

Rare Inherited and De Novo CNVs Reveal Complex Contributions to ASD Risk in Multiplex Families

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Rare mutations, including copy-number variants (CNVs), contribute significantly to autism spectrum disorder (ASD) risk. Although their importance has been established in families with only one affected child (simplex families), the contribution of both de novo and inherited CNVs to ASD in families with multiple affected individuals (multiplex families) is less well understood. We analyzed 1,532 families from the Autism Genetic Resource Exchange (AGRE) to assess the impact of de novo and rare CNVs on ASD risk in multiplex families. We observed a higher burden of large, rare CNVs, including inherited events, in individuals with ASD than in their unaffected siblings (odds ratio [OR] = 1.7), but the rate of de novo events was significantly lower than in simplex families. In previously characterized ASD risk loci, we identified 49 CNVs, comprising 24 inherited events, 19 de novo events, and 6 events of unknown inheritance, a significant enrichment in affected versus control individuals (OR = 3.3). In 21 of the 30 families (71%) in whom at least one affected sibling harbored an established ASD major risk CNV, including five families harboring inherited CNVs, the CNV was not shared by all affected siblings, indicating that other risk factors are contributing. We also identified a rare risk locus for ASD and language delay at chromosomal region 2q24 (implicating *NR4A2*) and another lower-penetrance locus involving inherited deletions and duplications of *WWOX*. The genetic architecture in multiplex families differs from that in simplex families and is complex, warranting more complete genetic characterization of larger multiplex ASD cohorts.

Introduction

Genetic variation accounts for a major proportion of the liability to autism spectrum disorder (ASD). Twin studies have estimated the heritability of ASD to be at least 50%, given that concordance of ASD in monozygotic twins ranges from 37% to 95% depending on the study design and the diagnostic criteria used.^{1–4} The importance of genetics in ASD susceptibility is also reflected by the recent success of microarray and whole-exome sequencing studies, which have established the role of de novo copy-number variants (CNVs) and de novo protein-disrupting single-nucleotide variants (SNVs) in ASD pathogenesis. Similar contributions have been identified in individuals with intellectual disability (ID) without ASD.^{5–15} Approximately 3.7% of affected individuals carry a large (>500 kb) de novo CNV, whereas only 0.4%–0.8% of their unaffected siblings do,^{9–11,13,16} implying that the rate of large de novo CNVs is approximately five times higher in individuals with ASD.

Despite their rarity in ASD, several recurrent large CNVs have been identified and include loci at 1q21.1 (MIM: 612475 and 612474), 3q29 (MIM: 609425), 7q11.23 (MIM: 609757), 15q11–13 (MIM: 608636), 15q13.3

(MIM: 612001 and 608636), 16p11.2 (MIM: 611913 and 614671), and 22q11.2 (MIM: 608363),^{11,13,17} as well as several other very rare CNVs, including the 5q35 deletion (Sotos syndrome [MIM: 117550]) and the 17q12 deletion (MIM: 614527). Although the overall signal for statistical enrichment comes from rare, de novo CNVs in ASD, some known recurrent CNVs can be inherited, as seen with 15q11–13 duplications or 1q21.1 CNVs.^{18,19} Some studies have suggested an excess of maternally inherited pathogenic CNVs,^{15,20} but an excess of maternal transmission appears to vary by locus rather than being generalizable.^{9,13,16,20}

Some studies have included individuals from families with multiple affected children (multiplex families) in a case-control design^{9,12,21–23} but have not focused specifically on analyzing the role of CNVs in these families. In fact, most major studies have focused primarily on simplex families who have been carefully selected for the absence of observable relevant clinical phenotypes in first-degree relatives—a select cohort that is likely to have less inherited genetic variation than the general ASD population and especially multiplex families. Generalization from studies in simplex or mixed family types provides most of what we know about specific genetic contributions to ASD.^{10,11,24} Moreover, heritable variation

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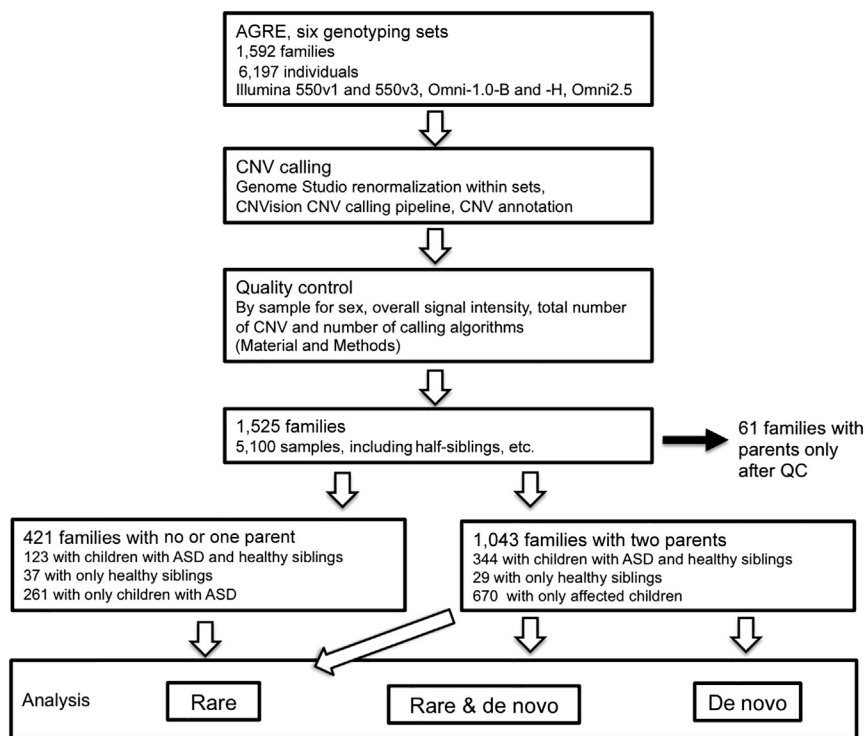


Figure 1. Overview of the Analysis Pipeline

We started by renormalizing intensities according to manufacturer recommendations and continued with the CNVision pipeline, followed by quality control (QC) with strict recommended criteria. After QC, we proceeded to annotate CNVs by type and annotate samples by family structure and analyzed the samples in multiplex (at least two affected children) and combined (all samples and family types) analyses for rare (<1% frequency in the DGV) and de novo CNVs. Families in whom the child or children failed QC were excluded from the analyses. Analyses were performed by CNV size (≥ 500 kb, 100–500 kb, and combined) in the mentioned CNV categories. Inheritance patterns for CNVs could be determined only in families with both parents, and only these families were included in the de novo analyses.

conservative pipeline or a different focus in earlier studies³⁴ (Table S1). Of the available families, 1,189 (78%) are multiplex, and 343 (22%) are simplex. No restrictions

is estimated to provide a significant contribution to ASD risk,^{4,25} but studies of simplex families most likely underestimate this component. Multiplex families are estimated to constitute about 11% of ASD-affected families and are hypothesized to have a different genetic architecture.^{12,26–30} One prominent model posits that they are enriched with inherited, potentially dominant variation and therefore exhibit a smaller contribution from de novo events than do simplex families.³⁰ Stoppage, the decision to stop having more children after a diagnosis in one, is also an issue in ASD-affected families.³¹ In some cases, multiplex families are more likely to include children with milder ASD symptoms, therefore reducing the likelihood of stoppage. This provides an additional hypothesis that multiplex families are enriched with inherited variants of lower impact.

Despite the predicted differences in the genetic architecture of ASD between simplex and multiplex families, few large studies of CNVs have been conducted in large multiplex cohorts.^{12,32,33} We undertook such a study by using the Autism Genetic Resource Exchange (AGRE), the largest cohort of predominantly multiplex ASD-affected families who have been genotyped on microarray platforms that permit genome-wide CNV detection, allowing us to focus on the genetic architecture in multiplex families in a well-powered cohort.

