Early expression of CD94 and loss of CD96 on CD8+ T cells after allogeneic stem cell tranplantation is predictive of subsequent relapse and survival

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Supplemental Data

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Supplementary Figure S1. Read and Feature count overview from scRNAseq. Quality control metrics from the smart-seq2 sequencing run. Plots show the number of reads, reads not aligning to the human genome, total counts and total features for defined wells from the sequencing experiment. Blank = wells not containing a cell; CD4_100_cells_Pt/HD = CD4 T cells from patient/HD samples (100 cells randomly selected); CD8_100_cells_Pt/HD = CD8 T cells from patient/HD samples (100 cells randomly selected); mousecontrol = control wells containing mouse cells; SC_lysate = single cell lysate from non-control wells; SC_WELLS = all non-control wells.



Supplementary Figure S2. Functional enrichments and interactions in T cells at WK2 post transplant. (A) Top 30 significant CD4 Marker genes and CD8 marker genes (FDR<0.05; logFC>1); (B) Selected cluster identifying genes within CD8+ T cells (C) GO term: Biological Process (D) KEGG Pathway; and (E), Transcription factor (TF) targets) within marker genes overexpressed in WK2 CD8+ T cell Effector (E) and Naïve (N) cell populations. (F) Significant estimated interactions between T cell subsets at WK2. Colour scale indicates the means of the average expression of interacting molecule 1 in subset 1 and interacting molecule 2 in subset 2.



Supplementary Figure S3. CD8+ T cell within-cluster Relapse vs No Relapse differential expression. Within-cluster Relapse vs No Relapse differentially expressed genes (Coloured points, FDR<0.01 & absolute logFC > 0.5).



Supplementary Figure S4. Functional enrichments within Relapse-expressed genes in CD8+ T cells at 2 weeks post transplant. Selected enrichments of KEGG Pathway (A) and Transcription factor targets (B) within Relapse-overexpressed genes identified from within-cluster differential expression analysis.

A Signatures with maximum proportion difference betwe en Clusters



THE CITRIC ACID TCA CYCLE AND RESPIRATORY ELECTRON TRANSPORT OME AXON GUIDANCE ENIC ESCHERICHIA COLI INFECTION RHO GTPASE EFFECTORS PLATELET ACTIVATION SIGNALING AND AGGREGATION FORMYL PEPTIDE RECEPTORS BIND FORMYL PEPTIDE CORE MATRISOME ABA ECM GLYCOPROTEINS ADA EUM GLICUPROLEINS LEACTOME NAPULIS CL DEPENDENT NEUROTRANSMITTER TRANSPORTERS LEACTOME FORMATION OF THE CORNIFIED ENVELOPE LEACTOME KERATINIZATION INCARTA FOSB PATHWAY GSE25087 TREG VS TCONV ADULT UP FERRARO Treg sig UP GSE22045 TREG VS TCONV UP GSE25087 TREG VS TCONV FETUS UP GSE7852 TREG VS TCONV UP GSE7882 TREG VS TCONV UP GSE43957 UNTREATED VS NACL TREATED ANTI CD3 CD28 STIM CD4 TCELL DN GSE9316 CD4 TCELL BALBC VS TH17 ENRI CD4 TCELL SKG PMA IONO STIM FR4NEG DN

BIOCARTA EPONFKB PATHWAY

REACTOME KERATINIZATION

NABA MATRISOME NABA CORE MATRISOME

REACTOME POST TRANSLATIONAL MODIFICATION: SYNTHESIS OF GPI ANCHORED PROTEINS

REACTOME SYNTHESIS OF GLYCOSYLPHOSPHATIDYLINOSITOL G REACTOME FORMATION OF THE CORNIFIED ENVELOPE

REACTOME SCAVENGING BY CLASS F RECEPTORS KEGG LONG TERM POTENTIATION

REACTOME NAPLUS CL DEPENDENT NEUROTRANSMITTER TRANSPORTERS

Cluster 2 3

Relapse Relapse No Relapse

Supplementary Figure S5. Profiles of selected MSigDB gene set signature assignments from AUCell for CD4+ T cells at WK2 post SCT. Cells are assigned as being active for a signature if the AUC signature score is above a threshold value (global k1 threshold). A, Binary gene set activity profile of Immunerelated signatures and pathways that showed the most divergence in the proportion of cells active between clusters. B, Binary gene set activity profile of Treg associated signature activity. C, Binary gene set activity profile of selected Immune-related signatures and pathways that showed the most divergence in the proportion of cells active between clusters.



