

Supplementary Information for

The MYCL and MXD1 transcription factors regulate the fitness of murine dendritic cells

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Gene Set	SIZE	NES	p-val	q-val
GO_RIBOSOME_BIOGENESIS	247	2.03	0.00	0.03
GO_RRNA_METABOLIC_PROCESS	203	2.02	0.00	0.02
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	98	2.02	0.00	0.01
GO_TRANSLATIONAL_INITIATION	122	1.99	0.00	0.02
GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	17	1.95	0.00	0.03
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	351	1.94	0.00	0.02
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	40	1.91	0.00	0.03
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	41	1.90	0.00	0.03
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	38	1.89	0.00	0.03
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	30	1.88	0.00	0.04
GO_NCRNA_PROCESSING	312	1.86	0.00	0.04
GO_MATURATION_OF_SSU_RRNA	31	1.86	0.00	0.04
GO_RNA_CATABOLIC_PROCESS	195	1.85	0.00	0.04
GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	44	1.85	0.00	0.04
GO_MATURATION_OF_5_8S_RRNA	25	1.85	0.00	0.04
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	85	1.84	0.00	0.04
GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	98	1.83	0.00	0.05
GO_NCRNA_METABOLIC_PROCESS	441	1.80	0.00	0.06
GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	15	1.79	0.00	0.07
GO_POSITIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	29	1.79	0.00	0.07
GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	24	1.78	0.00	0.07
GO_NCRNA_CATABOLIC_PROCESS	18	1.77	0.00	0.08
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	18	1.76	0.00	0.08
GO_CYTOPLASMIC_TRANSLATION	34	1.76	0.00	0.08
GO_MULTI_ORGANISM_METABOLIC_PROCESS	113	1.75	0.00	0.09
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	44	1.75	0.00	0.09
GO_OXIDATIVE_PHOSPHORYLATION	71	1.74	0.00	0.09
GO_REGULATION_OF_TRANSLATIONAL_ELONGATION	19	1.74	0.00	0.09
GO_EPITHELIAL_STRUCTURE_MAINTENANCE	18	1.73	0.01	0.10
GO_NEGATIVE_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	16	1.73	0.00	0.09
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	58	1.73	0.00	0.09
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	47	1.72	0.00	0.10
GO_CELLULAR_RESPIRATION	123	1.72	0.00	0.11
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	162	1.71	0.00	0.11
GO_REGULATION_OF_MRNA_METABOLIC_PROCESS	98	1.71	0.00	0.11
GO_RNA_SECONDARY_STRUCTURE_UNWINDING	38	1.71	0.00	0.11
GO_AMIDE_BIOSYNTHETIC_PROCESS	425	1.70	0.00	0.11
GO_TRNA_MODIFICATION	49	1.70	0.00	0.11
GO_RIBOSOME_ASSEMBLY	46	1.70	0.00	0.11
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	24	1.69	0.00	0.12
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	216	1.69	0.00	0.11
GO_NEGATIVE_REGULATION_OF_MRNA_METABOLIC_PROCESS	28	1.69	0.00	0.12
GO_RNA_MODIFICATION	93	1.69	0.00	0.12
GO_HISTONE_MONOUBIQUITINATION	18	1.69	0.01	0.12
GO_CALCIIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	17	-1.71	0.00	0.13
GO_CELLULAR_DEFENSE_RESPONSE	36	-1.79	0.00	0.09
GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	31	-1.82	0.00	0.07
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	25	-2.14	0.00	0.01
GO_MEMBRANE_RAFT_ORGANIZATION	16	-2.21	0.00	0.01
GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	21	-2.42	0.00	0.00

Table S1. GO-based GSEA results for expression microarray experiment on splenic cDC1s isolated at steady state from *Mycl*^{+/+} and *Mycl*^{gfp/gfp} mice. The top 50 gene sets are reported and their ranked normalized enrichment scores.

