

# Unlocking the Potential of Banked ADCUs A Matching Modelling Approach

Jürgen Sauter<sup>1</sup>, Ute V. Solloch<sup>1</sup>, Deborah Buk<sup>2</sup>, Henning Baldauf<sup>3</sup>, Johannes Schetelig<sup>3</sup>, Alexander Platz<sup>4</sup>

<sup>1</sup> DKMS Group, Tübingen, Germany; <sup>2</sup> DKMS Donor Center, Tübingen, Germany; <sup>3</sup> DKMS Group, Dresden, Germany; <sup>4</sup> DKMS Stem Cell Bank, Dresden, Germany

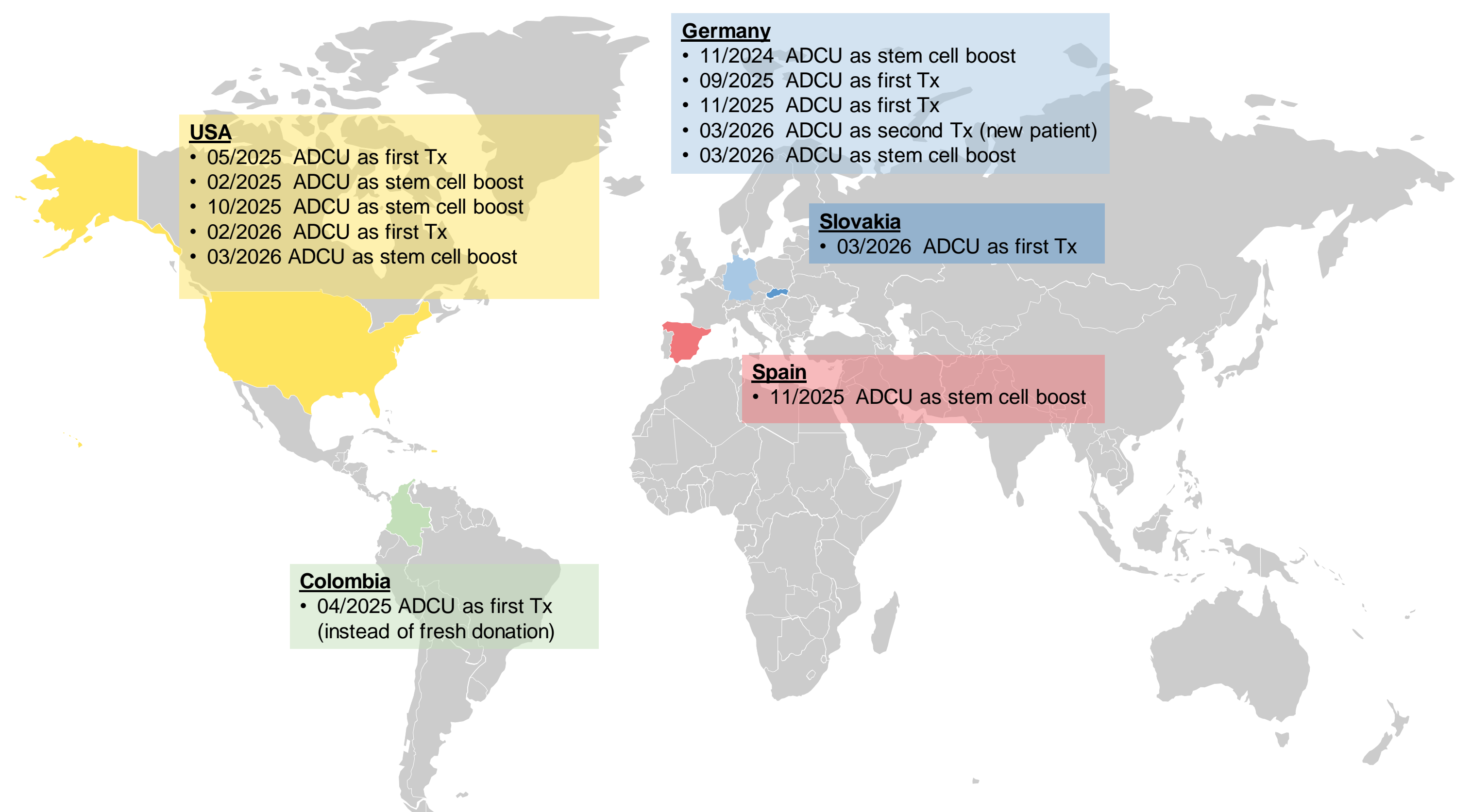
## Background

The timely availability of suitable HLA-matched stem cell products is a key determinant for successful outcome of hematopoietic stem cell transplantation. To address urgent graft requests, DKMS introduced adult donor cryopreserved stem cell units (ADCUs) as an additional allogeneic source.

As of April 2025, the DKMS Stem Cell Bank comprises 552 ADCUs generated from surplus material obtained during peripheral stem cell collection from DKMS Germany donors undergoing work-up.

Since 2024, a total of 13 ADCUs have been delivered.

This demonstrates the growing interest in these alternative graft sources.



