

Supplementary Material

How ancestry influences the chances of finding unrelated donors: an investigation in admixed Brazilians

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1. Supplementary Figures

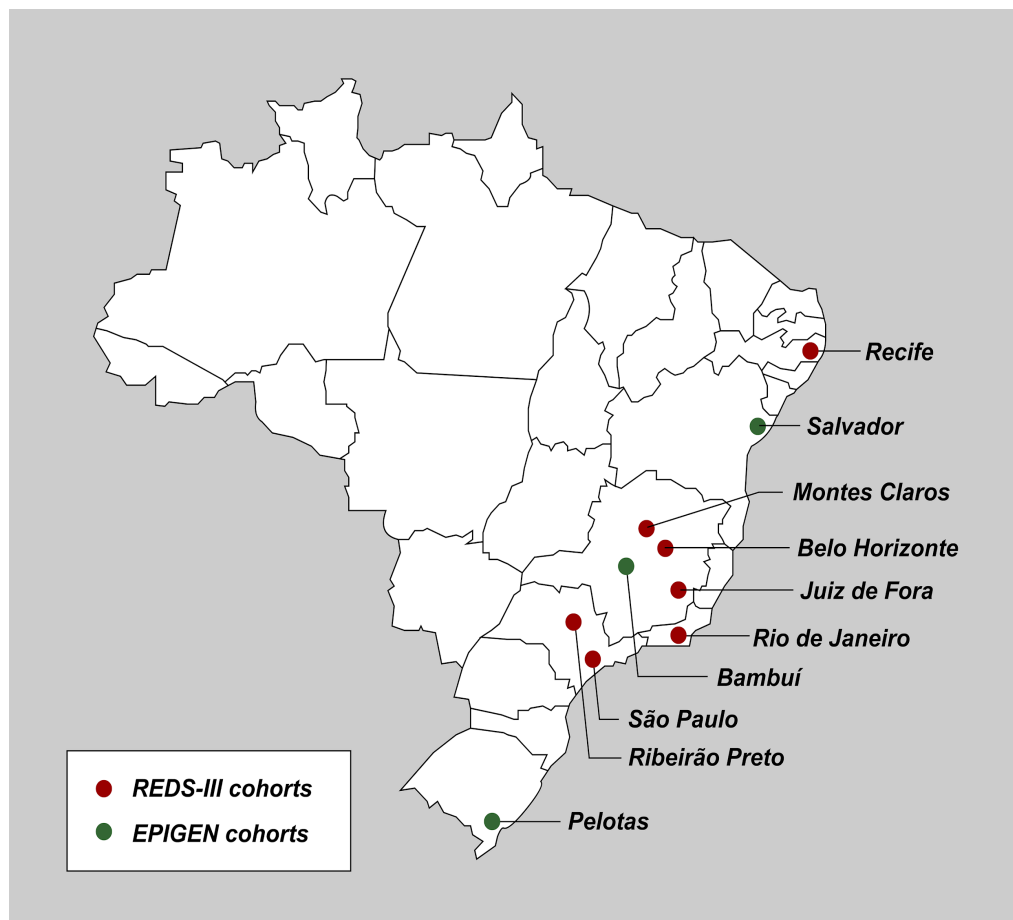


Figure S1. Geographic locations of the REDS-III and EPIGEN cohorts which compose the merged dataset used in our study.

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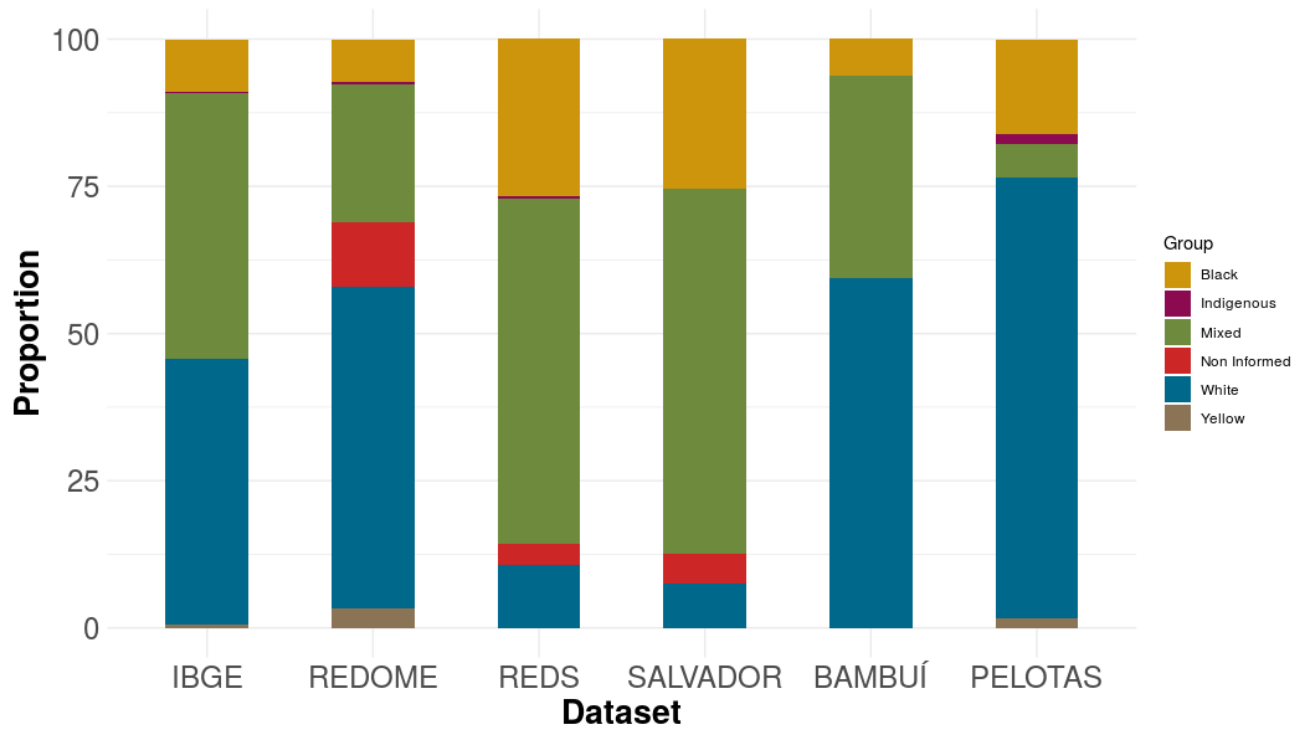


Figure S2. Self-Identification in the Brazilian population (IBGE) and in our datasets. Proportion of self-identified categories “Black”, “Indigenous”, “Mixed”, “White”, “Yellow” and “Non-Informed” for IBGE. REDOME, REDS-III and EPIGEN (Salvador, Bambuí and Pelotas).

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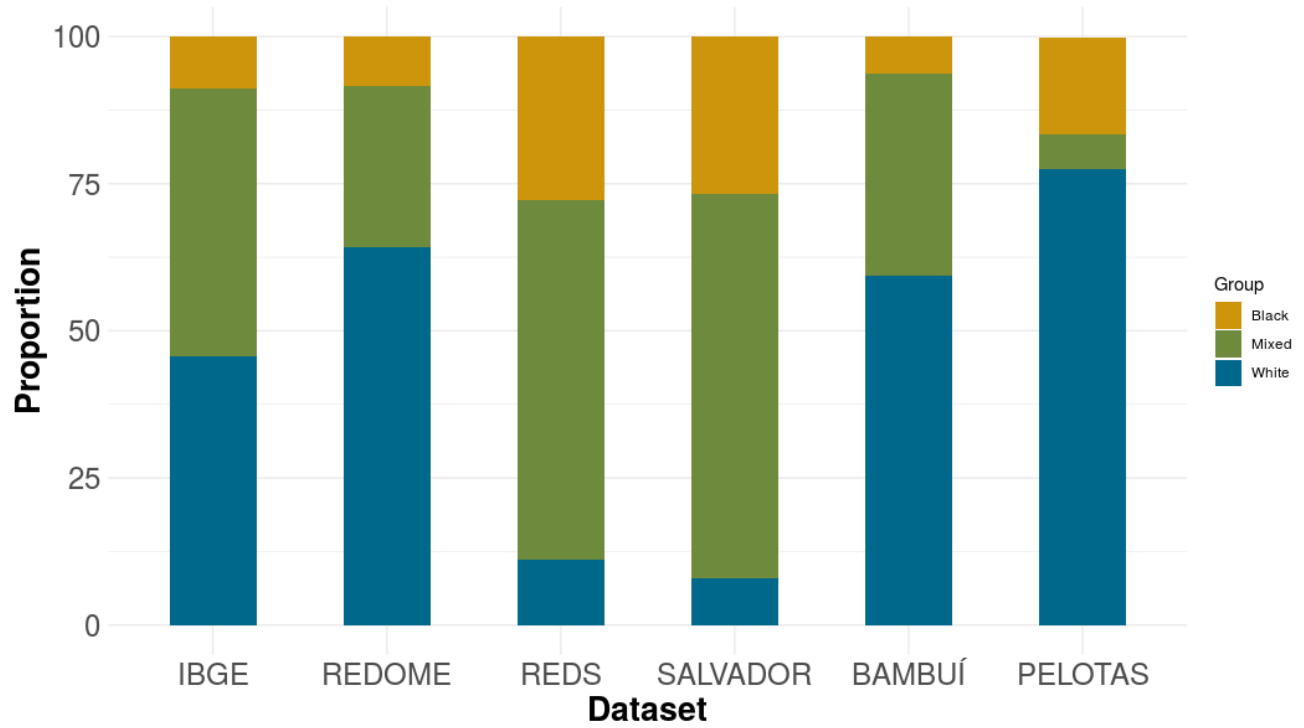


Figure S3. Self-Identification in the Brazilian population (IBGE) and in our datasets. Proportion of self-identified categories “Black”, “Mixed” and “White” for IBGE. REDOME, REDS-III and EPIGEN (BambuÍ, Salvador and Pelotas).

