Supplementary Material for:

Leu C, Balestrini S, et al. (2015) Genome-wide polygenic burden of rare deleterious variants in sudden unexpected death in epilepsy.

Corresponding Author:
Prof. Dr. Sanjay M Sisodiya
Department of Clinical and Experimental Epilepsy
UCL Institute of Neurology
33 Queen Square
London WC1N 3BG
United Kingdom
Tel: +44 (0) 20 3448 8612
Fax: +44 (0) 20 3448 8615
Email: s.sisodiya@ucl.ac.uk

Supplementary Methods

Supplementary Results

Supplementary Methods

1. Sample collection

Collection of SUDEP samples for genetic studies provides an unusual level of challenge. SUDEP cannot be predicted, so there is no 'target' population. Collection after SUDEP is difficult to systematize, as by definition death is unexpected and cannot be anticipated, leading to logistic difficulties of obtaining material after death (Smithson *et al.*, 2014).

National Hospital for Neurology and Neurosurgery

At the National Hospital for Neurology and Neurosurgery, DNA samples have been collected from thousands of patients for an approved broad study of epilepsy genetics and pharmacogenomics. By chance, some of the individuals who gifted DNA samples sadly succumbed to SUDEP. These were the samples used in this study.

Wales Epilepsy Research Network (WERN), Swansea University

WERN has an accredited epilepsy BioBank with 3,000 samples including epilepsy families and specific cohorts and has IRAS approval for the infrastructure project. Samples submitted to this study were gifted by consent prior to the tragic SUDEP event. We thank the families for their post-SUDEP advocacy of the research and their positive bravery in the search for the cause.

Royal College of Surgeons in Ireland

At Beaumont Hospital / RCSI, Dublin, DNA samples have been collected from over 1,500 of patients with different types of epilepsy for an approved broad study of epilepsy genetics and pharmacogenomics. Using our epilepsy electronic patient record database we identified two patients from whom DNA had been collected and who had died of SUDEP. These samples were used in this study.

Epilepsy Research Centre, Melbourne

The Epilepsy Genetics Research Program at the Epilepsy Research Centre, Austin Health, University of Melbourne, has been fortunate to have many thousands of participants with epilepsy provide DNA samples over 25 years. Sadly, some participants have subsequently passed away from SUDEP. We thank our participants and their families for their ongoing support of our research, especially following such a tragic event.

Royal Hospital for Sick Children

At the Royal Hospital for Sick Children, Glasgow DNA samples have been collected from patients for clinical testing of epilepsy genes. A cohort of patients with *SCN1A*-related epilepsy was enrolled in a research project. By chance some of the individuals who gifted DNA samples sadly succumbed to SUDEP. These were the samples used in this study.

2. Intellectual Disability Assessment

All available clinical information for epilepsy cases was reviewed. Presence of intellectual disability was defined as an intelligence quotient < 70 from a previous psychometric assessment, with onset under 18 years of age, or systematic mention of "learning/intellectual disability" or "mental retardation" in the medical notes.

3. Statistical analysis for clinical phenotype

To compare the clinical features of the SUDEP cases and epilepsy controls, two-sample t-test or Wilcoxon rank-sum test were used for continuous variables showing Gaussian or non-Gaussian distributions, respectively. Pearson χ^2 test or Fisher's exact test, as appropriate according to the sample size in any of the cells of contingency tables, were used to compare categorical variables. Two-tailed *P*-values of the Fisher's exact test were calculated. Raw *P*-values are given in Table 1 and in Supplementary Table 2. Bonferroni correction of the nominal threshold for significance of 0.05 was subsequently applied. We had less than 10% missing data and we performed sensitivity analyses of deviations from the assumption of missing at random. Sensitivity analyses showed that missing data did not cause any bias to our results. We therefore present results for subjects with complete data. The amount of missing data for each clinical variable is noted in the footnotes of Table 1 and Supplementary Table 2. Data were analyzed using Stata (http://www.stata.com).

4. University College London exomes consortium

The University College London exomes consortium (UCL-exomes) is a consortium of researchers within University College London (London, UK) designed to aggregate raw read-level data from multiple exome sequencing projects in order to facilitate case-control association studies. At the time of this study, the UCL-exomes dataset included 3,412 samples (21 SUDEP, 128 epilepsy, and 3,263 non-epilepsy disease samples). The 3,263 non-epilepsy disease samples had no diagnosis of cardiac disease.

5. Whole-exome sequencing

Whole-exome sequencing for all 3,412 UCL-exomes samples (including 21 SUDEP and 128 epilepsy controls; pre-QC) was performed using Agilent, NimbleGen, and Illumina sequence capture with Illumina sequencing on HiSeq or GAIIx instruments. Fastq files were aligned with Novoalign (http://www.novocraft.com) against the reference human genome (GRCh37). Duplicate read removal, format conversion, and indexing were performed using Picard (http://broadinstitute.github.io/picard). The Genome Analysis Toolkit (GATK) (McKenna *et al.*, 2010) was used for variant calling, with Variant Quality Score Recalibration (VQSR) and separate models for SNPs and indels, following best practice (DePristo *et al.*, 2011; Van der Auwera *et al.*, 2013). Multi-sample variant calling was performed using the GATK HaplotypeCaller on 3,412 samples of the UCL-exomes consortium. We used the union of the different target regions for variant calling, +/- 100 base-pairs on each side of the target regions. Read depth was excluded from the recalibration model because of the large read depth variability generated by the heterogeneous capture kits used in the multiple studies aggregated in the UCL-exomes cohort.

6. Quality control (QC)

6.1 Variant QC

The following QC thresholds were applied for all variant calls using VCFtools (Danecek *et al.*, 2011): (i) GATK truth sensitivity 99.5% for single nucleotide variants (SNVs) and 95% for indels; (ii) genotype quality (GQ) $\geq$ 20 for homozygous and $\geq$ 40 for heterozygous calls; (iii) maximum two alleles; (iv) sample read depth (DP) of high-quality reads $\geq$ 10; (v) Hardy-Weinberg equilibrium (HWE) with $P > 10^{-20}$; (vi) call rate (CR) $\geq$ 1% in the 3,412 samples of the multi-sample call. 2,122,400 out of 3,238,068 variants called in 3,412 samples passed the QC thresholds.

6.2 Individual-level QC

To minimize the type I error rate on rare variant burden analyses (Luedtke *et al.*, 2011), only individuals of white European ancestry were included (self-reported, and by inspecting the first 20 coordinates of a multidimensional scaling analysis (MDS), Supplementary Fig. 1). Related individuals with a proportion of alleles shared identically by descent according to second-degree relatives and higher (π-hat $\geq$ 25%) were excluded. In addition, extensive sample QC was applied to ensure technical (sequencing assay) homogeneity of the remaining samples. Samples were excluded for the following criteria: (i) low sample CR one standard deviation (SD) from the mean; (ii) singleton rate two SD from the mean; (iii) heterozygosity rate two SD from the mean. Sample QCs were performed using PLINK (Purcell *et al.*, 2007). For MDS, per-individual heterozygosity and pairwise relatedness estimation, we used a trimmed set of variants (autosomal variants only, call rate $\geq$ 90%, minor allele frequency (MAF) $\geq$ 0.1%, and linkage disequilibrium $r^2 < 0.5$ for the MDS only). Singleton rates were calculated using PLINK/SEQ

(https://atgu.mgh.harvard.edu/plinkseq). Out of 21 SUDEP samples, 18 passed the individual-level QC; 87 out of 128 epilepsy controls, and 1,479 out of 3,263 UCL-exomes non-epilepsy disease controls (Fig. 1) passed the same stringent QC.

7. Prediction of variant deleteriousness

We used the recently published Combined Annotation Dependent Depletion method (CADD) (Kircher *et al.*, 2014), to predict the deleteriousness of variants. The CADD framework integrates multiple annotations into one metric, with the advantage that it allows the ranking of every variant, based on the predicted deleteriousness, among all GRCh37/hg19 reference SNVs (~8.6 billion). We used pre-scored files provided for download (version 1.1) and the CADD web interface to generate the CADD raw and scaled scores for all sequenced and QC-filtered variants (n = 2,122,400). The CADD raw scores were used to generate the cumulative per-individual burden scores for the genome-wide burden analysis. Scaled CADD scores were used to select the most deleterious variants (scaled CADD score ≥ 15; median value for all possible canonical splice site changes and non-synonymous variants) for the gene-based association analyses.

