# Comparative evaluation of biological human leukocyte antigen DPB1 mismatch models for survival and graft-*versus*-host disease prediction after unrelated donor hematopoietic cell transplantation

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*doi:10.3324/haematol.2019.225177*

## Clinical endpoints definitions and statistical methods.

Acute GvHD (aGvHD) and chronic GvHD (cGvHD) were defined and scored according to the Glucksberg and Seattle criteria, respectively[1-2]. NRM was defined as death from any cause while in continuous remission of the primary disease. OS was defined as the interval from HSCT to death from any cause. GRFS events were defined as grade 3–4 acute GVHD, extensive chronic GVHD, disease relapse, or death from any cause after HSCT[3]. Actuarial probabilities were determined at 3 years. Baseline characteristics among groups were compared using the Chi-square test for categorical variables, while the distribution of continuous variables was compared using the Mann-Whitney U test. The probabilities of OS and GRFS were estimated using the Kaplan-Meyer estimator and groups were compared by the log-rank test[4-5]. Cumulative incidences (CI) were estimated for GvHD, NRM and relapse to accommodate competing risks, and tests of equality across groups were performed according to Gray[6-7]. Relapse was a competing risk for NRM, death from any cause was a competing risk for relapse. Both relapse and death from any causes were competing risks for GvHD. Multivariate analysis were built to test the independent prognostic value of DPB1 mismatch permissiveness: each DPB1 mismatch model was the main effect term and was held in all steps of model building. Cox proportional hazard models were adopted for OS and GRFS[8], while Fine-Gray proportional hazard regression models for competing events were adopted for aGvHD, cGvHD, relapse and NRM. Covariates included: patient age, disease phase, HCT-CI, female donor to male recipient, host-donor CMV serostatus, conditioning intensity, stem cell source, ATG use, HLA-matching on 5 loci (HLA-A, -B, -C, -DRB1 and –DQB1), center effect (>10 HSCT performed each year Vs ≤10). Interactions between each covariate and each DPB1 mismatch model were tested and not found. In particular, no interaction was found between HLA matching on 5 loci and each model. The proportional hazard assumption was met for all variables. The type I error was fixed at 0.05. Statistical analyses were performed with R version 3.3.3 (R Development Core Team, Vienna, Austria).

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**Supplemental Table 1a.** Patient, donor and transplant characteristics in DPB1 typed or non-typed cases.

| | **Non-DPB1 typed (N=582)** | **DPB1 typed (N=422)** | **p** |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.1 (0.3-6.1) | 3.2 (0.3-6.2) | 0.7 |
| **HSCT year, median (range)** | 2014 (2012-2015) | 2013 (2012-2015) | 0.001 |
| **Patient age, years, median (range)** | 51 (18-69) | 49 (18-71) | 0.003 |
| **Patient gender, male, n** | 345 | 245 | 0.7 |
| **Type of diagnosis, n** | | | 0.2 |
| AML or ALL | 308 | 232 | |
| MDS or MPN | 127 | 69 | |
| Lymphoma or Myeloma | 138 | 109 | |
| CLL | 9 | 12 | |
| **Disease status at HSCT, n** | | | 0.3 |
| Early | 293 | 191 | |
| Intermediate | 135 | 114 | |
| Advanced | 145 | 105 | |
| **HCT-CI score, median (range)** | 1 (0-7) | 1 (0-7) | 0.1 |
| **Karnofsky PS, median (range)** | 90% (40-100) | 90% (50-100) | 0.4 |
| **Donor age, years, median (range)** | 28 (18-57) | 29 (18-57) | 0.6 |
| **Donor gender, male, n** | 415 | 306 | 0.7 |
| **Female donor/male recipient, n** | 97 | 61 | 0.3 |
| **Host/donor CMV serostatus, n** | | | 0.3 |
| Pos/pos | 206 | 156 | |
| Pos/neg | 266 | 167 | |
| Neg/pos | 38 | 36 | |
| Neg/neg | 72 | 53 | |
| **Type of conditioning, n** | | | 0.3 |
| MAC | 390 | 296 | |
| RIC | 192 | 126 | |
| **Source of stem cells, n** | | | 0.1 |
| PB | 492 | 342 | |
| BM | 90 | 80 | |
| **ATG-based GvHD prophylaxis, n** | 476 | 350 | 0.6 |

