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(54) **DIAGNOSTIC TEST FOR CARDIOMYOPATHY**

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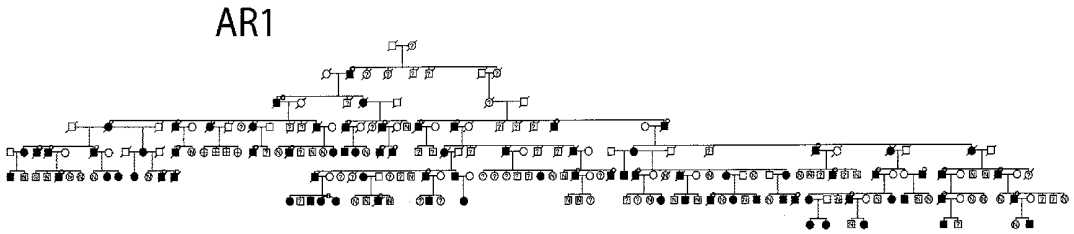
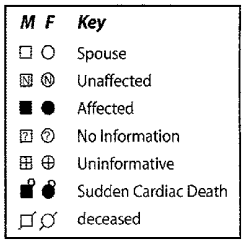
C12Q 1/68	(2006.01)
C07H 21/04	(2006.01)
G01N 33/53	(2006.01)
G01N 33/566	(2006.01)

(52) **U.S. Cl.** **506/9**; 435/4; 435/6; 536/24.31; 435/7.1; 436/501

(57) **ABSTRACT**

Methods and compositions relating to diagnosing and treating cardiomyopathy and particularly relating to methods and compositions for diagnosing and treating arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) are described. Provided are methods for screening for, diagnosing or detecting a risk of developing arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) comprising detecting the presence of a transmembrane protein 43 (TMEM43) disease associated variant in a sample of a subject, wherein the presence of a TMEM43 disease variant is indicative that the subject has ARVD/C or an increased risk of developing ARVD/C compared to an individual having wild type TMEM43.





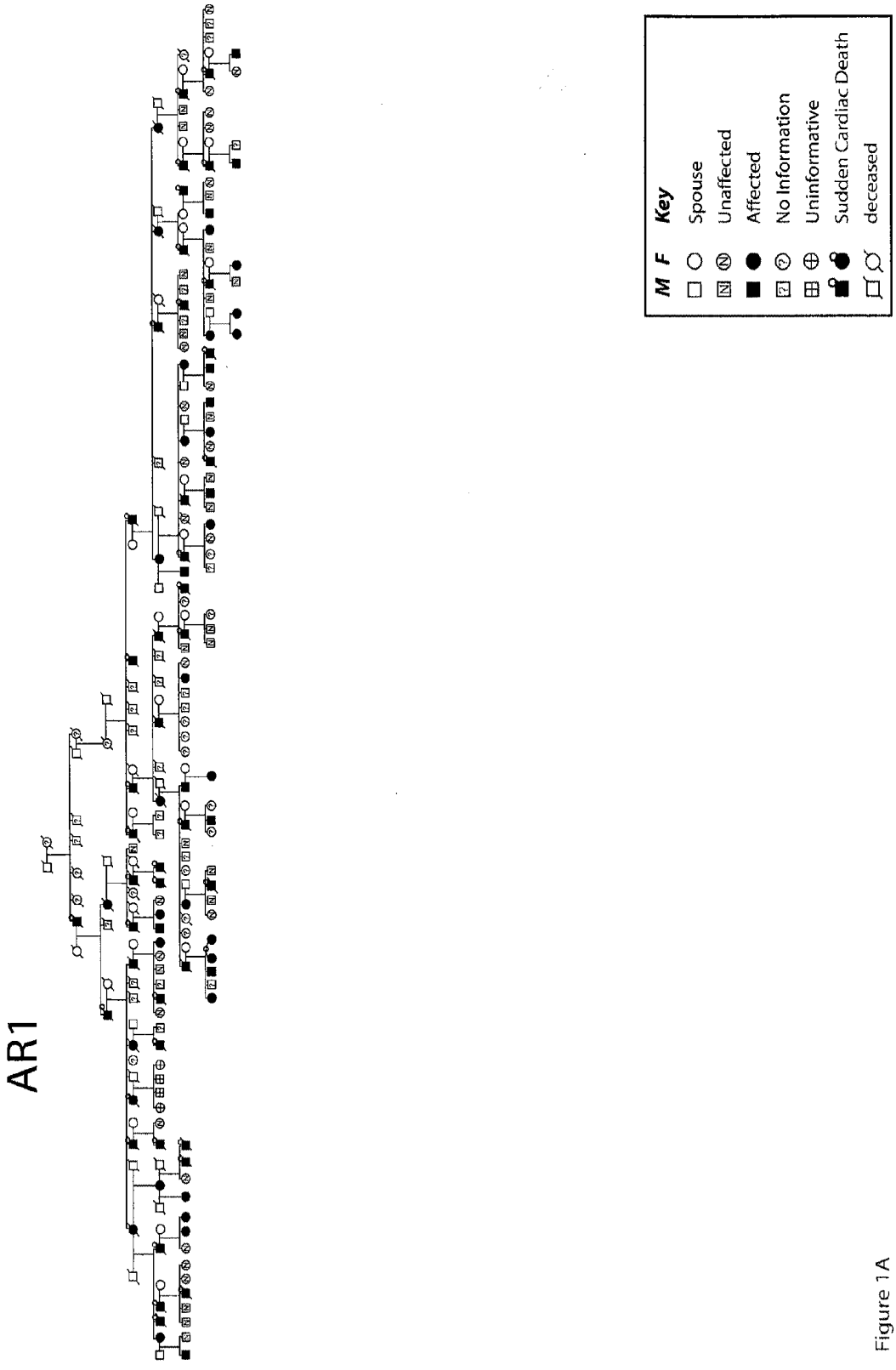

AR1
M F Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

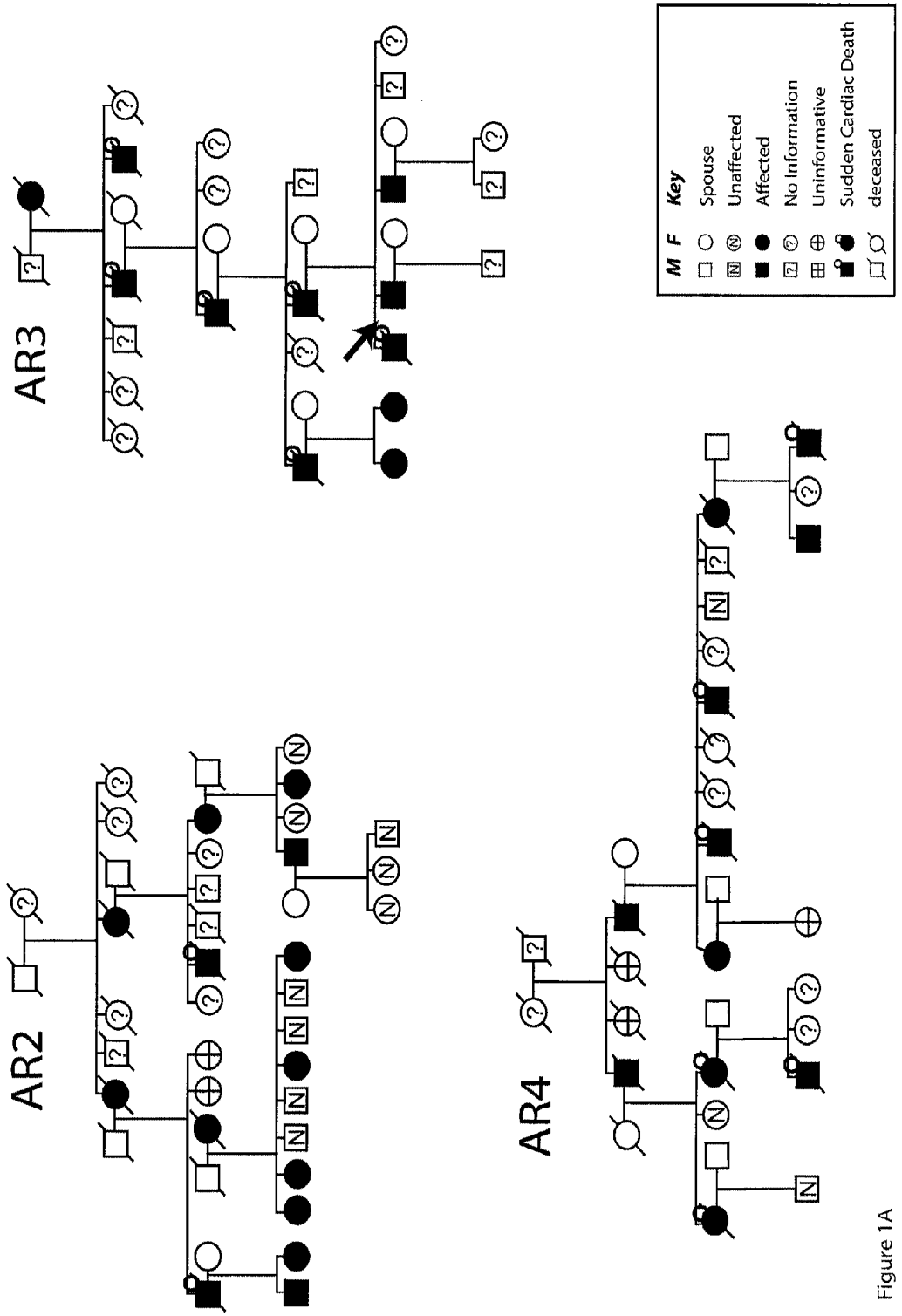

AR3
AR2
AR4
Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

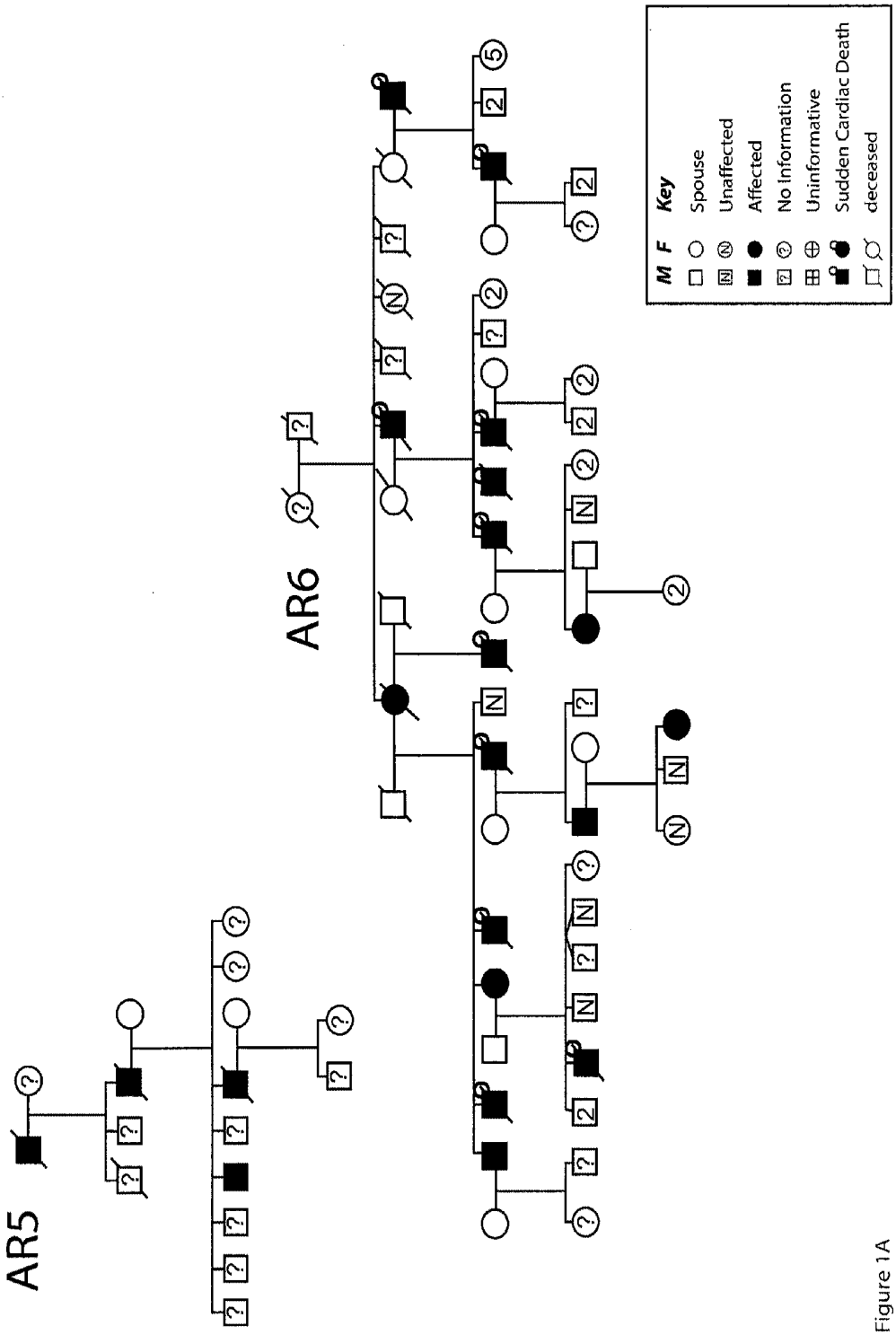

AR5
AR6
Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

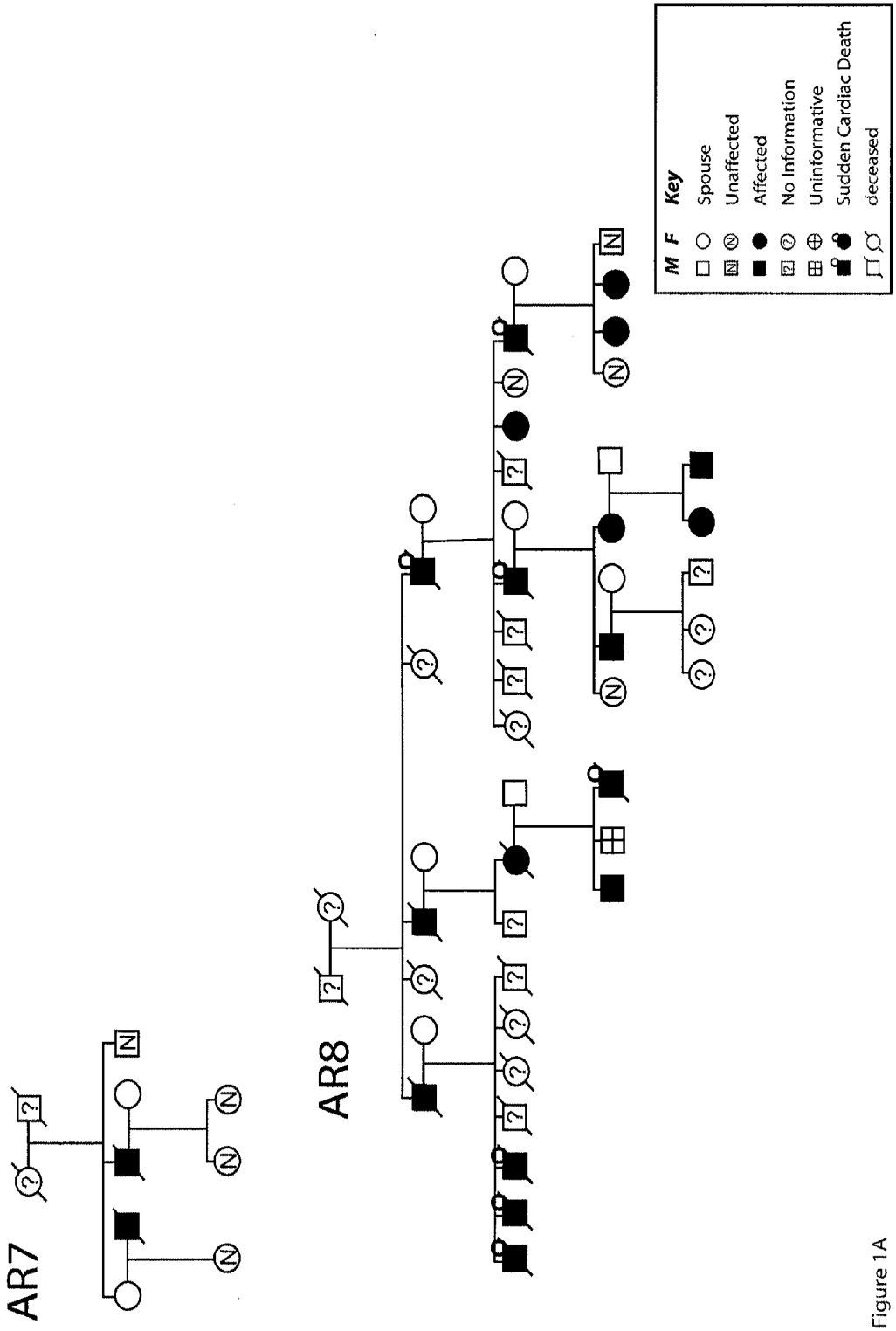

AR7
AR8
M F Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

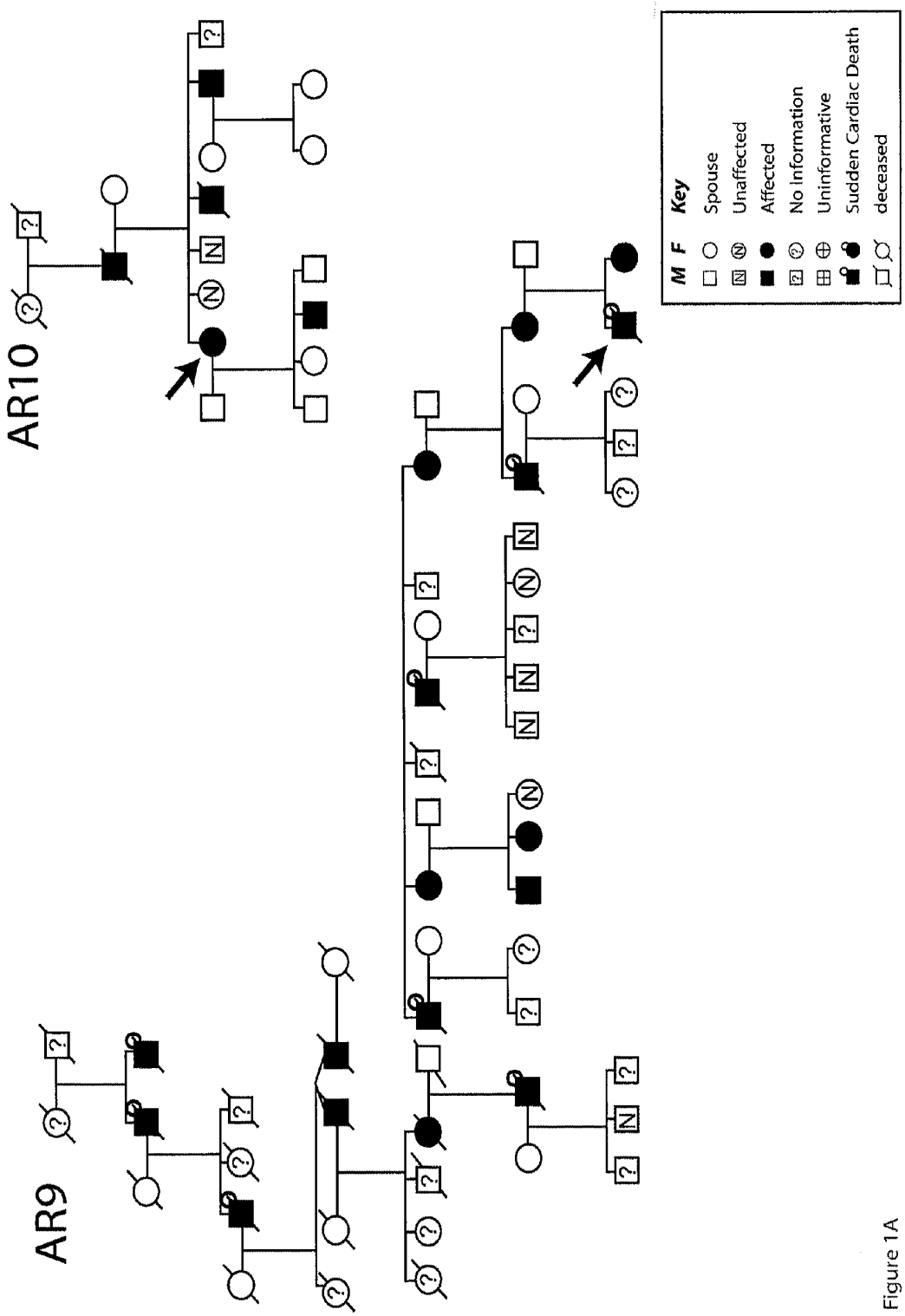

AR10
AR9
Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

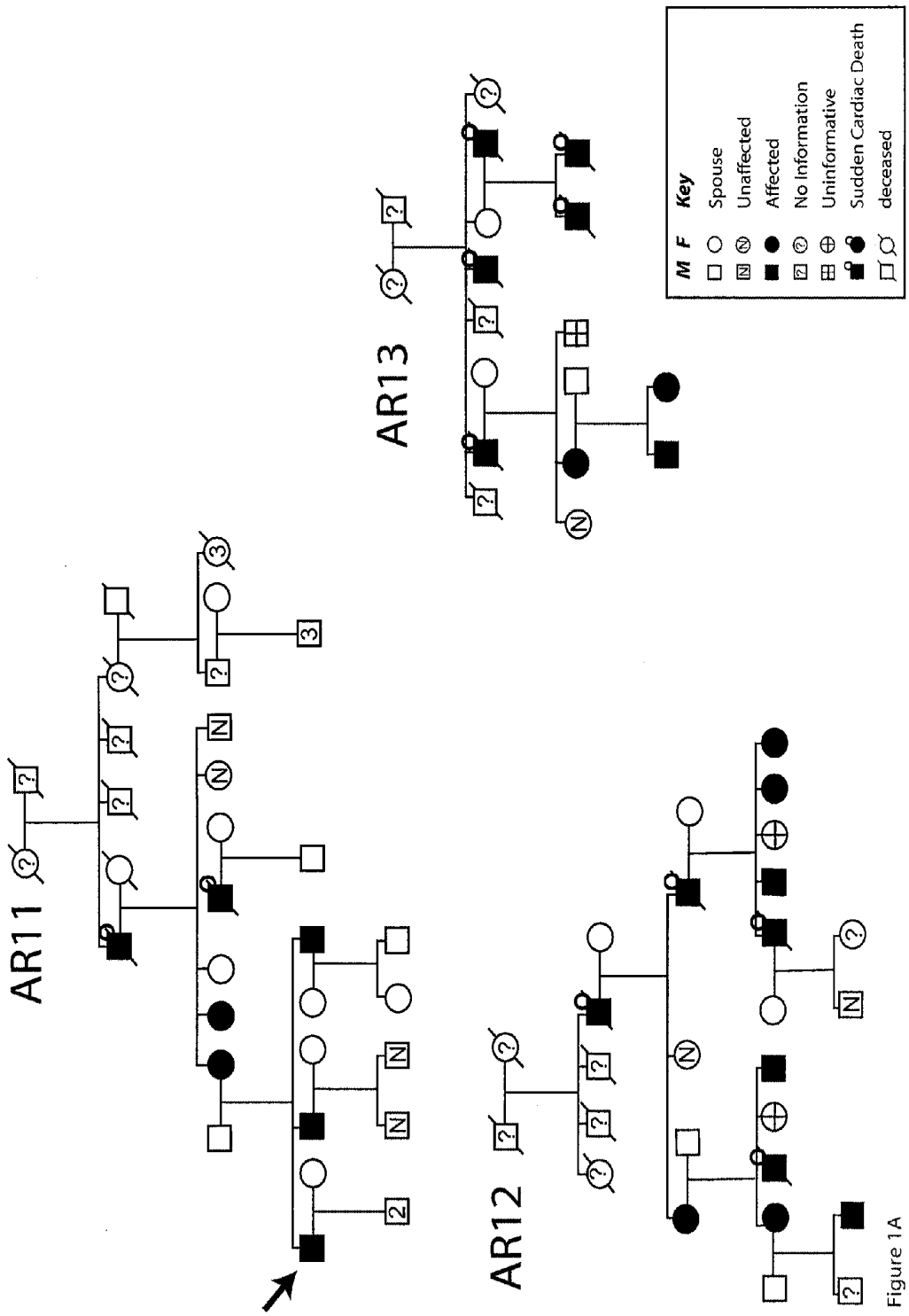

AR11
AR12
AR13
Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

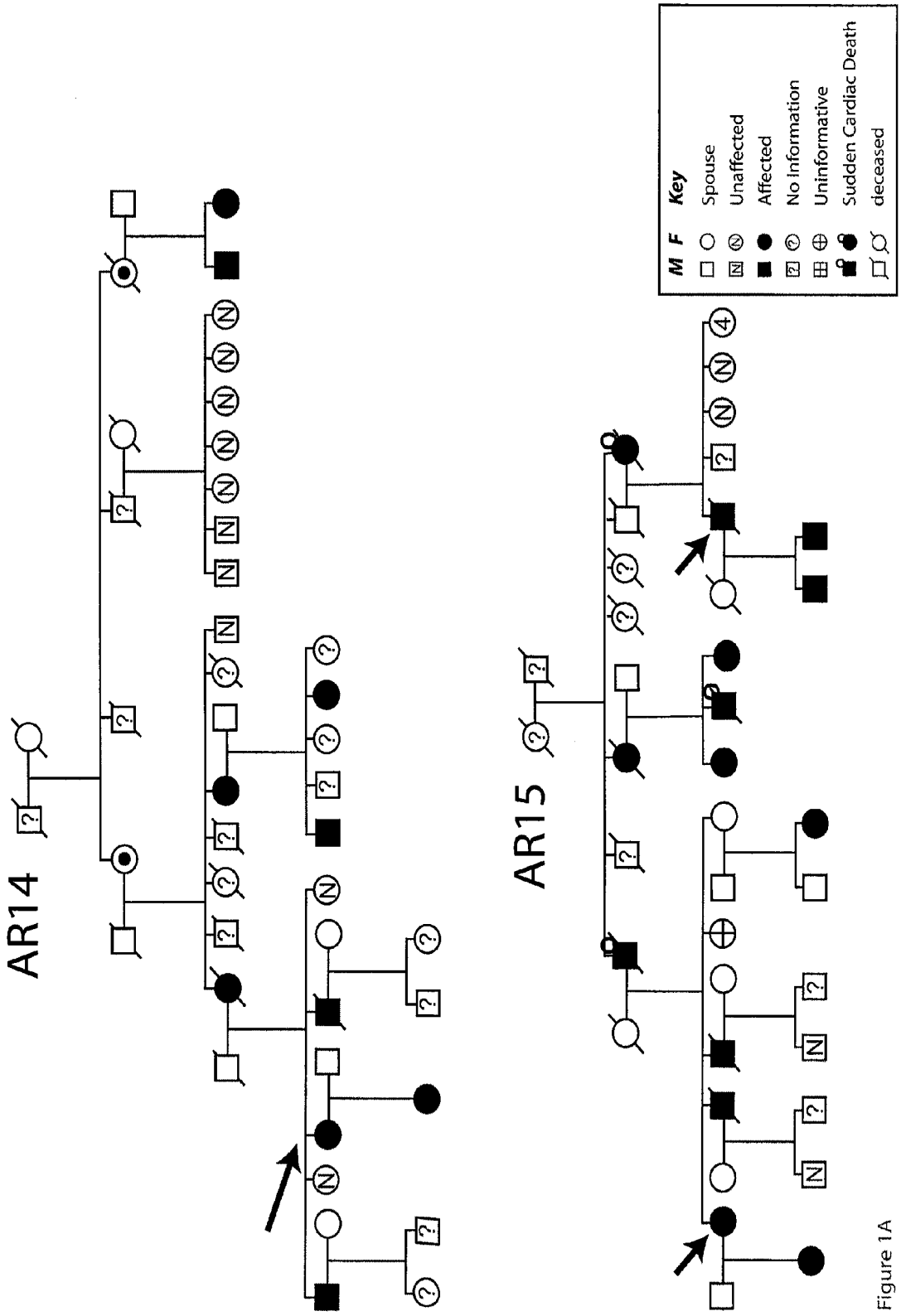
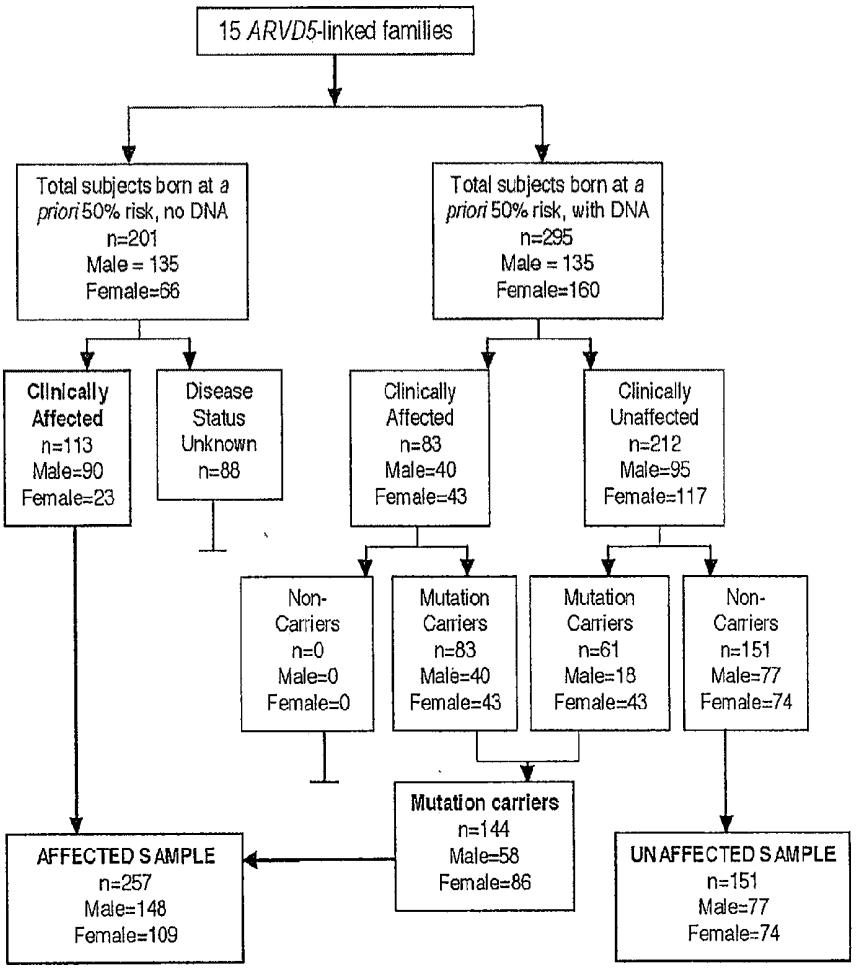

AR14
AR15
Key
Spouse
Unaffected
Affected
No Information
Uninformative
Sudden Cardiac Death
deceased

Figure 1A

B

Figure1B



Disease status criteria pre mutation testing:

Clinically Affected: (at least one of)	(1) Sudden cardiac death consistent with ARVC under 50 years of age (2) VT or VF under 50 years of age + treatment with drugs or ICD or cardioversion (3) Obligate carrier status (has a clinically affected parent and a child)
Clinically unaffected:	(1) Presented for screening based on family history

Disease status criteria post mutation testing:

Affected: (at least one of)	(1) Clinically affected (2) Mutation positive
Unaffected:	(1) Mutation negative
Unknown:	(1) Unavailable for analysis

Figure 2

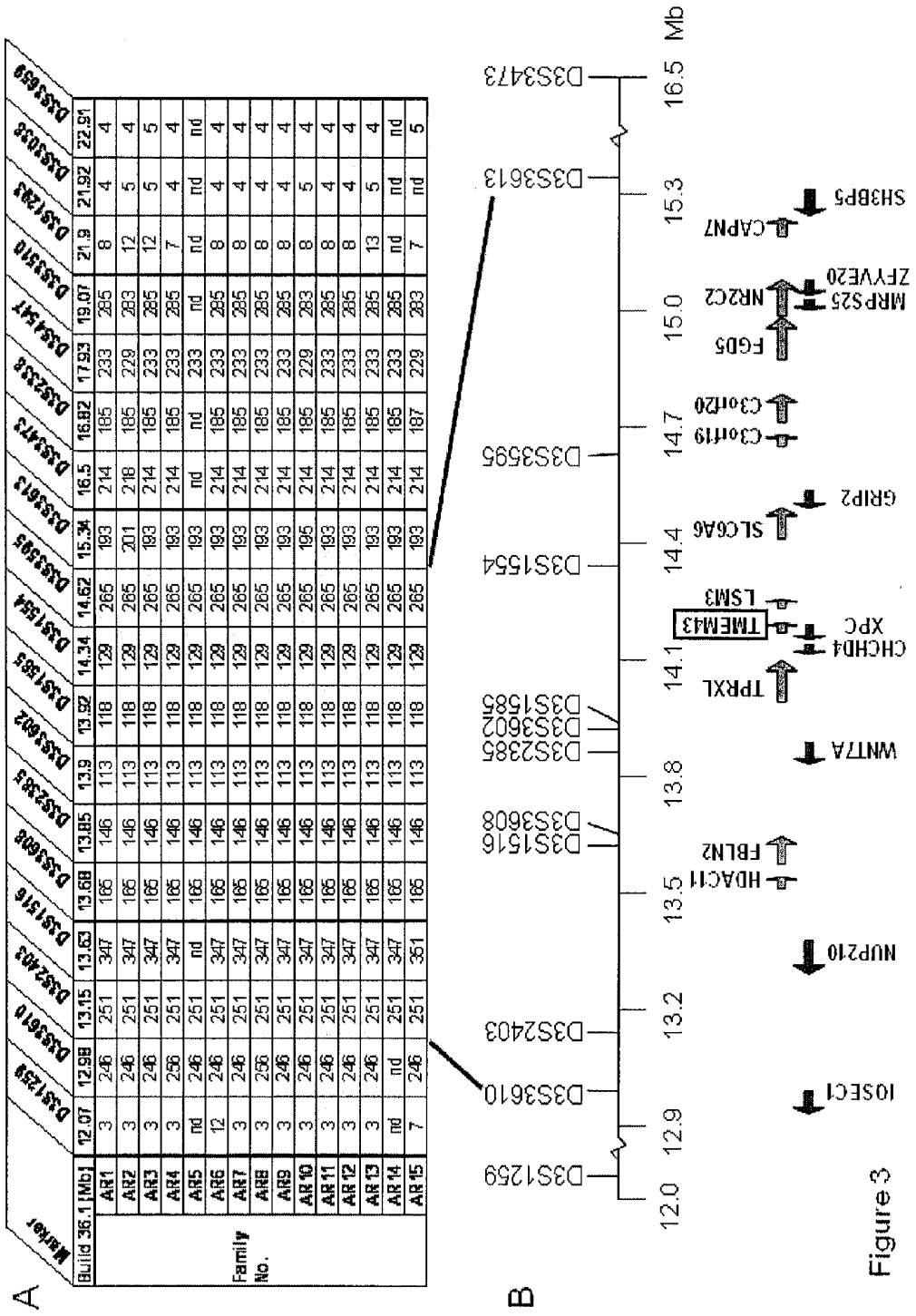

A
Marker
Build 36.1 (Mb)
Family No.
D3S1259
D3S3610
D3S2403
D3S1316
D3S3608
D3S2385
D3S1585
D3S3602
D3S1554
D3S3595
D3S3613
D3S3473
D3S2328
D3S1547
D3S1310
D3S1283
D3S1038
D3S1659
AR1 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR2 3 246 251 347 185 146 113 118 129 265 201 218 185 229 283 12 5 4 4
AR3 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 12 5 5 4
AR4 3 256 251 347 185 146 113 118 129 265 193 214 185 233 285 7 4 4 4
AR5 nd 246 251 nd 185 146 113 118 129 265 193 nd nd 233 nd nd nd nd nd
AR6 12 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR7 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR8 3 256 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR9 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR10 3 246 251 347 185 146 113 118 129 265 195 214 185 229 283 8 5 4 4
AR11 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR12 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 8 4 4 4
AR13 3 246 251 347 185 146 113 118 129 265 193 214 185 233 285 13 5 4 4
AR14 nd nd 251 347 185 146 113 118 129 265 193 214 185 233 285 nd nd nd nd
AR15 7 246 251 351 185 146 113 118 129 265 193 214 187 229 283 7 nd 5 5
B
D3S1259
D3S3610
D3S2403
D3S1516
D3S3608
D3S2385
D3S3602
D3S1585
D3S1554
D3S3595
D3S3613
D3S3473
12.0
12.9
13.2
13.5
13.8
14.1
14.4
14.7
15.0
15.3
16.5 Mb
IOSEC1
NUP210
HDAC11
FBLN2
WNT7A
TPRXL
CHCHD4
XPC
TMEM43
LSM3
SLC6A6
GRIP2
C3orf19
C3orf20
FGD5
NR2C2
MRPS25
ZFYVE20
CAPN7
SH3BP5

