

Supplemental material Table II. Genes downregulated after stimulation with SEI and SEB.

Gene Symbol ^a	Gene Title	NCBI Accession No	probe set ID	SEI		SEB	
				mean fold change ^b	FDR	mean fold change ^b	FDR
HEY1 ^c	hairy/enhancer-of-split related with YRPW motif 1	NM_012258	218839_at	-6.2	< 0.0001	-3.9	0.0015
ST3GAL6 ^c	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	AI989567	213355_at	-6.1	< 0.0001	-4.2	0.0005
CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	206336_at	-5.7	< 0.0001	-4.8	0.0010
NT5DC2	5'-nucleotidase domain containing 2	NM_022908	218051_s_at	-5.6	< 0.0001	-2.6	0.0490
MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	BC001875	223723_at	-5.3	< 0.0001	-3.7	0.0036
VCAN ^c	versican	BF590263	204619_s_at	-4.6	0.0001	-5.2	0.0003
---	Transcribed locus	AI494347	240393_at	-4.5	0.0003	-2.6	0.0413
NOG	Noggin	AL575177	231798_at	-4.5	0.0002	-2.6	0.0413
HNMT ^c	histamine N-methyltransferase	BC005907	211732_x_at	-4.2	0.0006	-3.2	0.0093
LOC285181	hypothetical protein LOC285181	AA002166	1561334_at	-4.1	0.0005	-2.9	0.0212
OLIG1	oligodendrocyte transcription factor 1	AL355743	228170_at	-3.9	0.0002	-3.8	0.0021
TFPI	Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AL080215	215447_at	-3.8	0.0011	-3.2	0.0092
C5AR1	complement component 5a receptor 1	NM_001736	220088_at	-3.8	0.0012	-2.7	0.0418
---	---	AA805633	230175_s_at	-3.7	0.0011	-2.8	0.0326
SIGLEC9	sialic acid binding Ig-like lectin 9	AF247180	210569_s_at	-3.7	0.0011	-3.1	0.0136
KCNE3	potassium voltage-gated channel, Isk-related family, member 3	AI692703	227647_at	-3.7	0.0012	-4.2	0.0005
---	MRNA; cDNA DKFZp313E1515 (from clone DKFZp313E1515)	AL833097	1560034_a_at	-3.7	0.0017	-2.3	0.1028
VNN1 ^c	vanin 1	BG120535	1558549_s_at	-3.6	0.0008	-3.4	0.0073
STON2	stonin 2	AA632295	227461_at	-3.6	0.0011	-2.4	0.0806
TIMP2 ^c	TIMP metalloproteinase inhibitor 2	BE968786	231579_s_at	-3.6	0.0015	-2.5	0.0600
EPHA4 ^c	EPH receptor A4	T15545	228948_at	-3.5	0.0015	-2.8	0.0297
---	MRNA full length insert cDNA clone EUROIMAGE 85905	AL080280	1559910_at	-3.5	0.0016	-2.1	0.1945
RNASEH2C	ribonuclease H2, subunit C	AI990526	227543_at	-3.5	0.0024	-1.3	0.8072
CXCL2	chemokine (C-X-C motif) ligand 2	BC005276	1569203_at	-3.3	0.0031	-2.2	0.1344
C4orf18	chromosome 4 open reading frame 18	AF260333	223204_at	-3.3	0.0025	-4.0	0.0016
OLIG2	oligodendrocyte lineage transcription factor 2	AA757419	213825_at	-3.3	0.0017	-2.8	0.0263
---	Transcribed locus	BF724178	229613_at	-3.3	0.0015	-1.5	0.6611
SLC16A6 ^c	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	AI873273	230748_at	-3.3	0.0029	-2.5	0.0483
---	Homo sapiens, clone IMAGE:4105785, mRNA	BC016361	1558871_at	-3.2	0.0064	-2.9	0.0293
EREG	epiregulin	BC035806	1569583_at	-3.2	0.0064	-2.4	0.0777
HAS1	hyaluronan synthase 1	NM_001523	207316_at	-3.2	0.0064	-4.7	0.0021
DOCK5 ^{cd}	dedicator of cytokinesis 5	BF447954	230263_s_at	-3.2	0.0052	-2.1	0.1649
FPRL2 ^c	formyl peptide receptor-like 2	AW026543	230422_at	-3.1	0.0061	-3.6	0.0025
CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1	NM_000784	203979_at	-3.1	0.0051	-2.6	0.0575
HECTD1	HECT domain containing 1	BC016947	1570251_at	-3.0	0.0084	-2.1	0.1259
FLJ46446	Hypothetical gene supported by AK128305	CA425190	1556402_at	-3.0	0.0060	-2.0	0.1950
---	---	AI694722	242397_at	-3.0	0.0064	-2.9	0.0290
PLK2	polo-like kinase 2 (Drosophila)	NM_006622	201939_at	-3.0	0.0060	-2.4	0.0770
ZFP36L2 ^c	zinc finger protein 36, C3H type-like 2	AI356398	201367_s_at	-3.0	0.0096	-3.0	0.0173
---	Transcribed locus	AI401017	244874_at	-3.0	0.0068	-1.7	0.4029
SPON1	spondin 1, extracellular matrix protein	AI885290	213993_at	-3.0	0.0073	-1.4	0.8303
TXLNB	taxilin beta	AL589605	227834_at	-3.0	0.0074	-2.2	0.1358

