Copy number variants implicate cardiac function and development pathways in earthquake-induced stress cardiomyopathy.

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Abstract

The pathophysiology of stress cardiomyopathy (SCM), also known as takotsubo syndrome, is poorly understood. SCM usually occurs sporadically, often in association with a stressful event, but clusters of cases are reported after major natural disasters. There is some evidence that this is a familial condition. We have examined three possible models for an underlying genetic predisposition to SCM. Our primary study cohort consists of 28 women who suffered SCM as a result of two devastating earthquakes that struck the city of Christchurch, New Zealand, in 2010 and 2011. To seek possible underlying genetic factors we carried out exome analysis, Cardio-MetaboChip genotyping array analysis and array comparative genomic hybridization on these subjects. The most striking finding from these analyses was the observation of a markedly elevated rate of rare, heterogeneous copy number variants (CNV) of uncertain clinical significance (in 12/28 subjects). Several of these CNVs clearly impacted on genes of cardiac relevance including *RBFOX1*, *GPC5*, *KCNRG*, *CHODL*, and *GPBP1L1.* There is no physical overlap between the CNVs, and the genes they impact do not fall into a clear pathophysiological pathway. However, the recognition that SCM cases display a high rate of unusual CNV, and that SCM predisposition may therefore be associated with these CNVs, offers a novel perspective and a new approach by which to understand this enigmatic condition.

Introduction

Stress cardiomyopathy (SCM), also known as "broken heart syndrome" or takotsubo syndrome,[1; 2] is a condition that captures widespread public interest.

The cardiomyopathy is distinctive and the precipitating emotional event is typically clearly defined, however the mechanism for the cardiomyopathy and links between the psychological event and the physical illness are not understood.

Sporadic cases of SCM are estimated to account for 1-5% of acute coronary syndrome presentations.[3-5] Predominantly the condition occurs in post-menopausal women,[6; 7] and because of this, 5-10% of female presentations with suspected acute coronary syndrome are attributed to SCM.[8-11] Although SCM can be fatal, the symptoms are commonly transient and patients generally have a good prognosis and recover well over a period of days to weeks.[12] In classic descriptions the cardiomyopathy has a typical pattern but a number of variations are now widely recognised and it is increasingly apparent that cases can be quite heterogeneous.[13]

SCM occurring in clusters around the time of major disasters such as earthquakes, floods and bushfires is also well recognised.[6; 14-16] Due to the large impact these events have upon hospital resources and medical infrastructure, it is rare for such clusters of SCM to be studied in any depth. This was made clear in reports from the Great East Japan Earthquake.[17] In the Canterbury (New Zealand) earthquake sequence of 2010 and 2011 the two main events precipitated large case clusters of SCM.[17-22] Unusually for a major natural disaster, the tertiary hospital in Christchurch continued to function, allowing the collection of a relatively large homogenous cohort of cases which have been followed over several years.[18-23] Most research around this disorder has focused

on sporadic SCM associated with heterogenous triggers.[4; 24-26] Although the presentation of earthquake-associated SCM (EqSCM) appears to be similar to that of sporadic cases, a key difference is the homogenous nature of the trigger.

Various mechanisms have been postulated for takotsubo cardiomyopathy, including that the syndrome arises from stunning of the heart muscle (myocardium) as a result of either ischemia from spasm of the coronary arteries, or from the direct effect of catecholamines (dopamine, adrenaline or noradrenaline) on cardiac myocytes.[4; 24; 27; 28] Despite suggestive pathophysiological observations and theories, most authors conclude that the aetiology of SCM is poorly understood, and we do not yet have satisfactory explanations for the origins of this condition.[27; 29-32 26; 32] Some retrospective case series have suggested that the incidence of SCM is increased in patients with anxiety conditions, but in our studies we did not find any correlation with psychiatric or anxiety disorders.[19; 23]

Amongst the models that may be proposed for SCM aetiology, it is worth considering the possible contribution of genetic factors. Many forms of cardiomyopathy have genetic origins.[33; 34] Hypertrophic cardiomyopathy is the most common form of familial heart disease and a leading cause of sudden cardiac death. It is inherited in an autosomal dominant Mendelian manner with variable expressivity and age-related penetrance.[33] These cardiomyopathies show considerable genetic heterogeneity, with cases now attributed to some 1400 mutations in 11 genes, all of which contribute to cardiac sarcomere function. Familial dilated cardiomyopathy is also frequently attributable to an

underlying genetic predisposition and at least 50 genes have now been implicated, with most eliciting disease as dominant mutations.[34]

Evidence for genetic contributions to SCM are not as strong as for other cardiomyopathies. However, there are several examples of familial occurrence of SCM involving siblings[35-37] or mother-daughter pairs,[38-42] and a large Swedish study of SCM identified three families in which several close relatives developed the condition.[43] The overall rarity of SCM would suggest that these familial clusters are significant, and it is quite possible that more overt familial relationships in this disorder are obscured by the simultaneous requirement for two key circumstances (in most cases): post-menopausal status and environmental exposure to a sudden major stressful event. Occasional cases of SCM occur in younger women or males, and a proportion of patients report no preceding stressor,[44] suggesting that an intrinsic pathogenic mechanism is involved. The recurrence of SCM in some patients, including one Christchurch EqSCM case,[22] also implies a biological vulnerability.

These observations have prompted consideration of genetic susceptibility to this condition.[39; 42; 45; 46] Until recently, genetic studies were restricted to candidate gene analysis in case series of sporadic SCM patients,[47-51] but these have yielded mainly negative findings. One candidate gene study reported a significant difference in the frequency of a *GRK5* polymorphism in cases,[52] but this has not been replicated and past history of single gene association studies suggests it is unlikely to be meaningful.[53] More recently, another candidate gene study has implicated estrogen receptor genes as potential risk factors for

SCM.[54] In an effort to capture genome-wide data, exome sequencing[55-58] was recently applied to a sample of sporadic SCM cases.[42] Although this analysis did not reveal any difference in allele frequency or burden between SCM cases and population controls (28 adults with normal echocardiograms), it was noted that two thirds of the cases carried a rare deleterious variant within at least one gene of a large set of adrenergic pathway genes, and 11 genes harboured a variant in two or more cases. However, the significance of these rare variants remains unclear.

