

Supplementary Table S1a: Characteristics of Human Donor Eyes Used for the Present Study

DEX Treatment (nM)	Code	Age	Sex	Cause of Death	Time B/W Death & Enucleation (h)	Time B/W Enucleation & Culture (h)	Experiment Eye	HOCAS/ Culture	Treatment	Remarks
100nM (N=16)	OCHD18-29	76	F	Natural	0.45	30.5	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD18-49	48	M	Heart Disease	2.5	30.66	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD18-52	55	F	Vascular accident	2.75	67.91	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD18-53	67	M	Diabetes	4.33	27	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD18-56	82	M	Cardiac arrest	4	23	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD18-57	80	F	Respiratory disease	3	28.5	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD19-01	73	M	Natural	4.5	30.8	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD19-02	66	M	Road traffic injury	2.75	8.33	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD19-03	65	F	Heart Disease	5.8	47.33	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD19-04	72	M	Heart Disease	3.5	41	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established
	OCHD20-04	65	M	Chronic obstructive	0.33	28.5	OD	HOCAS	DEX	Data included
							OS	Cell culture	ETH/DEX	TM Culture established

pulmonary disease									
OCHD20-05	50	M	Kidney failure	2	71.58	OD	HOCAS	DEX	Data included
						OS	Cell culture	ETH/DEX	TM Culture established
OCHD20-06	59	M	Chronic Kidney Disease	0.5	29.16	OD	HOCAS	DEX	Data included
						OS	Cell culture	ETH/DEX	TM Culture established
OCHD20-09	46	M	Accidental fall	2.25	31	OD	HOCAS	DEX	Data included
						OS	Cell culture	ETH/DEX	TM Culture established
OCHD20-10	38	M	Chronic Kidney Disease	1.41	47.5	OD	HOCAS	DEX	Data included
						OS	Cell culture	ETH/DEX	TM Culture established
OCHD20-14	56	M	Heart Disease	3.91	72.25	OD	HOCAS	DEX	Data included
						OS	Cell culture	ETH/DEX	TM Culture established
HTM Cell used for RNA-Sequencing									
OCHD18-39	82	F	Respiratory disease	0.75	-	OS	Cell culture	ETH/DEX	TM Culture established

A total of 16 paired eyes were used for the study with the mean (\pm) SD age was 62.38 ± 12.82 years. The mean (\pm) SD elapsed time between (b/w) death and enucleation was 2.75 ± 1.58 h and the mean elapsed time between enucleation and culture was 38.44 ± 18.39 h. DEX- Eyes treated with dexamethasone; ETH/DEX- HTM Cells treated with either 0.1% ethanol or dexamethasone. * HTM Cells used for RNA-sequencing.

Supplementary Table S1b: Trabecular Meshwork Cells Used for the RNA Sequence

R/NR	Code	Experiment Eye	Treatment	RAN Seq
R	OCHD18-39	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD18-53	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD19-03	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD19-04	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD18-29	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
NR	OCHD18-52	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD18-56	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes
	OCHD19-02	OS	ETH (0.1%)	Yes
			DEX (100nM)	Yes

Note: Responder; NR- Non-responder

Supplementary Table S2. List of Genes Selected from RNA Sequencing for Validation by RT²- PCR Array

S.No	Ref seq	Symbol	Description
1	NM_000681	<i>ADRA2A</i>	Adrenergic, alpha-2A-, receptor
2	NM_004673	<i>ANGPTL1</i>	Angiopoietin-like 1
3	NM_001647	<i>APOD</i>	Apolipoprotein D
4	NM_031911	<i>CIQTNF7</i>	C1q and tumor necrosis factor related protein 7
5	NM_004355	<i>CD74</i>	CD74 molecule, major histocompatibility complex, class II invariant chain
6	NM_001276	<i>CHI3L1</i>	Chitinase 3-like 1 (cartilage glycoprotein-39)
7	NM_022131	<i>CLSTN2</i>	Calsyntenin 2
8	NM_001855	<i>COL15A1</i>	Collagen, type XV, alpha 1
9	NM_001874	<i>CPM</i>	Carboxypeptidase M
10	NM_004419	<i>DUSP5</i>	Dual specificity phosphatase 5
11	NM_006350	<i>FST</i>	Follistatin
12	NM_000618	<i>IGF1</i>	Insulin-like growth factor 1 (somatomedin C)
13	NM_000612	<i>IGF2</i>	Insulin-like growth factor 2 (somatomedin A)
14	NM_000261	<i>MYOC</i>	Myocilin, trabecular meshwork inducible glucocorticoid response
15	NM_015039	<i>NMNAT2</i>	Nicotinamide nucleotide adenyltransferase 2
16	NM_000905	<i>NPY</i>	Neuropeptide Y
17	NM_005010	<i>NRCAM</i>	Neuronal cell adhesion molecule
18	NM_006180	<i>NTRK2</i>	Neurotrophic tyrosine kinase, receptor, type 2
19	NM_000275	<i>OCA2</i>	Oculocutaneous albinism II
20	NM_002612	<i>PDK4</i>	Pyruvate dehydrogenase kinase, isozyme 4
21	NM_002820	<i>PTHLH</i>	Parathyroid hormone-like hormone
22	NM_004103	<i>PTK2B</i>	PTK2B protein tyrosine kinase 2 beta
23	NM_014059	<i>RGCC</i>	Regulator Of Cell Cycle
24	NM_000331	<i>SAA1</i>	Serum amyloid A1
25	NM_006922	<i>SCN3A</i>	Sodium channel, voltage-gated, type III, alpha subunit
26	NM_016932	<i>SIX2</i>	SIX homeobox 2
27	NM_012391	<i>SPDEF</i>	SAM pointed domain containing ets transcription factor
28	NM_024636	<i>STEAP4</i>	STEAP family member 4

29	NM_003256	<i>TIMP4</i>	TIMP metallopeptidase inhibitor 4
30	NM_170744	<i>UNC5B</i>	Unc-5 homolog B
31	NM_004385	<i>VCAN</i>	Versican
32	NM_006006	<i>ZBTB16</i>	Zinc finger and BTB domain containing 16

Supplementary Table S3: The Raw Data of the IOP of Perfusion Cultured Indian Cadaveric Eyes

Dose group (nM)	R/NR	ID	Stabilization period (h)	Pressure change before and after drug treatment (mmHg)								mΔ IOP (mmHg)
				D0	D1	D2	D3	D4	D5	D6	D7	
100	R	OCHD18-53	51.3	22.89	30.72	35.47	49.43	54.96	39.82	22.77	24.63	13.94
		OCHD18-57	40.8	17.57	16.47	17.94	18.62	18.16	22.73	35.99	37.21	6.30
		OCHD19-03	43.1	18.20	33.94	34.10	32.25	30.54	31.32	32.50	32.96	14.32
		OCHD19-04	35.5	21.62	21.71	23.49	28.47	33.03	33.80	33.61	31.81	7.80
		OCHD20-04	65.1	10.29	12.27	23.35	43.61	55.56	56.21	54.71	56.20	32.84
		OCHD20-09	37.8	11.94	15.47	24.34	20.79	22.40	23.70	12.74	15.63	7.36
		OCHD20-14	68.3	22.75	23.96	28.84	35.16	42.68	42.76	41.77	43.33	14.18
	Baseline IOP (IOP on day 0): mean= 17.89, SEM= 1.93, mΔ IOP: mean= 13.82, SEM= 3.4.10; N= 7											
	NR	OCHD18-29	62.3	22.61	23.48	24.43	23.22	22.20	23.13	23.05	23.82	0.72
		OCHD18-49	33.3	13.25	13.61	16.96	14.58	19.37	15.68	14.84	17.65	2.85
		OCHD18-52	48.1	20.75	20.86	23.22	24.63	25.66	25.12	25.32	22.98	3.22
		OCHD18-56	40.8	21.71	21.90	18.18	14.83	13.40	13.13	13.20	13.23	0 ^a
		OCHD19-01	55.6	11.73	16.28	12.19	15.07	10.34	11.59	14.53	11.65	1.36
		OCHD19-02	27	12.50	13.18	16.60	13.34	12.42	11.78	10.09	10.61	0.07
		OCHD20-05	50.5	19.27	18.91	20.26	19.39	17.28	16.14	15.92	16.08	0 ^a
		OCHD20-06	48.5	11.99	11.86	10.71	7.71	6.83	6.73	8.81	9.32	0 ^a
		OCHD20-10	47.8	15.45	13.42	10.89	10.01	7.97	8.44	9.94	9.65	0 ^a
	Baseline IOP (IOP on day 0): mean= 16.59, SEM= 1.7, mΔ IOP: mean= 0.91, SEM = 0.43; N= 9											

Note: ^aMinus values are given as 0; Day 0 represents the day before respective drug treatments; R - Responder; NR- Non-responder

Supplementary Table S4: Alignment Statistics of RNA Sequencing Data

S. No	R/NR	ID	mRNA				
			Total Reads (In millions)	% Of Mapped Reads	% Of Unmapped Reads	No. of Genes	
1	R	18-39	ETH	21.1	85.08	14.92	15765
			DEX	29.3	84.79	15.11	17079
2		18-53	ETH	22.5	85.76	14.24	17371
			DEX	36.2	82.11	17.89	16415
3		19-03	ETH	23.4	84.91	15.09	15353
			DEX	30.5	87.00	13.00	16396
4		19-04	ETH	27.5	87.40	12.60	14515
			DEX	30.7	85.38	14.62	16334
5		18-49	ETH	26.8	84.30	15.70	15439
			DEX	30.3	85.22	14.78	15637
6	NR	18-52	ETH	23.1	84.42	15.58	14682
			DEX	28.4	86.27	13.73	15997
7		18-56	ETH	24.8	86.28	13.72	15852
			DEX	36.2	86.28	13.72	16654
8		19-02	ETH	23.4	88.60	11.40	16039
			DEX	32.7	85.84	14.16	16828
		Mean	28	86	14.4	16022	

Supplementary Table S5a. List of top 50 Up/Down-regulated Genes from Group #1

Up-regulated genes				Down-regulated genes			
Gene	logFC	logCPM	P Value	Gene	logFC	logCPM	P Value
<i>SAA1</i>	6.34	2.81	0.000	<i>UPK3A</i>	-8.49	0.36	0.001
<i>ZBTB16</i>	5.60	4.66	0.000	<i>RLN1</i>	-8.02	1.24	0.001
<i>FRG2C</i>	5.27	-2.07	0.002	<i>FAM110D</i>	-7.42	-0.59	0.002
<i>NPSR1-AS1</i>	5.07	-2.19	0.016	<i>PRSS22</i>	-7.38	-0.62	0.002
<i>BHLHE22</i>	5.04	0.77	0.012	<i>NPY</i>	-7.26	3.41	0.000
<i>SAA4</i>	4.75	-2.34	0.028	<i>GIMAP1</i>	-6.96	-0.98	0.001
<i>SAA2</i>	4.71	0.71	0.003	<i>ST14</i>	-6.81	1.52	0.001
<i>OCA2</i>	4.71	1.61	0.000	<i>LRRC26</i>	-6.79	1.53	0.002
<i>PRODH</i>	4.46	3.17	0.000	<i>KRT15</i>	-6.67	3.39	0.000
<i>H19</i>	4.44	7.60	0.000	<i>FXYD3</i>	-6.59	2.02	0.001
<i>PRR33</i>	4.22	1.04	0.000	<i>PRAC1</i>	-6.58	-0.09	0.003
<i>HIF3A</i>	4.20	4.11	0.000	<i>HOXB13</i>	-6.57	2.99	0.003
<i>P2RY14</i>	4.14	1.13	0.001	<i>TPSB2</i>	-6.50	0.98	0.002
<i>LINC01088</i>	4.14	1.46	0.000	<i>ACPP</i>	-6.48	6.82	0.002
<i>FKBP5</i>	3.99	7.23	0.000	<i>LCN2</i>	-6.47	0.44	0.001
<i>MYOC</i>	3.95	6.57	0.014	<i>KLK3</i>	-6.39	7.58	0.002
<i>CPM</i>	3.93	4.02	0.000	<i>KCNH2</i>	-6.34	0.38	0.002
<i>ANGPTL7</i>	3.93	8.01	0.016	<i>AQP1</i>	-6.33	7.61	0.000
<i>LSP1</i>	3.91	5.22	0.000	<i>DOC2B</i>	-6.30	-0.33	0.001
<i>LINC00702</i>	3.82	3.76	0.000	<i>LINC01297</i>	-6.30	1.17	0.002
<i>TUSC5</i>	3.79	-1.37	0.015	<i>TPSAB1</i>	-6.26	0.71	0.001
<i>LEP</i>	3.75	-0.16	0.012	<i>RBBP8NL</i>	-6.22	-1.54	0.009
<i>SLC16A12</i>	3.72	1.63	0.000	<i>CHRNA2</i>	-6.21	1.31	0.002
<i>RNA5SP111</i>	3.63	-2.00	0.049	<i>SLC52A3</i>	-6.20	-0.35	0.002
<i>IGF2</i>	3.56	6.66	0.000	<i>KLK4</i>	-6.20	3.10	0.006
<i>KCNE1</i>	3.55	0.74	0.010	<i>KRT5</i>	-6.19	2.48	0.001
<i>ANGPTL1</i>	3.54	3.59	0.000	<i>MT1H</i>	-6.18	-1.57	0.005
<i>RPL7P57</i>	3.49	-2.06	0.019	<i>KLK2</i>	-6.17	6.41	0.004
<i>TLDC2</i>	3.48	1.28	0.000	<i>CCDC64B</i>	-6.03	0.46	0.001
<i>NTRK2</i>	3.39	5.15	0.002	<i>SFN</i>	-6.02	1.83	0.000
<i>ADH1B</i>	3.39	7.72	0.001	<i>DES</i>	-5.98	6.03	0.001
<i>FMO2</i>	3.38	3.38	0.002	<i>MSMB</i>	-5.97	4.06	0.006
<i>SAMHD1</i>	3.36	7.81	0.000	<i>COL9A1</i>	-5.96	2.75	0.000
<i>GIP</i>	3.36	-1.29	0.008	<i>C2orf54</i>	-5.94	-1.73	0.012
<i>APOD</i>	3.35	7.28	0.018	<i>PAGE4</i>	-5.94	0.47	0.004
<i>RN7SKP69</i>	3.30	-1.68	0.004	<i>EVX2</i>	-5.90	-1.76	0.008
<i>MIR5690</i>	3.22	-1.75	0.012	<i>PLVAP</i>	-5.87	1.64	0.002
<i>SCN3A</i>	3.09	0.86	0.008	<i>RAMP3</i>	-5.83	0.30	0.002
<i>TNFAIP8L3</i>	3.09	3.20	0.001	<i>RAB25</i>	-5.81	0.28	0.002
<i>MAP1LC3C</i>	3.01	3.54	0.026	<i>HOXA9</i>	-5.78	-0.78	0.007
<i>FHL5</i>	2.99	-0.36	0.016	<i>CHRM1</i>	-5.77	0.88	0.003

