

ORIGINAL ARTICLE

Recurrent Rearrangements of Chromosome 1q21.1 and Variable Pediatric Phenotypes

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ABSTRACT

BACKGROUND

Duplications and deletions in the human genome can cause disease or predispose persons to disease. Advances in technologies to detect these changes allow for the routine identification of submicroscopic imbalances in large numbers of patients.

METHODS

We tested for the presence of microdeletions and microduplications at a specific region of chromosome 1q21.1 in two groups of patients with unexplained mental retardation, autism, or congenital anomalies and in unaffected persons.

RESULTS

We identified 25 persons with a recurrent 1.35-Mb deletion within 1q21.1 from screening 5218 patients. The microdeletions had arisen *de novo* in eight patients, were inherited from a mildly affected parent in three patients, were inherited from an apparently unaffected parent in six patients, and were of unknown inheritance in eight patients. The deletion was absent in a series of 4737 control persons ($P=1.1\times 10^{-7}$). We found considerable variability in the level of phenotypic expression of the microdeletion; phenotypes included mild-to-moderate mental retardation, microcephaly, cardiac abnormalities, and cataracts. The reciprocal duplication was enriched in nine children with mental retardation or autism spectrum disorder and other variable features ($P=0.02$). We identified three deletions and three duplications of the 1q21.1 region in an independent sample of 788 patients with mental retardation and congenital anomalies.

CONCLUSIONS

We have identified recurrent molecular lesions that elude syndromic classification and whose disease manifestations must be considered in a broader context of development as opposed to being assigned to a specific disease. Clinical diagnosis in patients with these lesions may be most readily achieved on the basis of genotype rather than phenotype.

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RECENT ADVANCES IN TECHNOLOGIES such as comparative genomic hybridization (CGH; see Glossary) allow for the routine detection of submicroscopic deletions and duplications. Several studies of persons with mental retardation or congenital anomalies of unknown cause have led to the identification of new genomic disorders.¹⁻¹⁰ Classically, criteria that have been applied to determine whether a given rearrangement is causative include de novo appearance of the deletion or duplication in an affected individual (i.e., it is not present in unaffected parents), recurrence of the same or an overlapping event in similarly affected persons, and absence of the deletion or duplication in a control population. Examples of genomic disorders with these features include the Williams–Beuren syndrome, the 17q21.31 microdeletion syndrome, and the Prader–Willi and Angelman syndromes.

As more patients are identified with a given unbalanced microrearrangement, it has become clear that some genomic disorders have high penetrance but a wide range of phenotypic severity. For example, although 90% of persons with the 22q11 deletion syndrome have the same 3-Mb deletion on chromosome 22, the phenotypic features are highly variable. Congenital heart disease is found in most (74%) but not all carriers of the deletion, and cleft palate is found in 27% of carriers (reviewed in Robin and Shprintzen¹¹). More recently, reports of microdeletions or duplications with apparently incomplete penetrance and vari-

able expressivity have been identified in mental retardation–multiple congenital anomalies, autism, and other psychiatric disorders.¹²⁻¹⁶ The 1q21.1 microdeletions associated with the thrombocytopenia–absent radius syndrome are necessary but not sufficient to cause disease.¹⁷ As these reports accumulate, it is becoming clear that the phenotypes associated with imbalances of some regions of the genome can be variable, and modifiers probably play an important role. The ascertainment and description of patients with a specific chromosomal rearrangement critically affects the spectrum of phenotypes associated with it.

METHODS

POPULATIONS OF PATIENTS

DNA samples were obtained from the series described in Tables 1A and 1B in the Supplementary Appendix (available with the full text of this article at www.nejm.org) after approval by local institutional review boards at each of the participating centers in Europe and the United States. Series 1 and 2, 4 through 11, 13 through 15, and the Dutch series of 788 patients came from diagnostic referral centers to which the majority of patients (95%) were referred for mental retardation with or without other features. Series 3 and 12 comprise probands with a diagnosis of autism according to Autism Diagnostic Interview–Revised (ADI-R) and Autism Diagnostic Observation Schedule (ADOS) criteria. Written informed consent was provided by all patients or, if children, by their parent or guardian.

DETERMINING VARIATION IN COPY NUMBER

Affected Persons

The method of screening for changes in copy number for each series is included in Table 1A in the Supplementary Appendix. The Dutch series of patients was screened using array-based CGH involving a bacterial artificial chromosome microarray, as described in Table 1B in the Supplementary Appendix. Rearrangements of 1q21.1 were further analyzed with the use of custom oligonucleotide arrays (NimbleGen Systems). Details are given in the Methods section of the Supplementary Appendix.¹⁸⁻²⁰

Unaffected Persons

We evaluated 2063 unaffected persons, using HumanHap 300, HumanHap 550, or HumanHap 650Y Genotyping BeadChips (Illumina) (Table 2

Glossary

Comparative genomic hybridization (CGH): An assay in which DNA samples from patients and from reference genomes are labeled with different fluorescent dyes and cohybridized to an array containing known DNA sequences. Differences in relative fluorescence intensities of hybridized DNA on the microarray reflect differences in copy number between the genome of the patients and reference DNA.

Nonallelic homologous recombination: Aberrant meiotic recombination between nonallelic segmental duplications that are highly homologous but located at different places on the chromosome. This recombination causes duplication, deletion, or inversion of the sequence between the homologous blocks of DNA.

