Supplementary Table I. AcP-dependent responses in reconstituted cortical neurons

ProbeSet_ID	GeneName	Description	Accession#	Category	AcP FC	error%	AcP+AcPb FC	error%
1419209_at	Cxcl1	chemokine	NM_008176	chemokine	100.0	2%	74.6	13%
1418930_at	Cxcl10	chemokine	NM_021274	chemokine	89.0	6%	67.3	10%
1457644_s_at	Cxcl1	chemokine	NM_008176	chemokine	24.6	7%	17.2	7%
1420380_at	Ccl2	chemokine	NM_011333	chemokine	14.1	19%	13.6	14%
1449984_at	Cxcl2	chemokine	NM_009140	chemokine	13.6	21%	12.7	29%
1419728_at	Cxcl5	chemokine	NM_009141	chemokine	10.0	27%	8.8	22%
1421228_at	Ccl7	chemokine	NM_013654	chemokine	7.5	43%	3.2	33%
1418240_at	Gbp2	G-binding protein	NM_010260	signaling	36.8	13%	38.5	22%
1435906_x_at	Gbp2	G-binding protein	NM_010260	signaling	36.8	16%	26.2	26%
1417483_at	Nfkbiz	NFkB inhibitor, zeta	NM_030612	signaling	11.8	6%	7.7	10%
1448728_a_at	Nfkbiz	NFkB inhibitor, zeta	NM_030612	signaling	8.3	17%	5.9	29%
1419647_a_at	Ier3	anti-apoptotic target of NFKB	NM_133662	signaling	6.6	10%	3.6	9%
1418392_a_at	Gbp3	G-binding protein	NM_018734	signaling	4.5	13%	2.7	12%
1449773_s_at	Gadd45b	anti-apoptotic target of NFKB	NM_008655	signaling	3.9	7%	2.9	9%
1425156_at	Gbp6	G-binding protein	NM_145545	signaling	3.6	16%	3.3	19%
1450173_at	Ripk2	TNFRSF-interacting serine-threonine kinase	NM_138952	signaling	3.5	7%	2.9	6%
1450971_at	Gadd45b	anti-apoptotic target of NFKB	NM_008655	signaling	3.4	14%	3.2	16%
1434380_at	Gbp6	G-binding protein	NM_145545	signaling	3.4	9%	3.0	13%
1455899_x_at	Socs3	suppressor of cytokine signaling	NM_007707	signaling	3.2	10%	2.2	12%
1456212_x_at	Socs3	suppressor of cytokine signaling	NM_007707	signaling	3.2	24%	2.3	17%
1458299_s_at	Nfkbie	NFkB inhibitor, epsilon	NM_008690	signaling	3.0	9%	3.5	17%

1449731_s_at	Nfkbia	NFkB inhibitor, alpha	NM_010907	signaling	2.8	4%	2.0	4%
1418825_at	Irgm	immunity-related GTPase family, M	NM_008326	signaling	2.7	10%	1.8	7%
1431843_a_at	Nfkbie	NFkB inhibitor, epsilon	NM_008690	signaling	2.2	16%	1.6	17%
1421236_at	Ripk2	TNFRSF-interacting serine-threonine kinase 2	NM_138952	signaling	2.2	10%	3.2	14%
1418571_at	Tnfrsf12a	TNF receptor superfamily	NM_013749	cytokine or receptor	39.3	50%	1.9	29%
1418572_x_at	Tnfrsf12a	TNF receptor superfamily	NM_013749	cytokine or receptor	18.7	59%	2.1	31%
1421207_at	Lif	cytokine	NM_001039537	cytokine or receptor	8.4	37%	2.4	54%
1419132_at	Tlr2	toll-like receptor 2	NM_011905	cytokine or receptor	5.2	13%	5.0	14%
1438658_a_at	Edg3	S1P receptor	NM_010101	cytokine or receptor	4.7	5%	2.5	10%
1437173_at	Edg3	S1P receptor	NM_010101	cytokine or receptor	4.5	9%	2.4	12%
1452483_a_at	Cd44	CD44 antigen	NM_001039150	cytokine or receptor	3.5	12%	1.1	14%
1460251_at	Fas	TNF receptor superfamily	NM_007987	cytokine or receptor	3.5	27%	2.3	22%
1460220_a_at	Csf1	cytokine	NM_007778	cytokine or receptor	3.3	9%	2.4	12%
1460661_at	Edg3	S1P receptor	NM_010101	cytokine or receptor	3.2	22%	3.0	21%
1418674_at	Osmr	oncostatin M receptor	NM_011019	cytokine or receptor	2.6	9%	1.0	10%
1425107_a_at	Lifr	LIF receptor	NM_013584	cytokine or receptor	2.1	22%	1.2	21%
1449363_at	Atf3	transcription factor	NM_007498	gene regulation	22.4	37%	3.8	19%
1423233_at	Cebpd	transcription factor	NM_007679	gene regulation	12.7	9%	4.1	14%
1427682_a_at	Egr2	transcription factor	NM_010118	gene regulation	8.8	14%	8.1	13%