Material and Methods

Samples

We analyzed an AGRE sample set consisting of 1,532 families, a subset of whom had been previously analyzed with a different, less

regarding family structure were imposed during sample collection, which included both extended families and half-siblings in addition to nuclear families. The number of individuals with available biomaterials was at minimum one individual per family, which led to a collection of mixed family structures (Figure 1 and Table S1). Pedigrees of families affected by ASD-associated CNVs were drawn with the Madeline 2.0 Pedigree Drawing Engine.³⁵

Sample diagnostic criteria are provided on the Internet System of Accessing Autistic Children website (see Web Resources). In summary, the Autism Diagnostic Observation Schedule and Autism Diagnostic Interview-Revised were used for assigning individuals into three categories: (1) a strict autism diagnosis, (2) not quite autism, (3) or broad spectrum. In this study, all individuals in any of these categories were considered affected, in accordance with standard AGRE practice.³⁶ The term “broad spectrum” includes phenotypes that fit former Asperger syndrome and pervasive developmental disorder – not otherwise specified, which are currently considered a part of the ASD spectrum. A more detailed description is available online at the AGRE website (see Web Resources) and in previous publications.³⁶ This study was approved by institutional review boards at the AGRE, University of Washington, and University of California, Los Angeles (UCLA). Written informed consent was obtained from all adult participants, and assent with agreement from their parents was obtained from all underage participants.

Microarrays

Individuals were genotyped on six different platforms according to manufacturer protocols over multiple years. We initially included 4,013 samples from the AGRE Illumina Human 550v1 and 550v3 genotyping set from Wang et al.³⁷ but were only able to retain 2,974 samples after quality control (see below and Table S1). The remainder of the samples ($n = 2,284$) were genotyped at the UCLA Neuroscience Genomics Core on three different versions of Illumina HumanHap Omni1 arrays ($n = 1,265$) or the

Illumina HumanHap Omni2.5 array ($n = 1,019$) (Figure 1 and Table S1). DNA for microarrays was extracted from lymphoblastoid cell lines (LCLs) at the Rutgers Repository according to standard protocols. All individual arrays were recalled and calibrated by batch, and sex chromosomes were recalled on GenomeStudio according to manufacturer protocols.

CNV Calling and Annotation

CNVs were called with CNVision¹¹ (a pipeline that uses two “gold-standard” CNV-calling algorithms for microarray data), PennCNV,³⁸ QuantiSNP,³⁹ and GNOSIS, an algorithm based on CNVision integrated outlier detection. All CNVs on each microarray batch were annotated to their respective genome versions with the Bamotate annotation tool¹¹ for overlapping genes, regions with recurrent syndrome-causing CNVs, and select genomic features (such as telomeres, centromeres, and human leukocyte antigen). After annotation to their respective genome versions, all CNVs were lifted from hg18 to hg19 (UCSC Genome Browser) with the UCSC LiftOver tool.

CNV Quality Control

Sample-based quality-metric thresholds were based on the standard recommendations from the developers of PennCNV and QuantiSNP.^{38,39} In addition to controlling for basic noise, we excluded all 88 samples whose sex chromosome log R ratios (LRRs) fell over 3 SDs from the mean of the dataset or whose number of CNVs was more or less than 3 SDs from the mean of the respective genotyping set to remove samples with potentially wide-ranging LCL artifacts or poor-quality genotypes. No unexpected sex chromosome syndromes were identified.

Previous studies have shown that CNV calls from microarrays are sensitive to the algorithms used and the size of the CNV. Using overlapping calls from several algorithms increases the reliability of CNV detection.^{40,41} CNVs were included initially if they were >50 kb, identified by at least two of the three algorithms, and spanned a minimum number of probes (10 for Illumina 550K arrays and 15 for Illumina HumanHap Omni1 and Omni2.5 arrays). CNVs that overlapped repetitive or rearranged regions and potential LCL artifacts (such as antibody-coding fragments, T cell receptors, telomeres, centromeres, array or genome gap regions, or segmental duplications encompassing >50% of their length) were excluded.

We used two additional validation steps for the CNV calls: visual inspection from microarray intensity data and qPCR validation for all de novo CNVs. We found that although it was conservative and time consuming, visual inspection of intensity data was still an important step in estimating the reliability of CNV calls. We plotted the LRR and B allele frequency by using custom scripts for all available family members of the CNV carrier. False-negative CNVs were added to the data with the same size and location to match the true-positive calls of family members. We excluded ambiguous calls with no clear CNV signal, most of which were located in pericentromeric regions, telomeres, common CNV regions, or regions close to array and genome gap regions, which often represent non-unique regions of the genome. Our visual-inspection step resulted in the inclusion of 53% of all CNV calls, and we found a false-negative rate of 2% with the automatic calling algorithms. For each AGRE genotyping set, 65%–89% of samples remained after quality control (Figure 1 and Table S1). This is comparable to other studies that used similar array types. Our CNV calls were consistent with published data from an earlier analysis

in a subset of the AGRE cohorts;^{12,34} one exception was a CNV previously called in a telomeric region because it was too noisy to call in our data. Five individuals included in this previous analysis were excluded from our analysis on the basis of general quality metrics. All CNV calls are available in the National Database for Autism Research (see Accession Numbers).

qPCR Validation

All CNVs that were predicted to be de novo events by CNVision and large recurrent events with uncertain inheritance were validated by qPCR. In addition, a randomly chosen set of inherited events of smaller sizes was included for qPCR validation. All primers were designed with Primer3 default settings. Samples were run in quadruplicate with 1 ng/ μ L DNA for the CNV and RNaseP reference. Each primer was also run in 0.5 and 1 ng/ μ L of reference DNA mix from ten unaffected individuals, and primers for duplications were also run in 2 ng/ μ L of reference DNA mix. The accuracy of visual inspection is clear given that all visually confirmed de novo CNVs passed qPCR testing (15/15) (Table S2); however, only 13/42 (31%) of 50–100 kb de novo CNVs and 34/189 (18%) of <50 kb de novo CNVs that were not confirmed by visual inspection were experimentally confirmed, consistent with previous experience.¹¹

In Situ Hybridization

In situ hybridization was performed with radioactive probes for *NR4A2* (MIM: 601828; GenBank: BC009288, base pairs 4–2,175]) as previously described.^{42–44} Regional annotation of expression was performed with the *Atlas of Human Central Nervous System Development*.⁴⁵

Statistical Analyses

All statistical analyses were performed with R (3.0.2). We used a non-linear mixed model and general regression model with affection status as the response variable. The linear mixed model was also used for testing the association between the de novo CNVs and the Raven's nonverbal IQ score, the Social Responsiveness Scale population-normalized Z score,⁴⁶ the Vineland Adaptive Behavior Scales, the Stanford-Binet Intelligence Scales, and the Peabody Picture Vocabulary Test. For tests of de novo burden, we included all children from all families in whom two parents had array data. For tests of overall burden, we selected one random affected and one random unaffected sample from each family to control for relatedness. Gene- and locus-based analyses were family based, and only one CNV per affected and unaffected sibling was taken into account for each family.

We used the non-parametric Kruskal-Wallis test⁴⁷ to estimate differences in all tested CNV categories between different arrays for possible detection bias (Table S2 and Figure S1) and discovered a significant effect. Therefore, we included the genotyping set and the first three components of multidimensional-scaling analysis as covariates to account for array effects and population stratification, respectively. For IQ analyses, we also included sex as a covariate. Regression models were fit with the R package lme4, which includes a function to fit general regression models.⁴⁸

Power analyses were conducted with the DSS Researcher's Toolkit's online two-sample estimation tool for percentage values. We used our current sample size, de novo rates from an analysis of the Simons Simplex Collection (SSC),¹³ and a 5% alpha rate in our estimations.

