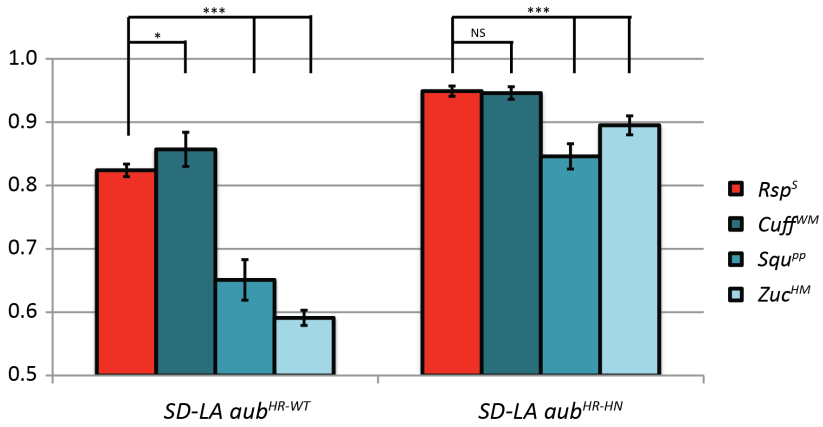

Figure S1 Chromosomes carrying *zuc*^{HM} and *squ*^{PP} suppress distortion by *SD*-LA in both *aub*$^{HR\text{-}wt}$ and *aub*$^{HR\text{-}HN}$ backgrounds. Females of the genotype *SD-LA aub*$^{HR\text{-}wt}$ and *aub*$^{HR\text{-}HN}$ were crossed with males carrying either a mutation in either *zuc, cuff* or *squ.* The 15-30 individual male F1 were then backcrossed to *cn bw* females to test for distortion. The *squ*^{pp} and *zuc*^{HM} chromosomes significantly suppressed distortion when paired with either the *aub*$^{HR\text{-}HN}$ or *aub*$^{HR\text{-}wt}$ chromosome. The *cuff*^{WM} chromosome gave a small but significant enhancement of distortion($p < 0.05$) with the wild type allele and there was no significant change with the *aub*$^{HR\text{-}HN}$ mutant (*** $p < 0.0005$, * $p < 0.05$, 2-tailed Z-test).

