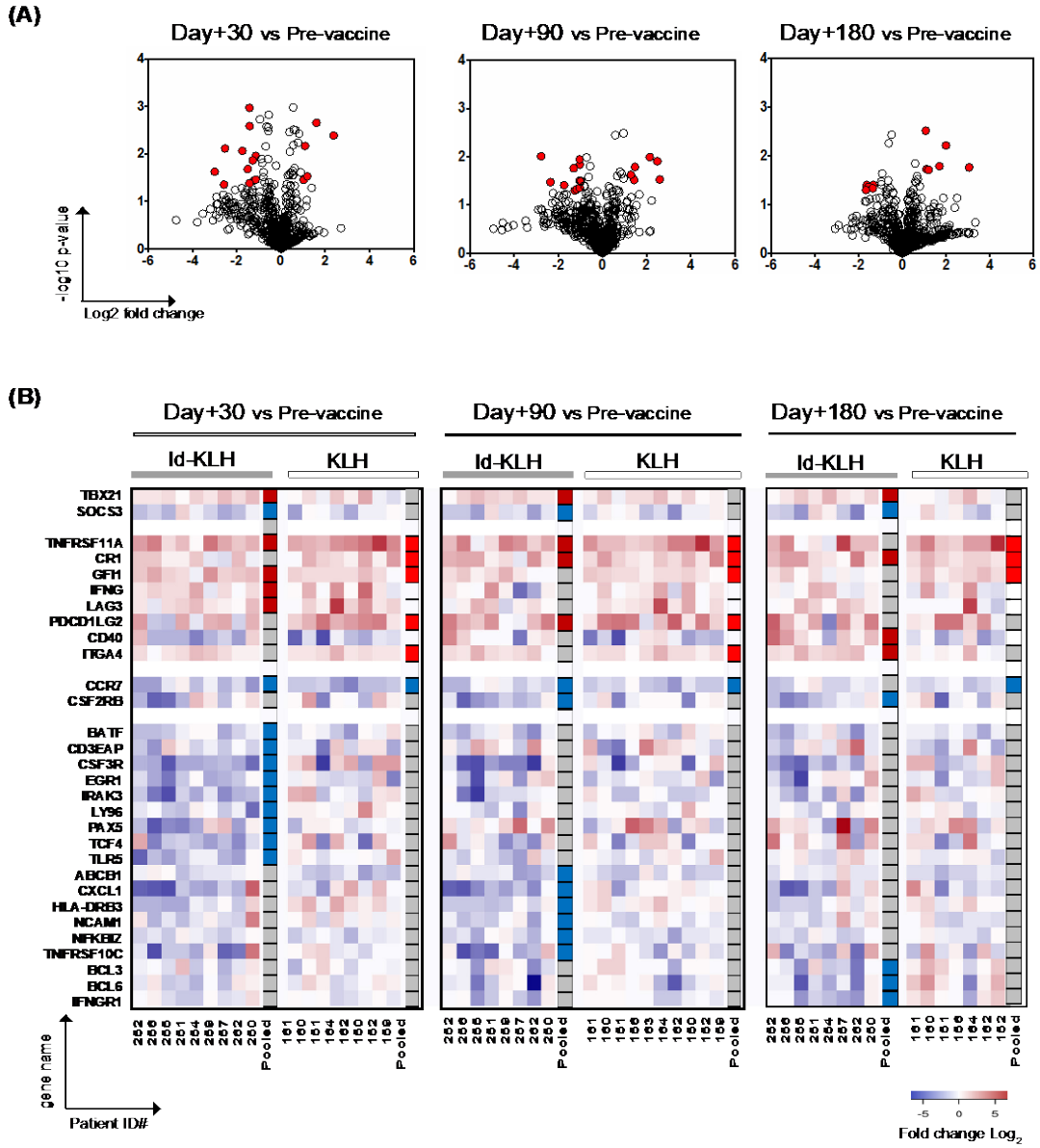


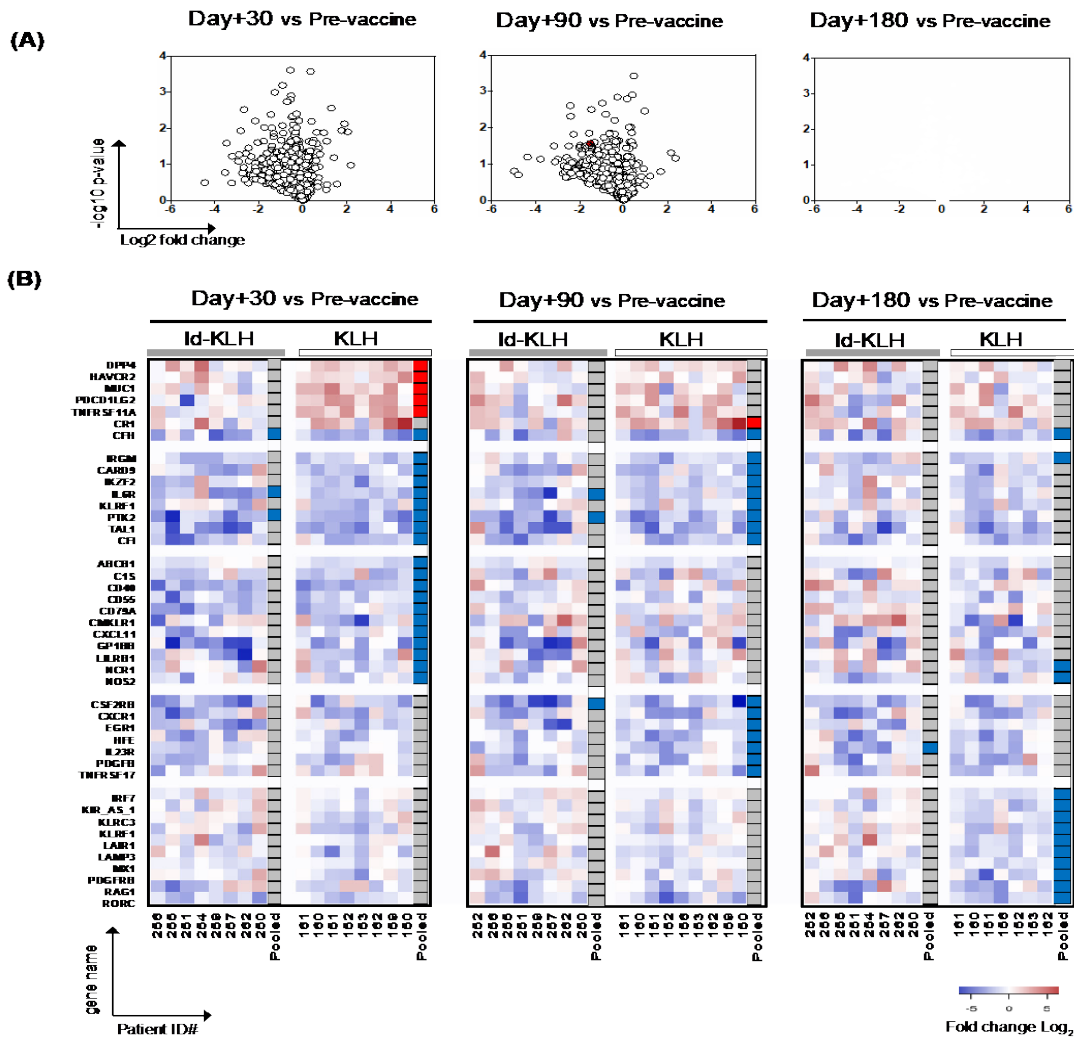
Supplemental Figure 1.



Supplemental Figure 1. Differential CD4⁺ T cells immune gene expression between vaccine and control vaccine patients.

(A) Volcano plots illustrate the Log₂ fold change in gene expression (x-axis) and paired P values from student t tests between pre-vaccine [T0] and Id-KLH post-vaccine samples [T30, T90, and T180] (y-axis). Differentially expressed genes [p < 0.05 and Log₂ fold-change > 2 or < -1/2] are indicated in