**Supplementary Figure S1. Structure of the *Drosophila melanogaster mip120* locus.** A schematic diagram of *mip120* region was generated using the JBrowse viewer in FlyBase [http://flybase.org/reports/FBgn0033846.html]. Boxes indicate exons. Purple shading indicates open reading frames. Nucleotide numbers for chromosome arm 2R are shown above. The black bar below indicates the extent of the deletion in *mip120^{67}*. The large upward arrow indicates the location of the piggyBac transposon insertion in *mip120^{LL07629}*.
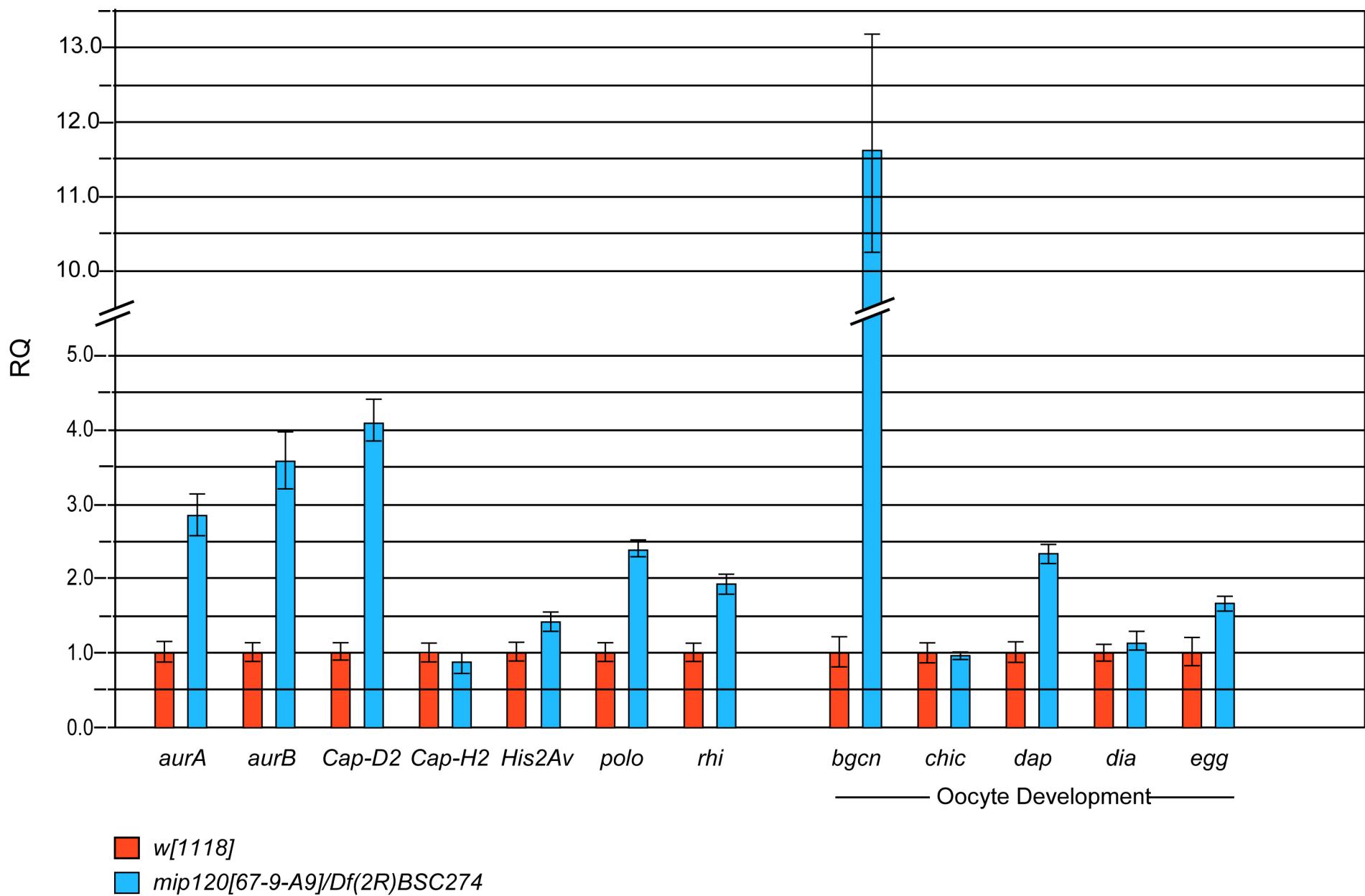
Supplementary Figure S2. Alterations in gene expression in *mip120* null ovaries. Ovaries from *mip120^WT* control (*w^1118*) and *mip120^67-9a-9* / *Df(2R)BSC274* mutant females were dissected and qPCR was used to quantitate RNA levels the indicated genes. The five genes marked as "Oocyte Development" were identified from a bioinformatics screen for promoter occupancy by Mip120 but not Myb, followed by a DAVID search for "gamete generation" or "oogenesis". Errors bars indicate RQ min and RQ max values for three technical replicates.