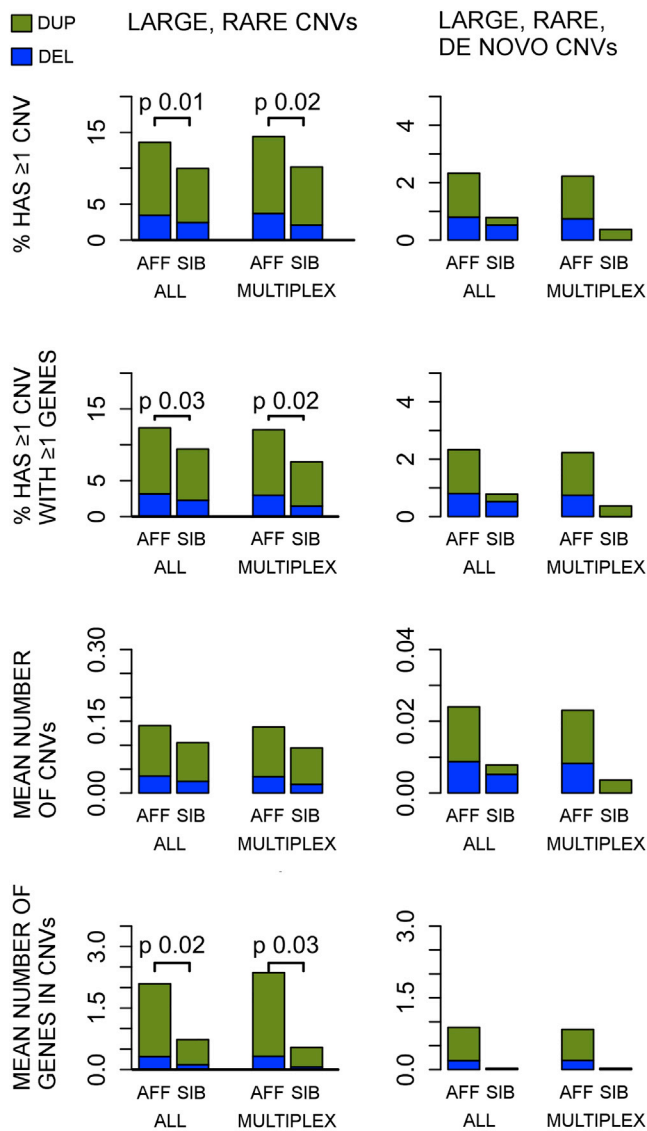


Figure 2. Summary of CNV Association Results in the AGRE

Summary of results for all samples combined (simplex and multiplex) and multiplex families only. Detailed sample sizes and summaries by array are available in Table S2. CNVs over 500 kb were considered large, and CNVs with a population frequency below 1% in the DGV were considered rare. CNVs found in a child but not in the parents were considered de novo. Analyses for large, rare CNVs contained inherited or de novo CNVs, whereas de novo analyses contained only de novo CNVs. Only p values smaller than 0.05 are shown in the figure. The fraction of deletions is shown in blue, and the fraction of duplications is shown in green. Abbreviations are as follows: Aff, affected sibling; and Sib, unaffected sibling.

Samples from the Database of Genomic Variants

The Database of Genomic Variants (DGV) is a public repository of structural chromosomal variation, and its datasets are not necessarily uniformly curated or checked for overlap. We downloaded the DGV data and only included studies with genome-wide detection methods. All samples were inspected for overlap, and after careful pruning, we were left with 27,263 independent human samples.

Results

Using the CNVision pipeline,¹¹ we applied a CNV-calling approach that is based on integrating three algorithms: PennCNV,³⁸ QuantiSNP,³⁹ and GNOSIS¹¹ (Figure 1). This approach has been shown to increase reliability of CNV detection^{11,40,41} and also permits more direct comparisons with studies that use this same pipeline to analyze SSC families.^{11,13} Given the resolution of SNP microarrays and our aim of focusing on events more likely to be reliable and pathogenic in neurodevelopmental disorders, we targeted CNVs of ≥ 100 kb⁴⁹ and carefully controlled for biases introduced by array type or population structure. After quality control, our dataset consisted of 1,464 families with 1,764 affected and 572 unaffected children (Figure 1). We used all children from the 1,043 families with data from both parents for the de novo CNV analyses.

Large, Rare CNVs in the AGRE

We found 524 rare (population frequency below 1% in the DGV), large (≥ 500 kb) inherited or de novo CNVs at 214 non-overlapping loci in the non-repetitive unique regions of the genome. We tested all 15 de novo deletions and 10 of 22 duplications in this class by qPCR, and all were confirmed for a 100% validation rate (Table S3).

Overall, large, rare CNVs, either inherited or de novo, are more frequent in affected children than in their unaffected siblings (147/1,122 [13.1%] versus 36/402 [8.9%], odds ratio [OR] = 1.7, $p = 0.016$, logistic regression) (Figure 2 and Tables S4, S5, and S6), as previously observed.^{11,13,22,23} 28% of all large, rare CNVs that we observed in the AGRE are in previously ASD-associated loci (Figure 3A). Consistent with previous studies, we only observed maternal over-transmission of large, rare CNVs at the imprinted 15q11–13 locus, where 7 of 16 such events were maternal, six were de novo, one was paternal, and two were of unknown inheritance because biomaterials were unavailable from the parents.

Out of a total of 163 non-overlapping large, rare CNV loci identified in either affected or unaffected siblings, 143 were present in affected and 41 were observed in unaffected siblings. 20 of the 143 CNV loci in affected children (13.9%) were not previously associated with ASD and contained one or more additional overlapping CNVs in at least one other affected child, but not in any unaffected sibling in the AGRE. 13 of these 20 were not observed in unaffected siblings in either the SSC or AGRE cohorts and thus are potential candidate ASD risk loci (Table S7). In contrast, none of the loci found in unaffected siblings were restricted to them. Thus, we observed a significant enrichment of these large, rare CNVs as a class in affected siblings (13/143 [13.9%] versus 0/41 [0%], $p = 0.041$, Fisher's exact test).

Because the events are rare, present only in a few families, and have a $< 1\%$ frequency in the DGV, we combined these with published data from the SSC¹³ to assess their

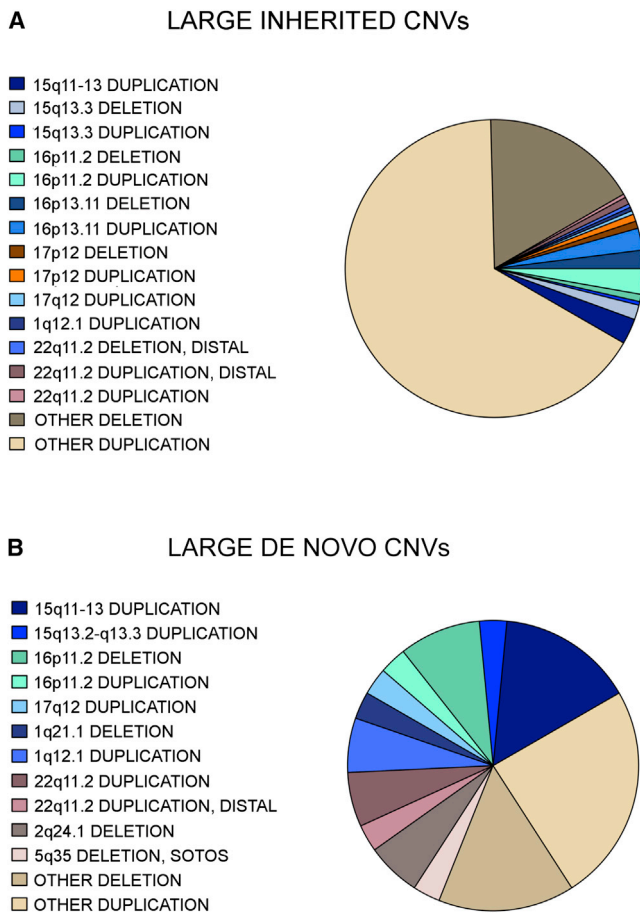


Figure 3. Distribution of Large, Rare CNVs

The majority of large, rare de novo CNVs in the AGRE are in loci considered to be associated with ASD (55%), and only a minority of the CNVs are loci of unknown pathogenicity (not presently associated with ASD). Inherited CNVs, however, are mostly of unknown pathogenicity, and only 28% are in known ASD-associated loci. Most ASD-associated CNV loci have been identified through the recurrence of de novo events, which would bias our findings toward de novo CNVs. Also, because these loci have large effect sizes on behavior and cognition, we would expect a larger percentage of the CNVs to be de novo at these loci as a result of potential effects on fecundity. Table 1 shows a breakdown of all known ASD-associated loci found in the AGRE, Table S3 shows all large, rare de novo CNVs, and Table S4 shows large, rare inherited CNVs.

potential association with ASD (Table S7). We found evidence for one locus: CNVs (deletions or duplications) overlapping *WWOX* (MIM: 605131) were found in affected children in 12 of 3,565 families (0.34%) but in only one unaffected sibling out of 2,633 families (0.04%, $p = 0.01$, OR = 8.8, Fisher's exact test) (Figure S2). Published affected individuals from the Autism Genome Project (AGP) did not carry any rare CNVs overlapping *WWOX*.²³ The overall frequency of >100 kb CNVs overlapping *WWOX* in the DGV is 26/27,263 (0.10%), which is significantly lower than in the ASD individuals. The combined association test for all datasets was nominally significant ($p = 0.0148$, OR = 2.6, 95% confidence interval [CI] = 1.1–5.4, Fisher's exact test). Recessive mutations in *WWOX* have been linked to infantile epileptic encephalopathy,

delayed development, and poor eye contact,⁵⁰ but a history of seizures was reported in only two of the AGRE individuals harboring a CNV that overlaps *WWOX* (Table S11). Nine of the other large, rare CNVs that were only observed in affected children in the AGRE were also found in affected children from the SSC (and not in unaffected siblings), but none of these loci individually reach statistical significance because of their low frequency. We list these in Table S7 and consider them potential candidate risk loci that require more evidence from future family cohorts. Several of these CNVs contain single genes, including *FAM19A*, *CDH18* (MIM: 603019), *CDH13* (MIM: 601364), *IGF1R* (MIM: 147370), and *ARSK* (MIM: 610011).

