



(12) **DEMANDE DE BREVET CANADIEN**
CANADIAN PATENT APPLICATION
(13) **A1**

(86) Date de dépôt PCT/PCT Filing Date: 2018/03/21
(87) Date publication PCT/PCT Publication Date: 2018/09/27
(85) Entrée phase nationale/National Entry: 2019/08/23
(86) N° demande PCT/PCT Application No.: US 2018/023631
(87) N° publication PCT/PCT Publication No.: 2018/175636
(30) Priorité/Priority: 2017/03/22 (US62/475,024)

(51) Cl.Int./Int.Cl. *C12N 15/11* (2006.01)
(71) Demandeurs/Applicants:
NOVARTIS AG, CH;
INTELLIA THERAPEUTICS, INC., US
(72) Inventeurs/Inventors:
BROGDON, JENNIFER, US;
CHEN, MING-WEI, US;
LIM, HYUNGWOOK, US;
YANG, YI, US;
STEWART, MORAG, US;
HESSE, SARAH, US
(74) Agent: FETHERSTONHAUGH & CO.

(54) Titre : COMPOSITIONS ET PROCEDES D'IMMUNO-ONCOLOGIE
(54) Title: COMPOSITIONS AND METHODS FOR IMMUNOONCOLOGY

(57) **Abrégé/Abstract:**

The present disclosure is directed to genome editing systems, reagents and methods for immunooncology.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau

(43) International Publication Date
27 September 2018 (27.09.2018)



(10) International Publication Number
WO 2018/175636 A3

(51) International Patent Classification:
C12N 15/11 (2006.01)

(21) International Application Number:
PCT/US2018/023631

(22) International Filing Date:
21 March 2018 (21.03.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/475,024 22 March 2017 (22.03.2017) US

(71) Applicants: **NOVARTIS AG** [CH/CH]; Lichtstrasse 35, 4056 Basel (CH). **INTELLIA THERAPEUTICS, INC.** [US/US]; 40 Erie Street, Suite 130, Cambridge, MA 02139 (US).

(72) Inventors: **BROGDON, Jennifer**; 250 Massachusetts Avenue, Cambridge, MA 02139 (US). **CHEN, Ming-Wei**; 250 Massachusetts Avenue, Cambridge, MA 02139 (US). **LIM, Hyungwook**; 250 Massachusetts Avenue, Cambridge, MA 02139 (US). **YANG, Yi**; 250 Massachusetts Avenue, Cambridge, MA 02139 (US). **STEWART, Morag**; 40 Erie Street, Suite 130, Cambridge, MA 02139 (US). **HESSE, Sarah**; 40 Erie Street, Suite 130, Cambridge, MA 02139 (US).

(74) Agent: **MCDONELL, Leslie, A.** et al.; Finnegan, Henderson, Farabow, Garrett & Dunner, LLP, 901 New York Avenue, NW, Washington, DC 20001 (US).

(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

(88) Date of publication of the international search report:

22 November 2018 (22.11.2018)

(54) Title: COMPOSITIONS AND METHODS FOR IMMUNOONCOLOGY

(57) Abstract: The present disclosure is directed to genome editing systems, reagents and methods for immunooncology.

WO 2018/175636 A3

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 3
CONTENANT LES PAGES 1 À 215

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 3
CONTAINING PAGES 1 TO 215

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

COMPOSITIONS AND METHODS FOR IMMUNOONCOLOGY**RELATED APPLICATIONS**

[001] This application claims priority to U.S. Provisional patent application number 62/475024, filed March 22, 2017. The entire content of this application is incorporated herein by reference.

SEQUENCE LISTING

[002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on March 15, 2018, is named PAT057662-WO-PCT_SL.txt and is 3,460,141 bytes in size.

BACKGROUND

[003] CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats) evolved in bacteria as an adaptive immune system to defend against viral attack. Upon exposure to a virus, short segments of viral DNA are integrated into the CRISPR locus of the bacterial genome. RNA is transcribed from a portion of the CRISPR locus that includes the viral sequence. That RNA, which comprises a sequence complementary to the viral genome, mediates targeting of a Cas9 protein to the sequence in the viral genome. The Cas9 protein cleaves and thereby silences the viral target.

[004] Recently, the CRISPR/Cas system has been adapted for genome editing in eukaryotic cells. The introduction of site-specific single-strand breaks (SSBs) or double-strand breaks (DSBs) allows for target sequence alteration through, for example, non-homologous end-joining (NHEJ) or homology-directed repair (HDR).

SUMMARY

[005] In an aspect, the disclosure provides a gRNA molecule including a tracr and crRNA, wherein the crRNA includes a targeting domain that is complementary with a target sequence of a TET2 intron or TET2 intron-exon junction.

[006] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from: a) chr4:105146980-105190359; b) chr4:105190506-105233896; c) chr4:105237352-105241338; d) chr4:105241430-105242833; e) chr4:105242928-105243569; f) chr4:105243779-105259618; g) chr4:105259770-105261758; h) chr4:105261849-105269609; i)

chr4:105269748-105272563; and j) chr4:105272919-105275047, wherein said genomic region is according to human reference genome hg38, for example, wherein the genomic region is chr4:105269748-105272563 (the intron between exon 9 and exon 10 of TET2).

[007] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; chr4:105272465-105272485; chr4:105271387-105271407; chr4:105272436-105272456; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; chr4:105271845-105271865; chr4:105271849-105271869; and chr4:105271056-105271076.

[008] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271387-105271407; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; and chr4:105271056-105271076.

[009] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485. In some embodiments, the gRNA molecule is capable of generating the editing repair pattern described in Table 22 and/or >75% indel frequencies as described in Table 23.

[0010] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from

chr4:105271340-105271360; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485. In some embodiments, the gRNA molecule is capable of generating the editing repair pattern described in Table 22 and/or >80% indel frequencies as described in Table 23.

[0011] In an aspect, the disclosure provides a gRNA molecule, wherein the targeting domain is complementary to a sequence within a genomic region selected from chr4:105270624-105270643, chr4:105270630-105270649, and chr4:105271863-105271883. In an aspect, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain includes, e.g., consists of, any one of SEQ ID NO: 1000 to SEQ ID NO: 10514, e.g., of Table 1 or Table 2, e.g., includes, e.g., consists of, any one of SEQ ID NO: 10102 to SEQ ID NO: 10324.

[0012] In an aspect of the gRNA molecule, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that includes, e.g., consists of, a targeting domain sequence listed in Table 2, for example, includes, e.g., consists of, any one of SEQ ID NO: 10148, SEQ ID NO: 10184, SEQ ID NO: 10185, SEQ ID NO: 10188, SEQ ID NO: 10209, SEQ ID NO: 10212, SEQ ID NO: 10317, SEQ ID NO: 10318, SEQ ID NO: 10187, SEQ ID NO: 10224, SEQ ID NO: 10292, SEQ ID NO: 10149, SEQ ID NO: 10177, SEQ ID NO: 10151, SEQ ID NO: 10225 or SEQ ID NO: 10509.

[0013] In an aspect of the gRNA, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that comprises or consists of SEQ ID NO: 10148, 10149, 10206, 10191, 10515, 10203, 10259, 10136, 10314, 10234, 10290, 10233, 10209, 10224, 10212, 10317, 10318, 10225, 10184, 10185, 10188, 10187, 10292, 10151, 10509, 10281, 10299, 10301, or 10177; or a fragment thereof.

[0014] In an aspect of the gRNA, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that comprises or consists of SEQ ID NO: 10148, 10149, 10290, 10209, 10224, 10212, 10317, 10318, 10225, 10184, 10185, 10188, 10187, 10292, 10151, 10509, 10281, or 10177; or a fragment thereof.

[0015] In an aspect of the gRNA, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that comprises or consists of SEQ ID NO: 10206, 10191, 10515, 10203, 10259, 10136, 10314, or 10234; or a fragment thereof.

[0016] In an aspect of the gRNA, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that comprises or consists of SEQ ID

NO: 10191, 10203, 10259, 10136, 10314, or 10234; or a fragment thereof. In some embodiments, the gRNA molecule is capable of generating the editing repair pattern described in Table 22 and/or >75% indel frequencies as described in Table 23.

[0017] In an aspect of the gRNA, including in any of the previous aspects, a gRNA molecule of the disclosure includes a targeting domain that comprises or consists of SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206; or a fragment thereof. In some embodiments, the gRNA molecule is capable of generating the editing repair pattern described in Table 22 and/or >80% indel frequencies as described in Table 23.

[0018] In some embodiments, the gRNA molecules are capable of generating the editing repair pattern described in Table 22 and/or the indel frequencies described in Table 23. In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain includes 17, 18, 19 or, 20 consecutive nucleic acids of any one of the recited targeting domain sequences. In an aspect, including in any of the previous aspects, the targeting domain consists of 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences. In an aspect, the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences are the 17, 18, 19, or 20 consecutive nucleic acids disposed at the 3' end of the recited targeting domain sequence. In another aspect, the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences are the 17, 18, 19, or 20 consecutive nucleic acids disposed at the 5' end of the recited targeting domain sequence. In another aspect, the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences do not include either the 5' or 3' nucleic acid of the recited targeting domain sequence.

[0019] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain consists of the recited targeting domain sequence.

[0020] In an aspect of the gRNA molecule, including in any of the previous aspects, a portion of the crRNA and a portion of the tracr hybridize to form a flagpole including SEQ ID NO: 50 or SEQ ID NO: 51. In an aspect of the gRNA molecule, including in any of the previous aspects, the flagpole further includes a first flagpole extension, located 3' to the crRNA portion of the flagpole, wherein said first flagpole extension includes SEQ ID NO: 55. In an aspect of the gRNA molecule, including in any of the previous aspects, the flagpole further includes a second flagpole extension located 3' to the crRNA portion of the flagpole

and, if present, the first flagpole extension, wherein said second flagpole extension includes SEQ ID NO: 57.

[0021] In an aspect of the gRNA molecule, including in any of the previous aspects, the tracr includes: (a) SEQ ID NO: 87, optionally further including, at the 3' end, an additional 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides; (b) SEQ ID NO: 65; or (c) SEQ ID NO: 84.

[0022] In an aspect of the gRNA molecule, including in any of the previous aspects, the crRNA portion of the flagpole includes SEQ ID NO: 79 or SEQ ID NO: 80.

[0023] In an aspect of the gRNA molecule, including in any of the previous aspects, the tracr includes SEQ ID NO: 53 or SEQ ID NO: 54, and optionally, if a first flagpole extension is present, a first tracr extension, disposed 5' to SEQ ID NO: 53 or SEQ ID NO: 54, said first tracr extension including SEQ ID NO: 56.

[0024] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain and the tracr are disposed on separate nucleic acid molecules.

[0025] In an aspect of the gRNA molecule, including in any of the previous aspects, the crRNA includes, from 5' to 3', [targeting domain]-: a) SEQ ID NO: 50; b) SEQ ID NO: 51; c) SEQ ID NO: 77; d) SEQ ID NO: 78; e) SEQ ID NO: 79; f) SEQ ID NO: 80; or g) SEQ ID NO: 81.

[0026] In an aspect of the gRNA molecule, including in any of the previous aspects, the tracr includes, from 5' to 3': a) SEQ ID NO: 53; b) SEQ ID NO: 54; c) SEQ ID NO: 82; d) SEQ ID NO: 83; e) SEQ ID NO: 65; f) SEQ ID NO: 84; g) SEQ ID NO: 87; h) SEQ ID NO: 76; i) SEQ ID NO: 85; j) SEQ ID NO: 86; k) any of a) to j), above, further including, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides; l) any of a) to k), above, further including, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides; or m) any of a) to l), above, further including, at the 5' end (e.g., at the 5' terminus), at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides.

[0027] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain and the tracr are disposed on separate nucleic acid molecules, and wherein the nucleic acid molecule including the targeting domain includes SEQ ID NO: 79, optionally disposed immediately 3' to the targeting domain, and the nucleic acid molecule including the tracr includes, e.g., consists of, SEQ ID NO: 65.

[0028] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein the tracr is disposed 3' to the targeting domain. In an aspect of the gRNA molecule, including in any of the previous aspects involving a sgRNA, the gRNA molecule further includes a loop, disposed 3' to the targeting domain and 5' to the tracr, for example a loop that includes SEQ ID NO: 52.

[0029] In an aspect of the gRNA molecule, including in any of the previous aspects, the gRNA molecule includes, from 5' to 3', [targeting domain]-: (a) SEQ ID NO: 71; (b) SEQ ID NO: 72; (c) SEQ ID NO: 73; (d) SEQ ID NO: 74; (e) SEQ ID NO: 75; or (f) any of (a) to (e), above, further including, at the 3' end, 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides.

[0030] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein said nucleic acid molecule includes, e.g., consists of, said targeting domain and SEQ ID NO: 71, optionally disposed immediately 3' to said targeting domain.

[0031] In an aspect of the gRNA molecule, including in any of the previous aspects, the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein said nucleic acid molecule includes, e.g., consists of, said targeting domain and SEQ ID NO: 75, optionally disposed immediately 3' to said targeting domain.

[0032] In an aspect of the gRNA molecule, including in any of the previous aspects, one, or optionally more than one, of the nucleic acid molecules including the gRNA molecule includes: a) a, e.g., three, phosphorothioate modification(s) at the 3' end of said nucleic acid molecule or molecules; b) a, e.g., three, phosphorothioate modification(s) at the 5' end of said nucleic acid molecule or molecules; c) a, e.g., three, 2'-O-methyl modification(s) at the 3' end of said nucleic acid molecule or molecules; d) a, e.g., three, 2'-O-methyl modification(s) at the 5' end of said nucleic acid molecule or molecules; e) a 2' O-methyl modification at each of the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues of said nucleic acid molecule or molecules; or f) any combination thereof.

[0033] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a cell, an indel is formed at or near the target sequence complementary to the targeting domain of the gRNA molecule, for example, an indel that includes a deletion of

greater than 10 nucleotides, e.g., 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides.

[0034] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a population of cells, an indel is formed at or near the target sequence complementary to the targeting domain of the gRNA molecule in at least about 40%, e.g., at least about 50%, e.g., at least about 60%, e.g., at least about 70%, e.g., at least about 80%, e.g., at least about 90%, e.g., at least about 95%, e.g., at least about 96%, e.g., at least about 97%, e.g., at least about 98%, e.g., at least about 99%, of the cells of the population, for example, as measured by next generation sequencing (NGS). In an aspect of the gRNA molecule, including in any of the previous aspects, the indel that includes a deletion of greater than 10 nucleotides, e.g., 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides is detected in at least about 5%, e.g., at least about 10%, 15%, 20%, 25%, 30% or more of the cells of the population, for example, as measured by next generation sequencing (NGS).

[0035] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a cell, expression of TET2, e.g., at least one isoform of TET2, is reduced or eliminated in said cell.

[0036] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a cell, a function, e.g., a catalytic function, of TET2 is reduced or eliminated in said cell.

[0037] In an aspect of the gRNA molecule, including in any of the previous aspects, the function, e.g., the catalytic function, of TET2 is reduced, e.g., by at least about 10%, 20%, 30%, 40% or 50%, but said function, e.g., said catalytic function, is not reduced by more than about 80%, e.g., is not eliminated, in said cell.

[0038] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a cell, TET2 expression, e.g., expression of at least one TET2 isoform, and/or at least one TET2 function is not altered relative to the level of expression and/or function in

the same type of cell but to which said CRISPR system is not introduced (e.g., an unaltered cell of the same type).

[0039] In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a cell, no off-target indels are formed in said cell, e.g., as detectable by next generation sequencing and/or a nucleotide insertional assay. In an aspect of the gRNA molecule, including in any of the previous aspects, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule is introduced into a population of cells, an off-target indel is detected in no more than about 5%, e.g., no more than about 1%, e.g., no more than about 0.1%, e.g., no more than about 0.01%, of the cells of the population of cells e.g., as detectable by next generation sequencing and/or a nucleotide insertional assay.

[0040] In some embodiments, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule (e.g., described herein) is introduced into a cell, e.g., a T cell, a non-naturally occurring indel at or near the target sequence of a gRNA described herein is formed, e.g., an indel comprising a non-naturally occurring indel as described in Table 22 is formed. In some embodiments, when a CRISPR system (e.g., an RNP as described herein) including the gRNA molecule (e.g., described herein) is introduced into a population of cells, e.g., a population of T cells, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the cells of the population comprise one or more non-naturally occurring indels at or near the target sequence of a gRNA described herein, e.g., comprise one or more non-naturally occurring indels selected from the indels described in Table 22 (e.g., the indels described in Table 2 associated with a gRNA targeting domain sequence).

[0041] In some embodiments, when a CRISPR system (e.g., an RNP as described herein) including a gRNA molecule (e.g., described herein) and a template nucleic acid molecule (e.g., as described herein) is introduced into a cell, e.g., a T cell, a cell comprising heterologous sequence inserted at or near the target sequence of a gRNA is formed. In some embodiments, the heterologous sequence comprises sequence encoding a CAR, e.g., as described herein. In some embodiments, the heterologous sequence comprises sequence encoding a CAR, e.g., as described herein, operably linked to sequence encoding a promoter, e.g., an EF1-alpha promoter, e.g., as described herein. In an aspect the disclosure provides a composition including a first gRNA molecule of any of the preceding gRNA aspects and embodiments. In an aspect, the composition further includes a Cas9 molecule, for example, a Cas9 molecule that includes,

e.g., consists of, any one of SEQ ID NO: 90 or SEQ ID NO: 111 to SEQ ID NO: 121 or SEQ ID NO: 123, or for example, an active or inactive *S. pyogenes* Cas9.

[0042] In an aspect of the composition, including in any of the previous composition aspects, the first gRNA molecule and Cas9 molecule are present in a ribonuclear protein complex (RNP).

[0043] In an aspect of the composition, including in any of the previous composition aspects, the composition further includes a template nucleic acid, for example, a template nucleic acid that is double-stranded or single stranded, or for example, wherein the template nucleic acid is or is included in a vector, for example, a lentivirus vector, and AAV vector, an adenovirus vector, a plasmid, a minicircle or a nanoplasmid. In an aspect of the composition, including in any of the previous composition aspects, the template nucleic acid includes at least one (e.g., at least a 5' or at least a 3') homology arm, and wherein said homology arm includes sequence homologous to sequence of a TET2 intron. In an aspect of the composition, including in any of the previous composition aspects, the template nucleic acid includes both a 5' and a 3' homology arm, and wherein at least one of the homology arms includes sequence homologous to sequence of a TET2 intron. In an aspect of the composition, including in any of the previous composition aspects, the composition the template nucleic acid includes nucleic acid encoding a chimeric antigen receptor (CAR), for example, a CAR as described herein. In aspects, the CAR is: (a) a CD19 CAR, e.g., as described in herein; or (b) a BCMA CAR, e.g., as described herein. In aspects, the CAR is a CD19 CAR including an antigen binding domain including any one of SEQ ID NO: 160 to SEQ ID NO: 172 or SEQ ID NO: 175. In aspects, the CAR is a CD19 CAR and includes any one of SEQ ID NO: 185 to SEQ ID NO: 197. In other aspects, the CAR is a BCMA CAR including an antigen binding domain including any one of SEQ ID NO: 239 to SEQ ID NO: 412. In aspects, the CAR is a BCMA CAR and includes any one of SEQ ID NO: 849 to SEQ ID NO: 863 or SEQ ID NO: 879 to SEQ ID NO: 899, e.g., includes SEQ ID NO: 859. In an aspect of the composition, including in any of the previous composition aspects, the composition includes a template nucleic acid that includes a promotor, e.g., an EF1-alpha promotor, operably linked to the nucleic acid sequence encoding the CAR.

[0044] In an aspect of the composition, including in any of the previous composition aspects, the composition further includes at least one additional gRNA molecule (e.g., a second gRNA molecule; a second gRNA molecule and a third gRNA molecule; or a second gRNA molecule, a third gRNA molecule, and a fourth gRNA molecule), and wherein each gRNA

molecule of the composition is complementary to a different target sequence. In an aspect, the at least one additional gRNA molecule, e.g., a second gRNA molecule, the third gRNA molecule (if present), and the fourth gRNA molecule (if present), are complementary to target sequences within the same TET2 intron. In another aspect, the first gRNA molecule, the second gRNA molecule, the third gRNA molecule (if present), and the fourth gRNA molecule (if present) are complementary to target sequence within different genes, for example, the first gRNA molecule is a gRNA molecule of any of the previous gRNA aspects and embodiments (e.g., as described herein), and the second gRNA molecule includes a targeting domain complementary to a target sequence of an inhibitory molecule (e.g., PDCD1), a component of the T cell receptor (e.g., TRAC or TRBC), B2M, or CIITA.

[0045] In an aspect of the composition, including in any of the previous composition aspects, the composition is formulated in a medium suitable for electroporation, for example, wherein each of said gRNA molecules is in a RNP complex with a Cas9 molecule described herein, and wherein each of said RNP complexes is at a concentration of less than about 10uM, e.g., less than about 3uM, e.g., less than about 1uM, e.g., less than about 0.5uM, e.g., less than about 0.3uM, e.g., less than about 0.1uM.

[0046] In an aspect, the disclosure provides a nucleic acid sequence that encodes a gRNA molecule of any of the preceding gRNA aspects and embodiments or a, e.g., all, components of a composition of any of the preceding composition aspects and embodiments.

[0047] In an aspect, the disclosure provides a vector including a nucleic acid of any of the preceding nucleic acid aspects and embodiments, for example, wherein in the vector is selected from the group consisting of a lentiviral vector, an adenoviral vector, an adeno-associated viral (AAV) vector, a herpes simplex virus (HSV) vector, a plasmid, a minicircle, a nanoplasmid, and an RNA vector.

[0048] In an aspect, the disclosure provides a method of altering e.g., altering the structure, e.g., sequence of, a target sequence of a cell, including contacting said cell with: a) a gRNA molecule, e.g., more than one gRNA molecule, of any of the preceding gRNA aspects and embodiments and a Cas9 molecule; b) a gRNA molecule, e.g., more than one gRNA molecule, of any of the preceding gRNA aspects and embodiments and nucleic acid encoding a Cas9 molecule; c) nucleic acid encoding a gRNA molecule, e.g., more than one gRNA molecule, of any of the preceding gRNA aspects and embodiments and a Cas9 molecule; d) nucleic acid encoding a gRNA molecule, e.g., more than one gRNA molecule, of any of the preceding

gRNA aspects and embodiments and nucleic acid encoding a Cas9 molecule; e) any of a) to d), above, and a template nucleic acid, e.g., a template nucleic acid as described in any of the preceding aspects and embodiments, e.g., as described herein; g) the composition of any of the preceding composition aspects and embodiments; or h) the vector of any of the preceding vector aspects and embodiments.

[0049] In an aspect of the method, including in any of the previous method aspects, the gRNA molecule of any of the preceding gRNA aspects and embodiments (or nucleic acid encoding the gRNA molecule of any of the preceding gRNA aspects and embodiments), and the Cas9 molecule or nucleic acid encoding the Cas9 molecule, are formulated in a single composition.

[0050] In an aspect of the method, including in any of the previous method aspects, when the composition includes a template nucleic acid, e.g., a template nucleic acid as described in any of the preceding aspects and embodiments (e.g., as described herein), the template nucleic acid is formulated in a separate composition from the gRNA molecule of any of the preceding gRNA aspects and embodiments (or nucleic acid encoding the gRNA molecule of any of the preceding gRNA aspects and embodiments) and the Cas9 molecule or nucleic acid encoding the Cas9 molecule. In an aspect the more than one compositions are delivered (to a cell) sequentially.

[0051] In an aspect of the method, including in any of the previous method aspects, the method results in insertion of at least a portion of the template nucleic acid at or near the target sequence of the gRNA molecule of any of the preceding gRNA aspects and embodiments. In an aspect, insertion occurs at only at one allele.

[0052] In an aspect, the disclosure provides a method of engineering a cell to express a chimeric antigen receptor (CAR), including: (a) introducing into said cell a CRISPR system including a gRNA molecule of any of the preceding gRNA aspects and embodiments or a composition of any of the preceding composition aspects and embodiments; and (b) introducing into said cell a template nucleic acid including nucleic acid sequence encoding a CAR; wherein said nucleic acid sequence encoding a CAR is integrated into the genome, e.g., optionally at only a single allele of the genome, at or near the target sequence of said gRNA molecule. In an aspect, the method further includes introducing into said cell one or more CRISPR systems including one or more gRNA molecules complementary to a target sequence of an inhibitory molecule, a component of the T cell receptor, B2M and/or CIITA.

[0053] In an aspect of the method, including in any of the previous method aspects, the cell is an animal cell, for example, a mammalian, primate, or human cell, for example, an immune effector cell (e.g., a population of immune effector cells), for example, a T cell or NK cell, e.g., a T cell, e.g., a CD4⁺ T cell, a CD8⁺ T cell, or a combination thereof.

[0054] In an aspect of the method, including in any of the previous method aspects, the CAR is a CAR described herein, for example: (a) a CD19 CAR, e.g., as described in herein; or (b) a BCMA CAR, e.g., as described herein. In aspects, the CAR is: (a) a CD19 CAR, e.g., as described in herein; or (b) a BCMA CAR, e.g., as described herein. In aspects, the CAR is a CD19 CAR including an antigen binding domain including any one of SEQ ID NO: 160 to SEQ ID NO: 172 or SEQ ID NO: 175. In aspects, the CAR is a CD19 CAR and includes any one of SEQ ID NO: 185 to SEQ ID NO: 197. In other aspects, the CAR is a BCMA CAR including an antigen binding domain including any one of SEQ ID NO: 239 to SEQ ID NO: 412. In aspects, the CAR is a BCMA CAR and includes any one of SEQ ID NO: 849 to SEQ ID NO: 863 or SEQ ID NO: 879 to SEQ ID NO: 899, e.g., includes SEQ ID NO: 859.

[0055] In an aspect of the method, including in any of the previous method aspects, the cell is autologous or allogeneic with respect to a patient to be administered said cell.

[0056] In an aspect, the disclosure provides a cell as described herein, for example, a cell altered by the method of any of the herein method aspects and embodiments (e.g., by a method described herein). In aspects, the cell includes a first gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), or a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid, e.g., as described herein, or a vector of any of the preceding vector aspects and embodiments. In aspects, the cell is an animal cell, e.g., a mammalian, primate, or human cell. In aspects, the cell is an immune effector cell (e.g., a population of immune effector cells), e.g., a T cell or NK cell, e.g., a T cell, e.g., a CD4⁺ T cell, a CD8⁺ T cell, or a combination thereof.

[0057] In an aspect of the cell, including in any of the previous cell aspects, the cell has reduced or eliminated expression of an inhibitory molecule, a component of the T cell receptor (e.g., TRAC, TRBC1, TRBC2, CD3E, CD3D, or CD3G), B2M, CIITA, or combinations thereof, e.g., relative to an unmodified cell of the same type.

[0058] In an aspect of the cell, including in any of the previous cell aspects, the cell includes nucleic acid sequence encoding a chimeric antigen receptor (CAR) (e.g., a CAR as

described herein) integrated into the genome at a TET2 intron or intron-exon junction, e.g., integrated at only a single allele.

[0059] In an aspect of the cell, including in any of the previous cell aspects, the cell includes reduced or eliminated TET2 expression, e.g., expression of at least one TET2 isoform, and/or reduced or eliminated function of TET2, e.g., at least one function of TET2, e.g., catalytic function of TET2, relative to the level of expression and/or function of an unaltered cell of the same cell type.

[0060] In an aspect of the cell, including in any of the previous cell aspects, the cell is a T cell and exhibits: (a) enhanced proliferative capacity; (b) enhanced cytotoxicity; (c) a less-exhausted phenotype (e.g., reduced expression of an inhibitory molecule, e.g., PD1, TIM3, LAG3, PD-L1, or combinations thereof); or (d) a Tscm phenotype (e.g., is CD45RA+CD62L+CD27+CD95+), relative to an unaltered cell of similar type.

[0061] In an aspect of the cell, including in any of the previous cell aspects, the cell is autologous with respect to a patient to be administered said cell. In other aspects of the cell, including in any of the previous cell aspects, the cell is allogeneic with respect to a patient to be administered said cell.

[0062] In an aspect, the disclosure provides a modified cell, which has reduced or eliminated expression and/or function of TET2, and includes heterologous nucleic acid sequence (e.g., nucleic acid sequence encoding a chimeric antigen receptor, e.g., as described herein) integrated at a site within a TET2 intron, wherein said site within a TET2 intron is selected from: a) chr4:105146980-105190359; b) chr4:105190506-105233896; c) chr4:105237352-105241338; d) chr4:105241430-105242833; e) chr4:105242928-105243569; f) chr4:105243779-105259618; g) chr4:105259770-105261758; h) chr4:105261849-105269609; i) chr4:105269748-105272563; and j) chr4:105272919-105275047, wherein the coordinates above are according to hg38.

[0063] In an aspect of the cell, including in any of the previous cell aspects, the cell has reduced or eliminated expression and/or function of a component of the T cell receptor, B2M, CIITA or a combination thereof, relative to an unmodified cell of the same type.

[0064] In some embodiments, including in any of the previous cell aspects and embodiments, the cell, e.g., the T cell, comprises a non-naturally occurring indel at or near the target sequence of a gRNA described herein, e.g., comprises an indel comprising a non-naturally occurring indel as described in Table 22. In some embodiments, including in any of

the previous cell aspects and embodiments, the disclosure provides a population of cells, e.g., a population of T cells, wherein at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the cells of the population comprise one or more non-naturally occurring indels at or near the target sequence of a gRNA described herein, e.g., comprise one or more non-naturally occurring indels selected from the indels described in Table 22 (e.g., the indels described in Table 2 associated with a gRNA targeting domain sequence).

[0065] In some embodiments, the disclosure provides a cell comprising heterologous sequence inserted at or near the target sequence of a gRNA, e.g., a gRNA described herein. In some embodiments, the heterologous sequence comprises sequence encoding a CAR, e.g., as described herein. In some embodiments, the heterologous sequence comprises sequence encoding a CAR, e.g., as described herein, operably linked to sequence encoding a promoter, e.g., an EF1-alpha promoter, e.g., as described herein. In preferred embodiments, the CAR is expressed in said cell.

[0066] In an aspect, the disclosure provides a method of providing an anti-tumor immunity in a subject, the method including administering to the subject an effective amount of a cell of any of the preceding cell aspects and embodiments (e.g., as described herein).

[0067] In an aspect, the disclosure provides a method of treating a subject having a disease associated with expression of a tumor antigen, e.g., a proliferative disease, a precancerous condition, a cancer, and a non-cancer related indication associated with expression of the tumor antigen, the method including administering to the subject an effective amount of a cell of any of the preceding cell aspects and embodiments (e.g., as described herein), for example, wherein the disease associated with expression of a tumor antigen is cancer or a non-cancer related indication, for example, wherein the disease is cancer, for example, a cancer selected from colon cancer, rectal cancer, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, melanoma, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, Hodgkin's Disease, non-Hodgkin's lymphoma, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the bladder, cancer of the

kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers, chronic lymphocytic leukemia (CLL), acute leukemias, acute lymphoid leukemia (ALL), B-cell acute lymphoid leukemia (B-ALL), T-cell acute lymphoid leukemia (T-ALL), chronic myelogenous leukemia (CML), acute myeloid leukemia (AML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and pre-leukemia, combinations of said cancers, and metastatic lesions of said cancers.

[0068] In an aspect of the method, including in any of the previous method aspects, the method further includes administering a chemotherapeutic agent, for example, cyclophosphamide, fludarabine, or cyclophosphamide and fludarabine.

[0069] In an aspect of the method, including in any of the previous method aspects, the method includes administering a lympho-depleting agent or immunosuppressant prior to administering to the subject an effective amount of the cell of any of the preceding cell aspects and embodiments (e.g., as described herein).

[0070] In an aspect, the disclosure provides a population of cells including the cell of any of the previous cell aspects and embodiments (e.g., as described herein), wherein at least about 30% of the cells, e.g., at least about 40%, 50%, 60%, 70%, 80% or 90% of the cells, are a cell of any of the preceding cell aspects and embodiments (e.g., as described herein).

[0071] In an aspect, the disclosure provides a gene editing system which binds a sequence of a TET2 intron or intron-exon junction, for example, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: a) chr4:105146980-105190359; b) chr4:105190506-105233896; c) chr4:105237352-105241338; d) chr4:105241430-105242833; e) chr4:105242928-105243569; f) chr4:105243779-105259618; g) chr4:105259770-105261758; h) chr4:105261849-105269609; i) chr4:105269748-105272563; and j) chr4:105272919-105275047, wherein said genomic region is according to hg38, for example, wherein the genomic region is chr4:105269748-105272563.

In an aspect, the gene editing system is a zinc finger nuclease (ZFN) gene editing system, a TALEN gene editing system, a CRISPR gene editing system, or a meganuclease gene editing system. In an aspect, the gene editing system further includes a template nucleic acid (e.g., as described herein), for example, a template nucleic acid including nucleic acid sequence encoding a CAR (e.g., as described herein). In an aspect of the gene editing system, including in any of the previous gene editing system aspects, when said gene editing system (and/or nucleic acid sequence encoding one or more components of the gene editing system) is introduced into a cell, the nucleic acid sequence encoding the CAR is integrated into the genome of said cell at or near the sequence of a TET2 intron or intron-exon junction bound by said genome editing system.

[0072] In an aspect, the disclosure provides a cell, modified by the gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein).

[0073] In an aspect, the disclosure provides a cell including the gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein).

[0074] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use as a medicament.

[0075] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use in the manufacture of a medicament.

[0076] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the

preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use in the treatment of a disease.

[0077] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use in the treatment of a disease, wherein the disease is a disease associated with expression of a tumor antigen, e.g., a proliferative disease, a precancerous condition, a cancer, and a non-cancer related indication associated with expression of the tumor antigen.

[0078] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use in the treatment of a cancer, wherein the cancer is a hematologic cancer selected from the group consisting of chronic lymphocytic leukemia (CLL), acute leukemias, acute lymphoid leukemia (ALL), B-cell acute lymphoid leukemia (B-ALL), T-cell acute lymphoid leukemia (T-ALL), chronic myelogenous leukemia (CML), acute myeloid leukemia (AML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin's

lymphoma, Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and pre-leukemia.

[0079] In an aspect, the disclosure provides a gRNA molecule of any of the preceding gRNA aspects and embodiments (e.g., as described herein), a composition of any of the preceding composition aspects and embodiments (e.g., as described herein), a nucleic acid of any of the preceding nucleic acid aspects and embodiments (e.g., as described herein), a vector of any of the preceding vector aspects and embodiments (e.g., as described herein), a cell (or population of cells) of any of the preceding cell aspects and embodiments (e.g., as described herein), or a gene editing system of any of the preceding gene editing system aspects and embodiments (e.g., as described herein), for use in the treatment of a cancer, e.g., wherein the cancer is selected from the group consisting of mesothelioma, adenocarcinoma, glioblastoma, colon cancer, rectal cancer, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, melanoma, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, Hodgkin's Disease, non-Hodgkin's lymphoma, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers, combinations of said cancers, and metastatic lesions of said cancers.

BRIEF DESCRIPTION OF THE DRAWINGS

[0080] Fig. 1: Editing efficiency at targeted B2M locus in CD34+ hematopoietic stem cells by different Cas9 variants, as evaluated by NGS and Flow cytometry. NLS = SV40 NLS; His6 (SEQ ID NO: 108) or His8 (SEQ ID NO: 109) refers to 6 or 8 histidine residues, respectively; TEV = tobacco etch virus cleavage site; Cas9 = wild type *S. pyogenes* Cas9 – mutations or variants are as indicated).

[0081] Fig. 2: Editing efficiency at targeted B2M locus in primary human T cells by different Cas9 variants and a range of concentrations, as measured by flow cytometry.

[0082] Fig. 3: Editing efficiency of two different Cas9 variants, at various concentrations, in primary human T cells using two different gRNAs targeting either B2M (left panel) or TRAC (right panel). Editing efficiency (% editing) was measured by flow cytometry by measuring the loss of cell surface expression of B2M (left panel) or TCR (right panel).

[0083] Fig. 4: Schematic for gRNA design targeting intron 9-10 (the intron between exon 9 and exon 10) of hTET2.

[0084] Fig. 5: Schematic for AAV targeting construct (not drawn to scale).

[0085] Fig. 6: FACS staining shows that 11.4% of CD3⁺ cells were BCMA10_CAR⁺ using g1-RNA and 13.5% using g45-RNA at day 7. The percentage of BCMA10_CAR⁺ cells increased over time.

[0086] Fig. 7: FACS staining shows CD3⁺ cells that were BCMA10_CAR⁺ using g45 and a different donor than used in Fig. 6. The percentage of BCMA10_CAR⁺ cells increased over time.

[0087] Fig. 8: The total cell fold change is shown for RNP-AAV treated, RNP treated, and debeaded only groups. The expansion of BCMA-CAR⁺ cells from day 7 to day 10 was slightly faster than the total population (4.3 vs 2.7 fold)

[0088] Fig. 9: Schematic of PCR primers designed to amplify from outside of the homology region to the BCMA10_CAR insert in order to confirm correct integration at both 5' and 3' sites (SEQ ID NOS 10557-10558, 10557-10558, 10559-10560, and 10559-10560, respectively, in order of appearance).

[0089] Fig. 10A and Fig. 10B: Exemplary guides were evaluated in CD3⁺ T cells. For each target site, two sets of primers were designed to amplify each locus. The total percent editing, the percent of insertion and the deletion at each target sequence was determined using NGS.

[0090] Fig. 11: An oligo insertion-based assay (see, e.g., Tsai et al., Nature Biotechnology. 33, 187–197; 2015) was used to determine potential off-target genomic sites cleaved by Cas9 targeting TET2. Exemplary gRNAs targeting TET2 and control guides were screened in Cas9-expressing HEK293 cells. High-efficiency editing at the expected target

sequences, potential off-targets for some of the guides, and no off-targets for three of the guides were detected.

DEFINITIONS

[0091] The terms “gene editing system” or “genome editing system” refer to a system of one or more molecules comprising at least a nuclease (or nuclease domain) and a programmable nucleotide binding domain, which necessary and sufficient to direct and effect modification (e.g., single or double-strand break) of nucleic acid at a target sequence by the nuclease (or nuclease domain). In embodiments, the gene editing system is a CRISPR system. In embodiments, the gene editing system is a zinc finger nuclease system (ZFN). In embodiments, the gene editing system is a TALEN system. In embodiments, the gene editing system is a meganuclease system. In embodiments, the gene editing system modifies a site within a TET2 intron. In embodiments, the gene editing system further comprises a template nucleic acid, e.g., a template nucleic acid comprising sequence encoding a chimeric antigen receptor, e.g., as described herein. In embodiments, one or more of the components of the gene editing system may be introduced into cells as nucleic acid encoding said component or components. Without being bound by theory, upon expression of said component or component, the gene editing system is constituted, e.g., in the cell.

[0092] The terms “CRISPR system,” “Cas system” or “CRISPR/Cas system” refer to a set of molecules comprising an RNA-guided nuclease or other effector molecule and a guide RNA molecule that together are necessary and sufficient to direct and effect modification of nucleic acid at a target sequence by the RNA-guided nuclease or other effector molecule. In one embodiment, a CRISPR system comprises a guide RNA and a Cas protein, e.g., a Cas9 protein. Such systems comprising a Cas9 or modified Cas9 molecule are referred to herein as “Cas9 systems” or “CRISPR/Cas9 systems.” In one example, the guide RNA molecule and Cas molecule may be complexed, to form a ribonuclear protein (RNP) complex.

[0093] The terms “guide RNA,” “guide RNA molecule,” “gRNA molecule” or “gRNA” are used interchangeably, and refer to a set of nucleic acid molecules that promote the specific directing of a RNA-guided nuclease or other effector molecule (typically in complex with the gRNA molecule) to a target sequence. In some embodiments, said directing is accomplished through hybridization of a portion of the gRNA to DNA (e.g., through the gRNA targeting domain), and by binding of a portion of the gRNA molecule to the RNA-guided nuclease or other effector molecule (e.g., through at least the gRNA tracr). In embodiments, a gRNA

molecule consists of a single contiguous polynucleotide molecule, referred to herein as a “single guide RNA,” “sgRNA,” or “single-molecule DNA-targeting RNA” and the like. In other embodiments, a gRNA molecule consists of a plurality, usually two, polynucleotide molecules, which are themselves capable of association, usually through hybridization, referred to herein as a “dual guide RNA,” “dgRNA,” or “double-molecule DNA-targeting RNA” and the like. gRNA molecules are described in more detail below, but generally include a targeting domain and a tracr. In embodiments the targeting domain and tracr are disposed on a single polynucleotide. In other embodiments, the targeting domain and tracr are disposed on separate polynucleotides.

[0094] The term “targeting domain” as used herein in connection with a gRNA, is the portion of the gRNA molecule that recognizes, e.g., is complementary to, a target sequence, e.g., a target sequence within the nucleic acid of a cell, e.g., within a gene.

[0095] The term “crRNA” as used herein in connection with a gRNA molecule, is a portion of the gRNA molecule that comprises a targeting domain and a region that interacts with a tracr to form a flagpole region.

[0096] The term “target sequence” refers to a sequence of nucleic acids complementary, for example fully complementary, to a gRNA targeting domain. In embodiments, the target sequence is disposed on genomic DNA. In an embodiment the target sequence is adjacent to (either on the same strand or on the complementary strand of DNA) a protospacer adjacent motif (PAM) sequence recognized by a protein having nuclease or other effector activity, e.g., a PAM sequence recognized by Cas9. The PAM sequence and length may depend on the Cas9 protein used. Non-limiting examples of PAM sequences include 5'-NGG-3', 5'-NGGNG-3', 5'-NG-3', 5'-NAAAAN-3', 5'-NNAAAAN-3', 5'-NNNNACA-3', 5'-GNNNCNNA-3', and 5'-NNNNGATT-3' where N represents any nucleotide, and W represents A or T.

[0097] In embodiments, the target sequence is a target sequence of an allogeneic T cell target. In embodiments, the target sequence is a target sequence of an inhibitory molecule. In embodiments, the target sequence is a target sequence of a downstream effector of an inhibitory molecule.

[0098] The term “flagpole” as used herein in connection with a gRNA molecule, refers to the portion of the gRNA where the crRNA and the tracr bind to, or hybridize to, one another.

[0099] The term “tracr” or “tracrRNA” as used herein in connection with a gRNA molecule refers to the portion of the gRNA that binds to a nuclease or other effector molecule.

In embodiments, the tracr comprises nucleic acid sequence that binds specifically to Cas9. In embodiments, the tracr comprises nucleic acid sequence that forms part of the flagpole.

[00100] The term “Cas” refers to an RNA-guided nuclease of the CRISPR system that together with a guide RNA molecule are necessary and sufficient to direct and effect modification of nucleic acid at a target sequence. One non-limiting example is a Cas molecule from the Type II CRISPR system, e.g., a Cas9 molecule. Another non-limiting example is a Cas molecule is from a Type V CRISPR system, e.g., a Cpf1 molecule.

[00101] The terms “Cas9” and “Cas9 molecule” refer to an enzyme from bacterial Type II CRISPR/Cas system responsible for DNA cleavage. In embodiments, Cas9 also includes wild-type protein, mutant protein, variant protein, including non-catalytic protein, and functional fragments thereof. Non-limiting examples of Cas9 sequences are known in the art and provided herein. In some embodiments, Cas9 refers to a Cas9 sequence that comprises at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% homology with; differs at no more than 1%, 2%, 5%, 10%, 15%, 20%, 30%, or 40% of the amino acid residues when compared with; differs by at least 1, 2, 5, 10 or 20 amino acids but by no more than 100, 80, 70, 60, 50, 40 or 30 amino acids from; or is identical to any Cas9 sequence, e.g., wild-type, mutant, variant, non-catalytic, or functional fragment thereof, known in the art or disclosed herein.

[00102] The terms “Cpf1” and “Cpf1 molecule” refer to an enzyme from a bacterial Type V CRISPR/Cas system responsible for DNA cleavage. In embodiments, Cpf1 also includes wild-type protein, mutant protein, variant protein, including non-catalytic protein, and functional fragments thereof. Non-limiting examples of Cpf1 sequences are known in the art. In some embodiments, Cpf1 refers to a Cpf1 sequence that comprises at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% homology with; differs at no more than 1%, 2%, 5%, 10%, 15%, 20%, 30%, or 40% of the amino acid residues when compared with; differs by at least 1, 2, 5, 10 or 20 amino acids but by no more than 100, 80, 70, 60, 50, 40 or 30 amino acids from; or is identical to any Cpf1 sequence, e.g., wild-type, mutant, variant, non-catalytic, or functional fragment thereof, known in the art.

[00103] The term “complementary” as used in connection with nucleic acid, refers to the pairing of bases, A with T or U, and G with C. The term complementary can also refer to nucleic acid molecules that are completely complementary, that is, form A to T or U pairs and

G to C pairs across the entire reference sequence, as well as molecules that are at least about 80%, 85%, 90%, 95%, or 99% complementary.

[00104] As used herein, “template nucleic acid” refers to a nucleic acid sequence which can be used with a gene editing system, e.g., a CRISPR system, to insert nucleic acid sequence at or near a target sequence e.g., in homology-directed repair or homologous recombination. In embodiments, part of the template nucleic acid sequence is inserted at or near a target sequence. In embodiments, all or substantially all of the template nucleic acid sequence is inserted at or near a target sequence. The template nucleic acid can be single- or double-stranded RNA or DNA. In embodiments, the template nucleic acid is a vector, or is included in a vector, for example an AAV vector, plasmid DNA, minicircle or nanoplasmid. In aspects, the template nucleic acid comprises nucleic acid sequence encoding a chimeric antigen receptor (CAR), e.g., as described herein. In aspects, the template nucleic acid comprises or is included in a vector comprising nucleic acid sequence encoding a chimeric antigen receptor (CAR), e.g., as described herein. In embodiments, the template nucleic acid comprises nucleic acid sequence which is complementary to nucleic acid sequence at or near the target sequence.

[00105] An “indel,” as the term is used herein, refers to a nucleic acid comprising one or more insertions of nucleotides, one or more deletions of nucleotides, or a combination of insertions and deletions of nucleotides, relative to an unmodified reference nucleic acid, that results from being exposed to a composition comprising a gRNA molecule, e.g., a CRISPR system. In some embodiments, an indel comprises nucleotides outside of the target sequence. Indels can be determined by sequencing nucleic acid after being exposed to a composition comprising a gRNA molecule, for example, by NGS. With respect to the site of an indel, an indel is said to be “at or near” a reference site (e.g., a site complementary to a targeting domain of a gRNA molecule) if it comprises at least one insertion or deletion within about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 nucleotide(s) of the reference site, or is overlapping with part or all of said reference site (e.g., comprises at least one insertion or deletion overlapping with, or within 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 nucleotides of a site complementary to the targeting domain of a gRNA molecule, e.g., a gRNA molecule described herein). In embodiments, indels are non-naturally occurring, for example, do not correspond to any naturally-occurring genetic mutation (e.g., insertion, deletion or combination thereof), for example, in the target cell.

[00106] An “indel pattern,” as the term is used herein, refers to a set of indels that results after exposure to a composition comprising a gene editing system, e.g., a CRISPR system, or gRNA molecule. In an embodiment, the indel pattern comprises or consists of, the top three

indels, by frequency of appearance. In an embodiment, the indel pattern comprises or consists of, the top five indels, by frequency of appearance. In an embodiment, the indel pattern comprises or consists of, the indels which are present at greater than about 5% frequency relative to all sequencing reads. In an embodiment, the indel pattern comprises or consists of, the indels which are present at greater than about 10% frequency relative to total number of indel sequencing reads (i.e., those reads that do not consist of the unmodified reference nucleic acid sequence). In an embodiment, the indel pattern includes of any 3 of the top five most frequently observed indels. The indel pattern may be determined, for example, by sequencing cells of a population of cells which were exposed to a gene editing system, e.g., a CRISPR system, e.g., a CRISPR system comprising a gRNA molecule described herein.

[00107] An “off-target indel,” as the term I used herein, refers to an indel at or near a site other than the target sequence of the targeting domain of the gRNA molecule. Such sites may comprise, for example, 1, 2, 3, 4, 5 or more mismatch nucleotides relative to the sequence complementary to the targeting domain of the gRNA. In exemplary embodiments, such sites are detected using targeted sequencing of in silico predicted off-target sites, or by an insertional method known in the art.

[00108] The term “inhibitory molecule” refers to a molecule, which when activated causes or contributes to an inhibition of cell survival, activation, proliferation and/or function. The term also refers to the gene encoding said molecule and its associated regulatory elements, e.g., promoters, enhancers, etc. In embodiments, an inhibitory molecule is a molecule expressed on an immune effector cell, e.g., on a T cell. Non-limiting examples of inhibitory molecules are PD-1, PD-L1, PD-L2, CTLA4, TIM3, LAG3, CEACAM (e.g., CEACAM-1, CEACAM-3 and/or CEACAM-5), VISTA, BTLA, TIGIT, LAIR1, CD160, 2B4, CD80, CD86, B7-H3 (CD276), B7-H4 (VTCN1), HVEM (TNFRSF14 or CD107), KIR, A2aR, MHC class I, MHC class II, GAL9, adenosine, and TGF beta. It will be understood that the term inhibitory molecule may refer to the gene (and its associated regulatory elements) encoding an inhibitory molecule protein when it is used in connection with a target sequence or gRNA molecule. In some embodiments, gene editing systems, e.g., CRISPR systems, comprising one or more gRNA molecules comprising a targeting domain to a sequence of an inhibitory molecule are used in conjunction with the other features disclosed herein (e.g., a CRISPR system to a TET2 intron).

[00109] The terms “allogeneic T cell target” and “allogeneic T-cell target” are used interchangeably herein, and refer to a protein that mediates or contributes to a host versus graft

response, mediates or contributes to a graft versus host response, or is a target for an immunosuppressant; and the gene encoding said molecule and its associated regulatory elements, e.g., promoters. It will be understood that the term allogeneic T cell target may refer to the gene (and its associated regulatory elements) encoding an allogeneic T cell target protein when it is used in connection with a target sequence or gRNA molecule. Without being bound by theory, inhibition or elimination of one or more allogeneic T cell targets, e.g., by use of gene editing systems, e.g., CRISPR systems, to such targets, may improve the efficacy, survival, function and/or viability of, e.g., an allogeneic cell, e.g., an allogeneic T cell, for example, by reducing or eliminating undesirable immunogenicity (such as a host versus graft response or a graft versus host response). An allogeneic T cell target may also refer to a functional fragment, splice variant, or domain of a specified target.

[00110] In some embodiments, immunogenicity refers to the initiation of a humoral or cell-mediated immune response. In certain embodiments, undesirable immunogenicity may result from graft versus host disease (GvHD) or graft versus host response, e.g., following an allogeneic transplant, in which the donor/grafted cells or tissues attack the donee/host cells or tissues as foreign. In other embodiments, undesirable immunogenicity may result from host versus graft disease (HvGD), e.g., following an allogeneic transplant, in which the donee/host cells or tissues attack the donor/grafted cells or tissues as foreign.

[00111] In a non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is one or more components of the T cell receptor. In an embodiment, the component of the T cell receptor is the T cell receptor alpha, for example the constant domain of the TCR alpha. In an embodiment, the component of the T cell receptor is the T cell receptor beta chain, for example the constant domain 1 or constant domain 2 of the TCR beta. In an embodiment, the component of the T cell receptor is the T cell receptor delta chain. In an embodiment, the component of the T cell receptor is the T cell receptor epsilon chain. In an embodiment, the component of the T cell receptor is the T cell receptor zeta chain. In an embodiment, the component of the T cell receptor is the T cell receptor gamma chain. Thus, in embodiments where the protein encoded by the allogeneic T cell target is a component of the TCR, the gene encoding the allogeneic T cell target may be, for example, TRAC, TRBC1, TRBC2, CD3D, CD3E, CD3G or CD247, and combinations thereof.

[00112] In a non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is an HLA protein or B2M. Examples of HLA

proteins include HLA-A, HLA-B and HLA-C. Thus, in embodiments where the allogeneic T cell target protein is a HLA or B2M protein, the gene encoding the allogeneic T cell target may be, for example, *HLA-A*, *HLA-B*, *HLA-C* or *B2M*, and combinations thereof. In other embodiments, the allogeneic T cell target protein is NLRC5, and the gene encoding the allogeneic T cell target may be, for example, *NLRC5*.

[00113] In some embodiments, the protein that mediates or contributes to a graft versus host response or a host versus graft response is selected from: HLA-DM, HLA-DO, HLA-DR, HLA-DQ, HLA-DP, CIITA, RFXANK, RFXAP, RFX1, RFX5, NF-YA, NF-YB, NF-YC, X2BP, OCAB, HLA-A, HLA-B, HLA-C, B2M, NLRC5, TRAC, TRBC1, TRBC2, CD247, CD3, CD3D, CD3E, CD3G, DCK, CD52, FKBP1A, and NR3C1. In a non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is a major histocompatibility complex class II (MHC II) molecule (e.g., HLA-Dx (where x refers to a letter of a MHC II protein, e.g., HLA-DM, HLA-DO, HLA-DR, HLA-DQ and/or HLA-DP)), or a regulatory factor for expression of a MHC II, and combinations thereof. A non-limiting example is CIITA (also referred to herein as C2TA). Thus, in embodiments where the allogeneic T cell target protein is a CIITA, the gene encoding the allogeneic T cell target may be, for example, *CIITA*. In another non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is RFXANK. In another non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is RFXAP. In another non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is RFX5. In another non-limiting example, the protein that mediates or contributes to a graft versus host response or host versus graft response is RFX1.

[00114] In some embodiments, gene editing systems, e.g., CRISPR systems, comprising one or more gRNA molecules comprising a targeting domain to a sequence of an allogeneic T cell target are used alone or in conjunction with the other features disclosed herein (e.g., a CRISPR system to a TET2 intron). In embodiments, CRISPR systems targeting TRAC, B2M and/or CIITA are used in conjunction with the other features disclosed herein (e.g., a CRISPR system to a TET2 intron).

[00115] The term “target for an immunosuppressant” as used herein refers to a molecular target, for example a receptor or other protein, for an immunosuppressant agent (the terms, “immunosuppressant” and “immunosuppressive” are used interchangeably herein in connection with an agent, or target for an agent). An immunosuppressant agent is an agent that

suppresses immune function by one or more mechanisms of action. In other words, an immunosuppressive agent is a role played by a compound which is exhibited by a capability to diminish the extent and/or voracity of an immune response. One example of a type of activity exhibited by an immunosuppressant agent is eliminating T-cells, for example, activated T-cells. Another example of a type of activity exhibited by an immunosuppressant agent is reducing the activity or activation level of T-cells.

[00116] As a non-limiting example, an immunosuppressive agent can be a calcineurin inhibitor, a target of rapamycin, an interleukin-2 α -chain blocker, an inhibitor of inosine monophosphate dehydrogenase, an inhibitor of dihydrofolic acid reductase, a corticosteroid, cyclosporine, or an immunosuppressive antimetabolite. Classical cytotoxic immunosuppressants act by inhibiting DNA synthesis. Others may act through activation of T-cells or by inhibiting the activation of helper cells. As non-limiting examples, targets for immunosuppressive agent can be a receptor for an immunosuppressive agent such as: deoxycytidine kinase, CD52, glucocorticoid receptor (GR), a FKBP family gene member, e.g., FKBP12, and a cyclophilin family gene member. In an embodiment, the target for an immunosuppressant is deoxycytidine kinase (DCK), and the immunosuppressant is a nucleoside analog-based drug such as cytarabine (cytosine arabinoside) or gemcitabine. In an embodiment, the target for an immunosuppressant is GR, and the immunosuppressant is a corticosteroid such as dexamethasone. In an embodiment, the target for an immunosuppressant is CD52, and the immunosuppressant is an anti-CD52 antibody or antigen-binding fragment thereof such as alemtuzumab (CAMPATH®). In an embodiment, the target for an immunosuppressant is FKBP12, and the immunosuppressant is FK506 (or analog or FKBP12-binding fragment thereof), cyclosporine, rapamycin or rapalog, or mTor inhibitor such as RAD001. Thus, in embodiments where the allogeneic T cell target is a target for an immunosuppressant protein, the gene encoding the allogeneic T cell target may be, for example, *NR3C1*, *FKBP1A*, *CD52*, or *DCK*, and combinations thereof. In some embodiments, gene editing systems, e.g., CRISPR systems, comprising one or more gRNA molecules comprising a targeting domain to a sequence of allogeneic T cell target are used in conjunction with the other features disclosed herein (e.g., a CRISPR system to a TET2 intron). In embodiments, CRISPR systems targeting TRAC and FKBP1A are used in conjunction with the other features disclosed herein (e.g., a CRISPR system to a TET2 intron).

[00117] “Tet” as the term is used herein, refers to the family of genes, and the proteins encoded by said genes, of the ten-eleven translocation methylcytosine dioxygenase family. Tet includes, for example, Tet1, Tet2 and Tet3.

[00118] “Tet2” as the term is used herein, refers to gene, tet methylcytosine dioxygenase 2, and the protein encoded by said gene, the tet2 methylcytosine dioxygenase, which catalyzes the conversion of methylcytosine to 5-hydroxymethylcytosine. It is sometimes also referred to as “KIAA1546,” “FLJ20032” and “tet oncogene family member 2.” The encoded protein is involved in myelopoiesis, and defects in this gene have been associated with several myeloproliferative disorders. In the human genome, TET2 is located on chromosome 4q24. The Tet2 gene includes both the introns and exons of the associated gene. Currently six TET2 isoforms have been described and their Genbank numbers are: NM_001127208.2; XM_005263082.1; XM_006714242.2; NM_017628.4; XM_011532044.1; and XM_011532043.1.

[00119] An example of the protein sequence of human Tet2 is provided as UniProt accession number Q6N021:

10	20	30	40	50
MEQDRTNHVE	GNRLSPFLIP	SPPICQTEPL	ATKLQNGSPL	PERAHPEVNG
60	70	80	90	100
DTKWHSFKSY	YGIPCMKGSQ	NSRVSPDFTQ	ESRGYSKCLQ	NGGIKRTVSE
110	120	130	140	150
PSLSGLLQIK	KLKQDQKANG	ERRNFGVSQE	RNPGESSQPN	VSDLSDKKES
160	170	180	190	200
VSSVAQENAV	KDFTSFSTHN	CSGPENPELQ	ILNEQEGKSA	NYHDKNIVLL
210	220	230	240	250
KNKAVLMPNG	ATVSASSVEH	THGELLEKTL	SQYYPDCVSI	AVQKTTSHIN
260	270	280	290	300
AINSQATNEL	SCEITHPSHT	SGQINSAQTS	NSELPPKPAA	VVSEACDADD
310	320	330	340	350
ADNASKLAAM	LNTCSFQKPE	QLQQQKSVFE	ICPSPAENNI	QGTTKLASGE
360	370	380	390	400
EFCSGSSSNL	QAPGGSSERY	LKQNEMNAY	FKQSSVFTKD	SFSATTTPPP
410	420	430	440	450
PSQLLLSPPP	PLPQVPQLPS	EGKSTLNGGV	LEEHHHYPNQ	SNTTLLREVK
460	470	480	490	500
IEGKPEAPPS	QSPNPSTHVC	SPSPMLSERP	QNNCVNRNDI	QTAGTMTVPL
510	520	530	540	550
CSEKTRPMSE	HLKHNPPIFG	SSGELQDNCQ	QLMRNKEQEI	LKGRDKEQTR
560	570	580	590	600
DLVPPTQHYL	KPGWIELKAP	RFHQAESHLK	RNEASLPSIL	QYQPNLSNQM
610	620	630	640	650
TSKQYTGNSN	MPGGLPRQAY	TQKTTQLEHK	SQMYQVEMNQ	GQSQGTVDQH
660	670	680	690	700

WO 2018/175636

PCT/US2018/023631

LQFQKPSHQV	HFSKTDHLPK	AHVQSLCGTR	FHFQQRADSQ	TEKLMSPVLK
710	720	730	740	750
QHLNQQASET	EPFSNSHLLQ	HKPHKQAAQT	QPSQSSHLPQ	NQQQQQKLQI
760	770	780	790	800
KNKEEILQTF	PHPQSNNDQQ	REGSFFGQTK	VEECFHGENQ	YSKSSEFETH
810	820	830	840	850
NVQMGLEEVQ	NINRRNSPYS	QTMKSSACKI	QVSCSNNTHL	VSENKEQTTH
860	870	880	890	900
PELFAGNKTQ	NLHHMQYFPN	NVIPKQDLLH	RCFQEQEQKS	QQASVLQGYK
910	920	930	940	950
NRNQDMSGQQ	AAQLAQORYL	IHNHANVFPV	PDQGGSHQT	PPQKDTQKHA
960	970	980	990	1000
ALRWHLLOKQ	EQQQTQQPQT	ESCHSQMHRP	IKVEPGCKPH	ACMHTAPPEN
1010	1020	1030	1040	1050
KTWKKVTKQE	NPPASCDNVQ	QKSIIETMEQ	HLKQFHAKSL	FDHKALTLKS
1060	1070	1080	1090	1100
QKQVKVEMSG	PVTVLTRQTT	AAELDSHTPA	LEQQTTSSEK	TPTKRRTAASV
1110	1120	1130	1140	1150
LNNFIESPSK	LLDTPIKNLL	DTPVKTYQDF	PSCRCVEQII	EKDEGPFYTH
1160	1170	1180	1190	1200
LGAGPNVAAI	REIMEERFGQ	KGKAIRIERV	IYTGKEGKSS	QGCPIAKWVV
1210	1220	1230	1240	1250
RRSSSEEKLL	CLVRERAGHT	CEAAVIVILI	LVWEGIPLSL	ADKLYSELTE
1260	1270	1280	1290	1300
TLRKYGTLTN	RRCALNEERT	CACQGLDPET	CGASFSGCS	WSMYNGCKF
1310	1320	1330	1340	1350
ARSKIPRKF	LLGDDPKEEE	KLESHLQNL	TLMAPTYKKL	APDAYNNQIE
1360	1370	1380	1390	1400
YEHRAPECRL	GLKEGRPFSG	VTACLDFCAH	AHRDLHNMQN	GSTLVCTLTR
1410	1420	1430	1440	1450
EDNREFGGKP	EDEQLHVLPL	YKVSDVDEFG	SVEAQEEKKR	SGAIQVLSSF
1460	1470	1480	1490	1500
RRKVRMLAEP	VKTCRQRKLE	AKKAAAEKLS	SLNSSNKNE	KEKSAPSRTK
1510	1520	1530	1540	1550
QTENASQAKQ	LAELLRLSGP	VMQQSQPPQP	LQKQPPQPQQ	QQRPPQQQPH
1560	1570	1580	1590	1600
HPQTESVNSY	SASGSTNPYM	RRPNPVSPYP	NSSHTSDIYG	STSPMNFYST
1610	1620	1630	1640	1650
SSQAAGSYLN	SSNPMNPYPG	LLNQNTQYPS	YQCNGNLSVD	NCSPYLGSYS
1660	1670	1680	1690	1700
PQSQPMDLR	YPSQDPLSKL	SLPPIHTLYQ	PRFGNSQSFT	SKYLGYNQON
1710	1720	1730	1740	1750
MQGDGFSSCT	IRPNVHHVGK	LPPYPTHEMD	GHFMGATSRL	PPNLSNPNMD
1760	1770	1780	1790	1800
YKNGEHHSPS	HIIHNYSAAP	GMFNSSLHAL	HLQNKENDML	SHTANGLSKM
1810	1820	1830	1840	1850
LPALNHDRTA	CVQGGLHKLS	DANGQEKQPL	ALVQGVASGA	EDNDEVWSDS
1860	1870	1880	1890	1900
EQSFLDPDIG	GVAVAPTHGS	ILIECAKREL	HATTPLKNPN	RNHPTRISLV
1910	1920	1930	1940	1950
FYQHKSMNEP	KHGLALWEAK	MAEKAREKEE	ECEKYGPDYV	PQKSHGKKVK
1960	1970	1980	1990	2000
REPAEPHETS	EPTYLRFIKS	LAERTMSVTT	DSTVTTSPYA	FTRVTGPYNR

2002

YI

[SEQ ID NO: 950]

[00120] The tet2 gene is located on chromosome 4, location GRCh38.p2 (GCF_000001405.28) (NC_000004.12 (105145875 to 105279803); Gene ID 54790.

[00121] Examples of nucleic acid sequences encoding Tet2 are provided below. There are 6 identified isoforms of human Tet2 have been identified. The mRNA sequences are provided below (In embodiments, in each sequence, T may be replaced with U). In embodiments, Tet2 includes the proteins encoded by each of the sequences below:

Name	NCBI Reference Sequence	Sequence
Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant 1, mRNA [SEQ ID NO: 951]	NM_001127208.2	GGCAGTGGCAGCGGCGAGAGCTTGGGCGGCCGCGCCG CCTCCTCGCGAGCGCCGCGCGCCCGGGTCCCG CTCGCATGCAAGTCACGTCCGCCCCCTCGGCGCGGCCGC CCCGAGACGCCGGCCCCGCTGAGTGATGAGA ACAGACGTCAAACCTGCCTTATGAATATTGATGCGGAGGC TAGGCTGCTTTCGTAGAGAAGCAGAAGGAAG CAAGATGGCTGCCCTTTAGGATTTGTTAGAAAGGAGACC CGACTGCAACTGCTGGATTGCTGCAAGGCTG AGGGACGAGAACGAGGCTGGCAAACATTCAGCAGCACA CCCTCTCAAGATTGTTTACTTGCCTTTGCTCC TGTTGAGTTACAACGCTTGGAAGCAGGAGATGGGCTCAG CAGCAGCCAATAGGACATGATCCAGGAAGAG CAGTAAGGGACTGAGCTGCTGAATTCAACTAGAGGGCA GCCTTGTTGGATGGCCCCGAAGCAAGCCTGATG GAACAGGATAGAACCAACCATGTTGAGGGCAACAGACT AAGTCCATTCTGATAACCATCACCTCCCATT GCCAGACAGAACCTCTGGCTACAAAGCTCCAGAATGGA AGCCCACTGCCTGAGAGAGCTCATCCAGAAGT AAATGGAGACACCAAGTGGCACTCTTTCAAAAGTTATTA TGGAATACCCTGTATGAAGGGAAGCCAGAAT AGTCGTGTGAGTCCTGACTTTACACAAGAAAGTAGAGGG TATTCCAAGTGTTTGCAAAATGGAGGAATAA AACGCACAGTTAGTGAACCTTCTCTCTCTGGGCTCCTTCA GATCAAGAAATTGAAACAAGACCAAAAGGC TAATGGAGAAAGACGTAACCTTCGGGGTAAGCCAAGAAA GAAATCCAGGTGAAAGCAGTCAACCAAAATGTC TCCGATTTGAGTGATAAGAAAGAATCTGTGAGTTCTGTA GCCCAAGAAAATGCAGTTAAAGATTTACCA GTTTTTCAACACATAACTGCAGTGGGCCTGAAAATCCAG AGCTTCAGATTCTGAATGAGCAGGAGGGGAA AAGTGCTAATTACCATGACAAGAACATTGTATTACTTAA AAACAAGGCAGTGCTAATGCCTAATGGTGCT ACAGTTTCTGCCTCTTCCGTGGAACACACACATGGTGAA CTCCTGGAAAAAACACTGTCTCAATATTATC CAGATTGTGTTTCCATTGCGGTGCAGAAAACCACATCTC ACATAAATGCCATTAACAGTCAGGCTACTAA TGAGTTGTCCTGTGAGATCACTACCCATCGCATACCTCA GGGCAGATCAATTCCGCACAGACCTCTAAC

		TCTGAGCTGCCTCCAAAGCCAGCTGCAGTGGTGAGTGAG GCCTGTGATGCTGATGATGCTGATAATGCCA GTAAACTAGCTGCAATGCTAAATACCTGTTCTTTCAGA AACCAGAACAACTACAACAACAAAAATCAGT TTTTGAGATATGCCCATCTCCTGCAGAAAATAACATCCA GGGAACCACAAAGCTAGCGTCTGGTGAAGAA TTCTGTTTCAGGTTCAGCAGCAATTTGCAAGCTCCTGGTG GCAGCTCTGAACGGTATTTAAAACAAAATG AAATGAATGGTGCTTACTTCAAGCAAAGCTCAGTGTTCA CTAAGGATTCTTTTTCTGCCACTACCACACC ACCACCACCATCACAATTGCTTCTTTCTCCCCCTCCTCCT CTTCCACAGGTTCCTCAGCTTCCTTCAGAA GGAAAAAGCACTCTGAATGGTGGAGTTTTAGAGAACA CCACCACTACCCCAACCAAAGTAACACAACAC TTTAAAGGGAAGTGAAAATAGAGGGTAAACCTGAGGCA CCACCTTCCCAGAGTCCTAATCCATCTACACA TGTATGCAGCCCTTCTCCGATGCTTTCTGAAAGGCCTCAG AATAATTGTGTGAACAGGAATGACATACAG ACTGCAGGGACAATGACTGTTCCATTGTGTTCTGAGAAA ACAAGACCAATGTCAGAACACCTCAAGCATA ACCCACCAATTTTTGGTAGCAGTGGAGAGCTACAGGACA ACTGCCAGCAGTTGATGAGAAACAAAGAGCA AGAGATTCTGAAGGGTCGAGACAAGGAGCAAACACGAG ATCTTGTGCCCCCAACACAGCACTATCTGAAA CCAGGATGGATTGAATTGAAGGCCCTCGTTTTTCACCAA GCGGAATCCCATCTAAAACGTAATGAGGCAT CACTGCCATCAATTCTTCAGTATCAACCCAATCTCTCCAA TCAAATGACCTCCAAACAATACTGGA TTCCAACATGCCTGGGGGGCTCCCAAGGCAAGCTTACAC CCAGAAAACAACACAGCTGGAGCACAAGTCA CAAATGTACCAAGTTGAAATGAATCAAGGGCAGTCCCAA GGTACAGTGGACCAACATCTCCAGTTCCAAA AACCCTCACACCAGGTGCACTTCTCCAAAACAGACCATT TACCAAAGCTCATGTGCAGTCACTGTGTGG CACTAGATTTTCATTTTCAACAAAGAGCAGATTCCCAAAC TGAAAAACTTATGTCCCCAGTGTTGAAACAG CACTTGAATCAACAGGCTTCAGAGACTGAGCCATTTTCA AACTCACACCTTTTGCAACATAAGCCTCATA AACAGGCAGCACAAACACAACCATCCCAGAGTTTACATC TCCCTCAAACAGCAACAGCAGCAAAAATT ACAAATAAAGAATAAAGAGGAAATACTCCAGACTTTTCC TCACCCCCAAAGCAACAATGATCAGCAAAGA GAAGGATCATTCTTTGGCCAGACTAAAGTGGAAGAATGT TTTCATGGTGAAAATCAGTATTCAAAATCAA GCGAGTTCGAGACTCATAATGTCCAAATGGGACTGGAGG AAGTACAGAATATAAATCGTAGAAATTCCCC TTATAGTCAGACCATGAAATCAAGTGCATGCAAAATACA GGTTTCTTGTTCAAACAATACACACCTAGTT TCAGAGAATAAAGAACAGACTACACATCCTGAACTTTTT GCAGGAAACAAGACCCAAAACCTTGCATCACA TGCAATATTTTCCAAATAATGTGATCCCAAAGCAAGATC TTCTTCACAGGTGCTTTCAAGAACAGGAGCA GAAGTCACAACAAGCTTCAGTTCTACAGGGATATAAAAA TAGAAACCAAGATATGTCTGGTCAACAAGCT GCGCAACTTGCTCAGCAAAGGTAATTGATACATAACCAT
--	--	---

		GCAAATGTTTTTCCTGTGCCTGACCAGGGAG GAAGTCACACTCAGACCCCTCCCCAGAAGGACACTCAA AGCATGCTGCTCTAAGGTGGCATCTCTTACA GAAGCAAGAACAGCAGCAAACACAGCAACCCCCAACTG AGTCTTGCCATAGTCAGATGCACAGGCCAATT AAGGTGGAACCTGGATGCAAGCCACATGCCTGTATGCAC ACAGCACACCAGAAAAACAAAACATGGAAAA AGGTAACCTAAGCAAGAGAATCCACCTGCAAGCTGTGATA ATGTGCAGCAAAAAGAGCATCATTGAGACCAT GGAGCAGCATCTGAAGCAGTTTCACGCCAAGTCGTTATT TGACCATAAGGCTCTTACTCTCAAATCACAG AAGCAAGTAAAAGTTGAAATGTCAGGGCCAGTCACAGTT TTGACTAGACAAACCACTGCTGCAGAACTTG ATAGCCACACCCCAGCTTTAGAGCAGCAAACAACCTTCTT CAGAAAAGACACCAACCAAAAAGAACAGCTGC TTCTGTTCTCAATAATTTTATAGAGTCACCTTCCAAATTA CTAGATACTCCTATAAAAAAATTTATTGGAT ACACCTGTCAAGACTCAATATGATTTCCCATCTTGCAGAT GTGTAGAGCAAATTATTGAAAAAGATGAAG GTCCTTTTTATACCCATCTAGGAGCAGGTCCTAATGTGGC AGCTATTAGAGAAATCATGGAAGAAAGGTT TGGACAGAAGGGTAAAGCTATTAGGATTGAAAGAGTCA TCTATACTGGTAAAGAAGGCCAAAAGTTCTCAG GGATGTCCTATTGCTAAGTGGGTGGTTCGCAGAAGCAGC AGTGAAGAGAAGCTACTGTGTTTGGTGCGGG AGCGAGCTGGCCACACCTGTGAGGCTGCAGTGATTGTGA TTCTCATCCTGGTGTGGGAAGGAATCCCGCT GTCTCTGGCTGACAACTCTACTCGGAGCTTACCGAGAC GCTGAGGAAATACGGCACGCTCACCAATCGC CGGTGTGCCTTGAATGAAGAGAGAACTTGCGCCTGTCAG GGGCTGGATCCAGAAACCTGTGGTGCCTCCT TCTCTTTTGGTTGTTTCATGGAGCATGTACTACAATGGATG TAAGTTTGCCAGAAGCAAGATCCCAAGGAA GTTTAAGCTGCTTGGGGATGACCCAAAAGAGGAAGAGA AACTGGAGTCTCATTGCAAAACCTGTCCACT CTTATGGCACCAACATATAAGAACTTGACCTGATGCA TATAATAATCAGATTGAATATGAACACAGAG CACCAGAGTGCCGTCTGGGTCTGAAGGAAGGCCGTCCAT TCTCAGGGGTCACCTGCATGTTTGGACTTCTG TGCTCATGCCCACAGAGACTTGCACAACATGCAGAATGG CAGCACATTGGTATGCACTCTCACTAGAGAA GACAATCGAGAATTTGGAGGAAAACCTGAGGATGAGCA GCTTCACGTTCTGCCTTTATACAAAGTCTCTG ACGTGGATGAGTTTGGGAGTGTGGAAGCTCAGGAGGAG AAAAACGGAGTGGTGCCATTGAGGTACTGAG TTCTTTTCGGCGAAAAGTCAGGATGTTAGCAGAGCCAGT CAAGACTTGCCGACAAAGGAACTAGAAGCC AAGAAAGCTGCAGCTGAAAAGCTTTCCTCCCTGGAGAAC AGCTCAAATAAAAAATGAAAAGGAAAAGTCAG CCCCATCACGTACAAAACAACTGAAAACGCAAGCCAG GCTAAACAGTTGGCAGAACTTTTGCGACTTTC AGGACCAGTCATGCAGCAGTCCCAGCAGCCCCAGCCTCT ACAGAAGCAGCCACCACAGCCCCAGCAGCAG CAGAGACCCCAGCAGCAGCAGCCACATCACCTCAGAC AGAGTCTGTCAACTCTTATTCTGCTTCTGGAT
--	--	---

		CCACCAATCCATACATGAGACGGCCCAATCCAGTTAGTC CTTATCCAAACTCTTCACACACTTCAGATAT CTATGGAAGCACCAGCCCTATGAACTTCTATTCCACCTC ATCTCAAGCTGCAGGTTTCATATTTGAATTCT TCTAATCCCATGAACCCTTACCCTGGGCTTTTGAATCAGA ATACCCAATATCCATCATATCAATGCAATG GAAACCTATCAGTGGACAACCTGCTCCCCATATCTGGGT CCTATTCTCCCCAGTCTCAGCCGATGGATCT GTATAGGTATCCAAGCCAAGACCCTCTGTCTAAGCTCAG TCTACCACCCATCCATACACTTTACCAGCCA AGGTTTGGAAATAGCCAGAGTTTACATCTAAATACTTA GGTTATGGAAACCAAAATATGCAGGGAGATG GTTTCAGCAGTTGTACCATTAGACCAAATGTACATCATG TAGGGAAATTGCCTCCTTATCCCACCTCATGA GATGGATGGCCACTTCATGGGAGCCACCTCTAGATTACC ACCCAATCTGAGCAATCCAAACATGGACTAT AAAAATGGTGAACATCATTACCTTCTCACATAATCCAT AACTACAGTGCAGCTCCGGGCATGTTCAACA GCTCTCTTCATGCCCTGCATCTCCAAAACAAGGAGAATG ACATGCTTTCCACACAGCTAATGGGTTATC AAAGATGCTTCCAGCTCTTAACCATGATAGAAGCTGCTTG TGTCCAAGGAGGCTTACACAAATTAAGTGAT GCTAATGGTCAGGAAAAGCAGCCATTGGCACTAGTCCAG GGTGTGGCTTCTGGTGCAGAGGACAACGATG AGGTCTGGTCAGACAGCGAGCAGAGCTTTCTGGATCCTG ACATTGGGGGAGTGGCCGTGGCTCCAACCTCA TGGGTCAATTCTCATTGAGTGTGCAAAGCGTGAGCTGCA TGCCACAACCCCTTTAAAGAATCCCAATAGG AATCACCCCACCAGGATCTCCCTCGTCTTTTACCAGCATA AGAGCATGAATGAGCCAAAACATGGCTTGG CTCTTTGGGAAGCCAAAATGGCTGAAAAAGCCCGTGAGA AAGAGGAAGAGTGTGAAAAGTATGGCCCAGA CTATGTGCCTCAGAAATCCCATGGCAAAAAAGTGAAACG GGAGCCTGCTGAGCCACATGAACTTCAGAG CCCACTTACCTGCGTTTCATCAAGTCTCTTGCCGAAAGGA CCATGTCCGTGACCACAGACTCCACAGTAA CTACATCTCCATATGCCTTCACTCGGGTCACAGGGCCTTA CAACAGATATATATGATATCACCCCCTTTT GTTGGTTACCTCACTTGAAAAGACCACAACCAACCTGTC AGTAGTATAGTTCTCATGACGTGGGCAGTGG GGAAAGGTCACAGTATTCATGACAAATGTGGTGGGAAA AACCTCAGCTCACCAGCAACAAAAGAGGTTAT CTTACCATAGCACTTAATTTTCACTGGCTCCCAAGTGGTC ACAGATGGCATCTAGGAAAAGACCAAAGCA TTCTATGCAAAAAGAAGGTGGGGAAGAAAGTGTTCCGC AATTTACATTTTTTAAACACTGGTTCTATTATT GGACGAGATGATATGTAAATGTGATCCCCCCCCCGCT TACAACCTCTACACATCTGTGACCCTTTTAA TAATATCAAGTTTGCATAGTCATGGAACACAAATCAAAC AAGTACTGTAGTATTACAGTGACAGGAATCT TAAAATACCATCTGGTGCTGAATATATGATGTACTGAAA TACTGGAATTATGGCTTTTTTGAAATGCAGTT TTTACTGTAATCTTAACCTTTTATTTATCAAAATAGCTACA GGAAACATGAATAGCAGGAAAACACTGAAT TTGTTTGGATGTTCTAAGAAATGGTGCTAAGAAAATGGT
--	--	--

		GTCTTTAATAGCTAAAAATTTAATGCCTTTA TATCATCAAGATGCTATCAGTGTACTCCAGTGCCCTTGA ATAATAGGGGTACCTTTTTCATTCAAGTTTTT ATCATAATTACCTATTCTTACACAAGCTTAGTTTTTAAAA TGTGGACATTTTAAAGGCCTCTGGATTTTG CTCATCCAGTGAAGTCCTTGTAGGACAATAAACGTATAT ATGTACATATATACACAAACATGTATATGTG CACACACATGTATATGTATAAATATTTTAAATGGTGTTTT AGAAGCACTTTGTCTACCTAAGCTTTGACA ACTTGAACAATGCTAAGGTACTGAGATGTTTAAAAACA AGTTTACTTTTCATTTTAGAATGCAAAGTTGA TTTTTTTAAGGAAACAAAGAAAGCTTTTAAATATTTTTG CTTTGTAGCCATGCATCTGCTGATGAGCAAT TGTGTCCATTTTAAACACAGCCAGTTAAATCCACCATGG GGCTTACTGGATTCAAGGGAATACGTTAGTC CACAAAACATGTTTTCTGGTGCTCATCTCACATGCTATAC TGTAAAACAGTTTTATACAAAATTGTATGA CAAGTTCATTGCTCAAAAATGTACAGTTTTAAGAATTTTC TATTAAGTGCAGGTAATAATTAGCTGCATG CTGCAGACTCAACAAAGCTAGTTCCTGAAGCCTATGCT ATTTTATGGATCATAGGCTCTTCAGAGAAGT GAATGGCAGTCTGCCTTTGTGTTGATAATTATGTACATTG TGACGTTGTCAATTTCTTAGCTTAAGTGTCC TCTTTAACAAGAGGATTGAGCAGACTGATGCCTGCATAA GATGAATAAACAGGGTTAGTTCCATGTGAAT CTGTCAGTTAAAAAGAAACAAAAACAGGCAGCTGGTTTG CTGTGGTGGTTTTAAATCATTAATTTGTATA AAGAAGTGAAAGAGTTGTATAGTAAATTAAATTGTAAAC AAAACTTTTTTAATGCAATGCTTTAGTATTT TAGTACTGTAAAAAAATTAATATATACATATATATATA TATATATATATATATATATATGAGTTTGAAG CAGAATTCACATCATGATGGTGCTACTCAGCCTGCTACA AATATATCATAATGTGAGCTAAGAATTCATT AAATGTTTGAGTGATGTTCTACTTGTTCATATACCTCAAC ACTAGTTTGGCAATAGGATATTGAACTGAG AGTGAAAGCATTGTGTACCATCATTTTTTTTCCAAGTCCTT TTTTTTATTGTTAAAAAAAAGCATAACCT TTTTTCAATACTTGATTTCTTAGCAAGTATAACTTGAAC TCAACCTTTTTGTTCTAAAAATTCAGGGAT ATTTAGCTCATGCTCTCCCTATGCCAACATGTCACCTGT GTTTATGTAAAATTGTTGTAGGTTAATAAA TATATTCTTTGTCAGGGATTTAACCCTTTTATTTTGAATC CCTTCTATTTTACTTGTACATGTGCTGATG TAACTAAACTAATTTTGTAAATCTGTTGGCTCTTTTTAT TGTAAGAAAAGCATTTTAAAAGTTTGAGG AATCTTTTGACTGTTTCAAGCAGGAAAAAAAATTACAT GAAAATAGAATGCACTGAGTTGATAAAGGGA AAAATTGTAAGGCAGGAGTTTGGCAAGTGGCTGTTGGCC AGAGACTTACTTGTAACCTCTCTAAATGAAGT TTTTTTGATCCTGTAATCACTGAAGGTACATACTCCATGT GGACTTCCCTTAAACAGGCAAACACCTACA GGTATGGTGTGCAACAGATTGTACAATTACATTTTGGCC TAAATACATTTTTGCTTACTAGTATTTAAAA TAAATTCTTAATCAGAGGAGGCCTTTGGGTTTTATTGGTC AAATCTTTGTAAGCTGGCTTTTGTCTTTTT
--	--	--

		AAAAAATTTCTTGAATTTGTGGTTGTGTCCAATTTGCAAA CATTTCCAAAAATGTTTGCTTTGCTTACAA ACCACATGATTTTAATGTTTTTTGTATAACCATAATATCTA GCCCCAACATTTGATTACTACATGTGCAT TGGTGATTTTGATCATCCATTCTTAATATTTGATTTCTGT GTCACCTACTGTCATTTGTAAACTGCTGG CCAACAAGAACAGGAAGTATAGTTTGGGGGGTTGGGGA GAGTTTACATAAGGAAGAGAAGAAATTGAGTG GCATATTGTAAATATCAGATCTATAATTGTAAATATAAA ACCTGCCTCAGTTAGAATGAATGGAAAGCAG ATCTACAATTTGCTAATATAGGAATATCAGGTTGACTAT ATAGCCATACTTGAAAATGCTTCTGAGTGGT GTCAACTTTACTTGAATGAATTTTTTCATCTTGATTGACGC ACAGTGATGTACAGTTCACTTCTGAAGCTA GTGGTTAACTTGTGTAGGAACTTTTGCAGTTTGACACTA AGATAACTTCTGTGTGCATTTTTCTATGCT TTTTTAAAACTAGTTTCATTTTCATTTTCATGAGATGTTT GGTTTATAAGATCTGAGGATGGTTATAAAT ACTGTAAGTATTGTAATGTTATGAATGCAGGTTATTTGA AAGCTGTTTATTATTATATCATTCCTGATAA TGCTATGTGAGTGTTTTTAATAAAATTTATATTTATTAA TGCACTCTAAAAAAAAAAAAAAAAAAAAA
PREDICTED: Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant X1, mRNA [SEQ ID NO: 952]	XM_005263 082.1	AAGCAGAAGGAAGCAAGATGGCTGCCCTTTAGGATTTGT TAGAAAGGAGACCCGACTGCAACTGCTGGAT TGCTGCAAGGCTGAGGGACGAGAACGAGAATTCAACTA GAGGGCAGCCTTGTGGATGGCCCCGAAGCAAG CCTGATGGAACAGGATAGAACCAACCATGTTGAGGGCA ACAGACTAAGTCCATTTCCTGATACCATCACCT CCCATTTGCCAGACAGAACCTCTGGCTACAAAGCTCCAG AATGGAAGCCCCTGCTGAGAGAGCTCATC CAGAAGTAAATGGAGACACCAAGTGGCACTCTTTCAAAA GTTATTATGGAATACCCTGTATGAAGGGAAG CCAGAATAGTCGTGTGAGTCCTGACTTTACACAAGAAAG TAGAGGGTATTCCAAGTGTTTGCAAAATGGA GGAATAAAACGCACAGTTAGTGAACCTTCTCTCTCTGGG CTCCTTCAGATCAAGAAATTGAAACAAGACC AAAAGGCTAATGGAGAAAGACGTAACCTTCGGGGTAAGC CAAGAAAGAAATCCAGGTGAAAGCAGTCAACC AAATGTCTCCGATTTGAGTGATAAGAAAGAATCTGTGAG TTCTGTAGCCCAAGAAAATGCAGTTAAAGAT TTCACCAGTTTTTCAACACATAACTGCAGTGGGCCTGAA AATCCAGAGCTTCAGATTCTGAATGAGCAGG AGGGGAAAAGTGCTAATTACCATGACAAGAACATTGTAT TACTTAAAAACAAGGCAGTGCTAATGCCTAA TGGTGCTACAGTTTCTGCCTCTTCCGTGGAACACACACAT GGTGAACCTCCTGGAAAAAACACTGTCTCAA TATTATCCAGATTGTGTTTCCATTGCGGTGCAGAAAACC ACATCTCACATAAATGCCATTAACAGTCAGG CTACTAATGAGTTGTCCTGTGAGATCACTCACCCATCGC ATACCTCAGGGCAGATCAATTCCGCACAGAC CTCTAACTCTGAGCTGCCTCCAAAGCCAGCTGCAGTGGT GAGTGAGGCCTGTGATGCTGATGATGCTGAT AATGCCAGTAAACTAGCTGCAATGCTAAATACCTGTTCC TTTCAGAAACCAGAACAACTACAACAACAAA

		AATCAGTTTTTTGAGATATGCCCATCTCCTGCAGAAAATA ACATCCAGGGAACCACAAAGCTAGCGTCTGG TGAAGAATTCTGTTTCAGGTTCCAGCAGCAATTTGCAAGC TCCTGGTGGCAGCTCTGAACGGTATTTAAAA CAAAATGAAATGAATGGTGCTTACTTCAAGCAAAGCTCA GTGTTCACTAAGGATTTCCTTTTCTGCCACTA CCACACCACCACCACCATCACAATTGCTTCTTTCTCCCC TCCTCCTCTTCCACAGGTTCCCTCAGCTTCC TTCAGAAGGAAAAAGCACTCTGAATGGTGGAGTTTTAGA AGAACACCACCCTACCCCAACCAAAGTAAC ACAACACTTTTAAGGGAAGTGAAAATAGAGGGTAAACC TGAGGCACCACCTTCCCAGAGTCCTAATCCAT CTACACATGTATGCAGCCCTTCTCCGATGCTTTCTGAAAG GCCTCAGAATAATTGTGTGAACAGGAATGA CATACAGACTGCAGGGACAATGACTGTTCCATTGTGTTC TGAGAAAACAAGACCAATGTCAGAACACCTC AAGCATAACCCACCAATTTTTGGTAGCAGTGGAGAGCTA CAGGACAACCTGCCAGCAGTTGATGAGAAACA AAGAGCAAGAGATTCTGAAGGGTCGAGACAAGGAGCAA ACACGAGATCTTGTGCCCCCAACACAGCACTA TCTGAAACCAGGATGGATTGAATTGAAGGCCCTCGTTT TCACCAAGCGGAATCCCATCTAAAACGTAAT GAGGCATCACTGCCATCAATTCTTCAGTATCAACCCAAT CTCTCCAATCAAATGACCTCCAAACAATACA CTGGAAATTCCAACATGCCTGGGGGGCTCCCAAGGCAAG CTTACACCCAGAAAACAACACAGCTGGAGCA CAAGTCACAAATGTACCAAGTTGAAATGAATCAAGGGC AGTCCCAAGGTACAGTGGACCAACATCTCCAG TTCCAAAAACCCTCACACCAGGTGCACTTCTCCAAAACA GACCATTTACCAAAAAGCTCATGTGCAGTCAC TGTGTGGCACTAGATTTTCATTTTCAACAAAGAGCAGATT CCCAAACCTGAAAAACTTATGTCCCCAGTGTT GAAACAGCACTTGAATCAACAGGCTTCAGAGACTGAGCC ATTTTCAAACCTCACACCTTTTGCAACATAAG CCTCATAAACAGGCAGCACAAACACAACCATCCCAGAGT TCACATCTCCCTCAAAACCAGCAACAGCAGC AAAAATTACAAATAAAGAATAAAGAGGAAATACTCCAG ACTTTTCCTCACCCCCAAAGCAACAATGATCA GCAAAGAGAAGGATCATTCTTTGGCCAGACTAAAGTGGA AGAATGTTTTTCATGGTGAAAATCAGTATTCA AAATCAAGCGAGTTCGAGACTCATAATGTCCAAATGGGA CTGGAGGAAGTACAGAATATAAATCGTAGAA ATTCCCCTTATAGTCAGACCATGAAATCAAGTGCATGCA AAATACAGGTTTCTTGTTCAAACAATACACA CCTAGTTTCAGAGAATAAAGAACAGACTACACATCCTGA ACTTTTTGCAGGAAACAAGACCCAAAACCTTG CATCACATGCAATATTTTCCAAATAATGTGATCCCAAAG CAAGATCTTCTTCACAGGTGCTTTCAAGAAC AGGAGCAGAAGTCACAACAAGCTTCAGTTCTACAGGGAT ATAAAAATAGAAACCAAGATATGTCTGGTCA ACAAGCTGCGCAACTTGCTCAGCAAAGGTACTTGATACA TAACCATGCAAATGTTTTTCTGTGCCTGAC CAGGGAGGAAGTCACACTCAGACCCCTCCCCAGAAGGA CACTCAAAGCATGCTGCTCTAAGGTGGCATC TCTTACAGAAGCAAGAACAGCAGCAAACACAGCAACCC
--	--	--

		CAAACTGAGTCTTGCCATAGTCAGATGCACAG GCCAATTAAGGTGGAACCTGGATGCAAGCCACATGCCTG TATGCACACAGCACCACCAGAAAACAAAACA TGGAAAAAGGTAACTAAGCAAGAGAATCCACCTGCAAG CTGTGATAATGTGCAGCAAAAGAGCATCATTG AGACCATGGAGCAGCATCTGAAGCAGTTTTCACGCCAAGT CGTTATTTGACCATAAGGCTCTTACTCTCAA ATCACAGAAGCAAGTAAAAGTTGAAATGTCAGGGCCAG TCACAGTTTTGACTAGACAAACCACTGCTGCA GAACTTGATAGCCACACCCAGCTTTAGAGCAGCAAACA ACTTCTTCAGAAAAGACACCAACCAAAAAGAA CAGCTGCTTCTGTTCTCAATAATTTTATAGAGTCACCTTC CAAATTACTAGATACTCCTATAAAAAAATTT ATTGGATACACCTGTCAAGACTCAATATGATTTCCCATCT TGCAGATGTGTAGAGCAAATTATTGAAAAA GATGAAGGTCCTTTTTTATACCCATCTAGGAGCAGGTCCT AATGTGGCAGCTATTAGAGAAATCATGGAAG AAAGGTTTGGACAGAAGGGTAAAGCTATTAGGATTGAA AGAGTCATCTATACTGGTAAAGAAGGCAAAAAG TTCTCAGGGATGTCCTATTGCTAAGTGGGTGGTTCGCAG AAGCAGCAGTGAAGAGAAGCTACTGTGTTTG GTGCGGGAGCGAGCTGGCCACACCTGTGAGGCTGCAGTG ATTGTGATTCTCATCCTGGTGTGGGAAGGAA TCCCGCTGTCTCTGGCTGACAACTCTACTCGGAGCTTAC CGAGACGCTGAGGAAATACGGCACGCTCAC CAATCGCCGGTGTGCCTTGAATGAAGAGAGAACTTGCGC CTGTCAGGGGCTGGATCCAGAAACCTGTGGT GCCTCCTTCTCTTTTGGTTGTTTCATGGAGCATGTACTACA ATGGATGTAAGTTTGCCAGAAGCAAGATCC CAAGGAAGTTTAAGCTGCTTGGGGATGACCCAAAAGAG GAAGAGAAACTGGAGTCTCATTGCAAAACCT GTCCACTCTTATGGCACCAACATATAAGAACTTGCACC TGATGCATATAATAATCAGATTGAATATGAA CACAGAGCACCAGAGTGCCGTCTGGGTCTGAAGGAAGG CCGTCCATTCTCAGGGGTCCTGTCATGTTTGG ACTTCTGTGCTCATGCCCACAGAGACTTGCACAACATGC AGAATGGCAGCACATTGGTATGCACTCTCAC TAGAGAAGACAATCGAGAATTTGGAGGAAAACCTGAGG ATGAGCAGCTTCACGTTCTGCCTTTATACAAA GTCTCTGACGTGGATGAGTTTGGGAGTGTGGAAGCTCAG GAGGAGAAAAAACGGAGTGGTGCCATTTCAGG TACTGAGTTCTTTTCGGCGAAAAGTCAGGATGTTAGCAG AGCCAGTCAAGACTTGCCGACAAAGGAACT AGAAGCCAAGAAAGCTGCAGCTGAAAAGCTTTCCTCCCT GGAGAACAGCTCAAATAAAAATGAAAAGGAA AAGTCAGCCCCATCACGTACAAAACAACTGAAAACGC AAGCCAGGCTAAACAGTTGGCAGAACTTTTGC GACTTTCAGGACCAGTCATGCAGCAGTCCCAGCAGCCCC AGCCTCTACAGAAGCAGCCACCACAGCCCCA GCAGCAGCAGAGACCCAGCAGCAGCAGCCACATCACC CTCAGACAGAGTCTGTCAACTCTTATTCTGCT TCTGGATCCACCAATCCATACATGAGACGGCCCAATCCA GTTAGTCCTTATCCAACTCTTCACACACTT CAGATATCTATGGAAGCACCAGCCCTATGAACTTCTATT CCACCTCATCTCAAGCTGCAGGTTTCATATT
--	--	---

		GAATTCTTCTAATCCCATGAACCCTTACCCTGGGCTTTTG AATCAGAATACCCAATATCCATCATATCAA TGCAATGGAAACCTATCAGTGGACAACCTGCTCCCCATAT CTGGGTTCTTATTCTCCCCAGTCTCAGCCGA TGGATCTGTATAGGTATCCAAGCCAAGACCCTCTGTCTA AGCTCAGTCTACCACCCATCCATACACTTTA CCAGCCAAGGTTTGGAAATAGCCAGAGTTTACATCTAA ATACTTAGGTTATGGAAACCAAAATATGCAG GGAGATGGTTTCAGCAGTTGTACCATTAGACCAAATGTA CATCATGTAGGGAAATTGCCTCCTTATCCCA CTCATGAGATGGATGGCCACTTCATGGGAGCCACCTCTA GATTACCACCCAATCTGAGCAATCCAAACAT GGACTATAAAAAATGGTGAACATCATTACCTTCTCACAT AATCCATAACTACAGTGCAGCTCCGGGGCATG TTCAACAGCTCTCTTCATGCCCTGCATCTCCAAAACAAG GAGAATGACATGCTTTCCACACAGCTAATG GGTTATCAAAGATGCTTCCAGCTCTTAACCATGATAGAA CTGCTTGTGTCCAAGGAGGCTTACACAAATT AAGTGATGCTAATGGTCAGGAAAAGCAGCCATTGGCACT AGTCCAGGGTGTGGCTTCTGGTGCAGAGGAC AACGATGAGGTCTGGTCAGACAGCGAGCAGAGCTTTCTG GATCCTGACATTGGGGGAGTGGCCGTGGCTC CAACTCATGGGTCAATTCTCATTGAGTGTGCAAAGCGTG AGCTGCATGCCACAACCCCTTTAAAGAATCC CAATAGGAATCACCCACCAGGATCTCCCTCGTCTTTTAC CAGCATAAGAGCATGAATGAGCCAAAACAT GGCTTGGCTCTTTGGGAAGCCAAAATGGCTGAAAAAGCC CGTGAGAAAGAGGAAGAGTGTGAAAAGTATG GCCCAGACTATGTGCCTCAGAAATCCCATGGCAAAAAAG TGAAACGGGAGCCTGCTGAGCCACATGAAAC TTCAGAGCCCACTTACCTGCGTTTCATCAAGTCTCTTGCC GAAAGGACCATGTCCGTGACCACAGACTCC ACAGTAACTACATCTCCATATGCCTTCACTCGGGTCACA GGGCCTTACAACAGATATATATGATATCACC CCCTTTTGTGTTGGTTACCTCACTTGAAAAGACCACAACCA ACCTGTCAGTAGTATAGTTCTCATGACGTGG GCAGTGGGGAAAGGTCACAGTATTCATGACAAATGTGGT GGGAAAAACCTCAGCTCACCAGCAACAAAAG AGGTTATCTTACCATAGCACTTAATTTTCACTGGCTCCCA AGTGGTCACAGATGGCATCTAGGAAAAGAC CAAAGCATTCTATGCAAAAAGAAGGTGGGGGAAGAAAGT GTTCCGCAATTTACATTTTAAACACTGGTTC TATTATTGGACGAGATGATATGTAAATGTGATCCCCCCC CCCCGCTTACAACCTCTACACATCTGTGACCA CTTTTAATAATATCAAGTTTGCATAGTCATGGAACACAA ATCAAACAAGTACTGTAGTATTACAGTGACA GGAATCTTAAAATACCATCTGGTGCTGAATATATGATGT ACTGAAATACTGGAATTATGGCTTTTTTGAAA TGCAGTTTTTACTGTAATCTTAACTTTTATTTATCAAAAT AGCTACAGGAAACATGAATAGCAGGAAAAC ACTGAATTTGTTTGGATGTTCTAAGAAATGGTGCTAAGA AAATGGTGTCTTTAATAGCTAAAAATTTAAT GCCTTTATATCATCAAGATGCTATCAGTGTACTCCAGTGC CCTTGAATAATAGGGGTACCTTTTCATTCA AGTTTTTATCATAATTACCTATTCTTACACAAGCTTAGTT
--	--	---

	TTTAAAATGTGGACATTTTAAAGGCCTCTG GATTTTGCTCATCCAGTGAAGTCCTTGTAGGACAATAAA CGTATATATGTACATATATACACAAACATGT ATATGTGCACACACATGTATATGTATAAATATTTTAAAT GGTGTTTTAGAAGCACTTTGTCTACCTAAGC TTTGACAACCTTGAACAATGCTAAGGTACTGAGATGTTTA AAAAACAAGTTTACTTTTCATTTTAGAATGCA AAGTTGATTTTTTTAAGGAAACAAAGAAAGCTTTTAAAA TATTTTGTCTTTTAGCCATGCATCTGCTGAT GAGCAATTGTGTCCATTTTAAACACAGCCAGTTAAATCC ACCATGGGGCTTACTGGATTCAAGGGAATAC GTTAGTCCACAAAACATGTTTTCTGGTGCTCATCTCACAT GCTATACTGTAAAACAGTTTTTATACAAAAT TGTATGACAAGTTCATTGCTCAAAAATGTACAGTTTTTAA GAATTTTCTATTAAGTGCAGGTAATAATTAG CTGCATGCTGCAGACTCAACAAAGCTAGTTCAGTGAAGC CTATGCTATTTTATGGATCATAGGCTCTTCA GAGAACTGAATGGCAGTCTGCCTTTGTGTTGATAATTAT GTACATTGTGACGTTGTCATTTCTTAGCTTA AGTGTCCCTCTTTAACAAGAGGATTGAGCAGACTGATGCC TGCATAAGATGAATAAACAGGGTTAGTTCCA TGTGAATCTGTCAGTTAAAAAGAAACAAAAACAGGCAG CTGGTTTGCTGTGGTGGTTTTAAATCATTAAT TTGTATAAGAAGTGAAAGAGTTGTATAGTAAATTAAAT TGTAACAAAACCTTTTTTAATGCAATGCTTT AGTATTTTAGTACTGTAAAAAATTAAATATATACATAT ATATATATATATATATATATATATATATGAG TTTGAAGCAGAATTCACATCATGATGGTGCTACTCAGCC TGCTACAAATATATCATAATGTGAGCTAAGA ATTCATTAAATGTTTGAGTGATGTTCCCTACTTGTCATATA CCTCAACACTAGTTTGGCAATAGGATATTG AACTGAGAGTGAAAGCATTGTGTACCATCATTTTTTTTCCA AGTCCTTTTTTTTTATTGTTAAAAAAG CATACCTTTTTTCAATACTTGATTTCTTAGCAAGTATAAC TTGAACTTCAACCTTTTTGTTCTAAAAATT CAGGGATATTCAGCTCATGCTCTCCCTATGCCAACATGT CACCTGTGTTTATGTAAAATTGTTGTAGGT TAATAAATATATTCTTTGTCAGGGATTAAACCCTTTTATT TTGAATCCCTTCTATTTTACTTGTACATGT GCTGATGTAACATAAACTAATTTTGTAATCTGTTGGCTC TTTTTATTGTAAAGAAAAGCATTTTAAAAG TTTGAGGAATCTTTTGACTGTTTCAAGCAGGAAAAA ATTACATGAAAATAGAATGCACTGAGTTGAT AAAGGGAAAAATTGTAAGGCAGGAGTTTGGCAAGTGGC TGTTGGCCAGAGACTTACTTGTAACCTCTCTAA ATGAAGTTTTTTTGATCCTGTAATCACTGAAGGTACATAC TCCATGTGGACTTCCCTTAAACAGGCAAAC ACCTACAGGTATGGTGTGCAACAGATTGTACAATTACAT TTTGGCCTAAATACATTTTGTCTTACTAGTA TTTAAAATAAATTCTTAATCAGAGGAGGCCTTTGGGTTTT ATTGGTCAAATCTTTGTAAGCTGGCTTTTG TCTTTTTAAAAAATTTCTTGAATTTGTGGTTGTGTCCAAT TTGCAACATTTCCAAAAATGTTTGCTTTG CTTACAAACCACATGATTTTAATGTTTTTTGTATACCATA ATATCTAGCCCCAACATTTGATTACTACA
--	---

		TGTGCATTGGTGATTTTGTATCATCCATTCTTAATATTTGA TTTCTGTGTACCTACTGTCAATTTGTTAAA CTGCTGGCCAACAAGAACAGGAAGTATAGTTTGGGGGGT TGGGGAGAGTTTACATAAGGAAGAGAAGAAA TTGAGTGGCATATTGTAAATATCAGATCTATAATTGTAA ATATAAACCTGCCTCAGTTAGAATGAATGG AAAGCAGATCTACAATTTGCTAATATAGGAATATCAGGT TGACTATATAGCCATACTTGAAAATGCTTCT GAGTGGTGTCAACTTTACTTGAATGAATTTTTTCATCTTGA TTGACGCACAGTGATGTACAGTTCACCTTCT GAAGCTAGTGGTTAACTTGTGTAGGAACTTTTGCAGTT TGACACTAAGATAACTTCTGTGTGCATTTTT CTATGCTTTTTTTAAAACTAGTTTCATTTTCATTTTCATGA GATGTTTGGTTTATAAGATCTGAGGATGGT TATAAATACTGTAAGTATTGTAATGTTATGAATGCAGGT TATTTGAAAGCTGTTTATTATTATATCATTC CTGATAATGCTATGTGAGTGTTTTTAATAAAATTTATATT TATTTAATGCACTCTAA
PREDICTED: Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant X2, mRNA [SEQ ID NO: 953]	XM_006714 242.2	GTAGAGAAGCAGAAGGAAGCAAGATGGCTGCCCTTTAG GATTTGTTAGAAAGGAGACCCGACTGCAACTG CTGGATTGCTGCAAGGCTGAGGGACGAGAACGAGGCTG GCAAACATTCAGCAGCACACCCTCTCAAGATT GTTTACTTGCCTTTGCTCCTGTTGAGTTACAACGCTTGGA AGCAGGAGATGGGCTCAGCAGCAGCCAATA GGACATGATCCAGGAAGAGCAGTAAGGGACTGAGCTGC TGAATTCAACTAGAGGGCAGCCTTGTGGATGG CCCCGAAGCAAGCCTGATGGAACAGGATAGAACCAACC ATGTTGAGGGCAACAGACTAAGTCCATTCTG ATACCATCACCTCCCATTTGCCAGACAGAACCTCTGGCT ACAAAGCTCCAGAATGGAAGCCCACTGCCTG AGAGAGCTCATCCAGAAGTAAATGGAGACACCAAGTGG CACTCTTTCAAAGTTATTATGGAATACCCTG TATGAAGGGAAGCCAGAATAGTCGTGTGAGTCCTGACTT TACACAAGAAAGTAGAGGGTATTCCAAGTGT TTGCAAAATGGAGGAATAAAACGCACAGTTAGTGAACCT TCTCTCTCTGGGCTCCTTCAGATCAAGAAAT TGAAACAAGACCAAAAGGCTAATGGAGAAAGACGTAAC TTCGGGGTAAGCCAAGAAAGAAATCCAGGTGA AAGCAGTCAACCAAATGTCTCCGATTTGAGTGATAAGAA AGAATCTGTGAGTTCTGTAGCCCAAGAAAAT GCAGTTAAAGATTTACCCAGTTTTTCAACACATAACTGC AGTGGGCCTGAAAATCCAGAGCTTCAGATTC TGAATGAGCAGGAGGGGAAAAGTGCTAATTACCATGAC AAGAACATTGTATTACTTAAAAACAAGGCAGT GCTAATGCCTAATGGTGCTACAGTTTCTGCCTCTTCCGTG GAACACACACATGGTGAACCTCCTGGAAAAA ACACTGTCTCAATATTATCCAGATTGTGTTTCCATTGCGG TGCAGAAAACCATCTCACATAAATGCCA TTAACAGTCAGGCTACTAATGAGTTGTCCTGTGAGATCA CTCACCCATCGCATACCTCAGGGCAGATCAA TTCCGCACAGACCTCTAACTCTGAGCTGCCTCCAAAGCC AGCTGCAGTGGTGAGTGAGGCCTGTGATGCT GATGATGCTGATAATGCCAGTAAACTAGCTGCAATGCTA AATACCTGTTCTTTTCAGAAACCAGAACAAAC

		TACAACAACAAAAATCAGTTTTTTGAGATATGCCCATCTC CTGCAGAAAATAACATCCAGGGAACCACAAA GCTAGCGTCTGGTGAAGAATTCTGTTTCAGGTTCCAGCAG CAATTTGCAAGCTCCTGGTGGCAGCTCTGAA CGGTATTTAAAACAAAATGAAATGAATGGTGCTTACTTC AAGCAAAGCTCAGTGTTCACTAAGGATTTCCT TTTCTGCCACTACCACACCACCACCATCACAATTGCT TCTTTCTCCCCCTCCTCCTCTTCCACAGGT TCCTCAGCTTCCTTCAGAAGGAAAAAGCACTCTGAATGG TGGAGTTTTAGAAGAACACCACCCTACCCC AACCAAAGTAACACAACACTTTTAAGGGAAGTGAAAAT AGAGGGTAAACCTGAGGCACCACCTTCCCAGA GTCCTAATCCATCTACACATGTATGCAGCCCTTCTCCGAT GCTTTCTGAAAGGCCTCAGAATAATTGTGT GAACAGGAATGACATACAGACTGCAGGGACAATGACTG TTCCATTGTGTTCTGAGAAAACAAGACCAATG TCAGAACACCTCAAGCATAACCCACCAATTTTTGGTAGC AGTGGAGAGCTACAGGACAACCTGCCAGCAGT TGATGAGAAACAAAGAGCAAGAGATTCTGAAGGGTCGA GACAAGGAGCAAACACGAGATCTTGTGCCCCC AACACAGCACTATCTGAAACCAGGATGGATTGAATTGAA GGCCCCCTCGTTTTTACCAAGCGGAATCCCAT CTAAAACGTAATGAGGCATCACTGCCATCAATTCTTCAG TATCAACCCAATCTCTCCAATCAAATGACCT CCAAACAATACACTGGAAATTCCAACATGCCTGGGGGGC TCCAAGGCAAGCTTACACCCAGAAAACAAC ACAGCTGGAGCACAAAGTCACAAATGTACCAAGTTGAAAT GAATCAAGGGCAGTCCCAAGGTACAGTGGAC CAACATCTCCAGTTCCAAAAACCCTCACACCAGGTGCAC TTCTCCAAAACAGACCATTTACCAAAAAGCTC ATGTGCAGTCACTGTGTGGCACTAGATTTTCATTTTCAACA AAGAGCAGATTCCCAAACCTGAAAAACTTAT GTCCCCAGTGTTGAAACAGCACTTGAATCAACAGGCTTC AGAGACTGAGCCATTTTCAAACCTCACACCTT TTGCAACATAAGCCTCATAAACAGGCAGCACAAACACA ACCATCCCAGAGTTCACATCTCCCTCAAACCC AGCAACAGCAGCAAAAATTACAAATAAAGAATAAAGAG GAAATACTCCAGACTTTTCTCACCACCCCAAAG CAACAATGATCAGCAAAGAGAAGGATCATTCTTTGGCCA GACTAAAGTGGAAGAATGTTTTTCATGGTGAA AATCAGTATTCAAATCAAGCGAGTTCGAGACTCATAAT GTCCAAATGGGACTGGAGGAAGTACAGAATA TAAATCGTAGAAATTCCCCTTATAGTCAGACCATGAAAT CAAGTGCAATGCAAAATACAGGTTTCTTGTTT AAACAATACACACCTAGTTTCAGAGAATAAAGAACAGA CTACACATCCTGAACTTTTTGCAGGAAACAAG ACCCAAAACCTTGCATCACATGCAATATTTTCCAAATAAT GTGATCCCAAAGCAAGATCTTCTTCACAGGT GCTTTCAAGAACAGGAGCAGAAGTCACAACAAGCTTCA GTTCTACAGGGATATAAAAATAGAAACCAAGA TATGTCTGGTCAACAAGCTGCGCAACTTGCTCAGCAAAG GTACTTGATACATAACCATGCAAATGTTTTT CCTGTGCCTGACCAGGGAGGAAGTCACACTCAGACCCCT CCCCAGAAGGACACTCAAAGCATGCTGCTC TAAGGTGGCATCTCTTACAGAAGCAAGAACAGCAGCAA
--	--	--

		ACACAGCAACCCCCAAACTGAGTCTTGCCATAG TCAGATGCACAGGCCAATTAAGGTGGAACCTGGATGCAA GCCACATGCCTGTATGCACACAGCACCACCA GAAAACAAAACATGGAAAAAGGTAAC TAAGCAAGAGAA TCCACCTGCAAGCTGTGATAATGTGCAGCAAA AGAGCATCATTGAGACCATGGAGCAGCATCTGAAGCAGT TTCACGCCAAGTCGTTATTTGACCATAAGGC TCTTACTCTCAAATCACAGAAGCAAGTAAAAGTTGAAAT GTCAGGGGCCAGTCACAGTTTTTGACTAGACAA ACCACTGCTGCAGAACTTGATAGCCACACCCCAGCTTTA GAGCAGCAAACAACCTTCTTCAGAAAAGACAC CAACCAAAAAGAACAGCTGCTTCTGTTCTCAATAATTTTAT AGAGTCACCTTCCAAATTACTAGATACTCC TATAAAAAATTTATTGGATACACCTGTCAAGACTCAATA TGATTTCCCATCTTGCAGATGTGTAGGTTTG GACAGAAGGGTAAAGCTATTAGGATTGAAAGAGTCATCT ATACTGGTAAAGAAGGCCAAAAGTTCTCAGGG ATGTCCTATTGCTAAGTGGGAGAACTTGCGCCTGTCAGG GGCTGGATCCAGAAACCTGTGGTGCCTCCTT CTCTTTTGGTTGTTTCATGGAGCATGTACTACAATGGATGT AAGTTTGCCAGAAGCAAGATCCCAAGGAAG TTTAAGCTGCTTGGGGATGACCCAAAAGAGGAAGAGAA ACTGGAGTCTCATTGTGCAAAACCTGTCCACTC TTATGGCACCAACATATAAGAACTTGCACCTGATGCAT ATAATAATCAGATTGAATATGAACACAGAGC ACCAGAGTGCCGTCTGGGTCTGAAGGAAGGCCGTCCATT CTCAGGGGGTCACTGCATGTTTGGACTTCTGT GCTCATGCCCACAGAGACTTGCACAACATGCAGAATGGC AGCACATTGGTATGCACTCTCACTAGAGAAG ACAATCGAGAATTTGGAGGAAAACCTGAGGATGAGCAG CTTCACGTTCTGCCTTTATACAAAGTCTCTGA CGTGGATGAGTTTGGGAGTGTGGAAGCTCAGGAGGAGA AAAAACGGAGTGGTGCCATTCAGGTACTGAGT TCTTTTCGGCGAAAAGTCAGGATGTTAGCAGAGCCAGTC AAGACTTGCCGACAAAGGAACTAGAAAGCCA AGAAAGCTGCAGCTGAAAAGCTTTCCTCCCTGGAGAACA GCTCAAATAAAAAATGAAAAGGAAAAGTCAGC CCCATCACGTACAAAACAACTGAAAACGCAAGCCAGG CTAAACAGTTGGCAGAACTTTTGCGACTTTCA GGACCAGTCATGCAGCAGTCCCAGCAGCCCCAGCCTCTA CAGAAGCAGCCACCACAGCCCCAGCAGCAGC AGAGACCCCAGCAGCAGCAGCCACATCACCTCAGACA GAGTCTGTCAACTCTTATTCTGCTTCTGGATC CACCAATCCATACATGAGACGGCCCAATCCAGTTAGTCC TTATCCAACTCTTCACACACTTCAGATATC TATGGAAGCACCAGCCCTATGAACTTCTATTCCACCTCAT CTCAAGCTGCAGGTTTCATATTTGAATTCTT CTAATCCCATGAACCCTTACCCTGGGCTTTTGAATCAGA ATACCCAATATCCATCATATCAATGCAATGG AAACCTATCAGTGGACAACCTGCTCCCCATATCTGGGTTC CTATTCTCCCCAGTCTCAGCCGATGGATCTG TATAGGTATCCAAGCCAAGACCCTCTGTCTAAGCTCAGT CTACCACCCATCCATACACTTTACCAGCCAA GGTTTGGAAATAGCCAGAGTTTTACATCTAAATACTTAG GTTATGGAAACCAAAAATATGCAGGGAGATGG
--	--	--

