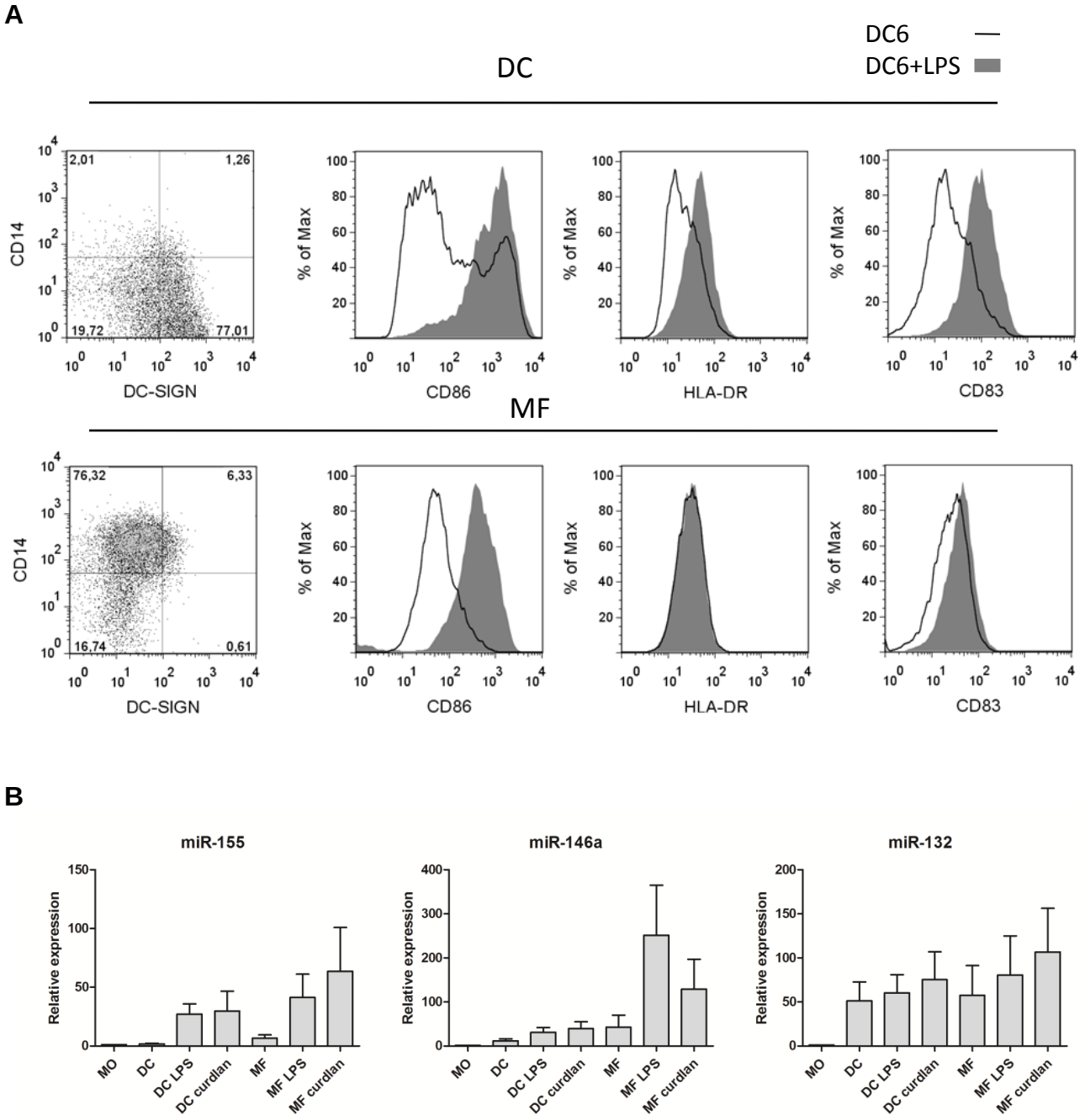
Online Supporting Information



Supplementary Fig. S1. Characteristics of MO derived DCs and MFs. (A) Flow cytometric analysis of MO derived DCs and MFs. Left panels show DCs and MFs characterized by the expression of CD14 and DC-SIGN on day 6 (DC6). The histograms represent the geometric mean fluorescent intensities of CD86, HLA-DR and CD83 shown as % of maximum in LPS stimulated DCs and MFs (filled gray) relative to respective