1427683_at	Egr2	transcription factor	NM_010118	gene regulation	8.1	10%	6.5	9%
1456605_at	Cebpd	transcription factor	NM_007679	gene regulation	4.9	12%	3.2	21%
1416564_at	Sox7	transcription factor	NM_011446	gene regulation	3.4	21%	1.8	17%
1451755_a_at	Apobec1	RNA editing enzyme	NM_031159	gene regulation	3.2	7%	1.8	12%
1427844_a_at	Cebpb	transcription factor	NM_009883	gene regulation	3.1	27%	2.5	12%
1423100_at	Fos	transcription factor	NM_010234	gene regulation	2.9	7%	1.5	7%
1418901_at	Cebpb	transcription factor	NM_009883	gene regulation	2.6	6%	1.9	6%
1432979_at	Gatad2b	transcription factor	NM_139304	gene regulation	2.1	21%	0.9	29%
1448734_at	Cp	ceruloplasmin	NM_001042611	enzyme	10.1	14%	2.5	22%
1449152_at	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	NM_007670	enzyme	6.9	47%	1.9	31%
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	NM_001044384	enzyme	3.6	14%	1.5	22%
1417494_a_at	Cp	ceruloplasmin	NM_001042611	enzyme	3.0	7%	2.4	21%
1451537_at	Chi3l1	chitinase 3-like 1	NM_007695	enzyme	3.0	22%	2.2	19%
1455393_at	Cp	ceruloplasmin	NM_001042611	enzyme	2.9	29%	2.1	31%
1450716_at	Adamts1	a disintegrin-like and metallopeptidase	NM_009621	enzyme	2.8	6%	1.8	6%
1418678_at	Has2	hyaluronan synthase 2	NM_008216	enzyme	2.6	14%	2.3	16%
1417496_at	Cp	ceruloplasmin	NM_001042611	enzyme	2.4	26%	1.4	29%
1417495_x_at	Cp	ceruloplasmin	NM_001042611	enzyme	2.3	22%	1.6	16%
1460197_a_at	Steap4	STEAP family member 4	NM_054098	other	81.2	10%	84.4	10%
1438855_x_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	NM_009396	other	56.6	9%	32.5	16%
1426784_at	Trim47	tripartite motif protein 47	NM_172570	other	25.3	26%	2.4	24%
1427747_a_at	Lcn2	lipocalin 2	NM_008491	other	18.1	31%	7.7	14%

1424067_at	Icam1	intercellular adhesion molecule	NM_010493	other	15.2	24%	3.8	14%
1418666_at	Ptx3	pentraxin related gene	NM_008987	other	11.7	9%	11.9	13%
1421321_a_at	Net1	neuroepithelial cell transforming gene 1	NM_001047159	other	2.9	7%	1.4	12%

The ProbeSet_ID is the unique Affymetrix identifier for the sequences on the array, where there can be more than one probe set per gene. The AcP fold change (FC) and AcP+AcPb FC values are the fold change as a result of IL-1 stimulation, evaluated from ratios built between triplicate samples. The error % is the mean log error in the ratio, where the error model allows only a maximum 100-fold change.

