Supp. Data Table S4 VUS4-VUS0 in our SIDS cohort

Case	Gender	Age (mo)	SIDS category	rs-Nr.	Gene	HGVS genomic RefSeq-Nr.	HGVS Refseq-Nr.	Coding Effect	Location	c.DNA	Protein change	dbSNP ALLMAF	espEAMAF	Human Gene Mutation Database (HGMD)-Phenotype	HGMD Variant class	associated disease	AGVGD	SIFT	MAPP	MutationTaster	Grantham distance	polyphen2	ExAC EURMAF (non-finnish)	1000 Genomes EURMAF	Coverage	Alternative Allele	Sanger confirmed	in-house database[a]	subclass based on scoring scheme
SIDS001	F	9	2	rs17848485	*CPT2*	NG_008035.1	NM_000098.2	missense	exon	c.1634A>C	p.(Glu545Ala)	0.0010	0.0000	Hypercholesterolaemia	DM?	SPCD	C65	Deleterious	bad	disease-causing	107	probably damaging	0.0000	0.0030	34	0.38	√	NA	VUS3
SIDS001	F	9	2	rs144848998	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.6228G>T	p.(Lys2076Asn)	0.0000	0.0000	-	-	LQTS	C0	Deleterious	good	disease-causing	94	possibly damaging	0.0000	0.0010	62	0.37	NA	NA	VUS2
SIDS001	F	9	2	rs149331873	*AGL*	NG_012865.1	NM_000028.2	missense	exon	c.2657C>T	p.(Pro886Leu)	0.0000	0.0000	-	-	GSD	C0	Tolerated	unknown	disease-causing	98	benign	0.0000	0.0000	87	0.43	NA	NA	VUS1
SIDS001	F	9	2	rs200130356	*FLNA*	NG_011506.1	NM_001110556.1	missense	exon	c.4451A>G	p.(Gln1484Arg)	0.0010	0.0015	Mental retardation	DM	heterotopia	C35	Deleterious	bad	polymorphism	43	benign	0.0016	0.0000	25	0.40	NA	NA	VUS1
SIDS004	M	7	2	rs199583774	*PKP2*	NG_009000.1	NM_004572.3	missense	exon	c.2083C>T	p.(Arg695Cys)	0.0000	0.0000	-	-	ARVC	C25	Deleterious	bad	disease-causing	180	probably damaging	0.0001	0.0010	70	0.43	NA	NA	VUS4
SIDS005	M	4	1	rs142890619	*COL5A1*	NG_008030.1	NM_000093.3	missense	exon	c.598G>A	p.(Asp200Asn)	0.0000	0.0010	-	-	EDS	C0	Deleterious	bad	disease-causing	23	probably damaging	0.0000	0.0010	107	0.47	NA	NA	VUS3
SIDS007	F	8	2	rs143641133	*DOLK*	NG_017009.1	NM_014908.3	missense	exon	c.1324G>A	p.(Ala442Thr)	0.0000	0.0000	-	-	DCM	C0	Deleterious	bad	disease-causing	58	probably damaging	0.0000	0.0010	131	0.36	√	NA	VUS3
SIDS007	F	8	2	rs121913013	*DSG2*	NG_007072.3	NM_001943.3	missense	exon	c.166G>A	p.(Val56Met)	0.0000	0.0035	ARVC	DM	ARVC	C0	Deleterious	good	disease-causing	105	probably damaging	0.0006	0.0010	46	0.35	NA	NA	VUS1
SIDS008	F	4	1	rs145425478	*DTNA*	NG_009201.1	NM_001390.4	missense	exon	c.1757C>T	p.(Pro586Leu)	0.0000	0.0000	-	-	LVNC	C0	Deleterious	good	disease-causing	98	probably damaging	0.0000	NA	54	0.50	NA	NA	VUS1
SIDS008	F	4	1	rs200130356	*FLNA*	NG_011506.1	NM_001110556.1	missense	exon	c.4451A>G	p.(Gln1484Arg)	0.0010	0.0015	Mental retardation	DM	heterotopia	C35	Deleterious	bad	polymorphism	43	benign	0.0016	0.0000	43	0.47	NA	NA	VUS1
SIDS009	M	2	2	rs151254520	*ACADVL*	NG_007975.1	NM_001270447.1	missense	exon	c.1963C>T	p.(Arg655Cys)	0.0000	0.0002	-	-	MCAD	C0	Deleterious	bad	disease-causing	180	possibly damaging	0.0006	NA	123	0.32	NA	NA	VUS2
SIDS009	M	2	2	~	*SMAD9*	NG_016963.1	NM_001127217.2	nonsense	exon	c.811C>T	p.(Gln271*)	NA	NA	-	-	PAH	NA	NA	NA	disease-causing	NA	NA	NA	NA	58	0.41	NA	0.0000	VUS2
SIDS010	F	3	2	rs200473206	*DSP*	NG_008803.1	NM_004415.2	splice site	splice site	c.273+5G>A	p.(?)	0.0000	0.0005	ARVC	DM	ARVC	NA	NA	NA	NA	NA	NA	0.0005	NA	62	0.48	NA	NA	VUS3
SIDS010	F	3	2	rs141121553	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.6062G>A	p.(Arg2021His)	0.0000	0.0000	-	-	MVP	C25	Deleterious	bad	polymorphism	29	possibly damaging	0.0000	0.0000	94	0.41	NA	NA	VUS2
SIDS010	F	3	2	rs117360770	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.9148C>G	p.(Leu3050Val)	0.0020	0.0010	-	-	EDMD	C25	Deleterious	bad	NA	32	probably damaging	0.0020	0.0020	115	0.46	NA	NA	VUS1
SIDS011	M	2	1	rs71352737	*TRPM4*	NG_027551.1	NM_017636.3	nonsense	exon	c.1575G>A	p.(Trp525*)	0.0010	0.0011	-	-	BrS	NA	NA	NA	disease-causing	NA	NA	0.0018	0.0010	23	0.48	√	NA	VUS4
SIDS012	M	10	2	rs145850743	*COL5A2*	NG_011799.1	NM_000393.3	missense	exon	c.1301C>T	p.(Thr434Met)	0.0000	0.0026	-	-	EDS	C65	Deleterious	bad	disease-causing	81	benign	0.0020	0.0000	30	0.50	NA	NA	VUS2
SIDS013	M	3	1	rs200015085	*SHOC2*	NG_028922.1	NM_007373.3	missense	exon	c.610A>G	p.(Ile204Val)	0.0000	0.0000	-	-	Noonan syndrome	C25	Deleterious	bad	disease-causing	29	benign	0.0000	0.0000	111	0.48	NA	NA	VUS2
SIDS014	M	3	1	rs141821444	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.9448G>A	p.(Ala3150Thr)	0.0000	0.0000	-	-	EDMD	C55	Deleterious	bad	NA	58	probably damaging	0.0000	NA	51	0.43	NA	NA	VUS1
SIDS015	M	1	2	rs143788120	*MRPL3*	NG_029207.1	NM_007208.3	missense	exon	c.862T>C	p.(Ser288Pro)	0.0000	0.0000	-	-	HCM	C65	Deleterious	bad	disease-causing	74	probably damaging	0.0006	0.0030	115	0.43	NA	NA	VUS3
SIDS016	M	8	1	rs142992009	*MYH6*	NG_023444.1	NM_002471.3	missense	exon	c.1763A>C	p.(Asp588Ala)	0.0000	0.0022	-	-	HCM	C65	Deleterious	bad	disease-causing	126	benign	0.0030	0.0030	108	0.40	NA	NA	VUS2
SIDS016	M	8	1	rs201082652	*SLC22A5*	NG_008982.1	NM_003060.3	missense	exon	c.364G>T	p.(Asp122Tyr)	0.0000	0.0003	systemic primary carnitine deficiency	DM	SPCD	C0	Deleterious	good	NA	160	probably damaging	0.0005	0.0000	74	0.45	NA	NA	VUS2
SIDS021	M	4	1	~	*TSFM*	NG_016971.1	NM_001172696.1	Frameshift	exon	c.971_972del	p.(Gln324Argfs*11)	NA	0.0000	-	-	DCM	NA	NA	NA	NA	NA	NA	NA	NA	40	0.40	√	0.0000	VUS3
SIDS021	M	4	1	rs147589613	*COL5A1*	NG_008030.1	NM_000093.4	missense	exon	c.341C>A	p.(Ala114Asp)	0.0000	0.0010	-	-	EDS	C0	Deleterious	bad	NA	126	possibly damaging	0.0000	0.0000	73	0.47	NA	NA	VUS2
SIDS021	M	4	1	rs183156491	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.4028C>T	p.(Ala1343Val)	0.0010	0.0010	Aortic valve disease	DM	AOVD	C0	Deleterious	bad	disease-causing	64	possibly damaging	0.0020	0.0010	36	0.50	NA	NA	VUS1