We next assessed the contribution of large, rare de novo CNVs to ASD risk in AGRE multiplex families. We found that siblings with ASD carry at least one large, rare, de novo CNV more frequently (27/1,217 [2.2%]) than their unaffected siblings (1/273 [0.4%]), although this must be considered a trend given that it does not reach our threshold for statistical significance (OR = 7.1, $p = 0.06$, logistic regression; Figure 2 and Tables S5 and S6). As expected, the enrichment in affected siblings was significantly lower in AGRE than in the SSC families (OR = 6.3; 3.8% in affected siblings versus 0.6% in unaffected SSC siblings),¹³ consistent with a significantly lower frequency of de novo events in multiplex ASD ($p = 0.01$, one-sided Fisher's exact test). We had the power to detect a similar difference for large, rare, de novo CNVs, as seen in the SSC (>95% power to observe 3.7% and 0.8% of ≥ 500 kb de novo CNVs in affected and unaffected individuals, respectively),^{11,13} and therefore this most likely represents a true difference between simplex and multiplex cohorts.

17 of 32 (53%) of all large, de novo events observed in affected children in the AGRE, but not in unaffected siblings, were in loci that have been previously associated with ASD^{11,13,17,51} (see Table 1, Figure 3B, Table S8, and below). CNVs in these previously identified ASD-associated loci were observed in affected children in 46 of 1,464 (3.1%) families (Table 1 and Table S8). The most frequent recurrent CNV loci in the AGRE were at 15q11–13 (1.1%), 16p13.11 (0.7%), 22q11.2 (0.5%), 16p11.2 (0.4%), and 1q21.1 (0.3%) (Table 1; see also Figure 4).

CNVs in ASD-Associated Genes and Candidate Genes

Recent exome sequencing studies in simplex families have identified several genes in which children with ASD carry disruptive de novo point mutations that are associated with the disorder.^{5,6,8,15,52,53} We scrutinized all CNVs in 71 regions and genes with ASD-associated or ASD candidate variants,¹³ such as *NRXN3* (MIM: 600568), down to 100 kb resolution. Because we were interested in gene-disrupting events, we included only CNVs spanning exons, promoter regions, and UTRs in our analyses (Table 2 and Table S8). We identified CNVs, most of which were inherited, in 20 genes that have been observed or suggested to carry most likely disruptive mutations in individuals

Table 1. Large, Rare, Recurrent ASD-Associated CNVs

Locus	Position (Mb) ^a	Frequency (n)	Affected	Siblings
1q21.1	146.5–147.8	0.34% (5)	one de novo deletion; three de novo and two maternal duplications	one paternal duplication
5q35	36.2–37.7	0.07% (1)	one de novo deletion	not observed
7q11.23	72.7–74.1	0.07% (1)	one paternal duplication	not observed
15q11–13	–	1.1% (16)	six de novo, seven maternal, one paternal, and two NA ² CNVs	
BP2-3 ^b	23.6–28.9	0.68% (10)	four de novo, four maternal, and two NA ² duplications	not observed
BP3-5 ^b	28.9–32.5	0.13% (2)	one maternal deletion and one de novo duplication	not observed
BP4-5 ^b	30.9–32.6	0.27% (4)	one de novo, two maternal, and one paternal deletion	not observed
16p13.11	14.9–16.3	0.66% (10)	two maternal and one paternal deletion; one maternal, three paternal, and two NA ² duplications	one paternal deletion one paternal duplication
16p11.2	29.6–30.2	0.35% (5)	three de novo deletions; one de novo and one maternal duplication	one maternal duplication
17q12	34.8–36.2	0.07% (1)	one de novo duplication	not observed
22q11.2	–	0.48% (7)	three de novo, one paternal, two maternal, and one NA ² CNVs	
Classic ^b	18.9–21.5	0.27% (4)	two de novo, one paternal, and one NA ² duplication	not observed
Distal ^b	23.0–25.0	0.20% (3)	one de novo and two maternal duplications	not observed
Total	–	3.1% (46)	19 de novo, 14 maternal, six paternal, and six NA ² CNVs	two maternal and two paternal CNVs

The table describes the total number (n) of families with known ASD-causing events and how often (frequency) these events occur in affected and unaffected children of these families. Out of a total 1,464 families, 1,398 have affected children, and 539 have unaffected siblings passing quality filters. Fisher's exact test gave $p = 0.02538$ for deletions and $p = 0.01130$ for duplications in affected versus unaffected siblings. The AGRE didn't contain any of the following known ASD-associated CNVs: 3q29 deletions, 17p11.2 deletions or duplications, 17q11.2 deletions, and 17q21.31 deletions. A significant proportion of the large, ASD-associated events that have a known mode of inheritance are de novo events (37%). This is interesting given that most of the AGRE families have two or more affected children, and the de novo events here are present only in one affected child. The following abbreviation is used: NA, no biomaterials were available from one or more parents.

^aPosition in the human reference sequence (UCSC Genome Browser hg19).

^bSub-loci within a larger ASD-associated CNV locus.

with ASD. The observed CNVs in affected children in the AGRE included events in *ANK2* (MIM: 106410), *CNTNAP2* (MIM: 604569), *CNTN4* (MIM: 607280), *RBFOX1* (MIM: 605104), *NRXN1* (MIM: 600565), *MACROD2* (MIM: 611567), and *AUTS2* (MIM: 607270) (Table 2 and Table S8).

We next assessed the frequency of all CNVs affecting these loci in both affected and unaffected siblings in the combined AGRE and SSC collections (Sanders et al.¹³) and found a higher number of CNVs in this set of ASD-associated genes in affected individuals than in their unaffected siblings (77 in ASD individuals in 3,565 families [2.2%] versus 18 in unaffected siblings in 2,633 families [0.07%], OR = 3.3, 95% CI = 1.9–5.7, $p = 9.4 \times 10^{-7}$) and a signal stronger in deletion carriers (38/3,565 [1.1%] in ASD versus 7/2,633 [0.2%] in unaffected siblings, OR = 4.0, 95% CI = 1.8–10.7, $p = 0.0001$) than in duplication carriers (Table S8). Most of the CNVs were small to medium sized (range = 57 kb to 4 Mb, median = 270 kb) and restricted to a single gene (Table S8). There was no bias for either maternal or paternal inheritance (21 maternal, 21 paternal, 6 de novo, and 5 with no parental information). Loci containing more than one gene included *ANK2* (which was contained within a duplication extending to *NEUROG1* [MIM: 601726]), deletions extending to neighboring genes in the *CYFIP1* (MIM: 606322) region in

several individuals, and a *KCNMA1* (MIM: 600150) duplication extending to *DLG5*. We detected three de novo, non-recurrent CNVs in ASD-associated genes: an exonic 480 kb duplication overlapping *CYFIP1* in an affected sibling, a previously identified deletion including the first exon of *RBFOX1* in another affected sibling,⁵⁵ and a 4 Mb duplication including *ANK2*, a gene harboring recurrent de novo SNV in the SSC, in an unaffected sibling.^{5,13,52}

De Novo Deletions at 2q24.1 Are Associated with ASD

Two affected individuals in the AGRE have overlapping large, rare de novo hemizygous deletions at 2q24.1 (Figure 5). CNVs greater than 100 kb are rare at the 2q24.1 locus, given that none have been reported in previous ASD studies or the DGV. We turned to DECIPHER⁵⁶ and the Clinical Genome Resource (ClinGen), which contain clinically discovered isolated cases, and searched for ≤ 5 Mb CNVs in 2q24.1; we identified five individuals with 2q24.1 CNVs (Table S9). All were deletions ranging from 170 kb to 4.7 Mb (Figure 5), and all overlapped the deletions in the two ASD individuals in the AGRE. Only two reporting sites had tested the parents for CNVs, and both reported a de novo deletion in the child (Table S9).

