**Table S1. Screen of Chromatin Regulators.** For each line, the regeneration index was calculated by summing the product of approximate wing size (0%, 25%, 50%, 75% and 100%) and the corresponding percentage of wings for each wing size. The  $\Delta$  Index, which is the difference between the regeneration indices of the line being tested and the control tested simultaneously, was calculated by subtracting the regeneration index of the control from the regeneration index of the mutant or RNAi line. A cutoff  $\Delta$  index of 10% was set, over which we considered the regenerative capacity to be affected. Green indicates lines that had a higher regeneration index compared to the control, purple indicates lines that had a lower regeneration index compared to the control. \* =  $\Delta$  Index ≥ 10 or ≤ -10, \*\* =  $\Delta$  Index ≥ 20 or ≤ -20, \*\*\* =  $\Delta$  Index ≥ 30 or ≤ -30.

#### Fig S1. Roles of the SWI/SNF components in regeneration and development

(A) Average  $\Delta$  regeneration index of chromatin regulator mutants and RNAi lines screen. The  $\Delta$  regeneration Index is the difference between the regeneration indices of the line being tested and the control tested simultaneously.  $\Delta$  regeneration index was calculated as described in materials and methods.

(B) Undamaged adult wings of *osa*<sup>308</sup>/+ animals.

(C) *Bap60* expression examined by qPCR of *Bap60*<sup>RNAi</sup> and control undamaged wing discs. The graph shows fold change relative to control discs. RNAi lines were crossed to  $w^{1118}$ ; +; *rn-GAL4*, *tubGAL80*<sup>ts</sup>/TM6B and kept at 18°C.

Temperature shift to 30°C at day 7 for 24 hours then back to 18°C. Wing discs of non-Tubby larvae were dissected at 24 hours after shifting back to 18°C.

(D) Complementation test for *mor*<sup>1</sup> and *mor*<sup>11</sup> mutants.

(E) *brm* expression examined by qPCR of *brm*<sup>RNAi</sup> and control undamaged wing discs. The graph shows fold change relative to control discs. RNAi lines were crossed to  $w^{1118}$ ; +; *rn-GAL4*, *tubGAL80<sup>ts</sup>/TM6B* and kept at 18°C. Temperature shift to 30°C at day 7 for 24 hours then back to 18°C. Wing discs of non-Tubby larvae were dissected at 24 hours after shifting back to 18°C.

(F-H) Undamaged adult wings of *Bap55<sup>LL05955</sup>*/+ (E), *mor*<sup>1</sup>/+ (F) and *mor*<sup>2</sup>/+ (G) animals.

Error bars are S.E.M.. Scale bars are 500 $\mu$ m for all adult wings images. \* p < 0.05, \*\* p < 0.01, \*\*\* p < 0.001 Student's *t*-test for (C) and (E).

# Fig S2. The PBAP complex is required for regenerative growth whereas the BAP complex is not.

(A) Wild-type ( $w^{1118}$ ) regenerating wing disc at R24 with wing pouch marked by anti-Nubbin immunostaining.

(B) *brm*<sup>2</sup>/+ regenerating wing disc at R24 with wing pouch marked by anti-Nubbin immunostaining.

(C) Comparison of regenerating wing pouch size at 24 hours after imaginal disc damage in  $brm^2/+$  and wild-type ( $w^{1118}$ ) animals. n = 11 wing discs ( $brm^2/+$ ) and 10 wing discs ( $w^{1118}$ ).

(D) Wild-type (*w*<sup>1118</sup>) regenerating wing disc at R24 with wing pouch marked by anti-Nubbinimmunostaining.

(E) *osa*<sup>308</sup>/+ regenerating wing disc at R24 with wing pouch marked by anti-Nubbin immunostaining.

(F) Wild-type ( $w^{1118}$ ) regenerating wing disc at R48 with wing pouch marked by anti-Nubbin immunostaining.

(G) *osa<sup>308</sup>*/+ regenerating wing disc at R48 with wing pouch marked by anti-Nubbin immunostaining.

(H) Comparison of regenerating wing pouch size at 24 and 48 hours after imaginal disc damage and regeneration in  $osa^{308}$ /+ and wild-type ( $w^{1118}$ ) animals. At R24, n = 26 wing discs ( $osa^{308}$ /+) and 27 wing discs ( $w^{1118}$ ). At R48, n = 6 wing discs ( $osa^{308}$ /+) and 21 wing discs ( $w^{1118}$ ).

(I) Average number of mitotic cells (marked with PH3 immunostaining) per  $\mu$ m<sup>2</sup> in the regenerating wing primordium at R24 in *Bap170*<sup> $\Delta$ 135</sup>/+ and wild-type (w<sup>1118</sup>) animals. n = 8 wing discs (*Bap170*<sup> $\Delta$ 135</sup>/+) and 10 wing discs (w<sup>1118</sup>).

