Supplementary Tables

Supplementary table 1: **Mass cytometry panel used for immunophenotyping.**

Metal Isotope /Fluorochrome	**Antigen**	**Clone**	**Manufacturer**
Barcoding and fluorescent			
^{89}Y or ^{113}In	CD45	30-F11	Biolegend
Biotin	CD86	IT2.2	BD
PE	CD223 (Lag3)	T47-530	BD
Remaining surface stain			
^{115}In	CD11c	Bu15	Biolegend
^{141}Pr	CD27	M-T271	BD
^{142}Nd	CD19	HIB19	BD
^{143}Nd	CD45RA	HI100	Biolegend
^{144}Nd	CCR5	HEK/1/8	Biolegend
^{145}Nd	CD4	RPA-T4	BD
^{146}Nd	CCR10	1B5	BD
^{147}Sm	CD20	2H7	Biolegend
^{148}Nd	CD16	3G8	BD
^{149}Sm	CD366 (Tim3)	7D3	BD
^{150}Nd	Biotin	1D4-C5	Biolegend
^{151}Eu	CD278 (ICOS)	DX29	BD
^{152}Sm	CD45RO	UCHL1	BD
^{153}Eu	CD62L	DREG	Biolegend
^{154}Gd	CD196 (CCR6)	11A9	BD
^{155}Gd	CD31	WM59	Biolegend
^{156}Gd	PE	PE001	Biolegend
^{158}Gd	CD194 (CCR4)	L291H4	Biolegend
^{159}Tb	CD197 (CCR7)	150503	RnD Systems
^{160}Gd	CD14	M5E2	Biolegend
^{161}Dy	CD274 (PD-L1)	29E.2A3	Biolegend
^{163}Dy	CD183 (CXCR3)	G025H7	Biolegend
^{164}Er	CD161	DX12	BD
^{165}Ho	CD127 (IL-7R)	A019D5	Biolegend
^{166}Er	CD185 (CXCR5)	RF8B2	BD
^{167}Er	CD38	HIT2	Biolegend
^{168}Er	CD8a	RPA-T8	BD
^{169}Tm	CD25	2A3	Fluidigm
^{170}Er	CD3	UCHT1	BD

^{171}Yb	CD335 (NKp46)	9E2	Biolegend
^{172}Yb	CD57	HCD57	Fluidigm
^{173}Yb	Integrin β7	FIB504	BD
^{174}Yb	HLA-DR	L243	BD
^{175}Lu	CD279 (PD-1)	EH12.2H7	Biolegend
^{176}Lu	CD56	NCAM16	BD
Intracellular stain			
^{162}Er	FOXP3	PCH101	BD
$^{191/193}Ir$	DNA Intercalator		Fluidigm