<i>SEMG1</i>	2.97	-1.56	0.047	<i>PDE9A</i>	-5.68	1.33	0.000
<i>ABRA</i>	2.93	0.31	0.012	<i>SHH</i>	-5.67	-1.91	0.010
<i>ADRA1B</i>	2.91	2.49	0.000	<i>GIMAP7</i>	-5.67	-0.28	0.004
<i>AFF2</i>	2.90	1.40	0.007	<i>SPOCK3</i>	-5.64	1.74	0.001
<i>ADH1A</i>	2.85	1.95	0.014	<i>LCN6</i>	-5.61	-1.94	0.011
<i>SLC16A10</i>	2.84	1.28	0.028	<i>GNA15</i>	-5.60	-0.92	0.002
<i>XRCC6P2</i>	2.82	-0.36	0.001	<i>HOXA10</i>	-5.59	0.11	0.001
<i>BCRP1</i>	2.82	-1.97	0.032	<i>MMP7</i>	-5.58	1.84	0.004
<i>HSPD1P11</i>	2.81	1.79	0.001	<i>GATA5</i>	-5.58	-0.87	0.009

Note: *Group #1*: DEGs between DEX and ETH treated GC-R HTM cells

Supplementary Table S5b. List of top 50 Up/Down-regulated Genes from Group #2

Up-regulated genes				Down-regulated genes			
Gene	logFC	logCPM	P Value	Gene	logFC	logCPM	P Value
<i>ZBTB16</i>	8.48	4.59	0.000	<i>MXRA5Y</i>	-5.08	-0.47	0.003
<i>RGCC</i>	7.75	1.95	0.000	<i>GRM5</i>	-5.05	-2.43	0.010
<i>OCA2</i>	6.89	2.24	0.000	<i>RARRES2</i>	-3.94	3.36	0.000
<i>H19</i>	6.67	8.47	0.000	<i>AQP1</i>	-3.91	4.05	0.000
<i>MYOC</i>	6.40	9.28	0.001	<i>SLC24A2</i>	-3.89	-1.78	0.025
<i>HIF3A</i>	6.19	2.63	0.000	<i>LAMP3</i>	-3.82	0.03	0.000
<i>APOD</i>	6.03	8.49	0.000	<i>GRIA2</i>	-3.82	0.29	0.001
<i>APCDD1</i>	5.95	2.15	0.000	<i>RBFOX1</i>	-3.80	-1.82	0.048
<i>IGF2-AS</i>	5.88	-1.83	0.002	<i>KRT17P1</i>	-3.77	-1.24	0.009
<i>PNMT</i>	5.76	-1.91	0.002	<i>TNFSF18</i>	-3.76	0.09	0.001
<i>SAA1</i>	5.75	1.16	0.000	<i>GRID2</i>	-3.67	-0.01	0.002
<i>RAMP2-AS1</i>	5.64	0.83	0.000	<i>VCAN-AS1</i>	-3.63	-1.95	0.003
<i>ALOX15B</i>	5.51	-0.80	0.000	<i>PADI2</i>	-3.55	0.96	0.000
<i>ADH1B</i>	5.38	6.06	0.000	<i>PII6</i>	-3.49	-0.82	0.008
<i>PTGDR2</i>	5.24	-2.22	0.003	<i>KLHDC7B</i>	-3.22	-0.85	0.003
<i>LINC00525</i>	5.13	-2.29	0.003	<i>LRRC15</i>	-3.21	4.55	0.017
<i>FKBP5</i>	4.87	7.62	0.000	<i>IGFL2</i>	-3.20	-2.15	0.040
<i>LSP1</i>	4.81	4.97	0.000	<i>C1orf87</i>	-3.10	-2.21	0.032
<i>PRODH</i>	4.58	2.59	0.000	<i>NPY6R</i>	-3.09	-2.22	0.036
<i>P2RY14</i>	4.57	0.98	0.000	<i>NMNAT2</i>	-3.02	3.71	0.014
<i>STEAP4</i>	4.57	3.40	0.000	<i>CLDN1</i>	-3.01	1.69	0.000
<i>SCN3A</i>	4.54	3.24	0.001	<i>ADM2</i>	-2.93	4.72	0.000
<i>SFTPC</i>	4.51	-2.59	0.021	<i>RIMS3</i>	-2.91	2.92	0.002
<i>MAOA</i>	4.44	4.35	0.000	<i>CCND2-AS1</i>	-2.91	-1.15	0.007
<i>FAM107A</i>	4.43	5.13	0.000	<i>IL32</i>	-2.91	2.34	0.007
<i>HMGN2P15</i>	4.37	-0.64	0.002	<i>TMEM63C</i>	-2.84	-1.45	0.003
<i>ANGPTL7</i>	4.31	9.66	0.007	<i>COL19A1</i>	-2.79	0.34	0.001
<i>FHL5</i>	4.24	-0.81	0.005	<i>NGEF</i>	-2.76	0.86	0.020
<i>SOAT2</i>	4.13	-0.86	0.001	<i>KAL1</i>	-2.75	2.99	0.007
<i>PRR33</i>	4.13	0.77	0.000	<i>WNT2</i>	-2.70	0.87	0.001
<i>CPM</i>	4.06	3.13	0.000	<i>VCAN</i>	-2.69	7.10	0.001
<i>SAA2</i>	4.06	-1.83	0.004	<i>CCND2-AS2</i>	-2.69	-1.72	0.032
<i>TRAV39</i>	4.03	-0.91	0.012	<i>C2orf40</i>	-2.67	1.60	0.000
<i>IGF2</i>	4.01	6.48	0.000	<i>NGFR</i>	-2.65	-1.76	0.020
<i>LGI3</i>	3.70	-0.07	0.001	<i>IPCEF1</i>	-2.64	-2.20	0.047
<i>INHBB</i>	3.67	1.41	0.000	<i>VNN1</i>	-2.63	-1.99	0.034
<i>SAMHD1</i>	3.57	7.45	0.000	<i>ARHGAP9</i>	-2.62	-0.48	0.003
<i>RPA4</i>	3.56	-2.16	0.006	<i>ADRA2A</i>	-2.60	2.91	0.001
<i>PDK4</i>	3.52	4.49	0.000	<i>RDH12</i>	-2.57	-1.62	0.012
<i>ANKRD2</i>	3.48	1.17	0.002	<i>PRSS35</i>	-2.57	3.69	0.001
<i>LINC00702</i>	3.44	4.81	0.000	<i>MYHAS</i>	-2.56	-1.50	0.012

<i>ANGPTL1</i>	3.42	2.28	0.000	<i>SLC14A1</i>	-2.53	0.08	0.047
<i>CHI3L2</i>	3.34	3.45	0.015	<i>EPHA3</i>	-2.52	0.55	0.007
<i>SCARA5</i>	3.34	-0.26	0.004	<i>CNGA1</i>	-2.49	-1.82	0.036
<i>GPRC5B</i>	3.26	5.02	0.000	<i>ELOVL2-AS1</i>	-2.46	-1.70	0.012
<i>USP2</i>	3.25	2.49	0.001	<i>KRT23</i>	-2.44	-1.92	0.036
<i>TNNT3</i>	3.12	-0.91	0.001	<i>RGS7BP</i>	-2.43	-0.27	0.031
<i>POM121L9P</i>	3.12	2.50	0.000	<i>CHAC1</i>	-2.43	4.19	0.000
<i>ISM1</i>	3.11	-0.30	0.001	<i>ATPIA3</i>	-2.43	-0.96	0.004
<i>NCAM1-AS1</i>	3.10	-2.39	0.046	<i>SEMA3D</i>	-2.42	1.49	0.026

Note: Group #2: DEGs between DEX and ETH treated GC-NR HTM cells

Supplementary Table S5c. List of Genes from Group #3

Gene	Group#1			Group#2		
	logFC	logCPM	P Value	logFC	logCPM	P Value
<i>ZBTB16</i>	5.60	4.66	0.000	8.48	4.59	0.000
<i>OCA2</i>	4.71	1.61	0.000	6.89	2.24	0.000
<i>H19</i>	4.44	7.60	0.000	6.67	8.47	0.000
<i>MYOC</i>	3.95	6.57	0.014	6.40	9.28	0.001
<i>HIF3A</i>	4.20	4.11	0.000	6.19	2.63	0.000
<i>APOD</i>	3.35	7.28	0.018	6.03	8.49	0.000
<i>SAA1</i>	6.34	2.81	0.000	5.75	1.16	0.000
<i>ADH1B</i>	3.39	7.72	0.001	5.38	6.06	0.000
<i>FKBP5</i>	3.99	7.23	0.000	4.87	7.62	0.000
<i>LSP1</i>	3.91	5.22	0.000	4.81	4.97	0.000
<i>PRODH</i>	4.46	3.17	0.000	4.58	2.59	0.000
<i>P2RY14</i>	4.14	1.13	0.001	4.57	0.98	0.000
<i>SCN3A</i>	3.09	0.86	0.008	4.54	3.24	0.001
<i>MAOA</i>	2.54	4.68	0.005	4.44	4.35	0.000
<i>ANGPTL7</i>	3.93	8.01	0.016	4.31	9.66	0.007
<i>FHL5</i>	2.99	-0.36	0.016	4.24	-0.81	0.005
<i>PRR33</i>	4.22	1.04	0.000	4.13	0.77	0.000
<i>CPM</i>	3.93	4.02	0.000	4.06	3.13	0.000
<i>SAA2</i>	4.71	0.71	0.003	4.06	-1.83	0.004
<i>IGF2</i>	3.56	6.66	0.000	4.01	6.48	0.000
<i>SAMHD1</i>	3.36	7.81	0.000	3.57	7.45	0.000
<i>PDK4</i>	2.24	5.55	0.000	3.52	4.49	0.000
<i>LINC00702</i>	3.82	3.76	0.000	3.44	4.81	0.000
<i>ANGPTL1</i>	3.54	3.59	0.000	3.42	2.28	0.000
<i>USP2</i>	2.22	2.21	0.015	3.25	2.49	0.001
<i>MRO</i>	2.68	1.62	0.037	3.10	1.99	0.003
<i>AOX1</i>	2.21	6.79	0.004	3.10	5.53	0.000
<i>GALNT15</i>	2.26	4.60	0.014	3.04	4.52	0.012
<i>NEDD9</i>	2.53	7.45	0.004	2.99	7.79	0.000
<i>ACA59</i>	2.04	-1.44	0.034	2.96	-1.20	0.007
<i>ADH1A</i>	2.85	1.95	0.014	2.95	0.45	0.000
<i>FGFR4</i>	2.50	3.10	0.029	2.92	1.76	0.001
<i>ADRA1B</i>	2.91	2.49	0.000	2.87	3.14	0.000
<i>PPP1R14A</i>	2.11	7.46	0.024	2.86	5.54	0.028
<i>XRCC6P2</i>	2.82	-0.36	0.001	2.84	-0.33	0.005
<i>ABCA6</i>	2.08	4.75	0.008	2.82	3.39	0.002
<i>TIMP4</i>	2.07	1.11	0.025	2.78	2.41	0.000
<i>SLC16A12</i>	3.72	1.63	0.000	2.75	-0.57	0.002
<i>ADH4</i>	2.54	-1.36	0.029	2.74	-0.95	0.005
<i>FAM46B</i>	2.15	4.36	0.001	2.53	4.96	0.001
<i>SLC16A10</i>	2.84	1.28	0.028	2.47	0.64	0.011