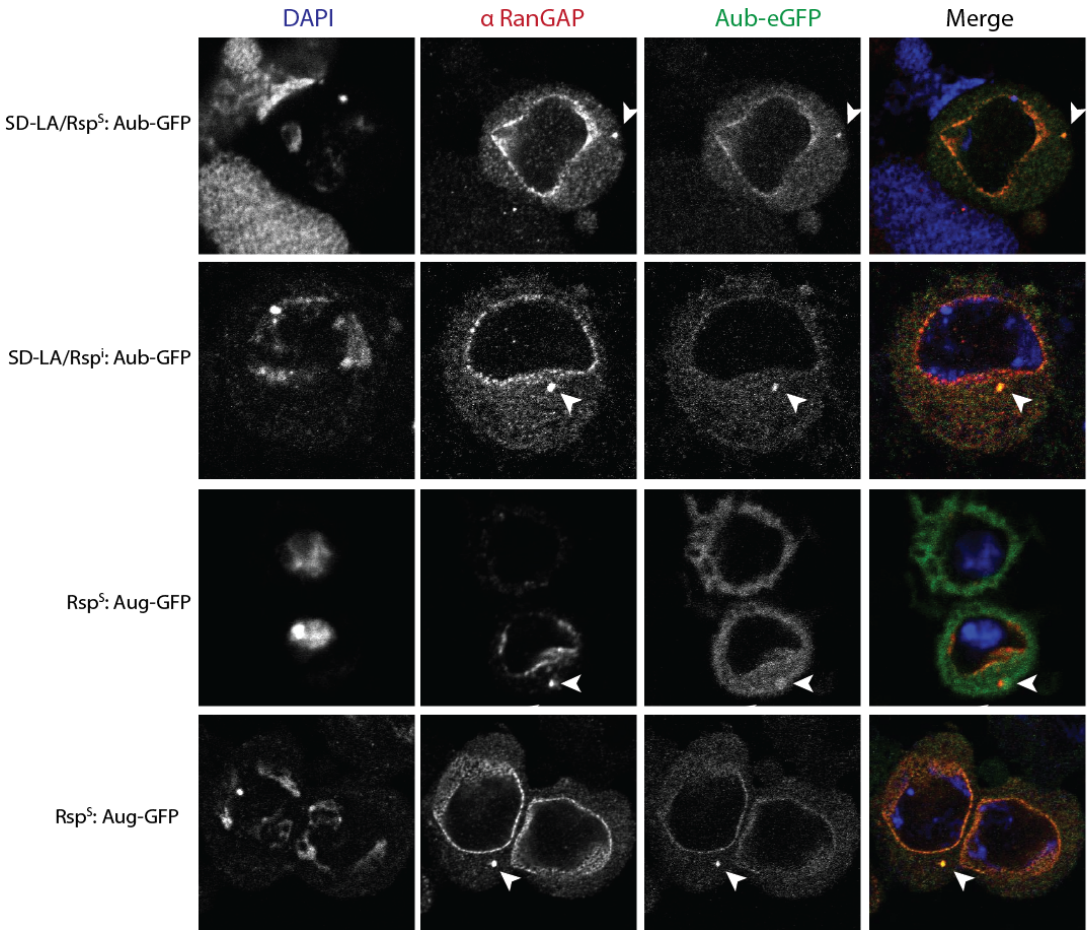

Figure S2 Aub-GFP and RanGAP colocalized in a single large body of primary spermatocytes. Whole mount testis of males expressing Aub-GFP were fixed with paraformaldyhide and stained with anti-RanGAP (1:1000) primary and Alexa Fluor (1:800) secondary antibodies. Confocal imaging was done on a Zeiss LSM 510. Spermatocytes in the testis of both distorting (SD-LA*/Rsp*^{S}) and non-distorting (*SD*$^{+}$ *Rsp*^{S}) males show a single large point of colocaliztion between Aub-GFP and Ran-GAP (arrowhead)

Table S1 Genetic stocks used in this study

Line	Notes on genotype	Source	Reference
HR stocks			
y w;FLP-I-SceI/TM6	y^1 w*; P{ $ry^{+t7.2}$=70FLP}11 P{ $v^{+t1.8}$=70I - SceI}2B noc^{Sco}/CyO, S^2	BSC 6930	Staber *et al.* 2011
y w ey-FLP	$y^{d2}w^{1118}$ P{ry[+t7.2]=ey-FLP.N}2	BSC 5580	Staber *et al.* 2011
y w Cre; noc^{Sco}/CyO	y^1 w^{67c23} P{$y^{+mDint2}$=Crey}1b; noc^{Sco}/CyO	BSC 766	Staber *et al.* 2011
w^1		BSC 145	Staber *et al.* 2011
w^{1118}		BSC 3605	Staber *et al.* 2011
Balancer Stocks			
w; TM3 *sb* /TM6 *tb*		B. Ganetzky	
+; $CyO^{lt\ dp\ pr\ cn}$ /Sco		B. Ganetzky	
w: $CyO^{\ cn\ bw\ Roi}$ /Sco		B. Ganetzky	
SD Stocks			
SD-5	Strong distortion phenotype and contains *Sd, E(SD), Rsp^i, M(SD)*and *St(SD) as well as two paracentric inversions on 2R.*	B. Ganetzky	*Sandler and Hiraizumi 1959; Sandler et al. 1959*
*SD-5**	Uncharacterized derivative of *SD-5** which exhibits an intermediate level of distortion	B. Ganetzky	
SD-72	Strong distorter with a both pericentric and paracentric inversions	B. Ganetzky	Sandler and Hiraizumi 1959)
SD-Mad lt cn	Derived from the original *SD-Mad* by recombination with chromosomes carrying the recessive markers *cn, lt*	B. Ganetzky	R.G. Temin 1979
SD-Mad bw^3	Derived from the original *SD-Mad* by recombination with chromosomes carrying the recessive markers *bw^3*	B. Ganetzky	R.G. Temin 1979
SD-Roma	Inversion free moderately distorting SD chromosome isolated in Italy	B. Ganetzky	Nicoletti and Trippa 1967)
SD-Los Arrenos	Weak distorter	B. Ganetzky	
Rsp^S cn bw	[*Sd^+, $E(SD)^+$, Rsp^S*] standard Rsp sensitive chromosome	B. Ganetzky	Lyttle 1991
Rsp^{i16} cn bw	[*Sd^+ $E(SD)^+$ Rsp^i*] Radiation-induced derivative of the Rsps cn bw chromosome where the Rsp locus has	B. Ganetzky	Ganetzky 1977

