## SUPPLEMENTAL FILES AND TABLES

SMAD2/3 signaling in the uterine epithelium controls endometrial cell homeostasis and regeneration

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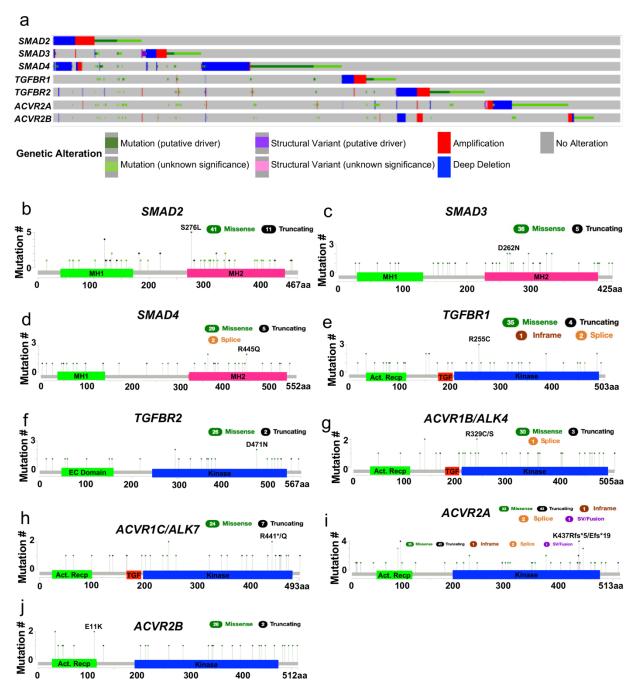
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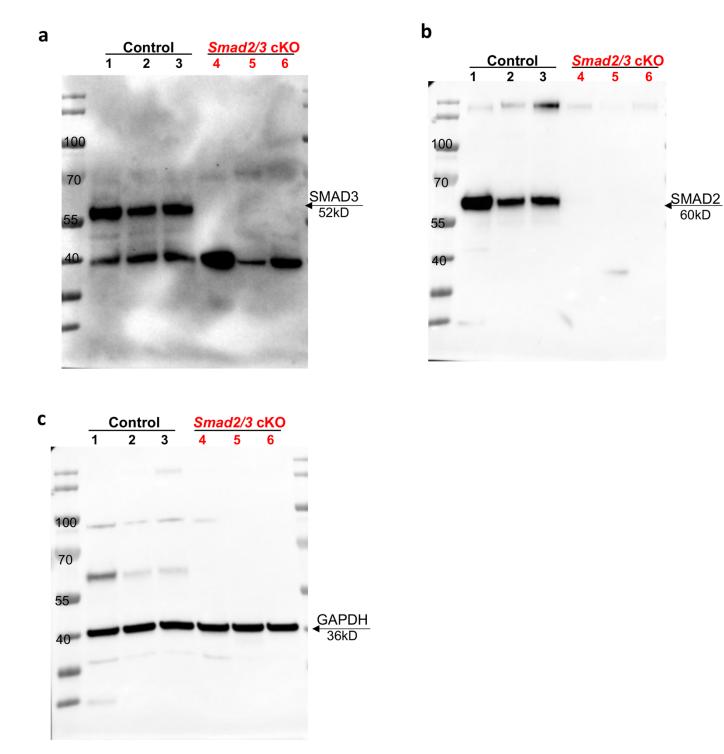
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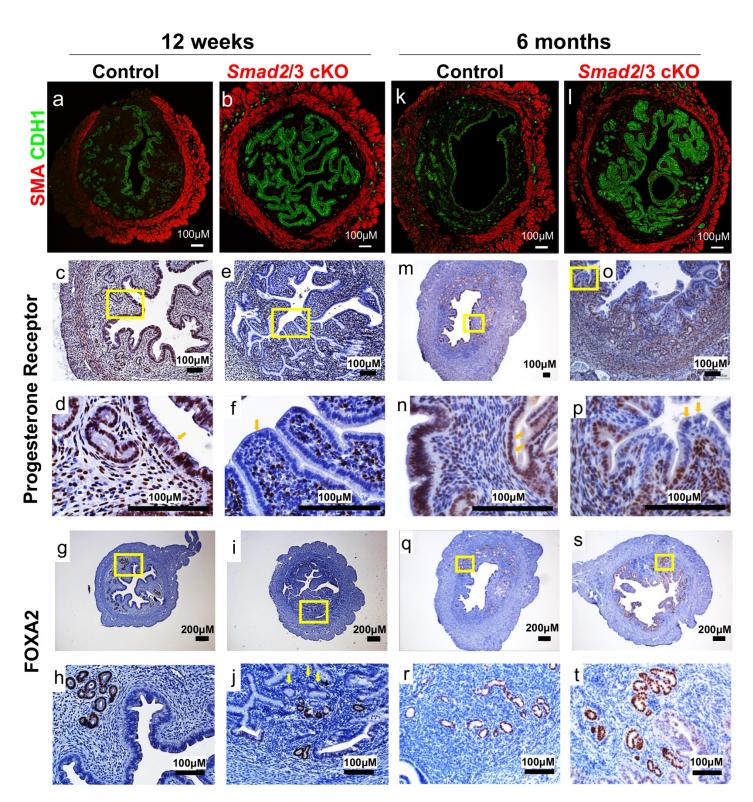
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Supplementary Fig. 1: Mutations in the TGF $\beta$  signaling pathway in endometrial tumors. A dataset of 894 patients was queried for the presence of mutations in the TGF $\beta$  signaling pathway (**a**). This figure shows an overview of the mutations found in the coding regions for *SMAD2*, *SMAD3*, *SMAD4* (**b-d**), and in the various TGF $\beta$  receptors (**e-j**) that can activate SMAD2/3 signaling. Data represent analysis of 894 patients from the cBioPortal consortium. **b-j** Individual mutations for each of the transcription factors, *SMAD2*, *SMAD3*, *SMAD4* and TGF $\beta$  receptors, *TGFBR1*, *TFGBR2*, *ACVR1B*, *ACVR1C*, *ACVR2A*, and *ACVR2B*. The most frequent mutation is noted as well as the predicted effect of the mutation (missense, truncating, in-frame, etc).

