**Table S1. Patients, donors and transplant characteristics of the overall cohort.**

| | **Entire population (n=509)** | **Subgroup with HLA allele level (n=418)** |
|---|---|---|
| Patient age y, median (range) | 45 (18 – 78) | 45 (18 – 78) |
| Patient sex, male (%) | 292 (57%) | 241 (58%) |
| Time from diagnosis to transplant, months, median (range) | 10 (2 – 192) | 10 (2 – 192) |
| AML/ALL, n (%) | 373 (73%)/136 (27%) | 312 (75%)/106 (25%) |
| Disease status at transplant, n (%) | | |
| CR1 | 182 (36%) | 145 (35%) |
| CR≥2 | 137 (27%) | 113 (27%) |
| Advanced (Primary induction failure, Relapse) | 190 (37%) | 160 (38%) |
| Cytogenetic risk stratification, n (%)* | | |
| AML: | | |
| Favorable: t(8;21)(q22;q22); RUNX1-RUNX1T1<br>inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB-MYH11<br>Mutated NPM1 without FLT3-ITD (normal karyotype)<br>Mutated CEBPA (normal karyotype) | 34 (12%) | 27 (11%) |
| Intermediate I: Mutated NPM1 and FLT3-ITD (normal karyotype)<br>Wild-type NPM1 and FLT3-ITD (normal karyotype)<br>Wild-type NPM1 without FLT3-ITD (normal karyotype) | 138 (47%) | 117 (46%) |
| Intermediate II: t(9;11)(p22;q23); MLLT3-MLL<br>Cytogenetic abnormalities not classified as favorable or Adverse | 52 (18%) | 46 (18%) |
| Adverse: inv(3)(q21q26.2) or t(3;3)(q21;q26.2); RPN1-EVI1<br>t(6;9)(p23;q34); DEK-NUP214<br>t(v;11)(v;q23); MLL rearranged<br>5 or del(5q); -7; abnl(17p); complex karyotype | 68 (23%) | 63 (25%) |
| ALL: | | |
| Standard | 38 (42%) | 31 (42%) |
| Poor: complex (>5 abn), t(9;22), t(4;11), t(8;14), hypodiploid | 52 (58%) | 42 (58%) |
| Donor age y, median (range) | 38 (12 – 74) | 39 (12 – 74) |
| Donor sex, male (%) | 271 (53%) | 225 (54%) |
| Female donor/male recipient, n (%) | 134 (26%) | 111 (27%) |
| CMV serostatus, donor/patient, n (%) | | |
| Negative/negative | 57 (11%) | 49 (12%) |
| Other combinations | 452 (89%) | 369 (88%) |
| Intensity of conditioning regimen, n (%) | | |
| RIC | 265 (52%) | 219 (52%) |
| MAC | 244 (48%) | 199 (48%) |
| Donor stem cell source, n (%) | | |
| PB | 309 (61%) | 250 (60%) |
| BM | 200 (39%) | 168 (40%) |
| GvHD prophylaxis regimen details: | | |
| PTCy | 313 (61%) | 258 (62%) |
| ATG | 196 (39%) | 160 (38%) |
| **HLA A locus:** | **Ag mismatch:** 430 (84%)<br>**Ag match:** 79 (16%) | **All mismatch:** 379 (90%)<br>**All match:** 39 (10%) |
| **HLA B locus:** | **Ag mismatch:** 454 (89%)<br>**Ag match:** 55 (11%) | **All mismatch:** 383 (91%)<br>**All match:** 35 (9%) |
| **HLA C locus:** | **Ag mismatch:** 417 (82%)<br>**Ag match:** 92 (18%) | **All mismatch:** 374 (89%)<br>**All match:** 44 (11%) |
| **HLA DRB1 locus:** | **Ag mismatch:** 418 (82%)<br>**Ag match:** 91 (18%) | **All mismatch:** 383 (91%)<br>**All match:** 35 (9%) |

