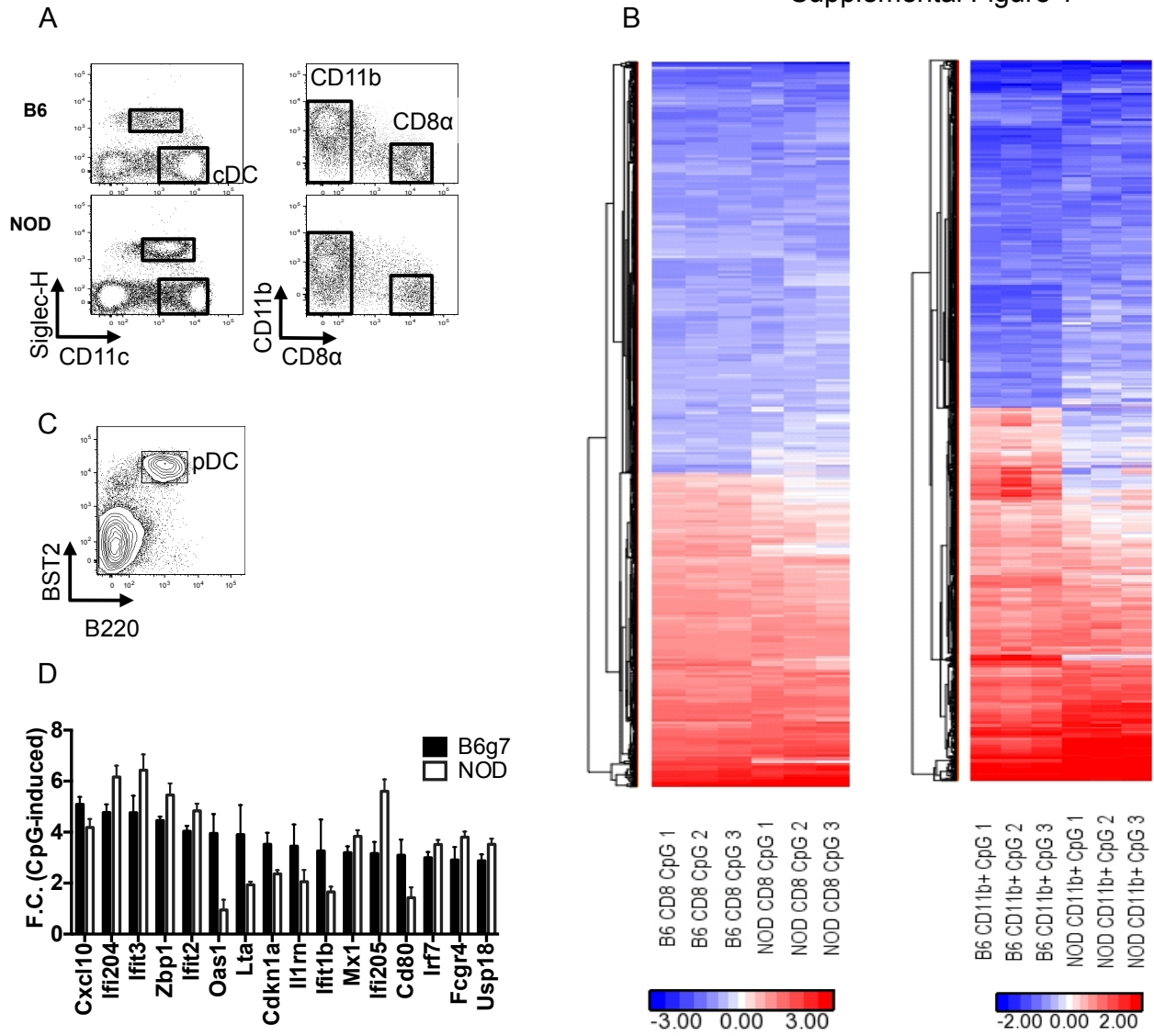


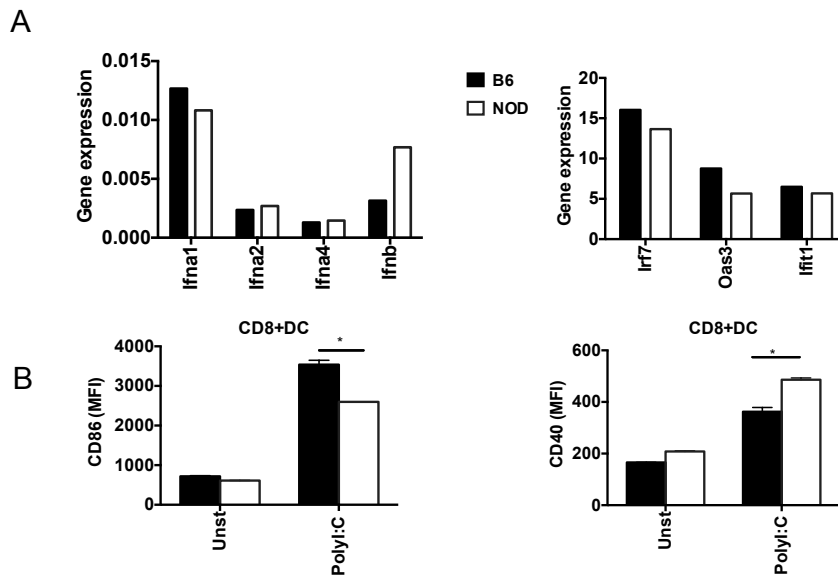
Supplemental Figure 1



Supplemental Figure 1: **Gene expression changes in DC subsets after CpG stimulation.**

(A) Sorting gate for data shown in Fig. 2. Lineage negative spleen cells (Aqua⁻, CD3⁻, CD19⁻, NKP46⁻ and Ly6c⁻) were gated for DC subset sorting. SiglecH⁻ CD11c⁺ cells were further gated for CD8⁺ cDC and CD11b⁺ cDC subset identification. (B) Heat map of DE genes was generated using microarray data for CD8⁺ cDC and CD11b⁺ cDC subsets. (C) Sorting gate for pDC data shown in D. From the lineage negative cells, CD11c⁺ cells were then gated for BST2⁺ B220⁺ as shown. (D) pDC data generated with a panel of 450 bar-coded probes run by NanoString technologies. The 25 genes with highest upregulation after CpG in the