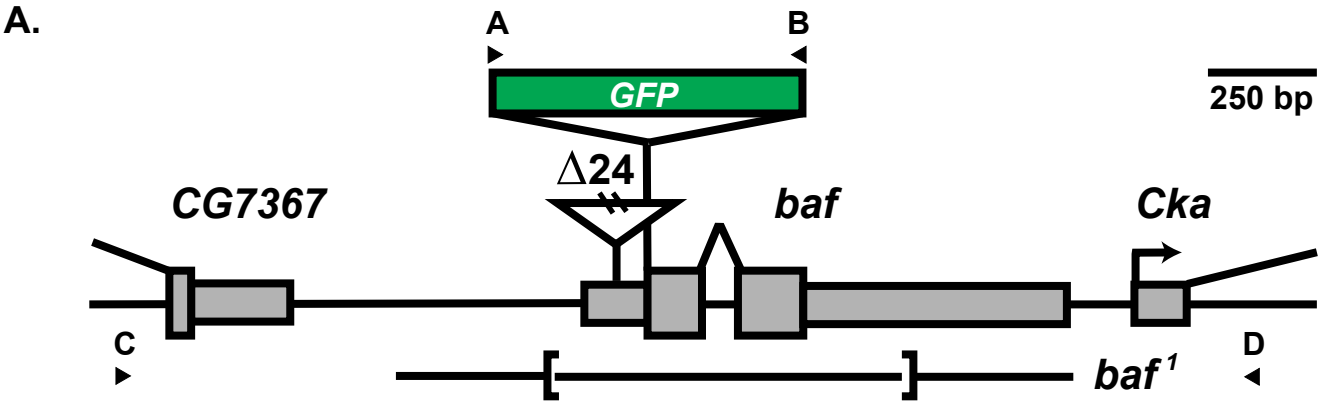
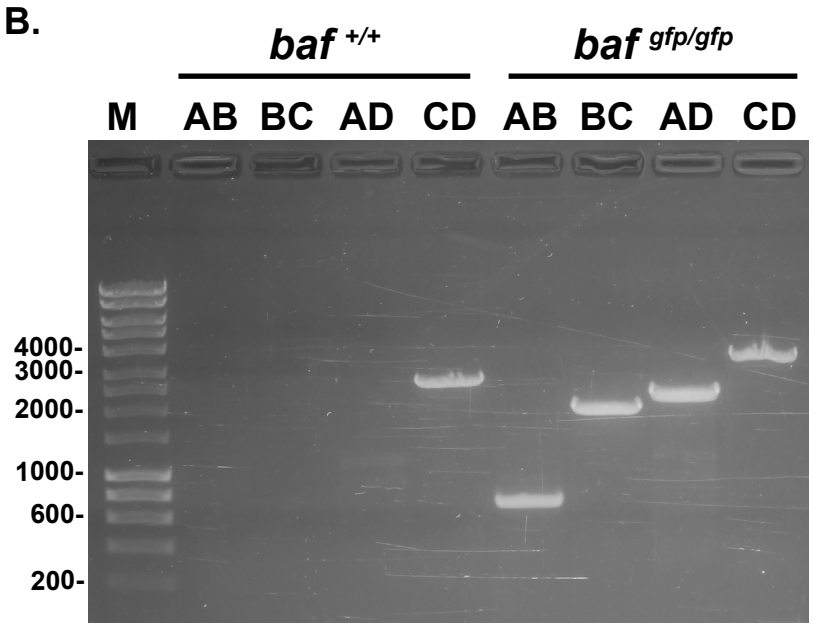




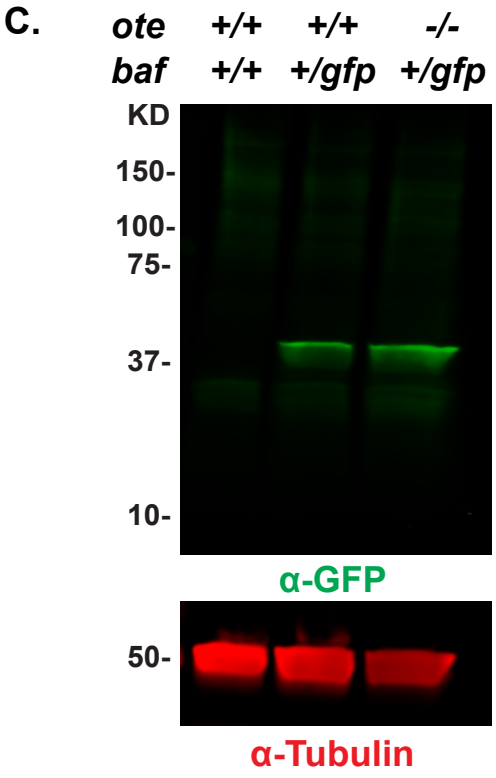


Figure S1. **Data supporting generation of a *gfp-baf* allele**. (A) Shown is a diagram of the *baf* locus, including *baf* and the 5' *CG7367* and 3' *Cka* genes. Gene symbols are described in Figure 1. Locations of genotyping primers are shown above (A,B) and underneath (C,D) the diagram. (B) Agarose gel showing PCR fragments obtained from amplification of $baf^{+/+}$ and $baf^{gfp/gfp}$ genomic DNA using the indicated primer pairs. (C) Western blot of proteins extracted from the anterior third of wandering third instar larvae of the indicated genotypes. Blots were probed with antibodies against GFP (green) to monitor levels of GFP-BAF production and α-Tubulin (red), as a loading control.