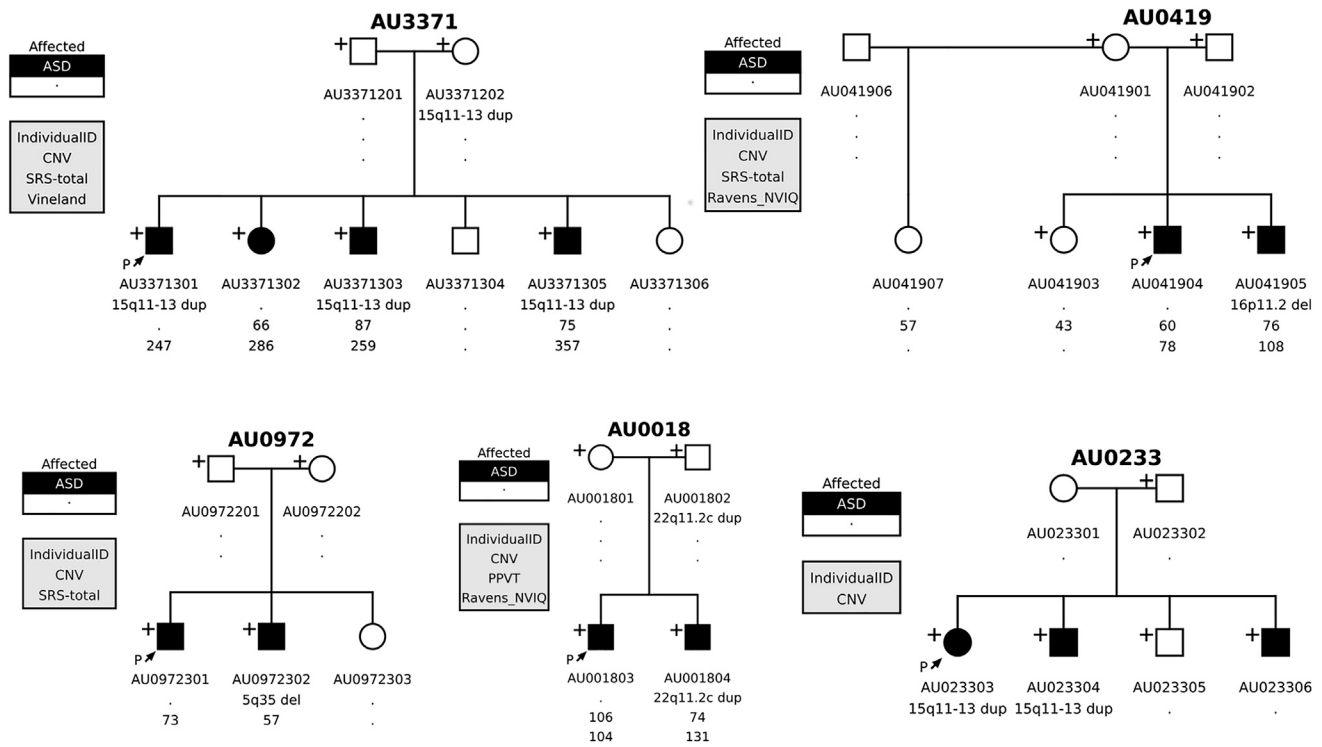


Figure 4. The Non-segregation of Established ASD Risk CNVs in Multiplex Families

We observed non-segregation of known pathogenic CNVs in multiplex families: all affected children in the same family did not necessarily share the CNV. Most of these ($n = 17/21$) were de novo CNVs and were present in only one affected child. The cause of ASD in the other affected child remains unknown. Thorough sequencing of all family members will be beneficial for determining the exact phenotypic effects of the pathogenic CNVs and assessing other possible genetic causes of ASD in these families. Plus signs indicate samples with available DNA for testing.

Both DECIPHER⁵⁶ and ClinGen, a genomic variant database funded by the National Human Genome Research Institute, are general databases for clinical data and have no restrictions on phenotype. Interestingly, the phenotype information available for four of five samples from the databases and from contact with the primary clinical sites that characterized the individuals revealed that they exhibit both ASD-like symptoms and language delay, similarly to the two affected siblings in the AGRE. More specifically, three of four affected individuals with phenotype data have speech or language delay, and the fourth is reported to have non-specific psychomotor delay. All individuals with the CNV manifest behavioral and/or cognitive symptoms, but only three are described as having either an ASD-like or Sotos-like phenotype (Table S9). Individuals with Sotos syndrome are characterized by pre- and postnatal overgrowth, characteristic facial features, learning disability including delayed language development,⁵⁷ and sometimes ASD or ASD-like behavior.⁵⁸ Combining AGRE, SSC (2,591 affected individuals and 2,100 siblings),¹³ AGP ASD samples (941 non-overlapping affected individuals),²³ and filtered DGV data (27,263 population samples) revealed an association between the 2q24.1 deletion and ASD ($p = 0.020$, Fisher's exact test). If we combine the ASD individuals with all clinical DECIPHER samples in which one de novo 2q24.1 deletion was observed in 18,819 clinical

samples, the signal is stronger ($p = 0.0076$, Fisher's exact). Overall, the 2q24.1 deletion is very rare ($<0.05\%$ in affected individuals) and thus far appears restricted to de novo events.

The 2q24.1 deletion critical region overlaps two genes (Figure 5A): *NR4A2* and *GPD2* (MIM: 138430), neither of which has been listed in the list of predicted ASD risk genes by Liu et al.⁵⁹ However, both mRNAs are bound by FMRP⁶⁰ and are potentially regulated by *CHD8* (MIM: 610528) in human neuronal stem cells, whose regulatory targets are enriched among genes that harbor ASD risk variants.^{60,61} Several truncating mutations or deletions have been reported in *GPD2* in the Exome Aggregation Consortium (ExAC) Browser and DGV. In contrast, disruptive SNVs are extremely rare in *NR4A2* in the ExAC Browser, and no CNVs overlap with *NR4A2* in the DGV despite adequate coverage on most microarray platforms. In fact, *NR4A2* is among the predicted loss-of-function (LoF)-intolerant (LI) constrained genes in the ExAC Browser ($pLI = 0.991$)⁶² and is far less tolerant of truncating and missense variants than most genes (Residual Variation Intolerance Score [RVIS] = -0.63 [17.3rd percentile]),⁶³ whereas *GPD2* is predicted to be tolerant of LoF ($pLI = 0.000101$) and missense and truncating variants (RVIS = 0.22 [68.5th percentile]). These genetic data provide support for mutations in *NR4A2* as the more plausible ASD-contributing factor at this two-gene locus.

