

Supplementary Figure S1

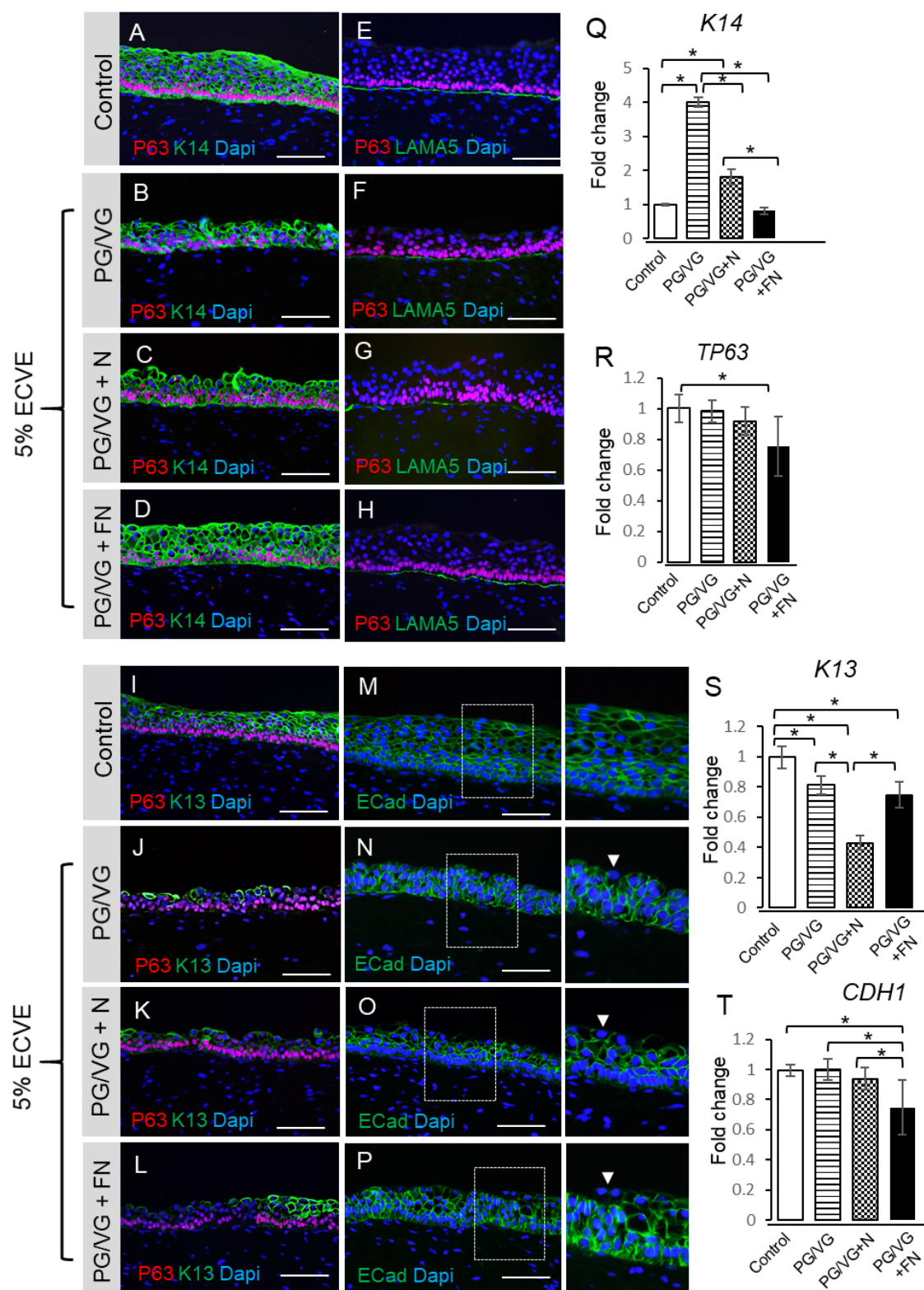


Fig. S1. Distribution and expression levels of VF structural epithelial genes. (A-D) Anti-Cytokeratin 14 (green) and anti-P63 staining (red) in control (A) and 5% ECVE exposed VF mucosae (B-D). (E-H) Anti-Laminin alfa 5 (green) co-stained with anti-P63 (red) in control (E) and 5% ECVE treated VF mucosae (F-H). (I-L) Anti-Cytokeratin 13 (in green) co-stained with anti-P63 (in red) in control (I) and 5% ECVE exposed VF mucosae (J-L). (M-P) Anti-E-Cadherin staining (in green) in control (M) and 5% ECVE exposed VF mucosae (N-P). Bracketed regions in the panels of M, N, O and P are magnified in the boxes on the right. White arrows point to apical cells with decreased expression of E-Cadherin. Scale bars = 100 μ m. (Q-T) Transcript levels of *KRT14* (Q), *TP63* (R), *KRT13* (S) and *CDH1* (T) in control and 5% ECVE exposed VF mucosae. Error bars represent \pm standard error of the mean obtained from three biological and three technical replicates. All histological data were performed in three biological replicates (n=3) and repeated twice in the laboratory by two investigators. One-Way ANOVA of variance for independent or correlated samples statistical analysis along with Plus Tukey HSD test were used to confirm statistical significance in gene expression, p-Value \leq 0.05 (*).

Supplemental Figure S2

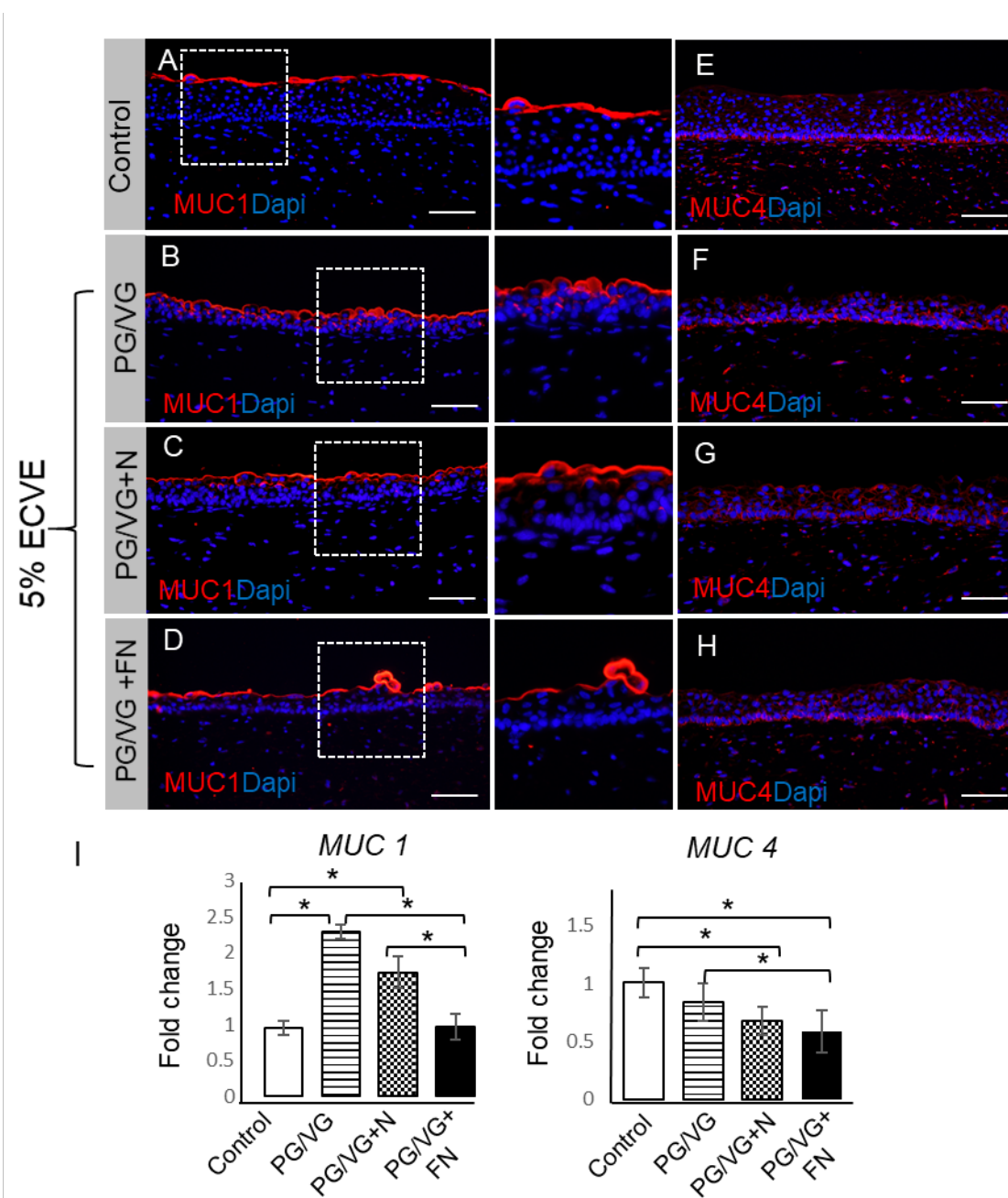


Fig. S2. Distribution and expression levels of functional VF epithelial genes. (A-D) Red immunofluorescent staining of Mucin 1 (MUC1) in control (A) and 5% ECVE exposed VF mucosae (B-D). Bracketed regions in the panels of A-D are magnified on the right respectively. (E-H) Red immunofluorescent staining of Mucin 4 (MUC4) in control (E) and 5% ECVE treated VF mucosae (F-H). Scale bar = 100 μ m. All histological data were performed in three biological replicates (n=3) and repeated twice in the laboratory by two investigators (I) Transcript levels of *MUC 1* and *MUC 4*. Error bars represent \pm standard error of the mean obtained from three biological and three technical replicates. One-Way ANOVA of variance for independent or correlated samples statistical analysis along with Plus Tukey HSD test were used to confirm statistical significance in gene expression, p-Value \leq 0.05 (*).