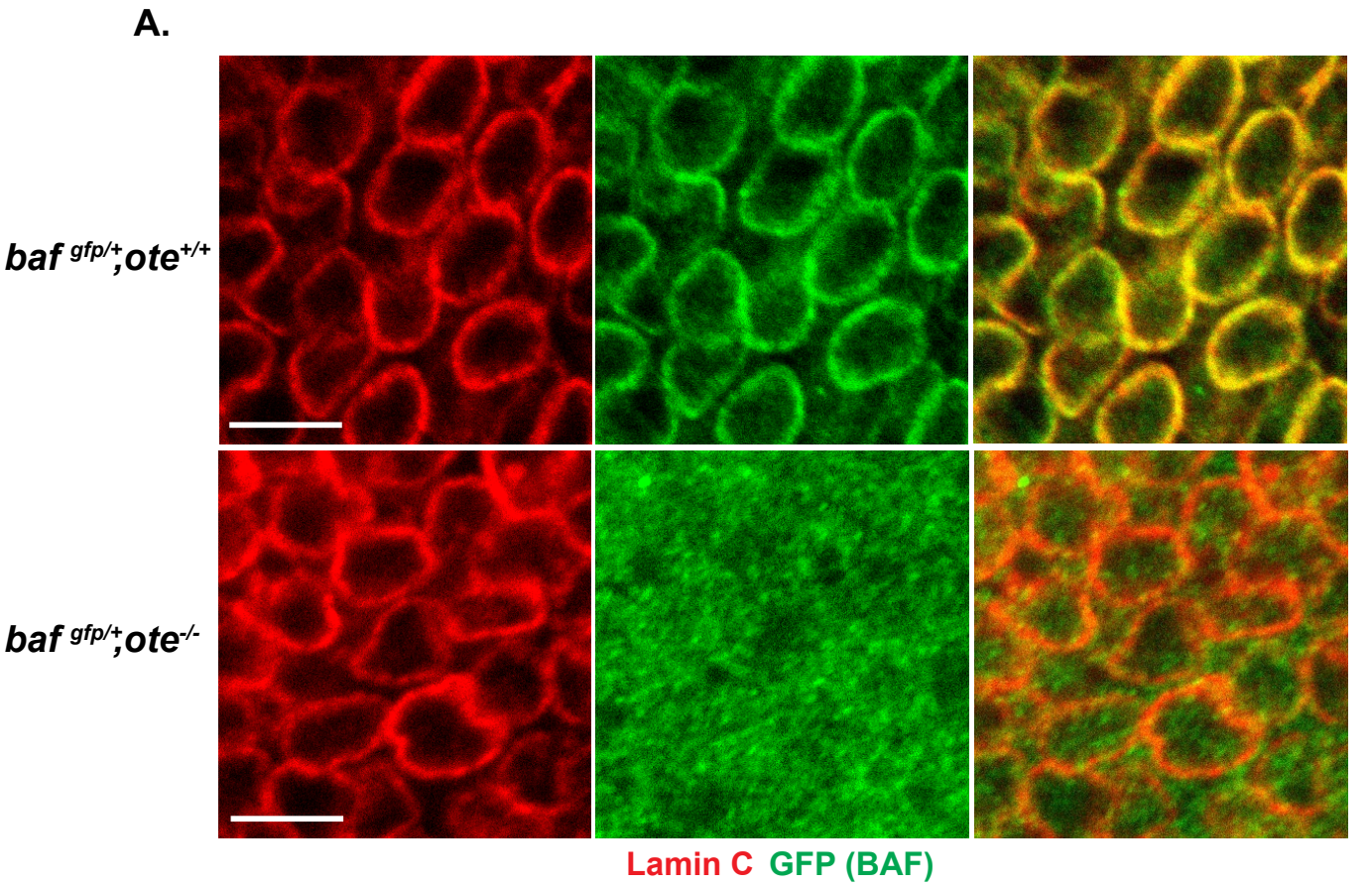


Figure S2. Nuclear localization of BAF depends on Drosophila emerin orthologues. (A) Shown are confocal images of imaginal wing discs from *baf-gfp, ote*$^{+/+}$ and *baf-gfp, ote*$^{-/-}$ animals that were stained with antibodies again the A-type lamin (Lamin C, red) and GFP (green). Scale bar: 5 µm. (B) Shown are confocal images of salivary gland nuclei from wild type and the indicated *lem-d* mutants that were stained with antibodies against GFP (green) and the B-type lamin (Lamin; red). Genotypes are noted at the top of each image. Below each image is a representative line scan of the relative fluorescent intensity (RFI) of GFP (green) and Lamin (red) across