values of un-stimulated cells (black line). Data from one representative donor are shown. (B) Expression of miR-155, miR-146a and miR-132 is induced during differentiation and/or maturation of DCs and MFs. Relative expression of each miRNA is shown compared to the level in MOs (=1). Data are mean with SEM of the results from three different donors.

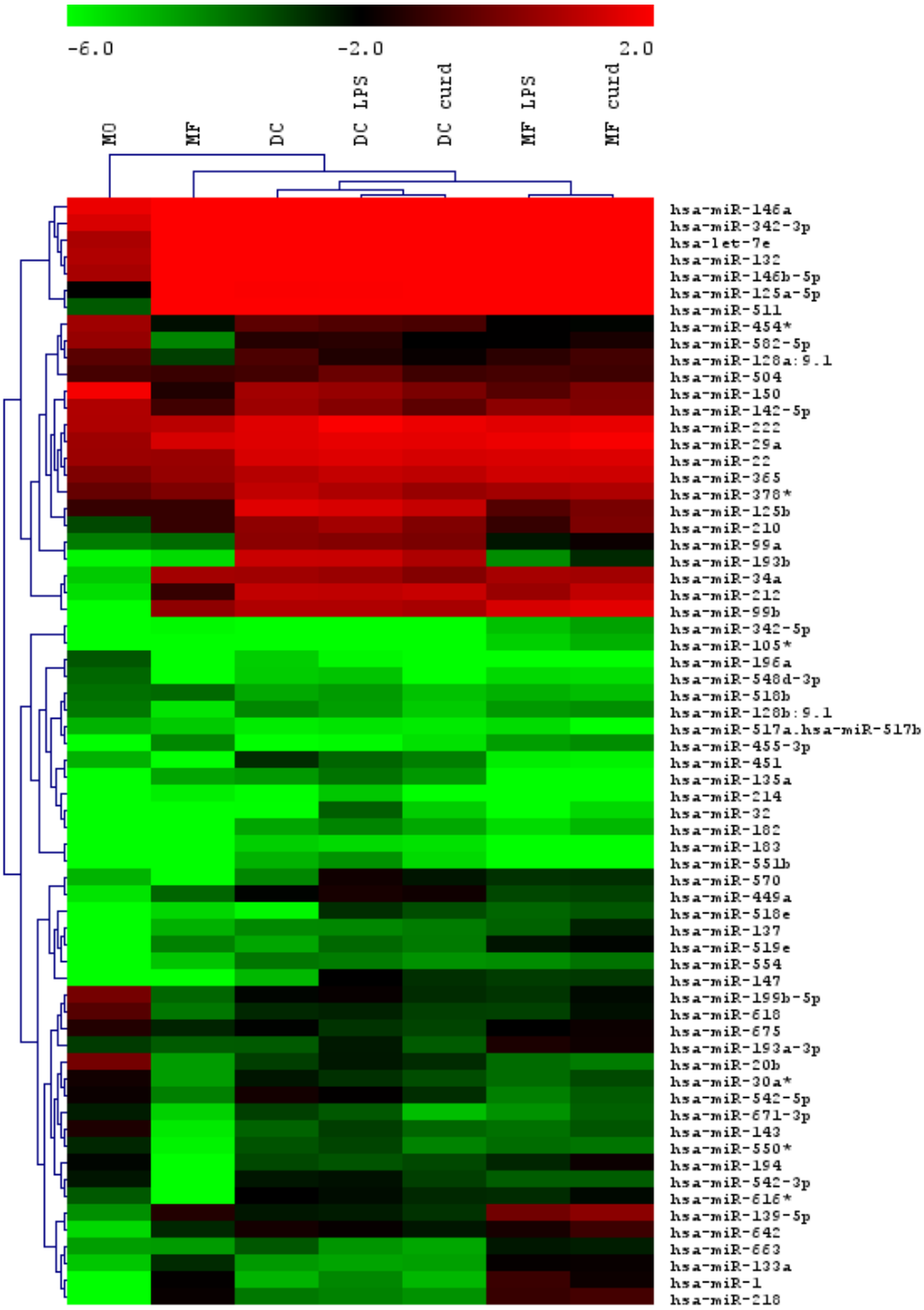
Supplementary Table S1: Number of miRNAs detected with Illumina miRNA array

