**Supplemental Table 1a.** Impact of conditioning intensity on HCT outcomes

| | MAC | | | RIC | | |
|---|---|---|---|---|---|---|
| | Haplo (N=358) | MUD (N=716) | p value | Haplo (N=129) | MUD (N=258) | p value |
| **Age at transplant, years** | | | 0.99 | | | <0.0001 |
| Median (Range) | 32 (18-68) | 32 (18-71) | | 39 (18-73) | 53 (18-76) | |
| Interquartile range | 23, 44 | 24, 43 | | 26, 54 | 36, 61 | |
| <30 | 166 (46%) | 326 (46%) | 0.60 | 42 (33%) | 45 (17%) | <0.0001 |
| 30-39 | 74 (21%) | 155 (22%) | | 24 (19%) | 28 (11%) | |
| 40-54 | 79 (22%) | 173 (24%) | | 32 (25%) | 66 (26%) | |
| ≥55 | 39 (11%) | 62 (9%) | | 31 (24%) | 119 (46%) | |
| **Recipient sex** | | | 1.0 | | | 1.0 |
| Male | 231 (65%) | 462 (65%) | | 72 (56%) | 144 (56%) | |
| Female | 127 (35%) | 254 (35%) | | 57 (44%) | 114 (44%) | |
| **KPS** | | | 0.0001 | | | 0.37 |
| 90-100 | 237 (66%) | 495 (69%) | | 84 (65%) | 162 (63%) | |
| ≤80 | 109 (30%) | 155 (22%) | | 42 (33%) | 82 (32%) | |
| NA | 12 (3%) | 66 (9%) | | 3 (2%) | 14 (5%) | |
| **Cytogenetic risk** | | | 1.0 | | | 1.0 |
| Poor risk | 114 (32%) | 228 (32%) | | 49 (38%) | 98 (38%) | |
| Not poor | 244 (68%) | 488 (68%) | | 80 (62%) | 160 (62%) | |
| **Ph (+) status** | | | 1.0 | | | 1.0 |
| Ph+ | 81 (23%) | 162 (23%) | | 36 (28%) | 72 (28%) | |
| Ph- | 277 (77%) | 554 (77%) | | 93 (72%) | 186 (72%) | |
| **Disease stage prior to HCT** | | | 1.0 | | | 1.0 |
| CR1 | 195 (54%) | 390 (54%) | | 61 (47%) | 122 (47%) | |
| CR2+ | 110 (31%) | 220 (31%) | | 46 (36%) | 92 (36%) | |
| Active disease | 53 (15%) | 106 (15%) | | 22 (17%) | 44 (17%) | |
| **ALL type** | | | 0.73 | | | 0.57 |
| B-ALL | 251 (70%) | 499 (70%) | | 94 (73%) | 200 (78%) | |
| T-ALL | 86 (24%) | 166 (23%) | | 27 (21%) | 43 (17%) | |
| Other | 21 (6%) | 51 (7%) | | 8 (6%) | 15 (6%) | |
| **From diagnosis to transplant** | | | 0.077 | | | 0.30 |
| ≤6 months | 90 (25%) | 220 (31%) | | 24 (19%) | 64 (25%) | |
| >6-12 months | 126 (35%) | 256 (36%) | | 42 (33%) | 86 (33%) | |
| >12 months | 142 (40%) | 240 (34%) | | 63 (49%) | 108 (42%) | |
| **HCT Comorbidity Index** | | | <0.0001 | | | <0.0001 |
| 0 | 76 (21%) | 40 (6%) | | 22 (17%) | 9 (3%) | |
| 1-2 | 56 (16%) | 12 (2%) | | 15 (12%) | 9 (3%) | |
| >2 | 39 (11%) | 6 (1%) | | 43 (33%) | 6 (2%) | |
| NA | 187 (52%) | 658 (92%) | | 49 (38%) | 234 (91%) | |
| **Donor age, years** | N=328 | N=331 | <0.0001 | N=122 | N=131 | 0.004 |
| Median (Range) | 38 (13-74) | 32 (18-57) | | 37 (15-76) | 31 (19-62) | |
| Interquartile range | 26, 50 | 26, 40 | | 26, 47 | 24, 40 | |
| <30 | 105 (29%) | 132 (18%) | <0.0001 | 41 (32%) | 64 (25%) | <0.0001 |
| 30-50 | 142 (40%) | 181 (25%) | | 58 (45%) | 62 (24%) | |
| ≥50 | 81 (23%) | 18 (3%) | | 23 (18%) | 5 (2%) | |
| NA | 30 (8%) | 385 (54%) | | 7 (5%) | 127 (49%) | |
| **Donor sex** | | | <0.0001 | | | 0.034 |
| Male | 196 (55%) | 505 (71%) | | 80 (62%) | 185 (72%) | |
| Female | 162 (45%) | 188 (26%) | | 49 (38%) | 69 (27%) | |
| NA | | 23 (3%) | | | 4 (2%) | |