<i>FPR1</i>	2.70	-0.01	0.007	2.46	0.79	0.024
<i>MOB3B</i>	2.61	2.14	0.001	2.45	2.31	0.020
<i>LINC01088</i>	4.14	1.46	0.000	2.45	0.41	0.005
<i>FMO2</i>	3.38	3.38	0.002	2.40	1.29	0.002
<i>TLDC2</i>	3.48	1.28	0.000	2.38	1.05	0.003
<i>ANGPTL5</i>	2.39	0.70	0.015	2.25	1.24	0.001
<i>OLAH</i>	2.57	2.30	0.004	2.20	0.37	0.004
<i>PER1</i>	2.11	6.11	0.000	2.20	5.87	0.000
<i>TRPV6</i>	-3.05	1.87	0.019	2.17	0.67	0.014
<i>DKK2</i>	2.46	3.59	0.016	2.17	3.54	0.017
<i>FST</i>	-2.08	6.67	0.000	-2.01	6.50	0.000
<i>TNFSF15</i>	-2.05	0.31	0.017	-2.05	-1.40	0.026
<i>CERS1</i>	-2.05	-0.45	0.033	-2.07	-0.49	0.018
<i>ARSI</i>	-2.42	3.36	0.001	-2.13	3.10	0.000
<i>TNNT2</i>	-2.29	1.92	0.026	-2.14	-0.86	0.049
<i>BST2</i>	-4.64	1.92	0.000	-2.20	-0.98	0.012
<i>RGS16</i>	-2.34	5.10	0.007	-2.21	5.59	0.028
<i>TAC3</i>	-3.33	-1.20	0.002	-2.23	-1.29	0.033
<i>FNDC1</i>	-2.67	4.35	0.005	-2.27	5.07	0.003
<i>SEMA6B</i>	-2.30	1.97	0.016	-2.28	1.15	0.001
<i>CPA4</i>	-2.42	3.57	0.002	-2.34	2.68	0.034
<i>CILP2</i>	-2.02	0.07	0.026	-2.34	0.13	0.024
<i>RGS7BP</i>	-2.34	-1.10	0.029	-2.43	-0.27	0.031
<i>KRT23</i>	-3.53	0.24	0.023	-2.44	-1.92	0.036
<i>SLC14A1</i>	-2.58	2.94	0.041	-2.53	0.08	0.047
<i>PRSS35</i>	-2.32	3.30	0.000	-2.57	3.69	0.001
<i>ADRA2A</i>	-4.16	4.99	0.002	-2.60	2.91	0.001
<i>NGFR</i>	-2.06	0.83	0.041	-2.65	-1.76	0.020
<i>C2orf40</i>	-5.16	2.72	0.000	-2.67	1.60	0.000
<i>WNT2</i>	-3.86	2.59	0.000	-2.70	0.87	0.001
<i>NGEF</i>	-2.86	-0.57	0.016	-2.76	0.86	0.020
<i>TMEM63C</i>	-2.25	-1.54	0.042	-2.84	-1.45	0.003
<i>LRRC15</i>	-2.42	2.19	0.026	-3.21	4.55	0.017
<i>PII6</i>	-3.79	2.47	0.019	-3.49	-0.82	0.008
<i>TNFSF18</i>	-4.19	0.95	0.000	-3.76	0.09	0.001
<i>LAMP3</i>	-3.62	0.92	0.002	-3.82	0.03	0.000
<i>AQP1</i>	-6.33	7.61	0.000	-3.91	4.05	0.000
<i>RARRES2</i>	-2.19	5.97	0.016	-3.94	3.36	0.000
<i>MXRA5Y</i>	-2.78	-1.55	0.043	-5.08	-0.47	0.003

Note: *Group #3*: DEGs that are common to *Group #1* and *Group #2*

Supplementary Table S5d: List of top 50 Up/Down-regulated Genes from Group #4

Up-regulated genes				Down-regulated genes			
Gene	logFC	logCPM	P Value	Gene	logFC	logCPM	P Value
<i>FRG2C</i>	5.27	-2.07	0.002	<i>UPK3A</i>	-8.49	0.36	0.001
<i>NPSRI-AS1</i>	5.07	-2.19	0.016	<i>RLN1</i>	-8.02	1.24	0.001
<i>BHLHE22</i>	5.04	0.77	0.012	<i>FAM110D</i>	-7.42	-0.59	0.002
<i>SAA4</i>	4.75	-2.34	0.028	<i>PRSS22</i>	-7.38	-0.62	0.002
<i>TUSC5</i>	3.79	-1.37	0.015	<i>NPY</i>	-7.26	3.41	0.000
<i>LEP</i>	3.75	-0.16	0.012	<i>GIMAP1</i>	-6.96	-0.98	0.001
<i>RNA5SP111</i>	3.63	-2.00	0.049	<i>ST14</i>	-6.81	1.52	0.001
<i>KCNE1</i>	3.55	0.74	0.010	<i>LRRC26</i>	-6.79	1.53	0.002
<i>RPL7P57</i>	3.49	-2.06	0.019	<i>KRT15</i>	-6.67	3.39	0.000
<i>NTRK2</i>	3.39	5.15	0.002	<i>FXYD3</i>	-6.59	2.02	0.001
<i>GIP</i>	3.36	-1.29	0.008	<i>PRAC1</i>	-6.58	-0.09	0.003
<i>RN7SKP69</i>	3.30	-1.68	0.004	<i>HOXB13</i>	-6.57	2.99	0.003
<i>MIR5690</i>	3.22	-1.75	0.012	<i>TPSB2</i>	-6.50	0.98	0.002
<i>TNFAIP8L3</i>	3.09	3.20	0.001	<i>ACPP</i>	-6.48	6.82	0.002
<i>MAP1LC3C</i>	3.01	3.54	0.026	<i>LCN2</i>	-6.47	0.44	0.001
<i>SEMG1</i>	2.97	-1.56	0.047	<i>KLK3</i>	-6.39	7.58	0.002
<i>ABRA</i>	2.93	0.31	0.012	<i>KCNH2</i>	-6.34	0.38	0.002
<i>AFF2</i>	2.90	1.40	0.007	<i>DOC2B</i>	-6.30	-0.33	0.001
<i>BCRP1</i>	2.82	-1.97	0.032	<i>LINC01297</i>	-6.30	1.17	0.002
<i>HSPD1P11</i>	2.81	1.79	0.001	<i>TPSAB1</i>	-6.26	0.71	0.001
<i>C5AR2</i>	2.76	0.11	0.006	<i>RBBP8NL</i>	-6.22	-1.54	0.009
<i>MARCH10</i>	2.75	-0.45	0.028	<i>CHRNA2</i>	-6.21	1.31	0.002
<i>KRT18P62</i>	2.74	-1.38	0.015	<i>SLC52A3</i>	-6.20	-0.35	0.002
<i>HNRNPA3P11</i>	2.73	-1.59	0.025	<i>KLK4</i>	-6.20	3.10	0.006
<i>LINC00664</i>	2.71	-2.02	0.035	<i>KRT5</i>	-6.19	2.48	0.001
<i>KIAA1456</i>	2.70	2.33	0.000	<i>MT1H</i>	-6.18	-1.57	0.005
<i>B3GALT2</i>	2.68	3.10	0.000	<i>KLK2</i>	-6.17	6.41	0.004
<i>PLCE1-AS1</i>	2.63	4.43	0.006	<i>CCDC64B</i>	-6.03	0.46	0.001
<i>CYP51A1P2</i>	2.62	-1.04	0.034	<i>SFN</i>	-6.02	1.83	0.000
<i>RAPGEF5</i>	2.62	3.56	0.010	<i>DES</i>	-5.98	6.03	0.001
<i>CCDC54</i>	2.60	-1.08	0.018	<i>MSMB</i>	-5.97	4.06	0.006
<i>KLF15</i>	2.58	4.75	0.000	<i>COL9A1</i>	-5.96	2.75	0.000
<i>ITGA10</i>	2.55	4.93	0.000	<i>C2orf54</i>	-5.94	-1.73	0.012
<i>PDLIM1P4</i>	2.54	-1.82	0.035	<i>PAGE4</i>	-5.94	0.47	0.004
<i>CYP7B1</i>	2.53	1.20	0.008	<i>EVX2</i>	-5.90	-1.76	0.008
<i>GPX3</i>	2.51	7.49	0.013	<i>PLVAP</i>	-5.87	1.64	0.002
<i>ANO3</i>	2.48	0.01	0.006	<i>RAMP3</i>	-5.83	0.30	0.002
<i>NKAIN2</i>	2.48	0.21	0.037	<i>RAB25</i>	-5.81	0.28	0.002
<i>LINC00547</i>	2.47	-0.51	0.013	<i>HOXA9</i>	-5.78	-0.78	0.007
<i>ST7-AS2</i>	2.44	-1.06	0.009	<i>CHRM1</i>	-5.77	0.88	0.003
<i>FAM65C</i>	2.38	3.31	0.012	<i>PDE9A</i>	-5.68	1.33	0.000

<i>ACTG1P3</i>	2.33	-1.48	0.038	<i>SHH</i>	-5.67	-1.91	0.010
<i>CIQTNF7</i>	2.30	3.78	0.000	<i>GIMAP7</i>	-5.67	-0.28	0.004
<i>GJA5</i>	2.26	0.01	0.049	<i>SPOCK3</i>	-5.64	1.74	0.001
<i>FRMD3</i>	2.21	1.81	0.006	<i>LCN6</i>	-5.61	-1.94	0.011
<i>RN7SL608P</i>	2.19	-1.55	0.028	<i>GNAI5</i>	-5.60	-0.92	0.002
<i>TSC22D3</i>	2.19	8.12	0.000	<i>HOXA10</i>	-5.59	0.11	0.001
<i>SLC38A11</i>	2.16	2.84	0.014	<i>MMP7</i>	-5.58	1.84	0.004
<i>LDHAL6B</i>	2.15	-1.43	0.036	<i>GATA5</i>	-5.58	-0.87	0.009
<i>FGF14</i>	2.13	3.26	0.023	<i>LADI</i>	-5.57	-0.94	0.006

Note: *Group #4*: Uniquely expressed DEGs of GC-R HTM cells (Group #1 minus Group #3)

