

Table S1. Results of laboratory analysis in children with HSCT procedure.

Parameter	Pre-HSCT, <i>n</i> = 27	Post-HSCT, <i>n</i> = 27	<i>p</i> / <i>p</i> ^{BH} -Value Pre-HSCT vs. Post-HSCT
Glc (mmol/L)	4.4 ± 0.6	4.5 ± 0.6	0.7/-
TC (mmol/L)	3.3 ± 1.0	3.9 ± 0.9	0.002/0.04
HDL-C (mmol/L)	1.0 ± 0.4	1.3 ± 0.5	0.02/0.4
LDL-C (mmol/L)	1.4 ± 0.9	1.9 ± 0.8	0.05/-
TG (mmol/L)	1.8 ± 0.7	1.5 ± 0.6	0.3/-
hsCRP (mg/L)	7.7 ± 10.4	7.0 ± 11.2	0.8/-

Table S2. The genes which expression changed most significantly after the HSCT procedure (as presented in Table 5). The groups of children with non-neoplastic and neoplastic disease as an indication for HSCT were considered separately here. The gene expression is shown as log₂ of signal RMA-normalized intensity.

Gene symbol	Locus and Affimetrix code	Non-neoplastic		Pre-HSCT vs post-HSCT		Neoplastic		Pre-HSCT vs post-HSCT	
		Pre-HSCT <i>n</i> = 9	Post-HSCT <i>n</i> = 9	<i>FC</i>	<i>p</i> / <i>p</i> ^{BH} -Value	Pre-HSCT <i>n</i> = 18	Post-HSCT <i>n</i> = 18	<i>FC</i>	<i>p</i> / <i>p</i> ^{BH} -Value
The most statistically significantly changed genes (FDR <0.05) after HSCT									
<i>DPP4</i>	2q24.2 8056222	9.18	8.05	-2.18	0.0009/0.3	8.81	7.71	-2.15	8*10 ⁻⁶ /0.02
<i>SLC4A10</i>	2q24.2 8045974	6.19	6.41	1.16	0.06/0.6	7.03	6.55	-1.40	0.002/0.1
<i>NR3C2</i>	4q31 8103094	6.71	5.69	-2.03	10 ⁻⁶ /0.032	6.18	5.71	-1.38	0.01/0.2
<i>AK5</i>	1p31.1 7902452	7.55	5.73	-3.53	0.001/0.3	6.88	5.79	-2.14	0.002/0.1
The genes which expression was most decreased after the HSCT procedure									
<i>AHSP</i>	16p11.2 7995237	9.11	6.75	-5.15	0.07/0.6	9.53	7.41	-4.34	0.0005/0.08
<i>CA1</i>	8q21.2 8151592	10.47	7.61	-7.26	0.08/0.7	10.24	8.02	-4.64	0.002/0.1
<i>ALAS2</i>	Xp11.21 8173135	9.73	7.25	-5.60	0.08/0.7	9.97	8.13	-3.57	0.003/0.1
The genes which expression was most increased after the HSCT procedure									
<i>MS4A1</i>	11q12.2 7940287	9.04	9.2	1.1	0.1/0.7	4.89	5.09	1.15	0.02/0.3
<i>TCL1A</i>	14q32.13 7981183	10.48	10.44	-1.03	0.6/0.9	7.44	10.03	6.02	3*10 ⁻⁵ /0.033
<i>CD22</i>	19q13.12 8027837	9.96	10.24	1.22	0.4/0.8	6.01	8.73	6.6	9*10 ⁻⁷ /0.009

Table S3. Table showing the analysis of GO enrichment from DEGs between children before and after performing the HSCT procedure.

Category	Term	Genes count (<i>n</i> , %)	<i>p</i> -Value	<i>p</i> ^{BH} -Value
CC	blood microparticle	18, 10.8%	2.2*10 ⁻¹⁷	2.5*10 ⁻¹⁵
	external side of plasma membrane	17, 10.2%	1.2*10 ⁻¹³	6.8*10 ⁻¹²
	extracellular region	33, 19.8%	3.7*10 ⁻¹⁰	1.5*10 ⁻⁸
	immunoglobulin complex, circulating	7, 4.2%	9.1*10 ⁻¹⁰	2.7*10 ⁻⁸
	plasma membrane	52, 31.1%	9.9*10 ⁻⁹	2.3*10 ⁻⁷
	extracellular exosome	39, 23.4%	2.5*10 ⁻⁷	4.8*10 ⁻⁶
	hemoglobin complex	4, 2.4%	4.2*10 ⁻⁵	7.0*10 ⁻⁴

