

Supplemental Table 1

GBP1	-5.05	NM_002053 // GBP1 // guanylate binding protein 1, interferon-inducible, 67kDa // 1p22.2 // 2633
IFIT1	-5.32	NM_001548 // IFIT1 // interferon-induced protein with tetratricopeptide repeats 1 // 10q25-q26 // 3434
COL14A1	-5.36	NM_021110 // COL14A1 // collagen, type XIV, alpha 1 (undulin) // 8q23 // 7373 // BC036192 // COL14A1 // collagen, type XIV, alpha 1 (undulin) // 8q23 // 7373 // Y11710 // COL14A1 // collagen, type XIV, alpha 1 (undulin) // 8q23 // 7373 // M64108 // COL14A1 // collagen, type XIV, alpha 1 (undulin) // 8q23 // 7373
C1QTNF7	-5.96	NM_031911 // C1QTNF7 // C1q and tumor necrosis factor related protein 7 // 4p16-p15 // 114905 // AF329839 // C1QTNF7 // C1q and tumor necrosis factor related protein 7 // 4p16-p15 // 114905
PTPLAD2	-6.04	NM_001010915 // PTPLAD2 // protein tyrosine phosphatase-like A domain containing 2 // 9p21.3 // 401494 // BC114215 // PTPLAD2 // protein tyrosine phosphatase-like A domain containing 2 // 9p21.3 // 401494 // ENST00000342195 // PTPLAD2 // protein tyrosine phosphatase-like A domain containing 2 (PTPLAD2), mRNA // 9p21.3 // 401494 // BX538052 // PTPLAD2 // protein tyrosine phosphatase-like A domain containing 2 // 9p21.3 // 401494
ACTG2	-6.05	NM_001615 // ACTG2 // actin, gamma 2, smooth muscle, enteric // 2p13.1 // 72 // AK124338 // ACTG2 // actin, gamma 2, smooth muscle, enteric // 2p13.1 // 72
PHGDH	-6.05	NM_006623 // PHGDH // phosphoglycerate dehydrogenase // 1p12 // 26227 // AK093306 // PHGDH // phosphoglycerate dehydrogenase // 1p12 // 26227 // AK129762 // PHGDH // phosphoglycerate dehydrogenase // 1p12 // 26227
PLXNC1	-6.08	NM_005761 // PLXNC1 // plexin C1 // 12q23.3 // 10154 // AB208934 // PLXNC1 // plexin C1 // 12q23.3 // 10154
SULF1	-6.10	NM_015170 // SULF1 // sulfatase 1 // 8q13.2-q13.3 // 23213 // BC068565 // SULF1 // sulfatase 1 // 8q13.2-q13.3 // 23213 // AK055467 // SULF1 // sulfatase 1 // 8q13.2-q13.3 // 23213
PSAT1	-6.17	NM_058179 // PSAT1 // phosphoserine aminotransferase 1 // 9q21.2 // 29968 // NM_021154 // PSAT1 // phosphoserine aminotransferase 1 // 9q21.2 // 29968
SLC38A4	-6.40	NM_018018 // SLC38A4 // solute carrier family 38, member 4 // 12q13 // 55089 // AK001053 // SLC38A4 // solute carrier family 38, member 4 // 12q13 // 55089
ACTA2	-6.72	NM_001613 // ACTA2 // actin, alpha 2, smooth muscle, aorta // 10q23.3 // 59 // BC017554 // ACTA2 // actin, alpha 2, smooth muscle, aorta // 10q23.3 // 59
SEMA3C	-7.12	NM_006379 // SEMA3C // sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C // 7q21-q31 // 10512
MXRA5	-13.86	NM_015419 // MXRA5 // matrix-remodelling associated 5 // Xp22.33 // 25878
TAGLN	-15.55	NM_001001522 // TAGLN // transgelin // 11q23.2 // 6876 // NM_003186 // TAGLN // transgelin // 11q23.2 // 6876 // BC093050 // TAGLN // transgelin // 11q23.2 // 6876 // BC065829 // TAGLN // transgelin // 11q23.2 // 6876 // AB209555 // TAGLN // transgelin // 11q23.2 // 6876 // AK223002 // TAGLN // transgelin // 11q23.2 // 6876

Table 2 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with 0.5mM cAMP for 96 hrs (hESFendo cAMP) versus hESF endo treated with vehicle

Gene symbol	FC (hESFendo cAMP/hESFendo Control)	Description
CXCR4	33.49	chemokine (C-X-C motif) receptor 4
STC1	13.14	stanniocalcin 1
PRL	8.82	prolactin
SLC16A6	8.43	solute carrier family 16, member 6 (monocarboxylic acid
SERPINB2	7.45	serpin peptidase inhibitor, clade B (ovalbumin), member 2
MT1A	7.31	metallothionein 1A
GDF15	6.97	growth differentiation factor 15
TNFRSF11B	6.66	tumor necrosis factor receptor superfamily, member 11b
MT2A	6.24	metallothionein 2A
IL24	4.85	interleukin 24
SHC4	4.73	SHC (Src homology 2 domain containing) family, member
RHOB	4.49	ras homolog gene family, member B
MUM1L1	4.40	melanoma associated antigen (mutated) 1-like 1
TMPRSS11E2	4.26	transmembrane protease, serine 11E2 (TMPRSS11E2),
RGS2	4.24	regulator of G-protein signaling 2, 24kDa
SMOX	4.12	spermine oxidase
PLCL2	4.08	phospholipase C-like 2
ID3	4.03	inhibitor of DNA binding 3, dominant negative helix-loop-
BMP2	3.97	bone morphogenetic protein 2
ABCG1	3.65	ATP-binding cassette, sub-family G (WHITE), member 1
SLC40A1	3.61	solute carrier family 40 (iron-regulated transporter),
KIAA1754	3.51	KIAA1754
IER3	3.38	immediate early response 3
MCC	3.37	mutated in colorectal cancers
BTG1	3.32	B-cell translocation gene 1, anti-proliferative
ABTB2	3.17	ankyrin repeat and BTB (POZ) domain containing 2
PPP2R1B	3.12	protein phosphatase 2 (formerly 2A), regulatory subunit A,
TBX3	3.11	T-box 3 (ulnar mammary syndrome)
IGFBP1	3.00	insulin-like growth factor binding protein 1
SLC46A3	2.89	solute carrier family 46, member 3
BCL2L11	2.89	BCL2-like 11 (apoptosis facilitator)
TNFRSF10D	2.83	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
PRDM1	2.62	PR domain containing 1, with ZNF domain
TSPAN12	2.58	tetraspanin 12
GAB2	2.56	GRB2-associated binding protein 2
GPR125	2.41	G protein-coupled receptor 125
DISP2	2.40	dispatched homolog 2 (Drosophila)
CYFIP2	2.34	cytoplasmic FMR1 interacting protein 2
PITPNC1	2.32	phosphatidylinositol transfer protein, cytoplasmic 1
SNF1LK2	2.31	SNF1-like kinase 2
KIAA0256	2.29	KIAA0256 gene product
RNF19A	2.16	ring finger protein 19A
EPHB6	2.15	EPH receptor B6