Table S1. Identification and rescue of a new *mip120* mutant allele.

Test crosses mated *mip120^{LL07629}, Cy+/ CyO* virgin parental females
with the parental males indicated below.

	males	males	females	females	males	males	females	females		
	Cy$^+$	*Cy$^+$*	*Cy$^+$*	*Cy$^+$*	*Cy*	*Cy*	*Cy*	*Cy*		
	Ser$^+$	*Ser*	*Ser$^+$*	*Ser*	*Ser$^+$*	*Ser*	*Ser$^+$*	*Ser*	Escapers	Rescued
Parental Males	F1	F1	F1	F1	F1	F1	F1	F1	NA	NA
Df(2R)BSC274 / CyO	0	NA	4	NA	13	NA	30	NA	9%	NA
mip120$^{67-9-A9}$ / CyO,ActGFP	0	NA	6 *	NA	75	NA	83	NA	4%	NA
mip120^{67-9-A} / CyO; P{Cherry-mip120^{WT}} / TM3,Ser,ActGFP	19	0	16 **	1	54	23	37	38	1%	19%

NA = not applicable   * Sterile

                                            **Fertile

Escapers may be overestimated because of incomplete expressivity of *Cy*.

Expected rescue in the cross in the bottom row is 20% of <u>viable</u> progeny as shown below.

Parents: *mip120^{LL07629}/ CyO   x   mip120$^{67-9-A9}$ / CyO; P{Cherry-mip120^{WT}} / TM3,Ser,ActGFP*

mip120^{LL0762}/ mip120$^{67-9-9A}$

↗ *P{Cherry-mip120^{WT}} / +* (12.5% => viable)

↘ *TM3,Ser,ActGFP / +* (12.5% => dead)
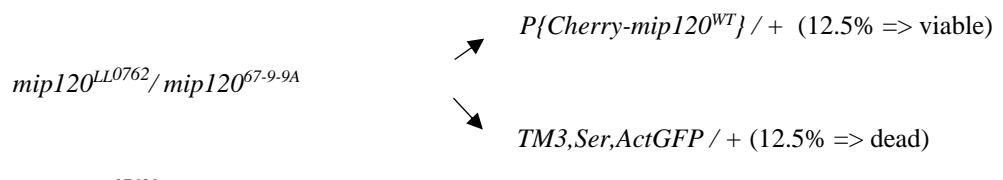
mip120^{LL07629}/ CyO (25% => viable)

mip120$^{67-9-A9}$ / CyO (25% => viable)

CyO/ CyO (25% => dead)

Expected rescue offspring among <u>viable</u> progeny = 12.5% / (12.5% + 25% + 25%) = 20%

Table S2. Predicted Protein Size and Extent of Mip120 Mutants

Protein	Predicted MW	Amino Acids of Mip120
Mip120	100,020	1-950
mCherry-Mip120-WT	126,965	1-950
mCherry-Mip120-N-Term	84,545	1-570
mCherry-Mip120-C-Term	69,383	571-950
mCherry-Mip120-CXC	42,847	727-860
mCherry-Mip120-HCH	36,885	865-950
Conserved CXC Domain	NA	738-848
Conserved HCH Domain	NA	885-930

