

Online Appendix for the following *JACC* article

TITLE: *SCN5A* Mutations Associate With Arrhythmic Dilated Cardiomyopathy and Commonly Localize to the Voltage-Sensing Mechanism

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APPENDIX

Table 1. Conservation Analysis of Residues T220, R222 of Domain I, S4, and R814 of Domain II, S4*

Protein	NCBI Identifier	Location	S4 Sequence
KHACN4	Q9Y3Q4	S4	T K I L S L L R L L R L S R L I R Y I H
BCNG1	O60741	S4	T K I L S L L R L L R L S R L I R Y I H
BCNG2	Q9UL51	S4	T K I L S L L R L L R L S R L I R Y I H Q
Kv11.1	Q12809	S4	L L K T A R L R L V R V A R K L D R Y Y
Kv11.2	Q9H252	S4	L L K T A R L R L V R V A R K L D R Y Y
KvH2C	NP_742054	S4	L L K T A R L R L V R V A R K L D R Y Y
Kv10.1	O95259	S4	S L K V V R L L R L G R V A R K L D H Y
Kv10.2	Q8NCM5	S4	S L K V V R L L R L G R V A R K L D H Y L
SCN11A	Q9UI33	Domain IV, S4	F R I V R L A R I G R I L R L V R A A R
SCN10A	Q9Y5Y9	Domain IV, S4	F R V I R L A R I G R I L R L I R A A K
SCN4A	P35499	Domain IV, S4	F R V I R L A R I G R V L R L I R G A K
SCN5A	Q14524	Domain IV, S4	F R V I R L A R I G R I L R L I R G A K
SCN1A	P35498	Domain IV, S4	F R V I R L A R I G R I L R L I K G A K
SCN2A	Q99250	Domain IV, S4	F R V I R L A R I G R I L R L I K G A K
SCN3A	Q9NY46	Domain IV, S4	F R V I R L A R I G R I L R L I K G A K
SCN8A	Q9UQD0	Domain IV, S4	F R V I R L A R I G R I L R L I K G A K
SCN9A	Q15858	Domain IV, S4	F R V I R L A R I G R I L R L V K G A K
CACNA1G	O43497	Domain III, S4	L R V L R L L R T L R P L R V I S R A Q
CACNA1I	Q9P0X4	Domain III, S4	L R V L R L L R T L R P L R V I S R A P
CACNA1S	Q13698	Domain III, S4	V K I L R V L R V L R P L R A I N R A K
CACNA1C	Q13936	Domain III, S4	V K I L R V L R V L R P L R A I N R A K
CACNA1G	O43497	Domain I, S4	F S A V R T V R V L R P L R A I N R V P
CACNA1S	Q13698	Domain I, S4	V K A L R A F R V L R P L R L V S G V P
CACNA1C	Q13936	Domain I, S4	V K A L R A F R V L R P L R L V S G V P
CACNA1I	Q9P0X4	Domain I, S4	L S A I R T V R V L R P L K A I N R V P
CACNA1A	O00555	Domain I, S4	L R T L R A V R V L R P L K L V S G I P
CACNA1E	NP_000712	Domain I, S4	L R T L R A V R V L R P L K L V S G I P
SCN1A	P35498	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN5A	Q14524	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN2A	Q99250	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN3A	Q9NY46	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN4A	P35499	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN8A	Q9UQD0	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN9A	Q15858	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN10A	Q9Y5Y9	Domain III, S4	L R T L R A L R P L R A L S R F E G M R
SCN11A	Q9UI33	Domain III, S4	F T R L R A L R P L R A L S Q F E G M K
CACNA1A	O00555	Domain III, S4	I K S L R V L R V L R P L K T I K R L P
CACNA1E	NP_000712	Domain III, S4	I K S L R V L R V L R P L K T I K R L P
SCN7A	Q01118	Domain I, S4	T L Q T A R T L R I L K I I P L N Q G L
SCN1A	P35498	Domain I, S4	A L R T F R V L R A L K T I S V I P G L
SCN2A	Q99250	Domain I, S4	A L R T F R V L R A L K T I S V I P G L
SCN3A	Q9NY46	Domain I, S4	A L R T F R V L R A L K T I S V I P G L
SCN4A	P35499	Domain I, S4	A L R T F R V L R A L K T I T V I P G L
SCN5A	Q14524	Domain I, S4	A L R T F R V L R A L K T I S V I S G L
SCN8A	Q9UQD0	Domain I, S4	A L R T F R V L R A L K T I S V I P G I
SCN9A	Q15858	Domain I, S4	A L R T F R V L R A L K T I S V I P G L
SCN10A	Q9Y5Y9	Domain I, S4	G L R T F R V L R A L K T V S V I P G L
SCN11A	Q9UI33	Domain I, S4	P L R T F R V F R A L K A I S V V S R L
SCN11A	Q9UI33	Domain II, S4	F L R S F R V L R V F K L A K S W P T L
SCN5A	Q14524	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN1A	P35498	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN2A	Q99250	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN3A	Q9NY46	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN4A	P35499	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN7A	Q01118	Domain II, S4	L L R L F R M L R I F K L G K Y W P T F
SCN8A	Q9UQD0	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN9A	Q15858	Domain II, S4	V L R S F R L L R V F K L A K S W P T L
SCN10A	Q9Y5Y9	Domain II, S4	V L R S F R L L R V F K L A K S W P T L

