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## Multicolor-FISH Characterization of a Prenatal Mosaicism for a Chromosomal Rearrangement Undetected by Molecular Cytogenetics

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1 **Novel Insights**

2 **Multicolor-FISH characterization of a prenatal mosaicism for a chromosomal rearrangement undetected**  
3 **by molecular cytogenetic**

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13  
14 Short Title: Multicolor-FISH characterization of a prenatal low-level mosaicism chromosomal  
15 rearrangement.

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31 **Established Facts and Novel Insights**

Established Facts

- Fetal mosaicism is frequent
- Most of these mosaics are aneuploidies
- Chromosomal microarray analysis (CMA) is now used as a first-tier technique in prenatal diagnosis

Novel Insights

- CNV diagnosed with CMA may be associated with additional genomic imbalances present in low level mosaicism,
- These rearrangements require morphological cytogenetic techniques to be properly diagnosed

33

34 **ABSTRACT**

35 Fetal mosaicism for chromosomal rearrangements remains a challenge to diagnose, even in the era of  
36 whole genome sequencing. We present here a case of fetal mosaicism for a chromosomal rearrangement  
37 explored in amniocytes and fetal muscle, consisting of a major cell population (95%) with 4q partial  
38 monosomy and a minor population (5%) with additional material replacing the 4qter deleted segment.  
39 Molecular techniques (MLPA, array-CGH) failed to assess the origin of this material. Only multicolor-FISH  
40 identified the additional segment on chromosome 4 as derived from chromosome 17. Due to the poor  
41 prognosis, the couple chose to terminate the pregnancy. Because of low-level mosaicism, chromosomal  
42 microarray analyses (CMA), now considered as first-tier prenatal genetic analysis, did not allow the  
43 identification of the minor cell. In case of large CNV (>5Mb) detected by CMA, realization of a karyotype  
44 may be considered to elucidate the mechanism of the underlying rearrangement and eliminate mosaicism.

45

46 **I) INTRODUCTION**

47 Fetal mosaicism (i.e. the presence, in an individual, of two or more distinct cellular populations) can  
48 concern 0.64% of amniotic fluid samples (AFS) and up to 2% of chorionic villus samples (CVS) (Grati et al.,  
49 2017). For these CVS, most of mosaicisms are confined to the placenta (Grati et al., 2017), and only fetal  
50 sampling (e.g. AFS or cord blood samples) can prove true fetal mosaicism (Malvestiti et al., 2015).

51 Mosaicism can also be the consequence of culture artifacts (Pipiras et al., 2004). Most fetal mosaicisms are  
52 aneuploidies (Grati et al., 2017) corresponding to mitotic, post-zygotic events, mainly underpinned by two  
53 mechanisms: chromosome missegregation in a somatic cell of a euploid conceptus and trisomy or  
54 monosomy rescue after a meiotic nondisjunction (Grati et al., 2017; Taylor et al., 2014). Mosaicism for  
55 small supernumerary marker chromosomes (sSMCs) are also described in prenatal samples and are  
56 involved in 14% of fetal mosaicisms (Grati et al., 2017). Mosaicism may finally also involve structural  
57 chromosomal abnormalities and thus are observed for balanced or unbalanced translocations (Malvestiti et

58 al., 2015; Pipiras et al., 2004; Stallings et al., 1997). Mosaicism remains a challenge to diagnose, even with  
59 routine techniques of prenatal testing. When diagnosed, the clinical consequences of such mosaicisms are  
60 also highly difficult to predict, depending both on the anomalies involved and the level of mosaicism in  
61 each tissue (Taylor et al., 2014).

62 Among cytogenetic techniques, multicolor-FISH (M-FISH), consisting in using up to 24 chromosome painting  
63 probes in a single FISH technique is overthrown by molecular techniques such as chromosomal microarray  
64 analyses (CMA) or high throughput sequencing. However, M-FISH is still of interest to supplement these  
65 techniques in some cases, such as characterizing small supernumerary marker chromosomes (sSMC,(Jang  
66 et al., 2016)) or mosaic complex chromosomal rearrangements (Lin et al., 2018).