red. (B) Heatmap displaying expression of 30 differentially expressed genes, as defined in (A). Pooled results for all patients are shown for each gene in the column to the far right for each treatment arm. Pooled results are classified as significantly upregulated (red), significantly down-regulated (blue) or no significant change (gray).

Supplemental Figure 2.

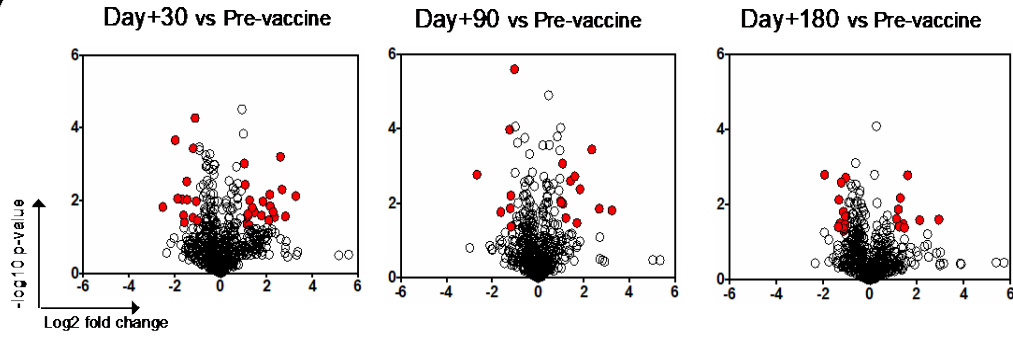


Supplemental Figure 2. Differential CD8⁺ T cells immune gene expression between vaccine and control vaccine patients.