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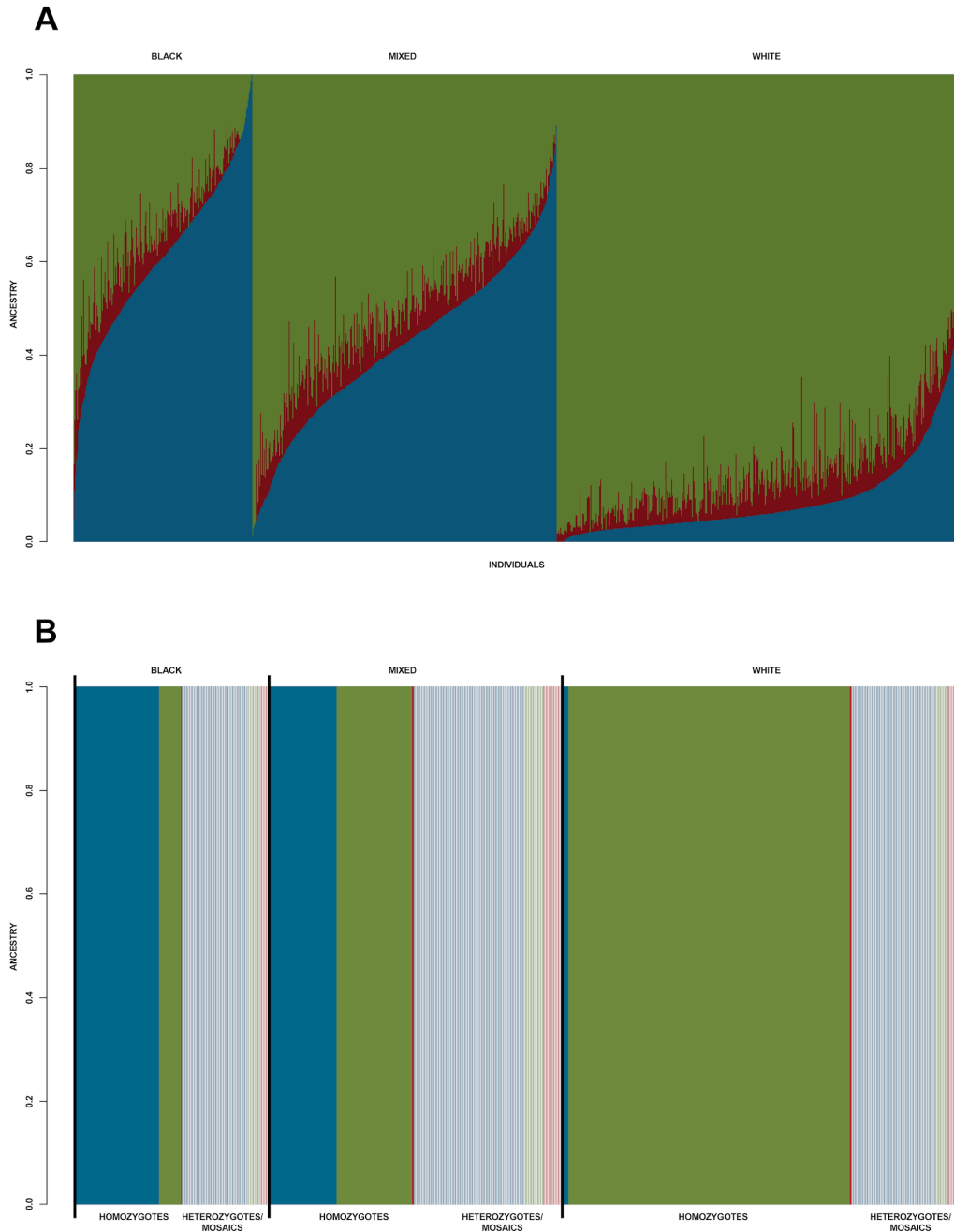


Figure S4. Ancestry inference. **A.** Self-identification and the proportion of genome wide ancestry for REDS+EPIGEN dataset samples. The vertical lines represent the proportion of ancestry inferred in each individual. The colors blue, green and red correspond to African, European and Native American ancestry respectively. **B.** Self-identification and the MHC ancestry for REDS+EPIGEN dataset samples. The vertical lines represent the proportion of ancestry inferred in each chromosome for the MHC region (each two lines represent one individual). The colors blue, green and red correspond to African, European and Native American ancestry respectively, Homozygotes correspond to a single ancestry in the MHC; heterozygotes refer to different ancestry between chromosome and mosaic to situations where there are more than one ancestry on the chromosome.

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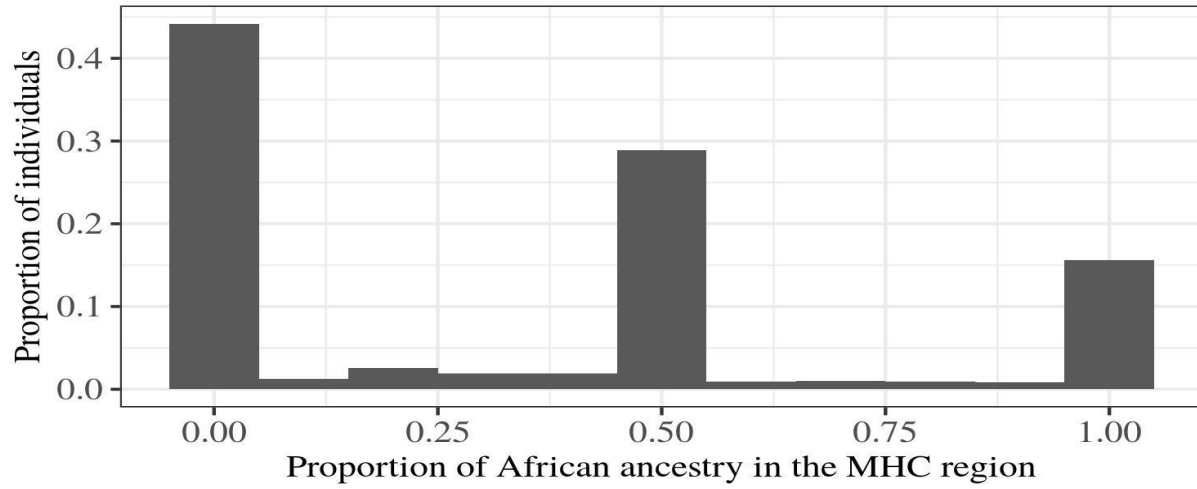


Figure S5. Histogram of the proportions of African ancestry in the MHC region. Proportions equal to 0, 0.5 and 1 correspond to 0, 1 and 2 chromosomes which are of African ancestry at the MHC, respectively. Intermediate values correspond to mosaics of different ancestries at the MHC.