67 We present here a case-report of a fetal mosaicism for an unexpected unbalanced translocation solved by  
68 M-FISH after failure of both MLPA and CMA to conclude on the complete nature of the rearrangement.

## 69 **II) CLINICAL REPORT**

### 70 **II.1) Case Presentation**

71 A 28 year-old primigravida woman was referred to our center at 15 gestation weeks (GW) for an isolated  
72 increased nuchal translucency (95<sup>th</sup> percentile). Familial and personal medical histories were unremarkable.  
73 Consanguinity was discounted. Amniotic fluid was sampled to find a possible genetic caused of the  
74 increased nuchal translucency.

### 75 **II.2) Methods and Results**

76 RHG -banding karyotype was performed on cultured amniocytes (for the fetus) and cultured lymphocytes  
77 obtained from peripheral blood (for the parents) according to standard cytogenetic procedures. Two  
78 abnormal cell populations were observed on both fetal karyotypes realized on two different amniotic fluid  
79 samples (performed at 15 gestation weeks (GW) and 23 GW respectively): one major population (95% of  
80 cells) carrying a distal deletion of the long arm of a chromosome 4 (Figure 1A), and a second population (5%  
81 of cells) presenting with additional material of unknown origin on the deleted chromosome 4 (Figure 1B).  
82 No normal cell was observed. FISH was performed using chromosome 4 whole chromosome painting and  
83 subtelomeric probes on cultured amniocytes according to manufacturers' protocols. FISH confirmed that  
84 the subtelomeric 4qter region was deleted in both populations and that the additional material did not  
85 originate from a chromosome 4 (data not shown). To identify the additional chromosomal material,  
86 different molecular techniques were used. DNA was extracted from cultured amniocytes. The MLPA kits  
87 SALSA P036B and P070 (MRC Holland, Amsterdam, The Netherlands) were used according to the  
88 manufacturer's protocol. Electrophoresis of the PCR products was run on an AbiPrism 3130xl and analyzed  
89 using Coffalyser.Net software. This analysis showed a homogeneous heterozygous deletion of chromosome  
90 4 long arm subtelomeric region and failed to detect a gain of another subtelomeric region (data not  
91 shown).

92 Oligonucleotide array-CGH (aCGH) was performed using the Agilent Human Genome CGH microarray  
93 4x180K (Agilent Technologies, Santa Clara, CA, USA), on DNA extracted from both cultured amniocytes and

94 frozen fetal muscle. Scanning, extraction and analysis methods were described elsewhere (Jaillard et al.,  
95 2011). The probes were mapped using GRCh37 genome version. Aberration detection was set as follow:  
96 minimal number of deviated probes = 3, with ADM-2 as aberration algorithm (threshold = 6) with fuzzy zero  
97 off. aCGH on both samples highlighted a terminal deletion starting at 4q33 and spanning 19.9Mb (Figure  
98 2A). The mean log ratio of the deletion was -0.92, a result in favor of a homogeneous heterozygous  
99 4q33q35.2 terminal deletion. The profiles of the other chromosomes showed no pathogenic gain, even in  
100 mosaic (assessed through multisample analyses).

101 Parental karyotypes were normal.

102 Due to the difficulties in identifying the additional material on fetal chromosome 4q with MLPA and aCGH,  
103 an M-FISH on cultured amniocytes was performed using the 24Xcyte-MetaSystems 24-color kit and  
104 according to the manufacturer's protocol. Counting 100 metaphases, we finally concluded that the  
105 additional material, present in 5% of the metaphases, originated from chromosome 17 (Figure 3B). In 95%  
106 of the metaphases, we only observed the terminal 4q deletion.

107 Retrospective analysis of the karyotype in light of the M-FISH findings suggested that the additional  
108 material corresponded to the long arm of a chromosome 17. Reanalysis of the aCGH profiles of  
109 chromosome 17 did not show any deviation (Figure 2B). We performed an additional FISH analysis using  
110 the ZytoLight® ERBB2/CEP17 probes (Zytovision GmBH, Bremerhaven, Germany) on frozen fetal muscle.  
111 Mosaicism for partial trisomy 17q was estimated to be 7-8% in this tissue. In all the cells carrying an extra  
112 signal of the ERBB2 probe (at 17q12q21.1 locus) we did not identify additional spots for the probe targeting  
113 the chromosome 17 centromere. Thus, these results discounted the presence of centromere of  
114 chromosome 17 in the additional segment of chromosome 17 located on 4q.