Segmental duplications: Large stretches of DNA (>1 kb in length), with more than 90% sequence identity, that are present at two or more places in the genome. These duplication blocks often include one or more genes and constitute approximately 5% of the human genome. They are also referred to as low-copy repeats or duplicons.

in the Supplementary Appendix; 91, 206, or 212 probes used, respectively, within the critical region). Hybridization, data analysis, and copy-number analysis, with particular reference to chromosome 1q21.1 (mapping between genome coordinates 143,500,000 and 145,000,000 on chromosome 1, according to National Center for Biotechnology Information [NCBI] build 35), were performed according to published protocols.²¹ We also evaluated 300 unaffected persons, using a quantitative real-time polymerase-chain-reaction (PCR) assay for changes in copy number at five loci within the region of minimal deletion (primer list available on request). Details about this assay, as well as information about the TaqMan quantitative PCR, DNA-methylation studies, sequence analysis, and fluorescence in situ hybridization (FISH), are given in the Supplementary Appendix.

RESULTS

CHROMOSOME 1Q21.1 REARRANGEMENTS IN AFFECTED PERSONS

We previously described one person with a deletion of 1q21.1 and another with an overlapping duplication in a series of 390 persons screened by array-based CGH involving a bacterial artificial chromosome microarray.^{2,8} These persons had global delay, growth retardation, and seizures (Patient 1) (Table 1) and mental retardation, growth retardation, and facial dysmorphism (Patient 2) (Table 3 in the Supplementary Appendix). In a collaborative study of 3788 patients from 12 centers in Europe and the United States using array-based CGH (Table 1A in the Supplementary Appendix), we identified an additional 22 probands with deletion and 8 probands with duplication. Targeted screening of another 1040 persons with unexplained mental retardation, by means of two TaqMan quantitative PCR assays within the commonly deleted region, resulted in detection of a deletion in two additional patients. Thus, from a total of 5218 persons with idiopathic mental retardation, autism, or congenital anomalies, we have a series of 25 unrelated probands with overlapping deletions of 1q21.1 (0.5%) (Fig. 1A) and 9 persons with the apparently reciprocal duplication (0.2%) (Fig. 1B). Five persons (four with a 1q21.1 deletion and one with a duplication) also carried one or more additional chromosome abnormalities that could have contributed to their phenotype and were therefore excluded from fur-

ther analysis (see Table 4 in the Supplementary Appendix for their phenotypic features).

The minimally deleted region spans approximately 1.35 Mb (on chromosome 1, 143.65 to 145 Mb [according to NCBI build 35], or 145 to 146.35 Mb [according to NCBI build 36]) and includes at least seven genes. The majority of persons studied have deletions with breakpoints (BP) in segmental-duplication blocks BP3 and BP4 (see Glossary and Fig. 1). Patient 12 has a larger, atypical deletion approximately 5.5 Mb in size that extends more proximally toward the centromere than the common deletion (on chromosome 1, 142.5 to 148.0 Mb [NCBI build 36]) (Fig. 1 in the Supplementary Appendix). Of the 21 probands without secondary karyotype abnormalities, the 1q21.1 deletion was *de novo* in 7 (3 with maternal origin, 1 with paternal origin, and 3 with undetermined parental origin), maternally inherited in 3, paternally inherited in 4, and of unknown inheritance (parents unavailable for study) in 7 (Table 1).

The phenotypes of persons with 1q21.1 deletions are described in Table 1 (21 patients without additional chromosomal abnormalities) and Table 4 in the Supplementary Appendix (4 patients with additional chromosomal abnormalities). Pedigrees of eight probands are shown in Figure 2. The majority of persons with a deletion have a history of mild-to-moderate developmental delay (16 of 21 [76.2%]) and dysmorphic features (17 of 21 [81.0%]), consistent with their ascertainment criteria. Three parents are also mildly affected; however, five probands had normal cognitive development, and four apparently unaffected parents have the same deletion. In addition, 14 of the 21 patients (66.7%) and 2 parents with the deletion have microcephaly or relative microcephaly. Other phenotypic features noted in more than one patient with the deletion include ligamentous laxity or joint hypermobility (five patients), congenital heart abnormality (six patients), hypotonia (five patients), seizures (three patients) and cataracts (three patients). There are no notable phenotypic differences among carriers of a deletion with different breakpoints. Consistent with variability of phenotypic outcome, we noted that the same region was recently described in an adult patient with schizophrenia²² (Table 4 in the Supplementary Appendix). We obtained DNA from this patient to map the breakpoints; our results show that the deletion in this patient with adult-onset schizophrenia is apparently identical to the common 1.35-Mb deletion found in

Table 1. Phenotypic Features of Probands with a Deletion in Chromosome 1q21.1.*

| Patient No. | Inheritance | Parental Origin | Cognitive Features | Growth Features | Facial Features | Skeletal Features | Features of Heart | Features of Eyes | Neurologic Features |
|-------------|-------------|-----------------|--|--|---|---|---|---|---|
| 1 | De novo | M | Severe global delay, autism, self-harming behavior, stereotypy | Height, 3rd percentile for age; weight, 3rd percentile for age; in childhood, 25th percentile for age from adolescence (truncal obesity); OFC normal | Prominent nasal bridge, prominent columella, grimacing smile | Marked ligamentous laxity | Normal | Hypermetropia, convergent squint | Seizures, hypotonia, sensorineural deafness |
| 2 | De novo | M | Mild DD | Height, 25th–50th percentile for age; weight, 50th percentile for age; OFC, <0.4th percentile for age | Epicanthic folds, full lower lip, wide-spaced teeth | Single palmar crease in left hand | Patent ductus arteriosus (diagnosed at 4 yr of age) | Subtle nuclear pulverulent cataracts (diagnosed at 4 yr of age) | No seizures |
| 3 | De novo | M | Normal cognition, mild speech delay | At birth: Normal height, weight, OFC At 7.5 yr: Height, 3rd percentile for age; weight, <3rd percentile for age; OFC, <3rd percentile for age | Prominent nose with long columella, flat philtrum | Normal | Normal | Strabismus in left eye | Normal |
| 4 | De novo | P | Moderate MR | Height, 50th percentile for age; weight, >97th percentile for age; OFC, 50th–75th percentile for age | Brachycephaly, large and deep nasal bridge, thin lips, prognathism, short neck | Brachydactyly, single palmar crease in left hand, small feet | Normal | Hypermetropia in right eye | Seizures since 8 mo of age, hypotonia, deep sulci in cortex on brain MRI |
| 5 | De novo | Unknown | Mild MR | Height, 50th percentile for age; weight, >97th percentile for age; OFC, 10th percentile for age | Brachycephaly, large and deep nasal bridge, synophrys, long philtrum, thin lips, high palate, wide-spaced teeth, short neck | Mild joint hypermobility, short distal phalanges on 2nd, 4th, and 5th fingers | Normal | Normal | Mild hypotonia, slow waves over the anterior and central areas of both hemispheres on EEG |

