Supplemental table 1

Cytokines protein and mRNA abundance in mice 16 hours after exposure to LPS

Cytokine	S360A+LPS (pg/ml)[a,c]	Relative Intensity (GeneChip Value)[b,c]	5A-aPC+LPS (pg/ml)[a,c]	Relative Intensity (GeneChip Value)[b,c]
IL-1a	408.1 ± 101.46	3.59 ± 0.05	779.76 ± 166.66 **	3.73 ± 0.17
IL-1b	2002.09 ± 236.97	9.71 ± 0.01	2441.66 ± 527.77	10.14 ± 0.01
IL-2	ND	2.66 ± 0.25	ND	2.75 ± 0.51
IL-3	3.25 ± 0.41	2.52 ± 0.11	4.05 ± 2.47	2.55 ± 0.12
IL-4	ND	2.81 ± 0.04	ND	2.98 ± 0.14
IL-5	ND	2.87 ± 0.04	ND	2.87 ± 0.05
IL-6	1682.7 ± 651.57	8.66 ± 0.13	1586.36 ± 672.29	8.79 ± 0.14
IL-9	489.62 ± 113.47	5.09 ± 0.29	517.63 ± 142.02	4.95 ± 0.22
IL-10	58.83 ± 13.14	4.49 ± 0.35	156.39 ± 53.88 **	4.63 ± 0.24
IL-12p40	7820.76 ± 1809.94	4.64 ± 0.09	10378.23 ± 1691.97	4.71 ± 0.09
IL-12p70	2062.08 ± 1114.22	6.36 ± 0.09	924.18 ± 547.48	5.43 ± 0.21
IL-13	125.89 ± 110.48	3.96 ± 0.11	433.01 ± 823.74	3.94 ± 0.11
IL-17	19.45 ± 4.55	3.76 ± 0.04	25.30 ± 4.89	3.84 ± 0.04
Eotaxin	1058.89 ± 1395.70	2.20 ± 0.11	5388.47 ± 1766.57 **	2.47 ± 0.21
G-CSF	4396.71 ± 631.31	3.55 ± 0.01	3820.44 ± 1062.35	3.84 ± 0.37
GM-CSF	31.01 ± 19.78	3.88 ± 0.04	67.57 ± 10.41 **	4.16 ± 0.71
IFNγ	40.59 ± 6.76	6.70 ± 0.33	69.57 ± 20.05 *	6.14 ± 0.74
KC	5998.81 ± 478.12	8.79 ± 0.06	6064.70 ± 678.59	8.85 ± 0.07
MCP-1	6416.40 ± 1606.08	5.09 ± 0.06	8827.74 ± 1232.02 *	5.54 ± 0.07
MIP-1α	2300.58 ± 293.50	9.88 ± 0.04	2773.84 ± 291.65	9.39 ± 0.13
MIP-1β	1404.79 ± 270.45	9.76 ± 0.21	1627.07 ± 249.67	9.47 ± 0.01
RANTES	1944.95 ± 153.78	12.77 ± 0.01	3897.17 ± 1540.56 *	12.76 ± 0.07
TNFα	42.71 ± 7.52	8.50 ± 0.07	43.09 ± 18.56	7.81 ± 0.02

[a.] Protein measurements are the mean of 5 mouse spleen samples run in duplicate. [b.] GeneChip measurements taken as the mean of the values from duplicate chips. [c.] Error is measured as standard deviation of the mean. **ND** means values were below the limit of detection within the range of the assay. * $p<0.05$; ** $p<0.01$. Significance was determined using non-paired *t* test.

