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Comprehensive chromosomal abnormality detection: integrating CNV-Seq with traditional karyotyping in prenatal diagnostics

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Abstract

Background This study aimed to evaluate the efficacy of copy number variation sequencing (CNV-Seq) in detecting chromosomal abnormalities in prenatal diagnosis, comparing its performance with traditional karyotype analysis.

Methods A retrospective analysis was conducted on 1001 prenatal samples collected between April 2021 and December 2023. Samples were analyzed using both CNV-Seq and karyotype analysis. The detection rates of chromosomal abnormalities were compared between the two methods across various prenatal diagnostic indications. Clinical follow-up was performed to assess pregnancy outcomes.

Results CNV-Seq detected chromosomal abnormalities in 89 of 1,001 cases (8.9%), compared to 50 cases (5.0%) identified by traditional karyotyping. CNV-Seq not only detected all abnormalities identified by karyotyping, including common aneuploidies such as trisomy 21 and sex chromosome abnormalities, but also uncovered 53 additional pathogenic submicroscopic CNVs associated with 33 known syndromes. The detection rates of CNV-Seq were significantly higher in high-risk groups, such as those identified by non-invasive prenatal testing (HR-NIPT) and maternal serum screening (HR-MSS), demonstrating superior sensitivity and accuracy in prenatal diagnostics.

Conclusion CNV-Seq demonstrated superior sensitivity in detecting chromosomal abnormalities, particularly submicroscopic alterations, compared to traditional karyotyping. The study highlights the potential of CNV-Seq as a valuable tool in prenatal diagnostics, offering improved detection of genetic abnormalities and guiding clinical decision-making. However, a combined approach using both CNV-Seq and karyotype analysis is recommended for comprehensive prenatal genetic screening.

Keywords CNV-Seq, Karyotyping, Prenatal diagnostics, Chromosomal abnormality

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Introduction

Prenatal diagnosis plays a crucial role in modern obstetrics, offering the ability to detect chromosomal abnormalities and genetic disorders in the developing fetus [1]. Early identification of such anomalies allows for informed decision-making, tailored medical management, and psychological preparedness for the expecting parents [2]. The primary techniques employed in prenatal diagnosis to detect chromosomal abnormalities include karyotype analysis, chromosomal microarray analysis (CMA), and CNV-Seq. [3]

Karyotype analysis has been the cornerstone of prenatal cytogenetic diagnostics for several decades [4]. It provides a visual assessment of the entire chromosome set, enabling the detection of aneuploidies, large deletions, duplications, and structural rearrangements [5]. However, its resolution is limited to detecting changes that affect large segments of the genome, typically greater than 5–10 megabases [6]. Moreover, karyotyping is time-consuming, labor-intensive, and requires viable cell cultures, which can sometimes fail to yield results due to poor cell growth or contamination [6].

CMA has emerged as a more sensitive alternative, capable of detecting submicroscopic chromosomal imbalances that are beyond the resolution of traditional karyotyping [7]. Despite its higher resolution, CMA has limitations, including its inability to detect balanced translocations and low-level mosaicism [8]. Furthermore, the interpretation of copy number variants (CNVs) identified by CMA can be challenging, particularly when they are of uncertain significance, leading to potential ambiguity in clinical outcomes [9].

Advancements in genomic technologies have introduced CNV-Seq as a promising tool in the field of prenatal diagnosis. CNV-Seq combines the high-resolution capabilities of microarray analysis with the comprehensive genomic coverage of next-generation sequencing (NGS) [10, 11]. This method not only detects a broader range of chromosomal abnormalities, including those that are submicroscopic, but it also identifies CNVs with greater accuracy and speed [11]. Additionally, CNV-Seq can provide insights into the genomic architecture at a level previously unattainable with conventional methods, making it a superior option for comprehensive prenatal genetic screening [12].

The progress of CNV-Seq in prenatal diagnostics represents a significant leap forward, addressing the shortcomings of karyotyping and CMA while offering a more detailed and efficient approach to detecting genetic abnormalities. In this retrospective study, samples of fetuses with puncture indications were analyzed with CNV-seq. We compared the results of karyotype analysis and CNV-seq and evaluated the incidence fetal chromosomal anomalies by clinical indication.

