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Increased Frequency of De Novo Copy Number Variations in Congenital Heart Disease by Integrative Analysis of SNP Array and Exome Sequence Data

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DISCLOSURES

None.

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Abstract

Rationale—Congenital heart disease (CHD) is among the most common birth defects. Most cases are of unknown etiology.

Objective—To determine the contribution of *de novo* copy number variants (CNVs) in the etiology of sporadic CHD.

Methods and Results—We studied 538 CHD trios using genome-wide dense single nucleotide polymorphism (SNP) arrays and/or whole exome sequencing (WES). Results were experimentally validated using digital droplet PCR. We compared validated CNVs in CHD cases to CNVs in 1,301 healthy control trios. The two complementary high-resolution technologies identified 63 validated *de novo* CNVs in 51 CHD cases. A significant increase in CNV burden was observed when comparing CHD trios with healthy trios, using either SNP array ($p=7 \times 10^{-5}$, Odds Ratio (OR)=4.6) or WES data ($p=6 \times 10^{-4}$, OR=3.5) and remained after removing 16% of *de novo* CNV loci previously reported as pathogenic ($p=0.02$, OR=2.7). We observed recurrent *de novo* CNVs on 15q11.2 encompassing *CYFIP1*, *NIPA1*, and *NIPA2* and single *de novo* CNVs encompassing *DUSP1*, *JUN*, *JUP*, *MED15*, *MED9*, *PTPRE*, *SREBF1*, *TOP2A*, and *ZEB2*, genes that interact with established CHD proteins *NKX2-5* and *GATA4*. Integrating *de novo* variants in WES and CNV data suggests that *ETSI* is the pathogenic gene altered by 11q24.2-q25 deletions in Jacobsen syndrome and that *CTBP2* is the pathogenic gene in 10q sub-telomeric deletions.

Conclusions—We demonstrate a significantly increased frequency of rare *de novo* CNVs in CHD patients compared with healthy controls and suggest several novel genetic loci for CHD.

Keywords

De novo copy number variation; congenital heart disease; SNP-array; whole exome sequencing; CNV burden; congenital cardiac defect; microarray; genomics

INTRODUCTION

Congenital heart disease (CHD) is the most frequent birth defect, affecting approximately 7 in 1000 live births,¹ and is a significant cause of childhood morbidity and mortality.² Rare Mendelian disorders, specific chromosomal abnormalities, and copy number variants

(CNVs) are known to explain a subset of CHD cases,²⁻⁴ but the cause of over 80% of CHD remains unexplained.⁵⁻¹²

The application of evolving technologies that detect structural variation throughout the genome has demonstrated a considerable contribution of CNVs to CHD. Early cytogenetic studies recognized an increased prevalence of *de novo* chromosomal abnormalities in syndromic CHD patients, observations that were replicated and extended to non-syndromic CHD with successive generations of CNV detection technologies including array CGH and low density SNP arrays. Using these techniques, researchers have demonstrated significant burden of large *de novo* CNV in some specific CHD lesions. Such CNVs are reported to occur in 13.9% of infants with single ventricles compared to 4.4% in controls,¹³ in 10% of non-syndromic tetralogy of Fallot (TOF) compared to 4% of controls,⁵ and in 12.7% children with hypoplastic left heart syndrome compared to 2% of controls.²⁰ Among different CHD lesions, the frequency of large *de novo* CNVs is similar.²⁰ While many large CNVs are unique to a single CHD patient, several are recurrent in CHD cohorts. A 3-Mb 22q11.2 deletion is the most common recurrent *de novo* CNV associated with syndromic conotruncal defects (CTDs) and is found overall in at least 10% of TOF, 35% of truncus and 50% of interrupted aortic arch (IAA) type B cases.²³ Recurrent *de novo* CNVs in CHD patients reported in multiple studies also occur at chromosomes 1q21.1, 3p25.1, 7q11.13, 8p23.1, 11q24-25, and 16p13.11.

The identification of CHD loci that are altered by CNVs provides opportunities to elucidate disease pathogenesis. However, discerning the causal gene(s) and inferring critical networks and pathways that cause or contribute to CHD has been difficult because low-resolution technologies used in many studies (array CGH and low-density SNP arrays) typically define large CNVs (>100kb) involving many genes. To address these issues, we capitalized on two independent strategies, high-density SNP genotyping arrays (Illumina Omni-1.0 and 2.5M) and whole exome sequencing (WES), to detect smaller *de novo* CNVs in a family-based trio study of sporadic CHD cases with conotruncal, heterotaxy, and left ventricular outflow tract defects.²⁴ We compared CNVs found in CHD trios to those identified in healthy control trios. Through these analyses we sought to compare the robustness of genome-wide CNV detection using array-based and sequence-based technologies to determine if there was an increased burden of smaller *de novo* CNVs in CHD patients as was demonstrated with larger CNVs, and to determine if fewer genes altered by these CNVs enabled more precise detection of gene networks and pathways contributing to the pathogenesis of CHD.

METHODS

Ethics statement

The protocol was approved by the Institutional Review Boards of Boston Children's Hospital, Brigham and Women's Hospital, Great Ormond St. Hospital, Children's Hospital of Los Angeles, Children's Hospital of Philadelphia, Columbia University Medical Center, Icahn School of Medicine and Mt. Sinai, Rochester School of Medicine and Dentistry, Steven and Alexandra Cohen Children's Medical Center of New York, and Yale School of Medicine. Written informed consent was obtained from each participating subject or their parent/guardian.

Patient cohorts

CHD probands and parents were recruited into the CHD Genes Study of the Pediatric Cardiac Genomics Consortium (CHD genes: ClinicalTrials.gov identifier NCT01196182) as previously described,²⁴ using protocols approved by Institutional Review Boards of each institution. Trios selected for this study had no history of CHD in first-degree relatives. CHD diagnoses were obtained from echocardiograms, catheterization and operative reports; extra-cardiac findings were extracted from medical records and included dysmorphic features, major anomalies, non-cardiac medical problems, and deficiencies in growth or developmental delay. The etiologies for CHD were unknown; patients with previously identified cytogenetic anomalies or pathogenic CNVs identified through routine clinical evaluation were excluded. Whole blood samples were collected and genomic DNA extracted.

CHD trios were studied by SNP arrays (n=414) or by WES (n=356), including a subset (n=233) that were analyzed by both methods. The distribution by CHD lesions in patients genotyped by arrays was: 403 (61%) left ventricular obstruction (LVO); 197 (30%) conotruncal defects (CTD); 49 (7%) heterotaxy (HTX); and 12 (2%) other cardiac diagnoses (Supplementary Table I). The distribution by CHD lesions in patients studied by WES was 284 (46.1%) left ventricular obstruction (LVO); 235 (38.1%) conotruncal defects (CTD); 78 (12.7%) heterotaxy (HTX); and 19 (3.1%) with other cardiac diagnoses (Supplemental Table II).

Control trios were the unaffected sibling and parents of a child with autism who were consented and recruited through the Simons Simplex Collection (SSC). CNVs were identified in the same way in the control trios as in the cases using SNP arrays (n=814) or WES (n=872), including a subset (n=385) analyzed by both methods.

Additional data on the distribution and prevalence of previously reported CNVs in the general population was derived from the Database of Genomic Variants (<http://dgv.tcag.ca>) and from 649 de-identified control subjects who had participated in an unrelated psychiatric case-control study, genotyped on the same high density SNP array platforms at the same genotyping center as the CHD probands (438 on the Illumina Omni-1M and 211 on the Illumina Omni-2.5M). These controls were used only to prioritize the *de novo* CNVs identified by SNP array methods that were selected for confirmation analyses.