Figure 3

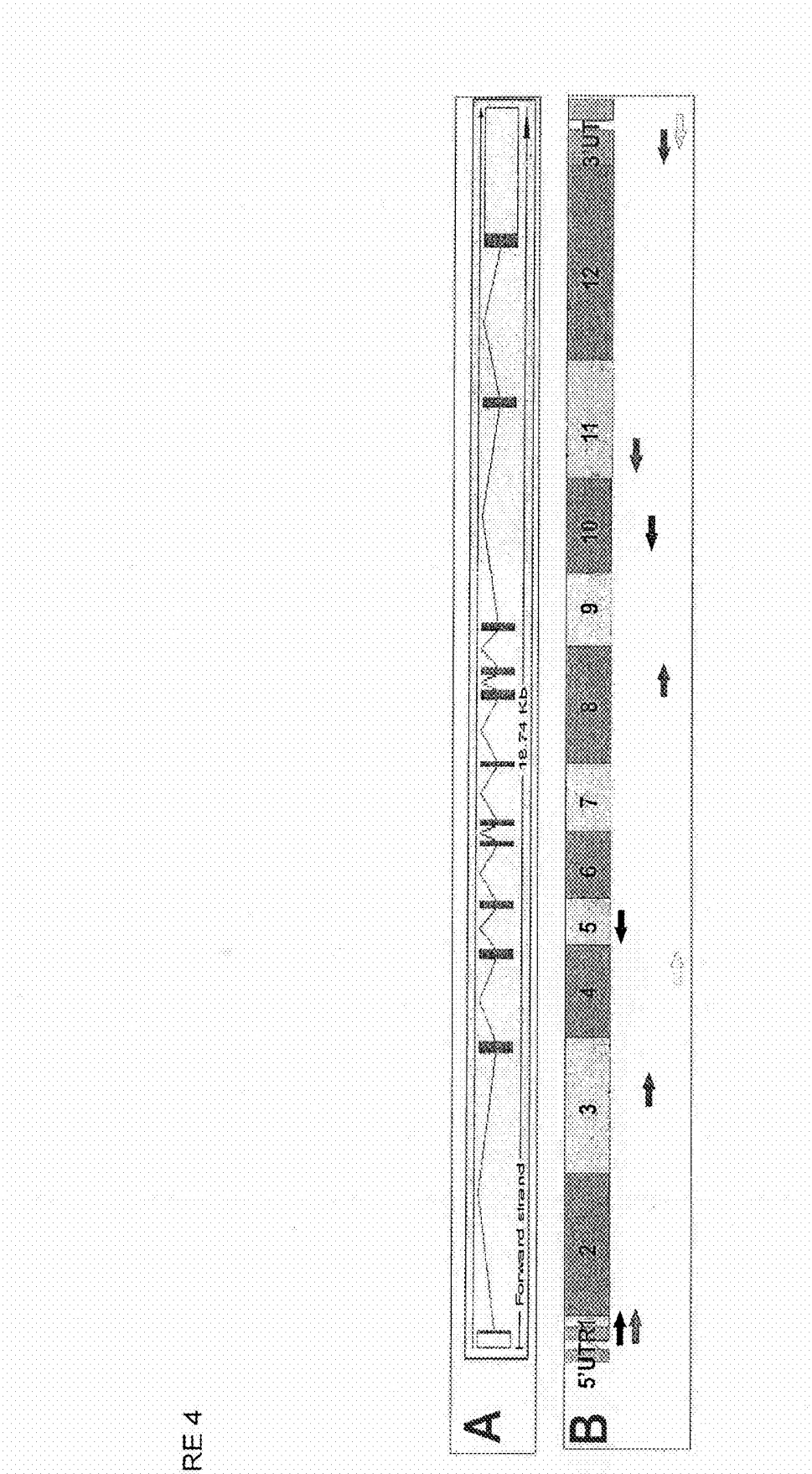
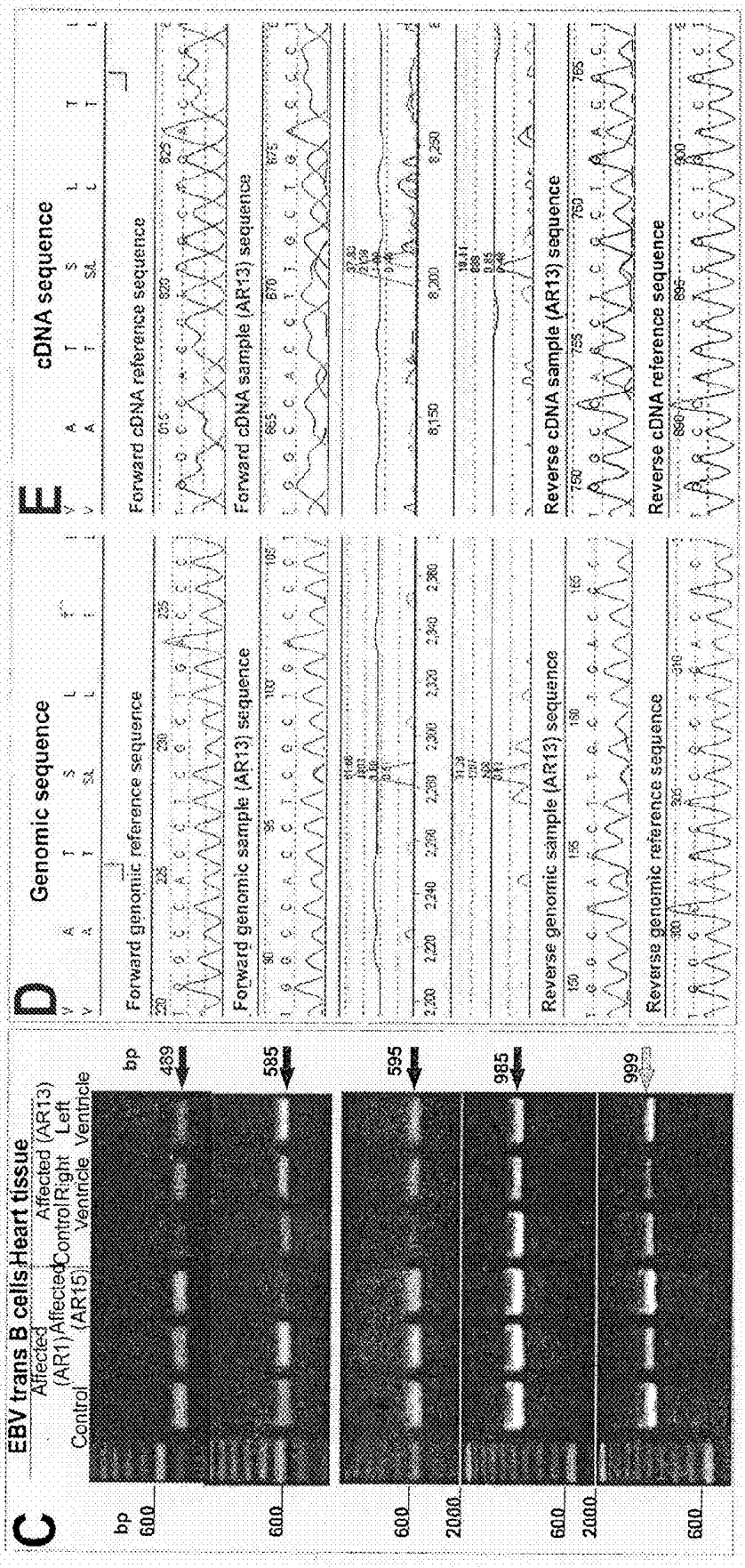


FIGURE 4

FIGURE 4 - CONTINUED



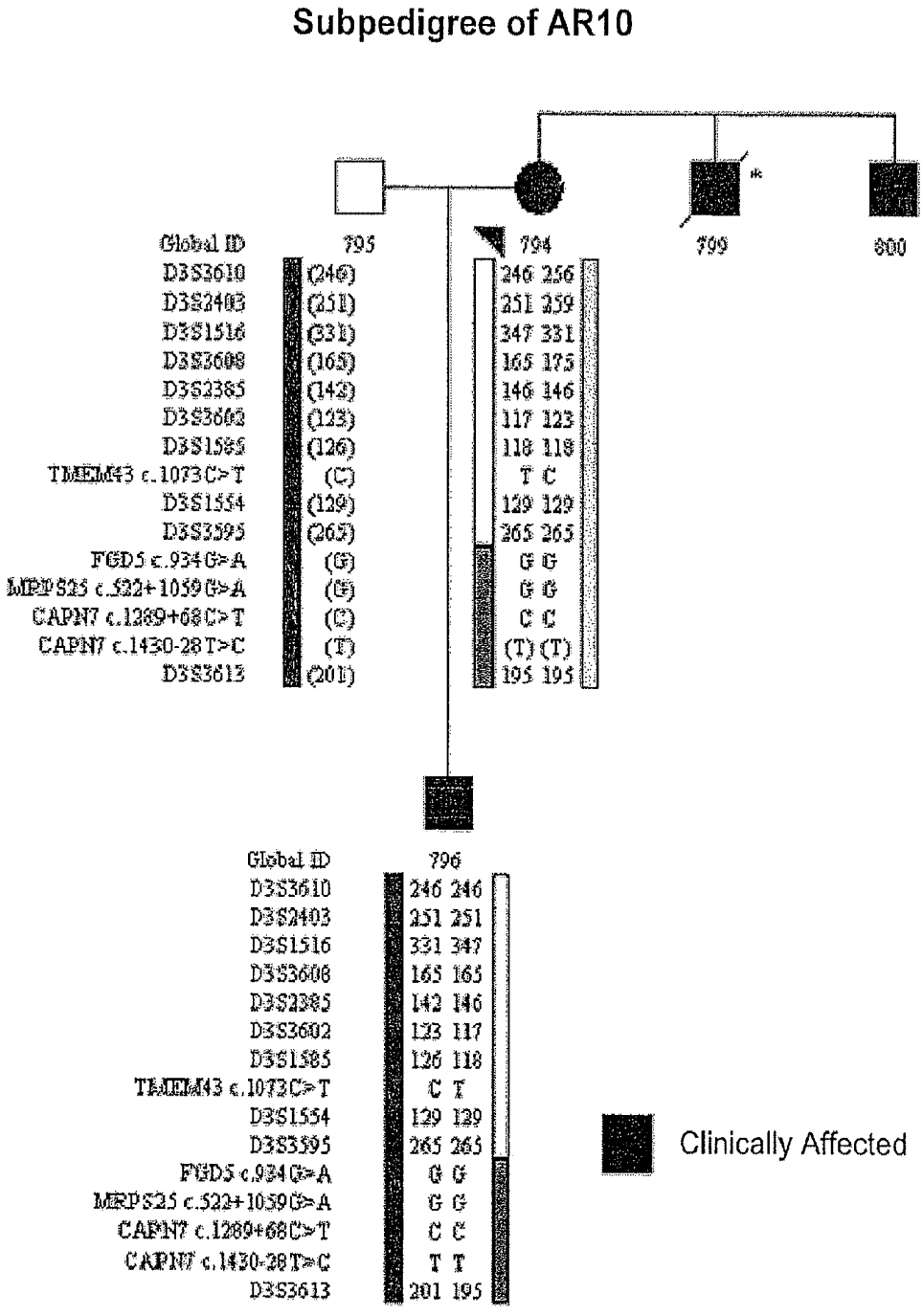
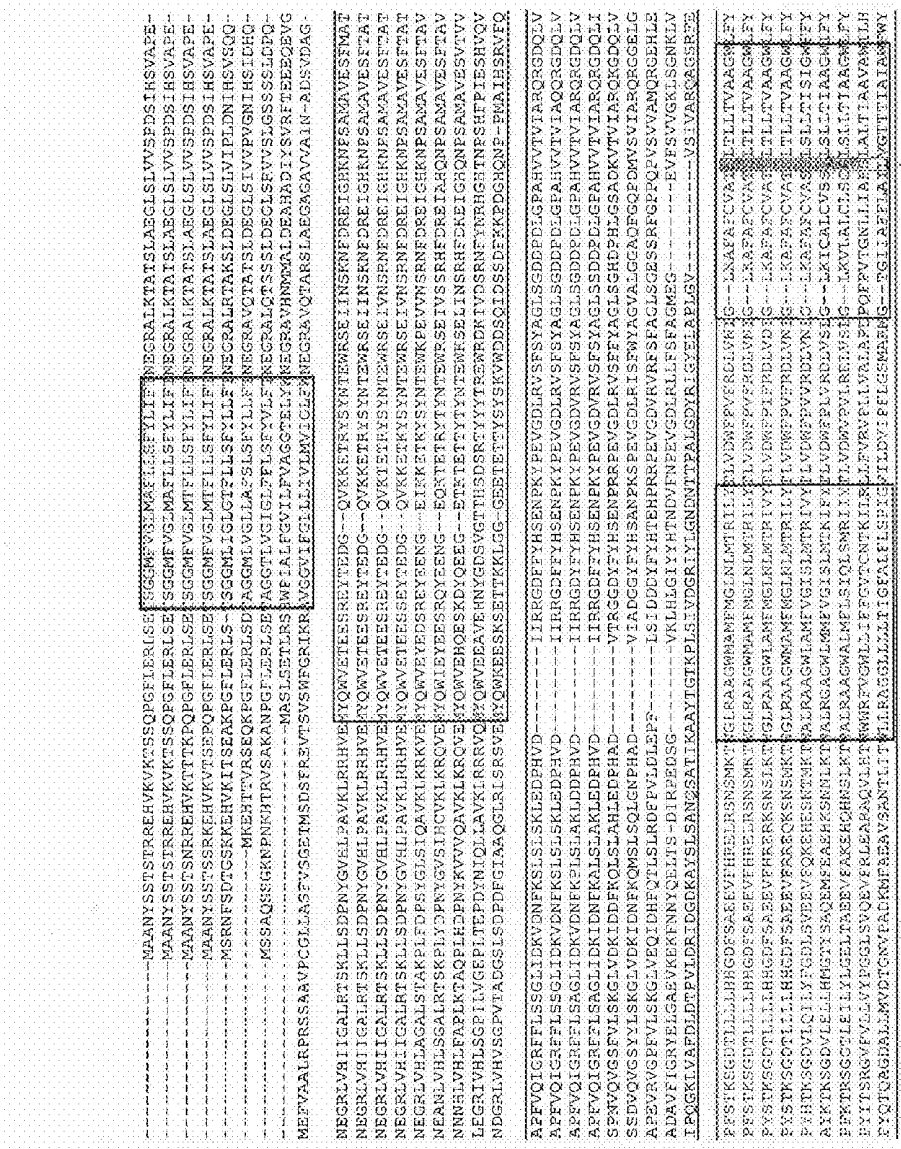

Subpedigree of AR10
Global ID
D3S3610
D3S2403
D3S1516
D3S3608
D3S2385
D3S3602
D3S1585
TMEM43 c.1073C>T
D3S1554
D3S3595
FGD5 c.934G>A
MRPS25 c.522+1059G>A
CAPN7 c.1289+68C>T
CAPN7 c.1430-28T>C
D3S3613
795
794
799
800
796
Clinically Affected

Figure 5

FIGURE 6


A
Homo sapien
Pan troglodytes
Canis familiaris
Mus musculus
Gallus gallus
Z. tropicalis
T. nigroviridis
D. melanogaster
Rhizobium loti
S3581

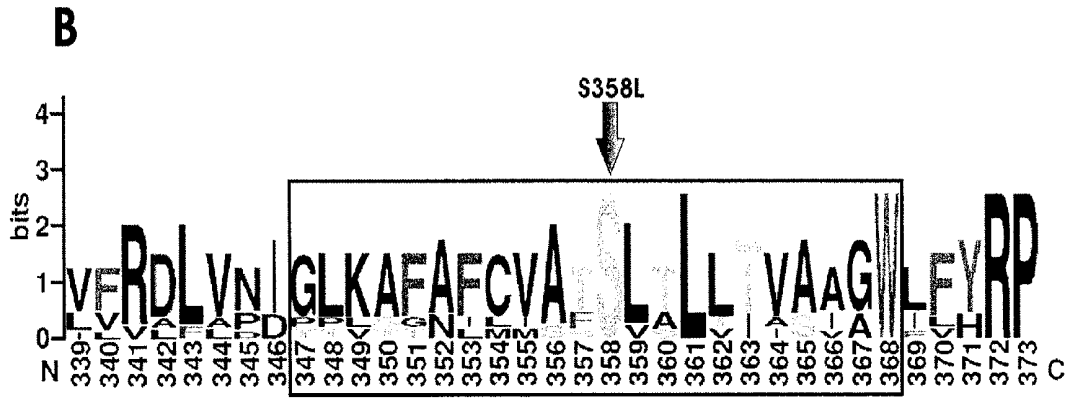


Figure 6 continued

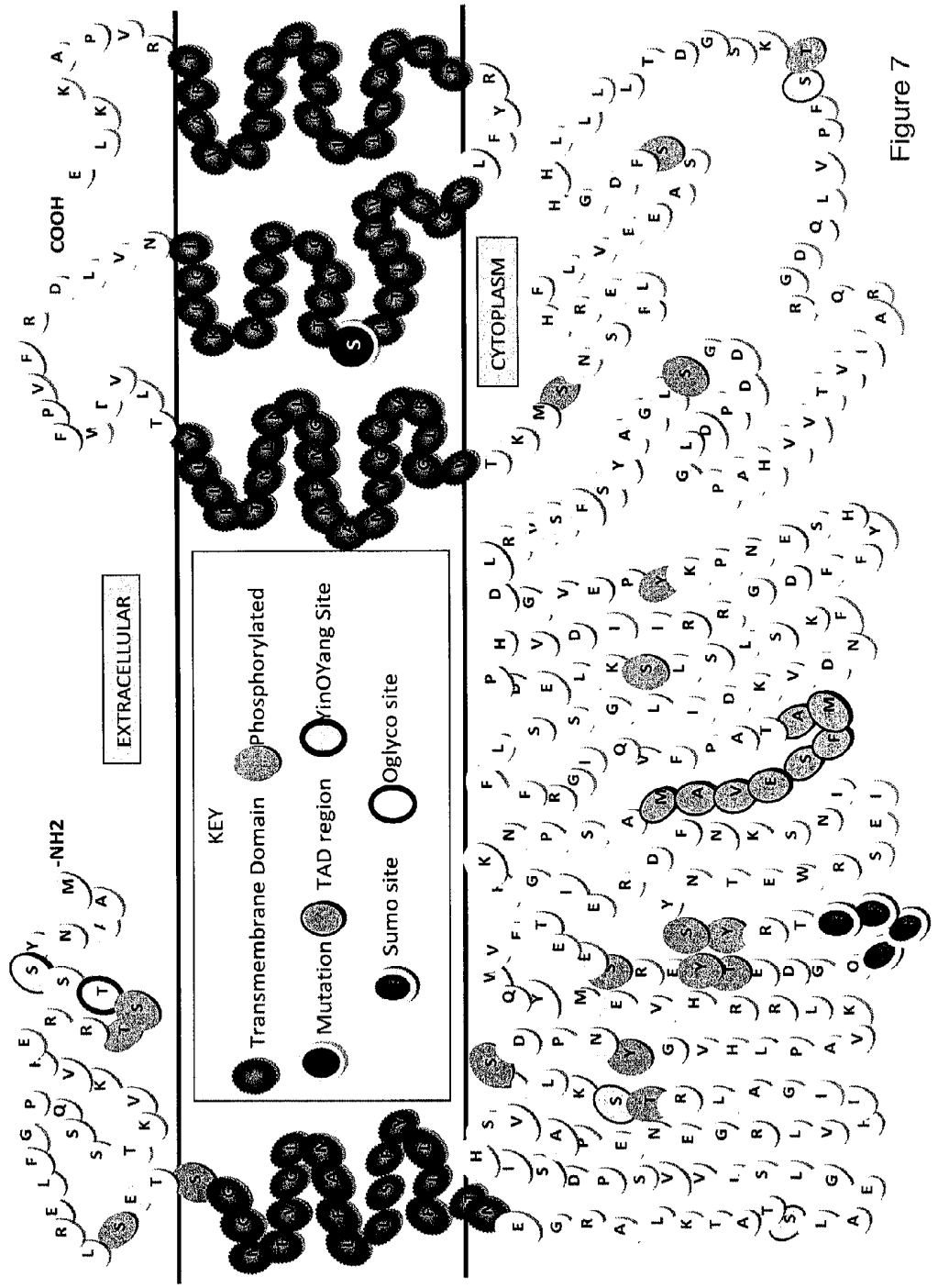

EXTRACELLULAR
CYTOPLASM
-NH2
COOH
KEY
Transmembrane Domain
Phosphorylated
Mutation
TAD region
YinOYang Site
Sumo site
Oglyco site

Figure 7

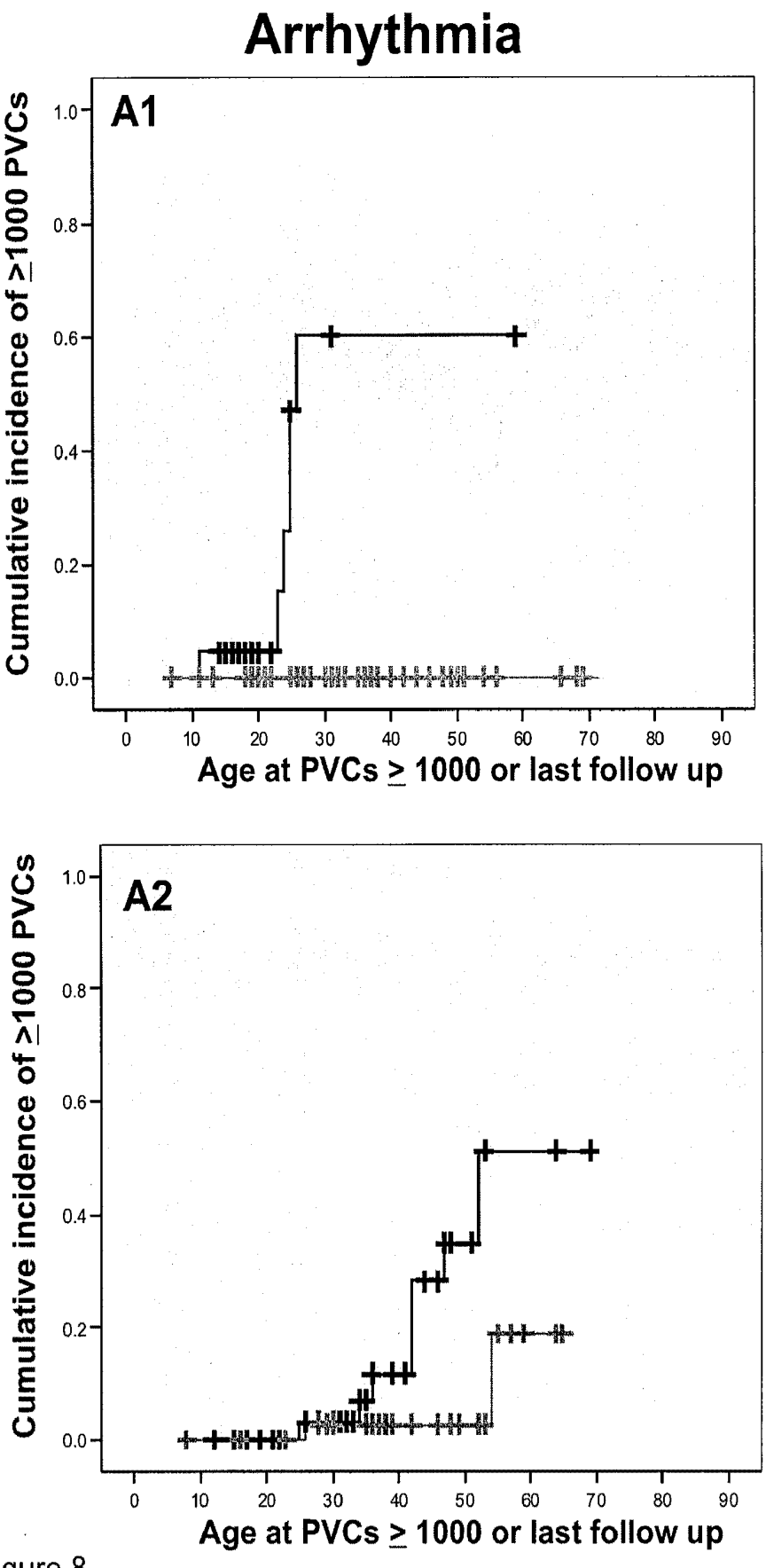
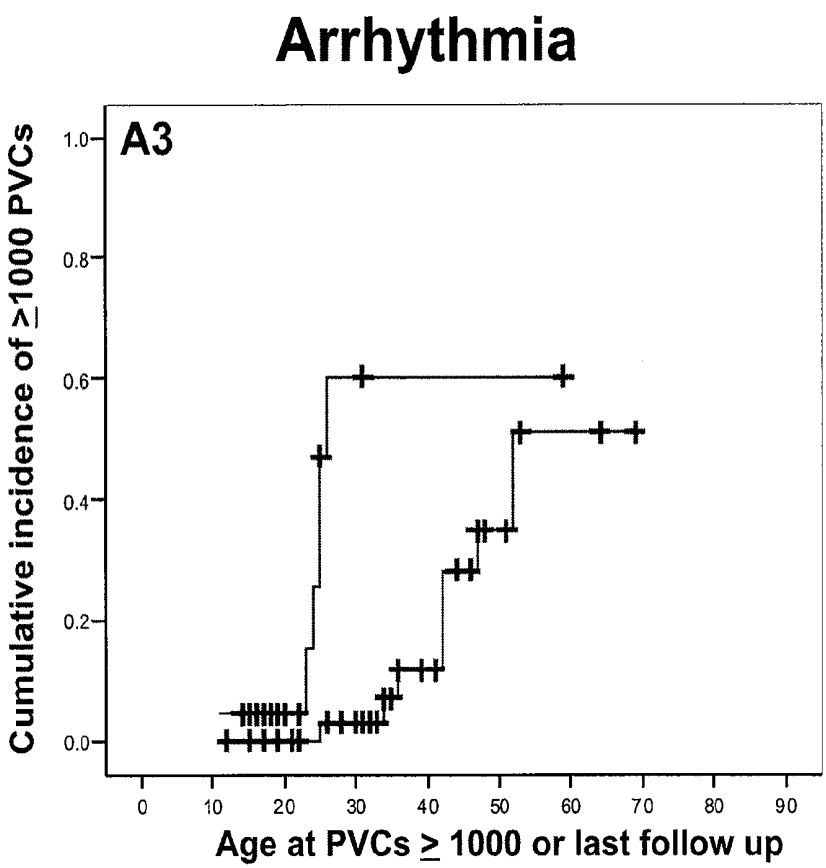

Arrhythmia
A1
Cumulative incidence of ≥1000 PVCs
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
60
70
80
90
Age at PVCs ≥ 1000 or last follow up
A2
Cumulative incidence of ≥1000 PVCs
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
60
70
80
90
Age at PVCs ≥ 1000 or last follow up

Figure 8



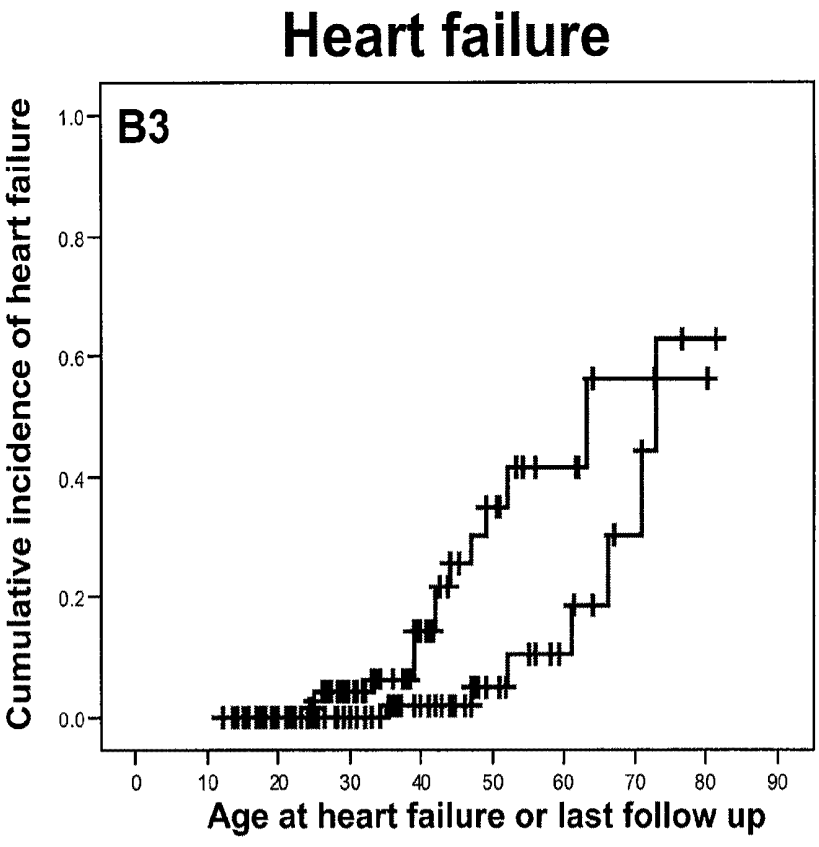
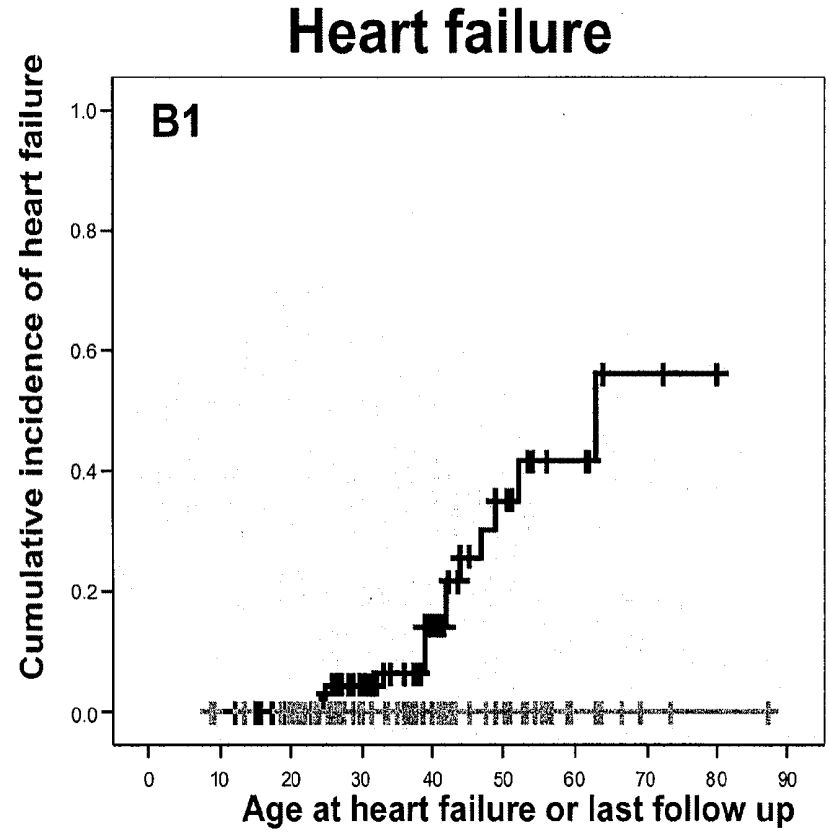
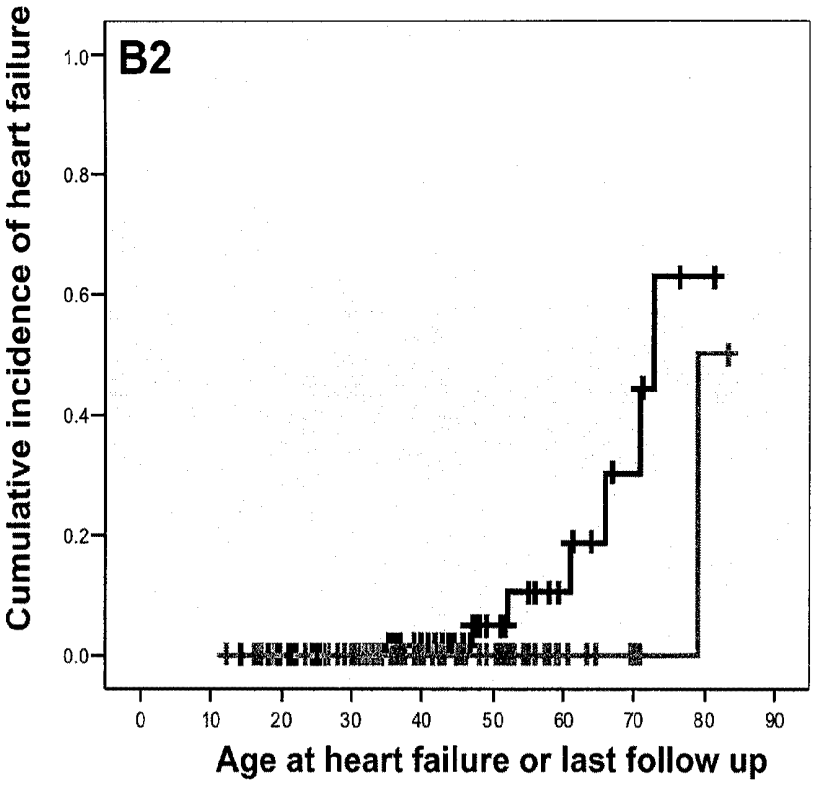


Figure 8 continued





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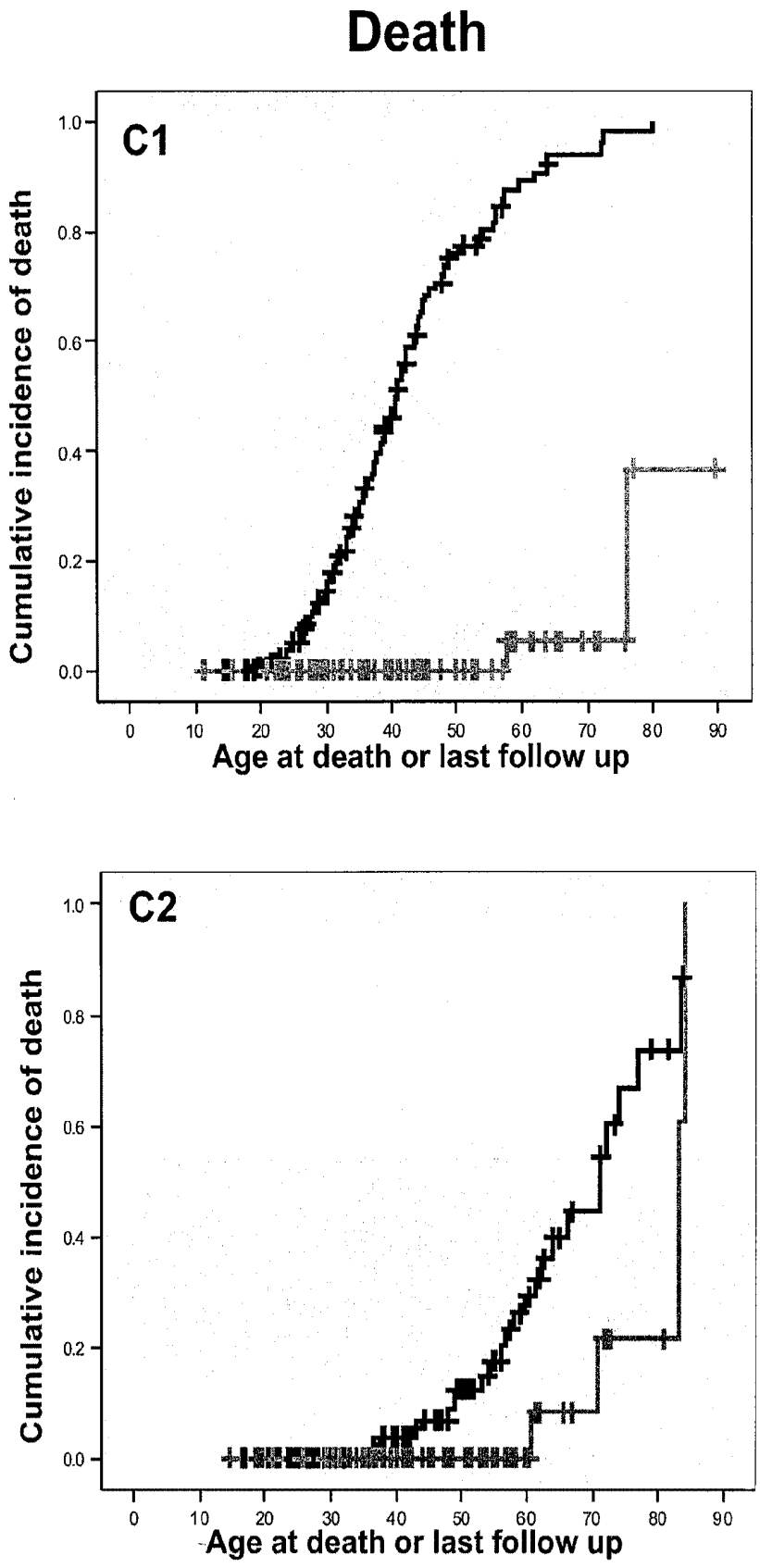


