Supplementary Materials

Fig. S1. Protein levels of cytokine and transcription factors in ILC3s at different points of the circadian cycle.

Fig. S2. Acute SW model disrupts circadian rhythm without altering food intake or bodyweight.

Fig. S3. REV-ERBα deficiency results in reduced NKp46^{+} ILC3 in multiple tissues

Fig. S4. REV-ERBβ deficiency alone does not affect ILC3s.

Fig. S5. Acute circadian disruption does not affect ILC3 mitochondria.

Fig. S6. Reduction of NKp46^{+} ILC3 in *Nr1d1*$^{-/-}$ mice is not due to increase in plasticity.

Fig. S7. Accessibility of *Nfil3, Il17,* and *Tbp* loci in *Nr1d1*$^{+/+}$ and *Nr1d1*$^{-/-}$ ILC3s.

Table S1. Motif enrichment of known motifs by HOMER in *Nr1d1*$^{+/+}$ NKp46^{-} ILC3s.

Table S2. *De novo* motif enrichment by HOMER in *Nr1d1*$^{+/+}$ NKp46^{-} ILC3s.

Table S3. Motif enrichment of known motifs by HOMER in *Nr1d1*$^{-/-}$ NKp46^{-} ILC3s.

Table S4. *De novo* motif enrichment by HOMER in *Nr1d1*$^{-/-}$ NKp46^{-} ILC3s.

Table S5. Sequences of primers used for qPCR.

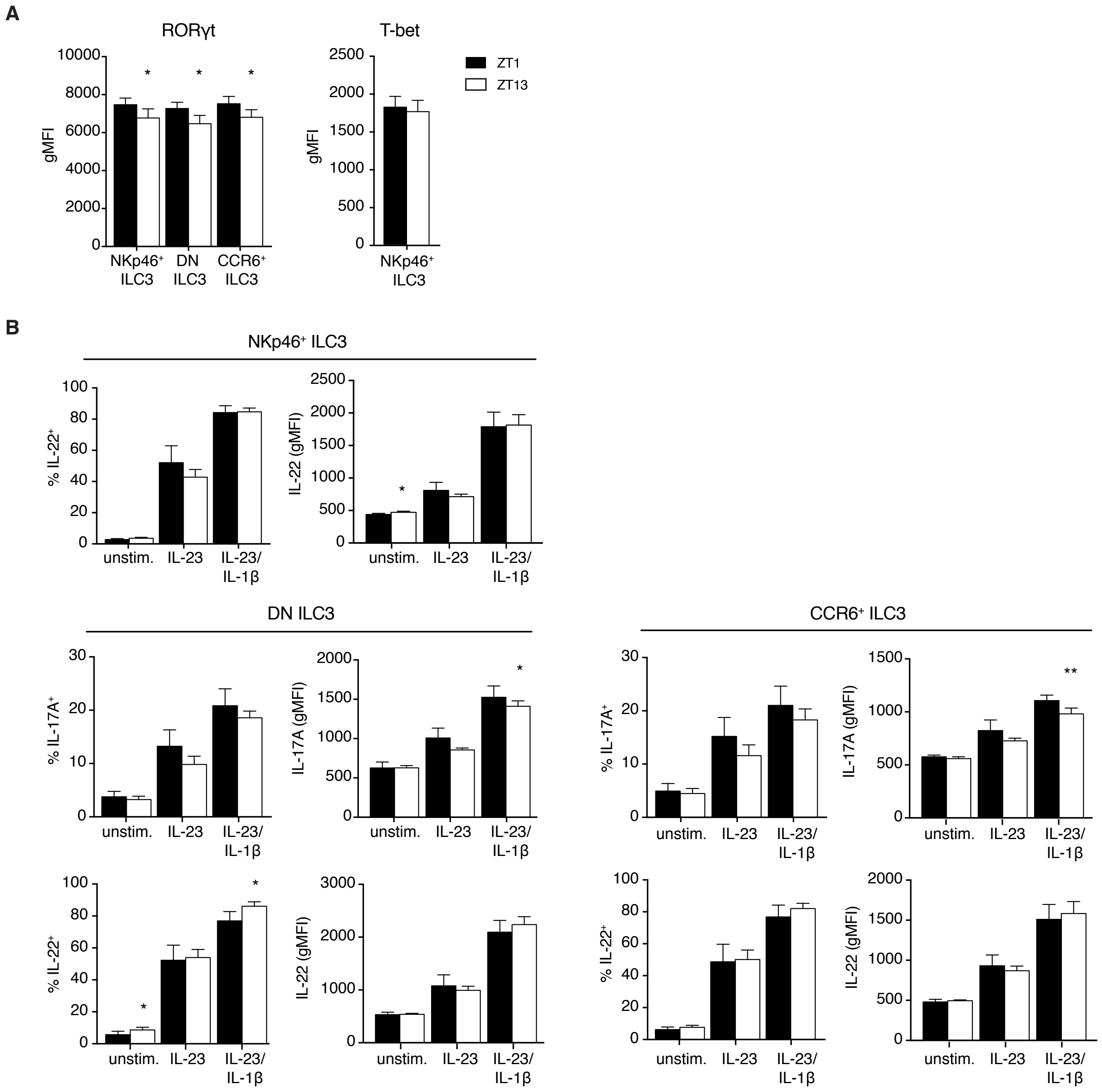

Figure S1. Protein levels of cytokine and transcription factors in ILC3s at different points of the circadian cycle.

C57Bl6/J mice were examined at ZT1 and ZT13. **A)** RORγt and T-bet expression by intracellular staining in ILC3 subsets. **B)** IL-17A and IL-22 production in ILC3 subsets in response to in vitro stimulation with 1 ng/mL IL-23 or 10 ng/mL IL-23/IL-1β. Frequency of cytokine producing cells and amount of cytokine per cell (gMFI) are shown. Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. Data are representative of two independent experiments, n=5 per group per experiment.

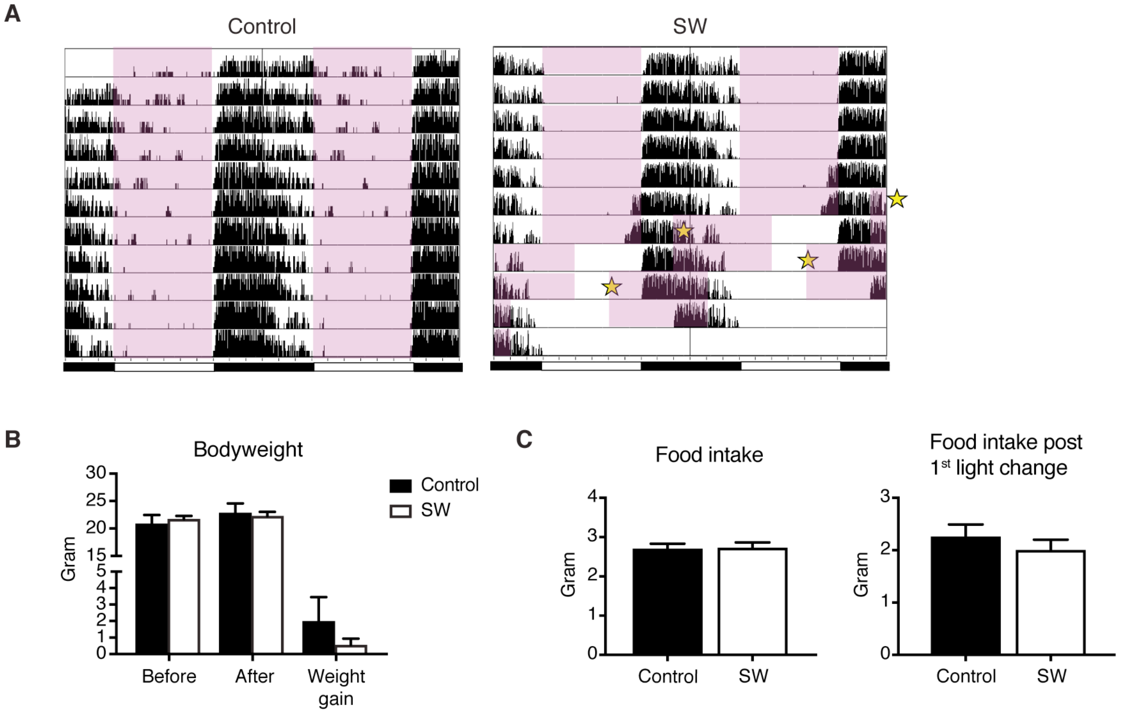

Figure S2. Acute SW model disrupts circadian rhythm without altering food intake or bodyweight.
A) Wheel-running activity of control and SW mice (colored blocks represent lighting schedule, stars indicate advance of light/dark cycle, double plotted for better visualization). **B)** Bodyweight and weight changes of control and SW mice. **C)** Average food intake per day during experiment (left) and food intake after first light change (right) of control and SW mice. Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. Data are representative of two independent experiments (A-B), n=5 per group per experiment.