	MO	DC	DC+ LPS	DC+ curdlan	MF	MF+ LPS	MF+ curdlan
Detected known miRNAs (detection p-value < 0.05)	355	380	317	307	332	332	372
high expression (Average signal > 1000)	142	142	142	133	115	135	141
average expression (Average signal 100...1000)	116	105	109	111	137	120	113
low expression (Average signal < 100)	97	133	66	63	80	77	118

Supplementary Table S2: Differential expression of miRNAs in MOs, DCs and MFs[a]

ILMN_GENE	MO	DC	DC LPS	DC curd	MF	MF LPS	MF curd
hsa-miR-193b	40,70	5 367,60	5 263,40	3 937,00	54,50	126,30	380,20
hsa-miR-551b	1,00	84,90	119,40	55,00	1,00	1,60	1,00
hsa-miR-548d-3p	192,50	64,00	70,00	31,30	1,00	55,50	52,50
hsa-miR-32	31,00	37,30	211,20	63,30	1,00	24,00	56,20
hsa-miR-616*	223,80	590,20	513,00	380,20	29,30	366,50	538,40
hsa-miR-194	558,70	268,20	236,00	268,70	15,80	392,00	676,10
hsa-miR-99a	152,90	2 723,20	2 486,70	2 257,10	184,70	466,80	680,20
hsa-miR-196a	231,30	62,40	40,10	22,40	7,20	31,30	10,40
hsa-miR-147	1,00	79,40	589,30	352,30	11,80	305,10	321,00
hsa-miR-582-5p	3 075,60	892,00	936,90	590,20	138,30	608,20	783,70
hsa-miR-125b	1 071,30	6 830,60	6 223,20	5 121,30	1 067,80	1 487,20	2 222,80
hsa-miR-182	8,00	97,90	140,10	94,30	18,70	54,60	79,60
hsa-miR-212	52,70	4 895,30	4 767,00	5 205,10	1 065,80	3 158,90	4 864,70
hsa-miR-143	822,00	200,30	303,80	193,20	46,10	172,80	233,50
hsa-miR-150	8 618,10	3 508,80	3 082,90	2 272,30	837,60	1 521,10	2 342,90
hsa-miR-570	83,00	135,60	718,40	470,00	34,00	346,20	354,70
hsa-miR-454*	3 370,60	1 635,40	1 436,80	1 332,40	502,40	608,90	562,50
hsa-miR-449a	49,40	565,80	773,90	710,60	196,80	270,40	290,60
hsa-miR-199b-5p	2 136,40	554,80	647,50	367,40	193,30	332,30	534,90
hsa-miR-20b	2 117,10	300,60	457,40	370,10	107,40	183,50	153,30
hsa-miR-210	269,30	2 815,90	3 501,00	2 426,20	1 066,40	1 070,50	2 310,40
hsa-miR-618	1 512,30	384,30	408,50	297,10	160,70	290,90	500,50
hsa-miR-554	17,50	164,70	152,10	120,40	69,90	127,10	167,70
hsa-miR-663	105,90	229,20	116,30	95,50	108,60	455,40	430,30
