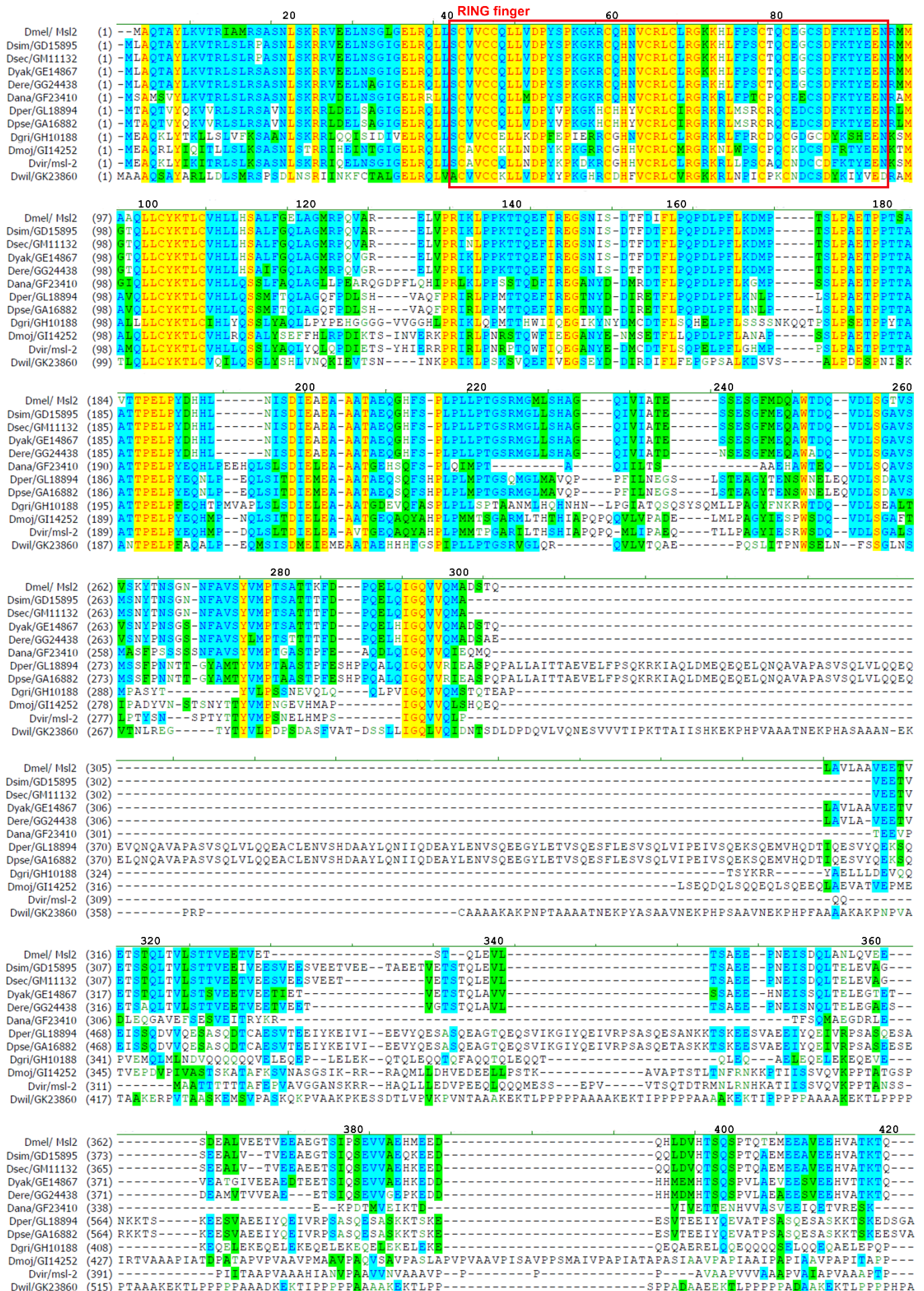


Supplementary Figures



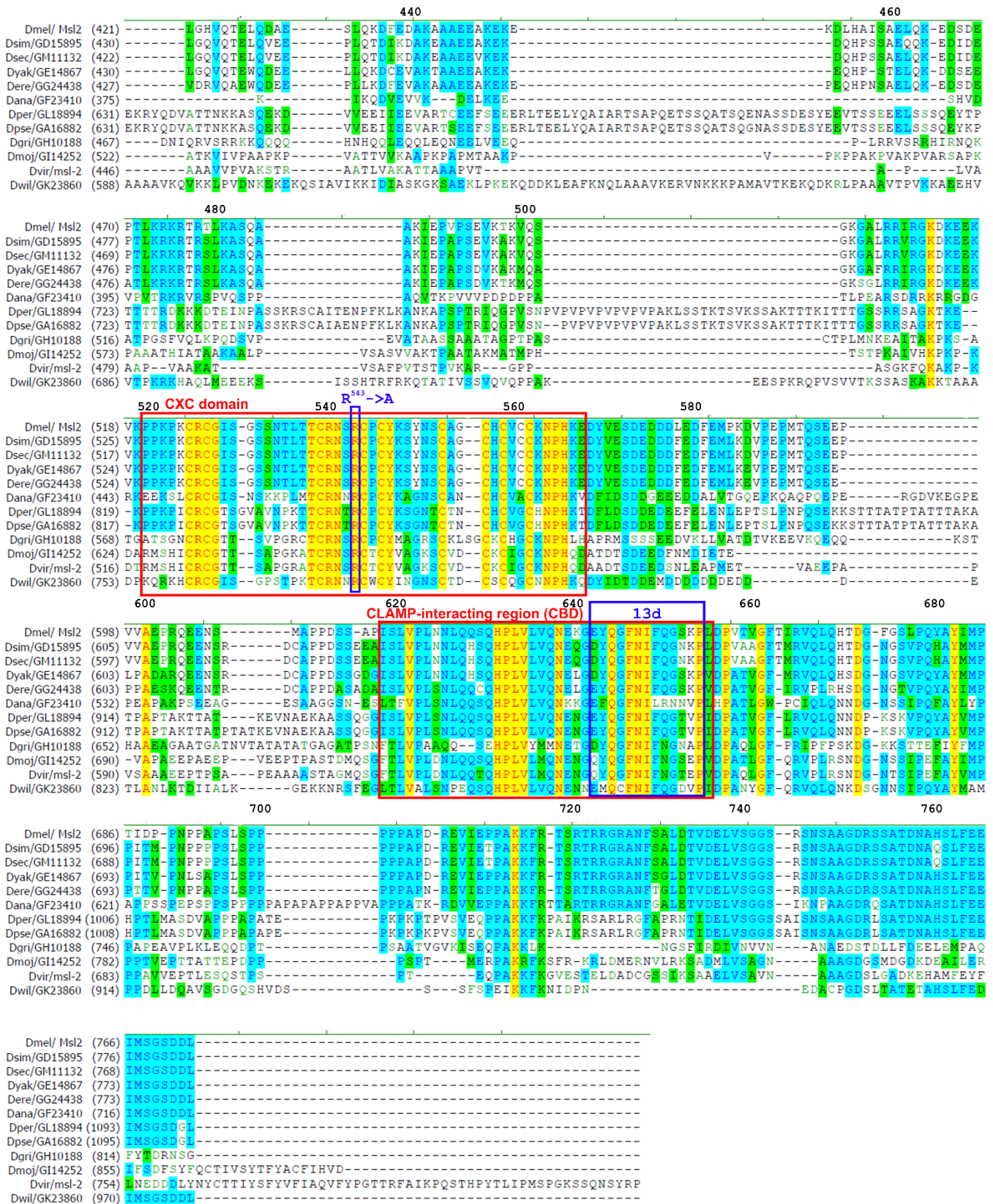


Figure S1. Alignment of MSL2 protein among Drosophilidae. Different regions are shown in the red frames. Also R543 amino acid residue and minimal 13 aa CLAMP-interacting region are marked in blue frames.

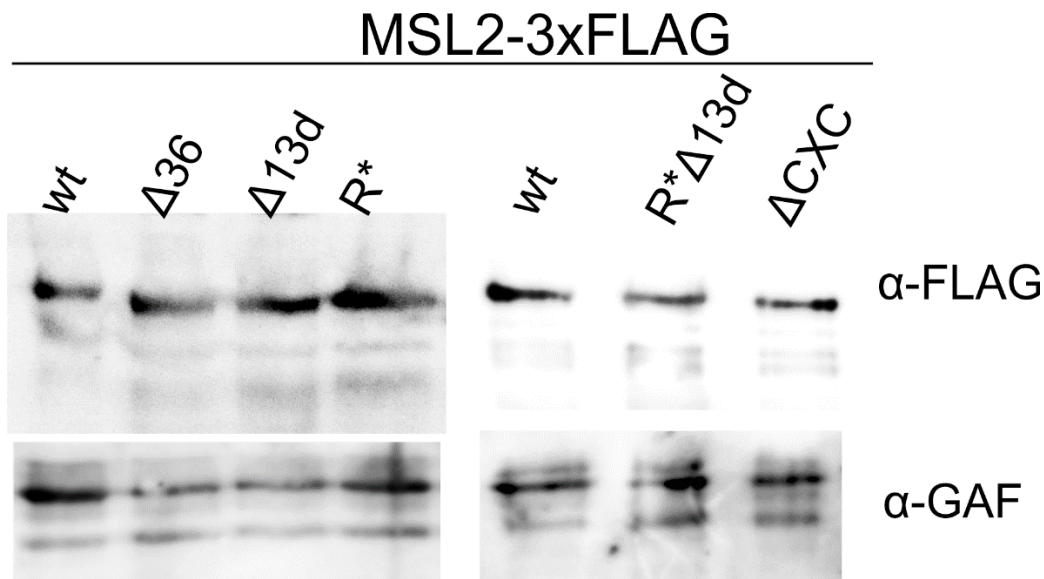


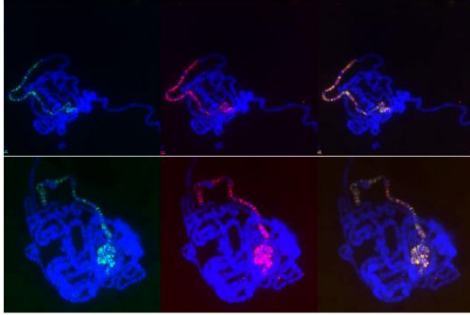
Figure S2.

Western blotting of protein extracts prepared from adult flies expressing different variants of 3xFLAG-tagged MSL2 protein (wild-type (wt), deletion of 36 ($\Delta 36$) and 13 ($\Delta 13d$) aa from CLAMP-binding region, substitution of arginine at the 543 position by alanine (R*), simultaneous substitution of arginine at the 543 position by alanine and deletion of 13 aa from CLAMP-binding region (R* $\Delta 13d$), deletion of CXC domain (ΔCXC)). Immunoblot analysis was performed with FLAG and GAF antibodies (internal control).

