

SUPPLEMENT

Comprehensive analysis of differences between samples. The analysis is based on determination of the distances between points in the multidimensional space of the studied parameters. A set of characteristics of one sample or group is taken as a point.

1. The data are presented in the form of a table: N number of observations (plasma samples, given repetitions: index $i = 1 \dots N$), in each observation X parameters (concentrations of cytokines and chemokines in plasma samples, index $j = 1 \dots X$).
2. All observations are divided into groups according to the criterion chosen by the researchers (donors D, patients before treatment (A), patients after treatment (B), index $g = 1, 2, 3$).
3. For each parameter, geometric mean of the group is calculated by the formula:

$$\bar{x}_{gj} = \sqrt[N_g]{\prod_{i=1}^{N_g} x_{gij}},$$

where x_{gij} value of parameter j in sample i of the group g .

4. For each sample in group g , its relative difference is calculated (ε_{gij}) from the geometric mean (how many times it differs regardless of whether up or down):

$$\varepsilon_{gij} = e^{\left| \ln \frac{x_{ij}}{\bar{x}_{gj}} \right|}.$$

5. The average value of the relative difference for each parameter of this group is calculated, respectively:

$$\bar{\varepsilon}_{gj} = \frac{\sum_{i=1}^{N_g} (\varepsilon_{gij})}{N}.$$

6. We take samples i corresponding to the plasma of one-person p , regardless of the group. We carry out points 3-5 for each p as if it were one group. Next, we need the values $\bar{x}_{pj}$ $\bar{\varepsilon}_{pj}$.

7. We introduce the relative units ($\bar{s}_{pgj}$) for the coordinate values for each sample relative to the average value of the appropriate parameter in the corresponding group:

$$\bar{s}_{pgj} = \frac{\bar{x}_{pj}}{\bar{x}_{gj}}.$$

8. Next, we apply the mapping strategy, where the distance (L'_{pg}) from the experimental point to the average value is used as a criterion. When calculating the distance between points, it is necessary to take into account effect of the accuracy of determining average values. The greater is the accuracy of determining the average value and the greater is the difference between the means, the more significant is this difference.

$$L'_{pg} = \sum_j \bar{s}_{pgj} / (\bar{\varepsilon}_{gj} \bar{\varepsilon}_{pj}).$$

The meaning of this is that $\bar{s}_{pgj} / (\bar{\varepsilon}_{gj} \bar{\varepsilon}_{pj})$ shows how many times the plasma

parameter j differs from the geometric mean group g , and how many times this difference exceeds the measurement error $\bar{\varepsilon}_{ij}$ $\bar{\varepsilon}_{gj}$.

10. To observe changes in the relationships between the studied cytokines and chemokines, we calculate the parameter T_{pjf} for each p . We consider deviation of the

parameter j_1 from the group average g^p , to which the studied plasma sample – p belongs. Next, we divide this deviation by the deviation according to parameter j_2 , for all $j_1 j_2$:

$$T_{ij_1j_2} = \frac{\bar{x}_{ij_1} - \bar{x}_{g^p j_1}}{\bar{x}_{ij_2} - \bar{x}_{g^p j_2}}.$$

If we introduce the parameters j_1 and j_2 on the plane, the linear relationship between them can be displayed as a straight line with the slope T (the slope coefficient).

For the convenience of further calculations, we transform the tilt coefficients to the tilt angles:

$$Ar_{ij_1j_2} = \arctg T_{ij_1j_2}.$$

11. For each pair of the parameters j_1, j_2 . the average is calculated $\overline{Ar}_{gj_1j_2}$ by group g by the formula:

$$\overline{Ar}_{gj_1j_2} = \frac{\sum_{i=1}^{N_g} Ar_{ij_1j_2}}{N_g}.$$

12. For each sample in group g , its relative difference is calculated ($\varepsilon_{gi_1j_2}^{Ar}$) from $\overline{Ar}_{gj_1j_2}$:

$$\varepsilon_{gi_1j_2}^{Ar} = |\overline{Ar}_{gj_1j_2} - Ar_{ij_1j_2}|.$$

13. We consider the average deviation $\bar{\varepsilon}_{gi_1j_2}^{Ar}$

14.

$$\bar{\varepsilon}_{gi_1j_2}^{Ar} = \frac{\sum_{i=1}^{N_g} (\varepsilon_{gi_1j_2}^{Ar})}{N}.$$

15. We take $Ar_{ij_1j_2}$ corresponding to the plasma of one-person p , regardless of the group. We carry out points nos. 11-13 for each p separately, as if it were one group. Next, we need the values:

$$\overline{Ar}_{pj_1j_2} \bar{\varepsilon}_{pi_1j_2}^{Ar}.$$

16. We calculate the difference for $\Delta \overline{Ar}_{pj_1j_2}$ the coordinate values for each sample relative to the average value of the corresponding parameter in the corresponding group:

$$\Delta \overline{Ar}_{pj_1j_2} = |\overline{Ar}_{pj_1j_2} - \overline{Ar}_{gj_1j_2}|.$$