hsa-miR-378*	1 808,70	4 861,20	3 922,30	3 110,20	2 357,70	3 518,00	3 982,00
hsa-miR-22	3 251,30	6 211,00	6 746,10	6 116,60	3 120,10	6 353,80	6 538,90
hsa-miR-642	55,60	743,10	638,30	461,50	382,50	767,10	1 155,70
hsa-miR-137	34,40	133,50	135,10	152,20	85,90	202,80	409,10
hsa-miR-222	3 998,10	6 821,20	9 217,40	7 845,10	4 493,40	6 929,80	7 511,90
hsa-miR-99b	15,30	4 023,10	4 042,00	3 680,10	2 809,90	6 120,90	7 056,00
hsa-miR-365	2 365,90	4 285,00	5 055,30	4 700,00	3 032,90	5 733,30	5 552,10
hsa-miR-132	4 071,00	15 177,70	15 138,60	16 988,90	11 307,00	14 735,20	14 608,00
hsa-miR-511	222,10	13 372,70	12 476,50	12 493,10	10 133,10	11 919,30	12 679,20
hsa-miR-342-3p	6 306,50	14 896,10	15 397,30	14 405,20	12 793,00	11 654,50	12 276,30
hsa-miR-146b-5p	3 703,00	15 830,20	16 210,30	15 930,60	13 775,10	16 574,70	15 348,10
hsa-miR-135a	20,40	112,40	168,50	112,50	99,20	21,70	23,70
hsa-miR-29a	3 299,00	6 692,90	7 404,90	7 209,30	6 153,50	7 881,40	8 886,40
hsa-miR-193a-3p	313,90	220,60	451,50	219,20	218,30	802,10	696,70
hsa-miR-34a	65,20	3 424,50	3 154,20	2 487,20	3 551,40	3 650,70	3 452,80
hsa-let-7e	3 822,80	11 357,00	12 381,90	13 072,40	12 464,70	15 568,90	14 345,10
hsa-miR-125a-5p	578,70	9 156,00	9 304,40	9 994,50	10 676,00	12 310,60	11 906,20
hsa-miR-146a	7 858,00	15 571,40	18 463,20	19 151,40	20 947,30	21 589,30	20 816,40
hsa-miR-518e	19,40	40,10	359,20	254,70	56,80	192,90	230,50
hsa-miR-519e	30,60	96,80	189,10	155,30	144,70	474,90	559,60
hsa-miR-139-5p	123,50	462,80	440,40	339,70	870,90	2 054,40	2 713,70
hsa-miR-133a	68,50	111,70	98,90	103,00	373,50	631,60	655,60
hsa-miR-455-3p	31,10	36,40	38,70	51,10	135,60	105,40	127,50
hsa-miR-218	1,00	159,90	143,30	119,60	656,50	1 088,10	1 263,90
hsa-miR-1	1,00	84,20	135,40	80,40	617,40	1 127,80	682,70

[a]Average expression signals of miRNAs with differential p-value<0.05 and which average expression level reached over 100 at least in one condition are shown.

