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

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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).

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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. (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).
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 log\(_{10}\)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).
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                  | 1.0              |
| 02         | Cytologic R | FLA-IDA     | 1.4                      | PR               | 23.8                        | 1.2x10E7                | 1.0              |
| 03         | Cytologic R | V-I-PEG-A-Dexa | 1.6                  | RD               | 8.8                         | 1x10E7                  | 1.0              |
| 04         | Molecular R | no          | -                        | -                | 19.1                        | 5x10E5                  | 3                |
| 05         | 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.

| Variable | 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) | 0.2556 | 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 | 0.2608 | 0.1059 | 0.1462 | 0.1744 |
| 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 | 0.8598 | 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.

| Variable                                | 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    | 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       | 0.000   | 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 Lower | 95% CI Upper | P value |
|----------------------|-------------|----------------|-----|--------------|--------------|---------|
| 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

| Term                                      | Coefficient | Standard error | HR    | 95% CI Lower | 95% CI Upper | P value  |
|-------------------------------------------|-------------|----------------|-------|--------------|--------------|----------|
| 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   |

| Term                                      | Coefficient | Standard error | HR    | 95% CI Lower | 95% CI Upper | P value  |
|-------------------------------------------|-------------|----------------|-------|--------------|--------------|----------|
| 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   |

| Term                                      | Coefficient | Standard error | HR    | 95% CI Lower | 95% CI Upper | P value  |
|-------------------------------------------|-------------|----------------|-------|--------------|--------------|----------|
| 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   |

| Term                                      | Coefficient | Standard error | HR    | 95% CI Lower | 95% CI Upper | P value  |
|-------------------------------------------|-------------|----------------|-------|--------------|--------------|----------|
| 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

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

| Variable                                      | Coefficient | Standard error | HR  | 95% CI     | P value |
|-----------------------------------------------|-------------|----------------|-----|------------|---------|
| 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  |