Supplementary Figure S6. Validation of selected genes by flow cytometry or qPCR in patients with disease Relapse (REL) or No relapse (NR) post allogeneic SCT. (A-K) Percentage of CD53+, NKG2D+, KLRG1+, CCL5+, CD63+, CD28+, CD95+, CD132+, CD164+ cells within the CD8+ T cell subset is depicted in REL patients (n=16) compared to NR patients (n=18), using flow cytometry. qPCR was used to determine relative expression of the phosphatase DUSP1 as well as KLRC4 which encodes the intracellular NKG2F. Mann Whitney-U test was performed for statistical analysis, * depicts p value <0.005; **** depicts p value <0.001.



Supplementary Figure S7. Violin plot depicting Mean Fluorescence Intensity (MFI) values for (A) CD94 and (B) CD96+ cells within the CD8+ T cell population in the Relapse (REL) and Non-relapse (NR) group of patients in the validation cohort. * depicts statistical significance of p<0.05.

Relapse

MRD Unknown

Sex match Mismatch

PSex M

Term	HR	CI	P.val	Adj.HR	Adj.Cl	Adj.P.val	
Age at transplant	1.01	(0.97 – 1.04)	0.75410	0.95	(0.9 – 1.01)	0.08044	-
CD94 CD94 ⁺ > 15%	4.71	(1.5 – 14.75)	0.00786	10.64	(1.88 – 60.28)	0.00754	
CD96 CD96 ⁺ > 95%	0.27	(0.08 – 0.85)	0.02602	0.29	(0.07 – 1.26)	0.09886	
CMV status Pos	1.58	(0.58 – 4.3)	0.37346	2.25	(0.58 – 8.71)	0.23982	
Disease Risk High	0.48	(0.18 – 1.3)	0.14737	1.06	(0.25 – 4.5)	0.93617	
Disease subgroup CR1_AML_or_MDS	1.57	(0.56 – 4.37)	0.38864	1.73	(0.26 – 11.65)	0.57135	
MRD Pos	0.82	(0.24 – 2.86)	0.76154	0.61	(0.11 – 3.31)	0.56713	
MRD Unknown	1.33	(0.4 – 4.4)	0.63960	1.34	(0.18 – 10.1)	0.77748	
PSex M	2.64	(0.93 – 7.48)	0.06711	0.95	(0.13 – 6.98)	0.95705	
Sex match Mismatch	0.34	(0.11 – 1.07)	0.06615	0.2	(0.02 – 1.56)	0.12447	
							-4 -3 -2 -1 0 1 2 3 4
							Coefficient
Overall Death							
Term	HR	CI	P.val	Adj.HR	Adj.Cl	Adj.P.val	
Age at transplant	1.02	(0.98 – 1.06)	0.3079	0.98	(0.93 – 1.04)	0.57432	+
CD94 CD94 ⁺ > 15%	5.3	(1.46 – 19.2)	0.0111	16.52	(2.06 – 132.65)	0.00834	
CD96 CD96⁺ > 95%	0.23	(0.06 – 0.84)	0.0261	0.19	(0.03 – 1.12)	0.0668	
CMV status Pos	2.9	(0.94 – 8.92)	0.0628	4.27	(0.91 – 19.98)	0.06518	
Disease Risk High	0.48	(0.16 – 1.39)	0.1750	1.26	(0.21 – 7.36)	0.80031	
Disease subgroup CR1_AML_or_MDS	1.4	(0.47 – 4.21)	0.5483	0.8	(0.13 – 4.89)	0.8075	
MRD Pos	0.83	(0.21 – 3.32)	0.7875	0.26	(0.03 – 2.09)	0.20325	

Supplementary Figure S8. Relapse and Overall Death covariate associations. Univariate p values and hazard ratios (P.val and HR) and multivariate p values and hazard ratios (Adj.P.val and Adj.HR) based on CoxPH model of Relapse and Overall Death with a 95% CI and adjusted regression coefficients.

1.06

0.62

0.32

(0.13 - 8.45)

(0.06 - 6.99)

(0.03 – 3.12)

1.75 (0.49 - 6.23) 0.3848

2.49 (0.82 - 7.55) 0.1057

0.46 (0.14 - 1.47) 0.1906

0.95476

0.69929

0.32547

-

Т -3 -2 -1 0 1 2 3 4 5 Coefficient

Supplementary Table 1. Patient characteristics and percentage CD94 high/low and CD96 high/low expression on T cells in each group of patients.