**Table S2. Univariate analysis of outcome according to HLA matching status.**

**PTCy regimens**

| | 60-d PMN> 500/mm3 | 100-d aGvHD ≥2 | 2-y cGvHD | 2-y Ext cGvHD | 2-y TRM | 2-y Relapse | 2-y OS | 2-y LFS |
|---|---|---|---|---|---|---|---|---|
| HLA-A antigenic match | 94 [82 – 98] | 40 [27 – 53] | 27 [15 – 40] | 12 [5 – 23] | 31 [19 – 44] | 32 [19 – 45] | 40 [26 – 53] | 36 [23 – 50] |
| HLA-A antigenic mismatch | 95 [91 – 97] | 29 [24 – 35] | 28 [22 – 34] | 16 [7 – 15] | 27 [21 – 33] | 33 [27 – 39] | 45 [38 – 51] | 40 [33 – 46] |
| **p** | 0.50 | 0.12 | 0.94 | 0.76 | 0.37 | 0.89 | 0.38 | 0.50 |
| HLA-A allelic match | 92 [70 – 98] | 35 [18 – 52] | 27 [12 – 46] | 16 [5 – 32] | 17 [6 – 33] | 28 [13 – 46] | 56 [36 – 72] | 53 [33 – 69] |
| HLA-A allelic mismatch | 95 [90 – 97] | 28 [22 – 34] | 27 [21 – 34] | 12 [8 – 17] | 28 [22 – 34] | 34 [27 – 40] | 42 [35 – 49] | 37 [30 – 44] |
| **p** | 0.49 | 0.45 | 0.96 | 0.63 | 0.35 | 0.36 | 0.42 | 0.48 |
| HLA-B antigenic match | 94 [76 – 98] | 42 [26 – 58] | 22 [10 – 38] | 10 [2 – 23] | 16 [5 – 30] | 34 [18 – 50] | 58 [38 – 73] | 49 [30 – 65] |
| HLA-B antigenic mismatch | 95 [91 – 97] | 30 [24 – 53] | 28 [23 – 34] | 11 [8 – 16] | 29 [23 – 35] | 32 [26 – 38] | 42 [36 – 48] | 38 [32 – 44] |
| **p** | 0.70 | 0.08 | 0.53 | 0.79 | 0.08 | 0.95 | 0.11 | 0.16 |
| HLA-B allelic match | 94 [71 – 99] | 38 [16 – 60] | 17 [4 – 39] | 12 [2 – 32] | 17 [4 – 39] | 22 [7 – 44] | 57 [30 – 77] | 58 [31 – 78] |
| HLA-B allelic mismatch | 94 [90 – 97] | 28 [22 – 34] | 28 [22 – 34] | 12 [8 – 17] | 27 [21 – 33] | 34 [28 – 40] | 43 [36 – 50] | 38 [31 – 45] |
| **p** | 0.61 | 0.27 | 0.43 | 0.99 | 0.35 | 0.36 | 0.28 | 0.18 |
| HLA-C antigenic match | 92 [79 – 97] | 33 [20 – 45] | 21 [11 – 34] | 10 [4 – 21] | 22 [11 – 35] | 28 [16 – 41] | 54 [39 – 67] | 49 [34 – 62] |
| HLA-C antigenic mismatch | 95 [91 – 97] | 31 [25 – 37] | 29 [23 – 35] | 11 [7 – 16] | 29 [23 – 35] | 33 [27 – 39] | 42 [35 – 48] | 37 [31 – 44] |
| **p** | 0.59 | 0.71 | 0.31 | 0.92 | 0.35 | 0.46 | 0.14 | 0.18 |
| HLA-C allelic match | 95 [69 – 99] | 19 [6 – 38] | 20 [6 – 40] | 20 [6 – 40] | 14 [3 – 33] | 30 [11 – 52] | 60 [35 – 78] | 53 [28 – 73] |
| HLA-C allelic mismatch | 95 [90 – 97] | 30 [24 – 36] | 28 [22 – 34] | 11 [7 – 16] | 28 [22 – 34] | 33 [27 – 40] | 42 [35 – 49] | 38 [31 – 45] |
| **p** | 0.60 | 0.31 | 0.50 | 0.21 | 0.19 | 0.64 | 0.17 | 0.17 |
| HLA-DRB1 antigenic match | 89 [75 – 95] | 17 [9 – 29] | 37 [24 – 51] | 19 [9 – 31] | 36 [23 – 49] | 20 [10 – 33] | 48 [34 – 61] | 44 [30 – 57] |
| HLA-DRB1 antigenic mismatch | 95 [92 – 98] | 34 [28 – 40] | 25 [20 – 31] | 9 [6 – 14] | 26 [20 – 31] | 35 [29 – 41] | 43 [36 – 49] | 38 [32 – 45] |
| **p** | 0.19 | 0.02 | 0.13 | 0.07 | 0.10 | 0.09 | 0.86 | 0.67 |
| HLA-DRB1 allelic match | 95 [66 – 99] | 19 [6 – 38] | 27 [9 – 49] | 21 [6 – 43] | 39 [18 – 60] | 25 [9 – 47] | 42 [20 – 62] | 36 [16 – 56] |
| HLA-DRB1 allelic mismatch | 95 [90 – 97] | 30 [24 – 36] | 27 [21 – 34] | 11 [7 – 16] | 25 [20 – 31] | 34 [27 – 40] | 44 [37 – 51] | 40 [33 – 47] |
| **p** | 0.69 | 0.33 | 0.74 | 0.28 | 0.08 | 0.31 | 0.68 | 0.77 |

