CLAIMS

1. A fusion protein comprising a zinc finger protein (ZFP) domain and a transcription repressor domain, wherein the ZFP domain binds to a target sequence of a human *SCN9A* gene, wherein the target sequence comprises any one of SEQ ID NOs: 16-24.

2. The fusion protein of claim 1, wherein the target sequence is within 1.5 kb of a transcription start site (TSS) in the *SCN9A* gene optionally within 1000 bps upstream of the TSS, and/or optionally within 500 bps downstream of the TSS of the SCN9A gene wherein the fusion protein optionally represses expression of the SCN9A gene by at least about 40%, 75%, 90%, 95%, or 99% with no or minimal detectable off-target binding or activity, wherein the transcription repressor domain optionally comprises a KRAB domain, wherein the KRAB domain optionally is from a human KOX1 protein, and wherein the ZFP domain optionally is linked to the transcription repressor domain through a peptide linker.

3. The fusion protein of any one of claims 1- 2, wherein the ZFP domain comprises a DNA-binding recognition helix sequence shown in the table below:

| **F1** | **F2** | **F3** | **F4** | **F5** | **F6** |
|---|---|---|---|---|---|
| DRSDLSR (25) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLAR (35) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| DRSYRNT (36) | RRSDLKR (37) | ERGTLAR (38) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| DRSNLSR (40) | LKFALAN (41) | RSDNLST (42) | RSAALAR (43) | RSDHLST (44) | QSAHRIT (45) |
| RSDDLSK (46) | RSDHRTN (47) | DRSHLTR (32) | TSANLSR (48) | RSDSLSR (49) | DRSVRTK (50) |
| YKHVLSD (51) | TSGSLTR (52) | RSDSLLR (53) | NYASRTW (54) | RSDSLLR (53) | NYASRTW (54) |
| RSDSLSQ (55) | RKADRTR (56) | QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) |

| F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|
| HKTSLKD (60) | | QSNHLTE (61) | QNATRTK (62) | DRSALSR (63) | RSDHLSR (64) |
| QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) | LRHHLTR (65) | LRHNLRA (66) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLAR (35) | |
| ^DRSDLSR (69) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ^DRSYRNT (70) | RRSDLKR (37) | ^ERGTLAR (71) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| ^ASKTRTN (67) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DSSHRTR (33) | |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |

wherein the symbol "^" indicates that the arginine (R) residue at the 4th position upstream of the 1st amino acid in the indicated recognition helix is changed to glutamine (Q).

4. The fusion protein of any one of claims 1- 3, wherein the ZFP domain comprises the DNA-binding recognition helix sequences as shown in a single row of the table below:

| F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|
| DRSDLSR (25) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLAR (35) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| DRSYRNT (36) | RRSDLKR (37) | ERGTLAR (38) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| DRSNLSR (40) | LKFALAN (41) | RSDNLST (42) | RSAALAR (43) | RSDHLST (44) | QSAHRIT (45) |
| RSDDLSK (46) | RSDHRTN (47) | DRSHLTR (32) | TSANLSR (48) | RSDSLSR (49) | DRSVRTK (50) |
| YKHVLSD (51) | TSGSLTR (52) | RSDSLLR (53) | NYASRTW (54) | RSDSLLR (53) | NYASRTW (54) |
| RSDSLSQ (55) | RKADRTR (56) | QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) |

| F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|
| HKTSLKD (60) | | QSNHLTE (61) | QNATRTK (62) | DRSALSR (63) | RSDHLSR (64) |
| QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) | LRHHLTR (65) | LRHNLRA (66) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLAR (35) | |
| ^DRSDLSR (69) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ^DRSYRNT (70) | RRSDLKR (37) | ^ERGTLAR (71) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| ^ASKTRTN (67) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DSSHRTR (33) | |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |

wherein the symbol "^" indicates that the arginine (R) residue at the 4th position upstream of the 1st amino acid in the indicated recognition helix is changed to glutamine (Q).