	been completely deleted		
Rsp^{SS} lt pk cn	[*Sd^{+} E(SD)$^{+}$ Rsp^{SS}*] the canonical RspSS chromosome	B. Ganetzky	Lyttle 1991
RNAi Mutants			
aub^{QC42}cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
aub^{HN2} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
aub^{HM23} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
aub^{AHN56} cn bw/CyO	EMS: Strong allele, has secondary mutation	T. Schüpbach	Schupbach and Wieschaus 1991
aub^{AHE13} cn bw/CyO	EMS: Strong allele, has secondary mutation	T. Schüpbach	Schupbach and Wieschaus 1991
zuc^{HM27} cn bw/CyO	EMS: Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
zuc^{SG63,rec2} pr c px sp/CyO	EMS: homozygotes poorly viable	T. Schüpbach	Schupbach and Wieschaus 1991
squ^{PP32} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
squ^{HE47} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
cuff^{WM25} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
cuff^{QQ37} cn bw/CyO	EMS; Strong allele	T. Schüpbach	Schupbach and Wieschaus 1991
w^{1}; aub^{N11}/CyO	110bp deletion	P. Macdonald	Harris and Macdonald 2001
piwi^{06843} cn /CyO	P{PZ} in first exon	BSC 12225	Cox et al 1998
nosGAL4, Aub-GFP	UAS-Aubergine-GFP recombined on to the same chromosome as nos-GAL4 VP16	P. Macdonald	Harris and Macdonald 2001

Table S2 Primer sequences used in this study

Name	Sequence
Cloning Primers	
AUBarm1-F *Bsi*WI	TCGTACGCTCTCCATGTAGCGAAAAGCGTATAG
AUBarm1-R *Asc*I	TGGCGCGCCAATGCATATATTCGTATGAAATGAGC
AUBarm2-F *Acc*65I	TGGTACCTTCCAGCAACGGAACTTTATAGAC
AUBarm2-R *Not*I	TGCGGCCGCTGGTTACGAAGAGTCGTGCTGGCG
Sequencing Primers	
AUBarm1-s1	GTGACAGTCGCTGCCATCGTATTATTGG
AUBarm1-s2	CTGACAAGTGGACTGTCTGCAGTGGGTG
AUBarm1-s3	CTTTATATCGAAGGGTAAGTACATG
AUBarm1-s4	GACTCGAACGATGAAGAAACAACACCAGCG
AUBarm2-s1	GTAGCGAGAATTAATGCGCTTGGATAC
AUBarm2-s2	GTGTCACCACCTGCGATGGCACCGGTC
AUBarm2-s3	CCGGTGGCAACACGCGTGCTGGAATCTC
AUBarm2-s4	CGATTGAAAGTCGACATCGTCAATGCG
aub arm1-RS1	GGGCAACTCAAAAAGTGGTAACAAG
aub arm2-RS1	GATATATGTATGTAGATATGTACATC
AUBarm1-R3	CTTGTTTATTTACATGTAAGTACTGTCC
AUBarm1-R4	CCTGGTCAACCCCTTAAATGCAGATGC
AUBarm1-R5	GCTTAGTAAATAAGTTAACACAATTTAC
AUB HN1 VR	CCGCAACGGCACTTACTCCCAAGCG
Mutagenic Primers	
AUB HN m1 F	GATGGGAGCTCCCTGGTAGGTAGTCATCCCCCTCCACGGTCTGA
AUB HN m1 R	TCAGACCGTGGAGGGGGATGACTACCTACCAGGGAGCTCCCATC
aub E721A R	GGTCAGCTCTACCAGGTGGTAAACAGCGCGGTGAACACCCTAAAGGACAGG
aub E721A F	CCTGTCCTTTAGGGTGTTCACCGCGCTGTTTACCACCTGGTAGAGCTGACC
Arm Specific Validation Primers	
AUBarm2-V1	CTTGTATGAACATAAAGGGATCC
AUBarm2-V2	CGTCGATTTTACGCCTGATGTGG
AUBarm2-V3	GGCACTCATATTACCGTGCAGGC
AUBarm1-V1	GGTTTATAATTCCACGGACTTC
AUBarm1-V2	CCATAGCGAATGTAGTGTG
AUBarm1-V3	CCCGGACCATCGCAAAGTAAACTGC
AUBarm2-VR2	CGGTGAACATGGCGTGCGCCCTGAGG
AUBarm1-R3	CTTGTTTATTTACATGTAAGTACTGTCC
AUBarm1-R4	CCTGGTCAACCCCTTAAATGCAGATGC
AUBarm1-R5	GCTTAGTAAATAAGTTAACACAATTTAC