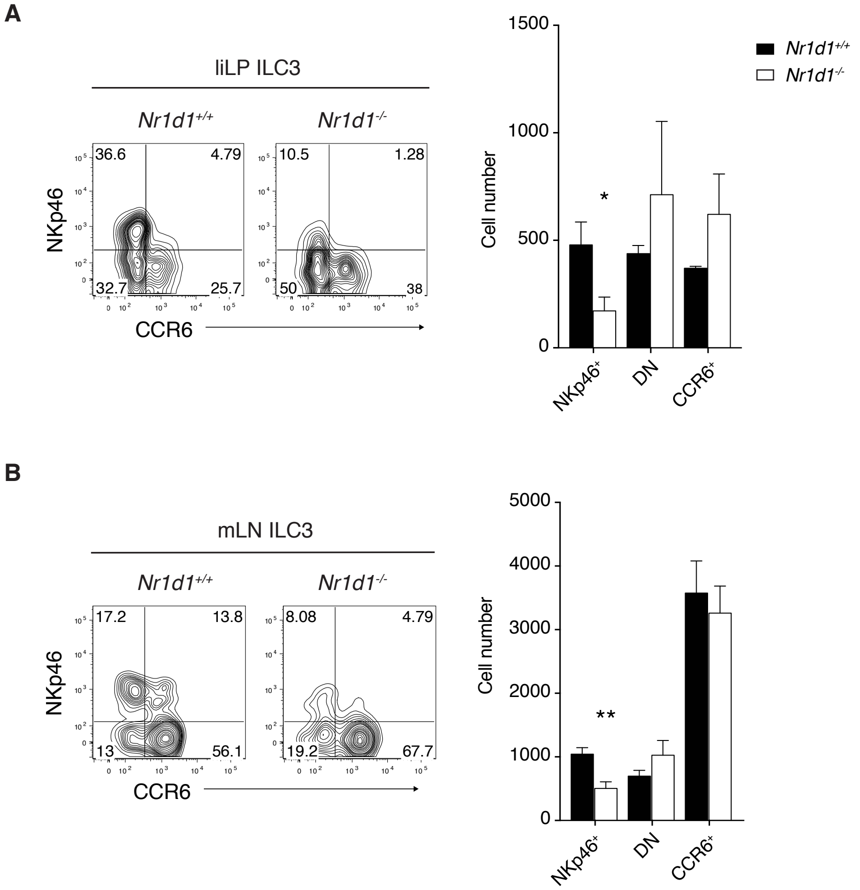

Figure S3. REV-ERBα deficiency results in reduced NKp46^{+} ILC3 in multiple tissues
Representative plots (left) and numbers (right) of ILC3 subsets in: **A)** large intestine lamina propria (liLP), **B)** mesenteric lymph nodes (mLN). Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. Data are representative of two independent experiments (A), n=3 per group per experiment.

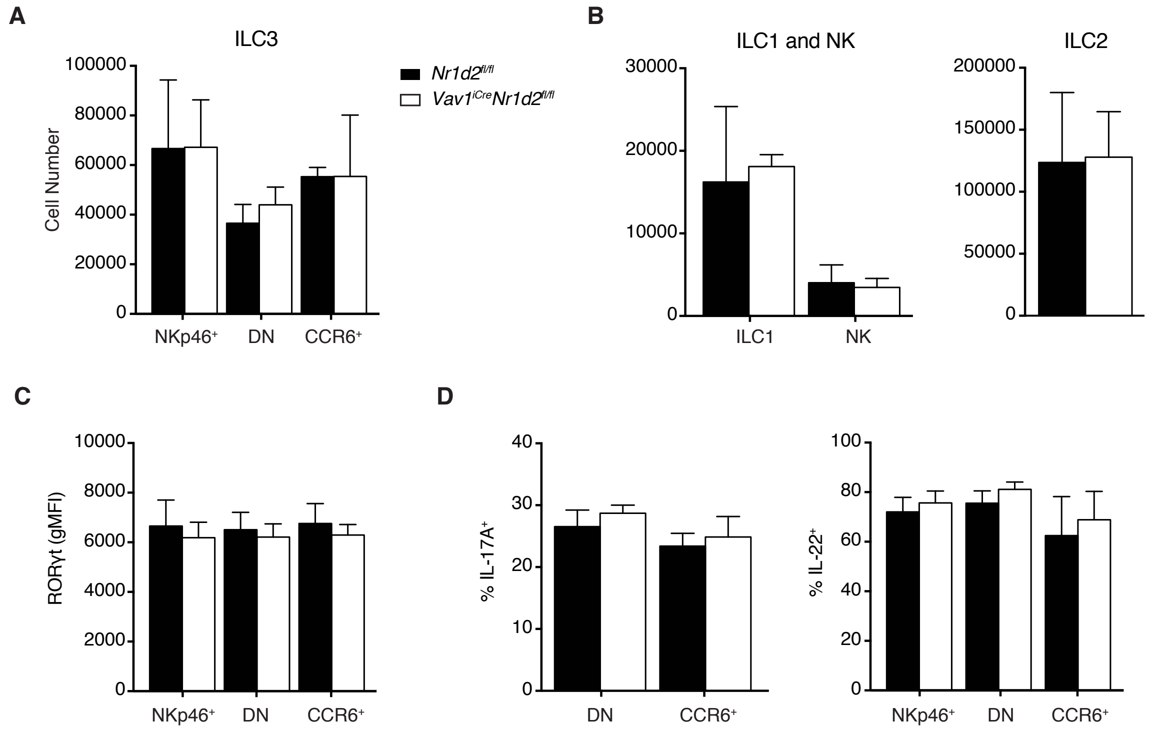

Figure S4. REV-ERBβ deficiency alone does not affect ILC3s.
ILCs were isolated from *Nr1d2*$^{fl/fl}$ and *Vav1*^{iCre}*Nr1d2*$^{fl/fl}$ siLP: Cell counts of **A)** ILC3s, **B)** ILC1s, NKs, and ILC2s. **C)** Quantification of RORγt levels by intracellular staining in ILC3 subsets. **D)** Frequency of IL-17A^{+} and IL-22^{+} ILC3s after in vitro stimulation with 10 ng/mL of IL-23 and IL-1β. Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). Data are representative of two independent experiments, n=3 per group per experiment.

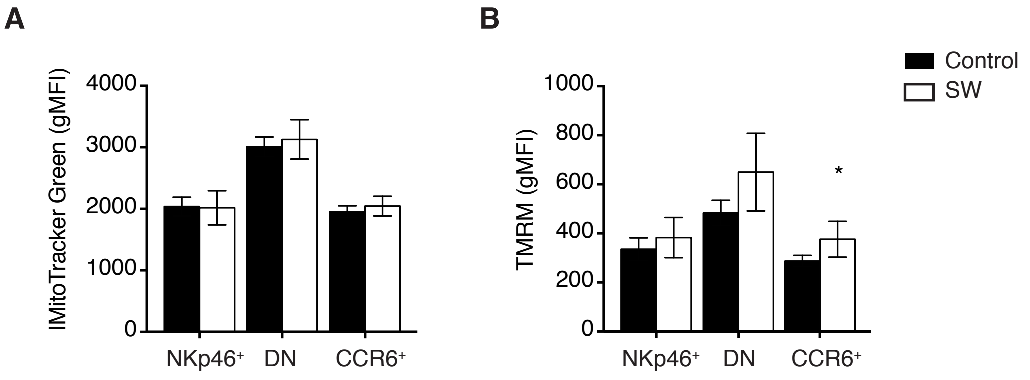

Figure S5. Acute circadian disruption does not affect ILC3 mitochondria.
Acute shift work model as in Fig. 2. Quantification of **A)** mitochondrial content by MitoTracker Green FM staining and **B)** mitochondrial potential by TMRM staining in ILC3 subsets. Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. Data are representative of two independent experiments (A-B), n=5 per group per experiment.