In this study, we set out to explore the role of genetic factors in predisposition to EqSCM. We specifically tested three discrete hypotheses for potential genetic contributions to risk of SCM: (i) an essentially Mendelian hypothesis that rare genetic variants in one or a few key genes cause predisposition, which was tested by whole exome sequencing (WES); (ii) that SCM was a complex disorder with genetic contributions from multiple common variants, which was tested using the Cardio-MetaboChip genotyping array; and (iii) that rare copy number variants (CNV) impacting on relevant genes contribute to risk, which was tested by array comparative genomic hybridization (aCGH).

Material and Methods

Cases

The September 2010 earthquake of magnitude 7.1 on the Richter scale (Mw 7.1) in Christchurch (New Zealand) triggered eight cases of EqSCM, and the shallow highly destructive quake (Mw 6.3) that followed in February 2011 triggered 21 cases over four days. One woman presented after both quakes [22],

and one was in hospital during the initial quake. Enrolment of this latter participant was delayed, and her sample was available for aCGH analysis (n=28) but not for Cardio-Metabolome analysis (n=27). The steps leading to recruitment of our EqSCM cohort are detailed elsewhere[20; 21], but briefly, our study commenced the day of the first earthquake with the creation of a register of prospectively identified earthquake stress cardiomyopathy cases. As our hospital was still functioning we could build a cohort with first-world data from complete single centre capture. After the second earthquake the study was extended.[20-22]

Inclusion criteria: i) Meeting modified Mayo criteria for stress cardiomyopathy and admitted to Christchurch Hospital within one week of either the September 2010 or February 2011 earthquake; ii) age over 18; iii) informed consent given. Exclusion criteria: i) unable to understand English sufficiently to be able to complete questionnaires.

All participants were recruited with informed consent, including discussion of the possibility of incidental findings from genetic analyses, and return of such findings after consultation with a medical geneticist. The Southern Health and Disability Ethics Committee (New Zealand) approved this study.

DNA extraction

Peripheral blood samples were obtained from consenting participants. Genomic DNA was extracted from 3 mL peripheral blood using NucleoMag extraction kits (Machery-Nagel GmbH, Düren, Germany) on a KingFisher™ Flex Magnetic

liquid-handling robot (Thermo Fisher Scientific, Inc, Waltham, MA). DNA was quantified by analysis with the Nanodrop™ (ThermoFisher), and, where appropriate, the Tapestation 4200 system (Agilent Technologies).

Exome analysis

We applied WES to a subset (24 of 28) EqSCM cases. The exome capture and sequencing was carried out in two batches of 12, during 2012-13 (New Zealand Genomics Limited, Dunedin, New Zealand). DNA was processed with Illumina TruSeq sample preparation and exome enrichment kits (which capture ~62Mb of genomic DNA), and sequencing (100bp paired-end reads) was carried out on an Illumina HiSeq2000 system. Good quality sequence was obtained across all exomes, with very few unassigned reads, and greater than 20 million sequence reads per sample at mean quality scores (Phred) of Q37. Raw read data were aligned to the GRCh37 human reference genome using the Burrows-Wheeler Aligner (BWA),[59] and processed through the Broad GATK pipeline.[60] The alignment process included removal of reads from duplicate fragments, realignment around known indels, and recalibration of all base quality scores. Joint variant calling was performed with GATK's HaplotypeCaller. This included *de novo* assembly at each potential variant locus. Variants were annotated and analysed using Ingenuity Variant Analysis (IVA) software (QIAGEN, Redwood City, CA, USA), MutationTaster2,[61] SnpEff,[62] SeattleSeq annotation server,[55] and Galaxy (via usegalaxy.org).[63] Allele frequencies and additional annotations were drawn from 1000 Genomes project,[64] NHLBI GO Exome Sequencing Project (ESP), Seattle, WA (URL: http://evs.gs.washington.edu/EVS/), ClinVar,[65] and Exome Aggregation Consortium (ExAC), Cambridge, MA (URL:

176 http://exac.broadinstitute.org). Promising gene variants were inspected by
177 Sanger sequence analysis on the appropriate genomic DNA samples.
178
179 *Cardio-MetaboChip Analysis*
180 Three groups were genotyped using the Illumina Cardio-MetaboChip: 27 out of
181 28 female Christchurch EqSCM cases, 133 heart-healthy controls from the
182 Canterbury Healthy Volunteers Study (HVOLs, 54 F / 79 M),[66] and 157 patients
183 recruited for an ongoing study of premature coronary heart disease and
184 consented for genotyping (CHD, 64 F / 93 M). DNA samples were run on the
185 Cardio-MetaboChip and scanned on the Illumina® iScan platform by
186 AgResearch Limited (Invermay, New Zealand).
187
188 Quality control with summary analysis of allele and genotype frequencies,
189 Hardy-Weinberg equilibrium tests, and missing genotype rates were performed
190 with PLINK version 1.07 software.[67] SNPs with a minor allele frequency of <0.05
191 and those that failed the Hardy-Weinberg equilibrium test ($p<0.001$) were
192 excluded from the analysis, leaving 141,095 SNPs in the analysis (Table 1).
193 Three samples from the CHD Study were also removed after analysis of
194 relatedness. Principal Component Analysis (PCA, Eigenstrat 4.2) was
195 performed on an independent subset of almost 50,000 SNPs; the first principal
196 component explained 6% of the variation, subsequent components all less than
197 0.5%, and matched self-reported ethnicity (visual inspection). Hence the first
198 principal component was subsequently included as a factor in the logistic
199 regression. Logistic regression was performed to evaluate differences in SNP
200 minor allele frequencies between groups, adjusted for ethnicity and gender,

using an additive genetic model (R 3.01 software[68]). P values were adjusted for false discovery rate (FDR) using the Benjamini Yekuteli method.[69] Pathway analysis was performed for the leading 100 SNPs in each pairwise group comparison, using MetaCore from GeneGo (Thomson Reuters).

CNV detection and analysis

Array comparative genomic hybridisation (aCGH) was undertaken on 28 EqSCM cases to examine structural variants in the cohort. For this analysis, we used either the Nimblegen 135k oligo array (CGX12) (Roche NimbleGen Inc, Madison, WI, USA), capable of genome-wide screening for CNV to a resolution of 10kb in well-categorised pathogenic genomic regions, and 50kb elsewhere or the Agilent 180k HD oligo array (Sureprint G3 Human 4x180k) (Agilent Technologies, Santa Clara, CA, USA), which has a similar resolution.

