

Human CCK Promoter: GenBank Reference No. AC018358.20 Gene ID: 885

TTCTAACCGAAAGAAGAAAAATAAAACCCACGAGATTAATAATAGTGTGAAAAAATATCCTAAAGGGAAGACTCC
GTGGGAGAAATGAGAACCCTGGGGAAAGCACTTTTCCAGATAGCTAACAAGCTTTCAATATGGAAATACAGTAAATG
ATGAAAAAGAGAAGCACAGTTTAAAAATGTAGGAGCAATAAATAAAGCCGTATTTATAAAGTTTTTCTCAAAGTGAC
GTGGGAAATGGCAATAAGCCACTACGCAGAACATAGGCAGTTTTTAAAAATCAGAAATATGTGCCACGCGCTCAGGCT
TCGAAAGCCCCGTGCATTTTAGATCGCTAGTGGATAAAACACCCTCAAGTTTCTATCCGTAAAGCCTCGAAATTTTC
TGCAGTATTTAGAAAAATGAATTTAAATCTTAAACCCCTCAATATTTTATTAGAAAAGATTGCAAAGTCCCCCGCAC
CGCTGTGTAACAGCTAGCAAACCTCAATCTGCATGCGAATCTTAGCGAATGGGTAGTTCATCCCTTAATGATGCTGGC
GTATGAAAGGCTCTAAAGCAGCTCTACCCACCCAGACCTCACTTTTAGACCCAGAGCCGTATTTCTGACTTCAAGA
AATGTCTTTCGAGCTCTCGGAGGAAGACACAGAAAATAGAAAAGCATAATGGAAATGGGCACAAAGCTGAAGACAG
CATCCTTCAAAGACACACGACACTTGGATCCCCCGCTGACGAAACCGAGGGACCTACCTTTTGGATTAGGACGCAGCT
GGCTTGGCGTTTCCAACCGGAGCAGCCCGGCAGCTGAGCCAAGTTCAGGGAGGACCAGCGGGCGGCTGTCTCTTAAA
TAGCCCCACCCGGCGGCTCGGCCAGTCATGTATTTACCAACCGCTGACGCAGACTGGCAGTAACACGTGCTCAGAG
GGCGGCCACTGGGGCGACAACCGGTTGAAGTGGCTCCTGGGAGAGAGGGGGAGGTGGTCTAGTGGGGTGGAGTTAAT
CCCTCCACGCGCGGTGCCGGGTGTCGCCCCCTCTGGTCCGAGAAGCTTCCGCCAACCCCTTTCAGGTGCCGCT
CCCCTGCGCATTCCAGAGCAGTACTCTCCAAGGTGGGAAACCTAGGAGTTTGGAGTCTCCTCCGGGATGGAGAAGCT
GCCGCTAGCTTAGTTCGCTTTGGGACCCGAGGGGCTAGAAAAGGAAACTGGGGCGGGGGTGGGGGGTGGACACTGG
GCAGGACTGAGCATCAGCAAGGCGTGATTCTGAAAGGGAGGGGGCGTCCGCCCCCTACCCCGGAGCGTCCGAGGCGC
TGGTCTTCATACTGTGTGGCTCTTTGGAAGGAGAGAGGAGGAGTCCGGGTCTTCACTTCTTCTCAGCCGCAATTA
AAAGCCCTCGCAGTTCTCCAGGTTTCCGAGGGCCAGTGTCTGGGTCACTGAAAGGGCTCTGGCCACAGCTGGCTCT
TGGTGTCTTGGGCTCTCTTGACGCAGCTGTAAAATGCGGATGACACCATCTGGTTTTGCTCAGAGGAATCCGGTTT
GGAAAGGGATGTGTTTTCTCCCGGCCAAGTTACCACCACCCCGCGGCCACTGTTCCCCGTTGTGACAAAGCG
GCCCCAGCGAGGGTCTGGGGAACCTTGACCACCGCACCCCCGCAAGCTCGGGTAGACCACGGCATCCGCCCTCGCA
CCTTCTGAGGGCCACACACTCACACCCCCAGGACAGTACCTTCCAGAACTCAGCTGCGCAGCCTGGAGGTGAGG
ACCTCACCCCTAGTCAGTCACCCGTCCGGTGGAGGGAAGGGAGGCACCGAGGCTGCCGTGCGCCTTTCCTGACACGC
GGTACTCTCCCGGCTCCGGAGCGGGCCGACCTGGAGCCCTCAGTGGCTCTGGTCTTACACCCTGAAACCTT
TGAGTTCGAGTCCGCTTGTGTTGCTTGAGTTCGCCCGCTCCCTGCAAAGGCACCTGCCAACCCCATTTACAGACCG
CAAACCAGGGCGCGAGGAAGAGCAGCGCCTTGCCAAGGCTCCACAACACGCCCTCGCCCTCTCCGTGCACCGAGGC
CGCCCAGCCTGGGACCTGGAGATCACCAGGCCTTGAACCTTGGGACCTCAACTCCTCTCCCTTTCTTCCCCACCC
GTCTTAGATGCAAGGAGAAAGATTTAGAAGCGCTATTTTAAAAATCGGAATCCGTATTCGGCTCTGGAATTCCTCT
GGAATGGAGGGACTGTGGCAACGCCAGTGTGAGGGTGGAGTGGGCGAGGCGGGTGGGGGGTGGGGGGCGGCC
AGAGACGCTCCGGTTGCTGCTCCACTTCTAATCCTGAGAGGCAGCTGCGTTTTCTGCAACCTATGGGCAACATGTT
TGAAAGAGCTGAAGCTGATTAATGCTTTCCAGTGGTTTCGCCACGAGCCTGCTAAGGTTTGTGTAGTTCAAGTTCGC
AAAAAGAGTCTTATTTGTGATTGTGGCAAGACATGTCTGGAACATAAACTTGTATCGAAATACCCCCAGAGCTTC
TAATTCAGTAGGCTGAGGAAGGGCCCAAGAATCCGAATTCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
CTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
TCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
CCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
TTCTTTCTTTCTTTCTTTATTTCTTTCTTTCTTTCTTTCAATTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
TCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT

Fig. 1A

Human Tacl Promoter GenBank Reference No. AC004140.2 Gene ID: 6863
AAACATAGGTCATAAATATTTAGAAAAAATGCATCCGTGCTAAACACATACAGACTTTTTCCCTTTGTGTTATTCC
CCACATAATACAGTATAACAACATTTTACACTGCCTTTATATTTATATTAAGTATCATAAGTAATCTAGAGATTATTT
AAAATATATGAGACGATGTGCATAGGTTATATTTCAAATACCACACCATTTTGCATCAGGGACTTGAGCATCCACAGG
TTTTGATACCTACAGGAGGTCCTACAGCCAATCCCCTATGCATACTGAGTGATGACTGTATGTCAAATGTGTTTAAA
TCCAGGAAGTCATAATAATCCTAATTTTTTAAAGTGGGCTTATTTAAAGGTGTTAATTTACCAATTCATTATTTTC
AAAATTGGTAGAGAGACATAATCAAGCATTTATCCCATCTTTCCTATATTAATAATGCTTTAGAATAACTAGTTGCT
GAGAAACATGAAAGAAACAAGTCTGCCTACCAGACAAAATAATGAATGATAAAAATCAACATAGCACTGTTTTGAAAA
ACTAATGAATTAATGATCTAGAAAATGATAGTCAATGGCTGCTAACAACTCAAAGGAGAAACAACCACATATCAT
GTGCTTCCCTACCAGAACAACACACATGTGAAGTAGTCTCATCAAAAAAAAAAAAAAAAAAGAAAAAGAAAGGAAAA
AGAAAAAATGTACAGAGGATCAAACCTCTAGATACAACCTACCAATTAACAGGAAATAATCGAAACAGAGAAACAAG
TTAAAGGCAATCAGCAAAGTCCAGAATGCGGTACACTCTCTGACCTGTCTTATCAATAAACTACAATAGAGAGAG
AAAGAGAGAGCGAATTACAGATTCAGGGAGATTTAAGAAACATGCAGTAGAAGGAATGTTGCTGTCCTCCAAAATG
CATGTGTTGAAATCGTAACCCCTAAGGTTATGGTATTAGGAAGTGGGGTCTTTGGAAGATAATTAGATCATGATGGT
GCAGCTCTTATGAATGAGATCAGTGCCTGATAAAAGGGACTTTGAAGAGCTCTCTCATTCTTTCTGCCATGTGAG
GATATAACAAGGAGACAATATGACAGTCTGTAACCTGGAAGAGGGCCTTAAACACAACCAGACCATGCTGACACCAC
GATCTCAGACTTCCAACCTTCGAAACTGTGAGAAATAAATTTCTGTTGTTTACGTCACCCAGACCAGGTACTTTCT
TACAGCAGCCTGAACTAACAAAACCAATTGTAATGTATGGACTTCATTATAAATCTGATTTCAAAGTAGTAAACGTG
TGGGCCGGAATTAGGAAGCAATGAGAAATATTTGAATGCTAACTGGATATTTAATGTAAGGAATATTTTTATGTTGT
TTTAGGTGGGATAATGGCGTGGATATGTTTTTATTTTTTTAATTCCTACCTTTATACAGACATGCTGAAATATTTA
CAGTTGAAATGATTAACGTCTGGGATTTTTTTCAAATAATCTCAGTGCAGAGGAACTGGAAGGGTTGTAGATGA
AACTTGAAGTGGATGTTTCTCTACTTTTTGGATATGCTPATAATTTTCCATATAAAAGTTCTGAAAACGGAAAT
AAAATGCTCACATTTGTGAGGCTAAGGCCAAAAGAAATCAGAGATGCATGAGAATTTCCAAATTCAGGATTATTTAAG
AACACATAGAGAAAAAATACTTCTGGTTTTGAGTTGCAAAAATTTATTTCTTTTATGCAATATACTAAAAAATCAT
AATTAATTGAAAAATATAATACTTCATATGTAAGGGGAGAAAACTACTCCACCAAAGATGTCACATCTTTTAATTC
ATTTGGAGATCAAAGAAATGTGTCTGCCAGGCAACCAAGGGCTCATGGAAAGGTGTGGTTTCTGTACAAATGCTATT
TGTCTAATATTTTGTGCTGTTAATGACTGTCCATTAGCATCTTCACTACACTTACTTTCATAGAAAGGAGAAACAT
GATTTATAGAGCCCTTTAGTGACAAGGGTGAGGATCCTACACACTATGTTGCTGGTTTCCTAGTCTTCAGCAAGAAA
GTGTAGGAGAGAAGCAAAAACGTCCTGTTCAACCCCTGCTCCTGGATGTGGCAAGGAAGAGGAGTTACCCGGCTTG
AAACAAAAGAAATCCTAAGTCTGACACACAATGTCATGTTTAAATTTCCCTTTCTCCAAAATGTAATAAATAATCTGC
TTCCATCTTCTAAAATACTATGGGACTAAACATCCTTTTTGTTATGCTAAGGAAAAGCCAGTATTCGCGTTGATTTAG
AAGAGGGATGTTCTGGTTATAGAACGATGCTGTGTCTCAGAAACACTTAAATACTATTAAGCTAGAAATAGAAGGGA
AAATAATGCTTCCCGCATCTCCCTCAAGTGTAGTCTCTTTTTTTAGCCTGATTTCCGACGAAATGTCTGAATGC
CTACAGTTATTTGGCCATCCTGAAAAGTGCAACTTATCCTGACGTCTCGAGGGACGGAAAAGTTACCGAAGTCCAAG
GAATGAGTCACTTTGCTCAAATTTGATGAGTAATATCAGGTGTCATGAAACCCAGTTTCAAGGAGAGGGGAGGGGG
CGTCAGATCTGCAGACGGAAGCAGGCGCTCCGGATTGGATGGCGAGACCTCGATTTTCTAAAATTGCGTCATTTA
GAACCAATTTGGGTCCAGATGTTATGGGCATCGACGAGTTACCGTCTCGGAACTCTCAATCACGCAAGCGAAAGGA
GAGGAGGCGGCTAATTAATATGAGCAGAAAGTCCGCTGGGGAGAATGTCACGTGGGTCTGGAGGCTCAAGGAGGC
TGGGATAAATACCGCAAGGCACTGAGCAGGCGAAAGAGCGCTCGGACCTCCTTCCCGGCGGCAGCTACCGAGAGT
GCGGAGCGACCAGCGTGCCTCGGAGGAACAGAGAAGTACGACCCCGGGACTGTCCGTGCGAGTAAGTGC

Fig. 1B

Human Nts Promoter GenBank Reference No. NG_047010.1 Gene ID: 4922

GATTATTTTCAGCAATTACCTAATAAAGGTCTGACATAAGTAACAGTACAAGCTTAGAAATCTACCTACTTTAGAGA
TGTTGTAATCAACAGGTACCTAACAGGTAACATCCACTTAAGAAGGCCAACACAGGAATATTATTAAGGACAAATGC
TTAAAACTTTTATCAGATATTTTAAGAACTAGGTAACCCCTAGAAGGATCTAAGGTATGCCGGGCATGGTGGCTCAC
GCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCATGAGGTCAAGAGATCGAGACCATCCTGGCCAACA
TGGTGAAACCCCGTCTCTACTAAAAATACAAGAATTAGCTGGGCTGGTGGTGTGCCTGTAGTCCCAGCTACTCGGG
GGGCTGAGGCAGGAGAGTTGCTTGAACCCAGGAGGTGGAGACTGCAGTGAGCCGAGATCACACCCTGCCTCCAGC
CTGGTGACAGAGAGAAGCTCCATCTCAAAAAAAAAAAAAAAAAAGAAAAAAAAAGAAAGGATCTGGGGTAAAAAGCCTTTA
AAATAAAAAACAGTTACCCATCTCCATAGCAAGGTGCTACAATCCTGCATTAAAGGCATCATTTAGGAAGTTCGTA
GGTACTTTTTAAGTGAAAAATACATACTTAACCTTTATCCCTACAACAAATGTTTTATTGGTTTTATGTGTAGCT
TGAAGGCATTAGATTAGAGCAAGAAACAAAAAGCCTAACACATTAAGAAAAATACCAATTAGAGGTCAAAGTTATC
TACATCATAATTTTACCAAAGTTATACATCTTTTTTCCCCAAAAGAAAAGTAGCATATAGCATCTATTTGAATTTGA
ATTATTTGACATAACTTAATGTTTCCCTATTCTTGAATATTTATCACATATCTCAATTTTACATTAACAACATAAT
ATCCATGTTATATATTTAAAATGAATTTCCATTAATCTTCTCCCCCTTTTTTCTAATTAATTAGGGATCAATTTTG
TCAACATATTGAAGAAATCATCTGAGGAAAATAAGAATCACATTTCCCTTTTTTACTATTAGACTGCTATCACACATTT
TAAAAGATCATTCTTTGTATTTGCAATTCAAAAGCAGAGAAAACAATAATTTAATATCATGCAAAGTATATATAA
TTTTCCCGATTTGTTAATCAAAGTGGCTTTAAGAGGATTCGTGCACAAAGATGCTCTGATAGTAACAGGAAAGTAAG
CACAAATCTCACTGAGACTCTGTTAAGTGAAAACCAAGTGTTCAGCTTCCATTGCTCCCCCTAATGGTAGGAAA
GCAGAAAAACATAGACGTATGTATTTACATTTTGTCACTAAATACTTTACAGAAACCTTCCCTCCATGTGAGTATG
TTCAATATTTGTGTTTTTATGTAAGTTCAGAAAAACAACTAAAAGTAATAATATATCAGTTATTATTAATTTCTGGT
ATTATATGAAAGACTCCTTGCTATTCTAAGTAATTTAATGTTTGGATTTAATCGCTTTGCTTAAGTTTTGGGTA
AAGGTGAAAAAGTTAAACTCATAGATGTATAATATAAATCAATATCTATAGGAACCAATCCTATTTTTTCTCAAC
TGTTACTACATGATTGATTTATTTAAAATTAACAAGACTCAGACAACCTTACATTCAAATATTCACATCTCTAAC
AGCACTGACTTGTCAAATTACCCCATGTATCTTGAATGCTTACTACAAGAAGAAAGTTTTACTCTAAAAGGCATTT
TGAACAATTTCTTTTGGAGAACTCAGACAAAGAATGGGTATCAGTGTAACCTCATGAAATACATGAAGACTATCATAG
AAAAGTGACTTTGGTGAATGGTGGTTATTTAGGATTGCTCCTTTCCAAAAGTACAATCTCTTTTTTTATGGTGAAA
AGAGTATTATAACAGGGAAAGAAAGCCGATGCAATAGTAAAACTGTTGAGAAGGGAATTATACAAAGAGTGAGACA
TGGCATCAAGAATGAATTCAAAAAGAGCAGAAAAATATAGGCATAAAAAAGAGATAATGTACAGAAAAAAGTCAGTG
ATACAACAACACAAAATTTTTACCTGCTAGAATGTAAGTAATTTAGAGCTGGATTTTATAAACATGAAATGTTTTTC
TAATACATTCAAACAAAAGTCCAGCACACATAGTTCAGTCACTCTCATTACTTACAATAAAAATATTTTTCTATTTGTT
AGGAAATAATATCTTATTTCCCTGGATCTATTTTCTTTTTATTTGATTTTCTTTCTATTTCTTAAACTTAATTTGCTT
AATTTTTATAACTGATTCTCTGTCTCTATTCCATCTTATTTCCAGCATGGATTATTTAAAACCTGTATTAGTTTTGGA
ACCACTAAACATTTGCTCAGAAGTTTGAATACCAGAGAAGCACCCCTAACTCTTCAAGAACTTCCAAGCCTAAGGAA
TCACTGATTTTCATGCATTCATCCTGGAGATTTTCCCTAAAAATAGAAATAACAGATCTCATGTTTCAAAAAATCAA
AATGACAACCTTTTGGAGTGGGGGAATGAGAAGTGGGAAAAGGATGATACTGGGGTTCTTTGTGAGTATGCTGTATG
TATGCTGTATGTCAGTGCAGTTGAATGACTCCTTCTGTGCGTCAGAAATCCAAGCAGCAGCAGCAGCAATTAGGGA
AGATCGTCACTTTCACTCAAGTTTCAGAAATGGGGGAGGAGAGCAGGGGGGACAAAGGAAAAGGGGAGGAGAAAGCA
GGCAAAAGAGGGGAGGGATGGAGGTGAAGATAGGGCACATCTGCAAAAGATAATGTCTGTACAATCAATGACATCAT
CCTCTGCTTATATATATAGGGGAATGGCCAGAGCACCTCTCATAGTTCACTCACTTTCAAAGCCAGCTGAAGGAAA
GAGGAAGTGCTAGAGAGAGCCCCCTTCAGTGTGCTTCTGACTTTTACGGACTTGGCTTGTAGAAGGCTGAAAG

Fig. 1C

Human Parvalbumin Promoter: GenBank Reference No. Z82185.2 Gene ID: 5816
CCAAAGGACTTGGACCTGAAAGTTTGTAGCATTGCAGGGACAGCCATCTTGCCACCCTCAGGGGTCAACCAGTTTGA
GAGAGTGGCACAAGGTATTGCTGAGAAGTAAGAGAAACAGCATCTTCCCTGACAGCATTGAGTTCTGGATCAAACCA
TGCTTGAACTTTCGTGGACTTTTCAGTTGCACGAGTTAGCAAATCCCCACTGTCTTAAGCCAGCCCAAGTCAGACT
TTCTCATCACTTACAGGCAAAAACAGACCTGACTGATAAACCCATTTTCTGGCATCAAGGCCCTGTATAATTAACC
AAATTAATAAAATGAAGCCTGCTTCAATCAGCACAGATTGAGAGCAAAAAAACAACAAAACAAAAAATAAAACT
AGATCATGTTTCCAGATATATGACTCGGGTTTTAGGACATCTTACCCTACTTTAAGTATTGTAGGGGGAAAGATCC
TCCAGAATCAGAAGTGTCTAGTTTAAATCCTAGCTCTCCCACCTACTTCCCTACCTGTGTGACCTTAGGTAAGTCACT
AAACCTCTCTGAGATTCTATTTCTCGAACGTCTGAGATAAAGCACATAAAGCACTAGGTACGCAGTAGGTGCTCAA
TAAATGCACCCCCCCCCAACACACACACACACACGATATGGTTTCAGCCCATTCAGATTTGCTTAATTAGAGGTA
CATGAAGAAGACCTATGGGGACAAAGAGGAAGGCCATCTGGGCTCCTGAGAATTCAACCACAGTAGGTGCTGCTCCC
GTCTTCCGGTCTTATTCTGGAAGCAGGATAGTGTGGTAGAAAGGAGCAAGTGTCTTGGAGTCAGAGAACCAGGGGCTG
AAATCCTACCTCCATTTCTGTGATCTTAGGCAAGTTGCCCAATCTCTCTGAGCCTTGTTCTTCCATCATTAGTAAAA
AGAGAGGGTTTTGCTACCTCTTAAGGGGATACAAGAATCAAAGTGCATGCTGTGCACACAGAACCAGCACACTG
TTCAACAAAAGTGTAAATTTTCCCAGGCCCCAGCCAGCGATCTTCTCAAGGGTTCATCTCAAGGTTCTCTCT
GCATCCCGGCTCCCTGAGCTCAGCCATGCCACGACTTGACGAGATCAACTCCTTGACTTCTCTGATGACAAAGCCC
CCAGGGTCCAGCCCTGACCTCACTCCAGAGTTCCAGACACATCTCCGCCAGGGTGTCTTCAGGTCCCCTAAACCCAG
CATCAGCTCTTGGCTCTTCCACTACTCTCTGGGGATTTGGGTAAGTCACCCTGGCCTTGGTTTTCTTCATCTATAAC
ATGATGTCATTTGTAGAAGTTGTAGCCGATCACCACGGAGGCTGTCCCAGCCCTAACATCCTAGGATTCAACACCA
CTTACTCTATCATCCCTTCGACTGAGCACTACCTCCTCCCTACACTCCCTGCCTCAAAGTCAACACCTTCTTCTT
CAGCAAACCCACCTTGAATATTTAGGGTCAGCTTGGATTTGTCCTCTTGTTCATGCCACAGCCCCAATTTCTGGAA
GCTTCTCTCCAAGAGGTGCTCCCTATCTGACACTCCTTCTGTGTTGCCACCACCAGCAACCTAGCTCAGGCCCCAG
CACCACACCTCAAGGAGGCCCCAGTCCCAGCTTCCCCATGCAGCCTGCCCTCGGCCCTTCTATCCATGGAGCTTC
CAAACAGCCTTTGCATGGAGCCTGGGATTCTCGTGTCACTGTGAAGAAGTACAGCCCAACATTGACAATCTTCGTG
CCCTGGAGATTCTTTTTCAGGTTAGGGATGAGGAGAGGAACATTCATGGTGGTCAGATTAGATATTTCACTACGTATT
TATTGAATTCATTTGGTTCATTCATGCTTCTCAAACACATCCCTCAGCTGGTCCCTCTCCAATCCAAAACAGACAATG
TCAGAGATCTCTTTGCAAATCATGAAGGGCTTGGGCCTTTGTGCCTCAATGTCACACGCATACAATTTAGGGGGTC
CATCTTCCCCTCGCCCTAGACCATCTATAGGGCACAGTTTACCTCTGATTGAGCTCATGTTACAGGTGGAAAGACTG
AGAAAGAGAGAGGAAGGGACTTGCTGAGAATATGCGGAACATTTCTTCTACCAGGCACTAGATCCTCGCACAAAA
GTGCTGAGTCCGCTCCCAACCCAGGCCCGTGGCTTTGAGCAGCAGGTCACTTAACATCTAACGTCTTTATGCTGTT
TCCTCACTGTGCGAGAGCAGCTATGTCTACCTGGCAAGGCTGTAGTGAGAGATCATATCAGCATAGGAATGGGGCT
CAGCCCCATGCACAGAGGACAGTTCTTGTTTTATTCTTTTCCCTTGCTGTTTTCTTCTTCTTCTTCCCTTCCCTGGCAGAAATGGA
GGAAGGAAGCATCGCTGCCATCTACAGTGGTCACGGAAGGCTTCATGGAAGAGGGCAGCCCTGCCTGGGCCTCAATT
TTGGGTGCTGGAGGGAAGCAGGGGCCAAGAGTTATTAATAGTCTTGGCCTGATGGGCCAGGGAGGCTGAATGTGAT
ACAGACACCCAGCACCACGGTTGGGGAGTACCTGACACCGGAAGGGGAGGGGGCCGGGGCTACGGGGAGTGCCACCT
CCCAAAATAGCCAGAGCAGAAGCCTATATAGGTGGCCATCCACCTCCAGGCTCACTTCCCGACAGGACTTCCCACC
AGCCCAGCCTTTCAGTGCAGGCTCCAGCCCTCCACCCCCACCCGAGGTGAGTGGCAGCTACCGAGGTTGGAGGATAG
AGGGATGCAGCAGGATGAGCCAGCTGGAAGGGAGAGCTACATCTCCCCTGTCCGTAGTGACCCGGGGAGGGGGTGC
GGTGGGGGTGCTGGAGGCAGGGCAGCTGTGGAATGTAGGGCTGAGAGCATGCATTCCTGCTTCTCCACCAGACTCC
TGGTGTGCCTGGGGCAAACTCCCCCACCCACCGCCCCCGTGGCTGGGCCTCAGATTTCCCAGCCTTAGAAC