115 In conclusion, the fetal karyotype presented with a major cellular population showing a terminal deletion  
116 4q33qter (95% of cells), and a minor population showing the same 4q33qter deletion, replaced by a  
117 chromosome 17 long arm (5% of cells) leading to chromosome 17 partial trisomy. Both populations were  
118 otherwise disomic for normal chromosomes 17. The final formula was

119  $\text{mos } 46,XY,\text{del}(4)(q33)[95]/46,XY,\text{der}(4)t(4;17)(q33;q11)[5].\text{arr}[GRCh37]$

120  $4q33q35.2(170684863\_190679684)\times 1$

121

### 122 **II.3) Pregnancy outcome**

123 Due to the poor prognosis resulting from the chromosomal anomalies, the couple chose to terminate the  
124 pregnancy at 24 GW. A male fetus was delivered. He presented with a dolichocephaly associated with  
125 prefrontal edema, hypertelorism, retrognathism and a narrow palate. Careful examination of the  
126 extremities highlighted brachymesophalangia of the 5<sup>th</sup> fingers and a bilateral single palmar crease. At  
127 autopsy, the fetus also had a single left umbilical artery, cryptorchidism, a common mesentery with an  
128 intestinal malrotation and a small atrial septal defect. Delayed bone maturation (bone maturation  
129 compatible with a 22 GW-old fetus) was diagnosed at standard radiographies. Histopathological analyses

130 revealed asymmetric testes, with one normal testis and one showing an immature parenchyma.

131 Histological analyses of the other organs were unremarkable.

### 132 III) **DISCUSSION**

133 Mosaicism in prenatal samples is a phenomenon favored by advanced parental age (Taylor et al., 2014) that  
134 can reach up to 2% of CVS samples (Grati et al., 2017) but is more uncommon in AFS (between 0.3% and  
135 0.64% (Grati et al., 2017; Ing et al., 1999; Li et al., 2019; LI et al., 2019)). Most of these mosaicisms,  
136 especially when confirmed on fetal-derived tissues, are aneuploidies (Grati et al., 2017). However, some of  
137 these mosaic anomalies may involve structural chromosomal abnormalities. If most of these anomalies are  
138 sSMCs, mosaicism for balanced or unbalanced translocations are also observed (Pipiras et al., 2004;  
139 Stallings et al., 1997). We present here a case of mosaicism in a fetus presenting with a major cell  
140 population showing a 4q partial monosomy and a minor population with a 4q partial monosomy plus a 17q  
141 partial trisomy.

142 4q terminal deletions are rare and responsible for various phenotypes, combining cleft lip and palate,  
143 congenital heart defects and neurodevelopmental delay, as well as other minor anomalies depending on  
144 the size of the deletion (Tidrenczel et al., 2019). Large 17q duplications are also very rare and seem to  
145 generate more severe phenotypes, as Ellis-Van-Creveld-like features (Serotkin et al., 1988), delayed  
146 psychomotor development, micrognathia, skeletal anomalies, and central nervous system (CNS) defects  
147 and even hydrops fetalis (Lenzini et al., 1988). The fetus presented here had an association of several mild  
148 anomalies including facial dysmorphism, single left umbilical artery, cryptorchidism intestinal malrotation  
149 and small atrial septal defect. This phenotype may recall 4q terminal deletion syndrome rather than 17q  
150 duplication. This may be explained by the very low prevalence of cells carrying a 17q trisomy contrary to  
151 homogeneous 4qter deletion.

