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The karyotypes of the 70 cases using CMA, karyotype analysis, and cytogenetic G-banding were considered normal. There were no discrepancies between the CMA results and the results obtained with cytogenetic G-banding analysis. Twelve cases in the normal group were found to have benign clinical CNVs using whole genome sequencing and whole exome sequencing, but these variants were absent on cytogenetic G-banding analysis and CMA, which showed normal karyotype status (non-pathologic variants). There were 45 clinically significant pathogenic CNVs (pCNVs) in 21 cases of VOUS, and 3 clinically significant pCNVs were found in chromosomes and chromosomes including abnormal karyotypes: female, 15; male, 1. Furthermore, 15 CNVs were present in chromosomes that also had abnormal karyotypes; 11 were present in chromosomes with normal karyotypes (93.55%, 15/17). These results indicate that VOUS CNVs that do not show an association with abnormal karyotypes should be further evaluated using other methods (e.g., whole genome sequencing and exome sequencing) to identify other associated abnormalities, to elucidate the pathogenicity of the detected variants, and to determine whether there is a causal relationship between the pCNV and the abnormal karyotype [ 24 ]. Metaheuristic search-based techniques have also been widely used for the evolutionary engineering of synthetic chromosomes. The interested reader is referred to metaheuristics. In this section, we use a backtracking recombination algorithm [ 32 ] and generation of diploid chromosome sets to analyze karyotype data.

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## Karyotype Analysis Software Free Download

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