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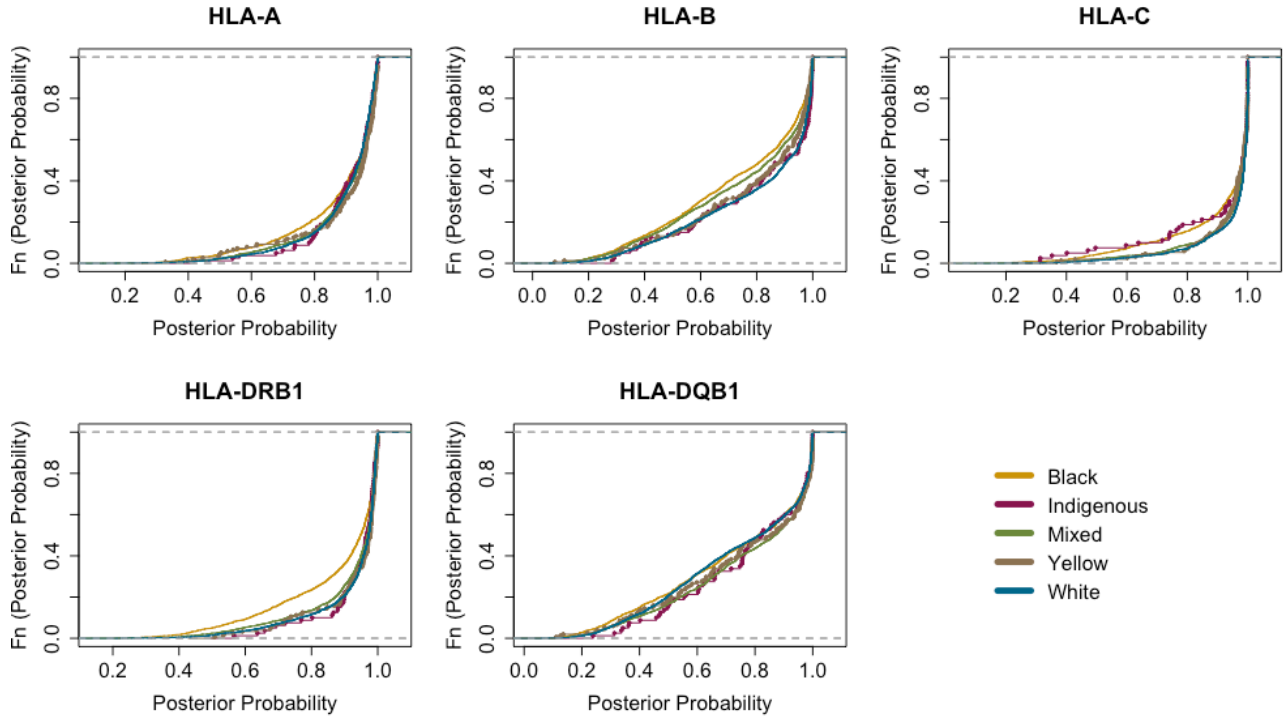


Figure S6. Empirical cumulative distribution function (ECDF) of HLA genotype (two-fields resolution) posterior probability for self-identification: Black (orange), Indigenous (purple), Mixed (green), Yellow (brown), White (blue). The ECDF organizes the posterior probabilities of the HLA genotypes, allowing the cumulative proportion of the genotypes to be observed throughout their distribution. In this case, we observed that self-declared individuals "Black", have lower posterior probabilities distribution than the other categories.

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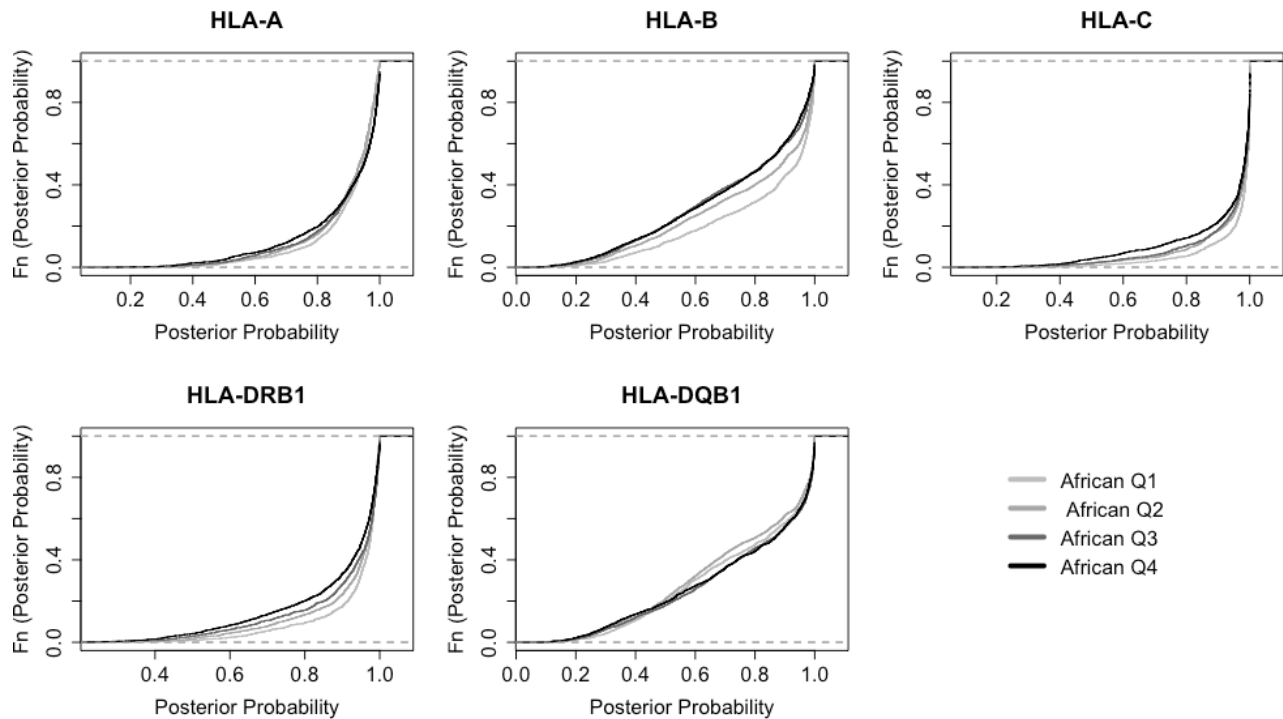


Figure S7. Empirical cumulative distribution function (ECDF) of HLA genotype (two-fields resolution) posterior probability for quartiles of African ancestry: Black (orange), Indigenous (purple), Mixed (green), Yellow (brown), White (blue). The ECDF organizes the posterior probabilities of the HLA genotypes, allowing the cumulative proportion of the genotypes to be observed throughout their distribution.

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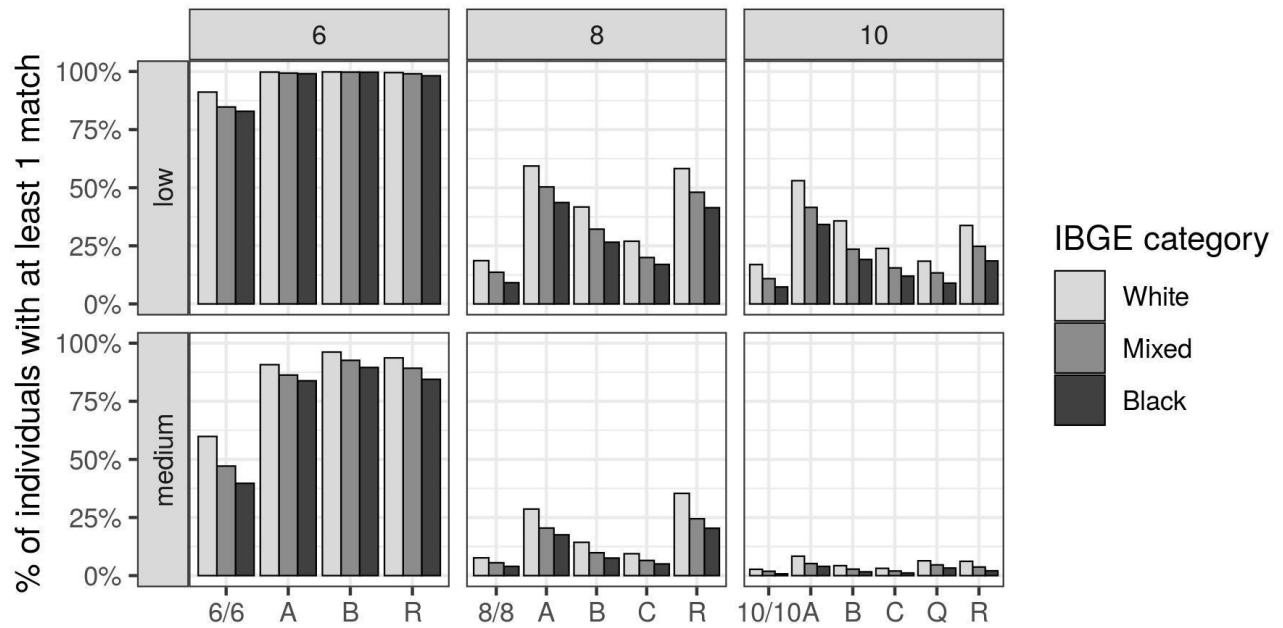