**Supplemental Table 1a.** Impact of conditioning intensity on HCT outcomes

| | MAC | | | RIC | | |
|---|---|---|---|---|---|---|
| | Haplo (N=358) | MUD (N=716) | p value | Haplo (N=129) | MUD (N=258) | p value |
| **Female donor to male recipient** | | | <0.0001 | | | 0.054 |
| Yes | 105 (29%) | 99 (14%) | | 26 (20%) | 32 (12%) | |
| No | 253 (71%) | 594 (83%) | | 103 (80%) | 222 (86%) | |
| NA | | 23 (3%) | | 0 (0%) | 4 (2%) | |
| **Donor/Recipient CMV serostatus** | | | <0.0001 | | | <0.0001 |
| D-/R- | 31 (9%) | 217 (30%) | | 12 (9%) | 58 (22%) | |
| D-/R+ | 58 (16%) | 197 (28%) | | 26 (20%) | 85 (33%) | |
| D+/R- | 28 (8%) | 71 (10%) | | 13 (10%) | 18 (7%) | |
| D+/R+ | 227 (63%) | 197 (28%) | | 76 (59%) | 81 (31%) | |
| Unknown | 14 (4%) | 34 (5%) | | 2 (2%) | 16 (6%) | |
| **Conditioning intensity** | | | | | | |
| TBI-based | 173 (49%) | 535 (75%) | <0.0001 | | | |
| Not TBI-based | 183 (51%) | 176 (25%) | | | | |
| **Stem cell source** | | | <0.0001 | | | <0.0001 |
| BM | 180 (50%) | 152 (21%) | | 57 (44%) | 16 (6%) | |
| PB | 178 (50%) | 564 (79%) | | 72 (56%) | 242 (94%) | |
| **GvHD prophylaxis** | | | | | | |
| Sirolimus-based | | 13 (2%) | | | 10 (4%) | |
| MTX-based | | 576 (80%) | | | 88 (34%) | |
| CellCept-based | | 127 (18%) | | | 160 (62%) | |
| PTCy/CellCept/CNI | 358 (100%) | | | 129 (100%) | | |
| ATG added | 0 | 463 (65%) | | 0 | 163 (63%) | |
| **Transplant period** | | | <0.0001 | | | <0.0001 |
| 2005-2012 | 58 (16%) | 477 (67%) | | 28 (22%) | 132 (51%) | |
| 2013-2018 | 300 (84%) | 239 (33%) | | 101 (78%) | 126 (49%) | |

