



Figure S1. The copy number of the HTT subfamilies in each strain, broken down by population and corrected by the estimated fraction of missing junctions. A) The percent of junctions for all HTT subfamilies inferred from posterior predictive simulations to have been missed in each strain due to read depth variation, broken down by population. To ensure interpretations of population structure are not driven by these missing junctions for the rest of this figure only, when assessing the presence of population structure we roughly corrected our copy number estimates by dividing by one minus the inferred fraction of missing junctions for each HTT subfamily. Inferred missing junctions for each HTT subfamily: B) *HeT-A*, C) *HeT-A1*, D) *HeT-A2*, E) *HeT-A3*, F) *HeT-A5*, G) *TAHRE*, H) *TART-A*, I) *TART-B*, J) *TART-C*.