♂ *msl2²²⁷*

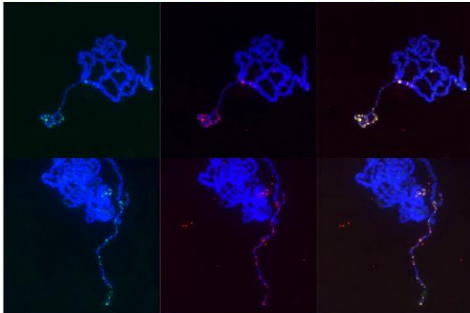
MSL2^{wt}-3xFLAG

FLAG MSL1 merged



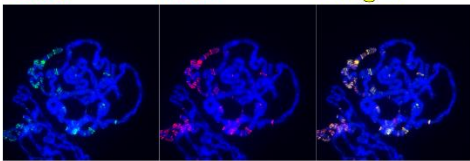
MSL2^{Δ13d}-3xFLAG

FLAG MSL1 merged



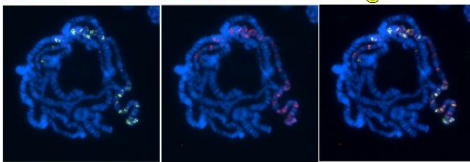
MSL2^{R*}-3xFLAG

FLAG MSL1 merged



MSL2^{ΔCXC}-3xFLAG

FLAG MSL1 merged



MSL2^{R*Δ13d}-3xFLAG

FLAG MSL1 merged

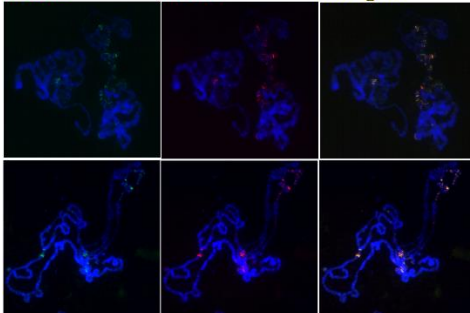
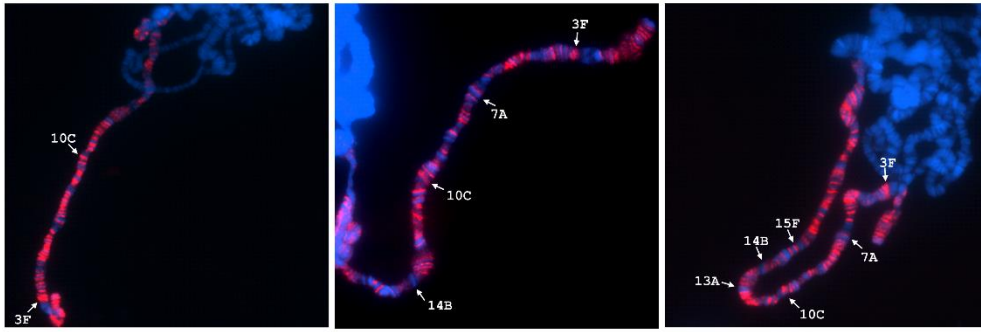


Figure S3. MSL1 and MSL2 localization on the polytene chromosomes from salivary glands of male 3rd instar larvae in the *msl2*-null (*msl2²²⁷*) background that express different FLAG-tagged variants of MSL2 protein: wild-type (wt), deletion of 13 aa from CLAMP-binding region ($\Delta 13d$), substitution of arginine at the 543 position by alanine (R*), deletion of CXC domain

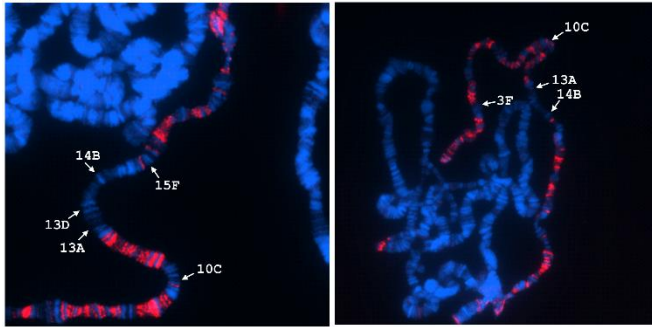
(Δ CXC), simultaneous substitution of arginine at the 543 position by alanine and deletion of 13 aa from CLAMP-binding region (R* Δ 13d). Panels show immunostaining of 3xFLAG-MSL2 protein with mouse anti-FLAG antibody (green) and MSL1 protein with corresponding rabbit antibody (red) on polytene chromosomes. DNA is stained with DAPI (blue).

♂ *msl2*²²⁷

MSL2^{wt}-3xFLAG

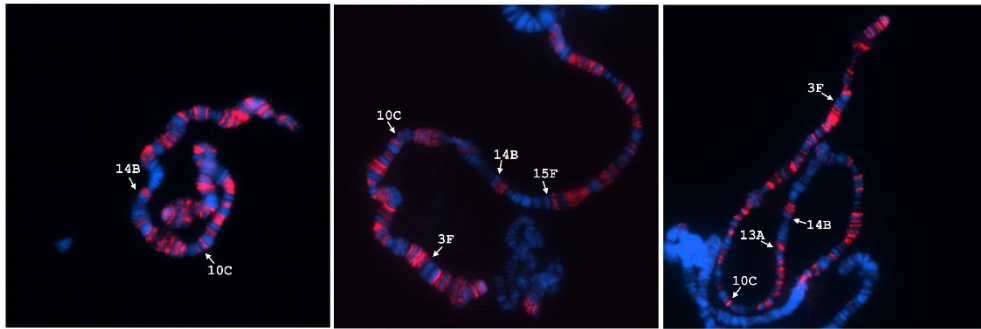


MSL2^{Δ13d}-3xFLAG

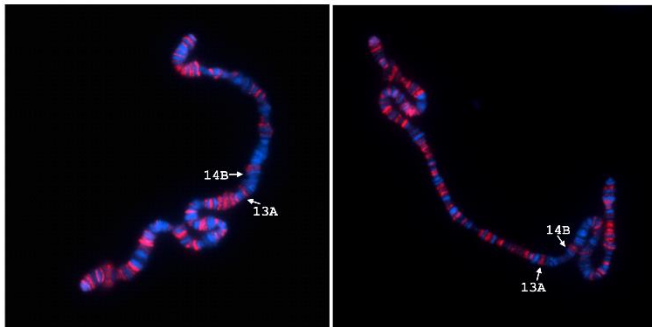


MSL2
DAPI

MSL2^{R+}-3xFLAG



MSL2^{ΔCXC}-3xFLAG



MSL2^{R+Δ13d}-3xFLAG

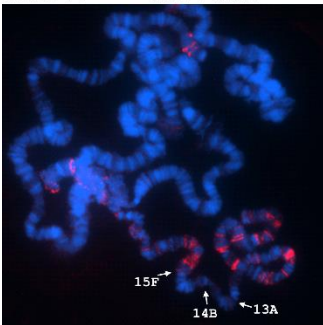


Figure S4. Comparing several sites of MSL complex binding at the high resolution cytological map on the polytene chromosomes from salivary glands of male 3rd instar larvae in the *msl2*-null (*msl2*²²⁷) background that expressed different FLAG-tagged variants of MSL2 protein: wild-

type (wt), deletion of 13 aa from CLAMP-binding region (Δ 13d), substitution of arginine at the 543 position by alanine (R*), deletion of CXC domain (Δ CXC), simultaneous substitution of arginine at the 543 position by alanine and deletion of 13 aa from CLAMP-binding region (R* Δ 13d). Panels show immunostaining of 3xFLAG-MSL2 protein with rabbit anti-MSL2 antibody (red) on polytene chromosomes. DNA is stained with DAPI (blue).