TNS1 ^c	tensin 1	AF116610	218864_at	-3.0	0.0073	-2.7	0.0317
FUCA1	fucosidase, alpha-L- 1, tissue	NM_000147	202838_at	-3.0	0.0109	-2.4	0.0781
CD14	CD14 molecule	NM_000591	201743_at	-3.0	0.0085	-2.6	0.0475
SULT1A3 /// SULT1A4	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /// sulfotransferase family, cytosolic, 1A, phenol-preferring, member 4	AI580112	222094_at	-3.0	0.0073	-1.3	0.7235
SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	W90718	243969_at	-2.9	0.0114	-1.9	0.1951
NPL	N-acetylneuraminase pyruvate lyase (dihydrodipicolinate synthase)	AI368358	240440_at	-2.9	0.0074	-2.9	0.0214
PER1	period homolog 1 (Drosophila)	NM_002616	202861_at	-2.9	0.0061	-2.2	0.1059
C20orf117	chromosome 20 open reading frame 117	NM_015377	207711_at	-2.9	0.0122	-2.9	0.0282
LOC440934 ^c	Hypothetical gene supported by BC008048	AW473883	244159_at	-2.9	0.0094	-2.4	0.0848
ETV5 ^c	ets variant gene 5 (ets-related molecule)	NM_004454	203349_s_at	-2.9	0.0099	-2.6	0.0607
CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	NM_005211	203104_at	-2.9	0.0104	-2.8	0.0324
IGSF2	immunoglobulin superfamily, member 2	NM_004258	207167_at	-2.9	0.0159	-2.1	0.2000
C5orf29	chromosome 5 open reading frame 29	NM_152687	1552386_at	-2.8	0.0114	-2.3	0.1080
PLD1	phospholipase D1, phosphatidylcholine- specific	AA132961	232530_at	-2.8	0.0098	-1.9	0.2779
---	Transcribed locus	AA573201	240099_at	-2.8	0.0132	-1.8	0.3658
ZBTB1	zinc finger and BTB domain containing 1	NM_014950	205092_x_at	-2.8	0.0103	-1.9	0.2764
TNFRSF8	tumor necrosis factor receptor superfamily, member 8	NM_001243	206729_at	-2.8	0.0052	-2.1	0.1582
PNKD	paroxysmal nonkinesigenic dyskinesia	AB033010	233177_s_at	-2.8	0.0158	-2.8	0.0319
LOC387763	hypothetical LOC387763	AW276078	227099_s_at	-2.7	0.0159	-2.4	0.0750
---	---	AI832594	244605_at	-2.7	0.0256	-1.2	0.9150
---	CDNA clone IMAGE:5787947	BC039553	1559544_s_at	-2.7	0.0251	-1.8	0.3998
TMEM45B	transmembrane protein 45B	AW242836	230323_s_at	-2.7	0.0135	-2.2	0.1381
VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	NM_016830	207100_s_at	-2.7	0.0200	-1.6	0.4263
YPEL2	yippee-like 2 (Drosophila)	AK097253	1556420_s_at	-2.7	0.0156	-1.4	0.6977
PASK	PAS domain containing serine/threonine kinase	U79240	216945_x_at	-2.7	0.0248	-1.9	0.2779
TTL4	tubulin tyrosine ligase-like family, member 4	NM_014640	203703_s_at	-2.6	0.0218	-2.2	0.1415
---	---	H94882	242936_at	-2.6	0.0269	-2.2	0.1587
DOK3	docking protein 3	BC004564	223553_s_at	-2.6	0.0217	-2.5	0.0520
FCAR	Fc fragment of IgA, receptor for	U56237	211306_s_at	-2.6	0.0209	-2.3	0.0894
RAB7B	RAB7B, member RAS oncogene family	AY094596	1553982_a_at	-2.6	0.0217	-1.7	0.4212
LDLRAP1	low density lipoprotein receptor adaptor protein 1	AL545035	221790_s_at	-2.6	0.0288	-1.5	0.5919
HHEX	hematopoietically expressed homeobox	Z21533	215933_s_at	-2.6	0.0359	-2.1	0.1948
LY9 ^{cd}	lymphocyte antigen 9	AL582804	215967_s_at	-2.6	0.0252	-2.3	0.0971
TFPI2	tissue factor pathway inhibitor 2	AL574096	209277_at	-2.6	0.0330	-1.8	0.2785
NR5A2	nuclear receptor subfamily 5, group A, member 2	AF228413	210174_at	-2.6	0.0381	-2.1	0.1491
ZNF587	zinc finger protein 587	AK055448	1558251_a_at	-2.5	0.0311	-2.0	0.2417
C20orf112	chromosome 20 open reading frame 112	AL034550	230954_at	-2.5	0.0344	-2.7	0.0422
NMT2	N-myristoyltransferase 2	AL134489	215743_at	-2.5	0.0381	-1.9	0.2999
INSR	insulin receptor	AA485908	213792_s_at	-2.5	0.0286	-2.3	0.0982
---	CDNA FLJ12187 fis, clone MAMMA1000831	AA572675	232286_at	-2.5	0.0266	-2.1	0.1412
RGS2	regulator of G-protein signaling 2, 24kDa	NM_002923	202388_at	-2.5	0.0331	-2.2	0.1164

