

**Supplementary Table 4:** Differentially expressed genes (cutoffs: P-value  $<10^{-10}$  and  $\log_2$  fold change  $\geq 1$ ) in SSA/Ps and cADNs (versus their matched samples of normal mucosa). Filtered by adjusted P-values. ENSEMBL ID based on GRCh37/hg19 assembly.

ENSEMBL ID	GENE SYMBOL	Chr	Log <sub>2</sub> Fold Change	Adjusted P-value
<b>SSA/Ps versus normal mucosa - UPREGULATED</b>				
ENSG00000179546	HTR1D	chr1	6.784624316	3.1614E-102
ENSG00000134193	REG4	chr1	6.925155251	8.4816E-100
ENSG00000167757	KLK11	chr19	4.931589618	2.74116E-97
ENSG00000100196	KDEL3	chr22	3.042914463	3.59112E-96
ENSG00000196188	CTSE	chr1	5.662937397	6.33465E-80
ENSG00000062038	CDH3	chr16	5.97783346	4.28969E-79
ENSG00000206075	SERPINB5	chr18	7.297953941	3.09375E-75
ENSG00000169903	TM4SF4	chr3	8.98547193	1.07571E-74
ENSG00000198203	SULT1C2	chr2	6.076038971	1.18279E-73
ENSG00000136542	GALNT5	chr2	2.620774989	1.18279E-73
ENSG00000137699	TRIM29	chr11	5.147015312	1.53684E-73
ENSG00000163347	CLDN1	chr3	4.176239592	1.31577E-71
ENSG00000087916	SLC6A14	chrX	6.636180331	1.41346E-71
ENSG00000163993	S100P	chr4	5.249263493	1.76413E-71
ENSG00000135046	ANXA1	chr9	3.641267623	4.21047E-69
ENSG00000170786	SDR16C5	chr8	4.772378211	5.32997E-69
ENSG00000221947	XKR9	chr8	4.206718353	9.77638E-67
ENSG00000221926	TRIM16	chr17	1.871647329	5.53623E-66
ENSG00000138772	ANXA3	chr4	2.638701672	1.68717E-64
ENSG00000181634	TNFSF15	chr9	3.63207314	7.94826E-63
ENSG00000188910	GJB3	chr1	4.651672224	5.95907E-62
ENSG00000112414	GPR126	chr6	2.626141702	1.27726E-61
ENSG00000242247	ARFGAP3	chr22	2.186479672	1.27726E-61
ENSG00000129451	KLK10	chr19	7.234575094	4.73099E-61
ENSG00000120875	DUSP4	chr8	5.137909308	1.89088E-60
ENSG00000164379	FOXQ1	chr6	3.829619982	2.59122E-57
ENSG00000112299	VNN1	chr6	4.992282993	3.11403E-56
ENSG00000189433	GJB4	chr1	5.92561767	7.04676E-56
ENSG00000005001	PRSS22	chr16	5.010363561	1.05087E-55
ENSG00000172031	EPHX4	chr1	5.363187919	1.8615E-55
ENSG00000139289	PHLDA1	chr12	3.37473192	2.57522E-55
ENSG00000182240	BACE2	chr21	2.042176472	7.80632E-55
ENSG00000128039	SRD5A3	chr4	2.141180748	1.47047E-54
ENSG00000169047	IRS1	chr2	3.500601623	6.08433E-54
ENSG00000165376	CLDN2	chrX	5.48632627	8.86125E-54

ENSG00000160181	<b>TFF2</b>	chr21	6.934814617	1.51836E-53
ENSG00000198788	<b>MUC2</b>	chr11	3.540997815	7.49033E-53
ENSG00000163191	<b>S100A11</b>	chr1	2.551714962	7.49033E-53
ENSG00000105976	<b>MET</b>	chr7	2.00975368	7.07644E-52
ENSG00000167755	<b>KLK6</b>	chr19	7.649490598	7.74393E-52
ENSG00000151364	<b>KCTD14</b>	chr11	2.290605055	1.28329E-51
ENSG00000124157	<b>SEMG2</b>	chr20	8.998154764	1.50675E-50
ENSG00000196352	<b>CD55</b>	chr1	3.638124906	5.73793E-50
ENSG00000133985	<b>TTC9</b>	chr14	3.852309574	9.50342E-50
ENSG00000105464	<b>GRIN2D</b>	chr19	4.37901515	7.88656E-49
ENSG00000181577	<b>C6orf223</b>	chr6	6.388734952	9.18923E-49
ENSG00000150403	<b>TMCO3</b>	chr13	1.623324349	3.97651E-48
ENSG00000135480	<b>KRT7</b>	chr12	5.778389864	8.39607E-48
ENSG00000109511	<b>ANXA10</b>	chr4	7.954750653	2.68717E-47
ENSG00000110427	<b>KIAA1549L</b>	chr11	6.231120499	2.10119E-46
ENSG00000215182	<b>MUC5AC</b>	chr11	8.222420874	2.86217E-46
ENSG00000146038	<b>DCDC2</b>	chr6	4.886544085	2.86217E-46
ENSG00000157613	<b>CREB3L1</b>	chr11	2.094090021	8.77313E-46
ENSG00000112559	<b>MDFI</b>	chr6	4.547198317	1.99264E-45
ENSG00000142661	<b>MYOM3</b>	chr1	2.525316635	2.54713E-45
ENSG00000189280	<b>GJB5</b>	chr1	7.282694571	3.3046E-45
ENSG00000197442	<b>MAP3K5</b>	chr6	1.9094081	3.50034E-45
ENSG00000140274	<b>DUOXA2</b>	chr15	6.551963011	7.75737E-45
ENSG00000134504	<b>KCTD1</b>	chr18	2.036536299	1.02951E-44
ENSG00000129455	<b>KLK8</b>	chr19	8.37155684	1.02951E-44
ENSG00000196228	<b>SULT1C3</b>	chr2	6.173010951	1.91637E-44
ENSG00000124602	<b>UNC5CL</b>	chr6	2.391905253	3.55585E-44
ENSG00000167653	<b>PSCA</b>	chr8	5.90973231	1.85545E-43
ENSG00000154217	<b>PITPNC1</b>	chr17	1.915692897	2.33578E-43
ENSG00000166396	<b>SERPINB7</b>	chr18	7.655269857	6.16662E-43
ENSG00000123684	<b>LPGAT1</b>	chr1	1.672005361	1.66126E-42
ENSG00000162366	<b>PDZK1IP1</b>	chr1	3.011288258	1.71545E-42
ENSG00000164542	<b>KIAA0895</b>	chr7	2.711928752	3.1555E-42
ENSG00000168631	<b>DPCR1</b>	chr6	7.969548009	3.4127E-42
ENSG00000146054	<b>TRIM7</b>	chr5	3.223520726	4.7448E-42
ENSG00000147041	<b>SYTL5</b>	chrX	2.265937066	5.34576E-42
ENSG00000160182	<b>TFF1</b>	chr21	5.899219964	6.9408E-42
ENSG00000140526	<b>ABHD2</b>	chr15	1.698598405	9.22135E-42
ENSG00000065833	<b>ME1</b>	chr6	2.966199679	1.6668E-41
ENSG00000184292	<b>TACSTD2</b>	chr1	4.080440788	1.69773E-41
ENSG00000100003	<b>SEC14L2</b>	chr22	3.787688649	5.44418E-41
ENSG00000102265	<b>TIMP1</b>	chrX	2.82226053	1.00837E-40
ENSG00000150961	<b>SEC24D</b>	chr4	1.930460871	1.02854E-40
ENSG00000089723	<b>OTUB2</b>	chr14	2.403555771	1.3634E-40
ENSG00000139629	<b>GALNT6</b>	chr12	2.826099881	3.95391E-40

ENSG00000168679	<b>SLC16A4</b>	chr1	2.886018755	6.10675E-40
ENSG00000138028	<b>CGREF1</b>	chr2	4.050828614	7.73465E-40
ENSG00000168615	<b>ADAM9</b>	chr8	1.539199471	8.71169E-40
ENSG00000139515	<b>PDX1</b>	chr13	5.534241706	1.2051E-39
ENSG00000161798	<b>AQP5</b>	chr12	9.105370015	1.7934E-39
ENSG00000140279	<b>DUOX2</b>	chr15	5.533917698	1.2324E-38
ENSG00000072422	<b>RHOBTB1</b>	chr10	2.305662522	1.46745E-38
ENSG00000181791	<b>AC009041.1</b>	chr16	5.244472188	1.96729E-38
ENSG00000253368	<b>TRNP1</b>	chr1	5.256122258	1.10552E-37
ENSG00000185567	<b>AHNAK2</b>	chr14	3.710423313	1.29501E-37
ENSG00000132357	<b>CARD6</b>	chr5	3.008457786	1.98789E-37
ENSG00000147206	<b>NXF3</b>	chrX	5.501392785	3.93234E-37
ENSG00000187231	<b>SESTD1</b>	chr2	2.091388342	5.54818E-37
ENSG00000169247	<b>SH3TC2</b>	chr5	3.297808397	7.90337E-37
ENSG00000153395	<b>LPCAT1</b>	chr5	1.712750969	8.18307E-37
ENSG00000198807	<b>PAX9</b>	chr14	5.0435467	8.45155E-37
ENSG00000159184	<b>HOXB13</b>	chr17	4.94878896	9.51256E-37
ENSG00000167767	<b>KRT80</b>	chr12	4.376532625	1.32676E-36
ENSG00000164171	<b>ITGA2</b>	chr5	2.160493622	4.4055E-36
ENSG00000112378	<b>PERP</b>	chr6	1.53892261	9.46824E-36
ENSG00000115648	<b>MLPH</b>	chr2	1.886577389	1.45423E-35
ENSG00000148346	<b>LCN2</b>	chr9	3.879225411	1.69051E-35
ENSG00000151012	<b>SLC7A11</b>	chr4	3.043383794	1.20848E-34
ENSG00000168785	<b>TSPAN5</b>	chr4	2.287002	1.68131E-34
ENSG00000128595	<b>CALU</b>	chr7	1.508804519	2.02798E-34
ENSG00000101842	<b>VSIG1</b>	chrX	7.119386177	2.81787E-34
ENSG00000160868	<b>CYP3A4</b>	chr7	5.106112636	4.17398E-34
ENSG00000111700	<b>SLCO1B3</b>	chr12	6.8176304	7.12828E-34
ENSG00000106089	<b>STX1A</b>	chr7	2.647626235	7.90747E-34
ENSG00000125657	<b>TNFSF9</b>	chr19	3.564063285	2.37037E-33
ENSG00000160862	<b>AZGP1</b>	chr7	2.736824836	2.4614E-33
ENSG00000023171	<b>GRAMD1B</b>	chr11	4.019809803	5.35867E-33
ENSG00000119547	<b>ONECUT2</b>	chr18	3.249605088	2.01803E-32
ENSG00000198363	<b>ASPH</b>	chr8	1.555369103	2.65505E-32
ENSG00000139800	<b>ZIC5</b>	chr13	6.801199661	3.17633E-32
ENSG00000029153	<b>ARNTL2</b>	chr12	2.876109229	3.53084E-32
ENSG00000229715	<b>EEF1DP3</b>	chr13	4.520312081	5.68124E-32
ENSG00000167105	<b>TMEM92</b>	chr17	3.403130702	6.0934E-32
ENSG00000124233	<b>SEMG1</b>	chr20	7.638409925	9.58794E-32
ENSG00000128203	<b>ASPHD2</b>	chr22	2.0857231	1.14893E-31
ENSG00000106541	<b>AGR2</b>	chr7	2.472673758	1.47523E-31
ENSG00000134070	<b>IRAK2</b>	chr3	2.564317966	1.99191E-31
ENSG00000114019	<b>AMOTL2</b>	chr3	1.702116808	3.12265E-31
ENSG00000128610	<b>FEZF1</b>	chr7	6.989618348	4.84032E-31
ENSG00000102934	<b>PLLP</b>	chr16	3.569016668	5.2889E-31