Supplementary Figure S3

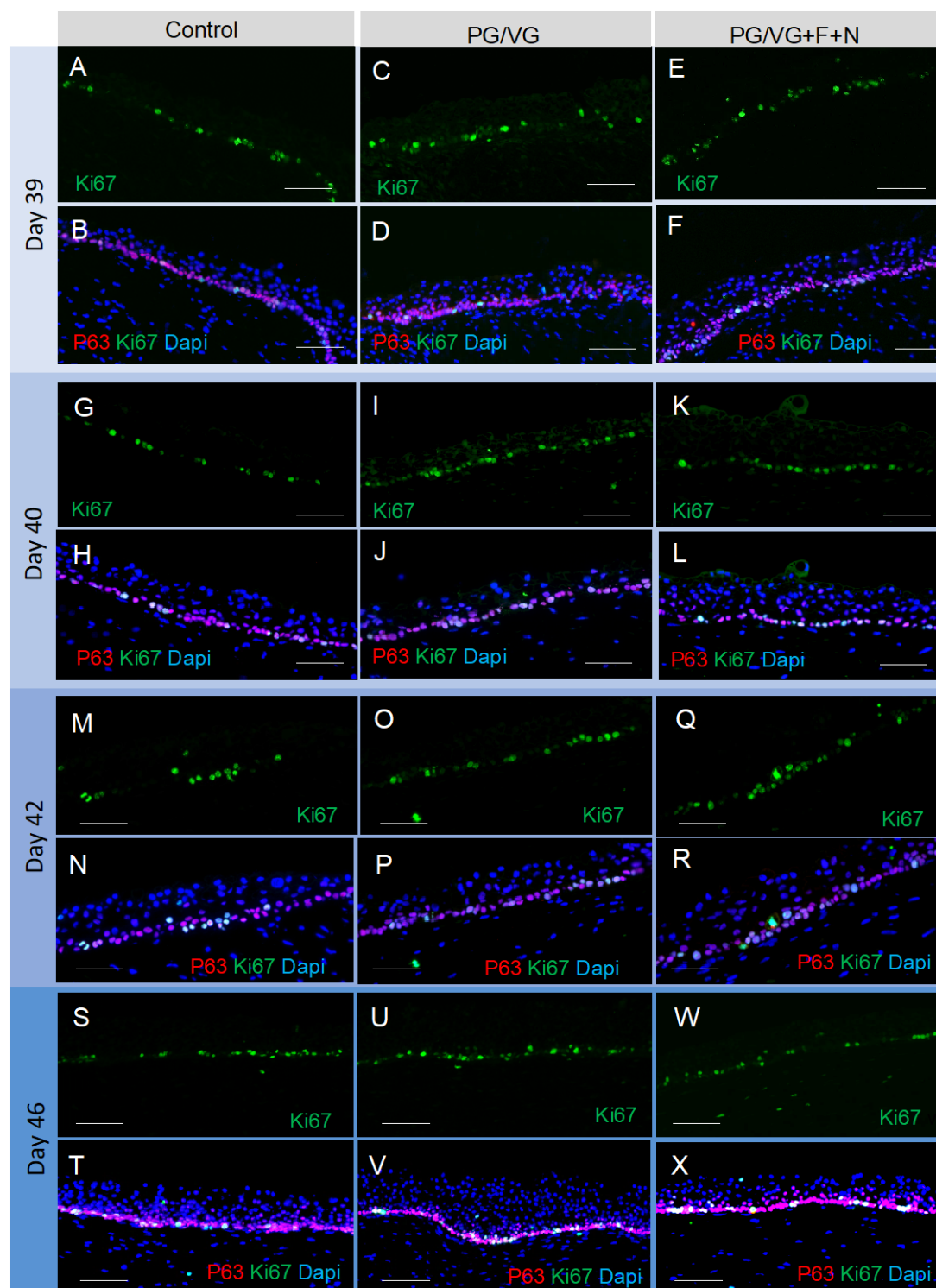


Fig. S3. Assessment of cell proliferation in control and 0.5% ECVE exposed VF mucosae at different stages of VF epithelial recovery (A -X). Anti-Ki67 staining (green) and anti-Ki67 co-stained with P63 (red) in control and 0.5% ECVE exposed VF mucosae at Day 39 (A-F), at Day 40 (G-L), at Day 42 (M-R), and at Day 46 (S-X). Scale bar = 100µm. All histological data were performed in three biological replicates (n=3) and repeated twice in the laboratory by two investigators

Table S1. Genes analyzed in the RT² Profiler PCR Arrays --Human Cytokine and Chemokines (PAHS-150Z).

Position	RefSeq Number	Symbol	Description
A01	NM_004797	ADIPOQ	Adiponectin, C1Q and collagen domain containing
A02	NM_001200	BMP2	Bone morphogenetic protein 2
A03	NM_130851	BMP4	Bone morphogenetic protein 4
A04	NM_001718	BMP6	Bone morphogenetic protein 6
A05	NM_001719	BMP7	Bone morphogenetic protein 7
A06	NM_001735	C5	Complement component 5
A07	NM_002981	CCL1	Chemokine (C-C motif) ligand 1
A08	NM_002986	CCL11	Chemokine (C-C motif) ligand 11
A09	NM_005408	CCL13	Chemokine (C-C motif) ligand 13
A10	NM_002987	CCL17	Chemokine (C-C motif) ligand 17
A11	NM_002988	CCL18	Chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
A12	NM_006274	CCL19	Chemokine (C-C motif) ligand 19
B01	NM_002982	CCL2	Chemokine (C-C motif) ligand 2
B02	NM_004591	CCL20	Chemokine (C-C motif) ligand 20
B03	NM_002989	CCL21	Chemokine (C-C motif) ligand 21
B04	NM_002990	CCL22	Chemokine (C-C motif) ligand 22
B05	NM_002991	CCL24	Chemokine (C-C motif) ligand 24
B06	NM_002983	CCL3	Chemokine (C-C motif) ligand 3
B07	NM_002985	CCL5	Chemokine (C-C motif) ligand 5
B08	NM_006273	CCL7	Chemokine (C-C motif) ligand 7

B09	NM_005623	CCL8	Chemokine (C-C motif) ligand 8
B10	NM_000074	CD40LG	CD40 ligand
B11	NM_000614	CNTF	Ciliary neurotrophic factor
B12	NM_000757	CSF1	Colony stimulating factor 1 (macrophage)
C01	NM_000758	CSF2	Colony stimulating factor 2 (granulocyte-macrophage)
C02	NM_000759	CSF3	Colony stimulating factor 3 (granulocyte)
C03	NM_002996	CX3CL1	Chemokine (C-X3-C motif) ligand 1
C04	NM_001511	CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
C05	NM_001565	CXCL10	Chemokine (C-X-C motif) ligand 10
C06	NM_005409	CXCL11	Chemokine (C-X-C motif) ligand 11
C07	NM_000609	CXCL12	Chemokine (C-X-C motif) ligand 12
C08	NM_006419	CXCL13	Chemokine (C-X-C motif) ligand 13
C09	NM_022059	CXCL16	Chemokine (C-X-C motif) ligand 16
C10	NM_002089	CXCL2	Chemokine (C-X-C motif) ligand 2
C11	NM_002994	CXCL5	Chemokine (C-X-C motif) ligand 5
C12	NM_002416	CXCL9	Chemokine (C-X-C motif) ligand 9
D01	NM_000639	FASLG	Fas ligand (TNF superfamily, member 6)
D02	NM_000175	GPI	Glucose-6-phosphate isomerase
D03	NM_000605	IFNA2	Interferon, alpha 2
D04	NM_000619	IFNG	Interferon, gamma
D05	NM_000572	IL10	Interleukin 10
D06	NM_000641	IL11	Interleukin 11
D07	NM_000882	IL12A	Interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
D08	NM_002187	IL12B	Interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)