Pooled reference DNA samples (catalogue numbers G147A and G152A) were purchased from Promega (Madison, WI, USA). EqSCM case and reference DNA samples (0.5-1 μg each) were labelled with Cy3 and Cy5 dyes respectively, purified, hybridized, and washed according to Nimblegen and Agilent protocols. Microarrays were scanned on a GenePix 4000B laser scanner (Axon Instruments, CA, USA) or a G2600D Agilent SureScan microarray scanner (Agilent Technologies). Data was processed using Nimblescan (Roche Nimblegen Inc) or Cytogenomics software (Agilent Technologies) with the default algorithms and analysis settings, but with a 5 probe minimum calling threshold. All arrays passed QC metrics for derivative log ratio spread (DLRS) values of <0.2. CNV data was visualised and interpreted using Genoglyphix

software (Perkin Elmer) and NCBI genome browser software (genome build hg19 (GRCh37)). The EqSCM aCGH data were assessed against many CNV databases including Genoglyphix Chromosome Aberration Database (containing over 14,000 validated variants from 50,000 samples) (Perkin Elmer, Waltham, MA, USA),[70] DECIPHER,[71] and the Database of Genomic Variation (DGV, containing CNV data from over 35,000 unaffected individuals).[72] CNVs were classified as thought to be benign (TBB), uncertain clinical significance (UCS), or clinically significant (CS) using an evidence-based approach[73-76] which included database comparisons (frequency in cases/controls and relation to phenotype), gene content, gene function and dosage sensitivity. A broad summary of our CNV interpretation algorithm is depicted in Figure S1. Rare CNVs are defined as those that occur at a frequency of ≤ 1%. We classified our rare CNV frequency using larger DGV studies containing >1000 individuals.[77-81]

Results

Exome Analysis

To test the potential for an essentially Mendelian predisposition to EqSCM, WES was carried out on 24 of the 28 Christchurch EqSCM cases. Several approaches to analysis of the identified variants were used, all of them hypothesising the involvement of gene variants with a low population minor allele frequency (MAF), that were over-represented in the EqSCM cohort. We carried out various iterations of filtering using variant allele frequency data derived from large population databases (1000 Genomes; NHBLI Exome Sequencing Project), followed by careful manual inspection of remaining variants. For example, excluding all variants present in these databases with an

allele frequency > 3%, and selecting for any present in at least 4/24 EqSCM exomes, identified variants in 131 genes, none of which proved to be convincing on closer analysis. We also carried out ranking of gene variants by predicted functional impact using various approaches.[61; 62; 82] Once again, none of the variants identified in these analyses proved to be significantly enriched amongst our EqSCM exomes.

Mitochondrial DNA reads can be recovered from exome data [83]. We carried out manual inspection of BAM files of mitochondrial DNA for our exome data compared with non-disease control exomes [84]. No unusual variants were detected in mitochondrial sequences of the EqSCM samples.

Finally, the 11 genes listed in Figure 2 of Goodloe et al (2014),[42] as well as a gene recently proposed to play a role in SCM, *BAG3*,[46] were carefully examined for presence of any rare variants in the EqSCM dataset. None of the previously identified variants,[42; 46] and no other convincing rare variants in these genes, were detected.

Cardio-MetaboChip Analysis

To test the possibility of a more complex, polygenetic basis to SCM risk, involving multiple variants of small effect size, Cardio-MetaboChip analysis was carried out. The Cardio-MetaboChip data for 27 EqSCM cases and 133 heart-healthy controls were compared by logistic regression (adjusted for ethnicity and gender, additive genetic model), first performed for pairwise comparisons across groups. No SNPs reached statistical significance of <0.05 after adjusting for

false discovery rate (FDR) when comparing either the EqSCM and HVOLs, or the EqSCM and CHD samples. To investigate whether the top 100 of these SNPs mapped to gene pathways that might assist in understanding potential disease mechanisms underlying SCM, pathway analysis of the leading 100 SNPs in the EqSCM versus HVOLs pairwise comparison was performed in MetaCore. Disease Biomarker Pathway analysis identified Myocardial Ischemia as the third most enriched pathway (FDR-adjusted $p=1.3e^{-2}$), featuring 11 SNP loci on our list out of 886 pathway objects, including annexin V, ANRIL, COL4A1, dynein, HXK4, nectin-2, PPAR-gamma, prolidase, Tcf(Lef), UGT, and VEGFR-2 .

aCGH Analysis

To test for potential involvement of CNVs in SCM, we applied aCGH to all cases. Of the 28 EqSCM cases examined by aCGH, twelve (42%) showed evidence of large, rare heterozygous CNVs classified as being of unclear clinical significance (Table 2), meaning that insufficient evidence is available for unequivocal determination of clinical significance.[73] Of these CNVs, seven were deletions and six were duplications. All of the CNVs were different, and there was no physical overlap between the various CNVs. Each of these rare CNVs encompasses one or more genes, or their immediate upstream regulatory regions, and many of the genes included within the CNVs have functions of cardiac relevance. A full list of all CNVs detected in the cohort is presented in Table S1.

Three cases (EqSCM 01, 06 and 19) harboured deletions very likely to impact genes of high relevance to cardiomyopathy or cardiac function. In EqSCM 01, intragenic deletion of *RBFOX1* results in a single copy loss of one exon used by the majority of transcripts predicted for the gene (Figure 1). This exon contains the start methionine for the RBFOX1 protein, meaning the gene is most likely rendered non-functional. *RBFOX1* is an important RNA-binding protein mediating the incorporation of microexons into many transcripts associated with neurological patterning and tissue development,[85; 86] particularly in the brain, heart and muscles. Intragenic deletions in *RBFOX1* have been observed in a range of conditions, including occasional cases with cardiac defects.[87; 88; 89] Furthermore, RBFOX1-mediated RNA splicing was also recently shown to be an important regulator of cardiac hypertrophy and heart failure[90].