| | | | | | | | | | |
|----|--|---------|---|---|--|---|--|---|---|
| 6 | Inherited (mother with B1F; grandfather also carries deletion) | M | Mild MR (IQ 55) | Height, <3rd percentile for age; weight, <10th percentile for age; OFC, <3rd percentile for age | Brachycephaly, prominent ears, long columella, fine upper lip, pointed chin | Wide thumbs, duplicated left hallux | Normal | Normal | Normal |
| 7 | Inherited (mother normal) | M | Severe DD | At birth: Height and weight normal In childhood: Microcephaly | Fine features, triangular face; micrognathia, hypertelorism, low-set ears | Severe scoliosis, severe ligamentous laxity | Truncus arteriosus, multiple muscular VSDs of moderate size requiring early intervention | Microphthalmia, strabismus | Tonic-clonic seizures since 4 mo of age; absence seizures since 3 yr of age |
| 8 | Inherited (mother normal) | M | Mild global delay | Height, weight, and OFC all <0.4th percentile for age | Epicanthic folds, mild micrognathia, high palate, bifid uvula, turri-cephaly | Amputation deformity of left hand and foot; talipes of the right foot | Normal | Duane anomaly | Truncal hypotonia |
| 9 | Inherited (father with growth 2nd-9th percentile for age and no cataracts; affected sister carries same 1q21.1 deletion) | P | Normal | Growth measures, 9th percentile for age (sister's growth measures, 2nd-9th percentile for age) | Normal | Normal | Unknown | Bilateral congenital anterior sutural cataracts, dense congenital cataracts in sister | Unknown |
| 10 | Inherited (father mildly affected, with OFC <3rd percentile for age) | P | Mild MR (IQ, 65) | Height and OFC, <3rd percentile for age | Long columella, wide-spaced teeth | Broad thumbs, great toes, and fetal pads | Normal echocardiogram | Exophoria | Normal neurologic examination |
| 11 | Unknown | Unknown | Mild DD at 1 yr of age, resolved by 4 yr of age | OFC normal at 4 yr of age | Deep-set eyes, flat nasal bridge | Bilateral bifid great toes (required surgery) | Unknown | Unknown | Unknown |
| 12 | Unknown (son with speech delay) | Unknown | Mild MR (IQ, 59) | OFC, 80th-85th percentile for age | Round facies | Normal | Normal | Normal | Normal |

Table 1. (Continued.)

| Patient No. | Inheritance | Parental Origin | Cognitive Features | Growth Features | Facial Features | Skeletal Features | Features of Heart | Features of Eyes | Neurologic Features |
|-------------|--|-----------------|--|--|---|--|---|---|---|
| 13 | Unknown | Unknown | Severe MR (IQ, 33) | Height, weight, and OFC all <3rd percentile for age | Micrognathia, full nose, fine lips, simple ears | Bilateral clinodactyly of 5th finger | Normal | Strabismus | Fine tremor, heel stomping, stereotypic behaviors |
| 14 | Unknown | Unknown | Developmental delay; ADHD | Failure to thrive, microcephaly | Prominent occiput, high palate, micrognathia | Unknown | Unknown | Unknown | Unknown |
| 15 | Inherited (father and brother with deletion both have OFC <3rd percentile for age, mild learning disability, and similar facies) | P | Mild MR; schoolwork 2 yr behind that for chronological age | At birth: Weight, 10th–25th percentile for age At 8 yr: Height and weight, 0.4th percentile for age; OFC, <3rd percentile for age | Prominent metopic suture, up-slanting palpebral fissures, thin upper lip, full lower lip | Normal | Normal echocardiogram | Normal | Normal brain CT |
| 16† | Unknown | Unknown | BIF | Height, 75th–90th percentile for age, weight, 97th percentile for age | Up-slanting palpebral fissures, malar hypoplasia, arched palate, orthodontic correction | Joint laxity, pes planus | Bicuspid aortic valve, dilation of ascending aorta, aortic insufficiency | Cataracta complicata | Behavioral abnormalities |
| 17 | De novo | Unknown | Mild MR (IQ, 63) and ADHD | Height and OFC, <3rd percentile for age; weight, 50th percentile for age | Frontal balding, arched eyebrows, deeply set eyes, thin upper lip | Fingers with mild camptodactyly, mild interdigital webbing | Aortic coarctation diagnosed at 1 wk of age, surgically repaired at 8 yr of age | Strabismus (surgical intervention at 2 yr of age) | Normal |
| 18 | Inherited (father normal) | P | Normal at 9 mo of age | Height, weight, and OFC all <3rd percentile for age | Hypotelorism, short palpebral fissures, low nasal bridge | Mesaxial polydactyly of right foot | Normal | Normal | Normal |
| 19 | De novo | Unknown | Moderate MR, aggressive behavior | Height, 3rd–10th percentile for age; weight, 10th–25th percentile for age; OFC, 3rd–10th percentile for age | High, prominent forehead, long eyelashes, low nasal bridge, anteverted nares, small teeth | Overlapping toes | Patent ductus arteriosus | Normal | Unknown |