ENSG00000165388	<b>ZNF488</b>	chr10	3.023986458	6.8406E-31
ENSG00000154845	<b>PPP4R1</b>	chr18	1.111206756	1.12714E-30
ENSG00000110244	<b>APOA4</b>	chr11	6.942986183	1.32958E-30
ENSG00000198535	<b>C2CD4A</b>	chr15	4.296246528	2.92064E-30
ENSG00000145391	<b>SETD7</b>	chr4	1.570462393	3.61953E-30
ENSG00000078114	<b>NEBL</b>	chr10	2.08040478	4.94628E-30
ENSG00000110080	<b>ST3GAL4</b>	chr11	4.559781683	6.36705E-30
ENSG00000138119	<b>MYOF</b>	chr10	2.207167871	6.48882E-30
ENSG00000100342	<b>APOL1</b>	chr22	2.206241115	1.03024E-29
ENSG00000128342	<b>LIF</b>	chr22	1.854013068	1.20484E-29
ENSG00000163739	<b>CXCL1</b>	chr4	3.319861077	1.21356E-29
ENSG00000120889	<b>TNFRSF10B</b>	chr8	1.197453239	1.25283E-29
ENSG00000103888	<b>KIAA1199</b>	chr15	2.641272073	1.32488E-29
ENSG00000164951	<b>PDP1</b>	chr8	1.814090057	1.32798E-29
ENSG00000169403	<b>PTAFR</b>	chr1	2.587338482	2.38116E-29
ENSG00000165816	<b>VWA2</b>	chr10	2.648232385	3.31891E-29
ENSG00000107819	<b>SFXN3</b>	chr10	1.8634026	8.09937E-29
ENSG00000088826	<b>SMOX</b>	chr20	2.350176604	1.05685E-28
ENSG00000111981	<b>ULBP1</b>	chr6	2.150030337	1.08479E-28
ENSG00000215864	<b>NBPF7</b>	chr1	2.716104769	1.16561E-28
ENSG00000176485	<b>PLA2G16</b>	chr11	2.735319341	1.41793E-28
ENSG00000169248	<b>CXCL11</b>	chr4	4.406958054	1.78573E-28
ENSG00000177508	<b>IRX3</b>	chr16	6.080918676	2.79915E-28
ENSG00000135919	<b>SERPINE2</b>	chr2	2.61981934	4.00099E-28
ENSG00000169035	<b>KLK7</b>	chr19	7.064692316	4.99012E-28
ENSG00000157227	<b>MMP14</b>	chr14	1.316405924	9.39631E-28
ENSG00000124588	<b>NQO2</b>	chr6	1.510102421	1.05078E-27
ENSG00000157224	<b>CLDN12</b>	chr7	1.577706047	1.74262E-27
ENSG00000137203	<b>TFAP2A</b>	chr6	3.575532635	2.23661E-27
ENSG00000132911	<b>NMUR2</b>	chr5	6.52122452	2.84626E-27
ENSG00000169213	<b>RAB3B</b>	chr1	2.577152506	3.44279E-27
ENSG00000128578	<b>STRIP2</b>	chr7	2.989087688	3.76233E-27
ENSG00000166401	<b>SERPINB8</b>	chr18	1.730029227	4.57607E-27
ENSG00000152766	<b>ANKRD22</b>	chr10	1.511015626	4.99598E-27
ENSG00000120149	<b>MSX2</b>	chr5	2.653078067	5.08242E-27
ENSG00000067177	<b>PHKA1</b>	chrX	1.645263046	6.1103E-27
ENSG00000175832	<b>ETV4</b>	chr17	3.469168707	7.42832E-27
ENSG00000251493	<b>FOXD1</b>	chr5	6.057557323	7.93133E-27
ENSG00000173898	<b>SPTBN2</b>	chr11	2.523975322	9.62045E-27
ENSG00000197265	<b>GTF2E2</b>	chr8	1.083256304	1.08802E-26
ENSG00000182158	<b>CREB3L2</b>	chr7	1.409993363	1.16536E-26
ENSG00000123843	<b>C4BPB</b>	chr1	2.434908041	1.19831E-26
ENSG00000107159	<b>CA9</b>	chr9	3.822182898	1.50114E-26
ENSG00000111696	<b>NT5DC3</b>	chr12	1.770568204	1.94663E-26
ENSG00000100170	<b>SLC5A1</b>	chr22	1.552522131	1.96775E-26

ENSG00000137033	<b>IL33</b>	chr9	3.39980259	2.06078E-26
ENSG00000007171	<b>NOS2</b>	chr17	2.906118668	3.52043E-26
ENSG00000014257	<b>ACPP</b>	chr3	1.952881982	3.96081E-26
ENSG00000166670	<b>MMP10</b>	chr11	5.082000195	3.97112E-26
ENSG00000138823	<b>MTTP</b>	chr4	5.450478222	6.25504E-26
ENSG00000134317	<b>GRHL1</b>	chr2	2.862255262	6.49143E-26
ENSG00000006534	<b>ALDH3B1</b>	chr11	2.112112268	6.9363E-26
ENSG00000196611	<b>MMP1</b>	chr11	3.755711156	8.92541E-26
ENSG00000163947	<b>ARHGEF3</b>	chr3	1.559525972	9.54111E-26
ENSG00000105219	<b>CNTD2</b>	chr19	4.360347903	9.54291E-26
ENSG00000180398	<b>MCFD2</b>	chr2	1.085911068	9.91092E-26
ENSG00000163817	<b>SLC6A20</b>	chr3	3.386252718	1.14549E-25
ENSG00000167695	<b>FAM57A</b>	chr17	1.452141485	1.51477E-25
ENSG00000124920	<b>MYRF</b>	chr11	1.862898764	1.88204E-25
ENSG00000213822	<b>CEACAM18</b>	chr19	6.68580372	2.25829E-25
ENSG00000143217	<b>PVRL4</b>	chr1	2.087473732	2.72895E-25
ENSG00000136448	<b>NMT1</b>	chr17	1.088156277	3.25092E-25
ENSG00000111907	<b>TPD52L1</b>	chr6	1.614613136	3.49422E-25
ENSG00000183900	<b>AC099522.1</b>	chr5	5.50411163	3.50944E-25
ENSG00000159263	<b>SIM2</b>	chr21	3.170820677	4.25254E-25
ENSG00000196754	<b>S100A2</b>	chr1	2.438633519	4.63514E-25
ENSG00000177409	<b>SAMD9L</b>	chr7	1.506715718	4.63514E-25
ENSG00000100078	<b>PLA2G3</b>	chr22	6.690035828	5.15021E-25
ENSG00000198964	<b>SGMS1</b>	chr10	1.373777231	5.54996E-25
ENSG00000169129	<b>AFAP1L2</b>	chr10	1.157000038	8.0841E-25
ENSG00000115507	<b>OTX1</b>	chr2	5.407671462	8.20877E-25
ENSG00000164111	<b>ANXA5</b>	chr4	1.428774233	1.07107E-24
ENSG00000105514	<b>RAB3D</b>	chr19	1.532297786	1.35876E-24
ENSG00000169908	<b>TM4SF1</b>	chr3	2.638011809	1.71521E-24
ENSG00000134827	<b>TCN1</b>	chr11	6.557574541	2.13567E-24
ENSG00000100522	<b>GNPNAT1</b>	chr14	1.482680062	2.32516E-24
ENSG00000162699	<b>DNAJA1P5</b>	chr1	6.650697211	3.11448E-24
ENSG00000079337	<b>RAPGEF3</b>	chr12	2.158112954	4.16094E-24
ENSG00000085117	<b>CD82</b>	chr11	2.176337055	6.05687E-24
ENSG00000180801	<b>ARSJ</b>	chr4	2.692252089	8.32668E-24
ENSG00000033170	<b>FUT8</b>	chr14	1.28238125	1.01695E-23
ENSG00000244503	<b>RP11-278L15.6</b>	chr3	7.295961205	1.09906E-23
ENSG00000160183	<b>TMPRSS3</b>	chr21	2.675745283	1.35508E-23
ENSG00000072864	<b>NDE1</b>	chr16	1.150682903	1.56449E-23
ENSG00000118898	<b>PPL</b>	chr16	1.798738249	1.88374E-23
ENSG00000183914	<b>DNAH2</b>	chr17	2.423875737	1.98896E-23
ENSG00000106038	<b>EVX1</b>	chr7	5.795495008	1.98896E-23
ENSG00000163734	<b>CXCL3</b>	chr4	2.549941631	2.39654E-23
ENSG00000113645	<b>WWC1</b>	chr5	1.459202608	3.15476E-23
ENSG00000171004	<b>HS6ST2</b>	chrX	2.858745041	3.51297E-23

ENSG00000166068	<b>SPRED1</b>	chr15	1.477749381	4.42944E-23
ENSG00000168502	<b>SOGA2</b>	chr18	3.10985519	4.67232E-23
ENSG00000102854	<b>MSLN</b>	chr16	4.267072905	4.76157E-23
ENSG00000172927	<b>MYEOV</b>	chr11	2.916817535	5.35047E-23
ENSG00000006327	<b>TNFRSF12A</b>	chr16	2.203393075	6.57774E-23
ENSG00000163577	<b>EIF5A2</b>	chr3	2.428758616	7.32584E-23
ENSG00000171060	<b>C8orf74</b>	chr8	5.52242919	1.01362E-22
ENSG00000136155	<b>SCEL</b>	chr13	3.483510871	1.14889E-22
ENSG00000131746	<b>TNS4</b>	chr17	2.21437697	1.25585E-22
ENSG00000136869	<b>TLR4</b>	chr9	1.577260404	1.66383E-22
ENSG00000099769	<b>IGFALS</b>	chr16	4.493102771	1.92748E-22
ENSG00000186188	<b>FFAR4</b>	chr10	1.685939113	2.05711E-22
ENSG00000088992	<b>TESC</b>	chr12	3.024517707	2.19977E-22
ENSG00000069011	<b>PITX1</b>	chr5	2.215686794	2.3793E-22
ENSG00000157193	<b>LRP8</b>	chr1	2.279412381	3.28958E-22
ENSG00000043355	<b>ZIC2</b>	chr13	6.041091736	3.60454E-22
ENSG00000075618	<b>FSCN1</b>	chr7	2.928765175	3.66411E-22
ENSG00000169876	<b>MUC17</b>	chr7	5.250402479	3.68788E-22
ENSG00000124102	<b>PI3</b>	chr20	3.73655983	3.75833E-22
ENSG00000159871	<b>LYPD5</b>	chr19	2.058670673	4.30115E-22
ENSG00000186591	<b>UBE2H</b>	chr7	1.003222911	5.0478E-22
ENSG00000064042	<b>LIMCH1</b>	chr4	1.803924035	5.64983E-22
ENSG00000198835	<b>GJC2</b>	chr1	3.467893509	6.92751E-22
ENSG00000196954	<b>CASP4</b>	chr11	1.227651757	7.69869E-22
ENSG00000060558	<b>GNA15</b>	chr19	2.395914435	8.51077E-22
ENSG00000196730	<b>DAPK1</b>	chr9	1.906508276	1.24137E-21
ENSG00000167460	<b>TPM4</b>	chr19	1.496381634	1.25053E-21
ENSG00000136141	<b>LRCH1</b>	chr13	1.247516647	1.48487E-21
ENSG00000136026	<b>CKAP4</b>	chr12	1.110562979	1.51172E-21
ENSG00000197506	<b>SLC28A3</b>	chr9	2.825865948	1.66494E-21
ENSG00000166268	<b>MYRFL</b>	chr12	3.654193515	1.68957E-21
ENSG00000235750	<b>KIAA0040</b>	chr1	1.126459145	2.99406E-21
ENSG00000134278	<b>SPIRE1</b>	chr18	2.20559172	3.00933E-21
ENSG00000164181	<b>ELOVL7</b>	chr5	1.268254466	3.13932E-21
ENSG00000134323	<b>MYCN</b>	chr2	2.480763413	3.47987E-21
ENSG00000197930	<b>ERO1L</b>	chr14	1.952596445	5.23578E-21
ENSG00000166002	<b>SMCO4</b>	chr11	1.023961238	7.36397E-21
ENSG00000091409	<b>ITGA6</b>	chr2	1.236174517	8.19492E-21
ENSG00000151929	<b>BAG3</b>	chr10	1.492104185	9.70109E-21
ENSG00000128165	<b>ADM2</b>	chr22	2.42668364	9.70109E-21
ENSG00000138606	<b>SHF</b>	chr15	1.931181598	1.05922E-20
ENSG00000003147	<b>ICA1</b>	chr7	1.168565328	1.84115E-20
ENSG00000089327	<b>FXD5</b>	chr19	1.51191605	1.9468E-20
ENSG00000151135	<b>C12orf23</b>	chr12	1.319095384	2.26064E-20
ENSG00000124107	<b>SLPI</b>	chr20	2.720169832	2.65927E-20