8. Variant Annotation and filtering

We used ANNOVAR (Wang *et al.*, 2010) to select variants based on the following criteria: (i) protein-changing variants according to the hg19 Reference Sequence (RefSeq) gene transcripts (UCSC Genome Browser, http://genome.ucsc.edu) (stop-gain/loss, splice-site variants within 2bp of an exon-intron boundary, frameshift/non-frameshift indels, and non-synonymous variants); (ii) not located within segmental duplications, to avoid artifacts due to paralogous sequence variation (Bailey *et al.*, 2001; Wang *et al.*, 2010). Out of 2,122,400 post-QC variants, 402,181 were classified as protein-changing. Out of 402,181 protein-changing variants, 203,089 variants, present with at least one non-reference allele in the samples which passed individual-level QC (18 SUDEP patients, 87 epilepsy controls, 1,479 UCL-exomes non-epilepsy disease controls), were selected for subsequent analyses. ANNOVAR was also used for subsequent filtering based on the MAF.

8.1 Variant filtering for genome-wide burden analyses only

The selected 203,089 protein-changing variants were filtered to be rare, defined by a MAF ≤ 0.5% (arbitrary, but commonly-used, threshold to define a rare variant (Tennessen *et al.*, 2012; Hunt *et al.*, 2013)) according to three publicly-available datasets: Exome Aggregation Consortium (ExAC) v0.2 non-Finnish Europeans (n = 34,427), NHLBI-ESP European-Americans (n = 4,300), and 1000genomes October 2014 Europeans (n = 503). Out of 203,089 protein-changing variants, 166,603 were selected as protein-changing and rare (or novel) variants for the genome-wide burden analyses.

Additional variant QC was applied for the genome-wide analyses to mitigate batch effects. Variant missing data rates were calculated using VCFtools in the SUDEP, epilepsy, and disease control samples separately. The generated missing data rates were used as custom databases for the annotation with ANNOVAR. Subsequently, only variants sequenced in more than 80% of each test group were retained. This method was more efficient in removing sequencing batch effects than a correction method based on target interval mean coverage of the three groups, as indicated by the coefficients of variation of the cumulative per-individual burden scores (Supplementary Table 5). A higher sequencing threshold for filtering did not lead to a lower variance of the values around their mean. Finally, 89,512 variants were included in the analysis.

8.2 Variant filtering for gene-based association analyses only

The selected 203,089 protein-changing variants were filtered to be novel according to (i.e. not present in) the ExAC v0.2 non-Finnish Europeans, NHLBI-ESP European-Americans, and 1000genomes October 2014 Europeans. Variants present in the epilepsy control cohort were also excluded. Following our unique variant strategy, we filtered the remaining variants to be exclusive to the SUDEP or exclusive to the disease control samples. We then selected the most deleterious variants, following the recommendations of the prediction software used (scaled CADD score ≥ 15; median value for all possible canonical splice site changes and non-synonymous variants).

VCFtools was used to generate the filtered datasets for association testing.

9. Variant validation for the gene-based association analyses

Aligned sequence data for 12 variants selected from six genes significantly associated with SUDEP in the gene-based association analyses and six singletons observed in genes implicated in either cardiac death or epilepsy, were visually inspected using the IGV browser (Robinson *et al.*, 2011).

9.1 Sanger sequencing

Confirmatory Sanger sequencing in the SUDEP samples was performed for the variants which passed the visual inspection. Primers for the regions of interest were designed using primer3 software (http://bioinfo.ut.ee/primer3/). Polymerase chain reaction (PCR) was performed according to the optimal conditions of the designed primers. PCR products were purified using ExoSAP-IT (Affymetrix, Santa Clara, CA, USA), and sequenced using BigDye v. 3.1 (Applied Biosystems) on an ABI3730xl automated DNA sequencer.

Supplementary Results

Supplementary Table 1. Details of the 18 SUDEP cases.

ID	Gender	Age of death	Epilepsy syndrome	SUDEP
4	F	7	DS	Definite
5	F	11	DS	Definite
6	M	6	DS	Definite
1	M	12	DS	Definite
37	F	42	Focal S.	Definite
39	M	20	Focal S.	Definite
48	M	18	Focal U.	Definite
38	F	32	GGE	Definite
3	F	3	DS	Probable
2	M	20	DS	Probable
41	M	44	Focal S.	Probable
46	M	46	Focal S.	Probable
47	M	67	Focal S.	Probable
43	M	35	Focal U.	Probable
40	M	38	Focal U.	Probable
45	M	40	Focal U.	Probable
44	M	32	UE	Probable
42	M	56	UE	Probable

Abbreviations: ID = identification number, SUDEP = sudden unexpected death in epilepsy, M = male, F = female, DS = Dravet Syndrome, Focal U. = Focal unknown aetiology, Focal S. = Focal symptomatic, GGE = Genetic Generalised Epilepsy, UE = Unclassified Epilepsy (Berg *et al.*, 2010).

Supplementary Table 2. Demographic and clinical features of Dravet Syndrome cases comparing those who died of SUDEP with living cases.
Bonferroni method was applied to correct for exposure to each AED and for the following known risk factors for SUDEP: gender, age at first seizure, epilepsy duration, total number of AEDs taken, subjects living alone in the 12-month period before last appointment or death, convulsive or nocturnal seizures in the 12-month period before last follow-up or death. Threshold for statistical significance after Bonferroni correction was set to $\alpha = 0.002$.

	Dravet Syndrome cases who died of SUDEP *n* = 6	**Living Dravet Syndrome cases *n* = 30**	**Uncorrected *P*-value**	**Test**
Mean age at last recorded follow-up/death, years (SD)	10 (6)	36 (11)	<0.001	t-test
Gender, n male (%)	3 (50)	12 (40)	0.677	Fisher's exact
Median age at first seizure occurrence, years (IQR)	0.7 (0.4-0.9)	0.6 (0.5-0.7)	0.732	Wilcoxon rank-sum
Mean epilepsy duration, years (SD)	9 (6)	35 (11)	<0.001	t-test
Intellectual disability	6 (100)	29 (97)	1	Fisher's exact
Total number of AEDs taken, median (IQR)	8 (5-10)	10 (9-11)	0.095	Wilcoxon rank-sum
Exposure to acetazolamide (%)	1 (17)	8 (27)	1	Fisher's exact
Exposure to carbamazepine (%)	4 (67)	29 (97)	0.066	Fisher's exact
Exposure to clobazam (%)	5 (83)	20 (67)	0.643	Fisher's exact
Exposure to ethosuximide (%)	0 (0)	8 (27)	0.302	Fisher's exact
Exposure to gabapentin (%)	1 (17)	9 (30)	0.655	Fisher's exact
Exposure to lacosamide (%)	0 (0)	4 (13)	1	Fisher's exact
Exposure to levetiracetam (%)	3 (50)	23 (77)	0.317	Fisher's exact
Exposure to lamotrigine (%)	5 (83)	26 (87)	1	Fisher's exact
Exposure to oxcarbazepine (%)	1 (17)	3 (10)	0.535	Fisher's exact
Exposure to phenobarbitone (%)	4 (67)	21 (70)	1	Fisher's exact
Exposure to phenytoin (%)	2 (33)	22 (73)	0.149	Fisher's exact
Exposure to pregabalin (%)	0 (0)	2 (7)	1	Fisher's exact
Exposure to primidone (%)	0 (0)	9 (30)	0.303	Fisher's exact
Exposure to stiripentol (%)	4 (67)	8 (27)	0.149	Fisher's exact
Exposure to topiramate (%)	5 (83)	20 (67)	0.643	Fisher's exact
Exposure to vigabatrin (%)	2 (33)	14 (47)	0.672	Fisher's exact
Exposure to sodium valproate (%)	6 (100)	29 (97)	1	Fisher's exact
Exposure to zonisamide (%)	0 (0)	7 (23)	0.317	Fisher's exact
Subject living alone in the 12-month period before last follow-up/death, n (%)	0 (0)	0 (0)	Not applicable	Not applicable
Convulsive seizures in the 12-month period before last follow-up/death, n (%)*	6 (100)	22 (82)	0.556	Fisher's exact
History of nocturnal seizures in the 12-month period before last follow-up/death, n (%)*	2 (33)	19 (70)	0.159	Fisher's exact

Abbreviations: SUDEP = sudden unexpected death in epilepsy, SD = standard deviation, IQR = interquartile range, *n* = number.

***** Missing data**:** convulsive seizures in the 12-month period before last follow-up/death (*n* = 3); history of nocturnal seizures in the 12-month period before last follow-up/death (*n* = 3)

Supplementary Table 3. *SCN1A* mutations identified prior to WES in the Dravet Syndrome patients who died of SUDEP.