Fig. 1E

Human NPY Promoter: GenBank Reference No. NG_016148.1 Gene ID: 4852

AGGTATAAGGTGCAAAATACACTGGATAGGATTGGCAGTAATCAGATATTACAGAAGAAAACATTAGTGAACTCACA
GACATAGCAATAGAGACTATCCAAAATAAAATATGAAGGAAAAAATGAGCAAAACAGAAAGCAAAAACAGATCACCAA
CAAACCTGTGGCCAAATATACACTCACCGTCTGACTCAGCCATTCTGGTTTTAAGTATTTTCCAAGAGAATTAAGGC
TTTATGTCCATACAAAGACTTGCATATGAATGTCAAGGCAGCTTTATTTCGTAAAAGTTTCAAGTGAAAATAACCCAAA
AATTCATGAGCAGTAGAATTGATTA AAAATTTTGAAGTATATCATATAATGAAATACTGCCAGCAATAAAAAAGAA
TAAACTATTGCTACATTTAACAATGTGAGTGGATTCAAAAATAATGATGCTAAGTGAAAGAAGTCAGACAAAGAGTA
CCTACCGTGGAACTATATTTATGTCAATTCTAGAAAACGCAAAACAAATCTCTAGTGATAGCAGATCAATGGAGGAG
GGGGTGAGGAAGAGGCAAAAGGAAGGAATTACAAAGGTACATGTGGAAATTTGGGGAAAGTGATGTATAATCTTCATT
TTCTTGGTTTTAGTGATGGCTTCTGAGCATATAACACACATGCATATGTGTAAGAATATATCCAATTTGAATATTTT
ACACATTTGTAGCTTTGTATATATTCAGCAGTATCTATTCATTCCTTCTGCTTCTTTACCTTAGGTTTTAGTCATGAA
ACCCTGGGTTTTATGTGGTCCAGGTTCTATCTGAATCAAGCTATGAACCTGCTATCAGTAAGACCTCCTAATTGCA
AACCACATGGACCTTTACCGGTTATTTGACTTCTCTCGGTCAATACCTTCTCTAGTCTCCACTGATTCACCTCCTTT
TGAATCTCAACAAGCTCAACAGTATCTCAATGTTATCTTAAACAAAGCTGTTAGAAAATAACAACCTTGACTTTGAAAC
AAAGGAGAGAAATGGCTCAGCAGCTAGGAGAAGATGCAGGGTTGAGTTGCCAACAGTTGGTTTTGTTTGTATTTGG
CCAGGGGATGTGGCTTGGACTGGAGAGAAAGGAGATAAGGATGTAAGCACATGTAGGGCATATCACCCCTATTTTT
TATTCCTGAATCCTTAAACCCTCAGAATAAGTTCTTATTTCTTGAGAATCAATGACATTATCTTAAAGCTAAATTAATC
AAGCCTCCACAGTGTCTTCTCAATAGTGGTGTGGGCCCTTCTAGAAAGTAATTTTTCCCAAATTCAGTGATACAT
TTTAAAGTTCAGATTTTAAATTGATATGAATCTGTGATACACTCTAAAATAAGATTATTTTATTGAAAAGTGGACTGTA
ACTTTCCCTTTATCTAGGAAGAGCTCTAAGTTAGAAGATGTTTTGCACCTTTTACCGAAGGCTGTGTCTTGTAAAGCAC
CCCCGAGCAACTCTGAGAGCCTTGATTTTTGTGTCTCAGCATATGTTTGTGTAATACAGAAAAGAGAAGCAGTTGGC
AAGTGAAAAGGGATGTTGGTCTCCAAAATATAGTTTTGATCCCAAAACACACAAAACACATACATGCAAAGGATTTGTT
TGCTTCACGGTTTTTTGATATTTAATTC AATGCTGTTGGAACAGCACAAAACTAAGTGTCAAGTTTAAACAGAATCACT
TGTCCTTTTAGCATTAAAATAACATGGAACCTAATGCTTTAATTTCCCAACATGCCCTTTTATTTAGAAAGATTCAG
ACTTATATTTTCAATTTAGAAATAAAATGCCATTTTTATTTAGAAAAGATACAGGAGCATTTCATTCACGGAACCTTTCAGAT
CTCAGTCCACTGCATAAAATCTTGATCCTGTAATAATAGTTTCTGTATCTTGCATATTCATTCAACAGGTTTTAACGC
GATGAGCAAATTAATGTTTCATCGTTTTTAAACATGTTTCACTTAATCAGAACCACATTCCTCAACGTTAATTGAACG
TACATAGGACTATACAAGGGTTAGTAAATAAGACAGAAACTGTTGTTCAATTTAACCACCGTCACCTTTGGACCAAAAA
AGAAAAATATATATTTTTAAAATTTGAGCTTAAAAGAGTCTCTAGAAGCTGGAAGCGTGGCTCTTTTTTTCAGCAAACCT
GGGGGAATAGGTTTTACCGTGTTCCTCTGGGGAATTTTGAATCGCCACACTCATGTCTCGACCGAGCCTGGCTCG
CTGCGTCTGAGCGAGTACTTTGAGGAAGGCTGATCTAGAAAAACCAGCTGAGAGAAGGGGCAGAAAGCCCTGAAACCA
CGGGCGGGGTGGGGTGGGGAGCGCAGCTTTGGGACCCTCTAGCCGGAGACTTCCGGCAGCTGCCTCCGACTTGTTT
TAAGTACAGGAAAAATCTGTGCGCCAGTTGCCTCACTCCAACAGCGCGCAGTTGTGCCCGGCGAGGATGCCGCGCT
AGTCGTGGAGATGCCCCACCACAAAGAGGATTCAGGTGCTTCCTACTCCGGCACCCAGTGGGTTGGTAGTCTCTGTTG
GCAGGAGACAAGAATCGTCTGGGCTGCTCCTATCTCTGGCAGGACTAGACGGGGCGTGAAGGAAAGAAGGAAAGAAG
GAAAGCAGGGATCGGGCACTGCCCGAGGGCAGATACTTTGGGCTTTGGTGTGTCCAGCGCGCTCGGAGTGGCTGCC
TCGCTCACGCGGTCCAGGCCCCGCTTCTTCAGGCAGTGCTTGGGGCGGGAGGGTTGGGGTGTGGGTGGCTCCCTAA
GTCGACACTCGTGC GGCTGCGGTTCCAGCCCCCTCCCCCGCCACTCAGGGGCGGGAAGTGGCGGGTGGGAGTCACC
CAAGCGTACTGCCCGAGGCCCTCCTGCCGCGGCGAGGAAGCTCCATAAAAGCCCTGTCCGACCCGCTCTCTGCA
CCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGCCGCCCAGCCACGCCCGCGCG

Fig. 1G

Human SST Promoter: GenBank Reference No. AC072022.19 Gene ID: 6750

CCTGCCCTGTGTGCCCTCTTGTAAAGCACTGAAGGTCTCAGGACCTCAGTTTCCTCCTCTGTGAGGTGGGAATAGCAT
GCCCTGAAGTGTGGATGAGAAAAGTGTGTTTGTGAGCAACAGAGGACTGGGTAAGGATTCCTAGTGAGTTTGGTTGGT
CTGGGCAATAGCGTCCCCAATACAACCACAAAACACTTTACCCCTCCAGCTTTGAGACTTTGGGAGAGATGCCCTGGG
GGTTGATTACAGAAGGCTCAGGTTGGGAAAGTGTGAAGTGTTCATGCTAAACCAACCTTTAAGCTATAACTGGCCA
TGGAGGGCTTAAGGGAGAATTTATGTCCCTTTTTGTCCCTGGCTTCTCTGATAAGTGGTTCTCAGACTCATAACTCTC
CAGGAGTTATAAAACAACAAAAGCAAACCCCTTAAGTCACTCTCATTTACAGCTTCAGCTCTTCAGCAGGGTATGAGG
GAAGCAACTGTTTACTATTTCATAAGTAGATACTTAAACAGATAGACATCATGAGGTTTTTGTGTTGTTTGGT
TGAGAAGCAGTTGAGGAGGGGAAGAAAGAAAAGAGGAGAGAAAAGAGAGGGGAGAGATGTCTTGAGGCAGAGACTG
GGATAGGCACTGGCTAAGCAGGGTGAGAAGGCAGGGAAAGAGCCGGGCTGACCCAAACCAAGTCAGAAAATGATTG
AGAAGAGCAAGAAAACAAAGGAATGAGGATACAGAGTCAAGAGAGGAGACAAAAGAAGGATTGAGTGAGGAAAAT
CTGAAACATAAAATTTGCAGAAAAGGTTAAGGAAAAGGAGGAATAAGAAGGAGGAGAAAAGTGTAGAGGGAGAGCACAAG
GATGTGGAAGGAGGGGAGCAAGCGTCTGGGGAAGGAGACAGAAGAGATCCTAGAGCACAGGGGAAGATGGGGAGCTG
CTATTTGTTCTTCGGCTGGCTCCTGCTTTGGAAAATCCTCGTTTCCTACTCAGTGGGTATGCCAAAGACCACATCC
TGGGTACAGGAGATATGAGATCATTGGAGGTACCTAGAGACAGTCCACAGTGATAGAACTAAACTCTGAGTCCTTAG
AGGCCAGAGAGAGTTGCAAGATTTAGAGAAATAACATGTATTTCCCTAGGACTGGGTCCACAGCTCCAGATTCATT
GATCTCTTAGACTACTCCAACACATGTGAATGACTTTTTAATGCCCCACTTTGTGCTTAGTCTTGGCTGGCCTTGTC
AAGACCTGGAAACTTTAACACTTCTTGCTGTGCATTTCCGCTTTGCCTTGGATTACAAGCACAAAAGAATAAGTGA
CAATTTCAAGCCATTCAGGATACTTCCCAACCCCTTCTGCCTCTCAACACTGTGGTTCGGGTCTAAGTACTGAGA
ATATTTTAATACCTAATATGAGCTTCGCATGGTTTTCCAGAGATGCAGCATATCTTTTTAGCTAATATTGGCTTTTT
GAAGCTCATAAGATAACAGCTCTTAAAGATCCTGTAGGGATCATCTCGTCCATGCTAGGAAATTAGTGGTCTTCC
TCAGTAAAGAACTATTTAGATAAAAAGCAGTCAAGACTCTGGCCTGAACAGTAAACATTTAACCAGAGTTCAATCAGA
ATTC AAGGACAGGTTTTCTTAAACTTTCTTTGTTTCTAGGAGATCAGGCAGAGCTGAATTTAACCAAGAATCTTTTG
ATCCTTTCCACATATAGATATAAATAGTGGTCAATATGTTCTGGGAGTTCCTAGACCTTATATGTCTAAACTGGG
GCTTCCTGACATAAAACTATGCTTACCGGCCAGGAATCTGTAGAAAACCTCAGAGCTCAGTAGAAGGAACACTGGCT
TTGGAATGTGGAGGTCTGGTTTTGCTCAAAGTGTGCAGTATGTGAAGGAGAACAATTTACTGACCATTACTCTGCCT
TACTGATTCAAATCTGAGGTTTATGAAATAATTTCTTAGATTTGCCTTCCAGCTCTAAATTTCTCAGCACCAAAATG
AAGTCCATTTCAATCTCTCTCTCTCTCTTTCCCTCCCGTACATATACACACACTCATACATATATATGGTCAACAATA
GAAAGGCAGGTAGATCAGAAGTCTCAGTTGCTGAGAAAAGAGGGAGGGGAGGGTGAGCCAGAGGTACCTTCTCCCCAT
TGTAGAGAAAAGTGAAGTCTTTTAGAGCCCCGTTACATCTTCAAGGCTTTTTATGAGATAATGGAGGAAATAAAGA
GGGCTCAGTCTCTACTGTCCATAATTCATTCTCAAATCTGTTATTAGAGGAATGATTTCTGATCTCCACCTACCAT
ACACATGCCCTGTTGCTTGTGGGCCCTTCTAAAATGTTAGAGTATGATGACAGATGGAGTTGTCTGGGTACATTTG
TGTGCATTTAAGGGTGATAGTGTATTTGCTCTTTAAGAGCTGAGTGTGTTGAGCCTCTGTTGTGTGTAATTGAGTGT
GCATGTGTGGGAGTGAATTTGGAATGTGTATGCTCATAGCACTGAGTGAAAATAAAAGATTGTATAAATCGTGGG
GCATGTGGAATTTGTGTGTGCCTGTGCGTGTGCAGTATTTTTTTTTTTTTAAGTAAGCCACTTTAGATCTTGTACCT
CCCCTGCTCTCTGTGATTGATTTTGCAGGGCTAATGGTGCCTAAAAGGGCTGGTGAGATCTGGGGGGCGCTCCTAGC
CTGACGTGAGAGAGAGTTTTAAAACAGAGGGAGACGGTTGAGAGCACACAAGCCGCTTTAGGAGCGAGGTTCCGAG
CCATCGCTGCTGCCTGTGATCCGCGCTAGAGTTTGACCAGCCACTCTCCAGCTCGGCTTTTCGCGGCGCCGAGATG
CTGTCTGCCGCTCCAGTGCAGGCTGGCTGCGCTGTCCATCGTCTTGGCCCTGGGCTGTGTACCCGGCGCTCCCTC
GGACCCAGACTCCGTCAGTTTTCTGCAGAAGTCCCTGGCTGCTGCCGCGGGGAAGCAGGTAAGGAGACTCCCTC

Fig. 1H

Human GRPR Promoter: GenBank Reference No. NG_012512.1 Gene ID: 2925
GCCTGAAGCCAAATTCAGCCTTCCCTCCAGAAGCTTCCCTTTTGACCTTGCTCATAGCCAGTGGGAAGAGGCTTTG
TCTCCACACTCTGTGGTCCCATTGAACTACCTGTTCTCTAAATTTCTATCAAGTCACTGTTGCCACCTCATGTTA
GAGCCCCACAGAAAATCCAGTCTTTTGGAAAGATGAAAAAGGTGACTCTATTGACTGAAATAGAAAACAGAAGTGACA
ACCCTGTCCCAACACATAAGAAAAGATGCTGAGTCATACTCCAATTTCTATTTCAGAAAATGGACTCCCTGGGGACAGA
GATTTTATATTACATTTGGTTCCATGTTCATGTTTACATGTTCAGAGGCATCTCATGTTTACCAGTAAATAAAAAGCTAA
GCAAATGTCTGAATACGTTTGGTGTTTGGTGTTCGGCTCTGCCGGAAGGTGACACATAATGGTAGGGATGGAAAAGA
GTCATTATAGTTAATTAGTTGAAATGACATAGAAATTAIGGAATTAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGAG
GGAGTCTTGCTGTGTCGACAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTCAC
CGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGTGCCCATCACCACGCTTGGTTAATTTTTTGTAT
TTTTAGTACAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCATGATCCACCCGCTCGGC
CTCCCAAAGTGTGGGATTACATGCGTGAGCCACCGCACCTGGCCGAATTAGCTTTTTAAAGCATCCTTGATCCCC
GAAAATATTAGATGTCAAACCTCAACGCACCTTTACTCTAAAATACCATTAGAAGAACTATAAGTGTGTGGAACA
CATAATGCTAACACCAGCTATGAGAAAATCAATATCTATCAGCATCCCCTTAACCTTACATTGGAAGAAAACACTAACCA
CCCAATTAGATTTAAGTAGTGAGGCTGACTCAGCACACAGGGGTGTCTAAAGAAATAAAGGGAAAACAACATCCAGAA
GTTCTCTTTGTGAACCAAAAATATGCCTTTTAGACCAAACCTTCTTAGCAAGAATACAAGAATCCATCACAATCTCACC
CAAACCTGCTCTAGTGCATTTACAGCTGTTCTTTTCCACCCCTGTCTTCCAATCTGGGTGACCCCTCTGGATTTA
TAGATGTCCTCTGCTCAATGTCAATGCTCTTTCCCTTTATGCCTTGATCCTAGGCACATATGATTTTCTTCAATCAA
AGACCTTGTC AACACTTAACTTTAAAGATATCGTCTTTTCTGGAGAAAAGGTAGTTGCTTCACTCCAGAGAGGGGT
TGGGGTCTAAAGAGCTGTGAGAGTACACATCTTATGCTATTTTTCTCAGCCTCTGCTCAGTGCCTGGCAACTGGT
AGATGTTTGATAAATTTTTTCAAGTAAATAAAGGAGTGTCTAATCACTCGTATGAGTGCCTTGCCTATTGATCTGA
GGTCAATCACTCTTCTGAATCATTGGGCTTTTCCAAAGTAAGCCTTTCCCCCTCAATCTAATAATGATAATAATAA
TAAGTGTCTAATATTAATTGAGCACTTACTATGTGCCAAATACTATGCAATCTTAACATGAATCATTTTCACTAECTT
CATAAGTTCTCCTCACCTGCAGATGAGGAACCTGAAGCTTAAGACACTAAGTAACTTGCCATAATATAAATGAGG
GAGCCAGGATGAAGCAGAGCCTGTGACTGTATCATTAAAGCTATATTGCTGGCAACTAATCAACACCCTGGGCTC
ATGGCTATTGGCTGGTTACTGGTGCTACTGATCTTCTGCCGAGAAGCTCTTCCACCTTAGCCATGCAGCATGACTCT
CCCTCCTGCTGGCAGAGAGGGGGCTGAGCCTTTCTATTTACATAGAAAAGCATGGCAGCAGCCTCAGTGTGGAAAC
CTGCCACTGGAAATGTCCATAACAACACAGTTGGGGGCTTCTTTGTGGGCCCTGGCATGGTAAGTGCAAGTTTTGT
TATTCCTTATGGGTTCTGAAAAATGAGACTTACCTGTTAGTGACTGGCTTACGTCATGTACCTGGAGGAGCTGGC
TTCACATACGTCATAAAGATGCACTCTAATAATGTATTTAGAAGTTGTTGGCTAAAGGTCTAAGCCTGATTCTAATA
GCACTTCTCAATTAAGCTTTTTCTAGCACTCCTTCAACGATAACTTACTTCTTTTACCACCCACTCAATTCCTCAG
TATTGTATCTATCAGCCTTTTATAGTCTTTATTTTTCCACACAGGGCTATAAAGAGGATATTTGCTATAAAAACATGG
CAAACATTAATTAATAAATGCAAAATAGCTGCATCAAAATGCCGATTATAAAAATTTTTAGATCAGATGAGAAAAGAC
CCATTTTTCTGGAAAAGACTATTGATCATTGAGAGTTAAGAATACAGCTGGTTCCCAATTTAATTTCTCCCTGGTAA
ACAGAAATAGGAATGGCTTGGCAAACTACAGGAAAGAACATGTGTGCATTGTCTTCTGGCTTTCCAGATGTCAGT
TGCTGAAAGTTTAAAGGTGTGAGTCTGTGCATGTGTTTTCTGAGGATCAGTCCCTGTTCAAAGAGGCAGTGGGAAGACT
GAGTGGGATAAATCACACATGGACACCCTGTGCATCAGTGTGCGTTTAAATCAAAGACAGACCTCATTGATAGCAA
TATTGACATGTCATTCTAATGAATAGAAAAAATGAGAAAAATGGGATGTAAATCCCCATCTGGATTATGGGGATAG
TATCAGAAAAGATTTTTCAGTGCCTTTGCAGAATGCTAGCAACATTTATTAATAACCTACCCTAGGTGCTATGTGCTTA
CATGAGAAGCCAAAGGTATCTGTTAAGCTAGGTAGGAATGCACTCGGCTGGTTGCTTCTCATCTGGAGAAAGCCTA
CACATGCTGCTGCCAGCGGCCAGCTGATCTTAGGTGTTTAGGCCTAGAAGACCAACCAGCTCCAAATCACTTAAAG
CCTAAACGTTCCCTGTCTCTACTAAAAATACAAACATTAGCCACGCATGGTGGCGGGCGCCTGTAATCCCAGCTACT
TGGGAGGCTGAGGGAGGAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCAGAGATTGCCCATTTGCACTC
TAGTCTGGGGCAGAGAGTGGACACACAGAC
ACACACACGCTAAACATTTCAAGGCCAGGATGCTTGACAGATGTGATTATAAAAATGACAAAAAGCACAAAATCC
AAAATCTCGTATAAGCTCAGTGGCTGTGGCAGCGAGGTTGAAGAGCAAAGGCAGGCCGGGCACCTGGCTGATGATGT
GTGGACCCGTGTCACAGCAGGGCCCCGAGTGCAGGTGTGGGTGGGGCCAGTCTCTGCCGCTCACCCCTATTCC
AGGGACACAGTCTGCTTGGCTCTTCTGGACTGAGCCATCTCATCACCGAGATCTCCCTGAATTCAGCCCACGACA
GCCACCCCGGGCGTTTTCTTGTGTTGTTGTTGGGGAGGGAGGCAGCGGTTGTTATCAACCTCACCCCTGCAGAGGAG
GCACCTGAGGCCCAGAGACGAGGAGGGATGGGTCTAACCAGAAACCACAGATGGCTCTGAGCCGGGGCCCTGTCCAC
CCTCCAGGCCGACGTCAGTGGCCGAGGACTGCCTGGGCCCTGCTAGGCCTGCTCACCTCTGAGGCCTCTGGGGTG
AGAGGTTTCACTCTGGAAACACTTCACTTCTAGGGGGCTGGGGGCAGCAGCAAGTTGGAGTTTTGGGGTACCCCTGCT
TCACAGGGCCCTTGGCAAGGAGGGCAGGTGGGGTCTAAGGACAAGCAGTCTTACTTTGGGAGTCAACCCCGCGGTG
GTGGCTGCTGCAGGTTGCACACTGGGCCACAGAGGATCCAGCAAGG

Fig. 11

Human PRKCG Promoter GenBank Reference No. NG_009114.1 Gene ID: 5582
CCCGCCAGCCTCGCGGGGCACGCCGGGAGGCGGAGTTCTCGGTCTGTCCCGAGAGTGGCTGGTCCGCGAGGCTCGG
ACTACCAGTCCCAGAATGCACTGCGCCCGCAGCCCGGGGCGGGCCGTGGTTGCCCTGGCAACAGAGAGGGCTCCCG
GGAGCGGGGACTGGGAAGCGCTCCCGAGCCGGGGAGGCGCAGAGCCCGACCAGAGAGAGGGCGGGGACGCGGGTAGAG
CGACCAAGAGGTGTGGAGGCCGGAAGAGACTGACCGCGCCGCCCTTGGAGAGACCCCTTTCTGAGAGGGGGCGCA
CAGAGAGGATGCCGAAGCCAGCGAGATCTAGAGAGAGGGAGACAGGGATTGAATCACAGAGACACTTAGAGGGAGGG
AGAGACCTCAAAGACAGAGAGATTCACAGGGCCAGAGAGACACGTAGAGTGGGTTCAGAGAAGAGGACAGAGGACAGA
GACATAGAAAAGACAGGAGGGGAGAGAGACTGAATCACAGAGACACAGGGAGAGAGGGGAGAGACCTCAGAGATGGAGA
GAGACTCACAGGGCCAGATAGACACATGGAGTGGGTTCAGAGAAGGGGACAGAGAGAGAGACACAGAAAAGGGAAGAG
GGAGAGAGACTGAATCACAGAGACACAGAGAGGGAAGTCTCTATCTAGAGACCCTCGACAGAGATTCCTAGAGCCAG
AGACAGAGATTCAGAGAGCCAGAGACACAGAGAGATTCATAGAGACATATAGAGAGATTCAGAGAGCCTGAATCACA
GAGATTCACAGAGCCAACGAGACAAAACAGAGAGATTCATAGAGCCAGAGACACAGATTCGGAGAGTCAGAGAGACAT
AGAAAGATTCATAGAGCCAGAGACACAGAGATTCAGAGAGTCAGAGAGACATAGAGAGACATTCATAGAGCCAGAGA
CACAGAGAGATTCATAGACATATAGAGAGATTCAGAGAGCCTGAATCACAGAGATTCACAGAGCCAAAGAGACAAAC
AGAGAGATTCATAGAGCCAGAGACACAGAGGGGATTCGGAGAGTCAGAGAGACATAGAAAGAGATTCATAGAGCCAGA
GACACAGAGATTCATAGAGACATAGAGATTCATAGAGCCAGAGACACAGAGATTCAGAGAGTCAGAGAGACATAGAA
AGACATTCATAGAGCCAGAGACACAGAGAGATTCAGAGTCAGAGAAACATAGAGATTCATAGAGCCAGAGACACAGA
GAGATTCAGAGTCAGAGAGACATAGAGAGACATTCATAGAGCCGGAGACACAGAGAGATTCAGAGTCAGAGAGACAT
AGATTTATAGAGCCAGAGACACAGATTCAGGGAGTCAGAGAGACATAGAGAGACATTCATAGAGCCGGAGACACAGA
TTCAGAGTCAGAGAGACATAGACATTCATAGAGCCAGAGACACAGATTCAGAGAGTCAGAGAGTGAATGATTCAG
AGAGCCAGAGACACAGGGAGAGTGAATCACAGACACAGAGGGACGGGGAGATCCCCAGAAAACAGAAAGAGATTCATA
GAGCCAGAGAGACAAATAGAGATTCGGGTTCAGAGAGAAAGGGACAGAGACAGAGACAGAGAAGAGAAGAGGGGAGAGAG
ATTGGGTTCAGAGAGAAAGGGACAGAGACAGAGAAGAGAAGAGGGAGAGAGAGACTGAGTCATAGACAGGAGAGAGAC
CCCCCTAGCATCAGAGAGAGAGAGAGATCAACAGAGCCAGAGAGGGACAAGTACAGAGAAACAGATGGAACCAGA
GAGATATAGGAAGAGACAAACAAAACAGAGACGGAGTTGCAGAACCAGGGAAGGGAGAGAGACAGAGACAAAGGC
ATTTATAAAGACCGGTGGAGGTGAGGAGAGAGAGGGGAGAGACAGGGGCAAGCATTTAGAGAGTACTCCCAGAGAGG
AAGACAGAGACGGACTCCCAAAGAGATCAAGTTGCAGAGGGAGGGGGAGACAGAGTCACAGCCTGAGAGAGAAATAGA
GATTCACAGAGCCAGAGAGACAAAAGACAGGGAAAGAAACAACTCAGGGAGACAGAGGCGGAAGAATTTATCAGACG
TAGAGGGAGAGACAGAGGGGAGACTGATTCACAGTGGGAGAGACCAAGACCCCGAGAAGAACCCACGACACCAAGACCC
AGAGATGGCGACAGATACAGATGGAGACACACAGCAGAGGAAATAGAGAAATAGAAAGAAATAGAAACAGCATTCT
CGGAGACAGGAAAAGAAAACAGATCCACTGAGAGGCAGAAAACAGAGACACATCGAGAAAAGCTCGCTCCAGGAATAG
AGGGAGAGGGACAGAGGTACAAGAAAGACACACGCAGGCAGAGAGCTACACAAATAATGGAGAGGGCCAGGGGAGGA
AATAAAGACTCAGCCGGCATCGGAGAAAGTGAGAACCTTAGCGCCCTGCCTGTCCACTGCTGGACCCCTAGCGTGG
GCATAAAGTTTGTGTAAGGAAGGAGAGGGGAGGGTTCAGACACAGGGACCCAGGGCGCCACAGGACACACGAGGC
ACCCTAGTGGGGGAGGAACGCGGGGCAGGATGACAGATTGCAGGGTGGTGGGGGGGAGCCAGGCTCAGAGGATGCCC
CTCCCTCCAGCCAGCCCCGGAGTGGGTGTGTGCACGTGTGGGGGGCGGGGAGGGAGGACATTTGTCCCGTGTCTCC
GGGAGGGGAGCGCCTTTAAGCCGAAACCCCGCCCTCTCGGTCTGTCTGGCAACGCCCTCCCCAACCCGGGGCTCCCA
CATTTACAGAGGTGCCGGAGCTGGAGCTCCACCCGCGCCCGCCGTGCCTCCGGCTGCCGGCGCCCTGCCTTTGGC
TCTTCTCCCCACTCGCCCGCTCCCCCTGGCGGAGCCGCGCGCCCGGGGTGCCGCTCCCTGCCTGGCGCGCTCCCG
ACCTGGAGGTGCCTTGCCCCCTCTCTGCCACCTCGGAATTTCCCTGTGGCTCCTTTGATCCTTCGAGTCTCC

