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Supplementary Figure 1. Overall study design.

Supplementary Figure 2. Expansion of TEMRA CD8 in KT with biopsy-proven ABMR.

KT were recruited 1 year after their transplantation and with either biopsy-proven ABMR (n=12) or normal histological biopsy (n=52; recipient age and gender matched) (A) Absolute number per mL of blood of subsets of CD8 T cells. (B) Spearman correlation between the frequency of TEMRA CD8 among CD8 T cells and the percentage of CD107a⁺ among CD8 T cells. Data represents the median±IQR[25%-75%] and the value (point) of a single patient and one representative patient. The p-values were calculated using the Mann-Whitney test ** p<0.01.

Supplementary Figure 3. Migratory properties of memory CD8 T cell (TEMRA and EM): adhesion to activated HDMECs and chemokine screening by transmigration assays. (A)

Transcriptomic profiling of chemokine receptor expression by EM and TEMRA CD8 T cells according to published RNA-seq data¹⁰. (B) Targeted proteomic analysis of chemokine receptor expression by EM and TEMRA CD8 T cells based on the ImmunoProt database²⁴. (C) Transmigration of CD8 T cell subsets across TNF α (100 U/ml, O/N)-treated HDMEC monolayers in response to the indicated chemokines and cytokines. (D) Impact of CXCL12 (50 ng/ml) on the roundness of CD8 T cell subsets from KT and HVs. The roundness was tracked for all cells during the entire observational period using Fiji- and MATLAB-based scripts. A roundness of 1 is obtained for a perfect circular shape and 0 for a flat shape. (E) Migration of Fura-2-labeled CD8 T cell subsets from KT and HV onto TNF α -treated HDMEC monolayers. Average velocity of CD8 T cell subsets is shown. The p-values were calculated using Wilcoxon matched-pairs signed rank test (A), nonparametric ANOVA (Kruskal-Wallis) with Dunn's multiple comparisons test (C) and the Wilcoxon matched-pairs signed rank test. * p<0.05, ** p<0.01.

Supplementary Figure 4. Accumulation of TEMRA CD8 T cells in the kidney graft of KT with ABMR. (A) GSEA analysis of TEMRA gene signature derived from the literature (**Supplementary Table 3**) in gene expression data of kidney biopsies from kidney transplanted patients with or without ABMR (n= 56 and 168, respectively)¹ (GSE147089). The normalized enrichment score (NES) is the degree to which a gene set is overrepresented, normalized across analyzed gene sets. The nominal P-value (NOM P-val) is the statistical significance of the enrichment score. (B) Correlation between expression of *CD8* and TEMRA-associated genes in patients with ABMR (pink) and normal biopsy (shaded gray). Correlation was calculated using nonparametric Spearman correlation.

Supplementary Figure 5. Combined stimulation with CXCL12 and TCR results in the selective activation of memory CD8 T cells (TEMRA and EM). Frequency of CD69⁺CD107a⁺ among the EM (green dot), TEMRA (red dot) and NAÏVE (black dot) CD8 T cells from KT (A, B) or HVs (B) after 4 h of stimulation with plate-bound anti-CD3 mAb (2 µg/ml) or aCD3 + CXCL12 (50 ng/ml). Data represent the median (gray histogram) and the value (point) of a single HV. The p-values were calculated using nonparametric ANOVA (Kruskal-Wallis) with Dunn's multiple comparisons test. * p<0.05, ** p<0.01, **** p<0.0001

Supplementary Figure 6. Short-term IL-15 stimulation enhances the selectivity of memory (TEMRA and EM) CD8 T cells to P-selectin. (A) CD8 T cell subsets (NAÏVE, black; EM, green; TEMRA, red) were purified from HVs and stimulated, when indicated, O/N with IL-15 (10 ng/ml). Binding of CD8 T cell subsets to P-selectin chimeric proteins was quantified. Data represent the median (gray histogram), the value (point) of a single HV and one representative histogram. The p-values were calculated using nonparametric ANOVA (Kruskal-Wallis) with Dunn's multiple comparisons test. * p<0.05, **** p<0.0001. (B) Gating strategy to analyze the incorporation of ManAc by purified CD8 T cells incubated O/N with Click-IT ManNAz (ManAc) and, when indicated, IL-15 (10 ng/ml). CD8 T cells were then

treated with 2-DG (50 μ M, 4 h, 37°C) before the quantification of the incorporation of ManAc after cell permeabilization (intra) or cell fixation (extra). Incorporation of ManAc was quantified after cell permeabilization (Intracellular) or cell fixation (Extracellular).

