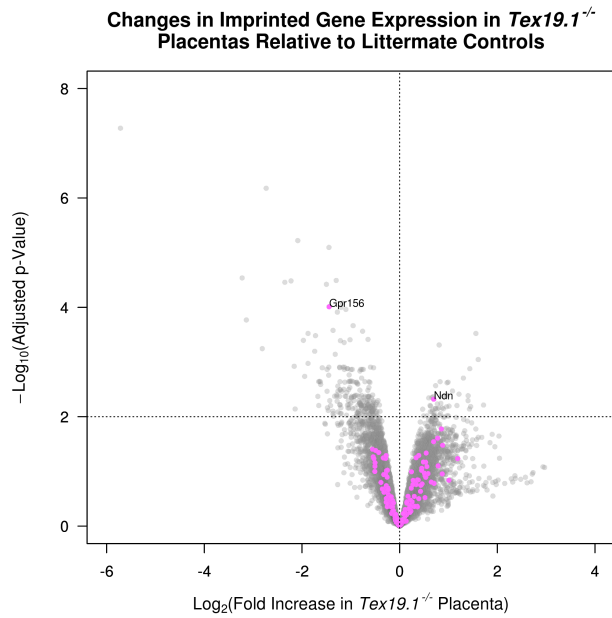


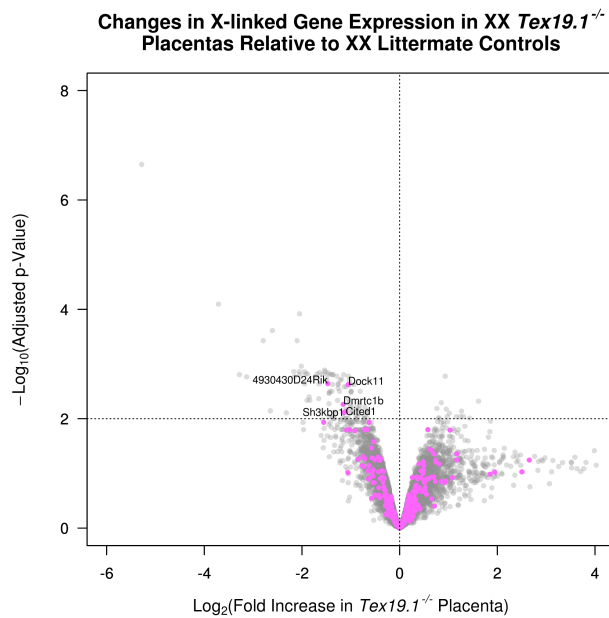
Supplementary Figure S1. TEX19.1 Protein is Present in E9.5 Placenta

Anti-TEX19.1 immunostaining (A,C) and non-specific IgG control staining (B,D) of E9.5 embryos. Anti-TEX19.1 immunostaining (brown precipitate) is restricted to the placenta (pl). Within the E9.5 placenta, anti-TEX19.1 immunostaining is present in the parietal trophoblast giant cells (TGC) and future junctional zone (Jz) and labyrinth (L) layers. Sections were counterstained with haematoxylin. Scale bars 500 μ m.



Supplementary Figure S2. Imprinted Genes Are Not Specifically Derepressed in *Tex19.1*^{-/-} Placentas

Volcano plot of gene expression microarray data showing the probability that each gene on the microarray is differentially expressed, and its level of upregulation in *Tex19.1*^{-/-} placentas (n=6) relative to littermate controls (n=6). Non-imprinted genes are shown in grey, and the 150 imprinted genes in the mouse genome (http://www.har.mrc.ac.uk/research/genomic_imprinting/) are highlighted in pink. An adjusted p-value threshold of 0.01 is indicated by the horizontal dotted line, and the separation between gene expression increasing and decreasing in *Tex19.1*^{-/-} placentas indicated by the vertical dotted line. Similar proportions of imprinted genes (2/150) and non-imprinted genes (266/13153) are expressed at significantly (p<0.01) different levels in *Tex19.1*^{-/-} placentas (χ^2 -test, p=0.76). The significantly different imprinted genes are annotated with their gene names.



