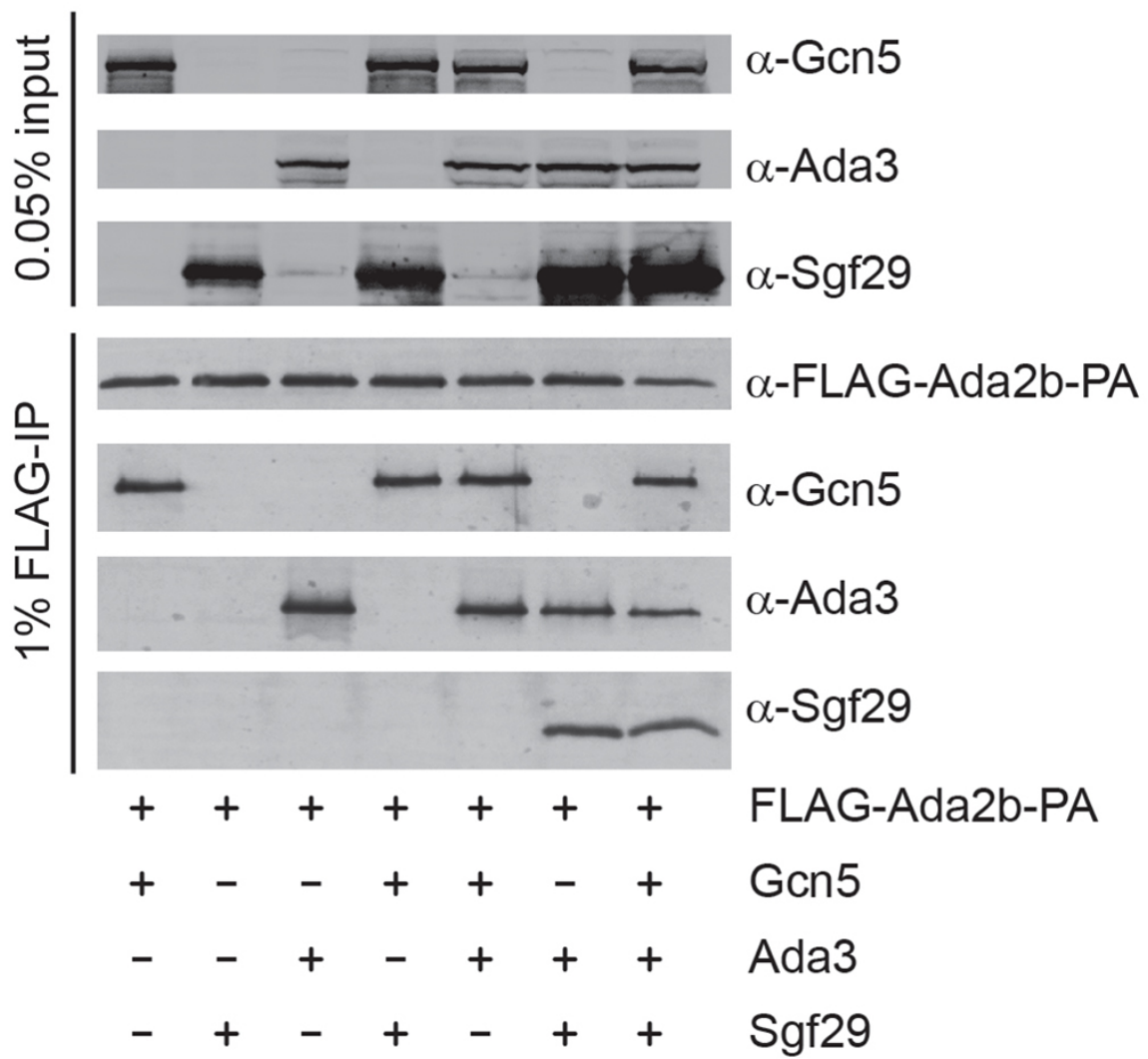