D09	NM_002188	IL13	Interleukin 13
D10	NM_000585	IL15	Interleukin 15
D11	NM_004513	IL16	Interleukin 16
D12	NM_002190	IL17A	Interleukin 17A
E01	NM_052872	IL17F	Interleukin 17F
E02	NM_001562	IL18	Interleukin 18 (interferon-gamma-inducing factor)
E03	NM_000575	IL1A	Interleukin 1, alpha
E04	NM_000576	IL1B	Interleukin 1, beta
E05	NM_000577	IL1RN	Interleukin 1 receptor antagonist
E06	NM_000586	IL2	Interleukin 2
E07	NM_021803	IL21	Interleukin 21
E08	NM_020525	IL22	Interleukin 22
E09	NM_016584	IL23A	Interleukin 23, alpha subunit p19
E10	NM_006850	IL24	Interleukin 24
E11	NM_145659	IL27	Interleukin 27
E12	NM_000588	IL3	Interleukin 3 (colony-stimulating factor, multiple)
F01	NM_000589	IL4	Interleukin 4
F02	NM_000879	IL5	Interleukin 5 (colony-stimulating factor, eosinophil)
F03	NM_000600	IL6	Interleukin 6 (interferon, beta 2)
F04	NM_000880	IL7	Interleukin 7
F05	NM_000584	CXCL8	Interleukin 8
F06	NM_000590	IL9	Interleukin 9
F07	NM_002309	LIF	Leukemia inhibitory factor (cholinergic differentiation factor)
F08	NM_000595	LTA	Lymphotoxin alpha (TNF superfamily, member 1)
F09	NM_002341	LTB	Lymphotoxin beta (TNF superfamily, member 3)
F10	NM_002415	MIF	Macrophage migration inhibitory factor (glycosylation-inhibiting factor)

F11	NM_005259	MSTN	Myostatin
F12	NM_018055	NODAL	Nodal homolog (mouse)
G01	NM_020530	OSM	Oncostatin M
G02	NM_002704	PPBP	Pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
G03	NM_000582	SPP1	Secreted phosphoprotein 1
G04	NM_003238	TGFB2	Transforming growth factor, beta 2
G05	NM_000460	THPO	Thrombopoietin
G06	NM_000594	TNF	Tumor necrosis factor
G07	NM_002546	TNFRSF11B	Tumor necrosis factor receptor superfamily, member 11b
G08	NM_003810	TNFSF10	Tumor necrosis factor (ligand) superfamily, member 10
G09	NM_003701	TNFSF11	Tumor necrosis factor (ligand) superfamily, member 11
G10	NM_006573	TNFSF13B	Tumor necrosis factor (ligand) superfamily, member 13b
G11	NM_003376	VEGFA	Vascular endothelial growth factor A
G12	NM_002995	XCL1	Chemokine (C motif) ligand 1
H01	NM_001101	ACTB	Actin, beta
H02	NM_004048	B2M	Beta-2-microglobulin
H03	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H04	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H05	NM_001002	RPLP0	Ribosomal protein, large, P0
H06	SA_00105	HGDC	Human Genomic DNA Contamination
H07	SA_00104	RTC	Reverse Transcription Control
H08	SA_00104	RTC	Reverse Transcription Control
H09	SA_00104	RTC	Reverse Transcription Control
H10	SA_00103	PPC	Positive PCR Control
H11	SA_00103	PPC	Positive PCR Control
H12	SA_00103	PPC	Positive PCR Control

Table S2. List of CT values of human cytokines and chemokines uploaded on to the data analysis web portal at <http://www.qiagen.com/geneglobe>

	Control Group	Control Group	Control Group	PG/VG Test Group 1	PG/VG Test Group 1	PG/VG Test Group 1	PG/VG+N Test Group 2	PG/VG+N Test Group 2	PG/VG+N Test Group 2	PG/VG+N Test Group 3	PG/VG+N Test Group 3	PG/VG+N Test Group 3
A01	34.69	35.26	33.19	32.75	35.37	33.31	34.02	34.20	33.79	34.18	34.83	34.92
A02	26.76	30.27	27.15	29.55	29.60	26.59	27.40	28.55	27.19	27.15	29.63	26.95
A03	27.22	28.81	27.23	25.69	26.43	23.47	25.81	28.06	27.14	26.52	28.30	26.62
A04	28.82	29.82	28.60	29.21	28.57	26.89	26.97	28.59	28.68	27.31	28.92	27.74
A05	28.90	28.23	26.85	26.13	26.45	24.38	26.76	28.28	27.24	28.05	30.05	28.34
A06	28.75	40	28.14	30.70	40	27.85	27.24	28.81	29.23	26.98	28.71	27.65
A07	30.55	40	32.39	30.43	30.58	29.29	29.08	30.20	29.47	28.94	29.81	29.82
A08	32.12	33.44	31.04	34.58	31.63	30.66	27.92	29.42	29.51	28.08	30.06	28.46
A09	31.70	31.66	30.35	30.38	30.40	29.59	28.64	30.60	29.81	29.84	29.61	29.07
A10	33.58	33.11	33.38	32.00	34.11	31.91	33.22	34.29	32.55	34.68	33.79	32.24
A11	32.61	30.82	32.93	31.83	30.22	31.36	32.89	29.98	31.27	33.59	30.44	33.80
A12	37.71	35.72	31.67	34.27	32.71	31.91	33.47	31.44	35.16	36.19	31.72	33.57
B01	26.31	27.03	25.41	24.86	24.83	23.13	23.62	25.97	24.01	24.33	26.58	24.55
B02	27.14	27.90	27.27	27.90	27.18	25.89	26.11	27.45	26.32	25.53	26.29	25.60
B03	31.60	33.37	32.96	34.65	33.59	32.41	31.46	31.89	32.63	32.38	32.84	31.81
B04	40	34.60	40	40	36.92	40	35.05	40	40	40	40	33.58
B05	34.80	33.22	34.10	33.26	30.81	32.57	32.66	35.59	32.79	33.09	30.72	32.94
B06	33.99	34.21	33.55	34.55	33.68	33.14	32.85	33.28	32.68	33.28	33.19	32.84
B07	32.49	32.86	31.82	32.85	32.29	31.36	30.37	31.93	31.26	32.18	33.77	32.77
B08	29.00	29.61	28.18	29.80	30.20	29.58	26.61	28.27	27.60	29.39	27.14	27.17
B09	35.71	35.74	35.50	34.23	34.48	32.28	34.46	33.74	33.73	33.68	33.67	35.51
B10	32.59	31.98	32.54	31.75	32.06	31.27	31.28	32.28	31.50	31.46	32.41	32.49
B11	29.36	29.38	29.13	29.48	28.88	27.94	28.87	29.16	29.66	30.49	29.48	29.47
B12	27.58	26.34	25.37	26.64	26.29	25.26	25.02	24.98	25.14	25.17	25.30	23.84

C01	30.04	29.61	30.59	27.91	29.20	30.54	28.20	29.29	29.47	28.85	29.24	30.28
C02	31.53	32.41	31.33	31.79	32.19	29.95	30.91	32.20	31.73	31.95	31.89	30.53
C03	28.92	29.56	28.97	28.84	30.63	28.12	27.62	29.09	28.18	28.60	29.43	28.72
C04	26.25	29.59	27.53	28.44	29.79	24.64	22.66	27.25	25.51	23.06	27.57	23.45
C05	32.76	32.11	30.85	33.47	29.10	30.00	29.92	30.96	30.65	29.99	30.05	29.40
C06	36.42	37.32	36.16	34.73	35.41	33.67	36.53	36.50	35.35	36.69	36.15	34.88
C07	23.23	23.75	23.00	24.51	24.79	23.41	23.40	22.57	22.85	21.34	22.92	21.99
C08	29.72	29.75	28.96	30.60	29.80	29.50	27.66	28.12	27.86	26.47	27.91	27.49
C09	37.66	36.07	34.16	35.91	33.78	33.03	33.14	34.25	33.88	35.90	33.66	33.99
C10	27.44	28.00	24.67	25.93	26.00	23.51	24.99	24.43	24.28	27.04	24.57	22.52
C11	33.62	34.44	34.09	34.08	32.30	32.65	32.65	32.99	32.92	33.74	33.19	31.47
C12	31.79	32.27	31.26	31.50	30.75	30.50	30.75	31.32	30.51	29.62	31.00	30.59
D01	31.68	31.65	32.16	31.35	30.74	31.38	30.01	30.38	30.87	30.00	30.91	33.19
D02	23.28	23.57	23.22	22.99	22.27	20.86	21.10	22.92	21.31	20.93	22.88	21.18
D03	35.13	36.09	35.42	36.60	36.51	33.96	34.41	36.34	36.32	35.51	36.41	35.33
D04	32.53	33.45	34.08	35.35	32.99	32.45	34.43	34.22	33.17	34.60	34.72	34.32
D05	32.18	30.45	29.97	34.77	26.93	30.70	31.59	32.13	32.59	31.38	26.25	31.50
D06	27.90	27.21	26.23	29.10	29.20	27.85	25.57	27.13	27.48	25.22	26.82	25.84
D07	32.28	32.23	30.51	31.56	30.61	29.09	29.99	32.27	31.39	32.72	31.94	30.47
D08	32.98	32.71	33.84	33.35	33.23	31.62	32.70	33.10	32.51	32.17	33.41	31.25
D09	29.46	30.85	30.76	30.34	29.78	29.09	30.62	30.54	29.22	29.01	29.85	30.78
D10	28.45	28.34	27.72	28.88	28.28	27.96	27.22	26.89	27.50	27.74	26.87	26.42
D11	33.14	31.93	31.33	33.58	33.68	31.74	32.69	31.84	31.25	33.41	33.81	29.95
D12	36.91	35.22	35.38	36.81	34.49	34.49	34.62	38.03	36.07	37.01	33.77	34.46
E01	30.27	30.25	30.95	30.19	30.12	29.52	29.60	29.41	29.69	30.14	30.27	30.19
E02	29.96	31.01	31.34	32.18	31.24	29.98	30.14	31.57	29.35	29.50	30.67	30.09
E03	31.12	32.52	32.37	33.02	31.78	29.82	29.96	31.31	31.20	31.11	31.97	30.64
E04	27.69	30.92	29.21	32.43	32.85	30.84	27.44	30.11	30.28	28.57	30.95	29.31
E05	29.86	28.82	28.16	29.63	30.24	27.56	25.96	28.20	27.74	26.42	28.38	26.85
E06	35.88	35.56	35.73	34.64	33.93	33.78	34.00	33.90	34.06	33.84	34.23	34.88
E07	24.00	25.26	25.19	26.98	26.51	26.55	26.81	25.98	25.29	26.63	26.51	26.44
E08	28.36	28.79	28.92	28.78	29.60	28.96	25.99	29.69	28.61	29.86	29.95	28.73
E09	29.40	30.66	29.45	33.18	32.12	30.32	28.69	31.15	30.55	31.48	31.68	30.61
E10	30.00	29.53	28.33	29.57	29.35	27.64	27.99	28.23	27.91	28.82	27.55	25.94

