Figure S1. Expression of *RAC1* and *FSCN1* in A549 cells following transfection with *SEMA5A* plasmid. Relative expression levels of (A) *RAC1* and (B) *FSCN1* in A549 cells overexpressing *SEMA5A* measured by microarray. Bars represent the means ± SD of 3 independent experiments. Total RNA was extracted 24 h following transfection and genomic profiling was examined by Illumina Human HT-12 v4 Bead Chips.

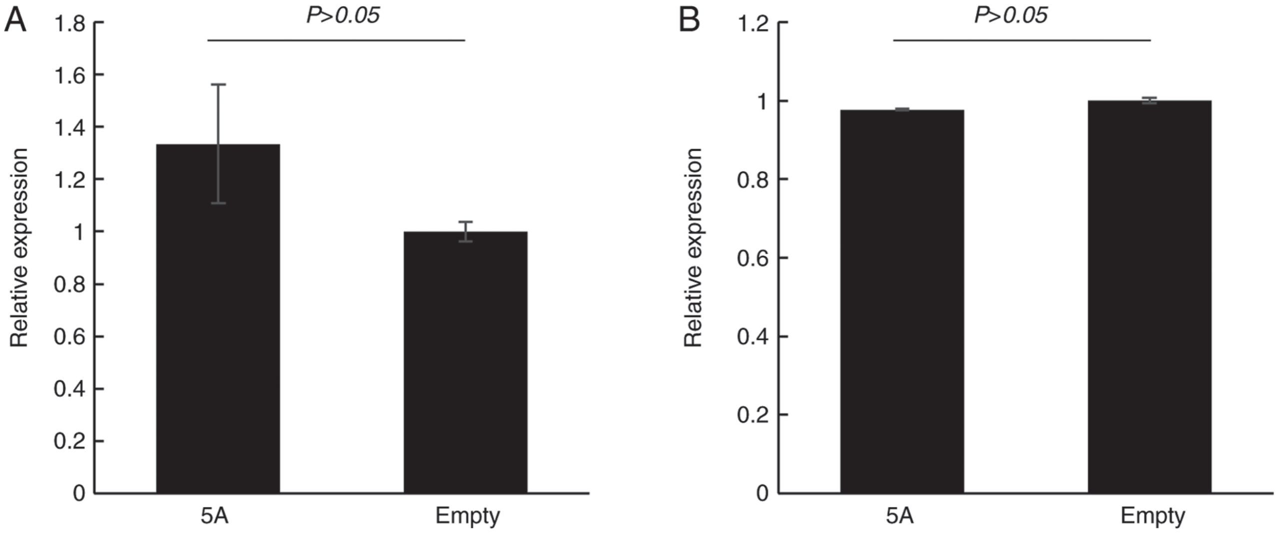

Table SI. Differential expression genes in A549 cells overexpressing *SEMA5A*.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
OAS2	ILMN_1674063	8.73	426.01	$6.72x10^{-6}$	12q24.13b	*Homo sapiens* 2'-5'-oligoadenylate synthetase 2, 69/71kDa (OAS2), transcript variant 1, mRNA.
IFI27	ILMN_2058782	8.71	418.65	$1.17x10^{-6}$	14q32.13a	*Homo sapiens* interferon, alpha-inducible protein 27 (IFI27), transcript variant 2, mRNA.
OASL	ILMN_1674811	8.26	306.72	$2.28x10^{-6}$	12q24.31a	*Homo sapiens* 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, mRNA.
MX1	ILMN_1662358	8.06	267.38	$1.78x10^{-8}$	21q22.3a	*Homo sapiens* myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA.
IFIT3	ILMN_1701789	7.71	209.37	$6.67x10^{-6}$	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.
IFIT3	ILMN_2239754	7.39	167.91	$3.79x10^{-6}$	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.
IFI44L	ILMN_1723912	6.99	127.18	$2.17x10^{-6}$	1p31.1e	*Homo sapiens* interferon-induced protein 44-like (IFI44L), mRNA.
IFIT2	ILMN_1739428	6.96	124.11	$1.06x10^{-8}$	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 2 (IFIT2), mRNA.
IFNB1	ILMN_1682245	6.73	106.19	$2.19x10^{-6}$	9p21.3d	*Homo sapiens* interferon, beta 1, fibroblast (IFNB1), mRNA.
IFI44	ILMN_1760062	6.69	103.22	$1.41x10^{-5}$	1p31.1e	*Homo sapiens* interferon-induced protein 44 (IFI44), mRNA.
IRF7	ILMN_2349061	6.46	88.31	$2.56x10^{-6}$	11p15.5d	*Homo sapiens* interferon regulatory factor 7 (IRF7), transcript variant b, mRNA.
CCL5	ILMN_1773352	6.23	75.28	$6.16x10^{-5}$	17q12b	*Homo sapiens* chemokine (C-C motif) ligand 5 (CCL5), mRNA.
IFIT1	ILMN_1707695	6.16	71.38	$3.95x10^{-7}$	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 2, mRNA.
OAS2	ILMN_2248970	6.13	70.19	$1.11x10^{-6}$	12q24.13b	*Homo sapiens* 2'-5'-oligoadenylate synthetase 2, 69/71kDa (OAS2), transcript variant 3, mRNA.
BATF2	ILMN_1690241	6.08	67.54	$6.52x10^{-6}$	11q13.1c	*Homo sapiens* basic leucine zipper transcription factor, ATF-like 2 (BATF2), mRNA.
ISG15	ILMN_2054019	5.97	62.58	$3.34x10^{-7}$	1p36.33b	*Homo sapiens* ISG15 ubiquitin-like modifier (ISG15), mRNA.
IFITM1	ILMN_1801246	5.92	60.71	$5.49x10^{-8}$	11p15.5d	*Homo sapiens* interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.
RSAD2	ILMN_1657871	5.83	56.95	$3.05x10^{-6}$	2p25.2a	*Homo sapiens* radical S-adenosyl methionine domain containing 2 (RSAD2), mRNA.
VTRNA1-1	ILMN_3309759	5.83	56.72	$2.99\ x10^{-5}$		*Homo sapiens* vault RNA 1-1 (VTRNA1-1), non-coding RNA.
OASL	ILMN_1681721	5.65	50.32	$1.11x10^{-6}$	12q24.31a	*Homo sapiens* 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 1, mRNA.
IRF7	ILMN_1798181	5.63	49.56	$1.82x10^{-6}$	11p15.5d	*Homo sapiens* interferon regulatory factor 7 (IRF7), transcript variant b, mRNA.
LAMP3	ILMN_2170814	5.62	49.22	$3.63x10^{-6}$	3q27.1a	*Homo sapiens* lysosomal-associated membrane protein 3 (LAMP3), mRNA.
VTRNA1-2	ILMN_3310441	5.58	47.70	$1.04x10^{-5}$		*Homo sapiens* vault RNA 1-2 (VTRNA1-2), non-coding RNA.
SAMD9L	ILMN_1799467	5.48	44.68	$3.26x10^{-6}$	7q21.2b-q21.3a	*Homo sapiens* sterile alpha motif domain containing 9-like (SAMD9L), mRNA.
LOC100129681	ILMN_3259146	5.39	41.91	$8.33x10^{-5}$	19p13.11d	PREDICTED: *Homo sapiens* similar to NPC-A-7 (LOC100129681), mRNA.
CCL5	ILMN_2098126	5.17	35.97	$2.54x10^{-5}$	17q12b	*Homo sapiens* chemokine (C-C motif) ligand 5 (CCL5), mRNA.
TNFSF10	ILMN_1801307	5.14	35.27	$3.37x10^{-6}$	3q26.31b	*Homo sapiens* tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA.
IFI6	ILMN_2347798	5.13	34.95	$7.51x10^{-7}$	1p35.3b	*Homo sapiens* interferon, alpha-inducible protein 6 (IFI6), transcript variant 2, mRNA.
MX2	ILMN_2231928	5.10	34.40	$3.14\ x10^{-5}$	21q22.3a	*Homo sapiens* myxovirus (influenza virus) resistance 2 (mouse) (MX2), mRNA.
OAS1	ILMN_1672606	5.08	33.85	$2.67x10^{-5}$	12q24.13b	*Homo sapiens* 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 1, mRNA.
IFIH1	ILMN_1781373	5.00	32.06	$2.88x10^{-6}$	2q24.2d	*Homo sapiens* interferon induced with helicase C domain 1 (IFIH1), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
RASGRP3	ILMN_1727045	4.93	30.46	1.12×10^{-5}	2p22.3d	*Homo sapiens* RAS guanyl releasing protein 3 (calcium and DAG-regulated (RASGRP3), mRNA.
DDX58	ILMN_1797001	4.92	30.28	5.72×10^{-5}	9p21.1a	*Homo sapiens* DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (DDX58), mRNA.
IL28A	ILMN_1662302	4.88	29.38	1.75×10^{-5}	19q13.2a	*Homo sapiens* interleukin 28A (interferon, lambda 2) (IL28A), mRNA.
IFI6	ILMN_1687384	4.67	25.54	4.55×10^{-6}	1p35.3b	*Homo sapiens* interferon, alpha-inducible protein 6 (IFI6), transcript variant 3, mRNA.
CMPK2	ILMN_1783621	4.66	25.34	8.93×10^{-7}	2p25.2a	*Homo sapiens* cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (CMPK2), nuclear gene encoding mitochondrial protein, mRNA.
OAS2	ILMN_1736729	4.59	24.11	5.97×10^{-8}	12q24.13b	*Homo sapiens* 2'-5'-oligoadenylate synthetase 2, 69/71kDa (OAS2), transcript variant 2, mRNA.