ID	Variant Type	cDNA position	Predicted protein change	Inheritance	Number of mutations	SUDEP classification
1	splice site	c.4339-14T>G	unknown	de novo	1	Definite
2	nonsense	c.1738C>T	p.Arg580Ter	de novo	1	Probable
3	frameshift	c.5536_5539delAAAC	p.Lys1846SerfsTer11	de novo	1	Probable
4	nonsense	c.1837C>T	p.Arg613Ter	de novo	1	Definite
5	frameshift	c.5536_5539delAAAC	p.Lys1846SerfsX11	de novo	1	Definite
6	missense	c.4181C>T	p.Thr1394lle	de novo	1	Definite

Abbreviations: WES = whole exome sequencing, SUDEP = sudden unexpected death in epilepsy, ID = identification number, cDNA = complementary DNA.

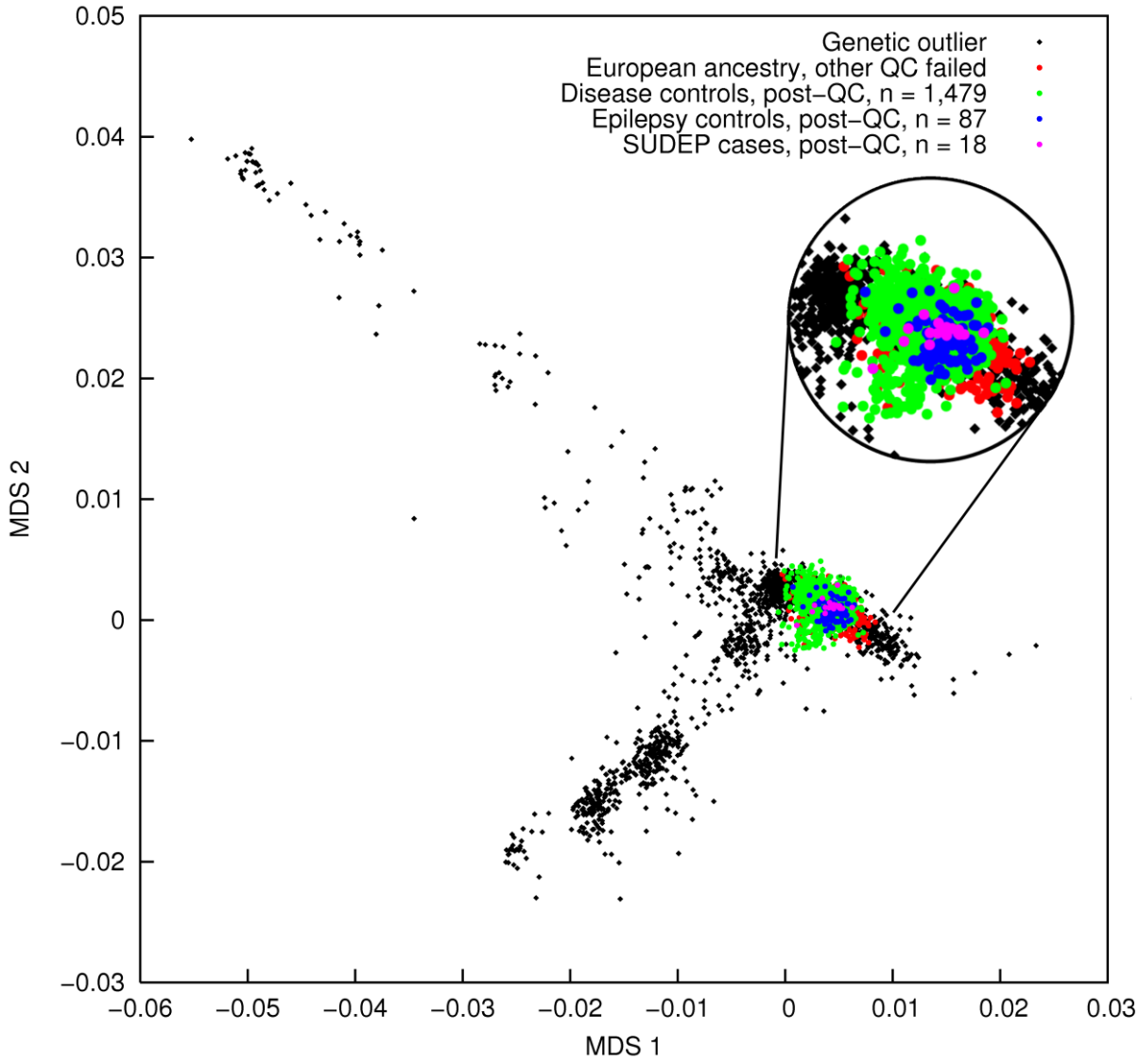
Supplementary Table 4. *SCN1A* mutations identified prior to WES in the living Dravet Syndrome cohort.

ID	Type	cDNA position	Predicted protein change	Inheritance	Number of mutations
7	frameshift	c.1714_1718delACAAG	p.Thr572ProfsTer5	de novo	1
8	in-frame deletion	c.2725_2727delATG	p.Met909del	not determined	1
9	missence	c.2729A>C	p.Glu910Pro	de novo	1
10	missense	c.3797A>C	p.Glu1266Ala	de novo	1
11	missense	c.4384T>C	p.Tyr1462His	de novo	1
12	missense	c.4568T>C	p.lle1523Thr	de novo	1
13	splice site	c.264+4_264+7delAGTG	unknown	de novo	1
14	missense	c.5639G>A	p.Gly1880Glu	One parent analysed, mother negative	1
15	nonsense	c.992delT	p.Leu331Ter	de novo	1
16	missense	c.2792G>A	p.Arg931His	not determined	1
17	premature stop codon	c.4369_4372dupCTGT	p.Tyr1458SerfsTer29	de novo	1
18	frameshift	c.111delC	p.Lys38AsnfsTer54	de novo	1
19	nonsense	c.1152G>A	p.Trp384Ter	father deceased, mother negative	1
20	missense	c.512T>A	p.Ile171Lys	de novo	1
21	frameshift	c.4062delT	p.Ile1356TyrfsTer4	de novo	1
22	frameshift	c.1209delT	p.Phe403LeufsTer12	father deceased, mother negative	1
23	nonsense	c.664C>T	p.Arg222Ter	de novo	1
24	missense	c.2792G>A	p.Arg931His	de novo	1
25	missense	c.302G>A	p.Arg101Gln	father deceased, mother negative	1
26	frameshift	c.4949dupT	p.Lys1651GlnfsTer22	de novo	1
27	missense	c.5119T>G	p.Phe1707Val	One parent analysed, mother negative	1
28	missense	c.2831T>A	p.Val944Glu	de novo	1
29	nonsense	c.4933C>T	p.Arg1645Ter	de novo	1
30	missense; nonsense	c.1811G>A; c.4573C>T	p.Arg604His; p.Arg1525Ter	father deceased, mother negative	2
31	nonsense	c.5436G>A	p.Trp1812Ter	de novo	1
32	splice site	c.2589+3A>T	unknown	de novo	1
33	Mutation not detected				
34	Mutation not detected				
35	Mutation not detected				
36	Mutation not detected				