p[W25.2] Specific Validation Primers	
pW-Not 1	CACTGTTCACGTCGCACTCGAGGGTAC
pW-Not 2	GCACTCGAGAGCTCGTTACAGTCCG
pW-Bsi 1	CGCACCGGACTGTAACGAGCTAC
pW-Bsi 2	GGCGACTCAACGCAGATGCCGTACC
pW-Asc 1	GTATGCTATACGAAGTTATCTAGACTAGTCTAGGGCG
pW-Asc 2	GCTTGGCTGCAGGTCGACTCTAGAGG
pW-Asc 3	CGATCATTCATTATTCGCTGCATGAATTAGC
pW-Acc 1	CATTATACGAAGTTATCTAGACTAGTCTAGGGTAC
pW-Acc 2	GACGCTCCGTCGACGAAGCGCCTC
pW-Acc 3	GCTCAGCTTGCTTCGCGATGTGTTCAC
WTPR	CGCGAACATTCGAGGCGCGCTCTCTCG
Wt SQ10F	GTGACCTGTTCGGAGTGATTAGCG
Southern Blotting	
SP6	GCCAAGCTATTTAGGTGACACTATAG
T7	GAATTGTAATACGACTCACTATAGGG
Rsp13 clone sequence	GGAGCTCCACCGCGGTGGCGGCCGGCCCTGCAGATCTGCGGCCGCTCTAGAAGGTGTCTTCTGTTCGCCT GGTACTTGAAATCGAAAAATCACTCATTTGACCGCTAAAATGACATAACTTAGTCAATTTATTGTTTTTGTG TACCAGGTTTAAATAATCTGTAGAAGGTATCTTCTGTTTGTCTGGTACTTGAAATCGGAAAATCACTCATTT TGACCGCTTAAAATGTAAAACTTAGGCAATTTACTGTTTTTCCTTACCAGTTGAACAGAATCTCTAGAAGG TGTCTTCTGTTCGCCTGGTACTTGAAATCGAAAAATCACTCATTTGACCGCTAAAATGACATAACTTAGTCA ATTTATTGTTTTTGTGTACCAGGTTTAAATAATCTGTAGAAGGTATCTTCTGTTTGTCTGGTACTTGAAATC GGAAAATCACTCATTTTGACCGCTTAAAATGTAAAACTTAGGCAATTTACTGTTTTTCCTTACCAGTTGAAC AGAATCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACC TCGAGGGGGGGCCCGGTACCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATG GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC