

Table S1. Top 25 up- and downregulated genes in Nur77-KO vs WT BMM

Gene Symbol	Log2 Fold Change (KO/WT)	p-value	Entrez Gene ID
Upregulated genes			
<i>Npy</i>	5.6062	4.07E-04	109648
<i>M34473</i>	5.4207	9.67E-05	243469
<i>Eif2s3y</i>	4.6783	8.92E-04	26908
<i>abParts</i>	4.2134	5.56E-04	16142
<i>Ighg</i>	2.8760	1.14E-05	16019
<i>S100a9</i>	2.8396	1.62E-03	20202
<i>Col1a1</i>	2.6363	1.11E-02	12842
<i>Itga11</i>	2.6357	2.18E-03	319480
<i>Ltf</i>	2.5876	5.07E-03	17002
<i>Serping1</i>	2.5568	1.96E-02	12258
<i>Cxcl12</i>	2.5079	2.00E-02	20315
<i>Dkk3</i>	2.3926	2.97E-02	50781
<i>Ogn</i>	2.3816	6.60E-03	18295
<i>Igh-A (1g2)</i>	2.3501	2.30E-02	16061
<i>Actg2</i>	2.3012	5.30E-02	11468
<i>Knq2</i>	2.2874	1.42E-03	385643
<i>Gfpt1</i>	2.2597	4.73E-06	14583
<i>Wisp2</i>	2.2514	2.50E-03	22403
<i>Chac1</i>	2.2337	7.28E-02	69065
<i>Thbs2</i>	2.0130	9.57E-02	21826
<i>Ccdc80</i>	2.0016	8.76E-03	67896
<i>Dcn</i>	1.9975	9.20E-02	13179
<i>Timp3</i>	1.9637	2.82E-02	21859
<i>Mxd1</i>	1.9573	1.71E-03	17119
<i>Bicc1</i>	1.9430	1.18E-03	83675
Downregulated genes			
<i>Tgfb1</i>	-1.0752	0.12214	21810
<i>Cav</i>	-1.0835	0.01927	12389
<i>Fcrls</i>	-1.0933	0.00038	80891
<i>Cd74</i>	-1.1044	0.00368	16149
<i>Cytip</i>	-1.1077	0.00286	227929
<i>Stap1</i>	-1.1086	0.04858	56792
<i>T</i>	-1.1582	0.00591	20997
<i>Gpr84</i>	-1.1593	0.00394	80910
<i>3110002H16Rik</i>	-1.1687	0.04292	76482
<i>Uchl1</i>	-1.1945	0.06995	22223
<i>H2-Eb1</i>	-1.3139	0.00026	14969
<i>Fos</i>	-1.3209	0.01022	14281
<i>H2-Ab1</i>	-1.3297	0.00025	14961
<i>Ttc15</i>	-1.3564	0.01063	217449
<i>Olfm1</i>	-1.3627	0.07107	56177
<i>Ahr</i>	-1.3669	0.00426	11624
<i>Xist</i>	-1.4229	0.02179	213742
<i>Pde1c</i>	-1.4947	0.02739	18575
<i>Ciita</i>	-1.5196	0.01751	12265
<i>Clec4b1</i>	-1.5515	0.00063	69810
<i>Gdf3</i>	-1.6907	0.00001	14562
<i>Pou6f1</i>	-1.7861	0.00009	19009
<i>Spint1</i>	-1.8194	0.00188	20732
<i>Anxa4</i>	-1.9455	0.00001	11746
<i>Cx3cr1</i>	-2.4795	<0.00001	13051

Table S2. Top 25 canonical pathways associated with differentially expressed genes in Nur77-KO vs WT BMM

