Supplementary Material

Table S1. Amino acid sequences of six voltage-gated sodium channels from *Th. sirtalis*. When two copies of exon 5 are present (fig. 1), exon 5a, which varies in sequence across paralogs, is shown.

Na$_v$1.1 (partial amino acid sequence, GenBank accession BK008860)

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MEQPVLVPPGPDSFHYFTRESLAAIEQRIAAEKAKQSKQDHKDNDENGPKPSSDLEAGKSLPFIYGDIPA
GMVATPLEDLDPFYINTKTFIVLNRGKAIFRFSATPALYILTPFNPLRKVAIKILVHSLFSMLIMCTILT
NCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKIIARGFCIDGFTFLRDPWNWLDFTVITFAYITEFVNLG
NVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRHKCLYW
NPPNATDNDTDIFNATFGENSTLNATQFDWNAYIQDENNFYFLEGQNDALLCGNSSDAGQCPEGYFCIKA
GRNPNYDYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLILAVVAM
AYDEQNQATMEEADHKEAEFQQMLEQLKKHQEGVQAAAIAAATASAESNDPSVRGGTGGHSESSSETSKL
SSKSAKERRNRRKKRKQKEQCGGEEKDEDEFHRSESEESFRRKGCRFSIEGNRLTLERKHSSPHQSLLSM
RGSLFSPRRNSRTSLFSFRGRAKDIGSENDFADDEHSTFEDNDSRRDSLFVPRRHGERRNSNISQASRSS
RMLAVFPVNGKMHSTVDCNGVVSLVGGPSVPTSPVGQLLPEVIIDKPATDDNATTTETELKKRRSSSFHI
SMDFLEDPNLRDRAMSVASILTNTMEELEESRQKCPPCWYKFANIFLIWDCCPHWLKIKHVVNIIVMDPF
VDLAITICIVLNTLFMAMEHYPMTERFAEVLNVGNLVFTGIFTGEMFLKLVAKDPYYYFQEGWNIFDGFI
VTLSLVELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGM
QLFGKSYKECVCKIAKDCELPRWHMHDFFHSFLIVFRVLCGEWIETMWDCMEVAGQAMCLTVFMMVMVIG
NLVVLNLFLALLLSSFSADNLAATDDDNEMNNLQIAMARIDKGIDFMKRKMHEFIQKSFVKKQKALDETK
PLEELHNKNTCISNHTIEICKEIDYFRDRNGTTTSGIGTGSSVGKYVVDESDYMSFINNPSLTVTVPIAV
GESDFENLNTEEFSSESDSEESKEKLNSSSSSEGSTVDIGLPAEEQAVVEPEEALEPEACFTEGCVQRFK
CCQVSVEDGRGKQWWSLRKTCFRIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFT
YIFILEMLLKWVAYGYQTYFTNAWCWLDFLIVDVSLISLTANALGYSELGAIKSLRTLRALRPLRALSRF
EGMRVVVNALLGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGNMFEVDEVANKSECESLI
LANETARWKNVKVNFDNVGFGYLSLLQVATFKGWMDIMYAAVDSRKVLEQPIYEDNLYMYIYFVIFIIFG
SFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPGNKYQGMVFDFVTQ
QVFDISIMILICLNMITMMVETDDQSKQTEDILYRINFIFIVLFTGECVLKLISLRYYYFTIGWNIFDFV
VVILSIVGMFLAEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLV
MFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFMITTSAGWDGLLAPILNSGPPDCDPKKDHPGS
SVKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFGVATEESAEPLSEDDFEMFYEVWEKFDPDAT
QFMEFEKLSEFAAALEPPLHLPKPNKV
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Na$_v$1.2 (partial amino acid sequence, GenBank accession BK008861)

