

Supplemental Table I. Immune response genes down-regulated in anti-miR33 treated plaque macrophages.

ID	Gene Name	fold change (anti-miR33 vs. control)	p-value
Oas1c	2'-5' oligoadenylate synthetase 1C	-1.48	0.0119
Oas1f	2'-5' oligoadenylate synthetase 1F	-1.23	0.0252
Clec4n	C-type lectin domain family 4, member n	-2.37	0.0392
Clec5a	C-type lectin domain family 5, member a	-1.87	0.0112
Cd8a	CD8 antigen, alpha chain	-2.57	0.0247
Cd8b1	CD8 antigen, beta chain 1	-1.76	0.0032
Fcgr3	Fc receptor, IgG, low affinity III	-1.2	0.021
Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.36	0.0016
Pou2f2	POU domain, class 2, transcription factor 2	-1.17	0.0461
AF251705	cDNA sequence AF251705	-1.43	0.0235
Ccl9	chemokine (C-C motif) ligand 9	-1.43	0.0218
Cxcl15	chemokine (C-X-C motif) ligand 15	-1.34	0.0098
C1qb	complement component 1, q subcomponent, beta polypeptide	-1.11	0.0363
C9	complement component 9	-1.33	0.012
Lilrb4, Gp49a	glycoprotein 49 A; leukocyte immunoglobulin-like receptor, subfamily B, member 4	-1.16	0.0254
H2-M9	histocompatibility 2, M region locus 9	-1.21	0.0161
H2-Q5	histocompatibility 2, Q region locus 5	-1.2	0.0452
Irf8	interferon regulatory factor 8	-1.39	0.0037
Il1rl2	interleukin 1 receptor-like 2	-1.45	0.0446
Il18	interleukin 18	-1.51	0.041
Lcp1	lymphocyte cytosolic protein 1	-1.21	0.0106
Pf4	platelet factor 4	-1.67	0.0268
Prkcd	protein kinase C, delta	-1.27	0.0269
Ptpn6	protein tyrosine phosphatase, non-receptor type 6	-1.22	0.0463
Ptprc	protein tyrosine phosphatase, receptor type, C	-1.32	0.0093
Prg2	proteoglycan 2, bone marrow	-1.66	0.0423
Lilrb3	similar to Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member	-1.44	0.0067
Tlr13	toll-like receptor 13	-1.41	0.0192
Tlr6	toll-like receptor 6	-1.33	0.0101
Tnf	tumor necrosis factor	-1.51	0.025
Tnfrsf1b	TNF receptor superfamily, member 1b	-1.29	0.0354
Tnfaip8l2	TNF, alpha-induced protein 8-like 2	-1.37	0.0136

Plaque CD68+ macrophages from mice treated with PBS, control anti-miR or anti-miR33 oligonucleotides for 4 weeks were laser captured, RNA extracted and analyzed with the Affymetrix Mouse 430 2.0 arrays. Data are expressed as fold-change compared to control anti-miR. Immune response genes were significantly down-regulated in anti-miR33 compared to controls according to gene ontology (GO) analysis (Benjamini corrected p-value=8.1x10⁻³).