Supplemental Data

Supplemental Figure 1. Details of study recruitment and number of samples.

Supplemental Figure 2. Study plan.

Supplemental Figure 3. $CD8^+$ T cells numbers do not differ in GvL samples compared to noGvL and in patients with developing relapse compared to no relapse.

Supplemental Figure 4. Publicity of $CD8^+$ CDR3 sequences does not differ in GvL samples compared to noGvL.

Supplemental Figure 5. Analysis of all GvL samples shows differences in $CD8^+$ *TRB* diversity, clonal space, top 20 clones and overlap.

Supplemental Figure 6. Individual temporal course of $CD8^+$ diversity grouped by patient outcome to DLI.

Supplemental Figure 7. CD8+ T cell clones originating from DLI input do not differ over time in samples with continuous GvL and do not predict relapse.

Supplemental Figure 8. Absolute $CD8^+$ T cell numbers and $CD8^+$ T cell diversity of DLI input do not predict response to DLI.

Supplemental Figure 9. $CD4^+$ and $CD3^+$ *TRB* diversity is not different in patients with and without relapse.

Supplemental Figure 10. Relapse incidence is not predicted by expansion of $CD4^+$ or $CD3^+$ T cell clones 14 days after DLI.

Supplemental Table 1. Patient samples.

Supplemental Table 2. Disease and Transplant Characteristics.

Supplemental Table 3. DLI Characteristics.

Supplemental Table 4. Response to DLI.

Supplemental Table 5A. Univariate comparison of clinical characteristics for the GvL and noGvL subgroup.

Supplemental Table 5B. Multivariate analysis of difference in TRB $CD8^+$ 1/D (Figure 2B).

Supplemental Table 5C. Multivariate analysis of delta number of clones of the top 25% TRB $CD8^+$ repertoire (Figure 3B).

Supplemental Table 5D. Multivariate analysis of delta number of clones of the top 50% TRB CD8$^+$ repertoire (Figure 3B).

Supplemental Table 5E. Multivariate analysis of delta number of clones of the top 75% TRB CD8$^+$ repertoire (Figure 3B).

Supplemental Table 5F. Multivariate analysis of delta number of clones of the whole TRB CD8$^+$ repertoire (Figure 3B).

Supplemental Table 5G. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 20 clones (Figure 4B).

Supplemental Table 5H. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-50 clones (Figure 4B).

Supplemental Table 5I. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 51-N clones (Figure 4B).

Supplemental Table 5J. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 20 overlapping clones (Figure 5B).

Supplemental Table 5K. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-N overlapping clones (Figure 5B).

Supplemental Table 5L. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by all overlapping clones (Figure 5B).

Supplemental Table 5M. Multivariate analysis of change of overlapping DLI input CD8$^+$ T cell clones (Figure 5F).

Supplemental Table 5N. Multivariate analysis of change of new DLI input CD8$^+$ T cell clones (Figure 5G).

Supplemental Table 6A. Univariate comparison of clinical characteristics for the no relapse and relapse subgroup.

Supplemental Table 6B. Univariate analysis of clinical variables with Figure 6B-H.

Supplemental Table 6C. Multivariate analysis of difference in TRB CD8$^+$ 1/D (Figure 6B).

Supplemental Table 6D. Multivariate analysis of delta number of clones of the top 25% TRB CD8$^+$ repertoire (Figure 6D).

Supplemental Table 6E. Multivariate analysis of delta number of clones of the top 50% TRB CD8$^+$ repertoire (Figure 6D).

Supplemental Table 6F. Multivariate analysis of delta number of clones of the top 75% TRB CD8$^+$ repertoire (Figure 6D).

Supplemental Table 6G. Multivariate analysis of delta number of clones of the whole TRB CD8$^+$ repertoire (Figure 6D).

Supplemental Table 6H. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 20 clones (Figure 6F).

Supplemental Table 6I. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-50 clones (Figure 6F).

Supplemental Table 6J. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 51-N clones (Figure 6F).

Supplemental Table 6K. Multivariate analysis of difference in $CD8^+$ TRB repertoire occupation by top 20 overlapping clones (Figure 6H).

Supplemental Table 6L. Multivariate analysis of difference in $CD8^+$ TRB repertoire occupation by top 21-N overlapping clones (Figure 6H).

Supplemental Table 6M. Multivariate analysis of difference in $CD8^+$ TRB repertoire occupation by all overlapping clones (Figure 6H).

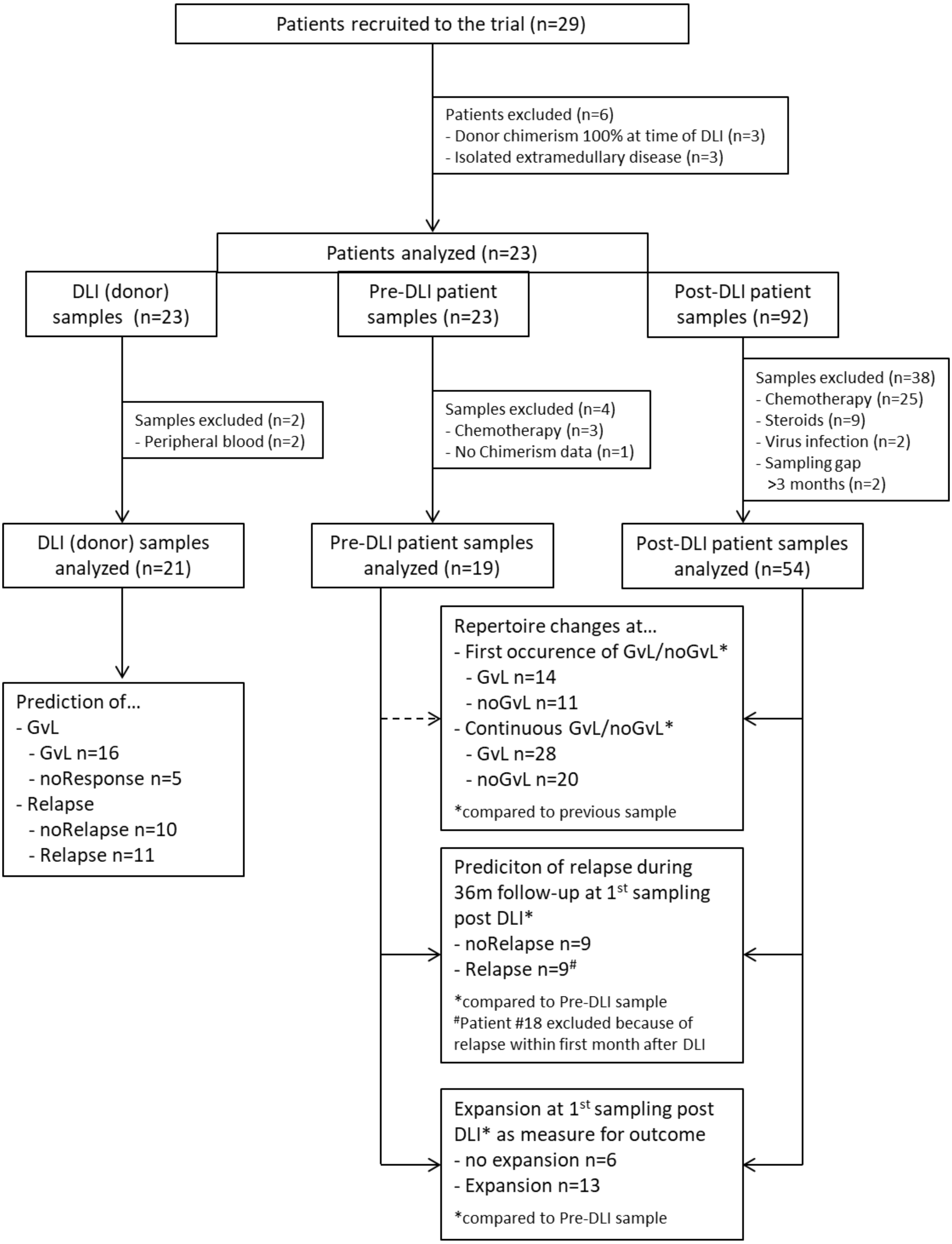
Supplemental Table 7A. Univariate comparison of clinical characteristics for the d+14 post DLI $CD8^+$ expansion vs no expansion subgroup.

Supplemental Table 7B. Results of univariate Cox regression for cumulative incidence of relapse (Figure 7A).

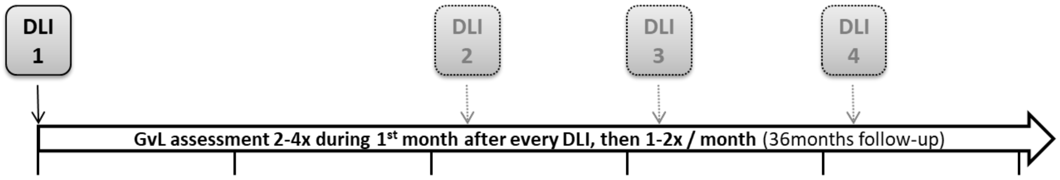
Supplemental Table 7C. Results of multivariate Cox regression model for cumulative incidence of relapse (Figure 7A).

Supplemental Table 7D. Results of univariate Cox regression for relapse free survival (Figure 7B).

Supplemental Table 7E. Results of multivariate Cox regression model for relapse free survival (Figure 7B).

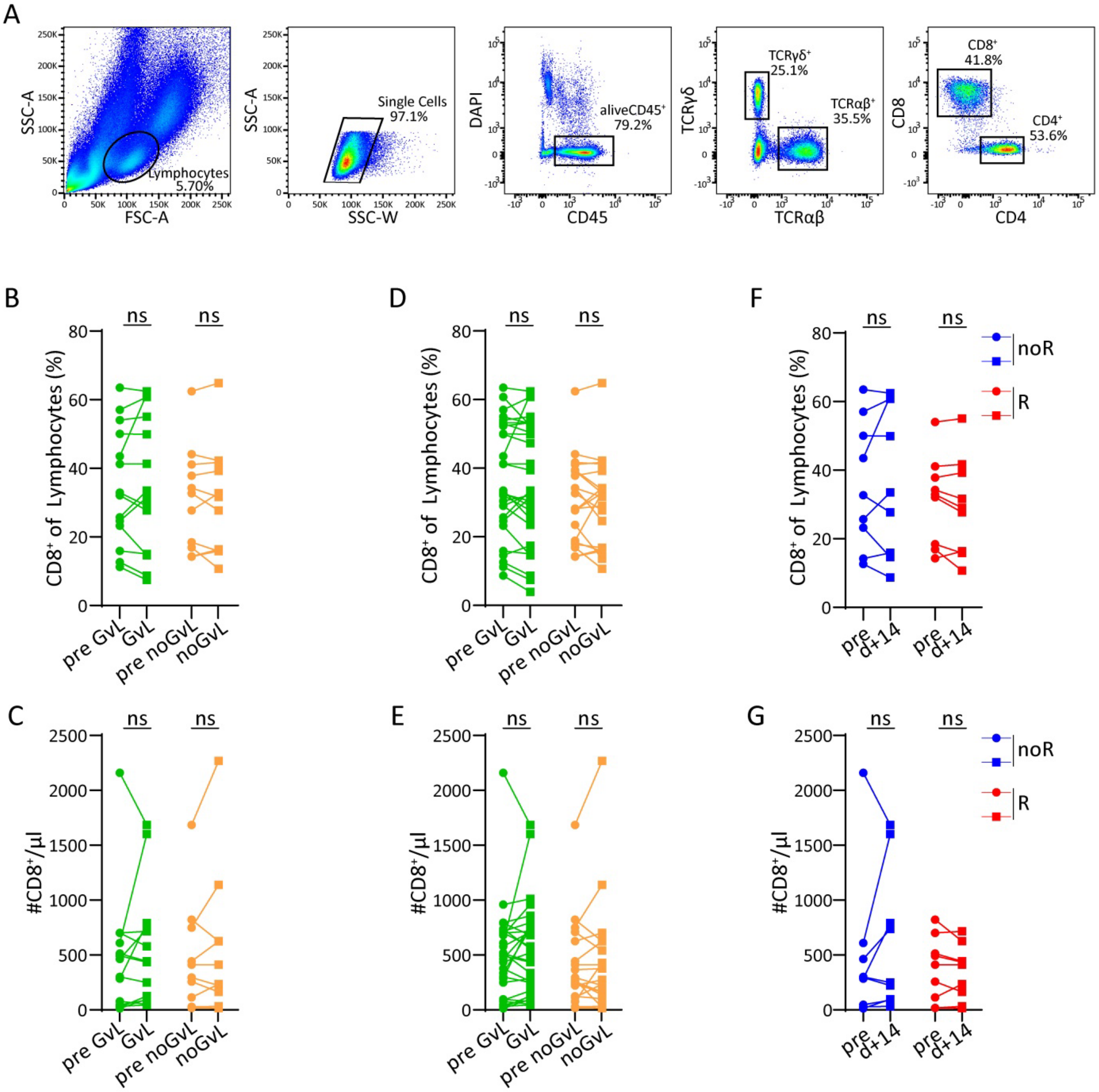


Supplemental Figure 1. Details of study recruitment and number of samples.