In the second case (EqSCM 06, Figure. 2), a heterozygous deletion encompassed exon 2 and the majority of intron 2 of the *Glypican 5* (*GPC5*) locus. *GPC5* encodes a cell surface proteoglycan, which binds to the outer surface of the plasma membrane in the cardiovascular system and displays diverse functions including blood vessel formation after ischemic injury and proliferation of smooth muscle cells during atherogenesis.[91] *GPC5* was also implicated by GWAS as a protective locus for sudden cardiac arrest,[92] and other glypicans (GPC3, 4 and 6) have been associated with cardiac dysfunction.[93] This case (EqSCM 06) also harbours a duplication on 4q21.21 involving the ANXA3 gene, which encodes a member of the annexin family, annexin A3. Members of this calcium-dependent phospholipid-binding protein family have a range of functions in the regulation of cellular growth and signal transduction

pathways. Annexin A6 for example is the most abundant annexin expressed in the heart and its overexpression in mice has been shown to cause physiological alterations in contractility leading to dilated cardiomyopathy, while Annexin A6 knockout has been found to induce faster changes in Ca2+ transience and increased contractility.[94; 95] Alterations in expression and activity of annexins A5 and A7 have also been found to be associated with regulation of Ca2+ handling in the heart.[96] The function of annexin A3 is not fully understood, however it has been shown to play a role in endothelial migration and vascular development.[97]

The third case (EqSCM 19), contained a deletion at chr13q14.3. This region harbours at least 10 genes (*DLEU2, TRIM13, KCNRG, MIR16-1, MIR15A, DLEU1, DLEU1AS-1, ST13P4, DLEU7AS-1, DLEU7,* and *RNASEH2B-AS1*), including several non-coding RNAs (DLEU genes and micro-RNA genes) and a gene (*KCNRG*) encoding a protein involved in the regulation of voltage-gated potassium channel activity. The micro-RNA genes mir-16-1 and mir-15a in this interval have been implicated in a range of cardiovascular phenotypes, including a role for mir-15a in postnatal mitotic arrest of cardiomyocytes.[98-100] Two further chromosome 13 duplicated CNVs of approximately 150kb were classified as uncertain significance - one involving LINC00346 and ANKRD10 and the other containing ENOX1, postulated to affect vascular development based on zebrafish expression patterns[101] (Table 2).

Beyond these three cases, cardiac or relevant neurological impacts appeared likely for many of the other rare CNVs identified in EqSCM cases (Table 2, Figure 2, Table S1), several of which are discussed below.

A 96kb heterozygous deletion in EqSCM 03 disrupts all predicted transcripts of the chondrolectin gene (*CHODL*), a membrane bound C-type lectin involved in muscle organ development, whose protein product is detected in heart and skeletal muscle by immunohistochemistry.[102] In addition to this CNV, this patient carries a 1.94Mb duplication at 22q11.25, a locus containing 45 genes or miRNAs, associated with learning difficulties.[103; 104] This individual, who exhibited a degree of cognitive impairment, had consented for clinically relevant findings to be forwarded to their General Practice clinician, who subsequently recommended genetic counselling for this individual.

A 455kb duplication within EqSCM 04 at 1p34.1 affects the genes *GPBP1L1, TMEM69, IPP, MAST2,* and *PIK3R3*. Smaller rare duplications in this region have been reported by the DGV database[105] but none span the genes within this CNV. *GPBP1L1* is widely expressed in many tissues, including heart muscle[106] and predicted to be involved in transcriptional regulation. *TMEM69*, a gene of unknown function, is most strongly expressed in heart tissue.[106] IPP is a transcription factor with a 50 amino acid Kelch repeat known to interact with actin, while *MAST2* contains a PDZ domain and is another gene highly expressed in heart and skeletal muscle.[106] The protein product of *PIK3R3,* phosphoinositide-3-kinase regulatory subunit 3, acts downstream of G-protein-coupled receptors in cardiac function,[107] and is also a target for isoproterenol, which can trigger SCM-like conditions in humans and rodents.[12; 108-110]

374 Duplication of a long non-coding RNA (LOC101928358), the 3' segment of
375 *COL4A5* and the entire *IRS4* gene at Xq22.3 (9 probes, 113kb) was identified
376 within case EqSCM 05. IRS4 is an insulin receptor molecule expressed in heart
377 and skeletal muscle cells[111] and other tissues such as brain, kidney and liver.[112]
378 Duplication of *IRS4* may be of functional significance, although copy number
379 increases on the X chromosome of females may be counteracted to a degree by
380 random X inactivation. Of note is a Genoglyphix Chromosome Aberration
381 Database (GCAD[70]) case 52414 with a phenotype of low muscle tone, which
382 has an identical duplication at this locus (as well as a 1p33 deletion). With
383 regard to *IRS4*, Schreyer et al. (2003)[111] found a more restricted tissue
384 distribution than *IRS1* and *IRS2*, in primary human skeletal muscle cells and rat
385 cardiac muscle and isolated cardiomyocytes. Although IRS4 protein function is
386 still relatively unknown, the role of IRS proteins in general, acting as mediators
387 of intracellular signalling from insulin and insulin-like growth factor 1 receptors,
388 implicates IRS4 in cell growth and survival.[113] It is interesting to note that PI 3-
389 kinase (PI3K) signalling in HEH293T cells depends on IRS4, and that the IRS
390 proteins relay signals from receptor tyrosine kinases to downstream
391 components of signalling pathways,[111] which we note is a connection with the
392 *PIK3R3* gene duplicated in one of our other cases, EqSCM 04.
393
394 EqSCM 10 harboured a 130kb duplication of *NLRP7, NLRP2, GP6* and *RDH13*
395 at 19q13.42. One similar DGV duplication has been seen in this area
396 (nsv1062047[105]), but otherwise duplicated CNVs are generally much smaller
397 and rare. *NLRP2* and *NLRP7* are genes that encode members of the NACHT,
398 leucine rich repeat, and PYD containing (NLRP) protein family. These proteins