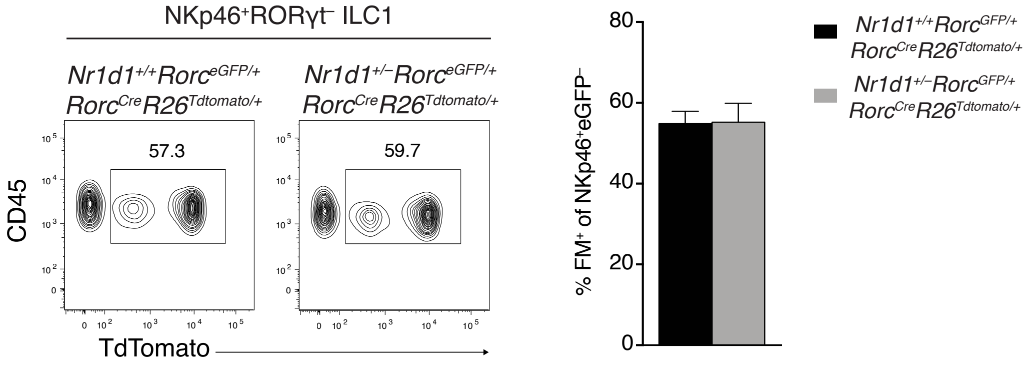

Figure S6. Reduction of NKp46$^+$ ILC3 in *Nr1d1*$^{-/-}$ mice is not due to increase in plasticity. Representative plot (left) and frequency (right) of RORγt-FM$^+$ ILC1s (CD45$^+$Lin$^-$ (CD3/CD5/CD19)RORγt-eGFP$^-$NKp46$^+$) from siLP of *Nr1d1*$^{+/+}$ and *Nr1d1*$^{-/-}$ RORγt-reporter-FM mice. Statistical analysis was performed using Student's t-test. Bars indicate mean (±SD). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. Data are representative of two independent experiments, n=3-4 per genotype per experiment.

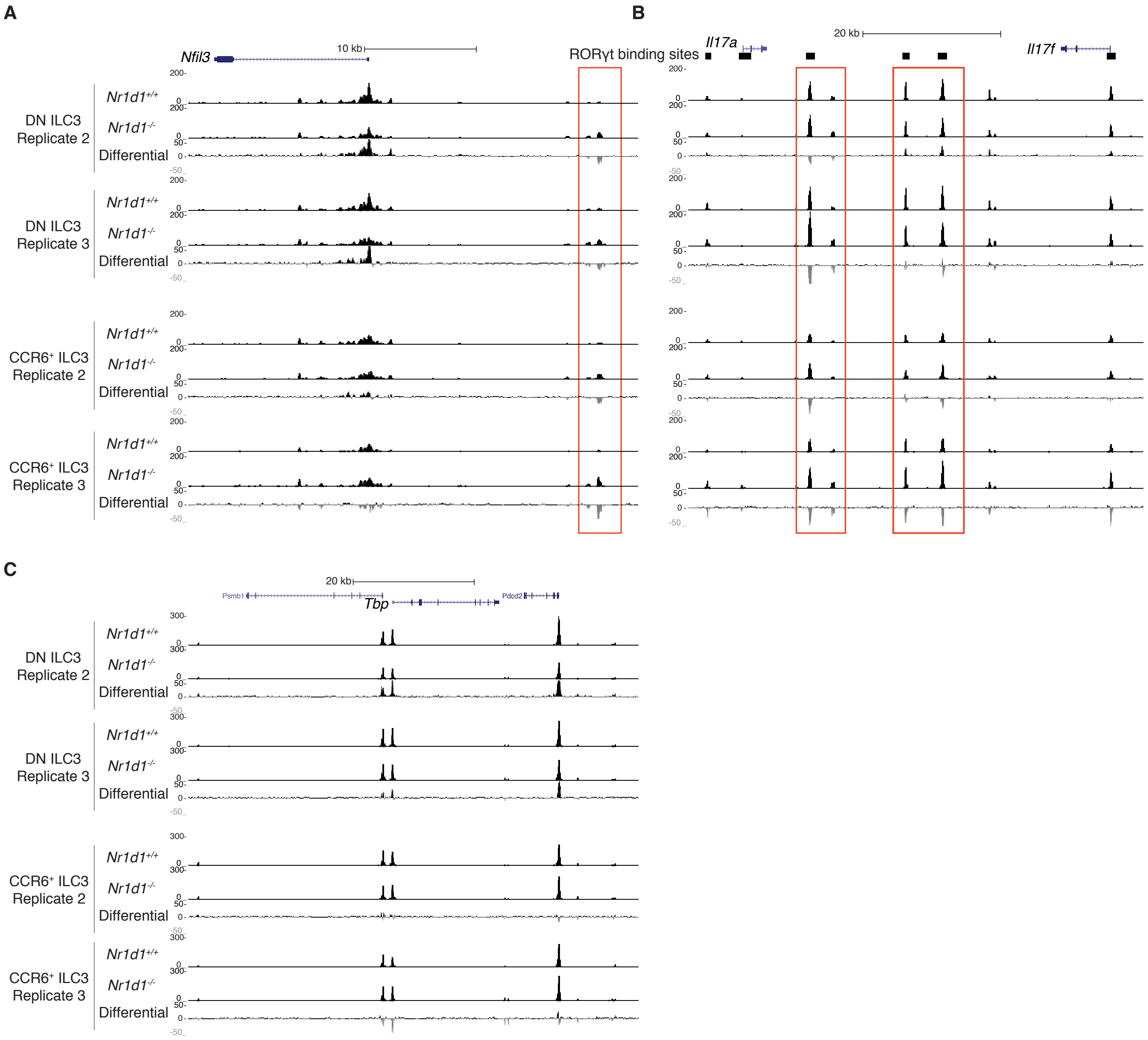

Figure S7. Accessibility of *Nfil3*, *Il17*, and *Tbp* loci in *Nr1d1*$^{+/+}$ and *Nr1d1*$^{–/–}$ ILC3s.
UCSC genome browser view of ATAC-seq tracks at the **A)** *Nfil3*, **B)** *Il17*, and **C)** *Tbp* loci in biological replicates of *Nr1d1*$^{+/+}$ and *Nr1d1*$^{–/–}$ ILC3s.

Motif Name	Consensus	P-value	Log P-value	q-value (Benjamini)	# of Target Sequences with Motif(of 1138)	% of Target Sequences with Motif	# of Background Sequences with Motif(of 48512)	% of Background Sequences with Motif
RORgt(NR)/EL4-RORgt.Flag-ChIP-Seq(GSE56019)/Homer	AAYTAGGTCA	1.00E-79	-1.84E+02	0	208	18.28%	1780.4	3.67%
RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer	AAACCACARM	1.00E-61	-1.41E+02	0	617	54.22%	14760.2	30.45%
RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer	SAAACCACAG	1.00E-59	-1.37E+02	0	500	43.94%	10707.5	22.09%
RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer	NWAACCACADNN	1.00E-58	-1.35E+02	0	556	48.86%	12753.2	26.31%
RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer	GCTGTGGTTW	1.00E-54	-1.26E+02	0	499	43.85%	11056.3	22.81%
NFkB-p65(RHD)/GM12787-p65-ChIP-Seq(GSE19485)/Homer	WGGGGATTTCCC	1.00E-52	-1.21E+02	0	355	31.20%	6563.7	13.54%
NFkB-p65-Rel(RHD)/ThioMac-LPS-Expression(GSE23622)/Homer	GGAAATTCCC	1.00E-44	-1.03E+02	0	96	8.44%	637	1.31%
NFkB-p50,p52(RHD)/Monocyte-p50-ChIP-Chip(Schreiber_et_al.)/Homer	GGGGGAATCCCC	1.00E-18	-4.19E+01	0	86	7.56%	1210.6	2.50%
Tcf4(HMG)/Hct116-Tcf4-ChIP-Seq(SRA012054)/Homer	ASATCAAAGGVA	1.00E-15	-3.67E+01	0	253	22.23%	6441.2	13.29%
Atf7(bZIP)/3T3L1-Atf7-ChIP-Seq(GSE56872)/Homer	NGRTGACGTCAY	1.00E-12	-2.82E+01	0	235	20.65%	6312.2	13.02%
Atf2(bZIP)/3T3L1-Atf2-ChIP-Seq(GSE56872)/Homer	NRRTGACGTCAT	1.00E-11	-2.73E+01	0	181	15.91%	4514.4	9.31%
Atf1(bZIP)/K562-ATF1-ChIP-Seq(GSE31477)/Homer	GATGACGTCA	1.00E-11	-2.70E+01	0	297	26.10%	8618.8	17.78%
c-Jun-CRE(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer	ATGACGTCATCY	1.00E-11	-2.67E+01	0	168	14.76%	4116.1	8.49%
Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.967)	NNAYTTCCTGHN	1.00E-10	-2.51E+01	0	412	36.20%	13142.3	27.12%
BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer	DATGASTCAT	1.00E-10	-2.39E+01	0	286	25.13%	8442.9	17.42%
Egr2(Zf)/Thymocytes-Egr2-ChIP-Seq(GSE34254)/Homer	NGCGTGGGCGGR	1.00E-10	-2.38E+01	0	93	8.17%	1890.4	3.90%
Jun-AP1(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer	GATGASTCATCN	1.00E-10	-2.38E+01	0	129	11.34%	2995.3	6.18%
Fosl2(bZIP)/3T3L1-Fosl2-ChIP-Seq(GSE56872)/Homer	NATGASTCABNN	1.00E-09	-2.29E+01	0	168	14.76%	4322.4	8.92%

