SUPPLEMENTARY MATERIAL

Supplementary Table I. Primers used for quantitative real-time PCR.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
Apitd1	TCTCTGCCAGGAAGTCACG	GAAAAGTCACCTCGGAGATCG
Ccdc21	GACAAGCAAAGGAAGCATATCTC	AGTGTTCTCTCGCTGCAACTC
Ccdc28b	CAATTCCATACAGAAGCTACACTTG	CACAGTTTGAAGAGGAGAGTAGCAG
Ephb2	CTGTCCTCTGGCATCAACCT	AAAGCTGGTGTAGTCCGGTATC
Lrp8	CTCCAGTGAAGAGTGTCCTGC	CACAGTCCTTCTCTCCGTCG
Mtor	ACAGATCCTGACCCTGATATGC	ATTCAGAGCCACAAACAGAGC
Padi2	AGCGACAAGGTCACTGTCAATACT	ATGCCTTCTTAGGATTGTTCTTCTC
Ptprf	AGCTGTGCCCTTCAAGATCC	CGCTACTGCCACGATTATC
Tceb3	GGTTCCAGTAGAGCGAAATAGTG	CCAGAGGGTTTCCAGCTTTC
Zfp69	CCAGAGGATCCCATTTTAGATGTG	CCTCGTGATGCCATGATCG
Hprt	CAATGCAAACTTTGCTTTCCC	AAATCCAACAAAGTCTGGCC

Supplementary Table II. Microarray probes detecting differentially expressed transcripts between NOD vs. NR4 B cells.

Probe	Gene	Chr: Position (bases)	NOD vs NR4 fold-change[a]	q-value (FDR)[b]
1449038_at	*Hsd11b1*	1:195047829-195068553	-2.41	8.73E-03
1442347_at	*Lrp8*	4:107547998-107549437	-2.13	3.68E-02
1420044_at	*Osbpl9*	4:108733579-108734079	2.49	2.24E-02
1420843_at	*Ptprf*	4:117880771-117964010	-1.58	4.08E-02
1458274_at	*Zfp69*	4:120602743-120603230	7.92	2.24E-02
1454913_at	*9930104L06Rik*	4:124621223-124621905	-2.60	3.58E-02
1459840_s_at	*Ccdc28b*	4:129296518-129296771	-7.36	1.91E-03
1454861_at	*Txlna*	4:129303323-129305534	-2.18	1.19E-02
1418630_at	*Khdrbs1*	4:129391062-129419549	-2.82	2.03E-02
1435982_at	*Stx12*	4:132409417-132410076	-2.14	4.46E-02
1442318_at	*Nudc*	4:133087684-133088210	7.33	2.03E-03
1432391_at	*Ccdc21*	4:133720120-133743000	-15.16	1.57E-06
1434117_at	*Tceb3*	4:135559282-135560774	1.72	2.95E-03
1454022_at	*Ephb2*	4:136325304-136391889	-2.53	3.93E-02
1418252_at	*Padi2*	4:140462258-140508501	3.51	2.03E-03
1448390_a_at	*Dhrs3*	4:144482695-144517545	9.41	2.24E-02
1436574_at	*1700029I01Rik*	4:145420139-146555866	-2.83	4.27E-03
1442183_at	*Gm13238*	4:145430789-146566430	-5.47	1.25E-03
1451477_at	*Gm13139*	4:145371445-146555000	3.91	2.94E-03
1446175_at	-	4:145425823-146561350	-9.38	4.41E-03
1428604_at	*2610305D13Rik*	4:146986045-147076644	38.06	5.08E-06
1424213_at	*Ubiad1*	4:147808603-147818888	1.45	4.15E-02
1451478_at	*Mtor*	4:147869291-147874571	2.41	1.26E-02
1453067_at	*Apitd1*	4:148502307-148511728	4.22	6.18E-03
1423994_at	*Kif1b*	4:148550427-148681740	2.27	4.79E-02
1424588_at	*Srgap3*	6:112667964-112670977	-13.16	1.55E-04
1445537_at	*2310039F13Rik*	6:112708194-112708767	-20.41	5.48E-04
1460442_at	*Rps19*	7:25669654-25674825	3.83	1.55E-04
1435703_at	*Ubash3b*	9:40819175-40820310	-1.54	3.58E-02
1448862_at	*Icam2*	11:106238969-106244292	14.94	1.02E-02
1417826_at	*Akr1e1*	13:4591735-4608407	-3.99	2.24E-02
1435088_at	*Nsd1*	13:55417742-55419687	-3.69	1.25E-03
1452452_at	-	Unmapped	-5.97	1.66E-03
1452426_x_at	-	Unmapped	-29.55	6.98E-06

[a] Mean fold-change (FC) in expression between five NOD and six NR4 B cell samples (combination of BCR-stimulated and unstimulated samples). Positive fold changes shown for probes where NOD>NR4, while negative fold changes denote probes where NR4>NOD.