| | | | | | | | | | | |
|----|---------|---------|-----------------------|---|--------|--|--|---------|---------|------------------------------|
| 20 | Unknown | Unknown | DD, autistic features | Height, 25th–50th percentile for age; weight, 10th–25th percentile for age; OFC, 3rd percentile for age | Normal | Bilateral mild clinodactyly of 5th finger, palmar and plantar erythema, single palmar crease in right hand, joint hypermobility, mild pectus excavatum | Normal | Normal | Normal | Normal |
| 21 | Unknown | Unknown | Normal at 1 mo of age | At birth: Height, 25th percentile for age; weight and OFC, 50th percentile for age | Normal | Normal | Transposition of the great vessels, 6 mm ASD, 2 mm perimembranous VSD, surgically repaired | Unknown | Unknown | Normal brain ultrasonography |

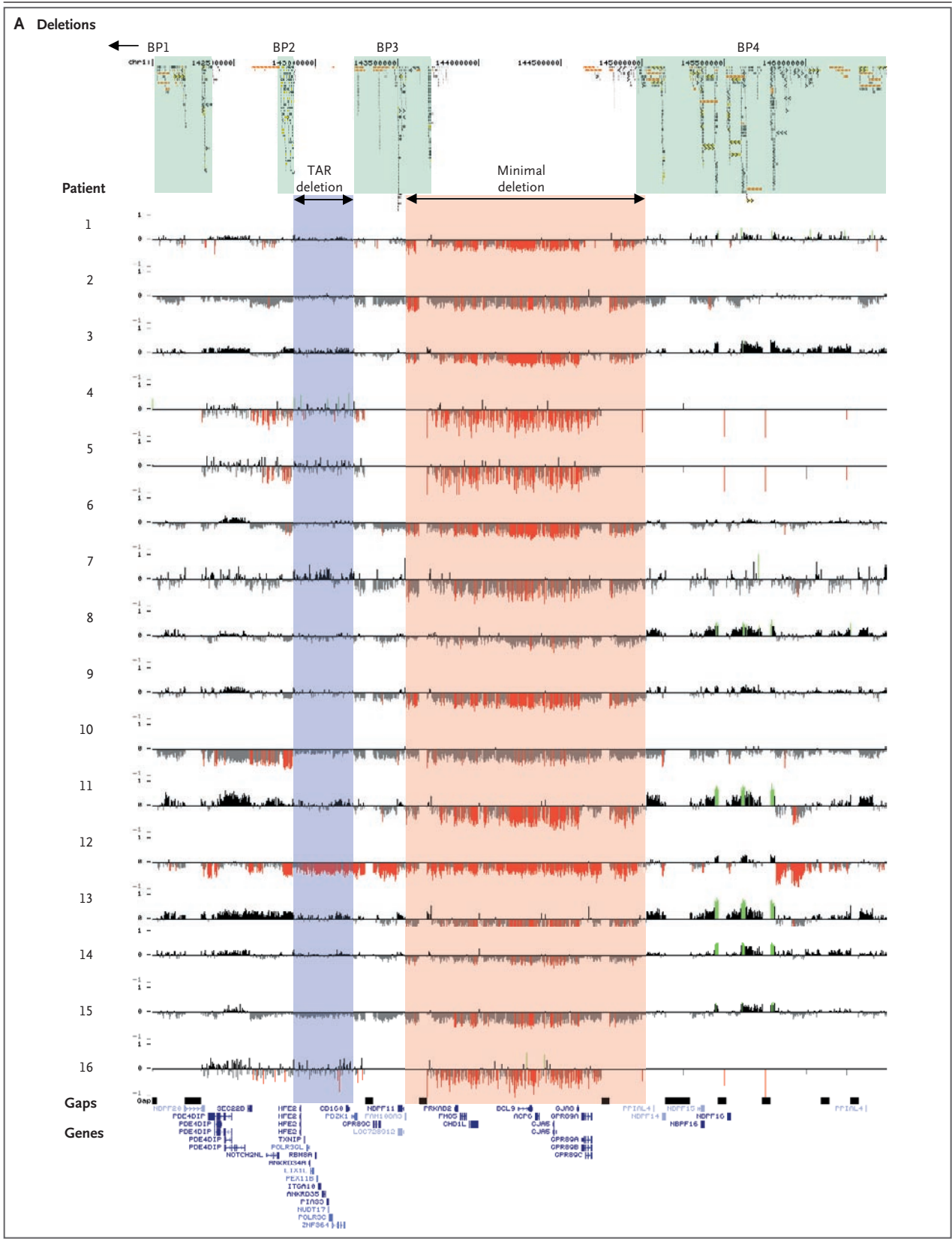
* ADHD denotes attention deficit–hyperactivity disorder, ASD autism spectrum disorder, BIF borderline intellectual function, CT computed tomography, DD developmental delay, EEG electroencephalography, M maternal, MR mental retardation, MRI magnetic resonance imaging, OFC occipitofrontal circumference, P paternal, and VSD ventricular septal defect.
 † Because of Patient 16’s marfanoid features, complete sequencing of the fibrillin 1 gene *FBN1* was performed; no mutations were detected.