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ARSG	2.13	arylsulfatase G
ATP6V0B	2.09	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b
C1orf75	2.03	chromosome 1 open reading frame 75
USP31	2.02	ubiquitin specific peptidase 31
FNDC3A	1.98	fibronectin type III domain containing 3A
ARHGAP24	1.98	Rho GTPase activating protein 24 /
GSTO1	1.98	glutathione S-transferase omega 1
ZBTB38	1.91	zinc finger and BTB domain containing 38
TNFRSF10B	1.91	tumor necrosis factor receptor superfamily, member 10b
CLN8	1.90	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive
OSGIN2	1.87	oxidative stress induced growth inhibitor family member 2
MAFG	1.86	v-maf musculoaponeurotic fibrosarcoma oncogene
ZFYVE27	1.86	zinc finger, FYVE domain containing 27
ZNF295	1.85	zinc finger protein 295
IFRD1	1.84	interferon-related developmental regulator 1
RBM24	1.83	RNA binding motif protein 24
FAS	1.83	Fas (TNF receptor superfamily, member 6)
KLHL23	1.82	kelch-like 23 (Drosophila)
ZNF468	1.80	zinc finger protein 468
UPF3B	1.79	UPF3 regulator of nonsense transcripts homolog B (yeast)
PCK2	1.75	PCK2 protein kinase 2
GADD45A	1.73	growth arrest and DNA-damage-inducible, alpha
DDX52	1.72	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
TMEM161B	1.72	transmembrane protein 161B
GABARAPL1	1.71	GABA(A) receptor-associated protein like 1
KLHDC8B	1.71	kelch domain containing 8B
SLC24A6	1.71	solute carrier family 24 (sodium/potassium/calcium
SERPINB8	1.69	serpin peptidase inhibitor, clade B (ovalbumin), member 8
ZCCHC14	1.69	zinc finger, CCHC domain containing 14
VPS18	1.69	vacuolar protein sorting 18 homolog (S. cerevisiae)
GDPD1	1.67	glycerophosphodiester phosphodiesterase domain
ACY1	-1.78	aminoacylase 1
COQ5	-1.78	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)
CCDC111	-1.79	coiled-coil domain containing 111
MPI	-1.80	mannose phosphate isomerase
TRIM6-TRIM34	-1.80	tripartite motif-containing 34 (TRIM34), transcript variant 3,
CAPN2	-1.81	calpain 2, (m/II) large subunit
ARL15	-1.82	ADP-ribosylation factor-like 15
RPL10	-1.83	ribosomal protein L10
SEMA5A	-1.85	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short
CTA-216E10.6	-1.86	hypothetical FLJ23584
APOBEC3F	-1.87	apolipoprotein B mRNA editing enzyme, catalytic
THG1L	-1.94	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)
FAM111A	-1.95	family with sequence similarity 111, member A

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ADAM23	-1.97	ADAM metallopeptidase domain 23
DPH5	-2.01	DPH5 homolog (S. cerevisiae)
RFX5	-2.04	regulatory factor X, 5 (influences HLA class II expression)
BCL2L13	-2.06	BCL2-like 13 (apoptosis facilitator)
HIST2H4A	-2.07	histone cluster 2, H4a
HIST2H2AA3	-2.08	histone cluster 2, H2aa3
ANXA3	-2.09	annexin A3
BFSP1	-2.10	beaded filament structural protein 1, filensin
IMPDH2	-2.11	IMP (inosine monophosphate) dehydrogenase 2
FMO4	-2.17	flavin containing monooxygenase 4
MGAT5	-2.18	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-
CLSPN	-2.19	claspin homolog (Xenopus laevis)
HIST1H4C	-2.20	histone cluster 1, H4c
C13orf3	-2.23	chromosome 13 open reading frame 3
LOC729197	-2.24	similar to Dynamin-1 (D100) (Dynamin, brain) (B-dynamin)
ARHGAP11A	-2.26	Rho GTPase activating protein 11A
RPL22L1	-2.29	ribosomal protein L22-like 1
NDC80	-2.30	NDC80 homolog, kinetochore complex component (S.
BRCA1	-2.32	breast cancer 1, early onset
ATAD2	-2.38	ATPase family, AAA domain containing 2
SSPN	-2.40	sarcospan (Kras oncogene-associated gene)
C15orf51	-2.41	chromosome 15 open reading frame 51
NRP1	-2.44	neuropilin 1
DPYSL3	-2.45	dihydropyrimidinase-like 3
LOC339803	-2.47	hypothetical protein LOC339803
KIF23	-2.53	kinesin family member 23
TPM2	-2.55	tropomyosin 2 (beta)
DKFZp434H141	-2.58	hypothetical protein DKFZp434H1419
CEP55	-2.62	centrosomal protein 55kDa
THBS3	-2.65	thrombospondin 3
ALDH1B1	-2.69	aldehyde dehydrogenase 1 family, member B1
MYL9	-2.70	myosin, light chain 9, regulatory
BRIP1	-2.71	BRCA1 interacting protein C-terminal helicase 1
PDCD1LG2	-2.76	programmed cell death 1 ligand 2
KIF2C	-2.79	kinesin family member 2C
KIF11	-2.81	kinesin family member 11
RASGRP3	-2.83	RAS guanyl releasing protein 3 (calcium and DAG-
FOXM1	-2.84	forkhead box M1
AHNAK	-2.85	AHNAK nucleoprotein
BUB1	-2.86	BUB1 budding uninhibited by benzimidazoles 1 homolog
CASP4	-2.87	caspase 4, apoptosis-related cysteine peptidase
CDKN3	-2.88	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
FLNB	-2.89	filamin B, beta (actin binding protein 278)
UBA7	-2.97	ubiquitin-like modifier activating enzyme 7

Table 2 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with 0.5mM cAMP for 96 hrs (hESFendo cAMP) versus hESF endo treated with vehicle