**Supplemental Table 1b.** Univariate analysis for transplant outcomes in DPB1 typed or non-typed cases.[1]

| | **3-y OS** | **3-y GRFS** | **3-y Relapse** | **3-y NRM** | **100-d aGvHD≥2** | **100-d aGvHD≥3** | **3-y cGvHD** | **3-y ext cGvHD** |
|---|---|---|---|---|---|---|---|---|
| **DPB1 typing** | | | | | | | | |
| DPB1 typed (n=422) | 52 (46-56) | 32 (27-36) | 30 (25-35) | 27 (23-31) | 21 (17-25) | 7 (5-10) | 28 (24-32) | 9 (6-12) |
| Non-DPB1 typed (N=582) | 56 (52-61) | 35 (31-39) | 34 (30-38) | 23 (20-29) | 22 (18-25) | 7 (5-10) | 27 (23-30) | 9 (6-11) |
| p | 0.15 | 0.45 | 0.08 | 0.08 | 0.60 | 0.85 | 0.68 | 0.80 |

[1] shown are mean percentages (range in parenthesis) for each outcome.

**Supplemental Table 2.** Patient, donor and transplant characteristics in permissive and non permissive DPB1 mismatched pairs according to the **TCE3 model**

| | **Permissive (N=208)** | **Non-permissive (N=174)** | **p** |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.4 (0.3-6) | 3.1 (0.3-6) | 0.28 |
| **HSCT year, median (range)** | 2013 (2012-2015) | 2013 (2012-2015) | 0.12 |
| **Patient age, years, median (range)** | 48 (18-71) | 50 (19-66) | 0.49 |
| **Patient gender, male, n** | 101 | 117 | 0.72 |
| **Type of diagnosis, n** | | | 0.16 |
| AML or ALL | 121 | 85 | |
| MDS or MPN | 35 | 32 | |
| Lymphoma and Myeloma | 52 | 57 | |
| **Disease status at HSCT, n** | | | 0.43 |
| Early | 100 | 74 | |
| Intermediate | 54 | 45 | |
| Advanced | 54 | 55 | |
| **HCT-CI score, median (range)** | 0 (0-7) | 1 (0-5) | 0.97 |
| **Karnofsky PS, median (range)** | | | 0.39 |
| **Donor age, years, median (range)** | 27 (19-55) | 30 (20-56) | 0.23 |
| **Donor gender, male, n** | 149 | 126 | 0.87 |
| **Female donor/male recipient, n** | 28 | 29 | 0.38 |
| **Host/donor CMV serostatus, n** | 90% (60-100) | 90% (50-100) | 0.35 |
| Pos/pos | 71 | 71 | |
| Pos/neg | 81 | 71 | |
| Neg/pos | 19 | 11 | |
| Neg/neg | 31 | 19 | |
| **Type of conditioning, n** | | | 0.58 |
| MAC | 150 | 121 | |
| RIC | 58 | 53 | |
| **Source of stem cells, n** | | | 0.01 |
| PB | 179 | 132 | |
| BM | 29 | 42 | |
| **ATG-based GvHD prophylaxis, n** | 189 | 156 | 0.69 |

**Supplemental Table 3.** Patient, donor and transplant characteristics in in permissive and non permissive DPB1 mismatched pairs according to the **TCE4 model**

| | Permissive (N=135) | Non-permissive (N=247) | p |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.4 (0.3-6) | 3.3 (0.3-6) | 0.17 |
| **HSCT year, median (range)** | 2014 (2012-2015) | 2013 (2012-2015) | 0.45 |
| **Patient age, years, median (range)** | 48 (18-68) | 49 (19-71) | 0.46 |
| **Patient gender, male, n** | 80 | 138 | 0.52 |
| **Type of diagnosis, n** | | | 0.86 |
| AML or ALL | 75 | 131 | |
| MDS or MPN | 22 | 45 | |
| Lymphoma or Myeloma | 38 | 71 | |
| **Disease status at HSCT, n** | | | 0.80 |
| Early | 62 | 112 | |
| Intermediate | 37 | 62 | |
| Advanced | 36 | 73 | |
| **HCT-CI score, median (range)** | 0 (0-7) | 1 (0-5) | 0.96 |
| **Karnofsky PS, median (range)** | 90% (70-100) | 90% (50-100) | 0.77 |
| **Donor age, years, median (range)** | 29 (19-55) | 28 (19-56) | 0.68 |
| **Donor gender, male, n** | 94 | 181 | 0.45 |
| **Female donor/male recipient, n** | 23 | 34 | 0.39 |
| **Host/donor CMV serostatus, n** | | | 0.35 |
| Pos/pos | 50 | 92 | |
| Pos/neg | 51 | 101 | |
| Neg/pos | 15 | 15 | |
| Neg/neg | 16 | 34 | |
| **Type of conditioning, n** | | | 0.86 |
| MAC | 95 | 176 | |
| RIC | 40 | 71 | |
| **Source of stem cells, n** | | | 0.03 |
| PB | 118 | 193 | |
| BM | 17 | 54 | |
| **ATG-based GvHD prophylaxis, n** | 127 | 230 | 0.13 |