ENSG00000131910	<b>NR0B2</b>	chr1	4.048199561	2.92125E-20
ENSG00000167880	<b>EVPL</b>	chr17	1.460771407	3.37773E-20
ENSG00000171017	<b>LRRC8E</b>	chr19	2.327392187	5.00948E-20
ENSG00000103855	<b>CD276</b>	chr15	1.602700714	6.32474E-20
ENSG00000104522	<b>TSTA3</b>	chr8	1.615134515	6.39535E-20
ENSG00000134324	<b>LPIN1</b>	chr2	1.241064663	6.92292E-20
ENSG00000181652	<b>ATG9B</b>	chr7	4.320134579	7.41913E-20
ENSG00000124570	<b>SERPINB6</b>	chr6	1.213178151	7.84285E-20
ENSG00000123130	<b>ACOT9</b>	chrX	1.052675602	1.18591E-19
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ENSG00000164211	<b>STARD4</b>	chr5	1.476672458	1.89153E-19
ENSG00000145730	<b>PAM</b>	chr5	1.558916988	1.89211E-19
ENSG00000241322	<b>CDRT1</b>	chr17	2.665699546	1.94801E-19
ENSG00000164761	<b>TNFRSF11B</b>	chr8	2.243542908	1.98662E-19
ENSG00000139318	<b>DUSP6</b>	chr12	1.592192308	1.99997E-19
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ENSG00000066405	<b>CLDN18</b>	chr3	3.52423328	4.23989E-19
ENSG00000131620	<b>ANO1</b>	chr11	2.131468706	4.3945E-19
ENSG00000152056	<b>AP1S3</b>	chr2	1.822146742	4.3945E-19
ENSG00000134851	<b>TMEM165</b>	chr4	1.022514565	5.32071E-19
ENSG00000125798	<b>FOXA2</b>	chr20	2.051885671	5.78906E-19
ENSG00000175592	<b>FOSL1</b>	chr11	3.228321255	7.23263E-19
ENSG00000155660	<b>PDIA4</b>	chr7	1.232966802	7.55057E-19
ENSG00000101187	<b>SLCO4A1</b>	chr20	1.734811122	8.1159E-19
ENSG00000110492	<b>MDK</b>	chr11	2.104731684	8.61639E-19
ENSG00000186007	<b>LEMD1</b>	chr1	5.569211517	8.93046E-19
ENSG00000231274	<b>SBK3</b>	chr19	4.817477397	9.65902E-19
ENSG00000100558	<b>PLEK2</b>	chr14	1.147974662	1.09207E-18
ENSG00000106348	<b>IMPDH1</b>	chr7	1.614869882	1.15183E-18
ENSG00000185624	<b>P4HB</b>	chr17	1.161407601	1.27664E-18
ENSG00000104312	<b>RIPK2</b>	chr8	1.169480817	1.31018E-18
ENSG00000135111	<b>TBX3</b>	chr12	1.350130987	1.31202E-18
ENSG00000185332	<b>TMEM105</b>	chr17	3.813884992	1.31202E-18
ENSG00000058085	<b>LAMC2</b>	chr1	2.022046764	1.33709E-18
ENSG00000184979	<b>USP18</b>	chr22	1.464336968	1.44937E-18
ENSG00000198088	<b>NUP62CL</b>	chrX	1.611931812	1.44937E-18
ENSG00000138759	<b>FRAS1</b>	chr4	2.380582009	1.46473E-18
ENSG00000092445	<b>TYRO3</b>	chr15	1.940503705	1.57263E-18
ENSG00000143013	<b>LMO4</b>	chr1	1.096544164	1.67652E-18
ENSG00000125207	<b>PIWIL1</b>	chr12	6.294535486	1.77174E-18
ENSG00000107338	<b>SHB</b>	chr9	1.542743217	1.91549E-18
ENSG00000165046	<b>LETM2</b>	chr8	2.166066784	2.45492E-18
ENSG00000182718	<b>ANXA2</b>	chr15	1.322768217	2.64573E-18
ENSG00000065618	<b>COL17A1</b>	chr10	1.643809403	2.87892E-18

ENSG00000238271	<b>IFNWP19</b>	chr9	5.238619685	3.55866E-18
ENSG00000151689	<b>INPP1</b>	chr2	1.191440078	3.5848E-18
ENSG00000140263	<b>SORD</b>	chr15	1.611386821	3.59944E-18
ENSG00000129474	<b>AJUBA</b>	chr14	2.048202358	3.81273E-18
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ENSG00000165507	<b>C10orf10</b>	chr10	1.753938234	7.28839E-18
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ENSG00000163297	<b>ANTXR2</b>	chr4	1.092996438	7.83427E-18
ENSG00000125629	<b>INSIG2</b>	chr2	1.061603408	8.1929E-18
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ENSG00000181409	<b>AATK</b>	chr17	2.61199466	1.02653E-17
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ENSG00000163737	<b>PF4</b>	chr4	2.359042874	6.4604E-17
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ENSG00000155093	<b>PTPRN2</b>	chr7	1.55716758	1.00743E-16
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ENSG00000147592	<b>LACTB2</b>	chr8	1.217343084	1.69341E-16
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ENSG00000203727	<b>SAMD5</b>	chr6	1.895835248	3.2658E-14
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ENSG00000006704	<b>GTF2IRD1</b>	chr7	1.243577616	2.77589E-13
ENSG00000169174	<b>PCSK9</b>	chr1	2.771911865	2.7791E-13
ENSG00000079819	<b>EPB41L2</b>	chr6	1.234697764	3.15837E-13
ENSG00000109501	<b>WFS1</b>	chr4	1.408557702	3.2949E-13
ENSG00000162174	<b>ASRGL1</b>	chr11	1.148315822	3.33767E-13
ENSG00000176842	<b>IRX5</b>	chr16	4.834516775	3.52555E-13
ENSG00000143498	<b>TAF1A</b>	chr1	1.249978405	3.89328E-13
ENSG00000124496	<b>TRERF1</b>	chr6	1.402798232	4.17017E-13
ENSG00000042493	<b>CAPG</b>	chr2	1.139765657	4.19589E-13
ENSG00000172461	<b>FUT9</b>	chr6	2.560943971	4.21481E-13
ENSG00000104537	<b>ANXA13</b>	chr8	1.379875212	4.33858E-13
ENSG00000171346	<b>KRT15</b>	chr17	2.156938177	4.42832E-13
ENSG00000214814	<b>FER1L6</b>	chr8	1.413543447	4.79985E-13
ENSG00000101188	<b>NTSR1</b>	chr20	4.302478297	5.11005E-13
ENSG00000107807	<b>TLX1</b>	chr10	3.143401136	5.37751E-13
ENSG00000122711	<b>SPINK4</b>	chr9	2.636331797	5.55432E-13
ENSG00000128567	<b>PODXL</b>	chr7	1.384920099	5.77149E-13
ENSG00000197119	<b>SLC25A29</b>	chr14	1.5241345	5.87861E-13
ENSG00000114771	<b>AADAC</b>	chr3	3.420931715	5.98808E-13
ENSG00000100665	<b>SERPINA4</b>	chr14	5.374310408	6.1094E-13
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ENSG00000134508	<b>CABLES1</b>	chr18	1.158561614	6.4918E-13
ENSG00000120068	<b>HOXB8</b>	chr17	1.479201225	7.02339E-13
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ENSG00000070190	<b>DAPP1</b>	chr4	1.69141457	8.01345E-13
ENSG00000112541	<b>PDE10A</b>	chr6	3.054099602	8.25302E-13

ENSG00000197279	<b>ZNF165</b>	chr6	1.480353676	8.51341E-13
ENSG00000078900	<b>TP73</b>	chr1	1.832392917	8.53572E-13
ENSG00000121653	<b>MAPK8IP1</b>	chr11	1.889239881	8.78022E-13
ENSG00000160188	<b>RSPH1</b>	chr21	1.158857679	8.78653E-13
ENSG00000128268	<b>MGAT3</b>	chr22	1.614854108	8.95163E-13
ENSG00000155269	<b>GPR78</b>	chr4	5.178128062	9.84937E-13
ENSG00000171552	<b>BCL2L1</b>	chr20	1.143527986	1.00306E-12
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ENSG00000111701	<b>APOBEC1</b>	chr12	1.672857449	1.18301E-12
ENSG00000204876	<b>AC021218.2</b>	chr7	3.567238206	1.30635E-12
ENSG00000129226	<b>CD68</b>	chr17	1.225419499	1.33821E-12
ENSG00000112759	<b>SLC29A1</b>	chr6	1.452553157	1.34748E-12
ENSG00000111331	<b>OAS3</b>	chr12	1.133078359	1.58628E-12
ENSG00000204334	<b>ERICH2</b>	chr2	2.553586708	1.59379E-12
ENSG00000176720	<b>BOK</b>	chr2	1.296770767	1.6104E-12
ENSG00000137225	<b>CAPN11</b>	chr6	2.210534257	1.92599E-12
ENSG00000236699	<b>ARHGEF38</b>	chr4	1.131580464	1.94433E-12
ENSG00000130827	<b>PLXNA3</b>	chrX	1.455486044	2.0709E-12
ENSG00000214376	<b>VSTM5</b>	chr11	1.808338251	2.14573E-12
ENSG00000035862	<b>TIMP2</b>	chr17	1.341850594	2.32511E-12
ENSG00000239754	<b>CFB</b>	chrHSCCHR6_MHC_COX	1.356925539	2.38614E-12
ENSG00000128683	<b>GAD1</b>	chr2	3.357188935	2.44673E-12
ENSG00000196420	<b>S100A5</b>	chr1	2.649770338	2.65463E-12
ENSG00000164690	<b>SHH</b>	chr7	1.400556009	2.66802E-12
ENSG00000050344	<b>NFE2L3</b>	chr7	1.478750629	2.72338E-12
ENSG00000106258	<b>CYP3A5</b>	chr7	1.201724151	2.99098E-12
ENSG00000071575	<b>TRIB2</b>	chr2	1.48609701	3.19381E-12
ENSG00000204335	<b>SP5</b>	chr2	2.782234431	3.1939E-12
ENSG00000214274	<b>ANG</b>	chr14	1.049453357	3.21015E-12
ENSG00000161647	<b>MPP3</b>	chr17	2.044575785	3.46994E-12
ENSG00000179403	<b>VWA1</b>	chr1	1.825502318	4.17323E-12
ENSG00000135318	<b>NT5E</b>	chr6	1.418477351	5.26573E-12
ENSG00000177119	<b>ANO6</b>	chr12	1.980514478	5.33368E-12
ENSG00000085063	<b>CD59</b>	chr11	1.133975489	5.61717E-12
ENSG00000067225	<b>PKM</b>	chr15	1.02546311	5.78014E-12
ENSG00000269636	<b>AC010441.1</b>	chr5	1.231920604	5.93754E-12
ENSG00000183018	<b>SPNS2</b>	chr17	2.609477255	6.06578E-12
ENSG00000013588	<b>GPRC5A</b>	chr12	2.106439117	6.254E-12
ENSG00000237223	<b>SULT1C2P1</b>	chr2	2.148616952	6.37903E-12
ENSG00000112494	<b>UNC93A</b>	chr6	3.971439769	6.63272E-12
ENSG00000160752	<b>FDPS</b>	chr1	1.020097666	7.0356E-12
ENSG00000163975	<b>MFI2</b>	chr3	1.390488175	7.29144E-12
ENSG00000152669	<b>CCNO</b>	chr5	2.455611999	7.35792E-12