SIDS023	M	4	2	rs199473233	*SCN5A*	NG_008934.1	NM_001099404.1	missense	exon	c.4057G>A	p.(Val1353Met)	0.0000	0.0000	Brugada syndrome	DM	BrS, HCM, LQTS	C15	Deleterious	bad	disease-causing	21	probably damaging	0.0000	NA	110	0.46	NA	NA	VUS1
SIDS024	M	2	2	rs140470576	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.10118C>A	p.(Ser3373Tyr)	0.0000	0.0020	-	-	LQTS	C65	Deleterious	bad	disease-causing	144	probably damaging	0.0000	0.0000	84	0.48	NA	NA	VUS4
SIDS024	M	2	2	rs121913013	*DSG2*	NG_007072.3	NM_001943.3	missense	exon	c.166G>A	p.(Val56Met)	0.0000	0.0035	ARVC	DM	ARVC	C0	Deleterious	good	disease-causing	21	probably damaging	0.0006	0.0010	28	0.46	NA	NA	VUS1
SIDS024	M	2	2	rs150290283	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.17089C>T	p.(Arg5697Trp)	0.0000	0.0000	-	-	EDMD	C65	Deleterious	bad	NA	101	possibly damaging	0.0000	NA	51	0.47	NA	NA	VUS1
SIDS025	F	3	2	rs200742016	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.9230C>T	p.(Pro3077Leu)	0.0010	0.0019	-	-	EDMD	C65	Deleterious	bad	disease-causing	98	probably damaging	0.0017	0.0020	50	0.50	NA	NA	VUS2
SIDS029	M	7	1	~	*DCHS1*	NG_033858.1	NM_003737.2	nonsense	exon	c.4672C>T	p.(Gln1558*)	NA	NA	-	-	MVP	NA	NA	NA	disease-causing	NA	NA	NA	NA	148	0.45	NA	0.0000	VUS2
SIDS029	M	7	1	rs181059522	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.15865G>A	p.(Val5289Met)	0.0000	0.0000	-	-	EDMD	C0	Deleterious	good	disease-causing	21	possibly damaging	0.0000	0.0000	87	0.38	NA	NA	VUS2
SIDS029	M	7	1	rs141443652	*TMPO*	NG_021393.1	NM_003276.2	missense	exon	c.1277C>T	p.(Pro426Leu)	0.0010	0.0015	Muscular dystrophy	DM	DCM	C0	Deleterious	bad	disease-causing	98	probably damaging	0.0020	0.0010	41	0.39	NA	NA	VUS2
SIDS031	F	4	2	rs141131535	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.344G>A	p.(Arg115His)	0.0000	0.0002	-	-	HCM	C25	Deleterious	bad	disease-causing	29	possibly damaging	0.0001	0.0010	38	0.37	√	NA	VUS3
SIDS031	F	4	2	rs373665895	*RYR2*	NG_008799.2	NM_001035.2	missense	exon	c.2828T>C	p.(Leu943Ser)	0.0000	0.0001	-	-	CPVT	C65	Deleterious	bad	disease-causing	145	benign	0.0003	NA	84	0.49	NA	NA	VUS2
SIDS031	F	4	2	rs35912339	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.1007C>T	p.(Pro336Leu)	0.0000	0.0013	-	-	HCM	C15	Deleterious	bad	polymorphism	98	possibly damaging	0.0017	0.0020	53	0.49	NA	NA	VUS1
SIDS031	F	4	2	rs752038761	*RYR2*	NG_008799.2	NM_001035.2	missense	exon	c.4798C>T	p.(Pro1600Ser)	0.0000	NA	-	-	CPVT	C65	Deleterious	bad	disease-causing	74	probably damaging	0.0000	NA	42	0.50	NA	NA	VUS1
SIDS032	M	3	2	~	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.2966T>A	p.(Leu989His)	NA	0.0000	-	-	LQTS	C65	Deleterious	bad	disease-causing	99	probably damaging	NA	NA	122	0.42	NA	0.0000	VUS2
SIDS032	M	3	2	rs199909093	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.7886T>C	p.(Val2629Ala)	0.0000	0.0000	-	-	LQTS	C25	Deleterious	good	polymorphism	64	benign	0.0000	0.0010	85	0.45	NA	NA	VUS1
SIDS037	F	4	1	rs139965373	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.3580G>A	p.(Ala1194Thr)	0.0010	0.0000	-	-	LQTS	C55	Deleterious	bad	disease-causing	58	probably damaging	0.0000	0.0000	29	0.41	√	NA	VUS4
SIDS037	F	4	1	rs749544930	*DLG1*	NG_029099.1	NM_004087.2	missense	exon	c.2455C>G	p.(Arg819Gly)	0.0000	NA	-	-	LQTS	C45	Deleterious	bad	disease-causing	125	probably damaging	0.0000	0.0000	23	0.26	NA	NA	VUS2
SIDS037	F	4	1	rs199681901	*DSG2*	NG_007072.3	NM_001943.3	missense	exon	c.1781T>C	p.(Leu594Pro)	0.0000	0.0000	-	-	ARVC	C0	Tolerated	good	disease-causing	98	possibly damaging	0.0005	0.0020	20	0.40	NA	NA	VUS1
SIDS037	F	4	1	rs138004884	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.6934T>C	p.(Phe2312Leu)	0.0000	0.0000	-	-	EDMD	C0	Tolerated	bad	NA	22	probably damaging	0.0012	0.0010	121	0.46	NA	NA	VUS1
SIDS040	F	8	2	rs201971987	*TXNRD2*	NG_011835.1	NM_006440.4	missense	exon	c.1174T>C	p.(Tyr392His)	0.0000	0.0006	-	-	DCM	C65	Deleterious	NA	polymorphism	83	probably damaging	0.0005	NA	156	0.33	NA	NA	VUS1
SIDS041	F	4	2	rs185947256	*AGL*	NG_012865.1	NM_000028.2	missense	exon	c.3290G>A	p.(Arg1097His)	0.0000	0.0000	-	-	GSD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	73	0.36	√	NA	VUS3
SIDS041	F	4	2	rs139790539	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.18185C>T	p.(Ser6062Leu)	0.0010	0.0000	-	-	EDMD	C0	Deleterious	good	disease-causing	145	possibly damaging	0.0000	0.0000	54	0.46	NA	NA	VUS2
SIDS041	F	4	2	rs200383755	*GATA5*	NA	NM_080473.4	missense	exon	c.56C>G	p.(Ser19Trp)	0.0000	0.0000	Bicuspid aortic valve	DM?	Afib	C0	Deleterious	unknown	disease-causing	177	probably damaging	0.0280	0.0010	87	0.41	NA	NA	VUS1
SIDS041	F	4	2	rs367825691	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.839A>G	p.(Asn280Ser)	0.0000	0.0000	-	-	AOVD	C45	Deleterious	bad	disease-causing	46	probably damaging	0.0015	NA	185	0.48	NA	NA	VUS1
SIDS044	M	3	2	rs137953195	*ELN*	NG_009261.1	NM_001278939.1	missense	exon	c.328G>A	p.(Ala110Thr)	0.0000	0.0000	-	-	connective tissue?	C0	Tolerated	NA	disease-causing	58	probably damaging	0.0000	0.0010	95	0.49	NA	NA	VUS1
SIDS044	M	3	2	rs376263577	*ETFDH*	NG_007078.2	NM_004453.3	missense	exon	c.358G>C	p.(Asp120His)	0.0000	0.0000	-	-	GA	C0	Deleterious	NA	NA	81	possibly damaging	0.0000	0.0000	67	0.34	NA	NA	VUS1
SIDS044	M	3	2	~	*MYH6*	NG_023444.1	NM_002471.3	missense	exon	c.2819C>A	p.(Ala940Asp)	NA	NA	-	-	HCM	C65	Deleterious	bad	disease-causing	126	probably damaging	NA	NA	183	0.47	NA	0.0000	VUS1