**Supplemental Table 1b.** Conditioning regimen

| | **Haplo (N=487)** | **MUD (N=974)** | **Total (N=1461)** |
|---|---|---|---|
| **Conditioning regimen** | | | |
| TBI based MAC | 173 (36%) | 535 (55%) | 708 (48%) |
| FluBu MAC | 162 (33%) | 47 (5%) | 209 (14%) |
| FluTreo MAC | 4 (1%) | 18 (2%) | 22 (2%) |
| FluBu RIC | 21 (4%) | 107 (11%) | 128 (9%) |
| FluMel | 28 (6%) | 0 (0%) | 28 (2%) |
| FluTBI RIC | 85 (17%) | 63 (6%) | 148 (10%) |
| FluTReo RIC | 3 (1%) | 9 (1%) | 12 (1%) |
| other MAC | 4 (1%) | 116 (12%) | 120 (8%) |
| other RIC | 7 (1%) | 79 (8%) | 86 (6%) |
| | | | |
| **Conditioning regimen** | | | |
| FluBu | 183 (38%) | 154 (16%) | 337 (23%) |
| FluMel | 28 (6%) | 0 (0%) | 28 (2%) |
| FluTBI | 85 (17%) | 63 (6%) | 148 (10%) |
| FluTreo | 7 (1%) | 27 (3%) | 34 (2%) |
| TBI based MAC | 173 (36%) | 535 (55%) | 708 (48%) |
| other | 11 (2%) | 195 (20%) | 206 (14%) |

**Supplemental Table 2.** Neutrophil engraftment

| | | | Neutrophil Engraftment | | |
|---|---|---|---|---|---|
| | | N | 28 Days (95%CI) | *HR (95%CI)** | *P* value* |
| Donor type | MUD | 974 | 0.88(0.86,0.90) | Reference | 0.24 |
| | Haplo | 487 | 0.86(0.83,0.89) | 1.08(0.95,1.24) | |
| Recipient age, years | <30 | 579 | 0.87(0.84,0.90) | Reference | 0.22 |
| | 30-39 | 281 | 0.88(0.83,0.91) | 0.94(0.82,1.09) | |
| | 40-54 | 350 | 0.88(0.84,0.91) | 0.90(0.79,1.03) | |
| | ≥55 | 251 | 0.86(0.82,0.90) | 0.84(0.70,1.00) | |
| KPS† | 90-100 | 978 | 0.89(0.87,0.91) | Reference | **0.047** |
| | ≤80 | 388 | 0.83(0.79,0.87) | 0.88(0.78,1.00) | |
| ALL subtype | B-ALL | 1044 | 0.88(0.86,0.90) | Reference | 0.44 |
| | T-ALL | 322 | 0.87(0.82,0.90) | 1.05(0.91,1.22) | |
| | Other | 95 | 0.85(0.76,0.91) | 0.90(0.72,1.13) | |
| Months from dx to HCT | ≤6 | 398 | 0.90(0.86,0.92) | Reference | 0.98 |
| | >6-12 | 510 | 0.87(0.84,0.90) | 1.01(0.89,1.16) | |
| | >12 | 553 | 0.86(0.83,0.89) | 1.01(0.84,1.21) | |
| HCTCI† | 0 | 147 | 0.90(0.84,0.94) | Reference | 0.96 |
| | 1-2 | 92 | 0.90(0.82,0.95) | 1.03(0.75,1.42) | |
| | >2 | 94 | 0.94(0.86,0.97) | 1.04(0.79,1.38) | |
| Donor age, years† | <30 | 342 | 0.90(0.86,0.93) | Reference | 0.50 |
| | 30-49 | 443 | 0.88(0.85,0.91) | 0.95(0.82,1.10) | |
| | ≥50 | 127 | 0.88(0.81,0.93) | 1.06(0.88,1.28) | |
| F donor to M recipient† | No | 1172 | 0.87(0.85,0.89) | Reference | **0.020** |
| | Yes | 262 | 0.88(0.83,0.91) | 1.18(1.03,1.36) | |
| CMV serostatus† | D+/R+ | 581 | 0.87(0.84,0.89) | Reference | 0.15 |
| | D+/R- | 130 | 0.92(0.86,0.96) | 1.13(0.96,1.33) | |
| | D-/R+ | 366 | 0.89(0.85,0.92) | 1.08(0.94,1.23) | |
| | D-/R- | 318 | 0.87(0.83,0.90) | 0.93(0.81,1.07) | |
| Stem cell source | PB | 1056 | 0.90(0.88,0.92) | Reference | **<0.001** |
| | BM | 405 | 0.81(0.77,0.84) | 0.61(0.55,0.69) | |
| Transplant period | 2005-2012 | 695 | 0.86(0.83,0.89) | Reference | **0.024** |
| | 2013-2018 | 766 | 0.89(0.86,0.91) | 1.13(1.02,1.26) | |

*Based on multivariable proportional subdistribution hazards model for competing risks adjusted for KPS, F donor to M recipient, stem cell source, and transplant period, and stratified by matching variables: sex, cytogenetic risk, Ph status, disease stage, and conditioning intensity. The robust sandwich covariance matrix estimate was used to adjust for within center correlation.