Figure S8. Percentage of individuals from different IBGE categories which found at least one match in REDOME. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed, A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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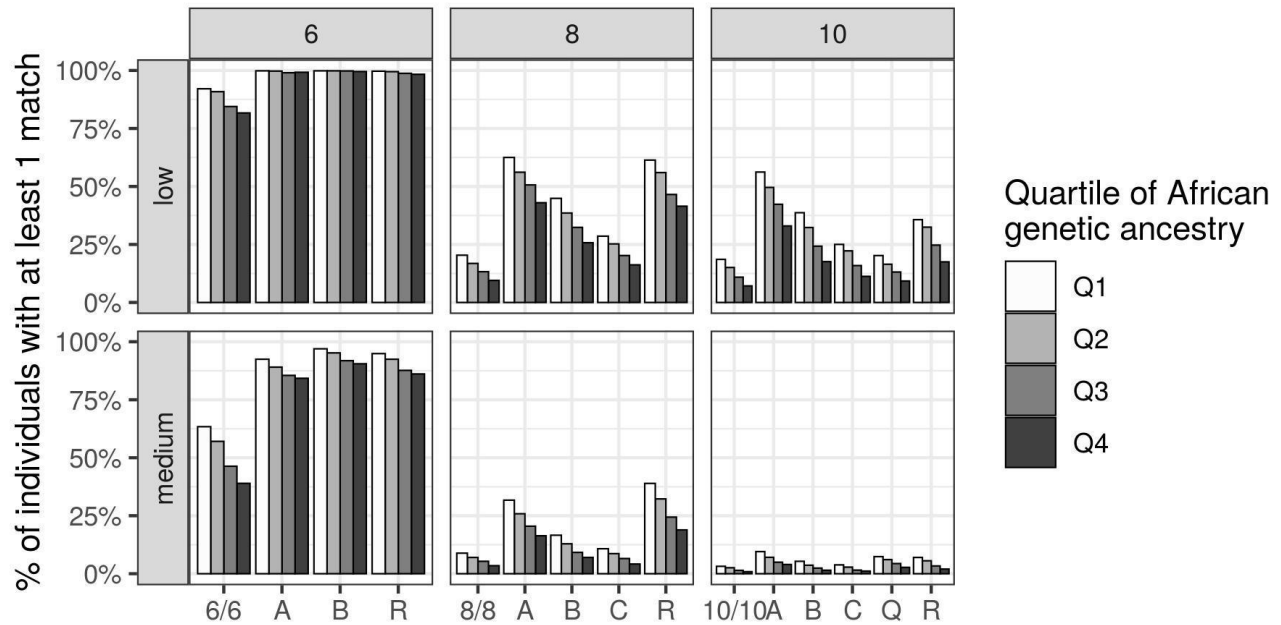


Figure S9. Percentage of individuals at different quartiles of African genetic ancestry which found at least one match in REDOME. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed, A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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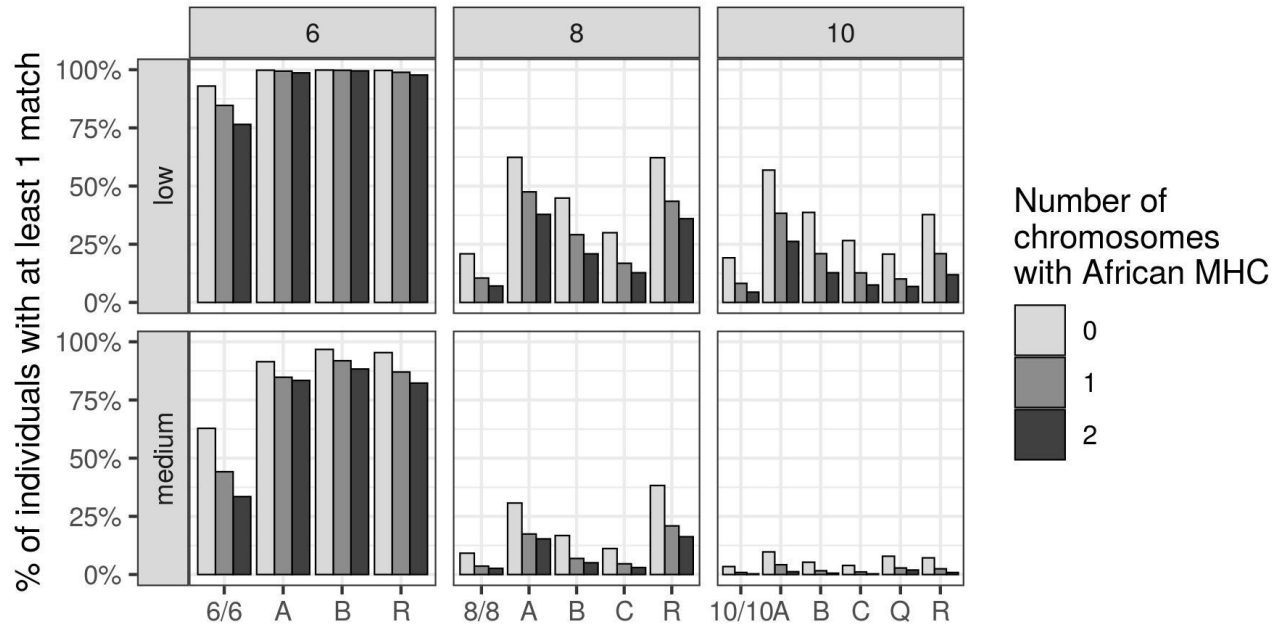


Figure S10. Percentage of individuals who found at least one match in REDOME, according to the number of chromosomes with African MHC which they carry. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed. A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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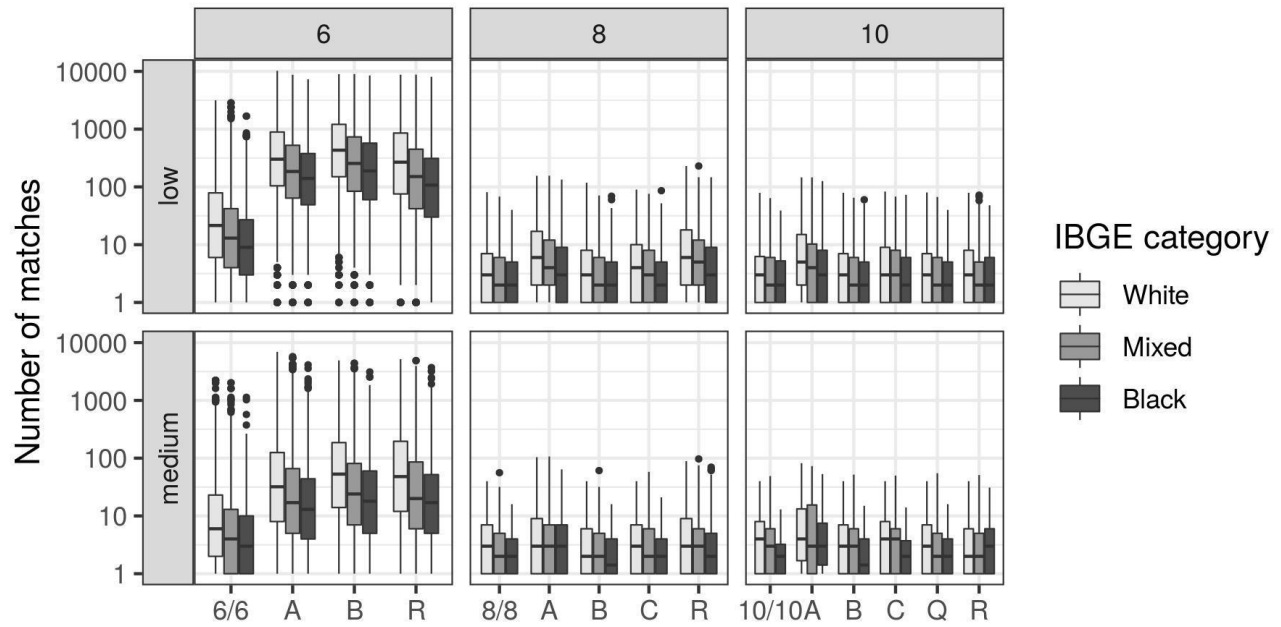


Figure S11. Boxplot of the number of matches in REDOME for individuals from different IBGE categories. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed. A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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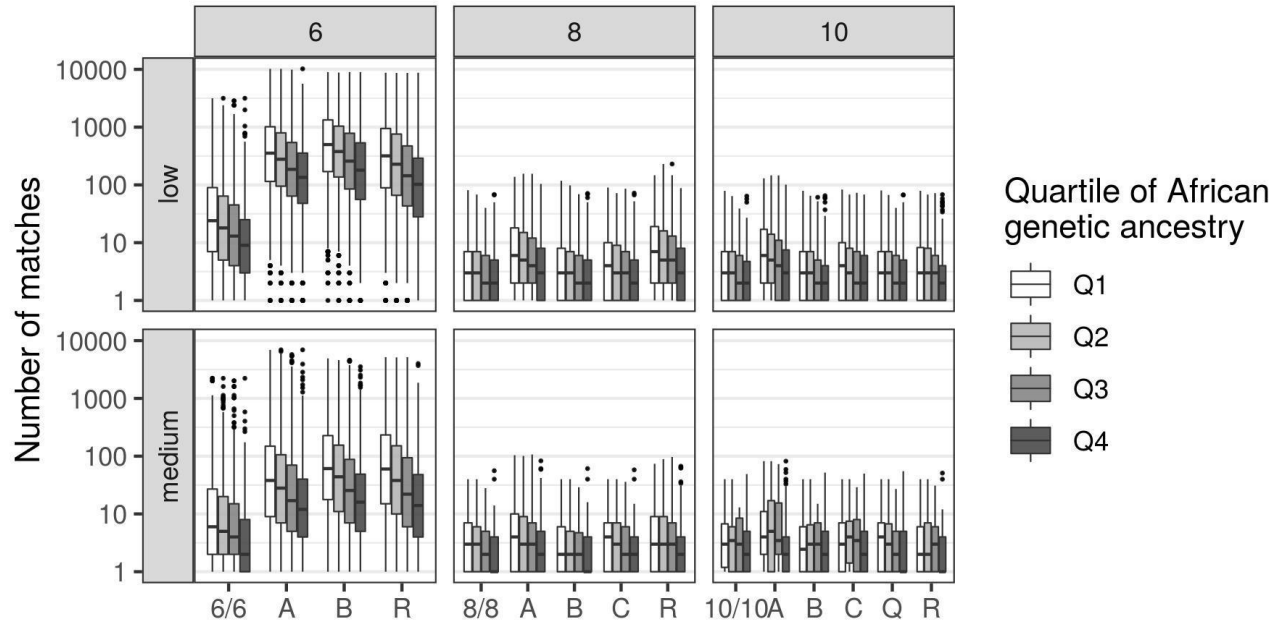