Methods

Participants

A cohort of 1685 fetuses were subjected to invasive prenatal diagnostic procedures from April 2021 and December 2023 at the Prenatal Diagnosis Unit of the Central Hospital in Fujian Province, China. We retrospectively collected clinical and karyotype information from 1001 subjects with abnormal CNV-seq results. The Indications for prenatal diagnosis included pregnant women aged 35 years or older, fetuses with elevated risk of Down syndrome as indicated by maternal serum screening, high-risk results from non-invasive prenatal testing (NIPT) using cell-free fetal DNA, and the presence of fetal abnormalities detected via ultrasonography. Samples were collected between the 18th and 24^{+5}th weeks of gestation and included amniotic fluid, and umbilical cord blood. Informed consent was obtained from both parents after a detailed genetic counseling session, which outlined the benefits and limitations of karyotyping and CNV-Seq. To mitigate the risk of maternal cell contamination and aid in the characterization of CNVs, peripheral blood samples from both parents were also collected for each case.

Karyotype analysis

Karyotyping was performed on amniotic fluid samples using standardized cytogenetic techniques. Samples were cultured in AmnioMAX-II (Gibco, Carlsbad, CA) medium to promote cell growth. After a 7-day incubation period, during which the culture medium was refreshed to maintain optimal conditions, cells were harvested for chromosome analysis.

Metaphase chromosome spreads were prepared from the cultured cells and subsequently G-banded using the trypsin-Giemsa staining method to visualize chromosomal structures. Each specimen underwent a detailed examination of at least 10 metaphases, achieving a band resolution between 400 and 500 bands per haploid set, which allowed for the identification of both numerical and structural chromosomal abnormalities.

Chromosome images were captured and analyzed using an automated metaphase chromosome analysis system (MetaSystems, Göttingen, Germany). Chromosomes were classified and reported following the guidelines of the International System for Human Cytogenetic Nomenclature (ISCN). This rigorous approach ensured high accuracy in the detection and characterization of chromosomal abnormalities.

CNV-Seq

CNV-Seq was conducted following established protocols with slight modifications to optimize results. Genomic DNA was extracted from amniotic fluid samples using the DNAeasy Blood and Tissue Kit (Qiagen, Valencia, CA, USA), ensuring a minimum DNA concentration of

50 ng/μL. The extracted DNA was then processed to create sequencing libraries through enzymatic fragmentation, end repair, adapter ligation, and PCR amplification. Library quality was assessed through two rounds of cycle quality control, ensuring that the starting DNA quantity of 50 ng was sufficient for downstream applications.

Sequencing was performed on the MGISEQ-2000 platform (MGI, Shenzhen, China), generating approximately 5 million reads with a read length of 36 base pairs. Post-sequencing, raw data underwent rigorous quality control, with a Q30 score exceeding 85% to ensure high fidelity. The resulting sequences were aligned to the human genome reference sequence (hg19, UCSC Genome Browser), utilizing the Burrows-Wheeler Aligner (BWA) for accurate mapping of the reads.

CNVs were identified by applying a CNV detection algorithm called EXCAVATOR based on binning and comparison across 20-kilobase (kb) intervals along each chromosome [13]. Identified CNVs were then annotated and cross-referenced with public databases, including DECIPHER, Database of Genomic Variants (DGV), and Online Mendelian Inheritance in Man (OMIM), for pathogenicity assessment. Variants were classified according to the American College of Medical Genetics and Genomics (ACMG) guidelines into pathogenic, likely pathogenic, variants of uncertain significance (VUS), likely benign, and benign categories. For clinical reporting, only pathogenic, likely pathogenic, and VUS anomalies were considered relevant.

All detected chromosomal abnormalities were corroborated with traditional karyotyping or quantitative fluorescent PCR (QF-PCR) to ensure the accuracy and clinical relevance of the CNV-Seq findings.

Follow-up and statistical analysis

All participating pregnant women were followed up via telephone to monitor pregnancy outcomes and assess the health status of their newborns. This follow-up allowed for the collection of data regarding delivery and postnatal health conditions.

For statistical analysis, R software (version 4.0) was utilized. Descriptive statistics were employed to summarize the data, with measurement data expressed as the mean ± standard deviation (SD). The chi-squared (χ^2) test was conducted to compare the detection rates between different diagnostic methods, with a P-value of less than 0.05 considered statistically significant. This analysis helped to evaluate the effectiveness and reliability of the diagnostic approaches used in the study.

