Figure S1.

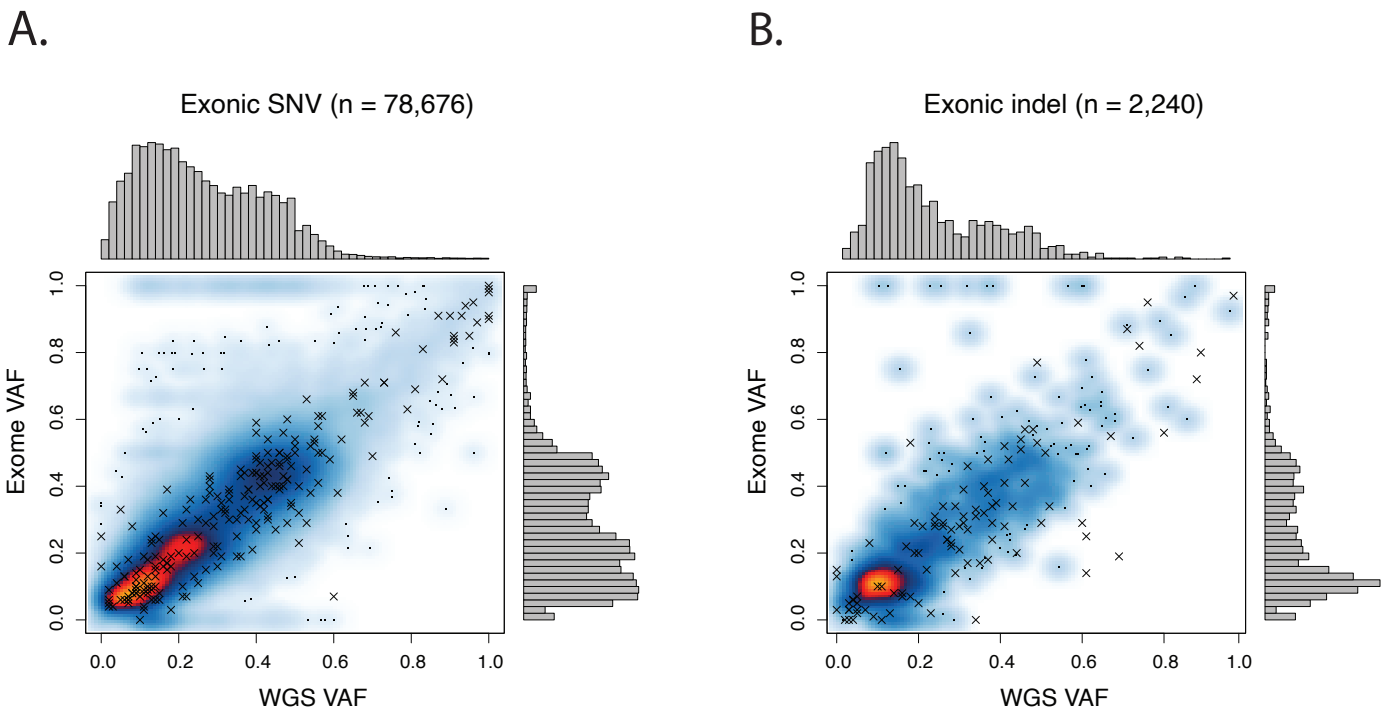

Figure S1. Somatic SNV and indel variant allele frequencies from WGS and WES. **A.** Density plot showing the variant allele fraction (VAF) detected in whole genome (WGS; x-axis) and whole exome (WES; y-axis) of 78,676 manually verified somatically acquired SNVs in the G4K cohort (hypermutator samples were removed from this analysis). White to blue to red color gradient approximates the density of points on the scatterplot; density of points on the x and y-axes are also represented as grey histograms adjacent to the axes. Black 'X's show P/LP clinically reported variants (n=323) superimposed on to the plot and showing the same approximate VAF distribution as the whole dataset. **B.** VAF data for identified indels is presented in the same way for 2,240 manually reviewed short insertion deletion variants.