B6g7 strain were filtered for the 16 genes that were induced differently in NOD pDCs (p<0.05). Fold change with CpG of these 16 genes is shown; 9 were upregulated more in NOD.

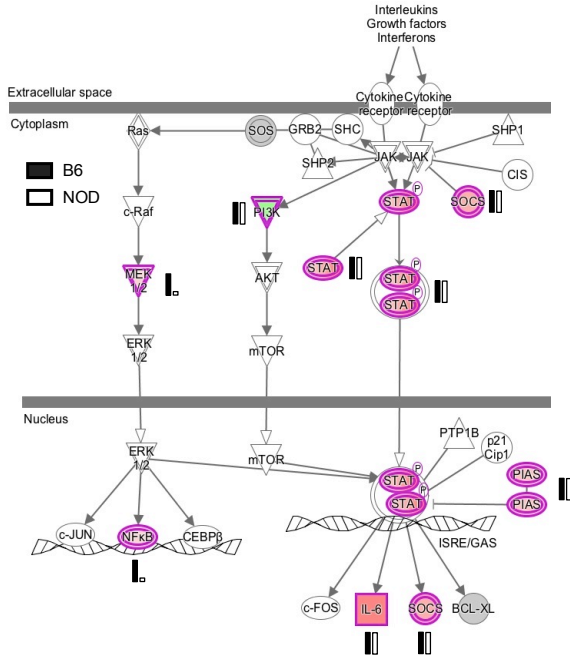
Supplemental Figure 2



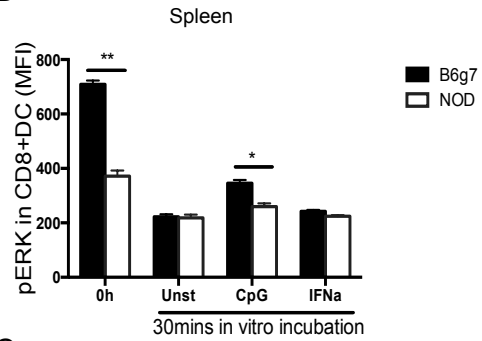
Supplemental Figure 2: **Muted response to Poly I:C in NOD DCs.** (A) CD11c⁺ spleen cells from NOD and B6 mice were analyzed after Poly I:C stimulation for 6 h by quantitative gene expression analysis for Type 1 IFN genes and IFN-response genes. (B) NOD or B6 mice were treated with Poly I:C i.v., for 6 h and spleen cells were stained for CD86 and CD40 and DC subset markers (CD8⁺ cDC, CD11b⁺ cDC and pDC subsets). Data presented here showed geometric mean MFI presented as one representative experiment from two experiments.