	TTTCAGCAGTTGTACCATTAGACCAAATGTACATCATGT AGGGAAATTGCCTCCTTATCCCACCTCATGAG ATGGATGGCCACTTCATGGGAGCCACCTCTAGATTACCA CCCAATCTGAGCAATCCAAACATGGACTATA AAAATGGTGAACATCATTACCTTCTCACATAATCCATA ACTACAGTGCAGCTCCGGGCATGTTCAACAG CTCTCTTCATGCCCTGCATCTCCAAAACAAGGAGAATGA CATGCTTTCCACACAGCTAATGGGTTATCA AAGATGCTTCCAGCTCTTAACCATGATAGAACTGCTTGT GTCCAAGGAGGCTTACACAAATTAAGTGATG CTAATGGTCAGGAAAAGCAGCCATTGGCACTAGTCCAGG GTGTGGCTTCTGGTGCAGAGGACAACGATGA GGTCTGGTCAGACAGCGAGCAGAGCTTTCTGGATCCTGA CATTGGGGGAGTGGCCGTGGCTCCAACCTCAT GGGTCAATTCTCATTGAGTGTGCAAAGCGTGAGCTGCAT GCCACAACCCCTTTAAAGAATCCCAATAGGA ATCACCCCACCAGGATCTCCCTCGTCTTTTACCAGCATAA GAGCATGAATGAGCCAAAACATGGCTTGGC TCTTTGGGAAGCCAAAATGGCTGAAAAAGCCCGTGAGA AAGAGGAAGAGTGTGAAAAGTATGGCCCAGAC TATGTGCCTCAGAAATCCCATGGCAAAAAGTGAAACGG GAGCCTGCTGAGCCACATGAAACTTCAGAGC CCACTTACCTGCGTTTCATCAAGTCTCTTGCCGAAAGGAC CATGTCCGTGACCACAGACTCCACAGTAAC TACATCTCCATATGCCTTCACTCGGGTCACAGGGCCTTAC AACAGATATATATGATATCACCCCCTTTTG TTGGTTACCTCACTTGAAAAGACCACAACCAACCTGTCA GTAGTATAGTTCTCATGACGTGGGCAGTGGG GAAAGGTCACAGTATTCATGACAAATGTGGTGGGAAAA ACCTCAGCTCACCAGCAACAAAAGAGGTTATC TTACCATAGCACTTAATTTTCACTGGCTCCCAAGTGGTCA CAGATGGCATCTAGGAAAAGACCAAAGCAT TCTATGCAAAAAGAAGGTGGGGAAGAAAGTGTTCCGCA ATTTACATTTTAAACACTGGTTCTATTATTG GACGAGATGATATGTAAATGTGATCCCCCCCCCGCTT ACAACCTCTACACATCTGTGACCACCTTTTAAT AATATCAAGTTTGCATAGTCATGGAACACAAATCAAACA AGTACTGTAGTATTACAGTGACAGGAATCTT AAAATACCATCTGGTGCTGAATATATGATGTACTGAAAT ACTGGAATTATGGCTTTTTGAAATGCAGTTT TACTGTAATCTTAACCTTTTATTTATCAAAATAGCTACAG GAAACATGAATAGCAGGAAAACACTGAATT TGTTTGGATGTTCTAAGAAATGGTGCTAAGAAAATGGTG TCTTTAATAGCTAAAAATTTAATGCCTTTAT ATCATCAAGATGCTATCAGTGTACTCCAGTGCCCTTGAA TAATAGGGGTACCTTTTCATTCAAGTTTTTA TCATAATTACCTATTCTTACACAAGCTTAGTTTTTAAAT GTGGACATTTTAAAGGCCTCTGGATTTTGC TCATCCAGTGAAGTCCTTGTAGGACAATAAACGTATATA TGTACATATATACACAAACATGTATATGTGC ACACACATGTATATGTATAAATATTTTAAATGGTGTTTTA GAAGCACTTTGTCTACCTAAGCTTTGACAA CTTGAACAATGCTAAGGTACTGAGATGTTTAAAAAACAA GTTTACTTTTCATTTTAGAATGCAAAGTTGAT TTTTTTAAGGAAACAAAGAAAGCTTTTAAATATTTTGC
--	---

	TTTTAGCCATGCATCTGCTGATGAGCAATT GTGTCCATTTTAAACACAGCCAGTTAAATCCACCATGGG GCTTACTGGATTCAAGGGAATACGTTAGTCC ACAAAACATGTTTTCTGGTGCTCATCTCACATGCTATACT GTAAAACAGTTTTATACAAAATTGTATGAC AAGTTCATTGCTCAAAAATGTACAGTTTTAAGAATTTTCT ATTAAGTGCAGGTAATAATTAGCTGCATGC TGCAGACTCAACAAAGCTAGTTCAGTGAAGCCTATGCTA TTTTATGGATCATAGGCTCTTCAGAGAACTG AATGGCAGTCTGCCTTTGTGTTGATAATTATGTACATTGT GACGTTGTCATTTCTTAGCTTAAGTGTCCT CTTTAACAAGAGGATTGAGCAGACTGATGCCTGCATAAG ATGAATAAACAGGGTTAGTTCCATGTGAATC TGTCAGTTAAAAAGAAACAAAAACAGGCAGCTGGTTTGC TGTGGTGGTTTTAAATCATTAATTTGTATAA AGAAGTGAAAGAGTTGTATAGTAAATTAAATTGTAAACA AACTTTTTTAATGCAATGCTTTAGTATTTT AGTACTGTAAAAAAATTAAATATATACATATATATATAT ATATATATATATATATATATGAGTTTGAAGC AGAATTCACATCATGATGGTGCTACTCAGCCTGCTACAA ATATATCATAATGTGAGCTAAGAATTCATTA AATGTTTGAGTGATGTTCCCTACTTGTGCATATACCTCAACA CTAGTTTGGCAATAGGATATTGAACTGAGA GTGAAAGCATTGTGTACCATCATTTTTTTTCCAAGTCCTTT TTTTTATTGTTAAAAAAAAGCATAACCTT TTTTCAATACTTGATTTCTTAGCAAGTATAACTTGAACTT CAACCTTTTTGTCTAAAAAATTCAGGGATA TTTCAGCTCATGCTCTCCCTATGCCAACATGTCACCTGTG TTTATGTAAAATTGTTGTAGGTTAATAAAT ATATTCTTTGTCAGGGATTAAACCCTTTTATTTTGAATCC CTTCTATTTTACTTGTACATGTGCTGATGT AACTAAAATAATTTTGTAAATCTGTTGGCTCTTTTTTATT GTAAAGAAAAGCATTTTTAAAAGTTTGAGGA ATCTTTTGACTGTTTCAAGCAGGAAAAAAAATTACATG AAAATAGAATGCACTGAGTTGATAAAGGGAA AAATTGTAAGGCAGGAGTTTGGCAAGTGGCTGTTGGCCA GAGACTTACTTGTAACCTCTCTAAATGAAGTT TTTTTGATCCTGTAATCACTGAAGGTACATACTCCATGTG GACTTCCCTTAAACAGGCAAACACCTACAG GTATGGTGTGCAACAGATTGTACAATTACATTTTGGCCT AAATACATTTTGTCTTACTAGTATTTAAAAT AAATTCTTAATCAGAGGAGGCCTTTGGGTTTTATTGGTCA AATCTTTGTAAGCTGGCTTTTGTCTTTTAA AAAAATTTCTTGAATTTGTGGTTGTGTCCAATTTGCAAAC ATTTCCAAAAATGTTTGCTTTGCTTACAAA CCACATGATTTTAATGTTTTTTGTATACCATAATATCTAG CCCCAAACATTTGATTACTACATGTGCATT GGTGATTTTGATCATCCATTCTTAATATTTGATTTCTGTG TCACCTACTGTCATTTGTAAACTGCTGGC CAACAAGAACAGGAAGTATAGTTTGGGGGGTGGGGAG AGTTTACATAAGGAAGAGAAGAAATTGAGTGG CATATTGTAAATATCAGATCTATAATTGTAAATATAAAA CCTGCCTCAGTTAGAATGAATGGAAAGCAGA TCTACAATTTGCTAATATAGGAATATCAGGTTGACTATAT AGCCATACTTGAAAATGCTTCTGAGTGGTG
--	---

		TCAACTTTACTTGAATGAATTTTTTCATCTTGATTGACGCA CAGTGATGTACAGTTCACCTTCTGAAGCTAG TGGTTAACTTGTGTAGGAACTTTTGCAGTTTGACACTAA GATAACTTCTGTGTGCATTTTTCTATGCTT TTTTAAAACTAGTTTCATTTTCATTTTCATGAGATGTTTG GTTTATAAGATCTGAGGATGGTTATAAATA CTGTAAGTATTGTAATGTTATGAATGCAGGTTATTTGAA AGCTGTTTATTATTATATCATTCTGATAAT GCTATGTGAGTGTTTTTAATAAAATTTATATTTATTTAAT GCACTCTAA
Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant 2, mRNA [SEQ ID NO: 954]	NM_017628. 4	AAACAGAAGGTGGGCCGGGGCGGGGAGAAACAGAAGCTC GGTCAATTTCCCAGTTTGTCTGGGTCTTTAAAA ATACAGGCCCTAAAGCACTAAGGGCATGCCCTCGGTGA AACAGGGGAGCGCTTCTGCTGAATGAGATTA AAGCGACAGAAAAGGGAAAGGAGAGCGCGGGCAACGG GATCTAAAGGGAGATAGAGACGCGGGCCTCTGA GGGCTGGCAAACATTCAGCAGCACACCCTCTCAAGATTG TTTACTTGCCTTTGCTCCTGTTGAGTTACAA CGCTTGGAAGCAGGAGATGGGCTCAGCAGCAGCCAATA GGACATGATCCAGGAAGAGCAGTAAGGGACTG AGCTGCTGAATTCAACTAGAGGGCAGCCTTGTGGATGGC CCCGAAGCAAGCCTGATGGAACAGGATAGAA CCAACCATGTTGAGGGCAACAGACTAAGTCCATTCCTGA TACCATCACCTCCCATTGTCAGACAGAAACC TCTGGCTACAAAGCTCCAGAATGGAAGCCCCTGCCTGA GAGAGCTCATCCAGAAGTAAATGGAGACACC AAGTGGCACTCTTTCAAAGTTATTATGGAATACCCTGT ATGAAGGGAAGCCAGAATAGTCGTGTGAGTC CTGACTTTACACAAGAAAGTAGAGGGTATTCCAAGTGTT TGCAAAATGGAGGAATAAAACGCACAGTTAG TGAACCTTCTCTCTCTGGGCTCCTTCAGATCAAGAAATTG AAACAAGACCAAAAGGCTAATGGAGAAAGA CGTAACTTCGGGGTAAGCCAAGAAAGAAATCCAGGTGA AAGCAGTCAACCAAATGTCTCCGATTTGAGTG ATAAGAAAGAATCTGTGAGTTCTGTAGCCCAAGAAAATG CAGTTAAAGATTTACCAGTTTTTTCAACACA TAACTGCAGTGGGCCTGAAAATCCAGAGCTTCAGATTCT GAATGAGCAGGAGGGGAAAAGTGCTAATTAC CATGACAAGAACATTGTATTACTTAAAAACAAGGCAGTG CTAATGCCTAATGGTGCTACAGTTTCTGCCT CTTCCGTGGAACACACACATGGTGAACCTCCTGGAAAAAA CACTGTCTCAATATTATCCAGATTGTGTTTC CATTGCGGTGCAGAAAACCACATCTCACATAAATGCCAT TAACAGTCAGGCTACTAATGAGTTGTCCTGT GAGATCACTACCCATCGCATACCTCAGGGCAGATCAAT TCCGCACAGACCTCTAACTCTGAGCTGCCTC CAAAGCCAGCTGCAGTGGTGAGTGAGGCCTGTGATGCTG ATGATGCTGATAATGCCAGTAACTAGCTGC AATGCTAAATACCTGTTCTTTTCAGAAACCAGAACAACT ACAACAACAAAATCAGTTTTTTGAGATATGC CCATCTCCTGCAGAAAATAACATCCAGGGAACCACAAAG CTAGCGTCTGGTGAAGAATTCTGTTTCAGGTT CCAGCAGCAATTTGCAAGCTCCTGGTGGCAGCTCTGAAC GGTATTTAAACAAAATGAAATGAATGGTGTC

		TTACTTCAAGCAAAGCTCAGTGTTCACTAAGGATTCCTTT TCTGCCACTACCACACCACCACCACCATCA CAATTGCTTCTTTCTCCCCCTCCTCCTTCCACAGGTTCC TCAGCTTCCTTCAGAAGGAAAAAGCACTC TGAATGGTGGAGTTTTAGAAAGAACACCACCCTACCCCA ACCAAAGTAACACAACACTTTTAAGGGAAGT GAAAATAGAGGGTAAACCTGAGGCACCACCTTCCCAGA GTCCTAATCCATCTACACATGTATGCAGCCCT TCTCCGATGCTTTCTGAAAGGCCTCAGAATAATTGTGTG AACAGGAATGACATACAGACTGCAGGGACAA TGACTGTTCCATTGTGTTCTGAGAAAACAAGACCAATGT CAGAACACCTCAAGCATAACCCACCAATTTT TGGTAGCAGTGGAGAGCTACAGGACAACCTGCCAGCAGTT GATGAGAAACAAAGAGCAAGAGATTCTGAAG GGTCGAGACAAGGAGCAAACACGAGATCTTGTGCCCCC AACACAGCACTATCTGAAACCAGGATGGATTG AATTGAAGGCCCTCGTTTTTCACCAAGCGGAATCCCATC TAAAACGTAATGAGGCATCACTGCCATCAAT TCTTCAGTATCAACCCAATCTCTCCAATCAAATGACCTCC AAACAATACACTGGAAATTCCAACATGCCT GGGGGGCTCCCAAGGCAAGCTTACACCCAGAAAACAAC ACAGCTGGAGCACAAGTCACAAATGTACCAAG TTGAAATGAATCAAGGGCAGTCCCAAGGTACAGTGGACC AACATCTCCAGTTCCAAAAACCCTCACACCA GGTGCACCTTCTCCAAAACAGACCATTTACCAAAAGCTCA TGTGCAGTCACTGTGTGGCACTAGATTTTCAT TTTCAACAAAGAGCAGATTCCCAAACCTGAAAACTTATG TCCCCAGTGTTGAAACAGCACTTGAATCAAC AGGCTTCAGAGACTGAGCCATTTTCAAACCTCACACCTTTT GCAACATAAGCCTCATAAACAGGCAGCACA AACACAACCATCCCAGAGTTTACATCTCCCTCAAAACCA GCAACAGCAGCAAAAATTACAAATAAAGAAT AAAGAGGAAATACTCCAGACTTTTCCTCACCCCCAAAGC ACAATGATCAGCAAAGAGAAGGATCATTCT TTGGCCAGACTAAAGTGGAAGAATGTTTTTCATGGTGAAA ATCAGTATTCAAAATCAAGCGAGTTCGAGAC TCATAATGTCCAAATGGGACTGGAGGAAGTACAGAATAT AAATCGTAGAAATTCCCCTTATAGTCAGACC ATGAAATCAAGTGCATGCAAAATACAGGTTTCTTGTTCA ACAATACACACCTAGTTTCAGAGAATAAAG AACAGACTACACATCCTGAACTTTTTGCAGGAAACAAGA CCCAAACTTGCATCACATGCAATATTTTCC AAATAATGTGATCCCAAAGCAAGATCTTCTTCACAGGTG CTTTCAAGAACAGGAGCAGAAGTCACAACAA GCTTCAGTTCTACAGGGATATAAAAATAGAAACCAAGAT ATGTCTGGTCAACAAGCTGCGCAACTTGCTC AGCAAAGGTACTTGATACATAACCATGCAAATGTTTTTC CTGTGCCTGACCAGGGAGGAAGTCACACTCA GACCCCTCCCCAGAAGGACACTCAAAGCATGCTGCTCT AAGGTGGCATCTCTTACAGAAGCAAGAACAG CAGCAAACACAGCAACCCCAAACCTGAGTCTTGCCATAGT CAGATGCACAGGCCAATTAAGGTGGAACCTG GATGCAAGCCACATGCCTGTATGCACACAGCACCACCAG AAAACAAAACATGGAAAAAGGTAACCTAAGCA AGAGAATCCACCTGCAAGCTGTGATAATGTGCAGCAAAA
--	--	---

		GAGCATCATTGAGACCATGGAGCAGCATCTG AAGCAGTTTTCACGCCAAGTCGTTATTTGACCATAAGGCT CTTACTCTCAAATCACAGAAGCAAGTAAAAG TTGAAATGTCAGGGCCAGTCACAGTTTTGACTAGACAAA CCACTGCTGCAGAACTTGATAGCCACACCCC AGCTTTAGAGCAGCAAACAACCTTCTTCAGAAAAGACACC AACCAAAAGAACAGCTGCTTCTGTTCTCAAT AATTTTATAGAGTCACCTTCCAAATTACTAGATACTCCTA TAAAAAATTTATTGGATACACCTGTCAAGA CTCAATATGATTTCCCATCTTGCAGATGTGTAGGTAAGTG CCAGAAATGTACTGAGACACATGGCGTTTA TCCAGAATTAGCAAATTTATCTTCAGATATGGGATTTTCC TTCTTTTTTTTAAATCTTGAGTCTGGCAGCA ATTTGTAAAGGCTCATAAAAATCTGAAGCTTACATTTTTT GTCAAGTTACCGATGCTTGTGTCTTGTGAA AGAGAAGTTCACTTACATGCAGTTTTTCCAAAAGAATTA AATAATCGTGCATGTTTATTTTTCCCTCTCT TCAGATCCTGTAAAATTTGAATGTATCTGTTTTAGATCAA TTCGCCTATTTAGCTCTTTGTATATTATCT CCTGGAGAGACAGCTAGGCAGCAAAAAACAATCTATT AAAATGAGAAAATAACGACCATAGGCAGTCTA ATGTACGAACTTTAAATATTTTTTAATTCAAGGTAAAATA TATTAGTTTCAAGATTTCTGGCTAATAG GGAAATTATTATCTTCAGTCTTCATGAGTTGGGGGAAAT GATAATGCTGACACTCTTAGTGCTCCTAAAG TTTCCTTTTCTCCATTTATACATTTGGAATGTTGTGATTTA TATTCATTTTGATTCCCTTTTCTCTAAAA TTTCATCTTTTTTGATTAAAAAATATGATACAGGCATACCT CAGAGATATTGTGGGTTTGGCTCCATACCA CAATAAAATGAATATTACAATAAAGCAAGTTGTAAGGAC TTTTTGGTTTCTCACTGTATGTAAAAGTTAT TTATATACTATACTGTAACTACTAAGTGTGCAATAGCA TTGTGTCTAAAAAATATATACTTTAAAAAATA ATTTATTGTTAAAAAAATGCCAACAATTATCTGGGCCTTT AGTGAGTGCTAATCTTTTTGCTGGTGGAGG GTCGTGCTTCAGTATTGATCGCTGTGGACTGATCATGGTG GTAGTTGCTGAAGGTTGCTGGGATGGCTGT GTGTGTGGCAATTTCTTAAAATAAGACAACAGTGAAGTG CTGTATCAATTGATTTTTCCATTACAAAAG ATTTCTCTGTAGCATGCAATGCTGTTTGATAGCATTTAAC CCACAGCAGAATTTCTTTGAAAATTGGACT CAGTCCTCTCAAACCTGTGCTGCTGCTTTATCAACTAAGTT TTTGTAATTTTCTGAATCCTTTGTTGTCAT TTCAGCAGTTTACAGCATCTTCATTGGAAGTATATTCCAT CTCAAACATTCTTTGTTTCATCCATAAGAAG CAACTTCTTATCAAGTTTTTTTCATGACATTGCAGTAACTC AGCCCCATCTTCAGGCTCTACTTCTAATTC TGGTTCTCTTGCTACATCTCCCTCATCTGCAGTGACCTCT CCACGGAAGTCTTGAACCTCCTCAAAGTAAT CCATGAGGGTTGGAATCAACTTCTAAACTCCTGTTAATG TTGATATATTGACCCCCTCCCATGAATTATG AATGTTCTTAATAACTTCTAAATGGTGATACCTTTCCAGA AGGCTTTCAATGTACTTTGCCCGGATCCAT CAGAAGACTATCTTGGCAGCTGTAGACTAACAATATATT TCTTAAATGATAAGACTTGAAAGTCAAAAGT
--	--	--

		ACTCCTTAATCCATAGGCTGCAGAATCAATGTTGTATTA ACAGGCACGAAAACAGCATTAAATCTTGTGCA TCTCCATCGGAGCTCTTGGGTGACTAGGTGCCTTGAGCA GTAATATTTTGAAAGGAGGTTTTGGTTTTGT TTTTGTTTTTTTTTTTTGTTTTTTAGCAGTAAGTCTCAAC ACTGGGCTTAAAATATTCAGTAAACTATG TTGTAAAAAGATGTGTTATCATCCAGACTTTGTTGTTCCA TTA CTCTACACAAGCAGGGTACACTTAGCA TAATTCTTAAGGGCCTTGGAATTTTCAGAATGGTAAATG AGTATGGGCTTCAACTTAAAATCATCAACTG CATTAGCCTGTAACAAGAGAGTCAGCCTGTCCTTTGAAG CAAGGCATTGACTTCTATCTATGAAAGTCTT AGATGGCACCTTGTTTCAATAGTAGGCTGTTTAGTACAG CCACCTTCATCAGTGATCTTAGCTAGATCTT CTGCATAACTTGCTGCAGCTTCTACATCAGCACTTGCTGC CTCACCTTGTCCTTTTATGTTATAGAGACA GCTGCGCTTCTTAACTTTATAAACCAACTTCTGCTAGCT TCCA ACTTCTCTTCTGCAGCTTCCTCATTC TCTTCATAGAACTGAAGGGAGTCAAGGCCTTGCTCTGGA TTAAGCTTTGGCTTAAGGAATGTTGTGGCTG ACGTGATCTTCTATCCAGACCACTAAAGCGCTCTCCATAT CAGCAATAAGGCCGTTTTGCTTTCTTACCT TTCATGTGTTCACTGGAGTAATTTCTTCAAGAATTTTTC CTTTACATTCACAACTTGGCTAACTGGCAT GCAAGGCCTAGCTTTCAGCCTGTCTTGGCTTTTGACATGC CTTCTCACTTAGCTCGTCATATCTAGCTT TTGATTTAAAGTGGCAGGCATACAACTCTTCTTCACTT GAACACTTAGAGGCCACTGTAGGGTTATTA ATTGGCCTAATTTCAATATTGTTGTGTTTTAGGGAATAGA GAGGCCCAGGGAGAGGGAGAGAGCCCAAAC GGCTGGTTGATAGAGCAGGCAGAATGCACACAACATTTA TCAGATTATGTTTGCACCATTACCAGATTA TGGGTACGGTTTGTGGCACCCCCCAA AATTAGAATAGT AACATCAAAGATCACTGATCACAGATCGCCA TAACATAAATAATAATAAACTTTAAAATACTGTGAGAAT TACCAA AATGTGATACAGAGACATGAAGTGA GCACATGCTGTTGAAAAAAATGACACTGATAGACATACT TAACACGTGGGATTGCCACAAACCTTCAGTT TGTA AAAGTCACAGTAACTGTGACTCACAAAAGAACAA AGCACAATAAAACGAGGTATGCCTGTATTTTT AAAAAAAGCTTTTTGT TAAAATTCAGGATATGTAATAGG TCTGTAGGAATAGTGAAATATTTTTGCTGAT GGATGTAGATATATACGTGGATAGAGATGAAGATCTTAA TTATAGCTATGCAGCATAGATTTAGTCAAAG ACATTTGAAAAGACAAATGT TAAATTAGTGTGGCTAATG ACCTACCCGTGCCATGTTTTCCCTCTTGCAA TGAGATACCCACACTGTGTAGAAGGATGGAGGGAGGA CTCCTACTGTCCCTCTTTGCGTGTGGTTATTA AGTTGCCTCACTGGGCTAAAACACCACACATCTCATAGA TAATATTTGGTAAGTTGTAATCGTCTTCACT CTTCTCTTATCACCCACCCCTATCTTCCCACTTTTCCATCT TTGTTGGTTTGCAACAGCCCCCTTCTTTTT GCCTGACTCTCCAGGATTTTCTCTCATCATAAATTGTTCT AAAGTACATACTAATATGGGTCTGGATTGA CTATTCTTATTTGCAAAACAGCAATTAAATGTTATAGGG
--	--	--

		AAGTAGGAAGAAAAAGGGGTATCCTTGACAA TAAACCAAGCAATATTCTGGGGGTGGGATAGAGCAGGA AATTTTATTTTAAATCTTTTAAAATCCAAGTA ATAGGTAGGCTTCCAGTTAGCTTTAAATGTTTTTTTTTC CAGCTCAAAAAAATTGGATTGTAGTTGATAC TACATATAATACATTCTAATTCCCTCACTGTATTCTTTGT TTAGTTTCATTTATTTGGTTTAAAATAATT TTTTATCCCATATCTGAAATGTAATATATTTTTATCCAAC AACCAGCATGTACATATACTTAATTATGTG GCACATTTTCTAATAGATCAGTCCATCAATCTACTCATTT TAAAGAAAAAAAATTTTAAAGTCACTTTT AGAGCCCTTAATGTGTAGTTGGGGGTAAAGCTTTGTGGA TGTAGCCTTTATATTTAGTATAATTGAGGTC TAAAATAATAATCTTCTATTATCTCAACAGAGCAAATTA TTGAAAAAGATGAAGGTCCTTTTTATACCCA TCTAGGAGCAGGTCCTAATGTGGCAGCTATTAGAGAAAT CATGGAAGAAAGGTAATTAACGCAAAGGCAC AGGGCAGATTAACGTTTATCCTTTTGTATATGTCAGAATT TTCCAGCCTTCACACACAAAGCAGTAAAC AATTGTAAATTGAGTAATTATTAGTAGGCTTAGCTATTCT AGGGTTGCCAACACTACACACTGTGCTATT CACCAGAGAGTCACAATATTTGACAGGACTAATAGTCTG CTAGCTGGCACAGGCTGCCCCTTTGCGATG GATGCCAGAAAACCCAGGCATGAACAGGAATCGGCCAG CCAGGCTGCCAGCCACAAGGTACTGGCACAGG CTCCAACGAGAGGTCCCCTCTGGCTTTCCACCTGATA ATAAAGTGTCAAAGCAGAAAGACTGGTAAAG TGTGGTATAAGAAAAGAACCCTGAATTAAATTCACCTA GTGTTGCAAATGAGTACTTATCTCTAAGTTT TCTTTTACCATAAAAAGAGAGCAAGTGTGATATGTTGAA TAGAAAGAGAAACATACTATTTACAGCTGCC TTTTTTTTTTTTTTTCGCTATCAATCACAGGTATACAAGTA CTTGCCTTTACTCCTGCATGTAGAAGACT CTTATGAGCGAGATAATGCAGAGAAGGCCTTTCATATAA ATTTATACAGCTCTGAGCTGTTCTTCTTCTA GGGTGCCTTTTTCATTAAGAGGTAGGCAGTATTATTATTA AAGTACTTAGGATACATTGGGGCAGCTAGGA CATATTCAGTATCATTCTTGCTCCATTTCCAAATTATTCA TTTCTAAATTAGCATGTAGAAGTTCATAA ATAATCATCTAGTGGCCTGGCAGAAATAGTGAATTTCCC TAAGTGCCTTTTTTTTGTGTTTTTTTTGTGTTT TGTTTTTTAAACAAGCAGTAGGTGGTGCTTTGGTCATAA GGGAAGATATAGTCTATTTCTAGGACTATTC CATATTTTCCATGTGGCTGGATACTAACTATTTGCCAGCC TCCTTTTCTAAATTGTGAGACATTCTTGGA GGAACAGTTCTAACTAAAATCTATTATGACTCCCCAAGT TTTAAAATAGCTAAATTTAGTAAGGGAAAAA ATAGTTTATGTTTTAGAAGACTGAACTTAGCAAATAAC CTGAATTTTGTGCTTTGTGAAATTTTATATC GAAATGAGCTTTCCCATTTTACCCACATGTAATTTACAA AATAGTTCATTACAATTATCTGTACATTTT GATATTGAGGAAAAACAAGGCTTAAAAACCATTATCCAG TTTGCTTGGCGTAGACCTGTTTAAAAAATAA
--	--	---

		TAAACCGTTCATTTCTCAGGATGTGGTCATAGAATAAAG TTATGCTCAAATGTTCAAATATTTAAA
PREDICTED: Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant X9, mRNA [SEQ ID NO: 955]	XM_011532 044.1	TCAGGCTCTACTTCTAATTCTGGTTCTCTTGCTACATCTC CCTCATCTGCAGTGACCTCTCCACGGAAGT CTTGAACCTCTCAAAGCAAATTATTGAAAAAGATGAAG GTCCTTTTTATACCCATCTAGGAGCAGGTCC TAATGTGGCAGCTATTAGAGAAATCATGGAAGAAAGGTT TGGACAGAAGGGTAAAGCTATTAGGATTGAA AGAGTCATCTATACTGGTAAAGAAGGCAAAAGTTCTCAG GGATGTCCTATTGCTAAGTGGGTGGTTTCGCA GAAGCAGCAGTGAAGAGAAGCTACTGTGTTTGGTGCGG GAGCGAGCTGGCCACACCTGTGAGGCTGCAGT GATTGTGATTCTCATCCTGGTGTGGGAAGGAATCCCGCT GTCTCTGGCTGACAACTCTACTCGGAGCTT ACCGAGACGCTGAGGAAATACGGCACGCTCACCAATCG CCGGTGTGCCTTGAATGAAGAGAGAACTTGCG CCTGTCAGGGGCTGGATCCAGAAACCTGTGGTGCCTCCT TCTCTTTTGGTTGTTTCATGGAGCATGTACTA CAATGGATGTAAGTTTGCCAGAAGCAAGATCCCAAGGA AGTTTAAGCTGCTTGGGGATGACCCAAAAGAG GAAGAGAAACTGGAGTCTCATTTGCAAAACCTGTCCACT CTTATGGCACCAACATATAAGAAACTTGCAC CTGATGCATATAATAATCAGATTGAATATGAACACAGAG CACCAGAGTGCCGTCTGGGTCTGAAGGAAGG CCGTCCATTCTCAGGGGTCCTGCATGTTTGGACTTCTGT GCTCATGCCACAGAGACTTGCACAACATG CAGAATGGCAGCACATTGGTATGCACTCTCACTAGAGAA GACAATCGAGAATTTGGAGGAAAACCTGAGG ATGAGCAGCTTCACGTTCTGCCTTTATACAAAGTCTCTGA CGTGGATGAGTTTGGGAGTGTGGAAGCTCA GGAGGAGAAAAAACGGAGTGGTGCCATTCAGGTACTGA GTTCTTTTCGGCGAAAAGTCAGGATGTTAGCA GAGCCAGTCAAGACTTGCCGACAAAGGAACTAGAAAGC CAAGAAAGCTGCAGCTGAAAAGCTTTCCTCCC TGGAGAACAGCTCAAATAAAAATGAAAAGGAAAAGTCA GCCCCATCACGTACAAAACAACTGAAAACGC AAGCCAGGCTAAACAGTTGGCAGAACTTTTGCGACTTTC AGGACCAGTCATGCAGCAGTCCCAGCAGCCC CAGCCTCTACAGAAGCAGCCACCACAGCCCCAGCAGCA GCAGAGACCCCAGCAGCAGCAGCCACATCACC CTCAGACAGAGTCTGTCAACTCTTATTCTGCTTCTGGATC CACCAATCCATACATGAGACGGCCCAATCC AGTTAGTCCTTATCCAAACTCTTCACACACTTCAGATATC TATGGAAGCACCAGCCCTATGAACTTCTAT TCCACCTCATCTCAAGCTGCAGGTTCATATTTGAATTCTT CTAATCCCATGAACCTTACCCTGGGCTTT TGAATCAGAATACCCAATATCCATCATATCAATGCAATG GAAACCTATCAGTGGACAACCTGCTCCCCATA TCTGGGTTCCTATTCTCCCCAGTCTCAGCCGATGGATCTG TATAGGTATCCAAGCCAAGACCTCTGTCT AAGCTCAGTCTACCACCCATCCATACACTTTACCAGCCA AGGTTTGGAAATAGCCAGAGTTTTACATCTA AATACTTAGGTTATGGAAACCAAAATATGCAGGGAGATG

		GTTTCAGCAGTTGTACCATTAGACCAAATGT ACATCATGTAGGGAAATTGCCTCCTTATCCCACATGA GATGGATGGCCACTTCATGGGAGCCACCTCT AGATTACCACCCAATCTGAGCAATCCAAACATGGACTAT AAAAATGGTGAACATCATTACCTTCTCACA TAATCCATAACTACAGTGCAGCTCCGGGCATGTTCAACA GCTCTCTTCATGCCCTGCATCTCCAAAACAA GGAGAATGACATGCTTTCCACACAGCTAATGGGTTATC AAAGATGCTTCCAGCTCTTAACCATGATAGA ACTGCTTGTGTCCAAGGAGGCTTACACAAATTAAGTGAT GCTAATGGTCAGGAAAAGCAGCCATTGGCAC TAGTCCAGGGTGTGGCTTCTGGTGCAGAGGACAACGATG AGGTCTGGTCAGACAGCGAGCAGAGCTTTCT GGATCCTGACATTGGGGGAGTGGCCGTGGCTCCAACCTCA TGGGTCAATTCTCATTGAGTGTGCAAAGCGT GAGCTGCATGCCACAACCCCTTTAAAGAATCCCAATAGG AATCACCCCACCAGGATCTCCCTCGTCTTTT ACCAGCATAAGAGCATGAATGAGCCAAAACATGGCTTG GCTCTTTGGGAAGCCAAAATGGCTGAAAAAGC CCGTGAGAAAGAGGAAGAGTGTGAAAAGTATGGCCCAG ACTATGTGCCTCAGAAATCCCATGGCAAAAAA GTGAAACGGGAGCCTGCTGAGCCACATGAAACTTCAGA GCCCACTTACCTGCGTTTCATCAAGTCTCTTG CCGAAAGGACCATGTCCGTGACCACAGACTCCACAGTAA CTACATCTCCATATGCCTTCACTCGGGTCAC AGGGCCTTACAACAGATATATATGATATCACCCCCTTTT GTTGGTTACCTCACTTGAAAAGACCACAACC AACCTGTCAGTAGTATAGTTCTCATGACGTGGGCAGTGG GGAAAGGTCACAGTATTCATGACAAATGTGG TGGGAAAAACCTCAGCTCACCAGCAACAAAAGAGGTTA TCTTACCATAGCACTTAATTTTCACTGGCTCC CAAGTGGTCACAGATGGCATCTAGGAAAAGACCAAAGC ATTCTATGCAAAAAGAAGGTGGGGAAGAAAGT GTTCCGCAATTTACATTTTAAACACTGGTTCTATTATTG GACGAGATGATATGTAAATGTGATCCCCC CCCCCGCTTACAACCTCTACACATCTGTGACCACTTTTAAT AATATCAAGTTTGCATAGTCATGGAACACA AATCAAACAAGTACTGTAGTATTACAGTGACAGGAATCT TAAATACCATCTGGTGCTGAATATATGATG TACTGAAATACTGGAATTATGGCTTTTTTGAAATGCAGTTT TACTGTAATCTTAACTTTTATTTATCAA ATAGCTACAGGAAACATGAATAGCAGGAAAACACTGAA TTTGTTTGGATGTTCTAAGAAATGGTGCTAAG AAAATGGTGTCTTTAATAGCTAAAAATTTAATGCCTTTAT ATCATCAAGATGCTATCAGTGTACTCCAGT GCCCTTGAATAATAGGGGTACCTTTTCATTCAAGTTTTTA TCATAATTACCTATTCTTACACAAGCTTAG TTTTTAAAATGTGGACATTTTAAAGGCCTCTGGATTTTGC TCATCCAGTGAAGTCCTTGTAAGGACAATAA ACGTATATATGTACATATATACACAAACATGTATATGTG CACACACATGTATATGTATAAATATTTTAAA TGGTGTTTTAGAAGCACTTTGTCTACCTAAGCTTTGACAA CTTGAACAATGCTAAGGTACTGAGATGTTT AAAAACAAGTTTACTTTTATTTTAGAAATGCAAAGTTGA TTTTTTTAAAGGAAACAAAGAAAGCTTTTAAA
--	--	---

		ATATTTTGTCTTTTAGCCATGCATCTGCTGATGAGCAATT GTGTCCATTTTAAACACAGCCAGTTAAATC CACCATGGGGCTTACTGGATTCAAGGGAATACGTTAGTC CACAAAACATGTTTTCTGGTGCTCATCTCAC ATGCTATACTGTAAAACAGTTTTATACAAAATTGTATGA CAAGTTCATTGCTCAAAAATGTACAGTTTTA AGAATTTTCTATTAAGTGCAGGTAATAATTAGCTGCATG CTGCAGACTCAACAAAGCTAGTTCCTACTGAAG CCTATGCTATTTTATGGATCATAGGCTCTTCAGAGAACTG AATGGCAGTCTGCCTTTGTGTTGATAATTA TGTACATTGTGACGTTGTCATTTCTTAGCTTAAGTGTCCT CTTTAACAAGAGGATTGAGCAGACTGATGC CTGCATAAGATGAATAAACAGGGTTAGTTCCATGTGAAT CTGTCAGTTAAAAAGAAACAAAAACAGGCAG CTGGTTTGCTGTGGTGGTTTTAAATCATTAATTTGTATAA AGAAGTGAAAGAGTTGTATAGTAAATTA TTGTAAACAAAACCTTTTTTAATGCAATGCTTTAGTATTTT AGTACTGTAAAAAAATTAATATATACATA TATATATATATATATATATATATATATATGAGTTTGAAGC AGAATTCACATCATGATGGTGCTACTCAGC CTGCTACAAATATATCATAATGTGAGCTAAGAATTCATT AAATGTTTGAGTGATGTTCCCTACTTGTCATA TACCTCAACACTAGTTTGGCAATAGGATATTGAAGTGAAG AGTGAAAGCATTGTGTACCATCATTTTTTTTC CAAGTCCTTTTTTTTATTGTTAAAAAAAAGCATACTT TTTTCAATACTTGATTTCTTAGCAAGTATA ACTTGAAGTTCAACCTTTTTGTTCTAAAAATTCAGGGATA TTTCAGCTCATGCTCTCCCTATGCCAACAT GTCACCTGTGTTTATGTAAAATTGTTGTAGGTTAATAAAT ATATTCTTTGTCAGGGATTAAACCTTTTA TTTTGAATCCCTTCTATTTTACTTGTACATGTGCTGATGT AACTAAAATAATTTTGTAATCTGTTGGC TCTTTTTATTGTAAAGAAAAGCATTTTTAAAAGTTTGAGG AATCTTTTGACTGTTTCAAGCAGGAAAAAAA AATTACATGAAAATAGAATGCACTGAGTTGATAAAGGG AAAAATTGTAAGGCAGGAGTTTGGCAAGTGCC TGTTGGCCAGAGACTTACTTGTAAGTCTCTAAATGAAGTT TTTTTGATCCTGTAATCACTGAAGGTACAT ACTCCATGTGGACTTCCCTTAAACAGGCAAACACCTACA GGTATGGTGTGCAACAGATTGTACAATTACA TTTTGGCCTAAATACATTTTTGCTTACTAGTATTAAAAT AAATTCTTAATCAGAGGAGGCCTTTGGGTT TTATTGGTCAAATCTTTGTAAGCTGGCTTTTGTCTTTTTA AAAAATTTCTTGAATTTGTGGTTGTGTCCA ATTTGCAAACATTTCCAAAAATGTTTGCTTTGCTTACAAA CCACATGATTTTAATGTTTTTTGTATACCA TAATATCTAGCCCCAACATTTGATTACTACATGTGCATT GGTGATTTTGATCATCCATTCTTAATATTT GATTTCTGTGTCACCTACTGTCATTTGTTAAACTGCTGGC CAACAAGAACAGGAAGTATAGTTTGGGGGG TTGGGGAGAGTTTACATAAGGAAGAGAAGAAATTGAGT GGCATATTGTAAATATCAGATCTATAATTGTA AATATAAACCTGCCTCAGTTAGAATGAATGGAAAGCAG ATCTACAATTTGCTAATATAGGAATATCAGG TTGACTATATAGCCATACTTGAAAATGCTTCTGAGTGGT
--	--	---

		GTCAACTTTACTTGAATGAATTTTTTCATCTT GATTGACGCACAGTGATGTACAGTTCACTTCTGAAGCTA GTGGTTAACTTGTGTAGGAACTTTTGCAGT TTGACACTAAGATAACTTCTGTGTGCATTTTTCTATGCTT TTTTAAAACTAGTTTCATTTTCATTTTCAT GAGATGTTTGGTTTATAAGATCTGAGGATGGTTATAAAT ACTGTAAGTATTGTAATGTTATGAATGCAGG TTATTTGAAAGCTGTTTATTATTATATCATTCTGATAAT GCTATGTGAGTGTTTTTAATAAAATTTATA TTTATTTAATGCACTCTAA
PREDICTED: Homo sapiens tet methylcytosine dioxygenase 2 (TET2), transcript variant X7, mRNA [SEQ ID NO: 956]	XM_011532 043.1	GTAGAGAAGCAGAAGGAAGCAAGATGGCTGCCCTTTAG GATTTGTTAGAAAGGAGACCCGACTGCAACTG CTGGATTGCTGCAAGGCTGAGGGACGAGAACGAGGCTG GCAAACATTCAGCAGCACACCCTCTCAAGATT GTTTACTTGCCTTTGCTCCTGTTGAGTTACAACGCTTGGA AGCAGGAGATGGGCTCAGCAGCAGCCAATA GGACATGATCCAGGAAGAGCAGTAAGGGACTGAGCTGC TGAATTCAACTAGAGGGCAGCCTTGTGGATGG CCCCGAAGCAAGCCTGATGGAACAGGATAGAACCAACC ATGTTGAGGGCAACAGACTAAGTCCATTCTG ATACCATCACCTCCCATTTGCCAGACAGAACCTCTGGCT ACAAAGCTCCAGAATGGAAGCCCCTGCCTG AGAGAGCTCATCCAGAAGTAAATGGAGACACCAAGTGG CACTCTTTCAAAGTTATTATGGAATACCCTG TATGAAGGGAAGCCAGAATAGTCGTGTGAGTCCTGACTT TACACAAGAAAGTAGAGGGTATTCCAAGTGT TTGCAAAATGGAGGAATAAAACGCACAGTTAGTGAACCT TCTCTCTCTGGGCTCCTTCAGATCAAGAAAT TGAAACAAGACCAAAAAGGCTAATGGAGAAAGACGTAAC TTCGGGGTAAGCCAAGAAAGAAATCCAGGTGA AAGCAGTCAACCAAATGTCTCCGATTTGAGTGATAAGAA AGAATCTGTGAGTTCTGTAGCCCAAGAAAAT GCAGTTAAAGATTTACCCAGTTTTTTCAACACATAACTGC AGTGGGCCTGAAAATCCAGAGCTTCAGATTC TGAATGAGCAGGAGGGGAAAAGTGCTAATTACCATGAC AAGAACATTGTATTACTTAAAAACAAGGCAGT GCTAATGCCTAATGGTGCTACAGTTTCTGCCTCTTCCGTG GAACACACACATGGTGAACCTCCTGGAAAAA ACACTGTCTCAATATTATCCAGATTGTGTTTCCATTGCGG TGCAGAAAACCACATCTCACATAAATGCCA TTAACAGTCAGGCTACTAATGAGTTGTCCTGTGAGATCA CTCACCCATCGCATACCTCAGGGCAGATCAA TTCCGCACAGACCTCTAACTCTGAGCTGCCTCCAAAGCC AGCTGCAGTGGTGAGTGAGGCCTGTGATGCT GATGATGCTGATAATGCCAGTAAACTAGCTGCAATGCTA AATACCTGTTCTTTTCAGAAACCAGAACAAAC TACAACAACAAAAATCAGTTTTTTGAGATATGCCCATCTC CTGCAGAAAATAACATCCAGGGAACCAAAA GCTAGCGTCTGGTGAAGAATTCTGTTTCAGGTTCCAGCAG CAATTTGCAAGCTCCTGGTGGCAGCTCTGAA CGGTATTTAAAACAAAATGAAATGAATGGTGCTTACTTC AAGCAAAGCTCAGTGTTCACTAAGGATTCCT TTTCTGCCACTACCACACCACCACCACCATCACAATTGCT TCTTTCTCCCCCTCCTCCTCTTCCACAGGT

		TCCTCAGCTTCCTTCAGAAGGAAAAAGCACTCTGAATGG TGGAGTTTTAGAAAGAACACCACCCTACCCC AACCAAAGTAACACAACACTTTTAAGGGAAGTGAAAAT AGAGGGTAAACCTGAGGCACCACCTTCCCAGA GTCCTAATCCATCTACACATGTATGCAGCCCTTCTCCGAT GCTTTCTGAAAGGCCTCAGAATAATTGTGT GAACAGGAATGACATACAGACTGCAGGGACAATGACTG TTCCATTGTGTTCTGAGAAAACAAGACCAATG TCAGAACACCTCAAGCATAACCCACCAATTTTTGGTAGC AGTGGAGAGCTACAGGACAACCTGCCAGCAGT TGATGAGAAACAAAGAGCAAGAGATTCTGAAGGGTCGA GACAAGGAGCAAACACGAGATCTTGTGCCCCC AACACAGCACTATCTGAAACCAGGATGGATTGAATTGAA GGCCCCCTCGTTTTTCACCAAGCGGAATCCCAT CTAAAACGTAATGAGGCATCACTGCCATCAATTCTTCAG TATCAACCCAATCTCTCCAATCAAATGACCT CCAAACAATACACTGGAAATTCCAACATGCCTGGGGGGC TCCCAAGGCAAGCTTACACCCAGAAAACAAC ACAGCTGGAGCACAAGTCACAAATGTACCAAGTTGAAAT GAATCAAGGGCAGTCCCAAGGTACAGTGGAC CAACATCTCCAGTTCCAAAAACCCTCACACCAGGTGCAC TTCTCCAAAACAGACCATTTACCAAAAAGCTC ATGTGCAGTCACTGTGTGGCACTAGATTTTCATTTTCAACA AAGAGCAGATTCCCAAACCTGAAAAACTTAT GTCCCCAGTGTTGAAACAGCACTTGAATCAACAGGCTTC AGAGACTGAGCCATTTTCAAACCTCACACCTT TTGCAACATAAGCCTCATAAACAGGCAGCACAAACACA ACCATCCCAGAGTTACATCTCCCTCAAAACC AGCAACAGCAGCAAAAATTACAAATAAAGAATAAAGAG GAAATACTCCAGACTTTTCCTCACCCCCAAAG CAACAATGATCAGCAAAGAGAAGGATCATTCTTTGGCCA GACTAAAGTGGAAGAATGTTTTTCATGGTGAA AATCAGTATTCAAAATCAAGCGAGTTCGAGACTCATAAT GTCCAAATGGGACTGGAGGAAGTACAGAATA TAAATCGTAGAAATTCCCCTTATAGTCAGACCATGAAAT CAAGTGCATGCAAAATACAGGTTTCTTGTTT AAACAATACACACCTAGTTTCAGAGAATAAAGAACAGA CTACACATCCTGAACTTTTTGCAGGAAACAAG ACCCAAAACCTTGCATCACATGCAATATTTTCCAAATAAT GTGATCCCAAAGCAAGATCTTCTTCACAGGT GCTTTCAAGAACAGGAGCAGAAGTCACAACAAGCTTCA GTTCTACAGGGATATAAAAAATAGAAACCAAGA TATGTCTGGTCAACAAGCTGCGCAACTTGCTCAGCAAAG GTACTTGATACATAACCATGCAAATGTTTTT CCTGTGCCTGACCAGGGAGGAAGTCACACTCAGACCCCT CCCCAGAAGGACACTCAAAGCATGCTGCTC TAAGGTGGCATCTCTTACAGAAGCAAGAACAGCAGCAA ACACAGCAACCCCCAAACTGAGTCTTGCCATAG TCAGATGCACAGGCCAATTAAGGTGGAACCTGGATGCAA GCCACATGCCTGTATGCACACAGCACCACCA GAAAACAAAACATGGAAAAAGGTAAGTAAGCAAGAGAA TCCACCTGCAAGCTGTGATAATGTGCAGCAAA AGAGCATCATTGAGACCATGGAGCAGCATCTGAAGCAGT TTCACGCCAAGTCGTTATTTGACCATAAGGC TCTTACTCTCAAATCACAGAAGCAAGTAAAAGTTGAAAT
--	--	--

		GTCAGGGGCCAGTCACAGTTTTGACTAGACAA ACCACTGCTGCAGAACTTGATAGCCACACCCCAGCTTTA GAGCAGCAAACAACCTTCTTCAGAAAAGACAC CAACCAAAGAAGACAGCTGCTTCTGTTCTCAATAATTTTAT AGAGTCACCTTCCAAATTACTAGATACTCC TATAAAAAATTTATTGGATACACCTGTCAAGACTCAATA TGATTTCCCATCTTGCAGATGTGTAGAGCAA ATTATTGAAAAAGATGAAGGTCCTTTTTTATACCCATCTA GGAGCAGGTCCTAATGTGGCAGCTATTAGAG AAATCATGGAAGAAAGGTATACAAGTACTTGCCTTTACT CCTGCATGTAGAAGACTCTTATGAGCGAGAT AATGCAGAGAAGGCCTTTCATATAAATTTATACAGCTCT GAGCTGTTCTTCTTCTAGGGTGCCTTTTTCAT TAAGAGGTAGGCAGTATTATTATTAAAGTACTTAGGATA CATTGGGGCAGCTAGGACATATTCAGTATCA TTCTTGCTCCATTTCCAAATTATTCATTTCTAAATTAGCA TGTAAGAGTTCATAAATAATCATCTAGTG GCCTGGCAGAAATAGTGAATTTCCCTAAGTGCCTTTTTTT TGTTGTTTTTTTTGTTTTGTTTTTTTAAACAA GCAGTAGGTGGTGCTTTGGTCATAAGGGAAGATATAGTC TATTTCTAGGACTATTCCATATTTTCCATGT GGCTGGATACTAACTATTTGCCAGCCTCCTTTTCTAAATT GTGAGACATTCTTGGAGGAACAGTTCTAAC TAAAATCTATTATGACTCCCCAAGTTTTTAAAATAGCTAA ATTTAGTAAGGGAAAAAATAGTTTATGTTTT AGAAGACTGAACCTTAGCAAACCTGAATTTTGTGCT TTGTGAAATTTTATATCGAAATGAGCTTTCC CATTTTCACCCACATGTAATTTACAAAATAGTTCATTACA ATTATCTGTACATTTTGATATTGAGGAAAA ACAAGGCTTAAAAACCATTATCCAGTTTGCTTGGCGTAG ACCTGTTTAAAAAATAATAAACCGTTCATTT CTCAGGATGTGGTCATAGAATAAAGTTATGCTCAAATGT TCAA
--	--	--

[00122] The term “gene” or “gene sequence” is meant to refer to a genetic sequence, e.g., a nucleic acid sequence. The term “gene” is intended to encompass a complete gene sequence or a partial gene sequence. The term “gene” refers to a sequence that encodes a protein or polypeptide or a sequence that does not encode a protein or polypeptide, e.g., a regulatory sequence, leader sequence, signal sequence, intron, or other non-protein coding sequence.

The term “intron” refers to nucleic acid sequence within a gene which is noncoding for the protein expressed from said gene. Intronic sequence may be transcribed from DNA into RNA, but may be removed before the protein is expressed.

[00123] The term “exon” refers to nucleic acid sequence within a gene which encodes a protein expressed from said gene.

[00124] The term “intron-exon junction,” when used in connection with a gene editing system or gRNA molecule, refers to a sequence which includes nucleotides of an exon and nucleotides of an intron. In exemplary embodiments, an intron-exon junction is a gRNA target sequence, whereby, when recognized by a CRISPR system comprising a gRNA comprising a targeting domain complementary to the intron-exon junction target sequence, said CRISPR system modifies, e.g., produces a break, at or near the target sequence between two nucleotides of an intron. In other exemplary embodiments, an intron-exon junction is a gRNA target sequence, whereby, when recognized by a CRISPR system comprising a gRNA comprising a targeting domain complementary to the intron-exon junction target sequence, said CRISPR system modifies, e.g., produces a break, at or near the target sequence between two nucleotides of an exon. In other exemplary embodiments, an intron-exon junction is a gRNA target sequence, whereby, when recognized by a CRISPR system comprising a gRNA comprising a targeting domain complementary to the intron-exon junction target sequence, said CRISPR system modifies, e.g., produces a break, at or near the target sequence between a nucleotide of an exon and a nucleotide of an intron.

[00125] The term “a,” “an,” or “the” refers to one or to more than one of the grammatical object of the article. The term may mean “one,” “one or more,” “at least one,” or “one or more than one.” By way of example, “an element” means one element or more than one element. The term “or” means “and/or” unless otherwise stated. The term “including” or “containing” is not limiting.

[00126] The term “about” when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of $\pm 20\%$ or in some instances $\pm 10\%$, or in some instances $\pm 5\%$, or in some instances $\pm 1\%$, or in some instances $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

[00127] The term “Chimeric Antigen Receptor” or alternatively a “CAR” refers to a set of polypeptides, typically two in the simplest embodiments, which when in an immune effector cell, provides the cell with specificity for a target cell, typically a cancer cell, and with intracellular signal generation. In some embodiments, a CAR comprises at least an extracellular antigen binding domain, a transmembrane domain and a cytoplasmic signaling domain (also referred to herein as “an intracellular signaling domain”) comprising a functional signaling domain derived from a stimulatory molecule and/or costimulatory molecule as defined below. In some aspects, the set of polypeptides are contiguous with each other. In some embodiments, the set of polypeptides include a dimerization switch that, upon the

presence of a dimerization molecule, can couple the polypeptides to one another, e.g., can couple an antigen binding domain to an intracellular signaling domain. In one aspect, the stimulatory molecule is the zeta chain associated with the T cell receptor complex. In one aspect, the cytoplasmic signaling domain further comprises one or more functional signaling domains derived from at least one costimulatory molecule as defined below. In one aspect, the costimulatory molecule is chosen from the costimulatory molecules described herein, e.g., 41BB (i.e., CD137), CD27 and/or CD28. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising a functional signaling domain derived from a costimulatory molecule and a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising two functional signaling domains derived from one or more costimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect, the CAR comprises a chimeric fusion protein comprising an extracellular antigen binding domain, a transmembrane domain and an intracellular signaling domain comprising at least two functional signaling domains derived from one or more costimulatory molecule(s) and a functional signaling domain derived from a stimulatory molecule. In one aspect the CAR comprises an optional leader sequence at the amino-terminus (N-ter) of the CAR fusion protein. In one aspect, the CAR further comprises a leader sequence at the N-terminus of the extracellular antigen binding domain, wherein the leader sequence is optionally cleaved from the antigen binding domain (e.g., a scFv) during cellular processing and localization of the CAR to the cellular membrane.

[00128] A CAR that comprises an antigen binding domain (e.g., a scFv, or TCR) that targets a specific tumor marker X, such as those described herein, is also referred to as XCAR. For example, a CAR that comprises an antigen binding domain that targets CD19 is referred to as CD19CAR. As another example, a CAR that comprises an antigen binding domain that targets BCMA is referred to as a BCMA CAR.

[00129] The term “signaling domain” refers to the functional portion derived from protein which acts by transmitting information within a cell to regulate cellular activity via defined

signaling pathways, for example, by generating second messengers or functioning as effectors by responding to such messengers. In embodiments, a signaling domain refers to a variant or homolog, e.g., a functional variant or homolog, of a naturally occurring signaling domain, for example a signaling domain variant having at least about 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a naturally-occurring signaling domain.

[00130] The term “antibody,” as used herein, refers to one or more proteins or polypeptide sequence derived from an immunoglobulin molecule which specifically binds an antigen. Antibodies can be polyclonal or monoclonal, multiple or single chain, functional fragments (e.g., Fab fragments or scFv), or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be, e.g., dimers or tetramers of immunoglobulin molecules. Antibodies can be from any species or chimeric, including human or humanized antibodies.

[00131] The term “antibody fragment” refers to at least one portion of an antibody, that retains the ability to specifically interact with (e.g., by binding, steric hindrance, stabilizing/destabilizing, spatial distribution) an epitope of an antigen. In some embodiments, the antibody fragment retains an affinity for the epitope of an antigen broadly comparable to that of the intact immunoglobulin. For example, the antibody fragment may retain 80%, 85%, 90%, 95%, 99%, or more of the affinity seen with the intact immunoglobulin, as measured, e.g., by ELISA, Biacore, or other suitable assays. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, Fv fragments, scFv antibody fragments, disulfide-linked Fvs (sdFv), a Fd fragment consisting of the VH and CH1 domains, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, multi-specific antibodies formed from antibody fragments such as a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region, and an isolated CDR or other epitope binding fragments of an antibody. An antigen binding fragment can also be incorporated into single domain antibodies, maxibodies, minibodies, nanobodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, Nature Biotechnology 23:1126-1136, 2005). Antigen binding fragments can also be grafted into scaffolds based on polypeptides such as a fibronectin type III (Fn3) (see U.S. Patent No.: 6,703,199, which describes fibronectin polypeptide minibodies).

[00132] The term “scFv” refers to a fusion protein comprising at least one antibody fragment comprising a variable region of a light chain and at least one antibody fragment comprising a variable region of a heavy chain, wherein the light and heavy chain variable

regions are contiguously linked, e.g., directly or via a synthetic linker, e.g., a short flexible polypeptide linker, and capable of being expressed as a single chain polypeptide, and wherein the scFv retains the specificity of the intact antibody from which it is derived. Unless specified, as used herein an scFv may have the VL and VH variable regions in either order, e.g., with respect to the N-terminal and C-terminal ends of the polypeptide, the scFv may comprise VL-linker-VH or may comprise VH-linker-VL.

[00133] The portion of the CAR comprising an antibody or antibody fragment thereof may exist in a variety of forms where the antigen binding domain is expressed as part of a contiguous polypeptide chain including, for example, a single domain antibody fragment (sdAb), a single chain antibody (scFv), a humanized antibody or bispecific antibody (Harlow et al., 1999, In: *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, In: *Antibodies: A Laboratory Manual*, Cold Spring Harbor, New York; Houston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; Bird et al., 1988, *Science* 242:423-426). In one aspect, the antigen binding domain of a CAR composition comprises an antibody fragment. In a further aspect, the CAR comprises an antibody fragment that comprises a scFv. In another aspect, the CAR comprises a full antibody including the Fc region.

[00134] The portion of the CAR comprising a full antibody may be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), any class (e.g., IgG 1, IgG2, IgG 3, IgG4, IgA1 and IgA2) or any subclass. In some embodiments the Fc region is an IgG type constant region. In certain embodiments the Fc region of the full antibody includes an Fc region from IgG1, IgG2, IgG3, IgG4, IgA, IgA1, IgA2, IgM, IgE, IgD, and IgY, or a fragment thereof. In some embodiments the Fc region is an IgG1. The Fc region may be a native sequence Fc region, or a variant Fc region. In one embodiment, the Fc region is a human Fc region.

[00135] The portion of the CAR comprising an antibody or antibody fragment thereof may comprise the CDR sequences of an antibody coupled with human or other antibody framework sequences. The framework sequences may be the same or different from those in a starting antibody. The precise amino acid sequence boundaries of a given CDR can be determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), “*Sequences of Proteins of Immunological Interest*,” 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (“Kabat” numbering scheme), Al-Lazikani et al., (1997) *JMB* 273,927-948 (“Chothia” numbering scheme), or a combination thereof. As used herein, the term “binding domain” or “antibody molecule” refers to a protein, e.g., an

immunoglobulin chain or fragment thereof, comprising at least one immunoglobulin variable domain sequence. The term “binding domain” or “antibody molecule” encompasses antibodies and antibody fragments, as well as multispecific binding constructs. In an embodiment, an antibody molecule is a multispecific antibody molecule, e.g., it comprises a plurality of immunoglobulin variable domain sequences forming antigen-binding sites for different epitopes of antigens, when a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and at least a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, a multispecific antibody molecule is a bispecific antibody molecule. A bispecific antibody has specificity for no more than two antigens. A bispecific antibody molecule is characterized by a first immunoglobulin variable domain sequence which has binding specificity for a first epitope and a second immunoglobulin variable domain sequence that has binding specificity for a second epitope. In other embodiments, a “binding domain” or “antibody molecule” encompasses multivalent antibody molecules, e.g., it comprises a plurality of immunoglobulin variable domain sequences forming two or more antigen binding sites for the same epitope of an antigen.

[00136] The term “antibody heavy chain,” refers to the larger of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations, and which normally determines the class to which the antibody belongs.

[00137] The term “antibody light chain,” refers to the smaller of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations. Kappa (κ) and lambda (λ) light chains refer to the two major antibody light chain isotypes.

[00138] The term “recombinant antibody” refers to an antibody which is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage or yeast expression system or in any other host cell. The term also includes an antibody which has been generated by the synthesis of a DNA molecule encoding the antibody and which DNA molecule expresses an antibody protein, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using recombinant DNA or amino acid sequence technology which is available and well known in the art.

[00139] The term “antigen” or “Ag” refers to a molecule that provokes an immune response. This immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both. The term also refers to any peptide bound by an

antibody or antibody fragment thereof. The skilled artisan will understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. Furthermore, antigens can be derived from recombinant or genomic DNA. A skilled artisan will understand that any DNA, which comprises a nucleotide sequences or a partial nucleotide sequence encoding a protein that elicits an immune response therefore encodes an “antigen” as that term is used herein. Furthermore, one skilled in the art will understand that an antigen need not be encoded solely by a full length nucleotide sequence of a gene. It is readily apparent that the present disclosure includes, but is not limited to, the use of partial nucleotide sequences of more than one gene and that these nucleotide sequences are arranged in various combinations to encode polypeptides that elicit the desired immune response. Moreover, a skilled artisan will understand that an antigen need not be encoded by a “gene” at all. It is readily apparent that an antigen can be generated synthesized or can be derived from a biological sample, or might be macromolecule besides a polypeptide. Such a biological sample can include, but is not limited to a tissue sample, a tumor sample, a cell or a fluid with other biological components.

[00140] The term “anti-cancer effect” refers to a biological effect which can be manifested by various means, including but not limited to, e.g., a decrease in tumor volume, a decrease in the number of cancer cells, a decrease in the number of metastases, an increase in life expectancy, decrease in cancer cell proliferation, decrease in cancer cell survival, or amelioration of various physiological symptoms associated with the cancerous condition. An “anti-cancer effect” can also be manifested by the ability of the peptides, polynucleotides, cells and antibodies in prevention of the occurrence of cancer in the first place. The term “anti-tumor effect” refers to a biological effect which can be manifested by various means, including but not limited to, e.g., a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in tumor cell proliferation, or a decrease in tumor cell survival.

[00141] The term “autologous” refers to any material derived from the same individual into whom it is introduced.

[00142] The term “allogeneic” refers to any material derived from a different animal of the same species as the individual to whom the material is introduced. Two or more individuals are said to be allogeneic to one another when the genes at one or more loci are not identical. In some aspects, allogeneic material from individuals of the same species may be sufficiently unlike genetically to interact antigenically

[00143] The term “xenogeneic” refers to a graft derived from an animal of a different species.

[00144] The term “cancer” refers to a disease characterized by the uncontrolled growth of aberrant cells. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. Examples of various cancers are described herein and include but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer and the like. The terms “tumor” and “cancer” are used interchangeably herein, e.g., both terms encompass solid and liquid, e.g., diffuse or circulating, tumors. As used herein, the term “cancer” or “tumor” includes premalignant, as well as malignant cancers and tumors.

[00145] “Derived from” as that term is used herein, indicates a relationship between a first and a second molecule. It generally refers to structural similarity between the first molecule and a second molecule and does not connote or include a process or source limitation on a first molecule that is derived from a second molecule. For example, in the case of an intracellular signaling domain that is derived from a CD3zeta molecule, the intracellular signaling domain retains sufficient CD3zeta structure such that it has the required function, namely, the ability to generate a signal under the appropriate conditions. It does not connote or include a limitation to a particular process of producing the intracellular signaling domain, e.g., it does not mean that, to provide the intracellular signaling domain, one must start with a CD3zeta sequence and delete unwanted sequence, or impose mutations, to arrive at the intracellular signaling domain.

[00146] The phrase “disease associated with expression of a tumor antigen as described herein” includes, but is not limited to, a disease associated with expression of a tumor antigen as described herein or condition associated with cells which express a tumor antigen as described herein including, e.g., proliferative diseases such as a cancer or malignancy or a precancerous condition such as a myelodysplasia, a myelodysplastic syndrome or a preleukemia; or a noncancer-related indication associated with cells which express a tumor antigen as described herein. In one aspect, a cancer associated with expression of a tumor antigen as described herein is a hematological cancer. In one aspect, a cancer associated with expression of a tumor antigen as described herein is a solid cancer. Further diseases associated with expression of a tumor antigen described herein include, but not limited to, e.g., atypical and/or non-classical cancers, malignancies, precancerous conditions or proliferative diseases associated with expression of a tumor antigen as described herein. Non-cancer related

indications associated with expression of a tumor antigen as described herein include, but are not limited to, e.g., autoimmune disease, (e.g., lupus), inflammatory disorders (allergy and asthma) and transplantation. In some embodiments, the tumor antigen-expressing cells express, or at any time expressed, mRNA encoding the tumor antigen. In an embodiment, the tumor antigen-expressing cells produce the tumor antigen protein (e.g., wild-type or mutant), and the tumor antigen protein may be present at normal levels or reduced levels. In an embodiment, the tumor antigen-expressing cells produced detectable levels of a tumor antigen protein at one point, and subsequently produced substantially no detectable tumor antigen protein.

[00147] The term “conservative sequence modifications” refers to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody or antibody fragment containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into an antibody or antibody fragment described herein by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, one or more amino acid residues within a CAR of the disclosure can be replaced with other amino acid residues from the same side chain family and the altered CAR can be tested using the functional assays described herein.

[00148] The term “stimulation,” refers to a primary response induced by binding of a stimulatory molecule (e.g., a TCR/CD3 complex or CAR) with its cognate ligand (or tumor antigen in the case of a CAR) thereby mediating a signal transduction event, such as, but not limited to, signal transduction via the TCR/CD3 complex or signal transduction via the appropriate NK receptor or signaling domains of the CAR. Stimulation can mediate altered expression of certain molecules.

[00149] The term “stimulatory molecule,” refers to a molecule expressed by an immune cell (e.g., T cell, NK cell, B cell) that provides the cytoplasmic signaling sequence(s) that regulate

activation of the immune cell in a stimulatory way for at least some aspect of the immune cell signaling pathway. In one aspect, the signal is a primary signal that is initiated by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, and which leads to mediation of a T cell response, including, but not limited to, proliferation, activation, differentiation, and the like. A primary cytoplasmic signaling sequence (also referred to as a “primary signaling domain”) that acts in a stimulatory manner may contain a signaling motif which is known as immunoreceptor tyrosine-based activation motif or ITAM. Examples of an ITAM containing cytoplasmic signaling sequence that is of particular use includes, but is not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta (Fc Epsilon R1b), CD3 gamma, CD3 delta, CD3 epsilon, CD79a, CD79b, DAP10, and DAP12. In a specific CAR embodiment, the intracellular signaling domain in any one or more CARS of the disclosure comprises an intracellular signaling sequence, e.g., a primary signaling sequence of CD3-zeta. In a specific CAR of the disclosure, the primary signaling sequence of CD3-zeta is the sequence provided as SEQ ID NO:21, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In a specific CAR of the disclosure, the primary signaling sequence of CD3-zeta is the sequence as provided in SEQ ID NO: 24, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00150] The term “antigen presenting cell” or “APC” refers to an immune system cell such as an accessory cell (e.g., a B-cell, a dendritic cell, and the like) that displays a foreign antigen complexed with major histocompatibility complexes (MHC's) on its surface. T-cells may recognize these complexes using their T-cell receptors (TCRs). APCs process antigens and present them to T-cells.

[00151] An “intracellular signaling domain,” as the term is used herein, refers to an intracellular portion derived from a molecule, e.g., a stimulatory or costimulatory molecule. The intracellular signaling domain generates a signal that promotes an immune effector function of the CAR containing cell, e.g., a CART cell. Examples of immune effector function, e.g., in a CART cell, include cytolytic activity and helper activity, including the secretion of cytokines.

[00152] In an embodiment, the intracellular signaling domain can comprise a primary intracellular signaling domain. Exemplary primary intracellular signaling domains include those derived from the molecules responsible for primary stimulation, or antigen dependent stimulation. In an embodiment, the intracellular signaling domain can comprise a costimulatory

intracellular domain. Exemplary costimulatory intracellular signaling domains include those derived from molecules responsible for costimulatory signals, or antigen independent stimulation. For example, in the case of a CART, a primary intracellular signaling domain can comprise a cytoplasmic sequence of a T cell receptor, and a costimulatory intracellular signaling domain can comprise cytoplasmic sequence from co-receptor or costimulatory molecule.

[00153] A primary intracellular signaling domain can comprise a signaling motif which is known as an immunoreceptor tyrosine-based activation motif or ITAM. Examples of ITAM containing primary cytoplasmic signaling sequences include, but are not limited to, those derived from CD3 zeta, common FcR gamma (FCER1G), Fc gamma RIIa, FcR beta (Fc Epsilon R1b), CD3 gamma, CD3 delta, CD3 epsilon, CD79a, CD79b, DAP10, and DAP12.

[00154] The term “zeta” or alternatively “zeta chain”, “CD3-zeta” or “TCR-zeta” is defined as the protein provided as GenBan Acc. No. BAG36664.1, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, and a “zeta stimulatory domain” or alternatively a “CD3-zeta stimulatory domain” or a “TCR-zeta stimulatory domain” is defined as the amino acid residues from the cytoplasmic domain of the zeta chain, or functional derivatives thereof, that are sufficient to functionally transmit an initial signal necessary for T cell activation. In one aspect the cytoplasmic domain of zeta comprises residues 52 through 164 of GenBank Acc. No. BAG36664.1 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like, that are functional orthologs thereof. In one aspect, the “zeta stimulatory domain” or a “CD3-zeta stimulatory domain” is the sequence provided as SEQ ID NO: 21. In one aspect, the “zeta stimulatory domain” or a “CD3-zeta stimulatory domain” is the sequence provided as SEQ ID NO: 24.

[00155] The term “costimulatory molecule” refers to a cognate binding partner on a T cell that specifically binds with a costimulatory ligand, thereby mediating a costimulatory response by the T cell, such as, but not limited to, proliferation. Costimulatory molecules are cell surface molecules other than antigen receptors or their ligands that are contribute to an efficient immune response. Costimulatory molecules include, but are not limited to an MHC class I molecule, BTLA and a Toll ligand receptor, as well as OX40, CD27, CD28, CDS, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), and 4-1BB (CD137). Further examples of such costimulatory molecules include CDS, ICAM-1, GITR, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD160, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D,

ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, NKG2C, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, and a ligand that specifically binds with CD83.

[00156] A costimulatory intracellular signaling domain can be the intracellular portion of a costimulatory molecule. A costimulatory molecule can be represented in the following protein families: TNF receptor proteins, Immunoglobulin-like proteins, cytokine receptors, integrins, signaling lymphocytic activation molecules (SLAM proteins), and activating NK cell receptors. Examples of such molecules include CD27, CD28, 4-1BB (CD137), OX40, GITR, CD30, CD40, ICOS, BAFFR, HVEM, ICAM-1, lymphocyte function-associated antigen-1 (LFA-1), CD2, CDS, CD7, CD287, LIGHT, NKG2C, NKG2D, SLAMF7, NKp80, NKp30, NKp44, NKp46, CD160, B7-H3, and a ligand that specifically binds with CD83, and the like.

[00157] The intracellular signaling domain can comprise the entire intracellular portion, or the entire native intracellular signaling domain, of the molecule from which it is derived, or a functional fragment or derivative thereof.

[00158] The term “4-1BB” refers to a member of the TNFR superfamily with an amino acid sequence provided as GenBank Acc. No. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like; and a “4-1BB costimulatory domain” is defined as amino acid residues 214-255 of GenBank Acc. No. AAA62478.2, or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like. In one aspect, the “4-1BB costimulatory domain” is the sequence provided as SEQ ID NO: 16 or the equivalent residues from a non-human species, e.g., mouse, rodent, monkey, ape and the like.

[00159] “Immune effector cell,” as that term is used herein, refers to a cell that is involved in an immune response, e.g., in the promotion of an immune effector response. Examples of immune effector cells include T cells, e.g., alpha/beta T cells and gamma/delta T cells, B cells, natural killer (NK) cells, natural killer T (NKT) cells, mast cells, and myeloid-derived phagocytes.

[00160] “Immune effector function or immune effector response,” as that term is used herein, refers to function or response, e.g., of an immune effector cell, that enhances or promotes an immune attack of a target cell. E.g., an immune effector function or response refers a property of a T or NK cell that promotes killing or the inhibition of growth or proliferation, of a target cell. In the case of a T cell, primary stimulation and co-stimulation are examples of immune effector function or response.

[00161] The term “encoding” refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (e.g., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene, cDNA, or RNA, encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

[00162] Unless otherwise specified, a “nucleotide sequence encoding an amino acid sequence” includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase nucleotide sequence that encodes a protein or an RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

[00163] The term “effective amount” or “therapeutically effective amount” are used interchangeably herein, and refer to an amount of a compound, formulation, material, or composition, as described herein effective to achieve a particular biological result.

[00164] The term “endogenous” refers to any material from or produced inside an organism, cell, tissue or system.

[00165] The term “exogenous” refers to any material introduced from or produced outside an organism, cell, tissue or system.

[00166] The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by a promoter.

[00167] The term “transfer vector” refers to a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of

a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term “transfer vector” includes an autonomously replicating plasmid or a virus. The term should also be construed to further include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, a polylysine compound, liposome, and the like. Examples of viral transfer vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

[00168] The term “expression vector” refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, including cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

[00169] The term “homologous” or “identity” refers to the subunit sequence identity between two polymeric molecules, e.g., between two nucleic acid molecules, such as, two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit; e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous or identical at that position. The homology between two sequences is a direct function of the number of matching or homologous positions; e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (e.g., 9 of 10), are matched or homologous, the two sequences are 90% homologous.

[00170] “Humanized” forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies and antibody fragments thereof are human immunoglobulins (recipient antibody or antibody fragment) in which one or more, e.g., all six, complementary-determining regions (CDRs) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv

framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, a humanized antibody/antibody fragment can comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences as long as the same antigen specificity is retained. These modifications can further refine and optimize antibody or antibody fragment performance. In general, the humanized antibody or antibody fragment thereof will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or a significant portion of the FR regions are those of a human immunoglobulin sequence. The humanized antibody or antibody fragment can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature*, 321: 522-525, 1986; Reichmann et al., *Nature*, 332: 323-329, 1988; Presta, *Curr. Op. Struct. Biol.*, 2: 593-596, 1992.

[00171] “Fully human” refers to an immunoglobulin, such as an antibody or antibody fragment, where the whole molecule is of human origin or consists of an amino acid sequence identical to a human form of the antibody or immunoglobulin.

[00172] The term “isolated” means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not “isolated,” but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is “isolated.” An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

[00173] The term “operably linked” or “transcriptional control” refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. The promoter or regulatory sequence may be a cis-acting element or a trans-acting element. Operably linked DNA sequences can be contiguous with each other and, e.g., where necessary to join two protein coding regions, are in the same reading frame.

[00174] The term “parenteral” administration of an immunogenic composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, intratumoral, or infusion techniques.

[00175] The term “nucleic acid” or “polynucleotide” refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608 (1985); and Rossolini et al., *Mol. Cell. Probes* 8:91-98 (1994)).

[00176] The terms “peptide,” “polypeptide,” and “protein” are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein’s or peptide’s sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. “Polypeptides” include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. A polypeptide includes a natural peptide, a recombinant peptide, or a combination thereof.

[00177] The term “promoter” refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence.

[00178] The term “promoter/regulatory sequence” refers to a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence.

In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.

[00179] A “constitutive” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell.

[00180] An “inducible” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell.

[00181] A “tissue-specific” promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide encodes or specified by a gene, causes the gene product to be produced in a cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

[00182] The terms “cancer associated antigen” or “tumor antigen” interchangeably refers to a molecule (typically a protein, carbohydrate or lipid) that is expressed on the surface of a cancer cell, either entirely or as a fragment (e.g., MHC or peptide fragment), and which is useful for the preferential targeting of a pharmacological agent to the cancer cell. In some embodiments, a tumor antigen is a marker expressed by both normal cells and cancer cells, e.g., a lineage marker, e.g., CD19 on B cells. In some embodiments, a tumor antigen is a cell surface molecule that is overexpressed in a cancer cell in comparison to a normal cell, for instance, 1-fold over expression, 2-fold overexpression, 3-fold overexpression or more in comparison to a normal cell. In some embodiments, a tumor antigen is a cell surface molecule that is underexpressed in a cancer cell in comparison to a normal cell, for instance, 1-fold underexpression, 2-fold underexpression, 3-fold underexpression or more in comparison to a normal cell. In some embodiments, a tumor antigen is a cell surface molecule that is inappropriately synthesized in the cancer cell, for instance, a molecule that contains deletions, additions or mutations in comparison to the molecule expressed on a normal cell.

[00183] In some embodiments, a tumor antigen will be expressed exclusively on the cell surface of a cancer cell, entirely or as a fragment (e.g., MHC or peptide fragment), and not synthesized or expressed on the surface of a normal cell. In some embodiments, the CARs of

the present disclosure includes CARs comprising an antigen binding domain (e.g., antibody or antibody fragment) that binds to a tumor antigen or fragment, e.g., a MHC presented peptide.

[00184] Normally, peptides derived from endogenous proteins fill the pockets of Major histocompatibility complex (MHC) class I molecules, and are recognized by T cell receptors (TCRs) on CD8 + T lymphocytes. The MHC class I complexes are constitutively expressed by all nucleated cells. In cancer, virus-specific and/or tumor-specific peptide/MHC complexes represent a unique class of cell surface targets for immunotherapy. TCR-like antibodies targeting peptides derived from viral or tumor antigens in the context of human leukocyte antigen (HLA)-A1 or HLA-A2 have been described (see, e.g., Sastry et al., J Virol. 2011 85(5):1935-1942; Sergeeva et al., Blood, 2011 117(16):4262-4272; Verma et al., J Immunol 2010 184(4):2156-2165; Willemssen et al., Gene Ther 2001 8(21) :1601-1608 ; Dao et al., Sci Transl Med 2013 5(176) :176ra33 ; Tassev et al., Cancer Gene Ther 2012 19(2):84-100). For example, TCR-like antibody can be identified from screening a library, such as a human scFv phage displayed library.

[00185] The term “tumor-supporting antigen” or “cancer-supporting antigen” interchangeably refer to a molecule (typically a protein, carbohydrate or lipid) that is expressed on the surface of a cell that is, itself, not cancerous, but supports the cancer cells, e.g., by promoting their growth or survival e.g., resistance to immune cells. Exemplary cells of this type include stromal cells and myeloid-derived suppressor cells (MDSCs). The tumor-supporting antigen itself need not play a role in supporting the tumor cells so long as the antigen is present on a cell that supports cancer cells.

[00186] The term “flexible polypeptide linker” or “linker” as used in the context of a scFv refers to a peptide linker that consists of amino acids such as glycine and/or serine residues used alone or in combination, to link variable heavy and variable light chain regions together. In one embodiment, the flexible polypeptide linker is a Gly/Ser linker and comprises the amino acid sequence (Gly-Gly-Gly-Ser)_n, where n is a positive integer equal to or greater than 1. For example, n=1, n=2, n=3, n=4, n=5 and n=6, n=7, n=8, n=9 and n=10 (SEQ ID NO: 32). In one embodiment, the flexible polypeptide linkers include, but are not limited to, (Gly₄ Ser)₄ (SEQ ID NO: 34) or (Gly₄ Ser)₃ (SEQ ID NO: 35). In another embodiment, the linkers include multiple repeats of (Gly₂Ser), (GlySer) or (Gly₃Ser) (SEQ ID NO: 36). Also included within the scope of the disclosure are linkers described in WO2012/138475, incorporated herein by reference).

[00187] As used herein in connection with a messenger RNA (mRNA), a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m7G cap) is a modified guanine nucleotide that has been added to the “front” or 5' end of a eukaryotic messenger RNA shortly after the start of transcription. The 5' cap consists of a terminal group which is linked to the first transcribed nucleotide. Its presence is critical for recognition by the ribosome and protection from RNases. Cap addition is coupled to transcription, and occurs co-transcriptionally, such that each influences the other. Shortly after the start of transcription, the 5' end of the mRNA being synthesized is bound by a cap-synthesizing complex associated with RNA polymerase. This enzymatic complex catalyzes the chemical reactions that are required for mRNA capping. Synthesis proceeds as a multi-step biochemical reaction. The capping moiety can be modified to modulate functionality of mRNA such as its stability or efficiency of translation.

[00188] As used herein, “in vitro transcribed RNA” refers to RNA, preferably mRNA, that has been synthesized in vitro. Generally, the in vitro transcribed RNA is generated from an in vitro transcription vector. The in vitro transcription vector comprises a template that is used to generate the in vitro transcribed RNA.

[00189] As used herein, a “poly(A)” is a series of adenosines attached by polyadenylation to the mRNA. In the preferred embodiment of a construct for transient expression, the polyA is between 50 and 5000 (SEQ ID NO: 10517), preferably greater than 64, more preferably greater than 100, most preferably greater than 300 or 400. Poly(A) sequences can be modified chemically or enzymatically to modulate mRNA functionality such as localization, stability or efficiency of translation.

[00190] As used herein, “polyadenylation” refers to the covalent linkage of a polyadenylyl moiety, or its modified variant, to a messenger RNA molecule. In eukaryotic organisms, most messenger RNA (mRNA) molecules are polyadenylated at the 3' end. The 3' poly(A) tail is a long sequence of adenine nucleotides (often several hundred) added to the pre-mRNA through the action of an enzyme, polyadenylate polymerase. In higher eukaryotes, the poly(A) tail is added onto transcripts that contain a specific sequence, the polyadenylation signal. The poly(A) tail and the protein bound to it aid in protecting mRNA from degradation by exonucleases. Polyadenylation is also important for transcription termination, export of the mRNA from the nucleus, and translation. Polyadenylation occurs in the nucleus immediately after transcription of DNA into RNA, but additionally can also occur later in the cytoplasm. After transcription has been terminated, the mRNA chain is cleaved through the action of an

endonuclease complex associated with RNA polymerase. The cleavage site is usually characterized by the presence of the base sequence AAUAAA near the cleavage site. After the mRNA has been cleaved, adenosine residues are added to the free 3' end at the cleavage site.

[00191] As used herein, “transient” refers to expression of a non-integrated transgene for a period of hours, days or weeks, wherein the period of time of expression is less than the period of time for expression of the gene if integrated into the genome or contained within a stable plasmid replicon in the host cell.

[00192] As used herein, the terms “treat”, “treatment” and “treating” refer to a partial or complete reduction or amelioration of the progression, severity and/or duration of a proliferative disorder, or the amelioration of one or more symptoms (preferably, one or more discernible symptoms) of a proliferative disorder resulting from the administration of one or more therapies (e.g., one or more therapeutic agents such as a CAR of the disclosure). In specific embodiments, the terms “treat”, “treatment” and “treating” refer to the amelioration of at least one measurable physical parameter of a proliferative disorder, such as growth of a tumor, as well as parameters not necessarily discernible by the patient. In other embodiments the terms “treat”, “treatment” and “treating” -refer to the inhibition of the progression of a proliferative disorder, such as stabilization of a tumor size, either physically by, e.g., stabilization of a discernible symptom, physiologically by, e.g., stabilization of a physical parameter, or both. In other embodiments the terms “treat”, “treatment” and “treating” refer to the reduction or stabilization of tumor size or cancerous cell count.

[00193] A “signal transduction pathway” refers to the biochemical relationship between two or more signal transduction molecules that play a role in the transmission of a signal from one portion of a cell to another portion of the cell or to another cell. The phrase “cell surface receptor” includes molecules and complexes of molecules capable of receiving a signal and transmitting signal across the membrane of a cell.

[00194] A “subject” is intended to include living organisms in which an immune response can be elicited (e.g., a mammal such as a human).

[00195] A “substantially purified” cell refers to a cell that is essentially free of other cell types. A substantially purified cell also refers to a cell which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells. In other instances, this term refers simply to cell that have been separated from the cells with which

they are naturally associated in their natural state. In some aspects, the cells are cultured in vitro. In other aspects, the cells are not cultured in vitro.

[00196] A “therapeutic” as used herein means a treatment. A therapeutic effect is obtained by partial or complete reduction, suppression, remission, or eradication of a disease state or symptom.

[00197] The term “prophylaxis” as used herein means the partial or complete prevention of or protective treatment for a disease or disease state.

[00198] In the context of the present disclosure, “tumor antigen” or “hyperproliferative disorder antigen” or “antigen associated with a hyperproliferative disorder” refers to antigens that are common to specific hyperproliferative disorders. In certain aspects, the hyperproliferative disorder antigens of the present disclosure are derived from, cancers including but not limited to primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, non-Hodgkin lymphoma, Hodgkin lymphoma, leukemias, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast cancer, prostate cancer, ovarian cancer, pancreatic cancer, and the like.

[00199] The term “transfected” or “transformed” or “transduced” refers to a process by which exogenous nucleic acid is transferred or introduced into the host cell. A “transfected” or “transformed” or “transduced” cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny.

[00200] The term “specifically binds,” refers to a molecule that preferentially recognizes and binds a binding partner (e.g., a protein or nucleic acid) over other molecules present in a sample.

[00201] “Membrane anchor” or “membrane tethering domain”, as that term is used herein, refers to a polypeptide or moiety, e.g., a myristoyl group, sufficient to anchor an extracellular or intracellular domain to the plasma membrane.

[00202] The term “bioequivalent” refers to an amount of an agent other than the reference compound (e.g., RAD001), required to produce an effect equivalent to the effect produced by the reference dose or reference amount of the reference compound (e.g., RAD001). In an embodiment the effect is the level of mTOR inhibition, e.g., as measured by P70 S6 kinase inhibition, e.g., as evaluated in an in vivo or in vitro assay, e.g., as measured by an assay described herein, e.g., the Boulay assay. In an embodiment, the effect is alteration of the ratio

of PD-1 positive/PD-1 negative T cells, as measured by cell sorting. In an embodiment a bioequivalent amount or dose of an mTOR inhibitor is the amount or dose that achieves the same level of P70 S6 kinase inhibition as does the reference dose or reference amount of a reference compound. In an embodiment, a bioequivalent amount or dose of an mTOR inhibitor is the amount or dose that achieves the same level of alteration in the ratio of PD-1 positive/PD-1 negative T cells as does the reference dose or reference amount of a reference compound.

[00203] The term “low, immune enhancing, dose” when used in conjunction with an mTOR inhibitor, e.g., an allosteric mTOR inhibitor, e.g., RAD001 or rapamycin, or a catalytic mTOR inhibitor, refers to a dose of mTOR inhibitor that partially, but not fully, inhibits mTOR activity, e.g., as measured by the inhibition of P70 S6 kinase activity. Methods for evaluating mTOR activity, e.g., by inhibition of P70 S6 kinase, are discussed herein. The dose is insufficient to result in complete immune suppression but is sufficient to enhance the immune response. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in a decrease in the number of PD-1 positive T cells and/or an increase in the number of PD-1 negative T cells, or an increase in the ratio of PD-1 negative T cells/PD-1 positive T cells. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in an increase in the number of naive T cells. In an embodiment, the low, immune enhancing, dose of mTOR inhibitor results in one or more of the following:

[00204] an increase in the expression of one or more of the following markers: CD62L^{high}, CD127^{high}, CD27⁺, and BCL2, e.g., on memory T cells, e.g., memory T cell precursors;

[00205] a decrease in the expression of KLRG1, e.g., on memory T cells, e.g., memory T cell precursors; and

[00206] an increase in the number of memory T cell precursors, e.g., cells with any one or combination of the following characteristics: increased CD62L^{high}, increased CD127^{high}, increased CD27⁺, decreased KLRG1, and increased BCL2;

[00207] wherein any of the changes described above occurs, e.g., at least transiently, e.g., as compared to a non-treated subject.

[00208] “Refractory” as used herein refers to a disease, e.g., cancer, that does not respond to a treatment. In embodiments, a refractory cancer can be resistant to a treatment before or at the beginning of the treatment. In other embodiments, the refractory cancer can become resistant during a treatment. A refractory cancer is also called a resistant cancer.

[00209] “Relapsed” as used herein refers to the return of a disease (e.g., cancer) or the signs and symptoms of a disease such as cancer after a period of improvement, e.g., after prior treatment of a therapy, e.g., cancer therapy.

[00210] Ranges: throughout this disclosure, various aspects of the disclosure can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the disclosure. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. As another example, a range such as 95-99% identity, includes something with 95%, 96%, 97%, 98% or 99% identity, and includes subranges such as 96-99%, 96-98%, 96-97%, 97-99%, 97-98% and 98-99% identity. This applies regardless of the breadth of the range. All specified ranges also include the endpoints unless otherwise stated.

DETAILED DESCRIPTION

[00211] The gRNA molecules, compositions and methods described herein relate to genome editing, for example, gene editing in eukaryotic cells, in particular at a tet gene intron or intron-exon junction, for example at a TET2 intron or intron-exon junction, for example, using a CRISPR/Cas system, e.g., a Cas9 system, e.g., described herein. In particular embodiments, the gRNA molecules, compositions and methods described herein provide for the targeting of a CRISPR system to a target sequence of an intron, or intron-exon junction of a tet gene, for example a tet2 gene. In further aspects, the disclosure provides for modification (e.g., insertion or deletion) of a target sequence of an intron or intron-exon junction of a tet gene, for example, a tet2 gene. In further aspects, the disclosure provides for insertion of a nucleic acid sequence encoding a heterologous protein, for example a CAR molecule, for example as described herein, at or near the target sequence bound by a gene editing system, e.g., bound by a gRNA molecule described herein, e.g., at an intron, or intron-exon junction, of a tet gene, for example a tet2 gene. Such nucleic acid sequence encoding a heterologous protein may be separately introduced into the cell as a template nucleic acid as described herein, for example, including homology arms, or as part of a vector, or introduced at the same time as the gene editing system.

[00212] Missense, nonsense, and frameshift mutations (i.e., loss-of-function mutations) in the TET2 gene are associated with various cancers, e.g., hematological cancers. See, e.g., Pan et al., IUBMB Life 67(6): 438-45 (June 2015). Nevertheless, without being bound by theory, the disclosure is based in part on the finding that a CAR gene insertion into the TET2 gene, and in particular into an intron of the TET2 gene, for example the intron between exon 9 and exon 10, results in a CAR-expressing T cell with improved properties. For instance, in some embodiments, a CART cell comprising a CAR gene inserted into one or more copies of the TET2 gene, e.g., an intron of the TET2 gene, is capable of disrupting the expression and/or function of TET2. In some embodiments, the resulting CART cell with TET2 loss-of-function surprisingly is capable of avoiding uncontrolled proliferation and useful in the treatment of cancer, e.g., hematological cancers.

[00213] Without being bound by theory, the insertion of a CAR gene into one or more alleles of the TET2 gene, e.g., an intron of the TET2 gene, may be capable of producing a truncated and/or dominant negative form of TET2 that is capable of partially or fully disrupting full-length form(s) of TET2.

[00214] The disclosure is further based in part on the discovery that partial (but not full) inhibition of the function and/or expression of TET2 may be beneficial to immune effector cell function. In some embodiments, a CAR gene insertion into the TET2 gene, e.g., an intron of the TET2 gene, disrupts one allele of the TET2 gene and results in partial inhibition of the function and/or expression of TET2. In some embodiments, a CAR gene insertion into the TET2 gene, e.g., an intron of the TET2 gene, disrupts both alleles of the TET2 gene and results in full inhibition of the function and/or expression of TET2. The disclosure is also based in part on the recognition of the need for targeted insertion of nucleic acid encoding a heterologous protein, for example a CAR molecule, for example as described herein, into the genome of a cell, for example an immune effector cell, for example specifically at an intron of a tet gene, e.g., at an intron of a TET2 gene, e.g., at the intron between exon 9 and exon 10 of TET2. Thus, in an aspect, the disclosure provides gene editing systems, gRNA molecules, CRISPR systems and methods useful for insertion of nucleic acid sequence encoding a heterologous protein, for example a CAR molecule, for example as described herein, within an intron of the TET2 gene of a cell, for example an immune effector cell, for example as described herein.

[00215] The disclosure is further based in part on the discovery that targeting an intron, e.g., the intron between exon 9 and exon 10 of TET2, may provide a number of advantages. First,

for example, the disclosure provides gRNAs that are able to create indels, including 1- or 2-nucleotide deletion indels, at or near target sequences with surprisingly high frequencies, and in particular, combining CRISPR systems comprising these gRNA molecules with a template nucleic acid, e.g., a template nucleic acid encoding a CAR (e.g., as described herein), results in unexpectedly and surprisingly high frequencies of incorporation of sequence of the template nucleic acid at or near the site targeted by the gRNA molecule. These indels and insertions (e.g., insertions of sequence of the template nucleic acid), when created within an exon, can lead to a frameshift mutation and thus significant (e.g., total) inhibition of expression of the protein encoded by the gene. Because of the high frequency of indel formation by these gRNAs, such frameshifts can occur at both alleles of the gene in a high percentage of the cells. Without being bound by theory, targeting an intron sequence with a CRISPR system as disclosed herein, particularly as a site for insertion of nucleic acid encoding a heterologous protein (e.g., sequence of a template nucleic acid), may therefore be beneficial where reduced, but not eliminated, function and/or expression of the target gene is desired because, for example, indels of less than 50 nt, 100 nt, or 150 nt in an intronic region, even if occurring at both alleles of the gene, are not expected to disrupt expression of the functional protein. Because insertion may be a relatively low-frequency event, insertion of the nucleic acid encoding the heterologous protein (e.g., CAR molecule as described herein) may occur in most cells at only one allele of the gene targeted by the CRISPR system. In some embodiments, targeting an intron with a CRISPR system allows for targeted insertion of nucleic acid encoding a heterologous sequence (e.g., CAR molecule, e.g., as described herein) while preserving at least a portion of the expression and/or function of the gene, for example, through the allele which does not comprise the inserted nucleic acid sequence. In alternate embodiments, for example, using the gRNA molecules described herein which result in a surprisingly high rate of incorporation of sequence of the template nucleic acid, targeting an intron with a CRISPR system (e.g., as described herein) allows for targeted insertion of nucleic acid encoding a heterologous sequence (e.g., CAR molecule, e.g., as described herein) while disrupting the expression and/or function of both alleles of the gene. In an aspect, the cell is an immune effector cell, e.g., an NK cell or T cell. In an aspect, the cell is an autologous cell.

[00216] Thus, in an aspect, the disclosure provides a cell, e.g., an immune effector cell, e.g., an immune effector cell comprising a CAR molecule, comprising an indel at or near a target sequence within an intron of a Tet gene, for example within an intron of a Tet2 gene. In an aspect, the disclosure provides a cell, e.g., an immune effector cell, e.g., an immune effector

cell comprising a CAR molecule, comprising an indel at or near a target sequence complementary to the targeting domain of a gRNA molecule to a Tet intron sequence, e.g., a Tet2 intron sequence, e.g., complementary to the targeting domain of a gRNA molecule described herein. In an aspect, the disclosure provides a cell, e.g., an immune effector cell, e.g., an immune effector cell comprising a CAR molecule, comprising nucleic acid sequence encoding a heterologous protein (e.g., a CAR molecule, e.g., described herein) integrated into the genome of said cell at or near a target sequence complementary to the targeting domain of a gRNA molecule to a Tet intron sequence, e.g., Tet2 intron sequence, or intron-exon junction sequence, e.g., complementary to the targeting domain of a gRNA molecule described herein. The disclosure further provides methods and compositions useful in connection with said cells

[00217] In any of the aforementioned aspects and embodiments the cell is an autologous cell. Alternatively, In any of the aforementioned aspects and embodiments, the cell is an allogeneic cell. Examples of allogeneic cells include those in which expression and/or function of a T cell receptor chain, for example, TRAC or TRBC, has been reduced or eliminated, for example using a genome editing system (e.g., CRISPR system) targeted to said gene. The cell may further comprise reduced or eliminated expression of one or more additional genes, for example, B2M and/or CIITA. In any of the aforementioned embodiments and aspects, the cell is or will be engineered to express a chimeric antigen receptor (CAR), e.g., as described herein. In any of the aforementioned aspects and embodiments, the cell is a T cell.

[00218] Additional features of the gene editing systems, gRNA molecules, the CRISPR systems, Cas9 molecules, cells, CAR molecules, methods and other aspects of the disclosure are described in detail below.

Gene Editing Systems

[00219] In an aspect, the disclosure provides gene editing systems which target a TET, e.g., TET2, intron sequence, e.g., a sequence selected from the sequences listed in Table 3. Various gene editing systems are described more fully below.

[00220] In some embodiments, the disclosure provides gene editing systems comprising a template nucleic acid encoding a CAR and capable of integrating a CAR nucleic acid sequence such that CAR is expressed and/or TET, e.g., TET2, is disrupted. In some embodiments, the TET, e.g., TET2, is partially disrupted. In some embodiments, the TET, e.g., TET2, is fully disrupted. In some embodiments, only one allele of TET, e.g., TET2, is modified. In some embodiments, both alleles of TET, e.g., TET2, are modified.

TALEN gene editing systems

[00221] TALENs are produced artificially by fusing a TAL effector DNA binding domain to a DNA cleavage domain. Transcription activator-like effects (TALEs) can be engineered to bind any desired DNA sequence, including a sequence of a TET2 intron, e.g., a sequence within a sequence of Table 3. By combining an engineered TALE with a DNA cleavage domain, a restriction enzyme can be produced which is specific to any desired DNA sequence, including a TET2 intron. These can then be introduced into a cell, wherein they can be used for genome editing. Boch (2011) *Nature Biotech.* 29: 135-6; and Boch et al. (2009) *Science* 326: 1509-12; Moscou et al. (2009) *Science* 326: 3501.

[00222] TALEs are proteins secreted by *Xanthomonas* bacteria. The DNA binding domain contains a repeated, highly conserved 33-34 amino acid sequence, with the exception of the 12th and 13th amino acids. These two positions are highly variable, showing a strong correlation with specific nucleotide recognition. They can thus be engineered to bind to a desired DNA sequence.

[00223] To produce a TALEN, a TALE protein is fused to a nuclease (N), which is, for example, a wild-type or mutated FokI endonuclease. Several mutations to FokI have been made for its use in TALENs; these, for example, improve cleavage specificity or activity. Cermak et al. (2011) *Nucl. Acids Res.* 39: e82; Miller et al. (2011) *Nature Biotech.* 29: 143-8; Hockemeyer et al. (2011) *Nature Biotech.* 29: 731-734; Wood et al. (2011) *Science* 333: 307; Doyon et al. (2010) *Nature Methods* 8: 74-79; Szczeppek et al. (2007) *Nature Biotech.* 25: 786-793; and Guo et al. (2010) *J. Mol. Biol.* 200: 96.

[00224] The FokI domain functions as a dimer, requiring two constructs with unique DNA binding domains for sites in the target genome with proper orientation and spacing. Both the number of amino acid residues between the TALE DNA binding domain and the FokI cleavage domain and the number of bases between the two individual TALEN binding sites appear to be important parameters for achieving high levels of activity. Miller et al. (2011) *Nature Biotech.* 29: 143-8.

[00225] A TALEN to a TET2 intron sequence, e.g., a sequence listed in Table 3, can be used inside a cell to produce a double-stranded break (DSB). A mutation can be introduced at the break site if the repair mechanisms improperly repair the break via non-homologous end joining. For example, improper repair may introduce a frame shift mutation. Alternatively, template nucleic acid, e.g., as described herein, can be introduced into the cell along with the

TALEN, e.g., template nucleic acid encoding a CAR, e.g., as described herein; depending on the sequences of the template nucleic acid and chromosomal sequence, this process can be used to integrate heterologous nucleic acid sequence, e.g., sequence encoding the CAR, e.g., as described herein, at or near the site targeted by the TALEN. Without being bound by theory, such integration may lead to the expression of the CAR as well as disruption, e.g., partial disruption, e.g., disruption of one or more functions, e.g., disruption of only one allele of, TET2. In some embodiments, both alleles of TET, e.g., TET2, are disrupted.

[00226] TALENs specific to sequences in TET2 introns, can be constructed using any method known in the art, including various schemes using modular components. Zhang et al. (2011) *Nature Biotech.* 29: 149-53; Geibler et al. (2011) *PLoS ONE* 6: e19509; US 8,420,782 ; US 8,470,973, the contents of which are hereby incorporated by reference in their entirety.

Zinc finger nuclease (“ZFN”) gene editing systems to a TET2 intron

[00227] “ZFN” or “zinc finger nuclease” refers to an artificial nuclease which can be used to modify, e.g., delete one or more nucleic acids of, a desired nucleic acid sequence, e.g., a TET2 intron, e.g., a sequence listed in Table 3. Mutant and variant ZFNs are also encompassed.

[00228] Like a TALEN, a ZFN comprises a FokI nuclease domain (or derivative thereof) fused to a DNA-binding domain. In the case of a ZFN, the DNA-binding domain comprises one or more zinc fingers. Carroll et al. (2011) *Genetics Society of America* 188: 773-782; and Kim et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 1156-1160.

[00229] A zinc finger is a small protein structural motif stabilized by one or more zinc ions. A zinc finger can comprise, for example, Cys2His2, and can recognize an approximately 3-bp sequence. Various zinc fingers of known specificity can be combined to produce multi-finger polypeptides which recognize about 6, 9, 12, 15 or 18-bp sequences. Various selection and modular assembly techniques are available to generate zinc fingers (and combinations thereof) recognizing specific sequences, including phage display, yeast one-hybrid systems, bacterial one-hybrid and two-hybrid systems, and mammalian cells.

[00230] Like a TALEN, a ZFN must dimerize to cleave DNA. Thus, a pair of ZFNs are required to target non-palindromic DNA sites. The two individual ZFNs must bind opposite strands of the DNA with their nucleases properly spaced apart. Bitinaite et al. (1998) *Proc. Natl. Acad. Sci. USA* 95: 10570-5.

[00231] Also like a TALEN, a ZFN can create a double-stranded break in the DNA, which can create a frame-shift mutation if improperly repaired, leading to a decrease in the expression

and/or function, e.g., one or more functions, of TET2, e.g., from one allele, in a cell. ZFNs can also be used with homologous recombination to mutate the TET2 intron, or to introduce nucleic acid, e.g., encoding a CAR, at or near a site of the target sequence. As discussed above, the nucleic acid encoding a CAR may be introduced as part of a template nucleic acid. In embodiments, the template nucleic acid further comprises homology arms 5' to, 3' to, or both 5' and 3' to the nucleic acid of the template nucleic acid which encodes the molecule or molecules of interest (e.g., which encodes a CAR described herein), wherein said homology arms are complementary to genomic DNA sequence flanking the target sequence.

[00232] ZFNs specific to sequences in a TET2 intron, e.g., a sequence of Table 3, can be constructed using any method known in the art. See, e.g., Provasi (2011) *Nature Med.* 18: 807-815; Torikai (2013) *Blood* 122: 1341-1349; Cathomen et al. (2008) *Mol. Ther.* 16: 1200-7; and Guo et al. (2010) *J. Mol. Biol.* 400: 96; U.S. Patent Publication 2011/0158957; and U.S. Patent Publication 2012/0060230, the contents of which are hereby incorporated by reference in their entirety. In embodiments, The ZFN gene editing system may also comprise nucleic acid encoding one or more components of the ZFN gene editing system, e.g., a ZFN gene editing system targeted to a TET2 intron, e.g., a sequence listed in Table 3.

[00233] In a preferred aspect, the gene editing system is a CRISPR system. Additional features of the gRNA molecules, the CRISPR systems, Cas9 molecules, cells, CAR molecules, methods and other aspects of the disclosure are described in detail below.

I. gRNA Molecules

[00234] A gRNA molecule may have a number of domains, as described more fully below; however, a gRNA molecule typically comprises at least a crRNA domain (comprising a targeting domain) and a tracr. In embodiments, the crRNA and the tracr are provided on a single contiguous polynucleotide molecule. In other embodiments, the crRNA and the tracr are provided on separate polynucleotide molecules, which are themselves capable of association, e.g., through non-covalent hybridization. The gRNA molecules, used as a component of a CRISPR system, are useful for modifying (e.g., modifying the sequence) DNA at or near a target site. Such modifications include deletions and or insertions that result in, for example, reduced or eliminated expression of a functional product of the gene comprising the target site. Such modifications can also include insertion of heterologous nucleic acid sequence, for example, nucleic acid sequence encoding a heterologous protein (e.g., a CAR molecule, e.g., as described herein), that may be provided to said cell as a template nucleic

acid, as described herein. In some embodiments, the inserted heterologous nucleic acid also serves to eliminate expression of the functional product of the gene comprising the target site. In some embodiments, a separate gRNA molecule and CRISPR system are used to eliminate expression of the functional product of the gene comprising the target site before, at the same time as, or after the insertion of the heterologous nucleic acid. These uses, and others, are described more fully below.

[00235] In an embodiment, a unimolecular, or sgRNA comprises, preferably from 5' to 3': a crRNA (which comprises a targeting domain complementary to a target sequence and a region that forms part of a flagpole (i.e., a crRNA flagpole region)); a loop; and a tracr (which comprises a domain complementary to the crRNA flagpole region, and a domain which additionally binds a nuclease or other effector molecule, e.g., a Cas molecule, e.g., a Cas9 molecule), and may take the following format (from 5' to 3'):

[targeting domain] – [crRNA flagpole region] – [optional first flagpole extension] – [loop] – [optional first tracr extension] – [tracr flagpole region] – [tracr nuclease binding domain].

[00236] In embodiments, the tracr nuclease binding domain binds to a Cas protein, e.g., a Cas9 protein.

[00237] In an embodiment, a bimolecular, or dgRNA comprises two polynucleotides; the first, preferably from 5' to 3': a crRNA (which contains a targeting domain complementary to a target sequence and a region that forms part of a flagpole; and the second, preferably from 5' to 3': a tracr (which contains a domain complementary to the crRNA flagpole region, and a domain which additionally binds a nuclease or other effector molecule, e.g., a Cas molecule, e.g., Cas9 molecule), and may take the following format (from 5' to 3'):

Polynucleotide 1 (crRNA): [targeting domain] – [crRNA flagpole region] – [optional first flagpole extension] – [optional second flagpole extension]

Polynucleotide 2 (tracr): [optional first tracr extension] – [tracr flagpole region] – [tracr nuclease binding domain]

[00238] In embodiments, the tracr nuclease binding domain binds to a Cas protein, e.g., a Cas9 protein.

[00239] In some aspects, the targeting domain comprises or consists of a targeting domain sequence described herein, e.g., a targeting domain described in Table 1 or, preferably, a

targeting domain described in Table 2, or a targeting domain comprising or consisting of 17, 18, 19, or 20 (preferably 20) consecutive nucleotides of a targeting domain sequence described in Table 1, or Table 2.

[00240] In some aspects, the flagpole, e.g., the crRNA flagpole region, comprises, from 5' to 3': GUUUUAGAGCUA (SEQ ID NO: 50).

[00241] In some aspects, the flagpole, e.g., the crRNA flagpole region, comprises, from 5' to 3': GUUUAAGAGCUA (SEQ ID NO: 51).

[00242] In some aspects the loop comprises, from 5' to 3': GAAA (SEQ ID NO: 52).

[00243] In some aspects the tracr comprises, from 5' to 3':

UAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGCACCGAG
UCGGUGC (SEQ ID NO: 53) and is preferably used in a gRNA molecule comprising SEQ ID NO: 50.

[00244] In some aspects the tracr comprises, from 5' to 3':

UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGCACCGAG
UCGGUGC (SEQ ID NO: 54) and is preferably used in a gRNA molecule comprising SEQ ID NO: 51.

[00245] In some aspects, the gRNA may also comprise, at the 3' end, additional U nucleic acids. For example the gRNA may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 U nucleic acids at the 3' end (SEQ ID NO: 58). In an embodiment, the gRNA comprises an additional 4 U nucleic acids at the 3' end. In the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) may comprise, at the 3' end, additional U nucleic acids. For example, the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 U nucleic acids at the 3' end (SEQ ID NO: 58). In an embodiment, in the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) comprises an additional 4 U nucleic acids at the 3' end. In an embodiment of a dgRNA, only the polynucleotide comprising the tracr comprises the additional U nucleic acid(s), e.g., 4 U nucleic acids. In an embodiment of a dgRNA, only the polynucleotide comprising the targeting domain comprises the additional U nucleic acid(s). In an embodiment of a dgRNA, both the polynucleotide comprising the targeting domain and

the polynucleotide comprising the tracr comprise the additional U nucleic acids, e.g., 4 U nucleic acids.

[00246] In some aspects, the gRNA may also comprise, at the 3' end, additional A nucleic acids. For example the gRNA may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 A nucleic acids at the 3' end (SEQ ID NO: 59). In an embodiment, the gRNA comprises an additional 4 A nucleic acids at the 3' end. In the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) may comprise, at the 3' end, additional A nucleic acids. For example, the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 A nucleic acids at the 3' end (SEQ ID NO: 59). In an embodiment, in the case of dgRNA, one or more of the polynucleotides of the dgRNA (e.g., the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr) comprises an additional 4 A nucleic acids at the 3' end. In an embodiment of a dgRNA, only the polynucleotide comprising the tracr comprises the additional A nucleic acid(s), e.g., 4 A nucleic acids. In an embodiment of a dgRNA, only the polynucleotide comprising the targeting domain comprises the additional A nucleic acid(s). In an embodiment of a dgRNA, both the polynucleotide comprising the targeting domain and the polynucleotide comprising the tracr comprise the additional U nucleic acids, e.g., 4 A nucleic acids.

[00247] In embodiments, one or more of the polynucleotides of the gRNA molecule may comprise a cap at the 5' end.

[00248] In an embodiment, a unimolecular, or sgRNA comprises, preferably from 5' to 3' : a crRNA (which contains a targeting domain complementary to a target sequence; a crRNA flagpole region; first flagpole extension; a loop; a first tracr extension (which contains a domain complementary to at least a portion of the first flagpole extension); and a tracr (which contains a domain complementary to the crRNA flagpole region, and a domain which additionally binds a Cas9 molecule). In some aspects, the targeting domain comprises a targeting domain sequence described herein, e.g., a targeting domain described in Table 1 or Table 2, or a targeting domain comprising or consisting of 17, 18, 19, 20 (preferably 20) consecutive nucleotides of a targeting domain sequence described in Table 1 or Table 2, for example the 3' 17, 18, 19 or 20 (preferably 20) consecutive nucleotides of a targeting domain sequence described in Table 1 or Table 2.

[00249] In aspects comprising a first flagpole extension and/or a first tracr extension, the flagpole, loop and tracr sequences may be as described above. In general any first flagpole extension and first tracr extension may be employed, provided that they are complementary. In embodiments, the first flagpole extension and first tracr extension consist of 3, 4, 5, 6, 7, 8, 9, 10 or more complementary nucleotides.

[00250] In some aspects, the first flagpole extension comprises, from 5' to 3': UGCUG (SEQ ID NO: 55). In some aspects, the first flagpole extension consists of SEQ ID NO: 55.

[00251] In some aspects, the first tracr extension comprises, from 5' to 3': CAGCA (SEQ ID NO: 56). In some aspects, the first tracr extension consists of SEQ ID NO: 56.

[00252] In an embodiment, a dgRNA comprises two nucleic acid molecules. In some aspects, the dgRNA comprises a first nucleic acid which contains, preferably from 5' to 3' : a targeting domain complementary to a target sequence; a crRNA flagpole region; optionally a first flagpole extension; and, optionally, a second flagpole extension; and a second nucleic acid (which may be referred to herein as a tracr), and comprises at least a domain which binds a Cas molecule, e.g., a Cas9 molecule) comprising preferably from 5' to 3': optionally a first tracr extension; and a tracr (which contains a domain complementary to the crRNA flagpole region, and a domain which additionally binds a Cas, e.g., Cas9, molecule). The second nucleic acid may additionally comprise, at the 3' end (e.g., 3' to the tracr) additional U nucleic acids. For example the tracr may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 U nucleic acids at the 3' end (e.g., 3' to the tracr) (SEQ ID NO: 58). The second nucleic acid may additionally or alternately comprise, at the 3' end (e.g., 3' to the tracr) additional A nucleic acids. For example the tracr may comprise an additional 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 A nucleic acids at the 3' end (e.g., 3' to the tracr) (SEQ ID NO: 59). In some aspects, the targeting domain comprises a targeting domain sequence described herein, e.g., a targeting domain described in Table 1 or Table 2, or a targeting domain comprising or consisting of 17, 18, 19, or 20 (preferably 20) consecutive nucleotides of a targeting domain sequence described in Table 1 or Table 2.

[00253] In aspects involving a dgRNA, the crRNA flagpole region, optional first flagpole extension, optional first tracr extension and tracr sequences may be as described above.

[00254] In some aspects, the optional second flagpole extension comprises, from 5' to 3': UUUUG (SEQ ID NO: 57).

[00255] In embodiments, the 3' 1, 2, 3, 4, or 5 nucleotides, the 5' 1, 2, 3, 4, or 5 nucleotides, or both the 3' and 5' 1, 2, 3, 4, or 5 nucleotides of the gRNA molecule (and in the case of a dgRNA molecule, the polynucleotide comprising the targeting domain and/or the polynucleotide comprising the tracr) are modified nucleic acids, as described more fully in section XIII, below.