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MAQSVLVPPGPDSFNFFTKESLAAIEQRIAEEKAKKSKQERKDVDDDENGPKPNSDLEAGKSLPFIYGDI
PPGMVSEPLEDLDPYYVNKKTFIVLNRGKAIFRFSATSAVYLLTPFNPLRKIAIKILVHSLFSMLIMCTI
LTNCVFMTMSNPPEWTKNVEYTFTGIYTFESLIKILARGFCLENFTFLRDPWNWLDFTVITFAYVTEFVN
LGNVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRHKCL
LWPPDNSTYTINVVSYFNSSMGENGTFVNTTVTTFNWEEYVRDDSHFYFLEGQNDALLCGNGSDAGQCPE
GYMCVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINL
ILAVVAMAYEEQNQATMEEAEQKEAEFQQMLEQLKKQQEEAQAAALAAAAGESREFSEIGGVGGFSESSS
ATSKLSSKSAKERKNRRKKRKQREQSEGDEKDDEFHKSESEDSIRRKGFRFSIEGNRLTYEKRFSSPHQS
LLSIRGSLFSPRRSSKTSLFSFRGRAKDFGSENDFADDEHSTFEDNESRRDSLFVPHRHSERRNSTISQA
SRSSRVMPILPANGKMHSTVDCNGVVSLVGGPPPLMSPTGQLLPEGTTTETELRKRRSSSYHMSMDFLSD
PTARQRAMSIASILTNTMEELEESRQKCPPCWYKFANMCLIWDCWAPWLKIKHIVNLIVMDPFVDLAITI
CIVLNTLFMAMEHYPMTQQFNNVLSVGNLVFTGIFTAEMFLKIIAKDPYYYFQEGWNIFDGIIVSLSLME
LGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNY
KECVCKISNDCELPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQPMCLTVFMMVMVIGNLVVLNL
FLALLLSSFSSDNLAATDDDNEMNNLQIAVARIQKGIDFIKRKAHECVEKAFVRKQKALDEIKPLEDLNN
KKDSCISNHVIVDIAKDFNYLKDGNGTTSGIGSSVEKYIIDESDYMSFINNPSVTVTVPIAVGESDFENL
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NTEEFSSESDLEESKEKLNASSSSEGSTVDVGLPPIGEQPEAEPEESLEPEACFTEGCIRKFKCCQVSLE
DGKGKLWWNLRKTCYKIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTVLEYADKVFTYIFILEM
LLKWVAYGFQVYFTNAWCWLDFLIVDVSIVSLTANALGYSELGAIKSLRTLRALRPLRALSRFEGMRVVV
NALLGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGEMFSIDEVDNQTECENLIERNETAR
WKNVKVNFDNVGLGYLSLLQVATFKGWMDIMYAAVDSRNVEQQPHYEDNLYMYLYFVIFIIFGSFFTLNL
FIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTKQAFDISI
MILICLNMVTMMVETDDQTDAMETILYRINFIFIVLFTGECVLKLISLRYYYFTIGWNIFDFVVVILSIV
GMFLAEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYAIF
GMSNFAYVKREVGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSGPPDCDPEIDHPGSSVKGDCG
NPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFAK
LSDFAASLDPPLLIPKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESDEMDALRVQMEDRFMAAN
PSKASYEPITTTLKRKQEEVSAVII
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Na_v1.3 (complete amino acid sequence, GenBank accession BK008862)

Na$_v$1.3 (complete amino acid sequence, GenBank accession BK008862)

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MAQTLLVPPGPDSFCFFTRESLAAIEKRCTEEKAKRPKQEHTDNDDESGPKPNSDLEAGKTLPFIYGDIP
PGMGSEPLEDLDPYYSNKKTFIVLNRGKTIFRFSATSALYILTPFNPLRKIAIKILVHSLFSMLIMCTIL
TNCVFMTMSNPPEWTKNVEYTFTGIYTFESLIKILARGFCLEGFTFLRDPWNWLDFSVILMAYVTEFVNL
GNVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRHKCLL
WPLDNSTLEGNITSHFNSTEGDNDTFVNMTVTTFNWEEYIEDESHFYVLEGQRDALLCGNSSDAGQCPEG
YMCVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLINLI
LAVVAMAYEEQNQATMEEAEQKEAEFQQMLEQLKKQQEEAQTTAAVAAASVASRDFSGVGGLGELLESSS
EASKLSSKSAKDRRNKRKKKKQKELSEAEDKEEAERYPKSESEDSIRRGGRLSYEKRTSTHQSLLSFRGS
LFSPRRNSRTSIFSFRGRVKDIGSENDFADDEHSTLEDNESRRDSLFVPNRQTSERRNSTTSQISLSSKM
VPVLPANGKMHSTVDCNGVVSLMGGPPALPSPTGQFLPEGTTTETEIRKRRLSSYQISMELMEESAARQR
AMSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCWLPWLKVKHIVNLIVMDPFVDLAITICIVLNT
LFMAMEHYPMTSDFYQVLSVGNLVFTGIFTAEMILKIIAMDPYYYFQEGWNIFDGIIVSLSLMELGLANV
EGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCK
IAEDCELPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLL
SSFSSDNLAATDDDNETNNLQIAVARIQKGIDYIKKKLGEIVQKGTVRKQKAIDDIKVLEELNHKKDVCI
SNHTMAEITKDVNYLRDGNGTTSGLGTGSSVEKYIIDENDYLSFINNPGLTVTVPIAVGESDFENINTEE
FSSESELEGSKEKINATSSSEGSTVDVALPGEGEQAEIEPEEALEPEACFTEGCIQKFPCCQVSIEDGKG
KIWWNFRKTCYCIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYSDKVFTYIFILEMLLKW
VAYGFQIYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALV
GAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGEMFNISDVNNKTECDELIHNNQQARWKNV
KVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVEEQPYYEDNLYMYLYFVIFIIFGSFFTLNLFIGV
IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPGNKFQGLVFDFVTKQAFDITIMILI
CLNMVTMMVETDDQSKEMEIILSRINLVFIILFTGECVLKLISLRHYYFTIGWNIFDFVVVILSIVGMFL
AEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYAIFGMSN
FAYVKREVGIDDLFNFETFGNSMLCLFQITTSAGWDGLLAPILNSGPPDCDPEIDHPGSSVKGDCGNPSV
GIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDASQFIEYSKLSDF
AASLDPPLLIAKPNNVQLISMDLPMVSGDRIHCLDILFAFTKRVLGESEEMDLLRVQMEDRFMAANPSKV
SYEPITTTLKRKQEEVSATIIQRAFRHFLLKQKVKKVTSMYNKEKCRDGEVLPIKDVTSDRFNGNSSPEK
TNESSSTTSPPSYDSVTKPNKEKYEKGKTERDFKGKDIKISKK
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Na_v1.4 (complete amino acid sequence, GenBank accession BK008863)