Supplementary Figure S3. X-linked Genes Are Not Specifically Derepressed in XX *Tex19.1*^{-/-} Placentas

Volcano plot of gene expression microarray data showing the probability that each gene on the microarray is differentially expressed, and its level of upregulation in XX *Tex19.1*^{-/-} placentas (n=4) relative to XX littermate controls (n=4). Autosomal genes are shown in grey, and X-linked genes are highlighted in pink. An adjusted p-value threshold of 0.01 is indicated by the horizontal dotted line, and the separation between gene expression increasing and decreasing in XX *Tex19.1*^{-/-} placentas indicated by the vertical dotted line. Similar proportions of X-linked (5/312) and autosomal genes (106/9411) are expressed at significantly ($p < 0.01$) different levels in XX *Tex19.1*^{-/-} placentas (χ^2 -test, $p = 0.61$). The significantly different X-linked genes are annotated with their gene names.

	Male	Female	All
<i>Tex19.1</i> ^{+/+}	135 (29 %)	119 (26 %)	254 (28 %)
<i>Tex19.1</i> ^{+/-}	250 (53 %)	258 (57 %)	508 (55 %)
<i>Tex19.1</i> ^{-/-}	88 (19 %) *	73 (16 %) *	161 (17 %) *
Total	473	450	923

Supplementary Table 1. Loss of *Tex19.1* Impairs Embryo Viability

The number (and percentage) of *Tex19.1*^{+/+}, *Tex19.1*^{+/-} and *Tex19.1*^{-/-} animals born from heterozygous crosses. Asterisks indicate significant deviation from the expected 1:2:1 Mendelian ratio in all animals, male animals or female animals (χ^2 test). The sex ratio for each of the three genotypes is not significantly different from expected (1:1).

	Concurrent Pregnancy and Lactation			Pregnancy Without Concurrent Lactation		
	Male	Female	All	Male	Female	All
<i>Tex19.1</i> ^{+/+}	35 (35 %)	25 (25 %)	60 (30 %)	100 (27 %)	94 (27 %)	194 (27 %)
<i>Tex19.1</i> ^{+/-}	52 (52 %)	73 (72 %)	125 (62 %)	198 (53 %)	185 (53 %)	383 (53 %)
<i>Tex19.1</i> ^{-/-}	14 (14 %) *#	3 (3 %) *#	17 (8 %) *	74 (20 %)	70 (20 %)	144 (20 %) *
Total	101	101	202	372	349	721

Supplementary Table 2. Concurrent Pregnancy and Lactation Induces Severe Female-Biased Lethality in *Tex19.1*^{-/-} Embryos

The number (and percentage) of *Tex19.1*^{+/+}, *Tex19.1*^{+/-} and *Tex19.1*^{-/-} animals born from heterozygous crosses where mothers were either nursing a pre-existing litter during pregnancy (concurrent pregnancy and lactation) or not. The 'pregnancy without concurrent lactation' group includes mothers giving birth to their first litters, and mating pairs where the mother and father were separated during pregnancy and post-partum lactation; no difference was observed in the lethality of *Tex19.1*^{-/-} animals between these two subgroups. Asterisks indicate significant deviation from the expected 1:2:1 Mendelian ratio in all animals, male animals or female animals (χ^2 test). Hashes indicate genotypes with significant deviation from the expected 1:1 sex ratio (χ^2 test).