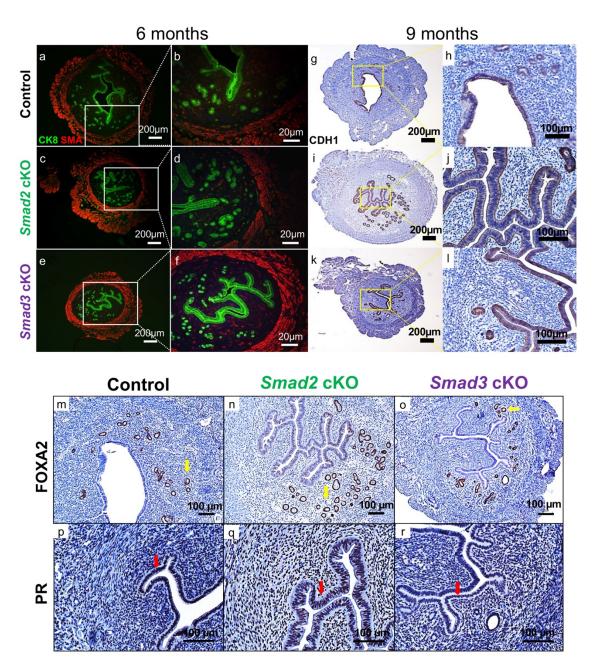


Supplementary Fig. 2: Uncropped western blot images for Fig. 1d. Western blot images for SMAD3 (a), SMAD2 (b), and GAPDH (c), respectively.