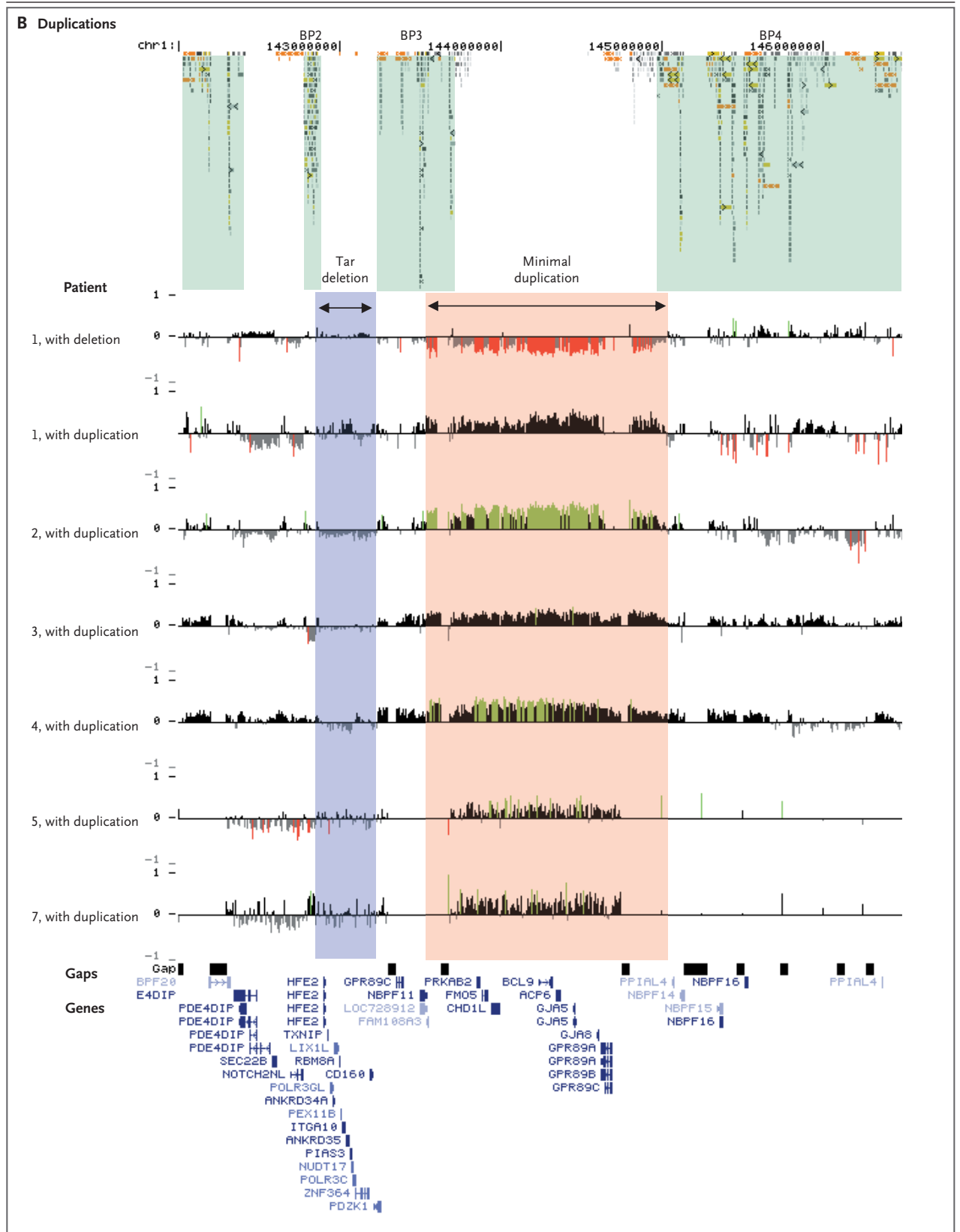
Figure 1 (following pages). High-Density Oligonucleotide-Array Mapping of Chromosome 1q21.1 Rearrangements in the Study Patients.
 Sixteen 1q21.1 deletions (Panel A) and seven 1q21.1 duplications (Panel B) from patients without other chromosomal abnormalities were identified on chromosome 1q21.1. The region of minimal rearrangement is located from approximately 143,650,000 to 145,000,000 bp (pink shading) and contains two assembly gaps and eight genes in the National Center for Biotechnology Information Reference Sequence (RefSeq) collection. In Panel B, a patient with a microdeletion (Patient 1) is shown for comparison with the duplication carriers (Patients 1 through 7 shown). Segmental-duplication blocks are shown, with the approximate breakpoint (BP) regions indicated with green shading. The microdeletion associated with the thrombocytopenia-absent radius (TAR) syndrome¹⁷ is shaded in blue. For each patient, deviations from 0 of probe log₂ ratios are depicted by vertical bars, with those exceeding a threshold of 1.5 SD from the mean probe ratio shown in green or red to represent relative gains or losses, respectively; bars below this threshold are black (gains) or gray (losses). Segmental duplications of increasing similarity are also shown, as horizontal bars highlighted with green shading: 90 to 98% (gray bars), >98 to 99% (yellow bars), and >99% (orange bars). Results for Patients 17 through 20 with deletions and Patient 8 with a duplication are shown in Figure 3 in the Supplementary Appendix. Patient 21 with a deletion and Patient 6 with a duplication were evaluated only by means of the screening platform listed in Table 1A in the Supplementary Appendix, because of insufficient DNA for additional oligonucleotide-array analysis (data not shown).