**ATG regimens**

| | 60-d PMN> 500/mm3 | 100-d aGvHD ≥2 | 2-y cGvHD | 2-y Ext cGvHD | 2-y TRM | 2-y Relapse | 2-y OS | 2-y LFS |
|---|---|---|---|---|---|---|---|---|
| HLA-A antigenic match | 92 [71 – 98] | 27 [12 – 45] | 29 [12 – 48] | 12 [3 – 28] | 24 [9 – 43] | 48 [27 – 67] | 44 [25 – 63] | 28 [12 – 46] |
| HLA-A antigenic mismatch | 98 [94 – 99] | 35 [28 – 42] | 33 [26 – 41] | 14 [9 – 19] | 30 [23 – 37] | 37 [29 – 44] | 40 [32 – 47] | 34 [27 – 41] |
| **p** | 0.12 | 0.36 | 0.47 | 0.61 | 0.46 | 0.46 | 0.62 | 0.79 |
| HLA-A allelic match | 90 [70 – 98] | 22 [3 – 53] | 25 [7 – 47] | 12 [3 – 27] | 29 [12 – 52] | 33 [13 – 62] | 27 [4 – 58] | 25 [2 – 56] |
| HLA-A allelic mismatch | 98 [93 – 99] | 35 [28 – 43] | 34 [27 – 42] | 15 [10 – 21] | 32 [25 – 40] | 34 [26 – 42] | 39 [30 – 47] | 34 [26 – 42] |
| **p** | 0.18 | 0.35 | 0.59 | 0.81 | 0.54 | 0.55 | 0.81 | 0.42 |
| HLA-B antigenic match | 94 [70 – 99] | 26 [9 – 47] | 36 [13 – 59] | 5 [1 – 22] | 22 [6 – 43] | 39 [16 – 60] | 45 [22 – 65] | 40 [18 – 61] |
| HLA-B antigenic mismatch | 97 [93 – 99] | 35 [28 – 42] | 32 [25 – 40] | 14 [9 – 20] | 30 [23 – 37] | 38 [31 – 46] | 40 [32 – 47] | 32 [25 – 39] |
| **p** | 0.84 | 0.52 | 0.86 | 0.27 | 0.55 | 0.75 | 0.55 | 0.15 |
| HLA-B allelic match | 93 [69 – 99] | 13 [2 – 35] | 22 [5 – 48] | 7 [2 – 27] | 28 [8 – 53] | 36 [12 – 61] | 43 [18 – 67] | 36 [13 – 60] |
| HLA-B allelic mismatch | 98 [93 – 99] | 37 [29 – 45] | 35 [27 – 43] | 15 [10 – 22] | 34 [26 – 42] | 35 [27 – 43] | 37 [29 – 46] | 31 [24 – 39] |
| **p** | 0.73 | 0.10 | 0.43 | 0.41 | 0.46 | 0.45 | 0.49 | 0.81 |
| HLA-C antigenic match | 97 [81 – 99] | 31 [17 – 46] | 35 [19 – 52] | 11 [3 – 23] | 24 [12 – 38] | 31 [17 – 47] | 51 [34 – 66] | 45 [29 – 60] |
| HLA-C antigenic mismatch | 97 [93 – 99] | 35 [27 – 42] | 32 [25 – 40] | 14 [9 – 20] | 30 [23 – 38] | 40 [32 – 48] | 37 [30 – 45] | 30 [33 – 37] |
| **p** | 0.71 | 0.63 | 0.62 | 0.75 | 0.60 | 0.43 | 0.21 | 0.15 |
| HLA-C allelic match | 95 [72 – 99] | 29 [11 – 49] | 26 [9 – 48] | 15 [3 – 34] | 30 [12 – 52] | 30 [12 – 51] | 44 [21 – 64] | 40 [19 – 60] |
| HLA-C allelic mismatch | 98 [93 – 99] | 36 [27 – 44] | 35 [27 – 43] | 14 [9 – 21] | 34 [26 – 42] | 35 [27 – 44] | 37 [28 – 45] | 31 [23 – 39] |
| **p** | 0.78 | 0.51 | 0.70 | 0.59 | 0.83 | 0.74 | 0.48 | 0.48 |
| HLA-DRB1 antigenic match | 92 [76 – 97] | 30 [16 – 46] | 30 [15 – 46] | 11 [3 – 24] | 17 [7 – 31] | 46 [29 – 62] | 47 [29 – 62] | 37 [22 – 53] |
| HLA-DRB1 antigenic mismatch | 98 [95 – 99] | 35 [27 – 42] | 34 [26 – 41] | 14 [9 – 20] | 32 [25 – 40] | 36 [29 – 44] | 39 [31 – 47] | 32 [25 – 40] |
| **p** | 0.62 | 0.54 | 0.59 | 0.77 | 0.04 | 0.11 | 0.31 | 0.64 |
| HLA-DRB1 allelic match | 92 [71 – 99] | 58 [25 – 81] | 33 [9 – 61] | 8 [2 – 33] | 38 [8 – 69] | 35 [9 – 63] | 29 [5 – 60] | 27 [5 – 56] |
| HLA-DRB1 allelic mismatch | 98 [94 – 99] | 33 [25 – 40] | 34 [26 – 42] | 15 [10 – 21] | 33 [25 – 41] | 35 [27 – 43] | 38 [30 – 46] | 32 [25 – 40] |
| **p** | 0.73 | 0.08 | 0.82 | 0.52 | 0.98 | 0.87 | 0.86 | 0.83 |