ENSG00000153292	<b>GPR110</b>	chr6	2.332619508	7.3809E-12
ENSG00000087253	<b>LPCAT2</b>	chr16	1.012926959	8.75042E-12
ENSG00000006453	<b>BAIAP2L1</b>	chr7	1.023445444	9.38695E-12
ENSG00000173227	<b>SYT12</b>	chr11	2.934964787	9.9626E-12
ENSG00000271361	<b>HTATSF1P2</b>	chr6	2.669327921	1.0607E-11
ENSG00000092929	<b>UNC13D</b>	chr17	1.640364087	1.06339E-11
ENSG00000172819	<b>RARG</b>	chr12	1.20078174	1.12738E-11
ENSG00000104689	<b>TNFRSF10A</b>	chr8	1.013388752	1.1569E-11
ENSG00000136295	<b>TTYH3</b>	chr7	1.375227832	1.22214E-11
ENSG00000052802	<b>MSMO1</b>	chr4	1.652820851	1.44382E-11
ENSG00000149243	<b>KLHL35</b>	chr11	2.077313366	1.51162E-11
ENSG00000132329	<b>RAMP1</b>	chr2	2.360619136	1.71255E-11
ENSG00000166455	<b>C16orf46</b>	chr16	1.347230112	1.72041E-11
ENSG00000130475	<b>FCHO1</b>	chr19	1.350334419	1.76699E-11
ENSG00000188487	<b>INSC</b>	chr11	1.765913895	1.86456E-11
ENSG00000169258	<b>GPRIN1</b>	chr5	2.038198032	2.28489E-11
ENSG00000272939	<b>CEACAM6</b>	chrHG1350 _HG959_PA TCH	2.046219485	2.29216E-11
ENSG00000143369	<b>ECM1</b>	chr1	1.454243743	2.3325E-11
ENSG00000114378	<b>HYAL1</b>	chr3	1.938650631	2.40698E-11
ENSG00000021488	<b>SLC7A9</b>	chr19	2.846819213	2.40698E-11
ENSG00000171617	<b>ENC1</b>	chr5	1.223935026	2.64004E-11
ENSG00000181649	<b>PHLDA2</b>	chr11	2.53177466	2.73735E-11
ENSG00000130751	<b>NPAS1</b>	chr19	2.261988233	2.79068E-11
ENSG00000117834	<b>SLC5A9</b>	chr1	1.777057771	3.29137E-11
ENSG00000180730	<b>SHISA2</b>	chr13	1.899855435	3.36235E-11
ENSG00000183778	<b>B3GALT5</b>	chr21	1.970296683	3.55472E-11
ENSG00000135702	<b>CHST5</b>	chr16	1.710919342	3.7651E-11
ENSG00000187800	<b>PEAR1</b>	chr1	1.256094373	4.29829E-11
ENSG00000271225	<b>RP11-460N11.3</b>	chr9	2.84746509	4.34551E-11
ENSG00000110092	<b>CCND1</b>	chr11	1.013820874	4.35391E-11
ENSG00000184956	<b>MUC6</b>	chr11	3.459481067	4.51291E-11
ENSG00000138075	<b>ABCG5</b>	chr2	1.727245062	4.82507E-11
ENSG00000244405	<b>ETV5</b>	chr3	1.48563056	6.01965E-11
ENSG00000168993	<b>CPLX1</b>	chr4	2.094823206	6.2572E-11
ENSG00000178597	<b>PSAPL1</b>	chr4	4.255931239	7.00112E-11
ENSG00000114346	<b>ECT2</b>	chr3	1.120179083	7.45662E-11
ENSG00000116132	<b>PRRX1</b>	chr1	2.740285664	7.54875E-11
ENSG00000161249	<b>DMKN</b>	chr19	1.714219744	7.99475E-11
ENSG00000054598	<b>FOXC1</b>	chr6	1.876087784	9.1182E-11
ENSG00000108379	<b>WNT3</b>	chr17	1.752558089	9.44266E-11
ENSG00000109107	<b>ALDOC</b>	chr17	1.501863656	1.10953E-10
ENSG00000135862	<b>LAMC1</b>	chr1	1.160877743	1.15058E-10
ENSG00000068650	<b>ATP11A</b>	chr13	1.051077985	1.16309E-10

ENSG00000168209	<b>DDIT4</b>	chr10	1.451940529	1.3011E-10
ENSG00000168955	<b>TM4SF20</b>	chr2	2.839685908	1.33349E-10
ENSG00000117016	<b>RIMS3</b>	chr1	1.337859847	1.35799E-10
ENSG00000003249	<b>DBNDD1</b>	chr16	2.086504241	1.362E-10
ENSG00000185022	<b>MAFF</b>	chr22	1.646130411	1.39622E-10
ENSG00000183010	<b>PYCR1</b>	chr17	1.284293761	1.4379E-10
ENSG00000169583	<b>CLIC3</b>	chr9	2.685870637	1.44585E-10
ENSG00000169469	<b>SPRR1B</b>	chr1	5.323749472	1.45174E-10
ENSG00000134107	<b>BHLHE40</b>	chr3	1.381153167	1.71541E-10
ENSG00000119403	<b>PHF19</b>	chr9	1.095716972	1.80302E-10
ENSG00000136158	<b>SPRY2</b>	chr13	1.061843441	2.00619E-10
ENSG00000099960	<b>SLC7A4</b>	chr22	2.100898598	2.12334E-10
ENSG00000131015	<b>ULBP2</b>	chr6	3.774161082	2.14815E-10
ENSG00000100557	<b>C14orf105</b>	chr14	4.930284411	2.23372E-10
ENSG00000002587	<b>HS3ST1</b>	chr4	1.726884848	2.30787E-10
ENSG00000197905	<b>TEAD4</b>	chr12	1.092143326	2.36184E-10
ENSG00000164086	<b>DUSP7</b>	chr3	1.024859062	2.4649E-10
ENSG00000182795	<b>C1orf116</b>	chr1	1.328232171	2.50937E-10
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ENSG00000146233	<b>CYP39A1</b>	chr6	1.497779802	2.7439E-10
ENSG00000166840	<b>GLYATL1</b>	chr11	2.042078081	3.13053E-10
ENSG00000137267	<b>TUBB2A</b>	chr6	1.791297973	3.14511E-10
ENSG00000026508	<b>CD44</b>	chr11	1.359286652	3.22186E-10
ENSG00000132481	<b>TRIM47</b>	chr17	1.342255439	3.37386E-10
ENSG00000183196	<b>CHST6</b>	chr16	1.785635507	3.44479E-10
ENSG00000111057	<b>KRT18</b>	chr12	1.101518094	3.46858E-10
ENSG00000157350	<b>ST3GAL2</b>	chr16	1.185589385	3.56224E-10
ENSG00000188037	<b>CLCN1</b>	chr7	2.826356515	3.65062E-10
ENSG00000136305	<b>CIDEB</b>	chr14	1.730017933	4.04256E-10
ENSG00000028137	<b>TNFRSF1B</b>	chr1	1.182403889	4.23577E-10
ENSG00000254521	<b>SIGLEC12</b>	chr19	1.564079977	4.23592E-10
ENSG00000159423	<b>ALDH4A1</b>	chr1	1.168349727	4.39154E-10
ENSG00000140465	<b>CYP1A1</b>	chr15	4.488842313	4.48653E-10
ENSG00000197046	<b>SIGLEC15</b>	chr18	1.810900566	4.49193E-10
ENSG00000114854	<b>TNNC1</b>	chr3	2.542398955	4.88734E-10
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ENSG00000073067	<b>CYP2W1</b>	chr7	2.899854562	4.9707E-10
ENSG00000141582	<b>CBX4</b>	chr17	1.0174719	5.31293E-10
ENSG00000115919	<b>KYNU</b>	chr2	1.896849864	5.44621E-10
ENSG00000164294	<b>GPX8</b>	chr5	1.43550667	5.81661E-10
ENSG00000187642	<b>C1orf170</b>	chr1	2.510517391	6.80634E-10
ENSG00000116791	<b>CRYZ</b>	chr1	1.148300867	7.29575E-10
ENSG00000004848	<b>ARX</b>	chrX	2.443574042	7.51838E-10
ENSG00000197520	<b>FAM177B</b>	chr1	1.505771118	7.58968E-10
ENSG00000142733	<b>MAP3K6</b>	chr1	1.145531588	7.96442E-10

ENSG00000173557	<b>C2orf70</b>	chr2	2.399410233	8.35247E-10
ENSG00000182747	<b>SLC35D3</b>	chr6	2.29443671	9.04014E-10
ENSG00000133019	<b>CHRM3</b>	chr1	1.621461569	9.4267E-10