		ScRNA-			<15%		>15%		<95%		>95%	
		sea	Validation		CD94+		CD94+		CD96+		CD96+	
		n (N=3)	n (N=34)	%	n (N=18)	%	n (N=16)	%	n (N=17)	%	n (N=17)	%
Gender	Male	1	19	55,9	10	55,6	9	56,3	9	52,9	10	58,8
	Female	2	15	44,1	8	44,4	7	43,8	8	47,1	7	41,2
						,				,		
Disease	AML	3	15	44,1	8	44,4	7	43,8	7	41,2	8	47,1
	CML	0	4	11,8	2	11,1	2	12,5	3	17,6	1	5,9
	MDS	0	5	14,7	2	11,1	3	18,8	2	11,8	3	17,6
	ALL	0	5	14,7	2	11,1	3	18,8	3	17,6	2	11,8
	CLL	0	1	2,9	1	5,6	0	0,0	0	0,0	1	5,9
	HL	0	2	5,9	1	5,6	1	6,3	2	11,8	0	0,0
	NHL	0	1	2,9	1	5,6	0	0,0	0	0,0	1	5,9
	Myelofibrosis	0	1	2,9	1	5,6	0	0,0	0	0,0	1	5,9
Age			49 (22-73)		49(24-64)		50(22-73)		48(24-67)		50 (22-73)	
<u></u>		2	22	011	10	100.0		07.5	45	00.2	47	100.0
Source of graft	PBSC	3	32	94,1	18	100,0	14	87,5	15	88,2	17	100,0
	Cord	0	1	2,9	0	0,0	1	6,3	1	5,9	0	0,0
	BIVI	0	1	2,9	0	0,0	L	6,3	1	5,9	0	0,0
Tuno	MUD	2	26	76 5	12	72.2	12	91.2	12	76 5	12	76 5
туре	MRD	0	20	20.6	5	27.8	2	12 5	3	17.6	15	23 5
	Cord	0	, 1	20,0	0	0.0	1	63	1	59		0.0
	coru	0	1	2,5	0	0,0	1	0,5		5,5	0	0,0
Conditioning	FLU/BU	3	9	26.5	6	33.3	3	18.8	6	35.3	3	17.6
	FLAMSA/BU	0	5	14.7	2	11.1	3	18.8	2	11.8	3	17.6
	CYCLO/TBI	0	3	8,8	1	5,6	2	12,5	0	0,0	3	17,6
	CYCLO/FLU	0	2	5,9	1	5,6	1	6,3	1	5,9	1	5,9
	FLU/MELPH	0	12	35,3	6	33,3	6	37,5	6	35,3	6	35,3
	BEAM	0	3	8,8	2	11,1	1	6,3	2	11,8	1	5,9
										0,0		0,0
	ATG	3	14	41,2	7	38,9	7	43,8	7	41,2	7	41,2
	CAMPATH	0	17	50,0	9	50,0	8	50,0	9	52,9	8	47,1
CMV	R+/D+	0	11	32,4	5	27,8	6	37,5	6	35,3	5	29,4
	R+/D-	1	6	17,6	5	27,8	1	6,3	3	17,6	3	17,6
	<u>R-/D+</u>	0	1	2,9	1	5,6	0	0,0	0	0,0	1	5,9
	R-/D-	2	16	47,1	/	38,9	y	56,3	8	47,1	8	47,1
Minal												
viral	CMV	2	2	00	С	11 1	1	6.2	2	176	0	0.0
Teactivation	ERV		1	<u>0,0</u>		0.0	1	6.2	<u> </u>	50	0	0,0
	LDV	0	1	2,9	0	0,0	1	0,3		5,5	0	0,0
Relapse		2	16	47.1	3	16.7	13	81.3	11	64.7	5	29.4
neiupse	Median days		10	17,1	5	10,7	15	01,0		01,7		23,1
	to relapse	47	250		211		242					
	•											
GvHD	acute	0	12	35,3	6	33,3	6	37,5	4	23,5	8	47,1
	chronic	0	3	8,8	1	5,6	2	12,5	0	0,0	3	17,6
Survival		1	20	58,8	15	83,3	5	31,3	7	41,2	13	76,5
	Median days											
	to death	79	377		449		361					

Supplementary Table 2 Univariate CoxPH results summarising effect of covariates on Overall Death and Relapse.