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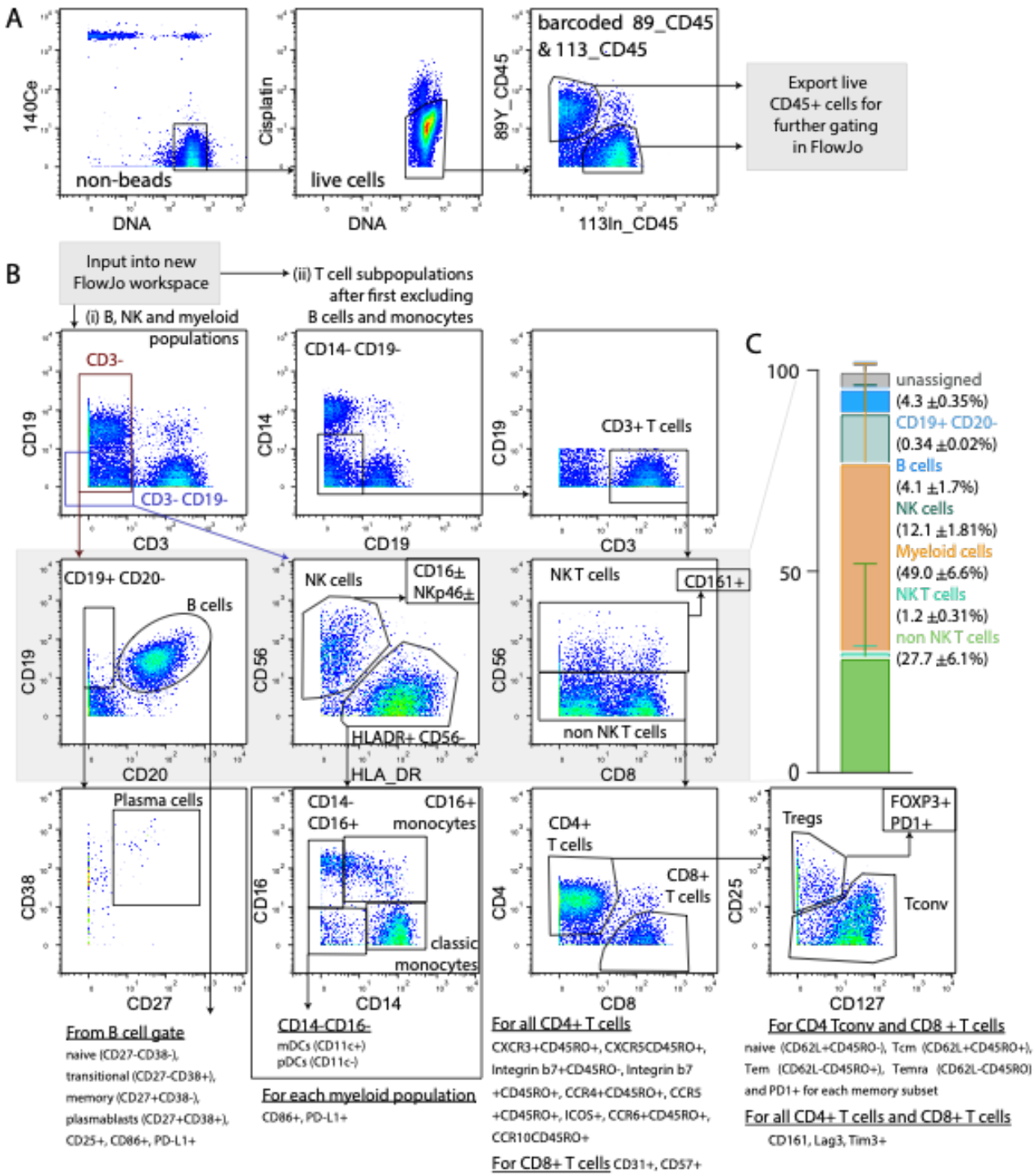
Supplementary Figures

Supplementary figure 1. Gating Strategy. PBMCs were stained as per antibodies and steps outlined in Supplementary table S1 and subsequently analysed by mass cytometry. **A**) Cells were pre-gated prior to population analysis. Cells were first distinguished as positive for DNA-intercalated events (detected in channels 191 and 193) and negative for EQ-beads (detected in 140 channel), and with subsequent demarcation for exclusion of dead (cisplatin positive) cells and differential CD45 antibody staining to distinguish barcoded, concurrently analysed samples. **B**) The gating strategy allows for distinguishing major immune lineages and particular subsets of interest following haemopoietic stem cell transplantation immune reconstitution. **C**) Summarising the collective gated population occupancy as demarcated by populations in second row of Supplementary figure 1B (boxed in grey), with median frequency ± sem across a batch of healthy controls (n = 4) and patients receiving HSCT alone (n = 10).

