**Figure S1:** Distribution of GFP expression in the *MommeD41* colony. The percentage of red blood cells expressing GFP was assessed in 107 mice from the *MommeD41* colony at weaning, and grouped by genotype for the *Morc3* mutation. Wild types are shown in blue and heterozygotes are shown in orange.
Figure S2: Characterization of Morc3MD41/MD41 mESCs (MommeD line). a Representative images of cellular morphology and alkaline phosphatase (AP) staining of the WT and the Morc3MD41/MD41 derived mESCs grown in 2i and serum. b Pluripotent gene expression levels in WT and the Morc3MD41/MD41. Error bars represent 1 standard deviation. c RNA-seq validates the downregulation of Morc3 in Morc3MD41/MD41. Error bars represent 1 standard deviation.
**Figure S3:** Characterization of Morc3<sup>−/−</sup> mESCs (CRISPR line).  

**a** Sanger sequencing shows a 58-bp deletion in exon 2 of Morc3 gene.  

**b** Genome browser shot of mapped RNAseq reads shows absence of exon 2 in the Morc3<sup>−/−</sup> mutant lines.  

**c** Western blot in Morc3<sup>−/−</sup> and WT mESC lines shows absence of MORC3 protein in the mutant line.  

**d** Pluripotent gene expression levels in WT and the Morc3<sup>−/−</sup>. Error bars represent 1 standard deviation.
Figure S4: MORC3 enrichment at IAPEz-ints in WT mESCs (left) and Morc3−/− mESCs (right).
Figure S5: Boxplots comparing the length of TEs bound by MORC3 with the length of all TEs in that subfamily. Mann–Whitney U test was used to test for significance (p-value = 9.33e-48 for IAPEz-int, p-value = 3.2e-68 for RLTR27, p-value = 2e-11 for LTRIS2, p-value = 0.5 for IAPLTR1a_Mm and p-value = 1.4e-05 for IAPA_MM-int)
**Figure S6:** Coverage of MORC3, H3K4me3 and H3K9me3 at MORC3 bound promoters (a) and at IAPEz-int (b).
Figure S7: MORC3 ChIP-qPCR to validate the presence of MORC3 at the *Cdca7* promoter, at exon 1 of *Gapdh* and at an IAPLTR2a. RLTRETN_Mm, ORR1B2-int, *Gapdh* exon6 and *Dpp6* intron are loci where MORC3 is absent and were used as negative control for MORC3 ChIP-qPCR.
Figure S8: Distribution of MORC2A ChIP-seq peaks over genomic features.
Figure S9: Heatmaps showing the enrichment of H3K9me3 over TEs in MommeD and CRISPR lines.
Figure S10: a Meta plot and heatmaps showing enrichment of ATAC-seq read coverage around TSS of mouse genes. Coverage is measured in rpkm. b Metaplot and heatmaps showing the enrichment of TRIM28 at DAL. c
Representative genome browser tracks showing examples of DAL. A black arrow indicates a locus identified as differentially accessible. DAL are covered with H3K9me3 as indicated by the H3K9me3 ChIP-seq tracks.
Figure S11: 

a) Metaplot showing ATAC-seq read coverage at all MORC3 peaks. 

b,c) Metaplots and heatmaps showing ATAC-seq read coverage at MORC3 bound promoters (b) and at MORC3 bound IAPEz-int (c) in WT and Morc3MD41/MD41.
Figure S12: TRIM28 ChIP-qPCR to validate the presence of TRIM28 at the Mest and Nnat. MERVL-LTR and MERVL-pol loci were used as negative control of the TRIM28 ChIP-qPCR. TRIM28 ChIP-qPCR was performed at DALs IAPEz-int and LTRIS2.