### SSA/Ps versus normal mucosa - DOWNREGULATED

ENSEMBL ID	GENE SYMBOL	Chr	Log <sub>2</sub> Fold Change	Adjusted P-value
ENSG00000132915	<b>PDE6A</b>	chr5	-2.926345507	8.7081E-47
ENSG00000214189	<b>ZNF788</b>	chr19	-2.564213658	1.44363E-45
ENSG00000111846	<b>GCNT2</b>	chr6	-2.291104006	2.60423E-38
ENSG00000269190	<b>FBXO17</b>	chr19	-2.011606389	1.75902E-37
ENSG00000124615	<b>MOCS1</b>	chr6	-2.742465629	2.5999E-37
ENSG00000197375	<b>SLC22A5</b>	chr5	-1.590346489	4.10047E-36
ENSG00000119042	<b>SATB2</b>	chr2	-1.355501475	1.55727E-34
ENSG00000167080	<b>B4GALNT2</b>	chr17	-3.739469135	3.02542E-34
ENSG00000176273	<b>SLC35G1</b>	chr10	-1.541908787	5.76232E-34
ENSG00000108187	<b>PBLD</b>	chr10	-1.872524992	1.59138E-33
ENSG00000175600	<b>SUGCT</b>	chr7	-3.182058587	2.23035E-33
ENSG00000108576	<b>SLC6A4</b>	chr17	-4.065876468	7.60447E-33
ENSG00000168734	<b>PKIG</b>	chr20	-1.471979254	8.95775E-33
ENSG00000152078	<b>TMEM56</b>	chr1	-2.124575146	1.66253E-32
ENSG00000109182	<b>CWH43</b>	chr4	-3.354763348	2.50404E-32
ENSG00000122694	<b>GLIPR2</b>	chr9	-1.902384283	4.11774E-32
ENSG00000156345	<b>CDK20</b>	chr9	-1.988092391	4.76444E-32
ENSG00000066468	<b>FGFR2</b>	chr10	-1.502563289	9.0373E-32
ENSG00000214357	<b>NEURL1B</b>	chr5	-2.062770867	1.36151E-31
ENSG00000179750	<b>APOBEC3B</b>	chr22	-2.55121722	1.43363E-31
ENSG00000188373	<b>C10orf99</b>	chr10	-2.350939354	4.04847E-31
ENSG00000111863	<b>ADTRP</b>	chr6	-2.889375151	7.05006E-31
ENSG00000167107	<b>ACSF2</b>	chr17	-2.010204122	7.25099E-31
ENSG00000185432	<b>METTL7A</b>	chr12	-1.846513429	2.00743E-30
ENSG00000006740	<b>ARHGAP44</b>	chr17	-2.079132895	2.60326E-30
ENSG00000155850	<b>SLC26A2</b>	chr5	-3.632355678	1.15499E-29
ENSG00000248144	<b>ADH1C</b>	chr4	-2.894849634	2.12628E-29
ENSG00000135083	<b>CCNJL</b>	chr5	-1.984303891	3.7169E-29
ENSG00000139163	<b>ETNK1</b>	chr12	-2.104477851	2.41629E-28
ENSG00000203401	<b>AC009061.1</b>	chr16	-2.276044233	2.4398E-28
ENSG00000249948	<b>GBA3</b>	chr4	-2.658790995	3.09693E-28
ENSG00000156298	<b>TSPAN7</b>	chrX	-1.811552858	6.08085E-28
ENSG00000064655	<b>EYA2</b>	chr20	-3.67595295	4.87276E-27
ENSG00000175356	<b>SCUBE2</b>	chr11	-2.098223593	8.30884E-27
ENSG00000066230	<b>SLC9A3</b>	chr5	-2.727871125	5.20194E-26
ENSG00000172572	<b>PDE3A</b>	chr12	-2.45426916	5.73208E-26
ENSG00000171612	<b>SLC25A33</b>	chr1	-1.592077847	8.22092E-26
ENSG00000164093	<b>PITX2</b>	chr4	-2.298082659	1.4214E-25

ENSG00000075239	<b>ACAT1</b>	chr11	-1.538925268	1.85977E-25
ENSG00000150054	<b>MPP7</b>	chr10	-1.220046032	2.83118E-25
ENSG00000143416	<b>SELENBP1</b>	chr1	-1.978405061	3.85065E-25
ENSG00000073711	<b>PPP2R3A</b>	chr3	-1.486994906	3.91723E-25
ENSG00000082397	<b>EPB41L3</b>	chr18	-3.003792307	3.94315E-25
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ENSG00000121769	<b>FABP3</b>	chr1	-2.357656835	5.05099E-25
ENSG00000196268	<b>ZNF493</b>	chr19	-1.37879505	8.59512E-25
ENSG00000272398	<b>CD24</b>	chrHG357_ PATCH	-1.344414553	1.00366E-24
ENSG00000198125	<b>MB</b>	chr22	-2.498108244	2.53839E-24
ENSG00000164039	<b>BDH2</b>	chr4	-1.400296474	3.37405E-24
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ENSG00000101470	<b>TNNC2</b>	chr20	-2.731521868	8.31836E-24
ENSG00000170482	<b>SLC23A1</b>	chr5	-2.803957038	1.2304E-23
ENSG00000109814	<b>UGDH</b>	chr4	-1.292047549	1.53201E-23
ENSG00000040199	<b>PHLPP2</b>	chr16	-1.755296629	1.70892E-23
ENSG00000258679	<b>RP11-74M13.4</b>	chr12	-2.252648257	3.66246E-23
ENSG00000039987	<b>BEST2</b>	chr19	-3.027888637	4.09132E-23
ENSG00000178163	<b>ZNF518B</b>	chr4	-1.928341965	5.0338E-23
ENSG00000250506	<b>CDK3</b>	chr17	-1.64133264	5.37752E-23
ENSG00000088280	<b>ASAP3</b>	chr1	-1.578943068	5.3963E-23
ENSG00000171208	<b>NETO2</b>	chr16	-2.179446357	5.68181E-23
ENSG00000183049	<b>CAMK1D</b>	chr10	-1.811462655	1.14889E-22
ENSG00000123643	<b>SLC36A1</b>	chr5	-1.185037104	1.64238E-22
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ENSG00000186198	<b>SLC51B</b>	chr15	-2.00027714	5.71872E-11
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ENSG00000137727	<b>ARHGAP20</b>	chr11	-1.907906188	5.85828E-11
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ENSG00000233087	<b>AC073869.1</b>	chr2	-1.801604239	6.40419E-11
ENSG00000167434	<b>CA4</b>	chr17	-3.091202537	6.45908E-11
ENSG00000106351	<b>AGFG2</b>	chr7	-1.129437836	6.50489E-11
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ENSG00000123612	<b>ACVR1C</b>	chr2	-1.915594804	7.14152E-11
ENSG00000163106	<b>HPGDS</b>	chr4	-1.670970672	7.19638E-11
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ENSG00000117519	<b>CNN3</b>	chr1	-1.126081337	7.63284E-11
ENSG00000116141	<b>MARK1</b>	chr1	-1.782006437	7.72885E-11
ENSG00000229676	<b>ZNF492</b>	chr19	-2.163571294	8.37667E-11
ENSG00000162409	<b>PRKAA2</b>	chr1	-2.438290009	9.33387E-11
ENSG00000155659	<b>VSIG4</b>	chrX	-1.450170597	9.50733E-11
ENSG00000185345	<b>PARK2</b>	chr6	-1.286467478	9.61945E-11
ENSG00000189037	<b>DUSP21</b>	chrX	-4.101535484	1.16418E-10
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ENSG00000135437	<b>RDH5</b>	chr12	-1.375093829	1.3522E-10
ENSG00000203858	<b>HSD3BP2</b>	chr1	-3.372802447	1.36843E-10
ENSG00000144648	<b>ACKR2</b>	chr3	-1.392912596	1.41276E-10
ENSG00000184368	<b>MAP7D2</b>	chrX	-2.530799239	1.41276E-10
ENSG00000133134	<b>BEX2</b>	chrX	-1.958787229	1.52009E-10
ENSG00000181374	<b>CCL13</b>	chr17	-2.284641601	1.52213E-10
ENSG00000143995	<b>MEIS1</b>	chr2	-1.426058593	1.54519E-10

ENSG00000113580	<b>NR3C1</b>	chr5	-1.280248613	1.6367E-10
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ENSG00000016490	<b>CLCA1</b>	chr1	-2.286503623	1.76768E-10
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ENSG00000160111	<b>CPAMD8</b>	chr19	-1.546844852	1.82441E-10
ENSG00000072133	<b>RPS6KA6</b>	chrX	-1.487324299	1.91294E-10
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ENSG00000176884	<b>GRIN1</b>	chr9	-1.757199432	2.50937E-10
ENSG00000115896	<b>PLCL1</b>	chr2	-2.02244017	2.71977E-10
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ENSG00000106404	<b>CLDN15</b>	chr7	-1.515175363	2.82468E-10
ENSG00000162949	<b>CAPN13</b>	chr2	-1.669470104	2.83816E-10
ENSG00000010282	<b>HHATL</b>	chr3	-3.121490568	2.92958E-10
ENSG00000157111	<b>TMEM171</b>	chr5	-1.387419738	3.07145E-10
ENSG00000179774	<b>ATOX7</b>	chr10	-3.39143351	3.13053E-10
ENSG00000230873	<b>STMND1</b>	chr6	-1.696250276	3.22186E-10
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ENSG00000135905	<b>DOCK10</b>	chr2	-1.367471813	3.53335E-10
ENSG00000176472	<b>ZNF575</b>	chr19	-1.358792256	3.73727E-10
ENSG00000240995	<b>RP11-708H21.1</b>	chr17	-3.831772131	3.74147E-10
ENSG00000164175	<b>SLC45A2</b>	chr5	-2.329204355	3.78101E-10
ENSG00000164794	<b>KCNV1</b>	chr8	-1.803492336	4.6295E-10
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ENSG00000169918	<b>OTUD7A</b>	chr15	-1.908110495	4.9743E-10
ENSG00000188227	<b>ZNF793</b>	chr19	-1.560953921	5.07214E-10
ENSG00000153898	<b>MCOLN2</b>	chr1	-1.319014327	6.01556E-10
ENSG00000251209	<b>LINC00923</b>	chr15	-1.064404586	6.03258E-10
ENSG00000100092	<b>SH3BP1</b>	chr22	-1.139730923	6.06787E-10
ENSG00000065717	<b>TLE2</b>	chr19	-1.449071226	6.21908E-10
ENSG00000100146	<b>SOX10</b>	chr22	-1.689025891	6.71221E-10
ENSG00000117318	<b>ID3</b>	chr1	-1.096225528	6.7207E-10
ENSG00000171303	<b>KCNK3</b>	chr2	-1.521427631	6.80267E-10
ENSG00000101850	<b>GPR143</b>	chrX	-2.199392122	8.64566E-10
ENSG00000182636	<b>NDN</b>	chr15	-1.370881139	8.64566E-10
ENSG00000104081	<b>BMF</b>	chr15	-1.352257703	8.82894E-10
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### Conventional Adenomas versus normal mucosa - UPREGULATED

ENSEMBL ID	GENE SYMBOL	Chr	Log <sub>2</sub> Fold Change	Adjusted P-value
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ENSG00000165376	<b>CLDN2</b>	chrX	7.937352047	3.87696E-84
ENSG00000120149	<b>MSX2</b>	chr5	5.383206356	4.778E-82
ENSG00000186377	<b>CYP4X1</b>	chr1	4.70105642	3.44712E-72
ENSG00000140807	<b>NKD1</b>	chr16	5.764129621	6.73705E-65
ENSG00000103888	<b>KIAA1199</b>	chr15	4.208312893	1.92188E-59
ENSG00000164379	<b>FOXQ1</b>	chr6	4.092999106	1.39737E-57
ENSG00000167767	<b>KRT80</b>	chr12	5.62405369	1.24792E-52
ENSG00000163347	<b>CLDN1</b>	chr3	3.69156306	3.5105E-52
ENSG00000062038	<b>CDH3</b>	chr16	5.094235042	6.22052E-52
ENSG00000078114	<b>NEBL</b>	chr10	2.979520853	1.85516E-51
ENSG00000165816	<b>VWA2</b>	chr10	3.806875049	1.65756E-50
ENSG00000183734	<b>ASCL2</b>	chr11	3.932432853	2.20322E-49
ENSG00000167755	<b>KLK6</b>	chr19	7.772038112	1.13213E-48
ENSG00000135111	<b>TBX3</b>	chr12	2.338153475	4.61263E-47
ENSG00000105976	<b>MET</b>	chr7	2.016128956	1.59064E-46
ENSG00000139292	<b>LGR5</b>	chr12	4.143818539	6.40054E-45
ENSG00000108375	<b>RNF43</b>	chr17	2.526485371	5.11456E-42
ENSG00000182240	<b>BACE2</b>	chr21	1.899069078	1.46192E-41
ENSG00000157557	<b>ETS2</b>	chr21	1.882003115	3.14909E-41
ENSG00000137699	<b>TRIM29</b>	chr11	3.872949067	9.10091E-41
ENSG00000169247	<b>SH3TC2</b>	chr5	3.661807444	1.08587E-40
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ENSG00000185269	<b>NOTUM</b>	chr17	5.911759802	8.73887E-40
ENSG00000182580	<b>EPHB3</b>	chr3	2.550411872	2.27259E-39
ENSG00000154856	<b>APCDD1</b>	chr18	3.368671467	5.80625E-39
ENSG00000124766	<b>SOX4</b>	chr6	1.799205923	8.27378E-39
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ENSG00000146411	<b>SLC2A12</b>	chr6	4.09064919	1.17688E-37
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ENSG00000137673	<b>MMP7</b>	chr11	8.185802717	9.06848E-37
ENSG00000171617	<b>ENC1</b>	chr5	2.396515104	1.08184E-35
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ENSG00000178773	<b>CPNE7</b>	chr16	2.912777539	8.99103E-27
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ENSG00000163975	<b>MFI2</b>	chr3	2.158298552	1.27692E-24
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ENSG00000100170	<b>SLC5A1</b>	chr22	1.485642791	1.80675E-21
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ENSG00000153071	<b>DAB2</b>	chr5	1.470219687	5.49907E-21