Results

Patient characteristics

The study included 1001 pregnant women with a mean age of 34.4 years (range: 20–49) and a mean gestational period of 19^{+6} weeks (range: 18–24^{+5}). The primary indications for fetal sampling were categorized as follows: 10.5% (105/1001) presented fetal abnormalities detected by ultrasound, 38.8% (388/1001) were flagged as high-risk for Down syndrome through screening, 40.1% (401/1001) were of advanced maternal age, 4.0% (40/1001) had NIPT results suggesting partial chromosome duplications or deletions, 5.7% (57/1001) had other indication such as both parents carrying the same type of thalassemia or had a history of giving birth to children with anomalies (Table 1). inheritable risk of a single gene disease, prior risk of an abnormal pregnancy outcome, an abnormal amniotic fluid volume,

Detection results of CNV-Seq

Of the 1001 fetal samples analyzed using CNV-Seq, 36 cases (3.6%) were found to have whole chromosome aneuploidies, and 53 samples (5.3%) were pathogenic CNVs. The sizes of these CNVs ranged from 107 kb to 40.75 Mb. Among the 53 pathogenic CNVs, 15 cases (1.5%; 15/1001) involved microduplications, and 38 cases (3.8%; 38/1001) involved microdeletions (Table 2). These CNVs were associated with 33 known syndromes, including DiGeorge syndrome ($n=4$), 22q11.2 microduplication syndrome ($n=4$), 15q11.2 microdeletion syndrome ($n=4$), Williams-Beuren syndrome ($n=3$), 1q21.1 microduplication syndrome ($n=2$), 16p13.11 microdeletion syndrome ($n=2$), 1q21.1 microdeletion syndrome ($n=2$), Kagami-Ogata syndrome ($n=1$), Prader-Willi syndrome ($n=1$), Russell-Silver syndrome ($n=1$), Cri du Chat

Table 1 Patient characteristics

	AMA ($N=401$)	HR-MSS ($N=388$)	USM ($N=105$)	Others ($N=57$)	HR-NIPT ($N=40$)	Mixed[1] ($N=10$)	Total ($N=1001$)
Age							
Mean	39.2	31.3	31.0	31.0	32.3	36.9	34.4
Range	24–49	20–38	20–40	20–37	24–40	25–42	20–49
Gestational age wk^{+d}							
Mean	19^{+4}	20	20^{+6}	19^{+3}	20^{+3}	19^{+3}	19^{+6}
Range	18–24^{+4}	18–24^{+5}	18–24^{+4}	18–22^{+3}	18–24	18^{+4}– 21^{+1}	18–24^{+5}

AMA, advanced maternal age; HR-MSS, high-risk maternal serum screening; USM, ultrasound soft marker; HR-NIPT, high-risk non-invasive prenatal testing.

[1]This group consisted of patients with mixed indications, including AMA, HRMSS, USM, HR-NIPT, inheritable risk of a single gene disease and prior risk of an abnormal pregnancy outcome.

Table 2 Summary of CNV-Seq results of 1001 prenatal diagnostic samples grouped by prenatal diagnostic indications

	AMA	HR-MSS	USM	Others	HR-NIPT	Mixed	Total
Chromosomal aneuploidy	10 (2.5%)	6 (1.5%)	5 (4.8%)	2 (3.5%)	12 (30%)	1 (10%)	36 (3.6%)
T21	6 (1.5%)	4 (1.0%)	4 (3.8%)	1 (1.8%)	4 (10.0%)	1 (10.0%)	20 (2.0%)
T18	2 (0.5%)	1 (0.3%)	0 (0.0%)	0 (0.0%)	1 (2.5%)	0 (0.0%)	4 (0.4%)
T13	0 (0.0%)	0 (0.0%)	1 (1.0%)	1 (1.8%)	0 (0.0%)	0 (0.0%)	2 (0.2%)
Sex chromosome abnormality	2 (0.5%)	1 (0.3%)	0 (0.0%)	0 (0.0%)	7 (17.5%)	0 (0.0%)	10 (1.0%)
P/LP CNVs	10 (2.5%)	25 (6.4%)	9 (8.6%)	2 (3.5%)	7 (17.5%)	0 (0.0%)	53 (5.3%)
Microdeletion	6 (1.5%)	20 (5.2%)	5 (4.8%)	0 (0.0%)	7 (17.5%)	0 (0.0%)	38 (3.8%)
microduplication	4 (1.0%)	5 (1.3%)	4 (3.8%)	2 (3.5%)	0 (0.0%)	0 (0.0%)	15 (1.5%)
VUS	381 (95.0%)	357 (92.0%)	91 (86.7%)	53 (93.0%)	21 (52.5%)	9 (90.0%)	912 (91.2%)
Total	401	388	105	57	40	10	1001