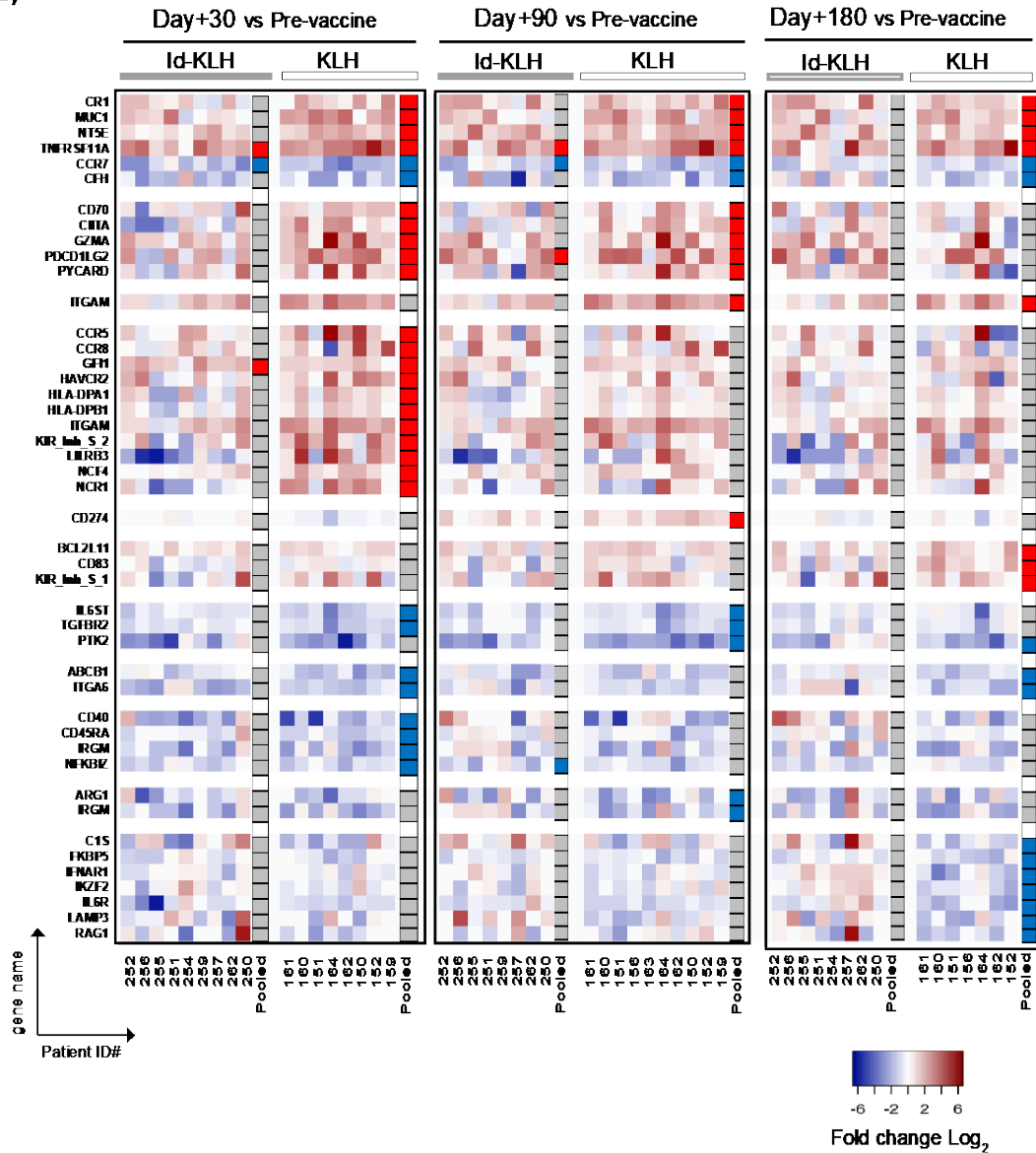
CD8 T cells were isolated from PBMC obtained pre- (T0) and at three time points post-vaccine [30 (T30), 90 (T90), and 180 (T180) days after activated T cell infusion] from 16 patients (8 patients treated with Id-KLH and 8 patients treated with KLH control). Gene expression profiling was batched, performed by NanoString and post-vaccine results for each patient were compared against corresponding T0 pre-vaccine samples. (A) Volcano plots illustrate the Log₂ fold change in gene expression (x-axis) and paired P values from student t tests between pre-vaccine [T0] and KLH post-vaccine samples [T30, T90, and T180] (y-axis). Differentially expressed genes [p < 0.05 and Log₂ fold-change > 2 or < -1/2] are indicated in red. (B) Heatmap displaying expression of 43 differentially expressed genes, as defined in (A). Pooled results for all patients are shown for each gene in the column to the far right for each treatment arm. Pooled results are classified as significantly upregulated (red), significantly down-regulated (blue) or no significant change (gray).