**Supplemental Table 4.** Patient, donor and transplant characteristics in in permissive and non-permissive DPB1 mismatched pairs according to the **ΔFD model**[1]

| | **<2.665 (N=259)** | **≥2.665 (N=123)** | **p** |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.5 (0.3-6) | 2.9 (0.3-5) | 0.12 |
| **HSCT year, median (range)** | 2013 (2012-2015) | 2014 (2012-2015) | 0.97 |
| **Patient age, years, median (range)** | 48 (18-71) | 52 (19-66) | 0.48 |
| **Patient gender, male, n** | 155 | 63 | 0.11 |
| **Type of diagnosis, n** | | | 0.59 |
| AML or ALL | 144 | 62 | |
| MDS or MPN | 45 | 22 | |
| Lymphoma or Myeloma | 70 | 39 | |
| **Disease status at HSCT, n** | | | 0.78 |
| Early | 120 | 54 | |
| Intermediate | 68 | 31 | |
| Advanced | 71 | 38 | |
| **HCT-CI score, median (range)** | 0 (0-7) | 1 (0-6) | 0.38 |
| **Karnofsky PS, median (range)** | 90% (60-100) | 90% (50-100) | 0.25 |
| **Donor age, years, median (range)** | 28 (19-56) | 30 (20-52) | 0.98 |
| **Donor gender, male, n** | 184 | 91 | 0.55 |
| **Female donor/male recipient, n** | 40 | 17 | 0.68 |
| **Host/donor CMV serostatus, n** | | | 0.60 |
| Pos/pos | 93 | 49 | |
| Pos/neg | 105 | 47 | |
| Neg/pos | 23 | 7 | |
| Neg/neg | 32 | 18 | |
| **Type of conditioning, n** | | | 0.59 |
| MAC | 186 | 85 | |
| RIC | 73 | 38 | |
| **Source of stem cells, n** | | | 0.15 |
| PB | 216 | 95 | |
| BM | 43 | 28 | |
| **ATG-based GvHD prophylaxis, n** | 233 | 112 | 0.74 |

[1] shown are data for cut-off 2.665; data for cut-off 1.64 were not significantly different.

**Supplemental Table 5.** Patient, donor and transplant characteristics in in low risk and high risk DPB1 mismatched pairs according to the **Expression model**

| | **Low risk (N=153)** | **High risk (N=76)** | **p** |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.5 (0.3-6) | 3.3 (0.3-6) | 0.59 |
| **HSCT year, median (range)** | 2013 (2012-2015) | 2013 (2012-2015) | 0.31 |
| **Patient age, years, median (range)** | 49 (18-71) | 49 (19-68) | 0.98 |
| **Patient gender, male, n** | 93 | 45 | 0.82 |
| **Type of diagnosis, n** | | | 0.68 |
| AML or ALL | 80 | 44 | |
| MDS or MPN | 27 | 13 | |
| Lymphoma or Myeloma | 46 | 19 | |
| **Disease status at HSCT, n** | | | 0.94 |
| Early | 71 | 37 | |
| Intermediate | 39 | 19 | |
| Advanced | 43 | 20 | |
| **HCT-CI score, median (range)** | 1 (0-6) | 0 (0-7) | 0.26 |
| **Karnofsky PS, median (range)** | 90% (50-100) | 90% (70-100) | 0.49 |
| **Donor age, years, median (range)** | 28 (19-56) | 29 (19-54) | 0.19 |
| **Donor gender, male, n** | 105 | 53 | 0.86 |
| **Female donor/male recipient, n** | 28 | 12 | 0.64 |
| **Host/donor CMV serostatus, n** | | | 0.47 |
| Pos/pos | 62 | 24 | |
| Pos/neg | 53 | 33 | |
| Neg/pos | 13 | 5 | |
| Neg/neg | 21 | 12 | |
| **Type of conditioning, n** | | | 0.73 |
| MAC | 112 | 54 | |
| RIC | 41 | 22 | |
| **Source of stem cells, n** | | | 0.09 |
| PB | 129 | 57 | |
| BM | 24 | 19 | |
| **ATG-based GvHD prophylaxis, n** | 136 | 72 | 0.15 |