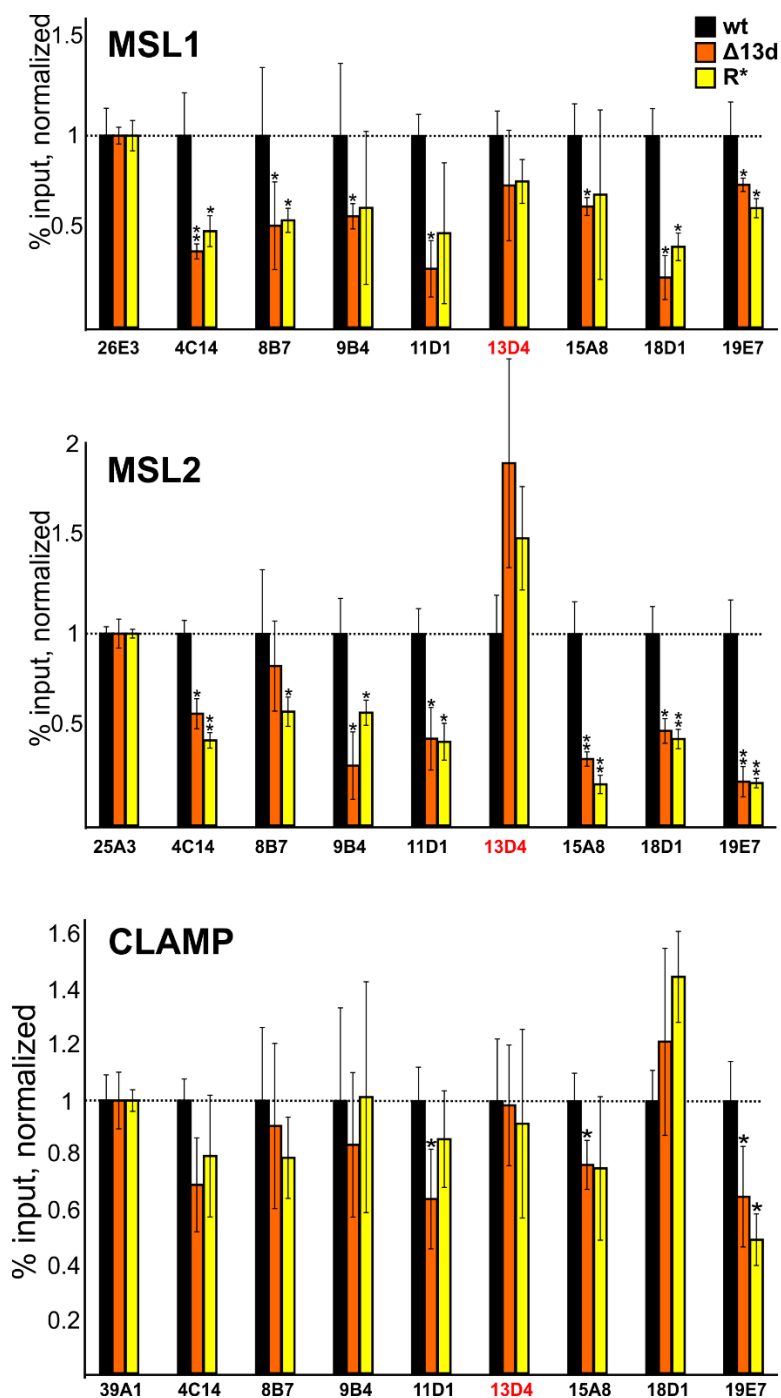


Figure S5. Comparing binding of MSL1, MSL2, and CLAMP at different CES and PionX (marked with red) regions in the MSL2-expressing males in the *msl2* ^{γ 227} background. Histograms show ChIP enrichments at the CES regions on chromatin isolated from male flies expressing different variants (wt, $\Delta 13d$, R*) of MSL2 protein. The results are presented as a percentage of input genomic DNA normalized to corresponding positive autosomal genome regions for MSL1(26E3) and MSL2 (25A3), and compared with binding levels in the flies with expressed wild type MSL2 protein (corresponding to the “1” on the scale). Error bars show standard deviations of quadruplicate PCR measurements for three independent experiments. Asterisks indicate significance levels: * $p < 0.05$, ** $p < 0.01$.