SupplementaryTable II. AcPb-dependent responses are also induced in AcP cultures

ProbeSet_ID	GeneName	Accession#	AcP FC	AcP p-val	AcP+AcPb FC	AcP+AcPb p-val	AcPb FC	AcPb p-val
1435508_x_at	0610009D07Rik	NM_025323	1.25	4.3E-01	2.02	4.6E-06	1.99	2.7E-11
1437452_x_at	Vdac1	NM_011694	1.5	5.0E-02	1.86	5.0E-05	1.9	2.6E-04
1420042_at	Thoc1	NM_153552	1.3	6.0E-02	1.97	1.3E-04	1.88	7.3E-06
1441788_s_at	BC068171	NM_001030307	1.16	1.1E-01	1.26	3.9E-04	1.42	6.5E-14
1453245_at	9130024F11Rik	XM_978942	1.2	1.0E-01	1.29	2.4E-04	1.38	4.7E-04
1433733_a_at	Cry1	NM_007771	1.26	6.0E-02	1.47	1.1E-04	1.36	4.0E-07
1428224_at	Hnrpdl	NM_016690	1.12	2.7E-01	1.27	1.5E-04	1.34	8.3E-07
1433453_a_at	Abtb2	NM_178890	1.13	3.0E-02	1.32	1.1E-04	1.31	8.5E-09
1452063_at	2410081M15Rik	NM_028603	1.15	3.0E-02	1.21	8.5E-04	1.27	6.4E-04
1454793_x_at	Ddx5	NM_007840	1.06	4.5E-01	1.21	9.1E-04	1.26	2.7E-05
1438487_s_at	Zzz3	NM_198416	1.15	9.0E-02	1.18	6.0E-04	1.25	1.1E-04
1433960_at	Isg20l2	NM_177663	1.21	2.0E-02	1.22	1.1E-04	1.25	3.7E-04
1443524_x_at	Bcl10	NM_009740	1.17	1.8E-04	1.19	8.9E-04	1.24	1.5E-04
1451641_at	Dbr1	NM_031403	1.14	1.4E-01	1.18	6.1E-04	1.23	1.1E-10

1417930_at	Nab2	NM_008668	1.35	8.9E-05	1.34	7.4E-05	1.23	3.0E-03
1433771_at	5730446C15Rik	NM_146096	1.04	6.5E-01	1.12	1.8E-04	1.21	2.3E-04
1420840_at	Plekha3	NM_031256	1.19	1.0E-02	1.15	1.7E-04	1.2	2.6E-05
1425562_s_at	Trnt1	NM_027296	1.11	1.0E-01	1.19	3.1E-04	1.2	2.3E-04
1454136_a_at	4921524J17Rik	NM_025722	1.07	1.4E-01	1.17	1.8E-06	1.2	8.3E-09
1436566_at	Rab40b	NM_139147	1.15	8.0E-02	1.11	5.4E-04	1.18	2.6E-04
1426964_at	3110003A17Rik	XM_125510	1.12	4.0E-02	1.18	1.5E-07	1.18	3.5E-04
1452534_a_at	Hmgb2	NM_008252	1.13	1.2E-01	1.32	7.4E-06	1.18	1.2E-04
1415908_at	Tspyl1	NM_009433	1.05	3.0E-01	1.15	4.9E-04	1.18	1.6E-04
1417625_s_at	Cxcr7	NM_007722	1.23	7.5E-04	1.28	1.7E-05	1.17	5.2E-07
1455557_at	LOC553095	BB751199	1.14	5.0E-02	1.27	1.9E-04	1.17	9.3E-05
1436759_x_at	Cnn3	NM_028044	1.24	1.7E-09	1.29	6.5E-04	1.16	6.3E-07
1420537_at	Kctd4	NM_026214	1.05	3.1E-01	1.18	2.4E-04	1.16	9.1E-05
1416499_a_at	Dctn6	NM_011722	1.07	2.1E-01	1.14	1.1E-04	1.16	1.4E-04
1455643_s_at	Tsr1	NM_177325	1.07	1.7E-01	1.19	8.7E-05	1.16	5.7E-04
1438171_x_at	Mettl9	NM_021554	1.09	1.0E-01	1.22	6.2E-04	1.14	2.5E-04
1437009_a_at	Zfp364	NM_026406	1.04	3.3E-01	1.17	3.6E-04	1.14	6.2E-07
1425460_at	Mtmr2	NM_023858	1.05	2.4E-01	1.17	8.2E-04	1.13	1.3E-04
1419655_at	Tle3	NM_009389	1.2	1.9E-03	1.12	8.3E-04	1.12	6.3E-06
1455959_s_at	1455959_s_at	AW825835	1.09	4.0E-02	1.15	7.5E-04	1.12	3.7E-05
1423130_a_at	Sfrs5	NM_001079694	1.16	1.2E-01	1.11	1.2E-04	1.12	5.6E-05
1433883_at	Tpm4	NM_001001491	1.08	1.9E-01	1.14	1.2E-04	1.1	1.1E-04
1448694_at	Jun	NM_010591	1.27	3.3E-04	1.29	7.1E-05	1.08	3.5E-01
1417968_a_at	Mbd1	NM_013594	1.18	3.7E-05	1.17	3.4E-06	1.07	2.0E-01
1426994_at	Phlpp	XM_129968	0.89	3.3E-04	0.89	1.9E-04	0.99	7.8E-01
1423740_a_at	Rbm10	NM_145627	0.84	9.8E-05	0.9	1.6E-04	0.97	5.4E-01
1452366_at	4732435N03Rik	NM_172753	0.85	6.3E-04	0.87	2.2E-05	0.95	7.0E-02
1436876_at	Rgs7bp	NM_029879	0.92	7.0E-02	0.87	2.1E-05	0.9	8.6E-04
1419286_s_at	Ift81	NM_009879	0.89	5.0E-02	0.89	8.2E-04	0.89	3.7E-05
1417115_at	Map3k12	NM_009582	0.92	1.3E-01	0.89	1.6E-04	0.89	9.1E-04
1457412_at	Scn8a	NM_001077499	0.87	4.1E-04	0.85	4.1E-04	0.89	2.5E-03
1449465_at	Reln	NM_011261	0.88	1.6E-03	0.8	6.7E-05	0.88	6.6E-04