**Supplemental Table 6.** Patient, donor and transplant characteristics in low risk or high risk DPB1 mismatched pairs according to the **DP2/DP5 model**

| | **DP2 (N=118)** | **DP5 (N=31)** | **p** |
|---|---|---|---|
| **Median follow-up for survivors, years (range)** | 3.4 (0.3-6.2) | 2.8 (0.3-6.1) | 0.39 |
| **HSCT year, median (range)** | 2013 (2012-2015) | 2013 (2012-2015) | 0.74 |
| **Patient age, years, median (range)** | 49 (18-69) | 45 (19-66) | 0.16 |
| **Patient gender, male, n** | 74 | 20 | 0.85 |
| **Type of diagnosis, n** | | | 0.67 |
| AML or ALL | 58 | 18 | |
| MDS or MPN | 22 | 5 | |
| Lymphoma or Myeloma | 38 | 8 | |
| **Disease status at HSCT, n** | | | 0.83 |
| Early | 57 | 14 | |
| Intermediate | 28 | 9 | |
| Advanced | 33 | 8 | |
| **HCT-CI score, median (range)** | 1 (0-6) | 1 (0-5) | 0.58 |
| **Karnofsky PS, median (range)** | 90% (50-100) | 90% (70-100) | 0.98 |
| **Donor age, years, median (range)** | 28 (19-56) | 29 (23-54) | 0.09 |
| **Donor gender, male, n** | 84 | 22 | 0.98 |
| **Female donor/male recipient, n** | 20 | 4 | 0.41 |
| **Host/donor CMV serostatus, n** | | | 0.35 |
| Pos/pos | 48 | 8 | |
| Pos/neg | 37 | 14 | |
| Neg/pos | 11 | 2 | |
| Neg/neg | 18 | 6 | |
| **Type of conditioning, n** | | | 0.07 |
| MAC | 91 | 19 | |
| RIC | 27 | 12 | |
| **Source of stem cells, n** | | | 0.39 |
| PB | 96 | 24 | |
| BM | 22 | 7 | |
| **ATG-based GvHD prophylaxis, n** | 104 | 29 | 0.39 |

**Supplemental Table 7.** Univariate analysis for transplant outcomes and different models of DPB1 mismatch permissivity.[1]