ENSG00000107159	<b>CA9</b>	chr9	3.524152225	5.8324E-21
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ENSG00000168785	<b>TSPAN5</b>	chr4	1.835559144	1.05086E-20
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ENSG00000134193	<b>REG4</b>	chr1	2.864178187	1.16983E-20
ENSG00000128683	<b>GAD1</b>	chr2	4.738235513	2.22287E-20
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ENSG00000179546	<b>HTR1D</b>	chr1	2.758983422	1.0184E-19
ENSG00000127418	<b>FGFRL1</b>	chr4	1.76603866	1.02717E-19
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ENSG00000187556	<b>NANOS3</b>	chr19	4.146353248	1.31647E-19
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ENSG00000130147	<b>SH3BP4</b>	chr2	1.654026333	1.3897E-19
ENSG00000008300	<b>CELSR3</b>	chr3	2.152125495	1.6814E-19
ENSG00000119771	<b>KLHL29</b>	chr2	1.854007916	1.80219E-19
ENSG00000009950	<b>MLXIPL</b>	chr7	2.563190469	1.99249E-19
ENSG00000119280	<b>C1orf198</b>	chr1	1.238848618	2.75347E-19
ENSG00000186474	<b>KLK12</b>	chr19	3.554556881	3.7973E-19
ENSG00000187535	<b>IFT140</b>	chr16	1.585130991	3.84476E-19
ENSG00000082512	<b>TRAF5</b>	chr1	1.589654799	3.91901E-19
ENSG00000197905	<b>TEAD4</b>	chr12	1.563696928	4.74065E-19
ENSG00000144730	<b>IL17RD</b>	chr3	3.186345997	5.04331E-19
ENSG00000152104	<b>PTPN14</b>	chr1	1.36938423	5.1431E-19
ENSG00000100105	<b>PATZ1</b>	chr22	1.333345477	6.21674E-19
ENSG00000196187	<b>TMEM63A</b>	chr1	1.439135171	6.28132E-19
ENSG00000215012	<b>C22orf29</b>	chr22	1.222272832	6.28132E-19
ENSG00000120068	<b>HOXB8</b>	chr17	1.91991229	7.44048E-19
ENSG00000137747	<b>TMPRSS13</b>	chr11	3.34879805	8.05774E-19
ENSG00000259479	<b>CTD-2008A1.2</b>	chr15	2.016260453	8.18707E-19
ENSG00000129455	<b>KLK8</b>	chr19	6.451378598	9.98751E-19
ENSG00000179294	<b>C17orf96</b>	chr17	2.103797671	1.02898E-18
ENSG00000003147	<b>ICA1</b>	chr7	1.171057122	1.54866E-18
ENSG00000088992	<b>TESC</b>	chr12	2.883226588	1.89846E-18
ENSG00000033170	<b>FUT8</b>	chr14	1.187824889	2.14589E-18
ENSG00000125864	<b>BFSP1</b>	chr20	2.305539759	2.18246E-18
ENSG00000081059	<b>TCF7</b>	chr5	1.88077543	2.21227E-18
ENSG00000170454	<b>KRT75</b>	chr12	6.5089993	2.21227E-18
ENSG00000141101	<b>NOB1</b>	chr16	1.476680696	2.33073E-18
ENSG00000165071	<b>TMEM71</b>	chr8	2.236371955	2.60904E-18
ENSG00000169429	<b>IL8</b>	chr4	3.199389182	2.62154E-18

ENSG00000168065	<b>SLC22A11</b>	chr11	2.946119548	2.85376E-18
ENSG00000128849	<b>CGNL1</b>	chr15	1.947098784	5.09927E-18
ENSG00000133519	<b>ZDHHC8P1</b>	chr22	2.777612853	5.8286E-18
ENSG00000136997	<b>MYC</b>	chr8	1.869202779	6.01011E-18
ENSG00000122547	<b>EEPD1</b>	chr7	1.304024359	1.11844E-17
ENSG00000129946	<b>SHC2</b>	chr19	2.65241338	1.14518E-17
ENSG00000196411	<b>EPHB4</b>	chr7	1.57871107	1.20668E-17
ENSG00000105989	<b>WNT2</b>	chr7	7.1596582	1.23317E-17
ENSG00000156219	<b>ART3</b>	chr4	2.52948874	1.26811E-17
ENSG00000182489	<b>XKRX</b>	chrX	1.627513324	1.34774E-17
ENSG00000059377	<b>TBXAS1</b>	chr7	1.539645929	1.53462E-17
ENSG00000135472	<b>FAIM2</b>	chr12	3.994455639	1.8674E-17
ENSG00000198835	<b>GJC2</b>	chr1	3.510866522	1.90126E-17
ENSG00000164398	<b>ACSL6</b>	chr5	3.416319831	1.95622E-17
ENSG00000115363	<b>EVA1A</b>	chr2	2.28459777	1.99879E-17
ENSG00000180869	<b>C1orf180</b>	chr1	2.722678901	2.02467E-17
ENSG00000137693	<b>YAP1</b>	chr11	1.181606107	2.31883E-17
ENSG00000168772	<b>CXXC4</b>	chr4	2.571816759	2.38969E-17
ENSG00000178035	<b>IMPDH2</b>	chr3	1.335273865	2.44195E-17
ENSG00000106178	<b>CCL24</b>	chr7	2.523411444	2.53728E-17
ENSG00000159337	<b>PLA2G4D</b>	chr15	1.992036732	2.66564E-17
ENSG00000205502	<b>C2CD4B</b>	chr15	2.762080898	2.73432E-17
ENSG00000181026	<b>AEN</b>	chr15	1.249689134	2.86418E-17
ENSG00000163629	<b>PTPN13</b>	chr4	2.607175614	3.39188E-17
ENSG00000169035	<b>KLK7</b>	chr19	5.078085523	4.92886E-17
ENSG00000106089	<b>STX1A</b>	chr7	1.943720697	5.27667E-17
ENSG00000170373	<b>CST1</b>	chr20	4.569459669	8.22833E-17
ENSG00000203727	<b>SAMD5</b>	chr6	2.120024643	8.22833E-17
ENSG00000159216	<b>RUNX1</b>	chr21	1.141351119	8.69792E-17
ENSG00000185479	<b>KRT6B</b>	chr12	5.710395969	9.36931E-17
ENSG00000183248	<b>CTD-3193O13.9</b>	chr19	3.27579267	1.12528E-16
ENSG00000153395	<b>LPCAT1</b>	chr5	1.200595824	1.14178E-16
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ENSG00000213923	<b>CSNK1E</b>	chr22	1.234742723	1.22518E-16
ENSG00000133985	<b>TTC9</b>	chr14	2.159849525	1.51523E-16
ENSG00000137198	<b>GMPR</b>	chr6	2.0729624	1.5309E-16
ENSG00000174136	<b>RGMB</b>	chr5	1.611813406	1.5309E-16
ENSG00000104783	<b>KCNN4</b>	chr19	1.608754969	1.59495E-16
ENSG00000189431	<b>RASSF10</b>	chr11	5.156825678	2.59451E-16
ENSG00000072110	<b>ACTN1</b>	chr14	1.192838884	2.61229E-16
ENSG00000165434	<b>PGM2L1</b>	chr11	1.464106756	2.85556E-16
ENSG00000130035	<b>GALNT8</b>	chr12	1.831872371	3.06165E-16
ENSG00000165388	<b>ZNF488</b>	chr10	2.129837197	3.15216E-16
ENSG00000149968	<b>MMP3</b>	chr11	4.003027203	3.36456E-16
ENSG00000125485	<b>DDX31</b>	chr9	1.235784787	3.5446E-16

ENSG00000187079	<b>TEAD1</b>	chr11	1.096636634	3.8216E-16
ENSG00000142102	<b>ATHL1</b>	chr11	2.070812756	4.82052E-16
ENSG00000265817	<b>FSBP</b>	chr8	4.238076461	5.06601E-16
ENSG00000184584	<b>TMEM173</b>	chr5	1.069612399	5.48815E-16
ENSG00000120256	<b>LRP11</b>	chr6	1.066835371	5.68029E-16
ENSG00000184428	<b>TOP1MT</b>	chr8	1.435539764	6.23474E-16
ENSG00000029153	<b>ARNTL2</b>	chr12	2.082829035	6.35993E-16
ENSG00000088826	<b>SMOX</b>	chr20	1.765285257	6.4382E-16
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ENSG00000257046	<b>LST3</b>	chr12	6.689329134	7.04511E-16
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ENSG00000205336	<b>GPR56</b>	chr16	1.383211149	7.94355E-16
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ENSG00000241186	<b>TDGF1</b>	chr3	2.75705804	9.18157E-16
ENSG00000148735	<b>PLEKHS1</b>	chr10	2.188609283	1.01713E-15
ENSG00000196793	<b>ZNF239</b>	chr10	1.788912485	1.25887E-15
ENSG00000173557	<b>C2orf70</b>	chr2	3.256353461	1.83253E-15
ENSG00000183914	<b>DNAH2</b>	chr17	2.032498206	2.46934E-15
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ENSG00000169891	<b>REPS2</b>	chrX	1.265462888	2.74148E-15
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ENSG00000159184	<b>HOXB13</b>	chr17	3.306256157	5.55255E-15
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ENSG00000109255	<b>NMU</b>	chr4	2.285330164	1.20559E-14
ENSG00000180884	<b>ZNF792</b>	chr19	1.411785412	1.36362E-14
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ENSG00000174939	<b>ASPHD1</b>	chr16	2.126869619	1.53761E-14
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ENSG00000111696	<b>NT5DC3</b>	chr12	1.346388946	1.67032E-14
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ENSG00000171017	<b>LRRC8E</b>	chr19	1.997594334	2.15605E-14
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ENSG00000162174	<b>ASRGL1</b>	chr11	1.233353959	6.0099E-14
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ENSG00000167747	<b>C19orf48</b>	chr19	1.066350638	1.01048E-13
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ENSG00000175065	<b>DSG4</b>	chr18	3.302298852	1.76138E-13
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ENSG00000238271	<b>IFNWP19</b>	chr9	5.080904045	5.41617E-13
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ENSG00000137573	<b>SULF1</b>	chr8	1.580491612	7.26727E-13
ENSG00000086159	<b>AQP6</b>	chr12	4.062527088	8.05364E-13
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ENSG00000073536	<b>NLE1</b>	chr17	1.10829469	1.34395E-12
ENSG00000271363	<b>PHF16</b>	chrHG29_P ATCH	1.04682804	1.36823E-12
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ENSG00000102854	<b>MSLN</b>	chr16	3.119273847	1.43449E-12
ENSG00000108773	<b>KAT2A</b>	chr17	1.069501614	1.48957E-12