5. The fusion protein of any one of claims 1- 4, wherein the ZFP domain of the fusion protein

comprises five or six zinc fingers;

binds to a target sequence shown in one ofSEQ ID Nos: 16-24;

comprises the DNA-binding recognition helix sequences of a ZFP transcription factor shown in the table below:

| F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|
| DRSDLSR (25) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLAR (35) | |
| ASKTRTN (31) | QSGSLTR (26) | QSGDLTR (27) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| DRSYRNT (36) | RRSDLKR (37) | ERGTLAR (38) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| DRSNLSR (40) | LKFALAN (41) | RSDNLST (42) | RSAALAR (43) | RSDHLST (44) | QSAHRIT (45) |

| F1 | F2 | F3 | F4 | F5 | F6 |
|---|---|---|---|---|---|
| RSDDLSK (46) | RSDHRTN (47) | DRSHLTR (32) | TSANLSR (48) | RSDSLSR (49) | DRSVRTK (50) |
| YKHVLSD (51) | TSGSLTR (52) | RSDSLLR (53) | NYASRTW (54) | RSDSLLR (53) | NYASRTW (54) |
| RSDSLSQ (55) | RKADRTR (56) | QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) |
| HKTSLKD (60) | | QSNHLTE (61) | QNATRTK (62) | DRSALSR (63) | RSDHLSR (64) |
| QSGDLTR (27) | LKDTLRR (57) | RSANLAR (58) | QSSDLRR (59) | LRHHLTR (65) | LRHNLRA (66) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLAR (35) | |
| ^DRSDLSR (69) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DRSHLSR (29) | TSGHLSR (30) |
| ^DRSYRNT (70) | RRSDLKR (37) | ^ERGTLAR (71) | DRSALAR (39) | DRSHLTR (32) | QSGDLTR (27) |
| ^ASKTRTN (67) | QSGSLTR (26) | QSGDLTR (27) | DSSNRAK (28) | DSSHRTR (33) | |
| ASKTRTN (31) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DSSHRTR (33) | |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DRSNLTR (34) | DRSHLSR (29) | TSGHLSR (30) |
| ^ASKTRTN (67) | QSGSLTR (26) | ^QSGDLTR (68) | DSSNRAK (28) | DRSHLTR (32) | TSGHLSR (30) |

wherein the symbol "^" indicates that the arginine (R) residue at the 4th position upstream of the 1st amino acid in the indicated recognition helix is changed to glutamine (Q);

comprises the DNA-binding recognition helix sequences linked as shown in the table below:

| DNA-Recognition Helix Amino Acid Sequence Within Each Finger | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| F1 | L 1 | F2 | L 2 | F3 | L 3 | F4 | L 4 | F5 | L 5 | F6 | L 6 |
| DRSDLSR (25) | 0 | QSGSLTR (26) | 0c | QSGDLTR (27) | 0 | DSSNRAK (28) | 0c | DRSHLSR (29) | 0 | TSGHLSR (30) | C 1 |
| ASKTRTN (31) | 0 | QSGSLTR (26) | 0c | QSGDLTR (27) | 0 | DSSNRAK (28) | 0c | DRSHLTR (32) | 0 | TSGHLSR (30) | C 1 |
| ASKTRTN (31) | 0 | QSGSLTR (26) | 0c | QSGDLTR (27) | 0 | DSSNRAK (28) | 0a | DSSHRTR (33) | | | C 1 |
| ASKTRTN (31) | 0 | QSGSLTR (26) | 0c | QSGDLTR (27) | 0 | DRSNLTR (34) | 0a | DRSHLAR (35) | | | C 1 |
| ASKTRTN (31) | 0 | QSGSLTR (26) | 0c | QSGDLTR (27) | 0 | DRSNLTR (34) | 0c | DRSHLSR (29) | 0 | TSGHLSR (30) | C 1 |

