SUPPLEMENTAL DATA

Table S1. Baseline clinical characteristics of all treated patients.

	Nonresponders		**Responders**		**Total**		
	N	%	N	%	N	%	*P*
Total	7	100	22	100	29	100	
Age median (range)	48 (30 - 52)		48 (27 - 62)		48 (27 - 62)		0.81
Gender (male)	3	43	10	45	13	45	1
Sex mismatch (male patient, female donor)	2	29	4	18	6	21	0.61
Prior Transplant	2	29	1	5	3	10	0.14
Transplant Type							0.24
Myeloablative	6	86	22	100	28	97	
Non-myeloablative	1	14	-	-	1	3	
Cell Source							0.24
Bone Marrow	6	86	22	100	28	97	
Peripheral Blood Stem Cells	1	14	-	-	1	3	
Donor Type							1
Matched Related	7	100	21	95	28	97	
Matched Unrelated	-	-	1	5	1	3	

Table S2. Baseline clinical characteristics of microarray samples

Patient	Age at DLI	Gender	Transplant Type	Time from Transplant to Relapse (mo)	Time from Transplant to DLI (mo)	Timepoints after DLI (mo)
R1	59	F	Myeloablative	17	18	0 and 3
R2	63	F	Myeloablative	37	38	0 and 6
R3	40	F	Myeloablative	24	27	0 and 3
R4	40	F	Myeloablative	22	24	0 and 12
NR1	48	M	Non-myeloablative	13	14	0 and 6
NR2	50	M	Myeloablative	48	49	0 and 3

Table S3. Gene probes differentially regulated between responders and nonresponders before and after DLI therapy.

Pretreatment		**Response to treatment**	
Gene Probe	*Fold Change*	*Gene Probe*	*Fold Change*
CD247	5.4	SNHG3	3.3
TNFAIP3	5.2	TSEN2	3.2
LAIR2	3.8	ZBED2	3
PSMB9	2.9	GPM6B	2.7
NCALD	2.6	SACS	2.6
VAMP5	2.6	CBLB	2.3
PPDPF	2.5	PDSS1	2.2
PRKX	2.5	PTTG2	2.2
LITAF	2.4	ZNF451	2
AMZ2	2.4	TMEM177	2
LY6E	2.4	KIAA0317	1.9
EIF5A2	2.4	CAD	1.9
NUAK1	2.4	H1FX	-2.3
ANKRA2	2.3	TPPP3	-2.4
RABAC1	2.3	AP1S2	-2.5
PPP1R2	2.2	DUSP3	-2.6
WWP1	2.1	HLA-DQB1	-2.6
CD81	2	PTAFR	-2.6
UBL3	2	EMR2	-2.6
IFITM2	1.9	LST1	-2.7
HLA-F	1.9	LGALS1	-2.7
AKIRIN1	1.9	HCK	-2.8
TBCB	1.8	TSPO	-2.8
TAP2	1.8	FCGR2A	-2.8
TNIP2	1.7	LILRB4	-2.9
PRLR	-1.5	LY86	-3
KRT13	-1.7	TGFBI	-3.1
MPL	-1.7	LILRA1	-3.1
LMNB1	-1.8	FGL2	-3.1
KIF2C	-1.8	TNFAIP2	-3.1
ENTPD7	-1.9	TMEM176A	-3.2
LTA4H	-2	AIF1	-3.4
TMEM177	-2	BST2	-3.4
RAB3D	-2.1	CYBB	-3.4
TKT	-2.1	SLC15A3	-3.5
SMAD1	-2.2	GPX1	-3.6
ASGR2	-2.4	TLR8	-4
FPR2	-2.4	TYROBP	-4.4
ACPP	-2.4	CSF1R	-4.6
KIF14	-2.4	FCER1G	-4.6
POLQ	-2.5	CST3	-5.4
ZNF193	-2.7	CD9	-6
TROAP	-2.8		
PADI2	-3.7		
LOC100272216	-3.8		
HP	-4		
PADI4	-4.1		
ASPM	-4.2		
P2RY2	-4.2		
MOSC1	-5.3		
CHI3L1	-5.5		

Table S4. Description of curated T cell exhaustion gene sets.