Gene Set	SIZE	NES	p-val	q-val
GO_RRNA_METABOLIC_PROCESS	203	2.62	0.00	0.00
GO_RIBOSOME_BIOGENESIS	247	2.56	0.00	0.00
GO_TRANSLATIONAL_INITIATION	122	2.47	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	351	2.45	0.00	0.00
GO_NCRNA_PROCESSING	312	2.40	0.00	0.00
GO_MULTI_ORGANISM_METABOLIC_PROCESS	113	2.40	0.00	0.00
GO_NCRNA_METABOLIC_PROCESS	441	2.35	0.00	0.00
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	98	2.34	0.00	0.00
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	41	2.32	0.00	0.00
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	85	2.28	0.00	0.00
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	38	2.23	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	89	2.21	0.00	0.00
GO_RNA_CATABOLIC_PROCESS	195	2.21	0.00	0.00
GO_TRANSLATIONAL_TERMINATION	84	2.20	0.00	0.00
GO_MITOCHONDRIAL_TRANSLATION	96	2.19	0.00	0.00
GO_AMIDE_BIOSYNTHETIC_PROCESS	426	2.19	0.00	0.00
GO_MRNA_METABOLIC_PROCESS	490	2.19	0.00	0.00
GO_MATURATION_OF_SSU_RRNA	31	2.18	0.00	0.00
GO_TRNA_METABOLIC_PROCESS	151	2.18	0.00	0.00
GO_AMINO_ACID_ACTIVATION	46	2.17	0.00	0.00
GO_MATURATION_OF_5_8S_RRNA	25	2.17	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	162	2.16	0.00	0.00
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	16	2.16	0.00	0.00
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	110	2.15	0.00	0.00
GO_RNA_3_END_PROCESSING	76	2.15	0.00	0.00
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	216	2.15	0.00	0.00
GO_OXIDATIVE_PHOSPHORYLATION	71	2.14	0.00	0.00
GO_NUCLEAR_EXPORT	114	2.14	0.00	0.00
GO_TRANSLATIONAL_ELONGATION	99	2.14	0.00	0.00
GO_REGULATION_OF_TRANSLATIONAL_ELONGATION	19	2.13	0.00	0.00
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	17	2.13	0.00	0.00
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	80	2.13	0.00	0.00
GO_MRNA_3_END_PROCESSING	56	2.12	0.00	0.00
GO_RNA_LOCALIZATION	141	2.11	0.00	0.00
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	24	2.10	0.00	0.00
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	2.08	0.00	0.00
GO_DNA_REPLICATION_INITIATION	21	2.08	0.00	0.00
GO_RNA_SPLICING	284	2.08	0.00	0.00
GO_RIBOSOME_ASSEMBLY	46	2.08	0.00	0.00
GO_MRNA_PROCESSING	339	2.07	0.00	0.00
GO_RRNA_MODIFICATION	18	2.07	0.00	0.00
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	30	2.06	0.00	0.00
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	46	2.06	0.00	0.00
GO_NEURON_FATE_SPECIFICATION	29	-2.09	0.00	0.01
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	22	-2.21	0.00	0.00
GO_ORGAN_MATURATION	16	-2.25	0.00	0.00
GO_REGULATION_OF_MYOBLAST_FUSION	17	-2.34	0.00	0.00
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	49	-2.48	0.00	0.00
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	67	-2.48	0.00	0.00
GO_CALCIUM_INDEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	19	-2.68	0.00	0.00

Table S2. GO-based GSEA results for expression microarray experiment on splenic cDC1s isolated at steady state from *MycI^{gfp/+}* and *MycI^{gfp/gfp}* mice. The top 50 gene sets are reported and their ranked normalized enrichment scores.