[00256] The domains are discussed briefly below:

1) The Targeting Domain:

[00257] Guidance on the selection of targeting domains can be found, e.g., in Fu Y et al. NAT BIOTECHNOL 2014 (doi: 10.1038/nbt.2808) and Sternberg SH et al. NATURE 2014 (doi: 10.1038/nature13011).

[00258] The targeting domain comprises a nucleotide sequence that is complementary, e.g., at least 80, 85, 90, 95, or 99% complementary, or e.g., fully complementary, to the target sequence on the target nucleic acid. The targeting domain is part of an RNA molecule and will therefore comprise the base uracil (U), while any DNA encoding the gRNA molecule will comprise the base thymine (T). While not wishing to be bound by theory, it is believed that the complementarity of the targeting domain with the target sequence contributes to specificity of the interaction of the gRNA molecule/Cas9 molecule complex with a target nucleic acid. It is understood that in a targeting domain and target sequence pair, the uracil bases in the targeting domain will pair with the adenine bases in the target sequence.

[00259] In an embodiment, the targeting domain is 5 to 50, e.g., 10 to 40, e.g., 10 to 30, e.g., 15 to 30, e.g., 15 to 25 nucleotides in length. In an embodiment, the targeting domain is 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides in length. In an embodiment, the targeting domain is 16 nucleotides in length. In an embodiment, the targeting domain is 17 nucleotides in length. In an embodiment, the targeting domain is 18 nucleotides in length. In an embodiment, the targeting domain is 19 nucleotides in length. In an embodiment, the targeting domain is 20 nucleotides in length. In an embodiment, the targeting domain is 21 nucleotides in length. In an embodiment, the targeting domain is 22 nucleotides in length. In an embodiment, the targeting domain is 23 nucleotides in length. In an embodiment, the targeting domain is 24 nucleotides in length. In an embodiment, the targeting domain is 25 nucleotides in length. In embodiments, the aforementioned 16, 17, 18, 19, or 20 nucleotides comprise the 5'- 16, 17, 18, 19 or 20 nucleotides from a targeting domain described in Table 1 or Table 2. In embodiments, the aforementioned 16, 17, 18, 19, or 20 nucleotides comprise the 3'- 16, 17,

18, 19 or 20 nucleotides from a targeting domain described in Table 1 or Table 2. In embodiments, the aforementioned 16, 17, 18, 19, or 20 nucleotides consist of the 3' - 16, 17, 18, 19 or 20 nucleotides from a targeting domain described in Table 1 or Table 2. In embodiments, the targeting domain consists of a targeting domain described in Table 1 or Table 2.

[00260] Without being bound by theory, it is believed that the 8, 9 or 10 nucleic acids of the targeting domain disposed at the 3' end of the targeting domain may be important for targeting the target sequence, and may thus be referred to as the “core” region of the targeting domain. In an embodiment, the core domain is fully complementary with the target sequence.

[00261] The strand of the target nucleic acid with which the targeting domain is complementary is referred to herein as the target sequence. In some aspects, the target sequence is disposed on a chromosome, e.g., is a target within a gene. In some aspects the target sequence is disposed within an exon of a gene. In some aspects the target sequence is disposed within an intron of a gene. In some aspects, the target sequence comprises, or is proximal (e.g., within 10, 20, 30, 40, 50, 100, 200, 300, 400, 500, or 1000 nucleic acids) to a binding site of a regulatory element, e.g., a promoter or transcription factor binding site, of a gene of interest. Some or all of the nucleotides of the targeting domain can have a modification, e.g., modification found in Section XIII herein.

2) crRNA Flagpole Region:

[00262] The flagpole comprises a portion of gRNA in which the crRNA and the tracr bind or hybridize to one another. The crRNA flagpole region is complementary with a portion of the tracr, and in an embodiment, has sufficient complementarity to a portion of the tracr to form a duplexed region under at least some physiological conditions, for example, normal physiological conditions. In an embodiment, the crRNA flagpole region is 5 to 30 nucleotides in length. In an embodiment, the crRNA flagpole region is 5 to 25 nucleotides in length. The crRNA flagpole region can share homology with, or be derived from, a naturally occurring portion of the repeat sequence from a bacterial CRISPR system. In an embodiment, it has at least 50% homology with a crRNA flagpole region disclosed herein, e.g., an *S. pyogenes*, or *S. thermophilus*, crRNA flagpole region.

[00263] In an embodiment, the flagpole, e.g., the crRNA flagpole region, comprises SEQ ID NO: 50. In an embodiment, the flagpole, e.g., the crRNA flagpole region, consists of SEQ ID NO: 50. In an embodiment, the flagpole, e.g., the crRNA flagpole region, comprises sequence

having at least 50%, 60%, 70%, 80%, 85%, 90%, 95% or 99% homology with SEQ ID NO: 50. In an embodiment, the flagpole, e.g., the crRNA flagpole region, comprises at least 5, 6, 7, 8, 9, 10, or 11 nucleotides of SEQ ID NO: 50. In an embodiment, the flagpole, e.g., the crRNA flagpole region, comprises SEQ ID NO: 51. In an embodiment, the flagpole, e.g., the crRNA flagpole region, consists of SEQ ID NO: 51. In an embodiment, the flagpole comprises sequence having at least 50%, 60%, 70%, 80%, 85%, 90%, 95% or 99% homology with SEQ ID NO: 51. In an embodiment, the flagpole, e.g., the crRNA flagpole region, comprises at least 5, 6, 7, 8, 9, 10, or 11 nucleotides of SEQ ID NO: 51.

[00264] Some or all of the nucleotides of the domain can have a modification, e.g., modification described in Section XIII herein.

3) First Flagpole Extension

[00265] When a tracr comprising a first tracr extension is used, the crRNA may comprise a first flagpole extension. In general any first flagpole extension and first tracr extension may be employed, provided that they are complementary. In embodiments, the first flagpole extension and first tracr extension consist of 3, 4, 5, 6, 7, 8, 9, 10 or more complementary nucleotides.

[00266] The first flagpole extension may comprise nucleotides that are complementary, e.g., 80%, 85%, 90%, 95% or 99%, e.g., fully complementary, with nucleotides of the first tracr extension. In some aspects, the first flagpole extension nucleotides that hybridize with complementary nucleotides of the first tracr extension are contiguous. In some aspects, the first flagpole extension nucleotides that hybridize with complementary nucleotides of the first tracr extension are discontinuous, e.g., comprises two or more regions of hybridization separated by nucleotides that do not base pair with nucleotides of the first tracr extension. In some aspects, the first flagpole extension comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more nucleotides. In some aspects, the first flagpole extension comprises, from 5' to 3': UGCUG (SEQ ID NO: 55). In some aspects, the first flagpole extension consists of, from 5' to 3': UGCUG (SEQ ID NO: 55). In some aspects, the first flagpole extension consists of SEQ ID NO: 55. In some aspects the first flagpole extension comprises nucleic acid that is at least 80%, 85%, 90%, 95% or 99% homology to SEQ ID NO: 55.

[00267] Some or all of the nucleotides of the first tracr extension can have a modification, e.g., modification found in Section XIII herein.

3) The Loop

[00268] A loop serves to link the crRNA flagpole region (or optionally the first flagpole extension, when present) with the tracr (or optionally the first tracr extension, when present) of a sgRNA. The loop can link the crRNA flagpole region and tracr covalently or non-covalently. In an embodiment, the linkage is covalent. In an embodiment, the loop covalently couples the crRNA flagpole region and tracr. In an embodiment, the loop covalently couples the first flagpole extension and the first tracr extension. In an embodiment, the loop is, or comprises, a covalent bond interposed between the crRNA flagpole region and the domain of the tracr which hybridizes to the crRNA flagpole region. Typically, the loop comprises one or more, e.g., 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides.

[00269] In dgRNA molecules the two molecules can be associated by virtue of the hybridization between at least a portion of the crRNA (e.g., the crRNA flagpole region) and at least a portion of the tracr (e.g., the domain of the tracr which is complementary to the crRNA flagpole region).

[00270] A wide variety of loops are suitable for use in sgRNAs. Loops can consist of a covalent bond, or be as short as one or a few nucleotides, e.g., 1, 2, 3, 4, or 5 nucleotides in length. In an embodiment, a loop is 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 or more nucleotides in length. In an embodiment, a loop is 2 to 50, 2 to 40, 2 to 30, 2 to 20, 2 to 10, or 2 to 5 nucleotides in length. In an embodiment, a loop shares homology with, or is derived from, a naturally occurring sequence. In an embodiment, the loop has at least 50% homology with a loop disclosed herein. In an embodiment, the loop comprises SEQ ID NO: 52. In an embodiment, the loop consists of SEQ ID NO: 52.

[00271] Some or all of the nucleotides of the domain can have a modification, e.g., modification described in Section XIII herein.

4) The Second Flagpole Extension

[00272] In an embodiment, a dgRNA can comprise additional sequence, 3' to the crRNA flagpole region or, when present, the first flagpole extension, referred to herein as the second flagpole extension. In an embodiment, the second flagpole extension is 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, or 2-4 nucleotides in length. In an embodiment, the second flagpole extension is 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more nucleotides in length. In an embodiment, the second flagpole extension comprises SEQ ID NO: 57. In an embodiment, the second flagpole extension consists of SEQ ID NO: 57.

5) The Tracr:

[00273] The tracr is a nucleic acid sequence that can provide for nuclease, e.g., Cas9, binding. Without being bound by theory, it is believed that each Cas9 species is associated with a particular tracr sequence. Tracr sequences are utilized in both sgRNA and in dgRNA systems. The exemplary gRNA targeting domain sequences provided in Table 1 and Table 2 may be utilized in both sgRNA and in dgRNA systems.

[00274] In an embodiment, the tracr comprises sequence from, or derived from, an *S. pyogenes* tracr. See Jinek et al. (2012). In some aspects, the tracr has a portion that hybridizes to the flagpole portion of the crRNA, e.g., it has sufficient complementarity to the crRNA flagpole region to form a duplexed region under at least some physiological conditions (sometimes referred to herein as the tracr flagpole region or a tracr domain complementary to the crRNA flagpole region). In embodiments, the domain of the tracr that hybridizes with the crRNA flagpole region comprises at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides that hybridize with complementary nucleotides of the crRNA flagpole region. In some aspects, the tracr nucleotides that hybridize with complementary nucleotides of the crRNA flagpole region are contiguous. In some aspects, the tracr nucleotides that hybridize with complementary nucleotides of the crRNA flagpole region are discontinuous, e.g., comprises two or more regions of hybridization separated by nucleotides that do not base pair with nucleotides of the crRNA flagpole region. In some aspects, the portion of the tracr that hybridizes to the crRNA flagpole region comprises, from 5' to 3': UAGCAAGUUAAAA (SEQ ID NO: 61). In some aspects, the portion of the tracr that hybridizes to the crRNA flagpole region comprises, from 5' to 3': UAGCAAGUUAAAA (SEQ ID NO: 62). In embodiments, the sequence that hybridizes with the crRNA flagpole region is disposed on the tracr 5' - to the sequence of the tracr that additionally binds a nuclease, e.g., a Cas molecule, e.g., a Cas9 molecule.

[00275] The tracr further comprises a domain that additionally binds to a nuclease, e.g., a Cas molecule, e.g., a Cas9 molecule. Without being bound by theory, it is believed that Cas9 from different species bind to different tracr sequences. In some aspects, the tracr comprises sequence that binds to a *S. pyogenes* Cas9 molecule. See Jinek et al. (2012). In some aspects, the tracr comprises sequence that binds to a Cas9 molecule disclosed herein. In some aspects, the domain that additionally binds a Cas9 molecule comprises, from 5' to 3': UAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC (SEQ ID NO: 63). In some aspects the domain that additionally binds a Cas9 molecule comprises, from 5' to 3':

UAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU
(SEQ ID NO: 64).

In some embodiments, the tracr comprises SEQ ID NO: 53. In some embodiments, the tracr comprises SEQ ID NO: 54. In some embodiments, the tracr consists of SEQ ID NO: 53. In some embodiments, the tracr consists of SEQ ID NO: 54.

[00276] Some or all of the nucleotides of the tracr can have a modification, e.g., modification found in Section XIII herein.

[00277] In embodiments, the gRNA or any of the gRNA components described above comprises an inverted abasic residue at the 5' end, the 3' end or both the 5' and 3' end (e.g., in the sgRNA or in the tracr and/or crRNA of a dgRNA). In embodiments, the gRNA or any of the gRNA components described above comprises one or more phosphorothioate bonds. For example, the one or more phosphorothioate bonds can be between residues at the 5' end of the polynucleotide, for example, a phosphorothioate bond between the first two 5' residues, between each of the first three 5' residues, between each of the first four 5' residues, or between each of the first five 5' residues (e.g., in the sgRNA or in the tracr and/or crRNA of a dgRNA). In embodiments, the gRNA or gRNA component may alternatively or additionally comprise one or more phosphorothioate bonds between residues at the 3' end of the polynucleotide, for example, a phosphorothioate bond between the first two 3' residues, between each of the first three 3' residues, between each of the first four 3' residues, or between each of the first five 3' residues. In an embodiment, the gRNA or gRNA components described above, comprises a phosphorothioate bond between each of the first four 5' residues (e.g., comprises or consists of, three phosphorothioate bonds at the 5' end(s)), and a phosphorothioate bond between each of the first four 3' residues (e.g., comprises or consists of, three phosphorothioate bonds at the 3' end(s)). In an embodiment, any of the phosphorothioate modifications described above can be combined with an inverted abasic residue at the 5' end, the 3' end, or both the 5' and 3' ends of the polynucleotide. In such embodiments, the inverted abasic nucleotide may be linked to the 5' and/or 3' nucleotide by a phosphate bond or a phosphorothioate bond.

[00278] In embodiments, the gRNA or gRNA components described above, comprises one or more nucleotides that include a 2' O-methyl modification. In embodiments, each of the first 1, 2, 3, or more of the 5' residues comprise a 2' O-methyl modification. In embodiments, each of the first 1, 2, 3, or more of the 3' residues comprise a 2' O-methyl modification. In

embodiments, the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues comprise a 2' O-methyl modification. In embodiments, each of the first 1, 2, 3 or more of the 5' residues comprise a 2' O-methyl modification, and each of the first 1, 2, 3 or more of the 3' residues comprise a 2' O-methyl modification. In an embodiment, each of the first 3 of the 5' residues comprise a 2' O-methyl modification, and each of the first 3 of the 3' residues comprise a 2' O-methyl modification. In embodiments, each of the first 3 of the 5' residues comprise a 2' O-methyl modification, and the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues comprise a 2' O-methyl modification. In embodiments, any of the 2' O-methyl modifications described above may be combined with one or more phosphorothioate modifications, e.g., as described above, and/or one or more inverted abasic modifications, e.g., as described above.

[00279] In an embodiment, the gRNA or gRNA components described above, comprises or consists of, a phosphorothioate bond between each of the first four 5' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a phosphorothioate bond between each of the first four 3' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a 2' O-methyl modification at each of the first three 5' residues, and a 2' O-methyl modification at each of the first three 3' residues.

[00280] In an embodiment, the gRNA or gRNA components described above, comprises or consists of, a phosphorothioate bond between each of the first four 5' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a phosphorothioate bond between each of the first four 3' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a 2' O-methyl modification at each of the first three 5' residues, and a 2' O-methyl modification at each of the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues.

[00281] In an embodiment, the gRNA or gRNA components described above, comprises or consists of, a phosphorothioate bond between each of the first four 5' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a phosphorothioate bond between each of the first four 3' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a 2' O-methyl modification at each of the first three 5' residues, a 2' O-methyl modification at each of the first three 3' residues, and an additional inverted abasic residue at each of the 5' and 3' ends.

[00282] In an embodiment, the gRNA or gRNA components described above, comprises or consists of, a phosphorothioate bond between each of the first four 5' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a phosphorothioate bond between each of the first four 3' residues (e.g., comprises or consists of three phosphorothioate bonds at the 5' end of the polynucleotide(s)), a 2' O-methyl modification at each of the first three 5' residues, and a 2' O-methyl modification at each of the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues, and an additional inverted abasic residue at each of the 5' and 3' ends.

[00283] Specific embodiments of gRNA molecules are described in detail below. Although each is shown with 20 nucleic acid residues of the targeting domain (N's in each of the sequences below), it will be understood that the targeting domain may comprise or consist of 5-50 residues, e.g., 15-30 residues, e.g., 15-25 residues, e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 residues. In embodiments, the gRNA is a dgRNA and comprises or consists of:

crRNA:

[00284] mN*mN*mN*NNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAU*mG*mC*mU (SEQ ID NO: 66), where m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein (optionally with an inverted abasic residue at the 5' and/or 3' terminus); and

tracr:

[00285] AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAA AAGUGGCACCGAGUCGGUGCUUUUUUUU (SEQ ID NO: 65) (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

[00286] In embodiments, the gRNA is a dgRNA and comprises or consists of:

crRNA:

[00287] mN*mN*mN*NNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAU*mG*mC*mU (SEQ ID NO: 66), where m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein, (optionally with an inverted abasic residue at the 5' and/or 3' terminus); and

tracr:

[00288] mA*mA*mC*AGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUUUU*mU*mU*mU (SEQ ID NO: 67), where

m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

[00289] In embodiments, the gRNA is a dgRNA and comprises or consists of:

crRNA:

[00290] mN*mN*mN*NNNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAUGCUGUU*mU*mU*mG (SEQ ID NO: 68), where m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein, (optionally with an inverted abasic residue at the 5' and/or 3' terminus); and

tracr:

[00291] AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAA AAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 65) (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

[00292] In embodiments, the gRNA is a dgRNA and comprises or consists of:

crRNA:

[00293] mN*mN*mN*NNNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAUGCUGUU*mU*mU*mG (SEQ ID NO: 68), where m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein, (optionally with an inverted abasic residue at the 5' and/or 3' terminus); and

tracr:

[00294] mA*mA*mC*AGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUUUU*mU*mU*mU (SEQ ID NO: 67), where m indicates a base with 2'O-Methyl modification, and * indicates a phosphorothioate bond (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

[00295] In embodiments, the gRNA is a sgRNA and comprises or consists of:

[00296] mN*mN*mN*NNNNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAGAAAUAGCA AGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCU*mU*mU*mU (SEQ ID NO: 69), where m indicates a base with 2'O-Methyl

modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein, (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

[00297] In embodiments, the gRNA is a sgRNA and comprises or consists of:

[00298] mN*mN*mN*NNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U (SEQ ID NO: 70, where m indicates a base with 2'O-Methyl modification, * indicates a phosphorothioate bond, and N's indicate the residues of the targeting domain, e.g., as described herein, (optionally with an inverted abasic residue at the 5' and/or 3' terminus).

6) First Tracr Extension

[00299] Where the gRNA comprises a first flagpole extension, the tracr may comprise a first tracr extension. The first tracr extension may comprise nucleotides that are complementary, e.g., 80%, 85%, 90%, 95% or 99%, e.g., fully complementary to nucleotides of the first flagpole extension. In some aspects, the first tracr extension nucleotides that hybridize with complementary nucleotides of the first flagpole extension are contiguous. In some aspects, the first tracr extension nucleotides that hybridize with complementary nucleotides of the first flagpole extension are discontinuous, e.g., comprises two or more regions of hybridization separated by nucleotides that do not base pair with nucleotides of the first flagpole extension. In some aspects, the first tracr extension comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more nucleotides. In some aspects, the first tracr extension comprises SEQ ID NO: 56. In some aspects the first tracr extension comprises nucleic acid that is at least 80%, 85%, 90%, 95% or 99% homology to SEQ ID NO: 56.

[00300] Some or all of the nucleotides of the first tracr extension can have a modification, e.g., modification found in Section XIII herein.

[00301] In some embodiments, the sgRNA may comprise, from 5' to 3' and disposed 3' to the targeting domain:

a)

GUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC (SEQ ID NO: 71);

b)

GUUUAAGAGCUAGAAAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUG
AAAAAGUGGCACCGAGUCGGUGC (SEQ ID NO: 72);

c)

GUUUUAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGU
UAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC (SEQ ID NO: 73);

d)

GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGU
UAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC (SEQ ID NO: 74);

[00302] e) any of a) to d), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides;

[00303] f) any of a) to d), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides; or

[00304] g) any of a) to f), above, further comprising, at the 5' end (e.g., at the 5' terminus, e.g., 5' to the targeting domain), at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides.

[00305] In an embodiment, a sgRNA of the disclosure comprises or consists of, from 5' to 3': [targeting domain]-

GUUUUAGAGCUAGAAAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUG
AAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 75).

[00306] In an embodiment, a sgRNA of the disclosure comprises or consists of, from 5' to 3': [targeting domain]-

GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGU
UAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 76).

[00307] In embodiments, any of a) to g) above is disposed directly 3' to the targeting domain.

[00308] In some embodiments, the dgRNA may comprise:

[00309] A crRNA comprising, from 5' to 3', preferably disposed directly 3' to the targeting domain:

a) GUUUUAGAGCUA (SEQ ID NO: 50);

- b) GUUUAAGAGCUA (SEQ ID NO: 51);
- c) GUUUUAGAGCUAUGCUG (SEQ ID NO: 77);
- d) GUUUAAGAGCUAUGCUG (SEQ ID NO: 78);
- e) GUUUUAGAGCUAUGCUGUUUUG (SEQ ID NO: 79);
- f) GUUUAAGAGCUAUGCUGUUUUG (SEQ ID NO: 80); or
- g) GUUUUAGAGCUAUGC (SEQ ID NO: 81):

[00310] and a tracer comprising, from 5' to 3':

- a)
UAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG
UCGGUGC (SEQ ID NO: 53);
- b)
UAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG
UCGGUGC (SEQ ID NO: 54);
- c)
CAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA
CCGAGUCGGUGC (SEQ ID NO: 82);
- d)
CAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA
CCGAGUCGGUGC (SEQ ID NO: 83);
- e)
AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 65);
- f)
AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 84);
- g)
GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGU
UAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 76);
- h)
AGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCAC
CGAGUCGGUGCUUU (SEQ ID NO: 85);

i)

GUUGGAACCAUUCAAAACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUC
AACUUGAAAAAGUGGCACCGAGUCGGUGCUUU (SEQ ID NO: 86);

j)

AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGC (SEQ ID NO: 87);

[00311] k) any of a) to j), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides;

[00312] l) any of a) to j), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides; or

[00313] m) any of a) to l), above, further comprising, at the 5' end (e.g., at the 5' terminus), at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides.

[00314] In an embodiment, the sequence of k), above comprises the 3' sequence UUUUUU, e.g., if a U6 promoter is used for transcription. In an embodiment, the sequence of k), above, comprises the 3' sequence UUUU, e.g., if an HI promoter is used for transcription. In an embodiment, sequence of k), above, comprises variable numbers of 3' U's depending, e.g., on the termination signal of the pol-III promoter used. In an embodiment, the sequence of k), above, comprises variable 3' sequence derived from the DNA template if a T7 promoter is used. In an embodiment, the sequence of k), above, comprises variable 3' sequence derived from the DNA template, e.g., if in vitro transcription is used to generate the RNA molecule. In an embodiment, the sequence of k), above, comprises variable 3' sequence derived from the DNA template, e.g., if a pol-II promoter is used to drive transcription.

[00315] In an embodiment, the crRNA comprises SEQ ID NO: 79 and the tracr comprises or consists of

AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGCUUUUUUUU (SEQ ID NO: 65).

[00316] In an embodiment, the crRNA comprises SEQ ID NO: 80 and the tracr comprises or consists of,

AACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGCUUUUUUUU (SEQ ID NO: 84).

[00317] In an embodiment, the crRNA comprises or consists of, a targeting domain and, disposed 3' to the targeting domain (e.g., disposed directly 3' to the targeting domain), a sequence comprising, e.g., consisting of, GUUUUAGAGCUAUGCU (SEQ ID NO: 81), and the tracr comprises or consists of, GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 76).

[00318] In an embodiment, the crRNA comprises or consists of, a targeting domain and, disposed 3' to the targeting domain (e.g., disposed directly 3' to the targeting domain), a sequence comprising, e.g., consisting of, GUUUUAGAGCUAUGCU (SEQ ID NO: 81), and the tracr comprises or consists of, AGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUU (SEQ ID NO: 85).

[00319] In an embodiment, the crRNA comprises or consists of, a targeting domain and, disposed 3' to the targeting domain (e.g., disposed directly 3' to the targeting domain), a sequence comprising, e.g., consisting of, GUUUUAGAGCUAUGCUGUUUUG (SEQ ID NO: 79), and the tracr comprises or consists of, GUUGGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUUAACUUGAAAAAGUGGCACCGAGUCGGUGCUUU (SEQ ID NO: 86).

[00320] Targeting Domains Useful for gRNA molecules and other aspects of the disclosure.

[00321] Provided in the tables below are targeting domains for gRNA molecules for use in the CRISPR systems, cells, compositions and methods of the present disclosure, for example, in reducing or eliminating the expression and/or function of TET2 and/or insertion of heterologous nucleic acid sequence (e.g., nucleic acid sequence encoding a CAR, e.g., as described herein) at or near a target sequence of TET2, e.g., of a TET2 intron or intron-exon junction.

Table 1: gRNA Targeting Domains for TET2 introns and intron-exon junctions. In the "Id" field, the first number relates to the target gene, here, indicating human TET2; the second number indicates the intron number (for example, a "1" indicates the gRNA targets a target sequence in the intron between exon 1 and exon 2); the final number is a unique identifier for the gRNA.

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_6	+	chr4:105147018-105147038	UUCUCCCCUUCGCUUUUUCU	1000
54790_1_8	+	chr4:105147019-105147039	UCUCCCCUUCGCUUUUUCUC	1001
54790_1_12	+	chr4:105147027-105147047	UCGCUUUUUCUCGGGCUUCC	1002
54790_1_13	+	chr4:105147028-105147048	CGCUUUUUCUCGGGCUUCCA	1003
54790_1_16	+	chr4:105147033-105147053	UUUCUCGGGCUUCCAGGGAC	1004
54790_1_18	+	chr4:105147034-105147054	UUCUCGGGCUUCCAGGGACU	1005
54790_1_22	+	chr4:105147035-105147055	UCUCGGGCUUCCAGGGACUG	1006
54790_1_30	+	chr4:105147072-105147092	UGUCACCCACAAAUACCAAG	1007
54790_1_32	+	chr4:105147073-105147093	GUCACCCACAAAUACCAAGA	1008
54790_1_36	+	chr4:105147079-105147099	CACAAAUACCAAGAGGGAAG	1009
54790_1_38	+	chr4:105147080-105147100	ACAAAUACCAAGAGGGAAGA	1010
54790_1_40	+	chr4:105147099-105147119	AGGGAAGCUUCACAAAUUAC	1011
54790_1_43	+	chr4:105147115-105147135	UUACUGGAGCCUCUUCAACA	1012
54790_1_59	+	chr4:105147240-105147260	CCUUUGUGCCUCCGACGAGC	1013
54790_1_63	+	chr4:105147248-105147268	CCUCCGACGAGCCGGUUUCC	1014
54790_1_83	+	chr4:105147314-105147334	UUUCUAAAAUAGUUCAGCUU	1015
54790_1_84	+	chr4:105147315-105147335	UUCUAAAAUAGUUCAGCUUU	1016
54790_1_86	+	chr4:105147316-105147336	UCUAAAAUAGUUCAGCUUUG	1017
54790_1_88	+	chr4:105147317-105147337	CUAAAAUAGUUCAGCUUUGG	1018
54790_1_112	+	chr4:105147415-105147435	ACCUCAGAGAGAACACUGAU	1019
54790_1_113	+	chr4:105147416-105147436	CCUCAGAGAGAACACUGAUA	1020
54790_1_116	+	chr4:105147445-105147465	UCGACCCUUUUUAUCAGCUGU	1021
54790_1_119	+	chr4:105147446-105147466	CGACCCUUUUUAUCAGCUGUA	1022
54790_1_122	+	chr4:105147451-105147471	CUUUUAUCAGCUGUAGGGUC	1023
54790_1_123	+	chr4:105147452-105147472	UUUUUAUCAGCUGUAGGGUCU	1024
54790_1_127	+	chr4:105147457-105147477	UCAGCUGUAGGGUCUGGGUC	1025
54790_1_129	+	chr4:105147458-105147478	CAGCUGUAGGGUCUGGGUCU	1026
54790_1_134	+	chr4:105147498-105147518	CUACCUUCUUAUCCCCCUUU	1027
54790_1_136	+	chr4:105147499-105147519	UACCUUCUUAUCCCCCUUUA	1028
54790_1_137	+	chr4:105147500-105147520	ACCUUCUUAUCCCCCUUAG	1029
54790_1_138	+	chr4:105147501-105147521	CCUUCUUAUCCCCCUUAGG	1030
54790_1_147	+	chr4:105147524-105147544	CUGUACGAAGUGAAUGUCAC	1031
54790_1_149	+	chr4:105147525-105147545	UGUACGAAGUGAAUGUCACA	1032
54790_1_152	+	chr4:105147530-105147550	GAAGUGAAUGUCACAGGGAG	1033
54790_1_155	+	chr4:105147536-105147556	AAUGUCACAGGGAGUGGAAU	1034
54790_1_158	+	chr4:105147550-105147570	UGGAAUUGGAGUACACUGAG	1035
54790_1_159	+	chr4:105147551-105147571	GGAAUUGGAGUACACUGAGU	1036
54790_1_170	+	chr4:105147588-105147608	AAGUCCGCGCGUUUUGUUAG	1037
54790_1_179	+	chr4:105147604-105147624	UUAGCGGCGCUGAGUGAAAG	1038
54790_1_184	+	chr4:105147622-105147642	AGAGGAAAGAAUAGUUUCUC	1039
54790_1_189	+	chr4:105147658-105147678	ACCAGAACUCACUUUUCUCA	1040
54790_1_194	+	chr4:105147676-105147696	CAAGGUACAUAAGUCAGCGC	1041
54790_1_195	+	chr4:105147677-105147697	AAGGUACAUAAGUCAGCGCU	1042
54790_1_198	+	chr4:105147695-105147715	CUGGGCUGAGCCUUCCAGCC	1043
54790_1_201	+	chr4:105147696-105147716	UGGGCUGAGCCUUCCAGCCU	1044
54790_1_203	+	chr4:105147697-105147717	GGGCUGAGCCUUCCAGCCUG	1045
54790_1_209	+	chr4:105147720-105147740	AAUGUAUGUAAGAGAAUUUA	1046
54790_1_210	+	chr4:105147737-105147757	UUAUGGACAAAUCUGUGUCC	1047

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_216	+	chr4:105147769-105147789	UCUCCCCGAAUCAGCUUCGUU	1048
54790_1_218	+	chr4:105147777-105147797	AUCAGCUUCGUUUUGGUUCCU	1049
54790_1_220	+	chr4:105147788-105147808	UUGGUUCCUUGGUAAGUGAC	1050
54790_1_225	+	chr4:105147800-105147820	UAAGUGACAGGCAGACACAA	1051
54790_1_226	+	chr4:105147804-105147824	UGACAGGCAGACACAAAGGC	1052
54790_1_227	+	chr4:105147810-105147830	GCAGACACAAAGGCAGGCGC	1053
54790_1_229	+	chr4:105147815-105147835	CACAAAGGCAGGCGCAGGCC	1054
54790_1_231	+	chr4:105147816-105147836	ACAAAGGCAGGCGCAGGCC	1055
54790_1_233	+	chr4:105147817-105147837	CAAAGGCAGGCGCAGGCCCG	1056
54790_1_236	+	chr4:105147820-105147840	AGGCAGGCGCAGGCCCGGGG	1057
54790_1_239	+	chr4:105147821-105147841	GGCAGGCGCAGGCCCGGGGA	1058
54790_1_240	+	chr4:105147822-105147842	GCAGGCGCAGGCCCGGGGAG	1059
54790_1_241	+	chr4:105147823-105147843	CAGGCGCAGGCCCGGGGAGG	1060
54790_1_243	+	chr4:105147826-105147846	GCGCAGGCCCGGGGAGGGGG	1061
54790_1_246	+	chr4:105147827-105147847	CGCAGGCCCGGGGAGGGGGC	1062
54790_1_248	+	chr4:105147830-105147850	AGGCCCGGGGAGGGGGCGGG	1063
54790_1_251	+	chr4:105147831-105147851	GGCCCGGGGAGGGGGCGGGA	1064
54790_1_252	+	chr4:105147832-105147852	GCCCGGGGAGGGGGCGGGAG	1065
54790_1_253	+	chr4:105147833-105147853	CCCGGGGAGGGGGCGGGAGG	1066
54790_1_256	+	chr4:105147836-105147856	GGGGAGGGGGCGGGAGGGGG	1067
54790_1_257	+	chr4:105147837-105147857	GGGAGGGGGCGGGAGGGGGU	1068
54790_1_260	+	chr4:105147838-105147858	GGAGGGGGCGGGAGGGGGUG	1069
54790_1_263	+	chr4:105147851-105147871	GGGGGUGGGGAGCGCAGCGU	1070
54790_1_264	+	chr4:105147869-105147889	GUUGGAGUUGCAAGACUGCA	1071
54790_1_268	+	chr4:105147874-105147894	AGUUGCAAGACUGCAAGGUC	1072
54790_1_269	+	chr4:105147875-105147895	GUUGCAAGACUGCAAGGUCA	1073
54790_1_270	+	chr4:105147876-105147896	UUGCAAGACUGCAAGGUCAG	1074
54790_1_280	+	chr4:105147955-105147975	GUCCCAUCCAAAUUUCUCUU	1075
54790_1_281	+	chr4:105147968-105147988	UUCUCUUUUGGCUUCUCUCUU	1076
54790_1_298	+	chr4:105148092-105148112	AUCUUGCUGAAUCUUUUCAC	1077
54790_1_300	+	chr4:105148093-105148113	UCUUGCUGAAUCUUUUCACU	1078
54790_1_306	+	chr4:105148124-105148144	UCUAGUUUUUAUUAAGCUAAU	1079
54790_1_308	+	chr4:105148125-105148145	CUAGUUUUUAUUAAGCUAAUA	1080
54790_1_313	+	chr4:105148134-105148154	UUAAGCUAAUAGGGUUUGUA	1081
54790_1_323	+	chr4:105148167-105148187	ACCUAUGACAUAAGAAGUG	1082
54790_1_325	+	chr4:105148172-105148192	UGACAUAAGAAGUGUGGCC	1083
54790_1_328	+	chr4:105148184-105148204	GUGUGGCCUGGAUAGACUCC	1084
54790_1_329	+	chr4:105148189-105148209	GCCUGGAUAGACUCCUGGAA	1085
54790_1_332	+	chr4:105148220-105148240	GAAAUUAAGUGUUUUUUGC	1086
54790_1_340	+	chr4:105148257-105148277	AUAUACUUUUAAUUACAUUG	1087
54790_1_343	+	chr4:105148258-105148278	UAUACUUUUAAUUACAUUGA	1088
54790_1_357	+	chr4:105148300-105148320	AAUGUUUAAGAAUUGAGAAA	1089
54790_1_360	+	chr4:105148315-105148335	AGAAAAGGCUUAUUUCCAG	1090
54790_1_373	+	chr4:105148368-105148388	AUUUAUAUUUUACGUGUCU	1091
54790_1_375	+	chr4:105148369-105148389	UUUAUAUUUUACGUGUCUA	1092
54790_1_380	+	chr4:105148374-105148394	AUAUUUACGUGUCUAGGGAG	1093
54790_1_388	+	chr4:105148434-105148454	GUGCUUUUUCCCCUUCAGUC	1094
54790_1_390	+	chr4:105148435-105148455	UGCUUUUUCCCCUUCAGUCA	1095

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_398	+	chr4:105148445-105148465	CCUUCAGUCAGGGAUUAUAA	1096
54790_1_399	+	chr4:105148446-105148466	CUUCAGUCAGGGAUUAUAAU	1097
54790_1_406	+	chr4:105148491-105148511	AUCAACAAAUGAUCCAUCAU	1098
54790_1_410	+	chr4:105148511-105148531	AGGAAUAAGAUUGUAUCUUA	1099
54790_1_411	+	chr4:105148512-105148532	GGAAUAAGAUUGUAUCUUA	1100
54790_1_415	+	chr4:105148519-105148539	GAUUGUAUCUUAAGGGAAGU	1101
54790_1_416	+	chr4:105148520-105148540	AUUGUAUCUUAAGGGAAGUU	1102
54790_1_423	+	chr4:105148542-105148562	GAUUCACAGAGAAAAGACAU	1103
54790_1_424	+	chr4:105148547-105148567	ACAGAGAAAAGACAUUGGUU	1104
54790_1_426	+	chr4:105148552-105148572	GAAAAGACAUUGGUUUGGUU	1105
54790_1_429	+	chr4:105148565-105148585	UUUGGUUUGGUGUGAUACUG	1106
54790_1_430	+	chr4:105148566-105148586	UUGGUUUGGUGUGAUACUGU	1107
54790_1_435	+	chr4:105148579-105148599	AUACUGUGGGUAUUGUUGCC	1108
54790_1_441	+	chr4:105148611-105148631	UCAUUACAUUUGCAUUUUAA	1109
54790_1_450	+	chr4:105148629-105148649	AAUGGAAAGUUGAAAUACUA	1110
54790_1_451	+	chr4:105148630-105148650	AUGGAAAGUUGAAAUACUAA	1111
54790_1_455	+	chr4:105148631-105148651	UGGAAAGUUGAAAUACUAAG	1112
54790_1_464	+	chr4:105148677-105148697	UAUGUGUGCUUAAUAAUGUU	1113
54790_1_482	+	chr4:105148741-105148761	AAAUGUUAUAAGCAGAGAA	1114
54790_1_487	+	chr4:105148756-105148776	GAGAACGGUUAUGAAGUGU	1115
54790_1_493	+	chr4:105148791-105148811	AAGUUUAGAAGACAAUUUAU	1116
54790_1_497	+	chr4:105148803-105148823	CAAUUUAUAGGAUUAAAAAA	1117
54790_1_503	+	chr4:105148811-105148831	AGGAUUAAAAAUGGAUAGA	1118
54790_1_526	+	chr4:105148942-105148962	UUGC UUAAUCAUUGAUACG	1119
54790_1_528	+	chr4:105148943-105148963	UGC UUAAUCAUUGAUACGU	1120
54790_1_529	+	chr4:105148944-105148964	GCUUUAAUCAUUGAUACGUG	1121
54790_1_537	+	chr4:105148965-105148985	GGUUCUUUCACAUGAUUACA	1122
54790_1_539	+	chr4:105148966-105148986	GUUCUUUCACAUGAUUACAA	1123
54790_1_547	+	chr4:105148989-105149009	AGAAGCAUUACUCAUCUCUG	1124
54790_1_551	+	chr4:105149000-105149020	UCAUCUCUGUGGAAUAGAAA	1125
54790_1_552	+	chr4:105149008-105149028	GUGGAAUAGAAACGGUUCAU	1126
54790_1_561	+	chr4:105149047-105149067	CUAAAAUUAAAACAAAAAUU	1127
54790_1_564	+	chr4:105149072-105149092	UUUACCAUUAAUGCUGUUCA	1128
54790_1_573	+	chr4:105149094-105149114	GUAAACUAUCGAGAAAACUA	1129
54790_1_587	+	chr4:105149162-105149182	ACAAACUAAUAUUUACUUUU	1130
54790_1_589	+	chr4:105149163-105149183	CAAACUAAUAUUUACUUUUU	1131
54790_1_590	+	chr4:105149164-105149184	AAACUAAUAUUUACUUUUUG	1132
54790_1_597	+	chr4:105149185-105149205	GGACAACUUUCAAUGUUG	1133
54790_1_601	+	chr4:105149202-105149222	UUGUGGUAAUACUGUCUUC	1134
54790_1_609	+	chr4:105149262-105149282	AUAAAUAAAGAAUACUACAU	1135
54790_1_614	+	chr4:105149290-105149310	AAUUUUGAAUACAACUAUGA	1136
54790_1_638	+	chr4:105149401-105149421	AAAGUAUUUCAGUGAUUAUA	1137
54790_1_645	+	chr4:105149438-105149458	UUAGUCACUUUAUCCUUUGU	1138
54790_1_658	+	chr4:105149466-105149486	AGAAAUUAUUUAAUAAGUA	1139
54790_1_659	+	chr4:105149467-105149487	GAAAUUAUUUAAUAAGUAU	1140
54790_1_660	+	chr4:105149468-105149488	AAAUUAUUUAAUAAGUAUG	1141
54790_1_672	+	chr4:105149533-105149553	UAUAUGUGAUCAUACUACCU	1142
54790_1_674	+	chr4:105149553-105149573	AGGUGCUCCAAAAAUCCAU	1143

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_676	+	chr4:105149563-105149583	AAAAUUCCAUAGGACUGUCU	1144
54790_1_677	+	chr4:105149564-105149584	AAAUUCCAUAGGACUGUCUU	1145
54790_1_682	+	chr4:105149579-105149599	GUCUUGGGUUAUUGAAUUUU	1146
54790_1_686	+	chr4:105149592-105149612	GAAUUUUAGGAACAUGAUAA	1147
54790_1_721	+	chr4:105149739-105149759	UAUUUGCCAAACUCUUCUUA	1148
54790_1_724	+	chr4:105149750-105149770	CUCUUCUUAAAGGCUUUAUU	1149
54790_1_732	+	chr4:105149780-105149800	UGCCAGUUUAUGCCAGAAGC	1150
54790_1_735	+	chr4:105149783-105149803	CAGUUUAUGCCAGAAGCCGG	1151
54790_1_740	+	chr4:105149802-105149822	GAGGAAUUGAUUGAUUUUG	1152
54790_1_741	+	chr4:105149808-105149828	UUGAUUGAUUUUGAGGCAG	1153
54790_1_743	+	chr4:105149815-105149835	GAUUUUGAGGCAGUGGCACA	1154
54790_1_747	+	chr4:105149831-105149851	CACAUGGUCCUACUAGACAU	1155
54790_1_755	+	chr4:105149876-105149896	CAAGUGAAGUGCACCUGCCA	1156
54790_1_762	+	chr4:105149910-105149930	AAGAAUUCCAAAGUCCUUAU	1157
54790_1_763	+	chr4:105149911-105149931	AGAAUUCCAAAGUCCUUAUU	1158
54790_1_764	+	chr4:105149917-105149937	CCAAAGUCCUUAUUGGGCAC	1159
54790_1_767	+	chr4:105149929-105149949	UUGGGCACUGGUCUUGUAUU	1160
54790_1_771	+	chr4:105149942-105149962	UUGUAUUAGGUAACAACAAC	1161
54790_1_796	+	chr4:105150097-105150117	AAGCCCUUCUUAUGAUUCAU	1162
54790_1_806	+	chr4:105150146-105150166	AUCCUGCCCAAAGUCUGAGU	1163
54790_1_817	+	chr4:105150205-105150225	UAAAAUAUCUUCAAAAGUUA	1164
54790_1_856	+	chr4:105150368-105150388	AUCUAGCAAUUUCAAAUCGC	1165
54790_1_867	+	chr4:105150434-105150454	AAUGUUAUUGUUUCCUACCU	1166
54790_1_872	+	chr4:105150435-105150455	AUGUUAUUGUUUCCUACCUU	1167
54790_1_874	+	chr4:105150441-105150461	UUGUUUCCUACCUUGGGAAC	1168
54790_1_879	+	chr4:105150453-105150473	UUGGGAACAGGCUAAAACUU	1169
54790_1_893	+	chr4:105150529-105150549	CCAUUGCACAGUAGUUCUUA	1170
54790_1_895	+	chr4:105150539-105150559	GUAGUUCUUAAGGAUAGUAA	1171
54790_1_902	+	chr4:105150589-105150609	UCCCAAGCCAACUUUACAAU	1172
54790_1_904	+	chr4:105150603-105150623	UACAAUUGGAGCCUUCACUG	1173
54790_1_907	+	chr4:105150604-105150624	ACAAUUGGAGCCUUCACUGU	1174
54790_1_913	+	chr4:105150630-105150650	GACCAGUUGCCAAGUAGAGC	1175
54790_1_914	+	chr4:105150633-105150653	CAGUUGCCAAGUAGAGCUGG	1176
54790_1_917	+	chr4:105150641-105150661	AAGUAGAGCUGGUGGUUAUC	1177
54790_1_919	+	chr4:105150642-105150662	AGUAGAGCUGGUGGUUAUCU	1178
54790_1_926	+	chr4:105150701-105150721	CCAAAUAUACAGUAUUUACU	1179
54790_1_939	+	chr4:105150768-105150788	GAAUACUGUGACAUAUUGA	1180
54790_1_941	+	chr4:105150771-105150791	UACUGUGACAUAUUGAAGG	1181
54790_1_944	+	chr4:105150791-105150811	AGGUUAUGCAGUACAUCUGU	1182
54790_1_945	+	chr4:105150796-105150816	AUGCAGUACAUCUGUUGGUU	1183
54790_1_948	+	chr4:105150807-105150827	CUGUUGGUUUGGUUAUAGU	1184
54790_1_954	+	chr4:105150815-105150835	UUGGUUAUAGUAGGAGAGA	1185
54790_1_955	+	chr4:105150816-105150836	UGGUUAUAGUAGGAGAGAA	1186
54790_1_960	+	chr4:105150823-105150843	UAGUAGGAGAGAAGGGUCC	1187
54790_1_963	+	chr4:105150826-105150846	UAGGAGAGAAGGGUCCAGG	1188
54790_1_964	+	chr4:105150827-105150847	AGGAGAGAAGGGUCCAGGA	1189
54790_1_968	+	chr4:105150832-105150852	AGAAGGGUCCAGGAGGGAA	1190
54790_1_969	+	chr4:105150833-105150853	GAAGGGUCCAGGAGGGAAA	1191

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_971	+	chr4:105150834-105150854	AAGGGUUCCAGGAGGGAAAG	1192
54790_1_994	+	chr4:105150989-105151009	UUCUCAAAAGAAUAGAUUU	1193
54790_1_1002	+	chr4:105151016-105151036	CCAUUCCAAAUAAACAAUUU	1194
54790_1_1004	+	chr4:105151020-105151040	UCCAAAUAAACAAUUUUGGA	1195
54790_1_1005	+	chr4:105151021-105151041	CCAAAUAAACAAUUUUGGAU	1196
54790_1_1007	+	chr4:105151026-105151046	UAACAAAUUUUUGGAUGGGCG	1197
54790_1_1013	+	chr4:105151056-105151076	UGCCUGUAAUCCUAGCACUU	1198
54790_1_1014	+	chr4:105151057-105151077	GCCUGUAAUCCUAGCACUUU	1199
54790_1_1016	+	chr4:105151060-105151080	UGUAAUCCUAGCACUUUGGG	1200
54790_1_1017	+	chr4:105151066-105151086	CCUAGCACUUUGGGAGGCCA	1201
54790_1_1023	+	chr4:105151083-105151103	CCAAGGUGAGAGAUCACUUG	1202
54790_1_1025	+	chr4:105151088-105151108	GUGAGAGAUACAUUGAGGCC	1203
54790_1_1030	+	chr4:105151106-105151126	CCAGGAGUUUGAAACCACCC	1204
54790_1_1031	+	chr4:105151107-105151127	CAGGAGUUUGAAACCACCCU	1205
54790_1_1034	+	chr4:105151120-105151140	CCACCCUGGGCAACACAGUC	1206
54790_1_1037	+	chr4:105151155-105151175	CAAAAAAUUUAAAAAGUUAG	1207
54790_1_1038	+	chr4:105151156-105151176	AAAAAAUUUAAAAAGUUAGU	1208
54790_1_1039	+	chr4:105151157-105151177	AAAAAUUUAAAAAGUUAGUG	1209
54790_1_1040	+	chr4:105151162-105151182	UUUAAAAAGUUAGUGGGGCA	1210
54790_1_1041	+	chr4:105151165-105151185	AAAAAGUUAGUGGGGGCAUGG	1211
54790_1_1046	+	chr4:105151193-105151213	UCCUGUAGUCCCAGCUACUC	1212
54790_1_1051	+	chr4:105151206-105151226	GCUACUCAGGAGACUGAGAU	1213
54790_1_1054	+	chr4:105151209-105151229	ACUCAGGAGACUGAGAUAGG	1214
54790_1_1056	+	chr4:105151213-105151233	AGGAGACUGAGAUAGGAGGA	1215
54790_1_1062	+	chr4:105151275-105151295	ACACCACUGCGCUCCAGCCC	1216
54790_1_1066	+	chr4:105151282-105151302	UGC GCUCCAGCCCAGGCAAG	1217
54790_1_1068	+	chr4:105151283-105151303	GCGCUCCAGCCCAGGCAAGA	1218
54790_1_1085	+	chr4:105151426-105151446	AAAAAGAAGAAACAGAUAGU	1219
54790_1_1088	+	chr4:105151429-105151449	AAGAAGAAACAGAUAGUAGG	1220
54790_1_1100	+	chr4:105151548-105151568	GUUUUAAGAAUUCAGAACUC	1221
54790_1_1102	+	chr4:105151553-105151573	AAGAAUUCAGAACUCAGGCC	1222
54790_1_1105	+	chr4:105151558-105151578	UUCAGAACUCAGGCCAGGUG	1223
54790_1_1106	+	chr4:105151561-105151581	AGAACUCAGGCCAGGUGUGG	1224
54790_1_1110	+	chr4:105151571-105151591	CCAGGUGUGGUGGCUCAUUC	1225
54790_1_1112	+	chr4:105151572-105151592	CAGGUGUGGUGGCUCAUUCU	1226
54790_1_1114	+	chr4:105151575-105151595	GUGUGGUGGCUCAUUCUGGG	1227
54790_1_1116	+	chr4:105151576-105151596	UGUGGUGGCUCAUUCUGGGA	1228
54790_1_1119	+	chr4:105151577-105151597	GUGGUGGCUCAUUCUGGGAG	1229
54790_1_1120	+	chr4:105151581-105151601	UGGCUCAUUCUGGGAGGGGA	1230
54790_1_1123	+	chr4:105151585-105151605	UCAUUCUGGGAGGGGAAGGC	1231
54790_1_1125	+	chr4:105151588-105151608	UUCUGGGAGGGGAAGGCAGG	1232
54790_1_1128	+	chr4:105151599-105151619	GAAGGCAGGAGGAUCACUUG	1233
54790_1_1132	+	chr4:105151622-105151642	CCAGAAGUUCUAGACCAGCC	1234
54790_1_1133	+	chr4:105151623-105151643	CAGAAGUUCUAGACCAGCCU	1235
54790_1_1152	+	chr4:105151771-105151791	GAGAAUUAAGUAAGAGACG	1236
54790_1_1153	+	chr4:105151775-105151795	AUUAAGUAAGAGACGAGGC	1237
54790_1_1155	+	chr4:105151781-105151801	GUAAGAGACGAGGCCGGUUG	1238
54790_1_1156	+	chr4:105151784-105151804	AGAGACGAGGCCGGUUGUGG	1239

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_1160	+	chr4:105151811-105151831	UGCCUGUAAUCCCAGCACUU	1240
54790_1_1161	+	chr4:105151812-105151832	GCCUGUAAUCCCAGCACUUU	1241
54790_1_1162	+	chr4:105151821-105151841	CCCAGCACUUUGGGACGACA	1242
54790_1_1163	+	chr4:105151825-105151845	GCACUUUGGGACGACAAGGC	1243
54790_1_1165	+	chr4:105151828-105151848	CUUUGGGACGACAAGGCAGG	1244
54790_1_1169	+	chr4:105151839-105151859	CAAGGCAGGUGGAUGACCUG	1245
54790_1_1171	+	chr4:105151844-105151864	CAGGUGGAUGACCUGAGGUC	1246
54790_1_1174	+	chr4:105151862-105151882	UCAGGAGUUUGAGACCAGCC	1247
54790_1_1175	+	chr4:105151871-105151891	UGAGACCAGCCUGGCCAACA	1248
54790_1_1180	+	chr4:105151910-105151930	CUAAAAAUACAAAAAUUAGC	1249
54790_1_1181	+	chr4:105151911-105151931	UAAAAAUACAAAAAUUAGCC	1250
54790_1_1182	+	chr4:105151916-105151936	AUACAAAAAUUAGCCGGGCA	1251
54790_1_1183	+	chr4:105151919-105151939	CAAAAAUUAGCCGGGCAUGG	1252
54790_1_1187	+	chr4:105151947-105151967	ACCAGUAAUCCCAGCUACUC	1253
54790_1_1188	+	chr4:105151950-105151970	AGUAAUCCCAGCUACUCAGG	1254
54790_1_1190	+	chr4:105151956-105151976	CCCAGCUACUCAGGAGGCUG	1255
54790_1_1196	+	chr4:105151978-105151998	GCCCGAGAAUCACUUGAGCC	1256
54790_1_1197	+	chr4:105151979-105151999	CCCGAGAAUCACUUGAGCCU	1257
54790_1_1198	+	chr4:105151984-105152004	GAAUCACUUGAGCCUGGGCA	1258
54790_1_1199	+	chr4:105151987-105152007	UCACUUGAGCCUGGGCAUGG	1259
54790_1_1203	+	chr4:105152014-105152034	UACCUAUAUCCCAGCACUU	1260
54790_1_1204	+	chr4:105152015-105152035	ACCUAUAUCCCAGCACUUU	1261
54790_1_1206	+	chr4:105152018-105152038	UAUAAUCCCAGCACUUUGGG	1262
54790_1_1208	+	chr4:105152024-105152044	CCCAGCACUUUGGGAGGCCG	1263
54790_1_1209	+	chr4:105152028-105152048	GCACUUUGGGAGGCCGAGGC	1264
54790_1_1211	+	chr4:105152031-105152051	CUUUGGGAGGCCGAGGCAGG	1265
54790_1_1215	+	chr4:105152047-105152067	CAGGUGGAUCACCUGACGUC	1266
54790_1_1218	+	chr4:105152065-105152085	UCAGGAUUCGAGACCAGUC	1267
54790_1_1219	+	chr4:105152074-105152094	CGAGACCAGUCUGGCCAACA	1268
54790_1_1223	+	chr4:105152112-105152132	ACUAAACAUACAAAAUAGC	1269
54790_1_1224	+	chr4:105152113-105152133	CUAAACAUACAAAAUAGCU	1270
54790_1_1225	+	chr4:105152118-105152138	CAUACAAAAUAGCUGGGUG	1271
54790_1_1226	+	chr4:105152121-105152141	ACAAAAUAGCUGGGUGUGG	1272
54790_1_1229	+	chr4:105152149-105152169	GCCUGUAGUCUCAGCUAUUC	1273
54790_1_1231	+	chr4:105152152-105152172	UGUAGUCUCAGCUAUUCUGG	1274
54790_1_1234	+	chr4:105152162-105152182	GCUAUUCUGGAGGCUGAUAC	1275
54790_1_1241	+	chr4:105152184-105152204	GAGAAUUGCUUGAACCCUCC	1276
54790_1_1243	+	chr4:105152185-105152205	AGAAUUGCUUGAACCCUCCC	1277
54790_1_1244	+	chr4:105152188-105152208	AUUGCUUGAACCCUCCCGGG	1278
54790_1_1247	+	chr4:105152194-105152214	UGAACCCUCCCGGGAGGCAG	1279
54790_1_1249	+	chr4:105152200-105152220	CUCCCGGGAGGCAGAGGCUG	1280
54790_1_1252	+	chr4:105152213-105152233	GAGGCUGCGGUGAGCCGAGA	1281
54790_1_1254	+	chr4:105152234-105152254	GGCUCUGCUGCACUCCAGCC	1282
54790_1_1255	+	chr4:105152235-105152255	GCUCUGCUGCACUCCAGCCU	1283
54790_1_1257	+	chr4:105152240-105152260	GCUGCACUCCAGCCUGGGCG	1284
54790_1_1263	+	chr4:105152287-105152307	GAAAAUAAUAAUAAUAAU	1285
54790_1_1267	+	chr4:105152302-105152322	UAAAUAGGAGAUGAAUAAU	1286
54790_1_1269	+	chr4:105152303-105152323	AAAUAGGAGAUGAAUAAU	1287

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_1272	+	chr4:105152321-105152341	UUGGGAUAAAGUGUUUUUGA	1288
54790_1_1275	+	chr4:105152331-105152351	GUGUUUUUGAAGGACAGUCU	1289
54790_1_1281	+	chr4:105152347-105152367	GUCUAGGAUAUAAAUGAAC	1290
54790_1_1290	+	chr4:105152408-105152428	UACAUUUCUUUUUUGUCUAU	1291
54790_1_1293	+	chr4:105152412-105152432	UUUCUUUUUUGUCUAUUGGA	1292
54790_1_1296	+	chr4:105152416-105152436	UUUUUUGUCUAUUGGAAGGU	1293
54790_1_1310	+	chr4:105152484-105152504	ACCUCUCAGUCAAUUUUAA	1294
54790_1_1339	+	chr4:105152599-105152619	UUUUUUUUUUUUUUUUUGAGA	1295
54790_1_1356	+	chr4:105152620-105152640	GGUAUCUUGCUCUGUCACCU	1296
54790_1_1359	+	chr4:105152624-105152644	UCUUGCUCUGUCACCUAGGC	1297
54790_1_1361	+	chr4:105152634-105152654	UCACCUAGGCUGGAGUGCAG	1298
54790_1_1362	+	chr4:105152645-105152665	GGAGUGCAGUGGUGUGAUCU	1299
54790_1_1363	+	chr4:105152670-105152690	CACUGCAACCUCUGCCUCC	1300
54790_1_1369	+	chr4:105152708-105152728	UUCUCAGCCCCCAGAGUAGC	1301
54790_1_1371	+	chr4:105152709-105152729	UCUCAGCCCCCAGAGUAGCU	1302
54790_1_1375	+	chr4:105152715-105152735	CCCCCAGAGUAGCUGGGACU	1303
54790_1_1377	+	chr4:105152736-105152756	GGAGCGUGCCCCACCACACC	1304
54790_1_1380	+	chr4:105152765-105152785	UUUCUAUUUUUAUUAGAGAC	1305
54790_1_1381	+	chr4:105152766-105152786	UUCUAUUUUUAUUAGAGACA	1306
54790_1_1390	+	chr4:105152780-105152800	GAGACAGGGUUUCACCAUGU	1307
54790_1_1392	+	chr4:105152785-105152805	AGGGUUUCACCAUGUUGGCC	1308
54790_1_1396	+	chr4:105152803-105152823	CCAGGCUGAUCUCGUACUCC	1309
54790_1_1397	+	chr4:105152810-105152830	GAUCUCGUACUCCUGGUCUC	1310
54790_1_1399	+	chr4:105152826-105152846	UCUCAGGUGAUCUGCCUGCC	1311
54790_1_1400	+	chr4:105152827-105152847	CUCAGGUGAUCUGCCUGCCC	1312
54790_1_1402	+	chr4:105152843-105152863	GCCCGGGUCUCCCAAAGUGC	1313
54790_1_1404	+	chr4:105152844-105152864	CCCGGGUCUCCCAAAGUGCU	1314
54790_1_1405	+	chr4:105152852-105152872	UCCCAAAGUGCUGGGAUUAC	1315
54790_1_1407	+	chr4:105152871-105152891	CAGGCAUGAGCCACUGCACC	1316
54790_1_1415	+	chr4:105152920-105152940	AAAAAUAGUGUUAAGUGUCU	1317
54790_1_1416	+	chr4:105152926-105152946	AGUGUUAAGUGUCUUGGUGA	1318
54790_1_1418	+	chr4:105152935-105152955	UGUCUUGGUGAUGGUGAUGA	1319
54790_1_1421	+	chr4:105152939-105152959	UUGGUGAUGGUGAUGAUGGU	1320
54790_1_1423	+	chr4:105152947-105152967	GGUGAUGAUGGUAGGAGUAA	1321
54790_1_1424	+	chr4:105152977-105152997	UCCUUAACAUUUAAUUUCUAC	1322
54790_1_1428	+	chr4:105152983-105153003	CAUUUAAUUUCUACAGGCUA	1323
54790_1_1436	+	chr4:105153029-105153049	AUUUUAAGCACAAAAGUGAA	1324
54790_1_1442	+	chr4:105153049-105153069	UGGUUUUUAGUAAACUUAUA	1325
54790_1_1443	+	chr4:105153050-105153070	GGUUUUUAGUAAACUUAUAU	1326
54790_1_1469	+	chr4:105153160-105153180	ACUUGCUCAAUUUCCCCCAG	1327
54790_1_1475	+	chr4:105153247-105153267	CCAUGAUACUGACAUUGAUG	1328
54790_1_1526	+	chr4:105153484-105153504	AAGUCCUUUUUUUGAUAGAA	1329
54790_1_1546	+	chr4:105153567-105153587	CUCAUCACAACCCUAGAGAU	1330
54790_1_1553	+	chr4:105153597-105153617	CUUAUCCCUAUUUAUGAGUG	1331
54790_1_1560	+	chr4:105153616-105153636	GAGGAAACUGAAGCCCAGUG	1332
54790_1_1563	+	chr4:105153654-105153674	AAGUUCAUACAGCCUAUACA	1333
54790_1_1565	+	chr4:105153660-105153680	AUACAGCCUAUACAUGGCUU	1334
54790_1_1581	+	chr4:105153766-105153786	AGCUGUAAAAGUGUAUAAUG	1335

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_1587	+	chr4:105153791-105153811	UAUGUAGAGAAAGUCAUAAA	1336
54790_1_1594	+	chr4:105153864-105153884	CAUUACAGCAUUAUUAUAA	1337
54790_1_1599	+	chr4:105153874-105153894	UUAUUAUAAUUGGUAAAAAA	1338
54790_1_1604	+	chr4:105153922-105153942	AUGAGUGAAUAAACAAAUUG	1339
54790_1_1609	+	chr4:105153961-105153981	AAUAUUAUUAAGUAGUAUAA	1340
54790_1_1611	+	chr4:105153966-105153986	UAUUAAGUAGUAUAAAGGAA	1341
54790_1_1614	+	chr4:105153992-105154012	AUUGAUAAAUGCUGUCACAU	1342
54790_1_1620	+	chr4:105154005-105154025	GUCACAUAGGUGAAUCUGAG	1343
54790_1_1623	+	chr4:105154016-105154036	GAAUCUGAGAGGCACAAGAA	1344
54790_1_1628	+	chr4:105154060-105154080	UUUUAAGUAACGUCCAGAAU	1345
54790_1_1633	+	chr4:105154071-105154091	GUCCAGAAUAGGCAAAUCUA	1346
54790_1_1637	+	chr4:105154085-105154105	AAUCUAAGGAGACAGAAAGU	1347
54790_1_1639	+	chr4:105154100-105154120	AAAGUUGGCUAGUUAUUACU	1348
54790_1_1641	+	chr4:105154101-105154121	AAGUUGGCUAGUUAUUACUA	1349
54790_1_1642	+	chr4:105154102-105154122	AGUUGGCUAGUUAUUACUAG	1350
54790_1_1646	+	chr4:105154107-105154127	GCUAGUUAUUACUAGGGGCU	1351
54790_1_1647	+	chr4:105154108-105154128	CUAGUUAUUACUAGGGGCUA	1352
54790_1_1650	+	chr4:105154112-105154132	UUAUUACUAGGGGCUAGGGA	1353
54790_1_1651	+	chr4:105154113-105154133	UAUUACUAGGGGCUAGGGAU	1354
54790_1_1655	+	chr4:105154116-105154136	UACUAGGGGCUAGGGAUGGG	1355
54790_1_1657	+	chr4:105154117-105154137	ACUAGGGGCUAGGGAUGGGA	1356
54790_1_1660	+	chr4:105154120-105154140	AGGGGCUAGGGAUGGGAGGG	1357
54790_1_1662	+	chr4:105154151-105154171	AAUAAGUAUGAGAUUUCUUU	1358
54790_1_1678	+	chr4:105154240-105154260	ACUGAAUUAUAUGCUUUA	1359
54790_1_1694	+	chr4:105154312-105154332	AUGAAUGUAGUUGAGUUAU	1360
54790_1_1711	+	chr4:105154362-105154382	AUCUCAUGCAAAAGAAU	1361
54790_1_1713	+	chr4:105154372-105154392	AAAGAAUAGCAGGAACUAU	1362
54790_1_1716	+	chr4:105154383-105154403	GGAACUAUUUGGAUUGAAU	1363
54790_1_1721	+	chr4:105154402-105154422	GAGGCUAAGCAUAUCUUUCU	1364
54790_1_1723	+	chr4:105154409-105154429	AGCAUAUCUUUCUAGGAAGA	1365
54790_1_1726	+	chr4:105154417-105154437	UUUCUAGGAAGAUGGCAUCA	1366
54790_1_1729	+	chr4:105154442-105154462	UUUUAUUAUGCCUGUAAUCC	1367
54790_1_1734	+	chr4:105154450-105154470	UGCCUGUAAUCCUGGCACUU	1368
54790_1_1738	+	chr4:105154451-105154471	GCCUGUAAUCCUGGCACUUU	1369
54790_1_1739	+	chr4:105154454-105154474	UGUAAUCCUGGCACUUUGGG	1370
54790_1_1740	+	chr4:105154460-105154480	CCUGGCACUUUGGGAGGCCA	1371
54790_1_1743	+	chr4:105154463-105154483	GGCACUUUGGGAGGCCAAGG	1372
54790_1_1744	+	chr4:105154464-105154484	GCACUUUGGGAGGCCAAGGC	1373
54790_1_1751	+	chr4:105154490-105154510	CCAGAAGUUUGAGAUUAGUC	1374
54790_1_1752	+	chr4:105154491-105154511	CAGAAGUUUGAGAUUAGUCU	1375
54790_1_1759	+	chr4:105154516-105154536	ACAUCCUCUUAUAGAUGAGA	1376
54790_1_1761	+	chr4:105154539-105154559	AUACUUAUUCACUCAAAGU	1377
54790_1_1770	+	chr4:105154581-105154601	AAUAGCCUUUAGAGCUCAUA	1378
54790_1_1773	+	chr4:105154582-105154602	AUAGCCUUUAGAGCUCAU	1379
54790_1_1776	+	chr4:105154605-105154625	AAGAUUCAUAGAUAGUGAU	1380
54790_1_1778	+	chr4:105154618-105154638	UAGUGAUAGGUUAUAUGACU	1381
54790_1_1781	+	chr4:105154626-105154646	GGUUAUAUGACUUGGUAAAG	1382
54790_1_1782	+	chr4:105154627-105154647	GUUAUAUGACUUGGUAAAGA	1383

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_1785	+	chr4:105154640-105154660	GUAAAGAGGGCUUAAUGUAAU	1384
54790_1_1793	+	chr4:105154690-105154710	GUUACCUAGCCAUCAGUUC	1385
54790_1_1801	+	chr4:105154714-105154734	GAUGUAACCCAAGUGUAAA	1386
54790_1_1803	+	chr4:105154725-105154745	AGUGUAAAAGGAAUGUGAC	1387
54790_1_1804	+	chr4:105154726-105154746	GUGUAAAAGGAAUGUGACU	1388
54790_1_1805	+	chr4:105154731-105154751	AAAAGGAAUGUGACUGGGUG	1389
54790_1_1807	+	chr4:105154734-105154754	AGGAAUGUGACUGGGUGCGG	1390
54790_1_1809	+	chr4:105154765-105154785	UGUAAUCCCAGCACUUUGCG	1391
54790_1_1811	+	chr4:105154768-105154788	AAUCCCAGCACUUUGCGAGG	1392
54790_1_1814	+	chr4:105154774-105154794	AGCACUUUGCGAGGCGGAAG	1393
54790_1_1815	+	chr4:105154775-105154795	GCACUUUGCGAGGCGGAAGU	1394
54790_1_1817	+	chr4:105154778-105154798	CUUUGCGAGGCGGAAGUGGG	1395
54790_1_1818	+	chr4:105154779-105154799	UUUGCGAGGCGGAAGUGGGU	1396
54790_1_1824	+	chr4:105154794-105154814	UGGGUGGGUCUCUUGAGCUC	1397
54790_1_1827	+	chr4:105154800-105154820	GGUCUCUUGAGCUCAGGAGU	1398
54790_1_1830	+	chr4:105154812-105154832	UCAGGAGUUGGAGACAAGCC	1399
54790_1_1831	+	chr4:105154813-105154833	CAGGAGUUGGAGACAAGCCU	1400
54790_1_1832	+	chr4:105154821-105154841	GGAGACAAGCCUGGGCAACA	1401
54790_1_1835	+	chr4:105154860-105154880	CAAAAAAUGCACAAAUUAGC	1402
54790_1_1836	+	chr4:105154861-105154881	AAAAAAUGCACAAAUUAGCU	1403
54790_1_1837	+	chr4:105154866-105154886	AUGCACAAAUUAGCUGGGUG	1404
54790_1_1838	+	chr4:105154869-105154889	CACAAAUUAGCUGGGUGUGG	1405
54790_1_1840	+	chr4:105154889-105154909	UGGCACAUCCCUGUAGUUCC	1406
54790_1_1842	+	chr4:105154898-105154918	CCUGUAGUUCCAGGUACUUG	1407
54790_1_1844	+	chr4:105154899-105154919	CUGUAGUUCCAGGUACUUGU	1408
54790_1_1845	+	chr4:105154900-105154920	UGUAGUUCCAGGUACUUGUG	1409
54790_1_1847	+	chr4:105154906-105154926	UCCAGGUACUUGUGGGGCUG	1410
54790_1_1850	+	chr4:105154909-105154929	AGGUACUUGUGGGGCUGAGG	1411
54790_1_1853	+	chr4:105154910-105154930	GGUACUUGUGGGGCUGAGGC	1412
54790_1_1855	+	chr4:105154913-105154933	ACUUGUGGGGCUGAGGCGGG	1413
54790_1_1856	+	chr4:105154917-105154937	GUGGGGCUGAGGCGGGAGGA	1414
54790_1_1861	+	chr4:105154928-105154948	GCGGGAGGAUGGCUCGAGCC	1415
54790_1_1862	+	chr4:105154929-105154949	CGGGAGGAUGGCUCGAGCCU	1416
54790_1_1865	+	chr4:105154938-105154958	GGCUCGAGCCUGGGAAGUUG	1417
54790_1_1867	+	chr4:105154957-105154977	GAGGCUGCAGUGAGCCAUGU	1418
54790_1_1870	+	chr4:105154978-105154998	GGUGCCCCCACACUUCAGCC	1419
54790_1_1871	+	chr4:105154979-105154999	GUGCCCCCACACUUCAGCCU	1420
54790_1_1887	+	chr4:105155091-105155111	UAAUAACAAAUUACUAGAUAU	1421
54790_1_1889	+	chr4:105155092-105155112	AAUAACAAAUUACUAGAUUU	1422
54790_1_1890	+	chr4:105155093-105155113	AUAACAAAUUACUAGAUUUG	1423
54790_1_1892	+	chr4:105155094-105155114	UAACAAAUUACUAGAUUUGG	1424
54790_1_1893	+	chr4:105155095-105155115	AACAAAUUACUAGAUUUGGG	1425
54790_1_1902	+	chr4:105155128-105155148	CUUAUCUAUGUGAAAACAGA	1426
54790_1_1903	+	chr4:105155129-105155149	UUAUCUAUGUGAAAACAGAA	1427
54790_1_1906	+	chr4:105155138-105155158	UGAAAACAGAAGGGCAAUGC	1428
54790_1_1907	+	chr4:105155139-105155159	GAAAACAGAAGGGCAAUGCA	1429
54790_1_1927	+	chr4:105155237-105155257	AAA AUGACAAAGUAUCUCAU	1430
54790_1_1928	+	chr4:105155238-105155258	AAAUGACAAAGUAUCUCAUA	1431

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_1932	+	chr4:105155278-105155298	UUUCCUGUUAACUGAUACUG	1432
54790_1_1938	+	chr4:105155301-105155321	CAUGUUGAAGAUGUAAAAUA	1433
54790_1_1943	+	chr4:105155310-105155330	GAUGUAAAAUAAGGUUGAAA	1434
54790_1_1948	+	chr4:105155343-105155363	GCAGCAGUCUUCAUAAUGCC	1435
54790_1_1955	+	chr4:105155360-105155380	GCCAGGACAAAGUGAGAAAC	1436
54790_1_1956	+	chr4:105155361-105155381	CCAGGACAAAGUGAGAAACA	1437
54790_1_1959	+	chr4:105155376-105155396	AAACAGGGUCAGAAUGAUGA	1438
54790_1_1960	+	chr4:105155399-105155419	CUCUCCAUCUUUGCUACACA	1439
54790_1_1966	+	chr4:105155448-105155468	AACUUCUACAAACCACUUAC	1440
54790_1_1972	+	chr4:105155485-105155505	AUUUUUAAACACUAGUCCCUA	1441
54790_1_1978	+	chr4:105155506-105155526	GGAACUAUGACUUGUAGUUU	1442
54790_1_1980	+	chr4:105155515-105155535	ACUUGUAGUUUUGGACACAC	1443
54790_1_1981	+	chr4:105155516-105155536	CUUGUAGUUUUGGACACACA	1444
54790_1_1989	+	chr4:105155528-105155548	GACACACAGGGUGAAUUACU	1445
54790_1_1990	+	chr4:105155529-105155549	ACACACAGGGUGAAUUACUU	1446
54790_1_1991	+	chr4:105155530-105155550	CACACAGGGUGAAUUACUUG	1447
54790_1_2011	+	chr4:105155628-105155648	UUUUAUUCUCAUGAGAAUGC	1448
54790_1_2012	+	chr4:105155629-105155649	UUUAUUCUCAUGAGAAUGCU	1449
54790_1_2018	+	chr4:105155639-105155659	UGAGAAUGCUGGGUUGCAGC	1450
54790_1_2020	+	chr4:105155643-105155663	AAUGCUGGGUUGCAGCCGGU	1451
54790_1_2024	+	chr4:105155657-105155677	GCCGGUUGGAUCCCAUACCU	1452
54790_1_2025	+	chr4:105155658-105155678	CCGGUUGGAUCCCAUACCUU	1453
54790_1_2028	+	chr4:105155676-105155696	UUGGGACCAUGACUGAUAAC	1454
54790_1_2033	+	chr4:105155681-105155701	ACCAUGACUGAUAACUGGAG	1455
54790_1_2038	+	chr4:105155700-105155720	GUGGAGAAAAUUCACUGAUC	1456
54790_1_2039	+	chr4:105155705-105155725	GAAAAUUCACUGAUCUGGAA	1457
54790_1_2043	+	chr4:105155717-105155737	AUCUGGAAAGGUUGAGCUUU	1458
54790_1_2044	+	chr4:105155718-105155738	UCUGGAAAGGUUGAGCUUUA	1459
54790_1_2047	+	chr4:105155737-105155757	AGGGUUCAGAGACUUAUUUA	1460
54790_1_2055	+	chr4:105155763-105155783	ACAUGUGAUUGUACCCAAUA	1461
54790_1_2058	+	chr4:105155774-105155794	UACCCAAUAAGGAAGUAUAU	1462
54790_1_2077	+	chr4:105155861-105155881	UGAUCAUAGCAUCUACUUGU	1463
54790_1_2086	+	chr4:105155923-105155943	UGUUAGACCCAUUAAGAAGU	1464
54790_1_2088	+	chr4:105155934-105155954	UUAAGAAGUUGGUGUAGUGA	1465
54790_1_2092	+	chr4:105155940-105155960	AGUUGGUGUAGUGAUGGUUA	1466
54790_1_2097	+	chr4:105155963-105155983	AAAGCAGUAAGAUAGAAUUU	1467
54790_1_2100	+	chr4:105155981-105156001	UUAGGUUCUGUUCUCCUUAC	1468
54790_1_2138	+	chr4:105156175-105156195	UAAAUCUGUUCUCGCAUAUU	1469
54790_1_2158	+	chr4:105156235-105156255	UUUAUAGUAAUUUAUACAGA	1470
54790_1_2168	+	chr4:105156263-105156283	CAUAUUCAAAAGAAGAAAAA	1471
54790_1_2169	+	chr4:105156264-105156284	AUAUUCAAAAGAAGAAAAAU	1472
54790_1_2178	+	chr4:105156301-105156321	UGAUGUACUACUCUCUUCAA	1473
54790_1_2180	+	chr4:105156302-105156322	GAUGUACUACUCUCUUCAAA	1474
54790_1_2181	+	chr4:105156319-105156339	AAAGGGAAUUGCCUAUGUUC	1475
54790_1_2186	+	chr4:105156333-105156353	AUGUUCAGGCAUAGAAAUGC	1476
54790_1_2188	+	chr4:105156349-105156369	AUGCAGGCAGUCUGACAUUU	1477
54790_1_2207	+	chr4:105156424-105156444	AUUUGUCACAGUUUGUUCUG	1478
54790_1_2208	+	chr4:105156425-105156445	UUUGUCACAGUUUGUUCUGU	1479

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_2210	+	chr4:105156428-105156448	GUCACAGUUUGUUCUGUGGG	1480
54790_1_2213	+	chr4:105156429-105156449	UCACAGUUUGUUCUGUGGGU	1481
54790_1_2216	+	chr4:105156441-105156461	CUGUGGGUGGGUAAAAGUAA	1482
54790_1_2231	+	chr4:105156546-105156566	UAAAUCUAGCUUCUAUGUCC	1483
54790_1_2239	+	chr4:105156585-105156605	ACAUUCACCCAUCUCUCAAA	1484
54790_1_2240	+	chr4:105156586-105156606	CAUUCACCCAUCUCUCAAAU	1485
54790_1_2249	+	chr4:105156649-105156669	AAAAGUAAAAAAGCUUCAAU	1486
54790_1_2251	+	chr4:105156650-105156670	AAAGUAAAAAAGCUUCAUA	1487
54790_1_2254	+	chr4:105156678-105156698	GAAAGCCAGAUACAUAAGCA	1488
54790_1_2262	+	chr4:105156726-105156746	CUUACCUGUCUGCACUAAGA	1489
54790_1_2265	+	chr4:105156727-105156747	UUACCUGUCUGCACUAAGAA	1490
54790_1_2278	+	chr4:105156840-105156860	CUAUCCAUAACAUACUGUCC	1491
54790_1_2310	+	chr4:105156941-105156961	AGAAUUUUUAUAUUUGCCA	1492
54790_1_2323	+	chr4:105156995-105157015	UUCAUUUAUUUGCAUUA	1493
54790_1_2373	+	chr4:105157234-105157254	GAAAAGAAGAAUACCAUAA	1494
54790_1_2374	+	chr4:105157235-105157255	AAAAGAAGAAUACCAUAAU	1495
54790_1_2378	+	chr4:105157254-105157274	UGGGUACCUUUCAAAAUGA	1496
54790_1_2394	+	chr4:105157346-105157366	ACAAACAGAUACAUUUUAGC	1497
54790_1_2411	+	chr4:105157411-105157431	UCCAAUCUAGCCACUGAAA	1498
54790_1_2422	+	chr4:105157463-105157483	CAUAAGUUGAAUUUAAAACA	1499
54790_1_2435	+	chr4:105157506-105157526	UGUCUGCCACAUAACGCUUG	1500
54790_1_2437	+	chr4:105157517-105157537	UUACGCUUGUGGAAAAACAC	1501
54790_1_2442	+	chr4:105157551-105157571	GCUAAUAGACAUUUUGCUGU	1502
54790_1_2446	+	chr4:105157567-105157587	CUGUUGGCUCACCUUAUUA	1503
54790_1_2457	+	chr4:105157621-105157641	GCAAACUUGAAAAAGACGUU	1504
54790_1_2461	+	chr4:105157634-105157654	AGACGUUUGGUUACUAACUG	1505
54790_1_2463	+	chr4:105157635-105157655	GACGUUUGGUUACUAACUGU	1506
54790_1_2471	+	chr4:105157675-105157695	UAUUUUUAUUUUUUUAUUUU	1507
54790_1_2489	+	chr4:105157699-105157719	AGAGUCUCACUCUCUUGCCC	1508
54790_1_2492	+	chr4:105157703-105157723	UCUCACUCUCUUGCCCAGGC	1509
54790_1_2493	+	chr4:105157713-105157733	UUGCCCAGGCUGGAGUGCAG	1510
54790_1_2495	+	chr4:105157724-105157744	GGAGUGCAGUGGCAUGAUCU	1511
54790_1_2498	+	chr4:105157748-105157768	UCACUGCAGCCUCCUCCUUC	1512
54790_1_2499	+	chr4:105157749-105157769	CACUGCAGCCUCCUCCUUCU	1513
54790_1_2505	+	chr4:105157788-105157808	GUCUCAGCCUCCCGAGUAGC	1514
54790_1_2507	+	chr4:105157789-105157809	UCUCAGCCUCCCGAGUAGCU	1515
54790_1_2508	+	chr4:105157797-105157817	UCCCGAGUAGCUGGGAUUAU	1516
54790_1_2510	+	chr4:105157816-105157836	UAGGCACCAGCCACCAUGCC	1517
54790_1_2521	+	chr4:105157860-105157880	GAAACAGCGUUUCGCCAUGU	1518
54790_1_2522	+	chr4:105157865-105157885	AGCGUUUCGCCAUGUAGGCU	1519
54790_1_2523	+	chr4:105157869-105157889	UUUCGCCAUGUAGGCUAGGC	1520
54790_1_2529	+	chr4:105157923-105157943	CCUUCUGCUUCCUAAAGUGC	1521
54790_1_2530	+	chr4:105157924-105157944	CUUCUGCUUCCUAAAGUGCU	1522
54790_1_2532	+	chr4:105157932-105157952	UCCUAAAGUGCUGGGAUUAC	1523
54790_1_2535	+	chr4:105157945-105157965	GGAUUACAGGCAUGAGCCAU	1524
54790_1_2536	+	chr4:105157950-105157970	ACAGGCAUGAGCCAUCGGCC	1525
54790_1_2547	+	chr4:105158014-105158034	UUAUUUACUGUUA	1526
54790_1_2553	+	chr4:105158040-105158060	UUAUUUCAAAUAAGAUUUUA	1527

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_2574	+	chr4:105158110-105158130	ACCAACAUUUUUCAAGAGCA	1528
54790_1_2578	+	chr4:105158111-105158131	CCAACAUUUUUCAAGAGCAU	1529
54790_1_2582	+	chr4:105158120-105158140	UUCAAGAGCAUGGGAAAUCU	1530
54790_1_2584	+	chr4:105158121-105158141	UCAAGAGCAUGGGAAAUCUA	1531
54790_1_2587	+	chr4:105158126-105158146	AGCAUGGGAAAUCUAGGGUA	1532
54790_1_2592	+	chr4:105158158-105158178	GUGACUUUAAAGACACUUCU	1533
54790_1_2593	+	chr4:105158159-105158179	UGACUUUAAAGACACUUCUU	1534
54790_1_2630	+	chr4:105158269-105158289	AUUAGUCAUGCCUUAUCCU	1535
54790_1_2631	+	chr4:105158270-105158290	UUAGUCAUGCCUUAUCCUC	1536
54790_1_2632	+	chr4:105158271-105158291	UAGUCAUGCCUUAUCCUCG	1537
54790_1_2635	+	chr4:105158278-105158298	GCCUUAUCCUCGGGGUUUU	1538
54790_1_2638	+	chr4:105158279-105158299	CCUUAUCCUCGGGGUUUUU	1539
54790_1_2642	+	chr4:105158293-105158313	GUUUUUGGGAAACUAUAUUU	1540
54790_1_2643	+	chr4:105158294-105158314	UUUUUUGGGAAACUAUAUUUA	1541
54790_1_2644	+	chr4:105158295-105158315	UUUUUGGGAAACUAUAUUUAG	1542
54790_1_2655	+	chr4:105158338-105158358	AUUGUAAUUUUUCUCAGUAU	1543
54790_1_2662	+	chr4:105158350-105158370	CUCAGUAUUGGUAAGAAUUC	1544
54790_1_2665	+	chr4:105158359-105158379	GGUAAGAAUUCAGGUGUUUA	1545
54790_1_2669	+	chr4:105158364-105158384	GAAUUCAGGUGUUUAAGGAA	1546
54790_1_2684	+	chr4:105158424-105158444	GAUAUAAUGAAUGUAGAUGA	1547
54790_1_2688	+	chr4:105158440-105158460	AUGAAGGUGAAAUCCGAGAU	1548
54790_1_2692	+	chr4:105158448-105158468	GAAAUCCGAGAUAGGAAGAG	1549
54790_1_2695	+	chr4:105158480-105158500	ACUUUUUUUUCUUCACCCA	1550
54790_1_2707	+	chr4:105158502-105158522	GAAAGCCAUUGAAUACUGAA	1551
54790_1_2708	+	chr4:105158503-105158523	AAAGCCAUUGAAUACUGAAU	1552
54790_1_2711	+	chr4:105158523-105158543	GGGUCAUGUUGUAAUUUAAU	1553
54790_1_2712	+	chr4:105158524-105158544	GGUCAUGUUGUAAUUUAAUU	1554
54790_1_2721	+	chr4:105158574-105158594	GCCUACUUAGUGUAUAUCUC	1555
54790_1_2734	+	chr4:105158635-105158655	ACUGAAGUAAAUAAGCAAGC	1556
54790_1_2738	+	chr4:105158656-105158676	GGAAUAAGUCCUGCAAUAG	1557
54790_1_2748	+	chr4:105158719-105158739	AACUGAUCCUAAAUUGAAUU	1558
54790_1_2756	+	chr4:105158756-105158776	UAGAUUACAAGAAAUGCAAC	1559
54790_1_2762	+	chr4:105158788-105158808	UUACAGUUCUCCUCUUUUU	1560
54790_1_2780	+	chr4:105158868-105158888	ACAUCUGUAUGCUCAUUUUU	1561
54790_1_2782	+	chr4:105158869-105158889	CAUCUGUAUGCUCAUUUUUA	1562
54790_1_2783	+	chr4:105158884-105158904	UUUUAGGGCCAAAAAUAGU	1563
54790_1_2789	+	chr4:105158895-105158915	AAAAAUAGUAGGCUUCUCUU	1564
54790_1_2795	+	chr4:105158933-105158953	UCUCUCCUCCAGUUACACG	1565
54790_1_2801	+	chr4:105158956-105158976	UCACAUCAACAUUUGACACG	1566
54790_1_2802	+	chr4:105158957-105158977	CACAUCAACAUUUGACACGU	1567
54790_1_2804	+	chr4:105158971-105158991	ACACGUGGGUACCGUGCACG	1568
54790_1_2807	+	chr4:105158999-105159019	GUAUUUACAAACACCAUCCU	1569
54790_1_2814	+	chr4:105159026-105159046	CAGAGACUCUUAUGUAAACAG	1570
54790_1_2820	+	chr4:105159052-105159072	GAGUAAGCUUUGAGUGUCUG	1571
54790_1_2821	+	chr4:105159053-105159073	AGUAAGCUUUGAGUGUCUGU	1572
54790_1_2824	+	chr4:105159056-105159076	AAGCUUUGAGUGUCUGUGGG	1573
54790_1_2827	+	chr4:105159059-105159079	CUUUGAGUGUCUGUGGGCGG	1574
54790_1_2832	+	chr4:105159087-105159107	ACACAGUUUAAUUCAUUGUC	1575

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_2834	+	chr4:105159088-105159108	CACAGUUUAAUUCAUUGUCC	1576
54790_1_2837	+	chr4:105159101-105159121	AUUGUCCGGGAGCCCUUGUC	1577
54790_1_2841	+	chr4:105159111-105159131	AGCCCUUGUCUGGCUCUGAU	1578
54790_1_2842	+	chr4:105159112-105159132	GCCCUUGUCUGGCUCUGAUA	1579
54790_1_2845	+	chr4:105159132-105159152	GGGUCAUGAACC AAAGAUCA	1580
54790_1_2846	+	chr4:105159140-105159160	AACCAAAGAUCAAGGUGUUU	1581
54790_1_2848	+	chr4:105159145-105159165	AAGAUCAAGGUGUUUAGGUC	1582
54790_1_2851	+	chr4:105159163-105159183	UCAGGAUAUUCCCUAACGCA	1583
54790_1_2870	+	chr4:105159253-105159273	UUUUUUUUUUUUUUUUUGAGA	1584
54790_1_2888	+	chr4:105159275-105159295	GAGUUUCGCUCUUGCUGCCA	1585
54790_1_2891	+	chr4:105159279-105159299	UUCGCUCUUGCUGCCAAGGU	1586
54790_1_2895	+	chr4:105159289-105159309	CUGCCAAGGUUGGAGUGCAG	1587
54790_1_2897	+	chr4:105159303-105159323	GUGCAGUGGCGCCGCGAUCU	1588
54790_1_2898	+	chr4:105159328-105159348	CACUGCAACCUC CGCCUCAC	1589
54790_1_2903	+	chr4:105159367-105159387	GCCUCAGACACCCAAGUAGC	1590
54790_1_2904	+	chr4:105159368-105159388	CCUCAGACACCCAAGUAGCU	1591
54790_1_2905	+	chr4:105159376-105159396	ACCCAAGUAGCUGGGAUU AU	1592
54790_1_2907	+	chr4:105159395-105159415	UAGGCAUGCGCCACCACGCC	1593
54790_1_2910	+	chr4:105159422-105159442	UUUUGUAUUUUUAGUACAGA	1594
54790_1_2911	+	chr4:105159423-105159443	UUUGUAUUUUUAGUACAGAC	1595
54790_1_2912	+	chr4:105159424-105159444	UUGUAUUUUUAGUACAGACG	1596
54790_1_2920	+	chr4:105159438-105159458	CAGACGGGGUUUCUCCAUGU	1597
54790_1_2921	+	chr4:105159447-105159467	UUUCUCCAUGUUGGUCAGCC	1598
54790_1_2926	+	chr4:105159468-105159488	GGUGUUGAACUCCCGACUUA	1599
54790_1_2928	+	chr4:105159485-105159505	UUAAGGUGAUCCGCUUGCUU	1600
54790_1_2932	+	chr4:105159501-105159521	GCUUCGGCCCCC CAAAGUGC	1601
54790_1_2934	+	chr4:105159502-105159522	CUUCGGCCCCC CAAAGUGCU	1602
54790_1_2936	+	chr4:105159510-105159530	CCCCAAAGUGCUGGGAUUAC	1603
54790_1_2946	+	chr4:105159595-105159615	GCCAAACCAUUUUUGUGAUU	1604
54790_1_2949	+	chr4:105159596-105159616	CCAAACCAUUUUUGUGAUUU	1605
54790_1_2950	+	chr4:105159597-105159617	CAAACCAUUUUUGUGAUUUG	1606
54790_1_2960	+	chr4:105159621-105159641	AACAUGAGCAGAUGAUGCUU	1607
54790_1_2971	+	chr4:105159716-105159736	GCCUUUAAAAA AUACAUCU	1608
54790_1_2973	+	chr4:105159721-105159741	UAAAAAAUUA CAUCUUGGCC	1609
54790_1_2976	+	chr4:105159725-105159745	AAAUUACAUCU UGGCCAGGA	1610
54790_1_2979	+	chr4:105159744-105159764	AUGGCUCACGCCUGUAAUCC	1611
54790_1_2982	+	chr4:105159752-105159772	CGCCUGUAAUCC CGGCAUUU	1612
54790_1_2983	+	chr4:105159753-105159773	GCCUGUAAUCC CGGCAUUUU	1613
54790_1_2985	+	chr4:105159756-105159776	UGUAAUCCCGG CAAUUUUGGG	1614
54790_1_2986	+	chr4:105159762-105159782	CCCGGCAUUUUG GGAGGCCA	1615
54790_1_2988	+	chr4:105159765-105159785	GGCAUUUUGGG AGGCCAAGG	1616
54790_1_2989	+	chr4:105159766-105159786	GCAUUUUGGG AGGCCAAGGC	1617
54790_1_2990	+	chr4:105159769-105159789	UUUUGGGAGGCC AAGGCGGG	1618
54790_1_2996	+	chr4:105159791-105159811	GCAAGAGAUCG AGAUCAUCC	1619
54790_1_2997	+	chr4:105159800-105159820	CGAGAUCAUCC UGGCCAACA	1620
54790_1_3000	+	chr4:105159839-105159859	CUAAAAAUACA AAAAAUAGC	1621
54790_1_3001	+	chr4:105159840-105159860	UAAAAAUACA AAAAAUAGCU	1622
54790_1_3002	+	chr4:105159845-105159865	AUACAAAAAUU AGCUGGGCG	1623

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_3003	+	chr4:105159848-105159868	CAAAAAUUAGCUGGGCGUGG	1624
54790_1_3005	+	chr4:105159851-105159871	AAAUUAGCUGGGCGUGGUGG	1625
54790_1_3006	+	chr4:105159852-105159872	AAUUAGCUGGGCGUGGUGGC	1626
54790_1_3010	+	chr4:105159875-105159895	CGCCUGUAAUCCCAGCUACU	1627
54790_1_3011	+	chr4:105159876-105159896	GCCUGUAAUCCCAGCUACUU	1628
54790_1_3013	+	chr4:105159885-105159905	CCCAGCUACUUGGGAGACUG	1629
54790_1_3016	+	chr4:105159889-105159909	GCUACUUGGGAGACUGUGGC	1630
54790_1_3021	+	chr4:105159907-105159927	GCAGGAGAAUCGCUUGACCC	1631
54790_1_3023	+	chr4:105159908-105159928	CAGGAGAAUCGCUUGACCCC	1632
54790_1_3025	+	chr4:105159911-105159931	GAGAAUCGCUUGACCCCGGG	1633
54790_1_3027	+	chr4:105159914-105159934	AAUCGCUUGACCCCGGGAGG	1634
54790_1_3029	+	chr4:105159917-105159937	CGCUUGACCCCGGGAGGCGG	1635
54790_1_3034	+	chr4:105159957-105159977	CGCGCCACUGCACUCCAGCC	1636
54790_1_3047	+	chr4:105160057-105160077	GAUUGACUUCCCAAACUAAA	1637
54790_1_3054	+	chr4:105160089-105160109	AAAACACUCAAGAAAACUCU	1638
54790_1_3071	+	chr4:105160237-105160257	AGCUUUAAGUCUCUAUAUUU	1639
54790_1_3074	+	chr4:105160238-105160258	GCUUUAAGUCUCUAUAUUUA	1640
54790_1_3095	+	chr4:105160321-105160341	GCAAGUUGAAAUAAAAAAAAA	1641
54790_1_3099	+	chr4:105160357-105160377	AAUGUCUAACCACGUUAUUU	1642
54790_1_3100	+	chr4:105160371-105160391	UAUAUUUUGGUAUAUGUAUAC	1643
54790_1_3103	+	chr4:105160399-105160419	UGUAUUAGCUGUAAGCAGAC	1644
54790_1_3117	+	chr4:105160454-105160474	UUCUUUUUGUAUUGCAUCUA	1645
54790_1_3125	+	chr4:105160468-105160488	CAUCUAAGGAUCAUUUGAGA	1646
54790_1_3155	+	chr4:105160628-105160648	UACACUACCUUUCUAAAGAU	1647
54790_1_3163	+	chr4:105160689-105160709	AUAUGUAUUUUUUUAAAAUAA	1648
54790_1_3175	+	chr4:105160733-105160753	CAAGCACCAAUUCUGUUUUUU	1649
54790_1_3177	+	chr4:105160734-105160754	AAGCACCAAUUCUGUUUUUUU	1650
54790_1_3178	+	chr4:105160735-105160755	AGCACCAAUUCUGUUUUUUUG	1651
54790_1_3179	+	chr4:105160736-105160756	GCACCAAUUCUGUUUUUUUGG	1652
54790_1_3180	+	chr4:105160744-105160764	UCUGUUUUUUGGGGGUUUUU	1653
54790_1_3182	+	chr4:105160752-105160772	UUGGGGGUUUUUUGGUUUGU	1654
54790_1_3208	+	chr4:105160799-105160819	AGAGUCUCCCUCUGUCGCCC	1655
54790_1_3211	+	chr4:105160803-105160823	UCUCCCUCUGUCGCCCAGGC	1656
54790_1_3215	+	chr4:105160813-105160833	UCGCCCAGGCUGGAGUGAAG	1657
54790_1_3217	+	chr4:105160823-105160843	UGGAGUGAAGCGGAGCGAUC	1658
54790_1_3218	+	chr4:105160824-105160844	GGAGUGAAGCGGAGCGAUCU	1659
54790_1_3220	+	chr4:105160848-105160868	UCACCGCAACCUCCGCCUCC	1660
54790_1_3221	+	chr4:105160849-105160869	CACCGCAACCUCCGCCUCCU	1661
54790_1_3222	+	chr4:105160872-105160892	UUCAGCAAUUCUCUGCCUC	1662
54790_1_3225	+	chr4:105160878-105160898	CAAUUCUCUGCCUCAGGCUU	1663
54790_1_3230	+	chr4:105160887-105160907	GCCUCAGGCUUCGGAGUAGC	1664
54790_1_3231	+	chr4:105160888-105160908	CCUCAGGCUUCGGAGUAGCU	1665
54790_1_3232	+	chr4:105160896-105160916	UUCGGAGUAGCUGGGAUUAC	1666
54790_1_3235	+	chr4:105160915-105160935	CAGGCACUCGCCACCACGCC	1667
54790_1_3237	+	chr4:105160940-105160960	AAUUUUUGUAUUUUUAGUAG	1668
54790_1_3239	+	chr4:105160943-105160963	UUUUGUAUUUUUAGUAGAGG	1669
54790_1_3241	+	chr4:105160944-105160964	UUUGUAUUUUUAGUAGAGGC	1670
54790_1_3243	+	chr4:105160945-105160965	UUGUAUUUUUAGUAGAGGCG	1671

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_3251	+	chr4:105160959-105160979	GAGGCGGGGUUUUACCAUCU	1672
54790_1_3252	+	chr4:105160964-105160984	GGGGUUUUACCAUCUUGGUC	1673
54790_1_3253	+	chr4:105160968-105160988	UUUUACCAUCUUGGUCAGGC	1674
54790_1_3259	+	chr4:105160987-105161007	CUGGUUUUGAACUCCUGACC	1675
54790_1_3264	+	chr4:105161020-105161040	GCCUCAGCCUCCCAAAGUGC	1676
54790_1_3266	+	chr4:105161021-105161041	CCUCAGCCUCCCAAAGUGCU	1677
54790_1_3267	+	chr4:105161029-105161049	UCCCAAAGUGCUGGGAUUAC	1678
54790_1_3269	+	chr4:105161053-105161073	GUUUUUCUUUAAGUAAUACU	1679
54790_1_3281	+	chr4:105161075-105161095	GUAUAAGAGAACUUUAUAUC	1680
54790_1_3290	+	chr4:105161128-105161148	UUAUUCACAUAUAGAAACUC	1681
54790_1_3301	+	chr4:105161168-105161188	CUAAAGCUGUUCUCAUUUAG	1682
54790_1_3309	+	chr4:105161214-105161234	UUAACUAACAAUAAAUCUA	1683
54790_1_3320	+	chr4:105161259-105161279	GCAGAGCAAAGCAGCCUUC	1684
54790_1_3340	+	chr4:105161348-105161368	AAUUAAAGAUGCGAUGAGAGU	1685
54790_1_3354	+	chr4:105161407-105161427	UCUACUUGCUUUUUUAGUGU	1686
54790_1_3361	+	chr4:105161442-105161462	GUAUUUCUCUCAAUUAUCCU	1687
54790_1_3366	+	chr4:105161462-105161482	CGGCCUAAAUAGUAAAAGCU	1688
54790_1_3367	+	chr4:105161463-105161483	GGCCUAAAUAGUAAAAGCUU	1689
54790_1_3388	+	chr4:105161583-105161603	UUAUAUUUUUCCCUCUUUCU	1690
54790_1_3396	+	chr4:105161612-105161632	GUUUCACAGUAAAUCAUAUA	1691
54790_1_3403	+	chr4:105161646-105161666	AAGUGCUCAGAAUUUGAUUA	1692
54790_1_3408	+	chr4:105161673-105161693	AAGUUAUUUUCUACUAAAAA	1693
54790_1_3410	+	chr4:105161674-105161694	AGUUAUUUUCUACUAAAAAA	1694
54790_1_3415	+	chr4:105161697-105161717	AUUCAAAUAAGAACUUUCAUU	1695
54790_1_3424	+	chr4:105161721-105161741	UGUACUGUAGUUUCACUUGA	1696
54790_1_3425	+	chr4:105161722-105161742	GUACUGUAGUUUCACUUGAA	1697
54790_1_3426	+	chr4:105161723-105161743	UACUGUAGUUUCACUUGAAG	1698
54790_1_3430	+	chr4:105161761-105161781	CAUUGACUUUAUCAAUGCAU	1699
54790_1_3440	+	chr4:105161822-105161842	UGUAUUUAUAAAUAUCAGAA	1700
54790_1_3444	+	chr4:105161848-105161868	AUUGAAUCUGAUGCAUACCA	1701
54790_1_3449	+	chr4:105161858-105161878	AUGCAUACCAAGGAGCAAUG	1702
54790_1_3450	+	chr4:105161868-105161888	AGGAGCAAUGUGGAAAUUUU	1703
54790_1_3460	+	chr4:105161910-105161930	UACUACUAAGUGUGUGUAUG	1704
54790_1_3470	+	chr4:105161957-105161977	UAUUUAAGCUGAAUCCUCUU	1705
54790_1_3475	+	chr4:105161966-105161986	UGAAUCCUCUUUGGUAGAAA	1706
54790_1_3491	+	chr4:105162068-105162088	UUGAAAGUGCACAGAAUCCU	1707
54790_1_3492	+	chr4:105162069-105162089	UGAAAGUGCACAGAAUCCUU	1708
54790_1_3493	+	chr4:105162070-105162090	GAAAGUGCACAGAAUCCUUG	1709
54790_1_3496	+	chr4:105162097-105162117	UUGUAUAAACUGUUUUUAUA	1710
54790_1_3506	+	chr4:105162119-105162139	GUUCCUGUAGAAGACAGCUG	1711
54790_1_3508	+	chr4:105162155-105162175	CACAAAACAAACAGCUUGCU	1712
54790_1_3512	+	chr4:105162177-105162197	GUGAUGAUAAACAUUCGUGCA	1713
54790_1_3515	+	chr4:105162178-105162198	UGAUGAUAAACAUUCGUGCAA	1714
54790_1_3518	+	chr4:105162196-105162216	AAGGGAGUUCUCUCUUGCAU	1715
54790_1_3520	+	chr4:105162205-105162225	CUCUCUUGCAUAGGAGUCCC	1716
54790_1_3523	+	chr4:105162229-105162249	UACCCUAAUGCCUUCCCACA	1717
54790_1_3527	+	chr4:105162241-105162261	UUCCCAUAUGGUCAAACACA	1718
54790_1_3539	+	chr4:105162299-105162319	AGCCUGCAGUUGUUUAUCAG	1719

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_3540	+	chr4:105162300-105162320	GCCUGCAGUUGUUUAUCAGU	1720
54790_1_3542	+	chr4:105162307-105162327	GUUGUUUAUCAGUGGGAUAC	1721
54790_1_3545	+	chr4:105162308-105162328	UUGUUUAUCAGUGGGAUACA	1722
54790_1_3552	+	chr4:105162319-105162339	UGGGAUACAGGGAGAAAGAG	1723
54790_1_3554	+	chr4:105162350-105162370	UUACUAAACUGUUUAAUGACC	1724
54790_1_3563	+	chr4:105162385-105162405	GAUACAGAAUAAGAAAGCAC	1725
54790_1_3566	+	chr4:105162397-105162417	GAAAGCACUGGCCUGACUGC	1726
54790_1_3568	+	chr4:105162398-105162418	AAAGCACUGGCCUGACUGCA	1727
54790_1_3569	+	chr4:105162399-105162419	AAGCACUGGCCUGACUGCAG	1728
54790_1_3571	+	chr4:105162407-105162427	GCCUGACUGCAGGGGAAACA	1729
54790_1_3574	+	chr4:105162421-105162441	GAAACAUGGUAGAUGCCUAA	1730
54790_1_3575	+	chr4:105162424-105162444	ACAUGGUAGAUGCCUAAAGG	1731
54790_1_3587	+	chr4:105162476-105162496	AACUAUCAUUAUCACCUGAA	1732
54790_1_3596	+	chr4:105162530-105162550	UUUAACCCUGACAAGCAAGU	1733
54790_1_3602	+	chr4:105162555-105162575	CUUUAGUAUUCAAGAACUGA	1734
54790_1_3608	+	chr4:105162570-105162590	ACUGAAGGUGACAAGCCCUG	1735
54790_1_3622	+	chr4:105162678-105162698	CAUGCCUUCAUAGAAACAGU	1736
54790_1_3659	+	chr4:105162812-105162832	GAACUAUUUUGCUUAACAUI	1737
54790_1_3670	+	chr4:105162847-105162867	AGCCUAUAUCUGCAAUAAUA	1738
54790_1_3672	+	chr4:105162848-105162868	GCCUAUAUCUGCAAUAAUAC	1739
54790_1_3674	+	chr4:105162849-105162869	CCUAUAUCUGCAAUAAUACG	1740
54790_1_3686	+	chr4:105162898-105162918	UAAUGAUAAAGAGAAAGAAA	1741
54790_1_3691	+	chr4:105162914-105162934	GAAAAGGUGAGAAGUAAUUU	1742
54790_1_3694	+	chr4:105162915-105162935	AAAAGGUGAGAAGUAAUUUU	1743
54790_1_3698	+	chr4:105162939-105162959	AAUAUGCAAUGAUAAACUAG	1744
54790_1_3704	+	chr4:105162979-105162999	ACCAGCAGCUGUGCUUAGCA	1745
54790_1_3706	+	chr4:105162995-105163015	AGCAUGGAUAAUUGCCUAAA	1746
54790_1_3713	+	chr4:105163020-105163040	GAGAAAAAAAAGUAAAAAUC	1747
54790_1_3777	+	chr4:105163278-105163298	GCUUAUAAGACAUUGCCACC	1748
54790_1_3789	+	chr4:105163356-105163376	UAUUUUCAAACAUAGAAUCA	1749
54790_1_3797	+	chr4:105163375-105163395	AUGGAUUGCUACAAGCUGAA	1750
54790_1_3807	+	chr4:105163426-105163446	UGCAUUUACAGAUAGAGAAA	1751
54790_1_3810	+	chr4:105163429-105163449	AUUUACAGAUAGAGAAAUGG	1752
54790_1_3814	+	chr4:105163434-105163454	CAGAUAGAGAAAUGGAGGCA	1753
54790_1_3816	+	chr4:105163435-105163455	AGAUAGAGAAAUGGAGGCAU	1754
54790_1_3822	+	chr4:105163519-105163539	UAUUGAUUAAGUUCUUAUGU	1755
54790_1_3823	+	chr4:105163520-105163540	AUUGAUUAAGUUCUUAUGUU	1756
54790_1_3834	+	chr4:105163585-105163605	UAUGUCAUCUAUAUUUUUGU	1757
54790_1_3843	+	chr4:105163613-105163633	UUACUCUCCUCACUUUACUA	1758
54790_1_3850	+	chr4:105163630-105163650	CUAAGGAAGAAACCAAGACA	1759
54790_1_3852	+	chr4:105163631-105163651	UAAGGAAGAAACCAAGACAU	1760
54790_1_3853	+	chr4:105163632-105163652	AAGGAAGAAACCAAGACAUG	1761
54790_1_3857	+	chr4:105163669-105163689	UAUAAAUUUUGAAUUAUCUU	1762
54790_1_3871	+	chr4:105163743-105163763	UAAAUCAACUCUUAACAGU	1763
54790_1_3873	+	chr4:105163762-105163782	UUGGAUGCCAACAAGCAGUC	1764
54790_1_3876	+	chr4:105163769-105163789	CCAACAAGCAGUCUGGUGUU	1765
54790_1_3908	+	chr4:105163881-105163901	UGUGUGUCCAGCUUUGUUG	1766
54790_1_3921	+	chr4:105163977-105163997	GUGAAGUGAUUAUUACUAUC	1767

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_3926	+	chr4:105164023-105164043	UCAGUCAUUUUUUGUGUUUA	1768
54790_1_3939	+	chr4:105164059-105164079	GAGCUACUCAA AUGUAGUCA	1769
54790_1_3943	+	chr4:105164131-105164151	GAAUGUAUUAAAUAUUCAUC	1770
54790_1_3949	+	chr4:105164189-105164209	UUCCCCUACUACCCAGCCCA	1771
54790_1_3963	+	chr4:105164265-105164285	UAUAAGUGAGAUCAUGCAAU	1772
54790_1_3973	+	chr4:105164323-105164343	UAGCUGUGUAUGUCAUAUUC	1773
54790_1_3985	+	chr4:105164393-105164413	AACUAAUAAUUCUUAUCUCA	1774
54790_1_3989	+	chr4:105164405-105164425	UUAUCUCAUGGAUUACUGAG	1775
54790_1_3994	+	chr4:105164449-105164469	AAAACAUCCAGCAUGUUACU	1776
54790_1_4007	+	chr4:105164517-105164537	GUGUUGAGCAUCUAUGUAUC	1777
54790_1_4013	+	chr4:105164549-105164569	AGCCAUCAUCUUUACCCUUC	1778
54790_1_4015	+	chr4:105164559-105164579	UUUACCCUUCUGGAAUAUAC	1779
54790_1_4019	+	chr4:105164567-105164587	UCUGGAAUAUACAGGCUCAU	1780
54790_1_4033	+	chr4:105164621-105164641	CAUAAUGAGAU GAAAAUUAU	1781
54790_1_4034	+	chr4:105164634-105164654	AAAUUAUAGGACUCAUAGAC	1782
54790_1_4038	+	chr4:105164644-105164664	ACUCAUAGACUGGUCAGUUG	1783
54790_1_4041	+	chr4:105164655-105164675	GGUCAGUUGAGGAAUUUCCC	1784
54790_1_4045	+	chr4:105164680-105164700	GCUUCCAGCCUCUGCUCAAA	1785
54790_1_4049	+	chr4:105164706-105164726	GAAUUCCCAGUUGCCUGAAU	1786
54790_1_4052	+	chr4:105164718-105164738	GCCUGAAUAGGCGCCAGAGU	1787
54790_1_4056	+	chr4:105164738-105164758	UGGCAUAGCUUUCUCAGUAU	1788
54790_1_4057	+	chr4:105164739-105164759	GGCAUAGCUUUCUCAGUAUU	1789
54790_1_4060	+	chr4:105164749-105164769	UCUCAGUAUUGGGACCUGAC	1790
54790_1_4062	+	chr4:105164750-105164770	CUCAGUAUUGGGACCUGACA	1791
54790_1_4069	+	chr4:105164789-105164809	ACAGCACAGCCUCUGAAGAU	1792
54790_1_4072	+	chr4:105164796-105164816	AGCCUCUGAAGAUUGGCUCA	1793
54790_1_4073	+	chr4:105164797-105164817	GCCUCUGAAGAUUGGCUCAA	1794
54790_1_4076	+	chr4:105164798-105164818	CCUCUGAAGAUUGGCUCAAG	1795
54790_1_4078	+	chr4:105164799-105164819	CUCUGAAGAUUGGCUCAAGG	1796
54790_1_4082	+	chr4:105164811-105164831	GCUCAAGGGGGAAGAGAUGA	1797
54790_1_4107	+	chr4:105164955-105164975	UAGAAAUAUUAAAUGAUAGC	1798
54790_1_4110	+	chr4:105164977-105164997	GCAUGAUUUAAAAAGUACUA	1799
54790_1_4120	+	chr4:105165024-105165044	CUAUUUUGUAUCAUAUUUUC	1800
54790_1_4129	+	chr4:105165044-105165064	AGGAAGAAGAGACAACAUUU	1801
54790_1_4134	+	chr4:105165075-105165095	GCUUAAAGAUAGAUGAUAGC	1802
54790_1_4135	+	chr4:105165076-105165096	CUUAAAGAUAGAUGAUAGCC	1803
54790_1_4138	+	chr4:105165081-105165101	AGAUAGAUGAUAGCCGGGUG	1804
54790_1_4139	+	chr4:105165084-105165104	UAGAUGAUAGCCGGGUGUGG	1805
54790_1_4142	+	chr4:105165111-105165131	GACCUGUAAUUCCAGCACUU	1806
54790_1_4144	+	chr4:105165112-105165132	ACCUGUAAUUCCAGCACUUU	1807
54790_1_4145	+	chr4:105165115-105165135	UGUAAUUCCAGCACUUUGGG	1808
54790_1_4147	+	chr4:105165121-105165141	UCCAGCACUUUGGGAGGCCG	1809
54790_1_4150	+	chr4:105165124-105165144	AGCACUUUGGGAGGCCGAGG	1810
54790_1_4151	+	chr4:105165125-105165145	GCACUUUGGGAGGCCGAGGC	1811
54790_1_4155	+	chr4:105165139-105165159	CGAGGCGGGCAGAUCACCUG	1812
54790_1_4157	+	chr4:105165144-105165164	CGGGCAGAUCACCUGAGGUC	1813
54790_1_4160	+	chr4:105165162-105165182	UCAGGAGUUUGAAACCAACC	1814
54790_1_4166	+	chr4:105165212-105165232	AAAAAAUACAAAAAUUAGCC	1815