	Gene Set	Description	References	Genes
Exhaustion	*Exh vs rest in LCMV*	Genes up in LCMV-specific CD8+ T cells in chronic infection (exhausted) vs acute (effector, memory)	26	EEA1 BC039093 GPD2 ENTPD1 GPR65 D0H8S2298E CD244 RSAD2 D17H6S56E-5 IFIH1 STK39 PDCD1 H2-T23 5830471E12RIK PLSCR1 1110067D22RIK LYCAT GAS2 CCRL2 PTPN13 VAMP8 RPA3 MLLT3 ITGAV CCL3 CPEB2 MDFIC LITAF CASP3 ZFP91 RGS16 LIMS1 LAMP2 KCTD9 SCD2 SH2D2A GP49A TRAF5 ACADL EIF3S1 CYFIP1 6530401D17RIK TACSTD1 GJB2 4631408O11RIK IRAK1 PBX3 SP1 HIF1A SPG21 FASLG NOL7 AHR APOA1BP PTGER4 4930429A08RIK TGN TANK 1810035L17RIK NFATC1 PSMB8 RNF11 DHX36 2010100O12RIK SLC27A4 RDBP SEC14L1 PGLYRP1 PHLDA1 PPP2R5C 4-Sep TCRB-J LOC381765 NUCB1 HRB TM2D3 ZFP207 DDIT4 ZDHHC5 HCCS 1300007C21RIK LO NR4A2 H2-Q1 2510002D24RIK FYN MYO5A XPO1 PTGER2 IIGP1 2610020H08RIK DDEF1 PTK2B VCP NDUFAB1 RAB28 2210409M21RIK LO DOCK7 CD9 2510002A14RIK RBL2 A030007L17RIK C80638 COX6C RFC3 GYG CBFA2T2H RWDD1 MGAT2 RCN1 KIF5B NCOA6 LIN9 ZAP70 IFI204 PRKDC CD160 EOMES SPOCK2 YSG2 NDUFA5 2610209M04RIK MAP3K7 LSM3 RPL7L1 D6WSU176E TRG@ SART3 PERP CD7 ENPP1 MTHFD2 CAMK2B PARP1 LYSMD2 RER1 NAB1 GPM6B ZFP239 TNFRSF4 2310003F16RIK CRRY SYT1 MYO1E CCR6 4633402D15RIK NRP1 NFYB HIST1H3F 4833441D16RIK 1110008H02RIK ATPIF1 ZFP37 NUDCD2 CAPZB RHOQ SPG20 TXNDC9 XCL1 A130052D22 IFNA11 SEZ6 RAB37 P ALS2CR3 C330007P06RIK AA675035 ATTP 8430420C20RIK ALCAM X83313 ATP5G2 LOC546080 D10BWG0791E PGM1 CENPC1 CBX6 AZIN1 PIGQ 2700088M22RIK 5730420B22RIK TIMM17A LRRC6 IL10 CCR5 MGI:1914262 RBBP4 NEK7 UBB D10627 WNK1 SLC6A6 D10ERTD322E LOC2 LAT2 PIGF ZFP54 PSMB1 SLC31A1 SNAP23 BRCA2 LIAS 1200009F10RIK BC054822 PLAGL1 NDUFB3 ITGA6 ZRF1 TRIM17 HIST3H2A EWSR1 PRSS2 4930564D15RIK NDUFS4 TERF1 MRPS31 RBBP6 MRPL51 6720463E02RIK 2310015N07RIK LOC544986 LOC544 2610524H06RIK DHFR WBP5 TNFRSF7 BC003993 LOC4324 LOC544991 LOC544 CD200 PHKG2 DCTN2 1700013H19RIK GCM2 TNFRSF9 NCOA1 COX7C ILF3 HNRPA2B1 VAMP5 AP3B1 IFI27 SLK COCH