Supplementary Figure 7. Inhibition of glycolysis impairs the generation of functional PSGL-1. CD8 T cell were purified from HVs and stimulated O/N with IL-15 (10 ng/ml) and , when indicated, in the presence of 2-DG (50 μ M). Expression by EM and TEMRA of total and functional PSGL-1 was quantified by flow cytometry using KPL-1 and CHO131 anti-PSGL-1 mAb respectively. Data represent the value (point) of a single HV and one representative histogram. The p-values were calculated using nonparametric paired Wilcoxon test. * $p < 0.05$.

Target	Fluorochrome	Clone Name	Provider
CD3	BV421	UCHT1	BD Biosciences
CD3	VioBlue	HIT3a	BD Biosciences
CD3		OKT3	Invitrogen
CD3	FITC	UCHT1	BD Biosciences
CD8	VioGreen	BW135/80	Miltenyi
CD8	PE-Cy7	RPA-T8	BD Biosciences
CD8	Purified	C8/144B	Dako
CD28	PE-CF594	CD28.2	BD Biosciences
CD28	Purified	CD28.2	Invitrogen
CD45RA	APC-Vio770	TD611	Miltenyi
CD162	PE	KPL1	BD Biosciences
CD11a	APC	HI111	BD Biosciences
CD49d	FITC	9F10	BD Biosciences
CD162	Purified	CHO131	R&D Systems
PERF1	PE	B-D48	Diaclone
GZMB	PE-C7	QA18A28	Biolegend

Caspase-3	PE	C92 605	BD Biosciences
IgM	PE	C48-6	BD Biosciences
VLA-4	PE-Cy7	9F10	Biolegend
LFA-1	PE	G4325B	Biolegend

Supplementary Table 1. Listing of monoclonal antibodies

Reagent or Resource	Provider
Oligomycin	Sigma
6-Diazo-5-oxo-L-norleucine (DON)	Sigma
2-Deoxy-D-glucose (2-DG)	Sigma
Neuraminidase	Sigma
CXCL10	PeptoTech
CXCL9	PeptoTech
IL-8	PeptoTech
CXCL12 (SDF1 α)	R&D Systems
¹⁰ Panx	R&D Systems
Recombinant human P-selectin	R&D Systems
P2X1 (NF023)	R&D Systems
P2X4 (5-BDBD)	R&D Systems
P2X7 (A438079)	R&D Systems
TNF α	R&D Systems
IL-15	Miltenyi
CD8 T cell Isolation Kit human	Miltenyi
Human REAlease CD8 MicroBead Kit	Miltenyi
TexMacs medium	Miltenyi
Endothelial Cell Growth Medium	Lonza
CCCP	Sigma
123count eBeads™ Counting Beads	Thermo Fisher
Fura2	Thermo Fisher
ApoSENSOR™ ATP Cell Viability Bioluminescence Assay Kit	BioVision
PE-anti-human IgG Fc	Thermo Fisher
Click-iT® Cell Reaction Buffer Kit and alkyne Alexa Fluor® 488	Invitrogen
Click-IT™ ManNAz Metabolic Glycoprotein Labeling Reagent (tetraacetylated N-Azidoacetyl-D-Mannosamine)	Invitrogen

BD Cytotfix/Cytoperm™ kit	BD Bioscience
μ-Slide 8 well	ibidi
Poly-L-Lysine precoated μ-Slide 8 well	ibidi
RPMI 1640 medium	Thermo Fisher
FBS	Sigma
Glutamax	Thermo Fisher
Penicillin-Streptomycin-Neomycin Solution	Sigma
IL-2	Biologend
Trypan blue	Gibco
Ficoll-Paque Plus	GE Healthcare
Cell Proliferation Dye eFluor V450	Thermo Fisher
Fixable Viability Dye 440UV	BD Bioscience
Fc Block	BD Bioscience
OPAL 520	Akoya
DAPI	Invitrogen
TR1, TR2	Impath
Poly-E and HRP-2-Step	Impath
Vectashield® Vibrance™ Antifade Mounting Medium	Vector

Supplementary Table 2. List of reagents

Gene Name	References
CD3D	2
CD3E	2
CD3G	2
CD8A	2
CD8B	2
TBX21	2-4
IFNG	2
CX3CR1	2-6
GZMB	2
GZMH	2
GNLY	2
PRF1	2
FCGR3A	2-7
PRDM1	2
HK2	8
Zeb2	9
Ezh2	8
Bcl6	8
EOMES	8
ID3	8
TNFa	2-6
KLRD1	10
IL7R	10-12
CD28	10-12

Supplementary Table 3. Gene signature of TEMRA CD8 based on a review of literature.