the selected nucleus. At least five nuclei were studied for each genotype, with similar results obtained. X-axis, distance, Y-axis RFI. Scale bar: 5 µm.

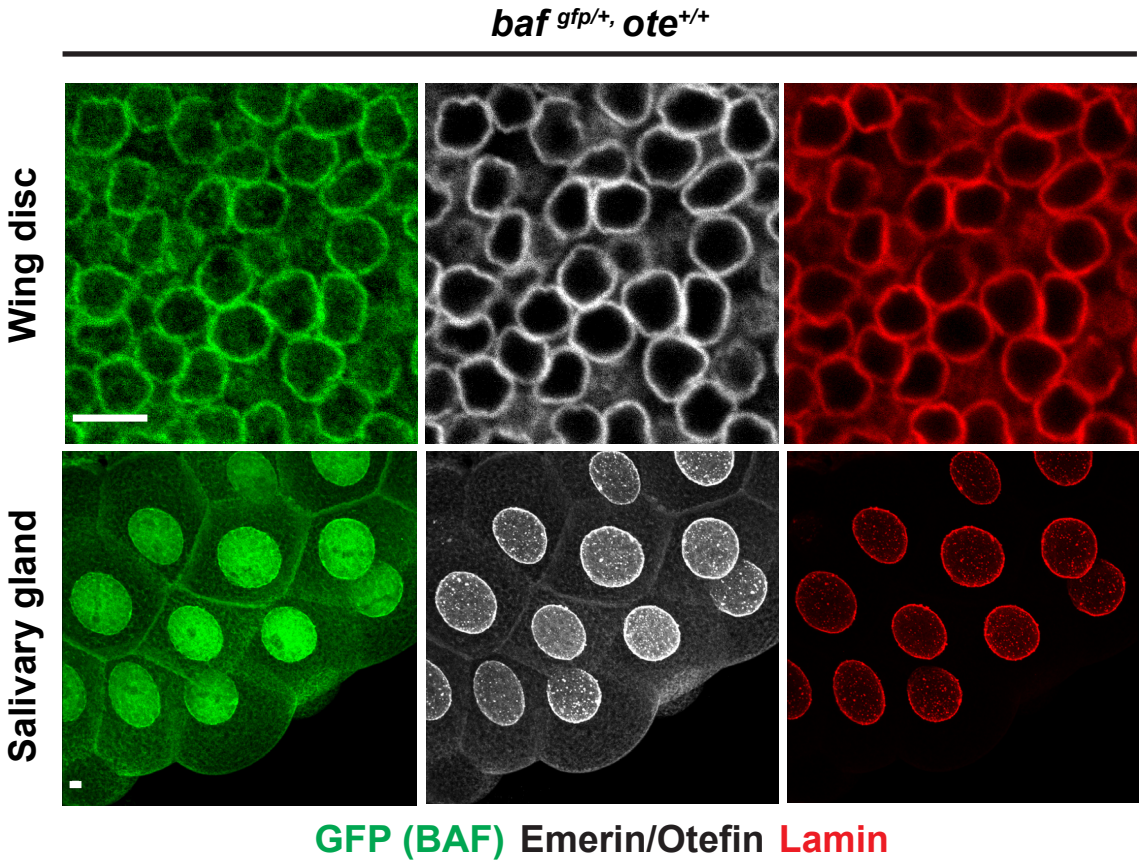
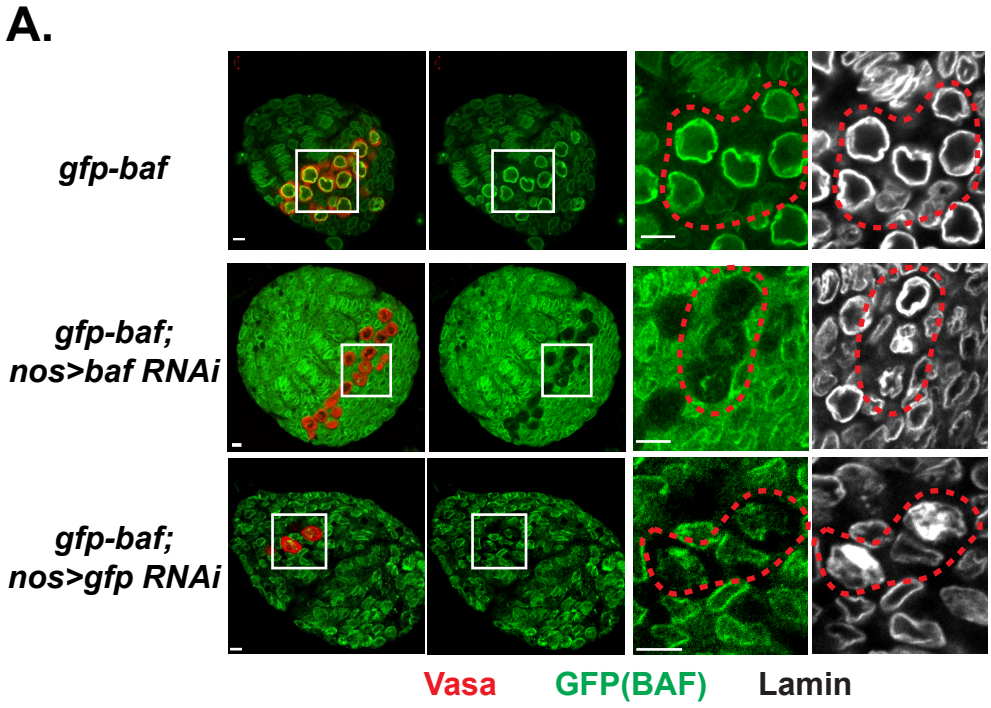
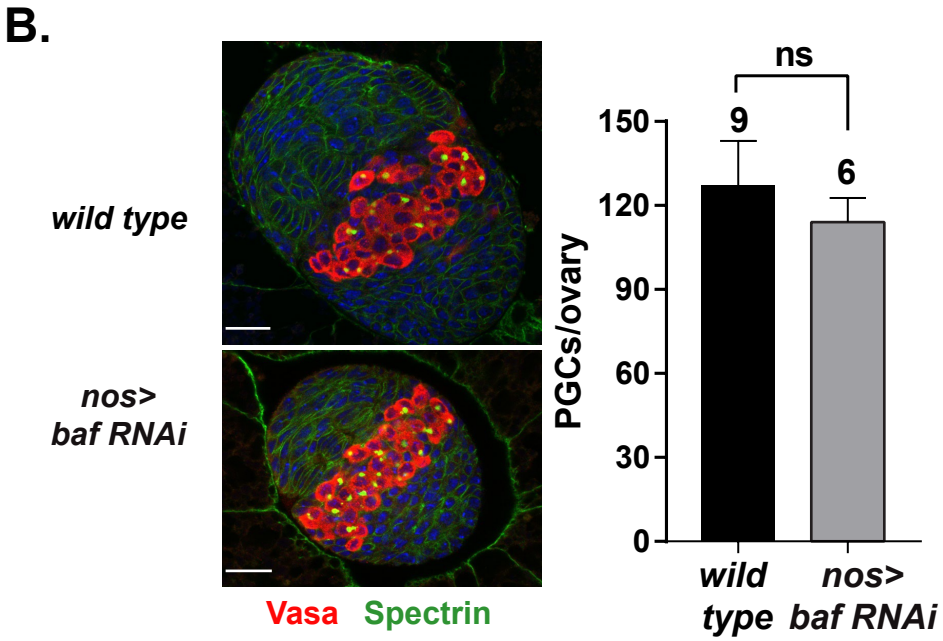


Figure S3. D-emerin/Otefin shows nucleoplasmic localization in the salivary gland. Shown are confocal images of fields of nuclei from bafgfp third instar wing discs and salivary glands. Larval tissues were stained with antibodies against GFP (green), D-emerin/Otefin (white) and the B-type lamin (Lamin; red). Scale bar: 5 μm.





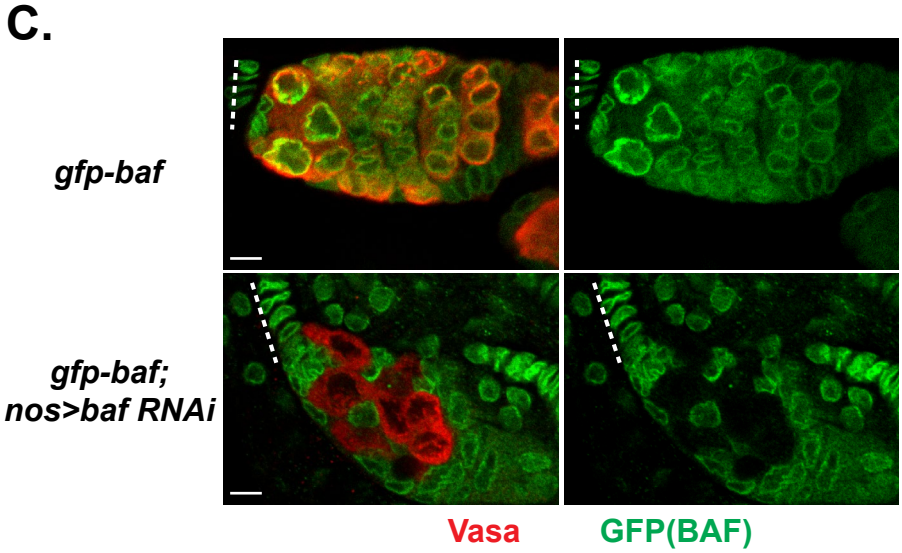


Figure S4. **Efficiency of germline knockdown of BAF depends upon source of the RNAi responder.