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_4167	+	chr4:105165217-105165237	AUACAAAAAUUAGCCAGGCG	1816
54790_1_4168	+	chr4:105165220-105165240	CAAAAAUUAGCCAGGCGUGG	1817
54790_1_4170	+	chr4:105165223-105165243	AAAUUAGCCAGGCGUGGUGG	1818
54790_1_4171	+	chr4:105165224-105165244	AAUUAGCCAGGCGUGGUGGU	1819
54790_1_4174	+	chr4:105165248-105165268	GCCUGUAAUUCCAGCCACUC	1820
54790_1_4177	+	chr4:105165257-105165277	UCCAGCCACUCAGGAGACUG	1821
54790_1_4185	+	chr4:105165280-105165300	CACGAGAAUCACUUGAACCC	1822
54790_1_4186	+	chr4:105165283-105165303	GAGAAUCACUUGAACCCAGG	1823
54790_1_4188	+	chr4:105165289-105165309	CACUUGAACCCAGGAGGCAG	1824
54790_1_4194	+	chr4:105165329-105165349	CGUGCCAUUGCACUCCAGCC	1825
54790_1_4195	+	chr4:105165330-105165350	GUGCCAUUGCACUCCAGCCU	1826
54790_1_4199	+	chr4:105165339-105165359	CACUCCAGCCUGGGUGACAG	1827
54790_1_4201	+	chr4:105165340-105165360	ACUCCAGCCUGGGUGACAGA	1828
54790_1_4204	+	chr4:105165385-105165405	AAAAUAAAAAAUAAUUGUCU	1829
54790_1_4206	+	chr4:105165398-105165418	AUUGUCUUGGUGUGCUAAUC	1830
54790_1_4213	+	chr4:105165416-105165436	UCAGGAGCUUCCUGUGAGAG	1831
54790_1_4216	+	chr4:105165431-105165451	GAGAGUGGAAAUUCCUACA	1832
54790_1_4220	+	chr4:105165451-105165471	UGGCAGUGUCAUGAAAUUUU	1833
54790_1_4229	+	chr4:105165494-105165514	GAGUGUCUCAAAAUAGUUA	1834
54790_1_4247	+	chr4:105165562-105165582	UUGAAGUUUCUUUGAGAACU	1835
54790_1_4261	+	chr4:105165670-105165690	GAUUAUUGCCAUGUAUAAGU	1836
54790_1_4263	+	chr4:105165671-105165691	AUUAUUGCCAUGUAUAAGUU	1837
54790_1_4271	+	chr4:105165706-105165726	ACCUUUCUAAGUCUGCAUUU	1838
54790_1_4272	+	chr4:105165707-105165727	CCUUUCUAAGUCUGCAUUUA	1839
54790_1_4280	+	chr4:105165740-105165760	CACAAAUGAAAUGUUUGAU	1840
54790_1_4289	+	chr4:105165778-105165798	AGUGACUUUUCAAAAUGUAU	1841
54790_1_4291	+	chr4:105165785-105165805	UUUCAAAAUGUAUAGGAGCA	1842
54790_1_4330	+	chr4:105166026-105166046	AAUUUAUAAUAUUUAUAUUC	1843
54790_1_4350	+	chr4:105166147-105166167	CACUGUAACACCUAGCAGUA	1844
54790_1_4357	+	chr4:105166165-105166185	UAUGGUUGAACAUGUAGAAA	1845
54790_1_4360	+	chr4:105166207-105166227	CUAAAAUUUAGCUUGUUCUA	1846
54790_1_4366	+	chr4:105166227-105166247	AGGAUGCUACUUUAAGCAUU	1847
54790_1_4367	+	chr4:105166228-105166248	GGAUGCUACUUUAAGCAUUA	1848
54790_1_4369	+	chr4:105166236-105166256	CUUUAAGCAUUAGGGUAAAA	1849
54790_1_4383	+	chr4:105166303-105166323	AUUUUUGUUUCUUUCACAUU	1850
54790_1_4452	+	chr4:105166507-105166527	GUUUCUUCUCAUUUUUCUCC	1851
54790_1_4490	+	chr4:105166610-105166630	AAAAAAAAAGAAAAAAAAAAC	1852
54790_1_4491	+	chr4:105166611-105166631	AAAAAAAAAGAAAAAAAAACA	1853
54790_1_4492	+	chr4:105166612-105166632	AAAAAAAAAGAAAAAAAAACAG	1854
54790_1_4515	+	chr4:105166735-105166755	AGUAAUUUUCUCUCAGAGCU	1855
54790_1_4517	+	chr4:105166736-105166756	GUAAUUUUCUCUCAGAGCUU	1856
54790_1_4521	+	chr4:105166745-105166765	UCUCAGAGCUUGGGAAACAU	1857
54790_1_4526	+	chr4:105166768-105166788	UACGUUGUUACCCUUCAUCU	1858
54790_1_4543	+	chr4:105166851-105166871	UCCCUAUUCAUAUGUUUAUU	1859
54790_1_4556	+	chr4:105166890-105166910	UUCUGAAAUUCCUCCAGAU	1860
54790_1_4564	+	chr4:105166940-105166960	CUUGAUGAUUCUGUACAAUC	1861
54790_1_4567	+	chr4:105166967-105166987	AACUGCCUUUAUUUAGCUUA	1862
54790_1_4592	+	chr4:105167044-105167064	CUUUAUGAAACUCAUGUUA	1863

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_4639	+	chr4:105167212-105167232	CUCUGAUUGAUUCUUUUUAA	1864
54790_1_4643	+	chr4:105167227-105167247	UUUAAUGGUAGCCUAUUUCG	1865
54790_1_4652	+	chr4:105167260-105167280	AUAAAAUGUAUUAAAUUUUG	1866
54790_1_4654	+	chr4:105167261-105167281	UAAAAUGUAUUAAAUUUUGU	1867
54790_1_4655	+	chr4:105167270-105167290	UUAAAUUUUGUGGGGAAA AUU	1868
54790_1_4684	+	chr4:105167581-105167601	ACUGACUAAUUUUCAGAACU	1869
54790_1_4685	+	chr4:105167590-105167610	UUUUCAGAACUUGGUGUGUA	1870
54790_1_4694	+	chr4:105167639-105167659	GCUUUAGUAUUACAGUGCCC	1871
54790_1_4698	+	chr4:105167700-105167720	GUUCAUCCUGUACAGAUCUA	1872
54790_1_4701	+	chr4:105167721-105167741	GGUGUAAACUAUUUUCAUUUC	1873
54790_1_4702	+	chr4:105167722-105167742	GUGUAAACUAUUUUCAUUUCU	1874
54790_1_4704	+	chr4:105167729-105167749	UAUUUUCAUUUCUGGGCCCU	1875
54790_1_4710	+	chr4:105167740-105167760	CUGGGCCCUUGGAGAUUCUU	1876
54790_1_4721	+	chr4:105167782-105167802	CUAUCUUGCUGUUCAAUAAC	1877
54790_1_4726	+	chr4:105167794-105167814	UCAAUAAACAGGUAAUAGAAA	1878
54790_1_4737	+	chr4:105167864-105167884	AAAUAAAUGUGAAACCCGUA	1879
54790_1_4740	+	chr4:105167888-105167908	CGUAAUCUUGCCUAGCUUUA	1880
54790_1_4744	+	chr4:105167896-105167916	UGCCUAGCUUUAAGGAAUGA	1881
54790_1_4755	+	chr4:105167924-105167944	CUAGAAACAACAGAGAGAAA	1882
54790_1_4760	+	chr4:105167978-105167998	UCUACCUGUAAAGUAUAUUC	1883
54790_1_4774	+	chr4:105168069-105168089	AAAGUGCAGUUUCCCUGUCA	1884
54790_1_4775	+	chr4:105168070-105168090	AAGUGCAGUUUCCCUGUCAU	1885
54790_1_4785	+	chr4:105168114-105168134	UCCCCCUUCUUACCUCACCG	1886
54790_1_4786	+	chr4:105168115-105168135	CCCCCUUCUUACCUCACCGU	1887
54790_1_4794	+	chr4:105168163-105168183	GAUCAUUUAAAAAUUAAGUC	1888
54790_1_4799	+	chr4:105168196-105168216	CCUCUGCUUAAAACCAUUA	1889
54790_1_4800	+	chr4:105168197-105168217	CUCUGCUUAAAACCAUUAU	1890
54790_1_4811	+	chr4:105168263-105168283	CCACCAGUCCUCAAGUGAAU	1891
54790_1_4822	+	chr4:105168330-105168350	UCAUUCUAUUCUAAUUUCCU	1892
54790_1_4826	+	chr4:105168347-105168367	CCUUGGUUUUCUUGCUGUCC	1893
54790_1_4835	+	chr4:105168377-105168397	AAGAGCAUCCUUUUUCCUCC	1894
54790_1_4844	+	chr4:105168406-105168426	CACUUGCUGUUCCCUCUUCC	1895
54790_1_4850	+	chr4:105168433-105168453	CCCUUCCUUCAGAGAGCCAC	1896
54790_1_4885	+	chr4:105168584-105168604	UUUUUAUUUUUUUAUUCCCA	1897
54790_1_4891	+	chr4:105168591-105168611	UUUUUAUUCCCAUAGGUUAU	1898
54790_1_4893	+	chr4:105168592-105168612	UUUUUAUUCCCAUAGGUUAU	1899
54790_1_4895	+	chr4:105168593-105168613	UUUAUUCCCAUAGGUUAUUG	1900
54790_1_4902	+	chr4:105168599-105168619	CCCAUAGGUUAUUGGGGAAC	1901
54790_1_4904	+	chr4:105168602-105168622	AUAGGUUAUUGGGGAACAGG	1902
54790_1_4905	+	chr4:105168609-105168629	AUUGGGGAACAGGUGGUAAU	1903
54790_1_4909	+	chr4:105168617-105168637	ACAGGUGGUAAUUUGGUUACA	1904
54790_1_4910	+	chr4:105168618-105168638	CAGGUGGUAAUUUGGUUACA	1905
54790_1_4913	+	chr4:105168633-105168653	UACAUGGGUAAGUUCUUUAG	1906
54790_1_4917	+	chr4:105168651-105168671	AGUGGUGAAUUUGUGAGAUCU	1907
54790_1_4945	+	chr4:105168819-105168839	GAGUGAGAACAUAGAUGUU	1908
54790_1_4957	+	chr4:105168873-105168893	AAUAGUCUCCAGUCUUAUCC	1909
54790_1_4959	+	chr4:105168909-105168929	CAUUA AUUCAUCCUUUUUA	1910
54790_1_4976	+	chr4:105168978-105168998	CUCACCGAUUGACGAGCAU	1911

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_4977	+	chr4:105168979-105168999	UCACCGAUUGACGAGCAUUU	1912
54790_1_4978	+	chr4:105168983-105169003	CGAUUGACGAGCAUUUGGGU	1913
54790_1_4995	+	chr4:105169066-105169086	AUAUAAUGACUUUUUCCUC	1914
54790_1_4996	+	chr4:105169067-105169087	UAUAAUGACUUUUUCCUCU	1915
54790_1_5004	+	chr4:105169084-105169104	UCUGGGUAGAUACCCAGUAG	1916
54790_1_5005	+	chr4:105169085-105169105	CUGGGUAGAUACCCAGUAGU	1917
54790_1_5007	+	chr4:105169093-105169113	AUACCCAGUAGUGGGAUUGC	1918
54790_1_5008	+	chr4:105169102-105169122	AGUGGGAUUGCUGGAUCAA	1919
54790_1_5012	+	chr4:105169127-105169147	GUUGUACUUUUAGUUAUUUA	1920
54790_1_5020	+	chr4:105169153-105169173	CUCCACACUGUUUUCCAAG	1921
54790_1_5036	+	chr4:105169257-105169277	UUUUUUAAUUGCCGUUCUUGC	1922
54790_1_5046	+	chr4:105169277-105169297	AGGAGUAAAGUAUUGCAUUG	1923
54790_1_5059	+	chr4:105169337-105169357	ACAUUUUCUCAUAUGUUUGU	1924
54790_1_5076	+	chr4:105169398-105169418	UCCUUAGCCCACUUUUUGAU	1925
54790_1_5086	+	chr4:105169430-105169450	UUUUUUCCUUGCUAAUUUGU	1926
54790_1_5101	+	chr4:105169467-105169487	UCUAGAUAUUAGUCCUUUGC	1927
54790_1_5109	+	chr4:105169503-105169523	GAAGAUUUUCUCCCACUCUG	1928
54790_1_5110	+	chr4:105169504-105169524	AAGAUUUUCUCCCACUCUGU	1929
54790_1_5118	+	chr4:105169547-105169567	CUGUCCCUAUUGCUGUGCAG	1930
54790_1_5130	+	chr4:105169606-105169626	GUUUUUGUUGCAUUUGCUUU	1931
54790_1_5133	+	chr4:105169607-105169627	UUUUUGUUGCAUUUGCUUUU	1932
54790_1_5138	+	chr4:105169614-105169634	UGCAUUUGCUUUUGGGUUCU	1933
54790_1_5150	+	chr4:105169649-105169669	UACCUAAGCCAAUGUCUAGA	1934
54790_1_5152	+	chr4:105169650-105169670	ACCUAAGCCAAUGUCUAGAA	1935
54790_1_5175	+	chr4:105169738-105169758	CUUGAGUUGAUUUUUUAUAUA	1936
54790_1_5182	+	chr4:105169750-105169770	UUUAUAUAAGGUGAGAGAUG	1937
54790_1_5187	+	chr4:105169776-105169796	UAGUUUCAUUCUUCUAUAUG	1938
54790_1_5195	+	chr4:105169811-105169831	CCCAGCACCAUUUGUUGAAU	1939
54790_1_5196	+	chr4:105169812-105169832	CCAGCACCAUUUGUUGAAUA	1940
54790_1_5204	+	chr4:105169857-105169877	GUUUUUGUUGCUUUGUCAAA	1941
54790_1_5209	+	chr4:105169865-105169885	UUGCUUUGUCAAAAGGUCAGU	1942
54790_1_5215	+	chr4:105169879-105169899	GUCAGUUGGCUGUAAGUAUG	1943
54790_1_5216	+	chr4:105169880-105169900	UCAGUUGGCUGUAAGUAUGU	1944
54790_1_5218	+	chr4:105169892-105169912	AAGUAUGUGGGUUUCUUUCU	1945
54790_1_5223	+	chr4:105169911-105169931	UUGGUUCUCUAUCCCCCAU	1946
54790_1_5230	+	chr4:105169951-105169971	AUACCAGUACCAUGCUGUUU	1947
54790_1_5232	+	chr4:105169960-105169980	CCAUGCUGUUUUGGUGUCUA	1948
54790_1_5236	+	chr4:105169980-105170000	UGGCCUUCUAGUAUAAAGUC	1949
54790_1_5241	+	chr4:105170027-105170047	CUUUGUGCUUAGUUUUGCUU	1950
54790_1_5246	+	chr4:105170035-105170055	UUAGUUUUGCUUUGGCUCUG	1951
54790_1_5247	+	chr4:105170036-105170056	UAGUUUUGCUUUGGCUCUGU	1952
54790_1_5273	+	chr4:105170097-105170117	CCUAAUUCUGUGAAGAAUGA	1953
54790_1_5276	+	chr4:105170100-105170120	AAUUCUGUGAAGAAUGAUGG	1954
54790_1_5280	+	chr4:105170111-105170131	GAAUGAUGGUGGUUUUUGA	1955
54790_1_5282	+	chr4:105170112-105170132	AAUGAUGGUGGUUUUUGAU	1956
54790_1_5286	+	chr4:105170137-105170157	UUGCAUAGUUUAUCAACCCU	1957
54790_1_5309	+	chr4:105170212-105170232	GAUGUGAGUUCUAUGAGAUG	1958
54790_1_5312	+	chr4:105170224-105170244	AUGAGAUGAGGAACAUGUU	1959

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_5313	+	chr4:105170225-105170245	UGAGAUGAGGAACAUUGUUU	1960
54790_1_5317	+	chr4:105170260-105170280	AUUGUCAGCAUACCAAACAG	1961
54790_1_5319	+	chr4:105170271-105170291	ACCAAACAGUGGCUAGCACA	1962
54790_1_5321	+	chr4:105170293-105170313	GUGAGCACUCAAUAAAUAUU	1963
54790_1_5327	+	chr4:105170318-105170338	AAAGUUGCAGUGAAUGAAAA	1964
54790_1_5329	+	chr4:105170330-105170350	AAUGAAAAUGGUUUCUAAAA	1965
54790_1_5333	+	chr4:105170360-105170380	UAUAGUCCCAGCUACUCUGA	1966
54790_1_5335	+	chr4:105170366-105170386	CCCAGCUACUCUGAAGGCUG	1967
54790_1_5338	+	chr4:105170370-105170390	GCUACUCUGAAGGCUGAGGC	1968
54790_1_5342	+	chr4:105170397-105170417	UUGCCUGAGUCUCAAAGUU	1969
54790_1_5343	+	chr4:105170398-105170418	UGCCUGAGUCUCAAAGUUU	1970
54790_1_5344	+	chr4:105170399-105170419	GCCUGAGUCUCAAAGUUUG	1971
54790_1_5351	+	chr4:105170450-105170470	AUAGCUGCUGCAUUGUAGCC	1972
54790_1_5355	+	chr4:105170486-105170506	AACCCAUCUCUUUAAAAAAA	1973
54790_1_5360	+	chr4:105170526-105170546	UUUUACUGCUUUUCUCUUUA	1974
54790_1_5375	+	chr4:105170567-105170587	CUCUGCUGAUUUAUCCUCAU	1975
54790_1_5382	+	chr4:105170607-105170627	AAUAUCCAUGAUUAUUUAU	1976
54790_1_5384	+	chr4:105170617-105170637	GAUUAUUUAUAGGUGAAAUU	1977
54790_1_5388	+	chr4:105170624-105170644	UAUAGGUGAAAUUAGGCUUU	1978
54790_1_5393	+	chr4:105170634-105170654	AUUAGGCUUUUGGAUCCAUG	1979
54790_1_5402	+	chr4:105170657-105170677	AAUAGCUGAGACAAUCUCC	1980
54790_1_5404	+	chr4:105170666-105170686	GACAAUCUUCAGGAGCUUC	1981
54790_1_5409	+	chr4:105170674-105170694	UCCAGGAGCUUCUGGAGCCG	1982
54790_1_5411	+	chr4:105170683-105170703	UUCUGGAGCCGAGGAAACAU	1983
54790_1_5414	+	chr4:105170707-105170727	CACUAAAAUACCAUUUAUUAU	1984
54790_1_5423	+	chr4:105170761-105170781	AAUUACAUUGUGCAUUUAAA	1985
54790_1_5425	+	chr4:105170770-105170790	GUGCAUUUAAAAGGCUGUUG	1986
54790_1_5437	+	chr4:105170844-105170864	ACUGAUUUUAUAAAUAGACUU	1987
54790_1_5438	+	chr4:105170845-105170865	CUGAUUUUAUAAAUAGACUUA	1988
54790_1_5453	+	chr4:105170945-105170965	CUUCCUCCUCCUUCUACACU	1989
54790_1_5467	+	chr4:105171009-105171029	UGAUGAGAAAAUAUCUUUUC	1990
54790_1_5474	+	chr4:105171046-105171066	CUUCAUUCUUUUUUUUUAAA	1991
54790_1_5478	+	chr4:105171049-105171069	CAUUCUUUUUUUUUAAAUGG	1992
54790_1_5494	+	chr4:105171101-105171121	UUUCUUCUGCUGUUAUUGC	1993
54790_1_5501	+	chr4:105171114-105171134	UUAUUGCUGGCUCAAAUCC	1994
54790_1_5509	+	chr4:105171148-105171168	GUUAUUUCUGAGCUCCAUGA	1995
54790_1_5510	+	chr4:105171149-105171169	UUAUUUCUGAGCUCCAUGAU	1996
54790_1_5523	+	chr4:105171205-105171225	CCAGUGUCUAGCACAGUGCC	1997
54790_1_5526	+	chr4:105171237-105171257	AGCCUAUAAUGUUUAUCUAG	1998
54790_1_5532	+	chr4:105171284-105171304	UUAUCAUUGCAAAGAUUUAG	1999
54790_1_5539	+	chr4:105171327-105171347	UAAUGCUCUACUCCAUGCUA	2000
54790_1_5565	+	chr4:105171468-105171488	AUAACCAAUAAGAUAAACAC	2001
54790_1_5568	+	chr4:105171497-105171517	UUUGUUCUUUAAAAAAUGAC	2002
54790_1_5581	+	chr4:105171526-105171546	AGAAUAAGAGAAAAAAUAG	2003
54790_1_5597	+	chr4:105171646-105171666	CUACAACUGCCUCUUGAUAA	2004
54790_1_5598	+	chr4:105171653-105171673	UGCCUCUUGAUAAAGGAUGC	2005
54790_1_5602	+	chr4:105171691-105171711	UAAUGUUUGCUCAUUUACAG	2006
54790_1_5608	+	chr4:105171712-105171732	GGAAUGUACAAUAUAGUACC	2007

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_5610	+	chr4:105171713-105171733	GAAUGUACAAUAGUACCU	2008
54790_1_5611	+	chr4:105171717-105171737	GUACAAUAGUACCUGGGA	2009
54790_1_5614	+	chr4:105171726-105171746	AGUACCUGGGAUGGUGAAGA	2010
54790_1_5617	+	chr4:105171754-105171774	CAACAAUUUAAAAUAGCUG	2011
54790_1_5618	+	chr4:105171755-105171775	AACAAUUUAAAAUAGCUGU	2012
54790_1_5635	+	chr4:105171834-105171854	AUGCCUGCCUUUAUCUGCUU	2013
54790_1_5646	+	chr4:105171905-105171925	AUAGCAUGCAUUUCUCAGAC	2014
54790_1_5651	+	chr4:105171919-105171939	UCAGACAGGUAAGAUAGAAU	2015
54790_1_5652	+	chr4:105171930-105171950	AGAUAGAAUUGGUUAUAUUAU	2016
54790_1_5654	+	chr4:105171948-105171968	UUUGGUUAUAGCAAAAAGUCA	2017
54790_1_5657	+	chr4:105171971-105171991	UUGUCUUUAGAUAUAUCCU	2018
54790_1_5661	+	chr4:105171983-105172003	UAUAUCCUUGGUUUUUC AUG	2019
54790_1_5665	+	chr4:105171989-105172009	CUUGGUUUUUC AUGUGGUAC	2020
54790_1_5666	+	chr4:105171990-105172010	UUGGUUUUUC AUGUGGUACU	2021
54790_1_5668	+	chr4:105171991-105172011	UGGUUUUUC AUGUGGUACUG	2022
54790_1_5679	+	chr4:105172027-105172047	UUUCUUC AUCAAUAAAUGA	2023
54790_1_5683	+	chr4:105172033-105172053	CAUCUAUAAAUGAAGGACC	2024
54790_1_5685	+	chr4:105172034-105172054	AUCUAUAAAUGAAGGACCU	2025
54790_1_5693	+	chr4:105172085-105172105	AACUUUGAGCUCAGCAAAGU	2026
54790_1_5695	+	chr4:105172086-105172106	ACUUUGAGCUCAGCAAAGUA	2027
54790_1_5704	+	chr4:105172159-105172179	CAGUUGACCCUUGAAUAACA	2028
54790_1_5705	+	chr4:105172162-105172182	UUGACCCUUGAAUAACAUGG	2029
54790_1_5716	+	chr4:105172253-105172273	ACUAAUAGCCUGCUGUUGUC	2030
54790_1_5718	+	chr4:105172256-105172276	AAUAGCCUGCUGUUGUCUGG	2031
54790_1_5734	+	chr4:105172374-105172394	CUGUUAUUAAGAAAAUCGUA	2032
54790_1_5741	+	chr4:105172406-105172426	UAUAUUUACUAUUUAUUAAA	2033
54790_1_5757	+	chr4:105172470-105172490	CCUUGAGUAUGCUGAAGAAG	2034
54790_1_5760	+	chr4:105172473-105172493	UGAGUAUGCUGAAGAAGAGG	2035
54790_1_5764	+	chr4:105172479-105172499	UGCUGAAGAAGAGGAGGAAA	2036
54790_1_5766	+	chr4:105172483-105172503	GAAGAAGAGGAGGAAAAGGA	2037
54790_1_5767	+	chr4:105172484-105172504	AAGAAGAGGAGGAAAAGGAU	2038
54790_1_5768	+	chr4:105172488-105172508	AGAGGAGGAAAAGGAUGGGU	2039
54790_1_5771	+	chr4:105172503-105172523	UGGGUUGGUCUUGCUGUUCC	2040
54790_1_5772	+	chr4:105172504-105172524	GGGUUGGUCUUGCUGUUCCA	2041
54790_1_5773	+	chr4:105172505-105172525	GGUUGGUCUUGCUGUUCCAG	2042
54790_1_5774	+	chr4:105172508-105172528	UGGUCUUGCUGUUCCAGGGG	2043
54790_1_5779	+	chr4:105172517-105172537	UGUUCCAGGGGUGGCAGAAG	2044
54790_1_5785	+	chr4:105172568-105172588	CAGUCAAACCUGUAUUUUA	2045
54790_1_5787	+	chr4:105172575-105172595	AACCUGUAUUUUAAGGUCAA	2046
54790_1_5819	+	chr4:105172699-105172719	AACUAUGAAAGUUGAAUUCA	2047
54790_1_5835	+	chr4:105172760-105172780	UCAUAUAAUGAGAAUACUAA	2048
54790_1_5847	+	chr4:105172829-105172849	AAAAAGAAAUCUUUCAGUG	2049
54790_1_5855	+	chr4:105172874-105172894	UCUAGUAGAUGACAUUUUU	2050
54790_1_5859	+	chr4:105172891-105172911	UUUUGGUAAUGAAAUUGAUA	2051
54790_1_5860	+	chr4:105172892-105172912	UUUGGUAAUGAAAUUGAUUA	2052
54790_1_5866	+	chr4:105172917-105172937	AUUAACAGCUUUUCCAAGU	2053
54790_1_5906	+	chr4:105173084-105173104	AUAUAAAUUUUCUUCUUAAG	2054
54790_1_5915	+	chr4:105173113-105173133	AUUCUUGCAUGCCAACACAA	2055

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_5923	+	chr4:105173147-105173167	ACCUAUCCUUAGUUUCUAAG	2056
54790_1_5931	+	chr4:105173216-105173236	GAUAAGUUCCAACUCAAUUCU	2057
54790_1_5933	+	chr4:105173220-105173240	AGUUCCAACUCAAUUCUUGGU	2058
54790_1_5934	+	chr4:105173221-105173241	GUUCCAACUCAAUUCUUGGUU	2059
54790_1_5936	+	chr4:105173226-105173246	AACUCAAUUCUUGGUUGGGUG	2060
54790_1_5937	+	chr4:105173229-105173249	UCAAUCUUGGUUGGGUGUGG	2061
54790_1_5940	+	chr4:105173248-105173268	GUGGCUCACGCCUGUGAUCC	2062
54790_1_5942	+	chr4:105173256-105173276	CGCCUGUGAUCCCGGCACUU	2063
54790_1_5945	+	chr4:105173257-105173277	GCCUGUGAUCCCGGCACUUU	2064
54790_1_5946	+	chr4:105173260-105173280	UGUGAUCCCGGCACUUUGGG	2065
54790_1_5948	+	chr4:105173266-105173286	CCCGGCACUUUGGGAGGCCG	2066
54790_1_5950	+	chr4:105173269-105173289	GGCACUUUGGGAGGCCGAGG	2067
54790_1_5951	+	chr4:105173270-105173290	GCACUUUGGGAGGCCGAGGU	2068
54790_1_5957	+	chr4:105173287-105173307	GGUGGGCAGAUACGAGCUC	2069
54790_1_5959	+	chr4:105173305-105173325	UCAGGAGUUUGAGACCAGCC	2070
54790_1_5960	+	chr4:105173314-105173334	UGAGACCAGCCUGGCCAAUA	2071
54790_1_5964	+	chr4:105173369-105173389	AAAAAAAAAACAACUAGCC	2072
54790_1_5965	+	chr4:105173374-105173394	AAAACAAAACUAGCCCGGCA	2073
54790_1_5966	+	chr4:105173377-105173397	ACAAAACUAGCCCGGCAUGG	2074
54790_1_5969	+	chr4:105173404-105173424	CUCCCGUAGUCCCAGCUACU	2075
54790_1_5971	+	chr4:105173405-105173425	UCCCGUAGUCCCAGCUACUU	2076
54790_1_5972	+	chr4:105173408-105173428	CGUAGUCCCAGCUACUUGGG	2077
54790_1_5974	+	chr4:105173414-105173434	CCCAGCUACUUGGGAGGCUG	2078
54790_1_5977	+	chr4:105173418-105173438	GCUACUUGGGAGGCUGAGGC	2079
54790_1_5984	+	chr4:105173437-105173457	CAGGAGAAUCGAUUGAACCC	2080
54790_1_5985	+	chr4:105173440-105173460	GAGAAUCGAUUGAACCCAGG	2081
54790_1_5987	+	chr4:105173443-105173463	AAUCGAUUGAACCCAGGAGG	2082
54790_1_5989	+	chr4:105173446-105173466	CGAUUGAACCCAGGAGGUGG	2083
54790_1_5994	+	chr4:105173486-105173506	UGCACCACUGCACUCCAGCC	2084
54790_1_5995	+	chr4:105173487-105173507	GCACCACUGCACUCCAGCCU	2085
54790_1_6000	+	chr4:105173496-105173516	CACUCCAGCCUGGGCAAAG	2086
54790_1_6002	+	chr4:105173497-105173517	ACUCCAGCCUGGGCAAAGA	2087
54790_1_6010	+	chr4:105173579-105173599	UGAGUCAUUUUAGUCAAUAA	2088
54790_1_6024	+	chr4:105173634-105173654	AAUUUGCUACAAGAAUGCAA	2089
54790_1_6029	+	chr4:105173647-105173667	AAUGCAAAGGUGAUGACAUG	2090
54790_1_6032	+	chr4:105173655-105173675	GGUGAUGACAUGAGGAAAAA	2091
54790_1_6034	+	chr4:105173656-105173676	GUGAUGACAUGAGGAAAAA	2092
54790_1_6035	+	chr4:105173657-105173677	UGAUGACAUGAGGAAAAAAG	2093
54790_1_6041	+	chr4:105173696-105173716	CUCUACUACUCAGCAAUUGC	2094
54790_1_6046	+	chr4:105173701-105173721	CUACUCAGCAAUUGCAGGCC	2095
54790_1_6047	+	chr4:105173731-105173751	UUAUUCAAAUAUUUAUUACA	2096
54790_1_6054	+	chr4:105173757-105173777	AUUAACAUAUUUAUAAAAUU	2097
54790_1_6066	+	chr4:105173817-105173837	UAAACAAGAUUAUAAUCUAA	2098
54790_1_6069	+	chr4:105173830-105173850	AAUCUAAUGGAGAUUAAUUAU	2099
54790_1_6082	+	chr4:105173887-105173907	GUUUAAUAAAAUAUUGACUU	2100
54790_1_6088	+	chr4:105173902-105173922	GACUUAGGUAGAUUAUUGUG	2101
54790_1_6095	+	chr4:105173960-105173980	UAUGUAUUUCUAAAAGAGU	2102
54790_1_6100	+	chr4:105173978-105173998	GUAGGUAGCAAUGACUUCAA	2103

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_6116	+	chr4:105174112-105174132	UCAUAUAUAAGUAAAAUUUUU	2104
54790_1_6117	+	chr4:105174113-105174133	CAUAUAUAAGUAAAAUUUUUA	2105
54790_1_6119	+	chr4:105174114-105174134	AUAUAUAAGUAAAAUUUUUAG	2106
54790_1_6159	+	chr4:105174312-105174332	AGUAUUUCCUAAGAUUUUAUU	2107
54790_1_6169	+	chr4:105174336-105174356	AUAGAAGAUCGAUAUUUUUUC	2108
54790_1_6170	+	chr4:105174337-105174357	UAGAAGAUCGAUAUUUUUUCU	2109
54790_1_6171	+	chr4:105174348-105174368	UAUUUUUCUGGGAUGACAUA	2110
54790_1_6183	+	chr4:105174420-105174440	AAGUAAAAAGCUGAAUGAAU	2111
54790_1_6193	+	chr4:105174467-105174487	UGUCAGAAAAAUGAGAUUAU	2112
54790_1_6194	+	chr4:105174468-105174488	GUCAGAAAAAUGAGAUUAUA	2113
54790_1_6198	+	chr4:105174504-105174524	CAAUAUUUAGAGAAGCAGAC	2114
54790_1_6205	+	chr4:105174531-105174551	UAGAAAGAAUCACAACUUAG	2115
54790_1_6207	+	chr4:105174532-105174552	AGAAAGAAUCACAACUUAGU	2116
54790_1_6208	+	chr4:105174533-105174553	GAAAGAAUCACAACUUAGUG	2117
54790_1_6211	+	chr4:105174548-105174568	UAGUGGGGCAAAAACCUACA	2118
54790_1_6215	+	chr4:105174561-105174581	ACCUACAAGGAAAAUUUUUG	2119
54790_1_6217	+	chr4:105174562-105174582	CCUACAAGGAAAAUUUUUGU	2120
54790_1_6218	+	chr4:105174568-105174588	AGGAAAAUUUUUGUGGGAAC	2121
54790_1_6219	+	chr4:105174575-105174595	UUUUUGUGGGAACCGGUGCC	2122
54790_1_6223	+	chr4:105174579-105174599	UGUGGGAACCGGUGCCAGGU	2123
54790_1_6230	+	chr4:105174616-105174636	AAUUGAAAAAUUGUUCAGUG	2124
54790_1_6231	+	chr4:105174617-105174637	AUUGAAAAAUUGUUCAGUGU	2125
54790_1_6232	+	chr4:105174620-105174640	GAAAAAUUGUUCAGUGUGGG	2126
54790_1_6236	+	chr4:105174633-105174653	GUGUGGGCGGUUGUUCAGUG	2127
54790_1_6239	+	chr4:105174644-105174664	UGUUCAGUGUGGCAAGUCUG	2128
54790_1_6240	+	chr4:105174645-105174665	GUUCAGUGUGGCAAGUCUGA	2129
54790_1_6245	+	chr4:105174659-105174679	GUCUGAGGGUUA AAAACUCC	2130
54790_1_6247	+	chr4:105174662-105174682	UGAGGGUUA AAAACUCCAGG	2131
54790_1_6251	+	chr4:105174674-105174694	ACUCCAGGAGGACUCACUUA	2132
54790_1_6253	+	chr4:105174678-105174698	CAGGAGGACUCACUUACGGA	2133
54790_1_6254	+	chr4:105174679-105174699	AGGAGGACUCACUUACGGAA	2134
54790_1_6258	+	chr4:105174708-105174728	CUUUUGUGAGUUUAACCUCC	2135
54790_1_6267	+	chr4:105174729-105174749	GGAGUGUUCACAGUGACUAC	2136
54790_1_6273	+	chr4:105174745-105174765	CUACUGGAGAAAAUUCCCUA	2137
54790_1_6274	+	chr4:105174746-105174766	UACUGGAGAAAAUUCCCUAA	2138
54790_1_6277	+	chr4:105174747-105174767	ACUGGAGAAAAUUCCCUAAG	2139
54790_1_6282	+	chr4:105174758-105174778	UUCCCUAAGGGGAGAAGAAA	2140
54790_1_6289	+	chr4:105174792-105174812	AAUAUGUCAGAGCAUUUUGU	2141
54790_1_6297	+	chr4:105174843-105174863	UUUACCAGAGCCUAAACUUU	2142
54790_1_6299	+	chr4:105174844-105174864	UUACCAGAGCCUAAACUUUU	2143
54790_1_6310	+	chr4:105174872-105174892	AUAAGAGUGUAACCUCCCAA	2144
54790_1_6313	+	chr4:105174873-105174893	UAAGAGUGUAACCUCCCAA	2145
54790_1_6316	+	chr4:105174877-105174897	AGUGUAACCUCCCAAAGGGA	2146
54790_1_6319	+	chr4:105174878-105174898	GUGUAACCUCCCAAAGGGAA	2147
54790_1_6322	+	chr4:105174918-105174938	CCCUUUUAGCUUCCACAUA	2148
54790_1_6325	+	chr4:105174919-105174939	CCCUUUUAGCUUCCACAUA	2149
54790_1_6328	+	chr4:105174924-105174944	UUAGCUUCCACAUAAGGGAA	2150
54790_1_6335	+	chr4:105174941-105174961	GAAAGGAAAAUAUAUAACUC	2151

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_6337	+	chr4:105174970-105174990	CAAACCAUCCUGUCCACGUU	2152
54790_1_6340	+	chr4:105174971-105174991	AAACCAUCCUGUCCACGUUA	2153
54790_1_6341	+	chr4:105174972-105174992	AACCAUCCUGUCCACGUUAG	2154
54790_1_6342	+	chr4:105174973-105174993	ACCAUCCUGUCCACGUUAGG	2155
54790_1_6345	+	chr4:105174979-105174999	CUGUCCACGUUAGGGGGCCU	2156
54790_1_6347	+	chr4:105174980-105175000	UGUCCACGUUAGGGGGCCUA	2157
54790_1_6349	+	chr4:105174981-105175001	GUCCACGUUAGGGGGCCUAG	2158
54790_1_6354	+	chr4:105174996-105175016	CCUAGGGGAACUGAGAAAAC	2159
54790_1_6357	+	chr4:105175015-105175035	CUGGUGAAGUUCAUAGUCCA	2160
54790_1_6358	+	chr4:105175016-105175036	UGGUGAAGUUCAUAGUCCA	2161
54790_1_6362	+	chr4:105175035-105175055	UGGGUACAGUUUCACCAAAG	2162
54790_1_6365	+	chr4:105175036-105175056	GGGUACAGUUUCACCAAAGA	2163
54790_1_6368	+	chr4:105175052-105175072	AAGAGGGAGACCAAUUAUA	2164
54790_1_6387	+	chr4:105175167-105175187	CAUUCAACCAAAAAAUUAUA	2165
54790_1_6389	+	chr4:105175179-105175199	AAAUUAUAAGGCAUGCUIAA	2166
54790_1_6391	+	chr4:105175183-105175203	UAUAAGGCAUGCUIAAAGGC	2167
54790_1_6400	+	chr4:105175234-105175254	AUCAGAAGCAGAGUCIAAAUA	2168
54790_1_6403	+	chr4:105175246-105175266	GUCAAAUAUGGCAGUGACAU	2169
54790_1_6408	+	chr4:105175281-105175301	AGAAACUUAUAIAAAAAACUA	2170
54790_1_6409	+	chr4:105175290-105175310	AUAAAAAACUAUGGUUAAUA	2171
54790_1_6415	+	chr4:105175295-105175315	AAACUAUGGUUAAUAUGGUG	2172
54790_1_6416	+	chr4:105175296-105175316	AACUAUGGUUAAUAUGGUGA	2173
54790_1_6421	+	chr4:105175326-105175346	AAAUAGACAUACAAGAACAGA	2174
54790_1_6424	+	chr4:105175347-105175367	GGAUAAUGUAAAUUAUAGAGA	2175
54790_1_6428	+	chr4:105175357-105175377	AAUAUAGAGACGGAAAUUUU	2176
54790_1_6438	+	chr4:105175425-105175445	AUGAUUAAAAUGUCUUUGAU	2177
54790_1_6446	+	chr4:105175453-105175473	AAGUAGAUUGAACAUAGCCG	2178
54790_1_6450	+	chr4:105175474-105175494	GGAAAAAAUCUUUGAAGUUA	2179
54790_1_6453	+	chr4:105175487-105175507	GAAGUUAAGGAUAUGAUAAU	2180
54790_1_6466	+	chr4:105175559-105175579	AGAGAUUAUUCAGAACUCGC	2181
54790_1_6471	+	chr4:105175573-105175593	AACUGCAGGAGAACUACAAA	2182
54790_1_6473	+	chr4:105175592-105175612	AAGGUUAUAUGUACGUGCAA	2183
54790_1_6474	+	chr4:105175593-105175613	AGGUUAUAUGUACGUGCAAU	2184
54790_1_6482	+	chr4:105175616-105175636	CAUACUAGAAAAAGAAAGAA	2185
54790_1_6496	+	chr4:105175716-105175736	GAGCUCAAAGAACACCAAGC	2186
54790_1_6498	+	chr4:105175741-105175761	AAAUGUCCCAAAACUACUCA	2187
54790_1_6499	+	chr4:105175742-105175762	AAUGUCCCAAAACUACUCAU	2188
54790_1_6512	+	chr4:105175803-105175823	AAAUAU CGAAAGAAUCCAGA	2189
54790_1_6516	+	chr4:105175821-105175841	GAAGGAAAAAACACCUAUAG	2190
54790_1_6528	+	chr4:105175915-105175935	AAGAUGUUGAAAGAAAAAUC	2191
54790_1_6532	+	chr4:105175931-105175951	AAUCCGGCAGUGUACGAUUC	2192
54790_1_6545	+	chr4:105175997-105176017	CUUAAAGAAACAAAAAUUUC	2193
54790_1_6548	+	chr4:105176013-105176033	UUUCAGGAAUUUGUUGCCAG	2194
54790_1_6558	+	chr4:105176054-105176074	GUUUAAAGUUCUUUAGAGAG	2195
54790_1_6562	+	chr4:105176068-105176088	AGAGAGAGGUAAAAUGAUAC	2196
54790_1_6568	+	chr4:105176092-105176112	UAGAAACUCAGAUCCACAUA	2197
54790_1_6573	+	chr4:105176106-105176126	CACAUAAAGGAAAAUAAAAUU	2198
54790_1_6574	+	chr4:105176107-105176127	ACAUAAAGGAAAAUAAAAUUA	2199

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_6592	+	chr4:105176223-105176243	UAAGAUCAAGAACAAGACAA	2200
54790_1_6595	+	chr4:105176254-105176274	CUUACCACUUUGUUUCCUAC	2201
54790_1_6602	+	chr4:105176283-105176303	UACCUGAAUGCAAUAAGACAA	2202
54790_1_6609	+	chr4:105176312-105176332	AAUGAAAAGCAUACAGAUUC	2203
54790_1_6612	+	chr4:105176315-105176335	GAAAAGCAUACAGAUUCCGG	2204
54790_1_6617	+	chr4:105176342-105176362	AAUCAAAACUGUCUUUGUUCA	2205
54790_1_6623	+	chr4:105176361-105176381	ACGGAUGACAGUUGUUUAUA	2206
54790_1_6625	+	chr4:105176373-105176393	UGUUUAUAUGGAAUAUCCAA	2207
54790_1_6635	+	chr4:105176393-105176413	AGGAUCAGAAAAAAGAAAAC	2208
54790_1_6636	+	chr4:105176417-105176437	ACUAAUAAAUGAUUAUUGUA	2209
54790_1_6679	+	chr4:105176727-105176747	AAACACAGCACGAUAUUUUA	2210
54790_1_6681	+	chr4:105176741-105176761	AUUUUAUGGAUAUCAACAAA	2211
54790_1_6686	+	chr4:105176759-105176779	AAAGGAUUCUAAAGUUUAUA	2212
54790_1_6689	+	chr4:105176764-105176784	AUUCUAAAGUUUAUAUGGAG	2213
54790_1_6699	+	chr4:105176798-105176818	AAUAGCCAACUCAGUAUUUG	2214
54790_1_6704	+	chr4:105176817-105176837	GAGGAGAACAACAAAGUCAG	2215
54790_1_6706	+	chr4:105176832-105176852	GUCAGAGGACUGACACUACC	2216
54790_1_6711	+	chr4:105176873-105176893	AGCUCAGAUAAUCAAUUGUAG	2217
54790_1_6712	+	chr4:105176874-105176894	GCUCAGAUAAUCAAUUGUAGU	2218
54790_1_6713	+	chr4:105176880-105176900	AUAAUCAAUUGUAGUGGGUAC	2219
54790_1_6718	+	chr4:105176907-105176927	AGAAUAUUCAAAUAAGACCAA	2220
54790_1_6726	+	chr4:105176966-105176986	UAAUCAAAUGAUCUUUGACA	2221
54790_1_6727	+	chr4:105176967-105176987	AAUCAAAUGAUCUUUGACAA	2222
54790_1_6729	+	chr4:105176975-105176995	GAUCUUUGACAAGGGAGCAA	2223
54790_1_6733	+	chr4:105176986-105177006	AGGGAGCAAAGGCAAUACAA	2224
54790_1_6735	+	chr4:105176997-105177017	GCAAUACAAUGGAGCAAAGA	2225
54790_1_6737	+	chr4:105177019-105177039	GUCUUUUAACAAAUAAUGC	2226
54790_1_6759	+	chr4:105177168-105177188	AAACUCCCAGAAGAUAACAC	2227
54790_1_6761	+	chr4:105177189-105177209	GGAAAAAUCCUAGAUGACUU	2228
54790_1_6762	+	chr4:105177194-105177214	AAUCCUAGAUGACUUUGGUA	2229
54790_1_6763	+	chr4:105177200-105177220	AGAUGACUUUGGUAUGGCAG	2230
54790_1_6766	+	chr4:105177225-105177245	UUUUUUAGAUACAGCUCCAA	2231
54790_1_6775	+	chr4:105177240-105177260	UCCAAAGGCACGAUACAUGA	2232
54790_1_6777	+	chr4:105177258-105177278	GAAGGAAUGAUUGACAAGC	2233
54790_1_6791	+	chr4:105177331-105177351	AUGAGAAGACAAGCCACAGA	2234
54790_1_6796	+	chr4:105177365-105177385	GCAAAAGAUACUUCUCAUAA	2235
54790_1_6814	+	chr4:105177499-105177519	CACAAGUGUCAAGAAAGCAU	2236
54790_1_6816	+	chr4:105177528-105177548	UGUUAAACAUCAUAGUCAUU	2237
54790_1_6817	+	chr4:105177529-105177549	GUUAAACAUCAUAGUCAUUA	2238
54790_1_6826	+	chr4:105177580-105177600	CCGCUACAUACCUGUUAGAA	2239
54790_1_6831	+	chr4:105177614-105177634	ACACUGAUGAAACCAAGUGC	2240
54790_1_6837	+	chr4:105177625-105177645	ACCAAGUGCUGGUGAGAAUG	2241
54790_1_6840	+	chr4:105177634-105177654	UGGUGAGAAUGUGGAGCAAC	2242
54790_1_6841	+	chr4:105177653-105177673	CAGGAACCUUCAUUCAUUGC	2243
54790_1_6846	+	chr4:105177669-105177689	UUGCUGGUAAGAAUUCAAAA	2244
54790_1_6850	+	chr4:105177683-105177703	UCAAAAUGGCAUAGUCACUU	2245
54790_1_6852	+	chr4:105177695-105177715	AGUCACUUUGGAAGACAGUU	2246
54790_1_6861	+	chr4:105177753-105177773	GAUUCAGCAAUAGCGCUCCU	2247

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_6864	+	chr4:105177758-105177778	AGCAAUAGCGCUCCUUGGUA	2248
54790_1_6867	+	chr4:105177779-105177799	GGACUUGAAAACUUAUGUCC	2249
54790_1_6869	+	chr4:105177783-105177803	UUGAAAACUUAUGUCCUGGC	2250
54790_1_6870	+	chr4:105177784-105177804	UGAAAACUUAUGUCCUGGCC	2251
54790_1_6874	+	chr4:105177819-105177839	CGCCUGUAAUUGCAGCACUU	2252
54790_1_6876	+	chr4:105177820-105177840	GCCUGUAAUUGCAGCACUUU	2253
54790_1_6878	+	chr4:105177823-105177843	UGUAAUUGCAGCACUUUGGG	2254
54790_1_6879	+	chr4:105177829-105177849	UGCAGCACUUUGGGAGGCCC	2255
54790_1_6881	+	chr4:105177833-105177853	GCACUUUGGGAGGCCCAGGC	2256
54790_1_6883	+	chr4:105177836-105177856	CUUUGGGAGGCCCAGGCAGG	2257
54790_1_6887	+	chr4:105177847-105177867	CCAGGCAGGUGGAUCAUUUG	2258
54790_1_6889	+	chr4:105177852-105177872	CAGGUGGAUCAUUUGAGGUC	2259
54790_1_6893	+	chr4:105177870-105177890	UCAGGAGUUCAAGACCAGCC	2260
54790_1_6896	+	chr4:105177883-105177903	ACCAGCCUGGUGAAAUCCCA	2261
54790_1_6899	+	chr4:105177923-105177943	UAAAGAUACAAAAAAGUAGC	2262
54790_1_6900	+	chr4:105177924-105177944	AAAGAUACAAAAAAGUAGCU	2263
54790_1_6901	+	chr4:105177929-105177949	UACAAAAAAGUAGCUGGGUG	2264
54790_1_6904	+	chr4:105177959-105177979	CGCCUGUAAUCUCAGCUACU	2265
54790_1_6906	+	chr4:105177960-105177980	GCCUGUAAUCUCAGCUACUA	2266
54790_1_6907	+	chr4:105177963-105177983	UGUAAUCUCAGCUACUAGGG	2267
54790_1_6909	+	chr4:105177969-105177989	CUCAGCUACUAGGGAGGCUG	2268
54790_1_6912	+	chr4:105177973-105177993	GCUACUAGGGAGGCUGAGGC	2269
54790_1_6917	+	chr4:105177992-105178012	CAGGAGAAUCACUUGAGCCC	2270
54790_1_6919	+	chr4:105177995-105178015	GAGAAUCACUUGAGCCCAGG	2271
54790_1_6921	+	chr4:105177998-105178018	AAUCACUUGAGCCCAGGAGG	2272
54790_1_6923	+	chr4:105178001-105178021	CACUUGAGCCCAGGAGGCGG	2273
54790_1_6936	+	chr4:105178163-105178183	UUUACAUAUUUGCCAAAACU	2274
54790_1_6937	+	chr4:105178164-105178184	UUACAUAUUUGCCAAAACUU	2275
54790_1_6944	+	chr4:105178196-105178216	GAUAUCCUUUAAUAAUUUGAG	2276
54790_1_6947	+	chr4:105178207-105178227	AUAUUUGAGUGGAUAAACUG	2277
54790_1_6958	+	chr4:105178273-105178293	UAUCACAUCAUAAAACGACA	2278
54790_1_6965	+	chr4:105178322-105178342	UGAAAGAAGCUAAUCCGAAA	2279
54790_1_6967	+	chr4:105178359-105178379	AUUCCAACUAUAUGACAUUC	2280
54790_1_6971	+	chr4:105178376-105178396	UUCCGGAAAAGCCAAAUAUA	2281
54790_1_6979	+	chr4:105178407-105178427	AAAAGAGCAGUGUUUUCCAG	2282
54790_1_6981	+	chr4:105178408-105178428	AAAGAGCAGUGUUUUCCAGA	2283
54790_1_6984	+	chr4:105178411-105178431	GAGCAGUGUUUUCCAGAGGG	2284
54790_1_6985	+	chr4:105178421-105178441	UUCCAGAGGGAGGAAUGUAU	2285
54790_1_6995	+	chr4:105178466-105178486	GAAUCUAUGUAAUACUAUAG	2286
54790_1_6997	+	chr4:105178469-105178489	UCUAUGUAAUACUAUAGUGG	2287
54790_1_6999	+	chr4:105178504-105178524	AUACAUUUGUCCAAACACGU	2288
54790_1_7005	+	chr4:105178542-105178562	GUGAACCCUAAUGUAAACUA	2289
54790_1_7007	+	chr4:105178543-105178563	UGAACCCUAAUGUAAACUAU	2290
54790_1_7008	+	chr4:105178544-105178564	GAACCCUAAUGUAAACUAUG	2291
54790_1_7010	+	chr4:105178549-105178569	CUAAUGUAAACUAUGGGGUU	2292
54790_1_7011	+	chr4:105178550-105178570	UAAUGUAAACUAUGGGGUUU	2293
54790_1_7014	+	chr4:105178572-105178592	GUAUCAAAAUGCAUCAAUUGU	2294
54790_1_7017	+	chr4:105178603-105178623	UUGUAACAAAUAUACCACUC	2295

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_7020	+	chr4:105178608-105178628	ACAAAUAUACCACUCUGGUA	2296
54790_1_7022	+	chr4:105178609-105178629	CAAUAUACCACUCUGGUAU	2297
54790_1_7024	+	chr4:105178622-105178642	CUGGUAUGGGAUGUUGAUAA	2298
54790_1_7027	+	chr4:105178623-105178643	UGGUAUGGGAUGUUGAUAAU	2299
54790_1_7028	+	chr4:105178624-105178644	GGUAUGGGAUGUUGAUAAUG	2300
54790_1_7030	+	chr4:105178628-105178648	UGGGAUGUUGAUAAUGGGGA	2301
54790_1_7032	+	chr4:105178634-105178654	GUUGAUAAUGGGGAAGGUUG	2302
54790_1_7033	+	chr4:105178635-105178655	UUGAUAAUGGGGAAGGUUGU	2303
54790_1_7036	+	chr4:105178642-105178662	UGGGGAAGGUUGUGGGUCUG	2304
54790_1_7038	+	chr4:105178643-105178663	GGGGAAGGUUGUGGGUCUGU	2305
54790_1_7040	+	chr4:105178644-105178664	GGGAAGGUUGUGGGUCUGUG	2306
54790_1_7043	+	chr4:105178649-105178669	GGUUGUGGGUCUGUGGGGAC	2307
54790_1_7044	+	chr4:105178650-105178670	GUUGUGGGUCUGUGGGGACA	2308
54790_1_7045	+	chr4:105178651-105178671	UUGUGGGUCUGUGGGGACAG	2309
54790_1_7049	+	chr4:105178658-105178678	UCUGUGGGGACAGGGGUUAUA	2310
54790_1_7050	+	chr4:105178659-105178679	CUGUGGGGACAGGGGUUAUAU	2311
54790_1_7068	+	chr4:105178774-105178794	AAUAAUAAUAAAUAUUUU	2312
54790_1_7084	+	chr4:105178879-105178899	UGAGACUGAGUAAUUUAUAA	2313
54790_1_7089	+	chr4:105178912-105178932	AAUUGACUCACAGUUUAGCA	2314
54790_1_7093	+	chr4:105178916-105178936	GACUCACAGUUUAGCAUGGC	2315
54790_1_7097	+	chr4:105178917-105178937	ACUCACAGUUUAGCAUGGCU	2316
54790_1_7098	+	chr4:105178918-105178938	CUCACAGUUUAGCAUGGCUG	2317
54790_1_7100	+	chr4:105178921-105178941	ACAGUUUAGCAUGGCUGGGG	2318
54790_1_7102	+	chr4:105178928-105178948	AGCAUGGCUGGGGAGGUCUC	2319
54790_1_7106	+	chr4:105178945-105178965	CUCAGGAAACUUAACAGUCA	2320
54790_1_7107	+	chr4:105178949-105178969	GGAAACUUAACAGUCAUGGC	2321
54790_1_7109	+	chr4:105178965-105178985	UGGCAGGUGACUUCACAAAG	2322
54790_1_7111	+	chr4:105178969-105178989	AGGUGACUUCACAAAGUGGC	2323
54790_1_7114	+	chr4:105178973-105178993	GACUUCACAAAGUGGCAGGA	2324
54790_1_7127	+	chr4:105179059-105179079	UCCCUAUGAUGAGAACAGCA	2325
54790_1_7130	+	chr4:105179060-105179080	CCCUAUGAUGAGAACAGCAU	2326
54790_1_7131	+	chr4:105179061-105179081	CCUAUGAUGAGAACAGCAUG	2327
54790_1_7132	+	chr4:105179062-105179082	CUAUGAUGAGAACAGCAUGG	2328
54790_1_7133	+	chr4:105179096-105179116	AUGAUCCAAUUACUUCCACC	2329
54790_1_7137	+	chr4:105179115-105179135	CUGGUCUCUGCCUUGACACA	2330
54790_1_7138	+	chr4:105179116-105179136	UGGUCUCUGCCUUGACACAU	2331
54790_1_7140	+	chr4:105179124-105179144	GCCUUGACACAUGGGUAUUA	2332
54790_1_7145	+	chr4:105179133-105179153	CAUGGGUAUUAUGGAGAUUA	2333
54790_1_7147	+	chr4:105179134-105179154	AUGGGUAUUAUGGAGAUUAU	2334
54790_1_7148	+	chr4:105179135-105179155	UGGGUAUUAUGGAGAUUAUG	2335
54790_1_7153	+	chr4:105179159-105179179	UUAUAAUUCAAGAUGAGAUU	2336
54790_1_7154	+	chr4:105179160-105179180	UAUAAUUCAAGAUGAGAUUU	2337
54790_1_7157	+	chr4:105179163-105179183	AAUUCAAGAUGAGAUUUGGG	2338
54790_1_7160	+	chr4:105179164-105179184	AUUCAAGAUGAGAUUUGGGU	2339
54790_1_7161	+	chr4:105179165-105179185	UUCAAGAUGAGAUUUGGGUG	2340
54790_1_7167	+	chr4:105179215-105179235	AAACUAUGUCUUUUCUUUUA	2341
54790_1_7168	+	chr4:105179216-105179236	AACUAUGUCUUUUCUUUUAU	2342
54790_1_7169	+	chr4:105179217-105179237	ACUAUGUCUUUUCUUUUAUG	2343

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_7183	+	chr4:105179272-105179292	GACCUCCAUUUCCAAUUUC	2344
54790_1_7188	+	chr4:105179277-105179297	CCAUUUCCAAUUUCUGGUU	2345
54790_1_7209	+	chr4:105179363-105179383	AAUCUUUCAUUAAAAGAAAU	2346
54790_1_7211	+	chr4:105179364-105179384	AUCUUUCAUUAAAAGAAUA	2347
54790_1_7213	+	chr4:105179365-105179385	UCUUUCAUUAAAAGAAUAG	2348
54790_1_7214	+	chr4:105179368-105179388	UUCAUUAAAAGAAUAGGGG	2349
54790_1_7219	+	chr4:105179374-105179394	AAAAGAAUAGGGGAGGUGA	2350
54790_1_7222	+	chr4:105179375-105179395	AAAGAAUAGGGGAGGUGAU	2351
54790_1_7224	+	chr4:105179376-105179396	AAGAAUAGGGGAGGUGAUG	2352
54790_1_7225	+	chr4:105179377-105179397	AGAAUAGGGGAGGUGAUGG	2353
54790_1_7228	+	chr4:105179397-105179417	GGGAUAUCCAUGAGUGUCCA	2354
54790_1_7229	+	chr4:105179398-105179418	GGAUUAUCCAUGAGUGUCCA	2355
54790_1_7234	+	chr4:105179450-105179470	AUGAUACUGCAAAGCCUACA	2356
54790_1_7243	+	chr4:105179532-105179552	AUCUUGUUUCAUUUUAUGUG	2357
54790_1_7259	+	chr4:105179583-105179603	UGAAAAUAUCCUCUUCAUU	2358
54790_1_7260	+	chr4:105179584-105179604	GAAAAUAUCCUCUUCAUUU	2359
54790_1_7277	+	chr4:105179688-105179708	AUAAUGCAUGACUUCAUUC	2360
54790_1_7278	+	chr4:105179697-105179717	GACUUCAUUC AUGGCUCUCU	2361
54790_1_7281	+	chr4:105179719-105179739	GUGACCUGUGUACCCUGACC	2362
54790_1_7283	+	chr4:105179753-105179773	AGAGUAUUAAGUCAUUUCAG	2363
54790_1_7288	+	chr4:105179766-105179786	AUUUCAGUGGCACAUGUUUG	2364
54790_1_7289	+	chr4:105179767-105179787	UUUCAGUGGCACAUGUUUGA	2365
54790_1_7296	+	chr4:105179786-105179806	AGGGAAGAUUGACAUCCAC	2366
54790_1_7301	+	chr4:105179835-105179855	AAGCAGCUGCAUUCUAGUG	2367
54790_1_7303	+	chr4:105179862-105179882	AUUAAGUUUAUCCACUAUU	2368
54790_1_7307	+	chr4:105179868-105179888	UUUAUCCACUAUUAGGUUC	2369
54790_1_7314	+	chr4:105179893-105179913	UAUUACUUGUCAUGCCCAAG	2370
54790_1_7319	+	chr4:105179922-105179942	UUUCUAGCAUGCAGAGUAUC	2371
54790_1_7324	+	chr4:105179932-105179952	GCAGAGUAUCUGGUUUUUA	2372
54790_1_7332	+	chr4:105179965-105179985	GAAAUAAA AUGUGCCUACUA	2373
54790_1_7333	+	chr4:105179966-105179986	AAAUAAA AUGUGCCUACUAA	2374
54790_1_7339	+	chr4:105180011-105180031	UCUUUCACUGUUUUUUUCU	2375
54790_1_7342	+	chr4:105180014-105180034	UUCACUGUUUUUUUCUUGG	2376
54790_1_7353	+	chr4:105180037-105180057	UUACAGUAGUUAUGCCUUC	2377
54790_1_7355	+	chr4:105180045-105180065	GUUAUGCCUUUCUGGUCAGC	2378
54790_1_7363	+	chr4:105180093-105180113	CUUUCACAUCUUAAGUGUA	2379
54790_1_7375	+	chr4:105180168-105180188	CUUUCAGUAUUGAUUUCUCA	2380
54790_1_7383	+	chr4:105180191-105180211	CCUAUGAACCUGAGUCAACU	2381
54790_1_7385	+	chr4:105180199-105180219	CCUGAGUCAACUUGGCAUAA	2382
54790_1_7391	+	chr4:105180237-105180257	UUCUCUAAAUGCAGAGUCAG	2383
54790_1_7399	+	chr4:105180284-105180304	GCUCAGUGAUAAAUUAAAA	2384
54790_1_7410	+	chr4:105180351-105180371	AAAUUCAGUCAUUAUACA	2385
54790_1_7413	+	chr4:105180354-105180374	UCUCAGUCAUUAUACAUGG	2386
54790_1_7415	+	chr4:105180388-105180408	UAUUACAUGCCUGUGCUUCU	2387
54790_1_7430	+	chr4:105180472-105180492	UUAUCUUUUUUUGUUUUACC	2388
54790_1_7460	+	chr4:105180574-105180594	AAUAUUCUCCAUGAUCUCCA	2389
54790_1_7469	+	chr4:105180637-105180657	UAUCAUUUUUUUUUUUUUCU	2390
54790_1_7486	+	chr4:105180662-105180682	ACAGUCUCACUCUGUUGCCC	2391

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_7489	+	chr4:105180666-105180686	UCUCACUCUGUUGCCCAGGC	2392
54790_1_7490	+	chr4:105180667-105180687	CUCACUCUGUUGCCCAGGCU	2393
54790_1_7497	+	chr4:105180743-105180763	AUUCUCCUGCCUCAGCCUGC	2394
54790_1_7498	+	chr4:105180744-105180764	UUCUCCUGCCUCAGCCUGCC	2395
54790_1_7502	+	chr4:105180760-105180780	UGCCGGGUAGCUAGAAUUAC	2396
54790_1_7503	+	chr4:105180779-105180799	CAGGCAUGUGCCACCACACC	2397
54790_1_7507	+	chr4:105180807-105180827	UCUGUAUUUUUAGUAGAGAC	2398
54790_1_7508	+	chr4:105180808-105180828	CUGUAUUUUUAGUAGAGACA	2399
54790_1_7514	+	chr4:105180822-105180842	GAGACAGGGUUUCACGAUGU	2400
54790_1_7515	+	chr4:105180831-105180851	UUUCACGAUGUUGGCCAGAC	2401
54790_1_7520	+	chr4:105180852-105180872	GGUCUUGAACUCCUGACCUC	2402
54790_1_7523	+	chr4:105180885-105180905	ACCGCAGCCUCCCAAAGUGC	2403
54790_1_7525	+	chr4:105180894-105180914	UCCCAAAGUGCUGGAAUUAC	2404
54790_1_7527	+	chr4:105180901-105180921	GUGCUGGAAUUACAGGCGUG	2405
54790_1_7529	+	chr4:105180913-105180933	CAGGCGUGAGGCACUGCAUC	2406
54790_1_7568	+	chr4:105181171-105181191	GCUACGAUCUAUAUACUCCU	2407
54790_1_7577	+	chr4:105181226-105181246	UGUGUGUGUCUGUAUAGUAG	2408
54790_1_7585	+	chr4:105181266-105181286	UAGUCACAAUAUGCUUUUUG	2409
54790_1_7590	+	chr4:105181282-105181302	UUUGAGGAUUUCCUUUUCC	2410
54790_1_7592	+	chr4:105181283-105181303	UUGAGGAUUUCCUUUUCCU	2411
54790_1_7626	+	chr4:105181394-105181414	CUCUCCAUCUUAGAAGAGC	2412
54790_1_7629	+	chr4:105181425-105181445	AACCGACUCUUCUUUUAUCU	2413
54790_1_7635	+	chr4:105181442-105181462	UCUUGGUUUCUACAACACAG	2414
54790_1_7641	+	chr4:105181475-105181495	ACUUUAAUCCCUUUUAAACAC	2415
54790_1_7659	+	chr4:105181548-105181568	AAAAUCUAGCAAUAAAAAA	2416
54790_1_7676	+	chr4:105181663-105181683	AUUAUGAU AUGCUUAUUCAU	2417
54790_1_7682	+	chr4:105181703-105181723	GCAAUAGUGUAGCCCUUCU	2418
54790_1_7695	+	chr4:105181796-105181816	UUGUUAUAAAAAUACUCAU	2419
54790_1_7713	+	chr4:105181876-105181896	UUAUACUACUUUCUUUAUUU	2420
54790_1_7716	+	chr4:105181877-105181897	UAUACUACUUUCUUUAUUUA	2421
54790_1_7722	+	chr4:105181880-105181900	ACUACUUUCUUUAUUUAGGG	2422
54790_1_7729	+	chr4:105181906-105181926	GUAUUUAAAUUCUGUUAUCU	2423
54790_1_7774	+	chr4:105182067-105182087	UUUCCCUAUCAUUUGUUCUC	2424
54790_1_7783	+	chr4:105182112-105182132	CAUUUUUUUCCAGUGACAAA	2425
54790_1_7806	+	chr4:105182194-105182214	UGCAAACAACCAGAGCUGAU	2426
54790_1_7807	+	chr4:105182201-105182221	AACCAGAGCUGAUAGGCAGC	2427
54790_1_7809	+	chr4:105182216-105182236	GCAGCAGGUGCACAUGAGUG	2428
54790_1_7810	+	chr4:105182228-105182248	CAUGAGUGUGGCUGUGCUGA	2429
54790_1_7812	+	chr4:105182248-105182268	UGGUUACUGAAAGAUUUGCA	2430
54790_1_7818	+	chr4:105182304-105182324	GCUCCUCCCCCAUUACUCCC	2431
54790_1_7819	+	chr4:105182305-105182325	CUCCUCCCCCAUUACUCCCU	2432
54790_1_7824	+	chr4:105182340-105182360	CCUGCAGCUAGAAUAAUAAA	2433
54790_1_7825	+	chr4:105182348-105182368	UAGAAUAAUAAAUGGCAUGU	2434
54790_1_7827	+	chr4:105182358-105182378	AAUGGCAUGUAGGUUCCUCU	2435
54790_1_7830	+	chr4:105182389-105182409	CCAGCACUAUGUCUCAUGCC	2436
54790_1_7833	+	chr4:105182431-105182451	UUUUGAUUAUCACUCCUGUG	2437
54790_1_7839	+	chr4:105182436-105182456	AUUAUCACUCCUGUGUGGUA	2438
54790_1_7840	+	chr4:105182437-105182457	UUAUCACUCCUGUGUGGUAA	2439

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_7858	+	chr4:105182551-105182571	UAGUUUGUUUUUUAACAAACC	2440
54790_1_7906	+	chr4:105182695-105182715	UUAGAGAAUAUUGUUACUGA	2441
54790_1_7941	+	chr4:105182864-105182884	CUUUAAACCUUAGCUCAUUAU	2442
54790_1_7948	+	chr4:105182902-105182922	CAUCCUAGAUGAAGAUAAUU	2443
54790_1_7949	+	chr4:105182903-105182923	AUCCUAGAUGAAGAUAAUUU	2444
54790_1_7964	+	chr4:105182973-105182993	UCCAUUUUGAAGAAAUUGUA	2445
54790_1_7966	+	chr4:105182977-105182997	UUUUGAAGAAAUUGUAAGGU	2446
54790_1_7967	+	chr4:105182978-105182998	UUUGAAGAAAUUGUAAGGUA	2447
54790_1_7976	+	chr4:105183043-105183063	AAAACAUUUUUUAAAAUAUC	2448
54790_1_7977	+	chr4:105183044-105183064	AAAUCAUUUUUAAAAUAUCU	2449
54790_1_7983	+	chr4:105183061-105183081	UCUGGGUAAUGCUAUAGAU	2450
54790_1_7992	+	chr4:105183117-105183137	GUUUAUUGAUCCUCAUCUG	2451
54790_1_7997	+	chr4:105183130-105183150	CAAUCUGUGGCUGUUUAAA	2452
54790_1_8004	+	chr4:105183164-105183184	AGUUCAGUCUAAGAGAACCA	2453
54790_1_8015	+	chr4:105183230-105183250	AUAUAAAUAUACUAAAUAUA	2454
54790_1_8021	+	chr4:105183261-105183281	AUAUAUUGUAAAAAUUGCUU	2455
54790_1_8026	+	chr4:105183282-105183302	GGAAUCAAUAAUAAGUAUUG	2456
54790_1_8032	+	chr4:105183315-105183335	UAGUUAUAUAUUACAAUGUA	2457
54790_1_8033	+	chr4:105183316-105183336	AGUUAUAUAUUACAAUGUAA	2458
54790_1_8067	+	chr4:105183465-105183485	AUUCGAUAGUAUCUAAAUCA	2459
54790_1_8070	+	chr4:105183487-105183507	GAAUCAUAAAACCUUAAAGC	2460
54790_1_8071	+	chr4:105183488-105183508	AAUCAUAAAACCUUAAAGCU	2461
54790_1_8074	+	chr4:105183492-105183512	AUAAAACCUUAAAGCUGGGU	2462
54790_1_8079	+	chr4:105183524-105183544	AAUACAAUUUAACAUCUUUAU	2463
54790_1_8083	+	chr4:105183556-105183576	CCUCAGUUUCCCUAAGUGAU	2464
54790_1_8088	+	chr4:105183577-105183597	GGCUCAAGAUCUAUGAAUUUA	2465
54790_1_8091	+	chr4:105183580-105183600	UCAAGAUCAUGAAUUUAUGG	2466
54790_1_8108	+	chr4:105183660-105183680	CUACCCCUUAGUUUGCCUG	2467
54790_1_8109	+	chr4:105183661-105183681	UACCCCUUAGUUUGCCUGU	2468
54790_1_8111	+	chr4:105183668-105183688	UUAGUUUGCCUGUGGGUUUA	2469
54790_1_8117	+	chr4:105183678-105183698	UGUGGGUUUAUGGAAGUUAC	2470
54790_1_8155	+	chr4:105183894-105183914	AUACUACUUGAAAUUUCUAG	2471
54790_1_8156	+	chr4:105183895-105183915	UACUACUUGAAAUUUCUAGC	2472
54790_1_8158	+	chr4:105183896-105183916	ACUACUUGAAAUUUCUAGCG	2473
54790_1_8163	+	chr4:105183913-105183933	GCGGGGAUCUCUAAAUGCC	2474
54790_1_8166	+	chr4:105183921-105183941	CUCUAAAUGCCUGGAUGUU	2475
54790_1_8167	+	chr4:105183926-105183946	AAAUGCCUGGAUGUUAGGAA	2476
54790_1_8174	+	chr4:105183965-105183985	AAUUUAUUUUUCUAUUUUAG	2477
54790_1_8184	+	chr4:105183993-105184013	AAAUAAACCAUACCCUUAAG	2478
54790_1_8191	+	chr4:105184031-105184051	AUUUUGAGCACAUCCUUCAU	2479
54790_1_8197	+	chr4:105184052-105184072	GGCCCAGUCUCUGACCAGUG	2480
54790_1_8218	+	chr4:105184141-105184161	AUUUUCUGUGUGAUGUUUAU	2481
54790_1_8219	+	chr4:105184142-105184162	UUUUCUGUGUGAUGUUUAUA	2482
54790_1_8229	+	chr4:105184172-105184192	UUCUGAAAUUUUUCCAUCU	2483
54790_1_8245	+	chr4:105184231-105184251	UCAUAACUUCUUUUUAUUUU	2484
54790_1_8260	+	chr4:105184311-105184331	ACCUCUCAUGUCCAGUGUU	2485
54790_1_8267	+	chr4:105184338-105184358	UAAAUAAUCACUUUGUAUAA	2486
54790_1_8271	+	chr4:105184367-105184387	UAUGUUAAAUUGUUUAUAAC	2487

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_8272	+	chr4:105184370-105184390	GUUAAAUUGUUUAUAAACUGG	2488
54790_1_8277	+	chr4:105184392-105184412	GUUGAUUUUCAGCCUUGUU	2489
54790_1_8287	+	chr4:105184439-105184459	UAAUUAGAAACAACCUCAUA	2490
54790_1_8292	+	chr4:105184464-105184484	UAUGCUUGUUUUUAUCUUCA	2491
54790_1_8305	+	chr4:105184497-105184517	GCAAACACUGAGUUCUUUAC	2492
54790_1_8306	+	chr4:105184498-105184518	CAAACACUGAGUUCUUUACU	2493
54790_1_8313	+	chr4:105184522-105184542	GUCACCACUUUGUCUAUGUU	2494
54790_1_8316	+	chr4:105184525-105184545	ACCACUUUGUCUAUGUUAGG	2495
54790_1_8319	+	chr4:105184531-105184551	UUGUCUAUGUUAGGAGGAGC	2496
54790_1_8324	+	chr4:105184549-105184569	GCAGGAAGUGAAUACAUUUA	2497
54790_1_8333	+	chr4:105184588-105184608	UAAAACUUUGACUACUGUAG	2498
54790_1_8339	+	chr4:105184608-105184628	UGGUUUUUUAAAGCAUUAAC	2499
54790_1_8349	+	chr4:105184663-105184683	CUGAAAUAGCACUUCCCUUU	2500
54790_1_8353	+	chr4:105184677-105184697	CCCUUUAGGCACUGUACAGU	2501
54790_1_8359	+	chr4:105184698-105184718	GGAAUCAUUUACUUGCAGAG	2502
54790_1_8370	+	chr4:105184750-105184770	GUACUCAUGUGUAUAAGAAU	2503
54790_1_8374	+	chr4:105184765-105184785	AGAAUAGGAGAAACACUUUG	2504
54790_1_8375	+	chr4:105184766-105184786	GAAUAGGAGAAACACUUUGU	2505
54790_1_8377	+	chr4:105184781-105184801	UUUGUGGGCAUAUCCUGCUG	2506
54790_1_8384	+	chr4:105184831-105184851	AGUCUCAUCCCAUUUAAACC	2507
54790_1_8387	+	chr4:105184834-105184854	CUCAUCCCAUUUAAACCUGG	2508
54790_1_8395	+	chr4:105184880-105184900	AGCCAAAGCAGCAUUUCAAC	2509
54790_1_8398	+	chr4:105184884-105184904	AAAGCAGCAUUUCAACAGGA	2510
54790_1_8402	+	chr4:105184900-105184920	AGGAAGGAAACAUCUAUUAC	2511
54790_1_8404	+	chr4:105184901-105184921	GGAAGGAAACAUCUAUUACU	2512
54790_1_8405	+	chr4:105184902-105184922	GAAGGAAACAUCUAUUACUG	2513
54790_1_8411	+	chr4:105184926-105184946	UUUGAAGAAACAUGCCAUGA	2514
54790_1_8416	+	chr4:105184945-105184965	AAGGUGUACUAAUAUCACAA	2515
54790_1_8418	+	chr4:105184946-105184966	AGGUGUACUAAUAUCACAAA	2516
54790_1_8421	+	chr4:105184950-105184970	GUACUAAUAUCACAAAGGGA	2517
54790_1_8422	+	chr4:105184951-105184971	UACUAAUAUCACAAAGGGAA	2518
54790_1_8425	+	chr4:105184955-105184975	AAUAUCACAAAGGGAAGGGA	2519
54790_1_8428	+	chr4:105184997-105185017	ACAAAGUCCCUUUUUUGUAA	2520
54790_1_8435	+	chr4:105185024-105185044	GUUUGAUGAUGUUUGAUCAA	2521
54790_1_8437	+	chr4:105185027-105185047	UGAUGAUGUUUGAUCAAUGG	2522
54790_1_8444	+	chr4:105185044-105185064	UGGUGGAUCUAUCUCUUGAA	2523
54790_1_8449	+	chr4:105185068-105185088	AA AUGCAUUUAAACCCCAA	2524
54790_1_8451	+	chr4:105185071-105185091	UGCAUUUAAACCCCAAUGG	2525
54790_1_8454	+	chr4:105185085-105185105	AA AUGGAGGAUUCUUAUAUA	2526
54790_1_8458	+	chr4:105185120-105185140	AAUGAUUAUUAUGUUUAUA	2527
54790_1_8460	+	chr4:105185132-105185152	AUGUUUAUAGGUAGAGUGAC	2528
54790_1_8467	+	chr4:105185147-105185167	GUGACUGGUUUUUAGAGAAG	2529
54790_1_8489	+	chr4:105185194-105185214	ACGAAAACUUGUCUGUCUCU	2530
54790_1_8507	+	chr4:105185264-105185284	CUGAAUCUCCUACAAGCUUG	2531
54790_1_8508	+	chr4:105185267-105185287	AAUCUCCUACAAGCUUGUGG	2532
54790_1_8513	+	chr4:105185296-105185316	AGCAUGUUGAAUAAGAGCAC	2533
54790_1_8515	+	chr4:105185302-105185322	UUGAAUAAGAGCACAGGCUC	2534
54790_1_8518	+	chr4:105185305-105185325	AAUAAGAGCACAGGCUCUGG	2535

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 1 8520	+	chr4:105185323-105185343	GGAGGCCCUGCCACCCACAA	2536
54790 1 8521	+	chr4:105185324-105185344	GAGGCCCUGCCACCCACAAA	2537
54790 1 8522	+	chr4:105185334-105185354	CACCCACAAAGGGUGUGCUA	2538
54790 1 8541	+	chr4:105185429-105185449	CUUUUUUUUCUAAAUCUAUU	2539
54790 1 8554	+	chr4:105185482-105185502	UUCUAAAACACAGUGAGACC	2540
54790 1 8557	+	chr4:105185490-105185510	CACAGUGAGACCAGGCGCAG	2541
54790 1 8559	+	chr4:105185518-105185538	GCCUGUAAUCCCAGCACUUU	2542
54790 1 8561	+	chr4:105185521-105185541	UGUAAUCCCAGCACUUUCGG	2543
54790 1 8563	+	chr4:105185527-105185547	CCCAGCACUUUCGGAGGCCG	2544
54790 1 8565	+	chr4:105185534-105185554	CUUUCGGAGGCCGAGGU AUG	2545
54790 1 8569	+	chr4:105185543-105185563	GCCGAGGU AUGCGGAUCACG	2546
54790 1 8572	+	chr4:105185548-105185568	GGU AUGCGGAUCACGAGGUC	2547
54790 1 8574	+	chr4:105185566-105185586	UCAGGAGAU CGAGACCAUCC	2548
54790 1 8575	+	chr4:105185575-105185595	CGAGACCAUCCUGGCUAACA	2549
54790 1 8577	+	chr4:105185615-105185635	UAAAAAUACAAAAAUUAGCC	2550
54790 1 8580	+	chr4:105185620-105185640	AUACAAAAAUUAGCCAGGCG	2551
54790 1 8581	+	chr4:105185621-105185641	UACAAAAAUUAGCCAGGCGU	2552
54790 1 8583	+	chr4:105185622-105185642	ACAAAAAUUAGCCAGGCGUG	2553
54790 1 8584	+	chr4:105185623-105185643	CAAAAAAUUAGCCAGGCGUGG	2554
54790 1 8587	+	chr4:105185651-105185671	GCCUGUAAUCCCAGCUACUC	2555
54790 1 8589	+	chr4:105185654-105185674	UGUAAUCCCAGCUACUCAGG	2556
54790 1 8591	+	chr4:105185660-105185680	CCCAGCUACUCAGGAGGCUG	2557
54790 1 8593	+	chr4:105185664-105185684	GCUACUCAGGAGGCUGAGGC	2558
54790 1 8597	+	chr4:105185671-105185691	AGGAGGCUGAGGCAGGAGAA	2559
54790 1 8601	+	chr4:105185681-105185701	GGCAGGAGAAUGGCGUGAAC	2560
54790 1 8602	+	chr4:105185682-105185702	GCAGGAGAAUGGCGUGAACC	2561
54790 1 8605	+	chr4:105185683-105185703	CAGGAGAAUGGCGUGAACCG	2562
54790 1 8606	+	chr4:105185686-105185706	GAGAAUGGCGUGAACCGGGG	2563
54790 1 8609	+	chr4:105185689-105185709	AAUGGCGUGAACCGGGGAGG	2564
54790 1 8613	+	chr4:105185732-105185752	CGCACCACUGCACUCCAGCC	2565
54790 1 8614	+	chr4:105185733-105185753	GCACCACUGCACUCCAGCCU	2566
54790 1 8620	+	chr4:105185814-105185834	UUAUAAAGAUAAAAUAGAAU	2567
54790 1 8625	+	chr4:105185826-105185846	AAUAGAAUAGGCUUCAUUU	2568
54790 1 8626	+	chr4:105185827-105185847	AUAGAAUAGGCUUCAUUUA	2569
54790 1 8629	+	chr4:105185835-105185855	GGCUUCAUUUAGGGAACAA	2570
54790 1 8635	+	chr4:105185849-105185869	GAACAAAGGAAAAUAUGUUU	2571
54790 1 8640	+	chr4:105185886-105185906	CAAAAU GAUUGCAACUUUGA	2572
54790 1 8648	+	chr4:105185923-105185943	UUCAAUUAAAAUGUAGAU A	2573
54790 1 8651	+	chr4:105185927-105185947	AUUAAAAAUGUAGAU AUGGC	2574
54790 1 8652	+	chr4:105185928-105185948	UUAAAAAUGUAGAU AUGGCU	2575
54790 1 8654	+	chr4:105185933-105185953	AAUGUAGAU AUGGCUGGGCG	2576
54790 1 8655	+	chr4:105185936-105185956	GUAGAU AUGGCUGGGCGUGG	2577
54790 1 8658	+	chr4:105185963-105185983	CACCUGUAAUCCCAGCACUU	2578
54790 1 8659	+	chr4:105185967-105185987	UGUAAUCCCAGCACUUUGGA	2579
54790 1 8660	+	chr4:105185977-105185997	GCACUUUGGAAGGUUGACGC	2580
54790 1 8662	+	chr4:105185980-105186000	CUUUGGAAGGUUGACGCAGG	2581
54790 1 8666	+	chr4:105185991-105186011	UGACGCAGGUGGAUCACUUG	2582
54790 1 8669	+	chr4:105185996-105186016	CAGGUGGAUCACUUGAGGUU	2583

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_8674	+	chr4:105186014-105186034	UUAGGAGUUUGAGACCUGCC	2584
54790_1_8675	+	chr4:105186015-105186035	UAGGAGUUUGAGACCUGCCU	2585
54790_1_8681	+	chr4:105186065-105186085	AAAAUAAACAAAAAAUGUGC	2586
54790_1_8682	+	chr4:105186066-105186086	AAAUAAACAAAAAAUGUGCU	2587
54790_1_8683	+	chr4:105186071-105186091	AACAAAAAAUGUGCUGGGUG	2588
54790_1_8684	+	chr4:105186074-105186094	AAAAAAUGUGCUGGGUGUGG	2589
54790_1_8687	+	chr4:105186101-105186121	UGCCUGUAGUCCUAGCCACU	2590
54790_1_8689	+	chr4:105186102-105186122	GCCUGUAGUCCUAGCCACUU	2591
54790_1_8693	+	chr4:105186114-105186134	AGCCACUUGGGAGACUGAGA	2592
54790_1_8695	+	chr4:105186118-105186138	ACUUGGGAGACUGAGAUGGA	2593
54790_1_8700	+	chr4:105186133-105186153	AUGGAAGGAUAGCUUGAGUC	2594
54790_1_8702	+	chr4:105186134-105186154	UGGAAGGAUAGCUUGAGUCU	2595
54790_1_8703	+	chr4:105186137-105186157	AAGGAUAGCUUGAGUCUGGG	2596
54790_1_8709	+	chr4:105186183-105186203	CGUGCCACUGCACUUGAGCC	2597
54790_1_8710	+	chr4:105186184-105186204	GUGCCACUGCACUUGAGCCU	2598
54790_1_8717	+	chr4:105186252-105186272	AACAACAGUAGAU AUGUGUG	2599
54790_1_8719	+	chr4:105186253-105186273	ACAACAGUAGAU AUGUGUGU	2600
54790_1_8722	+	chr4:105186281-105186301	GAACAUUUA AUGUGCUCAU	2601
54790_1_8726	+	chr4:105186310-105186330	UUUUUCUUUAACCCCUUCA	2602
54790_1_8747	+	chr4:105186405-105186425	UUAUAACUCUCA AUGUAUCA	2603
54790_1_8754	+	chr4:105186412-105186432	UCUCA AUGUAUCAUGGCAGA	2604
54790_1_8766	+	chr4:105186477-105186497	UUUUUUUUUUUUUUUUGAGA	2605
54790_1_8785	+	chr4:105186498-105186518	GGAGUCUCACUCUGUCACCC	2606
54790_1_8787	+	chr4:105186502-105186522	UCUCACUCUGUCACCCAGGC	2607
54790_1_8789	+	chr4:105186512-105186532	UCACCCAGGCUGGAGUGCAG	2608
54790_1_8792	+	chr4:105186547-105186567	UUAUUGCAACCUC CGCCUCC	2609
54790_1_8794	+	chr4:105186550-105186570	UUGCAACCUC CGCCUCCUGG	2610
54790_1_8798	+	chr4:105186583-105186603	GCCUCAGCCUCCCCAGUAGC	2611
54790_1_8800	+	chr4:105186584-105186604	CCUCAGCCUCCCCAGUAGCU	2612
54790_1_8801	+	chr4:105186592-105186612	UCCCCAGUAGCUGGGACUAC	2613
54790_1_8803	+	chr4:105186611-105186631	CAGGCUUGCACCACCAUGCC	2614
54790_1_8807	+	chr4:105186639-105186659	UUUUUAU AUUUUUA GUAGAGA	2615
54790_1_8809	+	chr4:105186640-105186660	UUUAUAU AUUUUUA GUAGAGAC	2616
54790_1_8810	+	chr4:105186641-105186661	UUAUAU AUUUUUA GUAGAGACG	2617
54790_1_8819	+	chr4:105186660-105186680	GGGGUUUCAUCAUGUUGUCU	2618
54790_1_8820	+	chr4:105186664-105186684	UUUCAUCAUGUUGUCUAGGC	2619
54790_1_8824	+	chr4:105186702-105186722	CUCAAGUGAUCCACCCACCU	2620
54790_1_8826	+	chr4:105186718-105186738	ACCUUGGCCUCCCAAAGUGC	2621
54790_1_8828	+	chr4:105186719-105186739	CCUUGGCCUCCCAAAGUGCU	2622
54790_1_8830	+	chr4:105186727-105186747	UCCCAAAGUGCUGGGAUUGC	2623
54790_1_8832	+	chr4:105186742-105186762	AUUGCAGGCAUGAGCCACCG	2624
54790_1_8834	+	chr4:105186747-105186767	AGGCAUGAGCCACCGCGGCC	2625
54790_1_8845	+	chr4:105186844-105186864	UUAUCAGAAUAUUAUCAUAU	2626
54790_1_8855	+	chr4:105186880-105186900	CUGAACAAAGCCAGAAUUAU	2627
54790_1_8858	+	chr4:105186889-105186909	GCCAGAAUUAUUGGCUACUG	2628
54790_1_8866	+	chr4:105186925-105186945	CAAGAGACUAUUCUAUUUGU	2629
54790_1_8867	+	chr4:105186926-105186946	AAGAGACUAUUCUAUUUGUU	2630
54790_1_8869	+	chr4:105186927-105186947	AGAGACUAUUCUAUUUGUUG	2631

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_8876	+	chr4:105186948-105186968	GGAUCACCUCUUUUUACUAA	2632
54790_1_8878	+	chr4:105186949-105186969	GAUCACCUCUUUUUACUAAA	2633
54790_1_8879	+	chr4:105186950-105186970	AUCACCUCUUUUUACUAAAG	2634
54790_1_8881	+	chr4:105186960-105186980	UUUACUAAAGGGGACUGUUU	2635
54790_1_8883	+	chr4:105186961-105186981	UUACUAAAGGGGACUGUUUU	2636
54790_1_8892	+	chr4:105186983-105187003	GCAUAUAAAACUAGAAUUCA	2637
54790_1_8901	+	chr4:105187036-105187056	CCAGUCAACCAGAUAACUGC	2638
54790_1_8903	+	chr4:105187059-105187079	UAGUGACACUCAUGUCCUCC	2639
54790_1_8907	+	chr4:105187088-105187108	AAUCUUGUGCCAGCUCAGAG	2640
54790_1_8910	+	chr4:105187089-105187109	AUCUUGUGCCAGCUCAGAGA	2641
54790_1_8915	+	chr4:105187142-105187162	AAGAACCACAAGCACCACCU	2642
54790_1_8940	+	chr4:105187262-105187282	UAUUUUAAACAGAAAACAGA	2643
54790_1_8944	+	chr4:105187293-105187313	CCUCUGCCUUCUCAGUAUU	2644
54790_1_8953	+	chr4:105187339-105187359	UUAAGAGUCUAAUCAUAUAC	2645
54790_1_8974	+	chr4:105187463-105187483	CUGCCUGAUGAAUAUUUAUU	2646
54790_1_9045	+	chr4:105187802-105187822	UUCUACCACUUCACACUCAC	2647
54790_1_9047	+	chr4:105187803-105187823	UCUACCACUUCACACUCACU	2648
54790_1_9050	+	chr4:105187807-105187827	CCACUUCACACUCACUGGGA	2649
54790_1_9052	+	chr4:105187836-105187856	UUUUUAAAACAUAACUAAC	2650
54790_1_9058	+	chr4:105187847-105187867	UACAAUAACAGGUGUUAGUG	2651
54790_1_9061	+	chr4:105187853-105187873	AACAGGUGUUAGUGCGGAUA	2652
54790_1_9063	+	chr4:105187862-105187882	UAGUGCGGAUAUGGAAAAAU	2653
54790_1_9069	+	chr4:105187884-105187904	GAACCCUGACACAUUGCUGAG	2654
54790_1_9070	+	chr4:105187896-105187916	AUUGCUGAUGGAAUGUAAAA	2655
54790_1_9072	+	chr4:105187922-105187942	AGCCACUUUGCAAAACAGUU	2656
54790_1_9079	+	chr4:105187947-105187967	GUUCAUCAAAAGAUUAAGCA	2657
54790_1_9084	+	chr4:105187981-105188001	GACCCAGUAGUUUCGCUCUU	2658
54790_1_9085	+	chr4:105187982-105188002	ACCCAGUAGUUUCGCUCUUA	2659
54790_1_9100	+	chr4:105188081-105188101	CAUUAUUCACAAUAGCCUAA	2660
54790_1_9105	+	chr4:105188109-105188129	GCAACCCAAAUGCCUACAGA	2661
54790_1_9108	+	chr4:105188117-105188137	AAUGCCUACAGAUGGAUGAA	2662
54790_1_9111	+	chr4:105188132-105188152	AUGAAUGGAUAAACAGAAUG	2663
54790_1_9113	+	chr4:105188148-105188168	AAUGUGGUUAUAGACAUACAA	2664
54790_1_9116	+	chr4:105188171-105188191	ACUAUUAUUCAACCUUAAAG	2665
54790_1_9127	+	chr4:105188205-105188225	GACACAUGCUAGAAAAUAAA	2666
54790_1_9129	+	chr4:105188230-105188250	CUUGUAUACAUUCUACUAAG	2667
54790_1_9136	+	chr4:105188279-105188299	AUUAUGAUUCCACUUACAUG	2668
54790_1_9143	+	chr4:105188306-105188326	UAGAAUAGUCAAAUUAUAG	2669
54790_1_9149	+	chr4:105188332-105188352	ACAGUAGAAUAAUGAUUGCC	2670
54790_1_9151	+	chr4:105188333-105188353	CAGUAGAAUAAUGAUUGCCA	2671
54790_1_9152	+	chr4:105188334-105188354	AGUAGAAUAAUGAUUGCCAG	2672
54790_1_9155	+	chr4:105188338-105188358	GAAUAAUGAUUGCCAGGGGC	2673
54790_1_9156	+	chr4:105188339-105188359	AAUAAUGAUUGCCAGGGGCU	2674
54790_1_9159	+	chr4:105188342-105188362	AAUGAUUGCCAGGGGCUGGG	2675
54790_1_9162	+	chr4:105188345-105188365	GAUUGCCAGGGGCUGGGAGG	2676
54790_1_9167	+	chr4:105188354-105188374	GGGCUGGGAGGAGGAGCAAA	2677
54790_1_9168	+	chr4:105188355-105188375	GGCUGGGAGGAGGAGCAAAU	2678
54790_1_9178	+	chr4:105188392-105188412	UGAGUAUAGAAUUUCUGUUU	2679

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_9184	+	chr4:105188410-105188430	UUAGGAAGAUGAAAAAGUUC	2680
54790_1_9189	+	chr4:105188416-105188436	AGAUGAAAAAGUUCUGGAGA	2681
54790_1_9190	+	chr4:105188417-105188437	GAUGAAAAAGUUCUGGAGAU	2682
54790_1_9191	+	chr4:105188420-105188440	GAAAAAGUUCUGGAGAUGGG	2683
54790_1_9192	+	chr4:105188429-105188449	CUGGAGAUGGGUGGCAGUGA	2684
54790_1_9199	+	chr4:105188483-105188503	CAGAAUAGUAUACUUAUAUA	2685
54790_1_9201	+	chr4:105188492-105188512	AUACUUAUAUAUGGUUUGAA	2686
54790_1_9218	+	chr4:105188566-105188586	CCAAAGAAGCAUUAUUUAUG	2687
54790_1_9221	+	chr4:105188576-105188596	AUUAUUUAUGAGGCUAAAAG	2688
54790_1_9226	+	chr4:105188611-105188631	AGUUCAUCAUUGAUAGCUAA	2689
54790_1_9229	+	chr4:105188619-105188639	AUUGAUAGCUAAAGGAAACA	2690
54790_1_9234	+	chr4:105188654-105188674	GUAGAAUAUUAGUCAUACAA	2691
54790_1_9242	+	chr4:105188733-105188753	UGAAAGAAACCAGACGUAAA	2692
54790_1_9243	+	chr4:105188748-105188768	GUAAAAGGCCAAAUUUUGUA	2693
54790_1_9251	+	chr4:105188778-105188798	UAUAUAAAGUCGUUCAAAAU	2694
54790_1_9255	+	chr4:105188810-105188830	AAAGACUGAAAGUUGAUUAG	2695
54790_1_9256	+	chr4:105188819-105188839	AAGUUGAUUAGUGGUCACCA	2696
54790_1_9259	+	chr4:105188824-105188844	GAUUAGUGGUCACCAAGGCC	2697
54790_1_9261	+	chr4:105188825-105188845	AUUAGUGGUCACCAAGGCC	2698
54790_1_9264	+	chr4:105188826-105188846	UUAGUGGUCACCAAGGCCCG	2699
54790_1_9266	+	chr4:105188827-105188847	UAGUGGUCACCAAGGCCCGG	2700
54790_1_9269	+	chr4:105188830-105188850	UGGUCACCAAGGCCCGGGGG	2701
54790_1_9273	+	chr4:105188846-105188866	GGGGAGGAAUGAAUGAAAAC	2702
54790_1_9275	+	chr4:105188856-105188876	GAAUGAAAACUGGCUCCUAA	2703
54790_1_9276	+	chr4:105188857-105188877	AAUGAAAACUGGCUCCUAAU	2704
54790_1_9278	+	chr4:105188863-105188883	AACUGGCUCCUAAUGGGUAC	2705
54790_1_9279	+	chr4:105188864-105188884	ACUGGCUCCUAAUGGGUACU	2706
54790_1_9282	+	chr4:105188872-105188892	CUAAUGGGUACUGGGUUUUU	2707
54790_1_9283	+	chr4:105188873-105188893	UAAUGGGUACUGGGUUUUUU	2708
54790_1_9284	+	chr4:105188874-105188894	AAUGGGUACUGGGUUUUUUUG	2709
54790_1_9288	+	chr4:105188879-105188899	GUACUGGGUUUUUUUGGGGCG	2710
54790_1_9289	+	chr4:105188880-105188900	UACUGGGUUUUUUUGGGGCGA	2711
54790_1_9291	+	chr4:105188881-105188901	ACUGGGUUUUUUUGGGGCGAG	2712
54790_1_9293	+	chr4:105188882-105188902	CUGGGUUUUUUUGGGGCGAGG	2713
54790_1_9304	+	chr4:105188925-105188945	UAGAAUUUGAUAGUAAUGAU	2714
54790_1_9308	+	chr4:105188934-105188954	AUAGUAAUGAUAGGUGAGAG	2715
54790_1_9318	+	chr4:105188985-105189005	ACUGACUCAUAUACUUUACA	2716
54790_1_9319	+	chr4:105188998-105189018	CUUUACAAGGAUGUAUUUUA	2717
54790_1_9327	+	chr4:105189043-105189063	ACCCCUUAAAUUUUAACGUA	2718
54790_1_9338	+	chr4:105189105-105189125	AGUCUCAGCUUACUAUUUCU	2719
54790_1_9351	+	chr4:105189158-105189178	UCCCUUCUACUCUGUAAAAA	2720
54790_1_9352	+	chr4:105189159-105189179	CCCUUCUACUCUGUAAAAAU	2721
54790_1_9359	+	chr4:105189226-105189246	AUUUUUUUGAGUGUAAAUG	2722
54790_1_9367	+	chr4:105189259-105189279	AGUGCAUCUAGCAUAGUGUC	2723
54790_1_9370	+	chr4:105189278-105189298	CUGGCAUUUACCAAGAACCC	2724
54790_1_9373	+	chr4:105189279-105189299	UGGCAUUUACCAAGAACCCC	2725
54790_1_9380	+	chr4:105189327-105189347	ACUAUUCAGAUACUAUUUC	2726
54790_1_9386	+	chr4:105189357-105189377	AAUACUGUUCCAUAUAUUC	2727

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_9388	+	chr4:105189364-105189384	UUUCCAUUAUUAUCAGGACAA	2728
54790_1_9397	+	chr4:105189417-105189437	CUUUAGAUUCUGUUUCAAAU	2729
54790_1_9422	+	chr4:105189557-105189577	UCCUCUUUUCUCUCUGCCCU	2730
54790_1_9429	+	chr4:105189567-105189587	UCUCUGCCCUUGGAACUCUG	2731
54790_1_9447	+	chr4:105189676-105189696	UUGACCAAUUAAGUCUUACU	2732
54790_1_9448	+	chr4:105189677-105189697	UGACCAAUUAAGUCUUACUU	2733
54790_1_9453	+	chr4:105189695-105189715	UUGGGUUAUGUUUUUAAAGU	2734
54790_1_9456	+	chr4:105189707-105189727	UUUAAAGUAGGUUUCUUAAU	2735
54790_1_9459	+	chr4:105189710-105189730	AAAGUAGGUUUCUUAAUAGG	2736
54790_1_9478	+	chr4:105189825-105189845	CUUAGCAUGUUACCUUGACA	2737
54790_1_9494	+	chr4:105189889-105189909	UGCCACAUCUCAUGAAGUAC	2738
54790_1_9495	+	chr4:105189890-105189910	GCCACAUCUCAUGAAGUACA	2739
54790_1_9499	+	chr4:105189933-105189953	GACUUCAUCUUACAGUCACC	2740
54790_1_9511	+	chr4:105190001-105190021	AAAUCCUCAACUUCUUACCU	2741
54790_1_9517	+	chr4:105190035-105190055	UAAGCCACACUGUGAACCAC	2742
54790_1_9520	+	chr4:105190066-105190086	GAUGAAGUAAUUAAGCCAC	2743
54790_1_9521	+	chr4:105190092-105190112	UUAAGCCUCAUUGAUUAUUG	2744
54790_1_9529	+	chr4:105190121-105190141	UGUGAAGACUAAAGAUGCUU	2745
54790_1_9530	+	chr4:105190122-105190142	GUGAAGACUAAAGAUGCUUU	2746
54790_1_9531	+	chr4:105190127-105190147	GACUAAAGAUGCUUUGGGCA	2747
54790_1_9537	+	chr4:105190163-105190183	AGAUUUAGAAUUGUUAUUA	2748
54790_1_9554	+	chr4:105190229-105190249	UUUUAAACAGCCACACUGUAA	2749
54790_1_9561	+	chr4:105190246-105190266	UAAUGGAAAUUCCAAUUUAU	2750
54790_1_9563	+	chr4:105190278-105190298	CCUUUUAAACUCUUUAUAUC	2751
54790_1_9576	-	chr4:105147002-105147022	AGAAGAAAGGGAGAGUUUCG	2752
54790_1_9578	-	chr4:105147014-105147034	AAAGCGAAGGGGAGAAGAAA	2753
54790_1_9581	-	chr4:105147015-105147035	AAAAGCGAAGGGGAGAAGAA	2754
54790_1_9586	-	chr4:105147025-105147045	AAGCCCGAGAAAAAGCGAAG	2755
54790_1_9588	-	chr4:105147026-105147046	GAAGCCCGAGAAAAAGCGAA	2756
54790_1_9591	-	chr4:105147027-105147047	GGAAGCCCGAGAAAAAGCGA	2757
54790_1_9599	-	chr4:105147048-105147068	AGGGUUUGCUCUCCCAGUCCC	2758
54790_1_9604	-	chr4:105147067-105147087	UAUUUGUGGGUGACACUACA	2759
54790_1_9605	-	chr4:105147068-105147088	GUAUUUGUGGGUGACACUAC	2760
54790_1_9609	-	chr4:105147080-105147100	UCUUCCCUCUUGGUUUUUGU	2761
54790_1_9610	-	chr4:105147081-105147101	CUCUUCCCUCUUGGUUUUUG	2762
54790_1_9614	-	chr4:105147090-105147110	GAAGCUUCCCUCUUCCCUCU	2763
54790_1_9619	-	chr4:105147127-105147147	AUUUGUCAGCCAUGUUGAAG	2764
54790_1_9625	-	chr4:105147162-105147182	ACAGGUUUAAAAGGGGUAGA	2765
54790_1_9627	-	chr4:105147163-105147183	UACAGGUUUAAAAGGGGUAG	2766
54790_1_9631	-	chr4:105147169-105147189	CAGAACUACAGGUUUAAAAG	2767
54790_1_9632	-	chr4:105147170-105147190	ACAGAACUACAGGUUUAAA	2768
54790_1_9634	-	chr4:105147171-105147191	CACAGAACUACAGGUUUAAA	2769
54790_1_9636	-	chr4:105147180-105147200	AGAAGAGAACACAGAACUAC	2770
54790_1_9647	-	chr4:105147205-105147225	AUGAGGGGACGAGCAUUAGG	2771
54790_1_9649	-	chr4:105147208-105147228	GAGAUGAGGGGACGAGCAUU	2772
54790_1_9656	-	chr4:105147220-105147240	UAAGUUUUCUGGGAGAUGAG	2773
54790_1_9658	-	chr4:105147221-105147241	GUAAGUUUUCUGGGAGAUGA	2774
54790_1_9660	-	chr4:105147222-105147242	GGUAAGUUUUCUGGGAGAUG	2775

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_9663	-	chr4:105147230-105147250	GGCACAAAGGUAAGUUUUCU	2776
54790_1_9666	-	chr4:105147231-105147251	AGGCACAAAGGUAAGUUUUC	2777
54790_1_9668	-	chr4:105147243-105147263	CCGGCUCGUCGGAGGCACAA	2778
54790_1_9669	-	chr4:105147251-105147271	CCGGGAAACCGGCUCGUCGG	2779
54790_1_9671	-	chr4:105147254-105147274	AGGCCGGGAAACCGGCUCGU	2780
54790_1_9674	-	chr4:105147262-105147282	AUUAAAAAAGGCCGGGAAAC	2781
54790_1_9678	-	chr4:105147269-105147289	UCUGAGGAUUAAAAAAGGCC	2782
54790_1_9681	-	chr4:105147270-105147290	UUCUGAGGAUUAAAAAAGGC	2783
54790_1_9683	-	chr4:105147274-105147294	ACUUUUCUGAGGAUUAAAAA	2784
54790_1_9686	-	chr4:105147285-105147305	AUUUAAAAAUCACUUUUCUG	2785
54790_1_9692	-	chr4:105147315-105147335	AAAGCUGAACUAUUUUAGAA	2786
54790_1_9699	-	chr4:105147353-105147373	AACAGGGGAAGAGGAUUAAA	2787
54790_1_9701	-	chr4:105147354-105147374	AAACAGGGGAAGAGGAUUAA	2788
54790_1_9704	-	chr4:105147362-105147382	CACGAAAGAAACAGGGGAAG	2789
54790_1_9710	-	chr4:105147368-105147388	CACUACACGAAAGAAACAG	2790
54790_1_9712	-	chr4:105147369-105147389	UCACUACACGAAAGAAACA	2791
54790_1_9713	-	chr4:105147370-105147390	UUCACUACACGAAAGAAAC	2792
54790_1_9721	-	chr4:105147401-105147421	UGAGGUUGUUCAGGAUAAAC	2793
54790_1_9723	-	chr4:105147402-105147422	CUGAGGUUGUUCAGGAUAAA	2794
54790_1_9726	-	chr4:105147410-105147430	UGUUCUCUCUGAGGUUGUUC	2795
54790_1_9728	-	chr4:105147419-105147439	CCCUAUCAGUGUUCUCUCUG	2796
54790_1_9731	-	chr4:105147452-105147472	AGACCCUACAGCUGAUAAAA	2797
54790_1_9732	-	chr4:105147453-105147473	CAGACCCUACAGCUGAUAAA	2798
54790_1_9734	-	chr4:105147494-105147514	GGGGAUAAGAAGGUAGGAGG	2799
54790_1_9736	-	chr4:105147497-105147517	AAGGGGGAUAAGAAGGUAGG	2800
54790_1_9738	-	chr4:105147500-105147520	CUAAAGGGGGAUAAGAAGGU	2801
54790_1_9741	-	chr4:105147504-105147524	CCCCCUAAAGGGGGAUAAGA	2802
54790_1_9746	-	chr4:105147513-105147533	UUCGUACAGCCCCCUAAAGG	2803
54790_1_9748	-	chr4:105147514-105147534	CUUCGUACAGCCCCCUAAAG	2804
54790_1_9749	-	chr4:105147515-105147535	ACUUCGUACAGCCCCCUAAA	2805
54790_1_9752	-	chr4:105147516-105147536	CACUUCGUACAGCCCCCUAA	2806
54790_1_9757	-	chr4:105147587-105147607	UAACAAAACGCGCGGACUUA	2807
54790_1_9759	-	chr4:105147595-105147615	AGCGCCGCUAACAAAACGCG	2808
54790_1_9773	-	chr4:105147650-105147670	GUGAGUUCUGGUCUUGUUUG	2809
54790_1_9775	-	chr4:105147651-105147671	AGUGAGUUCUGGUCUUGUUU	2810
54790_1_9777	-	chr4:105147652-105147672	AAGUGAGUUCUGGUCUUGUU	2811
54790_1_9781	-	chr4:105147662-105147682	ACCUUGAGAAAAGUGAGUUC	2812
54790_1_9787	-	chr4:105147708-105147728	CAUACAUUCCCCAGGCUGGA	2813
54790_1_9789	-	chr4:105147712-105147732	CUUACAUACAUUCCCCAGGC	2814
54790_1_9792	-	chr4:105147716-105147736	UUCUCUACAUACAUUCCCC	2815
54790_1_9796	-	chr4:105147758-105147778	UUCGGGAGAAGCACAAAGCC	2816
54790_1_9798	-	chr4:105147759-105147779	AUUCGGGAGAAGCACAAAGC	2817
54790_1_9802	-	chr4:105147775-105147795	GAACCAAACGAAGCUGAUUC	2818
54790_1_9805	-	chr4:105147776-105147796	GGAACCAAACGAAGCUGAUU	2819
54790_1_9811	-	chr4:105147797-105147817	UGUCUGCCUGUCACUACCA	2820
54790_1_9814	-	chr4:105147836-105147856	CCCCUCCCGCCCCCUCCC	2821
54790_1_9815	-	chr4:105147837-105147857	ACCCCUCCCGCCCCCUCCC	2822
54790_1_9827	-	chr4:105147904-105147924	GGAUUGGGUUUCAUUUCUUU	2823

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_9831	-	chr4:105147919-105147939	UUCACUUCUUUGCUGGGAUU	2824
54790_1_9832	-	chr4:105147920-105147940	CUUCACUUCUUUGCUGGGAU	2825
54790_1_9834	-	chr4:105147925-105147945	CUGCUCUUCACUUCUUUGC	2826
54790_1_9836	-	chr4:105147926-105147946	UCUGCUCUUCACUUCUUUGC	2827
54790_1_9841	-	chr4:105147960-105147980	UCGGUUUCUCUAAUUUGGAU	2828
54790_1_9842	-	chr4:105147961-105147981	UUCGGUUUCUCUAAUUUGGA	2829
54790_1_9845	-	chr4:105147965-105147985	UCUCUUCGGUUUCUCUAAUU	2830
54790_1_9856	-	chr4:105148009-105148029	CUCUCCUCUGUGUCUCUCUU	2831
54790_1_9860	-	chr4:105148026-105148046	UCUCUCUUCUUUCUCAUCUC	2832
54790_1_9875	-	chr4:105148085-105148105	GAUUCAGCAAGAUGCGAGUG	2833
54790_1_9884	-	chr4:105148171-105148191	GCCACACUUCAUUAUGUCAU	2834
54790_1_9889	-	chr4:105148193-105148213	GCCUUUCCAGGAGUCUAUCC	2835
54790_1_9894	-	chr4:105148205-105148225	AUUUCAUUUUCGGCCUUUCC	2836
54790_1_9897	-	chr4:105148215-105148235	U AACACUUAUAUUUCAUUUU	2837
54790_1_9900	-	chr4:105148251-105148271	AAUUAAAAGUAUAUCAUGAG	2838
54790_1_9901	-	chr4:105148252-105148272	UAAUUAAAAGUAUAUCAUGA	2839
54790_1_9904	-	chr4:105148253-105148273	GUA AUUAAAAGUAUAUCAUG	2840
54790_1_9912	-	chr4:105148290-105148310	CUUAAACA UAGAUGAAGAA	2841
54790_1_9914	-	chr4:105148291-105148311	UCUUAACA UAGAUGAAGA	2842
54790_1_9929	-	chr4:105148334-105148354	UAUGCACUAAAUUUUACCGC	2843
54790_1_9945	-	chr4:105148446-105148466	AUUAUAAUCCCUGACUGAAG	2844
54790_1_9946	-	chr4:105148447-105148467	CAUUAUAAUCCCUGACUGAA	2845
54790_1_9949	-	chr4:105148448-105148468	CCAUAUAAUCCCUGACUGA	2846
54790_1_9959	-	chr4:105148475-105148495	UGAUGAAUAUCUUUGAAUUU	2847
54790_1_9960	-	chr4:105148476-105148496	UUGAUGAAUAUCUUUGAAUU	2848
54790_1_9967	-	chr4:105148507-105148527	AUACAAUCUUAUUCCUAUGA	2849
54790_1_9977	-	chr4:105148600-105148620	AUGUAAUGAUUUCAUUAGCC	2850
54790_1_10028	-	chr4:105148861-105148881	AGUUUUGGAAAUUCGACUUA	2851
54790_1_10032	-	chr4:105148876-105148896	CUAUCGAGGACAAAUAGUUU	2852
54790_1_10035	-	chr4:105148890-105148910	AGUUACAAAGUGAACUAUCG	2853
54790_1_10066	-	chr4:105149048-105149068	UAAUUUUUGUUUUAUUUUUA	2854
54790_1_10067	-	chr4:105149049-105149069	CUAAUUUUUGUUUUAUUUUU	2855
54790_1_10072	-	chr4:105149079-105149099	UUUACCAUGAACAGCAUUA	2856
54790_1_10086	-	chr4:105149129-105149149	UGUUUUUAAUUCUGAAUUGC	2857
54790_1_10094	-	chr4:105149155-105149175	AAUAUUAGUUUGUUAGCAA	2858
54790_1_10113	-	chr4:105149258-105149278	AGUUAUUCUUAUUUAUUGAG	2859
54790_1_10123	-	chr4:105149326-105149346	AAGAAUCUAAAUUUGAUGAC	2860
54790_1_10131	-	chr4:105149363-105149383	GCUAUUUUCAGUAUAAAAGU	2861
54790_1_10145	-	chr4:105149454-105149474	UAAUUUCUCUUUUCCAACAA	2862
54790_1_10153	-	chr4:105149516-105149536	AUAUGGUAAAGAAAGAACUG	2863
54790_1_10158	-	chr4:105149533-105149553	AGGUAGUAUGAUCACAUUA	2864
54790_1_10163	-	chr4:105149553-105149573	AUGGAAUUUUUGGAGCACC	2865
54790_1_10165	-	chr4:105149563-105149583	AGACAGUCCUAUGGAAUUUU	2866
54790_1_10169	-	chr4:105149572-105149592	AAUAACCCAAGACAGUCCUA	2867
54790_1_10189	-	chr4:105149719-105149739	UGACAAUUUAAACAAAGCAA	2868
54790_1_10191	-	chr4:105149720-105149740	AUGACAAUUUAAACAAAGCA	2869
54790_1_10197	-	chr4:105149748-105149768	UUAAGCCUUAAGAAGAGUU	2870
54790_1_10203	-	chr4:105149785-105149805	CUCCGGCUUCUGGCAUAAAC	2871

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_10204	-	chr4:105149795-105149815	AUAUCAAUUCCUCCGGCUUC	2872
54790_1_10205	-	chr4:105149802-105149822	CAAAAUCAUAUCAAUUCCUC	2873
54790_1_10208	-	chr4:105149842-105149862	UUCACUUGCCAAUGUCUAGU	2874
54790_1_10215	-	chr4:105149873-105149893	CAGGUGCACUUCACUUGUUC	2875
54790_1_10220	-	chr4:105149892-105149912	UUUCAUAACAACUCCUUGGC	2876
54790_1_10223	-	chr4:105149896-105149916	AUUCUUUCAUAACAACUCCU	2877
54790_1_10224	-	chr4:105149920-105149940	CCAGUGCCCAAUAAGGACUU	2878
54790_1_10227	-	chr4:105149927-105149947	UACAAGACCAGUGCCCAAUA	2879
54790_1_10241	-	chr4:105150006-105150026	GAGUCUUAGAAGAAUUGAUA	2880
54790_1_10242	-	chr4:105150007-105150027	GGAGUCUUAGAAGAAUUGAU	2881
54790_1_10255	-	chr4:105150028-105150048	CUUACAACAUUGUUUGGGGG	2882
54790_1_10257	-	chr4:105150031-105150051	UGACUUACAACAUUGUUUGG	2883
54790_1_10258	-	chr4:105150032-105150052	UUGACUUACAACAUUGUUUG	2884
54790_1_10260	-	chr4:105150033-105150053	UUUGACUUACAACAUUGUUU	2885
54790_1_10262	-	chr4:105150034-105150054	AUUUGACUUACAACAUUGUU	2886
54790_1_10270	-	chr4:105150077-105150097	CUUAAUGAGGUCAGUAAUUA	2887
54790_1_10272	-	chr4:105150090-105150110	AUAAGAAGGGCUUCUAAUG	2888
54790_1_10274	-	chr4:105150103-105150123	GUGCCUAUGAAUCAUAAGAA	2889
54790_1_10275	-	chr4:105150104-105150124	UGUGCCUAUGAAUCAUAAGA	2890
54790_1_10282	-	chr4:105150127-105150147	UGGAAAUAUAGAGUUUCUGUG	2891
54790_1_10288	-	chr4:105150147-105150167	UACUCAGACUUUGGGCAGGA	2892
54790_1_10292	-	chr4:105150151-105150171	UACCUACUCAGACUUUGGGC	2893
54790_1_10294	-	chr4:105150155-105150175	AAUUUACCUACUCAGACUUU	2894
54790_1_10295	-	chr4:105150156-105150176	GAAUUUACCUACUCAGACUU	2895
54790_1_10310	-	chr4:105150200-105150220	UUUGAAGAUUUUUUUAUUUCA	2896
54790_1_10339	-	chr4:105150421-105150441	UAACAUUAAAACAGUCUACA	2897
54790_1_10344	-	chr4:105150450-105150470	UUUUAGCCUGUUCCCAAGGU	2898
54790_1_10347	-	chr4:105150454-105150474	AAAGUUUUAGCCUGUUCCCA	2899
54790_1_10349	-	chr4:105150480-105150500	GAUGAACAAAUACUGACAGC	2900
54790_1_10355	-	chr4:105150532-105150552	CCUUAAGAACUACUGUGCAA	2901
54790_1_10363	-	chr4:105150567-105150587	UAUUCUAUUGCUGCUGGCUU	2902
54790_1_10365	-	chr4:105150573-105150593	GGGAGAUAUUCUAUUGCUGC	2903
54790_1_10368	-	chr4:105150593-105150613	UCCAAUUGUAAAGUUGGCUU	2904
54790_1_10371	-	chr4:105150594-105150614	CUCCAAUUGUAAAGUUGGCU	2905
54790_1_10373	-	chr4:105150599-105150619	GAAGGCUCCAAUUGUAAAGU	2906
54790_1_10377	-	chr4:105150617-105150637	ACUGGUCUUUCCACAGUGA	2907
54790_1_10379	-	chr4:105150635-105150655	CACCAGCUCUACUUGGCAAC	2908
54790_1_10382	-	chr4:105150642-105150662	AGAUAAACCACCAGCUCUACU	2909
54790_1_10390	-	chr4:105150689-105150709	AUAUUUGGCAAAAUCAUUUG	2910
54790_1_10391	-	chr4:105150704-105150724	CCAAGUAAAUACUGUAUAUU	2911
54790_1_10397	-	chr4:105150736-105150756	CAGUGAGUAGAAAUAAGAAU	2912
54790_1_10403	-	chr4:105150759-105150779	UCACAGUAUUCACUCAGUUU	2913
54790_1_10411	-	chr4:105150844-105150864	UGACUUUCCCCUUCUCCUCC	2914
54790_1_10420	-	chr4:105150894-105150914	CAGACAUACAUAUUUCUUUU	2915
54790_1_10422	-	chr4:105150923-105150943	AUAUAGGACAAAAUAAUGC	2916
54790_1_10425	-	chr4:105150939-105150959	GUCUCUGCAAUGUACAAUAU	2917
54790_1_10442	-	chr4:105151019-105151039	CCAAAAUUUGUUAUUUGGAA	2918
54790_1_10444	-	chr4:105151024-105151044	GGGAUCCAAAAUUUGUUAUU	2919