152 The threshold of mosaicism detection for prenatal cytogenetic techniques is around 19% for karyotype (for  
153 a routine number of 15 metaphases analyzed, with 95% degree of confidence, reaching 5% with 99%  
154 degree of confidence if 100 cells are analyzed (Hook, 1977)), 40% for MLPA (Chen et al., 2014) and 20% for  
155 BoBs (BACs on Beads, (Cheng et al., 2013)). The use of CMA lowered the capacities of mosaic detection, and  
156 the sensitivity of this technique for both gains and losses is around 10% (9-15% (Ballif et al., 2006; Carey et  
157 al., 2014)). The lowest level of prenatal mosaicism detected previously reported in the literature was 6% in a  
158 case of trisomy 21 (detected through karyotype on amniocytes, (Sifakis et al., 2008)). In our case, karyotype  
159 identified 2 cell populations but MLPA and aCGH failed to identify the nature of the additional material  
160 located on chromosome 4q, because of a very low level of mosaicism for the cell line with the der(4)t(4;17)  
161 chromosome (5%). Only M-FISH led to the identification of the additional material, corresponding to  
162 additional chromosome 17 long arm material on chromosome 4q. As previously mentioned, M-FISH is now  
163 used in rare pre- and postnatal cases of sSMC when CMA does not allow to characterize the abnormal  
164 chromosome (Jang et al., 2016), by painting all chromosomes in one experiment. However, M-FISH shows  
165 limitations when exact localization of a chromosomal breakpoint is required or intrachromosomal

166 aberrations are present. Another limitation is the size of the chromosomal segment involved in a  
167 rearrangement. Apart from M-FISH, massive parallel sequencing MPS with Whole Genome Sequencing  
168 (WGS), is predicted helpful to shed light on chromosomal rearrangements but CNV smaller than 100 kb may  
169 still be challenging to diagnose in routine practice (Gross et al., 2019) and repetitive DNA sequences, such  
170 as centromeres, cannot be explored. Moreover, WGS detection threshold for mosaicism is estimated  
171 between 10 and 20% depending on the anomaly (Hochstenbach et al., 2019), lower detection thresholds  
172 being currently achieved only for point variations through targeted MPS (Brewer et al., 2020; Liu et al.,  
173 2020). These statements suggest that MPS is probably not suitable for an accurate characterization of our  
174 rearrangement.

175

176 Chromosomal rearrangements are a common finding in early human embryos (Vanneste et al., 2009).  
177 These rearrangements include segmental terminal imbalances or double-strand breaks (DSB) within the  
178 centromeric regions, whole arm deletions and duplications. Multiple rearrangements can coexist in the  
179 same blastomere, revealing a high chromosomal instability (Vanneste et al., 2009). Most of these anomalies  
180 may be rescued through various mechanisms or be overwhelmed by normal cells (Popovic et al., 2020), but  
181 milder anomalies can persist and generate mosaicism (Grati et al., 2017). Four hypotheses can be  
182 formulated to elucidate the mechanism generating the rearrangement observed in our case (Figure 4).  
183 A) A balanced translocation (4;17)(q33;q11) appeared in one parent's gamete and the zygote received the  
184 der(4) chromosome. Then, during the early mitotic divisions of the embryo, a break occurred on the  
185 derivative chromosome with loss of the additional segment of 17q attached to 4q. The broken der(4) is  
186 then stabilized by neotelomere formation, resulting in a minor "native" cell line with the der(4) and a major  
187 "derived" cell line with a pure 4q deletion (Figure 4A). This hypothesis has been proposed by (Kulikowski et  
188 al., 2006) as a statement for a similar mosaicism observed in a patient, which associated a pure monosomy  
189 9p23pter in a major cell line and a minor cell line showing additional material from chromosome 1  
190 (1q41qter) in place of the deleted 9p23pter segment. This hypothesis seems to be the most relevant to  
191 explain the results obtained in this case.

192 B) A DSB occurred at 4q33 during early embryogenesis. Microhomology Mediated Break-Induced Repair  
193 (MMBIR) mechanism took place to repair the DSB during replication. Briefly, MMBIR allows a collapsed  
194 replication fork to invade any single stranded template in close physical proximity that it shares  
195 microhomology to (Colnaghi et al., 2011). Here, instead of using a replication fork on chromosome 4 as a  
196 template to correct the DSB, the cell used a fork on chromosome 17, resulting in an aberrant chromosome  
197 4 in which the 4q33q35 region is replaced by a segment originating from chromosome 17 (Figure 4B).  
198 These previous hypotheses may be promoted by the abundance of segmental duplications and Low-Copy-  
199 Repeats (LCR) on chromosome 17 (Cardone et al., 2008), some of them having strong homologies with LCR  
200 on distal chromosome 4q. The presence of intrachromosomal telomeric-like sequences at both centromeric  
201 region of chromosome 17 and 4q32q33 band may favor telomere capture as a way to "heal" broken