Array genotyping and CNV identification

A total of 360 CHD parental samples genotyped on the Omni1M and 654 on Omni2.5M arrays were applied for cluster definition using Illumina Genome Studio clustering algorithm. Raw data is publicly available through the database of genotypes and phenotypes (dbGaP) National Heart, Lung, and Blood Institute (NHLBI) Bench to Bassinet Program: The Pediatric Cardiac Genetics Consortium (PCGC) under dbGaP Study Accession: phs000571.v1.p1. We removed clusters with outlier values of SNP call rate, Hardy-Weinberg equilibrium, AA/AB/BB cluster means, and minor allele frequency to improve the intensity noise (Log R ratio standard deviation) from a mean of 0.2 (using the default cluster file from Illumina) to 0.1 for CHD samples. Briefly, individual samples were filtered through a

standard quality control pipeline.²⁵ B-allele frequency (BAF) and Log R ratio (LRR) values were exported from Illumina Genome Studio. Only samples with SNP call rate > 98%, standard deviation (SD) of normalized intensity (LRR) < 0.3, absolute value of GC-corrected LRR < 0.005, as well as CNV call count < 800 for Omni1-Quadv1 or < 300 for Omni2.5-8v1 were included.⁶³ Samples with high inbreeding coefficients, that were duplicated, or had gender mismatches, and trios with Mendelian errors > 1% were removed from analyses. We started with 1,536 genotyped samples (512 trios), including 561 on the Illumina Omni-1M and 969 on the Illumina Omni-2.5M. Four hundred and sixty-one trios had the same array version for all family members. Upon completion of these QC procedures 1,245 samples, including 447 genotyped on the Illumina Omni-1M and 798 on the Illumina Omni-2.5M high-density SNP array platforms, were taken forward for analysis, constituting 415 complete trios (Supplemental Table III).

Three groups (CHOP, Harvard, Yale) independently analyzed genotyping data using slightly different algorithms to detect putative *de novo* CNVs. For each of the three independent analyses, CNVs were called for each subject using PennCNV⁶⁴ with the hidden Markov model algorithm and custom-made population frequency of B-allele (PFB) and GC model files. CNVs were called when 10 or more consecutive probes demonstrated consistent copy number change. The PennCNV detect_cnv --trio option was used to boost transmission probability of CNV calling for initially *de novo* scored CNVs. Fragmented CNV calls were merged using clean_cnv. All candidate CNVs were visually inspected to ensure the appropriate pattern of LRR and B-allele frequency was consistent with the CNV call. Additionally, Gnosis,²⁵ QuantiSNP,⁶⁵ and Nexus (biodiscovery.com) were used to increase specificity. *De novo* CNVs were prioritized for quality by genomic length, number of probes, confidence score based on signal strength, 50% overlap of two or more algorithms, low parental origin p-value using infer_snp_allele, and visual BAF/LRR review. CNVs with a minor allele frequency > 1% were removed, leaving rare CNVs. All putative *de novo* CNVs were experimentally evaluated by digital droplet PCR (ddPCR, Supplemental Figure I), and only validated CNVs are reported.

De novo CNV loci that were previously reported as pathogenic were defined by reported recurrence in at least two publications using independent data. Although some of the CNVs reported here overlap with previously reported CNVs in CHD patients based on review of the literature,⁶⁶ they do not meet our frequency constraint for previously reported pathogenic *de novo* CNV loci.

CNV identification and variant calling from WES data

WES data from 356 CHD trios were analyzed for *de novo* CNVs (Supplemental Table II). WES samples were captured with the Nimblegen SeqCap Exome V2 chemistry and sequenced on the Illumina HiSeq 2000 platform as previously described.²⁶ Sequence reads were aligned to the human reference genome hg19 using Novoalign (<http://novocraft.com>), BWA,⁶⁷ and ELAND.⁶⁸ Duplicates were marked with Picard (<http://picard.sourceforge.net>). Indel realignment and Base Quality Score Recalibration was done with GATK. XHMM is an algorithm to detect exon-level copy number variation and assign CNV quality metrics³⁸ and was used at four of the PCGC analysis sites (CHOP, Harvard, Columbia and Mount

Sinai) to identify *de novo* CNVs (Supplemental Figure II). Candidate *de novo* CNVs were inspected visually. Putative *de novo* CNVs were prioritized for confirmation based on genomic length, low sequence depth variability and low prevalence in theXHMM call set data (AF<1%). All putative *de novo* CNVs were independently confirmed by ddPCR.

SNVs and short insertions/deletions (indels) were called from the Novoalign alignment of WES trios using a pipeline derived from GATK version 2.7 best practices.⁶⁹ Briefly, aligned reads were first compressed using the GATK ReducedReads module and variants were called on all CHD WES trios using the UnifiedGenotyper joint variant calling module. Identified variants were filtered using GATK variant quality score recalibration. Variants were annotated using SnpEff.⁷⁰ *De novo* SNVs and indels were independently confirmed using Sanger sequencing.

CNV confirmation with digital droplet PCR

Putative CNVs were experimentally confirmed with ddPCR as previously reported⁷¹ using an 18-27 base pair FAM probe designed within each candidate CNV region, avoiding homopolymer runs or probes that began with G. A VIC probe targeting the RPP30 gene was used as reference. Reaction mixtures of 20 μ L volume comprising ddPCR Master Mix (Bio-Rad), relevant forward and reverse primers and probe(s) and 100 ng of digested DNA were prepared, ensuring that approximately 25-75% of the 10,000 droplets ultimately produced were positive for FAM or VIC signal. For *de novo* CNV confirmations, DNA from the CHD patient and parents was used. After thermal cycling, plates were transferred to a droplet reader (Bio-Rad) that flows droplets single-file past a two-color fluorescence detector. Differentiation between droplets that contain target and those that did not was achieved by applying a global fluorescence amplitude threshold in QuantaSoft (Bio-Rad). The threshold was set manually based on visual inspection at approximately the midpoint between the average fluorescence amplitude of positives and negative droplet clusters on each of the FAM and VIC channels. Confirmed CNV duplications had approximately 50% increase in the ratio of positive to negative droplets as did the reference channel. Conversely confirmed CNV deletions had approximately half the ratio of positive to negative droplets as did the reference channel.

Network analysis

Three bioinformatic algorithms were utilized: DAVID,³⁵ DAPPLE,³⁶ and WebGestalt.³⁷ Four different gene lists derived from the *de novo* CNV loci were used (Supplemental Table IV). The lists were constructed as follows: (1) All genes contained within *de novo* CNV intervals; (2) Published “causative” genes from previously reported CHD CNVs intervals in addition to all genes in novel CHD CNV intervals. “Causal” genes in previously reported CNV intervals included *ELN* (Williams syndrome), *RAI1* (Smith-Magenis syndrome), *TBX1* (22q11 deletion), *GATA4* (8p23.1 deletion), *GJA5* (1q21.1 duplication), and *NKX2.5* (5q35.1 deletion); (3) Genes contained solely within novel CHD CNV intervals (e.g., exclude genes from previously published CNVs); (4) Genes contained within *de novo* CNV intervals that are highly expressed in the developing mouse heart (top quartile of all genes expressed E14.5 mouse heart).²⁶ We anticipated that genes in list 2 and list 4 would

have increased specificity for CHD in comparison to genes in list 1 and that genes in list 3 would be biased towards new disease networks.

We expanded network analysis input gene lists by including both *de novo* CNV genes and *de novo* single nucleotide variants (SNV) that were previously identified in CHD probands by WES.²⁶ Only *de novo* SNVs predicted to be deleterious (e.g., loss of function (LOF): nonsense, frame-shift, and splice site mutations and missense variants that alter highly conserved amino acid residues or predicted to be deleterious by SIFT or PolyPhen2) were included in the expanded gene list. The additional gene lists included: (5) All genes within a *de novo* CNV interval (e.g., list 1) and protein-altering SNVs and (6) Published “causative” genes from previously reported CHD CNVs intervals in addition to all genes in novel CHD CNV intervals (e.g., list 2) and protein altering SNVs.

