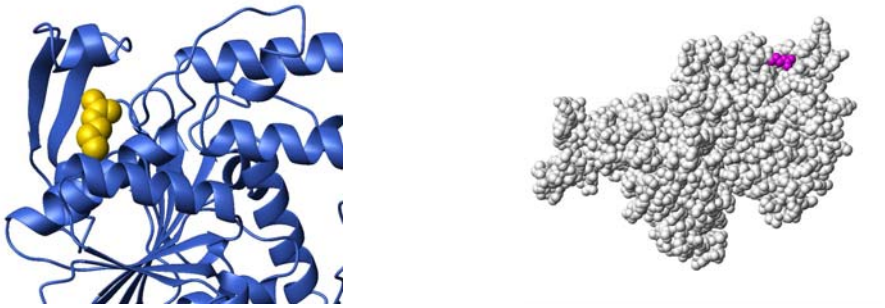
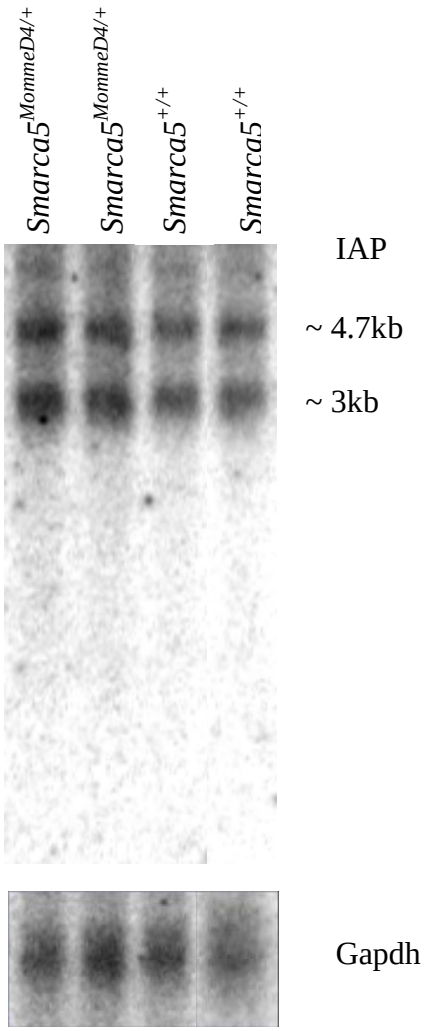
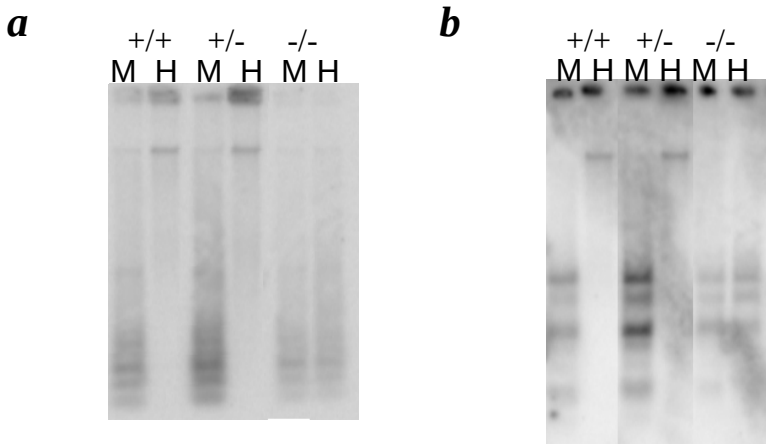
a ***b***



Supplementary Figure 1. Homology model of mut-snf2h. a. Ribbon representation showing the sidechain of Arg520 in yellow. **b**. CPK representation showing the sidechain of Arg520 in magenta on the surface of the molecule.