202 chromosomes but also chromosomal rearrangements and breakages (Ruiz-Herrera et al., 2005). The  
203 characterization of the breakpoints in the minor cell line would have been of interest to explore the  
204 hypothesis of the invasion of a chromosome 17 template by a collapsed fork on chromosome 4, but  
205 unfortunately, we did not have enough fetal material to do so.

206 C) A balanced translocation (4;17)(q33;q11) appears in early embryogenesis. The centromere of the  
207 chromosome 17 was included in the translocation leading to the generation of an acentric chromosome 17  
208 derivative (lost during mitoses) and a dicentric chromosome 4 derivative. Endoreplication or similar  
209 mechanisms rescues the monosomy 17 (Taylor et al., 2014). Then, absence of centromere inactivation in  
210 some cells may result in a breakage of the chromosome 4 derivative during mitosis and thus to a pure  
211 4q33qter-deleted population (Figure 4C). This hypothesis was discounted by complementary FISH analyses  
212 showing the absence of chromosome 17 centromere in the der(4) of the minor cell line.

213 D) Finally, it has also been recently demonstrated that chromoanagenesis may occur in the germline,  
214 resulting in high complexity rearrangements. These rearrangements are often stable, but rare cases of  
215 instability generating mosaicism are described. In an autistic patient, Collins *et al.* found a somatic mosaic  
216 unbalanced chromoanasythesis of chromosome 19, resulting from a *de novo* duplication-inversion-  
217 duplication in the germline (or in early embryogenesis) followed by mitotic missegregation leading to 6  
218 mosaic duplications (Collins et al., 2017). Due to the extensive explorations performed, this hypothesis  
219 seems very unlikely (Figure 4D).

#### 220 **IV) CONCLUSION**

221 Chromosomal mosaicism is frequent in prenatal period but remains a challenge to diagnose. After assessing  
222 the presence of a mosaicism in a fetal-derived sample, determining the nature of the chromosomal  
223 anomaly can raise unexpected issues, even in the era of WGS. For prenatal diagnosis, CMA analysis should  
224 now be considered as a gold standard technique performed in first tier, as recommended by the  
225 Association des Cytogénéticiens de Langue Française (ACLF) in some indications presented in the  
226 guidelines. Its limitations in detecting low-level mosaicisms is now well described but may be tolerated,  
227 given the fact that low-mosaic anomalies are very rare, thus chromosomal mosaic anomalies overlooked by  
228 CMA are estimated less than 1% (Tuke et al., 2019). However, the case reported here highlights the  
229 limitations of aCGH analysis for the detection of multiple abnormal cell lines and the necessity to associate  
230 morphological techniques with CMA (as karyotype or M-FISH) to conclude properly on the mechanism  
231 underlying the anomaly. In case of large CNV (>5Mb) detected by CMA, the realization of a karyotype may  
232 be considered to elucidate the mechanism of the underlying rearrangement and eliminate low-level  
233 mosaicism.

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#### 239 **Statement of Ethics**

240 The research was conducted ethically in accordance with the World Medical Association Declaration of  
241 Helsinki. Written informed consent was obtained from the parents of the fetus for publication of this case  
242 report and any accompanying images.

#### 243 **Conflict of Interest**

244 The authors have no conflicts of interest to declare.

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#### 248 **Author Contributions**

249 SJ conceived and designed the study. SO, DA and GLB were involved in the patient care and evaluation. EL,  
250 CH and LM acquired the cytogenetic data. SJ, LM, CH and EL analyzed and interpreted the data. PL  
251 performed the fetal autopsy. LM wrote the manuscript. SJ and MABR critically reviewed the manuscript and  
252 all authors read and approved the final manuscript.