Fig. 1J

Human Calb2 Promoter GenBank Reference No. AC106736.4 Gene ID: 794
CGCTCATGAGATCACTGTGCGAGATACTTCCCTTCATTTCCCTTCTGTGACCTTGAAGGGTCTGGGCTACATCATCT
CCATGTCTCCATCCCATTCCGATATTCTTGAAGATCAAGACCCTGGGTGGCCATTAAAGGGGAATGGAAGGGAGGT
GGTAGATTTTGATACGTTTGGCAAAGAGGTTGACATTCCTGTTGTTGCAGGCTTGGCGGAAGTACGACACAGACA
GGAGTGGCTACATCGAAGCCAATGAGCTCAAGGTAGGATGGGCCTTGGGAGGGTGTGAGGCCAGAGTGGCGGTGGG
CTTAAGTGCCTGAGGAGGGAGGAGATGTTGGATGAGGGGCATGAGTTTGCGGGCTGCTTAGGAATACTCAGACCTG
GCACTGAATTGTTGGACTTGTGTTAGAGAAGTCAGGGGAAATCAGTAACATAGAGCTGCCAGGCTGTAGATTTCAACG
AAACCCAGCTCTTCTGCACCTCCATGCTCGGGACAGGAGTCCCTCCAGGCAATTCAGAAAGATTGGCCTCTGGCTCCT
AGGTCCACCTCCAAATTCCTCTGGCTATCACCCAGTGATCCCCAGGCACTGCTTAGCTCCGTATACTGGTCTCCCA
GGAGGCAGAGCCAATCTCTAGCGCCTATTCTGTGAGGCAGGGTTGCACCACCAGCTAGTACAGCCTTAAAAGTCACT
CCCCAAGAGTTAGGAATTATGAGGGCCCTGAGTCATAGAACTGGTAGACCTGAAAAACACACACACACACATTGAGA
GACTGTCTGAATGAGCAAGTAAGGAAATGAATGAGGGACCGAATGCACGAGTCAGGAGTACTAAAGAGGCCCTTTTGT
GTTGCAGGGATTCTGTGACACCTGCTGAAGAAGGCCAACCAGGCTACGATGAGCCCAAGCTCCAGGAATACACCC
AAACCATAGTGAAGTGAACAGAAGTGTCCCTCTCCCCAGGGTGCAGGACTTGTGCCCAAGCCACTTGGGCTCTGGT
GTGCAGGGTCCCTTGTGTTGCTGATTCTTCAGGCCCAAGGGAAGTGATTACAGTGGCAGCTGGCAAAAAGGGATGCT
ACTTCGTGGCTTACATAACCTTTGAGGTCCTGGGTGTGAGCTGACTCGTGGGCCAATGTGATTGTCTGTCTCCATG
GCAACCTCTGCAGCTCTAGGAGAGGATGATCTTGGAGAGAGTGGGCCTTTAGTGCCGGCTGCTGTGCCTCAGCTGC
CCCTGTCCCTGAGGAGGGGAGAGAGGAGCAGTGAACGAGTCCCTGTGGTCCACCCAGGGGACCCCGTACTGATTT
AGCCCATGTTGGTTCTTGGCCCTACGGACCTCAGAGGAAGCATGAGCACGTGTCAACCGTCCCTCTCCATCCCTC
TCCAGTAAAAGGGGATGTCAGGTCAGAGAAATTCACAGCAAATAACCCAGGCACCTTTCTGTCCCAACAGCTACGG
ATGTTGACTTGAACGGGGATGGCAAATTTGGCCCTCTCAGAGATGTCCCGGTAAGCACCTCACCCCGGGGTCAGT
ATACTGGCTCCCACAGTCACTTCCCTGTGTTATCCGTCTCTGAGATCCATTGGTGGGAAAGTGACAGGTGGGGTGT
AAGAAGCTCAAGACAAAGCAAGATAGAATTGTGACCGTCAACACCTCACCTTGTCTGTCTCCCTCGTTTTTGA
ACTTCCCCTGATTCAATTATGTGTGAAGTGCTCAGAAATCATTCTGTAAGTGCAGGCACCGCTCTGCCTTCCCCTC
CGCTTGCCCTTGCCCTGTGCAGTCTCTCATCTCTGCTCTAACATTTTCTCCCCAGACTCCTGCCTGTCCAGGAAA
AC TTCTGCTTAAATTTTCAAGTAAAATTTGCTTTTCCCTTCCCTTCCCTCATCCCTCTGAGCCTGGCCCTGCAC
CCTCCTTCCCCCAACGCACCACACACAACACACTACACACACCCACACACACCACACACACAAAACACACCACAC
ACACAACACACACAGATCACACACACAAAACACACACAGACCACACACACCACATAACACAACACACGCAGACCACAC
ACACTACATATCACACGCACACACCCACACATACACAGAGACATCACACACACCACACAGACCACACACCACACAC
AACACACACATCACACATGCACACACCACACACATAAACACACACACAAAACGCACACCACACACACACCCTGC
GCTTCTGCTTCTGTCTTTAATACCCTGGTTCTTGCAGGGCATGAAGCTGACCTCAGAGGAGTTAAACGCGATCTCA
CATTTTACGACAAGGTAAGAGAGGGAGTTGGCATGGCAGGGAAAAATCAGAAGCCCATCAGCCCGTCCAGAAGGGCTC
AGCTTCATCCCTGGGAAGAGACAGCTTTCCAGGGTGGCCGGGCCGTGTGGTTTCTTCTGCCGCATCTTCTGCTG
TATGAGAAGGCAAATGTCAATCTCCACCGGTGGCCTATGGAGCCCAAGGGGTGGTTTCTGCAGAGTGCAGCCGAGA
ATCGTTGGGGGAGGACTATGCTTAGAACTAGGGTGTGACCAGCTGTCCGGAGCCAAAGGGAAGAGACACTCAGAAC
TGCCCTGGTGCCAGATCACAATCTGCCAGGGCCAAGTCTTCTCTGGGAAGTTGGAAGTTAGATGATCTCCATAC
CCACCCCTCCCTGGGCTGTCCCTGCCACATGACTCCGGTGGTTTTCTTTCATAACCAAGTGTGGAGGTAACTTTA
AATAGCCCCGGACTCAGGGAGTTAACCAAATGCTTCTTGAATCTCACTTAAATTTTCAACGCACATGAAAAGCACC
ACAATGAAAGGCTACCCAAAGCTTGACCCACTGCCACCTTCTGCCATGACTGGTTAAGGCAGAAGGGACACATTA
TTTTGTCAATTACACGATCTGAACACCCCTTTTGCACAGAGTAATGGAGAGGCTAGACTCTTAGACATCCCTGG

Fig. 1K

Mouse CCK Promoter (2441 bp) (GenBank Reference No. AC131660.4 Gene ID: 12424
GAATTCCCAGGGAAGATCCCAGGGAAGATGAAGAAACCATGGCTACAATATTTTATTAAATAAAGAGTCCATTGTGC
CACCTTCTCCAGCTTCTAACTGTCCCTTGACACCTTTGGCTCTCCTGGTGGCTTTTCTACTCTGGCCTTTGACCCT
GCCTGTGGTCAGGTGCTGGACCCCTTCTCCCGTTCCCTTCCCTGGCTGTACACCTGGGAATCTGGGCAGAGATGCCT
TTTCTCTCCCTCGCTTCCACCTTTTGAGTCTCTTCTACAGCTTCCAGGTGGGAAGCCACCATCTACAGAAAGAG
TCTTGGGTGTACCTCCAGTGTCCCTCTGTCCAGGACTTGAGATCACAACCTTCTCTAGCTGTCCACCCATAACCTG
GATTCATCCCCACGCCCCGCCAGACACACACCAGTTGGTGTGTTTTCTTCTGAACCTCCCTGTGGCCAATACACT
CCCACCACCCCTTGTCTCTCAGCCAGAACCTTACAGTCAGCCCCAGACACGGAGTACCTTTGGGTTTTCTTGAAGAG
CAAGATGCTGCTTCCATGCCTGGAAGTTTCTGCTTATGCTACTGTTCTAGCTATTTCGGATGTTCTATTGTAGGCAC
TTAGGACTCGTATAGTGTCTGTACATTTTCATGATAGTGAATAAATTTACAAAAGCATATTAGGCTTCTATAAAT
CTGTCTCATTCTCAATGGCCCTCCCATCTCCTGTCTTCTAACCTGTCTCTGGTCTCCCGTGTCTGCCCTAGGGAC
ACCTCCATGTCCACCAGACTCAGTGGAAATCCTTACTCCGCCCTTGGCTATTAGTGCAGATCTGAACCTCAGTTC
TTGTACTTGCAGGCAAGCACTTCACTGGCTGAGCCGCCCTCCAGTTCCAGCTCCAGGCCCGGCTCCCAAAGGTGT
TTATTTGTGTGGGTATTTATTTTGTCCAGTCTTGGTTCACCCGCATCCTCAGGGGCTGGGCACAGTTTATAAATCTT
GAGGCAAGCGATGGAGGGAAGGAGGCAGCTAAGCGTCCATATCTCAGCCACCGACCCAGGGAAGTCAGCGCTGTGG
ATTCTGACCATATCGAACAGCCTTGTGCCAGCTGCTTTATCCACAATTCGGGACATGCTCGATCTGTACAGATAC
ATTCCCACAACCTGAGCTGTCTTGTGCGGGAAATCACCCACAGCATTTAATCTGTTGCTGTTTAAAACATGTTGCC
TCTAGGTTGCAGACACCGCTAGAGCCACAACCATGAACCTAAACTCTTGGCATCACTTGTGTTTTCTCATAGTCCCC
CTCAGCCGGAAGTCCCCAACTGTGTGCCTTTTCTATTTAGAAAAGAGTTTCTAACCTTTCTCCATTACCCTAGCT
TGACAGGGTTGAGGGCATTGGTTGCCCTGGCTGGTGGTGGTACCCTCAAGTTACAAGCTAGCAGCAAGGAGGTTGCTGTG
GGCTTCTCAGTATGTGTTCTGTGGAATGGGGTTAGAGGATTCAGCAAATTTCTAGCACCTTGGGCATAGATAATCA
CTTTGTTATGTGAGAAGTGGGGTTGCAGGATTGTGCGCACTACAGCAGAGAGAGCCCCCTCTCTCCTTCTGCTTG
GTAAGAGTCTTTTTCTCAGCCAAGATCCTCATCACCCAGCGAAATCCATAACTTTAGAGGGACTAGACTGGAAAGG
GTGATCTGAGCTCTTGGGAAGGTGCGAGCCAGCCCGCATGGCTCAGCCAGCCAGAGCTTGGGAGTGCCTGAGACAC
TCTCTGGCGCCACTTACAGACAAAAGCATCAGTAGATGATAGGCCCTGGGAAGTCTGCTGGAAAGAAATTACAA
ATCTTTTTCCAGAGGCTTTTCGAGAAAAGGCAGGAGCTGCACCCGATCTTACAATTTGTGTAAGAATAGAATCCAGG
ATGCCAACTGCAATTGAGTTCTGAAAAATTGGGAGCCCGATTTCCCTCTCTTACTTGTGAGAGCCCACTCAGGCTG
AGGTGGTCCCAGAGAACACACCAGGATACATCTGCTGACACCCAGCCTGTGAGGGTCCCCAGTTCCTTGAAGGA
TTTGATCCCCAAAGCTCACTGAACCTGGTTCAGTCTTCCATTCAGATAAACTCCTGTTTTTACCAGAGAGTGGAGG
TGGCACCTCCCTGAGGTGGACTCTGCACAGGCGCCGACAGGATGGGAAGGAAGCTCTTGTAGATAAAGAGTAAAGACC
CATGCAAAGTGCCCCCTGGGAGGGGCTATCCTCATTCACTGGGACGCTTCCCTTCTCTCCGGAGGGCCACATCAAT
CGGTGGTCCCTCCAGTGGCTGCCCTGAGCACGTGTCTGCTGGACTGCGTCAGCACTGGGTAAACAGATGACTGGC
TGCGAACCGGGAGGAGCTATTTAAGAGCAGTCACCCTCCCGCTGCCCTCACCT

Mouse Calb2 Promoter Region: Genbank Accession No. U34818.1 Gene ID: 12308
CCATGGCGATGGAAAGCTGACCAGTGTCTCCCTCTGATCAAGGAATCCTTTCCAAGCTCACCAGAGAGCACAAGCATA
AAGGACAGGAACACAGACTCATGTAATCCCCAGAACAATCCAAGATGTCAATACCCACACACCCATTTTACAGACTC
GGAAAGCCAAGGCACAGACAGGCTGTGTAAGCCAAACAACGTTGTGGAGGTTTTGTTGTTGTTGTTGTTAGGAACTAG
ACCCGAGGAGTTTTGATTTCTATTGCAACTGTCTTTAGGACTGAGCCTTCTTGCCTTCTCGAAGGCAAGACTCAGGCT
GGGGACTCTAGCTTAGTAATTTCTCAGCCCTGGCAGCAAGGAATGCTGGGTTACAGAAGCCCCAACAGTTAGCCTA
TTTTGCTGCGTCTTTCCAGTCTGTCTTTGTAACAACCTCAAACCTGTGTGCCTGGGCAACACACCAGCAGTTTTGA
AACTTGGGCTCCATGTTGCCCTTTGAGGTTAGCTCCGAGCTACCTCAAACCTGACCCAGGAAACAGCCTGCTCTTCT
CCGCTCCCCCCCCCTCCCCCACCACCCCGGGTTCTCTCTCCCTAGCGACCTGCTTTAGATTCTCACCTCCTT
CTCTTTTGTCTCTCCCTTTCGAAGGCAGCTCAGCTAACACTCATTAGCACATGTTAATGAGCAGCAATTAAGTCTCTG
TCCTTCTTTTTAGGGGCAGGGTGTCTGTGTTGCTCTGAAGGTAAGGTGTCCAAGAAGCAAGCACACACTGCAGACC
TTTAGAGTAGGGAGGATATGGGACGGAGGCTGGCTCTGTGATTGAGGAGACCCACGGTGTGCTGTGCTTGTCTGTCT
GTTTTCTTTAACAGAAGTTTCAACATCTTTGGGTCAGAGTTTACCAGCATCTACCTACGGGACTACGGGAGGCTCC
AGTCTGCTACTACTGGATAAAGGTCTAAAAGTCTGCAGGATGTGACAGATAACCGGAGGGAAGTGGGTTACTGAACA
GTGGAGTAGTTCTCCATTCCCATCTGAATCCTCATTGCACCTTGTGATTCCAGTTGTCCACCTACGGTAAAACCT
TGAGAACCCTGCTTTCTGCAATCCTGGTACCCTCGAGGGAGTACAGGACAGGAAGAGTCTGGGCTCAAATCTT
AGCTTTGCTACTTGTAAATAATGCTATTGCTGCGACTAGAACTGGGTGTGCTCAAGATGGACAGAGGGAAGGGAAG
GCAGGAGTGCCTCTCCCATTTCCAGCTAAATACCTGCGGTGTCCCCGGAGGGCACCAGAAGTCTCATTGAACAC
TCTCTCCCGGTCCCAGGAACCTTGGCAGAGAAGAGCCCCCGCCGTCAGCGCCCGCCCTGCGCGATTCCCTGAG
TGTGCGCGCCCCCTTCCGGCGGCCGACCGGGCGCAGCTCCGGGCTGCATATAAAGGCAGCGTGGCGCGCAGCCCCA
CGCGAGAACCAGAGCCAAGCGGCACCGAGTGACAGCGCTGAGAGAGAGGCTTAAGATCTCCGGAGCGGCTCGCC
ATGG

Fig. 1L

Mouse PRKCG Promoter Region: Genbank Accession No. AC245272.2, Gene ID: 18752
GGACTAGATCCTGGATCCCTGGGTATGAGGAAGGAGGGGAGTTGTGCCTAGATTCCCTAGATCCTGAGAGACAAGGGA
CCTGGAGGAGTTCCAAAGGATAGAATCAGAGGCATCCATGTGTGTAAGAAGTTGTATCCAGAAGCTGGCTCCTGTGT
ACTTCGGGAGCTGTTCTGGGACAGTGTGAGCTTCCAGAGGTTAAAGCAAGCCCTTCTGTCTTTCCGTGGGCTTGACC
TTAGCACGACTTTTCTTCGGGGGAAAGTTATGAATAATTCTGTGTTTCATCACAGAACACAGGATGATGGGCTGCCGC
GCGGTGGTGGCTACACCTTTAATTACAGCACTCCAAAGACAGAGGCAGGCAGATCTCTTTGAGTTCGAGGCCAGCCA
GCCTGATCTGCATAGTGAAGTCCAGTACAGCCACAACAGAACAACAACAACAACAAGATGCAAGGTCAAAGAGACC
AAAGTTAACCAAGTGCACCTGGGTGAGCCAGTGAAGTGGACTGAAAATACTTGCAGGGGCATAGAGAAGCCACCCCA
ACATGGAAAGACTCATGAAGACGCATTTCTGGGGTACACTGCTCAACTTGTAGTCAGCTGGGCAGAAGACTTCTCCT
GTCCTCTCTTAATTGTTTGGCTGCTCATATAATTACTTCAGCTTTGGGAGGGGCCTCATAGCACAGCCCTGTAACCTTC
TGAGCCTTGGGGGTTCTATGGTTTGTCTTTCTAACATGTAATTATTGTGTGTGTGCATGTATGTGTACACCCCATAG
CCAGTGTATGGAGGTCAGAGGACAATTTGCAGAATCCACATGGTCTATCCACCATGTGGGTCTTGGGGACAGAACT
CAGCTTATCATGCTCTGTTGTAAGTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCAATTTATTTATTT
ATTTTCCATATATGAGTACATTGTAGCTATACAGATGGTTGTGAGCCATCATGTGGTGTCTGGGAATTGAACTCAGG
ACCTCTGCTTGGCTCCAGCCCTGCTTGGCTCCAGCCCAAAGATTTATTTATTATTATATGTACGCTGTACATATAATAA
TAAATACATACATAAGTAATATATTTATTTATAATAATAAATAAGTACACTGTAGCTGTTTTCCGACCCACCAGAAGA
GGGTGTCAGATCTCATTACGGATGGTGTGTGAGCCACCATGTGGTGTCTGGGATTTGAACTCAGGACCTTTAGTTG
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GCCCTTAGTCTCTATAGCTTTTGGAGTTAATTGAGTCCCTCCCTCCCTCTATCAGCTGATGTTCAATTCAGAAGAAA
TAACTACAGAAGTACAATAGTAATAAGAAAATTGGACCTGGAAAACCACCTTCTCATATCTTTAGTGGCATCAGCCG
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TGGTACACTAGAAGGCCGAGAGGCCTGTCTGAGGTCTAGCCCTGCATGACTGATCTCGAAAAGTACAGATTTTCAAGT
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GATAAGCTCAGAGATAAGAAAAGCAGAAACTGAGCAGTCTTCAATTTCTCCAGGTCAGAGTGGATTGGGGGTGGGGT
GGGTGAAGCTTGAAGGAGGGGAGAAAAGAAAGCATAATGTTCTGGTCAAGATCTCTGGAAGAGGAGTGAAGGA
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Fig. 1M

Mouse Calb1 Promoter: GenBank Reference No. L42901.1 Gene ID: 12307
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ACTAGCCAGTACATGCCAGTAGGGCCTAAGTCTAAATACAGATGCAATAATTCAGTAACATGAAATGGGAAAGAGTT
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AAAAATGTATATCTAAAATAAATATCTGAAGATATTTGTTGCAGCTGTTTGTACAGTAGAACACTAAAAAGATGG
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CGGGATAAATACAGAGAAGTGGGTGCGGGGTGCGGAGAACTCCGGAGGACGCCCGAACGGAGCAGCACCGCGGACAG
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Fig. 1N

Mouse Nmu Promoter Region: GenBank Reference No. AC133184.3 Gene ID: 56183
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CACTCATATACATAAAATAAATAAATAAATCTAAAAAAGAGAAAAGAAGGAAGGAAGGAAGGAAGGAAGGAAG
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CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT
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TGCCCTTTCTCCGAGCTCCTCGCCTTTCAAAGGAGGTTAAACAAGATCAGATGCCCTTTTTTTCTGCAGAAGGAA
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GCTACCCCTCCGGCTCCCACCCAAGTCCTTCCACAGGTGGGAGTGGACCGCCATGGTTTAATTCCATTCTCCAGCT
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AAAAGTTGGTGGCGCGCGGAGATGGTCACTTTGGTGTCTGAGCTCAGCAAGAGGAGGCGCACAGGACACGCTGAGGG
ACAGCTAAAACACCCGCACAACACAGGG

Fig. 10

MRCSPGGVWLALAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQP
LTVYFSL SLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNVSEY PGVKTV
RFPDGGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSC
YIDVRWF PFDVQHCKLKFGSWSYGGWSLDLQM QEADISGYIPNGEWDLVG
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MRCSPGGVWLALAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQP
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RFPDGGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSC
YIDVRWF PFDVQHCKLKFGSWSYGGWSLDLQM QEADISGYIPNGEWDLVG
IPGKR SERFYECCKEYPDPVTF TVTMR RR (SEQ ID NO: 19)

MRCSPGGVWLALAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQP
LTVYFSL SLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNVSEY PGVKTV
RFPDGGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSC
YIDVRWF PFDVQHCKLKFGSWSYGGWSLDLQM QEADISGYIPNGEWDLVG
IPGKR SERFYECCKEYPDPVTF TVTMR RR TLYY (SEQ ID NO: 20)

Fig 2.

MRCSPGGVWLALAAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQPLTVYFSL SLL
QIMDVDEKNQVLT TTNIW LQMSWTDHYLQWNVSEYPGVKTRVFPDGGQIWKPDILLYNSADE
RFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPPFDVQHCKLKFGSWSYGGW SLDL
QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTF TVI IRRRPLFYAVS LLLP
SIFLMVVDIVGFCLPPDSGERVSFKITLLLGYSVFLIIVSDTLPATIGTPLIGVYFVVC M
ALLVISLAETIFIVRLVHKQDLQRPVPDWRHLVLDRIAWILCLGEQPM AHRPPATFQAN
KTDDCSGSDLLPAMGNHCSHVGGPQDLEKTPRGRGSPLPPPREASLAVRGLLQELSSIRH
FLEKRDEMREVARDWLRVGYVLDRLLFRIYLLAVLAYSITLVTLWSIWHYS

Fig. 3A

MRCSPGGVWLALAAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQPLTVYFSL SLL
QIMDVDEKNQVLT TTNIW LQMSWTDHYLQWNVSEYPGVKTRVFPDGGQIWKPDILLYNSADE
RFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPPFDVQHCKLKFGSWSYGGW SLDLQ
MQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTF TVTMRMRMGYYLIQMYIPS
LLIVILSWISFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVS YVKAIDIWMAVCL
LFVFSALLEYAAVN FVSRQHKE LLRFRKR RRRHHKED EAGEGRNF SAYGMGPACLOAKDG
ISVKGANN SNTTNPP PAPS KSP EEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWI IYK
IVRREDVHNQ

Fig. 3B

MRCSPGGVWLALAAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQPLTVYFSL SLL
QIMDVDEKNQVLT TTNIW LQMSWTDHYLQWNVSEYPGVKTRVFPDGGQIWKPDILLYNSADE
RFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPPFDVQHCKLKFGSWSYGGW SLDLQ
MQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTF TVI IRRRPLFYVVS LLLP
SIFLMVMDIVGFYLPNSGERVSFKITLLLGYSVFLIIVSDTLPATAIGTPLIGVYFVVC
MALLVISLAETIFIVRLVHKQDLQQPVPAWLRHLVLERIAWLLCLREQSTSORPPATSQA
TKTDDCSAMGNHCSHMGGPQDFEKSPRDRCSPPPPPREASLAVCGLLQELSSIRQFLEKR
DEIREVARDWLRVGSVLDKLLFHIYLLAVLAYSITLVM LWSIWQYA

Fig. 3C

MRCSPGGVWLALAAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQPLTVYFSL SLL
QIMDVDEKNQVLT TTNIW LQMSWTDHYLQWNVSEYPGVKTRVFPDGGQIWKPDILLYNSADE
RFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPPFDVQHCKLKFGSWSYGGW SLDLQ
MQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTF TVTMRRTLYYLLQTYFP
ATLMVMLSWSVFWIDRRAPARVPLGITTVLTMSTIITGVNASMPRVSYIKAVDIYLWVS
FVFVFLSVLEYAAVN YLTTVQERKEQKLREKL PCTSGLPPPTAMLDGNYSDGEVNDL DN
YMPENGEKPD RMMVQLTLASERS SPQRKSQRSSYVSMRIDTHAIDKYSRIIFPAAYILFN
LIYWSIFS

Fig. 3D

MGGGRGGIWLALAAALLHVS LQGEFQRRLYKELVKNYNPLERP VANDSQPLTVYFSL SLL
QIMDVDEKNQVLT TTNIW LQMSWTDHYLQWNMSEYPGVKNVRFPDGGQIWKPDILLYNSADE
RFDATFHTNVLVNASGHCQYLPPGIFKSSCYIDVRWFPPFDVQQCKLKFGSWSYGGW SLDLQ
QMQEADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTVTVMRRRTLYYGLNLLIP
CVLISALALLVFLLPADSGEKI SLGITVLLSLTFM LLLVAEIMPATSDSVPLIAQYFAST
MIIVGLSVVVTVIVLRYHHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGEDKVRPACQHK
PRRCSLASVELSAGAGPPT SGNLLYIGFRGLEGMHCAPT PDSGVVCGRLACSPTHDEHL
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Fig. 3E

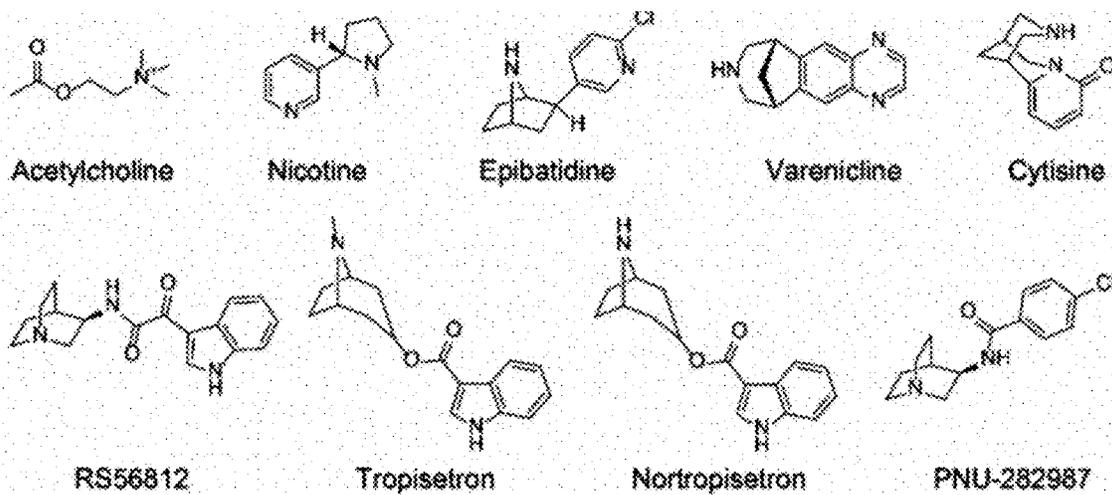


Fig. 4

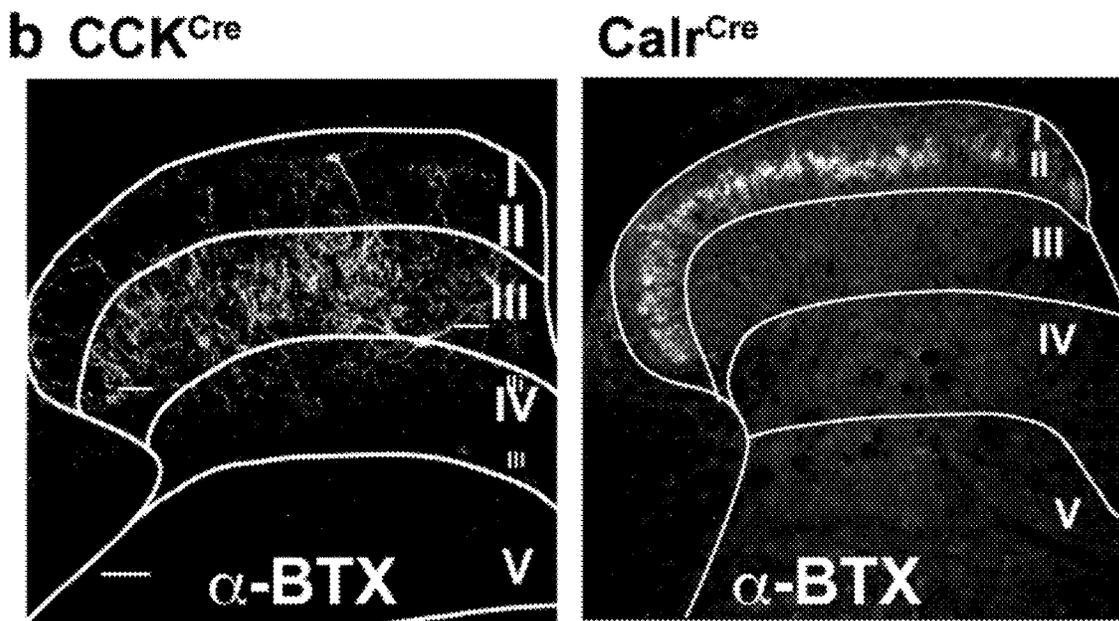
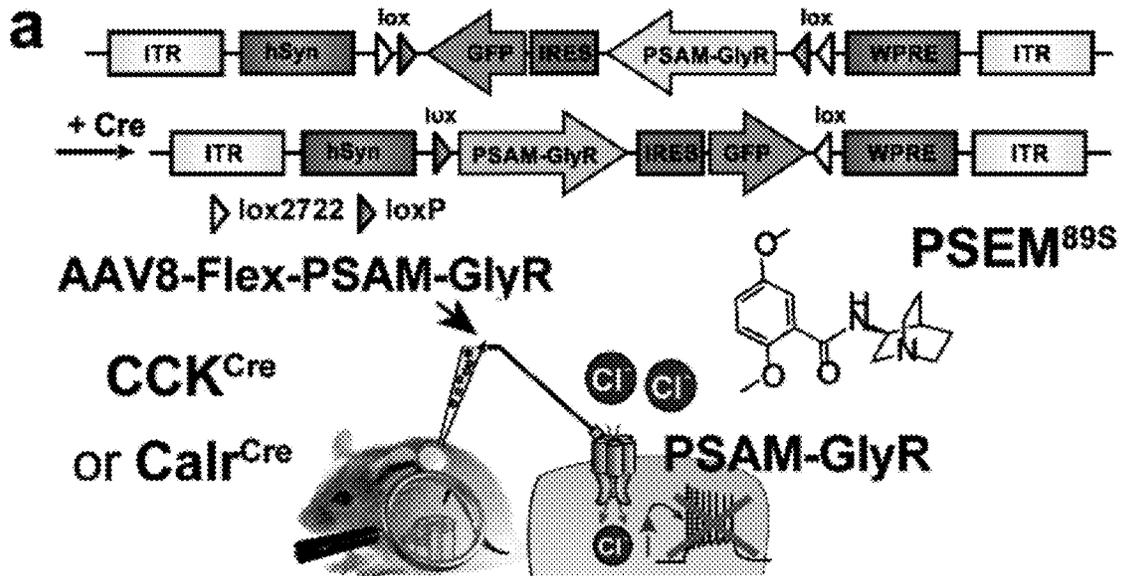