Na$_v$1.4 (complete amino acid sequence, GenBank accession BK008863)

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MAAVPYIPGPDCLRPFTRESLKAIEKRIAEREAEKLKNQHEEVLDEEKQPKPRCDLEQGKGLPLIYGEPP
PELIGVPLEDLDTFYSDQKTYIILNKGNTIFRFTAAPALYMLDPFNPIRNGAIKVLTHSLFSMFIMITIL
ANCVFMTMSNPPIWAKDVEYTFTGIYTFEAMIKVLARGFCIDSFTFLRDPWNWLDFSVIVMAYVTEFVDL
GNVSALRTFRVLRALKTITVIPGLKTIVGALIQSVKKLADVMILTVFCLAVFALIGLQLFMGNLRQKCVR
WPPFSNDTLQDALGPSFTSDSLQDVLWRDPLDNSTLNDNFTLTGTFDWHEYINNEDNFYFLDGALDALLC
GNSSDAGQCPEGFLCMKAGRNPNYGYTSYDTFSWAFLSLFRLMTQDYWENLFQLTLRAAGKTYMIFFVVI
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IFLGSFYLINLILAVVAMAYAEQNDATLQEEKEKEEEFQQMVEQLKKHQEEQQRLLQAQTATNSSAESII
VEKKQKGELDEKAQSDQEGPKDCNGRAIPRLVLERSATVRESNPREEHEKSHQNHLYVDGVEGKGLEKRV
GSAVSVVSSTLEELEEAHQKCPPWWYKFAHAVLIWNCCPVWVKLKHIIKLIVLDPFVDLGITICIVLNTV
FMAMEHYPMTEEFNNVLNVGNLVFTGIFTAEMVLKLIALDPYEYFQIGWNIFDSIIVTLSLVELGLANVQ
GLSVLRSFRLMRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYIECVCKI
SSDCELPRWHMHDFFHSFLIVFRILCGEWIETMWDCMEVAGQPMCLIVFLMVMVIGNLVVLNLFLALLLS
SFSADSLAGSDDDSEMNNLQIAIGRINRGIDFVKKHVLLLLHRELKEKTELSSEEPDDSKKENFVLNHMD
NLNHVDTGQDFKSEYMDGIVKNEQLIDELGQMNFINNPNLTINVPIASEESDLYDETDTGEETADDIKKP
LSDGTDSSICSTVDYKPPDPSEEKAEVEENMENDDPEECFTEACVQRCPFLYVDIKTEKGAKWWNLRKAC
FKIVEHNWFETFIIFMILLSSGALAFEDIYIERRHTIRTILEYADKIFTYVFILEMLLKWVAYGFKVYFT
NAWCWLDFLIVDVSLISLTANWLGYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALLGAIPSIMNVL
LVCLIFWLIFSIMGVNLFAGKYYRCVNTTTGDLFEIEHVNNKSDCINLINIENATDVRWVNVKVNFDNVG
LGYLSLLQVATFKGWMDIMYAAVDSREQEEQPQYEVNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQ
KKKFGGKDIFMTEEQKKYYNAMKKLGSKKPVKPIPRPQNKYQGMIFDFVTQQAFDIIIMILICLNMVTMM
VETDDQSQTKITILAQINLVFIIIFTSECFLKMIALRHYFFTNGWNIFDFVVVILSIVGLVLSDIIEKYF
VSPTLFRVIRLARIGRVLRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGMSNFAYVKKES
GIDDIFNFETFGNSIICLFEVTTSAAWDGLLNPILNSVPPDCDPHLDNPGSHVKGDCGNPSMGICFFCSY
IIVSFLIVVNMYIAIILENFNVATEESSEPLCEDDFEMFYETWEKFDPDATQFIAYSTLSDFVDTLQEPL
RIAKPNKIKLITLDLPMVPGDKIHCLDILFALTKEVLGDSGEMDALKQSMEEKFMAANPSKVSYEPITTT
LKRKQEEVCAIKIQRAFRRYLLKRSVKQASYLYRQSQDMDIPKENAPEKEGMIANKMNAMYSSQVEVEKS
PETAPSPVLEPLSSPEIKKDAGEMKEQDNNGKEGDDSGKTKKSENAKRGVKESSV
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Na$_v$1.6 (complete amino acid sequence, GenBank accession BK008864)