Supplementary Table S5e: List of top 50 Up/Down-regulated Genes from Group #5

Up-regulated genes				Down-regulated genes			
Gene	logFC	logCPM	P Value	Gene	logFC	logCPM	P Value
<i>RGCC</i>	7.75	1.95	0.000	<i>GRM5</i>	-5.05	-2.43	0.010
<i>APCDD1</i>	5.95	2.15	0.000	<i>SLC24A2</i>	-3.89	-1.78	0.025
<i>IGF2-AS</i>	5.88	-1.83	0.002	<i>GRIA2</i>	-3.82	0.29	0.001
<i>PNMT</i>	5.76	-1.91	0.002	<i>RBFOX1</i>	-3.80	-1.82	0.048
<i>RAMP2-AS1</i>	5.64	0.83	0.000	<i>KRT17P1</i>	-3.77	-1.24	0.009
<i>ALOX15B</i>	5.51	-0.80	0.000	<i>GRID2</i>	-3.67	-0.01	0.002
<i>PTGDR2</i>	5.24	-2.22	0.003	<i>VCAN-AS1</i>	-3.63	-1.95	0.003
<i>LINC00525</i>	5.13	-2.29	0.003	<i>PADI2</i>	-3.55	0.96	0.000
<i>STEAP4</i>	4.57	3.40	0.000	<i>KLHDC7B</i>	-3.22	-0.85	0.003
<i>SFTPC</i>	4.51	-2.59	0.021	<i>IGFL2</i>	-3.20	-2.15	0.040
<i>FAM107A</i>	4.43	5.13	0.000	<i>C1orf87</i>	-3.10	-2.21	0.032
<i>HMGN2P15</i>	4.37	-0.64	0.002	<i>NPY6R</i>	-3.09	-2.22	0.036
<i>SOAT2</i>	4.13	-0.86	0.001	<i>NMNAT2</i>	-3.02	3.71	0.014
<i>TRAV39</i>	4.03	-0.91	0.012	<i>CLDN1</i>	-3.01	1.69	0.000
<i>LGI3</i>	3.70	-0.07	0.001	<i>ADM2</i>	-2.93	4.72	0.000
<i>INHBB</i>	3.67	1.41	0.000	<i>RIMS3</i>	-2.91	2.92	0.002
<i>RPA4</i>	3.56	-2.16	0.006	<i>CCND2-AS1</i>	-2.91	-1.15	0.007
<i>ANKRD2</i>	3.48	1.17	0.002	<i>IL32</i>	-2.91	2.34	0.007
<i>CHI3L2</i>	3.34	3.45	0.015	<i>COL19A1</i>	-2.79	0.34	0.001
<i>SCARA5</i>	3.34	-0.26	0.004	<i>KAL1</i>	-2.75	2.99	0.007
<i>GPRC5B</i>	3.26	5.02	0.000	<i>VCAN</i>	-2.69	7.10	0.001
<i>TNNT3</i>	3.12	-0.91	0.001	<i>CCND2-AS2</i>	-2.69	-1.72	0.032
<i>POM121L9P</i>	3.12	2.50	0.000	<i>IPCEF1</i>	-2.64	-2.20	0.047
<i>ISM1</i>	3.11	-0.30	0.001	<i>VNN1</i>	-2.63	-1.99	0.034
<i>NCAM1-AS1</i>	3.10	-2.39	0.046	<i>ARHGAP9</i>	-2.62	-0.48	0.003
<i>STOX1</i>	3.10	2.24	0.023	<i>RDH12</i>	-2.57	-1.62	0.012
<i>MYBPHL</i>	3.09	-2.40	0.040	<i>MYHAS</i>	-2.56	-1.50	0.012
<i>C3</i>	3.06	5.98	0.023	<i>EPHA3</i>	-2.52	0.55	0.007
<i>LINC00704</i>	3.04	-1.95	0.038	<i>CNGA1</i>	-2.49	-1.82	0.036
<i>GGT5</i>	3.04	6.46	0.000	<i>ELOVL2-AS1</i>	-2.46	-1.70	0.012
<i>NR0B1</i>	2.92	-1.01	0.016	<i>CHAC1</i>	-2.43	4.19	0.000
<i>TRPC3</i>	2.82	2.14	0.002	<i>ATPIA3</i>	-2.43	-0.96	0.004
<i>FAM150B</i>	2.80	-0.05	0.040	<i>SEMA3D</i>	-2.42	1.49	0.026
<i>EDNRB</i>	2.79	1.64	0.014	<i>CTNNA3</i>	-2.37	1.35	0.003
<i>STAR</i>	2.76	-1.13	0.002	<i>ERICH2</i>	-2.33	-1.49	0.036
<i>WSCD1</i>	2.74	0.98	0.034	<i>CCND2</i>	-2.32	2.26	0.019
<i>RPL23AP81</i>	2.74	-2.15	0.031	<i>LPHN3</i>	-2.30	2.21	0.043
<i>ALDH1L1-AS2</i>	2.64	-2.19	0.035	<i>INA</i>	-2.30	2.04	0.038
<i>NRCAM</i>	2.61	3.46	0.001	<i>UNC5B</i>	-2.28	5.69	0.009
<i>AKR1B15</i>	2.60	0.70	0.009	<i>CA3</i>	-2.27	-1.49	0.042
<i>B3GNT7</i>	2.60	1.89	0.009	<i>RIMS2</i>	-2.25	-1.14	0.045

<i>SYN2</i>	2.60	-0.79	0.002	<i>PLXNC1</i>	-2.23	2.68	0.003
<i>PLIN5</i>	2.59	-1.93	0.041	<i>LINC01133</i>	-2.21	2.67	0.003
<i>SIX2</i>	2.58	4.07	0.019	<i>LRRN4CL</i>	-2.19	2.88	0.005
<i>MTSS1</i>	2.51	4.67	0.008	<i>KCNS1</i>	-2.17	-0.42	0.010
<i>DGKG</i>	2.48	1.57	0.010	<i>KCTD16</i>	-2.17	2.93	0.002
<i>MREG</i>	2.47	2.69	0.001	<i>SLC7A5</i>	-2.14	6.66	0.004
<i>SPPI</i>	2.45	0.63	0.000	<i>KCNMB2</i>	-2.12	-1.25	0.033
<i>HEYL</i>	2.44	2.28	0.039	<i>BEX2</i>	-2.12	-0.68	0.018
<i>TLE6</i>	2.43	0.12	0.003	<i>CNTN6</i>	-2.11	1.58	0.010

Note: *Group #5*: Uniquely expressed DEGs of GC-NR HTM cells (Group #2 minus Group #3)

Supplementary Table S6a. List of Enriched Pathways in Group #1

Pathway	Fold Enrichment	P Value	Genes
Phosphatidylinositol signaling system	1.76	2E-03	<i>DGKG, PI4K2B, MTMR2, DGKE, DGKB, ITPR1, MTMR8, PIK3CD, ITPR2, PIK3CB, PIK3R1, PIK3C2A, MTMR6, MTMR7, MTM1, IMPA1, IMPA2, PPIP5K2, PIP4K2A, PLCE1, IP6K3, IPMK, INPP4B, PIKFYVE, PIK3CA, IMPAD1, PIK3C3, PLCB1, DGKI, DGKH</i>
Focal adhesion	1.73	7E-06	<i>ITGB1, GSK3B, FLT1, ITGB4, PIK3CD, PIK3CB, ARHGAP5, ACTB, IGF1R, PPP1CB, CCND3, AKT3, CAPN2, KDR, TNR, ITGAV, VAV3, PPP1R12A, ITGA4, ITGA2, ITGA1, ACTN4, PIK3CA, COL4A4, COL4A3, COL6A6, ITGA6, COL6A5, ITGA5, PPP1R12B, TLN1, MET, CRK, SOS2, BIRC2, SHC3, LAMA2, ROCK1, ROCK2, COL11A1, LAMA3, PDGFB, XIAP, PIK3R1, MYL12A, MYL12B, MAPK8, RAPIA, CHAD, SPPI, FLNA, MYL10, FLNB, PAK2, CAV2, CAV1, LAMB4, FN1, BRAF, PTK2, ITGA10, COL5A3</i>
TGF-beta signaling pathway	1.65	1E-02	<i>TGIF1, SMAD2, SMAD4, BMPR2, ROCK1, ZFYVE9, NOG, CUL1, BMP8A, INHBB, INHBA, GDF6, LTBP1, SMAD5, ACVR2B, TGFBRI, TGFBRI2, BMP2, ZFYVE16, RBL1, RPS6KB1, MYC, BMPRI1, NODAL</i>
p53 signaling pathway	1.63	3E-02	<i>GADD45B, APAF1, SERPINE1, CCNB3, CCND3, SESN3, CCNE2, RRM2B, ZMAT3, CHEK2, CASP3, CCNG2, CCNG1, CHEK1, MDM2, FAS, MDM4, ATM, ATR</i>
mTOR signaling pathway	1.59	7E-02	<i>PRKAA1, PRKAA2, CAB39, STRADA, IRS1, PIK3CD, BRAF, TSC1, PIK3CB, PIK3R1, PIK3CA, RPS6KB1, RPS6KA2, DDIT4, AKT3, RICTOR</i>
Cell cycle	1.58	6E-03	<i>CDKN1C, RB1, GSK3B, CCNH, PRKDC, CUL1, SMC3, CDC14B, CCNB3, CCND3, CHEK2, MYC, ORC3, RAD21, ORC2, CHEK1, CDC27, BUB3, BUB1, SMAD2, SMAD4, GADD45B, RBL2, CCNA1, STAG1, WEE1, RBL1, DBF4, STAG2, CCNE2, MDM2, ANAPC4, ATM, ATR</i>
Adherens junction	1.54	6E-02	<i>SMAD2, SMAD4, YES1, INSR, ACTN4, SORBS1, IQGAP1, TGFBRI, ACTB, TGFBRI2, IGF1R, TJP1, SNAI1, SNAI2, CTNNA2, WASF1, MAP3K7, MET, WASF3</i>
Regulation of actin cytoskeleton	1.51	1E-03	<i>ITGB1, CHRM2, NCKAP1, ITGB4, PIK3CD, PIK3CB, FGF1, FGF2, ACTB, FGF5, PPP1CB, CFL2, PIP4K2A, ITGAV, VAV3, PPP1R12A, ARHGEF12, ITGA4, ITGA2, ITGA1, ACTN4, ENAH, PIK3CA, ITGA6, ITGA5, PPP1R12B, CRK, SOS2, ARHGEF6, ROCK1, ROCK2, PDGFB, PIK3R1, IQGAP1, MYL12A, MYL12B, GNAI3, NRAS, MYL10, WASF1, PAK2, FGF22, RDX, FN1, BRAF, ARPC5, SSH2, PTK2, PIKFYVE, DIAPH2, FGF14, APC, ITGA10, KRAS, FGFR4</i>
TNF signaling pathway	1.51	2E-02	<i>ATF2, CEBPB, TNFAIP3, PIK3CD, PIK3CB, PIK3R1, CXCL2, MAPK8, BAG4, CASP3, AKT3, MAP3K8, DNMI1, MAP3K7, MAP3K5, EDN1, CHUK, CFLAR, FOS, TNFRSF1B, NFKBIA, ITCH, PIK3CA, TRAF5, FAS, TAB3, TAB2, BIRC2</i>
MAPK signaling pathway	1.48	7E-04	<i>ATF2, ZAK, HSPB1, FGF1, FGF2, FGF5, MECOM, MYC, RPS6KA2, CASP3, AKT3, MAP3K8, MAP3K6, MAP3K7, MAP3K5, DUSP4, DUSP5, MEF2C, CHUK, DUSP1, CACNA2D3, CACNA2D4, FOS, TGFBRI, DUSP6, TGFBRI2, CACNB2, PPM1A, PPM1B, TRAF6, RASA1, RASA2, RAPGEF2, CRK, SOS2, PDGFB, RASGRP2, RASGRP1, CACNG8, NRAS, PPP3R1, MAPK8, RAPIA, MAPK7, NTF3, FLNA, FLNB, CD14, PAK2, MAP4K3, FGF22, MAP3K2, NTRK2, GADD45B, NFATC3, BRAF, HSPA2, PPP5C, FGF14, TAOK1, NF1, FAS, KRAS, TAB2, FGFR4</i>
Pathways in cancer	1.32	3E-03	<i>RB1, ITGB1, GSK3B, WNT2B, HHIP, PIK3CD, CBLB, PIK3CB, FGF1, ETS1, FGF2, IGF1R, FGF5, EDNRB, MECOM, MYC, CASP3, AKT3, ITGAV, JAK1, APPL1, ARHGEF12, CHUK, ITGA2, WNT5A, MITF, FOS, TGFBRI, TGFBRI2, MSH6, PIK3CA, CCNE2, MSH2, MSH3, COL4A4, TRAF6, COL4A3, TRAF5, AGTR1, RARB, ITGA6, PLCB1, MET, CRK, SOS2, BIRC2, LAMA2, ROCK1, ROCK2, CUL2, LAMA3, PTGER3, PDGFB, GNAI3, LPAR1, WNT8B, XIAP, PIK3R1, CBL, RASGRP2, RASGRP1, HIF1A, FOXO1, GNAI3, NRAS, MAPK8, TPR, CTNNA2, FGF22, RUNX1T1, EGLN1, SMAD2, STAT5A, SMAD4, ZBTB16, PTCH1, FZD6, LAMB4, FN1, BRAF, PTK2, NFKBIA, BMP2, FGF14, APC, GNAQ, GNB4, MDM2, FAS, KRAS</i>