FANCI	-3.02	Fanconi anemia, complementation group I
DIAPH3	-3.27	diaphanous homolog 3 (Drosophila)
LMOD1	-3.28	leiomodin 1 (smooth muscle)
CENPI	-3.33	centromere protein I
SERPINE1	-3.36	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
CCNB1	-3.45	cyclin B1
PSMB9	-3.46	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)
TMEM171	-3.47	transmembrane protein 171
APOL6	-3.47	apolipoprotein L, 6
TPX2	-3.50	TPX2, microtubule-associated, homolog (Xenopus laevis)
NCAPG	-3.85	non-SMC condensin I complex, subunit G
GBP2	-3.90	guanylate binding protein 2, interferon-inducible
KIF20A	-3.90	kinesin family member 20A
CAV1	-3.97	caveolin 1, caveolae protein, 22kDa
MELK	-4.02	maternal embryonic leucine zipper kinase
ASPM	-4.30	asp (abnormal spindle) homolog, microcephaly associated
GRIA1	-4.65	glutamate receptor, ionotropic, AMPA 1
HIST1H3B	-4.69	histone cluster 1, H3b
C10orf107	-4.81	chromosome 10 open reading frame 107
S100A10	-5.25	S100 calcium binding protein A10
DLG7	-5.53	discs, large homolog 7 (Drosophila)
ANLN	-5.76	anillin, actin binding protein
SHCBP1	-6.05	SHC SH2-domain binding protein 1
ACTA2	-6.34	actin, alpha 2, smooth muscle, aorta
TOP2A	-7.09	topoisomerase (DNA) II alpha 170kDa
KIAA0101	-7.21	KIAA0101
TNC	-8.15	tenascin C (hexabrachion)
TAGLN	-11.29	transgelin

Table 3 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

Gene symbol	FC (hESFendo Control/hESFnon-endo Control)	Description
ANGPT2	4.27	angiopoietin 2
MMP10	3.88	matrix metalloproteinase 10 (stromelysin 2)
HSD17B2	3.84	hydroxysteroid (17-beta) dehydrogenase 2
CST1	3.81	cystatin SN
MMP3	3.40	matrix metalloproteinase 3 (stromelysin 1, progelatinase)
C20orf82	3.34	chromosome 20 open reading frame 82
MMP12	3.23	matrix metalloproteinase 12 (macrophage elastase)
PSG4	3.03	pregnancy specific beta-1-glycoprotein 4
ABCB1	2.72	ATP-binding cassette, sub-family B (MDR
IGFBP5	2.47	insulin-like growth factor binding protein 5
ARHGDIB	2.42	Rho GDP dissociation inhibitor (GDI) beta
MDGA2	2.42	MAM domain containing glycosylphosphatidylinositol anchor 2
MMP1	2.38	matrix metalloproteinase 1 (interstitial collagenase)
PLCH1	2.35	phospholipase C, eta 1
FMO2	2.34	flavin containing monooxygenase 2 (non-functional)
GRIA4	2.26	glutamate receptor, ionotropic, AMPA 4
ROBO2	2.25	roundabout, axon guidance receptor, homolog 2 (Drosophila)
PDE8B	2.25	phosphodiesterase 8B
CBLN2	2.24	cerebellin 2 precursor
COCH	2.22	coagulation factor C homolog, cochlin (Limulus polyphemus)
CHRM2	2.15	cholinergic receptor, muscarinic 2
TMEM26	2.15	transmembrane protein 26
ABCB4	2.08	ATP-binding cassette, sub-family B (MDR
CNTN5	2.05	contactin 5
ITGA8	2.04	integrin, alpha 8
ZSWIM5	2.03	zinc finger, SWIM-type containing 5
DSC3	2.00	desmocollin 3
SLC38A4	1.98	solute carrier family 38, member 4
MMP27	1.94	matrix metalloproteinase 27
CD274	1.94	CD274 molecule

Table 3 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

CCDC81	1.93	coiled-coil domain containing 81
DBC1	1.93	deleted in bladder cancer 1
PDK4	1.93	pyruvate dehydrogenase kinase, isozyme 4
CD24	1.90	CD24 molecule
A2M	1.90	alpha-2-macroglobulin
PTN	1.90	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)
ST3GAL5	1.89	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
SLC16A6	1.87	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)
KIAA0888	1.86	KIAA0888 protein
APCDD1	1.84	adenomatosis polyposis coli down-regulated 1
L1CAM	1.83	L1 cell adhesion molecule
OSAP	1.82	ovary-specific acidic protein
MMP7	1.81	matrix metalloproteinase 7 (matrilysin, uterine)
SYTL5	1.81	synaptotagmin-like 5
MYCN	1.81	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
C17orf28	1.80	chromosome 17 open reading frame 28
C18orf58	1.78	chromosome 18 open reading frame 58
GRAMD1C	1.78	GRAM domain containing 1C
CCRL1	1.77	chemokine (C-C motif) receptor-like 1
PFKFB3	1.77	6-phosphofructo-2-kinase
AK5	1.75	adenylate kinase 5
GSTM5	1.74	glutathione S-transferase M5
PHKA1	1.74	phosphorylase kinase, alpha 1 (muscle)
NRK	1.74	Nik related kinase
DEPDC1	1.72	DEP domain containing 1
DSG2	1.72	desmoglein 2
POLR2J3	1.72	RPB11b2 protein
PSG7	1.72	pregnancy specific beta-1-glycoprotein 7
MGC35361	1.71	hypothetical MGC35361
BMP4	1.70	bone morphogenetic protein 4
DOCK4	1.70	dedicator of cytokinesis 4
TRPC6	1.69	transient receptor potential cation channel, subfamily C, member 6

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List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

CCND2	1.68	cyclin D2
ESCO2	1.67	establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)
HIST1H4F	1.67	histone cluster 1, H4f
APOD	1.66	apolipoprotein D
KRTAP1-5	1.66	keratin associated protein 1-5
KRTAP1-5	1.66	keratin associated protein 1-5
MEOX1	1.66	mesenchyme homeobox 1
C10orf107	1.65	chromosome 10 open reading frame 107
DLG7	1.64	discs, large homolog 7 (<i>Drosophila</i>)
MGAT5	1.63	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase
ATP1B1	1.62	ATPase, Na ⁺
KRT34	1.62	keratin 34
NUSAP1	1.62	nucleolar and spindle associated protein 1
COP1	1.62	caspase-1 dominant-negative inhibitor pseudo-ICE
SEMA6A	1.61	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
SPRY4	1.61	sprouty homolog 4 (<i>Drosophila</i>)
TSPAN13	1.61	tetraspanin 13
CCDC144A	1.61	coiled-coil domain containing 144A
DUSP6	1.61	dual specificity phosphatase 6
KIF5C	1.60	kinesin family member 5C
CNIH3	1.60	cornichon homolog 3 (<i>Drosophila</i>)
SEMA3A	1.60	3A
NEDD4L	1.60	neural precursor cell expressed, developmentally down-regulated 4-like
ITGB3	1.59	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
HIST1H1A	1.59	histone cluster 1, H1a
CCDC144A	1.58	coiled-coil domain containing 144A
ZDHHC15	1.58	zinc finger, DHHC-type containing 15
CPE	1.58	carboxypeptidase E
KLHL2	1.57	kelch-like 2, Mayven (<i>Drosophila</i>)
TNFSF4	1.57	glycoprotein 1, 34kDa)
LEPREL1	1.56	leprecan-like 1
ZNF724P	1.56	zinc finger protein 724 pseudogene