E11	31.80	31.83	31.39	32.06	31.32	29.78	30.74	31.02	30.13	31.27	31.38	30.59
E12	34.25	29.91	32.65	33.99	28.34	30.18	32.31	27.56	32.11	33.62	25.98	31.14
F01	29.45	30.53	30.19	29.00	31.35	30.66	29.92	30.81	30.07	29.87	30.83	30.27
F02	32.76	34.80	34.81	32.64	34.19	33.44	32.34	33.41	33.10	32.41	34.69	34.51
F03	23.57	23.94	23.02	23.71	23.80	22.13	19.99	21.60	21.41	19.59	21.01	19.87
F04	32.75	34.61	35.17	33.74	34.10	34.61	33.92	36.58	33.90	34.04	36.51	33.50
F05	24.58	24.33	22.83	23.90	24.71	22.33	20.48	23.06	22.69	20.56	23.09	20.86
F06	35.65	36.91	35.37	37.16	36.05	34.95	34.30	38.13	36.37	34.37	37.45	35.98
F07	29.33	28.44	26.67	29.57	28.78	26.71	24.88	27.65	27.37	28.76	26.97	26.00
F08	32.08	33.27	32.46	34.49	31.77	31.00	32.72	32.45	31.69	31.99	32.42	31.32
F09	32.38	32.49	31.81	32.09	32.39	30.21	31.85	32.58	31.14	32.33	32.77	31.46
F10	22.40	21.56	20.25	20.82	21.02	19.83	21.19	21.57	20.50	20.57	19.90	19.57
F11	32.24	32.78	31.74	31.92	32.14	29.95	31.90	32.32	31.05	31.55	32.29	31.74
F12	33.28	33.83	31.82	33.39	32.83	30.64	31.70	32.14	31.68	34.11	33.56	30.82
G01	32.62	32.32	33.60	33.20	33.76	31.20	31.31	30.99	31.82	31.84	31.19	33.61
G02	30.70	32.92	31.90	34.04	33.29	32.93	32.93	31.32	34.35	30.91	29.23	30.97
G03	25.93	26.61	25.82	27.17	27.15	25.97	24.33	25.92	25.89	27.63	27.35	26.62
G04	26.16	26.86	26.10	25.75	25.46	23.84	23.96	25.50	26.00	24.15	26.02	24.90
G05	30.20	31.47	30.63	31.25	30.85	29.55	29.82	30.83	30.61	29.37	31.17	29.14
G06	40	35.58	34.07	10.58	34.42	40	35.52	40	38.63	33.45	32.87	33.30
G07	28.38	29.40	26.67	28.71	31.66	25.89	22.30	27.14	26.61	25.96	26.76	24.13
G08	31.23	30.44	30.00	29.30	29.52	28.40	28.29	30.82	29.78	29.46	30.85	30.11
G09	32.88	31.61	31.41	31.34	31.28	29.63	30.51	31.95	31.44	31.72	32.50	31.33
G10	28.63	27.84	27.61	29.38	28.89	27.88	27.64	27.17	27.62	28.26	27.31	26.59
G11	24.36	24.46	23.44	25.53	23.13	22.22	24.36	24.19	23.83	24.19	23.21	22.33
G12	35.76	35.57	35.57	37.72	31.79	31.78	37.69	32.51	36.57	38.26	31.15	32.88
H01	20.61	23.63	20.89	21.00	22.56	17.22	18.59	22.03	19.25	19.56	22.22	19.52
H02	20.60	22.05	20.97	21.73	21.13	20.09	17.46	20.20	18.46	18.33	20.24	18.79
H03	20.37	22.68	20.18	21.63	19.69	19.69	19.13	19.86	21.15	19.50	19.79	19.50
H04	26.30	26.68	25.93	26.23	25.80	25.16	24.96	26.13	26.35	25.25	26.14	25.32
H05	22.68	21.40	20.23	19.92	19.64	18.31	16.57	19.10	20.49	17.44	19.49	17.63
H06	35.22	35.67	36.41	34.31	34.93	34.44	35.26	35.75	35.50	35.17	35.68	34.62
H07	22.40	23.64	23.88	23.71	25.29	23.19	21.12	25.39	26.30	21.13	24.90	22.89
H08	22.50	23.83	24.00	24.51	25.68	22.81	21.40	25.11	25.96	21.22	24.80	22.732

H09	22.59	23.77	23.65	24.38	25.36	22.84	25.84	24.87	23.68	26.77	25.12	22.97
H10	27.66	23.23	27.91	27.13	23.89	25.71	28.59	23.52	26.43	28.30	22.87	24.21
H11	28.17	23.90	27.31	28.16	22.66	23.92	29.17	24.15	25.87	27.64	22.27	23.71
H12	28.80	22.92	27.84	27.73	23.81	24.25	29.33	23.82	26.68	28.15	22.17	23.90

Table S3. Fold regulation and p-values of genes associated mucosal inflammation. Fold regulation is compared to controls

Position	Gene Symbol	Group 1		Group 2		Group 3	
		Fold Regulation	p-Value	Fold Regulation	p-Value	Fold Regulation	p-Value
A01	ADIPOQ	-1.34	0.949612	-2.65	0.07756	-4.34	0.022261
A02	BMP2	-2.93	0.162542	-2.56	0.214097	-3.07	0.150726
A03	BMP4	2.89	0.048146	-1.93	0.019491	-2.22	0.007207
A04	BMP6	-1.13	0.333216	-1.62	0.024908	-1.6	0.015384
A05	BMP7	2.49	0.044874	-2.19	0.15756	-5.99	0.051444
A06	C5	-2.99	0.26999	1.42	0.521938	2.12	0.946686
A07	CCL1	2.87	0.296137	2.57	0.391479	2.56	0.40323
A08	CCL11	-2.17	0.211494	2.93	0.009991	2.97	0.003055
A09	CCL13	1.06	0.855139	-1.1	0.634625	-1	0.89173
A10	CCL17	-1.27	0.847791	-3.24	0.228373	-3.95	0.188997
A11	CCL18	-1.03	0.717673	-1.94	0.633077	-4.78	0.471747
A12	CCL19	-1.08	0.653829	-2.16	0.832994	-2.47	0.749384
B01	CCL2	1.93	0.005131	1.01	0.765233	-1.59	0.049993
B02	CCL20	-1.49	0.161355	-1.85	0.180155	-1.1	0.733896
B03	CCL21	-3.81	0.076845	-2.06	0.224412	-2.76	0.11197
B04	CCL22	-2.23	0.29771	-3.56	0.192872	-2.69	0.229169
B05	CCL24	1.74	0.560675	-2.2	0.38765	1.02	0.733473
B06	CCL3	-1.87	0.158638	-1.65	0.368825	-1.93	0.216966
B07	CCL5	-1.75	0.090679	-1.41	0.254146	-4.87	0.010946
B08	CCL7	-3.88	0.008	-1.2	0.425252	-1.66	0.946204
B09	CCL8	1.24	0.778056	-1.6	0.610014	-1.85	0.510117
B10	CD40LG	-1.28	0.57854	-2.02	0.329164	-2.86	0.238628
B11	CNTF	-1.41	0.364815	-3.11	0.121358	-4.88	0.090452
B12	CSF1	-1.57	0.295875	-1.24	0.661535	-1.08	0.72296
C01	CSF2	-1.12	0.769752	-1.52	0.413178	-2.21	0.358839
C02	CSF3	-1.5	0.0961	-2.94	0.007822	-2.76	0.021024
C03	CX3CL1	-2.11	0.219691	-1.8	0.153513	-2.89	0.038237
C04	CXCL1	-1.82	0.646625	1.93	0.39189	2.51	0.224539

