Table 1: Na$_v$1.1 sequencing primers.

Name	5' - Sequence - 3'	Length (Bases)
hNav1.1-620F	TGGACCTGGGCAATGTCTCG	20
hNav1.1-1017	CTCTGATGCAGGCCAATGTC	20
hNav1.1-1467F	GAGTTCCAAGAGTGCTAAGG	20
hNav1.1-1734F	AGGGCGAGCAAAGGATGTGG	20
hNav1.1-1833R	GGGCACAAACAAGGAATCTC	20
hNav1.1-2316F	GGCCATCACCATCTGTATTG	20
hNav1.1-3046F	GTGGATAGGATGCACAAAGG	20
hNav1.1-3607F	CAATGGTGGAACCTGAGAAG	20
hNav1.1-4337F	ATGTGGAACTCCAGCCTAAG	20
hNav1.1-4896F	TACCCTGTTCCGAGTGATCC	20
hNav1.1-5442F	GTTTGATCCCGATGCAACTC	20
hNav1.1-6356R (3' UTR)	TGGATCTCCATTCGCCATTC	20

Primer identifiers are made up of the protein name and a numeral that stands for the primer's first 5' base with respect to the open reading frame position. The letters "F" and "R" indicate forward and reverse priming, respectively. The tables in this article do not claim to be comprehensive and serve only as recommendations. Regions that have proven to be problematic may be covered by several primers. Upstream sequencing with a vector primer may be necessary where reverse priming of the reading frame 5' end is not provided. Owing to the research focus in our laboratory, we address only select human Na$_v$ channels (Na$_v$1.1, Na$_v$1.2, Na$_v$1.4, Na$_v$1.5, Na$_v$1.6, and Na$_v$1.7). Note that, due to sequence similarities between the different Na$_v$ channels, some of the primers can be used on several different isoforms. For Na$_v$1.1, this includes hNav1.2-656F, hNav1.7-2576F, hNav1.7-4802R, and hNav1.2-4972F.

Table 2: Na$_v$1.2 sequencing primers

Name	5' - Sequence - 3'	Length (Bases)
hNav1.2-319R	GGGTGGCACTGAATCGAGAG	20
hNav1.2-656F	TCAGAGTTCTCCGAGCATTG	20
hNav1.2-783R	CACGCTTAGACAGAACACAG	20
hNav1.2-1278F	GGCCTATGAGGAACAGAATC	20
hNav1.2-1840F	CCGCACAGACATGGAGAACG	20
hNav1.2-2325F	CATGGCTATGGAGCACTATC	20
hNav1.2-2863F	GGCCAAACCATGTGCCTTAC	20
hNav1.2-3420F	ATCTGAAGGCAGCACGGTTG	20
hNav1.2-3952F	TCCCGGTTTGAAGGAATGAG	20
hNav1.2-4190R	CTGGCAGTTTGATTGCTCTC	20
hNav1.2-4535F	CCATACCTCGACCTGCTAAC	20
hNav1.2-4972F	CCTGCGTTGTTTAACATCGG	20
hNav1.2-5421F	CGATGCGACCCAGTTTATAG	20

Primers not originally intended but functional for Na$_v$1.2 include hNav1.7-4802R and hNav1.1-4896F (Table 6 and 1, respectively).

Table 3: Na$_v$1.4 sequencing primers

Name	5' - Sequence - 3'	Length (Bases)
hNav1.4-370F	GCCATCAAGGTGCTCATCC	19
hNav1.4-500R	ATCCCTGTGAAGGTGTACTC	20
hNav1.4-855F	GCCGTTCAACGACACCAACAC	21
hNav1.4-1386F	GGAGAAAGAGGAGGAGTTTCAG	22
hNav1.4-1832F	CTGTGGGCAACCTGGTCTTC	20
hNav1.4-2360F	TCATCGGCAATCTTGTGGTC	20
hNav1.4-2894F	GCAGCACAGCTGACTACAAG	20
hNav1.4-3372F	CATCAAATCCCTGCGGACAC	20
hNav1.4-3856F	ACCCTCAACCTCTTCATTGG	20
hNav1.4-4332F	CACGCTGTTCCGTGTGATCC	20
hNav1.4-4894F	ACCCAGTTCATCGCCTACAG	20
hNav1.4-5330F	GCAAGATGTATGGCCACGAG	20

Details as explained in Table Legend 1.

Table 4: Na$_v$1.5 sequencing primers

Name	5' - Sequence - 3'	Length (Bases)
hNav1.5-416F	GCACCATCCTCACCAACTG	20
hNav1.5-903F	GGAATCCCTGGACCTTTACC	20
hNav1.5-1402F	CCAGTAAACAGCCATGAGAG	20
hNav1.5-1776F	CAGCACTGTGGACTGCAATG	20
hNav1.5-2443F	GTCTTCAAGCTGGCCAAATC	20
hNav1.5-2923F	CGGACCACCTGGGATTTCTG	20
hNav1.5-3415F	GGCAGCACAGCAGACATGAC	20
hNav1.5-3943F	TCACGATTTGAGGGCATGAG	20
hNav1.5-4444F	GGCCAGGACATCTTCATGAC	20
hNav1.5-4893F	CCGCATCCTCAGACTGATCC	20
hNav1.5-5433F	TTCGGTCCTGTCTGACTTTG	20

Details as explained in Table Legend 1.

Table 5: $Na_v1.6$ sequencing primers

Name	5' - Sequence - 3'	Length (Bases)
hNav1.6-317F	TTAGTGCCACGCCTGCCTTG	20
hNav1.6-852F	GCCCATAAACTTCAACGAGAGC	20
hNav1.6-1374F	CTCAGAAGATGCCATAGAGG	20
hNav1.6-1918F	AACAGCACGGTGGACTGCAACG	22
hNav1.6-2411F	TCATAGCCATGGATCCCTAC	20
hNav1.6-2900F	TGGTGCTGAACCTGTTTCTG	20
hNav1.6-3393F	CTCTGAAGGAAGCACCATTG	20
hNav1.6-3868F	GGTGCCATAAAGTCCCTTAG	20
hNav1.6-4363F	ACCCTGAACCTGTTCATTGG	20
hNav1.6-4908F	GATTCGTACCCTGCTCTTTG	20
hNav1.6-5412F	GTACTGTAAGCTGGCAGAC	19

Details as explained in Table Legend 1.

Table 6: Na$_v$1.7 sequencing primers

Name	5' - Sequence - 3'	Length (Bases)
hNav1.7-680R	ACAGAAATAGTTTTCAAAGC	20
hNav1.7-707F	GGGCTTTGATCCAGTCAGTG	20
hNav1.7-1029R	GCTCGTGTAGCCATAATCAG	20
hNav1.7-1359F	CAGAATTATGGGCCTCTCAG	20
hNav1.7-2095F	TGTCCACCTTGGTGGTACAG	20
hNav1.7-2276R	TCAGTCATTGGGTGGTGTTC	20
hNav1.7-2576F	TGTTGGCCATCATCGTCTTC	20
hNav1.7-4038F	ACGGTTTCCTGCAAGTCAAG	20
hNav1.7-4222R	CAGAATCCACTGCTGCATAC	20
hNav1.7-4228F	GTAGACAAGCAGCCCAAA	18
hNav1.7-4802R	ATCACTCGGAACAGGGTAGG	20

Details as explained in Table Legend 1. Primers not originally intended but functional for Na$_v$1.7 include hNav1.1-4896F (Table 1) as well as hNav1.2-4972F and hNav1.2-5421F (Table 2).