** (A) Confocal images of 3rd instar larval ovaries stained with antibodies against Vasa (red), GFP (green) and the B-type Lamin (white). Genotypes are noted on the left of the image. Boxed regions are enlarged on the right, and germ cells are circled with red dash lines. Scale bar: 5 μm. BAF knockdown is incomplete using the *baf RNAi* responder retains BAF (GFP) staining. Knockdown using the *gfp RNAi* responder causes loss of primordial germ cells (PGCs), with the few remaining PGCs showing BAF (GFP) staining. (B) Left: Confocal images of third instar larval ovaries stained with antibodies against Vasa (red) and Spectrin (green). Genotypes are noted on the left of the image. Scale bar: 20 μm. Right: Bar graph of the number of PGCs per ovary in third instar larvae. Genotypes are noted below the graph and the number of ovaries assessed is noted above each bar. Significance was assessed by Student's t-test; ns: not significant. (C) Confocal images of ovaries from less than one-day-old females stained with antibodies against Vasa (red) and GFP (green). BAF knockdown appears complete in adult ovaries, using the *baf RNAi* responder. GSC niches are denoted by dash lines. Genotypes are noted on the left. Scale bar: 5 μm.

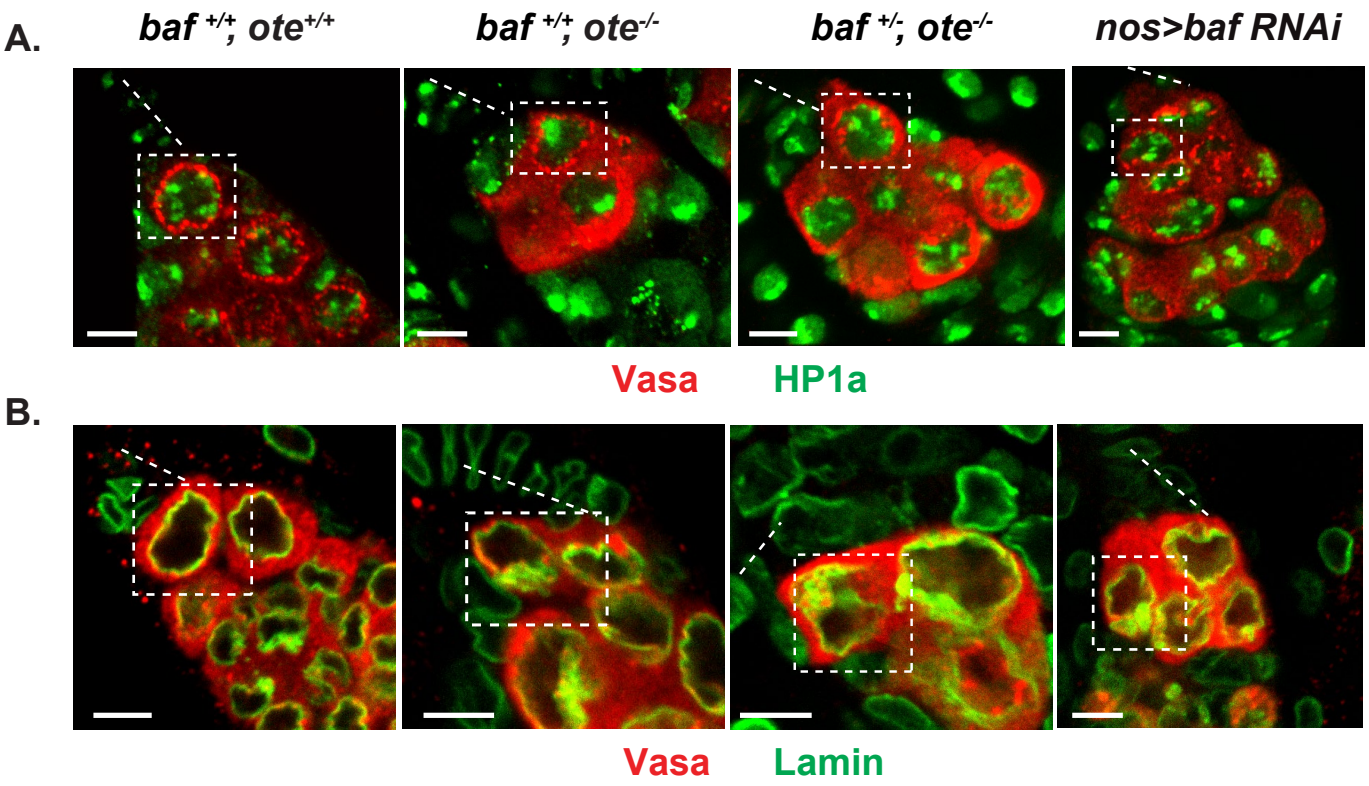


Figure S5: Germline knockdown of BAF alters nuclear structure. (A, B). Shown are confocal images of germaria in ovaries dissected from less than one-day-old females of the indicated genotypes. Ovaries were stained for Vasa (red) and either HP1a (green, A) or the B-type lamin (Lamin, green, B). GSC niches are denoted by the dashed lines. Boxed nuclei are shown in Fig. 5. Scale bar: 5 μm.