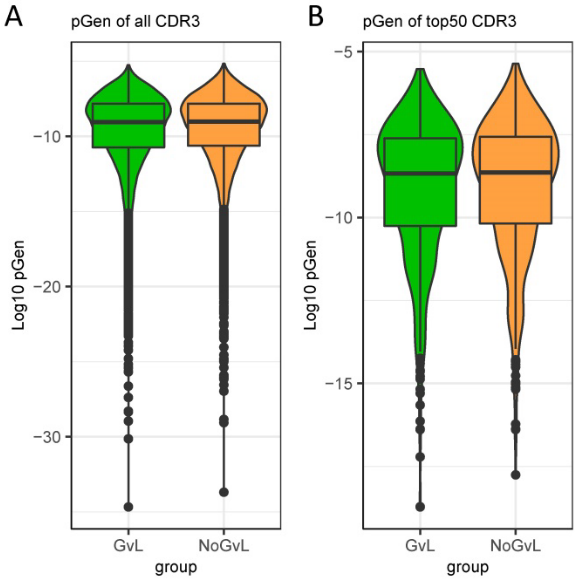


Sampling time point:	d0	d+14	d+30	d+60	d+90	d+120
Sample name:	(pre-DLI)	(A)	(B)	(C)	(D)	(E)
Samples amount:	23	21	22	10	11	11
Median day post DLI (range):	0 (-7-0)	14 (12-23)	30 (24-44)	59 (42-77)	96 (84-112)	124 (110-136)
1st occurence of GvL, median day post DLI (range):	-	15 (12-21), n=11	32 (27-36), n=4	51, n=1	-	132, n=1
Median difference between GvL detection and sampling in days (range):	-	0 (0-13)	0 (0-0)	26 (-)	-	4 (-)

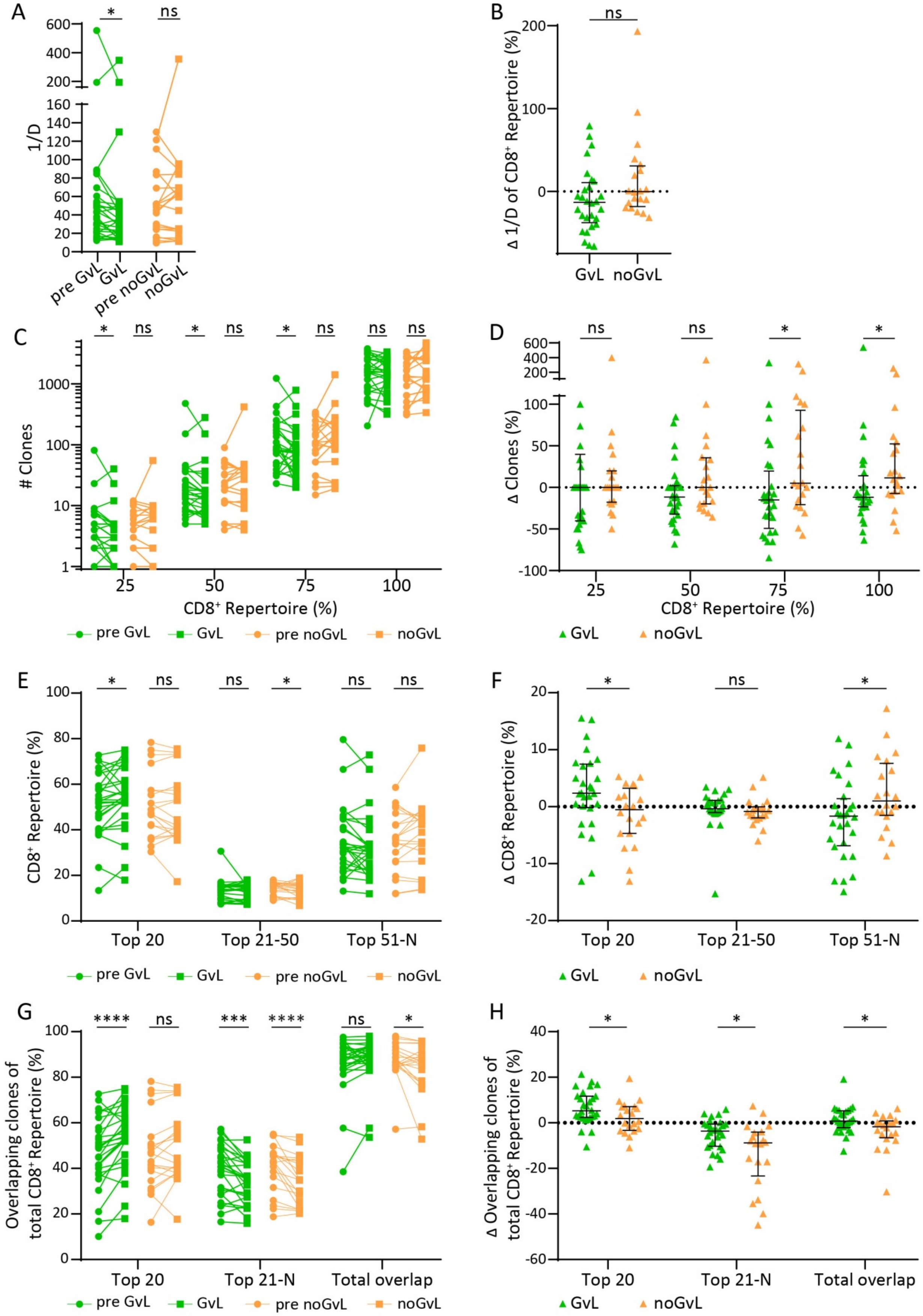
Supplemental Figure 2. Study plan.



Supplemental Figure 3. CD8$^+$ T cells numbers do not differ in GvL samples compared to noGvL and in patients with developing relapse compared to no relapse. (A) Gating strategy. (B-G) CD8$^+$ T cells are shown as percentage of lymphocytes (B, D, F) and absolute numbers (C, E, G); (B, C) Comparing patients with GvL effect (green) and those without (orange). The graphs show the time point prior to first GvL/ noGvL (closed circles) and the first time point of GvL/noGvL (closed squares) for each patient. (D, E) Displayed are all GvL/ noGvL (closed squares) time points in comparison with the previous time point (closed circles). **(**F, G) Comparing pre DLI samples (filled circles) and d+14 post DLI samples (filled squares) in patients without relapse (noR) after DLI during the study follow-up (blue) and patients with relapse (R) after DLI (red). Statistical analysis was performed by Wilcoxon matched-pairs signed ranked test (two-tailed); ns: not significant.

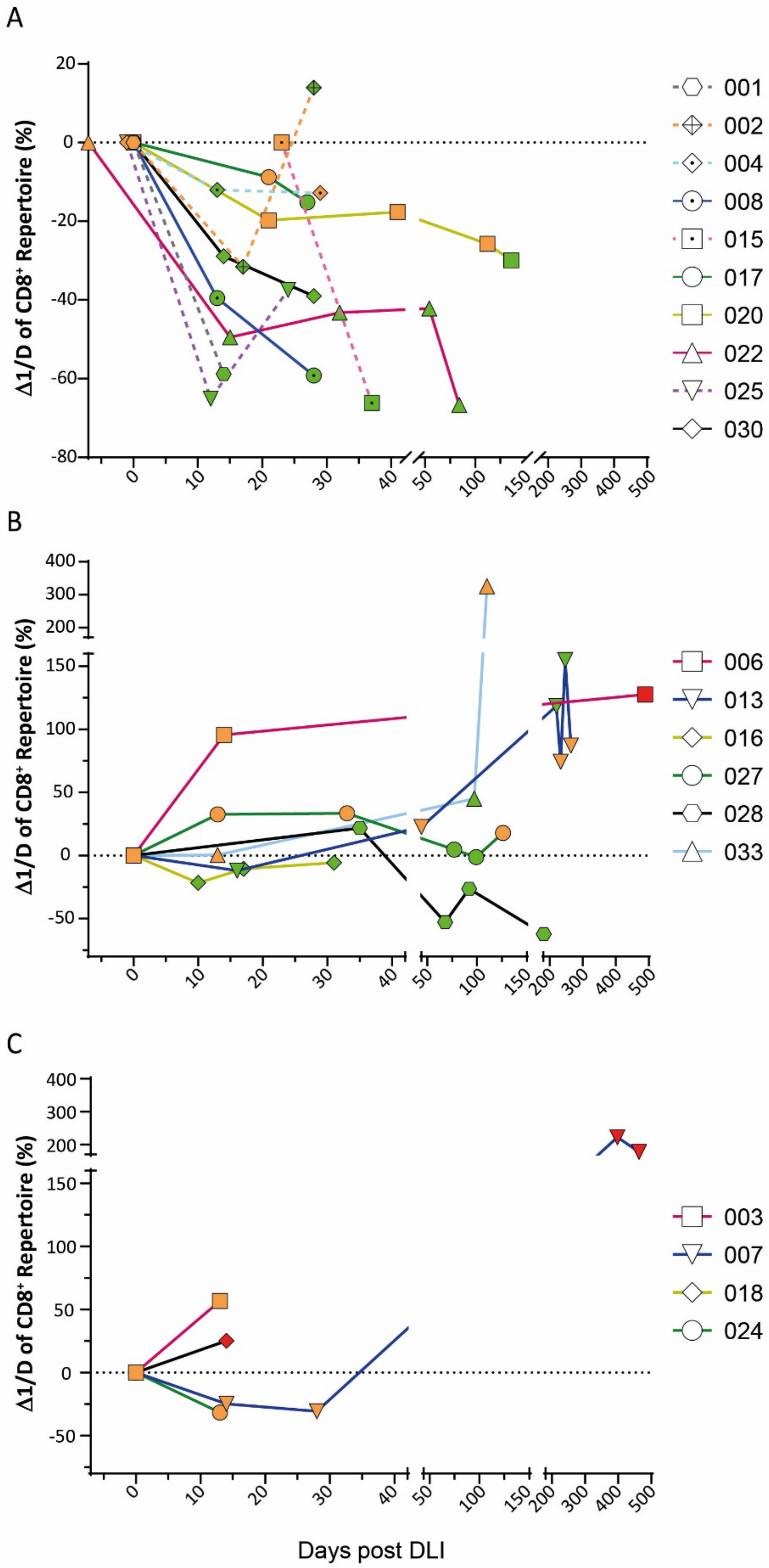


Supplemental Figure 4. Publicity of CD8$^+$ CDR3 sequences does not differ in GvL samples compared to noGvL. Publicity is displayed via $_{\log10}$pGen (Y axis) of all CDR3 sequences (A) and top 50 sequences only (B) in samples with first occurrence of GvL (n=14, green) compared to noGvL (n=11, orange).