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_10449	-	chr4:105151061-105151081	AGGGUUUCACGAUCCUAAUG	2920
54790_1_10451	-	chr4:105151069-105151089	GGAACCGGAGGGUUUCACGA	2921
54790_1_10453	-	chr4:105151086-105151106	GGAGUUCACUAGAGAGUGGA	2922
54790_1_10457	-	chr4:105151109-105151129	GGUCCCACCAAAGUUUGAGG	2923
54790_1_10458	-	chr4:105151123-105151143	GGACUGACACAACGGGUCCC	2924
54790_1_10459	-	chr4:105151126-105151146	CCCGGACUGACACAACGGGU	2925
54790_1_10460	-	chr4:105151127-105151147	CCCCGGACUGACACAACGGG	2926
54790_1_10471	-	chr4:105151146-105151166	AUUUAAAAAACAUCUCUGAC	2927
54790_1_10472	-	chr4:105151147-105151167	AAUUUAAAAAACAUCUCUGA	2928
54790_1_10474	-	chr4:105151148-105151168	AAAUUUAAAAAACAUCUCUG	2929
54790_1_10477	-	chr4:105151197-105151217	AGGACUCAUCGACCCUGAUG	2930
54790_1_10480	-	chr4:105151205-105151225	AGAGUCAGAGGACUCAUCGA	2931
54790_1_10482	-	chr4:105151206-105151226	UAGAGUCAGAGGACUCAUCG	2932
54790_1_10492	-	chr4:105151281-105151301	AACGGACCCGACCUCGCGUC	2933
54790_1_10494	-	chr4:105151291-105151311	AGAGAGGGAGAACGGACCCG	2934
54790_1_10496	-	chr4:105151295-105151315	UCCCAGAGAGGGAGAACGGA	2935
54790_1_10498	-	chr4:105151296-105151316	AUCCCAGAGAGGGAGAACGG	2936
54790_1_10505	-	chr4:105151314-105151334	ACAACACGCUGAAACUCUAU	2937
54790_1_10507	-	chr4:105151315-105151335	AACAACACGCUGAAACUCUA	2938
54790_1_10519	-	chr4:105151343-105151363	AAUGUGCUUAAAACAAACAA	2939
54790_1_10552	-	chr4:105151541-105151561	GAAUUCUUAACUCGCAGGU	2940
54790_1_10554	-	chr4:105151545-105151565	UUCUGAAUUCUUAACUCGC	2941
54790_1_10557	-	chr4:105151574-105151594	GGUCUUACUCGGUGGUGUGG	2942
54790_1_10563	-	chr4:105151625-105151645	GGUCCGACCAGAUUCUGAAG	2943
54790_1_10566	-	chr4:105151639-105151659	AGAGUGAUACAACGGGUCCG	2944
54790_1_10567	-	chr4:105151643-105151663	CCAUAGAGUGAUACAACGGG	2945
54790_1_10577	-	chr4:105151664-105151684	AUAAAAAUAAACUUAUCUCUG	2946
54790_1_10597	-	chr4:105151737-105151757	AUGAUUUAAGUCAGUUUAG	2947
54790_1_10609	-	chr4:105151763-105151783	ACUUUAAUUCUCAGUUUAUU	2948
54790_1_10612	-	chr4:105151797-105151817	GUCCGUACUCGGUGGUGUUG	2949
54790_1_10614	-	chr4:105151816-105151836	AGGGUUUCACGACCCUAAUG	2950
54790_1_10616	-	chr4:105151824-105151844	GGAACAGCAGGGUUUCACGA	2951
54790_1_10617	-	chr4:105151825-105151845	CGGAACAGCAGGGUUUCACG	2952
54790_1_10620	-	chr4:105151858-105151878	CCAGAGUUUGAGGACUGGAG	2953
54790_1_10624	-	chr4:105151879-105151899	AAAGUGGUACAACCGGUCCG	2954
54790_1_10625	-	chr4:105151883-105151903	UCCCAAAGUGGUACAACCGG	2955
54790_1_10626	-	chr4:105151888-105151908	CUCUGUCCCAAAGUGGUACA	2956
54790_1_10635	-	chr4:105151902-105151922	AACAUAAAAAUCAUCUCUGU	2957
54790_1_10636	-	chr4:105151903-105151923	AAACAUAAAAAUCAUCUCUG	2958
54790_1_10640	-	chr4:105151932-105151952	GACCACACACGGUGGUACGG	2959
54790_1_10641	-	chr4:105151951-105151971	AGGACUCAUCGACCCUAAUG	2960
54790_1_10642	-	chr4:105151959-105151979	GGAGUCGGAGGACUCAUCGA	2961
54790_1_10643	-	chr4:105151960-105151980	CGGAGUCGGAGGACUCAUCG	2962
54790_1_10648	-	chr4:105151982-105152002	GGGUCCGAGUUCACUAAGAG	2963
54790_1_10649	-	chr4:105151983-105152003	CGGGUCCGAGUUCACUAAGA	2964
54790_1_10652	-	chr4:105151999-105152019	UCCAUACUCGGUGGUACGGG	2965
54790_1_10654	-	chr4:105152019-105152039	AGGGUUUCACGACCCUAAUA	2966
54790_1_10655	-	chr4:105152027-105152047	GGAGCCGGAGGGUUUCACGA	2967

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_10657	-	chr4:105152028-105152048	CGGAGCCGGAGGGUUUCACG	2968
54790_1_10659	-	chr4:105152044-105152064	CAGUCCACUAGGUGGACGGA	2969
54790_1_10661	-	chr4:105152061-105152081	CCAGAGCUUAAGGACUGCAG	2970
54790_1_10666	-	chr4:105152082-105152102	AAAGUGGUACAACCGGUCUG	2971
54790_1_10667	-	chr4:105152091-105152111	CUCUACCCCAAAGUGGUACA	2972
54790_1_10673	-	chr4:105152105-105152125	AACAUACAAAUCACCUCUAC	2973
54790_1_10674	-	chr4:105152106-105152126	AAACAUACAAAUCACCUCUA	2974
54790_1_10676	-	chr4:105152107-105152127	AAAACAUACAAAUCACCUCU	2975
54790_1_10678	-	chr4:105152113-105152133	UCGAUUAAAACAUACAAAUC	2976
54790_1_10681	-	chr4:105152153-105152173	AGGUCUUAUCGACUCUGAUG	2977
54790_1_10686	-	chr4:105152201-105152221	CGUCGGAGACGGAGGGCCCU	2978
54790_1_10687	-	chr4:105152202-105152222	GCGUCGGAGACGGAGGGCCC	2979
54790_1_10690	-	chr4:105152205-105152225	GUGGCGUCGGAGACGGAGGG	2980
54790_1_10691	-	chr4:105152206-105152226	AGUGGCGUCGGAGACGGAGG	2981
54790_1_10694	-	chr4:105152230-105152250	CCUCACGUCGUCUCGGUAGA	2982
54790_1_10696	-	chr4:105152251-105152271	AGAGAGACGGAGCGGGUCCG	2983
54790_1_10699	-	chr4:105152255-105152275	UCUCAGAGAGACGGAGCGGG	2984
54790_1_10714	-	chr4:105152279-105152299	UUAUUA AAAAAGAAAAAAC	2985
54790_1_10745	-	chr4:105152466-105152486	GUCAACAGUAGGUUCUAUUA	2986
54790_1_10746	-	chr4:105152467-105152487	GGUCAACAGUAGGUUCUAUU	2987
54790_1_10750	-	chr4:105152477-105152497	UUGACUGAGAGGUCAACAGU	2988
54790_1_10752	-	chr4:105152488-105152508	UCCAUUAAAUAUUGACUGAG	2989
54790_1_10770	-	chr4:105152532-105152552	UUUUUUCUAGUUAAAUUGCA	2990
54790_1_10774	-	chr4:105152577-105152597	UUUCUUUCUUUGAAAGAAAA	2991
54790_1_10782	-	chr4:105152640-105152660	UGUGGUGACGUGAGGUCGGA	2992
54790_1_10787	-	chr4:105152681-105152701	GUGAACUUGGACCUUCCGUC	2993
54790_1_10789	-	chr4:105152687-105152707	CUCUUAGUGAACUUGGACCU	2994
54790_1_10790	-	chr4:105152691-105152711	CUUUCUCUUAGUGAACUUGG	2995
54790_1_10798	-	chr4:105152718-105152738	GGAUCAGGGUCGAUGAGACC	2996
54790_1_10799	-	chr4:105152719-105152739	AGGAUCAGGGUCGAUGAGAC	2997
54790_1_10801	-	chr4:105152720-105152740	GAGGAUCAGGGUCGAUGAGA	2998
54790_1_10803	-	chr4:105152721-105152741	CGAGGAUCAGGGUCGAUGAG	2999
54790_1_10806	-	chr4:105152747-105152767	UUUUAAUCGGUCCACACCAC	3000
54790_1_10807	-	chr4:105152748-105152768	UUUUUAAUCGGUCCACACCA	3001
54790_1_10808	-	chr4:105152749-105152769	CUUUUUAUCGGUCCACACC	3002
54790_1_10811	-	chr4:105152752-105152772	UAUCUUUUUAAUCGGUCCAC	3003
54790_1_10812	-	chr4:105152757-105152777	AUUUUUAUCUUUUUAAUCGG	3004
54790_1_10815	-	chr4:105152797-105152817	GCUCUAGUCGGACCGGUUGU	3005
54790_1_10816	-	chr4:105152806-105152826	GGUCCUCAUGCUCUAGUCGG	3006
54790_1_10818	-	chr4:105152824-105152844	GUCCGUCUAGUGGACUCUGG	3007
54790_1_10824	-	chr4:105152843-105152863	CGUGAAACCCUCUGGGCCCG	3008
54790_1_10825	-	chr4:105152847-105152867	GGGUCGUGAAACCCUCUGGG	3009
54790_1_10826	-	chr4:105152848-105152868	AGGGUCGUGAAACCCUCUGG	3010
54790_1_10828	-	chr4:105152856-105152876	CGGACAUUAGGGUCGUGAAA	3011
54790_1_10831	-	chr4:105152857-105152877	ACGGACAUUAGGGUCGUGAA	3012
54790_1_10834	-	chr4:105152884-105152904	AUAGAUUACUGGUCCACGUC	3013
54790_1_10837	-	chr4:105152892-105152912	CAUUGAAAAUAGAUUACUGG	3014
54790_1_10847	-	chr4:105152981-105153001	GCCUGUAGAAAUUAAAUGUA	3015

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_10855	-	chr4:105153015-105153035	UAAAAUGGGUGGCUUUUAUA	3016
54790_1_10857	-	chr4:105153016-105153036	UUAAAAUGGGUGGCUUUUAU	3017
54790_1_10862	-	chr4:105153026-105153046	ACUUUUGUGCUUAAAAUGGG	3018
54790_1_10863	-	chr4:105153029-105153049	UUCACUUUUGUGCUUAAAAU	3019
54790_1_10864	-	chr4:105153030-105153050	AUUCACUUUUGUGCUUAAAA	3020
54790_1_10876	-	chr4:105153127-105153147	GAGACAUAAUAAAGUAUGUU	3021
54790_1_10878	-	chr4:105153155-105153175	CCUUUAAACUCGUUCAUAUGC	3022
54790_1_10887	-	chr4:105153176-105153196	AACGUUUCACAACGGUGACC	3023
54790_1_10889	-	chr4:105153177-105153197	AAACGUUUCACAACGGUGAC	3024
54790_1_10892	-	chr4:105153178-105153198	AAAACGUUUCACAACGGUGA	3025
54790_1_10894	-	chr4:105153179-105153199	CAAACGUUUCACAACGGUG	3026
54790_1_10901	-	chr4:105153250-105153270	GGUGUAGUUACAGUCAUAGU	3027
54790_1_10903	-	chr4:105153273-105153293	CUGUAGACUUAUUCUAAUCA	3028
54790_1_10906	-	chr4:105153295-105153315	UUACUCAUGUUCAAUUUGAC	3029
54790_1_10910	-	chr4:105153338-105153358	UAUGUGAUGUACACUGAUUU	3030
54790_1_10917	-	chr4:105153369-105153389	UUCUCUGUUUUGAGAAAAAA	3031
54790_1_10930	-	chr4:105153443-105153463	UUCUGACACACAUUUUAUA	3032
54790_1_10936	-	chr4:105153491-105153511	AAGGCCAUUCUAUCAAAAAA	3033
54790_1_10943	-	chr4:105153510-105153530	UUAAAAUAUUUUUAACAUAA	3034
54790_1_10949	-	chr4:105153580-105153600	UUCUUAUUAUGGAUAGAGAU	3035
54790_1_10950	-	chr4:105153581-105153601	AUUCUUAUUAUGGAUAGAGA	3036
54790_1_10956	-	chr4:105153605-105153625	UCAAAGGAGUGAGUAUUUAU	3037
54790_1_10958	-	chr4:105153606-105153626	GUCAAAGGAGUGAGUAUUUA	3038
54790_1_10964	-	chr4:105153632-105153652	CCUUCAAUAAAUUGGAGUGA	3039
54790_1_10965	-	chr4:105153633-105153653	UCCUUCAAUAAAUUGGAGUG	3040
54790_1_10968	-	chr4:105153653-105153673	CAUAUCCGACAUACUUGAAU	3041
54790_1_10971	-	chr4:105153669-105153689	CGAUUCGGAUUCGGUACAUA	3042
54790_1_10973	-	chr4:105153691-105153711	UCUGACGAAUUGAGUUUACG	3043
54790_1_10978	-	chr4:105153724-105153744	UUUAUAUCACUAAUUUUCUAA	3044
54790_1_11000	-	chr4:105153858-105153878	UAUUACGACAUUACUUGUAA	3045
54790_1_11011	-	chr4:105153906-105153926	AGUACUGUACUAUCUGUAGA	3046
54790_1_11012	-	chr4:105153907-105153927	GAGUACUGUACUAUCUGUAG	3047
54790_1_11021	-	chr4:105153953-105153973	GAAUUAUUAUAAAGUGACAU	3048
54790_1_11034	-	chr4:105154042-105154062	UUAACUUUCGUAUAGUAUAC	3049
54790_1_11041	-	chr4:105154076-105154096	GAGGAAUCUAAACGGAUAAG	3050
54790_1_11047	-	chr4:105154151-105154171	UUUCUUUAGAGUAUGAAUAA	3051
54790_1_11062	-	chr4:105154216-105154236	AAGUCGUAAUAGUUUCUCAA	3052
54790_1_11063	-	chr4:105154217-105154237	AAAGUCGUAAUAGUUUCUCA	3053
54790_1_11070	-	chr4:105154240-105154260	AAAUUUCGUAAUUAAGUCA	3054
54790_1_11071	-	chr4:105154241-105154261	AAAAUUUCGUAAUUAAGUC	3055
54790_1_11102	-	chr4:105154455-105154475	AGGGUUUCACGGUCCUAAUG	3056
54790_1_11103	-	chr4:105154463-105154483	GGAACCGGAGGGUUUCACGG	3057
54790_1_11106	-	chr4:105154480-105154500	UUUGAAGACCAGAGGGCGGA	3058
54790_1_11108	-	chr4:105154493-105154513	GGUCUGAUUAGAGUUUGAAG	3059
54790_1_11111	-	chr4:105154523-105154543	GUAUCCUUCUCAUCUAUAAG	3060
54790_1_11122	-	chr4:105154589-105154609	UCUUCCCAUAUGAGCUCUAA	3061
54790_1_11134	-	chr4:105154697-105154717	AUCUCCUGAACUGAAUGGCU	3062
54790_1_11136	-	chr4:105154702-105154722	GUUACAUCUCCUGAACUGAA	3063

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_11143	-	chr4:105154724-105154744	AGACAUUCCUUUUUAAACACUU	3064
54790_1_11144	-	chr4:105154725-105154745	CAGACAUUCCUUUUUAAACACU	3065
54790_1_11148	-	chr4:105154766-105154786	AGCGUUUCACGACCCUAAUG	3066
54790_1_11150	-	chr4:105154774-105154794	GAAGGCGGAGCGUUUCACGA	3067
54790_1_11152	-	chr4:105154775-105154795	UGAAGGCGGAGCGUUUCACG	3068
54790_1_11161	-	chr4:105154833-105154853	CCCCAAAACGGUACAACGGG	3069
54790_1_11169	-	chr4:105154852-105154872	CACGUAAAAAACAUCCCUAC	3070
54790_1_11170	-	chr4:105154853-105154873	ACACGUAAAAAACAUCCCUA	3071
54790_1_11172	-	chr4:105154854-105154874	AACACGUAAAAAACAUCCCU	3072
54790_1_11174	-	chr4:105154858-105154878	AUUA AACACGUAAAAAACA	3073
54790_1_11176	-	chr4:105154859-105154879	GAUUA AACACGUAAAAAACA	3074
54790_1_11178	-	chr4:105154900-105154920	GUGUUCAUGGACCUUGAUGU	3075
54790_1_11180	-	chr4:105154901-105154921	GGUGUUCAUGGACCUUGAUG	3076
54790_1_11182	-	chr4:105154910-105154930	CGGAGUCGGGGUGUUCAUGG	3077
54790_1_11187	-	chr4:105154949-105154969	GUGACGUCGGAGUUGAAGGG	3078
54790_1_11188	-	chr4:105154974-105154994	CUUCACACCCCCGUGGUUGU	3079
54790_1_11192	-	chr4:105154985-105155005	AGUGGGUCCGACUUCACACC	3080
54790_1_11193	-	chr4:105154986-105155006	CAGUGGGUCCGACUUCACAC	3081
54790_1_11195	-	chr4:105154987-105155007	ACAGUGGGUCCGACUUCACA	3082
54790_1_11197	-	chr4:105154988-105155008	AACAGUGGGUCCGACUUCAC	3083
54790_1_11200	-	chr4:105154999-105155019	UCCCAGAGUAAAACAGUGGG	3084
54790_1_11212	-	chr4:105155018-105155038	UAGAAAAAAAAAAACUCUCUCU	3085
54790_1_11214	-	chr4:105155019-105155039	AUAGAAAAAAAAAAACUCUCUC	3086
54790_1_11250	-	chr4:105155211-105155231	AAA AUCUGAAACAUGACAAG	3087
54790_1_11264	-	chr4:105155284-105155304	AUGCCACAGUAUCAGUUAAC	3088
54790_1_11284	-	chr4:105155364-105155384	CCCUGUUUCUCACUUUGUCC	3089
54790_1_11288	-	chr4:105155406-105155426	GCAGCCAUGUGUAGCAAAGA	3090
54790_1_11295	-	chr4:105155444-105155464	GUGGUUUGUAGAAGUUCUGC	3091
54790_1_11301	-	chr4:105155463-105155483	GCACUCAUUUUACCUGUAAG	3092
54790_1_11304	-	chr4:105155503-105155523	CUACAAGUCAUAGUCCAU	3093
54790_1_11305	-	chr4:105155504-105155524	ACUACAAGUCAUAGUCCAU	3094
54790_1_11313	-	chr4:105155578-105155598	CUGGUAUCUAGAAUUACAUA	3095
54790_1_11316	-	chr4:105155597-105155617	CAUUGCACAACAAGAAUGUC	3096
54790_1_11322	-	chr4:105155627-105155647	CAUUCUCAUGAGAAUAAAAA	3097
54790_1_11324	-	chr4:105155628-105155648	GCAUUCUCAUGAGAAUAAAAA	3098
54790_1_11329	-	chr4:105155661-105155681	CCAAGGU AUGGGAUCCAAC	3099
54790_1_11331	-	chr4:105155671-105155691	CAGUCAUGGUCCCAAGGU AU	3100
54790_1_11332	-	chr4:105155672-105155692	UCAGUCAUGGUCCCAAGGUA	3101
54790_1_11335	-	chr4:105155677-105155697	AGUUAUCAGUCAUGGUCCCA	3102
54790_1_11339	-	chr4:105155685-105155705	UCCACUCCAGUUAUCAGUCA	3103
54790_1_11348	-	chr4:105155779-105155799	AGCCAAUAUACUCCCUUAU	3104
54790_1_11349	-	chr4:105155780-105155800	AAGCCAAUAUACUCCCUUAU	3105
54790_1_11359	-	chr4:105155909-105155929	CUAACAUGAGCAUCUAUCUU	3106
54790_1_11360	-	chr4:105155910-105155930	UCUAACAUGAGCAUCUAUCU	3107
54790_1_11365	-	chr4:105155933-105155953	CACUACACCAACUUCUUAU	3108
54790_1_11366	-	chr4:105155934-105155954	UCACUACACCAACUUCUUA	3109
54790_1_11379	-	chr4:105155998-105156018	AGCUAGUCAUUUCUCCAGUA	3110
54790_1_11394	-	chr4:105156064-105156084	AAAUUUAUAGUCAGCUGAGG	3111

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_11395	-	chr4:105156067-105156087	CAAAA AUUU AUAGUCAGCUG	3112
54790_1_11405	-	chr4:105156101-105156121	GAACAACUUUUUUAAAAUUA	3113
54790_1_11417	-	chr4:105156168-105156188	GAGAACAGAUUUACA UUUUU	3114
54790_1_11435	-	chr4:105156265-105156285	CAUUUUUCUUCUUUUGAAUA	3115
54790_1_11446	-	chr4:105156333-105156353	GCAUUUCUAUGCCUGAACAU	3116
54790_1_11449	-	chr4:105156379-105156399	AAAAAUAUCAAUACUCUGUA	3117
54790_1_11462	-	chr4:105156490-105156510	GGUUUUAGCAAUGGCUAAUG	3118
54790_1_11466	-	chr4:105156499-105156519	GGUAAGGCAGGUUUUAGCAA	3119
54790_1_11467	-	chr4:105156511-105156531	AAUAAGUGAUUUGGUAAGGC	3120
54790_1_11468	-	chr4:105156515-105156535	AGAAAAUAAGUGAUUUGGUA	3121
54790_1_11469	-	chr4:105156520-105156540	CAUCAAGAAAAUAAGUGAUU	3122
54790_1_11477	-	chr4:105156567-105156587	GUUCUCAUUA AUGUAUAACC	3123
54790_1_11482	-	chr4:105156595-105156615	UAAUAACCCA UUGAGAGAU	3124
54790_1_11483	-	chr4:105156596-105156616	AUAAUAACCCA UUGAGAGA	3125
54790_1_11497	-	chr4:105156629-105156649	UUUUAUGCAUCAUCUAUUUC	3126
54790_1_11511	-	chr4:105156686-105156706	AUAUACCAUGCUAUGUUAUC	3127
54790_1_11513	-	chr4:105156717-105156737	AGACAGGUAAGAAAAACGGG	3128
54790_1_11517	-	chr4:105156720-105156740	UGCAGACAGGUAAGAAAAAC	3129
54790_1_11519	-	chr4:105156721-105156741	GUGCAGACAGGUAAGAAAAA	3130
54790_1_11523	-	chr4:105156733-105156753	GUGCCCUUCU UAGUGCAGAC	3131
54790_1_11527	-	chr4:105156755-105156775	UAAUAAUUAUGGUAUUUAAU	3132
54790_1_11528	-	chr4:105156756-105156776	CUAAUAAUUAUGGUAUUUAA	3133
54790_1_11530	-	chr4:105156766-105156786	GGCAGCACAA CUAUA AUUA	3134
54790_1_11533	-	chr4:105156787-105156807	AUUCUGGUGCUCUACUUCAG	3135
54790_1_11537	-	chr4:105156803-105156823	AUUGUAUUA CUCUCACA UUC	3136
54790_1_11539	-	chr4:105156830-105156850	UUAUGGAUAGA AUCUGGGUG	3137
54790_1_11540	-	chr4:105156835-105156855	GUAUGUUAUGGAUAGAAUCU	3138
54790_1_11541	-	chr4:105156836-105156856	AGUAUGUUAUGGAUAGAAUC	3139
54790_1_11545	-	chr4:105156847-105156867	AAGACCAGGACAGUAUGUUA	3140
54790_1_11548	-	chr4:105156861-105156881	UUAAAAAAAUUAAUAAGACC	3141
54790_1_11550	-	chr4:105156884-105156904	AAAGUGC UAAAAGAACAAAC	3142
54790_1_11554	-	chr4:105156908-105156928	AAGAGACUUC AAACAAAAGC	3143
54790_1_11562	-	chr4:105156960-105156980	UGAGAUAA CUUUACAGCCAA	3144
54790_1_11572	-	chr4:105157034-105157054	AAUCAUCUGAAUUA AUUACA	3145
54790_1_11573	-	chr4:105157035-105157055	UAAUCAUCUGAAUUA AUUAC	3146
54790_1_11587	-	chr4:105157090-105157110	UCUUCUGUUAUAAUGUAU AU	3147
54790_1_11591	-	chr4:105157118-105157138	AGACACUGUAUUUGUAGAAA	3148
54790_1_11612	-	chr4:105157208-105157228	UACAUUUGGUACA UAAAAAU	3149
54790_1_11619	-	chr4:105157222-105157242	UUCUUUUCAU CAGUUACA UU	3150
54790_1_11627	-	chr4:105157250-105157270	UUUUGAAAGGUACCCA UUUUA	3151
54790_1_11636	-	chr4:105157263-105157283	UUUUUUC CUUCAUUUUUGAA	3152
54790_1_11647	-	chr4:105157310-105157330	ACUAAAAUAAAUA AUUUUAUA	3153
54790_1_11658	-	chr4:105157389-105157409	AAGAUAAAAUCUAUAAAACA	3154
54790_1_11663	-	chr4:105157416-105157436	AACCAUUUCAGUGGCUAGAU	3155
54790_1_11667	-	chr4:105157425-105157445	UGGAGAAAAA ACCAUUUCAG	3156
54790_1_11670	-	chr4:105157445-105157465	UGUAGAUAAUAUAACUUCAC	3157
54790_1_11683	-	chr4:105157515-105157535	GUUUUUC CACAAGCGUAAUG	3158
54790_1_11693	-	chr4:105157581-105157601	UUAAAUCU UAGCCA UUAUA	3159

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_11713	-	chr4:105157719-105157739	UACGGUGACGUGAGGUCGGA	3160
54790_1_11714	-	chr4:105157720-105157740	GUACGGUGACGUGAGGUCGG	3161
54790_1_11718	-	chr4:105157760-105157780	GCGAACUUGGGUCUUCCUCC	3162
54790_1_11719	-	chr4:105157763-105157783	UUAGCGAACUUGGGUCUUCC	3163
54790_1_11723	-	chr4:105157766-105157786	CUCUUAGCGAACUUGGGUCU	3164
54790_1_11730	-	chr4:105157788-105157808	CGAUGAGCCCUCGACUCUG	3165
54790_1_11733	-	chr4:105157798-105157818	AUAUUAGGGUCGAUGAGCCC	3166
54790_1_11735	-	chr4:105157801-105157821	CGGAUAAUAGGGUCGAUGAG	3167
54790_1_11737	-	chr4:105157802-105157822	ACGGAUAAUAGGGUCGAUGA	3168
54790_1_11740	-	chr4:105157825-105157845	UAAUCGGUCCGUACCACCG	3169
54790_1_11741	-	chr4:105157829-105157849	GUUUUUAAUCGGUCCGUACC	3170
54790_1_11742	-	chr4:105157832-105157852	UACGUUUUUAAUCGGUCCGU	3171
54790_1_11743	-	chr4:105157837-105157857	AUUUUUACGUUUUUAAUCGG	3172
54790_1_11748	-	chr4:105157877-105157897	GCUCUGGUCGGAUCGGAUGU	3173
54790_1_11750	-	chr4:105157904-105157924	CCCCACCUAGUGAUCUCCAG	3174
54790_1_11753	-	chr4:105157909-105157929	UCUUCUUUUACCUAGUGAUC	3175
54790_1_11757	-	chr4:105157920-105157940	GAAAUCCUUCGUCUUUUUUU	3176
54790_1_11759	-	chr4:105157923-105157943	CGUGAAAUCCUUCGUCUUC	3177
54790_1_11760	-	chr4:105157924-105157944	UCGUGAAAUCCUUCGUCUUC	3178
54790_1_11761	-	chr4:105157925-105157945	GUCGUGAAAUCCUUCGUCUU	3179
54790_1_11763	-	chr4:105157926-105157946	GGUCGUGAAAUCCUUCGUCU	3180
54790_1_11768	-	chr4:105157936-105157956	CGGACAUUAGGGUCGUGAAA	3181
54790_1_11772	-	chr4:105157964-105157984	AAAUAAAGUCCGGUCCGGCU	3182
54790_1_11774	-	chr4:105157971-105157991	UACAGUAAAUAAAGUCCGG	3183
54790_1_11775	-	chr4:105157976-105157996	AGUUGUAAACAGUAAAUAAAGU	3184
54790_1_11802	-	chr4:105158114-105158134	CCCAUGCUCUUGAAAAAUGU	3185
54790_1_11824	-	chr4:105158282-105158302	CCCAAAAACCCCGAGGAUUA	3186
54790_1_11825	-	chr4:105158289-105158309	AUAGUUUCCCAAAAACCCCG	3187
54790_1_11849	-	chr4:105158415-105158435	UUCAUUAAUUCUUUUACAAU	3188
54790_1_11850	-	chr4:105158416-105158436	AUUCAUUAAUUCUUUUACAA	3189
54790_1_11859	-	chr4:105158456-105158476	UUUUACCUUCUUCUUAUCU	3190
54790_1_11865	-	chr4:105158493-105158513	CAAUGGCUUCCUUGGGUGA	3191
54790_1_11870	-	chr4:105158499-105158519	AGUAUUCAAUGGCUUCCUU	3192
54790_1_11871	-	chr4:105158500-105158520	CAGUAUUCAAUGGCUUCCU	3193
54790_1_11873	-	chr4:105158510-105158530	AUGACCCAUUCAGUAUUCAA	3194
54790_1_11881	-	chr4:105158578-105158598	ACCAGAGAUAUACACUAAGU	3195
54790_1_11888	-	chr4:105158618-105158638	AGUGUAAACUGAGAUUUUAU	3196
54790_1_11889	-	chr4:105158619-105158639	CAGUGUAAACUGAGAUUUUA	3197
54790_1_11904	-	chr4:105158668-105158688	UUUCUACUUCUUAUUUGC	3198
54790_1_11917	-	chr4:105158729-105158749	UGCUCUACCUAAUUCAAUUU	3199
54790_1_11944	-	chr4:105158802-105158822	AAAAAAAAAAACCAAAAAG	3200
54790_1_11955	-	chr4:105158847-105158867	AAGGAAUUAUCACUAAUUA	3201
54790_1_11956	-	chr4:105158848-105158868	CAAGGAAUUAUCACUAAUUA	3202
54790_1_11958	-	chr4:105158866-105158886	AAAUAGCAUACAGAUUGUCA	3203
54790_1_11969	-	chr4:105158895-105158915	AAGAGAAGCCUACUAAUUUU	3204
54790_1_11976	-	chr4:105158941-105158961	UGUGACCGCGUGUAAUUGGA	3205
54790_1_11979	-	chr4:105158945-105158965	UUGAUGUGACCGCGUGUAAU	3206
54790_1_11984	-	chr4:105158985-105159005	AAAUACUGCUGCCACGUGCA	3207

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_11985	-	chr4:105159015-105159035	GAGUCUCUGGAAUCCUAGGA	3208
54790_1_11987	-	chr4:105159019-105159039	AUAAGAGUCUCUGGAAUCCU	3209
54790_1_11989	-	chr4:105159028-105159048	CACUGUUACAUAAGAGUCUC	3210
54790_1_11998	-	chr4:105159109-105159129	CAGAGCCAGACAAGGGCUCC	3211
54790_1_12000	-	chr4:105159116-105159136	ACCCUAUCAGAGCCAGACAA	3212
54790_1_12002	-	chr4:105159117-105159137	GACCCUAUCAGAGCCAGACA	3213
54790_1_12008	-	chr4:105159145-105159165	GACCUAAACACCUUGAUCUU	3214
54790_1_12013	-	chr4:105159176-105159196	GGUAGGAAAACCAUGCGUUA	3215
54790_1_12014	-	chr4:105159177-105159197	UGGUAGGAAAACCAUGCGUU	3216
54790_1_12020	-	chr4:105159193-105159213	ACAGCUUUUGAGGCUUUGGU	3217
54790_1_12025	-	chr4:105159197-105159217	AGGCACAGCUUUUGAGGCUU	3218
54790_1_12027	-	chr4:105159203-105159223	GUAUUUAGGCACAGCUUUUG	3219
54790_1_12030	-	chr4:105159217-105159237	AAAAGAUUAAUCUUGUAUUU	3220
54790_1_12038	-	chr4:105159295-105159315	CGCGGUGACGUGAGGUUGGA	3221
54790_1_12040	-	chr4:105159317-105159337	CAACGUCACUCGGCUCUAGC	3222
54790_1_12044	-	chr4:105159339-105159359	GCGAACUUGGCCACUCCGCC	3223
54790_1_12046	-	chr4:105159342-105159362	UUAGCGAACUUGGCCACUCC	3224
54790_1_12048	-	chr4:105159345-105159365	CUCUUAGCGAACUUGGCCAC	3225
54790_1_12050	-	chr4:105159350-105159370	CCGACCUCUUAGCGAACUUG	3226
54790_1_12054	-	chr4:105159367-105159387	CGAUGAACCCACAGACUCCG	3227
54790_1_12057	-	chr4:105159371-105159391	GGGUCGAUGAACCCACAGAC	3228
54790_1_12059	-	chr4:105159380-105159400	CGGAUAUUAGGGUCGAUGAA	3229
54790_1_12060	-	chr4:105159381-105159401	ACGGAUAUUAGGGUCGAUGA	3230
54790_1_12063	-	chr4:105159408-105159428	UGUUUUAAUCGGCCCCGCACC	3231
54790_1_12064	-	chr4:105159411-105159431	UUAUGUUUUAAUCGGCCCCGC	3232
54790_1_12065	-	chr4:105159416-105159436	GAUUUUUAUGUUUUAAUCGG	3233
54790_1_12066	-	chr4:105159417-105159437	UGAUUUUUUAUGUUUUAAUCG	3234
54790_1_12070	-	chr4:105159455-105159475	GUUGUGGUCCGACUGGUUGU	3235
54790_1_12074	-	chr4:105159468-105159488	AUUCAGCCCUCAAGUUGUGG	3236
54790_1_12076	-	chr4:105159482-105159502	GUUCGCCUAGUGGAAUUCAG	3237
54790_1_12077	-	chr4:105159483-105159503	CGUUCGCCUAGUGGAAUUCA	3238
54790_1_12082	-	chr4:105159498-105159518	GAAACCCCCCGGCUUCGUUC	3239
54790_1_12085	-	chr4:105159511-105159531	ACAUUAGGGUCGUGAAACCC	3240
54790_1_12086	-	chr4:105159512-105159532	GACAUUAGGGUCGUGAAACC	3241
54790_1_12087	-	chr4:105159513-105159533	GGACAUUAGGGUCGUGAAAC	3242
54790_1_12090	-	chr4:105159514-105159534	CGGACAUUAGGGUCGUGAAA	3243
54790_1_12092	-	chr4:105159515-105159535	UCGGACAUUAGGGUCGUGAA	3244
54790_1_12096	-	chr4:105159542-105159562	UUAACUUAACGACCCGCGCC	3245
54790_1_12097	-	chr4:105159545-105159565	AGAUUAAUCUUAACGACCCGC	3246
54790_1_12098	-	chr4:105159550-105159570	UAAAAAGAUUAAUCUUAACGA	3247
54790_1_12099	-	chr4:105159551-105159571	AUAAAAAGAUUAAUCUUAACG	3248
54790_1_12106	-	chr4:105159575-105159595	AUGACUAGUUGUUUGCUGCA	3249
54790_1_12107	-	chr4:105159576-105159596	CAUGACUAGUUGUUUGCUGC	3250
54790_1_12111	-	chr4:105159599-105159619	CCCAAUCACAAAAAUGGUU	3251
54790_1_12112	-	chr4:105159604-105159624	GUUUCCCCAAAUACAAAAA	3252
54790_1_12120	-	chr4:105159696-105159716	AUUUUGUGAGGCUGGGAGGC	3253
54790_1_12123	-	chr4:105159700-105159720	AGGCAUUUUGUGAGGCUGGG	3254
54790_1_12127	-	chr4:105159703-105159723	UAAAGGCAUUUUGUGAGGCU	3255

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_12130	-	chr4:105159704-105159724	UUAAAGGCAUUUUGUGAGGC	3256
54790_1_12132	-	chr4:105159708-105159728	UUUUUUAAAGGCAUUUUGUG	3257
54790_1_12134	-	chr4:105159720-105159740	CGGAAGAUGUAAUUUUUUAA	3258
54790_1_12136	-	chr4:105159742-105159762	UAAUGUCCGCACUCGGUAGG	3259
54790_1_12138	-	chr4:105159757-105159777	AGGGUUUUACGGCCCUAAUG	3260
54790_1_12140	-	chr4:105159765-105159785	GGAACCGGAGGGUUUUACGG	3261
54790_1_12141	-	chr4:105159766-105159786	CGGAACCGGAGGGUUUUACG	3262
54790_1_12145	-	chr4:105159782-105159802	GCUAGAGAACGGUGGGCGGA	3263
54790_1_12150	-	chr4:105159812-105159832	CCCAAAGUGGCACAACCGG	3264
54790_1_12153	-	chr4:105159817-105159837	CUCUGCCCAAAAGUGGCACA	3265
54790_1_12161	-	chr4:105159832-105159852	AAACAUAAAAAUCGUCUCUG	3266
54790_1_12162	-	chr4:105159833-105159853	AAAACAUAAAAAUCGUCUCU	3267
54790_1_12166	-	chr4:105159880-105159900	AGGGUUCAUCGACCCUAAUG	3268
54790_1_12167	-	chr4:105159888-105159908	GGUGUCAGAGGGUUCAUCGA	3269
54790_1_12169	-	chr4:105159889-105159909	CGGUGUCAGAGGGUUCAUCG	3270
54790_1_12172	-	chr4:105159927-105159947	UGACGUUGGAGGCGGAGGGC	3271
54790_1_12173	-	chr4:105159928-105159948	GUGACGUUGGAGGCGGAGGG	3272
54790_1_12174	-	chr4:105159929-105159949	AGUGACGUUGGAGGCGGAGG	3273
54790_1_12177	-	chr4:105159953-105159973	CCUCACGUCACCGCGCUAGA	3274
54790_1_12179	-	chr4:105159964-105159984	CAGCGGUCCGACCUCACGUC	3275
54790_1_12180	-	chr4:105159974-105159994	CAGAGCAAGACAGCGGUCCG	3276
54790_1_12183	-	chr4:105159978-105159998	GCCUCAGAGCAAGACAGCGG	3277
54790_1_12196	-	chr4:105159998-105160018	GAAAAAAAAAAAAAAGACUCU	3278
54790_1_12213	-	chr4:105160069-105160089	CUGGUCAGACCGUUUAGUUU	3279
54790_1_12215	-	chr4:105160070-105160090	UCUGGUCAGACCGUUUAGUU	3280
54790_1_12222	-	chr4:105160088-105160108	GAGUUUUCUUGAGUGUUUUC	3281
54790_1_12226	-	chr4:105160126-105160146	GCAGGUAAUAAUGGUAAUACUA	3282
54790_1_12229	-	chr4:105160136-105160156	AAGGGGAGAGGCAGGUAAUA	3283
54790_1_12230	-	chr4:105160144-105160164	GAUGGGGAAAGGGGAGAGGC	3284
54790_1_12233	-	chr4:105160148-105160168	AGAGGAUGGGGAAAGGGGAG	3285
54790_1_12235	-	chr4:105160153-105160173	UUUACAGAGGAUGGGGAAAG	3286
54790_1_12237	-	chr4:105160154-105160174	AUUUACAGAGGAUGGGGAAA	3287
54790_1_12239	-	chr4:105160155-105160175	AAUUUACAGAGGAUGGGGAA	3288
54790_1_12243	-	chr4:105160160-105160180	GAGAGAAUUUACAGAGGAUG	3289
54790_1_12246	-	chr4:105160161-105160181	UGAGAGAAUUUACAGAGGAU	3290
54790_1_12247	-	chr4:105160162-105160182	UUGAGAGAAUUUACAGAGGA	3291
54790_1_12250	-	chr4:105160166-105160186	AAGGUUGAGAGAAUUUACAG	3292
54790_1_12258	-	chr4:105160185-105160205	AUGAAAUUAAAAAUGAGAGA	3293
54790_1_12270	-	chr4:105160209-105160229	GUUGUUUUAGCUCUAGGUCU	3294
54790_1_12273	-	chr4:105160215-105160235	GUUGUUGUUGUUUUAGCUCU	3295
54790_1_12279	-	chr4:105160270-105160290	AAAAAUCAAUUUGGGAUAGG	3296
54790_1_12281	-	chr4:105160273-105160293	UCUAAAAAUCAAUUUGGGAU	3297
54790_1_12283	-	chr4:105160278-105160298	AAAGCUCUAAAAAUCAAUUU	3298
54790_1_12285	-	chr4:105160279-105160299	AAAAGCUCUAAAAAUCAAUU	3299
54790_1_12309	-	chr4:105160369-105160389	AUACAUAAUACCAAUAUACG	3300
54790_1_12327	-	chr4:105160511-105160531	AGGCAAGAAGGCUUCUAUUU	3301
54790_1_12331	-	chr4:105160523-105160543	CAAUUCUUUGUUAGGCAAGA	3302
54790_1_12334	-	chr4:105160531-105160551	UCUAAUUACAAUUCUUUGUU	3303

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_12354	-	chr4:105160638-105160658	GAUUUUUCCUAUCUUUAGAA	3304
54790_1_12374	-	chr4:105160722-105160742	UGGUGCUUGGUUUAGCUCUU	3305
54790_1_12377	-	chr4:105160723-105160743	UUGGUGCUUGGUUUAGCUCU	3306
54790_1_12379	-	chr4:105160735-105160755	CAAAAAACAGAUUUGGUGCU	3307
54790_1_12380	-	chr4:105160742-105160762	AAACCCCCAAAAACAGAUU	3308
54790_1_12382	-	chr4:105160809-105160829	UGAGGUCGGACCCGCUGUCU	3309
54790_1_12385	-	chr4:105160810-105160830	GUGAGGUCGGACCCGCUGUC	3310
54790_1_12388	-	chr4:105160819-105160839	CGAGGCGAAGUGAGGUCGGA	3311
54790_1_12389	-	chr4:105160820-105160840	GCGAGGCGAAGUGAGGUCGG	3312
54790_1_12393	-	chr4:105160854-105160874	UUGGGUCCUCCGCCUCCAAC	3313
54790_1_12395	-	chr4:105160860-105160880	ACGACCUUGGGUCCUCCGCC	3314
54790_1_12396	-	chr4:105160863-105160883	UUAACGACCUUGGGUCCUCC	3315
54790_1_12399	-	chr4:105160866-105160886	CUCUUAACGACCUUGGGUCC	3316
54790_1_12400	-	chr4:105160869-105160889	CGUCUCUUAACGACCUUGGG	3317
54790_1_12404	-	chr4:105160877-105160897	UCGGACUCCGUCUCUUAACG	3318
54790_1_12408	-	chr4:105160891-105160911	GGGUCGAUGAGGCUUCGGAC	3319
54790_1_12413	-	chr4:105160928-105160948	GUUUUUAUUCGGCCCGCACC	3320
54790_1_12414	-	chr4:105160931-105160951	UAUGUUUUUAAUCGGCCCGC	3321
54790_1_12415	-	chr4:105160936-105160956	AUUUUUAUGUUUUUAAUCGG	3322
54790_1_12416	-	chr4:105160937-105160957	GAUUUUUAUGUUUUUAAUCG	3323
54790_1_12419	-	chr4:105160976-105160996	GUUUUGGUCGGACUGGUUCU	3324
54790_1_12420	-	chr4:105161003-105161023	CCGCUCACCUAGUGGUCCAG	3325
54790_1_12423	-	chr4:105161008-105161028	CGACUCCGCUCACCUAGUGG	3326
54790_1_12426	-	chr4:105161017-105161037	GAAACCCUCCGACUCCGCUC	3327
54790_1_12429	-	chr4:105161024-105161044	GGGUCGUGAAACCCUCCGAC	3328
54790_1_12431	-	chr4:105161030-105161050	ACAUAAGGGUCGUGAAACCC	3329
54790_1_12433	-	chr4:105161033-105161053	UGGACAUUAGGGUCGUGAAA	3330
54790_1_12434	-	chr4:105161034-105161054	GUGGACAUUAGGGUCGUGAA	3331
54790_1_12449	-	chr4:105161122-105161142	CUAU AUGUGAAUAUAUAGAUU	3332
54790_1_12455	-	chr4:105161160-105161180	GAACAGCUUUAGAUGUUA AAA	3333
54790_1_12467	-	chr4:105161200-105161220	AGUUA AAUAAGUCACUCUUU	3334
54790_1_12480	-	chr4:105161277-105161297	AAUAUCUUUUCAUAUCCAGA	3335
54790_1_12505	-	chr4:105161462-105161482	AGCUUUUACUAUUUAGGCCG	3336
54790_1_12510	-	chr4:105161468-105161488	CACCCAAGCUUUUACUAUUU	3337
54790_1_12512	-	chr4:105161514-105161534	GUAAUGGCUCUGCUCUGUGC	3338
54790_1_12516	-	chr4:105161530-105161550	AGCUCGAGAGUGUUCAGUAA	3339
54790_1_12525	-	chr4:105161567-105161587	UUAAUAUUCUAAUAUAAGAU	3340
54790_1_12527	-	chr4:105161596-105161616	AAACAAAGGUCCGAGAAAGA	3341
54790_1_12529	-	chr4:105161597-105161617	GAAACAAAGGUCCGAGAAAG	3342
54790_1_12537	-	chr4:105161610-105161630	UAUGAUUUACUGUGAAACAA	3343
54790_1_12577	-	chr4:105161868-105161888	AAAAUUUCCACAUUGCUCU	3344
54790_1_12589	-	chr4:105161974-105161994	UUUAACCAUUUCUACCAAAG	3345
54790_1_12611	-	chr4:105162061-105162081	UGUGCACUUUCAACAUUAUA	3346
54790_1_12612	-	chr4:105162062-105162082	CUGUGCACUUUCAACAUUAU	3347
54790_1_12617	-	chr4:105162088-105162108	AGUUUAUACAAAAGACCCCA	3348
54790_1_12623	-	chr4:105162125-105162145	GUGCCUCAGCUGUCUUCUAC	3349
54790_1_12630	-	chr4:105162147-105162167	GUUUGUUUUGUGUGUGUGUU	3350
54790_1_12639	-	chr4:105162225-105162245	GGAAGGCAUUAAGGGUAACCU	3351

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_12640	-	chr4:105162226-105162246	GGGAAGGCAUUAGGGUAACC	3352
54790_1_12645	-	chr4:105162234-105162254	GACCAUGUGGGAAGGCAUUA	3353
54790_1_12646	-	chr4:105162235-105162255	UGACCAUGUGGGAAGGCAUU	3354
54790_1_12648	-	chr4:105162242-105162262	AUGUGUUUGACCAUGUGGGA	3355
54790_1_12650	-	chr4:105162246-105162266	CUCCAUGUGUUUGACCAUGU	3356
54790_1_12651	-	chr4:105162247-105162267	GCUCCAUGUGUUUGACCAUG	3357
54790_1_12657	-	chr4:105162290-105162310	AACUGCAGGCUUCAGAAUUC	3358
54790_1_12661	-	chr4:105162304-105162324	UCCACUGAUAAACAACUGC	3359
54790_1_12669	-	chr4:105162371-105162391	UGUAUCAGUAUUCAUGAUCC	3360
54790_1_12674	-	chr4:105162411-105162431	ACCAUGUUUCCCCUGCAGUC	3361
54790_1_12677	-	chr4:105162439-105162459	GGCAGGGAAAAGCCUCCUUU	3362
54790_1_12680	-	chr4:105162455-105162475	AAAAUAAACAGUGUGGGGCA	3363
54790_1_12683	-	chr4:105162456-105162476	UAAAAUAAACAGUGUGGGGC	3364
54790_1_12685	-	chr4:105162460-105162480	AGUUUAAAAUAAACAGUGUG	3365
54790_1_12686	-	chr4:105162461-105162481	UAGUUUAAAAUAAACAGUGU	3366
54790_1_12687	-	chr4:105162462-105162482	AUAGUUUAAAAUAAACAGUG	3367
54790_1_12693	-	chr4:105162493-105162513	CAAAGUGAAAAGCUCCUUUC	3368
54790_1_12701	-	chr4:105162538-105162558	AAGUGCCUACUUGCUUGUCA	3369
54790_1_12702	-	chr4:105162539-105162559	AAAGUGCCUACUUGCUUGUC	3370
54790_1_12710	-	chr4:105162588-105162608	AAAGAGAGUAACACUCCUCA	3371
54790_1_12711	-	chr4:105162589-105162609	GAAAGAGAGUAACACUCCUC	3372
54790_1_12720	-	chr4:105162616-105162636	UAAAAGAGUUUGAGUCAGCU	3373
54790_1_12727	-	chr4:105162660-105162680	UGCAGCAACAUUAUUAGAGA	3374
54790_1_12732	-	chr4:105162685-105162705	UGCUGCAACUGUUUCUAUGA	3375
54790_1_12741	-	chr4:105162767-105162787	AUUUCUAUAUGUAAUAGGAA	3376
54790_1_12745	-	chr4:105162772-105162792	GAAGUAUUUCUAUAUGUAAU	3377
54790_1_12749	-	chr4:105162794-105162814	UCUAUACAAACAGUGAUUUU	3378
54790_1_12752	-	chr4:105162795-105162815	UUCUAUACAAACAGUGAUUU	3379
54790_1_12762	-	chr4:105162852-105162872	CCCCGUAAUUAUUGCAGAUAU	3380
54790_1_12765	-	chr4:105162882-105162902	AUUAUUCUAUCACACAAAAG	3381
54790_1_12767	-	chr4:105162883-105162903	CAUUAUUCUAUCACACAAAA	3382
54790_1_12769	-	chr4:105162884-105162904	UCAUUAUUCUAUCACACAAA	3383
54790_1_12788	-	chr4:105162983-105163003	UCCAUGCUAAGCACAGCUGC	3384
54790_1_12802	-	chr4:105163012-105163032	CUUUUUUUUCUCAUCCUUUU	3385
54790_1_12822	-	chr4:105163124-105163144	UCUGAUAAUUUGUUACAAGU	3386
54790_1_12826	-	chr4:105163159-105163179	AAAGAUGAAAAGCUCAAAAA	3387
54790_1_12831	-	chr4:105163184-105163204	AGAAUUAAAUCUAUAAUUCA	3388
54790_1_12832	-	chr4:105163185-105163205	CAGAAUUAAAUCUAUAAUUC	3389
54790_1_12842	-	chr4:105163296-105163316	GAAAGUGGUGGCAAUCCAGG	3390
54790_1_12843	-	chr4:105163299-105163319	AGUGAAAGUGGUGGCAAUCC	3391
54790_1_12845	-	chr4:105163308-105163328	AAAUACUGGAGUGAAAGUGG	3392
54790_1_12848	-	chr4:105163311-105163331	UUGAAAUACUGGAGUGAAAG	3393
54790_1_12854	-	chr4:105163322-105163342	UGAAGUGUUUAUUGAAAUAC	3394
54790_1_12869	-	chr4:105163419-105163439	UAGACAUUUACGUUCCUUA	3395
54790_1_12872	-	chr4:105163420-105163440	GUAGACAUUUACGUUCCUUA	3396
54790_1_12874	-	chr4:105163421-105163441	AGUAGACAUUUACGUUCCUU	3397
54790_1_12877	-	chr4:105163426-105163446	AAAAGAGUAGACAUUUACGU	3398
54790_1_12887	-	chr4:105163477-105163497	AAUCGAACAAUGCGAUAAAC	3399

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_12899	-	chr4:105163553-105163573	AGAAACCUUUCACGAAUCGU	3400
54790_1_12901	-	chr4:105163569-105163589	GUAUUCUUAUUCUAUUAGAA	3401
54790_1_12911	-	chr4:105163623-105163643	CAAAGAAGGAAUCAUUUCAC	3402
54790_1_12918	-	chr4:105163645-105163665	UCAAUAAAUUGGGGUACAGA	3403
54790_1_12923	-	chr4:105163669-105163689	AAGAUAUUUCAAUUUUAAU	3404
54790_1_12925	-	chr4:105163670-105163690	AAAGAUAAUUCAAAUUUAA	3405
54790_1_12929	-	chr4:105163703-105163723	ACAAUGGAGAUUUGCAAUA	3406
54790_1_12931	-	chr4:105163704-105163724	GACAAUGGAGAUUUGCAAU	3407
54790_1_12936	-	chr4:105163719-105163739	GAUUACGAACAAAGAGACAA	3408
54790_1_12949	-	chr4:105163772-105163792	CCAAACACCAGACUGCUUGU	3409
54790_1_12957	-	chr4:105163892-105163912	GUUAAUAUGGAGUUGUUUCG	3410
54790_1_12965	-	chr4:105163928-105163948	GAAUUUACACAUGUCAAAAC	3411
54790_1_12971	-	chr4:105164016-105164036	UUUUUUACUGACUCUCCACU	3412
54790_1_12973	-	chr4:105164022-105164042	UUUGUGUUUUUUACUGACUC	3413
54790_1_12983	-	chr4:105164088-105164108	ACUGAUGUCAAUCAUGACAU	3414
54790_1_12985	-	chr4:105164111-105164131	ACCUCUAGAUUACAUGUCGU	3415
54790_1_12988	-	chr4:105164131-105164151	CUACUUAUAAAUAUGUAAG	3416
54790_1_12997	-	chr4:105164176-105164196	UCCCCUUUAUCCAAACAGUU	3417
54790_1_12999	-	chr4:105164187-105164207	CCGACCCAUCAUCCCCUUUA	3418
54790_1_13001	-	chr4:105164194-105164214	ACGGUACCCGACCCAUCAUC	3419
54790_1_13003	-	chr4:105164195-105164215	AACGGUACCCGACCCAUCAU	3420
54790_1_13005	-	chr4:105164196-105164216	CAACGGUACCCGACCCAUCA	3421
54790_1_13008	-	chr4:105164203-105164223	GUACCACCAACGGUACCCGA	3422
54790_1_13009	-	chr4:105164204-105164224	UGUACCACCAACGGUACCCG	3423
54790_1_13011	-	chr4:105164208-105164228	UCAUUGUACCACCAACGGUA	3424
54790_1_13012	-	chr4:105164209-105164229	CUCAUUGUACCACCAACGGU	3425
54790_1_13014	-	chr4:105164218-105164238	UUUGCGUCUCUCAUUGUACC	3426
54790_1_13015	-	chr4:105164221-105164241	GUAUUUGCGUCUCUCAUUGU	3427
54790_1_13024	-	chr4:105164263-105164283	ACGUACUAGAGUGAAUAUAC	3428
54790_1_13028	-	chr4:105164308-105164328	UCGAUUUUUUUCCUUUCAG	3429
54790_1_13031	-	chr4:105164317-105164337	CUGUAUGUGUCGAUUAUUUU	3430
54790_1_13035	-	chr4:105164352-105164372	UUCGUCUAAGUGUUUACGAU	3431
54790_1_13046	-	chr4:105164380-105164400	UAAUCAACAAGAGUAAAUG	3432
54790_1_13059	-	chr4:105164459-105164479	UUAAAACGGUUCAUUGUACG	3433
54790_1_13070	-	chr4:105164554-105164574	UUCGAGAAGGGUAAAGAUGA	3434
54790_1_13071	-	chr4:105164566-105164586	UGAGCCUGUAUAUUCCAGAA	3435
54790_1_13073	-	chr4:105164567-105164587	AUGAGCCUGUAUAUUCCAGA	3436
54790_1_13092	-	chr4:105164675-105164695	CGUCUCCGACCUUCGUAGGA	3437
54790_1_13094	-	chr4:105164676-105164696	UCGUCUCCGACCUUCGUAGG	3438
54790_1_13098	-	chr4:105164687-105164707	GUGUGGAAAACUCGUCUCCG	3439
54790_1_13101	-	chr4:105164691-105164711	UUAAGUGUGGAAAACUCGUC	3440
54790_1_13106	-	chr4:105164714-105164734	ACCGCGGAUAAGUCCGUUGA	3441
54790_1_13107	-	chr4:105164715-105164735	GACCGCGGAUAAGUCCGUUG	3442
54790_1_13110	-	chr4:105164722-105164742	CGGUUGAGACCGCGGAUAAG	3443
54790_1_13111	-	chr4:105164734-105164754	ACUCUUUCGAUACGGUUGAG	3444
54790_1_13116	-	chr4:105164766-105164786	UGAACACGUUAGAGGGACAG	3445
54790_1_13120	-	chr4:105164801-105164821	GGGGAACUCGGUUAGAAGUC	3446
54790_1_13126	-	chr4:105164844-105164864	CUAACUUUGUUAUUUUCCCU	3447

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_13129	-	chr4:105164848-105164868	AGAACUAAACUUUGUUAUUUU	3448
54790_1_13130	-	chr4:105164849-105164869	UAGAACUAAACUUUGUUAUUU	3449
54790_1_13135	-	chr4:105164893-105164913	UUUCCUACUAGUACUUUCCU	3450
54790_1_13136	-	chr4:105164897-105164917	GUUAUUUCCUACUAGUACUU	3451
54790_1_13141	-	chr4:105164911-105164931	CAUAGAUUAUUUCUGUUAUU	3452
54790_1_13151	-	chr4:105164955-105164975	CGAUAGUAAAUAUAAAGAU	3453
54790_1_13159	-	chr4:105165024-105165044	CUUUUAUACUAUGUUUUAUC	3454
54790_1_13168	-	chr4:105165074-105165094	GAUAGUAGAUAGAAAUUCGU	3455
54790_1_13170	-	chr4:105165097-105165117	GUCCAGACUCGGUGGUGUGG	3456
54790_1_13172	-	chr4:105165116-105165136	AGGGUUUCACGACCUUAAUG	3457
54790_1_13174	-	chr4:105165125-105165145	CGGAGCCGGAGGGUUUCACG	3458
54790_1_13176	-	chr4:105165141-105165161	GAGUCCACUAGACGGGCGGA	3459
54790_1_13180	-	chr4:105165158-105165178	CCAAAGUUUGAGGACUGGAG	3460
54790_1_13184	-	chr4:105165179-105165199	AAAGAGAUGCAACCGGUCCA	3461
54790_1_13185	-	chr4:105165183-105165203	CCCCAAAGAGAUGCAACCGG	3462
54790_1_13187	-	chr4:105165188-105165208	GUCUGCCCCAAAGAGAUGCA	3463
54790_1_13196	-	chr4:105165202-105165222	ACAUAAAAAACCAUGUCUGC	3464
54790_1_13197	-	chr4:105165203-105165223	AACAUAAAAAACCAUGUCUG	3465
54790_1_13198	-	chr4:105165204-105165224	AAACAUAAAAAACCAUGUCU	3466
54790_1_13201	-	chr4:105165213-105165233	ACCGAUUAAAAACAUA AAAA	3467
54790_1_13203	-	chr4:105165233-105165253	GUCCGCGGGUGGUGGUGCGG	3468
54790_1_13204	-	chr4:105165252-105165272	AGGACUCACCGACCUUAAUG	3469
54790_1_13205	-	chr4:105165261-105165281	CGGAGUCAGAGGACUCACCG	3470
54790_1_13209	-	chr4:105165265-105165285	AGCACGGAGUCAGAGGACUC	3471
54790_1_13212	-	chr4:105165300-105165320	GUGACGUUGGAGACGGAGGA	3472
54790_1_13213	-	chr4:105165301-105165321	AGUGACGUUGGAGACGGAGG	3473
54790_1_13215	-	chr4:105165336-105165356	AGUGGGUCCGACCUCACGUU	3474
54790_1_13217	-	chr4:105165346-105165366	AGAGGGAGACAGUGGGUCCG	3475
54790_1_13219	-	chr4:105165350-105165370	CUUCAGAGGGAGACAGUGGG	3476
54790_1_13236	-	chr4:105165377-105165397	UAAAAAAUA AAAAUAAAAAA	3477
54790_1_13238	-	chr4:105165378-105165398	AUAAAAAAUA AAAAUAAAAAA	3478
54790_1_13244	-	chr4:105165429-105165449	AUUCCUUA AAGGUGAGAGUG	3479
54790_1_13249	-	chr4:105165447-105165467	AAAGUACUGUGACGGUACAU	3480
54790_1_13254	-	chr4:105165477-105165497	GAGUUUUUGUAGAAAGUGUA	3481
54790_1_13255	-	chr4:105165478-105165498	UGAGUUUUUGUAGAAAGUGU	3482
54790_1_13281	-	chr4:105165615-105165635	GCUUGCGUGAUAAUUGUUGU	3483
54790_1_13283	-	chr4:105165616-105165636	UGC UUGCGUGAUAAUUGUUG	3484
54790_1_13288	-	chr4:105165652-105165672	UCAUCAGUAAGUGUUAUUGA	3485
54790_1_13289	-	chr4:105165653-105165673	AUCAUCAGUAAGUGUUAUUG	3486
54790_1_13293	-	chr4:105165681-105165701	AGAGUAUCCCAACUUAUACA	3487
54790_1_13298	-	chr4:105165710-105165730	CCCUAAAUGCAGACUUAAGAA	3488
54790_1_13310	-	chr4:105165777-105165797	UACAUUUUGAAAAGUCACUG	3489
54790_1_13323	-	chr4:105165848-105165868	AUUGUGGGUAAGAAUAAUAA	3490
54790_1_13330	-	chr4:105165863-105165883	UUAAAGCAAUGCAUUAUUGU	3491
54790_1_13331	-	chr4:105165864-105165884	UUUAAAGCAAUGCAUUAUUG	3492
54790_1_13333	-	chr4:105165908-105165928	UCAUCUCUGAGUCUUUCCAU	3493
54790_1_13335	-	chr4:105165913-105165933	AUGUAUCAUCUCUGAGUCUU	3494
54790_1_13344	-	chr4:105165963-105165983	CCGUCCUUUUCUUUUCAUCG	3495

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_13349	-	chr4:105165980-105166000	AUGUCCUCAAACUGUCUCCG	3496
54790_1_13352	-	chr4:105165984-105166004	CCUUAUGUCCUCAAACUGUCU	3497
54790_1_13355	-	chr4:105165997-105166017	CUUCAUUACUUAUACCUUAUG	3498
54790_1_13361	-	chr4:105166005-105166025	UCGUUAUUCUUCAUUACUUAU	3499
54790_1_13388	-	chr4:105166127-105166147	UUAAAAUAAAUAAUGUUAGU	3500
54790_1_13394	-	chr4:105166160-105166180	UGUACAAGUUGGUAUGACGA	3501
54790_1_13403	-	chr4:105166201-105166221	UUCGAUUUAAAAUCACAGUG	3502
54790_1_13415	-	chr4:105166265-105166285	ACUGUUUCUUAUAAUCGUUUU	3503
54790_1_13418	-	chr4:105166266-105166286	AACUGUUUCUUAUAAUCGUUUU	3504
54790_1_13425	-	chr4:105166289-105166309	AAAAAUGUGGCAUAAUUUUUG	3505
54790_1_13428	-	chr4:105166302-105166322	AUGUGAAAGAAACAAAAAUG	3506
54790_1_13436	-	chr4:105166340-105166360	AAGAAAAAUUGAAUGCUUAC	3507
54790_1_13454	-	chr4:105166450-105166470	AGUGUAUUUCAUUCAUCAA	3508
54790_1_13468	-	chr4:105166528-105166548	AAGCAAUAAUAGACAUAGCC	3509
54790_1_13497	-	chr4:105166671-105166691	UCCUUUUUAUUAUCCGUAAA	3510
54790_1_13499	-	chr4:105166679-105166699	CAUGAUAUUCCUUUUUAUUAU	3511
54790_1_13502	-	chr4:105166691-105166711	AUUAUAAUACUUAUACAUGAU	3512
54790_1_13512	-	chr4:105166726-105166746	UCUUUUAAUGAAACUUAUAAU	3513
54790_1_13519	-	chr4:105166781-105166801	GUAUUCGUUAGGAUCUACUU	3514
54790_1_13520	-	chr4:105166782-105166802	AGUAUUCGUUAGGAUCUACU	3515
54790_1_13524	-	chr4:105166820-105166840	AUUUUUUCUGUCUUAGUCUG	3516
54790_1_13526	-	chr4:105166855-105166875	AGGAUUAUUUGUAUACUUAU	3517
54790_1_13529	-	chr4:105166856-105166876	UAGGAUUAUUUGUAUACUUA	3518
54790_1_13540	-	chr4:105166903-105166923	AAAUUGUCUCGGUAUAGACC	3519
54790_1_13543	-	chr4:105166906-105166926	GUAAAAUUGUCUCGGUAUAG	3520
54790_1_13557	-	chr4:105166975-105166995	UUCAUGGAAUUCGAUUUAUU	3521
54790_1_13559	-	chr4:105167003-105167023	UCUUUAUUAGUUUCCAUGUU	3522
54790_1_13562	-	chr4:105167011-105167031	UUCUUCUUCUUAUUUAUUAGUU	3523
54790_1_13564	-	chr4:105167027-105167047	UUCUAUCCCACUUUUUUUCU	3524
54790_1_13573	-	chr4:105167041-105167061	UGUACUCAAAGUAUUUCUAU	3525
54790_1_13574	-	chr4:105167042-105167062	UUGUACUCAAAGUAUUUCUA	3526
54790_1_13582	-	chr4:105167112-105167132	UUGUCUACUUUUUAUACACU	3527
54790_1_13597	-	chr4:105167194-105167214	UCUUAUCUUUUUACCUGAAGA	3528
54790_1_13599	-	chr4:105167203-105167223	UAGUUAGUCUCUUAUCUUUU	3529
54790_1_13611	-	chr4:105167241-105167261	UAUGAUUUGAGCCACGAUUA	3530
54790_1_13635	-	chr4:105167319-105167339	UAUUGUUUUUAGAUAUAGUU	3531
54790_1_13657	-	chr4:105167551-105167571	AGCACUGUUAUUUUUAAAAG	3532
54790_1_13658	-	chr4:105167552-105167572	UAGCACUGUUAUUUUUAAAA	3533
54790_1_13660	-	chr4:105167553-105167573	CUAGCACUGUUAUUUUUAAA	3534
54790_1_13671	-	chr4:105167628-105167648	UACUAAAGCAUUAUUAUUGA	3535
54790_1_13672	-	chr4:105167629-105167649	AUACUAAAGCAUUAUUAUUG	3536
54790_1_13676	-	chr4:105167659-105167679	CACAGUCACUGACUAUGCCU	3537
54790_1_13677	-	chr4:105167660-105167680	GCACAGUCACUGACUAUGCC	3538
54790_1_13679	-	chr4:105167690-105167710	CAGGAUGAACUGCUACUGCU	3539
54790_1_13684	-	chr4:105167709-105167729	GUUACACCUUAGAUCUGUAC	3540
54790_1_13688	-	chr4:105167748-105167768	GACAACCAAAGAAUCUCCAA	3541
54790_1_13689	-	chr4:105167749-105167769	AGACAACCAAAGAAUCUCCA	3542
54790_1_13696	-	chr4:105167784-105167804	CUGUUAUUGAACAGCAAGAU	3543

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_13712	-	chr4:105167845-105167865	UUUAAAGACUGUUAAGCAGU	3544
54790_1_13716	-	chr4:105167846-105167866	UUUUAAAGACUGUUAAGCAG	3545
54790_1_13722	-	chr4:105167881-105167901	AGGCAAGAUUACGUCCUUAAC	3546
54790_1_13723	-	chr4:105167882-105167902	UAGGCAAGAUUACGUCCUUA	3547
54790_1_13730	-	chr4:105167901-105167921	UUCCUUCAUUCCUUAAGCU	3548
54790_1_13740	-	chr4:105167960-105167980	CUCAGUUGUCUUGUACAACC	3549
54790_1_13743	-	chr4:105167963-105167983	CAUCUCAGUUGUCUUGUACA	3550
54790_1_13750	-	chr4:105167985-105168005	UCUAGGACUUAUAUGAAAUG	3551
54790_1_13755	-	chr4:105168020-105168040	CCUCUACCUUUAACCACUUU	3552
54790_1_13758	-	chr4:105168028-105168048	CAAACUUAACCUCUACCUUUA	3553
54790_1_13760	-	chr4:105168035-105168055	CUUCCACCAAACUUAACCUCU	3554
54790_1_13762	-	chr4:105168041-105168061	UGUGUACUUCCACCAAACUU	3555
54790_1_13769	-	chr4:105168050-105168070	AAGUUUCAUUGUGUACUCC	3556
54790_1_13770	-	chr4:105168053-105168073	GAAAAGUUUCAUUGUGUACU	3557
54790_1_13773	-	chr4:105168084-105168104	UUUGUCCCUUUGGGUACUGU	3558
54790_1_13774	-	chr4:105168085-105168105	CUUUGUCCCUUUGGGUACUG	3559
54790_1_13777	-	chr4:105168099-105168119	CCCCUCGUUUCGAUCUUUGU	3560
54790_1_13779	-	chr4:105168100-105168120	CCCCCUCGUUUCGAUCUUUG	3561
54790_1_13783	-	chr4:105168118-105168138	GGGUGCCACUCCAUUCUCC	3562
54790_1_13786	-	chr4:105168119-105168139	UGGGUGCCACUCCAUUCUUC	3563
54790_1_13787	-	chr4:105168120-105168140	UUGGGUGCCACUCCAUUCUU	3564
54790_1_13789	-	chr4:105168121-105168141	UUUGGGUGCCACUCCAUUCU	3565
54790_1_13799	-	chr4:105168129-105168149	AACCCAUUUUUGGGUGCCAC	3566
54790_1_13802	-	chr4:105168134-105168154	AAACAAACCCAUUUUUGGGU	3567
54790_1_13804	-	chr4:105168147-105168167	CUAGUGAACUUA AAAACAAA	3568
54790_1_13807	-	chr4:105168148-105168168	ACUAGUGAACUUA AAAACAA	3569
54790_1_13817	-	chr4:105168194-105168214	UUACCAAAAUUCGUCUCCUC	3570
54790_1_13819	-	chr4:105168199-105168219	GGUAAUUAACCAAAAUUCGUC	3571
54790_1_13823	-	chr4:105168212-105168232	CACUUUGUCUCUGGGUAAUU	3572
54790_1_13831	-	chr4:105168247-105168267	CACCCAGUACUUUUCGCGAA	3573
54790_1_13833	-	chr4:105168253-105168273	CCUGACCACCCAGUACUUUU	3574
54790_1_13834	-	chr4:105168254-105168274	UCCUGACCACCCAGUACUUU	3575
54790_1_13838	-	chr4:105168265-105168285	GUUAAGUGAACUCCUGACCA	3576
54790_1_13839	-	chr4:105168266-105168286	GGUUAAGUGAACUCCUGACC	3577
54790_1_13841	-	chr4:105168269-105168289	GUCGGUUAAGUGAACUCCUG	3578
54790_1_13842	-	chr4:105168274-105168294	UUAUCGUCGGUUAAGUGAAC	3579
54790_1_13847	-	chr4:105168310-105168330	CCCUCUUAUCACCGUUCUUU	3580
54790_1_13851	-	chr4:105168320-105168340	UUAUCUUAUCUCCUUCUUAUC	3581
54790_1_13853	-	chr4:105168330-105168350	UCCUUUAAUCUUAUCUUAUCU	3582
54790_1_13855	-	chr4:105168331-105168351	UUCCUUUAAUCUUAUCUUAAC	3583
54790_1_13863	-	chr4:105168350-105168370	GGUCCUGUCGUUCUUUUGGU	3584
54790_1_13868	-	chr4:105168368-105168388	UCCUACGAGAAGAACAACGG	3585
54790_1_13870	-	chr4:105168388-105168408	ACGUUUCGACCUCCUUUU	3586
54790_1_13872	-	chr4:105168395-105168415	GUCGUUCACGUUUCGCGACC	3587
54790_1_13875	-	chr4:105168398-105168418	CUUGUCGUUCACGUUUCGCG	3588
54790_1_13878	-	chr4:105168403-105168423	UCUCCCUUGUCGUUCACGUU	3589
54790_1_13880	-	chr4:105168420-105168440	CCUUCCACGAGGUCCUUCU	3590
54790_1_13881	-	chr4:105168421-105168441	UCCUUCCACGAGGUCCUUC	3591

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_13885	-	chr4:105168427-105168447	GAGACUUCCUUCCCACGAGG	3592
54790_1_13888	-	chr4:105168436-105168456	GGACACCGAGAGACUUCCUU	3593
54790_1_13889	-	chr4:105168437-105168457	UGGACACCGAGAGACUUCCU	3594
54790_1_13891	-	chr4:105168441-105168461	GUUAUGGACACCGAGAGACU	3595
54790_1_13895	-	chr4:105168452-105168472	UUUCUAUCUUUGUUAUGGAC	3596
54790_1_13898	-	chr4:105168475-105168495	UGUGAGUUCCUCUCUAAUCU	3597
54790_1_13906	-	chr4:105168488-105168508	GAGACUUUUUCAUUGUGAGU	3598
54790_1_13913	-	chr4:105168518-105168538	UCUGAAUCUAUCUUACCAAU	3599
54790_1_13915	-	chr4:105168519-105168539	UUCUGAAUCUAUCUUACCAA	3600
54790_1_13918	-	chr4:105168524-105168544	CAGAGUUCUGAAUCUAUCUU	3601
54790_1_13921	-	chr4:105168555-105168575	AAAAGAGAGAAAUAAGCA	3602
54790_1_13930	-	chr4:105168602-105168622	GGACAAGGGGUUAUUGGAUA	3603
54790_1_13932	-	chr4:105168603-105168623	UGGACAAGGGGUUAUUGGAU	3604
54790_1_13937	-	chr4:105168681-105168701	CACAU AUGACGAGCCACUA	3605
54790_1_13938	-	chr4:105168688-105168708	CCCACUUCACAU AUGACGAG	3606
54790_1_13939	-	chr4:105168689-105168709	UCCACUUCACAU AUGACGA	3607
54790_1_13942	-	chr4:105168708-105168728	CCUUAUUUUCUGAUGCUUAU	3608
54790_1_13943	-	chr4:105168709-105168729	UCCUUAUUUUCUGAUGCUUA	3609
54790_1_13946	-	chr4:105168729-105168749	UUUUCCCACCCUCCCCCAC	3610
54790_1_13950	-	chr4:105168734-105168754	UCCCUUUUCCCACCCUUC	3611
54790_1_13951	-	chr4:105168735-105168755	GUCCCCUUUCCCACCCUUC	3612
54790_1_13952	-	chr4:105168736-105168756	AGUCCCCUUUCCCACCCUU	3613
54790_1_13955	-	chr4:105168737-105168757	GAGUCCCCUUUCCCACCCU	3614
54790_1_13957	-	chr4:105168741-105168761	CCCUGAGUCCCCUUUCCCA	3615
54790_1_13960	-	chr4:105168742-105168762	UCCUGAGUCCCCUUUCCC	3616
54790_1_13962	-	chr4:105168745-105168765	AGAUCCCUGAGUCCCCUUU	3617
54790_1_13963	-	chr4:105168746-105168766	GAGAUCCCUGAGUCCCCUUU	3618
54790_1_13965	-	chr4:105168752-105168772	UUACCUGAGA UCCCUGAGUC	3619
54790_1_13968	-	chr4:105168753-105168773	GUUACCUGAGA UCCCUGAGU	3620
54790_1_13970	-	chr4:105168754-105168774	UGUUACCUGAGA UCCCUGAG	3621
54790_1_13972	-	chr4:105168761-105168781	CUUACUGUGUU ACCUGAGAU	3622
54790_1_13974	-	chr4:105168762-105168782	UCUUACUGUGUU ACCUGAGA	3623
54790_1_13976	-	chr4:105168770-105168790	UUCCGU AUUCUUACUGUGUU	3624
54790_1_13979	-	chr4:105168789-105168809	CGAUGCGAU ACUCCUACGUU	3625
54790_1_13980	-	chr4:105168798-105168818	AUUCACCCUCGAUGCGAUAC	3626
54790_1_13984	-	chr4:105168813-105168833	UAUACAAGAGUGAGUAUUCA	3627
54790_1_13987	-	chr4:105168814-105168834	GUAUACAAGAGUGAGUAUUC	3628
54790_1_13992	-	chr4:105168849-105168869	AUUCACUUCAUUGAGUCCCU	3629
54790_1_13994	-	chr4:105168853-105168873	UAAGAUUCACUUCAUUGAGU	3630
54790_1_13995	-	chr4:105168854-105168874	AUAAGAUUCACUUCAUUGAG	3631
54790_1_14001	-	chr4:105168884-105168904	ACGUCACUGGACCUAUUCUG	3632
54790_1_14005	-	chr4:105168894-105168914	AUUACCGUAAACGUCACUGG	3633
54790_1_14007	-	chr4:105168911-105168931	GUAUUUUUCCCUACUUAUUAU	3634
54790_1_14010	-	chr4:105168924-105168944	UUAUGAUGAGUCGGUAUUUU	3635
54790_1_14014	-	chr4:105168947-105168967	UGACACCAUAUAAAUAUUCU	3636
54790_1_14018	-	chr4:105168963-105168983	CACUCAUCAAUUUCUUUGAC	3637
54790_1_14021	-	chr4:105168985-105169005	GUUGGGUUUACGAGCAGUUA	3638
54790_1_14026	-	chr4:105169011-105169031	UUAACGUUAACGUUUUUAC	3639

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_14034	-	chr4:105169085-105169105	UGAUGACCCAUAGAUGGGUC	3640
54790_1_14039	-	chr4:105169099-105169119	CUAGGUCGUUAGGGUGAUGA	3641
54790_1_14040	-	chr4:105169100-105169120	ACUAGGUCGUUAGGGUGAUG	3642
54790_1_14044	-	chr4:105169158-105169178	UCGGUGAUACCUUUUGUCAC	3643
54790_1_14048	-	chr4:105169170-105169190	CAUUUGAUCAUGUCGGUGAU	3644
54790_1_14051	-	chr4:105169196-105169216	UUGUGAAGAUGUGACGACCA	3645
54790_1_14054	-	chr4:105169197-105169217	CUUGUGAAGAUGUGACGACC	3646
54790_1_14056	-	chr4:105169200-105169220	UCUCUUGUGAAGAUGUGACG	3647
54790_1_14062	-	chr4:105169228-105169248	UCAUCUGCAACCGUACCUAU	3648
54790_1_14063	-	chr4:105169234-105169254	UUUUUAUCAUCUGCAACCGU	3649
54790_1_14065	-	chr4:105169239-105169259	UUAGUUUUUAUCAUCUGCA	3650
54790_1_14068	-	chr4:105169270-105169290	UAUGAAAUAGAGGACGUUCUU	3651
54790_1_14072	-	chr4:105169318-105169338	AAGUUAUAGUGAUUACUAGU	3652
54790_1_14075	-	chr4:105169319-105169339	CAAGUUAUAGUGAUUACUAG	3653
54790_1_14085	-	chr4:105169402-105169422	AGGAUAGUUUUUCACCCGAU	3654
54790_1_14087	-	chr4:105169408-105169428	UUUGUUAGGAUAGUUUUUCA	3655
54790_1_14088	-	chr4:105169409-105169429	GUUUGUUAGGAUAGUUUUUC	3656
54790_1_14092	-	chr4:105169439-105169459	CCUUGAGGUUGUUUAAUCGU	3657
54790_1_14095	-	chr4:105169460-105169480	UGAUUAUAGAUCUUAGAUGU	3658
54790_1_14099	-	chr4:105169483-105169503	UGUUAGAUACGUAGGCCGUU	3659
54790_1_14101	-	chr4:105169489-105169509	UAGAAGUGUUAGAUACGUAG	3660
54790_1_14104	-	chr4:105169517-105169537	UUUGUCUGUUGGGUGUCUCA	3661
54790_1_14105	-	chr4:105169518-105169538	AUUUGUCUGUUGGGUGUCUC	3662
54790_1_14109	-	chr4:105169555-105169575	UUCUCGGAGACGUGUCGUUA	3663
54790_1_14116	-	chr4:105169596-105169616	GUUGUUUUUGUUUCUAUUUA	3664
54790_1_14123	-	chr4:105169654-105169674	UGGGAAGAUCUGUAACCGAA	3665
54790_1_14124	-	chr4:105169660-105169680	UCUUUUUGGGAAGAUCUGUA	3666
54790_1_14132	-	chr4:105169737-105169757	UAUAUUUUUAGUUGAGUUCU	3667
54790_1_14139	-	chr4:105169806-105169826	UGUUUACCACGACCCUAUCG	3668
54790_1_14140	-	chr4:105169814-105169834	GGAUAAGUUGUUUACCACGA	3669
54790_1_14142	-	chr4:105169815-105169835	GGGAUAAGUUGUUUACCACG	3670
54790_1_14144	-	chr4:105169821-105169841	UCCUGUGGGAUAAGUUGUUU	3671
54790_1_14146	-	chr4:105169841-105169861	UUUGUAUUUAAUCAUCCAUI	3672
54790_1_14148	-	chr4:105169847-105169867	UUUGUUUUUGUAUUUAAUCA	3673
54790_1_14157	-	chr4:105169926-105169946	AUCCAUGUCUCUGGUUACCC	3674
54790_1_14158	-	chr4:105169927-105169947	UAUCCAUGUCUCUGGUUACC	3675
54790_1_14161	-	chr4:105169928-105169948	UUAUCCAUGUCUCUGGUUAC	3676
54790_1_14163	-	chr4:105169929-105169949	UUUAUCCAUGUCUCUGGUUA	3677
54790_1_14165	-	chr4:105169930-105169950	UUUUAUCCAUGUCUCUGGUU	3678
54790_1_14168	-	chr4:105169945-105169965	GUACCAUGACCAUAUUUUUA	3679
54790_1_14169	-	chr4:105169957-105169977	UGUGGUUUUGUCGUACCAUG	3680
54790_1_14170	-	chr4:105169963-105169983	GGUAUCUGUGGUUUUGUCGU	3681
54790_1_14174	-	chr4:105169986-105170006	AAUGGACUGAAUAUGAUCU	3682
54790_1_14179	-	chr4:105170019-105170039	GAUUCGUGUUUCUUGUUUAA	3683
54790_1_14180	-	chr4:105170020-105170040	UGAUUCGUGUUUCUUGUUUA	3684
54790_1_14195	-	chr4:105170100-105170120	GGUAGUAAGAAGUGUCUUA	3685
54790_1_14203	-	chr4:105170156-105170176	AAGCAGAAACACUUUGCCAA	3686
54790_1_14204	-	chr4:105170157-105170177	AAAGCAGAAACACUUUGCCA	3687

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_14212	-	chr4:105170209-105170229	GAGUAUCUUGAGUGUAGAUG	3688
54790_1_14220	-	chr4:105170275-105170295	UGGUACACGAUCGGUGACAA	3689
54790_1_14238	-	chr4:105170369-105170389	GGAGUCGGAAGUCUCAUCGA	3690
54790_1_14240	-	chr4:105170370-105170390	CGGAGUCGGAAGUCUCAUCG	3691
54790_1_14246	-	chr4:105170403-105170423	UGGGGUUUGAAAACUCUGAG	3692
54790_1_14249	-	chr4:105170446-105170466	UGUUACGUCGUCGAUAAGUG	3693
54790_1_14252	-	chr4:105170471-105170491	CCCAAGAGUGACACAACUGG	3694
54790_1_14261	-	chr4:105170491-105170511	UGCCAAAAAAAAAUUUCUCUA	3695
54790_1_14263	-	chr4:105170492-105170512	UUGCCAAAAAAAAAUUUCUCU	3696
54790_1_14270	-	chr4:105170555-105170575	CAGCAGAGAAAAGACAACAC	3697
54790_1_14279	-	chr4:105170584-105170604	UCUAUCUUCAAUUUCCAAUG	3698
54790_1_14284	-	chr4:105170615-105170635	UUUCACCUAUAAAUAUCAA	3699
54790_1_14288	-	chr4:105170652-105170672	AUUGUCUCAGCUAUUCCUCA	3700
54790_1_14293	-	chr4:105170678-105170698	UCCUCGGCUCCAGAAGCUCC	3701
54790_1_14300	-	chr4:105170694-105170714	UUUAGUGACCAAUGUUUCCU	3702
54790_1_14302	-	chr4:105170720-105170740	AGUACAGUUGCCAAUAUAAA	3703
54790_1_14306	-	chr4:105170748-105170768	UGUAAUUGAAACACUAGCAU	3704
54790_1_14317	-	chr4:105170799-105170819	CACAUCAUGUUUAUAUUUUG	3705
54790_1_14326	-	chr4:105170879-105170899	GGCAGUGCUCUUCUUGCAGG	3706
54790_1_14327	-	chr4:105170882-105170902	ACAGGCAGUGCUCUUCUUGC	3707
54790_1_14330	-	chr4:105170900-105170920	GGAAGCAGAAGGAAGAACAC	3708
54790_1_14334	-	chr4:105170911-105170931	GCUGAAAUAAAGGAAGCAGA	3709
54790_1_14339	-	chr4:105170921-105170941	UAGACACACAGCUGAAAUAA	3710
54790_1_14343	-	chr4:105170944-105170964	GUGUAGAAGGAGGAGGAAGU	3711
54790_1_14346	-	chr4:105170951-105170971	UCUCCUAGUGUAGAAGGAGG	3712
54790_1_14350	-	chr4:105170954-105170974	AUUUCUCCUAGUGUAGAAGG	3713
54790_1_14353	-	chr4:105170957-105170977	GCAAUUUCUCCUAGUGUAGA	3714
54790_1_14359	-	chr4:105170987-105171007	AUAGCAGAUGUUAAGAUUAU	3715
54790_1_14370	-	chr4:105171045-105171065	UUAAAAAAAAAAGAAUGAAGA	3716
54790_1_14385	-	chr4:105171110-105171130	UUUGAGCCAGCAAUAACAGC	3717
54790_1_14388	-	chr4:105171135-105171155	AAAUAACACUGAAAUGCUC	3718
54790_1_14393	-	chr4:105171165-105171185	GUCUUUACCUUGAGGGUAGU	3719
54790_1_14398	-	chr4:105171179-105171199	GUGAAACUUAUUUUGUCUUU	3720
54790_1_14402	-	chr4:105171208-105171228	GGUCCGUGACACGAUCUGUG	3721
54790_1_14407	-	chr4:105171226-105171246	AAUAUCCGAUAUUACACGG	3722
54790_1_14408	-	chr4:105171242-105171262	UAGGUGAUCUAUUUGUAAUA	3723
54790_1_14414	-	chr4:105171270-105171290	UGAUAAUUCUUAAUAGUAU	3724
54790_1_14431	-	chr4:105171342-105171362	UGCACUUCAUUUCCUAGCA	3725
54790_1_14441	-	chr4:105171385-105171405	UUCAGAAAGUUCUCUAUACU	3726
54790_1_14458	-	chr4:105171475-105171495	AUGGCCUGUGUUAUCUUAUU	3727
54790_1_14464	-	chr4:105171494-105171514	AUUUUUUAAGAACAAGAA	3728
54790_1_14483	-	chr4:105171572-105171592	AUCUCAGUAAGUUACACUAC	3729
54790_1_14490	-	chr4:105171607-105171627	UAGCAUCAAUACAGAAUUUA	3730
54790_1_14495	-	chr4:105171630-105171650	GUAGCUCAAGAGUUGCAUCU	3731
54790_1_14499	-	chr4:105171658-105171678	GACCAGCAUCCUUUAUCAAG	3732
54790_1_14502	-	chr4:105171680-105171700	CAAACAUAACACUGGCAGCA	3733
54790_1_14503	-	chr4:105171681-105171701	GCAAACAUAACACUGGCAGC	3734
54790_1_14506	-	chr4:105171688-105171708	UAAAUAGAGCAAACAUAACAC	3735

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_14514	-	chr4:105171733-105171753	UUCACCUUCUUCACCAUCCC	3736
54790_1_14524	-	chr4:105171785-105171805	AGAGAAUAGUCUGUUUCUGU	3737
54790_1_14529	-	chr4:105171813-105171833	UGAAAAUGAAUAAUGCAAUC	3738
54790_1_14534	-	chr4:105171840-105171860	CUUCCAAAGCAGAUAAAGGC	3739
54790_1_14535	-	chr4:105171844-105171864	UAGGCUUCCAAAGCAGAUAA	3740
54790_1_14538	-	chr4:105171863-105171883	AUCUUGGAAGAUUAGGAAAU	3741
54790_1_14540	-	chr4:105171870-105171890	AUGAUAAAUUCUUGGAAGAUU	3742
54790_1_14543	-	chr4:105171879-105171899	AUGAAGGUGAUGAUAAAUCU	3743
54790_1_14545	-	chr4:105171895-105171915	UGCAUGCUAUGGACAUAUGA	3744
54790_1_14548	-	chr4:105171906-105171926	UGUCUGAGAAAUGCAUGCUA	3745
54790_1_14558	-	chr4:105171991-105172011	CAGUACCACAUGAAAAACCA	3746
54790_1_14567	-	chr4:105172023-105172043	AAAUUUCUACUUCUUUGUCA	3747
54790_1_14574	-	chr4:105172054-105172074	CACAGAAUGAAUAGAACGGG	3748
54790_1_14587	-	chr4:105172149-105172169	CCCAGUUGACUAUUUAUUUA	3749
54790_1_14590	-	chr4:105172169-105172189	AAUUGGAGGUACAAUAAGUU	3750
54790_1_14591	-	chr4:105172170-105172190	GAAUUGGAGGUACAAUAAGU	3751
54790_1_14598	-	chr4:105172197-105172217	AAAAACUGUCACGUCCCCCA	3752
54790_1_14599	-	chr4:105172201-105172221	ACCUAAAAACUGUCACGUCC	3753
54790_1_14601	-	chr4:105172202-105172222	CACCUAAAAACUGUCACGUC	3754
54790_1_14603	-	chr4:105172203-105172223	ACACCUAAAAACUGUCACGU	3755
54790_1_14604	-	chr4:105172204-105172224	UACACCUAAAAACUGUCACG	3756
54790_1_14611	-	chr4:105172221-105172241	CCCCUCAGUUUUUAAUGUAC	3757
54790_1_14616	-	chr4:105172240-105172260	AUAAUCAUCAAUUCAAAC	3758
54790_1_14617	-	chr4:105172241-105172261	GAUAAUCAUCAAUUCAAAC	3759
54790_1_14619	-	chr4:105172242-105172262	CGAUAAUCAUCAAUUCAAAC	3760
54790_1_14622	-	chr4:105172264-105172284	GUCCCGGAGGUCUGUUGUCG	3761
54790_1_14624	-	chr4:105172282-105172302	UUGACACACACAAUAGUCGU	3762
54790_1_14626	-	chr4:105172283-105172303	GUUGACACACACAAUAGUCG	3763
54790_1_14655	-	chr4:105172458-105172478	UGAGUUCCACUUCUGUUGUU	3764
54790_1_14662	-	chr4:105172473-105172493	GGAGAAGAAGUCGUUAGAGU	3765
54790_1_14669	-	chr4:105172524-105172544	AGAAGGUGAAGACGGUGGGG	3766
54790_1_14677	-	chr4:105172566-105172586	UUUAUGUCCAAACUUGACGU	3767
54790_1_14681	-	chr4:105172580-105172600	UACCCAACUGGAUUUUUAUG	3768
54790_1_14691	-	chr4:105172629-105172649	UUCAUUGAAAAAAAUUAACA	3769
54790_1_14697	-	chr4:105172664-105172684	UAAACAUCAGGCAUUUGAA	3770
54790_1_14702	-	chr4:105172675-105172695	AAUGUUUCUCAUAAACAUAC	3771
54790_1_14742	-	chr4:105172934-105172954	GAGUAGCAGCAUAGCCAACU	3772
54790_1_14760	-	chr4:105173018-105173038	CUAAAGGGAUAAUUAAAAUU	3773
54790_1_14768	-	chr4:105173033-105173053	CAUAAUUUCUAUUCUCUAAA	3774
54790_1_14769	-	chr4:105173034-105173054	UCAUAAUUUCUAUUCUCUAA	3775
54790_1_14780	-	chr4:105173077-105173097	AGAAAAUUUAUAUUGUUGAG	3776
54790_1_14796	-	chr4:105173127-105173147	AAACUUUUUAUCCUUUGUGU	3777
54790_1_14801	-	chr4:105173151-105173171	UCCUCUAGAAACUAAGGAU	3778
54790_1_14802	-	chr4:105173156-105173176	CAUUUUCUCUUAAGAAACUA	3779
54790_1_14811	-	chr4:105173191-105173211	GGUAACUGGCACACAGCAGA	3780
54790_1_14816	-	chr4:105173205-105173225	GAACUUAUCGUUUUGGUAAC	3781
54790_1_14818	-	chr4:105173212-105173232	UGAGUUGGAACUUAUCGUUU	3782
54790_1_14819	-	chr4:105173227-105173247	UGUGGGUUGGAAGAUUGAGU	3783

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_14824	-	chr4:105173261-105173281	AGGGUUUCACGGCCCUAGUG	3784
54790_1_14825	-	chr4:105173269-105173289	GGAGCCGGAGGGUUUCACGG	3785
54790_1_14826	-	chr4:105173270-105173290	UGGAGCCGGAGGGUUUCACG	3786
54790_1_14829	-	chr4:105173286-105173306	UCGAGCACUAGACGGGUGGA	3787
54790_1_14835	-	chr4:105173322-105173342	AAAGUGGUUAUAACCGGUCCG	3788
54790_1_14836	-	chr4:105173326-105173346	CCCAAAAGUGGUUAUAACCGG	3789
54790_1_14838	-	chr4:105173331-105173351	CUCUGCCCCAAAAGUGGUUAUA	3790
54790_1_14849	-	chr4:105173346-105173366	AAACAUA AAAAUCAUCUCUG	3791
54790_1_14852	-	chr4:105173347-105173367	AAAACAUA AAAAUCAUCUCU	3792
54790_1_14863	-	chr4:105173390-105173410	GCCCUCGUGUGGUGGUACGG	3793
54790_1_14864	-	chr4:105173391-105173411	UGCCCUCGUGUGGUGGUACG	3794
54790_1_14867	-	chr4:105173409-105173429	AGGGUUCAUCGACCCUGAUG	3795
54790_1_14869	-	chr4:105173410-105173430	GAGGGUUCAUCGACCCUGAU	3796
54790_1_14871	-	chr4:105173417-105173437	GGAGUCGGAGGGUUCAUCGA	3797
54790_1_14872	-	chr4:105173418-105173438	CGGAGUCGGAGGGUUCAUCG	3798
54790_1_14878	-	chr4:105173457-105173477	GUGACGUUGGAGGUGGAGGA	3799
54790_1_14879	-	chr4:105173458-105173478	AGUGACGUUGGAGGUGGAGG	3800
54790_1_14881	-	chr4:105173482-105173502	CCUCACGUCACCACGUUAGA	3801
54790_1_14885	-	chr4:105173493-105173513	AACGGGUCCGACCUCACGUC	3802
54790_1_14886	-	chr4:105173503-105173523	AGAGGGAGAAAACGGGUCCG	3803
54790_1_14889	-	chr4:105173507-105173527	UCUCAGAGGGAGAAAACGGG	3804
54790_1_14943	-	chr4:105173722-105173742	UAUUUGAAUAAAUGGGUUC	3805
54790_1_14944	-	chr4:105173729-105173749	UAAUAAAUAAUUGAAUAAU	3806
54790_1_14945	-	chr4:105173730-105173750	GUAUAUAUAUUGAAUAAA	3807
54790_1_14966	-	chr4:105173800-105173820	UUAUAUGUCACUUUGUUAAC	3808
54790_1_14989	-	chr4:105173942-105173962	UACAUCAUUUUUGCAUGCAU	3809
54790_1_14990	-	chr4:105173943-105173963	AUACAUCAUUUUUGCAUGCA	3810
54790_1_15001	-	chr4:105174005-105174025	UAUGUUGAUAGGGACAGCUA	3811
54790_1_15006	-	chr4:105174015-105174035	UGUUAUAUAUAUGUUGAUA	3812
54790_1_15009	-	chr4:105174016-105174036	UUGUUAUAUAUAUGUUGAU	3813
54790_1_15018	-	chr4:105174081-105174101	AUAGAACAAAUUGAGGCUUU	3814
54790_1_15019	-	chr4:105174082-105174102	UAUAGAACAAAUUGAGGCUU	3815
54790_1_15021	-	chr4:105174088-105174108	UAUAGCUAUAGAACAAAUUG	3816
54790_1_15040	-	chr4:105174188-105174208	GAUCUAUCAAAUUAAGGGAU	3817
54790_1_15042	-	chr4:105174193-105174213	UUUAAGAUCUAUCAAAUUA	3818
54790_1_15044	-	chr4:105174194-105174214	UUUUAAGAUCUAUCAAAUUA	3819
54790_1_15058	-	chr4:105174271-105174291	CAUAGUCUACUUCUCAAAA	3820
54790_1_15059	-	chr4:105174272-105174292	UCAUAGUCUACUUCUCAAAA	3821
54790_1_15063	-	chr4:105174310-105174330	UAAAUCUUAGGAAAUACUAG	3822
54790_1_15067	-	chr4:105174322-105174342	UUCUAUUCCAAUAAAUCUU	3823
54790_1_15119	-	chr4:105174498-105174518	AAGAGAUUAUAAACUACGUC	3824
54790_1_15133	-	chr4:105174565-105174585	GGGUGUUUUUAAAAGGAACA	3825
54790_1_15138	-	chr4:105174590-105174610	GUACAAAAGGAUGGACCGUG	3826
54790_1_15140	-	chr4:105174596-105174616	UGUCAAGUACAAAAGGAUGG	3827
54790_1_15154	-	chr4:105174680-105174700	GAAGGCAUUCACUCAGGAGG	3828
54790_1_15158	-	chr4:105174705-105174725	CCAAUUUGAGUGUUUUCAUG	3829
54790_1_15159	-	chr4:105174726-105174746	CAGUGACACUUGUGAGGACC	3830
54790_1_15160	-	chr4:105174729-105174749	CAUCAGUGACACUUGUGAGG	3831

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_15174	-	chr4:105174763-105174783	AAGGAAAAGAAGAGGGGGAU	3832
54790_1_15176	-	chr4:105174764-105174784	CAAGGAAAAGAAGAGGGGGA	3833
54790_1_15180	-	chr4:105174786-105174806	ACGAGACUGUAUAAAGUUCU	3834
54790_1_15186	-	chr4:105174825-105174845	UUUAUCAAAAGUGAACUCUCG	3835
54790_1_15192	-	chr4:105174850-105174870	UUAGGGUUUUCAAAUCCGAG	3836
54790_1_15193	-	chr4:105174856-105174876	AAUAUUUUUAGGGUUUUCAAA	3837
54790_1_15201	-	chr4:105174887-105174907	CAUAAAGGGAAGGGAAACCC	3838
54790_1_15202	-	chr4:105174890-105174910	AUCCAUAAGGGGAAGGGAAA	3839
54790_1_15204	-	chr4:105174891-105174911	AAUCCAUAAGGGGAAGGGAA	3840
54790_1_15207	-	chr4:105174909-105174929	CGAUUUUCCCCCGACUUGAA	3841
54790_1_15211	-	chr4:105174920-105174940	GAUACACCUUUCGAUUUUC	3842
54790_1_15212	-	chr4:105174921-105174941	GGAUACACCUUUCGAUUUUC	3843
54790_1_15213	-	chr4:105174922-105174942	GGGAUACACCUUUCGAUUUU	3844
54790_1_15216	-	chr4:105174923-105174943	AGGGAUACACCUUUCGAUUU	3845
54790_1_15223	-	chr4:105174935-105174955	AUAUAAAAGGAAAGGGAUAC	3846
54790_1_15230	-	chr4:105174977-105174997	CGGGGGAUUGCACCUGUCCU	3847
54790_1_15232	-	chr4:105174981-105175001	GAUCCGGGGGAUUGCACCUG	3848
54790_1_15234	-	chr4:105174986-105175006	AAGGGGAUCCGGGGGAUUGC	3849
54790_1_15240	-	chr4:105174999-105175019	GGUCAAAGAGUCAAGGGGA	3850
54790_1_15244	-	chr4:105175035-105175055	GAAACCACUUUGACAUGGGU	3851
54790_1_15250	-	chr4:105175052-105175072	AUAUUAACCAGAGGGAGAA	3852
54790_1_15252	-	chr4:105175065-105175085	GUAAGACAUCGGAUAUUA	3853
54790_1_15254	-	chr4:105175091-105175111	UAUCAUUUCCACACCCUUU	3854
54790_1_15255	-	chr4:105175092-105175112	CUAUCAUUUUCCACACCCUU	3855
54790_1_15261	-	chr4:105175097-105175117	UUAUACUAUCAUUUCCACA	3856
54790_1_15263	-	chr4:105175098-105175118	AUUAUACUAUCAUUUCCAC	3857
54790_1_15266	-	chr4:105175103-105175123	AAAUCAUUAUACUAUCAUUU	3858
54790_1_15267	-	chr4:105175128-105175148	AUUUUCUUUGACGACGUUA	3859
54790_1_15280	-	chr4:105175177-105175197	AUCGUACGGAAUAUUA	3860
54790_1_15297	-	chr4:105175282-105175302	UAUCAAAAAAUUUUCAAG	3861
54790_1_15321	-	chr4:105175389-105175409	ACUAUGAACCGUAAAGAGAA	3862
54790_1_15324	-	chr4:105175402-105175422	ACAUGUGAUACGAACUAUGA	3863
54790_1_15338	-	chr4:105175473-105175493	UUGAAGUUUCUAAAAAGGA	3864
54790_1_15390	-	chr4:105175681-105175701	ACCACAGACUGUAAUUAACC	3865
54790_1_15392	-	chr4:105175682-105175702	AACCACAGACUGUAAUUAAC	3866
54790_1_15394	-	chr4:105175683-105175703	AAACCACAGACUGUAAUUA	3867
54790_1_15396	-	chr4:105175684-105175704	CAAACCACAGACUGUAAUUA	3868
54790_1_15401	-	chr4:105175701-105175721	UCGAGAGACCUCUUCAUCAA	3869
54790_1_15407	-	chr4:105175714-105175734	AACCACAAGAAACUCGAGAG	3870
54790_1_15415	-	chr4:105175733-105175753	AAACCCUGUAAAUAGGACGA	3871
54790_1_15416	-	chr4:105175750-105175770	UAUACGGGUACUCAUAAAA	3872
54790_1_15418	-	chr4:105175751-105175771	UUAUACGGGUACUCAUAAA	3873
54790_1_15445	-	chr4:105175821-105175841	GAUAUCCACAAAAAGGAAG	3874
54790_1_15454	-	chr4:105175837-105175857	AUAAUAAAAACGAGGAGUA	3875
54790_1_15460	-	chr4:105175877-105175897	AGAAUAAACAUACCAAUAC	3876
54790_1_15463	-	chr4:105175886-105175906	UGAGAUGAGAGAAUAAACAU	3877
54790_1_15472	-	chr4:105175937-105175957	CCAGGUCUUAGCAUGUGACG	3878
54790_1_15479	-	chr4:105175958-105175978	AAGACUCCUGUUAAAACGU	3879

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_15484	-	chr4:105175972-105175992	GAAAUAAAGAAUUGAAGACU	3880
54790_1_15502	-	chr4:105176032-105176052	AAAAACGUUCCCACCAGGUG	3881
54790_1_15505	-	chr4:105176040-105176060	AAUUUGUAAAAAACGUUCCC	3882
54790_1_15506	-	chr4:105176043-105176063	UGAAAUUUGUAAAAAACGUU	3883
54790_1_15507	-	chr4:105176044-105176064	UUGAAAUUUGUAAAAAACGU	3884
54790_1_15524	-	chr4:105176108-105176128	GAUUAAAAUAAAAGGAAUAC	3885
54790_1_15536	-	chr4:105176146-105176166	CAUAAAAGAAAUAGUUCAAC	3886
54790_1_15537	-	chr4:105176147-105176167	ACAUAAAAGAAAUAGUUCAA	3887
54790_1_15540	-	chr4:105176148-105176168	CACAUAAAAGAAAUAGUUCA	3888
54790_1_15545	-	chr4:105176177-105176197	AAUUCAUACUACAUUUGACA	3889
54790_1_15557	-	chr4:105176221-105176241	CAGAACAAGAACUAGAAUCG	3890
54790_1_15561	-	chr4:105176254-105176274	CAUCCUUUGUUUCACCAUUC	3891
54790_1_15565	-	chr4:105176261-105176281	UGAAGGUCAUCCUUUGUUUC	3892
54790_1_15568	-	chr4:105176272-105176292	GUAAUCCAUCGUGAAGGUCA	3893
54790_1_15579	-	chr4:105176288-105176308	AAGGAAACAGAAUAAACGUAA	3894
54790_1_15589	-	chr4:105176334-105176354	CUGUCAAAACUAAAGAAGGAG	3895
54790_1_15604	-	chr4:105176392-105176412	AAAAGAAAAAAGACUAGGAA	3896
54790_1_15621	-	chr4:105176473-105176493	GACCAUAUGUCCUUUCACUA	3897
54790_1_15625	-	chr4:105176484-105176504	GAACAAUAACGACCAUAUG	3898
54790_1_15629	-	chr4:105176492-105176512	UUUAAUGUGAACAAAUAAACG	3899
54790_1_15638	-	chr4:105176532-105176552	AGAACCCACGAAUACAUUU	3900
54790_1_15642	-	chr4:105176547-105176567	GUUUUCAUAAAGUAAAGAAC	3901
54790_1_15643	-	chr4:105176548-105176568	UGUUUUCAUAAAGUAAAGAA	3902
54790_1_15645	-	chr4:105176549-105176569	AUGUUUUCAUAAAGUAAAGA	3903
54790_1_15666	-	chr4:105176635-105176655	GAGAAGUAAUAAAUCAAGUG	3904
54790_1_15673	-	chr4:105176692-105176712	GACUUAGAUUUCUAGUUCAA	3905
54790_1_15676	-	chr4:105176693-105176713	UGACUUAGAUUUCUAGUUCA	3906
54790_1_15684	-	chr4:105176722-105176742	AUAGCACGACACAAAAAAUU	3907
54790_1_15700	-	chr4:105176806-105176826	CAAGAGGAGUUUAUGACUCA	3908
54790_1_15707	-	chr4:105176853-105176873	AAUAUCAUUCGAAAUUUCGG	3909
54790_1_15724	-	chr4:105176926-105176946	CCGAGAAAUAAAGAUAAAGUA	3910
54790_1_15731	-	chr4:105176947-105176967	UAUAAAUGUACCCAAACAAA	3911
54790_1_15733	-	chr4:105176948-105176968	AUAUAAAUGUACCCAAACAA	3912
54790_1_15735	-	chr4:105176957-105176977	AGUAAACUAAUAUAAAUGUA	3913
54790_1_15736	-	chr4:105176958-105176978	UAGUAAACUAAUAUAAAUGU	3914
54790_1_15767	-	chr4:105177087-105177107	UAGACACAAUUGUGAGUUA	3915
54790_1_15775	-	chr4:105177116-105177136	AAGUUCAAUUA AAAACGUUU	3916
54790_1_15776	-	chr4:105177117-105177137	UAAGUUCAAUUA AAAACGUU	3917
54790_1_15787	-	chr4:105177146-105177166	AUCAAGACGUAAA AUGUAAA	3918
54790_1_15794	-	chr4:105177176-105177196	AAAAAGGACACAAUAGAAGA	3919
54790_1_15797	-	chr4:105177177-105177197	UAAAAGGACACAAUAGAAG	3920
54790_1_15799	-	chr4:105177200-105177220	GACGGUAUGGUUUCAGUAGA	3921
54790_1_15806	-	chr4:105177244-105177264	AGGAAGUACAUAGCACGGAA	3922
54790_1_15834	-	chr4:105177347-105177367	CGUUUAUUA AAAAGGUAGAC	3923
54790_1_15871	-	chr4:105177473-105177493	GAAACCACUCAACAGACAAG	3924
54790_1_15877	-	chr4:105177490-105177510	ACUGUGAACACAUAGAAGAA	3925
54790_1_15893	-	chr4:105177583-105177603	GGUAAGAUUGUCCAUAACAUC	3926
54790_1_15895	-	chr4:105177593-105177613	GACUGAAGUCGGUAAGAUUG	3927

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_15901	-	chr4:105177629-105177649	AGGUGUAAGAGUGGUCGUGA	3928
54790_1_15906	-	chr4:105177662-105177682	AAGAAUGGUCGUUACUUACU	3929
54790_1_15921	-	chr4:105177749-105177769	CGCGAUAAACGACUUAGUAUA	3930
54790_1_15923	-	chr4:105177750-105177770	UCGCGAUAAACGACUUAGUAU	3931
54790_1_15930	-	chr4:105177773-105177793	UUCAAAAGUUCAGGUAUGGU	3932
54790_1_15933	-	chr4:105177800-105177820	CACUCGAUGACACGGGCCGG	3933
54790_1_15936	-	chr4:105177805-105177825	GUCCGCACUCGAUGACACGG	3934
54790_1_15938	-	chr4:105177824-105177844	AGGGUUUCACGACGUUAAUG	3935
54790_1_15939	-	chr4:105177849-105177869	GAGUUUACUAGGUGGACGGA	3936
54790_1_15940	-	chr4:105177850-105177870	GGAGUUUACUAGGUGGACGG	3937
54790_1_15948	-	chr4:105177887-105177907	UGGUACCCUAAAGUGGUCCG	3938
54790_1_15949	-	chr4:105177891-105177911	AAAGUGGUACCCUAAAGUGG	3939
54790_1_15952	-	chr4:105177902-105177922	AUCUCGACCCCAAAGUGGUA	3940
54790_1_15954	-	chr4:105177903-105177923	CAUCUCGACCCCAAAGUGGU	3941
54790_1_15961	-	chr4:105177914-105177934	AACAUAGAAAUCAUCUCGAC	3942
54790_1_15962	-	chr4:105177915-105177935	AAACAUAGAAAUCAUCUCGA	3943
54790_1_15964	-	chr4:105177916-105177936	AAAACAUAGAAAUCAUCUCG	3944
54790_1_15968	-	chr4:105177964-105177984	AGGGAUCAUCGACUCUAAUG	3945
54790_1_15971	-	chr4:105178012-105178032	GUGACGUUGGAGGCGGAGGA	3946
54790_1_15972	-	chr4:105178013-105178033	AGUGACGUUGGAGGCGGAGG	3947
54790_1_15974	-	chr4:105178048-105178068	AGUGAGUCCGACCUCACGUU	3948
54790_1_15979	-	chr4:105178058-105178078	AAAACGAGACAGUGAGUCCG	3949
54790_1_15981	-	chr4:105178062-105178082	CCUCAAAACGAGACAGUGAG	3950
54790_1_15998	-	chr4:105178083-105178103	AAAACGAAAAAAAAAACUCU	3951
54790_1_16016	-	chr4:105178133-105178153	UUACACACGUCCAAAAAUAC	3952
54790_1_16018	-	chr4:105178144-105178164	UCGACAAUUUGUUACACACG	3953
54790_1_16025	-	chr4:105178178-105178198	AGAACUAACGUGGGUUCAAA	3954
54790_1_16029	-	chr4:105178204-105178224	AAAUAGGUGAGUUUAUAAU	3955
54790_1_16033	-	chr4:105178238-105178258	GACUUAUUUAUAGAAUGUAG	3956
54790_1_16057	-	chr4:105178339-105178359	GUAUGUCAUAAAUCGGAAAA	3957
54790_1_16063	-	chr4:105178365-105178385	AAAGGCCUACAGUAUAUCA	3958
54790_1_16070	-	chr4:105178381-105178401	GAGGUAUUAAAACCGAAAAG	3959
54790_1_16076	-	chr4:105178390-105178410	AAA AUGACAGAGGU AUUAAA	3960
54790_1_16081	-	chr4:105178426-105178446	ACGGAUAUGUAAGGAGGGAG	3961
54790_1_16089	-	chr4:105178497-105178517	ACCUGUUUACAU AUUACUGU	3962
54790_1_16093	-	chr4:105178517-105178537	CACCAAUGUAGGAUGCACAA	3963
54790_1_16099	-	chr4:105178536-105178556	UGUAAUCCCAAGUGAUAAACC	3964
54790_1_16100	-	chr4:105178539-105178559	AA AUGUAAUCCCAAGUGAU A	3965
54790_1_16101	-	chr4:105178550-105178570	UUUGGGGU AUCAA AUGUAAU	3966
54790_1_16102	-	chr4:105178551-105178571	GUUUGGGGU AUCAA AUGUAA	3967
54790_1_16112	-	chr4:105178620-105178640	UAGUUGUAGGGU AUGGUCUC	3968
54790_1_16136	-	chr4:105178759-105178779	AAUAAUAUGAAAUUCAA AAU	3969
54790_1_16138	-	chr4:105178760-105178780	UAAUAAUAUGAAAUUCA AAA	3970
54790_1_16171	-	chr4:105178880-105178900	AAAU AUUAAUGAGUCAGAG	3971
54790_1_16192	-	chr4:105179022-105179042	GACUACCAAAAU AUUCACAA	3972
54790_1_16194	-	chr4:105179038-105179058	ACUCAAGAGUACUCUAGACU	3973
54790_1_16200	-	chr4:105179063-105179083	GGGUACGACAAGAGUAGUAU	3974
54790_1_16202	-	chr4:105179064-105179084	GGGGUACGACAAGAGUAGUA	3975