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List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

LIPN	1.56	lipase, family member N
GLRX	1.56	glutaredoxin (thioltransferase)
FAM111B	1.56	family with sequence similarity 111, member B
ASTN2	1.55	astrotactin 2
IGFBP7	1.54	insulin-like growth factor binding protein 7
TNFRSF19	1.51	tumor necrosis factor receptor superfamily, member 19
DTL	1.46	denticleless homolog (Drosophila)
AOX1	-1.45	aldehyde oxidase 1
MATN2	-1.52	matrilin 2
CSF1	-1.54	colony stimulating factor 1 (macrophage)
OR2J3	-1.55	olfactory receptor, family 2, subfamily J, member 3
DDIT4	-1.55	DNA-damage-inducible transcript 4
C9orf19	-1.56	chromosome 9 open reading frame 19
METTL7A	-1.60	methyltransferase like 7A
PIP5K1B	-1.60	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
FAM49A	-1.61	family with sequence similarity 49, member A
NAV2	-1.61	neuron navigator 2
SLC7A8	-1.61	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
9-Sep	-1.62	septin 9
FMOD	-1.62	fibromodulin
LONRF2	-1.62	LON peptidase N-terminal domain and ring finger 2
C6orf141	-1.63	chromosome 6 open reading frame 141
DMKN	-1.64	dermokine
ANKRD30B	-1.64	ankyrin repeat domain 30B
GEM	-1.64	GTP binding protein overexpressed in skeletal muscle
BNC1	-1.64	basonuclin 1
CD226	-1.65	CD226 molecule
IGF1	-1.65	insulin-like growth factor 1 (somatomedin C)
TNC	-1.65	tenascin C (hexabrachion)
LIFR	-1.65	leukemia inhibitory factor receptor alpha
PPAP2B	-1.68	phosphatidic acid phosphatase type 2B
AKR1C3	-1.69	II)

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EGR1	-1.69	early growth response 1
SERPINE2	-1.70	member 2
BHLHB3	-1.70	basic helix-loop-helix domain containing, class B, 3
ABCC9	-1.70	ATP-binding cassette, sub-family C (CFTR
TMEM16D	-1.70	transmembrane protein 16D
THSD7A	-1.70	thrombospondin, type I, domain containing 7A
TLL1	-1.71	tolloid-like 1
IL19	-1.71	interleukin 19
PRKAR2B	-1.71	protein kinase, cAMP-dependent, regulatory, type II, beta
MKX	-1.71	mohawk homeobox
SLC7A3	-1.71	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
RORB	-1.72	RAR-related orphan receptor B
IL17RD	-1.73	interleukin 17 receptor D
CLIC2	-1.73	chloride intracellular channel 2
LRRC2	-1.73	leucine rich repeat containing 2
NFIX	-1.73	nuclear factor I
RHOJ	-1.73	ras homolog gene family, member J
ID2	-1.73	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
CHI3L1	-1.74	chitinase 3-like 1 (cartilage glycoprotein-39)
PODN	-1.74	podocan
IL1R1	-1.75	interleukin 1 receptor, type I
DACH1	-1.75	dachshund homolog 1 (Drosophila)
STK17B	-1.75	serine
TNIK	-1.75	TRAF2 and NCK interacting kinase
ECM2	-1.76	extracellular matrix protein 2, female organ and adipocyte specific
LRRK2	-1.76	leucine-rich repeat kinase 2
HSPB6	-1.79	heat shock protein, alpha-crystallin-related, B6
ATP8B4	-1.80	ATPase, class I, type 8B, member 4
LRRC32	-1.80	leucine rich repeat containing 32
PMP22	-1.82	peripheral myelin protein 22
SERPINF1	-1.83	factor), member 1
MFAP5	-1.83	microfibrillar associated protein 5

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C13orf33	-1.84	chromosome 13 open reading frame 33
KCNE4	-1.84	potassium voltage-gated channel, Isk-related family, member 4
FOS	-1.85	v-fos FBJ murine osteosarcoma viral oncogene homolog
PGM5	-1.85	phosphoglucomutase 5
HECW1	-1.85	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1
THBS2	-1.86	thrombospondin 2
AKR1C2	-1.87	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2)
SGK1	-1.87	serum
KLHL13	-1.87	kelch-like 13 (Drosophila)
ZDHHC14	-1.88	zinc finger, DHHC-type containing 14
INHBA	-1.89	inhibin, beta A
FBN2	-1.89	fibrillin 2 (congenital contractural arachnodactyly)
PAK3	-1.89	p21 (CDKN1A)-activated kinase 3
EMX2	-1.89	empty spiracles homeobox 2
LAMA4	-1.89	laminin, alpha 4
PCDH10	-1.91	protocadherin 10
CDH2	-1.92	cadherin 2, type 1, N-cadherin (neuronal)
DPP4	-1.92	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)
DLX5	-1.93	distal-less homeobox 5
SEMA6D	-1.94	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
KCNJ2	-1.96	potassium inwardly-rectifying channel, subfamily J, member 2
CPM	-1.96	carboxypeptidase M
TGFB3	-1.96	transforming growth factor, beta 3
VLDLR	-1.99	very low density lipoprotein receptor
MCOLN3	-1.99	mucolipin 3
IL33	-2.00	interleukin 33
RDH10	-2.00	retinol dehydrogenase 10 (all-trans)
ABCA6	-2.00	ATP-binding cassette, sub-family A (ABC1), member 6
FAM20A	-2.03	family with sequence similarity 20, member A
ANK2	-2.03	ankyrin 2, neuronal
EDG2	-2.04	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
EDNRA	-2.05	endothelin receptor type A

