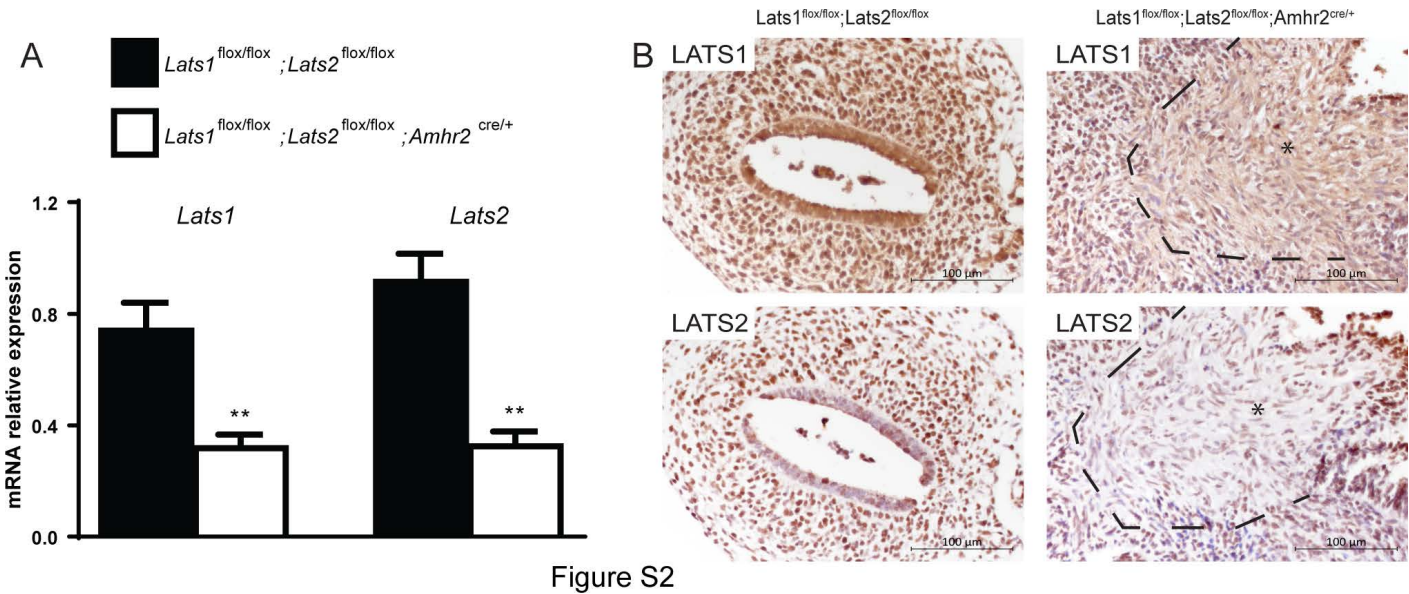
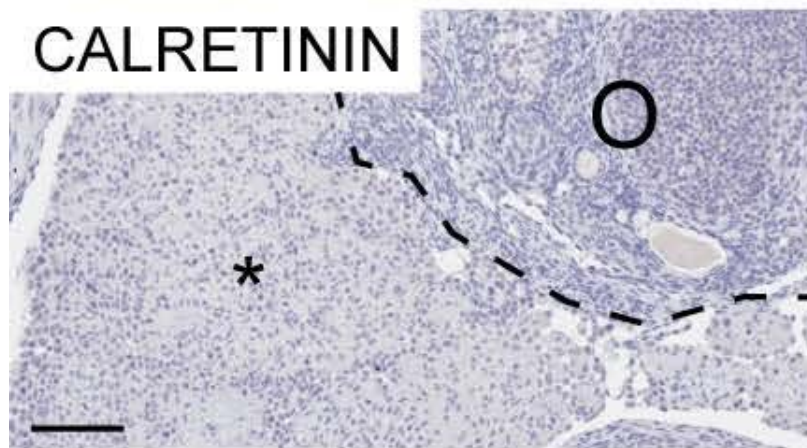
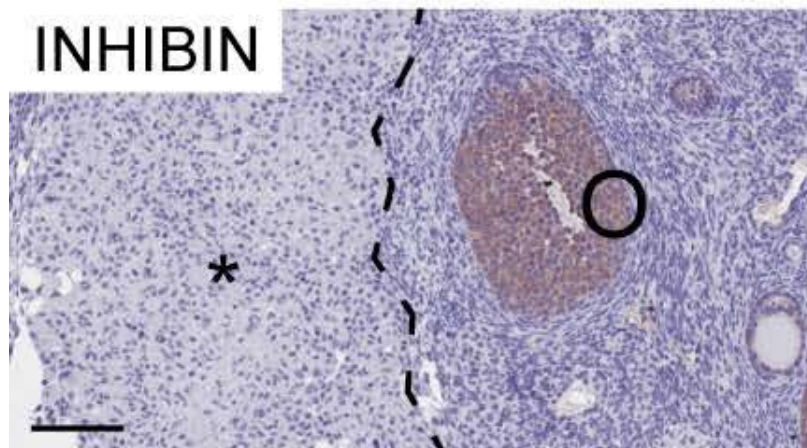