IPA canonical pathway	p-value	Adjusted p-value	Ratio	z-score	Genes
Inhibition of Matrix Metalloproteinases	1.45E-07	5.89E-05	0.31	n/a	HSPG2,TIMP3,MMP7,MMP23B,SDC1,SDC2, MMP14,THBS2,MMP2,MMP9, TIMP2
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.00E-05	0.002	0.12	n/a	VCAM1,FN1,COL6A2,COL12A1,FGFR2, VEGFB,MMP2,IGFBP5,PDGFC,COL1A2, VEGFA,COL1A1,IGF2,IGF1,CD40,TGFB3, CD14,EDNRA,MMP9,TNFSF14,TIMP2, COL3A1
Inhibition of Angiogenesis by TSP1	3.55E-04	0.033	0.21	0.000	VEGFA,HSPG2,SDC1,SDC2,MAPK10,AKT3, MMP9
Dendritic Cell Maturation	3.80E-04	0.033	0.11	n/a	CREB3L4,HLA-DQB1,CREB5,DDR1,COL1A2, TRAF6,PIK3R3,COL1A1,CD40,HLA-DMA, IL1RN,FSCN1,MAPK10, AKT3,HLA-DRB5, COL3A1
Granulocyte Adhesion and Diapedesis	4.37E-04	0.033	0.11	n/a	ITGB1,VCAM1,MMP7,SDC1,Ppbb,MMP14, CXCL12,MMP2,MMP23B,ITGAM,ICAM2, Ccl8,SDC2,IL1RN,MMP9,HSPB1
HIF1α Signaling	0.001	0.033	0.13	n/a	VEGFA,PIK3R3,MMP7,MMP23B,MMP14, MAPK10,AKT3,VEGFB,MMP2,TCEB1, PDGFC,MMP9
Bladder Cancer Signaling	0.001	0.033	0.13	n/a	VEGFA,CDKN2A,MMP7,MMP23B,MMP14, FGF14,VEGFB,MMP2,PDGFC, MMP9,FGF13
Intrinsic Prothrombin Activation Pathway	0.001	0.033	0.22	n/a	KNG1,COL1A2,COL1A1,KLK3,F8, COL3A1
ILK Signaling	0.001	0.033	0.10	1.500	ITGB1,SNAI2,FN1,VEGFB,CREB3L4,CREB5, RICTOR,PDGFC,VEGFA,PIK3R3,FOS, PPAP2B,IRS1,MAPK10,AKT3, ACTG2,MMP9
Pancreatic Adenocarcinoma Signaling	0.001	0.050	0.12	1.265	VEGFA,CDKN2A,PIK3R3,HMOX1,MAPK10, TGFB3,AKT3,VEGFB,E2F3,NOTCH1,PDGFC, MMP9
Atherosclerosis Signaling	0.002	0.068	0.11	n/a	COL1A2,COL1A1,VCAM1,CD40,IL1RN, CXCL12,ALOX12,S100A8,PDGFC,TNFSF14, MMP9,COL3A1
Agranulocyte Adhesion and Diapedesis	0.002	0.068	0.10	n/a	ITGB1,AOC3,VCAM1,MMP7,FN1,Ppbb, MMP14,CXCL12,MMP2,MMP23B,ICAM2, Ccl8,IL1RN,ACTG2,MMP9
Role of IL-17A in Psoriasis	0.002	0.068	0.43	n/a	S100A9,IL17RC,S100A8
Acute Phase Response Signaling	0.002	0.068	0.10	0.905	SOCS3,SERPING1,FN1,CP,TRAF6,PIK3R3, HMOX1,FOS,HP,F8,IL1RN,AKT3OSMR, CRABP2,C2
Aryl Hydrocarbon Receptor Signaling	0.003	0.069	0.10	1.890	AHRR,GSTA3,CDKN2A,FOS,GSTM1,CCND2, NFIC,ALDH1L2,GSTM5,NQO1,TGFB3,NFIB, HSPB1
Role of IL-17F in Allergic Inflammatory Airway Diseases	0.003	0.089	0.17	n/a	TRAF6,RPS6KA6,IGF1,IL17RC,CREB3L4, CREB5
Leukocyte Extravasation Signaling	0.005	0.116	0.09	1.604	ITGB1,TIMP3,VCAM1,ARHGAP6,MMP7, MMP14,CXCL12,RAPGEF3,MMP2,PIK3R3, MMP23B,ITGAM,MAPK10,ACTG2,MMP9, TIMP2
IL-6 Signaling	0.007	0.139	0.10	1.000	VEGFA,TRAF6,PIK3R3,COL1A1,SOCS3,FOS, IL1RN,MAPK10,AKT3,CD14,HSPB1