AMA, advanced maternal age; HR-MSS, high-risk maternal serum screening; USM, ultrasound soft marker; HR-NIPT, high-risk non-invasive prenatal testing; P/LP, pathogenic/likely pathogenic; VUS: variants of uncertain significance

Table 3 Comparison of detection rates of karyotype and CNV-SEQ classified according to prenatal diagnostic indications

Indications	CNV-Seq abnormal	Detection rate	Karyotype abnormal	Detection rate
AMA ($N=401$)	20	5.0%	12	2.9%
HR-MSS ($N=388$)	31	8.0%	11	2.8%
USM ($N=105$)	14	13.3%	7	6.7%
HR-NIPT ($N=40$)	19	47.5%	16	40.0%
Others ($N=57$)	4	7.0%	3	5.3%
Mixed ($N=10$)	1	10.0%	1	10.0%
Total ($N=1001$)	89	8.9%	50	5.0%

AMA, advanced maternal age; HR-MSS, high-risk maternal serum screening; USM, ultrasound soft marker; HR-NIPT, high-risk non-invasive prenatal testing.

Syndrome ($n=1$), 2q37 microdeletion syndrome ($n=1$), 18q microdeletion syndrome ($n=1$), 16p13.11 microdeletion syndrome ($n=1$), etc. (Table S1).

Comparison of CNV-Seq and karyotype analysis

In this study, a detailed comparison between CNV-Seq and karyotype analysis was conducted to evaluate their respective efficacies in detecting chromosomal abnormalities across different prenatal diagnostic indications. Overall, CNV-Seq demonstrated a higher detection rate, identifying chromosomal abnormalities in 8.9% (89/1001) of cases compared to 5.0% (50/1001) identified by karyotype analysis (Table 3).

In specific diagnostic categories, CNV-Seq exhibited superior performance. For instance, in cases with high-risk non-invasive prenatal testing (HR-NIPT), CNV-Seq detected abnormalities in 47.5% of cases, while karyotype analysis identified abnormalities in 40.0%. Similarly, in cases with high-risk maternal serum screening (HR-MSS), CNV-Seq detected abnormalities in 8.0% of cases, more than double the 2.8% detection rate of karyotyping (Table 3).

The analysis also highlighted that CNV-Seq was consistent with karyotyping in detecting common aneuploidies, such as trisomy 21 ($n=19$), trisomy 18 ($n=4$), and sex chromosome abnormalities ($n=9$) like Turner syndrome (Table 4). For deletions and duplications, all deletions and duplications detected by karyotyping were confirmed by CNV-seq, except for one case of extra genetic material of unknown origin on the long arm of chromosome 13 (q)33, where CNV-seq detected a duplication of 7.77 M on chromosome 1 (Table 4). In addition, CNV-seq detected 47 microdeletions and microduplications in small segments that could not be detected by karyotype (Table S1). However, for the three cases of balanced translocations detected by karyotype, CNV-seq was unable to detect any of them. In addition, for the five cases with mosaicism, CNV-seq could only detect one mosaicism chromosomal abnormality at levels up to 55%.

Clinical follow-up

Of these 1001 cases, 958 had follow-up results for pregnancy outcomes and were included in the clinical pregnancy outcome analysis. Among the 88 fetuses identified with chromosomal abnormalities (35 chromosomal aneuploidy and 53 P/LP CNVs) via CNV-Seq, 63 pregnancies (31 chromosomal aneuploidy group and 32 P/LP CNVs group) were terminated following extensive genetic counseling. Of these, 31 involved fetuses with whole chromosome aneuploidies, while 32 had pathogenic CNVs. In cases where CNVs were classified as likely pathogenic, 32 out of 53 women chose to terminate the pregnancy. For fetuses with variants of uncertain significance (VUS), 829 pregnancies were continued after parental studies indicated no associated disease phenotype, while 41 were terminated due to the potential risks (Table 5).