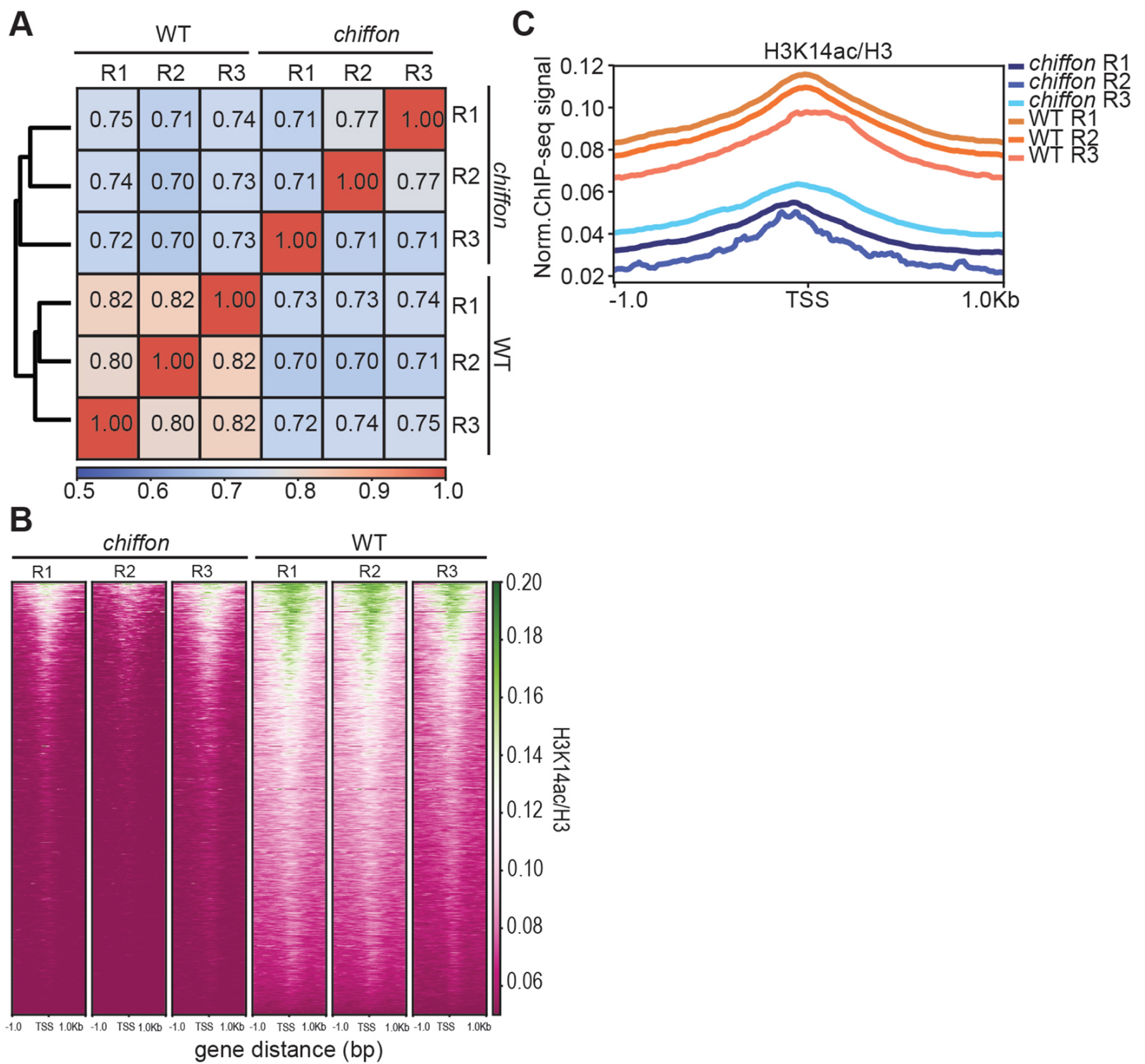