PRIC285	ILMN_1787509	4.41	21.25	7.77×10^{-7}	20q13.33e	*Homo sapiens* peroxisomal proliferator-activated receptor A interacting complex 285 (PRIC285), transcript variant 2, mRNA.
PLEKHA4	ILMN_1755173	4.41	21.22	8.04×10^{-4}	19q13.33a	*Homo sapiens* pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA.
IFIT1	ILMN_1699331	4.40	21.14	2.82×10^{-4}	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 2, mRNA.
DDX60	ILMN_1795181	4.35	20.38	1.28×10^{-4}	4q32.3e	*Homo sapiens* DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 (DDX60), mRNA.
RN5S9	ILMN_3234762	4.34	20.27	1.94×10^{-7}		*Homo sapiens* RNA, 5S ribosomal 9 (RN5S9), ribosomal RNA.
DTX3L	ILMN_1784380	4.28	19.41	3.94×10^{-4}	3q21.1a	*Homo sapiens* deltex 3-like (*Drosophila*) (DTX3L), mRNA.
OAS1	ILMN_2410826	4.15	17.80	7.21×10^{-8}	12q24.13b	*Homo sapiens* 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 3, mRNA.
IFI16	ILMN_1710937	4.13	17.54	2.42×10^{-4}	1q23.1g	*Homo sapiens* interferon, γ-inducible protein 16 (IFI16), mRNA.
SP110	ILMN_1813455	4.12	17.40	8.14×10^{-6}	2q37.1a	*Homo sapiens* SP110 nuclear body protein (SP110), transcript variant c, mRNA.
GBP1	ILMN_1701114	4.10	17.11	1.89×10^{-6}	1p22.2c	*Homo sapiens* guanylate binding protein 1, interferon-inducible, 67 kDa (GBP1), mRNA.
SLC15A3	ILMN_2085862	4.06	16.71	1.50×10^{-4}	11q12.2a	*Homo sapiens* solute carrier family 15, member 3 (SLC15A3), mRNA.
USP18	ILMN_3240420	4.02	16.25	4.19×10^{-4}	22q11.21b	*Homo sapiens* ubiquitin specific peptidase 18 (USP18), mRNA.
OAS3	ILMN_2184262	4.01	16.09	2.94×10^{-4}	12q24.13b	*Homo sapiens* 2'-5'-oligoadenylate synthetase 3, 100 kDa (OAS3), mRNA.
MIR886	ILMN_3310643	3.99	15.93	9.78×10^{-7}	5q31.2a	*Homo sapiens* microRNA 886 (MIR886), microRNA.
BST2	ILMN_1723480	3.95	15.42	8.50×10^{-4}	19p13.11d	*Homo sapiens* bone marrow stromal cell antigen 2 (BST2), mRNA.
SAMD9	ILMN_1814305	3.93	15.23	6.03×10^{-6}	7q21.2b	*Homo sapiens* sterile alpha motif domain containing 9 (SAMD9), mRNA.
CASP1	ILMN_2326509	3.92	15.19	3.92×10^{-5}	11q22.3b	*Homo sapiens* caspase 1, apoptosis-related cysteine peptidase (interleukin 1, β, convertase) (CASP1), transcript variant δ, mRNA.
PARP10	ILMN_2262044	3.91	14.98	7.05×10^{-5}	8q24.3g	*Homo sapiens* poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA.
TRIM22	ILMN_1779252	3.90	14.88	2.47×10^{-4}	11p15.4c	*Homo sapiens* tripartite motif-containing 22 (TRIM22), mRNA.
IFITM3	ILMN_1805750	3.85	14.38	1.25×10^{-4}	11p15.5d	*Homo sapiens* interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA.
OAS1	ILMN_1675640	3.84	14.37	8.30×10^{-7}	12q24.13b	*Homo sapiens* 2',5'-oligoadenylate synthetase 1, 40/46kDa (OAS1), transcript variant 3, mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
DDX60L	ILMN_3243928	3.80	13.92	1.34x10^{-4}	4q32.3e	*Homo sapiens* DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like (DDX60L), mRNA.
LOC144383	ILMN_1724628	3.80	13.89	1.24x10^{-4}	12p11.21b	PREDICTED: *Homo sapiens* similar to Interferon-induced transmembrane protein 3 (Interferon-inducible protein 1-8U) (LOC144383), mRNA.
IFIT3	ILMN_1664543	3.79	13.81	2.91x10^{-4}	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), mRNA.
TXNIP	ILMN_1697448	3.77	13.61	1.03x10^{-5}	1q21.1b	*Homo sapiens* thioredoxin interacting protein (TXNIP), mRNA.
CXCL10	ILMN_1791759	3.74	13.32	2.16x10^{-4}	4q21.1a	*Homo sapiens* chemokine (C-X-C motif) ligand 10 (CXCL10), mRNA.
GBP1	ILMN_2148785	3.73	13.25	1.14x10^{-4}	1p22.2c	*Homo sapiens* guanylate binding protein 1, interferon-inducible, 67kDa (GBP1), mRNA.
REC8	ILMN_2317751	3.65	12.51	4.96x10^{-4}	14q12a	*Homo sapiens* REC8 homolog (yeast) (REC8), transcript variant 1, mRNA.
UBA7	ILMN_1794612	3.64	12.44	1.06x10^{-4}	3p21.31c	*Homo sapiens* ubiquitin-like modifier activating enzyme 7 (UBA7), mRNA.
HERC5	ILMN_1729749	3.64	12.43	3.75x10^{-6}	4q22.1b	*Homo sapiens* hect domain and RLD 5 (HERC5), mRNA.
TMEM140	ILMN_1736863	3.63	12.34	1.25x10^{-4}	7q33b	*Homo sapiens* transmembrane protein 140 (TMEM140), mRNA.
IL28B	ILMN_1768900	3.60	12.13	5.11x10^{-5}	19q13.2a	*Homo sapiens* interleukin 28B (interferon, λ 3) (IL28B), mRNA.
GBP4	ILMN_1771385	3.59	12.06	2.49x10^{-3}	1p22.2c	*Homo sapiens* guanylate binding protein 4 (GBP4), mRNA.
IL12A	ILMN_1671353	3.59	12.03	6.76x10^{-4}	3q25.33b	*Homo sapiens* interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lympho cyte maturation factor 1, p35) (IL12A), mRNA.
XAF1	ILMN_2370573	3.58	11.98	4.64x10^{-5}	17p13.2a	*Homo sapiens* XIAP associated factor 1 (XAF1), transcript variant 2, mRNA.
SP100	ILMN_1690920	3.57	11.89	2.37x10^{-4}	2q37.1a	*Homo sapiens* SP100 nuclear antigen (SP100), transcript variant 2, mRNA.
HLA-B	ILMN_1778401	3.54	11.60	4.62x10^{-7}	6p21.33a	*Homo sapiens* major histocompatibility complex, class I, B (HLA-B), mRNA.
PARP9	ILMN_1731224	3.51	11.41	5.47x10^{-6}	3q21.1a	*Homo sapiens* poly (ADP-ribose) polymerase family, member 9 (PARP9), mRNA.
PARP10	ILMN_1721411	3.49	11.21	4.37x10^{-5}	8q24.3g	PREDICTED: *Homo sapiens* poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA.
TLR3	ILMN_2155708	3.45	10.93	5.72x10^{-5}	4q35.1f	*Homo sapiens* Toll-like receptor 3 (TLR3), mRNA.
SP110	ILMN_2415144	3.43	10.78	5.50x10^{-7}	2q37.1a	*Homo sapiens* SP110 nuclear body protein (SP110), transcript variant b, mRNA.
LMO2	ILMN_1800078	3.39	10.49	3.61x10^{-4}	11p13c	*Homo sapiens* LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA.
OAS1	ILMN_1658247	3.36	10.28	9.37x10^{-6}	12q24.13b	*Homo sapiens* 2',5'-oligoadenylate synthetase 1, 40/46 kDa (OAS1), transcript variant 2, mRNA.
GEM	ILMN_1677092	3.33	10.08	1.91x10^{-4}	8q22.1b	*Homo sapiens* GTP binding protein overexpressed in skeletal muscle (GEM), transcript variant 2, mRNA.
SP100	ILMN_2284998	3.33	10.04	1.27x10^{-4}	2q37.1a	*Homo sapiens* SP100 nuclear antigen (SP100), transcript variant 1, mRNA.
LOC729231	ILMN_3298716	3.32	10.01	4.96x10^{-4}	4q28.2a	PREDICTED: *Homo sapiens* misc_RNA (LOC729231), miscRNA.
GEM	ILMN_2367883	3.30	9.86	2.43x10^{-5}	8q22.1b	*Homo sapiens* GTP binding protein overexpressed in skeletal muscle (GEM), transcript variant 2, mRNA.
LOC642393	ILMN_1745214	3.30	9.82	1.53x10^{-5}		PREDICTED: *Homo sapiens* similar to mitochondrial ribosomal protein L20, transcript variant 2 (LOC642393), mRNA.
PARP9	ILMN_2053527	3.27	9.66	2.54x10^{-5}	3q21.1a	*Homo sapiens* poly (ADP-ribose) polymerase family, member 9 (PARP9), mRNA.
SP110	ILMN_1672661	3.26	9.60	1.23x10^{-5}	2q37.1a	*Homo sapiens* SP110 nuclear body protein (SP110), transcript variant b, mRNA.
IL29	ILMN_2149624	3.22	9.34	1.61x10^{-4}	19q13.2a	*Homo sapiens* interleukin 29 (interferon, lambda 1) (IL29), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
CASP1	ILMN_2326512	3.21	9.25	$5.45\text{x}10^{-5}$	11q22.3b	*Homo sapiens* caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) (CASP1), transcript variant delta, mRNA.