PI3K-Akt signaling pathway	1.30	9E-03	<i>ITGB1, CHRM2, ATF2, GSK3B, FLT1, IRS1, ITGB4, PIK3CD, BRCA1, PIK3CB, FGF1, FGF2, IGF1R, GHR, FGF5, CCND3, MYC, AKT3, KDR, TNF, ITGAV, JAK2, IL6R, JAK1, ITGA4, CHUK, ITGA2, ITGA1, TSC1, PRLR, RBL2, PIK3CA, CCNE2, COL4A4, COL4A3, DDIT4, MTCPI, COL6A6, ITGA6, SGK3, COL6A5, ITGA5, MET, TLR4, SOS2, TLR2, PHLPP2, PRKAA1, PRKAA2, LAMA2, COL11A1, LAMA3, PDGFB, LPAR1, PIK3R1, FOXO3, NRAS, BCL2L1, PPP2R3C, CHAD, SPP1, FGF22, MCL1, ANGPT1, INSR, LAMB4, FN1, PPP2R3A, PTK2, FGF14, RPS6KB1, ITGA10, COL5A3, GNB4, MDM2, KRAS, PKN2, FGFR4</i>
Cell adhesion molecules (CAMs)	-1.94	5E-10	<i>CD86, CNTNAP2, CNTNAP1, ITGAM, ITGB2, ICAM2, F11R, ITGAL, CLDN1, PTPRF, ICAM1, SPN, CDH5, CDH3, CDH1, ITGB7, HLA-DOA, NEO1, CD34, ICOSLG, HLA-DPA1, HLA-B, HLA-C, HLA-A, HLA-F, CLDN11, CLDN6, CLDN5, CLDN4, CLDN3, CD8A, CLDN8, CLDN7, PECAM1, CDH15, HLA-DQB1, ITGA9, NLGN3, SELPLG, NLGN2, SDC4, NRXN1, SDC2, SDC3, NRXN2, GLG1, HLA-DMA, HLA-DMB, LRRC4C, HLA-DQA2, CD99, HLA-DQA1, LRRC4B, CD276, NTNG2, HLA-DRB5, VCAM1, CADM1, SELE, SELP, CD2, CD4, OCLN, PTPRC, SELL, CD6, HLA-DPB1, HLA-DRA, CNTN2, ESAM, SIGLEC1, CD22, HLA-DRB1</i>
Calcium signaling pathway	-1.68	2E-07	<i>RYR1, CHRM3, RYR2, MYLK2, CHRM1, CALML6, HTR2B, ATP2A3, ADRA1D, CALML3, ATP2A1, GRPR, ADRA1A, SLC8A2, MYLK4, PPP3CA, CYSLTR1, CYSLTR2, BDKRB2, CD38, BDKRB1, NOS1, PRKACA, PDGFRA, PRKCB, TNNC1, TACR2, AVPR1A, TACR1, ITPKB, ADCY9, LTB4R2, ADORA2B, STIM2, ORAI2, SLC25A5, PLCB2, SLC25A6, CAMK2B, PDE1B, PTGER1, PDE1A, CHRNA7, CAMK2A, PTAFR, CACNA1B, ADCY4, CACNA1A, CACNA1D, ADRB1, ADCY2, ADCY1, CACNA1E, ADCY7, CACNA1G, GNA14, HRH1, GNA15, PLN, PHKG1, ERBB3, TBXA2R, PHKG2, ERBB2, PLCG2, DRD1, NTSR1, NOS3, ATP2B3, GRIN2C, GRIN1, P2RX7, P2RX6, P2RX4, P2RX2, P2RX1, CAMK4, CALM3, PLCD3, PLCD4</i>
Axon guidance	-1.63	6E-05	<i>ROBO3, RND1, PPP3CA, RGS3, NCK2, RAC2, RAC3, PLXNC1, EPHB2, EPHB1, EPHB4, EPHB3, SEMA6B, EPHA7, SEMA6A, UNC5B, UNC5D, RHOD, EPHA1, NGEF, EPHA3, EPHA2, SEMA3D, SEMA3A, SEMA3B, SEMA3G, CXCR4, SEMA3E, SEMA3F, EFNA4, NTN3, EFNB1, PAK1, EFNB3, ABL1, PAK6, PLXNA1, SLIT3, SLIT2, SRGAP3, PAK3, LRRC4C, PAK4, NTNG2, SEMA4A, SEMA4D, NFATC2, SEMA4F, SEMA4G, EFNA1, EFNA3, CXCL12, CDK5, FES, PLXNB2</i>
Inflammatory mediator regulation of TRP channels	-1.50	5E-03	<i>CAMK2B, CALML6, CAMK2A, ADCY4, HTR2B, PIK3R3, CALML3, ADCY2, PIK3R2, ADCY1, ADCY7, PIK3CG, PIK3R5, ADCY5, HRH1, PLCG2, BDKRB2, BDKRB1, TRPM8, PRKACA, ASIC1, CYP2J2, NTRK1, PLA2G4F, PRKCH, PRKCB, PRKCE, PRKCD, PLA2G4C, IGF1, NGF, MAPK12, MAPK11, ADCY9, TRPV4, IL1B, F2RL1, CALM3, PLCB2</i>
ECM-receptor interaction	-1.47	1E-02	<i>LAMA5, TNXB, SDC4, LAMC3, LAMA1, ITGA2B, TNC, LAMC2, THBS2, THBS4, THBS3, VTN, RELN, SV2B, SV2A, DAG1, ITGB7, ITGB6, CD36, LAMB3, COL24A1, VWF, COL1A1, COL3A1, COL1A2, COL4A2, COL5A1, ITGA11, COL4A6, COL6A3, ITGA7, AGRN, CD44, ITGA9</i>
Wnt signaling pathway	-1.39	7E-03	<i>FZD10, PPP3CA, FRAT2, CCND2, SOX17, RAC2, RAC3, PRKACA, MMP7, PRKCB, CTNBNBIP1, WNT9A, WNT16, DKK1, SFRP4, SFRP1, SFRP2, PLCB2, TP53, CAMK2B, CTBP1, TCF7, CAMK2A, LEF1, LRP5, CXXC4, NKD2, sFRP2, WNT11, WIF1, DVL1, TBL1Y, DVL2, DVL3, GPC4, WNT2, WNT3, WNT4, FZD1, WNT10B, WNT10A, FZD2, WNT3A, FZD7, WNT7B, FZD9, FZD8, NFATC2, NFATC1, VANGL2, BAMBI</i>
cAMP signaling pathway	-1.33	5E-03	<i>RYR2, VIPR2, CHRM1, CALML6, PDE3B, CALML3, GLI1, PIK3CG, GLI3, CREB3L4, AKT2, CREB3L1, ADORA1, PDE4B, CNGA1, RAC2, RAC3, FFAR2, SOX9, PRKACA, PDE4C, NPY1R, SSTRI, ATP1B2, SSTRI, VAV1, VAV2, TIAM1, CREB3, ADCY9, RAPGEF3, CFTR, CREB5, CAMK2B, GRIA2, ADCYAP1R1, GIPR, NPRI, CAMK2A, ADCY4, PIK3R3, ATP1A3, CACNA1D, ADRB1, PIK3R2, ATP1A2, ADCY2, ADCY1, ADCY7, PIK3R5, ADCY5, PAK1, HCARI, PLN, NPY, DRD1, GRIA4, BAD, BDNF, HTR1D, ATP2B3, NFATC1, GRIN2C, GRIN2B, TSHR, GRIN1, GRIN3B, CAMK4, FXD2, CALM3</i>
Ras signaling pathway	-1.30	6E-03	<i>CALML6, FLT4, RASGRF2, RASGRF1, CALML3, PIK3CG, FGF7, SYNGAP1, FGF9, RASSF5, AKT2, RAC2, RAC3, PRKACA, PDGFRA, PLA2G4F, KSR1, PRKCB, HGF, PLA2G4C, NGF, PGF, PLA2G16, TIAM1,</i>

MRAS, KIT, RIN1, PLA1A, EPHA2, SHC2, SHC1, PLA2G1B, PDGFA, PIK3R3, PIK3R2, PLA2G5, RASAL3, EFNA4, RASGRP4, PIK3R5, PAK1, GNG4, GNG7, PDGFC, ABL1, PLCG2, PAK6, PAK3, RALGDS, PAK4, ANGPT4, NGFR, ANGPT2, EGF, BAD, PLA2G2A, VEGFB, VEGFC, IGF1, GRIN2B, GNG11, GRIN1, VEGFA, EFNA1, FGF17, EFNA3, FGF18, CALM3, GNB5, RGL1, FGF13, FGF12, FGFR3, RGL2, FGF11, FGFR2, FGF10, FGFR1

Note: Group #1: The pathways enriched from DEGs between ETH and DEX-treated GC- R HTM cells; Size: Number of genes enriched. Fold enrichment is defined as the ratio of two proportions i.e. input genes/background information

Supplementary Table S6b. List of Enriched Pathways in Group #2.

Pathway	Fold Enrichment	P Value	Genes
TNF signaling pathway	1.65	2E-03	<i>CEBPB, TNFAIP3, PIK3R3, CXCL1, PIK3CB, PIK3R1, CXCL3, PTGS2, CXCL2, BAG4, CASP8, RPS6KA5, CASP10, CASP3, CCL2, MAPK1, RIPK1, MAP3K8, DNMI1, MAP3K5, JUN, EDN1, MLKL, CHUK, IL15, MMP3, CFLAR, FOS, TNFRSF1B, NFKBIA, ITCH, PIK3CA, IL1B, FAS, TAB3</i>
Cell cycle	1.50	9E-03	<i>CDKN1C, RB1, HDAC2, CDKN1B, PRKDC, CDC14A, ORC5, CCND3, PTTG1, YWHAQ, CHEK2, MYC, CDC26, RAD21, ORC2, CHEK1, E2F3, BUB3, SKP1, SMAD4, GADD45B, CDC25C, YWHAZ, GADD45G, RBL2, CCNA2, STAG1, WEE1, CDK7, RBL1, DBF4, CCNE2, CDK2, CDK1, MDM2, ANAPC4, MAD2L1</i>
Steroid biosynthesis	2.52	1E-02	<i>CYP27B1, EBP, SOAT1, SOAT2, CYP51A1, DHCR24, CEL, DHCR7, HSD17B7, LIPA</i>
MAPK signaling pathway	1.29	2E-02	<i>HSPB1, FGF1, RPS6KA6, RPS6KA5, MECOM, MYC, RPS6KA2, CASP3, MAP3K8, MAP3K6, MAP3K4, MAP3K5, DUSP4, PDGFRA, DUSP5, DUSP3, CHUK, DUSP1, IL1R1, PLA2G4B, RRAS2, PLA2G4A, PRKCA, FOS, MAPK8IP2, TGFBRI, DUSP6, TGFBRI, DUSP7, CACNB2, PPM1A, PPM1B, TRAF6, IL1B, RAPGEF2, RAF1, CRK, SOS2, RASGRP2, RASGRP4, CACNA1H, CACNA1G, CDC42, CACNG8, PPP3R1, RAP1A, MAPK7, FLNA, MAPK1, FLNB, MAP4K3, FGF22, NTRK2, JUN, GADD45B, BDNF, NFATC3, BRAF, HSPA2, GADD45G, PPP5C, FGF14, FAS, MAP3K13, FGFR4</i>
mTOR signaling pathway	1.65	3E-02	<i>PRKAA1, PRKAA2, CAB39, CAB39L, IRS1, RPS6, PIK3R3, BRAF, PRKCA, TSC1, PIK3CB, PIK3R1, MTOR, RPS6KA6, PIK3CA, RPS6KA2, ULK2, MAPK1, RICTOR</i>
Phosphatidylinositol signaling system	1.44	4E-02	<i>DGKG, PI4K2B, MTMR2, DGKB, ITPR1, MTMR8, PIK3R3, PIK3CB, PIK3R1, MTM1, IMPA1, IMPA2, PIP4K2A, PLCE1, PLCG1, IP6K3, IPMK, ITPK1, PRKCA, OCRL, INPP4B, SYNJI, PIK3CA, IMPAD1, PIK3C3, CALM1, DGKI, DGKH</i>
Vascular smooth muscle contraction	1.38	5E-02	<i>GUCY1B3, RAMP2, ROCK1, ROCK2, NPR1, ITPR1, ADCY3, ADCY2, ADRA1B, ACTG2, PPP1CB, PPP1CC, KCNMB3, MAPK1, PPP1R14A, PTGIR, PLA2G4B, PLA2G4A, PRKCA, BRAF, ACTA2, ADORA2A, ADORA2B, GNAQ, KCNMA1, AGTR1, MRV1, RAF1, CALM1, PPP1R12B, RAMP1, PPP1R12C</i>
VEGF signaling pathway	1.49	8E-02	<i>PLA2G4B, PXN, NFATC2, PLA2G4A, HSPB1, PIK3R3, PRKCA, PIK3CB, PIK3R1, PTGS2, PTK2, CDC42, PPP3R1, PIK3CA, KDR, MAPK1, PLCG1, RAF1</i>
TGF-beta signaling pathway	1.38	1E-01	<i>TGIF1, SMAD4, ROCK1, ZFYVE9, NOG, BMP8A, SMAD9, INHBB, GDF5, LTBP1, ACVR2B, DCN, TGFBRI, BMP6, TGFBRI, GDF7, PPP2CA, BMP2, RBL1, PPP2R1B, MYC, MAPK1, SKP1</i>
ECM-receptor interaction	-2.37	5E-09	<i>LAMA5, TNXB, LAMA2, SDC4, LAMA1, ITGA2B, TNC, LAMC2, THBS2, THBS4, THBS3, COMP, VTN, RELN, SV2A, DAG1, TNR, ITGB8, ITGB6, CD36, COL27A1, LAMB3, LAMB2, ITGA3, HSPG2, COL1A1, COL3A1, COL1A2, COL4A2, COL5A1, COL4A1, COL6A2, COL5A2, COL6A1, ITGA11, ITGA8, COL4A5, COL6A3, ITGA7, COL6A6, COL6A5, AGRN, CD44, ITGA9</i>
Axon guidance	-2.14	2E-09	<i>SEMA5A, ROBO3, LRRC4, RND1, RGS3, NCK2, RAC2, RAC3, PLXNC1, EPHB2, HRAS, EPHB1, EPHB4, EPHB3, SEMA6B, EPHA5, UNC5B, EPHA8, UNC5C, UNC5D, RHOD, RASA1, MET, NGEF, EPHA3, EPHA2, SEMA3D, SEMA3B, NTN4, SEMA3E, SEMA3F, EFNA4, NTN3, GNAI2, EFNB2, EFNB1, PAK1, EFNB3, ABL1, PAK6, PLXNA1, SLIT3, FYN, SRGAP3, PAK3, SRGAP2, LRRC4C, NTNG1, NTNG2, SEMA4A, LIMK1, SEMA4F, SEMA4G, L1CAM, EFNA3, CXCL12, PLXNB3, PLXNB2</i>
ABC transporters	-1.81	2E-02	<i>ABCD4, ABCA2, ABCD2, ABCB1, ABCA3, ABCB4, TAP2, TAP1, ABCA7, ABCC9, ABCB9, ABCB11, ABCA12, ABCC11, ABCA13, ABCG1, CFTR</i>
Notch signaling pathway	-1.75	2E-02	<i>JAG2, NUMBL, JAG1, CTBP1, PSEN2, DTX1, DTX2, RFNG, DLL1, DLL3, APH1A, DLL4, LFNG, NCSTN, DVLI, DVL2, DVL3, HES5</i>