SIDS045	M	5	1	rs369588692	*SCN1B*	NG_013359.1	NM_199037.3	missense	exon	c.673C>T	p.(Arg225Cys)	0.0000	0.0000	-	-	BrS, Afib	C0	Deleterious	bad	disease-causing	142	probably damaging	0.0001	0.0000	117	0.46	NA	NA	VUS4
SIDS046	F	3	2	rs374137476	*DSP*	NG_008803.1	NM_004415.2	missense	exon	c.8531G>T	p.(Gly2844Val)	0.0000	0.0001	-	-	ARVC	C0	Deleterious	bad	disease-causing	109	probably damaging	0.0000	NA	71	0.48	NA	NA	VUS2
SIDS046	F	3	2	rs147173048	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.16178C>T	p.(Ala5393Val)	0.0000	0.0000	-	-	EDMD	C0	Tolerated	bad	disease-causing	64	possibly damaging	0.0000	0.0000	37	0.46	NA	NA	VUS2
SIDS049	F	3	1	rs587780334	*FKRP*	NG_008898.2	NM_024301.4	missense	exon	c.1027G>C	p.(Glu343Gln)	NA	NA	-	-	CMD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	78	0.38	NA	NA	VUS1
SIDS049	F	3	1	rs139203363	*SLC22A5*	NG_008982.1	NM_003060.3	missense	exon	c.34G>A	p.(Gly12Ser)	0.0010	0.0016	systemic primary carnitine deficiency	DM	SPCD	C0	Deleterious	good	NA	56	probably damaging	0.0007	0.0010	141	0.48	NA	NA	VUS1
SIDS050	M	2	1	~	*ACTN2*	NG_009081.1	NM_001103.2	nonsense	exon	c.2671G>T	p.(Glu891*)	NA	0.0000	-	-	DCM	NA	NA	NA	disease-causing	NA	NA	NA	NA	41	0.44	√	0.0000	VUS4
SIDS050	M	2	1	rs199732064	*TRPM7*	NG_021363.1	NM_017672.4	missense	exon	c.4084C>T	p.(Pro1362Ser)	0.0000	0.0009	-	-	DCM	C0	Deleterious	bad	disease-causing	74	possibly damaging	0.0005	0.0010	127	0.46	NA	NA	VUS3
SIDS050	M	2	1	rs35912339	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.1007C>T	p.(Pro336Leu)	0.0000	0.0013	-	-	HCM	C15	Deleterious	bad	polymorphism	98	possibly damaging	0.0017	0.0020	32	0.50	NA	NA	VUS1
SIDS050	M	2	1	rs147146713	*TGFBR1*	NG_007461.1	NM_004612.2	missense	exon	c.470G>A	p.(Arg157Gln)	0.0000	0.0000	-	-	LDS1	C35	Deleterious	bad	disease-causing	43	benign	0.0004	NA	47	0.40	NA	NA	VUS1
SIDS051	M	2	2	rs140704891	*RANGRF*	NG_028189.1	NM_016492.4	nonsense	exon	c.181G>T	p.(Glu61*)	0.0020	0.0054	Altered function	FP	Afib	NA	NA	NA	disease-causing	NA	NA	0.0053	0.0050	47	0.45	NA	NA	VUS2
SIDS051	M	2	2	rs201148126	*RBM20*	NG_021177.1	NM_001134363.2	missense	exon	c.850G>A	p.(Gly284Arg)	0.0000	0.0006	-	-	DCM	C0	NA	NA	disease-causing	125	probably damaging	0.0000	0.0010	78	0.47	NA	NA	VUS2
SIDS052	F	4	1	rs774949123	*GJD4*	NA	NM_153368.2	Frameshift	exon	c.215dup	p.(Ser73Valfs*180)	0.0000	0.0000	-	-	Afib	NA	NA	NA	NA	NA	NA	NA	NA	134	0.46	NA	NA	VUS1
SIDS055	M	2	2	rs140322345	*ILK*	NG_029702.1	NM_001014794.2	missense	exon	c.631C>T	p.(Arg211Cys)	0.0010	0.0014	-	-	DCM	C25	Deleterious	NA	disease-causing	180	possibly damaging	0.0008	0.0010	48	0.40	NA	NA	VUS2
SIDS056	M	6	2	rs28383480	*SLC22A5*	NG_008982.1	NM_003060.3	missense	exon	c.1451G>T	p.(Gly484Val)	0.0000	0.0000	-	-	SPCD	C0	Deleterious	bad	disease-causing	109	probably damaging	0.0000	NA	19	0.47	NA	NA	VUS2
SIDS056	M	6	2	rs751300489	*ACTA2*	NG_011541.1	NM_001141945.1	missense	exon	c.403T>C	p.(Tyr135His)	0.0000	NA	Thoracic aortic aneurysms	DM	TAAD	C65	Deleterious	bad	disease-causing	83	probably damaging	0.0000	NA	41	0.46	NA	NA	VUS1
SIDS056	M	6	2	rs748609148	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.8399C>T	p.(Ser2800Leu)	NA	NA	-	-	MVP	C0	Deleterious	bad	polymorphism	145	probably damaging	0.0000	0.0000	28	0.46	NA	NA	VUS1
SIDS057	M	3	1	rs138714806	*HCN4*	NG_009063.1	NM_005477.2	missense	exon	c.1703G>C	p.(Ser568Thr)	0.0000	0.0010	-	-	BrS	C0	Deleterious	bad	disease-causing	58	benign	0.0000	0.0010	42	0.38	NA	NA	VUS2
SIDS060	M	4	2	rs570425717	*PTPN3*	NA	NM_002829.3	missense	exon	c.2329G>A	p.(Glu777Lys)	NA	NA	-	-	schizophrenia	C0	Deleterious	bad	disease-causing	119	possibly damaging	0.0000	0.0000	62	0.48	NA	NA	VUS1
SIDS061	M	4	2	rs143767864	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.704G>A	p.(Arg235Gln)	0.0000	0.0000	-	-	MVP	C0	Deleterious	bad	disease-causing	43	probably damaging	0.0000	0.0010	114	0.46	NA	NA	VUS3
SIDS061	M	4	2	rs142217269	*SCN10A*	NG_031891.2	NM_006514.2	missense	exon	c.4568G>A	p.(Cys1523Tyr)	0.0010	0.0027	Brugada syndrome	DM?	BrS	C65	Deleterious	bad	disease-causing	194	probably damaging	0.0018	0.0010	134	0.46	NA	NA	VUS3
SIDS061	M	4	2	rs78727187	*FBN2*	NG_008750.1	NM_001999.3	missense	exon	c.4141C>A	p.(His1381Asn)	0.0030	0.0050	-	-	MFS	C65	Deleterious	bad	disease-causing	68	benign	0.0000	0.0010	104	0.39	NA	NA	VUS2
SIDS062	M	3	1	rs139539832	*ABCC9*	NG_012819.1	NM_005691.3	missense	exon	c.1859G>A	p.(Arg620Gln)	0.0000	0.0000	-	-	DCM	C0	Deleterious	NA	NA	43	possibly damaging	0.0000	0.0010	34	0.32	NA	NA	VUS1
SIDS062	M	3	1	~	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.4697C>T	p.(Pro1566Leu)	NA	NA	-	-	AOVD	C65	Deleterious	bad	disease-causing	98	probably damaging	NA	NA	31	0.45	NA	0.0000	VUS1
SIDS063	F	3	1	~	*COL5A2*	NG_011799.1	NM_000393.3	missense	exon	c.2459C>G	p.(Pro820Arg)	NA	0.0000	-	-	EDS	C65	Deleterious	bad	disease-causing	103	probably damaging	NA	NA	19	0.21	NA	0.0000	VUS2
SIDS064	F	3	1	rs779096534	*MYOM1*	NG_032120.1	NM_003803.3	missense	exon	c.2309G>A	p.(Gly770Glu)	NA	NA	-	-	HCM	C0	Deleterious	bad	polymorphism	98	probably damaging	0.0000	0.0000	128	0.40	NA	NA	VUS1
SIDS064	F	3	1	rs372607729	*SGCD*	NG_008693.2	NM_000337.5	missense	exon	c.761C>A	p.(Thr254Lys)	0.0000	0.0000	-	-	DCM	C0	Tolerated	good	disease-causing	78	benign	0.0000	0.0000	68	0.24	NA	NA	VUS1
SIDS066	M	4	2	rs147896322	*CACNA1C*	NG_008801.2	NM_199460.3	missense	exon	c.5263G>A	p.(Val1755Ile)	0.0000	0.0001	-	-	BrS	C0	Tolerated	NA	disease-causing	29	probably damaging	0.0007	0.0010	70	0.46	NA	NA	VUS1
SIDS069	M	3	2	rs200893930	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.7645C>T	p.(Arg2549Cys)	0.0000	0.0001	-	-	AOVD	C25	Deleterious	bad	disease-causing	180	possibly damaging	0.0000	0.0000	113	0.26	√	NA	VUS4