Figure 8 continued

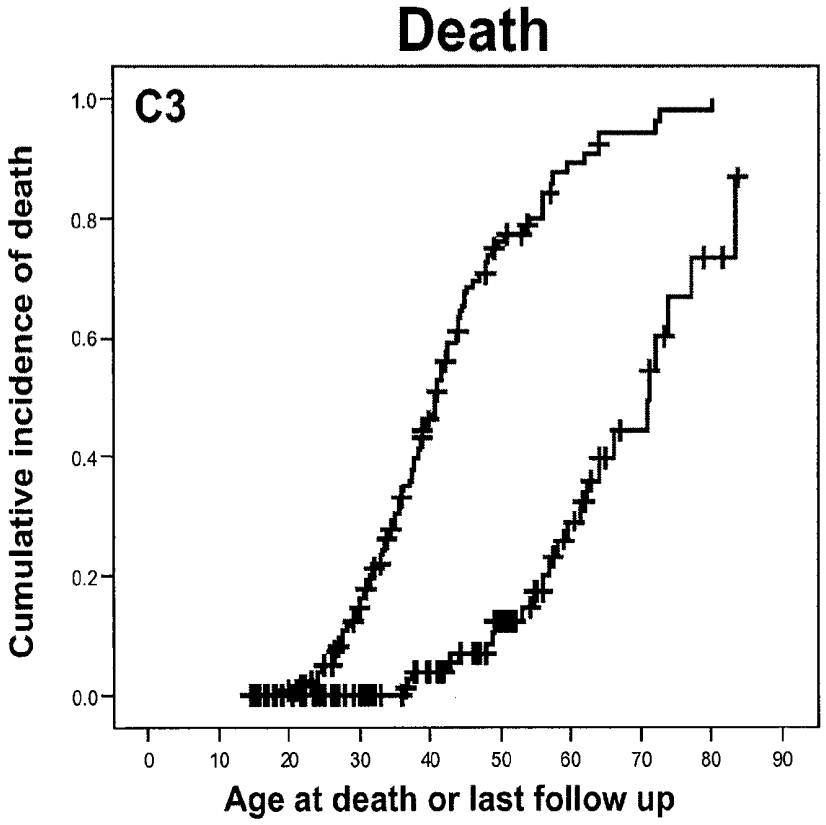


Figure 8 continued

Locus	Accession number	Primer Exon name	Variation Name		Amino acid change	Genomic number of variant	Samples	BB04--66		WP05-218		CH04-81		GT04-141		GP05-219		MH05-244		MS06-114	
							Family	AR1		AR15		AR1		AR8		AR15		AR1		AR2	
							Clinical Status	affected		affected		affected		affected		unaffected		unaffected		unaffected	
			IVS and mRNA naming	HGV name			Chromosome	1	2	1	2	1	2	1	2	1	2	1	2	1	2
IQSEC1	NM_014869	14c	3'UTR A>G	2892+1060A>G		12914829		A	A	nd	nd	A	A	A	A	A	A	nd	nd	A	G
IQSEC1	NM_014869	14c	3'UTR C>T	2892+1343 C>T		12914546		T	T	T	T	T	T	T	T	T	T	T	T	T	T
IQSEC1	NM_014869	9	IVS9+60 T>C	2358+60T>C		12929868		C	C	nd	nd	C	C	C	C	C	C	C	C	C	C
IQSEC1	NM_014869	8	IVS8+73C>T	2232+73 C>T		12931531		T	T	T	C	T	T	T	T	T	C	T	C	T	T
Marker	*D3S3610*			Start 12980656	End	12980996		246	246	256	242	nd	nd	246	242	256	242	246	242	nd	nd
IQSEC1	NM_014869	1	IVS1+73C>G	65+73C>G		12983814		nd	nd	nd	nd	C	C	C	G	C	C	C	C	C	C
Marker	*D3S2403*			Start 13147397	End	13147709		251	279	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
NUP210	NM_024923	40d	3'UTR T>C	5664+1195 T>C		13332986		C	C	C	T	C	C	C	T	C	T	C	T	C	T
NUP210	NM_024923	40c	3'UTR G>A	5664+1051 G>A		13333130		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	40c	3'UTR A>C	5664+1010 A>C		13333171		C	C	C	A	C	C	C	A	C	A	C	A	C	A
NUP210	NM_024923	40c	3'UTR C>T	5664+977 C>T		13333204		T	T	T	C	T	T	T	C	T	C	T	C	T	C
NUP210	NM_024923	40b	3'UTR A>T	5664+365A>T		13333816		A	A	A	A	A	A	A	T	A	A	A	A	A	A
NUP210	NM_024923	38&39	IVS39+59 G>A	5563+59G>A		13335513		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	38&39	IVS39+9 C>G	5563+9C>G		13335563		C	G	C	G	C	G	C	G	C	C	C	G	C	C
NUP210	NM_024923	37	IVS37+25 G>A	5383+25G>A		13336238		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	37	5339 G>A	5339 G>A	V>M	13336287		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	37	5225 T>C	5225 T>C	L>S	13336391		C	C	C	C	C	C	C	C	C	C	C	T	C	T
NUP210	NM_024923	34	4701 C>A	4701 C>A	T>T	13339876		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	33	4582 C>T	4582 C>T	R>W	13342357		C	C	C	C	C	C	C	T	C	C	C	C	C	C
NUP210	NM_024923	33	4533 G>A	4533 G>A	S>S	13342406		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	32	4332C>T	4332C>T	C>C	13343892		C	C	C	T	C	C	C	T	C	T	C	T	C	T
NUP210	NM_024923	26	3489 G>A	3489 G>A	E>E	13354400		G	G	G	A	G	G	G	A	G	A	G	A	G	A
NUP210	NM_024923	26	IVS25 -35 C>T	3472 -35 C>T		13354452		C	C	C	C	C	C	C	T	C	T	C	C	C	C
NUP210	NM_024923	22&23	3048 T>C	3048 T>C	F>F	13358540		T	T	T	C	T	T	T	C	T	C	T	C	T	C
NUP210	NM_024923	22&23	IVS21 -26 C>T	2965 -26 C>T		13358649		C	C	C	C	C	C	C	C	C	T	C	C	C	C
NUP210	NM_024923	21	IVS21 +143 C>T	2964 +143 C>T		13359532		C	C	C	T	C	C	C	C	C	C	C	C	C	C
NUP210	NM_024923	17	2461 C>G	2461 C>G	P>A	13370475		C	C	C	C	C	C	C	G	C	G	C	C	C	C
NUP210	NM_024923	17	2357 G>T	2357 G>T	R>L	13370579		G	G	G	T	G	G	G	T	G	T	G	T	G	T
NUP210	NM_024923	16	2264 C>T	2264 C>T	A>V	13374786		C	C	C	T	C	C	C	C	C	C	C	T	C	T
NUP210	NM_024923	16	IVS15 -53 A>G	2155 -53 A>G		13374948		A	A	A	G	A	A	A	A	A	A	A	G	A	G
NUP210	NM_024923	14	1822 A>G	1822 A>G	I>V	13382556		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	9	IVS8 -64 ins	1046 -64 ins		13394126		wt	wt	wt	ins	wt	wt	wt	wt	wt	wt	wt	ins	wt	ins
NUP210	NM_024923	8	IVS8 +29 G>T	1045 +29 G>T		13395383		G	T	G	G	G	G	G	G	G	G	G	G	G	T
NUP210	NM_024923	7	IVS7 +39 G>A	976 +39 G>A		13396024		G	G	G	G	G	G	G	G	G	A	G	G	G	G
NUP210	NM_024923	7	889 G>A	889 G>A	A>T	13396150		G	G	G	A	G	G	G	A	G	A	G	A	G	A
NUP210	NM_024923	7	IVS6 -98 A>G	818 -98 A>G		13396320		A	A	A	G	A	A	A	G	A	G	A	G	A	G
NUP210	NM_024923	6	IVS5 -91 C>A	685 -91 C>A		13402998		C	C	C	A	C	C	C	C	C	C	C	A	C	A
NUP210	NM_024923	3	IVS3 +27 T>C	436 +27 T>C		13413830		T	T	T	C	T	T	T	C	T	C	T	C	T	C
NUP210	NM_024923	3	IVS2 -17 T>C	305 -17 T>C		13414005		T	T	T	C	T	T	T	T	T	T	T	T	T	T

Figure 9

NUP210	NM_024923	1	IVS1+130G>A	166 +130G>A		13436430	G	G	G	A	G	G	G	G	G	G	G	G	G	G
HDAC11	NM_024827	2	IVS2 +79 C>T	151 +79 C>T		13497973	C	C	C	C	C	T	C	C	C	C	C	T	C	T
HDAC11	NM_024827	3	IVS3 +24 G>T	252 +24 G>T		13500088	G	G	G	G	G	G	G	G	G	G	G	G	G	T
HDAC11	NM_024827	4	IVS4 +19 insG	369 +19 insG		13513371	ins	wt	ins	ins	ins	wt	ins	wt	wt	wt	wt	wt	wt	wt
HDAC11	NM_024827	7	IVS6 -97 C>T	490 -97 C>T		13518274	C	C	C	C	C	C	C	T	C	C	C	C	C	C
HDAC11	NM_024827	8	IVS7 -74 G>A	553 -74 G>A		13519310	G	G	G	G	G	G	G	A	G	G	G	G	G	G
FBLN2	DA856838	EST 4	del GT			13586337	del	del	del	wt	del	wt	del	wt	wt	wt	wt	wt	del	wt
FBLN2	DA856838	EST 4	G>A			13586424	G	G	G	G	G	G	G	G	G	A	G	G	G	G
FBLN2	NM_MMMMMM	Ex2C#2	del**			13587794	del	del	del	del	del	del	del	del	del	del	del	del	del	del
FBLN2	MM_MMMMMM	Ex2C#2	1081 A>G			1MMMMMM	A	A	A	A	A	A	A	A	A	G	A	A	A	A
FBLN2	BC111426	EST1	G>A			13627967	G	G	G	A	G	A	G	G	G	G	G	G	G	G
FBLN2	BC111426	EST1	A>G			13628401	A	A	A	G	A	G	A	A	A	G	A	A	A	G
Marker	*D3S1516*			Start 13628628	End	13629103	347	359	351	359	347	351	347	335	351	343	351	363	nd	nd
FBLN2	NM_001004019	5	IVS5 +18 C>T			13630683	C	C	C	C	C	C	C	C	C	T	C	C	C	C
FBLN2	BF368851	EST 6	C>G			13637585	G	G	G	G	G	G	G	G	G	G	G	C	G	C
FBLN2	NM_001004019	11	IVS11 +68 T>G			13644538	G	G	G	G	G	G	G	G	G	G	G	T	G	T
FBLN2	NM_001004019	12	2646 A>G			13645482	G	G	G	G	G	G	G	G	G	A	G	A	G	A
FBLN2	NM_001004019	12	2701 A>G			13645537	G	G	G	G	G	G	G	G	G	A	G	A	G	A
FBLN2	NM_001004019	13	2826 T>C			13645777	C	C	C	C	C	C	C	C	C	C	C	T	C	T
FBLN2	NM_001004019	13	IVS13 +45 T>G	2842 +45 T>G		13645838	G	G	G	G	G	G	G	G	T	G	T	G	T	G
FBLN2	NM_001004019	15	IVS15 +77G>C	3085 +77 G>C		13647393	G	C	G	C	G	C	G	C	G	G	G	C	G	C
FBLN2	W70042	EST 2	A>T			13649190	T	A	T	A	T	A	T	A	A	A	T	A	A	A
FBLN2	NM_001004019	Ex 17	IVS17 +105 G>T	3338 +105 G>T		13653174	G	G	G	T	G	T	G	G	T	T	G	T*	G	T*
FBLN2	NM_001004019	18a	IVS17 -18 G>A	3339 -18 G>A		13654045	G	G	G	A	G	G	G	G	A	A	G	G	G	G
FBLN2	NM_001004019	18a	3480 G>A			13654204	G	G	G	A	G	G	G	G	A	A	G	G	G	G
FBLN2	NM_001004019	18a	3612 C>T			13654336	C	C	C	T	C	C	C	C	T	T	C	C	C	C
FBLN2	NM_001004019	18b-3'UTR	G>A			13654616	G	A	G	A	G	G	nd	nd	G	G	G	A	G	A
FBLN2	NM_001004019	18b-3'UTR	T>A			13654689	T	A	T	T	T	T	nd	nd	T	T	T	T	T	A
FBLN2	NM_001004019	18b-3'UTR	C>A			13654696	C	A	C	C	C	C	nd	nd	C	C	C	C	C	A?
FBLN2	NM_001004019	18b-3'UTR	C>A			13654709	C	A	C	C	C	A	nd	nd	C	C	C	C	C	A
FBLN2	NM_001004019	18b-3'UTR	C>T			13654830	C	T	C	T	C	T	nd	nd	T	T	C	C	C	T
FBLN2	NM_001004019	18b-3'UTR	del TA			13654852	wt	del	wt	wt	wt	del	nd	nd	wt	wt	wt	wt	wt	del
FBLN2	NM_001004019	18b-3'UTR	T>A			13654856	T	T	T	A	T	T	nd	nd	A	A	T	T	T	T
Marker	*D3S3608*			Start 13670236	End	13679541	165	165	165	165	165	175	165	165	165	165	nd	nd	nd	nd
WNT7A	NM_004625	4a#1	IVS3 -37 T>C	571 -37T>C	End	13835958	T	T	T	C	T	T	T	T	T	T	T	C	T	T
Marker	*D3S2385*			Start 13853945		13854287	146	142	nd	nd	nd	nd	146	146	nd	nd	nd	nd	nd	nd
WNT7A	NM_004625	3	459 T>C	459 T>C	S>S	13871141	C	T	C	C	C	T	C	T	C	T	T	T	T	T
WNT7A	NM_004625	3	315 G>A	315 G>A	A>A	13871285	A	G	A	A	A	G	A	G	A	G	G	G	G	G
WNT7A	NM_004625	2	IVS2 +37 C>A	298 +37 C>A		13891408	C	A	C	C	C	C	nd	nd	nd	nd	C	A	C	A
WNT7A	AA405144	EST1-Ex2	A>G			13892334	A	G	A	G	A	A	A	G	G	G	A	G	A	G
WNT7A	AA405144	EST1-Ex1	delG			13893611	wt	wt	wt	delG	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt
WNT7A	NM_004625	1b	5'UTR C>A	1 -164 C>A		13896478	C	C	C	A	C	C	C	C	C	C	C	C	C	C
Marker	*D3S3602*		Start 13900968		End	13901215	113	119	113	111	113	113	113	123	119	119	119	107	nd	nd
Marker	*D3S1585*		Start 13916682		End	13916861	118	126	118	118	118	118	118	126	126	126	118	138	nd	nd

Figure 9 Continued

TPRXL	AK092426	Ex2	IVS1 -9 ins/delTTT	ATTT microsatelitte		14079871	8	6	8	9	8	8	8	6	6	6	8	6	8	7
TPRXL	AK092426	Ex2	IVS2 +81 A>G	5' UTR		14080090	A	G	A	A	A	A	A	G	G	G	G	G	nd	nd
CHCHD4	NM_144636	BC033775 Ex3	3'UTR A>C			14129232	A	A	A	A	A	A	A	C	C	C	A	C	C	C
CHCHD4	NM_144636	BC033775 Ex2	IVS3 +36 G>C	160 +36 G>C		14132891	G	G	G	G	G	G	G	G	G	G	C	G	G	G
CHCHD4	NM_144636	BC033775 Ex2	IVS3 +13 T>C	160 +13 T>C		14132914	T	T	T	T	T	T	T	T	T	T	C	T	T	T
CHCHD4	NM_144636	BC033775 Ex1	5'UTR A>G			14141281	G	G	G	G	G	G	G	G	G	G	G	G	A	G
TMEM43	NM_024334	4	IVS3 -106 C>T	298 -106 C>T		14147975	C	C	C	C	C	C	C	T	C	T	C	C	C	C
TMEM43	NM_024334	5&6	IVS5 +51 T>C	442 +51 T>C		14149147	T	T	T	T	T	T	T	T	nd	nd	T	T	C	C
TMEM43	NM_024334	7	IVS6 -90 G>A	513 -90 G>A		14150150	G	G	G	G	G	G	G	G	G	G	G	A	G	G
TMEM43	NM_024334	7	536 T>C		M>T	14150263	T	T	T	T	T	T	T	C	C	C	T	T	T	C
TMEM43	NM_024334	8&9	IVS8 +55 G>A	705 +55 G>A		14151447	G	G	G	G	G	G	G	A	A	A	G	G	G	A
TMEM43	NM_024334	10	IVS9 -56 G>A	781 -56 G>A		14152252	G	G	G	G	G	G	G	A	A	A	G	G	G	A
TMEM43	NM_024334	11	IVS10 -47 C>T	883 -47 C>T		14155634	C	C	C	C	C	C	C	C	C	C	C	T	C	T
TMEM43	NM_024334	12a	1073 C>T		S>L	14158166	T	C	T	C	T	C	T	C	C	C	C	C	C	C
TMEM43	NM_024334	12a	3' UTR T>C	c.1203 +115 T>C		14158411	T	T	T	T	T	T	T	C	C	C	C	C	C	C
TMEM43	NM_024334	12b	3' UTR C>T			14158573	C	C	C	C	C	T	C	C	C	C	C	C	C	C
TMEM43	NM_024334	12b	3' UTR A>G			14158759	A	A	A	A	A	A	A	A	A	A	A	G	A	G
TMEM43	NM_024334	12c	3' UTR A>C			14159075	A	A	A	A	A	A	A	A	A	A	A	C	A	C
TMEM43	NM_024334	12d	3' UTR T>C			14159670	T	T	T	T	T	T	T	T	T	T	T	C	T	C
TMEM43	NM_024334	12d	3' UTR T>C			14159720	T	T	T	T	T	T	T	T	T	T	T	C	T	C
TMEM43	NM_024334	12e	IVS12 +58 ins/del	1203 +1942		14160264	12	11	12	11	12	11	12	11	13	14	11	13	12	14
XPC	NM_004628	16b	IVS16 +30 ins/del T	2823 +821		14161621	12	13	12	13	12	13	12	14	nd	nd	nd	nd	12	14
XPC	NM_004628	16b	3'UTR G>C	c.2823 +684 G>C		14161759	G	C	G	C	G	C	G	C	C	C	nd	nd	C	C
XPC	NM_004628	16b	3'UTR A>G			14161824	A	A	A	A	A	A	A	A	A	A	A	A	A	G
XPC	NM_004628	16b	3'UTR T>A			14161831	T	T	T	T	T	T	T	T	T	T	T	T	T	A
XPC	NM_004628	16a	3'UTR C>G			14162346	C	C	C	C	C	C	C	C	C	C	C	G	C	G
XPC	NM_004628	16a	2815 C>A		Q>K	14162450	C	C	C	C	C	C	C	A	A	A	C	A	A	A
XPC	NM_004628	16a	IVS15 -40 A>G	2605 -40 A>G		14162700	A	A	A	A	A	A	A	G	G	G	A	G	G	G
XPC	NM_004628	16a	IVS15 -51 A>G	2605 -51 A>G		14162711	A	A	A	A	A	A	A	G	G	G	A	A	A	G
XPC	NM_004628	15	IVS15 +90 G>T	2604 +90 G>T		14163701	G	G	G	G	G	G	G	T	T	T	nd	nd	T	T
XPC	NM_004628	15	IVS15 +28 C>G	2604 +28 C>G		14163763	C	C	C	C	C	C	C	G	G	G	nd	nd	G	G
XPC	NM_004628	14	IVS14 +68 T>C	2514 +68 T>C		14164341	T	T	T	T	T	T	T	C	C	C	T	C	C	C
XPC	NM_004628	12&13	IVS 12 -6 A>C	2251 -6 A>C		14165238	A	A	A	A	A	A	A	C	C	C	A	C	C	C
XPC	NM_004628	12&13	IVS 12 +46 C>G	2250 +46 C>G		14165269	C	C	C	C	C	C	C	G	G	G	C	G	G	G
XPC	NM_004628	11	2061 G>A		R>R	14168890	G	G	G	G	G	G	G	A	A	A	G	G	G	A
XPC	NM_004628	10	del C			14172877	del	del	del	del	del	del	del	del	del	del	del	del	del	del
XPC	NM_004628	10	1881 T>A		A>A	14172989	A	A	A	A	A	A	A	A	A	A	A	A	A	A
XPC	NM_004628	9b	1496 C>T		A>V	14174889	C	C	C	C	C	C	C	C	C	C	C	T	C	T
XPC	NM_004628	9a	1415 A>C		D>A	14174970	C	C	C	C	C	C	C	C	C	C	C	C	C	C
XPC	NM_004628	9a	del G			14174971	del	del	del	del	del	del	del	del	del	del	del	del	del	del
XPC	NM_004628	9a	del G			14175043	del	del	del	del	del	del	del	del	del	del	del	del	del	del
XPC	NM_004628	8	IVS7 -70 A>C	901 -70 A>C		14176404	A	A	A	A	A	A	A	C	C	C	A	A	A	C
XPC	NM_004628	5	IVS5 +44 C>G	621 +44 C>G		14183629	C	C	C	C	C	C	C	G	G	G	C	C	C	G
XPC	NM_004628	3	IVS3 +73 G>T	412 +73 G>T		14186869	G	G	G	G	C	nd	G	T	T	T	G	G	G	T

Figure 9 Continued

XPC	NM_004628	1	G>C 5' UTR																								
LSM3	NM_014463		No SNP's	No SNP's	1.4E+07	14195099	C	nd	G	G	G	G	C	C	C	C	C	C	C	C	C	C	C	C	C
Marker	*D3S1554*			Start 14342778	End	-1.4E+07	129	129	129	129	129	129	129	129	129	131	129	129	129	129	129	129	129	129	129	nd	nd
SLC6A6	NM_003043	1	G>T 5'UTR	1 - 41125 G>T		14343106	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G
SLC6A6	NM_003043	1	del 5'UTR	1 - 40888 del		14419021	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40882 del		14419248	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40854 del		14419254	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40846 del		14419282	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40823 del		14419290	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40813 del		14419313	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40805 del		14419323	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	1	del 5'UTR	1 - 40802 del		14419331	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	NM_003043	2	G>A 5'UTR	1 - 27420		14419334	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del
SLC6A6	BC038790	mRNA1a	C>G 5'UTR			14432716	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G
SLC6A6	BC038790	mRNA1b	C>T 5'UTR			14435728	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
SLC6A6	BC111489	5	IVS5+46 G>T	599+46 G>T		14435919	T	T	T	nd	T	T	T	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C
SLC6A6	BC111489	5	IVS5+370 A>G	c.599+370 A>G		14464374	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
SLC6A6	AK023516-Ex1a	mRNA2	IV6-1745 G>A	733-1745 G>A		14464898	G	G	G	G	A	G	T	G	T	G	A	G	A	G	A	G	A	G	A	G	A	G
SLC6A6	AK023516-Ex1a	mRNA2	IV6-1541 T>C	733-1541 T>C		14481263	A	A	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G
SLC6A6	AK023516-Ex1a	mRNA2	IV6-1521 C>A	733-1521 C>A		14481487	C	C	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T
SLC6A6	AK023516-Ex1a	mRNA2	IV6-1392 G>A	733-1392 G>A		14481507	A	A	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C
SLC6A6	AK023516-Ex1a	mRNA2	IV6-1363 G>A	733-1363 G>A		14481638	A	A	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G
SLC6A6	AK023516-Ex1b	mRNA2	IV6-1226 A>G	733-1226 A>G		1471777	G	G	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A
SLC6A6	AK023516-Ex1c	mRNA2	IV6-280 del A	733-280 del A		14477777	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt
SLC6A6	NM_003043	15a	3'UTR del			14501629	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt
SLC6A6	NM_003043	15b	3'UTR G>A			14502367	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
SLC6A6	NM_003043	15c	3'UTR C>G			14502940	C	C	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G
SLC6A6	NM_003043	15c	3'UTR C>G			14502943	G	G	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C	G	C
SLC6A6	NM_003043	15c	3'UTR T>C			14503008	C	C	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T
SLC6A6	NM_003043	15c	3'UTR T>C			14503032	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T
SLC6A6	NM_003043	15c	3'UTR del			14503092	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del
SLC6A6	NM_003043	15d	3'UTR C>T			14503260	T	T	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C
SLC6A6	NM_003043	15e	3'UTR G>T			14503788	G	G	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T	G	T
SLC6A6	NM_003043	15g	3'UTR del			14505435	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del
SLC6A6	NM_003043	15h	3' UTR A>G			14505725	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
GRIP2	NM_001080423	23	IVS22 -5 del	2974 -5 del		14513077	nd	wt	wt	del	wt	wt	nd	nd	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt	wt
GRIP2	NM_001080423	22	IVS22+20A>G	2973+20A>G		14520058	A	A	A	A	A	A	A	A	A	A	A	A	A	G	A	A	A	G	A	A	A	A
GRIP2	NM_001080423	21	2808 C>T		T>T	14522186	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
GRIP2	NM_001080423	20	IVS20 +101 C>T	2692 +101 C>T		14523212	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	nd	nd	nd	nd
GRIP2	NM_001080423	20	IVS19 -6 T>C	2513 -6 T>C		14523498	T	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	nd	nd	nd	nd
GRIP2	NM_001080423	18	2256 T>C		S>S	14526448	T	T	T	C	T	T	T	T	C	T	C	T	C	T	C	T	C	T	nd	nd	T	C
GRIP2	NM_001080423	16	IVS15 -7 T>C	2015 -7 T>C		14527998	T	C	T	C	T	T	T	C	T	C	T	C	T	C	T	C	T	C	C	C	C	C
GRIP2	NM_001080423	14	1890 A>G		A>A	14530220	A	A	A	G	A	A	A	G	A	G	A	G	A	G	A	G	A	G	nd	nd	A	G
GRIP2	NM_001080423	14	IVS13 -49 A>G	1787 -49 A>G		14530371	nd	A	A	G	A	A	A	G	A	G	A	G	A	G	A	G	A	G	nd	nd	A	G

Figure 9 Continued

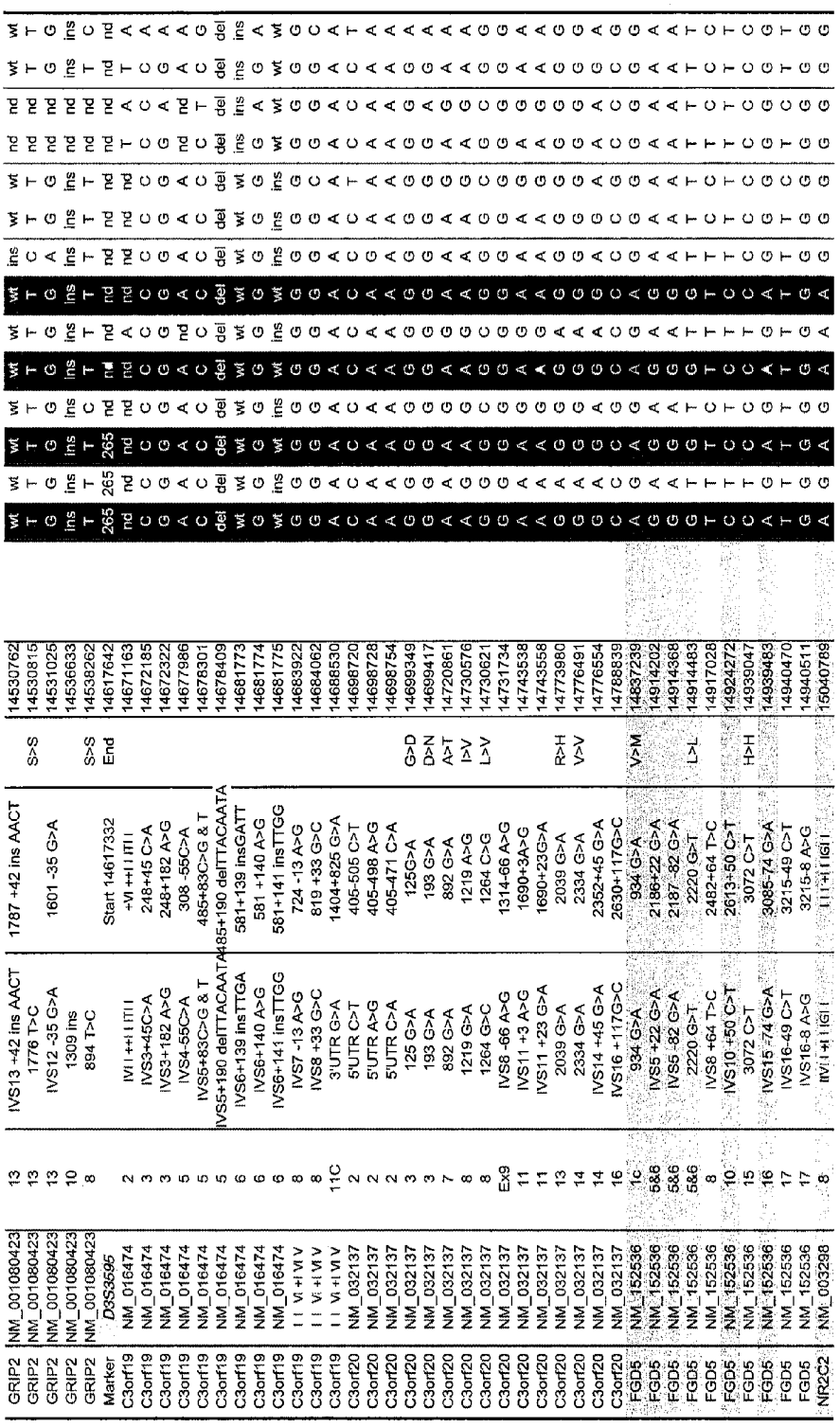


Figure 9 Continued

NR2C2	NM_003298	12	A/A++AAVACAT	+AAAAAVACAT		15051147	C	C	C	C	C	C	C	T	C	C	C	C	C	T
NR2C2	NM_003298	14c	A+AAAACAAA	A+AAAACAAA	Q/Q	15055700	G	G	G	G	G	G	G	A	G	G	G	G	G	A
NR2C2	NM_003298	15b	AV+TAAAAC			15059873	A	A	A	A	A	A	A	A	A	G	A	A	A	A
NR2C2	NM_003298	15b	AV+TAATAA			15059884	A	T	A	T	A	A	A	T	T	T	T	T	T	T
NR2C2	NM_003298	15e	AAV+TAACAT			15061256	C	C	C	C	C	C	C	T	C	C	C	C	C	T
NR2C2	NM_003298	15g	AAV+TAAAVCATA			15062484	ins	wt	ins	wt	ins	isn	ins	wt	wt	wt	ins	wt	wt	wt
NR2C2	NM_003298	15k	AAV+TAACAC			15064207	C	C	C	C	C	G	C	C	C	C	C	C	C	C
NR2C2	NM_003298	15k	AAV+TAACAA			15064452	G	G	G	G	G	G	G	G	G	G	G	G	G	A
MRPS25	NM_022497	4f	3' UTR A>G	522 +2704A>G		15066248	A	A	A	A	A	A	A	A	A	A	A	A	A	G
MRPS25	NM_022497	4f	3' UTR T>C	522 +2700T>C		15066252	C	T	C	T	C	C	C	T	T	T	C	T	T	T
MRPS25	NM_022497	4d	3' UTR T>C	522 +1875T>C		15067077	T	T	T	T	T	T	T	C	T	T	T	T	T	C
MRPS25	NM_022497	4c	3' UTR G>A	522+1059G>A		15067893	A	G	A	G	A	G	A	G	G	G	G	G	G	G
MRPS25	NM_022497	4a	3' UTR A>T	522+192A>T		15068761	A	A	A	A	A	A	A	T	A	A	A	A	A	A
MRPS25	NM_022497	2	IVS2 +75 C>T	241+75 C>T		15075805	nd	nd	C	T	C	T	C	T	C	C	C	T	C	C
ZFYVE20	NM_022340	14g	AAV+TAATAC			15088127	C	T	C	T	C	C	C	C	T	T	C	T	C	T
ZFYVE20	NM_022340	14g	AAV+TAATAA			15088307	T	T	T	T	T	T	T	T	T	T	T	T	T	A
ZFYVE20	NM_022340	14g	AAV+TAACAA			15088523	A	G	A	G	A	A	A	A	G	G	A	G	A	G
ZFYVE20	NM_022340	14e	AAV+TAAAVAAAAAAA			15089241	wt	wt	wt	wt	wt	ins	nd	nd	wt	wt	wt	wt	wt	ins
ZFYVE20	NM_022340	14c	AAV+TAACAA			15090274	A	C	A	C	A	A	A	A	C	C	A	C	A	C
ZFYVE20	NM_022340	14b	+AAVACAC		AAA	15090914	C	C	C	C	C	C	C	C	C	C	C	C	C	G
ZFYVE20	NM_022340	6	A/AAAAAAACAATC	AAAAAAAACAATC		15102527	del	wt	del	wt	del	del	del	del	wt	wt	del	wt	del	wt
CAPN7	NM_014296	1	5'UTR A>G			15222800	G	G	nd	nd	nd	nd	nd	nd	G	A	G	G	G	G
CAPN7	NM_014296	6	IVS5-160A>G	639-160A>G		15239826	A	A	A	A	A	G	A	A	A	A	A	A	A	A
CAPN7	NM_014296	11	IVS11+68 C>T	1286 +68 C>T		15250552	T	C	T	C	T	C	T	C	C	C	C	C	C	C
CAPN7	NM_014296	12	IVS12+150 G>A	1407 +150G>A		15251806	G	A	G	A	G	A	G	A	G	A	G	A	G	A
CAPN7	NM_014296	13&14	IVS12-28 T>C	1408 -28 T>C		15256956	C	T	C	T	C	T	C	T	T	T	T	T	nd	nd
CAPN7	NM_014296	19	AAVA+AAAAACAA	AAAVAAAACAA		15263760	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del	wt	del
SH3BP5	NM_004844	9b	AV+TAACAA	+AAA+VAAACAA		15272099	nd	nd	wt	del	nd	nd	wt	del	wt	del	wt	del	wt	del
SH3BP5	NM_004844	9a	AV+TAACAA	+AAA+AAACAA		15272574	G	G	G	G	G	G	G	G	G	A	G	G	G	G
SH3BP5	NM_004844	8	AA+ACAA		VAA	15273553	G	G	G	G	G	G	G	G	G	G	G	A	G	G
SH3BP5	NM_004844	6	IVS5-53 C>T	AAAAAAACAT		15276367	T	C	nd	nd	T	T	T	C	T	C	T	T	T	T
SH3BP5	NM_004844	6	IVS5-79 G>C	627-79G>C		+AAAAAAA	G	C	nd	nd	G	C	G	C	G	C	G	C	G	C
SH3BP5	NM_004844	4	390 T>C		R>R	+AAAAAAA	C	T	C	C	C	C	C	C	T	T	C	T	C	T
SH3BP5	NM_004844	4	IVS3-80 C>A	331-80 C>A		+AAAAVAA	A	A	A	A	A	A	A	A	A	A	A	A	A	A
Marker	D3S3613			Start 15336926	End	15337204	193	197	193	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
SH3BP5	NM_001018009	1	5'UTR A>G	1-71626 A>G		+AAAAAAV	A	A	A	A	A	A	A	A	A	A	A	G	A	A

Figure 9 Continued

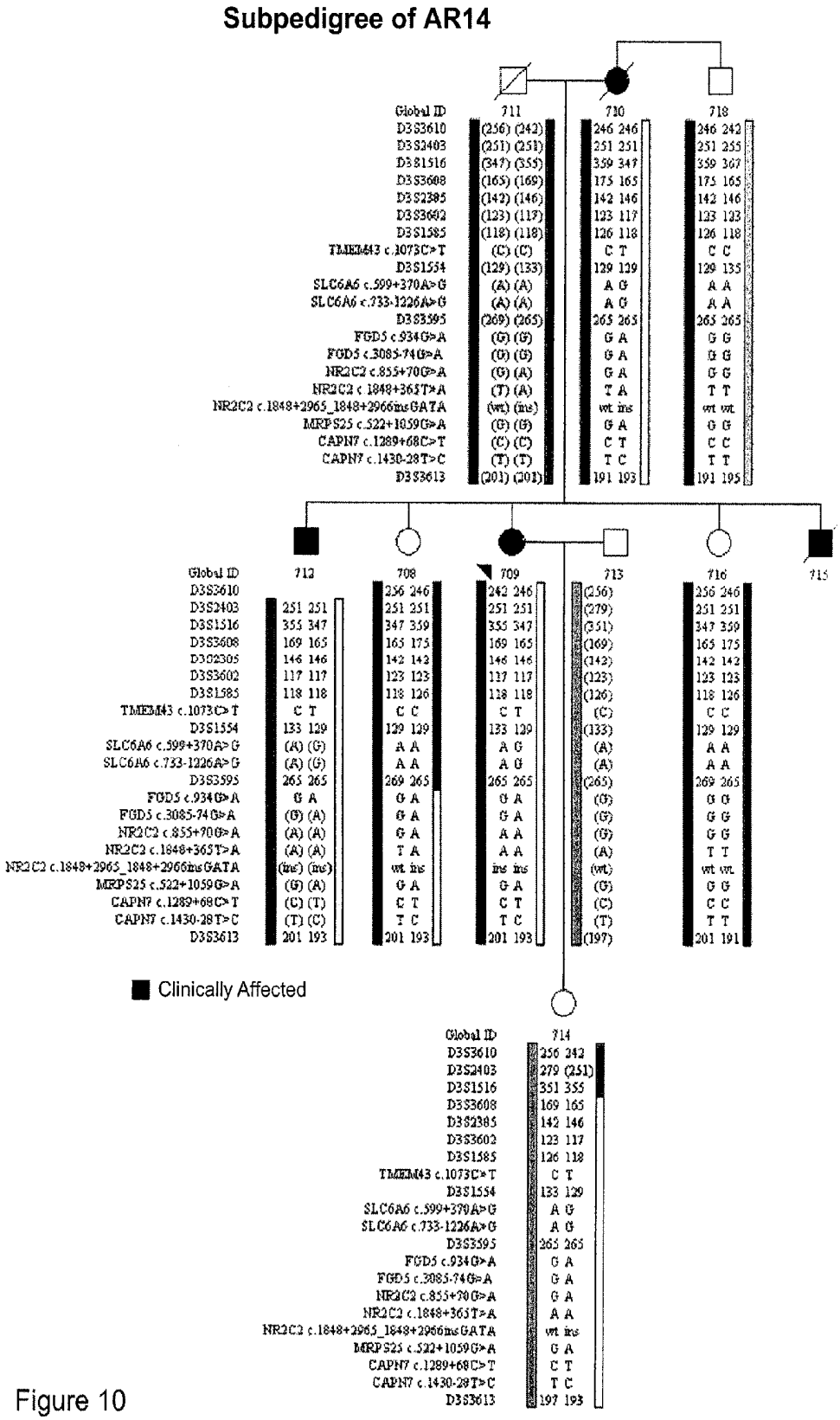
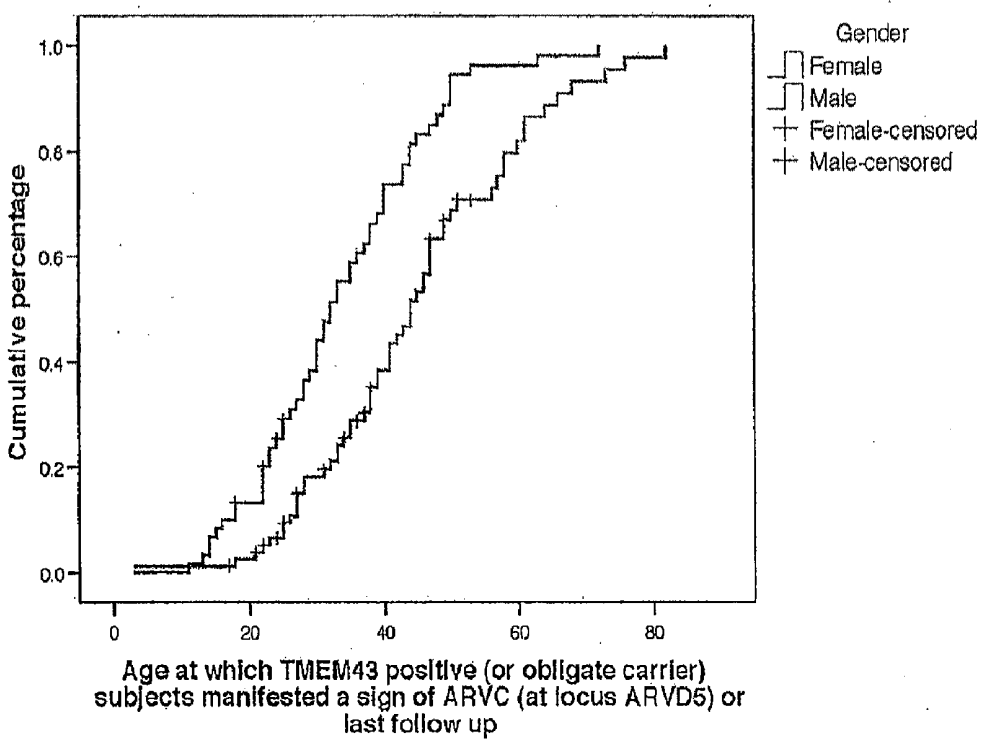

Subpedigree of AR14
Global ID
D3S3610
D3S2403
D3S1516
D3S3608
D3S2385
D3S3602
D3S1585
TMEM43 c.1073C>T
D3S1554
SLC6A6 c.599+370A>G
SLC6A6 c.733-1226A>G
D3S3595
FGD5 c.934G>A
FGD5 c.3085-74G>A
NR2C2 c.855+70G>A
NR2C2 c.1848+36ST>A
NR2C2 c.1848+2965_1848+2966insGATA
MRPS25 c.522+1059G>A
CAPN7 c.1289+68C>T
CAPN7 c.1430-28T>C
D3S3613
711
710
718
712
708
709
713
716
715
714
Clinically Affected

Figure 10

Markers	3p25 location	Affected haplotype	Unaffected recombinants	
			AR14	AR6
D3S2403	13147397 - 13147709	251	251	251
D3S1516	13628628 - 13629103	347	359	347
D3S3608	13670236 - 13679541	165	175	165
D3S2385	13853945 - 13854287	146	142	146
D3S3602	13900968 - 13901215	113	123	113
D3S1585	13916682 - 13916861	118	126	118
TMEM43	**14158166 C>T**	**T**	**C**	**C**
D3S1554	14342778 - 14343106	129	129	133
D3S3595	14617332 - 14617642	265	265	265
D3S3613	15271250 - 15357905	193	193	187

Figure 11

A



B

Percentage of subject's penetrant by each age

Age (years)	11-20	21-30	31-40	41-50	51-60	61-70	71-80
Males	13	39	68	89	96	100	100
Females	3	18	38	67	80	97	100

Figure 12

DIAGNOSTIC TEST FOR CARDIOMYOPATHY

FIELD

[0001] The disclosure relates to methods and compositions for diagnosing and treating cardiomyopathy and particularly to methods and compositions for diagnosing and treating arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C).