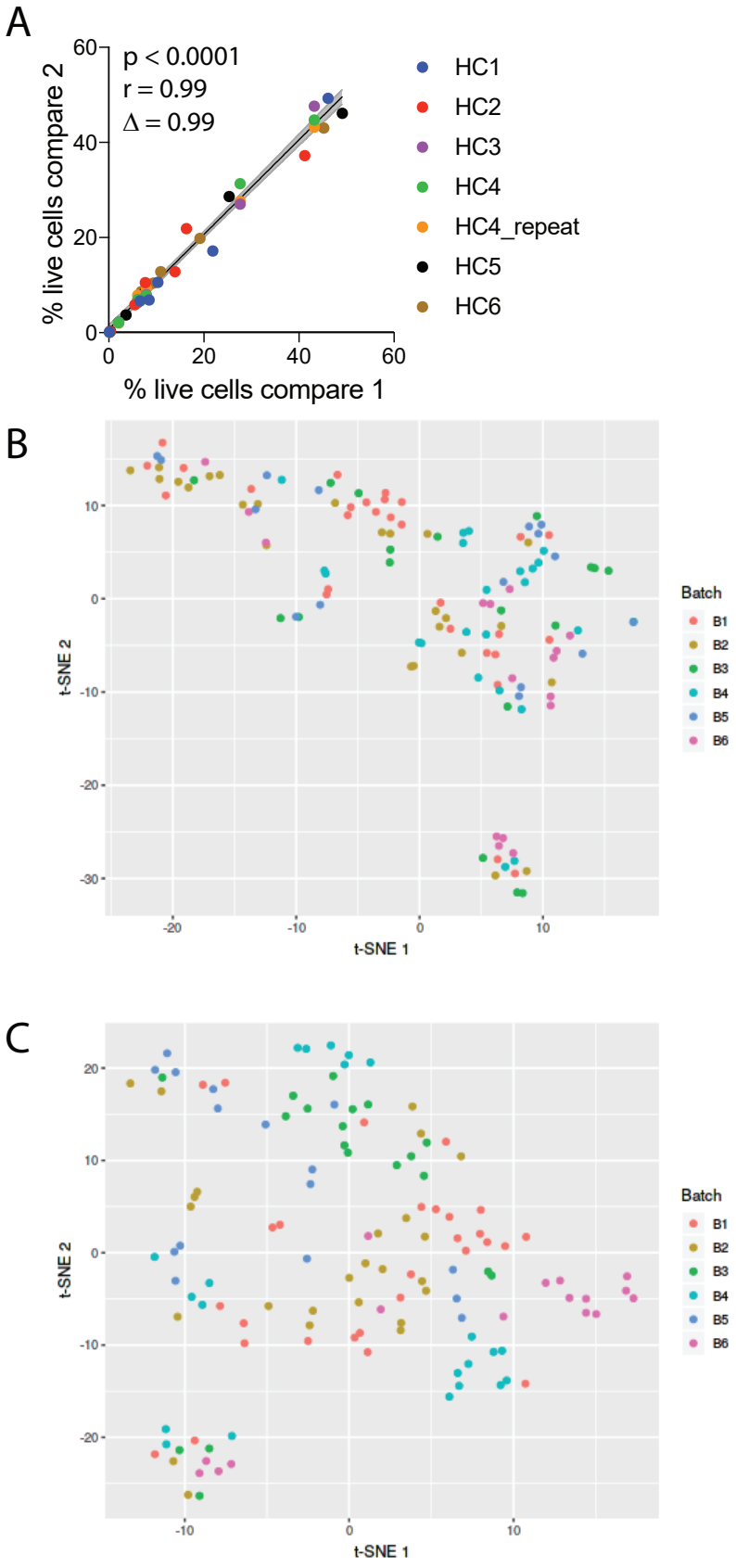
Supplementary figure 2. The mass cytometry immunophenotyping assay is robust across experimental batches. **A**) Correlation showing consistency of population frequencies for the 6 healthy control (HC) samples analysed across two different batches, with HC4 analysed in three independent batches. Colour identifies healthy control correlated across the frequency of major immune populations (Supplementary figure **1B**, row 2). Linear regression line is shown in black with the 95% confidence intervals shaded. Coefficient, *P*-value and slope was calculated on data from all healthy control batch comparisons. t-SNE shows good mixing of batches across clusters when analysed for **B**) scaled populations or **C**) frequencies of parental gates.

Supplementary figure 3. Density plot, CD3, CD4, CD8, CD19, CD56, HLA-DR and CD16 intensity of signal are shown across viSNE space occupancy from a time series of Patient 1 and Patient 2 who had divergent clinical outcomes following VST treatment. Day post-transplant annotated on Figure, with day post-VST infusion in brackets.

Supplementary figure 1



Supplementary figure 2



Supplementary figure 3