Supplemental Figure 3.

(A)



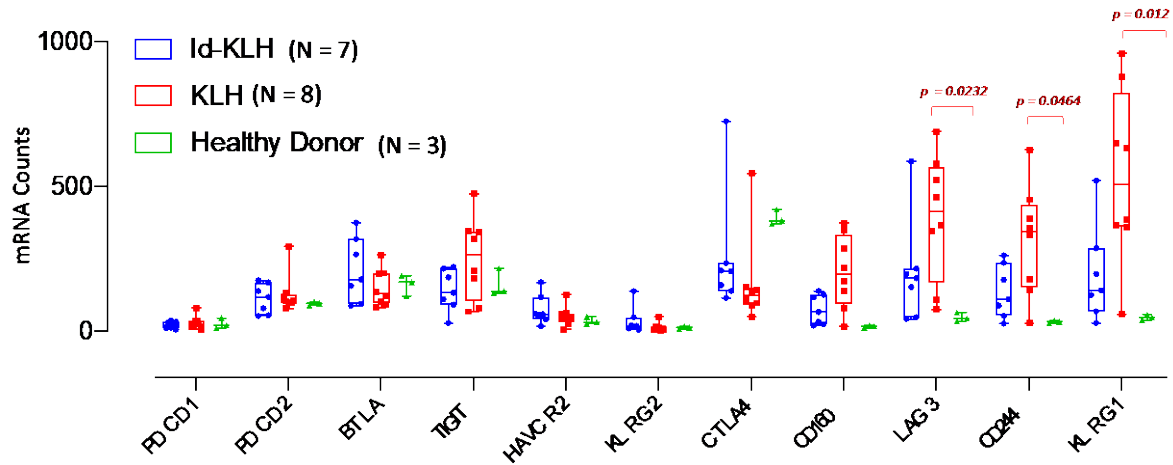
(B)



Supplemental Figure 3. Differential CD4⁺ T cells immune gene expression between vaccine and control vaccine patients.

(A) Volcano plots illustrate the Log₂ fold change in gene expression (x-axis) and paired P values from student t tests between pre-vaccine [T0] and KLH post-vaccine samples [T30, T90, and T180] (y-axis). Differentially expressed genes [p < 0.05 and Log₂ fold-change > 2 or < -1/2] are indicated in red. (B) Heatmap displaying expression of 47 differentially expressed genes, as defined in (A). Pooled results for all patients are shown for each gene in the column to the far right for each treatment arm. Pooled results are classified as significantly upregulated (red), significantly down-regulated (blue) or no significant change (gray).

Supplementary Figure 4.



Supplementary Figure 4. CD8+ T cells from patients treated with KLH control or Id-KLH vaccine exhibited significantly greater mRNA expression of multiple exhaustion markers compared with healthy donors at baseline. Comparisons of mRNA expression levels for individual exhaustion marker genes analyzed at the T1 timepoint by healthy donors in green (N=3), Id-KLH treated patients in blue (N=7), and KLH treated patients in red (N=8). The Dunn's multiple comparisons test was employed to determine adjusted p values indicated for comparisons between the Id-KLH treatment, KLH, and healthy donor groups.