BACKGROUND

[0002] Arrhythmogenic right ventricular cardiomyopathy (ARVC) causes ventricular tachyarrhythmias, heart failure and sudden cardiac death (SCD), with fibro-fatty replacement of the ventricular myocardium. Diagnosis relies upon descriptive diagnostic criteria[1], and remains difficult because gene carriers manifest different phenotypes (variable expressivity) and may show no signs of disease (reduced penetrance). This recognized clinical heterogeneity[2] makes the potential use of genetic diagnosis (either by linkage or mutation analysis), to determine those at risk prior to malignant clinical sequalea, extremely important. ARVC is also genetically heterogeneous, with eleven ARVC mapped loci and seven identified genes to date,[3-7] several coding for desmosomal proteins (desmoplakin, plakophilin, desmoglein and plakoglobin) that are predicted to succumb to mechanical stress.[5, 7]

[0003] A novel locus for ARVC (ARVD5) was mapped to chromosome 3p in 1998 as the result of a genome-wide scan in an extended family from Newfoundland, Canada with an autosomal dominant form of ARVC.[8] Since then, 14 additional Newfoundland families have been identified where a disease-associated haplotype (ARVD5 haplotype) is shared with the family used to map the ARVD5 locus. This ARVD5 haplotype has been used to predict disease risk status, allowing prophylactic treatment with implantable cardioverter defibrillator (ICD) therapy that greatly improved survival.[9]

[0004] Identification of the ARVD5 gene would allow improved diagnosis and therapeutic treatment of individuals with ARVD/C.

SUMMARY

[0005] The inventors have identified a minimal critical region of the ARVD5 haplotype associated with the cardiomyopathy, ARVD/C and have further identified a gene, TMEM43, disease associated variants of which are diagnostic of ARVD/C. The inventors have found that various markers that map to the ARVD5 region are useful for predicting if an individual is affected when other family members are available for testing. These include microsatellite markers: D3S3610, D3S2403, D3S1516, D3S3608, D3S2385, D3S3602, D3S1585, D3S1554, D3S3595, D3S3613. In addition the inventors have shown that detection of TMEM43 disease associated variants is useful for diagnosing individuals with ARVD/C and for prognosing individuals at risk of developing ARVD/C. Early detection is advantageous as the inventors have previously shown that improved survival occurs in patients with an implantable cardioverter defibrillator (ICD). The inventors disclose that at risk families are readily screened for TMEM43 disease associated variants through, for example, genetic mutation analysis.

[0006] The inventors have further demonstrated that a serine to leucine substitution in amino acid 358 of TMEM43 at locus ARVD5 is the cause of ARVD/C in 15 families analyzed. Both arrhythmogenic and cardiomyopathic disease occurs, leading to early death and heart failure, particularly in males. Pre-symptomatic diagnosis by molecular testing facilitates early recognition of subjects within the population at risk for sudden death, and allows for therapeutic intervention.

[0007] Accordingly, an aspect of the disclosure provides a method of screening for, diagnosing or detecting a risk of developing cardiomyopathy in a subject by detecting the presence of a transmembrane protein 43 (TMEM43) disease associated variant in a sample of the subject, where the presence of the TMEM43 disease associated variant is indicative that the subject has cardiomyopathy or an increased risk of developing cardiomyopathy compared to an individual not having the TMEM43 disease associated variant. In an embodiment, the cardiomyopathy is ARVD/C. In another embodiment, the cardiomyopathy is ARVD/C, associated with ARVD5.

[0008] Another aspect provides a method of screening for, diagnosing or detecting a risk of developing arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) in a subject by detecting the presence of a transmembrane protein 43 (TMEM43) disease associated variant in a sample of the subject, where the presence of the TMEM43 disease associated variant is indicative that the subject has ARVD/C or an increased risk of developing ARVD/C compared to an individual not having the TMEM43 disease associated variant.

[0009] A further aspect provides a method of identifying subjects with an increased risk of and/or predisposition for developing cardiomyopathy, by detecting the presence of a TMEM43 disease associated variant in a sample of the subject, where the presence of the TMEM43 disease associated is indicative that the subject has an increased risk of developing cardiomyopathy. In an embodiment, the cardiomyopathy is ARVD/C. In another embodiment, the cardiomyopathy is ARVD/C, associated with ARVD5.

[0010] In an embodiment the TMEM43 disease associated variant detected has a gene mutation.

[0011] A gene mutation is optionally detected in genomic sequence. Accordingly, in one embodiment the gene mutation is mutation of a nucleotide corresponding to genome position 14158166. In another embodiment the mutation is the nucleotide corresponding to genome position 14158166 and is a missense mutation. In another embodiment the missense mutation at this position is a mutation to thymidine (nucleotide 171, SEQ ID NO:4). In yet another embodiment the gene mutation is 14158166C>T.

[0012] A gene mutation is optionally detected in nucleic acid gene products. Accordingly, in one embodiment the gene mutation detected is mutation of a nucleotide corresponding to position 1073 in TMEM43 mRNA. In one embodiment the mutation of the nucleotide corresponding to position 1073 in TMEM43 mRNA is a missense mutation. In another embodiment the missense mutation at this position is mutation to thymidine (nucleotide 1073, SEQ ID NO:5). In a further embodiment the gene mutation is 1073C>T.

[0013] A gene mutation is optionally detected in polypeptide gene products. Accordingly, in one embodiment the gene mutation encodes a mutation of an amino acid corresponding to position 358 in TMEM43 polypeptide. In one embodiment the amino acid corresponding to position 358 is leucine (SEQ ID NO:5). In a further embodiment the gene mutation encodes S358L.

[0014] In alternate embodiments the gene mutation is a deletion mutation that results in deletion of: a nucleotide corresponding to genome position 14158166, a nucleotide corresponding to position 1073 in TMEM43 mRNA, or an amino acid corresponding to position 358 in TMEM43 polypeptide.

[0015] In certain embodiments the TMEM43 disease associated variant is detected in a sample of a subject where the sample contains blood. In other embodiments, the sample contains white blood cells. In yet other embodiments, the sample contains cardiac tissue.

[0016] The methods are useful for screening for, diagnosing or detecting a risk of developing ARVD/C in pre-symptomatic subjects and in subjects having a relative with an ARVD5 haplotype associated with ARVD/C.

[0017] In certain embodiments, the methods employ isolated nucleic acids and antibodies described herein. In other embodiments, the methods employ genotyping, PCR and RT-PCR, and/or use of microarrays.

[0018] Another aspect provides an isolated nucleic acid molecule comprising a nucleic acid sequence comprising a TMEM43 gene or transcript disease associated variant.

[0019] Another aspect provides a reagent for detecting a TMEM43 disease associated variant, such as an isolated nucleic acid primer or probe. In an embodiment, the isolated nucleic acid molecule comprises:

[0020] a) any one of SEQ ID NOs: 1-54 and/or combinations thereof; and/or

[0021] b) a nucleic acid molecule with at least 80%, 90%, 95%, or 99% sequence identity to a), characterized in that the nucleic acid molecule is capable of binding TMEM43 under moderately stringent conditions. In an embodiment, the nucleic acid with at least 80%, 90%, 95%, or 99% sequence identity to a) binds TMEM43 under moderately stringent conditions and is capable of priming strand synthesis. Isolated nucleic acid molecules including for example SEQ ID NOs: 1-52 are useful as primers to amplify TMEM43. In an embodiment, the isolated nucleic acid molecule is an amplified which is produced by amplification of a TMEM43 disease associated variant containing template. Isolated nucleic acid molecules including for example SEQ ID NO: 53 and/or 54, are useful for as probes to detect TMEM43 disease associated variants.

[0022] Another aspect provides a composition comprising at least one isolated nucleic acid sequence that hybridizes to:

[0023] a) a RNA product of TMEM43;

[0024] b) a nucleic acid complementary to a); and/or

[0025] c) a nucleic acid corresponding to a);

where the composition is used to detect a TMEM43 disease associated variant. In an embodiment, a) comprises a TMEM43 disease associated variant. In an embodiment, a nucleic acid complementary to a) and/or corresponding to a) comprises genomic TMEM43. In certain embodiments, the isolated nucleic acid is a probe. In one embodiment the probe comprises SEQ ID NO: 53 or 54. In other embodiments the isolated nucleic acid is a primer optionally a primer pair useful for amplifying a TMEM43 disease associated variant. In certain embodiments the primers comprise SEQ ID NO:43 and/or SEQ ID NO:44.

[0026] The disclosure also describes kits containing one or more isolated nucleic acids and/or antibodies useful for detecting a TMEM43 disease associated variant and instructions for use.

[0027] A further aspect relates to a commercial package comprising one or more isolated nucleic acids and/or antibodies useful for detecting a TMEM43 disease associated variant and instructions for use.

[0028] Yet a further aspect relates to identifying TMEM43 disease associated variants comprising amplifying a TMEM43, gene or transcript or part thereof from a sample of a subject, comparing the amplified region to a control population, wherein a mutation that is detected in the sample and is rare or undetected in the control population is a TMEM43 disease associated variant.

[0029] Another aspect relates to a screening assay for identifying agents that target and/or bind a TMEM43 disease associated variant.

[0030] Other features and advantages of the disclosure will become apparent from the following detailed description. It should be understood, however, that the description and the specific examples while indicating preferred embodiments are given by way of illustration only, since various changes and modifications within the spirit and scope of the disclosure will become apparent to those skilled in the art from this description of various embodiments.

DRAWINGS

[0031] Embodiments are described below in relation to the drawings in which:

[0032] FIG. **1** is a schematic demonstrating that ARVC families are linked to 3p25. Panel A shows the pedigrees of 15 autosomal dominant ARVC families from Newfoundland linked to ARVD5 on 3p25. Patients diagnosed with ARVC are indicated by blackened squares (male) and circles (female). Panel B is the photomicrographs of paraffin-embedded post mortem right ventricular myocardium stained with masson trichrome showing fibrofatty replacement of myocytes where darker staining is the normal myocardium, lighter grey is fiber and white is fat, from a male teenager who had a SCD (left: ×40 magnification) and his second degree blood relative who also died suddenly in his 8th decade (right: ×20 magnification).

[0033] FIG. **2** is a schematic showing workflow and mutation status of subjects born at a priori 50% risk of ARVC.

[0034] FIG. **3** is a physical map of the ARVD5 critical region. Panel A shows a summary of recombinant ARVD5 haplotypes identified in patients across 15 ARVC families from Newfoundland. Eighteen microsatellite markers across the top, and summary family haplotypes on the side. Numbers in cells are alleles in base pairs. Panel B is the physical map of the ARVD5 critical region. Physical distances were captured from the March 2006 freeze of The UCSC Genome Browser. Arrows show the direction of transcription of each annotated gene in the ARVD5 critical region on chromosome 3p.

[0035] FIG. **4** is a comparison of TMEM43 cDNA in myocardium and leukocytes. (Panel A) Gene structure of TMEM43. (Panel B) Coverage of primers designed to amplify cDNA showing position of PCR primer pairs: Exons 1-4 (darkest grey), Exons 4-9 (light grey), Exons 9-12 (lighter grey); Exons 1-10 (medium grey) 5-12 (white). (Panel C) PCR products amplified from cDNA of EBV transfected B cells of affected subjects from the mutation screening panel (Affected AR1 & Affected AR15) and unaffected (control) subjects and cDNA of heart tissue from the left and right ventricle of an affected subject (Affected Left Ventricle and Affected Right Ventricle) and heart biopsy from a control subject. (Panel D&E) Sequencing traces of genomic and

complimentary DNA including amino acid translations (top) and both forward and reverse traces (output from Mutation Surveyor) of an affected subject (Family AR13).

[0036] FIG. **5** is a haplotype analysis of the rare sequencing variants in ARVC families identified with key recombinations to the ARVD5 ancestral haplotype. Only one variant, TMEM43 1073 C>T, is retained on the ARVD5-ancestral haplotype (white) in subjects with primary affection status from families AR2 and AR10. Haplotypes consist of both microsatellite markers (D names) and the five rare variants (gene named followed by the variant description).

[0037] FIG. **6** is a schematic showing multiple alignment of the TMEM43 gene with eight other vertebrate and invertebrate homologous sequences Panel A: Large light grey box outlines the DUF1625 domain and black boxes outline predicted transmembrane domains. Completely conserved residues are in lightest grey, strongly similar residues are in gray and weakly similar residues are in dark grey. The mutation in ARVC families is shown highlighted in black. Panel B: shows the alignment of Eukaryotic species in Web logo format, where the third transmembrane domain is outlined (black box). The white arrow gives the position of the S358L mutation. Clustal W align was used to align orthologues from *Homo sapiens* (NP_077310) (SEQ ID NO:3), Pan troglodytes (XP_516299) (SEQ ID NO:7), *Canis familiaris* (XP_541751) (SEQ ID NO:8), *Mus musculus* (NP_083042) (SEQ ID NO:9), *Gallus gallus* (XP_414378) (SEQ ID NO:10), *Zenopus tropicalis* (UP10004D5297) (SEQ ID NO:11), *Tetraodon nigroviridis* (Q4RXL8) (SEQ ID NO:12), *Drosophila melanogaster* (NP_64162) (SEQ ID NO:13), *Rhizobium loti* (Q98HF3) (SEQ ID NO:14).[11]

[0038] FIG. **7** is a schematic showing the predicted topography of the TMEM43 protein showing four transmembrane domains (white) with predicted phoshorylation sites (pale grey), transactivation domain (medium grey), YingOYang sites (pale grey) SUMO attachment (dark grey), and the O-glycosylation sites (open grey), S358L mutation (black). The extracellular and cytoplasmic regions can switched for there is equal evidence supporting either orientation.

[0039] FIG. **8** is an analysis of clinical data in affected and non-affected individuals. A) Cumulative incidence of PVC's >1000 in 24 hours in: A1) Affected n=11 and unaffected n=18 males without >1000 PVC's at baseline. A2) Affected n=24 and unaffected n=21 females without >1000 PVC's at baseline. A3) Affected males vs. affected females without >1000 PVC's at baseline. B) Cumulative incidence of Heart Failure in: B1) Affected n=89 and unaffected n=71 males without heart failure at baseline. B2) Affected n=87 and unaffected n=68 females without heart failure at baseline. B3) Affected males vs. affected females without heart failure at baseline. C) Cumulative incidence of death in: C1) Affected n=148 and unaffected n=77 males. C2) Affected n=109 and unaffected 74=X females. C3) Affected males vs. affected females.

[0040] FIG. **9** is a schematic showing sequence variants identified through sequencing using the Mutation Screening Panel. All sequencing variants (n=240) identified in the 20 ARVD5 candidate genes. 19 variants were found exclusively in subjects with primary affection status.

[0041] FIG. **10** is a segregation analysis through family AR14 illustrates that eleven of the nineteen variants are on the ARVD5-associated haplotype (white).

[0042] FIG. **11** is schematic showing that clinically unaffected subjects from two ARVC families share distal regions of the ARVD5 ancestral haplotype that do not include the TMEM43 gene.

[0043] FIG. **12** is a graph (A) and table (B) showing age penetrance of TMEM43 positive subjects.

DESCRIPTION OF VARIOUS EMBODIMENTS

[0044] Arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) in its most severe presentation, causes sudden cardiac death and early death due to arrhythmias and heart failure. This is seen particularly in males. Clinical diagnosis of ARVD/C is difficult. Various loci including the ARVD5 locus have previously been identified. The inventors have identified a reduced minimal critical region of the ARVD5 haplotype associated with ARVD/C and have further identified a gene, TMEM43, disease associated variants of which are diagnostic of ARVD/C. For example a modification of serine to leucine at position 358 (S358L) was found in all affected individuals and in less than 1% of the population at large, indicating that detection of TMEM43 disease associated variants, such as S358L is diagnostic for ARVD/C and/or developing ARVD/C. At risk families are readily screened for TMEM43 disease associated variants through for example genetic mutation analysis. Detection of TMEM43 disease associated variants is useful for diagnosing individuals with ARVD/C and for prognosing individuals at risk of developing ARVD/C. Early detection is advantageous as the inventors have previously shown that improved survival occurs in patients with an implantable cardioverter defibrillator (ICD).

[0045] Accordingly, an aspect of the disclosure provides a method of screening for, diagnosing and/or detecting cardiomyopathy or an increased risk of developing cardiomyopathy in a subject comprising detecting the presence of a TMEM43 disease associated variant in a sample of the subject, wherein the presence of the TMEM43 disease associated variant is indicative of cardiomyopathy and/or an increased risk or developing cardiomyopathy.

[0046] Another embodiment provides a method of diagnosing ARVD/C comprising detecting the presence of a TMEM43 disease associated variant in a sample of the subject, wherein the presence of the TMEM43 disease associated variant is indicative of ARVD/C. In an embodiment, the subject has at least one clinical feature associated with cardiomyopathy, for example arrhythmias. In another embodiment, the subject has been diagnosed with a cardiomyopathy.

[0047] In another embodiment, the disclosure provides a method of screening for, diagnosing or detecting ARVD/C and/or an increased risk of developing ARVD/C in a subject comprising detecting the presence of a TMEM43 disease associated variant in a sample of the subject, wherein the presence of the TMEM43 disease associated variant is indicative of ARVD/C and/or an increased risk of developing ARVD/C.

[0048] A further embodiment provides a method of diagnosing a predisposition for ARVD/C in a subject comprising detecting the presence of a TMEM43 disease associated variant in a sample of the subject, wherein the presence of the TMEM43 disease associated variant is indicative of a predisposition for ARVD/C. Another embodiment provides a method of identifying a subject with an increased risk of and/or predisposition for ARVD/C comprising detecting in a sample from the subject, a TMEM43 disease associated variant, wherein the presence of the TMEM43 disease associated

variant is indicative of an increased risk of ARVD/C. The presence of a TMEM43 disease associated variant is indicative that the subject has ARVD/C or an increased risk of developing ARVD/C compared to an individual not having the TMEM43 disease associated variant.

[0049] As used herein the phrase "screening for, diagnosing or detecting ARVD/C" refers to a method or process of determining if a subject has ARVD/C.

[0050] As used herein the phrase "screening for, diagnosing or detecting a risk of developing ARVD/C" refers to a method or process of determining if a subject has an increased risk of developing ARVD/C.

[0051] As used herein "cardiomyopathy" refers to diseases of the heart muscle and includes ARVD/C including ARVD/C, associated with ARVD5.

[0052] As used herein "ARVD/C" or arrhythmogenic right ventricular dysplasia/cardiomyopathy refers to a cardiomyopathy in which normal myocardium appears to be replaced by fibrofatty tissue. Although ARVD/C was initially described as a disease of the right ventricle it is also a biventricular disorder. ARVD/C has a genetic component. Hence the methods, compositions and kits described are useful for identifying presymptomatic subjects and/or subjects with an increased risk of and/or predisposition for developing ARVD/C as well as diagnosing subjects with ARVD/C. Symptoms associated with ARVD/C may include palpitations ventricular tachycardia, pre-syncope or light headedness, syncope or fainting, which are all vague symptoms found in the general population. A final outcome can include heart failure and sudden death. ARVD/C is alternatively referred to as ARVC or arrhythmic cardiomyopathy.

[0053] As used herein "ARVD/C associated with ARDV5" refers to ARVD/C associated with and/or caused by mutations in the ARVD5 locus. For example, the methods, compositions and kits described herein are useful for identifying subjects who are negative for mutations associated with loci other than ARVD5 e.g. in desmosomal genes such as mutations in desmoplakin, plakophilin, desmoglein and/or plakoglobin not associated with ARVD5. A person skilled in the art would recognize that ARVD/C associated with may be related to deficiencies in desmosomal pathways, eg through functional interactions.

[0054] As used herein "TMEM43" or "transmembrane protein 43" refers to a TMEM43 gene including gene introns and its gene products including transcribed nucleic acids and translated polypeptides (such as TMEM43 gene, TMEM43 transcripts, TMEM43 polypeptides). TMEM43 is also known as LUMA and has been suggested to reside in the inner nuclear membrane and ER[43]. TMEM43 optionally refers to the full sequence or a portion thereof which retains TMEM43 activity. In a preferred embodiment TMEM43 refers to human TMEM43.

[0055] "Wild-type TMEM43 gene" or "wild-type TMEM43 gene products" as used herein refers to common naturally occurring forms of the TMEM43 gene or gene products that are not associated with disease. In one embodiment, wild type TMEM43 has the genomic sequence (SEQ ID NO:1) wherein nucleotide at genomic position 14158166 is cytosine. In one embodiment, wild type TMEM43 has the nucleic acid sequence identified by Genbank Accession number NM_024334 (SEQ ID NO:2). In another embodiment wild type TMEM43 has the protein sequence identified by Genbank Accession number NP_077310 protein (SEQ ID NO:3). Protein and polypeptide are used herein interchangeably. Various isoforms of TMEM43 exist.

[0056] In addition, the inventors have conducted extensive database analysis using ECGene Model and EMBL-EBI databases. ECGene Model with alternative splicing reports 953 sequences corresponding to TMEM43 that include 1 RefSeq, 12 mRNA, 940 EST sequences. According to ECgene bioinformatic analysis, this gene produces 34 transcript variants encoding 18 distinct proteins for human TMEM43 The transcript variants include Transcript ID's: H3C1779.1, H3C1779.2, H3C1779.3#R, H3C1779.4, H3C1779.5, H3C1779.6, H3C1779.7, H3C1779.8, H3C1779.9, H3C1779.10, H3C1779.11, H3C1779.12, H3C1779.13, H3C1779.14, H3C1779.15, H3C1779.16, H3C1779.17, H3C1779.18, H3C1779.19, H3C1779.20, H3C1779.21, H3C1779.22, H3C1779.23, and H3C1779.24. Searches in EMBL-EBI database reports 6 transcripts. A person skilled in the art will recognize that the TMEM43 disease associated variants are readily detected in any of the above variants and/or in any of the encoded polypeptides.

[0057] The Ensembl data base EBI IDs are identified by searching for ENSG00000170876743.

[0058] As used herein "TMEM43 disease associated variant" means any TMEM43 molecule, nucleic acid, including an allele, or polypeptide that comprises at least one modification and/or alteration compared to wild-type TMEM43 that is associated with or useful for screening, diagnosing or detecting an increased risk of developing ARVD/C. The modification and/or alteration is optionally a TMEM43 gene mutation, for example a germline mutation. As used herein, a "TMEM43 gene mutation" refers to a nucleotide change (and/or nucleotide changes) in the TMEM43 gene allele or alleles that is/are reflected in nucleic acid and polypeptide gene products that is/are not present in wild-type TMEM43 gene or gene products which are not associated with disease. The gene mutation is in one embodiment inherited e.g. a germline mutation. In another embodiment, the gene mutation is sporadic (eg. a somatic mutation). TMEM43 gene mutations include without limitation, missense mutations, deletion mutations, point mutations, and/or insertion mutations. Accordingly TMEM43 gene mutations include nucleotide polymorphisms such as single nucleotide polymorphisms associated with disease.

[0059] In an embodiment, the TMEM43 disease associated variants comprise TMEM43 polypeptide mutated at serine 358, TMEM43 transcripts mutated at cytosine 1073 and/or TMEM43 gene mutated at cytosine at genomic position 14158166, including missense mutations, deletions, and insertions.

[0060] In another embodiment, the TMEM43 disease associated variants consist of TMEM43 polypeptide mutated at serine 358, TMEM43 transcripts mutated at cytosine 1073 and/or TMEM43 gene mutated at cytosine at genomic position 14158166, including missense mutations, deletions, and insertions.

[0061] In an embodiment, the TMEM43 disease associated variants comprise S358L, 1073 C>T, and/or 14158166 C>T.

[0062] In another embodiment, the TMEM43 disease associated variants is selected from S358L, 1073 C>T and 14158166 C>T. In another embodiment, the TMEM43 disease associated variant comprises a S358L mutation. In a further embodiment, the TMEM43 disease associated variant

comprises a 1073 C>T mutation. In yet a further embodiment, the TMEM43 disease associated variant comprises a 14158166 C>T mutation.

[0063] A person skilled in the art would recognize that the genomic mutation, 14158166 C>T is optionally detected in the opposite DNA strand. A person skilled in the art will understand that primers probes and other reagents can be designed to detect the corresponding mutation in the non-coding allele.

[0064] TMEM43 gene mutations are readily detected by analyzing the TMEM43 gene or its gene products. For example nucleic acids and/or polypeptides corresponding to a TMEM43 gene are optionally sequenced and compared to corresponding wild-type sequences. Gene mutations are optionally detected by analyzing genomic sequence.

[0065] In the general population, the predominant nucleotide found at genome position 14158166 in subjects without ARVD/C or an increased risk of developing ARVD/C is cytosine (for example, see position 171 in SEQ ID NO:1 and SEQ ID NO:4). The inventors have shown that the nucleotide corresponding to genome position 14158166 is modified in subjects with ARVD/C or an increased risk of developing ARVD/C from cytosine (C) to thymidine (T).

[0066] In an embodiment, the TMEM43 disease associated variant is a germline mutation. In an embodiment, the germline mutation comprises 14158166 C>T. In another embodiment, detecting a TMEM43 disease associated variant comprises determining whether there is a germline alteration in the TMEM43 gene and/or TMEM43 gene regulatory sequence. The inventors have further shown that the gene mutation that results in thymidine at the nucleotide corresponding to genome position 14158166 is typically a missense mutation.

[0067] A "missense mutation" as used herein refers to a mutation in a nucleotide that changes a codon for one amino acid into a codon for a different amino acid. The TMEM43 disease associated variant comprising this gene mutation is optionally referred to as 14158166C>T and it changes the coded for amino acid from serine to leucine in the TMEM43 polypeptide. Accordingly, in an embodiment the TMEM43 disease associated variant comprises a gene mutation of a nucleotide corresponding to genome position 14158166 (genome build NCBI Build 36.1 (May 2006) accessed online through Genome Browser http://genome.ucsc.edu/). In another embodiment, the gene mutation of the nucleotide corresponding to genome position 14158166 is a missense mutation. In another embodiment, the missense mutation is mutation to thymidine (T) (for example, see position 1073 in SEQ ID NO:4). In yet a further embodiment the TMEM43 disease associated variant is 14158166C>T.

[0068] The term "corresponding to" as used herein means situated in a different sequence position but having sequence characteristics in common, including identical, or substantially identical, nucleotide sequence flanking the mutation (eg. substantial identity is optionally at least 75% identity over four or more contiguous nucleotides). For example, "a nucleotide corresponding to genome position 14158166" refers to a nucleotide that is equivalently situated in terms of flanking sequence and relative position number in TMEM43 but that may be identified by a different genome position in another build (eg the related context). Similarly, "corresponding to position 1073 in TMEM43 mRNA" refers to a nucleotide that is equivalently situated in terms of flanking sequence and relative position in TMEM43 but that may be identified by a different nucleotide number in a different transcript. Further "corresponding to" can refer to derived from or related to, for example a nucleic acid corresponding to a gene refers to a nucleic acid derived from the gene such as a transcript and/or an amplified or synthetic copy related to the gene. Similarly, an amino acid sequence corresponding to a nucleic acid refers to an amino acid that is coded for by the nucleic acid.

[0069] A person skilled in the art will recognize that mutations at this position such as deletion of one or more nucleotides comprising the nucleotide at position 14158166 will also be associated with ARVD/C or an increased risk of developing ARVD/C. Similarly, it is expected that modification of this nucleotide to guanine or adenosine would also be associated with ARVD/C or an increased risk of developing ARVD/C.

[0070] Accordingly in an embodiment, the gene mutation comprises a deletion of a nucleotide at genome position 14158166. In another embodiment, the nucleotide detected at genome position 14158166 is guanine or adenine.

[0071] Gene mutations are optionally detected by analyzing nucleic acids corresponding to the TMEM43 gene such as RNA transcripts e.g. mRNA or complementary DNA (cDNA). In the general population, the predominant nucleotide found in TMEM43 mRNA at position 1073 in subjects without ARVD/C or an increased risk of developing ARVD/C is cytosine (SEQ ID NO:2). The inventors have shown that the nucleotide found at position 1073 in TMEM43 mRNA (NM_0234334) is modified in subjects with ARVD/C or an increased risk of developing ARVD/C, from cytosine (C) to thymidine (T). The inventors have shown that this mutation is a missense mutation. The TMEM43 disease associated variant comprising this gene mutation is optionally referred to as 1073C>T (SEQ ID NO:5). Accordingly, in one embodiment the TMEM43 disease associated variant detected comprises a gene mutation in a nucleotide corresponding to position 1073 in TMEM43 mRNA. In one embodiment the gene mutation is a missense mutation. In another embodiment, the nucleotide detected at position 1073 is thymidine (SEQ ID NO:5). In yet a further embodiment, the TMEM43 diseases associated variant is 1073C>T. A person skilled in the art will recognize nucleotide mutations in mRNA can be detected using corresponding cDNA. Further a person skilled in the art will recognize that mutations at this position such as deletion of one or more nucleotides comprising the nucleotide at position 1073 will also be associated with ARVD/C or an increased risk of developing ARVD/C. Similarly, it is expected that modification of this nucleotide to guanine or adenosine would also be associated with ARVD/C or an increased risk of developing ARVD/C. Accordingly in one embodiment, the modification comprises a deletion of nucleotide at position 1073 in TMEM43 mRNA. In another embodiment, the nucleotide detected at 1073 is guanine or adenine.

[0072] Gene mutations are optionally detected by analyzing polypeptides corresponding to the TMEM43 gene. The inventors have shown that the amino acid found at position 358 in TMEM43 protein (NP_077310) (SEQ ID NO:3) is modified in subjects with ARVD/C or an increased risk of developing ARVD/C from serine (Ser) to leucine (Leu) (SEQ ID NO:6). The TMEM43 disease associated variant comprising this mutation is optionally referred to as Ser358Leu and or S358L. Accordingly, in an embodiment the TMEM43 disease associated variant detected comprises a modification in the amino acid corresponding to position 358 in TMEM43

polypeptide. In another embodiment, the amino acid detected at position 358 is leucine (SEQ ID NO:6). In yet a further embodiment, the TMEM43 disease associated variant is S358L. A person skilled in the art will recognize that modifications at this position such as deletion of one or more amino acids comprising the amino acid at position 358 will also be associated with ARVD/C or an increased risk of developing ARVD/C. Similarly, it is expected that modification of this amino acid to other branched amino acids would also be associated with ARVD/C or an increased risk of developing ARVD/C. For example, it is shown that a nucleotide change in TMEM43 mRNA at position 1073 results in introduction of leucine (i.e nucleotide change to thymidine) as mentioned above, a stop codon (i.e. nucleotide change to adenine) or tryptophan (i.e. nucleotide change to guanine). A person skilled in the art will understand that additional amino acid changes result from changes in the first (i.e nucleotide 1072) and third (i.e. nucleotide 1074) nucleotides of the codon coding for the amino acid at position 358. Accordingly in one embodiment, the modification comprises a deletion of amino acid at position 358 in TMEM43 polypeptide. In another embodiment, the amino acid detected at a position 358 is tryptophan. In another embodiment the amino acid at 358 is replaced by a stop codon.

[0073] Other modifications can include post-translational modifications of serine 358 in TMEM43.

[0074] A person skilled in the art will understand that positions of mutations provided are relative to the particular accession numbers and SEQ ID NOS provided. A person skilled in the art would readily be able to determine corresponding position in any TMEM43 isoforms, TMEM43 homologues, TMEM43 sequence fragments or other related sequences.

[0075] The terms "risk" and "increased risk" as used herein refer to a subject having a predisposition to developing a disease e.g increased risk compared to the average risk of a population. The predisposition is optionally inherited, or optionally acquired (e.g sporadic mutation). The increased risk is relative to a subject not having a TMEM43 disease associated variant.

[0076] The term "sample" and "sample of a subject" as used herein refer to any sample of a subject that comprises nucleic acids or polypeptide and/or includes sequence or sequence data corresponding to TMEM43 gene, RNA or protein sequence. For example, a priori sequenced TMEM43 gene, RNA or protein sequence is optionally used to detect TMEM43 disease associated variants. In one embodiment, the sample comprises blood, whole blood or a fraction thereof. As the inventors have shown that TMEM43 is expressed in white blood cells, in one embodiment the sample is any fluid, cell preparation or tissue comprising white blood cells. In a further embodiment, the sample comprises B-lymphocytes. In another embodiment, the sample comprises cardiac tissue, and/or cardiac cells. In another embodiment, the sample is selected from the group consisting of fresh tissue such as a biopsy, frozen tissue and paraffin embedded tissue. In other embodiments, the sample comprises any nucleated cell from the human body and any cell lines generated to express TMEM43.

[0077] The term "subject" as used herein includes all members of the animal kingdom including multicellular organisms, including mammals, and preferably means humans.

[0078] As mentioned previously, ARVD/C is difficult to diagnose. The inventors have determined that the methods described herein identify individuals presymptomatically. Accordingly, in one embodiment, the individual is presymptomatic.

[0079] ARVD/C is associated with several known loci and cloned genes. The ARVD5 haplotype, which is associated with an autosomal dominant form of ARVD/C, maps to chromosome 3p. As used herein "ARVD5 haplotype" and/or "ARVD5 locus" means the allele or alleles of ARVD5 that are associated with ARVD/C. Given the severity of the ARVD/C, its variable presentation and penetrence, the methods described herein are useful, for example, for screening relatives of individuals known to have ARVD/C and/or known to be carriers of the ARVD5 haplotype.

[0080] As used herein, "a relative" or "blood relation" is a relative genetically related, or related by birth, and includes without limitation 1^{st}, 2^{nd}, 3^{rd}, 4^{th}, 5^{th}, 6^{th}, 7^{th}, 8^{th}, 9^{th} and 10^{th} degree relations, for example but not limited to parents, children, grandchildren, grandparents, cousins and/or 2^{nd} cousins related by blood.

Isolated Nucleic Acids and Compositions

[0081] TMEM43 disease associated variants are readily detected using isolated nucleic acids and/or compositions comprising isolated nucleic acids or polypeptides that are specific for a TMEM43 disease associated variant.

[0082] Accordingly in one aspect, the application provides compositions comprising isolated nucleic acids useful for detecting TMEM43 disease associated variants. Another aspect provides an isolated nucleic acid molecule comprising a nucleic acid sequence comprising a TMEM43 gene or transcript disease associated variant.

[0083] Another aspect provides a reagent for detecting a TMEM43 disease associated variant, such as an isolated nucleic acid primer or probe. In an embodiment, the isolated nucleic acid molecule comprises:

[0084] a) any one of SEQ ID NOs: 1-54, and/or combinations thereof; and/or

[0085] b) a nucleic acid molecule with at least 80%, 90%, 95%, or 99% sequence identity to a), characterized in that the nucleic acid molecule is capable of binding TMEM43 under moderately stringent conditions. In an embodiment, the nucleic acid with at least 80%, 90%, 95%, or 99% sequence identity to a) binds TMEM43 under moderately stringent conditions and is capable of priming strand synthesis. Isolated nucleic acid molecules including for example SEQ ID NOs: 1-52 are useful as primers to amplify TMEM43. In an embodiment, the isolated nucleic acid molecule is an amplified which is produced by amplification of a TMEM43 disease associated variant containing template. Isolated nucleic acid molecules including for example SEQ ID NO: 53 and/or 54, are useful for as probes to detect TMEM43 disease associated variants.

[0086] The term "isolated nucleic acid sequence" and/or "oligonucleotide" as used herein refers to a nucleic acid substantially free of cellular material or culture medium when produced by recombinant DNA techniques, or chemical precursors, or other chemicals when chemically synthesized. The term "nucleic acid" and/or "oligonucleotide" as used herein refers to a sequence of nucleotide or nucleoside monomers consisting of naturally occurring bases, sugars, and intersugar (backbone) linkages, and is intended to include DNA and RNA which can be either double stranded or single stranded, represent the sense or antisense strand. The term

also includes modified or substituted oligomers comprising non-naturally occurring monomers or portions thereof, which function similarly, which are referred to herein as "chemical analogues" and/or "oligonucleotide analogues" such as "peptide nucleic acids". Such modified or substituted nucleic acids may be preferred over naturally occurring forms because of properties such increased stability in the presence of nucleases.

[0087] One aspect of the application provides a composition comprising at least one isolated nucleic acid sequence, wherein the at least one isolated nucleic acid molecule hybridizes to:

[0088] a) a RNA product of TMEM43;

[0089] b) a nucleic acid sequence complementary to a); and/or

[0090] c) a nucleic acid sequence corresponding to a);

wherein the composition is used to detect a TMEM43 disease associated variant. In an embodiment, a) comprises a TMEM43 disease associated variant. In an embodiment, the nucleic acid complementary to or corresponding a) comprises genomic sequence.

[0091] The term "hybridize" refers to the sequence specific non-covalent binding interaction with a complementary nucleic acid. One aspect of the application provides an isolated nucleotide sequence, which hybridizes to a RNA product of TMEM43 or a nucleic acid sequence which is complementary to an RNA product of a gene of TMEM43. In one embodiment the hybridization is conducted under at least moderately stringent conditions. In a preferred embodiment, the hybridization is under high stringency conditions. Appropriate stringency conditions which promote hybridization are known to those skilled in the art, or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1 6.3.6. For example, 6.0× sodium chloride/sodium citrate (SSC) at about 45° C. for 15 minutes, followed by a wash of 2.0×SSC at 50° C. for 15 minutes may be employed.

[0092] The stringency may be selected based on the conditions used in the wash step. For example, the salt concentration in the wash step can be selected from a high stringency of about 0.2×SSC at 50° C. for 15 minutes. In addition, the temperature in the wash step can be at high stringency conditions, at about 65° C. for 15 minutes.

[0093] By "at least moderately stringent hybridization conditions" it is meant that conditions are selected which promote selective hybridization between two complementary nucleic acid molecules in solution. Hybridization may occur to all or a portion of a nucleic acid sequence molecule. The hybridizing portion is typically at least 15 (e.g. 20, 25, 30, 40 or 50) nucleotides in length. Those skilled in the art will recognize that the stability of a nucleic acid duplex, or hybrids, is determined by the Tm, which in sodium containing buffers is a function of the sodium ion concentration and temperature (Tm=81.5° C.−16.6 (Log 10[Na+])+0.41(% (G+C)−600/l), or similar equation). Accordingly, the parameters in the wash conditions that determine hybrid stability are sodium ion concentration and temperature. In order to identify molecules that are similar, but not identical, to a known nucleic acid molecule a 1% mismatch may be assumed to result in about a 1° C. decrease in Tm, for example if nucleic acid molecules are sought that have a >95% sequence identity, the final wash temperature will be reduced by about 5° C. Based on these considerations those skilled in the art will be able to readily select appropriate hybridization conditions. In preferred embodiments, stringent hybridization conditions are selected. By way of example the following conditions may be employed to achieve stringent hybridization: hybridization at 5× sodium chloride/sodium citrate (SSC)/5×Denhardt's solution/1.0% SDS at Tm −5° C. based on the above equation, followed by a wash of 0.2×SSC/0.1% SDS at 60° C. for 15 minutes. Moderately stringent hybridization conditions include a washing step in 3×SSC at 42° C. for 15 minutes. It is understood, however, that equivalent stringencies may be achieved using alternative buffers, salts and temperatures. Additional guidance regarding hybridization conditions may be found in: Current Protocols in Molecular Biology, John Wiley & Sons, N.Y., 1989, 6.3.1-6.3.6 and in: Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2000, Third Edition.