Supplemental table 2

Cytokines protein and mRNA abundance in mice 3 hours after exposure to LPS

Cytokine	S360A+LPS (pg/ml)[a,c]	Relative Intensity (GeneChip Value)[b,c]	5A-aPC+LPS (pg/ml)[a,c]	Relative Intensity (GeneChip Value)[b,c]
IL-1a	22696.58 ± 9445.98	5.13 ± 1.39	26698.1 ± 8964.57	5.25 ± 0.17
IL-1b	36054.32 ± 14214.47	8.76 ± 1.32	34269.7 ± 5061.34	10.43 ± 0.85
IL-2	55.95 ± 12.94	2.69 ± 0.25	45.75 ± 4.17	2.38 ± 0.19
IL-3	128.04 ± 40.22	2.82 ± 0.49	145.96 ± 21.49	2.35 ± 0.08
IL-4	ND	2.77 ± 0.14	ND	2.68 ± 0.14
IL-5	277.38 ± 104.92	2.94 ± 0.15	309.64 ± 79.14	2.49 ± 0.12
IL-6	2515.46 ± 3738.14	8.28 ± 0.84	2976.90 ± 2482.86	8.39 ± 0.25
IL-9	9458.06 ± 1688.32	4.91 ± 0.18	9788 ± 1846.87	4.74 ± 0.41
IL-10	4340.12 ± 1280.70	4.05 ± 0.12	4699.58 ± 1554.67	4.05 ± 0.01
IL-12p40	20481.34 ± 4744.95	4.04 ± 0.42	21586.54 ± 3616.94	3.78 ± 0.07
IL-12p70	5085.96 ± 2711.66	4.48 ± 1.17	5687.60 ± 962.70	4.73 ± 1.15
IL-13	3311.08 ± 1071.42	3.78 ± 0.03	3252.12 ± 547.12	3.73 ± 0.07
IL-17	2715.34 ± 2999.83	3.98 ± 0.42	4003.48 ± 2710.07	3.90 ± 0.07
Eotaxin	31813.40 ± 12949.41	2.53 ± 0.31	29853.38 ± 12807.11	2.23 ± 0.12
G-CSF	462411± 218887	3.59 ± 0.01	571672 ± 172941	3.51 ± 0.16
GM-CSF	1400.84 ± 454.12	3.26 ± 0.11	1423.52 ± 586.35	3.63 ± 0.10
IFNγ	3074.54 ± 1967.87	7.81 ± 0.28	3625.48 ± 1535.17	8.83 ± 0.87
KC	126104 ± 59267	7.46 ± 0.15	144590 ± 41865	7.76 ± 0.67
MCP-1	80195.4 ± 41909.7	4.89 ± 0.29	99483.88 ± 29126.28	4.93 ± 0.05
MIP-1α	57031.14 ± 13002.14	7.57 ± 0.11	55944.28 ± 12601.61	7.80 ± 0.43
MIP-1β	13405.32 ± 6805.21	7.50 ± 0.61	14676.12 ± 4400.93	7.28 ± 0.18
RANTES	ND	13.51 ± 0.05	ND	13.41 ± 0.07
TNFα	13445.98 ± 3638.45	7.18 ± 0.40	14962.08 ± 2168.06	7.20 ± 0.06

[a.] Protein measurements are the mean of 5 mouse spleen samples run in duplicate. [b.] GeneChip measurements taken as the mean of the values from duplicate chips. [c.] Error is measured as standard deviation of the mean. **ND** means values were below the limit of detection within the range of the assay. No significant difference was measured in any of the samples.