(J) Wild-type ( $w^{1118}$ ) regenerating wing disc at R24 with Nubbin (green) (J') and cleaved caspase Dcp1 (magenta)(J'') immunostaining marking the debris field, and DNA (blue) was detected with Topro3 here in subsequent panel. (J'''). (K) *bap170*<sup> $\Delta$ 135</sup>/+ regenerating wing disc at R24 with Nubbin (green)(K') and cleaved caspase Dcp1 (magenta)(K'') immunostaining, and DNA (blue)(K'''). Error bars are S.E.M.. Scale bars are 100µm for all wing discs images. \* p < 0.05, \*\* p < 0.01, Student's *t*-test.

## Fig S3. The PBAP complex regulates Myc in regeneration whereas the BAP complex does not.

(A) Wild-type ( $w^{1118}$ ) undamaged wing disc with Myc (magenta) (A') and Nubbin

(green) (A") immunostaining. DNA (blue) (A") was detected with Topro3.

(B-C) Wild-type  $(w^{1118})$  (B) and  $brm^2/+$  (C) regenerating wing discs at R24 with Myc immunostaining.

(D) Quantification of anti-Myc immunostaining fluorescence intensity in the wing pouch in *brm*<sup>2</sup>/+ and wild-type ( $w^{1118}$ ) regenerating wing discs at R24. n = 11 wing discs (*brm*<sup>2</sup>/+) and 12 wing discs ( $w^{1118}$ ).

(E-F) Wild-type  $(w^{1118})$  (E) and  $osa^{308}/+$  (F) regenerating wing discs at R24 with Myc immunostaining.

(G) Quantification of anti-Myc immunostaining fluorescence intensity in the wing pouch in *osa*<sup>308</sup>/+ and wild-type ( $w^{1118}$ ) regenerating wing discs at R24. n = 28 wing discs (*osa*<sup>308</sup>/+) and 27 wing discs ( $w^{1118}$ ).

(H) Comparison of the size of adult wings after imaginal disc damage and regeneration in wild-type ( $w^{1118}$ ),  $Bap170^{\Delta 135}/+$ ,  $Bap170^{\Delta 135}/+$ ; UAS-Myc/+, and UAS-Myc/+ animals. n = 364 wings ( $w^{1118}$ ), 194 wings ( $Bap170^{\Delta 135}/+$ ), 194 wings ( $Bap170^{\Delta 135}/+$ ; UAS-Myc/+) and 294 wings (UAS-Myc/+) from 3 independent experiments. Chi-square test for  $Bap170^{\Delta 135}/+$  and  $Bap170^{\Delta 135}/+$ ; UAS-Myc/+ has p < 0.001

Error bars are S.E.M.. Scale bars are 100 $\mu$ m for all wing discs images. \* p < 0.05, \*\* p < 0.01, Student's *t*-test for (D) and (G).

#### Fig S4. The function of BAP and PBAP in regeneration and development

(A) Pupariation rates of animals during normal development at 18°C. n = 103 pupae ( $Bap170^{\Delta 135}$ /+) and 227 pupae ( $w^{1118}$ ) from 3 independent experiments. Student's *t*-test not significant.

(B) Pupariation rates of animals after tissue damage (30°C) and regeneration (18°C). n = 117 pupae ( $Bap170^{\Delta 135}/+$ ) and 231 pupae ( $w^{1118}$ ) from 3 independent experiments. Because the temperature shift to 30°C in the ablation protocol increases the developmental rate, the pupariation timing of regenerating animals (B) cannot be compared to the undamaged control animals (A). Chi-square test p < 0.001.

(C-E) *mmp1* expression examined by immunofluorescence in wild-type ( $w^{1118}$ )

(C) and  $Bap170^{\Delta 135}$ + (D) regenerating wing discs at R24. Quantification in (E).

n= 19 ( $w^{1118}$ ) and 17 (*Bap170*<sup> $\Delta$ 135</sup>/+), error bars are S.E.M., p=0.00041.

(F) Wild-type (*w*<sup>1118</sup>) regenerating wing disc at R48 with Ptc (green)(F') and Ci (magenta)(F'') immunostaining.

(G) *osa*<sup>308</sup>/+ regenerating wing disc at R48 with Ptc (green)(G') and Ci (magenta)(G'') immunostaining.

(H-K) Wild-type ( $w^{1118}$ ) regenerating wing discs at 0, 24, 48, and 72 hours after imaginal disc damage with Osa immunostaining.

(L-M) Wild-type (*w*<sup>1118</sup>) (L) and *tara*<sup>1</sup>/+ (M) regenerating wing discs at R48 with Osa immunostaining.

