

**SUPPLEMENTAL TABLE 2: GENES DIFFERENTIALLY REGULATED BY EC SECRETIONS**

Gene ID	Gene Symbol	Gene Name	Fold Change (Transmigrated/ Untreated)	Fold Change (Unmigrated Above/Untreated)	Fold Change (Unmigrated Below/Untreated)
THC2374741	--	Unannotated	24.24	12.07	16.79
THC2283842	--	Unannotated	15	4.612	2.738
NM_002982	CCL2	chemokine (C-C motif) ligand 2	14.83	8.569	11.42
NM_006273	CCL7	chemokine (C-C motif) ligand 7	14.43	5.424	8.318
NM_001423	EMP1	epithelial membrane protein 1	13.63	6.416	5.5
ENST00000354530	CTSL3	cathepsin L family member 3	9.275	4.3	3.37
NM_006399	BATF	basic leucine zipper transcription factor, ATF-like	9.14	7.302	2.815
ENST00000342020	CTSL1	PREDICTED: Homo sapiens similar to Cathepsin L, preproprotein	8.739	4.004	3.548
NM_001912	CTSL1	cathepsin L (CTSL), transcript variant 1	8.315	4.405	3.413
NM_024607	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	7.696	5.099	5.632
NM_145071	CISH	cytokine inducible SH2-containing protein	7.089	8.974	8.353
NM_173842	IL1RN	interleukin 1 receptor antagonist	6.878	4.824	3.512
A_24_P375550	A_24_P375550	Unannotated	6.698	3.429	3.136
NM_018349	MCTP2	multiple C2-domains with two transmembrane regions 2	6.531	4.083	2.788
NM_014317	PDSS1	trans-prenyltransferase	6.194	3.486	2.829
AI094165	IL1RN	interleukin 1 receptor antagonist protein precursor	5.949	3.502	3.664
A_32_P145515	--	Unannotated	5.711	2.676	6.076
A_24_P755069	--	Unannotated	5.64	2.772	3.105
NM_003955	SOCS3	suppressor of cytokine signaling 3	5.026	6.684	8.971
AK091994	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	5.015	5.402	4.507
NM_001781	CD69	CD69 antigen (p60, early T-cell activation antigen)	4.817	4.928	5.748
NM_016354	SLCO4A1	solute carrier organic anion transporter family, member 4A1	4.588	3.474	3.23
BC024020	TMEM49	transmembrane protein 49	4.548	3.465	5.242
THC2404028	--	Unannotated	4.34	3.591	2.733
NM_183013	CREM	cAMP responsive element modulator	4.022	3.593	3.641
THC2438999	--	Unannotated	3.984	3.245	3.256
NM_032784	RSPO3	thrombospondin, type I, domain containing 2 (THSD2)	3.899	4.343	2.552
BC060766	SLC2A14	solute carrier family 2 (facilitated glucose transporter), member 14	3.89	3.542	3.09
BX109076	--	Unannotated	3.769	2.371	2.89
NM_005239	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2	3.66	2.784	2.946
BF238843	--	Unannotated	3.651	2.882	3.4
NM_153758	IL19	interleukin 19 (IL19)	3.632	2.917	2.207
NM_170736	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	3.506	2.313	2.771
AK098753	MIAT	myocardial infarction associated transcript	3.462	3.584	2.647
NM_005239	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2	3.29	2.553	2.927
NM_006931	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	3.26	2.747	2.372
XM_372040	--	PREDICTED: Homo sapiens similar to asparagine synthetase	3.047	2.232	2.071
AL713762	FGD4	FYVE, RhoGEF and PH domain containing 4	3.045	2.298	2.184
AK127258	--	Unannotated	3.027	2.179	2.357