Cell adhesion molecules (CAMs)	-1.71	4E-05	<i>CNTNAP2, CNTNAP1, ITGB2, ICAM2, LRRC4, ITGAL, PVR, CLDN1, PTPRF, ICAM1, CDH5, CDH3, CDH2, CDH1, MPZ, ITGB8, NEO1, CD34, HLA-B, HLA-C, HLA-A, HLA-F, VCAN, CLDN7, ITGA8, CDH15, ITGA9, NLGN3, SELPLG, NLGN2, SDC4, NRXN1, SDC2, SDC3, NRXN2, GLG1, HLA-DMA, LRRC4C, CD99, JAM2, LRRC4B, CD276, NTNG1, NTNG2, CADM3, VCAM1, CADM1, L1CAM, CD4, OCLN, PTPRC, SIGLEC1</i>
Gap junction	-1.65	4E-03	<i>ADCY4, HTR2B, HTR2A, ADCY1, ADCY8, ADCY7, GRM1, GNAI2, ADCY5, TUBA1C, TUBB6, GRM5, TUBA1A, TUBB3, PDGFC, PRKACA, HRAS, PRKG1, MAP2K5, GUCY1A3, GUCY1A2, MAP2K1, PRKCB, EGF, TUBB, PLCB4, ADCY9, GNAS, GRB2, SOS1, PLCB2</i>
Inflammatory mediator regulation of TRP channels	-1.57	6E-03	<i>CALML6, CAMK2A, ADCY4, HTR2B, PIK3R2, HTR2A, ADCY1, ADCY8, ADCY7, ADCY5, PLCG2, BDKRB2, BDKRB1, PRKACA, MAP2K6, ASIC1, MAP2K3, NTRK1, PRKCH, PRKCB, PRKCE, PLA2G4C, IGF1, NGF, MAPK10, MAPK11, PLCB4, ADCY9, TRPV4, GNAS, PRKCQ, PLCB2, CALM2</i>
Long-term depression	-1.48	7E-02	<i>GUCY1A3, GUCY1A2, GRIA2, GNAZ, MAP2K1, GRID2, PRKCB, PLA2G4C, CACNA1A, IGF1, GRM1, GNAI2, PLCB4, GNAI2, GNAS, HRAS, PLCB2, GRIA3, PRKG1</i>
Ras signaling pathway	-1.43	1E-03	<i>CALML6, RASGRF2, ELK1, FGF7, RASSF5, RAC2, RAC3, PRKACA, HRAS, MAP2K1, KSR1, PRKCB, HGF, PLA2G4C, NGF, PLA2G16, TIAM1, MRAS, RASA1, KIT, SOS1, MET, PLA1A, EPHA2, SHC4, SHC2, SHC1, PLA2G1B, PIK3R2, PLD1, RASGRP1, EFNA4, RELA, RASGRP3, PAK1, GNG4, GNG7, PDGFC, ABL1, PLCG2, PAK6, PAK3, RALGDS, ANGPT4, NGFR, ANGPT2, EGF, BAD, VEGFB, VEGFC, IGF1, GRIN2B, GNG11, NFKB1, VEGFA, MAPK10, FGF17, EFNA3, KITLG, FGF18, GRB2, GNB5, TEK, CALM2, FGF12, FGFR3, RGL2, FGFR2, FGFR1</i>
PI3K-Akt signaling pathway	-1.42	5E-05	<i>EPO, ITGA2B, TNC, COMP, STK11, FGF7, CCND2, CCND1, CREB3L4, CREB3L1, TNF, IFNAR2, MAP2K1, COL27A1, IL4R, HGF, F2R, COL4A2, COL4A1, DDIT4, COL4A5, MTCP1, TP53, EPHA2, ATF4, PIK3R2, EFNA4, VTN, PDGFC, EIF4EBP1, PCK2, NGFR, IGF1, GNG11, NFKB1, FGF17, COL1A1, EFNA3, IL6, CDK6, COL1A2, COL5A1, IL7, CDK4, COL5A2, ITGA11, FGF18, GRB2, GNB5, IL7R, FGF12, FGFR3, FGFR2, FGFR1, CDKN1A, LAMC2, CASP9, MLST8, ITGB8, ITGB6, JAK3, HRAS, ITGA3, NGF, CREB3, COL6A2, COL6A1, KIT, ITGA8, COL6A3, ITGA7, COL6A6, COL6A5, SOS1, MET, ITGA9, CREB5, LAMA5, PHLPP1, TNXB, LAMA2, ATF6B, LAMA1, THBS2, RELA, THBS4, THBS3, RELN, GNG4, GNG7, ANGPT4, ANGPT2, LAMB3, BAD, LAMB2, EGF, VEGFB, VEGFC, PPP2R3B, VEGFA, COL3A1, KITLG, TEK, PKN1, PIK3AP1</i>
cGMP-PKG signaling pathway	-1.42	8E-03	<i>ATF6B, CALML6, ADCY4, ATP1A4, ATP2A3, ATP1A3, ATP1A2, ADRB2, ADCY1, ADCY8, ADCY7, SLC8A1, GNAI2, ADCY5, CREB3L4, CREB3L1, KCNMB2, GNAI2, ADORA1, CNGA1, BDKRB2, KCNMB4, CACNA1S, PRKG1, GUCY1A3, GUCY1A2, MAP2K1, MEF2C, KCNJ8, BAD, PRKCE, PDE2A, ATP2B3, ATP2B1, ADRA2B, ADRA2A, CREB3, KCNU1, PLCB4, ADCY9, PDE3A, PDE5A, SLC25A5, PLCB2, CALM2, ATF4, SLC25A6, CREB5</i>
Calcium signaling pathway	-1.38	9E-03	<i>CHRM3, RYR2, CALML6, CHRM5, HTR2B, ATP2A3, HTR2A, HTR4, SLC8A1, GRM1, GRM5, CYSLTR2, BDKRB2, BDKRB1, PRKACA, PRKCB, TNNC1, TNNC2, F2R, TACR1, ITPKB, PLCB4, ADCY9, ITPKA, ORA12, SLC25A5, PLCB2, SLC25A6, PTGER1, PDE1A, CAMK2A, ADCY4, CACNA1A, ADRB2, ADCY1, ADCY8, CACNA1E, ADCY7, GNAI4, PHKG1, ERBB3, TBXA2R, PLCG2, CACNA1S, ATP2B3, ATP2B1, P2RX7, P2RX6, P2RX4, GNAS, PLCD3, CALM2, PLCD4</i>
Regulation of actin cytoskeleton	-1.25	5E-02	<i>CYFIP2, CHRM3, ARPC1B, ITGA2B, ITGB2, CHRM5, ARPC5L, ITGAL, FGF7, BDKRB2, RAC2, BDKRB1, ITGB8, RAC3, PIP4K2B, ITGB6, HRAS, APC2, MAP2K1, ITGA3, INSRR, F2R, VAV2, TIAM1, MRAS, ITGA8, PFN4, ARHGEF4, ITGA7, SOS1, ITGA9, PFN2, PIK3R2, IQGAP2, IQGAP3, FGD1, PAK1, GNAI2, PDGFC, PIP5K1A, PAK6, NCKAP1L, PAK3, EGF, LIMK1, BAIAP2, SSH3, MYLPF, FGF17, DIAPH3, ITGA11, FGF18, FGF12, FGFR3, FGFR2, FGFR1</i>

Note: Group #2: The pathways Enriched from DEGs between ETH and DEX-treated GC- NR HTM cells; Size: Number of genes enriched.

Supplementary Table S6c. List of Enriched Pathways in Group #3.

Pathway	Fold Enrichment	P Value	Genes
Focal adhesion	1.86	1E-04	<i>FLT1, SHC3, ROCK1, ROCK2, ITGB4, COL11A1, LAMA3, XIAP, PIK3CB, PIK3R1, MYL12A, ACTB, MYL12B, PPP1CB, CCND3, RAPIA, KDR, SPP1, CAPN2, FLNA, MYL10, FLNB, VAV3, ITGA4, CAV2, CAV1, ITGA2, LAMB4, BRAF, PTK2, PIK3CA, ITGA10, COL4A4, COL4A3, ITGA6, ITGA5, PPP1R12B, TLN1, CRK, SOS2</i>
Phosphatidylinositol signaling system	2.05	2E-03	<i>DGKG, PI4K2B, MTMR2, DGKB, IPMK, ITPR1, MTMR8, PIK3CB, PIK3R1, MTM1, INPP4B, PIK3CA, IMPA1, IMPA2, IMPAD1, PIP4K2A, PLCE1, PIK3C3, IP6K3, DGKI, DGKH</i>
MAPK signaling pathway	1.59	2E-03	<i>HSPB1, FGF1, RASGRP2, CACNG8, PPP3R1, RAPIA, MAPK7, MECOM, MYC, CASP3, RPS6KA2, FLNA, FLNB, MAP3K8, MAP3K6, MAP4K3, FGF22, MAP3K5, DUSP4, NTRK2, DUSP5, GADD45B, CHUK, DUSP1, NFATC3, BRAF, HSPA2, FOS, TGFBRI, DUSP6, TGFB2, CACNB2, PPM1A, PPP5C, PPM1B, FGF14, TRAF6, RAPGEF2, FAS, FGFR4, CRK, SOS2</i>
Pathways in cancer	1.39	8E-02	<i>RB1, WNT2B, PIK3CB, FGF1, ETS1, EDNRB, MECOM, MYC, CASP3, JAK1, CHUK, ITGA2, WNT5A, MITF, FOS, TGFBRI, TGFB2, MSH6, PIK3CA, CCNE2, COL4A4, TRAF6, COL4A3, AGTR1, RARB, ITGA6, CRK, SOS2, ROCK1, ROCK2, LAMA3, GNAI3, LPAR1, WNT8B, XIAP, PIK3R1, CBL, RASGRP2, HIF1A, FOXO1, FGF22, STAT5A, SMAD4, ZBTB16, PTCH1, FZD6, LAMB4, BRAF, PTK2, NFKBIA, BMP2, FGF14, APC, GNAQ, GNB4, MDM2, FAS</i>
TNF signaling pathway	1.79	1E-02	<i>EDN1, CEBPB, CHUK, TNFAIP3, CFLAR, PIK3CB, PIK3R1, FOS, TNFRSF1B, CXCL2, NFKBIA, ITC, BAG4, PIK3CA, CASP3, FAS, TAB3, MAP3K8, DNM1L, MAP3K5</i>
p53 signaling pathway	2.00	2E-02	<i>GADD45B, APAF1, SERPINE1, CCND3, SESN3, CCNE2, CHEK2, CASP3, CCNG2, CCNG1, CHEK1, MDM2, FAS, MDM4</i>
Drug metabolism - cytochrome P450	1.97	2E-02	<i>MAOA, ADH1B, ADH1A, MGST1, FMO2, FMO3, FMO4, FMO5, ADH5, ADH6, ADH4, CYP2A6, ALDH3B1, AOX1</i>
Adipocytokine signaling pathway	1.91	3E-02	<i>PRKAA1, PRKAB2, PRKAA2, CHUK, ACSL1, IRS1, PRKAG2, IRS2, PTPN11, TNFRSF1B, NFKBIA, ACSBG1, JAK2, PPARA</i>
Regulation of actin cytoskeleton	1.46	3E-02	<i>ROCK1, ROCK2, ITGB4, PIK3CB, PIK3R1, FGF1, MYL12A, ACTB, MYL12B, PPP1CB, MYL10, PIP4K2A, FGF22, VAV3, ITGA4, ITGA2, BRAF, ARPC5, SSH2, PTK2, ENAH, DIAPH2, FGF14, APC, PIK3CA, ITGA10, ITGA6, ITGA5, FGFR4, PPP1R12B, CRK, SOS2</i>
Thyroid hormone signaling pathway	1.58	5E-02	<i>NCOA2, MED1, NCOA3, SLC16A10, PIK3CB, PIK3R1, ATP1B1, ESR1, HIF1A, FOXO1, ACTB, MED13L, MED14, NCOR1, PIK3CA, TBC1D4, MYC, MDM2, PLCE1</i>
Cell cycle	1.54	5E-02	<i>CDKN1C, RB1, SMAD4, GADD45B, PRKDC, RBL2, CCND3, STAG1, WEE1, RBL1, DBF4, CCNE2, CHEK2, MYC, RAD21, ORC2, CHEK1, MDM2, ANAPC4, BUB3</i>
mTOR signaling pathway	1.81	8E-02	<i>PRKAA1, PRKAA2, CAB39, PIK3CA, IRS1, RPS6KA2, TSC1, BRAF, RICTOR, PIK3CB, PIK3R1</i>
PI3K-Akt signaling pathway	1.25	9E-02	<i>PRKAA1, FLT1, PRKAA2, IRS1, ITGB4, COL11A1, LAMA3, LPAR1, BRCA1, PIK3CB, PIK3R1, FOXO3, FGF1, CCND3, BCL2L11, MYC, KDR, SPP1, JAK2, IL6R, FGF22, JAK1, MCL1, ANGPT1, ITGA4, CHUK, ITGA2, INSR, LAMB4, TSC1, PRLR, PTK2, RBL2, FGF14, PIK3CA, CCNE2, ITGA10, COL4A4, COL4A3, GNB4, MDM2, ITGA6, ITGA5, FGFR4, SOS2</i>
TGF-beta signaling pathway	1.59	9E-02	<i>TGIF1, SMAD4, ROCK1, ZFYVE9, NOG, BMP8A, INHBB, LTBP1, ACVR2B, TGFBRI, TGFB2, BMP2, RBL1, MYC</i>
Axon guidance	-2.25	5E-07	<i>ROBO3, SEMA3D, SEMA3B, SEMA3E, SEMA3F, EFNA4, RND1, NTN3, EFNBI, PAK1, EFNBI, RGS3, ABL1, NCK2, RAC2, PAK6, PLXNA1, RAC3, SLIT3, PLXNC1, SRGAP3, EPHB2, PAK3, LRRC4C, EPHB1, EPHB4, EPHB3, SEMA6B, NTNG2, SEMA4A, UNC5B, SEMA4F, UNC5D, SEMA4G, RHOD, EFNA3, CXCL12, PLXNB2, EPHA3, NGEF, EPHA2</i>

