## Supplementary

**Table S1:** Correlation of KIR genes and haplotype in child mother and father with the occurrence of FM. Fisher's exact test with risk calculation of odds ratio and 95% confidence analysis was performed. Odds ratios were calculated as follows odds ratio = ((FM-/KIR+)/(FM+/KIR+))/(FM-/KIR-)/(FM+KIR-). Odds ratio >1 = occurrence or absence of gene affects FM. KIR2DL1, KIR2DL4, KIR3DL2 and KIR2DL3 are present in all donors and therefore were excluded. ** Genes are constantly present and therefore were excluded. Significance level p<0.05.

| KIR | Child | | | Mother | | | Father | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | p-value | odds ratio (95% CI) | N | p-value | odds ratio (95% CI) | N | p-value | odds ratio (95% CI) |
| 2DL2 | 51 | 0.765 | 1.388 (0.432-4.459) | 51 | 0.202 | 0.358 (0.085-1.500) | 18 | 1 | 0.9 (0.133-6.08) |
| 2DL3 | 51 | 0.623 | 1.765 (0.228-13.685) | 51 | 0.04 | 6.923 (1.23-35.956) | 18 | 1 | 0.909 (0.754-1.096) |
| 2DL5 | 50 | 0.145 | 0.368 (0.113-1.198) | 51 | 0.065 | 0.241 (0.058-0.995) | 18 | 0.627 | 0.500 ( 0.068-3.696) |
| 2DP1 | ** | | | 51 | 1 | 0.969 (0.91-1.031) | ** | | |
| 2DS1 | 51 | 0.08 | 0.306 (0.094-0.998) | 51 | 0.565 | 0.642 (0.204-2.017) | 18 | 0.627 | 0.500 (0.068-3.696) |
| 2DS2 | 51 | 0.771 | 0.75 (0.234-2.404) | 51 | 0.543 | 0.595 (0.171-2.071) | 18 | 1 | 1.111 (0.164-7.506) |
| 2DS3 | 44 | 0.738 | 1.447 (0.365-5.735) | 44 | 0.456 | 2.571 (0.475-13.913) | 18 | 1 | 0.600 (0.031-11.473) |
| 2DS4 | 51 | 0.373 | 1.056 (0.949-1.174) | 51 | 0.373 | 1.056 (0.949-1.174) | ** | | |
| 2DS5 | 51 | 0.106 | 0.317 (0.089-1.132) | 51 | 0.563 | 0.667 (0.211-2.106) | 18 | 1 | 2.250 (0.185-27.369) |
| 3DL1 | 51 | 0.134 | 1.118 (0.958-1.304) | 51 | 0.373 | 1.056 (0.949-1.174) | ** | | |
| 3DP1 | 0 | 0.285 | 0.906 (0.811-1.013) | 51 | 1 | 0.969 (0.91-1.031) | 18 | 1 | 0.909 (0.754-1.096) |
| 3DS1 | 51 | 0.07 | 0.311 (0.091-1.065) | 51 | 0.561 | 0.616 (0.196-1.933) | 18 | 1 | 1.333 (0.098-18.192) |
| Haplotype | 51 | 0.128 | 6 (0.687-52.383) | 51 | 0.236 | 4.154 (0.4637-37.513) | 18 | 1 | 1 (0.072-13.868) |