RNF149 TNFSF10 PACSIN1 1810054D07RIK MYO6 DBNL CTLA4 USMG5 POLR3K SERPINA3G 2700097O09RIK GPR56 UBE2T CXCL10 D3ERTD229E TNFRSF1B PRNP EGR1 CKMT1 KIT FGL2 SOX2 RYR1 CCL4 DXERTD242E COMT SPP1 PCBD2 SFRS2IP TAP1 ZCCHC10 PGM2 LAG3 TNFSF11 PENK1 IGH-V IGH IG SDC4 HBB HBB-B1 H PGF ABCB10 PTPRS ZCCHC3 ARPC4 HOXA7 KLF3 ATP13A2 NOS3 AZI1 CAP1 MYCS MGI:1932697 PVRL3 ZFP162 MAFK PIPOX AP1B1 PER3 LEF1 NEDD4L 1110038D17RIK LDLR D6ERTD365E LMNB2 ALDOA-PS1 HKR3 KLF13
	Exh vs mem in LCMV	Genes up in LCMV-specific CD8+ T cells in chronic infection (exhausted) vs acute (memory)	26	GPD2 BC039093 ENTPD1 LAMP2 RSAD2 EEA1 5830471E12RIK GPR65 PLSCR1 SPG21 SCD2 D17H6S56E-5 LITAF IFIH1 D0H8S2298E STK39 LIMS1 CD244 LAT2 AZIN1 RPA3 LYCAT 4930429A08RIK HIF1A ITGAV TCERG1 IFI27 LOC14433 LOC3806 KCTD9 PDCD1 APOA1BP SP1 H2-T23 SMC4L1 CCRL2 NRIP1 PTPN13 SEC14L1 1810010N17RIK 2610002J02RIK ISGF3G DDIT4 MLLT3 VAMP8 GAS2 CASP3 BCL2A1A BCL2A1B CPEB2 IRF8 AU022220 BRCA2 1110067D22RIK MDFIC VCP PPP2R5C IFIT1 CCL3 NUDCD2 IRF4 ZCCHC6 ZFP91 PTPRJ AW125753 SH2D2A NAPSA ACADL CHD1 AHR ZA20D2 MYB RNF19 HCCS TACSTD1 IIGP1 4631408O11RIK ALCAM RAB28 RYR1 GMFG NAB1 1810035L17RIK RBL2 PERP CLIC4 TRAF5 RGS16 RHOQ TCRB-J LOC381765 SH3BGRL SLC27A4 RFC3 TXN1 ATPIF1 GYG FASLG NUCB1 PSMB8 1300007C21RIK LO TANK WASPIP 5230400G24RIK GP49A BC003993 LOC4324 C330027G06RIK A030007L17RIK RNF11 ANKRD28 SNX9 ILF3 EIF3S1 ZFP207 H2-Q1 MS4A1 TIMM17A RBX1 BAT4 LOC434585 CD9 6530401D17RIK DDX6 2510002A14RIK MGAT2 MRVI1 CYFIP1 ZFP54 CCR6 2610020H08RIK PGLYRP1 NDUFB5 APBB1IP NFATC1 SMARCC1 GJB2 NMT1 COX7B LOC14433 LOC2294 PRSS2 PRPF19 GZMA TM2D3 ENPP1 TGN ZFP265 NFYC SOLT COX6C DHX36 SLC6A6 1110008H02RIK PSMA4 TRIM17 HIST3H2A MAP3K7 PPIC AV011803 PBX3 BCL2A1A BCL2A1C BMP2K ZAP70 MYO5A 5730420B22RIK MAD2L1BP MYO1E PSCD3 EGR2 5031425D22RIK PGM1 V2R14 CASP7 CHEK2 SYPL IRF5 ZNF617 TNFRSF4 2310040A13RIK D3ERTD789E WNK1 IRAK1 2610524H06RIK FYN 4633402D15RIK WEE1 2010100O12RIK 2210409M21RIK LO SLC4A7 RER1 AU020206 IL10 NDUFS4 AP3S1 SLK NR4A2 4930564D15RIK BC021442 EWSR1 RAB1A TYKI CD200 KPNA2 0610010E21RIK NOL7 EZH2 DNAJC13