Table 1, continued

Protein	NCBI Identifier	Location		S4 Sequence																						
CACNA1A	O00555	Domain II, S4	579	I	S	V	L	R	A	L	R	L	L	R	I	F	K	V	T	K	Y	W	A			
CACNA1E	NP_000712	Domain II, S4	568	I	S	V	L	R	A	L	R	L	L	R	I	F	K	I	T	K	Y	W	A			
CACNA1S	Q13698	Domain II, S4	524	I	S	V	L	R	C	I	R	L	L	R	I	F	K	I	T	K	Y	W	T			
CACNA1C	Q13936	Domain II, S4	616	I	S	V	L	R	C	V	R	L	L	R	I	F	K	I	T	R	Y	W	N			
Kv1.2	NP_000710.4	S4	293	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.1	NP_000208	S4	291	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.3	NP_002223	S4	311	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.5	NP_002225	S4	398	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.6	NP_002226	S4	340	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.7	NP_114092	S4	276	I	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S			
Kv1.10	NP_005540	S4	334	I	L	R	I	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S			
Kv1.4	P15385	S4	445	L	R	I	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
Kv1.4	NP_002224	S4	443	L	R	I	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S				
KvSHAL3-2	NP_751948	S4	286	F	V	T	L	R	V	F	R	V	F	R	I	F	K	F	S	R	H	S				
KvSHAL3-1	NP_004971	S4	286	F	V	T	L	R	V	F	R	V	F	R	I	F	K	F	S	R	H	S				
KvSHAL2	NP_036413	S4	293	F	V	T	L	R	V	F	R	V	F	R	I	F	K	F	S	R	H	S				
KvSHAL1	AAH45659	S4	289	S	G	A	F	V	T	L	R	V	F	R	I	F	K	L	S	R	H	S				
Kv3.4	Q03721	S4	345	L	R	V	V	R	F	V	R	I	L	R	I	F	K	L	T	R	H	F				
KvDRect	NP_002243	S4	291	I	L	R	L	M	R	I	F	R	I	L	K	L	A	R	H	S						
KvG3-1	AAH71558	S4	288	L	R	V	L	R	M	M	R	I	F	W	V	I	K	L	A	R	H	F				
CACNA1I	Q9P0X4	Domain II, S4	727	L	S	V	L	R	T	F	R	L	L	R	V	L	K	L	V	R	F	M	P			
CACNA1G	O43497	Domain II, S4	833	L	S	V	L	R	T	F	R	L	M	R	V	L	K	L	V	R	F	L	P			
CACNA1C	Q13936	Domain IV, S4	1373	I	T	F	F	R	L	F	R	V	M	R	L	V	K	L	L	S	R	G	E			
CACNA1G	O43497	Domain IV, S4	1708	I	R	I	M	M	R	V	L	R	I	A	R	V	L	K	L	L	K	M	A	V		
CACNA1I	Q9P0X4	Domain IV, S4	1584	I	R	I	M	M	R	V	L	R	I	A	R	V	L	K	L	L	K	M	A	T		
CACNA1A	O00555	Domain IV, S4	1657	L	S	F	L	R	L	F	R	A	A	R	L	I	K	L	L	R	Q	G	Y			
CACNA1E	NP_000712	Domain IV, S4	1572	M	S	F	L	K	L	F	R	A	A	R	L	I	K	L	L	R	Q	G	Y			
KvSHAL1	AAH46629	S4	342	V	L	R	V	L	R	A	L	R	I	L	Y	V	M	R	L	A	R	H	S			
Kv7.1	P51787	S4	228	R	G	I	R	F	L	Q	I	L	R	M	L	H	V	D	R	Q	G	G	T	W	K	
Kv7.2	O88943	S4	198	R	S	L	R	F	L	Q	I	L	R	M	I	R	M	D	R	R	G	G	T	W	K	
Kv7.4	P56696	S4	202	R	S	M	R	F	L	Q	I	L	R	M	V	R	M	D	R	R	G	G	T	W	F	I
TRPM1	NP_002411	S4	848	G	R	V	I	Y	C	V	D	I	I	F	W	Y	I	R	V	L	D	I	F	T	V	
TRPM2	O94759	S4	897	G	R	V	I	Y	C	V	D	I	L	F	C	L	R	L	M	H	I	F	G	V		
TRPM3	NP_002411	S4	996	G	R	V	I	Y	C	V	N	I	I	Y	W	Y	I	R	L	L	D	I	F	T	I	
TRPM4	NP_060106	S4	893	G	R	T	V	L	C	I	D	F	M	V	F	T	V	R	L	L	H	I	F	A	V	
TRPM5	NP_055370	S4	833	G	R	T	V	L	A	M	D	F	M	V	F	T	L	R	L	I	H	I	F	A	V	
TRPM6	Q9BX84	S4	940	G	R	L	I	Y	C	I	D	I	I	F	W	F	S	R	L	L	D	F	L	A	V	
TRPM7	Q96QT4	S4	963	G	R	L	I	Y	C	L	N	I	I	F	W	Y	V	R	L	L	D	F	F	T		
TRPM8	Q7Z2W7	S4	830	G	R	V	I	F	C	L	D	Y	I	I	F	T	L	R	L	I	H	I				