**Table S2:** n values to figures 1 - 6.

| Figure | Group | n | | | |
|---|---|---|---|---|---|
| 1 A + B | female | 23 | | | |
| | male | 28 | | | |
| 1 C + D | age | 51 | | | |
| 2 A | **FM$^{+/-}$** | **child** | **mother** | **father** | |
| | FM$^-$ | 32 | 32 | 13 | |
| | FM$^+$ | 19 | 19 | 7 | |
| 2 B | **child** | **C1/C1** | **C1/C2** | **C2/C2** | |
| | mother | | | | |
| | C1/C1 | 11 | 4 | 0 | |
| | C1/C2 | 10 | 15 | 7 | |
| | C2/C2 | 0 | 4 | 1 | |
| 2 C | **FM$^{+/-}$** | **match** | **mismatch** | | |
| | FM$^-$ mother | 11 | 21 | | |
| | FM$^+$ mother | 14 | 4 | | |
| | FM$^-$ father | 7 | 6 | | |
| | FM$^+$ father | 4 | 3 | | |
| 2 D | match | 26 | | | |
| | mismatch | 25 | | | |
| 2 E + F | C1/C1 match | 11 | | | |
| | C1/C2 match | 15 | | | |
| | non-self | 9 | | | |
| | missing self | 16 | | | |
| 3 A | **FM$^{+/-}$** | **2DL3+** | **2DL3-** | | |
| | FM$^-$ | 31 | 2 | | |
| | FM$^+$ | 16 | 6 | | |
| 3 B | all | 51 | | | |
| 3 C | 2DL3 only | 8 | | | |
| | 2DL2 and 2DL3 | 29 | | | |
| | 2DL2 only | 14 | | | |
| 3 D + E | **FM$^{+/-}$** | **child** | **mother** | | |
| | FM$^-$ | 32 | 32 | | |
| | FM$^+$ | 19 | 19 | | |
| 3 F | **KIR gene motif** | **child** | **mother** | | |
| | A/A cen | 13 | 16 | | |
| | A/B cen | 29 | 31 | | |
| | B/B cen | 9 | 4 | | |
| 3 F | A/A tel | 25 | 27 | | |
| | A/B tel | 24 | 23 | | |
| | B/B tel | 2 | 1 | | |
| 4 | **KIR** | **FM$^-$** | **FM$^+$** | **FM$^-$ act** | **FM$^+$ act** |
| | all act | - | - | 42 | 10 |
| | 2DL1/S1 | 42 | 10 | 42 | 10 |
| | 2DL1/S5 | 30 | 8 | 30 | 8 |
| | 2DL1 | 39 | 9 | 39 | 9 |
| | 2DL2/3/S2(DX27) | 36 | 10 | 36 | 10 |
| | 2DL3 | 42 | 10 | 42 | 10 |
| | 2DL2/3/S2(CH-L) | 18 | 3 | 18 | 3 |
| | 2DL5 | 31 | 9 | 31 | 9 |
| | 2DS4 | 41 | 10 | 41 | 10 |
| | 2DS3/S4 | 31 | 9 | 31 | 9 |
| | NKG2A | 26 | 7 | 26 | 7 |
| 5 A | FM$^-$ | 23 | | | |
| | FM$^+$ | 10 | | | |
| 5 B | FM$^-$ | 23 | | | |
| | FM$^+$ | 13 | | | |
| | father | 16 | | | |
| 6 A | | **mother** | **father** | | |
| | match | 25 | 12 | | |
| | mismatch | 20 | 9 | | |
| 6 B | | **blast** | **K562** | | |
| | HLA-C1/C1 | 19 | 15 | | |
| | HLA-C1/C2 | 16 | 15 | | |
| | HLA-C2/C2 | 4 | 4 | | |
| 6 C | 2DL2+ | 4 | | | |
| | 2DL2/L3+ | 19 | | | |
| | 2DL3+ | 12 | | | |
| 6 D | cen A/A | 16 | | | |
| | cen A/B | 23 | | | |
| | cen B/B | 5 | | | |
| | tel A/A | 23 | | | |
| | tel A/B | 21 | | | |
| | tel B/B | 0 | | | |

**Table S3:** n-values to supplementary figure 1 -4.

| Figure | Group | N | | |
|---|---|---|---|---|
| S1 A | HLA-C | Child | Mother | Father |
| | C1/C1 | 23 | 24 | 16 |
| | C1/C2 | 37 | 38 | 13 |
| | C2/C2 | 10 | 7 | 4 |
| S1 C | FM+/- | non-self | missing-self | |
| | FM- | 8 | 13 | |
| | FM+ | 1 | 3 | |
| S2 | B content score | Child | Mother | Father |
| | 0 | 15 | 10 | 8 |
| | 1 | 27 | 30 | 14 |
| | 2 | 26 | 26 | 3 |
| | 3+4 | 2 | 4 | 3 |
| S3 A | 0 | 7 | | |
| | 1 | 21 | | |
| | 2 | 15 | | |
| | 3+4 | 1 | | |
| S3 B | 0 | 0 | | |
| | 1 | 4 | | |
| | 2 | 7 | | |
| | 3+4 | 1 | | |
| S3 C | 0 | 4 | | |
| | 1 | 13 | | |
| | 2 | 6 | | |
| | 3+4 | 1 | | |
| S3 D | Haplotype | FM- | FM+ | |
| | A | 4 | 0 | |
| | Bx | 19 | 12 | |