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MAGRLLAPPGPDSFRPFTPESLANIEKRIAEDKKKRPKQDSSHRDDDEDNKPKPNSDLEAGKSLPFIYGD
IPKGLVAVPLEDFDPYYMTQKTFVVLNRGKTLFRFSATPALYILSPFNLLRRIAIKILIHSVFSMIIMCT
ILTNCVFMTFSNPPEWSKQVEYTFTGIYTFESLVKIIARGFCIDGFTFLRDAWNWLDFSVIMMAYITEFV
NLGNVSALRTFRVLRALKTISVIPGLKTIVGALVQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKC
VVWPIDLNETYLENGTKGFDWEEYSNNMSNFYTIPGFLDPLLCGNSSDAGQCPEGYTCMKAGRNPNYGYT
SFDTFSWAFLALFRLMTQDFWENLYQLTLRAAGKTYMIFFVLVIFVGSFYLVNLILAVVAMAYEEQNQAT
LEEAEQKEAEFKAMLEQLKKQQEEAQAAAMATSAGTVSDDAAEEGGGGRMSHTSSEFSKLSSKSAKERRN
RRKKRKEKELSEGEEKGDLEKVFKSESEDGMRRKVFRLPDNRLGRKLSIMNQSLLSIPGSPYLSRHNSKS
SIFSFKRGFRDPGSENEFADDEHSTVEESEGRRDSLFIPIRGYDRKSSYSGYSGYSQGSRSSRIFPSIRR
NMKRNSTVDCNGVVSLIGGPTSNIPSGRLLPEVKIDKAATDDSATTEVEIKKKSTGSLLVSMDQLNASYG
RKDRTNSIMTVITNTLVEELEESQRKCPPCWYKFANTFLIWECHPHWVKLKEIVNLIVMDPFVDLAITIC
IVLNTLFMAMEHHPMTPTFEHVLAVGNLVFTGIFTAEMFLKLIAMDPYYYFQEGWNIFDGFIVSLSLLEL
MLADVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYK
ECVCKINPDCDLPRWHMHDFFHSFLIVFRVLCGEWIETMWDCMEVAGQAMCLIVFMMVMVIGNLVVLNLF
LALLLSSFSADNLAASDDDGEMNNLQISVIRIKKGIAWIKIKVHEFVQTHFKQREADEVKPLDELYDKKM
NCIANHTGADINREIDYQKNGNGTTSGIGSSVEKYIIDEDHMSFINNPHLTVRVPIAVGESDFENLNTED
FSSDTDAGGSKEKLDDTSSSEGSTIDIKPEVEEVPVEAPEEYLDPDACFTEGCVQRFKICQVSIEDGLGK
SWWNLRKTCFLIVEHNWFETFIIFMILLSSGALAFEDIYIEQRKTIRTVLEYADKVFTYIFILEMLLKWC
AYGFVKFFTNAWCWLDFLIVAVSLVSLIANALGYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALVG
AIPSIMNVLLVCLIFWLIFSIMGVNLFAGKYHYCFNETAEYRFEIEEVNNKTECEKLMDPNGTEIRWKNV
KINFDNVGAGYLALLQIATFKGWMDIMYAAVDSRKQEEQPKYEDNIYMYIYFVIFIIFGSFFTLNLFIGV
IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNRIQGAVFDFVTQQAFDIVIMLLI
CLNMVTMMVETDTQSKQMEEILYWINFVFVIFFTCECVLKMFALRHYYFTIGWNIFDFVVVILSVVGMFL
AEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIFSIFGMSN
FAYVKHEAGIDDMFNFETFGNSMICLFQVTTSAGWDGLLLPILNRPPDCDLEKEHPGSGFKGDCGNPSVG
IFFFVSYIIISFLIVVNMYIAIILENFSVATEESADPLSEDDFETFYEIWEKFDPDATQFIEYCKLADFA
DALEHPLRVPKPNTIELIAMDLPMVSGDRIHCLDILFAFTKRVLGDSGELDILRQQMEERFVASNPSKVS
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YEPITTTLRRKQEEVSAVVIQRAYRVRLARRGFICRKNVSNAIENGGTNREKKEGTPSTASLPSYDSVTK
PEKEKQRAEEGRRERAKRQKDARESKC
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Na$_v$1.7 (complete amino acid sequence, GenBank accession BK008865)