| | **3-y OS** | **3-y GRFS** | **3-y Relapse** | **3-y NRM** | **100-d aGvHD≥2** | **100-d aGvHD≥3** | **3-y cGvHD** | **3-y ext cGvHD** |
|---|---|---|---|---|---|---|---|---|
| **DPB1 allele matching status** | | | | | | | | |
| Matched (n=40) | 43 (26-59) | 34 (20-49) | 38 (23-54) | 26 (13-40) | 0 | 0 | 18 (8-31) | 5 (1-16) |
| Mismatched (n=382) | 53 (47-58) | 32 (27-37) | 29 (24-34) | 27 (22-31) | 23 (19-27) | 8 (6-11) | 29 (24-33) | 9 (7-13) |
| p | 0.81 | 0.68 | 0.16 | 0.81 | **<0.01** | **0.05** | 0.10 | 0.35 |
| **TCE3** | | | | | | | | |
| Permissive mismatch (n= 208) | 53 (46-60) | 33 (26-40) | 30 (24-37) | 26 (20-32) | 22 (16-28) | 7 (4-11) | 27 (21-33) | 6 (4-10) |
| Non Permissive mismatch (n=174) | 52 (44-60) | 30 (23-38) | 27 (20-34) | 28 (21-35) | 24 (18-31) | 9 (6-14) | 31 (24-38) | 13 (8-19) |
| p | 0.50 | 0.35 | 0.64 | 0.43 | 0.48 | 0.57 | 0.31 | **0.03** |
| **TCE4** | | | | | | | | |
| Permissive mismatch (n=135) | 60 (51-68) | 36 (28-45) | 30 (22-38) | 21 (15-29) | 21 (15-29) | 7 (3-12) | 26 (19-34) | 4 (2-9) |
| Non Permissive mismatch (n=247) | 49 (42-55) | 29 (24-35) | 28 (22-34) | 30 (24-36) | 24 (19-29) | 9 (5-12) | 30 (25-37) | 12 (8-17) |
| p | **0.05** | **0.04** | 0.96 | 0.09 | 0.56 | 0.58 | 0.3 | **0.01** |
| **ΔFD** | | | | | | | | |
| <2.65 (n=259) | 54 (47-60) | 31 (26-38) | 28 (23-34) | 27 (22-33) | 23 (18-28) | 8 (5-12) | 28 (23-34) | 9 (6-13) |
| ≥2.65 (n=123) | 51 (41-60) | 32 (24-41) | 30 (22-39) | 25 (18-33) | 23 (16-31) | 7 (4-13) | 29 (21-38) | 10 (6-17) |
| p | 0.83 | 0.71 | 0.57 | 0.71 | 0.90 | 0.65 | 0.88 | 0.75 |
| **Expression model** | | | | | | | | |
| low risk (n=153) | 56 (47-63) | 27 (20-35) | 34 (26-42) | 23 (17-30) | 16 (10-22) | 5 (2-9) | 29 (22-36) | 9 (5-14) |
| high risk (n=76) | 57 (45-68) | 39 (28-50) | 23 (14-34) | 26 (16-36) | 32 (22-43) | 9 (4-17) | 34 (24-45) | 12 (6-20) |
| p | 0.95 | 0.23 | 0.23 | 0.81 | **<0.01** | 0.32 | 0.30 | 0.42 |
| **DP2/DP5 model** | | | | | | | | |
| low risk (n=118) | 59 (49-67) | 29 (21-38) | 27 (19-36) | 25 (17-33) | 15 (9-22) | 4 (2-9) | 32 (24-41) | 11 (6-17) |
| high risk (n=31) | 62 (42-77) | 39 (21-56) | 31 (15-49) | 23 (10-40) | 43 (25-60) | 20 (8-36) | 26 (12-42) | 16 (6-31) |
| p | 0.76 | 0.47 | 0.62 | 0.80 | **0.001** | **0.01** | 0.67 | 0.32 |

[1] shown are mean percentages (range in parenthesis) for each outcome.