	PD-1 ligation	200 upregulated genes upon anti-PD-1/CD3/CD28 ligation in PD-1 expressing Jurkat cells (*P*<0.01)	27	SDHC P2RX2 IFI16 POU3F2 SP110 ZNF195 NARFL MRPS18A ADORA2B NOSIP TRBV21-1 TRBV19 CD53 SEPW1 KIAA0256 GOLT1B BACE2 COBL LOC650610 PGR DAD1 ZNF580 LOC51035 MR1 TSPAN5 ARL4C VRK3 KIAA0748 FDPS C4ORF30 CNIH3 DKFZP434H1419 SLC25A22 NKG7 IL4R EEF1D LOC126037 LASS4 ZFP30 GCHFR CDKL1 FLJ20850 THTPA CD52 TFPT PACS1 ATP5J PRKCE ZDHHC13 TBL1Y CSAD C19ORF42 TAF13 TRA@ TRAC COX6C OTOF IL15 TNFRSF1A KIAA0152 CCRL2 LOC642312 LAX1 RP11-484I6.3 RPS27L POLD4 GP1BB SCN1A CCDC28B TLX1 LOC123876 ACSM2 IFIH1 ARPC2 HSD17B7 OAS3 MYLPF NMI ENSA ANXA2 WDR78 PTP4A2 SOD1 IL10RB RPS26 RPS26L CES4 CAPNS1 B3GNT2 ISLR DYNC2LI1 GIMAP5 ERAL1 CD3D ABHD11 TRA@ CGA CKS2 APOL6 GTF2H5 CACNA1C LY96 C1ORF54 HLA-A CKB DDAH2 RER1 ENY2 IL7R CKMT1B CKMT1A ANTXR1 IGHM LOC652494 / MED6 HLA-C SLA LOC441259 LOC641 PUS3 CD58 RRAGA SPA17 YPEL1 GRB2 GSTK1 C9ORF95 BTN3A2 PFDN5 CLIC1 RBM17 GDF15 CHI3L2 FMOD BAMBI GRM2 RARRES3 HMGCS1 IFIT3 RHOH LCP2 COX7B CCR1 SEC61G PSME1 FBXW7 TRGC2 TRGV2 NOLA3 ANXA1 HLA-B SNRPD2 GABARAPL2 CNOT7 TRBV19 TRBC1 SNFT S100A10 GMFG LAT ECM1 DEFB1 IRF1 CLEC2B PSME2 MXRA7 H3F3B MT1X MT2A IFI6 PSMB8 TMC7 ALOX5AP ISG20 DFNA5 PSMB9 CD28 CD1C CST7 PTPRC TRAC ATP6V1D TIMP1 ITM2A EMP3 SH3BGRL3 HLA-E NT5E TMEM50B SH2D2A TRIM21 TAP1 CES2 GSTO1 ISGF3G LOC92482 PHLDA1 RAB27A JARID2 VIM PSMB10 UBE2L6 STAT1 IFI35 STAT4 LGALS1 GBP1 ENPP1 GZMA TNFSF10 GZMB
	PD-1 NN	Genes correlated with *PD-1* expression (gene neighbors)	26	PDCD1 CCL3 PTPN13 CASP3 CD244 GP49A NR4A2 TRG@ EEA1 GPD2 4-Sep FASLG CD160 IFIH1 TANK MDFIC WBP5 PTGER4 SH2D2A 4631408O11RIK NRP1 ISG20 GPR56 CD7 1110067D22RIK CCL4 GAS2 ENTPD1 NR1I4 NFATC1 RSAD2 FGL2 COCH PBX3 GPR65 EOMES LITAF SERPINA3G CCRL2 PTGER2 FYN LAG3 PERP SPP1 TNFRSF1B 1300007C21RIK