17. Next, we apply a similar mapping strategy, where the distance (L'_{pg}) from the experimental point to the average mean of the groups is used as a criterion. When calculating the distance between points, it is necessary to take into account effect of the accuracy of determining average values. The greater is the accuracy of determining the average value and the greater is the difference between the means, the more significant this difference is.

$$L''_{pg} = \sum_j \Delta \overline{Ar}_{pj_1j_2} / (\bar{\varepsilon}_{pi_1j_2}^{Ar} + \bar{\varepsilon}_{gi_1j_2}^{Ar}).$$

18. Summarize $L'_{pg} \subset L''_{pg}$

$$L_{pg} = L'_{pg} + L''_{pg}.$$

You can enter axes that show how many times the distance from a point to one center is greater than to another:

$$k_{pB} = \frac{L_{pB}}{L_{pD}} \quad k_{pA} = \frac{L_{pA}}{L_{pD}}.$$

19. We display in the figure the points with the calculated coordinates $k_{pB} \ k_{pA}$.

Table S1. Characteristics of the patients with DLBCL, volume of tumor involvement, treatment, CFU-F, MSCs, and PDT before treatment

No.	Age	Gender	Treatment	IPI	ECOG	CFU-F per 10 ⁶ BM cells	MSC, ×10 ⁶ per 4 passages	PDT	Volume of tumor involvement in primary patients
1	30	male	R-(DA)-EPOCH (6 cycles)	2	1	3	13.9	6.4	palatine and lingual tonsil, root of the tongue, soft palate with invasion of the oropharynx, epiglottis, cervical lymph nodes
2	60	female	R-NHL BFM-90 (6 cycles) + aut o HSCT	3	1	20	7.6	4.7	stomach, abdominal lymph nodes
3	68	female	R-CHOP-21 (6 cycles)	5	3	4	6.2	4.5	left humerus bone, surrounding tissues, axillary, intrathoracic lymph nodes
4	60	female	R-(DA)-EPOCH (6 cycles) + R-DHAP (2 cycles)	5	4	7	6.5	4.2	hepato-pancreatic-duodenal zone with intergrowth in the liver, gallbladder, right adrenal, kidneys, the mesentery of the small intestine, aorta, inferior vena cava, intraperitoneal and retroperitoneal lymph nodes
5	64	female	R-CHOP-21 (6 cycles)	2	1	3	21.3	7.1	tissue of the nose
6	38	female	R-(DA)-EPOCH (6 cycles) + aut o HSCT	4	1	4	16.9	5.7	lungs, submandibular, axillary, hilar lymph nodes
7	47	female	R-CHOP-21 (4 cycles)	1	1	3	7.1	5.1	pharyngeal and palatine tonsils, axillary lymph nodes
8	61	female	R-(DA)-EPOCH (5 cycles) + DH AP (1 cycle)	5	3	7	4.7	4.5	lungs, right humerus bone, liver, heart, pancreatic, uterus, intraperitoneal and retroperitoneal lymph nodes
9	79	female	R-CHOP-21 (6 cycles) + DH	4	2	2	4	4.5	cervical, thoracic lymph nodes, stomach, small

			AP (2 cycle)						intestine, thyroid gland
10	49	female	R-(DA)-EPOCH (6 cycles) + aut o HSCT	3	2	0.5	5.8	4.5	breast
11	42	male	NHL BFM-90 (6 cycles)	3	2	51	24	6.9	right tibia and soft tissue
12	60	female	NHL BFM-90 (6 cycles)	3	1	9.5	29.8	7.1	peripheral, intrathoracic, intra-abdominal lymph nodes, palatine and pharyngeal tonsils
13	54	female	R-NHL BFM-90 (4 cycles)	0	1	1	5.9	3.8	pharyngeal tonsil, lymph nodes of the neck
14	54	male	R-NHL BFM-90 (6 cycles)	4	2	1	30.4	8.3	L2 vertebra, spleen, ileum and cecum
15	54	male	R-NHL BFM-90 (4 cycles) + aut o HSCT	4	2	3	12.2	6.6	peripheral, intraperitoneal, retroperitoneal lymph nodes, liver, spleen, ileum
16	79	female	R-CHOP-21 (6 cycles) + DH AP (2 cycle)	5	2	18.5	4.02	2.2	axillary intrathoracic, inguinal, axillary lymph nodes, spleen, skeleton bones, lung
17	72	female	R-CHOP (4 cycles), R-DHAP (2 cycles), ESHAP (2 cycles)	4	1	19	5.4	3.7	cervical, intrathoracic, retroperitoneal lymph nodes, diaphragm, stomach, pancreas, spleen, adrenal glands, formation in the right iliac region
18	64	female	R-DA-EPOCH(6 cycles) + aut o HSCT	3	3	2	4.8	3.4	intraperitoneal and retroperitoneal lymph nodes, spleen
19	51	male	R-NHL BFM-90 (4 cycles) + 2R	0	1	3	8.1	4.3	skin, soft tissues of the gluteal region, inguinal lymph nodes
20	37	male	R-NHL BFM-90 (6 cycles)	3	2	14	6	3.4	axillary, cervical lymph node, palatine and lingual tonsils, tongue root
21	70	female	R-CHOP-21	5	3	41	6.6	4.5	sacrum, ilium