399 are implicated in the activation of pro-inflammatory caspases. Recessive
400 mutations ininin NLRP2/7 in humans are associated with reproductive
401 disorders.[114] Another gene in this duplicated cluster associated with disease is
402 *GP6*, a platelet membrane glycoprotein, involved in collagen-induced platelet
403 aggregation and thrombus formation, which is expressed at high levels in heart,
404 kidney and whole blood.[106] A *GP6* SNP (c.13254TC) has been implicated in
405 recurrent cardiovascular events and mortality.[115] Another study involving this
406 SNP,[116] found that hormone replacement therapy (HT) reduced the hazard ratio
407 (HR) of CHD) events in patients with the *GP6* 13254TT genotype by 17% but
408 increased the HR in patients with the TC+CC genotypes by 35% (adjusted
409 interaction $P < 0.001$). The authors found that in postmenopausal women with
410 established CHD, the *GP6* polymorphism, and another in *GP1B*, were predictors
411 of CHD events and significantly modified the effects of HT on CHD risk.[116]
412
413 Duplication of *PPL2*, *YPEL1* and *MAPK1* on chromosome 22q11.21 (180kb)
414 observed in EqSCM 11, does not appear in the DGV catalogue of CNVs in
415 healthy individuals, and the consequences of overexpression of these genes,
416 miRNAs or regulatory sequences are unknown. One of the affected genes,
417 *MAPK1* (previously named *ERK* or *ERK2*), may constitute a link to another
418 kinase intracellular signalling pathway – the RAF-MEK-ERK kinase cascade,
419 which in mice and human has an established role in the induction of cardiac
420 tissue hypertrophy.[117] Although not the kind of left ventricular enlargement seen
421 in SCM, subtle copy number variation at *MAPK1* may influence signalling
422 through this pathway. Another duplication in EqSCM 11 involving the 3' half of
423 *TSPAN7*, a member of the tetraspanin protein superfamily (Xp11.4) was noted

as rare, and a similar (though larger) duplication was recently observed in a patient with Rolandic epilepsy.[118]

An agenic duplication 50kb upstream from *NRG3* (10q23.1) was seen in case EqSCM 15. This CNV could conceivably disrupt upstream regulatory regions of *NRG3*, which encodes an important ligand for the transmembrane tyrosine kinase receptor ERBB4. NRG3 has been shown to activate tyrosine phosphorylation of its cognate receptor, ERBB4, and is thought to influence neuroblast proliferation, migration and differentiation by signalling through ERBB4. *NRG3* is a strong candidate gene for schizophrenia, and neuregulin molecules and their receptors are involved in rat cardiac development and maintenance.[119]

Finally, the two rare deletions observed on chromosome 13 (13q21.33 and 13q33.1) in case EqSCM 17, fall into largely uncharacterised areas of the genome. The first is agenic, although there is a prediction of a spliced EST in the NCBI database, and the second occurs as two 50kb blocks within the *ITGBL1* gene. *ITGBL1* is most strongly expressed in aorta.[120; 121]

Discussion

Monogenic and polygenic models of risk

The Christchurch earthquakes repeatedly exposed the entire population of the city, approximately 350,000 people, to major stress and life disruption. Almost all patients presenting with EqSCM were post-menopausal females, consistent with

449 other reports.[122] We set out to explore three categories of genetic contributions
450 to SCM predisposition, using WES to explore Mendelian models of risk, Cardio-
451 MetaboChip analysis to test for polygenic risk factors, and aCGH analysis to
452 evaluate the role of genomic structural variants.
453
454 Extensive analysis of the WES data did not yield any apparent enrichment of
455 rare, damaging variants within exome regions amongst the EqSCM cases.
456 Therefore, it seems unlikely that point mutations or small insertion-deletion
457 (indels) in a single gene underlie predisposition to earthquake SCM. A limitation
458 of this analysis is that it would have been unable to detect regulatory mutations,
459 or other important variants, not included or well represented within the captured
460 exome regions. Whole genome sequencing may therefore be warranted to
461 further test the hypothesis of Mendelian underpinnings of SCM, as this approach
462 could identify any regulatory variants not obtained with WES, and due to the
463 absence of a DNA capture step, would also provide more uniform coverage of
464 exons.
465
466 In a second approach, we explored the alternative hypothesis of polygenic risk
467 alleles of small effect size using a case-control association study, with
468 genotypes generated by the Cardio-MetaboChip. This chip allowed genotyping
469 of ~200,000 SNPs previously identified through genome‐wide association
470 studies (GWAS) for risk of metabolic, atherosclerotic and cardiovascular
471 diseases and traits.[123] The traits covered by the panel of genetic variants on the
472 chip include myocardial infarction (MI) and coronary heart disease (CHD), type 2
473 diabetes (T2D), T2D age diagnosed, T2D early onset, mean platelet volume,

474 platelet count, white blood cell, HDL cholesterol, LDL cholesterol, triglycerides,
475 total cholesterol, body mass index, waist hip ratio (BMI adjusted), waist
476 circumference (BMI adjusted), height, percent fat mass, fasting glucose, fasting
477 insulin, 2-hour glucose, HbA1c, systolic blood pressure, diastolic blood pressure
478 and QT interval. This analysis did not yield variants of genome-wide
479 significance in the SCM cases compared to either healthy controls or patients
480 with coronary disease. Exploratory pathway analysis suggested that the EqSCM
481 cases carried a greater burden of SNPs that mapped to a myocardial ischemia
482 pathway compared to the healthy controls, although this must be interpreted
483 with caution as our small sample set meant very limited statistical power. Two
484 limitations of this analysis were the relatively constrained content of the Cardio-
485 MetaboChip, which is less able to provide a rich dataset of genome-wide SNP
486 genotypes than the chips commonly used for GWAS, and the relatively small
487 cohort of cases available for study. Recruitment of a much larger SCM cohort
488 with a view to a well-powered GWAS with a more extensive genotyping chip
489 would therefore be a worthwhile future goal to more fully explore possible
490 polygenic underpinnings of this disorder. We note the recent publication of a
491 preliminary GWAS on 96 SCM cases and 475 healthy controls,[124] and believe
492 extension of this approach to larger cohorts is an important goal.
493
494 *Involvement of copy number variants*
495 CNVs have been implicated in many diseases since the recognition a decade
496 ago of their widespread distribution through the genome.[125-127] Of note, rare
497 CNVs are implicated in autism, epilepsy, schizophrenia, developmental delay
498 and intellectual disability.[105; 128-132] Cardiac conditions which involve CNVs

include congenital left-sided heart disease,[133; 134] congenital heart disease,[135; 136] some cases of long QT syndrome,[137] and Tetralogy of Fallot.[138] Our final analysis, therefore, was to explore the potential involvement of CNV in risk of EqSCM, using aCGH analysis of all cases. Results from this analysis were striking, with 42% of EqSCM cases having a rare CNV of unclear clinical significance. The CNV detection rate for diagnostic aCGH in childhood developmental disorders such as autism, developmental delay and intellectual disabilities, is approximately 20-30%.[139-141] A recent report of a large New Zealand aCGH case series (5,300 pre- and post-natal tests) reported CNVs in 28.3% of these clinically-selected cases.[142] Our observation of a rate of 42% for the EqSCM case series is significantly greater ($P < 0.02$) than rates for the enriched case cohorts normally referred for clinical aCGH testing[139-142]. The CNVs detected in EqSCM cases were all different, and there were no physical overlaps between them. This situation is similar to the pattern of CNVs seen in other conditions, including rolandic epilepsies[118] and congenital heart disease.[133; 135; 136] Many of the CNVs we observed are likely to impact genes of potential relevance to physiological processes implicated in SCM.