Figure S12. Boxplot of the number of matches in REDOME for individuals at different quartiles of African genetic ancestry. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed. A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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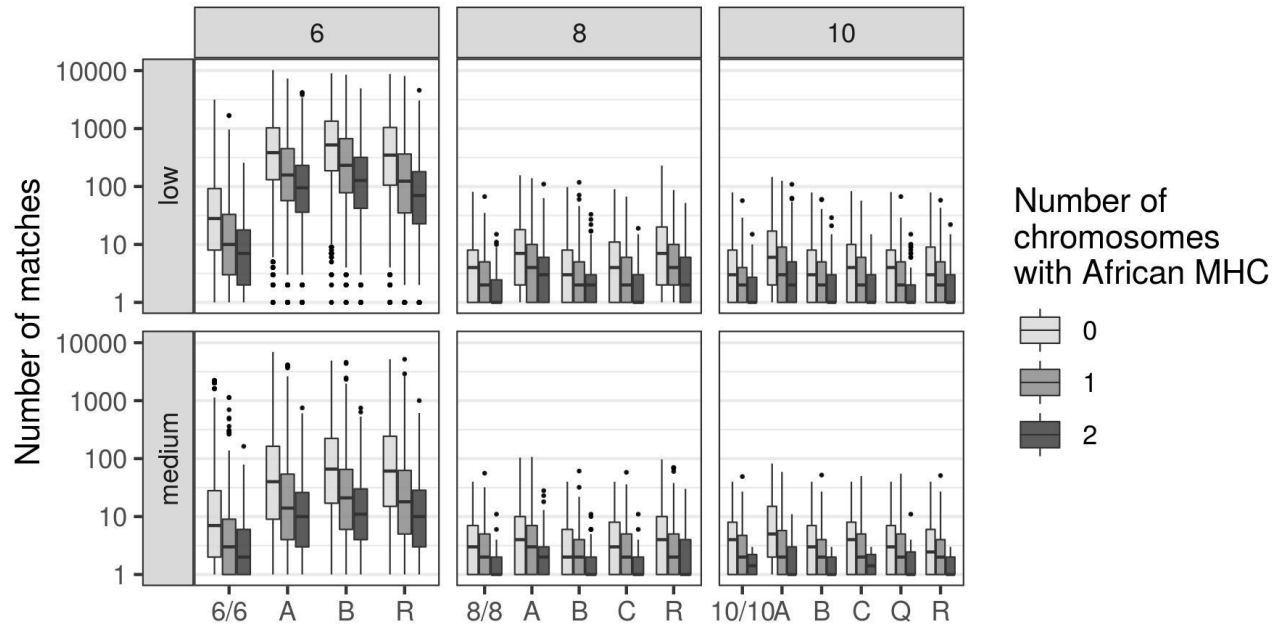


Figure S13. Boxplot of the number of matches in REDOME for individuals with a different number of chromosomes with African MHC. Columns correspond to matches at 6, 8, 10 alleles. Rows correspond to low and medium HLA typing resolution. The x-axis labels refer to either full matches (6/6, 8/8, 10/10) or the locus where a mismatch was allowed. A: *HLA-A*; B: *HLA-B*; C: *HLA-C*; Q: *HLA-DQB1*; R: *HLA-DRB1*.

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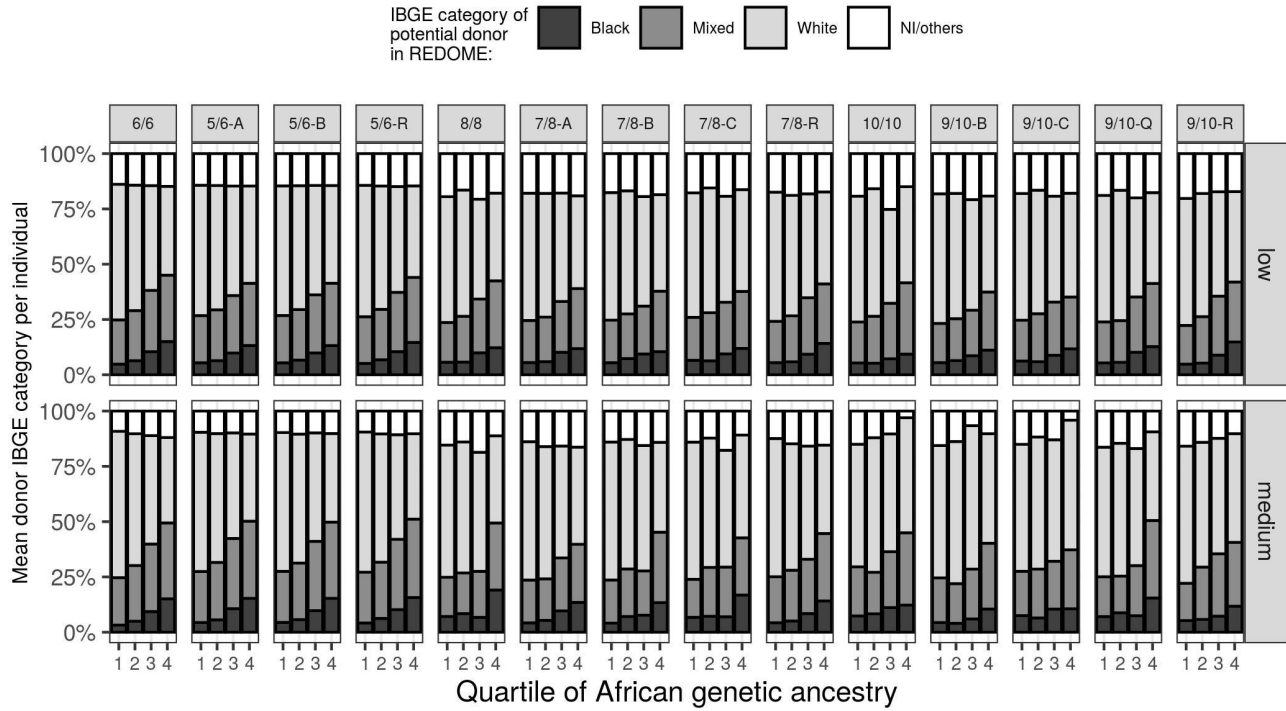


Figure S15. Mean IBGE category of donor in REDOME for individuals at different quartiles of African genetic ancestry. Columns correspond to the number of alleles with full or partial match. For example, “6/6” refers to a full match at *HLA-A*, *HLA-B*, and *HLA-DRB1*, whereas “5/6-A” refers to a mismatch at *HLA-A*. Rows correspond to low and medium HLA typing resolution.

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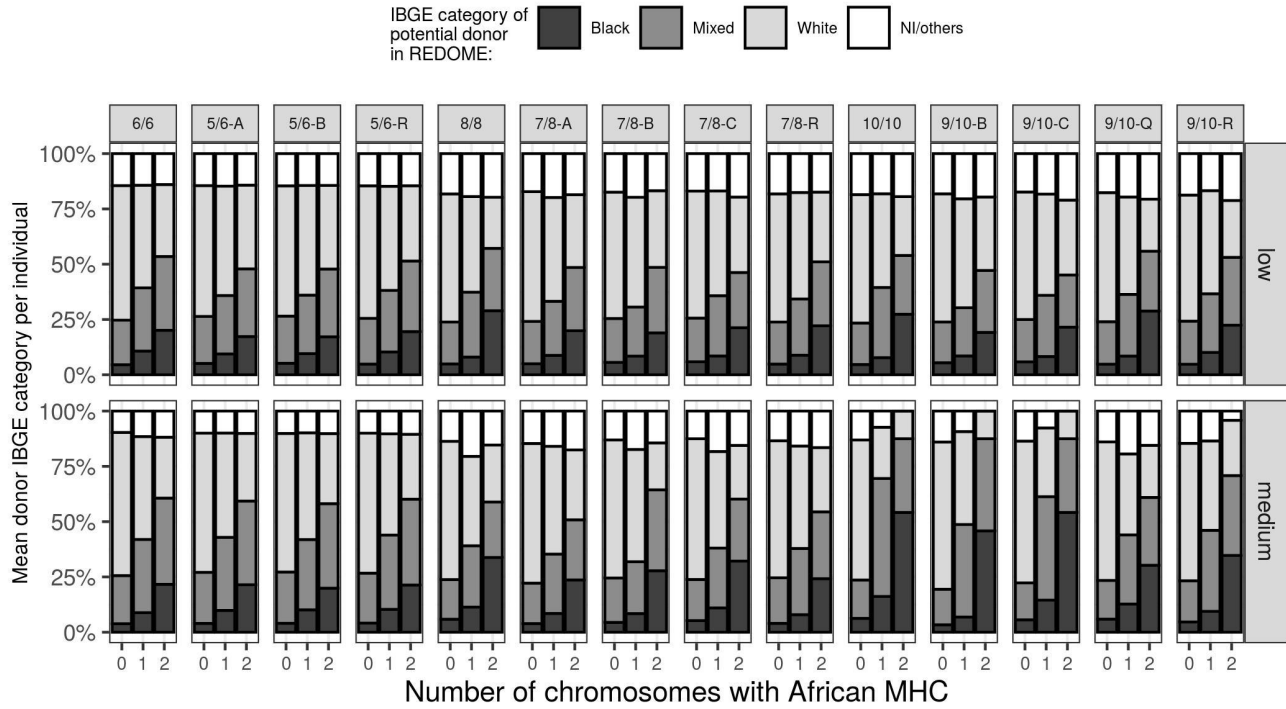