ETS:RUNX(ETS,Runt)/Jurkat-RUNX1-ChIP-Seq(GSE17954)/Homer	RCAGGATGTGGT	1.00E-09	-2.29E+01	0	69	6.06%	1239.3	2.56%
Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer	NNATGASTCATH	1.00E-09	-2.28E+01	0	245	21.53%	7030.3	14.51%
PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	AGAGGAAGTG	1.00E-09	-2.21E+01	0	250	21.97%	7264.3	14.99%
Atf3(bZIP)/GBM-ATF3-ChIP-Seq(GSE33912)/Homer	DATGASTCATHN	1.00E-09	-2.17E+01	0	283	24.87%	8513.1	17.56%
Fra2(bZIP)/Striatum-Fra2-ChIP-Seq(GSE43429)/Homer	GGATGACTCATC	1.00E-09	-2.12E+01	0	215	18.89%	6073.9	12.53%
Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer	MACAGGAAGT	1.00E-09	-2.11E+01	0	182	15.99%	4915.7	10.14%
EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq(SRA014231)/Homer	ATTTCCTGTN	1.00E-08	-2.01E+01	0	319	28.03%	10010.7	20.65%
JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer	RATGASTCAT	1.00E-07	-1.84E+01	0	239	21.00%	7160.6	14.77%
ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	ACAGGAAGTG	1.00E-07	-1.69E+01	0	421	36.99%	14339.8	29.59%
GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	RACCGGAAGT	1.00E-07	-1.66E+01	0	376	33.04%	12577	25.95%
TCFL2(HMG)/K562-TCF7L2-ChIP-Seq(GSE29196)/Homer	ACWTCAAAGG	1.00E-07	-1.64E+01	0	58	5.10%	1140	2.35%
Tcf3(HMG)/mES-Tcf3-ChIP-Seq(GSE11724)/Homer	ASWTCAAAGG	1.00E-07	-1.63E+01	0	137	12.04%	3672.6	7.58%
Gata2(Zf)/K562-GATA2-ChIP-Seq(GSE18829)/Homer	BBCTTATCTS	1.00E-07	-1.62E+01	0	277	24.34%	8785	18.13%
Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	NRYTTCCGGH	1.00E-06	-1.54E+01	0	425	37.35%	14670.3	30.27%
EWS:FLI1-fusion(ETS)/SK_N_MC-EWS:FLI1-ChIP-Seq(SRA014231)/Homer	VACAGGAAAT	1.00E-06	-1.45E+01	0	257	22.58%	8188.1	16.89%
ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	ACAGGAAGTG	1.00E-06	-1.43E+01	0	585	51.41%	21425.3	44.21%
GATA(Zf),IR4/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer	NAGATWNBNATCTNN	1.00E-06	-1.41E+01	0	50	4.39%	991.1	2.04%
AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	VTGACTCATC	1.00E-06	-1.40E+01	0	296	26.01%	9740.5	20.10%
JunD(bZIP)/K562-JunD-ChIP-Seq/Homer	ATGACGTCATCN	1.00E-06	-1.40E+01	0	58	5.10%	1232.1	2.54%
COUP-TFII(NR)/Artia-Nr2f2-ChIP-Seq(GSE46497)/Homer	AGRGGTCA	1.00E-06	-1.39E+01	0	605	53.16%	22327.3	46.07%
Gata6(Zf)/HUG1N-GATA6-ChIP-Seq(GSE51936)/Homer	YCTTATCTBN	1.00E-05	-1.37E+01	0	349	30.67%	11856	24.46%
IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	GAAASYGAAASY	1.00E-05	-1.30E+01	0	57	5.01%	1239.9	2.56%

IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer	GAAAGTGAAAGT	1.00E-05	-1.30E+01	0	71	6.24%	1677.8	3.46%
Brn1(POU,Homeobox)/NPC-Brn1-ChIP-Seq(GSE35496)/Homer	TATGCWAATBAV	1.00E-05	-1.25E+01	0	118	10.37%	3275.6	6.76%
Reverb(NR),DR2/RAW-Reverba.biotin-ChIP-Seq(GSE45914)/Homer	GTRGGTCASTGGGTCA	1.00E-05	-1.25E+01	0	82	7.21%	2060.2	4.25%
X-box(HTH)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer	GGTTGCCATGGCAA	1.00E-05	-1.24E+01	0	67	5.89%	1580.3	3.26%
Rfx2(HTH)/LoVo-RFX2-ChIP-Seq(GSE49402)/Homer	GTTGCCATGGCAACM	1.00E-05	-1.16E+01	0.0001	58	5.10%	1334.7	2.75%
MafA(bZIP)/Islet-MafA-ChIP-Seq(GSE30298)/Homer	TGCTGACTCA	1.00E-04	-1.13E+01	0.0001	339	29.79%	11764.9	24.27%
Rfx1(HTH)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer	KGTTGCCATGGCAA	1.00E-04	-1.11E+01	0.0001	102	8.96%	2824.1	5.83%
Gata1(Zf)/K562-GATA1-ChIP-Seq(GSE18829)/Homer	SAGATAAGRV	1.00E-04	-1.10E+01	0.0001	237	20.83%	7813.2	16.12%
ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	AACCGGAAGT	1.00E-04	-1.10E+01	0.0001	503	44.20%	18490.3	38.15%
GATA(Zf),IR3/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer	NNNNNBAGATAWYATCTVHN	1.00E-04	-1.07E+01	0.0002	72	6.33%	1831.3	3.78%
RFX(HTH)/K562-RFX3-ChIP-Seq(SRA012198)/Homer	CGGTTGCCATGGCAAC	1.00E-04	-1.05E+01	0.0002	51	4.48%	1169.4	2.41%
RAR:RXR(NR),DR5/ES-RAR-ChIP-Seq(GSE56893)/Homer	RGGTCADNNAGAGGTCAV	1.00E-04	-1.02E+01	0.0003	25	2.20%	422.7	0.87%
Gata4(Zf)/Heart-Gata4-ChIP-Seq(GSE35151)/Homer	NBWGATAAGR	1.00E-04	-1.00E+01	0.0003	364	31.99%	12945.3	26.71%
IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	AGTTTCAKTTTC	1.00E-04	-9.45E+00	0.0005	135	11.86%	4137.9	8.54%
IRF4(IRF)/GM12878-IRF4-ChIP-Seq(GSE32465)/Homer	ACTGAAACCA	1.00E-04	-9.30E+00	0.0006	178	15.64%	5755	11.87%
GATA3(Zf),DR8/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer	AGATSTNDNNDSAGATAASN	1.00E-03	-9.02E+00	0.0008	40	3.51%	894.3	1.85%
Chop(bZIP)/MEF-Chop-ChIP-Seq(GSE35681)/Homer	ATTGCATCAT	1.00E-03	-9.00E+00	0.0008	84	7.38%	2350.9	4.85%
CArG(MADS)/PUER-Srf-ChIP-Seq(Sullivan_et_al.)/Homer	CCATATATGGNM	1.00E-03	-8.60E+00	0.0012	124	10.90%	3815.3	7.87%
Egr1(Zf)/K562-Egr1-ChIP-Seq(GSE32465)/Homer	TGCGTGGGYG	1.00E-03	-8.49E+00	0.0013	238	20.91%	8164.3	16.84%
ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer	AGTTTCASTTTC	1.00E-03	-8.39E+00	0.0014	33	2.90%	708.7	1.46%
Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	HACTTCCGGY	1.00E-03	-8.37E+00	0.0014	206	18.10%	6936.9	14.31%
Esrrb(NR)/mES-Esrrb-ChIP-Seq(GSE11431)/Homer	KTGACCTTGA	1.00E-03	-8.33E+00	0.0014	278	24.43%	9762.6	20.14%