ENSG00000168264	<b>IRF2BP2</b>	chr1	1.037411015	1.52046E-12
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ENSG00000173918	<b>C1QTNF1</b>	chr17	1.624955789	1.72542E-12
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ENSG00000197958	<b>RPL12</b>	chr9	1.041648005	1.94403E-12
ENSG00000170786	<b>SDR16C5</b>	chr8	1.894315455	1.99108E-12
ENSG00000183742	<b>MACC1</b>	chr7	1.344838516	2.13438E-12
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ENSG00000103257	<b>SLC7A5</b>	chr16	1.699843968	2.26466E-12
ENSG00000184949	<b>FAM227A</b>	chr22	2.07200084	2.4015E-12
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ENSG00000183963	<b>SMTN</b>	chr22	1.108137927	2.91985E-12
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ENSG00000139515	<b>PDX1</b>	chr13	3.113999503	3.48144E-12
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ENSG00000125798	<b>FOXA2</b>	chr20	1.719240679	3.62925E-12
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ENSG00000115828	<b>QPCT</b>	chr2	1.881909656	4.22722E-12
ENSG00000006606	<b>CCL26</b>	chr7	3.005930388	4.7518E-12
ENSG00000181577	<b>C6orf223</b>	chr6	3.085641366	5.0122E-12
ENSG00000167914	<b>GSDMA</b>	chr17	1.918125694	5.5997E-12
ENSG00000135245	<b>HILPDA</b>	chr7	1.221619164	6.16168E-12
ENSG00000135749	<b>PCNXL2</b>	chr1	1.15760488	6.32155E-12
ENSG00000165659	<b>DACH1</b>	chr13	1.982885112	6.32325E-12
ENSG00000197119	<b>SLC25A29</b>	chr14	1.513373818	6.59206E-12
ENSG00000105948	<b>TTC26</b>	chr7	1.654113282	7.05936E-12
ENSG00000257594	<b>GALNT4</b>	chr12	1.135947828	7.42393E-12
ENSG00000211892	<b>IGHG4</b>	chr14	2.641858341	7.7025E-12
ENSG00000163132	<b>MSX1</b>	chr4	2.18309781	8.06542E-12
ENSG00000154217	<b>PITPNC1</b>	chr17	1.019094677	8.12256E-12
ENSG00000186160	<b>CYP4Z1</b>	chr1	5.075157002	8.15686E-12
ENSG00000159714	<b>ZDHHC1</b>	chr16	1.514829356	8.44858E-12
ENSG00000080546	<b>SESN1</b>	chr6	1.064272398	8.45291E-12
ENSG00000126016	<b>AMOT</b>	chrX	1.448485157	8.66146E-12
ENSG00000114019	<b>AMOTL2</b>	chr3	1.054718919	9.09503E-12
ENSG00000112796	<b>ENPP5</b>	chr6	1.535233716	9.20027E-12
ENSG00000187486	<b>KCNJ11</b>	chr11	1.672266408	9.20142E-12
ENSG00000163515	<b>RETNLB</b>	chr3	2.510014055	1.02714E-11
ENSG00000165810	<b>BTNL9</b>	chr5	1.66062199	1.11119E-11

ENSG00000171224	<b>C10orf35</b>	chr10	1.304575969	1.12046E-11
ENSG00000108557	<b>RAI1</b>	chr17	1.211751482	1.12489E-11
ENSG00000134812	<b>GIF</b>	chr11	3.722800345	1.12489E-11
ENSG00000099889	<b>ARVCF</b>	chr22	1.612579771	1.13144E-11
ENSG00000143126	<b>CELSR2</b>	chr1	1.152137537	1.40403E-11
ENSG00000118898	<b>PPL</b>	chr16	1.292199671	1.42245E-11
ENSG00000168679	<b>SLC16A4</b>	chr1	1.553935754	1.44944E-11
ENSG00000124225	<b>PMEPA1</b>	chr20	1.473318843	1.50017E-11
ENSG00000166455	<b>C16orf46</b>	chr16	1.37372347	1.58613E-11
ENSG00000196497	<b>IPO4</b>	chr14	1.063415384	1.59459E-11
ENSG00000137033	<b>IL33</b>	chr9	2.302088908	1.60293E-11
ENSG00000113946	<b>CLDN16</b>	chr3	3.790958703	1.66523E-11
ENSG00000137054	<b>POLR1E</b>	chr9	1.044677478	1.7737E-11
ENSG00000198720	<b>ANKRD13B</b>	chr17	1.801560108	1.88338E-11
ENSG00000159708	<b>LRRC36</b>	chr16	2.04492405	1.93599E-11
ENSG00000142700	<b>DMRTA2</b>	chr1	6.528885947	1.98918E-11
ENSG00000179241	<b>LDLRAD3</b>	chr11	1.268703035	2.13769E-11
ENSG00000167880	<b>EVPL</b>	chr17	1.132845497	2.29892E-11
ENSG00000166922	<b>SCG5</b>	chr15	1.675360866	2.31098E-11
ENSG00000110944	<b>IL23A</b>	chr12	1.784171357	2.40772E-11
ENSG00000161326	<b>DUSP14</b>	chr17	1.515389364	2.46627E-11
ENSG00000179104	<b>TMTC2</b>	chr12	1.195692534	2.56054E-11
ENSG00000129103	<b>SUMF2</b>	chr7	1.008185916	2.5798E-11
ENSG00000148225	<b>WDR31</b>	chr9	1.42370189	2.71275E-11
ENSG00000273045	<b>C2ORF15</b>	chr2	1.498392365	2.79043E-11
ENSG00000103021	<b>CCDC113</b>	chr16	1.574641209	2.89922E-11
ENSG00000103811	<b>CTSH</b>	chr15	1.0469847	2.89922E-11
ENSG00000011523	<b>CEP68</b>	chr2	1.116275253	3.08205E-11
ENSG00000135821	<b>GLUL</b>	chr1	1.142635313	3.086E-11
ENSG00000132357	<b>CARD6</b>	chr5	1.671608797	3.15112E-11
ENSG00000123104	<b>ITPR2</b>	chr12	1.431172222	3.2056E-11
ENSG00000100196	<b>KDEL3</b>	chr22	1.008068864	3.37789E-11
ENSG00000173473	<b>SMARCC1</b>	chr3	1.13598557	3.63519E-11
ENSG00000134258	<b>VTCN1</b>	chr1	4.631179387	3.77242E-11
ENSG00000271225	<b>RP11-460N11.3</b>	chr9	3.013427297	3.77996E-11
ENSG00000198298	<b>ZNF485</b>	chr10	1.238347235	3.78107E-11
ENSG00000132205	<b>EMILIN2</b>	chr18	1.046029098	4.2059E-11
ENSG00000128342	<b>LIF</b>	chr22	1.148842655	4.21411E-11
ENSG00000107130	<b>NCS1</b>	chr9	1.664982261	4.80677E-11
ENSG00000112578	<b>BYSL</b>	chr6	1.091343986	4.82261E-11
ENSG00000116106	<b>EPHA4</b>	chr2	1.512271296	4.99336E-11
ENSG00000100077	<b>ADRBK2</b>	chr22	1.473118572	5.32468E-11
ENSG00000125657	<b>TNFSF9</b>	chr19	2.064093699	5.52457E-11
ENSG00000176842	<b>IRX5</b>	chr16	4.577763408	5.68323E-11
ENSG00000139998	<b>RAB15</b>	chr14	1.398590516	5.97829E-11



ENSG00000179409	<b>GEMIN4</b>	chr17	1.039388942	6.05447E-11
ENSG00000110195	<b>FOLR1</b>	chr11	3.629622369	6.18672E-11
ENSG00000185008	<b>ROBO2</b>	chr3	3.321133352	6.27723E-11
ENSG00000060718	<b>COL11A1</b>	chr1	3.67972134	6.33667E-11
ENSG00000140939	<b>NOL3</b>	chr16	1.213961283	6.34593E-11
ENSG00000187607	<b>ZNF286A</b>	chr17	1.043589212	6.73137E-11
ENSG00000105810	<b>CDK6</b>	chr7	1.49958005	6.80508E-11
ENSG00000180354	<b>MTURN</b>	chr7	1.295449824	7.80844E-11
ENSG00000111752	<b>PHC1</b>	chr12	1.3086743	7.8256E-11
ENSG00000105514	<b>RAB3D</b>	chr19	1.04404888	8.04576E-11
ENSG00000104998	<b>IL27RA</b>	chr19	1.166909807	8.3148E-11
ENSG00000128567	<b>PODXL</b>	chr7	1.327704631	8.47791E-11
ENSG00000168234	<b>TTC39C</b>	chr18	1.092093109	8.76787E-11
ENSG00000109158	<b>GABRA4</b>	chr4	2.393499433	8.84442E-11
ENSG00000128422	<b>KRT17</b>	chr17	5.889723645	9.3292E-11
ENSG00000130475	<b>FCHO1</b>	chr19	1.370343582	9.81824E-11
ENSG00000135919	<b>SERPINE2</b>	chr2	1.593387063	1.06218E-10
ENSG00000170231	<b>FABP6</b>	chr5	3.129747334	1.29074E-10
ENSG00000164764	<b>SBSPON</b>	chr8	2.057867888	1.30109E-10
ENSG00000124177	<b>CHD6</b>	chr20	1.04158721	1.32189E-10
ENSG00000144354	<b>CDCA7</b>	chr2	1.460833675	1.39064E-10
ENSG00000137124	<b>ALDH1B1</b>	chr9	1.248741922	1.39724E-10
ENSG00000138795	<b>LEF1</b>	chr4	1.443037016	1.44727E-10
ENSG00000166840	<b>GLYATL1</b>	chr11	2.104385391	1.47997E-10
ENSG00000138031	<b>ADCY3</b>	chr2	1.185274213	1.58047E-10
ENSG00000205420	<b>KRT6A</b>	chr12	5.68686394	1.66432E-10
ENSG00000188763	<b>FZD9</b>	chr7	4.016134345	1.73958E-10
ENSG00000120800	<b>UTP20</b>	chr12	1.183540066	1.83517E-10
ENSG00000147251	<b>DOCK11</b>	chrX	1.434610259	2.04474E-10
ENSG00000158528	<b>PPP1R9A</b>	chr7	1.156193582	2.19449E-10
ENSG00000021826	<b>CPS1</b>	chr2	3.870039363	2.2761E-10
ENSG00000172023	<b>REG1B</b>	chr2	4.417950659	2.50958E-10
ENSG00000007402	<b>CACNA2D2</b>	chr3	1.827589543	2.70252E-10
ENSG00000111012	<b>CYP27B1</b>	chr12	1.318614465	2.82769E-10
ENSG00000126249	<b>PDCD2L</b>	chr19	1.173330061	3.08558E-10
ENSG00000069011	<b>PITX1</b>	chr5	1.495779731	3.40269E-10
ENSG00000166670	<b>MMP10</b>	chr11	3.080563896	3.50652E-10
ENSG00000161921	<b>CXCL16</b>	chr17	1.093983786	3.58806E-10
ENSG00000160183	<b>TMPRSS3</b>	chr21	1.770115438	3.64478E-10
ENSG00000239521	<b>GATS</b>	chr7	1.428422527	3.77408E-10
ENSG00000138119	<b>MYOF</b>	chr10	1.298938913	3.94606E-10
ENSG00000148734	<b>NPFFR1</b>	chr10	1.288550101	4.08159E-10
ENSG00000187867	<b>PALM3</b>	chr19	2.083246873	4.34615E-10
ENSG00000101255	<b>TRIB3</b>	chr20	1.597060801	4.57018E-10
ENSG00000137834	<b>SMAD6</b>	chr15	1.288231021	4.59306E-10