Overall Death outcome covariates	coef	exp(coef)	se(coef)	z	Pr(> z)	lower	upper	cox.zph.p
CD94 CD94+ > 15%	1.67	5.30	0.66	2.54	0.01	1.46	19.20	0.92
CD96 CD96+ > 95%	-1.48	0.23	0.66	-2.23	0.03	0.06	0.84	0.56
Psex M	0.91	2.49	0.57	1.62	0.11	0.82	7.55	0.45
Age at transplant	0.02	1.02	0.02	1.02	0.31	0.98	1.06	0.87
Dsex M	-0.56	0.57	0.65	-0.86	0.39	0.16	2.05	0.16
Disease risk High	-0.74	0.48	0.54	-1.36	0.18	0.16	1.39	0.78
Disease Subgroup CR1_AML_or_MDS	0.34	1.40	0.56	0.60	0.55	0.47	4.21	0.01
HCT-CI 1	-0.31	0.73	1.07	-0.29	0.77	0.09	5.94	0.53
HCT-CI 2	-0.59	0.55	0.79	-0.75	0.45	0.12	2.61	0.53
HCT-CI 3+	0.42	1.52	0.69	0.60	0.55	0.39	5.91	0.53
MRD UNKNOWN	0.56	1.75	0.65	0.87	0.38	0.49	6.23	0.86
MRD POS	-0.19	0.83	0.71	-0.27	0.79	0.21	3.32	0.86
CR CR1	0.22	1.24	0.62	0.35	0.72	0.37	4.15	0.49
CR CR2	-0.47	0.63	0.87	-0.54	0.59	0.11	3.44	0.49
SexMatch MISMATCH	-0.78	0.46	0.60	-1.31	0.19	0.14	1.47	0.81
TBI YES	0.24	1.27	0.76	0.31	0.76	0.28	5.67	0.12
CMVStatus POS	1.07	2.90	0.57	1.86	0.06	0.94	8.92	0.68
Campath NO	-0.61	0.54	1.08	-0.56	0.57	0.07	4.52	0.04
Campath YES	-0.23	0.80	0.56	-0.41	0.68	0.27	2.38	0.04
GvHDProphylaxis COMBINATION	0.40	1.49	0.56	0.71	0.48	0.49	4.46	0.74
Relapse outcome covariates	coef	exp(coef)	se(coef)	z	Pr(> z)	lower	upper	cox.zph.p
Relapse outcome covariates CD94 CD94+ > 15%	coef 1.55	exp(coef) 4.71	se(coef) 0.58	z 2.66	Pr(> z) 0.01	lower 1.50	upper 14.75	cox.zph.p 0.99
Relapse outcome covariates CD94 CD94+ > 15% CD96 CD96+ > 95%	coef 1.55 -1.32	exp(coef) 4.71 0.27	se(coef) 0.58 0.59	z 2.66 -2.23	Pr(> z) 0.01 0.03	lower 1.50 0.08	upper 14.75 0.85	cox.zph.p 0.99 0.39
Relapse outcome covariates CD94 CD94+ > 15% CD96 CD96+ > 95% Psex M	coef 1.55 -1.32 0.97	exp(coef) 4.71 0.27 2.64	se(coef) 0.58 0.59 0.53	z 2.66 -2.23 1.83	Pr(> z) 0.01 0.03 0.07	lower 1.50 0.08 0.93	upper 14.75 0.85 7.48	cox.zph.p 0.99 0.39 0.11
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplant	coef 1.55 -1.32 0.97 0.01	exp(coef) 4.71 0.27 2.64 1.01	se(coef) 0.58 0.59 0.53 0.02	z 2.66 -2.23 1.83 0.31	Pr(> z) 0.01 0.03 0.07 0.75	lower 1.50 0.08 0.93 0.97	upper 14.75 0.85 7.48 1.04	cox.zph.p 0.99 0.39 0.11 0.57
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex M	coef 1.55 -1.32 0.97 0.01 -0.71	exp(coef) 4.71 0.27 2.64 1.01 0.49	se(coef) 0.58 0.59 0.53 0.02 0.58	z 2.66 -2.23 1.83 0.31 -1.22	Pr(> z) 0.01 0.03 0.07 0.75 0.22	lower 1.50 0.08 0.93 0.97 0.16	upper 14.75 0.85 7.48 1.04 1.54	cox.zph.p 0.99 0.39 0.11 0.57 0.74
Relapse outcome covariates CD94 CD94+ > 15% CD96 CD96+ > 95% Psex M Age at transplant Dsex M Disease risk High	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51	z 2.66 -2.23 1.83 0.31 -1.22 -1.45	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15	lower 1.50 0.08 0.93 0.97 0.16 0.18	upper 14.75 0.85 7.48 1.04 1.54 1.30	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDS	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.11	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.11 0.57	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.26
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWN	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.11 0.57 0.40	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.26 0.52
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POS	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.19	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.11 0.57 0.40 0.24	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.26 0.52
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.19 0.29	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.64	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.48	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76 0.63	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.52 0.58