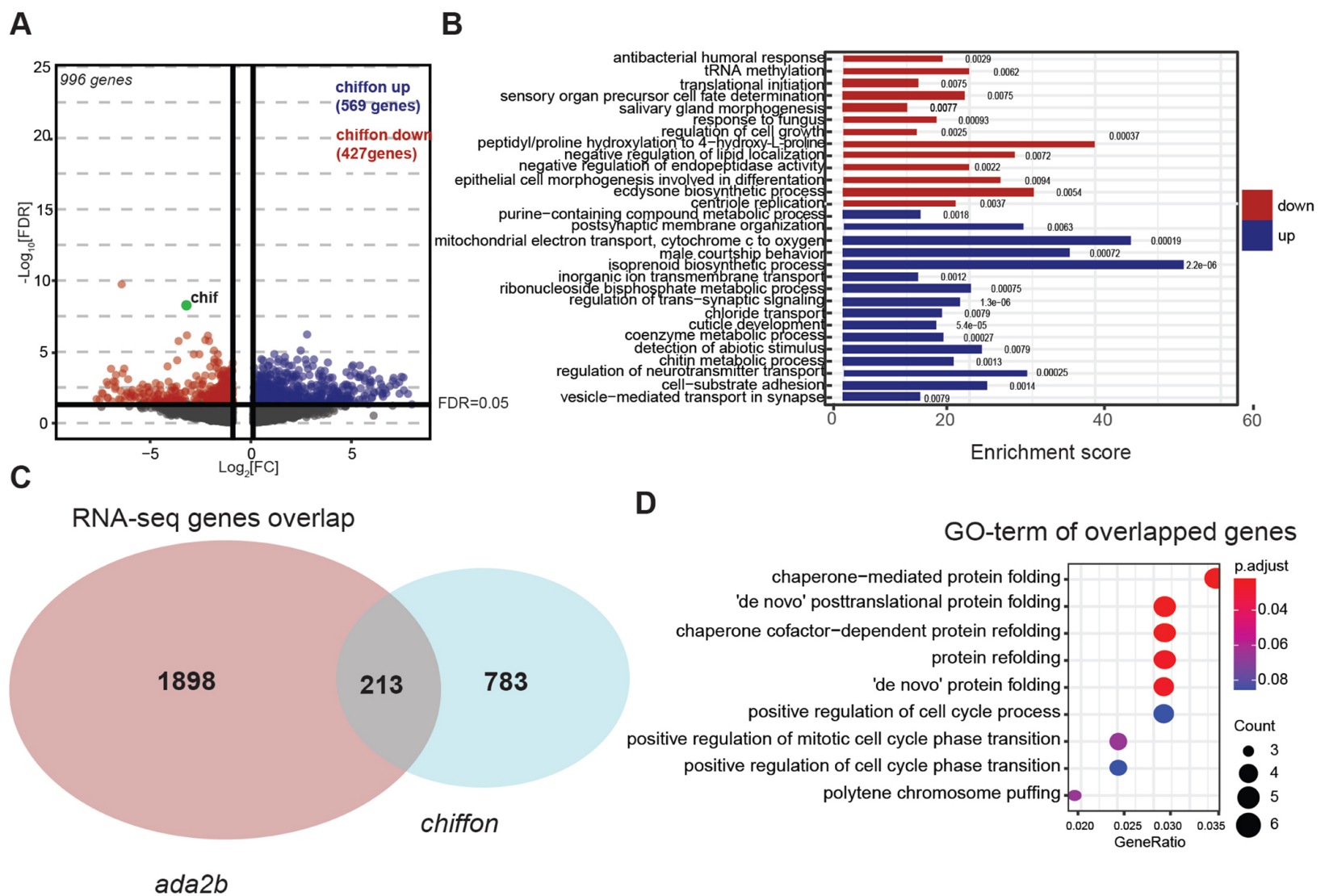
**Fig. S1. Chiffon is required for H3K14ac in embryos to a greater extent than Ada2b.** (A) Stage 10 – 13 *ada2b* embryos were examined for DAPI and H3K14ac. GFP-positive embryos are *ada2b* null. Scale bars: 20  $\mu$ m. (B) Stage 11 - 13 *chiffon* embryos were examined for DAPI and H3K14ac. GFP-positive embryos are *chiffon* null. Scale bars: 20  $\mu$ m. (C) Box plots showing relative H3K14ac levels in GFP versus non-GFP (heterozygote siblings) embryos. 5 independent embryos were quantified. *p*-value (\*\*\*, *p* < 0.0001) for the indicated comparison was determined by t-test. (D) Stage 10 – 13 *chiffon* embryos were examined for DAPI and H3K18ac. GFP-positive embryos are *chiffon* null. Scale bars: 20  $\mu$ m. (E) Box plots showing relative H3K18ac levels in GFP versus non-GFP (heterozygote siblings) embryos. 5 independent embryos were quantified. *p*-value (\*\*, *p* < 0.0016) for the indicated comparison was determined by t-test.