C05	CXCL10	1.02	0.615737	-1.23	0.522227	1.25	0.685628
C06	CXCL11	-1.41	0.413821	-3.25	0.14523	-3.31	0.134927
C07	CXCL12	-3.83	0.02162	-2.49	0.18512	-1.44	0.200292
C08	CXCL13	-2.86	0.074479	-1.07	0.980486	1.34	0.426084
C09	CXCL16	-1.18	0.626293	-1.67	0.221699	-2.4	0.319296
C10	CXCL2	1.44	0.761869	1.35	0.610594	1.17	0.492224
C11	CXCL5	1.01	0.81883	-1.42	0.487189	-1.43	0.658705
C12	CXCL9	-1.13	0.838286	-1.72	0.288454	-1.31	0.369544
D01	FASLG	-1.28	0.71466	-1.22	0.660594	-2.46	0.386366
D02	GPI	1.22	0.645905	-1.08	0.946249	-1.05	0.721945
D03	IFNA2	-1.6	0.316888	-2.84	0.149693	-3.4	0.133243
D04	IFNG	-2.22	0.203707	-4.87	0.106166	-7.76	0.068464
D05	IL10	-1.95	0.562303	-7.67	0.137885	-1.53	0.501363
D06	IL11	-6.18	0.062115	-2.48	0.13037	-1.53	0.280914
D07	IL12A	1.17	0.723315	-2.36	0.071131	-3.48	0.071281
D08	IL12B	-1.5	0.380721	-2.45	0.284113	-1.82	0.332568
D09	IL13	-1.33	0.399013	-2.76	0.212357	-2.44	0.181454
D10	IL15	-2.34	0.136928	-1.66	0.493474	-1.52	0.603639
D11	IL16	-3.72	0.139453	-2.81	0.272895	-4.06	0.244233
D12	IL17A	-1.61	0.392563	-2.97	0.147803	-2.26	0.414697
E01	IL17F	-1.4	0.462483	-1.71	0.43161	-2.77	0.209698
E02	IL18	-2.62	0.111179	-2.43	0.273233	-2.11	0.153393
E03	IL1A	-1.47	0.328236	-1.43	0.303056	-2	0.144028
E04	IL1B	-13.84	0.135316	-3.26	0.214877	-4.29	0.184107
E05	IL1RN	-2.34	0.19862	-1.04	0.648971	-1.03	0.673274
E06	IL2	-1.11	0.78615	-1.61	0.473853	-2.12	0.285518
E07	IL21	-7.39	0.041969	-7.5	0.050909	-11.12	0.035929
E08	IL22	-2.73	0.169701	-2.15	0.199245	-6.02	0.062789
E09	IL23A	-8.35	0.001218	-3.98	0.002164	-9.1	0.001272
E10	IL24	-1.51	0.238463	-1.37	0.578921	1.06	0.614469
E11	IL27	-1.33	0.380075	-1.57	0.533096	-2.25	0.15919
E12	IL3	1.33	0.95802	-1.06	0.815109	1.2	0.484133
F01	IL4	-2.48	0.566347	-3.77	0.046445	-4.1	0.035901

F02	IL5	-1.26	0.866017	-1.44	0.388842	-2.85	0.189438
F03	IL6	-1.66	0.108928	1.75	0.049729	3.01	0.001628
F04	IL7	-2.08	0.337616	-3.61	0.146737	-3.55	0.134236
F05	CXCL8	-1.69	0.20717	1.1	0.942692	1.57	0.262679
F06	IL9	-2.01	0.281961	-2.77	0.1509	-2.94	0.14391
F07	LIF	-2.35	0.144571	-1.14	0.521211	-1.82	0.501239
F08	LTA	-1.79	0.352771	-2.61	0.128913	-2.1	0.06198
F09	LTB	-1.28	0.403547	-2.51	0.184707	-3.31	0.055584
F10	MIF	-1.13	0.592163	-2.6	0.184788	-1.3	0.683908
F11	MSTN	-1.08	0.686789	-2.3	0.180819	-2.59	0.024663
F12	NODAL	-1.26	0.392322	-1.47	0.451274	-3.06	0.1661
G01	OSM	-1.87	0.323128	-1.17	0.740635	-2.19	0.552686
G02	PPBP	-6.1	0.0713	-6.65	0.144067	-1.23	0.78631
G03	SPP1	-3.18	0.019935	-1.94	0.054915	-7.17	0.009913
G04	TGFB2	1.26	0.291319	-1.39	0.263056	-1.33	0.261376
G05	THPO	-1.75	0.070771	-2.54	0.037897	-1.85	0.06717
G06	TNF	127.49	0.373901	-4.02	0.050591	-1.22	0.969815
G07	TNFRSF11B	-3.09	0.268953	2.14	0.359668	1.7	0.344565
G08	TNFSF10	1.37	0.659453	-1.71	0.292383	-2.54	0.176298
G09	TNFSF11	1.14	0.847909	-2.05	0.280084	-3.14	0.196984
G10	TNFSF13B	-3.29	0.158789	-2.22	0.331585	-2.18	0.332172
G11	VEGFA	-1.48	0.522086	-3.33	0.065147	-1.89	0.334883
G12	XCL1	2.17	0.328343	-1.83	0.947324	1.17	0.480846
H01	ACTB	1.34	0.498357	1.04	0.823407	-1.4	0.424168
H02	B2M	-1.74	0.069622	1.75	0.198236	1.25	0.304749
H03	GAPDH	-1.22	0.842034	-1.59	0.393738	-1.22	0.668975
H04	HPRT1	-1.37	0.36067	-2.31	0.067216	-2.04	0.08229
H05	RPLP0	2.17	0.136325	2.02	0.292426	2.79	0.046283

Table S4. Table of genes involved in the Fatty Acid Metabolism (PAHS-007Z).

Position	RefSeq Number	Symbol	Description
A01	NM_001607	ACAA1	Acetyl-CoA acyltransferase 1
A02	NM_006111	ACAA2	Acetyl-CoA acyltransferase 2
A03	NM_025247	ACAD10	Acyl-CoA dehydrogenase family, member 10
A04	NM_032169	ACAD11	Acyl-CoA dehydrogenase family, member 11
A05	NM_014049	ACAD9	Acyl-CoA dehydrogenase family, member 9
A06	NM_001608	ACADL	Acyl-CoA dehydrogenase, long chain
A07	NM_000016	ACADM	Acyl-CoA dehydrogenase, C-4 to C-12 straight chain
A08	NM_000017	ACADS	Acyl-CoA dehydrogenase, C-2 to C-3 short chain
A09	NM_001609	ACADSB	Acyl-CoA dehydrogenase, short/branched chain
A10	NM_000018	ACADVL	Acyl-CoA dehydrogenase, very long chain
A11	NM_000019	ACAT1	Acetyl-CoA acetyltransferase 1
A12	NM_005891	ACAT2	Acetyl-CoA acetyltransferase 2
B01	NM_001037161	ACOT1	Acyl-CoA thioesterase 1
B02	NM_130767	ACOT12	Acyl-CoA thioesterase 12
B03	NM_001037162	ACOT6	Acyl-CoA thioesterase 6
B04	NM_181866	ACOT7	Acyl-CoA thioesterase 7
B05	NM_005469	ACOT8	Acyl-CoA thioesterase 8
B06	NM_001033583	ACOT9	Acyl-CoA thioesterase 9
B07	NM_004035	ACOX1	Acyl-CoA oxidase 1, palmitoyl
B08	NM_003500	ACOX2	Acyl-CoA oxidase 2, branched chain
B09	NM_003501	ACOX3	Acyl-CoA oxidase 3, pristanoyl
B10	NM_015162	ACSBG1	Acyl-CoA synthetase bubblegum family member 1
B11	NM_030924	ACSBG2	Acyl-CoA synthetase bubblegum family member 2
B12	NM_001995	ACSL1	Acyl-CoA synthetase long-chain family member 1
C01	NM_004457	ACSL3	Acyl-CoA synthetase long-chain family member 3
C02	NM_004458	ACSL4	Acyl-CoA synthetase long-chain family member 4