			(6 cycles)						
22	33	male	R-CHOP-21 (4 cycles)	0	1	0	6.1	4.3	pharynx
23	34	male	R-NHL BFM-90 (6 cycles) + aut o HSCT	2	2	38	15.4	6	cervical, iliac lymph nodes, soft tissues of the abdominal wall
24	78	male	R-CHOP-21 (6 cycles)	4	2	1	5.5	3	axillary, bronchopulmonary, axillary lymph nodes, ribs, formation in the chest, posterior mediastinum, bronchi, lungs
25	48	female	R-NHL BFM-90 (4 cycles)	1	1	1	6.4	3.4	left shoulder blade
26	34	female	R-CHOP-21 (6 cycles)	0	1	1	19.6	7.3	stomach
27	49	male	R-DA- EPOCH(6 cycles) + aut o HSCT	3	1	5	6.2	2.2	soft tissue of the neck, submandibular, cervical lymph node, Th5, soft tissues of the scapular region
28	78	female	R-CHOP-21 (3 cycles)	4	4	3	3.9	3.1	spleen
29	69	female	R-CHOP-21 (6 cycles)	1	1	13	6.2	4.6	stomach
30	59	female	R-DA- EPOCH(4 cycles) + aut o HSCT	3	2	9	3.3	3.5	kidney, adrenal gland
31	55	female	R-CHOP-21 (6 cycles)	1	1	2	10.1	7.03	tonsil
32	61	female	R-CHOP-21 (6 cycles)	1	1	6	4.8	3.7	thyroid
33	72	male	R-CHOP-21 (6 cycles)	5	2	26	4.4	2.5	stomach, spleen
34	47	male	R-DA- EPOCH (6 cycles)	2	4	34	6.6	4.46	ilium
35	63	female	R-CHOP-21 (6 cycles)	2	1	17	1.3		breast

Notes. Designations: IPI, international prognostic index; CFU-F, concentration per 10^6 BM cells; MSC, number of cells for 4 passages, $\times 10^6$; PDT, population doubling time.

Table S2. Primers and probes

Gene	Primer	5'-3' sequences
<i>BACT</i>	F	CAACCGCGAGAAGATGACC
	R	CAGAGGCGTACAGGGATAGC
	probe	ROX-AGACCTTCAACACCCCAGCCATGTACG-BHQ2
<i>GAPDH</i>	F	GGTGAAGGTCGGAGTCAACG
	R	TGGGTGGAATCATATTGGAACA
	probe	ROX-CTCTGGTAAAGTGGATATTGTTGCCATCA-BHQ2
<i>MMP2</i>	F	TGAGAAGGATGGCAAGTACG
	R	TGCGGCCCTCAGTGGTGC
	probe	FAM-CCGCTTCCAGGGCACATCCTATGAC-RTQ1
<i>IL6</i>	F	ACCTGAACCTTCCAAAGATG
	R	CTCCAAAAGACCAGTGATGA
	probe	FAM-ATTCAATGAGGAGACTTGCCTGGTG-RTQ1
<i>TGFB1</i>	F	TGCGTCTGCTGAGGCTCAA
	R	CGGTGACATCAAAAGATAACC
	probe	FAM-AGGAATTGTTGCTGTATTTCTGGTAC-RTQ1
<i>PDGFRb</i>	F	CTCCCTTATCATCCTCATCA
	R	TCCACGTAGATGTACTCATG
	probe	FAM-TCACAGACTCAATCACCTTCCATC-RTQ1
<i>PPARG</i>	F	TACTGTTCGGTTTCAGAAATGC
	R	CAACAGCTTCTCCTTCTCG
	probe	FAM-CCATCAGGTTTGGGCGGATGCC-RTQ1
<i>SOX9</i>	F	AGCAAGACGCTGGGCAAG
	R	GTTCTTCACCGACTTCCTC
	probe	FAM-CTGGAGACTTCTGAACGAGAGC-RTQ1
<i>bFGF</i>	F	GAAGAGCGACCCTCACATCAAG
	R	TCCGTAACACATTTAGAAGCCAGTA
	probe	FAM-TCATAGCCAGGTAACGGTTAGCACACACTCCT-RTQ1
<i>FGFR1</i>	F	CAGAATTGGAGGCTACAAGG
	R	TGATGCTGCCGTACTCATTC
	probe	FAM-CATCATAATGGACTCTGTGGTGC-RTQ1
<i>FGFR2</i>	F	CTCATTATGGAAAGTGTGGTC
	R	TGGGCCGGTGAGGCGATC
	probe	FAM-CAGGTGGTACGTGTGATTGATGGA -RTQ1
<i>VEGF</i>	F	CCGAAAGGCCCAGTTGAAG
	R	ACCCTGAGGGAGGCTCCTT
	probe	FAM-CCTCGGCTTGTCACATCTGCAAGTACGT-RTQ1
<i>SPP1</i>	F	ATAGTGTGGTTTATGGACTGAG
	R	ATTCAACTCCTCGCTTTCC
	probe	FAM-CCAGTACCCTGATGCTACAGACGAG-RTQ1
<i>ICAM1</i>	F	GCAATGTGCAAGAAGATAGC
	R	CTCCACCTGGCAGCGTAG