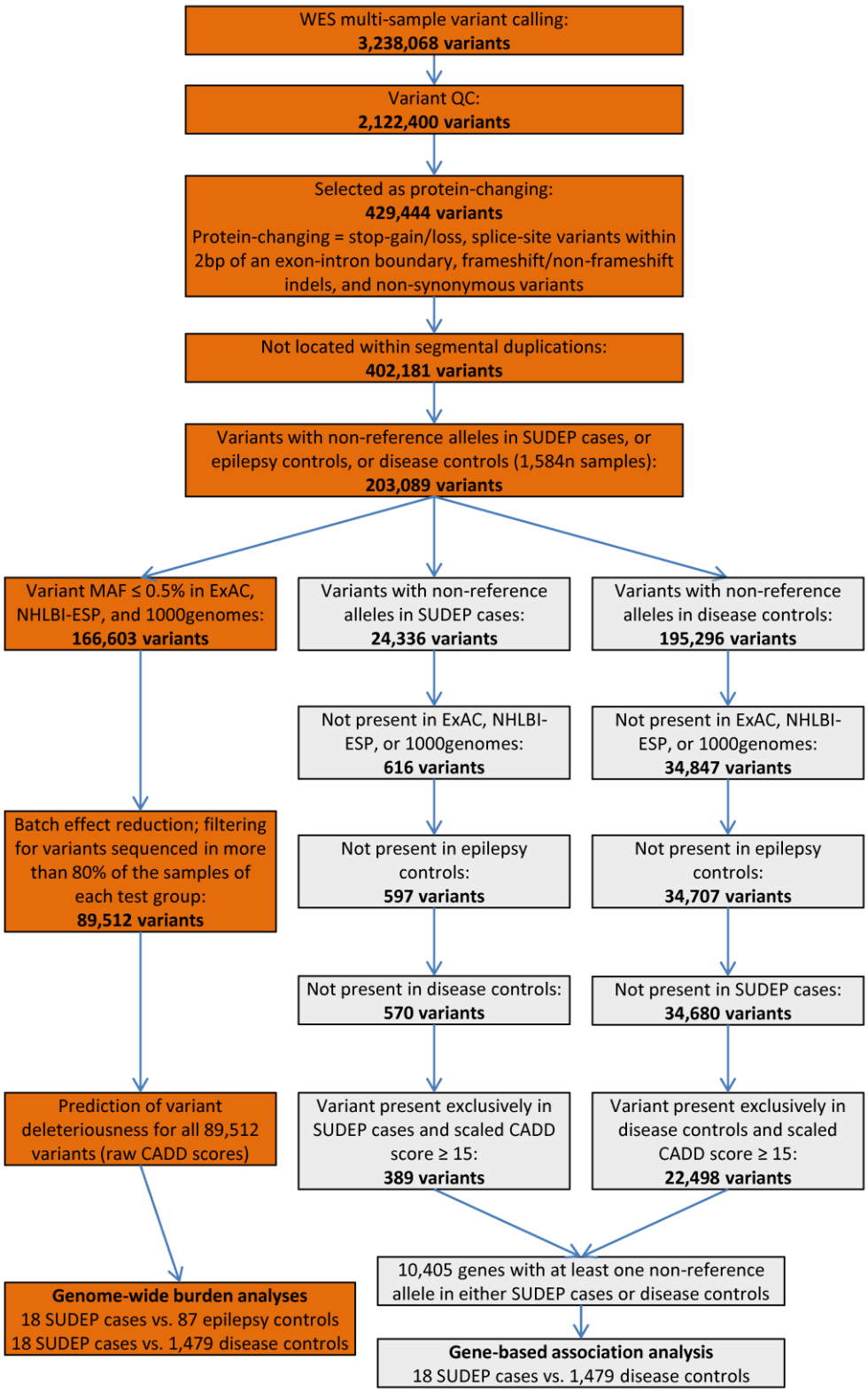
Abbreviations: WES = whole-exome sequencing, ID = identification number, cDNA = complementary DNA.

Supplementary Table 5. Coefficients of variation of the cumulative per-individual burden scores after applying different methods for batch correction.
The selected batch correction method with the lowest coefficient of variation in all samples (SUDEP, *n* = 18; epilepsy controls, *n* = 87; disease controls, *n* = 1,479) is shown in bold.

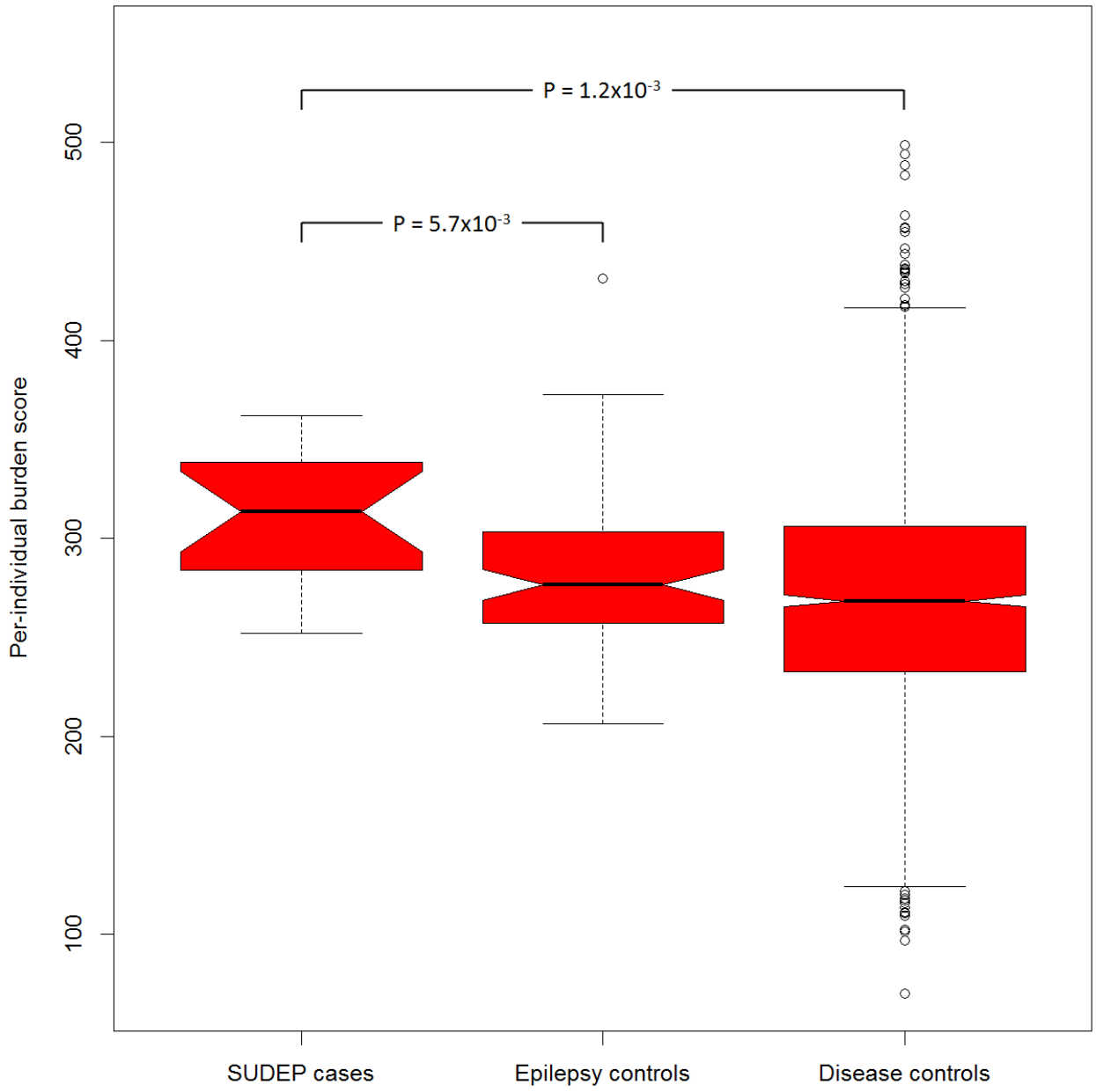
Batch correction method	Observations	Mean	Standard deviation	Coefficient of variation
Per variant				
Sequencing rate ≥ 70%	1,584	324.81	74.06	22.80
Sequencing rate ≥ 80%	**1,584**	**271.44**	**61.15**	**22.53**
Sequencing rate ≥ 90%	1,584	165.98	38.81	23.38
Per target interval				
Mean average coverage ≥ 10	1,584	444.92	101.27	22.76
Mean average coverage ≥ 30	1,584	350.56	82.78	23.61
Mean average coverage ≥ 50	1,584	180.57	45.58	25.24