ENSG00000142765	<b>SYTL1</b>	chr1	1.659616118	4.59614E-10
ENSG00000132746	<b>ALDH3B2</b>	chr11	2.866436109	4.59859E-10
ENSG00000064666	<b>CNN2</b>	chr19	1.090643998	4.79265E-10
ENSG00000173239	<b>LIPM</b>	chr10	1.264431277	4.96117E-10
ENSG00000060558	<b>GNA15</b>	chr19	1.614823791	5.31136E-10
ENSG00000168758	<b>SEMA4C</b>	chr2	1.023523331	5.46895E-10
ENSG00000118965	<b>WDR35</b>	chr2	1.304211477	6.22915E-10
ENSG00000163577	<b>EIF5A2</b>	chr3	1.592277011	6.33753E-10
ENSG00000168269	<b>FOXI1</b>	chr5	2.523089038	6.60305E-10
ENSG00000164761	<b>TNFRSF11B</b>	chr8	1.692165428	6.91755E-10
ENSG00000065989	<b>PDE4A</b>	chr19	1.084882924	7.25464E-10
ENSG00000179603	<b>GRM8</b>	chr7	2.389746238	7.41254E-10
ENSG00000156697	<b>UTP14A</b>	chrX	1.007461269	7.44035E-10
ENSG00000119403	<b>PHF19</b>	chr9	1.101663371	7.44262E-10
ENSG00000162849	<b>KIF26B</b>	chr1	2.285791534	7.58929E-10
ENSG00000205084	<b>TMEM231</b>	chr16	1.023723412	7.64487E-10
ENSG00000081041	<b>CXCL2</b>	chr4	2.006940239	8.42506E-10
ENSG00000109089	<b>CDR2L</b>	chr17	1.360073091	8.50267E-10
ENSG00000169248	<b>CXCL11</b>	chr4	2.527371648	8.50267E-10
ENSG00000166261	<b>ZNF202</b>	chr11	1.015732474	8.50927E-10
ENSG00000204060	<b>FOXO6</b>	chr1	2.206050522	8.88489E-10
ENSG00000111912	<b>NCOA7</b>	chr6	1.113027864	9.29578E-10
ENSG00000183036	<b>PCP4</b>	chr21	3.469472793	9.61456E-10

### Conventional Adenomas versus normal mucosa - DOWNREGULATED

ENSEMBL ID	GENE SYMBOL	Chr	Log <sub>2</sub> Fold Change	Adjusted P-value
ENSG00000187699	<b>C2orf88</b>	chr2	-3.003931779	3.66286E-75
ENSG00000006747	<b>SCIN</b>	chr7	-2.529152257	2.24615E-71
ENSG00000155545	<b>MIER3</b>	chr5	-2.59080811	4.11232E-56
ENSG00000080493	<b>SLC4A4</b>	chr4	-3.450882076	1.23845E-55
ENSG00000118777	<b>ABCG2</b>	chr4	-5.495413351	1.61262E-51
ENSG00000111846	<b>GCNT2</b>	chr6	-2.941838228	3.2457E-51
ENSG00000040199	<b>PHLPP2</b>	chr16	-2.786623474	4.94727E-48
ENSG00000163586	<b>FABP1</b>	chr2	-2.975139237	3.71266E-45
ENSG00000249948	<b>GBA3</b>	chr4	-3.904558014	4.9511E-45
ENSG00000164825	<b>DEFB1</b>	chr8	-2.602683926	1.31185E-44
ENSG00000163959	<b>SLC51A</b>	chr3	-3.846804914	5.32816E-43
ENSG00000066230	<b>SLC9A3</b>	chr5	-3.825027323	2.01791E-42
ENSG00000176273	<b>SLC35G1</b>	chr10	-1.859220159	3.74724E-42
ENSG00000169764	<b>UGP2</b>	chr2	-1.844412828	4.56163E-41
ENSG00000139163	<b>ETNK1</b>	chr12	-2.744064617	5.67322E-41
ENSG00000101049	<b>SGK2</b>	chr20	-1.89720977	8.09753E-41
ENSG00000186198	<b>SLC51B</b>	chr15	-4.764790121	1.00765E-40
ENSG00000073734	<b>ABCB11</b>	chr2	-4.927906667	8.73887E-40
ENSG00000075142	<b>SRI</b>	chr7	-2.0428555	1.20404E-39

ENSG00000142959	<b>BEST4</b>	chr1	-4.543659136	2.00104E-39
ENSG00000181751	<b>C5orf30</b>	chr5	-1.492652663	2.27259E-39
ENSG00000168748	<b>CA7</b>	chr16	-4.949323886	7.55211E-38
ENSG00000132915	<b>PDE6A</b>	chr5	-2.759780573	1.54423E-37
ENSG00000189221	<b>MAOA</b>	chrX	-1.722132872	1.58802E-37
ENSG00000153233	<b>PTPRR</b>	chr12	-3.836659639	2.10599E-37
ENSG00000158467	<b>AHCYL2</b>	chr7	-2.172365102	3.25029E-37
ENSG00000164120	<b>HPGD</b>	chr4	-3.23449687	5.84871E-37
ENSG00000144136	<b>SLC20A1</b>	chr2	-3.130455398	7.9181E-37
ENSG00000108242	<b>CYP2C18</b>	chr10	-2.783036653	9.06848E-37
ENSG00000233441	<b>CYP2AB1P</b>	chr3	-4.928446468	1.4607E-36
ENSG00000104267	<b>CA2</b>	chr8	-4.185134204	2.7067E-36
ENSG00000138678	<b>AGPAT9</b>	chr4	-2.561157045	2.85659E-36
ENSG00000111802	<b>TDP2</b>	chr6	-1.681719754	2.98532E-36
ENSG00000147883	<b>CDKN2B</b>	chr9	-3.6635267	5.28934E-36
ENSG00000065809	<b>FAM107B</b>	chr10	-1.80727512	5.50217E-36
ENSG00000182271	<b>TMIGD1</b>	chr17	-6.930464476	6.18146E-36
ENSG00000146039	<b>SLC17A4</b>	chr6	-3.087252593	6.2862E-36
ENSG00000196660	<b>SLC30A10</b>	chr1	-6.34443567	9.9722E-36
ENSG00000171431	<b>KRT20</b>	chr17	-3.11154501	1.01383E-35
ENSG00000183034	<b>OTOP2</b>	chr17	-7.068754566	1.12867E-35
ENSG00000110887	<b>DAO</b>	chr12	-6.228899522	1.47228E-35
ENSG00000145384	<b>FABP2</b>	chr4	-2.364930472	2.03728E-35
ENSG00000161533	<b>ACOX1</b>	chr17	-1.587899373	7.70155E-35
ENSG00000164237	<b>CMBL</b>	chr5	-1.449846236	9.66101E-35
ENSG00000166825	<b>ANPEP</b>	chr15	-5.324471319	1.39455E-34
ENSG00000184434	<b>LRRC19</b>	chr9	-2.106307332	2.89052E-34
ENSG00000141338	<b>ABCA8</b>	chr17	-3.006346613	7.81899E-34
ENSG00000072657	<b>TRHDE</b>	chr12	-2.010627508	8.19977E-34
ENSG00000141434	<b>MEP1B</b>	chr18	-3.976870169	1.06755E-33
ENSG00000162545	<b>CAMK2N1</b>	chr1	-1.69091351	2.18119E-33
ENSG00000071203	<b>MS4A12</b>	chr11	-5.701923136	3.7971E-33
ENSG00000133742	<b>CA1</b>	chr8	-6.259160441	7.9743E-33
ENSG00000156298	<b>TSPAN7</b>	chrX	-2.124541296	1.28599E-32
ENSG00000134028	<b>ADAMDEC1</b>	chr8	-3.259980757	1.40852E-32
ENSG00000091138	<b>SLC26A3</b>	chr7	-5.584046731	4.28708E-32
ENSG00000076641	<b>PAG1</b>	chr8	-2.289473777	5.43384E-32
ENSG00000188242	<b>CTD-2228K2.5</b>	chr5	-4.185258106	5.52137E-32
ENSG00000086696	<b>HSD17B2</b>	chr16	-3.248687118	9.67983E-32
ENSG00000114455	<b>HHLA2</b>	chr3	-2.564969439	1.22028E-31
ENSG00000036672	<b>USP2</b>	chr11	-4.422319488	1.49005E-31
ENSG00000135549	<b>PKIB</b>	chr6	-3.496733185	6.11916E-31
ENSG00000243064	<b>ABCC13</b>	chr21	-2.630335855	6.6862E-31
ENSG00000174992	<b>ZG16</b>	chr16	-5.215836412	7.49628E-31
ENSG00000181061	<b>HIGD1A</b>	chr3	-2.294908078	8.79019E-31

ENSG00000120498	<b>TEX11</b>	chrX	-3.666279161	1.23648E-30
ENSG00000162992	<b>NEUROD1</b>	chr2	-4.256366889	2.11114E-30
ENSG00000155850	<b>SLC26A2</b>	chr5	-3.983829482	4.09086E-30
ENSG00000108576	<b>SLC6A4</b>	chr17	-4.241251935	5.06237E-30
ENSG00000113303	<b>BTNL8</b>	chr5	-2.828669523	8.47377E-30
ENSG00000166869	<b>CHP2</b>	chr16	-3.33832402	8.81153E-30
ENSG00000138109	<b>CYP2C9</b>	chr10	-2.861339132	1.13554E-29
ENSG00000153902	<b>LGI4</b>	chr19	-3.352963103	1.35252E-29
ENSG00000204936	<b>CD177</b>	chr19	-5.882684571	1.99E-29
ENSG00000116833	<b>NR5A2</b>	chr1	-1.761208361	4.23631E-29
ENSG00000197165	<b>SULT1A2</b>	chr16	-3.731520495	4.74019E-29
ENSG00000133328	<b>HRASLS2</b>	chr11	-4.720850444	9.01589E-29
ENSG00000198944	<b>SOWAHA</b>	chr5	-2.074211941	1.12401E-28
ENSG00000123560	<b>PLP1</b>	chrX	-3.304005419	1.40847E-28
ENSG00000012504	<b>NR1H4</b>	chr12	-2.66655236	1.45982E-28
ENSG00000099139	<b>PCSK5</b>	chr9	-2.102726683	1.45982E-28
ENSG00000119686	<b>FLVCR2</b>	chr14	-2.560822308	1.58368E-28
ENSG00000155380	<b>SLC16A1</b>	chr1	-1.494088559	2.01262E-28
ENSG00000122756	<b>CNTFR</b>	chr9	-5.495439229	2.51148E-28
ENSG00000242515	<b>UGT1A10</b>	chr2	-1.52557888	3.08789E-28
ENSG00000162398	<b>C1orf177</b>	chr1	-3.056438632	4.20813E-28
ENSG00000137251	<b>TINAG</b>	chr6	-2.366415385	4.636E-28
ENSG00000123643	<b>SLC36A1</b>	chr5	-1.409304933	7.53896E-28
ENSG00000178537	<b>SLC25A20</b>	chr3	-1.583230015	1.00429E-27
ENSG00000164099	<b>PRSS12</b>	chr4	-1.763348694	1.30113E-27
ENSG00000224321	<b>RP11-169K16.6</b>	chr1	-3.525092584	2.24162E-27
ENSG00000054277	<b>OPN3</b>	chr1	-1.559828045	3.24369E-27
ENSG00000057704	<b>TMCC3</b>	chr12	-2.410951005	3.80364E-27
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ENSG00000096060	<b>FKBP5</b>	chr6	-1.017132659	5.13712E-12
ENSG00000181804	<b>SLC9A9</b>	chr3	-1.195907342	5.2702E-12
ENSG00000120913	<b>PDLIM2</b>	chr8	-2.035849459	6.4619E-12
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ENSG00000120129	<b>DUSP1</b>	chr5	-1.968845836	1.0111E-11
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ENSG00000105784	<b>RUNDC3B</b>	chr7	-1.630953485	5.02781E-10
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