Supplemental Figure 3

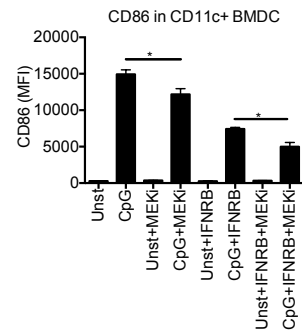
A



B



C



Supplemental Figure 3: **Differential activation of MEK1 after CpG stimulation.** (A) Pathway analysis of the cDC microarray data identifies differential MEK signal in NOD and B6 DCs, with more signal in B6 DCs after CpG stimulation. (B) Spleen cells from NOD or B6g7 mice were stimulated as indicated, and the level of phosphorylated ERK (pERK) was measured in CD8+ DCs by flow cytometry. (C) The MEK pathway inhibitor PD98059 was added as indicated to Flt3L BMDC cells from B6g7 mice and CD86 expression was measured by flow cytometry.

Supplemental Table 1: CpG-induced gene expression in pDCs

Gene ID	NOD pDC log ₂ -transformed values Gene differentially expressed with CpG (p<0.05 listed significant)				B6g7 pDC log ₂ -transformed values Gene differentially expressed with CpG (p<0.05 listed significant)					p-values (t-test)
	NOD-1	NOD-2	NOD-3	NOD-4	B6g7-1	B6g7-2	B6g7-3	B6g7-4	B6g7-5	
	Cxcl10	4.96	4.49	3.50	3.78	4.60	5.21	5.08	5.32	
Ifi204	7.11	6.74	5.31	5.49	4.82	5.22	4.85	4.59	4.35	0.014
Ifi3	7.59	7.16	4.79	6.18	4.16	4.63	4.13	5.44	5.48	0.035
Zbp1	6.31	6.16	4.60	4.76	4.50	4.67	4.49	4.29	4.33	0.042
Oas2	5.39	5.26	3.87	4.22	3.58	4.21	3.93	5.07	4.98	0.500
Ifi2	5.57	4.91	4.31	4.57	3.93	4.21	3.86	4.31	3.88	0.019
Tnf	4.22	3.26	2.96	3.37	5.04	4.88	4.89	2.69	2.28	0.511
Oas1	1.26	1.88	0.59	0.07	2.75	3.95	3.85	4.68	4.52	0.001
Lta	1.59	1.94	2.17	2.04	4.72	4.73	4.79	2.71	2.56	0.013
Cxcl9	5.80	4.88	3.55	3.23	3.75	3.92	4.01	3.66	3.68	0.326
Ifih1	5.39	4.79	3.90	3.77	3.75	4.30	3.86	3.05	3.06	0.089
Cdkn1a	2.31	2.06	2.77	2.33	3.14	4.12	3.60	3.74	3.00	0.003
Ifi1	4.50	4.23	3.33	4.14	2.95	3.42	2.94	4.19	3.92	0.163
Ilim	3.01	2.01	0.83	2.37	4.06	2.31	2.92	4.41	3.56	0.050
Ccl5	5.43	5.12	3.51	3.52	3.28	3.93	3.45	2.69	3.00	0.062
Ifihb	2.24	1.53	1.27	1.60	2.53	2.59	2.02	4.57	4.61	0.042
Gbp2	5.07	4.45	2.75	3.95	3.02	3.16	3.08	3.53	3.53	0.121
Mx1	4.38	4.11	3.49	3.35	3.21	3.56	3.28	2.98	2.95	0.038
Gpr33	2.63	2.54	2.36	2.38	3.18	3.82	3.53	3.14	2.23	0.056
Ifi205	6.58	6.20	4.98	4.65	3.18	3.77	3.16	3.21	2.50	0.001
Cd80	2.17	1.14	0.43	1.99	3.21	4.11	2.64	2.62	2.91	0.010
Caspa4	4.34	3.69	2.41	2.81	3.26	3.54	3.29	2.78	2.62	0.628
Ifi7	3.86	3.78	3.26	3.18	3.15	3.25	3.05	2.82	2.71	0.029
Fcgr4	4.21	3.87	3.18	3.96	2.74	2.13	3.30	3.41	2.97	0.028
Usp18	2.77	3.26	3.02	2.67	2.68	3.99	3.80	3.27	3.02	0.029