Fig. 5

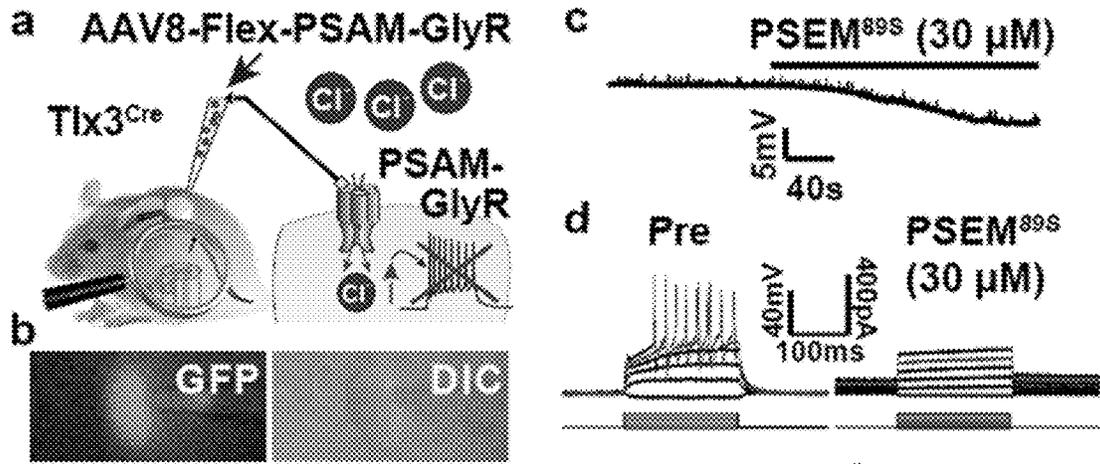


Fig. 6A

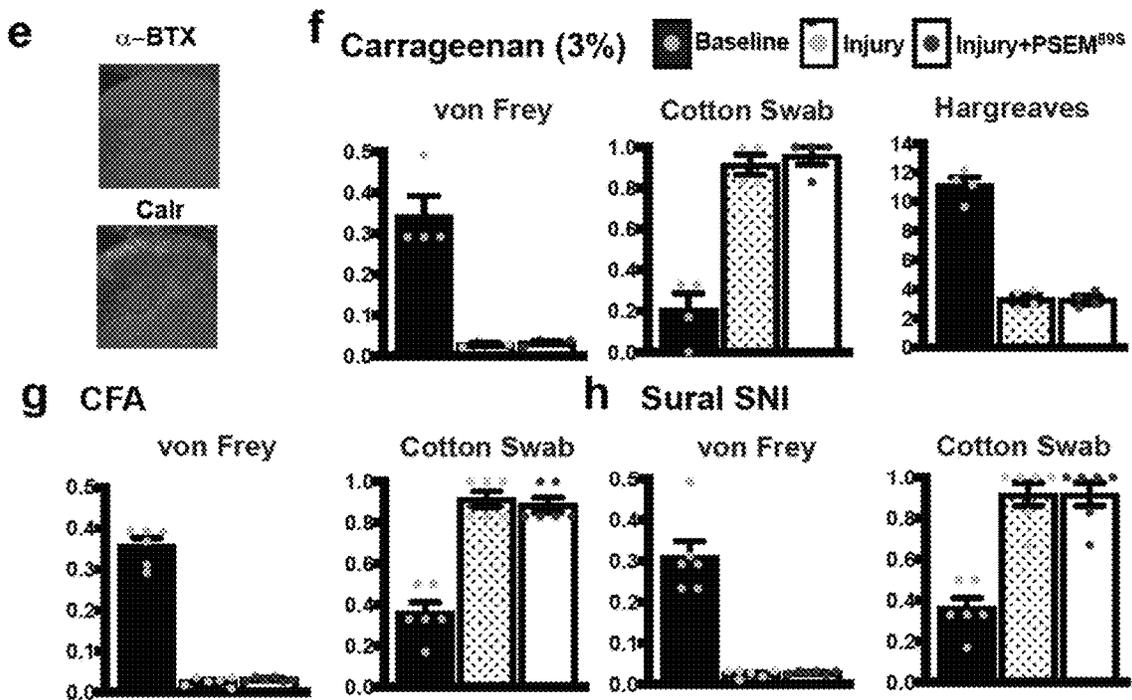


Fig. 6B

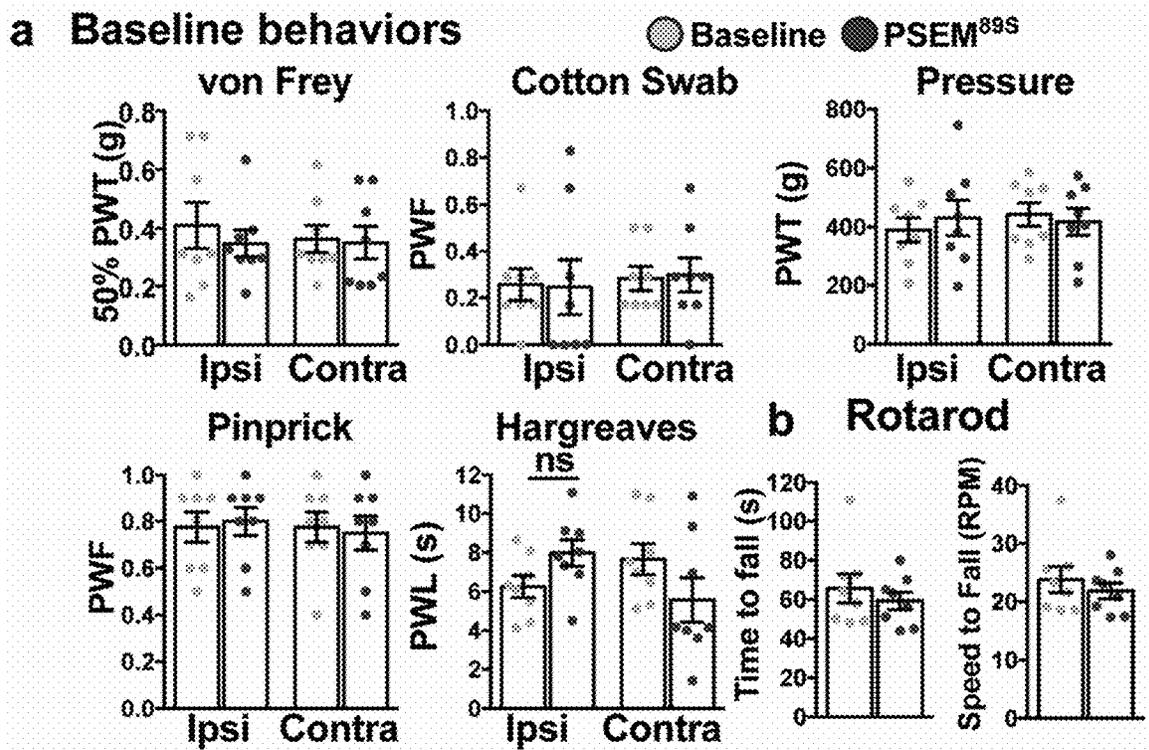


Fig. 7

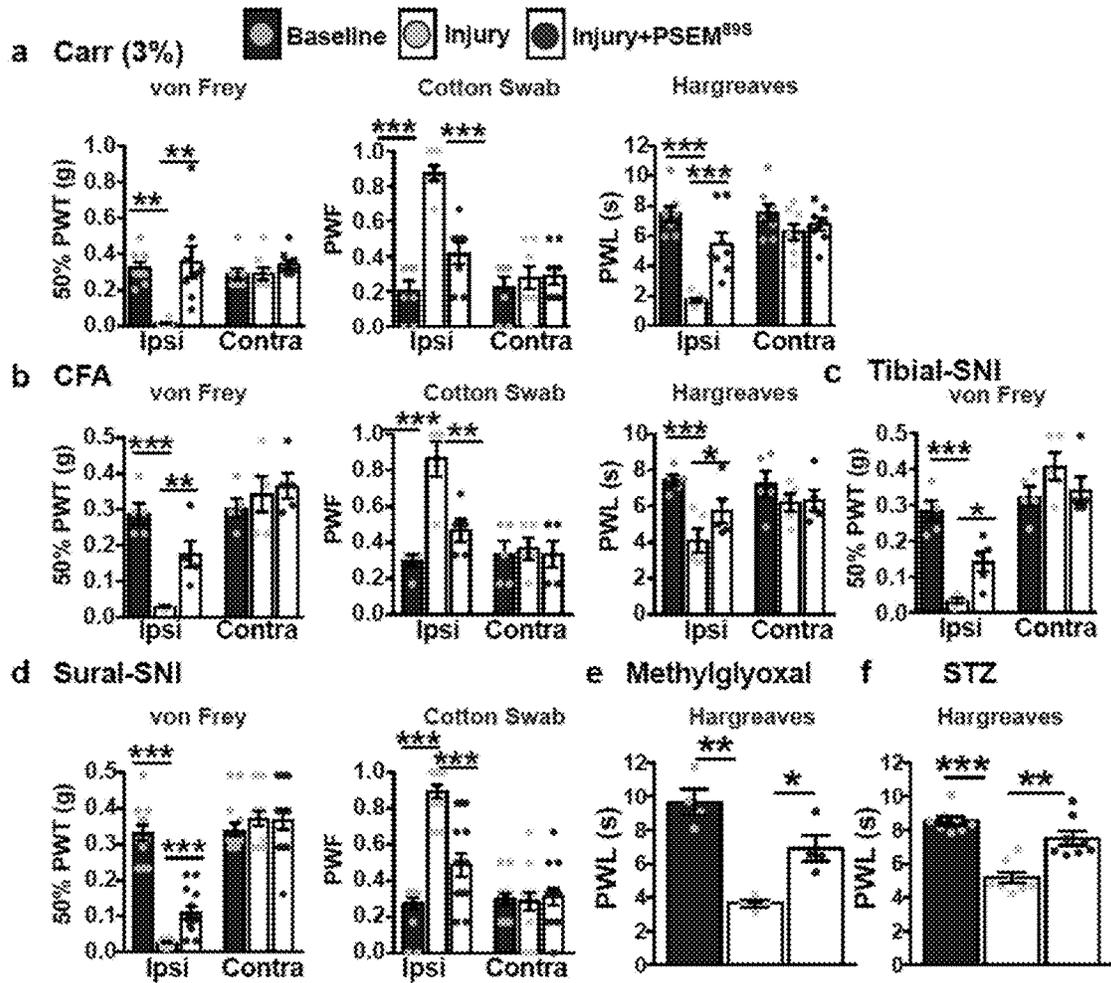


Fig. 8

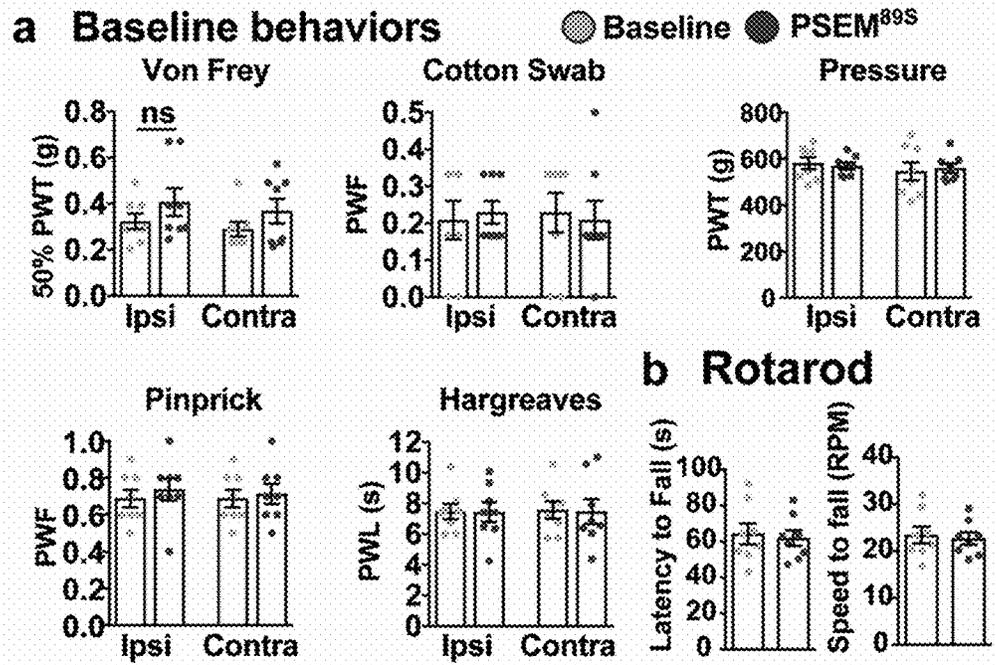


Figure 9

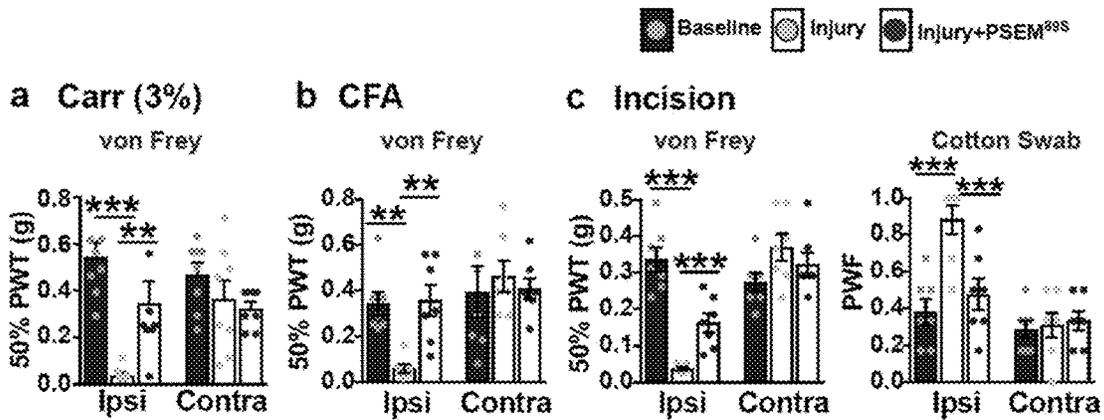


Fig. 10

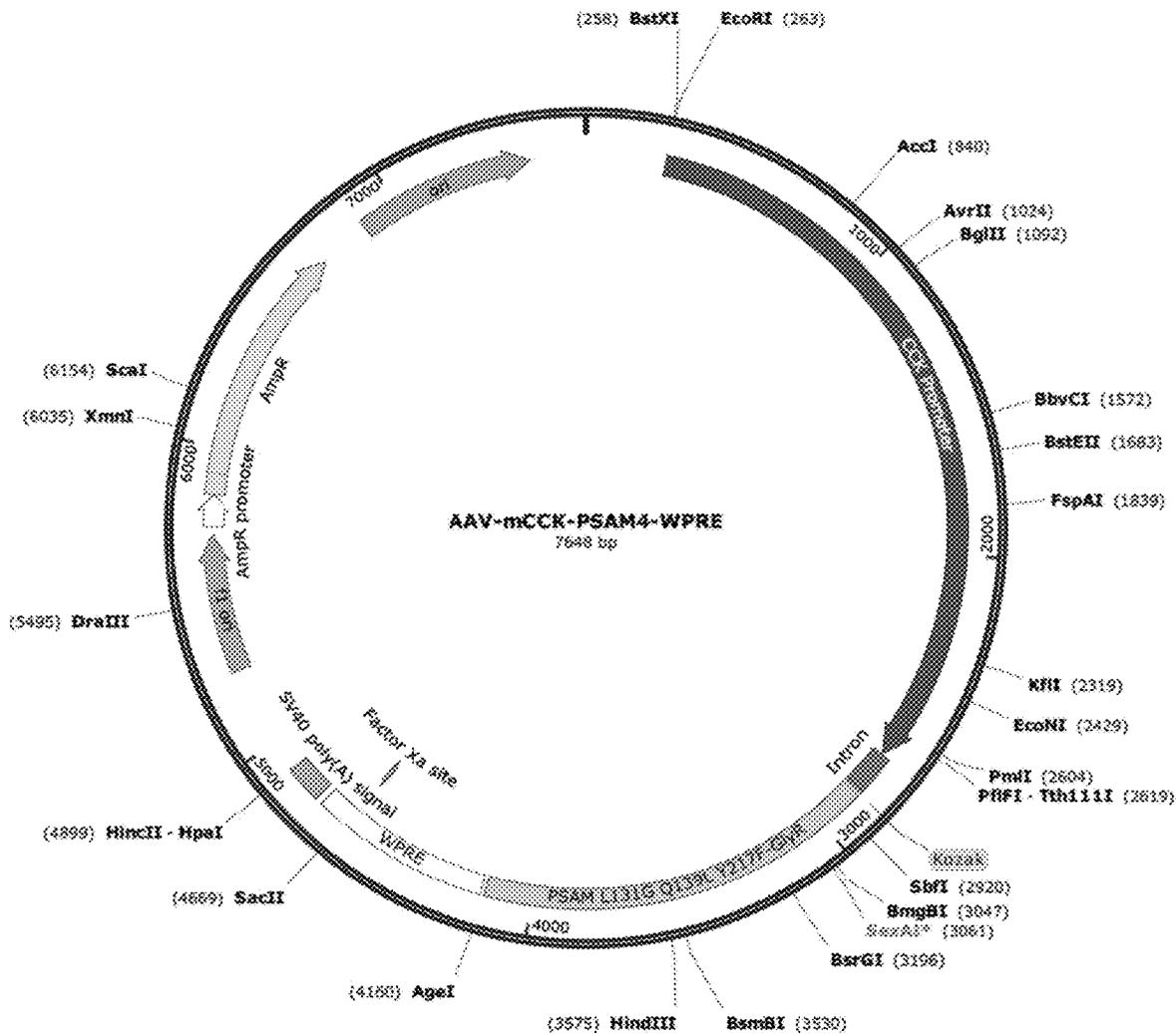


Fig. 11

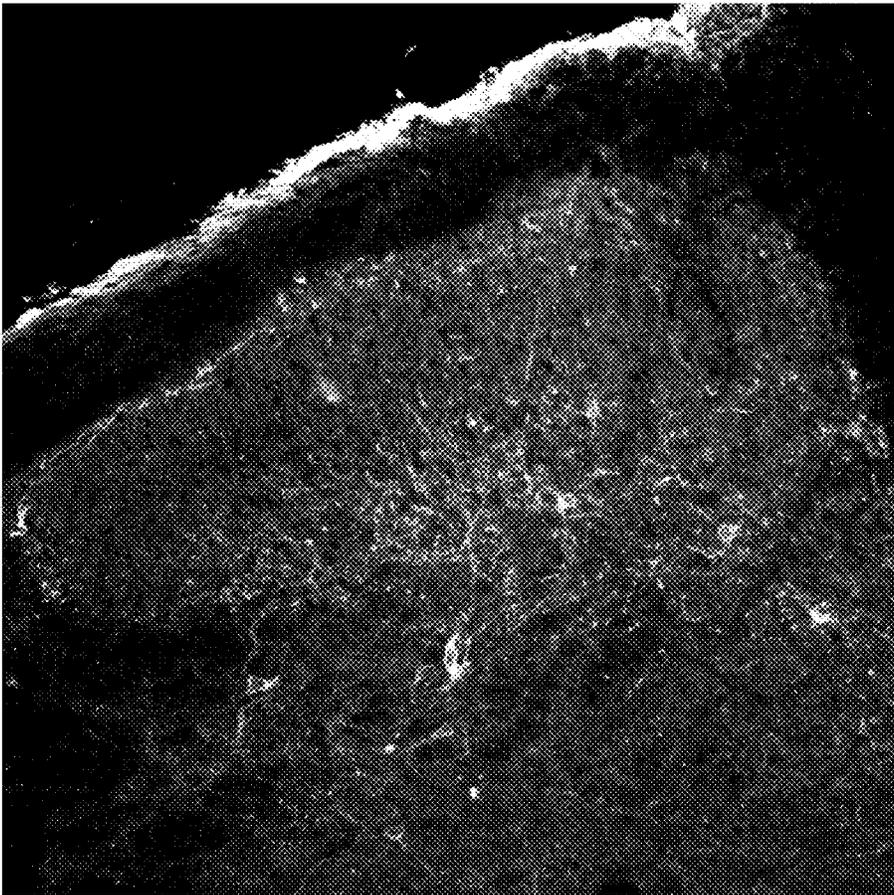
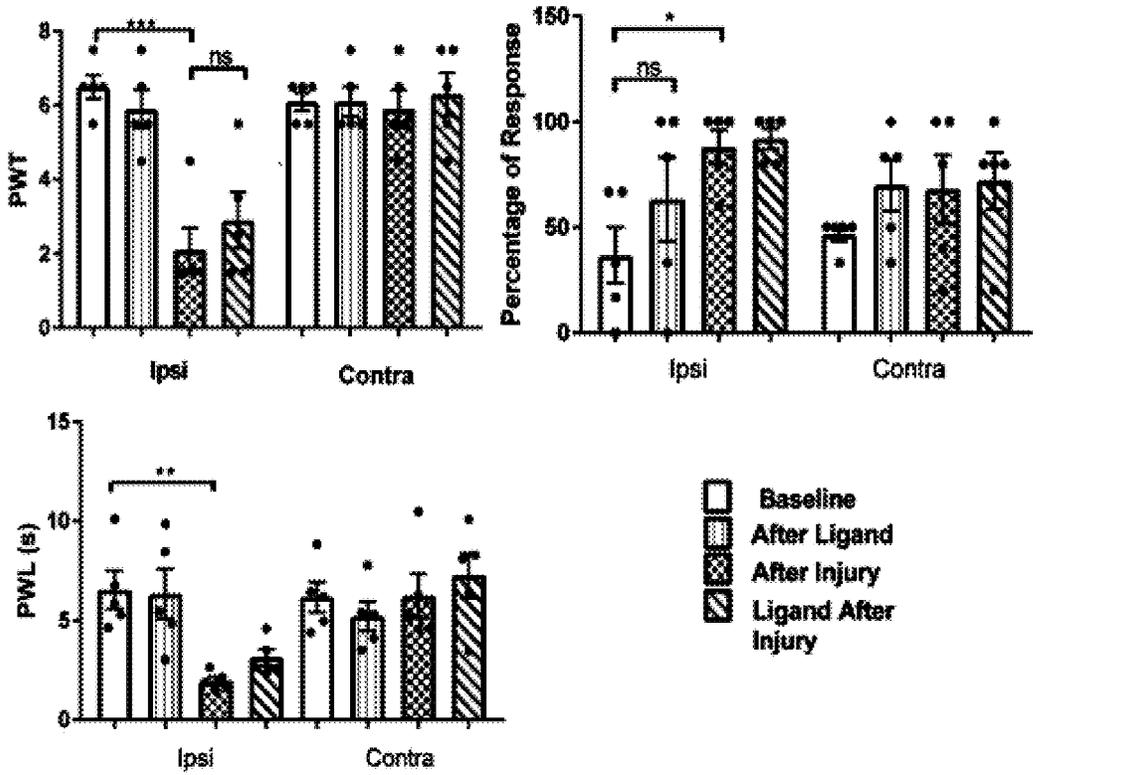


Fig. 12.