A
1/D
600
400
200
160
140
120
100
80
60
40
20
0
*
ns
pre GvL
GvL
pre noGvL
noGvL
B
Δ 1/D of CD8⁺ Repertoire (%)
200
100
0
ns
GvL
noGvL
C
Clones
1000
100
10
1
* ns * ns * ns ns ns
25
50
75
100
CD8⁺ Repertoire (%)
pre GvL
GvL
pre noGvL
noGvL
D
Δ Clones (%)
600
400
200
100
50
0
-50
-100
ns ns * *
25
50
75
100
CD8⁺ Repertoire (%)
GvL
noGvL
E
CD8⁺ Repertoire (%)
100
80
60
40
20
0
* ns ns * ns ns
Top 20
Top 21-50
Top 51-N
pre GvL
GvL
pre noGvL
noGvL
F
Δ CD8⁺ Repertoire (%)
20
10
0
-10
-20
* ns *
Top 20
Top 21-50
Top 51-N
GvL
noGvL
G
Overlapping clones of total CD8⁺ Repertoire (%)
100
80
60
40
20
0
**** ns *** **** ns *
Top 20
Top 21-N
Total overlap
pre GvL
GvL
pre noGvL
noGvL
H
Δ Overlapping clones of total CD8⁺ Repertoire (%)
40
20
0
-20
-40
-60
* * *
Top 20
Top 21-N
Total overlap
GvL
noGvL

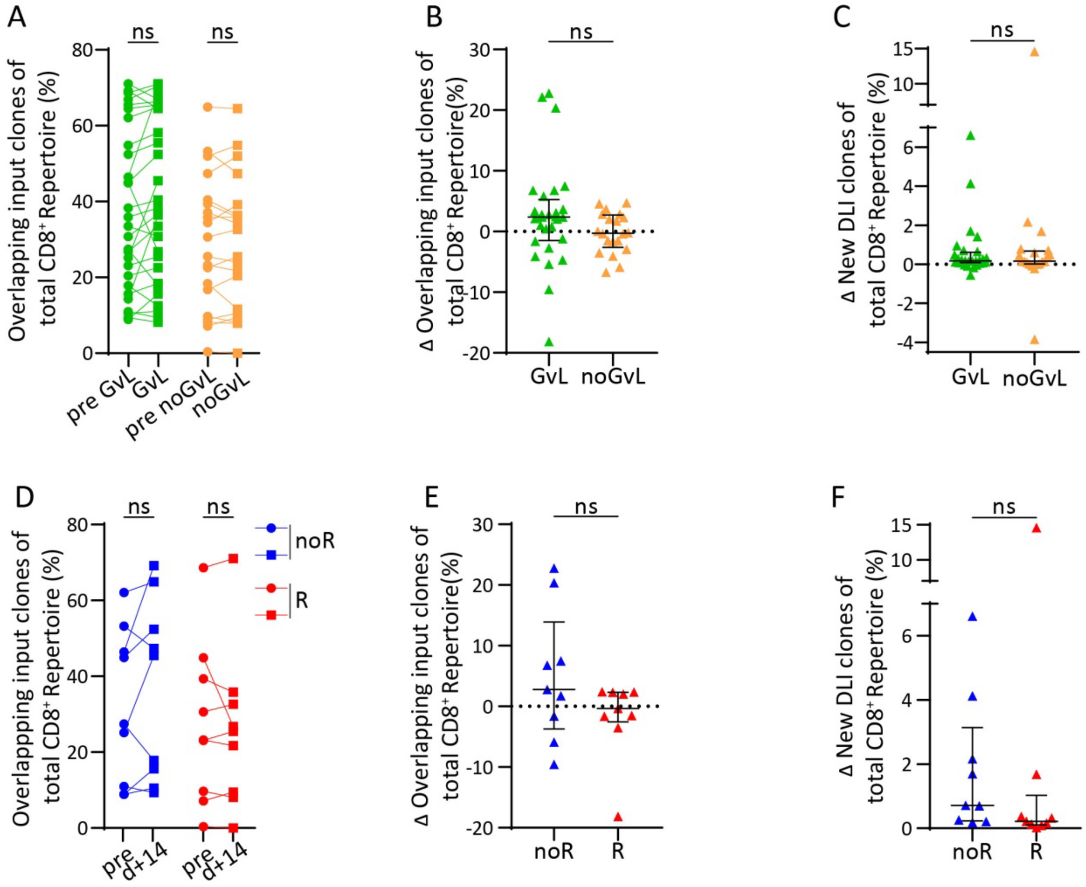
Supplemental Figure 5. Analysis of all GvL compared to noGvL samples shows differences in CD8$^+$ *TRB* diversity, clonal space, top 20 clones and overlap. (A) Comparison of CD8$^+$ *TRB* diversity in all samples with GvL effect (green, n=28) and those without (orange, n=20). The graph shows the time point prior to GvL/ noGvL (closed circles) and at occurrence of GvL/ noGvL (closed squares). (B) Change of CD8$^+$ TCR diversity in samples with GvL and noGvL in percent is displayed. (C) Number of unique clonotypes (Y axis) is displayed individually for each quartile of the CD8$^+$ repertoire comparing samples with GvL effect (green) and those without GvL effect (orange). Two time points are compared with closed circles displaying the pre GvL/ pre noGvL time point and closed squares displaying the GvL/ noGvL time point. (D) Difference in number of clones (Y axis) between pre GvL/ pre noGvL and GvL/ noGvL (Y axis) is displayed individually for each quartile of the CD8$^+$ repertoire. (E) CD8$^+$ TCR repertoire proportions are displayed for the top 20, 21-50 and 51-N CD8$^+$ T cell clones showing all samples with GvL effect (green) and those without GvL (orange). Two time points are compared with closed circles displaying the pre GvL/ pre noGvL time point and closed squares displaying the GvL/ noGvL time point. (F) Difference in CD8$^+$ TCR repertoire (Y axis) occupied by top 20, 21-50 and 51-N clones between all pre GvL/ pre noGvL and GvL/ noGvL time points. (G) Top 20, 21-N and total overlapping CD8$^+$ T cell clones as percent of total CD8$^+$ TCR repertoire (Y axis) is shown for samples with GvL (green) and without GvL (orange). Two time points are compared with closed circles displaying the pre GvL/ pre noGvL time point and closed squares displaying GvL/ noGvL time point. (H) Change of overlapping CD8$^+$ TCR repertoire proportions is compared between samples with GvL effect (green) and those without GvL effect (orange). Black lines represent median, error bars show the interquartile range. Statistical analysis was performed by Wilcoxon matched-pairs signed ranked test (two-tailed) for A, C, E, G and

Mann-Whitney test (two-tailed) for B, D, F, H. *$P< 0.05$, ***$P< 0.001$, ****$P< 0.0001$; ns: not significant.

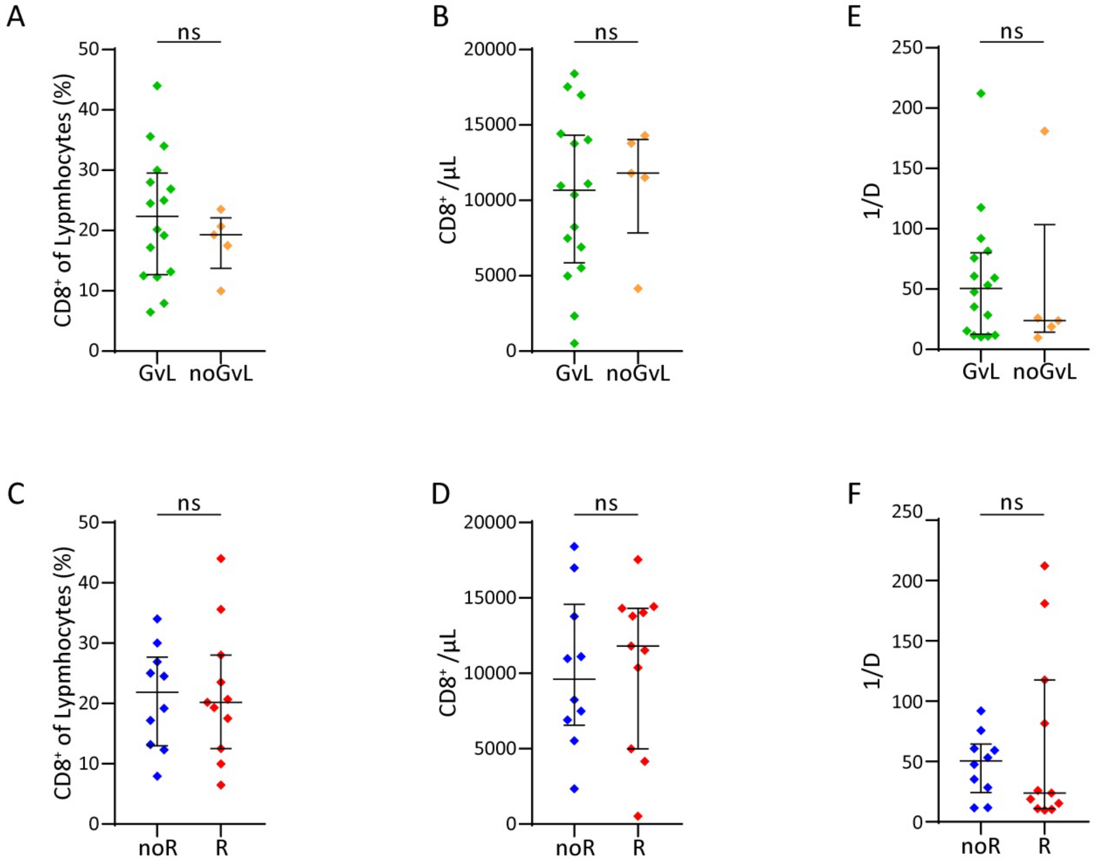


Supplemental Figure 6. Individual temporal course of CD8$^+$ diversity grouped by patient outcome to DLI. Displayed is the change in CD8$^+$ *TRB* diversity compared to the base line sample in percent (Y axis) for the course of the study (days post DLI, X axis) for

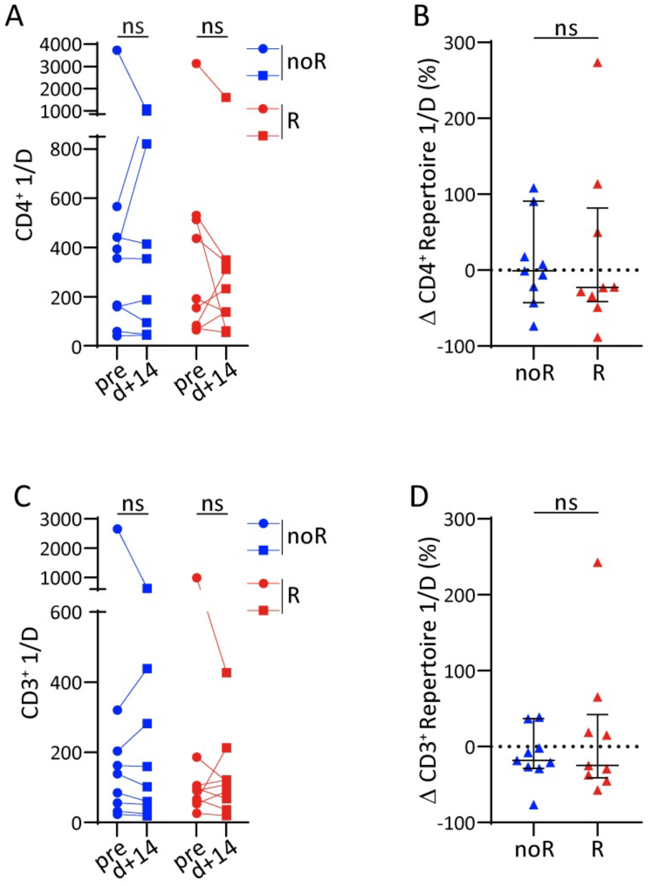
(A) patients with continuous GvL response (as defined in Table 1), (B) patients with intermittent GvL response and (C) patients not responding to DLI. Only patients were included with at least two available sample time points (as shown in Supplemental Table 1). Every symbol displays one individual patient with green fill indicating GvL effect (compared to the previous time point), orange fill indicating noGvL effect and red fill indicating relapse.