(N) Pupariation rates of animals during normal development at 18°C. n = 79 pupae ( $osa^{308}$ /+) and 173 pupae ( $w^{1118}$ ) from 3 independent experiments. Chisquare test p < 0.001, student's t-test at day 11 p<0.01.

(O) Pupariation rates of animals after tissue damage (30°C) and regeneration (18°C). n = 101 pupae ( $osa^{308}$ /+) and 155 pupae ( $w^{1118}$ ) from 3 independent

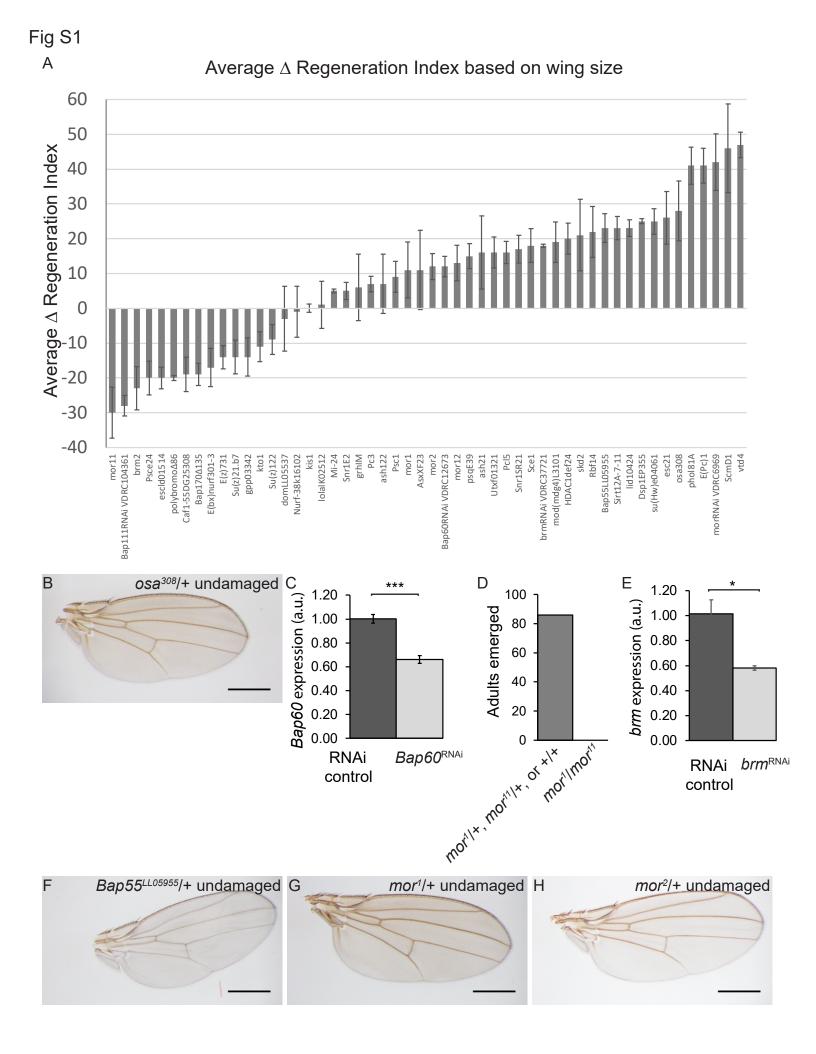
experiments. Chi-square test p < 0.001, student's t-test at day 3 p<0.01. Because the temperature shift to 30°C in the ablation protocol increases the developmental rate, the pupariation timing of regenerating animals (O) cannot be compared to the undamaged control animals (N).

Scale bars are 100 $\mu$ m for all wing discs images. Scale bars are 100 $\mu$ m for all wing discs images. Error bars are S.E.M. except where noted. \* p < 0.05, \*\* p < 0.01, \*\*\*<0.001 for Student's *t*-test.