Table 3 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

TSHZ3	-2.07	teashirt zinc finger homeobox 3
ST6GAL2	-2.08	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2
ROR2	-2.08	receptor tyrosine kinase-like orphan receptor 2
SFRP4	-2.10	secreted frizzled-related protein 4
FIBIN	-2.10	fin bud initiation factor
CNTN3	-2.11	contactin 3 (plasmacytoma associated)
KDR	-2.12	kinase insert domain receptor (a type III receptor tyrosine kinase)
HGF	-2.14	hepatocyte growth factor (hepapoietin A)
TNFAIP6	-2.14	tumor necrosis factor, alpha-induced protein 6
CXCL12	-2.17	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
CDH11	-2.17	cadherin 11, type 2, OB-cadherin (osteoblast)
PDE1A	-2.18	phosphodiesterase 1A, calmodulin-dependent
EBF1	-2.22	early B-cell factor 1
IFI44L	-2.23	interferon-induced protein 44-like
POSTN	-2.26	periostin, osteoblast specific factor
CCDC80	-2.29	coiled-coil domain containing 80
FST	-2.32	follistatin
ABCA9	-2.34	ATP-binding cassette, sub-family A (ABC1), member 9
MFAP4	-2.35	microfibrillar-associated protein 4
SMPDL3A	-2.38	sphingomyelin phosphodiesterase, acid-like 3A
RSPO3	-2.38	R-spondin 3 homolog (<i>Xenopus laevis</i>)
CLDN11	-2.39	claudin 11 (oligodendrocyte transmembrane protein)
KCNK2	-2.40	potassium channel, subfamily K, member 2
SNCA	-2.42	synuclein, alpha (non A4 component of amyloid precursor)
CYP1B1	-2.43	cytochrome P450, family 1, subfamily B, polypeptide 1
PRSS12	-2.45	protease, serine, 12 (neurotrypsin, motopsin)
IGFBP3	-2.45	insulin-like growth factor binding protein 3
PSAT1	-2.46	phosphoserine aminotransferase 1
RXFP1	-2.46	relaxin
CHODL	-2.48	chondrolectin
SLIT2	-2.53	slit homolog 2 (<i>Drosophila</i>)
ASPN	-2.55	asporin

Table 3 Supplemental Data

List of up- and down-regulated genes in comparison of hESFendo treated with vehicle for 96 hrs (control) versus hESF non-endo control, expressed as fold change (FC).

FLRT2	-2.61	fibronectin leucine rich transmembrane protein 2
KGFLP1	-2.62	keratinocyte growth factor-like protein 1
KGFLP1	-2.62	keratinocyte growth factor-like protein 1
KGFLP1	-2.62	keratinocyte growth factor-like protein 1
NOX4	-2.64	NADPH oxidase 4
SLC7A14	-2.64	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14
ALDH1A1	-2.66	aldehyde dehydrogenase 1 family, member A1
TMOD1	-2.68	tropomodulin 1
ALDH1A2	-2.69	aldehyde dehydrogenase 1 family, member A2 (ALDH1A2), transcript variant 3, mRNA
ERAP2	-2.81	endoplasmic reticulum aminopeptidase 2
ITGBL1	-2.85	integrin, beta-like 1 (with EGF-like repeat domains)
LTBP1	-2.93	latent transforming growth factor beta binding protein 1
PRLR	-2.93	prolactin receptor
ODZ3	-2.93	odz, odd Oz
ADAM12	-3.00	ADAM metallopeptidase domain 12 (meltrin alpha)
SFRP1	-3.07	secreted frizzled-related protein 1
FGF7	-3.28	fibroblast growth factor 7 (keratinocyte growth factor)
DKK1	-3.28	dickkopf homolog 1 (Xenopus laevis)
SILV	-3.50	silver homolog (mouse)
SEMA3C	-3.57	3C
CCL2	-4.02	chemokine (C-C motif) ligand 2
PLXNC1	-4.19	plexin C1
TFPI2	-6.87	tissue factor pathway inhibitor 2

Supplemental Table 4

Ingenuity Canonical Pathways hESFnon-endo cAMP vs. hESFnon-endo vehicle control

Pathways	-Log(P-value)	p-value	Molecules
Hepatic Fibrosis / Hepatic Stellate Cell Activation	3.87E00	0.00013	VEGFA, MYL9 (includes EG:10398), IGFBP4, MYH10, FN1, EDNRB, ACTA2, KDR, TGFB2, EDNRA, IL1R1, TNFRSF11B
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	2.43E00	0.00372	CCNB1, GADD45A, TOP2A, CCNB2, CDC2
Caveolar-mediated Endocytosis	2.34E00	0.00457	FLNB, FLNC, FLNA, ACTA2, CAV1, ACTG2 (includes EG:72), PTRF
cAMP-mediated Signaling	2.1E00	0.00794	AKAP12, RGS2, PDE7B, PDE3B, DUSP1, RGS10, DUSP4, PDE8B, ADRA2C, PDE4B
G-Protein Coupled Receptor Signaling	1.88E00	0.01318	RGS2, PDE7B, EDNRB, PDE3B, DUSP1, RGS10, EDNRA, DUSP4, PDE8B, ADRA2C, PDE4B
Sphingolipid Metabolism	1.68E00	0.02089	SULF1, PPAP2A, ARSG, SPHK1, SGMS2
VEGF Signaling	1.66E00	0.02188	VEGFA, FOXO1, ACTA2, KDR, HIF1A, ACTG2 (includes EG:72)
Tight Junction Signaling	1.65E00	0.02239	MYLK, MYL9 (includes EG:10398), MYH10, ACTA2, JAM2, TGFB2, ACTG2 (includes EG:72), PPP2R1B, TNFRSF11B
Nicotinate and Nicotinamide Metabolism	1.47E00	0.03388	NP, CDK6, NAMPT, AOX1, CDC2, BST1
IL-8 Signaling	1.45E00	0.03548	VEGFA, ANGPT1, RHOB, KDR, RHOJ, PTGS2, CCND1, TEK, PLD1
Cardiac β -adrenergic Signaling	1.43E00	0.03715	AKAP12, PDE7B, PDE3B, PDE8B, PDE4B, SLC8A1, PPP2R1B
Aminosugars Metabolism	1.32E00	0.04786	PDE7B, PDE3B, PDE8B, PDE4B
VDR/RXR Activation	1.25E00	0.05623	FOXO1, GADD45A, IL1RL1, TGFB2, HES1
Coagulation System	1.17E00	0.06761	PLAUR, SERPINE1, BDKRB1
Aryl Hydrocarbon Receptor Signaling	1.14E00	0.07244	CCNA2, NFIX, ALDH1L2, CDK6, TGFB2, CCND1, GSTO1
TR/RXR Activation	1.14E00	0.07244	AKR1C3, SLC2A1, PDE3B, RCAN2, HIF1A
Regulation of Actin-based Motility by Rho	1.14E00	0.07244	MYLK, RHOB, ACTA2, RHOJ, ACTG2 (includes EG:72)
Acute Phase Response Signaling	1.11E00	0.07762	SOCS3, SOD2, FN1, C4A, IL1R1, MAP3K5 (includes EG:4217), SERPINE1, TNFRSF11B
Notch Signaling	1.09E00	0.08128	CNTN1, MAML3, HES1
Endoplasmic Reticulum Stress Pathway	1.08E00	0.08318	ERN1 (includes EG:2081), MAP3K5 (includes EG:4217)
Calcium Signaling	1.08E00	0.08318	MYL9 (includes EG:10398), MYH10, GRIA1, ACTA2, RCAN2, TPM2, SLC8A1, ATP2B4
Lysine Degradation	1.01E00	0.09772	ACAT2, AASS, REN, KYNU
Glycine, Serine and Threonine Metabolism	9.93E-01	0.10162	PSAT1, PHGDH, SMOX, PLCL2
C21-Steroid Hormone Metabolism	9.31E-01	0.11722	AKR1C3, HSD11B1
Nitric Oxide Signaling in the Cardiovascular System	8.91E-01	0.12853	VEGFA, PDE3B, KDR, CAV1
LPS/IL-1 Mediated Inhibition of RXR Function	8.6E-01	0.13804	FABP5, FMO2, ALDH1L2, ABCG1, SMOX, IL1R1, GSTO1, TNFRSF11B
BMP signaling pathway	8.6E-01	0.13804	FST, BMP3, BMP2, NOG
Tryptophan Metabolism	8.48E-01	0.14191	WARS, ACAT2, DHCR24, SMOX, AOX1, KYNU
TGF- β Signaling	8.15E-01	0.15311	BMP2, TGFB2, SERPINE1, INHBA
Phospholipid Degradation	8.01E-01	0.15812	PPAP2A, SPHK1, PLCL2, PLD1
Axonal Guidance Signaling	7.85E-01	0.16406	PLXNC1, CXCR4, BMP3, BMP2, SEMA6A, SLIT2, VEGFA, MYL9 (includes EG:10398), EPHB6, SEMA3D, SEMA3C, NRP1, FZD7
Actin Cytoskeleton Signaling	7.65E-01	0.17179	MYLK, MYL9 (includes EG:10398), MYH10, FN1, CYFIP2 (includes EG:26999), DIAPH3, ACTA2, ACTG2 (includes EG:72)
Interferon Signaling	7.61E-01	0.17338	IFIT1, IFIT3