Upregulated genes in TEMRA CD8 vs EM CD8

Gene Symbol	log ₂ FC	AveExpr	P.Value	adj.P.Val
SH2D1B	5,67	1,553	4,44E-07	0,0022
RAMP1	5,17	1,702	9,54E-06	0,0072
LAT2	4,18	2,250	1,05E-05	0,0072
KLRF1	4,01	3,263	3,83E-06	0,0057
FCGR3A	4,01	2,942	1,44E-06	0,0034
FGFBP2	3,87	5,475	4,95E-06	0,0059
NCR1	3,83	3,236	1,43E-06	0,0034
ZEB2-AS1	3,75	1,650	3,01E-04	0,0440
GNLY	3,61	10,829	1,35E-04	0,0282
SPON2	3,45	2,101	3,56E-04	0,0451
KIR3DL2	3,40	1,305	1,49E-04	0,0300
LAIR2	3,40	0,589	3,46E-04	0,0451
KIR3DL1	3,36	0,614	1,65E-04	0,0313
SYNGR1	3,33	1,641	1,57E-05	0,0082
TYROBP	3,17	6,038	2,13E-04	0,0361
CX3CR1	3,09	1,235	4,57E-07	0,0022
PRSS23	3,06	1,597	9,19E-06	0,0072
HAVCR2	3,00	2,797	5,03E-05	0,0154
CD38	2,93	1,507	2,61E-04	0,0409
GSN	2,89	1,716	3,38E-04	0,0451
GPR56	2,78	2,958	2,00E-05	0,0087
AKR1C3	2,54	0,962	3,83E-05	0,0139
FHL3	2,34	1,366	4,67E-05	0,0153
CXXC5	2,29	1,691	2,02E-04	0,0352
TTC38	2,09	3,052	2,04E-04	0,0352
SPINK2	2,09	0,224	1,06E-04	0,0245
CCL4	2,01	5,263	4,57E-05	0,0153
FGR	1,99	3,102	3,49E-04	0,0451
CD160	1,97	1,944	1,79E-04	0,0327
MTSS1	1,97	2,094	8,67E-05	0,0227
LAYN	1,77	0,492	6,97E-05	0,0200
PION	1,76	1,625	3,63E-04	0,0452
UBE2F	1,72	4,388	1,25E-05	0,0074
PTPN12	1,71	1,708	3,08E-04	0,0443
NMUR1	1,54	0,554	9,36E-05	0,0228
IFIT2	1,52	2,793	2,14E-05	0,0087
CERS4	1,51	1,909	9,94E-05	0,0236
PDLIM1	1,50	2,536	4,10E-04	0,0498
IFIT3	1,45	3,120	8,50E-05	0,0227
GNPTAB	1,41	2,380	8,85E-05	0,0227
LIMK1	1,40	1,365	2,68E-04	0,0409
FAM46A	1,39	1,317	8,23E-05	0,0227
TTC28-AS1	1,32	1,955	4,86E-05	0,0154
GEMIN7	1,26	2,982	1,37E-04	0,0282
C5orf56	1,05	5,291	2,67E-04	0,0409