C03	NM_016234	ACSL5	Acyl-CoA synthetase long-chain family member 5
C04	NM_001009185	ACSL6	Acyl-CoA synthetase long-chain family member 6
C05	NM_005622	ACSM3	Acyl-CoA synthetase medium-chain family member 3
C06	NM_001080454	ACSM4	Acyl-CoA synthetase medium-chain family member 4
C07	NM_017888	ACSM5	Acyl-CoA synthetase medium-chain family member 5
C08	NM_000690	ALDH2	Aldehyde dehydrogenase 2 family (mitochondrial)
C09	NM_004051	BDH1	3-hydroxybutyrate dehydrogenase, type 1
C10	NM_020139	BDH2	3-hydroxybutyrate dehydrogenase, type 2
C11	NM_001876	CPT1A	Carnitine palmitoyltransferase 1A (liver)
C12	NM_004377	CPT1B	Carnitine palmitoyltransferase 1B (muscle)
D01	NM_152359	CPT1C	Carnitine palmitoyltransferase 1C
D02	NM_000098	CPT2	Carnitine palmitoyltransferase 2
D03	NM_000755	CRAT	Carnitine O-acetyltransferase
D04	NM_021151	CROT	Carnitine O-octanoyltransferase
D05	NM_001359	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial
D06	NM_020664	DECR2	2,4-dienoyl CoA reductase 2, peroxisomal
D07	NM_004092	ECHS1	Enoyl CoA hydratase, short chain, 1, mitochondrial
D08	NM_006117	ECI2	Enoyl-CoA delta isomerase 2
D09	NM_001966	EHHADH	Enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase
D10	NM_001443	FABP1	Fatty acid binding protein 1, liver
D11	NM_000134	FABP2	Fatty acid binding protein 2, intestinal
D12	NM_004102	FABP3	Fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)
E01	NM_001442	FABP4	Fatty acid binding protein 4, adipocyte
E02	NM_001444	FABP5	Fatty acid binding protein 5 (psoriasis-associated)
E03	NM_001445	FABP6	Fatty acid binding protein 6, ileal
E04	NM_001446	FABP7	Fatty acid binding protein 7, brain
E05	NM_004104	FASN	Fatty acid synthase
E06	NM_000159	GCDH	Glutaryl-CoA dehydrogenase

E07	NM_000167	GK	Glycerol kinase
E08	NM_033214	GK2	Glycerol kinase 2
E09	NM_005276	GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)
E10	NM_000408	GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
E11	NM_000182	HADHA	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
E12	NM_000191	HMGCL	3-hydroxymethyl-3-methylglutaryl-CoA lyase
F01	NM_002130	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)
F02	NM_005518	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
F03	NM_005357	LIPE	Lipase, hormone-sensitive
F04	NM_000237	LPL	Lipoprotein lipase
F05	NM_032601	MCEE	Methylmalonyl CoA epimerase
F06	NM_000255	MUT	Methylmalonyl CoA mutase
F07	NM_022120	OXCT2	3-oxoacid CoA transferase 2
F08	NM_018441	PECR	Peroxisomal trans-2-enoyl-CoA reductase
F09	NM_021129	PPA1	Pyrophosphatase (inorganic) 1
F10	NM_006251	PRKAA1	Protein kinase, AMP-activated, alpha 1 catalytic subunit
F11	NM_006252	PRKAA2	Protein kinase, AMP-activated, alpha 2 catalytic subunit
F12	NM_006253	PRKAB1	Protein kinase, AMP-activated, beta 1 non-catalytic subunit
G01	NM_005399	PRKAB2	Protein kinase, AMP-activated, beta 2 non-catalytic subunit
G02	NM_002730	PRKACA	Protein kinase, cAMP-dependent, catalytic, alpha
G03	NM_182948	PRKACB	Protein kinase, cAMP-dependent, catalytic, beta
G04	NM_002733	PRKAG1	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit
G05	NM_016203	PRKAG2	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit
G06	NM_017431	PRKAG3	Protein kinase, AMP-activated, gamma 3 non-catalytic subunit
G07	NM_198580	SLC27A1	Solute carrier family 27 (fatty acid transporter), member 1
G08	NM_003645	SLC27A2	Solute carrier family 27 (fatty acid transporter), member 2
G09	NM_024330	SLC27A3	Solute carrier family 27 (fatty acid transporter), member 3

G10	NM_005094	SLC27A4	Solute carrier family 27 (fatty acid transporter), member 4
G11	NM_012254	SLC27A5	Solute carrier family 27 (fatty acid transporter), member 5
G12	NM_014031	SLC27A6	Solute carrier family 27 (fatty acid transporter), member 6
H01	NM_001101	ACTB	Actin, beta
H02	NM_004048	B2M	Beta-2-microglobulin
H03	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H04	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H05	NM_001002	RPLP0	Ribosomal protein, large, P0
H06	SA_00105	HGDC	Human Genomic DNA Contamination
H07	SA_00104	RTC	Reverse Transcription Control
H08	SA_00104	RTC	Reverse Transcription Control
H09	SA_00104	RTC	Reverse Transcription Control
H10	SA_00103	PPC	Positive PCR Control
H11	SA_00103	PPC	Positive PCR Control
H12	SA_00103	PPC	Positive PCR Control

Table S5. List of CT values of genes involved in fatty acid metabolism that was uploaded on to the data analysis web portal at <http://www.qiagen.com/geneglobe>

Position	Control Group	Control Group	Control Group	PG/V G Test Group 1	PG/V G Test Group 1	PG/V G Test Group 1	PG/VG+ N Test Group 2	PG/VG+ N Test Group 2	PG/VG+ N Test Group 2	PG/VG+N+ F Test Group 3	PG/VG+N+ F Test Group 3	PG/VG+N+ F Test Group 3
A01	25.455	24.70	26.12	25.91	25.70	25.38	25.24	25.12	25.79	25.82	25.69	25.68
A02	24.443	25.43	24.87	23.59	24.43	24.53	23.21	23.33	23.75	23.45	23.69	24.34
A03	26.68	36.24	26.78	25.67	26.24	26.21	25.07	24.84	25.64	25.71	25.62	25.53
A04	25.21	27.57	25.77	24.94	24.57	24.99	24.46	24.63	24.86	24.84	24.89	25.20
A05	26.45	22.39	26.23	25.83	25.89	25.63	25.29	25.33	25.54	25.71	25.70	25.79
A06	38.00	26.35	33.81	40	33.85	36.47	30.53	29.66	29.64	31.18	30.24	30.75
A07	40	35.86	38.31	34.61	35.86	32.92	28.13	28.43	28.71	30.29	31.16	31.21
A08	27.35	27.25	26.89	26.83	27.25	26.57	26.28	26.39	26.51	27.06	27.12	27.18
A09	27.27	26.50	26.78	26.31	26.50	25.87	25.71	25.84	25.70	26.59	26.46	26.71
A10	22.31	22.24	22.35	22.54	22.24	21.60	20.92	21.09	21.73	21.58	22.23	22.42
A11	25.74	24.72	25.65	25.09	24.72	24.94	23.77	23.86	25.11	24.76	25.12	25.37
A12	26.31	25.62	26.35	25.28	25.62	25.02	24.75	25.14	25.25	26.16	25.21	25.57
B01	32.18	23.13	31.57	31.27	31.13	31.29	31.20	31.14	31.20	31.64	30.71	30.95
B02	30.62	36.61	31.78	32.62	30.61	31.23	30.42	29.57	30.63	31.54	32.28	31.17
B03	34.80	32.33	35.21	39.10	34.33	34.29	34.38	34.94	33.89	34.54	34.07	33.65
B04	27.04	26.73	26.93	25.17	25.43	25.45	26.15	25.73	25.78	25.98	26.31	25.68
B05	27.12	24.91	27.29	25.94	26.91	27.08	26.00	26.53	26.54	26.32	26.42	26.71
B06	26.21	31.34	26.52	24.96	25.34	25.40	24.26	24.40	25.14	25.65	25.59	25.64
B07	26.27	25.67	26.44	25.18	25.67	25.23	24.86	24.76	25.00	25.81	25.71	26.36
B08	31.36	31.43	30.87	30.72	31.43	30.47	29.37	29.32	30.21	29.63	31.45	31.15
B09	27.56	27.19	27.76	27.34	27.19	26.94	26.93	27.16	26.68	27.89	27.44	27.38
B10	30.81	31.54	31.26	29.84	31.54	30.21	28.17	30.06	29.93	29.20	30.97	30.91
B11	27.33	27.52	28.02	27.79	27.52	27.75	28.29	28.67	28.59	28.22	28.94	28.70
B12	25.64	24.51	25.52	26.10	24.51	24.44	25.17	25.72	22.94	25.98	24.35	24.54
C01	25.35	23.74	26.25	26.12	26.74	25.46	24.14	24.76	23.95	25.86	25.55	25.07
C02	23.00	30.74	24.13	23.78	23.74	23.45	22.30	22.73	23.41	22.62	23.66	25.08
C03	28.60	28.10	28.51	31.34	29.10	28.96	28.52	28.52	28.49	28.24	28.11	28.58
C04	37.39	35.16	35.92	33.68	34.16	33.97	33.80	33.19	32.97	32.65	30.94	30.90