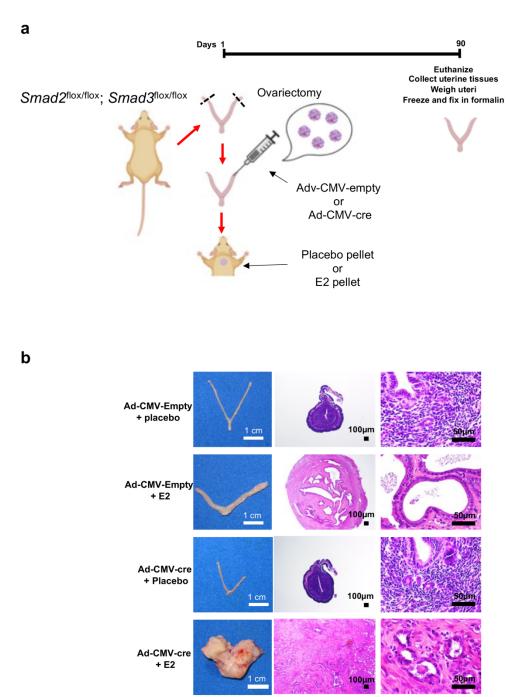


Supplementary Fig. 3: Mice with double SMAD2/3 conditional deletion develop hyperplasia and lose progesterone receptor expression. Uterine cross-sections from 12-week-old mice (**a**,**b**) and 6-month-old mice (**k**, **I**) stained with the myometrial marker, smooth muscle actin (SMA, red) and the epithelial cell marker, E-cadherin (CDH1, green) in control (**a**, **k**) and *Smad2/3* cKO (**b**, **I**) mice. E-

cadherin staining shows that hyperplasia is detected in the uteri of *Smad2/3* cKO mice starting at 12weeks of age and worsening by 6-months of age. **c-f**, **m-p** Progesterone receptor (PR) immunohistochemistry (IHC) in uterine cross-sections from 12-week-old (**c-f**) and 6-month-old (**m-p**) mice. Results show that compared to controls (**c-d**, **m-n**), *Smad2/3* cKO mice (**e-f**, **o-p**) had decreased PR levels in the uterine epithelium (indicated by yellow arrows in **d**, **f**, **n**, **p**). **g-j**, **q-t** Uterine cross sections from control (**g-h**, **q-r**) and *Smad2/3* cKO mice (**i-j**, **s-t**) showing that FOXA2 expression is expressed in the uterine glands of both genotypes at 12 weeks (**g-j**) and 6 months of age (**q-t**).

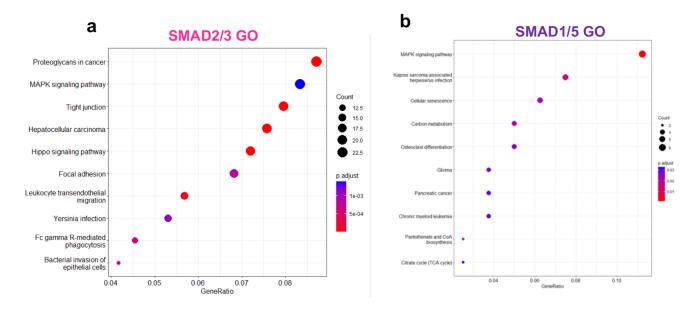


Supplementary Fig. 4: Morphological analysis of uteri from control and single *Smad2* cKO and *Smad3* cKO mice. a-f Cross sections of 6-month-old virgin mice from control (a-b), *Smad2* cKO (c-d), and *Smad3* cKO (e-f) mice stained with cytokeratin 8 (CK8, green) and smooth muscle actin (SMA, red). g-i Histological analysis of 9-month-old control (g-h), *Smad2* cKO (i-j), and *Smad3* cKO (k-l) stained with E-cadherin. Mice had been mated during 6 months as part of a breeding trial. m-n Uterine cross sections of control (m), *Smad2* cKO (n), and *Smad3* cKO (o) mice stained with the glandular cell marker, FOXA2. p-r Uterine cross-sections from control (p), *Smad2* cKO (q) and *Smad3* cKO (r) mice stained with progesterone receptor (PR) antibody.