SIDS073	M	3	2	rs200473206	*DSP*	NG_008803.1	NM_004415.2	splice site	splice site	c.273+5G>A	p.(?)	0.0000	0.0005	ARVC	DM	ARVC	NA	NA	NA	NA	NA	NA	0.0005	NA	50	0.40	NA	NA	VUS3
SIDS075	F	3	2	rs121434557	*GJA5*	NG_009369.2	NM_005266.6	missense	exon	c.286G>T	p.(Ala96Ser)	0.0000	0.0000	Atrial fibrillation	DM	Afib	C65	Deleterious	NA	disease-causing	99	probably damaging	0.0001	0.0010	239	0.45	NA	NA	VUS3
SIDS075	F	3	2	rs149272010	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.19534G>A	p.(Ala6512Thr)	NA	0.0000	-	-	EDMD	C55	Deleterious	bad	NA	58	probably damaging	0.0000	0.0000	71	0.41	NA	NA	VUS3
SIDS075	F	3	2	rs398123072	*ACADM*	NG_007045.2	NM_001286043.1	missense	exon	c.157C>T	p.(Arg53Cys)	0.0000	0.0000	MCAD deficiency	DM	MCAD	C25	Deleterious	NA	disease-causing	180	probably damaging	0.0000	NA	31	0.48	NA	NA	VUS2
SIDS075	F	3	2	rs139046510	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.10664A>T	p.(Asp3555Val)	0.0010	0.0012	-	-	LQTS	C65	Deleterious	bad	disease-causing	152	probably damaging	0.0014	0.0030	23	0.22	NA	NA	VUS2
SIDS075	F	3	2	rs370428679	*NEXN*	NG_016625.1	NM_144573.3	missense	exon	c.616G>C	p.(Glu206Gln)	0.0000	0.0000	-	-	DCM	C25	Deleterious	bad	polymorphism	29	possibly damaging	0.0000	0.0000	35	0.49	NA	NA	VUS2
SIDS075	F	3	2	rs766824318	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.2776C>T	p.(Arg926Cys)	0.0000	NA	-	-	HCM	C65	Deleterious	bad	disease-causing	180	probably damaging	0.0000	NA	147	0.44	NA	NA	VUS1
SIDS080	F	0	2	rs104894565	*G6PC*	NG_011808.1	NM_000151.3	missense	exon	c.113A>T	p.(Asp38Val)	0.0000	0.0070	Glycogen storage disease 1a	DM	GSD	C0	Deleterious	NA	disease-causing	152	probably damaging	0.0000	0.0000	33	0.48	NA	NA	VUS2
SIDS080	F	0	2	rs151090729	*SCN10A*	NG_031891.2	NM_006514.2	missense	exon	c.4984G>A	p.(Gly1662Ser)	0.0000	0.0019	Small fibre neuropathy	DM	BrS	C55	Deleterious	good	disease-causing	56	probably damaging	0.0007	0.0010	133	0.48	NA	NA	VUS2
SIDS080	F	0	2	rs146389405	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.26299A>G	p.(Met8767Val)	0.0000	0.0000	-	-	EDMD	C0	Deleterious	bad	NA	21	possibly damaging	0.0000	0.0000	98	0.38	NA	NA	VUS2
SIDS084	M	9	2	rs150955173	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.19415C>T	p.(Ser6472Leu)	0.0000	0.0020	-	-	EDMD	C0	Deleterious	bad	disease-causing	145	probably damaging	0.0030	0.0000	161	0.46	NA	NA	VUS2
SIDS084	M	9	2	rs377192523	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.8960A>G	p.(Gln2987Arg)	0.0000	0.0000	-	-	MVP	C0	Deleterious	bad	disease-causing	43	probably damaging	0.0000	NA	41	0.49	NA	NA	VUS1
SIDS085	F	2	2	rs148791938	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.5503C>T	p.(Leu1835Phe)	0.0000	0.0000	-	-	MVP	C0	Tolerated	good	disease-causing	22	probably damaging	0.0010	0.0010	75	0.49	NA	NA	VUS1
SIDS087	M	4	1	~	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.1490C>T	p.(Ser497Phe)	NA	0.0000	-	-	HCM	C65	Deleterious	bad	disease-causing	155	probably damaging	NA	NA	25	0.28	√	0.0000	VUS3
SIDS087	M	4	1	rs199654211	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.311A>G	p.(Asn104Ser)	0.0000	0.0200	-	-	AOVD	C15	Deleterious	bad	disease-causing	46	benign	0.0000	0.0000	56	0.25	NA	NA	VUS1
SIDS089	F	5	1	rs199800922	*MYH11*	NG_009299.1	NM_001040114.1	missense	exon	c.3624C>G	p.(His1208Gln)	0.0000	0.0001	-	-	HCM, TAA	C15	Deleterious	bad	disease-causing	24	possibly damaging	0.0000	0.0010	124	0.45	NA	NA	VUS3
SIDS089	F	5	1	rs562115547	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.7396C>T	p.(Arg2466Cys)	0.0000	NA	-	-	LQTS	C65	Deleterious	bad	disease-causing	180	possibly damaging	0.0000	0.0000	61	0.48	NA	NA	VUS2
SIDS089	F	5	1	rs138693624	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.10022T>C	p.(Val3341Ala)	0.0060	0.0000	-	-	EDMD	C25	Deleterious	good	NA	64	benign	0.0000	0.0000	53	0.36	NA	NA	VUS1
SIDS091	M	2	2	rs200899037	*CASQ2*	NG_008802.1	NM_001232.3	missense	exon	c.1052A>G	p.(Asp351Gly)	0.0000	0.0000	-	-	CPVT	C0	Deleterious	bad	disease-causing	94	probably damaging	0.0000	0.0010	58	0.35	√	NA	VUS3
SIDS091	M	2	2	rs201104206	*MYOM1*	NG_032120.1	NM_003803.3	missense	exon	c.1978C>G	p.(Pro660Ala)	0.0000	0.0016	-	-	HCM	C0	Deleterious	bad	disease-causing	27	probably damaging	0.0030	0.0020	32	0.47	NA	NA	VUS1
SIDS092	F	2	1	rs12720457	*KCNQ1*	NG_008935.1	NM_000218.2	missense	exon	c.1179G>T	p.(Lys393Asn)	0.0000	0.0008	LQTS	DM	LQTS	C35	Deleterious	bad	disease-causing	94	possibly damaging	0.0012	0.0040	86	0.47	NA	NA	VUS2
SIDS092	F	2	1	rs754717867	*ANKRD1*	NG_023227.1	NM_014391.2	missense	exon	c.544C>T	p.(Arg182Cys)	0.0000	NA	-	-	HCM	C55	Deleterious	bad	disease-causing	180	probably damaging	0.0000	NA	48	0.50	NA	NA	VUS1
SIDS093	F	8	2	rs2234916	*KCNE2*	NG_008804.1	NM_172201.1	missense	exon	c.22A>G	p.(Thr8Ala)	0.0020	0.0069	LQTS, drug induced	DP	LQTS	C55	Deleterious	bad	disease-causing	58	probably damaging	0.0054	0.0000	143	0.43	NA	NA	VUS1
SIDS096	F	2	1	rs71352737	*TRPM4*	NG_027551.1	NM_017636.3	nonsense	exon	c.1575G>A	p.(Trp525*)	0.0010	0.0011	-	-	BrS	NA	NA	NA	disease-causing	NA	NA	0.0018	0.0010	63	0.40	NA	NA	VUS4
SIDS097	F	2	1	rs200286058	*ABCC8*	NG_008867.1	NM_001287174.1	missense	exon	c.2152G>A	p.(Gly718Ser)	0.0000	0.0020	-	-	IVF	C55	Deleterious	NA	disease-causing	56	probably damaging	0.0000	0.0000	87	0.46	NA	NA	VUS2
SIDS097	F	2	1	rs147589613	*COL5A1*	NG_008030.1	NM_000093.4	missense	exon	c.341C>A	p.(Ala114Asp)	0.0000	0.0010	-	-	EDS	C0	Deleterious	bad	NA	126	possibly damaging	0.0000	0.0000	117	0.44	NA	NA	VUS2