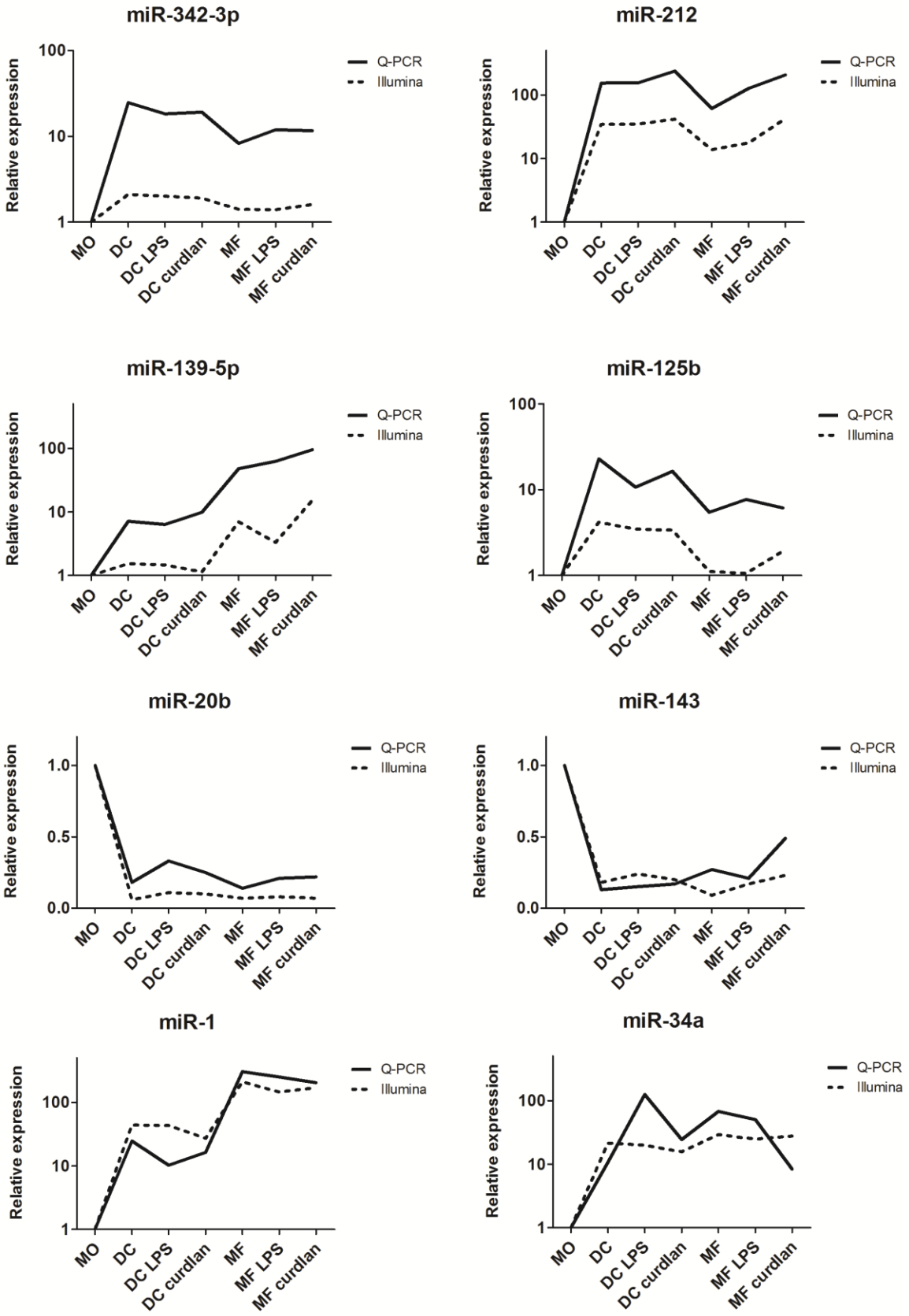


Supplementary Fig. S2. Hierarchical clustering of up- and down-regulated miRNAs. Only miRNA-s with average expression level over 100 at least in one condition are shown. Each column represents expression level of miRNAs (shown right) in each sample (shown above). Log2 expression values for each miRNA are mean-centered across all the analyzed miRNA expression values. Color scale from green (lower) to red (higher) represents deviation from the mean (black).