Gene Set	SIZE	NES	p-val	q-val
GO_RIBOSOME_BIOGENESIS	247	3.66	0.00	0.00
GO_RRNA_METABOLIC_PROCESS	203	3.66	0.00	0.00
GO_TRANSLATIONAL_INITIATION	122	3.64	0.00	0.00
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	85	3.64	0.00	0.00
GO_MULTI_ORGANISM_METABOLIC_PROCESS	113	3.58	0.00	0.00
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	98	3.57	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	351	3.53	0.00	0.00
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	3.48	0.00	0.00
GO_NCRNA_PROCESSING	312	3.41	0.00	0.00
GO_NCRNA_METABOLIC_PROCESS	441	3.31	0.00	0.00
GO_RNA_CATABOLIC_PROCESS	195	3.29	0.00	0.00
GO_PROTEIN_TARGETING_TO_MEMBRANE	132	3.23	0.00	0.00
GO_MRNA_METABOLIC_PROCESS	487	3.12	0.00	0.00
GO_RIBOSOME_ASSEMBLY	46	3.01	0.00	0.00
GO_AMIDE_BIOSYNTHETIC_PROCESS	425	2.99	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	162	2.94	0.00	0.00
GO_VIRAL_LIFE_CYCLE	236	2.90	0.00	0.00
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	41	2.89	0.00	0.00
GO_PEPTIDE_METABOLIC_PROCESS	469	2.89	0.00	0.00
GO_TRNA_METABOLIC_PROCESS	151	2.86	0.00	0.00
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	38	2.84	0.00	0.00
GO_AMINO_ACID_ACTIVATION	46	2.82	0.00	0.00
GO_CHROMOSOME_SEGREGATION	211	2.76	0.00	0.00
GO_CYTOPLASMIC_TRANSLATION	34	2.71	0.00	0.00
GO_SISTER_CHROMATID_SEGREGATION	147	2.66	0.00	0.00
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	296	2.65	0.00	0.00
GO_MITOCHONDRIAL_TRANSLATION	96	2.64	0.00	0.00
GO_MATURATION_OF_SSU_RRNA	31	2.63	0.00	0.00
GO_RNA_SECONDARY_STRUCTURE_UNWINDING	38	2.62	0.00	0.00
GO_NUCLEAR_CHROMOSOME_SEGREGATION	176	2.62	0.00	0.00
GO_SISTER_CHROMATID_COHESION	98	2.62	0.00	0.00
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	224	2.59	0.00	0.00
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	22	2.57	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	89	2.56	0.00	0.00
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	215	2.56	0.00	0.00
GO_RNA_SPLICING	282	2.53	0.00	0.00
GO_RNA_LOCALIZATION	141	2.52	0.00	0.00
GO_TRANSLATIONAL_ELONGATION	99	2.51	0.00	0.00
GO_MRNA_PROCESSING	336	2.51	0.00	0.00
GO_RNA_MODIFICATION	93	2.50	0.00	0.00
GO_TRNA_MODIFICATION	49	2.49	0.00	0.00
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	74	2.48	0.00	0.00
GO_TRANSLATIONAL_TERMINATION	84	2.47	0.00	0.00
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	24	2.45	0.00	0.00
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	349	2.45	0.00	0.00
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	111	2.45	0.00	0.00
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	63	2.44	0.00	0.00
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	46	2.42	0.00	0.00
GO_OXIDATIVE_PHOSPHORYLATION	71	2.41	0.00	0.00
GO_MULTI_ORGANISM_LOCALIZATION	54	2.40	0.00	0.00

Table S3. GO-based GSEA results for expression microarray experiment on splenic cDC1s isolated after activation with poly I:C from *Myel^{+/+}* and *Myel^{gfp/gfp}* mice. The top 50 gene sets are reported and their ranked normalized enrichment scores.

