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(57) Abstract: The present invention provides a non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.



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OMNI 263, 264, 266, 268, 269, 271, 274, 275, 276, 278, 279, 280, 281, 283, 284, 286, 287, 288, 290, 291, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 375, 376, 377, 378, 380, 381, 382, 383, 384, 385, AND 386 CRISPR

NUCLEASES

[0001] This application claims the benefit of U.S. Provisional Application No. 63/281,390, filed November 19, 2021, the contents of which are hereby incorporated by reference.

[0002] Throughout this application, various publications are referenced, including referenced in parenthesis. The disclosures of all publications mentioned in this application in their entireties are hereby incorporated by reference into this application in order to provide additional description of the art to which this invention pertains and of the features in the art which can be employed with this invention.

REFERENCE TO SEQUENCE LISTING

[0003] This application incorporates-by-reference nucleotide sequences which are present in the file named “221117_91815-A-PCT_Sequence_Listing_AWG.xml”, which is 4,464 kilobytes in size, and which was created on November 15, 2022 in the IBM-PC machine format, having an operating system compatibility with MS-Windows, which is contained in the XML file filed November 17, 2022 as part of this application.

FIELD OF THE INVENTION

[0004] The present invention is directed to, *inter alia*, composition and methods for genome editing.

BACKGROUND OF THE INVENTION

[0005] The Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) systems of bacterial and archaeal adaptive immunity show extreme diversity of protein composition and genomic loci architecture. The CRISPR systems have become important tools for research and genome engineering. Nevertheless, many details of CRISPR systems have not been determined

and the applicability of CRISPR nucleases may be limited by sequence specificity requirements, expression, or delivery challenges. Different CRISPR nucleases have diverse characteristics such as: size, PAM site, on target activity, specificity, cleavage pattern (e.g. blunt, staggered ends), and prominent pattern of indel formation following cleavage. Different sets of characteristics may be useful for different applications. For example, some CRISPR nucleases may be able to target particular genomic loci that other CRISPR nucleases cannot due to limitations of the PAM site. In addition, some CRISPR nucleases currently in use exhibit pre-immunity, which may limit *in vivo* applicability. See Charlesworth et al., Nature Medicine (2019) and Wagner et al., Nature Medicine (2019). Accordingly, discovery, engineering, and improvement of novel CRISPR nucleases is of importance.

SUMMARY OF THE INVENTION

[0006] Disclosed herein are compositions and methods that may be utilized for genomic engineering, epigenomic engineering, genome targeting, genome editing of cells, and/or in vitro diagnostics.

[0007] The disclosed compositions may be utilized for modifying genomic DNA sequences. As used herein, genomic DNA refers to linear and/or chromosomal DNA and/or plasmid or other extrachromosomal DNA sequences present in the cell or cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments, the cell of interest is a prokaryotic cell. In some embodiments, the methods produce double-stranded breaks (DSBs) at pre-determined target sites in a genomic DNA sequence, resulting in mutation, insertion, and/or deletion of a DNA sequence at the target site(s) in a genome.

[0008] Accordingly, in some embodiments, the compositions comprise a Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) nucleases. In some embodiments, the CRISPR nuclease is a CRISPR-associated protein.

OMNI CRISPR Nucleases

[0009] Embodiments of the present invention provide for CRISPR nucleases designated as an “OMNI” nuclease as provided in Table 1.

[0010] This invention provides a method of modifying a nucleotide sequence at a target site in the genome of a mammalian cell comprising introducing into the cell (i) a composition comprising a CRISPR nuclease having at least 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding a CRISPR nuclease which sequence has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 109-324 and (ii) a DNA-targeting RNA molecule, or a DNA polynucleotide encoding a DNA-targeting RNA molecule, comprising a nucleotide sequence that is complementary to a sequence in the target DNA.

[0011] This invention also provides a non-naturally occurring composition comprising a CRISPR associated system comprising:

- a) one or more RNA molecules comprising a guide sequence portion linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence, or one or more nucleotide sequences encoding the one or more RNA molecules; and
- b) an CRISPR nuclease comprising an amino acid sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and

wherein the one or more RNA molecules hybridize to the target sequence, wherein the target sequence is adjacent to the 3' end of a complimentary sequence of a Protospacer Adjacent Motif (PAM), and the one or more RNA molecules form a complex with the RNA-guided nuclease.

[0012] This invention also provides a non-naturally occurring composition comprising:

- a) a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and
- b) one or more RNA molecules, or one or more DNA polynucleotide encoding the one or more RNA molecules, comprising at least one of:
 - i) a nuclease-binding RNA nucleotide sequence capable of interacting with/binding to the CRISPR nuclease; and

- ii) a DNA-targeting RNA nucleotide sequence comprising a sequence complementary to a sequence in a target DNA sequence,

wherein the CRISPR nuclease is capable of complexing with the one or more RNA molecules to form a complex capable of hybridizing with the target DNA sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] **Figs. 1A-C: The predicted secondary structure of a single guide RNA (sgRNA) (crRNA-tracrRNA) from sgRNA-279, sgRNA-281 and sgRNA-280.** **Fig. 1A:** A representation of a crRNA–tracrRNA duplex for OMNI-279, the crRNA and tracrRNA portions of the sgRNA are noted. **Fig. 1B:** Examples of V1 and V2 of sgRNA design for OMNI-281. **Fig. 1C:** Examples of V1 of sgRNA design for OMNI-280 (sgRNA listed in Table 2)

[0014] **Figs. 2-109: *In vitro* TXTL PAM depletion results for OMNI nucleases.** The PAM logo is a schematic representation of the ratio of the depleted site (top panel). Depletion ratio (bottom panel, left) of specific PAM sequences (bottom panel, right) from the PAM plasmid library were calculated following NGS of the TXTL reaction. The calculation for each OMNI is based on a 4N window along the 8bp sequence of the PAM library. The required PAM of the tested OMNI and the level of nuclease activity under the reaction conditions is inferred from the depletion ratio. *In vitro* PAM depletion results for: Fig 2: OMNI-263. Fig 3: OMNI-264. Fig 4: OMNI-266. Fig 5: OMNI-268. Fig 6: OMNI-269. Fig 7: OMNI-271. Fig 8: OMNI-274. Fig 9: OMNI-275. Fig 10: OMNI-276. Fig 11: OMNI-278. Fig 12: OMNI-279. Fig 13: OMNI-280. Fig 14: OMNI-281. Fig 15: OMNI-283. Fig 16: OMNI-284. Fig 17: OMNI-286. Fig 18: OMNI-287. Fig 19: OMNI-288. Fig 20: OMNI-290. Fig 21: OMNI-291. Fig 22: OMNI-293. Fig 23: OMNI-294. Fig 24: OMNI-295. Fig 25: OMNI-296. Fig 26: OMNI-297. Fig 27: OMNI-298. Fig 28: OMNI-299. Fig 29: OMNI-300. Fig 30: OMNI-301. Fig 31: OMNI-302. Fig 32: OMNI-303. Fig 33: OMNI-304. Fig 34: OMNI-305. Fig 35: OMNI-307. Fig 36: OMNI-308. Fig 37: OMNI-309. Fig 38: OMNI-310. Fig 39: OMNI-311. Fig 40: OMNI-312. Fig 41: OMNI-313. Fig 42: OMNI-314. Fig 43: OMNI-315. Fig 44: OMNI-316. Fig 45: OMNI-317. Fig 46: OMNI-318. Fig 47: OMNI-319. Fig 48: OMNI-320. Fig 49: OMNI-321. Fig 50: OMNI-322. Fig 51: OMNI-323. Fig 52: OMNI-324. Fig 53: OMNI-325. Fig 54: OMNI-326. Fig 55: OMNI-327. Fig 56: OMNI-329. Fig 57: OMNI-330. Fig 58: OMNI-331. Fig 59: OMNI-332. Fig 60: OMNI-333. Fig 61: OMNI-334. Fig 62:

OMNI-336. Fig 63: OMNI-337. Fig 64: OMNI-338. Fig 65: OMNI-339. Fig 66: OMNI-340. Fig 67: OMNI-341. Fig 68: OMNI-342. Fig 69: OMNI-343. Fig 70: OMNI-344. Fig 71: OMNI-345. Fig 72: OMNI-346. Fig 73: OMNI-347. Fig 74: OMNI-348. Fig 75: OMNI-349. Fig 76: OMNI-350. Fig 77: OMNI-351. Fig 78: OMNI-352. Fig 79: OMNI-353. Fig 80: OMNI-354. Fig 81: OMNI-356. Fig 82: OMNI-357. Fig 83: OMNI-358. Fig 84: OMNI-359. Fig 85: OMNI-360. Fig 86: OMNI-361. Fig 87: OMNI-362. Fig 88: OMNI-363. Fig 89: OMNI-364. Fig 90: OMNI-365. Fig 91: OMNI-366. Fig 92: OMNI-367. Fig 93: OMNI-368. Fig 94: OMNI-369. Fig 95: OMNI-370. Fig 96: OMNI-371. Fig 97: OMNI-372. Fig 98: OMNI-373. Fig 99: OMNI-375. Fig 100: OMNI-376. Fig 101: OMNI-377. Fig 102: OMNI-378. Fig 103: OMNI-380. Fig 104: OMNI-381. Fig 105: OMNI-382. Fig 106: OMNI-383. Fig 107: OMNI-384. Fig 108: OMNI-385. Fig 109: OMNI-386.

DETAILED DESCRIPTION

[0015] According to some aspects of the invention, the disclosed compositions comprise a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) nuclease and/or a nucleic acid molecule comprising a sequence encoding the same.

[0016] Table 1 lists novel CRISPR nucleases, as well as substitutions at one or more positions within each nuclease which convert the nuclease to a nickase or catalytically dead nuclease.

[0017] Table 2 provides crRNA, tracrRNA, and single-guide RNA (sgRNA) sequences, and portions of crRNA, tracrRNA, and sgRNA sequences, that are compatible with each listed CRISPR nuclease. Accordingly, a crRNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 as part of a crRNA:tracrRNA complex may comprise any crRNA sequence listed in Table 2. Similarly, a tracrRNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 as part of a crRNA:tracrRNA complex may comprise any tracrRNA sequence listed in Table 2. Also, a single-guide RNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 may comprise any sequence listed in Table 2.

[0018] For example, a crRNA molecule of OMNI-263 nuclease (SEQ ID NO: 1) may comprise a sequence of any one of SEQ ID NOs: 326-329; a tracrRNA molecule of OMNI-263 nuclease may comprise a sequence of any one of SEQ ID NOs: 330-338; and a sgRNA molecule of OMNI-263 nuclease may comprise a sequence of any one of SEQ ID NOs: 325-338. Other crRNA

molecules, tracrRNA molecules, or sgRNA molecules for each OMNI nuclease may be derived from the sequences listed in Table 2 in the same manner.

[0019] Any one of these nucleases can target a desired DNA target sequence via a guide RNA molecule. The nuclease-guide complex will also carry any molecule attached to the complex to the target site. Thus, this disclosure also contemplates fusion proteins comprising CRISPR nucleases and a DNA modifying domain (e.g., a deaminase, a nuclease, a nickase, a recombinase, a methyltransferase, a methylase, an acetylase, an acetyltransferase, a transcriptional activator, or a transcriptional repressor domain), as well as the use of such fusion proteins in correcting mutations in a genome (e.g., the genome of a human subject) that are associated with disease, or generating mutations in a genome (e.g., the human genome) to decrease or prevent expression of a gene.

[0020] In some embodiments, any of the CRISPR nucleases provided herein may be fused to a protein that has an enzymatic activity. In some embodiments, the enzymatic activity modifies a target DNA. In some embodiments, the enzymatic activity is nuclease activity, methyltransferase activity, demethylase activity, DNA repair activity, DNA damage activity, deamination activity, dismutase activity, alkylation activity, depurination activity, oxidation activity, pyrimidine dimer forming activity, integrase activity, transposase activity, recombinase activity, polymerase activity, ligase activity, helicase activity, photolyase activity or glycosylase activity. In some cases, the enzymatic activity is nuclease activity. In some cases, the nuclease activity introduces a double strand break in the target DNA. In some cases, the enzymatic activity modifies a target polypeptide associated with the target DNA. In some cases, the enzymatic activity is methyltransferase activity, demethylase activity, acetyltransferase activity, deacetylase activity, kinase activity, phosphatase activity, ubiquitin ligase activity, deubiquitinating activity, adenylation activity, deadenylation activity, SUMOylating activity, deSUMOylating activity, ribosylation activity, deribosylation activity, myristoylation activity or demyristoylation activity. In some cases, the target polypeptide is a histone and the enzymatic activity is methyltransferase activity, demethylase activity, acetyltransferase activity, deacetylase activity, kinase activity, phosphatase activity, ubiquitin ligase activity or deubiquitinating activity.

[0021] Thus, any one of the CRISPR nucleases, nickases, or dead-nucleases may be fused (e.g. directly fused or fused via a linker) to another DNA modulating or DNA modifying enzyme, including, but not limited to, base editors such as a deaminase, a reverse transcriptase (e.g. for use

in prime editing, see Anzaolone et al. (2019)), an enzyme that modifies the methylation state of DNA (e.g. a methyltransferase), or a modifier of histones (e.g. a histone acetyl transferase). Indeed, the OMNI-50 nucleases, nickases, inactive nucleases described herein may be fused to a DNA modifying enzyme or an effector domain thereof. Examples of DNA modifiers include but are not limited to: a deaminase, a nuclease, a nickase, a recombinase, a methyltransferase, a methylase, an acetylase, an acetyltransferase, a reverse transcriptase, an helicase, an integrase, a ligase, a transposase, a demethylase, a phosphatase, a transcriptional activator, or a transcriptional repressor. In some embodiments, any of the CRISPR nucleases provided herein are fused to a protein that has an enzymatic activity. In some embodiments, the enzymatic activity modifies a target DNA molecule. In some embodiments, the CRISPR nucleases described herein or fusion proteins thereof, may be used to correct or generate one or more mutations in a gene associated with disease, or to increase, correct, decrease or prevent expression of a gene.

[0022] The invention provides a non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 90% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 1-12, and 14-108, or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.

[0023] In some embodiments, the composition further comprises one or more RNA molecules, or a DNA polynucleotide encoding any one of the one or more RNA molecules, wherein the one or more RNA molecules and the CRISPR nuclease do not naturally occur together and the one or more RNA molecules are configured to form a complex with the CRISPR nuclease and/or target the complex to a target site.

[0024] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 325-338.

[0025] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 326-329.

[0026] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 330-338.

[0027] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 325-338.

[0028] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 339-352.

[0029] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 340-343.

[0030] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 344-352.

[0031] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 339-352.

[0032] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 353-368.

[0033] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 354-357.

[0034] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 358-368.

[0035] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 353-368.

[0036] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 369-380.

[0037] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 370-373 and 114.

[0038] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 374-380.

[0039] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 369-380.

[0040] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 381-395.

[0041] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 382-385.