Numbers correspond to % [95% CI].

**Table S3. Univariate analysis for engraftment outcome according to the direction of HLA mismatches.**

| **PTCy regimens** | |
|---|---|
| | **60-d PMN> 500/mm3** |
| HLA-A match or GvH-directed mismatch (antigenic) (n=76) | 93 [83 – 97] |
| HLA-A bidirectional or HvG-directed mismatch (antigenic) (n=237) | 95 [91 – 97] |
| **p** | 0.62 |
| HLA-A match or GvH -directed mismatch (allelic) (n=56) | 92 [78 – 97] |
| HLA-A bidirectional or HvG -directed mismatch (allelic) (n=202) | 95 [91 – 98] |
| **p** | 0.40 |
| HLA-B match or GvH -directed mismatch (antigenic) (n=51) | 93 [80 – 98] |
| HLA-B bidirectional or HvG -directed mismatch (antigenic) (n=262) | 95 [91 – 97] |
| **p** | 0.15 |
| HLA-B match or GvH -directed mismatch (allelic) (n=36) | 96 [76 – 99] |
| HLA-B bidirectional or HvG -directed mismatch (allelic) (n=222) | 94 [90 – 97] |
| **p** | 0.23 |
| HLA-C match or GvH -directed mismatch (antigenic) (n=80) | 94 [85 – 98] |
| HLA-C bidirectional or HvG -directed mismatch (antigenic) (n=233) | 95 [90 – 97] |
| **p** | 0.98 |
| HLA-C match or GvH -directed mismatch (allelic) (n=55) | 98 [85 – 100] |
| HLA-C bidirectional or HvG -directed mismatch (allelic) (n= 203) | 94 [89 – 96] |
| **p** | 0.57 |
| HLA-DRB1 match or GvH -directed mismatch (antigenic) (n=82) | 92 [81 – 96] |
| HLA-DRB1 bidirectional or HvG -directed mismatch (antigenic) (n=231) | 95 [91 – 97] |
| **p** | 0.86 |
| HLA-DRB1 match or GvH -directed mismatch (allelic) (n=53) | 93 [79 – 98] |
| HLA-DRB1 bidirectional or HvG -directed mismatch (allelic) (n=205) | 95 [91 – 97] |
| **p** | 0.98 |
| **ATG regimens** | |
| | **60-d PMN> 500/mm3** |
| HLA-A match or GvH -directed mismatch (antigenic) (n=44) | 96 [83 – 99] |
| HLA-A bidirectional or HvG H-directed mismatch (antigenic) (n=152) | 98 [93 – 99] |
| p | 0.13 |
| HLA-A match or GvH -directed mismatch (allelic) (n=24) | 96 [74 – 99] |
| HLA-A bidirectional or HvG -directed mismatch (allelic) (n=136) | 98 [94 – 99] |
| p | 0.18 |
| HLA-B match or GvH -directed mismatch (antigenic) (n=30) | 97 [76 – 99] |
| HLA-B bidirectional or HvG -directed mismatch (antigenic) (n=166) | 97 [92 – 99] |
| p | 0.69 |
| HLA-B match or GvH -directed mismatch (allelic) (n=22) | 95 [71 – 99] |
| HLA-B bidirectional or HvG -directed mismatch (allelic) (n=138) | 98 [93 – 99] |
| p | 0.44 |
| HLA-C match or GvH -directed mismatch (antigenic) (n=54) | 98 [86 – 99] |
| HLA-C bidirectional or HvG -directed mismatch (antigenic) (n=142) | 97 [92 – 99] |
| p | 0.98 |
| HLA-C match or GvH -directed mismatch (allelic) (n=39) | 97 [81 – 99] |
| HLA-C bidirectional or HvG -directed mismatch (allelic) (n=121) | 97 [92 – 99] |
| p | 0.99 |
| HLA-DRB1 match or GvH -directed mismatch (antigenic) (n=52) | 94 [83 – 98] |
| HLA-DRB1 bidirectional or HvG -directed mismatch (antigenic) (n=144) | 98 [94 – 99] |
| p | 0.34 |
| HLA-DRB1 match or GvH -directed mismatch (allelic) (n=31) | 97 [77 – 99] |
| HLA-DRB1 bidirectional or HvG -directed mismatch (allelic) (n=129) | 98 [93 – 99] |
| p | 0.51 |