CFA (n=5)



SNI (n=5)

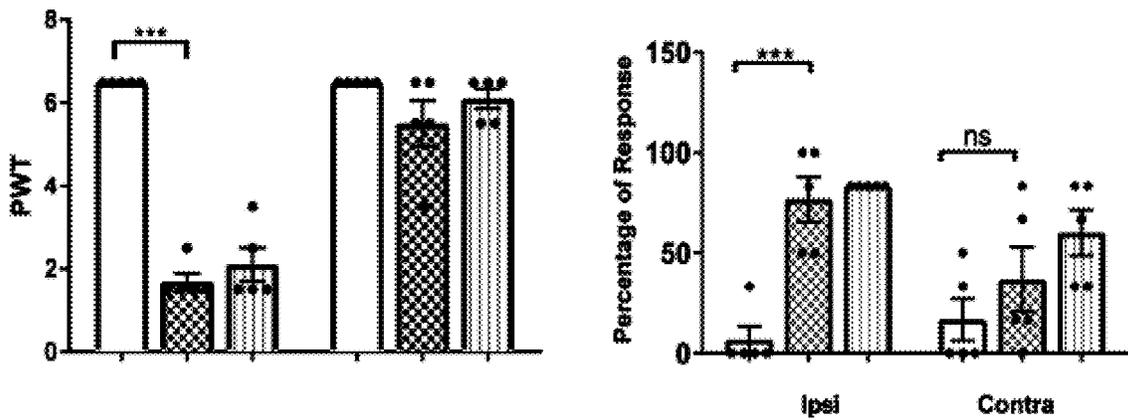


Fig. 13

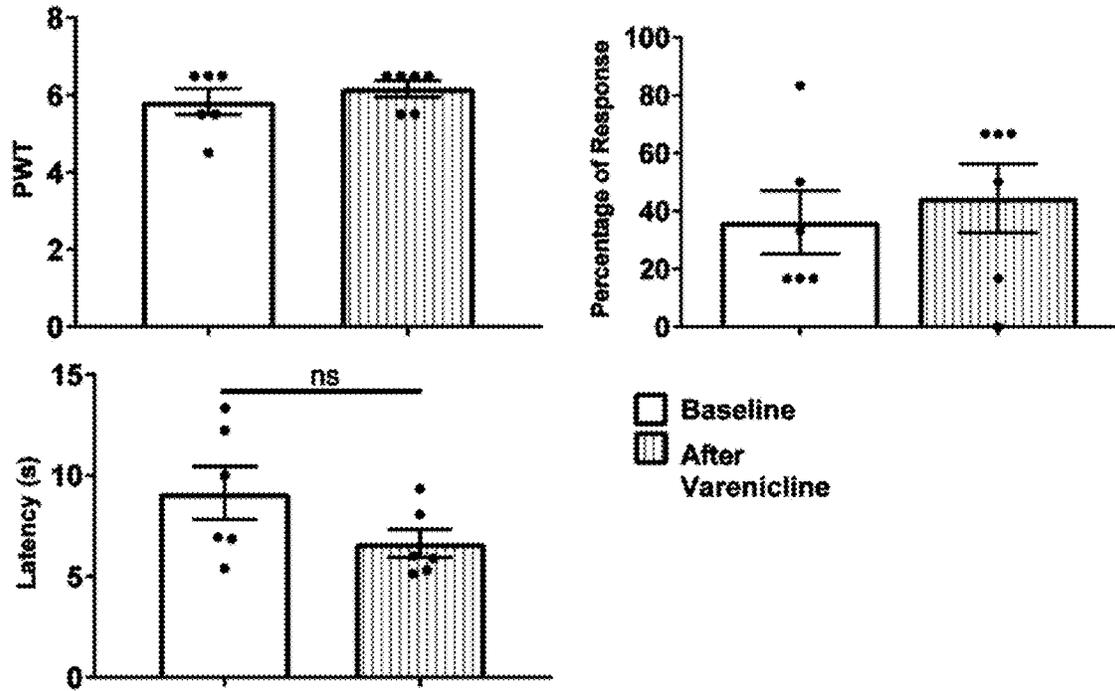


Fig. 14

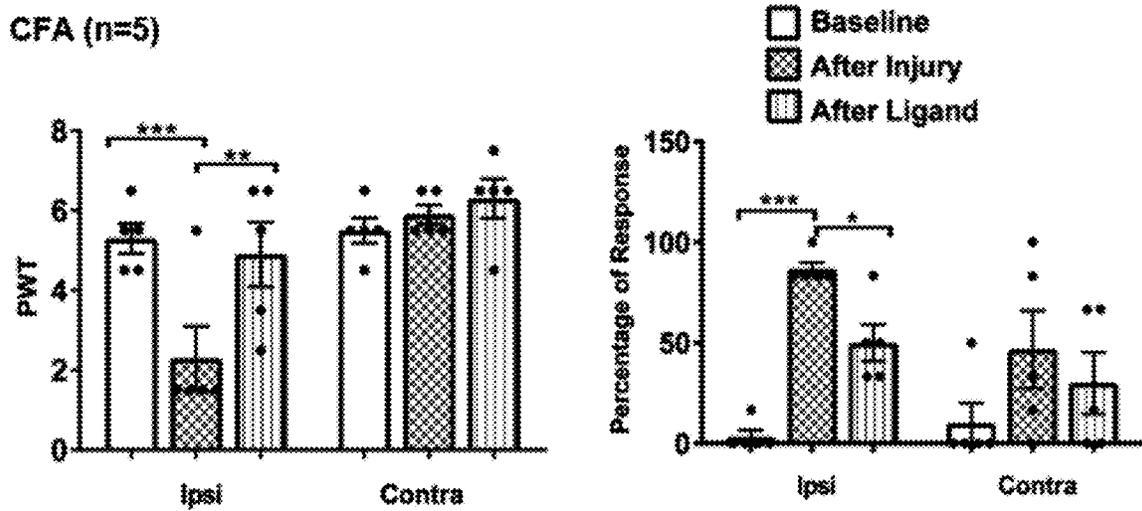


Fig. 15

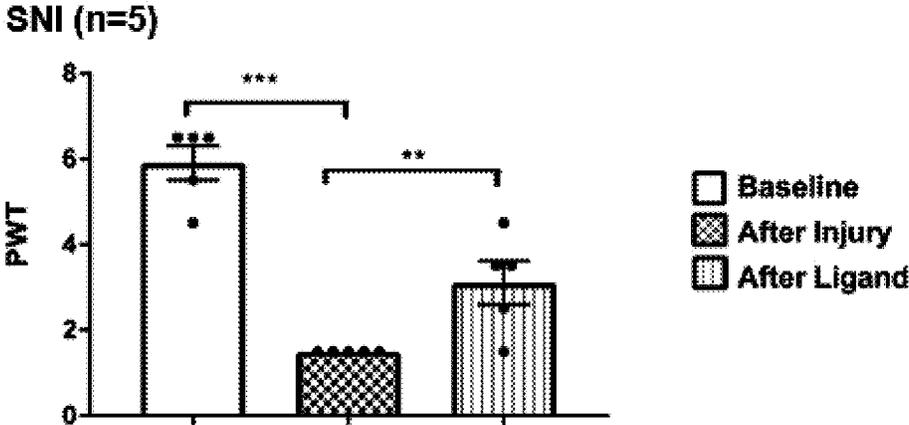


Fig. 16

**TARGETED GENE THERAPIES FOR PAIN
AND OTHER NEURO-RELATED DISORDERS****CROSS REFERENCE TO RELATED
APPLICATIONS**

[0001] This application is a divisional application of U.S. patent application Ser. No. 16/493,387, filed Mar. 20, 2018, which is the United States national phase of International Application No. PCT/US2018/023364 filed Mar. 20, 2018, and claims the benefit of U.S. Provisional Patent Application No. 62/473,630 filed Mar. 20, 2017, each of which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] The Sequence Listing associated with this application is filed in electronic format via Patent Center and is hereby incorporated by reference into the specification in its entirety. The name of the file containing the Sequence Listing is 2304751.xml. The size of the file is 73,585 bytes, and the file was created on Jun. 1, 2023.

[0003] Provided herein are compositions and related methods useful for treatment of pain, especially chronic pain.

[0004] Over 100 million people in the U.S. suffer from debilitating pain caused by disease and trauma. Current therapies are focused on opioids and NSAIDs, but these treatments lose efficacy or produce serious side effects. Addiction to opioid-based prescription painkillers has led to an epidemic level rise in opioid-related overdose deaths. Because of the lack of adequate treatment options, pain continues to be a major clinical problem. Therapeutic solutions to the lack of adequate pain treatment, especially for chronic pain, are needed.

SUMMARY

[0005] Provided herein are nucleic acids for tissue-specific delivery of modified ligand-gated ion channels (LGICs) that can be selectively activated with tailored compound ligands. Such LGICs, once delivered to the neurons of interest by gene therapy methods, would render those neurons sensitive to a ligand selective for such novel LGICs and would obviate the need for local delivery of the ligand, since the tailored ligand would have no effect on native LGICs. Furthermore, selective activation of those tissue-targeted LGICs would eliminate the non-specific effects arising from activation of neighboring populations of neurons that inevitably occur due to the ubiquitous expression of native LGICs. This provides specificity for control of neuron activity that can be used therapeutically to treat neurological diseases and conditions, such as chronic pain or itch. Therefore, development of novel tissue-targeted LGICs with unique pharmacology has therapeutic utility. Related methods also are provided.

[0006] According to a first aspect of the invention, a nucleic acid is provided, comprising a gene for expressing a modified ligand-gated ion channel. The gene comprises an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of transcriptional control elements governing cell-specific expression in CNS neurons, such as dorsal horn neurons, spinal cord cells, or brain cells, or in inhibitory neurons or nerve cells. Examples of transcription control elements include: a CCK promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a

Calb1 promoter, an SST promoter, a GRPR promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a PKC γ promoter, or a Calb2 promoter. The modified ligand-gated ion channel comprises a modified ligand binding domain activatable by an exogenous ligand, and optionally selective to the exogenous ligand, and an ion pore domain.

[0007] In another aspect of the invention, a method is provided of modulating (increasing or decreasing) the membrane potential of an excitable cell or a secretory cell. The method comprises expressing in the cell a genetic construct comprising a gene for expressing a modified ligand-gated ion channel, comprising an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of transcriptional control elements governing cell-specific expression in CNS neurons, such as dorsal horn neurons, spinal cord cells, or brain cells, or in inhibitory neurons or nerve cells, such as a CCK promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, an SST promoter, a GRPR promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a PKC γ promoter, or Calb2 promoter and a modified ligand-gated ion channel comprising a modified ligand binding domain activatable by an exogenous ligand, and optionally selective to the exogenous ligand, and an ion pore domain, and contacting the cell with an amount of the exogenous ligand effective to activate the modified ligand gated ion channel thereby modulating the membrane potential of the cell.

[0008] In a further aspect of the invention, a method is provided of treating a disease or disorder associated with the nervous system in a patient. The method comprises delivering a nucleic acid as described below, and administering the exogenous ligand to the patient in an amount effective to activate a modified ligand gated ion channel in a patient thereby treating the disease or disorder associated with the nervous system in the patient. The nucleic acid comprises a gene for expressing the modified ligand-gated ion channel. The gene comprises an open reading frame encoding the modified ligand-gated ion channel under transcriptional control of transcriptional control elements governing cell-specific expression in CNS neurons, such as dorsal horn neurons, spinal cord cells, or brain cells, or in inhibitory neurons or nerve cells. Examples of transcription control elements include: a CCK promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, an SST promoter, a GRPR promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a PKC γ promoter, or a Calb2 promoter. The modified ligand-gated ion channel comprises a modified ligand binding domain activatable by an exogenous ligand, and optionally selective to the exogenous ligand, and an ion pore domain.

BRIEF DESCRIPTION OF THE DRAWINGS

[0009] FIGS. 1A-1 depict exemplary nucleic acid sequences, continuous over FIGS. 1A-10, comprising promoter sequences useful in the genetic constructs described herein, as follows: Human CCK Promoter (SEQ ID NO: 1), Human Tac1 Promoter (SEQ ID NO: 2), Human Nts Promoter (SEQ ID NO: 3), Human Nmu Promoter (SEQ ID NO: 4), Human Calb1 Promoter (SEQ ID NO: 5), Human Parvalbumin Promoter (SEQ ID NO: 6), Human Gal Promoter (SEQ ID NO: 7), Human NPY Promoter (SEQ ID NO: 8), Human SST Promoter (SEQ ID NO: 9), Human GRPR Promoter (SEQ ID NO: 10), Human PRKCG Promoter (SEQ ID NO: 11), Human Calb2 Promoter (SEQ ID

NO: 12), Mouse CCK Promoter (SEQ ID NO: 13), Mouse Calb2 Promoter (SEQ ID NO: 14), Mouse PRKCG Promoter (SEQ ID NO: 15), Mouse Calb1 Promoter (SEQ ID NO: 16), and Mouse Nmu Promoter (SEQ ID NO: 17).

[0010] FIG. 2 provides amino acid sequences of exemplary $\alpha 7$ -nicotinic acetylcholine receptor ligand binding domains (SEQ ID NOs: 18-20 as indicated in the figure).

[0011] FIGS. 3A-3E provide exemplary amino acid sequences for chimeric LGICs. FIG. 3A provides an exemplary amino acid sequence of an $\alpha 7$ -5HT3 chimeric receptor (SEQ ID NO: 21), including a human $\alpha 7$ nAChR LBD and a murine 5HT3 IPD components. FIG. 3B provides an exemplary amino acid sequence of $\alpha 7$ -GlyR chimeric receptor (SEQ ID NO: 22) including a human $\alpha 7$ nAChR LBD and a human GlyR IPD components. FIG. 3C provides an exemplary amino acid sequence of $\alpha 7$ -5HT3 chimeric receptor (SEQ ID NO: 23, including human $\alpha 7$ nAChR LBD and a human 5HT3 IPD components. FIG. 3D provides an exemplary amino acid sequence of $\alpha 7$ -GABAC chimeric receptor (SEQ ID NO: 24), including a human $\alpha 7$ nAChR LBD and a human GABAC IPD components. FIG. 3E provides an exemplary amino acid sequence of rat nAChR sequence (SEQ ID NO: 25).

[0012] FIG. 4 provides exemplary exogenous ligands (U.S. 2018/0009862 A1).

[0013] FIG. 5. (a) Cre-dependent construct for expressing PSAM-GlyR in neurons using AAV delivery. PSEM^{89S} activates the PSAM-GlyR channel, preventing action potential firing of the cells expressing PSAM-GlyR. (b) Dorsal horns of CCK^{Cre} and Calr^{Cre} mice injected intraspinally with AAV8-Flex-PSAM-GlyR virus shows binding of alpha-bungarotoxin-Alexa647 (α -BTX-Alexa647) to PSAM-GlyR in patterns consistent with the distribution of these two genes.

[0014] FIGS. 6A and 6B. Positive and negative controls for PSAM-GlyR and PSEM^{89S}. (a) Schematic of PSAM-GlyR construct with GFP reporter used to make AAV8-hSyn-Flex-PSAM-GlyR. Virus was injected into Tlx3^{Cre} mice for electrophysiological slice recordings. (b) Electrode impaling a GFP+ cell (also shown as DI, image) in a transverse slice of the dorsal horn from a Tlx3^{Cre} mouse injected with AAV8-hSyn-Flex-PSAMGlyR virus. (c) Bath application of 30 μ M PSEM^{89S} induces a sustained hyperpolarization specifically in GFP-expressing cells. (d) Current injected into GFP+ cell produces action potentials (Pre) that are completely blocked after application of PSEM^{89S} (30 μ M) to the slice. (e) Control for the specificity of α -BTX-Alexa647. Contralateral dorsal horn lacks staining for α -BTX-Alexa647. Calretinin; PKC γ . Scale bar=50 μ m. Box indicates area of inset. (f) In mice lacking PSAM-GlyR, mechanical allodynia and heat hypersensitivity induced by the carrageenan pain model are not altered by injection of PSEM^{89S} (30 mg/kg, i.p.) (p>0.999, n=4) (g) Punctate and dynamic allodynia induced by CFA are also not altered by injection of PSEM^{89S} (p>0.999, n=6). (h) In the mice lacking PSAM-GlyR, punctate and dynamic allodynia induced by the sural-SNI model are not altered by injection of PSEM^{89S} (30 mg/kg, i.p.) (n>0.999, n=6). Data are mean \pm standard error of the mean (SEM). ***P<0.001; ns=not significant (i.e. p>0.05)

[0015] FIG. 7. CCK⁺ excitatory neurons in the dorsal horn primarily lamina III-IV are not required for baseline somatosensory behavior or motor behavior on rotarod. (a) Injection of PSEM^{89S} into CCK^{Cre} mice expressing PSAM-GlyR

ipsilaterally in the dorsal horn has no effect on baseline von Frey threshold (p=0.2192, n=8), response to cotton swab (p=0.7293, n=8), pressure with calibrated calipers (p=0.7450, n=8) or pinprick (p=0.5983, n=8). Hargreaves latencies are unchanged (p=0.9746, n=8). (b) Performance on the rotarod is also not altered by injection of PSEM^{89S}. Data are mean \pm SEM. None are significantly different.

[0016] FIG. 8. CCK+ excitatory dorsal horn neurons are required for the transmission of persistent forms of pain. Mice expressing PSAM-GlyR in CCK+ dorsal horn neurons were tested in persistent pain behaviors. (a) In the carrageenan pain model, injection of PSEM^{89S} (30 mg/kg, i.p.) reversed punctate (p=0.0017, n=8) and dynamic allodynia (p=0.0001, n=8) as well as heat hypersensitivity (p=0.0002, n=8). (b) In the CFA model, PSEM^{89S} injection also markedly reversed punctate (p=0.0034, n=5) and dynamic allodynia (p=0.0016, n=5) as well as heat hypersensitivity (p=0.0368, n=5). (c,d) Inhibiting the CCK population reversed punctate allodynia in the sural-SNI (p=0.0003, n=12) and tibial-SNI (p=0.0054, n=5) models. Dynamic allodynia in sural-SNI is also reversed (p=0.0001, n=12). (e,f) PSEM^{89S} also reversed heat hypersensitivity induced by MG (p=0.0272, n=4) or multi-dose STZ (p=0.010, n=9). Data are mean \pm SEM. *p<0.05, **p<0.01, ***P<0.001.

[0017] FIG. 9. Calretinin⁺ excitatory neurons in the dorsal horn lamina II are not required for baseline somatosensory behavior or motor behavior on the rotarod. (a) Injection of PSEM^{89S} (30 mg/kg, i.p.) into Calr^{Cre} mice expressing PSAM-GlyR ipsilaterally in the dorsal horn has no effect on ipsilateral von Frey threshold (p=0.3988, n=8), response to cotton swab (p=0.7963, n=8), pressure with calibrated calipers (p=0.8350, n=8) sticky tape (p=0.9346, n=8) or pinprick (p=0.7689, n=8). Hargreaves latencies are also unchanged (p=0.6125, n=8). (b) Motor behavior measured by rotarod is not altered by inhibition of dorsal horn calretinin neurons with PSEM^{89S}. Data are mean \pm SEM. None are significantly different.

[0018] FIG. 10. Calretinin⁺ excitatory neurons in lamina II of the dorsal horn convey mechanical allodynia induced by inflammatory, but not neuropathic pain models. Inhibition of PSAM-GlyR expressing calretinin neurons in the dorsal horn lamina II by injection of PSEM^{89S} (30 mg/kg, i.p.) reverses mechanical allodynia induced by models of inflammatory pain including (a) carrageenan (p=0.0074, n=8), (b) CFA (p=0.0026, n=8), (c) incision (punctate, p=0.0028, n=7; dynamic p=0.0001, n=7) Data are mean \pm SEM. **p<0.01, ***P<0.001.

[0019] FIG. 11: AAV-mCCK-PSAM4-WPRE construct. A 2.5 kb fragment of the mouse CCK promoter was sub-cloned upstream of the PSAM (L131G Q139L Y217F)-GlyR (PSAM4) gene with a chimeric intron (135 bp) located in between the promoter and the PSAM4 gene.

[0020] FIG. 12. Expression of PSAM4 in the dorsal horn of an adult wildtype C57Bl/6 mouse. α -bungarotoxin-Alexa647 (α -BTX-Alexa-647) staining of the lumbar dorsal horn of a mouse unilaterally injected with the AAV8 mCCK-PSAM4-WPRE virus in the dorsal horn (1¹³ vg/ml, custom packaged).

[0021] FIG. 13. Varenicline has no effect on baseline mechanical and heat sensitivity or CFA or sural SNI induced hypersensitivity in mice lacking PSAM4. PWT, frequency of response and PWL were tested in adult wildtype C57Bl/6 mice (not expressing PSAM4) before and after injection of varenicline (0.1 mpk, i.p.) at baseline and 3 and 7 days after

injection of CFA or sural-SNI surgery, respectively. Data are mean±SEM. N=5 mice. *p<0.05, **p<0.01, ***p<0.001; ns=not significant (i.e. p>0.05).

[0022] FIG. 14. Control showing effect of varenicline on mechanical and heat sensitivity at baseline in mice injected with mCCK-PSAM4 virus. The effect of varenicline (0.3 mpk, i.p) on baseline mechanical and heat hypersensitivity was tested 2 weeks after injection of AAV8 mCCK-PSAM4 unilaterally into the dorsal horn. Injection of varenicline had no effect on baseline PWT, percentage response or PWL (measured 30-60 minutes following injection of the drug) in mice expressing PSAM4 in dorsal horn CCK+ neurons. Data are mean±SEM. N=5-6 mice. **p<0.05, **p<0.01, ***p<0.001; ns=not significant (i.e. p>0.05).

[0023] FIG. 15. Varenicline reverses mechanical allodynia induced by CFA in mice expressing mCCK-PSAM4 in the dorsal horn. Adult wildtype C57Bl/6 mice injected with AAV8 mCCK-PSAM4-WPRE virus unilaterally in the dorsal horn. PWT to von Frey filaments and percentage of response to cotton swab were measured before and 3 days after CFA injection in plantar hindpaw and after injection of varenicline (0.3 mpk, i.p). Injection of varenicline reversed both PWT and response frequency to cotton swab after CFA. Data are mean±SEM. N=5 mice. *p<0.05, **p<0.01, ***p<0.001.

[0024] FIG. 16. Varenicline reverses mechanical allodynia induced by the sural model of SNI in mice expressing mCCK-PSAM4 in the dorsal horn. Adult wildtype C57Bl/6 mice injected with mCCK-PSAM4 unilaterally in the dorsal horn. Three weeks later, PWT to von Frey filaments was measured before and 7 days after sural-SNI surgery on the ipsilateral side and then again after injection of varenicline (0.3 mpk, i.p). Injection of varenicline reversed PWT after SNI. Data are mean±SEM. N=5 mice. *p<0.01, ***p<0.001.

DETAILED DESCRIPTION

[0025] The use of numerical values in the various ranges specified in this application, unless expressly indicated otherwise, are stated as approximations as though the minimum and maximum values within the stated ranges are both preceded by the word “about”. In this manner, slight variations above and below the stated ranges can be used to achieve substantially the same results as values within the ranges. Also, unless indicated otherwise, the disclosure of ranges is intended as a continuous range including every value between the minimum and maximum values. As used herein “a” and “an” refer to one or more.

[0026] As used herein, the term “comprising” is open-ended and may be synonymous with “including”, “containing”, or “characterized by”. The term “consisting essentially of” limits the scope of a claim to the specified materials or steps and those that do not materially affect the basic and novel characteristic(s) of the claimed invention. The term “consisting of” excludes any element, step, or ingredient not specified in the claim. As used herein, embodiments “comprising” one or more stated elements or steps also include, but are not limited to embodiments “consisting essentially of” and “consisting of” these stated elements or steps.

[0027] A “patient” is a human or animal, e.g., vertebrates or mammals, including rat, mouse, rabbit, pig, monkey, chimpanzee, cat, dog, horse, goat, guinea pig, and birds, and does not imply or require a doctor-patient or veterinarian-patient relationship.

[0028] The terms “transfect”, “transfection”, “transfected”, and like terms refer to the introduction of a gene into a eukaryotic cell, such as a keratinocyte, and includes “transduction,” which is viral-mediated gene transfer, for example, by use of recombinant AAV, adenovirus (Ad), retrovirus (e.g., lentivirus), or any other applicable viral-mediated gene transfer platform.

[0029] By “expression” or “gene expression,” it is meant the overall flow of information from a gene. A “gene” is a functional genetic unit for producing a gene product, such as RNA or a protein in a cell, or other expression system encoded on a nucleic acid and generally comprising: a transcriptional control sequence, such as a promoter and other cis-acting elements, such as transcriptional response elements (TREs) and/or enhancers; an expressed sequence that typically encodes a protein (referred to as an open-reading frame or ORF) or functional/structural RNA; and a polyadenylation sequence). A gene produces a gene product (typically a protein, optionally post-translationally modified or a functional/structural RNA) when transcribed. By “expression of genes under transcriptional control of,” or alternately “subject to control by,” a designated sequence such as a promoter, it is meant gene expression from a gene containing the designated sequence operably linked (functionally attached, typically in cis) to the gene. A gene that is “under transcriptional control” of a promoter or transcription control element, is a gene that is transcribed at detectably different levels in the presence of a transcription factor, e.g., in specific cells, as further described below, and in the context of the present disclosure, produces a difference in transcription levels when expressed in a specific cell type (e.g., where the promoter is a CCK promoter, the gene is preferentially expressed in cells that express CCK natively. A “gene for expression of” a stated gene product is a gene capable of expressing that stated gene product when placed in a suitable environment, that is, for example, when transformed, transfected, transduced, etc. into a cell, and subjected to suitable conditions for expression. In the case of a constitutive promoter “suitable conditions” means that the gene typically need only be introduced into a host cell. In the case of an inducible promoter, such as the tissue specific promoters described herein, “suitable conditions” means when factors that regulate transcription, such as DNA-binding proteins, are present or absent, for example, an amount of the respective inducer is available to the expression system (e.g., cell), or factors causing suppression of a gene are unavailable or displaced—effective to cause expression of the gene.

[0030] Transcriptional control elements include promoters, enhancers, transcription factor-responsive elements (TREs, e.g., transcription factor binding sequences), suppressors, introns, etc., as are broadly-known. Additional transcription control elements, such as a WPRE (woodchuck hepatitis virus post-transcriptional regulatory element), or an intron, e.g., as shown below, which can increase expression from certain viral vectors, can be included in the gene.

[0031] Exemplary tissue specific promoters, specific to excitable cells or secretory cells, e.g. of the central nervous system (CNS), such as, without limitation, neurons, sensory neurons, dorsal horn cells, spinal cord cells, brain cells, and inhibitory neurons, include, for example and without limitation, those promoter sequences depicted in FIGS. 1A-1L, and described in Table 1.

TABLE 1

Promoter	Location for Expression	Inhibitory or excitatory LGIC	Physiological Effect
Cholecystokinin (CCK)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Tachykinin (Tac1)	Dorsal horn neuron	inhibitory	Blocks persistent pain
PKC γ (PRKCG)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Neurotensin (NTS)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Neuromedin U (NMU)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Calbindin 1 (Calb1)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Calbindin 2 (Calb2)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Somatostatin (SST)	Dorsal horn neuron	inhibitory	Blocks persistent pain
Gastrin related peptide receptor (GRPR)	Dorsal horn neuron	inhibitory	Blocks itch
Galanin (GAL)	Dorsal horn neuron	Excitatory	Blocks persistent pain or itch
Neuropeptide Y (NPY)	Dorsal horn neuron	Excitatory	Blocks persistent pain or itch
Parvalbumin (PV)	Dorsal horn neuron	Excitatory	Blocks persistent pain or itch

[0032] A promoter is “specific” to specified excitable cells or secretory cells if it causes gene expression in those cells of a gene to a sufficient extent for production of useful or therapeutically effective amounts of the described modified LGICs described herein in the specified excitable cells or secretory cells, and insignificant expression elsewhere in the context of the use, e.g. therapeutic use.

[0033] Although these are human sequences and consensus sequences, there is conservation among species and many promoter sequences that function in human cells will also be expected to do so in mice, or any mammal or vertebrate, and many promoter sequences that function in mice, or any mammal or vertebrate will also be expected to do so in human cells. The sequences also may be modified, e.g., shortened, for virion packaging purposes and optimal expression, so long as tissue-specificity of the construct remains.

[0034] One of the advantages of using highly circumscribed cell-type specific promoters described herein, for example, Calb2 or CCK to drive expression of PSAM4 or another LGIC (e.g., an inhibitory LGIC in Calb2 or CCK expressing dorsal horn neurons), is that baseline mechanical or heat sensitivity are not affected (see, Examples 1 and 2, below) with exogenous ligand-mediated activation of the LGIC. These promoters provide an important advantage over pan neuronal or pan excitatory neuron or pan inhibitory neuron promoters, or also primary afferent promoters such as TRPV1 (those neurons fibers are required for all heat sensation), which will negatively impact acute pain or touch in the area innervated by the targeted neurons with exogenous ligand-mediated activation of the LGIC. The ability to feel acute pain is important to protect the patient from bodily harm.

[0035] Production of useful nucleic acid constructs, such as recombinant viral vectors for production of nucleic acids, such as the genetic constructs and recombinant viral genomes described herein, is routine, in that molecular cloning and gene assembly methods are routine. Further, a

number of companies can custom-synthesize and verify multi-kilobase genes, making the production of genes or genomes as described herein, such as rAAV or scAAV genomes, routine (See, e.g., Gene Synthesis Handbook, 2d Edition, 2014, GenScript USA, Inc.).