LO SFRS2IP CD200 CXCL10 H2-T23 1810035L17RIK PENK1 IIGP1 AHR 2010100O12RIK D17H6S56E-5 RNF11 LYCAT ADAM19 CD9 ART3 PGLYRP1 GM1066 IFIT1 TCRB-J LOC381765 BC039093 TNFRSF7 GZMK MLLT3 RGS16 IFIT3 CBX6 ITM2C ALCAM BCL2A1A BCL2A1B C330007P06RIK IRF8 GP49A LILRB4 TRIM17 HIST3H2A IFI204 RBL2 ITGAV CASP1 CTLA4 EIF3S1 SPG21 CAPZB ACADL MX1 NDUFA5 RASA1 SERPINB6A RCN1 TNFSF11 HCCS CCR5 2310015N07RIK 5830471E12RIK CPEB2 NUCB1
	BATF NN	Genes correlated with *BATF* expression (gene neighbors)	27	PLAUR PRSS3 C3AR1 CTNNA1 KRT18P44 TSPAN2 DAPK2 BMP10 FAM108A1 FAM108A3 CCHCR1 KIAA1045 ETV7 ANXA9 KIR2DS4 CDK2AP2 KIF22 LOC728037 PLEKHG6 PRSS2 FUT3 GINS4 NUSAP1 TACR3 SEPT4 KIR3DL2 NCAPG SOX2 GTSE1 HGFAC RUNX1T1 TESK1 TRIO GADD45GIP1 PRRX2 DKKL1 CHST2 GJB3 LRP12 SYT5 RCN3 EMILIN1 ABHD8 ZHX3 CDH6 AHDC1 MAPT EPO HTR7 HTR7P TRIM3 POU3F1 VGLL1 ALLC TSKS CDK5RAP2 AP1S1 TNNT2 NPAS1 CHIT1 ABCC6 DNAJC17 CNOT3 KCNB2 PTPRB MBL1P1 MDM2 FZD1 MYH13 KIR2DL4 ZNF669 CSF1 RICS C1orf76 CYP4F2 CYP4F3 GP1BB SEPT5 FOXL1 CCL21 TBX1 FCGR2C SERPINA2 HIST1H1E MTMR3 EXOC7 CHRNA1 KLF13 RRBP1 SSX5 ATP2B3 GABRA5 LOC727729 LOC643224 LOC728247 TUBB4Q TUBB8 MLL2 LMF1 C17orf88 ZNF668 OSBP2 CC2D1A SLC4A10 LOC90925 CST1 TRIM29 IFNA13 CRH SLC1A4 FRY KCNQ4 HIST1H2BB PVRL1 GPR35 SH2D3C KCNQ1 ZFX NOL3 PTN KRT20 JAKMIP2 HOXB13 RAPSN SF3A1 RRP1 TCL6 POLDIP3 TGFA PTPRN2 PCDH9 LMO3 MMP24 C20orf32 CRY2 PAPOLB LOC646677 LOC650674 BCR HBA1 HBA2 ZNF688 ZNF133 FOXI1 PRY MRE11A ASB4 MVK FLJ21511 MMP20 NAT8 NAT8B C16orf42 MAPK11 CCL24 DLGAP1 NEUROG1 ANKRD53 EVI1 LMO4 LILRB4 MGAT4B BRMS1 FKBP15 COL13A1 SCN2B PPP2R2B CCNA1 ITGA2B XAGE1 XAGE1B XAGE1C XAGE1D XAGE1E ADAMTS8 MYH6 MYH7 TAGLN MCM5 TPM1 TTLL1 CFHR5 LRRC42 EPB41L4A RIBC2 TSPY1 TLX2 GP1BB SEPT5 DKFZP564C196 OLFM1 PVR ELA2A EPHA3 LCN1 TCL1A TRA@ TRD@ KLK13 OSBPL10 CCKAR ACP1 EPX CSHL1 GOSR2 ST3GAL6 CCL14 CCL15 NRXN3 KIR2DS1 PBX2 DLG1 HAMP FCAR