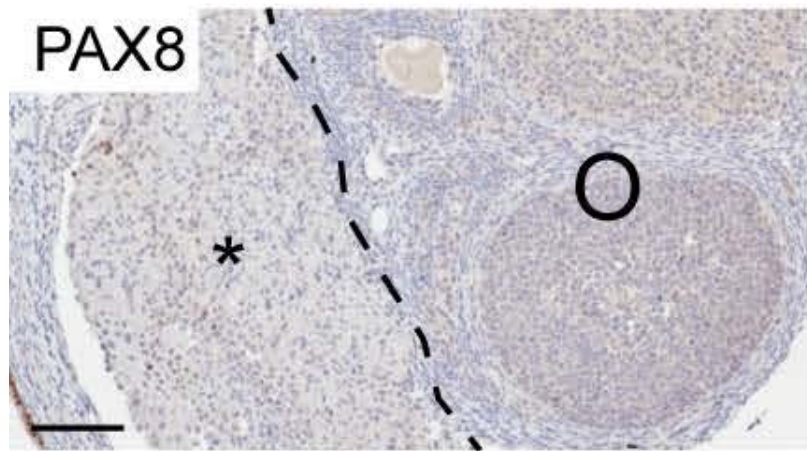
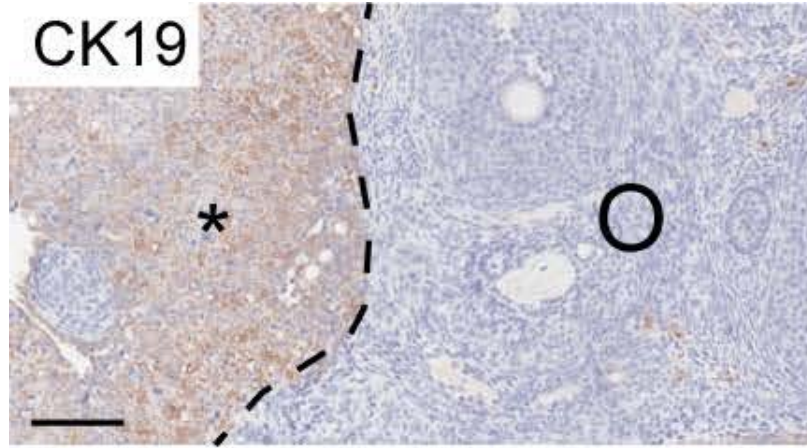