bZIP:IRF(bZIP,IRF)/Th17-BatF-ChIP-Seq(GSE39756)/Homer	NAGTTTCABTHTGACTNW	1.00E-03	-8.01E+00	0.0019	171	15.03%	5639.1	11.63%
CRE(bZIP)/Promoter/Homer	CSGTGACGTCAC	1.00E-03	-7.85E+00	0.0022	99	8.70%	2975.7	6.14%
EKLF(Zf)/Erythrocyte-Klf1-ChIP-Seq(GSE20478)/Homer	NWGGGTGTGGCY	1.00E-03	-7.78E+00	0.0023	104	9.14%	3163.7	6.53%
MafK(bZIP)/C2C12-MafK-ChIP-Seq(GSE36030)/Homer	GCTGASTCAGCA	1.00E-03	-7.68E+00	0.0026	105	9.23%	3209.5	6.62%
Oct6(POU,Homeobox)/NPC-Pou3f1-ChIP-Seq(GSE35496)/Homer	WATGCAAATGAG	1.00E-03	-7.62E+00	0.0027	141	12.39%	4549.3	9.39%
THRb(NR)/Liver-NR1A2-ChIP-Seq(GSE52613)/Homer	TRAGGTCA	1.00E-03	-7.36E+00	0.0034	962	84.53%	39170	80.82%
Sp5(Zf)/mES-Sp5.Flag-ChIP-Seq(GSE72989)/Homer	RGKGGGCGGAGC	1.00E-03	-7.13E+00	0.0042	309	27.15%	11196.3	23.10%
KLF6(Zf)/PDAC-KLF6-ChIP-Seq(GSE64557)/Homer	MKGGGYGTGGCC	1.00E-03	-7.06E+00	0.0045	346	30.40%	12705.9	26.22%
Atf4(bZIP)/MEF-Atf4-ChIP-Seq(GSE35681)/Homer	MTGATGCAAT	1.00E-03	-7.04E+00	0.0045	98	8.61%	3015.7	6.22%
Mef2a(MADS)/HL1-Mef2a.biotin-ChIP-Seq(GSE21529)/Homer	CYAAAAATAG	1.00E-02	-6.68E+00	0.0064	144	12.65%	4774.7	9.85%
ELF3(ETS)/PDAC-ELF3-ChIP-Seq(GSE64557)/Homer	ANCAGGAAGT	1.00E-02	-6.66E+00	0.0064	292	25.66%	10593.7	21.86%
E-box(bHLH)/Promoter/Homer	SSGGTCACGTGA	1.00E-02	-6.50E+00	0.0074	36	3.16%	890.7	1.84%
ERE(NR),IR3/MCF7-ERa-ChIP-Seq(Unpublished)/Homer	VAGGTCACNSTGACC	1.00E-02	-6.30E+00	0.0089	121	10.63%	3948.9	8.15%
KLF3(Zf)/MEF-Klf3-ChIP-Seq(GSE44748)/Homer	NRGCCCCRCCCHBNN	1.00E-02	-6.29E+00	0.0089	181	15.91%	6252.6	12.90%
MITF(bHLH)/MastCells-MITF-ChIP-Seq(GSE48085)/Homer	RTCATGTGAC	1.00E-02	-5.97E+00	0.0121	353	31.02%	13202.6	27.24%
Pdx1(Homeobox)/Islet-Pdx1-ChIP-Seq(SRA008281)/Homer	YCATYAATCA	1.00E-02	-5.66E+00	0.0163	312	27.42%	11591.9	23.92%
GATA3(Zf)/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer	AGATAASR	1.00E-02	-5.63E+00	0.0166	480	42.18%	18536.9	38.25%
CEBP:AP1(bZIP)/ThioMac-CEBPb-ChIP-Seq(GSE21512)/Homer	DRTGTTGCAA	1.00E-02	-5.59E+00	0.017	253	22.23%	9220.5	19.02%
Bach2(bZIP)/OCILy7-Bach2-ChIP-Seq(GSE44420)/Homer	TGCTGAGTCA	1.00E-02	-5.47E+00	0.019	83	7.29%	2622.1	5.41%
Mef2d(MADS)/Retina-Mef2d-ChIP-Seq(GSE61391)/Homer	GCTATTTTTAGC	1.00E-02	-5.44E+00	0.0194	65	5.71%	1967.7	4.06%
IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	GRAASTGAAAST	1.00E-02	-5.40E+00	0.0199	120	10.54%	4022.7	8.30%
Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	NRYTTCCGGY	1.00E-02	-5.39E+00	0.0199	194	17.05%	6904.6	14.25%
MafB(bZIP)/BMM-Mafb-ChIP-Seq(GSE75722)/Homer	WNTGCTGASTCAGCANWTTY	1.00E-02	-5.17E+00	0.0243	163	14.32%	5719.2	11.80%

Mef2b(MADS)/HEK293-Mef2b.V5-ChIP-Seq(GSE67450)/Homer	GCTATTTTTGGM	1.00E-02	-5.12E+00	0.0253	252	22.14%	9269.1	19.12%
VDR(NR),DR3/GM10855-VDR+vitD-ChIP-Seq(GSE22484)/Homer	ARAGGTCANWGAGTTCANNN	1.00E-02	-5.04E+00	0.0271	96	8.44%	3156.6	6.51%
ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer	AVCCGGAAGT	1.00E-02	-5.00E+00	0.028	186	16.34%	6654.6	13.73%
EHF(ETS)/LoVo-EHF-ChIP-Seq(GSE49402)/Homer	AVCAGGAAGT	1.00E-02	-5.00E+00	0.028	455	39.98%	17642	36.40%
Srebp2(bHLH)/HepG2-Srebp2-ChIP-Seq(GSE31477)/Homer	CGGTCACSCCAC	1.00E-02	-4.98E+00	0.028	63	5.54%	1938	4.00%
MafF(bZIP)/HepG2-MafF-ChIP-Seq(GSE31477)/Homer	HWWGTCAGCAWWTTT	1.00E-02	-4.94E+00	0.0287	97	8.52%	3206.2	6.62%
ZNF136(Zf)/HEK293-ZNF136.GFP-ChIP-Seq(GSE58341)/Homer	YTKGATAHAGTATTCTWGGTNGGCA	1.00E-02	-4.93E+00	0.0287	40	3.51%	1122.3	2.32%
ELF5(ETS)/T47D-ELF5-ChIP-Seq(GSE30407)/Homer	ACVAGGAAGT	1.00E-02	-4.93E+00	0.0287	280	24.60%	10441.5	21.54%
Nrf2(bZIP)/Lymphoblast-Nrf2-ChIP-Seq(GSE37589)/Homer	HTGCTGAGTCAT	1.00E-02	-4.74E+00	0.0337	24	2.11%	595.7	1.23%
Rfx5(HTH)/GM12878-Rfx5-ChIP-Seq(GSE31477)/Homer	SCCTAGCAACAG	1.00E-02	-4.72E+00	0.0343	133	11.69%	4619.7	9.53%

Table S1. Motif enrichment of known motifs by HOMER in *Nr1d1*$^{+/+}$ NKp46$^{–}$ ILC3s.

Rank	Motif	Best match	P-value	Log P-value	# of Target Sequences with Motif(of 1138)	% of Target Sequences with Motif	# of Background Sequences with Motif(of 48512)	% of Background Sequences with Motif
1	AWBTAGGTCA	RORgt(NR)/EL4-RORgt.Flag-ChIP-Seq(GSE56019)/Homer(0.976)	1.00E-108	-250.39	495	43.50%	7614.6	15.71%
2	GGAAATCCCC	MF0003.1_REL_class/Jaspar(0.976)	1.00E-85	-196.83	341	29.96%	4498.2	9.28%
3	NNHRACCACA	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer(0.938)	1.00E-67	-155.98	464	40.77%	8934.4	18.43%
4	AATCATAATAAC	PB0064.1_Sox14_1/Jaspar(0.712)	1.00E-18	-41.74	10	0.88%	3.5	0.01%
5	CTTTGAWCTT	TCF7L2/MA0523.1/Jaspar(0.930)	1.00E-17	-40.78	212	18.63%	4874.8	10.06%
6	GCCAAAGGGTTA	PB0191.1_Tcfap2c_2/Jaspar(0.625)	1.00E-15	-35.14	8	0.70%	2.8	0.01%
7	AWTAGGACGG	8-AWTAGGACGG,BestGuess:ZNF382(Zf)/HEK293-ZNF382.GFP-ChIP-Seq(GSE58341)/Homer(0.649)	1.00E-15	-34.66	161	14.15%	3523	7.27%
8	TTCAAAAAGTGC	13-TTCAAAAAGTGC,BestGuess:PB0146.1_Mafk_2/Jaspar(0.684)	1.00E-13	-30.17	81	7.12%	1357.2	2.80%
9	AGTGACTCAC	10-AGTGACTCAC,BestGuess:FOSL1/MA0477.1/Jaspar(0.850)	1.00E-12	-27.92	101	8.88%	1978.9	4.08%

Table S2. ***De novo*** **motif enrichment by HOMER in** ***Nr1d1***$^{+/+}$ **NKp46**$^{–}$ **ILC3s.**

