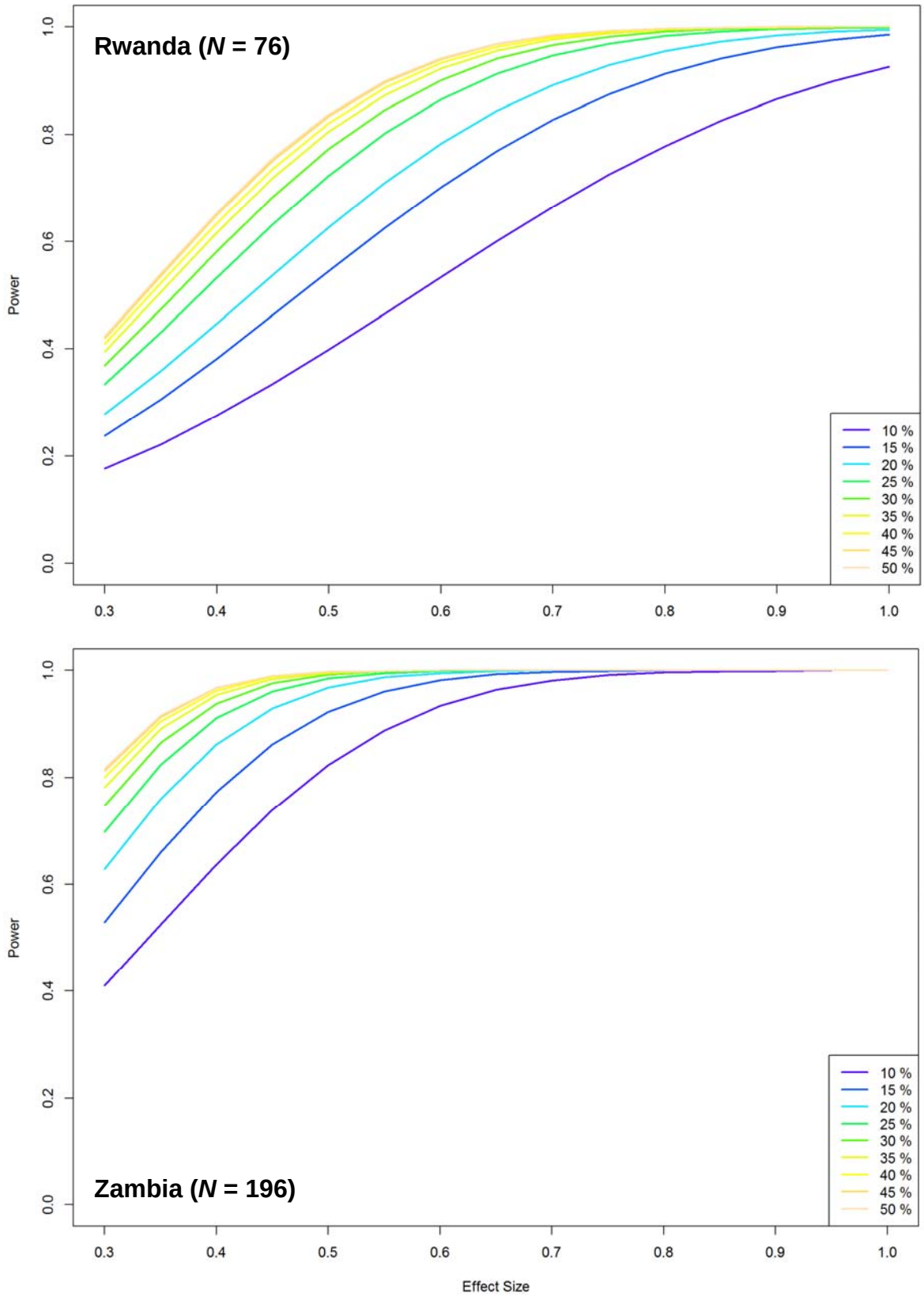

Figure S1. **Statistical power in confirming previously reported HLA-I AAR variants associated with HIV-1 viral load (alpha = 0.05).** In the Rwandan and Zambian cohorts (*N* = 76 and 196, respectively), statistical power (the Y-axis) varies by estimated effect sizes (regression beta, from 0.3-1.0 $\log_{10}$ viral load) and frequencies of AAR variants (from 10% to 50%).