We have taken a relatively conservative approach to categorising CNVs, in terms of rarity and predicted functional significance. For example, we did not include two CNVs located at 9p24.3, involving individuals EqSCM 14 and 28 - a deletion and duplication, respectively. These CNVs encompassed a region including the large isoform of *DOCK8* gene. *DOCK8* encodes a protein implicated in the regulation of the actin cytoskeleton,[143] and *DOCK8* mutations cause autosomal recessive hyper-IgE syndrome.[144] One reported case of a

524 homozygous 129kb deletion in this region was associated with Graves's disease
525 and aortic aneurysm.[145] However, several deletions of *DOCK8* are recorded in
526 the DGV for unaffected individuals, therefore the CNVs in EqSCM 14 and 28
527 were categorised as TBB (thought to be benign). The approximately160kb
528 duplication in EqSCM 28 was larger than the 44kb deletion in EqSCM 14, and it
529 encompassed a second gene, *KANK1*. A small number of similar duplications
530 have been recorded in the DGV, and therefore we did not consider this to be
531 pathogenic. However, it is of interest that we see two relatively rare CNVs at this
532 locus in our small EqSCM cohort.
533
534 Of the twelve EqSCM cases with rare CNVs, we consider that three (EqSCM 01,
535 06 and 19) contain CNVs that affect genes of high relevance to cardiomyopathy
536 or cardiac function. The remaining candidate CNVs are also strong candidates
537 with potential functional relevance. In one of our most highly-ranked candidate
538 CNV containing cases (EqSCM 01) a large genomic deletion removes an exon
539 of *RBFOX1* which contains the start codon used by the majority of transcripts
540 predicted for the gene. A recent report by Gao *et al*. (2016) provided strong
541 functional data that would support our hypothesis of this gene's involvement as
542 a susceptibility locus for SCM[90]. Their work with mouse models has shown
543 RBFox1 deficiency in the heart promoted pressure overload–induced heart
544 failure, and induction of *RBFox1* over-expression in these murine pressure-
545 overload models, substantially attenuated cardiac hypertrophy and pathological
546 manifestations[90]. The haploinsufficiency seen in EqSCM 01 at the *RBFOX1*
547 locus may, in concert with other environmental or genetic factors, contribute to
548 SCM through reduced global RNA splicing changes in the heart.

Conclusion

Beginning with a cohort of 28 SCM cases triggered by two major earthquakes that caused extensive death and damage in Christchurch (New Zealand), we carried out exploratory analyses of three models for genetic predisposition to this disorder. Using WES and Cardio-MetaboChip genotyping analyses we did not detect an obvious role for exonic mutations in a monogenic model, or SNPs in a polygenic model, for SCM risk. However, our analysis of copy number variation in SCM cases revealed a high rate of occurrence of CNV categorised as of uncertain clinical significance. Most of the CNV we detected in SCM cases were rare, or not previously seen (Table 2).

These observations lead us to propose that SCM is a copy number variant disorder, whereby haploinsufficiency of genes overlapping deletions or over-expression of duplicated genes leads to relatively subtle modification of cardiac or adrenergic physiology, such that these individuals are at increased risk of suffering SCM when exposed to specific environmental triggers. Although no obvious single pathway relationships between the genes affected by these CNVs is apparent, most of the CNVs encompass loci relevant to cardiac function or cardioneuronal development.

In order to confirm whether SCM predisposition does indeed arise from CNVs, four key areas for future work need to be pursued. First, more widespread analysis is required of CNVs in many SCM cases. This would confirm whether our observation of a high rate of CNV in EqSCM also prevails in sporadic cases, and it will broaden the catalog of affected genes, helping to discern underlying

574 signalling networks and physiological processes. In addition, with increasing
575 numbers of cases, physical overlaps between CNVs in different individuals
576 should become apparent, pinpointing key genomic regions for more intensive
577 analysis. Second, the inheritance patterns of these CNVs must be established. It
578 is unclear what proportion are *de novo* versus inherited from either parent.
579 Third, there is a clear need for detailed physiological and gene expression
580 analyses on appropriate cells, including cardiomyocytes, derived from SCM
581 cases. Given the diversity of CNV seen in our SCM cases, this goal would most
582 effectively be achieved by generation of induced-pluripotent stem cell (iPSC)
583 lines from many patients and appropriate controls.[146; 147] Finally, although our
584 data implicate CNV as a significant genetic factor underlying SCM risk, it would
585 seem wise to pursue an effective GWAS strategy to identify other genetic
586 contributors to SCM and build on the initial study in this area.[124] International
587 initiatives to collate SCM cases[13] should therefore ensure that consented DNA is
588 available to provide appropriately large numbers of well phenotyped cases and
589 controls to facilitate this goal.
590
591 Finally, we hope our observations implicating CNV in this unique case series of
592 EqSCM will stimulate further studies of copy number variation in other SCM
593 cohorts, and lead to an improved understanding of this perplexing and intriguing
594 condition.
595

596 **Supplemental Data**

597 Supplemental Data include one figure and one table and can be found with this
598 article online at….

599

600 **Acknowledgements**

601 This study was supported by an Earthquake research grant jointly awarded by
602 the Health Research Council of New Zealand and Canterbury Medical Research
603 Foundation. This study makes use of data generated by the DECIPHER
604 community. A full list of centres who contributed to the generation of the data is
605 available from http://decipher.sanger.ac.uk and via email from
606 decipher@sanger.ac.uk. Funding for the project was provided by the Wellcome
607 Trust. We thank all participants for their agreement to be involved in this study,
608 and Alan Aitchison and Allison Miller for preparation of DNA samples and
609 Sanger sequencing analyses.