Table 4 Chromosomal abnormalities detected by karyotype and their corresponding CNV-Seq results in the samples detected by both karyotype analysis and CNV-Seq

Categories Of Variation	Karyotype	CNV-Seq	Consistency of the two results	Number	Pregnancy outcome
Deletion/Duplication	45,X	del(Yp11.32q11.21,14.54 M)	Yes	1	Live birth
Deletion/Duplication	46,XX, add(13)(q33)	dup(1q43q44,7.77 M)	No	1	Termination
Deletion/Duplication	46,XX, del(1)(p32p22)	del(1p32.1p22.2,28.03 M)	Yes	1	Termination
Deletion/Duplication	46,XX, del(18)(q22.1q23)	del(18q22.1q23,13.67 M)	Yes	1	Termination
Deletion/Duplication	46,XX, del(6)(q26q27)	del(6q26q27,8.24 M)	Yes	1	Termination
Deletion/Duplication	46,XY, del(15)(q11.2q13)	del(15q11.2q13.1,5.72 M)	Yes	1	Termination
Deletion/Duplication	46,XY, del(5)(p14)	del(5p15.33p14.2,23.65 M)	Yes	1	Termination
Deletion/Duplication	47,XX, der(3;11;13)t(3;13;9;11)(p13;p12;q31;p15.5),+13mat	dup(9p24.3q31.1,102.76 M)	Yes	1	Termination
Translocation	46,XY, t(11;22)(q25;q13)mat	dup(16p13.13p13.13,104.12 K)	No	1	Live birth
Translocation	46,XY, t(3;7)(p14;p21)pat	dup(1p31.1p31.1,223.36 K)	No	1	Live birth
Translocation	46,XY, t(6;19)(p21.1;q13.4)	dup(1p31.1p22.3,116.60 K)	No	1	Live birth
Mosaicism	46,XY, del(11)(q23)[9]/46,XY[11]	dup(1q44q44,523.83 K)	No	1	Live birth
Mosaicism	45,X[55]/46,XY[33]	del(Yp11.32q11.221,19.54 M)	Yes	1	Termination
Mosaicism	45,X[21]/46,X, add(X)(p22.3)[38]/46,XX[105]	del(Xp22.33p22.33,3.64 M)	No	1	Termination
Mosaicism	47,XXX[2]/46,XX[105]	del(15q11.2q11.2,860.54 K)	No	1	Termination
Mosaicism	47,XY,+mar[30]/46,XY[35]	dup(2q11.2q11.2,1.15 M)	No	1	Termination
Aneuploidy	47,XX,+13	T13	Yes	2	Termination
Aneuploidy	47,XY,+18 or 47,XX,+18	T18	Yes	4	Termination
Aneuploidy	47,XY,+21 or 47,XX,+21	T21	Yes	19	Termination
Aneuploidy	47,XXY	XXY	Yes	4	Termination
Aneuploidy	47,XXX	XXX	Yes	3	1 Live birth and 2 Termination
Aneuploidy	47,XYY	XYY	Yes	2	1 Live birth and 1 NA

NA: not available

Table 5 Pregnancy outcomes of 958 participants with follow-up data

	Live birth (*N* = 854)	Termination (*N* = 104)	Total (*N* = 958)
Chromosomal aneuploidy	4 (11.4%)	31 (88.6%)	35 (100.0%)
T21	1 (5.0%)	19 (95.0%)	20 (100.0%)
T18	0 (0.0%)	4 (100.0%)	4 (100.0%)
T13	0 (0.0%)	2 (100.0%)	2 (100.0%)
Sex chromosome abnormality	3 (33.3%)	6 (66.7%)	9 (100.0%)
P/LP CNVs	21 (39.6%)	32 (60.4%)	53 (100.0%)
Microdeletion	13 (34.2%)	25 (65.8%)	38 (100.0%)
microduplication	8 (53.3%)	7 (46.7%)	15 (100.0%)
VUS	829 (95.3%)	41 (4.7%)	870 (100.0%)