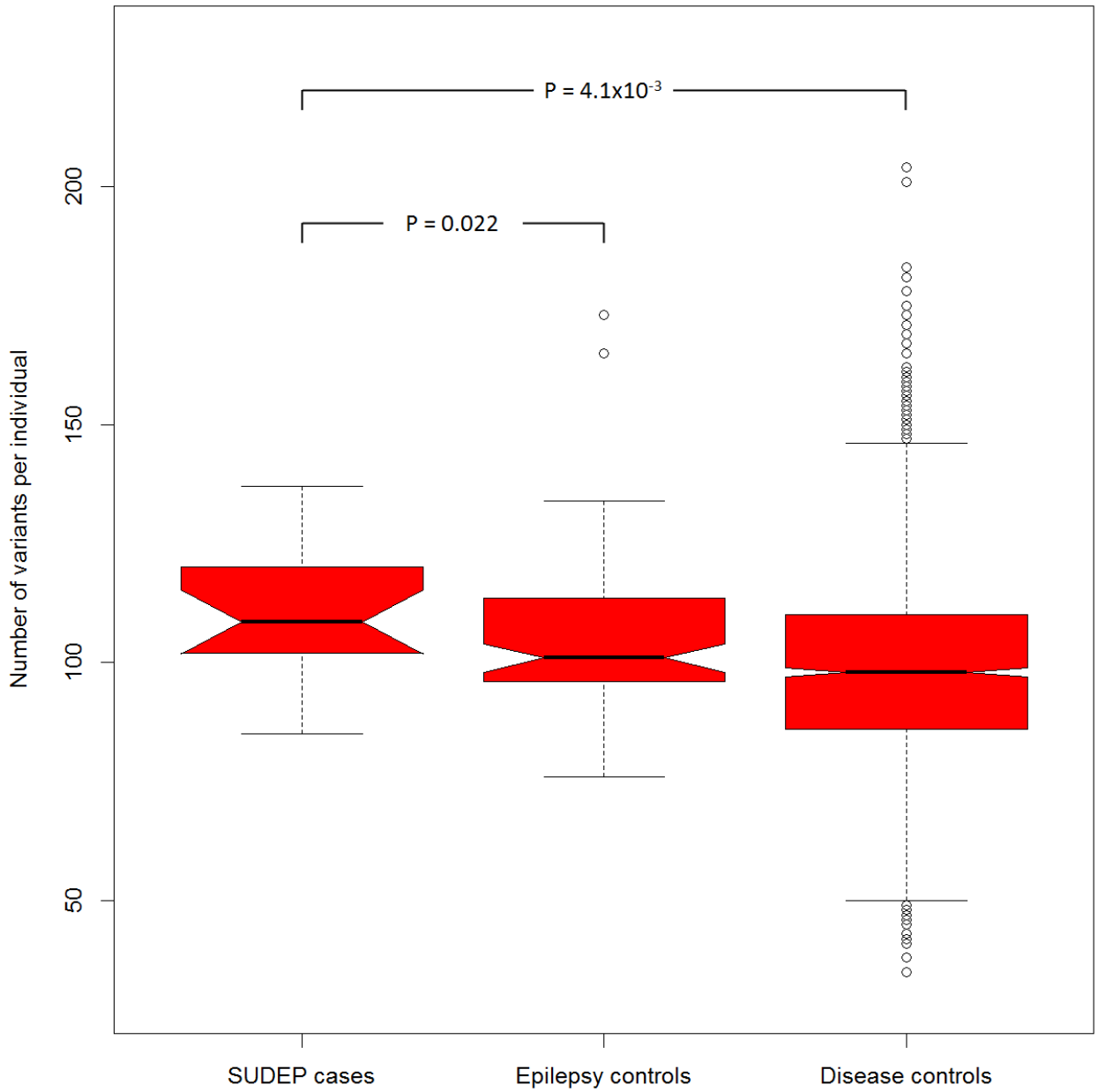
Supplementary Figure 1. Multidimensional scaling analysis. Plotted are 3,344 UCL-exomes samples after the first individual-level QC step (68 samples with low call rate filtered out). Each point within the scatter plot represents the individual coordinates of the first two dimensions of MDS analysis using 43,710 high-quality and uncorrelated variants. Genetic outliers for 20 MDS dimensions, indicated by black symbols, were removed as non-European samples from subsequent analyses. The zoomed area of the European cluster is indicated by black lines.



Supplementary Figure 2. Study design and variant filtering flowchart. Main part of the study (genome-wide burden analyses) is highlighted in dark orange. Secondary part (gene-based burden analyses) is highlighted in light grey. Abbreviations: WES = whole-exome sequencing, SUDEP = sudden unexpected death in epilepsy, ExAC = Exome Aggregation Consortium v0.2 non-Finnish Europeans (n = 34,427), NHLBI-ESP = NHLBI Grand Opportunity Exome Sequencing Project European-Americans (n = 4,300), 1000genomes = 1000 Genomes Phase 3 October 2014 Europeans (n = 503), MAF = minor allele frequency.



Supplementary Figure 3. Notched boxplot of the per-individual burden scores. Plotted are the per-individual burden scores for each test group. The thick black horizontal line is the median. The notched section represents the confidence interval around the median (median +/- 1.57 x IQR/$n^{0.5}$). According to Chambers *et al.* (1983) (Graphical Methods for Data Analysis, p. 62), there is "strong evidence" (95% confidence) that their medians differ when the notches of two boxes do not overlap. The box represents the IQR, while the whiskers extend to the furthest observations within ± 1.5 IQR of the lower (first) quartile and the upper (third) quartile. Empty dots represent outliers beyond 1.5 IQRs.



Supplementary Figure 4. Notched boxplot of the number of variants per individual. Plotted are the numbers of variants per individual of each test group. The thick black horizontal line is the median. The notched section represents the confidence interval around the median (median +/- 1.57 x IQR/$n^{0.5}$). According to Chambers *et al.* (1983) (Graphical Methods for Data Analysis, p. 62), there is "strong evidence" (95% confidence) that their medians differ when the notches of two boxes do not overlap. The box represents the IQR, while the whiskers extend to the furthest observations within ± 1.5 IQR of the lower (first) quartile and the upper (third) quartile. Empty dots represent outliers beyond 1.5 IQRs.

Supplementary Result 10: Whole exome sequencing coverage

Coverage information was generated using the DepthOfCoverage module in GATK. The union of the Agilent, NimbleGen, and Illumina target regions was used in order to obtain uniform coverage statistics across all samples corresponding to the multi-sample call.

SUDEP samples: The mean average coverage across the union of all target intervals was 55x. On average, 56% of all target bases achieved 20x or greater coverage (range 47-60%). The mean average coverage across all hg19 Reference Sequence exons was 68x.

Epilepsy samples: The mean average coverage across the union of all target intervals was 40x. On average, 48% of all target bases achieved 20x or greater coverage (range 33-81%). The mean average coverage across all hg19 Reference Sequence exons was 50x.

UCL-exomes (disease control) samples: The mean average coverage across the union of all target intervals was 45x. On average, 51% of all target bases achieved 20x or greater coverage (range 16-88%). The mean average coverage across all hg19 Reference Sequence exons was 56x.

Supplementary Result 11: Deleterious singleton variants in genes implicated in cardiac death or epilepsy causation

Of 373 genes with at least one non-reference variant present in the SUDEP cohort only (Supplementary Table 7), we also found deleterious variants in one gene implicated in sudden cardiac death (*CACNB2* (Antzelevitch *et al.*, 2007)) and five genes implicated in different epilepsy syndromes (*CNTN2* (Stogmann *et al.*, 2013), *GABRG2* (Baulac *et al.*, 2001), *MAGI2* (Marshall *et al.*, 2008), *POLG* (Uusimaa *et al.*, 2013), and *SYNGAP1* (Carvill *et al.*, 2013)), each present as a singleton in the SUDEP cohort.

Supplementary Table 6. Burden scores and variant numbers for the SUDEP and epilepsy control samples. The burden scores are calculated by summing the CADD scores for deleteriousness of every selected variant carried per individual**.**

ID	Group	Overall burden score	Number of variants
1	SUDEP	359.717	137
2	SUDEP	252.147	92
3	SUDEP	361.877	128
4	SUDEP	325.648	107
5	SUDEP	267.083	98
6	SUDEP	340.553	108
37	SUDEP	284.007	101
38	SUDEP	338.335	120
39	SUDEP	298.502	110
40	SUDEP	259.949	102
41	SUDEP	326.775	109
42	SUDEP	297.342	121
43	SUDEP	345.866	119
44	SUDEP	295.796	107
45	SUDEP	309.682	108
46	SUDEP	329.256	112
47	SUDEP	256.889	85
48	SUDEP	316.987	120
7	Epilepsy control	252.542	100
8	Epilepsy control	302.804	108
9	Epilepsy control	330.097	112
10	Epilepsy control	333.787	125
11	Epilepsy control	323.071	118
12	Epilepsy control	271.17	118
13	Epilepsy control	372.639	173
14	Epilepsy control	354.713	120
15	Epilepsy control	288.767	98
16	Epilepsy control	291.89	104
17	Epilepsy control	260.218	101
18	Epilepsy control	255.89	94
19	Epilepsy control	249.289	100
20	Epilepsy control	326.59	117
21	Epilepsy control	290.896	100
22	Epilepsy control	323.711	115
23	Epilepsy control	262.273	102
24	Epilepsy control	347.718	117
25	Epilepsy control	299.316	99
26	Epilepsy control	289.297	98
27	Epilepsy control	338.482	115
28	Epilepsy control	234.981	100
29	Epilepsy control	302.517	119
30	Epilepsy control	210.459	76

