

Supplementary data 5: Neutralization epitopes in VP7 and VP4

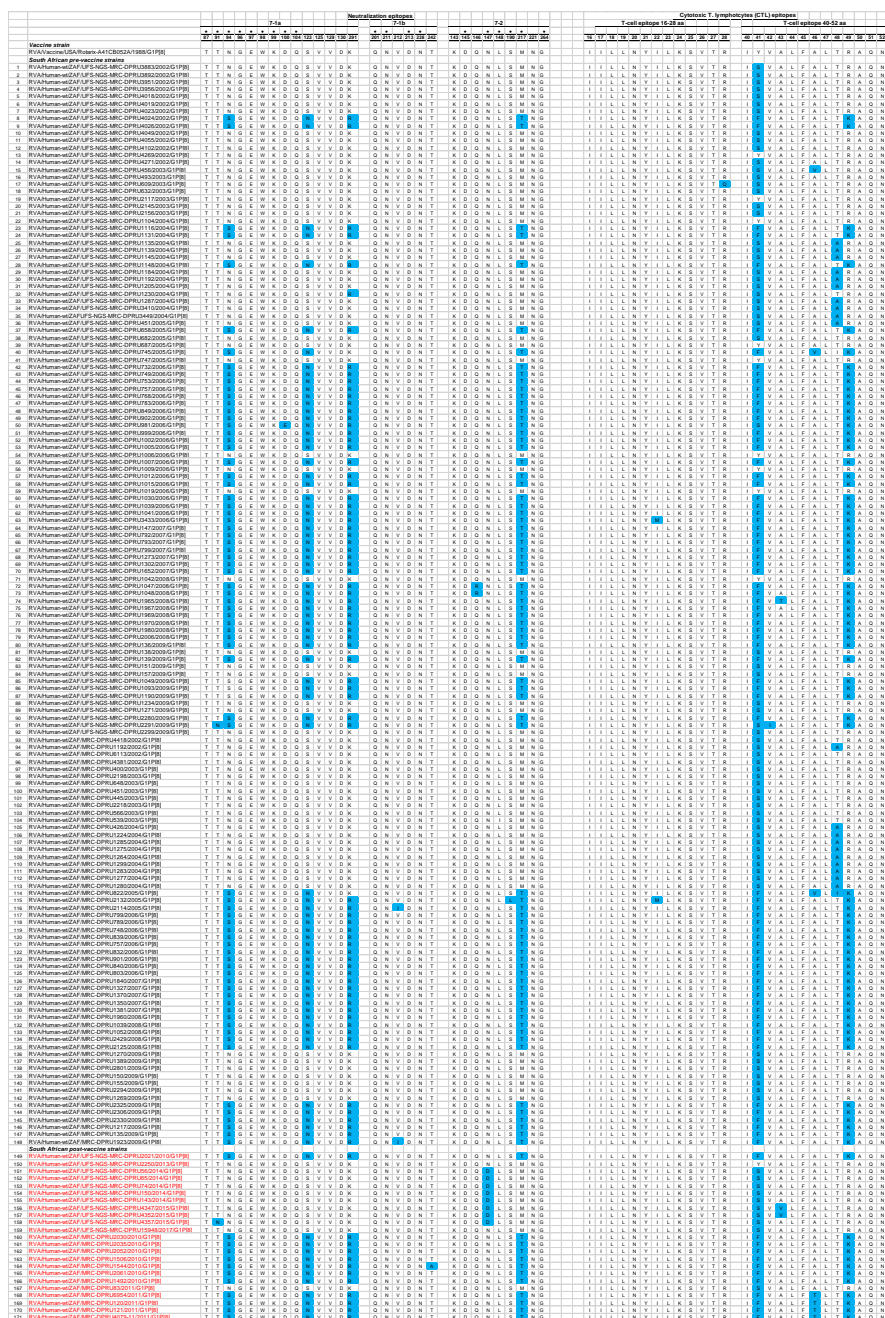


Figure S1: Alignment of VP7 neutralizing and cytotoxic T-cell lymphocytic epitopes residues of Rotarix® strain against wild type South African G1P[8] strains. Antigenic residues are divided in three epitopes (7-1a, 7-1b, and 7-2). Amino acids that differ with Rotarix® are colored in sky blue. Amino acid changes that have been shown to escape neutralization with monoclonal antibodies are indicated with a black dot. South Africa pre-vaccine G1 genotypes are indicated in boldface while post-vaccine strains are indicated in red.

Figure S2: Alignment of antigenic residues in VP4 between the P[8] component of Rotarix® and wild type P[8] strains. Antigenic residues are divided into four antigenic epitopes in VP8* (8-1, 8-2, 8-3 and 8-4) and five antigenic epitopes in VP5* (5-1, 5-2, 5-3, 5-4 and 5-5). Amino acid changes that have been shown to escape neutralization with monoclonal antibodies are indicated with a black dot. Amino acids residues colored in sky blue differ from Rotarix®.