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_16205	-	chr4:105179094-105179114	ACCUUCAUUAACCUAGUACC	3976
54790_1_16206	-	chr4:105179095-105179115	CACCUUCAUUAACCUAGUAC	3977
54790_1_16208	-	chr4:105179096-105179116	CCACCUUCAUUAACCUAGUA	3978
54790_1_16210	-	chr4:105179097-105179117	UCCACCUUCAUUAACCUAGU	3979
54790_1_16212	-	chr4:105179104-105179124	UCUCUGGUCCACCUUCAUUA	3980
54790_1_16214	-	chr4:105179114-105179134	CACAGUCCGUCUCUGGUCC	3981
54790_1_16217	-	chr4:105179117-105179137	GUACACAGUCCGUCUCUGG	3982
54790_1_16219	-	chr4:105179128-105179148	AGGUAUUAUGGGUACACAGU	3983
54790_1_16229	-	chr4:105179199-105179219	GUUUUAUCACACUAUACCAA	3984
54790_1_16230	-	chr4:105179204-105179224	ACAUAGUUUUAUCACACUAU	3985
54790_1_16238	-	chr4:105179277-105179297	AACCAGAAAUUGGAAAUGG	3986
54790_1_16241	-	chr4:105179280-105179300	CCUAACCAGAAAUUGGAAA	3987
54790_1_16246	-	chr4:105179287-105179307	UAUUUUUCCUAACCAGAAU	3988
54790_1_16252	-	chr4:105179319-105179339	AGGUUGUGGGUCAAUUAAGG	3989
54790_1_16254	-	chr4:105179322-105179342	ACAAGGUUGUGGGUCAAUUA	3990
54790_1_16260	-	chr4:105179332-105179352	UUCAUUGCAAACAAGGUUGU	3991
54790_1_16262	-	chr4:105179333-105179353	CUUCAUUGCAAACAAGGUUG	3992
54790_1_16265	-	chr4:105179339-105179359	UUGAUUCUUCAUUGCAAACA	3993
54790_1_16274	-	chr4:105179407-105179427	AUUAUGCCCAUGGACACUCA	3994
54790_1_16276	-	chr4:105179417-105179437	AGGCAACUGAAUUAUGCCCA	3995
54790_1_16282	-	chr4:105179437-105179457	GUAUCAUUGGCAUUGAAUGA	3996
54790_1_16288	-	chr4:105179450-105179470	UGUAGGCUUUGCAGUAUCAU	3997
54790_1_16290	-	chr4:105179467-105179487	GGUACAUGAAUUUGCCUUGU	3998
54790_1_16292	-	chr4:105179488-105179508	AAAGGAUGGAGUCUGUCUGU	3999
54790_1_16296	-	chr4:105179502-105179522	GAAUAGUUUGAGAAAAGGA	4000
54790_1_16302	-	chr4:105179506-105179526	UCUUGAAUAGUUUGAGAAA	4001
54790_1_16320	-	chr4:105179568-105179588	UUUCAUUUUUUGAGGAUAGA	4002
54790_1_16321	-	chr4:105179576-105179596	AGGAUAUUUUUCAUUUUUUG	4003
54790_1_16326	-	chr4:105179596-105179616	CACUCAUUUCCCAAUGAAG	4004
54790_1_16335	-	chr4:105179673-105179693	AUUAUCAGAAAGCAGGUCAG	4005
54790_1_16337	-	chr4:105179680-105179700	GUCAUGCAUUAUCAGAAAGC	4006
54790_1_16345	-	chr4:105179726-105179746	AUACGGUCCAGUCCCAUGUG	4007
54790_1_16346	-	chr4:105179734-105179754	AUCACCAAUACGGUCCAGU	4008
54790_1_16347	-	chr4:105179735-105179755	GAUCACCAAUACGGUCCAG	4009
54790_1_16350	-	chr4:105179740-105179760	UAUGAGAUCACCAAUACGG	4010
54790_1_16351	-	chr4:105179751-105179771	CUUUACUGAAUUAUGAGAUC	4011
54790_1_16355	-	chr4:105179804-105179824	UGACAUCUAUCAGAAGGUCA	4012
54790_1_16357	-	chr4:105179805-105179825	GUGACAUCUAUCAGAAGGUC	4013
54790_1_16361	-	chr4:105179832-105179852	UAGGAAUGCAGCUGCUUUAG	4014
54790_1_16366	-	chr4:105179851-105179871	AAACUUAUCAUGCCUCACU	4015
54790_1_16368	-	chr4:105179876-105179896	AUACUCCAGAACCUAAUAGU	4016
54790_1_16370	-	chr4:105179877-105179897	AAUACUCCAGAACCUAAUAG	4017
54790_1_16377	-	chr4:105179910-105179930	GCUAGAAAAACUUUCCUCUU	4018
54790_1_16378	-	chr4:105179911-105179931	UGCUAGAAAAACUUUCCUCU	4019
54790_1_16388	-	chr4:105179981-105180001	ACAAAUAGAACAACCCUUAGU	4020
54790_1_16390	-	chr4:105180010-105180030	GAAAAAAAACAGUGAAAGAA	4021
54790_1_16393	-	chr4:105180011-105180031	AGAAAAAAAACAGUGAAAGA	4022
54790_1_16399	-	chr4:105180054-105180074	CAACAGCCAGCUGACCAGAA	4023

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_16403	-	chr4:105180078-105180098	GAAAGUGUCAUUUCUAUGAU	4024
54790_1_16411	-	chr4:105180130-105180150	AUGAGAAACAAAGUGAAGGC	4025
54790_1_16415	-	chr4:105180134-105180154	UUGGAUGAGAAACAAAGUGA	4026
54790_1_16423	-	chr4:105180153-105180173	GAAAGUUUUGUCAUUGAUUU	4027
54790_1_16431	-	chr4:105180194-105180214	CCAAGUUGACUCAGGUUCAU	4028
54790_1_16433	-	chr4:105180202-105180222	CCUUUAUGCCAAGUUGACUC	4029
54790_1_16446	-	chr4:105180273-105180293	UCACUGAGCAAAGUGGAGUU	4030
54790_1_16450	-	chr4:105180280-105180300	AAUGUUAUCACUGAGCAAAG	4031
54790_1_16460	-	chr4:105180324-105180344	UGAGGAAGUAUUUUUAGACU	4032
54790_1_16467	-	chr4:105180342-105180362	GACUGAGAUUUUGGAAUAUG	4033
54790_1_16471	-	chr4:105180351-105180371	UGUAUUAAUGACUGAGAUUU	4034
54790_1_16479	-	chr4:105180400-105180420	CUACAACAGCCGAGAAGCAC	4035
54790_1_16497	-	chr4:105180493-105180513	AUAAACAUAUUUUUGCUUCC	4036
54790_1_16511	-	chr4:105180562-105180582	AGAAUAUUUACGUUUUAGAA	4037
54790_1_16516	-	chr4:105180585-105180605	GUUUGUGACCAUGGAGAUCA	4038
54790_1_16520	-	chr4:105180594-105180614	UGAAAUACUGUUUGUGACCA	4039
54790_1_16526	-	chr4:105180634-105180654	UUUUUUUUUUUUUGAUAAAA	4040
54790_1_16531	-	chr4:105180682-105180702	CACGAAGACGUAGGGUCGGA	4041
54790_1_16532	-	chr4:105180683-105180703	GCACGAAGACGUAGGGUCGG	4042
54790_1_16535	-	chr4:105180712-105180732	UCCUCCACCUCCAACGUCAC	4043
54790_1_16538	-	chr4:105180723-105180743	GCGAACUUGAGUCCUCCACC	4044
54790_1_16539	-	chr4:105180726-105180746	UUAGCGAACUUGAGUCCUCC	4045
54790_1_16542	-	chr4:105180729-105180749	CUCUUAGCGAACUUGAGUCC	4046
54790_1_16544	-	chr4:105180732-105180752	GUCCUCUUAGCGAACUUGAG	4047
54790_1_16549	-	chr4:105180751-105180771	CGAUGGGCCGUCCGACUCCG	4048
54790_1_16552	-	chr4:105180755-105180775	AGAUCGAUGGGCCGUCCGAC	4049
54790_1_16554	-	chr4:105180761-105180781	ACAUUAAGAUCGAUGGGCCG	4050
54790_1_16555	-	chr4:105180765-105180785	ACGGACAUAUAAGAUCGAUGG	4051
54790_1_16557	-	chr4:105180792-105180812	UGUCUUAUUCGGUCCACACC	4052
54790_1_16558	-	chr4:105180795-105180815	UUAUGUCUUAUUCGGUCCAC	4053
54790_1_16559	-	chr4:105180800-105180820	GAUUUUUAUGUCUUAUUCGG	4054
54790_1_16563	-	chr4:105180848-105180868	AGUCCUCAAGUUCUGGUCAG	4055
54790_1_16565	-	chr4:105180866-105180886	ACCCACCUAGUGGACUCCAG	4056
54790_1_16567	-	chr4:105180871-105180891	ACGCCACCCACCUAGUGGAC	4057
54790_1_16571	-	chr4:105180882-105180902	GAAACCCUCCGACGCCACCC	4058
54790_1_16574	-	chr4:105180885-105180905	CGUGAAACCCUCCGACGCCA	4059
54790_1_16575	-	chr4:105180886-105180906	UCGUGAAACCCUCCGACGCC	4060
54790_1_16577	-	chr4:105180889-105180909	AGGUCGUGAAACCCUCCGAC	4061
54790_1_16578	-	chr4:105180895-105180915	ACAUUAAGGUCGUGAAACCC	4062
54790_1_16580	-	chr4:105180898-105180918	CGGACAUAUAAGGUCGUGAAA	4063
54790_1_16581	-	chr4:105180899-105180919	GCGGACAUAUAAGGUCGUGAA	4064
54790_1_16587	-	chr4:105180939-105180959	GAGUUA AAAAGAAAGAUAAA	4065
54790_1_16588	-	chr4:105180940-105180960	UGAGUUA AAAAGAAAGAUAAA	4066
54790_1_16595	-	chr4:105180966-105180986	CACAUGGAGGGAUUAUUUUG	4067
54790_1_16599	-	chr4:105180978-105180998	GGAAGGCAACUUCACAUGGA	4068
54790_1_16601	-	chr4:105180979-105180999	GGGAAGGCAACUUCACAUGG	4069
54790_1_16604	-	chr4:105180982-105181002	UUAGGGAAGGCAACUUCACA	4070
54790_1_16606	-	chr4:105180995-105181015	GGACAGUACAUAUUAGGGA	4071

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_16608	-	chr4:105180999-105181019	ACUAGGACAGUACAUAAUUA	4072
54790_1_16610	-	chr4:105181000-105181020	AACUAGGACAGUACAUAAUU	4073
54790_1_16613	-	chr4:105181016-105181036	CAAGGAAUGAAGAUUAAACU	4074
54790_1_16621	-	chr4:105181034-105181054	UGGUUUUAUAGAGGCAAACA	4075
54790_1_16627	-	chr4:105181043-105181063	UUUUAAACUUGGUUUUAUAG	4076
54790_1_16629	-	chr4:105181054-105181074	UCAGAGACUAUUUUUAAACU	4077
54790_1_16643	-	chr4:105181133-105181153	UAGUAGAAACUUUGUUACAA	4078
54790_1_16646	-	chr4:105181165-105181185	AUAUAGAUCGUAGCUGAGAA	4079
54790_1_16649	-	chr4:105181191-105181211	UAUAACAAAAGACAUGGCCA	4080
54790_1_16652	-	chr4:105181197-105181217	UGUGUGUAUAACAAAAGACA	4081
54790_1_16658	-	chr4:105181264-105181284	AAAAGCAUAUUGUGACUAAA	4082
54790_1_16661	-	chr4:105181297-105181317	AUCAAGAAAUUCCCAGGAAA	4083
54790_1_16665	-	chr4:105181303-105181323	AAAUAUCAAGAAAUUCCC	4084
54790_1_16674	-	chr4:105181362-105181382	GAAAAGCACUAUUUCUGCAG	4085
54790_1_16679	-	chr4:105181402-105181422	UAUCACCAGCUCUUCUAAGA	4086
54790_1_16682	-	chr4:105181430-105181450	AACCAAGAUAAAAGAAGAGU	4087
54790_1_16694	-	chr4:105181486-105181506	UUGAUUGUCCUGUGUUAAAA	4088
54790_1_16697	-	chr4:105181487-105181507	GUUGAUUGUCCUGUGUUAAA	4089
54790_1_16701	-	chr4:105181518-105181538	UAUCUGAAUCUAAAGAAAGA	4090
54790_1_16733	-	chr4:105181612-105181632	GGGGCAGGGGUUACAGAUUGU	4091
54790_1_16735	-	chr4:105181625-105181645	GUAAAAAAUAUUUGGGGCAG	4092
54790_1_16736	-	chr4:105181626-105181646	AGUAAAAAAUAUUUGGGGCA	4093
54790_1_16737	-	chr4:105181627-105181647	AAGUAAAAAAUAUUUGGGGC	4094
54790_1_16740	-	chr4:105181631-105181651	GCAUAAGUAAAAAAUAUUUG	4095
54790_1_16741	-	chr4:105181632-105181652	AGCAUAAGUAAAAAAUAUUU	4096
54790_1_16743	-	chr4:105181633-105181653	UAGCAUAAGUAAAAAAUAUU	4097
54790_1_16756	-	chr4:105181718-105181738	CAUCUUCGAUUUCCUAGAAG	4098
54790_1_16758	-	chr4:105181719-105181739	ACAUCUUCGAUUUCCUAGAA	4099
54790_1_16760	-	chr4:105181720-105181740	CACAUCUUCGAUUUCCUAGA	4100
54790_1_16766	-	chr4:105181748-105181768	AACUCAUUAUCACAUUAAAC	4101
54790_1_16783	-	chr4:105181843-105181863	CAAUCAUACUUAAGGUUGGA	4102
54790_1_16784	-	chr4:105181844-105181864	UCAAUCAUACUUAAGGUUGG	4103
54790_1_16787	-	chr4:105181847-105181867	AAUUCAAUCAUACUUAAGGU	4104
54790_1_16789	-	chr4:105181851-105181871	UAUAAAUUCAAUCAUACUUA	4105
54790_1_16800	-	chr4:105181951-105181971	UAUAUAAAAAUGAAAGUAUG	4106
54790_1_16821	-	chr4:105182073-105182093	UAGCCAGAGAACAAAUGAUA	4107
54790_1_16824	-	chr4:105182074-105182094	GUAGCCAGAGAACAAAUGAU	4108
54790_1_16832	-	chr4:105182099-105182119	AAAAAUGUAACUAUUAACUU	4109
54790_1_16838	-	chr4:105182124-105182144	UGCAAAUUACCAUUUGUCAC	4110
54790_1_16848	-	chr4:105182180-105182200	UUUGCAUGAUUCUUAUAAUA	4111
54790_1_16849	-	chr4:105182181-105182201	GUUUGCAUGAUUCUUAUAAUA	4112
54790_1_16852	-	chr4:105182206-105182226	CACCUGCUGCCUAUCAGCUC	4113
54790_1_16858	-	chr4:105182268-105182288	AGCAGAAUUACUAGCUACCU	4114
54790_1_16862	-	chr4:105182292-105182312	GAAGGAGCUAUAGUGGCUUA	4115
54790_1_16863	-	chr4:105182293-105182313	GGAAGGAGCUAUAGUGGCUU	4116
54790_1_16865	-	chr4:105182299-105182319	UAAUGGGGAAGGAGCUAUAG	4117
54790_1_16867	-	chr4:105182310-105182330	GACCCAGGGAGUAAUGGGGA	4118
54790_1_16870	-	chr4:105182314-105182334	GGUAGACCCAGGGAGUAAUG	4119

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_16872	-	chr4:105182315-105182335	GGGUAGACCCAGGGAGUAAU	4120
54790_1_16874	-	chr4:105182316-105182336	UGGGUAGACCCAGGGAGUAA	4121
54790_1_16876	-	chr4:105182324-105182344	CAGGAUGGUGGGUAGACCCA	4122
54790_1_16878	-	chr4:105182325-105182345	GCAGGAUGGUGGGUAGACCC	4123
54790_1_16885	-	chr4:105182335-105182355	UAUUCUAGCUGCAGGAUGGU	4124
54790_1_16886	-	chr4:105182336-105182356	UUAUUCUAGCUGCAGGAUGG	4125
54790_1_16888	-	chr4:105182339-105182359	UUAUUAUUCUAGCUGCAGGA	4126
54790_1_16889	-	chr4:105182343-105182363	CCAUUUAUUAUUCUAGCUGC	4127
54790_1_16891	-	chr4:105182376-105182396	GUGCUGGAGGAGGAUCCUAG	4128
54790_1_16895	-	chr4:105182386-105182406	UUGAGACAUAGUGCUGGAGG	4129
54790_1_16898	-	chr4:105182389-105182409	CCGUUGAGACAUAGUGCUGG	4130
54790_1_16900	-	chr4:105182392-105182412	GGUCCGUUGAGACAUAGUGC	4131
54790_1_16906	-	chr4:105182410-105182430	UAAAUUGUCGAGUAUACAGG	4132
54790_1_16909	-	chr4:105182448-105182468	AGACGUCUCCCUUACCACAG	4133
54790_1_16919	-	chr4:105182513-105182533	AAGUGUCUACUUUUAUCAUA	4134
54790_1_16927	-	chr4:105182572-105182592	ACUCUGCAGUUAUGUUUACC	4135
54790_1_16936	-	chr4:105182598-105182618	UUAAGAUUUCAAAACGUAU	4136
54790_1_16943	-	chr4:105182639-105182659	CUAAUCUAUUUCUAAUAGAA	4137
54790_1_16949	-	chr4:105182672-105182692	UCAUUCUAAAAAUUGAAACA	4138
54790_1_16967	-	chr4:105182796-105182816	AAUUCUAAUGCUUAAUGGGA	4139
54790_1_16969	-	chr4:105182800-105182820	UAAAAAUUCUAAUGCUUAAU	4140
54790_1_16971	-	chr4:105182801-105182821	AUAAAAAUUCUAAUGCUUAA	4141
54790_1_16974	-	chr4:105182831-105182851	AUCAUGAAUAUAAACAUCAA	4142
54790_1_16980	-	chr4:105182874-105182894	CAUAUGACCUAUUAUGAGCUA	4143
54790_1_16987	-	chr4:105182908-105182928	AGCCCAAUAUCUUCAUCUA	4144
54790_1_17002	-	chr4:105182973-105182993	UACAAUUUCUUCAAAUGGA	4145
54790_1_17004	-	chr4:105182977-105182997	ACCUUACAAUUUCUUCAAA	4146
54790_1_17013	-	chr4:105183014-105183034	AUUUUGGGGGGAUAAGUAUU	4147
54790_1_17019	-	chr4:105183026-105183046	UUUAUUUUUCGUUUUUGGG	4148
54790_1_17021	-	chr4:105183027-105183047	UUUUUAUUUUUCGUUUUUGG	4149
54790_1_17023	-	chr4:105183028-105183048	AUUUUAUUUUUCGUUUUUG	4150
54790_1_17024	-	chr4:105183029-105183049	GAUUUUAUUUUUCGUUUUU	4151
54790_1_17026	-	chr4:105183030-105183050	UGAUUUUAUUUUUCGUUUU	4152
54790_1_17041	-	chr4:105183117-105183137	CAGAUUGAGGAUCAUAAAC	4153
54790_1_17044	-	chr4:105183130-105183150	UUUAAAACAGCCACAGAUUG	4154
54790_1_17051	-	chr4:105183184-105183204	GAGUAAUGAGUCUACUACCA	4155
54790_1_17056	-	chr4:105183206-105183226	AAAUUGAUGUAAUGGUUUCUG	4156
54790_1_17059	-	chr4:105183207-105183227	AAAUGAUGUAAUGGUUUCU	4157
54790_1_17060	-	chr4:105183208-105183228	CAAAUGAUGUAAUGGUUUC	4158
54790_1_17065	-	chr4:105183215-105183235	AAUAUUACAAAUGAUGUAA	4159
54790_1_17086	-	chr4:105183346-105183366	UGUGAUUUUAAGUUUAUAAA	4160
54790_1_17093	-	chr4:105183389-105183409	CACAAGCAAAUUAUAUUAA	4161
54790_1_17097	-	chr4:105183420-105183440	AAAGAGUUAUUGAAAUGAAU	4162
54790_1_17104	-	chr4:105183445-105183465	UUGAGAUAAAAAUUAUAUAU	4163
54790_1_17120	-	chr4:105183501-105183521	AGACAAGGUUGGGUCGAAAU	4164
54790_1_17127	-	chr4:105183559-105183579	GGCUAGUGAAUCCCUUUGAC	4165
54790_1_17131	-	chr4:105183568-105183588	CUAGAACUCGGCUAGUGAAU	4166
54790_1_17134	-	chr4:105183569-105183589	ACUAGAACUCGGCUAGUGAA	4167

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_17141	-	chr4:105183625-105183645	UGUUUCAUAUUUAAUUAGAA	4168
54790_1_17142	-	chr4:105183626-105183646	UUGUUUCAUAUUUAAUUAGA	4169
54790_1_17147	-	chr4:105183662-105183682	CACAGGCAAACUAAGGGGGU	4170
54790_1_17148	-	chr4:105183666-105183686	AACCCACAGGCAAACUAAGG	4171
54790_1_17149	-	chr4:105183667-105183687	AAACCCACAGGCAAACUAAG	4172
54790_1_17151	-	chr4:105183668-105183688	UAAACCCACAGGCAAACUAA	4173
54790_1_17153	-	chr4:105183669-105183689	AUAAACCCACAGGCAAACUA	4174
54790_1_17156	-	chr4:105183679-105183699	UGUAACUCCAUAACCCAC	4175
54790_1_17165	-	chr4:105183731-105183751	CAAUAAUUCUAUUGGGAGCU	4176
54790_1_17167	-	chr4:105183738-105183758	UACAGGGCAAUAAUUCUAUU	4177
54790_1_17168	-	chr4:105183739-105183759	CUACAGGGCAAUAAUUCUAU	4178
54790_1_17174	-	chr4:105183754-105183774	UAUUUGCGCGGCUGACUACA	4179
54790_1_17175	-	chr4:105183755-105183775	GUAUUUGCGCGGCUGACUAC	4180
54790_1_17179	-	chr4:105183766-105183786	UAUUUGUGAUUGUAUUUGCG	4181
54790_1_17187	-	chr4:105183789-105183809	UUCUUCACACAAGGAACUUC	4182
54790_1_17190	-	chr4:105183798-105183818	AUUUUCUUUUUCUUCACACA	4183
54790_1_17200	-	chr4:105183853-105183873	GGGAAGAAAGGGGCAAAGAA	4184
54790_1_17202	-	chr4:105183863-105183883	GGAGUGAAAGGGGAAGAAAG	4185
54790_1_17203	-	chr4:105183864-105183884	AGGAGUGAAAGGGGAAGAAA	4186
54790_1_17204	-	chr4:105183865-105183885	AAGGAGUGAAAGGGGAAGAA	4187
54790_1_17208	-	chr4:105183873-105183893	GGAGAAGAAAGGAGUGAAAG	4188
54790_1_17210	-	chr4:105183874-105183894	AGGAGAAGAAAGGAGUGAAA	4189
54790_1_17213	-	chr4:105183875-105183895	UAGGAGAAGAAAGGAGUGAA	4190
54790_1_17218	-	chr4:105183884-105183904	CAAGUAGUAUAGGAGAAGAA	4191
54790_1_17225	-	chr4:105183894-105183914	CUAGAAAUUUCAAGUAGUAU	4192
54790_1_17234	-	chr4:105183934-105183954	ACUUACCAUUCCUAACAUC	4193
54790_1_17246	-	chr4:105184003-105184023	UGAAAAGCCUCUUAAGGGUA	4194
54790_1_17248	-	chr4:105184008-105184028	AACUUUGAAAAGCCUCUUA	4195
54790_1_17249	-	chr4:105184009-105184029	UAACUUUGAAAAGCCUCUUA	4196
54790_1_17252	-	chr4:105184047-105184067	GUCAGAGACUGGGCCAAUGA	4197
54790_1_17256	-	chr4:105184057-105184077	GACCUCACUGGUCAGAGACU	4198
54790_1_17257	-	chr4:105184058-105184078	UGACCUCACUGGUCAGAGAC	4199
54790_1_17260	-	chr4:105184069-105184089	UGGCUAUACUUGACCUCAC	4200
54790_1_17265	-	chr4:105184089-105184109	UUUUCACGACAUUCUGACAC	4201
54790_1_17279	-	chr4:105184189-105184209	GAUAUUUUUAAAAACCAAGA	4202
54790_1_17289	-	chr4:105184231-105184251	AAAAUAAAAAGAAGUUAUGA	4203
54790_1_17291	-	chr4:105184232-105184252	GAAAAUAAAAAGAAGUUAUG	4204
54790_1_17303	-	chr4:105184294-105184314	GGUACAGGUAAUAAUUCACA	4205
54790_1_17304	-	chr4:105184309-105184329	CACUGGAACAUGAGAGGUAC	4206
54790_1_17305	-	chr4:105184315-105184335	ACCAAACACUGGAACAUGAG	4207
54790_1_17312	-	chr4:105184326-105184346	AUUAUUUAAGAACCAAACAC	4208
54790_1_17325	-	chr4:105184408-105184428	AUAACUACGAUAGCCAAACA	4209
54790_1_17330	-	chr4:105184455-105184475	AAACAAGCAUACACCAUAUG	4210
54790_1_17340	-	chr4:105184529-105184549	UCCUCCUAACAUAGACAAAG	4211
54790_1_17356	-	chr4:105184641-105184661	UGUCAGCUACUUGGCAGUGA	4212
54790_1_17359	-	chr4:105184650-105184670	AUUUCAGAAUGUCAGCUACU	4213
54790_1_17362	-	chr4:105184680-105184700	CCAACUGUACAGUGCCUAAA	4214
54790_1_17365	-	chr4:105184681-105184701	UCCAACUGUACAGUGCCUAA	4215

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_17373	-	chr4:105184797-105184817	AGCACGUUACUCACCUCAGC	4216
54790_1_17378	-	chr4:105184832-105184852	AGGUUUAAAUGGGAUGAGAC	4217
54790_1_17383	-	chr4:105184842-105184862	GUUCUCCUCCAGGUUUAAAU	4218
54790_1_17385	-	chr4:105184843-105184863	GGUUCUCCUCCAGGUUUAAA	4219
54790_1_17389	-	chr4:105184852-105184872	GCUUGAUGUGGUUCUCCUCC	4220
54790_1_17392	-	chr4:105184864-105184884	GGCUGCUUCUGUGCUUGAUG	4221
54790_1_17397	-	chr4:105184885-105184905	UUCCUGUUGAAAUGCUGCUU	4222
54790_1_17406	-	chr4:105184943-105184963	GUGAUAAUAGUACACCUUCA	4223
54790_1_17418	-	chr4:105185007-105185027	AACACUCCGUUACAAAAAA	4224
54790_1_17419	-	chr4:105185008-105185028	AAACACUCCGUUACAAAAA	4225
54790_1_17434	-	chr4:105185084-105185104	AUAUAAGAAUCCUCCAUUUG	4226
54790_1_17435	-	chr4:105185085-105185105	UAUAUAAGAAUCCUCCAUUU	4227
54790_1_17437	-	chr4:105185086-105185106	UUAUAUAAGAAUCCUCCAUU	4228
54790_1_17441	-	chr4:105185113-105185133	UGAAUAUAUCAUUACAAGCU	4229
54790_1_17448	-	chr4:105185184-105185204	AAGUUUUCGUUCAAAAUGA	4230
54790_1_17461	-	chr4:105185242-105185262	AAACAUUUCAUUUUGGGGAA	4231
54790_1_17464	-	chr4:105185247-105185267	CAGUGAAACAUUUCAUUUUG	4232
54790_1_17465	-	chr4:105185248-105185268	UCAGUGAAACAUUUCAUUUU	4233
54790_1_17467	-	chr4:105185249-105185269	UUCAGUGAAACAUUUCAUUU	4234
54790_1_17473	-	chr4:105185275-105185295	CAUGGCCUCCACAAGCUUGU	4235
54790_1_17478	-	chr4:105185293-105185313	CUCUUAUUCAACAUGCUUCA	4236
54790_1_17483	-	chr4:105185331-105185351	CACACCCUUUGUGGGUGGCA	4237
54790_1_17484	-	chr4:105185332-105185352	GCACACCCUUUGUGGGUGGC	4238
54790_1_17488	-	chr4:105185336-105185356	CUUAGCACACCCUUUGUGGG	4239
54790_1_17490	-	chr4:105185339-105185359	UACCUUAGCACACCCUUUGU	4240
54790_1_17491	-	chr4:105185340-105185360	UUACCUUAGCACACCCUUUG	4241
54790_1_17500	-	chr4:105185401-105185421	AAUAGCUAAAAUUUAUUGAA	4242
54790_1_17515	-	chr4:105185482-105185502	CCAGUCACUGUGUUUUAGAA	4243
54790_1_17518	-	chr4:105185503-105185523	GUCCGUACUCGGUGACGCGG	4244
54790_1_17520	-	chr4:105185522-105185542	AGGCUUUCACGACCCUAAUG	4245
54790_1_17521	-	chr4:105185530-105185550	GGAGCCGGAGGCUUUCACGA	4246
54790_1_17522	-	chr4:105185531-105185551	UGGAGCCGGAGGCUUUCACG	4247
54790_1_17526	-	chr4:105185547-105185567	UGGAGCACUAGGCGUAUGGA	4248
54790_1_17530	-	chr4:105185583-105185603	AAAGUGGCACAAUCGGUCCU	4249
54790_1_17531	-	chr4:105185587-105185607	CCCUAAAGUGGCACAAUCGG	4250
54790_1_17541	-	chr4:105185607-105185627	AAACAUAAAAAUCAUCUCUG	4251
54790_1_17542	-	chr4:105185608-105185628	AAAACAUAAAAAUCAUCUCU	4252
54790_1_17547	-	chr4:105185636-105185656	GUCCGCGUACGGGGGUGCGG	4253
54790_1_17548	-	chr4:105185655-105185675	AGGACUCAUCGACCCUAAUG	4254
54790_1_17549	-	chr4:105185663-105185683	GGAGUCGGAGGACUCAUCGA	4255
54790_1_17550	-	chr4:105185664-105185684	CGGAGUCGGAGGACUCAUCG	4256
54790_1_17556	-	chr4:105185703-105185723	GUGACGUUCGAGGCGGAGGG	4257
54790_1_17558	-	chr4:105185728-105185748	CCUCACGUCACCACGCUAGA	4258
54790_1_17559	-	chr4:105185739-105185759	AUCGGGUCCGACCUCACGUC	4259
54790_1_17562	-	chr4:105185749-105185769	AGAACGAGACAUCGGGUCCG	4260
54790_1_17564	-	chr4:105185753-105185773	UCUCAGAACGAGACAUCGGG	4261
54790_1_17613	-	chr4:105185968-105185988	AAGGUUUCACGACCCUAAUG	4262
54790_1_17614	-	chr4:105185976-105185996	GCAGUUGGAAGGUUUCACGA	4263

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_17616	-	chr4:105185977-105185997	CGCAGUUGGAAGGUUUCACG	4264
54790_1_17619	-	chr4:105186031-105186051	AGAGUGAUACAACGGGUCCG	4265
54790_1_17620	-	chr4:105186035-105186055	CUCCAGAGUGAUACAACGGG	4266
54790_1_17632	-	chr4:105186054-105186074	CAAAUAAAAACAUCUCUAC	4267
54790_1_17636	-	chr4:105186106-105186126	AGGGUUCACCGAUCCUGAUG	4268
54790_1_17638	-	chr4:105186114-105186134	AGAGUCAGAGGGUUCACCGA	4269
54790_1_17640	-	chr4:105186119-105186139	AAGGUAGAGUCAGAGGGUUC	4270
54790_1_17641	-	chr4:105186179-105186199	GUUCACGUCACCGUGCUAGA	4271
54790_1_17642	-	chr4:105186190-105186210	AGUGGGUCCGAGUUCACGUC	4272
54790_1_17644	-	chr4:105186204-105186224	UCCCAGAACGAGACAGUGGG	4273
54790_1_17657	-	chr4:105186223-105186243	AACAAACAAAAGAACUCUGU	4274
54790_1_17658	-	chr4:105186224-105186244	AAACAAACAAAAGAACUCUG	4275
54790_1_17674	-	chr4:105186324-105186344	UAAGAUAAAGGGCCAUGAAGG	4276
54790_1_17675	-	chr4:105186325-105186345	UUAAGAUAAAGGGCCAUGAAG	4277
54790_1_17676	-	chr4:105186326-105186346	GUUAAGAUAAAGGGCCAUGAA	4278
54790_1_17679	-	chr4:105186327-105186347	GGUUAAGAUAAAGGGCCAUGA	4279
54790_1_17682	-	chr4:105186336-105186356	GAAGACAGAGGUUAAGAUAA	4280
54790_1_17683	-	chr4:105186337-105186357	UGAAGACAGAGGUUAAGAUAA	4281
54790_1_17685	-	chr4:105186348-105186368	AAGGGUAGUGCUGAAGACAG	4282
54790_1_17688	-	chr4:105186366-105186386	AAACGGAACAAACAUAUGAA	4283
54790_1_17689	-	chr4:105186367-105186387	AAAACGGAACAAACAUAUGA	4284
54790_1_17694	-	chr4:105186383-105186403	AAAUACAUUAGAAGAUAAAA	4285
54790_1_17711	-	chr4:105186518-105186538	CGUGGUGACGUGAGGUCGGA	4286
54790_1_17712	-	chr4:105186519-105186539	GCGUGGUGACGUGAGGUCGG	4287
54790_1_17716	-	chr4:105186559-105186579	CUUAGCGGAGGUCCUCCGCC	4288
54790_1_17717	-	chr4:105186562-105186582	CCUCUUAGCGGAGGUCCUCC	4289
54790_1_17720	-	chr4:105186565-105186585	CGCCCUCUUAGCGGAGGUCC	4290
54790_1_17721	-	chr4:105186568-105186588	CUCCGCCUCUUAGCGGAGG	4291
54790_1_17725	-	chr4:105186583-105186603	CGAUGACCCCUCCGACUCCG	4292
54790_1_17728	-	chr4:105186584-105186604	UCGAUGACCCCUCCGACUCC	4293
54790_1_17730	-	chr4:105186587-105186607	GGGUCGAUGACCCCUCCGAC	4294
54790_1_17732	-	chr4:105186593-105186613	ACAUCAGGGUCGAUGACCCC	4295
54790_1_17733	-	chr4:105186596-105186616	CGGACAUCAGGGUCGAUGAC	4296
54790_1_17735	-	chr4:105186597-105186617	UCGGACAUCAGGGUCGAUGA	4297
54790_1_17737	-	chr4:105186598-105186618	UUCGGACAUCAGGGUCGAUG	4298
54790_1_17741	-	chr4:105186624-105186644	AUUUUUAAUAGGUCCGUACC	4299
54790_1_17742	-	chr4:105186627-105186647	UAUAUUUUUAAUAGGUCCGU	4300
54790_1_17743	-	chr4:105186632-105186652	AUUUUUAAUAAUUUUUAAUAGG	4301
54790_1_17749	-	chr4:105186699-105186719	ACCCACCUAGUGAACUCCAG	4302
54790_1_17752	-	chr4:105186704-105186724	GUUCCACCCACCUAGUGAAC	4303
54790_1_17756	-	chr4:105186715-105186735	GAAACCCUCCGGUUCCACCC	4304
54790_1_17758	-	chr4:105186718-105186738	CGUGAAACCCUCCGGUUCCA	4305
54790_1_17759	-	chr4:105186719-105186739	UCGUGAAACCCUCCGGUUCC	4306
54790_1_17761	-	chr4:105186722-105186742	GGGUCGUGAAACCCUCCGGU	4307
54790_1_17762	-	chr4:105186728-105186748	ACGUUAGGGUCGUGAAACCC	4308
54790_1_17763	-	chr4:105186731-105186751	CGGACGUUAGGGUCGUGAAA	4309
54790_1_17765	-	chr4:105186732-105186752	ACGGACGUUAGGGUCGUGAA	4310
54790_1_17770	-	chr4:105186759-105186779	AUCAUGAACGGUCCGGCGCC	4311

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_17772	-	chr4:105186762-105186782	UGGAUCAUGAACGGUCCGGC	4312
54790_1_17773	-	chr4:105186768-105186788	CUAUUUUGGAUCAUGAACGG	4313
54790_1_17776	-	chr4:105186782-105186802	GAAGCUUAAUGAUGCUAUUU	4314
54790_1_17786	-	chr4:105186827-105186847	UAAAUACAGUGAUGACUCAC	4315
54790_1_17795	-	chr4:105186893-105186913	UCCUCAGUAGCCAAUAAUUC	4316
54790_1_17801	-	chr4:105186957-105186977	CAGUCCCCUUUAGUAAAAG	4317
54790_1_17809	-	chr4:105187014-105187034	AUCAAGCUGGCAAACUAUCA	4318
54790_1_17814	-	chr4:105187027-105187047	UGGUUGACUGGGAAUCAAGC	4319
54790_1_17816	-	chr4:105187038-105187058	CAGCAGUUAUCUGGUUGACU	4320
54790_1_17817	-	chr4:105187039-105187059	CCAGCAGUUAUCUGGUUGAC	4321
54790_1_17820	-	chr4:105187047-105187067	UGUCACUACCAGCAGUUAUC	4322
54790_1_17823	-	chr4:105187077-105187097	CACAAGAUUGGGAGUCCUGG	4323
54790_1_17825	-	chr4:105187080-105187100	UGGCACAAGAUUGGGAGUCC	4324
54790_1_17829	-	chr4:105187088-105187108	CUCUGAGCUGGCACAAGAUU	4325
54790_1_17832	-	chr4:105187089-105187109	UCUCUGAGCUGGCACAAGAU	4326
54790_1_17835	-	chr4:105187100-105187120	GGGGAUUUCCCUCUCUGAGC	4327
54790_1_17839	-	chr4:105187119-105187139	AUGGUGUGAGCAGUUCUAGG	4328
54790_1_17840	-	chr4:105187120-105187140	AAUGGUGUGAGCAGUUCUAG	4329
54790_1_17842	-	chr4:105187121-105187141	GAAUGGUGUGAGCAGUUCUA	4330
54790_1_17845	-	chr4:105187122-105187142	GGAAUGGUGUGAGCAGUUCU	4331
54790_1_17850	-	chr4:105187138-105187158	GGUGCUUGUGGUUCUUGGAA	4332
54790_1_17851	-	chr4:105187143-105187163	AAGGUGGUGCUUGUGGUUCU	4333
54790_1_17856	-	chr4:105187150-105187170	CUAUACCAAGGUGGUGCUUG	4334
54790_1_17859	-	chr4:105187159-105187179	CAUUUUUAACUAUACCAAGG	4335
54790_1_17861	-	chr4:105187162-105187182	UCACAUUUUUAACUAUACCA	4336
54790_1_17869	-	chr4:105187187-105187207	GUUUUUAUCAGAAUUUGAGU	4337
54790_1_17891	-	chr4:105187296-105187316	CCAAAUACUGAGGAAGGCAG	4338
54790_1_17894	-	chr4:105187302-105187322	GACAAACCAAUACUGAGGA	4339
54790_1_17897	-	chr4:105187306-105187326	AACUGACAAACCAAUACUG	4340
54790_1_17908	-	chr4:105187371-105187391	ACAUUAUUAAGAUUAGAAGA	4341
54790_1_17909	-	chr4:105187372-105187392	AACAUUAUUAAGAUUAGAAG	4342
54790_1_17927	-	chr4:105187431-105187451	AGGUCAGGGUUGGAGUCAAU	4343
54790_1_17928	-	chr4:105187441-105187461	GAAGUACAGGAGGUCAGGGU	4344
54790_1_17931	-	chr4:105187445-105187465	AGGUGAAGUACAGGAGGUCA	4345
54790_1_17932	-	chr4:105187446-105187466	CAGGUGAAGUACAGGAGGUC	4346
54790_1_17935	-	chr4:105187451-105187471	UCAGGCAGGUGAAGUACAGG	4347
54790_1_17937	-	chr4:105187454-105187474	UCAUCAGGCAGGUGAAGUAC	4348
54790_1_17941	-	chr4:105187465-105187485	CAAAUAAAUUUCaucagGC	4349
54790_1_17943	-	chr4:105187469-105187489	AUCCAAAUAAAUUUCauc	4350
54790_1_17951	-	chr4:105187541-105187561	AUAAAUAGAUAAUUCUAGAA	4351
54790_1_17965	-	chr4:105187593-105187613	AGUGAUAAAGCUUUUGAGUU	4352
54790_1_17978	-	chr4:105187663-105187683	AUUACUGAUAAAGAAAUGAA	4353
54790_1_17985	-	chr4:105187720-105187740	CAAUAGUUGGAAUGAGAGGG	4354
54790_1_17986	-	chr4:105187723-105187743	AAGCAAUAGUUGGAAUGAGA	4355
54790_1_17987	-	chr4:105187724-105187744	UAAGCAAUAGUUGGAAUGAG	4356
54790_1_17992	-	chr4:105187733-105187753	ACUCAAGUAUAAGCAAUAGU	4357
54790_1_17998	-	chr4:105187767-105187787	AAUAAUCAUAUGCAAGAUAU	4358
54790_1_18001	-	chr4:105187797-105187817	ACACUUCACCAUGAAGAUUU	4359

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_18004	-	chr4:105187810-105187830	GGUAGGGUCACUCACACUUC	4360
54790_1_18022	-	chr4:105187890-105187910	UAAGGUGAUCGUUACACAGU	4361
54790_1_18024	-	chr4:105187891-105187911	GUAAGGUGAUCGUUACACAG	4362
54790_1_18029	-	chr4:105187927-105187947	ACGGUUUGACAAAACGUUUC	4363
54790_1_18037	-	chr4:105187978-105187998	UCGCUUUGAUGACCCAGAAU	4364
54790_1_18038	-	chr4:105187986-105188006	AGGGAUUCUCGCUUUGAUGA	4365
54790_1_18039	-	chr4:105187987-105188007	UAGGGAUUCUCGCUUUGAUG	4366
54790_1_18049	-	chr4:105188011-105188031	CAAAAGUUAAGAGAACUCUC	4367
54790_1_18059	-	chr4:105188039-105188059	UACAAAUUAUUCAAAAACAUA	4368
54790_1_18060	-	chr4:105188040-105188060	UUACAAAUUAUUCAAAAACAU	4369
54790_1_18063	-	chr4:105188069-105188089	CUUAUUACGACGUUGUUUGU	4370
54790_1_18072	-	chr4:105188099-105188119	AAACCCAACGAAGAUGGAAA	4371
54790_1_18074	-	chr4:105188116-105188136	AGUAGGUAGACAUCCGUAAA	4372
54790_1_18075	-	chr4:105188117-105188137	AAGUAGGUAGACAUCCGUAA	4373
54790_1_18079	-	chr4:105188124-105188144	AAUAGGUAAGUAGGUAGACA	4374
54790_1_18090	-	chr4:105188186-105188206	GUCUUA AAAAGAAGGAGAAAU	4375
54790_1_18108	-	chr4:105188262-105188282	UUAUAAAAAAGAAACACACUA	4376
54790_1_18111	-	chr4:105188291-105188311	AAGAUUCAUGGAGUACAUUC	4377
54790_1_18120	-	chr4:105188353-105188373	AACGAGGAGGAGGGUCGGGG	4378
54790_1_18138	-	chr4:105188483-105188503	AUAAAUUCAUAUGAUAAGAC	4379
54790_1_18155	-	chr4:105188569-105188589	GGAGUAUUUAUUACGAAGAA	4380
54790_1_18165	-	chr4:105188608-105188628	CGAUAGUUACUACUUGAAAA	4381
54790_1_18166	-	chr4:105188609-105188629	UCGAUAGUUACUACUUGAAA	4382
54790_1_18189	-	chr4:105188715-105188735	GUGAAUCACAUAUACAAAAAU	4383
54790_1_18196	-	chr4:105188745-105188765	UUUUAAACCGGAAAAUGCAG	4384
54790_1_18198	-	chr4:105188759-105188779	UAUAUUUUGGUAUGUUUUAA	4385
54790_1_18211	-	chr4:105188808-105188828	UUAGUUGAAAGUCAGAAUA	4386
54790_1_18212	-	chr4:105188809-105188829	AUUAGUUGAAAGUCAGAAAU	4387
54790_1_18220	-	chr4:105188839-105188859	AAGUAAGGAGGGGGCCCGGA	4388
54790_1_18221	-	chr4:105188845-105188865	AAAAGUAAGUAAGGAGGGGG	4389
54790_1_18222	-	chr4:105188846-105188866	CAAAAGUAAGUAAGGAGGGGG	4390
54790_1_18225	-	chr4:105188874-105188894	GUUUUUUGGGUCAUGGGUAA	4391
54790_1_18239	-	chr4:105188985-105189005	ACAUUUCAUAUACUCAGUCA	4392
54790_1_18240	-	chr4:105188986-105189006	AACAUUUCAUAUACUCAGUC	4393
54790_1_18251	-	chr4:105189047-105189067	GCCAUACGUUAAAAUUUAAG	4394
54790_1_18252	-	chr4:105189048-105189068	AGCCAUACGUUAAAAUUUAA	4395
54790_1_18253	-	chr4:105189049-105189069	AAGCCAUACGUUAAAAUUUA	4396
54790_1_18260	-	chr4:105189080-105189100	ACGUUGCUCUUUAGAAACA	4397
54790_1_18262	-	chr4:105189105-105189125	UCUUUAUCAUUCGACUCUGA	4398
54790_1_18263	-	chr4:105189106-105189126	AUCUUUAUCAUUCGACUCUG	4399
54790_1_18278	-	chr4:105189159-105189179	UAAA AUGUCUCAUUCUCCC	4400
54790_1_18281	-	chr4:105189162-105189182	GGGUAAA AUGUCUCAUUCUU	4401
54790_1_18283	-	chr4:105189163-105189183	AGGGUAAA AUGUCUCAUUCU	4402
54790_1_18296	-	chr4:105189225-105189245	UAAAUUGUGAGUUUUUUUAG	4403
54790_1_18302	-	chr4:105189291-105189311	GCUCAGGUUCCCGGGGUUGA	4404
54790_1_18303	-	chr4:105189298-105189318	AGUUGAAGCUCAGGUUCCCG	4405
54790_1_18304	-	chr4:105189299-105189319	CAGUUGAAGCUCAGGUUCCC	4406
54790_1_18305	-	chr4:105189300-105189320	GCAGUUGAAGCUCAGGUUCC	4407

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790_1_18308	-	chr4:105189307-105189327	AUCAGAAGCAGUUGAAGCUC	4408
54790_1_18313	-	chr4:105189336-105189356	GAAUAUCCUGAAAUAGUAUC	4409
54790_1_18319	-	chr4:105189358-105189378	UGAAUAUAUGGAAACAGUAU	4410
54790_1_18322	-	chr4:105189370-105189390	GGUCCAUUGUCCUGAAUAUA	4411
54790_1_18329	-	chr4:105189391-105189411	GAUAAAAUGGCUAAAGGAGU	4412
54790_1_18331	-	chr4:105189397-105189417	AGUUUUGAUAAAAUGGCUAA	4413
54790_1_18333	-	chr4:105189404-105189424	UCUAAAGAGUUUUGAUAAAA	4414
54790_1_18342	-	chr4:105189448-105189468	AAAGGAGCACAGAAGACUU	4415
54790_1_18347	-	chr4:105189466-105189486	UGACUGAAGAGUGUCUACAA	4416
54790_1_18353	-	chr4:105189507-105189527	AUACAGCUGCAGCAAAUUGG	4417
54790_1_18356	-	chr4:105189510-105189530	CAGAUACAGCUGCAGCAAAU	4418
54790_1_18363	-	chr4:105189535-105189555	GGGGAGAAAGCGUUGUUUUG	4419
54790_1_18367	-	chr4:105189554-105189574	GCAGAGAGAAAAGAGGAAUG	4420
54790_1_18368	-	chr4:105189555-105189575	GGCAGAGAGAAAAGAGGAAU	4421
54790_1_18372	-	chr4:105189556-105189576	GGGCAGAGAGAAAAGAGGAA	4422
54790_1_18375	-	chr4:105189561-105189581	UCCAAGGGCAGAGAGAAAAG	4423
54790_1_18381	-	chr4:105189576-105189596	AGAAGUCCACAGAGUUCCAA	4424
54790_1_18382	-	chr4:105189577-105189597	GAGAAGUCCACAGAGUUCCA	4425
54790_1_18390	-	chr4:105189612-105189632	AUGCACUGAUAAAAGGGAGU	4426
54790_1_18392	-	chr4:105189618-105189638	GAUGACAUGCACUGAUAAAA	4427
54790_1_18393	-	chr4:105189619-105189639	AGAUGACAUGCACUGAUAAA	4428
54790_1_18398	-	chr4:105189642-105189662	UAUUGGGUGCUACAAAUAAAG	4429
54790_1_18400	-	chr4:105189658-105189678	AAAGAUGUAGUAAAAAUUU	4430
54790_1_18402	-	chr4:105189659-105189679	CAAAGAUGUAGUAAAAAUUU	4431
54790_1_18405	-	chr4:105189683-105189703	UAACCCAAGUAAGACUUAUU	4432
54790_1_18410	-	chr4:105189737-105189757	CUGACCUGUAUAUCUUUAAA	4433
54790_1_18417	-	chr4:105189754-105189774	AAAUUAAAUUCGACCUCUCUG	4434
54790_1_18421	-	chr4:105189763-105189783	GAGUUCCCAAAAUUAAAUUCG	4435
54790_1_18423	-	chr4:105189778-105189798	GUACACCAGAGACACGAGUU	4436
54790_1_18425	-	chr4:105189779-105189799	UGUACACCAGAGACACGAGU	4437
54790_1_18427	-	chr4:105189794-105189814	UCCAUUUUGUAAUAUUGUAC	4438
54790_1_18428	-	chr4:105189814-105189834	GUACGAUUCACGAUACCUUU	4439
54790_1_18429	-	chr4:105189820-105189840	UCCAUUGUACGAUUCACGAU	4440
54790_1_18434	-	chr4:105189840-105189860	UAAGUCAUAUACGGUACAGU	4441
54790_1_18437	-	chr4:105189894-105189914	UCCCUGUACUUC AUGAGAUG	4442
54790_1_18442	-	chr4:105189933-105189953	CCACUGACAUUCUACUUCAG	4443
54790_1_18448	-	chr4:105189954-105189974	UUCUCCUUUGAAAUAAGAGG	4444
54790_1_18453	-	chr4:105189971-105189991	AAGACUGAACAACUCGAUUC	4445
54790_1_18462	-	chr4:105190008-105190028	UAGUGGAUCCAUCUUC AAC	4446
54790_1_18468	-	chr4:105190021-105190041	CCGAAUGUUCUCAUAGUGGA	4447
54790_1_18472	-	chr4:105190042-105190062	GAAUCGUCACCAAGUGUCAC	4448
54790_1_18475	-	chr4:105190054-105190074	ACUUCAUCUGUUGAAUCGUC	4449
54790_1_18479	-	chr4:105190085-105190105	CAAUGAGGCUUAAGAGCCAG	4450
54790_1_18482	-	chr4:105190100-105190120	CUUCACCGCAAUAUCAAUG	4451
54790_1_18502	-	chr4:105190241-105190261	UGGAUAUUUCCAUAUACAGUG	4452
54790_1_18507	-	chr4:105190261-105190281	AGGUUUUGGAUACCUAUAAU	4453
54790_1_18510	-	chr4:105190275-105190295	AUAAAGAGUUUAAAAGGUUU	4454
54790_1_18512	-	chr4:105190281-105190301	CCUGAUAAUAAAGAGUUUAAA	4455

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 1 18519	-	chr4:105190312-105190332	UAAGUUAGCAAAAAGGAACA	4456
54790 1 18520	-	chr4:105190313-105190333	UUAAGUUAGCAAAAAGGAAC	4457
54790 1 18525	-	chr4:105190319-105190339	ACAUUUUUAAGUUAGCAAAA	4458
54790 2 2	+	chr4:105190494-105190514	CUGAGCUGCUGGUAAGACAG	4459
54790 2 9	+	chr4:105190544-105190564	UGAAUUUAUUCCUAAUGUAA	4460
54790 2 17	+	chr4:105190620-105190640	UUUCUUUAUUGUCUAUGCUU	4461
54790 2 23	+	chr4:105190628-105190648	UUGUCUAUGCUUAGGACACA	4462
54790 2 37	+	chr4:105190697-105190717	UAUGUAUAGCUGUAUUUUUC	4463
54790 2 48	+	chr4:105190734-105190754	UUAUCAAUUCUCAUGUCUA	4464
54790 2 55	+	chr4:105190750-105190770	UCUAUGGAGUUUUUAAAAAG	4465
54790 2 57	+	chr4:105190755-105190775	GGAGUUUUUAAAAAGAGGUA	4466
54790 2 77	+	chr4:105190871-105190891	ACUUCGUCUCAAUUCUGUUA	4467
54790 2 79	+	chr4:105190884-105190904	CUUGUUAAGGACCAAUAAA	4468
54790 2 82	+	chr4:105190893-105190913	GACCAAUAUAAUGGUUUUG	4469
54790 2 89	+	chr4:105190933-105190953	AAGUGAGUACCUCUGCACC	4470
54790 2 90	+	chr4:105190957-105190977	UAGUCAGUCUUGUGACAAUU	4471
54790 2 98	+	chr4:105190989-105191009	ACUAGCAGAGAACUAAAUUA	4472
54790 2 100	+	chr4:105190994-105191014	CAGAGAACUAAAUUAUGGAA	4473
54790 2 103	+	chr4:105191005-105191025	AUUAUGGAAUGGCAGAUUC	4474
54790 2 105	+	chr4:105191030-105191050	CAGCUAUGUGAUUUUACAUA	4475
54790 2 107	+	chr4:105191044-105191064	UACAUACGGUUUGUUUUUAA	4476
54790 2 116	+	chr4:105191061-105191081	UAAUGGAUAGAGACAGAGUC	4477
54790 2 120	+	chr4:105191075-105191095	AGAGUCUGGCUAUGUUGCCC	4478
54790 2 124	+	chr4:105191093-105191113	CCAGGCUGCUCUGAAACUCC	4479
54790 2 125	+	chr4:105191094-105191114	CAGGCUGCUCUGAAACUCCU	4480
54790 2 129	+	chr4:105191127-105191147	CAUCCUGCCUAGCCUCUUA	4481
54790 2 132	+	chr4:105191133-105191153	GCCUAGCCUCUUAAGGAGC	4482
54790 2 133	+	chr4:105191134-105191154	CCUAGCCUCUUAAGGAGCU	4483
54790 2 135	+	chr4:105191142-105191162	UCUUAAGGAGCUGGGAUUAC	4484
54790 2 137	+	chr4:105191156-105191176	GAUUACAGGUGCAUGCCCCC	4485
54790 2 147	+	chr4:105191196-105191216	UCUGAAAAUACAAAAGAAAG	4486
54790 2 149	+	chr4:105191197-105191217	CUGAAAAUACAAAAGAAAGA	4487
54790 2 166	+	chr4:105191294-105191314	CUGCUGAGUGUCCCAACCUA	4488
54790 2 167	+	chr4:105191295-105191315	UGCUGAGUGUCCCAACCUAA	4489
54790 2 174	+	chr4:105191336-105191356	AUAUAUGCAUGUAUAGAAGU	4490
54790 2 177	+	chr4:105191337-105191357	UAUAUGCAUGUAUAGAAGUA	4491
54790 2 196	+	chr4:105191448-105191468	UAAAAUUUAUAGAGACAUUGC	4492
54790 2 202	+	chr4:105191459-105191479	AGACAUUGCAGGAGAGACUC	4493
54790 2 208	+	chr4:105191476-105191496	CUCUGGAUUAGAUAGAAAAA	4494
54790 2 212	+	chr4:105191486-105191506	GAUAGAAAAAAGGAAGAAUU	4495
54790 2 219	+	chr4:105191517-105191537	UUGUCUAUAAUCCUUUUAGU	4496
54790 2 237	+	chr4:105191622-105191642	UGCCUACUGCAGACACCUG	4497
54790 2 241	+	chr4:105191670-105191690	AUACUUCUCAGAGACUGUUC	4498
54790 2 251	+	chr4:105191722-105191742	AGUUGAACUCCCAUGAUUCC	4499
54790 2 255	+	chr4:105191746-105191766	UGUUGCCAUUUUCAAGACAC	4500
54790 2 256	+	chr4:105191747-105191767	GUUGCCAUUUUCAAGACACA	4501
54790 2 262	+	chr4:105191782-105191802	UCUAGAUAUACCUCUCUACCU	4502
54790 2 265	+	chr4:105191783-105191803	CUAGAUAUACCUCUCUACCUU	4503

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 270	+	chr4:105191805-105191825	GAAUUUUAAGUCACUCUGUG	4504
54790 2 273	+	chr4:105191806-105191826	AAUUUUAAGUCACUCUGUGA	4505
54790 2 295	+	chr4:105191923-105191943	UCCUCUUUCCCCUCUCAUGC	4506
54790 2 300	+	chr4:105191934-105191954	CUCUCAUGCUGGAAAAUCUU	4507
54790 2 327	+	chr4:105192067-105192087	CUGAGAGCGCAUUUUUAAGA	4508
54790 2 342	+	chr4:105192134-105192154	CUCUUCUUGAACGUUAAGCC	4509
54790 2 345	+	chr4:105192135-105192155	UCUUCUUGAACGUUAAGCCU	4510
54790 2 349	+	chr4:105192140-105192160	UUGAACGUUAAGCCUGGGUA	4511
54790 2 354	+	chr4:105192162-105192182	GAAUAAAGUGCAGAAGUUUA	4512
54790 2 364	+	chr4:105192224-105192244	AAUUAAAAUAUUAGCCAUUG	4513
54790 2 366	+	chr4:105192225-105192245	AUUAAAAUAUUAGCCAUUGA	4514
54790 2 368	+	chr4:105192231-105192251	AUAUUAGCCAUUGAGGGAAA	4515
54790 2 370	+	chr4:105192240-105192260	AUUGAGGGAAAAGGUUUUAC	4516
54790 2 374	+	chr4:105192253-105192273	GUUUUACAGGUAGCUCUCUG	4517
54790 2 384	+	chr4:105192311-105192331	UGCAUUUAAUUUUUUACAGU	4518
54790 2 401	+	chr4:105192381-105192401	UUAUUUUUAGUACAUUUUAU	4519
54790 2 411	+	chr4:105192394-105192414	AUUUAUUAGGAAUGUGUUCU	4520
54790 2 412	+	chr4:105192395-105192415	UUUAUUAGGAAUGUGUUCUU	4521
54790 2 422	+	chr4:105192432-105192452	UCUGUAAGCCCUGCUUUAAA	4522
54790 2 426	+	chr4:105192448-105192468	UAAAUGGCAAAGAAGAAAGU	4523
54790 2 430	+	chr4:105192468-105192488	AGGUAAUAAUAGAUAAUAAC	4524
54790 2 437	+	chr4:105192529-105192549	GUAAGUUCUCAAUUUUAU	4525
54790 2 468	+	chr4:105192628-105192648	UUGAGCACCUGCCAAAUACC	4526
54790 2 473	+	chr4:105192640-105192660	CAAAUACCAGGCACUCUUCU	4527
54790 2 475	+	chr4:105192651-105192671	CACUCUUCUAGGAACUAGAG	4528
54790 2 479	+	chr4:105192668-105192688	GAGUGGCAUUAUAGAGUAAG	4529
54790 2 495	+	chr4:105192794-105192814	UAAAAAUGUAAAGCAGAAAA	4530
54790 2 501	+	chr4:105192805-105192825	AGCAGAAAAAGGAAAUUGAG	4531
54790 2 503	+	chr4:105192809-105192829	GAAAAAGGAAAUUGAGUGGC	4532
54790 2 504	+	chr4:105192810-105192830	AAAAAGGAAAUUGAGUGGCA	4533
54790 2 505	+	chr4:105192815-105192835	GGAAAUUGAGUGGCAGGGUU	4534
54790 2 509	+	chr4:105192846-105192866	GAAGAUAUAGUAGUCAAGUA	4535
54790 2 519	+	chr4:105192922-105192942	CAAGCCAUGAAGUUAUCUGA	4536
54790 2 521	+	chr4:105192931-105192951	AAGUUAUCUGAAGGAAUUGC	4537
54790 2 523	+	chr4:105192937-105192957	UCUGAAGGAAUUGCAGGUAG	4538
54790 2 529	+	chr4:105192957-105192977	UGGAGAACAGCCAAAAGACC	4539
54790 2 531	+	chr4:105192969-105192989	AAAAGACCUGGAGUAGUAAA	4540
54790 2 544	+	chr4:105193052-105193072	AUACACUUAAGUAAGUGAUA	4541
54790 2 549	+	chr4:105193065-105193085	AGUGAU AUGGACAAGAACUU	4542
54790 2 551	+	chr4:105193081-105193101	ACUUUGGAAGUUGAAUAGCA	4543
54790 2 555	+	chr4:105193090-105193110	GUUGAAUAGCAAGGUCCAUC	4544
54790 2 560	+	chr4:105193103-105193123	GUCCAUCUGGACUAUAACAG	4545
54790 2 561	+	chr4:105193106-105193126	CAUCUGGACUAUAACAGAGG	4546
54790 2 564	+	chr4:105193117-105193137	UAACAGAGGAGGCUUCACAA	4547
54790 2 565	+	chr4:105193121-105193141	AGAGGAGGCUUCACAAAGGA	4548
54790 2 567	+	chr4:105193128-105193148	GCUUCACAAAGGAAGGUGAC	4549
54790 2 568	+	chr4:105193129-105193149	CUUCACAAAGGAAGGUGACA	4550
54790 2 570	+	chr4:105193134-105193154	CAAAGGAAGGUGACAGGGCA	4551

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 572	+	chr4:105193139-105193159	GAAGGUGACAGGGCAUGGCC	4552
54790 2 575	+	chr4:105193149-105193169	GGGCAUGGCCUGGAUCCUGA	4553
54790 2 577	+	chr4:105193154-105193174	UGGCCUGGAUCCUGAAGGAC	4554
54790 2 583	+	chr4:105193163-105193183	UCCUGAAGGACAGGAAGAAU	4555
54790 2 584	+	chr4:105193164-105193184	CCUGAAGGACAGGAAGAAUU	4556
54790 2 589	+	chr4:105193193-105193213	AACAAAGAAUGACAUCCCAG	4557
54790 2 595	+	chr4:105193203-105193223	GACAUCCCAGUGGAGAGAAG	4558
54790 2 598	+	chr4:105193206-105193226	AUCCCAGUGGAGAGAAGUGG	4559
54790 2 600	+	chr4:105193207-105193227	UCCCAGUGGAGAGAAGUGGA	4560
54790 2 601	+	chr4:105193208-105193228	CCCAGUGGAGAGAAGUGGAG	4561
54790 2 605	+	chr4:105193224-105193244	GGAGGGGAAACAGCAUGAAA	4562
54790 2 610	+	chr4:105193243-105193263	AUGGAGUGAAAUAAAGAAUGU	4563
54790 2 612	+	chr4:105193251-105193271	AAAUAAAGAAUGUUGGCCUUU	4564
54790 2 613	+	chr4:105193252-105193272	AAUAAGAAUGUUGGCCUUUA	4565
54790 2 615	+	chr4:105193256-105193276	AGAAUGUUGGCCUUUAGGGC	4566
54790 2 618	+	chr4:105193261-105193281	GUUGGCCUUUAGGGCAGGAA	4567
54790 2 619	+	chr4:105193262-105193282	UUGGCCUUUAGGGCAGGAAU	4568
54790 2 621	+	chr4:105193267-105193287	CUUUAGGGCAGGAAUGGGCC	4569
54790 2 626	+	chr4:105193273-105193293	GGCAGGAAUGGGCCAGGCAG	4570
54790 2 627	+	chr4:105193274-105193294	GCAGGAAUGGGCCAGGCAGA	4571
54790 2 630	+	chr4:105193281-105193301	UGGGCCAGGCAGAGGGCAAG	4572
54790 2 632	+	chr4:105193282-105193302	GGGCCAGGCAGAGGGCAAGU	4573
54790 2 635	+	chr4:105193289-105193309	GCAGAGGGCAAGUGGGAAGC	4574
54790 2 636	+	chr4:105193296-105193316	GCAAGUGGGAAGCAGGAAAA	4575
54790 2 637	+	chr4:105193321-105193341	ACCUUGUAUAAAGUUCAUGU	4576
54790 2 645	+	chr4:105193339-105193359	GUUGGC AAAUAGAGAGAAGA	4577
54790 2 647	+	chr4:105193340-105193360	UUGGC AAAUAGAGAGAAGAU	4578
54790 2 650	+	chr4:105193348-105193368	UAGAGAGAAGAUGGGAAAGC	4579
54790 2 651	+	chr4:105193349-105193369	AGAGAGAAGAUGGGAAAGCA	4580
54790 2 652	+	chr4:105193354-105193374	GAAGAUGGGAAAGCAGGGUA	4581
54790 2 659	+	chr4:105193417-105193437	GCAUGCUAUCCUGAAAAUAU	4582
54790 2 661	+	chr4:105193418-105193438	CAUGCUAUCCUGAAAAUAUU	4583
54790 2 664	+	chr4:105193419-105193439	AUGCUAUCCUGAAAAUAUUG	4584
54790 2 670	+	chr4:105193446-105193466	AUUAGAGCAGAUGAGUAGAA	4585
54790 2 680	+	chr4:105193499-105193519	UUUACAAAUUUAAACAAUA	4586
54790 2 686	+	chr4:105193505-105193525	AAUUUAAACAAUAAGGAAA	4587
54790 2 688	+	chr4:105193508-105193528	UUAAACAAUAAGGAAUUGG	4588
54790 2 692	+	chr4:105193518-105193538	AAGGAAUUGGAGGCAGUAGU	4589
54790 2 695	+	chr4:105193529-105193549	GGCAGUAGUUGGAGUAAUUU	4590
54790 2 700	+	chr4:105193546-105193566	UUUAGGAGAUAAAUUGAAAA	4591
54790 2 709	+	chr4:105193565-105193585	AUGGAUUUUUGUUAAGAGAGA	4592
54790 2 711	+	chr4:105193566-105193586	UGGAUUUUUGUUAAGAGAGAA	4593
54790 2 717	+	chr4:105193591-105193611	GAUAGA UUUUAUAUAUUUUA	4594
54790 2 724	+	chr4:105193604-105193624	UAUUUUAAAGGAAAAUCAUG	4595
54790 2 737	+	chr4:105193642-105193662	GCACGUAAGAGAUAAAAGAG	4596
54790 2 741	+	chr4:105193689-105193709	CAAAAUGAUUAAUUACGUGU	4597
54790 2 750	+	chr4:105193705-105193725	GUGUUGGUAAUUAAAAGAAAU	4598
54790 2 751	+	chr4:105193706-105193726	UGUUGGUAAUUAAAAGAAUA	4599

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 755	+	chr4:105193713-105193733	AUUAAAAGAAAUAGGGAAGU	4600
54790 2 757	+	chr4:105193714-105193734	UUAAAAGAAAUAGGGAAGUU	4601
54790 2 767	+	chr4:105193775-105193795	AUCAGAUGCAGAUAUUCUUA	4602
54790 2 770	+	chr4:105193808-105193828	UCAUUUGAUUUUUGUCAUUAU	4603
54790 2 790	+	chr4:105193917-105193937	UUUGUAUUUUUAUAAUAAGU	4604
54790 2 806	+	chr4:105193949-105193969	GAAUCAAAAAAUUAUUGAUU	4605
54790 2 813	+	chr4:105193990-105194010	AGUCCAAUUAGUUCAUUUUG	4606
54790 2 817	+	chr4:105193994-105194014	CAAUUAGUUCAUUUUGUGGA	4607
54790 2 820	+	chr4:105194001-105194021	UUCAUUUUGUGGAAGGAAAA	4608
54790 2 829	+	chr4:105194058-105194078	CCUCUAGCUAGUAUCUAACU	4609
54790 2 830	+	chr4:105194069-105194089	UAUCUAACUUGGUCUAGCCC	4610
54790 2 833	+	chr4:105194126-105194146	AAAUAAUAAAAAGUAUUAG	4611
54790 2 834	+	chr4:105194141-105194161	AUUAGUGGUUUGUAUUUUGC	4612
54790 2 838	+	chr4:105194152-105194172	GUAUUUUGCUGGCUUGCUUG	4613
54790 2 847	+	chr4:105194160-105194180	CUGGCUUGCUUGUGGAGAAU	4614
54790 2 850	+	chr4:105194169-105194189	UUGUGGAGAAUAGGAUUAGA	4615
54790 2 892	+	chr4:105194367-105194387	UUUAUCUUUCAGUAGUAUA	4616
54790 2 898	+	chr4:105194370-105194390	AUCUUUUCAGUAGUAUAAGG	4617
54790 2 918	+	chr4:105194438-105194458	AGAAAAAUAGCUUUUCUUAU	4618
54790 2 925	+	chr4:105194462-105194482	CCAAAAACCAUCACCCUAC	4619
54790 2 927	+	chr4:105194500-105194520	UUUGCUUGAUUUUCCUGAUC	4620
54790 2 942	+	chr4:105194568-105194588	CUUCAUUGUUACUUCCUAC	4621
54790 2 956	+	chr4:105194639-105194659	CAGUUUAUUCUUUGAGUCAC	4622
54790 2 993	+	chr4:105194837-105194857	UCUCCAUUACACAUGCCACA	4623
54790 2 996	+	chr4:105194891-105194911	AGCAAAACCACUCUUAUACA	4624
54790 2 998	+	chr4:105194912-105194932	GGUGUCUUGCAUAUAUAUUA	4625
54790 2 1001	+	chr4:105194922-105194942	AUAUAUAUUAAGGCCCAGAG	4626
54790 2 1006	+	chr4:105194982-105195002	CAAGACUGUUGACCUUCUUG	4627
54790 2 1009	+	chr4:105195002-105195022	UGGCAUUUAUCUGACAACCU	4628
54790 2 1035	+	chr4:105195166-105195186	GUUUCAGUUUCCUCAUCAA	4629
54790 2 1042	+	chr4:105195197-105195217	CAGCUGCCUCUGUUGAUCUC	4630
54790 2 1048	+	chr4:105195216-105195236	CAGGAUCUUUUAAGUAGAAA	4631
54790 2 1061	+	chr4:105195273-105195293	GAAAAUUGCAAUGUAAAUAC	4632
54790 2 1074	+	chr4:105195348-105195368	CUCAAAUUGUGAAAAUAGUA	4633
54790 2 1092	+	chr4:105195450-105195470	CAGUUGUCCUUCAGUAUCUG	4634
54790 2 1095	+	chr4:105195451-105195471	AGUUGUCCUUCAGUAUCUGU	4635
54790 2 1097	+	chr4:105195458-105195478	CUUCAGUAUCUGUGGGAGAU	4636
54790 2 1100	+	chr4:105195465-105195485	AUCUGUGGGAGAUUGGUUCC	4637
54790 2 1102	+	chr4:105195476-105195496	AUUGGUUCCAGGACCCCCCA	4638
54790 2 1106	+	chr4:105195492-105195512	CCCAUGGAUAUCAAAUUCUG	4639
54790 2 1118	+	chr4:105195636-105195656	GUUAUUACACUGUAUUGUUU	4640
54790 2 1120	+	chr4:105195637-105195657	UUAUUACACUGUAUUGUUUA	4641
54790 2 1146	+	chr4:105195741-105195761	UUGAUUGAAUCCACAGAUGC	4642
54790 2 1152	+	chr4:105195760-105195780	CUGGAAUCCAUGAAUACCCA	4643
54790 2 1154	+	chr4:105195761-105195781	UGGAAUCCAUGAAUACCCA	4644
54790 2 1155	+	chr4:105195762-105195782	GGAAUCCAUGAAUACCCAUG	4645
54790 2 1157	+	chr4:105195763-105195783	GAAUCCAUGAAUACCCAUGG	4646
54790 2 1158	+	chr4:105195764-105195784	AAUCCAUGAAUACCCAUGGG	4647

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 1161	+	chr4:105195816-105195836	AAUUUUGUAAUUCUCAACCA	4648
54790 2 1167	+	chr4:105195840-105195860	CACGUAAUAGUCCUUGAAUCU	4649
54790 2 1169	+	chr4:105195844-105195864	UAUAGUCCUUGAAUCUUGGU	4650
54790 2 1173	+	chr4:105195852-105195872	UUGAAUCUUGGUAGGAGUCU	4651
54790 2 1175	+	chr4:105195853-105195873	UGAAUCUUGGUAGGAGUCUU	4652
54790 2 1176	+	chr4:105195854-105195874	GAAUCUUGGUAGGAGUCUUG	4653
54790 2 1237	+	chr4:105196244-105196264	UCUUAAUAUCCUUUCUUUUA	4654
54790 2 1246	+	chr4:105196270-105196290	CCCAUUUCAGACUUUAUUAA	4655
54790 2 1249	+	chr4:105196275-105196295	UUCAGACUUUAUUAAAGGAG	4656
54790 2 1261	+	chr4:105196325-105196345	UGAAGUUUUUGCAAUUAGAA	4657
54790 2 1268	+	chr4:105196336-105196356	CAAUUAGAAUGGAGUUUAUU	4658
54790 2 1279	+	chr4:105196371-105196391	UAGAUGUGAUGUAGAAUUCU	4659
54790 2 1281	+	chr4:105196372-105196392	AGAUGUGAUGUAGAAUUCUU	4660
54790 2 1282	+	chr4:105196373-105196393	GAUGUGAUGUAGAAUUCUUG	4661
54790 2 1286	+	chr4:105196401-105196421	UACUUAUCCCCUUUUCAGAG	4662
54790 2 1295	+	chr4:105196426-105196446	CUGAAUAGCUCUGUGAACCC	4663
54790 2 1302	+	chr4:105196504-105196524	UAUGCUUGAUAUUCCUGAUC	4664
54790 2 1303	+	chr4:105196511-105196531	GAUAUUCCUGAUCUGGCUC	4665
54790 2 1330	+	chr4:105196665-105196685	CACAGCUCAGAUUUCUCAUA	4666
54790 2 1333	+	chr4:105196666-105196686	ACAGCUCAGAUUUCUCAUAA	4667
54790 2 1336	+	chr4:105196686-105196706	GGGAAGCUUCAUAUUUGUUG	4668
54790 2 1351	+	chr4:105196766-105196786	UUGCAGAUUCUGAAAUUCCU	4669
54790 2 1352	+	chr4:105196767-105196787	UGCAGAUUCUGAAAUUCCUA	4670
54790 2 1355	+	chr4:105196773-105196793	UUCUGAAAUUCCUAGGGCAA	4671
54790 2 1361	+	chr4:105196817-105196837	CUAAUAUUUUACACAGUAUC	4672
54790 2 1366	+	chr4:105196829-105196849	ACAGUAUCUGGUUACAUAGU	4673
54790 2 1371	+	chr4:105196858-105196878	AUCAUACAAUUUAAAAGAAG	4674
54790 2 1381	+	chr4:105196908-105196928	UUAUUUCCCUCUCCCCCUAC	4675
54790 2 1393	+	chr4:105196958-105196978	UACAGCACUUGCCCACUAAG	4676
54790 2 1395	+	chr4:105196961-105196981	AGCACUUGCCCACUAAGUGG	4677
54790 2 1397	+	chr4:105196962-105196982	GCACUUGCCCACUAAGUGGA	4678
54790 2 1400	+	chr4:105196968-105196988	GCCCACUAAGUGGAGGGAAG	4679
54790 2 1403	+	chr4:105196973-105196993	CUAAGUGGAGGGAAGAGGUG	4680
54790 2 1405	+	chr4:105196974-105196994	UAAGUGGAGGGAAGAGGUGU	4681
54790 2 1410	+	chr4:105196988-105197008	AGGUGUGGGAGUCGAGUAGU	4682
54790 2 1415	+	chr4:105197041-105197061	UUUGCAAAGUUACAUUAUUAU	4683
54790 2 1424	+	chr4:105197084-105197104	UUAAUUAUAAGCAACACUUG	4684
54790 2 1440	+	chr4:105197159-105197179	UGUUGCAGUUGAGAUUUGUG	4685
54790 2 1447	+	chr4:105197183-105197203	UUUAGCUAUUUAGAGACUUU	4686
54790 2 1449	+	chr4:105197184-105197204	UUAGCUAUUUAGAGACUUUA	4687
54790 2 1475	+	chr4:105197288-105197308	AAUGAUUUUGAUGUCUAUU	4688
54790 2 1499	+	chr4:105197412-105197432	UUUUCUUAUCCAGCAGUUUU	4689
54790 2 1518	+	chr4:105197451-105197471	ACUGUCAGAGAAGCAGAAAG	4690
54790 2 1520	+	chr4:105197458-105197478	GAGAAGCAGAAAGUGGUCAG	4691
54790 2 1523	+	chr4:105197473-105197493	GUCAGUGGACUUUAGAAUGU	4692
54790 2 1526	+	chr4:105197483-105197503	UUUAGAAUGUAGGCUCUUGU	4693
54790 2 1528	+	chr4:105197486-105197506	AGAAUGUAGGCUCUUGUAGG	4694
54790 2 1533	+	chr4:105197512-105197532	UAUGUUUGAGAGUGCUGUCC	4695

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 1536	+	chr4:105197527-105197547	UGUCCAGGUGCUUUGUGAUG	4696
54790 2 1541	+	chr4:105197537-105197557	CUUUGUGAUGUGGCUGAGAA	4697
54790 2 1544	+	chr4:105197544-105197564	AUGUGGCUGAGAAUGGAUGC	4698
54790 2 1546	+	chr4:105197552-105197572	GAGAAUGGAUGCAGGCUUGC	4699
54790 2 1548	+	chr4:105197553-105197573	AGAAUGGAUGCAGGCUUGCA	4700
54790 2 1554	+	chr4:105197591-105197611	AGAUCUCUAGAGAGCAUUUU	4701
54790 2 1558	+	chr4:105197611-105197631	AGGAAAGACUUCUAAGCUUU	4702
54790 2 1567	+	chr4:105197662-105197682	CUUAAUAUCCAUAGCUAUAG	4703
54790 2 1574	+	chr4:105197708-105197728	AAAUGUAGAAUUAUAAUUAUUU	4704
54790 2 1587	+	chr4:105197778-105197798	UAAUGAAAUAUAAAACCAGA	4705
54790 2 1589	+	chr4:105197789-105197809	AAAACCAGAUGGUCUCUGAA	4706
54790 2 1595	+	chr4:105197819-105197839	CUUUACUCACUUUCAGAGUA	4707
54790 2 1600	+	chr4:105197824-105197844	CUCACUUUCAGAGUAAGGCA	4708
54790 2 1656	+	chr4:105198032-105198052	AGUAUUUAAUAAAUGUUUUU	4709
54790 2 1657	+	chr4:105198033-105198053	GUAUUUAAUAAAUGUUUUU	4710
54790 2 1658	+	chr4:105198038-105198058	UAAUAAAUGUUUUUUGGGCC	4711
54790 2 1662	+	chr4:105198043-105198063	AAUGUUUUUUGGGCCAGGUG	4712
54790 2 1669	+	chr4:105198073-105198093	CUCCUGUAAUCCCAGCAAUU	4713
54790 2 1671	+	chr4:105198074-105198094	UCCUGUAAUCCCAGCAAUUU	4714
54790 2 1673	+	chr4:105198077-105198097	UGUAAUCCCAGCAAUUUGGG	4715
54790 2 1675	+	chr4:105198083-105198103	CCCAGCAAUUUGGGAGGCCG	4716
54790 2 1677	+	chr4:105198086-105198106	AGCAAUUUGGGAGGCCGAGG	4717
54790 2 1678	+	chr4:105198087-105198107	GCAAUUUGGGAGGCCGAGGC	4718
54790 2 1680	+	chr4:105198090-105198110	AUUUUGGGAGGCCGAGGCGGG	4719
54790 2 1684	+	chr4:105198101-105198121	CGAGGCGGGUGGAUCACCUG	4720
54790 2 1687	+	chr4:105198133-105198153	UGAGACCAGCCUGACCAGUA	4721
54790 2 1692	+	chr4:105198171-105198191	ACUAAAAAUGCAAAAUUAGC	4722
54790 2 1695	+	chr4:105198172-105198192	CUAAAAAUGCAAAAUUAGCU	4723
54790 2 1696	+	chr4:105198173-105198193	UAAAAAUGCAAAAUUAGCUG	4724
54790 2 1697	+	chr4:105198174-105198194	AAAAAUGCAAAAUUAGCUGG	4725
54790 2 1698	+	chr4:105198177-105198197	AAUGCAAAAUUAGCUGGGGG	4726
54790 2 1699	+	chr4:105198180-105198200	GCAAAAUUAGCUGGGGGUGG	4727
54790 2 1702	+	chr4:105198207-105198227	UGCCUAUAAUACCAGCUACU	4728
54790 2 1705	+	chr4:105198208-105198228	GCCUAUAAUACCAGCUACUC	4729
54790 2 1706	+	chr4:105198211-105198231	UAUAAUACCAGCUACUCGGG	4730
54790 2 1708	+	chr4:105198217-105198237	ACCAGCUACUCGGGAGGCUG	4731
54790 2 1710	+	chr4:105198221-105198241	GCUACUCGGGAGGCUGAGGC	4732
54790 2 1713	+	chr4:105198222-105198242	CUACUCGGGAGGCUGAGGCA	4733
54790 2 1715	+	chr4:105198223-105198243	UACUCGGGAGGCUGAGGCAG	4734
54790 2 1718	+	chr4:105198240-105198260	CAGGGGAUUCGCUUGAACUC	4735
54790 2 1720	+	chr4:105198243-105198263	GGGAAUCGCUUGAACUCAGG	4736
54790 2 1723	+	chr4:105198246-105198266	AAUCGCUUGAACUCAGGAGG	4737
54790 2 1724	+	chr4:105198249-105198269	CGCUUGAACUCAGGAGGUGG	4738
54790 2 1734	+	chr4:105198369-105198389	AAUGCUUUUUGAUUUAACGA	4739
54790 2 1744	+	chr4:105198390-105198410	GGUGUCAUUGUCCUAUGAAA	4740
54790 2 1752	+	chr4:105198440-105198460	CUUAGCUUUUGAUAAUGAUA	4741
54790 2 1768	+	chr4:105198524-105198544	AAAUUUUGAGACCAGUUAA	4742
54790 2 1774	+	chr4:105198534-105198554	GACCAGUUAAGGAGACAGA	4743

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 1778	+	chr4:105198543-105198563	AAGGAGACAGAAGGAAGUUA	4744
54790 2 1786	+	chr4:105198571-105198591	GAAGCAGUAGCCAGAAAAUA	4745
54790 2 1787	+	chr4:105198572-105198592	AAGCAGUAGCCAGAAAAUAA	4746
54790 2 1803	+	chr4:105198638-105198658	AAAUUGCUAUUAUUAUCAUC	4747
54790 2 1808	+	chr4:105198657-105198677	CUGGAAAAAAUAUGCCUUGU	4748
54790 2 1814	+	chr4:105198694-105198714	AUCCCCUUUCCAUAACCAUGC	4749
54790 2 1820	+	chr4:105198721-105198741	UUCUUUACUGCAUUCCUAAG	4750
54790 2 1826	+	chr4:105198742-105198762	GGACUAGUCUAGCACCUAU	4751
54790 2 1827	+	chr4:105198752-105198772	AGCACCUAUUGGAUACUUG	4752
54790 2 1830	+	chr4:105198762-105198782	UGGAUACUUGUGGUAAUAUU	4753
54790 2 1832	+	chr4:105198763-105198783	GGAUACUUGUGGUAAUAUUU	4754
54790 2 1835	+	chr4:105198778-105198798	UAUUUGGGAACUCACUGAUC	4755
54790 2 1839	+	chr4:105198791-105198811	ACUGAUCUGGUACAUCAGUG	4756
54790 2 1842	+	chr4:105198792-105198812	CUGAUCUGGUACAUCAGUGU	4757
54790 2 1875	+	chr4:105198979-105198999	UGUUGCAGUUGAGAGUUGUG	4758
54790 2 1880	+	chr4:105198993-105199013	GUUGUGAGGUUUUAGCUAUU	4759
54790 2 1884	+	chr4:105199003-105199023	UUUAGCUAUUUGGAAACUUU	4760
54790 2 1885	+	chr4:105199004-105199024	UUAGCUAUUUGGAAACUUUA	4761
54790 2 1913	+	chr4:105199106-105199126	GAGCAAGAAUCUGUCACUCU	4762
54790 2 1919	+	chr4:105199134-105199154	UACUCUUUAUUAAAGAAUGU	4763
54790 2 1923	+	chr4:105199154-105199174	UGGAUUCAUUUAUAACUUAC	4764
54790 2 1929	+	chr4:105199176-105199196	GUCCCUUAAAUAUUAAGUU	4765
54790 2 1930	+	chr4:105199183-105199203	AAAUAUUAAAGUUUGGUGUU	4766
54790 2 1938	+	chr4:105199212-105199232	AAACAUGAUUACAUCCUUAU	4767
54790 2 1940	+	chr4:105199213-105199233	AACAUGAUUACAUCCUUAUA	4768
54790 2 1944	+	chr4:105199232-105199252	AGGGCUCUCUUCUAAUUGCC	4769
54790 2 1958	+	chr4:105199326-105199346	ACAUUGAAGUUAGUCCGCAA	4770
54790 2 1961	+	chr4:105199345-105199365	AAGGUUUUUGUCUUUUUUUC	4771
54790 2 1978	+	chr4:105199413-105199433	GUGAUUUUCUAAAUAAAUGU	4772
54790 2 1995	+	chr4:105199472-105199492	UUCUUCAAGUCCCUCCUUUA	4773
54790 2 2001	+	chr4:105199482-105199502	CCCUCCUUUAAGGAAAUUUA	4774
54790 2 2007	+	chr4:105199508-105199528	UCUUUUUCCAUAACCAUCAAG	4775
54790 2 2018	+	chr4:105199543-105199563	UAACUUUUUCCCUUAAGUUC	4776
54790 2 2027	+	chr4:105199557-105199577	AAGUUCAGGAGUACACGUGC	4777
54790 2 2030	+	chr4:105199570-105199590	CACGUGCAGGUUUGUUGCAU	4778
54790 2 2032	+	chr4:105199579-105199599	GUUUGUUGCAUAGGCAACCU	4779
54790 2 2033	+	chr4:105199580-105199600	UUUGUUGCAUAGGCAACCUU	4780
54790 2 2037	+	chr4:105199586-105199606	GCAUAGGCAACCUUGGGUCA	4781
54790 2 2039	+	chr4:105199587-105199607	CAUAGGCAACCUUGGGUCAU	4782
54790 2 2043	+	chr4:105199602-105199622	GUCAUGGGAGUUUGUUGUAC	4783
54790 2 2046	+	chr4:105199619-105199639	UACAGGUUAUUUCAUCACCC	4784
54790 2 2058	+	chr4:105199690-105199710	CCCACCCUCCACCCUCUGAU	4785
54790 2 2059	+	chr4:105199696-105199716	CUCCACCCUCUGAUAGGCCC	4786
54790 2 2067	+	chr4:105199773-105199793	AAGUGAGAACAUGCAGUAUU	4787
54790 2 2074	+	chr4:105199802-105199822	GUUCCUAUGUUAGUUUGCUA	4788
54790 2 2076	+	chr4:105199809-105199829	UGUUAGUUUGCUAUGGAUAA	4789
54790 2 2080	+	chr4:105199863-105199883	CAUGAUCUUAUUCUCUUAUA	4790
54790 2 2083	+	chr4:105199881-105199901	UAUGGCUGCAUGUUAUUCCA	4791

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 2087	+	chr4:105199923-105199943	UUUUUUUAUCCAGUCUAUUUAU	4792
54790 2 2093	+	chr4:105199926-105199946	UUUAUCCAGUCUAUUAAUUGG	4793
54790 2 2095	+	chr4:105199927-105199947	UUAUCCAGUCUAUUAAUUGGU	4794
54790 2 2099	+	chr4:105199935-105199955	UCUAUUAAUUGGUGGGCAUUU	4795
54790 2 2108	+	chr4:105199966-105199986	AUGUCUUUGCUAUUGUGAAU	4796
54790 2 2117	+	chr4:105200026-105200046	AGAAUAAUUUUUUUUUCCCUU	4797
54790 2 2128	+	chr4:105200043-105200063	CUUUGGUAAUAUACCCAGUAG	4798
54790 2 2129	+	chr4:105200044-105200064	UUUGGUAAUAUACCCAGUAGU	4799
54790 2 2130	+	chr4:105200045-105200065	UUGGUAAUAUACCCAGUAGUG	4800
54790 2 2134	+	chr4:105200052-105200072	AUACCCAGUAGUGGGGUUGC	4801
54790 2 2135	+	chr4:105200053-105200073	UACCCAGUAGUGGGGUUGCU	4802
54790 2 2139	+	chr4:105200077-105200097	UGAAUAGUAUUUCUGUCUUG	4803
54790 2 2144	+	chr4:105200086-105200106	UUUCUGUCUUGAGGUCUUUG	4804
54790 2 2150	+	chr4:105200112-105200132	CGCUACACUGUCUUCCACAA	4805
54790 2 2168	+	chr4:105200218-105200238	UUAUAUAUAGCCGUCCUGAC	4806
54790 2 2174	+	chr4:105200228-105200248	CCGUCCUGACUGGUGUGAGA	4807
54790 2 2175	+	chr4:105200241-105200261	UGUGAGAUGGUAUCUCAUUG	4808
54790 2 2186	+	chr4:105200301-105200321	GCUUUAUUUCAUAUGUUUGU	4809
54790 2 2201	+	chr4:105200362-105200382	UCCUUUGCCCACUUUUUCAA	4810
54790 2 2202	+	chr4:105200363-105200383	CCUUUGCCCACUUUUUCAAU	4811
54790 2 2204	+	chr4:105200364-105200384	CUUUGCCCACUUUUUCAAUG	4812
54790 2 2224	+	chr4:105200419-105200439	UUUAAGAUCUUAUAGAUGC	4813
54790 2 2230	+	chr4:105200469-105200489	AAAUUUUUCUCCCAUUCUGU	4814
54790 2 2257	+	chr4:105200560-105200580	UGUGAAUUUUUGCUAUGAAC	4815
54790 2 2264	+	chr4:105200597-105200617	UAUGUUUAAUUUUAAACUCCC	4816
54790 2 2290	+	chr4:105200657-105200677	UGUUUUUGUUUUUGUUUUUU	4817
54790 2 2298	+	chr4:105200663-105200683	UGUUUUUGUUUUUUUGGAGA	4818
54790 2 2312	+	chr4:105200687-105200707	GUCUCACGCUGUCACCAGUC	4819
54790 2 2314	+	chr4:105200694-105200714	GCUGUCACCAGUCUGGAGUG	4820
54790 2 2315	+	chr4:105200708-105200728	GGAGUGUGGUGAUACAAUCU	4821
54790 2 2318	+	chr4:105200732-105200752	UCAUUGCAACCUCCACAUUC	4822
54790 2 2319	+	chr4:105200733-105200753	CAUUGCAACCUCCACAUUCC	4823
54790 2 2328	+	chr4:105200772-105200792	GCCUCAGCCUCCUGAGUAGC	4824
54790 2 2329	+	chr4:105200773-105200793	CCUCAGCCUCCUGAGUAGCU	4825
54790 2 2330	+	chr4:105200781-105200801	UCCUGAGUAGCUGGGACUAC	4826
54790 2 2333	+	chr4:105200828-105200848	UUUUGUAUUUUUAGUAAAGA	4827
54790 2 2334	+	chr4:105200829-105200849	UUUGUAUUUUUAGUAAAGAU	4828
54790 2 2335	+	chr4:105200830-105200850	UUGUAUUUUUAGUAAAGAU	4829
54790 2 2344	+	chr4:105200844-105200864	AAGAUGGGGUUUCACCAUGU	4830
54790 2 2346	+	chr4:105200849-105200869	GGGGUUUCACCAUGUUGGCC	4831
54790 2 2347	+	chr4:105200853-105200873	UUUCACCAUGUUGGCCAGGA	4832
54790 2 2354	+	chr4:105200905-105200925	GCCUCAGCCUCCCAAAGUGC	4833
54790 2 2356	+	chr4:105200906-105200926	CCUCAGCCUCCCAAAGUGCU	4834
54790 2 2357	+	chr4:105200914-105200934	UCCCAAAGUGCUGGGAUUAC	4835
54790 2 2360	+	chr4:105200933-105200953	CAGGCUUGAGCCACCACACC	4836
54790 2 2361	+	chr4:105200940-105200960	GAGCCACCACACCUGGCCCC	4837
54790 2 2371	+	chr4:105200983-105201003	AGAAAAAAGAUUGACUUCAC	4838
54790 2 2391	+	chr4:105201067-105201087	UGAGUUACUUGAUAAUACCA	4839

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 2400	+	chr4:105201105-105201125	UUGAAUCCUUCAACCCCUUG	4840
54790 2 2423	+	chr4:105201204-105201224	CUUGAUACAUUUUUUAAAGC	4841
54790 2 2432	+	chr4:105201250-105201270	UUAUCUCUUCUUCAAAAAAA	4842
54790 2 2438	+	chr4:105201281-105201301	CCCCCACAAUGUGUAAUUU	4843
54790 2 2441	+	chr4:105201297-105201317	AUUUAGGAAUUGUUUUCUUAU	4844
54790 2 2445	+	chr4:105201302-105201322	GGAAUUGUUUUCUUAUUGGAG	4845
54790 2 2453	+	chr4:105201338-105201358	AUUUUAGUUGCUCUAAUGCA	4846
54790 2 2460	+	chr4:105201359-105201379	GGUGUUUCCUAAAAAGUUUA	4847
54790 2 2471	+	chr4:105201405-105201425	AUGAUAGUAAAUAUACAAU	4848
54790 2 2474	+	chr4:105201406-105201426	UGAUAGUAAAUAUACAAUA	4849
54790 2 2475	+	chr4:105201407-105201427	GAUAGUAAAUAUACAAUAG	4850
54790 2 2476	+	chr4:105201408-105201428	AUAGUAAAUAUACAAUAGG	4851
54790 2 2493	+	chr4:105201519-105201539	AAAUCAAACAGUUCCACAAG	4852
54790 2 2508	+	chr4:105201572-105201592	UUUUAAACUUAACCUUACUG	4853
54790 2 2510	+	chr4:105201573-105201593	UUUAAACUUAACCUUACUGA	4854
54790 2 2511	+	chr4:105201574-105201594	UUAAACUUAACCUUACUGAG	4855
54790 2 2517	+	chr4:105201582-105201602	AACCUUACUGAGGGGUUUUA	4856
54790 2 2526	+	chr4:105201629-105201649	GCAAAGUAUAAAGUAAUAGA	4857
54790 2 2528	+	chr4:105201643-105201663	AAUAGAAGGUUACCAAGUUG	4858
54790 2 2534	+	chr4:105201678-105201698	UAGUGCCAAUACAGUUAAAA	4859
54790 2 2539	+	chr4:105201706-105201726	UUAACAGAACAUUCUUCAUCC	4860
54790 2 2552	+	chr4:105201743-105201763	UUUUUUUUUUUUUUUCAGAC	4861
54790 2 2553	+	chr4:105201744-105201764	UUUUUUUUUUUUUUUCAGACA	4862
54790 2 2571	+	chr4:105201770-105201790	CACUCCUGUUGCCCAGACUG	4863
54790 2 2573	+	chr4:105201778-105201798	UUGCCCAGACUGCGGUGCAG	4864
54790 2 2576	+	chr4:105201789-105201809	GCGGUGCAGUGGCCUGAUUG	4865
54790 2 2578	+	chr4:105201814-105201834	CACUGCAGCCUCAACUUCCC	4866
54790 2 2579	+	chr4:105201820-105201840	AGCCUCAACUUCCCAGGCUC	4867
54790 2 2584	+	chr4:105201862-105201882	UCCAGAGUAGCUGAGACCAC	4868
54790 2 2586	+	chr4:105201863-105201883	CCAGAGUAGCUGAGACCACA	4869
54790 2 2588	+	chr4:105201864-105201884	CAGAGUAGCUGAGACCACAG	4870
54790 2 2589	+	chr4:105201881-105201901	CAGGGGCAUGCCACCACCCC	4871
54790 2 2592	+	chr4:105201911-105201931	UUUGUAUUUUUUGUAGAGAC	4872
54790 2 2595	+	chr4:105201912-105201932	UUGUAUUUUUUGUAGAGACA	4873
54790 2 2604	+	chr4:105201931-105201951	AGGGUUUUGCCAUGUUGCCC	4874
54790 2 2609	+	chr4:105201949-105201969	CCAGGCUGUUCGCAAACUCC	4875
54790 2 2611	+	chr4:105201973-105201993	CUCAAGCAAUCCACCUGCCU	4876
54790 2 2613	+	chr4:105201989-105202009	GCCUCGGCUUCCCAAAGUGC	4877
54790 2 2617	+	chr4:105201997-105202017	UUCCCAAAGUGCUGGAAUUA	4878
54790 2 2619	+	chr4:105201998-105202018	UCCCAAAGUGCUGGAAUUAU	4879
54790 2 2625	+	chr4:105202026-105202046	GCUGCCACACCCAGCCCCUC	4880
54790 2 2628	+	chr4:105202058-105202078	AUUACCAACUUCUGUCUUCC	4881
54790 2 2633	+	chr4:105202073-105202093	CUUCCAGGUUUUUUAUGUCCU	4882
54790 2 2641	+	chr4:105202096-105202116	AAAUUUUAUGCAUAUUUUUAG	4883
54790 2 2659	+	chr4:105202216-105202236	AUACUUUAACUUAUUAUAGA	4884
54790 2 2665	+	chr4:105202232-105202252	UAGAAGGCUUACAAAACUG	4885
54790 2 2691	+	chr4:105202391-105202411	GUGAAGCAGCGAAUUUCUAG	4886
54790 2 2693	+	chr4:105202395-105202415	AGCAGCGAAUUUCUAGAGGC	4887

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 2694	+	chr4:105202396-105202416	GCAGCGAAUUUCUAGAGGCU	4888
54790 2 2697	+	chr4:105202409-105202429	AGAGGCUGGGUUCACGCUUC	4889
54790 2 2699	+	chr4:105202425-105202445	CUUCAGGUCCUCUAAAUCCU	4890
54790 2 2717	+	chr4:105202527-105202547	AAUUUUUAUUGAACAAAUAC	4891
54790 2 2730	+	chr4:105202566-105202586	CUCAUUGCUCUUGAAUACAU	4892
54790 2 2741	+	chr4:105202606-105202626	UGAAAUUCUGUUUUCCUUA	4893
54790 2 2745	+	chr4:105202620-105202640	CCUUAAGGCAGUCAUUUUU	4894
54790 2 2756	+	chr4:105202670-105202690	UAGUAACAUCUAACUUCAG	4895
54790 2 2765	+	chr4:105202718-105202738	AUAUGCCUACUUUUCAUAUC	4896
54790 2 2789	+	chr4:105202806-105202826	AAUUGCUGUCAACAAAGUAG	4897
54790 2 2794	+	chr4:105202849-105202869	UUCAUUGUGAAAACAUGAAA	4898
54790 2 2798	+	chr4:105202868-105202888	AUGGCUGUUAACUAUACAUC	4899
54790 2 2802	+	chr4:105202883-105202903	ACAUCAGGCAAAAUAAAAC	4900
54790 2 2805	+	chr4:105202902-105202922	CAGGAAAUUAAACAUAUCC	4901
54790 2 2807	+	chr4:105202908-105202928	AUAUAAACAUAUCCUGGAAC	4902
54790 2 2808	+	chr4:105202909-105202929	UAUAAACAUAUCCUGGAACA	4903
54790 2 2813	+	chr4:105202928-105202948	AGGGCAGAGUAUGAGUAAUA	4904
54790 2 2815	+	chr4:105202944-105202964	AAUAAGGUUAUCAAUAUAAU	4905
54790 2 2824	+	chr4:105202988-105203008	AAUGUCUUAAGAAAUGUCAC	4906
54790 2 2828	+	chr4:105202997-105203017	AGAAAUUGUCACUGGAAAGAC	4907
54790 2 2831	+	chr4:105203006-105203026	ACUGGAAAGACUGGAGUACU	4908
54790 2 2838	+	chr4:105203049-105203069	UUGAUUCCUAACACUGUGCU	4909
54790 2 2843	+	chr4:105203056-105203076	CUAACACUGUGCUUGGCACA	4910
54790 2 2844	+	chr4:105203060-105203080	CACUGUGCUUGGCACAUGGU	4911
54790 2 2847	+	chr4:105203081-105203101	GGUAAUUAUAAAUGUGUGA	4912
54790 2 2855	+	chr4:105203123-105203143	CAAUUAGUGACUAAGAGAGU	4913
54790 2 2858	+	chr4:105203128-105203148	AGUGACUAAGAGAGUUGGAA	4914
54790 2 2859	+	chr4:105203129-105203149	GUGACUAAGAGAGUUGGAAA	4915
54790 2 2862	+	chr4:105203147-105203167	AAGGGCUAUCAAUUUCAAU	4916
54790 2 2871	+	chr4:105203178-105203198	AGACAUUUUUACGUAAGAUU	4917
54790 2 2872	+	chr4:105203179-105203199	GACAUUUUUACGUAAGAUUU	4918
54790 2 2888	+	chr4:105203250-105203270	CCAUUCCUACAUUGACCAUG	4919
54790 2 2891	+	chr4:105203262-105203282	UGACCAUGUGGACUCAUAUU	4920
54790 2 2901	+	chr4:105203304-105203324	AUAAACAAAGCACCAAAGU	4921
54790 2 2904	+	chr4:105203310-105203330	AAAGCACCAAAGUUGGAAA	4922
54790 2 2906	+	chr4:105203323-105203343	UUGGAAAAGGAAGUAGUAGU	4923
54790 2 2911	+	chr4:105203328-105203348	AAAGGAAGUAGUAGUAGGAG	4924
54790 2 2912	+	chr4:105203329-105203349	AAGGAAGUAGUAGUAGGAGA	4925
54790 2 2914	+	chr4:105203351-105203371	GUUUUAAGCUAUGUAUUUAC	4926
54790 2 2917	+	chr4:105203352-105203372	UUUUUAAGCUAUGUAUUUACU	4927
54790 2 2934	+	chr4:105203409-105203429	UAAACAGUACUGUAAUCACU	4928
54790 2 2935	+	chr4:105203410-105203430	AAACAGUACUGUAAUCACUU	4929
54790 2 2940	+	chr4:105203439-105203459	AUGUGCUUUGUGUCAGACAA	4930
54790 2 2951	+	chr4:105203495-105203515	AAUACAUAUACAUAACACAGA	4931
54790 2 2953	+	chr4:105203496-105203516	AUACAUAUACAUAACACAGAA	4932
54790 2 2956	+	chr4:105203505-105203525	AUUACACAGAAGGGAGUGCC	4933
54790 2 2966	+	chr4:105203560-105203580	AAUACAUAUACAUAACACAGA	4934
54790 2 2969	+	chr4:105203561-105203581	AUACAUAUACAUAACACAGAA	4935

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 2971	+	chr4:105203570-105203590	AUUACACAGAAGGGAGUGCC	4936
54790 2 2982	+	chr4:105203625-105203645	AAUACAUUACAUUACACAGA	4937
54790 2 2984	+	chr4:105203626-105203646	AUACAUUACAUUACACAGAA	4938
54790 2 2986	+	chr4:105203635-105203655	AUUACACAGAAGGGAGUGCC	4939
54790 2 2990	+	chr4:105203641-105203661	CAGAAGGGAGUGCCUGGCUU	4940
54790 2 2991	+	chr4:105203642-105203662	AGAAGGGAGUGCCUGGCUUU	4941
54790 2 2996	+	chr4:105203689-105203709	CAUAGCACAAUGCUGCCAUA	4942
54790 2 2997	+	chr4:105203693-105203713	GCACAAUGCUGCCAUACGGU	4943
54790 2 2999	+	chr4:105203713-105203733	AGGUAAUACCAAGACAAAUC	4944
54790 2 3000	+	chr4:105203714-105203734	GGUAAUACCAAGACAAUUA	4945
54790 2 3003	+	chr4:105203735-105203755	GGCCGUUAUUAACAACCUUG	4946
54790 2 3007	+	chr4:105203746-105203766	ACAACCUUGAGGAAAUGUCU	4947
54790 2 3011	+	chr4:105203747-105203767	CAACCUUGAGGAAAUGUCUU	4948
54790 2 3018	+	chr4:105203783-105203803	AUUUUUGUUUAAUUUAUAUA	4949
54790 2 3028	+	chr4:105203823-105203843	AAGUCAUCCCAAACUCUUCG	4950
54790 2 3033	+	chr4:105203868-105203888	CUGUUUUUUAAUGUUUCUAA	4951
54790 2 3044	+	chr4:105203897-105203917	UGUAUAAUCUAUUAGAAAAC	4952
54790 2 3045	+	chr4:105203910-105203930	AGAAAACUGGCCAAGUGCAG	4953
54790 2 3049	+	chr4:105203937-105203957	UGCCUGUAAUCGCAGCACUU	4954
54790 2 3050	+	chr4:105203938-105203958	GCCUGUAAUCGCAGCACUUU	4955
54790 2 3052	+	chr4:105203941-105203961	UGUAAUCGCAGCACUUUGGG	4956
54790 2 3053	+	chr4:105203947-105203967	CGCAGCACUUUGGGAGGCCA	4957
54790 2 3055	+	chr4:105203950-105203970	AGCACUUUGGGAGGCCAAGG	4958
54790 2 3056	+	chr4:105203951-105203971	GCACUUUGGGAGGCCAAGGC	4959
54790 2 3060	+	chr4:105203965-105203985	CAAGGCGGGUAGAUAUACCUG	4960
54790 2 3063	+	chr4:105203970-105203990	CGGGUAGAUAUACCUGAGGUC	4961
54790 2 3066	+	chr4:105203997-105204017	UGAGACCAGCCUAGCCAAUA	4962
54790 2 3070	+	chr4:105204035-105204055	UAAAAAUACAAAAAUUAGCC	4963
54790 2 3071	+	chr4:105204043-105204063	CAAAAAUUAAGCCAGGCGUAG	4964
54790 2 3074	+	chr4:105204071-105204091	GCCUGUAAUCCCAGCUACUC	4965
54790 2 3076	+	chr4:105204074-105204094	UGUAAUCCCAGCUACUCAGG	4966
54790 2 3078	+	chr4:105204080-105204100	CCCAGCUACUCAGGAGGCUG	4967
54790 2 3081	+	chr4:105204084-105204104	GCUACUCAGGAGGCUGAGGC	4968
54790 2 3086	+	chr4:105204102-105204122	GCAGGAGAAUCUCUUGAACC	4969
54790 2 3088	+	chr4:105204103-105204123	CAGGAGAAUCUCUUGAACCC	4970
54790 2 3090	+	chr4:105204106-105204126	GAGAAUCUCUUGAACCCGGG	4971
54790 2 3092	+	chr4:105204111-105204131	UCUCUUGAACCCGGGAGGCG	4972
54790 2 3099	+	chr4:105204151-105204171	CGCGUCACUGCAUUCCAGCC	4973
54790 2 3100	+	chr4:105204152-105204172	GCGUCACUGCAUUCCAGCCU	4974
54790 2 3104	+	chr4:105204158-105204178	CUGCAUUCCAGCCUGGGCGA	4975
54790 2 3117	+	chr4:105204316-105204336	UUAAGCAUCUCUCUUCCUCA	4976
54790 2 3126	+	chr4:105204348-105204368	UUGAAUCCUUAUGUGCAUAUG	4977
54790 2 3135	+	chr4:105204419-105204439	AUUAGACAUCAUGUAAUAUC	4978
54790 2 3145	+	chr4:105204469-105204489	AACUAAGAAUAAUUUACCAA	4979
54790 2 3168	+	chr4:105204543-105204563	ACAUUAAGAGUUACGUUUCU	4980
54790 2 3177	+	chr4:105204566-105204586	AAAAUUGAAAAGAAUAUCUG	4981
54790 2 3180	+	chr4:105204574-105204594	AAAGAAUAUCUGUGGCACAA	4982
54790 2 3181	+	chr4:105204575-105204595	AAGAAUAUCUGUGGCACAAU	4983

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 3183	+	chr4:105204581-105204601	AUCUGUGGCACAAUGGGCUC	4984
54790 2 3184	+	chr4:105204582-105204602	UCUGUGGCACAAUGGGCUCU	4985
54790 2 3186	+	chr4:105204594-105204614	UGGGCUCUGGGUAUAAUUGC	4986
54790 2 3193	+	chr4:105204629-105204649	GUUUAAAGAAU AUUUUCAAU	4987
54790 2 3197	+	chr4:105204645-105204665	CAAUAGGUUAUAAGUUUAUUU	4988
54790 2 3208	+	chr4:105204692-105204712	UUUAGCAGUAUAUAUUUCCC	4989
54790 2 3213	+	chr4:105204710-105204730	CCUGGAACACCAUGCACUCU	4990
54790 2 3214	+	chr4:105204726-105204746	CUCUAGGUUUUCUAAUUUAU	4991
54790 2 3218	+	chr4:105204740-105204760	AUUUAUUGGUUUAAAAUACA	4992
54790 2 3227	+	chr4:105204775-105204795	UAAAUAUUCUCUGUAUCUGU	4993
54790 2 3242	+	chr4:105204861-105204881	AUUCACUAGAUUAUUUCCA	4994
54790 2 3277	+	chr4:105204986-105205006	GUUUUCCUAAAUAUAGUGAUU	4995
54790 2 3308	+	chr4:105205080-105205100	UAUAGCCAAUGCAUUUUGAG	4996
54790 2 3330	+	chr4:105205156-105205176	CUUUGAACAAAGAGUUAUUU	4997
54790 2 3338	+	chr4:105205166-105205186	AGAGUUAUUUAGGAAAAGAA	4998
54790 2 3360	+	chr4:105205262-105205282	UACUUCUUUAUAUUUUGUUG	4999
54790 2 3392	+	chr4:105205373-105205393	CUAAGAAAAUUUUCUUUGUC	5000
54790 2 3393	+	chr4:105205379-105205399	AAAUUUUCUUUGUCAGGAUA	5001
54790 2 3398	+	chr4:105205388-105205408	UUGUCAGGAUAAGGCACAUG	5002
54790 2 3422	+	chr4:105205502-105205522	GAAGUCCCCCCCCAACCCAAU	5003
54790 2 3431	+	chr4:105205543-105205563	UCCUAUUCACACAUUCUUGA	5004
54790 2 3462	+	chr4:105205654-105205674	GUUUUUCACUCUUGUUGCCU	5005
54790 2 3466	+	chr4:105205658-105205678	UUCACUCUUGUUGCCUAGGC	5006
54790 2 3470	+	chr4:105205668-105205688	UUGCCUAGGCUGGAGUGCAA	5007
54790 2 3474	+	chr4:105205672-105205692	CUAGGCUGGAGUGCAAUGGC	5008
54790 2 3475	+	chr4:105205703-105205723	UCACUGCAACCUCCGCCUCC	5009
54790 2 3482	+	chr4:105205743-105205763	GCCUCAGCCUCCCGAGUAGC	5010
54790 2 3484	+	chr4:105205744-105205764	CCUCAGCCUCCCGAGUAGCU	5011
54790 2 3485	+	chr4:105205752-105205772	UCCCGAGUAGCUGGGAUUUAU	5012
54790 2 3487	+	chr4:105205771-105205791	UAGGCAUGCACCACCACUCC	5013
54790 2 3491	+	chr4:105205801-105205821	UUUUCUAUUUUUAGUAGAGA	5014
54790 2 3502	+	chr4:105205817-105205837	GAGACGGAGUUUCUCCAUGU	5015
54790 2 3503	+	chr4:105205822-105205842	GGAGUUUCUCCAUGUUGGUC	5016
54790 2 3504	+	chr4:105205826-105205846	UUUCUCCAUGUUGGUCAGGC	5017
54790 2 3508	+	chr4:105205847-105205867	GGUCUCAACUCCCAACCUC	5018
54790 2 3510	+	chr4:105205881-105205901	CUUCAGCCUCCUAAAGUGCU	5019
54790 2 3512	+	chr4:105205889-105205909	UCCUAAAGUGCUAGGAUUAC	5020
54790 2 3518	+	chr4:105205929-105205949	AGCCGAAAACAUUAUCUUA	5021
54790 2 3532	+	chr4:105205992-105206012	AAAAUACUGCUUAAAAGAUC	5022
54790 2 3535	+	chr4:105206045-105206065	UAUUUCUCUUUUACUUGUCU	5023
54790 2 3544	+	chr4:105206070-105206090	UCUAGUUCAGAUUUUAUAGUU	5024
54790 2 3553	+	chr4:105206110-105206130	UGUUAGUGCUUCAGCCCAUC	5025
54790 2 3558	+	chr4:105206114-105206134	AGUGCUUCAGCCCAUCUGGU	5026
54790 2 3559	+	chr4:105206115-105206135	GUGCUUCAGCCCAUCUGGUU	5027
54790 2 3562	+	chr4:105206116-105206136	UGCUUCAGCCCAUCUGGUUG	5028
54790 2 3567	+	chr4:105206135-105206155	GGGGAACAGCUCUAUCCCAC	5029
54790 2 3568	+	chr4:105206136-105206156	GGGAACAGCUCUAUCCCACU	5030
54790 2 3572	+	chr4:105206167-105206187	CUUUCCUCAUGAGUGACGCC	5031