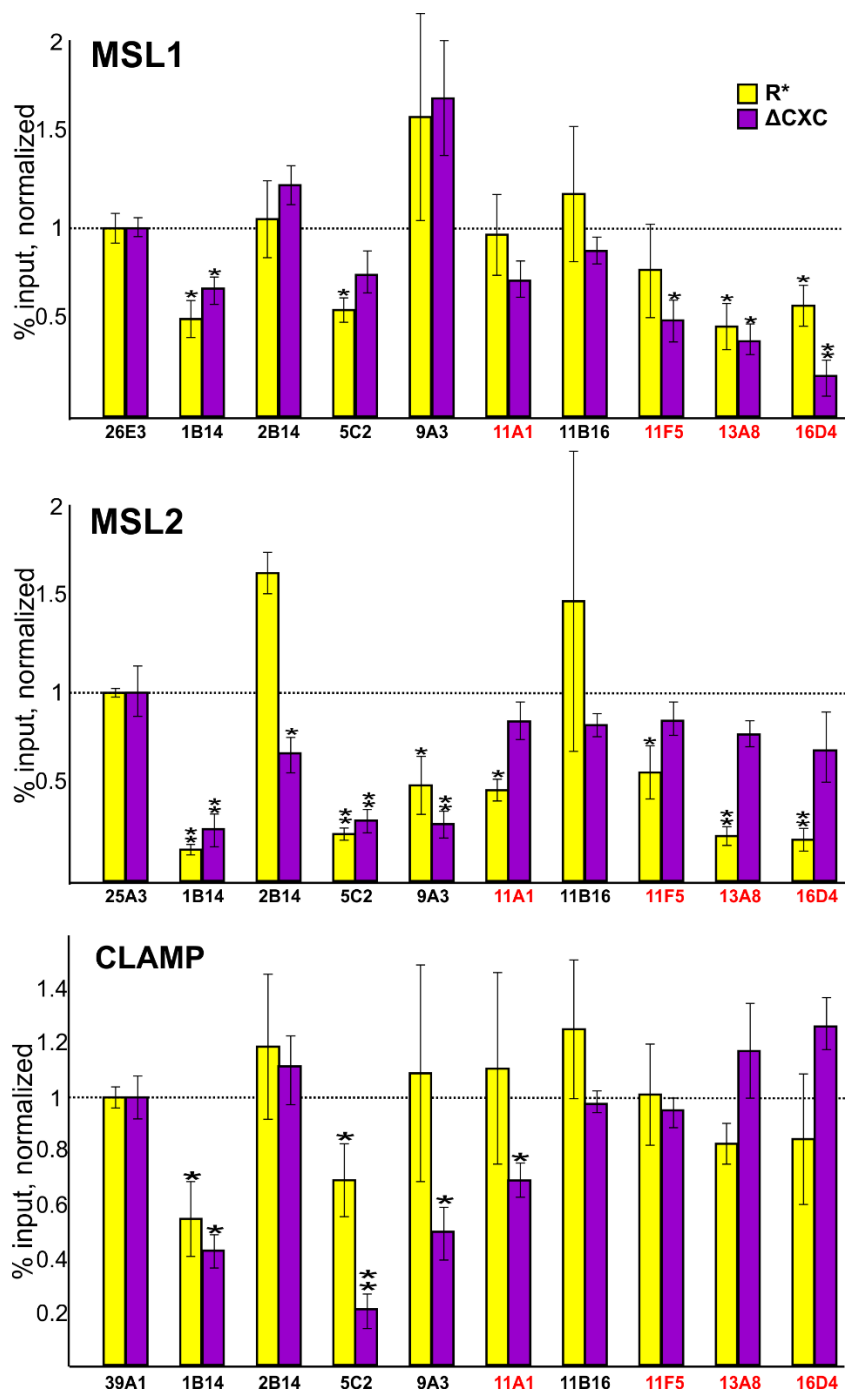


Figure S6. Comparing binding of MSL1, MSL2, and CLAMP at different CES and PionX (marked with red) regions in the MSL2-expressing flies in the *msl2*^{γ227} background. Histograms show comparison of ChIP enrichments at the CES regions on chromatin isolated from male flies expressed MSL2 protein with substitution of arginine at the 543 position by alanine (R*) and deletion of CXC domain (ΔCXC). The results are presented as a percentage of input genomic DNA normalized to corresponding positive autosomal genome regions for MSL1(26E3), MSL2 (25A3) and CLAMP (39A1), and compared with binding levels in the flies with expressed wild type MSL2 protein (corresponding to the “1” on the scale). Error bars show standard deviations of quadruplicate PCR measurements for three independent experiments. Asterisks indicate significance levels: *p < 0.05, **p < 0.01.