†Patients who had missing values were included in the model when the variable as covariates, but were excluded when the variable as predictor of interest

**Supplemental Table 3.** Survival outcomes and Neutrophil engraftment subgroup analysis

| | | | OS | | | RFS | | | Neutrophil engraftment | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | N | 3 Year (95%CI) | HR (95%CI)* | P* | 3 Year (95%CI) | HR (95%CI)* ‡ | P* | 28 Days (95%CI) | HR (95%CI)* ‡ | P* |
| MAC† | MUD | 716 | 0.51(0.47,0.55) | Reference | 0.56 | 0.46(0.42,0.49) | Reference | 0.87 | 0.88(0.86,0.91) | Reference | 0.11 |
| | Haplo | 358 | 0.44(0.38,0.50) | 1.07(0.86,1.33) | | 0.41(0.36,0.47) | 1.02(0.83,1.25) | | 0.87(0.83,0.90) | 1.14(0.97,1.34) | |
| RIC | MUD | 258 | 0.42(0.35,0.48) | Reference | 0.60 | 0.31(0.25,0.38) | Reference | 0.34 | 0.88(0.83,0.91) | Reference | 0.47 |
| | Haplo | 129 | 0.43(0.33,0.53) | 0.91(0.64,1.29) | | 0.31(0.22,0.41) | 0.88(0.68,1.14) | | 0.84(0.77,0.90) | 0.92(0.74,1.15) | |
| CR1 | MUD | 512 | 0.59(0.54,0.63) | Reference | 0.91 | 0.53(0.49,0.58) | Reference | 0.99 | 0.90(0.87,0.92) | Reference | 0.079 |
| | Haplo | 256 | 0.57(0.49,0.64) | 1.02(0.74,1.40) | | 0.51(0.43,0.57) | 1.00(0.75,1.33) | | 0.91(0.86,0.94) | 1.17(0.98,1.40) | |
| Ph+ | MUD | 234 | 0.57(0.50,0.63) | Reference | 0.74 | 0.46(0.39,0.53) | Reference | 0.68 | 0.90(0.85,0.93) | Reference | 0.58 |
| | Haplo | 117 | 0.53(0.41,0.63) | 1.07(0.72,1.60) | | 0.50(0.39,0.59) | 0.92(0.62,1.37) | | 0.86(0.79,0.91) | 1.08(0.83,1.39) | |
| Ph- | MUD | 740 | 0.46(0.42,0.49) | Reference | 0.62 | 0.41(0.37,0.44) | Reference | 0.47 | 0.88(0.85,0.90) | Reference | 0.38 |