Motif Name	Consensus	P-value	Log P-value	q-value (Benjamini)	# of Target Sequences with Motif(of 926)	% of Target Sequences with Motif	# of Background Sequences with Motif(of 48705)	% of Background Sequences with Motif
Etv2(ETS)/ES-ER71-ChIP-Seq(GSE59402)/Homer(0.967)	NNAYTTCCTGHN	1.00E-61	-1.41E+02	0	517	55.83%	14392.3	29.55%
ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer	ACAGGAAGTG	1.00E-55	-1.27E+02	0	529	57.13%	15565.5	31.95%
Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer	MACAGGAAGT	1.00E-53	-1.22E+02	0	278	30.02%	5475.8	11.24%
Fli1(ETS)/CD8-FLI-ChIP-Seq(GSE20898)/Homer	NRYTTCCGGH	1.00E-51	-1.18E+02	0	522	56.37%	15647.7	32.12%
EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq(SRA014231)/Homer	ATTTCCTGTN	1.00E-50	-1.16E+02	0	424	45.79%	11333.1	23.27%
NF1(CTF)/LNCAP-NF1-ChIP-Seq(Unpublished)/Homer	CYTGGCABNSTGCCAR	1.00E-48	-1.13E+02	0	281	30.35%	5857.2	12.02%
EWS:FLI1-fusion(ETS)/SK_N_MC-EWS:FLI1-ChIP-Seq(SRA014231)/Homer	VACAGGAAAT	1.00E-44	-1.03E+02	0	358	38.66%	9103.4	18.69%
ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer	ACAGGAAGTG	1.00E-40	-9.26E+01	0	642	69.33%	23169.8	47.57%
GABPA(ETS)/Jurkat-GABPa-ChIP-Seq(GSE17954)/Homer	RACCGGAAGT	1.00E-38	-8.96E+01	0	448	48.38%	13609	27.94%
RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer	AAACCACARM	1.00E-38	-8.96E+01	0	493	53.24%	15713.9	32.26%
ETV1(ETS)/GIST48-ETV1-ChIP-Seq(GSE22441)/Homer	AACCGGAAGT	1.00E-38	-8.88E+01	0	576	62.20%	19884.7	40.82%
RUNX(Runt)/HPC7-Runx1-ChIP-Seq(GSE22178)/Homer	SAAACCACAG	1.00E-38	-8.86E+01	0	398	42.98%	11429.1	23.46%
Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer	NNATGASTCATH	1.00E-37	-8.54E+01	0	309	33.37%	7874.5	16.17%
Fra2(bZIP)/Striatum-Fra2-ChIP-Seq(GSE43429)/Homer	GGATGACTCATC	1.00E-36	-8.38E+01	0	281	30.35%	6847.9	14.06%
ETS:RUNX(ETS,Runt)/Jurkat-RUNX1-ChIP-Seq(GSE17954)/Homer	RCAGGATGTGGT	1.00E-35	-8.25E+01	0	108	11.66%	1308	2.69%
Atf3(bZIP)/GBM-ATF3-ChIP-Seq(GSE33912)/Homer	DATGASTCATHN	1.00E-35	-8.13E+01	0	342	36.93%	9389.4	19.28%
Jun-AP1(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer	GATGASTCATCN	1.00E-34	-8.05E+01	0	181	19.55%	3423.2	7.03%
JunB(bZIP)/DendriticCells-Junb-ChIP-Seq(GSE36099)/Homer	RATGASTCAT	1.00E-34	-7.93E+01	0	303	32.72%	7892.6	16.20%
Fosl2(bZIP)/3T3L1-Fosl2-ChIP-Seq(GSE56872)/Homer	NATGASTCABNN	1.00E-33	-7.82E+01	0	223	24.08%	4912.4	10.08%
AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	VTGACTCATC	1.00E-32	-7.44E+01	0	366	39.52%	10746	22.06%

BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer	DATGASTCAT	1.00E-31	-7.20E+01	0	330	35.64%	9331.6	19.16%
RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer	NWAACCACADNN	1.00E-31	-7.17E+01	0	425	45.90%	13535.9	27.79%
PU.1(ETS)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer	AGAGGAAGTG	1.00E-30	-6.92E+01	0	289	31.21%	7779.1	15.97%
RORgt(NR)/EL4-RORgt.Flag-ChIP-Seq(GSE56019)/Homer	AAYTAGGTCA	1.00E-30	-6.92E+01	0	123	13.28%	1943	3.99%
Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer	HACTTCCGGY	1.00E-29	-6.87E+01	0	274	29.59%	7203.9	14.79%
RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer	GCTGTGGTTW	1.00E-29	-6.81E+01	0	386	41.68%	11968.9	24.57%
Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer	NRYTTCCGGY	1.00E-27	-6.36E+01	0	263	28.40%	6995.2	14.36%
ETS(ETS)/Promoter/Homer	AACCGGAAGT	1.00E-27	-6.30E+01	0	197	21.27%	4523.1	9.29%
ELF3(ETS)/PDAC-ELF3-ChIP-Seq(GSE64557)/Homer	ANCAGGAAGT	1.00E-25	-5.91E+01	0	366	39.52%	11600.9	23.82%
ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer	AVCCGGAAGT	1.00E-24	-5.61E+01	0	252	27.21%	6913.2	14.19%
Tlx?(NR)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer	CTGGCAGSCTGCCA	1.00E-23	-5.41E+01	0	253	27.32%	7050.8	14.47%
Bach2(bZIP)/OCILy7-Bach2-ChIP-Seq(GSE44420)/Homer	TGCTGAGTCA	1.00E-21	-5.04E+01	0	142	15.33%	3045	6.25%
EHF(ETS)/LoVo-EHF-ChIP-Seq(GSE49402)/Homer	AVCAGGAAGT	1.00E-20	-4.81E+01	0	505	54.54%	19024.8	39.06%
ELF5(ETS)/T47D-ELF5-ChIP-Seq(GSE30407)/Homer	ACVAGGAAGT	1.00E-16	-3.91E+01	0	331	35.75%	11354.2	23.31%
SPDEF(ETS)/VCaP-SPDEF-ChIP-Seq(SRA014231)/Homer	ASWTCCTGBT	1.00E-14	-3.31E+01	0	414	44.71%	15789.2	32.41%
USF1(bHLH)/GM12878-Usf1-ChIP-Seq(GSE32465)/Homer	SGTCACGTGR	1.00E-10	-2.35E+01	0	191	20.63%	6321.2	12.98%
HLF(bZIP)/HSC-HLF.Flag-ChIP-Seq(GSE69817)/Homer	RTTATGYAAB	1.00E-10	-2.32E+01	0	287	30.99%	10670.8	21.91%
c-Myc(bHLH)/LNCAP-cMyc-ChIP-Seq(Unpublished)/Homer	VCCACGTG	1.00E-10	-2.31E+01	0	164	17.71%	5203.3	10.68%
SpiB(ETS)/OCILY3-SPIB-ChIP-Seq(GSE56857)/Homer	AAAGRGGAAGTG	1.00E-09	-2.30E+01	0	122	13.17%	3494.3	7.17%
bHLHE40(bHLH)/HepG2-BHLHE40-ChIP-Seq(GSE31477)/Homer	KCACGTGMCN	1.00E-09	-2.29E+01	0	132	14.25%	3895.5	8.00%
CLOCK(bHLH)/Liver-Clock-ChIP-Seq(GSE39860)/Homer	GHCACGTG	1.00E-09	-2.11E+01	0	223	24.08%	7927.4	16.27%
MafK(bZIP)/C2C12-MafK-ChIP-Seq(GSE36030)/Homer	GCTGASTCAGCA	1.00E-08	-2.02E+01	0	121	13.07%	3623.7	7.44%
Bach1(bZIP)/K562-Bach1-ChIP-Seq(GSE31477)/Homer	AWWNTGCTGAGTCAT	1.00E-08	-1.85E+01	0	43	4.64%	835.3	1.71%
MITF(bHLH)/MastCells-MITF-ChIP-Seq(GSE48085)/Homer	RTCATGTGAC	1.00E-07	-1.76E+01	0	350	37.80%	14302	29.36%

NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq(Unpublished)/Homer	YTGCCAAG	1.00E-06	-1.61E+01	0	537	57.99%	24076.9	49.43%
IRF3(IRF)/BMDM-Irf3-ChIP-Seq(GSE67343)/Homer	AGTTTCAKTTTC	1.00E-06	-1.57E+01	0	134	14.47%	4482.6	9.20%
Reverb(NR),DR2/RAW-Reverba.biotin-ChIP-Seq(GSE45914)/Homer	GTRGGTCASTGGGTCA	1.00E-06	-1.49E+01	0	82	8.86%	2395.7	4.92%
NPAS2(bHLH)/Liver-NPAS2-ChIP-Seq(GSE39860)/Homer	KCCACGTGAC	1.00E-06	-1.46E+01	0	379	40.93%	16146.6	33.15%
MafF(bZIP)/HepG2-MafF-ChIP-Seq(GSE31477)/Homer	HWWGTCAGCAWWTTT	1.00E-06	-1.41E+01	0	109	11.77%	3549.8	7.29%
Max(bHLH)/K562-Max-ChIP-Seq(GSE31477)/Homer	RCCACGTGGYYN	1.00E-05	-1.36E+01	0	249	26.89%	9936.6	20.40%
ETS:E-box(ETS,bHLH)/HPC7-Scl-ChIP-Seq(GSE22178)/Homer	AGGAARCAGCTG	1.00E-05	-1.36E+01	0	62	6.70%	1696.4	3.48%
IRF4(IRF)/GM12878-IRF4-ChIP-Seq(GSE32465)/Homer	ACTGAAACCA	1.00E-05	-1.32E+01	0	167	18.03%	6166.8	12.66%
Usf2(bHLH)/C2C12-Usf2-ChIP-Seq(GSE36030)/Homer	GTCACGTGGT	1.00E-05	-1.31E+01	0	132	14.25%	4624.1	9.49%
Atf1(bZIP)/K562-ATF1-ChIP-Seq(GSE31477)/Homer	GATGACGTCA	1.00E-05	-1.28E+01	0	238	25.70%	9510.8	19.52%
Atf2(bZIP)/3T3L1-Atf2-ChIP-Seq(GSE56872)/Homer	NRRTGACGTCAT	1.00E-05	-1.26E+01	0	140	15.12%	5021.5	10.31%
NF-E2(bZIP)/K562-NFE2-ChIP-Seq(GSE31477)/Homer	GATGACTCAGCA	1.00E-05	-1.15E+01	0.0001	38	4.10%	913.3	1.88%
Rfx5(HTH)/GM12878-Rfx5-ChIP-Seq(GSE31477)/Homer	SCCTAGCAACAG	1.00E-04	-1.14E+01	0.0001	137	14.79%	5012.5	10.29%
n-Myc(bHLH)/mES-nMyc-ChIP-Seq(GSE11431)/Homer	VRCCACGTGG	1.00E-04	-1.12E+01	0.0001	239	25.81%	9769.6	20.06%
Tcf4(HMG)/Hct116-Tcf4-ChIP-Seq(SRA012054)/Homer	ASATCAAAGGVA	1.00E-04	-1.06E+01	0.0002	182	19.65%	7158.1	14.69%
E-box(bHLH)/Promoter/Homer	SSGGTCACGTGA	1.00E-04	-1.05E+01	0.0002	36	3.89%	885.9	1.82%
Nrf2(bZIP)/Lymphoblast-Nrf2-ChIP-Seq(GSE37589)/Homer	HTGCTGAGTCAT	1.00E-04	-1.05E+01	0.0002	32	3.46%	747.8	1.54%
STAT5(Stat)/mCD4+-Stat5-ChIP-Seq(GSE12346)/Homer	RTTTCTNAGAAA	1.00E-04	-1.04E+01	0.0002	144	15.55%	5430.6	11.15%
Atf7(bZIP)/3T3L1-Atf7-ChIP-Seq(GSE56872)/Homer	NGRTGACGTCAY	1.00E-04	-1.04E+01	0.0002	175	18.90%	6862.2	14.09%
FOXP1(Forkhead)/H9-FOXP1-ChIP-Seq(GSE31006)/Homer	NYYTGTTTACHN	1.00E-04	-1.03E+01	0.0002	165	17.82%	6412.1	13.16%
MafA(bZIP)/Islet-MafA-ChIP-Seq(GSE30298)/Homer	TGCTGACTCA	1.00E-04	-1.01E+01	0.0002	305	32.94%	13172.5	27.04%
NPAS(bHLH)/Liver-NPAS-ChIP-Seq(GSE39860)/Homer	NVCACGTG	1.00E-04	-9.60E+00	0.0004	477	51.51%	22018	45.20%

Gata2(Zf)/K562-GATA2-ChIP-Seq(GSE18829)/Homer	BBCTTATCTS	1.00E-04	-9.45E+00	0.0004	231	24.95%	9648.8	19.81%
MafB(bZIP)/BMM-Mafb-ChIP-Seq(GSE75722)/Homer	WNTGCTGASTCAGCANWTTY	1.00E-04	-9.38E+00	0.0005	166	17.93%	6570	13.49%
BMAL1(bHLH)/Liver-Bmal1-ChIP-Seq(GSE39860)/Homer	GNCACGTG	1.00E-03	-9.05E+00	0.0006	527	56.91%	24757.9	50.83%
PU.1-IRF(ETS:IRF)/Bcell-PU.1-ChIP-Seq(GSE21512)/Homer	MGGAAGTGAAAC	1.00E-03	-8.72E+00	0.0008	411	44.38%	18773.1	38.54%
c-Jun-CRE(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer	ATGACGTCATCY	1.00E-03	-8.50E+00	0.001	119	12.85%	4515.6	9.27%
NFkB-p50,p52(RHD)/Monocyte-p50-ChIP-Chip(Schreiber_et_al.)/Homer	GGGGGAATCCCC	1.00E-03	-8.49E+00	0.001	42	4.54%	1213.2	2.49%
ISRE(IRF)/ThioMac-LPS-Expression(GSE23622)/Homer	AGTTTCASTTTC	1.00E-03	-8.41E+00	0.0011	30	3.24%	765.9	1.57%
GATA(Zf),IR4/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer	NAGATWNBNATCTNN	1.00E-03	-8.37E+00	0.0011	41	4.43%	1181.4	2.43%
PRDM1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer	ACTTTCACTTTC	1.00E-03	-8.31E+00	0.0012	189	20.41%	7806.4	16.03%
Gata1(Zf)/K562-GATA1-ChIP-Seq(GSE18829)/Homer	SAGATAAGRV	1.00E-03	-8.12E+00	0.0014	206	22.25%	8653	17.76%
NFAT:AP1(RHD,bZIP)/Jurkat-NFATC1-ChIP-Seq(Jolma_et_al.)/Homer	SARTGGAAAAWRTGAGTCAB	1.00E-03	-8.03E+00	0.0015	74	7.99%	2568.8	5.27%
PAX5(Paired,Homeobox)/GM12878-PAX5-ChIP-Seq(GSE32465)/Homer	GCAGCCAAGCRTGACH	1.00E-03	-7.96E+00	0.0016	136	14.69%	5361.1	11.01%
Tcf3(HMG)/mES-Tcf3-ChIP-Seq(GSE11724)/Homer	ASWTCAAAGG	1.00E-03	-7.74E+00	0.002	108	11.66%	4105.9	8.43%
ZNF322(Zf)/HEK293-ZNF322.GFP-ChIP-Seq(GSE58341)/Homer	GAGCCTGGTACTGWGCCTGR	1.00E-03	-7.52E+00	0.0025	122	13.17%	4771.2	9.79%
FOXK2(Forkhead)/U2OS-FOXK2-ChIP-Seq(E-MTAB-2204)/Homer	SCHTGTTTACAT	1.00E-03	-7.32E+00	0.003	221	23.87%	9514.8	19.53%
Hoxc9(Homeobox)/Ainv15-Hoxc9-ChIP-Seq(GSE21812)/Homer	GGCCATAAATCA	1.00E-03	-7.18E+00	0.0034	157	16.95%	6457.2	13.26%
TCFL2(HMG)/K562-TCF7L2-ChIP-Seq(GSE29196)/Homer	ACWTCAAAGG	1.00E-03	-7.15E+00	0.0035	43	4.64%	1339.1	2.75%
TFE3(bHLH)/MEF-TFE3-ChIP-Seq(GSE75757)/Homer	GTCACGTGACYV	1.00E-03	-7.13E+00	0.0035	39	4.21%	1179.7	2.42%
X-box(HTH)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer	GGTTGCCATGGCAA	1.00E-03	-7.04E+00	0.0038	54	5.83%	1802.4	3.70%
IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer	GRAASTGAAAST	1.00E-03	-6.96E+00	0.004	113	12.20%	4429.5	9.09%
PU.1:IRF8(ETS:IRF)/pDC-Irf8-ChIP-Seq(GSE66899)/Homer	GGAAGTGAAAST	1.00E-03	-6.91E+00	0.0042	78	8.42%	2852.8	5.86%
Pax8(Paired,Homeobox)/Thyroid-Pax8-ChIP-Seq(GSE26938)/Homer	GTCATGCHTGRCTGS	1.00E-02	-6.90E+00	0.0042	126	13.61%	5040.4	10.35%