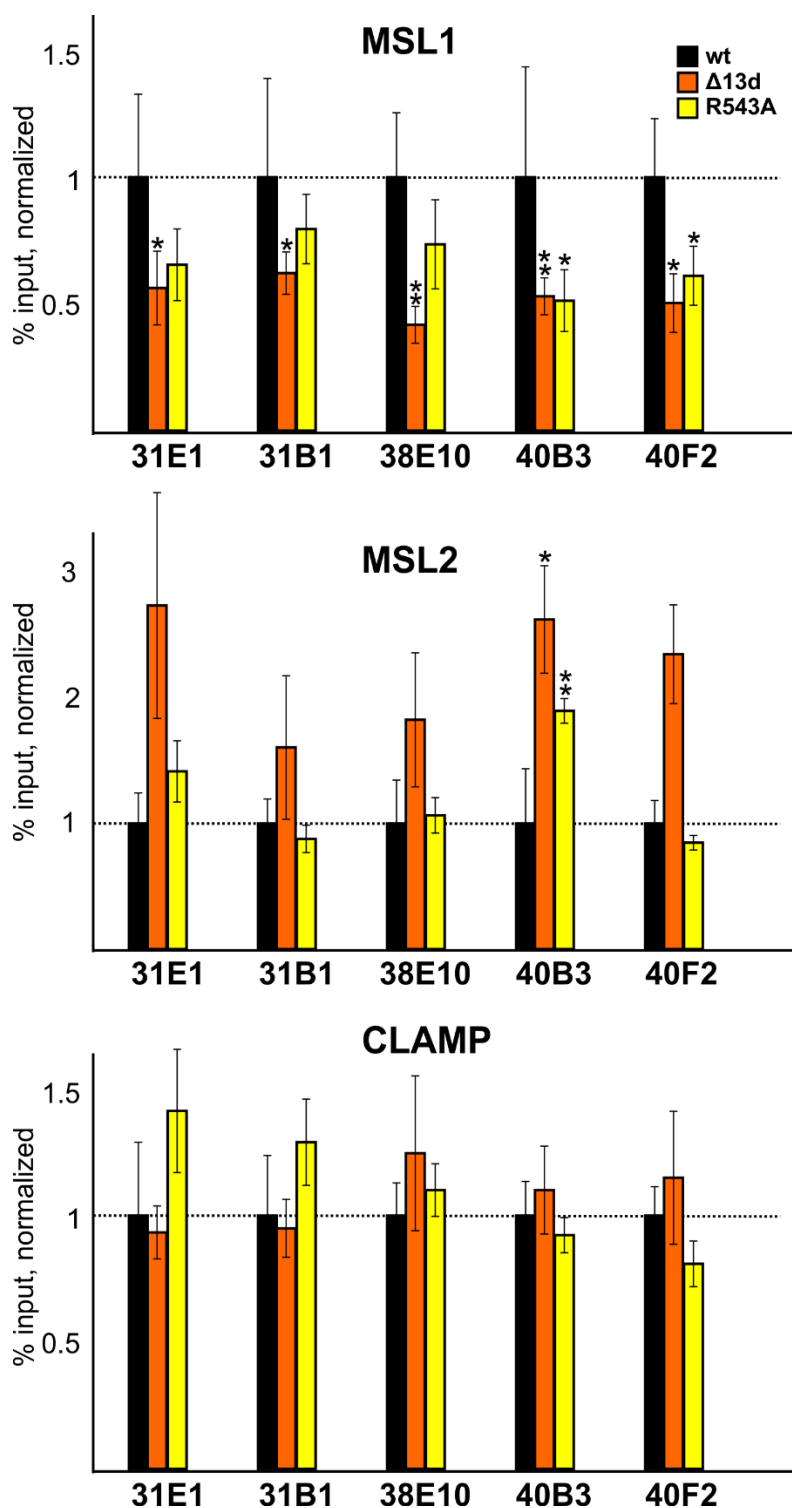


Figure S7. Comparing binding of MSL1, MSL2 and CLAMP at different autosomal genome regions in the MSL2-expressing flies in the *msl2^{γ227}* background. Histograms show ChIP enrichments at the CES regions on chromatin isolated from male flies expressing different variants (wt, $\Delta 13d$, R543A) of MSL2 protein. The results are presented as a percentage of input genomic DNA normalized to corresponding positive autosomal genome regions for MSL1(26E3), MSL2 (25A3), and compared with binding levels in the flies with expressed wild type MSL2 protein (corresponding to the “1” on the scale). Error bars show standard deviations of quadruplicate PCR measurements for three independent experiments. Asterisks indicate significance levels: * $p < 0.05$, ** $p < 0.01$.