| DNA-Recognition Helix Amino Acid Sequence Within Each Finger | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **F1** | **L 1** | **F2** | **L 2** | **F3** | **L 3** | **F4** | **L 4** | **F5** | **L 5** | **F6** | **L 6** |
| DRSYRN T (36) | 0 | RRSDL KR (37) | 1c | ERGTLA R (38) | 0 | DRSALA R (39) | 1c | DRSHL TR (32) | 0 | QSGDLT R (27) | C 1 |
| DRSNLS R (40) | 0 | LKFAL AN (41) | 0c | RSDNLS T (42) | 0 | RSAALA R (43) | 0c | RSDHLS T (44) | 0 | QSAHRI T (45) | C 1 |
| RSDDLS K (46) | 0 | RSDHR TN (47) | 0c | DRSHLT R (32) | 0 | TSANLS R (48) | 0c | RSDSLS R (49) | 0 | DRSVRT K (50) | C 1 |
| YKHVLS D (51) | 0 | TSGSLT R (52) | 1c | RSDSLL R (53) | 0 | NYASRT W (54) | 0c | RSDSLL R (53) | 0 | NYASRT W (54) | C 1 |
| RSDSLS Q (55) | 0 | RKADR TR (56) | 0c | QSGDLT R (27) | 0 | LKDTLR R (57) | 0c | RSANL AR (58) | 0 | QSSDLR R (59) | C 1 |
| HKTSLK D (60) | | | 0a | QSNHLT E (61) | 0 | QNATRT K (62) | 0c | DRSALS R (63) | 0 | RSDHLS R (64) | C 1 |
| QSGDLT R (27) | 0 | LKDTL RR (57) | 0c | RSANLA R (58) | 0 | QSSDLR R (59) | 0c | LRHHL TR (65) | 0 | LRHNLR A (66) | C 1 |
| ^ASKTR TN (67) | 0 | QSGSLT R (26) | 0c | ^QSGDL TR (68) | 0 | DRSNLT R (34) | 0a | DRSHL AR (35) | | | C 1 |
| ^DRSDL SR (69) | 0 | QSGSLT R (26) | 0c | QSGDLT R (27) | 0 | DSSNRA K (28) | 0c | DRSHLS R (29) | 0 | TSGHLS R (30) | C 1 |
| ^DRSYR NT (70) | 0 | RRSDL KR (37) | 1c | ^ERGTL AR (71) | 0 | DRSALA R (39) | 1c | DRSHL TR (32) | 0 | QSGDLT R (27) | C 1 |
| ^ASKTR TN (67) | 0 | QSGSLT R (26) | 0c | QSGDLT R (27) | 0 | DSSNRA K (28) | 0a | DSSHRT R (33) | | | C 1 |
| ASKTRT N (31) | 0 | QSGSLT R (26) | 0c | ^QSGDL TR (68) | 0 | DSSNRA K (28) | 0a | DSSHRT R (33) | | | C 1 |
| ^ASKTR TN (67) | 0 | QSGSLT R (26) | 0c | ^QSGDL TR (68) | 0 | DRSNLT R (34) | 0c | DRSHLS R (29) | 0 | TSGHLS R (30) | C 1 |
| ^ASKTR TN (67) | 0 | QSGSLT R (26) | 0c | ^QSGDL TR (68) | 0 | DSSNRA K (28) | 0c | DRSHL TR (32) | 0 | TSGHLS R (30) | C 1 |

wherein the symbol "^" indicates that the arginine (R) residue at the 4th position upstream of the 1st amino acid in the indicated recognition helix is changed to glutamine (Q);

comprises the DNA-binding recognition helix sequences linked as shown in the table below wherein DNA-binding recognition helix sequences are in boldface, zinc finger linkers are underlined, and interdomain linkers are double underlined:

| |
|---|
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**DRSDLSR**HIRTHTGEKPFACDICGRK FA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGRK FA**DSSNRAK**HTKIHTGSQKPFQCRICMRNFS**DRSHLSR**HIRTHTGEKPFACDICGRK FA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWKL LDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPD SETAFEIKSSVRS (SEQ ID NO:72) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGSQKPFQCRICMRNFS**DRSHLTR**HIRTHTGEKPFACDICGR KFA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWK LLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHP DSETAFEIKSSVRS (SEQ ID NO:73) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGEKPFQCRICMRKFA**DSSHRTR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:74) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DRSNLTR**HTKIHTGEKPFQCRICMRKFA**DRSHLAR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:76) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DRSNLTR**HTKIHTGSQKPFQCRICMRNFS**DRSHLSR**HIRTHTGEKPFACDICGR KFA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWK LLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHP DSETAFEIKSSVRS (SEQ ID NO:77) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**DRSYRNT**HIRTHTGEKPFACDICGR KFA**RRSDLKR**HTKIHTHPRAPIPKPFQCRICMRNFS**ERGTLAR**HIRTHTGEKPFACD ICGRKFA**DRSALAR**HTKIHTHPRAPIPKPFQCRICMRNFS**DRSHLTR**HIRTHTGEKPF ACDICGRKFA**QSGDLTR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVD FTREEWKLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVER EIHQETHPDSETAFEIKSSVRS (SEQ ID NO:78) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**DRSNLSR**HIRTHTGEKPFACDICGRK FA**LKFALAN**HTKIHTGSQKPFQCRICMRNFS**RSDNLST**HIRTHTGEKPFACDICGRK FA**RSAALAR**HTKIHTGSQKPFQCRICMRNFS**RSDHLST**HIRTHTGEKPFACDICGRK FA**QSAHRIT**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWKL LDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPD SETAFEIKSSVRS (SEQ ID NO:79) |