NAME	SIZE	NES	p-val	q-val
GO_SISTER_CHROMATID_COHESION	101	-2.16	0.00	0.00
GO_DNA_REPLICATION_INITIATION	21	-2.15	0.00	0.00
GO_SISTER_CHROMATID_SEGREGATION	150	-2.14	0.00	0.00
GO_MITOTIC_RECOMBINATION	36	-2.12	0.00	0.00
GO_NUCLEAR_CHROMOSOME_SEGREGATION	182	-2.11	0.00	0.00
GO_DNA_DEPENDENT_DNA_REPLICATION	77	-2.08	0.00	0.00
GO_DNA_GEOMETRIC_CHANGE	67	-2.07	0.00	0.00
GO_CHROMOSOME_SEGREGATION	218	-2.06	0.00	0.00
GO_DNA_REPLICATION	166	-2.04	0.00	0.00
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	74	-2.02	0.00	0.00
GO_MITOTIC_NUCLEAR_DIVISION	306	-2.02	0.00	0.00
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	30	-2.01	0.00	0.00
GO_MEIOTIC_CHROMOSOME_SEGREGATION	45	-1.97	0.00	0.00
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	80	-1.97	0.00	0.00
GO_TRNA_METABOLIC_PROCESS	151	-1.95	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	351	-1.95	0.00	0.00
GO_ORGANELLE_FISSION	400	-1.94	0.00	0.00
GO_MEIOTIC_CELL_CYCLE_PROCESS	113	-1.94	0.00	0.00
GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	93	-1.94	0.00	0.00
GO_MITOTIC_SPINDLE_ORGANIZATION	55	-1.93	0.00	0.00
GO_SPINDLE_CHECKPOINT	24	-1.93	0.00	0.00
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	55	-1.92	0.00	0.00
GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	35	-1.92	0.00	0.00
GO_DNA_BIOSYNTHETIC_PROCESS	92	-1.91	0.00	0.00
GO_DNA_CONFORMATION_CHANGE	185	-1.91	0.00	0.00
GO_RNA_MODIFICATION	93	-1.91	0.00	0.00
GO_RECOMBINATIONAL_REPAIR	57	-1.91	0.00	0.00
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	19	-1.90	0.00	0.00
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	30	-1.90	0.00	0.00
GO_RECIPROCAL_DNA_RECOMBINATION	31	-1.90	0.00	0.00
GO_DOUBLE_STRAND_BREAK_REPAIR	124	-1.89	0.00	0.00
GO_TRNA_PROCESSING	95	-1.89	0.00	0.00
GO_RRNA_MODIFICATION	18	-1.89	0.00	0.00
GO_RIBOSOME_BIOGENESIS	247	-1.89	0.00	0.00
GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	17	-1.89	0.00	0.00
GO_STRAND_DISPLACEMENT	22	-1.88	0.00	0.00
GO_MITOTIC_SPINDLE_ASSEMBLY	32	-1.88	0.00	0.00
GO_CHROMOSOME_LOCALIZATION	47	-1.88	0.00	0.00
GO_HISTONE_MRNA_METABOLIC_PROCESS	26	-1.87	0.00	0.00
GO_SPINDLE_ASSEMBLY	58	-1.87	0.00	0.00
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	162	-1.87	0.00	0.00
GO_NCRNA_PROCESSING	312	-1.87	0.00	0.00
GO_MATURATION_OF_5_8S_RRNA	25	-1.87	0.00	0.00
GO_DNA_INTEGRITY_CHECKPOINT	122	-1.86	0.00	0.00
GO_COENZYMES_BIOSYNTHETIC_PROCESS	108	-1.86	0.00	0.00
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	74	-1.86	0.00	0.00
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	33	-1.86	0.00	0.00
GO_CELL_CYCLE_PHASE_TRANSITION	213	-1.86	0.00	0.00
GO_CELLULAR_RESPIRATION	124	-1.86	0.00	0.00
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	22	-1.85	0.00	0.00

Table S4. GO-based GSEA results for expression microarray experiment on splenic cDC1s isolated after activation with poly I:C from *Mxd1*^{+/+} and *Mxd1*^{-/-} mice. The top 50 gene sets are reported and their ranked normalized enrichment scores.