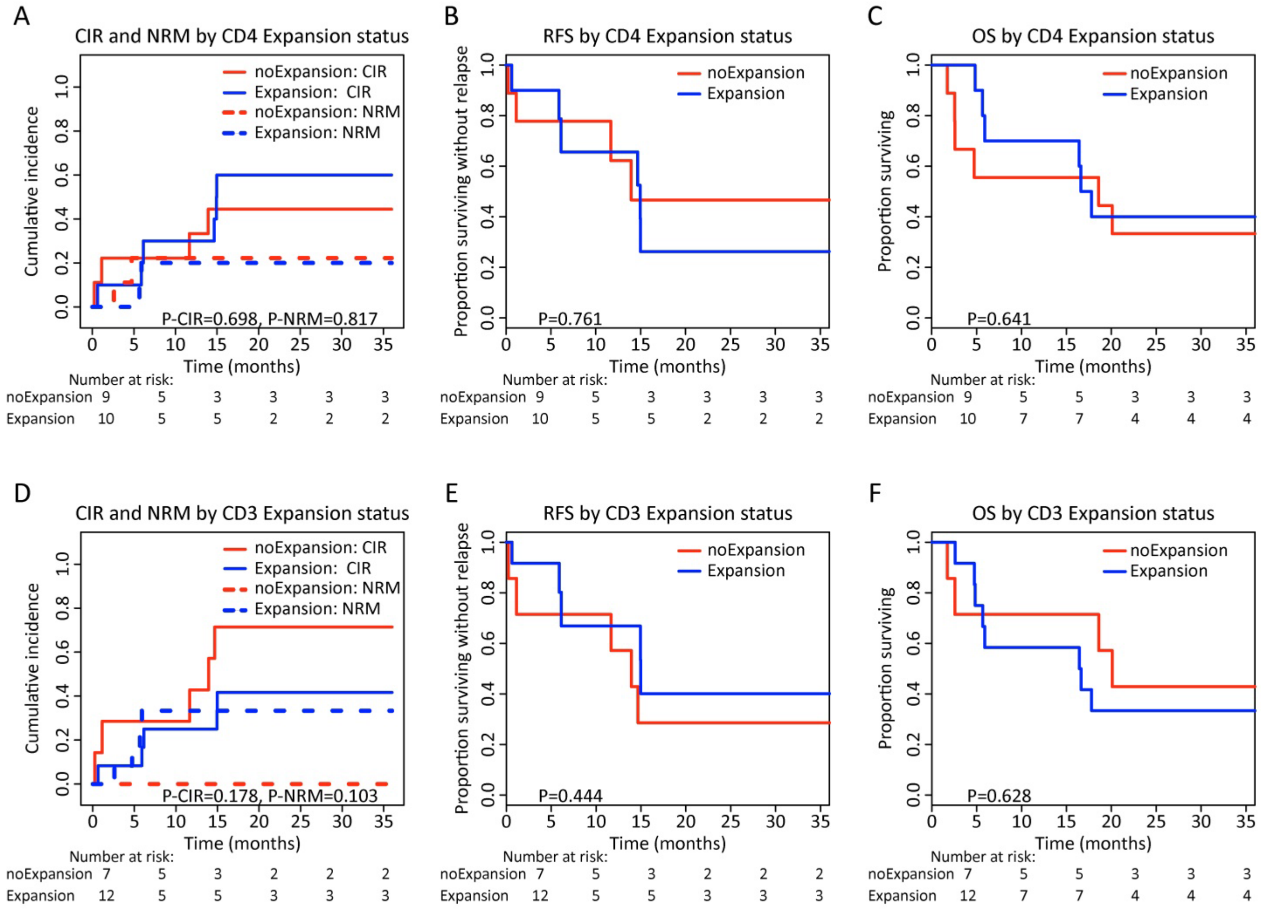
Supplemental Figure 7. CD8$^+$ T cell clones originating from DLI input do not differ over time in samples with continuous GvL and do not predict relapse. (A) Proportion of overlapping CD8$^+$ T cell DLI input clones in all samples with GvL effect (green, n=28) and those without (orange, n=20). The graph shows the time point prior to GvL/ noGvL (closed circles) and at occurrence of GvL/ noGvL (closed squares). (B) Change of overlapping DLI input CD8$^+$ T cell clones between all pre GvL/ pre noGvL and all GvL/ noGvL time points is shown for patients with GvL (green) and without GvL (orange). (C) Change of new DLI input CD8$^+$ T cell clones (clones were not detected in pre DLI sample) between all pre GvL/ pre noGvL and all GvL/ noGvL time points is shown for patients with GvL (green) and without GvL (orange). (D) Proportion of overlapping CD8$^+$ T cell DLI input clones in pre DLI samples (filled circles) and d+14 post DLI samples (filled squares) in patients without relapse (noR) after DLI during the study follow-up (blue, n=9) and patients with relapse (R) after DLI (red, n=9). (E) Change of overlapping input CD8$^+$ T cell clones between pre DLI and d+14 time point is shown for patients without (blue) and with relapse after DLI (red). (F) Change of new DLI CD8$^+$ T cell clones (clones were not present in pre DLI sample) between pre DLI and d+14 time point is shown for patients without relapse (blue) and with relapse (red) after DLI during study follow up. Statistical analysis was performed by Wilcoxon matched-pairs signed ranked test (two-tailed) for A, D and Mann-Whitney test (two-tailed) for B, C, E, F. *$P < 0.05$; ns: not significant. Black lines represent median, error bars show the interquartile range.



Supplemental Figure 8. Absolute CD8$^+$ T cell numbers and CD8$^+$ T cell diversity of DLI input do not predict response to DLI. (A, B) CD8$^+$ T cells as percentage of lymphocytes (A) and absolute numbers of CD8$^+$ T cells of DLI input samples in patients with occurrence of at least one sample with GvL (green diamonds, n=16) to those patients without GvL (orange diamonds, n=5) during the study follow-up. (C, D) Comparing DLI input samples in patients without relapse (noR, blue diamonds, n=10) and patients with relapse (R, red diamonds, n=11) after DLI during the study follow-up. (E) Comparison of CD8$^+$ TCR diversity of DLI input samples in patients with GvL (green diamonds) and without GvL (orange diamonds) during study follow up. (F) Comparison of CD8$^+$ TCR diversity of DLI input samples in patients without relapse (noR, blue diamonds) and with relapse (R, red diamonds) during study follow up. Black lines represent median, error bars show the interquartile range. Statistical analysis was performed by Mann-Whitney test (two-tailed). ns: not significant.



Supplemental Figure 9. CD4$^+$ and CD3$^+$ *TRB* diversity is not different in patients with and without relapse. (A, C) Comparison of CD4$^+$ (A) and CD3$^+$ (C) *TRB* diversity in pre DLI samples (filled circles) and d+14 post DLI samples (filled squares) in patients without relapse (noR) after DLI during the study follow-up (blue, n=9) and patients with relapse (R) after DLI (red, n=9). (B, D) Change of CD4$^+$ (B) and CD3$^+$ (D) *TRB* diversity in patients without (blue) and with relapse (red) in percent is displayed. Statistical analysis was performed by Wilcoxon matched-pairs signed ranked test (two-tailed) for A and Mann-Whitney test (two-tailed) for B. Black lines represent median, error bars show the interquartile range; ns: not significant. CD3$^+$ diversity data was calculated based on the cell frequencies of CD8$^+$ and CD4$^+$ cells (e.g. CD3$^+$ 1/D was calculated as sum of CD8$^+$ 1/D * frequency of CD8$^+$ of CD3$^+$ and CD4$^+$ 1/D * frequency of CD4$^+$ of CD3$^+$).



Supplemental Figure 10. Relapse incidence is not predicted by expansion of CD4^{+} or CD3^{+} T cell clones 14 days after DLI. (A, D) Cumulative incidence curves are shown with relapse incidence (CIR, solid lines) and non-relapse mortality (NRM, dotted lines) as competing events for patients without clonal expansion (A: n=9, D n=7) in red and for patients with clonal expansion (A: n=10, D: n=12) in blue of (A) CD4^{+} and (D) CD3^{+} *TRB* repertoire at first sampling time point after DLI (on average d+14). Expansion was assessed via inverse Simpson's index (1/D) and compared to the pre DLI time point. CIR and NRM were analyzed by means of cumulative incidence curves using Gray's test. (B, E) Analysis of relapse free survival (RFS) between patients without clonal expansion in red and for patients with clonal expansion in blue of (B) CD4^{+} and (E) CD3^{+} *TRB* repertoire at first sampling time point after DLI (on average d+14). Statistical analysis was done with univariate Cox regression model. (C, F) Analysis of overall survival (OS) between patients without clonal expansion in red and for patients with clonal expansion in blue of CD8$^+$ *TRB* repertoire at first sampling time point after DLI (on average d+14). Statistical analysis was done with univariate Cox regression model. CD3$^+$ diversity data was calculated based on the cell frequencies of CD8$^+$ and CD4$^+$ cells (e.g. CD3$^+$ 1/D was calculated as sum of CD8$^+$ 1/D * frequency of CD8$^+$ of CD3$^+$ and CD4$^+$ 1/D * frequency of CD4$^+$ of CD3$^+$).

Supplemental Table 1. Patient samples.

Given is the time point (days from DLI) of all available blood samples per patient in days post DLI. In case of exclusion of a sample from analysis, the reason is stated in parenthesis right next to the respective day. E.g. 28 (S) = sample at day +28 post DLI was excluded because of administration of steroids.

Abbreviations: Chim: no chimerism data; CTx: chemotherapy; G: sampling gap >3 months; PB: peripheral blood; S: steroid; V: virus infection.

Patient ID	Blood Samples	DLI Sample
01	0, 14, 28 (S)	yes
02	0, 17, 28	yes
03	0, 13, 27 (CTx)	yes
04	-1, 13, 29, 428 (S), 483 (S)	yes
06	0, 14, 28 (S), 489, 530 (CTx)	yes
07	0, 14, 28, 398, 463	yes
08	0, 13, 28	yes
09	0 (CTx), 18 (CTx), 33	yes
13	0, 16, 44, 220, 233, 247, 264	yes
15	0 (Chim), 23, 37	yes
16	0, 10, 17, 31, 135 (G), 248 (CTx), 261 (CTx)	yes
17	0, 21, 27, 105 (S), 125 (S)	yes
18	0, 14, 27 (CTx)	no (PB)
20	0, 21, 41, 112, 136, 164 (V), 240 (G)	yes
22	-7, 15, 32, 54, 84, 123 (S)	yes
23	0 (CTx), 8 (CTx), 14 (CTx), 43 (CTx), 64 (CTx), 91 (CTx), 117 (CTx)	yes
24	0, 13, 34 (CTx), 63 (CTx), 90 (CTx), 119 (CTx)	yes
25	-1, 12, 24, 54 (CTx), 96 (CTx), 124 (CTx), 180 (CTx)	yes
27	0, 13, 33, 77, 99, 126, 191 (V)	no (PB)
28	0, 35, 68, 92, 182	yes
30	0, 14, 28, 61 (S), 97 (S)	yes
32	0 (CTx), 56 (CTx), 84 (CTx), 118 (CTx)	yes
33	0, 13, 31 (CTx), 56 (CTx), 97, 110	yes

Supplemental Table 2. Disease and Transplant Characteristics.

aHSCT indicates allogeneic hematopoietic stem cell transplantation; BM bone marrow; f female; aGVHD acute graft-versus-host disease; cGVHD chronic graft-versus-host disease; m male; mye myeloablative; PBSC peripheral blood stem cell; RIC reduced intensity conditioning;

*Disease risk according to ELN [23] and IPSS-R [32].

Patient ID	Gender	Age at DLI	Disease Details	Disease risk*	HLA-Matching	Donor Gender	Donor Age at aHSCT	Graft source	Conditioning regimen	Total grade aGVHD post aHSCT (pre DLI)	Total grade cGVHD post aHSCT (pre DLI)
01	f	36	AML	intermediate	10/10	f	43	PBSC	mye	1	-
02	m	63	MDS	high	10/10	m	22	PBSC	RIC	-	-
03	f	23	c-ALL	standard	10/10	m	29	PBSC	mye	-	-
04	m	55	sAML from MPN	adverse	9/10	f	26	PBSC	RIC	1	limited
06	m	46	sAML from MDS	intermediate	9/10	f	23	PBSC	RIC	1	-
07	f	55	PMF/MPS-MDS	intermediate	10/10	m	57	PBSC	RIC	-	-
08	f	57	MDS	intermediate	10/10	m	58	PBSC	RIC	-	-
09	m	72	sAML from MDS	intermediate	10/10	m	22	PBSC	RIC	1	-
13	f	64	sAML from MDS	intermediate	10/10	f	64	PBSC	RIC	1	-
15	m	22	AML	intermediate	9/10	f	49	PBSC	RIC	-	-
16	f	36	sAML from MPN	intermediate	10/10	m	31	PBSC	RIC	-	limited
17	f	48	ET/sMF	-	10/10	m	31	PBSC	RIC	-	limited
18	m	36	AML	adverse	10/10	f	27	BM	RIC	1	-
20	m	55	P. vera	-	10/10	m	26	PBSC	RIC	-	-
22	m	50	AML	favorable	10/10	m	51	PBSC	mye	-	-
23	m	65	AML	adverse	10/10	m	61	PBSC	RIC	1	-
24	f	29	AML	intermediate	5/10	m	33	PBSC	mye	-	-
25	m	41	AML	intermediate	10/10	m	29	PBSC	mye	-	-
27	f	39	sAML from AA	intermediate	10/10	f	35	BM	RIC	-	-
28	m	24	AML	adverse	10/10	m	14	BM	RIC	-	-
30	m	40	tAML	adverse	10/10	m	27	PBSC	RIC	-	-
32	m	61	sAML from MDS	adverse	10/10	f	21	PBSC	RIC	3	limited
33	f	33	AML	adverse	10/10	f	30	PBSC	mye	-	-

Supplemental Table 3. DLI Characteristics.

aHSCT indicates allogeneic hematopoietic stem cell transplantation; CR complete remission; CTx chemotherapy; DAC daunorubicin + Ara-C + cladribine; EM extramedullary; FLA-IDA Fludarabine + AraC + Idarubicin; iHC increased host chimerism; PD progressive disease; R Relapse; RD resistant disease; SAIL Selinexor + Ara-C + Idarubicin; V-I-PEG-A-Dexa Vindesine + Idarubicin + PEG-Asparaginase + Dexamethasone.

