

CORRECTION

Correction: High Levels of Sample-to-Sample Variation Confound Data Analysis for Non-Invasive Prenatal Screening of Fetal Microdeletions

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[Fig 1](#) is an incorrect duplication of Fig 2. The authors have provided a corrected version here.



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5p15.33

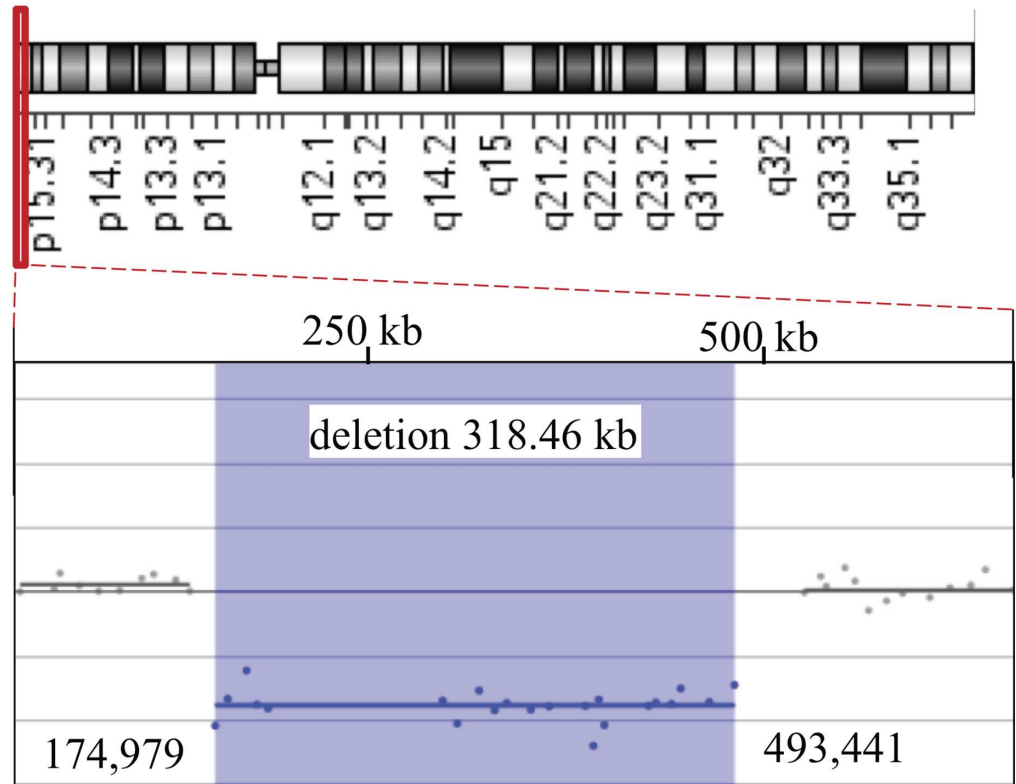


Fig 1. Comparative Genomic Hybridization Analysis of Affected Fetal Sample (First Pregnancy). Array CGH profile showing an interstitial deletion in the short arm of chromosome 5. Top: Ideogram of chromosome 5. The deleted 5p15.33 region is indicated by a red rectangle. Below: A magnified view of the 5p subtelomeric region. Positions are displayed according to GRCh37/hg19 Genome Browser. Shaded blue area indicates a loss in DNA copy number detected by 22 oligonucleotide probes (blue dots), located in the interval chr5:174,979–493,441 and encompassing an approximately 318 kb segment.

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Reference

1. Chu T, Yeniterzi S, Yatsenko SA, Dunkel M, Shaw PA, Bunce KD, et al. (2016) High Levels of Sample-to-Sample Variation Confound Data Analysis for Non-Invasive Prenatal Screening of Fetal Microdeletions. PLoS ONE 11(6): e0153182. doi: [10.1371/journal.pone.0153182](https://doi.org/10.1371/journal.pone.0153182) PMID: [27249650](https://pubmed.ncbi.nlm.nih.gov/27249650/)