

Table S5

	iM1 versus M2^{neg-siPool} (qPCR)			log2FC M1 versus M2 (adj. p value < 0.05)**
	24h*	48h	72h	
Cd86	2	2	0	5.9
Cxcl10	2	2	0	12.7
Cxcl9	2	2	0	13.1
Il12b	2	1	0	11.3
Il1b	2	2	2	9.1
Ldha	-1	0	-2	2.4
Nos2	2	2	2	13.5
Stat1	2	2	0	3.8
Arg1	-2	0	0	-1.5
Fizz1	-2	-2	-2	-3.5
Mrc1	-2	-2	0	-7.3
Ppat	2	0	-2	-1.1
Tgfb	-1	0	-2	-0.8
Ym1	-2	-2	-2	-8.3

* Transcriptional changes of M1 and M2 associated genes relative to M2 macrophages treated with a negative siRNA pool were experimentally determined by quantitative PCR. Samples were extracted 24 h, 48 h and 72 h after siRNA treatment (two replicates). Upregulation or downregulation of a gene was scored for each replicate by 1 or -1, respectively.

** 24 hours after siRNA treatment