Supplemental Table 4

Ingenuity Canonical Pathways hESFnon-endo cAMP vs. hESFnon-endo vehicle control

Glycerophospholipid Metabolism	7.46E-01	0.17947	PPAP2A, GPD2, SPHK1, PLCL2, PLD1
Sonic Hedgehog Signaling	7.38E-01	0.18281	CCNB1, CDC2
Cell Cycle: G1/S Checkpoint Regulation	7.35E-01	0.18408	CDK6, TGFB2, CCND1
PI3K/AKT Signaling	7.25E-01	0.18836	GAB2, FOXO1, MAP3K5 (includes EG:4217), CCND1, PPP2R1B
p53 Signaling	6.85E-01	0.20654	GADD45A, GADD45G, TNFRSF10B, CCND1
Lysine Biosynthesis	6.62E-01	0.21777	AASS
Amyotrophic Lateral Sclerosis Signaling	6.62E-01	0.21777	VEGFA, GRIA1, CAPN2, RNF19A
Phenylalanine Metabolism	6.53E-01	0.22233	DHCR24, SMOX
Purine Metabolism	6.33E-01	0.23281	AK5, ATP6V0B, IMPDH2, PDE7B, PDE3B, NP, RRM2, PDE8B, PDE4B, AOX1
p38 MAPK Signaling	6.18E-01	0.24099	DUSP1, TGFB2, IL1R1, MAP3K5 (includes EG:4217)
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	6.08E-01	0.24660	GAB2, ACTA2, ACTG2 (includes EG:72), PLD1
Integrin Signaling	5.93E-01	0.25527	MYLK, RHOB, ACTA2, CAV1, RHOJ, CAPN2, ACTG2 (includes EG:72)
LXR/RXR Activation	5.58E-01	0.27669	ABCG1, IL1R1, TNFRSF11B
Synthesis and Degradation of Ketone Bodies	5.54E-01	0.27925	ACAT2
Aminoacyl-tRNA Biosynthesis	5.34E-01	0.29242	WARS, IARS
NRF2-mediated Oxidative Stress Response	5.05E-01	0.31261	SOD2, ACTA2, MAP3K5 (includes EG:4217), AOX1, ACTG2 (includes EG:72), GSTO1
Valine, Leucine and Isoleucine Biosynthesis	4.98E-01	0.31769	IARS
Ceramide Signaling	4.84E-01	0.32810	SPHK1, PPP2R1B, TNFRSF11B
Androgen and Estrogen Metabolism	4.46E-01	0.35810	SULF1, ARSG, HSD11B1
Leukocyte Extravasation Signaling	4.31E-01	0.37068	CXCR4, MMP8, ACTA2, JAM2, MMP10, ACTG2 (includes EG:72)
N-Glycan Biosynthesis	4.19E-01	0.38107	MAN1C1, ARSG
14-3-3-mediated Signaling	4.1E-01	0.38905	FOXO1, CDK6, PLCL2, MAP3K5 (includes EG:4217), CDC2
Apoptosis Signaling	3.96E-01	0.40179	CAPN2, MAP3K5 (includes EG:4217), CDC2
IGF-1 Signaling	3.88E-01	0.40926	IGFBP4, NOV, FOXO1
PTEN Signaling	3.81E-01	0.41591	FOXO1, CCND1, BCL2L1
Wnt/ β -catenin Signaling	3.76E-01	0.42073	TGFB2, CCND1, PPP2R1B, LRP1, FZD7
SAPK/JNK Signaling	3.66E-01	0.43053	GADD45A, DUSP4, MAP3K5 (includes EG:4217)
Pantothenate and CoA Biosynthesis	3.6E-01	0.43652	DPYSL3
Glutamate Receptor Signaling	3.59E-01	0.43752	GRIA1, SLC38A1
Butanoate Metabolism	3.41E-01	0.45604	ACAT2, NLGN1
Glycosphingolipid Biosynthesis - Ganglioseries	3.31E-01	0.46666	ST3GAL5
Glycosphingolipid Biosynthesis - Globoseries	3.31E-01	0.46666	B3GALNT1
Death Receptor Signaling	3.24E-01	0.47424	TNFRSF10B, MAP3K5 (includes EG:4217)
Tyrosine Metabolism	3.24E-01	0.47424	SMOX, AOX1
Propanoate Metabolism	3.16E-01	0.48306	ACAT2, DHCR24
IL-10 Signaling	3.08E-01	0.49204	SOCS3, IL1R1
Glycosphingolipid Biosynthesis - Neolactoseries	3.06E-01	0.49431	ST3GAL5
Eicosanoid Signaling	3.01E-01	0.50003	AKR1C3, PTGS2
N-Glycan Degradation	2.94E-01	0.50816	MAN1C1
Activation of IRF by Cytosolic Pattern Recognition Receptors	2.93E-01	0.50933	RARRES3, IFIT2

