP (green). (H) *en-Gal4; UAS-Dcr2* with *UAS-RNAi-NcoA6 [vdrc36480]* showing expression of Diap1 (red) with posterior cells marked by Dcr2 (blue). (I and K) *F*lip-out clones with *ayGal4* expressing (I) *UAS-Dcr2, UAS-RNAi-NcoA6 [*TRiP.HMS00664; Bloomington 34964*] and (K) UAS-Dcr2, UAS-RNAi-trr[TRiP.JF03242; Bloomington 29563]* showing the expression of Diap1 (red) and bantam sensor-GFP (green), in which the clones are marked by Dcr2 (blue). Arrows point to examples of clones with altered gene expression. (J) *en-Gal4, bs-GFP; UAS-Dcr2* with *UAS-RNAi-trr[*TRiP.HMS01019*; Bloomington 36916]* showing expression of *Diap1* (red) with posterior cells marked by Dcr2 (blue).

Supplementary Figure S4 Oh et al

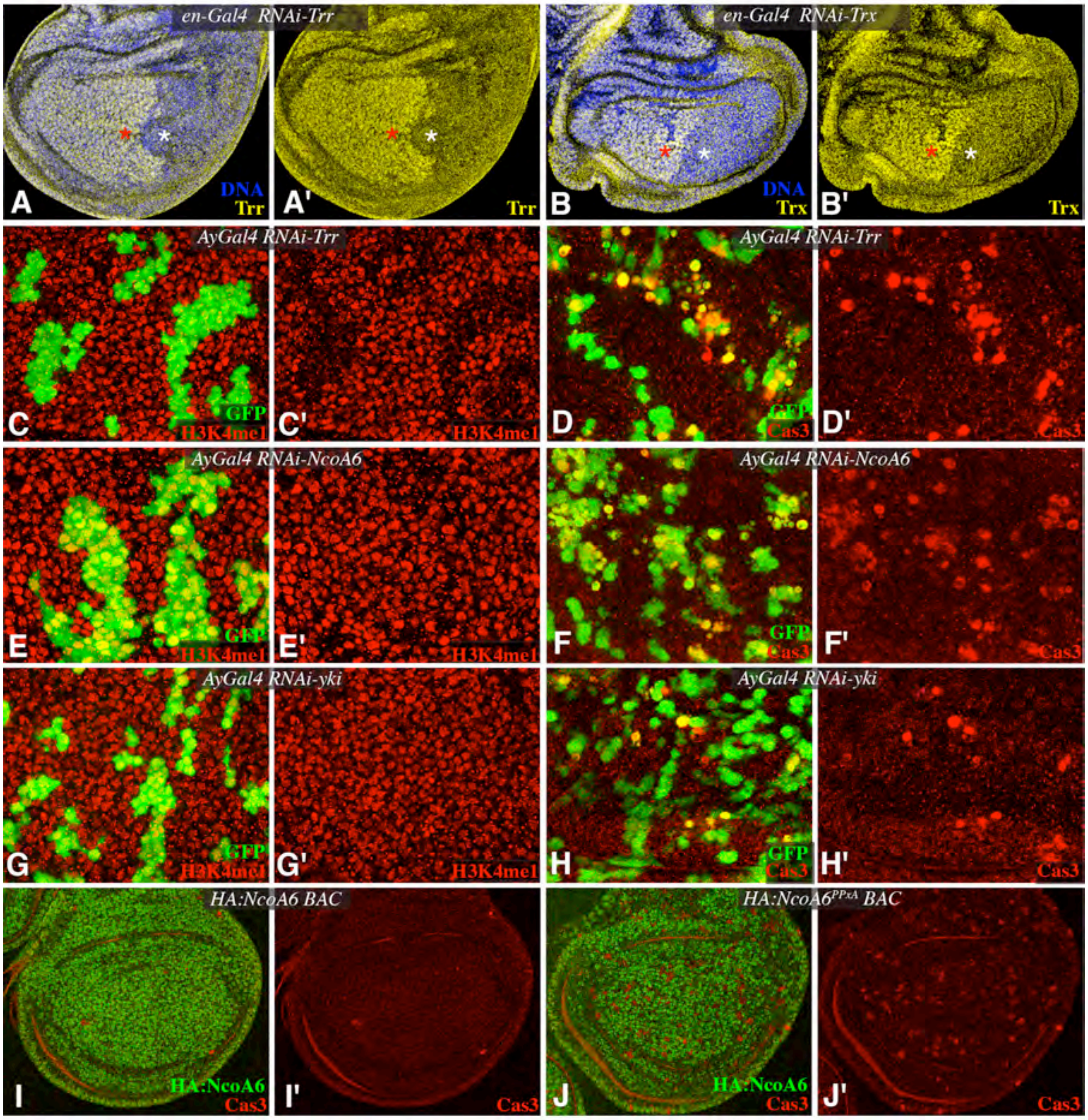

Figure S4, related to Figure 4. Additional Characterization of the Influence of Trr HMT complex on Apoptosis, and H3K4ME1.

(A) *en-Gal4 UAS-RNAi-Trr* showing Trr staining (yellow), in which anterior region is marked by red asterisks and posterior region is marked by white asterisks. (B) *en-Gal4 UAS-RNAi-trx [*TRiP.JF01557*; Bloomington 31092]* showing Trx staining (yellow), in which anterior region is marked by red asterisks and posterior region is marked by white asterisks. C-H) Clones of cells (marked by GFP, green) expressing, under actin-Gal4 (AyGal4) control C,D) *UAS-RNAi-Trr* E,F) *UAS-RNAi-NcoA6* G,H) *UAS-RNAi-yki* and stained for C,E,G) anti-H3K4me1 or D,F,H) anti-cleaved caspase3. I,J) Flies homozygous for an insertion of BAC CH322-05H20, encoding HA-tagged NcoA6 wild-type (I) or PPxA mutant (J), stained for expression of HA (green) and cleaved caspase 3 (red).