**Fig. S2. Ada2b-PA is necessary for formation of the Gcn5 core HAT module.** (A) Gcn5, Ada3, Sgf29, and Ada2b-PA (N-terminal FLAG tag) were expressed in Baculovirus-infected Sf21 cells, and cell lysates were mixed in the indicated pairwise combinations, and subjected to anti-FLAG affinity chromatography. The resulting immunopurified complexes were eluted, and assessed for presence of the indicated proteins by western blotting analysis.

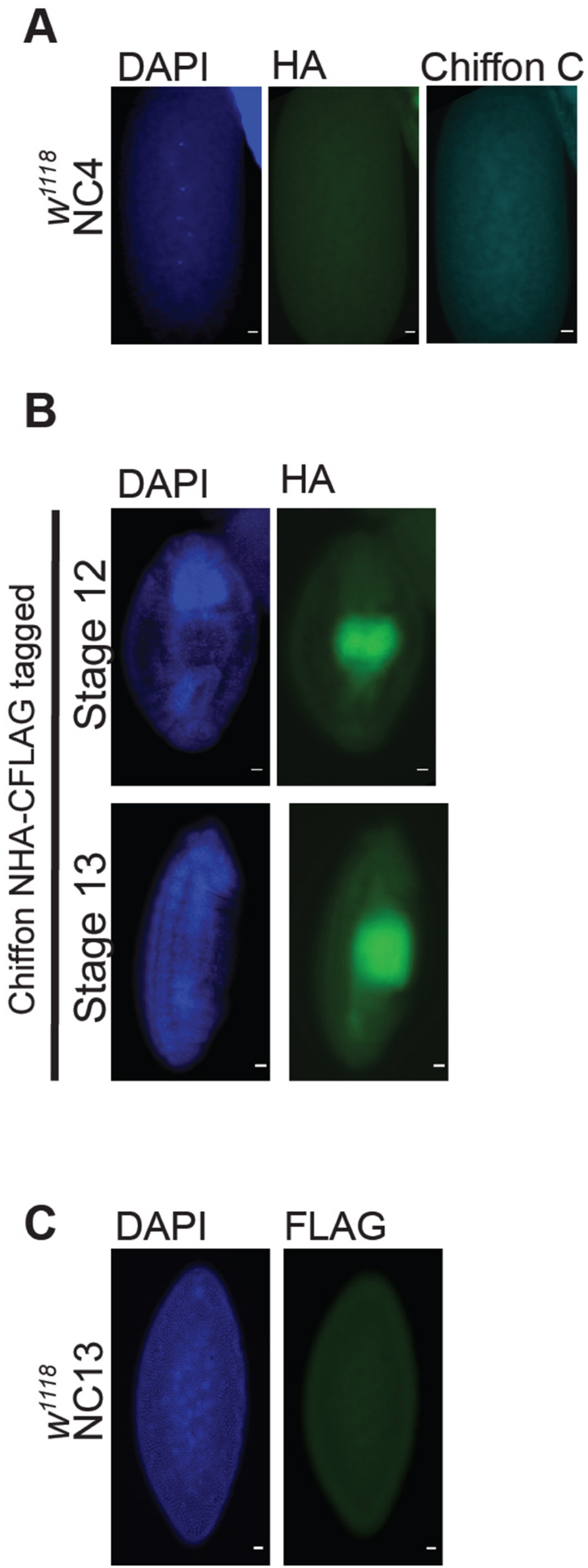


**Fig. S3. CHAT is required for global H3K14ac levels in embryos.** (A) Spearman correlation heatmap of H3K14ac ChIP-seq data comparing *chiffon* and WT (*chiffon* + FL) samples. (B) Heatmaps showing RRPm-normalized H3K14ac ChIP-seq signal around the TSS of protein-coding genes comparing *chiffon* and WT. (C) Metaplot of RRPm-normalized H3K14ac ChIP-seq signal around the transcription start site (TSS) averaged for all protein-coding genes in *chiffon* and WT samples for each replicate.



**Fig. S4. Chiffon is necessary for expression of developmental genes.** (A) Volcano plot showing the fold change of differential expressed genes of CHAT regulated genes plotted as  $\log_2(\text{fold change in counts per million reads, CPM})$  for each gene relative to its p-value ( $-\log_{10}[\text{FDR}]$ ). The dashed line shows the statistical significance cut-off ( $\text{FDR} < 0.05$ ) used for DEG analysis. (B) Over-represented GO terms ( $p < 0.01$ , Fisher's exact test) were identified for 427 downregulated or 569 upregulated genes relative to all 9765 expressed genes using TopGO. (C) Venn diagram indicating the overlapping genes detected in the *chiffon* and *ada2b* RNA-seq analysis. (D) GO terms analysis on *chiffon* and *ada2b* commonly regulated genes.





**Fig. S5. Specificity of the HA and FLAG antibodies for embryo immunostaining.