Table 2. Exon-, UTR-, or Promoter-Overlapping CNVs in ASD-Associated and Candidate Genes

Genes (MIM)	Families (n)	Families (%)	De Novo	Inheritance			Deletions	Duplications	Disrupted Elements
				Maternal	Paternal	Unknown ^a			
<i>ANK2</i> (106410) ^b	3	0.20	1	0	2	0	1	2	exon, 3' UTR, promoter
<i>ASXL3</i> (615115)	1	0.07	1	0	0	0	1	0	exon
<i>AUTS2</i> (607270) ^b	2	0.14	0	2	0	0	1	1	exon, promoter
<i>CNTNAP2</i> (604569) ^c	1	0.07	0	0	1	0	1	0	exon
<i>CNTN4</i> (607280)	5	0.34	0	1	3	1	2	3	exon, promoter
<i>CTTNBP2</i> (609772) ^b	1	0.07	0	1	0	0	0	1	exon, 3' UTR
<i>CYFIP1</i> (606322)	9	0.61	2	3	2	2	5	4	exon
<i>GABRB3</i> (137192) ^b	1	0.07	0	0	0	1	0	1	5' UTR
<i>GIGYF1</i> (612064) ^d	2	0.14	0	1	1	0	2	0	whole gene, <i>GNB2</i> (MIM: 139390)
<i>KCNMA1</i> (600150) ^{b,c}	1	0.07	0	1	0	0	0	1	5' UTR +
<i>MACROD2</i> (611567) ^c	6	0.41	1	2	1	2	6	0	3' UTR, ⁴ promoter, 5' UTR, exon
<i>MIB1</i> (608677) ^b	1	0.07	0	0	0	1	0	1	exon, 3' UTR, miR133
<i>MYO9B</i> (602129) ^b	1	0.07	0	0	0	1	1	0	exon, 3' UTR
<i>NCKAP1</i> (604891)	1	0.07	0	0	0	1	1	0	whole gene deleted
<i>NRXN1</i> (600565) ^c	7	0.48	0	3	2	2	7	0	exon, 5' UTR, promoter
<i>NRXN3</i> (600568) ^c	1	0.07	0	0	0	1	1	0	exon
<i>RBFOX1</i> (605104) ^{c,e}	6	0.41	1	3	2	0	3	3	exon, promoter
<i>SLC5A12</i> (612455)	1	0.07	0	1	0	0	0	1	exon, 3' UTR
<i>SHANK2</i> (603290) ^f	1	0.07	0	1	0	0	0	1	exon, promoter, <i>DHCR7</i> (MIM: 602858)
Total	51	3.48	6	19	14	12	32	19	–

A list of all candidate genes with >50 kb CNVs overlapping a functional region (all events overlap at least one exon, the 5' UTR, and the promoter or the 3' UTR). In total, 3.48% of families carry one of these events. Most of the CNVs are inherited.

^aThe parent(s) did not have biomaterials available for genotyping, and the mode of inheritance could not be assessed.

^bGene listed as a haploinsufficiency gene in Huang et al.⁵⁴ No information was available for *RBFOX1*.

^cSeveral families have CNVs in the intronic regions in this gene.

^dBoth parents carry the deletion in a heterozygous state, and the child is a heterozygote. It is not possible to identify the parent of origin.

^eFamilies with deletions in the 3' UTR contain unaffected children with this deletion.

^fDuplication also encompasses *DHCR7*. Disruptive mutations in this gene are known to cause ID and Smith-Lemli-Opitz syndrome (MIM: 270400).

Orthogonal neurobiological data also highlight the likely role of *NR4A2* in human brain development, given that a previous study suggested its involvement in the development of language-related brain regions during human fetal development.⁴⁴ This is perhaps even more remarkable in combination with the clinical observation that several individuals with the deletion have prominent language delay (Table S9). Therefore, we re-assessed the expression of *NR4A2* in the developing human brain, including some new samples along with those from our previous *in situ* hybridization study.⁴⁴ We observed strong expression in the claustrum, the habenula, and the deep cortical plate, especially in the frontal and perisylvian temporal regions and in the temporal entorhinal cortex (Figures 5B–5D). The expression pattern reflects the data in the Allen Brain Atlas,^{64,65} where *NR4A2* is highly expressed

in the fetal human posterior, superior temporal gyrus (a region critical for in speech and language),^{44,66,67} and claustrum in the adult human brain.

Intelligence in ASD Individuals Correlates with De Novo CNVs

ID is comorbid with ASD in 31% of cases,⁶⁸ and recent work has found an association between de novo variants and IQ, especially for protein-disrupting SNVs.^{5,7,30} A similar negative correlation has also been detected between IQ and de novo CNVs, as well as the number of genes contained within de novo CNVs.^{11,13}

We analyzed the correlation between IQ and de novo CNVs in 142 female and 644 male affected individuals whose Raven's non-verbal IQ (NVIQ) measurements were available. We observed a significant relationship between

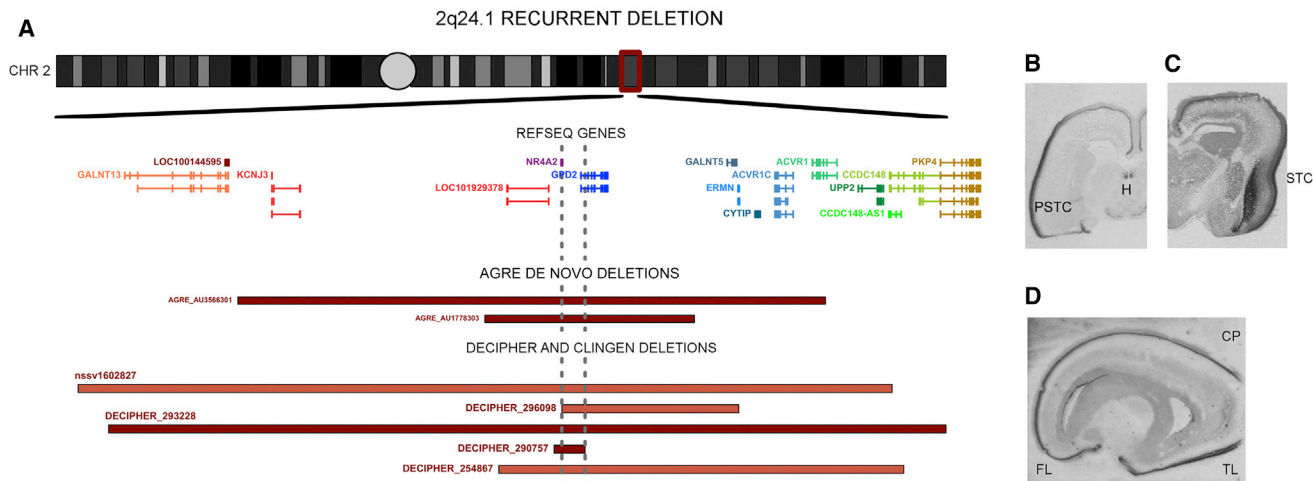


Figure 5. The 2q24.1 Recurrent De Novo Deletion Locus and *NR4A2* Expression in the Fetal Brain

(A) AGRE, DECIPHER, and ClinGen CNVs in 2q24.1 all overlap two genes: *NR4A2* and *GDP2*. All samples from DECIPHER or ClinGen were reviewed for additional CNVs, and only samples with no additional ASD risk CNVs were included. The minimal overlap area between gray dashed lines contains all of *NR4A2* and the beginning of *GDP2*. De novo deletions are marked in dark red, and deletions with no information on the mode of inheritance are marked in coral red.

(B–D) Using in situ hybridization, we looked at the localization of *NR4A2* expression in fetal brains from 19–20 gestational weeks. Coronal sections (B and C) showed strong expression in the deep layers of the cortical plate (CP; especially in the perisylvian temporal cortex [PSTC]), in the stratified transitional field (STF) (C) that runs through the claustrum and habenula (H) (B) and in the sagittal section (D) of the CP, especially in the frontal (FL) and temporal (TL) lobes.

lower IQ in affected individuals and the number of rare, de novo CNVs (effect size of -10 points per de novo CNV, $p = 0.0005$, linear regression). However, the signal was stronger for females (effect size of -26 points per de novo CNV, $p = 5.8 \times 10^{-5}$, linear regression) (Figures 6A–6D). No other psychometric tests were associated with CNV status. We then limited the analysis to large, rare, de novo events and observed an even stronger signal in females (effect size of -13.2 for both males and females [$p = 0.002$] and effect size of -43.1 for females only [$p = 0.00004$], linear regression) (Figures 6E and 6F). This was not due to a sex difference in IQ distributions because there was no overall difference in the measured Raven's IQ range between affected males and females (Figure 6G). Previous work in simplex families has shown that affected females are enriched with de novo CNVs, but we did not observe this in the AGRE cohort (Figure 6H). This could be due to diminished power, because power was comparable but low in both studies (50.1% [alpha 5%] in AGRE; 52.6% [alpha 5%] in SSC).¹³

Patterns of Inheritance and Segregation

One expectation that motivates the recruitment of multiplex families for genetic studies is that they will be enriched with inherited factors and subsequently that affected children in these families will share genetic risk factors or a single high-risk event.^{25,30,69–71} This prediction is supported by a trend toward an excess of inherited rare, large CNVs in affected children in the AGRE (Figure 2 and Tables S5 and S6). In contrast, affected children in simplex families (from the SSC) are enriched with de novo events and do not show a significant signal for the enrichment

of rare, inherited CNVs.¹³ A previous sequencing study in 85 quartet families found that many affected sibling pairs did not share rare, presumed damaging SNVs.³³ However, because the overwhelming majority of these variants are of unknown pathogenicity and it is expected that half of any such variants should be different between siblings by chance, the interpretation of these data³³ is unclear.