C05	28.58	24.69	28.61	28.97	28.69	28.31	28.31	27.99	27.51	28.45	27.95	28.58
C06	32.67	26.15	31.90	32.88	32.15	32.27	31.52	31.92	30.34	32.18	32.38	31.45
C07	29.02	29.30	29.03	29.47	29.30	29.11	29.65	29.60	29.07	30.03	29.75	29.90
C08	26.72	28.24	26.82	26.24	28.24	26.53	25.47	25.69	26.38	27.34	27.21	26.84
C09	30.86	30.85	31.23	30.35	30.85	30.48	30.15	29.51	28.22	30.92	30.39	30.01
C10	24.14	24.88	24.21	24.34	24.88	24.92	22.89	23.48	24.28	23.98	23.95	24.19
C11	26.46	26.12	26.82	26.50	26.12	26.07	24.58	24.78	26.63	25.24	26.34	26.50
C12	31.19	31.31	31.74	31.70	31.31	31.24	31.28	31.29	31.79	31.92	31.18	31.39
D01	25.49	26.92	25.57	25.21	26.92	26.15	24.60	24.66	25.39	25.50	26.25	25.77
D02	27.50	24.94	26.74	27.73	26.94	27.15	27.82	27.27	26.55	28.28	27.65	27.46
D03	26.30	32.19	25.84	24.74	25.19	24.87	24.58	24.58	24.24	24.56	24.84	24.53
D04	26.87	33.25	27.29	25.95	26.25	25.86	24.63	25.2	25.35	24.94	25.79	25.43
D05	24.27	29.44	24.92	23.90	24.44	23.25	22.41	23.10	24.36	22.71	24.84	24.89
D06	26.40	28.96	26.08	26.42	25.96	25.79	26.91	26.72	26.32	26.55	26.47	25.98
D07	24.70	24.40	24.79	23.19	24.40	23.72	23.65	23.47	22.84	24.33	24.60	24.53
D08	25.23	25.45	25.60	24.03	25.45	25.05	23.71	24.40	24.34	24.35	25.65	25.18
D09	29.29	30.39	29.75	29.49	30.39	29.53	27.24	28.26	28.18	28.26	29.52	29.25
D10	26.55	31.43	26.97	31.24	31.43	30.88	31.53	32.19	31.18	29.81	29.76	29.34
D11	33.23	34.21	32.88	34.34	34.21	34.66	33.30	34.45	39.65	32.99	37.15	36.84
D12	26.72	26.76	26.65	25.62	26.76	26.46	26.16	26.33	23.96	26.65	24.86	24.99
E01	28.90	28.43	29.36	28.72	28.43	28.67	26.64	26.68	30.76	27.21	29.90	29.50
E02	23.80	21.65	24.66	23.51	21.65	20.86	22.52	23.71	22.65	23.87	22.79	23.31
E03	30.63	29.81	29.42	30.48	29.81	29.95	30.73	30.27	29.73	30.14	29.65	29.87
E04	31.15	30.58	30.87	30.66	30.58	30.81	30.88	31.18	31.57	30.93	31.33	31.19
E05	24.93	23.67	25.37	24.31	23.67	23.32	24.12	24.09	23.46	24.41	24.40	25.28
E06	28.01	27.85	28.42	26.92	27.85	27.67	26.98	26.94	27.24	27.86	27.50	27.61
E07	34.91	34.42	34.39	35.91	34.42	32.45	31.41	32.78	32.95	32.97	34.74	34.60
E08	37.22	38.27	34.08	36.13	38.27	35.90	37.19	36.96	38.90	37.23	40	40
E09	31.69	35.65	33.30	29.17	35.65	32.66	31.95	31.85	31.77	33.41	32.98	33.72
E10	24.65	25.41	25.12	25.11	25.41	24.66	23.67	24.18	24.46	24.36	24.72	24.78
E11	24.60	24.39	24.67	23.84	24.39	24.21	23.28	23.73	23.78	24.17	24.33	24.35
E12	25.65	25.58	26.09	24.63	25.58	25.19	24.77	24.63	23.87	25.82	24.61	24.56
F01	22.74	23.07	23.40	23.15	23.07	22.69	22.78	22.80	21.90	24.10	22.56	22.33
F02	31.29	37.48	32.83	34.32	37.48	32.87	33.93	39.06	32.88	40	34.59	32.95
F03	27.67	27.73	27.39	27.60	27.73	27.43	27.59	27.33	27.25	27.74	27.74	27.66
F04	28.82	28.34	28.94	25.40	28.34	27.84	25.94	26.27	26.30	25.60	27.25	27.17

F05	28.00	27.52	28.24	27.52	27.52	27.18	26.05	26.52	26.53	26.41	27.47	27.57
F06	26.04	26.37	26.72	25.95	26.37	25.94	24.96	25.31	25.51	25.02	25.64	26.22
F07	30.48	30.67	29.12	29.74	30.67	29.58	28.59	28.44	29.25	29.23	29.42	30.28
F08	28.72	27.95	28.81	26.36	27.95	27.10	26.15	26.40	27.03	27.23	27.29	27.40
F09	23.92	24.18	24.39	22.94	24.18	23.58	22.42	23.06	22.99	23.36	23.81	23.58
F10	25.09	25.39	25.65	24.71	25.39	23.96	23.24	23.77	23.97	24.41	24.35	24.56
F11	28.49	30.09	29.92	27.47	30.09	28.71	27.56	28.34	28.08	28.54	29.33	28.91
F12	27.95	28.12	28.48	25.70	28.12	27.43	26.22	26.78	25.66	27.14	26.99	26.96
G01	26.45	27.10	27.46	26.66	27.10	27.14	25.61	26.20	25.39	25.87	26.00	26.20
G02	26.19	27.00	27.36	26.64	27.00	26.42	25.01	25.38	24.51	25.20	25.78	25.60
G03	26.70	25.88	26.08	24.79	25.88	25.79	24.62	24.93	24.72	24.70	25.17	24.86
G04	25.00	24.77	25.69	24.14	24.77	24.77	23.54	23.45	24.21	23.59	24.69	24.19
G05	27.61	27.37	27.62	26.18	27.37	27.10	25.87	26.39	25.95	26.42	26.56	26.98
G06	32.70	33.50	31.90	33.58	33.50	31.60	37.20	34.93	28.48	33.06	29.17	30.71
G07	28.39	28.21	28.16	27.42	28.21	27.75	27.50	27.64	26.91	28.42	27.85	28.51
G08	33.38	34.21	32.91	32.37	34.21	32.46	32.49	32.63	29.28	32.52	33.60	32.28
G09	28.50	28.88	28.97	27.31	28.88	28.08	27.85	27.51	27.08	28.44	28.29	28.07
G10	29.39	29.21	29.94	27.71	29.21	28.17	27.71	27.62	27.89	29.36	29.22	28.81
G11	28.11	27.69	27.75	28.07	27.69	27.41	28.32	28.24	27.94	28.55	27.59	27.87
G12	28.99	31.94	29.81	30.11	31.94	29.10	26.79	27.63	28.52	29.25	29.53	29.21
H01	19.61	19.82	20.21	18.52	19.82	18.97	18.95	18.88	17.82	19.50	19.18	18.97
H02	19.64	20.37	20.91	20.00	20.37	19.77	17.83	18.73	19.77	18.20	19.52	20.07
H03	20.97	19.78	20.17	19.61	19.78	19.19	20.01	19.23	17.95	20.16	20.12	19.39
H04	26.00	25.64	26.24	24.58	25.64	25.95	24.65	24.40	24.94	24.77	25.75	25.35
H05	20.42	19.06	20.44	18.15	19.06	18.37	18.23	17.30	17.63	17.80	18.91	18.96
H06	35.81	36.13	35.70	36.98	36.13	34.09	38.56	33.56	36.59	34.50	35.38	35.69
H07	21.89	23.77	23.15	21.52	23.77	23.15	24.99	22.83	22.82	23.57	22.54	24.70
H08	21.52	23.80	23.74	22.38	23.80	23.10	22.09	21.68	23.44	22.32	24.29	24.91
H09	20.87	24.34	23.44	20.48	24.34	23.17	20.62	21.13	23.24	21.19	23.09	23.90
H10	28.09	29.83	28.24	27.31	29.83	28.69	26.78	27.74	28.05	28.14	28.86	28.56
H11	27.68	28.87	29.02	27.21	28.87	27.76	26.82	28.89	28.11	28.13	28.78	28.57
H12	27.96	29.08	28.18	27.46	29.08	29.16	26.52	27.79	26.73	27.91	28.55	28.554

Table S6. Fold regulation and p-Values of genes associated with fatty acid metabolism analyzed in the study. Fold Regulation (comparing to control group)

Position	Gene Symbol	Group 1		Group 2		Group 3	
		Fold Regulation	p-Value	Fold Regulation	p-Value	Fold Regulation	p-Value
A01	ACAA1	-2.01	0.048542	-2.8	0.016388	-2.21	0.027894
A02	ACAA2	-1.03	0.776242	-1.03	0.792344	1.18	0.714739
A03	ACAD10	6.4	0.6315	6.82	0.524766	8.11	0.318698
A04	ACAD11	1.5	0.70867	1	0.607066	1.29	0.974287
A05	ACAD9	-2.88	0.344697	-3.72	0.322925	-2.93	0.342622
A06	ACADL	-12.68	0.369737	1.18	0.416386	1.11	0.417011
A07	ACADM	1.04	0.708738	32.85	0.006002	9.59	0.000668
A08	ACADS	-1.4	0.251221	-1.7	0.134504	-1.74	0.125277
A09	ACADSB	-1.11	0.649403	-1.35	0.168952	-1.5	0.139147
A10	ACADVL	-1.51	0.191533	-1.39	0.257033	-1.53	0.043931
A11	ACAT1	-1.24	0.5143	-1.33	0.557376	-1.47	0.071616
A12	ACAT2	1.02	0.859647	-1.4	0.137779	-1.31	0.524461
B01	ACOT1	-8.21	0.373023	-13.43	0.371535	-7.89	0.373397
B02	ACOT12	1.16	0.752789	1.66	0.866835	-1.03	0.429374
B03	ACOT6	-2.4	0.280458	-3.71	0.201734	-1.86	0.355934
B04	ACOT7	1.72	0.035566	-1.43	0.045815	1.05	0.767286
B05	ACOT8	-1.96	0.280723	-2.73	0.203106	-1.85	0.2926
B06	ACOT9	4.06	0.24632	3.71	0.354409	2.93	0.658994
B07	ACOX1	-1	0.99261	-1.22	0.111804	-1.6	0.04958
B08	ACOX2	-1.34	0.340069	1.04	0.927867	-1.29	0.561817
B09	ACOX3	-1.34	0.169607	-1.94	0.000816	-1.88	0.019001
B10	ACSBG1	-1.07	0.796352	1.22	0.574991	1	0.941453
B11	ACSBG2	-1.78	0.077905	-5.38	0.003044	-3.58	0.004257
B12	ACSL1	-1.48	0.607042	-1.89	0.535272	-1.49	0.552809
C01	ACSL3	-3.39	0.132828	-1.63	0.318414	-2.33	0.201804
C02	ACSL4	2.89	0.642993	3.05	0.750924	2.51	0.651126
C03	ACSL5	-4.49	0.009226	-3.12	0.000959	-1.68	0.035302