Numbers correspond to % [95% CI].

**Table S4. Univariate analysis for GvHD outcome according to the direction of HLA mismatches.**

| **PTCy regimens** | | |
|---|---|---|
| | **100-d aGvHD ≥2** | **2-y cGvHD** |
| HLA-A match or HvG-directed mismatch (antigenic) (n=76) | 37 [26 – 48] | 27 [17 – 38] |
| HLA-A bidirectional or GvH-directed mismatch (antigenic) (n=237) | 29 [23 – 35] | 28 [21 – 34] |
| **p** | 0.19 | 0.93 |
| HLA-A match or HvG-directed mismatch (allelic) (n=56) | 36 [23 – 49] | 28 [16 – 41] |
| HLA-A bidirectional or GvH-directed mismatch (allelic) (n=202) | 27 [21 – 34] | 27 [20 – 34] |
| **p** | 0.22 | 0.78 |
| HLA-B match or HvG-directed mismatch (antigenic) (n=51) | 39 [26 – 53] | 25 [13 – 38] |
| HLA-B bidirectional or GvH-directed mismatch (antigenic) (n=262) | 29 [24 – 35] | 28 [22 – 34] |
| **p** | 0.08 | 0.72 |
| HLA-B match or HvG-directed mismatch (allelic) (n=36) | 34 [19 – 49] | 19 [8 – 35] |
| HLA-B bidirectional or GvH-directed mismatch (allelic) (n=222) | 28 [22 – 35] | 28 [22 – 35] |
| **p** | 0.34 | 0.37 |
| HLA-C match or HvG-directed mismatch (antigenic) (n=80) | 27 [17 – 37] | 20 [12 – 30] |
| HLA-C bidirectional or GvH-directed mismatch (antigenic) (n=233) | 33 [27 – 39] | 30 [24 – 37] |
| **p** | 0.33 | 0.13 |
| HLA-C match or HvG-directed mismatch (allelic) (n=55) | 21 [11 – 32] | 17 [8 – 29] |
| HLA-C bidirectional or GvH-directed mismatch (allelic) (n= 203) | 32 [25 – 38] | 30 [23 – 37] |
| **p** | 0.11 | 0.08 |
| HLA-DRB1 match or HvG-directed mismatch (antigenic) (n=82) | 22 [14 – 32] | 32 [22 – 44] |
| HLA-DRB1 bidirectional or GvH-directed mismatch (antigenic) (n=231) | 34 [28 – 41] | 26 [20 – 32] |
| **p** | **0.05** | 0.37 |
| HLA-DRB1 match or HvG-directed mismatch (allelic) (n=53) | 21 [12 – 34] | 29 [16 – 42] |
| HLA-DRB1 bidirectional or GvH-directed mismatch (allelic) (n=205) | 31 [25 – 38] | 27 [20 – 33] |
| **p** | 0.19 | 0.93 |
| **ATG regimens** | | |
| | **aGvHD ≥2** | **cGvHD** |
| HLA-A match or HvG-directed mismatch (antigenic) (n=44) | 26 [14 – 40] | 25 [12 – 39] |
| HLA-A bidirectional or GvH-directed mismatch (antigenic) (n=152) | 36 [29 – 44] | 35 [27 – 43] |
| p | 0.18 | 0.36 |
| HLA-A match or HvG-directed mismatch (allelic) (n=24) | 22 [8 – 41] | 22 [8 – 41] |
| HLA-A bidirectional or GvH-directed mismatch (allelic) (n=136) | 36 [28 – 45] | 36 [27 – 44] |