Cell adhesion molecules (CAMs)	-2.01	1E-05	NLGN3, CNTNAP2, CNTNAP1, SELPLG, NLGN2, SDC4, NRXN1, SDC2, SDC3, ITGB2, ICAM2, NRXN2, ITGAL, CLDN1, PTPRF, GLG1, ICAM1, CDH5, HLA-DMA, CDH3, CDH1, LRRC4C, NEO1, CD34, CD99, LRRC4B, CD276, NTNG2, VCAM1, CADM1, HLA-B, HLA-C, HLA-A, HLA-F, CD4, OCLN, PTPRC, CLDN7, SIGLEC1, CDH15, ITGA9
ECM-receptor interaction	-2.24	5E-05	LAMA5, TNXB, SDC4, LAMA1, ITGA2B, TNC, LAMC2, THBS2, THBS4, THBS3, VTN, RELN, SV2A, DAG1, ITGB6, CD36, LAMB3, COL1A1, COL3A1, COL1A2, COL4A2, COL5A1, ITGA11, COL6A3, ITGA7, AGRN, CD44, ITGA9
Ras signaling pathway	-1.60	5E-04	CALML6, RASGRF2, FGF7, RASSF5, RAC2, RAC3, PRKACA, KSR1, PRKCB, HGF, PLA2G4C, NGF, PLA2G16, TIAM1, MRAS, KIT, PLA1A, EPHA2, SHC2, SHC1, PLA2G1B, PIK3R2, EFNA4, PAK1, GNG4, GNG7, PDGFC, ABL1, PLCG2, PAK6, PAK3, RALGDS, ANGPT4, NGFR, ANGPT2, EGF, BAD, VEGFB, VEGFC, IGF1, GRIN2B, GNG11, VEGFA, FGF17, EFNA3, FGF18, GNB5, FGF12, FGFR3, RGL2, FGFR2, FGFR1
Aldosterone synthesis and secretion	-1.98	2E-03	SCARB1, DAGLA, CAMK1D, CALML6, PRKCB, PRKCE, CAMK2A, PDE2A, ADCY4, ADCY1, ADCY7, ADCY5, CREB3, ADCY9, CREB3L4, CYP11A1, CREB3L1, CAMK1, PRKACA, PLCB2, CAMK1G, CREB5, ATF4
Thyroid hormone synthesis	-1.99	4E-03	GPX1, HSPA5, PRKCB, ADCY4, GPX7, ATP1A3, ATP1A2, ADCY1, ADCY7, TSHR, PDIA4, ADCY5, CREB3, ADCY9, CREB3L4, CREB3L1, PRKACA, PLCB2, CREB5, ATF4
Inflammatory mediator regulation of TRP channels	-1.70	1E-02	NTRK1, PRKCH, CALML6, PRKCB, PRKCE, CAMK2A, PLA2G4C, ADCY4, HTR2B, PIK3R2, ADCY1, IGF1, NGF, ADCY7, ADCY5, MAPK11, ADCY9, TRPV4, BDKRB2, PLCG2, BDKRB1, PRKACA, PLCB2, ASIC1
Notch signaling pathway	-2.03	2E-02	JAG2, CTBP1, PSEN2, DTX1, DTX2, RFNG, DLL1, DLL3, APH1A, DLL4, LFNG, DVL1, DVL2, DVL3
Glycine, serine and threonine metabolism	-2.14	2E-02	GAMT, AOC3, AOC2, PSAT1, SHMT2, CHDH, PGAM1, SARDH, PHGDH, SDSL, ALDH7A1, PSPH
Calcium signaling pathway	-1.44	2E-02	CHRM3, RYR2, PTGER1, CALML6, PDE1A, CAMK2A, ADCY4, HTR2B, ATP2A3, CACNA1A, ADCY1, CACNA1E, ADCY7, GNA14, CYSLTR2, PHKG1, ERBB3, TBXA2R, PLCG2, BDKRB2, BDKRB1, PRKACA, PRKCB, TNNC1, ATP2B3, TACR1, P2RX7, ITPKB, P2RX6, P2RX4, ADCY9, ORAI2, PLCD3, SLC25A5, PLCD4, PLCB2, SLC25A6
Protein processing in endoplasmic reticulum	-1.44	2E-02	RPN2, PRKCSH, RPN1, RRP1, HERPUD1, SEC61A1, GANAB, OS9, LMAN2, MAN1C1, FBXO6, BAK1, SIL1, UBQLN4, TXNDC5, PDIA3, SSR4, HSPA5, WFS1, SSR2, FBXO2, HSPA6, UBE2E2, TRAF2, CKAP4, DDOST, PDIA4, DNAJC5, DDIT3, ERP29, HYOU1, P4HB, CALR, MAN1B1, ATF4
Wnt signaling pathway	-1.46	3E-02	CTBP1, TCF7, LEF1, CAMK2A, LRP5, FZD10, FRAT2, WNT11, CCND2, DVL1, DVL2, RAC2, DVL3, RAC3, PRKACA, WNT2, WNT3, WNT4, WNT10B, FZD2, PRKCB, FZD7, CTNNBIP1, FZD8, WNT9A, SFRP4, VANGL2, PLCB2, TP53
ABC transporters	-1.74	9E-02	ABCA2, ABCB1, ABCA3, ABCB4, TAP2, TAP1, ABCA7, ABCB9, ABCC11, ABCG1, CFTR

Note: Group #3: The pathways Enriched from the overlapping DEGs between Group #1 and Group #2; Size: Number of genes enriched.

Supplementary Table S6d. List of Enriched Pathways in Group #4.

Pathway	Fold Enrichment	P Value	Genes
Axon guidance	1.94	1E-02	<i>ITGB1, GSK3B, SEMA7A, ARHGEF12, SEMA3C, LRRC4, NTN4, UNC5C, NRAS, RASA1, DPYSL2, CFL2, KRAS, PAK2, MET, SRGAP1, NCK1</i>
Regulation of actin cytoskeleton	1.59	3E-02	<i>ITGB1, CHRM2, NCKAP1, ARHGEF12, PPP1R12A, RDX, ITGA1, PDGFB, FN1, PIK3CD, ACTN4, IQGAP1, FGF2, FGF5, GNAI3, PIKFYVE, NRAS, CFL2, ITGAV, KRAS, WASF1, PAK2, ARHGEF6</i>
ECM-receptor interaction	2.00	3E-02	<i>ITGB1, LAMA2, COL5A3, ITGA1, CHAD, FN1, TNF, SDC1, COL6A6, ITGAV, GPIBA, COL6A5</i>
Focal adhesion	1.55	5E-02	<i>ITGB1, GSK3B, PPP1R12A, LAMA2, ITGA1, PDGFB, FN1, PIK3CD, ACTN4, ARHGAP5, IGF1R, MAPK8, COL5A3, CHAD, AKT3, TNF, COL6A6, ITGAV, COL6A5, PAK2, MET, BIRC2</i>
PI3K-Akt signaling pathway	1.39	5E-02	<i>ITGB1, CHRM2, PHLPP2, ATF2, GSK3B, LAMA2, PDGFB, PIK3CD, FGF2, IGF1R, GHR, FGF5, NRAS, PPP2R3C, CHAD, AKT3, TNF, ITGAV, ITGA1, FN1, PPP2R3A, RPS6KB1, COL5A3, DDIT4, MTCPI, KRAS, PKN2, COL6A6, SGK3, COL6A5, MET, TLR4, TLR2</i>
Adherens junction	2.04	5E-02	<i>SMAD2, TJP1, YES1, ACTN4, CTNNA2, IQGAP1, WASF1, MAP3K7, MET, IGF1R</i>
Protein processing in endoplasmic reticulum	1.54	7E-02	<i>SEC23A, SEC24A, SAR1B, SEL1L, CUL1, EIF2AK2, YOD1, EIF2S1, UBE2J1, DNAJC3, MAPK8, HSPH1, MAN1A2, MAN1A1, UGGT2, SEC62, ATF6, MBTPS2</i>
T cell receptor signaling pathway	1.74	8E-02	<i>GSK3B, DLG1, NRAS, AKT3, PIK3CD, KRAS, MAP3K7, PAK2, RASGRP1, LAT, MALTI, NCK1</i>
Cell cycle	1.64	8E-02	<i>SMAD2, GSK3B, CCNH, CUL1, SMC3, CDC14B, CCNB3, CCNA1, STAG2, ORC3, CDC27, ATM, BUB1, ATR</i>
Calcium signaling pathway	-1.98	1E-05	<i>CAMK2B, RYR1, MYLK2, CHRM1, PDE1B, CHRNA7, PTAFR, CACNA1B, CACNA1D, ADRA1D, ADRB1, ATP2A1, CALML3, ADCY2, GRPR, ADRA1A, SLC8A2, CACNA1G, MYLK4, PPP3CA, HRH1, GNAI5, CYSLTR1, PLN, PHKG2, ERBB2, CD38, DRD1, NOS1, NTSR1, PDGFRA, NOS3, TACR2, AVPR1A, GRIN2C, GRIN1, LTB4R2, ADORA2B, STIM2, P2RX2, P2RX1, CAMK4, CALM3</i>
Type I diabetes mellitus	-3.33	1E-05	<i>CD86, HLA-DRB5, PTPRN2, PTPRN, GAD1, PRF1, HLA-DMB, IL1B, HLA-DPB1, HLA-DRA, IL12A, HLA-DOA, HLA-DQA2, HLA-DQA1, HLA-DRB1, HLA-DPA1, HLA-DQB1</i>
Cell adhesion molecules (CAMs)	-1.85	7E-04	<i>CD86, ITGAM, F11R, SPN, HLA-DMB, ITGB7, HLA-DOA, HLA-DQA2, ICOSLG, HLA-DQA1, HLA-DPA1, HLA-DRB5, SELE, SELP, CLDN11, CD2, CLDN6, CLDN5, CLDN4, CLDN3, SELL, CD6, CD8A, CLDN8, HLA-DPB1, PECAM1, HLA-DRA, CNTN2, ESAM, CD22, HLA-DRB1, HLA-DQB1</i>
B cell receptor signaling pathway	-2.03	7E-03	<i>LYN, SYK, NFATC2, PIK3R3, NFATC1, PIK3CG, VAV1, PIK3R5, CD79B, CD79A, PPP3CA, AKT2, BLNK, PTPN6, FCGR2B, CD22, CARD11</i>
TNF signaling pathway	-1.69	2E-02	<i>MLKL, RIPK3, IL15, MMP3, LIF, PIK3R3, CXCL1, CXCL3, SELE, MMP9, PIK3CG, MAPK12, PIK3R5, TNFRSF1A, CXCL10, SOCS3, CASP10, IL1B, AKT2, CCL5, CCL2, PGAM5</i>
Chemokine signaling pathway	-1.37	6E-02	<i>CCL14, CCL13, CXCL6, GSK3A, CXCL9, NCF1, WAS, CXCR4, PIK3R3, CXCL1, ADCY2, ARRB2, CXCL13, CXCL3, CXCL14, PIK3CG, PIK3R5, PREX1, AKT2, CCL5, CCL2, CCL19, CCR1, LYN, PRKCD, VAV1, FGR, CXCL10, HCK, CXCL11, CCL26</i>

Note: Group #4: Uniquely expressed GC-R HTM cells specific pathways enriched from DEGs of Group #3 minus Group #1; Size: Number of genes enriched.

