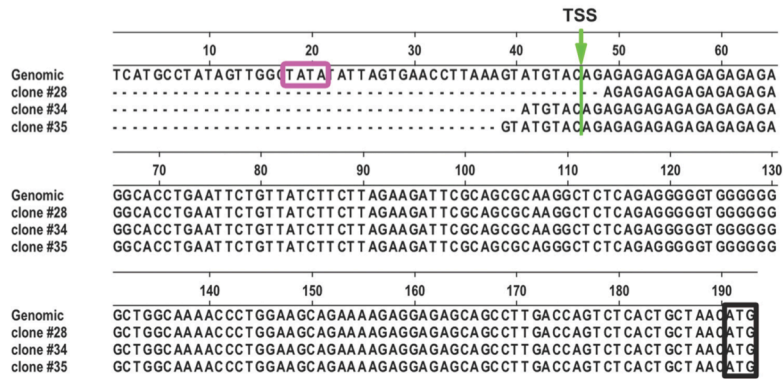


1 Supplementary Data

Gene Symbol	Fold change (from cHet UT)	
	cHet	cKO
2210411K11Rik	1.67	2.07
9130213B05Rik	1.80	1.80
A530088H08Rik	1.68	1.63
Abcc3	1.86	2.09
Abcc4	2.06	1.71
Acsf5	2.14	1.81
Acss1	1.93	2.02
Actg2	7.05	7.75
Ahnak	1.77	1.52
Ar	1.98	2.04
Arg2	2.46	2.07
Arhgef4	2.14	1.71
Arh4c	2.25	2.45
Atad4	2.10	2.13
Atp1a1	2.41	1.87
Atp1b1	1.93	2.18
Bace2	1.66	1.52
Bicc1	1.61	1.61
Bmp4	2.97	3.39
Capn6	1.58	1.76
Capsl	2.27	2.50
Car12	3.10	2.58
Cbr2	3.54	1.77
Cbr3	1.75	1.51
Ccdc3	1.91	1.93
Cond1	1.69	1.55
Cd9	2.13	2.27
Cd14	2.86	3.19
Cd44	1.91	1.86
Cd151	1.83	1.71
Cdc42se1	1.88	1.64
Cdh1	1.90	1.65
Ces3	3.48	3.26
Chodl	2.22	2.81
Claa3	1.82	3.82
Cldn3	1.81	2.15
Cldn4	2.95	2.26
Cldn6	1.65	2.05
Cldn10	7.49	9.22
Cldn11	3.53	3.06
Cntnap4	2.65	2.38
Col23a1	1.80	1.82
Cpe	1.51	1.52
Cpm	1.64	1.71
Crip2	1.63	1.81
Clsh	1.74	1.67
Ctsk	2.08	1.71
Cxcl15	3.11	8.74
Cyb561	2.18	2.06
Dkk3	2.06	1.87
Dpt	2.99	3.03
Dsg2	2.03	1.66
Dsp	2.20	1.96
Ebf3	2.01	1.75
Emb	3.21	3.50
Enpp2	4.79	5.44
Enpp5	1.80	1.66
Epb4.114b	1.62	1.52
Ern2	2.13	2.01
Erff1	1.77	1.64
Evx1	1.93	2.02
Faah	1.72	1.84
Fam134b	1.60	1.51
Fam3c	1.67	1.56
Fam46a	2.64	2.55
Fat1	2.40	1.80
Fgf10	2.35	2.35
Foxq1	2.68	1.65
Frk	1.63	1.72
Fxyd3	5.41	4.23
Gabrp	2.96	2.57
Gjb2	2.26	2.44
Gldc	2.54	2.06
Gm7665	1.63	1.82
Gm9746	2.38	2.10
Grb7	3.16	2.81
Grhl2	1.86	1.65
Gsta3	1.80	1.90
Gsta4	1.77	1.65
H2-D1	1.68	1.61
Hdc	8.37	7.61
Hexb	1.72	1.85
Hk2	2.09	2.07
Hopx	1.87	1.60
Hoxb7	2.10	2.00
Htalip2	1.56	1.67
Igf1	2.16	2.23
Igf2bp3	1.69	1.87
Igsf9	2.35	2.24
Inhba	2.07	1.78
Isl1	9.15	9.11
Itih2b	1.82	1.56
Kctd1	2.37	2.37
Klf5	2.22	1.70
Krt8	2.14	1.77
Krt15	6.09	2.65
Krt18	1.88	2.04
Krtcap3	1.89	2.15
Lad1	1.66	1.54