Gene	Downregulated genes in TEMRA CD8 vs EM CD8			
	Log2FC	Count	P-value	Adjusted P-value
DYNLT3	-1,00	4,237	3,39E-04	0,0451
S100A11	-1,00	6,683	3,57E-04	0,0451
KDSR	-1,14	2,795	3,14E-04	0,0444
CDC14A	-1,16	3,307	3,43E-04	0,0451
PLK3	-1,27	2,493	1,33E-04	0,0282
TMEM154	-1,33	2,298	4,28E-05	0,0150
INPP4B	-1,35	2,633	2,95E-04	0,0437
ANO9	-1,38	1,580	2,38E-04	0,0389
TNIP3	-1,48	1,893	2,50E-04	0,0402
TC2N	-1,54	4,425	2,81E-04	0,0422
CENPM	-1,73	2,021	1,11E-04	0,0245
ANTXR2	-1,91	1,828	2,53E-05	0,0096
SPON1	-1,93	0,678	3,87E-04	0,0477
HNRPLL	-1,98	1,937	5,88E-06	0,0062
FLT4	-2,06	0,072	1,88E-04	0,0336
NCF4	-2,16	1,192	1,61E-04	0,0310
AQP3	-2,16	3,847	1,09E-04	0,0245
CCR5	-2,22	1,929	1,54E-04	0,0304
HNMT	-2,23	-0,178	1,73E-04	0,0322
ELOVL4	-2,24	0,219	2,10E-05	0,0087
AMICA1	-2,25	4,414	9,40E-06	0,0072
CCR2	-2,35	-0,443	2,31E-04	0,0385
WDR86-AS1	-2,39	0,991	6,66E-05	0,0197
GPR183	-2,40	5,542	1,51E-05	0,0082
IL7R	-2,51	7,638	1,90E-05	0,0087
FAAH2	-2,52	1,387	3,38E-04	0,0451
CD28	-2,55	2,409	1,66E-05	0,0083
GPR15	-2,79	0,750	2,21E-05	0,0087
SLAMF1	-2,80	1,995	4,19E-06	0,0057
GZMK	-2,84	7,141	1,14E-05	0,0072
DPP4	-3,75	2,265	1,13E-05	0,0072
CCR4	-3,78	0,115	9,12E-05	0,0228
CCR6	-3,89	1,028	2,87E-06	0,0054

Supplementary Table 4. Differential expressed genes in TEMRA CD8 vs EM CD8 in KT patients.








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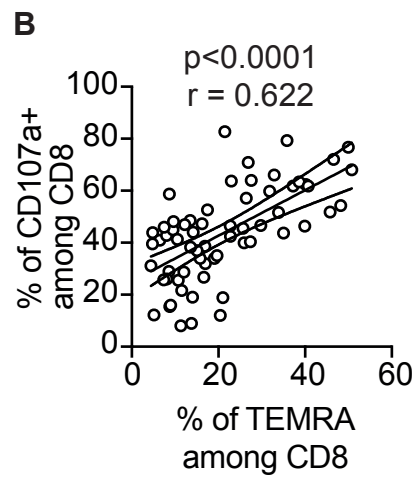
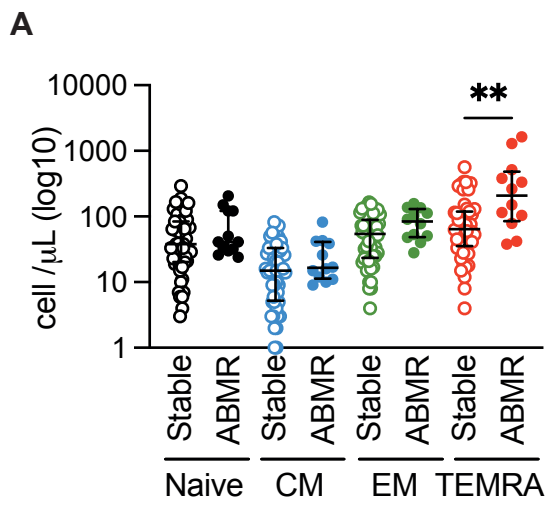
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Kidney recipient