*BLAST alignments of S4 transmembrane segments among homologous proteins

demonstrate sequence conservation of positions T220, R222, and R814 in *SCN5A*.

Relevant residues and segments of human *SCN5A* are in bold typeface and bracketed for easier identification. Colors were randomly selected and assigned to different amino acids to facilitate alignment.

Table 2. Conservation Analysis of SCN5A Residues E446 and F1520*

Species	Protein	NCBI Identifier	E446 Conservation										F1520 Conservation													
Human	SCN5A	Q14524	441	L	K	K	E	H	E	A	L	T	I	R	1515	N	K	Y	Q	G	F	I	F	D	I	V
Mus Musculus	SCN5A	84875498	441	L	K	K	E	H	E	A	L	T	I	R	1518	N	K	Y	Q	G	F	I	F	D	I	V
Canis Lupus	SCN5A	50950233	441	L	K	K	E	H	E	A	L	T	I	R	1512	N	K	Y	Q	G	F	L	F	D	I	V
Bos Taurus	SCN5A	27806135	444	L	K	K	E	Q	E	A	L	A	I	R	1520	N	K	Y	Q	G	F	I	F	D	I	V
Gallus Gallus	SCN5A	118085545	439	L	K	K	E	Q	E	A	L	A	A	K	1539	N	K	Y	Q	G	F	I	F	D	V	V
Pan Troglodytes	SCN5A	114586083	441	L	K	K	E	H	E	A	L	T	I	R	1515	N	K	Y	Q	G	F	I	F	D	I	V
Canis familiaris	SCN5A	29691680	442	L	K	K	E	H	E	A	L	T	I	R	1512	N	K	Y	Q	G	F	L	F	D	I	V
Rattus norvegicus	SCN5A	P15389.1	441	L	K	K	E	H	E	A	L	T	I	R	1517	N	K	Y	Q	G	F	I	F	D	I	V
Human	SCN1A	P35498	451	L	K	K	Q	Q	E	A	A	Q	Q	A	1528	N	K	F	Q	G	M	V	F	D	F	V
Human	SCN2A	Q99250	452	L	K	K	Q	Q	E	E	A	Q	A	A	1518	N	K	F	Q	G	M	V	F	D	F	V
Human	SCN3A	Q9NY46	451	L	K	K	Q	Q	E	E	A	Q	A	V	1513	N	K	F	Q	G	M	V	F	D	F	V
Human	SCN4A	P35499	472	F	K	K	H	Q	E	E	L	E	K	A	1340	N	K	I	Q	G	M	V	Y	D	L	V
Human	SCN7A	Q01118	422	L	Q	E	G	N	E	T	D	E	A	K	1238	N	K	L	Q	G	F	I	F	D	V	V
Human	SCN8A	Q9UQD0	439	L	K	K	Q	Q	E	E	A	Q	A	A	1509	N	K	I	Q	G	I	V	F	D	F	V
Human	SCN9A	Q15858	430	L	K	K	E	Q	E	E	A	E	A	I	1502	N	K	I	Q	G	C	I	F	D	L	V
Human	SCN10A	Q9Y5Y9	426	L	R	K	E	Q	E	V	L	A	A	L	1463	N	K	F	Q	G	F	V	F	D	I	V
Human	SCN11A	Q9UI33	428	L	K	E	E	K	E	A	L	V	A	M	1353	N	K	C	Q	G	L	V	F	D	I	V
Human	CAC1A	O00555	396	I	S	K	A	E	E	V	I	L	A	E	Poor Alignment / No Conservation											
Human	CAC1B	Q00975	392	I	F	K	A	E	E	V	M	L	A	E	Poor Alignment / No Conservation											
Human	CAC1C	Q13936	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1D	Q01668	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1E	Q15878	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1F	O60840	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1G	O43497.3	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1H	O95180	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1I	Q9P0X4.1	No alignment at this position										Poor Alignment / No Conservation													
Human	CAC1S	Q13698	No alignment at this position										405	N	K	I	I	Q	F	I	R	H	W	R		