Table S3

Gene Symbol	FlyBase ID	Sequence	Tm C	Product length	Intron Spanned
aTub84B_FWD	FBgn0003884	GCCTCATAGCCGGCAGTTCG	67	185bp	Exon1 - Exon2
aTub84B_REV		CTCCCAGCAGGCGTTTCCAA	67		
aurA_FWD	FBgn0000147	GCTCCGCACAGAATGCCAGA	67	210bp	Exon1 - Exon2
aurA_REV		CGGCACCATGGGTTTTTGGA	67		
aurB_FWD	FBgn0024227	ACGCCAACCGCAACCACCT	68	195bp	Exon1 - Exon2
aurB_REV		GCTCCCGCGCCAAGTAGACA	68		
bam_FWD	FBgn0000158	TCACCGGGCCAAAGCAGAAG	67	200bp	Exon1 - Exon2
bam_REV		AAGCCCAAATCGGCGGTCAG	67		
bam_FWD	FBgn0000158	CGGAAACTCGGGGAGCAATG	67	200bp	Exon2 - Exon3
bam_REV		CGGCACCGGACAAAAGGATG	67		
bgcn_FWD	FBgn0004581	AGAGCGCCAAGCCGGATTTC	68	190bp	Exon1 - Exon2
bgcn_REV		TCCTGCAGGCTGCCAGTGAG	68		
bgcn_FWD	FBgn0004581	GCTTCCGCACACCGTGGATT	68	200bp	Exon3 - Exon4
bgcn_REV		CTCCGCCGTAGCCTTGGACA	68		
Cap-D2_FWD	FBgn0039680	AGAAGCGTGCCAAGCCATCG	68	201bp	Exon2 - Exon3
Cap-D2_REV		CCATGCGAAGCGGCAAAAGT	68		
Cap-H2_REV	FBgn0037831	GAACCCGGCTCCCCCTGTAG	67	202bp	Exon6 - Exon7
Cap-H2_REV		TGGCGCTCGCGTCAGTTAAA	67		
chic_FWD	FBgn0000308	CCGCTTGTCGACGGTCACTC	66	223bp	Exon1 - Exon2
chic_REV		TGTTTGTCGTGGGTGCGGATT	66		
dia_FWD	FBgn0011202	CGGGCGTGGAGGACTTTGAG	67	201bp	Exon1 - Exon2
dia_REV		TTGGCGCTACGCTCCAGTGA	67		
dap_FWD	FBgn0010316	TGGCATGCGGTCGTCAGTTG	67	200bp	Exon1 - Exon2
dap_REV		GCTGACGCGCTCCCAAATGT	67		
egg_FWD	FBgn0086908	CGTGTCCGGTGGCACACAAA	67	202bp	Exon3 - Exon4
egg_REV		TTTCCGTTGATGGCGGTGCT	67		
Gapdh2_FWD	FBgn0001092	GGCGCTGCCCAGAACATCAT	67	201bp	Exon2 - Exon2
Gapdh2_REV		GTTGGCGGCCTCCTGAACCT	67		
His2Av_FWD	FBgn0001197	TGGCGGTAAAGCAGGCAAGG	66	190bp	Exon2 - Exon3
His2Av_REV		CTCGGCGGTCAGGTATTCCAA	66		
mip120_FWD	FBgn0033846	AGCATTGTGCCGCTGCCTTC	68	188bp	Exon2 - Exon3
mip120_REV		CTGCTGACCGAGGCCGATTG	68		
polo_FWD	FBgn0003124	TCGCCGGCAAGATCGTATCC	66	228bp	Exon2 - Exon3
polo_REV		AGCGGCATTCGAACTCCGTAA	66		
rhi_FWD	FBgn0004400	TGGAGCGGTTTTCCGAACGA	68	193bp	Exon1 - Exon1
rhi_REV		AGCTGCTGGGGCCATTCTCG	68		
tomB_FWD	FBgn0031715	CAACATGCCATCGCCCAAGA	67	206bp	Exon1 - Exon2
tomB_REV		CCACCAACTCGCGCACCTCT	67		
tut_FWD	FBgn0052364	CCGCGGTGGATTGTGGAAGT	67	200bp	Exon2 - Exon3
tut_REV		TCGCGATTGTTGGTCGATGG	67		
tut_FWD	FBgn0052364	GGCCAGCGAACTGGGTGAAG	68	186bp	Exon2 - Exon3
tut_REV		TCGCGATTGTTGGTCGATGG	68		