Supplementary Table 1: Top downregulated (positive NES values) and upregulated (negative NES values) pathways in bone marrow-derived *Rel*$^{-/-}$ MDSCs as determined by GSEA of the RNA-seq data.

Top enriched gene signatures in WT vs *Rel*$^{-/-}$ MDSCs	NES	NOM p-val	FDR q-val
CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.88	0.002	0.158
REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	1.84	0	0.139
CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	1.81	0	0.169
LIPID_OXIDATION	1.81	0	0.163
NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	1.78	0.006	0.198
LONG_CHAIN_FATTY_ACID_TRANSPORT	1.76	0.006	0.175
FATTY_ACID_CATABOLIC_PROCESS	1.71	0	0.268
GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	1.69	0.013	0.286
REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	1.68	0.002	0.287
G2M_CHECKPOINT	-2.62	0	0
E2F_TARGETS	-2.56	0	0
MITOTIC_SPINDLE	-2.16	0	0
TNFA_SIGNALING_VIA_NFKB	-2.07	0	2.86E-04
INTERFERON_GAMMA_RESPONSE	-1.99	0	2.29E-04
INFLAMMATORY_RESPONSE	-1.99	0	1.90E-04
ALLOGRAFT_REJECTION	-1.95	0	1.63E-04
IL6_JAK_STAT3_SIGNALING	-1.80	0	0.002
INTERFERON_ALPHA_RESPONSE	-1.68	0	0.008
SPERMATOGENESIS	-1.57	0.011	0.026

NES, normalized enrichment score; NOM p value, normalized p value; FDR, false discovery rate. Statistical significance was determined by Wald test with Benjamini-Hochberg's multiple-comparison correction.

Supplementary Table 2: Top upregulated pathways in bone marrow- derived RelA−/− MDSCs as determined by Ingenuity Pathway Analysis of the RNA-seq data.

Diseases or Functions Annotation	p-Value	Predicted Activation State	Activation z-score
Leukocyte migration	1.85E-25	Increased	4.111
Quantity of cells	2.06E-24	Increased	3.309
Cell movement of leukocytes	1.01E-22	Increased	3.571
Chemotaxis of leukocytes	1.58E-22	Increased	3.195
Quantity of leukocytes	1.86E-22	Increased	3.795
Cell movement of phagocytes	4.29E-22	Increased	3.785
Quantity of blood cells	4.88E-22	Increased	3.893
Proliferation of blood cells	7.28E-21		1.744
Inflammatory response	9.79E-21	Increased	2.774

Statistical significance was determined by right-tailed Fisher's Exact Test.