Primer Name	Sequence	Primer Name	Sequence
<i>LINE-1 a</i>	GTCTGCACCACAGAAGCTGA CTCTGCTGGCAAGCTCTCTT	<i>Gjb3</i>	GGGGCTCTCCATCAGACATA GTGCCAAACCTTCTCATGGT
<i>LINE-1 b</i>	ACAGGAGGAACAAGCTCCAA TTTTGGGTGTGTTGGGGTAT	<i>Pcdh12</i>	GCTCTGCATGTTTGGTCTCA AGACGAGCAGGAACTGGAA
<i>LINE-1 ORF2</i>	GGAGGGACATTTTCATTCTCATC GCTGCTCTTGATTTGGAGCATAGA	<i>Prl8a8</i>	AAATTATGTGGGTGCCTGGA TCACGCAGAATTTGTCTGTTG
<i>IAP</i>	GCACCCTCAAAGCCTATCTTA TCCCTTGGTCAGTCTGGATTT	<i>Prl3a1</i>	AGAGCGAAAGTGCATGTGTG GCACCTCTGTTTCCCTCAG
<i>MMVL30</i>	CAGCCTTGGCCTGAGAGTTT CTTTCTGGGCTGAAGTCCCT	<i>Cdx1</i>	AGCTAGCTAGCTAGCT GCTGGAAGAGGAGACAGGTG
<i>MMERVK10C</i>	GGTAAAGTCTCCGAGGGTCA AACTGGTCGCAGGAGCTG	<i>Cdx2</i>	GGGTGGGGGTAGCAATACTT CCCTTCCCTGATTTGTGGAGA
<i>Tex19.1</i>	AAAATGGGCCACCCACATCTC CCACTGGCCCTTGGACCAGAC	<i>Ctsm</i>	TGGATGTTGAATGGCAGAAA CCAAAGGCATTCATTTCCAT
<i>Tek</i>	AAGCATGCCCATCTGGTTAC GCCTGCCTTCTTTCTCACAC	<i>Psg18</i>	TGCAGGCAAACATTTTCAGAG GAGTATGACAGGGGCCTCAA
<i>Nr6a1</i>	GCAGCAGATTCCACAGAACA GGACTGGGTGCAGAAGACAT	<i>Psg29</i>	AGGGACAAGACAGAGGCTGA TGTGGTAGGAATGCAATGGA
<i>Dlx3</i>	ACTTTCTTCTGCCCCCTGAT GACCTGCTTCTCTTGGTTGC	<i>Prl5a1</i>	CTGGGGCAGTCCATACTGAT AATGAGTCAGGGGACAATGG
<i>Ctsq</i>	AGAACAGCTGGGGTAGACG GCCACATGCTTTCTTGTGAA	<i>Prl3c1</i>	GGATTCAGCCTGGAATTGAA TTGATTTTGCCATGCTTCAG
<i>Syna</i>	TTTCCCCCAAACCACAATAA AGTCATGAACCACACCACGA	<i>Dazl</i>	TCTTTGCCAGATATGGCTCAGT CTTCTGCACATCCACGTCATTA
<i>Synb</i>	CTGGGTCTGACATGAGGTT TGTCAGACAGTCCCTTGCAG	<i>Piwil2</i>	CATTATGGTCAAGTATCTGTT AGAGGTTGGCGAGGAATAAGG
<i>Hand1</i>	GTGCCAAACCTTCTCATGGT GGGGCTCTCCATCAGACATA	<i>Mov10l1</i>	TTCCCTCTATGCAGGTGACAA AAGTGCATAGTGACACCGTCT
<i>Tpbpa</i>	AAGTTAGGCAACGAGCGAAA AGTGCAGGATCCCCTTGT	<i>Asz1</i>	GAAGTTAACGCCAGGATGA GGTGTCTGCCATCTTTGGT
<i>BS_Tex19.1_1</i>	GGTTTTGTTTTTTGTTGTTG CATTACATATCTCCATAAAATC	<i>BS_Tex19.1_2</i>	TTATTAAAGAGATAGGGAAGAAG ATCCCAAACAACAAAAAAC
<i>BS_Dazl_1</i>	ATAAAAAAAAAAACCCACRACCAC GAGGTAATGATTTGAATAAA	<i>BS_Dazl_2</i>	AGGTAATGATTTGAATAAAT AAAAAACCAAAAAACCCAC
<i>BS_Piwil2_1</i>	GTTTGAGAGTAATTTTATATAG AAATCTAATACCACTAAACC	<i>BS_Piwil2_2</i>	AGGTTTATTTTAAAGAGGT TCCTTCCCTCCTATTCCAA
<i>BS_Mov10l1_1</i>	TTTTAAGTTTATATTGGGTAGTG TCCTTCCCTCAAAAAAAAAA	<i>BS_Mov10l1_2</i>	TTGGGTAGTGAAATTTTTTA TCAAAAAAAAAAACCAAC
<i>BS_Asz1_1</i>	TTTGAAGTTTAAAGAATGTAATT AATTACCTTCTCCACTACCTA	<i>BS_Asz1_2</i>	TTAAGAATGTAATTAATAA TTCTCCACTACCTAAAAAAA

Supplementary Table 3. Primer Sequences

Primers used for bisulphite sequencing are prefixed 'BS_', '_1' and '_2' suffixes for bisulphite sequencing primers indicate their use in the first and second round of the nested PCR respectively. Primers without a 'BS_' prefix were used for qRT-PCR.