	probe	ROX-CACGGTGAGGAAGGTTTTAGCTGTT-RTQ2
<i>BGLAP</i>	F	GCAGCGAGGTAGTGAAGAG
	R	GAAAGCCGATGTGGTCAG
	probe	FAM-CTCCCAGCCATTGATACAGGTAGC-RTQ1
<i>SMURF1</i>	F	AAACGGATTCGATAACCATTAG
	R	GTATCTGAGGGGTTTAGTTTG
	probe	FAM-CCAGCTCCCTGTTTCTTGTGAATTTTC-RTQ1
<i>BMP4</i>	F	CACAGCACTGGTCTTGAGTATCCT
	R	ACTGGTCCCTGGGATGTTCTC
	probe	FAM-CAACACCGTGAGGAGCTTCCACCAC-RTQ1
<i>BMP2</i>	F	AGCCGAGCCAACACTGTGC
	R	TCTCGGAAAACCTGAAGCTC
	probe	FAM-TTTAATTTAAGTTCTATCCCCACGG-RTQ1
<i>IL8</i>	F	ACCATCTCACTGTGTGTAAAC
	R	GTTTGGAGTATGTCTTTATGC
	probe	FAM-CAGTTTTGCCAAGGAGTGCTAAAG-RTQ1
<i>MCAM</i>	F	CACCACACTTCAGCATCAGC
	R	GTAGTTCCTGTGGTTCACCTC
	probe	FAM-CAGCACCAGGGAGGCAGAGGAAGAG-RTQ1

Table S3. Concentration of cytokines and chemokines in plasma from donors and patients with DLBCL in pg/ml

Cytokine	Donors	Patients before treatment	Patients one month after the end of the treatment
IL-1b	0.748 ± 0.361	0.827 ± 0.128	0.806 ± 0.083
IL-1ra	808.606 ± 539.387	1660.170 ± 752.279	247.370 ± 13.038
IL-2	6.283 ± 1.755	13.241 ± 2.763	10.641 ± 1.731
IL-4	2.721 ± 0.238	3.186 ± 0.294	3.073 ± 0.231
IL-5	21.316 ± 4.839	25.596 ± 3.869	36.170 ± 6.583
IL-6	3.341 ± 0.552	68.515 ± 32.844	7.213 ± 1.700
IL-7	28.213 ± 3.593	30.899 ± 2.285	33.137 ± 2.958
IL-8	7.469 ± 0.764	18.113 ± 6.006	7.492 ± 0.549
IL-9	47.254 ± 4.599	48.815 ± 2.937	46.662 ± 3.274
IL-10	13.482 ± 1.177	39.639 ± 12.164	11.010 ± 0.915
IL-12	5.785 ± 1.742	6.378 ± 1.363	10.959 ± 2.090
IL-13	8.947 ± 1.658	11.138 ± 0.952	13.355 ± 1.295
IL-15	385.025 ± 18.507	311.810 ± 35.618	410.444 ± 57.837
IL-17	8.541 ± 1.298	10.427 ± 1.566	10.006 ± 0.958
Eotaxin	83.053 ± 6.868	54.817 ± 4.791	59.360 ± 6.966
bFGF	29.326 ± 4.597	48.231 ± 3.540	50.293 ± 2.876
G-CSF	116.064 ± 11.837	310.278 ± 116.216	97.223 ± 8.611
GM-CSF	9.408 ± 1.557	5.966 ± 0.974	9.225 ± 1.573
IFN-γ	13.675 ± 3.690	14.740 ± 4.519	8.977 ± 1.427
IP-10	237.220 ± 17.364	1731.723 ± 457.463	964.957 ± 99.222
MCP-1	35.913 ± 3.320	31.453 ± 9.985	14.692 ± 1.185

MIP-1 α	1.695 $\pm$ 0.196	11.129 $\pm$ 4.486	2.253 $\pm$ 0.156
PDGF-bb	355.594 $\pm$ 80.813	2984.117 $\pm$ 578.425	1491.340 $\pm$ 190.877
MIP-1 β	50.619 $\pm$ 4.936	99.645 $\pm$ 22.668	53.826 $\pm$ 2.871
RANTES	5995.496 $\pm$ 745.809	4280.120 $\pm$ 233.258	4402.884 $\pm$ 252.002
TNF α	33.047 $\pm$ 4.996	99.489 $\pm$ 28.000	38.065 $\pm$ 3.135
VEGF	515.767 $\pm$ 52.028	298.351 $\pm$ 28.089	320.982 $\pm$ 26.357