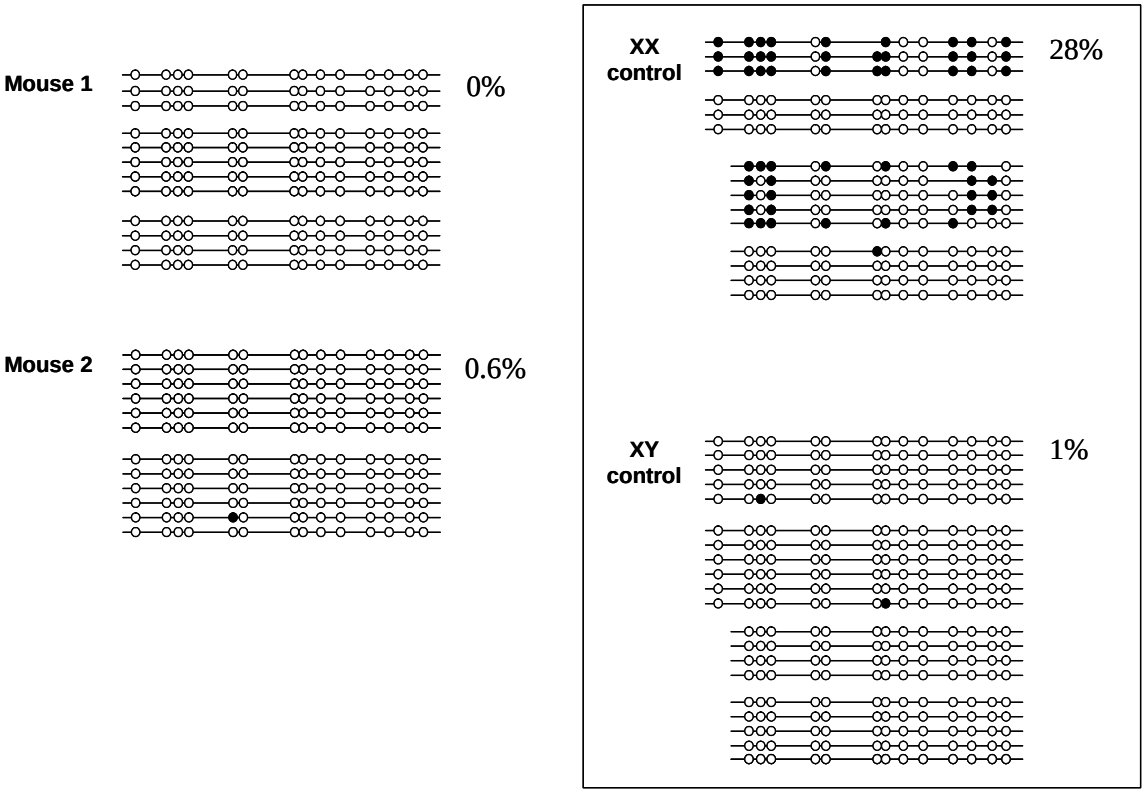


Supplementary Figure 2. Northern analysis of IAP RNA in *Smarca5*$^{Momme\ D4/+}$ testes. No abnormal IAP mRNA transcripts were detected in *Smarca5*$^{Momme\ D4/+}$testes.