**Supplemental Table 8. Multivariate analysis of clinical factors associated with HCT outcomes.**

| | **OS** | **GRFS** | **Relapse** | **NRM** | **aGvHD≥2** | **aGvHD≥3** | **cGvHD** | **Ext cGvHD** |
|---|---|---|---|---|---|---|---|---|
| | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p | HR (95% CI) p |
| **TCE4[1]: NP Vs P** | **1.7 (1.1-2.4) 0.008** | **1.4 (1.1-1.9) 0.01** | 1.1 (0.7-1.7) 0.7 | **1.9 (1.1-3.2) 0.01** | 1.3 (0.8-2.1) 0.2 | 1.5 (0.7-3.2) 0.3 | **1.7 (1.1-2.6) 0.02** | **3.6 (1.4-9.5) 0.01** |
| **Matched Vs P** | **2.1 (1.2-3.7) 0.01** | 1.5 (0.9-2.4) 0.09 | **2 (1.1-3.7) 0.03** | 2 (0.9-4.8) 0.09 | Not applicable[2] | Not applicable[2] | 0.8 (0.3-2) 0.6 | 0.9 (0.1-7.5) 0.9 |
| **Disease status: Intermediate Vs Early** | 1.4 (0.9-2.1) 0.09 | 1.3 (0.9-1.8) 0.1 | 1.5 (0.9-2.5) 0.09 | 1.6 (0.9-2.7) 0.09 | 1.1 (0.6-1.9) 0.7 | 0.7 (0.3-1.7) 0.4 | 1.1 (0.7-1.8) 0.6 | 2.4 (0.9-5.5) 0.09 |
| **Advanced Vs early** | **2.3 (1.6-3.3) $<10^{-3}$** | **1.5 (1.1-2) 0.01** | **2 (1.2-3.2) 0.005** | **1.9 (1.2-3.3) 0.01** | 0.7 (0.4-1.3) 0.3 | 0.6 (0.2-1.6) 0.3 | 1 (0.6-1.7) 0.9 | 1.2 (0.4-3.2) 0.7 |
| **Patient age** | 1 (0.9-1.1) 0.2 | 1 (0.9-1.1) 0.2 | 1 (0.9-1.1) 0.3 | 1 (0.9-1.1) 0.2 | 1 (0.9-1.1) 0.4 | 1 (0.9-1.1) 0.9 | 1 (0.9-1.1) 0.1 | 1 (0.9-1.1) 0.9 |
| **HCTI-Score: ≥1 Vs 0** | 1.3 (0.9-1.9) 0.09 | **1.4 (1.1-1.9) 0.008** | 1.1 (0.7-1.6) 0.7 | **1.6 (1.1-2.5) 0.04** | 1.2 (0.7-1.9) 0.5 | 1.5 (0.7-3.1) 0.3 | **2.2 (1.4-3.4) $<10^{-3}$** | **2.2 (1-5) 0.05** |
| **Female donor to male recipient** | 1.1 (0.7-1.8) 0.6 | 1.3 (0.9-1.1) 0.2 | 1.1 (0.6-2.1) 0.6 | 1.1 (0.6-2) 0.8 | 0.6 (0.3-1.3) 0.2 | 0.8 (0.3-2.3) 0.6 | 1.2 (0.7-2.1) 0.4 | 2.4 (1.1-5.4) 0.04 |
| **CMV status: neg/neg Vs other** | 0.7 (0.4-1.2) 0.2 | 0.9 (0.6-1.4) 0.7 | 0.6 (0.3-1.3) 0.2 | 0.8 (0.4-1.7) 0.6 | 1.1 (0.5-2.1) 0.9 | 1.3 (0.5-3.6) 0.6 | 1 (0.5-2) 0.9 | 1 (0.4-2.8) 0.9 |
| **Conditioning: MAC Vs RIC** | 1.3 (0.9-1.9) 0.1 | 1.1 (0.8-1.5) 0.5 | 1 (0.6-1.6) 0.9 | 1.3 (0.8-2.1) 0.4 | 1.4 (0.8-2.4) 0.2 | 1.9 (0.7-5.1) 0.2 | 1.1 (0.7-1.7) 0.8 | 0.5 (0.2-1.1) 0.08 |
| **Stem cell source: PB Vs BM** | 1.1 (0.7-1.6) 0.8 | 1.1 (0.8-1.6) 0.6 | 1 (0.6-1.7) 0.9 | 1.1 (0.6-1.9) 0.8 | 1.4 (0.7-2.7) 0.3 | 2.4 (0.7-8.4) 0.2 | 0.8 (0.4-1.3) 0.3 | 0.6 (0.2-1.7) 0.4 |
| **ATG use** | 1.2 (0.5-2.7) 0.7 | 0.9 (0.5-1.7) 0.8 | 2.6 (0.6-11) 0.2 | 1 (0.3-2.8) 0.9 | 0.5 (0.2-1.4) 0.2 | 0.4 (0.1-1.4) 0.1 | 1 (0.4-2.4) 0.9 | 0.9 (0.2-3.2) 0.8 |
| **Overall HLA-matching: 9/10 Vs 10/10** | 1.8 (1-3.3) 0.06 | 1.1 (0.7-1.7) 0.6 | 2 (0.9-4.2) 0.07 | 1.5 (0.7-3.3) 0.3 | 1.4 (0.6-3) 0.5 | 1.2 (0.4-4.1) 0.8 | 0.8 (0.4-1.4) 0.4 | 1.5 (0.3-6.6) 0.6 |
| **Center effect: ≥10 HCT/year Vs <10** | 0.9 (0.7-1.3) 0.7 | 1 (0.7-1.3) 0.8 | 0.8 (0.5-1.3) 0.4 | 0.9 (0.5-1.4) 0.6 | 0.9 (0.6-1.6) 0.9 | 0.7 (0.3-1.5) 0.3 | 1.1 (0.7-1.7) 0.7 | 1.9 (0.8-4.6) 0.2 |

[1] TCE4 NP, P and matched: N= 247, 135 and 40, respectively.
[2] Not applicable since no cases of aGvHD occurred in the DPB1 matched cohort.
Shown are the data for the TCE4 functional model as main effect term and covariates as described in Statistical methods.