[0042] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 386-395.

[0043] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 381-395.

[0044] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 396-409.

[0045] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 397-400.

[0046] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 401-409.

[0047] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 396-409.

[0048] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 410-433.

[0049] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 411-414.

[0050] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 415-433.

[0051] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 410-433.

[0052] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 434-447.

[0053] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 435-437.

[0054] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 438-447.

[0055] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 434-447.

[0056] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 448-461.

[0057] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 449-452.

[0058] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 453-461.

[0059] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 448-461.

[0060] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 462-475.

[0061] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 463-466.

[0062] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 467-475.

[0063] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 462-475.

[0064] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 476-491.

[0065] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 477-480.

[0066] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 481-491.

[0067] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 476-491.

[0068] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 492-512.

[0069] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 493-496 and 509-512.

[0070] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 497-507.

[0071] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 492-512.

[0072] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 513-535.

[0073] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 514-517 and 528-531.

[0074] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 518-526 and 532-535.

[0075] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 513-535.

[0076] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 536-549.

[0077] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 537-540.

[0078] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 541-549.

[0079] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 536-549.

[0080] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 550-575.

[0081] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 551-553.

[0082] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 554-563, 565-569, and 571-575.

[0083] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 550-575.

[0084] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 576-598.

[0085] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 577-580.

[0086] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 581-589 and 591-598.

[0087] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 576-598.

[0088] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 599-612.

[0089] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 600-603 and 201.

[0090] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 604-612.

[0091] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 599-612.

[0092] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 613-633.

[0093] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 614-617 and 630.

[0094] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 618-628 and 631-633.

[0095] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 613-633.

[0096] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 634-651.

[0097] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 635-638.

[0098] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 639-647 and 649-651.

[0099] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 634-651.

[00100] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 652-665.

[00101] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 653-656.

[00102] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 657-665.

[00103] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 652-665.

[00104] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 666-683 and UUGCUACAA.

[00105] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 667-670 and 680.

[00106] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 671-678, 681-683, and UUGCUACAA.

[00107] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 666-683 and UUGCUACAA.

[00108] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 684-707.

[00109] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 685-688.

[00110] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 689-697, 699-703, and 705-707.

[00111] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 684-707.

[00112] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 708-728.

[00113] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 709-712 and 721-724.

[00114] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 713-719 and 725-728.

[00115] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 708-728.

[00116] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 729-742.

[00117] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 730-733.

[00118] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 734-742.

[00119] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 729-742.

[00120] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 743-761.

[00121] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 744-747.

[00122] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 748-756 and 758-761.

[00123] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 743-761.

[00124] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 762-775.

[00125] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 763-766.

[00126] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 767-775.

[00127] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 762-775.

[00128] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 776-798.

[00129] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 777-780.

[00130] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 781-789, 791-794, and 796-798.

[00131] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 776-798.

[00132] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 799-816.

[00133] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 800-803.

[00134] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 804-812 and 814-816.

[00135] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 799-816.

[00136] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 817-830.

[00137] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 818-821.

[00138] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 822-830.

[00139] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 817-830.

[00140] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 831-844.

[00141] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 832-835.

[00142] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 836-844.

[00143] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 831-844.

[00144] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 845-862.

[00145] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 846-849.

[00146] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 850-858 and 860-862.

[00147] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 845-862.

[00148] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 863-883.

[00149] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 864-867 and 880-883.

[00150] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 868-878.

[00151] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 863-883.

[00152] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 884-901 and UUACUACAA.

[00153] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 885-888 and 898.

[00154] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 889-896, 899-901, and UUACUACAA.

[00155] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 884-901 and UUACUACAA.

[00156] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 902-915.

[00157] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 903-906.

[00158] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 907-915.

[00159] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 902-915.

[00160] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 916-931.

[00161] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 917-920 and 931.

[00162] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 921-929.

[00163] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 916-931.

[00164] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 932-947.

[00165] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 933-936.

[00166] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 937-947.

[00167] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 932-947.

[00168] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 948-962.

[00169] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 949-952.

[00170] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 953-962.

[00171] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 948-962.

[00172] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 963-985.

[00173] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 964-967 and 978-981.

[00174] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 968-976 and 982-985.

[00175] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 963-985.

[00176] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 986-1010.

[00177] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 987-990 and 1001-1004.

[00178] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 991-999 and 1005-1010.

[00179] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 986-1010.

[00180] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1011-1029.

[00181] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1012-1015 and 1026-1029.

[00182] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1016-1024.

[00183] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1011-1029.

[00184] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1030-1050, UUACUAAAA, and UUACUAGAA.

[00185] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1031-1034 and 1044-1047.

[00186] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1035-1042, 1048-1050, UUACUAAAA, and UUACUAGAA.

[00187] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1030-1050, UUACUAAAA, and UUACUAGAA.

[00188] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1051-1080.

[00189] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1052-1055 and 1068-1071.

[00190] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1056-1066, 1072-1074, and 1076-1079.

[00191] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1051-1080.

[00192] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1081-1101, UUACUAAAA, and UUACUAGAA.

[00193] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1082-1085 and 1095-1098.

[00194] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1086-1093, 1099-1101, UUACUAAAA, and UUACUAGAA.

[00195] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1081-1101, UUACUAAAA, and UUACUAGAA.

[00196] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1102-1115.

[00197] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1103-1106.

[00198] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1107-1115.

[00199] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1102-1115.

[00200] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1116-1135.

[00201] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1117-1120.

[00202] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1121-1130 and 1132-1135.

[00203] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1116-1135.

[00204] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1136-1167.

[00205] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1137-1140 and 1151-1154.

[00206] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1141-1149, 1155-1158, 1160-1163, and 1167-1167.

[00207] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1136-1167.

[00208] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1168-1186.

[00209] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1169-1172.

[00210] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1173-1181 and 1183-1186.

[00211] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1168-1186.

[00212] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1187-1211.

[00213] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1188-1191 and 1204-1207.

[00214] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1192-1202 and 1208-1211.

[00215] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1187-1211.

[00216] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1212-1243.

[00217] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1213-1216 and 1227-1230.

[00218] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1217-1225, 1231-1234, 1236-1239, and 1241-1243.

[00219] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1212-1243.

[00220] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1244-1255.

[00221] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1245-1247.

[00222] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1248-1255.

[00223] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1244-1255.

[00224] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1256-1284.

[00225] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1257-1260 and 1271-1274.

[00226] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1261-1269, 1276-1279, and 1281-1284.

[00227] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1256-1284.

[00228] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1285-1298.

[00229] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1286-1289.

[00230] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1290-1298.

[00231] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1285-1298.

[00232] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1299-1312.

[00233] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1300-1303.

[00234] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1304-1312.

[00235] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1299-1312.

[00236] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1313-1342.

[00237] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177 and 178.

[00238] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1314-1315 and 1334-1335.

[00239] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1316-1326, 1328-1332, and 1336-1342.

[00240] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1343-1362.

[00241] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1344-1347.

[00242] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1348-1356 and 1358-1362.

[00243] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1343-1362.

[00244] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1363-1378.

[00245] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1364-1367.

[00246] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1368-1378.

[00247] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1363-1378.

[00248] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1379-1397.

[00249] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1380-1383.

[00250] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1384-1394 and 1396-1397.

[00251] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1379-1397.

[00252] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1398-1413.

[00253] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1399-1402.

[00254] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1403-1413.

[00255] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1398-1413.

[00256] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1437.

[00257] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1415-1418 and 1431-1434.

[00258] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1419-1429 and 1436-1437.

[00259] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1414-1437.

[00260] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1438-1462.