[b] A FDR cutoff of $q<0.05$ was used to define differentially expressed transcripts between NOD and NR4 samples.

Supplementary Table III. Microarray probes detecting differentially expressed transcripts in BCR-stimulated vs. unstimulated B cells from NOD or NR4 strains only, or in both strains.

Probe	Gene	Chr: Position (b)	NOD FC (s vs. us)[a]	q-value[c]	NR4 FC (s vs. us)[b]	q-value[c]
1444878_at	-	1:80662178-80663151	2.52	8.89E-02		
1452666_a_at	*Tmcc2*	1:134252891-134287857	-2.01	5.24E-02		
1449363_at	*Atf3*	1:192994177-193007212	2.51	2.90E-02		
1449270_at	*Plxdc2*	2:16277917-16673950	2.24	7.08E-02		
1450749_a_at	*Nr4a2*	2:56959927-56967666	2.08	5.09E-02		
1450750_a_at	*Nr4a2*	2:56959927-56967666	2.49	8.08E-02		
1447863_s_at	*Nr4a2*	2:56960532-56960760	2.47	5.76E-02		
1432678_at	*Itgav*	2:83607291-83609658	2.44	7.20E-02		
1415874_at	*Spry1*	3:37538858-37543520	2.82	5.24E-02		
1416022_at	*Fabp5*	3:57331738-10016612	2.06	4.11E-02		
1436836_x_at	*Cnn3*	3:121160605-121161125	-2.16	3.34E-02		
1455570_x_at	*Cnn3*	3:121160772-121161113	-2.21	4.11E-02		
1417539_at	*Slc35a1*	4:34610505-34634676	-2.07	5.24E-02		
1429262_at	*Rassf6*	5:91032109-91060635	2.16	6.07E-02		
1446055_at	-	5:124915788-124916508	2.11	2.02E-02		
1454551_at	*9530034D02Rik*	6:31280626-31281731	2.40	2.02E-02		
1437671_x_at	*Prss23*	7:96657609-96657905	3.35	5.95E-02		
1431057_a_at	*Prss23*	7:96657618-96666049	2.19	4.51E-02		
1453547_at	*1810046K07Rik*	9:51097798-51137022	2.85	7.97E-02		
1444402_at	*Zc3h12c*	9:51920089-51920815	2.30	2.70E-02		
1457824_at	*Plscr1*	9:92147080-92147413	2.48	2.22E-02		
1440432_at	-	9:123621990-123622647	2.73	7.08E-02		
1438588_at	*Plagl1*	10:12835007-12835966	2.09	5.24E-02		
1430581_at	*Bclaf1*	10:20048836-20053697	2.49	4.92E-02		
1437992_x_at	*Gja1*	10:56110005-56110221	-2.59	2.22E-02		
1422708_at	*Pik3cg*	12:32857997-32893335	-2.01	2.02E-02		
1428851_at	*1300014I06Rik*	13:34719704-34758192	-2.31	4.11E-02		
1421477_at	*Cplx2*	13:54479945-54481604	-2.09	4.11E-02		
1436387_at	*Homer1*	13:94129653-94131011	2.02	4.08E-02		
1440573_at	*Erbb2ip*	13:104688064-104688764	2.67	7.11E-02		
1426156_at	*Lats2*	14:58341026-58353137	2.31	3.67E-02		
1443086_at	*Alcam*	16:52261222-52261845	-2.20	2.64E-02		
1440298_at	*Treml2*	17:48451176-48451863	-2.05	3.34E-02		
1444299_at	*A430093F15Rik*	19:10830372-10860533	2.07	8.73E-02		
1418248_at	*Gla*	X:131122894-131135505	2.13	4.95E-02		
1450330_at	*Il10*	1:132916423-132921547			3.19	2.82E-02
1428789_at	*Ralgps2*	1:158734296-158735895			-2.43	4.60E-02
1431704_a_at	*Ralgps2*	1:158743211-158869698			-2.12	4.16E-03
1457773_at	*Slamf6*	1:173882570-173883300			-2.74	2.90E-02
1454877_at	*Sertad4*	1:194670624-194677337			-3.12	3.97E-02
1426875_s_at	*Srxn1*	2:151935895-151937106			2.06	7.28E-02
1419942_at	*Npn3*	2:151936327-151936928			2.42	4.21E-02
1436480_at	*Dpp7*	2:25207809-25208394			2.12	4.21E-02
1416021_a_at	*Gm3601*	3:10012604-10016612			2.24	4.69E-02
1425454_a_at	*Il12a*	3:68495448-68502013			-2.56	2.90E-02
1449176_a_at	*Dck*	5:89194268-89212270			-2.06	2.02E-02
1448364_at	*Ccng2*	5:93696282-93705253			-2.19	3.68E-02
1458100_at	-	6:122538959-122539639			-2.10	4.67E-02
1419769_at	*Cd22*	7:31650847-31665288			-2.51	7.86E-02
1419768_at	*Cd22*	7:31650847-31665288			-2.18	8.19E-02
1443969_at	*Irs2*	8:10986976-11004939			2.04	2.90E-02