31	Epilepsy control	304.135	99
32	Epilepsy control	265.14	114
33	Epilepsy control	240.545	94
34	Epilepsy control	431.057	165
35	Epilepsy control	310.828	98
36	Epilepsy control	306.997	120
49	Epilepsy control	284.447	90
50	Epilepsy control	273.455	103
51	Epilepsy control	244.968	96
52	Epilepsy control	238.671	107
53	Epilepsy control	328.091	114
54	Epilepsy control	323.615	114
55	Epilepsy control	317.573	118
56	Epilepsy control	256.95	99
57	Epilepsy control	258.884	109
58	Epilepsy control	206.33	82
59	Epilepsy control	286.28	104
60	Epilepsy control	315.867	125
61	Epilepsy control	255.99	96
62	Epilepsy control	247.434	89
63	Epilepsy control	269.123	99
64	Epilepsy control	257.397	96
65	Epilepsy control	257.052	96
66	Epilepsy control	269.042	96
67	Epilepsy control	230.292	88
68	Epilepsy control	273.905	101
69	Epilepsy control	253.521	90
70	Epilepsy control	282.128	105
71	Epilepsy control	232.949	99
72	Epilepsy control	289.872	101
73	Epilepsy control	260.866	82
74	Epilepsy control	272.389	96
75	Epilepsy control	240.764	86
76	Epilepsy control	285.66	101
77	Epilepsy control	262.026	101
78	Epilepsy control	250.621	98
79	Epilepsy control	266.575	86
80	Epilepsy control	242.588	93
81	Epilepsy control	218.303	85
82	Epilepsy control	265.309	93
83	Epilepsy control	276.328	94
84	Epilepsy control	268.619	100
85	Epilepsy control	333.307	116
86	Epilepsy control	278.548	109
87	Epilepsy control	296.325	113
88	Epilepsy control	278.304	116
89	Epilepsy control	293.481	106

90	Epilepsy control	282.278	104
91	Epilepsy control	292.481	114
92	Epilepsy control	302.617	104
93	Epilepsy control	298.335	94
94	Epilepsy control	291.115	98
95	Epilepsy control	261.284	99
96	Epilepsy control	244.311	88
97	Epilepsy control	254.5	87
98	Epilepsy control	272.821	103
99	Epilepsy control	332.406	113
100	Epilepsy control	274.721	114
101	Epilepsy control	244.375	90
102	Epilepsy control	332.135	134
103	Epilepsy control	259.937	91
104	Epilepsy control	314.285	105
105	Epilepsy control	319.711	106

Supplementary Table 7. List of all 373 genes with at least one non-reference variant in the SUDEP cases. Genes with *P*-values surpassing the Bonferroni-corrected threshold for significance ($\alpha = 1.56 \times 10^{-3}$) are highlighted in grey. One gene with significant *P*-values but without Sanger confirmation is shown in red.

	Carrier of deleterious alleles				
Gene	Exclusive to SUDEP cases (*n*)	Exclusive to disease controls (*n*)	Burden *P*-value	C-alpha *P*-value	Comment
SCN1A	2	4	1.21E-03	1.61E-04	variants in SUDEP cases confirmed by Sanger sequencing
LGI1	2	2	3.12E-04	3.12E-04	variants in SUDEP cases confirmed by Sanger sequencing
PIK3C2A	2	1	3.12E-04	3.34E-04	one variant not confirmed by Sanger sequencing
SMC4	2	1	5.39E-04	5.39E-04	variants in SUDEP cases confirmed by Sanger sequencing
COL6A3	2	5	7.27E-04	7.27E-04	variants in SUDEP cases confirmed by Sanger sequencing
TIE1	2	4	1.48E-03	2.01E-03	variants in SUDEP cases confirmed by Sanger sequencing
MAGI2	1	3	8.93E-03	1.21E-02	epilepsy gene; variant in SUDEP case confirmed by Sanger sequencing
GABRG2	1	0	9.80E-03	1.40E-02	epilepsy gene; variant in SUDEP case confirmed by Sanger sequencing
CACNB2	1	1	2.14E-02	2.14E-02	sudden cardiac death gene; variant in SUDEP case confirmed by Sanger sequencing
CNTN2	1	6	2.67E-02	2.49E-02	epilepsy gene; variant in SUDEP case confirmed by Sanger sequencing
POLG	1	3	4.01E-02	3.12E-02	epilepsy gene; variant in SUDEP case confirmed by Sanger sequencing
SYNGAP1	1	2	4.71E-01	5.88E-01	epilepsy gene; variant in SUDEP case confirmed by Sanger sequencing
DNAH8	2	11	4.92E-03	3.62E-03	
VPS13D	2	7	3.61E-03	5.15E-03	
SYNE1	2	23	9.95E-03	6.64E-03	
MRPS6	2	1	1.02E-02	8.96E-03	
TENM3	2	9	7.33E-03	9.42E-03	
DNAH17	2	12	4.78E-01	3.91E-01	
ANO7	1	0	2.47E-03	2.03E-03	
HSPB7	1	0	2.34E-03	2.34E-03	
SLC9A3	1	0	3.12E-03	3.34E-03	
FLT3LG	1	0	4.04E-03	3.54E-03	
CENPP	1	1	3.17E-03	3.62E-03	
N4BP3	1	2	3.69E-03	3.69E-03	
CPE	1	0	3.95E-03	3.95E-03	
OSBPL6	1	0	7.39E-03	4.31E-03	
FCN1	1	2	1.22E-02	4.38E-03	
TOP3A	1	3	6.32E-03	4.42E-03	
POMGNT2	1	0	4.96E-03	4.63E-03	
TTC17	1	0	5.66E-03	4.67E-03	
PRAF2	1	0	5.45E-03	4.77E-03	

SLITRK2	1	1	1.48E-02	5.19E-03	
MPP7	1	0	7.69E-03	5.38E-03	
CD96	1	0	6.94E-03	5.40E-03	
RPL13A	1	0	7.23E-03	5.42E-03	
CYYR1	1	0	5.93E-03	5.53E-03	
FOPNL	1	0	4.86E-03	5.55E-03	
PITX2	1	0	4.25E-03	5.77E-03	
XPNPEP1	1	0	5.06E-03	5.78E-03	
R3HCC1L	1	0	7.87E-03	5.80E-03	
SFTPB	1	0	4.34E-03	5.88E-03	
PM20D2	1	0	6.31E-03	5.89E-03	
DHX32	1	0	5.57E-03	5.94E-03	
KLK7	1	0	6.38E-03	5.96E-03	
KIAA1549	1	0	8.13E-03	5.99E-03	
CRISP3	1	0	6.10E-03	6.10E-03	
CHMP2A	1	0	8.73E-03	6.11E-03	
TMED5	1	0	7.28E-03	6.37E-03	
ACTR10	1	0	8.70E-03	6.41E-03	
MAP10	1	0	6.42E-03	6.42E-03	
ZNF264	1	0	6.93E-03	6.47E-03	
ERCC1	1	0	8.49E-03	6.61E-03	
PKLR	1	0	8.51E-03	6.62E-03	
ST6GAL1	1	0	6.22E-03	6.66E-03	
PTGES2	1	0	8.63E-03	6.71E-03	
OTOA	1	0	5.59E-03	6.79E-03	
PSENEN	1	0	6.40E-03	6.86E-03	
THBS4	1	0	5.65E-03	6.87E-03	
SLC25A3	1	0	9.87E-03	6.91E-03	
TIMM9	1	0	7.90E-03	6.91E-03	
ZNF513	1	0	6.46E-03	6.92E-03	
OR2AP1	1	0	7.96E-03	6.96E-03	
C12orf10	1	0	6.53E-03	7.00E-03	
DNAJA3	1	0	8.01E-03	7.01E-03	
TERT	1	0	6.58E-03	7.05E-03	
ZNF451	1	0	6.18E-03	7.06E-03	
PDZD3	1	0	6.24E-03	7.13E-03	
HIST1H2BB	1	0	8.16E-03	7.14E-03	
TACC1	1	0	5.90E-03	7.16E-03	
PRSS21	1	0	8.29E-03	7.25E-03	
NSMAF	1	0	6.79E-03	7.27E-03	
SYAP1	1	0	8.44E-03	7.39E-03	
MON1A	1	0	5.77E-03	7.41E-03	
DMXL2	1	1	7.02E-03	7.53E-03	
BOLL	1	0	9.19E-03	7.57E-03	
MEX3A	1	1	1.03E-02	7.59E-03	
ACTA2	1	0	8.16E-03	7.61E-03	
WHSC1L1	1	1	7.71E-03	7.71E-03	

