

Supplementary Table 1: Inactivation of inflammatory responses of macrophages by pMSCs-CM

Affected gene transcripts	Fold changes by PMA/LPS (vs. Control)	P value (PMA/LPS vs. Control, n = 3)	Fold changed by pMSC-CM (vs PMA/LPS)	P value (PMA/LPS vs. PMA/LPS + 50%, n = 3)
CXCL8	535.95	0.009573	-9.14	0.083365
IL1B	500.8	0.048456	-6.25	0.123176
CXCL6	242.74	0.001276	-10.08	0.032372
CXCL1	235.55	0.116816	-5.27	0.247662
CXCL3	190.02	0.038563	-2.32	0.133338
IL1RN	177.15	0.004863	-4.02	0.037209
CXCL2	92.93	0.128867	-12.97	0.153547
CXCL5	78	0.09673	-6.37	0.401279
IL6	46.15	0.199307	-2.13	0.476512
CCL4	33.91	0.118846	-1.81	0.447106
IL1A	20.08	0.109787	-3.51	0.26583
NOS2	11.17	0.007915	-9.35	0.008181
PTGS2	9.8	0.106712	-2.33	0.302766
LY96	7.56	0.152586	-1.42	0.521316
CCL2	6.83	0.122509	-4.45	0.110069
RIPK2	6.02	0.013444	-5.35	0.058044
BCL6	5.27	0.029664	-2.39	0.085688
CSF1	4.9	0.080272	-1.88	0.270602
CCL3	4.12	0.224417	-2.59	0.273153
CCL7	4.01	0.209097	-2.64	0.251111
CCL5	3.8	0.065136	-8.77	0.017685
ITGB2	2.97	0.036245	-2.54	0.056093
NR3C1	2.45	0.234157	-7.81	0.043945
IL1R1	2.25	0.147725	-1.47	0.349567
MYD88	2.82	0.092337	-4.90	0.058324
TNF	1.98	0.052401	-1.46	0.140847
CEBPB	1.75	0.226914	-1.71	0.089656
CD14	1.68	0.268575	-1.03	0.593546
C3	1.35	0.284091	1.39	0.106648
C3AR1	-1.53	0.268667	1.07	0.593999
CCL11	-1.5	0.304463	1.73	0.069919
CCL13	1.25	0.489838	-1.26	0.173406
CCL16	-1.2	0.665358	1.69	0.108011
CCL17	-1.12	0.936866	1.68	0.186882
CCL19	-1.16	0.700046	1.82	0.142731
CCL21	-1.21	0.565338	1.24	0.466697
CCL22	1.27	0.185247	1.22	0.24265
CCL23	-1.79	0.327176	1.02	0.871449
CCL24	-1.12	0.575359	1.33	0.129974
CCL8	-1.26	0.548401	1.51	0.176782

CCR1	-1.27	0.428263	1.74	0.026517
CCR3	-1.43	0.4268	1.92	0.065713
CCR4	1.18	0.48383	1.92	0.01117
CCR7	1.05	0.887337	1.51	0.100115
CD40LG	-1.48	0.373571	1.39	0.397193
CRP	-1.07	0.929725	1.51	0.273909
CXCL10	-1.09	0.610765	-2.76	0.312984
CXCL9	-1.67	0.138019	1.97	0.000092
CXCR1	-1.11	0.662785	1.60	0.035095
CXCR2	-1.29	0.430072	1.49	0.109703
FASLG	-1.38	0.373761	1.51	0.091681
FOS	1.18	0.524644	1.37	0.256317
IL10	-1.38	0.309707	1.93	0.015066
IL10RB	1.24	0.285129	-1.19	0.366473
IL18	-1.16	0.622399	-1.29	0.303259
IL1RAP	1.05	0.916089	1.03	0.851851
IL23A	1.12	0.851924	1.60	0.016877
IL6R	-1.36	0.179679	1.65	0.004205
IL9	-1.25	0.522482	1.93	0.024161
KNG1	-1.25	0.320858	1.80	0.01354
LTA	-1.02	0.933977	1.53	0.197138
LTB	1.11	0.711759	1.24	0.311127
NFKB1	-1.23	0.454782	1.18	0.299521
SELE	-1.2	0.477778	1.86	0.005707
TIRAP	-1.04	0.820124	1.24	0.283465
TLR1	1.01	0.991327	1.34	0.24833
TLR2	1.23	0.73762	-1.72	0.183617
TLR3	-1.26	0.363668	2.17	0.008944
TLR4	-1.09	0.65828	-1.13	0.421518
TLR5	-1.38	0.298214	1.86	0.036134
TLR6	-1.24	0.410177	1.25	0.098511
TLR9	1.13	0.653286	1.50	0.20164
TNFSF14	1.09	0.63339	1.49	0.177894
TOLLIP	1.3	0.325699	1.13	0.740054
CXCR4	-2.14	0.127673	1.36	0.350269
CCR2	-2.42	0.076988	1.82	0.11419
TLR7	-8.43	0.285805	-1.02	0.833967

The regulatory effects of pMSCs-CM on expression of inflammation-related seventy-seven gene transcripts in PMA/LPS-activated THP1 cells was examined by using PCR array. The fold change of each transcript level in experimental group as compared to control group (PMA/LPS vs. Control, or PMA/LPS + 50% pMSCs-CM vs. PMA/LPS) was presented in mean of three separate RNA samples (n = 3). – (negative number) represented downregulation. A P value of less than 0.05 was highlighted in bold

Supplementary Table 1: Inactivation of inflammatory responses of macrophages by pMSCs-CM

The expression of a panel of monocyte/macrophage-expressing gene transcripts (total seventy-seven, as seen in the left column of the table) in THP1 cells from three different groups (Control, PMA/LPS, and PMA/LPS + 50% pMSCs-CM) was examined by using PCR array following manufacturer's instruction (SABiosciences – QIAGEN Inc., Valencia, CA, USA), and each group represented three separate samples. In brief, 1 µg of high quality total RNA from each sample was reverse transcribed to cDNA by using RT² First Strand Synthesis Kit (QIAGEN). The expression of selected genes was then amplified by real-time PCR using RT² Profile PCR arrays with PCR amplification conditions (10 min at 95°C, followed by 45 cycles of 15 s at 95°C and 60 s at 60°C) according to manufacturer's instruction (QIAGEN Inc.). The fold change of each target transcript and statistical comparison between groups were determined by using the manufacturer's online web analysis tools (www.SABiosciences.com/pcrarraydataanalysis.php). A negative number indicated a fold decrease, whereas a positive number implied a fold increase.