SepCNV results on whole-exome sequencing(WES) data.

All WES samples are downloaded from ftp://ftp.1000genomes.ebi.ac.uk. We use CNVs reported by Conrad et al. for validation. Like we did on Retinitis Pigmentosa data, considering multiple factors such as DNA quality, DNA extraction protocol and the possibly non-even reads distribution, we randomly selected three samples to pool together as control, and randomly select one sample as case.

control	NA19152_NA18973_NA19206
case	NA10847
precision	31%
recall	55%
false positive rate	10%