SLC22A15	solute carrier family 22 (organic cation transporter), member 15	AI279062	228497_at	-2.5	0.0381	-1.5	0.6454
CXCR7	chemokine (C-X-C motif) receptor 7	AI817041	212977_at	-2.5	0.0356	-2.5	0.0715
PTGFRN	prostaglandin F2 receptor negative regulator	BF311866	224937_at	-2.5	0.0286	-2.0	0.1772
CXCL5	chemokine (C-X-C motif) ligand 5	BG166705	215101_s_at	-2.5	0.0378	-2.4	0.0911
---	MRNA; cDNA DKFZp666P238 (from clone DKFZp666P238)	AL833038	1563597_at	-2.5	0.0286	-1.4	0.7700
---	Homo sapiens, clone IMAGE:5205388, mRNA	AW303397	229040_at	-2.5	0.0361	-1.5	0.5746
---	Transcribed locus	AI733470	240821_at	-2.5	0.0358	-1.2	0.9783
GLCE	glucuronic acid epimerase	W87398	213552_at	-2.5	0.0392	-1.5	0.5754
---	CDNA clone IMAGE:4544718	BC014231	1570607_at	-2.5	0.0347	-1.5	0.5624
HOM-TES-103	hypothetical protein LOC25900	BC002857	209721_s_at	-2.5	0.0395	-2.3	0.1110
---	Mir-223 transcript variant 1 mRNA, complete sequence	N39230	229934_at	-2.4	0.0390	-1.7	0.4093
TPST1	tyrosylprotein sulfotransferase 1	NM_003596	204140_at	-2.4	0.0420	-3.3	0.0298
CXCL3	chemokine (C-X-C motif) ligand 3	NM_002090	207850_at	-2.4	0.0388	-1.8	0.3705
SPIRE1	spire homolog 1 (Drosophila)	BC016825	1554807_a_at	-2.4	0.0415	-1.4	0.7458
PTCH1	patched homolog 1 (Drosophila)	BG054916	209815_at	-2.4	0.0396	-2.3	0.1031
---	Transcribed locus	AA416756	244677_at	-2.4	0.0425	-1.6	0.4845
CD244	CD244 molecule, natural killer cell receptor 2B4	NM_016382	220307_at	-2.4	0.0424	-1.7	0.3877
FRAT2	frequently rearranged in advanced T-cell lymphomas 2	AB045118	209864_at	-2.4	0.0387	-2.7	0.0312
ARRDC2	arrestin domain containing 2	AK000689	226055_at	-2.4	0.0423	-2.2	0.1087
IRS2	insulin receptor substrate 2	AF073310	209185_s_at	-2.4	0.0491	-2.1	0.1671
---	---	AA808178	235743_at	-2.4	0.0395	-1.5	0.5252
SIGLEC10	sialic acid binding Ig-like lectin 10	AF301007	1552807_a_at	-2.2	0.0705	-2.8	0.0421
LY9 ^{cd}	lymphocyte antigen 9	AF244129	210370_s_at	-2.2	0.0794	-2.9	0.0186
GAS2L3	Growth arrest-specific 2 like 3	AI860012	238756_at	-2.2	0.0799	-2.7	0.0460
KLHL24	kelch-like 24 (Drosophila)	AI961401	242088_at	-2.1	0.0911	-2.7	0.0415
DOCK5 ^{cd}	dedicator of cytokinesis 5	AK024569	222721_at	-2.1	0.1225	-2.6	0.0454
---	---	AW024087	239284_at	-2.0	0.0461	1.1	1.0232
SIGLEC5	sialic acid binding Ig-like lectin 5	NM_003830	220000_at	-2.0	0.1785	-3.4	0.0036