| p | 0.14 | 0.44 |
| HLA-B match or HvG-directed mismatch (antigenic) (n=30) | 24 [10 – 40] | 36 [18 – 54] |
| HLA-B bidirectional or GvH-directed mismatch (antigenic) (n=166) | 36 [28 – 43] | 32 [25 – 40] |
| p | 0.23 | 0.39 |
| HLA-B match or HvG-directed mismatch (allelic) (n=22) | 18 [6 – 35] | 30 [11 – 51] |
| HLA-B bidirectional or GvH-directed mismatch (allelic) (n=138) | 37 [29 – 45] | 34 [26 – 42] |
| p | 0.12 | 0.98 |
| HLA-C match or HvG-directed mismatch (antigenic) (n=54) | 33 [21 – 46] | 39 [25 – 53] |
| HLA-C bidirectional or GvH-directed mismatch (antigenic) (n=142) | 34 [26 – 42] | 30 [23 – 38] |
| p | 0.99 | 0.35 |
| HLA-C match or HvG-directed mismatch (allelic) (n=39) | 31 [17 – 46] | 39 [23 – 54] |
| HLA-C bidirectional or GvH-directed mismatch (allelic) (n=121) | 36 [27 – 44] | 32 [23 – 41] |
| p | 0.60 | 0.47 |
| HLA-DRB1 match or HvG-directed mismatch (antigenic) (n=52) | 33 [20 – 46] | 26 [14 – 39] |
| HLA-DRB1 bidirectional or GvH-directed mismatch (antigenic) (n=144) | 34 [27 – 42] | 35 [27 – 44] |
| p | 0.78 | 0.18 |
| HLA-DRB1 match or HvG-directed mismatch (allelic) (n=31) | 41 [23 – 59] | 20 [8 – 36] |
| HLA-DRB1 bidirectional or GvH-directed mismatch (allelic) (n=129) | 33 [25 – 41] | 37 [28 – 45] |
| p | 0.40 | 0.10 |

Numbers correspond to % [95% CI].

**Table S5. Univariate analysis of outcome according to the number of HLA mismatches.**

**PTCy regimens**

| | **60-d PMN> 500/mm3** | **100-d aGvHD ≥2** | **2-y cGvHD** | **2-y Ext cGvHD** | **2-y TRM** | **2-y Relapse** | **2-y OS** | **2-y LFS** |
|---|---|---|---|---|---|---|---|---|
| ≤2 antigenic mismatches (n=43) | 89 [74 – 96] | 39 [25 – 54] | 23 [11 – 38] | 16 [6 – 29] | 27 [14 – 42] | 28 [15 – 42] | 50 [33 – 65] | 44 [28 – 58] |
| >2 antigenic mismatches (n=270) | 95 [92 – 97] | 30 [24 – 35] | 28 [22 – 34] | 10 [7 – 14] | 27 [22 – 33] | 33 [27 – 39] | 42 [36 – 49] | 38 [32 – 45] |
| **p** | 0.80 | 0.12 | 0.49 | 0.34 | 0.86 | 0.34 | 0.45 | 0.46 |
| ≤2 allelic mismatches (n=21) | 95 [66 – 99] | 39 [18 – 60] | 17 [4 – 38] | 19 [6 – 39] | 19 [6 – 38] | 26 [9 – 48] | 56 [31 – 75] | 52 [27 – 72] |
| >2 allelic mismatches (n=237) | 95 [90 – 97] | 28 [22 – 34] | 28 [22 – 34] | 11 [7 – 16] | 27 [21 – 33] | 34 [27 – 40] | 42 [35 – 49] | 38 [31 – 45] |
| **p** | 0.75 | 0.21 | 0.28 | 0.31 | 0.95 | 0.39 | 0.44 | 0.51 |