Ketogenesis	0.007	0.139	0.30	n/a	ACAT2,HMGCS1,HADHA
IL-8 Signaling	0.007	0.139	0.08	1.807	VCAM1,VEGFB,MMP2,PDGFC,VEGFA,TRAF6,PIK3R3,FOS,HMOX1,ITGAM,CCND2,MPO,MAPK10,AKT3,MMP9
IL-12 Signaling and Production in Macrophages	0.008	0.139	0.10	n/a	TRAF6,PIK3R3,FOS,Ifna4,CD40,MAPK10,TGFB3,AKT3,ALOX12,S100A8,IFNA4
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	0.008	0.139	0.07	n/a	SOCS3,VCAM1,FN1,SFRP2,DAAM1,GNAQ,CXCL12,IL17RC,VEGFB,CREB3L4,CREB5,PDGFC,TRAF6,VEGFA,PIK3R3,FOS,IL1RN,DKK3,TLR7,AKT3,NFATC2
Ovarian Cancer Signaling	0.008	0.139	0.09	n/a	VEGFA,CDKN2A,PIK3R3,GJA1,MMP7,PTGS1AKT3,VEGFB,EDNRA,MMP2,PDGFC,MMP9
Glutaryl-CoA Degradation	0.009	0.158	0.27	n/a	ACAT2,HADHA,HSD17B8
IL-17A Signaling in Fibroblasts	0.010	0.162	0.16	n/a	TRAF6,NFKBID,FOS,LCN2,IL17RC

The pathways in bold involve matrix metalloproteinases (MMPs); red indicates upregulation, green indicates downregulation; n/a: not available

Table S3. Top 20 gene sets identified with GSEA that are upregulated in Nur77-KO vs WT BMM