| |
|---|
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**RSDDLSK**HIRTHTGEKPFACDICGR KFA**RSDHRTN**HTKIHTGSQKPFQCRICMRNFS**DRSHLTR**HIRTHTGEKPFACDICGR KFA**TSANLSR**HTKIHTGSQKPFQCRICMRNFS**RSDSLSR**HIRTHTGEKPFACDICGR KFA**DRSVRTK**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEW KLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETH PDSETAFEIKSSVRS (SEQ ID NO:80) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**YKHVLSD**HIRTHTGEKPFACDICGR KFA**TSGSLTR**HTKIHTHPRAPIPKPFQCRICMRNFS**RSDSLLR**HIRTHTGEKPFACDI CGRKFA**NYASRTW**HTKIHTGSQKPFQCRICMRNFS**RSDSLLR**HIRTHTGEKPFACDI CGRKFA**NYASRTW**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTR EEWKLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIH QETHPDSETAFEIKSSVRS (SEQ ID NO:81) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**RSDSLSQ**HIRTHTGEKPFACDICGRK FA**RKADRTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**LKDTLRR**HTKIHTGSQKPFQCRICMRNFS**RSANLAR**HIRTHTGEKPFACDICG RKFA**QSSDLRR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEW KLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETH PDSETAFEIKSSVRS (SEQ ID NO:82) |
| MAPKKKRKVGVPAAMAERPFQCRICMRKFA**HKTSLKD**HTKIHTGEKPFQCRICMR NFS**QSNHLTE**HIRTHTGEKPFACDICGRKFA**QNATRTK**HTKIHTGSQKPFQCRICM RNFS**DRSALSR**HIRTHTGEKPFACDICGRKFA**RSDHLSR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:83) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**LKDTLRR**HTKIHTGSQKPFQCRICMRNFS**RSANLAR**HIRTHTGEKPFACDICG RKFA**QSSDLRR**HTKIHTGSQKPFQCRICMRNFS**LRHHLTR**HIRTHTGEKPFACDICG RKFA**LRHNLRA**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREE WKLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQE THPDSETAFEIKSSVRS (SEQ ID NO:84) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICM***Q***NFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DRSNLTR**HTKIHTGEKPFQCRICMRKFA**DRSHLAR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:85) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**DRSDLSR**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGSQKPFQCRICMRNFS**DRSHLSR**HIRTHTGEKPFACDICGR KFA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWK LLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHP DSETAFEIKSSVRS (SEQ ID NO:86) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**DRSYRNT**HIRTHTGEKPFACDICGR KFA**RRSDLKR**HTKIHTHPRAPIPKPFQCRICM***Q***NFS**ERGTLAR**HIRTHTGEKPFACD ICGRKFA**DRSALAR**HTKIHTHPRAPIPKPFQCRICMRNFS**DRSHLTR**HIRTHTGEKPF ACDICGRKFA**QSGDLTR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVD |

| |
|---|
| FTREEWKLLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVER EIHQETHPDSETAFEIKSSVRS (SEQ ID NO:87) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICMRNFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGEKPFQCRICMRKFA**DSSHRTR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:88) |
| MAPKKKRKVGVPAAMAERPFQCRICMRNFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICM***Q***NFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGEKPFQCRICMRKFA**DSSHRTR**HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS (SEQ ID NO:89) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICM***Q***NFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DRSNLTR**HTKIHTGSQKPFQCRICMRNFS**DRSHLSR**HIRTHTGEKPFACDICGR KFA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWK LLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHP DSETAFEIKSSVRS (SEQ ID NO:90) |
| MAPKKKRKVGVPAAMAERPFQCRICM***Q***NFS**ASKTRTN**HIRTHTGEKPFACDICGR KFA**QSGSLTR**HTKIHTGSQKPFQCRICM***Q***NFS**QSGDLTR**HIRTHTGEKPFACDICGR KFA**DSSNRAK**HTKIHTGSQKPFQCRICMRNFS**DRSHLTR**HIRTHTGEKPFACDICGR KFA**TSGHLSR**HTKIHLRQKDAARGSGGDAKSLTAWSRTLVTFKDVFVDFTREEWK LLDTAQQIVYRNVMLENYKNLVSLGYQLTKPDVILRLEKGEEPWLVEREIHQETHP DSETAFEIKSSVRS (SEQ ID NO:91) |