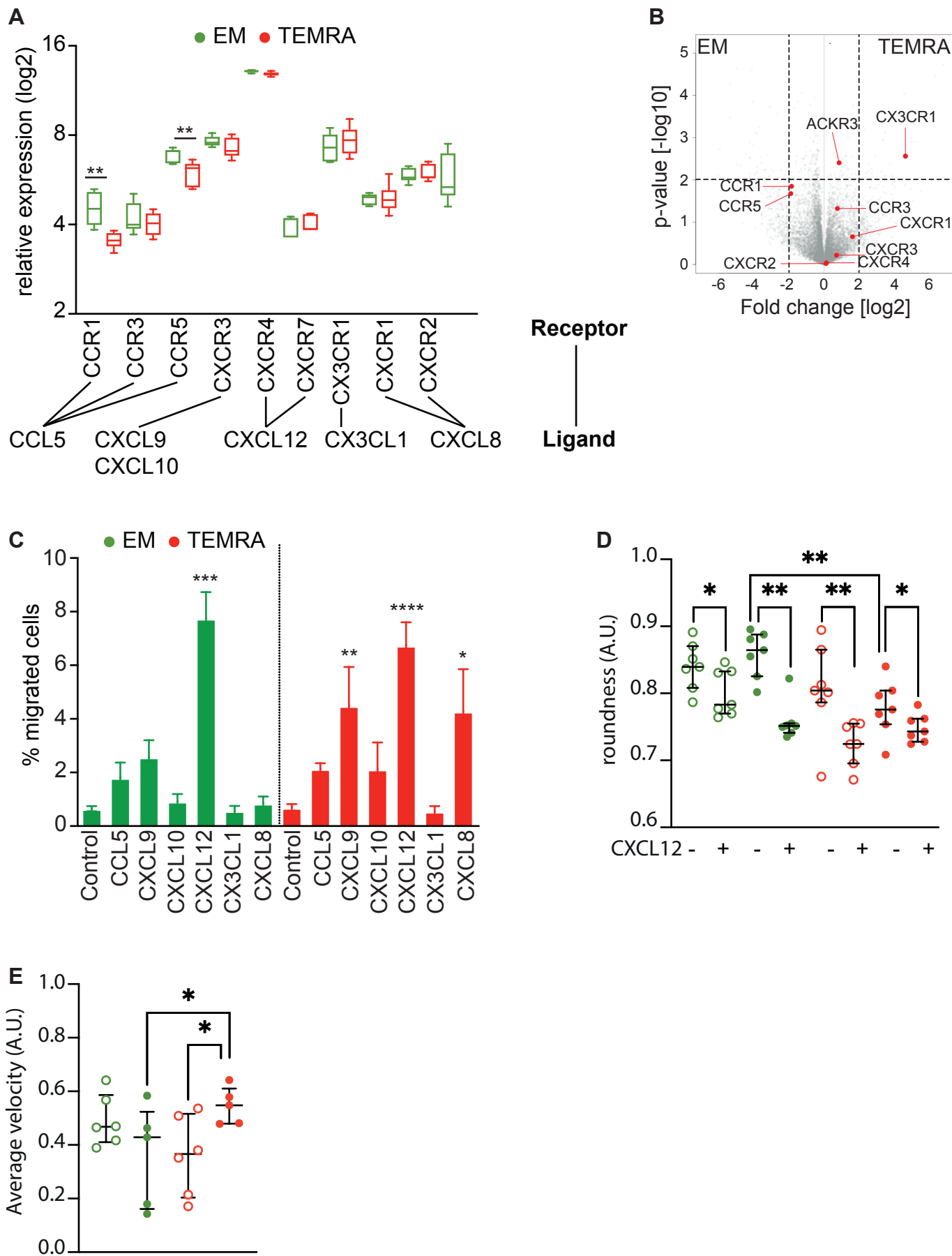
Healthy volunteer Humoral rejection Normal histology

		Blood	Adhesion to endothelium Transmigration across endothelium P-Selectin binding assay
		Blood	RNAseq of TEMRA/EM CD8
		Blood	Single-cell functional profiling of CD8 % of CD8 subsets Absolute number of CD8 subsets Cytotoxic function
		Kidney	CD8 T cell infiltration TEMRA CD8-related genes