Statistical analysis

Burden calculations were done with a Fisher exact test computed in the R statistical computing environment. For analyses using DAVID, networks with an enrichment of genes impacted by CNVs were assigned a *p*-value with Benjamini and Hochberg correction for multiple testing with a false discovery rate of 0.05. In DAPPLE, type I error was controlled through permutation. *p*-values of less than 0.05 were considered significant.

RESULTS

Identification of De Novo CNVs

We studied 415 CHD trios genotyped by SNP arrays and 356 trios by WES analysis, including 233 trios studied by both methods. No trios had an affected first-degree relative and the genetic cause of CHD in all studied children was unknown (Supplementary Tables 1 and 2).

Sixty-five *de novo* CNVs identified in CHD cases were independently confirmed by ddPCR. *De novo* CNVs were identified in 51 unique probands (9.8%). These CNVs ranged in size from 0.1 kb to 12.8 Mb. 48 of these (76%) were <500 kb and half were smaller than 110 kb. The number of genes in the CNV intervals ranged from 1 to 175 with 42 (67%) having 5 genes. Four *de novo* intervals contained no genes. Six probands had two *de novo* CNVs, two had three CNVs and one had four CNVs.

The parental origin of deletion CNVs was determined when the haplotype of the remaining copy could be uniquely assigned to one parent. Seven *de novo* CNVs arose on maternal chromosomes and 10 on paternal chromosomes. The remainder could not be assigned due to uninformative or insufficient numbers of informative parent-of-origin SNPs.

Comparison of SNP Array and WES CNV calling

To consider the accuracy of identifying *de novo* CNVs from SNP array data, we first considered a set of 40 high-confidence PennCNV *de novo* CNV calls that contained 10 adjacent SNPs, were >10 kb in length, and passed visual inspection. Among these 40 high-confidence putative CNVs, 40 were experimentally validated by ddPCR in the proband and 32 (80%) were experimentally confirmed to be *de novo*, representing a false positive rate of

20%. For smaller *de novo* CNVs identified using the high-density array data, we considered a set of 97 high-confidence PennCNV putative *de novo* CNV calls based on 7-9 SNPs. While 88% were experimentally validated by ddPCR in the proband, only four of the 97 (5%) were confirmed to be *de novo*.

From the WES data, we selected an initial set of 29 putative CNVs with a size range spanning six orders of magnitude from 530 bases in length (two exons) to more than 8 Mb in length covering hundreds of exons. Twenty-six of the 29 CNVs (90%) confirmed experimentally to be *de novo*, representing a false positive rate of 10%. The three false positive CNVs included one 530-bp region that contained only two exon targets and two different inherited CNVs that were miscalled as *de novo* because both parents harbored CNVs at the locus. Based on these considerations, we restricted subsequent WES *de novo* CNV calls to those containing ≥ 3 exons and for which each parental dataset contained no CNVs within the locus.

To evaluate false negative rates of the two platforms and analyses, we tested our ability to detect four CNVs (two 22q11 deletions, one 17p11 duplication, and one 10q terminal deletion; Supplemental Table V in clinical cases previously diagnosed with these CNVs. These four CNVs served as positive controls and were distinct from the PCGC cohort. Both the SNP array and WES platforms detected each of these four large, clinically significant CNVs.

We also compared the results of *de novo* CNVs analysis from the 233 trios studied by both SNP array and WES. Among 42 confirmed *de novo* CNVs in these trios, 24% (10/42) were identified by both platforms while 40% (17/42) were identified only with the SNP arrays and 35% (15/42) only by WES (Figure 1). The recognized technical limitations of each platform prevented detection of some CNVs. For example, CNVs that occur exclusively in noncoding sequences are not captured by WES whilst CNVs in coding or non-coding genomic regions where the SNP density is sparse can escape detection by SNP arrays.

From our studies we deduced that *de novo* CNVs were accurately detected by arrays when ≥ 10 adjacent SNPs were impacted or by WES when greater than three adjacent exons were impacted. In our dataset, 29 of 42 CNVs fulfilled both of these criteria and should have been identified by both technologies (Figure 1). However, only 34% (10/29) of these ddPCR confirmed CNVs were identified by both platforms. SNP arrays uniquely identified 34% (10/29) and WES analyses uniquely identified 31% (9/29). Taken together, the false negative rate of each methodology is approximately 30-35%. Overall, the genome-wide analyses of *de novo* CNVs identified by SNP arrays was reasonably concordant with WES data, but each also identified complementary CNVs. The minimum CNV size that we reliably detected by SNP arrays was 10 kb and by WES was 1 kb, although some smaller CNVs identified by these techniques were validated.

CNV burden analysis

The burden of *de novo* CNVs in CHD cases and control trios was initially compared using analyses from SNP arrays. *De novo* CNVs were assessed in 841 control trios, studied using the Illumina Omni1M array to match the case trio array resolution and called using the

PennCNV algorithm using computational parameters described previously²⁵. Nine *de novo* ddPCR-validated CNVs were identified among 841 control trios. Twenty-two *de novo* ddPCR-validated CNVs were identified among 462 CHD trios with SNP arrays. These data define a significant burden of CNVs in CHD cases compared to controls (OR: 4.6, Fisher p -value: 7×10^{-5} ; Table 2). After excluding nine previously identified CHD-associated CNVs, the calculated burden of novel CNVs identified in CHD cases remained modestly significant (OR: 2.7, Fisher $p=0.02$).

To provide further support for this finding, we analyzed the burden of *de novo* CNVs that were identified by WES. WES in CHD cases and control trios were technically comparable, including the same Nimblegen V2 exome capture chemistry and similar sequence read depths obtained on identical Illumina platforms. Sixty percent of control trios were sequenced at the same site (Yale Center for Genome Analysis) that sequenced the cases. Raw sequence reads were processed through the identical short read aligner (Novoalign) for CNV burden analysis. SNP genotyping of CHD and control datasets and principal component analysis did not identify any systematic biases (Supplemental Figure V). Cases and controls were matched for gender as best as possible with slight excess of male cases. Using an identical XHMM pipeline (CNVs involving 3 exons and no parental CNVs within 1 MB), we identified 19 *de novo* ddPCR-validated CNVs in 356 CHD trios, and 14 *de novo* ddPCR-validated CNVs in 872 control trios (OR: 3.5, Fisher $p=6 \times 10^{-4}$; Table 2). Excluding the six *de novo* CNVs previously identified as CHD-associated, we identified a similar OR and p -value as in the SNP array data (OR: 2.3, Fisher $p=0.03$).

Our data identify an increased burden of CNVs, detected by SNP arrays or WES, in CHD patients compared to controls. We observed a larger mean size of *de novo* CNVs with increased burden in CHD patients (3.6 Mb) than controls (495 kb; t -test $p=0.035$) with the distribution of CHD CNVs skewed towards the largest CNVs identified in CHD cases. The median size of *de novo* CNVs from CHD cases (522 kb) was also significantly larger than controls (118 kb; Mann-Whitney $p=0.028$). Of the CNVs identified by SNP array which were capable of detecting CNVs outside of coding regions, there was a trend towards an increased number of *de novo* CNVs in controls that contained no coding exon (4/9) compared to PCGC cases (3/22; Fisher $p=0.15$).