*Based on ELN response criteria [33]

Patient ID	DLI Trigger	CTx pre DLI	Months post CTx at 1st DLI	Response to CTx*	First DLI. Months post aHSCT	Dose 1st DLI. CD3+ /kg BW	Total Number DLI
01	Cytologic R	SAIL	1.4	CRi, iHC	7.9	1x10E7	1
02	Cytologic R	FLA-IDA	1.4	PR	23.8	1.2x10E7	1
03	Cytologic R	V-I-PEG-A-Dexa	1.6	RD	8.8	1x10E7	1
04	Molecular R	no		-	19.1	5x10E5	3
06	Molecular R	no		-	16.1	1x10E7	1
07	iHC	no		-	10.3	1x10E6	3
08	iHC	no		-	10.5	1x10E6	2
09	Cytologic R	Decitabine	0.2	PR	29.4	1x10E7	1
13	iHC	no		-	8.1	1x10E6	4
15	iHC	no		-	5.5	5x10E5	1
16	Histologic R	SAIL	1.9	CRi, iHC	22.0	5x10E6	7
17	Histologic R	no		-	24.0	1x10E6	3
18	Molecular R	no		-	9.6	5x10E6	1
20	Molecular R	no		-	9.3	1x10E6	4
22	Cytologic R	FLA-IDA	1.2	PR	14.2	1x10E7	2
23	Cytologic R	Azacitidine	0.3	PR	4.6	5x10E6	1
24	Cytologic R	no		-	6.5	1x10E6	4
25	Cytologic R	SAIL	0.9	CR, iHC	75.7	1x10E7	1
27	iHC	no		-	11.0	2.5x10E7	3
28	iHC	no			4.1	5x10E6	4
30	Molecular R	FLA-IDA	1.4	CR, iHC	26.3	1x10E7	2
32	Cytologic R	Azacitidine	0.3	RD	17.1	2x10E6	3
33	Cytologic R + EM R	DAC	1.1	CR, MC	11.5	1x10E7	1

Supplemental Table 4. Response to DLI.

Abbreviations are explained in supplemental Table 2 and 3.

Patient ID	First GvL [Months post DLI]	Relapse post DLI [Months post DLI]	Study Endpoint: Details	Study Endpoint/ Last follow-up [Months post DLI]	Overall GvL Response to DLI
01	0.5	no	Death: GVHD, Infection	2.6	continuous
02	0.9	no	Death: GVHD, Infection	4.7	continuous
03	noGvL	1.1	Death: PD, Infection	1.7	no response
04	0.4	no	-	36.0	continuous
06	0.7	14.7	-	36.0	intermittent
07	noGvL	5.9	Death: PD, Infection	16.6	no response
08	0.4	no	-	36.0	continuous
09	0.6	3.7	Death: PD, Infection	8.5	intermittent
13	0.5	15.0	Death: PD, Infection	16.4	intermittent
15	1.2	no	-	36.0	continuous
16	0.6	6.1	2nd aHSCT	17.8	intermittent
17	0.9	no	Death: GVHD, Infection	5.9	continuous
18	noGvL	0.2	2nd aHSCT	2.6	no response
20	4.4	no	-	36.0	continuous
22	0.5	no	Death: GVHD, Infection	5.7	continuous
23	noGvL	0.5	Death: PD, Infection	5.2	no response
24	noGvL	0.6	Death: PD, Infection	4.8	no response
25	0.6	no	-	36.0	continuous
27	1.7	11.7	2nd aHSCT	20.1	intermittent
28	0.7	14.9	-	36.0	intermittent
30	0.5	no	-	36.0	continuous
32	noGvL	1.9	Death: PD, Infection	5.2	no response
33	1.2	13.9	2nd aHSCT	18.6	intermittent

Supplemental Table 5A. Univariate comparison of clinical characteristics for the GvL and noGvL subgroup.

Given is the absolute number (%) for categorical variables and the median absolute value (range) for numerical variables. Categorical variables were compared with Fisher's exact test (two-tailed) and numerical variables were tested with Mann-Whitney test (two-tailed). Abbreviations: aHSCT indicates allogeneic hematopoietic stem cell transplantation; BW body weight; aGvHD acute Graft-versus-Host Disease; cGvHD chronic Graft-versus-Host Disease; PBSC peripheral blood stem cells; RIC reduced intensity conditioning.

	GvL n=14	**noGvL n=11**	**P value**
Gender (female)	6 (43)	7 (64)	0.4280
Age at DLI (years)	46 (22-64)	44.5 (23-64)	0.7355
Disease Details AML	10 (71)	7 (64)	1.0000
Disease risk high/adverse	4 (29)	3 (27)	1.0000
Donor HLA-Matching 10/10	12 (86)	8 (73)	0.6230
Female donor male recipient	2 (14)	3 (27)	0.6230
Donor Age at aHSCT	31 (14-64)	30 (23-64)	0.8400
Graft PBSC	12 (86)	9 (82)	1.0000
Conditioning Regimen RIC	11 (79)	8 (73)	1.0000
aGvHD post aHSCT	3 (21)	3 (27)	1.0000
cGvHD post aHSCT	3 (21)	2 (18)	1.0000
CTx pre DLI	6 (43)	2 (18)	0.2340
First DLI (Months post aHSCT)	12.6 (4.1-75.7)	10.3 (6.5-24.0)	0.5450
Dose 1st DLI (CD3+/kg BW)	5x10E6 (5x10E5-2.5x10E7)	1x10E6 (5x10E5-2.5x10E7)	0.7870
Total Number of DLI	2.5 (1-7)	3 (1-4)	0.9740
aGvHD post DLI	10 (71)	5 (45)	0.2410
cGvHD post DLI	6 (43)	3 (27)	0.6770
Sampling time point from 1st DLI (days)	15.5 (10-136)	14 (13-44)	0.5960

Supplemental Table 5B. Multivariate analysis of difference in TRB CD8$^+$ 1/D (Figure 2B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Numerical variables were categorized for the ANOVA. Abbreviations: Df indicates degrees of freedom for the independent variable; Sum_Sq sum of squares (the total variation between the group means and the overall mean); Mean_Sq mean of the sum of squares (calculated by dividing the sum of squares by the degrees of freedom for each parameter); F_value test statistic from the F test (mean square of each independent variable divided by the mean square of the residuals; the larger the F value, the more likely it is that the variation caused by the independent variable is real and not due to chance); Pr(>F) p-value of the F-statistic.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	10451	10451	8.86	**0.0309**
Gender	1	31	31	0.03	0.8775
Age at DLI	1	645	645	0.55	0.4929
Disease Details (AML vs. other)	1	0	0	0.00	0.9933
Disease risk (high/adverse vs. other)	1	153	153	0.13	0.7331
Donor HLA-Matching (10/10 vs. other)	1	60	60	0.05	0.8306
Female donor male recipient	1	1637	1637	1.39	0.2918
Donor Age Tx	1	2161	2161	1.83	0.2340
Graft (PBSC vs. BM)	1	1830	1830	1.55	0.2681
Conditioning Regimen (RIC vs. myeloablative)	1	367	367	0.31	0.6011
aGvHD post aHSCT	1	631	631	0.54	0.4974
cGvHD post aHSCT	1	4752	4752	4.03	0.1011
CTx pre DLI	1	1800	1800	1.53	0.2717
Months post aHSCT at 1st DLI	1	7	7	0.01	0.9411
Dose of 1st DLI	1	441	441	0.37	0.5675
Total Number of DLI	1	439	439	0.37	0.5684
aGvHD post DLI	1	747	747	0.63	0.4623
cGvHD post DLI	1	855	855	0.73	0.4335
Sampling Days from 1st DLI	1	206	206	0.17	0.6936
Residuals	5	5900	1180		

Supplemental Table 5C. Multivariate analysis of delta number of clones of the top 25% TRB CD8$^+$ repertoire (Figure 3B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	7150	7150	8.60	**0.0326**
Gender	1	366	366	0.44	0.5363
Age at DLI	1	185	185	0.22	0.6570
Disease Details (AML vs. other)	1	92	92	0.11	0.7535
Disease risk (high/adverse vs. other)	1	471	471	0.57	0.4857
Donor HLA-Matching (10/10 vs. other)	1	10	10	0.01	0.9149
Female donor male recipient	1	928	928	1.12	0.3392
Donor Age Tx	1	5514	5514	6.63	0.0498
Graft (PBSC vs. BM)	1	1912	1912	2.30	0.1899
Conditioning Regimen (RIC vs. myeloablative)	1	98	98	0.12	0.7455
aGvHD post aHSCT	1	185	185	0.22	0.6572
cGvHD post aHSCT	1	3417	3417	4.11	0.0985
CTx pre DLI	1	2532	2532	3.05	0.1415
Months post aHSCT at 1st DLI	1	123	123	0.15	0.7166
Dose of 1st DLI	1	712	712	0.86	0.3973
Total Number of DLI	1	726	726	0.87	0.3930
aGvHD post DLI	1	122	122	0.15	0.7178
cGvHD post DLI	1	487	487	0.59	0.4789
Sampling Days from 1st DLI	1	873	873	1.05	0.3527
Residuals	5	4159	832		

Supplemental Table 5D. Multivariate analysis of delta number of clones of the top 50% TRB CD8^{+} repertoire (Figure 3B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	Sum_Sq	Mean_Sq	F_value	Pr(>F)
GvL vs. noGvL	1	9547	9547	7.84	**0.0380**
Gender	1	0	0	0.00	0.9850
Age at DLI	1	284	284	0.23	0.6500
Disease Details (AML vs. other)	1	3	3	0	0.9640
Disease risk (high/adverse vs. other)	1	170	170	0.14	0.7240
Donor HLA-Matching (10/10 vs. other)	1	317	317	0.26	0.6320
Female donor male recipient	1	4161	4161	3.42	0.1240
Donor Age Tx	1	694	694	0.57	0.4840
Graft (PBSC vs. BM)	1	1975	1975	1.62	0.2590
Conditioning Regimen (RIC vs. myeloablative)	1	1066	1066	0.88	0.3920
aGvHD post aHSCT	1	731	731	0.60	0.4740
cGvHD post aHSCT	1	3026	3026	2.48	0.1760
CTx pre DLI	1	4002	4002	3.29	0.1300
Months post aHSCT at 1st DLI	1	1	1	0.00	0.9780
Dose of 1st DLI	1	247	247	0.20	0.6710
Total Number of DLI	1	142	142	0.12	0.7460
aGvHD post DLI	1	654	654	0.54	0.4970
cGvHD post DLI	1	4	4	0.00	0.9580
Sampling Days from 1st DLI	1	3	3	0.00	0.9650
Residuals	5	6091	1218		

Supplemental Table 5E. Multivariate analysis of delta number of clones of the top 75% TRB CD8$^+$ repertoire (Figure 3B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	13105	13105	6.78	**0.0480**
Gender	1	167	167	0.09	0.7808
Age at DLI	1	669	669	0.35	0.5820
Disease Details (AML vs. other)	1	62	62	0.03	0.8647
Disease risk (high/adverse vs. other)	1	1320	1320	0.68	0.4463
Donor HLA-Matching (10/10 vs. other)	1	3	3	0.00	0.9712
Female donor male recipient	1	3097	3097	1.60	0.2615
Donor Age Tx	1	199	199	0.10	0.7613
Graft (PBSC vs. BM)	1	2136	2136	1.11	0.3414
Conditioning Regimen (RIC vs. myeloablative)	1	392	392	0.20	0.6714
aGvHD post aHSCT	1	10928	10928	5.65	0.0634
cGvHD post aHSCT	1	1090	1090	0.56	0.4865
CTx pre DLI	1	4007	4007	2.07	0.2095
Months post aHSCT at 1st DLI	1	682	682	0.35	0.5783
Dose of 1st DLI	1	1588	1588	0.82	0.4064
Total Number of DLI	1	1462	1462	0.76	0.4243
aGvHD post DLI	1	6628	6628	3.43	0.1233
cGvHD post DLI	1	123	123	0.06	0.8112
Sampling Days from 1st DLI	1	1000	1000	0.52	0.5042
Residuals	5	9667	1933		