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MAHALHAQPGPDCFFQFTQESLAAIEQRITEEKAKQKVEQEQKEEDHDESKPKPNTDLEAGKSLPFIYGD
IPSRFVSQPLEDLDPYYANKKTFIVLNKGKTIFRFSATPALYMLSPFSTLRRISIKILVHSLFSIFIMFT
ILTNCVFMTLKDPPKWSWMVEYTFTGIYTFESLIKIFARGFCIDKFTFLRDPWNWLDFLVISFAYITEFV
KLGNVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTLFCLSVFALIGLQLFMGHLRHKC
LYWPNNTSPEDPRFKEYYNGTELLWSKYMENKDHFYYLEGAKDALLCGNSSDAGQCPEGYICVPYGRNPD
YGYTSFDSFSWAFLSLFRLMTQDYWENLYQQTLRAAGKGYMFFFVVVIFLGSFYLINLILAVVAMAYDEQ
NQATIEEALRKETEYQQMLEHLKRQQEEAQALMAAAAYKDFRDDGTLGRLSETSSELSSSKSAKERRNRR
KKRRQRELSVGEPGGNNKMFPKSESDSSIRRKGFRFSLEGNRLAYESRVISPYQSILFPTRSNSRASFSS
FKSPTVEGGSDADSEHSTFEENGSRNGSYFVVRSHSERRSSNISQTMFPMNGKMQSSVDCNGVVSLVGGP
PVLLSPTGQLLPEVIIDKATTDDSPTTSEMENKKRQSSSFQISMDLLEDPTIRERAMSIASIITNTMEEL
EESRQKCPPCWYKFAHKYLIWNCSDRWLQIKKIIHLIVMDPFVDLGITICIILNTLFMSMEHYPIDDSFS
SILKNGNLVFTGIFTAEMVLKIVAMDPYYYFQEGWNIFDSIIVTLSLMELGLQNVEGLSVLRSFRLLRVF
KLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYDMCKCKISEDCTLPRWHMNDF
FHSFLIVFRVLCGEWIETMWDCMEVSGQPLCLTVFMMVMVIGNLVLLNLFLALLLSSFSSDSLAAPEQET
EANNLQIAISRIQRGINYIKRKICEFVQIVFLQRCKATSGLSAADQQNDKEDQCIPNHTIVEINQTFGYQ
RPRMTTSCVDNTDHMSFINNPNLTVTVPIAVGESDFEHFNTEELTSISEVEETKEKTSLCSSTEGSTIIF
ASVGDKESDAAAKGPPQPKPCFTDGCVQKFKCCQIDIESGKGKCWWNLRKTCFKIVEHNWFETFIVFMIL
LSSGALAFEDIYIEQRKTIKTVLEYADKVFTYIFILEMLLKWVAYGFQAYFTNAWCWLDFVIVDVSLVSL
IANALDYSELGPIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLF
AGTFFECVNKTDGVRISHLIVPFKNVCETLDYARWRNVKVNFDNVAAGYLSLLQVATFKGWMEIMYAAVD
STGIEEQPQYEHNLYMYLYFVGFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQKKYYNAMKK
LGSKKPQKPIPRPSNKIQGFVFDFVTKQAFDIGIMILICLNMITMMVETADQDTSVEDILYWINLIFIVL
FTAECLLKLIALRYYYFTIGWNIFDFVVVIFSIVGMCLSKIIEKFFVSPTLFRVVRLARIGRILRLIKGA
KGIRTLLFALMMSLPALFNIGLLLFLVMFIYAIFGMSQFAYVKREAGIDDMFNFETFANSMICLFQITTS
GGWNYLLYPSLNKEPDCDPKKVHPGSSVLGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATE
ESAEPLGEDDFEMFYEVWEKFDPGATQFIELSKLFDFAASLEPPLLIPKPNKVQLIAMDLPIVSGDRIHC
LDILFAFTKRVLGESDEMDSLRVQMEDRFMAANPSKVSYEPITTTLKRKLEEQSARVIQRAFRHYRLRKP
VCNTDVQYLNRNIFPCKAEMEFDKFSLSLTLEKTERSSSTTSPPSYDSVTKPDKYEQEKSEKEEKGKDDK
DYRK
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Table S2. Overgos used in BAC library scan. Overgos were combined into one pool for the first scan and pooled as indicated below for the second scan.

Pool	Name	Expected paralog	Forward overgo	Reverse overgo	Source
1	78842	*SCN1/2/3/9A*	TGCCTTAATATGGTCACCATGATG	GGTCATCTGTTTCAACCATCATGG	1
1	34924B	*SCN1/2/3/9A*	CCAACACCAGGCATTTGTGAAATA	CTATGGCTTCCAGATTTATTTCAC	1
2	UProbe1799	*SCN1/2/3/9A*	GGCCAAACCATGTGCCTTATTG	GACCAGCATGAAAACAATAAGG	2
3	SCNAu1	*SCN1/2/3/9A*	AATGGTGTCTGAGCCATTGGAGGA	GTAATATGGGTCCAGGTCCTCCAA	3
3	SCNAu2	*SCN1/2/3/9A*	ACTTTCCTCCGGGATCCCTGGAAT	CTGTGAAGTCCAACCAATTCCAGG	3
3	SCNAu3	*SCN1/2/3/9A*	TGATACCTTCAGCTGGGCCTTCTT	CAGCCGAAATAGTGACAAGAAGGC	3
4	SCNAu5	*SCN1/2/3/9A*	AAACGAGCCTCTTCAGCTTCAGAG	AAATCCTTTGCTCGGCCTCTGAAG	3
4	SCNAu8	*SCN1/2/3/9A*	TGGGATTGTATGGAGGTTGCTGGA	TAAGGCACATGGGTTGTCCAGCAA	3
4	SCNAu9	*SCN1/2/3/9A*	ACCCAAGTGTAACTGTGACAGTAC	TCTCCAACAGCAATGGGTACTGTC	3
5	70621B	*SCN1/2/3/9A*	CAGACTGAATGAGAGCTCCCACAA	CCAGGTCTGAAGACAATTGTGGGA	1
5	UProbe1763	*SCN1/2/3/9A*	TCCTGGTTGGTCAAGCTGTGAA	AAGATGCAGGAGCATTCACAGC	2
6	75835	*SCN1/2/3/9A*	GATAAGTTTACTTTCCTTCGAGAT	CAAGCCAATTCCAAGGATCTCGAA	1
7	UProbe1757	*SCN1/2/3/9A*	CTAGGTGGTTGTGAATGCTCTT	GGGATTGCTCCAGTAAGAGCAT	2
8	UProbe1760	*SCN1/2/3/9A*	GTCTAGGTCAAGTGTAGGAGAG	CAGGCCAGCAGTGTCTCTCCTA	2
9	SCN4A1	*SCN4A*	ATTCCTGCGAGATCCTTGGAATTG	GACACTGAAATCCAGCCAATTCCA	4
9	SCN4A2	*SCN4A*	CAGTGTCCAGAAGGATTTCTCTGC	TTCGGCCAGCTTTCATGCAGAGAA	4
9	SCN4A3	*SCN4A*	CTCTGTGGAGAATGGATTGAGACC	CCATGCAATCCCACATGGTCTCAA	4
10	SCN4A4	*SCN4A*	GGTAACAATGATGGTGGAAACAGA	GGTTTGGCTTTGGTCATCTGTTTC	4
10	SCN4A5	*SCN4A*	CTTTGTATCGCCCACTCTCTTCAG	AGCCAATCGGATGACTCTGAAGAG	4
11	15010	*SCN5/10/11A*	GATGACACCAATGAAAAGATTCAA	CGGTTCTTTCTTCACTTTGAATCT	1
11	49514	*SCN5/10/11A*	GGATCGACGACATGTTCAACTTCG	CTGTTGGCAAACGTCTCGAAGTTG	1
11	64787	*SCN5/10/11A*	GGCATCCATTTCTCCAGATTCTCC	CACCAAAAGGGTTCTGGGAGAATC	1
12	42679	*SCN5/10/11A*	CACCAAGCATTGGTGAAGTACTTC	TCGCCTACGGCTTTAAGAAGTACT	1
13	20183	*SCN5/10/11A*	GACACACTTGTTCCTGAGGTTACC	ACTCCAGCTGTTCATGGGTAACCT	1
14	72073	*SCN5/10/11A*	CAGAAAAATCCAGCCAATTCCAGG	ACTTTCCTTCGAGACCCCTGGAAT	1
15	72073B	*SCN5/10/11A*	GGAGTGGCACTAAATCGAAAGATC	TGAACAAAGGGAAGACGATCTTTC	1
16	31048	*SCN5/10/11A*	CAGCACTCTCCAACTTTGCAGATG	AAAGGTTCTTCCAGGGCATCTGCA	1
17	24584	*SCN8A*	CATCTTCACTCAGTGGATCAGCAC	GTGGCTACAGAGGAAAGTGCTGAT	1
17	FT7MHCY03GU4OO	*SCN8A*	CAGTAGAGGATCTCCTCCATCTGT	CCGACACACAAAGCAAACAGATGG	1
18	UProbe1797	*SCN8A*	TGGAACTGGCTTGACTTCAGTG	CGCCATTAGAATGACACTGAAG	2
18	UProbe659	*SCN8A*	GCAGGTGTGGCACTAAATCGGA	AGGGAAAACACTCTTCCGATTT	2