VUS: variants of uncertain significance

Discussion

This study analyzed 1001 prenatal samples to assess the efficacy of CNV-Seq in detecting chromosomal abnormalities. The key findings indicate that CNV-Seq identified chromosomal abnormalities in 8.9% of cases, a higher detection rate compared to the 6.1% observed with karyotype analysis. Notably, CNV-Seq detected 53 LP/P CNVs in 5.3% of cases, with sizes ranging from 107 kb to 40.75 Mb, associated with 33 known syndromes. The clinical outcomes of these cases showed that 31 and 32 fetuses were terminated after detection of chromosomal aneuploidy and CNV, respectively, suggesting that prenatal diagnosis plays a crucial role in guiding clinical decision-making. The detection rate of CNV-Seq in this study is consistent with existing literature, which supports the higher sensitivity of CNV-Seq in identifying chromosomal abnormalities (2.8% increased yield) compared to conventional karyotyping [11]. Previous studies have reported similar findings, where CNV-Seq has shown superiority in detecting submicroscopic alterations, including microdeletions and microduplications that are often missed by karyotype analysis [14, 15]. The detection of 47.5% chromosomal abnormalities in high-risk NIPT cases by CNV-Seq, compared to 42.5% by karyotyping, aligns with the growing body of evidence that supports the enhanced capability of CNV-Seq in high-risk populations.

CNV-Seq offers several advantages over traditional karyotype analysis and CMA. The use of a sequencing platform allows CNV-Seq to detect smaller chromosomal aberrations that are below the resolution of karyotyping [16, 17]. Moreover, CNV-seq samples can be pooled with NIPT samples for sequencing, making NGS a versatile tool for prenatal diagnosis and reducing the cost of sequencing individual samples. This study demonstrated that CNV-Seq not only detected all abnormalities identified by karyotyping but also revealed additional submicroscopic changes, underscoring its superior sensitivity. The ability of CNV-Seq to identify pathogenic CNVs and their associated syndromes further emphasizes its diagnostic value. Despite its advantages, CNV-Seq has limitations in prenatal diagnostics. It may miss balanced chromosomal rearrangements, such as translocations and inversions, which are typically detected by karyotyping [17]. Therefore, a combined approach using both CNV-Seq and karyotype analysis is recommended to improve the overall detection rate of chromosomal abnormalities, ensuring a more comprehensive assessment.

The application of NGS technologies in prenatal diagnostics represents a significant advancement in the detection of genetic abnormalities. Among these, CNV-Seq, WES, and WGS each contribute distinct strengths to genetic analysis. CNV-Seq offers robust capabilities in identifying CNVs with high sensitivity, while WES focuses on protein-coding regions to uncover SNVs associated with Mendelian disorders. However, WGS stands out as the most comprehensive approach, capable of detecting CNVs, SNVs, and structural variations (SVs) across the entire genome [18]. This unparalleled scope allows for the identification of a broader spectrum of pathogenic mutations, including those in non-coding regions that may contribute to complex genetic disorders. By providing more precise and extensive genomic insights, WGS enhances the ability of clinicians to deliver accurate genetic counseling and guide pregnant women in making informed reproductive decisions [19]. The integration of these NGS technologies into prenatal care heralds a new era in precision medicine, promising improved diagnostic outcomes and personalized management strategies.

Conclusion

In conclusion, this study underscores the enhanced detection capability of CNV-Seq in prenatal diagnostics, particularly for submicroscopic chromosomal abnormalities that are often missed by karyotyping. While CNV-Seq offers significant advantages, including the ability to detect smaller chromosomal aberrations and compatibility with NIPT, its limitations necessitate a combined approach with traditional karyotype analysis. The potential of low-depth whole genome sequencing in non-invasive prenatal screening further highlights the evolving landscape of prenatal diagnostics, offering promises for more comprehensive and less invasive approaches in the future.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12920-025-02139-y.

Supplementary Material 1

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Author contributions

MY and FW: conception, design, manuscript draft and revision. YH and SF: data collection, variants classification, clinical consultation and manuscript draft. DS: data analysis, table preparation and manuscript draft. YY: data collection, table preparation. All authors have read and agreed to the published version of the manuscript.

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Data availability

The variation data and related clinical information have been uploaded to the China National GeneBank DataBase (CNGBdb, https://db.cngb.org/), with the accession number CNP0006387. The datasets are available upon reasonable request. Codes used to analyse the data and produce tables are accessible on GitHub (https://github.com/Di-Shao/Comprehensive_Chromosomal_Abnormality_Detection_Project).

Declarations

Ethics approval and consent to participate

All procedures performed in this study were in accordance with the Helsinki Declaration. This study protocol was approved by the Institutional Reviewer Board of SanMing First Hospital (IRB-2024-74). Written informed consent has been obtained from each patient.

Consent for publication

Written informed consent for publication of their clinical details was obtained from all participants.

Competing interests

Di Shao is an employee of BGI Genomics. The other authors declare no conflict of interest.

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