Supplementary Table 1. 36 up-regulated genes list

gene	description	Log2 (FC)	P-value FDR
PYCARD	PYD And CARD Domain Containing	4.69	0.0001
PPBP	Pro-Platelet Basic Protein	4.49	0.004
CCR5	C-C Motif Chemokine Receptor 5	4.41	0.022
CISH	Cytokine Inducible SH2 Containing Protein	4.22	0.001
KLRF1	Killer Cell Lectin Like Receptor F1	3.58	0.025
TCF4	Transcription Factor 4	3.54	0.001
KLRC2	Killer Cell Lectin Like Receptor C2	3.47	0.011
KLRC3	Killer Cell Lectin Like Receptor C3	3.33	0.033
PECAM1	Platelet And Endothelial Cell Adhesion Molecule 1	3.00	0.000
CYBB	Cytochrome B-245 Beta Chain	2.75	0.010
CMKLR1	Chemerin Chemokine-Like Receptor 1	2.73	0.015
SLAMF6	SLAM Family Member 6	2.66	0.003
KIR_Activating_Subgroup_1		2.56	0.007
KLRK1	Killer Cell Lectin Like Receptor K1	2.54	0.047
CD86	CD86 Molecule	2.31	0.035
LILRA4	Leukocyte Immunoglobulin Like Receptor A4	2.26	0.040
XCL1	X-C Motif Chemokine Ligand 1	2.18	0.012
B3GAT1	Beta-1,3-Glucuronyltransferase 1	2.05	0.028
KLRG1	Killer Cell Lectin Like Receptor G1	1.91	0.033
PAX5	Paired Box 5	1.74	0.047
G6PD	Glucose-6-Phosphate Dehydrogenase	1.73	0.000
BCL2	BCL2 Apoptosis Regulator	1.67	0.0001
IL6R	IL6R	1.65	0.041
STAT6	Signal Transducer And Activator Of Transcription 6	1.39	0.013
IFNAR1	Interferon Alpha And Beta Receptor Subunit 1	1.24	0.034
TIRAP	TIR Domain Containing Adaptor Protein	1.21	0.032
PSMB10	Proteasome 20S Subunit Beta 10	1.06	0.000
BCAP31	B Cell Receptor Associated Protein 31	1.03	0.00001
TAP2	Transporter 2, ATP Binding Cassette Subfamily B Member	0.94	0.009
TNFSF12	TNF Superfamily Member 12	0.90	0.001
CD74	CD74 Molecule	0.89	0.037
IKZF3	IKAROS Family Zinc Finger 3	0.87	0.042
IKZF2	IKAROS Family Zinc Finger 2	0.84	0.013
ITGAL	Integrin Subunit Alpha L	0.82	0.004
JAK3	Janus Kinase 3	0.60	0.009
NOD1	Nucleotide Binding Oligomerization Domain Containing 1	0.59	0.050

Supplementary Table 2. 29 down-regulated genes list

gene	description	Log2(FC)	P-value FDR
ILF3	Interleukin Enhancer Binding Factor 3	-0.58	0.038
CTNNB1	Catenin Beta 1	-0.68	0.003
CD5	CD5 Molecule	-0.82	0.000
CEBPB	CEBPB	-0.82	0.038
SMAD5	SMAD Family Member 5	-0.90	0.011
LGALS3	Galectin 3	-0.93	0.047
ITGAE	Integrin Subunit Alpha E	-1.00	0.001
BCL10	BCL10 Immune Signaling Adaptor	-1.01	0.032
ATG16L1	Autophagy Related 16 Like 1	-1.02	0.006
ATG5	Autophagy Related 5	-1.03	0.000
CXCR4	C-X-C Motif Chemokine Receptor 4	-1.06	0.005
SOCS1	Suppressor Of Cytokine Signaling 1	-1.07	0.050
STAT3	Signal Transducer And Activator Of Transcription 3	-1.17	0.000
BCL3	BCL3 Transcription Coactivator	-1.22	0.032
NFIL3	Nuclear Factor, Interleukin 3 Regulated	-1.22	0.026
PSMD7	Proteasome 26S Subunit, Non-ATPase 7	-1.23	0.007
RELA	RELA Proto-Oncogene, NF-KB Subunit	-1.34	0.025
PRDM1	PR/SET Domain 1	-1.36	0.009
PSMC2	Proteasome 26S Subunit, ATPase 2	-1.38	0.033
C1R	Complement C1r	-1.41	0.038
TRAF4	TNF Receptor Associated Factor 4	-1.54	0.007
NFKB1	Nuclear Factor Kappa B Subunit 1	-1.58	0.013
BCL6	BCL6 Transcription Repressor	-1.61	0.013
IFNGR1	Interferon Gamma Receptor 1	-1.67	0.004
MAPKAPK2	MAPK Activated Protein Kinase 2	-1.74	0.003
ZEB1	Zinc Finger E-Box Binding Homeobox 1	-1.86	0.028
RELB	RELB Proto-Oncogene, NF-KB Subunit	-2.17	0.008
DUSP4	Dual Specificity Phosphatase 4	-2.73	0.004
IL2	Interleukin 2	-3.04	0.004