Biocarta, KEGG, PID and Reactome pathways	NES	p-value	Adjusted p-value	Genes contributing to the pathway
Collagen formation (Reactome)	2.441	<0.001	<0.001	COL1A1,PCOLCE,COL12A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,COL16A1,COL4A2,BMP1,SERPINH1,PCOLCE2,COL4A1,ADAMTS2,COL14A1,PLOD2,COL6A3,COL8A1,COL5A2,COL17A1
Extracellular matrix organization (Reactome)	2.411	<0.001	<0.001	COL1A1,PCOLCE,COL12A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,MMP2,COL16A1,COL4A2,BMP1,SERPINH1,MMP3,PCOLCE2,COL4A1,ADAMTS2,COL14A1,PLOD2,COL6A3,PLG,MMP13,COL8A1,MMP9,TIMP1,COL5A2,COL17A1
Syndecan 1 pathway (PID)	2.191	<0.001	<0.001	COL1A1,COL12A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,CCL5,COL16A1,COL4A1,SDC1,COL14A1,COL6A3,COL8A1,MMP9,COL5A2,COL17A1
AVB3 integrin pathway (PID)	2.179	<0.001	<0.001	COL1A1,COL12A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,COL16A1,FN1,BCAR1,COL4A1,GPR124,SDC1,COL14A1,COL6A3,SRC,CSF1,COL8A1,COL5A2,COL17A1,VCL,RPS6KB1,COL2A1,EDIL3,RHOA
Signaling by PDGF (Reactome)	2.139	<0.001	<0.001	COL1A1,THBS2,COL3A1,PDGFRA,COL1A2,COL5A1,COL6A1,COL6A2,COL4A2,ADCY3,BCAR1,COL4A1,PDGFC,COL6A3,SRC,TRIB3,PLG,FOXO3,COL5A2,PLAT,STAT5A,ADCY6,GSK3A,THEM4,MAP2K1,COL2A1,PDGFRB,PDE1A,COL9A1,THBS1,RAPGEF1
ECM receptor interaction (KEGG)	2.114	<0.001	0.001	ITGA11,COL1A1,THBS2,COL3A1,SDC2,COL1A2,COL5A1,COL6A1,COL6A2,HSPG2,COL4A2,FN1,COL4A1,SDC1,COL6A3,TNC,ITGA9,LAMB2,LAMA4,COL5A2
Integrin1 pathway (PID)	2.096	<0.001	0.001	ITGA11,COL1A1,THBS2,COL3A1,FBN1,COL1A2,COL5A1,COL6A1,COL6A2,NID1,VCAM1,FN1,COL4A1,COL6A3,TNC,ITGA9,LAMB2,LAMA4,COL5A2
Focal adhesion (KEGG)	1.955	<0.001	0.017	ITGA11,COL1A1,THBS2,COL3A1,PDGFRA,COL1A2,COL5A1,COL6A1,COL6A2,CCND2,COL4A2,MYL9,FN1,BCAR1,MYLK,COL4A1,BRAF,PDGFC,COL6A3,TNC,SRC,EGFR,PAK3,PIK3R3,ITGA9,RAC3,LAMB2,LAMA4,COL5A2,FLT4,PARVG,VEGFC,VCL,MAPK8,DOCK1,VEGFB,FLNB,MAP2K1,SHC4,COMP,COL2A1,PDGFRB,VWF,RHOA,IBSP
Integrin3 pathway (PID)	1.933	<0.001	0.021	COL1A1,FBN1,COL1A2,CYR61,SPHK1,FN1,COL4A1,SDC1,TNC,LAMA4,PVR,EDIL3,PDGFRB,FGB,IBSP,THBS1,VEGFA
Smooth muscle contraction (Reactome)	1.915	<0.001	0.024	ACTG2,MYL9,CALD1,TPM2,MYLK,ACTA2,VCL
Integrin cell surface interactions (Reactome)	1.875	<0.001	0.041	ITGA11,COL1A1,FBN1,COL1A2,RAPGEF3,COL4A2,VCAM1,FN1,BCAR1,COL4A1,TNC,SRC,ITGAX,ITGA9,LAMB2,AMICA1,CDH1,COL2A1,VWF,FGB,IBSP,RAPGEF4
NCAM1 interactions (Reactome)	1.788	<0.001	0.112	COL1A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,COL4A2,COL4A1,COL6A3,NCAM1,COL5A2
Response to elevated platelet cytosolic Ca ²⁺ (Reactome)	1.772	<0.001	0.126	KNG1,SERPING1,SPARC,TGFB3,FN1,PPBP,SERPINF2,TGFB2,PLG,TIMP1,VEGFC,VCL,VEGFB,VWF,FGB
NCAM signaling for neurite out growth (Reactome)	1.765	<0.001	0.125	COL1A1,COL3A1,COL1A2,COL5A1,COL6A1,COL6A2,COL4A2,COL4A1,COL6A3,SRC,NCAM1,COL5A2,GDNF,MAP2K1,COL2A1
Sphingolipid de novo biosynthesis (Reactome)	1.757	0.002	0.128	PPAP2A,SPHK1,SGMS2,PPAP2B,SPTLC2,COL4A3BP
Platelet activation signaling and aggregation (Reactome)	1.749	<0.001	0.131	KNG1,COL1A1,SERPING1,COL1A2,RAPGEF3,MGLL,SPARC,TGFB3,ADRA2A,FN1,BCAR1,PPBP,GNA15,SERPINF2,SRC,TGFB2,F2R,PLG,PIK3R3,LCK,TIMP1,VEGFC,VCL,VEGFB,GNAI1,DAGLA,GP5,VWF,FGB,RHOA,RAPGEF4,LAT,P2RY1,THBS1,DGKE,VEGFA,RASGRP1

Keratan sulfate biosynthesis (Reactome)	1.747	0.013	0.127	OGN,CHST1,ST3GAL2
Intrinsic pathway (Biocarta)	1.732	0.012	0.143	KNG1,SERPING1,COL4A2,COL4A1,F2R
A tetrasaccharide linker sequence is required for gag synthesis (Reactome)	1.717	0.003	0.160	DCN,SDC2,HSPG2,SDC1,GPC4,BCAN,BGN,B3GAT2,B4GALT7,GPC1
CXCR4 pathway (Biocarta)	1.708	0.007	0.165	CXCL12,BCAR1,MAP2K1,GNAI1