[00261] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1439-1442 and 1455-1458.

[00262] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1443-1453 and 1459-1462.

[00263] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1438-1462.

[00264] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1463-1495.

[00265] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1464-1467 and 1478-1481.

[00266] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1468-1476, 1482-1490, and 1492-1495.

[00267] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1463-1495.

[00268] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1496-1533.

[00269] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1497-1500 and 1515-1518.

[00270] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1501-1513, 1519-1527, and 1529-1532.

[00271] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1496-1533.

[00272] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1534-1556.

[00273] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1535-1538.

[00274] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1539-1549, 1551-1553, and 1555-1556.

[00275] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1534-1556.

[00276] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1557-1572.

[00277] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1558-1561.

[00278] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1562-1572.

[00279] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1557-1572.

[00280] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1573-1617.

[00281] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1574-1577 and 1592-1595.

[00282] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1578-1590, 1596-1605, 1607-1612, and 1614-1617.

[00283] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1573-1617.

[00284] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1618-1634.

[00285] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1619-1622.

[00286] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1623-1631 and 1633-1634.

[00287] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1618-1634.

[00288] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1635-1655.

[00289] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1636-1639.

[00290] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1640-1652 and 1654-1655.

[00291] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1635-1655.

[00292] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1656-1674.

[00293] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1657-1660.

[00294] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1661-1671 and 1673-1674.

[00295] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1656-1674.

[00296] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1675-1701.

[00297] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1676-1679.

[00298] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1680-1692, 1694-1697, and 1699-1701.

[00299] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1675-1701.

[00300] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1702-1729.

[00301] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1703-1706.

[00302] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1707-1719, 1721-1722, 1724-1727, and 1729.

[00303] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1702-1729.

[00304] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1730-1747.

[00305] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1731-1734.

[00306] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1735-1747.

[00307] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1730-1747.

[00308] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1748-1774.

[00309] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1749-1752.

[00310] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1753-1763, 1765-1770, and 1772-1774.

[00311] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1748-1774.

[00312] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1775-1801.

[00313] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1776-1779 and 1792-1795.

[00314] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1780-1790 and 1796-1801.

[00315] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1775-1801.

[00316] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1802-1828.

[00317] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1803-1806.

[00318] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1807-1817, 1819-1820, 1822-1825, and 1827-1828.

[00319] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1802-1828.

[00320] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1829-1844.

[00321] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1830-1833.

[00322] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1834-1844.

[00323] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1829-1844.

[00324] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1845-1870.

[00325] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1846-1849.

[00326] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1850-1860, 1862-1863, 1865-1868, and 1870.

[00327] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1845-1870.

[00328] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1871-1895.

[00329] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1872-1875 and 1888-1891.

[00330] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1876-1886 and 1892-1895.

[00331] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1871-1895.

[00332] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1896-1911.

[00333] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1897-1900.

[00334] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1901-1911.

[00335] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1896-1911.

[00336] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1912-1930.

[00337] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1913-1916.

[00338] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1917-1927 and 1929-1930.

[00339] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1912-1930.

[00340] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1931-1942.

[00341] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1932-1934.

[00342] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1935-1942.

[00343] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1931-1942.

[00344] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1943-1971.

[00345] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1944-1947 and 1960-1963.

[00346] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1948-1958 and 1964-1971.

[00347] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1943-1971.

[00348] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1972-1999.

[00349] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1973-1976.

[00350] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1977-1989, 1991-1995, and 1997-1998.

[00351] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1972-1999.

[00352] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2000-2024.

[00353] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2001-2004.

[00354] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2005-2017, 2019-2020, and 2022-2023.

[00355] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2000-2024.

[00356] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2025-2045.

[00357] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2026-2029.

[00358] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2030-2042 and 2044-2045.

[00359] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2025-2045.

[00360] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2046-2063.

[00361] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2047-2050.

[00362] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2051-2063.

[00363] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2046-2063.

[00364] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2064-2088.

[00365] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2065-2068.

[00366] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2069-2081, 2083-2084, and 2086-2087.

[00367] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2064-2088.

[00368] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2089-2109.

[00369] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2090-2093.

[00370] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2094-2106 and 2108-2109.

[00371] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2089-2109.

[00372] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2110-2131.

[00373] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2111-2114.

[00374] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2115-2127, 2129, and 2131.

[00375] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2110-2131.

[00376] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2132-2156.

[00377] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2133-2136.

[00378] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2137-2149, 2151-2152, and 2154-2155.

[00379] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2132-2156.

[00380] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2157-2178.

[00381] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2158-2161.

[00382] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2162-2174 and 2176-2178.

[00383] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2157-2178.

[00384] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2179-2203.

[00385] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2180-2183.

[00386] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2184-2192, 2194-2196, and 2198-2203.

[00387] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2179-2203.

[00388] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2204-2230.

[00389] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2205-2208.

[00390] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2209-2221, 2223-2226, and 2228-2230.

[00391] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2204-2230.

[00392] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2231-2256.

[00393] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2232-2235.

[00394] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2236-2248, 2250-2252, and 2254-2255.

[00395] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2231-2256.

[00396] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2257-2277.

[00397] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2258-2261.

[00398] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2262-2274 and 2276-2277.

[00399] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2257-2277.

[00400] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2278-2304.

[00401] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2279-2282.

[00402] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2283-2295, 2297-2299, and 2301-2304.

[00403] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2278-2304.

[00404] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2305-2333.

[00405] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2306-2309.

[00406] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2310-2320, 2322-2325, 2327-2329, and 2331-2333.

[00407] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2305-2333.

[00408] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2334-2349.

[00409] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2335-2338.

[00410] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2339-2349.

[00411] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2334-2349.

[00412] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2350-2368.

[00413] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2351-2354.

[00414] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2355-2365 and 2367-2368.

[00415] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2350-2368.

[00416] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2369-2390.

[00417] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99 and at least one RNA molecule is

a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2370-2373.

[00418] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2374-2384 and 2386-2390.

[00419] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2369-2390.

[00420] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2391-2411.

[00421] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2392-2395.

[00422] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2396-2408 and 2410-2411.

[00423] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2391-2411.

[00424] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2412-2436.

[00425] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101 and at least one RNA molecule

is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2413-2416 and 2429-2432.

[00426] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2417-2427 and 2433-2436.

[00427] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2412-2436.

[00428] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2437-2452.

[00429] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2438-2441.

[00430] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2442-2452.

[00431] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2437-2452.

[00432] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 24523-2468.

[00433] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103 and at least one RNA molecule

is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2454-2457.

[00434] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2458-2468.

[00435] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 24523-2468.

[00436] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2469-2484.

[00437] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2470-2473.

[00438] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2474-2484.

[00439] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2469-2484.

[00440] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2485-2500.

[00441] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105 and at least one RNA molecule

is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2486-2489.

[00442] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2490-2500.

[00443] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2485-2500.

[00444] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2501-2536.

[00445] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2502-2505 and 2520-2523.

[00446] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2506-2518, 2524-2529, 2531-2534, and 2536.

[00447] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2501-2536.

[00448] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2537-2552.

[00449] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107 and at least one RNA molecule

is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2538-2541.

[00450] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2542-2552.

[00451] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2537-2552.

[00452] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2553-2574.

[00453] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2554-2557.

[00454] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2558-2566, 2568-2570, and 2572-2574.

[00455] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2553-2574.

[00456] In some embodiments, the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1.

[00457] In some embodiments, the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1.

[00458] In some embodiments, the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1.