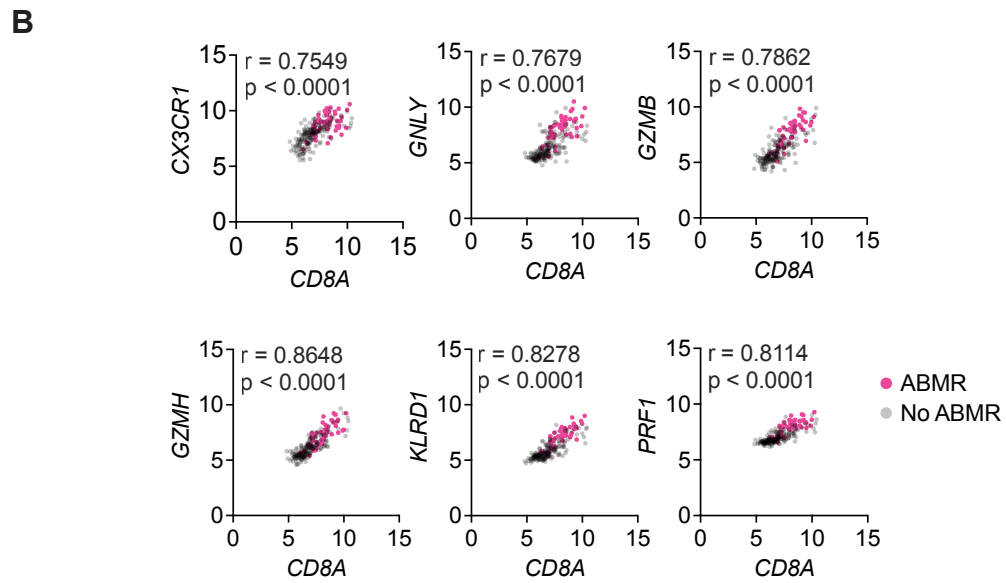
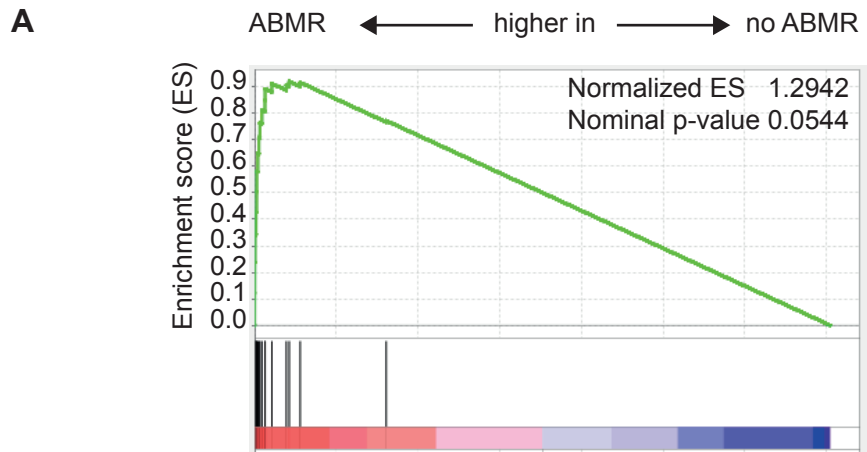
Supplementary Figure 1



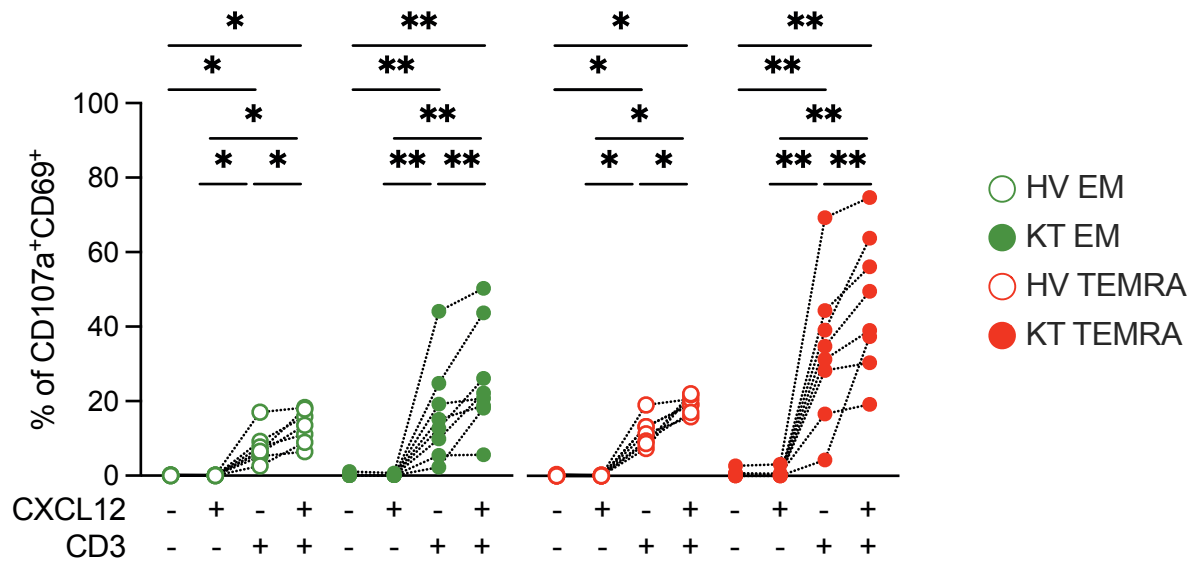
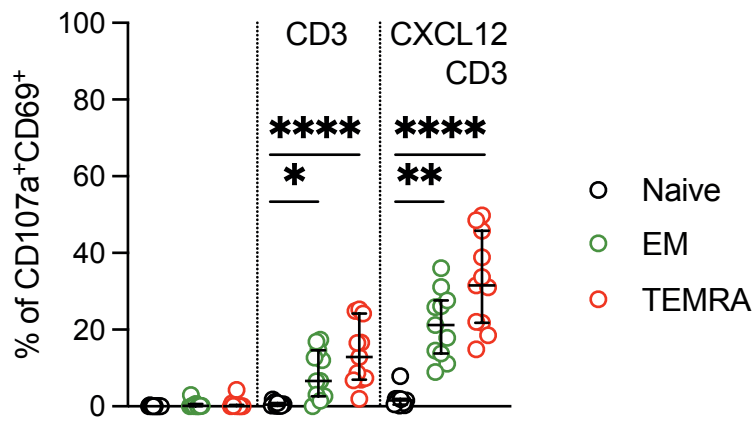
Supplementary Figure 2