*BLAST alignments of sequence immediately adjoining novel mutation sites E446 and F1520 in *SCN5A* demonstrate conservation among homologous, orthologous, and paralogous proteins. Pertinent positions within alignments are in boldface and bracketed for easier comparison.

Table 3, continued

Protein	NCBI Identifier	Location	S3 Segment																					
SCN2A	Q99250	Domain I, S3	190	P	W	N	W	L	D	F	T	V	I	T	F	A	Y	V	T	E	F	V	D	
SCN3A	Q9NY46	Domain I, S3	189	P	W	N	W	L	D	F	S	V	I	V	M	A	Y	V	T	E	F	V	S	
SCN4A	P35499	Domain I, S3	191	P	W	N	W	L	D	F	S	V	I	M	M	A	Y	L	T	E	F	V	D	
SCN7A	Q01118	Domain I, S3	180	P	W	N	W	L	D	F	S	V	T	V	F	E	V	I	I	R	Y	S	P	
SCN8A	Q9UQD0	Domain I, S3	193	P	W	N	W	L	D	F	S	V	I	M	M	A	Y	I	T	E	F	V	N	
SCN9A	Q15858	Domain I, S3	187	P	W	N	W	L	D	F	V	V	I	V	F	A	Y	L	T	E	F	V	N	
SCN10A	Q9Y5Y9	Domain I, S3	188	P	W	N	W	L	D	F	S	V	I	T	L	A	Y	V	G	T	A	I	D	
SCN11A	Q9UI33	Domain I, S3	193	P	W	N	W	L	D	S	I	V	I	G	I	A	I	V	S	Y	I	P	G	
CACNA1S	Q13698	Domain IV, S3	1181	P	W	N	V	F	D	F	L	I	V	I	G	S	I	I	D	V	I	L	S	
CACNA1C	Q13936	Domain IV, S3	1302	P	W	N	V	F	D	F	L	I	V	I	G	S	I	I	D	V	I	L	S	
TRPC3	Q13507	S3	468	L	W	N	V	L	D	F	G	M	L	S	I	F	I	A	A	F	T	A	R	F
CACNA1A	O00555	Domain III, S3	1312	L	W	N	V	L	I	L	D	F	V	V	S	G	A	L	V	A	F	A	F	T
CACNA1E	NP_000712	Domain III, S3	1221	L	W	N	V	L	I	L	D	F	V	V	V	G	A	L	V	A	F	A	L	N
CACNA1G	O43497	Domain III, S3	1345	S	W	N	V	L	D	G	L	L	V	L	I	S	V	I	D	I	L	V	S	
CACNA1I	Q9P0X4	Domain III, S3	1245	S	W	N	V	L	D	G	F	L	V	F	V	S	I	I	D	I	V	V	S	
SCN5A	Q14524	Domain IV, S3	1590	S	W	N	I	F	D	F	V	V	V	I	L	S	I	V	G	T	V	L		
CACNA1A	O00555	Domain IV, S3	1629	A	W	N	I	F	D	F	V	T	V	L	G	S	I	T	D	I	L	V	T	
SCN7A	Q01118	Domain IV, S3	1312	A	W	N	I	F	D	F	M	V	V	I	F	S	I	T	G	L	C	L		
SCN5A	Q14524	Domain III, S3	1270	A	W	C	W	L	D	F	L	I	V	D	V	S	L	V	S	L	V	A	N	
SCN1A	P35498	Domain III, S3	1283	A	W	C	W	L	D	F	L	I	V	D	V	S	L	V	S	L	T	A	N	