**Fig. S1. Immunohistochemical analyses of Hippo core component (LATS1, LATS2, YAP, TAZ, phosphoYAP) expression during female reproductive tract development.**

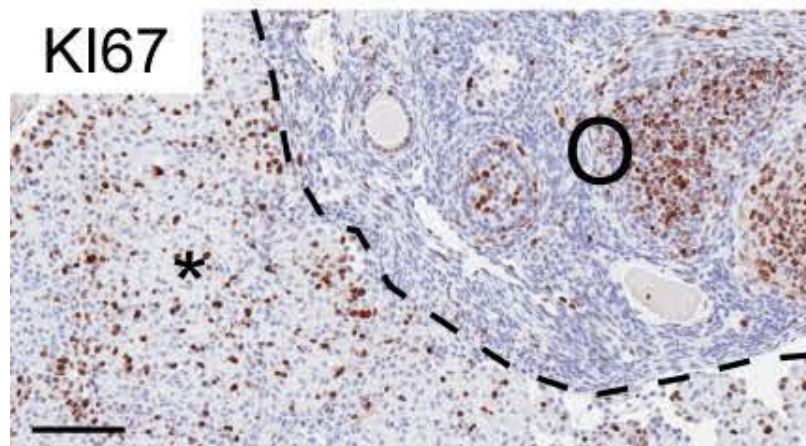
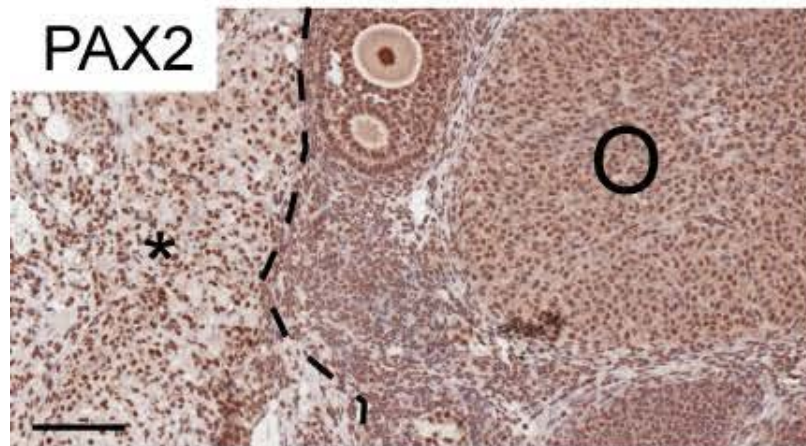
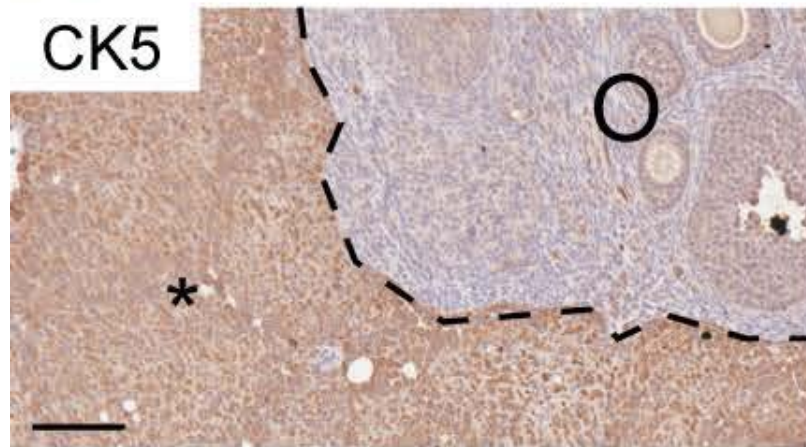
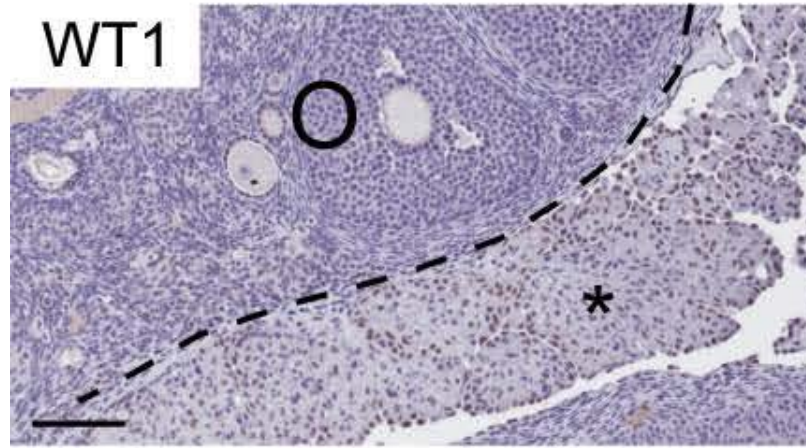