IL29	ILMN_1684570	3.20	9.16	$8.58\text{x}10^{-4}$	19q13.2a	*Homo sapiens* interleukin 29 (interferon, λ 1) (IL29), mRNA.
LBA1	ILMN_1750321	3.17	9.03	$4.53\text{x}10^{-5}$	3p22.2b	*Homo sapiens* lupus brain antigen 1 (LBA1), mRNA.
ATF3	ILMN_2374865	3.17	9.00	$1.71\text{x}10^{-3}$	1q32.3c	*Homo sapiens* activating transcription factor 3 (ATF3), transcript variant 4, mRNA.
MYH3	ILMN_1795119	3.16	8.91	$3.36\text{x}10^{-4}$	17p13.1a	*Homo sapiens* myosin, heavy chain 3, skeletal muscle, embryonic (MYH3), mRNA.
APOL2	ILMN_2325338	3.14	8.83	$4.22\text{x}10^{-3}$	22q12.3d	*Homo sapiens* apolipoprotein L, 2 (APOL2), transcript variant beta, mRNA.
CYP2J2	ILMN_1758731	3.12	8.69	$3.88\text{x}10^{-4}$	1p32.1c	*Homo sapiens* cytochrome P450, family 2, subfamily J, polypeptide 2 (CYP2J2), mRNA.
TLR3	ILMN_1689578	3.11	8.65	$1.32\text{x}10^{-3}$	4q35.1f	*Homo sapiens* Toll-like receptor 3 (TLR3), mRNA.
AURKAPS1	ILMN_2053650	3.09	8.52	$1.05\text{x}10^{-3}$	1q41d	*Homo sapiens* aurora kinase A pseudogene 1 (AURKAPS1), non-coding RNA.
XAF1	ILMN_1742618	3.06	8.34	$5.56\text{x}10^{-6}$	17p13.2a	*Homo sapiens* XIAP associated factor 1 (XAF1), transcript variant 2, mRNA.
C19ORF66	ILMN_1750400	3.04	8.25	$3.65\text{x}10^{-6}$	19p13.2c	*Homo sapiens* chromosome 19 open reading frame 66 (C19orf66), mRNA.
USP41	ILMN_1690365	2.99	7.92	$8.04\text{x}10^{-4}$	22q11.21d	PREDICTED: *Homo sapiens* ubiquitin specific peptidase 41 (USP41), mRNA.
APOL2	ILMN_2325337	2.98	7.91	$4.11\text{x}10^{-5}$	22q12.3d	*Homo sapiens* apolipoprotein L, 2 (APOL2), transcript variant β, mRNA.
OAS3	ILMN_1745397	2.98	7.88	$1.38\text{x}10^{-6}$	12q24.13b	*Homo sapiens* 2'-5'-oligoadenylate synthetase 3, 100 kDa (OAS3), mRNA.
PARP12	ILMN_1718558	2.96	7.78	$2.14\text{x}10^{-6}$	7q34c	*Homo sapiens* poly (ADP-ribose) polymerase family, member 12 (PARP12), mRNA.
ARL14	ILMN_2232463	2.95	7.75	$1.11\text{x}10^{-3}$	3q26.1a	*Homo sapiens* ADP-ribosylation factor-like 14 (ARL14), mRNA.
SP110	ILMN_1731418	2.95	7.73	$1.19\text{x}10^{-5}$	2q37.1a	*Homo sapiens* SP110 nuclear body protein (SP110), transcript variant b, mRNA.
GBP3	ILMN_1725314	2.93	7.64	$9.65\text{x}10^{-4}$	1p22.2c	*Homo sapiens* guanylate binding protein 3 (GBP3), mRNA.
CEACAM1	ILMN_1664330	2.92	7.55	$4.46\text{x}10^{-4}$	19q13.2c	*Homo sapiens* carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), transcript variant 1, mRNA.
MXD1	ILMN_2214678	2.91	7.51	$1.23\text{x}10^{-3}$	2p14a	*Homo sapiens* MAX dimerization protein 1 (MXD1), mRNA.
RN7SK	ILMN_1739423	2.85	7.19	$1.53\text{x}10^{-3}$	6p12.1d	*Homo sapiens* RNA, 7SK small nuclear (RN7SK), non-coding RNA.
CFB	ILMN_1774287	2.84	7.16	$6.84\text{x}10^{-5}$	6p21.32b	*Homo sapiens* complement factor B (CFB), mRNA.
EGR1	ILMN_1762899	2.82	7.07	$1.66\text{x}10^{-5}$	5q31.2c	*Homo sapiens* early growth response 1 (EGR1), mRNA.
LOC100128274	ILMN_3253787	2.81	7.02	$6.43\text{x}10^{-5}$	9p21.1a	PREDICTED: *Homo sapiens* hypothetical protein LOC100128274 (LOC100128274), mRNA.
RNY4	ILMN_3241021	2.79	6.91	$3.91\text{x}10^{-5}$		*Homo sapiens* RNA, Ro-associated Y4 (RNY4), small cytoplasmic RNA.
IL6	ILMN_1699651	2.78	6.88	$3.06\text{x}10^{-4}$	7p15.3c	*Homo sapiens* interleukin 6 (interferon, beta 2) (IL6), mRNA.
LGALS9	ILMN_2412214	2.77	6.83	$6.43\text{x}10^{-4}$	17q11.1c	*Homo sapiens* lectin, galactoside-binding, soluble, 9 (LGALS9), transcript variant 1, mRNA.
HERC6	ILMN_1654639	2.76	6.78	$5.84\text{x}10^{-6}$	4q22.1b	*Homo sapiens* hect domain and RLD 6 (HERC6), transcript variant 1, mRNA.
PARP10	ILMN_1710844	2.75	6.73	$2.08\text{x}10^{-3}$	8q24.3g	PREDICTED: *Homo sapiens* poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA.
LOC650029	ILMN_1760991	2.75	6.73	$4.14\text{x}10^{-4}$		PREDICTED: *Homo sapiens* similar to RNA-binding protein 4 (RNA-binding motif protein 4) (Lark homolog) (Hlark) (RNA-binding motif protein 4a), transcript variant 2 (LOC650029), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
STAT2	ILMN_1690921	2.74	6.68	$7.67x10^{-6}$	12q13.2c	*Homo sapiens* signal transducer and activator of transcription 2, 113 kDa (STAT2), mRNA.
PARP14	ILMN_1691731	2.70	6.52	$2.07x10^{-5}$	3q21.1a	*Homo sapiens* poly (ADP-ribose) polymerase family, member 14 (PARP14), mRNA.
LINCR	ILMN_2235851	2.69	6.47	$8.67x10^{-5}$	2q11.2a	*Homo sapiens* likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein (LINCR), mRNA.
UBQLNL	ILMN_1748907	2.67	6.37	$1.28x10^{-3}$	11p15.4c	*Homo sapiens* ubiquilin-like (UBQLNL), mRNA.
REC8	ILMN_1751886	2.66	6.33	$6.43x10^{-5}$	14q12a	*Homo sapiens* REC8 homolog (yeast) (REC8), transcript variant 1, mRNA.
CEACAM1	ILMN_2371724	2.64	6.23	$1.22x10^{-4}$	19q13.2c	*Homo sapiens* carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), transcript variant 2, mRNA.
ZC3HAV1	ILMN_1729973	2.64	6.22	$9.94x10^{-6}$	7q34b	*Homo sapiens* zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA.
GADD45A	ILMN_2052208	2.62	6.15	$3.10x10^{-4}$	1p31.3a	*Homo sapiens* growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA.
SOCS1	ILMN_1774733	2.61	6.12	$2.33x10^{-4}$	16p13.13c	*Homo sapiens* suppressor of cytokine signaling 1 (SOCS1), mRNA.
NLRC5	ILMN_1716704	2.59	6.03	$3.37x10^{-3}$	16q13b-q13c	*Homo sapiens* NLR family, CARD domain containing 5 (NLRC5), mRNA.
PLSCR1	ILMN_1745242	2.59	6.01	$4.82x10^{-6}$	3q24d	*Homo sapiens* phospholipid scramblase 1 (PLSCR1), mRNA.
USP36	ILMN_1697227	2.58	5.97	$1.38x10^{-4}$	17q25.3b	*Homo sapiens* ubiquitin specific peptidase 36 (USP36), mRNA.
TRIM21	ILMN_1678054	2.56	5.90	$1.04x10^{-5}$	11p15.4d	*Homo sapiens* tripartite motif-containing 21 (TRIM21), mRNA.
INDO	ILMN_1656310	2.53	5.78	$4.11x10^{-3}$	8p11.22a-p11.21c	*Homo sapiens* indoleamine-pyrrole 2,3 dioxygenase (INDO), mRNA.
GADD45A	ILMN_1694075	2.53	5.77	$8.62x10^{-5}$	1p31.3a	*Homo sapiens* growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA.
APOL3	ILMN_1756862	2.52	5.72	$2.64x10^{-5}$	22q12.3d	*Homo sapiens* apolipoprotein L, 3 (APOL3), transcript variant beta/a, mRNA.
TNFRSF10D	ILMN_1666022	2.51	5.68	$4.45x10^{-3}$	8p21.3a	*Homo sapiens* tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain (TNFRSF10D), mRNA.
RARRES3	ILMN_1701613	2.49	5.61	$1.13x10^{-6}$	11q12.3b	*Homo sapiens* retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA.
FST	ILMN_1700081	2.49	5.60	$6.93x10^{-5}$	5q11.2c	*Homo sapiens* follistatin (FST), transcript variant FST344, mRNA.