Supplementary Table S6e. List of Enriched Pathways in Group #5.

Pathway	Fold Enrichment	P Value	Genes
Long-term depression	2.31	9E-03	<i>RYR1, GUCY1B3, PLA2G4B, PLA2G4A, PRKCA, GNAI1, PPP2CA, GNAO1, PPP2R1B, PRKG2, MAPK1, NOS1, RAF1</i>
Vascular smooth muscle contraction	1.82	1E-02	<i>GUCY1B3, PTGIR, RAMP2, NPR1, PLA2G4B, PLA2G4A, ADCY3, PRKCA, ADCY2, ACTG2, PPP1CC, ADORA2A, ADORA2B, KCNMA1, MAPK1, MRV11, CALM1, RAF1, PPP1R12C, RAMP1</i>
Inflammatory mediator regulation of TRP channels	1.85	2E-02	<i>PTGER4, IL1R1, PTGER2, PLA2G4B, PLA2G4A, ADCY3, TRPV3, PIK3R3, PRKCA, ADCY2, ALOX12, PPP1CC, IL1B, F2RL1, PLCG1, CALM1, ASIC3</i>
Fatty acid metabolism	2.22	3E-02	<i>CPT1A, FASN, OXSM, ACSL6, ACSL5, ELOVL6, HADH, CPT1B, ACAT2, ACAT1</i>
VEGF signaling pathway	1.92	6E-02	<i>CDC42, PLA2G4B, PXN, NFATC2, PIK3R3, PLA2G4A, MAPK1, PRKCA, PLCG1, RAF1, PTGS2</i>
Oxytocin signaling pathway	1.49	7E-02	<i>RYR1, GUCY1B3, JUN, NPR1, PLA2G4B, KCNJ14, NFATC2, PLA2G4A, ADCY3, PRKCA, ADCY2, PTGS2, GNAI1, GNAO1, PPP1CC, RGS2, CAMK4, MAPK1, CALM1, RAF1, PPP1R12C</i>
Calcium signaling pathway	1.43	7E-02	<i>RYR1, PDGFRA, PTGFR, PDE1C, ATP2A2, ADCY3, ATP2A1, PRKCA, ADCY2, GRIN2C, CACNA1H, SLC8A2, CACNA1G, PLN, GNAL, STIM1, ADORA2A, ADORA2B, CAMK4, P2RX1, VDAC3, NOS1, PLCG1, CALM1</i>
ECM-receptor interaction	-2.62	9E-04	<i>COL27A1, LAMA2, LAMB2, ITGA3, HSPG2, COMP, COL4A1, COL6A2, COL5A2, COL6A1, ITGA8, COL4A5, TNF, ITGB8, COL6A6, COL6A5</i>
Focal adhesion	-1.94	1E-03	<i>SHC4, LAMA2, ELK1, COMP, CCND1, TNF, ITGB8, FYN, HRAS, MAP2K1, COL27A1, LAMB2, ITGA3, PARVA, MYLPP, MAPK10, COL4A1, COL6A2, COL5A2, COL6A1, ITGA8, COL4A5, GRB2, COL6A6, TLN2, COL6A5, SOS1, MET</i>
Gap junction	-2.43	3E-03	<i>MAP2K1, HTR2A, ADCY8, GRM1, GNAI2, GRM5, TUBB6, TUBA1A, PLCB4, GNAS, GRB2, SOS1, HRAS, MAP2K5, PRKG1</i>
Axon guidance	-1.91	2E-02	<i>NTNG1, SEMA5A, EPHA5, EPHA8, LIMK1, LRRC4, NTN4, UNC5C, L1CAM, GNAI2, EFNB2, RASA1, PLXNB3, FYN, SRGAP2, HRAS, MET</i>
PI3K-Akt signaling pathway	-1.45	2E-02	<i>PHLPP1, LAMA2, ATF6B, EPO, RELA, COMP, CCND1, EIF4EBP1, TNF, ITGB8, HRAS, JAK3, MAP2K1, COL27A1, LAMB2, ITGA3, F2R, NFKB1, KITLG, CDK6, COL4A1, COL6A2, COL5A2, COL6A1, DDIT4, ITGA8, COL4A5, MTCP1, GRB2, COL6A6, COL6A5, PKN1, TEK, SOS1, MET</i>
MAPK signaling pathway	-1.52	3E-02	<i>PPP5D1, ARRB1, ECSIT, RASGRP1, ELK1, RELA, RASGRP3, DUSP10, GNAI2, NTF3, CACNA1S, CD14, HRAS, MAP2K5, MAP2K6, MAP2K3, TGFB2, MAP2K1, MEF2C, DUSP2, MAP3K1, NFKB1, MAPK10, RASA1, GRB2, SOS1, MAP3K14</i>
Pathways in cancer	-1.38	4E-02	<i>LAMA2, EPAS1, BRCA2, ADCY8, RASGRP1, RELA, GNAI2, RASGRP3, CCND1, TPR, GNAI2, CTNNA1, VHL, CTNNA2, SKP2, HRAS, APC2, TCF7L2, TGFB2, MAP2K1, TCF7L1, CDKN2A, LAMB2, ITGA3, F2R, STAT3, NFKB1, PML, MAPK10, KITLG, PLCB4, CDK6, COL4A1, GNAS, COL4A5, GRB2, SOS1, MET</i>
Insulin secretion	-1.85	7E-02	<i>KCNU1, PLCB4, ATF6B, KCNMB2, ATP1A4, GNAS, KCNMB4, KCNN2, CACNA1S, ADCY8, TRPM4</i>
Cell cycle	-1.61	9E-02	<i>TGFB2, CDKN2A, BUB1B, TTK, CDC7, SMC1B, CCNA1, CDK6, CCND1, ATM, SKP2, E2F5, BUB1, MAD1L1</i>

Note: Group #5: Uniquely expressed GC-NR HTM cells specific pathways enriched from DEGs of Group #3 minus Group #2; Size: Number of genes enriched.

Supplementary Table S7: Comparison of Differentially Expressed Genes in TM Cells Treated with Glucocorticoid from Previous Reports and the Present Study

Study Design	Use of Postmortem Tissue	Age of the donors (Yrs)	Number of Donors used	Passage of Cells	Dexamethasone Treatment(nM)	Duration of Exposure (d)	Control medium	History of glaucoma	Microarray/RNA Seq	List of Up-regulated genes	References
Human Cultured TM cells	yes	7,16,21 and 28	4	4-5	100	7	0.1% Ethanol	Not specified	cDNA	<i>RGC32, OCA2, ANGPTL7, MYOC, FKBP5, SAA1, ZBTB16</i>	#7
Human Cultured TM cells	Yes	unknown	2	4-6	100	10	0.1% Ethanol	No history of glaucoma	Affymetrix Human Genome U95Av2 gene Chip microarrays	<i>SERPINA3, AKR1C1, IGFBP2, MYOC, PEDF, PCOLCE, AKR1C3, PTGDS, CHI3L1, ACTG2, CDT6, ASS, CTP, APOD, AP1G1</i>	#8
Human Cultured TM cells		unknown		8	100	10	Water in DMEM medium	Not specified	MicroMax Human cDNA System I	<i>GAS1, CDH4, MT1L, CST3, TSC22, LDHA, IGFbp2, TAGLN</i>	#9
Human Cultured TM cells	Yes	12,16 and 17	3	5	100	21	DMEM medium containing 10% fetal calf serum	No history of glaucoma	Affymetrix Human Genome U133A array	<i>MYOC, DCN, IGFBP2</i>	#10
Human Cultured TM cells	Yes	52	1	8	100	7	0.0025% and 0.025% Benzyl alcohol	No history of glaucoma	Standford Human cDNA SHEW	<i>GAS1, CDH4, MT1L, CST3, ATF4, ASNS/TS11, CHOP, HSPA5</i>	#11
Human Cultured TM cells	Yes	3 months old and 35	2	3-6	1000	24h	0.1% DMSO	Not specified	Agilent-014850 whole Human Genome Microarray 4X44K G4112F	<i>RGC32, OCA2, SAA1, ANGPTL7, ITGA10, LSP1, KCNB1, FKBP5, KLF15, ANGPTL4, MYOC, ZBTB16, PF4</i>	#12
Human Cultured TM cells	Yes	Not specified	3	Not specified	100	14	DMEM with 10% fetal calf serum	Not specified	Agilent - 028004 SurePrint G3 Human Gene Expression 8X60 K	<i>FKBP5, ZBTB16, SCNNIA, SAA1</i>	#13

										Microarray 039381	
Human Cultured TM cells	Yes	27	1	2	500	6	0.1% ethanol	Not specified	Affymetrix Human Gene 1.0 ST Array	<i>ITGB3, CHN1, PIK3R1, MFGE8</i>	#14
Bovine – Perfusion organ culture system -BTM cells with known GC responsiveness used	Yes-Bovine donor eyes	Adult cows	6 donors (paired eyes)	>3	100	7	0.1% ethanol	Not specified	Illumina Human Methylation 450K Chips	<i>DKK1, HMGA2, SOD2, STEAP4, SLC7A8</i>	#16
Human – Perfusion organ culture system -HTM cells with known GC responsiveness	Yes	67 (mean)	8 donors	3-4	100	7	0.1% Ethanol	No history of glaucoma	Illumina Next Seq 500	<i>ZBTB16, SAA1, MYOC, OCA2, H19, APOD, SAA2, HIF3A, PRODH, FKBP5, LSP1, ANGPTL7, CPM. STEAP4, MT2A, IRF7</i>	Present Study

Supplementary Table S8a. Comparison of Pathways Involved in DEX treated TM Cells from Previous Reports and the Present Study

Effect of DEX on TM cells		Present Study
Human Studies Combined*	Bovine[†]	
Collagen	Collagen	-
ECM	ECM	-
Adhesion	Adhesion	Adhesion
WNT signaling	WNT signaling	WNT signaling
Inflammation	Inflammation	-
Adipogenesis	Adipogenesis	-
Glucose metabolism	Glucose metabolism	-
NF-κB	NF-κB	-
Apoptosis	Apoptosis	-
GPCR	GPCR	-
Oxidative stress	Oxidative stress	-
		Phosphatidylinositol signaling system
		TGF Beta Signaling Pathway
		P53 Signaling Pathway
		mTOR signaling pathway
		Cell cycle
		Adherens junction
		Regulation of Actin Cytoskeleton
		TNF signaling pathway
		MAPK Signaling Pathway
		Pathways in Cancer
		PI3K-Akt signaling pathway
		Cell Adhesion Molecules Cams
		Calcium signaling pathway
		Axon Guidance
		Inflammatory mediator regulation of TRP channels

ECM-receptor interaction
cAMP signaling pathway
Ras signaling pathway
Steroid biosynthesis
Vascular smooth muscle contraction
VEGF Signaling Pathway
ABC transporters
Notch signaling pathway
Gap junction
cGMP-PKG signaling pathway

Note: **Ref. No.7-14*, [†]Ref.No.16, 35.

Supplementary Table S8b. Comparison of Pathways Enriched in Responder and Non-Responder HTM Cells from Previous Report and the Present Study.

Responder vs. non-responders Bovine †	Present Study	
	Responder	Non-Responder
Collagen	-	
ECM	-	
Adhesion	Adhesion	
WNT signaling	WNT signaling	
Inflammation	-	
Adipogenesis	-	
Glucose metabolism	-	
NF-κB	-	
Apoptosis	-	
Cell cycle	Cell cycle	
Senescence	-	
Oxidative stress	-	
	Axon guidance	Long-term depression
	Regulation of actin cytoskeleton	Vascular smooth muscle contraction
	ECM receptor interaction	Inflammatory mediator regulation of TRP channels
	Focal adhesion	Fatty acid metabolism
	PI3K-Akt signaling pathway	VEGF signaling pathway
	Adherens junction	Oxytocin signaling pathway
	Protein processing in endoplasmic reticulum	Calcium signaling pathway
	T cell receptor signaling pathway	ECM-receptor interaction
	Calcium signaling pathway	Focal adhesion
	Cell adhesion molecules (CAMs)	Gap junction
	B cell receptor signaling pathway	Axon guidance

TNF signaling pathway	PI3K-Akt signaling pathway
Chemokine signaling pathway	MAPK signaling pathway
	Pathways in cancer
	Insulin secretion
	Cell cycle

Note: [‡] Ref. No.16, 35