To further investigate assumptions about the genetic architecture of ASD on the basis of family structure, we analyzed the 30 AGRE multiplex families harboring a CNV at an ASD-associated locus, for example, 15q11–13 duplications and 16p11.2 duplications and deletions (Table 1 and Figures S3–S9). We observed that in the majority of AGRE multiplex families affected by these known risk CNVs (21/30 [70%]), a de novo or inherited event was not shared by all affected children. 16 of these de novo CNVs were observed in only one affected individual (76%), whereas the other five were inherited (24%) but did not fully segregate with ASD in the families. To demonstrate this phenomenon, we show multiple examples of CNVs at these loci, including the well-established causal duplication at 15q11–13 (Table 1, Figure 4, Figures S3–S9, and Tables S8 and S10). We observed no consistent effect on severity measures (such as IQ, adaptive functioning, or difficulty in social interactions) to explain the difference between the siblings carrying the known major risk allele and those without it (Table S10).

These results have two potential major interpretations in the case of de novo events: (1) that misfortune has struck twice, and the other affected children harbor undetected de novo events (CNVs or SNVs) or (2) that other inherited factors contribute to ASD in the family. In the latter case,

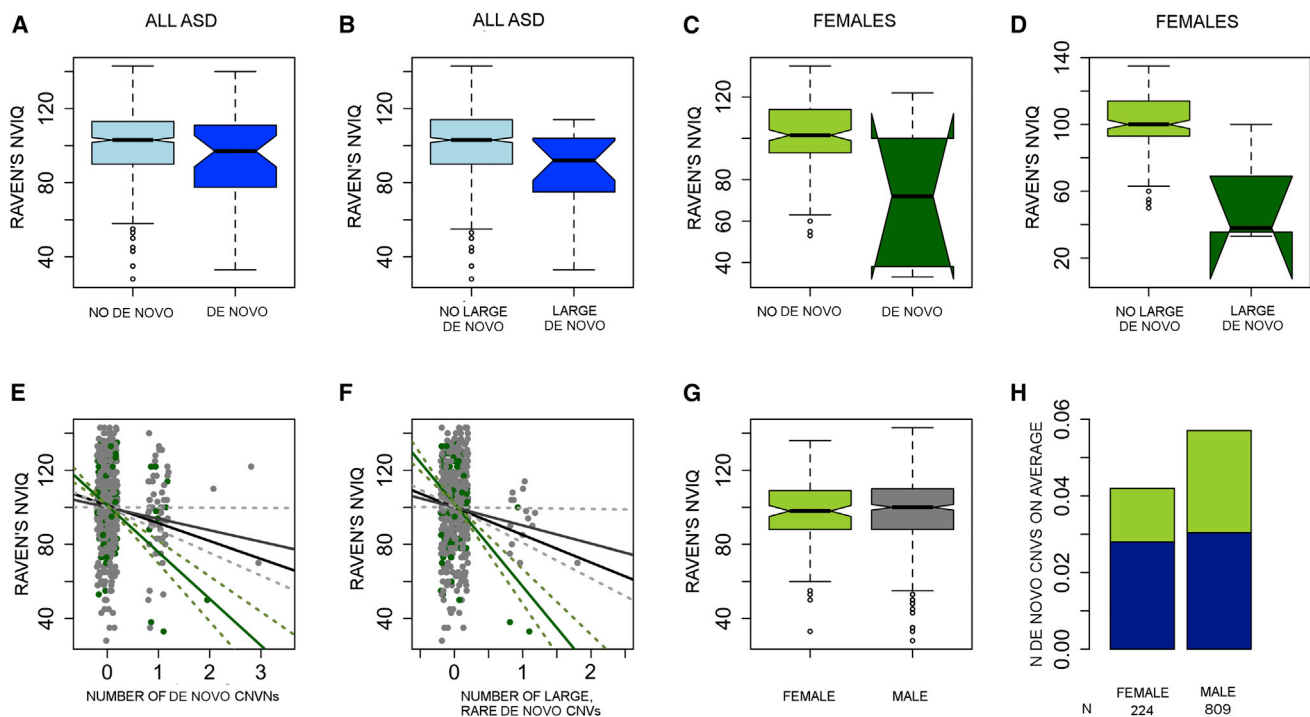


Figure 6. Raven's NVIQ Is Correlated with the Number of Rare De Novo CNVs in ASD

Overall, the effect of rare de novo CNVs (A) and large, rare de novo CNVs (B) on NVIQ is modest between de novo CNV carriers (light blue) and non-carriers (dark blue), but the effect is stronger in females with de novo CNVs (light green, C) than in females without de novo CNVs (dark green, D). The midline in the boxplots (A–D and E) represents the median, the notches show the 95% confidence interval, the solid box represents the middle 50% of the data points (quantiles two and three), the whiskers extend to show 1.5× the interquartile range, and the individual dots are outlier values. The number of rare de novo CNVs (E) or large, rare de novo CNVs (F) correlates clearly with NVIQ, more so in females (green) than in males (gray) or the total affected population (black line). SDs are shown with dashed lines. However, there is neither a difference in Raven's NVIQ between affected females (green) and males (gray) (G) nor an increased number of de novo CNVs in affected females (H) (the portion of large ≥ 500 kb, rare, de novo CNVs is shown in green, and rare, 100–500 kb de novo CNVs are in blue).

the prediction is that the CNV might also contribute to severity or overall developmental disability but might not be the primary cause of the ASD that is shared among the affected siblings. In other words, we are faced not with the commonly observed phenomenon of reduced penetrance of these major risk alleles but rather with the absence of the risk allele in other affected siblings in the family, even though the families were recruited under the expectation that risk variants would be shared. Such observations would be unlikely under a dominant model, where a single high-risk variant in an affected child is expected to cause ASD in a family.^{25,72}

To test the likelihood of the dominant single driving genetic factor assumed to be consistent with the structure of AGRE multiplex families,⁷² we conducted a Bayesian analysis under three priors representing a wide range of distributional assumptions by assuming a single dominant factor with high penetrance. In each case, the current assumption of a single dominant factor is highly unlikely (posterior probability of 1.7×10^{-24}). It is evident that in addition to de novo contributions, multiple ASD risk factors could segregate to different affected siblings even within multiplex families with heritable high-penetrance risk variants.

Discussion

Here, we have found that families ascertained for having two or more children with ASD and simplex families from the SSC show distinct patterns of genetic risk: the rate of large, rare de novo CNVs is lower in multiplex families, and there is an increased burden of large, rare inherited CNVs. For the AGRE cohort, we had power to detect a significant difference in the de novo mutation rate, under the assumption that the rates are comparable to those seen in SSC simplex families ($>95\%$ power for 3.7% and 0.8% of ≥ 500 kb de novo CNVs in affected and unaffected siblings, respectively, and $>80\%$ power for 2.3% and 0.5% of ≥ 1 Mb de novo CNVs in affected and unaffected siblings, respectively),^{11,13} but neither class of de novo events was significantly increased in affected individuals from AGRE multiplex families. Despite their lower frequency in ASD in multiplex families, de novo CNVs are correlated with lower IQ in both SSC simplex families and AGRE families.⁵⁵ The correlation is particularly strong in affected females.⁵⁵ However, unlike in simplex families, the proportion of affected females with de novo CNV is smaller (11/290 [3.8%]) than that of males (58/1,089 [5.3%]) in our data. A similar trend holds for

large, rare de novo events (4/290 [1.4%] for females versus 28/1,089 [2.6%] for males) and large, rare, gene-containing CNVs (41/371 [11.1%] for females versus 168/1,393 [12.1%] for males), although these differences do not reach statistical significance.⁵⁵

Another important observation is that many of the recurrent de novo CNVs identified in previous studies are present as de novo events in affected children in the AGRE as well. This contributes to the remarkable lack of co-inheritance of known ASD-associated CNVs in ASD-affected children in multiplex families. However, this observation is not exclusive to de novo events and also extends to five inherited events, including one duplication at 15q11.2–13.1 and two duplications at 22q11.2. Indeed, non-transmission of a CNV from a parent to an affected child at previously established ASD risk loci was observed in 41% (5/12) of families harboring such loci. These results indicate that affected children in multiplex families harbor a complex burden of risk factors, an important consideration for genetic counseling. The discovery of an ASD-associated de novo CNV in a family does not exclude the possibility that a second affected child in the same family will harbor a different set of genetic and environmental risk factors. This is similar to what has been observed in a smaller sample of 85 families in whom rare exonic variants, mostly of uncertain pathogenicity, showed a similar pattern of discordance in siblings with ASD.³³ In the AGRE, the pattern was observed in previously identified ASD risk genes with established pathogenicity, increasing confidence that we are observing discordance for major genetic risk among siblings in multiplex families.