[0036] AAV (adeno-associated virus), is a virus belonging to the genus Dependoparvovirus, and family Parvoviridae. The virus is a small replication-defective, non-enveloped virus. AAV is not currently known to cause any disease by itself. AAV requires a helper virus, such as adenovirus or herpes simplex virus, to facilitate productive infection and replication. In the absence of helper virus, AAVs establish a latent infection within the cell, either by site-specific integration into the host genome or by persisting in episomal forms. Gene therapy vectors using AAV can infect both dividing and quiescent cells. Furthermore, AAV serotypes have different tropism and can infect cells of multiple diverse tissue types. While eleven serotypes of AAV have been identified to date, AAV2 was among the first to be identified and has been consistently used for the generation of recombinant AAV vectors. Further certain natural or modified AAVs transduce specific organs or cell populations. In one example, AAV-PHP.eB and AAV-PHP.S, capsids efficiently transduce the central and peripheral nervous systems, respectively, when administered intravenously (Chan, K. Y., et al. Engineered AAVs for efficient noninvasive gene delivery to the central and peripheral nervous systems (2017) *Nat. Neurosci* 20(8):1172-1179). For example, compared to AAV9, AAV-PHP.B delivers genes to the brain and spinal cord at least 40 times more efficiently. See also, Tervo, D G, et al. A Designer AAV Variant Permits Efficient Retrograde Access to Projection Neurons (2016) *Neuron* 92, 372-382, describing engineered AAV variants, e.g., rAAV2-retro, which permit robust retrograde access to projection neurons with efficiency comparable to classical synthetic retrograde tracers, and enable sufficient sensor/effector expression for functional circuit interrogation and in vivo genome editing in targeted neuronal populations.

[0037] The AAV virion shell is approximately 25 nm in diameter and encapsulates a single-stranded DNA genome that consists of two large open reading frames (ORFs) flanked by inverted terminal repeats (ITR). The ITRs are the only cis-acting elements required for genome replication and packaging. In wild-type AAV, the left ORF encodes four replication proteins responsible for site-specific integration, nicking, and helicase activity, as well as regulation of promoters within the AAV genome. AAV possesses a 4.7 kb genome, and as such, efficient packaging of recombinant AAV (rAAV) vectors can be performed with constructs ranging from 4.1 kb to 4.9 kb in size (see, e.g., Samulski, R J, et al., AAV-Mediated Gene Therapy for Research and Therapeutic Purposes, *Annu. Rev. Virol.* 2014. 1:427-51).

[0038] Helper-free production of the rAAV requires transfection of the following components into host cells, typically 293 cells (HEK293 cells), which are broadly available, or similar cell lines: (1) an rAAV vector containing the transgene expression cassette flanked by the two ITRs; (2) expression of Rep and Cap proteins, typically provided by a helper plasmid in trans; and (3) adenovirus genes encoding E1, E2A, E4, and virus-associated RNA, also provided, at least in part by another helper plasmid in trans (293 cells produce the Ad E1 gene in trans). Rep and Cap proteins, which are necessary for viral packaging, are replication

proteins and capsid proteins, respectively. Rep proteins consist of rep 78, 68, 52 and 40. They specifically are involved with the replication of AAV. Cap proteins are comprised of three proteins, VP1, VP2 and VP3, with molecular weight of 87, 72 and 62 kDa, respectively. These capsid proteins assemble into a near-spherical protein shell of 60 subunits. Helper-free AAV packaging systems are broadly available, for example, from Clontech of Mountain View, California, from Cell Biolabs, Inc. of San Diego, CA, and see, e.g., U.S. Pat. Nos. 6,093,570, 6,458,587, 6,951,758, and 7,439,065. In scAAV (self-complementary AAV), the right ITR contains a deletion of D-sequence (the packaging signal) and a terminal resolution site mutation (Atrs), which prevent Rep-mediated nicking and force packaging of dimer or self-complementary genomes (see FIG. 8). Making dsAAV from scAAV vector renders much improved transduction both in vitro and in vivo (see, e.g., pscAAV-MCS Expression vector, Product Data Sheet, Cell Biolabs, Inc., San Diego, California (2012-2016)).

[0039] Preparation of rAAV transducing particles, such as scAAV transducing particles is routine. Since the transfection method is often considered unsuitable for large-scale production, the infection of cell lines stably expressing Rep and Cap with adenovirus carrying a vector genome has afforded the ability to scale-up. Another option includes infection of proviral cell lines with adenovirus or herpes simplex virus vector carrying an AAV Rep and Cap expression cassette. These methods still require the complete elimination of adenovirus (or herpesvirus) during the production process. However, in baculovirus expression vector systems for rAAV vector production in insect SF9 cells, the components of AAV production, including Rep and Cap proteins, as well as vector genomes are provided by separate recombinant baculoviruses. Ayuso, E., "Manufacturing of recombinant adeno-associated viral vectors: new technologies are welcome", *Molecular Therapy—Methods & Clinical Development* (2016) 3, 15049; doi:10.1038/mtm.2015.49, and Merten, O-W, et al., describe numerous robust current rAAV production methods, though commercial scale-up and validation needs improvement. High viral titers ($\sim 10^{12}$ – 10^{13} vp/mL) may be required for certain uses described herein. Protocols are available in the literature for concentration and purification of AAV vectors, allowing production of virus at these high concentrations (see, e.g., Gray S J, et al. (2011) Production of recombinant adeno-associated viral vectors and use in vitro and in vivo administration. *Curr Protoc Neurosci.* doi:10.1002/0471142301.ns0417s57 and Guo P, et al. (2012) Rapid and simplified purification of recombinant adeno-associated virus. *J Virol Methods* 183(2):139-146).

[0040] Once the virus has been produced in the, e.g., 293 cells, the cells are collected, lysed, and the resultant virus is purified. Density gradient ultracentrifugation, e.g., in cesium chloride or nonionic iodixanol (VISIPAQ™) gradients and column chromatography, such as ion-exchange, heparin-affinity, or mucin-affinity column chromatography, depending on the AAV serotype. Once the rAAV has been purified and concentrated to a suitable concentration, the virus can be used for in vitro cell transduction or for in vivo animal injection at an appropriate MOI (Multiplicity of Infection).

[0041] Numerous rAAV vectors have been made containing genes for expressing fluorescent proteins, and are commercially available. A "gene" is a genetic element for production of a gene product such as a protein or RNA. A

gene for production of a protein product includes, from 5' to 3' according to convention: one or more regulatory elements (transcription control elements) such as promoters, transcription response elements (TREs), repressors, enhancers; an open-reading frame (ORF) encoding a protein or a sequence encoding a functional RNA; and a polyadenylation (pA) site. Due to size limitations, genes for use in rAAV vectors typically do not include introns. rAAV vectors also include the 5' ITR and 3' ITR flanking the gene, which is referred to as a transgene. Thus a typical rAAV genome has the following structure, in order from 5' to 3' on the sense strand: ITR—promoter—transgene ORF—pA—ITR, and in one aspect of the present invention, the promoter includes a TRE and the transgene ORF is that of a colorimetric, e.g., fluorescent protein. Methods of molecular cloning of rAAV transgene constructs, preparation of rAAV particles, and storage and use thereof are broadly-known and further technical details are unnecessary for one of ordinary skill in the art to be able to construct useful rAAV vectors, and produce and use rAAV particles as described herein. As indicated above, so long as the gene sequence is less than the packaging limit of rAAV or scAAV, it is useful for production of a transduction particle as described herein.

[0042] AAV is but one of many robust and well-characterized viral vectors suited for gene therapy, which also includes, without limitation, gammaretroviruses, lentiviruses, adenovirus, and herpes simplex virus. While AAV is likely preferred in many instances, other safe and effective viral transducing particles can be developed based on the genes described herein for use in the devices, systems and methods described herein.

[0043] Likewise, DNA, such as plasmid or other forms of DNA, optionally combined with suitable transfection reagents, such as liposomes.

[0044] In aspects, compositions and methods are provided for delivery of a gene to excitable cells or secretory cells, such as nerve cells or neurons, e.g., to sensory neurons, or inhibitory neurons or nerve cells, that encodes a protein comprising a ligand binding domain fused to a functional or effector domain (transmembrane ion channel or ion pore domain). As described in further detail below, the protein may be a mutated native (non-chimeric) protein, such as a mutated GlyR or $\alpha 7$ -nicotinic acetylcholine receptor, or a chimeric protein, such as a protein comprising a mutated $\alpha 7$ -nicotinic acetylcholine receptor ligand binding domain (LBD) and a GlyR transmembrane ion channel domain.

[0045] In all instances, ligand-gated ion channels and their respective LBDs and transmembrane domains, are broadly-known, and their nucleotide and amino acid sequences, including a large number of mutated sequences that selectively bind exogenous ligands, and transcription control elements, such as promoters, are broadly-available in the literature and free databases and sources, such as GenBank, UniProt, Addgene, EPD (eukaryotic promoter database), see, U.S. Pat. No. 8,435,762 and U.S. Patent Application Publication No. 2018/0009862, etc., among many other literature and on-line sources, and do not need to be recited herein. Likewise, methods of preparing genes encoding such proteins and for expressing such proteins in a tissue-specific manner is routine and need not be described beyond what is provided herein. Nevertheless, exemplary nucleic acid constructs, nucleic acid and amino acid sequences, recombinant

virus particles, and related methods and reagents are provided herein for illustrative purposes, and as proof of concept.

[0046] Excitable cells or secretory cells include, for example and without limitation, sensory nerves and neurons including, without limitation, CNS neurons, such as spinal cord cells, such as dorsal horn cells and/or brain cells, including and without limitation a brainstem, hindbrain, midbrain or forebrain excitatory or inhibitory cell population.

[0047] The functional domain of the modified LGICs described herein is a transmembrane ion channel that can be cationic-selective or anion-selective. Cationic-selective (e.g., Na⁺—Ca²⁺-, and K⁺-selective) channels, such as that of the 5HT₃ receptor (also, 5-HT₃ receptor, or 5-hydroxytryptamine type 3 receptor), and the α 7-nicotinic acetylcholine receptor, have an excitatory, depolarizing effect on a neuron, while anion-selective (e.g., Cl⁻-selective) channels, such as that of the glycine receptor (e.g., GlyR) or GABA_A receptor, have an inhibitory, hyperpolarizing effect on the neuron. In one aspect, for pain management, the ion channel is hyperpolarizing, that is, when active, that is, when bound to the agonist ligand, the ion channel decreases a neuron's membrane potential to values more negative (e.g., -90 millivolts (mV)) than resting potential (e.g., -70 mV). In aspects, a hyperpolarizing ion channel is permeable to Cl⁻ or K⁺ ions, and thereby decreases neuron membrane potential when active. GlyR is permeable to Cl⁻, and therefore, when active, transfers Cl⁻ ions into the neuron. Suitable ion channels include transmembrane domains of members of the Cys-loop family of receptors. Non-limiting examples of suitable hyperpolarizing ion channels include: Glycine receptors; GABA receptors, such as GABA_A and GABA_C receptors; Glutamate-gated chloride receptors.

[0048] In another aspect, for pain management, the ion channel is depolarizing, and the cell is an inhibitory neuron. For example, as indicated in Table 1, NPPY, Gal, or PV promoters can be used to effectively target inhibitory neurons in the dorsal horn.

[0049] In one aspect, the protein is a mutated ligand-gated ion channel, such as GlyR, GABA_A, α 7-nicotinic acetylcholine receptor, or 5HT₃ receptor, having mutations in the protein causing enhanced selectivity of binding to exogenous ligands (ligands not naturally found in the cell in which the protein is expressed). In reference to binding of a ligand, by "selective to" it is meant either exclusive to or substantially or sufficiently exclusive binding to a ligand, such that the effect of the other ligand is insignificant or below a suitable or acceptable threshold level to achieve a desired purpose. For example, an LGIC having a mutated α 7-nicotinic acetylcholine LBD can be selective to an exogenous small molecule compound, such as varenicline, such that the LGIC is activated by the exogenous small molecule compound, and not to any clinically-relevant or physiologically-relevant extent by acetylcholine. Selective binding to an exogenous ligand is, compared to binding to an endogenous ligand, at least about 4-fold to at least about 200-fold enhanced potency as an agonist to the LGIC, including increments there between (see, e.g., U.S. 2018/0009862). Optionally, though preferably in many instances, the LGIC exhibits reduced binding to endogenous ligands (native ligands), such as in the case of the α 7-nicotinic acetylcholine ligand binding domain, reduced, negligible, or no binding to acetylcholine, but enhanced binding to exog-

enous ligands, such as, for example and without limitation, varenicline (e.g., CHANTIX®).

[0050] Methods of modification or mutation of ligand-gated ion channel proteins, including production of chimeric proteins, able to bind selectively to exogenous ligands, and examples of such proteins are broadly-known, and well within the skill of an ordinary artisan (see, e.g., U.S. Pat. No. 8,435,762; U.S. Patent Application Publication No. 2018/0009862; U.S. Pat. No. 8,957,036, incorporated herein by reference in its entirety; International Patent Publication No. 2017/049252, incorporated herein by reference for its description of additional modified LGICs; Weir et al., Using an engineered glutamate-gated chloride channel to silence sensory neurons and treat neuropathic pain at the source (2017) *Brain* 140; 2570-2585; Kynagh, T., et al., An Improved Ivermectin-activated Chloride Channel Receptor for Inhibiting Electrical Activity in Defined Neuronal Populations (2010) *J. Biol. Chem.* 285(20):14890-14897; and Sternson, S. M., et al. Chemogenetic Tools to Interrogate Brain Functions (2014) 37:387-407).

[0051] Chimeric ligand-gated ion channel proteins have ligand-binding domains and transmembrane ion channel domains from different proteins, either from the same or different species. In aspects, the protein is a chimeric protein comprising a LBD of a nicotinic acetylcholine receptor, such as a mutated ligand binding domain from the α 7 nicotinic acetylcholine receptor. In one aspect, the chimeric protein is a chimeric protein described in one of U.S. Pat. No. 8,435,762, or U.S. Patent Application Publication No. 2018/0009862, or International Patent Publication No. 2017/049252, each of which is incorporated herein by reference in its entirety for its technical disclosure of suitable chimeric proteins (modified LGICs) e.g., comprising a mutated α 7 nicotinic acetylcholine receptor binding domain (ligand binding domain, LBD) fused to an ion pore domain (IPD), e.g., from a 5HT₃, a GlyR, or a GABA_C receptor, as well as for disclosure of other modified LGICs. Non-limiting examples of LGICs include, without limitation, Cys-loop receptors, e.g., AChR such as a nAChR, e.g., a muscle-type nAChR or a neuronal-type nAChR, gamma-aminobutyric acid (GABA; such as GABA_A and GABA_{A-P}, (also referred to as GABA_C) receptors, GlyR, GluCl receptors, and 5HT₃ receptors), ionotropic glutamate receptors (iGluR; such as AMPA receptors, kainate receptors, NMDA receptors, and delta receptors), ATP-gated channels (e.g., P2X), and phosphatidylinositol 4,5-bisphosphate (PIP2)-gated channels, and the modified LGIC can comprise sequences of any appropriate combination of LBD and ion channel of the preceding, modified be selective for an exogenous ligand. LBD sequences and transmembrane ion channel sequences may be obtained from any species, such as human, mouse, rat, sheep, cow, pig, or simian species, so long as it is functional for the intended use, for example, in humans, when used to produce a modified LGIC. The LGIC may be homomeric, or multimeric, comprising one or more LGIC subunits that can be the same or different.

[0052] In some aspects, a modified LGIC subunit described herein can include a LBD from a α 7 nAChR. Exemplary amino acid sequences for α 7-nicotinic acetylcholine receptor LBDs are provided in FIG. 2 (obtained from U.S. Patent Application Publication No. 2018/0009862). In various aspects, an α 7-nicotinic acetylcholine receptor LBD is a homolog, orthologue, or paralog of the human α 7-nicotinic acetylcholine receptor LBD set forth in SEQ ID

NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20. In various aspects, an $\alpha 7$ -nicotinic acetylcholine receptor LBD has at least 75 percent sequence identity (e.g., at least 80%, at least 82%, at least 85%, at least 88%, at least 90%, at least 93%, at least 95%, at least 97% or at least 99% sequence identity) to SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20. Exemplary amino acid sequences for chimeric LGICs are provided in FIGS. 3A-3E (obtained from U.S. Patent Application Publication No. 2018/0009862). In various aspects, a modified LGIC has a sequence set forth in SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24. In aspects, a modified LGIC has an amino acid sequence having at least 75 percent sequence identity (e.g., at least 80%, at least 82%, at least 85%, at least 88%, at least 90%, at least 93%, at least 95%, at least 97% or at least 99% sequence identity) to SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

[0053] For purposes of generating a genetic construct for expressing these, or any amino acids, the nucleotide sequence of the ORF used can have any suitable sequence that can be translated to the desired amino acid sequence. Due to codon degeneracy, the nucleotide sequence can vary greatly, but codon usage may be the same or different from the natural gene, and can be optimized for increased, or optimal, expression.

[0054] In calculating percent sequence identity, two sequences are aligned and the number of identical matches of amino acid residues between the two sequences is determined. The number of identical matches is divided by the length of the aligned region (i.e., the number of aligned amino acid residues) and multiplied by 100 to arrive at a percent sequence identity value. The length of the aligned region can be a portion of one or both sequences up to the full-length size of the shortest sequence. Alignment of two or more sequences to determine percent sequence identity can be performed using the computer program ClustalW2 (EMBL-EBI) and default parameters, which calculates the best match between a query and one or more subject sequences, and aligns them.

[0055] FIGS. 3A-3E (excerpted from U.S. Patent Application Publication No. 2018/0009862) show exemplary amino acid sequences of chimeric LGICs. Mutation of amino acid residue 77 (e.g., W77F or W77Y) resulted in sensitivity to granisetron and tropisetron. Mutation of amino acid residue 79 (e.g., Q79G) was most effective for several agonists. Mutations of amino acid residue 131 (e.g., L131G, L131A, L131M, or L131N) altered sensitivity to varenicline, tropisetron, granisetron, and ACh. Potency was considerably enhanced when LBD mutations were combined with mutation at amino acid residue 298 in the GlyR or GABA_C IPD. Potency was also enhanced when $\alpha 7$ nAChR LBD mutations were combined with mutation at amino acid residue G175 and P216.

[0056] Specific, and non-limiting examples of modified LBDs of LGICs (relative to SEQ ID NOs: 18, 19, and 20) that change ligand binding specificity include, amino acid substitution at one or more of amino acid residues 77, 79, 115, 131, 139, 141, 175, 210, 216, 217, and 219, including, without limitation: W77F, W77Y, W77M, Q79A, Q79G, Q79C, Q79D, Q79E, Q79H, Q79L, Q79P, Q79R, Q79S, Q79T, Q79W, Y1 15F, Q1 39A, Q139C, Q139D, Q139F, Q139G, Q139H, Q139I, Q139K, Q139L, Q139M, Q139N, Q139R, Q139S, Q139V, Q139W, Q139Y, L141A, L141F, L141P, L141G, L141H, L141I, L141M, L141N, L141Q,

L141S, L141 V, L141W, G175K, G175A, G175F, G175H, G175M, G175R, G175S, G175V, P216I, and Y217F. In one aspect, the modified LBDs has the following combinations of point mutations: L131G and Q139L; L131G, Q139L, and Y217F; Q79G and L131G; L131G and Y217F; Q79S and L131G; or Q79S, L131G, and Q139L.

[0057] Point mutations that reduce binding to acetylcholine include Y1 15F, Q79R, Q139G, Q139V, Q1 39W, Q139Y, L141A, L141 Q, L141S, can be combined with any of the selectivity-inducing mutations as described herein, such as Q79G and L141 F. These modifications can be combined with amino acid substitutions to the ion channel domain that can alter conductance (See, U.S. Pat. No. 8,435,762 and U.S. Patent Application Publication No. 2018/0009862).

[0058] Various synthetic ligands, and the modified LGICs they bind to and activate, e.g., LGICs including modified $\alpha 7$ nAChR LBDs are provided in, see, U.S. Pat. No. 8,435,762 and U.S. Patent Application Publication No. 2018/0009862 A1, as well in the priority application to the present application, U.S. Provisional Patent Application No. 62/473,630 filed Mar. 20, 2017, which is incorporated herein by reference in its entirety.

[0059] The exogenous LGIC ligand can be a synthetic exogenous LGIC ligand selected from the group consisting of a quinuclidine, a tropane, a 9-azabicyclo[3.3.1]nonane, a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, and a 1,4-diazabicyclo[3.2.2]nonane. When the synthetic exogenous LGIC ligand is a tropane, the tropane can be tropisetron, pseudo-tropisetron, nortropisetron, compound 723, compound 725, compound 737, or compound 745. When the synthetic exogenous LGIC ligand is a quinuclidine, the quinuclidine can be PNU-282987, PHA-543613, compound 0456, compound 0434, compound 0436, compound 0354, compound 0353, compound 0295, compound 0296, compound 0536, compound 0676, or compound 702. When the synthetic exogenous LGIC ligand is a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, the ligand can be compound 765 or compound 770. When the synthetic exogenous LGIC ligand is a 1,4-diazabicyclo[3.2.2]nonane, the ligand can be compound 773 or compound 774 (U.S. Patent Application Publication No. 2018/0009862 A1).

[0060] Certain LGIC agonists associate increased potency with specific LBD substitutions in modified LGICs. FIG. 4A (from U.S. Patent Application Publication No. 2018/0009862 A1) shows LGIC agonists that exhibit enhanced potency with substituted $\alpha 7$ nAChR LBD having a Q79G amino acid substitution. Additional LGIC agonists are shown in FIG. 4B (also excerpted from U.S. Patent Application Publication No. 2018/0009862 A1). For example, $\alpha 7^{Q79G}$ -GlyR^{A298G} can be controlled by tropisetron, and $\alpha 7^{L131G, Q139L, Y217F}$ -GlyR can be controlled by varenicline. Further examples of modified LGICs include the ivermectin-responsive glutamate-gated chloride channels described in Weir et al., which were administered in AAV9 transducing particles intrathecally to mouse spinal cords (Weir et al., (2017) Brain 140; 2570-2585, see, also, Kynagh, T., et al., (2010) J. Biol. Chem. 285(20):14890-14897), and the ivermectin-responsive GlyR LGIC described in U.S. Pat. No. 8,957,036. Additional examples of the large number of known, specific modified LGICs and their specific agonists is beyond the scope of this disclosure, and is unnecessary.

[0061] According to one aspect of the invention, a method of modulating activity of excitable cells or secretory cells, such as nerve cells or neurons, e.g., to sensory neurons, e.g., depolarization or hyperpolarization of a neuron, in a patient is provided, comprising administering to an excitable cell or a secretory cell, such as a nerve cell or neuron of the patient a nucleic acid comprising a gene for expressing a modified LGIC that selectively binds, and is gated by an exogenous ligand to the cell, and where expression of the gene is under transcriptional control of a promoter specific to an excitable cell or a secretory cell, e.g., a sensory nerve cell or neuron, thereby expressing the modified LGIC in the cell, and administering the exogenous ligand to the patient, thereby activating the LGIC. The LGIC comprises an LBD and a transmembrane ion channel domain, for example and without limitation, according to any aspect described herein. Where hyperpolarization is desired, the modified LGIC comprises a transmembrane ion channel domain that is selective for Cl⁻ or K⁺ ions, such as a GlyR or GABA_A or GABA_C ion channel domain. Where depolarization is desired, the modified LGIC comprises a transmembrane ion channel domain that is selective for Na⁺ or Ca²⁺ ions. In aspects, the LBD is an α 7-nicotinic acetylcholine receptor LBD according to any aspect provided herein.

[0062] According to another aspect of the invention, a method of treating a disease or disorder associated with the nervous system in a patient. In one aspect, the disease or disorder associated with the nervous system is pain, such as chronic pain. In another aspect, the disease or disorder associated with the nervous system is itch. The method comprises administering to an excitable cell or a secretory cell of the patient, such as a nerve cell or neuron, e.g., to CNS cells, such as spinal cord cells or brain cells, such as a dorsal horn cell or a supraspinal cell, a nucleic acid comprising a gene for expressing a modified LGIC that selectively binds, and is gated by an exogenous ligand to the cell, and where expression of the gene is under transcriptional control of a promoter specific to a sensory neuron, thereby expressing the modified LGIC in the sensory neuron, and administering the exogenous ligand to the patient, thereby activating the LGIC. The LGIC comprises an LBD and a hyperpolarizing transmembrane ion channel domain introduced into an excitatory cell, or a depolarizing, excitatory transmembrane ion channel domain that is administered to inhibitory neurons. For example and without limitation, inhibitory ion channel domains according to any aspect described herein, include a transmembrane ion channel domain that is selective for Cl⁻ or K⁺ ions, such as a GlyR or GABA_A or GABA_C ion channel domain. For example and without limitation, excitatory ion channel domains according to any aspect described herein, include a transmembrane ion channel domain that is selective for Na⁺ or Ca²⁺ ions, such as a 5HT₃ ion channel domain. In aspects, the LBD is an α 7-nicotinic acetylcholine receptor LBD according to any aspect provided herein. In aspects, the pain is localized chronic pain in a patient, such as from osteoarthritic conditions, surgical implants, wounds, scarring, fibrotic conditions, nerve damage, or disease, visceral pain, muscle or deep tissue damage, spinal cord injury, post herpetic neuralgia, metabolic disease such as diabetes, chemotherapeutic neuropathy, idiopathic peripheral neuropathy.

[0063] In methods of delivering nucleic acids encoding modified LGICs, according to any aspect described herein to a cell or to a patient, the nucleic acid may be delivered by

any useful method, in any useful form, as is recognized by those of ordinary skill in the field of genetic therapies. The nucleic acid may be naked nucleic acid, such as a plasmid, deposited, for example and without limitation, by a colloidal drug delivery method, such as liposomes, e.g., cationic liposomes, or nanoparticles, or as part of a recombinant viral genome, as are broadly-known. In aspects, liposomes or nanoparticles comprising the nucleic acid are injected at a desired site, such as in or adjacent to specific neuronal tissue. In other aspects, a recombinant viral particle (transducing particle), is delivered, for example, injected, at a desired site, such as in or adjacent to, or otherwise targeting specific neuronal tissue. In one aspect, the nucleic acid comprising a gene for expressing the modified LGIC is an AAV (Adeno-Associated Virus) genome. In another aspect, the nucleic acid is injected into or adjacent to a tissue containing the target excitable or secretory cell, such as a CNS cell, e.g., a dorsal horn cell, a spinal cord cell, a brain cell, or a supraspinal cell. In another aspect, the nucleic acid is administered systemically, e.g., intravenously, and optionally in a delivery vehicle, such as an AAV particle that has a tropism to excitable or secretory cells, such as, for example and without limitation, AAV9, AAV-PHP.eB, AAV-PHP.S, or rAAV2-retro particles mentioned above, selective to brain, peripheral and/or spinal cord tissue. The nucleic acid may be injected once or more than once in order to establish sufficient expression of the modified LGIC in the target neuron cells. Suitable carriers or excipients for use in delivery of the nucleic acid, as are known in the related arts, may be included in the dosage form for delivery of the nucleic acid, such as in a liposomal or a recombinant viral transducing particle.

[0064] An “excipient” is an inactive substance used as a carrier for the active ingredients of a medication. Although “inactive,” excipients may facilitate and aid in increasing the delivery, stability or bioavailability of an active ingredient in a drug product. Non-limiting examples of useful excipients include: antiadherents, binders, rheology modifiers, coatings, disintegrants, emulsifiers, oils, buffers, salts, acids, bases, fillers, diluents, solvents, flavors, colorants, glidants, lubricants, preservatives, antioxidants, sorbents, vitamins, sweeteners, etc., as are available in the pharmaceutical/compounding arts. For example, for delivery to a nerve cell by injection, a drug product might comprise the nucleic acid in the form of a viral particle, nanoparticle, or liposome, in a suitable solvent, such as saline or phosphate-buffered saline, and including a rheology modifier or thixotropic agent.

