

# Comparative genomic hybridization

Comparative genomic hybridization (CGH) is a molecular cytogenetic method for analyzing copy number variations (CNVs) relative to ploidy level in the DNA of a test sample compared to a reference sample, without the need for culturing cells. The aim of this technique is to quickly and efficiently compare two genomic DNA samples arising from two sources, which are most often closely related, because it is suspected that they contain differences in terms of either gains or losses of either whole chromosomes or subchromosomal regions (a portion of a whole chromosome). This technique was originally developed for the evaluation of the differences between the chromosomal complements of solid tumors and normal tissue.

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