Supplementary Table S3. miRNAs up-regulated after stimulation with endotoxins[a]

Up-regulated after induction both in MFs and DCs				
	DC LPS/DC	DC curd/DC	MF LPS/MF	MF curd/MF
miR-518e	9.0	6.4	3.4	4.1
miR-147	7.4	4.4	25.9	27.2
miR-32	5.7	1.7	24.0	56.2
miR-570	5.3	3.5	10.2	10.4
miR-193a-3p	2.0	1.0	3.7	3.2
miR-519e	2.0	1.6	3.3	3.9
Up-regulated after induction only in MFs				
	DC LPS/DC	DC curd/DC	MF LPS/MF	MF curd/MF
miR-182	1.4	1.0	2.9	4.3
miR-22	1.1	1.0	2.0	2.1
miR-137	1.0	1.1	2.4	4.8
miR-99b	**1.0**	**0.9**	**2.2**	**2.5**
miR-193b	**1.0**	**0.7**	**2.3**	**7.0**
miR-212	**1.0**	**1.1**	**3.0**	**4.6**
miR-139-5p	**1.0**	**0.7**	**2.4**	**3.1**
miR-99a	**0.9**	**0.8**	**2.5**	**3.7**
miR-642	0.9	0.6	2.0	3.0
hmiR-663	0.5	0.4	4.2	4.0

[a]miRNA expression levels are shown as fold differences compared to the respective average values in DCs or MFs. For miRNAs designated with bold, induction with LPS and curdlan was also determined by RT-PCR. Up-regulation of miR-147 in response to LPS has been shown earlier in mouse [28]



Supplementary Fig. S3. Verification of Illumina array results with quantitative RT-PCR. Data from one representative donor are shown and are normalized to the value in MOs (=1).

Supplementary Table S4. Comparison of Illumina Array and qPCR results [a]

miRNA	DC/MO		DC+LPS/MO		DC+curd/MO		MF/MO		MF+LPS/MO		MF+curd/MO	
	Illum.	qPCR	Illum.	qPCR	Illum.	qPCR	Illum.	qPCR	Illum.	qPCR	Illum.	qPCR
miR-99b	263,6	173,9	264,8	170,9	241,1	214,7	184,1	505,1	401,0	1095,5	462,3	1047,0
miR-193b	131,8	85,1	129,3	94,6	96,7	82,5	NS	1,2	3,1	4,5	9,3	8,8
miR-212	93,0	85,6	90,5	92,7	98,8	130,9	20,2	36,8	60,0	71,6	92,4	113,9
miR-511	60,2	665,0	56,2	532,2	56,2	517,0	45,6	553,4	53,7	714,5	57,1	649,9
miR-34a	52,5	39,8	48,4	86,0	38,1	23,9	54,5	38,9	56,0	59,9	53,0	51,7
miR-99a	17,8	13,7	16,3	10,7	14,8	10,4	NS	2,7	3,1	4,7	4,4	4,3
miR-1	8,4	13,6	13,5	6,1	8,0	9,1	61,7	190,7	112,8	212,0	68,3	165,2
miR-125b	6,4	16,7	5,8	9,0	4,8	10,1	NS	3,0	NS	4,3	2,1	3,7
miR-139-5p	3,7	3,9	3,6	3,9	2,7	5,4	7,1	28,5	16,6	36,9	22,0	54,1
miR-132	3,7	48,0	3,7	46,7	4,2	55,3	2,8	24,4	3,6	39,2	3,6	68,1
miR-342-3p	2,4	14,1	2,4	12,0	2,3	10,8	2,0	4,9	NS	6,9	NS	6,8
miR-518e	2,1	NS	18,5	NS	13,1	NS	2,9	NS	9,9	NS	11,9	NS
miR-146a	2,0	7,6	2,3	20,3	2,4	24,1	2,7	15,3	2,7	207,4	2,6	60,9
miR-143	0,2	0,1	0,4	0,1	0,2	0,1	0,1	0,1	0,2	0,1	0,3	0,3
miR-20b	0,1	0,1	0,2	0,2	0,2	0,1	0,1	0,1	0,1	0,1	0,1	0,1
miR-155	NS	NS	NS	35,5	NS	44,4	NS	3,7	NS	31,3	NS	67,9

[a]miRNA expression levels are shown as average fold differences compared to the value in MOs, the results are average values of 2 or 3 different donor cells. NS means not signficant or less than 2 times up- or downregulation. Only miRNAs with the expression differences and studied by both methods are shown.