We also identified a risk locus for ASD and language impairment at chromosomal region 2q24.1, whose statistical association we confirmed via combined analysis of multiple cohorts. The clinical manifestations in individuals with a de novo 2q24.1 deletion (Table S9), including ASD or autism-like behavior and language delay, are quite similar, indicating that this CNV causes a distinct clinical syndrome. We also discovered one previous report of a single individual with a hemizygous deletion overlapping *NR4A2* and *GPD2*; this proband displayed intellectual delay and pervasive developmental disorder.⁷³ The authors focused on *GPD2* in their follow-up analyses and stated that “*NR4A2* is unlikely to cause significant clinical manifestations.”⁷³ On the contrary, we suggest that *NR4A2* is a more plausible candidate given its expression in language-related brain regions in both the adult and developing human brains and its intolerance of LoF, missense, and truncating mutations in human populations (e.g., in the ExAC Browser).^{62,63} The protein encoded by *GPD2* is involved in glycolysis, is broadly localized, and is located at the mitochondrial membrane within cells. It has been suggested to be involved in type II diabetes in rodents, but with the exception of one report of a 2q24.1 deletion overlapping both *NR4A2* and *GPD2*,⁷³ no additional report has suggested a connection between *GPD2* and neuropsychiatric or neurodevelopmental disorders. In summary,

our observations, when combined with those of previous studies, provide strong statistical support for 2q24.1 deletions as a cause of a highly penetrant form of syndromic ASD consisting of ID, language delay, and ASD-like behavioral and cognitive deficits. As more individuals with this rare mutation are identified and characterized, its penetrance in ASD and the range of its clinical manifestations can be further refined.

Similarly, our observed OR of 8.8 for *WWOX* suggests that CNVs in this gene are also a potential inherited risk factor for ASD. However, in contrast to *NR4A2*, *WWOX* is among the most mutation-tolerant genes according to both Genic Intolerance Score (RVIS = 1.1 [92.1st percentile])⁶³ and the ExAC Browser constraint score (pLI = 1.98×10^{-8}),⁶² indicating that heterozygous mutations in it are unlikely to be strong risk factors. Consistently, affected individuals with a *WWOX*-overlapping CNV have generally less severe ASD phenotypes and IQs in the mostly normal range (Table S11). Homozygous mutations in *WWOX* cause an epileptic encephalopathy (MIM: 616211).^{74,75} Interestingly, only 2 of 15 (13%) individuals with either a duplication or a deletion in *WWOX* had a history of seizures: one with febrile seizures and the other with infantile spasms (Table S11). This indicates that the association between *WWOX* CNVs and ASD is unlikely to be caused by comorbid epilepsy. This locus is reminiscent of the overlap between ASD and other epilepsy risk genes, such *SCN2A* (MIM: 182390) and *GABRB3* (MIM: 137192).^{52,76} Further investigation of potential modifier mutations and compound-heterozygous mutations, as well as large replication cohorts, will be needed for better understanding the putative contribution of *WWOX* to ASD.

Although slightly more than half of the AGRE collection has been included in previous studies (Table S1),^{17,19,20,22–24,32,34,77} neither the 2q24.1 de novo deletion nor CNVs in *WWOX* have been previously associated with ASD. This is not surprising, given that only one sample in the previously published AGRE studies had the 2q24.1 deletion, and neither the SSC nor the AGP contains samples with the 2q24.1 deletion. Although CNVs in *WWOX* are more common than 2q24.1 deletions, they are still rare, and obtaining adequate power to detect signal will require a combined analysis of two large datasets.

Previous studies in the SSC have observed that females with ASD have more de novo CNVs^{10,13} than males, which is consistent with the model whereby a larger genetic “hit” is needed to cause ASD in females.^{5,10,11,13} Yet, we did not observe this trend in the AGRE. In addition, the CNV burden between mothers and fathers did not reveal a bias toward female carriers of major risk alleles. These observations in the AGRE could reflect sample size or differences in genetic architecture in simplex and multiplex families¹⁰ and are consistent with a previously observed higher load of heritable factors in fathers from multiplex ASD-affected families,²⁸ but this needs to be replicated in larger cohorts.

In contrast to some previous studies,^{22,24,78} we did not observe any difference between affected children and control individuals (unaffected siblings or individuals from the general population) for the overall number of duplications and deletions; for gene-containing duplications or deletions; for exonic deletions, exonic duplications, or rare exonic CNVs; or for genes in CNVs in any other size category. Several potential explanations include differences between the genetic architectures in multiplex and simplex families, differences between control siblings and control individuals from the general population, or potential technical confounders introduced in previous studies by differences between platforms used in affected and control individuals (Table S2).^{21,22,78} In the current study, we were careful to control for the array platform used for case-control comparisons, and rather than using unrelated control individuals, we relied on siblings from multiplex families as our comparison set. This comparison set could also have reduced our chances of seeing true-positive signals, especially for inherited variants with small effect sizes and low penetrance. Because the number of families affected by ASD-associated high-risk CNVs is small and microarray platforms have a limited resolution for variant detection, further studies with deep sequencing and extensive phenotyping of multiplex families carrying ASD-associated CNVs are needed for fully assessing the roles of known high-risk ASD-associated factors and assumed inheritance patterns. It is possible that additional shared, strong, and highly penetrant risk factors exist in these families, but this seems unlikely given that a recent whole-genome sequencing study of 85 multiplex families found nearly the same rate of sibling discordance and found few shared risk factors in siblings with ASD.³³ Our findings indicate that it will be worthwhile to undertake both larger-scale collection of multiplex families subjected to whole-genome sequencing and larger-scale genome-wide association studies in ASD individuals for low-risk common variation to better define the role of specific heritable factors in ASD susceptibility and how they create risk in individuals.

Accession Numbers

The accession number for this study is NDAR: 393 (<http://dx.doi.org/10.15154/1238063>). The accession numbers for the 2q24.1 deletions reported in this paper are ClinVar: SCV000282106 and SCV000282167. The accession numbers for the ASD-associated CNVs and CNVs in genes with ASD-associated most likely gene-disrupting SNVs reported in this paper are ClinVar: SCV000282087–SCV000282105, SCV000282107–SCV000282151, SCV000282158–SCV000282166, and SCV000282168–SCV000282187.

Supplemental Data

Supplemental Data include nine figures and five tables and can be found with this article online at <http://dx.doi.org/10.1016/j.ajhg.2016.06.036>.

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Web Resources

Autism Genetic Research Exchange (AGRE) clinical information, <http://research.agre.org/program/diag.cfm>
Clinical Genome Resource (ClinGen) Structural Variation Database Search, <https://clinicalgenome.org>
ClinVar, <https://www.ncbi.nlm.nih.gov/clinvar/>
Database of Genomic Variants (DGV), <http://dgv.tcag.ca/dgv/app/home>
DECIPHER, <https://decipher.sanger.ac.uk>
DSS Research, <https://www.dssresearch.com/Home.aspx>
DSS Statistical Power calculators, <https://www.dssresearch.com/KnowledgeCenter/ToolkitCalculators/StatisticalPowerCalculators>
Internet System of Accessing Autistic Children, <http://www.autismtools.org>
National Database for Autism Research (NDAR), <https://ndar.nih.gov/>
UCSC Genome Browser, <https://genome.ucsc.edu/>

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