ZC3HAV1	ILMN_1724837	2.48	5.60	$8.36x10^{-5}$	7q34b	*Homo sapiens* zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA.
PLA2G4C	ILMN_1810191	2.48	5.57	$9.96x10^{-6}$	19q13.32c	*Homo sapiens* phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA.
PPM1A	ILMN_1727127	2.48	5.57	$3.34x10^{-4}$	14q23.1c	*Homo sapiens* protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), transcript variant 2, mRNA.
RETNLB	ILMN_1787379	2.46	5.49	$5.59x10^{-4}$	3q13.13a	*Homo sapiens* resistin like beta (RETNLB), mRNA.
DHX58	ILMN_1678422	2.44	5.41	$2.96x10^{-3}$	17q21.2b	*Homo sapiens* DEXH (Asp-Glu-X-His) box polypeptide 58 (DHX58), mRNA.
FOSL1	ILMN_1771841	2.42	5.36	$4.69x10^{-5}$	11q13.1d	*Homo sapiens* FOS-like antigen 1 (FOSL1), mRNA.
CEACAM1	ILMN_1716815	2.42	5.34	$1.40x10^{-4}$	19q13.2c	*Homo sapiens* carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), transcript variant 2, mRNA.
AMHR2	ILMN_1736412	2.41	5.33	$1.14x10^{-3}$	12q13.13e	*Homo sapiens* anti-Mullerian hormone receptor, type II (AMHR2), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
COL4A3BP	ILMN_2292123	2.41	5.31	3.62×10^{-3}	5q13.3b	*Homo sapiens* collagen, type IV, alpha 3 (Goodpasture antigen) binding protein (COL4A3BP), transcript variant 1, mRNA.
ECGF1	ILMN_1690939	2.38	5.20	2.76×10^{-3}	22q13.33b	*Homo sapiens* endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA.
LOC650799	ILMN_1715436	2.38	5.19	6.28×10^{-3}		PREDICTED: *Homo sapiens* similar to Ig λ chain V-I region BL2 precursor (LOC650799), mRNA.
ZNFX1	ILMN_1745148	2.37	5.17	2.78×10^{-5}	20q13.13c	*Homo sapiens* zinc finger, NFX1-type containing 1 (ZNFX1), mRNA.
IRF9	ILMN_1745471	2.36	5.15	3.32×10^{-5}	14q12a	*Homo sapiens* interferon regulatory factor 9 (IRF9), mRNA.
LOC729231	ILMN_3223813	2.36	5.14	7.69×10^{-3}	4q28.2a	PREDICTED: *Homo sapiens* misc_RNA (LOC729231), miscRNA.
ALOXE3	ILMN_1678255	2.36	5.12	9.43×10^{-3}	17p13.1c	*Homo sapiens* arachidonate lipoxygenase 3 (ALOXE3), mRNA.
IFI35	ILMN_1745374	2.36	5.12	5.35×10^{-6}	17q21.31a	*Homo sapiens* interferon-induced protein 35 (IFI35), mRNA.
SPHK1	ILMN_2357134	2.34	5.05	9.55×10^{-4}	17q25.1d	*Homo sapiens* sphingosine kinase 1 (SPHK1), transcript variant 1, mRNA.
TRIM69	ILMN_1813430	2.34	5.05	1.11×10^{-2}	15q21.1a	*Homo sapiens* tripartite motif-containing 69 (TRIM69), transcript variant a, mRNA.
TRIM25	ILMN_1813625	2.30	4.94	7.65×10^{-6}	17q22c	*Homo sapiens* tripartite motif-containing 25 (TRIM25), mRNA.
RMND5A	ILMN_1714093	2.30	4.92	4.49×10^{-4}	2p11.2e	*Homo sapiens* required for meiotic nuclear division 5 homolog A (S. cerevisiae) (RMND5A), mRNA.
LOC100132564	ILMN_3243644	2.30	4.92	3.26×10^{-5}	12q24.32b	PREDICTED: *Homo sapiens* hypothetical protein LOC100132564 (LOC100132564), mRNA.
VPS13A	ILMN_1789828	2.28	4.86	8.95×10^{-4}	9q21.13c	*Homo sapiens* vacuolar protein sorting 13 homolog A (S. cerevisiae) (VPS13A), transcript variant D, mRNA.
NT5C3	ILMN_1769734	2.27	4.83	1.28×10^{-4}	7p14.3c-p14.3b	*Homo sapiens* 5'-nucleotidase, cytosolic III (NT5C3), transcript variant 1, mRNA.
LOC643401	ILMN_1700280	2.26	4.79	3.01×10^{-3}		PREDICTED: *Homo sapiens* hypothetical protein LOC643401, transcript variant 2 (LOC643401), mRNA.
CARD9	ILMN_1712532	2.25	4.76	1.35×10^{-3}	9q34.3d	*Homo sapiens* caspase recruitment domain family, member 9 (CARD9), mRNA.
C5ORF41	ILMN_1776788	2.25	4.75	1.24×10^{-3}	5q35.2a	*Homo sapiens* chromosome 5 open reading frame 41 (C5orf41), mRNA.
MDM2	ILMN_1736829	2.24	4.71	3.65×10^{-3}	12q15b	*Homo sapiens* Mdm2 p53 binding protein homolog (mouse) (MDM2), transcript variant MDM2, mRNA.
IL32	ILMN_2368530	2.22	4.65	4.47×10^{-3}	16p13.3d	*Homo sapiens* interleukin 32 (IL32), transcript variant 4, mRNA.
RNY1	ILMN_3237623	2.21	4.61	7.81×10^{-6}		*Homo sapiens* RNA, Ro-associated Y1 (RNY1), small cytoplasmic RNA.
IFIT5	ILMN_1696654	2.20	4.58	6.65×10^{-5}	10q23.31b	*Homo sapiens* interferon-induced protein with tetratricopeptide repeats 5 (IFIT5), mRNA.
GIMAP2	ILMN_2135272	2.16	4.47	3.43×10^{-3}	7q36.1c	*Homo sapiens* GTPase, IMAP family member 2 (GIMAP2), mRNA.
FAM154B	ILMN_2184884	2.15	4.44	2.50×10^{-4}	15q25.2a	*Homo sapiens* family with sequence similarity 154, member B (FAM154B), mRNA.
TAP2	ILMN_1759250	2.14	4.41	4.50×10^{-4}	6p21.32a	*Homo sapiens* transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 2, mRNA.
ZEB2	ILMN_1688698	2.14	4.41	9.90×10^{-3}	2q22.3a	*Homo sapiens* zinc finger E-box binding homeobox 2 (ZEB2), mRNA.
PPP1R15A	ILMN_1659936	2.13	4.39	1.26×10^{-5}	19q13.33a	*Homo sapiens* protein phosphatase 1, regulatory (inhibitor) subunit 15A (PPP1R15A), mRNA.
TNFAIP3	ILMN_1702691	2.13	4.37	7.86×10^{-4}	6q23.3d	*Homo sapiens* tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
NR1D2	ILMN_1698668	2.12	4.35	9.13x10^{-4}	3p24.2b	PREDICTED: *Homo sapiens* nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA.
HLA-F	ILMN_1762861	2.12	4.33	2.18x10^{-3}	6p22.1a	*Homo sapiens* major histocompatibility complex, class I, F (HLA-F), transcript variant 1, mRNA.
ZNF79	ILMN_1794122	2.11	4.32	1.06x10^{-2}	9q33.3b	*Homo sapiens* zinc finger protein 79 (ZNF79), mRNA.
TRIM5	ILMN_1704972	2.10	4.30	5.17x10^{-5}	11p15.4c	*Homo sapiens* tripartite motif-containing 5 (TRIM5), transcript variant α, mRNA.
TMEM27	ILMN_1772894	2.10	4.27	1.17x10^{-3}	Xp22.2	*Homo sapiens* transmembrane protein 27 (TMEM27), mRNA.
SLC8A2	ILMN_1698846	2.09	4.26	1.80x10^{-3}	19q13.32c	*Homo sapiens* solute carrier family 8 (sodium/calcium exchanger), member 2 (SLC8A2), mRNA.
KLF4	ILMN_2137789	2.08	4.23	1.86x10^{-5}	9q31.2b	*Homo sapiens* Kruppel-like factor 4 (gut) (KLF4), mRNA.
FOSB	ILMN_1751607	2.07	4.20	7.16x10^{-4}	19q13.32a	*Homo sapiens* FBJ murine osteosarcoma viral oncogene homolog B (FOSB), mRNA.
NT5C3	ILMN_2352121	2.06	4.18	3.02x10^{-5}	7p14.3c-p14.3b	*Homo sapiens* 5'-nucleotidase, cytosolic III (NT5C3), transcript variant 1, mRNA.
HSH2D	ILMN_1788017	2.06	4.17	5.83x10^{-4}	19p13.11f	*Homo sapiens* hematopoietic SH2 domain containing (HSH2D), mRNA.
ARRDC3	ILMN_2198515	2.06	4.16	1.16x10^{-2}	5q14.3h	*Homo sapiens* arrestin domain containing 3 (ARRDC3), mRNA.
ARRDC4	ILMN_1660544	2.04	4.13	1.15x10^{-4}	15q26.3a	*Homo sapiens* arrestin domain containing 4 (ARRDC4), mRNA.
IRF2	ILMN_2090607	2.04	4.13	9.52x10^{-4}	4q35.1d	*Homo sapiens* interferon regulatory factor 2 (IRF2), mRNA.
HIST1H4H	ILMN_1751120	2.03	4.09	3.00x10^{-5}	6p22.1d	*Homo sapiens* histone cluster 1, H4h (HIST1H4H), mRNA.
