TLR9 vs. GFP expression data
Data underwent (1) Background correction, (2) Quantile normalization,
(3) Log2 transformation & (4) Mean aggregation of multiple gene copies
No graphical scaling

Expression value: 6 8 10 12

	GFP1	GFP1b	TLR9_1-rep	TLR9_1b	
	6.98	7.35	9.2	9.26	IFI35
	6.95	7.22	9.24	8.67	PLSCR1
	7.01	7.32	8.58	9.07	IFIH1
	6.24	6.75	8.74	8.68	ISG20
	6.93	7.01	7.98	8.02	IRF7
	8.13	8.19	8.79	8.36	ZC3HAV1
	8.35	8.58	7.73	7.71	LILRB1
	5.43	5.93	7.86	7.49	CCL5
	5.88	5.84	7.11	7.68	DDX58
	5.25	5.61	8.72	8.75	MX2
	4.84	5.13	6.36	6.52	RSAD2
	4.57	5.21	6.36	5.8	APOBEC3G
	4.58	4.5	6.12	6.25	IL29
	4.35	4.73	5.37	6	IFNB1
	5.97	6.1	6.05	6.49	BNIP3L
	5.34	5.31	4.47	4.45	CXCR4
	9.79	9.78	10.76	10.55	EIF2AK2
	9.79	9.91	10.58	10.45	IFNGR2
	9.84	10.12	10.92	10.84	BST2
	9.08	9.31	11	11.05	STAT1
	8.13	8.55	10.85	10.76	IRF9
	6.67	7.92	10.31	10.48	IFI44
	8.3	8.36	9.35	9.88	STAT2
	10.71	11.45	13.68	13.59	ISG15
	11.25	11.35	12.73	12.52	LCN2

Supplementary Figure 2

Figure 2: The true log2 of the quantile normalized expression signals in 4 samples belonging to 2 groups, GFP & TLR9 (No ratio & no scaling). In order to enhance data reading, color separation (blue = low & red = high) was based on the 50th theoretical percentile of the expression matrix. Here fold values are shown.