[0094] The term "sequence identity" as used herein refers to the percentage of sequence identity between two polypeptide sequences or two nucleic acid sequences. To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino acid or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity=number of identical overlapping positions/total number of positions.times.100%). In one embodiment, the two sequences are the same length. The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. U.S.A. 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., 1990, J. Mol. Biol. 215:403. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the present application. BLAST protein searches can be performed with the XBLAST program parameters set, e.g., to score-50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., of XBLAST and NBLAST) can be used (see, e.g., the NCBI website). The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted. In an embodiment, the isolated nucleic acids are useful as primers.

[0095] The term "primer" as used herein refers to a nucleic acid sequence, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand is induced (e.g. in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH). The primer must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon factors, including temperature, sequences of the primer and the methods used. A primer typically contains 15-25 or more nucleotides, although it can contain less. The factors involved in determining the appropriate length of primer are readily known to one of ordinary skill in the art.

[0096] The inventors designed a number of primers useful for detecting whether TMEM43 gene changes. These primers were custom designed with the assistance of Primer3 primer design program.

TABLE A

TMEM43 primers

Primer Name	Primer Sequence	
cDNA primers designed to cover the whole translated region		
NM_024334cDNA-Ex1-4-F	GTCAGCCCACTTCCTAGCTG	SEQ ID NO: 15
NM_024334cDNA-Ex1-4-R	CCTCGTCTCCTTCTTCACCT	SEQ ID NO: 16
NM_024334-cDNA-Ex4-9-F	AGAATGAAGGAAGGCTGGTG	SEQ ID NO: 17
NM_024334-cDNA-Ex4-9-R	TGGTGGAGAATGGGACTAGC	SEQ ID NO: 18
NM_024334-cDNA-Ex9-12-F	CGCCGTGGAGACTTTTTCTA	SEQ ID NO: 19
NM_024334-cDNA-Ex9-12-R	ACCTGGATCCTAGGGCTCAC	SEQ ID NO: 20
NM_024334-cDNA-Ex1-10-F	GTCAGCCCACTTCCTAGCTG	SEQ ID NO: 21
NM_024334-cDNA-Ex1-10-R	CCCAGGTCTTCATGGAGTTG	SEQ ID NO: 22
NM_024334-cDNA-Ex5-12-F	ATCTTCCGGCTGTGAAACTG	SEQ ID NO: 23
NM_024334-cDNA-Ex5-12-R	AGAGGGAGTGCAGAGTCCAA	SEQ ID NO: 24
Genomic DNA primers designed to cover the 5' and 3' untranslated regions all exons, intron exon boundaries and some flanking intronic sequence.		
NM_024334-Ex1-F	CAATGTCCCGGACCGTATAG	SEQ ID NO: 25
NM_024334-Ex1-R	GGCGAAATGGACCTAGAGGA	SEQ ID NO: 26
NM_024334-Ex2-F	AGTTTTCATTCTGTTACTGTTTCTTTT	SEQ ID NO: 27
NM_024334-Ex2-R	GGCCCTTGATTACCAAATCC	SEQ ID NO: 28
NM_024334-Ex3-F	AACTGTACGGTGGGGAGATG	SEQ ID NO: 29
NM_024334-Ex3-R	ATCACTCCCATGTGTGACCA	SEQ ID NO: 30
NM_024334-Ex4-F	AAGAACCTGGGACAGGGAGT	SEQ ID NO: 31
NM_024334-Ex4-R	CTCCTGGAGCCACTCTTCAC	SEQ ID NO: 32
NM_024334-Ex5&6-F	TGATCTGGTAGCCCTGAGGT	SEQ ID NO: 33
NM_024334-Ex5&6-R	CACGAGGCAGGATTAACTCAA	SEQ ID NO: 34
NM_024334-Ex7-F	CCTGGGCTAATCTGGACTTG	SEQ ID NO: 35
NM_024334-Ex7-R	CTGATCCTGTGCCTTTAGCC	SEQ ID NO: 36
NM_024334-Ex8&9-F	CGTGGACGAGACAGAGTCAG	SEQ ID NO: 37
NM_024334-Ex8&9-R	CGCTCCTGACATTGACCAAG	SEQ ID NO: 38
NM_024334-Ex10-F	GGGTTTCTGTGCTCACTTCC	SEQ ID NO: 39
NM_024334-Ex10-R	TGCCTCATTCACTGGCTATG	SEQ ID NO: 40

TABLE A-continued

TMEM43 primers		
Primer Name	Primer Sequence	
NM_024334-Ex11-F	TGTTCAGAAATGGCCAACAG	SEQ ID NO: 41
NM_024334-Ex11-R	CTCATCCCAAGGCTATGGAG	SEQ ID NO: 42
NM_024334-Ex12a-F	CCCATCCTCATCTAGGGACA	SEQ ID NO: 43
NM_024334-Ex12a-R	GGAAACAGCAGGAGAAGCTG	SEQ ID NO: 44
NM_024334-Ex12b-F	TGGTGTTCACCAGCTCATGT	SEQ ID NO: 45
NM_024334-Ex12b-R	TTCCTCTTGGGGTAGGAAAG	SEQ ID NO: 46
NM_024334-Ex12c-F	TCCTGAGGAGAAAAGCTGGA	SEQ ID NO: 47
NM_024334-Ex12c-R	CGTGGGCATTGTACAACCAG	SEQ ID NO: 48
NM_024334-Ex12d-F	CGATTAAGAGAAAAGGTTGGAA	SEQ ID NO: 49
NM_024334-Ex12d-R	GAGATTTGATGAAATTGCTCATGTA	SEQ ID NO: 50
NM_024334-Ex12e-F	TTGTGCCTGCTGGGAGTAAT	SEQ ID NO: 51
NM_024334-Ex12e-R	ATCCTATGGCTGAATTCTTTACA	SEQ ID NO: 52

[0097] In another aspect, the application describes probes that are useful for detecting a TMEM43 disease associated variant. Where the variation is only a single nucleotide change, for example 1073C>T shorter probes used at high stringency are useful. For example, oligonucleotide probes having a sequence length ranging from 16 to 20 nucleotides, comprising, within the sequence, for example, at the centre, a nucleotide specific for the alleleic variants of the gene coding for a TMEM43 disease associated variant, wherein the oligonucleotide probes hybridizes with the TMEM43 disease associated variant. In an embodiment the probe comprise ctgtgtggccacctTgctga (SEQ ID NO:53) to detect the disease variation. The normal variation is one embodiment detected using a probe comprising ctgtgtggccacctCgctga (SEQ ID NO:54)

[0098] A person skilled in the art will recognize that all or part of the above probes can be used.

[0099] The term "probe" as used herein refers to a nucleic acid sequence that will hybridize to a nucleic acid target sequence. In one example, the probe hybridizes to an RNA TMEM43 disease associated variant or a nucleic acid sequence complementary to the RNA TMEM43 disease associated variant. The length of probe depends on the hybridize conditions and the sequences of the probe and nucleic acid target sequence. In one embodiment, the probe is at least 8, 10, 15, 20, 25, 50, 75, 100, 150, 200, 250, 400, 500 or more nucleotides in length.

[0100] In certain embodiments the isolated nucleic acid comprises a detectable label, such as a fluorescent or radioactive label.

Detection Methods for the Presence of a TMEM43 Mutation

[0101] The presence of a TMEM43 disease associated variant are readily detected using methods that detect a gene mutation in a TMEM43 disease associated variant gene, RNA gene product, such as TMEM43 transcripts, and/or polypeptide gene product.

Detecting Nucleic Acid TMEM43 Disease Associated Variants

[0102] A person skilled in the art will appreciate that a number of methods are useful for detect the presence of a TMEM43 disease associated variant in a TMEM43 nucleic acid.

[0103] For example a variety of techniques are known in the art for detecting a gene mutation or alteration within a sample, including genotyping, microarrays, Restriction Fragment Length Polymorphism, Southern Blots, SSCP, dHPLC, single nucleotide primer extension, allele-specific hybridization, allele-specific primer extension, oligonucleotide ligation assay, and invasive signal amplification, Matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, and Fluorescence polarization (FP). Such methods optionally employ the isolated nucleic acid compositions of the disclosure. The TMEM43 disease associated variants, such as germline alterations, are readily detected by TMEM43 gene analysis. For example, this can be accomplished by gene amplification analysis such as polymerase chain reaction (PCR) analysis of TMEM43 or a part thereof, optionally followed by sequencing, and comparing the TMEM43 amplification profile or sequence to a wild-type TMEM43 amplification profile or wild-type TMEM43 sequence. In an embodiment, one or more TMEM43 exons are amplified by PCR, and analyzed for gene mutations, for example by single-strand conformation polymorphism (SSCP). In an embodiment, one or more TMEM43 exons are sequenced and analyzed for gene mutations, for example by comparing the sequence obtained from a sample of a subject, to wild-type TMEM43 sequence. The full exon or a part thereof, for example a part know to be associated with disease, for example a part comprising a nucleotide corresponding to the nucleotide shown at genome position 14158166, is optionally PCR amplified and/or sequenced. Detecting "T" at 14158166 is indicative of having ARVD/C or an increased risk of developing ARVD/C. In another embodiment, 2, 3, 4,

5, 6, 7, 8, 9, 10, 11, or 12 exons, or parts thereof, are PCR amplified and/or sequenced and the PCR profile and/or sequence analyzed for gene mutations. Accordingly, the presence of a TMEM43 gene mutation is detected in one embodiment by sequencing. Methods of sequencing are well known in the art. In one method, primers flanking a TMEM43 mutation are selected, for example primers which amplify exon 12 either in genomic sequence and/or corresponding transcripts, and used to amplify the gene region comprising a TMEM43 mutation. The amplified region is sequenced and analysed. In another embodiment the TMEM43 mutation comprises a thymidine corresponding to position 14158166 of genome build 36.1. In an embodiment the primers used to detect the mutation 14158166C>T or 1073 C>T mutation comprise:

Primer Name	Primer Sequence
NM_024334-Ex12a-F	CCCATCCTCATCTAGGGACA (SEQ ID NO: 43)
NM_024334-Ex12a-R	GGAAACAGCAGGAGAAGCTG (SEQ ID NO: 44)

[0104] Gene mutations can be detected by detecting the presence of the mutation in the gene or in a corresponding transcribed sequence. A variety of techniques are known in the art that are suitable for detecting mutations in the gene or in a corresponding transcribed sequence.

[0105] For example, primers which span one or more exons that comprise the putative location of a TMEM43 disease associated variant, are useful to detect TMEM43 disease associated variants. In an embodiment, a composition comprising SEQ ID NO: 19 and SEQ ID NO:20 is used to detect mutations at 1073, such as 1073C>T. In another embodiment, a composition comprising SEQ ID NO:23 and SEQ ID NO:24 is used to detect mutations at 1073. A person skilled in the art readily designs and uses suitable additional primers based on the sequences provided herein.

[0106] In another embodiment, TMEM43 disease associated variants are readily detected by polymerase chain reaction (PCR), real time PCR, multiplex ligation dependent probe amplification (MLPA), nucleic acid sequence based amplification (NASBA) and/or real time NASBA. As used herein "NASBA" refers to a sensitive isothermal transcription-based amplification method used for example for RNA research. NASBA technology is optionally applied to single nucleotide polymorphism (SNP) analysis using human genomic DNA as a template. For example combination of DNA NASBA with multiplex hybridization of specific molecular beacons makes it possible to discriminate the presence of mutations of interest (Berard, C, Cazalis M A, Leissner P, Mougin B., DNA nucleic acid sequence-based amplification-based genotyping for polymorphism analysis. Biotechniques. 2004, 37:680-2, 684, 686).

[0107] In another embodiment, the method of detecting the presence of a TMEM43 disease associated variant comprises a probe that specifically hybridizes a TMEM43 disease associated variant. The probe optionally hybridizes to an mRNA sequence, corresponding complementary DNA or copy DNA (cDNA) or a genomic sequence. The probe can hybridize a TMEM43 mutation directly or an amplified product comprising the TMEM43 gene mutation. In another embodiment the probe binds upstream or downstream of a TMEM43 gene mutation. For example, in one embodiment an amplified region comprising a TMEM43 gene mutation is hybridized using a composition comprising a probe specific for the TMEM43 gene mutation (e.g. "T") under stringent hybridization conditions. In an embodiment the probe comprises all or part (e.g. 10-19 nucleotides, or any number in between) of ctgtgtggccacctTgctga (SEQ ID NO:53) to detect the disease variation. The normal variation is in an embodiment detected using a probe comprising all or part (e.g. 10-19 nucleotides, or any number in between) of ctgtgtggccacctCgctga (SEQ ID NO:54). A person skilled in the art would recognize that a probe that hybridizes to a sequence in the non-coding (and/or corresponding sequence such as cDNA) comprising the TMEM43 disease associated variant is also useful with the methods, compositions and kits described herein.

[0108] In one embodiment, PCR or RT-PCR is employed to detect the presence of a TMEM 43 mutation. For example, PCR and RT-PCR and primers flanking the mutation are employed to amplify TMEM43 gene sequence and transcript sequence respectively in a sample comprising DNA (for PCR) or RNA (for RT-PCR). The amplified products are optionally sequenced to determine if a TMEM43 disease associated variant is present in the sample.

[0109] In another embodiment, the method of detecting the presence of a TMEM43 mutation comprises use of a restriction enzyme. For example amplified products can be digested with a restriction enzyme that specifically recognizes sequence comprising a TMEM43 disease associated variant but does not recognize sequence corresponding to the wild-type or non-disease associated TMEM43.

[0110] ARVD/C is an inheritable disease. Where a genetically related family member has been determined to have a TMEM43 disease associated variant, the genetic relation is readily screened specifically for mutations at cytosine 1073 of a TMEM43 transcript, and/or cytosine 14158166 of a TMEM43 genome. For example the genetic relation is optionally screened for 1073C>T and/or 14158166 C>T. Accordingly, in an embodiment, the subject has a genetic relation having a TMEM43 disease associated variant, such as mutation at 1073 of a TMEM43 transcript, mutation at 14158166 of TMEM43 genomic sequence, such as 1073C>T and 14158166C>T. In an embodiment primers flanking TMEM43 1073, and/or flanking TMEM43 14158166, for example, which hybridize within 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500 nucleotides upstream and within 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500 nucleotides downstream, are used to detect mutations at TMEM43 1073 or TMEM43 14158166.

[0111] A TMEM43 disease associated variant can also be detected using a DNA microarray.

Detecting Polypeptide TMEM43 Disease Associated Variants

[0112] A person skilled in the art will recognize that there are several methods known in the art for detecting a polypeptide TMEM43 disease associated variant.

[0113] A polypeptide TMEM43 disease associated variant is optionally detected using a binding agent that specifically binds a TMEM43 disease associated variant polypeptide gene products and not wild type TMEM43 polypeptide gene products. In one embodiment, the binding agent is an isolated polypeptide.

[0114] The term "isolated polypeptide" as used herein refers to a proteinaceous agent, such as a peptide, polypeptide

or protein, which is substantially free of cellular material or culture medium when produced recombinantly, or chemical precursors, or other chemicals, when chemically synthesized.

[0115] The phrase "bind to polypeptide products" as used herein refers to binding agents such as isolated polypeptides that specifically bind to TMEM43 disease associated variants described in the application. In an embodiment, isolated polypeptides are antibodies or antibody fragments.

[0116] The term "antibody" as used herein is intended to include monoclonal antibodies, polyclonal antibodies, and chimeric antibodies. The antibody may be from recombinant sources and/or produced in transgenic animals. The term "antibody fragment" as used herein is intended to include Fab, Fab', $F(ab')_2$, scFv, dsFv, ds-scFv, dimers, minibodies, diabodies, and multimers thereof and bispecific antibody fragments. Antibodies can be fragmented using conventional techniques. For example, $F(ab')_2$ fragments can be generated by treating the antibody with pepsin.

[0117] The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. Papain digestion can lead to the formation of Fab fragments. Fab, Fab' and $F(ab')_2$, scFv, dsFv, ds-scFv, dimers, minibodies, diabodies, bispecific antibody fragments and other fragments can also be synthesized by recombinant techniques.

[0118] To produce human monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from a human having cancer and fused with myeloma cells by standard somatic cell fusion procedures thus immortalizing these cells and yielding hybridoma cells. Such techniques are well known in the art, (e.g. the hybridoma technique originally developed by Kohler and Milstein (Nature 256:495-497 (1975)) as well as other techniques such as the human B-cell hybridoma technique (Kozbor et al., Immunol. Today 4:72 (1983)), the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Methods Enzymol, 121: 140-67 (1986)), and screening of combinatorial antibody libraries (Huse et al., Science 246:1275 (1989)). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with TMEM43 disease associated variants and the monoclonal antibodies can be isolated.

[0119] Specific antibodies, or antibody fragments, reactive against particular TMEM43 disease associated antigens, may also be generated by screening expression libraries encoding immunoglobulin genes, or portions thereof, expressed in bacteria with cell surface components. For example, complete Fab fragments, VH regions and FV regions can be expressed in bacteria using phage expression libraries (See for example Ward et al., Nature 341:544-546 (1989); Huse et al., Science 246:1275-1281 (1989); and McCafferty et al., Nature 348: 552-554 (1990)).

[0120] In one embodiment isolated polypeptides, antibodies or antibody fragments are used to detect a TMEM43 disease associated variant. In one embodiment the isolated polypeptides, antibodies or antibody fragments are labeled with a detectable marker.

[0121] The label is preferably capable of producing, either directly or indirectly, a detectable signal. For example, the label may be radio-opaque or a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{123}I, ^{125}I, ^{131}I; a fluorescent (fluorophore) or chemiluminescent (chromophore) compound, such as fluorescein isothiocyanate, rhodamine or luciferin; an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase; an imaging agent; or a metal ion.

[0122] In another embodiment, the detectable signal is detectable indirectly. For example, a secondary antibody that is specific for the isolated protein described in the application and contains a detectable label is useful to detect the isolated polypeptide described in the application.

[0123] A person skilled in the art will appreciate that a number of methods can be used to detect a polypeptide TMEM43 disease associated variant, including immunoassays such as Western blots, ELISA, and immunoprecipitation followed by SDS-PAGE, as well as immunocytochemistry or immunohistochemistry.

[0124] The application also contemplates the use of "peptide mimetics" for detecting polypeptide TMEM43 gene products. Peptide mimetics are structures which serve as substitutes for peptides in interactions between molecules (See Morgan et al (1989), Ann. Reports Med. Chem. 24:243-252 for a review). Peptide mimetics include synthetic structures which may or may not contain amino acids and/or peptide bonds but retain the structural and functional features of the isolated proteins described in the application, such as its ability to bind to the polypeptide product of a TMEM43 disease associated variant described in the application. Peptide mimetics also include peptoids, oligopeptoids (Simon et al (1972) Proc. Natl. Acad, Sci USA 89:9367); and peptide libraries containing peptides of a designed length representing all possible sequences of amino acids corresponding to the cleavage recognition sequence described in the application.

[0125] Peptide mimetics may be designed based on information obtained by systematic replacement of L-amino acids by D-amino acids, replacement of side chains with groups having different electronic properties, and by systematic replacement of peptide bonds with amide bond replacements. Local conformational constraints can also be introduced to determine conformational requirements for activity of a candidate peptide mimetic. The mimetics may include isosteric amide bonds, or D-amino acids to stabilize or promote reverse turn conformations and to help stabilize the molecule. Cyclic amino acid analogues may be used to constrain amino acid residues to particular conformational states. The mimetics can also include mimics of inhibitor peptide secondary structures. These structures can model the 3-dimensional orientation of amino acid residues into the known secondary conformations of proteins. Peptoids may also be used which are oligomers of N-substituted amino acids and can be used as motifs for the generation of chemically diverse libraries of novel molecules.

[0126] ARVD/C is an inheritable disease. Where a genetically related family member has been determined to have a TMEM43 disease associated variant, the genetic relation is readily screened specifically for mutations at serine 358 of a TMEM43 polypeptide. Accordingly in an embodiment, the subject has a genetic relation comprising a TMEM43 disease associated variant, such as mutation at serine 358, such as S358L.

[0127] In an embodiment the binding agents are fixed to a solid support. In a further embodiment the solid support is an ELISA plate.

[0128] Polypeptide TMEM43 disease associated variants can also be detected using tissue arrays.

Microarrays

[0129] As mentioned, the presence of a TMEM43 disease associated variant can optionally be detected using arrays

including DNA microarrays and tissue microarrays. A "microarray" as used herein refers to an ordered set of probes fixed to a solid surface that permits analysis such as gene analysis of a plurality of genes. A DNA microarray refers to an ordered set of DNA fragments fixed to the solid surface. For example, in one embodiment the microarray is a gene chip. A tissue microarray refers to an ordered set of tissue specimens fixed to a solid surface. For example, in one embodiment the tissue microarray comprises a slide comprising an array of arrayed tumor biopsy samples in paraffin. Tissue microarray technology optionally allows multiple specimens, such as biopsy samples, to be analysed in a single analysis at the DNA, RNA or protein level. Tissue microarrays are analysed by a number of techniques including immunohistochemistry, in situ hybridization, in situ PCR, RNA or DNA expression analysis and/or morphological and clinical characterization or a combination of techniques. The specimens are optionally from the same subject or from a plurality of subjects. Methods of detecting gene expression using arrays are well known in the art. Such methods are optionally automated. In one embodiment, a sample of an ARVC/D subject is analyzed using a tissue microarray.

Kits

[0130] Another aspect of the disclosure is a kit for screening for, diagnosing the presence of, or detecting a risk of developing, ARVD/C. In one embodiment the kits comprise, one or more isolated nucleic acid molecules and/or compositions described herein and instructions for use.

[0131] In an embodiment the kit comprises an isolated nucleic acid molecule or composition that specifically hybridizes to a TMEM43 disease associated variant, e.g. a probe. In an embodiment the nucleic acid molecule comprises SEQ ID NO:53. In another embodiment, the nucleic acid molecule comprises a detectable label such as a fluorescent molecule. In a further embodiment, the kit comprises an isolated nucleic acid molecule useful as a primer. In an embodiment, the primer is selected from all or part of (e.g. at least 10 or 15 nucleotides, or any number in between) of SEQ ID NO: 1-52. In another embodiment the kit comprises at least two nucleic acids wherein one hybridizes to a wildtype or non-disease associated TMEM43 containing molecule, for example SEQ ID NO:54 and the other hybridizes to a TMEM43 disease associated variant containing molecule, for example SEQ ID NO:53. In another embodiment the at least two isolated nucleic acids are primers for amplifying a sequence comprising a TMEM43 disease associated variant. In an embodiment, the at least two isolated nucleic acid molecules comprise two or more of all or part of SEQ ID NOs: 1-52. In a further embodiment, the at least two nucleic acid molecules comprise all or part of a primer pair listed in Table A. In a further embodiment, the primers are selected from the group comprising SEQ ID NOS: 43-44.

[0132] As used herein "all or part of" of a probe or primer refers to the portion sufficient for in the case a probe, sufficient to specifically hybridize to the intended target and in the case of a primer, sufficient to prime amplification of the intended template.

[0133] In other embodiments the kit comprises a binding agent such as an antibody that specifically binds a TMEM43 disease associated variant polypeptide and instructions for use. In a further embodiment the kit comprises an isolated antibody specific for an epitope present in a TMEM43 disease associated variant that is not present in a non-disease associated or wild-type TMEM43.

[0134] In certain embodiments, the kit is a diagnostic kit for medical use. In other embodiments, the kit is a diagnostic kit for laboratory use.

[0135] In another aspect the disclosure provides a commercial package comprising an isolated nucleic acid or composition described herein and instructions for use.

Assay for Identifying Additional TMEM43 Disease Associated Variants

[0136] Other TMEM43 disease associated variants are identified by screening other populations for TMEM43 mutations that are infrequently or not present in non-diseased subjects, e.g. normal population without ARVD/C. For example the primers in Table A are useful to screen individuals known to have ARVD/C. Sequence comparison between subjects known to have ARVD/C and subjects known not have ARVD/C readily identify additional mutations. For example, a pedigree is typically established as described in Example 1.

[0137] Accordingly, in an embodiment, the disclosure provides a method for identifying TMEM43 disease associated variants comprising determining whether there is a germline alteration in the sequence of TMEM43 gene or a TMEM43 gene regulatory sequence in a sample of a subject, wherein the subject has or is suspected of having ARVD/C. In an embodiment, the sequences of the TMEM43 gene or TMEM43 gene regulatory sequence in the sample is compared with the sequence of one or more wild type TMEM43 gene sequences, for example as in SEQ ID NO: 1. In another embodiment, determining the germline mutation comprises determining the sequence of a TMEM43 gene transcript. In another embodiment, the sequence of the TMEM43 gene transcript is compared with the sequence of one or more wild type TMEM43 gene transcript sequences, such as in SEQ ID NO:2, and/or a transcript described herein. In an embodiment, the disclosure provides a method for identifying TMEM43 disease associated variants comprising amplifying a TMEM43, gene or transcript or part thereof from a sample of a subject, comparing the amplified region to a control population, wherein a mutation that is detected in the sample and is rare or undetected in the control population is a TMEM43 disease associated variant. In an embodiment, one or more of the nucleic acids of Table A are used to amplify a TMEM43 gene or transcript or part thereof. In another embodiment, the part thereof comprises or corresponds to an exon and/or exon/intron boundary. In another embodiment, the part thereof comprises intronic TMEM43 sequence.

[0138] The TMEM43 mutation is optionally a deletion mutation, a missense mutation, a point mutation, and/or a mutation that affects TMEM43 expression levels.

[0139] In an embodiment, the method for identifying TMEM43 disease associated variants comprises detecting the level and/or sequence of an expression product of TMEM43 in the sample.

[0140] In another embodiment, the disclosure provides a method for identifying a TMEM43 disease associated variant comprising determining whether there is an amino acid alter-

ation in the TMEM43 polypeptide in the sample compared to the sequence of wild type TMEM43 polypeptide, for example SEQ ID NO:3.

Combination Testing

[0141] A person skilled in the art will recognize that the methods, isolated nucleic acids, compositions, and kits are optionally combined with methods, isolated nucleic acids, compositions and kits useful for detecting other forms of ARVD/C.

Screening Assay for Identifying Substances Useful for Treating ARVD/C

[0142] The application also includes screening assays for detecting substances that target or bind TMEM43. The application also includes screening assays for detecting substances that target or bind a TMEM43 disease associated variant, which are useful to treat ARVD/C. These assays may be in in vitro or in vivo format. In a suitable embodiment the application provides a cell based assay for evaluating whether a candidate compound is capable of binding a TMEM43 disease associated variant.

[0143] Accordingly, the application provides a method of identifying substances which bind a TMEM43 disease associated variant comprising:

[0144] a) contacting a TMEM43 disease associated variant with a test substance, under conditions which allow for formation of a complex between the TMEM43 disease associated variant and the test substance, and

[0145] b) detecting for complexes between TMEM43 disease associated variant and the test substance, wherein the presence of complexes indicates that the test substance binds the TMEM43 disease associated variant.

[0146] Detecting is optionally done by chemically detecting complexes, free test substance or non-complexed TMEM43 disease associated variant. In one embodiment, the TMEM43 disease associated variant contacted with a test substance is a polypeptide. Test substance-protein complexes, free test substance or non-complexed TMEM43 disease associated variant polypeptides may be isolated by conventional isolation techniques, for example, salting out, chromatography, electrophoresis, gel filtration, fractionation, absorption, polyacrylamide gel electrophoresis, agglutination, or combinations thereof. To facilitate the assay of the components, antibody against a TMEM43 disease associated variant or the test substance, or a labelled TMEM43 disease associated variant, or a labelled test substance may be utilized. The antibodies, proteins, or substances may be labelled with a detectable substance as described elsewhere.

[0147] Binding to a TMEM43 disease associated variant is optionally assessed using a TMEM43 disease associated variant or test substance that is insolubilized. For example, TMEM43 disease associated variant or a test substance may be bound to a suitable carrier. Examples of suitable carriers are agarose, cellulose, dextran, Sephadex, Sepharose, carboxymethyl cellulose polystyrene, filter paper, ion-exchange resin, plastic film, plastic tube, glass beads, polyamine-methyl vinyl-ether-maleic acid copolymer, amino acid copolymer, ethylene-maleic acid copolymer; nylon, silk, etc. The carrier may be in the shape of, for example, a tube, test plate, beads, disc, sphere etc. The proteins or substance may also be expressed on the surface of a cell.

[0148] The insolubilized protein or substance may be prepared by reacting the material with a suitable insoluble carrier using known chemical or physical methods, for example, cyanogen bromide coupling.

[0149] Another aspect involves use of animal ARVD/C models and TMEM43 disease associated variant transgenic mice and *Drosophila melanogaster* for identifying and testing compound that target or bind TMEM43 disease associated variants. Nucleic acids, polypeptides or small organic molecules are optionally tested in these assays. The application includes all compounds that are identified with the screening methods of the application and which are suitable for administration to subjects in pharmaceutical compositions.

Treatment

[0150] The inventors have previously reported that implantable cardioverter defibrillator (ICD) therapy increases survival in autosomal dominant arrhythmogenic right ventricular cardiomyopathy (including ARVD/C associated with ARVD5). Accordingly an aspect provides a method of identifying subjects that would benefit from ICD therapy comprising detecting a TMEM43 disease associated variant in a subject according to a method described herein, wherein the presence of the TMEM43 disease associated variant identifies that the subject would benefit from ICD therapy.

[0151] The disclosure also provides a method of treatment for subjects with ARVD/C and/or a risk of developing ARVD/C comprising:

[0152] a) detecting a TMEM43 disease associated variant in a subject according to a method described herein;

[0153] b) providing ICD therapy for the subject having the TMEM43 disease associated variant.

[0154] In a further embodiment, the disclosure provides use of ICD therapy for a subject comprising a TMEM43 disease associated variant, detected according to a method described herein. ARVD/C patients are typically treated with drugs that are part of a group of antiarrhythmic agents. These drugs are outlined below. In this population these drugs may also be used in conjunction with an ICD. In this case, the ICD is used to prevent sudden death due to ventricular fibrillation, while the antiarrhythmic agents are use to suppress ventricular tachyarrhythmia's so that the ICD doesn't shock the patient as often

[0155] There are five main classes in the Vaughan Williams classification which was introduced in 1970 and classifies a drug bases on the primary mechanism of its antiarryhythmic effect: a problem when many agents have multiple action mechanisms.

[0156] Class I agents—interfere with the sodium (Na+) channel

[0157] Class Ia—includes quinidin, procainamide and disopyramide

[0158] Class Ib—includes lidocaine, mexiletine, tocainide and phenytoin

[0159] Class Ic—includes encainide, flacainide, moricizine and propafenone

[0160] Class II agents—act by selectively blocking the effects of catecholamines at the β_1-adrenergic receptors. All agents in this class are beta blockers and include esmolol, propranolol and metoprolol, where metoprolol is most commonly prescribed for ARVC.

[0161] Class III agents predominantly block the potassium channels and prolong repolarization. These are generally prescribed for the treatment of refactory VT or VF or treatment of atrial or ventricular tachyarrhythmias and AV re-entrant arrhythmias. This class includes amiodarone, azimilide, bretylium, clofilium, dofetilide, tedisamil, ibutilide, sematilide and sotalol, where amiodarone and sotalol are the most commonly prescribed for ARVC.

[0162] Class IV agents affect the AV node as they are slow calcium channel blockers and include verapamil and diltiazem.

[0163] Class V agents work by other or unknown mechanisms and include digoxin (increase vagal activity via its action on the central nervous system, thus decreasing the conduction of electrical impulses through the AV node) and adenosine.

[0164] A "treatment" or "prevention" regime of a subject with a therapeutically effective amount of an agent, such as the drugs described herein may consist of a single administration, or alternatively comprise a series of applications. For example, the agent may be administered at least once a week. However, in another embodiment, the agent may be administered to the subject from about one time per week to about once daily for a given treatment. The length of the treatment period depends on a variety of factors, such as the severity of the disease, the age of the patient, the concentration and the activity of the agent, or a combination thereof. It will also be appreciated that the effective dosage of the agent used for the treatment or prophylaxis may increase or decrease over the course of a particular treatment or prophylaxis regime. Changes in dosage may result and become apparent by standard diagnostic assays known in the art. In some instances, chronic administration may be required.

[0165] It is to be understood that, as used herein "a", "an" and/or "the' includes one and/or more than one.

[0166] The following non-limiting examples are illustrative of the present disclosure:

EXAMPLES

Example 1

[0167] Arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) in its most severe presentation, causes sudden cardiac death. To date, there are 11 known loci and seven cloned genes. The ARVD5 locus was mapped to chromosome 3p in an extended Newfoundland family (AR1) in 1998. Subsequently, the inventors ascertained several other Newfoundland families that shared the ARVD5 haplotype with family AR1, and determined that improved survival occurred in patients with an implantable cardioverter defibrillator.

[0168] The inventors identified 15 ARVC families that shared the ARVD5 ancestral haplotype and used extensive genotyping and haplotype analyses to reduce the ARVD5 critical region on chromosome 3p. Twenty ARVD5 candidate genes were screened for mutations by direct sequencing. Once identified ARVD5 was identified, both retrospective and prospective clinical data from the past two decades was used to compare clinical outcomes in 257 affected versus 151 unaffected subjects.

[0169] Key recombinations to the ARVD5 haplotype reduced the minimal critical region from 9.98 Mb to 2.36 Mb (between markers D3S3610-D3S3613). Direct sequencing of 20 ARVD5 candidate genes revealed 240 variants. One of these, a missense mutation leading to an amino acid substitution in a highly conserved region of the novel protein TMEM43, was found exclusively in all patients across the 15 families, including key recombinants, and in no population controls. Affected and unaffected male and female subjects showed significant differences on first clinical testing for the presence of ectopy (multiple premature ventricular contractions and ventricular tachycardia), poor R wave progression, left ventricular enlargement and systolic dysfunction. A clear sex influence existed with males manifesting earlier clinical sequalea than females including arrhythmia (RR 5.5: 95% CI 1.7-16.8), heart failure (RR 3.4, 95% CI 1.4-8.6) and death (RR 6.8, 95% CI 1.3-10.9). Heart failure occurred in affected males at a later median age (63 years) than death (41 years) indicating that survivors of potentially lethal arrhythmias may develop heart failure. ARVC at locus ARVD5 is caused by the substitution of a serine to a leucine in a highly conserved region of TMEM43. This founder mutation in the Newfoundland genetic isolate frequently leads to early death due to arrhythmias and heart failure particularly in males. As clinical diagnosis of ARVC is difficult, at-risk families can now be screened for TMEM43 through genetic mutation analysis. The mutation has been traced back for nine generations in some of the ARVC families. Accordingly the mutation likely predates the settling of Newfoundland and would be expected to be present in other populations.

Methods

Study Population

[0170] Over the past nine years, approximately 150 families have been referred to either the Newfoundland Labrador provincial genetics program or the Newfoundland Labrador cardiomyopathy genetics clinic because of sudden cardiac death and a family history of cardiomyopathy. Fifteen of these families were determined to have an autosomal dominant form of ARVC based on established criteria[1], a shared haplotype on chromosome 3p and deep genealogies (up to eight generations) (FIG. **1**). Informed consent and blood samples were obtained from each subject in compliance with the Human Investigation Committee requirements of the Eastern Health Corporation of St. John's, Newfoundland (study number 00-176). A total of 425 genomic DNA samples were collected from subjects born at a priori 50% risk (obligate carriers and first degree relatives of affected subjects) and those born at less than a priori 50% risk (second and third degree relatives and spouses, a priori 25%, 12.5% and 0%, respectively). Subjects born at a priori 50% risk were further subdivided into three groups based on their affection status (primary, secondary and clinically unaffected) for the molecular arm of the study (FIG. **2**).

Refine Mapping of the ARVD5 Locus

[0171] A previous study that included a genomewide linkage analysis of Family AR1 (FIG. **1**) mapped a novel locus for ARVC to 3p23 and excluded other loci that had been identified for ARVC (14q23; ARVD1, 1q42; ARVD2, 14q12; ARVD3 and 2q32; ARVD4). Fine mapping with microsatellite markers defined a 9.3cM (9.98 Mb) region between markers D3S3610-D3S3659.[8] To further refine the critical region and identify the ARVD5 gene the inventors recruited extended members of family AR1 and 14 additional ARVC families from the Newfoundland population (FIG. **1**). Exten-

sive haplotyping using 18 polymorphic microsatellite markers was done on subjects at a priori 50% risk with primary affection status. In order to refine the critical region a recombination had to be detected in subjects from at least two families.

Screening Candidate ARVD5 Genes

[0172] A mutation screening panel comprised of seven genomic DNA samples from four subjects with primary affection status from three families (AR1, AR8, AR15) and three control samples (spouses) was established. All coding and non-coding exons and intron-exon boundaries of positional candidate genes for ARVD5 were sequenced. All sequences were amplified by polymerase-chain reaction (PCR) assay from genomic DNA in 25 μl reaction volume. The components for the PCR reactions are in μl:

10x PCR Buffer	2.50
2 mM dNTP's	2.50
50 mM MgCl2	0.75
3.75M Betaine	5.00/0.00
5 U/ul DMA Taq Polymerase	0.20
Water	11.05/16.05
Forward primer	1.00
Reverse primer	1.00
25 ng/ul DNA	1.00

[0173] These conditions were the standard trial conditions for each primer set +/−betaine and the temperature scheme for the PCR reaction was TD54 where the first 5 rounds of PCR decrease the annealing temperature by 2° C. starting at 64° C. for 30 seconds standard denaturing and extension temperatures of 95° C. and 72° C. respectively for 30 seconds each. The following 30 rounds of PCR have an annealing temperature of 54° C. and standard denaturing and extension temperatures of 95° C. and 72° C. respectively for 30 seconds each. These conditions along with the PCR mixture were adjusted if required to achieve the cleanest amplification per primer pair.

[0174] The PCR products were purified using 50% sephacryl (Amersham Biosciences) and MultiScreen HTS filter plates (Millipore Corporation). Purified PCR products were cycle sequenced in both forward and reverse directions with the use of BigDye Terminator V3.1 cycle sequencing kit on an automated ABI 3700 DNA analyzer (Applied Biosystems). Sequencing electropherograms were inspected manually and analyzed with Mutation Surveyor software (Transition Technologies). Sequencing variants found exclusively in ARVC subjects were experimentally verified to reside on the ARVC haplotype by segregation analysis in family AR14. The population frequencies of ARVD5-associated alleles were determined with population-based controls obtained through random phone dialing, as part of a large colorectal cancer study. Key recombinant families (AR2 and AR10) were analyzed to determine which rare variants (<1% of the population) were shared amongst subjects with primary affection status (FIG. **2**).