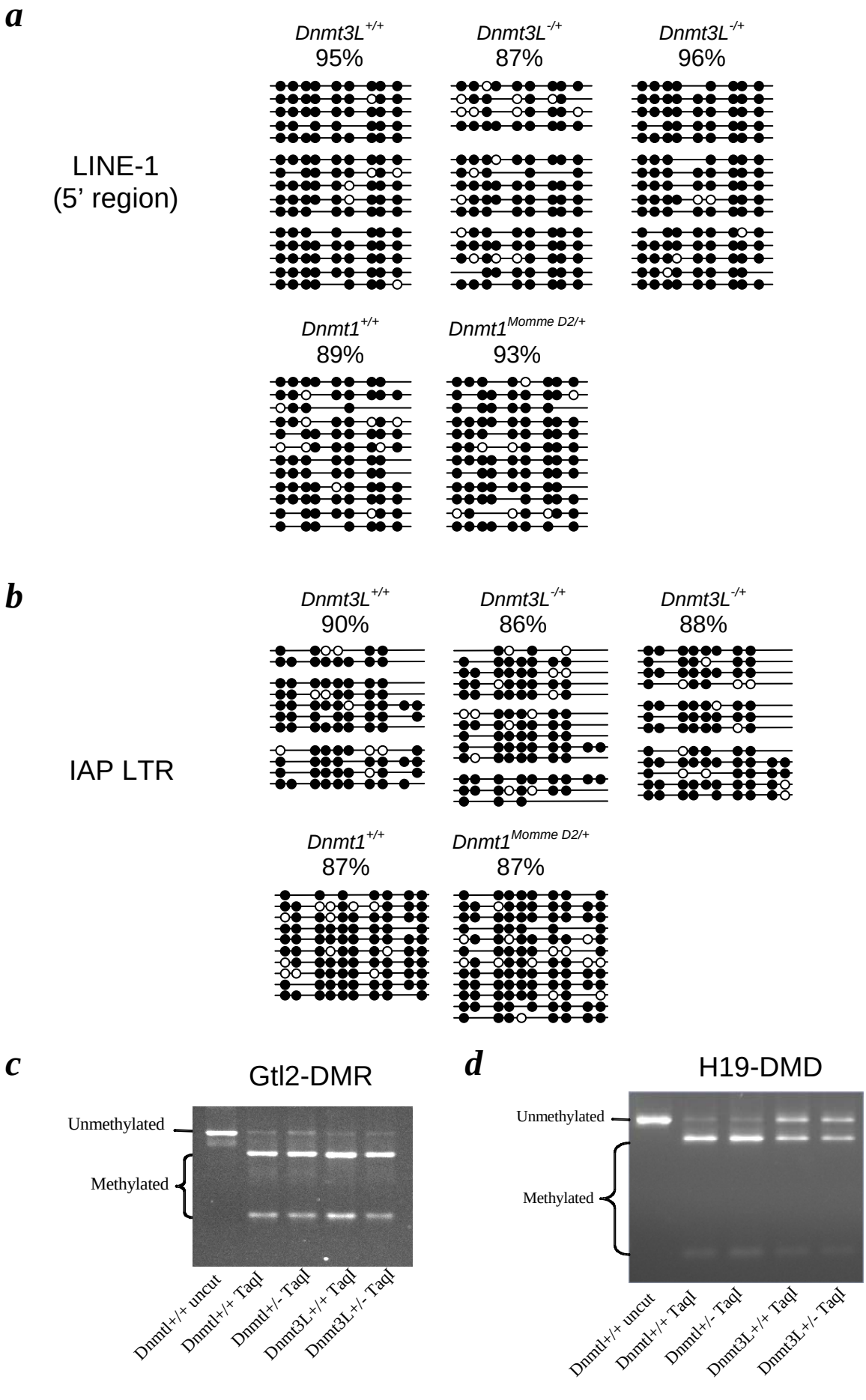


Supplementary Figure 3. DNA methylation analysis of repeats in *Dnmt1*^{MommeD2} embryos . DNA from *Dnmt1*^{MommeD2} wildtype, heterozygous and homozygous embryos (8.5 dpc) were digested with HpaII (H) and MspI (M) and hybridised with **a.** a probe for minor satellite DNA and **b.** a probe for an IAP retrotransposon.

Mtm1



Supplementary Figure 4. Methylation at the *Mtm1* CpG island in Mouse 1 and Mouse 2. Mouse 1 and Mouse 2 are two of the three female mice which displayed no methylation at the X-linked *Hprt* gene (see Figure 5). No DNA was available from Mouse 3.



Supplementary Figure 5. Methylation analysis of DNA from the sperm of *Dnmt1*$^{Momme\ D2/+}$ and *Dnmt3L*$^{-/+}$ mice. Bisulphite sequencing of ***a***. LINE-1 and ***b***. IAP LTR. (for primers see [46]) ***c***. Methylation at the Gtl2-DMR. ***d***. Methylation at the H19-DMD (for methods see [49]).

Supplementary Table 1. Genes in the *Momme D4* linked interval.

Gene	Ensembl Gene ID	Gene start (bp)	Gene end (bp)
HIP	ENSMUSG00000064325	82866417	82954078
	ENSMUSG00000044691	83006878	83007712
Gypa	ENSMUSG00000051839	83389800	83405220
4930505O20Rik	ENSMUSG00000044588	83408135	83408878
Frem3	ENSMUSG00000042353	83506826	83591102
Smarca5 (Snf2h)	**ENSMUSG00000031715**	**83595689**	**83635205**
Gab1	ENSMUSG00000031714	83660180	83776225
Usp38	ENSMUSG00000038250	83876479	83910652
	ENSMUSG00000037982	83909322	83934330
	ENSMUSG00000056170	84093373	84094094

Based on Ensembl build 36

Supplementary Table 2. *Smarca5*^{MommeD4} phenotypes.

a. Number of homozygous mutant embryos produced from *Smarca5*$^{Momme\ D4/+}$ intercross in the inbred FVB background

Genotype	14.5 dpc		17.5 dpc	
	Observed	Expected	Observed	Expected
Homozygous	15[†]	19	12[‡]	13.5
Heterozygous	40	38	30	27
Wildtype	22	19	12	13.5
Total	77		54	

[†] Three of these embryos displayed an abnormal phenotype
[‡] All but one of these embryos displayed an abnormal phenotype: four were white and regressing, consistent with macrophage invasion, and seven were anatomically normal but small.

b. Body weight at weaning of *Smarca5*$^{MommeD4/+}$ mice

Weight at 3 weeks of age (g)			
Male offspring		Female offspring	
Smarca5$^{+/+}$	*Smarca5*$^{MD4/+}$	*Smarca5*$^{+/+}$	*Smarca5*$^{MD4/+}$
11.9 ± 0.5	10.7 ± 0.9	11.5 ± 0.5	10.3 ± 0.8
n=10	n=20	n=13	n=12
$p<0.005$		$p<0.005$	

Offspring were generated from *Smarca5*$^{Momme\ D4}$ heterozygous males crossed with wildtype females

Supplementary Table 3. Primers

Name	Sequence
DXMit1F	caagcaaccgaggaagacat
DXMit1R	caggatgctaatcaccctgc
DXMit117F	gtaaaaccgcactgactaagcc
DXMit117R	ttcgcctctatcttactctggc
Hprt4-L	gatttttggagtttggttagatgtt
Hprt4-R	cacaaatataaattataacatctac
Hprt4-Lint	gtggggatgtttttttagtgagtt
Hprt4-Rint	caaacctaaacataccctctcatac
Mtm1SEQ-L	ggggatttaggattggaaaggtttgaagga
Mtm1SEQ-R	taacctttcctaaaccccaattcccccattc
Mtm1SEQLshort	aggaaaaagtagggatttttgaga
Mtm1SEQRshort	taacacaaaaacactaaccaaaaa
Mtm1L	ttggttttattgtttttatttgttttag
Mtm1R	acacttcttaataactattcacacttcc
MD4L	ggaatggctggcctaggta
MD4R	ctcgtatgcaatacaatacaaaca
MD2L	cggtcattccagatgattcc
MD2R	tgtcagcctcggctctaac
Smarca5-ex11L	cagcagggaagatggacaaa
Smarca5-ex11R	aacaccaccatcttgccact