	CTLA4	Genes in Biocarta pathway	Biocarta	ITK CD3G HLA-DRB1 CD3D CD3E GRB2 CD247 CTLA4 TRA@ TRB@ PTPN11 CD86 CD80 ICOS LCK PIK3CA PIK3R1 ICOSLG IL2 HLA-DRA CD28
	HIV Prog	Up in HIV progressors down in HIV elite controllers	27	RASA1 SPOCK2 RASA1 CDC14A TNFRSF25 PTGER4 PDCD4 TNFAIP3 GADD45A RGS1 BIRC3 SLC7A5 PDE4B NELL2 GNAQ TNFAIP3 HSPH1 LOC728198 TAF9B RGS1 SESN1 CCNH IFRD1 MED14 MRPS22 MC2R ACVR1B PDE4B SYNJ2 WRN ZNF238 SNX4 CDC14A RGPD4 RGPD5 RGPD6 RGPD8 PIK3IP1 CD28 JMJD6 KIAA0999 TACC1 SYPL1 C9orf97 PABPC3 ABCG1 TAPT1 YPEL5 FLJ32679 GOLGA8E GOLGA8G RBPJ ZNF136 PDE4B ARHGAP5 ZRF1 EIF1 LONRF3 AREG LOC727738 CTSO MASP2 TMEM184B DUSP4 SLC39A8 PLXDC1 BCAS2 MAP4K3 MED4 RIF1 PLXDC1 ZBTB10 LOC442215 SPATA2 CDK5R1 LRIG1 FAM102A RAB6IP1 DNAJB12 EIF4H CD44 OSBP IDI1 LOC146053 LOC391168 LOC391706 LOC400652 LOC439992 LOC643932 LOC644972 LOC646216 LOC646527 RPS3A TCEAL4 ZNF395 KLHL11 CBLB IL7R YIPF5 PBXIP1 GULP1 CCRN4L IHPK1 APOM APBA2 WDR48 RMND5A ETV3 ZMYM2 LOC151162 FLJ32679 GOLGA8E GOLGA8G PDCD4 THOC1 ARNTL C12orf41 TNF TMEM30B MBOAT5 SLC6A13 KIR2DS3 KIAA0831 C1QBP EIF4G1 MSH6 RIG N4BP3 FILIP1L NR4A2 IDI1 KLF9 C6orf64 PELO PFN2 TGIF1 RABGGTB CAND2 LIMK2 RWDD2A DKK3 RNF125 PELI2 CDCA4 PRKCI ATP2B1 SFRS3 LEPROTL1 PPP1R2 SYPL1 FAIM CD44 LOC653256 RABL3 LRRC40 CXCR3 NR4A2 SATB1 YTHDC2 CCT6B CKAP2 PABPC1 ADAM9 KLF7 RPAIN SNRPA1 WDR48 DHX29 SSX2IP C9orf82 CFHR2 GNAI3 TSFM FBXL11 PPP1CB NVL EIF4G2 INPP5A MRPL9 TM9SF1 LOC92482 ISCA1 SFRS18 RANBP10 ALG5 FKBP11 TSN POLR2J SCML2 GOLGA8A SF3B1 SLC7A6 EML4 ITSN2 HGSNAT MOAP1 CXCR4 MED14 LSR KTELC1 TBC1D2B ELL2 ISG20L1 SLC25A13

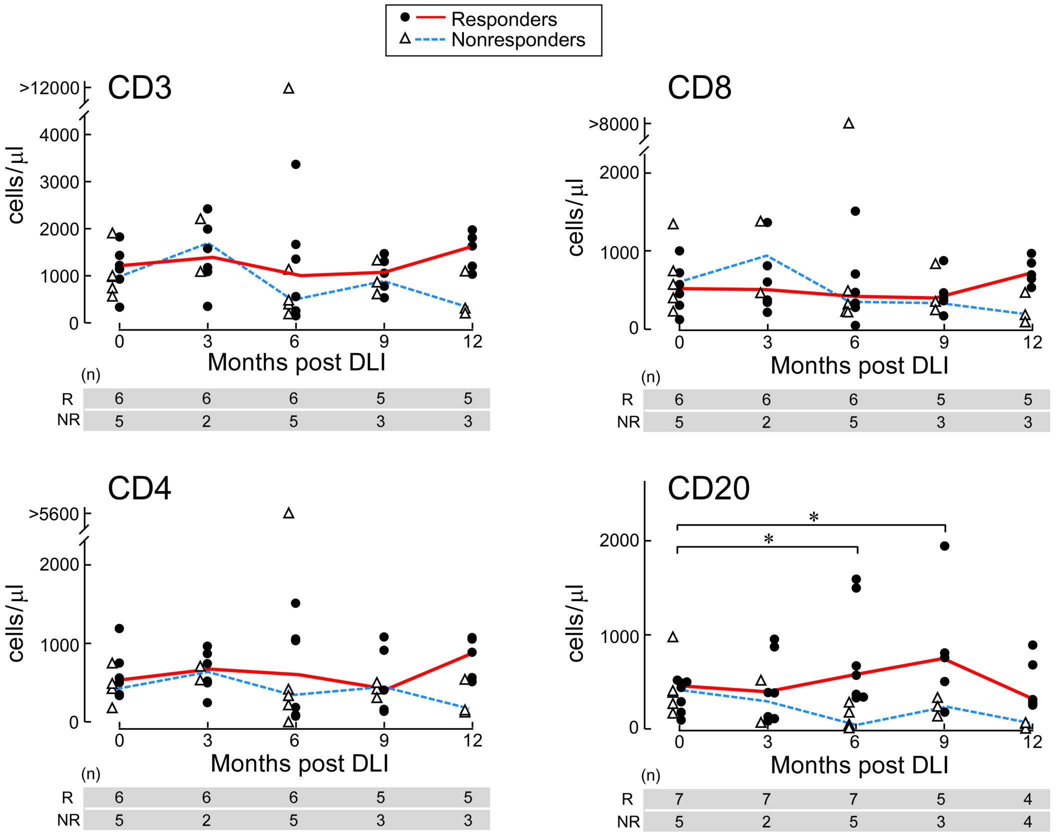

Figure S1. Characterization of immune cell subsets in peripheral blood over time following DLI. Flow cytometric analysis of immune populations in the peripheral blood from responders and nonresponders before and 3, 6, 9, and 12 months after DLI. For each immune cell subset, significant differences between 0 and 3, 6, 9, or 12 month timepoints are noted. *$P < 0.05$; Wilcoxon signed-rank test.