[00459] For example, a nickase may be generated for the OMNI-263 nuclease by inactivating its RuvC domain by substituting an aspartic acid residue (D) in position 9 of the amino acid sequence of OMNI-263 (SEQ ID NO: 1) for another amino acid e.g. alanine (A). Substitution to any other amino acid is permissible for each of the amino acid positions indicated in columns 5-7, unless otherwise indicated in Table 1. Other nickases or catalytically dead nucleases can be generated using the same notation in Table 1.

[00460] In some embodiments, the CRISPR nuclease utilizes a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in any one of columns 2-7 of Table 3. A CRISPR nuclease utilizes a PAM sequence as a targeting component in addition to a spacer sequence of a guide molecule.

[00461] The invention also provides a method for modifying a nucleotide sequence at a DNA target site in a cell-free system or the genome of a cell comprising introducing into the cell any one of the compositions described above. In some embodiments, the composition comprises a CRISPR nuclease and a crRNA:tracrRNA complex or a sgRNA molecule.

[00462] In some embodiments, the CRISPR nuclease effects a DNA break in a DNA strand adjacent to a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in any one of columns 2-7 of Table 3, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence. For example, the OMNI-263 nuclease with, the appropriate targeting sgRNA or crRNA:tracrRNA complex, is capable of forming a DNA break in strand adjacent to a NNNRCM or NNNRCC sequence and in a DNA strand adjacent to a sequence that is complementary to a NNNRCM or NNNRCC sequence. In another example, the OMNI-281 nuclease, with the appropriate targeting sgRNA or crRNA:tracrRNA complex, is capable of forming a DNA break in strand adjacent to a NNGRVNNN, NNGRVNNN, or NNGAVNNN sequence and in a DNA strand adjacent to a sequence that is complementary to a NNGRVNNN, NNGRVNNN, or NNGAVNNN sequence.

[00463] In some embodiments, the DNA strand is within a nucleus of a cell.

[00464] In some embodiments, the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.

[00465] In some embodiments, the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

[00466] In some embodiments, the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

[00467] In some embodiments, the cell is a eukaryotic cell or a prokaryotic cell.

[00468] In some embodiments, the cell is a mammalian cell.

[00469] In some embodiments, the cell is a human cell.

[00470] In some embodiments, the CRISPR nuclease comprises an amino acid sequence having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, or 82% amino acid sequence identity to a CRISPR nuclease as set forth in any of SEQ ID NOs: 1-108. In an embodiment the sequence encoding the CRISPR nuclease has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 109-324.

[00471] According to some aspects of the invention, the disclosed compositions comprise DNA constructs or a vector system comprising nucleotide sequences that encode the CRISPR nuclease or variant CRISPR nuclease. In some embodiments, the nucleotide sequence that encode the CRISPR nuclease or variant CRISPR nuclease is operably linked to a promoter that is operable in the cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments the cell of interest is a mammalian cell. In some embodiments, the nucleic acid sequence encoding the engineered CRISPR nuclease is codon optimized for use in cells from a particular organism. In some embodiments, the nucleic acid sequence encoding the nuclease is codon optimized for *E. coli*. In some embodiments, the nucleic acid sequence encoding the

nuclease is codon optimized for eukaryotic cells. In some embodiments, the nucleic acid sequence encoding the nuclease is codon optimized for mammalian cells.

[00472] In some embodiments, the composition comprises a recombinant nucleic acid, comprising a heterologous promoter operably linked to a polynucleotide encoding a CRISPR enzyme having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90% identity to any of SEQ ID NOs: 1-108. Each possibility represents a separate embodiment.

[00473] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 1 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 109 and 217.

[00474] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 2 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 110 and 218.

[00475] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 3 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 111 and 219.

[00476] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 4 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 112 and 220.

[00477] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 5 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 113 and 221.

[00478] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 6 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 114 and 222.

[00479] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 7 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 115 and 223.

[00480] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 8 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 116 and 224.

[00481] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 9 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 117 and 225.

[00482] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 10 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 118 and 226.

[00483] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 11 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 119 and 227.

[00484] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 12 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 120 and 228.

[00485] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 13 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 121 and 229.

[00486] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 14 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 122 and 230.

[00487] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 15 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 123 and 231.

[00488] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 16 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 124 and 232.

[00489] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 17 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 125 and 233.

[00490] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 18 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 126 and 234.

[00491] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 19 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 127 and 235.

[00492] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 20 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 128 and 236.

[00493] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 21 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 129 and 237.

[00494] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 22 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 130 and 238.

[00495] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 23 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 131 and 239.

[00496] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 24 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 132 and 240.

[00497] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 25 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 133 and 241.

[00498] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 26 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 134 and 242.

[00499] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 27 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 135 and 243.

[00500] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 28 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 136 and 244.

[00501] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 29 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 137 and 245.

[00502] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 30 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 138 and 246.

[00503] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 31 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 139 and 247.

[00504] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 32 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 140 and 248.

[00505] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 33 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 141 and 249.

[00506] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 34 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 142 and 250.

[00507] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 35 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 143 and 251.

[00508] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 36 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 144 and 252.

[00509] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 37 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 145 and 253.

[00510] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 38 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 146 and 254.

[00511] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 39 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 147 and 255.

[00512] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 40 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 148 and 256.

[00513] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 41 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 149 and 257.

[00514] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 42 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 150 and 258.

[00515] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 43 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 151 and 259.

[00516] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 44 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 152 and 260.

[00517] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 45 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 153 and 261.

[00518] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 46 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 154 and 262.

[00519] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 47 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 155 and 263.

[00520] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 48 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 156 and 264.

[00521] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 49 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 157 and 265.

[00522] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 50 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 158 and 266.

[00523] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 51 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 159 and 267.

[00524] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 52 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 160 and 268.

[00525] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 53 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 161 and 269.

[00526] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 54 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 162 and 270.

[00527] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 55 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 163 and 271.

[00528] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 56 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 164 and 272.

[00529] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 57 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 165 and 273.

[00530] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 58 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 166 and 274.

[00531] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 59 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 167 and 275.

[00532] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 60 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 168 and 276.

[00533] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 61 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 169 and 277.

[00534] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 62 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 170 and 278.

[00535] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 63 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 171 and 279.

[00536] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 64 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 172 and 280.

[00537] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 65 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 173 and 281.

[00538] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 66 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 174 and 282.

[00539] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 67 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 175 and 283.

[00540] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 68 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 176 and 284.

[00541] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 69 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 177 and 285.

[00542] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 70 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 178 and 286.

[00543] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 71 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 179 and 287.

[00544] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 72 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 180 and 288.

[00545] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 73 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 181 and 289.

[00546] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 74 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 182 and 290.

[00547] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 75 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 183 and 291.

[00548] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 76 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 184 and 292.

[00549] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 77 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 185 and 293.

[00550] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 78 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 186 and 294.

[00551] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 79 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 187 and 295.

[00552] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 80 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 188 and 296.

[00553] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 81 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 189 and 297.

[00554] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 82 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 190 and 298.

[00555] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 83 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 191 and 299.

[00556] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 84 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 192 and 300.

[00557] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 85 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 193 and 301.

[00558] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 86 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 194 and 302.

[00559] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 87 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 195 and 303.

[00560] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 88 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 196 and 304.

[00561] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 89 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 197 and 305.

[00562] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 90 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 198 and 306.

[00563] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 91 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 199 and 307.

[00564] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 92 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 200 and 308.

[00565] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 93 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 201 and 309.

[00566] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 94 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 202 and 310.

[00567] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 95 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 203 and 311.

[00568] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 96 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 204 and 312.

[00569] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 97 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 205 and 313.

[00570] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 98 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 206 and 314.