SCN2A	Q99250	Domain III, S3	1273	A	W	C	W	L	D	F	L	I	V	D	V	S	L	V	S	L	T	A	N	
SCN3A	Q9NY46	Domain III, S3	1271	A	W	C	W	L	D	F	L	I	V	D	V	S	L	V	S	L	V	A	N	
SCN4A	P35499	Domain III, S3	1096	A	W	C	W	L	D	F	L	I	V	D	V	S	I	I	S	L	V	A	N	
SCN8A	Q9UQD0	Domain III, S3	1263	A	W	C	W	L	D	F	L	I	V	A	V	S	L	V	S	L	I	A	N	
SCN9A	Q15858	Domain III, S3	1257	A	W	C	W	L	D	F	L	I	V	D	V	S	L	V	T	L	V	A	N	
SCN10A	Q9Y5Y9	Domain III, S3	1217	A	W	C	W	L	D	F	L	I	V	N	I	S	L	I	S	L	T	A	K	
SCN11A	Q9UI33	Domain III, S3	1121	A	W	C	C	L	D	F	I	I	V	V	S	V	T	T	L	I	N	L		
KHACN4	Q9Y3Q4	S3	341	W	F	M	V	D	F	I	S	S	I	P	V	D	Y	I	F	L	I	V	E	
BCNG1	O60741	S3	220	W	F	V	V	D	F	I	S	S	I	P	V	D	Y	I	F	L	I	V	E	
BCNG2	Q9UL51	S3	289	W	F	V	V	D	F	V	S	S	I	P	V	D	Y	I	F	L	I	V	E	
Kv10.1	O95259	S3	295	W	F	V	I	D	L	L	S	C	L	P	Y	D	V	I	N	A	F	E	N	
Kv10.2	Q8NCM4	S3	292	W	F	V	I	D	L	L	S	C	L	P	Y	D	I	I	N	A	F	E	V	
Kv11.1	Q12809	S3	496	W	F	L	I	D	M	V	A	A	I	P	F	D	L	L	I	F	G	S	G	
Kv11.2	Q9H252	S3	345	W	F	L	I	D	M	V	A	A	I	P	F	D	L	L	I	F	R	T	G	
KvH2C	NP_742054	S3	157	W	F	L	I	D	M	V	A	A	I	P	F	D	L	L	I	F	G	S	G	
KvG3-1	AAH71558	S3	254	L	N	I	I	D	L	L	A	I	T	P	Y	Y	I	S	V	L	M	T	V	F
KvSHAL1	AAH46629	S3	300	L	T	L	I	D	L	V	A	I	L	P	Y	Y	I	T	L	L	V	D	G	
Kv7.1	P51787	S3	197	I	S	I	D	L	I	V	V	V	A	S	M	V	V	L	C	V	G	S	K	
Kv7.4	P56696	S3	173	F	C	V	I	D	F	I	V	F	V	A	S	V	A	V	I	A	A	G	T	
TRPC1	P48995	S3	458	L	S	F	V	M	N	S	L	Y	L	A	T	F	A	L	K	V	V	A	H	
TRPM6	Q9BX84	S3	910	W	N	L	T	E	T	V	A	I	G	L	F	S	A	G	F	V	L	R	W	
PKD2L-2	Q9NZM6	S3	315	I	W	N	W	L	E	L	L	L	L	L	C	F	V	A	V	S	F	N		

*BLAST alignments of S3 transmembrane segments among homologous proteins

demonstrate sequence conservation of positions D1275, V1279, and D1595 in SCN5A.

Relevant residues and segments of human SCN5A are in boldface and bracketed for

easier identification. Colors were randomly selected and assigned to different amino acids to facilitate alignment.