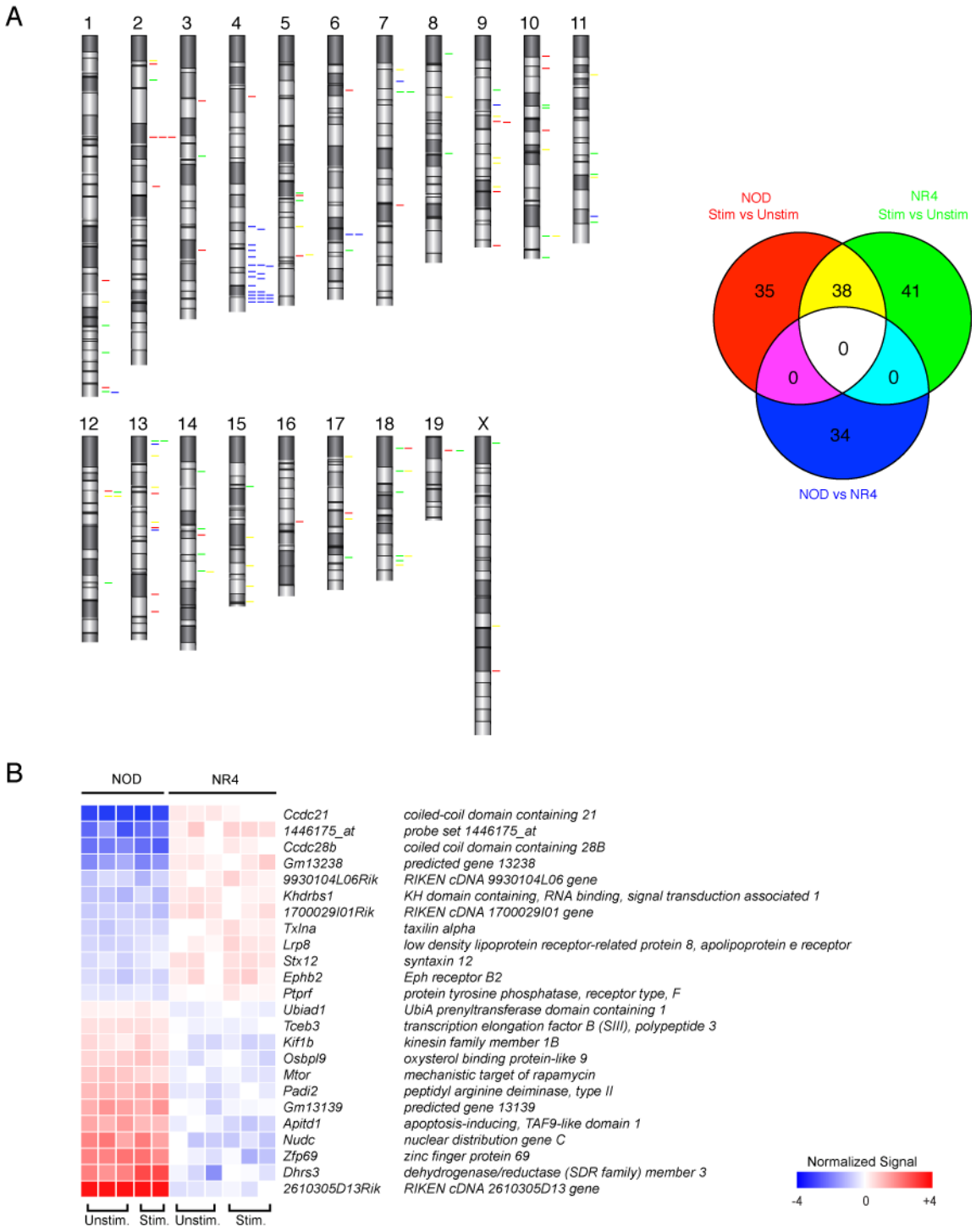
1434955_at	*March1*	8:68993022-68994332			-2.48	4.21E-02
1422027_a_at	*Ets1*	9:32503610-32562627			-2.02	2.90E-02
1440157_at	*Scml4*	10:42582798-42583132			-2.56	1.94E-02
1429413_at	*Cpm*	10:117066775-117122359			-4.08	7.04E-02
1457339_at	*Ccm2*	11:6446890-6496747			-2.02	1.94E-02
1418421_at	*Bcl6b*	11:70037628-70042674			2.70	1.94E-02
1423339_s_at	*Ccdc16*	11:82577846-82579757			-2.11	3.68E-02
1444376_at	*Sesn1*	10:41622229-41623046			-2.04	2.82E-02
1441482_at	-	11:110261063-110261748			-3.79	3.68E-02
1420342_at	*Gdap10*	12:33506736-33511770			2.20	2.02E-02
1450350_a_at	*Jdp2*	12:86940967-86980827			2.10	2.90E-02
1437221_at	*Rrm2b*	13:3352742-3353251			-2.00	9.01E-03
1437222_x_at	*Rrm2b*	13:3352742-3353251			-2.26	4.16E-03
1458206_at	*LOC218805*	14:21185185-21185948			-2.00	4.16E-03
1448860_at	*Rem2*	14:55094936-55099273			2.51	2.90E-02
1417750_a_at	*Slc25a37*	14:69859904-69903160			-2.04	4.31E-02
1442445_at	*2610027H17Rik*	14:79123667-79124134			2.71	2.90E-02
1453287_at	*Ankrd33b*	15:31253710-31297323			2.04	2.90E-02
1438030_at	*Rasgrp3*	17:75926335-75928391			-2.25	2.63E-02
1430143_at	*4930426D05Rik*	18:21810065-21814608			-2.59	2.90E-02
1421912_at	*Slc23a1*	18:35773951-35786881			-2.24	2.90E-02
1450188_s_at	*Lipg*	18:75099035-75120914			2.70	2.90E-02
1428114_at	*Slc14a1*	18:78296832-78298443			-4.47	2.90E-02
1418353_at	*Cd5*	19:10792632-10813464			-2.09	6.13E-02
1431106_a_at	*9530053H05Rik*	X:4789659-4791091			-2.12	1.94E-02
1442263_at	*Rgs13*	1:145985796-145986427	2.32	3.68E-02	2.27	5.80E-02
1417601_at	*Rgs1*	1:146091799-146096198	3.31	2.02E-02	2.79	1.94E-02
1442116_at	*Gm1012*	2:118102844-118103494	3.36	5.76E-02	5.80	4.21E-02
1453590_at	*Arl8*	2:14976908-14998230	2.78	3.34E-02	3.42	2.08E-02