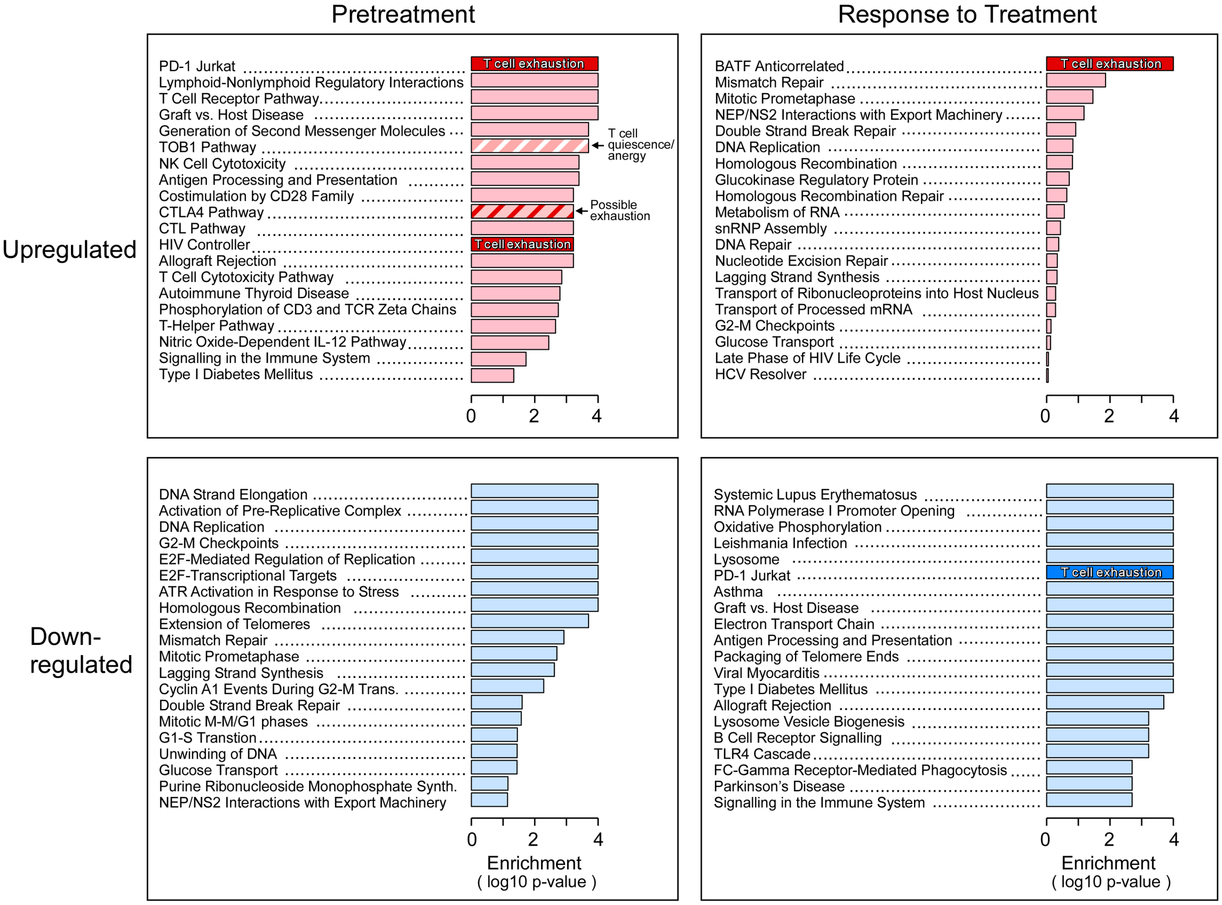

Figure S2. Gene set enrichment analysis (GSEA) of top 15 enriched gene sets in both 'pretreatment' and 'response to treatment' analyses. Gene sets are derived from ~880 curated gene sets from the CP (canonical pathways) collection of the Molecular Signatures Database, spiked with 11 specifically curated gene sets for T cell exhaustion, detailed in Table S4. Bar graphs show *P*-value of enrichment (signed according to enrichment score) for distinct gene sets. Dark red/blue bars indicate exhaustion gene sets; hatched bars indicate possible associate with T cell exhaustion.