Supplemental Table 5F. Multivariate analysis of delta number of clones of the whole TRB CD8$^+$ repertoire (Figure 3B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	644	644	0.39	0.5600
Gender	1	20442	20442	12.36	**0.0170**
Age at DLI	1	4172	4172	2.52	0.1732
Disease Details (AML vs. other)	1	23	23	0.01	0.9098
Disease risk (high/adverse vs. other)	1	1876	1876	1.13	0.3356
Donor HLA-Matching (10/10 vs. other)	1	957	957	0.58	0.4813
Female donor male recipient	1	4895	4895	2.96	0.1460
Donor Age Tx	1	7965	7965	4.81	0.0797
Graft (PBSC vs. BM)	1	12085	12085	7.30	**0.0427**
Conditioning Regimen (RIC vs. myeloablative)	1	17996	17996	10.88	**0.0215**
aGvHD post aHSCT	1	107394	107394	64.91	**0.0005**
cGvHD post aHSCT	1	14882	14882	9.00	**0.0301**
CTx pre DLI	1	5697	5697	3.44	0.1227
Months post aHSCT at 1st DLI	1	8104	8104	4.90	0.0778
Dose of 1st DLI	1	11594	11594	7.01	**0.0456**
Total Number of DLI	1	47055	47055	28.44	**0.0031**
aGvHD post DLI	1	24405	24405	14.75	**0.0121**
cGvHD post DLI	1	2566	2566	1.55	0.2682
Sampling Days from 1st DLI	1	2116	2116	1.28	0.3094
Residuals	5	8273	1655		

Supplemental Table 5G. Multivariate analysis of difference in CD8^{+} TRB repertoire occupation by top 20 clones (Figure 4B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	247.24	247.24	19.47	**0.0069**
Gender	1	1.87	1.87	0.15	0.7168
Age at DLI	1	5.06	5.06	0.40	0.5555
Disease Details (AML vs. other)	1	1.13	1.13	0.09	0.7778
Disease risk (high/adverse vs. other)	1	1.45	1.45	0.11	0.7494
Donor HLA-Matching (10/10 vs. other)	1	4.32	4.32	0.34	0.5851
Female donor male recipient	1	58.93	58.93	4.64	0.0838
Donor Age Tx	1	21.64	21.64	1.71	0.2485
Graft (PBSC vs. BM)	1	90.69	90.69	7.14	0.0442
Conditioning Regimen (RIC vs. myeloablative)	1	32.47	32.47	2.56	0.1707
aGvHD post aHSCT	1	18.98	18.98	1.49	0.2760
cGvHD post aHSCT	1	102.74	102.74	8.09	**0.0361**
CTx pre DLI	1	31.41	31.41	2.47	0.1766
Months post aHSCT at 1st DLI	1	3.37	3.37	0.27	0.6284
Dose of 1st DLI	1	9.59	9.59	0.76	0.4247
Total Number of DLI	1	1.82	1.82	0.14	0.7209
aGvHD post DLI	1	34.36	34.36	2.71	0.1609
cGvHD post DLI	1	4.58	4.58	0.36	0.5744
Sampling Days from 1st DLI	1	18.26	18.26	1.44	0.2841
Residuals	5	63.48	12.70		

Supplemental Table 5H. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-50 clones (Figure 4B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	0.47	0.47	0.27	0.6273
Gender	1	5.21	5.21	2.94	0.1469
Age at DLI	1	2.11	2.11	1.19	0.3249
Disease Details (AML vs. other)	1	1.58	1.58	0.90	0.3873
Disease risk (high/adverse vs. other)	1	3.86	3.86	2.19	0.1994
Donor HLA-Matching (10/10 vs. other)	1	1.79	1.79	1.01	0.3601
Female donor male recipient	1	1.74	1.74	0.98	0.3672
Donor Age Tx	1	12.98	12.98	7.34	**0.0423**
Graft (PBSC vs. BM)	1	3.15	3.15	1.78	0.2396
Conditioning Regimen (RIC vs. myeloablative)	1	3.27	3.27	1.85	0.2317
aGvHD post aHSCT	1	103.26	103.26	58.39	**0.0006**
cGvHD post aHSCT	1	32.01	32.01	18.10	**0.0081**
CTx pre DLI	1	11.69	11.69	6.61	**0.0499**
Months post aHSCT at 1st DLI	1	8.69	8.69	4.91	0.0775
Dose of 1st DLI	1	13.00	13.00	7.35	**0.0422**
Total Number of DLI	1	31.37	31.37	17.74	**0.0084**
aGvHD post DLI	1	32.21	32.21	18.22	**0.0080**
cGvHD post DLI	1	4.92	4.92	2.78	0.1561
Sampling Days from 1st DLI	1	15.70	15.70	8.88	**0.0308**
Residuals	5	8.84	1.77		

Supplemental Table 5I. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 51-N clones (Figure 4B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	225.94	225.94	11.77	**0.0186**
Gender	1	0.82	0.82	0.04	0.8440
Age at DLI	1	13.72	13.72	0.71	0.4366
Disease Details (AML vs. other)	1	5.37	5.37	0.28	0.6194
Disease risk (high/adverse vs. other)	1	0.58	0.58	0.03	0.8690
Donor HLA-Matching (10/10 vs. other)	1	11.60	11.60	0.60	0.4722
Female donor male recipient	1	81.04	81.04	4.22	0.0951
Donor Age Tx	1	1.11	1.11	0.06	0.8198
Graft (PBSC vs. BM)	1	59.97	59.97	3.12	0.1374
Conditioning Regimen (RIC vs. myeloablative)	1	15.15	15.15	0.79	0.4151
aGvHD post aHSCT	1	210.60	210.60	10.97	**0.0212**
cGvHD post aHSCT	1	20.00	20.00	1.04	0.3543
CTx pre DLI	1	81.49	81.49	4.24	0.0944
Months post aHSCT at 1st DLI	1	1.23	1.23	0.06	0.8102
Dose of 1st DLI	1	44.89	44.89	2.34	0.1868
Total Number of DLI	1	48.31	48.31	2.52	0.1735
aGvHD post DLI	1	132.99	132.99	6.93	**0.0464**
cGvHD post DLI	1	0.01	0.01	0.00	0.9857
Sampling Days from 1st DLI	1	0.10	0.10	0.01	0.9463
Residuals	5	96.00	19.20		

Supplemental Table 5J. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 20 overlapping clones (Figure 5B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	217.80	217.80	8.91	**0.0306**
Gender	1	1.00	1.00	0.04	0.8505
Age at DLI	1	21.40	21.40	0.88	0.3924
Disease Details (AML vs. other)	1	0.90	0.90	0.04	0.8534
Disease risk (high/adverse vs. other)	1	9.50	9.50	0.39	0.5596
Donor HLA-Matching (10/10 vs. other)	1	4.20	4.20	0.17	0.6941
Female donor male recipient	1	92.20	92.20	3.77	0.1098
Donor Age Tx	1	41.60	41.60	1.70	0.2488
Graft (PBSC vs. BM)	1	389.40	389.40	15.93	**0.0104**
Conditioning Regimen (RIC vs. myeloablative)	1	120.00	120.00	4.91	0.0776
aGvHD post aHSCT	1	121.20	121.20	4.96	0.0765
cGvHD post aHSCT	1	28.10	28.10	1.15	0.3324
CTx pre DLI	1	88.70	88.70	3.63	0.1151
Months post aHSCT at 1st DLI	1	7.90	7.90	0.32	0.5950
Dose of 1st DLI	1	20.20	20.20	0.83	0.4049
Total Number of DLI	1	46.60	46.60	1.91	0.2261
aGvHD post DLI	1	0.00	0.00	0.00	0.9996
cGvHD post DLI	1	1.10	1.10	0.04	0.8426
Sampling Days from 1st DLI	1	7.60	7.60	0.31	0.6018
Residuals	5	122.20	24.40		

Supplemental Table 5K. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-N overlapping clones (Figure 5B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	4.06	4.06	0.30	0.6098
Gender	1	8.08	8.08	0.59	0.4773
Age at DLI	1	16.57	16.57	1.21	0.3218
Disease Details (AML vs. other)	1	38.13	38.13	2.78	0.1563
Disease risk (high/adverse vs. other)	1	2.56	2.56	0.19	0.6836
Donor HLA-Matching (10/10 vs. other)	1	14.62	14.62	1.07	0.3492
Female donor male recipient	1	11.82	11.82	0.86	0.3958
Donor Age Tx	1	80.56	80.56	5.87	0.0599
Graft (PBSC vs. BM)	1	153.12	153.12	11.16	**0.0205**
Conditioning Regimen (RIC vs. myeloablative)	1	26.40	26.40	1.93	0.2240
aGvHD post aHSCT	1	76.78	76.78	5.60	0.0643
cGvHD post aHSCT	1	0.90	0.90	0.07	0.8085
CTx pre DLI	1	3.73	3.73	0.27	0.6242
Months post aHSCT at 1st DLI	1	130.48	130.48	9.51	0.0273
Dose of 1st DLI	1	144.21	144.21	10.51	0.0229
Total Number of DLI	1	183.60	183.60	13.39	0.0146
aGvHD post DLI	1	10.40	10.40	0.76	0.4237
cGvHD post DLI	1	2.17	2.17	0.16	0.7075
Sampling Days from 1st DLI	1	0.70	0.70	0.05	0.8304
Residuals	5	68.58	13.72		

Supplemental Table 5L. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by all overlapping clones (Figure 5B).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	277.61	277.61	14.73	**0.0121**
Gender	1	3.92	3.92	0.21	0.6676
Age at DLI	1	0.46	0.46	0.03	0.8816
Disease Details (AML vs. other)	1	29.11	29.11	1.55	0.2690
Disease risk (high/adverse vs. other)	1	2.90	2.90	0.15	0.7108
Donor HLA-Matching (10/10 vs. other)	1	34.77	34.77	1.85	0.2324
Female donor male recipient	1	36.59	36.59	1.94	0.2222
Donor Age Tx	1	6.97	6.97	0.37	0.5695
Graft (PBSC vs. BM)	1	53.49	53.49	2.84	0.1528
Conditioning Regimen (RIC vs. myeloablative)	1	34.34	34.34	1.82	0.2349
aGvHD post aHSCT	1	5.13	5.13	0.27	0.6242
cGvHD post aHSCT	1	19.46	19.46	1.03	0.3562
CTx pre DLI	1	61.86	61.86	3.28	0.1297
Months post aHSCT at 1st DLI	1	71.71	71.71	3.81	0.1086
Dose of 1st DLI	1	53.44	53.44	2.84	0.1530
Total Number of DLI	1	46.16	46.16	2.45	0.1783
aGvHD post DLI	1	10.82	10.82	0.57	0.4827
cGvHD post DLI	1	7.06	7.06	0.38	0.5672
Sampling Days from 1st DLI	1	13.48	13.48	0.72	0.4363
Residuals	5	94.21	18.84		

Supplemental Table 5M. Multivariate analysis of change of overlapping DLI input CD8^{+} T cell clones (Figure 5F).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	195.20	195.20	31.71	**0.0024**
Gender	1	6.10	6.10	1.00	0.3643
Age at DLI	1	31.50	31.50	5.11	0.0733
Disease Details (AML vs. other)	1	104.80	104.80	17.03	**0.0091**
Disease risk (high/adverse vs. other)	1	289.90	289.90	47.08	**0.0010**
Donor HLA-Matching (10/10 vs. other)	1	12.60	12.60	2.05	0.2119
Female donor male recipient	1	27.70	27.70	4.51	0.0872
Donor Age Tx	1	21.20	21.20	3.44	0.1226
Graft (PBSC vs. BM)	1	546.90	546.90	88.82	**0.0002**
Conditioning Regimen (RIC vs. myeloablative)	1	106.00	106.00	17.22	**0.0089**
aGvHD post aHSCT	1	24.30	24.30	3.94	0.1040
cGvHD post aHSCT	1	133.20	133.20	21.63	**0.0056**
CTx pre DLI	1	14.10	14.10	2.30	0.1901
Months post aHSCT at 1st DLI	1	18.70	18.70	3.03	0.1421
Dose of 1st DLI	1	101.60	101.60	16.51	**0.0097**
Total Number of DLI	1	117.30	117.30	19.05	**0.0073**
aGvHD post DLI	1	24.30	24.30	3.95	0.1036
cGvHD post DLI	1	143.30	143.30	23.27	**0.0048**
Sampling Days from 1st DLI	1	0.30	0.30	0.05	0.8405
Residuals	5	30.80	6.20		

Supplemental Table 5N. Multivariate analysis of change of new DLI input $CD8^+$ T cell clones (Figure 5G).