253

254

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## 370 LEGENDS TO FIGURES

371 **Figure 1:** Fetal karyotype on cultured amniocytes demonstrating the co-existence of 2 cell lines in the fetus.  
 372 Panel (A): karyotype of a metaphase with the del(4)(q33), indicated by the arrow. Panel B: karyotype of a  
 373 metaphase with the der(4)t(4;17)(q33;q11) chromosome, indicated by the arrow.

374  
 375 **Figure 2:** aCGH profile obtained from frozen fetal muscle DNA. Panel (A): 4q33qter non-mosaic  
 376 heterozygous loss. Panel (B): normal chromosome 17 profile.

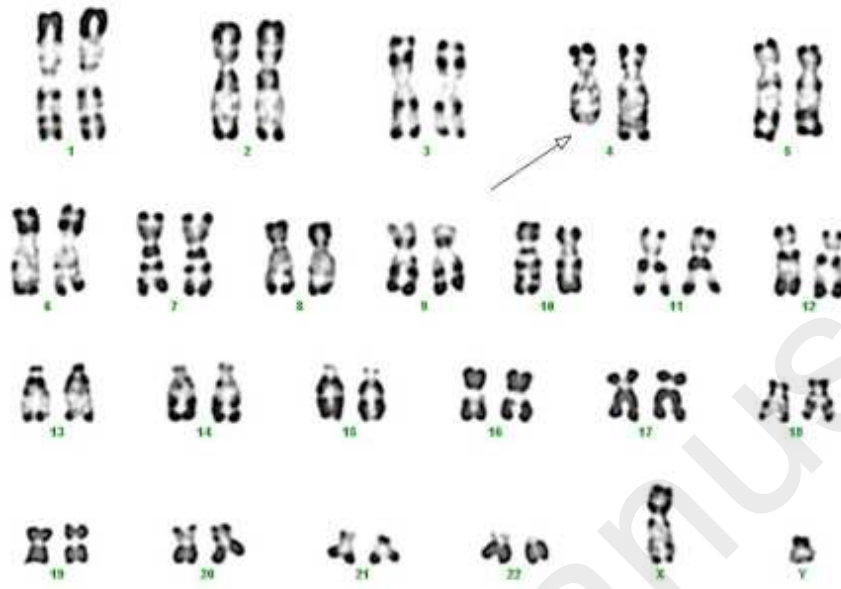
377  
 378 **Figure 3:** M-FISH results on cultured amniocytes. Panel (A): karyotype of a metaphase with the del(4)(q33).  
 379 Panel (B): karyotype of a metaphase with the der(4)t(4;17)(q33;q11) chromosome.

380

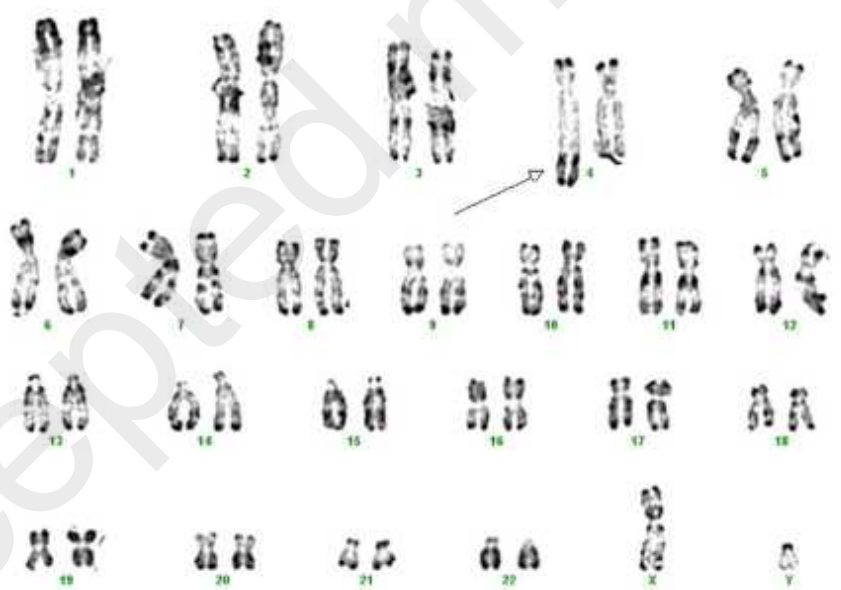
381 **Figure 4:** Schematic representation of the hypothesized mechanisms leading to the mosaic chromosomal  
382 rearrangement. Pane (A): der(4)t(4;17) breakage and neotelomere formation. Pane (B): DSB at  
383 chromosome 4q33 and aberrant MMBIR using a chromosome 17 template. Pane (C): t(4;17) with  
384 formation of a dicentric der(4) and loss of the der(17) acentric fragment, followed by secondary der(4)  
385 breakage in one cell line. Pane (D): chromoanagenesis. Fragmentation of one chromosome 4 and one  
386 chromosome 17. Chromoanagenesis rescue generates a major cell line with a fully recovered chromosome  
387 17 and an isolated 4qter deletion, and a minor cell line where the long arm of chromosome 17 replaces the  
388 4qter segment. The 4qter segment and chromosome 17 short arm are lost and the monosomy 17 is  
389 rescued.  
390