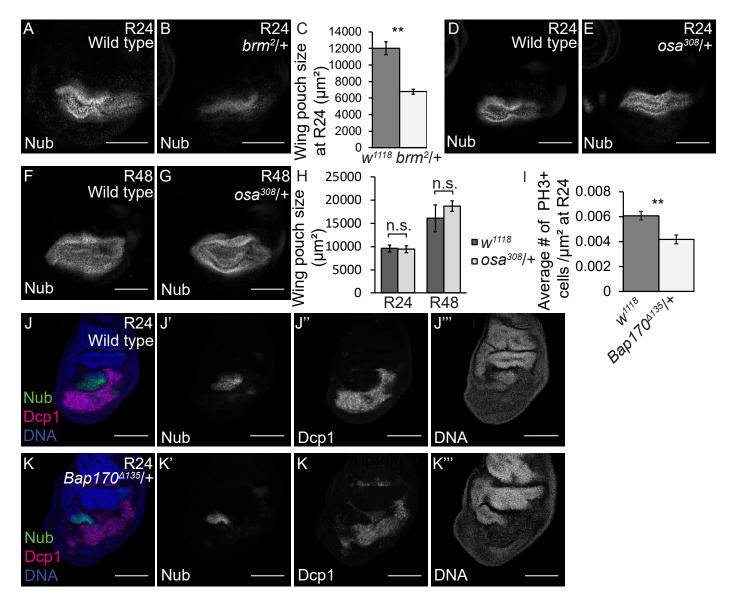
Allele or RNAi	Complex	Regeneration Phenotype	$\Delta$ Index	Phenotype Strength
Pc <sup>3</sup>	PRC1	••	7%	
Psc <sup>1</sup>	PRC1		9%	
Psc <sup>e24</sup>		Reduced	-20%	**
Sce <sup>1</sup>	PRC1	Enhanced	18%	*
Scm <sup>D1</sup>	PRC1	Enhanced	46%	***
<i>E</i> ( <i>z</i> ) <sup>731</sup>	PRC2	Reduced	-14%	*
Su(z)12 <sup>2</sup>	PRC2		-9%	
esc <sup>21</sup>	PRC2	Enhanced	26%	**
Caf1-55 <sup>DG25308</sup>	PRC2, NURF	Reduced	-19%	*
escl <sup>d01514</sup>	PRC2	Reduced	-20%	**
phol <sup>81A</sup>	PhoRC	Enhanced	41%	***
ash2 <sup>1</sup>	COMPASS, COMPASS-like	Enhanced	16%	*
<i>Utx</i> <sup>f01321</sup>	COMPASS-like	Enhanced	16%	*
ash1 <sup>22</sup>	ASH1		7%	
E(bx) <sup>nurf301-3</sup>	NURF	Reduced	-17%	*
Nurf-38 <sup>k16102</sup>	NURF		-1%	
Mi-2 <sup>4</sup>	NuRD		5%	
brm <sup>2</sup>	SWI/SNF (BAP & PBAP)	Reduced	-23%	**
brm <sup>RNAi VDRC37721</sup>	, ,	Enhanced	18%	*
osa <sup>308</sup>	SWI/SNF(BAP)	Enhanced	28%	**
Bap170 <sup>∆135</sup>	SWI/SNF(PBAP)	Reduced	-19%	*
, polybromo <sup>∆86</sup>	SWI/SNF(PBAP)	Reduced	-20%	**
Snr1 <sup>E2</sup>	SWI/SNF (BAP & PBAP)		5%	
Snr1 <sup>SR21</sup>		Enhanced	17%	*
mor <sup>1</sup>	SWI/SNF (BAP & PBAP)	Enhanced	11%	*
mor <sup>2</sup>	, , , , , , , , , , , , , , , , , , ,	Enhanced	12%	*
mor <sup>11</sup>		Reduced	-30%	***
mor <sup>12</sup>		Enhanced	13%	*
mor <sup>RNAi VDRC6969</sup>		Enhanced	42%	***
Bap55 <sup>LL05955</sup>	SWI/SNF (BAP & PBAP)	Enhanced	23%	**
Bap60 <sup>RNAi VDRC12673</sup>	SWI/SNF (BAP & PBAP)	Enhanced	12%	*
Bap111 <sup>RNAi VDRC104361</sup>	SWI/SNF (BAP & PBAP)	Reduced	-28%	**
psq <sup>E39</sup>				

S1 Table. Screen of chromatin regulators

Rbf <sup>14</sup>	dREAM	Enhanced	22%	**
Dsp1 <sup>EP355</sup>		Enhanced	25%	**
grh <sup>IM</sup>			6%	
Iolal <sup>K02512</sup>			1%	
Pcl <sup>5</sup>		Enhanced	16%	*
HDAC1 <sup>def24</sup>	Sin3A/HDAC complex	Enhanced	20%	**
Sirt1 <sup>2A-7-11</sup>	SIRT1-LSD1 complex	Enhanced	23%	**
vtd <sup>4</sup>	cohesin	Enhanced	47%	***
Su(z)2 <sup>1.b7</sup>		Reduced	-14%	*
gpp <sup>03342</sup>		Reduced	-14%	*
mod(mdg4) <sup>L3101</sup>		Enhanced	19%	*
su(Hw) <sup>e04061</sup>	gypsy chromatin insulator complex	Enhanced	25%	**
lid <sup>10424</sup>		Enhanced	23%	**
Asx <sup>XF23</sup>		Enhanced	11%	*
dom <sup>LL05537</sup>	TIP60 complex		-3%	
E(Pc) <sup>1</sup>	TIP60 complex	Enhanced	41%	***
kis <sup>1</sup>	·		0%	
kto <sup>1</sup>	mediator	Reduced	-11%	*
skd <sup>2</sup>	mediator	Enhanced	21%	**



### Fig S2



## Fig S3