| | Haplo | 370 | 0.41(0.35,0.46) | 1.05(0.86,1.30) | | 0.36(0.30,0.41) | 1.07(0.89,1.28) | | 0.86(0.82,0.89) | 1.07(0.92,1.24) | |
| PBSC | MUD | 806 | 0.49(0.45,0.53) | Reference | 0.27 | 0.42(0.39,0.46) | Reference | 0.46 | 0.89(0.87,0.91) | Reference | 0.77 |
| | Haplo | 250 | 0.43(0.36,0.51) | 1.18(0.88,1.58) | | 0.39(0.32,0.46) | 1.11(0.85,1.44) | | 0.92(0.88,0.95) | 1.02(0.88,1.18) | |
| BM | MUD | 168 | 0.44(0.36,0.52) | Reference | 0.32 | 0.40(0.32,0.48) | Reference | 0.41 | 0.83(0.76,0.88) | Reference | **0.038** |
| | Haplo | 237 | 0.43(0.36,0.51) | 0.86(0.64,1.15) | | 0.39(0.32,0.46) | 0.89(0.66,1.19) | | 0.80(0.74,0.84) | 1.27(1.01,1.59) | |
| 2013-2018 | MUD | 365 | 0.48(0.41,0.54) | Reference | 0.77 | 0.38(0.32,0.44) | Reference | 0.52 | 0.91(0.88,0.94) | Reference | 0.59 |
| | Haplo | 401 | 0.45(0.39,0.51) | 1.04(0.82,1.30) | | 0.41(0.35,0.46) | 0.94(0.76,1.15) | | 0.86(0.83,0.89) | 1.04(0.90,1.21) | |
| Ph+ B-ALL | MUD | 232 | 0.57(0.50,0.64) | Reference | 0.38 | 0.47(0.40,0.53) | Reference | 0.89 | 0.90(0.85,0.93) | Reference | 0.85 |
| | Haplo | 99 | 0.51(0.38,0.63) | 1.21(0.79,1.86) | | 0.47(0.35,0.58) | 1.03(0.68,1.56) | | 0.85(0.76,0.91) | 1.03(0.79,1.34) | |
| Ph- B-ALL | MUD | 467 | 0.46(0.41,0.51) | Reference | 0.64 | 0.42(0.37,0.46) | Reference | 0.35 | 0.88(0.85,0.91) | Reference | 0.13 |
| | Haplo | 246 | 0.39(0.32,0.46) | 1.06(0.83,1.36) | | 0.36(0.29,0.43) | 1.11(0.89,1.38) | | 0.87(0.82,0.91) | 1.15(0.96,1.37) | |
| T-ALL | MUD | 209 | 0.47(0.40,0.54) | Reference | 0.49 | 0.40(0.32,0.47) | Reference | 0.58 | 0.89(0.84,0.93) | Reference | 0.75 |
| | Haplo | 113 | 0.44(0.34,0.54) | 1.13(0.80,1.59) | | 0.36(0.27,0.45) | 1.10(0.79,1.52) | | 0.81(0.73,0.87) | 0.96(0.73,1.25) | |

