**Supplementary Methods Legend**

**Supplementary Program – 1.** [hg19.chrY.psr.py]. Sample program used to change the sequence of the pseudo-autosomal regions on chrY to N’s.

**Supplementary Program – 2.** [hg19.bowtie.build.bash]. Sample program used to prepare a bowtie index of the genome.

**Supplementary Program - 3a.** [hg19.generate.reads.k50.py]. Sample program used to simulate reads from the genome.

**Supplementary Program - 3b.** [chromlist.txt]. File used in the sample program  
hg19.generate.reads.k50.py

**Supplementary Program – 4.** [bowtie.qsub.py]. Sample program used to map reads back to the genome.

**Supplementary Program – 5.** [hg19.chrom.sizes.py]. Sample program used create a file listing the sizes of the chromosomes to be used for the copy number analysis

**Supplementary Program – 6.** [hg19.bowtie.goodzones.k50.py]. A sample program to create the list of goodzones from the mapped read files.

**Supplementary Program – 7.** [hg19.chrom.mappable.bowtie.k50.py]. A sample program used to compute the number of mappable positions on each chromosome.

**Supplementary Program – 8.** [hg19.bin.boundaries.50k.py]. Sample program used to compute bin boundaries.

**Supplementary Program – 9.** [hg19.varbin.gc.content.50k.bowtie.k50.py]. Sample program used to compute GC content in each bin.

**Supplementary Program – 10.** [barcode.split.sr01.py]. Sample program used to split barcoded samples.

**Supplementary Program – 11.** [varbin.50k.sam.py]. Varbin program used to compute the number of reads in each bin.

**Supplementary Program – 12.** [SRR054616.cbs.r]. Sample program used to perform GC content normalization, CBS segmentation and plot graphs.

**Supplementary Program – 13.** [SRR054616.copynumber.r]. Sample program used to estimate copy number