**Fig. S2. Evaluation of knockout efficiency in the female *Lats1*<sup>flox/flox</sup>; *Lats2*<sup>flox/flox</sup>; *Amhr2*<sup>cre/+</sup> reproductive tract.** (A). RT-qPCR analysis of *Lats1* and *Lats2* mRNA levels in Müllerian ducts from E17.5 mutant mice of the indicated genotypes. Data are presented as means (columns)  $\pm$  s.e.m (error bars). Columns labeled with asterisks are statistically significantly different from controls (\*\*= $P < 0.01$ ,  $n = 4$ , Student's t-test). (B). Immunohistochemistry analysis of LATS1 and LATS2 expression in uteri from P1 mice of the indicated genotypes. The ectopic myofibroblast cell population is delineated with a black dashed line. Apparent residual LATS1 and LATS2 staining in the myofibroblast population in the Müllerian ducts of *Lats1*<sup>flox/flox</sup>; *Lats2*<sup>flox/flox</sup>; *Amhr2*<sup>cre/+</sup> mice represents background signal.



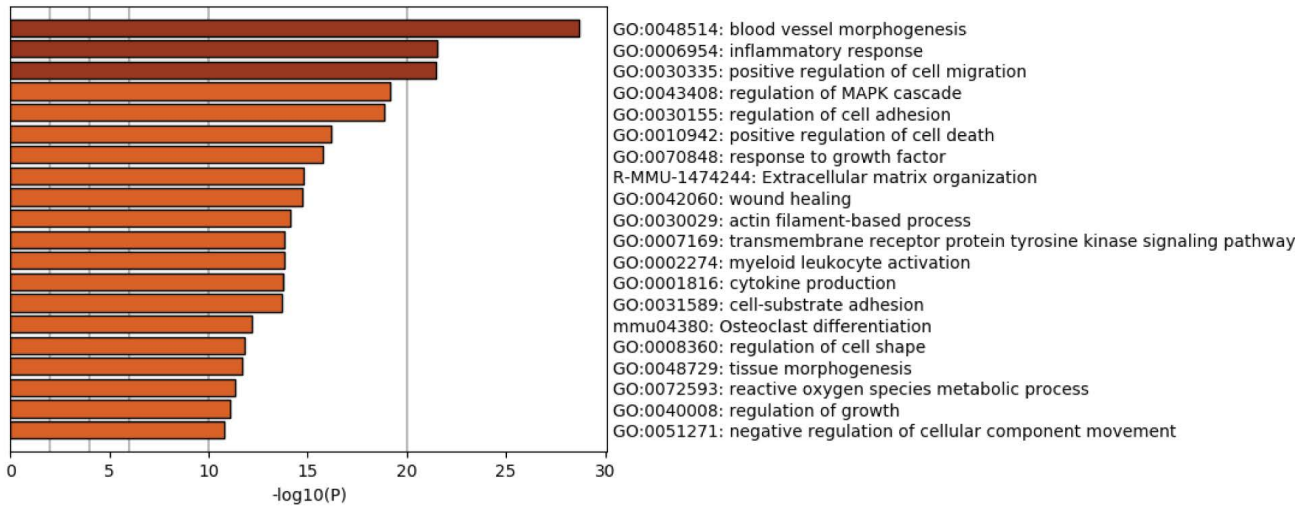




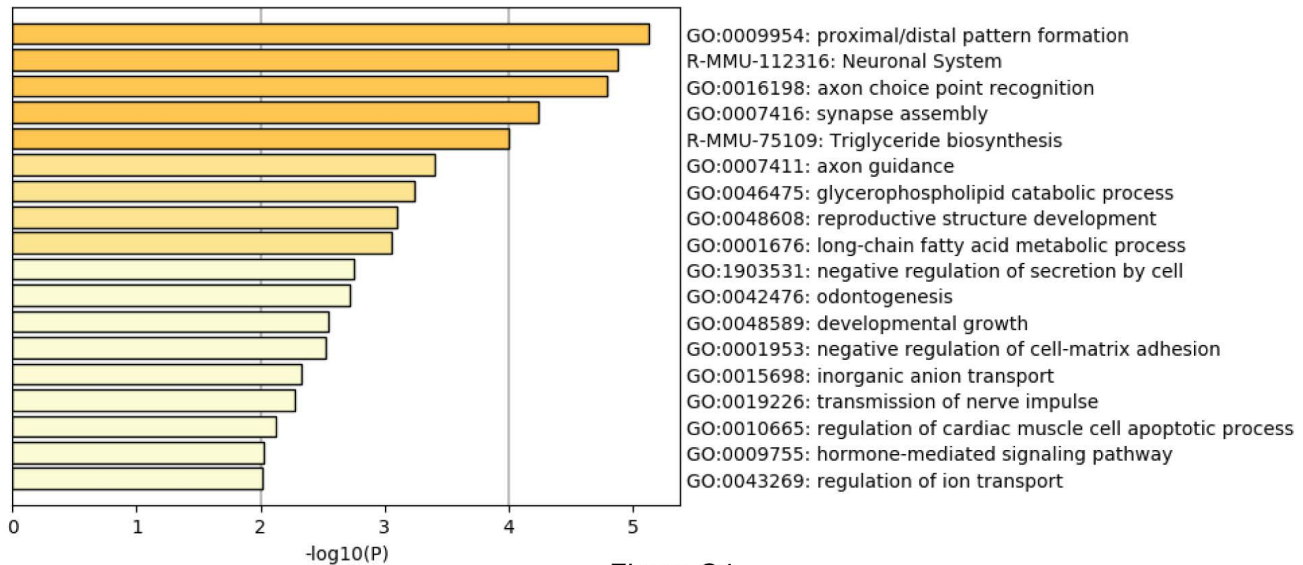


**Fig. S3. Representative tumor marker immunohistochemistry photomicrographs.** ○ = ovary, \* = neoplastic tissue. Bars = 100μM.