Table S4. Correlations between cytokines in plasma from donors and patients before and after treatment

Cytokine	Corr	Donors	Patients before treatment	Patients after treatment
IL-1b	IL-1Ra	R = 0.948, p = 0.0141	R = 0.909, p = 0.0007	R = 0.768, p = 0.0259
	IL-4	R = 0.968, p = 0.007	R = 0.95, p = 0.0001	
	IL-6		R = 0.917, p = 0.0005	
	IL-7	R = 0.915, p = 0.0293		R = 0.88, p = 0.0039
	IL-8	R = 0.94, p = 0.0177	R = 0.933, p = 0.0002	R = 0.753, p = 0.0312
	IL-10			R = 0.853, p = 0.0071
	IL-12	R = 0.905, p = 0.0348		
	IL-13			R = 0.927, p = 0.0009
	IL-17		R = 0.966, p < 0.0001	R = 0.91, p = 0.0017
	bFGF	R = 0.963, p = 0.0084	R = 0.672, p = 0.0474	
	G-CSF		R = 0.901, p = 0.0009	R = 0.738, p = 0.0365
	IFN- γ	R = 0.968, p = 0.0068	R = 0.949, p = 0.0001	R = 0.718, p = 0.0448
	MCP-1		R = 0.918, p = 0.0005	R = 0.753, p = 0.0309
	MIP-1 α		R = 0.895, p = 0.0011	R = 0.906, p = 0.0019
	MIP-1 β		R = 0.898, p = 0.001	
	TNF α		R = 0.894, p = 0.0012	
	VEGF		R = 0.926, p = 0.0003	
IL-1Ra	IL-2		R = 0.877, p = 0.0019	
	IL-4	R = 0.881,	R = 0.911,	R = 0.834,

		$p = 0.0485$	$p = 0.0006$	$p = 0.0101$
	IL-6		$R = 0.998,$ $p < 0.0001$	
	IL-7			$R = 0.864,$ $p = 0.0057$
	IL-8	$R = 0.918,$ $p = 0.0276$	$R = 0.997,$ $p < 0.0001$	
	IL-10			$R = 0.889,$ $p = 0.0031$
	IL-13			$R = 0.776,$ $p = 0.0236$
	IL-17		$R = 0.906,$ $p = 0.0008$	$R = 0.715,$ $p = 0.0463$
	G-CSF		$R = 0.999,$ $p < 0.0001$	$R = 0.838,$ $p = 0.0095$
	IFN- γ	$R = 0.901,$ $p = 0.0369$	$R = 0.973,$ $p < 0.0001$	
	MCP-1		$R = 0.998,$ $p < 0.0001$	$R = 0.71,$ $p = 0.0483$
	MIP-1 α		$R = 0.998,$ $p < 0.0001$	
	MIP-1 β		$R = 0.995,$ $p < 0.0001$	$R = 0.859,$ $p = 0.0063$
	TNF α		$R = 0.996,$ $p < 0.0001$	$R = 0.857,$ $p = 0.0066$
	VEGF		$R = 0.857,$ $p = 0.0031$	
IL-2	IL-4	$R = 0.913,$ $p = 0.0302$	$R = 0.929,$ $p = 0.0003$	
	IL-5	$R = 0.974,$ $p = 0.0049$	$R = 0.787,$ $p = 0.0119$	$R = 0.898,$ $p = 0.0025$
	IL-6	$R = 0.982,$ $p = 0.003$	$R = 0.873,$ $p = 0.0021$	$R = 0.726,$ $p = 0.0414$
	IL-7	$R = 0.941,$ $p = 0.0171$		$R = 0.857,$ $p = 0.0065$
	IL-8		$R = 0.889,$ $p = 0.0014$	$R = 0.899,$ $p = 0.0024$
	IL-10	$R = 0.906,$ $p = 0.0343$		$R = 0.781,$ $p = 0.0222$
	IL-12	$R = 0.991,$ $p = 0.0011$		$R = 0.86,$ $p = 0.0062$
	IL-13	$R = 0.988,$ $p = 0.0016$		$R = 0.92,$ $p = 0.0012$
	IL-15			$R = 0.813,$ $p = 0.0142$
	IL-17		$R = 0.963,$ $p < 0.0001$	$R = 0.827,$ $p = 0.0113$
	bFGF	$R = 0.937,$ $p = 0.019$	$R = 0.816,$ $p = 0.0073$	$R = 0.871,$ $p = 0.0048$