C5ORF41	ILMN_2195821	2.02	4.05	7.25x10^{-4}	5q35.2a	*Homo sapiens* chromosome 5 open reading frame 41 (C5orf41), mRNA.
WNK4	ILMN_1669114	2.00	4.00	2.13x10^{-4}	17q21.31a	*Homo sapiens* WNK lysine deficient protein kinase 4 (WNK4), mRNA.
ISG20	ILMN_1659913	1.99	3.97	1.20x10^{-5}	15q26.1a	*Homo sapiens* interferon stimulated exonuclease gene 20kDa (ISG20), mRNA.
KLRC2	ILMN_2059357	1.99	3.97	8.04x10^{-3}	12p13.2c	*Homo sapiens* killer cell lectin-like receptor subfamily C, member 2 (KLRC2), mRNA.
PLA1A	ILMN_1792506	1.98	3.95	1.62x10^{-2}	3q13.33a	*Homo sapiens* phospholipase A1 member A (PLA1A), mRNA.
KLF4	ILMN_1779857	1.98	3.94	2.10x10^{-4}	9q31.2b	*Homo sapiens* Kruppel-like factor 4 (gut) (KLF4), mRNA.
EID3	ILMN_1776000	1.98	3.93	3.05x10^{-4}	12q23.3a	*Homo sapiens* EP300 interacting inhibitor of differentiation 3 (EID3), mRNA.
MORC3	ILMN_1783702	1.96	3.90	1.87x10^{-3}	21q22.12b	*Homo sapiens* MORC family CW-type zinc finger 3 (MORC3), mRNA.
TAP2	ILMN_1777565	1.96	3.89	3.96x10^{-5}	6p21.32a	*Homo sapiens* transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 1, mRNA.
IDO1	ILMN_3239965	1.95	3.85	4.35x10^{-3}	8p11.22a-p11.21c	*Homo sapiens* indoleamine 2,3-dioxygenase 1 (IDO1), mRNA.
CSTF1	ILMN_1758339	1.93	3.82	7.03x10^{-4}	20q13.31a	*Homo sapiens* cleavage stimulation factor, 3'pre-RNA, subunit 1, 50kDa (CSTF1), transcript variant 1, mRNA.
LOC732450	ILMN_1724017	1.93	3.81	1.00x10^{-2}		PREDICTED: *Homo sapiens* similar to protein immuno-reactive with anti-PTH polyclonal antibodies (LOC732450), mRNA.
UBE2L6	ILMN_1703108	1.93	3.81	5.47x10^{-6}	11q12.1a	*Homo sapiens* ubiquitin-conjugating enzyme E2L 6 (UBE2L6), transcript variant 1, mRNA.
BTN3A1	ILMN_1802708	1.92	3.80	3.17x10^{-4}	6p22.1d	*Homo sapiens* butyrophilin, subfamily 3, member A1 (BTN3A1), mRNA.
CCL20	ILMN_1657234	1.92	3.78	1.39x10^{-2}	2q36.3c	*Homo sapiens* chemokine (C-C motif) ligand 20 (CCL20), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
CREB5	ILMN_1731714	1.92	3.78	$6.03\text{x}10^{-3}$	7p15.1d	*Homo sapiens* cAMP responsive element binding protein 5 (CREB5), transcript variant 1, mRNA.
CENTD2	ILMN_1786357	1.92	3.78	$1.87\text{x}10^{-3}$	11q13.4a-q13.4b	*Homo sapiens* centaurin, delta 2 (CENTD2), transcript variant 2, mRNA.
DDIT3	ILMN_1676984	1.91	3.77	$1.81\text{x}10^{-3}$	12q13.3b	*Homo sapiens* DNA-damage-inducible transcript 3 (DDIT3), mRNA.
LOC643896	ILMN_3239871	1.91	3.76	$1.93\text{x}10^{-3}$	2q11.2d	*Homo sapiens* similar to cAMP-regulated phosphoprotein 19 (LOC643896), mRNA.
JUN	ILMN_1806023	1.91	3.75	$3.81\text{x}10^{-4}$	1p32.1f	*Homo sapiens* jun oncogene (JUN), mRNA.
SP100	ILMN_2390586	1.89	3.72	$2.43\text{x}10^{-4}$	2q37.1a	*Homo sapiens* SP100 nuclear antigen (SP100), transcript variant 1, mRNA.
SP140L	ILMN_1658858	1.89	3.71	$1.25\text{x}10^{-2}$	2q37.1a	*Homo sapiens* SP140 nuclear body protein-like (SP140L), mRNA.
STAT1	ILMN_1690105	1.88	3.69	$2.58\text{x}10^{-5}$	2q32.2b	*Homo sapiens* signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant alpha, mRNA.
SERPINE1	ILMN_1744381	1.88	3.69	$4.83\text{x}10^{-4}$	7q22.1d	*Homo sapiens* serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA.
MYD88	ILMN_1738523	1.88	3.68	$1.88\text{x}10^{-6}$	3p22.2a	*Homo sapiens* myeloid differentiation primary response gene (88) (MYD88), mRNA.
BTG2	ILMN_1770085	1.88	3.68	$4.41\text{x}10^{-4}$	1q32.1e	*Homo sapiens* BTG family, member 2 (BTG2), mRNA.
TAP1	ILMN_1751079	1.88	3.67	$2.85\text{x}10^{-5}$	6p21.32a	*Homo sapiens* transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA.
IGFBPL1	ILMN_1677158	1.87	3.65	$2.57\text{x}10^{-3}$	9p13.1b	*Homo sapiens* insulin-like growth factor binding protein-like 1 (IGFBPL1), mRNA.
MAFF	ILMN_1680139	1.85	3.62	$7.41\text{x}10^{-6}$	22q13.1b	*Homo sapiens* v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) (MAFF), transcript variant 1, mRNA.
NHP2L1	ILMN_1709809	1.85	3.61	$8.37\text{x}10^{-3}$	22q13.2a-q13.2b	*Homo sapiens* NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), transcript variant 1, mRNA.
KLF11	ILMN_1673207	1.85	3.59	$5.97\text{x}10^{-3}$	2p25.1d	PREDICTED: *Homo sapiens* Kruppel-like factor 11 (KLF11), mRNA.
CNP	ILMN_1811758	1.83	3.56	$1.95\text{x}10^{-2}$	17q21.2b	*Homo sapiens* 2',3'-cyclic nucleotide 3'phosphodiesterase (CNP), mRNA.
PSMB9	ILMN_2376108	1.83	3.54	$2.64\text{x}10^{-5}$	6p21.32a	*Homo sapiens* proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) (PSMB9), transcript variant 1, mRNA.
PSMB8	ILMN_1767006	1.82	3.54	$8.27\text{x}10^{-4}$	6p21.32a	*Homo sapiens* proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) (PSMB8), transcript variant 2, mRNA.
HIPK3	ILMN_2337551	1.82	3.53	$1.49\text{x}10^{-2}$	11p13d	*Homo sapiens* homeodomain interacting protein kinase 3 (HIPK3), transcript variant 3, mRNA.
HS.553217	ILMN_1863484	1.82	3.52	$1.49\text{x}10^{-3}$		DA645971 MAMMA1 *Homo sapiens* cDNA clone MAMMA1000318 5, mRNA sequence
ACTA1	ILMN_2125869	1.80	3.48	$3.74\text{x}10^{-4}$	1q42.13e	*Homo sapiens* actin, alpha 1, skeletal muscle (ACTA1), mRNA.
SPTBN1	ILMN_1690708	1.79	3.47	$1.34\text{x}10^{-5}$	2p16.2a	*Homo sapiens* spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, mRNA.
COL27A1	ILMN_1788377	1.79	3.47	$3.67\text{x}10^{-3}$	9q32d	*Homo sapiens* collagen, type XXVII, alpha 1 (COL27A1), mRNA.
LAMA2	ILMN_1788019	1.79	3.45	$3.92\text{x}10^{-3}$	6q22.33d-q22.33e	*Homo sapiens* laminin, alpha 2 (LAMA2), transcript variant 2, mRNA.
EREG	ILMN_1657248	1.78	3.44	$3.38\text{x}10^{-3}$	4q13.3e	*Homo sapiens* epiregulin (EREG), mRNA.
PPM1K	ILMN_2070044	1.78	3.43	$1.46\text{x}10^{-2}$	4q22.1b	*Homo sapiens* protein phosphatase 1K (PP2C domain containing) (PPM1K), mRNA.
HRASLS2	ILMN_1809259	1.78	3.43	$1.54\text{x}10^{-2}$	11q12.3b	*Homo sapiens* HRAS-like suppressor 2 (HRASLS2), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
TYMP	ILMN_3223126	1.78	3.43	5.04x10^{-3}	22q13.33b	*Homo sapiens* thymidine phosphorylase (TYMP), transcript variant 3, mRNA.
ARHGAP30	ILMN_2408851	1.78	3.43	2.09x10^{-3}	1q23.3a	*Homo sapiens* Rho GTPase activating protein 30 (ARHGAP30), transcript variant 2, mRNA.
TDRD7	ILMN_1705241	1.77	3.41	9.96x10^{-5}	9q22.33a	*Homo sapiens* tudor domain containing 7 (TDRD7), mRNA.
IL32	ILMN_1778010	1.77	3.41	9.56x10^{-3}	16p13.3d	*Homo sapiens* interleukin 32 (IL32), transcript variant 7, mRNA.
TNFRSF9	ILMN_1813379	1.77	3.40	3.27x10^{-3}	1p36.23b	*Homo sapiens* tumor necrosis factor receptor superfamily, member 9 (TNFRSF9), mRNA.