Putative CHD loci at 15q11.2 and 2p13.3

Overlapping *de novo* CNVs found in multiple cases and not in controls likely contain disease genes. Sixteen of 65 (25%) *de novo* CNVs in CHD probands have been previously implicated in CHD⁵, including four 22q11.2 deletions, three 8p23 deletions (involving *GATA4*), two 1q21.1 duplications (involving *PRKAB2*, *PDIA3P*, *FMO5*, *CHD1L*, *BCL9*, *ACP6* and *GJA5*), one 22q11.2 distal duplication, one 2q22.3 deletion (that causes Mowat-Wilson syndrome), one 11q24.2-q25 deletion (that causes Jacobsen syndrome) and four with CNVs in 15q11.2.

CNVs in four CHD probands (two deletions, two duplications) at the BP1-BP2 15q11.2 locus that spans approximately 225 kb (chr15:22,836,000-23,062,000) were observed as recurrent *de novo* events (Supplemental Figures III and IV). Both patients with duplications (1-00192, 1-00315) and one with a deletion (1-00243) had LVO due to aortic coarctation.

The remaining proband (1-01396) had TOF with pulmonary atresia. As there was no *de novo* CNV identified in this region among 814 and 872 control trios studied respectively by SNP arrays or WES, this locus has a significant burden of *de novo* CNVs in CHD cases (4/538 CHD vs. 0/1301 controls; Fisher $p=0.007$). CNVs at the 15q11.2 locus were observed at low frequency (AF<1%) in the Database for Genomic Variants (DGV). Among the three genes altered by this CNV (*CYFIP1*, *NIPA1*, and *NIPA2*), only *CYFIP1* is highly expressed in the developing mouse heart.²⁶ *CYFIP1* encodes the cytoplasmic FMR1-interacting protein 1, which has dual roles in inhibiting local protein synthesis and in promoting actin remodeling.²⁷ An earlier study observed an increased burden of inherited deletions in CHD cases at 15q11.2¹ and a recent paper identified a single proband with a 6-Mb *de novo* duplication at 15q11.2-q13.1²⁰ and two additional cases with inherited 300-400-kb duplications at 15q11.2. Our data provide additional evidence that *de novo* CNVs at 15q11.2 may contribute to disease risk in CHD.

In addition, a recurrent CNV was observed to alter a novel locus at chromosome 2p13.3. A *de novo* 190-kb deletion was identified in a TOF proband (1-01536) and was maternally inherited in a proband with truncus arteriosus (1-01805). No 2p13.3 CNV was found in control samples or in DGV. Among three genes included in the CNV interval (*ASPRV1*, *PCBPI* and *PCBPI-AS1*), only *PCBPI* is highly expressed in the developing mouse heart.²⁶ *PCBPI* encodes a major cellular poly(rC)-binding protein, which controls translation from mRNAs containing the DICE (differentiation control element).²⁸ In DECIPHER, patient 257771 with an atrioventricular canal defect had a 7-Mb overlapping deletion of 2p13.3, suggesting this locus may also contribute to disease risk in CHD.

Integration of CNV and sequence data to identify CHD genes

To improve the identification of specific genes altered by CNVs that might cause or contribute to CHD, we searched the WES data for *de novo*, rare loss-of-function (LOF) variants in genes encoded in CNV intervals. We identified a terminal deletion of chromosome 11q24.2-q25, which causes Jacobsen syndrome in one CHD patient (1-01486) with clinical manifestations typical of this dominant disorder (hypoplastic left heart, coarctation of the aorta, mitral and aortic valve atresia, strabismus, and short stature). *ETS1* has been proposed as the critical CHD gene in the Jacobsen syndrome locus based on impaired ventricular development in an *Ets1*-null mouse.²⁹ WES analyses identified a *de novo* *ETS1* frameshift mutation (chr11:128350159GTCCT>G, c.1046_1049delAGGA, [p.K349fs]) in another CHD patient without the chromosome 11q24.2-q25 deletion with cardiac abnormalities observed in Jacobsen syndrome (hypoplastic left heart and mitral valve atresia). Our data provide the first human genetic evidence to suggest that *ETS1* mutations contribute to the cause of cardiac malformations in Jacobsen syndrome.

We also assessed whether *de novo* CNVs in combination with a rare or novel deleterious variant on the other allele might produce recessive forms of CHD. One CHD patient (1-01179) with a *de novo* 10q25-26 deletion also had a novel *CTBP2* variant (p.R134W) on the remaining allele. The hemizygous variant was absent from public genome databases, is predicted to be damaging (Polyphen2 score of 0.998), and altered a phylogenetically conserved residue (PhyloP score = 2.54). Cardiac abnormalities are present in approximately

one third of patients with subterminal chromosome 10q deletions and recently *CTBP2* was proposed as a candidate CHD gene.³² The clinical manifestations of our patient, truncus arteriosus and right aortic arch, resemble the phenotypes identified in a *Ctbp2*-null mouse (failure of vascular remodeling and cardiac looping).³³ We suggest that *CTBP2* sequence analyses in individuals with chromosome 10q deletions may identify additional variants in a subset of patients that modify phenotype.

Correlation of CHD phenotypes and CNVs

The frequency of *de novo* CNVs was 10% among conotruncal anomalies, 6% among left-sided obstructive lesions and 21% in heterotaxy. We observed a modest trend towards increased extra-cardiac manifestations such as developmental delay in patients with *de novo* CNVs (Supplemental Table VI). Approximately 31% of all CHD patients studied with SNP arrays or WES had extra-cardiac manifestations, whilst 40% (21/52; OR:1.5, Fisher $p=0.2$) of patients with *de novo* CNVs had extra-cardiac features. This association has been found in some,³⁴ but not all,²⁰ previous studies, perhaps due to differences in the ages of the CHD patients studied, methods of clinical data collection, and the definition of an extra-cardiac anomaly.

Gene networks impacted by CNVs in CHD

We employed pathway and network analysis with DAVID,³⁵ DAPPLE,³⁶ and WebGestalt,³⁷ using as input four different lists of genes encoded within all *de novo* CNV loci (Methods and Supplemental table IV). Initial gene lists contained: (1) all genes encoded in a *de novo* CNV interval; (2) genes previously defined as causative with CNVs intervals plus all genes in novel *de novo* CNV intervals; (3) only genes contained within novel *de novo* CNV intervals; (4) all genes contained within *de novo* CNV intervals that are highly expressed (top 25%) in the developing heart.²⁶

DAVID identified enrichment of a gene pathway implicated in acetylation $p<2.3\times 10^{-4}$; phosphoprotein $p<3.9\times 10^{-4}$, and G protein-activated inward rectifier potassium channel $p<2.5\times 10^{-2}$ (Benjamini-Hochberg corrected). WebGestalt implicated an enrichment of previously identified CHD genes including *ELN*, *NKX2.5*, *GATA4*, and *ZEB2* contributing to Gene Ontology processes: anatomical structure formation involved in morphogenesis $p<0.03$, cardioblast differentiation $p<0.03$, and septum secundum development $p<0.02$ (Benjamini-Hochberg corrected).

Using DAPPLE, we identified two additional sub-networks of direct protein/protein interactions that were consistently observed across four gene lists. Among genes encoded within CNVs that are highly expressed in the developing heart, a sub-network consisting of *NKX2.5* and *GATA4* ($p<0.1$, Figure 2a) and a sub-network consisting of *ETS1*, *JUN*, *TOP2A*, and *MKI67* ($p<0.01$, Figure 2b) were identified. By further expanding the CNV gene lists to include genes with *de novo* LOF mutations, the *ETS1/JUN/TOP2A* sub-network was significantly elaborated upon and enriched ($p<0.005$). Each of these three genes was directly linked through protein-protein interactions to sub-networks containing 10 additional genes identified in either CNV or WES datasets.²⁶ This entire network incorporated over 60 genes implicated in CHD (Figure 2c). As the *ETS1/JUN/TOP2A* sub-

network was robust to the specific *de novo* CNV gene list (criteria 2 above) and expanded with the addition of genes containing rare *de novo* LOF mutations, the data suggest that this sub-network contains genes and pathways involved in CHD.