Figure S16. Mean IBGE category of donor in REDOME for individuals with a different number of chromosomes with African MHC. Columns correspond to the number of alleles with full or partial match. For example, “6/6” refers to a full match at *HLA-A*, *HLA-B*, and *HLA-DRB1*, whereas “5/6-A” refers to a mismatch at *HLA-A*. Rows correspond to low and medium HLA typing resolution.

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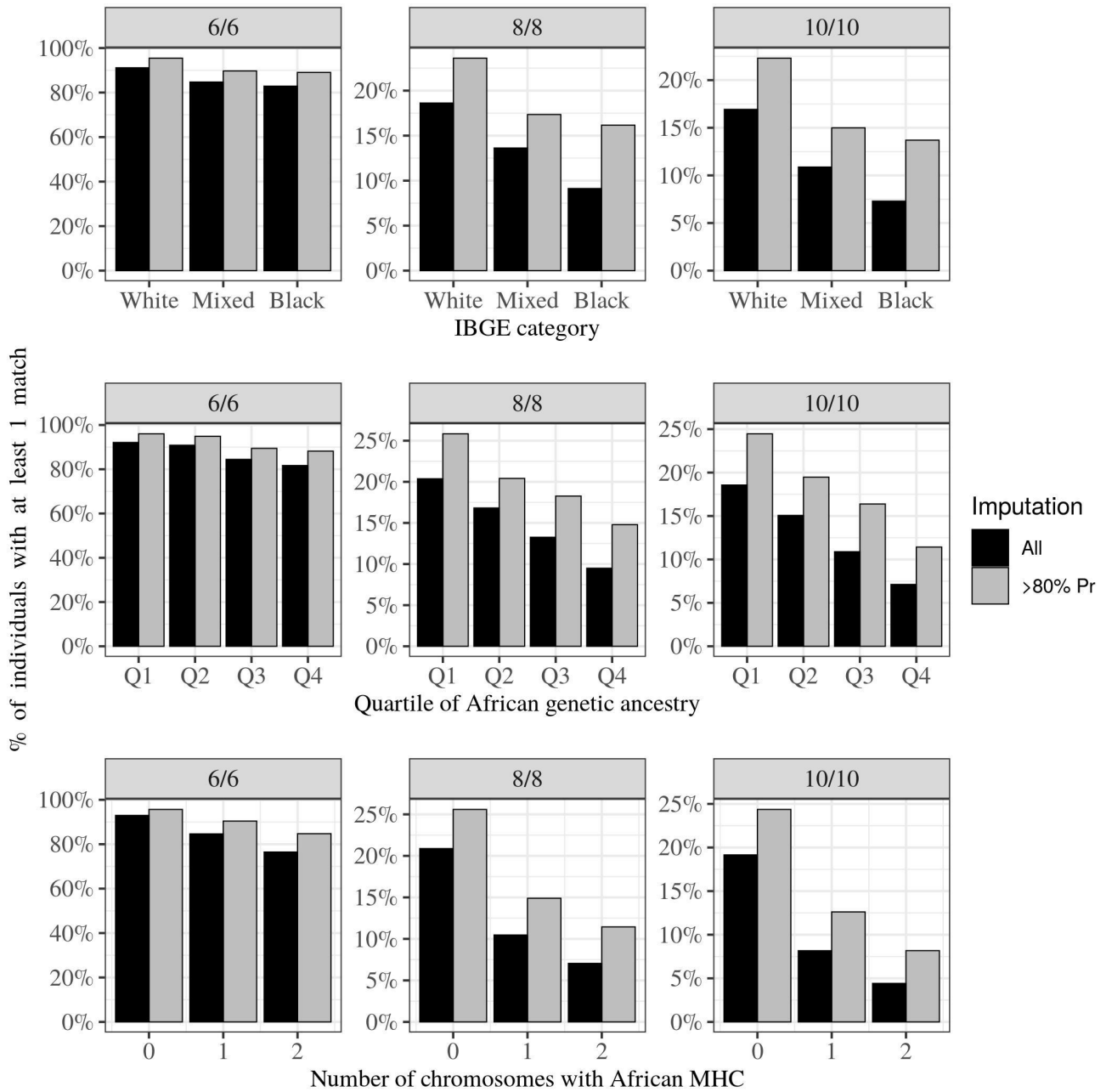


Figure S17. Percentage of individuals with at least one match in REDOME for low resolution 6/6, 8/8 and 10/10, in the whole merged dataset ("All") and in the subset of individuals with posterior probability of imputation >80% (">80% Pr"). Top row: IBGE categories; Middle row: Quartile of African ancestry; Bottom row: Number of chromosomes with African MHC per individual.

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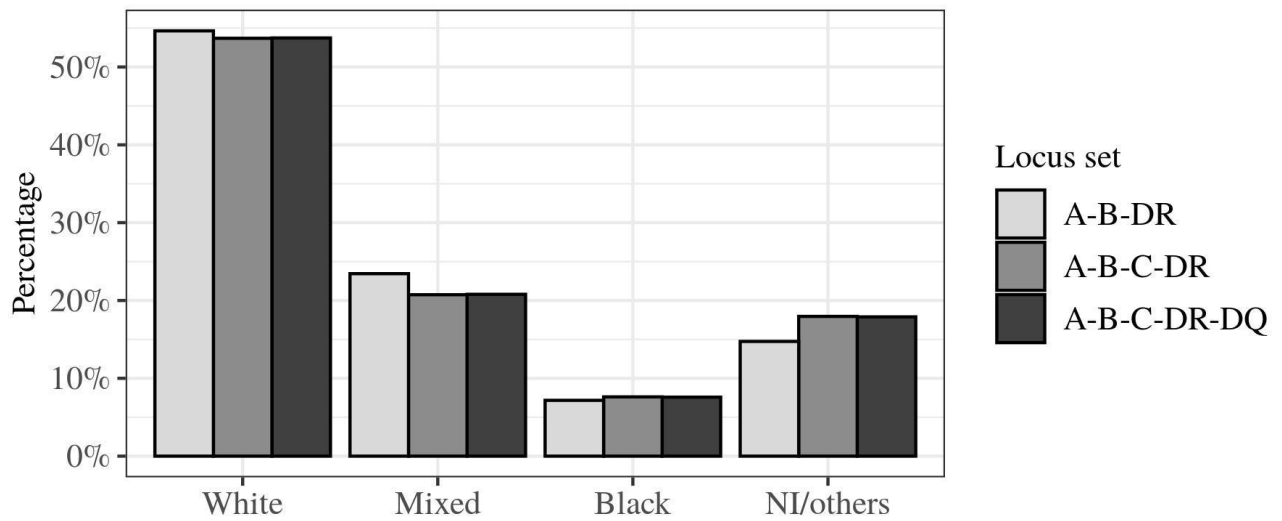


Figure S18. Percentage of "White", "Mixed", and "Black" individuals in the REDOME database according to the number of genotyped loci. NI/others: Non-informed category and other groups which are a minority in the database.

