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Introduction
To evaluate the diagnostic yield of prenatal whole exome sequencing (WES) for suspected monogenic disorders in continuous fetuses with similar structural malformations and normal results on cytogenetic testing, and to describe information on pathogenic variants that is provided by Whole Exome Sequencing (WES).

Methods
Karyotyping, chromosomal microarray analysis (CMA) and trio-based WES were performed sequentially on stored samples from two pedigrees with continuous similar sonographic abnormal pregnancies. Pedigree 1: three continuous abnormal pregnancies characterized by hydrocephalus; Pedigree 2: two continuous abnormal pregnancies characterized by Microcephaly.

Results
Two novel mutations in PNKP (cause Microcephaly, seizures, and development delay Syndrome) and two unreported mutations in CC2D2A (cause Joubert Syndrome, Type 9 or Meckel Gruber type 6) were found by WES and verified by Sanger Sequencing.

Conclusion
Whole exome sequencing is a useful diagnostic tool when fetal structural anomalies suggest a suspected Mendelian disorder, especially in the pedigree with continuous similar sonographic abnormal pregnancies, which show the normal results on karyotyping and CMA. And it has the potential to improve the clinical detection rate of genetics disorder.