The pathways in bold involve ECM interactions; NES: Normalized enrichment score

Table S4. Upstream Regulators in Nur77-KO vs WT BMM

Upstream regulator	Molecule type	*Activation Z-Score	**p-Value of Overlap
KRAS	enzyme	-2.575	1.49E-06
DICER1	enzyme	-2.538	1.81E-02
NR4A3	ligand-dependent nuclear receptor	-2.224	4.47E-02
NR4A1	ligand-dependent nuclear receptor	-2.216	2.67E-03
CIITA	transcription regulator	-2.190	1.30E-03
POMC	peptide hormone	-2.051	8.92E-03
AHR	ligand-dependent nuclear receptor	-2.013	8.04E-05
IRF1	transcription regulator	-2.013	2.35E-01
PAX5	transcription regulator	-2.000	2.00E-02
MYOG	transcription regulator	2.000	2.97E-03
IL17RA	transmembrane receptor	2.000	2.00E-02
F2RL1	g-protein coupled receptor	2.000	6.23E-02
EGFR	kinase	2.097	1.19E-09
RAC1	enzyme	2.120	1.49E-06
CTNNB1	transcription regulator	2.140	4.31E-09
TCF3	transcription regulator	2.158	2.28E-03
F2R	g-protein coupled receptor	2.176	1.62E-04
TFEB	transcription regulator	2.200	6.75E-03
SMARCA2	transcription regulator	2.213	1.21E-03
F2	peptidase	2.219	6.34E-03
SEMA7A	transmembrane receptor	2.236	1.63E-03
VGLL3	transcription regulator	2.236	6.88E-05
TP53	transcription regulator	2.341	8.74E-07
ATF4	transcription regulator	2.369	6.75E-02
HIF1A	transcription regulator	2.407	1.55E-07
EGR1	transcription regulator	2.609	1.44E-07
SMARCA4	transcription regulator	2.615	2.87E-05
FOSL1	transcription regulator	2.745	4.81E-04
PRDM1	transcription regulator	2.758	2.62E-01
NR1I2	ligand-dependent nuclear receptor	3.123	2.73E-02
ERBB3	kinase	3.167	1.95E-07

*The bias-corrected z-score is used to infer the activation states of upstream regulators. It is calculated from the proportions of genes that are differentially regulated in an expected direction based on the known interactions between the regulator and the genes present in the Ingenuity database. Those genes with a z-score greater than 2 or less than -2 are considered to be either activated or inhibited respectively.

**The p-value of overlap is the calculated statistical significance of overlap between genes from the dataset and genes that are known to be regulated by the upstream regulator using Fisher's Exact Test.

Table S5. Top 25 up- and downregulated genes in LPS-stimulated Nur77-KO vs WT BMM