SIDS097	F	2	1	rs142206385	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.15446G>A	p.(Arg5149His)	0.0010	0.0000	-	-	EDMD	C0	Tolerated	NA	disease-causing	29	possibly damaging	0.0000	0.0010	79	0.48	NA	NA	VUS1
SIDS098	M	11	1	rs201082652	*SLC22A5*	NG_008982.1	NM_003060.3	missense	exon	c.364G>T	p.(Asp122Tyr)	0.0000	0.0003	systemic primary carnitine deficiency	DM	SPCD	C0	Deleterious	good	NA	160	probably damaging	0.0005	0.0000	64	0.47	NA	NA	VUS2
SIDS098	M	11	1	rs35156360	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.1327C>T	p.(Pro443Ser)	0.0060	0.0205	-	-	HCM	C65	Deleterious	bad	disease-causing	74	probably damaging	0.0000	0.0130	44	0.45	NA	NA	VUS1
SIDS100	F	4	2	rs373347787	*SCN10A*	NG_031891.2	NM_006514.2	missense	exon	c.4780C>T	p.(Arg1594Cys)	0.0000	0.0000	-	-	BrS	C65	Deleterious	bad	disease-causing	180	probably damaging	0.0000	NA	100	0.45	NA	NA	VUS3
SIDS100	F	4	2	rs371316167	*ACADVL*	NG_007975.1	NM_001270447.1	missense	exon	c.1603C>T	p.(Arg535Trp)	0.0000	0.0000	-	-	MCAD	C0	Deleterious	good	disease-causing	101	probably damaging	0.0000	0.0000	152	0.49	NA	NA	VUS2
SIDS100	F	4	2	rs143842011	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.23659G>A	p.(Val7887Met)	0.0000	0.0000	-	-	EDMD	C0	Deleterious	bad	NA	21	probably damaging	0.0000	0.0000	62	0.47	NA	NA	VUS2

SIDS101	M	6	2	rs200899037	*CASQ2*	NG_008802.1	NM_001232.3	missense	exon	c.1052A>G	p.(Asp351Gly)	0.0000	0.0000	-	-	CPVT	C0	Deleterious	bad	disease-causing	94	probably damaging	0.0000	0.0010	50	0.32	√	NA	VUS3
SIDS102	F	9	2	rs77357563	*TBX5*	NG_007373.1	NM_000192.3	missense	exon	c.331G>T	p.(Asp111Tyr)	0.0020	0.0049	Holt-Oram syndrome	DM	ASD	C65	Deleterious	bad	disease-causing	160	probably damaging	0.0040	0.0060	98	0.49	NA	NA	VUS1
SIDS103	M	5	2	rs371564200	*MYBPC3*	NG_007667.1	NM_000256.3	missense	exon	c.1828G>C	p.(Asp610His)	0.0000	0.0000	HCM	DM	HCM, DCM, LVNC10	C65	Deleterious	bad	disease-causing	81	probably damaging	0.0000	NA	30	0.50	NA	NA	VUS2
SIDS103	M	5	2	rs36210417	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.9854T>C	p.(Ile3285Thr)	0.0050	0.0010	-	-	LQTS	C65	Deleterious	bad	disease-causing	89	probably damaging	0.0110	0.0080	103	0.49	NA	NA	VUS1
SIDS107	M	3	2	rs144605670	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.15781G>A	p.(Val5261Ile)	0.0010	0.0000	-	-	EDMD	C0	Deleterious	bad	polymorphism	29	benign	0.0000	0.0000	53	0.49	NA	NA	VUS1
SIDS111	M	3	2	~	*GUSB*	NG_016197.1	NM_000181.3	missense	exon	c.215G>T	p.(Gly72Val)	NA	0.0000	-	-	MPS VII	C0	Deleterious	bad	disease-causing	109	probably damaging	NA	NA	107	0.22	NA	0.0000	VUS2
SIDS111	M	3	2	~	*FBN1*	NG_008805.2	NM_000138.4	missense	exon	c.806T>C	p.(Phe269Ser)	NA	NA	-	-	MFS	C65	Deleterious	bad	disease-causing	155	probably damaging	NA	NA	55	0.22	NA	0.0000	VUS1
SIDS112	M	2	2	rs150147262	*COL5A1*	NG_008030.1	NM_000093.3	missense	exon	c.514G>T	p.(Val172Phe)	0.0000	0.0015	-	-	EDS	C0	Deleterious	bad	NA	50	benign	0.0000	0.0010	67	0.37	NA	NA	VUS1
SIDS114	M	6	2	rs35831865	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.20117G>A	p.(Arg6706Gln)	0.0050	0.0000	-	-	EDMD	C0	Deleterious	bad	disease-causing	43	possibly damaging	0.0000	0.0000	48	0.23	NA	NA	VUS2
SIDS115	F	2	2	rs146748294	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.280A>G	p.(Ile94Val)	0.0010	0.0000	-	-	EDMD	C0	Deleterious	bad	disease-causing	29	possibly damaging	0.0000	0.0020	70	0.44	NA	NA	VUS2
SIDS117	M	3	2	~	*DSP*	NG_008803.1	NM_004415.2	missense	exon	c.1577T>C	p.(Ile526Thr)	NA	NA	-	-	ARVC	C65	Deleterious	bad	disease-causing	89	probably damaging	NA	NA	23	0.35	NA	0.0000	VUS1
SIDS117	M	3	2	rs140413151	*HADH*	NG_008156.2	NM_001184705.2	missense	exon	c.643C>A	p.(Pro215Thr)	0.0020	0.0030	-	-	HHF	C35	Deleterious	bad	disease-causing	38	probably damaging	0.0000	0.0050	35	0.46	NA	NA	VUS1
SIDS119	F	1	2	~	*TRPM4*	NG_027551.1	NM_017636.3	Frameshift	exon	c.247dup	p.(Ala83Glyfs*13)	NA	0.0000	-	-	BrS	NA	NA	NA	NA	NA	NA	NA	NA	57	0.41	NA	0.0000	VUS3
SIDS120	M	3	2	rs121913013	*DSG2*	NG_007072.3	NM_001943.3	missense	exon	c.166G>A	p.(Val56Met)	0.0000	0.0035	ARVC	DM	ARVC	C0	Deleterious	good	disease-causing	21	probably damaging	0.0006	0.0010	26	0.42	NA	NA	VUS1
SIDS120	M	3	2	rs77357563	*TBX5*	NG_007373.1	NM_000192.3	missense	exon	c.331G>T	p.(Asp111Tyr)	0.0020	0.0049	Holt-Oram syndrome	DM	ASD	C65	Deleterious	bad	disease-causing	160	probably damaging	0.0040	0.0060	98	0.49	NA	NA	VUS1
SIDS120	M	3	2	rs749485028	*TGFB3*	NG_011715.1	NM_003239.2	missense	exon	c.1054C>T	p.(Arg352Cys)	NA	NA	-	-	ARVC	C0	Deleterious	bad	NA	180	probably damaging	0.0000	0.0000	43	0.35	NA	NA	VUS1
SIDS129	M	2	2	rs142191737	*LMNA*	NG_008692.2	NM_170707.2	missense	exon	c.1634G>A	p.(Arg545His)	0.0000	0.0004	Cardiac disease	DM	DCM	C25	Deleterious	bad	disease-causing	29	benign	0.0003	0.0010	53	0.47	NA	NA	VUS2
SIDS130	M	8	2	rs199473061	*SCN5A*	NG_008934.1	NM_001099404.1	missense	exon	c.436G>A	p.(Val146Met)	0.0000	0.0000	Brugada syndrome	-	BrS, HCM, LQTS	C15	Deleterious	bad	disease-causing	21	probably damaging	0.0000	NA	36	0.44	NA	NA	VUS1
SIDS131	F	2	2	rs368054375	*SCN3B*	NG_016283.1	NM_018400.3	missense	exon	c.415C>T	p.(Arg139Trp)	0.0000	0.0001	-	-	BrS	C35	Deleterious	bad	disease-causing	101	probably damaging	0.0001	NA	71	0.48	NA	NA	VUS2
SIDS133	F	10	2	rs587780334	*FKRP*	NG_008898.2	NM_024301.4	missense	exon	c.1027G>C	p.(Glu343Gln)	NA	NA	-	-	CMD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	53	0.25	NA	NA	VUS1
SIDS140	M	4	2	rs187029309	*FLNA*	NG_011506.1	NM_001110556.1	missense	exon	c.5972C>T	p.(Ser1991Leu)	0.0020	0.0035	-	-	heterotopia	C65	Deleterious	bad	disease-causing	145	probably damaging	0.0030	0.0040	37	homozygote	NA	NA	VUS1