**Supplementary Fig. 5: Adenoviral-cre mediated SMAD2/3 deletion in mice. a** Diagram showing the schematic used to obtain adenoviral cre-mediated deletion of SMAD2 and SMAD3 in *Smad2*<sup>flox/flox</sup>;*Smad3*<sup>flox/flox</sup> mice by injection into the uterus of ovariectomized mice treated with a placebo or estradiol (E2) releasing pellet. **b** Analysis of the reproductive tracts 3-months after Ad-cre injection and placebo or E2 treatment. Administration of Ad-cre + E2 led to tumor development, while Ad-cre administration without E2 did not results in endometrial tumors. Experiments were performed in 2-3 mice per genotype.

## Supplementary Fig. 6



Supplementary Fig. 6: Gene ontology classification in SMAD4-bound genes in endometrial organoids. **a-b** Gene ontology classifications in the 607 SMAD4-bound genes downregulated in control organoids (representative of SMAD2/3 direct target genes, **a**), and in the 185 SMAD4-bound genes upregulated in *Smad2/3* cKO organoids (representing SMAD1/5 target genes, **b**).

**Supplementary Table 1.** Development of tumors from *Smad2/3* cKO mice is E2-dependent.

Treatment	Genotype	Uterine Weight (g)	Uterine tumor	Lung Mets
	Control (n=4)	0.0185 ± 0.0034	0/4	0/4
No E2	S <i>mad2/3</i> cKO (n=4)	0.025 ± 0.002	0/4	0/4
E2 pellet	Control (n=4)	0.1079 ± 0.0382	0/4	0/4
	Smad2/3 cKO (n=4)	2.99 ± 0.66	4/4	2/4