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Supplementary Tables

Table S1. Out of bagging accuracy for each HLA imputation model (2 fields resolution).

| GENE | N individuals reference panel | N HLA alleles reference panel | Average out-of-bag accuracy (sd) – TM array | Average out-of-bag accuracy (sd) - HumanOmin 2.5 array |
|-----------------|-------------------------------|-------------------------------|---|--|
| <i>HLA-A</i> | 2.503 | 82 | 95.37% ± 0.50% | 95.62% ± 0.46% |
| <i>HLA-B</i> | 2.498 | 154 | 90.97% ± 0.84% | 89.60% ± 0.66% |
| <i>HLA-C</i> | 2.503 | 62 | 98.28% ± 0.30% | 97.88% ± 0.32% |
| <i>HLA-DRB1</i> | 2.502 | 72 | 92.29% ± 0.75% | 89.80% ± 0.67% |
| <i>HLA-DQB1</i> | 2.502 | 30 | 97.88% ± 0.33% | 98.22% ± 0.31% |

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Table S3. Summary statistics based on imputation posterior probabilities (2-fields resolution) by African ancestry quartile.

| African Ancestry | Q1 | Q2 | Q3 | Q4 |
|------------------|------|------|------|------|
| HLA-A | | | | |
| Min. | 0.15 | 0.17 | 0.24 | 0.13 |
| 1st Qu. | 0.87 | 0.86 | 0.85 | 0.84 |
| Median | 0.94 | 0.93 | 0.95 | 0.95 |
| Mean | 0.9 | 0.89 | 0.89 | 0.88 |
| 3rd Qu. | 0.97 | 0.98 | 0.99 | 0.99 |
| Max. | 1.00 | 1.00 | 1.00 | 1.00 |
| HLA-B | | | | |
| Min. | 0.11 | 0.06 | 0.06 | 0.05 |
| 1st Qu. | 0.7 | 0.6 | 0.55 | 0.55 |
| Median | 0.94 | 0.89 | 0.83 | 0.83 |
| Mean | 0.83 | 0.78 | 0.74 | 0.74 |
| 3rd Qu. | 0.99 | 0.98 | 0.97 | 0.96 |
| Max. | 1.00 | 1.00 | 1.00 | 1.00 |
| HLA-C | | | | |
| Min. | 0.16 | 0.2 | 0.12 | 0.15 |
| 1st Qu. | 0.97 | 0.95 | 0.94 | 0.92 |
| Median | 0.99 | 0.99 | 0.99 | 0.98 |
| Mean | 0.96 | 0.94 | 0.94 | 0.92 |
| 3rd Qu. | 1.00 | 1.00 | 1.00 | 1.00 |
| Max. | 1.00 | 1.00 | 1.00 | 1.00 |
| HLA-DRB1 | | | | |
| Min. | 0.29 | 0.21 | 0.14 | 0.2 |
| 1st Qu. | 0.93 | 0.91 | 0.89 | 0.85 |
| Median | 0.98 | 0.97 | 0.97 | 0.95 |
| Mean | 0.93 | 0.92 | 0.9 | 0.88 |
| 3rd Qu. | 0.99 | 0.99 | 0.99 | 0.99 |
| Max. | 1.00 | 1.00 | 1.00 | 1.00 |
| HLA-DQB1 | | | | |
| Min. | 0.11 | 0.06 | 0.08 | 0.09 |
| 1st Qu. | 0.56 | 0.54 | 0.59 | 0.57 |
| Median | 0.84 | 0.79 | 0.85 | 0.86 |
| Mean | 0.75 | 0.73 | 0.76 | 0.76 |
| 3rd Qu. | 0.98 | 0.97 | 0.98 | 0.98 |
| Max. | 1.00 | 1.00 | 1.00 | 1.00 |

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Table S4. Number of the HLA alleles in REDOME with low, medium and high resolution in each locus.

| RESOLUTION | <i>HLA-A</i> | | <i>HLA-B</i> | | <i>HLA-DRB1</i> | | <i>HLA-C</i> | | <i>HLA-DQB1</i> | |
|--------------------------------------|--------------|-----------|--------------------------|---------------------|---------------------|-----------|--------------|----------|-----------------|----------|
| | Allele 1 | Allele 2 | Allele 1 | Allele 2 | Allele 1 | Allele 2 | Allele 1 | Allele 2 | Allele 1 | Allele 2 |
| Low | 1,197,049 | 1,146,134 | 1,153,141 | 1,150,282 | 1,069,653 | 1,073,172 | 3,522 | 3,350 | 4,714 | 4,758 |
| Medium | 3,462,270 | 3,476,252 | 3,265,931 | 3,261,826 | 3,223,108 | 3,283,191 | 88,011 | 88,226 | 145,895 | 150,374 |
| High | 64,643 | 101,576 | 304,890 | 311,854 | 431,201 | 367,599 | 30,263 | 30,220 | 77,650 | 73,127 |
| Total (medium-high) | | | 4,723,962 (3,179,618) | | | | 121,796 | | 228,259 | |
| A~C~B~DRB1 (medium-high) | | | | 121,796 (76,184) | | | | | | |
| A~C~B~DRB1 ~DQB1 (medium-high) | | | | | 106,623 (65,129) | | | | | |

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Tables S5. Likelihood of having a low-resolution 6/6, 8/8, 10/10 matched donor by IBGE category

| Combination | Group | N | % Match | OR | 95% CI | p-value |
|-------------|-------|-------|---------|-------|---------------|----------|
| 6/6 | Black | 1,589 | 82.8 | - | - | - |
| 6/6 | Mixed | 2,620 | 84.7 | 0.849 | 0.720 - 1.00 | 0.05 |
| 6/6 | White | 3,544 | 91.1 | 0.450 | 0.379 - 0.532 | < 2e-16 |
| 8/8 | Black | 1,589 | 9.1 | - | - | - |
| 8/8 | Mixed | 2,620 | 13.6 | 0.629 | 0.515 - 0.764 | 3.8e-06 |
| 8/8 | White | 3,544 | 18.6 | 0.441 | 0.366 - 0.528 | <2e-16 |
| 10/10 | Black | 1,589 | 7.3 | - | - | - |
| 10/10 | Mixed | 2,620 | 10.8 | 0.632 | 0.507 - 0.782 | 3.17e-05 |
| 10/10 | White | 3,544 | 16.9 | 0.388 | 0.316 - 0.473 | <2e-16 |

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Table S6. Likelihood of having low-resolution 6/6, 8/8, 10/10 matched donor by African genetic ancestry quartile.

| Combination | African Quartile | N | % Match | OR | 95% CI | p-value |
|-------------|------------------|-------|---------|------|-------------|----------|
| 6/6 | Q4 | 2,206 | 82.00 | - | - | - |
| 6/6 | Q3 | 2,205 | 84.58 | 1.06 | 0.85 – 1.31 | 0.62 |
| 6/6 | Q2 | 2,205 | 90.87 | 1.95 | 1.61 – 2.38 | 1.83e-11 |
| 6/6 | Q1 | 2,206 | 92.10 | 2.57 | 2.13 – 3.12 | <2e-16 |
| 8/8 | Q4 | 2,206 | 9.6 | - | - | - |
| 8/8 | Q3 | 2,205 | 13.08 | 1.16 | 0.99 – 1.34 | 0.052 |
| 8/8 | Q2 | 2,205 | 17.21 | 1.66 | 1.44 – 1.95 | 5.19e-10 |
| 8/8 | Q1 | 2,206 | 20.36 | 2.35 | 1.98 – 2.80 | <2e-16 |
| 10/10 | Q4 | 2,206 | 7.3 | - | - | - |
| 10/10 | Q3 | 2,205 | 10.74 | 1.16 | 0.99 – 1.35 | 0.065 |
| 10/10 | Q2 | 2,205 | 15.32 | 1.87 | 1.58 – 2.22 | 8.03e-13 |
| 10/10 | Q1 | 2,206 | 18.52 | 2.83 | 2.34 – 3.43 | <2e-16 |

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Table S7. Number of potential donors between ancestries (Mann-Whitney test with Holm correction for multiple testing).

| Ancestry | Loci Set | Group1 | Group2 | p.value | signif_05 |
|------------------|----------|--------|--------|----------|-----------|
| IBGE categories | 6/6 | Mixed | Black | 4.99e-09 | TRUE |
| IBGE categories | 6/6 | White | Black | 1.06e-42 | TRUE |
| IBGE categories | 6/6 | White | Mixed | 2.29e-21 | TRUE |
| IBGE categories | 8/8 | Mixed | Black | 2.80e-01 | FALSE |
| IBGE categories | 8/8 | White | Black | 5.36e-03 | TRUE |
| IBGE categories | 8/8 | White | Mixed | 1.71e-02 | TRUE |
| IBGE categories | 10/10 | Mixed | Black | 4.56e-01 | FALSE |
| IBGE categories | 10/10 | White | Black | 9.02e-02 | FALSE |
| IBGE categories | 10/10 | White | Mixed | 1.10e-01 | FALSE |
| Genetic ancestry | 6/6 | Q2 | Q1 | 1.57e-05 | TRUE |
| Genetic ancestry | 6/6 | Q3 | Q1 | 4.68e-20 | TRUE |
| Genetic ancestry | 6/6 | Q4 | Q1 | 5.26e-56 | TRUE |
| Genetic ancestry | 6/6 | Q3 | Q2 | 5.73e-07 | TRUE |
| Genetic ancestry | 6/6 | Q4 | Q2 | 4.61e-32 | TRUE |
| Genetic ancestry | 6/6 | Q4 | Q3 | 2.81e-11 | TRUE |
| Genetic ancestry | 8/8 | Q2 | Q1 | 6.10e-01 | FALSE |
| Genetic ancestry | 8/8 | Q3 | Q1 | 1.83e-01 | FALSE |
| Genetic ancestry | 8/8 | Q4 | Q1 | 2.12e-04 | TRUE |