*Based on multivariable Cox regression model adjusted for covariates, and stratified by matching variables: sex, cytogenetic risk, Ph status, and disease stage. The robust sandwich covariance matrix estimate was used to adjust for within center correlation.

† Adjusted for TBI-based conditioning regimen too.

**Supplemental Table 4.** Relapse and non-relapse mortality subgroup analysis

| | | | | **Relapse** | | | **NRM** | |
|---|---|---|---|---|---|---|---|---|
| | | N | 3 Years (95%CI) | HR (95%CI)* | P* | 3 Years (95%CI) | HR (95%CI)* | P* |
| MAC | MUD | 716 | 0.31(0.28,0.35) | Reference | 0.53 | 0.23(0.20,0.26) | Reference | 0.32 |
| | Haplo | 358 | 0.35(0.29,0.40) | 0.91(0.67,1.22) | | 0.24(0.19,0.29) | 1.17(0.86,1.59) | |
| RIC | MUD | 258 | 0.42(0.36,0.49) | Reference | 0.24 | 0.26(0.21,0.32) | Reference | 0.86 |
| | Haplo | 129 | 0.42(0.32,0.52) | 0.79(0.53,1.18) | | 0.26(0.18,0.35) | 1.04(0.67,1.61) | |
| CR1 | MUD | 512 | 0.23(0.19,0.27) | Reference | 0.27 | 0.24(0.20,0.28) | Reference | 0.31 |
| | Haplo | 256 | 0.27(0.21,0.33) | 1.20(0.87,1.67) | | 0.23(0.17,0.29) | 0.83(0.58,1.18) | |
| Ph+ | MUD | 234 | 0.28(0.22,0.34) | Reference | 0.32 | 0.26(0.20,0.32) | Reference | 0.59 |
| | Haplo | 117 | 0.24(0.16,0.33) | 0.78(0.48,1.27) | | 0.26(0.18,0.35) | 1.13(0.73,1.74) | |
| Ph- | MUD | 740 | 0.36(0.32,0.40) | Reference | 0.72 | 0.23(0.20,0.27) | Reference | 0.43 |
| | Haplo | 370 | 0.41(0.35,0.46) | 1.05(0.81,1.35) | | 0.24(0.19,0.28) | 1.13(0.83,1.55) | |
| PBSC | MUD | 806 | 0.34(0.31,0.38) | Reference | 0.50 | 0.23(0.20,0.26) | Reference | 0.42 |
| | Haplo | 250 | 0.36(0.29,0.42) | 0.91(0.68,1.20) | | 0.25(0.20,0.31) | 1.16(0.81,1.65) | |
| BM | MUD | 168 | 0.33(0.26,0.41) | Reference | 0.68 | 0.27(0.20,0.34) | Reference | 0.93 |
| | Haplo | 237 | 0.38(0.31,0.44) | 1.08(0.74,1.59) | | 0.24(0.18,0.29) | 1.02(0.63,1.67) | |
| 2013-2018 | MUD | 365 | 0.42(0.36,0.48) | Reference | **0.018** | 0.20(0.15,0.24) | Reference | 0.070 |
| | Haplo | 401 | 0.34(0.29,0.39) | 0.75(0.59,0.95) | | 0.25(0.21,0.30) | 1.37(0.97,1.92) | |
| Ph+ B-ALL | MUD | 232 | 0.28(0.22,0.34) | Reference | 0.56 | 0.26(0.20,0.32) | Reference | 0.64 |
| | Haplo | 99 | 0.26(0.16,0.36) | 0.86(0.51,1.44) | | 0.27(0.18,0.37) | 1.12(0.70,1.81) | |
| Ph- B-ALL | MUD | 467 | 0.35(0.30,0.39) | Reference | 0.67 | 0.23(0.20,0.27) | Reference | 0.83 |
| | Haplo | 246 | 0.39(0.33,0.46) | 1.06(0.81,1.39) | | 0.25(0.19,0.31) | 1.04(0.74,1.46) | |
| T-ALL | MUD | 209 | 0.38(0.31,0.45) | Reference | 0.59 | 0.23(0.17,0.29) | Reference | 0.58 |
| | Haplo | 113 | 0.41(0.31,0.50) | 1.12(0.75,1.68) | | 0.23(0.16,0.32) | 0.86(0.50,1.47) | |

*Based on multivariable proportional subdistribution hazards model for competing risks adjusting covariates, and stratified by matching variables: sex, cytogenetic risk, Ph status, and disease stage. The robust sandwich covariance matrix estimate was used to adjust for within center correlation.

