Comparative genomic hybridization is a molecular cytogenetic method for analysing 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 tumor and normal tissue, and has an improved resolution of 5-10 megabases compared to the more traditional cytogenetic analysis techniques of giemsa banding and fluorescence in situ hybridization (FISH) which are limited by the resolution of the microscope utilized.