Figure 1

A



B

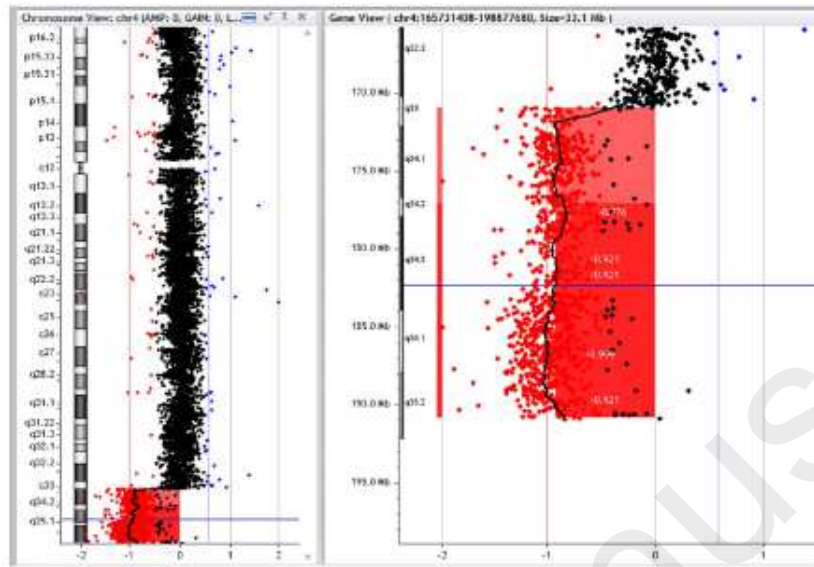


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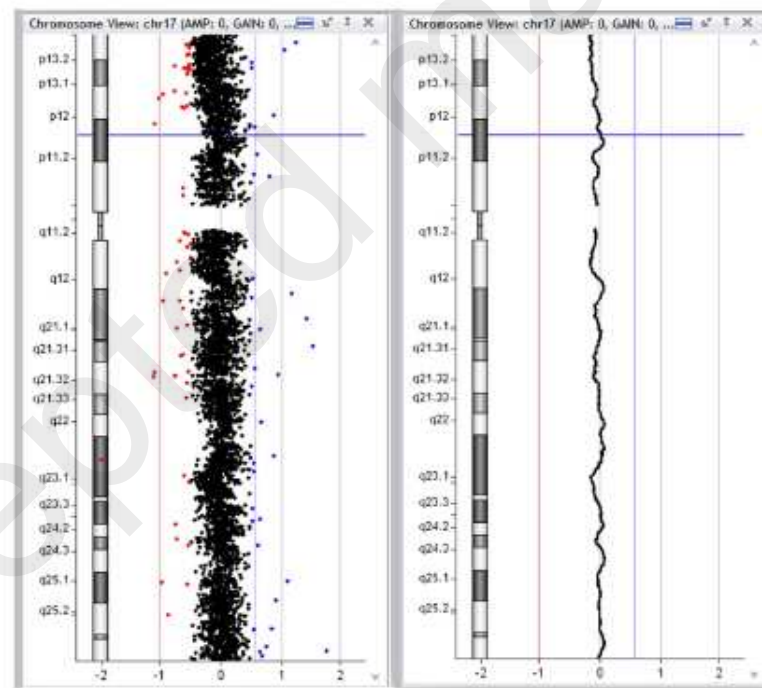
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Figure 2