** (A) Untagged wild-type embryos ( $w^{1118}$ ) at NC4 immunostained for DAPI, HA, and Chiffon C-terminal antibody showing lack of background signal under the conditions used, and no expression of Chiffon-B in early embryos. Identical immunostaining and imaging conditions were used for all other HA immunostaining experiments. (B) Epitope-tagged Chiffon-FL stage 12 and 13 embryos were examined for DAPI and HA. Scale bars: 20  $\mu\text{m}$ . The green signal represents auto-fluorescence from the gut tissue because we did not detect any HA (Chiffon-A) signal in this developmental stage. (C) Untagged wild-type embryo ( $w^{1118}$ ) at NC13 immunostained for DAPI and FLAG showing lack of background signal under the conditions used.

**Table S1.** Summary of DEGs in *ada2b* RNA-seq.

[Click here to download Table S1](#)

**Table S2.** Summary of DEGs in *chiffon* RNA-seq.

[Click here to download Table S2](#)

#### SUPPLEMENTAL REFERENCES FOR TABLE S2

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Torres-Zelada EF, Stephenson RE, Alpsoy A, Anderson BD, Swanson SK, Florens L, Dykhuizen EC, Washburn MP, Weake VM. 2019. The *Drosophila* Dbf4 ortholog Chiffon forms a complex with Gcn5 that is necessary for histone acetylation and viability. *J Cell Sci* **132**: jcs214072.

Weake VM, Dyer JO, Seidel C, Box A, Swanson SK, Peak A, Florens L, Washburn MP, Abmayr SM, Workman JL. 2011. Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. *Genes Dev* **25**: 1499–1509.

**Table S3.** Spike-in factors for ChIP-seq analysis. Spike-in factors for each ChIP-seq sample were calculated following the method described in (Orlando et al. 2014).

[Click here to download Table S3](#)

**Table S4. Summary of *Drosophila* stocks used in this study.** Genotypes and sources of stocks including original description of any transgenes (*ada2b*, *chiffon*) are indicated.