SIDS140	M	4	2	rs77357563	*TBX5*	NG_007373.1	NM_000192.3	missense	exon	c.331G>T	p.(Asp111Tyr)	0.0020	0.0049	Holt-Oram syndrome	DM	ASD	C65	Deleterious	bad	disease-causing	160	probably damaging	0.0040	0.0060	98	0.49	NA	NA	VUS1
SIDS142	M	3	2	rs45465995	*SCN5A*	NG_008934.1	NM_001099404.1	missense	exon	c.5689C>T	p.(Arg1897Trp)	0.0020	0.0004	LQTS	DM	BrS, HCM, LQTS	C65	Deleterious	bad	disease-causing	101	probably damaging	0.0000	0.0020	99	0.49	NA	NA	VUS4
SIDS142	M	3	2	rs140148322	*FHL2*	NG_008844.2	NM_001450.3	missense	exon	c.337C>T	p.(Arg113Cys)	0.0000	0.0005	-	-	DCM	C65	Deleterious	bad	disease-causing	180	probably damaging	0.0005	NA	30	0.27	√	NA	VUS3
SIDS142	M	3	2	rs138504021	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.1862G>A	p.(Arg621His)	0.0010	0.0010	-	-	AOVD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0019	0.0030	34	0.50	NA	NA	VUS1
SIDS142	M	3	2	rs144860423	*SNTA1*	NG_011622.1	NM_003098.2	missense	exon	c.566C>T	p.(Ser189Leu)	0.0000	0.0000	-	-	LQTS	C0	Tolerated	good	disease-causing	145	probably damaging	0.0000	0.0100	42	0.38	NA	NA	VUS1
SIDS143	M	6	2	rs369255950	*CACNA1C*	NG_008801.2	NM_199460.3	missense	exon	c.1487G>A	p.(Arg496Gln)	0.0000	0.0000	-	-	BrS	C0	Tolerated	NA	disease-causing	43	probably damaging	0.0000	0.0000	123	0.20	NA	NA	VUS1
SIDS143	M	6	2	rs112402535	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.379G>A	p.(Val127Ile)	0.0010	0.0070	-	-	MVP	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0070	0.0010	78	0.20	NA	NA	VUS1
SIDS148	M	5	2	rs148146011	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.4826G>A	p.(Arg1609Lys)	0.0000	0.0000	-	-	LQTS	C25	Deleterious	good	polymorphism	26	benign	0.0000	0.0010	227	0.44	NA	NA	VUS1
SIDS148	M	5	2	rs151021935	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.5369T>G	p.(Val1790Gly)	0.0000	0.0000	-	-	LQTS	C0	Tolerated	good	disease-causing	109	benign	0.0010	0.0000	23	0.43	NA	NA	VUS1
SIDS148	M	5	2	rs56208331	*GATA4*	NG_008177.1	NM_002052.3	missense	exon	c.1273G>A	p.(Asp425Asn)	0.0000	0.0000	Congenital heart defects	DM	ASD	C0	Tolerated	good	disease-causing	23	probably damaging	0.0003	0.0000	131	0.37	NA	NA	VUS1
SIDS149	M	2	2	rs375218723	*DES*	NG_008043.1	NM_001927.3	missense	exon	c.1123C>T	p.(Arg375Trp)	0.0000	0.0000	-	-	DCM	C65	Deleterious	bad	disease-causing	101	probably damaging	0.0000	NA	86	0.50	NA	NA	VUS2
SIDS149	M	2	2	rs142004123	*SOS1*	NG_007530.1	NM_005633.3	missense	exon	c.2371C>A	p.(Leu791Ile)	0.0000	0.0010	-	-	noonan syndrome	C0	Deleterious	bad	disease-causing	5	possibly damaging	0.0010	0.0010	54	0.48	NA	NA	VUS2
SIDS149	M	2	2	rs772783444	*TRDN*	NG_030438.1	NM_006073.3	missense	exon	c.812G>C	p.(Arg271Pro)	NA	NA	-	-	CPVT	C0	Deleterious	NA	disease-causing	103	probably damaging	0.0000	0.0000	39	0.31	NA	NA	VUS1
SIDS150	M	3	2	rs57629361	*LMNA*	NG_008692.2	NM_170707.2	missense	exon	c.1583C>T	p.(Thr528Met)	NA	0.0000	Hutchinson-Gilford progeria syndrome	DM	DCM, ARVC	C65	Deleterious	bad	disease-causing	81	probably damaging	NA	0.0000	38	0.29	NA	NA	VUS2
SIDS150	M	3	2	rs199589844	*CPT1A*	NG_011801.1	NM_001876.3	missense	exon	c.518G>A	p.(Arg173His)	0.0000	0.0000	-	-	SPCD	C0	Deleterious	good	disease-causing	29	benign	0.0000	0.0000	68	0.43	NA	NA	VUS1
SIDS150	M	3	2	rs201019894	*HADH*	NG_008156.2	NM_001184705.2	missense	exon	c.714C>G	p(.Phe238Leu)	0.0000	0.0008	-	-	HHF	C0	Deleterious	NA	disease-causing	22	NA	0.0000	0.0000	130	0.43	NA	NA	VUS1
SIDS150	M	3	2	rs76757102	*MYOZ2*	NG_029747.1	NM_016599.4	missense	exon	c.29A>C	p.(Gln10Pro)	0.0000	0.0001	-	-	HCM	C0	Deleterious	NA	polymorphism	76	possibly damaging	0.0000	0.0000	269	0.49	NA	NA	VUS1
SIDS150	M	3	2	rs113542007	*ZNF365*	NG_021209.1	NM_199451.2	missense	exon	c.1109C>A	p.(Thr370Lys)	NA	0.0000	-	-	others	C0	Tolerated	NA	disease-causing	78	benign	0.0000	0.0010	93	0.37	NA	NA	VUS1
SIDS156	F	2	2	rs139170018	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.15337G>A	p.(Val5113Ile)	0.0000	0.0012	-	-	EDMD	C25	Deleterious	bad	disease-causing	29	probably damaging	0.0010	0.0000	81	0.41	NA	NA	VUS3
SIDS156	F	2	2	rs16835270	*RYR2*	NG_008799.2	NM_001035.2	missense	exon	c.1519G>A	p.(Val507Ile)	0.0100	0.0004	-	-	CPVT	C25	Deleterious	bad	polymorphism	29	possibly damaging	0.0004	0.0000	64	0.33	NA	NA	VUS2
SIDS159	M	2	2	rs150955173	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.19415C>T	p.(Ser6472Leu)	0.0000	0.0020	-	-	EDMD	C0	Deleterious	bad	disease-causing	145	probably damaging	0.0030	0.0000	141	0.48	NA	NA	VUS2
SIDS159	M	2	2	rs138504021	*NOTCH1*	NG_007458.1	NM_017617.3	missense	exon	c.1862G>A	p.(Arg621His)	0.0010	0.0010	-	-	AOVD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0019	0.0030	54	0.39	NA	NA	VUS1
SIDS161	M	1	2	rs377061868	*TPM1*	NG_007557.1	NM_000366.5	splice site	splice site	c.375-5T>C	p.(?)	0.0000	0.0005	DCM	DM?	DCM	NA	NA	NA	NA	NA	NA	0.0004	NA	151	0.45	NA	NA	VUS3
SIDS161	M	1	2	rs371581038	*MYH11*	NG_009299.1	NM_001040114.1	missense	exon	c.5413C>T	p.(Arg1805Trp)	0.0000	0.0000	-	-	HCM, TAA	C35	Deleterious	bad	polymorphism	32	probably damaging	0.0000	NA	86	0.34	NA	NA	VUS1
SIDS172	F	8	2	rs111843122	*RYR2*	NG_008799.2	NM_001035.2	splice site	splice site	c.2907-1G>C	p.(?)	0.0000	0.0000	-	-	CPVT	NA	NA	NA	NA	NA	NA	0.0000	NA	34	0.47	√	NA	VUS3
SIDS172	F	8	2	rs202147520	*MYBPC3*	NG_007667.1	NM_000256.3	missense	exon	c.3742G>A	p.(Gly1248Arg)	0.0000	0.0000	HCM	DM	HCM, DCM, LVNC17	C65	Deleterious	bad	disease-causing	125	possibly damaging	0.0000	NA	35	0.46	NA	NA	VUS2