Sources: 1. *Th. elegans* transcriptome (Schwartz et al. 2010) 2. UProbe (Kellner et al. 2005; http://uprobe.genetics.emory.edu, last accessed April 2, 2014) 3. Unknown *SCNA* paralog identified in *Th. sirtalis* (Chuckalovcak 2010) 4. *Th. sirtalis SCN4A* (Geffeney et al. 2005)

Table S3. Putative positive clones identified from BAC library scanning and pooled for 454 sequencing. Clones marked with an asterisk were identified by Chuckalovcak (unpublished data) using *SCN4A*-specific probes.

Plate	Column	Row
2	M	7
2	N	7
4	C	17
7	B	13*
7	B	14
7	H	23*
13	N	15
15	C	14
15	C	15
16	G	15
16	H	16
16	O	15
19	N	15
22	H	1*
26	C	16*
27	D	22*
28	K	3*
29	K	24
39	D	7
39	E	7
47	H	18*
54	E	16*
75	G	4
77	E	8
80	F	20
80	G	19
97	J	4
107	E	10
109	E	5
112	E	5
114	E	14
115	E	5
130	K	3
130	N	18
130	N	19
133	M	17
133	O	18
133	P	17
137	C	6
145	I	2*

Table S4. Results of BLAT searches of full coding sequences of SCNA paralogs against the *Anolis carolinensis* genome. Searches using individual 454 contigs (including noncoding regions) provided consistent results.

Thamnophis paralog	Score	Start	End	Identity	Chromosome	Strand	Start	End	Span	*Anolis* paralog
SCN1A	**3600**	**265**	**5426**	**91.10%**	**Un_GL343214**	**+**	**989871**	**1053318**	**63448**	***SCN1A***
(Na$_v$1.1)	2414	145	5357	87.50%	Un_GL343214	-	1335760	1409172	73413	*SCN2A*
	2310	14	5357	87.20%	Un_GL343214	+	1520485	1608646	88162	*SCN3A*
	1193	603	5357	84.90%	Un_GL343214	+	798646	866464	67819	*SCN9A*
SCN2A	**4073**	**1**	**5648**	**89.80%**	**Un_GL343214**	**-**	**1335448**	**1409322**	**73875**	***SCN2A***
(Na$_v$1.2)	2743	14	5633	87.30%	Un_GL343214	+	1520485	1608943	88459	*SCN3A*
	2467	274	5356	87.10%	Un_GL343214	+	989874	1053269	63396	*SCN1A*
	1750	609	5627	84.50%	Un_GL343214	+	798646	866755	68110	*SCN9A*
SCN3A	**4083**	**14**	**5925**	**88.10%**	**Un_GL343214**	**+**	**1520485**	**1609235**	**88751**	***SCN3A***
(Na$_v$1.3)	2794	280	5905	87.40%	Un_GL343214	-	1335188	1401072	65885	*SCN2A*
	1920	280	5581	87.20%	Un_GL343214	+	989883	1053494	63612	*SCN1A*
	1293	606	5607	85.50%	Un_GL343214	+	798646	866732	68087	*SCN9A*
SCN4A	**2985**	**391**	**5622**	**86.50%**	**6**	**-**	**63466916**	**63528585**	**61670**	***SCN4A***
(Na$_v$1.4)	926	709	5234	81.00%	2	+	90897993	90950691	52699	*SCN8A*
	733	1177	4883	82.30%	Un_GL343214	-	1335853	1382727	46875	*SCN2A*
	587	2203	4976	81.00%	Un_GL343214	+	1022972	1053249	30278	*SCN1A*
SCN8A	**4553**	**1**	**5959**	**90.50%**	**2**	**+**	**90865054**	**90950972**	**85919**	***SCN8A***
(Na$_v$1.6)	1116	612	5666	81.60%	Un_GL343214	+	798646	1608892	810247	*SCN1/9A*
	694	1136	5587	81.30%	6	-	63466936	63519746	52811	*SCN4A*
	653	612	5345	82.70%	Un_GL343214	-	1335835	1392932	57098	*SCN2A*
SCN9A	**2996**	**157**	**5781**	**84.90%**	**Un_GL343214**	**+**	**790114**	**867023**	**76910**	***SCN9A***
(Na$_v$1.7)	1621	274	5775	85.30%	Un_GL343214	-	1335189	1401084	65896	*SCN2A*
	1475	612	5405	84.30%	Un_GL343214	+	1000209	1053429	53221	*SCN1A*
	1264	612	5451	85.80%	Un_GL343214	+	1531270	1608872	77603	*SCN3A*