Supplemental Table 4

Ingenuity Canonical Pathways hESFnon-endo cAMP vs. hESFnon-endo vehicle control

Valine, Leucine and Isoleucine Degradation	2.93E-01	0.50933	ACAT2, AOX1
Glycosaminoglycan Degradation	2.72E-01	0.53456	SULF1
Circadian Rhythm Signaling	2.72E-01	0.53456	BHLHB3
Hypoxia Signaling in the Cardiovascular System	2.66E-01	0.54200	VEGFA, HIF1A
PDGF Signaling	2.6E-01	0.54954	CAV1, SPHK1
Arginine and Proline Metabolism	2.41E-01	0.57412	SAT1, SMOX
Serotonin Receptor Signaling	2.26E-01	0.59429	SMOX
Complement System	2.26E-01	0.59429	C4A
Dopamine Receptor Signaling	2.25E-01	0.59566	SMOX, PPP2R1B
Antigen Presentation Pathway	2.03E-01	0.62661	PSMB9

Supplemental Table 5

Ingenuity Canonical Pathways hESFendo cAMP vs. hESFendo vehicle control

Pathways	-Log(P-value)	p-value	Molecules
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	2.44E00	0.00363	CCNB1, TOP2A, BRCA1
LPS/L-1 Mediated Inhibition of RXR Function	1.76E00	0.01738	ALDH1B1, ABCG1, SMOX, FMO4, TNFRSF11B
Caveolar-mediated Endocytosis	1.63E00	0.02344	FLNB, ACTA2, CAV1
Tight Junction Signaling	1.47E00	0.03388	MYL9 (includes EG:10398), ACTA2, PPP2R1B, TNFRSF11B
Calcium Signaling	1.35E00	0.04467	MYL9 (includes EG:10398), GRIA1, ACTA2, TPM2
Histidine Metabolism	1.34E00	0.04571	ALDH1B1, SMOX
N-Glycan Biosynthesis	1.24E00	0.05754	ARSG, MGAT5
β -alanine Metabolism	1.19E00	0.06457	ALDH1B1, DPYSL3
Actin Cytoskeleton Signaling	1.12E00	0.07586	MYL9 (includes EG:10398), CYFIP2 (includes EG:26999), DIAPH3, ACTA2
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.11E00	0.07762	MYL9 (includes EG:10398), ACTA2, TNFRSF11B
Glycine, Serine and Threonine Metabolism	1.01E00	0.09772	SMOX, PLCL2
LXR/RXR Activation	9.91E-01	0.10209	ABCG1, TNFRSF11B
Arginine and Proline Metabolism	9.59E-01	0.10990	ALDH1B1, SMOX
Dopamine Receptor Signaling	9.3E-01	0.11749	SMOX, PPP2R1B
Ceramide Signaling	9.2E-01	0.12023	PPP2R1B, TNFRSF11B
TGF- β Signaling	9.02E-01	0.12531	BMP2, SERPINE1
Xenobiotic Metabolism Signaling	8.95E-01	0.12735	ALDH1B1, SMOX, FMO4, PPP2R1B
Ascorbate and Aldarate Metabolism	8.5E-01	0.14125	ALDH1B1
Regulation of Actin-based Motility by Rho	8.49E-01	0.14158	RHOB, ACTA2
Axonal Guidance Signaling	8.11E-01	0.15453	EPHB6, MYL9 (includes EG:10398), CXCR4, BMP2, NRP1
Pantothenate and CoA Biosynthesis	8.1E-01	0.15488	DPYSL3
Amyotrophic Lateral Sclerosis Signaling	8.01E-01	0.15812	GRIA1, RNF19A
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	7.64E-01	0.17219	GAB2, ACTA2
Protein Ubiquitination Pathway	7.61E-01	0.17338	USP31, PSMB9, BRCA1
Integrin Signaling	7.09E-01	0.19543	RHOB, ACTA2, CAV1
Sonic Hedgehog Signaling	6.83E-01	0.20749	CCNB1
PI3K/AKT Signaling	6.43E-01	0.22751	GAB2, PPP2R1B
Serotonin Receptor Signaling	6.34E-01	0.23227	SMOX
Phenylalanine Metabolism	6.34E-01	0.23227	SMOX
Coagulation System	6.12E-01	0.24434	SERPINE1
Antigen Presentation Pathway	6.01E-01	0.25061	PSMB9
Bile Acid Biosynthesis	5.53E-01	0.27990	ALDH1B1
Tryptophan Metabolism	5.52E-01	0.28054	ALDH1B1, SMOX
Synaptic Long Term Depression	5.3E-01	0.29512	GRIA1, PPP2R1B
NF- κ B Signaling	5.13E-01	0.30690	BMP2, TNFRSF11B
Role of BRCA1 in DNA Damage Response	4.81E-01	0.33037	BRCA1
Glutamate Receptor Signaling	4.48E-01	0.35645	GRIA1
Butanoate Metabolism	4.35E-01	0.36728	ALDH1B1
Sphingolipid Metabolism	4.24E-01	0.37670	ARSG
Tyrosine Metabolism	4.24E-01	0.37670	SMOX
Acute Phase Response Signaling	4.21E-01	0.37931	SERPINE1, TNFRSF11B
Propanoate Metabolism	4.18E-01	0.38194	ALDH1B1
Ephrin Receptor Signaling	4.14E-01	0.38548	EPHB6, CXCR4

Supplemental Table 5

Ingenuity Canonical Pathways hESFendo cAMP vs. hESFendo vehicle control

Valine, Leucine and Isoleucine Degradation	4.01E-01	0.39719	ALDH1B1
Lysine Degradation	3.91E-01	0.40644	ALDH1B1
PDGF Signaling	3.76E-01	0.42073	CAV1
Leukocyte Extravasation Signaling	3.67E-01	0.42954	CXCR4, ACTA2
Chemokine Signaling	3.62E-01	0.43451	CXCR4
Nitric Oxide Signaling in the Cardiovascular System	3.58E-01	0.43853	CAV1
Pyruvate Metabolism	3.53E-01	0.44361	ALDH1B1
BMP signaling pathway	3.49E-01	0.44771	BMP2
Phospholipid Degradation	3.32E-01	0.46559	PLCL2
Androgen and Estrogen Metabolism	3.28E-01	0.46989	ARSG
VEGF Signaling	3.2E-01	0.47863	ACTA2
p53 Signaling	2.99E-01	0.50234	BRCA1
PTEN Signaling	2.99E-01	0.50234	BCL2L11
PPAR Signaling	2.99E-01	0.50234	TNFRSF11B
Glycerolipid Metabolism	2.99E-01	0.50234	ALDH1B1
IL-6 Signaling	2.95E-01	0.50699	TNFRSF11B
Glycolysis/Gluconeogenesis	2.76E-01	0.52966	ALDH1B1
Synaptic Long Term Potentiation	2.47E-01	0.56624	GRIA1
Glucocorticoid Receptor Signaling	2.33E-01	0.58479	PRL, SERPINE1
Glycerophospholipid Metabolism	2.29E-01	0.59020	PLCL2
Cardiac β -adrenergic Signaling	2.17E-01	0.60674	PPP2R1B

Supplemental Table 6

Canonical pathways uniquely activated by cAMP in hESF from women without (hESFnon-endo) and with (hESFendo) endometriosis.