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LOCUS       NM_138554                5667 bp    mRNA    linear   PRI 17-MAY-2009
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      121 acttcctctc acccttttagc ccagaactgc tttgaataca ccaattgctg tggggcggct
      181 cgaggaagag aagacaccag tgcctcagaa actgctcggt cagacggtga tagcgagcca
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      301 GCCTCGCGCC TGGCTGGGAC TCTGATCCCA GCCATGGCCT TCCTCTCCTG CGTGAGACCA
      361 GAAAGCTGGG AGCCCTGCGT GGAGGTGGTT CCTAATATTA CTTATCAATG CATGGAGCTG
      421 AATTTCTACA AAATCCCCGA CAACCTCCCC TTCTCAACCA AGAACCTGGA CCTGAGCTTT
      481 AATCCCCTGA GGCATTTAGG CAGCTATAGC TTCTTCAGTT TCCCAGAACT GCAGGTGCTG TLR4-1F
      541 GATTTATCCA GGTGTGAAAT CCAGACAATT GAAGATGGGG CATATCAGAG CCTAAGCCAC TLR4-1R
      601 CTCTCTACCT TAATATTGAC AGGAAACCCC ATCCAGAGTT TAGCCCTGGG AGCCTTTTCT
      661 GGACTATCAA GTTTACAGAA GCTGGTGGCT GTGGAGACAA ATCTAGCATC TCTAGAGAAC
          ..........