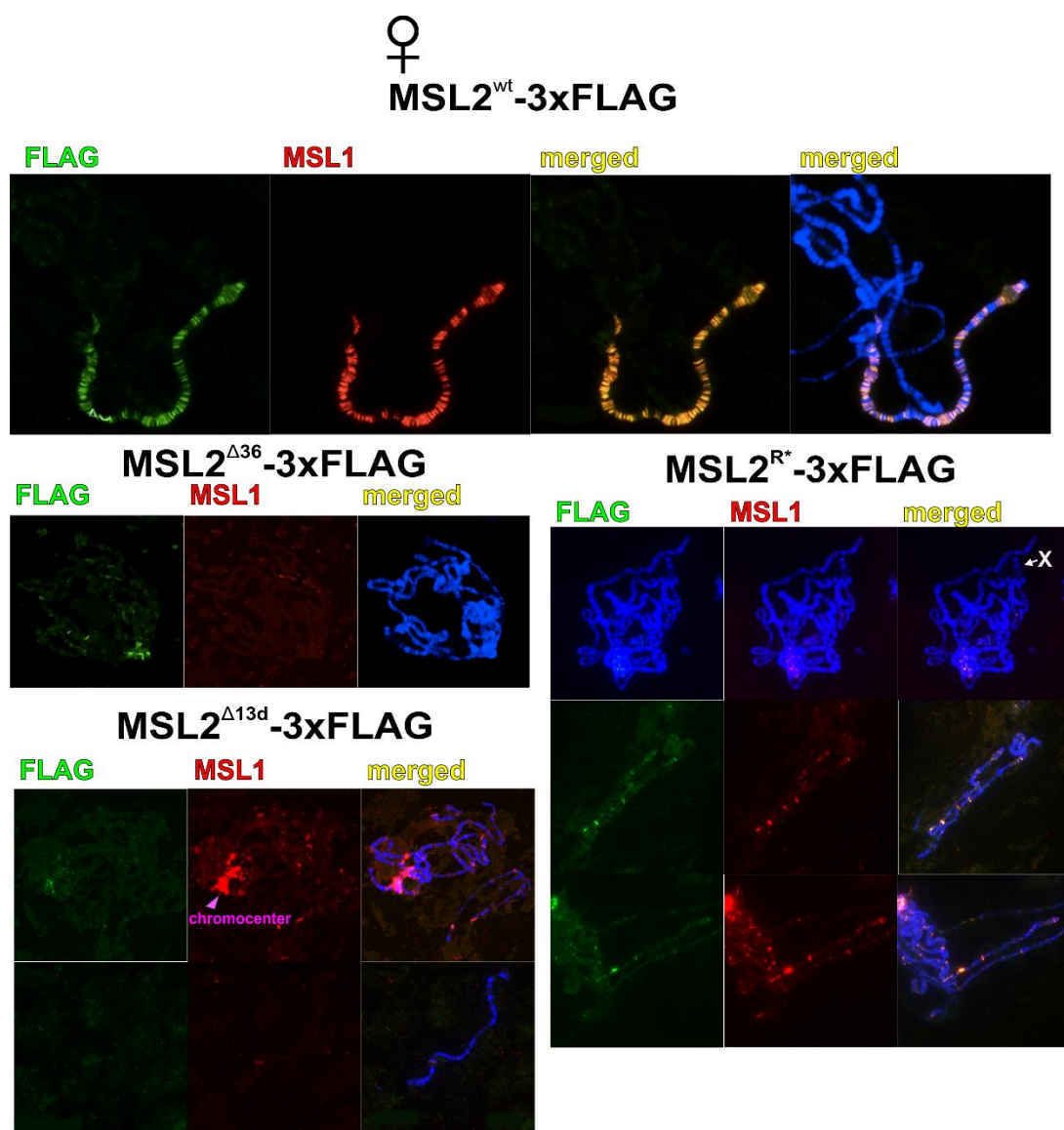


Figure S8. Distribution of MSL complex on the polytene chromosomes extracted from salivary glands of female 3rd instar larvae that express different FLAG-tagged variants of MSL2 protein: wild-type (wt), deletion of 36 ($\Delta 36$) and 13 ($\Delta 13d$) aa from CLAMP-binding region, substitution of arginine at the 543 position by alanine (R*). Panels show immunostaining of 3xFLAG-MSL2 protein with mouse anti-FLAG antibody (green) and MSL1 protein with corresponding rabbit antibody (red) on polytene chromosomes. DNA is stained with DAPI (blue).

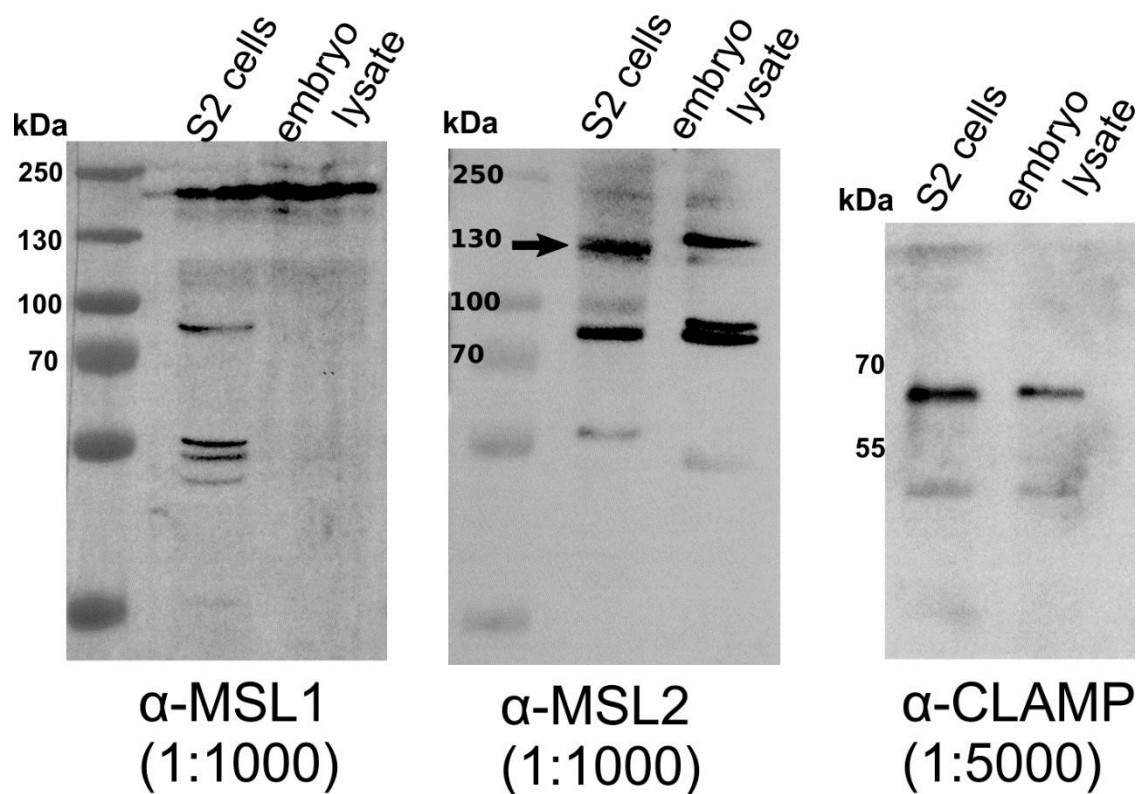


Figure S9. Immunoblot analysis of affinity-purified antibodies for MSL1, MSL2, CLAMP proteins.

Supplementary Table

Table S1. The list of used oligonucleotides.