Fly Stock	Description	Genotype	Source/Reference
<i>W<sup>1118</sup></i>	Control untagged stock for immunostaining and germline clones	<i>W<sup>1118</sup></i>	BDSC 3605
<i>chiffon<sup>DsRed</sup>, actin-Gal4</i>	<i>chiffon</i> null allele on chromosome 2 with actin-Gal4 for GFP sorting of <i>chiffon</i> mutant embryos	<i>P{w[+mC]=Act5C-GAL4}25FO1, chiff<sup>DsRed-attP</sup>/CyO</i>	This study
<i>chiffon<sup>DsRed</sup>, actin-Gal4; chiffonFL</i>	<i>chiffon</i> null allele on chromosome 2 with actin-Gal4 plus a transgene expressing full length (1 – 1695aa) for GFP sorting.	<i>yw; P{w[+mC]=Act5C-GAL4}25FO1, chiff<sup>DsRed-attP</sup>/CyO; P{w+mC =ChiffonFL}-NHACFLAG_ chiff}attP2</i>	This study; Chiffon transgenes described in (Torres-Zelada et al. 2019)
<i>chiffon<sup>DsRed</sup>, actin-Gal4; chiffonFL<sup>WF24</sup></i>	<i>chiffon</i> null allele on chromosome 2 with actin-Gal4 plus a transgene expressing FL <sup>WF24</sup> (1 – 1695aa) containing a nonsense mutation at 174aa (c.520C>T; p.174Q>X) for GFP sorting.	<i>yw; P{w[+mC]=Act5C-GAL4}25FO1, chiff<sup>DsRed-attP</sup>/CyO; P{w+mC =Chiffon FL<sup>WF24</sup>4-NHACFLAG_ chiff}attP2</i>	This study; Chiffon transgenes described in (Torres-Zelada et al. 2019)
<i>chiffon<sup>DsRed</sup>, actin-Gal4; chiffonΔN</i>	<i>chiffon</i> null allele on chromosome 2 as actin-Gal4 plus a transgene expressing ΔN (401 – 1695aa) for GFP sorting.	<i>yw; P{w[+mC]=Act5C-GAL4}25FO1, chiff<sup>DsRed-attP</sup>/CyO; P{w+mC =ChiffonΔN-NHACFLAG_ chiff}attP2</i>	This study; Chiffon transgenes described in (Torres-Zelada et al. 2019)
<i>chiff<sup>ETBE3</sup>, 10XUAS:GFP</i>	<i>chiffon</i> null allele on chromosome 2 with 10XUAS:GFP for GFP sorting of <i>chiffon</i> null mutants embryos	<i>chiff<sup>ETBE3</sup>, P{w[+mC]=10XUAS-IVS-mCD8::GFP}attP40</i>	This study
<i>10XUAS-IVS-mCD8:GFP</i>	GFP control stock for GFP sorting of <i>chiffon</i> mutants	<i>w<sup>1</sup>; P{y[+t7.7] w[+mC]=10XUAS-IVS-mCD8::GFP}attP40</i>	BDSC 32186
<i>Act5C-GAL4</i>	Actin-Gal4 control stock for GFP sorting of <i>chiffon</i> mutants	<i>y<sup>1</sup> w[*]; P{w[+mC]=Act5C-GAL4}25FO1/CyO, y[+]</i>	BDSC 4414
<i>ada2b<sup>1</sup>, 10XUAS:GFP</i>	<i>ada2b</i> null allele on chromosome 3 with 10XUAS:GFP for GFP sorting of <i>ada2b</i> mutant embryos	<i>ada2b<sup>1</sup>, P{w[+mC]=10XUAS-IVS-mCD8::GFP}su(Hw)attP1/TM3, Sb<sup>1</sup></i>	This study
<i>ada2b<sup>B42</sup>, elav-GAL4</i>	<i>ada2b</i> null allele on chromosome 3 with elav-GAL4 for GFP sorting of <i>ada2b</i> mutant embryos	<i>ada2b<sup>B42</sup>, w[*]; P{w[+mC]=elav-GAL4}LL7/TM3, Sb<sup>1</sup></i>	This study
<i>ada2b<sup>1</sup>, 10XUAS:GFP; ada2b-PA</i>	<i>ada2b</i> null allele on chromosome 3 with 10XUAS:GFP plus a transgene expressing Ada2b-PA isoform	<i>yw; P{w+mC =ADA2B-PA_ada2bEN}attP40; ada2b<sup>1</sup>, w<sup>+mC</sup>=10XUAS-IVS-mCD8::GFP}su(Hw)attP1</i>	This study; Ada2b transgenes described in (Weake et al. 2011)
<i>ada2b<sup>1</sup>, 10XUAS:GFP; ada2b-PB</i>	<i>ada2b</i> null allele on chromosome 3 with 10XUAS:GFP plus a transgene expressing Ada2b-PB isoform	<i>yw; P{w+mC =ADA2B-PB_ada2bEN}attP40; ada2b<sup>1</sup>, w[+mC]=10XUAS-IVS-mCD8::GFP}su(Hw)attP1ada2b<sup>1</sup></i>	This study; Ada2b transgenes described in (Weake et al. 2011)