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 3573	+	chr4:105206168-105206188	UUUCCUCAUGAGUGACGCCA	5032
54790 2 3584	+	chr4:105206239-105206259	UUCCCCAGCUUCGCUGCCUU	5033
54790 2 3596	+	chr4:105206309-105206329	UCGCCUUUAGUCCUUGAUGC	5034
54790 2 3599	+	chr4:105206310-105206330	CGCCUUUAGUCCUUGAUGCU	5035
54790 2 3601	+	chr4:105206311-105206331	GCCUUUAGUCCUUGAUGCUG	5036
54790 2 3604	+	chr4:105206320-105206340	CCUUGAUGCUGGGGACCUUU	5037
54790 2 3607	+	chr4:105206324-105206344	GAUGCUGGGGACCUUUUGGU	5038
54790 2 3609	+	chr4:105206325-105206345	AUGCUGGGGACCUUUUGGUU	5039
54790 2 3616	+	chr4:105206347-105206367	GAAGACAGCUUCCUUAUGUC	5040
54790 2 3617	+	chr4:105206348-105206368	AAGACAGCUUCCUUAUGUCA	5041
54790 2 3621	+	chr4:105206365-105206385	UCAGGGUGAGCCUGCUACAC	5042
54790 2 3628	+	chr4:105206431-105206451	GUUUCUUUGUCUCCCUCAA	5043
54790 2 3635	+	chr4:105206442-105206462	UCCCUCAA AUGGUACAAACG	5044
54790 2 3637	+	chr4:105206445-105206465	CUCAA AUGGUACAAACGUGG	5045
54790 2 3638	+	chr4:105206446-105206466	UCAA AUGGUACAAACGUGGA	5046
54790 2 3648	+	chr4:105206520-105206540	GCCCUCCAAUAAGAGAUGA	5047
54790 2 3657	+	chr4:105206569-105206589	UCCACAACUGACUUUAAAAG	5048
54790 2 3658	+	chr4:105206570-105206590	CCACAACUGACUUUAAAAGA	5049
54790 2 3660	+	chr4:105206575-105206595	ACUGACUUUAAAAGAGGGAC	5050
54790 2 3662	+	chr4:105206576-105206596	CUGACUUUAAAAGAGGGACU	5051
54790 2 3664	+	chr4:105206581-105206601	UUUAAAAGAGGGACUGGGAU	5052
54790 2 3665	+	chr4:105206582-105206602	UUAAAAGAGGGACUGGGAUU	5053
54790 2 3670	+	chr4:105206607-105206627	CUUAGUGAUGACUUUUA AUG	5054
54790 2 3682	+	chr4:105206659-105206679	UAAACUCUCUGCCUCUCAGC	5055
54790 2 3685	+	chr4:105206672-105206692	UCUCAGCUGGCACUAU UCCA	5056
54790 2 3687	+	chr4:105206689-105206709	CCAUGGUAUUUUAGUGCUAA	5057
54790 2 3689	+	chr4:105206690-105206710	CAUGGUAUUUUAGUGCUAAU	5058
54790 2 3693	+	chr4:105206691-105206711	AUGGUAUUUUAGUGCUAAUG	5059
54790 2 3694	+	chr4:105206692-105206712	UGGUAUUUUAGUGCUAAUGG	5060
54790 2 3711	+	chr4:105206740-105206760	UGACUGUUUAAAUCAUUUAC	5061
54790 2 3716	+	chr4:105206747-105206767	UUAAAUCAUUUACUGGAAAG	5062
54790 2 3717	+	chr4:105206748-105206768	UAAAUCAUUUACUGGAAAGA	5063
54790 2 3725	+	chr4:105206820-105206840	GAUUUUGUUCAUGAACAU GA	5064
54790 2 3732	+	chr4:105206851-105206871	UUCUUAAAUGCCUUUAAUAU	5065
54790 2 3738	+	chr4:105206866-105206886	AAUAUUGGAUACUGCUU UCA	5066
54790 2 3743	+	chr4:105206887-105206907	GGAAAUUUAAAAUAGCAAGC	5067
54790 2 3756	+	chr4:105206964-105206984	CAAGUCAUAUAAAACAAGUU	5068
54790 2 3779	+	chr4:105207068-105207088	AGAUUCCAAACAUAUAUAUA	5069
54790 2 3787	+	chr4:105207116-105207136	UACAUAAAUUUUACUAGAAG	5070
54790 2 3799	+	chr4:105207167-105207187	UCAAAAAGAUCUCAAUCUU	5071
54790 2 3801	+	chr4:105207168-105207188	CAAAAAGAUCUCAAUCUUA	5072
54790 2 3804	+	chr4:105207189-105207209	GGACUAAUAUUGUAAGUAUA	5073
54790 2 3806	+	chr4:105207190-105207210	GACUAAUAUUGUAAGUAUAC	5074
54790 2 3809	+	chr4:105207191-105207211	ACUAAUAUUGUAAGUAUACG	5075
54790 2 3816	+	chr4:105207234-105207254	UAUCUUGUGAGUUUUUAGUU	5076
54790 2 3840	+	chr4:105207319-105207339	ACUCUCCUUUUGAAGUACAA	5077
54790 2 3842	+	chr4:105207320-105207340	CUCUCCUUUUGAAGUACAAA	5078
54790 2 3849	+	chr4:105207346-105207366	CUAAAGUGAAUAACUCAAC	5079

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 3868	+	chr4:105207437-105207457	GUUUUAUUGCAUAGUUUCUU	5080
54790 2 3870	+	chr4:105207438-105207458	UUUUAUUGCAUAGUUUCUUU	5081
54790 2 3877	+	chr4:105207452-105207472	UUCUUUGGGAUAUACAUUGA	5082
54790 2 3885	+	chr4:105207459-105207479	GGAUAUACAUUGAAGGAGAA	5083
54790 2 3889	+	chr4:105207462-105207482	UAUACAUUGAAGGAGAAAGG	5084
54790 2 3893	+	chr4:105207465-105207485	ACAUUGAAGGAGAAAGGAGG	5085
54790 2 3894	+	chr4:105207466-105207486	CAUUGAAGGAGAAAGGAGGA	5086
54790 2 3898	+	chr4:105207485-105207505	AGGGAGUUUUAAAAGACAAG	5087
54790 2 3903	+	chr4:105207508-105207528	AAAGCCCUUUCUGCUUGUUU	5088
54790 2 3904	+	chr4:105207514-105207534	CUUUCUGCUUGUUUUUGGCUA	5089
54790 2 3913	+	chr4:105207541-105207561	CAUUUCAGUGUCUGUAUUUA	5090
54790 2 3915	+	chr4:105207542-105207562	AUUUCAGUGUCUGUAUUUAA	5091
54790 2 3919	+	chr4:105207553-105207573	UGUAUUUAAGGGAUCAUAAA	5092
54790 2 3922	+	chr4:105207559-105207579	UAAGGGAUCAUAAAAGGAAC	5093
54790 2 3926	+	chr4:105207568-105207588	AUAAAAGGAACUGGAAAGAC	5094
54790 2 3927	+	chr4:105207577-105207597	ACUGGAAAGACUGGUCACAA	5095
54790 2 3929	+	chr4:105207602-105207622	GCUCUGUACCUGUAUGAUUU	5096
54790 2 3940	+	chr4:105207649-105207669	CUUGUUAACCUAUACUGCUG	5097
54790 2 3943	+	chr4:105207672-105207692	AAGUCAUUCAUUAUGCAGUU	5098
54790 2 3950	+	chr4:105207706-105207726	CAAUAUAAGUUCACAGCUCU	5099
54790 2 3970	+	chr4:105207800-105207820	AAGAAGAUAGAAUCAAUACU	5100
54790 2 3971	+	chr4:105207811-105207831	AUCAAUACUUGGUGAUUGAU	5101
54790 2 3974	+	chr4:105207826-105207846	UUGAUAGGUUAUUUUUUAAA	5102
54790 2 3977	+	chr4:105207827-105207847	UGAUAGGUUAUUUUUUAAAA	5103
54790 2 3989	+	chr4:105207850-105207870	AAGAAAGAAUUAACAUCCA	5104
54790 2 3992	+	chr4:105207869-105207889	AUGGUUUCUUCUUAAGUAAC	5105
54790 2 3994	+	chr4:105207870-105207890	UGGUUUCUUCUUAAGUAACU	5106
54790 2 3997	+	chr4:105207871-105207891	GGUUUCUUCUUAAGUAACUG	5107
54790 2 3998	+	chr4:105207872-105207892	GUUUCUUCUUAAGUAACUGG	5108
54790 2 4000	+	chr4:105207873-105207893	UUUCUUCUUAAGUAACUGGG	5109
54790 2 4006	+	chr4:105207898-105207918	GAUAGUAUCCCUCACACCAA	5110
54790 2 4008	+	chr4:105207899-105207919	AUAGUAUCCCUCACACCAAU	5111
54790 2 4010	+	chr4:105207900-105207920	UAGUAUCCCUCACACCAAUG	5112
54790 2 4012	+	chr4:105207915-105207935	CAAUGGGGAGUAUAGAUGAC	5113
54790 2 4015	+	chr4:105207920-105207940	GGGAGUAUAGAUGACAGGUU	5114
54790 2 4021	+	chr4:105207947-105207967	AAAGACAGUGAAUUCCAUUU	5115
54790 2 4029	+	chr4:105207973-105207993	AGUUGAAUUUGAAGUGCCUA	5116
54790 2 4031	+	chr4:105207974-105207994	GUUGAAUUUGAAGUGCCUAU	5117
54790 2 4033	+	chr4:105207983-105208003	GAAGUGCCUAUGGGACAUAAC	5118
54790 2 4037	+	chr4:105207997-105208017	ACAUACAGGUACAGAUGACU	5119
54790 2 4050	+	chr4:105208079-105208099	UAAAUUGCUCUUGAGUUUCA	5120
54790 2 4051	+	chr4:105208080-105208100	AAAUUGCUCUUGAGUUUCAU	5121
54790 2 4055	+	chr4:105208091-105208111	UGAGUUCAUGGGAAUAAAAU	5122
54790 2 4058	+	chr4:105208106-105208126	AAAAUAGGUCAUUCUGCAAA	5123
54790 2 4060	+	chr4:105208126-105208146	UGGUUAUCUCAUAUCUCC	5124
54790 2 4063	+	chr4:105208137-105208157	AUAUCUCCUGGCCAUCUCU	5125
54790 2 4064	+	chr4:105208138-105208158	UAUCUCCUGGCCAUCUCUU	5126
54790 2 4074	+	chr4:105208194-105208214	UCUAAAUUCUCAUGUUUUUA	5127

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 4076	+	chr4:105208207-105208227	GUUUUUAAGGCUCUCAUCUU	5128
54790 2 4082	+	chr4:105208221-105208241	CAUCUUAGGCCAACUUAUCU	5129
54790 2 4083	+	chr4:105208222-105208242	AUCUUAGGCCAACUUAUCUU	5130
54790 2 4094	+	chr4:105208276-105208296	UCUCUAAAUUUGUGCUUUUA	5131
54790 2 4097	+	chr4:105208293-105208313	UUAAGGCCCCAUUCUCAAGC	5132
54790 2 4101	+	chr4:105208307-105208327	UCAAGCUGGCUUCUCUGUUU	5133
54790 2 4104	+	chr4:105208310-105208330	AGCUGGCUUCUCUGUUUUGG	5134
54790 2 4107	+	chr4:105208311-105208331	GCUGGCUUCUCUGUUUUGGU	5135
54790 2 4108	+	chr4:105208317-105208337	UUCUCUGUUUUGGUGGGAAC	5136
54790 2 4113	+	chr4:105208350-105208370	UCAUUUGUAAACAACCCAAA	5137
54790 2 4119	+	chr4:105208365-105208385	CCAAAUGGCUAGCAUUGAGC	5138
54790 2 4125	+	chr4:105208411-105208431	UUACAUUUUGAGUUAUCUGA	5139
54790 2 4133	+	chr4:105208430-105208450	AAGGAUCAUAUCUCAAAACU	5140
54790 2 4143	+	chr4:105208492-105208512	UUUUCUUGCCUUUAAGUAUA	5141
54790 2 4145	+	chr4:105208493-105208513	UUUCUUGCCUUUAAGUAUAA	5142
54790 2 4160	+	chr4:105208544-105208564	ACAAGUUAUUUUUUUAAUUAU	5143
54790 2 4187	+	chr4:105208658-105208678	AGCAUGAAGAAGAGUAAAAU	5144
54790 2 4190	+	chr4:105208663-105208683	GAAGAAGAGUAAAAUAGGAG	5145
54790 2 4191	+	chr4:105208670-105208690	AGUAAAAUAGGAGUGGAUAA	5146
54790 2 4192	+	chr4:105208678-105208698	AGGAGUGGAUAAAGGCACAG	5147
54790 2 4195	+	chr4:105208716-105208736	UCCAAUUAUUCUCAAGUUU	5148
54790 2 4210	+	chr4:105208768-105208788	UGUCUUCUGCUUUUUGACG	5149
54790 2 4218	+	chr4:105208788-105208808	UGGUAAACCUGCCAUAACAAA	5150
54790 2 4221	+	chr4:105208798-105208818	CCAUAACAAAAGGAAACAGC	5151
54790 2 4222	+	chr4:105208806-105208826	AAAGGAAACAGCAGGAAACU	5152
54790 2 4233	+	chr4:105208898-105208918	AAGUGUUUUAGAGUGAAACA	5153
54790 2 4238	+	chr4:105208912-105208932	GAAACAAGGAUAAAGAGACA	5154
54790 2 4240	+	chr4:105208936-105208956	UAUUAAAUUUUUACAUCUGC	5155
54790 2 4248	+	chr4:105208970-105208990	CAUGCCAGUAGAAUUAAGUU	5156
54790 2 4259	+	chr4:105209021-105209041	GAAAUAGAAUAGAUGCCUCA	5157
54790 2 4260	+	chr4:105209026-105209046	GAAAUAGAUGCCUCAAGGCA	5158
54790 2 4265	+	chr4:105209087-105209107	UAUAUAUAUAUGUUUGAGCG	5159
54790 2 4266	+	chr4:105209088-105209108	AUAUAUAUAUGUUUGAGCGA	5160
54790 2 4267	+	chr4:105209089-105209109	UAUAUAUAUGUUUGAGCGAG	5161
54790 2 4271	+	chr4:105209116-105209136	UCUAGCAAAACUGAAUACAC	5162
54790 2 4274	+	chr4:105209159-105209179	UUUUUUUAUCCAUCACUUU	5163
54790 2 4287	+	chr4:105209191-105209211	CAGCUGUGAGUUAUUCAACC	5164
54790 2 4293	+	chr4:105209227-105209247	AGUCUGAUUAAUAACGUUUA	5165
54790 2 4312	+	chr4:105209325-105209345	AAAUUGAAUUCCAUCCAAU	5166
54790 2 4314	+	chr4:105209326-105209346	AAUGAAUUCCAUCCAAUA	5167
54790 2 4317	+	chr4:105209329-105209349	GAAUUCCAUCCAAUAGGG	5168
54790 2 4326	+	chr4:105209371-105209391	CAGUGUUGACUGAGAUGCUC	5169
54790 2 4331	+	chr4:105209381-105209401	UGAGAUGCUCUGGAUGAGCC	5170
54790 2 4334	+	chr4:105209403-105209423	GACUCAGAGCUCACCAACUU	5171
54790 2 4338	+	chr4:105209427-105209447	UCUUUAUGUUAAGUAGUCAG	5172
54790 2 4340	+	chr4:105209428-105209448	CUUUAUGUUAAGUAGUCAGU	5173
54790 2 4341	+	chr4:105209429-105209449	UUUAUGUUAAGUAGUCAGUG	5174
54790 2 4348	+	chr4:105209477-105209497	UGUUCUACACCUCUUGAUAU	5175

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 4350	+	chr4:105209484-105209504	CACCUCUUGAUAUAGGUCAG	5176
54790 2 4358	+	chr4:105209544-105209564	AAACAGUACAUAUACCAAGU	5177
54790 2 4360	+	chr4:105209557-105209577	ACCAAGUUGGUUUGUCACAA	5178
54790 2 4363	+	chr4:105209558-105209578	CCAAGUUGGUUUGUCACAAU	5179
54790 2 4374	+	chr4:105209618-105209638	UUUGUGUGUAUGUUUCUGAA	5180
54790 2 4376	+	chr4:105209619-105209639	UUGUGUGUAUGUUUCUGAAU	5181
54790 2 4382	+	chr4:105209648-105209668	UACAUAUUUUACUCUCCU	5182
54790 2 4390	+	chr4:105209669-105209689	GGUGAAGAUGCUIIUUAUAAG	5183
54790 2 4400	+	chr4:105209701-105209721	AGAAAAUUAAGAAUGUUGU	5184
54790 2 4411	+	chr4:105209742-105209762	UUUAAACAGAAUUAGUAUAG	5185
54790 2 4419	+	chr4:105209761-105209781	GAGGUGUGAAGAUCUACUGA	5186
54790 2 4420	+	chr4:105209762-105209782	AGGUGUGAAGAUCUACUGAA	5187
54790 2 4423	+	chr4:105209778-105209798	UGAAGGGUGAUAAAGUAAGUG	5188
54790 2 4425	+	chr4:105209787-105209807	AUAAGUAAGUGUGGAAGAGA	5189
54790 2 4427	+	chr4:105209800-105209820	GAAGAGAUGGUGUUCAGCAU	5190
54790 2 4428	+	chr4:105209801-105209821	AAGAGAUGGUGUUCAGCAUU	5191
54790 2 4431	+	chr4:105209817-105209837	CAUUGGGCUUCAGUAUGAAU	5192
54790 2 4436	+	chr4:105209833-105209853	GAAUAGGUAGAAGAUGAGCA	5193
54790 2 4440	+	chr4:105209861-105209881	AGACAAGAAGUUCAUUCAAU	5194
54790 2 4441	+	chr4:105209870-105209890	GUUCAUUCAAUAGGCUGUUG	5195
54790 2 4445	+	chr4:105209889-105209909	GCGGUUAUCCAGCAAUGAGA	5196
54790 2 4449	+	chr4:105209907-105209927	GAUGGUGACAGCAUGAGCCA	5197
54790 2 4451	+	chr4:105209921-105209941	GAGCCAUGGUAGUAAAAGUA	5198
54790 2 4453	+	chr4:105209927-105209947	UGGUAGUAAAAGUAAGGACA	5199
54790 2 4455	+	chr4:105209938-105209958	GUAAGGACAUGGAUAAUUUG	5200
54790 2 4456	+	chr4:105209939-105209959	UAAGGACAUGGAUAAUUUGU	5201
54790 2 4462	+	chr4:105209972-105209992	AAUAAGAACAUAAGAACCGAU	5202
54790 2 4464	+	chr4:105209987-105210007	CCGAUAGGUUAUUUUUUAAA	5203
54790 2 4467	+	chr4:105209988-105210008	CGAUAGGUUAUUUUUUAAAC	5204
54790 2 4478	+	chr4:105210011-105210031	AAGAAAGAAUUAACAUCCA	5205
54790 2 4481	+	chr4:105210034-105210054	UUUCUUCUUAAGUAACUGCG	5206
54790 2 4488	+	chr4:105210059-105210079	GAUAGUACCCUCACACUGA	5207
54790 2 4490	+	chr4:105210060-105210080	AUAGUACCCUCACACUGAU	5208
54790 2 4491	+	chr4:105210061-105210081	UAGUACCCUCACACUGAUG	5209
54790 2 4493	+	chr4:105210076-105210096	UGAUGGGGAUGUAGAUGAC	5210
54790 2 4496	+	chr4:105210081-105210101	GGGAAUGUAGAUGACAGGUU	5211
54790 2 4504	+	chr4:105210106-105210126	UGAAAGAAUGAAUCCAUAUU	5212
54790 2 4512	+	chr4:105210132-105210152	AGUAGAGUUUGAAGUGCCUA	5213
54790 2 4514	+	chr4:105210133-105210153	GUAGAGUUUGAAGUGCCUAU	5214
54790 2 4516	+	chr4:105210142-105210162	GAAGUGCCUAUGGGACAUAC	5215
54790 2 4519	+	chr4:105210156-105210176	ACAUACAGGUACAGAUGACU	5216
54790 2 4525	+	chr4:105210194-105210214	CAAAUUGUGAACUCUGCUGA	5217
54790 2 4534	+	chr4:105210238-105210258	UGAAUUGCACUUGAGUUCA	5218
54790 2 4535	+	chr4:105210239-105210259	GAAUUGCACUUGAGUUCAU	5219
54790 2 4539	+	chr4:105210250-105210270	UGAGUUCAUGGGAAUAAAAU	5220
54790 2 4543	+	chr4:105210285-105210305	UUGUUAUCUCAUAUCUCC	5221
54790 2 4547	+	chr4:105210296-105210316	AUAUCUCCUGGCCAUCUCU	5222
54790 2 4548	+	chr4:105210297-105210317	UAUCUCCUGGCCAUCUCUU	5223

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 4556	+	chr4:105210342-105210362	UCUUUACAAUGUCAAAAUUC	5224
54790 2 4560	+	chr4:105210353-105210373	UCAAAAUUCUGGUGUUUUUA	5225
54790 2 4562	+	chr4:105210366-105210386	GUUUUUAAGGCCCCCAAUCUC	5226
54790 2 4564	+	chr4:105210370-105210390	UUAAGGCCCCCAAUCUCAGGC	5227
54790 2 4570	+	chr4:105210395-105210415	UCUCCAACUGUACUCUUACU	5228
54790 2 4571	+	chr4:105210396-105210416	CUCCAACUGUACUCUUACUU	5229
54790 2 4575	+	chr4:105210416-105210436	GGGAUGAUCUUAUCUAGUCA	5230
54790 2 4578	+	chr4:105210417-105210437	GGAUGAUCUUAUCUAGUCAU	5231
54790 2 4579	+	chr4:105210418-105210438	GAUGAUCUUAUCUAGUCAUG	5232
54790 2 4581	+	chr4:105210434-105210454	CAUGGGGCAUUAUUAAUACCAU	5233
54790 2 4582	+	chr4:105210438-105210458	GGGCAUUAUUAAUACCAUUGGU	5234
54790 2 4611	+	chr4:105210661-105210681	UUAGCUCAAGACAAAACUCU	5235
54790 2 4635	+	chr4:105210790-105210810	CCACUGCUAUUCUCUAGUUC	5236
54790 2 4639	+	chr4:105210821-105210841	UCCUUUCUCUUGUAUUACUG	5237
54790 2 4654	+	chr4:105210897-105210917	CUACCAGAGUGAUCUUUUAA	5238
54790 2 4659	+	chr4:105210942-105210962	CUUUUAUUAUAAUGCACCUA	5239
54790 2 4663	+	chr4:105210953-105210973	AUGCACCUAUGGCUUCCCAC	5240
54790 2 4667	+	chr4:105210990-105211010	CUUAACACUUUACUCCUCCA	5241
54790 2 4692	+	chr4:105211142-105211162	UCUAGCUGAAUCAUUCUUC	5242
54790 2 4693	+	chr4:105211157-105211177	CUUCCAGGUCAUUCUAUCAU	5243
54790 2 4719	+	chr4:105211310-105211330	UCUGAAAUUGUUUGUUUAUU	5244
54790 2 4727	+	chr4:105211340-105211360	UUUGUCUAGAUAAACUUCAC	5245
54790 2 4733	+	chr4:105211346-105211366	UAGAUAACUUCACUGGUGA	5246
54790 2 4749	+	chr4:105211444-105211464	GAAAGAAUGUUGAAGAGAAG	5247
54790 2 4750	+	chr4:105211445-105211465	AAAGAAUGUUGAAGAGAAGA	5248
54790 2 4753	+	chr4:105211465-105211485	GGGUCCAGUCCAGCCCCUG	5249
54790 2 4756	+	chr4:105211480-105211500	CCCUGAGGUGACCAGCAUUU	5250
54790 2 4758	+	chr4:105211481-105211501	CCUGAGGUGACCAGCAUUUA	5251
54790 2 4760	+	chr4:105211493-105211513	AGCAUUUAGGGAAUAAGCCG	5252
54790 2 4764	+	chr4:105211499-105211519	UAGGGAAUAAGCCGAGGCAG	5253
54790 2 4768	+	chr4:105211502-105211522	GGAAUAAGCCGAGGCAGAGG	5254
54790 2 4769	+	chr4:105211503-105211523	GAAUAAGCCGAGGCAGAGGA	5255
54790 2 4773	+	chr4:105211515-105211535	GCAGAGGAGGGCCAUUAAGA	5256
54790 2 4780	+	chr4:105211533-105211553	GAAGGAGCAAUGAGAGAUAG	5257
54790 2 4782	+	chr4:105211549-105211569	AUAGAGGAAAACUAAGAACA	5258
54790 2 4785	+	chr4:105211580-105211600	AAGUGAGAGUGUCCUAACAC	5259
54790 2 4788	+	chr4:105211593-105211613	CUAACACAGGUCUAAAUUGAA	5260
54790 2 4792	+	chr4:105211608-105211628	AUGAAAGGAUAGUUCAGAAG	5261
54790 2 4793	+	chr4:105211609-105211629	UGAAAGGAUAGUUCAGAAGA	5262
54790 2 4794	+	chr4:105211621-105211641	UCAGAAGAGGGCACUGCAGC	5263
54790 2 4801	+	chr4:105211641-105211661	UGGCUGAAAGAGAACAAGAA	5264
54790 2 4802	+	chr4:105211649-105211669	AGAGAACAAGAAAGGCUGUA	5265
54790 2 4804	+	chr4:105211652-105211672	GAACAAGAAAGGCUGUAAGG	5266
54790 2 4806	+	chr4:105211655-105211675	CAAGAAAGGCUGUAAGGUGG	5267
54790 2 4812	+	chr4:105211685-105211705	UUAUUUGAGCCGUGAAAGAU	5268
54790 2 4816	+	chr4:105211686-105211706	UAAUUGAGCCGUGAAAGAU	5269
54790 2 4822	+	chr4:105211702-105211722	GAUAGGGAAAUUCUGUAUGA	5270
54790 2 4825	+	chr4:105211711-105211731	AUUCUGUAUGAAGGAGUAAA	5271

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 4827	+	chr4:105211714-105211734	CUGUAUGAAGGAGUAAAUGG	5272
54790 2 4830	+	chr4:105211722-105211742	AGGAGUAAAUGGAGGCAUAG	5273
54790 2 4832	+	chr4:105211730-105211750	AUGGAGGCAUAGAGGCAUAG	5274
54790 2 4836	+	chr4:105211752-105211772	GCAGAAGAUGCAUGCCUGUU	5275
54790 2 4838	+	chr4:105211753-105211773	CAGAAGAUGCAUGCCUGUUU	5276
54790 2 4839	+	chr4:105211754-105211774	AGAAGAUGCAUGCCUGUUUG	5277
54790 2 4856	+	chr4:105211848-105211868	GUCACUAGAUUAAAAACAA	5278
54790 2 4859	+	chr4:105211858-105211878	UAAAAACAAAGGCUCCAUC	5279
54790 2 4865	+	chr4:105211884-105211904	ACACAGUAAACAGAAGAAUA	5280
54790 2 4868	+	chr4:105211894-105211914	CAGAAGAAUAUGGAUUUAAA	5281
54790 2 4873	+	chr4:105211953-105211973	UAAGUCAUUGAGAUUCCUUA	5282
54790 2 4881	+	chr4:105211996-105212016	AUAUAACAGUAUGCCAAUGU	5283
54790 2 4883	+	chr4:105212003-105212023	AGUAUGCCAAUGUAGGAAUG	5284
54790 2 4886	+	chr4:105212017-105212037	GGAAUGAGGCGUGAAUAAGC	5285
54790 2 4887	+	chr4:105212018-105212038	GAAUGAGGCGUGAAUAAGCA	5286
54790 2 4890	+	chr4:105212058-105212078	UCUCACCUUGAUUAUUCCUU	5287
54790 2 4895	+	chr4:105212069-105212089	UUAUUCCUUUGGUAGCUUCA	5288
54790 2 4897	+	chr4:105212070-105212090	UAUUCCUUUGGUAGCUUCA	5289
54790 2 4905	+	chr4:105212085-105212105	UUCAAGGGAAAUUGAGUUUG	5290
54790 2 4919	+	chr4:105212179-105212199	GCAGUUUUUAUCUAGUCAGA	5291
54790 2 4926	+	chr4:105212193-105212213	GUCAGAUGGUUGAGAAGUCC	5292
54790 2 4940	+	chr4:105212292-105212312	UCAGUGUACCUUUCAGAUUG	5293
54790 2 4952	+	chr4:105212369-105212389	AAUAAGCUCAUGUUAGUUUC	5294
54790 2 4963	+	chr4:105212418-105212438	UAAUAUUUACAUAUAUGAC	5295
54790 2 4972	+	chr4:105212471-105212491	CCUGUAUUUGCCUUUAUUUG	5296
54790 2 4973	+	chr4:105212472-105212492	CUGUAUUUGCCUUUAUUUGU	5297
54790 2 4988	+	chr4:105212567-105212587	CAAAAUUUUCAAAUUGUGUA	5298
54790 2 4989	+	chr4:105212571-105212591	AUUUUCAAAUUGUGUAUGGC	5299
54790 2 4995	+	chr4:105212586-105212606	AUGGCUGGUCUAUAUUUUCU	5300
54790 2 4996	+	chr4:105212600-105212620	UUUUCUAGGACUGUCCUUUC	5301
54790 2 5023	+	chr4:105212691-105212711	AAAAAUAAUAAUUUCCAGCC	5302
54790 2 5024	+	chr4:105212696-105212716	UAUUAAUUUCCAGCCAGGUG	5303
54790 2 5029	+	chr4:105212726-105212746	CGCCUGUAAUCCCAGCACUU	5304
54790 2 5032	+	chr4:105212727-105212747	GCCUGUAAUCCCAGCACUUU	5305
54790 2 5033	+	chr4:105212730-105212750	UGUAAUCCCAGCACUUUGGG	5306
54790 2 5035	+	chr4:105212736-105212756	CCCAGCACUUUGGGAGGCUG	5307
54790 2 5037	+	chr4:105212739-105212759	AGCACUUUGGGAGGCUGAGG	5308
54790 2 5038	+	chr4:105212740-105212760	GCACUUUGGGAGGCUGAGGC	5309
54790 2 5040	+	chr4:105212743-105212763	CUUUGGGAGGCUGAGGCGGG	5310
54790 2 5046	+	chr4:105212759-105212779	CGGGUGGAUCACCUGAAGUC	5311
54790 2 5047	+	chr4:105212777-105212797	UCAGGAGUUCAAAACCAGCC	5312
54790 2 5048	+	chr4:105212786-105212806	CAAAACCAGCCUGGCCAACA	5313
54790 2 5051	+	chr4:105212826-105212846	UAAAAAUACAAAACUAGCC	5314
54790 2 5052	+	chr4:105212831-105212851	AUACAAAACUAGCCAGGCA	5315
54790 2 5053	+	chr4:105212834-105212854	CAAAACUAGCCAGGCAUGG	5316
54790 2 5055	+	chr4:105212861-105212881	UGCCUGUAGUCCCAGAUACU	5317
54790 2 5056	+	chr4:105212865-105212885	UGUAGUCCCAGAUACUUGGA	5318
54790 2 5058	+	chr4:105212871-105212891	CCCAGAUACUUGGAUGGCUG	5319

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 5060	+	chr4:105212875-105212895	GAUACUUGGAUGGCUGAGGC	5320
54790 2 5067	+	chr4:105212894-105212914	CAGGAGAAUCACUUGAACCC	5321
54790 2 5069	+	chr4:105212897-105212917	GAGAAUCACUUGAACCCAGG	5322
54790 2 5072	+	chr4:105212900-105212920	AAUCACUUGAACCCAGGAGG	5323
54790 2 5073	+	chr4:105212903-105212923	CACUUGAACCCAGGAGGCGG	5324
54790 2 5078	+	chr4:105212943-105212963	UGUGCCACUGCACUCUAGCC	5325
54790 2 5086	+	chr4:105212971-105212991	AGAGUGAGAAUCUGUCUCAG	5326
54790 2 5094	+	chr4:105213028-105213048	CACCCACCAAAGACUCCA	5327
54790 2 5119	+	chr4:105213147-105213167	UUUCUGACAUAGAAUUAUAC	5328
54790 2 5127	+	chr4:105213184-105213204	GCUAAUAGUGACUAUUUUCU	5329
54790 2 5128	+	chr4:105213185-105213205	CUAAUAGUGACUAUUUUCUA	5330
54790 2 5138	+	chr4:105213274-105213294	UUUGUUAUUCUAAGUCAUAA	5331
54790 2 5148	+	chr4:105213284-105213304	UAAGUCAUAAAGGCAGAAU	5332
54790 2 5156	+	chr4:105213318-105213338	GCUUUUCAAAUAUGCAGAAG	5333
54790 2 5164	+	chr4:105213331-105213351	GCAGAAGAGGAAAAAUUGAG	5334
54790 2 5176	+	chr4:105213388-105213408	AAAUUGAGUUUGAAACUAC	5335
54790 2 5193	+	chr4:105213512-105213532	UAUACCUAUGCUUGACCAA	5336
54790 2 5212	+	chr4:105213590-105213610	UCAAGCAUUUCCCUUACCU	5337
54790 2 5225	+	chr4:105213663-105213683	ACUACCAAAGCCCUUCAU	5338
54790 2 5231	+	chr4:105213707-105213727	CUCCAUAGUUGCAUGUCUGA	5339
54790 2 5243	+	chr4:105213794-105213814	AAUUGUCAUUCUGUUUCCCA	5340
54790 2 5248	+	chr4:105213821-105213841	UAGUACAGUACUCUGCUCAC	5341
54790 2 5251	+	chr4:105213858-105213878	AGUUGAGCUACGUUUUUUA	5342
54790 2 5261	+	chr4:105213882-105213902	AGAGUCUCCCUCUGUCGCCC	5343
54790 2 5262	+	chr4:105213883-105213903	GAGUCUCCCUCUGUCGCCCA	5344
54790 2 5264	+	chr4:105213886-105213906	UCUCCCUCUGUCGCCCAGGG	5345
54790 2 5266	+	chr4:105213896-105213916	UCGCCCAGGGUGGAGUACAG	5346
54790 2 5268	+	chr4:105213930-105213950	CUCACUGCAACCUCUGCUGC	5347
54790 2 5269	+	chr4:105213931-105213951	UCACUGCAACCUCUGCUGCU	5348
54790 2 5275	+	chr4:105213970-105213990	GUCUCAGACUCCCGAGUAGC	5349
54790 2 5276	+	chr4:105213971-105213991	UCUCAGACUCCCGAGUAGCU	5350
54790 2 5277	+	chr4:105213998-105214018	UACCACCAUGCCACCAUGCC	5351
54790 2 5280	+	chr4:105214020-105214040	GCUAACUUUUAGUAGAAACA	5352
54790 2 5284	+	chr4:105214034-105214054	GAAACAAGGUUUCACCAUGU	5353
54790 2 5285	+	chr4:105214039-105214059	AAGGUUUCACCAUGUUGGCC	5354
54790 2 5286	+	chr4:105214043-105214063	UUUCACCAUGUUGGCCAGGC	5355
54790 2 5290	+	chr4:105214057-105214077	CCAGGCUGGUCUCCAACUCC	5356
54790 2 5291	+	chr4:105214081-105214101	CUCAAGUGAUCCACCUGCCU	5357
54790 2 5293	+	chr4:105214098-105214118	CCUUGGCCUCAUAAAGUGCU	5358
54790 2 5297	+	chr4:105214136-105214156	UGUCAUGUUACGAUAUAUAU	5359
54790 2 5300	+	chr4:105214149-105214169	UAUAUAUUGGUUUUUGUCCA	5360
54790 2 5301	+	chr4:105214156-105214176	UGGUUUUUGUCCAUGGUUUC	5361
54790 2 5316	+	chr4:105214202-105214222	UACAGUCUUUUGUUAGAAUG	5362
54790 2 5317	+	chr4:105214203-105214223	ACAGUCUUUUGUUAGAAUGU	5363
54790 2 5320	+	chr4:105214204-105214224	CAGUCUUUUGUUAGAAUGUG	5364
54790 2 5322	+	chr4:105214212-105214232	UGUUAGAAUGUGGGGUGUGU	5365
54790 2 5329	+	chr4:105214219-105214239	AUGUGGGGUGUGUUGGACCU	5366
54790 2 5330	+	chr4:105214220-105214240	UGUGGGGUGUGUUGGACCUC	5367

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 5331	+	chr4:105214221-105214241	GUGGGGUGUGUUGGACCU CG	5368
54790 2 5332	+	chr4:105214225-105214245	GGUGUGUUGGACCU CGGGGC	5369
54790 2 5342	+	chr4:105214274-105214294	UUCCUUUCACUUGUCCCCCG	5370
54790 2 5343	+	chr4:105214275-105214295	UCCUUUCACUUGUCCCCCGA	5371
54790 2 5372	+	chr4:105214329-105214349	AAGACUUCCCUGUGUCACCC	5372
54790 2 5374	+	chr4:105214333-105214353	CUUCCCUGUGUCACCCAGGC	5373
54790 2 5377	+	chr4:105214343-105214363	UCACCCAGGCUGGAGUGCAG	5374
54790 2 5378	+	chr4:105214379-105214399	CACCGCAGCCUCAGCCUCCU	5375
54790 2 5382	+	chr4:105214418-105214438	AUCUCAGCCUCCCAAGUACC	5376
54790 2 5383	+	chr4:105214419-105214439	UCUCAGCCUCCCAAGUACCU	5377
54790 2 5384	+	chr4:105214427-105214447	UCCCAAGUACCU GGGACUAC	5378
54790 2 5385	+	chr4:105214446-105214466	CAGGCACAUGCCACCACACC	5379
54790 2 5394	+	chr4:105214480-105214500	UUUUUUUUUUUUUUUGUAGAG	5380
54790 2 5411	+	chr4:105214503-105214523	UUUCGCCAUGUUGCCCAGUC	5381
54790 2 5416	+	chr4:105214517-105214537	CCAGUCUGGCCUCCAGCUCC	5382
54790 2 5417	+	chr4:105214518-105214538	CAGUCUGGCCUCCAGCUCCU	5383
54790 2 5418	+	chr4:105214541-105214561	CUCAAGUGAUCCACCCACCU	5384
54790 2 5423	+	chr4:105214568-105214588	AACCACCACACCCAACCCUG	5385
54790 2 5424	+	chr4:105214569-105214589	ACCACCACACCCAACCCUGA	5386
54790 2 5434	+	chr4:105214623-105214643	GAGUCUUAAAACCCCAGAGA	5387
54790 2 5439	+	chr4:105214641-105214661	GAAGGUCCCACCCUUUGCAC	5388
54790 2 5441	+	chr4:105214642-105214662	AAGGUCCCACCCUUUGCACU	5389
54790 2 5443	+	chr4:105214643-105214663	AGGUCCCACCCUUUGCACUG	5390
54790 2 5446	+	chr4:105214648-105214668	CCACCCUUUGCACUGGGGAA	5391
54790 2 5452	+	chr4:105214685-105214705	UGAAGCCUCCAUA AAAACUC	5392
54790 2 5454	+	chr4:105214688-105214708	AGCCUCCAUA AAAACUCAGG	5393
54790 2 5457	+	chr4:105214699-105214719	AAACUCAGGAGGAUUGAGUC	5394
54790 2 5460	+	chr4:105214700-105214720	AACUCAGGAGGAUUGAGUCU	5395
54790 2 5462	+	chr4:105214701-105214721	ACUCAGGAGGAUUGAGUCUG	5396
54790 2 5464	+	chr4:105214710-105214730	GAUUGAGUCUGGGGAGCUUC	5397
54790 2 5469	+	chr4:105214726-105214746	CUUCUGGAUAGCUGAACCAG	5398
54790 2 5470	+	chr4:105214729-105214749	CUGGAUAGCUGAACCAGUGG	5399
54790 2 5473	+	chr4:105214736-105214756	GCUGAACCAGUGGAGGUUCC	5400
54790 2 5475	+	chr4:105214740-105214760	AACCAGUGGAGGUUCCUGGA	5401
54790 2 5476	+	chr4:105214743-105214763	CAGUGGAGGUUCCUGGAAGG	5402
54790 2 5479	+	chr4:105214753-105214773	UCCUGGAAGGUGGCUCAUCC	5403
54790 2 5480	+	chr4:105214754-105214774	CCUGGAAGGUGGCUCAUCCA	5404
54790 2 5484	+	chr4:105214757-105214777	GGAAGGUGGCUCAUCCAGGG	5405
54790 2 5504	+	chr4:105214896-105214916	CAAACGU AUUGAACCCAAAG	5406
54790 2 5505	+	chr4:105214897-105214917	AAACGU AUUGAACCCAAAGA	5407
54790 2 5507	+	chr4:105214905-105214925	UGAACCCAAAGAGGGUGUUG	5408
54790 2 5509	+	chr4:105214906-105214926	GAACCCAAAGAGGGUGUUGU	5409
54790 2 5514	+	chr4:105214925-105214945	UGGGAACCCCAACUCGAAGC	5410
54790 2 5515	+	chr4:105214929-105214949	AACCCCAACUCGAAGCUGGU	5411
54790 2 5519	+	chr4:105214942-105214962	AGCUGGUUGGUCAGAAGUUC	5412
54790 2 5520	+	chr4:105214945-105214965	UGGUUGGUCAGAAGUUCUGG	5413
54790 2 5522	+	chr4:105214950-105214970	GGUCAGAAGUUCUGGAGGCC	5414
54790 2 5525	+	chr4:105214971-105214991	GGAUUUGUGACUUGUGUCUG	5415

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 5528	+	chr4:105214975-105214995	UUGUGACUUGUGUCUGUGGC	5416
54790 2 5534	+	chr4:105214985-105215005	UGUCUGUGGCAGGAGCAUCU	5417
54790 2 5536	+	chr4:105214986-105215006	GUCUGUGGCAGGAGCAUCUU	5418
54790 2 5540	+	chr4:105215007-105215027	GGAACUGAGCGUUUAAUCUA	5419
54790 2 5542	+	chr4:105215008-105215028	GAACUGAGCGUUUAAUCUAC	5420
54790 2 5543	+	chr4:105215009-105215029	AACUGAGCGUUUAAUCUACG	5421
54790 2 5547	+	chr4:105215026-105215046	ACGGGGUCUGACACUGUCUC	5422
54790 2 5550	+	chr4:105215027-105215047	CGGGGUCUGACACUGUCUCC	5423
54790 2 5553	+	chr4:105215038-105215058	ACUGUCUCCGGGAAUUAUAAU	5424
54790 2 5555	+	chr4:105215041-105215061	GUCUCCGGGAAUUAUAAUUGG	5425
54790 2 5560	+	chr4:105215073-105215093	UAGUGUCUGCUGCUUGUUUAU	5426
54790 2 5562	+	chr4:105215074-105215094	AGUGUCUGCUGCUUGUUUAU	5427
54790 2 5564	+	chr4:105215075-105215095	GUGUCUGCUGCUUGUUUAUUG	5428
54790 2 5569	+	chr4:105215095-105215115	GGGAGAAACCCUCACACAUU	5429
54790 2 5587	+	chr4:105215148-105215168	UUGUUGUGAUGUGAGAGCAG	5430
54790 2 5592	+	chr4:105215163-105215183	AGCAGAGGAAAAAUGCAUUU	5431
54790 2 5595	+	chr4:105215168-105215188	AGGAAAAAUGCAUUUUGGAG	5432
54790 2 5599	+	chr4:105215190-105215210	GUUUUUUCCUACACAGCCAU	5433
54790 2 5626	+	chr4:105215294-105215314	GCAUUUAAACUAAAAAGAAU	5434
54790 2 5667	+	chr4:105215503-105215523	CUUGUAAAUGUUUAUAAGAU	5435
54790 2 5670	+	chr4:105215514-105215534	UUAUAAGAUUGGUAGCUGUG	5436
54790 2 5671	+	chr4:105215515-105215535	UAUAAGAUUGGUAGCUGUGU	5437
54790 2 5696	+	chr4:105215588-105215608	UUUUGAAAAAAGAAACAGAA	5438
54790 2 5726	+	chr4:105215757-105215777	ACAAAGAGAACAUAUGAAACA	5439
54790 2 5729	+	chr4:105215758-105215778	CAAAGAGAACAUAUGAAACAU	5440
54790 2 5741	+	chr4:105215803-105215823	CCAGAAUGCCAACUCAUUUC	5441
54790 2 5743	+	chr4:105215804-105215824	CAGAAUGCCAACUCAUUUCU	5442
54790 2 5744	+	chr4:105215805-105215825	AGAAUGCCAACUCAUUUCUG	5443
54790 2 5756	+	chr4:105215866-105215886	UUUUUAUACGAUACCAUAAA	5444
54790 2 5758	+	chr4:105215870-105215890	UAUACGAUACCAUAAAUGGU	5445
54790 2 5793	+	chr4:105216068-105216088	AUGAUCUUGAUUACUAAACUG	5446
54790 2 5795	+	chr4:105216069-105216089	UGAUCUUGAUUACUAAACUGU	5447
54790 2 5807	+	chr4:105216128-105216148	AAUAUUAGAGCUAGUAUACU	5448
54790 2 5809	+	chr4:105216135-105216155	GAGCUAGUAUACUUGGAGUU	5449
54790 2 5812	+	chr4:105216148-105216168	UGGAGUUUGGCUAGUAUUUC	5450
54790 2 5813	+	chr4:105216149-105216169	GGAGUUUGGCUAGUAUUUCU	5451
54790 2 5817	+	chr4:105216150-105216170	GAGUUUGGCUAGUAUUUCUG	5452
54790 2 5818	+	chr4:105216151-105216171	AGUUUGGCUAGUAUUUCUGG	5453
54790 2 5820	+	chr4:105216154-105216174	UUGGCUAGUAUUUCUGGGGG	5454
54790 2 5827	+	chr4:105216163-105216183	AUUUCUGGGGGAGGUAGAAG	5455
54790 2 5838	+	chr4:105216216-105216236	GCCACGCUGACUAAAACAAA	5456
54790 2 5845	+	chr4:105216260-105216280	UCAUAGUACUUCUUUGAAAC	5457
54790 2 5849	+	chr4:105216264-105216284	AGUACUUCUUUGAAACAGGU	5458
54790 2 5852	+	chr4:105216265-105216285	GUACUUCUUUGAAACAGGUC	5459
54790 2 5854	+	chr4:105216266-105216286	UACUUCUUUGAAACAGGUCG	5460
54790 2 5856	+	chr4:105216267-105216287	ACUUCUUUGAAACAGGUCGG	5461
54790 2 5858	+	chr4:105216268-105216288	CUUCUUUGAAACAGGUCGGG	5462
54790 2 5861	+	chr4:105216271-105216291	CUUUGAAACAGGUCGGGGGG	5463

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 5873	+	chr4:105216316-105216336	UUUUAAUCAAAGUUCUUUCA	5464
54790 2 5877	+	chr4:105216325-105216345	AAGUUCUUUCAUGGAAUUGU	5465
54790 2 5880	+	chr4:105216334-105216354	CAUGGAAUUGUUGGUGCUUC	5466
54790 2 5896	+	chr4:105216414-105216434	AAUUCAGUGCUUGUCUUAAC	5467
54790 2 5898	+	chr4:105216417-105216437	UCAGUGCUUGUCUUAACUGG	5468
54790 2 5901	+	chr4:105216430-105216450	UACUGGGUGGACUUAUUUUA	5469
54790 2 5905	+	chr4:105216449-105216469	AUGGUAUUAUGUUUAUAAGA	5470
54790 2 5912	+	chr4:105216486-105216506	UUUUUUUAUACUCCUAAAAGA	5471
54790 2 5921	+	chr4:105216498-105216518	CUAAAAGAUGGAUACGAUAG	5472
54790 2 5922	+	chr4:105216499-105216519	UAAAAGAUGGAUACGAUAGA	5473
54790 2 5925	+	chr4:105216500-105216520	AAAAGAUGGAUACGAUAGAG	5474
54790 2 5928	+	chr4:105216505-105216525	AUGGAUACGAUAGAGGGGAA	5475
54790 2 5930	+	chr4:105216506-105216526	UGGAUACGAUAGAGGGGAAA	5476
54790 2 5931	+	chr4:105216507-105216527	GGAUACGAUAGAGGGGAAAG	5477
54790 2 5932	+	chr4:105216508-105216528	GAUACGAUAGAGGGGAAAGG	5478
54790 2 5933	+	chr4:105216526-105216546	GGGGGUAAGCUACAACUUUU	5479
54790 2 5934	+	chr4:105216533-105216553	AGCUACAACUUUUAGGUUGU	5480
54790 2 5953	+	chr4:105216618-105216638	UAAAAGUAAUGAUUUGCCAC	5481
54790 2 5973	+	chr4:105216703-105216723	UAUGAAAAAUGCCAUAAACU	5482
54790 2 5985	+	chr4:105216763-105216783	AAAGCUAAUUCAUCUUUUAG	5483
54790 2 5994	+	chr4:105216808-105216828	AGAUGUAUAGCUAAGUCUGU	5484
54790 2 5995	+	chr4:105216820-105216840	AAGUCUGUUGGACAAACUGU	5485
54790 2 6000	+	chr4:105216877-105216897	GUGAAUUUAUGAUUUUCCU	5486
54790 2 6003	+	chr4:105216888-105216908	AUAUUUCCUAGGUAAUGUUA	5487
54790 2 6007	+	chr4:105216896-105216916	UAGGUAAUGUUAAGGUUAUA	5488
54790 2 6010	+	chr4:105216911-105216931	UUUAUUGGAAAUUUCUUUGC	5489
54790 2 6024	+	chr4:105216960-105216980	UGUUAUUUUCAAUACAUACG	5490
54790 2 6064	+	chr4:105217145-105217165	GACCUUUCUCUUCAUUUCAA	5491
54790 2 6068	+	chr4:105217155-105217175	UUCAUUUCAAGGCAUAACU	5492
54790 2 6070	+	chr4:105217159-105217179	UUUCAAGGCAUAACUUGGA	5493
54790 2 6073	+	chr4:105217175-105217195	UGGAUGGUCUGUUUAGCUCA	5494
54790 2 6079	+	chr4:105217206-105217226	AAAAGUUAUGAUUUUGUAUU	5495
54790 2 6080	+	chr4:105217207-105217227	AAAGUUAUGAUUUUGUAUUU	5496
54790 2 6082	+	chr4:105217218-105217238	UUUGUAUUUGGGCAAAGUAC	5497
54790 2 6093	+	chr4:105217255-105217275	CAUUAGAACAGCAUAUAAC	5498
54790 2 6107	+	chr4:105217313-105217333	AGCUAAAGCAAAACUUGCAU	5499
54790 2 6116	+	chr4:105217363-105217383	CUCAGAACUCUACAUCUGAG	5500
54790 2 6121	+	chr4:105217395-105217415	UUUAUACUCUCCUAGUCCAC	5501
54790 2 6129	+	chr4:105217468-105217488	UCAUAUACUACAUCUGAAUU	5502
54790 2 6130	+	chr4:105217469-105217489	CAUAUACUACAUCUGAAUUA	5503
54790 2 6134	+	chr4:105217494-105217514	UCCAAAGUAUGCUAUUCCA	5504
54790 2 6140	+	chr4:105217512-105217532	CAUGGAAAUACUGUUUAUUC	5505
54790 2 6141	+	chr4:105217513-105217533	AUGGAAAUACUGUUUAUUCA	5506
54790 2 6147	+	chr4:105217553-105217573	UCCUGUGUUUCAUUAUGUCC	5507
54790 2 6154	+	chr4:105217608-105217628	UCAUCAUAUUAAGACUUUG	5508
54790 2 6174	+	chr4:105217686-105217706	ACAGAACUUUAUUUUUUCUC	5509
54790 2 6175	+	chr4:105217690-105217710	AACUUUAUUUUUUCUCAGGC	5510
54790 2 6194	+	chr4:105217777-105217797	AUGAUAAGAAUCUGUUUCA	5511

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 6195	+	chr4:105217783-105217803	AGAAUCUGUUUCAAUGGUGU	5512
54790 2 6198	+	chr4:105217801-105217821	GUUGGUGUACAUGUGUGUUC	5513
54790 2 6201	+	chr4:105217816-105217836	UGUUCAGGUACCUACACAUU	5514
54790 2 6208	+	chr4:105217860-105217880	ACUGCACUUAUAAAGAGACA	5515
54790 2 6213	+	chr4:105217889-105217909	CAUCAAGAAGACAUCAUUUU	5516
54790 2 6214	+	chr4:105217890-105217910	AUCAAGAAGACAUCAUUUUA	5517
54790 2 6216	+	chr4:105217893-105217913	AAGAAGACAUCAUUUUAGGG	5518
54790 2 6219	+	chr4:105217908-105217928	UAGGGUGGACACCAUUGCCU	5519
54790 2 6236	+	chr4:105217978-105217998	CGCAGAGUUGACUCGAGUGA	5520
54790 2 6264	+	chr4:105218103-105218123	AUUAUUUAUGUCCACUGUCC	5521
54790 2 6265	+	chr4:105218104-105218124	UUAUUUAUGUCCACUGUCCA	5522
54790 2 6270	+	chr4:105218118-105218138	UGUCCAGGGUACUUGC UUUA	5523
54790 2 6271	+	chr4:105218119-105218139	GUCCAGGGUACUUGC UUUA	5524
54790 2 6280	+	chr4:105218153-105218173	UCUUGAAGAUGAAGAGUCUU	5525
54790 2 6301	+	chr4:105218244-105218264	UCCUAGUGAUGUGAUCAUUAU	5526
54790 2 6305	+	chr4:105218269-105218289	AAUCCAGUGUUUCUUUCCA	5527
54790 2 6310	+	chr4:105218284-105218304	UUCCAAGGACAGUACUGAUA	5528
54790 2 6317	+	chr4:105218341-105218361	AUCUCCAUCUAUUCAUAGUU	5529
54790 2 6320	+	chr4:105218353-105218373	UCAUAGUUUGGCUCAGAAGU	5530
54790 2 6322	+	chr4:105218359-105218379	UUUGGCUCAGAAGUUGGACA	5531
54790 2 6328	+	chr4:105218392-105218412	UAUCUACUUCUCCUCAUGU	5532
54790 2 6339	+	chr4:105218445-105218465	GUUUACUUAUGUGUAAA AUG	5533
54790 2 6345	+	chr4:105218475-105218495	UACACCCUCAAACCGAAAG	5534
54790 2 6375	+	chr4:105218624-105218644	AAUUUUUAAAAAUUGAGAUG	5535
54790 2 6376	+	chr4:105218625-105218645	AUUUUUAAAAAUUGAGAUGU	5536
54790 2 6377	+	chr4:105218626-105218646	UUUUUAAAAAUUGAGAUGUG	5537
54790 2 6378	+	chr4:105218629-105218649	UUAAAAAUUGAGAUGUGGGG	5538
54790 2 6392	+	chr4:105218705-105218725	UGACUGUGUCUAUGUCCUGU	5539
54790 2 6401	+	chr4:105218778-105218798	ACCAUAUUUUAUGCAACUUC	5540
54790 2 6420	+	chr4:105218897-105218917	AAAACAUGCUAUAUAAUUUU	5541
54790 2 6435	+	chr4:105218964-105218984	AGAGUAAUCUUCAUCAUGUA	5542
54790 2 6438	+	chr4:105218965-105218985	GAGUAAUCUUCAUCAUGUAU	5543
54790 2 6443	+	chr4:105218997-105219017	GUAUUUUUCUGAUGAACACA	5544
54790 2 6452	+	chr4:105219050-105219070	UACUCUUUCUUCUGAUAGAC	5545
54790 2 6461	+	chr4:105219081-105219101	UUUAUGUUAUGAAAUA AUGU	5546
54790 2 6475	+	chr4:105219136-105219156	UUUCUUA AAUUGAUAGCUCA	5547
54790 2 6480	+	chr4:105219148-105219168	AUAGCUCAUGGAUGUGCAGU	5548
54790 2 6481	+	chr4:105219156-105219176	UGGAUGUGCAGUUGGUUUAA	5549
54790 2 6494	+	chr4:105219264-105219284	AUUGC UAGUUGU UCCAAA AU	5550
54790 2 6501	+	chr4:105219292-105219312	UAAAAAUGACCAGAUUGUUA	5551
54790 2 6506	+	chr4:105219322-105219342	UUGAUUAAGACUAGA UCAAU	5552
54790 2 6513	+	chr4:105219371-105219391	AAACUUCUCCAAAACAUAGA	5553
54790 2 6516	+	chr4:105219385-105219405	CAUAGAUGGCAUGCCUUUUG	5554
54790 2 6517	+	chr4:105219391-105219411	UGGCAUGCCUUUUGAGGCAA	5555
54790 2 6520	+	chr4:105219395-105219415	AUGCCUUUUGAGGCAAUGGU	5556
54790 2 6521	+	chr4:105219396-105219416	UGCCUUUUGAGGCAAUGGUA	5557
54790 2 6529	+	chr4:105219417-105219437	GGAACAAAUAUUUUUGAGA	5558
54790 2 6533	+	chr4:105219430-105219450	UUUGAGAAGGAGCAGAUUUU	5559

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 6535	+	chr4:105219431-105219451	UUGAGAAGGAGCAGAUUUUA	5560
54790 2 6543	+	chr4:105219474-105219494	GCCAAAUGCUUGUGUUACA	5561
54790 2 6545	+	chr4:105219482-105219502	GCUUGUGUUACAAGGAUCC	5562
54790 2 6550	+	chr4:105219509-105219529	GAGUUUUUAAAUAAAUGCU	5563
54790 2 6561	+	chr4:105219551-105219571	AUUAUAUUGUAGAGUCCCC	5564
54790 2 6563	+	chr4:105219552-105219572	UUAUAUUGUAGAGUCCCCU	5565
54790 2 6565	+	chr4:105219553-105219573	UAAUAUUGUAGAGUCCCCUG	5566
54790 2 6573	+	chr4:105219615-105219635	UCUACCUUUUGAUAGCUUUG	5567
54790 2 6575	+	chr4:105219616-105219636	CUACCUUUUGAUAGCUUUGU	5568
54790 2 6578	+	chr4:105219617-105219637	UACCUUUUGAUAGCUUUGUG	5569
54790 2 6595	+	chr4:105219659-105219679	GUUUUGCCAUUCUUGAUUUU	5570
54790 2 6597	+	chr4:105219660-105219680	UUUUGCCAUUCUUGAUUUUA	5571
54790 2 6612	+	chr4:105219722-105219742	UGCAUUGAUUAAGAUCU	5572
54790 2 6631	+	chr4:105219817-105219837	CUCAUUAUAUAGUAUUUAAU	5573
54790 2 6632	+	chr4:105219818-105219838	UCAUUAUAUAGUAUUUAAUA	5574
54790 2 6664	+	chr4:105219962-105219982	UUUCUCCUCAUAGAAUAUC	5575
54790 2 6672	+	chr4:105219976-105219996	AAUAUCAGGUCCAAGAAGAC	5576
54790 2 6674	+	chr4:105220001-105220021	UAUUUAUCUCUUUUGUUCAG	5577
54790 2 6677	+	chr4:105220012-105220032	UUUGUUCAGUGGUGUGUUAC	5578
54790 2 6709	+	chr4:105220195-105220215	UAUUUAUAGAACCCAUUUGU	5579
54790 2 6712	+	chr4:105220208-105220228	CAUUUGUUGGCCUUAUGUAA	5580
54790 2 6718	+	chr4:105220217-105220237	GCCUUAUGUAAUGGUUCU	5581
54790 2 6734	+	chr4:105220332-105220352	CCAUUAAUGUCUUCUUGACC	5582
54790 2 6738	+	chr4:105220359-105220379	AUAAUUUUUACAGCACCUUU	5583
54790 2 6763	+	chr4:105220466-105220486	CCCAGCACAAACUAAACAC	5584
54790 2 6766	+	chr4:105220479-105220499	UAAACACUGGCUCCAACCCU	5585
54790 2 6770	+	chr4:105220492-105220512	CAACCCUUGGAGUUGAAAGU	5586
54790 2 6773	+	chr4:105220493-105220513	AACCCUUGGAGUUGAAAGUA	5587
54790 2 6774	+	chr4:105220494-105220514	ACCCUUGGAGUUGAAAGUAG	5588
54790 2 6781	+	chr4:105220548-105220568	UACCGUGAGCACCAGUGCCU	5589
54790 2 6783	+	chr4:105220555-105220575	AGCACCAGUGCCUAGGAGAU	5590
54790 2 6784	+	chr4:105220556-105220576	GCACCAGUGCCUAGGAGAUU	5591
54790 2 6786	+	chr4:105220560-105220580	CAGUGCCUAGGAGAUUGGGC	5592
54790 2 6789	+	chr4:105220567-105220587	UAGGAGAUUGGGCAGGACUG	5593
54790 2 6792	+	chr4:105220571-105220591	AGAUUGGGCAGGACUGAGGA	5594
54790 2 6796	+	chr4:105220580-105220600	AGGACUGAGGAAGGAUGAAA	5595
54790 2 6799	+	chr4:105220588-105220608	GGAAGGAUGAAAAGGAGCUC	5596
54790 2 6800	+	chr4:105220589-105220609	GAAGGAUGAAAAGGAGCUCA	5597
54790 2 6804	+	chr4:105220615-105220635	CUUAAGCACCUGAACAAGAC	5598
54790 2 6806	+	chr4:105220618-105220638	AAGCACCUGAACAAGACUGG	5599
54790 2 6809	+	chr4:105220625-105220645	UGAACAAGACUGGAGGACUU	5600
54790 2 6811	+	chr4:105220647-105220667	GAUGUUGCUAUUUUUCUGCC	5601
54790 2 6814	+	chr4:105220657-105220677	UUUUUCUGCCUGGCAUUGAC	5602
54790 2 6820	+	chr4:105220664-105220684	GCCUGGCAUUGACUGGCUAU	5603
54790 2 6823	+	chr4:105220679-105220699	GCUAUUGGACGCCUCUGUG	5604
54790 2 6824	+	chr4:105220683-105220703	UUGGACGCCUCUGUGAGGC	5605
54790 2 6827	+	chr4:105220697-105220717	UGAGGCAGGCAUCCGAAUAC	5606
54790 2 6830	+	chr4:105220715-105220735	ACUGGCUUUCUUGACAUAUA	5607

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 6836	+	chr4:105220732-105220752	AUAUGGAGCGUUCUUUAGAG	5608
54790 2 6838	+	chr4:105220741-105220761	GUUCUUUAGAGAGGCCUACA	5609
54790 2 6839	+	chr4:105220742-105220762	UUCUUUAGAGAGGCCUACAA	5610
54790 2 6844	+	chr4:105220768-105220788	UCACUGCACAGUACCCUGAU	5611
54790 2 6857	+	chr4:105220850-105220870	ACCCACAGUCUCUUUCUGC	5612
54790 2 6858	+	chr4:105220851-105220871	CCCCACAGUCUCUUUCUGCU	5613
54790 2 6859	+	chr4:105220852-105220872	CCCACAGUCUCUUUCUGCUG	5614
54790 2 6862	+	chr4:105220866-105220886	CUGCUGGGGCAUCCUUGCCC	5615
54790 2 6878	+	chr4:105220953-105220973	UAAUUGAAAGUUUCAAGCAU	5616
54790 2 6886	+	chr4:105220990-105221010	UCCUAGACAGUGUUCAGUA	5617
54790 2 6890	+	chr4:105221024-105221044	ACAAUUAUCCAUUCUAAUAA	5618
54790 2 6891	+	chr4:105221025-105221045	CAAUUAUCCAUUCUAAUAAU	5619
54790 2 6920	+	chr4:105221158-105221178	UCCUUCAGUACACACUAGUU	5620
54790 2 6926	+	chr4:105221168-105221188	CACACUAGUUUGGUGAGACU	5621
54790 2 6930	+	chr4:105221175-105221195	GUUUGGUGAGACUUGGAGAA	5622
54790 2 6935	+	chr4:105221180-105221200	GUGAGACUUGGAGAAAGGCC	5623
54790 2 6938	+	chr4:105221211-105221231	CAAAUUCAAAAACAAUUC	5624
54790 2 6941	+	chr4:105221227-105221247	UUCAGGAUUAACAGAUAAAG	5625
54790 2 6950	+	chr4:105221278-105221298	UCAUUUUACCAAUAAGAAAC	5626
54790 2 6951	+	chr4:105221282-105221302	UUUACCAAUAAGAAACUGGU	5627
54790 2 6956	+	chr4:105221291-105221311	AAGAAACUGGUUGGUUAACU	5628
54790 2 6957	+	chr4:105221292-105221312	AGAAACUGGUUGGUUAACUU	5629
54790 2 6963	+	chr4:105221325-105221345	AAAGCAGAUUUUAUACUAAAC	5630
54790 2 6964	+	chr4:105221329-105221349	CAGAUUUUAUACUAAACUGGC	5631
54790 2 6969	+	chr4:105221391-105221411	AAUCUGCCUCUCAUCUUCAA	5632
54790 2 6991	+	chr4:105221488-105221508	AGAUUUUAAAACUUUAAACA	5633
54790 2 6994	+	chr4:105221489-105221509	GAUUUUUAAAACUUUAAACAU	5634
54790 2 6998	+	chr4:105221500-105221520	UUUAAACAUGGGAAUUAAAU	5635
54790 2 7003	+	chr4:105221511-105221531	GAAUUAAAUAGGCCCUACUG	5636
54790 2 7009	+	chr4:105221559-105221579	CUAUGCACAUGAUUUAGAUAU	5637
54790 2 7018	+	chr4:105221623-105221643	AAUUAACACCUUUUCAGAAA	5638
54790 2 7021	+	chr4:105221626-105221646	UACACCUUUUCAGAAUUGG	5639
54790 2 7028	+	chr4:105221640-105221660	AAAUGGAGGAACUUUCUCUG	5640
54790 2 7059	+	chr4:105221723-105221743	AUUAUUAUACUUUAAGUUUU	5641
54790 2 7061	+	chr4:105221724-105221744	UUAUUAUACUUUAAGUUUUA	5642
54790 2 7065	+	chr4:105221731-105221751	ACUUUAAGUUUUAGGGUACA	5643
54790 2 7066	+	chr4:105221732-105221752	CUUUAAAGUUUUAGGGUACAU	5644
54790 2 7072	+	chr4:105221745-105221765	GGUACAUGGGCACAAUGUGC	5645
54790 2 7075	+	chr4:105221777-105221797	UAUGUAUACAUGUGCCAUGC	5646
54790 2 7076	+	chr4:105221813-105221833	CUAACUCGUCAUCUAGCAUU	5647
54790 2 7089	+	chr4:105221939-105221959	CACCUAUGAGUGAGAAUAUG	5648
54790 2 7090	+	chr4:105221946-105221966	GAGUGAGAAUAUGCGGUGUU	5649
54790 2 7108	+	chr4:105222012-105222032	UUUCAUCCAUGUCCCUACAA	5650
54790 2 7112	+	chr4:105222036-105222056	CAUGAACUCAUCAUUUUUUA	5651
54790 2 7115	+	chr4:105222054-105222074	UAUGGCUGCAUAGUAUUGCA	5652
54790 2 7124	+	chr4:105222097-105222117	UUAUCCAGUCUAUCAUUGU	5653
54790 2 7127	+	chr4:105222105-105222125	GUCUAUCAUUGUUGGACAUA	5654
54790 2 7128	+	chr4:105222106-105222126	UCUAUCAUUGUUGGACAUA	5655

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 7129	+	chr4:105222110-105222130	UCAUUGUUGGACAUAUAGGGU	5656
54790 2 7142	+	chr4:105222196-105222216	CAGCAUGAUUUUAUAGUCCUU	5657
54790 2 7143	+	chr4:105222197-105222217	AGCAUGAUUUUAUAGUCCUUU	5658
54790 2 7147	+	chr4:105222214-105222234	UUUGGGUAUAAACCCAGUAA	5659
54790 2 7149	+	chr4:105222215-105222235	UUGGGUAUAAACCCAGUAAU	5660
54790 2 7152	+	chr4:105222219-105222239	GUAUAAACCCAGUAAUGGGA	5661
54790 2 7153	+	chr4:105222232-105222252	AAUGGGAUGGCUCAGUCAA	5662
54790 2 7157	+	chr4:105222257-105222277	UUUCUAGUUCUAGAUCUCCUG	5663
54790 2 7161	+	chr4:105222283-105222303	CGCCACACUGACUCCACAA	5664
54790 2 7172	+	chr4:105222391-105222411	UUAAGAUCGCCAUUCUAAC	5665
54790 2 7179	+	chr4:105222414-105222434	UGUGAGAUGAUUUCUCAUUG	5666
54790 2 7181	+	chr4:105222438-105222458	UUUGAUUUUCAUUUCUCUGA	5667
54790 2 7187	+	chr4:105222448-105222468	AUUUCUCUGAUGGCCAGUGA	5668
54790 2 7192	+	chr4:105222474-105222494	GCAUUUUUUC AUGUGUCUUU	5669
54790 2 7209	+	chr4:105222534-105222554	GUGCUUCGCCCACUUUUUGA	5670
54790 2 7211	+	chr4:105222535-105222555	UGCUCGCCCACUUUUUGAU	5671
54790 2 7231	+	chr4:105222585-105222605	UUUGAGUUCUUUGUAGAUUC	5672
54790 2 7239	+	chr4:105222612-105222632	UAGCCCUUUGUCAGAUAGU	5673
54790 2 7246	+	chr4:105222639-105222659	GAAAAUUUUCUGCCAUUUUG	5674
54790 2 7247	+	chr4:105222640-105222660	AAAAUUUUCUGCCAUUUUGU	5675
54790 2 7254	+	chr4:105222660-105222680	GGGUUGCCUGUUCACUCUGA	5676
54790 2 7266	+	chr4:105222720-105222740	UAGAUCCCAUUUGUCAAUUU	5677
54790 2 7273	+	chr4:105222742-105222762	GCUUUUGUUGCCAUUGCUUU	5678
54790 2 7287	+	chr4:105222786-105222806	GCCCGUGCCUAUGUCGUGAA	5679
54790 2 7289	+	chr4:105222797-105222817	UGUCGUGAAUGGUGUUGCCU	5680
54790 2 7291	+	chr4:105222809-105222829	UGUUGCCUAGGUUUUCUUCU	5681
54790 2 7292	+	chr4:105222810-105222830	GUUGCCUAGGUUUUCUUCUA	5682
54790 2 7294	+	chr4:105222819-105222839	GUUUUCUUCUAGGGUUUUUA	5683
54790 2 7298	+	chr4:105222826-105222846	UCUAGGGUUUUUAUGGUUUU	5684
54790 2 7312	+	chr4:105222874-105222894	CUUGAAUUGAUUUUUGUAUA	5685
54790 2 7315	+	chr4:105222881-105222901	UGAUUUUUGUAUAAGGUGUA	5686
54790 2 7320	+	chr4:105222885-105222905	UUUUGUAUAAGGUGUAAGGA	5687
54790 2 7321	+	chr4:105222886-105222906	UUUGUAUAAGGUGUAAGGAA	5688
54790 2 7326	+	chr4:105222912-105222932	CAGUUUCAGCUUCCACAUA	5689
54790 2 7333	+	chr4:105222947-105222967	CCCAGCACCAUUUAUUAAAU	5690
54790 2 7338	+	chr4:105222948-105222968	CCAGCACCAUUUAUUAAUA	5691
54790 2 7343	+	chr4:105222979-105222999	CCCCAUUUCUUGUUUUUCUC	5692
54790 2 7354	+	chr4:105223012-105223032	AUCAGAUAGUUGUAGAU AUG	5693
54790 2 7358	+	chr4:105223026-105223046	GAUAUGUGGCCUUAUUUCUG	5694
54790 2 7359	+	chr4:105223027-105223047	AUAUGUGGCCUUAUUUCUGA	5695
54790 2 7365	+	chr4:105223064-105223084	AUUGAUCUAUAUCUCUGUUU	5696
54790 2 7368	+	chr4:105223077-105223097	UCUGUUUUGGUACCAGCACC	5697
54790 2 7402	+	chr4:105223234-105223254	UCUCCAUA CUUAAUCCAUAU	5698
54790 2 7406	+	chr4:105223251-105223271	UAUAGGAAACAUAUAU UCC	5699
54790 2 7407	+	chr4:105223263-105223283	UAUAU UCCAGGUCUAACAUG	5700
54790 2 7418	+	chr4:105223305-105223325	CUGUUGAAAAUAUAUGUUU	5701
54790 2 7455	+	chr4:105223440-105223460	UUUACCUCAAGAGUGAGACU	5702
54790 2 7464	+	chr4:105223486-105223506	AAUUUUAAAGUCAACGAAA	5703

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 7475	+	chr4:105223538-105223558	AUUUAAACUAACAUUUUGCU	5704
54790 2 7477	+	chr4:105223539-105223559	UUUAAACUAACAUUUUGCUC	5705
54790 2 7487	+	chr4:105223561-105223581	GAUUUUAGAACACUAUACAG	5706
54790 2 7488	+	chr4:105223562-105223582	AUUUUAGAACACUAUACAGA	5707
54790 2 7502	+	chr4:105223652-105223672	AAGCUAUGUCCCAUGUUGAU	5708
54790 2 7508	+	chr4:105223673-105223693	GGAAGAAUCCAAAAUAGUUU	5709
54790 2 7514	+	chr4:105223695-105223715	GAGAAUAAUGCCAUCUAUGC	5710
54790 2 7517	+	chr4:105223698-105223718	AAUAAUGCCAUCUAUGCAGG	5711
54790 2 7518	+	chr4:105223703-105223723	UGCCAUCUAUGCAGGAGGUG	5712
54790 2 7530	+	chr4:105223781-105223801	ACACUCUGAAUUACUAAUAG	5713
54790 2 7535	+	chr4:105223797-105223817	AUAGAGGUGAAGCCUGUCAG	5714
54790 2 7550	+	chr4:105223929-105223949	AUCUGAAUGUAUAAAUAAAC	5715
54790 2 7551	+	chr4:105223940-105223960	UAAAUAAACAGGAUUCAUGA	5716
54790 2 7555	+	chr4:105223972-105223992	UUAUAUAUACUUGUAGUAUU	5717
54790 2 7561	+	chr4:105223994-105224014	GACAUGCAAAACUUAUUUUA	5718
54790 2 7567	+	chr4:105224024-105224044	UAAUUUACUACCUUAUAGUA	5719
54790 2 7592	+	chr4:105224217-105224237	AGCAUAUCUACAGCUUUAUG	5720
54790 2 7601	+	chr4:105224263-105224283	GAGUAAUCCGAAGAGUCAAA	5721
54790 2 7604	+	chr4:105224268-105224288	AUCCGAAGAGUCAAAUGGUA	5722
54790 2 7606	+	chr4:105224298-105224318	UUACAGUCCUAAAUGCAUUAU	5723
54790 2 7618	+	chr4:105224372-105224392	GCAUCAUAGCAUCUUCAAAG	5724
54790 2 7621	+	chr4:105224391-105224411	GAGGCCUGUCAUAAUUAUGA	5725
54790 2 7632	+	chr4:105224482-105224502	AUAAUAAAUUAUUUUCAGAG	5726
54790 2 7636	+	chr4:105224485-105224505	AUAAAUUAUUUUCAGAGAGG	5727
54790 2 7638	+	chr4:105224486-105224506	UAAAUUAUUUUCAGAGAGGC	5728
54790 2 7643	+	chr4:105224492-105224512	AUUUUCAGAGAGGCGGGAGA	5729
54790 2 7649	+	chr4:105224506-105224526	GGGAGAAGGAACAAAUAUCAA	5730
54790 2 7651	+	chr4:105224519-105224539	AAAUCAAAGGAAAACUGCUG	5731
54790 2 7652	+	chr4:105224535-105224555	GCUGUGGCUAAAACCUGUUU	5732
54790 2 7655	+	chr4:105224542-105224562	CUAAAACCUGUUUUGGUCUU	5733
54790 2 7660	+	chr4:105224572-105224592	AAUGUUAGCUAGUAGUCAAA	5734
54790 2 7669	+	chr4:105224636-105224656	GCCUCUGACAUAGAAGAUAA	5735
54790 2 7674	+	chr4:105224733-105224753	UAGCUUAUGAAAAUUUAUUC	5736
54790 2 7676	+	chr4:105224734-105224754	AGCUUAUGAAAAUUUAUUCU	5737
54790 2 7677	+	chr4:105224735-105224755	GCUUAUGAAAAUUUAUUCUG	5738
54790 2 7684	+	chr4:105224758-105224778	CAUUAGCUGAAAUUAUUGAG	5739
54790 2 7690	+	chr4:105224801-105224821	UCUAUUUAUGUUAUUAUUGCC	5740
54790 2 7703	+	chr4:105224837-105224857	UUUAGAAUUUCUGAAAAAAA	5741
54790 2 7705	+	chr4:105224840-105224860	AGAAUUUCUGAAAAAAAUGG	5742
54790 2 7713	+	chr4:105224871-105224891	GUAAAUAGAAAUAUUCUUUU	5743
54790 2 7715	+	chr4:105224879-105224899	AAAUAUUCUUUUUGGUUCCU	5744
54790 2 7726	+	chr4:105224914-105224934	UACAAAGAACAUUAGAUAUUAU	5745
54790 2 7730	+	chr4:105224923-105224943	CAUUAGAUUAUUGGAAUAAA	5746
54790 2 7736	+	chr4:105224949-105224969	GACAUACAUAUAUUGACUAG	5747
54790 2 7737	+	chr4:105224950-105224970	ACAUACAUAUAUUGACUAGU	5748
54790 2 7743	+	chr4:105225001-105225021	AUUUAAUUAAGUCUGUCAUUU	5749
54790 2 7767	+	chr4:105225117-105225137	AAUUCACUUUGUUGCCUUUU	5750
54790 2 7792	+	chr4:105225274-105225294	AACAUGCCAUGUAUUUUCU	5751

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 7794	+	chr4:105225280-105225300	CCAUGUAUUUCCUAGGUUA	5752
54790 2 7795	+	chr4:105225281-105225301	CAUGUAUUUCCUAGGUUAA	5753
54790 2 7815	+	chr4:105225364-105225384	CGCUCUAUGAGUUUUUAUG	5754
54790 2 7824	+	chr4:105225408-105225428	ACUGAUGCACAUUUCUCCUU	5755
54790 2 7825	+	chr4:105225415-105225435	CACAUUUCUCCUUAGGUCAC	5756
54790 2 7830	+	chr4:105225441-105225461	UCCUCCCUCAGCAAUGUUGU	5757
54790 2 7842	+	chr4:105225507-105225527	AGUGUUUUUCUCUCAUACUA	5758
54790 2 7854	+	chr4:105225546-105225566	UAAAUUUUACAAGAGUGACU	5759
54790 2 7855	+	chr4:105225547-105225567	AAAUUUUACAAGAGUGACUU	5760
54790 2 7857	+	chr4:105225550-105225570	UUUUACAAGAGUGACUUGGG	5761
54790 2 7863	+	chr4:105225572-105225592	GCUGAU AUGCCCACAUUGAC	5762
54790 2 7865	+	chr4:105225573-105225593	CUGAU AUGCCCACAUUGACA	5763
54790 2 7868	+	chr4:105225612-105225632	UCCCCUCUCCUGUAUUCCCA	5764
54790 2 7874	+	chr4:105225654-105225674	CCUCAACAUAACCACAGUUC	5765
54790 2 7875	+	chr4:105225655-105225675	CUCAACAUAACCACAGUUCA	5766
54790 2 7878	+	chr4:105225664-105225684	ACCACAGUUCAGGGCAGUAG	5767
54790 2 7882	+	chr4:105225698-105225718	UUUGUGUUAGCUCCAUGCCA	5768
54790 2 7889	+	chr4:105225716-105225736	CAUGGCAACUGCACUGAGUG	5769
54790 2 7891	+	chr4:105225736-105225756	AGGAUUCAACUCAGUGCAGC	5770
54790 2 7899	+	chr4:105225797-105225817	AUUCUCUGAGUGACAUUAUC	5771
54790 2 7902	+	chr4:105225798-105225818	UUCUCUGAGUGACAUUAUCA	5772
54790 2 7904	+	chr4:105225799-105225819	UCUCUGAGUGACAUUAUCAG	5773
54790 2 7914	+	chr4:105225870-105225890	CCAGCAUUGCAAAGAUAUAUC	5774
54790 2 7915	+	chr4:105225871-105225891	CAGCAUUGCAAAGAUAUAUCU	5775
54790 2 7917	+	chr4:105225875-105225895	AUUGCAAAGAUAUAUCUGGGA	5776
54790 2 7918	+	chr4:105225878-105225898	GCAAAGAUAUAUCUGGGAAGG	5777
54790 2 7922	+	chr4:105225887-105225907	AUCUGGGAAGGUGGCAAAGA	5778
54790 2 7924	+	chr4:105225888-105225908	UCUGGGAAGGUGGCAAAGAA	5779
54790 2 7927	+	chr4:105225906-105225926	AAGGGAUCAGAAUAACUCUG	5780
54790 2 7943	+	chr4:105225986-105226006	CACAUAAAGAAAUGAUUUGU	5781
54790 2 7956	+	chr4:105226099-105226119	AAAAAAAAAGCUUAAAUUGU	5782
54790 2 7968	+	chr4:105226163-105226183	GCACUUGUCUUAGUAUUGUG	5783
54790 2 7971	+	chr4:105226166-105226186	CUUGUCUUAGUAUUGUGUGG	5784
54790 2 7973	+	chr4:105226167-105226187	UUGUCUUAGUAUUGUGUGGU	5785
54790 2 7981	+	chr4:105226199-105226219	AGAGAGCUGCCAGAGUGCUU	5786
54790 2 7986	+	chr4:105226213-105226233	GUGCUUAGGCCUAGUCCCUG	5787
54790 2 7988	+	chr4:105226214-105226234	UGC UUAGGCCUAGUCCCUGU	5788
54790 2 7990	+	chr4:105226228-105226248	CCCUGUGGGAGCCUCUGUUU	5789
54790 2 7992	+	chr4:105226241-105226261	UCUGUUUUGGUGCUUCACCA	5790
54790 2 7993	+	chr4:105226242-105226262	CUGUUUUGGUGCUUCACCAU	5791
54790 2 8005	+	chr4:105226282-105226302	ACAUCUUUAAAUGAGAAAA	5792
54790 2 8011	+	chr4:105226327-105226347	UGAAAUGUUUAUACAUUGUU	5793
54790 2 8027	+	chr4:105226393-105226413	AAUUUCUUAGCCGUGUGAUA	5794
54790 2 8029	+	chr4:105226398-105226418	CUUAGCCGUGUGAUAUGGUU	5795
54790 2 8032	+	chr4:105226405-105226425	GUGUGAUAUGGUUUUGGUUGU	5796
54790 2 8039	+	chr4:105226446-105226466	UGAAAUAAAUCCCCAGUGU	5797
54790 2 8042	+	chr4:105226449-105226469	AAUAUAAUCCCCAGUGUUGG	5798
54790 2 8045	+	chr4:105226452-105226472	AUAAUCCCCAGUGUUGGAGG	5799

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 8046	+	chr4:105226453-105226473	UAAUCCCCAGUGUUGGAGGU	5800
54790 2 8048	+	chr4:105226454-105226474	AAUCCCCAGUGUUGGAGGUG	5801
54790 2 8049	+	chr4:105226455-105226475	AUCCCCAGUGUUGGAGGUGG	5802
54790 2 8050	+	chr4:105226460-105226480	CAGUGUUGGAGGUGGGGGGCC	5803
54790 2 8053	+	chr4:105226463-105226483	UGUUGGAGGUGGGGGGCCUGG	5804
54790 2 8055	+	chr4:105226464-105226484	GUUGGAGGUGGGGGGCCUGGU	5805
54790 2 8058	+	chr4:105226474-105226494	GGGGCCUGGUGGGAAGUGUU	5806
54790 2 8060	+	chr4:105226482-105226502	GUGGGAAGUGUUUGGAUUAU	5807
54790 2 8062	+	chr4:105226483-105226503	UGGGAAGUGUUUGGAUUAUU	5808
54790 2 8063	+	chr4:105226484-105226504	GGGAAGUGUUUGGAUUAUUG	5809
54790 2 8066	+	chr4:105226498-105226518	UUAUUGGGGCAGAUCCCUC	5810
54790 2 8068	+	chr4:105226503-105226523	GGGGCAGAUCCCUC AUGGCA	5811
54790 2 8072	+	chr4:105226540-105226560	UAGUGAGUUCUCAAGAGAUC	5812
54790 2 8074	+	chr4:105226546-105226566	GUUCUCAAGAGAUCUGGUUA	5813
54790 2 8075	+	chr4:105226547-105226567	UUCUCAAGAGAUCUGGUUAA	5814
54790 2 8077	+	chr4:105226554-105226574	GAGAUCUGGUUAAGGGUGUG	5815
54790 2 8094	+	chr4:105226712-105226732	CCAUGAUUAUAAGUUUUGUA	5816
54790 2 8113	+	chr4:105226855-105226875	AGCCUAACAUAACCUUUCAAA	5817
54790 2 8124	+	chr4:105226909-105226929	GAUCUCUUUGUCCAGAAUUC	5818
54790 2 8129	+	chr4:105226934-105226954	AUAAAGAUGCCAAAUAUAUA	5819
54790 2 8131	+	chr4:105226952-105226972	UAUGGCAUGUAUUUGAUCUC	5820
54790 2 8133	+	chr4:105226953-105226973	AUGGCAUGUAUUUGAUCUCA	5821
54790 2 8138	+	chr4:105226974-105226994	GGAAUUUUCAUUUUUUUCAAA	5822
54790 2 8142	+	chr4:105226977-105226997	AUUUUCAUUUUUUUCAAAAGG	5823
54790 2 8152	+	chr4:105227010-105227030	AAUAUAUUUUUUUAUAUUU	5824
54790 2 8168	+	chr4:105227065-105227085	GAGCACAUUGUGAAACUUUC	5825
54790 2 8171	+	chr4:105227083-105227103	UCAGGAAUUGCAUGAGCUGU	5826
54790 2 8179	+	chr4:105227129-105227149	ACCAUAAGAGCAUCUCCUG	5827
54790 2 8192	+	chr4:105227211-105227231	GACAUCAUGAAAAUCAUCCC	5828
54790 2 8193	+	chr4:105227212-105227232	ACAUCAUGAAAAUCAUCCCU	5829
54790 2 8195	+	chr4:105227233-105227253	GGUAAACAAUUAGUCACUCC	5830
54790 2 8197	+	chr4:105227245-105227265	GUCACUCCAGGUUUUCCCAA	5831
54790 2 8206	+	chr4:105227305-105227325	CAGUUUAACAACCCCAAAAA	5832
54790 2 8209	+	chr4:105227321-105227341	AAAAAGGCCUUAUUUUUGAU	5833
54790 2 8214	+	chr4:105227337-105227357	UGAUUGGCCAGCAUCCUCUU	5834
54790 2 8227	+	chr4:105227402-105227422	AAUAAGAAUUGUUUCCAUCU	5835
54790 2 8229	+	chr4:105227403-105227423	AUAAGAAUUGUUUCCAUCUA	5836
54790 2 8234	+	chr4:105227418-105227438	AUCUAGGGAAUGAUUUUUUAU	5837
54790 2 8237	+	chr4:105227433-105227453	UUUAUAGGUAGAAUCUUAUU	5838
54790 2 8243	+	chr4:105227438-105227458	AGGUAGAAUCUUAUUUGGCA	5839
54790 2 8252	+	chr4:105227487-105227507	UGUGUAGACCUUCAAUAGCA	5840
54790 2 8263	+	chr4:105227559-105227579	CAUAUUAAUUUUGUGUUCUC	5841
54790 2 8273	+	chr4:105227578-105227598	CUGGUGUAAGAAAAAAUAGA	5842
54790 2 8317	+	chr4:105227827-105227847	CUCUACUUUCACUGAAUAGC	5843
54790 2 8321	+	chr4:105227838-105227858	CUGAAUAGCAGGUGAAUAGC	5844
54790 2 8348	+	chr4:105228004-105228024	CUACAAUGAGCAAAAUGCAU	5845
54790 2 8364	+	chr4:105228095-105228115	UUGAAAGAGUACUGUGCAAG	5846
54790 2 8365	+	chr4:105228096-105228116	UGAAAGAGUACUGUGCAAGU	5847

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 8368	+	chr4:105228103-105228123	GUACUGUGCAAGUGGGUUAC	5848
54790 2 8370	+	chr4:105228119-105228139	UUACUGGAUCAUAAUAUUCC	5849
54790 2 8371	+	chr4:105228120-105228140	UACUGGAUCAUAAUAUUCCA	5850
54790 2 8379	+	chr4:105228194-105228214	GCAUUUUUCUCCUUCUAAAA	5851
54790 2 8406	+	chr4:105228320-105228340	CAUUAAACUUUUCACACAAA	5852
54790 2 8410	+	chr4:105228331-105228351	UCACACAAAUGGUUGUAUAA	5853
54790 2 8415	+	chr4:105228377-105228397	UUCUGUAUAAUGUUUAAAAA	5854
54790 2 8435	+	chr4:105228460-105228480	GUAGCUAUUAUUAUACUCAA	5855
54790 2 8447	+	chr4:105228501-105228521	AAAGAAUGUCCAAAAUUAUG	5856
54790 2 8450	+	chr4:105228506-105228526	AUGUCCAAAAUUAUGUGGAA	5857
54790 2 8471	+	chr4:105228669-105228689	UGAUUGCUCUGUAUAUGAAU	5858
54790 2 8482	+	chr4:105228707-105228727	AAAAGAAAAGUGCCUUUUUU	5859
54790 2 8484	+	chr4:105228717-105228737	UGCCUUUUUUUGGUAGUAUC	5860
54790 2 8485	+	chr4:105228722-105228742	UUUUUUGGUAGUAUCUGGAC	5861
54790 2 8493	+	chr4:105228744-105228764	GUA AUUGACUUUCUUUCUGC	5862
54790 2 8513	+	chr4:105228806-105228826	AAGUGAUAGUGUCCUGAUUU	5863
54790 2 8524	+	chr4:105228875-105228895	AAACCUAAAGUUUCUUUAUU	5864
54790 2 8542	+	chr4:105228952-105228972	GAAACAUA AUGUAAGCCACA	5865
54790 2 8585	+	chr4:105229145-105229165	AUAGAUACCACAUCUCAAUU	5866
54790 2 8588	+	chr4:105229163-105229183	UUUGGACUAGACACA UUUUA	5867
54790 2 8589	+	chr4:105229164-105229184	UUGGACUAGACACA UUUUAA	5868
54790 2 8596	+	chr4:105229196-105229216	UAUAUGUGACUAGUCACUGU	5869
54790 2 8600	+	chr4:105229230-105229250	CUAGACCAUCUCUUA AUGUA	5870
54790 2 8603	+	chr4:105229234-105229254	ACCAUCUCUUA AUGUAUGGA	5871
54790 2 8626	+	chr4:105229333-105229353	CAGAGUCUCGCUCUGUUGCC	5872
54790 2 8628	+	chr4:105229337-105229357	GUCUCGCUCUGUUGCCAGGC	5873
54790 2 8630	+	chr4:105229347-105229367	GUUGCCAGGCUGGAGUGCAG	5874
54790 2 8632	+	chr4:105229358-105229378	GGAGUGCAGUGGCGCGAUCU	5875
54790 2 8634	+	chr4:105229382-105229402	UCACUGCAACCUCCGCCUCC	5876
54790 2 8635	+	chr4:105229383-105229403	CACUGCAACCUCCGCCUCCU	5877
54790 2 8640	+	chr4:105229422-105229442	GCCUCAGCCUCCCAAGUAAC	5878
54790 2 8641	+	chr4:105229423-105229443	CCUCAGCCUCCCAAGUAACU	5879
54790 2 8642	+	chr4:105229431-105229451	UCCCAAGUAACUGGGACUAC	5880
54790 2 8643	+	chr4:105229475-105229495	ACUUUUUGUAUUUUUAGUAG	5881
54790 2 8644	+	chr4:105229478-105229498	UUUUGUAUUUUUAGUAGUGG	5882
54790 2 8653	+	chr4:105229494-105229514	GUGGCGGUGUUUGACCACGU	5883
54790 2 8654	+	chr4:105229503-105229523	UUUGACCACGUUGGCCAAGA	5884
54790 2 8661	+	chr4:105229555-105229575	GCCUCAGCCUCCCAAGUGC	5885
54790 2 8662	+	chr4:105229556-105229576	CCUCAGCCUCCCAAGUGCU	5886
54790 2 8663	+	chr4:105229564-105229584	UCCCAAGUGCUGGGACUAC	5887
54790 2 8665	+	chr4:105229583-105229603	CAGGCGUGAGCCACCGUGCC	5888
54790 2 8673	+	chr4:105229620-105229640	UAUUAAGUAAUACACAUGCU	5889
54790 2 8680	+	chr4:105229645-105229665	GUUAUUUAAAAAAAAAAAAA	5890
54790 2 8691	+	chr4:105229706-105229726	AGCUGCCCCAUUCCUUUCC	5891
54790 2 8692	+	chr4:105229709-105229729	UGCCCCAUUCCUUUCCUGG	5892
54790 2 8694	+	chr4:105229722-105229742	UUCUGGAGGCAAAUUAUUA	5893
54790 2 8704	+	chr4:105229772-105229792	GAUUUUUUUUUAUUUUACAA	5894
54790 2 8707	+	chr4:105229778-105229798	UUUUUAUUUUACAAAGGUAU	5895

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 8722	+	chr4:105229835-105229855	CCUUUAUUCCAUUUAAUUAC	5896
54790 2 8724	+	chr4:105229836-105229856	CUUUAUUCCAUUUAAUUACU	5897
54790 2 8736	+	chr4:105229886-105229906	UACUAAUUUUAAUAGCUACA	5898
54790 2 8740	+	chr4:105229901-105229921	CUACAUGGUAUUAUAUUGUG	5899
54790 2 8745	+	chr4:105229942-105229962	AACAUAACCCUUAUUGAUGU	5900
54790 2 8768	+	chr4:105230064-105230084	AGUGUCUCACUCUGUCACCC	5901
54790 2 8771	+	chr4:105230068-105230088	UCUCACUCUGUCACCCAGGC	5902
54790 2 8773	+	chr4:105230113-105230133	UCACUGCAGUGUCCACCUC	5903
54790 2 8774	+	chr4:105230114-105230134	CACUGCAGUGUCCACCUCU	5904
54790 2 8775	+	chr4:105230120-105230140	AGUGUCCACCUCUGGGUUC	5905
54790 2 8781	+	chr4:105230153-105230173	UCCUCAGCCUCCCAAGUAAC	5906
54790 2 8782	+	chr4:105230154-105230174	CCUCAGCCUCCCAAGUAACU	5907
54790 2 8784	+	chr4:105230162-105230182	UCCCAAGUAACUGGGAUUAC	5908
54790 2 8787	+	chr4:105230203-105230223	GCUAAUUUUUUGUAUCUUUUU	5909
54790 2 8791	+	chr4:105230211-105230231	UUGUAUCUUUUUAGGAGAGA	5910
54790 2 8794	+	chr4:105230212-105230232	UGUAUCUUUUUAGGAGAGAC	5911
54790 2 8802	+	chr4:105230227-105230247	GAGACGGGAUUUCACCAUGU	5912
54790 2 8803	+	chr4:105230232-105230252	GGGAUUUCACCAUGUUGGCC	5913
54790 2 8804	+	chr4:105230236-105230256	UUUCACCAUGUUGGCCAGGU	5914
54790 2 8809	+	chr4:105230250-105230270	CCAGGUUGGUCUAGAACUCC	5915
54790 2 8810	+	chr4:105230257-105230277	GGUCUAGAACUCCUGGCCUC	5916
54790 2 8812	+	chr4:105230268-105230288	CCUGGCCUCAGGUGAUCCAC	5917
54790 2 8815	+	chr4:105230290-105230310	GCCUUAGCUUCCCAAAGUGC	5918
54790 2 8816	+	chr4:105230291-105230311	CCUUAGCUUCCCAAAGUGCU	5919
54790 2 8818	+	chr4:105230299-105230319	UCCCAAAGUGCUGGGAUUUAU	5920
54790 2 8823	+	chr4:105230342-105230362	CUGUCAGAUAAAUUCUAAAA	5921
54790 2 8824	+	chr4:105230343-105230363	UGUCAGAUAAAUUCUAAAA	5922
54790 2 8827	+	chr4:105230349-105230369	AUAAAUUCUUAAAAGGGUCA	5923
54790 2 8837	+	chr4:105230408-105230428	GUCAUCCUACAUGAUUUUG	5924
54790 2 8852	+	chr4:105230506-105230526	GCUUACUGAUCUUCACUAAU	5925
54790 2 8886	+	chr4:105230654-105230674	CUUGUCCAUUUUUUAGUAUG	5926
54790 2 8893	+	chr4:105230673-105230693	GUGGUUAUUCAUUUUUUUGU	5927
54790 2 8909	+	chr4:105230734-105230754	CUCUUUUUACAUGUUUUUUU	5928
54790 2 8944	+	chr4:105230855-105230875	CUCAGAUUGUUUUUAACUUU	5929
54790 2 8947	+	chr4:105230856-105230876	UCAGAUUGUUUUUAACUUUU	5930
54790 2 8951	+	chr4:105230857-105230877	CAGAUUGUUUUUAACUUUUG	5931
54790 2 8953	+	chr4:105230858-105230878	AGAUUGUUUUUAACUUUUGG	5932
54790 2 8954	+	chr4:105230859-105230879	GAUUGUUUUUAACUUUUGGG	5933
54790 2 8955	+	chr4:105230860-105230880	AUUGUUUUUAACUUUUGGGG	5934
54790 2 8976	+	chr4:105230917-105230937	AGAAUUUAUCUUAAGUGUA	5935
54790 2 8977	+	chr4:105230918-105230938	GAAUUUAUCUUAAGUGUAA	5936
54790 2 8983	+	chr4:105230946-105230966	UCCCACUUUAUCAUUUUUUC	5937
54790 2 8998	+	chr4:105231018-105231038	UAUCUUGUAGCAUAUUUCUG	5938
54790 2 9001	+	chr4:105231023-105231043	UGUAGCAUAUUUCUGUGGUU	5939
54790 2 9002	+	chr4:105231024-105231044	GUAGCAUAUUUCUGUGGUUU	5940
54790 2 9026	+	chr4:105231136-105231156	CUUUUAAAUAUCUUUUAAU	5941
54790 2 9031	+	chr4:105231144-105231164	UAUCUUUUAAUUUGGCUACU	5942
54790 2 9039	+	chr4:105231176-105231196	AUUCUUUUUCAGAAUAUCC	5943

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 9050	+	chr4:105231212-105231232	UUAUUUUUCCAAAUGAACUU	5944
54790 2 9087	+	chr4:105231372-105231392	UUUUAAAGUUAUUAUAAAAU	5945
54790 2 9106	+	chr4:105231459-105231479	AUUCCAGUAAAACUUCUGAC	5946
54790 2 9110	+	chr4:105231481-105231501	GUUGAUGCUCUUAUAAAUCA	5947
54790 2 9122	+	chr4:105231552-105231572	CAUUUUUUACUUGAUUCUCU	5948
54790 2 9178	+	chr4:105231748-105231768	AAAUGUAAUGAGAAAGACUG	5949
54790 2 9180	+	chr4:105231749-105231769	AAUGUAAUGAGAAAGACUGU	5950
54790 2 9183	+	chr4:105231777-105231797	AAAGCAGACACCUUAUACAA	5951
54790 2 9186	+	chr4:105231806-105231826	UUUUUUAGUGCCAUUUCUUC	5952
54790 2 9195	+	chr4:105231822-105231842	CUUCUGGCUUUCUCUAUUAU	5953
54790 2 9197	+	chr4:105231823-105231843	UUCUGGCUUUCUCUAUUAUU	5954
54790 2 9211	+	chr4:105231886-105231906	AAUGAAUGCAAUCAGAUUCA	5955
54790 2 9212	+	chr4:105231887-105231907	AUGAAUGCAAUCAGAUUCA	5956
54790 2 9213	+	chr4:105231899-105231919	AGAUUCAAGGGUACAAGUGC	5957
54790 2 9215	+	chr4:105231908-105231928	GGUACAAGUGCAGGUUAUAU	5958
54790 2 9219	+	chr4:105231925-105231945	UAUAGGUGAAUUGCAUGCCU	5959
54790 2 9221	+	chr4:105231926-105231946	AUAGGUGAAUUGCAUGCCUU	5960
54790 2 9223	+	chr4:105231927-105231947	UAGGUGAAUUGCAUGCCUUG	5961
54790 2 9224	+	chr4:105231928-105231948	AGGUGAAUUGCAUGCCUUGG	5962
54790 2 9225	+	chr4:105231933-105231953	AAUUGCAUGCCUUGGGGGUU	5963
54790 2 9230	+	chr4:105231958-105231978	UACAGACUAUUUUGUCACCC	5964
54790 2 9234	+	chr4:105231981-105232001	UAAUAAGCGUAGUACUAAU	5965
54790 2 9252	+	chr4:105232096-105232116	CUGCCACUUAAGAGACAUG	5966
54790 2 9259	+	chr4:105232128-105232148	GUUCCUUUGUUAGUUUGUUU	5967
54790 2 9261	+	chr4:105232135-105232155	UGUUAGUUUGUUUAGGAUAA	5968
54790 2 9271	+	chr4:105232189-105232209	CACGAUUUUGUGUUUCUUUA	5969
54790 2 9277	+	chr4:105232207-105232227	UAUGGCUGUGUAGUAUUCCA	5970
54790 2 9284	+	chr4:105232248-105232268	UUUAUCCAGUCUACUACUUA	5971
54790 2 9287	+	chr4:105232257-105232277	UCUACUACUUACGGACAUUU	5972
54790 2 9296	+	chr4:105232325-105232345	ACGUGUGCAAUAUGCCUUUA	5973
54790 2 9302	+	chr4:105232348-105232368	UAGAAUGAUUUUAUAUCCCUU	5974
54790 2 9303	+	chr4:105232349-105232369	AGAAUGAUUUUAUAUCCCUUU	5975
54790 2 9308	+	chr4:105232367-105232387	UUGGGUAAUAUGCCGAAUAA	5976
54790 2 9310	+	chr4:105232368-105232388	UGGGUAAUAUGCCGAAUAAU	5977
54790 2 9313	+	chr4:105232377-105232397	UGCCGAAUAAUGGGAUUGCU	5978
54790 2 9314	+	chr4:105232385-105232405	AAUGGGAUUGCUCGGUCAGA	5979
54790 2 9323	+	chr4:105232462-105232482	UUACAUUCCCACAAGCAAUA	5980
54790 2 9325	+	chr4:105232463-105232483	UACAUUCCCACAAGCAAUAA	5981
54790 2 9327	+	chr4:105232464-105232484	ACAUUCCCACAAGCAAUAAG	5982
54790 2 9332	+	chr4:105232489-105232509	AAGUGUUCCCUUUUCUCUGC	5983
54790 2 9343	+	chr4:105232521-105232541	UUCUUUUAGAGAGUCAAGA	5984
54790 2 9350	+	chr4:105232530-105232550	AGAGUCAAGAUGGAAUCCU	5985
54790 2 9351	+	chr4:105232531-105232551	GAGUCAAGAUGGAAUCCUA	5986
54790 2 9354	+	chr4:105232547-105232567	CCUAGGGAAGAUGAUUCUG	5987
54790 2 9355	+	chr4:105232551-105232571	GGGAAGAUGAUUCUGAGGC	5988
54790 2 9358	+	chr4:105232565-105232585	UGAGGCAGGUUUAGAGUCAU	5989
54790 2 9359	+	chr4:105232566-105232586	GAGGCAGGUUUAGAGUCAUU	5990
54790 2 9362	+	chr4:105232575-105232595	UUAGAGUCAUUGGGCAAUA	5991

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 9364	+	chr4:105232576-105232596	UAGAGUCAUUGGGCAAUAA	5992
54790 2 9365	+	chr4:105232577-105232597	AGAGUCAUUGGGCAAUAAAG	5993
54790 2 9370	+	chr4:105232587-105232607	GGCAAUAAGGGGAUUAAGA	5994
54790 2 9371	+	chr4:105232596-105232616	GGGGAUUAAGAAGGCAUUCU	5995
54790 2 9375	+	chr4:105232614-105232634	CUAGGCAGACAGAAAACCAA	5996
54790 2 9380	+	chr4:105232646-105232666	CUGAAACAGCUUACUAUGUU	5997
54790 2 9386	+	chr4:105232673-105232693	UUAUAAGCUGUUGUUAUUGU	5998
54790 2 9397	+	chr4:105232698-105232718	UAUAAACUGUAAGAGAGAGU	5999
54790 2 9400	+	chr4:105232701-105232721	AAACUGUAAGAGAGAGUAGG	6000
54790 2 9404	+	chr4:105232725-105232745	CAGAAAAAACAGCCUGUAUG	6001
54790 2 9407	+	chr4:105232726-105232746	AGAAAAAACAGCCUGUAUGC	6002
54790 2 9408	+	chr4:105232727-105232747	GAAAAAACAGCCUGUAUGCG	6003
54790 2 9411	+	chr4:105232728-105232748	AAAAAACAGCCUGUAUGCGG	6004
54790 2 9413	+	chr4:105232729-105232749	AAAAACAGCCUGUAUGCGGG	6005
54790 2 9421	+	chr4:105232766-105232786	ACAGAAAUUCUCAAAGAUU	6006
54790 2 9422	+	chr4:105232767-105232787	CAGAAAUUCUCAAAGAUUU	6007
54790 2 9434	+	chr4:105232810-105232830	AAACAUAGAAUCACCUAGAA	6008
54790 2 9435	+	chr4:105232811-105232831	AACAUAGAAUCACCUAGAAA	6009
54790 2 9445	+	chr4:105232856-105232876	AUCACCCCUAUUCUGUCACC	6010
54790 2 9450	+	chr4:105232876-105232896	UGGAUAUUGAUAAACACUGA	6011
54790 2 9452	+	chr4:105232877-105232897	GGAAUAUUGAUAAACACUGAA	6012
54790 2 9454	+	chr4:105232897-105232917	GGGAGUGUGCCUUAUCUCUC	6013
54790 2 9456	+	chr4:105232906-105232926	CCUUAUCUCUCAGGUGUAUU	6014
54790 2 9463	+	chr4:105232932-105232952	AAAUAGUUUGAGAACCAUGC	6015
54790 2 9479	+	chr4:105233007-105233027	AAUCUUCCUUUUGAUAACAA	6016
54790 2 9480	+	chr4:105233008-105233028	AUCUUCCUUUUGAUAAACAAA	6017
54790 2 9486	+	chr4:105233019-105233039	GAUAACAAAGGGAACCUUAA	6018
54790 2 9487	+	chr4:105233020-105233040	AUAACAAAGGGAACCUUAAA	6019
54790 2 9491	+	chr4:105233024-105233044	CAAAGGGAACCUUAAAGGGC	6020
54790 2 9494	+	chr4:105233027-105233047	AGGGAACCUUAAAGGGCUGG	6021
54790 2 9496	+	chr4:105233028-105233048	GGGAACCUUAAAGGGCUGGA	6022
54790 2 9497	+	chr4:105233029-105233049	GGAACCUUAAAGGGCUGGAG	6023
54790 2 9500	+	chr4:105233033-105233053	CCUUAAGGGCUGGAGGGGA	6024
54790 2 9501	+	chr4:105233034-105233054	CUUAAAGGGCUGGAGGGGAA	6025
54790 2 9504	+	chr4:105233041-105233061	GGCUGGAGGGGAAGGGCAGA	6026
54790 2 9506	+	chr4:105233042-105233062	GCUGGAGGGGAAGGGCAGAC	6027
54790 2 9507	+	chr4:105233043-105233063	CUGGAGGGGAAGGGCAGACG	6028
54790 2 9509	+	chr4:105233048-105233068	GGGAAGGGCAGACGGGGCU	6029
54790 2 9511	+	chr4:105233049-105233069	GGGAAGGGCAGACGGGGCUA	6030
54790 2 9513	+	chr4:105233050-105233070	GGAAGGGCAGACGGGGCUAG	6031
54790 2 9516	+	chr4:105233053-105233073	AGGGCAGACGGGGCUAGGGG	6032
54790 2 9519	+	chr4:105233080-105233100	CCCUUUUAAAAAGCUACUGC	6033
54790 2 9522	+	chr4:105233083-105233103	UUUUAAAAAGCUACUGCAGG	6034
54790 2 9523	+	chr4:105233084-105233104	UUUAAAAAGCUACUGCAGGU	6035
54790 2 9524	+	chr4:105233085-105233105	UUAAAAAGCUACUGCAGGUG	6036
54790 2 9528	+	chr4:105233090-105233110	AAGCUACUGCAGGUGGGGUG	6037
54790 2 9529	+	chr4:105233093-105233113	CUACUGCAGGUGGGGUGCGG	6038
54790 2 9531	+	chr4:105233120-105233140	CACCUGUAAUCCCAGCACUU	6039

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 9534	+	chr4:105233121-105233141	ACCUGUAAUCCCAGCACUUU	6040
54790 2 9535	+	chr4:105233124-105233144	UGUAAUCCCAGCACUUUGGG	6041
54790 2 9536	+	chr4:105233130-105233150	CCCAGCACUUUGGGAGGCCA	6042
54790 2 9537	+	chr4:105233134-105233154	GCACUUUGGGAGGCCAAGGC	6043
54790 2 9541	+	chr4:105233148-105233168	CAAGGCAGGCAGAUCACCUG	6044
54790 2 9544	+	chr4:105233153-105233173	CAGGCAGAUCACCUGAGGUC	6045
54790 2 9545	+	chr4:105233171-105233191	UCAGGAGUUCAAGACCAGCC	6046
54790 2 9547	+	chr4:105233220-105233240	UAAAAAUACAAAAAUUAGCU	6047
54790 2 9548	+	chr4:105233225-105233245	AUACAAAAAUUAGCUAGGCA	6048
54790 2 9549	+	chr4:105233232-105233252	AAUUAGCUAGGCAUGGUAGC	6049
54790 2 9552	+	chr4:105233255-105233275	CACCUGUAAUCUCAGCUACU	6050
54790 2 9555	+	chr4:105233256-105233276	ACCUGUAAUCUCAGCUACUU	6051
54790 2 9556	+	chr4:105233259-105233279	UGUAAUCUCAGCUACUUGGG	6052
54790 2 9558	+	chr4:105233265-105233285	CUCAGCUACUUGGGAGGCUG	6053
54790 2 9561	+	chr4:105233269-105233289	GCUACUUGGGAGGCUGAGGC	6054
54790 2 9568	+	chr4:105233287-105233307	GCAGGAGAAUUGCUUGAACC	6055
54790 2 9570	+	chr4:105233288-105233308	CAGGAGAAUUGCUUGAACCU	6056
54790 2 9571	+	chr4:105233291-105233311	GAGAAUUGCUUGAACCUGGG	6057
54790 2 9573	+	chr4:105233297-105233317	UGCUUGAACCUGGGAGGCAG	6058
54790 2 9579	+	chr4:105233337-105233357	UGUGCCGCUGCACUCCAGCC	6059
54790 2 9580	+	chr4:105233338-105233358	GUGCCGCUGCACUCCAGCCU	6060
54790 2 9587	+	chr4:105233397-105233417	AAAAGCUACUGCAGUAGAUC	6061
54790 2 9590	+	chr4:105233400-105233420	AGCUACUGCAGUAGAUCAGG	6062
54790 2 9591	+	chr4:105233403-105233423	UACUGCAGUAGAUCAGGAGG	6063
54790 2 9596	+	chr4:105233439-105233459	AGAAGAUCUGAGCUAUGAAG	6064
54790 2 9599	+	chr4:105233458-105233478	GUGGCAGUCAAGAUGAUUAA	6065
54790 2 9602	+	chr4:105233468-105233488	AGAUGAUUAAAGGAAUUAU	6066
54790 2 9606	+	chr4:105233502-105233522	AUAGAACUUAGCAAGUGAUU	6067
54790 2 9615	+	chr4:105233529-105233549	UGAAGUGCUAGAGAAAAUAA	6068
54790 2 9616	+	chr4:105233530-105233550	GAAGUGCUAGAGAAAAUAAA	6069
54790 2 9618	+	chr4:105233531-105233551	AAGUGCUAGAGAAAAUAAAG	6070
54790 2 9620	+	chr4:105233560-105233580	UUCAAUUGUUUUUAGCAUUU	6071
54790 2 9630	+	chr4:105233576-105233596	AUUUUGGCAAAAAAUUAUUU	6072
54790 2 9642	+	chr4:105233626-105233646	UAUGAACUUCCCACAUUAGC	6073
54790 2 9666	+	chr4:105233761-105233781	AAUAUCAGUUUGCUAUGUCU	6074
54790 2 9688	-	chr4:105190557-105190577	AGAGAGAUUACCAUUACAUU	6075
54790 2 9696	-	chr4:105190580-105190600	GUAACUUGAAGUUGAAGUUU	6076
54790 2 9699	-	chr4:105190581-105190601	GGUAACUUGAAGUUGAAGUU	6077
54790 2 9705	-	chr4:105190602-105190622	AAAGUAUUUGAGAGGGUGCA	6078
54790 2 9706	-	chr4:105190603-105190623	AAAAGUAUUUGAGAGGGUGC	6079
54790 2 9708	-	chr4:105190609-105190629	AUAAAGAAAAGUAUUUGAGA	6080
54790 2 9709	-	chr4:105190610-105190630	AAUAAAGAAAAGUAUUUGAG	6081
54790 2 9741	-	chr4:105190827-105190847	GCGAUAAAUACUCUAACAAC	6082
54790 2 9742	-	chr4:105190849-105190869	CUACAAGUGAAGCAAAAUUGG	6083
54790 2 9744	-	chr4:105190852-105190872	UGGCUACAAGUGAAGCAAAA	6084
54790 2 9749	-	chr4:105190872-105190892	UUAACAAGAUUGAGACGAAG	6085
54790 2 9756	-	chr4:105190898-105190918	AACCACAAAUACCAUUUAUU	6086
54790 2 9760	-	chr4:105190945-105190965	ACUGACUAGCCAGGUGCAGG	6087