## Study setup, methods, and aims

To address increasing demand from transplant centers in the United States, we conducted a simulation study to estimate the probabilities for patients to match at least one available ADCU under a specific scenario. Scenarios were defined by these parameters

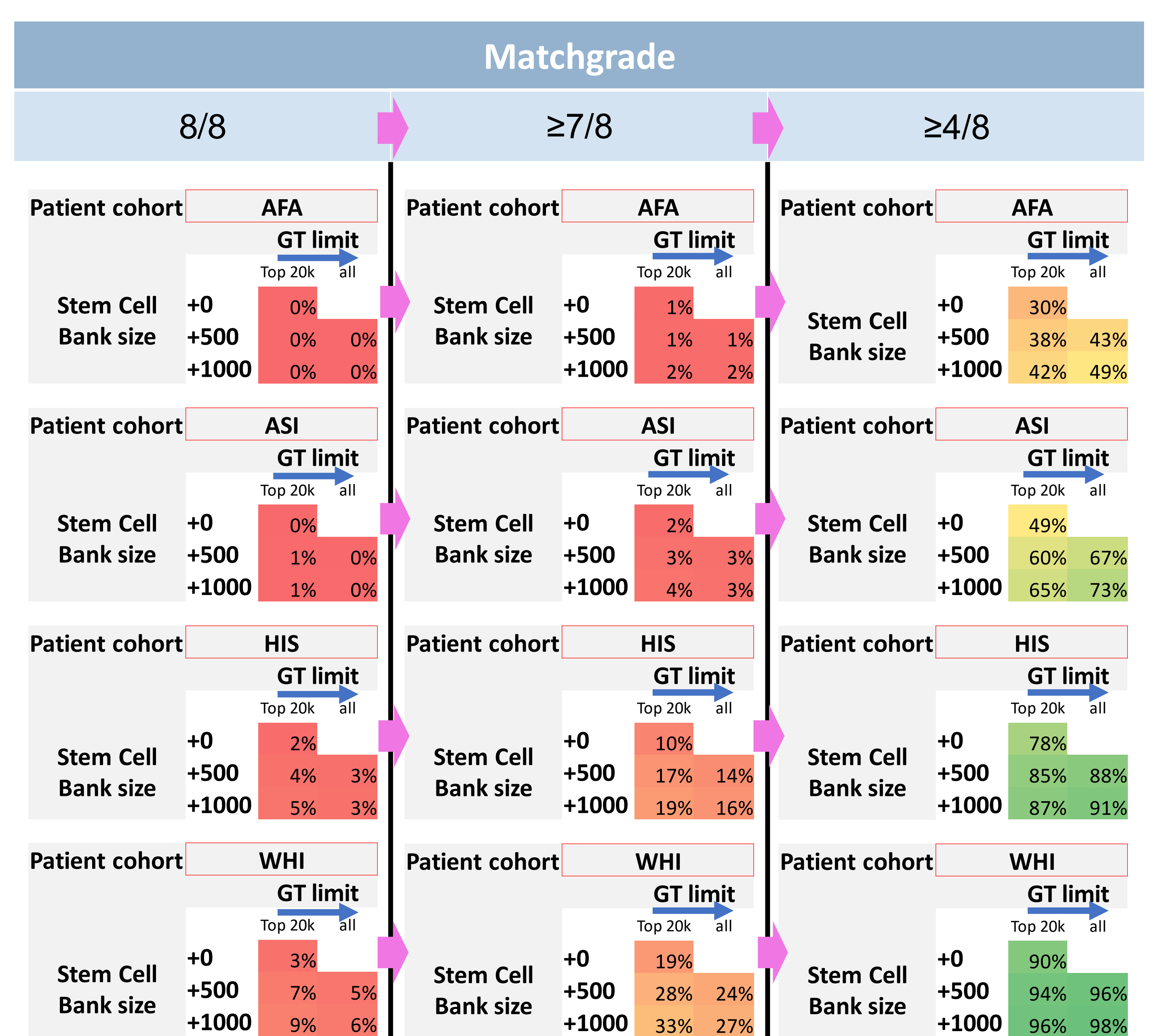
- **Bank size**
  - as is, 500 and 1,000 additional ADCUs
- **US Patient population**
  - African-American (AFA), Asian (ASI), Hispanic (HIS), and White (WHI)
- **Selection of eligible genotypes for ADCU storage**
  - Only most common genotypes (top 20,000) or all genotypes in DKMS DE
- **Match grade between patient and donors**
  - $\geq 4/8$ ,  $\geq 7/8$ ,  $8/8$ , with max. one mismatch per locus

For each scenario,  $n=500$  patient genotypes were generated under Hardy-Weinberg equilibrium to represent the population, using DKMS US donor haplotype frequencies.

For future ADCU bank size projections, additional genotypes were simulated under Hardy-Weinberg equilibrium, sampling either from the 20,000 most common genotypes or the full pool.

Each scenario was repeated 100 times to account for stochastic variation.

## Results



- Increased matching probabilities by accepting mismatches (→)
  - Largest relative effect for AFA and ASI patients
  - Absolute gain in matched patients highest for WHI, lowest for AFA
- ADCU genotype selection from top 20,000 to all genotypes (→)
  - lowers the chances of finding ADCUs matched  $8/8$  or  $\geq 7/8$
  - increases the chances at  $\geq 4/8$

## Conclusion

Our results demonstrate that the chance to find an  $8/8$ -matched ADCU at realistic bank sizes strongly depends on patient population, with particularly low probabilities for individuals of African-American ancestry. However, when permitting up to four mismatches (with no more than one mismatch per locus), the probability increases markedly for all population groups, exceeding 42% for bank sizes greater than 1,500 ADCUs.