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1CR CR2	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.11	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.89	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.64 0.64 0.60 0.77	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.48 -0.15	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.40 0.28 0.64 0.76 0.63 0.88	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1CR CR2SexMatch MISMATCH	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.11 -1.08	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.89 0.34	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.60 0.77 0.59	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.48 -0.15 -1.84	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.40 0.28 0.64 0.76 0.63 0.88 0.07	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.11 0.57 0.40 0.24 0.41 0.20 0.11	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01 1.07	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58 0.58 0.16
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1CR CR2SexMatch MISMATCHTBI YES	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.19 0.29 -0.11 -1.08 0.10	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.89 0.34 1.11	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.60 0.77 0.59 0.76	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.48 -0.15 -1.84 0.13	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76 0.63 0.88 0.07 0.89	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41 0.20 0.11 0.25	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01 1.07 4.89	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58 0.16
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1CR CR2SexMatch MISMATCHTBI YESCMV Status POS	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.19 0.29 -0.11 -1.08 0.10	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.89 0.34 1.11 1.58	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.61 0.59 0.77 0.59 0.76 0.51	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 1.08 0.85 1.08 0.47 -0.30 0.48 -0.15 -1.84 0.13 0.89	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76 0.63 0.88 0.07 0.89 0.37	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41 0.25 0.58	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01 1.07 4.89 4.30	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58 0.16 0.09 0.89
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-Cl 1HCT-Cl 2HCT-Cl 3+MRD UNKNOWNMRD POSCR CR1CR CR2SexMatch MISMATCHTBI YESCMV Status POSCampath NO	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.11 -1.08 0.10 0.46 -1.24	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.82 1.33 0.82 1.33 0.89 0.34 1.11 1.58 0.29	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.60 0.77 0.59 0.76 0.51 1.07	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.47 -0.30 0.48 -0.15 -1.84 0.13 0.89 -1.15	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76 0.63 0.88 0.07 0.89 0.37 0.25	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41 0.20 0.11 0.25 0.58 0.04	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01 1.07 4.89 4.30 2.37	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58 0.58 0.16 0.09 0.89 0.06
Relapse outcome covariatesCD94 CD94+ > 15%CD96 CD96+ > 95%Psex MAge at transplantDsex MDisease risk HighDisease Subgroup CR1_AML_or_MDSHCT-CI 1HCT-CI 2HCT-CI 3+MRD UNKNOWNMRD POSCR CR1CR CR2SexMatch MISMATCHTBI YESCMV Status POSCampath NOCampath YES	coef 1.55 -1.32 0.97 0.01 -0.71 -0.74 0.45 0.68 -0.67 0.69 0.29 -0.19 0.29 -0.11 -1.08 0.10 0.46 -1.24 -0.99	exp(coef) 4.71 0.27 2.64 1.01 0.49 0.48 1.57 1.97 0.51 2.00 1.33 0.82 1.33 0.82 1.33 0.89 0.34 1.11 1.58 0.29 0.37	se(coef) 0.58 0.59 0.53 0.02 0.58 0.51 0.52 0.80 0.79 0.64 0.61 0.64 0.61 0.59 0.77 0.59 0.76 0.51 1.07 0.55	z 2.66 -2.23 1.83 0.31 -1.22 -1.45 0.86 0.85 -0.85 1.08 0.47 -0.30 0.47 -0.30 0.48 -0.15 -1.84 0.13 0.89 -1.15 -1.80	Pr(> z) 0.01 0.03 0.07 0.75 0.22 0.15 0.39 0.40 0.40 0.28 0.64 0.76 0.63 0.88 0.07 0.89 0.37 0.25 0.07	lower 1.50 0.08 0.93 0.97 0.16 0.18 0.56 0.41 0.57 0.40 0.24 0.41 0.20 0.11 0.25 0.58 0.04 0.13	upper 14.75 0.85 7.48 1.04 1.54 1.30 4.37 9.49 2.43 6.98 4.40 2.86 4.35 4.01 1.07 4.89 4.30 2.37 1.09	cox.zph.p 0.99 0.39 0.11 0.57 0.74 0.43 0.13 0.26 0.26 0.52 0.52 0.58 0.16 0.09 0.89 0.06