Lamc1	1.57	1.68
Lcn2	3.14	4.14
Lgals3	4.92	3.92
Lin7a	1.54	1.52
Lig1	1.98	1.64
Lmo4	2.87	2.49
Lmo7	1.79	1.89
LOC100044677	1.59	1.75
LOC100045132	1.54	1.50
LOC100046616	1.80	1.71
LOC100047261	1.92	2.12
LOC100047936	1.70	1.52
LOC547041	2.36	2.31
Lrig1	1.56	1.50
Lrrc8d1	1.76	1.80
Lrrc15	1.61	1.78
Lrrc26	2.39	1.86
Lypd2	11.59	10.07
Med24	3.31	3.52
Mtfe8	2.31	1.68
Mtfe8	2.19	1.59
Mgst1	3.00	2.01
Mtap7	1.95	1.81
Mtus1	1.51	1.57
Myh11	2.83	3.59
Myo6	2.03	1.75
Nfkbi	1.52	1.58
Nipal2	1.82	1.63
Nr2f1	4.77	5.42
Nup210	1.82	1.92
Nupr1	2.09	2.17
Olfml2b	2.84	2.76
Pacrg	1.58	1.64
Padi1	6.38	6.62
Pamr1	2.41	2.51
Papss1	1.62	1.58
Pdcd4	1.78	1.84
Pdlim1	2.03	2.15
Pdlim3	2.40	2.60
Plk3r3	1.80	1.97
Plk4	2.12	1.98
Plec1	1.67	1.56
Plekha2	2.05	1.77
Plscr1	2.27	2.37
Pnliprp1	4.35	5.11
Ppap2b	1.80	1.74
Ppap2c	1.81	1.73
Ppp1r1b	2.49	2.71
Ppp1r3b	2.45	2.43
Ppp2r2b	2.31	2.65
Prkab1	1.99	1.78
Prss8	1.74	1.88
Ptprk	1.83	1.63
Rab15	2.15	1.87
Rab25	3.07	2.76
Rbm47	2.10	1.61
Reep6	1.65	1.66
Rerg	2.01	1.95
Rgs10	1.54	1.56
Rnaset2b	1.52	1.66
Runx1	1.70	1.57
S100a11	1.76	1.67
Scx	1.72	1.98
Sema3f	1.97	1.78
Sema4a	2.20	1.64
Serpib11	3.25	2.44
Serpinf1	1.87	1.96
Shisa2	3.54	3.63
Six1	1.98	1.94
Slc46a3	1.79	1.54
Sort1	2.48	2.36
Sox9	1.58	1.65
Sox11	2.07	1.79
Spata13	1.74	1.54
Spint1	3.25	2.49
Srd5a1	1.90	1.50
Srgap3	1.62	1.72
Srpx	1.57	1.76
St6gal1	1.76	1.55
St6galnac2	2.43	2.02
Stxbp2	1.63	1.59
Sv2b	1.52	1.77
Tes	1.91	1.62
Tfrc	1.65	1.72
Thbs2	2.12	1.79
Tle4	2.24	2.15
Tmem45b	1.64	1.58
Tmem50b	1.55	1.64
Tmem59	1.60	1.70
Tmem79	1.80	1.51
Tmem176b	1.67	1.97
Tmem213	1.72	1.93
Trp63	5.49	5.31
Tspan8	5.50	6.33
Twist2	2.30	2.11
Unc13b	1.92	1.89
Upk1a	2.13	1.82
Upk2	3.55	1.90
Vcam1	2.87	2.73
Wfdc2	1.97	1.95
Wfdc15b	5.49	5.91

