

JAX: copy number alteration - SNP,

Molecular Methods Description:

The copy number variation is analyzed from the Affymetrix Human SNP 6.0 array. PennCNV-Affy and ASCAT 2.2 is used to predict allele-specific copy number and ploidy. Gene-level copy number is obtained by intersecting copy number segments with genome coordinates of Ensembl genes. In cases where a segment boundary is contained within a gene's coordinates, the most conservative estimate of copy number is used.

Analysis Description:

The copy number of the CTP panel genes is displayed as a chart of $\log_2(\text{cn raw} / \text{sample ploidy})$. Other forms of copy number values (e.g. gain and loss relative to ploidy, loss of heterozygosity) and copy number of other genes not listed on the MTB site can be made available upon request.