SIDS172	F	8	2	rs140704891	*RANGRF*	NG_028189.1	NM_016492.4	nonsense	exon	c.181G>T	p.(Glu61*)	0.0020	0.0054	Altered function	FP	Afib	NA	NA	NA	disease-causing	NA	NA	0.0053	0.0050	22	0.36	NA	NA	VUS2
SIDS172	F	8	2	rs141488398	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.14528T>A	p.(Phe4843Tyr)	0.0000	0.0010	-	-	EDMD	C0	Deleterious	bad	disease-causing	22	possibly damaging	0.0000	0.0010	27	0.48	NA	NA	VUS2
SIDS172	F	8	2	rs751739709	*ANKRD1*	NG_023227.1	NM_014391.2	missense	exon	c.460C>T	p.(Arg154Trp)	0.0000	NA	-	-	HCM	C65	Deleterious	bad	disease-causing	101	probably damaging	0.0000	NA	60	0.45	NA	NA	VUS1
SIDS176	F	3	2	rs764169067	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.15366G>T	p.(Lys5122Asn)	NA	NA	-	-	EDMD	C65	Deleterious	bad	NA	94	probably damaging	0.0000	0.0000	83	0.31	NA	NA	VUS2
SIDS184	F	4	2	rs770002854	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.5639G>A	p.(Arg1880His)	NA	NA	-	-	LQTS	C25	Deleterious	bad	disease-causing	29	possibly damaging	0.0000	0.0000	36	0.22	NA	NA	VUS1
SIDS184	F	4	2	rs139547471	*ELN*	NG_009261.1	NM_001278939.1	missense	exon	c.2246G>A	p.(Gly749Glu)	0.0000	0.0000	-	-	connective tissue?	C0	Deleterious	NA	disease-causing	98	probably damaging	0.0000	NA	30	0.27	NA	NA	VUS1
SIDS194	F	5	2	rs72544141	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.4373A>G	p.(Glu1458Gly)	0.0010	0.0002	LQTS	DM	LQTS	C65	Deleterious	bad	disease-causing	98	possibly damaging	0.0006	0.0010	63	0.44	NA	NA	VUS4
SIDS194	F	5	2	rs587780334	*FKRP*	NG_008898.2	NM_024301.4	missense	exon	c.1027G>C	p.(Glu343Gln)	NA	NA	-	-	CMD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	55	0.44	NA	NA	VUS1
SIDS194	F	5	2	rs149617373	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.15248A>G	p.(Asp5083Gly)	0.0000	0.0016	-	-	EDMD	C0	Deleterious	bad	polymorphism	94	benign	0.0012	0.0010	122	0.49	NA	NA	VUS1
SIDS202	M	1	1	rs145169006	*LAMP2*	NG_007995.1	NM_001122606.1	missense	exon	c.661G>A	p.(Gly221Arg)	0.0010	0.0025	DCM	DM?	HCM	C0	Deleterious	bad	disease-causing	125	probably damaging	0.0017	0.0000	37	homozygote	NA	NA	VUS2
SIDS202	M	1	1	rs200056085	*DSC2*	NG_008208.2	NM_024422.3	Frameshift	exon	c.2686_2687dup	p.(Ala897Lysfs*4)	0.0060	0.0190	ARVC	DM?	ARVC	NA	NA	NA	NA	180	NA	0.0122	0.0100	168	0.45	NA	NA	VUS1
SIDS212	M	1	2	rs35973133	*BMPR1B*	NG_009245.1	NM_001256793.1	missense	exon	c.761G>A	p.(Arg254His)	0.0000	0.0012	-	-	others	C0	Deleterious	NA	disease-causing	29	possibly damaging	0.0015	0.0000	89	0.48	NA	NA	VUS1
SIDS212	M	1	2	rs759512753	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.25241C>T	p.(Thr8414Met)	NA	NA	-	-	EDMD	C0	Deleterious	bad	NA	81	probably damaging	0.0000	0.0000	76	0.47	NA	NA	VUS1
SIDS213	M	1	2	rs139203363	*SLC22A5*	NG_008982.1	NM_003060.3	missense	exon	c.34G>A	p(.Gly12Ser)	0.0010	0.0016	systemic primary carnitine deficiency	DM	SPCD	C0	Deleterious	good	NA	56	probably damaging	0.0007	0.0010	141	0.48	NA	NA	VUS1
SIDS216	M	7	2	rs763089587	*AKAP9*	NG_011623.1	NM_005751.4	missense	exon	c.4994A>T	p.(Gln1665Leu)	NA	NA	-	-	LQTS	C25	Deleterious	bad	disease-causing	113	benign	0.0000	0.0000	43	0.47	NA	NA	VUS1
SIDS217	M	3	2	rs35912339	*MYLK*	NG_029111.1	NM_053025.3	missense	exon	c.1007C>T	p.(Pro336Leu)	0.0000	0.0013	-	-	HCM	C15	Deleterious	bad	polymorphism	98	possibly damaging	0.0017	0.0020	39	0.38	NA	NA	VUS1
SIDS219	M	10	2	rs78727187	*FBN2*	NG_008750.1	NM_001999.3	missense	exon	c.4141C>A	p.(His1381Asn)	0.0030	0.0050	-	-	MFS	C65	Deleterious	bad	disease-causing	68	possibly damaging	0.0000	0.0010	93	0.49	NA	NA	VUS2
SIDS220	M	5	1	rs138797058	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.15848A>G	p.(Asp5283Gly)	0.0000	0.0000	-	-	EDMD	C0	Deleterious	bad	polymorphism	94	possibly damaging	0.0000	0.0010	57	0.47	NA	NA	VUS2
SIDS220	M	5	1	rs587780334	*FKRP*	NG_008898.2	NM_024301.4	missense	exon	c.1027G>C	p.(Glu343Gln)	NA	NA	-	-	CMD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	39	0.46	NA	NA	VUS1
SIDS220	M	5	1	rs140233643	*MYLK2*	NG_012847.1	NM_033118.3	missense	exon	c.463A>T	p.(Ile155Phe)	0.0000	0.0001	-	-	HCM	C0	Deleterious	good	polymorphism	21	possibly damaging	0.0000	0.0000	43	0.40	NA	NA	VUS1
SIDS223	F	2	1	rs148323523	*DCHS1*	NG_033858.1	NM_003737.2	missense	exon	c.6467T>A	p.(Val2156Glu)	0.0000	0.0006	-	-	MVP	C65	Deleterious	bad	disease-causing	121	possibly damaging	0.0002	0.0000	122	0.48	NA	NA	VUS4
SIDS225	F	3	2	rs141159831	*MYH11*	NG_009299.1	NM_001040114.1	missense	exon	c.3970C>A	p.(Leu1324Ile)	0.0030	0.0000	-	-	HCM, TAA	C0	Deleterious	bad	disease-causing	5	possibly damaging	0.0000	0.0000	66	0.33	NA	NA	VUS2
SIDS225	F	3	2	rs74120667	*NEBL*	NG_017092.1	NM_006393.2	missense	exon	c.2057T>C	p.(Val686Ala)	0.0070	0.0000	-	-	DCM	C0	Deleterious	bad	disease-causing	64	benign	0.0000	0.0000	124	0.32	NA	NA	VUS2
SIDS225	F	3	2	rs147173048	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.16178C>T	p.(Ala5393Val)	0.0000	0.0000	-	-	EDMD	C0	Tolerated	bad	disease-causing	64	possibly damaging	0.0000	0.0000	65	0.25	NA	NA	VUS2
SIDS225	F	3	2	rs587780334	*FKRP*	NG_008898.2	NM_024301.4	missense	exon	c.1027G>C	p.(Glu343Gln)	NA	NA	-	-	CMD	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	38	0.34	NA	NA	VUS1
SIDS226	F	2	1	rs151242451	*DMD*	NG_012232.1	NM_004006.2	missense	exon	c.2261G>T	p.(Gly754Val)	0.0020	0.0000	-	-	DCM	C0	Tolerated	good	disease-causing	109	probably damaging	0.0000	0.0000	126	0.44	NA	NA	VUS2
SIDS226	F	2	1	rs36026860	*SEMA3A*	NG_011489.1	NM_006080.2	missense	exon	c.1198A>G	p.(Ile400Val)	0.0010	0.0000	Kallmann syndrome	DM	IVF	C0	Deleterious	bad	disease-causing	29	benign	0.0000	0.0000	259	0.48	NA	NA	VUS2