Pathways unique to hESFnon-endo response to cAMP	-Log(P-value)	p-value	Molecules
cAMP-mediated Signaling	2.1E00	0.0079	AKAP12, RGS2, PDE7B, PDE3B, DUSP1, RGS10, DUSP4, PDE8B, ADRA2C, PDE4B
G-Protein Coupled Receptor Signaling	1.88E00	0.0132	RGS2, PDE7B, EDNRB, PDE3B, DUSP1, RGS10, EDNRA, DUSP4, PDE8B, ADRA2C, PDE4B
Aminosugars Metabolism	1.32E00	0.0479	PDE7B, PDE3B, PDE8B, PDE4B
VDR/RXR Activation	1.25E00	0.0562	FOXO1, GADD45A, IL1RL1, TGFB2, HES1
Aryl Hydrocarbon Receptor Signaling	1.14E00	0.0724	CCNA2, NFIX, ALDH1L2, CDK6, TGFB2, CCND1, GSTO1
TR/RXR Activation	1.14E00	0.0724	AKR1C3, SLC2A1, PDE3B, RCAN2, HIF1A
Notch Signaling	1.09E00	0.0813	CNTN1, MAML3, HES1
Endoplasmic Reticulum Stress Pathway	1.08E00	0.0832	ERN1 (includes EG:2081), MAP3K5 (includes EG:4217)
C21-Steroid Hormone Metabolism	9.31E-01	0.1172	AKR1C3, HSD11B1
Interferon Signaling	7.61E-01	0.1734	IFIT1, IFIT3
Cell Cycle: G1/S Checkpoint Regulation	7.35E-01	0.1841	CDK6, TGFB2, CCND1
Lysine Biosynthesis	6.62E-01	0.2178	AASS
Purine Metabolism	6.33E-01	0.2328	AK5, ATP6V0B, IMPDH2, PDE7B, PDE3B, NP, RRM2, PDE8B, PDE4B, AOX1
p38 MAPK Signaling	6.18E-01	0.2410	DUSP1, TGFB2, IL1R1, MAP3K5 (includes EG:4217)
Synthesis and Degradation of Ketone Bodies	5.54E-01	0.2793	ACAT2
Aminoacyl-tRNA Biosynthesis	5.34E-01	0.2924	WARS, IARS
NRF2-mediated Oxidative Stress Response	5.05E-01	0.3126	SOD2, ACTA2, MAP3K5 (includes EG:4217), AOX1, ACTG2 (includes EG:72), GSTO1
Valine, Leucine and Isoleucine Biosynthesis	4.98E-01	0.3177	IARS
14-3-3-mediated Signaling	4.1E-01	0.3890	FOXO1, CDK6, PLCL2, MAP3K5 (includes EG:4217), CDC2
Apoptosis Signaling	3.96E-01	0.4018	CAPN2, MAP3K5 (includes EG:4217), CDC2
IGF-1 Signaling	3.88E-01	0.4093	IGFBP4, NOV, FOXO1
Wnt/ β -catenin Signaling	3.76E-01	0.4207	TGFB2, CCND1, PPP2R1B, LRP1, FZD7
SAPK/JNK Signaling	3.66E-01	0.4305	GADD45A, DUSP4, MAP3K5 (includes EG:4217)
Glycosphingolipid Biosynthesis - Ganglioseries	3.31E-01	0.4667	ST3GAL5
Glycosphingolipid Biosynthesis - Globoseries	3.31E-01	0.4667	B3GALNT1
Death Receptor Signaling	3.24E-01	0.4742	TNFRSF10B, MAP3K5 (includes EG:4217)
IL-10 Signaling	3.08E-01	0.4920	SOCS3, IL1R1
Glycosphingolipid Biosynthesis - Neolactoseries	3.06E-01	0.4943	ST3GAL5
Eicosanoid Signaling	3.01E-01	0.5000	AKR1C3, PTGS2
N-Glycan Degradation	2.94E-01	0.5082	MAN1C1
Activation of IRF by Cytosolic Pattern Recognition Receptors	2.93E-01	0.5093	RARRES3, IFIT2
Glycosaminoglycan Degradation	2.72E-01	0.5346	SULF1
Circadian Rhythm Signaling	2.72E-01	0.5346	BHLHB3
Hypoxia Signaling in the Cardiovascular System	2.66E-01	0.5420	VEGFA, HIF1A
Complement System	2.26E-01	0.5943	C4A
Pathways unique to hESFendo response to cAMP	-Log(P-value)	p-value	Molecules
Histidine Metabolism	1.34E00	0.0457	ALDH1B1, SMOX
β -alanine Metabolism	1.19E00	0.0646	ALDH1B1, DPYSL3
Xenobiotic Metabolism Signaling	8.95E-01	0.1274	ALDH1B1, SMOX, FMO4, PPP2R1B
Ascorbate and Aldarate Metabolism	8.5E-01	0.1413	ALDH1B1
Protein Ubiquitination Pathway	7.61E-01	0.1734	USP31, PSMB9, BRCA1
Bile Acid Biosynthesis	5.53E-01	0.2799	ALDH1B1
Synaptic Long Term Depression	5.3E-01	0.2951	GRIA1, PPP2R1B

Supplemental Table 6

Canonical pathways uniquely activated by cAMP in hESF from women without (hESFnon-endo) and with (hESFendo) endometriosis.

NF-κB Signaling	5.13E-01	0.3069	BMP2, TNFRSF11B						
Role of BRCA1 in DNA Damage Response	4.81E-01	0.3304	BRCA1						
Ephrin Receptor Signaling	4.14E-01	0.3855	EPHB6, CXCR4						
PDGF Signaling	3.76E-01	0.4207	CAV1						
Chemokine Signaling	3.62E-01	0.4345	CXCR4						
Pyruvate Metabolism	3.53E-01	0.4436	ALDH1B1						
PPAR Signaling	2.99E-01	0.5023	TNFRSF11B						
Glycerolipid Metabolism	2.99E-01	0.5023	ALDH1B1						
IL-6 Signaling	2.95E-01	0.5070	TNFRSF11B						
Glycolysis/Gluconeogenesis	2.76E-01	0.5297	ALDH1B1						
Synaptic Long Term Potentiation	2.47E-01	0.5662	GRIA1						
Glucocorticoid Receptor Signaling	2.33E-01	0.5848	PRL, SERPINE1						