CCDC9	1	0	8.83E-03	7.73E-03	
ALOX12B	1	0	4.93E-03	7.75E-03	
NLK	1	1	8.86E-03	7.76E-03	
SPNS1	1	0	6.80E-03	7.77E-03	
PIGR	1	1	1.01E-02	7.88E-03	
SPTLC3	1	1	1.14E-02	8.01E-03	
ZCCHC9	1	0	8.07E-03	8.07E-03	
CPT1A	1	1	7.55E-03	8.09E-03	
MTAP	1	0	5.43E-03	8.15E-03	
PTPN5	1	0	1.05E-02	8.18E-03	
OR4B1	1	0	8.27E-03	8.27E-03	
SCML4	1	0	9.12E-03	8.51E-03	
TROVE2	1	0	9.74E-03	8.52E-03	
DYRK4	1	0	7.15E-03	8.68E-03	
SUCO	1	0	8.68E-03	8.68E-03	
GRHL3	1	0	6.43E-03	8.73E-03	
RBM12	1	0	7.30E-03	8.86E-03	
DLK2	1	1	1.46E-02	8.90E-03	
RPL32	1	0	7.79E-03	8.90E-03	
DSCAML1	1	0	1.02E-02	8.97E-03	
TBCEL	1	0	7.89E-03	9.01E-03	
WNT2B	1	1	1.10E-02	9.03E-03	
MFAP1	1	0	7.17E-03	9.22E-03	
TECPR2	1	1	1.08E-02	9.43E-03	
TMEM95	1	1	8.35E-03	9.54E-03	
CCDC60	1	0	7.47E-03	9.60E-03	
DACH2	1	0	1.03E-02	9.62E-03	
CORO1C	1	0	7.11E-03	9.65E-03	
NUP88	1	3	1.38E-02	1.01E-02	
NYNRIN	1	2	8.91E-03	1.02E-02	
ADAMTS12	1	5	1.32E-02	1.03E-02	
SLC24A4	1	1	1.03E-02	1.03E-02	
TANGO2	1	0	8.03E-03	1.03E-02	
NUMA1	1	2	1.48E-02	1.09E-02	
TCF7L2	1	0	8.62E-03	1.11E-02	
NR1H3	1	1	1.27E-02	1.11E-02	
TTC7A	1	1	9.77E-03	1.12E-02	
TSHZ3	1	0	1.05E-02	1.12E-02	
DENND6A	1	0	1.20E-02	1.12E-02	
INCA1	1	1	1.05E-02	1.13E-02	
SLC7A1	1	0	1.30E-02	1.13E-02	
OLFML2B	1	1	1.06E-02	1.14E-02	
SIPA1L2	1	1	1.73E-02	1.15E-02	
IPO5	1	1	1.57E-02	1.15E-02	
CTH	1	1	1.51E-02	1.18E-02	
NCKAP5	1	0	1.10E-02	1.18E-02	
NARF	1	2	1.65E-02	1.21E-02	

OR6C76	1	1	1.13E-02	1.21E-02	
GLB1L2	1	3	1.31E-02	1.22E-02	
PHKA2	1	1	1.22E-02	1.22E-02	
PRPH2	1	1	1.57E-02	1.22E-02	
CNBD2	1	1	8.63E-03	1.23E-02	
STRN	1	1	1.59E-02	1.24E-02	
MRPL50	1	0	1.25E-02	1.25E-02	
WDR12	1	1	1.04E-02	1.27E-02	
CWH43	1	1	1.12E-02	1.28E-02	
UNC13A	1	1	1.74E-02	1.28E-02	
VSIG8	1	0	8.97E-03	1.28E-02	
PRPF39	1	1	1.75E-02	1.29E-02	
NUDT9	1	1	1.29E-02	1.29E-02	
MASP2	1	3	1.21E-02	1.30E-02	
CSRNP3	1	0	1.08E-02	1.31E-02	
CHI3L2	1	0	1.34E-02	1.34E-02	
PPP3R1	1	1	1.64E-02	1.35E-02	
CEP97	1	1	1.05E-02	1.35E-02	
MFN1	1	1	1.11E-02	1.35E-02	
ZNF48	1	2	1.74E-02	1.35E-02	
STRIP2	1	2	1.55E-02	1.36E-02	
MTBP	1	1	1.45E-02	1.36E-02	
ACOXL	1	1	1.20E-02	1.37E-02	
KIF5C	1	1	1.29E-02	1.38E-02	
FN3KRP	1	1	1.08E-02	1.39E-02	
OR3A1	1	1	1.22E-02	1.39E-02	
KCNH1	1	1	1.09E-02	1.40E-02	
CTRL	1	1	1.83E-02	1.43E-02	
TNRC6C	1	1	1.14E-02	1.46E-02	
POLR3B	1	2	1.77E-02	1.46E-02	
ASXL1	1	1	1.67E-02	1.46E-02	
COG2	1	1	1.31E-02	1.50E-02	
SLC30A6	1	1	1.61E-02	1.50E-02	
CCDC33	1	1	1.11E-02	1.51E-02	
PPP1R12A	1	0	1.51E-02	1.51E-02	
PAPPA	1	1	1.62E-02	1.51E-02	
CHODL	1	2	1.53E-02	1.53E-02	
ERAP1	1	1	1.34E-02	1.53E-02	
TXNDC16	1	1	1.08E-02	1.55E-02	
HHAT	1	2	1.44E-02	1.55E-02	
LGALS13	1	1	1.67E-02	1.56E-02	
THAP1	1	1	1.56E-02	1.56E-02	
SCN11A	1	2	1.83E-02	1.60E-02	
NDST4	1	1	1.26E-02	1.62E-02	
ENOX1	1	1	1.86E-02	1.63E-02	
EBNA1BP2	1	1	1.87E-02	1.63E-02	
KCNB2	1	3	1.53E-02	1.64E-02	

FAM115A	1	1	1.76E-02	1.65E-02	
OLFML3	1	3	3.65E-02	1.65E-02	
CAD	1	7	1.49E-02	1.70E-02	
BAI3	1	1	1.19E-02	1.70E-02	
MRPS28	1	0	1.95E-02	1.71E-02	
RBM28	1	1	1.72E-02	1.72E-02	
EBF2	1	1	1.21E-02	1.72E-02	
RBCK1	1	1	1.42E-02	1.73E-02	
PZP	1	1	1.61E-02	1.73E-02	
CCNL2	1	1	1.85E-02	1.73E-02	
MDGA1	1	2	1.35E-02	1.73E-02	
BUB1B	1	3	2.12E-02	1.75E-02	
IL1RN	1	1	2.14E-02	1.76E-02	
TAC1	1	1	2.14E-02	1.77E-02	
TMED8	1	1	2.44E-02	1.79E-02	
TACR1	1	1	2.07E-02	1.81E-02	
BECN1	1	3	1.50E-02	1.82E-02	
KLHDC7A	1	2	1.61E-02	1.84E-02	
LRSAM1	1	2	1.85E-02	1.85E-02	
FAM171A1	1	2	2.12E-02	1.86E-02	
ZNF365	1	2	1.87E-02	1.87E-02	
LCMT2	1	3	1.92E-02	1.92E-02	
MAGEC2	1	1	2.89E-02	1.93E-02	
GOLGA4	1	4	2.50E-02	1.94E-02	
ART3	1	1	2.09E-02	1.96E-02	
GPALPP1	1	1	1.96E-02	1.96E-02	
DLC1	1	2	2.24E-02	1.96E-02	
RAB35	1	1	1.97E-02	1.97E-02	
CDK15	1	2	1.63E-02	1.98E-02	
NOC3L	1	1	2.12E-02	1.98E-02	
GLI2	1	3	2.83E-02	1.98E-02	
SIL1	1	3	2.13E-02	1.99E-02	
FAM168A	1	3	2.43E-02	2.00E-02	
DGKB	1	2	2.00E-02	2.00E-02	
NEMF	1	2	2.47E-02	2.03E-02	
SLC17A5	1	2	2.34E-02	2.04E-02	
CD97	1	1	1.69E-02	2.05E-02	
GAS2L3	1	1	1.92E-02	2.05E-02	
POLI	1	2	1.38E-02	2.07E-02	
CTNS	1	2	1.41E-02	2.11E-02	
MED12L	1	3	3.34E-02	2.12E-02	
ILF3	1	3	1.99E-02	2.14E-02	
HK2	1	2	2.60E-02	2.14E-02	
TPBG	1	1	2.01E-02	2.15E-02	
MAB21L1	1	1	2.62E-02	2.15E-02	
ETFA	1	2	2.47E-02	2.16E-02	
ZC3H7A	1	2	1.53E-02	2.19E-02	