**A** Biological processes associated with upregulated genes in müllerian ducts of *Lats1<sup>flox/flox</sup>; Lats2<sup>flox/flox</sup>; Amhr2<sup>cre/+</sup>* mice



**B** Biological processes associated with downregulated genes in müllerian ducts of *Lats1<sup>flox/flox</sup>; Lats2<sup>flox/flox</sup>; Amhr2<sup>cre/+</sup>* mice



**Fig. S4. Microarray gene ontology analysis (A).** Biological processes associated with genes upregulated in the uteri of *Lats1<sup>flox/flox</sup>; Lats2<sup>flox/flox</sup>; Amhr2<sup>cre/+</sup>* mice relative to controls. (B). Biological processes associated with genes downregulated in the uteri of *Lats1<sup>flox/flox</sup>; Lats2<sup>flox/flox</sup>; Amhr2<sup>cre/+</sup>* mice relative to controls. All results were obtained using Metascape (<http://metascape.org>) (Zhou et al., 2019).

Table S1. Fertility trial.

Genotype	n	Total litters	Total pups	Litter size
<i>Lats1</i> <sup>flox/flox</sup> ; <i>Lats2</i> <sup>flox/flox</sup>	7	7.57±0.30	67.29±5.06	8.88±0.37
<i>Lats1</i> <sup>flox/flox</sup> ; <i>Amhr2</i> <sup>cre/+</sup>	6	7.86±0.14	60.86±4.90	7.75±0.46
<i>Lats2</i> <sup>flox/flox</sup> ; <i>Amhr2</i> <sup>cre/+</sup>	6	7.83±0.17	55.33±4.36	7.06±0.34
<i>Lats1</i> <sup>flox/flox</sup> ; <i>Lats2</i> <sup>flox/flox</sup> ; <i>Amhr2</i> <sup>cre/+</sup>	6	0.0±0.0****	0.0±0.0****	0.0±0.0****

Values are expressed as means ± SEM

\*\*\*\* Means are significantly different (P<0.0001)

Table S2. Tumor marker immunohistochemistry analyses.