DISCUSSION

We report whole-genome CNV analyses using complementary detection technologies in a large cohort of CHD patients. CNV detection in WES has been investigated in schizophrenia³⁸ and autism,³⁹ but array-based and sequence-based strategies have not previously been directly compared, and our data highlight the differences between array-based and sequence-based strategies to detect *de novo* CNVs. By defining small CNVs with high resolution and integrating these findings with WES data that identified rare deleterious mutations, we identified novel *de novo* CNVs and genes involved in the pathogenesis of CHD. We show that 9.8% (53/538) of CHD patients without a previously identified genetic etiology have rare *de novo* CNVs. We previously demonstrated that 10% of CHD patients in our cohort have *de novo* single nucleotide or small insertion/deletion mutations in genes highly expressed in the developing heart that are likely to be damaging.²⁶ None of the CHD patients with rare *de novo* CNVs reported here carry these variants. Even if all the *de novo* CNVs and *de novo* predicted pathogenic sequence variants we have identified were causative, we do not yet know the etiology for the majority of CHD subjects in our study.

Our detection rate of approximately 10% *de novo* CNVs in CHD patients is equivalent to previous studies, despite identifying small CNVs. Had we not excluded patients with known pathogenic CNVs identified through clinical care, we expect that *de novo* CNVs would have been identified in approximately 15% of CHD patients, based on the prevalence of common *de novo* CNVs in CHD (e.g., 7% of TOF with chromosome 22q11 deletions, and 1% of TOF to 1q21 CNVs). In our study, these CNV loci accounted for <1% of CHD probands

Despite these exclusion criteria, we identified a four-fold increased frequency of rare *de novo* CNVs relative to the background frequencies of 1.2% (detected by SNP arrays) and 1.8% (detected by WES) of *de novo* CNVs in controls ($p=7 \times 10^{-5}$, $p=4 \times 10^{-4}$ respectively). Even after excluding previously defined CNVs, we still observed an approximate two-fold increase in novel rare *de novo* CNVs ($p=0.02$).

Since the odds ratio of *de novo* CNVs in cases vs controls was 3.5-4.6, we estimate that between 50-70% of *de novo* CNVs observed in cases may be disease causing. The possibility exists that a higher percentage of *de novo* CNVs increase the risk of CHD but may not be sufficient to cause CHD without other contributing genetic or environmental factors. Additionally, subtle anatomic defects in the heart may not have been diagnosed in the control group since controls were not systematically examined by echocardiogram. Overall, our evidence suggests a model in which *de novo* CNVs contribute to CHD

The comparison of dense array-based platforms and WES analyses to detect independently validated CNVs indicate that each strategy identifies only ~70% of the CNVs that should be within the detection limitations of each technology. As such, these two CNV methodologies provide substantial complementary information. An important corollary to this conclusion is

that previously published CNV analyses in human disease may have significantly underestimated the burden conveyed by these structural variants.

Amongst all confirmed *de novo* CNVs, 61% (41) were deletions and 39% (26) were duplications. The proportion of these classes of CNVs are not significantly different; whether or not the trend toward more CNV deletions in CHD is biologically meaningful or reflects greater sensitivity to detect deletions by these methods will require further analyses. *De novo* CNVs ranged in size from less than 1 kb to 12.8 Mb, with a median size of 110 kb. Thus, half of the independently confirmed CNVs were smaller than the reported detection limit of most prior studies. For example, four CHD patients had 200-kb *de novo* CNVs on chromosome 15. While the pathogenicity of the identified CNVs remains to be determined, we propose that the smaller CNVs involving fewer genes are particularly valuable in defining specific candidate CHD genes in comparison to larger CNVs that typically include many more candidates. The ability to reliably detect small CNVs is helpful, particularly if they fall within large CNVs previously identified and define a critical interval of overlap. For example, we identified one *de novo* CNV that only affected *JUN* and another that only altered *TOP2A*, two genes that were implicated by network analyses as interacting with transcription factors *SMAD2*, *SMAD4* and *ETS1*, molecules that play important roles in cardiovascular development.

Although there is considerable complexity in CHD phenotypes, we observed no significant difference in the frequencies of rare *de novo* CNVs among distinct CHD sub-classifications. While CHD patients with CNVs in our cohort were more likely to have extra-cardiac phenotypes (OR: 1.5), this trend fell short of significance. Whether this finding reflects shared developmental biologic pathways among different organ systems or the possibility that CNVs perturb multiple genes that individually contribute to organ system development is unknown.

We identified several *de novo* CNVs that impacted established CHD genes including *GATA4* and *GJA5*. We also identified a CHD patient with a deletion of chromosome 5q34-q35.2, encompassing *NKX2-5*. LOF *NKX2-5* mutations are an established cause of CHD, and CNVs encompassing *NKX2-5* have been previously recognized in CHD.

We identified recurrent *de novo* CNVs involving deletions or duplications at chromosome 15q11.2. As the proximal region of chromosome 15 is meiotically unstable due to the segmental duplications that serve as breakpoint hotspots, recurrent *de novo* events at this locus might reflect locus genomic instability. However, the excess burden of *de novo* CNVs at this locus in CHD patients compared to controls (Fisher $p=0.007$) suggests otherwise. The report of an excess burden of inherited deletions in CHD patients at this locus³ lends further evidence for pathogenicity although this study lacked information on inheritance. As CNVs at chromosome 15q11.2 CNV exhibit incomplete penetrance for both neuropsychiatric and CHD phenotypes, genes affected by this could participate in inherited and sporadic CHD.

Chromosome 15q11.2 deletions and duplications are implicated in neurodevelopmental disorders including schizophrenia, intellectual disability and autism.⁴³⁻⁴⁵ That chromosome 15q11.2 CNVs are also associated with CHD adds to a growing list of loci (22q11,⁴⁶ 1q21,

7q11.23,⁴⁸ 16p11.2, and 16p13.11) that link cardiac malformations and neurocognitive disorders. These (and other) genetic loci may explain in part the significant co-expression of heart and brain developmental phenotypes in many children.

By integrating CNV and sequencing data from WES, we also identified candidate genes within CNV regions that may cause dominant or recessive forms of CHD. We present the first human *ETS1* LOF mutation that likely contributes to Jacobsen syndrome. We also identified a rare inherited and predicted deleterious *CTBP2* missense variant that is hemizygous due to a *de novo* CNV deletion, associated with a CHD phenotype comparable to that observed in *Ctbp2*-null mice. Continued integration of CNV and sequence data should enable more comprehensive assessments of genetic causes of disease. The current study provides suggestive data, and sequencing large cohorts of CHD patients for mutations in these two genes will be necessary to unambiguously prove the role of these genes in CHD.

Network analyses by DAPPLE was more successful in elucidating novel network biology than DAVID and WebGestalt, which rely heavily on previously annotated gene sets and are challenged by the addition of unrelated genes encoded with CNV intervals along with pathogenic genes. If pathogenic CNVs on average contain one main causal gene and approximately five unrelated genes, then we might expect DAVID and WebGestalt to be less informative for CNV network analyses.⁵¹ Conversely, DAPPLE, based on proteome-wide protein-protein interaction data rather than previously curated gene lists, calculates p-values through within-degree node-label permutation, which is more permissive to background noise.³⁶

DAPPLE network analysis reinforced the central role of transcriptional regulation in congenital heart disease. The identification of one network, including NKX2.5/GATA4, provided a robust positive control as protein-protein interactions and substantial contributions by these molecules to CHD are previously described. Direct protein-protein interactions between ETS1/JUN/TOP2A have also been reported,⁵⁴⁻⁵⁶ but this network has not been previously implicated in CHD. In an expanded network analysis of these molecules that included rare LOF mutations identified from exome sequencing, JUN was linked to SMAD2 and SMAD4, molecules that participate in cardiac development through the TGF- β signaling pathway.⁵⁷⁻⁶⁰

We focused our current analysis solely on rare *de novo* CNVs. As the etiology of CHDs is known to be polygenic, and incomplete penetrance of genes for CHD has been previously described, future analyses of rare inherited CNVs may expand these findings.