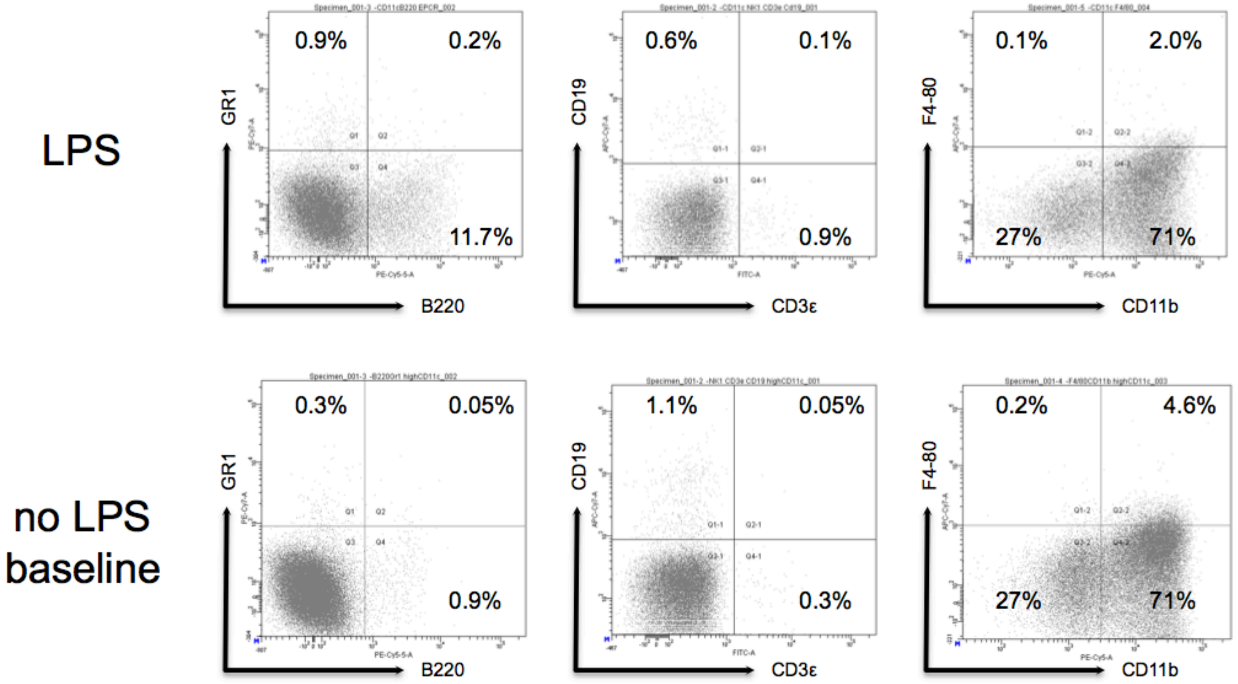
Supplemental Table 3

qRT-PCR performance parameters and primer sequences

Gene name	***UniGene***	***Slope***	***R2***	***E***	***Primer sequence***
Protein C receptor, endothelial	Mm.3243	-4.16	0.991	1.74	5’-CAACTCCAGGTCTGTCTGCCTAAG-3’ 5’-CCCAAGTCTATGGTCTGATTTCCAC-3’
Coagulation factor II receptor	Mm.24816	-3.91	00992	1.8	5’-GCTTCCACGAAAGTCCTATGGTTG-3’ 5’-GAGGGTGAACACAAAACAATGACG-3’
CD8 antigen, alpha chain	MM.1858	-4.43	0.996	1.68	5’-GCAGAGGGTGAGGTTTGACAGATAC-3’ 5’-GGTGCTAAGGAATGTTCTCCAAGG-3’
Lymphocyte antigen 75	mm.2074	-3.13	0.997	2.08	5’-AGACAATGAAACTCAGAACTCTG-3’ 5’-ATCTGGATCTTGTACAAAAATACTC-3’
S100 Calcium binding protein A8	mm.21567	-4.10	0.989	1.75	5’-CAAGGAAATCACCATGCCCTC-3’ 5’-CATCGCAAGGAACTCCTCGAAG-3
Neutrophilic granule protein	mm.236225	-1.61	0.997	4.16	5’-CCTCTTTACCTCCACTACCCATCTC-3’ 5’-CCCAGCAGAAGGAAGCAAATG-3’
Matrix metallopeptidase 8	mm.16415	-5.08	0.998	1.57	5’-CGCACCCTATGAGGACAAAAAG-3’ 5’-GGAATGCCAGATTACAAACGCTG-3’
Chitinase 3-like 3	mm.387173	-7.09	0.995	1.38	5’-TGGCTACACTGGAGAAAATAGTCCC-3’ 5’-GCTGGAAATCCCACAATGAGC-3’

Slope:	Slope of standard curve.
R2:	Linear regression of standard curve.
E:	Reaction efficiency, determined as previously described (71).

Supplemental Figure 1: Characterization of the CD11c *high* cell population: Splenocytes were pooled from 4 normal, unchallenged mice (“no LPS/baseline”) or from mice exposed to an LD50 of LPS (“LPS”), and selected on CD11c/PDCA-1 magnetic beads; live cells falling into the “CD11c-high/PDCA-1-low/negative” gate on a CD11c *versus* PDCA-1 scatter plot were selected by FACS and subsequently analyzed for surface expression of the indicated markers via flow cytometry. Gates for the indicated markers were selected conservatively (i.e. somewhat overestimating the fraction of cells expressing a given marker) based on control experiments with isotype matched non-immune antibody. Cells from LPS stimulated animals contain ~11% of $B220^{POS}$ cells corresponding to interferon-producing $NK1.1^{POS}$ “IK-CD” cells.



Supplemental Figure 2: Lack of EPCR-expression in CD11c/NK1.1 cells: **NK1.1-CD11c cells do not express EPCR. (a and b):** Splenocytes were collected from 4 wild type mice 14h after exposure to LPS, selected on CD11c/PDCA-1 magnetic beads, and analyzed via flow cytometry. Displayed is a scatter plot of live cells (gated for negative DAPI staining) by expression of CD11c *versus* PDCA-1. CD11c-positive cells in gate 2 (P2) were further characterized for expression of NK1.1 versus B220 in **(b). (c and d):** cells falling into gates P3 (NK1.1/B220 pos; figure d) and P4 (CD11c-positive/B220/NK1.1-negative; figure c) were analyzed for surface expression of EPCR. Solid line indicates reactivity with anti-EPCR AB; dotted line isotype matched non-immune AB. **(e and f):** cells in gate P2 of figure (a) were analyzed with anti-EPCR AB (e) or isotype-matched non-immune AB (f). EPCR-positive cells falling into gate P10 in (e) and (f) were analyzed for expression of NK1.1 and B220, as shown in (g) and (h), respectively.