Gene Symbol	Log2 Fold Change (KO/WT)	p-value	Entrez Gene ID
Upregulated genes			
<i>M34473</i>	3.8122	0.00239	243469
<i>Npy</i>	3.7195	0.00972	109648
<i>abParts</i>	3.6913	0.00000	16019
<i>abParts</i>	3.3032	0.00401	16142
<i>Slc11a2</i>	2.5333	0.00000	18174
<i>Eif2s3y</i>	2.3580	0.05844	26908
<i>Mxd1</i>	1.9684	0.00163	17119
<i>Ciita</i>	1.9550	0.00353	12265
<i>BC018473</i>	1.9113	0.00175	193217
<i>Gfpt1</i>	1.7600	0.00008	14583
<i>Serpinh1</i>	1.7300	0.26895	12406
<i>Kctd17</i>	1.7261	0.00088	72844
<i>R3hcc1</i>	1.6868	0.00003	71843
<i>Serping1</i>	1.5740	0.15043	12258
<i>Chi3l4</i>	1.5691	0.00938	104183
<i>Clic5</i>	1.5597	0.00666	224796
<i>Cxcl12</i>	1.5385	0.13358	20315
<i>Fnip1</i>	1.5297	0.02440	216742
<i>P4ha2</i>	1.5282	0.09063	18452
<i>Rragd</i>	1.4409	0.00002	52187
<i>abParts</i>	1.4149	0.01144	16098
<i>St6galnac2</i>	1.4055	0.09316	20446
<i>Actg2</i>	1.3902	0.22570	11468
<i>St5</i>	1.3678	0.14188	76954
<i>Nup210</i>	1.3633	0.00088	54563
Downregulated genes			
<i>Prpf39</i>	-1.2123	0.01697	328110
<i>Il16</i>	-1.2125	0.02781	16170
<i>Paqr9</i>	-1.2398	0.01637	75552
<i>Lrch4</i>	-1.2447	0.02609	231798
<i>Sla</i>	-1.2568	0.05813	20491
<i>Siglece</i>	-1.2666	0.00123	83382
<i>Shisa3</i>	-1.2847	0.01924	330096
<i>Rtn1</i>	-1.2852	0.06569	104001
<i>Ankrd37</i>	-1.2955	0.02359	654824
<i>Fmo3</i>	-1.3048	0.00930	14262
<i>Creb3l4</i>	-1.3095	0.00275	78284
<i>St7</i>	-1.3286	0.04667	64213
<i>Mdm1</i>	-1.3384	0.00766	17245
<i>Gm14378</i>	-1.3524	0.01689	100044509
<i>Gramd1a</i>	-1.3585	0.00324	52857
<i>Fos</i>	-1.3700	0.00814	14281
<i>Uchl1</i>	-1.3708	0.04040	22223
<i>Pou6f1</i>	-1.4433	0.00068	19009
<i>Bco2</i>	-1.4619	0.00237	170752
<i>Il6ra</i>	-1.5065	0.00012	16194
<i>1190003J15Rik</i>	-1.5252	0.00421	76974
<i>Jhdm1d</i>	-1.5279	0.17590	338523
<i>Gdf3</i>	-1.5795	0.00002	14562
<i>Anxa4</i>	-1.6957	0.00003	11746
<i>Il19</i>	-1.8319	0.00134	329244

Table S6. Top 25 canonical pathways associated with differentially expressed genes in LPS-stimulated Nur77-KO vs WT BMM