Supplementary Figure S5 Oh et al

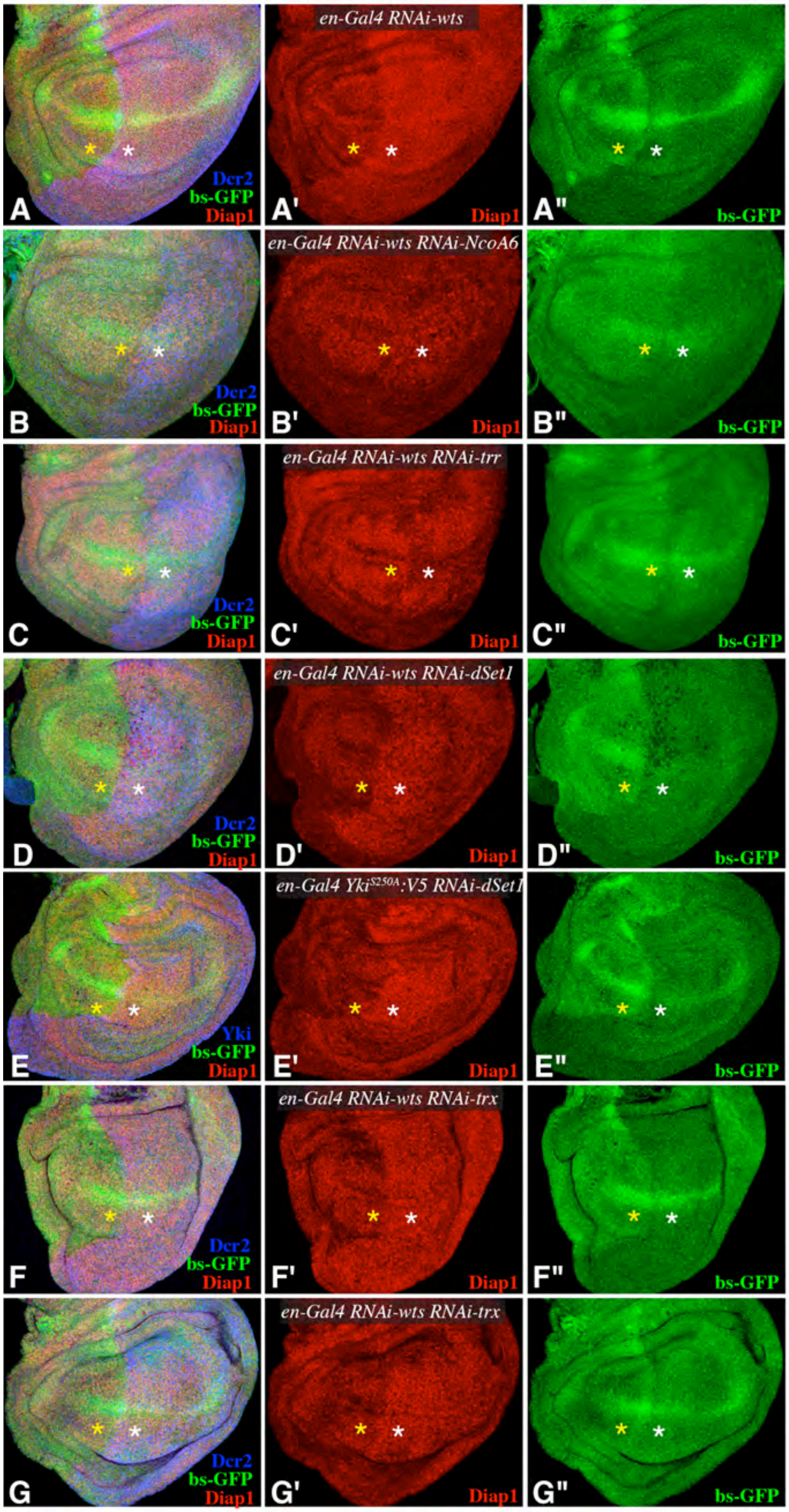

Figure S5, related to Figure 5. Trr HMT complex, not Set1 and Trx complex, is required for Yki activity. (A-G) Projections through five confocal sections of wing discs; panels marked by prime symbols show separated channels. Yellow asterisks identify regions with normal gene expression, and white asterisks identify regions with expression of RNAi lines and altered target gene expression. (A–G) *en-Gal4 bs-GFP; UAS-Dcr2* and with (A) *UAS-RNAi-Wts* (control) (B) *UAS-RNAi-Wts, UAS-RNAi-NcoA6* [TRiP.HMS00664; Bloomington 34964], (C) *UAS-RNAi-Wts, UAS-RNAi-trr* [TRiP.HMS01019*; Bloomington 36916],* (D) *UAS-RNAi-Wts, UAS-RNAi-Set1* [TRiP.HMS00581; *Bloomington 33704]*, (E) *UAS-Yki:V5*^{S250A} *UAS-RNAi-Set1* [TRiP.HMS00581; *Bloomington 33704], (F) UAS-RNAi-Wts, UAS-RNAi-trx* [TRiP.HMS00580; *Bloomington 33703], (G) UAS-RNAi-Wts, UAS-RNAi-trx* [TRiP.JF01557; *Bloomington 31092]* showing expression of Diap1 (red) and bs-GFP (green) and with posterior cells marked by Dcr2 (blue in A-D and F-G) or Yki (blue in E).

SUPPLEMENTAL Table

	Peaks	Peaks overlapping K4me1	Fraction overlap
Yki, no K4me3	1921	1534	0.8
Yki, +K4me3	2069	806	0.39
Yki, Total	3990	2340	0.59

Supplementary Table S1, related to Figure 1. Overlap of Yki-bound chromatin with H3K4me1.