**Supplementary Table 2.** Primer sequences used for genotyping and quantitative PCR.

Smad2FTACTTGGGGCAATCTTTTCGGenotypingRGTCACTCCCTGAACCTGAAGSmad3FCTCCAGATCGTGGGCATACAGCGenotypingRGGTCACAGGGTCCTCTGTGCCLtf-cre1GTTTCCTCCTTCTGGGCTCC2TTTAGTGCCCAGCTTCCCAG3CCTGTTGTTCAGCTTGCACCAldh1a1FATACTTGTCGGATTTAGGAGGCTRGGGCCTATCTTCCAAATGAACAAldh1a2FCAGAGAGTGGGAGAGTGTTCCRCAGACAGAACCAAGAAGAGAAGGAldh1a3FGGGTCACACTGGAGCTAGGACyp26a1FAAGCTCTGGGACCTGTACTGTRCTCCGCTCATGAAATCAGCTCRATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGGId1FCCTAGCTGTTCGCTGAAGGCRCTCCGACAGACCAAGTACCAC	Gene	Primer #	Sequence (5'-3')	
Smad3 GenotypingFCTCCAGATCGTGGGCATACAGC GGTCACAGGGTCCTCTGTGCCLtf-cre1GTTTCCTCCTTCTGGGCTCC TTTAGTGCCCAGCTTCCCAG 3Aldh1a1FATACTTGTCGGATTTAGGAGGCT GGGCCTATCTTCCAAATGAACAAldh1a1FCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAGGAldh1a2FCAGAGAGTGGGAGAGTGTTCC RCyp26a1FGGGTCACACTGGAGCTAGGA CTCGCGCTGTACTGT RLratFCCGTCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGAAGGCId1FCCTAGCTGTTCGCTGAAGGC	Smad2	F	TACTTGGGGCAATCTTTTCG	
GenotypingRGGTCACAGGGTCCTCTGTGCCLtf-cre1GTTTCCTCCTTCTGGGCTCC2TTTAGTGCCCAGCTTCCCAG3CCTGTTGTTCAGCTTGCACCAldh1a1FATACTTGTCGGATTTAGGAGGCTGGGCCTATCTTCCAAATGAACAGGGCCTATCTTCCAAATGAACAAldh1a2FCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAAGGAldh1a3FGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1FAAGCTCTGGGACCTGTACTGT RLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG RId1FCCTAGCTGTTCGCTGAAGGC	Genotyping	R	GTCACTCCCTGAACCTGAAG	
Ltf-cre1GTTTCCTCCTTCTGGGCTCC2TTTAGTGCCCAGCTTCCCAG3CCTGTTGTTCAGCTTGCACCAldh1a1FRATACTTGTCGGATTTAGGAGGCTGGCCTATCTTCCAAATGAACAAldh1a2FCAGAGAGTGGGAGAGTGTTCCRCAGAGAGTGGGAGAGTGTTCCAldh1a3FGGGTCACACTGGAGCTAGGACyp26a1FRAAGCTCTGGGACCTGTACTGTLratFCCGTCCCTATGAAATCAGCTCRbp4FCTAGCTGTTCGCTGAAGGCId1FCTAGCTGTTCGCTGAAGGC	Smad3	F	CTCCAGATCGTGGGCATACAGC	
2TTTAGTGCCCAGCTTCCCAGAldh1a1FATACTTGTCGGATTTAGGAGGCTRATACTTGTCGGATTTAGGAGGCTAldh1a2FCAGAGAGTGGGAGAGTGTTCCRCAGAGAGTGGGAGAGTGTTCCAldh1a3FGGGTCACACTGGAGCTAGGACyp26a1FAAGCTCTGGGACCTGTACTGTRCCGTCCCTATGAAATCAGCTCRCCGTCCCTATGAAATCAGCTCRRCCGTCCCTATGAAATCAGCTCRbp4FCCACTGGATCATCGACAGGAId1FCCTAGCTGTTCGCTGAAGGC	Genotyping	R	GGTCACAGGGTCCTCTGTGCC	
3CCTGTTGTTCAGCTTGCACCAldh1a1F RATACTTGTCGGATTTAGGAGGGCT GGGCCTATCTTCCAAATGAACAAldh1a2F RCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAGAGGAldh1a3F RGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1F RAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratF RCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACAGGAId1FCCTAGCTGTTCGCTGAAGCC	Ltf-cre	1	GTTTCCTCCTTCTGGGCTCC	
Aldh1a1F RATACTTGTCGGATTTAGGAGGCT GGGCCTATCTTCCAAATGAACAAldh1a2F RCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAGAGGGAldh1a2F RGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAAAldh1a3F RGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1F RAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratF RCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4F RCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		2	TTTAGTGCCCAGCTTCCCAG	
RGGGCCTATCTTCCAAATGAACAAldh1a2FCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAGAGGAldh1a3FGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1FAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		3	CCTGTTGTTCAGCTTGCACC	
Aldh1a2F RCAGAGAGTGGGAGAGTGTTCC CACACAGAACCAAGAGAGAGGGAldh1a3F RGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1F RAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratF RCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4F RCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC	Aldh1a1	F	ATACTTGTCGGATTTAGGAGGCT	
RCACACAGAACCAAGAGAGAGGGAldh1a3FGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1FAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		R	GGGCCTATCTTCCAAATGAACA	
Aldh1a3FGGGTCACACTGGAGCTAGGA CTGGCCTCTTCTTGGCGAACyp26a1FAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC	Aldh1a2	F	CAGAGAGTGGGAGAGTGTTCC	
RCTGGCCTCTTCTTGGCGAACyp26a1FAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		R	CACACAGAACCAAGAGAGAAGG	
Cyp26a1FAAGCTCTGGGACCTGTACTGT CTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC	Aldh1a3	F	GGGTCACACTGGAGCTAGGA	
RCTCCGCTGAAGCACCATCTLratFCCGTCCCTATGAAATCAGCTC RRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		R	CTGGCCTCTTCTTGGCGAA	
LratFCCGTCCCTATGAAATCAGCTC ATGGGCGACACGGTTTTCCRATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGG GCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC	Cyp26a1	F	AAGCTCTGGGACCTGTACTGT	
RATGGGCGACACGGTTTTCCRbp4FCCACTGGATCATCGACACGGRGCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		R	CTCCGCTGAAGCACCATCT	
Rbp4FCCACTGGATCATCGACACGGRGCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC	Lrat	F	CCGTCCCTATGAAATCAGCTC	
RGCCATTGGGGTCACGAGAAId1FCCTAGCTGTTCGCTGAAGGC		R	ATGGGCGACACGGTTTTCC	
Id1 F CCTAGCTGTTCGCTGAAGGC	Rbp4	F	CCACTGGATCATCGACACGG	
		R	GCCATTGGGGTCACGAGAA	
R CTCCGACAGACCAAGTACCAC	ld1	F	CCTAGCTGTTCGCTGAAGGC	
		R	CTCCGACAGACCAAGTACCAC	