The novel *de novo* CNVs we report should be considered provisional pending replication in independent studies. Replication of the overall effect and the magnitude of the risk of these identified variants is needed. While it is not yet possible to draw a conclusion about whether any particular *de novo* CNV is causal, the identification of additional CNVs and mutations in specific genes within the CNV intervals will be required to validate the new loci identified here.

In summary, integration of high resolution complementary platforms for CNV and sequence data on large numbers of patients with CHD has proven valuable to define the underlying genomic architecture of CHD and expand the genes and networks involved in cardiac development and is likely applicable to the study of other diseases.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Nonstandard Abbreviations and Acronyms

CTD	conotruncal defect
LVOT	Left Ventricular Outflow Tract Obstruction
TA	truncus arteriosus
TOF	tetralogy of Fallot
HLH	hypoplastic left heart syndrome
APVS	Absent pulmonary valve syndrome
ASD	Atrial septal defect
CoA	Coarctation of the Aorta
DTGA	dextro-Transposition of the great arteries
HTX	Heterotaxy

PA	Pulmonary Atresia
PS	Pulmonary Stenosis
TriAtrisia	Tricuspid atresia
VSD	Ventricular Septal Defect

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Novelty and Significance

What Is Known?

- Congenital heart disease (CHD) is among the most common birth defects.
- Many genomic loci are implicated in CHD, but most cases are of unknown etiology.

What New Information Does This Article Contribute?

- To determine impact of *de novo* CNVs in CHD, we found an increased *de novo* copy number variation (CNV) frequency in CHD families compared to healthy control families (termed burden).
- We found true recurrent *de novos* to find and define significant CHD CNV genes.
- We performed network analysis to assess biological gene function of single *de novo* CNVs.

CHD is among the most common birth defects. Many genomic loci are implicated in CHD, but most cases are of unknown etiology. A significant increase in CNV burden was observed when comparing CHD trios with healthy trios, using either SNP array ($p=7 \times 10^{-5}$, Odds Ratio (OR)=4.6) or WES data ($p=6 \times 10^{-4}$, OR=3.5) and remained after removing 16% of *de novo* CNV loci previously reported as pathogenic ($p=0.02$, OR=2.7). We observed recurrent *de novo* CNVs on 15q11.2 encompassing *CYFIP1*, *NIPA1*, and *NIPA2* and single *de novo* CNVs encompassing *DUSP1*, *JUN*, *JUP*, *MED15*, *MED9*, *PTPRE*, *SREBF1*, *TOP2A*, and *ZEB2*, genes that interact with established CHD proteins *NKX2-5* and *GATA4*. Integrating *de novo* variants in WES and CNV data suggests that *ETSI* is the pathogenic gene altered by 11q24.2-q25 deletions in Jacobsen syndrome and that *CTBP2* is the pathogenic gene in 10q sub-telomeric deletions. This is the first large cohort study of CHD families using WES and dense state of the art SNP arrays for integrative *de novo* CNV discovery. The new loci implicated here provide novel diagnostic markers for early detection of CHD and novel therapeutic drug targets.

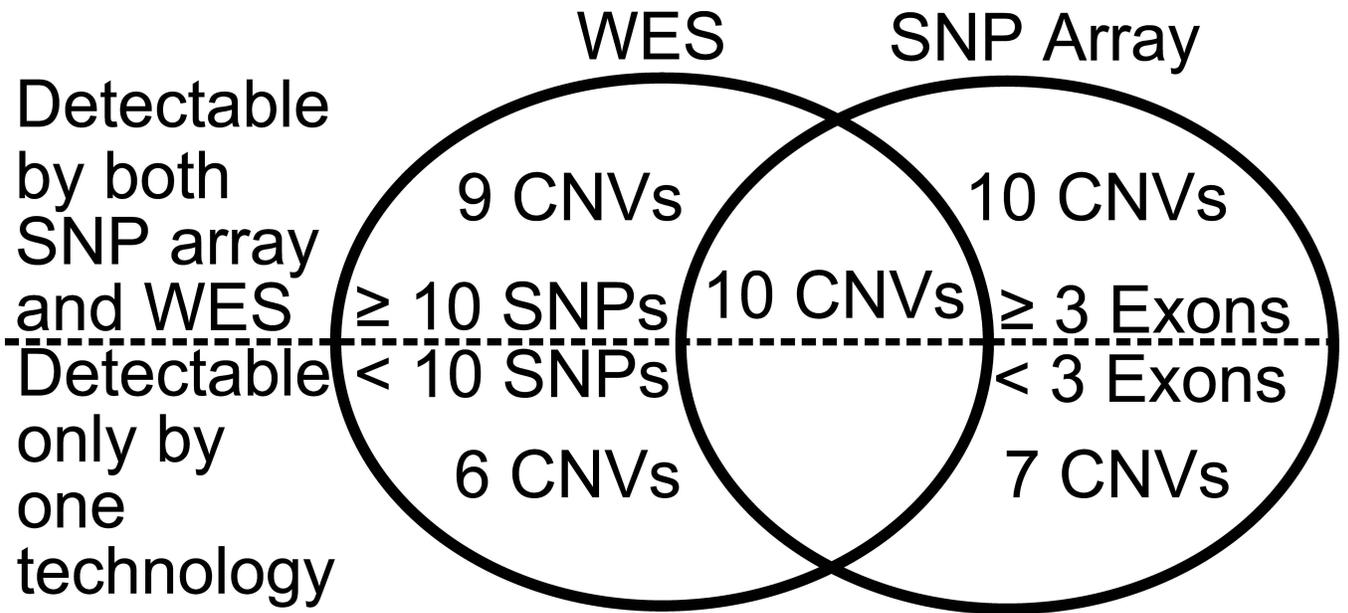


Figure 1. Comparison of SNP array and WES platforms in detection of the 42 validated de novo CNVs in the subset of 233 probands studied by both technologies. 10 of the 42 were detected by both methods, 32 were called by one method. The figures below the dotted line show the number of CNVs that were below the detection limits of the second platform (CNVs that span <10 SNPs on SNP arrays or <3 exons on WES) and hence could not have been called. The figures above the dotted line show the number of CNVs with sufficient SNPs and/or exons to enable high confirmation rates, but that were not called.