Expression of TMEM43 in Myocardium and Lymphocytes of ARVC Patients

[0175] Total RNA was extracted from Epstein Barr virus (EBV) transformed B lymphocytes from two affected subjects and one unaffected control and heart tissue from one affected subject and an unrelated control using Trizol (Invitrogen) followed by DNase1 treatment (Ambion). Complementary synthesis (Invitrogen) was performed and analyzed by both size fractionation and direct sequencing with overlapping primers designed to cover the complete coding sequence of TMEM43.

Bioinformatic Analysis

[0176] Conservation of the TMEM43 protein across species was determined using ClustalW and Weblogo[10-12]. Potential protein localization, function, structure and post-translational modification sites were predicted using the online tools via the ExPASy web site.[12] The effects of amino acid substitutions of protein function were predicted.[13-17]. Both the mutant and normal amino acid sequences of TMEM43 were used as input for these online tools to predict based on what is known about other similar proteins, the protein localization, function, structure and posttranslational modification sites. The web addresses of the sites used are available through accessing the main page at:

[0177] The following online tools were used:

[0178] 9aaTAD—Prediction of Nine Amino Acid Transactivation Domain

[0179] MITOPROT—Prediction of mitochondrial targeting sequences

[0180] Predotar—Prediction of mitochondrial and plastid targeting sequences

[0181] PTS1—Prediction of peroxisomal targeting signal 1 containing proteins

[0182] SignalP—Prediction of signal peptide cleavage sites

[0183] DictyOGlyc—Prediction of GlcNAc O-glycosylation sites in Dictyostelium

[0184] NetCGlyc—C-mannosylation sites in mammalian proteins

[0185] NetOGlyc—Prediction of O-GalNAc (mucin type) glycosylation sites in mammalian proteins

[0186] NetGlycate—Glycation of epsilon amino groups of lysines in mammalian proteins

[0187] NetNGlyc—Prediction of N-glycosylation sites in human proteins

[0188] YinOYang—O-beta-GlcNAc attachment sites in eukaryotic protein sequences

[0189] big-PI Predictor—GPI Modification Site Prediction

[0190] GPI-SOM—Identification of GPI-anchor signals by a Kohonen Self Organizing Map

[0191] Myristoylator—Prediction of N-terminal myristoylation by neural networks

[0192] NMT—Prediction of N-terminal N-myristoylation

[0193] PrePS—Prenylation Prediction Suite
[0194] NetAcet—Prediction of N-acetyltransferase A (NatA) substrates (in yeast and mammalian proteins)
[0195] NetPhos—Prediction of Ser, Thr and Tyr phosphorylation sites in eukaryotic proteins
[0196] NetPhosK—Kinase specific phosphorylation sites in eukaryotic proteins
[0197] Sulfinator—Prediction of tyrosine sulfation sites
[0198] SulfoSite—Prediction of tyrosine sulfation sites
[0199] SUMOplot—Prediction of SUMO protein attachment sites
[0200] TermiNator—Prediction of N-terminal modification
[0201] NetNES Leucine-rich nuclear export signals (NES) in eukaryotic proteins
[0202] PSORT—Prediction of protein subcellular localization
[0203] TargetP—Prediction of subcellular location
[0204] HMMTOP—Prediction of transmembrane helices and topology of proteins (Hungarian Academy of Sciences)
[0205] PredictProtein—Prediction of transmembrane helix location and topology (Columbia University)
[0206] SOSUI—Prediction of transmembrane regions (Nagoya University, Japan)
[0207] TMHMM—Prediction of transmembrane helices in proteins (CBS; Denmark)
[0208] TMpred—Prediction of transmembrane regions and protein orientation (EMBnet-Ch)
[0209] TopPred—Topology prediction of membrane proteins (France)
[0210] GlobPlot—Protein disorder/order/globularity/domain predictor
[0211] CLUSTALW [At EBI, PBIL, My Hits or at EMBnet-CH]
[0212] WebLogo—Sequence logos at Berkeley/USA

[0213] The potential effect of the amino acid substitution was assessed using the following tools:

SIFT, PANTHER, PolyPhen, SNPs3D and

PMut.

Clinical Assessment of TMEM43 Carriers and Non-Carriers

[0214] Only well-ascertained subjects born at a priori 50% risk were investigated for clinical outcomes. Subjects were categorized as affected, unaffected or unknown (FIG. **2**). Clinical data was collected prospectively over nine years. This involved annual visits by subjects to the cardiomyopathy genetics clinic where 12 lead ECGs, Holter monitors, MRI's, signal averaged ECG's and echocardiograms were done. All cardiac anomalies were noted following clinical testing. Clinical data was also obtained retrospectively from medical records including "at risk" relatives not seen in clinic. All available autopsy results from deceased subjects were obtained.

[0215] The prevalence of ECG abnormalities was determined by two physicians blind to disease status. The prevalence of structural cardiac abnormalities was determined on first echocardiogram. Left ventricular enlargement (LVE) was defined as 2 and 3 standard deviations (SD) above a predicted mean: left ventricular end diastolic diameter (LVEDD) >112% (>2SD) and LVEDD >117% (>3SD).[18] Those with echocardiography reports that did not include measurements were excluded. The prevalence of arrhythmias was determined on first Holter monitor. In subjects with serial Holter monitors, the age to onset of de novo ≧1000 premature ventricular contractions (PVCs) was calculated by time to event analysis, after excluding those with ≧1000 PVCs present at baseline.

Statistical Analysis

[0216] Comparisons between survival of affected versus unaffected subjects was calculated by the Kaplan Meier product limit method with censoring occurring at the time of ICD therapy, heart transplantation or last follow-up (defined as the age at the last clinic visit). Relative risk was calculated using Cox's Regression model. Proportions were assessed using Chi Square. A p-value of <0.05 was considered significant (SPSS software, version 14, Chicago USA).

Results

Refine Mapping

[0217] Extensive haplotype analysis both within and across the 15 extended ARVC families refined the genetic interval of ARVD5. Recombinations were identified in subjects in 8 (AR2, AR3, AR4, AR6, AR8, AR10, AR13 and AR15) of the 15 families, subjects from the other six families (AR5, AR7, AR9, AR11, AR12, AR14) shared the full-length ARVD5 haplotype identified in Family AR1 (FIG. **3**). Key recombinations in the ARVD5 haplotype reduced the shared haplotype to a physical region between markers D3S3610-D3S3613, reducing the ARVD5 critical region to 2.36 Mb (FIG. **3**A). This physical region on chromosome 3p includes 20 annotated genes (FIG. **3**B). The apparent recombination at D3S1516 in family AR15 was not taken into account as it was not observed in another family.

Mutation Screening

[0218] The characteristics of the 20 ARVD5 positional candidate genes, namely IQSEC1, NUP210, HDAC11, FBLN2, WNT7A, TPRXL, CHCHD4, TMEM43, XPC, LSM3, SLC6A6, GRIP2, C3orf19, C3orf20, FGD5, NR2C2, MRPS25, ZFYVE20, CAPN7, SH3BP5, are provided (Table 3). Direct sequencing of genomic DNA from subjects on the mutation screening panel revealed a total of 240 sequencing variants across the 20 ARVD5 candidate genes (FIG. **9**). Of these 240 variants, only 19 variants were found exclusively in subjects with primary affection status on the mutation screening panel, excluding 221 variants from further analysis (Table. 1). Of these 19 variants, 11 were determined to reside on the ARVD5 ancestral haplotype (FIG. **10**) and five were rare (<1% of population chromosomes; Table 1). Only one of the five rare variants, TMEM43 1073 C>T (S358L) (FIG. **4**D), was shared by all ARVC subjects with primary affection status across the 15 families. In fact, this was the only rare variant of the five that was still retained on the key recombinant ARVD5 haplotype identified in subjects with primary affection status from families AR2 and AR10 (FIG. **5**), which shows that TMEM43 is ARVD5. Additional support comes from the observation that clinically unaffected adults who share distal sections of the ARVD5 haplotype lack the TMEM43 mutation (FIG. **11**).

TABLE 1

Nineteen sequencing variants identified exclusively in ARVC subjects with primary affection status. Eleven variants (shaded) were determined to be in phase on the ARVD5-ancestral haplotype and were subsequently sequenced on population controls.

Gene Name	Accession #	Variant Nomenclature	Classification	Population Frequency
HDAC11	NM_024827	c. 369+ 18_369+ 19insG	Non-coding	nd
TMEM43	NM_024334	c. 1073C>T	Missense (S>L)	0% *
TMEM43	NM_024334	c. 1203+ 115T>C	Non-coding	nd
XPC	NM_004628	c. 2823+ 684G>C	Non-coding	nd
SLC6A6	NM_003043	c. 1-27420G>A	Non-coding	nd
SLC6A6	NM_003043	c. 599+ 370A>G	Non-coding	46%
SLC6A6	NM_003043	c. 733-1226A>G	Non-coding	55.60%
FGD5	NM_152536	c. 934G>A	Missense (V>M)	0.6% *
FGD5	NM_152536	c. 2186+ 22G>A	Non-coding	nd
FGD5	NM_152536	c. 2187-82G>A	Non-coding	nd
FGD5	NM_152536	c. 2220G>T	Synonymous (L>L)	nd
FGD5	NM_152536	c. 2613+ 50C>T	Non-coding	nd
FGD5	NM_152536	c. 3085-74G>A	Non-coding	9.00%
NR2C2	NM_003298	c. 855+70G>A	Non-coding	9.10%
NR2C2	NM_003298	c. 1848+ 365T>A	Non-coding	17.80%
NR2C2	NM_003298	c. 1848+ 2965_1848+ 2966insGATA	Non-coding	18.30%
MRPS25	NM_022497	c. 522+ 1059G>A	Non-coding	0% *
CAPN7	NM_014296	c. 1289+ 68C>T	Non-coding	0.01% *
CAPN7	NM_014296	c. 1430-28T>C	Non-coding	0% *

* rare variant (<1% of the population)

[0219] The assessment included the following features all of which were at a frequency of less than 10% in affected subjects: first degree AV block, T wave inversion in V2 and V3, ST depression anterior, lateral and inferior, ST elevation anterior, lateral and inferior, epsilon waves, tall R wave in V2, V3, left bundle branch block, right bundle branch block, flat/inferior/inverted lateral T waves, short PR interval, long and short QT interval, Inferior, lateral and anterior Q waves, atrial fibrillation, left atrial enlargement, right ventricular enlargement, left anterior and posterior hemiblock, left axis, FS<20% and left ventricular hypertrophy.

TABLE 3

Characteristics of the 20 physical candidate genes mapping within the ARVD5 critical region on 3p25

Gene Name	Accession Number	Strand	Genomic Position Start	Genomic Position End	Exons
IQSEC1	NM_014869	–	13,003,536	12,917,079	13
NUP210	NM_024923	–	13,436,809	13,332,737	40
HDAC11	NM_024827	+	13,496,824	13,521,834	10
FBLN2	NM_001004019	+	13,565,625	13,654,922	18
WNT7A	NM_004625	–	13,896,619	13,835,083	4
TPRXL	AK092426	+	13,953,902	14,082,480	3
CHCHD4	NM_144636	–	14,141,323	14,128,584	4
TMEM43	NM_024334	+	14,141,546	14,160,180	12
XPC	NM_004628	–	14,195,143	14,161,651	16
LSM3	NM_014463	+	14,195,341	14,214,840	4
SLC6A6	NM_003043	+	14,419,110	14,503,973	15
GRIP2	NM_001080423	–	14,558,592	14,510,177	25
C3orf19	NM_016474	+	14,668,278	14,689,167	11
C3orf20	NM_032137	+	14,691,658	14,789,544	17
FGD5	NM_152536	+	14,835,810	14,950,899	20
NR2C2	NM_003298	+	14,964,240	15,065,782	15
MRPS25	NM_022497	–	15,081,820	15,065,024	4
ZFYVE20	NM_022340	–	15,115,659	15,086,584	14
CAPN7	NM_014296	+	15,222,737	15,269,426	21
SH3BP5	NM_004844	–	15,349,108	15,271,250	9
				Total	275

ARVC at Locus ARVD5 is Caused by a Missense Mutation in TMEM43

[0220] Transmembrane protein 43 (TMEM43, Genbank Accession number NM_024334) is a conserved gene, found across all eukaryotic and prokaryotic species (FIG. **6**). The longest isoform has 12 exons producing a 400 amino acid protein (FIGS. **4**A&B) that is 98% similar to the mouse protein (FIG. **6**A). The TMEM43 transcript is expressed in white blood cells and heart tissue (FIG. **4**C). The cDNA from the heart muscle of an affected subject was the full-length transcript, unaltered as determined by size fraction analysis and direct sequencing, suggesting that TMEM43 1073 C>T does not affect splicing (FIG. **4**C, D&E).

[0221] Bioinformatic analysis of the amino acid sequence of TMEM43 predicts it to be a cytoplasmic membrane protein with a number of potential post-translation modification sites (FIG. **7**). The mutation (S358L) occurs within the third predicted transmembrane domain that is highly conserved in mammals, avian, amphibian, aquatic and insect orthologs (FIGS. **6**A&B, FIG. **7**). Interestingly, a leucine is tolerated in the bacterium *Rhizobium loti* but it is not found in any multicellular organisms (FIG. **6**A). The S358L mutation is predicted to be deleterious (FIG. **6**B, Table 4) but relatively little is known about the function of TMEM43.

TABLE 4

Prediction of the TMEM43 1073 C > T (S358L) mutation effect by five different bioinformatic programs.

	Method				
Mutation	SIFT	Panther	PolyPhen	SNPs3D	PMut
S358L	deleterious	deleterious	benign	deleterious	deleterious

Note:
Sequence homology for PolyPhen analyses was calculated with alignments of orthologs from Eukaryota and bacteria

TMEM43 Mutation Screening in Extended ARVD5 Family Members

[0222] Genomic DNA was sequenced from all available extended family members across the 15 ARVC families for the presence of the TMEM43 variant. All subjects at a priori 50% risk with primary or secondary affection status (n=106) were mutation carriers. Twenty-six subjects (3 male, 23 female) at a priori 50% risk who were clinically unaffected were mutation carriers as well. Median age of the males was 22 years, and for females 33 years: the absence of clinical signs is presumably due to age and sex dependent penetrance. The remaining 151 subjects at a priori 50% risk with no clinical signs who did not have the TMEM43 variant were considered unaffected. All subjects at less than a priori 50% risk (n=83) were also screened. Two subjects at a priori 25% risk had the TMEM43 variant. All spouses (n=47) were negative for the TMEM43 variant (FIG. **2**).

Clinical Assessment of ARVD5 Kindreds

Pathology

[0223] Thirty-nine autopsy reports were available. Of these, 18 were reviewed from deceased males (median age 30 years—range 25-56; mean heart weight=500 g) from family AR1 who died suddenly. Fifteen of these reported on right ventricular histology, 11 had fibro-fatty replacement of the myocardium and the remaining four showed primarily fibrotic changes (FIG. **1**B). No subject had critical coronary artery disease. For the 14 additional ARVD5 families 21 autopsy reports were reviewed, 17 males—median age 36.5 years (range 19-72) and 4 females—median age 52.5 years (range 36-65) were available. Mean heart weight was 525 g. Seven cases mentioned right ventricular histology all of which noted fibro-fatty replacement.

12-Lead ECG

[0224] Data on a total of 297 subjects (167 affected, 130 unaffected) that had at least one 12-lead surface ECG was available. The most prevalent features were poor R wave progression (PRWP), the presence of PVC's, and extended QRS 0.110 ms (Table 2). T wave inversion in leads V2-V3, and epsilon waves were noted in ≦3% of affected subjects. Of the 90 affected (35%), and 21 unaffected (14%) subjects with no ECG available for analysis, 73 affected and 2 unaffected were dead, the remaining subjects are in progress.

TABLE 2

12 lead ECG, Holter and Echocardiographic manifestations present on first ECG, first Holter and first echocardiogram in subjects from 15 families with ARVC due to a mutation in TMEM43 on chromosome 3

	12 lead ECG										
	Affected					Unaffected					
	Male		Female		Tot.	Male		Female		Tot.	X^2	X^2
N	78		89		167	64		66		130	Aff. Mv.	Aff. F v.
Mean Age	30		37.7			33.1		38.2			Unaff. M	Unaff. F
SD	12.1		15.8			16		13.2				
	n	%	n	%	N (%)	n	%	n	%	N (%)		
PRWP	23	30	25	28	48 (28.7)	0	0	2	3	2 (1.5)	P ≤ 0.001	P ≤ 0.001
PVCs	25	32	22	25	47 (28.1)	0	0	1	2	1 (0.7)	p ≤ 0.001	p ≤ 0.001

TABLE 2-continued

12 lead ECG, Holter and Echocardiographic manifestations present on first ECG, first Holter and first echocardiogram in subjects from 15 families with ARVC due to a mutation in TMEM43 on chromosome 3

QRS > 110	25	32	8	9	33 (19.8)	4	6	2	3	6 (4.6)	$p \leq 0.001$	$p \leqq 0.2$ ns
Septal Q	10	13	14	16	24 (14.4)	0	0	0	0	0	$p \leq 0.01$	$p \leq 0.001$

Holter Monitor

	Affected					Unaffected						
Sex	Male		Female		Total	Male		Female		Tot.	X^2	X^2
N	67		79		146	49		44		93	Aff. Mv.	Aff. F v.
Mean Age	31.1		37.7			33.1		38.2			Unaff. M.	Unaff. F
SD	13.3		15.5			15.9		12.8				
	n	%	n	%	N (%)	n	%	n	%	N (%)		
PVCs ≧ 200/24 hours	47	70	47	59	94 (64.4)	0	0	1	2.3	1.0	$P < 0.001$	$P < 0.001$
PVCs ≧ 1000/24 hours	45	67	37	47	82 (56.2)	0	0	1	2.3	1.0	$P < 0.001$	$P < 0.001$
≧ 1 run ns VT	13	19	18	23	31 (21.2)	0	0	0	0.0	0.0	$P < 0.01$	$P < 0.001$

Echocardiograph

	Affected					Unaffected						
	Male		Female		Tot.	Male		Female		Tot.	X^2	X^2
N	67		76		143	50		51		101	Aff. Mv.	Aff. Fv.
Mean Age	31.58		39.61			32.46		38.27			Unaff. M	Unaff. F
SD	13.15		15.14			14.91		13.28				
	n	%	n	%	N (%)	n	%	n	%	N (%)		
LVE > 2SD	35	52	27	20	62 (43.3)	10	20	4	8	14 (13.9)	$P < 0.001$	$P < 0.001$
LVE > 3SD	24	4	20	13	44 (30.8)	4	8	2	4	6 (5.9)	$P < 0.001$	$P < 0.001$
FS < 30%	24	36	17	22	41 (28.7)	5	10	4	8	9 (8.9)	$P < 0.01$	$P < 0.05$
Wall motion	18	27	15	20	33 (23.1)	2	4	0	0	2 (1.9)	$P < 0.01$	$P < 0.001$
LAE	16	24	8	10	24 (16.8)	4	8	3	6	7 (6.9)	$P < 0.025$	P < 1 ns

PVC: premature ventricular complex, VT: Ventricular tachycardia, PRWP: poor R wave progression defined as V3 less than 3 mm [32]LVE: Left ventricular enlargement indexed to height and weight [18,19]LAE: left atrial enlargement, FS: fractional shortening, M: males, F: females.

[0225] The assessment included the following features all of which were at a frequency of less than 10% in affected subjects: first degree AV block, T wave inversion in V2 and V3, ST depression anterior, lateral and inferior, ST elevation anterior, lateral and inferior, epsilon waves, tall R wave in V2, V3, left bundle branch block, right bundle branch block, flat/inferior/inverted lateral T waves, short PR interval, long and short QT interval, Inferior, lateral and anterior Q waves, atrial fibrillation, left atrial enlargement, right ventricular enlargement, left anterior and posterior hemiblock, left axis, FS<20% and left ventricular hypertrophy.

Holter Monitor

[0226] Of the 239 subjects (146 affected, 93 unaffected) with at least one Holter Monitor report, the most prevalent features were premature ventricular contractions (PVC's) ≧200 and ≧1000 in 24 hours, and the presence of at least one run of non sustained ventricular tachycardia (nsVT) (Table 2). Of the 111 affected (43%), and 58 unaffected (38%) subjects with no Holter monitor available for analysis, 76 affected and 2 unaffected were dead. The remaining subjects are in progress. Eighty-two affected subjects (56%: 45 male, 37 female) were determined to have ≧1000 PVC's on baseline Holter monitor (Table 2). Fifteen affected subjects (43%: six male, eight female) without ≧1000 PVC's at baseline subsequently developed ≧1000 PVC's (FIG. **8A1&A2**). One unaffected subject had ≧1000 PVC's at baseline (Table 2): two females developed ≧1000 PVC's on a subsequent Holter monitor (FIG. **8A2**). The median age to onset of de-novo

≧1000 PVC's for affected males was 26 years. There was a significant difference between affected and unaffected males for time to development of ≧1000 PVC's (p≦0.0001) (FIG. **8A1**). The median age to onset of de-novo ≧1000 PVC's for females in the affected group was 56 years with a significant difference between affected and unaffected females for time to development of ≧1000 PVC's (p=0.02, RR 5.9, 95% CI 1.2-28.5) (FIG. **8A2**). Affected males were five times more likely to develop ≧1000 PVC's than affected females (RR 5.467, (95% CI 1.769-16.889) p≦0.003) (FIG. **8A3**).

Echocardiography

[0227] Of the 244 subjects (143 affected and 101 unaffected) that had at least one 2D echocardiogram available for analysis. Five reports (three males, two females) from affected subjects were excluded because measurements were not available. Of these, three males and one female, all deceased, were reported to have a "massively dilated heart". The most prevalent feature was LVE based on LVEDD (Table 2) 19. Of the 114 (44%) affected, and 50 unaffected (33%) subjects with no echocardiogram, 86 affected and two unaffected were dead. The remaining subjects are in progress. Right ventricular echocardiography was unavailable for many echocardiograms from older subjects.

Heart Failure

[0228] Of 89 affected males with medical records, 14 developed heart failure at a median age of 63 years (95% CI 41 years-84 years) compared with none of the unaffected males (p≦0.0001: log rank) (FIG. **8B1**). Of 87 affected females with medical records, seven developed heart failure (median age 73 years, 95% CI 69 years-77 years), and one unaffected female at age 79 years (p≦0.001, log rank) (FIG. **8B2**). Affected males were three times more likely to develop heart failure than females (RR 3.4, 95% CI 1.36-8.57, p≦0.009) (FIG. **8B3**).

Life Expectancy

[0229] In the affected group (n=257) there were 123 (48%) deaths (99 males and 24 females). DNA was available from 10 deceased subjects, the remainder (n=113) made up the primary affection status group for whom no DNA was available (FIG. **2**). Sudden cardiac death occurred in 85 (86%) of the 99 males and 10 (42%) of the 24 females. Death was attributed to other cardiac causes in 14 (11%) subjects, (seven male, seven female) and non-cardiac conditions in seven (5%) subjects, three male and four female. For the remaining four deaths (two male, two female) the cause of death was unknown. The median survival was 41 years for affected males (95% CI 38 years-43 years) compared with a mean age of 83 years in unaffected males (p≦0.0001, log rank) (FIG. **8C1**). The median survival was 71 years for affected females (95% C.I. 64 years-78 years), compared with a median age of 83 years for unaffected females (95% CI 65 years-101 years) (FIG. **8C2**). The relative risk of dying was 6.8 times higher in affected males compared to affected females (95% C.I: 4.3-10.9, p≦0.0001) (FIG. **8C3**).

Discussion

[0230] The inventors have identified a mutation in TMEM43, as the cause of ARVC at locus ARVD5. Screening across 15 ARVD5-linked families for the S358L mutation show all subjects with primary affection status are heterozygous carriers, and the mutation was not detected in any population-based controls. This clearly is another Newfoundland founder mutation.[20] In addition, the serine at position 358 is well conserved across multicellular eukaryotic species and the effect of the amino acid change is predicted to be deleterious.

[0231] Without wishing to be bound by theory, mutations in desmosomal genes have been implicated in several genetic subtypes of ARVC, indicating that ARVC is primarily a disease of the desmosome.[5, 7] Mechanical stress has, therefore, been predicted to cause the ARVC phenotype. More recently signaling pathways have been implicated in ARVC pathogenesis.[7, 21] For example, plakoglobin, when freed from desmosomal complexes, translocates to the nucleus where it competes and opposes the action of β-catenin to down regulate the canonical Wnt/β-catenin signaling pathway, which in turn promotes adipogenesis, fibrogenesis and apoptosis.[5, 21] Suppression of the canonical Wnt/β-catenin signaling has been shown to up regulate two adipogenic transcription factors, C/EBP-α and PPARγ.[21]

[0232] In the case of ARVD5, the inventors have identified a gene that is highly conserved across animal phyla for which functional domains with known proteins yields no information to potential biochemical pathways. Interestingly, a genome wide scan for peroxisome proliferator response elements (PPREs) identified 1085 potential target genes of PPARγ, including TMEM43[22]. While the function of the TMEM43 protein is not well understood, and to date, it has not been associated with any known disease, TMEM43 appears to be regulated by PPARγ.

[0233] The inventors have defined ARVC at locus ARVD5 across at least eight generations from fifteen families. The phenotype included fibrofatty infiltration of both left and right ventricles, manifestations of arrhythmogenic disease and early death. The inventors showed that the arrhythmias were the earliest manifestation, followed by death. Heart failure occurred later in those who survived or experienced less ectopy. Subjects had LVE, with systolic manifestations, which lead in some instances to heart failure. This condition is alternatively called "arrhythmic cardiomyopathy."[23, 24, 25] ARVC was difficult to diagnose prior to the present disclosure.[1] A problem with prior approaches is that there has to be access to the relevant clinical testing, the subject needs to be alive, and a large enough family present to recognize disease despite variable expression and reduced penetrance. Although modifications to these criteria have been proposed[26] the continued reliance on multiple testing made diagnosis problematic in the prior art. The ability to define those with the gene, by molecular testing, presymptomatically (particularly as the first symptom may be SCD) now removes the uncertainly surrounding false negative clinical assessment, and allows for prophylactic treatment with ICD therapy.

[0234] Common diseases are those that most physicians will encounter in their practice over their lifetime. As a practical definition, Motulsky set a frequency of 1 affected per 1000 for a given disease to be considered common.[27] ARVC clearly approaches the frequency of a common disease in Newfoundland Labrador and a population-based approach for molecular genetic testing to identify individuals at risk of SCD is being considered. The high morbidity and mortality associated with the mutation in TMEM43 would be reduced by screening for ARVC.[28]

[0235] Many medically important genes and mutations have been identified in patients and families from Newfound-

land that are relevant to outbred populations. For example, the role of mismatch repair genes in colon cancer, a universal phenomenon, was discovered by genetic mapping in a multigenerational family from Newfoundland (33-34). The identification of multiple Newfoundland families with a rare, multisystem genetic disorder, Bardet-Biedl syndrome (BBS), included the mapping of a novel BBS gene (BBS5) and inspired a new medical field of inquiry, one of ciliary disease, involved in more common conditions (35-39). Hearing loss is the most common sensory disorder worldwide. A missense mutation in exon 8 of the WFS1 gene was first identified in a Newfoundland family with low frequency hearing loss (39). Since this report, missense mutations in the WFS1 gene have been found to underlie all reported cases for this type of hearing deficit except one (Costa Rican family) (40-41). These are but a few of many examples that both genes and specific mutations identified in patients and families with genetic disease from Newfoundland serve as a valuable resource for out bred populations. The Newfoundland founder population also has generalizability for more common (complex diseases). In a recent study of the genetic architecture of 12 of the worlds well established founder populations, the Newfoundland population was found to have the greatest generalizability of the founder populations, as all markers with an allele frequency greater than 10% in the NL population were also noted in a Caucasian out bred population (42).

[0236] The methods disclosed provide significant advantages because it they are based on a homogeneous population with almost total ascertainment of those at a priori 50% risk in the defined pedigrees. All the available past medical records from affected and unaffected subjects were examined, extensive genealogical data across multiple generations, and subjects are clinically screened at a single tertiary centre. An accurate knowledge of the disease process provides a basis for precise genetic counseling and clinical care of those at-risk. The TMEM43 mutations were made with a large and homogeneous ARVC population, which is well demarcated and well ascertained.

Example 2

ARVC Penetrance

[0237] One hundred and thirty seven subjects (60 affected males, 77 affected females) were used to determine penetrance. Median age to develop an ARVD5 associated phenotype was 32 years (95% CI 28-35) for males and 44 years (95% CI 39-48) for females, with 100% of males and females penetrant by 63 and 76 years respectively (FIGS. **12**A and B). Males were twice as likely to reveal the disease phenotype than females (RR 2, 99% CI 1.2-3.3) ($p \leqq 0.0001$). The commonest clinical features for which subjects were initially penetrant were ectopy (44%), and LVE (27%), then VT (9%), QRS >110 ms (9%), late potentials on SAECG (7%), SCD (2%) and heart failure (2%).

[0238] For the penetrance study, subjects who were alive at the start of the study (1996), who had a medical record and had a genetic diagnosis (mutation carriers or obligate carriers) were followed. The results showed that ARVC was fully penetrant in males by the age of 63 and in females by the age of 76; ectopy and LVE were often the first presenting features, and few presented with death or heart failure. Therefore, in order to assess the penetrance of heart failure and death, all affected subjects were used. Heart failure and death were morbid outcomes at early ages in both males and females, with far more serious early events in males. In both sexes heart failure occurs as a later manifestation in subjects who did not succumb to SCD. These major manifestations define ARVC, due to the TMEM43 mutation, as a lethal, fully penetrant, sex-influenced, autosomal dominant disorder.

Example 3

[0239] Subjects and/or families which have a family history of suspected ARVD/C eg a family history of cardiomyopathy and sudden cardiac death are identified. Blood samples from 1^{st}, 2^{nd} and third degree relatives of the affected subjects are obtained. One or more TMEM43 exons or parts thereof are sequenced and compared to normal subjects to identify putative mutations. The frequency and association of putative mutations in affected and control populations is determined, for example by assembling a pedigree. Mutations are confirmed, for example confirmed to be rare in a normal or non-ARVD/C population.

Example 4

[0240] TMEM43 transcripts identified by ECgene bioinformatic analysis are useful for designing probes and primers for use in the methods described herein.

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[0241] While the present disclosure has been described with reference to what are presently considered to be the preferred examples, it is to be understood that the disclosure is not limited to the disclosed examples. To the contrary, the disclosure is intended to cover various modifications and equivalent arrangements included within the spirit and scope of the appended claims.

[0242] All publications, patents and patent applications are herein incorporated by reference in their entirety to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety

FULL CITATIONS FOR REFERENCES REFERRED TO IN THE SPECIFICATION

[0243] 1. McKenna W J, Thiene G, Nava A, et al. Diagnosis of arrhythmogenic right ventricular dysplasia/cardiomyopathy. Task Force of the Working Group Myocardial and Pericardial disease of the European Society of Cardiology and the Scientific Council on Cardiomyopathies of the International Society and Federation of Cardiology. British Heart Journal 1994; 71:215-218.

[0244] 2. Fontaine G, Fontaliran F, Frank R. Arrhythmogenic right ventricular cardiomyopathies, clinical forms and main differential diagnoses. Circulation 1998; 97:1532-1535.

[0245] 3. Heuser A, Plovie E R, Ellinor P T, et al. Mutant Desmocollin-2 Causes Arrhythmogenic Right Ventricular Cardiomyopathy. Am J Hum Genet 2006; 79:1081-1088.

[0246] 4. Pilichou K, Nava A, Basso C, et al. Mutations in Desmoglein-2 Gene Are Associated With Arrhythmogenic Right Ventricular Cardiomyopathy 10.1161/CIRCULATIONAHA.105.583674. Circulation 2006; 113:1171-1179.

[0247] 5. Sen-Chowdhry S, Syrris P, McKenna W. Genetics of right ventricular cardiomyopathy. J Cardiovasc Electrophysiol 2005; 16:927-35.

[0248] 6. Dokuparti M V, Pamuru P R, Thakkar B, Tanjore R R, Nallari P. Etiopathogenesis of arrhythmogenic right ventricular cardiomyopathy. J Hum Genet 2005; 50:375-81.

[0249] 7. MacRae C A, Birchmeier W, Thierfelder L. Arrhythmogenic right ventricular cardiomyopathy: moving toward mechanism. J Clin Invest 2006; 116:1825-8.

[0250] 8. Ahmad F, Li D, Karibe A, et al. Localisation of a gene responsible for arrhythmogenic right ventricular dysplasia to chromosome 3p23. Circulation 1998; 98:2791-2795.

[0251] 9. Hodgkinson K, Parfrey P, Bassett A, et al. The impact of implantable cardioverter defibrillator therapy on survival in autosomal dominant arrhythmogenic right ventricular cardiomyopathy (ARVD5). The Journal of the American College of Cardiology 2005; 45:400-408.

[0252] 10. Crooks G E, Hon G, Chandonia J M, Brenner S E. WebLogo: a sequence logo generator. Genome Res 2004; 14:1188-90.

[0253] 11. Combet C, Blanchet C, Geourjon C, Deleage G. NPS@: network protein sequence analysis. Trends Biochem Sci 2000; 25:147-50.

[0254] 12. Gasteiger E, Gattiker A, Hoogland C, Ivanyi I, Appel R D, Bairoch A. ExPASy: The proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res 2003; 31:3784-8.

[0255] 13. Ramensky V, Bork P, Sunyaev S. Human non-synonymous SNPs: server and survey. Nucleic Acids Res 2002; 30:3894-900.

[0256] 14. Ng P C, Henikoff S. Accounting for human polymorphisms predicted to affect protein function. Genome Res 2002; 12:436-46.

[0257] 15. Thomas P D, Kejariwal A, Campbell M J, et al. PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. Nucleic Acids Res 2003; 31:334-41.

[0258] 16. Yue P, Melamud E, Moult J. SNPs3D: candidate gene and SNP selection for association studies. BMC Bioinformatics 2006; 7:166.

[0259] 17. Ferrer-Costa C, Gelpi J L, Zamakola L, Parraga I, de la Cruz X, Orozco M. PMUT: a web-based tool for the annotation of pathological mutations on proteins. Bioinformatics 2005; 21:3176-8.

[0260] 18. Henry W L, Gardin J M, Ware J H. Echocardiographic Measurements in Normal Subjects from Infancy to Old Age. Circulation 1980; 62:1054-1061.

[0261] 19. Henry W L, Ware J, Gardin J M, Hepner S I, McKay J, Weiner M. Echocardiographic measurements in normal subjects. Growth related changes that occur between infancy and early adulthood. Circulation 1978; 57:278-285.

[0262] 20. Rahman P, Jones A, Curtis J, et al. The Newfoundland population: a unique resource for genetic investigation of complex diseases. Hum. Mol. Genet. 2003; 12:167R-172.

[0263] 21. Garcia-Gras E, Lombardi R, Giocondo M J, et al. Suppression of canonical Wnt/beta-catenin signaling by nuclear plakoglobin recapitulates phenotype of arrhythmogenic right ventricular cardiomyopathy. J Clin Invest 2006; 116:2012-21.

[0264] 22. Lemay D G, Hwang D H. Genome-wide identification of peroxisome proliferator response elements using integrated computational genomics. J Lipid Res 2006; 47:1583-7.

[0265] 23. Pinamonti B, Pagnan L, Bussani R, Ricci C, Silvestri F, Camerini F. Right Ventricular Dysplasia With Biventricular Involvement. Circulation 1998; 98:1943-1945.

[0266] 24. Norman M, Simpson M, Mogensen J, et al. Novel Mutation in Desmoplakin Causes Arrhythmogenic

Left Ventricular Cardiomyopathy 10.1161/CIRCULATIONAHA.104.532234. Circulation 2005; 112:636-642.

[0267] 25. Sen-Chowdhry S, Syrris P, Ward D, Asimaki A, Sevdalis E, McKenna W. Clinical and genetic characterization of families with arrhythmogenic right ventricular dysplasia/cardiomyopathy provides novel insights into patterns of disease expression. Circulation 2007; 115:1710-20.

[0268] 26. Hamid M S, Norman M, Quraishi A, et al. Prospective Evaluation of Relatives for Familal Arrhythmogenic Right Ventricular Cardiomyopathy/Dysplasia Reveals a Need to Broaden Diagnostic Criteria. Journal of the American College of Cardiology 2002; 40:1445-1450.

[0269] 27. King R A, Rotter J I, Motulsky A G. The Genetic Basis of Common Diseases. Oxford: Oxford University Press, 2002:1096.

[0270] 28. Pullman D, Hodgkinson K. Genetic knowledge and moral responsibility: ethical concerns at the interface of genetic research and clinical practice. Clinical Genetics 2006; 69:199-203.

[0271] 29. Syrris P, Ward D, Asimaki A, et al. Clinical Expression of Plakophilin-2 Mutations in Familial Arrhythmogenic Right Ventricular Cardiomyopathy 10.1161/CIRCULATIONAHA.105.561654. Circulation 2006; 113:356-364.

[0272] 30. Syrris P, Ward D, Asimaki A, et al. Desmoglein-2 mutations in arrhythmogenic right ventricular cardiomyopathy: a genotype-phenotype characterization of familial disease 10.1093/eurheartj/ehl380. Eur Heart J 2007; 28:581-588.

[0273] 31. Protonotarios N, Tsatsopoulou A, Anastasakis A, et al. Genotype-phenotype assessment in autosomal recessive arrhythmogenic right ventricular cardiomyopathy (Naxos disease) caused by a deletion in plakoglobin. Journal of the American College of Cardiology 2001; 38:1477-1484.

[0274] 32. Gami A S, Holly T A, Rosenthal J E. Electrocardiographic poor R-wave progression: analysis of multiple criteria reveals little usefulness. American Heart Journal 2004; 148:80-85.

[0275] 33. Papadopoulos, N. et al. Mutation of a mutL homolog in hereditary colon cancer. Science 263, 1625-9 (1994).

[0276] 34. Green, R. C. et al. Hereditary nonpolyposis colon cancer: analysis of linkage to 2p15-16 places the COCA1 locus telomeric to D2S123 and reveals genetic heterogeneity in seven Canadian families. Am J Hum Genet 54, 1067-77 (1994).

[0277] 35. Young T L, Penney L, Woods M O, Parfrey P S, Green J S, Hefferton D, Davidson W S (1999) A fifth locus for Bardet-Biedl syndrome maps to chromosome 2q31. Am J Hum Genet 64: 900-904

[0278] 36. Young T L, Woods M O, Parfrey P S, Green J S, O'Leary E O, Hefferton D, Davidson W S (1998) Canadian Bardet-Biedl syndrome family reduces the critical region of BBS3 (3p) and presents with a variable phenotype. Am J Med Genet 78: 461-467

[0279] 37. Woods M O, Young T L, Parfrey P S, Hefferton D, Green J S, Davidson W S (1999) Genetic heterogeneity of BBS in a distinct Canadian population: Evidence for a fifth locus. Genomics 55: 2-9.

[0280] 38. Li, J B et al. Comparative and basal genomics identifies a flagellar and basal body proteome that includes the BBS in human disease gene. Cell 117: 541-52, 2004. (Citations: 130).