610

611

612 **Web Resources**

613 1000 Genomes project, http://www.internationalgenome.org/

614 ClinVar, https://www.ncbi.nlm.nih.gov/clinvar/

615 Database of Genomic Variation (DGV), http://dgv.tcag.ca/dgv/app/home

616 DECIPHER, https://decipher.sanger.ac.uk/

617 Exome Aggregation Consortium (ExAC), http://exac.broadinstitute.org

618 Galaxy, https://galaxyproject.org/

619 GTex, https://www.gtexportal.org/home/

620 HUGO Gene Nomenclature Committee, http://www.genenames.org

621 MutationTaster2, http://www.mutationtaster.org/

622 NHLBI GO Exome Sequencing Project (ESP),

623 https://esp.gs.washington.edu/drupal/

624 SeattleSeq annotation server, http://evs.gs.washington.edu/EVS/

625

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Figure titles and legends

Figure 1. CNV detected in EqSCM case 01. **A:** Chromosomal location of the CNV at the RBFOX1 locus of chromosome 16. **B:** Enlargement of the fifteen probe deletion (139kb, delimited by vertical green lines and blue shading) illustrating loss of the fMet-containing exon (pale blue vertical bar) for three major RBFOX1 isoforms. DGV track of known CNVs shown at bottom of figure, beneath the genes2 and regions of interest tracks. Graphical views from Genoglyphix (PerkinElmer) software.

Figure 2. Genome wide distribution of CNVs. CNVs detected in 12 (of 28) EqSCM individuals by aCGH analysis. Numbers beside arrows relate to EqSCM patient number. Red arrows denote deletions, blue arrows duplications. Note that EqSCM 03, EqSCM 06, EqSCM 11 carry two rare CNVs, while EqSCM 19 contains three.

Figure 1

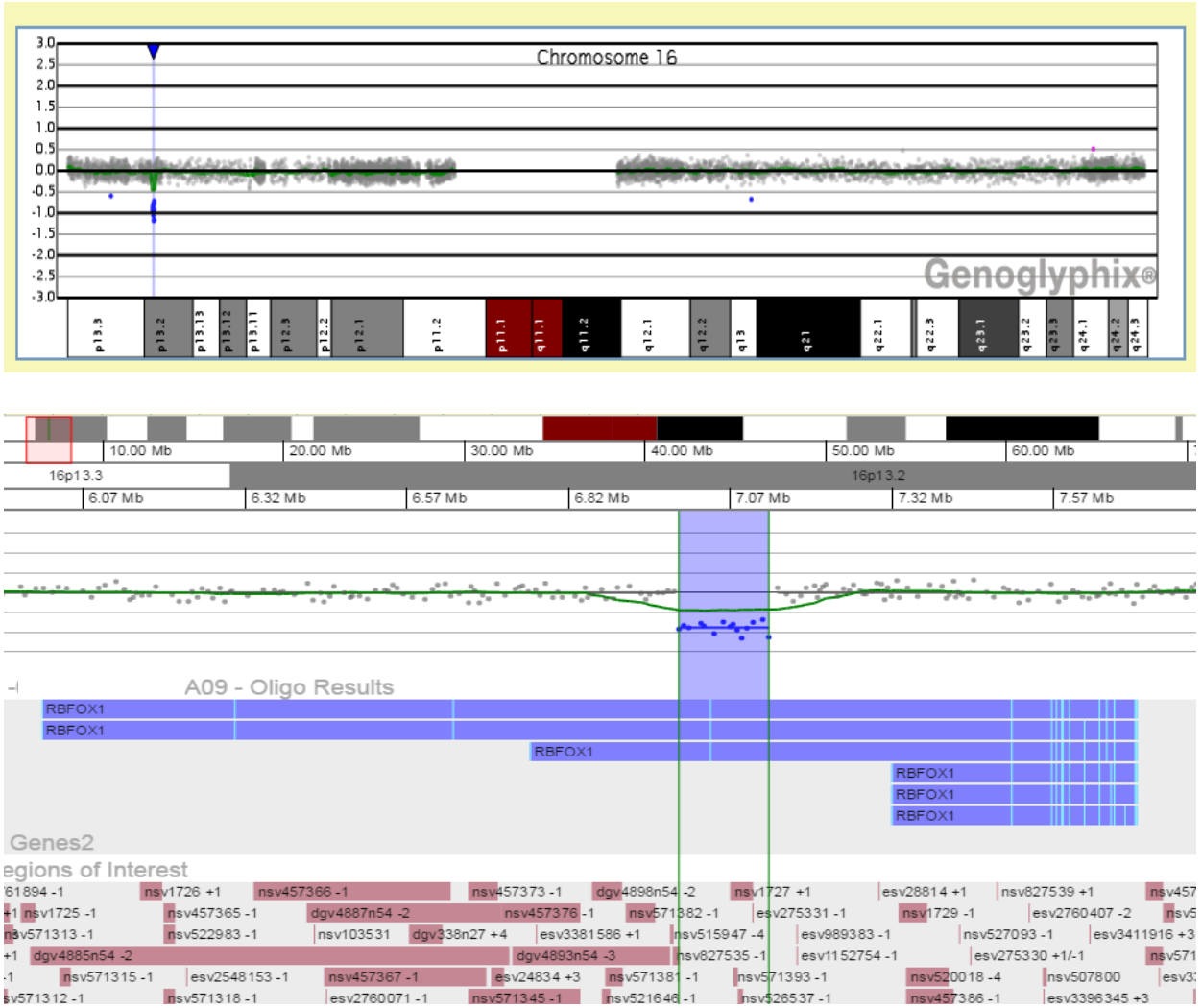

Figure 2.