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 9761	-	chr4:105190948-105190968	AAGACUGACUAGCCAGGUGC	6088
54790 2 9765	-	chr4:105190954-105190974	UGUCACAAGACUGACUAGCC	6089
54790 2 9770	-	chr4:105190985-105191005	UUAGUUCUCUGCUAGUUCUA	6090
54790 2 9776	-	chr4:105191095-105191115	GUCCUCAAGUCUCGUCGGA	6091
54790 2 9777	-	chr4:105191096-105191116	GGUCCUCAAGUCUCGUCGG	6092
54790 2 9781	-	chr4:105191114-105191134	GUCCUACUACCGAACUUGGG	6093
54790 2 9786	-	chr4:105191126-105191146	UUCUCCGAUUCGCUCCUACU	6094
54790 2 9787	-	chr4:105191133-105191153	CGAGGAAUUCUCCGAUUCG	6095
54790 2 9789	-	chr4:105191137-105191157	GGGUCGAGGAAUUCUCCGAU	6096
54790 2 9790	-	chr4:105191143-105191163	ACAUUAGGGUCGAGGAAUUC	6097
54790 2 9792	-	chr4:105191174-105191194	AUCAUAUGAAGACCCGGACC	6098
54790 2 9793	-	chr4:105191175-105191195	AAUCAUAUGAAGACCCGGAC	6099
54790 2 9795	-	chr4:105191176-105191196	AAAUCAUAUGAAGACCCGGA	6100
54790 2 9797	-	chr4:105191177-105191197	AAAAUCAUAUGAAGACCCGG	6101
54790 2 9802	-	chr4:105191182-105191202	UUCAGAAAAUCAUAUGAAGA	6102
54790 2 9804	-	chr4:105191183-105191203	UUUCAGAAAAUCAUAUGAAG	6103
54790 2 9829	-	chr4:105191290-105191310	UUGGGACACUCAGCAGGUCA	6104
54790 2 9830	-	chr4:105191296-105191316	CUUAGGUUGGGACACUCAGC	6105
54790 2 9831	-	chr4:105191308-105191328	GGUCUGACAACCCUUAGGUU	6106
54790 2 9832	-	chr4:105191309-105191329	UGGUCUGACAACCCUUAGGU	6107
54790 2 9835	-	chr4:105191313-105191333	AAA AUGGUCUGACAACCCUU	6108
54790 2 9837	-	chr4:105191329-105191349	UACAUGCAUAUAUGAGAAAA	6109
54790 2 9857	-	chr4:105191431-105191451	UUAACUGUCUUUAUAUAGUUC	6110
54790 2 9868	-	chr4:105191531-105191551	AAGCUGAAUUACCUACUAAA	6111
54790 2 9884	-	chr4:105191606-105191626	GGCAGAGAUUAGAGCUAUAC	6112
54790 2 9888	-	chr4:105191627-105191647	AUCCUCAGGUGUCUGCAGUA	6113
54790 2 9889	-	chr4:105191641-105191661	GAGUGGAUACUUAUAUCCUC	6114
54790 2 9890	-	chr4:105191658-105191678	AGAAGUAUCAAGUGGCAGAG	6115
54790 2 9893	-	chr4:105191666-105191686	AGUCUCUGAGAAGUAUCAAG	6116
54790 2 9902	-	chr4:105191707-105191727	CAACUGAGGACACACUGGAA	6117
54790 2 9904	-	chr4:105191712-105191732	GAGUUCAACUGAGGACACAC	6118
54790 2 9907	-	chr4:105191721-105191741	GAAUCAUGGGAGUUAACUG	6119
54790 2 9910	-	chr4:105191734-105191754	UGGCAACAUCCAGGAAUCAU	6120
54790 2 9913	-	chr4:105191735-105191755	AUGGCAACAUCCAGGAAUCA	6121
54790 2 9916	-	chr4:105191743-105191763	UCUUGAAAAUGGCAACAUCC	6122
54790 2 9920	-	chr4:105191754-105191774	CUUGCCCUGUGUCUUGAAAA	6123
54790 2 9924	-	chr4:105191794-105191814	UUAAAAUUCCCAAGGUAGAG	6124
54790 2 9927	-	chr4:105191802-105191822	AGAGUGACUAAAAUUCCCA	6125
54790 2 9941	-	chr4:105191875-105191895	UAAAAUAUUAACAUGCAAG	6126
54790 2 9944	-	chr4:105191876-105191896	CUAAAAUAUUAACAUGCAA	6127
54790 2 9947	-	chr4:105191877-105191897	UCUAAAAUAUUAACAUGCA	6128
54790 2 9956	-	chr4:105191927-105191947	UCCAGCAUGAGAGGGGAAAG	6129
54790 2 9960	-	chr4:105191934-105191954	AAGAUUUUCCAGCAUGAGAG	6130
54790 2 9962	-	chr4:105191935-105191955	UAAGAUUUUCCAGCAUGAGA	6131
54790 2 9965	-	chr4:105191936-105191956	CUAAGAUUUUCCAGCAUGAG	6132
54790 2 9973	-	chr4:105191989-105192009	AGCAAUCAUCAAGGGAGGAG	6133
54790 2 9976	-	chr4:105191990-105192010	AAGCAAUCAUCAAGGGAGGA	6134
54790 2 9978	-	chr4:105191991-105192011	AAAGCAAUCAUCAAGGGAGG	6135

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 9980	-	chr4:105191994-105192014	GGUAAAGCAAUCAUCAAGGG	6136
54790 2 9983	-	chr4:105191997-105192017	UGAGGUAAAGCAAUCACAA	6137
54790 2 9985	-	chr4:105191998-105192018	GUGAGGUAAAGCAAUCAUCA	6138
54790 2 9989	-	chr4:105192015-105192035	GUCACAGUUCUCACAGAGUG	6139
54790 2 10002	-	chr4:105192099-105192119	AUGUUAUGACUUCAUUAAGG	6140
54790 2 10005	-	chr4:105192102-105192122	CUAAUGUUAUGACUUCAUUA	6141
54790 2 10019	-	chr4:105192155-105192175	CUGCACUUUAUUCCCUACCC	6142
54790 2 10044	-	chr4:105192241-105192261	UGUAAAACCUUUUCCCUCAA	6143
54790 2 10054	-	chr4:105192286-105192306	AGAUUUUUGAGGAGAUUAUGA	6144
54790 2 10055	-	chr4:105192287-105192307	AAGAUUUUUGAGGAGAUUAUG	6145
54790 2 10060	-	chr4:105192297-105192317	AAUGCAAACAAGAUUUUUG	6146
54790 2 10070	-	chr4:105192347-105192367	UGCUAUUGAAAAUAUGUCAA	6147
54790 2 10071	-	chr4:105192348-105192368	UUGCUAUUGAAAAUAUGUCA	6148
54790 2 10074	-	chr4:105192376-105192396	UACUACUAAAAAUAAACUCU	6149
54790 2 10086	-	chr4:105192433-105192453	UAAAUUUCGUCCCGAUGUC	6150
54790 2 10092	-	chr4:105192443-105192463	GAAGAAACGGUAAAUUUCGU	6151
54790 2 10093	-	chr4:105192444-105192464	AGAAGAAACGGUAAAUUUCG	6152
54790 2 10101	-	chr4:105192510-105192530	GAUAUACAACCCGUUACAUG	6153
54790 2 10103	-	chr4:105192521-105192541	AACUCUUGAUGAUUAUACAA	6154
54790 2 10104	-	chr4:105192522-105192542	UACUCUUGAUGAUUAUACA	6155
54790 2 10111	-	chr4:105192573-105192593	AAAAGCAACAUUAAUAAAAG	6156
54790 2 10124	-	chr4:105192638-105192658	UUCUCACGGACCAUAAACCG	6157
54790 2 10126	-	chr4:105192642-105192662	GAUCUUCUCACGGACCAUAA	6158
54790 2 10127	-	chr4:105192649-105192669	GAUCAAGGAUCUUCUCACGG	6159
54790 2 10140	-	chr4:105192706-105192726	UACCUAAGAUUCGAGUUGUU	6160
54790 2 10142	-	chr4:105192707-105192727	UUACCUAAGAUUCGAGUUGU	6161
54790 2 10145	-	chr4:105192725-105192745	CACAGACAGAGAAUGAGAUU	6162
54790 2 10164	-	chr4:105192779-105192799	AAAAUUUUGAAUCGUGAAGA	6163
54790 2 10195	-	chr4:105192929-105192949	UUAAGGAAGUCUAUUGAAGU	6164
54790 2 10203	-	chr4:105192970-105192990	UUUUAGAUGAGGUCCAGAAA	6165
54790 2 10204	-	chr4:105192978-105192998	AUAAAACCUUUUAGAUGAGG	6166
54790 2 10220	-	chr4:105193108-105193128	CUCCUCUGUUAUAGUCCAGA	6167
54790 2 10229	-	chr4:105193160-105193180	CUUCCUGUCCUUCAGGAUCC	6168
54790 2 10230	-	chr4:105193167-105193187	CCCAAUUCUCCUGUCCUUC	6169
54790 2 10239	-	chr4:105193211-105193231	CCCCUCCACUUCUCUCCACU	6170
54790 2 10240	-	chr4:105193212-105193232	UCCCCUCCACUUCUCUCCAC	6171
54790 2 10250	-	chr4:105193269-105193289	CUGGCCCAUUCCUGCCCUAA	6172
54790 2 10253	-	chr4:105193288-105193308	CUUCCCACUUGCCCUCUGCC	6173
54790 2 10262	-	chr4:105193325-105193345	GCCAACAUGAACUUUAUACA	6174
54790 2 10276	-	chr4:105193380-105193400	CUUUAGGAUUUUACUAAAUU	6175
54790 2 10279	-	chr4:105193396-105193416	AUAAUCUUUAGCUUGACUUU	6176
54790 2 10286	-	chr4:105193429-105193449	AAUUAUUCCCCAAUAUUUUC	6177
54790 2 10358	-	chr4:105193876-105193896	UGUACUAUGUUAGUAUUACA	6178
54790 2 10364	-	chr4:105193914-105193934	UAUUAUAAAAAUACAAAUU	6179
54790 2 10374	-	chr4:105193977-105193997	AACCUGAUCGACUACAGAUU	6180
54790 2 10379	-	chr4:105193996-105194016	GAAGGUGUUUUACUUGAUUA	6181
54790 2 10383	-	chr4:105194030-105194050	AUUUCAGUACAUUGUAGAGA	6182
54790 2 10384	-	chr4:105194031-105194051	UAUUUCAGUACAUUGUAGAG	6183

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 10387	-	chr4:105194056-105194076	AAUCUAUGAUCGAUCUCCGU	6184
54790 2 10388	-	chr4:105194061-105194081	GGUUCAAUUCUAUGAUCGAUC	6185
54790 2 10390	-	chr4:105194089-105194109	GAGUCUCAGUAUCCUCUGGA	6186
54790 2 10391	-	chr4:105194090-105194110	AGAGUCUCAGUAUCCUCUGG	6187
54790 2 10396	-	chr4:105194098-105194118	GCAGGAGGAGAGUCUCAGUA	6188
54790 2 10411	-	chr4:105194113-105194133	AUUUUUUUUUUUUUUUUAGCAGG	6189
54790 2 10414	-	chr4:105194116-105194136	UUUAAUUUUUUUUUUUUUUAGC	6190
54790 2 10418	-	chr4:105194204-105194224	GGCUACAAGAGAGUGCUAAC	6191
54790 2 10423	-	chr4:105194225-105194245	GUGUAUGUUAAUUAGAAAAA	6192
54790 2 10428	-	chr4:105194254-105194274	UAGAUCUGUUUCAUGAGAAA	6193
54790 2 10429	-	chr4:105194255-105194275	UUAGAUCUGUUUCAUGAGAA	6194
54790 2 10441	-	chr4:105194323-105194343	CUUCAACAAUGACUAAAGGU	6195
54790 2 10444	-	chr4:105194324-105194344	ACUUCAACAAUGACUAAAGG	6196
54790 2 10446	-	chr4:105194327-105194347	GAAACUUCAACAAUGACUAA	6197
54790 2 10449	-	chr4:105194349-105194369	AAAAGAUAAACAUUGUAAAUC	6198
54790 2 10470	-	chr4:105194464-105194484	CUGUAGGGUGAUGGUUUUUU	6199
54790 2 10472	-	chr4:105194465-105194485	CCUGUAGGGUGAUGGUUUUU	6200
54790 2 10475	-	chr4:105194473-105194493	AUUUAAUUUCCUGUAGGGUGA	6201
54790 2 10476	-	chr4:105194479-105194499	AGUGUGAUUUAAUUUCCUGUA	6202
54790 2 10477	-	chr4:105194480-105194500	GAGUGUGAUUUAAUUUCCUGU	6203
54790 2 10482	-	chr4:105194516-105194536	GAGAAAUCAGUAGCCAGAUC	6204
54790 2 10491	-	chr4:105194551-105194571	AAGUCUUAAGAGUCUAAGUAU	6205
54790 2 10498	-	chr4:105194585-105194605	GUUCAUAAGAAUGACCUGUA	6206
54790 2 10502	-	chr4:105194614-105194634	GCUUGCUAGAACAACAAUGACUA	6207
54790 2 10506	-	chr4:105194636-105194656	ACUCAAGAAUAAACUGCUC	6208
54790 2 10517	-	chr4:105194685-105194705	GCACUGUAUUUAUGAUCUCUA	6209
54790 2 10533	-	chr4:105194777-105194797	UACAUGUCUGCUCACUUGCU	6210
54790 2 10541	-	chr4:105194843-105194863	AUACCAUGUGGCAUGUGUAA	6211
54790 2 10545	-	chr4:105194855-105194875	AUGACUUGUAUCAUACCAUG	6212
54790 2 10553	-	chr4:105194901-105194921	CAAGACACCAUGUAUAAGAG	6213
54790 2 10556	-	chr4:105194938-105194958	GAGACUACUGAUACCACUCU	6214
54790 2 10557	-	chr4:105194939-105194959	AGAGACUACUGAUACCACUC	6215
54790 2 10565	-	chr4:105194966-105194986	GAUGUUUAAUUCAGUCUCUU	6216
54790 2 10566	-	chr4:105194967-105194987	AGAUGUUUAAUUCAGUCUCU	6217
54790 2 10570	-	chr4:105194997-105195017	CAGUCUAUUUACGGUGUUCU	6218
54790 2 10578	-	chr4:105195022-105195042	ACACUUAACAUCCCUAACGGU	6219
54790 2 10579	-	chr4:105195032-105195052	AUGUCGAUAAACACUUAUAAU	6220
54790 2 10581	-	chr4:105195033-105195053	UAUGUCGAUAAACACUUAUAA	6221
54790 2 10585	-	chr4:105195081-105195101	AUCAAAGGACACAUCUAUAG	6222
54790 2 10591	-	chr4:105195096-105195116	UUUACUUGUUCUAAAUAUCAA	6223
54790 2 10598	-	chr4:105195139-105195159	AUCACUUUUACUGAAAGUAU	6224
54790 2 10607	-	chr4:105195179-105195199	ACUAUAAAGUGGAAACUAC	6225
54790 2 10612	-	chr4:105195206-105195226	UUUCUAGGACUCUAGUUGUC	6226
54790 2 10642	-	chr4:105195339-105195359	CACAUUUUGAGAAAAAUGUC	6227
54790 2 10661	-	chr4:105195460-105195480	GUUAGAGGGUGUCUAUGACU	6228
54790 2 10668	-	chr4:105195486-105195506	AACUAUAGGUACCCCCCAGG	6229
54790 2 10670	-	chr4:105195492-105195512	GUCUAAAACUAUAGGUACCC	6230
54790 2 10671	-	chr4:105195493-105195513	UGUCUAAAACUAUAGGUACC	6231

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 10672	-	chr4:105195494-105195514	GUGUCUAAAACUAUAGGUAC	6232
54790 2 10675	-	chr4:105195495-105195515	GGUGUCUAAAACUAUAGGUA	6233
54790 2 10677	-	chr4:105195496-105195516	AGGUGUCUAAAACUAUAGGU	6234
54790 2 10683	-	chr4:105195520-105195540	AUAAAAUAUUAUUCUCUGAAC	6235
54790 2 10688	-	chr4:105195572-105195592	UACUAAGCUUCAUAUACCCU	6236
54790 2 10689	-	chr4:105195573-105195593	CUACUAAGCUUCAUAUACCC	6237
54790 2 10691	-	chr4:105195576-105195596	UCUCUACUAAGCUUCAUAUA	6238
54790 2 10694	-	chr4:105195577-105195597	CUCUCUACUAAGCUUCAUAU	6239
54790 2 10702	-	chr4:105195623-105195643	AUUAUUGAUGAAUGUAUCGU	6240
54790 2 10714	-	chr4:105195713-105195733	GUUUUAUGAGUCUUUUUUUU	6241
54790 2 10720	-	chr4:105195754-105195774	AAGUACCUAAGGUCGUAGAC	6242
54790 2 10722	-	chr4:105195770-105195790	GUCGGGGGGGUACCCAUAAGU	6243
54790 2 10725	-	chr4:105195779-105195799	CAUUAUUCAGUCGGGGGGGUA	6244
54790 2 10726	-	chr4:105195780-105195800	ACAUAUUCAGUCGGGGGGGU	6245
54790 2 10735	-	chr4:105195836-105195856	UCAAGGACUAUACGUGUCCU	6246
54790 2 10736	-	chr4:105195853-105195873	AAGACUCCUACCAAGAUUCA	6247
54790 2 10743	-	chr4:105195901-105195921	GAGUCAAGAUCUUGAGAAGA	6248
54790 2 10747	-	chr4:105195923-105195943	GCACGUGUACAAGUGGGGGGU	6249
54790 2 10750	-	chr4:105195927-105195947	AUGUGCACGUGUACAAGUGG	6250
54790 2 10751	-	chr4:105195928-105195948	UAUGUGCACGUGUACAAGUG	6251
54790 2 10753	-	chr4:105195929-105195949	GUAUGUGCACGUGUACAAGU	6252
54790 2 10755	-	chr4:105195930-105195950	AGUAUGUGCACGUGUACAAG	6253
54790 2 10760	-	chr4:105195974-105195994	CCACUCGUCCUGAAUUCCUU	6254
54790 2 10761	-	chr4:105195975-105195995	ACCACUCGUCCUGAAUUCCU	6255
54790 2 10763	-	chr4:105195979-105195999	UUCGACCACUCGUCCUGAAU	6256
54790 2 10766	-	chr4:105195987-105196007	AUCCUUCGUUCGACCACUCG	6257
54790 2 10769	-	chr4:105195995-105196015	GUUACGUUAUCCUUCGUUCG	6258
54790 2 10772	-	chr4:105196006-105196026	AACUUAACGAGAGUUACGUUA	6259
54790 2 10777	-	chr4:105196029-105196049	CCAUCUUCAAGAACCAGAUG	6260
54790 2 10778	-	chr4:105196037-105196057	UUUUUAUACCAUCUUCAAGA	6261
54790 2 10784	-	chr4:105196050-105196070	GCCCAUCUCCACCUUUUUUAU	6262
54790 2 10786	-	chr4:105196060-105196080	ACUGUGUUUUGCCCAUCUCC	6263
54790 2 10788	-	chr4:105196063-105196083	UAAACUGUGUUUUGCCCAUC	6264
54790 2 10790	-	chr4:105196069-105196089	UAUGUCUAAACUGUGUUUUG	6265
54790 2 10791	-	chr4:105196070-105196090	AUAUGUCUAAACUGUGUUUU	6266
54790 2 10792	-	chr4:105196071-105196091	GAUAUGUCUAAACUGUGUUU	6267
54790 2 10795	-	chr4:105196093-105196113	ACUCUGAAGAAUGAAAAGAA	6268
54790 2 10805	-	chr4:105196123-105196143	UAGGAAAUAAUUUAUGGAAG	6269
54790 2 10807	-	chr4:105196129-105196149	AACAAUUAGGAAAUAAUUUA	6270
54790 2 10809	-	chr4:105196142-105196162	CAGAGGCAGAGGGAACAAUU	6271
54790 2 10812	-	chr4:105196152-105196172	AAAAAAAGAACAGAGGCAGA	6272
54790 2 10814	-	chr4:105196153-105196173	AAAAAAAAGAACAGAGGCAG	6273
54790 2 10818	-	chr4:105196159-105196179	AGAAAAAAGAAAGAACAG	6274
54790 2 10829	-	chr4:105196200-105196220	ACUUAAGAAUGGGCAUACAG	6275
54790 2 10831	-	chr4:105196210-105196230	UCAGAUUUGCACUUAAGAAU	6276
54790 2 10832	-	chr4:105196211-105196231	GUCAGAUUUGCACUUAAGAA	6277
54790 2 10836	-	chr4:105196233-105196253	AUAUUAAGAAGGGGUAGA	6278
54790 2 10837	-	chr4:105196242-105196262	AAAGAAAGGAUAUUAAGAAG	6279

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 10838	-	chr4:105196243-105196263	AAAAGAAAGGAU AUUAAGAA	6280
54790 2 10839	-	chr4:105196244-105196264	UAAAAGAAAGGAU AUUAAGA	6281
54790 2 10844	-	chr4:105196256-105196276	AAUGGGUAUCCA UAAAAGAA	6282
54790 2 10849	-	chr4:105196273-105196293	CCUUUAAUAAAGUCUGAAAU	6283
54790 2 10850	-	chr4:105196274-105196294	UCCUUUAAUAAAGUCUGAAA	6284
54790 2 10855	-	chr4:105196307-105196327	CAAGUGGUGAGGUGGGGAGG	6285
54790 2 10858	-	chr4:105196308-105196328	UCAAGUGGUGAGGUGGGGAG	6286
54790 2 10859	-	chr4:105196309-105196329	UUCAAGUGGUGAGGUGGGGA	6287
54790 2 10862	-	chr4:105196310-105196330	CUUCAAGUGGUGAGGUGGGG	6288
54790 2 10864	-	chr4:105196313-105196333	AAACUUCAAGUGGUGAGGUG	6289
54790 2 10868	-	chr4:105196314-105196334	AAAACUUCAAGUGGUGAGGU	6290
54790 2 10870	-	chr4:105196315-105196335	AAAAACUUCAAGUGGUGAGG	6291
54790 2 10872	-	chr4:105196318-105196338	UGCAAAAACUUCAAGUGGUG	6292
54790 2 10875	-	chr4:105196323-105196343	CUAAUUGCAAAAACUUCAAG	6293
54790 2 10883	-	chr4:105196402-105196422	ACUCUGAAAAGGGGAUAAGU	6294
54790 2 10885	-	chr4:105196411-105196431	UUCAGGGCCACUCUGAAAAG	6295
54790 2 10886	-	chr4:105196412-105196432	AUUCAGGGCCACUCUGAAAA	6296
54790 2 10888	-	chr4:105196413-105196433	UAUUCAGGGCCACUCUGAAA	6297
54790 2 10894	-	chr4:105196427-105196447	UGGGUUCACAGAGCUAUUCA	6298
54790 2 10895	-	chr4:105196428-105196448	CUGGGUUCACAGAGCUAUUC	6299
54790 2 10900	-	chr4:105196446-105196466	ACUGAGUUCUUCAGAUUCCU	6300
54790 2 10903	-	chr4:105196447-105196467	UACUGAGUUCUUCAGAUUCC	6301
54790 2 10911	-	chr4:105196477-105196497	AUCUACUUUCUGUAGGCUGA	6302
54790 2 10912	-	chr4:105196484-105196504	GAGUUUGAUCUACUUUCUGU	6303
54790 2 10915	-	chr4:105196520-105196540	GAGUAACCAGGAGCCAGAUUC	6304
54790 2 10920	-	chr4:105196532-105196552	GAGGAAUUUGAAGAGUAACC	6305
54790 2 10925	-	chr4:105196551-105196571	GAAGGGACAAUUAUAGUAAGG	6306
54790 2 10928	-	chr4:105196554-105196574	UCUGAAGGGACAAUUAUAGUA	6307
54790 2 10932	-	chr4:105196568-105196588	UAAAGAUUUACAAAUCUGAA	6308
54790 2 10933	-	chr4:105196569-105196589	GUAAAGAUUUACAAAUCUGA	6309
54790 2 10938	-	chr4:105196591-105196611	GUGUGUAAAAUACGAUGUCA	6310
54790 2 10939	-	chr4:105196618-105196638	GGAGAGGAACAGCGGUACAA	6311
54790 2 10941	-	chr4:105196626-105196646	GUUCAUCAGGAGAGGAACAG	6312
54790 2 10943	-	chr4:105196634-105196654	AAAGGGAAGUUCAUCAGGAG	6313
54790 2 10948	-	chr4:105196639-105196659	AGAGAAAAGGGAAGUUCAUC	6314
54790 2 10950	-	chr4:105196651-105196671	GCUGUGUAGUUAAGAGAAAA	6315
54790 2 10952	-	chr4:105196652-105196672	AGCUGUGUAGUUAAGAGAAA	6316
54790 2 10965	-	chr4:105196722-105196742	AUGUCAUUCAUCCUACAAAC	6317
54790 2 10969	-	chr4:105196732-105196752	UUGUUUACUGAUGUCAUUCA	6318
54790 2 10973	-	chr4:105196766-105196786	UCCUUAAAGUCUUAGACGUU	6319
54790 2 10979	-	chr4:105196786-105196806	GUUCUACGUCGGAACGGGA	6320
54790 2 10995	-	chr4:105196917-105196937	AAGUUGCCAGUAGGGGGAGA	6321
54790 2 10996	-	chr4:105196918-105196938	GAAGUUGCCAGUAGGGGGAG	6322
54790 2 11000	-	chr4:105196923-105196943	AGGAAGAAGUUGCCAGUAGG	6323
54790 2 11003	-	chr4:105196924-105196944	UAGGAAGAAGUUGCCAGUAG	6324
54790 2 11005	-	chr4:105196925-105196945	GUAGGAAGAAGUUGCCAGUA	6325
54790 2 11008	-	chr4:105196926-105196946	AGUAGGAAGAAGUUGCCAGU	6326
54790 2 11014	-	chr4:105196943-105196963	CUGUAUCUAUUUUUAGAAGU	6327

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 11021	-	chr4:105196972-105196992	ACCUCUUCCCUCACUUAGU	6328
54790 2 11022	-	chr4:105196973-105196993	CACCUCUUCCCUCACUUAG	6329
54790 2 11038	-	chr4:105197075-105197095	CUUAUAAUUAAGUAUCUCUG	6330
54790 2 11043	-	chr4:105197121-105197141	UACUUUAGUGAAAAAAUGU	6331
54790 2 11050	-	chr4:105197145-105197165	GCAACACAUUUAAUUUUGAU	6332
54790 2 11076	-	chr4:105197346-105197366	UAUUCAUGUAUUUCUCACUA	6333
54790 2 11083	-	chr4:105197424-105197444	AGAACACAACCAAAAACUGC	6334
54790 2 11093	-	chr4:105197512-105197532	GGACAGCACUCUCAACAUA	6335
54790 2 11095	-	chr4:105197533-105197553	CAGCCACAUCACAAAGCACC	6336
54790 2 11115	-	chr4:105197639-105197659	CACUUUUUACUCUUUGGUCA	6337
54790 2 11117	-	chr4:105197640-105197660	UCACUUUUUACUCUUUGGUC	6338
54790 2 11120	-	chr4:105197645-105197665	AAGAAUCACUUUUUACUCUU	6339
54790 2 11126	-	chr4:105197673-105197693	UUUACUUUCCUCUAUAGCUA	6340
54790 2 11134	-	chr4:105197703-105197723	UUUAAUUCUACAUUUGAUGU	6341
54790 2 11135	-	chr4:105197704-105197724	AUUUAAUUCUACAUUUGAUG	6342
54790 2 11157	-	chr4:105197796-105197816	AAAACCUUUCAGAGACCAUC	6343
54790 2 11161	-	chr4:105197820-105197840	UUACUCUGAAAGUGAGUAAA	6344
54790 2 11163	-	chr4:105197821-105197841	CUUACUCUGAAAGUGAGUAA	6345
54790 2 11174	-	chr4:105197887-105197907	AACUUUUGGAAAAACAGAAA	6346
54790 2 11175	-	chr4:105197888-105197908	AAACUUUUGGAAAAACAGAA	6347
54790 2 11181	-	chr4:105197901-105197921	CUUUCAAAAAAUAAAACUUU	6348
54790 2 11189	-	chr4:105197931-105197951	UAAUUUUUCAAAUGUCUAAA	6349
54790 2 11195	-	chr4:105197989-105198009	CUUUUCUACGUUGCUACUCU	6350
54790 2 11204	-	chr4:105198024-105198044	UUAUUAUAAUACUUACUAUGU	6351
54790 2 11206	-	chr4:105198059-105198079	GUCCUCACUCGAUGGAGUGG	6352
54790 2 11210	-	chr4:105198078-105198098	AGGGUUUAACGACCCUAAUG	6353
54790 2 11212	-	chr4:105198086-105198106	GGAGCCGGAGGGUUUAACGA	6354
54790 2 11213	-	chr4:105198087-105198107	CGGAGCCGGAGGGUUUAACG	6355
54790 2 11217	-	chr4:105198103-105198123	GAGUCCACUAGGUGGGCGGA	6356
54790 2 11218	-	chr4:105198120-105198140	CCAGAGUUUGAGAACUGGAG	6357
54790 2 11221	-	chr4:105198141-105198161	AAAGUGGUUAUGACCAGUCCG	6358
54790 2 11222	-	chr4:105198145-105198165	CCCCAAAGUGGUUAUGACCAG	6359
54790 2 11224	-	chr4:105198150-105198170	CUCUACCCCAAAGUGGUUAUG	6360
54790 2 11231	-	chr4:105198164-105198184	AACGUAAAAAUCAUCUCUAC	6361
54790 2 11232	-	chr4:105198165-105198185	AAACGUAAAAAUCAUCUCUA	6362
54790 2 11233	-	chr4:105198166-105198186	AAAACGUAAAAAUCAUCUCU	6363
54790 2 11238	-	chr4:105198212-105198232	AGGGCUCAUCGACCAUAAUA	6364
54790 2 11239	-	chr4:105198221-105198241	CGGAGUCGGAGGGCUCAUCG	6365
54790 2 11244	-	chr4:105198285-105198305	CCUCACGUUGCCGUGCUAGA	6366
54790 2 11247	-	chr4:105198296-105198316	AACGAGUCCGACCUCACGUU	6367
54790 2 11250	-	chr4:105198306-105198326	AAGUGAGAACAACGAGUCCG	6368
54790 2 11253	-	chr4:105198310-105198330	CUCAAAGUGAGAACAACGAG	6369
54790 2 11283	-	chr4:105198404-105198424	UUGAUAGUUUCCUUUUCAU	6370
54790 2 11300	-	chr4:105198486-105198506	CAUAUUUUAGUUUCUGACUU	6371
54790 2 11311	-	chr4:105198539-105198559	UUCCUUCUGUCUCCUUUAAC	6372
54790 2 11323	-	chr4:105198584-105198604	AUUUUCUUGCCCUUAUUUUC	6373
54790 2 11343	-	chr4:105198674-105198694	GUUCAUUUUUUCAGCCUACA	6374
54790 2 11346	-	chr4:105198700-105198720	CAAGGACGUACCAUACCUUU	6375

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 11347	-	chr4:105198701-105198721	CCAAGGACGUACCAUACCUU	6376
54790 2 11351	-	chr4:105198706-105198726	UUCUUCCAAGGACGUACCAU	6377
54790 2 11353	-	chr4:105198711-105198731	GUCAUUUCUUCCAAGGACGU	6378
54790 2 11355	-	chr4:105198722-105198742	AGAAUCCUUACGUCAUUUCU	6379
54790 2 11359	-	chr4:105198738-105198758	CCACGAUCUGAUCAGGAGAA	6380
54790 2 11363	-	chr4:105198759-105198779	UAAUGGUGUUCAUAGGUUAA	6381
54790 2 11378	-	chr4:105198893-105198913	AUUAUAAUUAAGUAUCUCUG	6382
54790 2 11389	-	chr4:105198965-105198985	GCAACACAUUUAAUUUUGGU	6383
54790 2 11391	-	chr4:105198969-105198989	AACUGCAACACAUUUAAUUU	6384
54790 2 11401	-	chr4:105199050-105199070	UUUAUGUUCAUCAUACUUAU	6385
54790 2 11423	-	chr4:105199181-105199201	CACCAAACUUUAAUAUUUAA	6386
54790 2 11425	-	chr4:105199182-105199202	ACACCAAACUUUAAUAUUUA	6387
54790 2 11430	-	chr4:105199229-105199249	AAUUAGAAGAGAGCCCUAUA	6388
54790 2 11437	-	chr4:105199253-105199273	AAUUAUCUACACGUCAUAGG	6389
54790 2 11446	-	chr4:105199343-105199363	UUUUUUCUGUUUUUGGAAAC	6390
54790 2 11455	-	chr4:105199400-105199420	UUUAGUGUCAGUGUUUCACU	6391
54790 2 11466	-	chr4:105199466-105199486	UCCCUGAACUUCUUUGUUCU	6392
54790 2 11475	-	chr4:105199485-105199505	GGUAUUUAAAGGAAUUUCCU	6393
54790 2 11477	-	chr4:105199486-105199506	AGGUAUUUAAAGGAAUUUCC	6394
54790 2 11480	-	chr4:105199489-105199509	UAAAGGUAUUUAAAGGAAUU	6395
54790 2 11483	-	chr4:105199518-105199538	UUUUUAGCCACUUGAUGGUA	6396
54790 2 11487	-	chr4:105199523-105199543	UUUUCUUUUUAAAGCCACUUGA	6397
54790 2 11490	-	chr4:105199556-105199576	GUGCACAUGAGGACUUGAAU	6398
54790 2 11495	-	chr4:105199599-105199619	GUUGUUUGAGGGUACUGGGU	6399
54790 2 11498	-	chr4:105199639-105199659	CCCAUGAUCCGAAUUAUGGA	6400
54790 2 11499	-	chr4:105199640-105199660	ACCAUGAUCCGAAUUAUGG	6401
54790 2 11501	-	chr4:105199652-105199672	UUUUUAUUGAUUACCCAUGA	6402
54790 2 11502	-	chr4:105199659-105199679	CUAGUCCUUUUUAUUGAUUA	6403
54790 2 11503	-	chr4:105199660-105199680	CCUAGUCCUUUUUAUUGAUU	6404
54790 2 11505	-	chr4:105199675-105199695	CACCCUCCUCCCUCCUAG	6405
54790 2 11508	-	chr4:105199681-105199701	ACCUCCCACCCUCCUCCUC	6406
54790 2 11511	-	chr4:105199686-105199706	CUCCCACCUCCCACCCUCCU	6407
54790 2 11513	-	chr4:105199687-105199707	UCUCCCACCUCCCACCCUCC	6408
54790 2 11516	-	chr4:105199690-105199710	UAGUCUCCCACCUCCCACCC	6409
54790 2 11520	-	chr4:105199693-105199713	GGAUAGUCUCCCACCUCCA	6410
54790 2 11521	-	chr4:105199694-105199714	CGGAUAGUCUCCCACCUCCC	6411
54790 2 11524	-	chr4:105199697-105199717	CCCCGGAUAGUCUCCCACCU	6412
54790 2 11525	-	chr4:105199698-105199718	GCCCCGGAUAGUCUCCCACC	6413
54790 2 11527	-	chr4:105199701-105199721	GUGGCCCCCGGAUAGUCUCCC	6414
54790 2 11530	-	chr4:105199704-105199724	UGUGUGGCCCCCGGAUAGUCU	6415
54790 2 11531	-	chr4:105199705-105199725	GUGUGUGGCCCCCGGAUAGUC	6416
54790 2 11534	-	chr4:105199716-105199736	CUCCCCUUGUUGUGUGUGGC	6417
54790 2 11535	-	chr4:105199717-105199737	UCUCCCCUUGUUGUGUGUGG	6418
54790 2 11536	-	chr4:105199718-105199738	GUCUCCCCUUGUUGUGUGUG	6419
54790 2 11540	-	chr4:105199733-105199753	CUCCUGUAUACCUUGUGUCUC	6420
54790 2 11541	-	chr4:105199734-105199754	ACUCCUGUAUACCUUGUGUCU	6421
54790 2 11543	-	chr4:105199735-105199755	UACUCCUGUAUACCUUGUGUC	6422
54790 2 11547	-	chr4:105199744-105199764	UCGAUUUACUACUCCUGUAU	6423

Id	strand	genomic location (hg38) of target sequence	gRNA targeting domain sequence	SEQ ID NO:
54790 2 11550	-	chr4:105199752-105199772	AUUCACCCUCGAUUUACUAC	6424
54790 2 11555	-	chr4:105199767-105199787	CGUACAAGAGUGAAUAUUCA	6425
54790 2 11556	-	chr4:105199768-105199788	ACGUACAAGAGUGAAUAUUC	6426
54790 2 11561	-	chr4:105199808-105199828	AUAGGUAUCGUUUGAUUGUA	6427
54790 2 11567	-	chr4:105199835-105199855	UACCUGUACCUACCUCGACC	6428
54790 2 11570	-	chr4:105199838-105199858	ACGUACCUGUACCUACCUCG	6429
54790 2 11573	-	chr4:105199844-105199864	CAAAAAACGUACCUGUACCU	6430
54790 2 11576	-	chr4:105199848-105199868	AGUACAAAAACGUACCUGU	6431
54790 2 11578	-	chr4:105199854-105199874	UAUUCUAGUACAAAAACGU	6432
54790 2 11583	-	chr4:105199901-105199921	UGACACAAUAUAUAUGUGGU	6433
54790 2 11586	-	chr4:105199934-105199954	UUACGGGUGGUUAUUAUCUG	6434
54790 2 11590	-	chr4:105199967-105199987	AUAAGUGUUUAUCGUUUCUGU	6435
54790 2 11599	-	chr4:105200045-105200065	GUGAUGACCCAUAUAUGGUU	6436
54790 2 11602	-	chr4:105200058-105200078	UUGGGUCGUUGGGGUGAUGA	6437
54790 2 11603	-	chr4:105200059-105200079	GUUGGGUCGUUGGGGUGAUG	6438
54790 2 11610	-	chr4:105200129-105200149	CAUUUAAUCAAGUUGGUAAC	6439
54790 2 11616	-	chr4:105200155-105200175	UUGUGAAUAUACGAUAACCA	6440
54790 2 11618	-	chr4:105200156-105200176	CUUGUGAAUAUACGAUAACC	6441
54790 2 11620	-	chr4:105200159-105200179	UUCCUUGUGAAUAUACGAUA	6442
54790 2 11624	-	chr4:105200178-105200198	AUCACUCCAACGCCUCUUUU	6443
54790 2 11627	-	chr4:105200187-105200207	UAUUGUGCAAUCACUCCAAC	6444
54790 2 11630	-	chr4:105200193-105200213	GUUUUUUAUUGUGCAAUCAC	6445
54790 2 11634	-	chr4:105200231-105200251	GGUAGAGUGUGGUCAGUCCU	6446
54790 2 11635	-	chr4:105200235-105200255	CUAUGGUAGAGUGUGGUCAG	6447
54790 2 11644	-	chr4:105200327-105200347	AUGUUUUCUUCUGUAUGUAC	6448
54790 2 11649	-	chr4:105200366-105200386	GGGUAACUUUUUCACCCGUU	6449
54790 2 11651	-	chr4:105200372-105200392	UUGUAGGGGUAACUUUUUCA	6450
54790 2 11652	-	chr4:105200373-105200393	UUUGUAGGGGUAACUUUUUC	6451
54790 2 11658	-	chr4:105200414-105200434	AUAUUCCUAGAAUUUAAAUG	6452
54790 2 11661	-	chr4:105200430-105200450	UUAUCAUAGGUCGUAGAUAU	6453
54790 2 11669	-	chr4:105200482-105200502	UUUGUCUGUUGGAUGUCUUA	6454
54790 2 11672	-	chr4:105200483-105200503	UUUUGUCUGUUGGAUGUCUU	6455
54790 2 11682	-	chr4:105200557-105200577	CAUUCGUUUUUUAAGUGUUUA	6456
54790 2 11684	-	chr4:105200558-105200578	UCAUUCGUUUUUUAAGUGUUU	6457
54790 2 11689	-	chr4:105200617-105200637	AAAAAAAAAACAGUGUGACCU	6458
54790 2 11692	-	chr4:105200618-105200638	CAAAAAAAAAACAGUGUGACC	6459
54790 2 11696	-	chr4:105200704-105200724	ACAUAGUGGUGUGAGGUCUG	6460
54790 2 11701	-	chr4:105200744-105200764	ACGAACUUGGGCCUUACACC	6461
54790 2 11702	-	chr4:105200747-105200767	UUAACGAACUUGGGCCUUAC	6462
54790 2 11706	-	chr4:105200754-105200774	CGUCUUCUUAACGAACUUGG	6463
54790 2 11712	-	chr4:105200776-105200796	GGGUCGAUGAGUCCUCCGAC	6464
54790 2 11714	-	chr4:105200782-105200802	ACAUCAGGGUCGAUGAGUCC	6465
54790 2 11716	-	chr4:105200785-105200805	CGGACAUCAGGGUCGAUGAG	6466
54790 2 11719	-	chr4:105200813-105200833	GUUUUUAAUCGACCCGUACC	6467
54790 2 11720	-	chr4:105200816-105200836	UAUGUUUUUAAUCGACCCGU	6468
54790 2 11723	-	chr4:105200821-105200841	AUUUUUAUGUUUUUAAUCGA	6469
54790 2 11724	-	chr4:105200822-105200842	GAUUUUUAUGUUUUUAAUCG	6470
54790 2 11727	-	chr4:105200861-105200881	UCUCUGGUAGGACCGGUUGU	6471

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 3
CONTENANT LES PAGES 1 À 215

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 3
CONTAINING PAGES 1 TO 215

NOTE: For additional volumes, please contact the Canadian Patent Office

NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS:

1. A gRNA molecule comprising a tracr and crRNA, wherein the crRNA comprises a targeting domain that is complementary with a target sequence selected from a TET2 intron and a TET2 intron-exon junction.
2. A gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105146980-105190359; chr4:105190506-105233896; chr4:105237352-105241338; chr4:105241430-105242833; chr4:105242928-105243569; chr4:105243779-105259618; chr4:105259770-105261758; chr4:105261849-105269609; chr4:105269748-105272563; and chr4:105272919-105275047, wherein said genomic region is according to human reference genome hg38.
3. The gRNA molecule of claim 2, wherein the genomic region is chr4:105269748-105272563.
4. The gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; chr4:105272465-105272485; chr4:105271387-105271407; chr4:105272436-105272456; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; chr4:105271845-105271865; chr4:105271849-105271869; and chr4:105271056-105271076.
5. The gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271387-105271407; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; and chr4:105271056-105271076.

6. The gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.
7. The gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105271340-105271360; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.
8. The gRNA molecule of claim 1, wherein the targeting domain is complementary to a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; and chr4:105271863-105271883.
9. The gRNA molecule any of claims 1-2, wherein the targeting domain comprises or consists of, any one of SEQ ID NO: 1000 to SEQ ID NO: 10514, e.g., of Table 1 or Table 2, or a fragment thereof.
10. The gRNA molecule of any of claims 1-8, wherein the targeting domain comprises any one of SEQ ID NO: 10102 to SEQ ID NO: 10324, or a fragment thereof.
11. The gRNA molecule of any of claims 1-9, wherein the targeting domain comprises a targeting domain sequence listed in Table 2, or a fragment thereof.
12. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of SEQ ID NO: 10148, SEQ ID NO: 10184, SEQ ID NO: 10185, SEQ ID NO: 10188, SEQ ID NO: 10209, SEQ ID NO: 10212, SEQ ID NO: 10317, SEQ ID NO: 10318, SEQ ID NO: 10187, SEQ ID NO: 10224, SEQ ID NO: 10292, SEQ ID NO: 10149, SEQ ID NO: 10177, SEQ ID NO: 10151, SEQ ID NO: 10225 or SEQ ID NO: 10509.
13. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of 10148, 10149, 10206, 10191, 10515, 10203, 10259, 10136, 10314, 10234, 10290, 10233, 10209, 10224, 10212, 10317, 10318, 10225, 10184, 10185, 10188, 10187, 10292, 10151, 10509, 10281, 10299, 10301, or 10177.
14. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of SEQ ID NOs: 10148, 10149, 10290, 10209, 10224, 10212, 10317, 10318, 10225, 10184, 10185, 10188, 10187, 10292, 10151, 10509, 10281, or 10177.

15. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of SEQ ID NOs: 10206, 10191, 10515, 10203, 10259, 10136, 10314, or 10234..
16. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of SEQ ID NOs: 10191, 10203, 10259, 10136, 10314, or 10234.
17. The gRNA molecule of any of claims 1-11, wherein the targeting domain comprises any one of SEQ ID NOs: 10148, 10149, and 10206.
18. The gRNA molecule of any of claims 1-17, wherein the targeting domain comprises 17, 18, 19 or, 20 consecutive nucleic acids of any one of the recited targeting domain sequences.
19. The gRNA molecule of any of claims 1-17, wherein the targeting domain consists of 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences.
20. The gRNA molecule of claim 18 or 19, wherein the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences are the 17, 18, 19, or 20 consecutive nucleic acids disposed at the 3' end of the recited targeting domain sequence.
21. The gRNA molecule of claim 18 or 99, wherein the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences are the 17, 18, 19, or 20 consecutive nucleic acids disposed at the 5' end of the recited targeting domain sequence.
22. The gRNA molecule of claim 18 or 19, wherein the 17, 18, 19, or 20 consecutive nucleic acids of any one of the recited targeting domain sequences do not comprise either the 5' or 3' nucleic acid of the recited targeting domain sequence.
23. The gRNA molecule of any of claims 1-17, wherein the targeting domain consists of the recited targeting domain sequence.
24. The gRNA molecule of any of the previous claims, wherein a portion of the crRNA and a portion of the tracr hybridize to form a flagpole comprising SEQ ID NO: 50 or SEQ ID NO: 51.
25. The gRNA molecule of claim 24, wherein the flagpole further comprises a first flagpole extension, located 3' to the crRNA portion of the flagpole, wherein said first flagpole extension comprises SEQ ID NO: 55.
26. The gRNA molecule of claim 24 or 25, wherein the flagpole further comprises a second flagpole extension located 3' to the crRNA portion of the flagpole and, if present, the first flagpole extension, wherein said second flagpole extension comprises SEQ ID NO: 57.

27. The gRNA molecule of any of claims 1-26, wherein the tracr comprises:

- (a) SEQ ID NO: 87, optionally further comprising, at the 3' end, an additional 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides;
- (b) SEQ ID NO: 65; or
- (c) SEQ ID NO: 84.

28. The gRNA molecule of claim 27, wherein the crRNA portion of the flagpole comprises SEQ ID NO: 79 or SEQ ID NO: 80.

29. The gRNA molecule of any of claims 1-26, wherein the tracr comprises SEQ ID NO: 53 or SEQ ID NO: 54, and optionally, if a first flagpole extension is present, a first tracr extension, disposed 5' to SEQ ID NO: 53 or SEQ ID NO: 54, said first tracr extension comprising SEQ ID NO: 56.

30. The gRNA molecule of any of claims 19-20, wherein the targeting domain and the tracr are disposed on separate nucleic acid molecules.

31. The gRNA molecule of any of claims 1-23, wherein the crRNA comprises, from 5' to 3', [targeting domain]-:

- (a) SEQ ID NO: 50;
- (b) SEQ ID NO: 51;
- (c) SEQ ID NO: 77;
- (d) SEQ ID NO: 78;
- (e) SEQ ID NO: 79;
- (f) SEQ ID NO: 80; or
- (g) SEQ ID NO: 81.

32. The gRNA molecule of any of claims 1-23 or 31, wherein the tracr comprises, from 5' to 3':

- (a) SEQ ID NO: 53;
- (b) SEQ ID NO: 54;
- (c) SEQ ID NO: 82;

(d) SEQ ID NO: 83;

(e) SEQ ID NO: 65;

(f) SEQ ID NO: 84;

(g) SEQ ID NO: 87;

(h) SEQ ID NO: 76;

(i) SEQ ID NO: 85;

(j) SEQ ID NO: 86;

(k) any of a) to j), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 uracil (U) nucleotides;

(l) any of a) to k), above, further comprising, at the 3' end, at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides; or

(m) any of a) to l), above, further comprising, at the 5' end (e.g., at the 5' terminus), at least 1, 2, 3, 4, 5, 6 or 7 adenine (A) nucleotides, e.g., 1, 2, 3, 4, 5, 6, or 7 adenine (A) nucleotides.

33. The gRNA molecule of any of claims 1-23, wherein the targeting domain and the tracr are disposed on separate nucleic acid molecules, and wherein the nucleic acid molecule comprising the targeting domain comprises SEQ ID NO: 79, optionally disposed immediately 3' to the targeting domain, and the nucleic acid molecule comprising the tracr comprises SEQ ID NO: 65.

34. The gRNA molecule of any of claims 27-28, wherein the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein the tracr is disposed 3' to the targeting domain.

35. The gRNA molecule of claim 34, further comprising a loop, disposed 3' to the targeting domain and 5' to the tracr.

36. The gRNA molecule of claim 35, wherein the loop comprises SEQ ID NO: 52.

37. The gRNA molecule of any of claims 1-33, comprising, from 5' to 3', [targeting domain]-:

(a) SEQ ID NO: 71;

(b) SEQ ID NO: 72;

(c) SEQ ID NO: 73;

(d) SEQ ID NO: 74;

(e) SEQ ID NO: 75; or

(f) any of (a) to (e), above, further comprising, at the 3' end, 1, 2, 3, 4, 5, 6 or 7 uracil (U) nucleotides.

38. The gRNA molecule of any of claims 1-23, wherein the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein said nucleic acid molecule comprises said targeting domain and SEQ ID NO: 71, optionally disposed immediately 3' to said targeting domain.

39. The gRNA molecule of any of claims 1-23, wherein the targeting domain and the tracr are disposed on a single nucleic acid molecule, and wherein said nucleic acid molecule comprises said targeting domain and SEQ ID NO: 75, optionally disposed immediately 3' to said targeting domain.

40. The gRNA molecule of any of claims 1-39 wherein one, or optionally more than one, of the nucleic acid molecules comprising the gRNA molecule comprises:

(a) a, e.g., three, phosphorothioate modification(s) at the 3' end of said nucleic acid molecule or molecules;

(b) a, e.g., three, phosphorothioate modification(s) at the 5' end of said nucleic acid molecule or molecules;

(c) a, e.g., three, 2'-O-methyl modification(s) at the 3' end of said nucleic acid molecule or molecules;

(d) a, e.g., three, 2'-O-methyl modification(s) at the 5' end of said nucleic acid molecule or molecules;

(e) a 2' O-methyl modification at each of the 4th-to-terminal, 3rd-to-terminal, and 2nd-to-terminal 3' residues of said nucleic acid molecule or molecules; or

(f) any combination thereof.

41. A gRNA molecule of any of claims 1-40, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a cell, an indel is formed at or near the target sequence complementary to the targeting domain of the gRNA molecule.

42. The gRNA molecule of claim 41, wherein the indel comprises a deletion of greater than 10 nucleotides, e.g., 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides.

43. A gRNA molecule of any of claims 1-42, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a population of cells, an indel is formed at or near the target sequence complementary to the targeting domain of the gRNA molecule in at least about 40%, e.g., at least about 50%, e.g., at least about 60%, e.g., at least about 70%, e.g., at least about 80%, e.g., at least about 90%, e.g., at least about 95%, e.g., at least about 96%, e.g., at least about 97%, e.g., at least about 98%, e.g., at least about 99%, of the cells of the population.

44. The gRNA molecule of claim 42, wherein the indel comprising a deletion of greater than 10 nucleotides, e.g., 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides is detected in at least about 5%, e.g., at least about 10%, 15%, 20%, 25%, 30% or more of the cells of the population.

45. A gRNA molecule of claim 41, wherein the indel is selected from those in Table 22.

46. A gRNA molecule of claim 41, wherein the indel forms at an indel frequency selected from those in Table 23.

47. The gRNA molecule of any of claims 41-46, wherein the indel is as measured by next generation sequencing (NGS).

48. A gRNA molecule of any of claims 1-47, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a cell, expression of at least one isoform of TET2 is reduced or eliminated in said cell.

49. A gRNA molecule of any of claims 1-48, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a cell, a function, e.g., a catalytic function, of TET2 is reduced or eliminated in said cell.

50. A gRNA molecule of claim 49, wherein the function, e.g., the catalytic function, of TET2 is reduced, e.g., by at least about 10%, 20%, 30%, 40% or 50%, but said function, e.g., said catalytic function, is not reduced by more than about 80%, e.g., eliminated, in said cell.

51. A gRNA molecule of any of claims 1-51, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a cell, TET2 expression, e.g., expression of at least one TET2 isoform, and/or at least one TET2 function is

not altered relative to the level of expression and/or function in the same type of cell but to which said CRISPR system is not introduced (e.g., an unaltered cell of the same type).

52. The gRNA molecule of any of claims 43-51, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a cell, no off-target indels are formed in said cell, e.g., as detectible by next generation sequencing and/or a nucleotide insertional assay.

53. The gRNA molecule of any of claims 43-51, wherein when a CRISPR system (e.g., an RNP as described herein) comprising the gRNA molecule is introduced into a population of cells, an off-target indel is detected in no more than about 5%, e.g., no more than about 1%, e.g., no more than about 0.1%, e.g., no more than about 0.01%, of the cells of the population of cells e.g., as detectible by next generation sequencing and/or a nucleotide insertional assay.

54. A composition comprising a first gRNA molecule of any of claims 1-53.

55. The composition of claim 54, further comprising a Cas9 molecule.

56. The composition of claim 55, wherein the Cas9 molecule comprises any one of SEQ ID NO: 90, SEQ ID NO: 111 to SEQ ID NO: 121 or SEQ ID NO: 123.

57. The composition of claim 55, wherein the Cas9 molecule is an active or inactive *S. pyogenes* Cas9.

58. The composition of any of claims 55-57, wherein the first gRNA molecule and Cas9 molecule are present in a ribonuclear protein complex (RNP).

59. The composition of any of claims 54-58, further comprising a template nucleic acid.

60. The composition of claim 59, wherein the template nucleic acid is double-stranded or single stranded.

61. The composition of any of claims 59-60, wherein the template nucleic acid is or is included in a vector.

62. The composition of claim 61, wherein the vector is a lentivirus vector, an AAV vector, an adenovirus vector, a plasmid, a minicircle or a nanoplasmid.

63. The composition of claim 62, wherein the vector is an AAV vector.

64. The composition of claim 63, wherein the AAV vector is an AAV6 vector.

65. The composition of any of claims 59-84, wherein the template nucleic acid comprises at least one (e.g., at least a 5' or at least a 3') homology arm, and wherein said homology arm comprises sequence homologous to sequence of a TET2 intron.

66. The composition of claim 65, wherein the template nucleic acid comprises both a 5' and a 3' homology arm, and wherein at least one of the homology arms comprises sequence homologous to sequence of a TET2 intron.

67. The composition of any of claims 59-66, wherein the template nucleic acid comprises nucleic acid encoding a chimeric antigen receptor (CAR).

68. The composition of claim 67, wherein the CAR is:

(a) a CD19 CAR, e.g., as described in herein; or

(b) a BCMA CAR, e.g., as described herein.

69. The composition of claim 68, wherein the CAR is a CD19 CAR comprising an antigen binding domain comprising any one of SEQ ID NO: 160 to SEQ ID NO: 172 or SEQ ID NO: 175.

70. The composition of any of claims 68-69, wherein the CAR is a CD19 CAR and comprises any one of SEQ ID NO: 185 to SEQ ID NO: 197.

71. The composition of claim 68, wherein the CAR is a BCMA CAR comprising an antigen binding domain comprising any one of SEQ ID NO: 239 to SEQ ID NO: 412.

72. The composition of any of claims 68 and 71, wherein the CAR is a BCMA CAR and comprises any one of SEQ ID NO: 849 to SEQ ID NO: 863 or SEQ ID NO: 879 to SEQ ID NO: 899, e.g., comprises SEQ ID NO: 859.

73. The composition of any of claims 67-72, wherein the template nucleic acid comprises a promotor, e.g., an EF1-alpha promotor, operably linked to the nucleic acid sequence encoding the CAR.

74. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; the template nucleic acid sequence further comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a

sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

75. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

76. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

77. The composition of any of claims 59-73, wherein the template nucleic acid sequence is in an AAV6 vector; the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; the template nucleic acid sequence further comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

78. The composition of any of claims 59-73, the template nucleic acid sequence is provided on an AAV6 vector; the template nucleic acid sequence comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

79. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; and the gRNA molecule is selected from a gRNA comprising a targeting domain complementary to

a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, chr4:105271863-105271883.

80. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; and the gRNA molecule is a gRNA comprising a targeting domain complementary to a sequence within a genomic region (according to hg38) of chr4:105269748-105272563, chr4:105270624-105270643, chr4:105270630-105270649, or chr4:105271863-105271883.

81. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; the template nucleic acid sequence further comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is selected from a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

82. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

83. The composition of any of claims 59-73, wherein the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

84. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; the template nucleic acid sequence further comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

85. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; the template nucleic acid sequence comprises a first homology arm comprising SEQ ID NO: 124 and a second homology arm comprising SEQ ID NO: 125; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

86. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; the template nucleic acid sequence comprises a nucleic acid sequence encoding a CAR selected from a CD19 CAR, a BCMA CAR, and a CD22 CAR; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

87. The composition of any of claims 59-73, wherein the template nucleic acid sequence is provided on an AAV6 vector; and the gRNA molecule is a gRNA comprising a targeting domain of any of the sequences in Table 1 or Table 2, SEQ ID NO: 10148, SEQ ID NO: 10149, or SEQ ID NO: 10206.

88. The composition of any of claims 54-87, further comprising at least one additional gRNA molecule, and wherein each gRNA molecule of the composition is complementary to a different target sequence.

89. The composition of claim 88, wherein the first gRNA molecule and the at least one additional gRNA molecule are complementary to target sequences within the same TET2 intron.

90. The composition of claim 88, wherein the first gRNA molecule and the at least one additional gRNA molecule are complementary to target sequence within different genes.

91. The composition of claim 90, wherein the first gRNA molecule is a gRNA molecule of any of claims 1-53, and at least one of the additional gRNA molecule(s) comprises a targeting domain complementary to a target sequence of an inhibitory molecule (e.g., PDCD1), a component of the T cell receptor (e.g., TRAC or TRBC), B2M, HLA-DM, HLA-DO, HLA-DR, HLA-DQ, HLA-DP, CIITA, RFXANK, RFXAP, RFX1, RFX5, NF-YA, NF-YB, NF-YC, X2BP, OCAB, HLA-A, HLA-B, HLA-C, NLRC5, CD247, CD3, CD3D, CD3E, CD3G, DCK, CD52, FKBP1A, or NR3C1.

92. The composition of any of claims 54-91, formulated in a medium suitable for electroporation.

93. The composition of any of claims 54-92, wherein each of said gRNA molecules is in a RNP complex with a Cas9 molecule described herein, and wherein each of said RNP complexes is at a concentration of less than about 10uM, e.g., less than about 3uM, e.g., less than about 1uM, e.g., less than about 0.5uM, e.g., less than about 0.3uM, e.g., less than about 0.1uM.

94. A nucleic acid sequence that encodes a gRNA molecule of any of claims 1-54 or a, e.g., all, components of a composition of any of claims 55-93.

95. A vector comprising the nucleic acid of claim 94.

96. The vector of claim 95, wherein in the vector is selected from the group consisting of a lentiviral vector, an adenoviral vector, an adeno-associated viral (AAV) vector, a herpes simplex virus (HSV) vector, a plasmid, a minicircle, a nanoplasmid, and an RNA vector.

97. A method of altering e.g., altering the structure, e.g., sequence of, a target sequence of a cell, comprising contacting said cell with:

- (a) a gRNA molecule, e.g., more than one gRNA molecule, of any of claims 1-54 and a Cas9 molecule;
- (b) a gRNA molecule, e.g., more than one gRNA molecule, of any of claims 1-54 and nucleic acid encoding a Cas9 molecule;
- (c) nucleic acid encoding a gRNA molecule, e.g., more than one gRNA molecule, of any of claims 1-54 and a Cas9 molecule;
- (d) nucleic acid encoding a gRNA molecule, e.g., more than one gRNA molecule, of any of claims 1-54 and nucleic acid encoding a Cas9 molecule;
- (e) any of a) to d), above, and a template nucleic acid, e.g., a template nucleic acid as described in any of claims 60-87;
- (f) the composition of any of claims 55-93; or
- (g) the vector of any of claims 95-96.

98. The method of claim 97, wherein the gRNA molecule of any of claims 1-54 or nucleic acid encoding the gRNA molecule of any of claims 1-54, and the Cas9 molecule or nucleic acid encoding the Cas9 molecule, are formulated in a single composition.

99. The method of claim 97 or 98, wherein the composition comprises a template nucleic acid, e.g., a template nucleic acid as described in any of claims 60-87, and the template nucleic acid

is formulated in a separate composition from the gRNA molecule of any of claims 1-54 or nucleic acid encoding the gRNA molecule of any of claims 1-54 and the Cas9 molecule or nucleic acid encoding the Cas9 molecule.

100. The method of claim 99, wherein the more than one compositions are delivered sequentially.

101. The method of claim 99, wherein the more than one compositions are delivered simultaneously.

102. The method of any of claims 97-101, wherein the method results in insertion of at least a portion of the template nucleic acid at or near the target sequence of the gRNA molecule of any of claims 1-54.

103. The method of claim 102, wherein said insertion occurs at only at one allele.

104. The method of claim 102, wherein said insertion occurs at both alleles.

105. A method of engineering a cell to express a chimeric antigen receptor (CAR), comprising:

(a) introducing into said cell a CRISPR system comprising a gRNA molecule of any of claims 1-54 or a composition of any of claims 55-58; and

(b) introducing into said cell a template nucleic acid comprising nucleic acid sequence encoding a CAR;

wherein said nucleic acid sequence encoding a CAR is integrated into the genome, e.g., optionally at only a single allele of the genome, at or near the target sequence of said gRNA molecule.

106. The method of claim 105, further comprising introducing into said cell one or more CRISPR systems comprising one or more gRNA molecules complementary to a target sequence of an inhibitory molecule, a component of the T cell receptor, B2M and/or CIITA.

107. The method of any of claims 97-106, wherein the cell is an animal cell.

108. The method of any of claims 97-107, wherein the cell is a mammalian, primate, or human cell.

109. The method of claim 108, wherein the cell is an immune effector cell (e.g., a population of immune effector cells).

110. The method of claim 109, wherein the immune effector cell is a T cell or NK cell, e.g., a T cell, e.g., a CD4⁺ T cell, a CD8⁺ T cell, or a combination thereof.

111. The method of any of claims 105-106, wherein the CAR is:

(a) a CD19 CAR, e.g., as described in herein; or

(b) a BCMA CAR, e.g., as described herein.

112. The method of claim 111, wherein the CAR is a CD19 CAR comprising an antigen binding domain comprising any one of SEQ ID NO: 160 to SEQ ID NO: 172 or SEQ ID NO: 175.

113. The method of any of claims 111-112, wherein the CAR is a CD19 CAR and comprises any one of SEQ ID NO: 185 to SEQ ID NO: 197.

114. The method of claim 111, wherein the CAR is a BCMA CAR comprising an antigen binding domain comprising any one of SEQ ID NO: 239 to SEQ ID NO: 412.

115. The method of any of claims 111 and 114, wherein the CAR is a BCMA CAR and comprises any one of SEQ ID NO: 849 to SEQ ID NO: 863 or SEQ ID NO: 879 to SEQ ID NO: 899, e.g., comprises SEQ ID NO: 859.

116. The method of any of claims 97-115, wherein the cell is autologous or allogeneic with respect to a patient to be administered said cell.

117. A cell, altered by the method of any of claims 97-116.

118. A cell, comprising a first gRNA molecule of any of claims 1-54, or a composition of any of claims 55-93, a nucleic acid of claim 94, or a vector of any of claims 95-96.

119. The cell of any of claims 117-118, wherein the cell is an animal cell, e.g., a mammalian, primate, or human cell.

120. The cell of claim 119, wherein the cell is an immune effector cell (e.g., a population of immune effector cells), e.g., a T cell or NK cell, e.g., a T cell, e.g., a CD4⁺ T cell, a CD8⁺ T cell, or a combination thereof.

121. The cell of any of claims 117-120, wherein the cell has reduced or eliminated expression of an inhibitory molecule, a component of the T cell receptor (e.g., TRAC, TRBC1, TRBC2, CD3E, CD3D, or CD3G), B2M, CIITA, or combinations thereof, e.g., relative to an unmodified cell of the same type.

122. A cell of any of claims 117-121, wherein the cell comprises nucleic acid sequence encoding a chimeric antigen receptor (CAR) integrated into the genome at a TET2 intron or intron-exon junction.

123. A cell of any of claims 117-122, wherein the cell comprises nucleic acid sequence encoding a chimeric antigen receptor (CAR) integrated into the genome at a TET2 intron 9-10 or an intron-exon junction at exon 9 and intron 9-10 or an intron-exon junction at exon 10 and intron 9-10.

124. A cell of any of claims 117-123, wherein the cell comprises reduced or eliminated TET2 expression, e.g., expression of at least one TET2 isoform, and/or reduced or eliminated function of TET2, e.g., at least one function of TET2, e.g., catalytic function of TET2, relative to the level of expression and/or function of an unaltered cell of the same cell type.

125. A cell of any of claims 117-124, wherein the cell is a T cell and exhibits:

- (a) enhanced proliferative capacity;
- (b) enhanced cytotoxicity;
- (c) a less-exhausted phenotype (e.g., reduced expression of an inhibitory molecule, e.g., PD1, TIM3, LAG3, PD-L1, or combinations thereof); or
- (d) a Tscm phenotype (e.g., is CD45RA+CD62L+CD27+CD95+),

relative to an unaltered cell of similar type.

126. The cell of any of claims 117-125, wherein the cell is autologous with respect to a patient to be administered said cell.

127. The cell of any of claims 117-125, wherein the cell is allogeneic with respect to a patient to be administered said cell.

128. A modified cell, which has reduced or eliminated expression and/or function of TET2, and comprises heterologous nucleic acid sequence (e.g., nucleic acid sequence encoding a chimeric antigen receptor) integrated at a site within a TET2 intron.

129. The modified cell of claim 128, wherein said site within a TET2 intron is selected from any one of chr4:105146980-105190359; chr4:105190506-105233896; chr4:105237352-105241338; chr4:105241430-105242833; chr4:105242928-105243569; chr4:105243779-105259618; chr4:105259770-105261758; chr4:105261849-105269609; chr4:105269748-

105272563; and chr4:105272919-105275047, wherein said genomic region is according to human reference genome hg38.

130. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105269748-105272563.

131. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; chr4:105272465-105272485; chr4:105271387-105271407; chr4:105272436-105272456; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; chr4:105271845-105271865; chr4:105271849-105271869; and chr4:105271056-105271076.

132. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271387-105271407; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; and chr4:105271056-105271076.

133. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.

134. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105271340-105271360;

chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.

135. The modified cell of claim 128 or 129, wherein the heterologous nucleic acid sequence is integrated at a site within a TET2 intron selected from: chr4:105270624-105270643; chr4:105270630-105270649; and chr4:105271863-105271883.

136. The cell of any one of claims 128-135, wherein the cell has reduced or eliminated expression and/or function of a component of the T cell receptor, B2M, CIITA or a combination thereof, relative to an unmodified cell of the same type.

137. A method of providing an anti-tumor immunity in a subject, the method comprising administering to the subject an effective amount of a cell of any of claims 117-136.

138. A method of treating a subject having a disease associated with expression of a tumor antigen, e.g., a proliferative disease, a precancerous condition, a cancer, and a non-cancer related indication associated with expression of the tumor antigen, the method comprising administering to the subject an effective amount of a cell of any of claims 117-136.

139. The method of claim 138, wherein the disease associated with expression of a tumor antigen is cancer or a non-cancer related indication.

140. The method of claim 139, wherein the disease is cancer selected from colon cancer, rectal cancer, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, melanoma, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, Hodgkin's Disease, non-Hodgkin's lymphoma, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers, chronic lymphocytic leukemia (CLL), acute leukemias, acute lymphoid leukemia (ALL), pediatric acute lymphoid leukemia, B-cell acute lymphoid leukemia (B-ALL), T-cell acute lymphoid leukemia (T-ALL), chronic myelogenous leukemia

(CML), acute myeloid leukemia (AML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and pre-leukemia, combinations of said cancers, and metastatic lesions of said cancers.

141. The method of claim 140, wherein the cancer is acute lymphoid leukemia (ALL).

142. The method of claim 140, wherein the cancer is pediatric ALL.

143. The method of claim 140, wherein the cancer is diffuse large B cell lymphoma.

144. The method of claim 140, wherein the cancer is chronic lymphocytic leukemia.

145. The method of claim 140, wherein the cancer is follicular lymphoma.

146. The method of claim 140, wherein the cancer is Hodgkin lymphoma.

147. The method of claim 140, wherein the cancer is non-Hodgkin lymphoma.

148. The method of any of claims 136-147, wherein the method further comprises administering a chemotherapeutic agent.

149. The method of claim 148, wherein the chemotherapeutic agent is cyclophosphamide, fludarabine, or cyclophosphamide and fludarabine.

150. The method of any of claims 136-149, wherein the method comprises administering a lymphodepleting agent or immunosuppressant prior to administering to the subject an effective amount of the cell of any of claims 117-136.

151. A population of cells comprising the cell of any of claims 117-136, wherein at least about 30% of the cells, e.g., at least about 40%, 50%, 60%, 70,%, 80% or 90% of the cells, are a cell according to any of claims 117-136.

152. A gene editing system which binds a sequence of a TET2 intron or intron-exon junction.

153. The gene editing system of claim 152, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from any one of chr4:105146980-105190359; chr4:105190506-105233896; chr4:105237352-105241338; chr4:105241430-105242833; chr4:105242928-105243569; chr4:105243779-105259618;

chr4:105259770-105261758; chr4:105261849-105269609; chr4:105269748-105272563; and chr4:105272919-105275047, wherein said genomic region is according to human reference genome hg38.

154. The gene editing system of claim 153, wherein the genomic region is chr4:105269748-105272563.

155. The gene editing system of claim 152 or 153, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; chr4:105272465-105272485; chr4:105271387-105271407; chr4:105272436-105272456; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; chr4:105271845-105271865; chr4:105271849-105271869; and chr4:105271056-105271076.

156. The gene editing system of claim 152 or 153, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; chr4:105271387-105271407; chr4:105271924-105271944; chr4:105272323-105272343; chr4:105272057-105272077; chr4:105272309-105272329; chr4:105272324-105272344; chr4:105272324-105272344; chr4:105271184-105271204; chr4:105271190-105271210; chr4:105271295-105271315; chr4:105271292-105271312; chr4:105271458-105271478; chr4:105270635-105270655; chr4:105271173-105271192; chr4:105271232-105271252; and chr4:105271056-105271076.

157. The gene editing system of claim 152 or 153, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: chr4:105271863-105271883; chr4:105271340-105271360; chr4:105271204-105271223; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.

158. The gene editing system of claim 152 or 153, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: chr4:105271340-

105271360; chr4:105271526-105271546; chr4:105270350-105270370; chr4:105270268-105270288; chr4:105272182-105272202; and chr4:105272465-105272485.

159. The gene editing system of claim 152 or 153, wherein the sequence of a TET2 intron or intron-exon junction is a sequence within a genomic region selected from: chr4:105270624-105270643; chr4:105270630-105270649; and chr4:105271863-105271883.

160. The gene editing system of any of claims 152-159, wherein the gene editing system is a zinc finger nuclease (ZFN) gene editing system, a TALEN gene editing system, a CRISPR gene editing system, or a meganuclease gene editing system.

161. The gene editing system of any of claims 152-160, wherein the gene editing system further comprises a template nucleic acid.

162. The gene editing system of claim 161, wherein the template nucleic acid comprises nucleic acid sequence encoding a CAR.

163. The gene editing system of claim 162, wherein when said gene editing system (and/or nucleic acid sequence encoding one or more components of the gene editing system) is introduced into a cell, the nucleic acid sequence encoding the CAR is integrated into the genome of said cell at or near the sequence of a TET2 intron or intron-exon junction bound by said genome editing system.

164. A cell, modified by the gene editing system of any of claims 152-163.

165. A cell comprising the gene editing system of any of claims 152-163.

166. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163, for use as a medicament.

167. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163, for use in the manufacture of a medicament.

168. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163, for use in the treatment of a disease.

169. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163, for use in the treatment of a disease, wherein the disease is a disease associated with expression of a tumor antigen, e.g., a proliferative disease, a precancerous condition, a cancer, and a non-cancer related indication associated with expression of the tumor antigen.

170. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163, for use in the treatment of a cancer, wherein the cancer is a hematologic cancer selected from the group consisting of chronic lymphocytic leukemia (CLL), acute leukemias, acute lymphoid leukemia (ALL), pediatric acute lymphoid leukemia, B-cell acute lymphoid leukemia (B-ALL), T-cell acute lymphoid leukemia (T-ALL), chronic myelogenous leukemia (CML), acute myeloid leukemia (AML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, marginal zone lymphoma, multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin's lymphoma, Hodgkin's lymphoma, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, and pre-leukemia.

171. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is acute lymphoid leukemia (ALL).

172. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is pediatric ALL.

173. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is diffuse large B cell lymphoma.

174. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is chronic lymphocytic leukemia.

175. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is follicular lymphoma.

176. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is Hodgkin lymphoma.

177. The gRNA molecule, composition, nucleic acid, vector, cell (or population of cells) or gene editing system for use of claim 170, wherein the disease is non-Hodgkin lymphoma.

178. A gRNA molecule of any of claims 1-54, a composition of any of claims 55-93, a nucleic acid of claim 94, a vector of any of claims 95-96, a cell (or population of cells) of any of claims 117-136, 151 or 164-165, or a gene editing system of any of claims 152-163 for use in the treatment of a cancer, e.g., wherein the cancer is selected from the group consisting of mesothelioma, adenocarcinoma, glioblastoma, colon cancer, rectal cancer, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, cancer of the small intestine, cancer of the esophagus, melanoma, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, Hodgkin's Disease, non-Hodgkin's lymphoma, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers, combinations of said cancers, and metastatic lesions of said cancers.

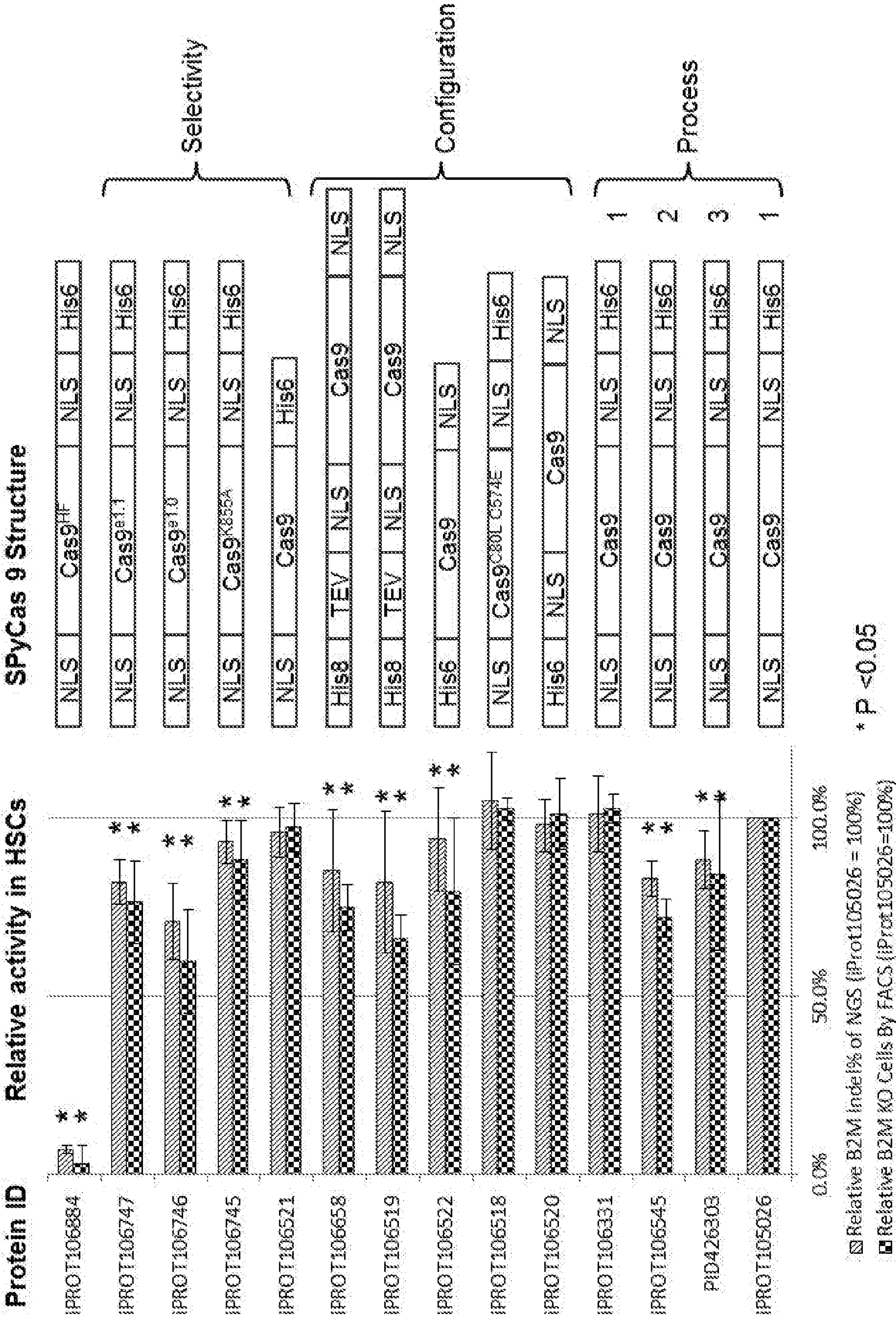


Fig. 1

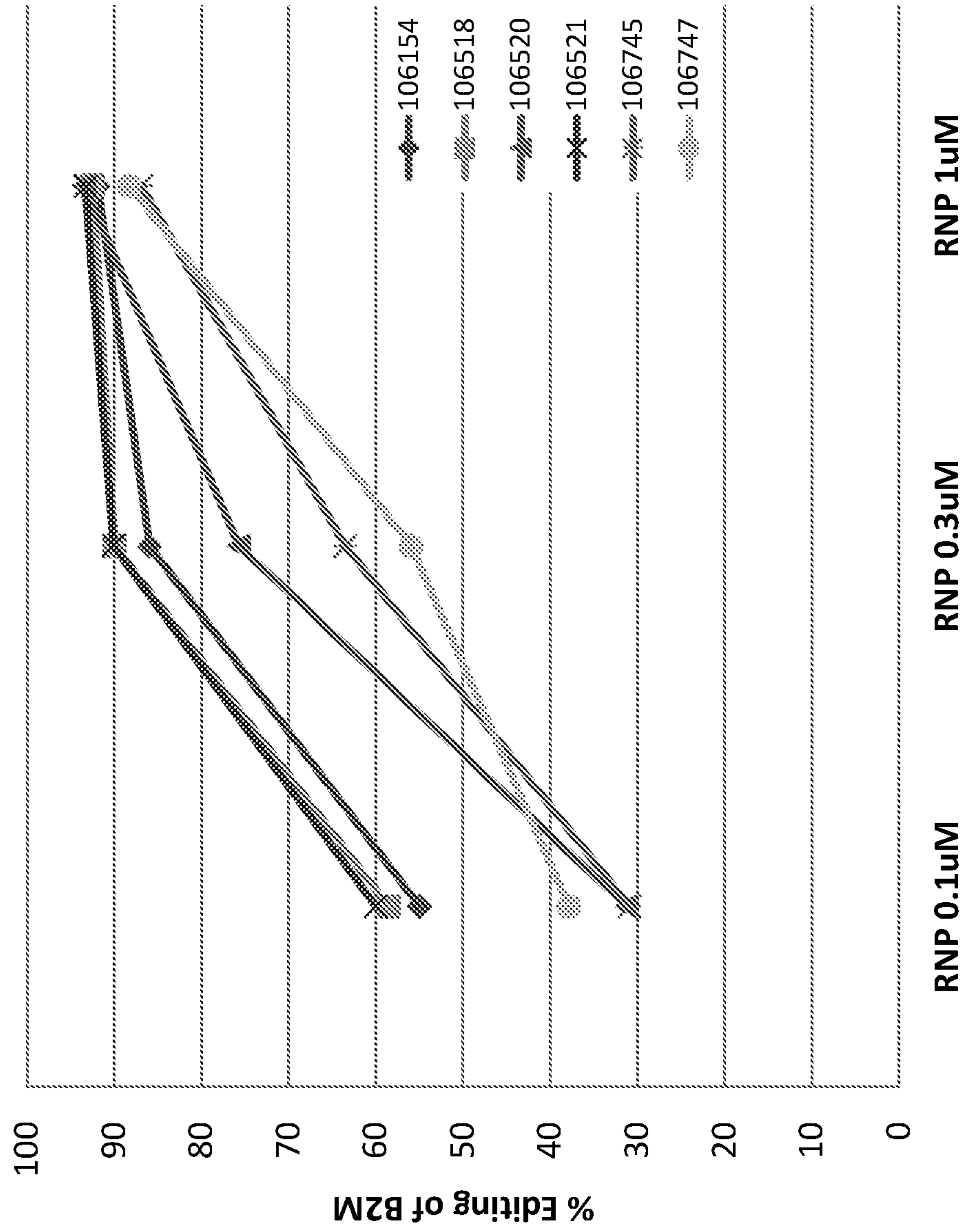


Fig. 2

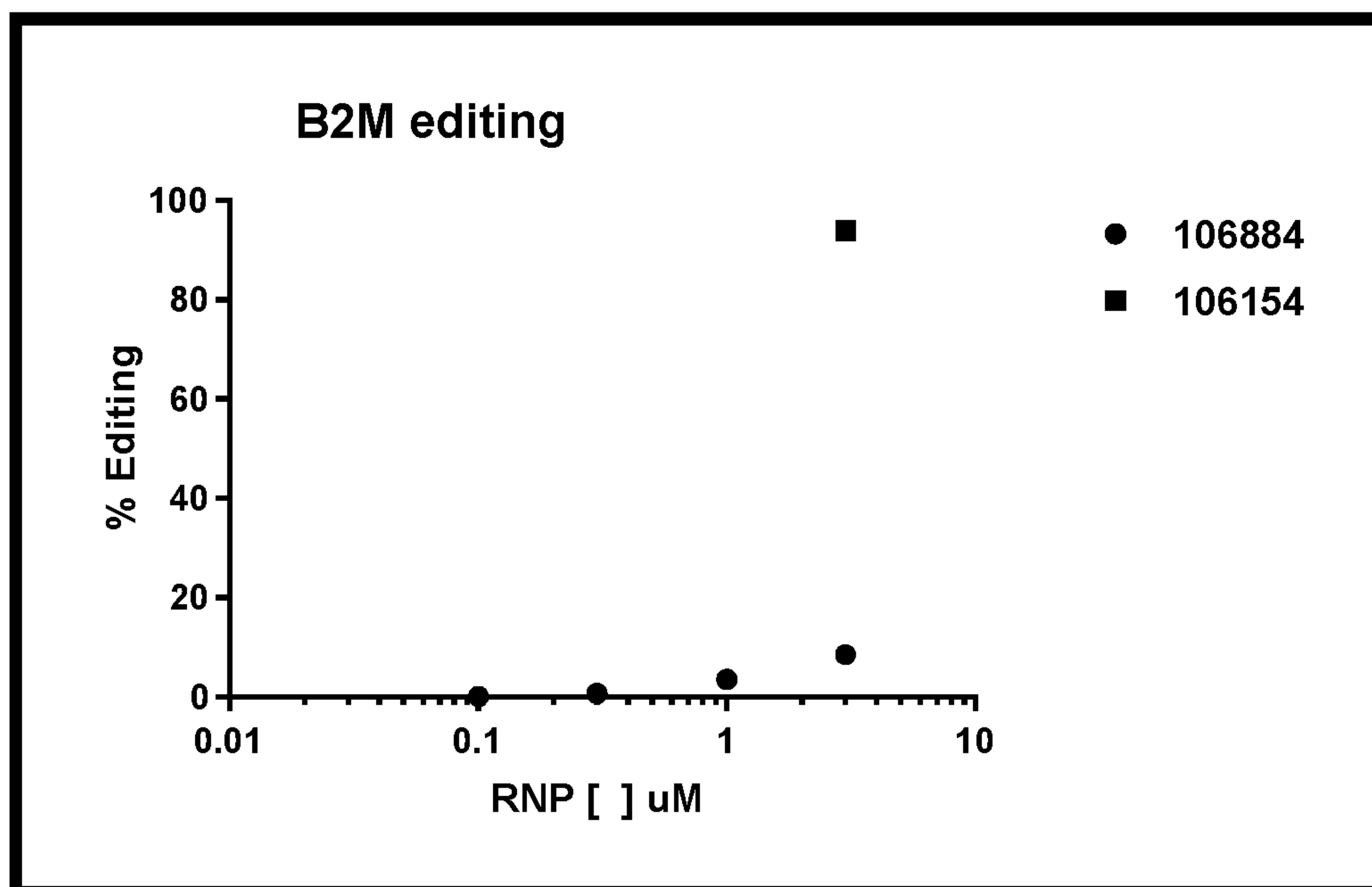
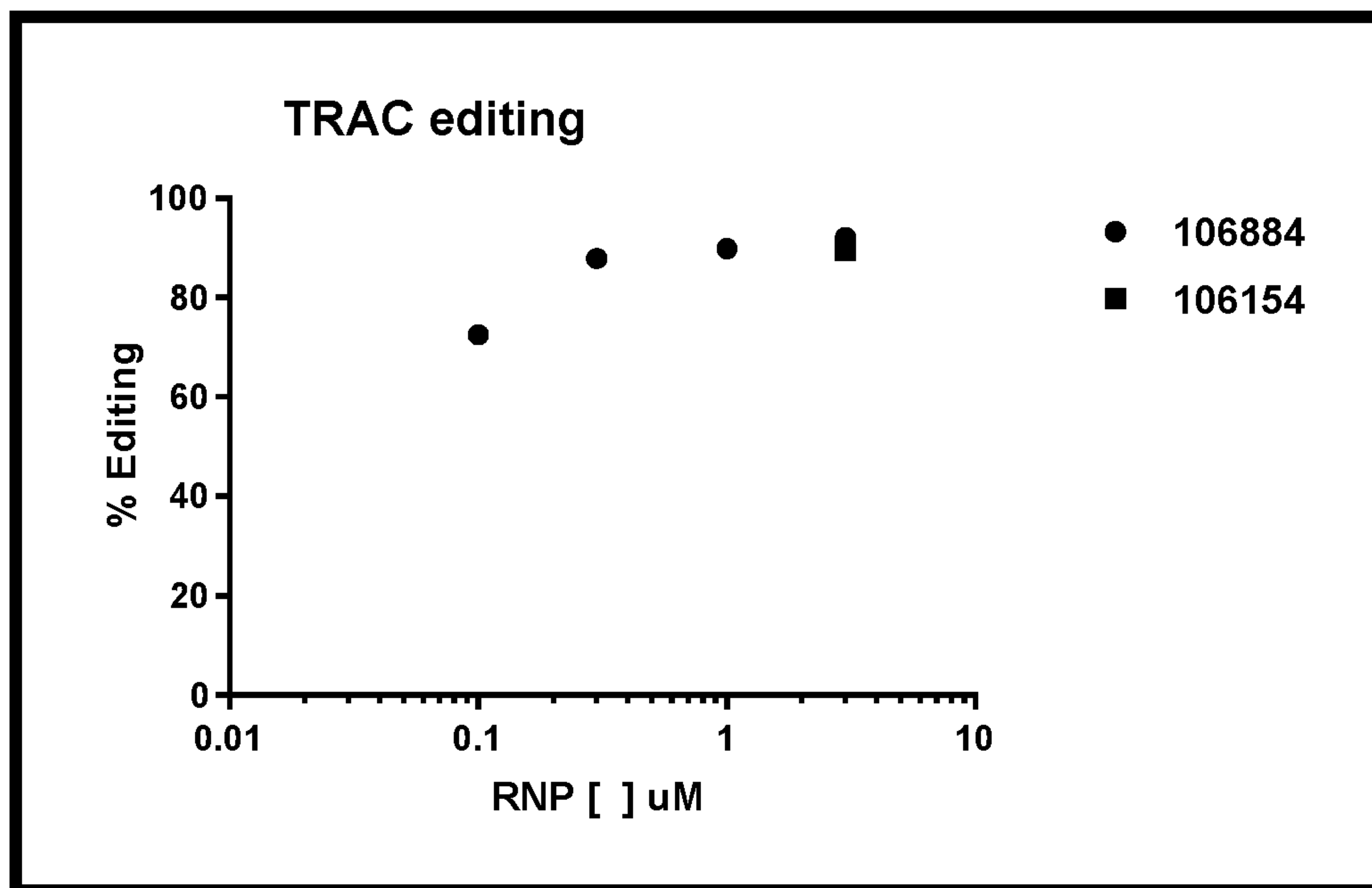


Fig. 3

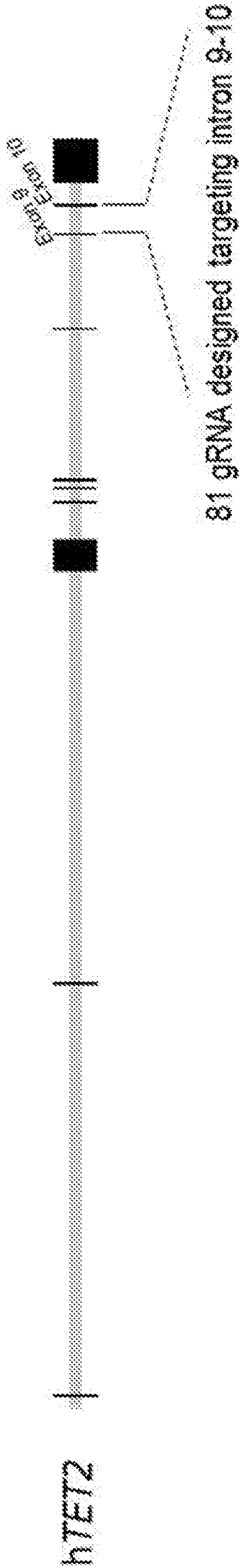


Fig. 4



FIG. 5

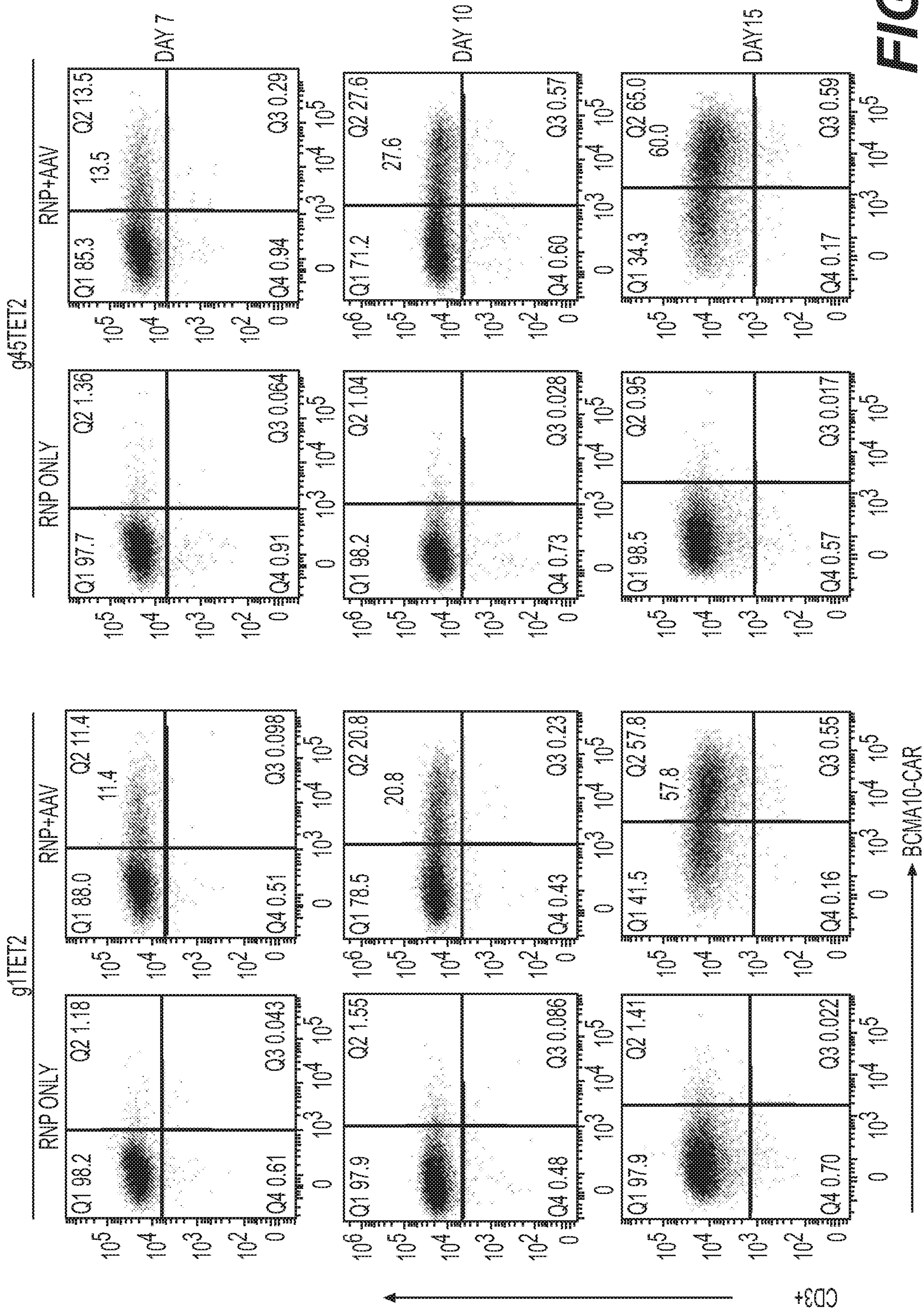


FIG. 6

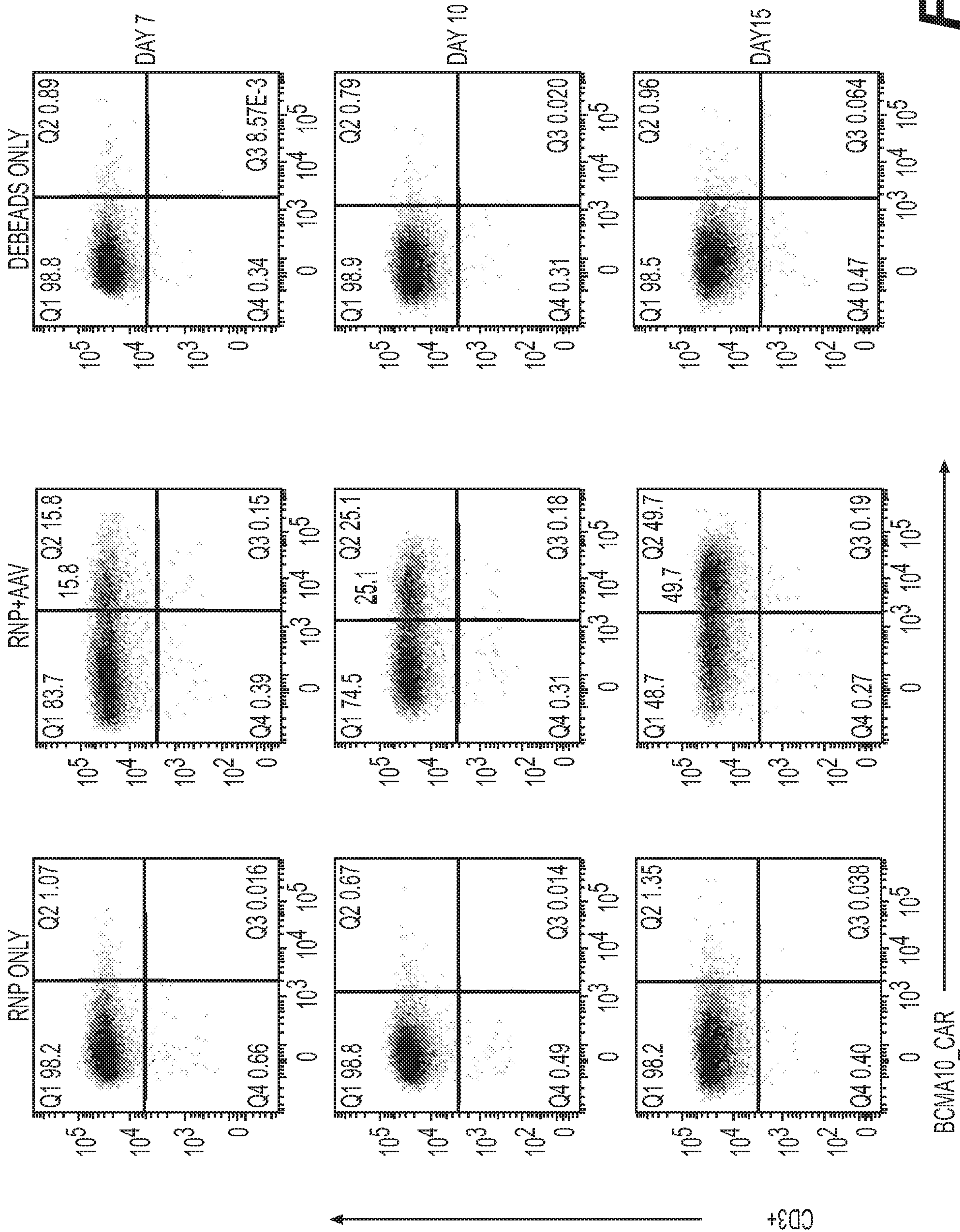


FIG. 7

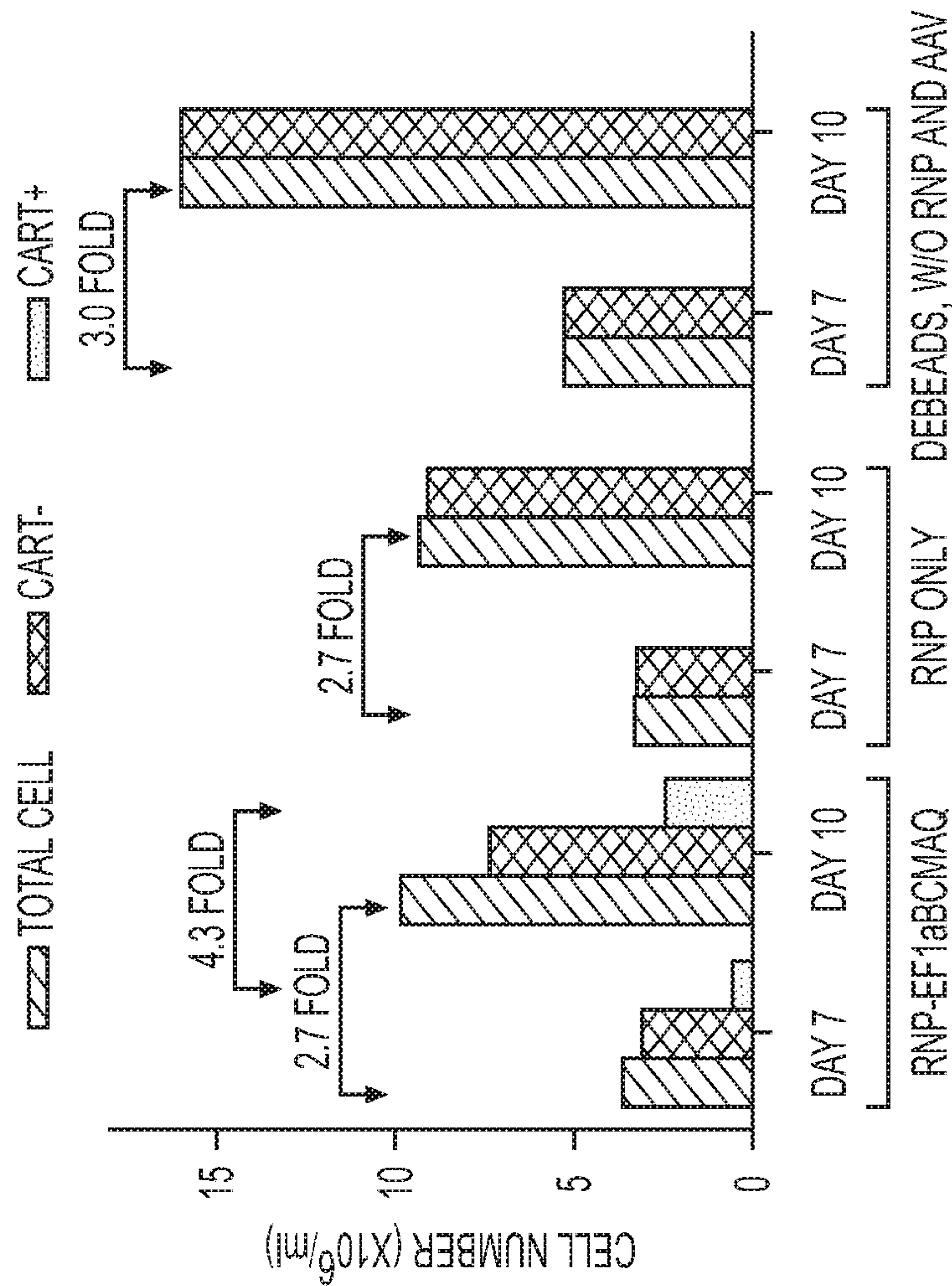


FIG. 8

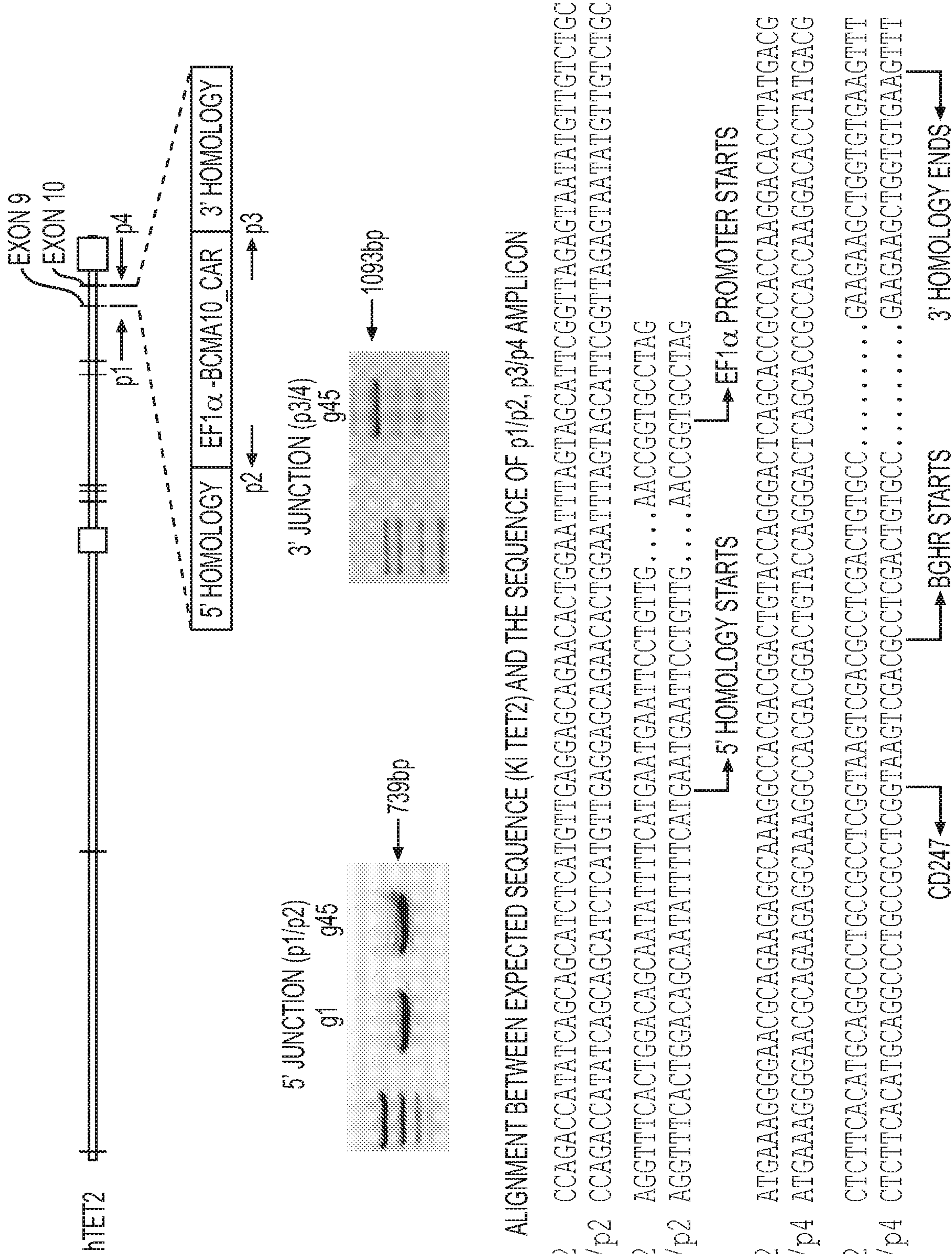


FIG. 9

Primer set 1

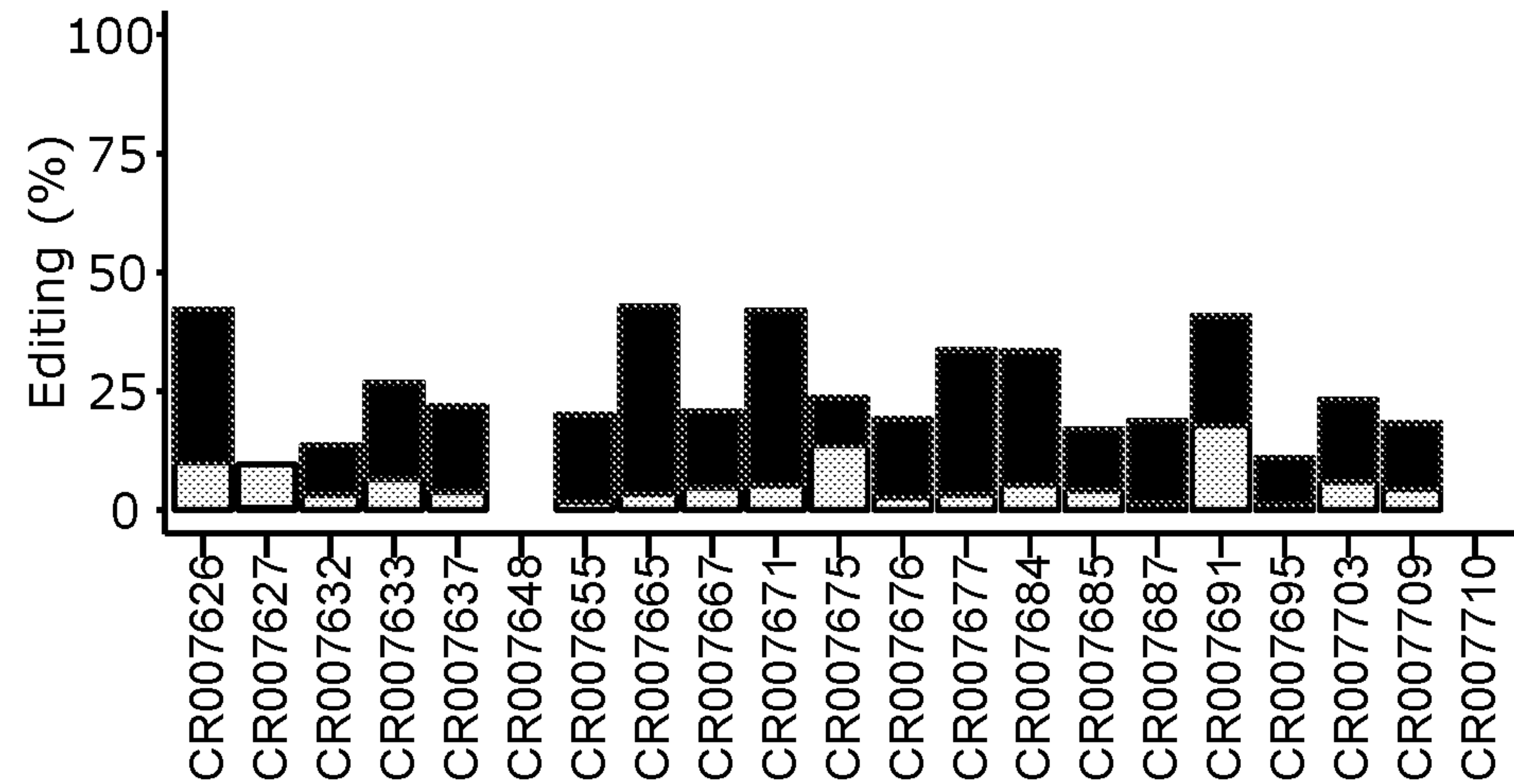


Fig. 10A

Primer set 2

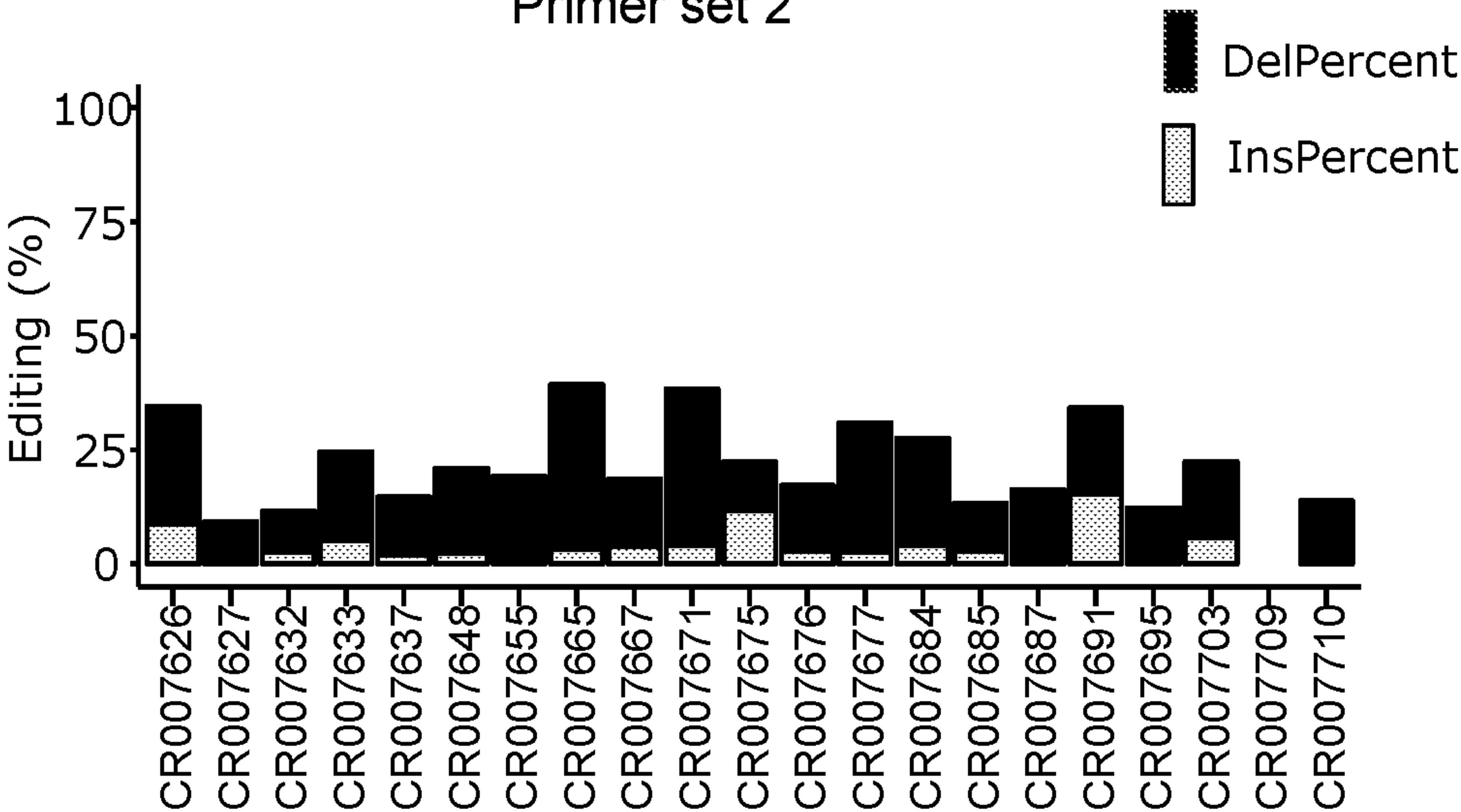


Fig. 10B

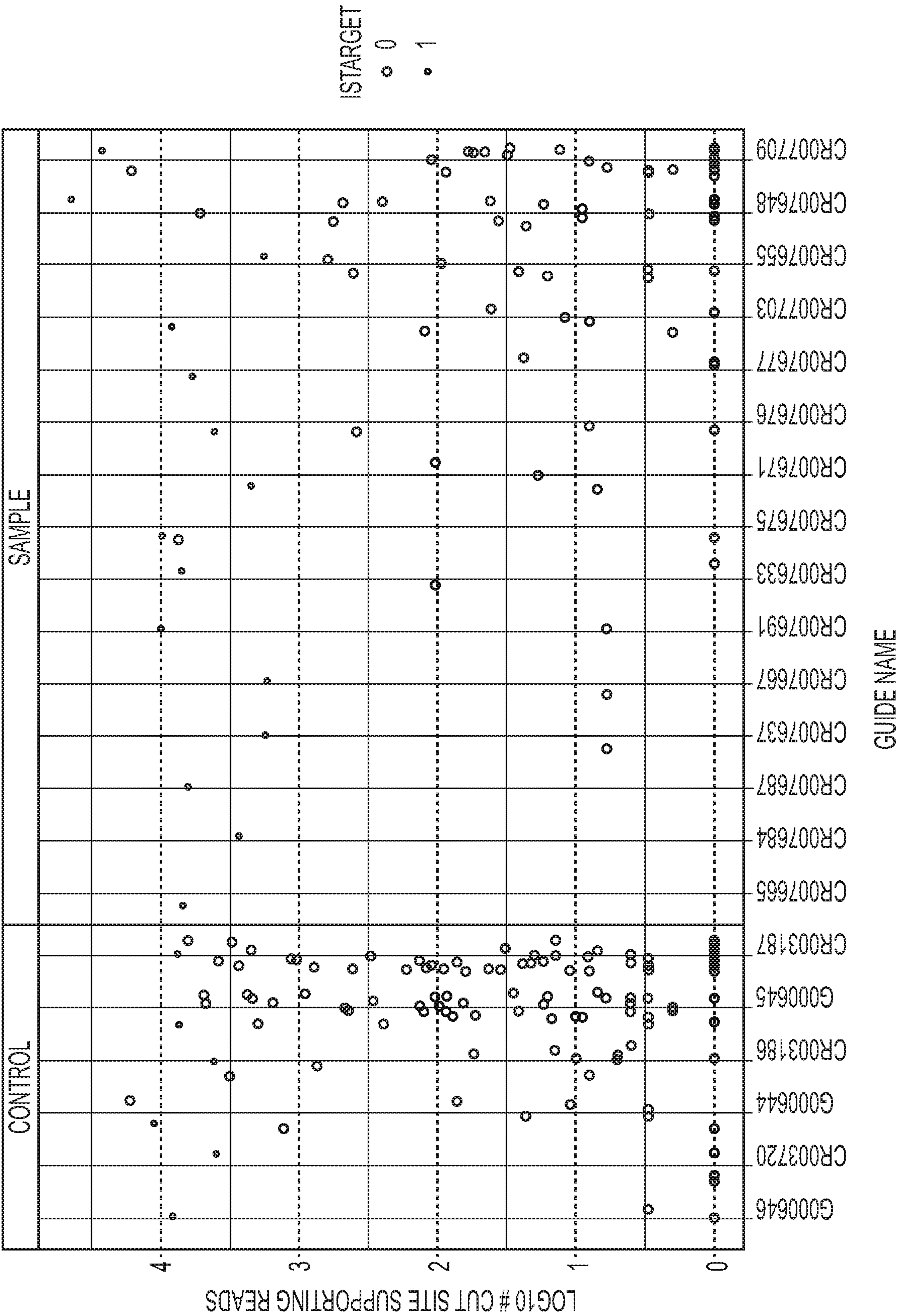


FIG. 11