

Supporting Information

Pinto et al. 10.1073/pnas.1308311110

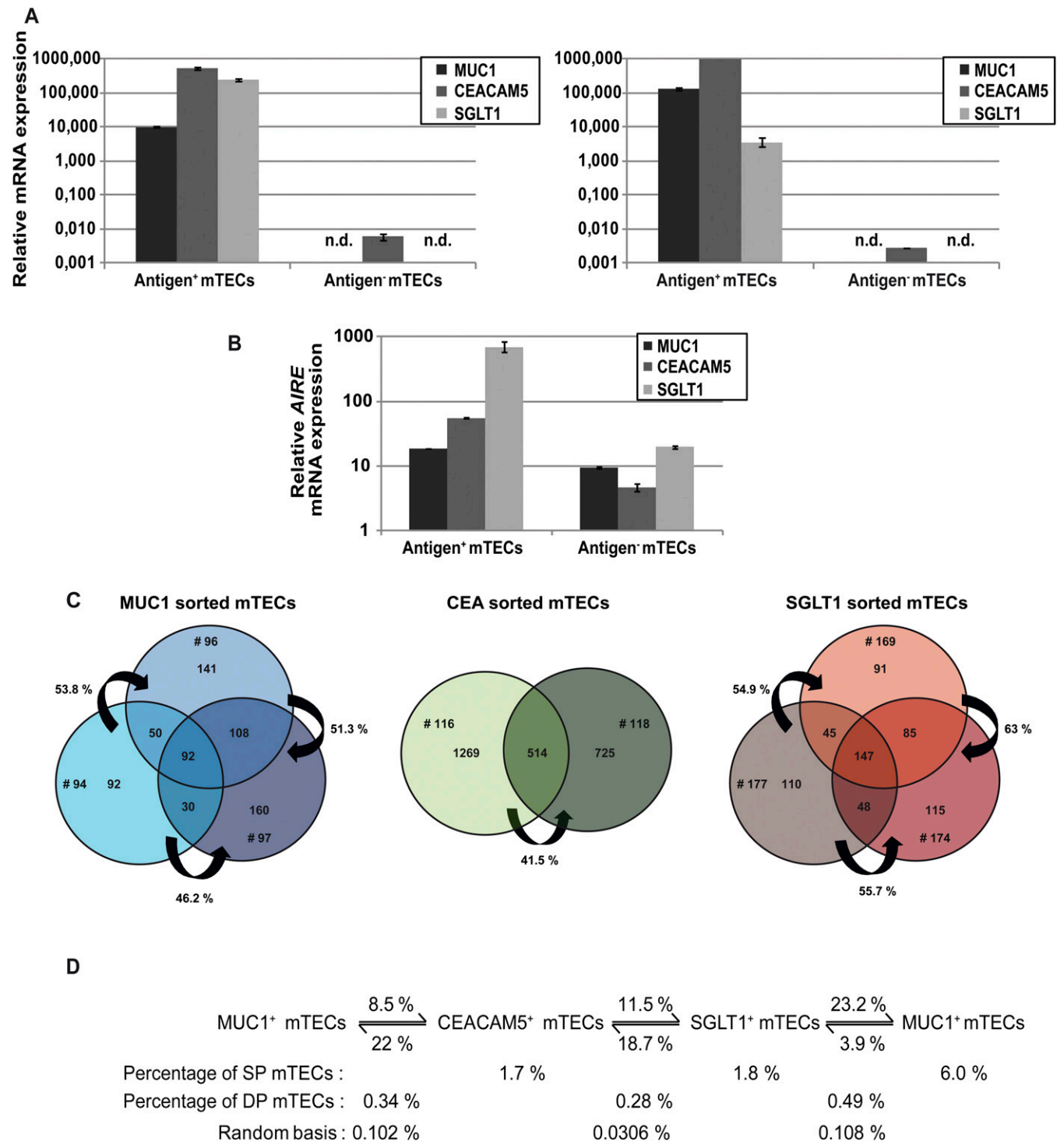


Fig. S1. Defining coexpression groups. (A) Enrichment of the sorted antigen-positive vs. antigen-negative medullary thymic epithelial cells (mTECs) by quantitative PCR. Shown are Mucin (*MUC1*) (#97, #96), carcinoembryonic antigen-related cell adhesion molecule (*CEACAM5*) (CEA) (#116, #118), and sodium/glucose co-transporter (*SGLT1*) (#177, #174). n.d., not detectable. (B) Additional example of autoimmune regulator (*AIRE*) mRNA levels within each mTEC subset. Shown MUC1 (#96), CEA, (#118), and SGLT1 (#177). (C) Example of two to three individuals sorted for MUC1⁺, CEA⁺, and SGLT1⁺ mTECs used for array hybridization. Numbers within circles refer to genes. (D) Additional example of protein coexpression patterns of the three antigens defining the mTEC subsets in one individual (#153).