NAME	SIZE	NES	p-val	q-val	
E2F1_Q6		193	-1.89	0.00	0.00
GKCGCNNNNNNTGAYG_UNKNOWN		49	-1.88	0.00	0.00
E2F_Q6		192	-1.87	0.00	0.00
E2F_Q2		195	-1.86	0.00	0.00
E2F_Q4		196	-1.85	0.00	0.00
E2F1DP1_01		195	-1.83	0.00	0.00
E2F_Q3		209	-1.83	0.00	0.00
E2F1DP2_01		195	-1.83	0.00	0.00
E2F_Q3		190	-1.82	0.00	0.00
E2F1_Q6_01		203	-1.82	0.00	0.00
E2F4DP1_01		198	-1.82	0.00	0.00
E2F1DP1RB_01		185	-1.82	0.00	0.00
E2F4DP2_01		195	-1.81	0.00	0.00
E2F1_Q3		200	-1.80	0.00	0.00
SGCGSSAAA_E2F1DP2_01		137	-1.80	0.00	0.00
E2F_Q4_01		204	-1.78	0.00	0.00
E2F1_Q4_01		198	-1.74	0.00	0.00
TMTCGCGANR_UNKNOWN		137	-1.74	0.00	0.00
E2F_Q3_01		203	-1.73	0.00	0.00
E2F_Q6_01		204	-1.72	0.00	0.00
CGGAARNGGCNG_UNKNOWN		45	-1.71	0.00	0.00
KTGGYRSGAA_UNKNOWN		58	-1.71	0.00	0.00
E2F_Q1		58	-1.71	0.00	0.00
E2F1_Q4		209	-1.65	0.00	0.00
GGAANCAGGAANY_UNKNOWN		81	-1.63	0.00	0.00
TCCCRNRTGC_UNKNOWN		175	-1.61	0.00	0.01
ELK1_Q2		209	-1.59	0.00	0.01
GABP_B		203	-1.58	0.00	0.01
YGCANTGCR_UNKNOWN		104	-1.56	0.00	0.01
KCCGNSWTTT_UNKNOWN		93	-1.56	0.00	0.01
ACTAYRNNNCCCR_UNKNOWN		363	-1.56	0.00	0.01
ETS_Q4		219	-1.54	0.00	0.01
GGCNKCCATNK_UNKNOWN		104	-1.52	0.00	0.02
NRF2_Q1		211	-1.52	0.00	0.02
GCCATNTTG_YY1_Q6		354	-1.52	0.00	0.02
NFMUE1_Q6		202	-1.51	0.00	0.02
NRF1_Q6		213	-1.51	0.00	0.02
KMCATNNWGA_UNKNOWN		73	-1.50	0.01	0.02
MYCMAX_Q1		210	-1.48	0.00	0.02
MYC_Q2		157	-1.47	0.00	0.03
USF_Q1		214	-1.47	0.00	0.03
MYCMAX_Q3		207	-1.47	0.00	0.03
CETS1P54_Q1		204	-1.46	0.00	0.03
TGCGCANK_UNKNOWN		448	-1.46	0.00	0.03
MAX_Q1		216	-1.45	0.00	0.03
AACWWCAANK_UNKNOWN		113	-1.45	0.00	0.04
GCGNNANTTCC_UNKNOWN		97	-1.44	0.00	0.04
YY1_Q2		203	-1.44	0.00	0.04
MYOGNF1_Q1		39	1.45	0.05	0.24
NFKB_Q6_Q1		203	1.57	0.00	0.23

Table S5. Transcription factor motif-based GSEA results for expression microarray experiment on splenic cDC1s isolated after activation with poly I:C from *Mxd1*^{+/+} and *Mxd1*^{-/-} mice. The top 50 gene sets and reported by their ranked normalized enrichment scores.

NAME	SIZE	NES	p-val	q-val
Maturation On	248	3.58	0	0
Cluster 30	66	-2.40	0	0
Cluster 31	67	-2.26	0	0

Table S6. cDC1 maturation gene set-based GSEA results for expression microarray experiment on splenic cDC1s isolated after activation with poly I:C from *Mxd1*^{+/+} and *Mxd1*^{-/-} mice.