1451680_at	*Srxn1*	2:151931260-151936197	2.58	7.97E-02	2.16	5.16E-02
1417679_at	*Gfi1*	5:108145672-108153363	2.25	2.02E-02	2.21	2.63E-02
1428207_at	*Bcl7a*	5:123794462-123824091	-2.55	2.02E-02	-3.20	1.90E-02
1422134_at	*Fosb*	7:19888045-19895100	2.55	5.76E-02	2.17	5.80E-02
1428834_at	*Dusp4*	8:35882847-35885006	2.98	8.31E-02	3.10	1.14E-02
1453220_at	*Fam55b*	9:48126088-48148943	-4.66	4.22E-02	-5.64	5.80E-03
1453360_a_at	*Tex9*	9:72308907-72339763	-2.14	8.73E-02	-2.02	5.86E-02
1429963_at	*Mapk6*	9:75256133-75257797	2.06	2.02E-02	2.04	3.08E-02
1419004_s_at	*Bcl2a1*	9:88618122-114239689	2.14	2.85E-02	2.23	4.80E-02
1427683_at	*Egr2*	10:67000625-67004935	2.57	2.02E-02	2.39	7.15E-03
1427682_a_at	*Egr2*	10:67000625-67004935	2.09	4.95E-02	2.22	4.16E-03
1453009_at	*Cpm*	10:117122298-117124401	-4.17	9.25E-02	-7.05	5.36E-02
1420710_at	*Rel*	11:23641516-23670970	2.2	3.34E-02	2.07	2.63E-02
1421578_at	*Ccl4*	11:83476088-83478182	3.51	4.95E-02	3.15	4.16E-03
1419561_at	*Ccl3*	11:83461344-83462880	4.11	4.95E-02	2.66	7.42E-02
1422631_at	*Ahr*	12:36182645-36219576	2.01	2.70E-02	2.05	1.94E-02
1450695_at	*Ahr*	12:36182645-36219576	2.18	4.95E-02	2.19	7.20E-02
1440162_x_at	*A630043P06*	13: 12569175-12612715	-3.11	9.04E-02	-3.08	3.44E-02
1437800_at	*Edaradd*	13:12569079-12569626	-4.52	4.95E-02	-6.63	3.71E-02
1421174_at	*Irf4*	13:30841126-30858850	2.64	3.34E-02	2.26	6.75E-03
1438658_a_at	*S1p3*	13:51517303-51517499	2.3	4.95E-02	2.24	1.03E-02
1438511_a_at	*1190002H23Rik*	14:79688553-79688817	2.66	4.95E-02	3.77	9.11E-02
1424942_a_at	*Myc*	15:61818976-61821802	3.09	4.46E-02	2.46	4.60E-02
1418936_at	*Maff*	15:79178119-79189504	3.59	4.95E-02	3.87	2.90E-02
1431394_a_at	*Lrrk2*	15:91610808-91646111	-2.43	3.34E-02	-4.43	1.14E-02
1416505_at	*Nr4a1*	15:101097281-101105230	2.72	4.95E-02	2.67	5.55E-02