Primers for cloning of <i>msl2</i> deletions			
Name	dir	rev	
<i>msl2</i> _full-sized	TTCGATATCATGGCCCAGACGGCATACTT	CCCGGGCAAGTCATCCGAGCCCGA	
<i>msl2</i> _d13	AAAGGCGAGGATCCGGTCACCGTTGG	GACCGGATCCTCGCCTTTCATTCT	
<i>msl2</i> _dB	CCACCGGCCCAACTTCTCGGCCCT	GAAGTTGGCGGCCGGTGGCTCGATGA	
<i>msl2</i> _dP	TATATAATGGCCAAGAAATTCAGGACC	TTTCTTGCCATTATATAAGCATACT	
Primers for RT-qPCR			
Name	dir	rev	Taqman probe
RoX1	CTTGTGCTTTCTCCTGAATGTG	TGTATTAGGCGGAGCTTCTTG	FAM-AGCCTATGAAATCCGGTCCAACCC-BHQ1
RoX2	TTCGAAACGTTCTCCGAAGC	AGTCGTACTCATCTCACTGTCC	FAM-AGCAAGAGTAACGATTTCGCGATAGTCG-BHQ1
RpL34	ACAACACACGCTCCAACA	GGGTGATACCCTTCAACTTCTC	FAM-TGGTAAACCAGACGACCACCGG-BHQ
Primers for ChIP analysis			
Genome region	dir	rev	
RoX1	AGGTCTGC AAGGTT CAGTTTAT	ATTCTTAAGGGTGGCGTCTTC	
RoX2	GGCTTAGAGAGAGATGGCAATAC	AGTTCTGGTACCCTGGA	
CES1B14	CAGGACAAGACTAGGACAAAAGG	GGTTTGGCGATTGAGGATTATTG	
CES2B14	CCCTCATATGCTTCTTCTGGTC	ACGTACGATCACGCACATATC	
CES4C14	ATTGGTATTCGGGCAAGGG	GAGCATATTTCTCTCGAGGATGG	
CES5C2	CAGAAATTCGAAGCGATCTCAAC	AATCGACTGCTAGGTTGGTAAA	
CES8B7	CAGCAGAACGCTCTTTGATTT	CCAACATTGCTTCACACAC	
CES9A3	TAATGCTGGATCTCGCTCAC	CTGATCGCCGGTCATAGAAA	
CES9B4	CGTGCCGCCTAACTATCTAAC	GGGATGAAAGAGAGAGCAAA	
CES11A1	GCCCGGAACCTCTTTAGTATG	TGATGCCACTGGATGAGTATG	
CES11B16	GGTGGTGGACATCTCGTTAAT	ACCAGCGAATATCGAGCATAAA	
CES11D1	AAGCCACTGATGCGTACAA	CAGAACGGCTGGCAAGATA	
CES11F5	TACAGTAGCTGAGAGCTGTACT	GTTTGGACTTGGCCTTTAC	
CES13A8	AATCTGAGCGAGATGGAAGAAC	GTGTCTAGTGGTTGGCTATGAC	
CES13D4	GCCGTGATTGTGGATCTCTT	CTCCAGACGTGCTGAATTGT	
CES15A8	CCAGGCTAAATAGTTCGC TACA	CGTAGTTGCATCTCGCTCTAAT	
CES16D4	CATCAACGACCTTGTACATTATC	GCACGAATCAGACAGAGAAGTA	
CES18D11	GCGCTTGCAATAGCTTCAATTA	GGAAATCCAAACAGTACAACCTCG	
CES19E7	GAGCGAGAGAGATTGCCAAATA	CGAATCGTGGAGTCTGAGAAAT	
26E3	CGTAACGGCACCCCTCAA	ACCGCACCGCACTACAAG	
25A3	GCTCCAGGAACCGATCTATTG	CTTGGCTTCCACTGAAGTTAGA	
39A1	CTCTGTTCACACAGCCATTTC	TACTCTTTCGGGCGGTATAA	
31E1	TGGATATGGCTTCTGGTTCATC	GGGCTGCATTCCGAGTTTA	
31B1	TTGTAAGGCGACTCGACTATTT	TGCTTTCGGCTGACTAATGA	
38E10	CGACACAAGTACCAGCTCTAAT	CGGCGAGGTAATTACCATATTC	
40B3	GCAGAAGGGGAACTGTGAAATA	CTTCGCGGAGGGTTAATTGT	
40F2	CAGAACAACGCTCAGAGATAGA	GGGCTCTAAGAAATCCTACCAG	

Table S2. Cloning procedures

Pull down assay			
	dir	rev	Restriction sites
TRX-His-MSL2 [573-708]	ttggaattcatggaggactacgttg	agtgtcgacctattccctgtcaggagca	EcoRI Sall
TRX-His-CLAMP [1-153]	ctggaattcatggaagaccttacaa	aacgtcgacttccccgtctgtatgcat	EcoRI Sall
TRX-His-CLAMP [40-153]	ctggaattcatgaaaacggagcagcagc	aacgtcgacttccccgtctgtatgcat	EcoRI Sall
TRX-His-CLAMP [86-153]	-	-	HincII Sall
TRX-His-CLAMP [116-153]	-	-	MunI Sall
GST-CLAMP [1-196]	tacccgggatggaagaccttacaaaaac	aacgtcgacagacacaatctgtatctgg	SmaI Sall
GST-MSL2 [573-708]	ttggaattcatggaggactacgttg	agtgtcgacctattccctgtcaggagca	EcoRI Sall
GST-MSL2 [618-642]	-	-	BamHI RsaI
GST-MSL2 [618-655]	-	-	BamHI DpnI
GST-MSL2 [618-667]	-	-	BamHI PvuII
GST-MSL2 [618-687]	-	-	BamHI MunI
GST-MSL2 [651-708]	cagggatccaagccctgatccggtc	agtgtcgacctattccctgtcaggagca	BamHI Sall
GST-MSL2 [630-655]	ctcgatccatgcagcatccttgggt	gtggaattcctaatacaaggggcttg	BamHI EcoRI
GST-MSL2 [641-655]	-	gtggaattcctaatacaaggggcttg	BamHI EcoRI
Fly constructs			
pSK msl2-Fx3 full	ttcgatatcatggcccagacggcactt	tctccgggcaagtcacccagcccga	EcoRV SmaI
pSK msl2-Fx3 Δ36	accgatatcatggaggcatggatctg	tggactagttaggcttatggggcagaa	EcoRV SpeI
	ctcactagtcttgatccggcaccgt	tctccgggcaagtcacccagcccga	SpeI SmaI
pSK msl2-Fx3 Δ13d	ttcgatatcatggcccagacggcactt	gaccggatcctgcctttctcattct	EcoRV SmaI
	aaaggcgaggatccggcaccgttgg	tctccgggcaagtcacccagcccga	
pSK msl2-Fx3 R543A	atcgaattccgcctgtcctt	tctccgggcaagtcacccagcccga	EcoRI SmaI
pSK msl2-Fx3 ΔCXC	ttcgatatcatggcccagacggcactt	cggattcttctcggcttcggaggct	EcoRV SmaI
	aagccgaagaagaatccgcacaagga	cccgggcaagtcacccagcccga	
pSK msl2-Fx3 R543A ΔCXC	atcgaattccgcctgtcctt	tctccgggcaagtcacccagcccga	EcoRI SmaI
yil Ubi msl2-Fx3 full attB	-	-	EcoRV NotI
yil Ubi msl2-Fx3 Δ36 attB	-	-	EcoRV NotI
yil Ubi msl2-Fx3 Δ13d attB	-	-	EcoRV NotI
yil Ubi msl2-Fx3 R543A attB	-	-	EcoRV NotI
yil Ubi msl2-Fx3 ΔCXC attB	-	-	EcoRV NotI
yil Ubi msl2-Fx3 R543A ΔCXC attB	-	-	EcoRV NotI