C04	ACSL6	1.22	0.250416	1.1	0.600237	6.3	0.073107
C05	ACSM3	-4.38	0.312885	-4.52	0.308799	-3.68	0.325518
C06	ACSM4	-7.8	0.359158	-5.88	0.363639	-6.1	0.362462
C07	ACSM5	-1.93	0.074261	-3.62	0.015483	-3.07	0.022552
C08	ALDH2	-1.43	0.374609	-1.08	0.667734	-1.64	0.252543
C09	BDH1	-1.27	0.067749	1.12	0.609952	-1.23	0.609427
C10	BDH2	-2.1	0.088246	-1.59	0.339097	-1.39	0.282793
C11	CPT1A	-1.45	0.160809	-1.31	0.862862	-1.32	0.160847
C12	CPT1B	-1.71	0.08074	-2.98	0.005024	-1.9	0.062988
D01	CPT1C	-1.82	0.207438	-1.34	0.403861	-1.61	0.227743
D02	CPT2	-3.14	0.168202	-5.11	0.11551	-4.74	0.122737
D03	CRAT	5.33	0.288872	4.32	0.550669	6.17	0.172267
D04	CROT	5.09	0.292138	5.71	0.248712	7.48	0.053914
D05	DECR1	2.98	0.60495	2.62	0.662377	2.33	0.838443
D06	DECR2	1.25	0.818553	-2.05	0.213949	-1.02	0.532141
D07	ECHS1	1.07	0.550888	-1.16	0.346152	-1.62	0.005287
D08	ECI2	-1.14	0.593853	-1.2	0.594086	-1.39	0.152046
D09	EHHADH	-1.7	0.162567	1.31	0.572161	-1.03	0.754397
D10	FABP1	-12.41	0.116284	-28.9	0.11077	-4.48	0.136404
D11	FABP2	-3.32	0.103371	-5.06	0.085761	-3.32	0.11947
D12	FABP3	-1.26	0.289409	-1.24	0.975776	1.29	0.390821
E01	FABP4	-1.39	0.235217	-1.58	0.773429	-1.76	0.452171
E02	FABP5	1.51	0.50594	-2.18	0.301157	-1.74	0.399356
E03	FABP6	-1.86	0.250142	-3.53	0.083747	-1.71	0.262328
E04	FABP7	-1.5	0.143765	-3.67	0.004842	-2.18	0.009357
E05	FASN	1.09	0.758268	-1.7	0.152533	-1.84	0.155805
E06	GCDH	-1.12	0.364784	-1.41	0.039111	-1.33	0.223062
E07	GK	-1.11	0.792326	1.58	0.368644	-1.3	0.554187
E08	GK2	-2.1	0.186509	-3.57	0.09803	-2.22	0.168222
E09	GPD1	1.22	0.595872	-1.04	0.519851	-1.84	0.319307
E10	GPD2	-1.7	0.131449	-1.48	0.283446	-1.32	0.263873
E11	HADHA	-1.28	0.069132	-1.49	0.103464	-1.49	0.027429
E12	HMGCL	-1.09	0.373878	-1.13	0.553173	-1.05	0.794041

F01	HMGCS1	-1.59	0.112293	-1.94	0.047888	-1.7	0.362526
F02	HMGCS2	-3.45	0.230846	-5.37	0.195291	-3.95	0.227631
F03	LIPE	-1.69	0.119489	-2.51	0.037891	-1.94	0.078766
F04	LPL	1.67	0.369455	1.99	0.029435	2.27	0.094906
F05	MCEE	-1.2	0.326859	1.01	0.827637	-1.05	0.828492
F06	MUT	-1.39	0.131583	-1.33	0.30076	-1.06	0.801114
F07	OXCT2	-1.59	0.369865	-1.15	0.616168	-1.32	0.50045
F08	PECR	1.51	0.115709	1.36	0.267124	1.27	0.154291
F09	PPA1	-1.13	0.492561	-1.14	0.69016	-1.2	0.252519
F10	PRKAA1	-1.06	0.941731	1.13	0.603804	1.06	0.766058
F11	PRKAA2	-1.02	0.943831	-1.01	0.805619	-1.21	0.505089
F12	PRKAB1	1.26	0.496432	1.35	0.255236	1.24	0.30915
G01	PRKAB2	-1.67	0.147342	-1.2	0.524918	1.1	0.82888
G02	PRKACA	-1.52	0.238998	1.28	0.522283	1.39	0.318521
G03	PRKACB	-1.02	0.887202	-1.05	0.776717	1.38	0.152692
G04	PRKAG1	-1.13	0.401189	-1.08	0.846456	1.11	0.465316
G05	PRKAG2	-1.09	0.663927	-1.05	0.852306	1.03	0.838065
G06	PRKAG3	-1.95	0.373751	-3.1	0.710624	1.84	0.372498
G07	SLC27A1	-1.24	0.239276	-1.55	0.105537	-1.8	0.112541
G08	SLC27A2	-1.21	0.576657	1.42	0.51309	-1.11	0.692374
G09	SLC27A3	-1.05	0.835354	-1.17	0.40721	-1.25	0.387841
G10	SLC27A4	1.3	0.17472	1.18	0.21304	-1.38	0.188936
G11	SLC27A5	-1.56	0.176814	-3.6	0.008332	-1.99	0.096795
G12	SLC27A6	-1.87	0.327645	2.1	0.434841	1.05	0.579324
H01	ACTB	1.01	0.988641	-1.15	0.684315	-1.13	0.692316
H02	B2M	-1.42	0.292702	-1	0.815027	1.15	0.712705
H03	GAPDH	1.01	0.952745	-1.22	0.796888	-1.34	0.41314
H04	HPRT1	-1.15	0.67802	-1.17	0.31048	-1.12	0.193351
H05	RPLP0	1.61	0.071266	1.65	0.123996	1.49	0.20647

Table S7. Genes and primers used in the study.

Gene	Forward (5'-3')	Reverse (5'-3')
TP63	CACCATGTGAGCTCTTCCTATC	AGGTAGCCTCTTACTTCTCCTT
Cytokeratin K14	AGTCCCTACTTCAAGACCATTGAG	GGTCCAACCTCTGTCTCATACTTGG
Cytokeratin K13	TCAAGACACGTCTGGAGCAG	AAGTCAGACAGTGAGGGGTCT
Beta-Actin	ACGTTGCTATCCAGGCTGTGCTAT	CTCGGTGAGGATCTTCATGAGGTAGT
CDH1	CGATTAAGGTGGAGAGAGGACTG	AATGAATGGTGGACAGACACAGG
MUC1	AGACGTCAGCGTGAGTGATG	GACAGCCAAGGCAATGAGAT
MUC4	GGGAAGAAAGGCCCAACTAC	CTATGCTGACGGGTTGGAAT
IL6	AAGCCAGAGCTGTGCAGATGAGTA	GCTGCGCAGAATGAGATGAGTTGT
IL8	AGACATACTCCAAACCTTTCCACCC	TCCAGACAGAGCTCTCTTCCATCA
MMP2	AGAAGGATGGCAAGTACGGCT	AGTGGTGCAGCTGTCATAGGATGT
CTNNB1 (Beta-Catenin)	TCTGAGGACAAGCCACAAGATTACA	TGGGCACCAATATCAAGTCCAA
LEF1	AATGAGAGCGAATGTCGTTGC	GCTGTCTTTCTTTCCGTGCTA
Wnt2	CTGACCTGATGCAGACGCAAG	AGGAGCCACCTGTAGCTCTCATGTA
Wnt7b	GTCAGGGATGTTTGTCCCACTTG	TCTGGTAGGTCCTTGTGCCACTC
LAMA5	CACCGCCCGGAAGGC	CAGGTGACTGGACAGGGAAC
CyclinD1	TCTACACCGACAACCTCCATCCG	TCTGGCATTGAGAGGAAGTG