ld2	F R	ATGAAAGCCTTCAGTCCGGTG AGCAGACTCATCGGGTCGT
ld3	F R	CGACCGAGGAGCCTCTTAG GGACGCGATAGGGAAGACC
ld4	F R	ATGAAAGCCTTCAGTCCGGTG AGCAGACTCATCGGGTCGT
<i>Smad2</i> Exon 10	F R	GCTCTTCTGGCTCAGTCTGTCA GGTGCACATTCGGGTTAGCT
Smad3 Exon 3	F R	TCACGTTATCTACTGCCGCC AGCTCCATGGCCCGTAATTC

Supplementary Table 3. Antibody information.

Antigen	Source	Cat. No.	Dilution
SMAD2	Cell Signaling	5339	WB 1:1000
SMAD3	Cell Signaling	9523	WB 1:1000
pSMAD2	Cell Signaling	3108S	WB 1:200
pSMAD2/3	Cell Signaling	8828S	IHC 1:100
SMA	Abcam	Ab5694	IHC 1:500
Progesterone Receptor	Cell Signaling	8757	IHC 1:200
FOXA2	Abcam	ab108422	IHC/IF 1:200
ERα	Cell Signaling	13258S	IHC 1:200
TTF1	Abcam	Ab76013	IHC, IF 1:200
CDH1	Cell Signaling	3195S	IHC: 1:200
CK8	DSHB	TROMA-I	IF 1:50
MUC1	Novusbio	NB120-15481	IHC 1:200
SMAD4	Abcam	Ab40759	0.678µg/reaction
ALDH1A1	Abcam	Ab52492	IHC 1:50
ALDH1A2	Sigma	HPA010022	IHC 1:500
ALDH1A3	GeneTex	GTX110784	IHC 1:100
pSMAD1/5	Cell Signaling	9516	IHC 1:200

## **Supplementary Data Files**

**Supplementary Data 1.** Gene ontology analysis of differentially expressed genes in endometrial organoids from control, control + A83-01, and *Smad2/3* cKO mice. *Attached as an excel spreadsheet.* 

**Supplementary Data 2.** SMAD4 bound genes that are up- or down-regulated in RNAseq datasets of control and *Smad2/3* cKO organoids. 607 SMAD4-bound genes downregulated in *Smad2/3* cKO vs control organoids (representing SMAD2/3 target genes) and 185 SMAD4-bound genes upregulated in *Smad2/3* cKO vs. control organoids (representing SMAD1/5 target genes). *Attached as an excel spreadsheet.* 

**Supplementary Data 3.** The source data behind the graphs in the paper. *Attached as an excel spreadsheet.*