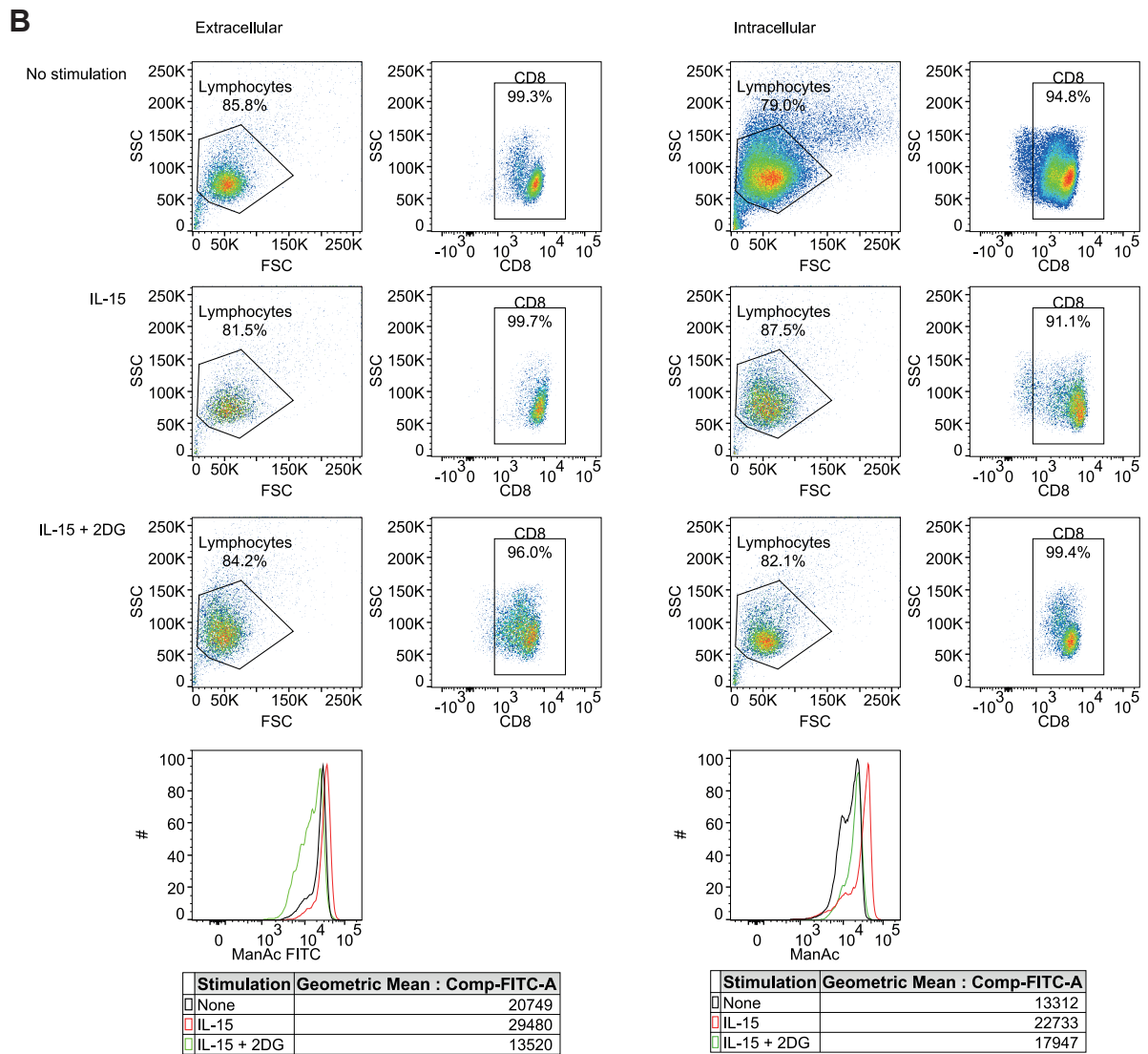
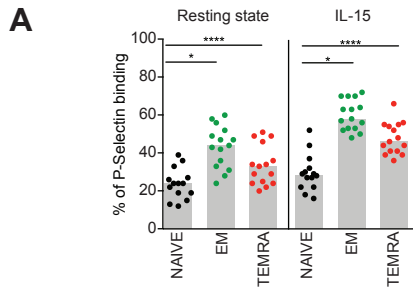
Supplementary Figure 3