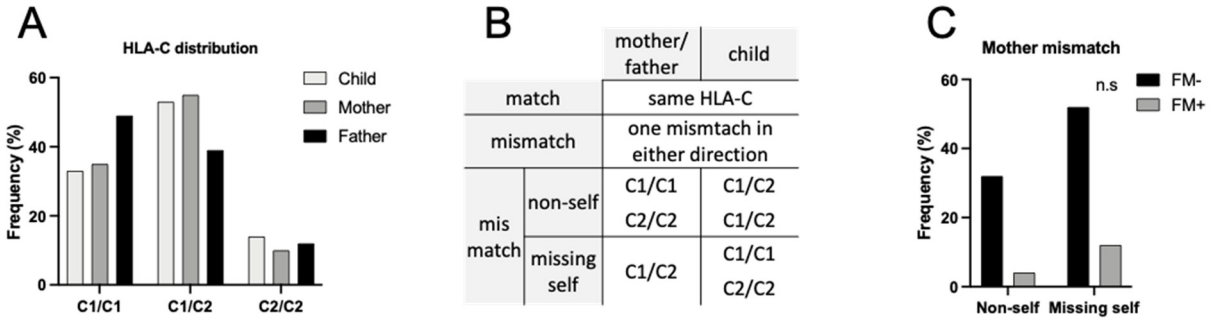


**Figure S1:** Child, mother and father were HLA-C genotyped and grouped according to their HLA-C genotype into HLA-C1/C1 (C1), HLA-C1/C2 (C1/2) or HLA-C2/C2 (C2). (A) HLA-C distribution of the analyzed cohort. (B) Criteria for grouping depending on HLA match or mismatch of mother and child. (C) Mismatched mothers were grouped into mismatch non-self or missing self. Statistical analysis of frequencies was performed using Fisher's exact test for two groups or Chi2 for more than two. Statistical significance $p<0.05$.

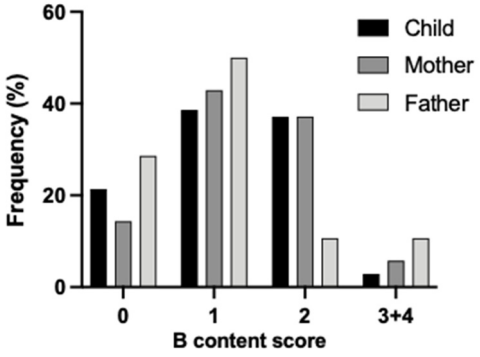


**Figure S2:** B content score frequencies in the analyzed cohort. B content score was determined after KIR genotyping in child, mother and father. Subsequently, they were grouped depending on their B content score.

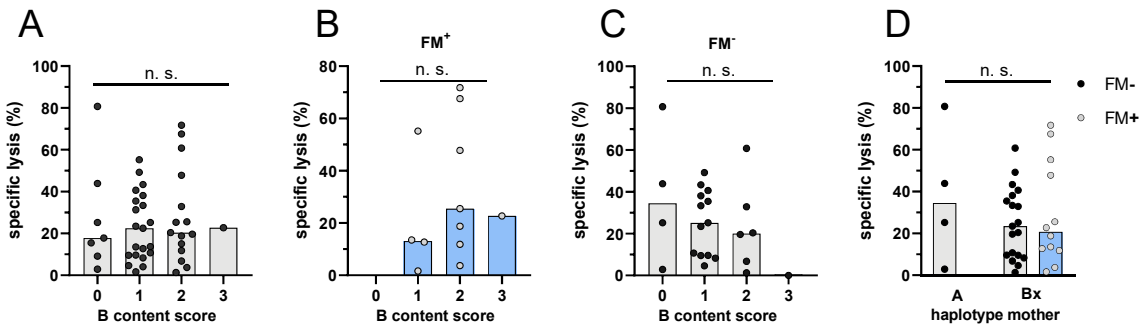


**Figure S3:** Parental cytotoxicity against filial leukemic blasts. Parental NK cells were isolated and IL-2/IL-15 pre-activated overnight. The next day their cytotoxicity was analyzed against filial blasts and the control cell line K562 in a FACS-based killing assay. (A) All mothers were grouped depending on their B content score and the lysis of leukemic blasts was compared between the groups. Mothers were further grouped into (B) FM+ and (C) FM- and the specific lysis was compared between the groups. (D) Mothers were grouped depending on their KIR haplotype and specific lysis of leukemic blasts was compared. Each dot resembles one sample, bars show mean of the group. Statistical analysis was performed using Kruskal-Wallis test followed by Dunn's multiple comparison test for more than two groups. Significance $p<0.05$, n. s. not significant.