Marker	Signal strength
CK19	++
PAX8	+
INHIBIN	-
CALRETININ	-
WT1	+/-
CK5	+++
PAX2	++
KI67	+

Table S3. qPCR primers

Gene	Forward	Reverse
<i>Acta2</i>	AGCCATCTTTCATTGGGATGG	CCCCTGACAGGACCTTGTTA
<i>Cald1</i>	GTTGCTGCCCTAGAGATAGTCA	AACCTTTGACTGTCCACCCC
<i>Cnn1</i>	TGCGCTTGTCTGTGTCATCT	TCTGGGCCAGCTTGTTCCTT
<i>Ctgf</i>	GAGGAAAACATTAAGAAGGGCAAAA	CCGCAGAACTTAGCCCTGTA
<i>Cyr61</i>	TTGACCAGACTGGCGCTCT	AGTTTTGCTGCAGTCCTCGT
<i>Lats1</i>	AGCAGCACGTAGAGAACGTC	TTCATTTGATCCTGGGCATCT
<i>Lats2</i>	TGCACTGGATTCAGGTGGACTCA	GAGAATGTGCCAGGCACCTCT
<i>Nanog</i>	ACCTGAGCTATAAGCAGGTTAAGA	TGAATCAGACCATTGCTAGTCTTC
<i>Oct4</i>	CCATGTTTCTGAAGTGCCCG	ACCATACTCGAACCACATCCTTC
<i>Prl8a2</i>	CTCACTTCTCAGGGGCACT	AGCCATTCTCTCCTGTTTGACA
<i>Ptgs2</i>	CCTGAAGCCGTACACATCATTGA	AGGCACTTGCATTGATGGTGGCT
<i>Rpl19</i>	CTGAAGGTCAAAGGGAATGTG	GGACAGAGTCTTGATGATCTC
<i>Sox2</i>	GCGGAGTGGAACTTTTGTC	CGGGAAGCGTGTACTTATCCTT
<i>Spp1</i>	CCTTGCTTGGGTTTGCAGTC	TGGTCGTAGTTAGTCCCTCAGA

Table S4. ChIP primers

Position	Forward	Reverse
<b>-3739</b>	CAAACATCCATGCTTCCTTCCAA	TTAAGGAGTGTGCCCTCTCACA
<b>-3639</b>	TCTGGCATAACGCCCCCTG	TGTGTCCTAGGTTTCAAGTCATGT
<b>-3539</b>	TGCTGACAGCCCAGTGTATG	GTGGAACGTGACTCAAAGCC
<b>-2292</b>	CACAACGCATCTGTTTCCTG	CTCGATTTTCGTTGCTCTCAGTG
<b>-1792</b>	GCCTCTTCTCTTTGAGGAATGCT	GTGTGAGTGGCTTGAAGTGTG
<b>-1242</b>	ACAACACAGGTCCTAAATGAATG	GAAGTGTACTTAGTTTCTGTAAGG
<b>-208</b>	CAGAACTGGCAAAGAGATTTTAAAG	TCCATATCATCTTCTCACCCCTC
<b>-108</b>	GCGAGCTAAAGTGTGCCAG	TTGACACTCCACATTCCTCCG
<b>-58</b>	GTGTCAAGGGGTCAGGATCAA	CCACCTTCTGCCTCATCAAC
<b>-43</b>	TGAGTTGATGAGGCAGGAAGG	CGCAAAGAAGTGAATGGAGTC
<b>462</b>	GAAGTGTGTACGGAGCGTGAC	CAGAAGAGGCCCTTGTGTGGG