NM_016389	IVNS1ABP	influenza virus NS1A binding protein	3.006	2.674	2.736
A_24_P581311	--	Unannotated	2.991	2.047	2.109
NM_183013	CREM	cAMP responsive element modulator	2.932	2.774	2.771
NM_032205	PHF20L1	PHD finger protein 20-like 1	2.879	2.674	2.077
X58747	TRAV6	T cell receptor V alpha gene segment V	2.808	2.116	3.205
NM_138557	TLR4	toll-like receptor 4	2.755	2.444	2.2
NM_016389	IVNS1ABP	influenza virus NS1A binding protein	2.741	2.603	2.444
THC2400121	PBEF	Pre-B cell enhancing factor precursor, partial	2.706	3.252	3.169
NM_003266	TLR4	toll-like receptor 4	2.693	2.207	2.184
NM_014522	PCDH11X	protocadherin 11 X-linked	2.662	2.236	2.594
NM_002357	MXD1	MAX dimerization protein 1	2.623	2.649	2.549
NM_032966	BLR1	Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)	2.547	2.284	3.459
NM_000361	THBD	thrombomodulin	2.505	2.978	3.165
AF147440	--	Unannotated	2.472	3.209	4.577
NM_152610	C1orf65	chromosome 1 open reading frame 65	2.435	2.25	2.635
ENST00000258775	NACAD	NAC alpha domain containing	2.348	2.355	2.868
THC2412698	--	Unannotated	2.302	2.296	2.003
NM_001004431	METRNL	meteorin, glial cell differentiation regulator-like	2.301	2.171	2.054
NM_004566	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	2.08	2.035	2.215
BC001892	C1orf63	chromosome 1 open reading frame 63	0.487	0.419	0.479
NM_052853	ADCK2	aarF domain containing kinase 2	0.466	0.402	0.452
NM_001009899	KIAA2018	Unannotated	0.465	0.361	0.293
AK055821	--	Unannotated	0.46	0.341	0.353
NM_006180	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	0.457	0.382	0.436
NM_138709	DAB2IP	DAB2 interacting protein	0.454	0.43	0.412
NM_006015	ARID1A	AT rich interactive domain 1A	0.451	0.482	0.472
ENST00000361063	--	Unannotated	0.443	0.495	0.466
ENST00000356730	--	PREDICTED: Homo sapiens similar to RIKEN	0.44	0.416	0.32
NM_032575	GLIS2	GLIS family zinc finger 2	0.437	0.417	0.412
NM_012083	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	0.43	0.446	0.477
NM_022340	ZFYVE20	zinc finger, FYVE domain containing 20	0.415	0.429	0.327
NM_033550	TP53RK	TP53 regulating kinase	0.41	0.456	0.338
NM_002978	SCNN1D	sodium channel, nonvoltage-gated 1, delta	0.41	0.489	0.369
NM_032829	C12orf34	hypothetical protein FLJ14721	0.405	0.394	0.308
NM_018282	PSPC1	paraspeckle component 1	0.404	0.306	0.5
NM_178172	LOC338328	high density lipoprotein-binding protein	0.402	0.456	0.417
NM_005481	THRAP5	thyroid hormone receptor associated protein 5	0.401	0.323	0.427
NM_001024858	SPTB	spectrin, beta, erythrocytic	0.4	0.449	0.381
NM_173078	SLITRK4	SLIT and NTRK-like family, member 4	0.395	0.428	0.495
A_32_P212939	--	Unannotated	0.395	0.431	0.379
THC2317353	--	Unannotated	0.375	0.314	0.188
AK023048	--	hypothetical protein FLJ12986	0.375	0.328	0.263
NM_022558	GH2	growth hormone 2	0.374	0.282	0.467
AL137712	--	hypothetical protein LOC90499	0.373	0.376	0.47
NM_000842	GRM5	glutamate receptor, metabotropic 5	0.372	0.459	0.373

NM_005574	LMO2	LIM domain only 2	0.369	0.348	0.479
AK123855	C1orf170	chromosome 1 open reading frame 170	0.369	0.325	0.372
AK025797	ANXA4	annexin A4	0.367	0.438	0.35
THC2319177	--	Unannotated	0.361	0.404	0.402
AL117443	PGM3	phosphoglucomutase 3	0.36	0.378	0.318
BC022205	C1orf79	chromosome 1 open reading frame 79	0.358	0.393	0.474
BC043547	--	hypothetical protein LOC730495	0.352	4.586	3.038
NM_000045	ARG1	arginase, liver	0.352	0.454	0.378
NM_003159	CDKL5	cyclin-dependent kinase-like 5	0.35	0.456	0.459
NM_014943	ZHX2	zinc fingers and homeoboxes 2	0.348	0.44	0.354
NM_006142	SFN	stratifin	0.345	0.358	0.385
BC041879	LOC390705	similar to protein phosphatase 2A	0.339	0.271	0.287
NM_016361	ACP6	acid phosphatase 6, lysophosphatidic	0.336	0.302	0.337
AB002384	C6orf32	chromosome 6 open reading frame 32	0.321	0.451	0.408
NM_152414	BHLHB5	basic helix-loop-helix domain containing, class B, 5	0.32	0.368	0.335
NR_001446	ANXA2P3	annexin A2 pseudogene 3	0.314	0.35	0.316
NM_018953	HOXC5	homeo box C5	0.314	0.158	0.27
THC2292455	--	Unannotated	0.31	0.343	0.425
NM_198794	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	0.308	0.278	0.386
NM_004088	DNTT	deoxynucleotidyltransferase, terminal	0.307	0.286	0.494
M69012	LOC346329	Human guanine nucleotide-binding regulatory protein (G-y-2-alpha) mRNA, partial cds. [M69012]	0.304	0.302	0.399
A_24_P7021	--	Unannotated	0.302	0.335	0.356
NM_012271	SETD2	huntingtin interacting protein B	0.298	0.241	0.348
AK023198	OPRK1	opioid receptor, kappa 1	0.278	0.35	0.208
NM_005898	CAPRN1	membrane component, chromosome 11, surface marker 1 (M11S1)	0.268	0.338	0.266
NM_080836	STK35	serine/threonine kinase 35	0.245	0.255	0.374
NM_001013711	LOC440905	hypothetical protein LOC440905	0.245	0.398	0.362
NM_000547	TPO	thyroid peroxidase	0.238	0.227	0.265
AK091289	ZNF367	zinc finger protein 367	0.235	0.294	0.347
BC020867	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	0.226	0.392	0.287
NM_053051	CNTROB	LYST-interacting protein LIP8	0.192	0.353	0.217
AK001072	FRMD4A	FERM domain containing 4A	0.189	0.256	0.235
ENST00000230559	MUC8	Human mucin (MUC8)	0.187	0.419	0.207
NM_007127	VIL1	villin 1	0.186	0.207	0.183
BC004277	FANCI	Fanconi anemia, complementation group I	0.167	0.262	0.152