SIDS226	F	2	1	rs150179494	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.12170C>T	p.(Pro4057Leu)	0.0010	0.0000	-	-	EDMD	C15	Deleterious	bad	NA	98	possibly damaging	0.0000	0.0010	83	0.36	NA	NA	VUS2
SIDS226	F	2	1	rs35530544	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.11218C>A	p.(Leu3740Ile)	0.0090	0.0001	Cardiac arrhythmia	DM	LQTS	C0	Tolerated	good	disease-causing	5	possibly damaging	0.0000	0.0010	131	0.47	NA	NA	VUS1
SIDS226	F	2	1	rs142873474	*CTGF*	NG_016131.1	NM_001901.2	missense	exon	c.645G>A	p.(Met215Ile)	0.0000	0.0000	-	-	cutix laxa	C0	Tolerated	good	disease-causing	10	possibly damaging	0.0000	0.0000	124	0.40	NA	NA	VUS1
SIDS226	F	2	1	rs76927619	*RAB3GAP1*	NG_016972.1	NM_001172435.1	missense	exon	c.669G>T	p.(Leu223Phe)	0.0090	0.0000	-	-	CMRH	C0	Tolerated	good	disease-causing	22	probably damaging	0.0000	0.0000	213	0.50	NA	NA	VUS1
SIDS226	F	2	1	rs35654757	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.19698G>T	p.(Met6566Ile)	0.0050	0.0000	-	-	EDMD	C0	Deleterious	bad	NA	10	benign	0.0000	0.0000	44	0.41	NA	NA	VUS1
SIDS226	F	2	1	rs144108695	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.10313G>A	p.(Cys3438Tyr)	0.0000	0.0000	-	-	EDMD	C0	Tolerated	good	polymorphism	194	possibly damaging	0.0000	0.0000	222	0.47	NA	NA	VUS1
SIDS227	M	4	2	rs765792077	*MYH6*	NG_023444.1	NM_002471.3	missense	exon	c.100C>T	p.(Arg34Cys)	0.0000	NA	-	-	HCM	C55	Deleterious	bad	polymorphism	180	probably damaging	0.0010	0.0000	91	0.35	NA	NA	VUS2
SIDS227	M	4	2	rs143584663	*NEBL*	NG_017092.1	NM_006393.2	missense	exon	c.2654C>T	p.(Ser885Phe)	0.0010	0.0040	-	-	DCM	C0	Deleterious	bad	disease-causing	155	probably damaging	0.0000	0.0050	48	0.33	NA	NA	VUS1
SIDS227	M	4	2	rs748204670	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.4168G>C	p.(Asp1390His)	NA	NA	-	-	EDMD	C0	Deleterious	bad	polymorphism	81	probably damaging	0.0000	0.0000	76	0.41	NA	NA	VUS1
SIDS234	M	2	2	rs771607178	*HMGCS2*	NG_013348.1	NM_005518.3	splice site	splice site	c.1016+1G>A	p.(?)	0.0000	NA	Mitochondrial HMG-CoA synthase deficiency	DM	HMGCS	NA	NA	NA	NA	NA	NA	0.0000	NA	35	0.49	NA	NA	VUS1
SIDS235	F	6	2	rs776254819	*ANK2*	NG_009006.2	NM_001148.4	missense	exon	c.229G>A	p.(Val77Met)	NA	NA	-	-	LQTS	C0	Deleterious	bad	disease-causing	21	probably damaging	0.0000	0.0000	49	0.47	NA	NA	VUS1
SIDS236	M	2	2	rs771703569	*KCND3*	NG_032011.2	NM_004980.4	missense	exon	c.1292G>A	p.(Arg431His)	NA	NA	-	-	BrS	C0	Deleterious	bad	disease-causing	29	probably damaging	0.0000	0.0000	22	0.32	NA	NA	VUS1
SIDS236	M	2	2	rs36083134	*TMEM43*	NG_008975.1	NM_024334.2	missense	exon	c.1096G>A	p.(Ala366Thr)	0.0060	0.0000	-	-	ARVC	C0	Tolerated	good	disease-causing	58	possibly damaging	0.0000	0.0000	60	0.47	NA	NA	VUS1
SIDS237	F	1	2	rs141159831	*MYH11*	NG_009299.1	NM_001040114.1	missense	exon	c.3970C>A	p.(Leu1324Ile)	0.0030	0.0000	-	-	HCM, TAA	C0	Deleterious	bad	disease-causing	5	possibly damaging	0.0000	0.0000	76	0.39	NA	NA	VUS2
SIDS237	F	1	2	rs74120667	*NEBL*	NG_017092.1	NM_006393.2	missense	exon	c.2057T>C	p.(Val686Ala)	0.0070	0.0000	-	-	DCM	C0	Deleterious	bad	disease-causing	64	benign	0.0000	0.0000	133	0.29	NA	NA	VUS2
SIDS237	F	1	2	rs147173048	*SYNE2*	NG_011756.1	NM_182914.2	missense	exon	c.16178C>T	p.(Ala5393Val)	0.0000	0.0000	-	-	EDMD	C0	Tolerated	bad	disease-causing	64	possibly damaging	0.0000	0.0000	32	0.28	NA	NA	VUS2
SIDS238	M	7	1	rs140704891	*RANGRF*	NG_028189.1	NM_016492.4	nonsense	exon	c.181G>T	p.(Glu61*)	0.0020	0.0054	Altered function	FP	Afib	NA	NA	NA	disease-causing	NA	NA	0.0053	0.0050	55	0.49	NA	NA	VUS2
SIDS239	M	2	1	rs374482089	*SYNE1*	NG_012855.1	NM_182961.2	missense	exon	c.6268G>C	p.(Glu2090Gln)	0.0000	0.0000	-	-	EDMD	C25	Deleterious	bad	NA	29	benign	0.0000	0.0000	26	0.31	NA	NA	VUS2

Abbreviations:

F: female, M: male, mo: months, NA: not available.

DM: disease-causing, DM?: Potentially disease-causing, DP: disease-causing polymorphisms reported to be significant association with diseases and assumed to be functional, FP: in vitro or in vivo functional polymorphism.

Afib: atrial fibrillation, AOVD: aortic valve disease, ARVC: arrhythmogenic right ventricular cardiomyopathy, ASD: aortic septal defect, BrS: Brugada syndrome, CMD: congenital muscular dystrophy, CMRH: cataract-mental retardation-hypgonadism, CPVT: catecholaminergic polymorphic ventricular tachycardia, CVDX: cardiac valvular dysplasia x-linked, DCM: dilated cardiomyopathy, EDMD: Emery-dreifuss muscular dystrophy, EDS: Ehlers-Danlos syndrome, GA: glutaric aciduria,GSD: glycogen storage disease, HCM:

hypertrophic cardiomyopathy, HHF: familial hyperinsulinemic hypoglycaemia, HMGCS: HMG-CoA synthase deficiency, IVF: idiopathic ventricular fibrillation, LQTS: long QT syndrome, LVNC: left ventricular noncompaction cardiomyopathy, MCAD: medium-chain-acyl-CoA-dehydrogenase deficiency, MVP: mitral valve prolapse, MFS: marfan syndrome, PAH: pulmonary hypertension, SPCD: systemic primary carnitine deficiency, TAAD: familiar thoracic aortic aneursym and aortic dissection.

AGVGD align Grantham variation and Grantham deviation, SIFT sorting intolerant from tolerant prediction, MAPP multivariate analysis of protein polymorphism prediction, MAF: minor allele frequency, dbSNP: MAF in general population in NCBI dbSNP, EspEAMAF: MAF in European American population in NHLBI GO Exome Sequencing Project, ExAC EURMAF: MAF in European population in exome aggregation consortium, 1000 Genomes Project EURMAF: MAF in Europan population in 1000 Genomes Project.

~ no dbSNP rs-nr. available.

- no information available.

[a]based on 118 in-house control exoms.