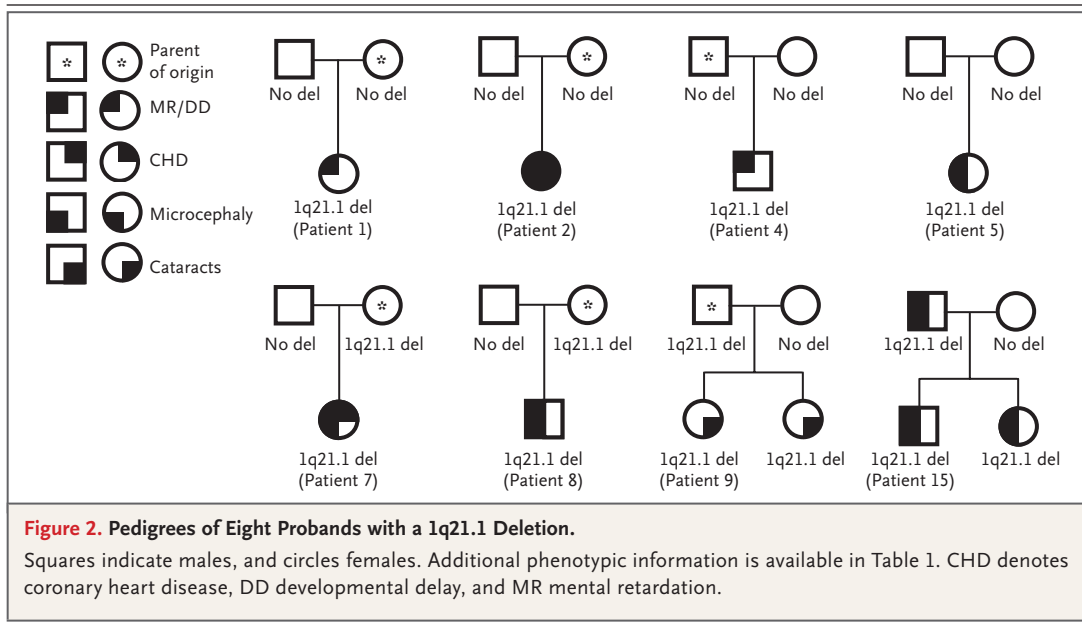
our sample of patients with primarily childhood-onset phenotypes (Fig. 3).

We also detected the reciprocal 1q21.1 duplication in nine persons (Fig. 1B), one of whom carried an additional large chromosomal abnormality and was thus excluded from further analysis (Table 4 in the Supplementary Appendix). Of the remaining eight patients with duplication, two had inheritance from an unaffected father, two had de novo duplication (parent of origin not known), and four did not have parental DNA available for analysis. Four of the eight patients with duplication (50.0%) had autism or autistic behaviors (Table 3 in the Supplementary Appendix). Other common phenotypic features of the eight duplication carriers include mild-to-moderate mental retardation (in five [62.5%]), macrocephaly or relative macrocephaly (in four [50.0%]), and mild dysmorphic features (in five [62.5%]).

In an independent sample of 788 patients with mental retardation and congenital anomalies from







the Netherlands, we identified deletion in 3 patients (0.4%) and duplication in another 3 patients (0.4%). The phenotypic features and inheritance patterns of these patients are listed in Table 1B in the Supplementary Appendix.

DELETIONS AND DUPLICATIONS IN UNAFFECTED PERSONS

To assess the frequency of 1q21.1 rearrangements in the general population, we evaluated data on copy number from three control populations: 2063 persons evaluated by means of single-nucleotide polymorphism (SNP)-genotyping bead arrays²¹ (Itsara A: personal communication), 300 persons evaluated by means of quantitative PCR performed on specimens from five different locations within the minimal-deletion region, and 2374 persons from previously published studies for which the copy-number variation of the 1q21.1 region was genotyped (Table 2 in the Supplementary Appendix).^{18,20,23-29} In this series of 4737 controls, we found no deletions of the 1q21.1 minimal-deletion region. Two controls each had one small duplication (117 kb and 184 kb) at the distal end of the minimal-deletion region, and only one control had confirmed duplication of the entire minimal 1q21.1 rearrangement region²⁹ (Feuk I: personal communication). Thus, the frequency of the 1.35-Mb deletion is clearly enriched in affected persons as compared with controls (25 of 5218 patients vs. 0 of 4737 controls,

$P=1.1\times 10^{-7}$ by Fisher's exact test). Although detected at a lower frequency in our series, the reciprocal duplication also appears to be enriched in affected persons (9 of 5218 patients, vs. 1 of 4737 controls; $P=0.02$ by Fisher's exact test).

GENOMIC STRUCTURE OF THE 1Q21.1 REGION

The genomic structure of the 1q21.1 breakpoint regions is extremely complex, with at least four large segmental-duplication blocks ranging in size from 270 kb to 2.2 Mb (Fig. 1, and Fig. 1 in the Supplementary Appendix), most of which exhibit copy-number polymorphism in the general population^{25,27} (see also the Database of Genomic Variants, <http://projects.tcag.ca/variation/>). A large inversion polymorphism that spans the recurrent deletion-duplication region, a feature associated with many other recurrent genomic disorders, has also been described.^{27,30} The complexity of 1q21.1 is underscored by the fact that there are still 15 assembly gaps, representing approximately 700 kb of missing sequence, in the most recent NCBI genome build (build 36). Of the 5.4 Mb of sequence within 1q21.1, only 25% represents unique (i.e., nonduplicated) sequence.

Although the complexity of the region complicates mapping efforts, our high-density array-based CGH results show that the proximal and distal breakpoints of the deletion-duplication events map within large segmental-duplication blocks. Our analysis reveals four possible break-

point regions, BP1 and BP4 (Fig. 1, and Fig. 1 in the Supplementary Appendix), as well as BP2 and BP3, which correspond to the previously described breakpoints associated with the thrombocytopenia-absent radius syndrome.¹⁷ Breakpoints of the most common 1.35-Mb deletion map to BP3 and BP4, which share 281 kb of sequence with more than 99.9% identity (Table 5 in the Supplementary Appendix). The structure of the 1q21.1 region (with multiple large blocks of highly homologous segmental duplication), the frequency of recurrent deletions or duplications, and the additional observation of reciprocal deletion and duplication events strongly suggest nonallelic homologous recombination as the mechanism that generates the deletion and duplication.