UBE2L6	ILMN_1769520	1.75	3.36	1.30x10^{-5}	11q12.1a	*Homo sapiens* ubiquitin-conjugating enzyme E2L 6 (UBE2L6), transcript variant 1, mRNA.
KANK3	ILMN_3241744	1.75	3.36	1.21x10^{-2}	19p13.2d	*Homo sapiens* KN motif and ankyrin repeat domains 3 (KANK3), mRNA.
RFX3	ILMN_1756102	1.75	3.35	6.21x10^{-3}	9p24.2b-p24.2a	*Homo sapiens* regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA.
LOC100132352	ILMN_3276395	1.74	3.35	8.72x10^{-3}	9q12i	PREDICTED: *Homo sapiens* similar to hCG1989297, transcript variant 1 (LOC100132352), mRNA.
MIR21	ILMN_3310840	1.74	3.35	9.28x10^{-4}	17q23.1a	*Homo sapiens* microRNA 21 (MIR21), microRNA.
IRF8	ILMN_1666594	1.74	3.34	2.85x10^{-2}	16q24.1b	*Homo sapiens* interferon regulatory factor 8 (IRF8), mRNA.
VAPA	ILMN_1690822	1.73	3.33	4.05x10^{-4}	18p11.22b	*Homo sapiens* VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 1, mRNA.
NPC1L1	ILMN_1787556	1.73	3.32	3.12x10^{-2}	7p13d	*Homo sapiens* NPC1 (Niemann-Pick disease, type C1, gene)-like 1 (NPC1L1), mRNA.
MED13	ILMN_1671067	1.73	3.31	7.17x10^{-4}	17q23.2c	*Homo sapiens* mediator complex subunit 13 (MED13), mRNA.
JUB	ILMN_1661372	1.72	3.29	4.84x10^{-3}	14q11.2f	*Homo sapiens* jub, ajuba homolog (Xenopus laevis) (JUB), transcript variant 1, mRNA.
LOC389386	ILMN_3295494	1.71	3.28	9.33x10^{-5}	6p21.31a	PREDICTED: *Homo sapiens* misc_RNA (LOC389386), partial miscRNA.
REV3L	ILMN_2199947	1.71	3.27	4.06x10^{-3}	6q21h	*Homo sapiens* REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA.
LOC388922	ILMN_1655462	1.71	3.26	3.04x10^{-2}		PREDICTED: *Homo sapiens* hypothetical LOC388922 (LOC388922), mRNA.
KLF11	ILMN_1751656	1.70	3.26	9.59x10^{-6}	2p25.1d	PREDICTED: *Homo sapiens* Kruppel-like factor 11 (KLF11), mRNA.
CNNM2	ILMN_1663975	1.70	3.26	2.56x10^{-3}	10q24.32b	*Homo sapiens* cyclin M2 (CNNM2), transcript variant 3, mRNA.
LAMP3	ILMN_2170813	1.70	3.25	1.10x10^{-5}	3q27.1a	*Homo sapiens* lysosomal-associated membrane protein 3 (LAMP3), mRNA.
RASSF1	ILMN_2393573	1.69	3.24	1.39x10^{-4}	3p21.31b	*Homo sapiens* Ras association (RalGDS/AF-6) domain family member 1 (RASSF1), transcript variant A, mRNA.
PTPN21	ILMN_1719664	1.69	3.24	7.84x10^{-3}	14q31.3d	*Homo sapiens* protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA.
KIAA1345	ILMN_1785036	1.69	3.23	4.64x10^{-3}	4p15.33a	PREDICTED: *Homo sapiens* KIAA1345 protein, transcript variant 8 (KIAA1345), mRNA.
ADRB2	ILMN_1695590	1.69	3.22	2.69x10^{-3}	5q33.1b	*Homo sapiens* adrenergic, beta-2-, receptor, surface (ADRB2), mRNA.
PLAC8L1	ILMN_1655341	1.69	3.22	6.19x10^{-4}	5q32c	*Homo sapiens* PLAC8-like 1 (PLAC8L1), mRNA.
NGF	ILMN_1716608	1.68	3.21	3.36x10^{-2}	1p13.2a	*Homo sapiens* nerve growth factor (β polypeptide) (NGF), mRNA.
FAM80B	ILMN_1681757	1.68	3.21	1.24x10^{-2}	12p13.31b	*Homo sapiens* family with sequence similarity 80, member B (FAM80B), mRNA.
TRIM5	ILMN_1737599	1.68	3.21	7.64x10^{-3}	11p15.4c	*Homo sapiens* tripartite motif-containing 5 (TRIM5), transcript variant gamma, mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
IL8	ILMN_2184373	1.68	3.21	3.61x10^{-3}	4q13.3d	*Homo sapiens* interleukin 8 (IL8), mRNA.
LAP3	ILMN_1683792	1.67	3.18	9.41x10^{-6}	4p15.32b	*Homo sapiens* leucine aminopeptidase 3 (LAP3), mRNA.
CCDC132	ILMN_2360362	1.67	3.17	4.41x10^{-2}	7q21.3a	*Homo sapiens* coiled-coil domain containing 132 (CCDC132), transcript variant 2, mRNA.
C4ORF49	ILMN_3236160	1.66	3.17	1.74x10^{-3}	4q31.1c	*Homo sapiens* chromosome 4 open reading frame 49 (C4orf49), mRNA.
HS.129244	ILMN_1844611	1.66	3.17	2.52x10^{-4}		os59g01.y5 NCI_CGAP_Br2 *Homo sapiens* cDNA clone IMAGE:1609680 5, mRNA sequence
AEN	ILMN_3240321	1.66	3.17	7.63x10^{-4}	15q26.1a	*Homo sapiens* apoptosis enhancing nuclease (AEN), mRNA.
GATA3	ILMN_2406656	1.66	3.15	1.21x10^{-2}	10p14d	*Homo sapiens* GATA binding protein 3 (GATA3), transcript variant 2, mRNA.
IL5	ILMN_1709300	1.65	3.14	4.03x10^{-2}	5q31.1b	*Homo sapiens* interleukin 5 (colony-stimulating factor, eosinophil) (IL5), mRNA.
IKZF5	ILMN_3307796	1.65	3.14	1.77x10^{-3}	10q26.13b	*Homo sapiens* IKAROS family zinc finger 5 (Pegasus) (IKZF5), mRNA.
TRAF1	ILMN_1698218	1.65	3.14	5.41x10^{-3}	9q33.2a	*Homo sapiens* TNF receptor-associated factor 1 (TRAF1), mRNA.
PPFIBP1	ILMN_2277252	1.65	3.13	1.33x10^{-3}	12p11.23a-p11.22b	*Homo sapiens* PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), transcript variant 1, mRNA.
KLHL15	ILMN_1701648	1.64	3.12	1.79x10^{-2}	Xp22.11a	*Homo sapiens* kelch-like 15 (*Drosophila*) (KLHL15), mRNA.
STAT1	ILMN_1777325	1.63	3.10	2.41x10^{-4}	2q32.2b	*Homo sapiens* signal transducer and activator of transcription 1, 91kDa (STAT1), tran script variant α, mRNA.
C15ORF48	ILMN_1654696	1.63	3.09	1.33x10^{-2}	15q21.1a	*Homo sapiens* chromosome 15 open reading frame 48 (C15orf48), transcript variant 2, mRNA.
HS.147562	ILMN_1872600	1.63	3.09	5.76x10^{-3}		601311935F1 NIH_MGC_44 *Homo sapiens* cDNA clone IMAGE:3658737 5, mRNA sequence
FLJ10996	ILMN_1694269	1.63	3.09	9.58x10^{-4}	2q14.1d	*Homo sapiens* hypothetical protein FLJ10996 (FLJ10996), mRNA.
PHC3	ILMN_2179873	1.63	3.09	8.52x10^{-4}	3q26.2b	*Homo sapiens* polyhomeotic homolog 3 (Drosophila) (PHC3), mRNA.
HS.121525	ILMN_1882112	1.62	3.08	1.25x10^{-3}		BX101252 NCI_CGAP_Lu24 *Homo sapiens* cDNA clone IMAGp998I115625, mRNA sequence
LOC389386	ILMN_3215715	1.62	3.08	2.82x10^{-4}	6p21.31a	PREDICTED: *Homo sapiens* misc_RNA (LOC389386), partial miscRNA.
DHDH	ILMN_1689200	1.60	3.04	4.73x10^{-3}	19q13.33a	*Homo sapiens* dihydrodiol dehydrogenase (dimeric) (DHDH), mRNA.
LOC727938	ILMN_3274465	1.60	3.04	3.25x10^{-2}	5q15d	PREDICTED: *Homo sapiens* misc_RNA (LOC727938), miscRNA.
CX3CR1	ILMN_2088437	1.60	3.03	4.78x10^{-2}	3p22.2a	*Homo sapiens* chemokine (C-X3-C motif) receptor 1 (CX3CR1), mRNA.
IRF1	ILMN_1708375	1.60	3.03	6.20x10^{-4}	5q31.1b	*Homo sapiens* interferon regulatory factor 1 (IRF1), mRNA.
PLEKHF2	ILMN_2106449	1.60	3.03	3.78x10^{-3}	8q22.1c	*Homo sapiens* pleckstrin homology domain containing, family F (with FYVE domain) member 2 (PLEKHF2), mRNA.
ZNF37A	ILMN_1774027	1.60	3.03	6.47x10^{-4}	10p11.21a	*Homo sapiens* zinc finger protein 37A (ZNF37A), transcript variant 2, mRNA.