[00571] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 99 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 207 and 315.

[00572] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 100 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 208 and 316.

[00573] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 101 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 209 and 317.

[00574] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 102 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 210 and 318.

[00575] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 103 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 211 and 319.

[00576] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 104 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 212 and 320.

[00577] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 105 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 213 and 321.

[00578] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 106 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 214 and 322.

[00579] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 107 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 215 and 323.

[00580] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% identity to the amino acid sequence as set forth in SEQ ID NO: 108 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 216 and 324.

[00581] According to some embodiments, there is provided an engineered or non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease. Each possibility represents a separate embodiment.

In an embodiment, the CRISPR nuclease is engineered or non-naturally occurring. The CRISPR nuclease may also be recombinant. Such CRISPR nucleases are produced using laboratory methods (molecular cloning) to bring together genetic material from multiple sources, creating sequences that would not otherwise be found in biological organisms.

[00582] In an embodiment, the CRISPR nuclease of the invention exhibits increased specificity to a target site compared to a SpCas9 nuclease when complexed with the one or more RNA molecules.

[00583] In an embodiment, the complex of the CRISPR nuclease of the invention and one or more RNA molecules exhibits at least maintained on-target editing activity of the target site and reduced off-target activity compared to SpCas9 nuclease.

[00584] In an embodiment, the CRISPR nuclease further comprises an RNA-binding portion capable of interacting with a DNA-targeting RNA molecule (gRNA) and an activity portion that exhibits site-directed enzymatic activity.

[00585] In an embodiment, the composition further comprises a DNA-targeting RNA molecule or a DNA polynucleotide encoding a DNA-targeting RNA molecule, wherein the DNA-targeting RNA molecule comprises a guide sequence portion, i.e. a nucleotide sequence that is complementary to a sequence in a target region, wherein the DNA-targeting RNA molecule and the CRISPR nuclease do not naturally occur together.

[00586] In an embodiment, the DNA-targeting RNA molecule further comprises a nucleotide sequence that can form a complex with a CRISPR nuclease.

[00587] This invention also provides a non-naturally occurring composition comprising a CRISPR associated system comprising:

- a) one or more RNA molecules comprising a guide sequence portion linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence, or one or more nucleotide sequences encoding the one or more RNA molecules; and
- b) a CRISPR nuclease comprising an amino acid sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease;

wherein the one or more RNA molecules hybridize to the target sequence, wherein the target sequence is 3' of a Protospacer Adjacent Motif (PAM), and the one or more RNA molecules form a complex with the RNA-guided nuclease.

[00588] In an embodiment, the composition further comprises an RNA molecule comprising a nucleotide sequence that can form a complex with a CRISPR nuclease (e.g. a tracrRNA molecule) or a DNA polynucleotide comprising a sequence encoding an RNA molecule that can form a complex with the CRISPR nuclease.

[00589] In an embodiment, the composition further comprises a donor template for homology directed repair (HDR).

[00590] In an embodiment, the composition is capable of editing the target region in the genome of a cell.

[00591] According to some embodiments, there is provided a non-naturally occurring composition comprising:

- (a) a CRISPR nuclease, or a polynucleotide encoding the CRISPR nuclease, comprising:
 - an RNA-binding portion; and
 - an activity portion that exhibits site-directed enzymatic activity, wherein the CRISPR nuclease has at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80% identity to any of SEQ ID NOs: 1-108; and

(b) one or more RNA molecules or a DNA polynucleotide encoding the one or more RNA molecules comprising:

- i) a DNA-targeting RNA sequence, comprising a nucleotide sequence that is complementary to a sequence in a target DNA sequence; and
- ii) a protein-binding RNA sequence, capable of interacting with the RNA-binding portion of the CRISPR nuclease,

wherein the DNA targeting RNA sequence and the CRISPR nuclease do not naturally occur together. Each possibility represents a separate embodiment.

[00592] In some embodiments, there is provided a single RNA molecule comprising the DNA-targeting RNA sequence and the protein-binding RNA sequence, wherein the RNA molecule can form a complex with the CRISPR nuclease and serve as the DNA targeting module. In some embodiments, the RNA molecule has a length of up to 1000 bases, 900 bases, 800 bases, 700 bases, 600 bases, 500 bases, 400 bases, 300 bases, 200 bases, 100 bases, 50 bases. Each possibility represents a separate embodiment. In some embodiments, a first RNA molecule comprising the DNA-targeting RNA sequence and a second RNA molecule comprising the protein-binding RNA sequence interact by base pairing or alternatively fused together to form one or more RNA molecules that complex with the CRISPR nuclease and serve as the DNA targeting module.

[00593] This invention also provides a non-naturally occurring composition comprising:

- a) a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and
- b) one or more RNA molecules, or one or more DNA polynucleotide encoding the one or more RNA molecules, comprising at least one of:
 - i) a nuclease-binding RNA nucleotide sequence capable of interacting with/binding to the CRISPR nuclease; and
 - ii) a DNA-targeting RNA nucleotide sequence comprising a sequence complementary to a sequence in a target DNA sequence,

wherein the CRISPR nuclease is capable of complexing with the one or more RNA molecules to form a complex capable of hybridizing with the target DNA sequence.

[00594] In an embodiment, the CRISPR nuclease and the one or more RNA molecules form a CRISPR complex that is capable of binding to the target DNA sequence to effect cleavage of the target DNA sequence.

[00595] In an embodiment, the CRISPR nuclease and at least one of the one or more RNA molecules do not naturally occur together.

[00596] In an embodiment:

- a) the CRISPR nuclease comprises an RNA-binding portion and an activity portion that exhibits site-directed enzymatic activity;
- b) the DNA-targeting RNA nucleotide sequence comprises a nucleotide sequence that is complementary to a sequence in a target DNA sequence; and
- c) the nuclease-binding RNA nucleotide sequence comprises a sequence that interacts with the RNA-binding portion of the CRISPR nuclease.

[00597] In an embodiment, the nuclease-binding RNA nucleotide sequence and the DNA-targeting RNA nucleotide sequence are on a single guide RNA molecule (sgRNA), wherein the sgRNA molecule can form a complex with the CRISPR nuclease and serve as the DNA targeting module.

[00598] In an embodiment, the nuclease-binding RNA nucleotide sequence is on a first RNA molecule and the DNA-targeting RNA nucleotide sequence is on a second RNA molecule, and wherein the first and second RNA molecules interact by base-pairing or are fused together to form a RNA complex or sgRNA that forms a complex with the CRISPR nuclease and serves as a DNA targeting module.

[00599] In an embodiment, the sgRNA has a length of up to 1000 bases, 900 bases, 800 bases, 700 bases, 600 bases, 500 bases, 400 bases, 300 bases, 200 bases, 100 bases, 50 bases.

[00600] In an embodiment, the composition further comprises a donor template for homology directed repair (HDR).

[00601]

[00602] In an embodiment, the CRISPR nuclease is non-naturally occurring.

[00603] In an embodiment, the CRISPR nuclease is engineered and comprises unnatural or synthetic amino acids.

[00604] In an embodiment, the CRISPR nuclease is engineered and comprises one or more of a nuclear localization sequences (NLS), cell penetrating peptide sequences, and/or affinity tags.

[00605] In an embodiment, the CRISPR nuclease comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of a CRISPR complex comprising the CRISPR nuclease in a detectable amount in the nucleus of a eukaryotic cell.

[00606] This invention also provides a method of modifying a nucleotide sequence at a target site in a cell-free system or the genome of a cell comprising introducing into the cell any of the compositions of the invention.