Shown is the analysis of variance (ANOVA) analysis for all variables from supplemental Table 5A. Abbreviations are explained in supplemental Table 5B.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
GvL vs. noGvL	1	4.50	4.50	7.42	**0.0415**
Gender	1	13.58	13.58	22.38	**0.0052**
Age at DLI	1	23.97	23.97	39.51	**0.0015**
Disease Details (AML vs. other)	1	0.50	0.50	0.82	0.4055
Disease risk (high/adverse vs. other)	1	27.86	27.86	45.92	**0.0011**
Donor HLA-Matching (10/10 vs. other)	1	3.55	3.55	5.84	0.0603
Female donor male recipient	1	1.09	1.09	1.79	0.2384
Donor Age Tx	1	10.15	10.15	16.72	**0.0095**
Graft (PBSC vs. BM)	1	15.36	15.36	25.32	**0.0040**
Conditioning Regimen (RIC vs. myeloablative)	1	0.64	0.64	1.05	0.3521
aGvHD post aHSCT	1	0.52	0.52	0.85	0.3991
cGvHD post aHSCT	1	18.92	18.92	31.19	**0.0025**
CTx pre DLI	1	4.29	4.29	7.07	**0.0450**
Months post aHSCT at 1st DLI	1	49.52	49.52	81.62	**0.0003**
Dose of 1st DLI	1	2.29	2.29	3.78	0.1094
Total Number of DLI	1	9.58	9.58	15.79	**0.0106**
aGvHD post DLI	1	21.56	21.56	35.54	**0.0019**
cGvHD post DLI	1	17.43	17.43	28.73	**0.0030**
Sampling Days from 1st DLI	1	10.15	10.15	16.74	**0.0094**
Residuals	5	3.03	0.61		

Supplemental Table 6A. Univariate comparison of clinical characteristics for the no relapse and relapse subgroup.

Given is the absolute number (%) for categorical variables and the median absolute value (range) for numerical variables. Categorical variables were compared with Fisher's exact test (two-tailed) and numerical variables were tested with Mann-Whitney test (two-tailed). Abbreviations: aHSCT indicates allogeneic hematopoietic stem cell transplantation; BW body weight; aGvHD acute Graft-versus-Host Disease; cGvHD chronic Graft-versus-Host Disease; PBSC peripheral blood stem cells; RIC reduced intensity conditioning.

	noRelapse n=9	**Relapse n=9**	**P value**
Gender (female)	3 (33)	7 (78)	0.1534
Age at DLI (years)	50 (36-63)	36 (23-64)	0.0653
Disease Details AML	5 (56)	7 (78)	0.6199
Disease risk high/adverse	3 (33)	2 (22)	1.0000
Donor HLA-Matching 10/10	8 (89)	7 (78)	1.0000
Female donor male recipient	1 (11)	1 (11)	1.0000
Donor Age at aHSCT	29 (22-58)	31 (14-64)	0.7141
Graft PBSC	9 (100)	7 (78)	0.4706
Conditioning Regimen RIC	6 (67)	6 (67)	1.0000
aGvHD post aHSCT	2 (22)	2 (22)	1.0000
cGvHD post aHSCT	2 (22)	1 (11)	1.0000
CTx pre DLI	5 (56)	3 (33)	0.6372
First DLI (Months post aHSCT)	19.1 (7.9-75.7)	10.3 (4.1-22.0)	0.0625
Dose 1st DLI (CD3+/kg BW)	1x10E7 (5x10E5-1.2x10E7)	5x10E6 (1x10E6-2.5x10E7)	0.9151
Total Number of DLI	2 (1-4)	3 (1-7)	0.2963
aGvHD post DLI	7 (78)	4 (44)	0.3348
cGvHD post DLI	4 (44)	2 (22)	0.6199
Sampling time point from 1st DLI (days)	14 (12-21)	13 (10-35)	0.4167

Supplemental Table 6B. Univariate analysis of clinical variables with Figure 6B-H.

Shown is the univariate analysis for all variables from supplemental Table 6A and numerical variables from Figure 6B-H. Abbreviations are explained in supplemental Table 6A. Statistical analysis was performed with Mann-Whitney test (two-tailed, exact). Variables used for multivariate analysis (supplemental Table 6C-M) are underscored (all no Relapse vs. Relapse values and for all other variables $P < 0.25$).

	Fig. 6B	**Fig. 6D 25%**	**Fig. 6D 50%**	**Fig. 6D 75%**	**Fig. 6D 100%**	**Fig. 6F Top 20**	**Fig. 6F Top 21-50**	**Fig. 6F Top 51-N**	**Fig. 6H Top 20**	**Fig. 6H Top 21-N**	**Fig. 6H Total overlap**
No Relapse vs. Relapse	**0.0142**	**0.0107**	**0.0242**	0.4363	0.8633	**0.0244**	1.0000	0.2581	**0.0503**	0.5613	0.0770
Gender	0.5636	0.3688	0.8239	0.9646	0.1976	0.7558	0.8242	0.8242	0.8940	1.0000	1.0000
Age at DLI	0.7911	0.5318	0.6582	0.7911	0.4268	0.8598	0.6588	1.0000	0.6588	0.8946	0.7239
Disease Details (AML vs. other)	0.9626	0.5697	0.6057	0.3736	0.1012	0.4824	0.1223	0.5427	0.6734	0.3026	0.1744
Disease risk (high/adverse vs. other)	0.6934	0.7271	0.9213	0.7674	0.1148	0.8437	0.7674	0.7674	1.0000	0.9214	0.8437
Donor HLA-Matching (10/10 vs. other)	0.6356	0.2308	0.3423	0.4069	1.0000	0.5536	0.5536	0.4069	0.2361	0.7221	0.4772
Female donor male recipient	0.1820	0.1357	0.0785	0.2324	1.0000	0.2324	0.3612	0.1820	0.1062	0.7253	0.2920
Donor Age at aHSCT	0.2893	0.4215	0.4790	0.5962	0.2893	0.1853	1.0000	0.5365	0.6588	0.5363	0.1853
Graft (PBSC vs. BM)	0.1062	0.2271	0.1394	0.1062	0.8331	0.1062	0.8331	0.1820	0.0579	0.2608	0.1402
Conditioning Regimen (RIC vs. myeloablative)	0.2417	0.5697	0.0825	0.3736	0.8883	0.2061	0.6065	0.4260	0.0351	0.1464	0.1744
aGvHD post aHSCT	0.3667	0.3075	0.2210	0.2220	0.3667	0.6327	0.3667	0.1236	0.3667	0.5590	1.0000
cGvHD post aHSCT	0.6356	0.4015	0.6349	0.6356	1.0000	1.0000	0.6356	1.0000	0.4772	0.1549	1.0000
CTx pre DLI	0.1976	0.3932	0.0680	0.1002	0.5052	0.0832	0.5636	0.1976	0.0295	0.3740	0.1002
First DLI (Months post aHSCT)	0.6588	1.0000	0.2500	0.0934	0.1120	0.3772	0.3772	0.1577	0.3772	0.7572	0.3772
Dose 1st DLI (CD3+/kg BW)	1.0000	0.8582	0.5955	0.7239	0.7239	0.8598	0.9296	0.8598	0.4799	0.2694	0.9296
Total Number of DLI	0.2893	0.4215	0.0927	0.5962	0.5365	0.2510	0.7239	0.4268	0.0774	0.0701	0.2164
aGvHD post DLI	0.6184	0.6469	0.9638	0.8209	0.6836	0.8919	0.5561	0.5561	0.4414	0.2212	0.8209
cGvHD post DLI	0.5121	0.8870	0.4528	0.3993	0.1601	0.4537	1.0000	0.5741	0.5121	0.4822	0.5121
Sampling Days from 1st DLI	1.0000	0.7402	0.9252	0.7787	0.5741	0.6396	0.9254	0.8514	0.8514	0.9253	0.5741

Supplemental Table 6C. Multivariate analysis of difference in TRB CD8$^+$ 1/D (Figure 6B).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations: Df indicates degrees of freedom for the independent variable; Sum_Sq sum of squares (the total variation between the group means and the overall mean); Mean_Sq mean of the sum of squares (calculated by dividing the sum of squares by the degrees of freedom for each parameter); F_value test statistic from the F test (mean square of each independent variable divided by the mean square of the residuals; the larger the F value, the more likely it is that the variation caused by the independent variable is real and not due to chance); Pr(>F) p-value of the F-statistic. P-values < 0.05 are shown in bold.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	8950	8950	10.774	**0.0066**
Female donor male recipient	1	5868	5868	7.063	**0.0209**
Graft (PBSC vs. BM)	1	1105	1105	1.331	0.2712
Conditioning Regimen (RIC vs. myeloablative)	1	4	4	0.005	0.9441
CTx pre DLI	1	225	225	0.270	0.6125
Residuals	12	9969	831		

Supplemental Table 6D. Multivariate analysis of delta number of clones of the top 25% TRB CD8$^+$ repertoire (Figure 6D).

Shown is the analysis of variance (ANOVA) analysis for all variables with $P < 0.25$ from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	8861	8861	12.794	**0.0034**
Donor HLA-Matching (10/10 vs. other)	1	1077	1077	1.556	0.2343
Female donor male recipient	1	4931	4931	7.119	**0.0193**
Graft (PBSC vs. BM)	1	344	344	0.496	0.4937
Residuals	13	9004	693		

Supplemental Table 6E. Multivariate analysis of delta number of clones of the top 50% TRB CD8$^+$ repertoire (Figure 6D).

Shown is the analysis of variance (ANOVA) analysis for all variables with $P < 0.25$ from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	8398	8398	9.440	**0.0133**
Female donor male recipient	1	7798	7798	8.766	**0.0159**
Graft (PBSC vs. BM)	1	334	334	0.376	0.5552
Conditioning Regimen (RIC vs. myeloablative)	1	355	355	0.399	0.5435
aGvHD post aHSCT	1	0	0	0.000	0.9963
CTx pre DLI	1	117	117	0.131	0.7256
First DLI (Months post aHSCT)	1	2320	2320	2.609	0.1407
Total Number of DLI	1	521	521	0.586	0.4637
Residuals	9	8006	890		

Supplemental Table 6F. Multivariate analysis of delta number of clones of the top 75% TRB CD8$^+$ repertoire (Figure 6D).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	3696	3696	2.035	0.1815
Female donor male recipient	1	5992	5992	3.299	0.0966
Graft (PBSC vs. BM)	1	6507	6507	3.582	0.0850
aGvHD post aHSCT	1	2734	2734	1.505	0.2455
CTx pre DLI	1	70	70	0.038	0.8482
First DLI (Months post aHSCT)	1	5983	5983	3.294	0.0969
Residuals	11	19980	1816		

Supplemental Table 6G. Multivariate analysis of delta number of clones of the whole TRB CD8$^+$ repertoire (Figure 6D).

