Online Resource Figure 1: Depth of coverage (DOC) distribution for cases (red), original control bams (blue) and down sampled (ds) control bams (green). The mean DOC is 60x for both cases and down sampled controls allowing us to compare the number of mosaic variants in each cohort

Online ResourceFigure 2: Distribution of the fraction of WES capture intervals with depth > = 15 (DIR 15 fraction) for WES cases (red), original control bams (blue) and down sampled (ds) control bams (green)

Online Resource Figure 3: Schematic illustrating how MuTect somatic variant caller was used with WES trio data to identify de novo variants in the child. For each trio we ran MuTect twice, designating the child as 'tumor' and each parent as 'normal.' The intersection of variants is the set of de novo variants in the child that are then filtered for mosaic variants

Online Resource Figure 4: A) Comparison of alternate allele depth in child versus total depth in child for variants that confirmed as mosaic and homozygous reference based on ddPCR results. Red squares represent confirmed mosaic variants. Blue diamonds represent homozygous loci. Dashed lines represent new filtering parameters to increase the positive predictive value. **B)** Comparison of minimum parental read depth compared to total depth in child

Online Resource Figure 5: Counts of variant types of CHD cases (blue) and controls (red)