	G-CSF		R = 0.876, $p = 0.002$	
	GM-CSF		R = 0.688, $p = 0.0404$	R = 0.901, $p = 0.0023$
	IFN- γ	R = 0.884, $p = 0.0467$	R = 0.958, $p < 0.0001$	R = 0.977, $p < 0.0001$
	MCP-1		R = 0.894, $p = 0.0012$	R = 0.835, $p = 0.0099$
	MIP-1 α	R = 0.916, $p = 0.0287$	R = 0.871, $p = 0.0022$	R = 0.803, $p = 0.0165$
	MIP-1 β		R = 0.859, $p = 0.003$	
	TNF α		R = 0.863, $p = 0.0027$	
	VEGF		R = 0.926, $p = 0.0003$	R = 0.826, $p = 0.0114$
IL-4	IL-6		R = 0.906, $p = 0.0008$	
	IL-7	R = 0.916, $p = 0.029$		
	IL-8	R = 0.892, $p = 0.0418$	R = 0.928, $p = 0.0003$	
	IL-10			R = 0.863, $p = 0.0058$
	IL-12	R = 0.935, $p = 0.0195$		
	IL-17		R = 0.984, $p < 0.0001$	
	bFGF	R = 0.929, $p = 0.0226$	R = 0.681, $p = 0.0435$	
	G-CSF		R = 0.91, $p = 0.0007$	R = 0.972, $p = 0.0001$
	IFN- γ	R = 0.91, $p = 0.0318$	R = 0.949, $p = 0.0001$	
	MCP-1		R = 0.921, $p = 0.0004$	
	MIP-1 α		R = 0.899, $p = 0.001$	R = 0.745, $p = 0.0338$
	MIP-1 β		R = 0.912, $p = 0.0006$	
	TNF α		R = 0.91, $p = 0.0007$	R = 0.869, $p = 0.0051$
	VEGF		R = 0.901, $p = 0.0009$	
IL-5	IL-12	R = 0.977, $p = 0.0041$	R = 0.765, $p = 0.0164$	R = 0.983, $p < 0.0001$
	IL-13	R = 0.982, $p = 0.0029$	R = 0.825, $p = 0.0062$	R = 0.811, $p = 0.0145$
	IL-15	R = 0.894,	R = 0.957,	R = 0.952,

		$p = 0.0406$	$p = 0.0001$	$p = 0.0003$
	IL-17	$R = 0.914,$ $p = 0.0299$	$R = 0.685,$ $p = 0.0419$	$R = 0.738,$ $p = 0.0365$
	bFGF	$R = 0.964,$ $p = 0.0083$	$R = 0.956,$ $p = 0.0001$	$R = 0.803,$ $p = 0.0165$
	GM-CSF	$R = 0.882,$ $p = 0.0475$	$R = 0.969,$ $p < 0.0001$	$R = 0.994,$ $p < 0.0001$
	IFN- γ	$R = 0.912,$ $p = 0.0309$		$R = 0.948,$ $p = 0.0003$
	MIP-1 α	$R = 0.9,$ $p = 0.0375$		
	VEGF		$R = 0.692,$ $p = 0.0389$	$R = 0.973,$ $p = 0.0001$
IL-6	IL-7	$R = 0.937,$ $p = 0.0188$		
	IL-8		$R = 0.998,$ $p < 0.0001$	
	IL-9	$R = -0.938,$ $p = 0.0182$		
	IL-10	$R = 0.949,$ $p = 0.0137$		
	IL-12	$R = 0.974,$ $p = 0.005$		$R = 0.925,$ $p = 0.001$
	IL-13	$R = 0.988,$ $p = 0.0016$		
	IL-15			$R = 0.97,$ $p = 0.0001$
	IL-17	$R = 0.883,$ $p = 0.0469$	$R = 0.903,$ $p = 0.0009$	
	bFGF	$R = 0.942,$ $p = 0.0168$		
	G-CSF		$R = 0.997,$ $p < 0.0001$	
	GM-CSF	$R = 0.886,$ $p = 0.0451$		$R = 0.937,$ $p = 0.0006$
	IFN- γ	$R = 0.887,$ $p = 0.0446$	$R = 0.968,$ $p < 0.0001$	$R = 0.798,$ $p = 0.0177$
	MCP-1		$R = 0.997,$ $p < 0.0001$	
	MIP-1 α	$R = 0.913,$ $p = 0.0305$	$R = 0.997,$ $p < 0.0001$	
	MIP-1 β		$R = 0.995,$ $p < 0.0001$	
	TNF α		$R = 0.995,$ $p < 0.0001$	
	VEGF		$R = 0.866,$ $p = 0.0025$	$R = 0.928,$ $p = 0.0009$
IL-7	IL-8			$R = 0.758,$ $p = 0.0292$