IPA canonical pathway	p-value	Adjusted p-value	Ratio	z-score	Genes
Glucocorticoid Receptor Signaling	0.003	0.465	0.100	n.a	IFNG,CD3E,SGK1,IL10,HSPA1A/HSPA1B,PIK3R5,GTF2F1,CCL11,NFATC1,MED14,TGFB2,FOS,TRAF2,POU2F1,POLR2A,NCOA2,DUSP1,SMARCA2,MAPK3,CREB1,HSP90AA1,NFATC2,PIK3R2,HLTF
Systemic Lupus Erythematosus Signaling	0.003	0.465	0.113	n.a	KNG1,CD3E,IL10,IL6R,PRPF39,PIK3R5FCGR2B,SART1,LSM2,NFATC1,CD28,FOS,LCK,MAPK3,CREM,NFATC2,PIK3R2
T Cell Receptor Signaling	0.005	0.465	0.128	n.a	FYN,FOS,CD28,LCK,CD3E,GRAP2,MAPK3,PIK3R5,NFATC2,PIK3R2,CD8BNFATC1
PKCθ Signaling in T Lymphocytes	0.006	0.465	0.120	-0.577	CD28,FOS,FYN,LCK,POU2F1,CD3E,HLA-DMA,GRAP2,MAPK3,PIK3R5,NFATC2,PIK3R2,NFATC1
CTLA4 Signaling in Cytotoxic T Lymphocytes	0.008	0.465	0.132	n.a	FYN,CD28,LCK,AP1G2,CD3E,GRAP2,CLTC,PIK3R5,PIK3R2,CD8B
Spermine and Spermidine Degradation I	0.009	0.465	0.667	n.a	SMOX,PAOX
Ascorbate Recycling (Cytosolic)	0.009	0.465	0.667	n.a	GSTO2,GLRX
L-serine Degradation	0.009	0.465	0.667	n.a	SRR,SDS
GDNF Family Ligand-Receptor Interactions	0.010	0.465	0.134	-1.667	FOS,DOK2,IRS1,MAPK3,CREB1,PIK3R5,IRS2,DOK3,PIK3R2
ILK Signaling	0.010	0.465	0.101	0.243	ITGB1,MYH10,FBLIM1,PIK3R5,VEGFB,CREB3L4,RICTOR,VEGFA,FOS,RHOT1,MAPK3,IRS1,CREB1,IRS2,ITGB4,PIK3R2,CTNNB1
Intrinsic Prothrombin Activation Pathway	0.014	0.557	0.185	n.a	KNG1,COL5A3,F9,KLK3,COL2A1
Role of BRCA1 in DNA Damage Response	0.020	0.682	0.127	1.000	IFNG,POU2F1,SMARCA2,RFC2,UIMC1RBL1,RFC5,HLTF
T Helper Cell Differentiation	0.020	0.682	0.127	n.a	TGFB2,IFNG,CD28,IL10,IL12RB1,HLA-DMA,IL6R,BCL6
AMPK Signaling	0.022	0.685	0.102	-1.265	ADRA2B,TSC1,GNAS,PIK3R5,SMARCA2,IRS1,FASN,IRS2,PIK3R2,INSR,HLTF,ADRA1A,PPAT
Prostate Cancer Signaling	0.029	0.776	0.112	n.a	CCNE1,KLK3,MAPK3,CREB1,PIK3R5,HSP90AA1,CREB3L4,PIK3R2,CTNNB1
CD28 Signaling in T Helper Cells	0.032	0.776	0.102	-1.667	FYN,FOS,CD28,LCK,CD3E,GRAP2,HLA-DMA,PIK3R5,NFATC2,PIK3R2,NFATC1
Vitamin-C Transport	0.037	0.776	0.214	n.a	GSTO2,GLRX,TXNRD2
GDP-glucose Biosynthesis	0.038	0.776	0.333	n.a	HK1,PGM1
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	0.039	0.776	0.085	n.a	ITGB1,IFNG,IL10,PIK3R5,MMP13,WNT6,TNFRSF11A,IL7,CSF1R,XIAP,NFATC1,FOS,TRAF2,MAPK3,NFATC2,PIK3R2,CTNNB1,SMAD1
RANK Signaling in Osteoclasts	0.041	0.776	0.106	n.a	FOS,TRAF2,MAPK3,PIK3R5,NFATC2,PIK3R2,TNFRSF11A,XIAP,NFATC1
Prolactin Signaling	0.041	0.776	0.111	-0.378	FYN,FOS,IRS1,MAPK3,PIK3R5,NMI,PIK3R2,IRF1
iCOS-iCOSL Signaling in T Helper Cells	0.043	0.776	0.101	-1.414	GAB2,CD28,LCK,CD3E,GRAP2,HLA-DMA,PIK3R5,NFATC2,PIK3R2,NFATC1
Role of IL-17F in Allergic Inflammatory Airway Diseases	0.044	0.776	0.139	n.a	TRAF3IP2,MAPK3,CREB1,MMP13,CREB3L4
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	0.050	0.776	0.107	n.a	TGFB2,FYN,FOS,CD28,CD3E,MAPK3,NFATC2,NFATC1
Glucose and Glucose-1-phosphate Degradation	0.051	0.776	0.286	n.a	HK1,PGM1

Genes that are upregulated in Nur77-deficient BMMs are shown in red and green indicates that the expression of the gene is reduced upon Nur77 deficiency.

Z-score: a positive z-score indicates an overall increase in the activity of the pathway while a negative z-score predicts a decreased activity of that specific pathway when Nur77 is absent.

n.a., not applicable, meaning that it cannot be predicted based on the available literature whether the pathway is up- or downregulated.