Table S1

Gene	Genotype	Nature of lesion	Source
ATR (meiosis-41)	*FM6a/sn^{3}, mei-41^{D9}; baf RNAi/Tb*	EMS, deletion of first 163 amino acids	BL#4174
ATR (meiosis-41)	*w*, mei-41^{29D};nosgal4vp16/Tb*	P excision, deletion of 975bp of coding region and frame shift	BL#4183
baf	*yw; baf^{1}/ CyO, y^{+}*	Imprecise excision of the P{lacW}l(2)k10210^{k10210} insertion, deletion 1kb of *baf* open reading frame, leaving 1kb of *P*-element.	K. Furukawa
baf	*yw; baf$^{\Delta 24}$/ CyO, y^{+}*	Imprecise excision of P-element 75bp downstream of TSS	BL#29496
baf	*y^{1} sc*v^{1} sev^{21}; P{y[+t7.7] v[+t1.8]=TRiP.HMS00195}attP2*	RNAi transgene	BL#36108
baf	*yw; baf^{gfp}*	CRISPR tagging	This work
chk2 (loki, mnk)	*y^{1}w^{67c23} ; loki^{P6}/ loki^{P6}*	P insertion and deletion in second exon	Y. Rong
chk2 (loki, mnk)	*y^{1}w^{67c23} ; loki^{P30}/CyO*	Deletion of 5'UTR and first two exons	Y. Rong
otefin (ote)	*y^{1}w^{67c23} ; ote^{B279-G}/CyO, y^{+}*	PB insertion at +764	BL#16189, Geyer lab
otefin (ote)	*y^{1}w^{67c23} ;ote^{halPK}/CyO, y^{+}*	EMS mutation, R127Stop	T. Schupbach
bocksbeutel (bocks)	*y^{1}w^{1118}; bocks$^{\Delta 10}$*	344 bp deletion from +11	Geyer lab
MAN1	*yw; MAN1$^{\Delta 81}$/ CyO, y^{+}*	P excision, 2325 bp deletion from +92	Geyer lab
nanos (nos)	*w^{1118}; P{GAL4::VP16-nos.UTR}CG6325MVD1*	Gal4 transgene	BL#4937
gfp	*y[1] sc[*] v[1] sev[21]; P{y[+t7.7] v[+t1.8]=VALIUM20-EGFP.shRNA.4}attP2*	RNAi transgene	BL#41553