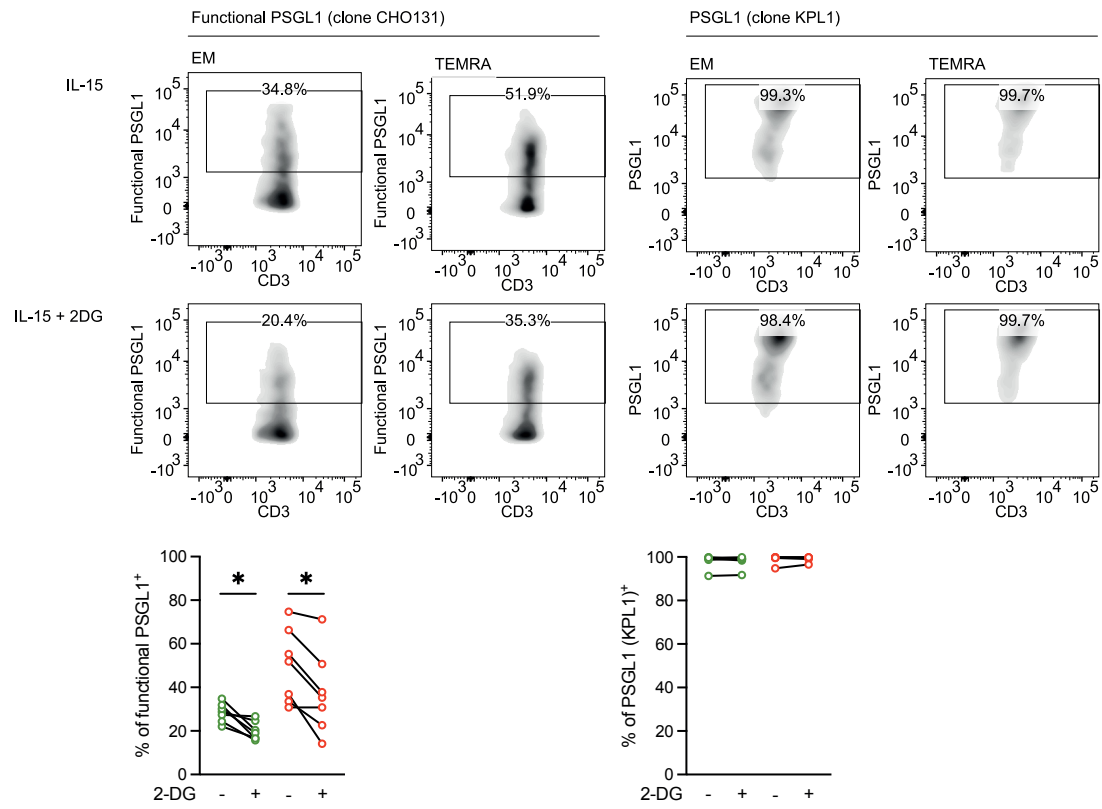
Supplementary Figure 4

A**B**

Supplementary Figure 5



Supplementary Figure 6



Supplementary Figure 7