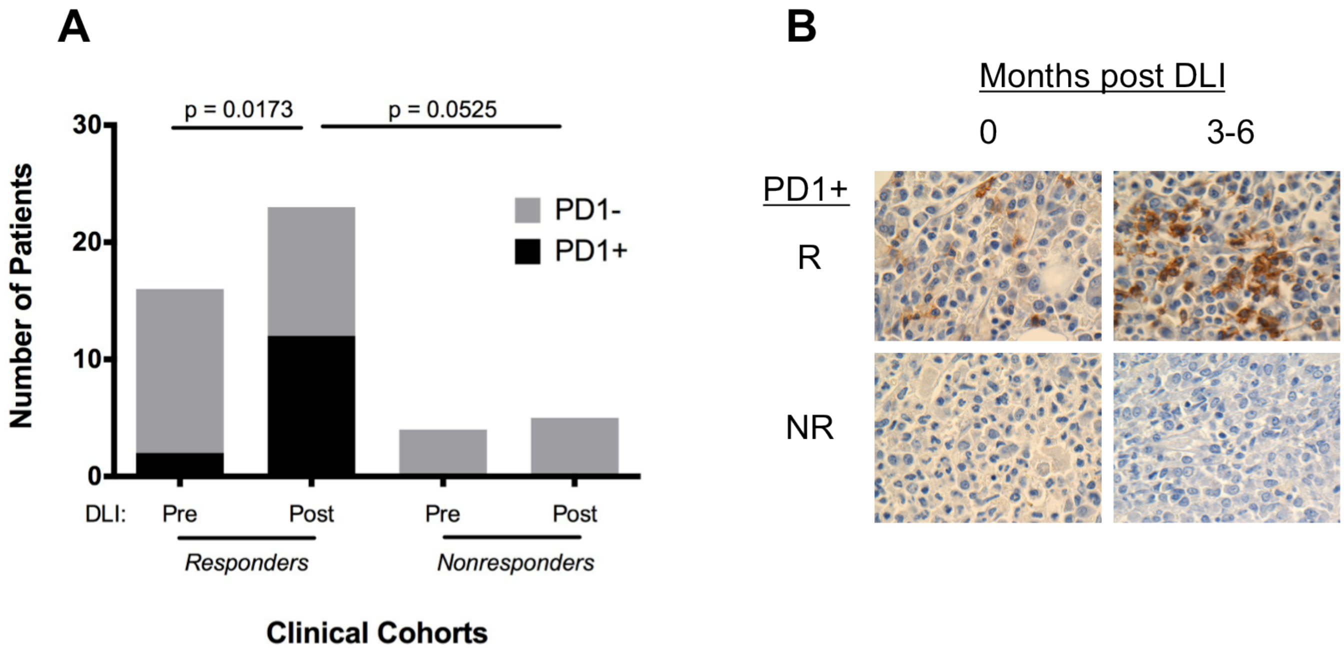

Figure S3. Association of PD1 expression and clinical response. (A) IHC staining analysis of $PD1^+$ cells in the marrow from responders and nonresponders before and after DLI. (B) Representative IHC of marrow samples from one responder and one nonresponder demonstrates robust marrow infiltration by $PD1^+$ cells in the responder before and subsequent increase after DLI. Fisher's exact test used for p-value calculation. The images were captured from an Olympus QColor 5 camera on an Olympus BX51 microscope with a 100X/1.30 objective at RT using acquisition software QCapture Pro.