PID1	1	2	2.19E-02	2.19E-02	
ZNF223	1	3	2.19E-02	2.19E-02	
IMPG2	1	1	2.36E-02	2.20E-02	
IPO9	1	1	2.06E-02	2.21E-02	
ATXN2	1	4	1.56E-02	2.22E-02	
MTMR3	1	1	2.54E-02	2.23E-02	
CDH7	1	1	2.24E-02	2.24E-02	
FRMPD3	1	4	1.31E-02	2.25E-02	
PHGDH	1	2	2.11E-02	2.26E-02	
NBEA	1	3	3.40E-02	2.27E-02	
NUB1	1	1	1.49E-02	2.34E-02	
LRRC17	1	2	2.51E-02	2.35E-02	
GPATCH3	1	2	1.96E-02	2.38E-02	
CCNB2	1	2	2.39E-02	2.39E-02	
ATM	1	6	3.42E-02	2.40E-02	
PRDM16	1	1	2.40E-02	2.40E-02	
CNTNAP5	1	3	2.59E-02	2.41E-02	
IL16	1	3	2.99E-02	2.46E-02	
NCOA2	1	2	2.07E-02	2.51E-02	
ATP9A	1	3	2.53E-02	2.53E-02	
ZNF470	1	2	2.72E-02	2.54E-02	
GNPDA1	1	2	2.76E-02	2.58E-02	
NDE1	1	2	2.96E-02	2.59E-02	
ERCC3	1	3	2.28E-02	2.61E-02	
PKD1L1	1	3	2.46E-02	2.64E-02	
RABGAP1L	1	4	3.21E-02	2.65E-02	
FNIP1	1	3	1.96E-02	2.66E-02	
CWF19L1	1	2	2.48E-02	2.66E-02	
NCF2	1	3	2.86E-02	2.67E-02	
TRAPPC9	1	2	1.97E-02	2.67E-02	
AKT1	1	3	2.69E-02	2.69E-02	
BRCA2	1	6	2.51E-02	2.69E-02	
NFAT5	1	3	2.36E-02	2.69E-02	
MLLT4	1	0	3.09E-02	2.71E-02	
RBM23	1	3	2.74E-02	2.74E-02	
NR1H4	1	2	3.23E-02	2.82E-02	
CAPN11	1	1	2.00E-02	2.85E-02	
FERMT1	1	4	2.51E-02	2.87E-02	
TBC1D15	1	1	2.37E-02	2.88E-02	
PNMAL1	1	3	2.03E-02	2.90E-02	
CCKAR	1	4	3.11E-02	2.90E-02	
CEP76	1	7	3.37E-02	2.95E-02	
ZDHHC5	1	1	3.24E-02	3.02E-02	
COL6A6	1	2	1.96E-02	3.08E-02	
RFX2	1	3	2.54E-02	3.09E-02	
ATXN7	1	3	4.95E-02	3.15E-02	
LDHAL6A	1	1	2.95E-02	3.16E-02	

PRCP	1	3	3.66E-02	3.20E-02	
CD207	1	3	3.90E-02	3.21E-02	
PARD3	1	3	3.45E-02	3.22E-02	
ITGAE	1	3	2.38E-02	3.23E-02	
PSD4	1	3	2.83E-02	3.23E-02	
GPR37	1	3	4.10E-02	3.33E-02	
SOX6	1	2	4.56E-02	3.36E-02	
PRKCH	1	3	3.38E-02	3.38E-02	
CFAP43	1	3	5.33E-02	3.39E-02	
MTRF1	1	3	2.81E-02	3.41E-02	
PSTK	1	2	3.95E-02	3.42E-02	
PRKD3	1	4	2.31E-02	3.47E-02	
SEC24C	1	5	3.48E-02	3.48E-02	
DLD	1	2	3.49E-02	3.49E-02	
VPS41	1	5	6.23E-02	3.52E-02	
SALL4	1	3	3.33E-02	3.57E-02	
CEP128	1	4	3.60E-02	3.60E-02	
TFDP2	1	1	3.01E-02	3.66E-02	
MSL2	1	3	3.26E-02	3.72E-02	
TTC3	1	4	4.87E-02	3.72E-02	
GUCY1A2	1	1	3.09E-02	3.75E-02	
NUP98	1	3	3.54E-02	3.80E-02	
ABHD8	1	1	3.53E-02	3.80E-02	
ANKRD50	1	4	3.82E-02	3.82E-02	
NBAS	1	4	4.19E-02	3.89E-02	
MKI67	1	6	5.42E-02	3.92E-02	
TRPM7	1	3	2.50E-02	3.92E-02	
PSMD13	1	3	4.02E-02	4.02E-02	
ARHGAP30	1	6	5.70E-02	4.11E-02	
MARCH8	1	4	5.43E-02	4.15E-02	
PIKFYVE	1	3	4.22E-02	4.22E-02	
PCNXL4	1	1	4.05E-02	4.36E-02	
PLCG2	1	4	2.83E-02	4.45E-02	
TDRD9	1	6	9.31E-02	4.48E-02	
NUP205	1	8	4.18E-02	4.50E-02	
NFATC3	1	5	3.14E-02	4.71E-02	
ATF7IP	1	4	4.17E-02	4.81E-02	
CLUH	1	3	3.06E-02	4.81E-02	
SLC25A32	1	2	4.92E-02	4.92E-02	
ITPR1	1	7	5.08E-02	5.08E-02	
GBA2	1	4	2.55E-02	5.10E-02	
OR5M10	1	2	6.00E-02	5.20E-02	
PIGN	1	3	4.00E-02	5.23E-02	
NCAPD3	1	3	4.87E-02	5.24E-02	
PHLDB2	1	4	6.15E-02	5.33E-02	
KIAA2018	1	6	4.68E-02	5.40E-02	
TTLL6	1	3	6.96E-02	5.65E-02	

EML5	1	4	6.70E-02	5.80E-02	
CYP2R1	1	5	8.52E-02	5.83E-02	
CCDC141	1	7	5.88E-02	5.88E-02	
PTPRT	1	3	3.83E-02	5.90E-02	
USP24	1	8	1.03E-01	6.07E-02	
MATN2	1	4	4.83E-02	6.32E-02	
GPR125	1	5	6.47E-02	6.47E-02	
LRP1B	1	14	9.60E-02	6.57E-02	
THADA	1	8	1.12E-01	6.95E-02	
KCNQ5	1	4	5.65E-02	6.96E-02	
ERICH2	1	2	6.07E-02	7.01E-02	
PCDH15	1	6	5.73E-02	7.05E-02	
DNAH3	1	11	8.20E-02	7.10E-02	
PTPRD	1	5	6.44E-02	7.43E-02	
MYO10	1	6	5.49E-02	7.59E-02	
PPL	1	38	7.30E-02	7.87E-02	
LAMA2	1	8	8.54E-02	7.93E-02	
FER1L6	1	7	9.76E-02	7.93E-02	
FRYL	1	6	6.63E-02	8.67E-02	
CDH1	1	6	7.18E-02	8.84E-02	
LAMC1	1	8	7.56E-02	1.05E-01	
PKHD1L1	1	14	2.37E-01	2.03E-01	
PITPNM1	1	2	5.33E-01	3.33E-01	
LOXHD1	1	14	5.00E-01	3.75E-01	
BEAN1	1	2	5.22E-01	3.91E-01	
TRIM56	1	1	6.09E-01	3.91E-01	
MARK2	1	2	2.86E-01	4.29E-01	
MKNK1	1	2	3.57E-01	4.29E-01	
PI4KA	1	2	4.44E-01	4.44E-01	
USP25	1	2	6.67E-01	4.44E-01	
MPP3	1	1	6.11E-01	4.44E-01	
ARHGEF1	1	2	4.29E-01	4.76E-01	
CACNA1B	1	7	6.25E-01	5.00E-01	
MICAL3	1	6	6.88E-01	5.00E-01	
RARG	1	2	5.63E-01	5.00E-01	
COL11A2	1	6	5.33E-01	5.33E-01	
ASB6	1	4	5.33E-01	5.33E-01	
EPHB2	1	3	5.33E-01	5.33E-01	
GLTPD2	1	3	6.92E-01	5.38E-01	
PPAPDC2	1	1	5.38E-01	5.38E-01	
MYO7A	1	9	4.44E-01	5.56E-01	
ZNF831	1	3	3.91E-01	5.65E-01	
JUN	1	2	8.33E-01	5.83E-01	
PHF2	1	3	8.00E-01	6.00E-01	
SYNPO2L	1	3	7.00E-01	6.00E-01	
GAREM	1	1	3.91E-01	6.09E-01	
NCOR2	1	9	5.00E-01	6.25E-01	

ZNF335	1	3	4.09E-01	6.36E-01	
TLE2	1	6	5.33E-01	6.67E-01	
LAMA5	1	4	6.67E-01	6.67E-01	
EMILIN1	1	2	4.44E-01	6.67E-01	
COL6A2	1	7	5.38E-01	6.92E-01	
TTN	1	85	7.14E-01	7.14E-01	
RNH1	1	2	7.14E-01	7.14E-01	
BLOC1S5	1	1	8.57E-01	7.14E-01	
FBRSL1	1	3	4.44E-01	7.78E-01	
OTOG	1	24	8.33E-01	8.33E-01	
MAST2	1	12	8.33E-01	8.33E-01	
STRA6	1	1	8.33E-01	8.33E-01	
ITGA4	1	7	7.14E-01	8.57E-01	

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