PLOS ONE

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.

Citation: Chu T, Yeniterzi S, Yatsenko SA, Dunkel M, Shaw PA, Bunce KD, et al. (2016) Correction: High Levels of Sample-to-Sample Variation Confound Data Analysis for Non-Invasive Prenatal Screening of Fetal Microdeletions. PLoS ONE 11(9): e0163578. doi:10.1371/journal.pone.0163578

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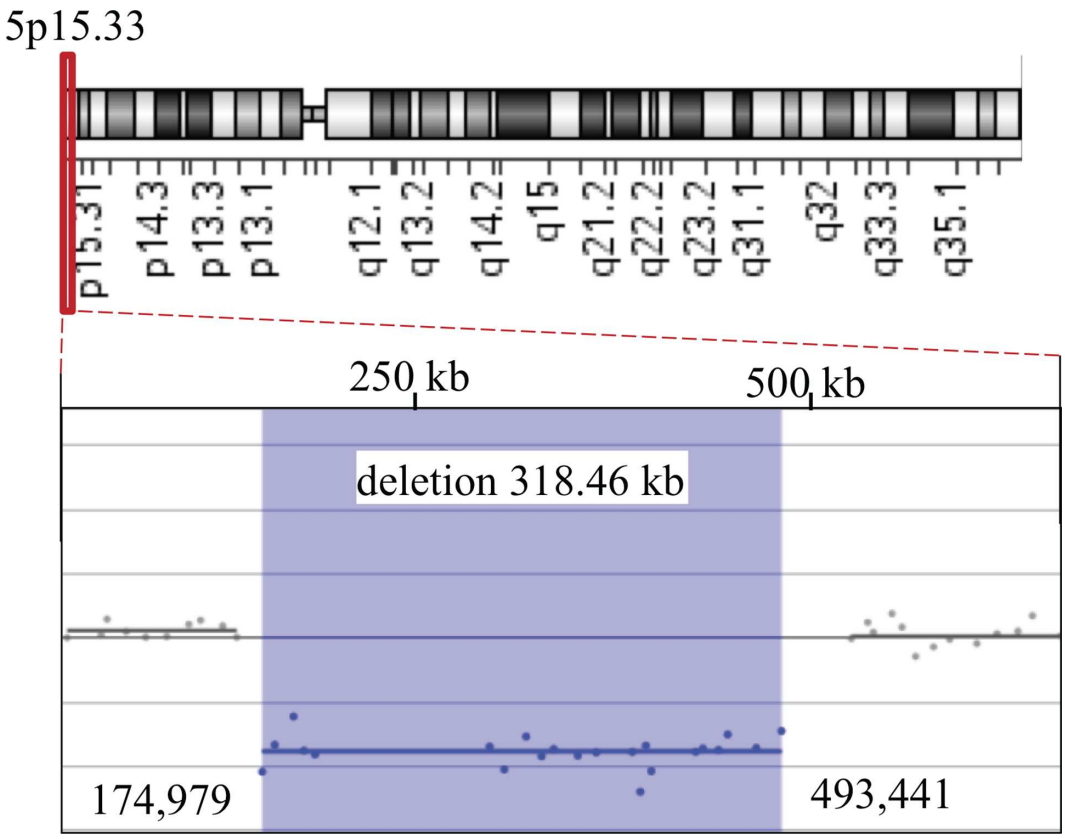

Fig 1. Comparative Genomic Hybridization Analysis of Affected Fetal Sample (First Pregnancy). Array CGH profile showing an interstitial deletion in the short arm of chromosome 5. Top: Ideogram of chromosome 5. The deleted 5p15.33 region is indicated by a red rectangle. Below: A magnified view of the 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.

doi:10.1371/journal.pone.0163578.g001

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 PMID: 27249650