**ATG regimens**

| | **60-d PMN> 500/mm3** | **100-d aGvHD ≥2** | **2-y cGvHD** | **2-y Ext cGvHD** | **2-y TRM** | **2-y Relapse** | **2-y OS** | **2-y LFS** |
|---|---|---|---|---|---|---|---|---|
| ≤2 antigenic mismatches (n=33) | 94 [76 – 98] | 30 [16 – 46] | 37 [19 – 54] | 12 [4 – 26] | 22 [9 – 38] | 40 [23 – 57] | 49 [30 – 65] | 38 [21 – 54] |
| >2 antigenic mismatches (n=163) | 98 [94 – 99] | 35 [27 – 42] | 31 [24 – 38] | 14 [9 – 20] | 30 [23 – 38] | 37 [30 – 45] | 38 [31 – 46] | 32 [25 – 39] |
| **p** | 0.47 | 0.68 | 0.86 | 0.64 | 0.25 | 0.76 | 0.21 | 0.29 |
| ≤2 allelic mismatches (n=15) | 94 [80 – 99] | 20 [5 – 43] | 21 [5 – 46] | 12 [2 – 34] | 31 [8 – 58] | 40 [15 – 64] | 35 [12 – 60] | 29 [8 – 54] |
| >2 allelic mismatches (n=145) | 98 [93 – 99] | 36 [28 – 44] | 34 [26 – 42] | 15 [9 – 21] | 33 [26 – 41] | 34 [26 – 42] | 38 [30 – 47] | 33 [25 – 41] |
| **p** | 0.89 | 0.25 | 0.41 | 0.79 | 0.44 | 0.46 | 0.64 | 0.75 |

Numbers correspond to % [95% CI].

**Table S6. Univariate analysis of outcome according to predicted NK alloreactivity in GvL vector.**

**PTCy regimens**

| | **60-d PMN> 500/mm3** | **100-d aGvHD ≥2** | **2-y cGvHD** | **2-y Ext cGvHD** | **2-y TRM** | **2-y Relapse** | **2-y OS** | **2-y LFS** |
|---|---|---|---|---|---|---|---|---|
| NK alloreactivity in GvL vector (n=97) | 94 [89 – 97] | 23 [15 – 31] | 24 [16 – 33] | 11 [6 – 19] | 25 [17 – 35] | 41 [31 – 52] | 37 [27 – 48] | 33 [23 – 43] |
| No NK alloreactivity in GvL vector (n=161) | 95 [88 – 98] | 33 [26 – 41] | 29 [22 – 37] | 12 [8 – 19] | 27 [20 – 35] | 28 [21 – 36] | 48 [39 – 56] | 43 [35 – 51] |
| **p** | 0.67 | 0.06 | 0.51 | 0.87 | 0.71 | 0.03 | 0.19 | 0.16 |

**ATG regimens**

| | **60-d PMN> 500/mm3** | **100-d aGvHD ≥2** | **2-y cGvHD** | **2-y Ext cGvHD** | **2-y TRM** | **2-y Relapse** | **2-y OS** | **2-y LFS** |
|---|---|---|---|---|---|---|---|---|
| NK alloreactivity in GvL vector (n=67) | 96 [89 – 99] | 43 [30 – 55] | 35 [23 – 47] | 14 [7 – 24] | 26 [16 – 37] | 40 [28 – 52] | 44 [24 – 44] | 34 [23 – 46] |
| No NK alloreactivity in GvL vector (n=93) | 98 [89 – 99] | 29 [20 – 38] | 33 [23 – 43] | 15 [8 – 23] | 39 [28 – 49] | 31 [21 – 40] | 34 [31 – 56] | 31 [22 – 41] |
| **p** | 0.75 | 0.09 | 0.93 | 0.96 | 0.10 | 0.30 | 0.29 | 0.60 |

Numbers correspond to % [95% CI].

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