---	Transcribed locus	AW016812	231644_at	-2.0	0.1629	-2.8	0.0303
MEGF9	multiple EGF-like-domains 9	BF110421	212831_at	-1.8	0.2279	-2.7	0.0329
HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	NM_005114	205466_s_at	-1.8	0.2294	-2.7	0.0414
---	CDNA FLJ34016 fis, clone FCBBF2002541	AI935334	235385_at	-1.8	0.2627	-2.6	0.0481
C1orf21	chromosome 1 open reading frame 21	NM_030806	221272_s_at	-1.7	0.2910	-2.9	0.0145
PDLIM7	PDZ and LIM domain 7 (enigma)	BC023629	1569149_at	-1.7	0.2875	-2.7	0.0309
SFRS11	Splicing factor, arginine/serine-rich 11	T90915	236948_x_at	-1.6	0.4361	-2.6	0.0449
DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	NM_020664	219664_s_at	-1.5	0.3851	-3.0	0.0221
ARRB1	arrestin, beta 1	NM_004041	218832_x_at	-1.5	0.4429	-3.4	0.0042
CCPG1	cell cycle progression 1	AK022459	222156_x_at	-1.5	0.4797	-2.6	0.0454
LOC286254	hypothetical protein LOC286254	AI471954	1559765_a_at	-1.5	0.4694	-2.6	0.0485
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	AF225513	223551_at	-1.4	0.5512	-2.8	0.0309
---	Transcribed locus	AI935541	236220_at	-1.4	0.4052	-3.0	0.0153
TTC3	tetratricopeptide repeat domain 3	BC026260	1569472_s_at	-1.3	0.7176	-2.6	0.0431
FANK1	fibronectin type III and ankyrin repeat domains 1	AU143929	232968_at	-1.3	0.7818	-2.7	0.0419
SOCS4	suppressor of cytokine signaling 4	NM_080867	1552792_at	-1.2	0.8851	-2.9	0.0227
PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	NM_017990	220236_at	-1.2	0.8907	-2.6	0.0468
ARHGAP24	Rho GTPase activating protein 24	AI743534	223422_s_at	-1.2	0.9224	-3.3	0.0042

MVD	mevalonate (diphospho) decarboxylase	AI189359	203027_s_at	-1.1	0.9687	-2.6	0.0429
BPI	bactericidal/permeability-increasing protein	NM_001725	205557_at	-1.1	0.9984	-2.6	0.0465

^aAll downregulated genes with an FDR less than 0.05 with at least one of the stimuli.

^bMean fold change of three blood donors.

^cGene represented by more than one probe set. The probe set with significant changes following both stimuli is shown. If none fulfilled this criterion, the probe set showing the highest fold change was selected.

^dGene represented by two probe sets, which are both included in this table.

Gene expression of human PBMC analyzed after 6 h stimulation with SEI and SEB. The vast majority of genes was influenced to a similar extend by SEI and SEB.