[0065] Suitable dosage forms for delivery of exogenous ligands as described herein, include, without limitation, oral, percutaneous, or inhaled dosage forms, the formulation of which is within the skill of an ordinary artisan (see, generally, Troy, DB, Editor, Remington: The Science and Practice of Pharmacy, 21st Ed., Lippincott Williams & Wilkins (2005), pp. 745-849, for descriptions of various compositions, solutions, and dosage forms useful for administration of the described compounds, as well as methods of making such compositions, solutions, and dosage forms). The exogenous ligand is delivered in an amount, and dosage regimen, effective to achieve a desired therapeutic end-point, such as lessening pain. Determination of safe and effective amounts of the exogenous ligand is routine, and within the skill of an ordinary artisan. Further, certain suitable exogenous ligands are approved for use for other indications, such as vareni-

cline, or tropisetron, and as such suitable safe dosage ranges are already established in humans.

Example 1—Calretinin⁺ and CCK⁺ Neurons in the Dorsal Horn are Required for Persistent Pain

[0066] Methods. Animals: All animals were kept on a standard 12:12 light/dark cycle in micro-isolator caging racks (Allentown Caging) with food and water provided ad libitum. Mouse strains obtained from Jackson Laboratories include C57Bl/6J (JAX #000664), Calr^{Cre} (JAX #010774) and CCK^{Cre} (JAX #012706). Adeno-associated viruses (AAV2/8) used in these experiments: hSyn-Flex-rev-PSAM^{L141F}-GlyR-IRES-eGFP (7¹² vg/ml) and hSyn-Flex-rev-PSAM^{L141F}-Y115F-GyR-IRES-eGFP (1.7¹³ vg/ml) were custom made by UNC Vector core based on plasmid material developed by Scott Sternson and provided by Addgene. The hSyn-Flex-rev-PSAM^{L141F}-GlyR-IRES-eGFP (7¹² vg/ml) was used in all experiments except FIG. 8 (e,f). For these experiments, hSyn-Flex-rev-PSAM^{L141F}-Y115F-GyR-IRES-eGFP (1.7¹³ vg/ml) was used. Methods including: intra-spinal virus injections, paw withdrawal threshold to von Frey filaments, to cotton swab, Hargreaves, pinprick and acute pain behaviors licking, guarding, flicking are all as previously described (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015); Seal, R. P. et al. Injury-induced mechanical hypersensitivity requires C-low threshold mechanoreceptors. *Nature* 462, 651-655, (2009)); For paw withdrawal threshold to pressure: mice were lightly restrained by hand such that their rear legs were allowed to freely hang. Using a Pressure Application Measurement device (Ugo Basile) the hind paw was grasped between the experimenter's forefinger and thumb (with pressure transducer on the thumb), and force was slowly applied to the paw until the mouse struggled or flicked its limb (paw withdrawal threshold, PWT). The final force in grams was recorded. Each mouse was tested on the left and right paw for three trials with a ten-minute inter-trial interval between applications, and the three results averaged for each paw. Injury Models including incision, complete Freund's adjuvant, spared nerve injury tibial and sural models, carrageenan, methylglyoxal and multi-dose streptozotocin are as previously described (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015); Seal, R. P. et al. Injury-induced mechanical hypersensitivity requires C-low threshold mechanoreceptors. *Nature* 462, 651-655, (2009); Decosterd, I. and Woolf, C. J. Spared nerve injury: an animal model of persistent peripheral neuropathic pain. *Pain* 87, 149-158 (2000); Bierhaus, A. et al. Methylglyoxal modification of Nav1.8 facilitates nociceptive neuron firing and causes hyperalgesia in diabetic neuropathy. *Nat Med* 18, 926-933 (2012); Cavanaugh, D. J. et al. Distinct subsets of unmyelinated primary sensory fibers mediate behavioral responses to noxious thermal and mechanical stimuli. *Proc Natl Acad Sci U S A* 106, 9075-9080, (2009)). Chemogenetic Activation of PSAM-GlyR Receptor: Behavior thresholds were performed as described above in AAV8-hSyn-DIO-PSAM-GlyR-IRES-GFP injected mice. PSEM^{89S} at 30 mg/kg was injected intraperitoneally 15 minutes prior to testing. Immunohistochemistry was performed as previously described (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015); Seal, R. P. et al. Injury-induced mechanical hypersensitivity requires C-low threshold mechanoreceptors. *Nature* 462, 651-655 (2009)).

α -bungarotoxin conjugated to Alexa-647 (1:1000; ThermoFisher B35450), α -bungarotoxin conjugated to Alexa-488 (1:1000; ThermoFisher B13422). Imaging: Spinal cord sections were imaged with a confocal laser-scanning microscope (Nikon A1R) and Nikon Elements software using 405-, 488-, 561- and 640 nm excitation laser light. In order to suppress emission crosstalk, the microscope was configured to perform all scanning in sequential mode. Z-series were scanned at 20 \times magnification with an oil immersion lens and a z-step of 5.0 μ m. Quantification and Statistical Analysis: all data are reported as mean \pm SEM. For acute behaviors, a two-tailed Student's t-test was used. The effect of chemogenetic activation on persistent pain behavior was analyzed by one-way repeated measures ANOVA with Bonferroni's Post hoc test. Significance was considered p<0.05. (*p<0.05, **p<0.01, ***p<0.001.) All quantitative analysis, graphs and statistical tests were performed on GraphPad Prism 7.0 (GraphPad).

[0067] Results. To determine the role of calretinin and cholecystokinin (CCK) excitatory dorsal horn neurons in persistent pain and baseline somatosensory behavior, we used the designer ligand-gated anion channel, PSAM-GlyR (FIGS. 5, 8, and 10), which allowed us to acutely and reversibly inhibit these specific populations of neurons. Somatosensory behavior was tested under chemogenetic control at baseline and after the induction of inflammatory and neuropathic pain models (FIGS. 8 and 10). The inhibitory designer receptor, PSAM-GlyR¹⁶, is engineered such that a mutated ligand-binding domain of the human α -7 nicotinic receptor is fused to the anion channel domain of the human glycine receptor (FIG. 5(a), that is, FIG. 1, panel (a)) (Magnus, C. J. et al. Chemical and genetic engineering of selective ion channel-ligand interactions. *Science* 333, 1292-1296, (2011)). This mutated receptor binding domain no longer recognizes physiological levels of acetylcholine, but instead binds the synthetic ligand PSEM^{89S} with high affinity. To selectively target the CCK and Calretinin neurons in the dorsal horn, a Cre-dependent adeno-associated virus (AAV) encoding PSAM-GlyR (AAV8-hSyn.FLEX. PSAM-GlyR.IRES.EGFP) was injected unilaterally into the dorsal horn of P21 CCK^{Cre} or Calretinin^{Cre} mice (FIG. 5(b)). Four weeks later, receptor expression was examined by staining spinal cord slices with α -bungarotoxin conjugated to Alexa Fluor-647 (α -BTX-Alexa647), which specifically recognizes the ligand binding domain of α -7 nicotinic acetylcholine receptors, including the ligand binding domain of PSAM-GlyR (FIG. 5(b)). Expression of PSAM-GlyR was largely limited to laminae III-IV (FIG. 5(b)) and did not overlap with PKC γ (PKC γ staining not shown). Specificity of α -BTX-Alexa647 staining for the exogenously expressed PSAM-GlyR was demonstrated by the lack of staining observed in the contralateral dorsal horn (FIG. 6e).

[0068] In Vitro and In Vivo Controls for the Specific Actions of PSEM89S on PSAM-GlyR

[0069] Prior to assessing the role of the neurons in somatosensory behavior, the ability of PSAM-GlyR to inhibit excitatory interneurons in the dorsal horn was tested using electrophysiological recordings in spinal cord slices. AAV8-Flex-PSAM-GlyR was injected intraspinally into the dorsal horn of P16 Tlx3^{Cre} mice. In this mouse line, the recombinase is strictly expressed by excitatory neurons located throughout laminae I-III. Three weeks later, neuronal excitability was measured using patch clamp electrophysiology in spinal cord slices in the presence and absence of PSEM^{89S}

(FIG. 6(a-d)). To identify PSAM-GlyR⁺ neurons, we identified cells expressing green fluorescent protein (GFP), which is also encoded by the PSAM-GlyR viral construct (FIG. 6(a,b)). Application of PSEM^{89S} (30 μM) to spinal cord slices significantly decreased the membrane potential (-7.3 ± 3.4 mV, n=3 cells from 2 mice) and blocked action potentials generated by current injection in GFP+(FIG. 6(c,d)), but not GFP⁻ neurons (data not shown). We also tested the effect of the ligand PSEM^{89S} on pain behavior in mice lacking the receptor (FIG. 6(f,h)). PSEM^{89S} injection had no effect on mechanical allodynia or heat hypersensitivity in the carrageenan, complete Freund's adjuvant or SNI pain model, suggesting the drug alone has no unintended behavioral effects.

[0070] CCK+ Dorsal Horn Neurons are Required for Conveying Persistent Pain, but not Baseline Somatosensory Behavior.

[0071] Three weeks after unilateral injection of AAV8-hSyn-Flex-PSAM-GlyR in the dorsal horn of CCK^{Cre} mice, we tested the effect of inhibiting the dorsal horn CCK neurons on baseline somatosensory behavior using von Frey threshold, cotton swab assay, pinprick assay, pressure test and Hargreaves assay (FIG. 7). We also tested motor behavior using rotarod (FIG. 7). All behaviors were normal and similar to the contralateral hindpaw (FIG. 7). We next tested the effect of inhibiting the dorsal horn CCK neurons on persistent pain in the carrageenan model of inflammatory pain. PSEM^{89S} injection significantly reversed punctate and dynamic mechanical allodynia as well as heat hypersensitivity (FIG. 8(a)). Similarly, using the more chronic inflammatory model, complete Freund's adjuvant (CFA), PSEM^{89S} injection again significantly reversed both punctate and dynamic allodynia (FIG. 8(b)) as well as heat hypersensitivity. Injection of PSEM^{89S} (30 mg/kg, i.p.) into mice lacking the receptor showed no effect on CFA-induced persistent pain (FIG. 6(g)). In the sural-SNI model of neuropathic pain, PSEM^{89S} injection significantly reversed both punctate and dynamic allodynia (FIG. 8(c)). Similarly, in the tibial-SNI model of neuropathic pain, PSEM^{89S} injection markedly reversed punctate allodynia (FIG. 8(d)).

[0072] We have shown here that the CCK population is essential for the transmission of carrageenan and CFA-induced heat hypersensitivity, but is dispensable for normal heat sensibility. Because heat hypersensitivity also develops in diabetic neuropathic pain models, we tested whether the CCK neurons are also required in this type of pain. Indeed, acute inhibition of the CCK population markedly reversed the heat hypersensitivity induced by methylglyoxal (MG) treatment as well as the heat hypersensitivity induced by the multi-dose STZ model of diabetic neuropathy (FIG. 8(e,f)). These data reveal for the first time an essential role for CCK excitatory dorsal horn neurons in conveying punctate and dynamic mechanical allodynia induced by inflammatory and neuropathic pain models. This population also has an important role in conveying heat hypersensitivity induced by inflammatory and polyneuropathic pain models.

[0073] Calretinin neurons in lamina II of the dorsal horn are required for conveying mechanical allodynia induced by inflammatory injuries. Here we show that calretinin expressing neurons in inner lamina II of the dorsal horn are required for conveying mechanical allodynia induced by inflammatory injury. We unilaterally injected Cre-dependent AAV8 PSAM-GlyR into the dorsal horn of Calr^{Cre} mice at P21 (FIGS. 5 and 10). Similar to what was observed when

expressing the excitatory designer receptor in this population, neurons expressing PSAM-GlyR were restricted to inner lamina II (FIG. 5(b)) and co-localized with calretinin, but not PKCγ (not shown). Baseline measures of mechanical and heat sensitivity showed no change after injection of PSEM^{89S} at either the ipsilateral or contralateral hindpaw. Motor behavior was also normal after PSEM^{89S} injection (FIGS. 9(a,b)). We next tested whether the calretinin neurons are required for conveying mechanical allodynia or heat hypersensitivity in the carrageenan model of inflammatory pain. Injection of PSEM^{89S} 24 hours after carrageenan injection significantly reversed punctate mechanical allodynia (FIG. 10(a)). We also tested whether the neurons are required for mechanical allodynia in the CFA model. Measured 5 days after injection of the inflammatory agent, injection of PSEM^{89S} resulted in a complete reversal of punctate mechanical allodynia at the ipsilateral hindpaw (FIG. 10(b)). To determine how generalizable the requirement for calretinin neurons is in conveying mechanical allodynia induced by inflammatory pain models, we tested the incision model of post-operative pain (FIG. 10(c)). Inhibition of the calretinin neurons also significantly reversed mechanical allodynia in this model. The data collected from a number of inflammatory pain models show that dorsal horn neurons expressing calretinin are required for conveying mechanical allodynia induced by inflammatory injuries.

[0074] Discussion Work shown here demonstrates that targeting of a designer ligand-gated anion channel (in this case PSAM-GlyR) to neurons that express CCK⁺ or calretinin⁺ in the dorsal horn markedly attenuates mechanical allodynia and/or heat hypersensitivity caused by models of inflammatory and neuropathic pain when the receptor is activated by the designer ligand (in this case PSEM^{89S}). The data also demonstrate that PSEM^{89S} and PSAM-GlyR mediated inhibition of the neurons does not affect baseline mechanical or thermal sensitivity. Finally, the data demonstrate that the ligand alone (i.e. in the absence of the receptor) does not affect mechanical or thermal sensitivity either before or after inflammatory or neuropathic injury. Therefore, the data suggest that inhibition of these neurons is sufficient to block persistent mechanical and heat pain.

Example 2—Mechanical Allodynia Induced by Inflammatory and Neuropathic Pain Models is Attenuated by Injection of Varenicline in Mice with mCCK-PSAM4 Delivered to the Dorsal Horn

[0075] As further proof of concept, a varenicline-responsive PSAM-GlyR receptor mutant that was directly under the transcriptional control of a CCK promoter and delivered to the dorsal horn was shown to markedly attenuate mechanical allodynia in persistent pain models. The mouse cholecystokinin (CCK) promoter with an added chimeric intron to drive expression of α7^{L131G, Q139L, Y217F} GlyR (PSAM4) was packaged into AAV2/8 and injected into the dorsal horn of 3-week-old wildtype C57Bl/6 male and female mice. Injection of AAV into the dorsal horn was performed as described previously (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015)). See FIG. 11 for a schematic of the plasmid used to produce these rAAV particles. Briefly, a 2.5 kb fragment of the mouse CCK promoter was subcloned upstream of the PSAM4 gene with the chimeric intron (135

bp) located in between. This construct expressed in AAV8 is sufficient to drive expression in neurons in the deep dorsal horn.

[0076] Expression of the PSAM4 in the dorsal horn was examined by immunostaining for α -BTX-Alexa647 (FIG. 12). α -BTX-Alexa647 staining was observed in cells in the deep dorsal horn below the PKC γ layer (PKC γ staining not shown). This expression pattern is similar to the pattern for CCK mRNA in the dorsal horn detected by in situ hybridization (Allen Spinal Cord Atlas) and by injecting AAV8 hSyn-Flex-PSAM-GlyR virus in the dorsal horn of CCK^{Cre} mice (see FIG. 5(a)).

[0077] Varenicline has no effect on mechanical or heat sensitivity at baseline or after CFA or sural-SNI in the absence of PSAM4. Mechanical and heat hypersensitivity was tested in adult wildtype male and female C57Bl/6 mice (not injected with mCCK-PSAM4 virus) before and after intraperitoneal injection of (i.p) varenicline (0.1 milligram per kilogram (mpk) (FIG. 13). We also tested these parameters before and 2-5 days after induction of the complete Freund's adjuvant (CFA)-model of inflammatory pain and 7 days after induction of the sural version of the spared nerve injury (SNI) model of neuropathic pain (FIG. 13). Sensitivity to mechanical stimuli was tested by measuring the paw withdrawal threshold to von Frey filaments (PWT) and the paw withdrawal response to a cotton swab (percentage of response) as described previously (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015)). Heat sensitivity was tested by measuring the withdrawal latency to a radiant heat source using the Hargreaves apparatus (PWL) as described previously (Peirs, C. et al. Dorsal Horn Circuits for Persistent Mechanical Pain. *Neuron* 87, 797-812 (2015)). As shown in FIG. 13, injection of varenicline (0.1 mpk, i.p) had no effect on baseline PWT, response frequency or PWL in uninjured mice (measured 30-60 minutes after injection). Injection of varenicline also had no effect on mechanical or heat hypersensitivity 3 and 2 days, respectively, after induction of CFA or 7 days after induction of sural-SNI models. PSAM4 ligands have no effect on baseline mechanical or heat sensitivity, but reverse mechanical allodynia induced by CFA and SNI in mice with targeted expression of PSAM4 in CCK+ neurons of the dorsal horn.

[0078] Mice were injected unilaterally in the dorsal horn with AAV8 mCCK-PSAM4 virus and tested two weeks later. As shown in FIG. 14, varenicline (0.3 mpk, i.p.) did not alter baseline PWTs, response frequencies or PWLs. Thus, inhibition of the dorsal horn CCK+ neurons does not alter mechanical or heat sensitivity. The ipsilateral plantar hind-paw of the mice was injected with CFA and PWTs and response frequencies tested 3 days later in the absence and presence of varenicline (0.3 mpk, i.p.). As shown in FIG. 15, varenicline (0.3 mpk, i.p.) markedly reversed both PWT and response frequency after CFA. As shown in FIG. 16, varenicline (0.3 mpk, i.p.) markedly reversed the PWT when measured 7 days following sural spared nerve injury. These results are similar to what we observed with PSEM^{89S} and PSAM-GlyR in FIGS. 7 and 8.

[0079] The following numbered clauses provide illustrative examples of aspects of the invention:

[0080] 1. A nucleic acid comprising a gene for expressing a modified ligand-gated ion channel, comprising an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of transcrip-

tional control elements governing cell-specific expression in CNS neurons, such as dorsal horn neurons, spinal cord cells, or brain cells, or in inhibitory neurons or nerve cells, such as a CCK promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, an SST promoter, a GRPR promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a PKC γ promoter or Calb2 promoter, wherein the modified ligand-gated ion channel comprises a modified ligand binding domain activatable by an exogenous ligand, and optionally selective to the exogenous ligand, and an ion pore domain.

[0081] 2. The nucleic acid of clause 1, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, an SST promoter, a GRPR promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a Calb2 promoter or a PKC γ promoter.

[0082] 3. The nucleic acid of clause 1, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, a Calb2 promoter, or a PKC γ promoter.

[0083] 4. The nucleic acid of clause 1, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter.

[0084] 5. The nucleic acid of any one of clauses 1-3, wherein the transcription control element comprises a human promoter sequence.

[0085] 6. The nucleic acid of clause 5, wherein the transcription control element is a promoter having at least 75 percent sequence identity to a sequence set forth in SEQ ID NOs: 1-17.

[0086] 7. The nucleic acid of any one of clauses 1-6, wherein the modified ligand binding domain is a modified α 7 nicotinic acetylcholine ligand binding domain. 8. The nucleic acid of clause 7, wherein the modified α 7 nicotinic acetylcholine ligand binding domain comprises a sequence having at least 75 percent sequence identity to a sequence set forth in SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20.

[0087] 9. The nucleic acid of clause 7, wherein the modified α 7 nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 131, 139, 141, 175, 210, 216, 217, and 219.

[0088] 10. The nucleic acid of clause 7, wherein the modified α 7 nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 139, and 141, such as Q79A, Q79G, L141A, L141 F, L141 P, W77F, W77Y, and W77M. 11. The nucleic acid of clause 7, wherein the modified α 7 nicotinic acetylcholine ligand binding domain comprises:

[0089] a L131G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution;

[0090] a W77F amino acid substitution, a Q79G amino acid substitution, and a G175K amino acid substitution;

[0091] a Q79G amino acid substitution, a Y1.15F amino acid substitution, and a G175K amino acid substitution;

- [0092] a Y115F amino acid substitution and a G175K amino acid substitution;
- [0093] a Q79G amino acid substitution and a P2161 amino acid substitution; or
- [0094] a R27D amino acid substitution and/or a E41R amino acid substitution.
- [0095] 12. The nucleic acid of clause 7, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises a L131 G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution.
- [0096] 13. The nucleic acid of clause 7, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain has reduced binding with endogenous acetylcholine (ACh) as compared to unmodified $\alpha 7$ -nAChR LBD.
- [0097] 14. The nucleic acid of clause one of clauses 1-13, wherein the ion pore domain is anion-selective, or cation-selective, and optionally is an ion pore domain of an ionotropic nicotinic acetylcholine receptor, an ionotropic serotonin receptor, an ionotropic glycine receptor, or an ionotropic GABA receptor.
- [0098] 15. The nucleic acid of any one of clauses 1-13, wherein the ion pore domain is an ion pore domain from a serotonin 3 receptor (5HT3) ion pore domain, a glycine receptor (GlyR) ion pore domain, a gamma-aminobutyric acid (GABA) receptor ion pore domain, or an $\alpha 7$ nicotinic acetylcholine receptor ion pore domain.
- [0099] 16. The nucleic acid of clause 15, wherein the ion pore domain is a GlyR ion pore domain comprising an amino acid substitution at residue 298.
- [0100] 17. The nucleic acid of clause 16, wherein the GlyR ion pore domain comprising an A298G amino acid substitution.
- [0101] 18. The nucleic acid of clause 1, wherein the exogenous ligand is selected from the group consisting of a quinuclidine, a tropane, a 9-azabicyclo[3.3.1]nonane, a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, and a 1,4-diazabicyclo[3.2.2]nonane.
- [0102] 19. The nucleic acid of any one of clauses 1-18, comprising a sequence of a packageable viral genome comprising the gene for expressing a modified ligand-gated ion channel.
- [0103] 20. The nucleic acid of clause 19, comprising Adeno-associated virus ITR sequences flanking the gene for expressing a modified ligand-gated ion channel, producing a sequence of a packageable recombinant AAV genome or a self-complementary AAV genome comprising the gene for expressing a modified ligand-gated ion channel.
- [0104] 21. A method of modulating (increasing or decreasing) the membrane potential of an excitable cell or a secretory cell, comprising expressing in the cell a genetic construct comprising a gene for expressing a modified ligand-gated ion channel, comprising an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of transcriptional control elements governing cell-specific expression in CNS neurons, such as dorsal horn neurons, spinal cord cells, or brain cells, or in inhibitory neurons or nerve cells, such as a CCK promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, an SST promoter, a GRPR promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a PKC γ promoter, or Calb2 promoter and a modified ligand-gated ion channel comprising a modified ligand binding domain activatable by an exogenous ligand, and optionally selective to the exogenous ligand, and an ion pore domain, and contacting the cell with an amount of the exogenous ligand effective to activate the modified ligand-gated ion channel thereby modulating the membrane potential of the cell.
- [0105] 22. The method of clause 21, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, an SST promoter, a GRPR promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, Calb2 promoter or a PKC γ promoter.
- [0106] 23. The method of clause 21, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, a Calb2 promoter, or a PKC γ promoter.
- [0107] 24. The method of clause 21, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter.
- [0108] 25. The method of any one of clauses 21-24, wherein the transcription control element comprises a human promoter sequence.
- [0109] 26. The method of clause 25, wherein the transcription control element is a promoter having at least 75 percent sequence identity to a sequence set forth in SEQ ID NOs: 1-17.
- [0110] 27. The method of any one of clauses 21-26, wherein the modified ligand binding domain is a modified $\alpha 7$ nicotinic acetylcholine ligand binding domain.
- [0111] 28. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises a sequence having at least 75 percent sequence identity to a sequence set forth in SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20.
- [0112] 29. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 131, 139, 141, 175, 210, 216, 217, and 219.
- [0113] 30. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 139, and 141, such as Q79A, Q79G, L141A, L141 F, L141 P, W77F, W77Y, and W77M.
- [0114] 31. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises:
- [0115] a L131G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution;
- [0116] a W77F amino acid substitution, a Q79G amino acid substitution, and a G175K amino acid substitution;
- [0117] a Q79G amino acid substitution, a Y1.15F amino acid substitution, and a G1.75K amino acid substitution;
- [0118] a Y115F amino acid substitution and a G175K amino acid substitution;

- [0119] a Q79G amino acid substitution and a P216I amino acid substitution; or
- [0120] a R27D amino acid substitution and/or a E41R amino acid substitution.
- [0121] 32. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises a L131 G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution, and, optionally, the exogenous ligand is varenicline.
- [0122] 33. The method of clause 27, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain has reduced binding with endogenous acetylcholine (ACh) as compared to unmodified $\alpha 7$ -nAChR LBD.
- [0123] 34. The method of clause one of clauses 21-33, wherein the ion pore domain is an ion pore domain of an ionotropic nicotinic acetylcholine receptor, an ionotropic serotonin receptor, an ionotropic glycine receptor, or an ionotropic GABA receptor.
- [0124] 35. The method of any one of clauses 21-33, wherein the ion pore domain is anion-selective, or cation-selective, and optionally is an ion pore domain from a serotonin 3 receptor (5HT3) ion pore domain, a glycine receptor (GlyR) ion pore domain, a gamma-aminobutyric acid (GABA) receptor ion pore domain, or an $\alpha 7$ nicotinic acetylcholine receptor ion pore domain.
- [0125] 36. The method of clause 35, wherein the ion pore domain is a GlyR ion pore domain comprising an amino acid substitution at residue 298.
- [0126] 37. The method of clause 36, wherein the GlyR ion pore domain comprising an A298G amino acid substitution.
- [0127] 38. The method of clause 37, wherein the exogenous ligand-gated ion channel ligand is selected from the group consisting of a quinuclidine, a tropane, a 9-azabicyclo[3.3.1]nonane, a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, and a 1,4-diazabicyclo[3.2.2]nonane.
- [0128] 39. The method of any one of clauses 21-38, comprising a sequence of a packageable viral genome comprising the gene for expressing a modified ligand-gated ion channel.
- [0129] 40. A method of treating a disease or disorder associated with the nervous system in a patient comprising: delivering a nucleic acid according to any one of clauses 1-20 to the patient, and administering the exogenous ligand to the patient in an amount effective to activate the modified ligand gated ion channel in a patient thereby treating the disease or disorder associated with the nervous system in the patient.
- [0130] 41. The method of clause 40, wherein the disease or disorder associated with the nervous system is itch.
- [0131] 42. The method of clause 40, wherein the disease or disorder associated with the nervous system is chronic pain, and transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, an SST promoter, a GRPR promoter, a Tac1 promoter, an NTS promoter, an NMU promoter, a Calb1 promoter, a parvalbumin promoter, a Gal promoter, an NPY promoter, a Calb2 promoter or a PKC γ promoter.
- [0132] 43. The method of clause 25, wherein transcription of the modified ligand-gated ion channel is controlled at least in part by a CCK promoter, a calb2 promoter, or a PKC γ promoter.
- [0133] 44. The method of any one of clauses 40-43, wherein the nucleic acid comprising the gene for expressing a modified ligand-gated ion channel is delivered to the patient as a recombinant AAV transducing particle.
- [0134] 45. The method of any one of clauses 40-44, wherein the exogenous ligand is selected from the group consisting of a quinuclidine, a tropane, a 9-azabicyclo[3.3.1]nonane, a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, and a 1,4-diazabicyclo[3.2.2]nonane.
- [0135] While the present invention is described with reference to several distinct aspects or embodiments, those skilled in the art may make modifications and alterations without departing from the scope and spirit. Accordingly, the above detailed description is intended to be illustrative rather than restrictive.