A



B

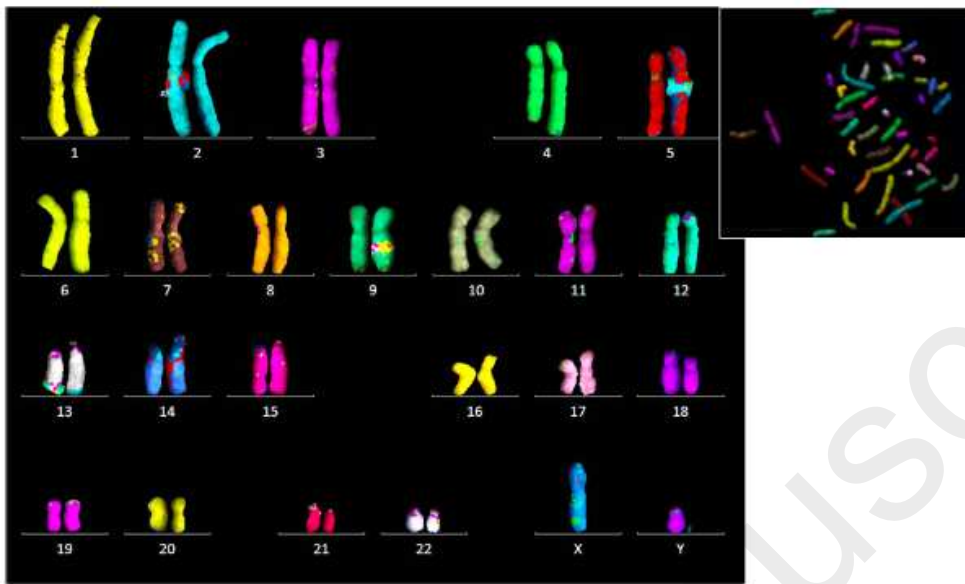


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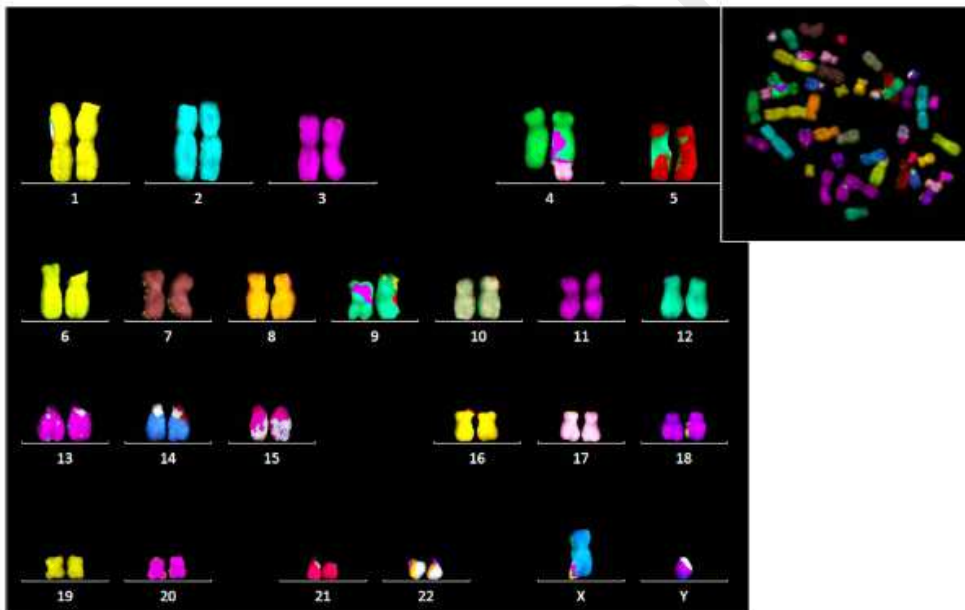
394

Figure 3

A



B



395

396

Figure 4