1427019_at	Ptprz1	XM_620293	0.89	1.1E-01	0.83	1.0E-04	0.88	4.1E-04
1417403_at	Elovl6	NM_130450	0.89	3.8E-03	0.87	4.1E-05	0.85	2.6E-04
1434530_at	Odz4	NM_011858	0.82	1.5E-03	0.79	6.6E-04	0.84	6.9E-06
1428204_at	C030002O17Rik	NM_172432	0.9	1.6E-01	0.85	6.4E-04	0.84	3.6E-04
1429240_at	Stard4	NM_133774	0.83	3.0E-06	0.85	2.8E-07	0.83	2.1E-03
1423626_at	Dst	NM_010081	0.84	1.3E-03	0.8	5.4E-06	0.83	7.0E-16
1433857_at	Fat1	XM_885736	0.81	1.1E-04	0.83	4.2E-04	0.83	1.5E-03
1442095_at	Asxl3	XM_140204	0.93	2.7E-01	0.89	5.4E-04	0.82	4.3E-07
1438207_at	Gbf1	NM_178930	0.86	1.0E-01	0.8	3.4E-04	0.82	2.4E-06
1426491_at	Herc2	NM_010418	0.86	3.0E-02	0.8	6.8E-04	0.8	2.4E-06
1455373_at	1455373_at	BE650990	0.72	3.0E-02	0.78	4.3E-04	0.8	4.3E-04
1419392_at	Pclo	NM_011995	0.76	3.2E-07	0.79	8.0E-04	0.79	5.4E-06
1439815_at	A230048G03Rik	XM_283480	0.87	2.0E-02	0.81	2.7E-05	0.79	8.7E-09
1440970_at	1440970_at	BM218863	0.83	3.6E-04	0.72	3.1E-05	0.74	1.9E-04
1460574_at	Fat4	NM_183221	0.82	4.2E-04	0.72	2.4E-04	0.74	8.7E-06
1448663_s_at	Mvd	NM_138656	0.86	7.8E-03	0.86	6.5E-05	0.73	7.4E-05
1428443_a_at	Rap1gap	XM_149500	0.89	1.9E-01	0.79	5.3E-05	0.66	2.9E-05

Columns are as in Supplementary Table I, with the p-values being the Resolver estimates for the changes occurring by chance, uncorrected for multiple testing. The probe sets were selected for having p–values less than 0.001 in either the AcPb-only or AcP+AcPb ratios.