Supplemental Figure Legends

Figure S1. Identification of *tis11* and *pan2* alleles.

(A) Over-expressing a dominant-negative form of Mastermind (Mam^{DN}) in immature INPs partially suppressed the supernumerary neuroblast phenotype in *numb* hypomorphic brains. Mam^{DN} antagonizes the activation of Notch target genes. Bar graph is represented as mean ± standard deviation. P-value: *** <0.005.

(B) Identification of the *tis11* locus as a genetic modifier of the supernumerary neuroblast phenotype in *brat* hypomorphic brains.

(C) Expression of *pan2* mRNA in wild-type or *pan2* homozygous mutant animals. *pan2*^{f00130} (*pan2*^{-/-}) is a null allele.

(D) Graphic illustration of the functional domains in Pan2. Asterisks correspond to the molecular lesions in enzymatically inactive Pan2^{D1039N,1041Q} transgenic protein. UCH: ubiquitin C-terminal hydrolase.

Figure S2. Brat likely recruits Tis11 to the BRE-ARE motif in the 3'UTRs of self-

renewal gene transcripts.

(A) The 3'UTRs of *dpn* and *klu* mRNA. High-affinity BREs: darker yellow. Lower-affinity BREs: lighter yellow. AREs: red.

(B) B-boxes are required for Brat to bind Tis11. This is the reciprocal IP-WB analysis of the lysate shown in Fig. 2B.

Figure S3. Conserved domains in Insb.

Illustration showing conserved motifs (marked in red) in Insb among 12 Drosophila species.

Figure S4. The Orange motif mediates Insb binding to Dpn.

C-terminally truncated Insb lacking the Orange motif fails to bind to Dpn. The Orange motif alone is sufficient to facilitate Insb binding to Dpn.



Α

BRE: U/AUGUUAU/A

dpn 3'UTR

ARE: AUUUA			
AUCAACCGCA	CAGGCCACUU	CU <mark>AUGUUAC</mark> G	UUUAUACAUU
GUUAAUUUAU	UUCAUUGCAA	UUUUUUCAAA	GAUCACUUCA
AUGCUUUAGA	ACCCCAUUAA	GUUUCAA CGA	UUUCUAU <mark>AUG</mark>
UUUUUAUGUA	UCCCCGUUUC	GCUUUCUUCA	UUUUAAGUUC
AGCUGTGAUU	UU GUAU AUUU	U UUGUGU AGU	UCUCGUUUAA
GCGCUUUAUA	CGACUAUUAU	GUAGUUCAUU	AAAUAAUUAU
GUUCUUUAAU	GUUUCAUUAA	CUGCUCAAGU	AUUUAAACAA
UUAAACGUGU	UUCU <mark>AUUUA</mark> A	GUUAUGUAGU	UUUCAUUGUA
UAGCGUUUAU	CAUUAGGUCA	UUCACGUUUC	UAUAUUAGUG
UUUUA <mark>AUUUA</mark>	ACGAUUGUAA	UUUUAACUUU	UAGGUAAUGC
AAAAUUCGAU	GGAGUGAAAA	UAA UGAU AAU	ААААААААА
UGCUGC			

klu 3'UTR

CGGUGUCUGU	AUGCAGCAGC	AUCCAGACCA	UUUAUGACCU	GUUAGGUAAA
AUCCAGUCCA	UCCAAUCUCC	AUUUGACAGG	CCCAGCUUAG	UGCUACAGAA
AAAUAUCUGA	AAAAAAAUA	GAGAAAAGAA	AUGAAAACAU	AUUAAACUAG
AGCAGUUUGU	ACUUGUACCG	GAAAUCUCUG	CGAAGACUGA	GGAACCUUAA
UACUACCUAC	AGUUUAAAUA	AUAGGCUAAA	GAACCAUCAA	CUAAUUUUGU
AAAAGAGGAG	UUAGAGGGCA	GCACUCAUAU	GACCACCCAA	CGUAUUAGAA
GUUUAACUAG	UUCUAGUUGC	UAGAUCCUUU	CGCGCGUCAA	AUGAACCCCC
AGGAGUUUAG	AUAGCCAGGA	UCUUCGAUAC	AGCUAGCAAU	UCCAUGUUCC
ACACCUAGGC	UAUACUACAC	UAUAUAUAGA	UAUAUAUAUA	UAGAUAUGGG
UCAGAUCCAU	CGUCCCGAUG	AUCUGAUCUC	UCAGCAUUUU	GAGCAACGUU
GAAAUUACUA	AGUUAGACUC	GCUACUUAGG	CUUCAUAGGC	ACGCCGCAUU
GGAAAAGGCA	UUACUUUUGU	ACUCCUAAUU	UUAAUUAAUU	CUUA <mark>AUUUA</mark> U
UUGUAACAUU	ACUCAGCAGA	AUGUAAACUU	AUACCACAAC	GAUUUGUAUU
A <mark>AUUUA</mark> AUUU	UACCUUAUUU	AAUAUUUAAU	UUAACUUAGU	UUUAAGGGAU
GCCUGCCUAC	ACAAGAACAC	AAACAAAAGA	CAAAGAAUUC	UCCCUAGGGC
UCAAAAAGAA	AAAAGAAACG	AACGCUACAC	AAAACUCAUU	UCUAUGGAAA
UCUUAAAUCU	UUAAUGGAAA	AGAAAGACAA	AAAGAAACAA	UUCCUUU <mark>UUU</mark>
UGUUCAACAA	AAACACUGUU	AA <mark>AUUUA</mark> CAU	UACCUUUGUA	AUUG <mark>AUUUA</mark> A
UGCUUGCUCU	UCUAUUAUCU	AAACUACUUU	UUGUUUUCAU	GAAAUGAAAU
AAAAACUUUU	AAGUUUUCUU	UAGUUUAUAA	ACCAUCUGGG	GAUUGGAAAC
ACCUCACCCC	CUUCCGCUCC	CGCAAGUGGG	GACACGUUAA	CCCGUUUCUG
CCCCCGGGGG	UGGGAAUCAC	CUCACCUUUC	GUGGUCGUUU	ACAUGUUUCA
AGUUAAAGUU	GUUCGUUAUU	UAUUAUAAAA	AGAAAUGAAA	CAAAGCCCCG
ACUCCCGAUU	AUUGAUUAUU	AGUUCUUAGC	UAAACGUUUA	AAUAAAUUAU
UAAUUU UGU	UAUUCUAGUU	GGUUAUGAUU	AGCACUUAGU	UAAAAACGUU
UUUCACAAAA	UAAAACAAAA	CAAAGUCUAU	ACAUGAUGGA	CAAUGUCAUA
CAAAACAGAA	UUUAAAGCC			