1443553_at	-	17:52002007-52002542	-2.27	8.73E-02	-2.37	8.19E-02
1452408_at	*LOC547214*	17:7515626-13535099	2.47	7.08E-02	2.31	4.60E-02
1428837_at	*Klhl14*	18:21708879-21810583	-2.83	2.02E-02	-4.53	2.98E-02
1421262_at	*Lipg*	18:75099035-75120914	2.1	8.31E-02	3.56	2.90E-02
1447084_at	*Nfatc1*	18:80844173-80844704	2.16	4.95E-02	2.09	4.08E-02
1425761_a_at	*Nfatc1*	18:80845197-80909810	2.17	4.11E-02	2.01	2.82E-02
1441887_x_at	*Sh3bgrl*	X:106395423-106395710	2.82	2.02E-02	3.17	3.04E-02
1448595_a_at	*Bex1*	X:132748510-132749998	7.48	8.89E-02	3.17	9.91E-02

[a] Mean fold-change (FC) in expression between two BCR-stimulated (s) and three unstimulated (us) NOD B cell samples. Positive fold-changes are shown for probes where transcripts were greater in stimulated vs. non-stimulated B cells; while negative fold-changes denote the reverse.

[b] Mean fold-change in expression between three BCR-stimulated and three unstimulated NR4 B cell samples.

[c] A fold change ≥ 2 and FDR cutoff of $q<0.1$ was used to identify differentially expressed transcripts between BCR stimulated and unstimulated groups for each strain. Grey areas denote no significant changes ($q>0.1$) of gene expression in NOD or NR4 B cell groups.



SUPPLEMENTARY FIGURE 1. Genes from distal Chr. 4 conditions the genome such that B cells from NOD and NR4 mice exhibit a different genetic response to stimulation. (A) The Venn diagram on the right shows the number of probes that detected differentially expressed transcripts by one-way ANOVA (FDR, $q<0.05$) between NOD (n=5) vs. NR4 (n=6) B cell samples (dark blue); or ≥2-fold (FDR, $q<0.1$) between BCR-stimulated (stim.) vs. unstimulated (unstim.) NOD (red; n=2 and 3, respectively) or NR4 (green; n=3 and 3, respectively) B cell samples. Probes deemed significant in multiple tests are shown in overlapping segments. Lists of significant probes for each category are shown in Tables II-V. No probes exhibited significance via two-way ANOVA (FDR, $q<0.1$) comparing the interaction between strain and stimulation. The approximate chromosomal locations of differentially expressed probes, colored according to Venn diagram, are illustrated in the schematic diagram on the left. (B) Heat-map depicting the normalized signal of individual NOD and NR4 samples for differentially expressed genes on Chr. 4.