**Supplemental Table 5a.** Acute GvHD subset analysis

| | | | **Grade II-IV aGVHD** | | | **Grade III-IV aGVHD** | | |
|---|---|---|---|---|---|---|---|---|
| | | N | 100 days (95%CI) | HR (95%CI) | P | 100 days (95%CI) | HR (95%CI) | P |
| MAC | MUD | 716 | 0.34(0.31,0.38) | Reference | 0.46 | 0.13(0.10,0.15) | Reference | 0.27 |
| | Haplo | 358 | 0.33(0.28,0.38) | 1.09(0.87,1.36) | | 0.14(0.10,0.18) | 1.23(0.85,1.76) | |
| RIC | MUD | 258 | 0.30(0.24,0.35) | Reference | 0.062 | 0.10(0.06,0.14) | Reference | **0.030** |
| | Haplo | 129 | 0.31(0.23,0.40) | 1.45(0.98,2.15) | | 0.13(0.08,0.19) | 2.19(1.08,4.44) | |
| CR1 | MUD | 512 | 0.34(0.30,0.39) | Reference | 0.34 | 0.12(0.10,0.15) | Reference | 0.46 |
| | Haplo | 256 | 0.34(0.28,0.40) | 1.14(0.87,1.50) | | 0.12(0.08,0.16) | 1.19(0.75,1.88) | |
| Ph+ | MUD | 234 | 0.37(0.31,0.43) | Reference | 0.87 | 0.14(0.10,0.19) | Reference | 0.51 |
| | Haplo | 117 | 0.41(0.32,0.50) | 1.03(0.72,1.48) | | 0.18(0.11,0.26) | 1.21(0.69,2.13) | |
| Ph- | MUD | 740 | 0.32(0.28,0.35) | Reference | 0.29 | 0.11(0.09,0.14) | Reference | 0.14 |
| | Haplo | 370 | 0.30(0.25,0.34) | 1.14(0.90,1.44) | | 0.12(0.09,0.16) | 1.34(0.91,1.98) | |
| PBSC | MUD | 806 | 0.34(0.31,0.38) | Reference | 0.11 | 0.12(0.10,0.15) | Reference | **0.041** |
| | Haplo | 250 | 0.39(0.33,0.45) | 1.20(0.96,1.50) | | 0.16(0.12,0.21) | 1.49(1.02,2.18) | |
| BM | MUD | 168 | 0.28(0.21,0.35) | Reference | 0.90 | 0.10(0.06,0.15) | Reference | 0.77 |
| | Haplo | 237 | 0.25(0.20,0.31) | 0.98(0.64,1.48) | | 0.11(0.07,0.15) | 1.11(0.56,2.16) | |
| 2013-2018 | MUD | 365 | 0.32(0.27,0.37) | Reference | 0.062 | 0.12(0.09,0.15) | Reference | 0.16 |
| | Haplo | 401 | 0.35(0.30,0.39) | 1.28(0.99,1.65) | | 0.15(0.11,0.18) | 1.32(0.90,1.94) | |
| Ph+ B-ALL | MUD | 232 | 0.37(0.31,0.43) | Reference | 0.61 | 0.14(0.10,0.19) | Reference | 0.30 |
| | Haplo | 99 | 0.39(0.29,0.49) | 1.10(0.76,1.61) | | 0.18(0.11,0.27) | 1.35(0.76,2.40) | |
| Ph- B-ALL | MUD | 467 | 0.29(0.25,0.34) | Reference | **0.034** | 0.11(0.08,0.14) | Reference | 0.30 |
| | Haplo | 246 | 0.34(0.28,0.40) | 1.37(1.02,1.82) | | 0.13(0.09,0.18) | 1.27(0.80,2.02) | |
| T-ALL | MUD | 209 | 0.37(0.30,0.43) | Reference | 0.15 | 0.11(0.07,0.16) | Reference | 0.92 |
| | Haplo | 113 | 0.21(0.14,0.29) | 0.65(0.36,1.17) | | 0.09(0.05,0.16) | 0.96(0.47,1.97) | |
| F to M HCT | MUD | 131 | 0.38(0.29,0.46) | Reference | **0.018** | 0.12(0.07,0.18) | Reference | 0.53 |
| | Haplo | 131 | 0.30(0.22,0.38) | 0.61(0.41,0.92) | | 0.11(0.06,0.17) | 0.80(0.40,1.60) | |

*Based on multivariable proportional subdistribution hazards model for competing risks adjusting time from ALL diagnosis to transplant, HCT CI, donor age, female donor to male recipient, and stem cell source, and stratified by matching variables: sex, cytogenetic risk, Ph status, and disease stage in MAC and RIC subgroups. The robust sandwich covariance matrix estimate was used to adjust for within center correlation.