<i>ada2b<sup>842</sup></i> , <i>elav4-GAL4</i> ; <i>ada2b-PB</i>	<i>Ada2b</i> null allele on chromosome 3 with <i>elav-GAL4</i> plus a transgene expressing <i>Ada2b-PA</i> isoform	<i>yw</i> ; <i>P{w+mC =ADA2B-PB_ada2bEN}attP40</i> ; <i>ada2b[842]</i> , <i>w[*]</i> ; <i>P{w[mC]=tubP-GAL4}LL7/TM3, Sb<sup>11</sup></i>	This study; <i>Ada2b</i> transgenes described in (Weake et al. 2011)
<i>10XUAS-IVS-mCD8::GFP</i>	GFP control stock for GFP sorting of <i>ada2b</i> mutants	<i>w<sup>1118</sup></i> ; <i>P{y[+t7.7] w[mC]=10XUAS-IVS-mCD8::GFP}su(Hw)attP1</i>	BDSC 32187
<i>Elav4-GAL4</i>	GFP control stock for GFP sorting of <i>ada2b</i> mutants	<i>w<sup>1118</sup></i> ; <i>P{y[+t7.7] w[mC]=GMR27E06-GAL4}attP2</i>	BDSC 45530
<i>Ada2b-PB-HF2</i>	<i>Ada2b-PB</i> HA and FLAG tagged in the C-terminal for immunostaining	<i>yw</i> ; <i>P{w+mC =ADA2B-PB-HF2_ada2bEN}attP40</i>	This study
<i>Ada2b-PA-HF2</i>	<i>Ada2b-PB</i> HA and FLAG tagged in the C-terminal for immunostaining	<i>yw</i> ; <i>P{w+mC =ADA2B-PA-HF2_ada2bEN}attP40</i>	This study
<i>chiffon<sup>ETBE3</sup>/chiffon<sup>DsRed</sup></i> ; <i>ChiffonFL-NHACFLAG</i>	<i>Chiffon FL</i> HA tagged in the N-terminal and FLAG tagged in the DN-terminal rescue on <i>chiffon</i> null mutant background	<i>yw</i> ; <i>chiff<sup>ETBE3</sup></i> , <i>P{ry[+t7.2]=neoFRT}40A/chiffon<sup>DsRed-attP</sup></i> ; <i>P{w+mC =ChiffonFL-NHACFLAG_chifp}attP2</i>	This study
<i>chiffon<sup>ETBE3</sup></i> , <i>FRT40A</i>	<i>chiffon</i> , <i>FRT40A</i> stock for germline clone experiment	<i>chiff<sup>ETBE3</sup></i> , <i>P{ry[+t7.2]=neoFRT}40A/CyO</i>	(Stephenson et al. 2015)
<i>chiffon<sup>ETBE3</sup></i> , <i>FRT40A</i> ; <i>chiffonΔN</i> (FLAG-HA)	<i>chiffon</i> , <i>FRT40A</i> stock plus transgene expressing ΔN (401 – 1695aa) for germline clone experiment	<i>yw</i> ; <i>chiff<sup>ETBE3</sup></i> , <i>P{ry[+t7.2]=neoFRT}40A/CyO</i> ; <i>P{w+mC =ChiffonDN-NHACFLAG_chifp}attP2</i>	This study