Table S5. Primer pairs used on *Th. sirtalis* cDNA for filling gaps in SCN1A-3A CDS.

Name	Paralog	Forward primer	Reverse primer
SCN1A01	*SCN1A*	CTCCGTTGGAAACTTGGTGT	TGACCTGCAACCTCCATACA
SCN1A02	*SCN1A*	CTGGCACATGCATGATTTTT	CTGGTGGTGGTTCCATTTCT
SCN1A03	*SCN1A*	CCTGCATCTCTAACCACACC	ACCATTGCTTTCCTCTTCCA
SCN1A04	*SCN1A*	TGCTTCTGAAATGGGTAGCAT	CATCTGGCAGTTTCATTTGC
SCN1A06	*SCN1A*	TCAAGAAAAGTGCTTGAACAGC	TTAGACGCAGGATTCGACCT
SCN1AEx9	*SCN1A*	GACGCAGGTCAATGTCCAGA	CCACCTCTTACGCTGGGATC
SCN1AEx1620	*SCN1A*	TTCAGTAGTGAGTCTGATTCG	TGCTCTCAGTGTCCTAAGGGA
SCN1AEx26	*SCN1A*	TTGTATCCCCCACCTTGTTC	AATCCCAACCGAAGGATTG
SCN1ASt1	*SCN1A*	GGAGCAATTCCATCCATCAT	TGACACCAATAAATAGATTCAGGGTA
SCN2A01	*SCN2A*	ACAAAAGGCTTTGGATGAAATC	TAGATGCATTTAGTTTCTCTTTGCTT
SCN2A02	*SCN2A*	GCAGTGAGTCAGATCTGGAAGA	TGTCTTGACCTCCAAACTTCTTT
SCN2A03	*SCN2A*	TCATCATAGATAACTTCAATCAGCAA	TTAGACGCAGGATTCGACCT
SCN2A05	*SCN2A*	GCCTCTTTGGATCCTCCTCT	CACCTAAAGGCTCGCTGAAT
SCN2A26	*SCN2A*	TGTGTCCCCTACCTTGTTCC	AATCCCAACTGAAGGATTGC
SCN2ASt1	*SCN2A*	ATAGGAAGCAGCGTGGAAAA	ACTTGAATTTCCGGATGCAG
SCN2ASt2	*SCN2A*	TGTGGGACTTGGCTACCTCT	TTTGCTGGCCTTGGTATAGG
SCN2ASt3	*SCN2A*	GCCTCCAGATTGTGATCCTG	AGGTCCATCGCAATAAGCTG
SCN3A01	*SCN3A*	TGGTCAGTTTAGTAGCCAATGC	GCAACTTGAAGCAGAGCAAG
SCN3A02	*SCN3A*	CCGATGGAAAAACGTGAAAG	TGTCAAAGGCTTGTTTGGTT
SCN3A03	*SCN3A*	TTTTATGACAGAGGAACAGAAAAA	TTAGACGCAGGATTCGACCT
SCN3A04	*SCN3A*	CTAGCGCCCATCCTAAACAG	TTCTTCGCTTTCTCCCAAGA
SCN3A05	*SCN3A*	TTCAGCTAATTTCAATGGACCT	TCTCTGTTTTGCCCTTTTTCA
SCN3A07	*SCN3A*	AGTTCCTCGACCACCTCTCC	CAAATGTGGCTGCTGAAGAA
SCN3AEx1620	*SCN3A*	TTTAGCAGTGAATCTGAGCTG	TGCTCTTAGTGTTCGAAGTGA
SCN3AEx26	*SCN3A*	GGAATGTTCCTCGCAGAGAT	GAAGGATTGCCACAGTCTCC
SCN3ASt1	*SCN3A*	ACCACAAAAGCCGATACCAA	TTAGACGCAGGATTCGACCT
SCN3ASt2	*SCN3A*	CTTTCCGATTTTGCTGCTTC	GTAGGACCTCGCCATCTCTG
SCN3ASt3	*SCN3A*	CAGCCTTTGAAGGGGATGTA	AGCAGCAATGTCGTTCCTTT

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Table S6. Primer pairs used on *Th. sirtalis* genomic DNA to assess interpopulation variation.