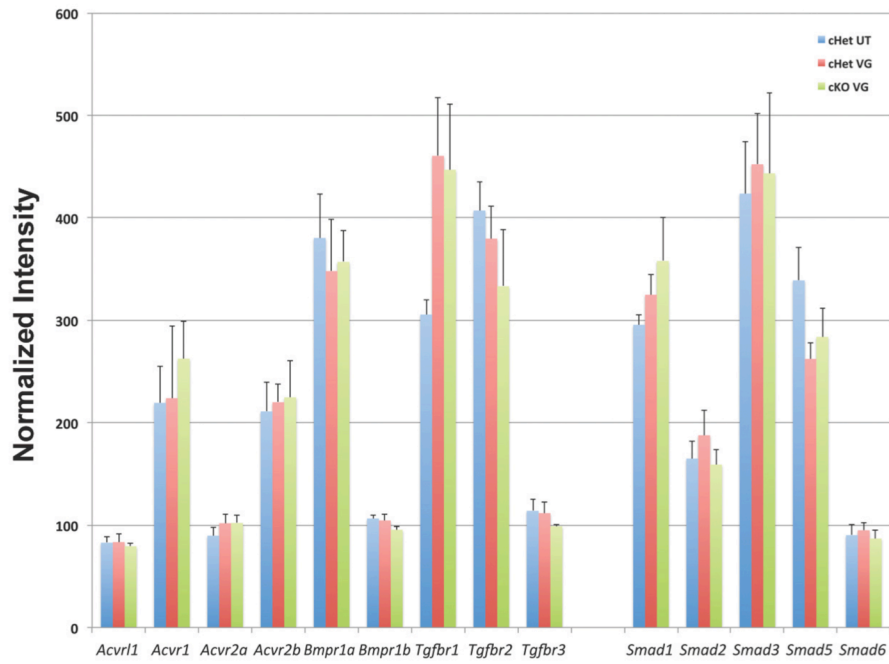
2 **Table S1. List of genes that are >1.5 fold higher in both *Trp63* cHet and cKO vaginae than *Trp63* cHet**
3 **uteri.** When multiple probes for a single gene are in the list, the signal for a probe that showed the highest fold
4 change is listed. The array data GEO # GSE44697 was further analyzed at the Genomic Core of the Center for
5 Genetic Medicine, Feinberg School of Medicine at Northwestern University, using the Bioconductor lumi and
6 limma packages for R [1,2,3,4]. The complete dataset was normalized by quantile normalization, and the probe-
7 set was filtered by present/absent calls based on the Illumina detection p-values – of these, 24003 out of 45281
8 probes were kept. Differentially expressed probes were identified by a modified t-test on each probe and
9 filtering them on the criteria that the change in expression was at least 1.5-fold and the p-value was less than
10 0.05.



11 **Figure S1. Identification of Trp63 promoter in vaginal epithelial cells.**

12 5' RACE analysis of *Trp63* was performed for P21 vaginal epithelial RNAs. The representative 3 sequences are
 13 aligned to genomic 5' sequence of *Trp63* exon 3', which contains ATG for Δ Np63. The TATA box (pink box),
 14 translational start site for Δ Np63 (black box), and the transcriptional start site (TSS) in reference sequences
 15 (GenBank AF075437.1, AF075438.1 and AF075439.1) are presented.

16
 17

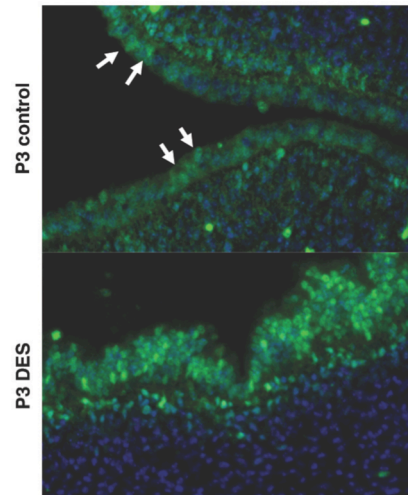


18 **Figure S2. Microarray analysis on TGF β family signaling related genes.**

19 The graph includes genes that were detected in at least one of 3 groups with detection p-value less than 0.05.

20 Type I and II receptors, Smads and Betaglycan (*Tgfb3*) were expressed in both uterus and vagina at similar

21 levels.



28 **Figure S4. RUNX1 expression in the uterus of P3 control and DES-treated mice.**

29 In P3 uterus, RUNX1 is expressed only in a small subset of uterine epithelial cells (arrows). However, DES-

30 treatment induces a high level of RUNX1 throughout the uterine epithelium.

31