	IL-10	R = 0.961, $p = 0.0092$		R = 0.888, $p = 0.0033$
	IL-12	R = 0.978, $p = 0.004$	R = 0.703, $p = 0.0345$	R = 0.714, $p = 0.0469$
	IL-13	R = 0.953, $p = 0.0122$	R = 0.734, $p = 0.0243$	R = 0.953, $p = 0.0002$
	IL-15		R = 0.668, $p = 0.0492$	
	IL-17	R = 0.91, $p = 0.032$		R = 0.884, $p = 0.0035$
	Eotaxin			
	bFGF	R = 0.967, $p = 0.0073$		R = 0.782, $p = 0.0219$
	GM-CSF		R = 0.717, $p = 0.0296$	R = 0.729, $p = 0.04$
	IFN- γ	R = 0.893, $p = 0.0411$		R = 0.88, $p = 0.004$
	MCP-1			R = 0.824, $p = 0.0119$
	MIP-1 α			R = 0.798, $p = 0.0176$
IL-8	MIP-1 β			R = 0.749, $p = 0.0326$
	IL-10			R = 0.724, $p = 0.0422$
	IL-12			R = 0.826, $p = 0.0115$
	IL-13			R = 0.842, $p = 0.0088$
	IL-17		R = 0.924, $p = 0.0004$	R = 0.92, $p = 0.0012$
	bFGF	R = 0.915, $p = 0.0295$		R = 0.842, $p = 0.0088$
	G-CSF		R = 0.996, $p < 0.0001$	
	GM-CSF			R = 0.831, $p = 0.0106$
	IFN- γ	R = 0.975, $p = 0.0048$	R = 0.975, $p < 0.0001$	R = 0.887, $p = 0.0033$
	MCP-1		R = 0.997, $p < 0.0001$	R = 0.81, $p = 0.0149$
	MIP-1 α	R = 0.916, $p = 0.029$	R = 0.994, $p < 0.0001$	R = 0.713, $p = 0.047$
	MIP-1 β		R = 0.994, $p < 0.0001$	
	TNF α		R = 0.994, $p < 0.0001$	
	VEGF		R = 0.882, $p = 0.0017$	R = 0.786, $p = 0.0207$

IL-9	IL-10	R = -0.931, $p = 0.0214$		
	IL-13	R = -0.914, $p = 0.0301$		
	IL-15	R = -0.901, $p = 0.0368$		
	IL-17	R = -0.888, $p = 0.0444$		
	GM-CSF	R = -0.881, $p = 0.0485$		
	VEGF	R = -0.904, $p = 0.0352$		
IL-10	IL-12	R = 0.934, $p = 0.02$		
	IL-13	R = 0.95, $p = 0.0132$		R = 0.906, $p = 0.0019$
	IL-15	R = 0.953, $p = 0.0121$	R = 0.864, $p = 0.0027$	
	IL-17	R = 0.966, $p = 0.0076$		R = 0.841, $p = 0.0089$
	bFGF	R = 0.92, $p = 0.0269$	R = 0.893, $p = 0.0012$	
	G-CSF			R = 0.859, $p = 0.0063$
	GM-CSF		R = 0.747, $p = 0.0206$	
	IFN- γ			R = 0.767, $p = 0.0262$
	MCP-1			R = 0.906, $p = 0.0019$
	MIP-1 α			R = 0.875, $p = 0.0044$
	TNF α			R = 0.802, $p = 0.0166$
IL-12	IL-13	R = 0.985, $p = 0.0021$	R = 0.901, $p = 0.0009$	R = 0.742, $p = 0.0352$
	IL-15		R = 0.821, $p = 0.0067$	R = 0.945, $p = 0.0004$
	Eotaxin		R = -0.767, $p = 0.0159$	
	bFGF	R = 0.963, $p = 0.0086$	R = 0.674, $p = 0.0465$	R = 0.851, $p = 0.0074$
	GM-CSF		R = 0.857, $p = 0.0032$	R = 0.989, $p < 0.0001$
	IFN- γ	R = 0.903, $p = 0.0359$		R = 0.93, $p = 0.0008$
	VEGF			R = 0.968, $p = 0.0001$
IL-13	IL-15		R = 0.782,	R = 0.719,

			$p = 0.0127$	$p = 0.0446$
	IL-17			$R = 0.917,$ $p = 0.0013$
	bFGF	$R = 0.922,$ $p = 0.0257$	$R = 0.688,$ $p = 0.0404$	$R = 0.765,$ $p = 0.0271$
	GM-CSF		$R = 0.865,$ $p = 0.0026$	$R = 0.78,$ $p = 0.0225$
	IFN- γ			$R = 0.9, p = 0.0023$
	MCP-1			$R = 0.819,$ $p = 0.013$
	MIP-1 α			$R = 0.924,$ $p = 0.001$
	RANTES		$R = -0.683,$ $p = 0.0426$	
	VEGF	$R = 0.88,$ $p = 0.0487$		$R = 0.711,$ $p = 0.0482$
IL-15	IL-17	$R = 0.996,$ $p = 0.0003$		
	bFGF		$R = 0.96,$ $p < 0.0001$	$R = 0.728,$ $p = 0.0407$
	GM-CSF		$R = 0.953,$ $p = 0.0001$	$R = 0.96,$ $p = 0.0002$
	IFN- γ			$R = 0.884,$ $p = 0.0036$
	VEGF			$R = 0.954,$ $p = 0.0002$
IL-17	bFGF	$R = 0.906,$ $p = 0.0341$	$R = 0.755,$ $p = 0.0186$	$R = 0.773,$ $p = 0.0246$
	G-CSF		$R = 0.906,$ $p = 0.0008$	
	IFN- γ		$R = 0.961,$ $p < 0.0001$	$R = 0.824,$ $p = 0.0119$
	MCP-1		$R = 0.917,$ $p = 0.0005$	$R = 0.815,$ $p = 0.0136$
	MIP-1 α		$R = 0.896,$ $p = 0.0011$	$R = 0.797,$ $p = 0.0179$
	MIP-1 β		$R = 0.903,$ $p = 0.0009$	
	TNF α		$R = 0.905,$ $p = 0.0008$	
	VEGF		$R = 0.922,$ $p = 0.0004$	
Eotaxin	GM-CSF	$R = -0.94,$ $p = 0.0174$		
	PDGF-bb		$R = 0.762,$ $p = 0.0169$	
	RANTES		$R = 0.749,$ $p = 0.0202$	

