bcftools; Use only dbSNP137 positions

HMMCopy: readCounter

Retrieve Read Count Data

HMMCopy: gcCounter

a) generateMap.pl
b) mapCounter

HMMCopy: readCounter

Retrieve Read Count Data

HMMCopy: readCounter

Tumor Allee Count

Tumor Sample

Heterozygous Germline Positions

Normal Sample

Normal Allee Count

Normal Coverage

Tumor Coverage

Tumor Sample

Normal Allee Count

Normal Coverage

GRCh37 Genome

Genome GC Content

Genome Mappability

TitanCNA Results

createTITANsegmentfiles.pl

Gene Centric sCNA

Segment Results

Mask for CNV

a) Normal Content Estimation from sSNV Data
b) numberClonalClusters (1-5)