**Table 5b.** Chronic GvHD subset analysis

| | | | **Any cGVHD** | | | **Extensive cGVHD** | | |
|---|---|---|---|---|---|---|---|---|
| | | N | 3-yr (95%CI) | HR (95%CI) | P* | 3-yr (95%CI) | HR (95%CI) | P* |
| MAC | MUD | 716 | 0.31(0.28,0.35) | Reference | 0.58 | 0.12(0.09,0.14) | Reference | 0.76 |
| | Haplo | 358 | 0.29(0.24,0.34) | 1.09(0.81,1.47) | | 0.09(0.06,0.12) | 1.08(0.65,1.79) | |
| RIC | MUD | 258 | 0.29(0.23,0.35) | Reference | 0.86 | 0.15(0.11,0.20) | Reference | 0.32 |
| | Haplo | 129 | 0.24(0.17,0.32) | 0.96(0.63,1.47) | | 0.11(0.06,0.17) | 0.73(0.40,1.34) | |
| CR1 | MUD | 512 | 0.36(0.31,0.40) | Reference | 0.68 | 0.15(0.12,0.18) | Reference | 0.89 |
| | Haplo | 256 | 0.32(0.26,0.38) | 1.07(0.77,1.48) | | 0.10(0.07,0.14) | 0.96(0.56,1.64) | |
| Ph+ | MUD | 234 | 0.37(0.31,0.44) | Reference | 0.63 | 0.14(0.10,0.19) | Reference | 0.77 |
| | Haplo | 117 | 0.34(0.25,0.43) | 1.11(0.72,1.73) | | 0.12(0.07,0.19) | 1.12(0.54,2.32) | |
| Ph- | MUD | 740 | 0.28(0.25,0.32) | Reference | 0.69 | 0.12(0.10,0.15) | Reference | 0.61 |
| | Haplo | 370 | 0.26(0.21,0.30) | 1.06(0.79,1.42) | | 0.09(0.06,0.12) | 0.89(0.57,1.39) | |
| PBSC | MUD | 806 | 0.30(0.27,0.34) | Reference | 0.48 | 0.12(0.10,0.15) | Reference | 0.74 |
| | Haplo | 250 | 0.29(0.23,0.35) | 1.11(0.82,1.51) | | 0.12(0.08,0.16) | 1.08(0.68,1.71) | |
| BM | MUD | 168 | 0.30(0.23,0.38) | Reference | 0.89 | 0.12(0.08,0.18) | Reference | 1.00 |
| | Haplo | 237 | 0.26(0.21,0.32) | 0.97(0.66,1.44) | | 0.07(0.04,0.11) | 1.00(0.41,2.43) | |
| 2013-2018 | MUD | 365 | 0.28(0.23,0.33) | Reference | 0.86 | 0.09(0.06,0.13) | Reference | 0.57 |
| | Haplo | 401 | 0.26(0.22,0.31) | 1.03(0.77,1.37) | | 0.08(0.06,0.12) | 1.16(0.69,1.97) | |
| Ph+ B-ALL | MUD | 232 | 0.37(0.31,0.44) | Reference | 0.69 | 0.14(0.10,0.19) | Reference | 0.44 |
| | Haplo | 99 | 0.36(0.26,0.46) | 1.10(0.68,1.78) | | 0.11(0.06,0.19) | 0.76(0.38,1.53) | |
| Ph- B-ALL | MUD | 467 | 0.28(0.24,0.33) | Reference | 0.94 | 0.13(0.10,0.16) | Reference | 0.93 |
| | Haplo | 246 | 0.26(0.21,0.32) | 1.01(0.73,1.41) | | 0.10(0.06,0.14) | 1.03(0.58,1.81) | |
| T-ALL | MUD | 209 | 0.29(0.23,0.36) | Reference | 0.71 | 0.11(0.07,0.16) | Reference | 0.60 |
| | Haplo | 113 | 0.24(0.17,0.33) | 1.10(0.67,1.81) | | 0.08(0.04,0.14) | 0.78(0.31,1.96) | |
| F to M HCT | MUD | 131 | 0.26(0.19,0.35) | Reference | 0.62 | 0.08(0.04,0.14) | Reference | 0.65 |
| | Haplo | 131 | 0.31(0.23,0.40) | 1.12(0.71,1.78) | | 0.12(0.07,0.18) | 1.21(0.54,2.69) | |

*Based on multivariable proportional subdistribution hazards model for competing risks adjusting covariates, and stratified by matching variables: sex, cytogenetic risk, Ph status, and disease stage. The robust sandwich covariance matrix estimate was used to adjust for within center correlation.