bFGF	GM-CSF		R = 0.92, $p = 0.0004$	R = 0.824, $p = 0.0118$
	IFN- γ	R = 0.978, $p = 0.0039$		R = 0.898, $p = 0.0025$
	VEGF		R = 0.779, $p = 0.0133$	R = 0.766, $p = 0.0266$
G-CSF	IFN- γ		R = 0.973, $p < 0.0001$	
	MCP-1		R = 0.998, $p < 0.0001$	
	MIP-1 α		R = 1, $p < 0.0001$	R = 0.809, $p = 0.015$
	MIP-1 β		R = 0.996, $p < 0.0001$	
	TNF α		R = 0.998, $p < 0.0001$	R = 0.934, $p = 0.0007$
	VEGF		R = 0.864, $p = 0.0027$	
GM-CSF	IFN- γ			R = 0.949, $p = 0.0003$
	MIP-1 α	R = 0.927, $p = 0.0235$		
	VEGF			R = 0.971, $p = 0.0001$
IFN- γ	MIP-1		R = 0.977, $p < 0.0001$	R = 0.818, $p = 0.0131$
	MIP-1 α	R = 0.901, $p = 0.037$	R = 0.97, $p < 0.0001$	R = 0.718, $p = 0.0448$
	MIP-1 β		R = 0.959, $p < 0.0001$	
	TNF α		R = 0.964, $p < 0.0001$	
	VEGF		R = 0.908, $p = 0.0007$	R = 0.898, $p = 0.0025$
IP-10	RANTES			R = 0.959, $p = 0.0002$
MCP-1	MIP-1 α		R = 0.997, $p < 0.0001$	R = 0.723, $p = 0.0428$
	MIP-1 β		R = 0.996, $p < 0.0001$	
	TNF α	R = 0.9, $p = 0.0374$	R = 0.995, $p < 0.0001$	
	VEGF		R = 0.878, $p = 0.0019$	
MIP-1 α	MIP-1 β		R = 0.995, $p < 0.0001$	
	RANTES		R = 0.669, $p = 0.0489$	
	TNF α		R = 0.997,	R = 0.73,

			$p < 0.0001$	$p = 0.0399$
	VEGF		R = 0.857, $p = 0.0031$	
PDGF-bb	MIP-1 β			R = 0.802, $p = 0.0168$
	RANTES		R = 0.76, $p = 0.0174$	
	TNF α	R = 0.887, $p = 0.0451$		
MIP-1 β	RANTES	R = 1, $p < 0.0001$	R = 0.68, $p = 0.0439$	
	TNF α	R = 0.902, $p = 0.0363$	R = 0.998, $p < 0.0001$	R = 0.729, $p = 0.0401$
	VEGF		R = 0.853, $p = 0.0035$	
RANTES	TNF α	R = 0.906, $p = 0.0342$	R = 0.688, $p = 0.0404$	
TNF α	VEGF		R = 0.86, $p = 0.0029$	

Table S5. Significant correlations between cytokines in plasma and gene expression in MSCs of patients before treatment

		Proteins									Gene expression													
		IL-5	IL-15	Eotaxin	FGFb	G-CSF	MCP-1	MIP-1b	RANTES	VEGF	MMP2	IL6	TGFB1	PDGFRb	SOX9	FGFb	FGFR1	FGFR2	VEGF	BGLAP	SMURF1	BMP4	IL8	MCAM
Gene expression	MMP2												0.902	0.901			0.929	0.944	0.900		0.972			
	IL6			−0.0878											0.940									
	TGFB1										0.902			0.925				0.926	0.924					
	PDGFRb										0.901		0.925				0.948		0.969			−0.886		0.971
	PPARG																							
	SOX9			−0.947								0.940												
	FGFb							−0.923															0.979	
	FGFR1										0.929			0.948					0.973		0.904			0.920
	FGFR2								−0.958		0.944		0.926						0.882					
	VEGF										0.900		0.924	0.969			0.973	0.882						0.931
	SPP1																							
	ICAM1					−0.908																		
	BGLAP																					0.975		
	SMURF1										0.972						0.904							
	BMP4													−0.886						0.975				
	BMP2	0.893	0.935		0.927		0.926			0.931														
	IL8							−0.934								0.979								
	MCAM													0.971			0.920		0.931					