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 organism = Homo sapiens

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FEATURE              Location/Qualifiers
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gcacactggg ccacagagga tccagcaagg                                     4050

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SEQ ID NO: 11      moltype = DNA length = 2999
FEATURE           Location/Qualifiers
source            1..2999
                  mol_type = genomic DNA
                  organism = Homo sapiens

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SEQUENCE: 11
cccgccagc ctcgcccggc acgcccgggag ggggagttct cggtcgtgtc ccgagagtgg 60
ctggtcccga ggctcggact accagtccca gaatgcactg cgcccgcagc ccggggcggg 120
ccgtgggtgc ccctggcaac agagaggggt cccgggagcg gggactggga agcgtcccgc 180
agccggggag ccgcagagcc cgaccagaga gaggcgggga cgcgggtaga gcgaccaaga 240
gggtgggagg ccggaagaga ctgaccgcgc cggcccttgg agagaccctt ttctctgagag 300
ggggcgcaca gagaggatgc cgaagccagc gagatctaga gagagggaga cagggattga 360
atcacagaga cacttagagg gagggagaga cctcaaaagc agagagattc acagggccag 420
agagacacgt agagtgggtc agagaagagg acagaggaca gagacataga aaagacagga 480
gggagagaga ctgaatcaca gagacacagg gagagagggg gagacctcag agatggagag 540
agactcacag ggccagatag acacatggag tgggtcagag aaggggacag agagagagac 600
acagaaaagg gaagaggagg agagactgaa tcacagagac acagagaggg aagtctctat 660
ctagagaccg tcgacagaga ttcttagagc cagagacaga gatctagaga gccagagaga 720
cagagagatt catagagaca tatagagaga ttcagagagc ctgaatcaca gagattcaca 780
gagccaacga gacaacacga gagattcata gagccagaga cacagatcgc gagagtccga 840
gagacataga aagattcata gagccagaga cacagagatt cagagagtca gagagacata 900
gagagacatt catagagcca gagacacaga gagattcata gacatataga gagattcaga 960
gagcctgaat cacagagatt cacagagcca aagagacaaa cagagagatt catagagcca 1020
gagacacaga gggattcggg gagtccagaga gacatagaaa gagattcata gagccagaga 1080
cacagagatt catagagaca tagagattca tagagcccga gacacagaga ttcagagagt 1140
cagagagaca tagaaagaca ttcatagagc cagagacaca gagagattca gagtccagaga 1200
aacatagaga tccatagagc cagagacaca gagagattca gagtccagaga gacatagaga 1260
gacattcata gagcccggag ccagagagaga ttcagagtca gagagacata gattttataga 1320
gccagagaca cagattcagg gagtccagaga gacatagaga gacattcata gagcccggaga 1380
cacagattca ggtccagaga gacatagaca ttcatagagc cagagacaca gattccagaga 1440
gtcagagaga tgaatagatt cagagagcca gagacacagg gagagtgaat cacagacaca 1500
gagggcgggg gagatcccca gaaacagaaa gagattcata gagccagaga gacaaataga 1560
gattgggtca gaaagaaagg gacagagaca gagacagaga agagaagagg gagagagatt 1620
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gacagggagag agacccccct agcatcagag agagagagag agatcaacag agccagagag 1740
ggacaagtac agagaaacag atggaaccag agagatatag gaagagacaa acaaaaaacag 1800
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actgattcac agtgagcgag accaaagacc cgagaagaac cagcacacca agaccagag 2160
atggcgagac atacagatgg agacacacag cagaggaat agagaaatag aaagaaatag 2220
aaacagcatt tctcggagac agggaaaaga aaacagatcc actgagaggg agaaacagag 2280
acacatcgag aaagctcgct ccaggaatag agggagaggg acagaggtca caaagaagac 2340
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cgcccacagg acacacaggg gaccctagtg ggggaggaac gccgggaggg atgacagatt 2580
gcagggtggt gggggggagc cagggtcaga ggatgccctt ccctccagcc agccccggga 2640
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SEQ ID NO: 12      moltype = DNA length = 3000
FEATURE           Location/Qualifiers
source            1..3000
                  mol_type = genomic DNA
                  organism = Homo sapiens

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SEQUENCE: 12
cgctcatgag atcactgtcg agatacttcc cttcatttcc ttctctgtga ccttgaaggg 60
tctgggctac atcatctcca tgtctccatc ccattccgat attcttgaag atcaagacc 120
tgggtggccc attaaagggg aatggaaggg aggtgggtag attttgatac gtctttgcaa 180
agaggttgac attctgtttg ttgcaggctt ggcggaagta cgacacagac aggagtggtc 240
acatcgaagc caatgagctc aaggtaggat gggccttggg gaggggtgtga ggcagagtg 300
gctgtgggct taaggtgctt gaggggggag gagatggttg atgaggggca tgagtttgcg 360
ggctgcttag gaatactcag acctggcact gaattgttgg acttgtttag agaagtcagg 420
ggaaatcagt aaacatagag tcaccaggct tagatttcaa cgaaacccag ctctttgca 480
cctccatgct cgggacagga gtcctccagg caattccaga agattggcct ctggctccta 540

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ggtccacctc caaattcttc tggetatcac ccagtgatcc cccaggeact gcttagctcc 600
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gcaccaccag ctagtacagc cttaaaagtc actcccacag agttaggaaat tatgagggcc 720
ctgagtcata gaactggtag acctgaaaa cacacacaca cacattgaga gactgtctga 780
atgagcaagt aaggaaatga atgagggacc gaatgcacga gtcaggagta ctaaagaggc 840
cttttgtggt gcaggggattc ctgtcagacc tgcctgaaga ggcgaaccgg ccgtacgatg 900
agcccaagct ccaggaatac acccaaacca tagtgagtga acagaagtgt ccctctcccc 960
caggggtcag gacttgtgcc ccaagccact tgggctctgg tgtgcagggt cccttgtttg 1020
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ttcgtggctt cacataccct ttgaggtcct ggggtgtgag tgactcgtgg gccaatgtga 1140
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ccttttagtgc cggcctgctg tcctcagct gccctgtcc ctgaggaggg gagagaggag 1260
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acacacacaa aacacaccac acacacacaa cacacagatc acacacacaa aacacacaca 2040
gaccacacac accacataca caacacacgc agaccacaca cactacatat cacacgcaca 2100
caccaccatc acacagagac atcacacaca ccacacagac cacacaccac acacacaaca 2160
cacacatcac acatgcacac accacacaca taaacacaca cacacaaaac cacaccaca 2220
cacacaccac tgccttctgt cttctgtctt taataacctg gttcttgcag ggcattgaagc 2280
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gcattggcagg gaaatcaga agcccatcag cccgtccaga agggctcagc ttcattcctg 2400
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cacgtgtcgg ggaaccaaag ggaagagaca ctcagaactg ccctgggtgc agatcacaaat 2640
tctgcccagg gccaaagtct tctctgggaa gttggaagtt agatgatctc cataccacc 2700
cctccctggg ctgtcccctg cccacatgac tccggtggtt ttcttcataa ccagtgttgg 2760
aggtaaactt taaatagccc ccggactcag ggagtttaacc aaatgcttct tgaatctcac 2820
ttaaattttc aacgcacatg aaaagcacca caatgaaagg ctaccocaaag cttgacccca 2880
ctgcccactt cctgctatga ctggtaaagg cagaaggggac acattatttt gtcattacac 2940
gatctgaaca cccctctttg ccacagagtaa tggagaggct agactcttag acatccctgg 3000

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SEQ ID NO: 13 moltype = DNA length = 2441
FEATURE Location/Qualifiers
source 1..2441
mol_type = genomic DNA
organism = Mus musculus

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SEQUENCE: 13
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taaagagtcc attgtgccac cttcttccag cttctaactg tccttgacac ctttggcttc 120
tcctgggtgc ttttctactc tggcctttga ccctgcctgt ggtcagggtc tggacccttc 180
tcccgttcct tcctctggct gtccacacct ggaatctggg cagagatgct ttttctcttc 240
cctcgtctcc caccttttga gtctcttctc acagettcca ggtgggaagc caccatctac 300
agaaagagtc ttgggttgta cctccaggtg cctctgtctc aggacttgag atcacacct 360
tctctagctg tccaccata accctgattc atccccacg ccccgccaga cacaccag 420
ttggtgtggt ttcttctgaa ctccccctgt ggccaataca ctccccacca cccttgtctc 480
tcagcccaga acttcacagt cagccccaga cacggagtac ctttgggttt cttgaagagc 540
aagatgctgc ttccatcgct ggaagtttct gcttatgtct actgttctag ctattcggat 600
gttctattgt aggcacttag gactcgtata gtgtctgcta catttcatga tagtgaataa 660
atttcacaaa agcatattag gcttctata aatctgtcct catctctcaa tggccctccc 720
atctcctgtc ttctcaacct ctccctggct cccgtgtctg ccctagggac acctccatgt 780
caccaccaga ctcagtgga atccttactc cgccttggc tattagtga gatctgaact 840
cagttccttg tacttgacag caagcacttc actgctgag ccgctccca gttccagctc 900
caggccccgg cctcccaag gtgtttatct gtgtgggtat ttattttgtc cagtcttgggt 960
cacaccgat cctcaggggc tgggcacagt tcataaatct tgaggcaagc gatggaggga 1020
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aaccatgaac ctaaacctct ggcatacact gctgtttctc atagtcccc tcagccggaa 1320
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ctagcttgac agggttgagg gcattgttgc cctggctggt ggtgacccca agttacaagc 1440
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gggattcagc aaattctagc accctgggca tagaataca ctttgttatg tgagaactgg 1560
gggttgacag attgtgcgca ctacagcaga gagagcccc tctctctctc ttgcttggta 1620
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ctagactgga aagggtgatc tgaactcttg ggaaggtgag agcccagccc gcatggctca 1740
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tcagtagatg ataggcccct gggaaagtcg cgtggaaaga aattacaat ctttttccca 1860
gaggcttttc gcagaaagge aggagctgca cccgatctta caattgtgta agaatagaat 1920
ccaggatgcc aactgcaatt gagttctgaa aaattgggag cccgatttcc ctctcttact 1980
tgtgagagcc cactcaggtc tgaagtggtc ccagagaaca caccaggatt acatctgctg 2040
acaccagacc tgtgagggtc ccccagtttc cttgaaggat ttgatcccca aagctcactg 2100
aacttggtea gcttctccat tgcagataaa ctctctgttt tcaccgagag tggaggtggc 2160
accctccctg aggtggactc tgcacaggcg ccgaacaggt gggaaaggag ctctttagat 2220
aaagagtaag acccatgcaa agtgccccc tgggaggggc tatcctcatt cactgggagc 2280
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acgtgtcctg ctggactgag tcagcactgg gtaaacagat gactggctgc gaaccgggag 2400
gagctattta agagcagtc cctcccgcgc tgcctcacc t 2441
    
```

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SEQ ID NO: 14      moltype = DNA length = 1544
FEATURE
source            Location/Qualifiers
                  1..1544
                  mol_type = genomic DNA
                  organism = Mus musculus
    
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SEQUENCE: 14
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gatgtcaata ccacacaccc cattttacag actcggaaag ccaaggcaca gacaggctgt 180
gtaagccaaa caacgttgtg gaggttttgt tgttgtttgt ttaggaacta gacccgagga 240
gtttgattct atgcaactg ttctttagga ctgagccttc ttgcctctc gaaggcaaga 300
ctcaggctgg gggactctag cttagtaatt tctcagccct ggcagcaagg aatgctgggt 360
tacagaagcc ccaacagttta gcctattttg ctgcgtctct cccagctctg tcttgtaaac 420
aacctcaaac ttgtgtcctg ggcaacacac cagcagtttt gaaaactggg ctccatggtg 480
ccctttgagg ttagctccga gctacctcaa cctgacccca ggaaacagcc tgctcttctc 540
cgctcccccc cctccccccc acccccaccc ggggtctcct ctcccctagc gacctgcttt 600
agattctcac ctctctctct ttgtctcctc cttcgaagge agctcagcta acactcatta 660
gcacatgtta atgagcagca attcaagtct ctgtcctctc ttttaggggc aggggtgctg 720
ctgttgctct gaaggtaagg tgtccaagaa gcaagcacac actcgagacc tttagagtag 780
ggaggatag ggacggagge tggctctctg attgaggaga cccacggtg tgcgtgctt 840
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agaaccctgc tttcctgcaa tctctgtacc cctcagggga gtcacaggac aggaagagtt 1140
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gggtgtctca agatggacag agggaaagga aggcaggagc tgcctctccc catttccagc 1260
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cctgagtggt cgcgccccct tccggcggcc cgacgctgag cagctccggg ctgcatataa 1440
aggcagcgtg gcgcgagccc ccagcgcgag aaccagagcc aagcggcacc gagtgcagac 1500
gctgtgagag agaggcttaa gatctccgga gcggctcgcgc atgg 1544
    
```

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SEQ ID NO: 15      moltype = DNA length = 3014
FEATURE
source            Location/Qualifiers
                  1..3014
                  mol_type = genomic DNA
                  organism = Mus musculus
    
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SEQUENCE: 15
ggactagatc ctggatccct gggatagagg aaggagggga gttgtgccta gattcctaga 60
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gtaagaagtt gatccagaa gctggctcct gtgtactctg ggagctgttc tgggacagtg 180
tgagcttcca ggggttaaag caagcccttc tgtctttccg tgggcttgac cttagacaga 240
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gctgcccgcg ggtgggtggct acacctttaa ttacagcact ccaaagacag aggcaggcag 360
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acagaacaaa caaacaacaa aagatgcaag gtcaaagaga ccaaagttaa ccaaagtgca 480
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catggaagac tcattggaaga cgcatttctg gggtagactg ctcaacttgt agtcagctgg 600
gcagaagagt cttcctgtcc tctcttaatt gtttgtgctc catatattac ttcagctttg 660
ggagggggcct catagcacag cccgtgaaat ttctgagcct tggggggttct atggtttgtc 720
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gaggtcagag gacaatttgc agaattccac atggctctac caccatgtgg gtcttgggga 840
cagaactcag cttatcatgc tctggtgtaa gtctctttct ttcttttctt ctttctttct 900
ttctttcttt caatttattt atttattttc catatatgag tacattgtag ctatacagat 960
ggttgtgagc catcatgtgg ttgctgggaa ttgaaactcag gacctctgct tgctccagcc 1020
ctgctgtctc cagcccaagg atttatttat tattatatgt acgctgtaca tataaataa 1080
aatacatata taagtaatat tattattata ataataaata agtacactgt agctgttttc 1140
ggacccacca gaagaggggt tcagatctca ttacggatgg ttgtgagcca ccatgtgggt 1200
ctcgggattt gaactcagga ccttcagaag agcaatcagt gctcttacct gctgagtcac 1260
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aagaataac tacagaactg acaatagtaa taagaaaatt ggacctggaa accaccttct 1440
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catttggtcc tagttctgag cctctaggac aaggagacag aagctgtggt ttgcagtgtg 1560
aaaaaagaga tgtggctggg cagtgggtgc acatgccttt aatcccagca catggaaggc 1620
agagccaggt ggtactctga gttcaaggcc agcctggctc acagagtggg ttccaggcca 1680
gccatggcta cacagagaaa cccctctcgg aaaaaacaaa acaaacaaaa agatggttagt 1740
ccttccactc acttcccact tcaagggtac atggtagact agaaggccga gaggcctgtc 1800
ctgaggtcta gcccctgatg actgatctcg aaaactagag atttcaagtgg actgctcaat 1860
gagaatggag ggagttgaat tttcctgtac ttgaggtacc tgtagctga gtccctggag 1920
gaagtgataa gctcagagat aagaaagcag aaactgagca gtctcaatt ctccaggtct 1980
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agactttaga ccatatcttt cattgctggg tgggtggttt tgtgtttgt tataaaacag 2400
ggtttggttg tttgtttggt tgtttgtaat aaaacagagt agccttgacc attctggaac 2460
tcaactgtga gccaggtgtg gctttgtttg ttttaaaggc agaaccacat tctgtagccc 2520
aagctagctt gacccttatt acagagcccga ggctggtctc catctcacag tagccttccc 2580
actttagctc cccaattctc aagatcatgg gtgtgcccct cttgacttgg tttgcgtagt 2640
gcagggttca gatccaagge ttctgaaat atatagacaa gcgtgttacc agctaagcca 2700
catccccacg gatcaaaagtt taggtgatg tttggggatg gctgtgatg gttcgcagtg 2760
aggtcagaag ttggtttttt ccttccagga gttatgtccc agtaagccag ctctagtttt 2820
ccagcatggc agcacacact cccgtggata ggatgctgac tccctgggaa agggaagcaa 2880
gaagtatagc tttgtagtgg tggattttgg gttttcttat gggtagggtc aggatgagcc 2940
tagaacctag atgaccaatt catttttata gtttatagac aagttccata tattaagaca 3000
catccttttc agaa 3014
    
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SEQ ID NO: 16      moltype = DNA length = 3171
FEATURE           Location/Qualifiers
source            1..3171
                 mol_type = genomic DNA
                 organism = Mus musculus
    
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SEQUENCE: 16
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 organism = Mus musculus

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RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWPFDP	VQHCKLKFGS	WSYGGWLDL	180
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 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 19

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RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWPFDP	VQHCKLKFGS	WSYGGWLDL	180
QMQEADISGY	IPNGEWDLVG	IPGKRSERFY	ECCKEPYPDV	TFTVTMRRR		229

SEQ ID NO: 20 moltype = AA length = 233
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 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 20

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RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWFPFD	VQHCKLKFGS	WSYGGWSDL	180
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 FEATURE Location/Qualifiers
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 note = alpha7-5HT3 chimeric receptor
 source 1..471
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 21

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RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWFPFD	VQHCKLKFGS	WSYGGWSDL	180
QMQEADISGY	IPNGEWDLVG	IPGKRSEPFY	ECCKEPYPDV	TFTVIIRRRR	LFYAVSLLP	240
SIFLMVVDIV	GFCLPPDSGE	RVSFKITLL	GYSVFLIIVS	DTLPATIGTP	LIGVYFVVC	300
ALLVISLAET	IFIVRLVHKQ	DLQRPVPDWL	RHLVLDRIAW	ILCLGEQPM	HRPPATFQAN	360
KTDDCSGSDL	LPAMGNHCSH	VGGPDLEKT	PRGRGSPLPP	PREASLAVRG	LLQELSSIRH	420
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 note = Alpha7-GlyR chimeric receptor
 source 1..430
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 22

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RFDATFHTNV	VNSSGHCQYL	PPGIFKSSCY	IDVRWFPFDV	QHCKLKFGSW	SYGGWSDLQ	180
MQEADISGYI	PNGEWDLVGI	PGKRSEPFYE	CCKEYPYDVT	FTVTMRRRM	YYLIQMYIPS	240
LLIVLISWIS	FWINMDAAPA	VVGLGITTVL	TMTQSSGSR	ASLPKVSVK	AIDIWMAVCL	300
LFVFSALLEY	AAVNFVSRQH	KELLRPRKR	RHHKEDEAGE	GRFNFSAYGM	GPACLOAKDG	360
ISVKGANNNS	TTNPPAPSK	SPEEMRKLFI	QRAKKIDKIS	RIGFPMFLI	FNMFYWIIYK	420
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SEQ ID NO: 23 moltype = AA length = 466
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 note = alpha7-5HT3 chimeric receptor
 source 1..466
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 23

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QIMDVDEKNQ	VLTTNIWLQM	SWTDHYLQWN	VSEYPGVKT	RFPDQIWKP	DILLYNSADE	120
RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWFPFD	VQHCKLKFGS	WSYGGWSDL	180
QMQEADISGY	IPNGEWDLVG	IPGKRSEPFY	ECCKEPYPDV	TFTVIIRRRR	LFYVVSLLP	240
SIFLMVMDIV	GFYLPPNSGE	RVSFKITLL	GYSVFLIIVS	DTLPATAIGT	PLIGVYFVC	300
MALLVISLAE	TIFIVRLVHK	QDLQQVPAW	LRHLVLERIA	WLLCLREQST	SQRPPATSQA	360
TKTDDCSAMG	NHCSHMGQP	DFEKSPRDRC	SPPPPPREAS	LAVCGLLQEL	SSIRQFLEKR	420
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SEQ ID NO: 24 moltype = AA length = 428
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 REGION 1..428
 note = alpha7-GABA_A chimeric receptor
 source 1..428
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 24

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RFDATFHTNV	LVNSSGHCQY	LPPGIFKSSC	YIDVRWFPFD	VQHCKLKFGS	WSYGGWSDL	180
QMQEADISGY	IPNGEWDLVG	IPGKRSEPFY	ECCKEPYPDV	TFTVTMRRRT	LYYLLQTYFP	240
ATLMVMSLVW	SFWIDRRAVP	ARVPLGITTV	LTMSTIITGV	NASMPRVSYI	KAVDIYLWVS	300
FVFPVLSVLE	YAAVNYLTTV	QERKEQKLRE	KLPCTSGLPP	PRTAMLGNY	SDGEVNDLDN	360
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SEQ ID NO: 25 moltype = AA length = 502
 FEATURE Location/Qualifiers
 source 1..502
 mol_type = protein

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organism = Rattus norvegicus

SEQUENCE: 25

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RFDATFHTNV	LVNASGHCQY	LPPGIFKSSC	YIDVRWFFPD	VQCKLKFSGS	WSYGGWSLDL	180
QMQEADISSY	IPNGEWDLMG	IPGKRNEKPY	ECCKEYPYDV	TYTVMRRRT	LYYGLNLLIP	240
CVLISALALL	VFLLPADSGE	KISLGITVLL	SLTVFMLLVA	EIMPATSDSV	PLIAQYFAST	300
MIIVGLSVVV	TVIVLRYHHH	DPDGGKMPKW	TRILLNWCWA	WFLMRKRPGE	DKVRPACQHK	360
PRRCSLASVE	LSAGAGPPTS	NGNLLYIGFR	GLEGMHCAPT	PDSGVVCGRL	ACSPHDEHL	420
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ICTIGILMSA	PNFVEAVSKD	FA				502

What is claimed is:

1. A nucleic acid comprising a gene for expressing a modified ligand-gated ion channel, comprising an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of a regulatory element governing cell-specific expression in dorsal horn neurons, wherein the modified ligand-gated ion channel comprises a modified ligand binding domain activatable by an exogenous ligand, and an ion pore domain,

wherein the modified ligand-gated ion channel is a modified $\alpha 7$ nicotinic acetylcholine ligand binding domain, and

wherein the ion pore domain is an ion pore domain of an ionotropic nicotinic acetylcholine receptor, an ionotropic serotonin receptor, an ionotropic glycine receptor, an ionotropic GABA receptor, a serotonin 3 receptor (5HT3) ion pore domain, a glycine receptor (GlyR) ion pore domain, a gamma-aminobutyric acid (GABA) receptor ion pore domain, or an $\alpha 7$ nicotinic acetylcholine receptor.

2. The nucleic acid of claim 1, wherein the regulatory element is a promoter, a transcription response element, a repressor, and/or an enhancer.

3. The nucleic acid of claim 1, wherein the modified ligand binding domain is a modified $\alpha 7$ nicotinic acetylcholine ligand binding domain.

4. The nucleic acid of claim 3, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises a sequence having at least 75 percent sequence identity to a sequence set forth in SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20.

5. The nucleic acid of claim 3, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 131, 139, 141, 175, 210, 216, 217, or 219 of SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20, such as Q79A, Q79G, L141A, L141 F, L141 P, W77F, W77Y, or W77M.

6. The nucleic acid of claim 3, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises:

- a. a L131G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution;
- b. a W77F amino acid substitution, a Q79G amino acid substitution, and a G175K amino acid substitution;
- c. a Q79G amino acid substitution, a Y115F amino acid substitution, and a G175K amino acid substitution;
- d. a Y115F amino acid substitution and a G175K amino acid substitution;
- e. a Q79G amino acid substitution and a P216I amino acid substitution; or

f. a R27D amino acid substitution and/or a E41R amino acid substitution.

7. The nucleic acid of claim 3, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain has reduced binding with endogenous acetylcholine (ACh) as compared to unmodified $\alpha 7$ -nAChR LBD.

8. The nucleic acid of claim 1, wherein the exogenous ligand is selected from the group consisting of a quinuclidine, a tropane, a 9-azabicyclo[3.3.1]nonane, a 6,7,8,9-tetrahydro-6,10-methano-6H-pyrazino(2,3-h)benzazepine, and a 1,4-diazabicyclo[3.2.2]nonane.

9. The nucleic acid of claim 1, comprising a sequence of a packageable viral genome comprising the gene for expressing a modified ligand-gated ion channel.

10. The nucleic acid of claim 9, comprising Adeno-associated virus ITR sequences flanking the gene for expressing a modified ligand-gated ion channel, producing a sequence of a packageable recombinant AAV genome or a self-complementary AAV genome comprising the gene for expressing a modified ligand-gated ion channel.

11. A method of preparing a patient for a treatment for relieving chronic pain, comprising:

delivering to the patient a nucleic acid comprising an open reading frame encoding a modified ligand-gated ion channel under transcriptional control of a regulatory element governing cell-specific expression in dorsal horn neurons, wherein the modified ligand-gated ion channel comprises a modified ligand binding domain activatable by an exogenous ligand, and an ion pore domain,

wherein the modified ligand-gated ion channel is a modified $\alpha 7$ nicotinic acetylcholine ligand binding domain, and

wherein the ion pore domain is an ion pore domain of an ionotropic nicotinic acetylcholine receptor, an ionotropic serotonin receptor, an ionotropic glycine receptor, an ionotropic GABA receptor, a serotonin 3 receptor (5HT3) ion pore domain, a glycine receptor (GlyR) ion pore domain, a gamma-aminobutyric acid (GABA) receptor ion pore domain, or an $\alpha 7$ nicotinic acetylcholine receptor.

12. The method of claim 11, wherein the nucleic acid is delivered to the dorsal horn of the spinal cord of the patient.

13. The method of claim 11, wherein the regulatory element is a promoter, a transcription response element, a repressor, and/or an enhancer.

14. The method of claim 11, wherein the modified ligand binding domain is a modified $\alpha 7$ nicotinic acetylcholine ligand binding domain.

15. The method of claim 14, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises a

sequence having at least 75 percent sequence identity to a sequence set forth in SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20.

16. The method of claim **14**, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises an amino acid substitution at one or more of amino acid residues 77, 79, 115, 131, 139, 141, 175, 210, 216, 217, or 219 of SEQ ID NO: 18, SEQ ID NO: 19, or SEQ ID NO: 20, such as Q79A, Q79G, L141A, L141 F, L141 P, W77F, W77Y, or W77M.

17. The method of claim **14**, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain comprises:

- a. a L131G amino acid substitution, a Q139L amino acid substitution, and a Y217F amino acid substitution;
- b. a W77F amino acid substitution, a Q79G amino acid substitution, and a G175K amino acid substitution;

- c. a Q79G amino acid substitution, a Y115F amino acid substitution, and a G175K amino acid substitution;
- d. a Y115F amino acid substitution and a G175K amino acid substitution;
- e. a Q79G amino acid substitution and a P216I amino acid substitution; or
- f. a R27D amino acid substitution and/or a E41R amino acid substitution.

18. The method of claim **14**, wherein the modified $\alpha 7$ nicotinic acetylcholine ligand binding domain has reduced binding with endogenous acetylcholine (ACh) as compared to unmodified $\alpha 7$ -nAChR LBD.

19. The method of claim **11**, further comprising administering the exogenous ligand to the patient in an amount effective to activate the modified ligand gated ion channel, thereby treating the chronic pain in the patient.

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