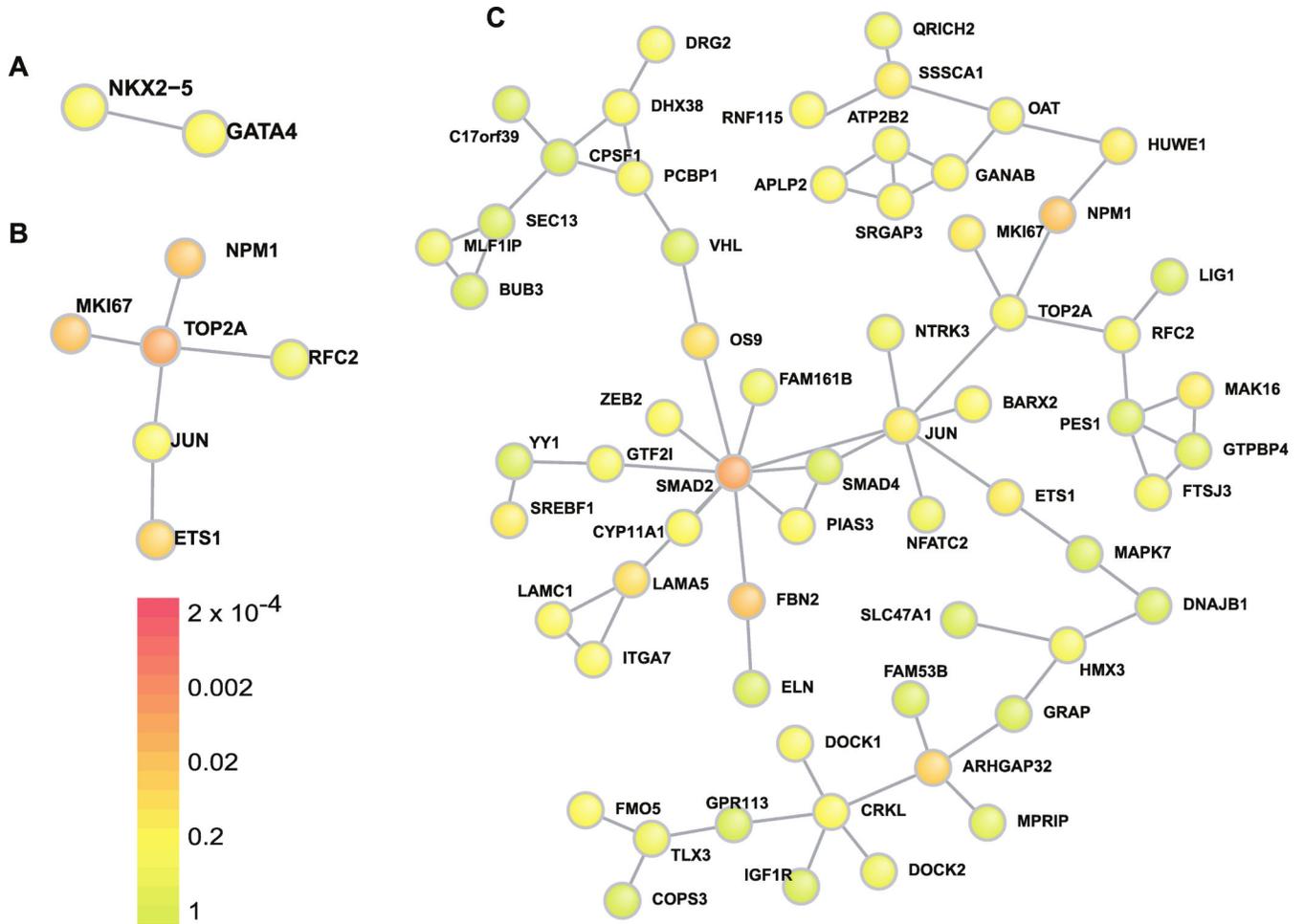


Figure 2.

Network analysis of CNV loci genes. Two networks of direct protein-protein interactions, (A) NKX2.5/Gata4 and (B) ETS1/JUN/TOP2A, were consistently identified in the DAPPLE *de novo* CNV loci analysis. P-values from the genes highly expressed in the developing heart, the most restrictive gene set list, are presented here. (C) The ETS1/JUN/TOP2A network was significantly elaborated upon by incorporating genes with deleterious *de novo* point mutations and indels in the WES exome sequencing analysis in addition to the CNV loci. Of note, two probands had *de novo* ETS1 variants (one CNV and one frameshift), two probands had *de novo* SMAD2 variants (a splice site mutation and a highly conserved missense variant) and two probands had *de novo* ELN variants (both Williams syndrome CNVs).

Table 1

Confirmed rare *de novo* CNVs in discovery cohort. Genomic coordinates refer to hg19.

ID	Chr	Start	End	Band	CNV ¹	Syndrome/ gene	Analysis Observed ²	Cardiac Lesion: (diagnosis) ³	Parent Origin	Extra-cardiac	N genes	Size (kb)
1-01401	1	59247993	59251097	p32.1	1	<i>JUN</i>	A	LVOT (HLHS)	-	-	1	3.1
1-03171	1	145586403	145799634	q21.1	3	1q21.1 dup/ <i>GIA5^A</i>	A/E	CTD (TOF/APVS)	-	-	7	213.2
1-01036	1	146631133	147416212	q21.1	3	1q21.1 dup/ <i>GIA5^A</i>	E	CTD (TOF)	M	-	15	785.1
1-01486	1	194201171	194304070	q24.2-q25	3	<i>CDC73</i>	A	LVOT (HLHS)	-	Yes	0	102.9
1-01518	1	248750565	248795110	q44	3	<i>OR2T10,OR2T11</i>	A	LVOT (HLHS)	-	-	2	44.5
1-01536	2	70168995	70359345	p13.3	1	<i>PCBP1</i>	A	CTD (TOF/PA)	-	-	5	190.4
1-01401	2	102493466	103001458	q11.2-q12.1	1	<i>MAP4K4</i>	E	LVOT (HLHS)	-	-	6	508.0
1-01401	2	145155868	145274931	q22.3	1	Mowat-Wilson/ <i>ZEB2^A</i>	E	LVOT (HLHS)	-	-	1	119.1
1-00762	3	60661	11712230	p26.1	3	<i>ARL8B,ARPC4,CAMK1,CAV3,CRBN,EMC3,ITPR1,SEC13,SETD5,VGLL4</i>	A	ASD/PS (ASD)	-	Yes	103	11651.6
1-01049	3	15637812	15643461	p25.1	3	<i>BTID,HACL1</i>	E	CTD (TOF)	-	-	2	5.6
1-01045	3	47780965	48309270	p21.31	3	<i>CDC25A,DHX30,MAP4,SMARCC1</i>	A	LVOT (HLHS)	-	-	14	528.3
1-02093	3	197143652	197186111	q29	3	<i>BDHI</i>	A	CTD (TOF/PA)	-	Yes	0	42.5
1-00771	4	185603346	185638397	q34.1	1	<i>CENPU,PRIMPOL</i>	E	CTD (DTGA/VSD)	P	Yes	2	35.1
1-00789	5	136464	232969	p15.33	3	<i>CCDC127,LRRC14B,PLEKHG4B,SDHA</i>	A	CTD (TOF)	-	-	4	96.5
1-00113	5	133706994	133730455	q31.1	1	<i>UBE2B</i>	A	CTD (TOF/PA)	-	Yes	1	23.5
1-00296	5	166386727	173073664	q34-q35.2	1	<i>NKX2.5^A</i>	A	CTD (TOF)	M	Yes	53	6686.9
1-01916	6	36646788	36651971	p21.2	1	<i>CDKN1A</i>	A	HTX (HTX)	-	-	1	5.2
1-01049	6	43484783	43485159	p21.1	3	<i>POLR1C</i>	E	CTD (TOF)	-	-	1	0.4
1-00096	7	50179707	50191153	p12.2	1	<i>C7orf72</i>	E	CTD (TOF/PA)	-	Yes	1	11.4
1-00800	7	72719386	74138603	q11.23	1	Williams syndrome ⁴	A	CTD (VSD/PS)	P	Yes	34	1419.2
1-00540	7	72721123	74140708	q11.23	1	Williams syndrome ⁴	A	LVOT (ASD)	M	Yes	34	1419.6
1-00977	7	138258252	143807632	q24-q25	1	<i>C7orf55,FAM115A,LUC7L2,MKRN1,NDUFB2,UBN2,ZC3HA VIL,ZYX</i>	E	CTD (TOF)	-	-	175	5549.4
1-01995	7	142334207	142460871	q34	1	<i>MTRNR2L6,PRSS1</i>	E	CTD (TOF)	M	-	15	126.7
1-01562	8	8067768	12530976	p22.1-p23.1	3	<i>GATA4^A</i>	A	CTD (TOF)	-	-	75	4463.2