ABL1	ILMN_1708922	1.60	3.03	1.35x10^{-2}	9q34.12a	*Homo sapiens* c-abl oncogene 1, receptor tyrosine kinase (ABL1), transcript variant b, mRNA.
HIST2H2BE	ILMN_1732071	1.60	3.02	3.89x10^{-4}	1q21.2a	*Homo sapiens* histone cluster 2, H2be (HIST2H2BE), mRNA.
ODF3B	ILMN_3241446	1.60	3.02	1.39x10^{-3}	22q13.33b	*Homo sapiens* outer dense fiber of sperm tails 3B (ODF3B), mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
LTA	ILMN_1795464	1.60	3.02	1.81×10^{-2}	6p21.33a	*Homo sapiens* lymphotoxin alpha (TNF superfamily, member 1) (LTA), transcript variant 2, mRNA.
LHX3	ILMN_1701340	1.59	3.02	2.12×10^{-2}	9q34.3d	*Homo sapiens* LIM homeobox 3 (LHX3), transcript variant 1, mRNA.
RASSF1	ILMN_1683239	1.59	3.02	3.75×10^{-3}	3p21.31b	*Homo sapiens* Ras association (RalGDS/AF-6) domain family member 1 (RASSF1), transcript variant C, mRNA.
EIF2AK2	ILMN_1706502	1.59	3.02	6.22×10^{-6}	2p22.2b	*Homo sapiens* eukaryotic translation initiation factor 2-alpha kinase 2 (EIF2AK2), mRNA.
EIF5	ILMN_2318430	1.59	3.01	2.09×10^{-3}	14q32.32b	*Homo sapiens* eukaryotic translation initiation factor 5 (EIF5), transcript variant 1, mRNA.
PMAIP1	ILMN_1689525	1.59	3.01	2.75×10^{-3}	18q21.32b	*Homo sapiens* phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA.
MARCH4	ILMN_1789991	1.59	3.00	4.59×10^{-5}	2q35b-q35c	*Homo sapiens* membrane-associated ring finger (C3HC4) 4 (MARCH4), mRNA.
DHRS9	ILMN_2384181	1.59	3.00	6.83×10^{-3}	2q31.1a	*Homo sapiens* dehydrogenase/reductase (SDR family) member 9 (DHRS9), transcript variant 1, mRNA.
LOC654174	ILMN_1696946	1.59	3.00	4.51×10^{-4}		PREDICTED: *Homo sapiens* similar to lethal (2) k00619 CG4775-PA (LOC654174), mRNA.
FNIP2	ILMN_3237329	-1.59	0.33	4.29×10^{-2}	4q32.1e	*Homo sapiens* folliculin interacting protein 2 (FNIP2), mRNA.
CSTF2T	ILMN_1807515	-1.60	0.33	5.15×10^{-3}	10q11.23c	*Homo sapiens* cleavage stimulation factor, 3'pre-RNA, subunit 2, 64kDa, tau variant (CSTF2T), mRNA.
CLDN3	ILMN_1723042	-1.62	0.32	1.14×10^{-2}	7q11.23b	*Homo sapiens* claudin 3 (CLDN3), mRNA.
C14ORF73	ILMN_1773017	-1.63	0.32	2.59×10^{-3}	14q32.32b	*Homo sapiens* chromosome 14 open reading frame 73 (C14orf73), mRNA.
SPATA17	ILMN_1686096	-1.63	0.32	8.18×10^{-3}	1q41b-q41c	*Homo sapiens* spermatogenesis associated 17 (SPATA17), mRNA.
CHAC1	ILMN_1739241	-1.63	0.32	3.63×10^{-3}	15q15.1b	*Homo sapiens* ChaC, cation transport regulator homolog 1 (E. coli) (CHAC1), mRNA.
ZADH2	ILMN_1795063	-1.63	0.32	3.61×10^{-3}	18q22.3d	*Homo sapiens* zinc binding alcohol dehydrogenase domain containing 2 (ZADH2), mRNA.
FLJ14712	ILMN_1699275	-1.65	0.32	4.72×10^{-4}	7p21.3a	PREDICTED: *Homo sapiens* hypothetical protein FLJ14712 (FLJ14712), mRNA.
NAV1	ILMN_1703374	-1.65	0.32	1.28×10^{-2}	1q32.1c	*Homo sapiens* neuron navigator 1 (NAV1), mRNA.
LOC643772	ILMN_1725327	-1.67	0.32	4.20×10^{-3}		PREDICTED: *Homo sapiens* similar to Contactin-associated protein-like 3 precursor (Cell recognition molecule Caspr3) (LOC643772), mRNA.
KIAA1333	ILMN_1680643	-1.67	0.31	1.33×10^{-3}	14q12d	*Homo sapiens* KIAA1333 (KIAA1333), mRNA.
LOC541469	ILMN_1702797	-1.68	0.31	8.46×10^{-4}	19q13.2a	*Homo sapiens* hypothetical protein LOC541469 (LOC541469), mRNA.
GAS2L3	ILMN_2211003	-1.68	0.31	1.77×10^{-2}	12q23.1d	*Homo sapiens* growth arrest-specific 2 like 3 (GAS2L3), mRNA.
KRT4	ILMN_1744765	-1.69	0.31	5.14×10^{-4}	12q13.13d	*Homo sapiens* keratin 4 (KRT4), mRNA.
SCARA5	ILMN_1751062	-1.72	0.30	5.51×10^{-4}	8p21.1e-p21.1d	*Homo sapiens* scavenger receptor class A, member 5 (putative) (SCARA5), mRNA.
FSIP1	ILMN_1716925	-1.72	0.30	6.94×10^{-3}	15q14d	*Homo sapiens* fibrous sheath interacting protein 1 (FSIP1), mRNA.
REEP1	ILMN_1733746	-1.72	0.30	1.28×10^{-2}	2p11.2f	*Homo sapiens* receptor accessory protein 1 (REEP1), mRNA.
LOC113230	ILMN_1803673	-1.73	0.30	1.12×10^{-2}	19p13.12c	PREDICTED: *Homo sapiens* hypothetical protein LOC113230 (LOC113230), mRNA.
GLS	ILMN_2188722	-1.74	0.30	9.29×10^{-6}	2q32.2b	*Homo sapiens* glutaminase (GLS), mRNA.
C9ORF100	ILMN_1681221	-1.74	0.30	6.54×10^{-3}	9p13.3a	*Homo sapiens* chromosome 9 open reading frame 100 (C9orf100), transcript variant 2, mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
HS.258266	ILMN_1879857	-1.75	0.30	4.15x10^{-3}		K-EST0220612 L18POOL1n1 *Homo sapiens* cDNA clone L18POOL1n1-33-F12 5, mRNA sequence
KIAA0232	ILMN_1795704	-1.76	0.30	9.91x10^{-3}	4p16.1e	*Homo sapiens* KIAA0232 (KIAA0232), transcript variant 1, mRNA.
FLJ10324	ILMN_2098297	-1.76	0.30	1.41x10^{-2}	7p22.1d	*Homo sapiens* hypothetical protein FLJ10324 (FLJ10324), mRNA.
KRT222	ILMN_1801090	-1.77	0.29	1.32x10^{-3}	17q21.2a	*Homo sapiens* keratin 222 (KRT222), mRNA.
CRYGS	ILMN_1792597	-1.78	0.29	9.13x10^{-3}	3q27.3a	*Homo sapiens* crystallin, γ S (CRYGS), mRNA.
SLC1A4	ILMN_1656904	-1.79	0.29	7.90x10^{-3}	2p14c	*Homo sapiens* solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4), mRNA.
TENC1	ILMN_1685042	-1.79	0.29	5.55x10^{-3}	12q13.13e	*Homo sapiens* tensin like C1 domain containing phosphatase (tensin 2) (TENC1), tran script variant 1, mRNA.
TRAIP	ILMN_1715540	-1.79	0.29	6.53x10^{-3}	3p21.31c	*Homo sapiens* TRAF interacting protein (TRAIP), mRNA.
CAMKV	ILMN_1667381	-1.80	0.29	7.76x10^{-5}	3p21.31c	*Homo sapiens* CaM kinase-like vesicle-associated (CAMKV), mRNA.
S1PR5	ILMN_2073184	-1.80	0.29	5.02x10^{-3}	19p13.2b	*Homo sapiens* sphingosine-1-phosphate receptor 5 (S1PR5), mRNA.
C21ORF58	ILMN_2310296	-1.80	0.29	5.05x10^{-3}	21q22.3f	*Homo sapiens* chromosome 21 open reading frame 58 (C21orf58), transcript variant 2, mRNA.
CD44	ILMN_1778625	-1.81	0.29	2.46x10^{-2}	11p13b	*Homo sapiens* CD44 molecule (Indian blood group) (CD44), transcript variant 1, mRNA.
RAB26	ILMN_1790317	-1.81	0.28	1.06x10^{-5}	16p13.3d	*Homo sapiens* RAB26, member RAS oncogene family (RAB26), mRNA.
FRAS1	ILMN_1671318	-1.82	0.28	1.93x10^{-4}	4q21.1c-q21.21a	*Homo sapiens* Fraser syndrome 1 (FRAS1), transcript variant 2, mRNA.
GPRIN2	ILMN_3241501	-1.83	0.28	3.77x10^{-3}	10q11.22a	*Homo sapiens* G protein regulated inducer of neurite outgrowth 2 (GPRIN2), mRNA.
TJP3	ILMN_1659610	-1.83	0.28	3.86x10^{-4}	19p13.3e	*Homo sapiens* tight junction protein 3 (zona occludens 3) (TJP3), mRNA.
C9ORF100	ILMN_1667405	-1.84	0.28	2.35x10^{-2}	9p13.3a	*Homo sapiens* chromosome 9 open reading frame 100 (C9orf100), mRNA.