[00607] In an embodiment, the cell is a eukaryotic cell.

[00608] In another embodiment, the cell is a prokaryotic cell.

[00609] In some embodiments, the one or more RNA molecules further comprises an RNA sequence comprising a nucleotide molecule that can form a complex with the RNA nuclease (tracrRNA) or a DNA polynucleotide encoding an RNA molecule comprising a nucleotide sequence that can form a complex with the CRISPR nuclease.

[00610] In an embodiment, the CRISPR nuclease comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the amino-terminus, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near carboxy-terminus, or a combination of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the amino-terminus and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near carboxy-terminus. In an embodiment 1-4 NLSs are fused with the CRISPR nuclease. In an embodiment, an NLS is located within the open-reading frame (ORF) of the CRISPR nuclease.

[00611] Methods of fusing an NLS at or near the amino-terminus, at or near carboxy-terminus, or within the ORF of an expressed protein are well known in the art. As an example, to fuse an NLS to the amino-terminus of a CRISPR nuclease, the nucleic acid sequence of the NLS is placed immediately after the start codon of the CRISPR nuclease on the nucleic acid encoding the NLS-fused CRISPR nuclease. Conversely, to fuse an NLS to the carboxy-terminus of a CRISPR nuclease the nucleic acid sequence of the NLS is placed after the codon encoding the last amino acid of the CRISPR nuclease and before the stop codon.

[00612] Any combination of NLSs, cell penetrating peptide sequences, and/or affinity tags at any position along the ORF of the CRISPR nuclease is contemplated in this invention.

[00613] The amino acid sequences and nucleic acid sequences of the CRISPR nucleases provided herein may include NLS and/or TAGs inserted so as to interrupt the contiguous amino acid or nucleic acid sequences of the CRISPR nucleases.

[00614] In an embodiment, the one or more NLSs are in tandem repeats.

[00615] In an embodiment, the one or more NLSs are considered in proximity to the N- or C-terminus when the nearest amino acid of the NLS is within about 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more amino acids along the polypeptide chain from the N- or C-terminus.

[00616] As discussed, the CRISPR nuclease may be engineered to comprise one or more of a nuclear localization sequences (NLS), cell penetrating peptide sequences, and/or affinity tags.

[00617] In an embodiment, the CRISPR nuclease exhibits increased specificity to a target site compared to the wild-type of the CRISPR nuclease when complexed with the one or more RNA molecules.

[00618] In an embodiment, the complex of the CRISPR nuclease and one or more RNA molecules exhibits at least maintained on-target editing activity of the target site and reduced off-target activity compared to the wild-type of the CRISPR nuclease.

[00619] In an embodiment, the composition further comprises a recombinant nucleic acid molecule comprising a heterologous promoter operably linked to the nucleotide acid molecule comprising the sequence encoding the CRISPR nuclease.

[00620] In an embodiment, the CRISPR nuclease or nucleic acid molecule comprising a sequence encoding the CRISPR nuclease is non-naturally occurring or engineered.

[00621] This invention also provides a non-naturally occurring or engineered composition comprising a vector system comprising the nucleic acid molecule comprising a sequence encoding any of the CRISPR nucleases of the invention.

[00622] This invention also provides use of any of the compositions of the invention for the treatment of a subject afflicted with a disease associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00623] This invention provides a method of modifying a nucleotide sequence at a target site in the genome of a mammalian cell comprising introducing into the cell (i) a composition comprising a CRISPR nuclease having at least 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108 or a nucleic acid molecule comprising a sequence encoding a CRISPR nuclease which sequence has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 109-324 and (ii) a DNA-targeting RNA molecule, or a DNA polynucleotide encoding a DNA-targeting RNA molecule, comprising a nucleotide sequence that is complementary to a sequence in the target DNA.

[00624] In some embodiments, the method is performed *ex vivo*. In some embodiments, the method is performed *in vivo*. In some embodiments, some steps of the method are performed *ex vivo* and some steps are performed *in vivo*. In some embodiments the mammalian cell is a human cell.

[00625] In an embodiment, the method further comprises introducing into the cell: (iii) an RNA molecule comprising a tracrRNA sequence or a DNA polynucleotide encoding an RNA molecule comprising a tracrRNA sequence.

[00626] In an embodiment, the DNA-targeting RNA molecule comprises a crRNA repeat sequence.

[00627] In an embodiment, the RNA molecule comprising a tracrRNA sequence is able to bind the DNA-targeting RNA molecule.

[00628] In an embodiment, the DNA-targeting RNA molecule and the RNA molecule comprising a tracrRNA sequence interact to form an RNA complex, and the RNA complex is capable of forming an active complex with the CRISPR nuclease.

[00629] In an embodiment, the DNA-targeting RNA molecule and the RNA molecule comprising a nuclease-binding RNA sequence are fused in the form of a single guide RNA molecule that is suitable to form an active complex with the CRISPR nuclease.

[00630] In an embodiment, the guide sequence portion comprises a sequence complementary to a protospacer sequence.

[00631] In an embodiment, the CRISPR nuclease forms a complex with the DNA-targeting RNA molecule and effects a double strand break in a region that is 3' or 5' of a Protospacer Adjacent Motif (PAM).

[00632] In an embodiment of any of the methods described herein, the method is for treating a subject afflicted with a disease associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00633] In an embodiment, the method comprises first selecting a subject afflicted with a disease associated with a genomic mutation and obtaining the cell from the subject.

[00634] This invention also provides a modified cell or cells obtained by any of the methods described herein. In an embodiment these modified cell or cells are capable of giving rise to progeny cells. In an embodiment these modified cell or cells are capable of giving rise to progeny cells after engraftment.

[00635] This invention also provides a composition comprising these modified cells and a pharmaceutically acceptable carrier. Also provided is an *in vitro* or *ex vivo* method of preparing this, comprising mixing the cells with the pharmaceutically acceptable carrier.

DNA-targeting RNA molecules

[00636] The “guide sequence portion” of an RNA molecule refers to a nucleotide sequence that is capable of hybridizing to a specific target DNA sequence, e.g., the guide sequence portion has a nucleotide sequence which is partially or fully complementary to the DNA sequence being targeted along the length of the guide sequence portion. In some embodiments, the guide sequence portion is 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 nucleotides in length, or approximately 17-50, 17-49, 17-48, 17-47, 17-46, 17-45, 17-44, 17-43, 17-42, 17-41, 17-40, 17-39, 17-38, 17-37, 17-36, 17-35, 17-34, 17-33, 17-31, 17-30, 17-29, 17-28, 17-27, 17-26, 17-25, 17-24, 17-22, 17-21, 18-25, 18-24, 18-23, 18-22, 18-21, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-22, 18-20, 20-21, 21-22, or 17-20 nucleotides in length. The entire length of the guide sequence portion is fully complementary to the DNA sequence being targeted along the length of the guide sequence portion. The guide sequence portion may be part of an RNA molecule that can form a complex with a CRISPR nuclease with the guide sequence portion serving as the DNA targeting portion of the CRISPR

complex. When the DNA molecule having the guide sequence portion is present contemporaneously with the CRISPR molecule the RNA molecule is capable of targeting the CRISPR nuclease to the specific target DNA sequence. Each possibility represents a separate embodiment. An RNA molecule can be custom designed to target any desired sequence. Accordingly, a molecule comprising a “guide sequence portion” is a type of targeting molecule. Throughout this application, the terms “guide molecule,” “RNA guide molecule,” “guide RNA molecule,” and “gRNA molecule” are synonymous with a molecule comprising a guide sequence portion, and the term “spacer” is synonymous with a “guide sequence portion.”