The presence of numerous assembly gaps in the 1q21.1 region hinders precise mapping of the chromosomal breakpoints that flank each duplication or deletion. Moreover, these gaps may contain genes that are absent from the current reference sequence and could potentially contribute to phenotypic differences between deletion carriers. One example is a partially duplicated copy of the hydrocephalus-inducing homologue (mouse) 2 gene *HYDIN2*, recently mapped to 1q21.1.³¹ We confirmed the presence of a *HYDIN* homologue within 1q21.1 by using FISH analysis involving two chromosome 16q22 fosmids containing the chromosome-16 *HYDIN* sequence (Fig. 2 in the Supplementary Appendix). Analysis of two deletion carriers (Patient 7 and her unaffected mother) revealed that the *HYDIN2* locus lies within the commonly deleted region and therefore may reside in one of the gaps between BP3 and BP4. Because probes designed to detect *HYDIN* also hybridize with *HYDIN2* sequence, data obtained through CGH studies, involving a whole-genome array, of persons with the 1q21.1 deletion suggest the existence of an approximately 35-kb deletion at 16q22 (Fig. 2 in the Supplementary Appendix) — that is, a false positive for the 16q22 deletion. FISH studies revealed only the 1q21.1 deletion and did not confirm the apparent 16q22 deletion.

ANALYSIS OF POTENTIAL MODIFIERS OF PHENOTYPE

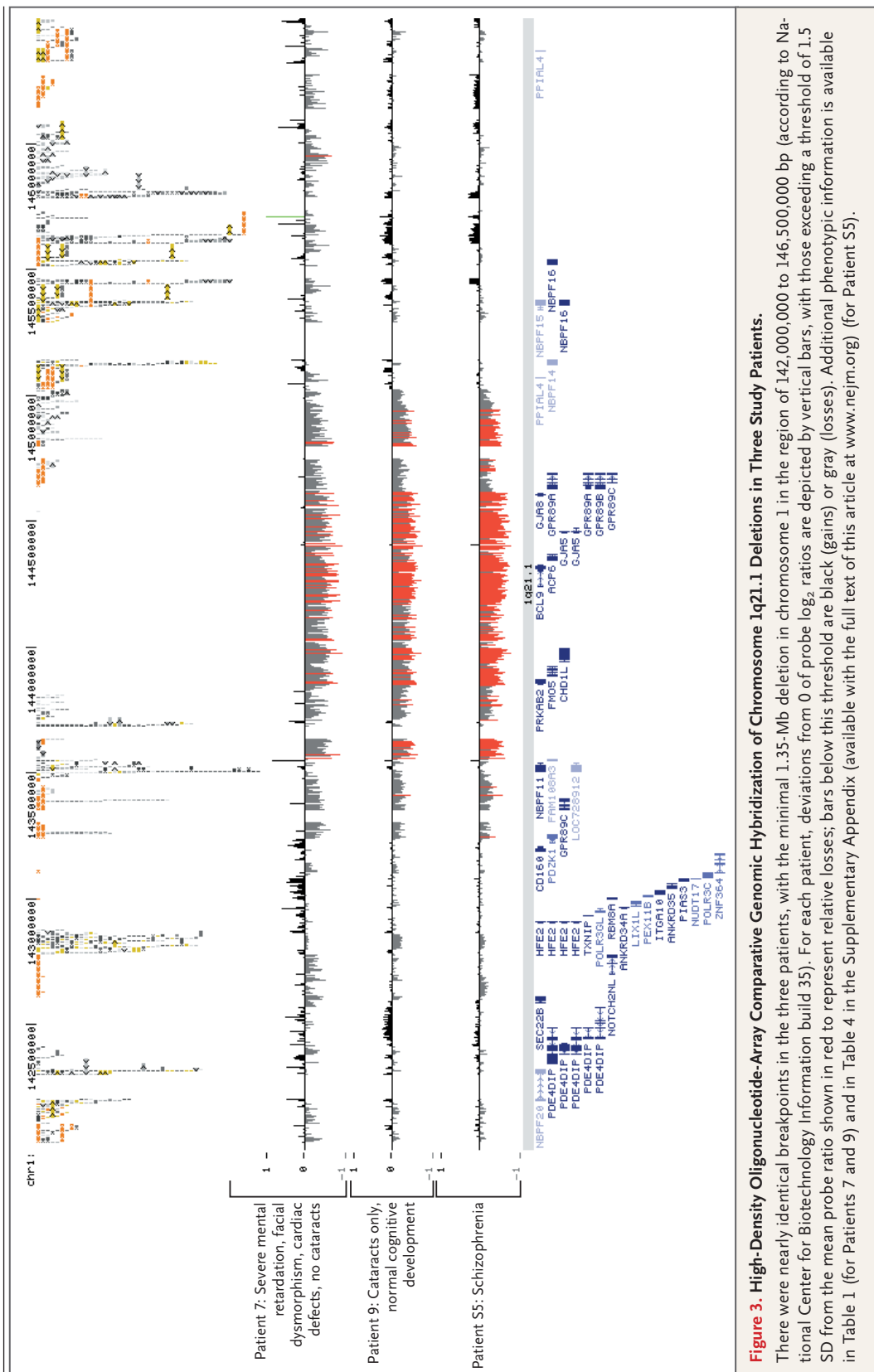
Given associations between *GJA5* (the gene encoding connexin 40) and cardiac phenotypes³²⁻³⁵ and between *GJA8* (the gene encoding connexin 50) and eye phenotypes,³⁶⁻³⁸ we hypothesized that coding variants on the remaining *GJA5* or *GJA8*

allele of deletion carriers may contribute to the cardiac or eye phenotypes, respectively, seen in some patients. However, we sequenced the coding and upstream regions of both genes in 11 deletion carriers and found no mutations (Table 6 in the Supplementary Appendix). We also investigated the possibility that epigenetic differences on the single remaining 1q21.1 allele might underlie the variable phenotype of those with 1q21.1 deletions. We analyzed the CpG (cytidine-phosphate-guanosine) methylation status within the deletion region in an affected 1q21.1 deletion carrier (Patient 7) and in her mother, who also carries the deletion but is unaffected. We found no significant differences between them (data not shown).