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| | | | | | |
|------------------|-------|----|----|----------|-------|
| Genetic ancestry | 8/8 | Q3 | Q2 | 3.88e-01 | FALSE |
| Genetic ancestry | 8/8 | Q4 | Q2 | 1.90e-03 | TRUE |
| Genetic ancestry | 8/8 | Q4 | Q3 | 6.29e-02 | FALSE |
| Genetic ancestry | 10/10 | Q2 | Q1 | 7.78e-01 | FALSE |
| Genetic ancestry | 10/10 | Q3 | Q1 | 1.82e-01 | FALSE |
| Genetic ancestry | 10/10 | Q4 | Q1 | 6.89e-03 | TRUE |
| Genetic ancestry | 10/10 | Q3 | Q2 | 3.00e-01 | FALSE |
| Genetic ancestry | 10/10 | Q4 | Q2 | 1.79e-02 | TRUE |
| Genetic ancestry | 10/10 | Q4 | Q3 | 3.00e-01 | FALSE |

| | | | | | |
|--------------|-------|---|---|-----------|------|
| MHC ancestry | 6/6 | 1 | 0 | 1.10e-81 | TRUE |
| MHC ancestry | 6/6 | 2 | 0 | 1.16e-116 | TRUE |
| MHC ancestry | 6/6 | 2 | 1 | 2.80e-15 | TRUE |
| MHC ancestry | 8/8 | 1 | 0 | 3.38e-06 | TRUE |
| MHC ancestry | 8/8 | 2 | 0 | 2.47e-11 | TRUE |
| MHC ancestry | 8/8 | 2 | 1 | 1.34e-04 | TRUE |
| MHC ancestry | 10/10 | 1 | 0 | 3.68e-05 | TRUE |
| MHC ancestry | 10/10 | 2 | 0 | 3.03e-07 | TRUE |
| MHC ancestry | 10/10 | 2 | 1 | 2.45e-03 | TRUE |

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Table S8. Proportion of SCD patients eligible for transplantation with at least one match in REDOME, median number of matches and the maximum number of matches at low and medium resolution.

| Loci | Low resolution | | | Medium resolution | | |
|-------|----------------------|--------------------------|---------------------------|----------------------|--------------------------|---------------------------|
| | % at least one match | Median number of matches | Maximum number of matches | % at least one match | Median number of matches | Maximum number of matches |
| 6/6 | 85.4 | 11 | 658 | 45.8 | 3 | 315 |
| 8/8 | 9.6 | 2 | 35 | 3.6 | 1 | 14 |
| 10/10 | 8.1 | 2 | 18 | 0.9 | 1 | 5 |

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Tables S9. Proportion of individuals with at least one match in REDOME for several dataset combinations.

| Dataset | 6/6 | 8/8 | 10/10 |
|--------------------------|---------------|---------------|---------------|
| LOW RESOLUTION | | | |
| REDS-III+EPIGEN | 7,024 (87.4%) | 1,211 (15.1%) | 1,042 (13.0%) |
| EPIGEN | 4,737 (88.8%) | 873 (16.4%) | 770 (14.4%) |
| Bambuí+Pelotas | 3,934 (89.1%) | 712 (16.2%) | 622 (14.1%) |
| REDS-III | 2,287 (84.6%) | 338 (12.5%) | 272 (10.1%) |
| REDS-Transplant* | 356 (85.37%) | 40 (9.6%) | 34 (8.1%) |
| MEDIUM RESOLUTION | | | |
| REDS-III+EPIGEN | 4,122 (51.3%) | 494 (6.1%) | 158 (2.0%) |
| EPIGEN | 2,887 (54.1%) | 365 (6.8%) | 122 (2.3%) |
| Bambuí+Pelotas | 2,510 (56.8%) | 314 (7.1%) | 104 (2.3%) |
| REDS-III | 1,235 (45.7%) | 129 (4.8%) | 36 (1.3%) |
| REDS-Transplant* | 191 (45.8%) | 15 (3.6%) | 4 (1.0%) |

* REDS-SCD patients eligible for transplantation based on the classification by Flor-Park and col. 2019.

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Table S10. Comparison of the proportion of at least one match between the datasets using the Z- test (p-value)

| Dataset I | Dataset II | 6/6 z-score (p-value) | 8/8 z-score (p-value) | 10/10 z-score (p-value) |
|-------------------|----------------|--------------------------|--------------------------|----------------------------|
| LOW RESOLUTION | | | | |
| REDS transplant* | REDS-III | 0.402 (0.689) | -1.696 (0.089) | -1.220 (0.222) |
| REDS transplant* | EPIGEN | -2.123 (0.034) | -3.646 (<0.0003) | -3.563 (0.0004) |
| REDS transplant* | BambuÍ+Pelotas | -2.295 (0.021) | -3.517 (0.0004) | -3.380 (0.00007) |
| REDS-III | EPIGEN | -5.357 (<0.0001) | -4.573 (<0.0001) | -4.970 (<0.0001) |
| REDS-III | BambuÍ+Pelotas | -5.519 (<0.0001) | -4.179 (<0.0001) | -5.513 (<0.0001) |
| MEDIUM RESOLUTION | | | | |
| REDS transplant* | REDS-III | 0.043 (0.968) | -1.065 (0.289) | -0.629 (0.5287) |
| REDS transplant* | EPIGEN | -3.281 (0.001) | -2.569 (0.010) | -1.784 (0.075) |
| REDS transplant* | BambuÍ+Pelotas | -4.338 (<0.0001) | -2.723 (0.006) | -1.843 (0.065) |
| REDS-III | EPIGEN | -7.147 (<0.0001) | -3.651 (0.0002) | -2.915 (0.003) |
| REDS-III | BambuÍ+Pelotas | -9.143 (<0.0001) | -3.963 (0.00008) | -3.017 (0.002) |

* REDS-SCD patients eligible for transplantation based on the classification by Flor-Park and col. 2019.

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Tables S11. Likelihood of having a 6/6, 8/8, 10/10 matched donor by IBGE category for high imputation quality dataset (posterior probability >0.8).

| Combination | Resolution | Group | N | % Match | OR | 95% CI | p-value |
|-------------|------------|-------|-------|---------|-------|---------------|----------|
| 6/6 | LOW | Black | 374 | 89.3 | - | - | - |
| 6/6 | LOW | Mixed | 870 | 90.2 | 0.904 | 0.612 - 1.00 | 0.619 |
| 6/6 | LOW | White | 1,223 | 95.9 | 0.356 | 0.231 - 0.531 | 2.95e-06 |
| 8/8 | LOW | Black | 374 | 16.6 | - | - | - |
| 8/8 | LOW | Mixed | 870 | 18.0 | 0.902 | 0.649 - 1.00 | 0.533 |
| 8/8 | LOW | White | 1,223 | 25.3 | 0.587 | 0.431 - 0.789 | 0.0005 |
| 10/10 | LOW | Black | 374 | 14.2 | - | - | - |
| 10/10 | LOW | Mixed | 870 | 15.9 | 0.876 | 0.617 - 1.00 | 0.448 |
| 10/10 | LOW | White | 1,223 | 23.9 | 0.524 | 0.377 - 0.715 | 7.15e-05 |

Supplementary Material

Table S12. Likelihood of having a 6/6, 8/8, 10/10 matched donor by African genetic ancestry quartile for high imputation quality dataset (posterior probability >0.8).

| Combination | Resolution | African Quartile | N | % Match | OR | 95% CI | p-value |
|-------------|------------|------------------|-----|---------|------|-------------|----------|
| 6/6 | LOW | Q4 | 639 | 88.9 | - | - | - |
| 6/6 | LOW | Q3 | 638 | 90.1 | 1.00 | 0.55 – 1.81 | 0.99 |
| 6/6 | LOW | Q2 | 638 | 96.4 | 2.93 | 1.82 – 4.89 | 1.72e-05 |
| 6/6 | LOW | Q1 | 639 | 96.4 | 3.34 | 2.09 – 5.54 | 9.86e-07 |
| 8/8 | LOW | Q4 | 639 | 14.7 | - | - | - |
| 8/8 | LOW | Q3 | 638 | 18.0 | 0.94 | 0.73 – 1.21 | 0.643 |
| 8/8 | LOW | Q2 | 638 | 25.5 | 1.56 | 1.19 – 2.04 | 0.001 |
| 8/8 | LOW | Q1 | 639 | 26.6 | 1.98 | 1.50 – 2.64 | 1.88e-06 |
| 10/10 | LOW | Q4 | 639 | 11.6 | - | - | - |
| 10/10 | LOW | Q3 | 638 | 16.6 | 0.92 | 0.71 – 1.18 | 0.507 |
| 10/10 | LOW | Q2 | 638 | 25.7 | 1.59 | 1.21 – 2.10 | 0.001 |
| 10/10 | LOW | Q1 | 639 | 24.1 | 2.42 | 1.79 – 3.29 | 9.71e-09 |