ID	Chr	Start	End	Band	CNV ¹	Syndrome/ gene	Analysis Observed ²	Cardiac Lesion: (diagnosis) ³	Parent Origin	Extra-cardiac	N genes	Size (kb)
1-02625	8	8102183	12190106	p23.1	3	<i>GATA4</i> ⁴	A	LVOT (CoA)	M	Yes	62	4087.9
1-00566	8	11606428	11710963	p23.1	1	<i>GATA4</i> ⁴	A E	CTD (TOF)	-	-	6	104.5
1-00948	8	119053343	119064098	q24.1	1	<i>EXT1</i>	A	LVOT (CoA)	P	Yes	1	10.8
1-02360	9	5302500	5337760	p24.1	3	<i>RLNI,RLN2</i>	A	CTD (ASD)	-	Yes	3	35.3
1-01852	11	34458230	34460862	p13	1	<i>CAT</i>	A	CTD (VSD)	-	-	1	2.6
1-00565	11	42968283	42970488	p12	3	<i>HNRNPKP3</i>	A	LVOTO (ASD)	-	-	0	2.2
1-01536	11	65157239	65408708	q13.1	1	<i>EHP1,IL1L1,TBP3,MAP3K11,PCNX1.3,SCYL1,SSSCA1</i>	A	CTD (TOF/PA)	-	-	14	251.5
1-00230	11	86939592	87025456	q14.2	1	<i>TMEM135</i>	A E	LVOT (ASD)	P	Yes	1	85.9
1-01486	11	125641368	134943190	q24.2-q25	1	Jacobsen / <i>ETS1</i> ⁴	A E	LVOT (HLHS)	P	Yes	73	9301.8
1-00795	11	134598043	134617838	q25	3	<i>LOC283177</i>	A	CTD (VSD)	M	-	0	19.8
1-00124	12	8003758	8123306	p13.31	3	<i>SLC2A14,SLC2A3</i>	A	LVOT (As/HLHS)	-	-	3	119.5
1-00050	12	52845952	52862783	q13.13	1	<i>KRT6C</i>	A	LVOT (HLHS)	-	-	1	16.8
1-02411	14	58860893	58881694	q23.1	1	<i>TMM9,TOMM20L</i>	A	CTD (TOF)	-	-	2	20.8
1-01049	14	74551632	74551731	q24.3	3	<i>LIN52</i>	E	CTD (TOF)	-	-	1	0.1
1-00192	15	22296985	23161330	q11.2	3	1 MB from <i>PW/ CYFIP1</i> ⁴	A	LVOT (CoA)	-	-	20	864.3
1-00315	15	22750305	23140114	q11.2	3	1 MB from <i>PW/ CYFIP1</i> ⁴	A	LVOT (CoA)	M	-	5	389.8
1-01396	15	22750305	23228712	q11.2	1	1 MB from <i>PW/ CYFIP1</i> ⁴	A E	CTD (TOF/PA)	P	-	6	478.4
1-00243	15	22835893	23062345	q11.2	1	1 MB from <i>PW/ CYFIP1</i> ⁴	E	LVOT (CoA)	P	Yes	4	226.5
1-01994	15	28389771	28446734	q13.2	1	<i>HERC2</i>	E	LVOT (ASD)	P	-	1	57.0
1-01696	15	44833588	44856873	q21.1	1	<i>EIF3,SPG11</i>	A E	CTD (TriAresia/DTGA)	-	-	2	23.3
1-01941	15	88761539	8879300	q25.3	3	<i>NTRK3</i>	A	CTD (TOF/DTGA)	P	-	1	17.8
1-01427	17	21562473	22252439	p11.2	1	<i>FAM27L,FLJ36000,MTRNR2L1</i>	A	HTX (HTX)	-	Yes	7	690.0
1-00561	17	27962393	28099002	q11.2	1	<i>SSH2</i>	A	LVOT (ASD)	-	Yes	3	136.6
1-01995	17	38544624	38548586	q21.1	1	<i>TOP2A</i>	A E	CTD (TOF)	-	-	1	4.0
1-01049	17	39845210	39846477	q21.2	3	<i>EIF1</i>	E	CTD (TOF)	-	-	2	1.3
1-01588	18	65138642	78015180	q22.1-q23	1	<i>NEFATC1</i> ⁴	A	LVOT (CoA)	-	Yes	58	12876.5

ID	Chr	Start	End	Band	CNV ¹	Syndrome/ gene	Analysis Observed ²	Cardiac Lesion: (diagnosis) ³	Parent Origin	Extra-cardiac	N genes	Size (kb)
1-02170	19	20601006	20717536	p12	1	<i>ZNF826P</i>	A	CTD (TOF)	-	Yes	1	116.5
1-00174	19	40515744	40681387	q13.2	1	<i>ZNF546,ZNF780A,ZNF780B</i>	A	CTD (TOF/PA)	-	Yes	4	165.6
1-01536	19	47792293	47905132	q13.33	1	<i>C5ARI,C5AR2,DHX34</i>	A	CTD (TOF/PA)	-	-	3	112.8
1-00730	20	14529657	14583899	p12.2	1	<i>MACROD2,MACROD2-IT1</i>	A	CTD (DTGA)	-	-	2	54.2
1-01194	22	18844632	21500000	q11.2	1	DiGeorge / <i>TBX1</i> ⁴	A	CTD (VSD)	P	Yes	80	2655.4
1-00113	22	18886915	22000000	q11.2	1	DiGeorge / <i>TBX1</i> ⁴	A E	CTD (TOF/PA)	P	Yes	96	3113.1
1-01836	22	19020529	21380382	q11.2	1	DiGeorge / <i>TBX1</i> ⁴	A E	CTD (TOF)	M	-	70	2359.9
1-00988	22	20733495	21464479	q11.2	1	DiGeorge / <i>TBX1</i> ⁴	A	CTD (HLHS/HTX)	M	Yes	31	731.0
1-02133	22	25661725	25919492	q11.23	3	22q11 distal duplication ⁴	A	CTD (TOF)	-	-	4	257.8
1-00425	22	36038076	36149338	q12.3	1	<i>APOL5,APOL6,RBFOX2</i>	A E	LVOT (HLHS)	-	-	4	111.3
1-01427	22	42522638	42531210	q13.2	3	<i>CYP2D6</i>	A	HTX (HTX)	-	Yes	2	8.6
1-01941	X	23003525	23086619	p22.11	3	<i>DDX53,RPI1-40F8.2</i>	A	CTD (TOF/DTGA)	-	-	1	83.1
1-00197	X	148685645	148693146	q28	3	<i>TMEM185A</i>	E	LVOT (HLHS)	-	Yes	1	7.5

¹ Copy number: 1- deletion; 3- duplication

² Analysis: A- identified with SNP Array; E- identified with WES

³ Parental Origin: M- maternal chromosome; P- paternal chromosome

⁴ De novo CNV loci that were previously reported as pathogenic.

Table 2Case Control *de novo* CNV Burden

		N Probands	N (%) CNVs	OR	P-value
SNP Array	SSC ¹	841	9 (1%)	-	-
	PCGC: all CNVs	462	22 (4.7%)	4.6	7×10^{-5}
	PCGC: novel loci		13 (2.8%)	2.7	0.02
WES	SSC ²	872	14 (1.6%)	-	-
	PCGC: all CNVs	356	19 (5.6%)	3.5	6×10^{-4}
	PCGC: novel loci		13 (3.9%)	2.3	0.03

¹Controls derived from State, 2011.²⁵

²Controls derived from three studies: Iossifov, 2012;⁷² Sanders, 2012;⁶² and an additional set of unpublished controls provided by Matthew State selected by the same criteria and sequenced as described in.⁶²