LOC442132	ILMN_1782116	-1.87	0.27	3.81x10^{-2}	5p15.31b	PREDICTED: *Homo sapiens* similar to hypothetical protein FLJ36144 (LOC442132), mRNA.
SFT2D3	ILMN_1765746	-1.87	0.27	6.68x10^{-4}	2q14.3e	*Homo sapiens* SFT2 domain containing 3 (SFT2D3), mRNA.
MAP2K6	ILMN_1697729	-1.87	0.27	2.68x10^{-2}	17q24.3a	*Homo sapiens* mitogen-activated protein kinase kinase 6 (MAP2K6), mRNA.
CCDC28B	ILMN_1778478	-1.88	0.27	2.34x10^{-2}	1p35.1b	*Homo sapiens* coiled-coil domain containing 28B (CCDC28B), mRNA.
SCARNA9	ILMN_1805064	-1.88	0.27	1.12x10^{-3}	11q21a	*Homo sapiens* small Cajal body-specific RNA 9 (SCARNA9), guide RNA.
USP9X	ILMN_2400583	-1.89	0.27	5.96x10^{-4}	Xp11.4b	*Homo sapiens* ubiquitin specific peptidase 9, X-linked (USP9X), transcript variant 3, mRNA.
MAPT	ILMN_2310814	-1.91	0.27	2.41x10^{-4}	17q21.31e	*Homo sapiens* microtubule-associated protein tau (MAPT), transcript variant 4, mRNA.
TC2N	ILMN_1734596	-1.92	0.26	1.23x10^{-2}	14q32.12a	*Homo sapiens* tandem C2 domains, nuclear (TC2N), mRNA.
FBXO43	ILMN_2344907	-1.93	0.26	6.80x10^{-3}	8q22.2b	*Homo sapiens* F-box protein 43 (FBXO43), transcript variant 2, mRNA.
LOC642333	ILMN_1696027	-1.93	0.26	3.87x10^{-2}		PREDICTED: *Homo sapiens* similar to M-phase phosphoprotein, mpp8 (LOC642333), mRNA.
KRT18P19	ILMN_3267748	-2.00	0.25	1.36x10^{-2}	2q32.2a	PREDICTED: *Homo sapiens* misc_RNA (KRT18P19), miscRNA.
SULT2B1	ILMN_1763520	-2.01	0.25	5.01 x10^{-4}	19q13.32c	*Homo sapiens* sulfotransferase family, cytosolic, 2B, member 1 (SULT2B1), transcript variant 2, mRNA.

Table SI. Continued.

Gene	Probe_ID	log2(SEMA5A/ CTL)	SEMA5A/ CTL	P-value	Cytoband	Definition
SLC22A3	ILMN_2048477	-2.03	0.25	$4.34\text{x}10^{-4}$	6q25.3f	*Homo sapiens* solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA.
C14ORF105	ILMN_2083789	-2.13	0.23	$1.04\text{x}10^{-2}$	14q23.1a	*Homo sapiens* chromosome 14 open reading frame 105 (C14orf105), mRNA.
TMEM107	ILMN_2413330	-2.13	0.23	$1.44\ \text{x}10^{-3}$	17p13.1c	*Homo sapiens* transmembrane protein 107 (TMEM107), transcript variant 1, mRNA.
MXD3	ILMN_1711904	-2.13	0.23	$2.96\text{x}10^{-5}$	5q35.3a	*Homo sapiens* MAX dimerization protein 3 (MXD3), mRNA.
DTX3	ILMN_1658677	-2.64	0.16	$1.13\text{x}10^{-3}$	12q13.3b	*Homo sapiens* deltex homolog 3 (Drosophila) (DTX3), mRNA.

Table SII. Molecular functions of differentially expression genes.

Category	P-value	No. of molecules	Molecules
Cell signaling	8.21×10^{-24}-1.83×10^{-3}	45	*SOCS1, GBP1, IL5, MX1, RSAD2, IFI16, IFNB1, LGALS9, TNFAIP3, TNFSF10, CX3CR1, IL6, CCL5, NGF, OASL, IFIT1, GADD45A, SPHK1, CASP1, PPM1A, TLR3, STAT1, TRIM5, ADRB2, PLSCR1, CXCL8, OAS1, PARP10, CNP, ZC3HAV1, OAS3, KLF4, BST2, ISG15, CARD9, IFITM3, MAPT, CD44, STAT2, IFIT5, TRIM22, EIF2AK2, TRIM25, ISG20, IFITM1*
Gene expression	3.64×10^{-15}-2.24×10^{-3}	81	*MED13, SOCS1, IL32, LMO2, IFI16, FNIP2, IL6, IFIH1, CXCL10, EIF5, FOSL1, PPM1A, LHX3, RFX3, IFNL2, KLF11, CXCL8, FST, ATF3, ZC3HAV1, IRF9, CREB5, KLF4, MAFF, BST2, IRF1, IKZF5, FOSB, NLRC5, IRF7, MAPT, DDX58, BTG2, RARRES3, STAT2, TRIM22, IRF8, IFNL1, EREG,* mir-21, *MAP2K6, IL5, DDIT3, MX1, VAPA, IFNB1, ABL1, TNFAIP3, TNFSF10, LGALS9, DDX60L, NGF, PARP9, SP100, LAMP3, IFI27, JUN, HERC5, MXD1, CASP1, TLR3, STAT1, IRF2, RASSF1, PLSCR1, PARP14, DHX58, OAS1, BATF2, HIPK3, MYD88, PARP10, EGR1, MDM2, NR1D2, APOL3, ZEB2, CD44, DTX3L, EIF2AK2, GATA3*
Cell death and survival	6.76×10^{-15}-2.63×10^{-3}	100	*SOCS1, TRAIP, LMO2, IL6, CXCL10, IFIH1, PPM1A, FOSL1, SERPINE1, IFNL2, IFIT3, TNFRSF9, TRIM21, IRF1, AEN, CARD9, BTG2, PPP1R15A, VTRNA2-1, IFNL1, IFIT2,* mir-21, *MAP2K6, USP18, SLC22A3, GBP1, DDIT3, MX1, IFNB1, TNFSF10, LGALS9, CCL5, IFI27, JUN, GADD45A, MXD1, IFI6, TLR3, IRF2, TRAF1, PMAIP1, OAS1, MYD88, EGR1, MDM2, REV3L, OAS3, SULT2B1, ISG15, LTA, XAF1, CD44, TRIM25, CLDN3, VPS13A, IFI16, ZNF79, IL32, TYMP, CX3CR1, UBA7, HLA-F, CEACAM1, KLF11, CXCL8, ATF3, FST, USP36, UBQLNL, IRF9, TNFRSF10D, KLF4, FOSB, NT5C3A, IRF7, MAPT, DDX58, IDO1, STAT2, IRF8, EREG, IL12A, IL5, VAPA, ABL1, TNFAIP3, NGF, CASP1, SPHK1, CFB, STAT1, RASSF1, PARP14, PLSCR1, HIPK3, GLS, TRIM69, TNS2, CYP2J2, EIF2AK2*
Cellular growth and proliferation	5.45×10^{-10}-2.35×10^{-3}	87	*SOCS1, TRAIP, IFI16, CCL20, IL6, IFIH1, CXCL10, SP110, AJUBA, EIF5, FOSL1, BTN3A1, SERPINE1, IFNL2, KLF11, CEACAM1, CXCL8, TNFRSF9, ATF3, TRIM21, FST, USP36, KLF4, IRF1, FOSB, NT5C3A, IFITM3, IRF7, SAMD9L, MAPT, PPP1R15A, BTG2, DDX58, RARRES3, IDO1, STAT2, TRIM22, IFNL1, IRF8, EREG,* mir-21, *MORC3, SPTBN1, MAP2K6, IFNL3, USP18, GEM, IL12A, DDIT3, IL5, GBP1, VAPA, ABL1, IFNB1, LGALS9, TNFAIP3, TNFSF10, CCL5, NGF, JUN, ARRDC3, GADD45A, MXD1, CASP1, SPHK1, STAT1, IRF2, RASSF1, BATF2, TXNIP, MYD88, EGR1, GLS, PARP10, MDM2, OAS3, ISG15, SULT2B1, TNS2, EXOC8, LTA, ZEB2, CD44, CYP2J2, EIF2AK2, GATA3, ISG20*
Cellular development	6.25×10^{-10}-2.35×10^{-3}	87	*SOCS1, TRAIP, IFI16, IL32, CCL20, IL6, PSMB8, CXCL10, SP110, AJUBA, EIF5, FOSL1, BTN3A1, SERPINE1, RFX3, IFNL2, KLF11, CEACAM1, CXCL8, TNFRSF9, FST, ATF3, TRIM21, USP36, KLF4, IRF1, FOSB, NT5C3A, IFITM3, IRF7, SAMD9L, MAPT, DDX58, BTG2, IDO1, RARRES3, STAT2, IRF8, IFNL1, EREG,* mir-21, *IFITM1, MORC3, MAP2K6, USP18, IFNL3, GEM, IL12A, DDIT3, GBP1, IL5, VAPA, ABL1, IFNB1, LGALS9, TNFAIP3, TNFSF10, CCL5, NGF, ARRDC3, JUN, GADD45A, CASP1, SPHK1, STAT1, IRF2, RASSF1, PLSCR1, BATF2, TXNIP, MYD88, EGR1, GLS, PARP10, MDM2, OAS3, ISG15, SULT2B1, TNS2, EXOC8, LTA, ZEB2, CD44, CYP2J2, EIF2AK2, GATA3, ISG20*