

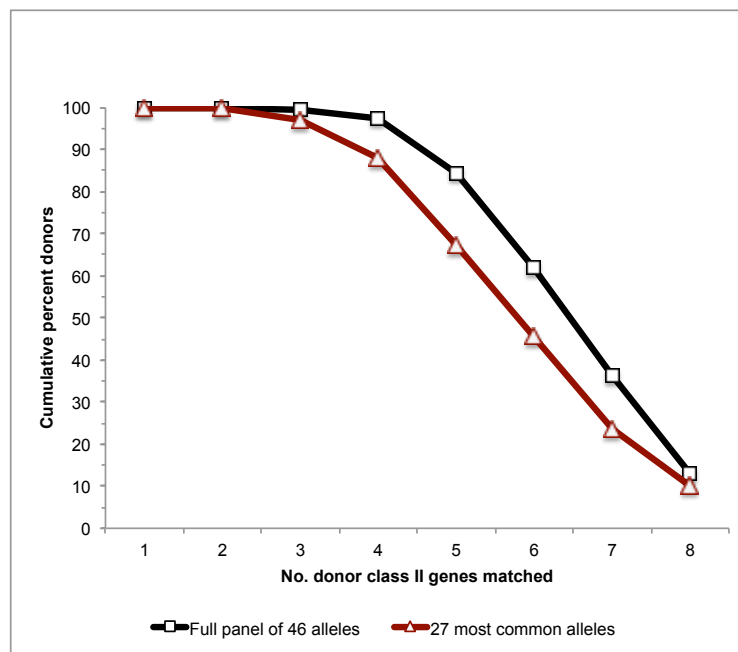
A strategy to determine HLA class II restriction broadly covering the DR, DP and DQ allelic variants most commonly expressed in the general population

Denise M. McKinney*, Scott Southwood*, Denise Hinz*, Carla Oseroff*, Cecilia S. Lindestam Arlehamn*, Veronique Schulten*, Randy Taplitz[†], David Broide[†], Willem A. Hanekom[‡], Thomas J. Scriba[‡], Robert Wood[§], Rafeul Alam[¶], Bjoern Peters*, John Sidney*, Alessandro Sette*

Corresponding Author: Alessandro Sette, La Jolla Institute for Allergy and Immunology, La Jolla, California, 92037; alex@liai.org

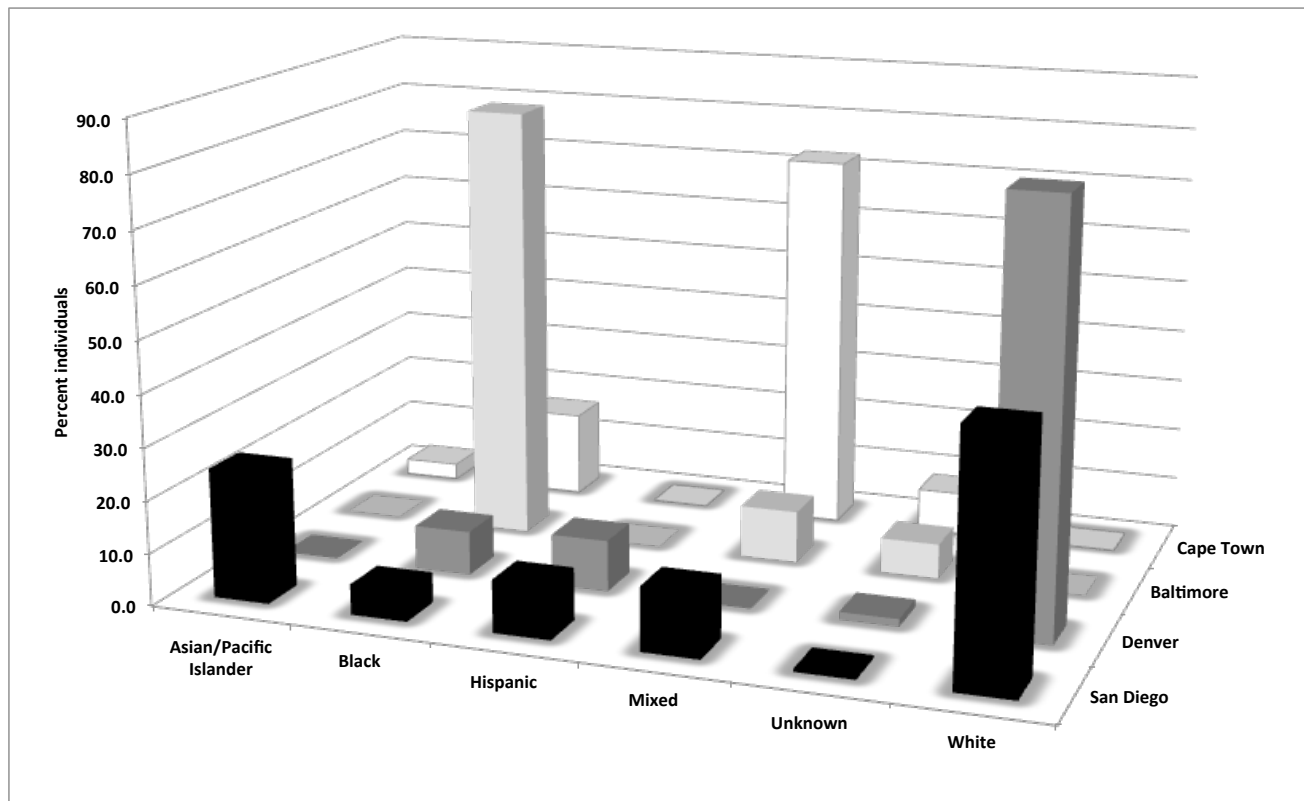
Online Resource 1. Comparison of population coverage afforded by the full panel and the sub-panel of the 27 most common alleles

The collective frequencies provided by the HLA class II alleles represented in the panel of 46 single transfected cell lines, and the sub-panel of the 27 most common alleles, are compared. Coverage was examined in a cohort of 190 donors recruited for two different studies in the San Diego area. The cumulative percent of all donors for which the panels provide coverage of 0 to 8 possible class II types expressed is shown.



Online Resource 2. Ethnic breakdown of four donor cohorts from different geographical areas

Representation of different ethnic groups, in terms of percent of individuals, in the San Diego, Denver, Baltimore and Cape Town cohorts. Ethnicity is as described by donors during clinical enrollment.



Online Resource 3. Correspondence between HLA frequencies in the donor cohort and the general population

The collective frequencies of alleles present in the San Diego, Denver, Baltimore and Cape Town cohorts examined largely match those found in the general worldwide population, based on HLA frequency data obtained from dbMHC (Middleton et al. 2003; Meyer et al. 2007).