Shown is the analysis of variance (ANOVA) analysis for all variables with $P < 0.25$ from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	9642	9642	0.618	0.4480
Gender (female)	1	49891	49891	3.198	0.1010
Disease Details (AML vs. other)	1	16914	16914	1.084	0.3200
Disease risk (high/adverse vs. other)	1	2932	2932	0.188	0.6730
First DLI (Months post aHSCT)	1	36399	36399	2.334	0.1550
aGvHD post DLI	1	10518	10518	0.674	0.4290
Residuals	11	171583	15598		

Supplemental Table 6H. Multivariate analysis of difference in CD8^{+} TRB repertoire occupation by top 20 clones (Figure 6F).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	210.47	210.47	11.246	**0.0073**
Female donor male recipient	1	105.90	105.90	5.658	**0.0387**
Donor Age at aHSCT	1	53.02	53.02	2.833	0.1233
Graft (PBSC vs. BM)	1	27.96	27.96	1.494	0.2497
Conditioning Regimen (RIC vs. myeloablative)	1	18.92	18.92	1.011	0.3383
CTx pre DLI	1	11.43	11.43	0.611	0.4526
Total Number of DLI	1	12.74	12.74	0.681	0.4286
Residuals	10	187.15	18.72		

Supplemental Table 6I. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 21-50 clones (Figure 6F).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	13.49	13.49	0.735	0.4050
Disease Details (AML vs. other)	1	0.02	0.02	0.001	0.9720
Residuals	15	275.07	18.34		

Supplemental Table 6J. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by top 51-N clones (Figure 6F).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	117.3	117.3	2.803	0.1220
Female donor male recipient	1	124.5	124.5	2.975	0.1120
Graft (PBSC vs. BM)	1	59	59.0	1.409	0.2600
aGvHD post aHSCT	1	56.3	56.3	1.346	0.2710
CTx pre DLI	1	0.1	0.1	0.001	0.9720
First DLI (Months post aHSCT)	1	106.2	106.2	2.538	0.1390
Residuals	11	460.3	41.9		

Supplemental Table 6K. Multivariate analysis of difference in CD8^{+} TRB repertoire occupation by top 20 overlapping clones (Figure 6H).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	200.7	200.7	6.313	**0.0308**
Donor HLA-Matching (10/10 vs. other)	1	55.1	55.1	1.733	0.2174
Female donor male recipient	1	81.2	81.2	2.555	0.1411
Graft (PBSC vs. BM)	1	89.7	89.7	2.822	0.1239
Conditioning Regimen (RIC vs. myeloablative)	1	188.9	188.9	5.943	**0.0350**
CTx pre DLI	1	0.7	0.7	0.023	0.8822
Total Number of DLI	1	0	0.0	0.000	0.9861
Residuals	11	317.9	28.9		

Supplemental Table 6L. Multivariate analysis of difference in CD8^{+} TRB repertoire occupation by top 21-N overlapping clones (Figure 6H).

Shown is the analysis of variance (ANOVA) analysis for all variables with P < 0.25 from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	2.68	2.68	0.094	0.7643
Graft (PBSC vs. BM)	1	25.29	25.29	0.893	0.3650
Conditioning Regimen (RIC vs. myeloablative)	1	83.23	83.23	2.939	0.1145
cGvHD post aHSCT	1	19.89	19.89	0.702	0.4198
Total Number of DLI	1	1.54	1.54	0.054	0.8202
aGvHD post DLI	1	200.3	200.3	7.073	**0.0222**
Residuals	11	311.52	28.32		

Supplemental Table 6M. Multivariate analysis of difference in CD8$^+$ TRB repertoire occupation by all overlapping clones (Figure 6H).

Shown is the analysis of variance (ANOVA) analysis for all variables with $P < 0.25$ from supplemental Table 6B. Abbreviations are explained in supplemental Table 6C.

	Df	**Sum_Sq**	**Mean_Sq**	**F_value**	**Pr(>F)**
No Relapse vs. Relapse	1	153.1	153.1	4.259	0.0660
Disease Details (AML vs. other)	1	170.4	170.4	4.740	0.0545
Donor Age at aHSCT	1	63.9	63.9	1.776	0.2122
Graft (PBSC vs. BM)	1	28.9	28.9	0.805	0.3908
Conditioning Regimen (RIC vs. myeloablative)	1	10.3	10.3	0.285	0.6049
CTx pre DLI	1	11.8	11.8	0.328	0.5792
Total Number of DLI	1	1.3	1.3	0.035	0.8544
Residuals	10	359.6	36.0		

Supplemental Table 7A. Univariate comparison of clinical characteristics for the d+14 post DLI $CD8^+$ expansion vs no expansion subgroup.

Given is the absolute number (%) for categorical variables and the median absolute value (range) for numerical variables. Categorical variables were compared with Fisher's exact test (two-tailed) and numerical variables were tested with Mann-Whitney test (two-tailed). Abbreviations: aHSCT indicates allogeneic hematopoietic stem cell transplantation; BW body weight; aGvHD acute Graft-versus-Host Disease; cGvHD chronic Graft-versus-Host Disease; PBSC peripheral blood stem cells; RIC reduced intensity conditioning.

	Expansion n=13	**no Expansion n=6**	**P value**
Gender (female)	7 (54)	3 (50)	1.000
Age at DLI (years)	50 (29-64)	34.5 (23-46)	0.012
Disease Details AML	8 (62)	5 (83)	0.605
Disease risk high/adverse	3 (23)	3 (50)	0.320
Donor HLA-Matching 10/10	11 (85)	5 (83)	1.000
Female donor male recipient	1 (8)	2 (33)	0.222
Donor Age at aHSCT	31 (22-64)	28 (14-35)	0.145
Graft PBSC	13 (100)	3 (50)	0.021
Conditioning Regimen RIC	9 (69)	4 (67)	1.000
aGvHD post aHSCT	3 (23)	2 (33)	1.000
cGvHD post aHSCT	3 (23)	0 (0)	0.517
CTx pre DLI	6 (46)	2 (33)	1.000
First DLI (Months post aHSCT)	14.2 (6.5-75.7)	10.3 (4.1-16.1)	0.282
Dose 1st DLI (CD3+/kg BW)	1x10E6 (5x10E5-1.2x10E7)	1x10E7 (5x10E6-2.5x10E7)	0.082
Total Number of DLI	3 (1-7)	1 (1-4)	0.186
aGvHD post DLI	8 (62)	3 (50)	1.000
cGvHD post DLI	4 (31)	2 (33)	1.000
Sampling time point from 1st DLI (days)	14 (10-21)	13.5 (13-35)	0.844

Supplemental Table 7B. Results of univariate Cox regression for cumulative incidence of relapse (Figure 7A).

Shown are the results of the univariate Cox regression model for the cumulative incidence of relapse including all variables from supplemental Table 7A which were assessable at d+14 post DLI. Variables with P < 0.25 are shown in bold. Abbreviations are explained in supplemental Table 7A

	Coefficient	**Standard error**	**HR**	**95% CI**		**P value**
				Lower	**Upper**	
CD8+ Expansion at d+14	-1.91	0.68	0.15	0.04	0.56	0.0040
Gender (female)	1.08	0.67	2.93	0.80	10.80	0.1059
Age at DLI (≥41 years)	-1.19	0.64	0.30	0.09	1.06	0.0620
Disease Details (AML)	0.67	0.83	1.95	0.39	9.85	0.4180
Disease risk (high/adverse)	-0.13	0.65	0.88	0.24	3.17	0.8458
Donor HLA-Matching (10/10)	-0.47	0.76	0.62	0.14	2.76	0.5350
Female donor male recipient	0.52	0.79	1.68	0.36	7.89	0.5114
Donor Age at aHSCT (≥30 years)	0.16	0.60	1.18	0.36	3.84	0.7866
Graft (PBSC)	-1.36	0.54	0.26	0.09	0.74	0.0118
Conditioning Regimen (RIC)	-0.06	0.70	0.94	0.24	3.70	0.9315
aGvHD post aHSCT	0.13	0.63	1.14	0.33	3.90	0.8368
cGvHD post aHSCT	-0.64	1.05	0.53	0.07	4.14	0.5444
CTx pre DLI	-0.65	0.67	0.52	0.14	1.95	0.3333
First DLI (≥11 months post aHSCT)	-1.09	0.64	0.34	0.10	1.18	0.0884
Dose 1st DLI (≤5x10E6)	-0.45	0.61	0.64	0.19	2.11	0.4619

Supplemental Table 7C. Results of multivariate Cox regression model for cumulative incidence of relapse (Figure 7A).

Shown are the results of the multivariate Cox regression model for the cumulative incidence of relapse including all variables with $P < 0.25$ from supplemental Table 7B. Cox regression was performed applying stepwise backward elimination. Abbreviations are explained in supplemental Table 7A

	Coefficient	**Standard error**	**HR**	**95% CI**		**P value**
				Lower	**Upper**	
CD8+ Expansion at d+14	-2.17	1.14	0.11	0.01	1.07	0.0570
Gender (female)	0.91	0.54	2.48	0.86	7.15	0.0940
Age at DLI (≥41 years)	-0.38	0.87	0.69	0.13	3.74	0.6600
Graft (PBSC)	0.63	0.70	1.88	0.48	7.37	0.3700
First DLI (≥11 months post aHSCT)	-0.95	0.73	0.39	0.09	1.61	0.1900
CD8+ Expansion at d+14	-2.33	0.92	0.10	0.02	0.59	0.0110
Gender (female)	1.00	0.53	2.73	0.97	7.65	0.0560
Graft (PBSC vs. BM)	0.52	0.76	1.68	0.38	7.40	0.4900
First DLI (≥11 months post aHSCT)	-0.95	0.75	0.39	0.09	1.68	0.2000
CD8+ Expansion at d+14	-2.05	0.77	0.13	0.03	0.58	0.0079
Gender (female)	1.13	0.54	3.11	1.08	8.94	0.0350
First DLI (≥11 months post aHSCT)	-0.67	0.55	0.51	0.17	1.50	0.2200
CD8+ Expansion at d+14	-2.07	0.78	0.13	0.03	0.58	0.0080
Gender (female)	1.25	0.49	3.50	1.33	9.21	0.0110

Supplemental Table 7D. Results of univariate Cox regression for relapse free survival (Figure 7B).

Shown are the results of the univariate Cox regression model for relapse free survival for all variables from supplemental Table 7A assessable at d+14 post DLI. Variables with P < 0.25 are shown in bold. Abbreviations are explained in supplemental Table 7A

	Coefficient	Standard error	HR	95% CI		P value
				Lower	Upper	
CD8+ Expansion at d+14	-1.60	0.67	0.20	0.05	0.76	0.0150
Gender (female)	1.23	0.67	3.41	0.92	12.65	0.0660
Age at DLI (≥41 years)	-1.03	0.62	0.36	0.11	1.21	0.0981
Disease Details (AML)	0.44	0.83	1.55	0.30	7.96	0.5980
Disease risk (high/adverse)	-0.25	0.65	0.78	0.22	2.80	0.7025
Donor HLA-Matching (10/10)	-0.16	0.79	0.85	0.18	4.05	0.8412
Female donor male recipient	0.20	0.83	1.22	0.24	6.17	0.8097
Donor Age at aHSCT (≥30 years)	0.57	0.62	1.78	0.53	5.98	0.3544
Graft (PBSC)	-1.10	0.57	0.33	0.11	1.03	0.0564
Conditioning Regimen (RIC)	-0.47	0.71	0.62	0.16	2.49	0.5035
aGvHD post aHSCT	0.07	0.61	1.08	0.32	3.57	0.9056
cGvHD post aHSCT	-0.51	1.06	0.60	0.07	4.80	0.6293
CTx pre DLI	-0.24	0.68	0.79	0.21	2.97	0.7256
First DLI (≥11 months post aHSCT)	-0.88	0.64	0.41	0.12	1.45	0.1689
Dose 1st DLI (≤5x10E6)	-0.12	0.61	0.89	0.27	2.95	0.8466

Supplemental Table 7E. Results of multivariate Cox regression model for relapse free survival (Figure 7B).

Shown are the results of the multivariate Cox regression model for relapse free survival including all variables with P < 0.25 from supplemental Table 7D. Cox regression was performed applying stepwise backward elimination. Abbreviations are explained in supplemental Table 7A

	Coefficient	**Standard error**	**HR**	**95% CI**		**P value**
				Lower	**Upper**	
CD8+ Expansion at d+14	-1.55	1.12	0.21	0.02	1.91	0.1700
Gender (female)	1.07	0.62	2.90	0.86	9.77	0.0850
Age at DLI (≥41 years)	-1.09	1.08	0.34	0.04	2.77	0.3100
Graft (PBSC)	0.85	0.73	2.33	0.56	9.78	0.2500
First DLI (≥11 months post aHSCT)	-1.08	0.75	0.34	0.08	1.49	0.1500
CD8+ Expansion at d+14	-1.93	0.88	0.15	0.03	0.82	0.0290
Gender (female)	1.19	0.58	3.29	1.05	10.24	0.0400
Graft (PBSC vs. BM)	0.31	0.79	1.36	0.29	6.39	0.6900
First DLI (≥11 months post aHSCT)	-0.68	0.81	0.51	0.10	2.50	0.4000
CD8+ Expansion at d+14	-1.76	0.75	0.17	0.04	0.75	0.0190
Gender (female)	1.27	0.58	3.57	1.15	11.13	0.0280
First DLI (≥11 months post aHSCT)	-0.50	0.59	0.61	0.19	1.93	0.4000
CD8+ Expansion at d+14	-1.74	0.75	0.18	0.04	0.77	0.0210
Gender (female)	1.39	0.54	4.00	1.40	11.43	0.0096