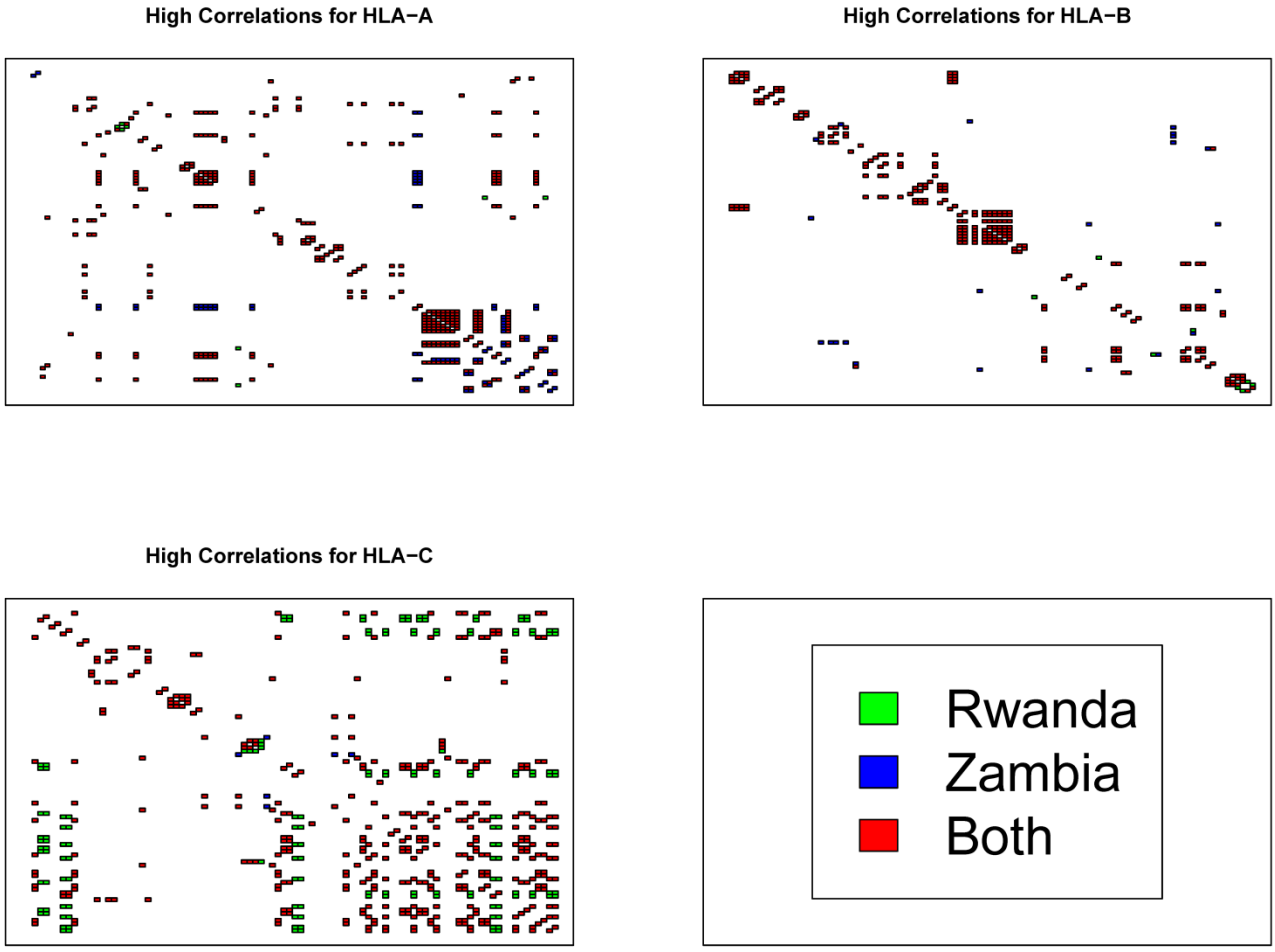

Figure S2. A graphical view of HLA-I AAR variants that are in strong linkage disequilibrium (r^2 >0.80) in either cohort (green = Rwanda only; blue = Zambia only) or both cohorts (red). Several AAR variants in exclusive LD are highlighted in **Table S1**.