DISCUSSION

Our data show that 1q21.1 deletions are associated with a broad array of pediatric developmental abnormalities. There is considerable phenotypic diversity associated with haploinsufficiency of 1q21.1, consistent with previous reports of apparently identical 1q21.1 deletions in patients with different phenotypes, including isolated heart defects,³⁹ cataracts,²⁷ müllerian aplasia,⁴⁰ autism,⁴¹ and schizophrenia.^{13,14,22} We identified several unaffected deletion carriers; however, it is possible that apparently unaffected parents who have a 1q21.1 deletion could also have subtle phenotypic features consistent with the deletion that would become evident on further clinical evaluation. In one of our patients (Patient 2), for example, subtle cataracts and a patent ductus arteriosus were detected only after directed studies were performed after discovery of the 1q21 deletion (Table 1).

The reciprocal duplication was detected less frequently in our series, a finding that is consistent with recent studies showing that rates of deletion mediated by nonallelic homologous recombination are higher than that for duplications in the male germ line.⁴² Nonetheless, the duplication is also enriched in affected persons as compared with controls ($P=0.02$). Seven of the eight duplication carriers have learning or developmental delay or mental retardation. Four of the eight duplication carriers have autistic behaviors or autism, consistent with previously reported 1q21.1 duplications in patients with autism.⁴¹ Two patients were initially identified among 141 patients with autism, a finding that suggests even greater



enrichment in this population (vs. 1 of 4737 controls, $P=0.002$ by Fisher's exact test). Other phenotypes described in the majority of patients for whom data are available include macrocephaly or relative macrocephaly. However, because of the small number of patients with a duplication event in our series, identification of additional carriers will be required to determine whether these clinical manifestations are consistent with the presence of the duplication.

Several possibilities may account for the phenotypic variability we found among carriers of 1q21.1 rearrangements, including variation in genetic background, epigenetic phenomena such as imprinting, expression or regulatory variation among genes in the rearrangement region, and (in the case of deletions) the unmasking of recessive variants residing on the single remaining allele. It is known, for example, that coding variants on the nondeleted allele in carriers of the velocardiofacial syndrome deletion can modify the phenotypes of patients.^{43,44} Sequence analysis of *GJA5* and *GJA8* (the genes previously implicated in cardiac and eye phenotypes, respectively) in 11 deletion carriers yielded no data to support the unmasking of recessive variants as a cause of phenotypic variability. Likewise, preliminary data from methylation analyses of an affected deletion carrier and her mother, who also carried the deletion but was unaffected, suggest that differences in the methylation status of the nondeleted 1q21.1 locus does not contribute to the variability in phenotype. Finally, parent-of-origin studies reveal both maternal and paternal transmission of the deletion, making it unlikely that imprinting plays a role in phenotypic variability.

Our results emphasize the importance of rare structural variants in human disease; they also demonstrate some of the challenges. First, large samples of patients and controls are required to show that a specific variant is pathogenic. Although there have been several reports of patients with 1q21.1 deletions in studies of specific diseases,^{22,39-41} our study shows that recurrent 1q21.1 microdeletions are significantly associated with pediatric disease, through systematic comparison of the frequency of rearrangements in affected and unaffected persons. Second, detailed clinical evaluations of affected persons disclosed a much broader spectrum of phenotypes than anticipated, dispelling any notion of syndromic disease. While this article was being reviewed before pub-

lication, two groups reported enrichment of 1q21.1 deletions in persons with schizophrenia^{13,14}; they report deletions in 0.26% of patients with schizophrenia, as compared with our finding of deletions in 0.5% of persons with developmental abnormalities. These results confirm the association of 1q21.1 rearrangements with a broad spectrum of phenotypes but also further dispel the notion that rare copy-number variants will necessarily follow the one gene (or one rearrangement)-one disease model.

The phenotypic diversity, incomplete penetrance, and lack of distinct syndromic features associated with 1q21 rearrangements will complicate genetic diagnosis and counseling. For clinicians caring for patients with developmental abnormalities, the identification of a 1q21 rearrangement by means of diagnostic array-based CGH should be considered a clinically significant finding and probably an influential genetic factor contributing to the phenotype. Evaluation of family members may reveal apparently unaffected (or mildly affected) persons carrying the same rearrangement. Given the spectrum of possible outcomes associated with 1q21 rearrangements, such persons should be monitored in the long term for learning disabilities, autism, or schizophrenia or other neuropsychiatric disorders. Counseling in the prenatal setting will present the greatest challenge: although the likelihood of an abnormal outcome is high in a person with a 1q21.1 rearrangement, current knowledge does not allow us to predict which abnormalities will occur in any given person. Further investigation of genetic and environmental modifiers may explain such variable expressivity but requires characterization of an even larger number of patients with a 1q21 deletion. Data on rare, de novo structural variants are collectively beginning to explain an increasingly greater fraction (approximately 15%) of patients with developmental delay, autism, schizophrenia, or other neuropsychiatric disorders, and our study adds 1q21.1 as a locus to include in screening panels for such patients.

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APPENDIX

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