and/or

comprises an amino acid sequence selected from the amino acid sequences shown in SEQ ID NOs: 25-71.

6. A nucleic acid construct comprising a coding sequence for the fusion protein of any one of claims 1-5, wherein the coding sequence is linked operably to a transcription regulatory element, wherein the transcription regulatory element is optionally a mammalian promoter that is constitutively active or inducible in neurons, wherein the construct is optionally a recombinant viral construct.

7. A recombinant virus comprising the nucleic acid construct of claim 6.

8. A pharmaceutical composition comprising the nucleic acid construct of claim 6 or the recombinant virus of claim 7, and a pharmaceutically acceptable carrier.

9. A host cell comprising the nucleic acid construct of claim 6, or the recombinant virus of claim 7, wherein the host cell is optionally a human cell, and optionally a neuronal cell or a pluripotent stem cell, wherein the stem cell is optionally an embryonic stem cell or an iPSC.

10. Use of a fusion protein of any one of claims 1-5 in the manufacture of a medicament for inhibiting expression of Nav1.7 in a human neuron, optionally through introduction of a nucleic acid construct of claim 6, a recombinant virus of claim 7, or the pharmaceutical composition of claim 8, thereby inhibiting the expression of Nav1.7 in the neuron, wherein the human neuron is optionally a nociceptive neuron in the dorsal root ganglia (DRG), wherein the introducing optionally comprises introducing into the neuron a recombinant adeno-associated virus (AAV) that expresses the fusion protein, and wherein the human neuron is optionally for use in the body of a human patient.

11. Use of a recombinant adeno-associated virus (AAV) or a nucleic acid construct encoding a fusion protein of any one of claims 1-5 in the manufacture of a medicament for treating a pain disorder in a patient in need thereof,
wherein the medicament is formulated for administration via an intravenous, intrathecal, intracerebral, intracerebroventricular, intra-cisternal magna, epidural, or intranasal route.

12. The use of a recombinant adeno-associated virus (AAV) or a nucleic acid of claim 11, wherein the patient is suffering from or at risk of developing a peripheral neuropathic pain disorder, optionally selected from

inherited erythromelalgia;

paroxysmal extreme pain disorder;

small fiber neuropathy, further optionally idiopathic small fiber neuropathy, small fiber neuropathy plus prediabetes, or diabetic small fiber neuropathy;

large fiber neuropathy;

trigeminal neuralgia;

post-herpetic neuralgia; and
painful diabetic neuropathy.

13. Use of a zinc finger, TALE, or CRISPR repressor in the manufacture of a medicament for inhibiting expression of Nav1.7 in a cell, preferably a human cell; wherein the repressor comprising a target site/sequence within or near a *SCN9A* gene, wherein the target sequence is optionally within 1.5 kb of a transcription start site (TSS) in the SCN9A gene, or optionally within 1000 bps upstream of the TSS, and/or optionally within 500 bps downstream of the TSS of the SCN9A gene; and
wherein the target sequence optionally:

i) comprises at least 8 contiguous bps of any of SEQ ID NOs: 16-24;
ii) comprises at least 8 non-contiguous bps of any of SEQ ID NOs: 16-24; or
iii) comprises any one of SEQ ID NOs: 16-24.

14. A fusion protein of any one of claims 1-5, a nucleic acid construct of claim 6, a recombinant virus of claim 7, or a pharmaceutical composition of claim 8, for use in the method of any one of claims 10-13.

15. Use of a fusion protein of any one of claims 1-5, or a nucleic acid construct of claim 6, or a recombinant virus of claim 7, for the manufacture of a medicament for use in the method of any one of claims 10-13.