Foxa3(Forkhead)/Liver-Foxa3-ChIP-Seq(GSE77670)/Homer	BSNTGTTTACWYWGN	1.00E-02	-6.78E+00	0.0046	120	12.96%	4777.2	9.81%
IRF2(IRF)/Erythroblas-IRF2-ChIP-Seq(GSE36985)/Homer	GAAASYGAAASY	1.00E-02	-6.71E+00	0.0049	42	4.54%	1329.1	2.73%
JunD(bZIP)/K562-JunD-ChIP-Seq/Homer	ATGACGTCATCN	1.00E-02	-6.63E+00	0.0053	42	4.54%	1335.8	2.74%
E2F4(E2F)/K562-E2F4-ChIP-Seq(GSE31477)/Homer	GGCGGGAAAH	1.00E-02	-6.23E+00	0.0078	76	8.21%	2837.6	5.83%
c-Myc(bHLH)/mES-cMyc-ChIP-Seq(GSE11431)/Homer	VVCCACGTGG	1.00E-02	-6.13E+00	0.0085	172	18.57%	7346.4	15.08%
Gata6(Zf)/HUG1N-GATA6-ChIP-Seq(GSE51936)/Homer	YCTTATCTBN	1.00E-02	-6.00E+00	0.0096	286	30.89%	13003.2	26.69%
CEBP(bZIP)/ThioMac-CEBPb-ChIP-Seq(GSE21512)/Homer	ATTGCGCAAC	1.00E-02	-5.79E+00	0.0117	184	19.87%	7991.7	16.41%
Stat3+il21(Stat)/CD4-Stat3-ChIP-Seq(GSE19198)/Homer	SVYTTCCNGGAARB	1.00E-02	-5.75E+00	0.012	241	26.03%	10806.5	22.18%
STAT1(Stat)/HelaS3-STAT1-ChIP-Seq(GSE12782)/Homer	NATTTCCNGGAAAT	1.00E-02	-5.69E+00	0.0126	111	11.99%	4512.2	9.26%
Tbox:Smad(T-box,MAD)/ESCd5-Smad2_3-ChIP-Seq(GSE29422)/Homer	AGGTGHCAGACA	1.00E-02	-5.48E+00	0.0156	87	9.40%	3428.6	7.04%
CHR(?)/Hela-CellCycle-Expression/Homer	SRGTTTCAAA	1.00E-02	-5.44E+00	0.016	191	20.63%	8402.6	17.25%
STAT6(Stat)/Macrophage-Stat6-ChIP-Seq(GSE38377)/Homer	TTCCKNAGAA	1.00E-02	-5.37E+00	0.0169	192	20.73%	8464.9	17.38%
CEBP:AP1(bZIP)/ThioMac-CEBPb-ChIP-Seq(GSE21512)/Homer	DRTGTTGCAA	1.00E-02	-5.30E+00	0.018	225	24.30%	10109.9	20.75%
ZNF264(Zf)/HEK293-ZNF264.GFP-ChIP-Seq(GSE58341)/Homer	RGGGCACTAACY	1.00E-02	-5.25E+00	0.0187	210	22.68%	9376	19.25%
Foxa2(Forkhead)/Liver-Foxa2-ChIP-Seq(GSE25694)/Homer	CYTGTTTACWYW	1.00E-02	-5.19E+00	0.0197	266	28.73%	12184.7	25.01%
E2F1(E2F)/Hela-E2F1-ChIP-Seq(GSE22478)/Homer	CWGGCGGGAA	1.00E-02	-5.17E+00	0.0198	39	4.21%	1324.4	2.72%
NFAT(RHD)/Jurkat-NFATC1-ChIP-Seq(Jolma_et_al.)/Homer	ATTTTCCATT	1.00E-02	-5.16E+00	0.02	269	29.05%	12343.9	25.34%
Gata4(Zf)/Heart-Gata4-ChIP-Seq(GSE35151)/Homer	NBWGATAAGR	1.00E-02	-5.13E+00	0.0204	305	32.94%	14170.4	29.09%
p53(p53)/Saos-p53-ChIP-Seq(GSE15780)/Homer	RRCATGYCYRGRCATGYYYN	1.00E-02	-5.03E+00	0.0221	44	4.75%	1552	3.19%
p53(p53)/Saos-p53-ChIP-Seq/Homer	RRCATGYCYRGRCATGYYYN	1.00E-02	-5.03E+00	0.0221	44	4.75%	1552	3.19%
CEBP:CEBP(bZIP)/MEF-Chop-ChIP-Seq(GSE35681)/Homer	NTNATGCAAYMNNHTGMAAY	1.00E-02	-5.01E+00	0.0224	49	5.29%	1771.7	3.64%
FOXK1(Forkhead)/HEK293-FOXK1-ChIP-Seq(GSE51673)/Homer	NVWTGTTTAC	1.00E-02	-4.88E+00	0.0251	315	34.02%	14742	30.26%
Stat3(Stat)/mES-Stat3-ChIP-Seq(GSE11431)/Homer	CTTCCGGGAA	1.00E-02	-4.79E+00	0.0273	169	18.25%	7456.8	15.31%

Table S3. Motif enrichment of known motifs by HOMER in *Nr1d1*$^{–/–}$ NKp46$^{–}$ ILC3s.

Rank	Motif	Best match	P-value	Log P-value	# of Target Sequences with Motif(of 1138)	% of Target Sequences with Motif	# of Background Sequences with Motif(of 48512)	% of Background Sequences with Motif
1	RACAGGAAGY	Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq(Barski_et_al.)/Homer(0.967)	1.00E-69	-160.02	334	36.07%	6378	13.09%
2	TGTGGTTT	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.981)	1.00E-48	-111.56	292	31.53%	6284.1	12.90%
3	VTGASTCAKN	Atf3(bZIP)/GBM-ATF3-ChIP-Seq(GSE33912)/Homer(0.985)	1.00E-39	-91.68	251	27.11%	5457.5	11.20%
4	TGGCACNVWGCC	Tlx?(NR)/NPC-H3K4me1-ChIP-Seq(GSE16256)/Homer(0.907)	1.00E-38	-88.04	225	24.30%	4665	9.58%
5	GTTATGTAAC	NFIL3/MA0025.1/Jaspar(0.920)	1.00E-34	-79.06	75	8.10%	636.2	1.31%
6	AACTAGGTCA	RORgt(NR)/EL4-RORgt.Flag-ChIP-Seq(GSE56019)/Homer(0.970)	1.00E-33	-76.48	136	14.69%	2154	4.42%
7	CTGGCAGCCA	NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq(Unpublished)/Homer(0.722)	1.00E-15	-35.35	296	31.97%	10046.2	20.62%
8	DTGACCTCATTT	JUND(var.2)/MA0492.1/Jaspar(0.767)	1.00E-13	-31.55	21	2.27%	113.3	0.23%
9	CACGTGAC	Arntl/MA0603.1/Jaspar(0.982)	1.00E-13	-30.55	219	23.65%	7012.8	14.40%

Table S4. ***De novo*** **motif enrichment by HOMER in** ***Nr1d1***$^{-/-}$ **NKp46**$^{-}$ **ILC3s.**

Primer	**Forward**	**Reverse**
Nr1d1	TGGCATGGTGCTACTGTGTAAGG	ATATTCTGTTGGATGCTCCGGCG
Nr1d1	GTCTCTCCGTTGGCATGTCT	CCAAGTTCATGGCGCTCT
Nr1d2	GGAGTTCATGCTTGTGAAGGCTGT	CAGACACTTCTTAAAGCGGCACTG
Clock	CACTCTCACAGCCCCACTGTAC	CCCCACAAGCTACAGGAGCAGT
Per1	TGAAGCAAGACCGGGAGAG	CACACACGCCATCACATCAA
Dbp	AATGACCTTTGAACCTGATCCCGCT	GCTCCAGTACTTCTCATCCTTCTGT
Nfil3	CTTTCAGGACTACCAGACATCCAA	GATGCAACTTCCGGCTACCA
Bmal1	TGACCCTCATGGAAGGTTAGAA	GGACATTGCATTGCATGTTGG
Rorc	TTCACCCCACCTCCACTG	GTGCAGGAGTAGGCCACATT
Eubacteria 16s rDNA	CGGCAACGAGCGCAACCC	CCATTGTAGCACGTGTGTAGCC
Actb	GACGGCCAGGTCATCACTATTG	AGGAAGGCTGGAAAAGAGCC
Il17a	CCAAGGACTTCCTCCAGAATG	CCCAGATCACAGAGGGATATCTA
Il22	TCCTGACCAAACTCAGCAATC	CTTGATCTCTCCACTCTCTCCA

Table S5. Sequences of primers used for qPCR