Genetic Results: The cytogenomic microarray analysis indicated that there was a gain involving chromosome 16 (1.7 Mb duplicated) within 16p13.11, suggesting partial trisomy for this region. This duplication has been reported as a risk factor for neurocognitive disorders as it appears to be enriched in children with intellectual disabilities, but is also observed, at a lower frequency, in normal individuals.

Method: CHROMOSOMAL MICROARRAY ANALYSIS (CMA).

Methodology: This CMA was performed using Affymetrix(R) Cytogenetics Whole-Genome 2.7M Array. The array offers a total of 2,141,868 markers across the entire genome, including 1,742,975 unique non-polymorphic markers, and 398,891 SNP markers.