[0281] 39. Kulaga H M, Leitch C C, Eichers E R, Badano J L, Lesemann A, Hoskins B E, Lupski J R, Beales P L, Reed R R, Katsanis N. Loss of BBS proteins causes anosmia in humans and defects in olfactory cilia structure and function in the mouse. *Nat Genet.* 2004 September; 36(9):994-8. Epub 2004 Aug. 22.

[0282] 40. Young T L, Ives E, Lynch E, Person R, Snook S, MacLaren L, Cator T, Griffin A, Fernandez B, Lee M K, King M C (2001) Non-syndromic progressive hearing loss DFNA38 is caused by heterozygous missense mutation in the Wolfram syndrome gene WFS1. Hum Mol Genet 10: 2509-14.

[0283] 41. Cryns K, Sivakumaran T A, Van den Ouweland J M, Pennings R J, Cremers C W, Flothmann K, Young T L, Smith R J, Lesperance M M, Van Camp G. Mutational spectrum of the WFS1 gene in Wolfram syndrome, non-syndromic hearing impairment, diabetes mellitus, and psychiatric disease. Hum Mutat. 2003 October; 22(4):275-87.

[0284] 42. Rahman P. Jones A. Curtis J. Bartlett S. Peddle L. Fernandez B. Freimer N. 2003. The Newfoundland population: a unique resource for genetic investigation of complex diseases. Hum. Mol. Genetics. 12(R2): R167-R172.

[0285] 43. Dreger, M Bengtsson, L Schoneberg T, Otto H, and Hucho F; Nuclear envelope proteomics: novel integral membrane proteins of the inner nuclear membrane, 2001 PNAS 98:11943-11948.

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ggtgcctgtg ctataaatga gtttcttcac atgaaaaaca cagccagccc aagatgactt 2940

atctgggttt aggattcaat agtattcact aactgcttat tacatgagca atttcatcaa 3000

atctccaaac tcttaaagga tgctttcgga aaacacgctg tatacctaga tgatgactaa 3060

atgcaaaatc cttgggcttt ggtttttttc tagtaaggat tttaaataac tgccgacttc 3120

aaaagtgttc ttaaaacgaa agataatgtt aagaaaaatt tgaaagcttt ggaaaaccaa 3180

atttgtaata tcattgtatt ttttattaaa agttttgtaa taaatttcta aattataaaa 3240

aaaaaaaaaa aaaa 3254

<210> SEQ ID NO 6
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu

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    50                  55                  60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65                  70                  75                  80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
                85                  90                  95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
            100                 105                 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
        115                 120                 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
    130                 135                 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145                 150                 155                 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
            180                 185                 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
        195                 200                 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
    210                 215                 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
            260                 265                 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Leu Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 7
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Pan troglodytes

<400> SEQUENCE: 7

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1               5                   10                  15
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Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65                  70                  75                  80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
                85                  90                  95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
            100                 105                 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
        115                 120                 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
    130                 135                 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145                 150                 155                 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Phe Thr Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
            180                 185                 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
        195                 200                 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
    210                 215                 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Gln Gln Arg Gly Asp Gln Leu
            260                 265                 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Ser Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 8
<211> LENGTH: 400
<212> TYPE: PRT
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<213> ORGANISM: Canis familiaris

<400> SEQUENCE: 8

```
Met Ala Ala Asn Tyr Ser Ser Thr Ser Asn Arg Arg Glu His Val Lys
1               5                  10                  15

Thr Thr Thr Lys Pro Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Thr Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65                  70                  75                  80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
                85                  90                  95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
            100                 105                 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
        115                 120                 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Thr Glu Thr Arg
    130                 135                 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Val Asn Ser Arg Asn
145                 150                 155                 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Phe Thr Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
            180                 185                 190

Ser Ala Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Pro Leu Ser Leu
        195                 200                 205

Ala Lys Leu Asp Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Tyr
    210                 215                 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Val Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
            260                 265                 270

Val Pro Tyr Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Arg Lys Ser Asn
    290                 295                 300

Ser Leu Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Leu Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Val Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Ile Phe Arg Asp Leu Val Asp Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Cys Ala Leu Phe Ile Ser Cys Leu Ala Leu
    370                 375                 380
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Val Pro Ile Ile Ile Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 9
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 9

Met Ala Ala Asn Tyr Ser Ser Thr Ser Ser Arg Lys Glu His Val Lys
1               5                   10                  15

Val Thr Ser Glu Pro Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Thr Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65                  70                  75                  80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
                85                  90                  95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
            100                 105                 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
        115                 120                 125

Glu Ser Ser Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Lys
    130                 135                 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Val Asn Ser Arg Asn
145                 150                 155                 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Phe Thr Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
            180                 185                 190

Ser Ala Gly Leu Ile Asp Lys Ile Asp Asn Phe Lys Ala Leu Ser Leu
        195                 200                 205

Ala Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
    210                 215                 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Val Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Ser Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
            260                 265                 270

Ile Pro Tyr Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe Arg Arg Glu Gln Lys Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350
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Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Ala Leu Ile Gly Cys Leu Ala Leu
    370                 375                 380

Val Pro Ile Ile Ile Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 10
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Gallus gallus

<400> SEQUENCE: 10

Met Ser Arg Asn Phe Ser Asp Thr Gly Ser Lys Lys Glu His Val Lys
1               5                   10                  15

Ile Thr Ser Glu Ala Lys Pro Gly Phe Leu Glu Arg Leu Ser Thr Ser
            20                  25                  30

Gly Gly Met Leu Ile Gly Leu Gly Thr Phe Leu Leu Ser Phe Tyr Leu
        35                  40                  45

Leu Phe Thr Asn Glu Gly Arg Ala Leu Arg Thr Ala Lys Ser Leu Asp
    50                  55                  60

Glu Gly Leu Ser Leu Val Ile Pro Leu Asp Asn Ile His Ser Val Ser
65                  70                  75                  80

Gln Gln Asn Glu Gly Arg Leu Val His Leu Ala Gly Ala Leu Ser Thr
                85                  90                  95

Ala Lys Pro Leu Phe Asp Pro Ser Tyr Gly Leu Ser Ile Gln Ala Val
            100                 105                 110

Lys Leu Lys Arg Lys Val Glu Met Tyr Gln Trp Val Glu Tyr Glu Asp
        115                 120                 125

Ser Arg Glu Tyr Glu Glu Asn Gly Glu Ile Lys Lys Glu Thr Lys Tyr
    130                 135                 140

Ser Tyr Asn Thr Glu Trp Lys Pro Glu Val Val Asn Ser Arg Asn Phe
145                 150                 155                 160

Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu Ser
                165                 170                 175

Phe Thr Ala Val Ser Pro Asn Val Gln Val Gly Ser Phe Val Leu Ser
            180                 185                 190

Lys Gly Leu Val Asp Lys Ile Asp Asp Phe Lys Gln Leu Ser Leu Ala
        195                 200                 205

His Leu Glu Asp Pro His Ala Asp Val Thr Arg Gly Gly Asp Tyr Phe
    210                 215                 220

Tyr His Ser Glu Asn Pro Arg Arg Pro Glu Val Gly Asp Leu Arg Val
225                 230                 235                 240

Ser Phe Phe Tyr Ala Gly Leu Ser Gly His Asp Pro His Leu Gly Ser
                245                 250                 255

Ala Asp Lys Val Thr Val Ile Ala Arg Gln Lys Gly Asp Gln Leu Val
            260                 265                 270

Pro Tyr His Thr Lys Ser Gly Asp Val Leu Gln Ile Leu Tyr Phe Gly
        275                 280                 285

Asp Leu Ser Val Glu Glu Val Phe Gln Lys Glu His Glu Ser Asn Thr
    290                 295                 300

Met Lys Thr Trp Ala Leu Arg Ala Ala Gly Trp Leu Ala Met Phe Val
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305                 310                 315                 320

Gly Ile Ser Leu Met Thr Arg Ile Val Tyr Thr Leu Val Asp Trp Phe
                325                 330                 335

Pro Val Val Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala Phe
            340                 345                 350

Cys Val Ala Ser Ser Leu Ser Leu Leu Thr Ile Ser Ile Gly Trp Phe
        355                 360                 365

Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Gly Leu Leu Ser Val Val
    370                 375                 380

Pro Ile Val Val Ala Lys Ser Arg Ile Pro Pro Lys Lys His Gln
385                 390                 395


<210> SEQ ID NO 11
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Zenopus tropicalis

<400> SEQUENCE: 11

Met Lys Glu His Thr Thr Val Arg Ser Glu Gln Lys Pro Gly Phe Leu
1               5                   10                  15

Glu Arg Leu Ser Asp Thr Ala Gly Gly Met Leu Val Gly Leu Leu Ala
            20                  25                  30

Phe Ser Leu Ser Phe Tyr Leu Leu Phe Thr Asn Glu Gly Arg Ala Val
        35                  40                  45

Gln Thr Ala Thr Ser Leu Asp Glu Gly Leu Ser Ile Val Val Pro Val
    50                  55                  60

Gly Asn Ile His Ser Ile Asp His Gln Asn Glu Ala Asn Leu Val His
65                  70                  75                  80

Leu Ser Gly Ala Leu Arg Thr Ser Lys Pro Leu Tyr Asp Pro Asn Tyr
                85                  90                  95

Gly Val Ser Ile His Cys Val Lys Leu Lys Arg Gln Val Glu Met Tyr
            100                 105                 110

Gln Trp Ile Glu Tyr Glu Glu Ser Arg Gln Tyr Glu Glu Asn Gly Glu
        115                 120                 125

Gln Lys Thr Glu Thr Arg Tyr Thr Tyr Asn Thr Glu Trp Arg Ser Glu
    130                 135                 140

Ile Val Ser Ser Arg His Phe Asp Arg Glu Ile Ala His Gln Asn Pro
145                 150                 155                 160

Ser Ala Met Ala Val Glu Ser Phe Thr Ala Val Ser Ser Asp Val Gln
                165                 170                 175

Val Gly Ser Tyr Tyr Leu Ser Lys Gly Leu Val Asp Lys Ile Asp Asn
            180                 185                 190

Phe Lys Gln Met Ser Leu Ser Gln Leu Gly Asn Pro His Ala Asp Val
        195                 200                 205

Ile Ala Asp Gly Gly Tyr Phe Tyr His Ser Ala Asn Pro Lys Ser Pro
    210                 215                 220

Glu Val Gly Asp Leu Arg Ile Ser Phe Trp Tyr Ala Gly Val Ala Leu
225                 230                 235                 240

Gly Gly Ala Gln Phe Gly Gln Pro Asp Met Val Ser Val Ile Ala Arg
                245                 250                 255

Gln Arg Gly Gly Glu Leu Gly Ala Tyr Lys Thr Lys Ser Gly Asp Val
            260                 265                 270
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Leu Glu Leu Leu His Met Gly Thr Tyr Ser Ala Gln Glu Met Phe Glu
        275                 280                 285

Ala Glu His Lys Ser Asn Asn Leu Lys Thr Trp Ala Leu Arg Gly Ala
    290                 295                 300

Gly Trp Leu Met Met Phe Val Gly Ile Ser Leu Met Thr Lys Ile Phe
305                 310                 315                 320

Tyr Thr Leu Val Asp Trp Phe Pro Leu Val Arg Asp Leu Val Ser Leu
                325                 330                 335

Gly Leu Lys Ile Cys Ala Leu Cys Val Ser Ser Ser Leu Ser Leu Leu
            340                 345                 350

Thr Ile Ala Ala Gly Trp Ile Phe Tyr Arg Pro Leu Leu Ala Leu Leu
        355                 360                 365

Leu Ser Ala Ala Ala Ile Gly Ile Ile Val Leu Ala Arg Ser Arg Val
    370                 375                 380

Pro Pro Lys Lys Tyr Gln
385                 390


<210> SEQ ID NO 12
<211> LENGTH: 402
<212> TYPE: PRT
<213> ORGANISM: Tetradon nigroviridis

<400> SEQUENCE: 12

Met Ser Ser Ala Gln Ser Ser Gly Lys Asn Pro Asn Lys His Thr Arg
1               5                   10                  15

Val Ser Ala Lys Ala Asn Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ala Gly Gly Thr Leu Val Gly Ile Gly Leu Phe Phe Leu Ser Phe Tyr
        35                  40                  45

Val Leu Phe Thr Asn Glu Gly Arg Ala Leu Gln Thr Ser Ser Ser Leu
    50                  55                  60

Asp Glu Gly Leu Ser Arg Val Val Ser Leu Gly Ser Ser Ser Ser Leu
65                  70                  75                  80

Asp Pro Gln Asn Asn Asn His Leu Val His Leu Phe Ala Pro Leu Lys
                85                  90                  95

Thr Ala Gln Pro Leu His Asp Pro Asn Tyr Lys Val Val Val Gln Ala
            100                 105                 110

Val Lys Leu Lys Arg Gln Val Glu Met Tyr Gln Trp Val Glu His Gln
        115                 120                 125

Glu Ser Lys Asp Tyr Gln Glu Glu Gly Glu Thr Lys Thr Glu Thr Thr
    130                 135                 140

Tyr Thr Tyr Asn Thr Glu Trp Lys Ser Glu Leu Ile Asn Ser Arg His
145                 150                 155                 160

Phe Asp Lys Glu Ile Gly His Gln Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Val Thr Val Val Ala Pro Glu Val Arg Val Gly Pro Phe Val Leu
            180                 185                 190

Ser Lys Gly Leu Val Glu Gln Ile Asp His Phe Gln Thr Leu Ser Leu
        195                 200                 205

Arg Asp Phe Pro Val Leu Asp Leu Glu Pro Phe Leu Ser Ile Asp Asp
    210                 215                 220

Asp Tyr Phe Tyr His Thr Glu His Pro Arg Arg Pro Glu Val Gly Asp
225                 230                 235                 240
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Val Arg Val Arg Phe Ser Phe Ala Gly Leu Ser Gly Glu Ser Ser Arg
                245                 250                 255

Phe Gly Pro Pro Gln Pro Val Ser Val Val Ala Met Gln Arg Gly Glu
            260                 265                 270

His Leu Glu Pro Phe Lys Thr Arg Ser Gly Gly Thr Leu Glu Ile Leu
        275                 280                 285

Tyr Leu Gly Glu Leu Thr Ala Glu Glu Val Phe Ala Lys Glu His Gln
    290                 295                 300

His Asn Ser Leu Lys Thr Trp Ala Leu Arg Ala Ala Gly Trp Ala Leu
305                 310                 315                 320

Met Phe Leu Ser Ile Gln Leu Ser Met Arg Ile Ile Tyr Thr Leu Val
                325                 330                 335

Asp Trp Val Pro Val Leu Arg Glu Leu Val Ser Leu Gly Leu Lys Val
            340                 345                 350

Leu Ala Leu Cys Leu Ser Cys Ser Leu Ser Leu Leu Thr Ile Ala Ala
        355                 360                 365

Gly Trp Leu Phe Tyr Arg Pro Leu Val Ala Ala Ala Leu Ala Ala Leu
    370                 375                 380

Ala Leu Val Pro Val Phe Leu Thr Arg Ser Gly Leu Pro Ala Lys Lys
385                 390                 395                 400

Asn Glu


<210> SEQ ID NO 13
<211> LENGTH: 376
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster

<400> SEQUENCE: 13

Met Ala Ser Leu Ser Glu Thr Leu Arg Ser His Trp Pro Ile Ala Leu
1               5                   10                  15

Phe Gly Val Ile Leu Phe Val Ala Gly Gly Thr Glu Leu Tyr Trp Asn
            20                  25                  30

Glu Gly Arg Ala Val His Asn Met Met Ala Leu Asp Glu Ala His Ala
        35                  40                  45

Asp Ile Tyr Ser Val Arg Phe Thr Glu Glu Glu Gln Glu Val Gly Leu
    50                  55                  60

Glu Gly Arg Ile Val His Leu Ser Gly Pro Ile Leu Val Gly Glu Pro
65                  70                  75                  80

Leu Thr Glu Pro Asp Tyr Asn Ile Gln Leu Leu Ala Val Lys Leu Arg
                85                  90                  95

Arg Arg Val Gln Met Tyr Gln Trp Val Glu Glu Ala Val Glu His Asn
            100                 105                 110

Tyr Gly Asp Ser Val Gly Thr Thr His Ser Asp Ser Arg Thr Tyr Tyr
        115                 120                 125

Tyr Thr Arg Glu Trp Arg Asp Lys Ile Val Asp Ser Arg Asn Phe Tyr
    130                 135                 140

Asn Arg His Gly His Thr Asn Pro Ser His Phe Pro Ile Glu Ser His
145                 150                 155                 160

Val Gln Val Ala Asp Ala Val Phe Ile Gly Arg Tyr Glu Leu Gly Ala
                165                 170                 175

Glu Val Lys Glu Lys Phe Asn Asn Tyr Gln Glu Leu Thr Ser Asp Ile
            180                 185                 190
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Arg Pro Glu Asp Ser Gly Val Lys Leu His Leu Gly Ile Tyr Tyr His
        195                 200                 205

Thr Asn Asp Val Phe Asn Pro Glu Val Gly Asp Leu Arg Leu Leu Phe
    210                 215                 220

Ser Phe Ala Gly Met Glu Gly Glu Val Phe Ser Val Val Gly Lys Leu
225                 230                 235                 240

Ser Gly Asn Lys Leu Val Pro Tyr Ile Thr Ser Arg Gly Val Pro Val
                245                 250                 255

Leu Leu Val Tyr Pro Gly Gly Leu Ser Val Gln Glu Val Phe Arg Leu
            260                 265                 270

Glu Ala Arg Ala Gln Val Leu His Thr Trp Trp Trp Arg Phe Val Gly
        275                 280                 285

Trp Leu Leu Ile Phe Phe Gly Val Thr Cys Asn Thr Lys Ile Leu Arg
    290                 295                 300

Leu Leu Phe Val Arg Val Pro Leu Leu Val Ala Leu Ala Pro Asp Pro
305                 310                 315                 320

Gln Phe Pro Val Thr Gly Asn Leu Leu Ile Ala Phe Ser Leu Ala Leu
                325                 330                 335

Thr Ile Ala Ala Val Ala Trp Ile Leu His Arg Pro Val Ile Gly Ala
            340                 345                 350

Cys Leu Leu Leu Ala Gly Ala Ser Pro Tyr Val Trp Phe Thr Arg Asn
        355                 360                 365

Leu Val Asp Tyr His Arg Leu Asp
    370                 375


<210> SEQ ID NO 14
<211> LENGTH: 425
<212> TYPE: PRT
<213> ORGANISM: Rhizobium loti

<400> SEQUENCE: 14

Met Glu Phe Val Ala Ala Leu Arg Pro Arg Ser Ser Ala Ala Val Pro
1               5                   10                  15

Cys Gly Leu Leu Ala Ser Phe Val Ser Gly Glu Thr Met Ser Asp Ser
            20                  25                  30

Phe Arg Glu Val Thr Ser Val Ser Trp Phe Gly Arg Ile Lys Arg Ala
        35                  40                  45

Val Gly Gly Val Ile Phe Gly Leu Leu Leu Ile Val Leu Met Val Ile
    50                  55                  60

Gly Leu Phe Trp Asn Glu Gly Arg Ala Val Gln Thr Ala Arg Ser Leu
65                  70                  75                  80

Ala Glu Gly Ala Gly Ala Val Val Ala Ile Asn Ala Asp Ser Val Asp
                85                  90                  95

Ala Gly Asn Asp Gly Arg Leu Val His Val Ser Gly Pro Val Thr Ala
            100                 105                 110

Asp Gly Ser Leu Ser Asp Pro Asp Phe Gly Ile Ala Ala Gln Gly Leu
        115                 120                 125

Arg Leu Ser Arg Ser Val Glu Met Tyr Gln Trp Lys Glu Glu Ser Lys
    130                 135                 140

Ser Glu Thr Thr Lys Lys Leu Gly Gly Gly Glu Glu Thr Glu Thr Thr
145                 150                 155                 160

Tyr Ser Tyr Ser Lys Val Trp Asp Asp Ser Gln Ile Asp Ser Ser Asp
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```
                165                 170                 175

Phe Lys Lys Pro Asp Gly His Gln Asn Pro Pro Met Ala Ile His Ser
            180                 185                 190

Arg Val Phe Gln Ile Pro Gln Gly Lys Leu Val Ala Phe Asp Leu Asp
        195                 200                 205

Thr Pro Val Leu Asp Arg Ile Asp Gly Asp Lys Ala Tyr Ser Leu Ser
    210                 215                 220

Ala Asn Gln Ser Ala Thr Ile Lys Ala Ala Tyr Thr Gly Thr Lys Pro
225                 230                 235                 240

Leu Ser Ile Val Asp Gly Arg Ile Tyr Leu Gly Asn Asp Asn Thr Thr
                245                 250                 255

Pro Ala Leu Gly Asp Tyr Arg Ile Gly Tyr Glu Leu Ala Pro Leu Gly
            260                 265                 270

Val Val Ser Ile Val Ala Arg Gln Ala Gly Ser Arg Phe Glu Pro Tyr
        275                 280                 285

Gln Thr Gln Ala Gly Asp Ala Leu Leu Met Val Asp Thr Gly Asn Val
    290                 295                 300

Pro Ala Asp Lys Met Phe Ala Glu Ala Val Ser Ala Asn Thr Leu Ile
305                 310                 315                 320

Thr Trp Leu Leu Arg Ala Gly Gly Leu Leu Leu Leu Thr Ile Gly Phe
                325                 330                 335

Ala Leu Phe Leu Ser Pro Ile Gly Val Ile Leu Asp Val Ile Pro Phe
            340                 345                 350

Leu Gly Ser Met Ala Arg Met Gly Thr Gly Ile Ile Ala Phe Phe Leu
        355                 360                 365

Ala Ile Leu Val Gly Thr Thr Thr Ile Ala Ile Ala Trp Phe Trp Tyr
    370                 375                 380

Arg Pro Val Leu Ala Ala Gly Ile Leu Ala Thr Gly Val Ile Ala Ala
385                 390                 395                 400

Ala Ala Val Tyr Tyr Leu Gly Arg Ser Arg Lys Ala Ala Ala Pro Met
                405                 410                 415

Ala Thr Pro Ser Thr Gly Thr Ala Thr
            420                 425


<210> SEQ ID NO 15
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 15

gtcagcccac ttcctagctg                                              20


<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 16

cctcgtctcc ttcttcacct                                              20


<210> SEQ ID NO 17
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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 17

agaatgaagg aaggctggtg 20

<210> SEQ ID NO 18
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 18

tggtggagaa tgggactagc 20

<210> SEQ ID NO 19
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 19

cgccgtggag acttttcta 20

<210> SEQ ID NO 20
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 20

acctggatcc tagggctcac 20

<210> SEQ ID NO 21
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 21

gtcagcccac ttcctagctg 20

<210> SEQ ID NO 22
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 22

cccaggtctt catggagttg 20

<210> SEQ ID NO 23
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 23

atcttccggc tgtgaaactg 20

<210> SEQ ID NO 24
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 24

agagggagtg cagagtccaa 20

<210> SEQ ID NO 25
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 25

caatgtcccg gaccgtatag 20

<210> SEQ ID NO 26
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 26

ggcgaaatgg acctagagga 20

<210> SEQ ID NO 27
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 27

agttttcatt ctgttactgt ttctttt 27

<210> SEQ ID NO 28
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 28

ggcccttgat taccaaatcc 20

<210> SEQ ID NO 29
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 29

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aactgtacgg tggggagatg 20

<210> SEQ ID NO 30
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 30

atcactccca tgtgtgacca 20

<210> SEQ ID NO 31
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 31

aagaacctgg gacagggagt 20

<210> SEQ ID NO 32
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 32

ctcctggagc cactcttcac 20

<210> SEQ ID NO 33
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 33

tgatctggta gccctgaggt 20

<210> SEQ ID NO 34
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 34

cacgaggcag gattaactca a 21

<210> SEQ ID NO 35
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 35

cctgggctaa tctggacttg 20

<210> SEQ ID NO 36

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequene
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 36

ctgatcctgt gcctttagcc 20

<210> SEQ ID NO 37
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 37

cgtggacgag acagagtcag 20

<210> SEQ ID NO 38
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 38

cgctcctgac attgaccaag 20

<210> SEQ ID NO 39
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 39

gggtttctgt gctcacttcc 20

<210> SEQ ID NO 40
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 40

tgcctcattc actggctatg 20

<210> SEQ ID NO 41
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 41

tgttcagaaa tggccaacag 20

<210> SEQ ID NO 42
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 42

ctcatcccaa ggctatggag 20

<210> SEQ ID NO 43
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 43

cccatcctca tctagggaca 20

<210> SEQ ID NO 44
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 44

ggaaacagca ggagaagctg 20

<210> SEQ ID NO 45
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 45

tggtgttcac cagctcatgt 20

<210> SEQ ID NO 46
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 46

ttcctcttgg ggtaggaaag 20

<210> SEQ ID NO 47
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 47

tcctgaggag aaaagctgga 20

<210> SEQ ID NO 48
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 48

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cgtgggcatt gtacaaccag 20

<210> SEQ ID NO 49
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 49

cgattaagag aaaaggttgg aa 22

<210> SEQ ID NO 50
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 50

gagatttgat gaaattgctc atgta 25

<210> SEQ ID NO 51
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 51

ttgtgcctgc tgggagtaat 20

<210> SEQ ID NO 52
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 52

atcctatggc tgaattcttt aca 23

<210> SEQ ID NO 53
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Probe

<400> SEQUENCE: 53

ctgtgtggcc accttgctga 20

<210> SEQ ID NO 54
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Probe

<400> SEQUENCE: 54

ctgtgtggcc acctcgctga 20

<210> SEQ ID NO 55

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<211> LENGTH: 2846
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (260)..(1459)

<400> SEQUENCE: 55

aaagctttgc agtgcgcagg cgcatcaatg aggtactgca atgtcccgga ccgtatagtt     60

tccaggacgt ctcgccgcgc gcatgcgcag aaacactggg cacaggggga ggtaactgca    120

gtaagtcccg cttggccctg gagtccacgc ggattttcga agctggggct ggcaagaggc    180

cgctggacac cacgctccag tcgtcagccc acttcctagc tgaacagcgc gaggcggcgg    240

cagcgagccg ggtcccacc atg gcc gcg aat tat tcc agt acc agt acc cgg     292

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg
1               5                   10

aga gaa cat gtc aaa gtt aaa acc agc tcc cag cca ggc ttc ctg gaa      340
Arg Glu His Val Lys Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu
            15                  20                  25

cgg ctg agc gag acc tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc      388
Arg Leu Ser Glu Thr Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe
        30                  35                  40

ctg ctc tcc ttc tac cta att ttc acc aat gag ggc cgc gca ttg aag      436
Leu Leu Ser Phe Tyr Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys
    45                  50                  55

acg gca acc tca ttg gct gag ggg ctc tcg ctt gtg gtg tct ccc gac      484
Thr Ala Thr Ser Leu Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp
60                  65                  70                  75

agc atc cac agt gtg gct ccg gag aat gaa gga agg ctg gtg cac atc      532
Ser Ile His Ser Val Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile
                80                  85                  90

att ggc gcc tta cgg aca tcc aag ctt ttg tct gat cca aac tat ggg      580
Ile Gly Ala Leu Arg Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly
            95                  100                 105

gtc cat ctt ccg gct gtg aaa ctg cgg agg cac gtg gag atg tac caa      628
Val His Leu Pro Ala Val Lys Leu Arg Arg His Val Glu Met Tyr Gln
        110                 115                 120

tgg gta gaa act gag gag tcc agg gag tac acc gag gat ggg cag gtg      676
Trp Val Glu Thr Glu Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val
    125                 130                 135

aag aag gag acg agg tat tcc tac aac act gaa tgg agg tca gaa atc      724
Lys Lys Glu Thr Arg Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile
140                 145                 150                 155

atc aac agc aaa aac ttc gac cga gag att ggc cac aaa aac ccc agt      772
Ile Asn Ser Lys Asn Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser
                160                 165                 170

gcc atg gca gtg gag tca ttc atg gca aca gcc ccc ttt gtc caa att      820
Ala Met Ala Val Glu Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile
            175                 180                 185

ggc agg ttt ttc ctc tcg tca ggc ctc atc gac aaa gtc gac aac ttc      868
Gly Arg Phe Phe Leu Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe
        190                 195                 200

aag tcc ctg agc cta tcc aag ctg gag gac cct cat gtg gac atc att      916
Lys Ser Leu Ser Leu Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile
    205                 210                 215
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cgc cgt gga gac ttt ttc tac cac agc gaa aat ccc aag tat cca gag      964
Arg Arg Gly Asp Phe Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu
220                 225                 230                 235

gtg gga gac ttg cgt gtc tcc ttt tcc tat gct gga ctg agc ggc gat     1012
Val Gly Asp Leu Arg Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp
                240                 245                 250

gac cct gac ctg ggc cca gct cac gtg gtc act gtg att gcc cgg cag     1060
Asp Pro Asp Leu Gly Pro Ala His Val Val Thr Val Ile Ala Arg Gln
            255                 260                 265

cgg ggt gac cag cta gtc cca ttc tcc acc aag tct ggg gat acc tta     1108
Arg Gly Asp Gln Leu Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu
        270                 275                 280

ctg ctc ctg cac cac ggg gac ttc tca gca gag gag gtg ttt cat aga     1156
Leu Leu Leu His His Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg
    285                 290                 295

gaa cta agg agc aac tcc atg aag acc tgg ggc ctg cgg gca gct ggc     1204
Glu Leu Arg Ser Asn Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly
300                 305                 310                 315

tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc tac     1252
Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr
                320                 325                 330

acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att ggc     1300
Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly
            335                 340                 345

ctg aaa gcc ttt gcc ttc tgt gtg gcc acc tcg ctg acc ctg ctg acc     1348
Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr
        350                 355                 360

gtg gcg gct ggc tgg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att     1396
Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile
    365                 370                 375

gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca     1444
Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro
380                 385                 390                 395

gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct gcgtgagccc     1499
Ala Lys Lys Leu Glu
                400

taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg agccccggtc   1559

aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc atgtgcacca   1619

ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa gcagctttgg   1679

tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt ccttcctctc   1739

ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac gcagacacgc   1799

tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct catcactgca   1859

cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa gggcggccgt   1919

tagtcattac tgctgagtcc tgggtcacca gcagacacac tgggcatgga cccctcaaag   1979

caggcacacc caaaacacaa gtctgtggct agaacctgat gtggtgttta aaagagaaga   2039

aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac acttatctta   2099

tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta agtttttctt   2159

cgttactttg ctgcttcatg tgtactttcc taccccaaga ggaagttttc tgaaataaga   2219

tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa acacccttta   2279

gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg gtttgattga   2339
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taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga tgcttttgaa 2399

acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag aaagcacttg 2459

ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta aaagattaaa 2519

gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc atggtgacgc 2579

cccgtcaacc acaatcaaga actgaggcct gaggctggtt gtacaatgcc cacgcctgcc 2639

tggctgcttt cacctgggag tgctttcgat gtgggcacct gggcttccta gggctgcttc 2699

tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa gatccaccca 2759

cacctaagtc acagaatttc taagttcccc aactactctc acacccttttt aaagataaag 2819

tatgttgtaa ccaggatgtc ttaaatg 2846

<210> SEQ ID NO 56
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
50 55 60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65 70 75 80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
85 90 95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
100 105 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
115 120 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
130 135 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145 150 155 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
165 170 175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
180 185 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
195 200 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
210 215 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225 230 235 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
245 250 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu

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            260                 265                 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 57
<211> LENGTH: 2243
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.2
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (260)..(1459)

<400> SEQUENCE: 57

aaagctttgc agtgcgcagg cgcatcaatg aggtactgca atgtcccgga ccgtatagtt     60

tccaggacgt ctcgccgcgc gcatgcgcag aaacactggg cacaggggga ggtaactgca    120

gtaagtcccg cttggccctg gagtccacgc ggattttcga agctggggct ggcaagaggc    180

cgctggacac cacgctccag tcgtcagccc acttcctagc tgaacagcgc gaggcggcgg    240

cagcgagccg ggtcccacc atg gcc gcg aat tat tcc agt acc agt acc cgg      292

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg
1               5                   10

aga gaa cat gtc aaa gtt aaa acc agc tcc cag cca ggc ttc ctg gaa      340
Arg Glu His Val Lys Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu
            15                  20                  25

cgg ctg agc gag acc tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc      388
Arg Leu Ser Glu Thr Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe
        30                  35                  40

ctg ctc tcc ttc tac cta att ttc acc aat gag ggc cgc gca ttg aag      436
Leu Leu Ser Phe Tyr Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys
    45                  50                  55

acg gca acc tca ttg gct gag ggg ctc tcg ctt gtg gtg tct ccc gac      484
Thr Ala Thr Ser Leu Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp
60                  65                  70                  75

agc atc cac agt gtg gct ccg gag aat gaa gga agg ctg gtg cac atc      532
Ser Ile His Ser Val Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile
                80                  85                  90

att ggc gcc tta cgg aca tcc aag ctt ttg tct gat cca aac tat ggg      580
Ile Gly Ala Leu Arg Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly
            95                  100                 105
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gtc cat ctt ccg gct gtg aaa ctg cgg agg cac gtg gag atg tac caa      628
Val His Leu Pro Ala Val Lys Leu Arg Arg His Val Glu Met Tyr Gln
        110                 115                 120

tgg gta gaa act gag gag tcc agg gag tac acc gag gat ggg cag gtg      676
Trp Val Glu Thr Glu Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val
    125                 130                 135

aag aag gag acg agg tat tcc tac aac act gaa tgg agg tca gaa atc      724
Lys Lys Glu Thr Arg Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile
140                 145                 150                 155

atc aac agc aaa aac ttc gac cga gag att ggc cac aaa aac ccc agt      772
Ile Asn Ser Lys Asn Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser
                160                 165                 170

gcc atg gca gtg gag tca ttc atg gca aca gcc ccc ttt gtc caa att      820
Ala Met Ala Val Glu Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile
            175                 180                 185

ggc agg ttt ttc ctc tcg tca ggc ctc atc gac aaa gtc gac aac ttc      868
Gly Arg Phe Phe Leu Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe
        190                 195                 200

aag tcc ctg agc cta tcc aag ctg gag gac cct cat gtg gac atc att      916
Lys Ser Leu Ser Leu Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile
    205                 210                 215

cgc cgt gga gac ttt ttc tac cac agc gaa aat ccc aag tat cca gag      964
Arg Arg Gly Asp Phe Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu
220                 225                 230                 235

gtg gga gac ttg cgt gtc tcc ttt tcc tat gct gga ctg agc ggc gat     1012
Val Gly Asp Leu Arg Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp
                240                 245                 250

gac cct gac ctg ggc cca gct cac gtg gtc act gtg att gcc cgg cag     1060
Asp Pro Asp Leu Gly Pro Ala His Val Val Thr Val Ile Ala Arg Gln
            255                 260                 265

cgg ggt gac cag cta gtc cca ttc tcc acc aag tct ggg gat acc tta     1108
Arg Gly Asp Gln Leu Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu
        270                 275                 280

ctg ctc ctg cac cac ggg gac ttc tca gca gag gag gtg ttt cat aga     1156
Leu Leu Leu His His Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg
    285                 290                 295

gaa cta agg agc aac tcc atg aag acc tgg ggc ctg cgg gca gct ggc     1204
Glu Leu Arg Ser Asn Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly
300                 305                 310                 315

tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc tac     1252
Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr
                320                 325                 330

acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att ggc     1300
Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly
            335                 340                 345

ctg aaa gcc ttt gcc ttc tgt gtg gcc acc tcg ctg acc ctg ctg acc     1348
Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr
        350                 355                 360

gtg gcg gct ggc tgg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att     1396
Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile
    365                 370                 375

gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca     1444
Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro
380                 385                 390                 395

gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct gcgtgagcct     1499
Ala Lys Lys Leu Glu
                400
```

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gaggctggtt gtacaatgcc cacgcctgcc tggctgcttt cacctgggag tgctttcgat 1559

gtgggcacct gggcttccta gggctgcttc tgagtggttc tttcacgtgt tgtgtccata 1619

gctttagtct tcctaaataa gatccaccca cacctaagtc acagaatttc taagttcccc 1679

aactactctc acacccttt aaagataaag tatgttgtaa ccaggatgtc ttaaatgatt 1739

ctttgtgtac cttttctgtc atattcagaa accgttttgt gcctgctggg agtaattcct 1799

ttagcaatta agtatttggt agctgaataa ggggtcagaa cttctgaaac cagagatctg 1859

taatcatctc tattggcctg gggtgcctgt gctataaatg agtttcttca catgaaaaac 1919

acagccagcc caagatgact tatctgggtt taggattcaa tagtattcac taactgctta 1979

ttacatgagc aatttcatca aatctccaaa ctcttaaagg atgctttcgg aaaacacgct 2039

gtatacctag atgatgacta aatgcaaaat ccttgggctt tggttttttt ctagtaagga 2099

ttttaaataa ctgccgactt caaaagtgtt cttaaaacga aagataatgt taagaaaaat 2159

ttgaaagctt tggaaaacca aatttgtaat atcattgtat tttttattaa aagttttgta 2219

ataaatttct aaattatctt ctgg 2243

<210> SEQ ID NO 58
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
50 55 60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65 70 75 80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
85 90 95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
100 105 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
115 120 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
130 135 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145 150 155 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
165 170 175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
180 185 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
195 200 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
210 215 220

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Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
            260                 265                 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 59
<211> LENGTH: 3353
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.3
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (260)..(1459)

