

Figure S1A. Genome-wide ROH distribution patterns in 3.5KJPNv2 dataset (on Chromosome 6 only). ROH segments longer than 1.5 Mb are inferred as red bars. ROH segments between 100 Kb and 1.5 Mb are inferred as black bars. Horizontal axis represents the base pair distances of ROHs detected by BCFtools on chromosome 6. Vertical axis represents each individual in the 3.5KJPNv2 dataset.

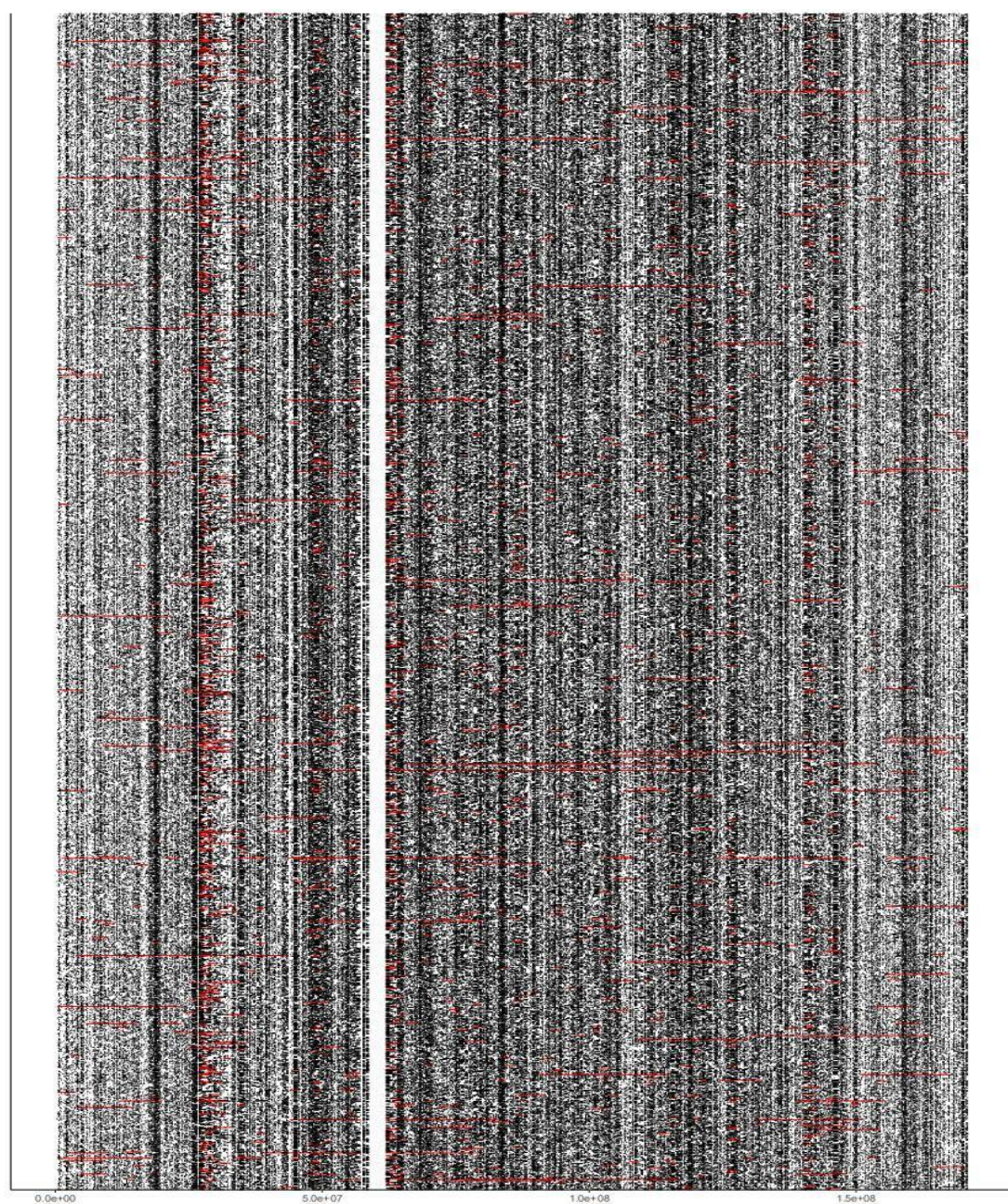


Figure S1B. OmniExpressExome array-based sites specific ROH distribution patterns in 3.5KJPNv2 dataset (on Chromosome 6 only). ROH segments longer than 1.5 Mb are inferred as red bars. ROH segments between 100 Kb and 1.5 Mb are inferred as black bars. Horizontal axis represents the base pair distances of ROHs detected by BCFtools on chromosome 6. Vertical axis represents each individual in the 3.5KJPNv2 dataset.