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BL stock #	Name	Deleted segment	Sequence coordinates	Phenotypic effect	Responsible gene	Reference
9299	Df(1)ED6565	2B14;2F5	X:1894112; 2317631	Suppressor	arm	Komori et al., Development 2014
422333	Df(1)BSC625	11B2;11D5	X:12583216;12974678	Enhancer	CKI α , tis 11	Komori et al., Development 2014; this study
2 nd						
BL stock #	Symbol	Deleted segment	Sequence coordinates	Phenotypic effect	Responsive gene	Reference
24118	Df(2L)ED105	21E2;22A1	2L:852854;1420528	Enhancer	unknown	This study
8068	Df(2L)ED94	21E2;21E3	2L:568095;1036969	Enhancer	unknown	This study
26540	Df(2L)BSC688	22B1;22D6	2L:1736964;22733842273572	Enhancer	erm	Jenssens et al., Development 2014
23677	Df(2L)BSC292	23F6;24A2	2L:3515462;3632008	Enhancer	unknown	This study
24133	Df(2L)ED690	30B3;30E4	2L:9437469;9918174	Enhancer	numb	This study
7859	Df(2R)Exel7094	44A4;44B5	2R:8061165; 8131743	Enhancer	unknown	This study
9063	Df(2R)ED1791	44F7;45F1	2R:8922730;9553252	Enhancer	pan2	This study
24912	Df(2R)BSC408	45D4;45F4	2R:9292659;9578616	Enhancer	not1	This study
9596	Df(2R)BSC161	54B2;54B17	2R:17304783;17484828	Enhancer	insb	This study
24379	Df(2R)BSC355	54B16;54C3	2R:17462347;17536673	Enhancer	insb	This study
3rd						
BL stock #	Symbol	Deleted segment	Sequence coordinates	Phenotypic effect	Responsive gene	Reference
8057	Df(3L)ED4288	63A6;63B7	3L:3070827; 3149091	Enhancer	pan3	This study
24401	Df(3L)BSC377	67E5;68A4	3L:1065471310654743; 11070652	Suppressor	klu	Xiao et al., Development 2012
25125	Df(3L)BSC574	68F1;68F1		Enhancer	pop2	This study
3640	Df(3L)brm11	71F1-4;72D1-10		Enhancer	brm	Jenssens et al., Development 2014
7982	Df(3R)Exel7327	89A8;89B1 (Df)	3R:1590143315901434; 16041562	Enhancer	mor	Jenssens et al., Development 2014
4431	Df(3R)DG2	89E1-F4;91B1-B2		Enhancer	osa	Jenssens et al., Development 2014
8583	Df(3R)BSC56	94E1-2;94F1-2		Enhancer	pnpp1	Komori et al., Development 2014
7990	Df(3R)Exel9012	94E9;94E13	3R:23279758; 23346387	Enhancer	pntp1	Komori et al., Development 2014
4432	Df(3R)crb-F89-4	95D7-D11;95F15		Enhancer	apc2	Komori et al., Development 2014
1910	Df(3R)TI-P	97A;98A1-2	3R:2605995426078012; 2738860827480200	Suppressor	unknown	This study
430	Df(3R)3450	98E3;99A6-8		Suppressor	unknown	This study
3547	Df(3R)L127	99B5-6;99F1	3R:2946894129565244; 3038780430459521	Enhancer	Axn	Komori et al., Development 2014