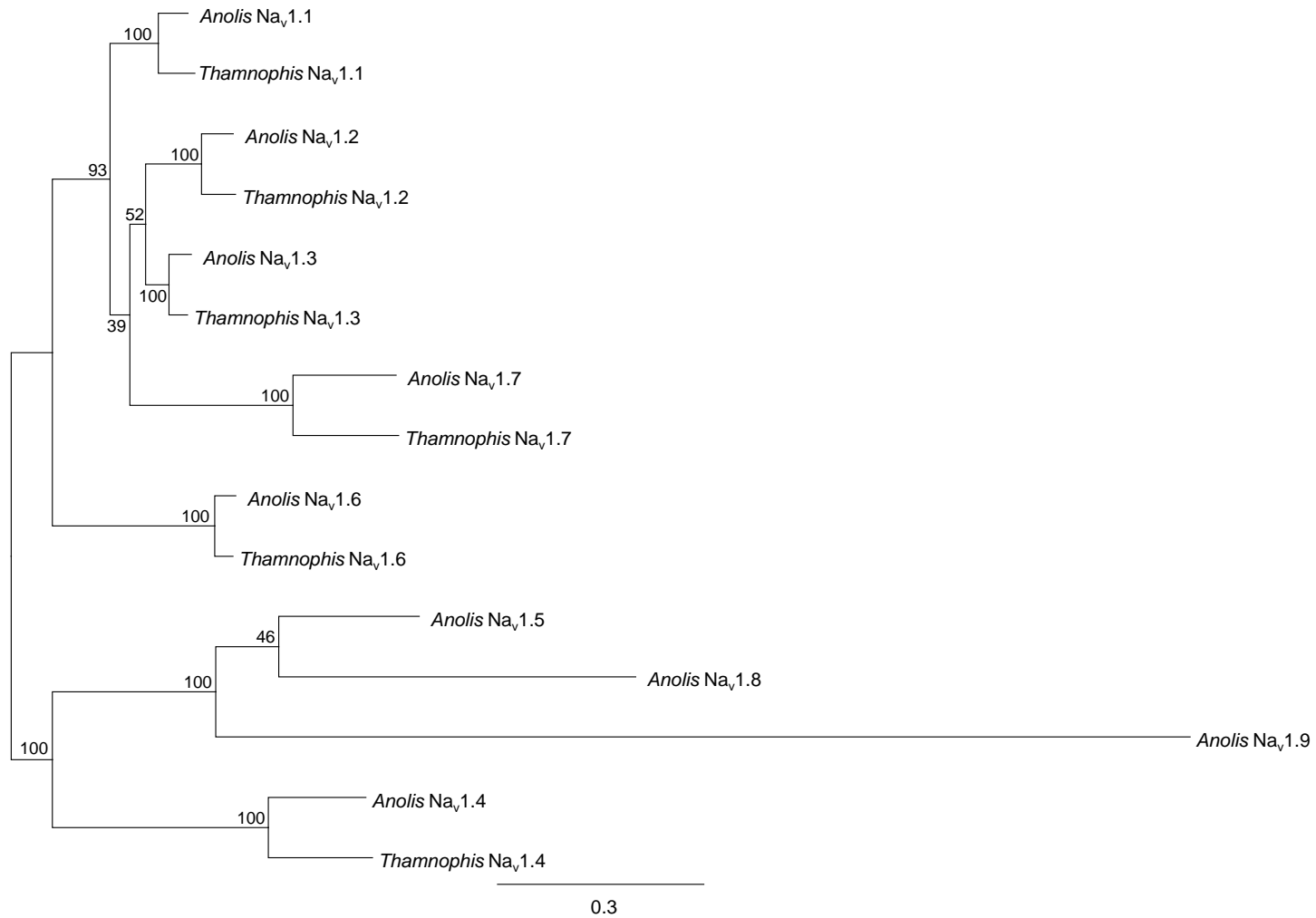| Name	Paralog	Forward primer	Reverse primer
SCN8A22	*SCN8A*	CCTCTGCCTTTGAGGTGAGTGGC	ACCCACTTGCCTTGTTTGGGCT
SCN8A26	*SCN8A*	CCGCCTGGCCCGTATTGGTC	ACTGGGTAGCGTCGGGGTCA
SCN9A22	*SCN9A*	TCTGTTAATGGAACAGCGTCTGCC	TGGGGCTCTCCCCAACATGGA
SCN9A26	*SCN9A*	AGGGGGATAGAGCCAATTTCGGA	TCCCAACCGAAGGATTGCCACA

Fig. S1. Maximum likelihood phylogeny of *Anolis carolinensis* (Zakon et al. 2011, accession nos. BK007953-BK007961) and *Thamnophis sirtalis* Na$_v$1 paralogs constructed using amino acid sequences in PhyML (Guindon and Gascuel 2003). Bootstrap values from 100 replicates are given at each node. Tree was rooted based on the topology of the larger tree in Zakon et al. (2011).