     2641 GAGCTGTACC GCCTTCTCAG CAGGAACACT TACCTGGAGT GGGAGGACAG TGTCCTGGGG
     2701 CGGCACATCT TCTGGAGACG ACTCAGAAAA GCCCTGCTGG ATGGTAAATC ATGGAATCCA
     2761 GAAGGAACAG TGGGTACAGG ATGCAATTGG CAGGAAGCAA CATCTATCTG aagaggaaaa
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     3061 aaagtcattt caactcttac ctcatcaagt tgaataaaga cagagaaaac agaaagagac miR-511 I
     3121 attgttcttt tcctgagtct tttgaatgga aattgtatta tgttatagcc atcataaaac
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     4681 catagaagca gagaatagaa cagtggttcc tagggaaaag gaggaaggga gaaatgagga
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     5641 ctctctctca aaaaaaaaaa aaaaaaa
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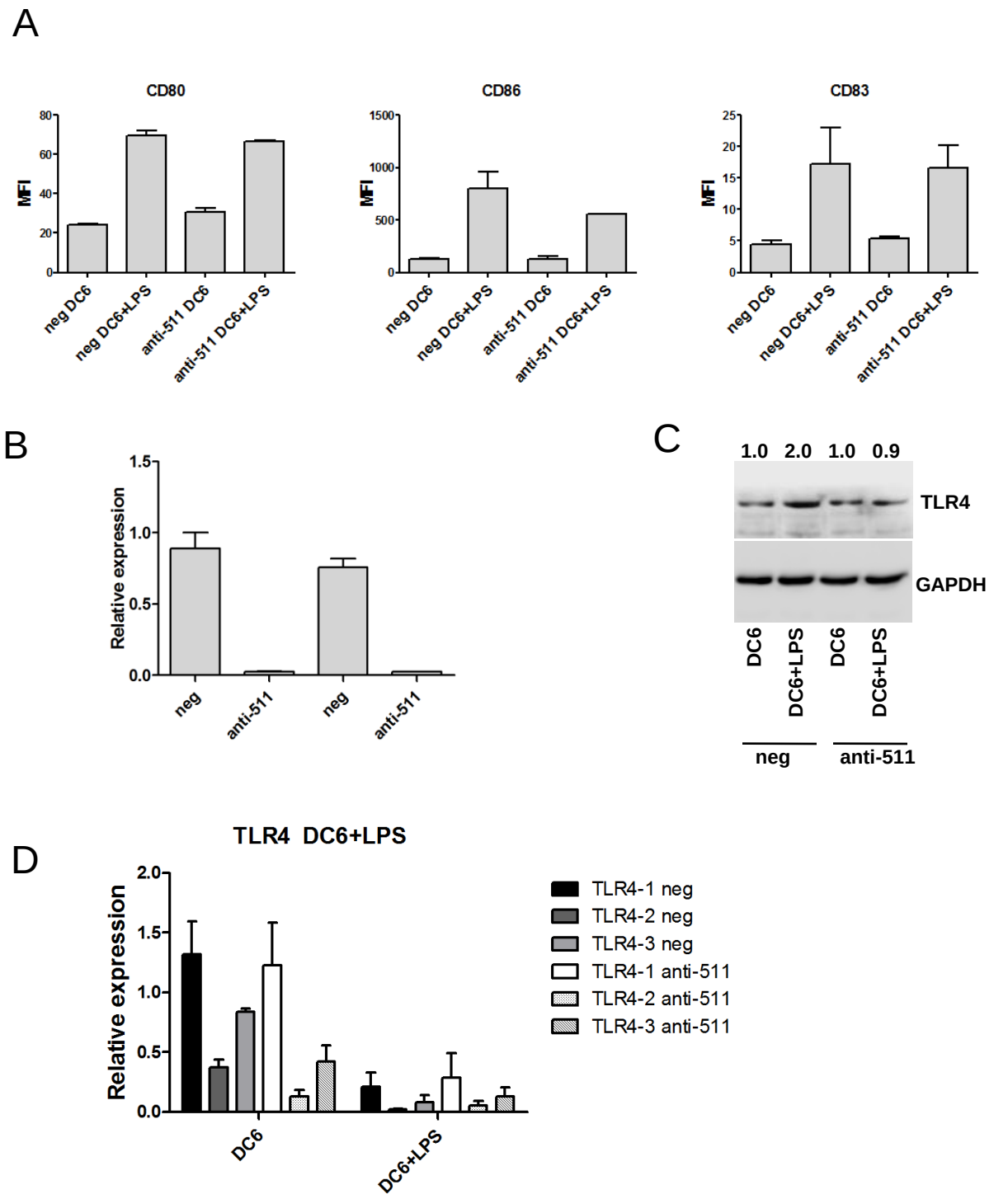
Supplementary Fig. S4. The partial sequence of the human TLR4 mRNA . Protein coding region is shown in uppercase and 3'UTR in lowercase. miR-511 target sequences are highlighted with blue and qPCR primer binding sites with red. Polyadenylation sites are underlined.



Supplementary Fig. S5. Knock-down of miR-511 does not lead to major changes in expression of DC cell activation markers. (A) The levels of CD80, CD86 and CD83 were measured on day 6 (DC6) during the DC differentiation and after 24 hours of LPS treatment (DC6+LPS). Average of geometric mean fluorecence intensities (MFI) with SEM of two parallel treatment are shown. (B) Inhibition of miR-511 is shown as average miRNA expression level with SEM of two parallel treatment normalized to the levels of control transfection on differentiation time point day 6 (DC6, neg, =1). (C) Western analyzis of DCs on day 6 (DC6) and after the LPS treatment, miR-511 inhibitor (anti-511) and the control inhibitor (neg) were used as indicated. Western blots are normalized to the GAPDH, the numbers indicate the fold difference compared to control transfected cells on day 6 (DC6, neg). (F) Analysis of TLR4 mRNA levels using indicated primers and conditions (D). Data are mean with SEM of two paralel transfections (D).