	secretory dimeric IgA immunoglobulin complex	3, 1.8%	1.0*10 ⁻⁴	1.2*10 ⁻³
	secretory IgA immunoglobulin complex	3, 1.8%	1.0*10 ⁻⁴	1.2*10 ⁻³
	monomeric IgA immunoglobulin complex	3, 1.8%	1.0*10 ⁻⁴	1.2*10 ⁻³
	extracellular space	19, 11.4%	8.2*10 ⁻⁴	8.7*10 ⁻³
	hexameric IgM immunoglobulin complex	2, 1.2%	1.2*10 ⁻²	1.1*10 ⁻¹
	pentameric IgM immunoglobulin complex	2, 1.2%	1.2*10 ⁻²	1.1*10 ⁻¹
	B cell receptor complex	2, 1.2%	1.2*10 ⁻²	1.1*10 ⁻¹
	integral component of plasma membrane	16, 9.6%	1.8*10 ⁻²	1.4*10 ⁻¹
	membrane raft	5, 3.0%	3.3*10 ⁻²	2.4*10 ⁻¹
	integral component of membrane	39, 23.4%	6.3*10 ⁻²	4.4*10 ⁻¹
MF	antigen binding	25, 15.0%	2.9*10 ⁻³²	5.9*10 ⁻³⁰
	immunoglobulin receptor binding	11, 6.6%	1.8*10 ⁻¹⁶	1.9*10 ⁻¹⁴
	serine-type endopeptidase activity	20, 12.0%	6.6*10 ⁻¹⁶	4.6*10 ⁻¹⁴
	oxygen transporter activity	3, 1.8%	3.1*10 ⁻³	1.6*10 ⁻¹
	heme binding	5, 3.0%	9.2*10 ⁻³	3.8*10 ⁻¹
	interleukin-8 receptor activity	2, 1.2%	1.2*10 ⁻²	4.1*10 ⁻¹
	interleukin-8 binding	2, 1.2%	1.8*10 ⁻²	5.3*10 ⁻¹
	oxygen binding	3, 1.8%	3.2*10 ⁻²	8.4*10 ⁻¹
	anion transmembrane transporter activity	2, 1.2%	5.3*10 ⁻²	1.0
	peptidoglycan binding	2, 1.2%	7.0*10 ⁻²	1.0
	FMN binding	2, 1.2%	8.6*10 ⁻²	1.0
	C2H2 zinc finger domain binding	2, 1.2%	8.6*10 ⁻²	1.0
	complement activation, classical pathway	24, 14.4%	1.6*10 ⁻³⁰	1.0*10 ⁻²⁷
BP	complement activation	19, 11.4%	5.1*10 ⁻²³	1.7*10 ⁻²⁰
	Fc-gamma receptor signaling pathway involved in phagocytosis	19, 11.4%	7.1*10 ⁻²⁰	1.6*10 ⁻¹⁷
	receptor-mediated endocytosis	19, 11.4%	7.6*10 ⁻¹⁷	1.2*10 ⁻¹⁴
	B cell receptor signaling pathway	13, 7.8%	4.5*10 ⁻¹⁶	5.9*10 ⁻¹⁴
	immune response	24, 14.4%	9.3*10 ⁻¹⁶	1.0*10 ⁻¹³
	positive regulation of B cell activation	10, 6.0%	2.7*10 ⁻¹⁴	2.5*10 ⁻¹²
	phagocytosis, recognition	10, 6.0%	5.9*10 ⁻¹⁴	4.9*10 ⁻¹²
	regulation of immune response	16, 9.6%	2.8*10 ⁻¹³	2.0*10 ⁻¹¹
	phagocytosis, engulfment	10, 6.0%	5.8*10 ⁻¹³	3.8*10 ⁻¹¹
	Fc-epsilon receptor signaling pathway	15, 9.0%	4.7*10 ⁻¹²	2.8*10 ⁻¹⁰
	proteolysis	21, 12.6%	2.6*10 ⁻¹¹	1.4*10 ⁻⁹
	adaptive immune response	8, 4.8%	3.7*10 ⁻⁵	1.9*10 ⁻³
	innate immune response	12, 7.2%	7.2*10 ⁻⁵	3.4*10 ⁻³
	defense response to bacterium	7, 4.2%	2.8*10 ⁻⁴	1.2*10 ⁻²
	positive regulation of respiratory burst	3, 1.8%	5.6*10 ⁻⁴	2.3*10 ⁻²
	glomerular filtration	3, 1.8%	1.3*10 ⁻³	5.1*10 ⁻²
	retina homeostasis	4, 2.4%	1.9*10 ⁻³	7.1*10 ⁻²
	antibacterial humoral response	4, 2.4%	2.5*10 ⁻³	8.8*10 ⁻²
	oxygen transport	3, 1.8%	3.8*10 ⁻³	1.2*10 ⁻¹
	dendritic cell chemotaxis	3, 1.8%	4.9*10 ⁻³	1.5*10 ⁻¹
	regulation of catalytic activity	4, 2.4%	8.0*10 ⁻³	2.3*10 ⁻¹
	cellular response to cytokine stimulus	3, 1.8%	8.1*10 ⁻³	2.3*10 ⁻¹
	interleukin-8-mediated signaling pathway	2, 1.2%	1.2*10 ⁻²	3.4*10 ⁻¹
	B cell proliferation	3, 1.8%	1.7*10 ⁻²	3.4*10 ⁻¹
	receptor internalization	3, 1.8%	2.9*10 ⁻²	7.2*10 ⁻¹
	bicarbonate transport	3, 1.8%	3.0*10 ⁻²	7.2*10 ⁻¹

inflammatory response	7, 4.2%	3.0*10 ⁻²	7.2*10 ⁻¹
hemoglobin metabolic process	2, 1.2%	3.7*10 ⁻²	8.3*10 ⁻¹
chemotaxis	4, 2.4%	4.0*10 ⁻²	8.7*10 ⁻¹
sensory perception of pain	3, 1.8%	4.1*10 ⁻²	8.7*10 ⁻¹
cellular response to organic cyclic compound	3, 1.8%	5.2*10 ⁻²	1.0
purine nucleotide metabolic process	2, 1.2%	6.0*10 ⁻²	1.0
locomotory exploration behaviour	2, 1.2%	7.2*10 ⁻²	1.0
positive regulation of cell-cell adhesion	2, 1.2%	7.2*10 ⁻²	1.0
oxidation-reduction process	8, 4.8%	7.5*10 ⁻²	1.0
homeostasis of number of cells	2, 1.2%	7.8*10 ⁻²	1.0
response to lipopolysaccharide	4, 2.4%	8.2*10 ⁻²	1.0
positive regulation of protein oligomerization	2, 1.2%	8.3*10 ⁻²	1.0
carbohydrate metabolic process	4, 2.4%	9.4*10 ⁻²	1.0