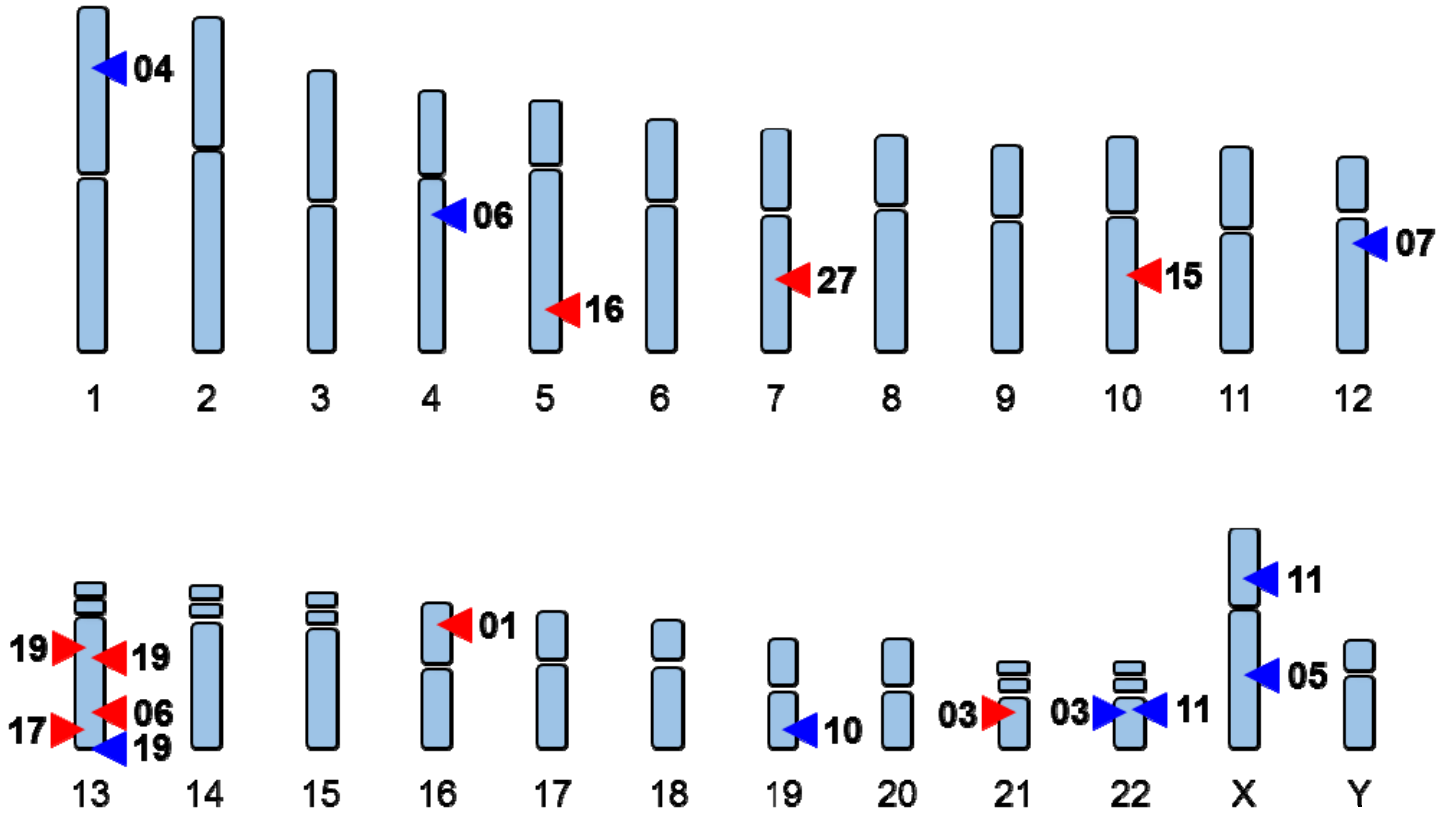

Table titles and legends

Table 1. SNP markers removed from Cardio-MetaboChip analysis in quality control

Stage of analysis	Number of SNPs	Comments
Assayed	196,725	
No genotype	10,927	
Mono allelic	28,367	
MAF <0.004	44,424	SNPs with only 1 minor allele found
Missing > 0.02 of samples	36,884	
HWE fail	130	HWE_P <1e-20 and 1.5x more heterozygotes than expected
Total Removed	65,622	Note that SNPs could fail on two or more of the criteria above
SNPs remaining in analysis	**131,103**	

Table 2. Rare CNVs detected in a cohort of 28 EqSCM cases.

Case ID	Prediction*	Location	Del/Dup	Key genes**	Size	Frequency	Location
EqSCM 01	UCS	16p13.2	DEL	RBFOX1**	139kb	1/20000	HG19 chr16:7,054,481-7,193,526
EqSCM 03	UCS	21q21.1	DEL	CHODL**	96kb	1/9000	HG19 chr21:19,537,178-19,633,275
	CS	22q11.26.1	DUP		2Mb		HG19 chr22:23,055,148-24,991,669
EqSCM 04	UCS	1p34.1	DUP	IPP** PIK3R3 (+3 others)	455kb	1/7000	HG19 chr1:46,144,479-46,599,815
EqSCM 05	UCS	Xq22.3	DUP	IRS4** COL4A5**	113kb	1/2000	HG19 chrX:107,896,435-108,009,609
EqSCM 06	UCS	13q31.5	DEL	GPC5**	207kb	1/5000	HG19 chr13:92,075,673-92,283,600
	UCS	4q21.21	DUP	FRAS1 ANX3** LINC01094	329kb	1/29000	HG19 chr4:79,281,048-79,610,796
EqSCM 07	UCS	12q13.13	DUP	17 Keratin genes	411kb	0	HG19 chr12:52,657,396-53,069,013
EqSCM 10	UCS	19q13.42	DUP	GP6**	130kb	1/15000	HG19 chr19:55,439,927-55,570,442
EqSCM 11	UCS	22q11.21	DUP	YPEL1** (+ 2 others)	180kb	0	HG19 chr22:22,008,249-22,189,094
	UCS	Xp11.4	DUP	TSPAN7**	140kb	1/1000	HG19 chrX:38,485,991-38,626,762
EqSCM 15	UCS	10q23.1	DUP	upstream NRG3**	78kb	0	HG19 chr10:83,506,502-83,585,097
EqSCM 17	UCS	13q33.1	DEL	ITGBL1**	148kb	0	HG19 chr13:102,148,514-102,296,766
EqSCM 19	?CS	13q14.2	DEL	KCNRG (+ 6 others)	886kb	0	HG19 chr13:50,585,186-51,452,033
	UCS	13q34	DUP	LINC00346, ANKRD10	146kb	0	HG19 chr13:111,385,673-111,532,564
	UCS	13q14.11	DUP	ENOX1**	149kb	0	HG19 chr13:89,219,432-89,359,036
EqSCM 27	UCS	7q31.1	DEL	LRRN3** IMMP2L	105kb	1/12000	HG19 chr7:110,744,611-110,849,681

*UCS = unclear clinical significance, ?CS = potential clinical significance. **Genes with clear cardiovascular association.
Frequency calculations are based on larger (>1000 individuals) studies included in the DGV.
A full list of all CNVs detected for each individual is presented in Supplementary Table 1.

Supplemental data

Table S1: Complete CNV detection list of EqSCM cases in this study. (Separate Excel spreadsheet).

Figure S1: CNV interpretation algorithm (Separate word file doc)