<i>chiffon<sup>ETBE3</sup></i> , <i>FRT40A</i> ; <i>chiffonN[376S&gt;X]</i> (FLAG-HA)	<i>chiffon</i> , <i>FRT40A</i> stock plus transgene expressing N (1 – 400aa) for germline clone experiment	<i>yw</i> ; <i>chiff<sup>ETBE3</sup></i> , <i>P{ry[+t7.2]=neoFRT}40A/CyO</i> ; <i>P{w+mC =ChiffonN[376S&gt;X]-NHACFLAG_chifp}attP2/MKRS</i>	This study
<i>chiffon<sup>ETBE3</sup></i> , <i>FRT40A</i> ; <i>chiffonFL</i> (FLAG-HA))	<i>chiffon</i> , <i>FRT40A</i> stock plus a transgene expressing full length (1 – 1695aa) for germline clone experiment	<i>yw</i> ; <i>chiff<sup>ETBE3</sup></i> , <i>P{ry[+t7.2]=neoFRT}40A/CyO</i> ; <i>P{w+mC =ChiffonFL-NHACFLAG_chifp}attP2/MKRS</i>	This study
<i>FRT40A</i> , <i>ubi-nlsGFP</i>	<i>FRT40A</i> control stock for germline clone experiment	<i>w<sup>1118</sup></i> ; <i>P{w[mC]=Ubi-GFP(S65T)nls}2L</i> <i>P{ry[+t7.2]=neoFRT}40A/CyO</i>	BDSC 5629
<i>hsFLP</i> ; <i>Adv<sup>1</sup>/CyO</i>	Heat-shock FLP, <i>Adv</i> stock for germline clone experiment	<i>P{ry[+t7.2]=hsFLP}1</i> , <i>w[1118]</i> ; <i>Adv[1]/CyO</i>	BDSC 6
<i>ovoD1</i> , <i>FRT40A</i>	<i>ovoD1 FRT40</i> stock used for germline clone analysis	<i>P{w[mC]=ovoD1-18}2La</i> , <i>P{ry[+t7.2]=neoFRT}40A/Dp(?;2)bw[D]</i> , <i>S[1] wg[Sp-1] Ms(2)M[1] bw[D]/CyO</i>	BDSC 2121



**Table S5.** Primer sequences used in this study. Primers used for qRT-PCR analysis in single embryos. Forward and Reverse primer sequences per each set of primer are indicated.

		Sequence
<i>Rpl32</i>	Forward	5'- CTTCTGGTTTCCGGCAAGGTA-3'
	Reverse	5'- GGTCGAAATACGAGCCGCA-3'
<i>Nanos</i>	Forward	5'-ACTTTGAGTCCGCCATTAC-3'
	Reverse	5'-GTGGTACTGTGCTGCATAA-3'
<i>even skipped</i>	Forward	5'-CCTGGTTGTGGACCTCTTG-3'
	Reverse	5'-TGCCGTTCAAGGAGTTATCC-3'
HA- <i>chiffon</i> ( <i>Chiffon-A</i> )	Forward	5'-TCCTTACGACGTACCAGACTAT-3'
	Reverse	5'-CTGCTGTTGAGTGGCTAGTT-3'
FLAG- <i>chiffon</i> ( <i>Chiffon-B</i> )	Forward	5'-ATCTCGCAGTTCCTGAAGAAG-3'
	Reverse	5'-TGTCATCATCGTCCTTGTAGTC-3'