<400> SEQUENCE: 59

aaagctttgc agtgcgcagg cgcatcaatg aggtactgca atgtcccgga ccgtatagtt     60

tccaggacgt ctcgccgcgc gcatgcgcag aaacactggg cacaggggga ggtaactgca    120

gtaagtcccg cttggccctg gagtccacgc ggattttcga agctggggct ggcaagaggc    180

cgctggacac cacgctccag tcgtcagccc acttcctagc tgaacagcgc gaggcggcgg    240

cagcgagccg ggtcccacc atg gcc gcg aat tat tcc agt acc agt acc cgg     292

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg
1               5                   10

aga gaa cat gtc aaa gtt aaa acc agc tcc cag cca ggc ttc ctg gaa      340
Arg Glu His Val Lys Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu
            15                  20                  25

cgg ctg agc gag acc tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc      388
Arg Leu Ser Glu Thr Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe
        30                  35                  40

ctg ctc tcc ttc tac cta att ttc acc aat gag ggc cgc gca ttg aag      436
Leu Leu Ser Phe Tyr Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys
    45                  50                  55

acg gca acc tca ttg gct gag ggg ctc tcg ctt gtg gtg tct ccc gac      484
Thr Ala Thr Ser Leu Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp
60                  65                  70                  75
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agc atc cac agt gtg gct ccg gag aat gaa gga agg ctg gtg cac atc      532
Ser Ile His Ser Val Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile
                80                  85                  90

att ggc gcc tta cgg aca tcc aag ctt ttg tct gat cca aac tat ggg      580
Ile Gly Ala Leu Arg Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly
            95                  100                 105

gtc cat ctt ccg gct gtg aaa ctg cgg agg cac gtg gag atg tac caa      628
Val His Leu Pro Ala Val Lys Leu Arg Arg His Val Glu Met Tyr Gln
        110                 115                 120

tgg gta gaa act gag gag tcc agg gag tac acc gag gat ggg cag gtg      676
Trp Val Glu Thr Glu Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val
    125                 130                 135

aag aag gag acg agg tat tcc tac aac act gaa tgg agg tca gaa atc      724
Lys Lys Glu Thr Arg Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile
140                 145                 150                 155

atc aac agc aaa aac ttc gac cga gag att ggc cac aaa aac ccc agt      772
Ile Asn Ser Lys Asn Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser
                160                 165                 170

gcc atg gca gtg gag tca ttc atg gca aca gcc ccc ttt gtc caa att      820
Ala Met Ala Val Glu Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile
            175                 180                 185

ggc agg ttt ttc ctc tcg tca ggc ctc atc gac aaa gtc gac aac ttc      868
Gly Arg Phe Phe Leu Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe
        190                 195                 200

aag tcc ctg agc cta tcc aag ctg gag gac cct cat gtg gac atc att      916
Lys Ser Leu Ser Leu Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile
    205                 210                 215

cgc cgt gga gac ttt ttc tac cac agc gaa aat ccc aag tat cca gag      964
Arg Arg Gly Asp Phe Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu
220                 225                 230                 235

gtg gga gac ttg cgt gtc tcc ttt tcc tat gct gga ctg agc ggc gat     1012
Val Gly Asp Leu Arg Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp
                240                 245                 250

gac cct gac ctg ggc cca gct cac gtg gtc act gtg att gcc cgg cag     1060
Asp Pro Asp Leu Gly Pro Ala His Val Val Thr Val Ile Ala Arg Gln
            255                 260                 265

cgg ggt gac cag cta gtc cca ttc tcc acc aag tct ggg gat acc tta     1108
Arg Gly Asp Gln Leu Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu
        270                 275                 280

ctg ctc ctg cac cac ggg gac ttc tca gca gag gag gtg ttt cat aga     1156
Leu Leu Leu His His Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg
    285                 290                 295

gaa cta agg agc aac tcc atg aag acc tgg ggc ctg cgg gca gct ggc     1204
Glu Leu Arg Ser Asn Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly
300                 305                 310                 315

tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc tac     1252
Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr
                320                 325                 330

acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att ggc     1300
Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly
            335                 340                 345

ctg aaa gcc ttt gcc ttc tgt gtg gcc acc tcg ctg acc ctg ctg acc     1348
Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr
        350                 355                 360

gtg gcg gct ggc tgg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att     1396
Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile
    365                 370                 375
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gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca     1444
Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro
380                 385                 390                 395

gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct gcgtgagccc     1499
Ala Lys Lys Leu Glu
                400

taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg agccccggtc   1559

aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc atgtgcacca   1619

ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa gcagctttgg   1679

tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt ccttcctctc   1739

ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac gcagacacgc   1799

tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct catcactgca   1859

cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa gggcggccgt   1919

tagtcattac tgctgagtcc tgggtcacca gcagacacac tgggcatgga cccctcaaag   1979

caggcacacc caaaacacaa gtctgtggct agaacctgat gtggtgttta aaagagaaga   2039

aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac acttatctta   2099

tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta agtttttctt   2159

cgttactttg ctgcttcatg tgtactttcc taccccaaga ggaagttttc tgaaataaga   2219

tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa acacccttta   2279

gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg gtttgattga   2339

taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga tgcttttgaa   2399

acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag aaagcacttg   2459

ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta aaagattaaa   2519

gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc atggtgacgc   2579

cccgtcaacc acaatcaaga actgaggcct gaggctggtt gtacaatgcc cacgcctgcc   2639

tggctgcttt cacctgggag tgctttcgat gtgggcacct gggcttccta gggctgcttc   2699

tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa gatccaccca   2759

cacctaagtc acagaatttc taagttcccc aactactctc acacccttt aaagataaag   2819

tatgttgtaa ccaggatgtc ttaaatgatt ctttgtgtac cttttctgtc atattcagaa   2879

accgttttgt gcctgctggg agtaattcct ttagcaatta agtatttggt agctgaataa   2939

ggggtcagaa cttctgaaac cagagatctg taatcatctc tattggcctg gggtgcctgt   2999

gctataaatg agtttcttca catgaaaaac acagccagcc caagatgact tatctgggtt   3059

taggattcaa tagtattcac taactgctta ttacatgagc aatttcatca aatctccaaa   3119

ctcttaaagg atgctttcgg aaaacacgct gtatacctag atgatgacta aatgcaaaat   3179

ccttgggctt tggttttttt ctagtaagga ttttaaataa ctgccgactt caaaagtgtt   3239

cttaaaacga aagataatgt taagaaaaat ttgaaagctt tggaaaacca aatttgtaat   3299

atcattgtat tttttattaa aagttttgta ataaatttct aaattatctt ctgg         3353
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<210> SEQ ID NO 60
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 60

```
Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1               5                  10                  15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65                  70                  75                  80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
                85                  90                  95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
            100                 105                 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
        115                 120                 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
    130                 135                 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145                 150                 155                 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
                165                 170                 175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
            180                 185                 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
        195                 200                 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
    210                 215                 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225                 230                 235                 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
                245                 250                 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
            260                 265                 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
        275                 280                 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
    290                 295                 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305                 310                 315                 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
                325                 330                 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
            340                 345                 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp
        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
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385                 390                 395                 400


<210> SEQ ID NO 61
<211> LENGTH: 2163
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.4
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (260)..(1459)

<400> SEQUENCE: 61

aaagctttgc agtgcgcagg cgcatcaatg aggtactgca atgtcccgga ccgtatagtt     60

tccaggacgt ctcgccgcgc gcatgcgcag aaacactggg cacaggggga ggtaactgca    120

gtaagtcccg cttggccctg gagtccacgc ggattttcga agctggggct ggcaagaggc    180

cgctggacac cacgctccag tcgtcagccc acttcctagc tgaacagcgc gaggcggcgg    240

cagcgagccg ggtcccacc atg gcc gcg aat tat tcc agt acc agt acc cgg      292

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg
1               5                   10

aga gaa cat gtc aaa gtt aaa acc agc tcc cag cca ggc ttc ctg gaa      340
Arg Glu His Val Lys Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu
            15                  20                  25

cgg ctg agc gag acc tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc      388
Arg Leu Ser Glu Thr Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe
        30                  35                  40

ctg ctc tcc ttc tac cta att ttc acc aat gag ggc cgc gca ttg aag      436
Leu Leu Ser Phe Tyr Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys
    45                  50                  55

acg gca acc tca ttg gct gag ggg ctc tcg ctt gtg gtg tct ccc gac      484
Thr Ala Thr Ser Leu Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp
60                  65                  70                  75

agc atc cac agt gtg gct ccg gag aat gaa gga agg ctg gtg cac atc      532
Ser Ile His Ser Val Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile
                80                  85                  90

att ggc gcc tta cgg aca tcc aag ctt ttg tct gat cca aac tat ggg      580
Ile Gly Ala Leu Arg Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly
            95                  100                 105

gtc cat ctt ccg gct gtg aaa ctg cgg agg cac gtg gag atg tac caa      628
Val His Leu Pro Ala Val Lys Leu Arg Arg His Val Glu Met Tyr Gln
        110                 115                 120

tgg gta gaa act gag gag tcc agg gag tac acc gag gat ggg cag gtg      676
Trp Val Glu Thr Glu Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val
    125                 130                 135

aag aag gag acg agg tat tcc tac aac act gaa tgg agg tca gaa atc      724
Lys Lys Glu Thr Arg Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile
140                 145                 150                 155

atc aac agc aaa aac ttc gac cga gag att ggc cac aaa aac ccc agt      772
Ile Asn Ser Lys Asn Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser
                160                 165                 170

gcc atg gca gtg gag tca ttc atg gca aca gcc ccc ttt gtc caa att      820
Ala Met Ala Val Glu Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile
            175                 180                 185

ggc agg ttt ttc ctc tcg tca ggc ctc atc gac aaa gtc gac aac ttc      868
Gly Arg Phe Phe Leu Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe
        190                 195                 200
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aag tcc ctg agc cta tcc aag ctg gag gac cct cat gtg gac atc att      916
Lys Ser Leu Ser Leu Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile
    205                 210                 215

cgc cgt gga gac ttt ttc tac cac agc gaa aat ccc aag tat cca gag      964
Arg Arg Gly Asp Phe Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu
220                 225                 230                 235

gtg gga gac ttg cgt gtc tcc ttt tcc tat gct gga ctg agc ggc gat     1012
Val Gly Asp Leu Arg Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp
                240                 245                 250

gac cct gac ctg ggc cca gct cac gtg gtc act gtg att gcc cgg cag     1060
Asp Pro Asp Leu Gly Pro Ala His Val Val Thr Val Ile Ala Arg Gln
            255                 260                 265

cgg ggt gac cag cta gtc cca ttc tcc acc aag tct ggg gat acc tta     1108
Arg Gly Asp Gln Leu Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu
        270                 275                 280

ctg ctc ctg cac cac ggg gac ttc tca gca gag gag gtg ttt cat aga     1156
Leu Leu Leu His His Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg
    285                 290                 295

gaa cta agg agc aac tcc atg aag acc tgg ggc ctg cgg gca gct ggc     1204
Glu Leu Arg Ser Asn Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly
300                 305                 310                 315

tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc tac     1252
Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr
                320                 325                 330

acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att ggc     1300
Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly
            335                 340                 345

ctg aaa gcc ttt gcc ttc tgt gtg gcc acc tcg ctg acc ctg ctg acc     1348
Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr
        350                 355                 360

gtg gcg gct ggc tgg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att     1396
Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile
    365                 370                 375

gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca     1444
Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro
380                 385                 390                 395

gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct gggcttccta     1499
Ala Lys Lys Leu Glu
                400

gggctgcttc tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa   1559

gatccaccca cacctaagtc acagaatttc taagttcccc aactactctc acacccttttt  1619

aaagataaag tatgttgtaa ccaggatgtc ttaaatgatt ctttgtgtac cttttctgtc   1679

atattcagaa accgttttgt gcctgctggg agtaattcct ttagcaatta agtatttggt   1739

agctgaataa ggggtcagaa cttctgaaac cagagatctg taatcatctc tattggcctg   1799

gggtgcctgt gctataaatg agtttcttca catgaaaaac acagccagcc caagatgact   1859

tatctgggtt taggattcaa tagtattcac taactgctta ttacatgagc aatttcatca   1919

aatctccaaa ctcttaaagg atgctttcgg aaaacacgct gtatacctag atgatgacta   1979

aatgcaaaat ccttgggctt tggttttttt ctagtaagga ttttaaataa ctgccgactt   2039

caaaagtgtt cttaaaacga aagataatgt taagaaaaat ttgaaagctt tggaaaacca   2099

aatttgtaat atcattgtat tttttattaa aagttttgta ataaatttct aaattatctt   2159

ctgg                                                               2163
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<210> SEQ ID NO 62
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
50 55 60

Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
65 70 75 80

Ala Pro Glu Asn Glu Gly Arg Leu Val His Ile Ile Gly Ala Leu Arg
85 90 95

Thr Ser Lys Leu Leu Ser Asp Pro Asn Tyr Gly Val His Leu Pro Ala
100 105 110

Val Lys Leu Arg Arg His Val Glu Met Tyr Gln Trp Val Glu Thr Glu
115 120 125

Glu Ser Arg Glu Tyr Thr Glu Asp Gly Gln Val Lys Lys Glu Thr Arg
130 135 140

Tyr Ser Tyr Asn Thr Glu Trp Arg Ser Glu Ile Ile Asn Ser Lys Asn
145 150 155 160

Phe Asp Arg Glu Ile Gly His Lys Asn Pro Ser Ala Met Ala Val Glu
165 170 175

Ser Phe Met Ala Thr Ala Pro Phe Val Gln Ile Gly Arg Phe Phe Leu
180 185 190

Ser Ser Gly Leu Ile Asp Lys Val Asp Asn Phe Lys Ser Leu Ser Leu
195 200 205

Ser Lys Leu Glu Asp Pro His Val Asp Ile Ile Arg Arg Gly Asp Phe
210 215 220

Phe Tyr His Ser Glu Asn Pro Lys Tyr Pro Glu Val Gly Asp Leu Arg
225 230 235 240

Val Ser Phe Ser Tyr Ala Gly Leu Ser Gly Asp Asp Pro Asp Leu Gly
245 250 255

Pro Ala His Val Val Thr Val Ile Ala Arg Gln Arg Gly Asp Gln Leu
260 265 270

Val Pro Phe Ser Thr Lys Ser Gly Asp Thr Leu Leu Leu Leu His His
275 280 285

Gly Asp Phe Ser Ala Glu Glu Val Phe His Arg Glu Leu Arg Ser Asn
290 295 300

Ser Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe
305 310 315 320

Met Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp
325 330 335

Phe Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala
340 345 350

Phe Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp

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        355                 360                 365

Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu
    370                 375                 380

Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
385                 390                 395                 400


<210> SEQ ID NO 63
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.5
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (178)..(375)

<400> SEQUENCE: 63

atgcgcagaa acactgggca caggggggagg taactgcagt aagtcccgct tggccctgga     60

gtccacgcgg attttcgaag ctggggctgg caagaggccg ctggacacca cgctccagtc    120

gtcagcccac ttcctagctg aacagcgcga ggcggcggca gcgagccggg tcccacc       177

atg gcc gcg aat cca aaa cct gga agc tgt caa gat acc cat cca ctg      225
Met Ala Ala Asn Pro Lys Pro Gly Ser Cys Gln Asp Thr His Pro Leu
1               5                   10                  15

acg aat gat tca gca cac tgt ggt ata gtc ata aat gga ata cta ctc      273
Thr Asn Asp Ser Ala His Cys Gly Ile Val Ile Asn Gly Ile Leu Leu
            20                  25                  30

agc cat gaa aag gaa caa att cct gat aaa cac cac aac atg aat gaa      321
Ser His Glu Lys Glu Gln Ile Pro Asp Lys His His Asn Met Asn Glu
        35                  40                  45

ttg caa aag cag tgc tct gag tcc aag aag ctg ggc aga aag gag ttg      369
Leu Gln Lys Gln Cys Ser Glu Ser Lys Lys Leu Gly Arg Lys Glu Leu
    50                  55                  60

gtg ccc tgattccatt tttctcaagt tgtagaagaa acaaactaat ctacgtattc       425
Val Pro
65

cagtaccagt acccggagag aacatgtcaa agttaaaacc agctcccagc caggctt       482


<210> SEQ ID NO 64
<211> LENGTH: 66
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

Met Ala Ala Asn Pro Lys Pro Gly Ser Cys Gln Asp Thr His Pro Leu
1               5                   10                  15

Thr Asn Asp Ser Ala His Cys Gly Ile Val Ile Asn Gly Ile Leu Leu
            20                  25                  30

Ser His Glu Lys Glu Gln Ile Pro Asp Lys His His Asn Met Asn Glu
        35                  40                  45

Leu Gln Lys Gln Cys Ser Glu Ser Lys Lys Leu Gly Arg Lys Glu Leu
    50                  55                  60

Val Pro
65


<210> SEQ ID NO 65
<211> LENGTH: 699
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.6
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (178)..(369)

<400> SEQUENCE: 65

atgcgcagaa acactgggca caggggggagg taactgcagt aagtcccgct tggccctgga 60

gtccacgcgg attttcgaag ctggggctgg caagaggccg ctggacacca cgctccagtc 120

gtcagcccac ttcctagctg aacagcgcga ggcggcggca gcgagccggg tcccacc 177

atg gcc gcg aat tat tcc agt acc agt acc cgg aga gaa cat gtc aaa 225
Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

gtt aaa acc agc tcc cag cca ggc ttc ctg gaa cgg ctg agc gag acc 273
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc ctg ctc tcc ttc tac 321
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

cta att ttc acc aat gag gta aaa tgt ctg ggg tct tcc tgt gca gag 369
Leu Ile Phe Thr Asn Glu Val Lys Cys Leu Gly Ser Ser Cys Ala Glu
50 55 60

tgagagtccc caccatgtca gagagcaaag gcgatgaacc cggaggctgg atttggtaat 429

caagggccta gattttaaaa agagaaagga ggatactgag ttaatcacag ttctttccat 489

tgtgatccat cccacagctg atgtgagcag gaaggggagt agatcagttc acacacctga 549

atatccaggg gttagcacct gcctcaggcg tagttggatc caggtgttca tgctgggtca 609

ccaggaatct ccatttcttc atcttttgcc tgtttttctc tattatggtg tttttcttgg 669

gcaggcactt catctgtgat ggcaaatgtg 699

<210> SEQ ID NO 66
<211> LENGTH: 64
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
20 25 30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
35 40 45

Leu Ile Phe Thr Asn Glu Val Lys Cys Leu Gly Ser Ser Cys Ala Glu
50 55 60

<210> SEQ ID NO 67
<211> LENGTH: 1861
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.7
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (178)..(474)

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<400> SEQUENCE: 67

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atgcgcagaa acactgggca caggggggagg taactgcagt aagtcccgct tggccctgga     60

gtccacgcgg attttcgaag ctggggctgg caagaggccg ctggacacca cgctccagtc    120

gtcagcccac ttcctagctg aacagcgcga ggcggcggca gcgagccggg tcccacc       177

atg gcc gcg aat tat tcc agt acc agt acc cgg aga gaa cat gtc aaa      225
Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1               5                  10                  15

gtt aaa acc agc tcc cag cca ggc ttc ctg gaa cgg ctg agc gag acc      273
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc ctg ctc tcc ttc tac      321
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

cta att ttc acc aat gag ggc cgc gca ttg aag acg gca acc tca ttg      369
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

gct gag ggg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att gcc ggc      417
Ala Glu Gly Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly
65                  70                  75                  80

ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca gcc aaa      465
Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys
                85                  90                  95

aag ttg gag tgaaaagacc ctggcacccg cccgacacct gcgtgagccc              514
Lys Leu Glu
taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg agccccggtc    574

aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc atgtgcacca    634

ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa gcagctttgg    694

tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt ccttcctctc    754

ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac gcagacacgc    814

tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct catcactgca    874

cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa gggcggccgt    934

tagtcattac tgctgagtcc tgggtcacca gcagacacac tgggcatgga cccctcaaag    994

caggcacacc caaaacacaa gtctgtggct agaacctgat gtggtgttta aaagagaaga   1054

aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac acttatctta   1114

tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta agtttttctt   1174

cgttactttg ctgcttcatg tgtactttcc taccccaaga ggaagttttc tgaaataaga   1234

tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa acacccttta   1294

gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg gtttgattga   1354

taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga tgcttttgaa   1414

acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag aaagcacttg   1474

ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta aaagattaaa   1534

gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc atggtgacgc   1594

cccgtcaacc acaatcaaga actgaggcct gaggctggtt gtacaatgcc cacgcctgcc   1654

tggctgcttt cacctgggag tgctttcgat gtgggcacct gggcttccta gggctgcttc   1714

tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa gatccaccca   1774
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cacctaagtc acagaatttc taagttcccc aactactctc acacccttt aaagataaag   1834

tatgttgtaa ccaggatgtc ttaaatg                                      1861


<210> SEQ ID NO 68
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1               5                   10                  15

Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly
65                  70                  75                  80

Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys
                85                  90                  95

Lys Leu Glu


<210> SEQ ID NO 69
<211> LENGTH: 2368
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.8
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (178)..(474)

<400> SEQUENCE: 69

atgcgcagaa acactgggca caggggggagg taactgcagt aagtcccgct tggccctgga     60

gtccacgcgg attttcgaag ctggggctgg caagaggccg ctggacacca cgctccagtc    120

gtcagcccac ttcctagctg aacagcgcga ggcggcggca gcgagccggg tcccacc       177

atg gcc gcg aat tat tcc agt acc agt acc cgg aga gaa cat gtc aaa      225
Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1               5                   10                  15

gtt aaa acc agc tcc cag cca ggc ttc ctg gaa cgg ctg agc gag acc      273
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

tcg ggt ggg atg ttt gtg ggg ctc atg gcc ttc ctg ctc tcc ttc tac      321
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

cta att ttc acc aat gag ggc cgc gca ttg aag acg gca acc tca ttg      369
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

gct gag ggg ctc ttc tac cga ccc ctg tgg gcc ctc ctc att gcc ggc      417
Ala Glu Gly Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly
65                  70                  75                  80

ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg cca gcc aaa      465
Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys
                85                  90                  95
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aag ttg gag tgaaaagacc ctggcacccg cccgacacct gcgtgagccc 514
Lys Leu Glu
taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg agccccggtc 574

aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc atgtgcacca 634

ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa gcagctttgg 694

tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt ccttcctctc 754

ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac gcagacacgc 814

tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct catcactgca 874

cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa gggcggccgt 934

tagtcattac tgctgagtcc tgggtcacca gcagacacac tgggcatgga cccctcaaag 994

caggcacacc caaaacacaa gtctgtggct agaacctgat gtggtgttta aaagagaaga 1054

aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac acttatctta 1114

tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta agtttttctt 1174

cgttactttg ctgcttcatg tgtactttcc taccccaaga ggaagttttc tgaaataaga 1234

tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa acacccttta 1294

gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg gtttgattga 1354

taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga tgcttttgaa 1414

acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag aaagcacttg 1474

ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta aaagattaaa 1534

gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc atggtgacgc 1594

cccgtcaacc acaatcaaga actgaggcct gaggctggtt gtacaatgcc cacgcctgcc 1654

tggctgcttt cacctgggag tgctttcgat gtgggcacct gggcttccta gggctgcttc 1714

tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa gatccaccca 1774

cacctaagtc acagaatttc taagttcccc aactactctc acacccttttt aaagataaag 1834

tatgttgtaa ccaggatgtc ttaaatgatt ctttgtgtac cttttctgtc atattcagaa 1894

accgttttgt gcctgctggg agtaattcct ttagcaatta agtatttggt agctgaataa 1954

ggggtcagaa cttctgaaac cagagatctg taatcatctc tattggcctg gggtgcctgt 2014

gctataaatg agtttcttca catgaaaaac acagccagcc caagatgact tatctgggtt 2074

taggattcaa tagtattcac taactgctta ttacatgagc aatttcatca aatctccaaa 2134

ctcttaaagg atgctttcgg aaaacacgct gtatacctag atgatgacta aatgcaaaat 2194

ccttgggctt tggtttttttt ctagtaagga ttttaaataa ctgccgactt caaaagtgtt 2254

cttaaaacga aagataatgt taagaaaaat ttgaaagctt tggaaaacca aatttgtaat 2314

atcattgtat tttttattaa aagttttgta ataaatttct aaattatctt ctgg 2368

<210> SEQ ID NO 70
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

Met Ala Ala Asn Tyr Ser Ser Thr Ser Thr Arg Arg Glu His Val Lys
1 5 10 15

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Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
            20                  25                  30

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
        35                  40                  45

Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
    50                  55                  60

Ala Glu Gly Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly
65                  70                  75                  80

Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys
                85                  90                  95

Lys Leu Glu


<210> SEQ ID NO 71
<211> LENGTH: 2718
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.9
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1047)..(1331)

<400> SEQUENCE: 71

atgtaggaag ctggccaggc atgactgcag gcaatcgttg taggcagagc aaacccacgc     60

gcagatacac aggcgagagg acacttgacc tggactgggg acagcagcca gcagggtcag    120

ggcactggca gcagggtcgg tgtccggggg gtgtggcagg gctctggcag gtgactgtgt    180

ggagaacaca gagtgggtga tagaagcagg gccagtgagg ctcctgcggg cagacagtgg    240

taagagactc gggaatatgt ggcctggact ggatggggtg gtaggggagg agcgagccat    300

gtctttccca tagatgtgag tgggtgggtg ggtgtgccat gtgctgagat ggagaaggcg    360

ccagtgtcag cactagacag gctgagatgt caagtggaaa tgtcaaggag gtggtggagg    420

tggtgggagc tgcagggctg tgaggcccgg gagagggcca gagctgcagc tttaaattgg    480

agggtcacgg catgtggagg ccaaggaagc agatgggatg tccggggaga gagtatggac    540

tgaagcagct aaagaattgc agcatctaat ggacaggaag aggggcagcg acagcgatgg    600

agcctgagaa ggagggtgca gtgtccccaa gccatgtgga gaggttctga gattaaacag    660

atcacacaca tagcgcagag catgctgccc agcagacatc ctccaacctg ctcaggggtg    720

gtgggcaggg tcctgctcat tccaggtgag accgtgggct gagggctcca ggtgctggca    780

ggctctgagc tgaggaaggc ccgtacgttc cacagagatc tcatgccttg ccctgtgctc    840

tgccagatgg gcagaaggac ttagccctat aggaggcttg cccccactcc gtctggcctg    900

ttcagaaatg gccaacagct cccgagttgg tacagccccc tcaggacctg ccctgccgac    960

tgggtacgcc actggccctc agcatcctga cctgccccca ccttgtcctg caggaggtgt   1020

ttcatagaga actaaggagc aactcc atg aag acc tgg ggc ctg cgg gca gct    1073

Met Lys Thr Trp Gly Leu Arg Ala Ala
1               5

ggc tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc     1121
Gly Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu
10                  15                  20                  25

tac acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att     1169
Tyr Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile
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               30                  35                  40

ggc ctg aaa gcc ttt gcc ttc tgt gtg gcc acc tcg ctg acc ctg ctg     1217
Gly Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu
            45                  50                  55

acc gtg gcg gct ggc tgg ctc ttc tac cga ccc ctg tgg gcc ctc ctc     1265
Thr Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu
        60                  65                  70

att gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg     1313
Ile Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val
    75                  80                  85

cca gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct            1361
Pro Ala Lys Lys Leu Glu
90                  95

gcgtgagccc taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg   1421

agccccggtc aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc   1481

atgtgcacca ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa   1541

gcagctttgg tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt   1601

ccttcctctc ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac   1661

gcagacacgc tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct   1721

catcactgca cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa   1781

gggcggccgt tagtcattac tgctgagtcc tgggtcacca gcagacacac tgggcatgga   1841

cccctcaaag caggcacacc caaaacacaa gtctgtggct agaacctgat gtggtgttta   1901

aaagagaaga aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac   1961

acttatctta tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta   2021

agtttttctt cgttactttg ctgcttcatg tgtactttcc taccccaaga ggaagttttc   2081

tgaaataaga tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa   2141

acacccttta gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg   2201

gtttgattga taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga   2261

tgcttttgaa acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag   2321

aaagcacttg ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta   2381

aaagattaaa gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc   2441

atggtgacgc cccgtcaacc acaatcaaga actgaggcct gaggctggtt gtacaatgcc   2501

cacgcctgcc tggctgcttt cacctgggag tgctttcgat gtgggcacct gggcttccta   2561

gggctgcttc tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa   2621

gatccaccca cacctaagtc acagaatttc taagttcccc aactactctc acacccttt   2681

aaagataaag tatgttgtaa ccaggatgtc ttaaatg                           2718


<210> SEQ ID NO 72
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

Met Lys Thr Trp Gly Leu Arg Ala Ala Gly Trp Met Ala Met Phe Met
1               5                  10                  15

Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp Phe
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           20                  25                  30

Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala Phe
        35                  40                  45

Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp Leu
    50                  55                  60

Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu Val
65                  70                  75                  80

Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
                85                  90                  95


<210> SEQ ID NO 73
<211> LENGTH: 2718
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: H3C1779.10
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1047)..(1331)

<400> SEQUENCE: 73

atgtaggaag ctggccaggc atgactgcag gcaatcgttg taggcagagc aaacccacgc     60

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ggcactggca gcagggtcgg tgtccggggg gtgtggcagg gctctggcag gtgactgtgt    180

ggagaacaca gagtgggtga tagaagcagg gccagtgagg ctcctgcggg cagacagtgg    240

taagagactc gggaatatgt ggcctggact ggatggggtg gtaggggagg agcgagccat    300

gtctttccca tagatgtgag tgggtgggtg ggtgtgccat gtgctgagat ggagaaggcg    360

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agcctgagaa ggagggtgca gtgtccccaa gccatgtgga gaggttctga gattaaacag    660

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gtgggcaggg tcctgctcat tccaggtgag accgtgggct gagggctcca ggtgctggca    780

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tgccagatgg gcagaaggac ttagccctat aggaggcttg cccccactcc gtctggcctg    900

ttcagaaatg gccaacagct cccgagttgg tacagccccc tcaggacctg ccctgccgac    960

tgggtacgcc actggccctc agcatcctga cctgccccca ccttgtcctg caggaggtgt   1020

ttcatagaga actaaggagc aactcc atg aag acc tgg ggc ctg cgg gca gct    1073

Met Lys Thr Trp Gly Leu Arg Ala Ala
1               5

ggc tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc     1121
Gly Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu
10                  15                  20                  25

tac acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att     1169
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Thr Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu
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Ile Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val
    75                  80                  85

cca gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct            1361
Pro Ala Lys Lys Leu Glu
90                  95

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atgtgcacca ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa   1541

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gcagacacgc tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct   1721

catcactgca cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa   1781

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acacccttta gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg   2201

gtttgattga taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga   2261

tgcttttgaa acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag   2321

aaagcacttg ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta   2381

aaagattaaa gaaacgatta agagaaaagg ttggaagctt tatactaaat gggctccttc   2441

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gggctgcttc tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa   2621

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<210> SEQ ID NO 74
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

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Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala Phe
```

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Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp Leu
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Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu Val
65                  70                  75                  80

Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
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<210> SEQ ID NO 75
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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tgccagatgg gcagaaggac ttagccctat aggaggcttg cccccactcc gtctggcctg    900

ttcagaaatg gccaacagct cccgagttgg tacagccccc tcaggacctg ccctgccgac    960

tgggtacgcc actggccctc agcatcctga cctgccccca ccttgtcctg caggaggtgt   1020

ttcatagaga actaaggagc aactcc atg aag acc tgg ggc ctg cgg gca gct    1073

Met Lys Thr Trp Gly Leu Arg Ala Ala
1               5

ggc tgg atg gcc atg ttc atg ggc ctc aac ctt atg aca cgg atc ctc     1121
Gly Trp Met Ala Met Phe Met Gly Leu Asn Leu Met Thr Arg Ile Leu
10                  15                  20                  25

tac acc ttg gtg gac tgg ttt cct gtt ttc cga gac ctg gtc aac att     1169
Tyr Thr Leu Val Asp Trp Phe Pro Val Phe Arg Asp Leu Val Asn Ile
                30                  35                  40

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Gly Leu Lys Ala Phe Ala Phe Cys Val Ala Thr Ser Leu Thr Leu Leu
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Thr Val Ala Ala Gly Trp Leu Phe Tyr Arg Pro Leu Trp Ala Leu Leu
        60                  65                  70

att gcc ggc ctg gcc ctt gtg ccc atc ctt gtt gct cgg aca cgg gtg     1313
Ile Ala Gly Leu Ala Leu Val Pro Ile Leu Val Ala Arg Thr Arg Val
    75                  80                  85

cca gcc aaa aag ttg gag tgaaaagacc ctggcacccg cccgacacct            1361
Pro Ala Lys Lys Leu Glu
90                  95

gcgtgagccc taggatccag gtcctctctc acctctgacc cagctccatg ccagagcagg   1421

agccccggtc aattttggac tctgcactcc ctctcctctt caggggccag acttggcagc   1481

atgtgcacca ggttggtgtt caccagctca tgtcttcccc acatctcttc ttgccagtaa   1541

gcagctttgg tgggcagcag cagctcatga atggcaagct gacagcttct cctgctgttt   1601

ccttcctctc ttggactgag tgggtacggc cagccactca gcccattggc agctgacaac   1661

gcagacacgc tctacggagg cctgctgata aagggctcag ccttgccgtg tgctgcttct   1721

catcactgca cacaagtgcc atgctttgcc accaccacca agcacatctg tgatcctgaa   1781

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aaagagaaga aacactgaag atgtcctgag gagaaaagct ggacatatac tgggcttcac   1961

acttatctta tggcttggca gaatctttgt agtgtgtggg atctctgaag gccctattta   2021

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tgaaataaga tttaaaaaca aaacaaaaaa aacacttaat atttcagact gttacaggaa   2141

acacccttta gtctgtcagt tgaattcaga gcactgaaag gtgttaaatt ggggtatgtg   2201

gtttgattga taaaaagtta cctctcagta ttttgtgtca ctgagaagct ttacaatgga   2261

tgcttttgaa acaagtatca gcaaaaggat ttgttttcac tctgggagga gagggtggag   2321

aaagcacttg ctttcatcct ctggcatcgg aaactcccct atgcacttga agatggttta   2381

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gggctgcttc tgagtggttc tttcacgtgt tgtgtccata gctttagtct tcctaaataa   2621

gatccaccca cacctaagtc acagaatttc taagttcccc aactactctc acacccttt    2681

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gggtgcctgt gctataaatg agtttcttca catgaaaaac acagccagcc caagatgact   2921

tatctgggtt taggattcaa tagtattcac taactgctta ttacatgagc aatttcatca   2981

aatctccaaa ctcttaaagg atgctttcgg aaaacacgct gtatacctag atgatgacta   3041

aatgcaaaat ccttgggctt tggttttttt ctagtaagga ttttaaataa ctgccgactt   3101

caaaagtgtt cttaaaacga aagataatgt taagaaaaat ttgaaagctt tggaaaacca   3161

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ctgg                                                                3225
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<210> SEQ ID NO 76
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

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Gly Leu Asn Leu Met Thr Arg Ile Leu Tyr Thr Leu Val Asp Trp Phe
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Pro Val Phe Arg Asp Leu Val Asn Ile Gly Leu Lys Ala Phe Ala Phe
35 40 45

Cys Val Ala Thr Ser Leu Thr Leu Leu Thr Val Ala Ala Gly Trp Leu
50 55 60

Phe Tyr Arg Pro Leu Trp Ala Leu Leu Ile Ala Gly Leu Ala Leu Val
65 70 75 80

Pro Ile Leu Val Ala Arg Thr Arg Val Pro Ala Lys Lys Leu Glu
85 90 95

1. A method of screening for, diagnosing and/or detecting an increased risk of developing arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) in a subject comprising detecting a presence of a transmembrane protein 43 (TMEM43) disease associated variant in a sample of the subject, wherein the presence of the TMEM43 disease variant is indicative that the subject has ARVD/C or an increased risk of developing ARVD/C.

2. The method of claim **1** wherein the TMEM43 disease associated variant comprises a modification selected from a gene mutation, a germline mutation, a sporadic mutation, a deletion mutation, a missense mutation, a point mutation, a coding mutation and an amino acid mutation.

3. The method of claim **1** wherein the TMEM43 disease associated variant comprises mutation/alteration of a nucleotide corresponding to genome position 14158166.

4. The method of claim **2** wherein the TMEM43 disease associated variant comprises 14158166C>T.

5. The method of claim **1** wherein the TMEM43 disease associated variant comprises mutation/alteration of a nucleotide corresponding to position 1073 in a TMEM43 transcript.

6. The method of claim **1** wherein the TMEM43 disease associated variant comprises 1073C>T.

7. The method of claim **1** wherein the TMEM43 disease associated variant comprises mutation of the amino acid corresponding to position 358 of TMEM43 polypeptide.

8. The method of claim **1** wherein the TMEM43 disease associated variant S358L.

9. The method of claim **1** wherein the sample comprises blood, a white blood cell, cardiac tissue, a cardiac cell and/or a nucleated cell.

10. The method of claim **1** wherein the subject is presymptomatic.

11. The method of claim **1** wherein the subject has at least one blood relation with ARVD/C.

12. A composition comprising at least one isolated nucleic acid sequence; wherein at least one isolated nucleic acid sequence hybridizes to:

a. a RNA product of TMEM43 disease associated variant; and/or

b. a nucleic acid complementary to a); and/or

c. a nucleic acid corresponding to a);

wherein the composition is used to detect a TMEM43 disease associated variant.

13. The composition of claim **12** wherein at least one isolated nucleic acid is useful for amplifying a TMEM43 disease associated variant.

14. The composition of claim **12** wherein at least one isolated nucleic acid comprises a probe that specifically hybridizes to a disease associated variant.

15. The composition of claim **12** comprising one or more isolated nucleic acids selected from SEQ ID NOS: 15-54.

16. The method of claim **15** wherein the TMEM43 disease associated variant is detected by one or more of genotyping, using a probe that hybridizes a TMEM43 disease associated variant and/or wildtype TMEM43, PCR, RT-PCR, NASBA, using a binding agent, or microarray.

17. A kit for screening for, diagnosing or detecting an increased risk of developing arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) comprising:

a. a TMEM43 disease associated variant detection agent; and

b. instructions for use.

18. The kit of claim **17** wherein the detection agent comprises an isolated nucleic acid, a probe, primer, a genotyping primer and/or an antibody.

19. A method of identifying TMEM43 disease associated variants comprising determining whether there is a germline alteration in the sequence of TMEM43 gene or a TMEM43 gene regulatory sequence in a sample of a subject, wherein the subject has ARVD/C.

20. A method of identifying substances which bind a TMEM43 disease associated variant comprising:

a. contacting a TMEM43 disease associated variant with a test substance, under conditions which allow for forma-

tion of a complex between the TMEM43 disease associated variant and the test substance, and

b. detecting for complexes between TMEM43 disease associated variant and the test substance;

c. wherein the presence of complexes indicates that the test substance binds the TMEM43 disease associated variant.

21. A method of treatment for subjects with ARVD/C and/or a risk of developing ARVD/C comprising:

a) detecting a TMEM43 disease associated variant according to a claim **1**;

b) providing ICD therapy for a subject having the TMEM43 disease associated variant.

* * * * *

专利名称(译)	心肌病的诊断试验		
公开(公告)号	US20090291856A1	公开(公告)日	2009-11-26
申请号	US12/339877	申请日	2008-12-19
申请(专利权)人(译)	GENESIS GROUP INC.		
当前申请(专利权)人(译)	纽芬兰纪念大学		
[标]发明人	HAYWOOD ANNIKA MERNER NANCY FRENCH VANESSA YOUNG TERRY LYNN HODGKINSON KATHY CONNORS SEAN PARFREY PATRICK		
发明人	HAYWOOD, ANNIKA MERNER, NANCY FRENCH, VANESSA YOUNG, TERRY-LYNN HODGKINSON, KATHY CONNORS, SEAN PARFREY, PATRICK		
IPC分类号	C40B30/04 C12Q1/00 C12Q1/68 C07H21/04 G01N33/53 G01N33/566		
CPC分类号	C12Q1/6883 G01N33/6893 G01N2800/325 G01N33/6887 C12Q2600/106 C12Q2600/156 C12Q2600/172 G01N2800/326		
优先权	61/016226 2007-12-21 US		
其他公开文献	US8409799		
外部链接	Espacenet USPTO		

摘要(译)

描述了与诊断和治疗心肌病相关的方法和组合物，特别涉及用于诊断和治疗致心律失常性右心室发育不良/心肌病（ARVD / C）的方法和组合物。提供了用于筛选，诊断或检测发生致心律失常性右心室发育不良/心肌病（ARVD / C）的风险的方法，包括检测受试者样品中跨膜蛋白43（TMEM43）疾病相关变体的存在，其中存在与具有野生型TMEM43的个体相比，TMEM43疾病变体的TM表示受试者具有ARVD / C或发展ARVD / C的风险增加。