[00637] In embodiments of the present invention, the CRISPR nuclease has its greatest cleavage activity when used with an RNA molecule comprising a guide sequence portion having 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides.

[00638] A single-guide RNA (sgRNA) molecule may be used to direct a CRISPR nuclease to a desired target site. The single-guide RNA comprises a guide sequence portion as well as a scaffold portion. The scaffold portion interacts with a CRISPR nuclease and, together with a guide sequence portion, activates and targets the CRISPR nuclease to a desired target site. A scaffold portion may be further engineered, for example, to have a reduced size.

[00639] According to some aspects of the invention, the disclosed methods comprise a method of modifying a nucleotide sequence at a target site in a cell-free system or the genome of a cell comprising introducing into the cell the composition of any one of the embodiments described herein.

[00640] In some embodiments, the cell is a eukaryotic cell, preferably a mammalian cell or a plant cell.

[00641] According to some aspects of the invention, the disclosed methods comprise a use of any one of the compositions described herein for the treatment of a subject afflicted with a disease associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00642] According to some aspects of the invention, the disclosed methods comprise a method of treating subject having a mutation disorder comprising targeting any one of the compositions described herein to an allele associated with the mutation disorder.

[00643] In some embodiments, the mutation disorder is related to a disease or disorder selected from any of a neoplasia, age-related macular degeneration, schizophrenia, neurological, neurodegenerative, or movement disorder, Fragile X Syndrome, secretase-related disorders, prion-related disorders, ALS, addiction, autism, Alzheimer's Disease, neutropenia, inflammation-related disorders, Parkinson's Disease, blood and coagulation diseases and disorders, beta thalassemia, sickle cell anemia, cell dysregulation and oncology diseases and disorders, inflammation and immune-related diseases and disorders, metabolic, liver, kidney and protein diseases and disorders, muscular and skeletal diseases and disorders, dermatological diseases and disorders, neurological and neuronal diseases and disorders, and ocular diseases and disorders.

Diseases and therapies

[00644] Certain embodiments of the invention target a nuclease to a specific genetic locus associated with a disease or disorder as a form of gene editing, method of treatment, or therapy. For example, to induce editing or knockout of a gene, a novel nuclease disclosed herein may be specifically targeted to a pathogenic mutant allele of the gene using a custom designed guide RNA molecule. The guide RNA molecule is preferably designed by first considering the PAM requirement of the nuclease, which as shown herein is also dependent on the system in which the gene editing is being performed. For example, a guide RNA molecule designed to target an OMNI-263 nuclease to a target site is designed to contain a spacer region complementary to a DNA strand of a DNA double-stranded region that neighbors a OMNI-263 PAM sequence, e.g. "NNNRCM" or "NNNRCC." The guide RNA molecule is further preferably designed to contain a spacer region (i.e. the region of the guide RNA molecule having complementarity to the target allele) of sufficient and preferably optimal length in order to increase specific activity of the nuclease and reduce off-target effects.

[00645] As a non-limiting example, the guide RNA molecule may be designed to target the nuclease to a specific region of a mutant allele, e.g. near the start codon, such that upon DNA damage caused by the nuclease a non-homologous end joining (NHEJ) pathway is induced and leads to silencing of the mutant allele by introduction of frameshift mutations. This approach to guide RNA molecule design is particularly useful for altering the effects of dominant negative mutations and thereby treating a subject. As a separate non-limiting example, the guide RNA molecule may be designed to target a specific pathogenic mutation of a mutated allele, such that

upon DNA damage caused by the nuclease a homology directed repair (HDR) pathway is induced and leads to template mediated correction of the mutant allele. This approach to guide RNA molecule design is particularly useful for altering haploinsufficiency effects of a mutated allele and thereby treating a subject.

[00646] Non-limiting examples of specific genes which may be targeted for alteration to treat a disease or disorder are presented herein below. Specific disease-associated genes and mutations that induce a mutation disorder are described in the literature. Such mutations can be used to design a DNA-targeting RNA molecule to target a CRISPR composition to an allele of the disease associated gene, where the CRISPR composition causes DNA damage and induces a DNA repair pathway to alter the allele and thereby treat the mutation disorder.

[00647] Mutations in the ELANE gene are associated with neutropenia. Accordingly, without limitation, embodiments of the invention that target ELANE may be used in methods of treating subjects afflicted with neutropenia.

[00648] CXCR4 is a co-receptor for the human immunodeficiency virus type 1 (HIV-1) infection. Accordingly, without limitation, embodiments of the invention that target CXCR4 may be used in methods of treating subjects afflicted with HIV-1 or conferring resistance to HIV-1 infection in a subject.

[00649] Programmed cell death protein 1 (PD-1) disruption enhances CAR-T cell mediated killing of tumor cells and PD-1 may be a target in other cancer therapies. Accordingly, without limitation, embodiments of the invention that target PD-1 may be used in methods of treating subjects afflicted with cancer. In an embodiment, the treatment is CAR-T cell therapy with T cells that have been modified according to the invention to be PD-1 deficient.

[00650] In addition, BCL11A is a gene that plays a role in the suppression of hemoglobin production. Globin production may be increased to treat diseases such as thalassemia or sickle cell anemia by inhibiting BCL11A. See for example, PCT International Publication No. WO 2017/077394A2; U.S. Publication No. US2011/0182867A1; Humbert et al. Sci. Transl. Med. (2019); and Canver et al. Nature (2015). Accordingly, without limitation, embodiments of the invention that target an enhancer of BCL11A may be used in methods of treating subjects afflicted with beta thalassemia or sickle cell anemia.

[00651] Embodiments of the invention may also be used for targeting any disease-associated gene, for studying, altering, or treating any of the diseases or disorders listed in Table A or Table B below. Indeed, any disease-associated gene may be studied, altered, or targeted by any one of the nucleases disclosed herein to treat the disease caused by the disease-associated gene. Non-limiting examples are those listed in U.S. Publication No. 2018/0282762A1 and European Patent No. EP3079726B1.

Table A - Diseases, Disorders and their associated genes

DISEASE / DISORDERS	GENE(S)
Neoplasia	PTEN; ATM; ATR; EGFR; ERBB2; ERBB3; ERBB4; Notch1; Notch2; Notch3; Notch4; AKT; AKT2; AKT3; HIF; HIF1a; HIF3a; Met; HRG; Bcl2; PPAR alpha; PPAR gamma; WT1 (Wilms Tumor); FGF Receptor Family members (5 members: 1, 2, 3, 4, 5); CDKN2a; APC; RB (retinoblastoma); MEN1; VHL; BRCA1; BRCA2; AR (Androgen Receptor); TSG101; IGF; IGF Receptor; Igf1 (4 variants); gf2 (3 variants); Igf 1 Receptor; Igf 2 Receptor; Bax; Bcl2; caspases family (9 members: 1, 2, 3, 4, 6, 7, 8, 9, 12); Kras; Apc
Age-related Macular Degeneration	Abcr; Ccl2; Cc2; cp (ceruloplasmin); Timp3; cathepsinD; Vldlr; Ccr2
Schizophrenia	Neuregulin1 (Nrg1); Erb4 (receptor for Neuregulin); Complexin1 (Cplx1); Tph1 Tryptophan hydroxylase; Tph2 Tryptophan hydroxylase 2; Neurexin 1; GSK3; GSK3a; GSK3b
Neurological, Neuro degenerative, and Movement Disorders	5-HTT (SLc6a4); COMT; DRD (Drd1a); SLC6A3; DAOA; DTNBP1; Dao (Dao1)
Trinucleotide Repeat Disorders	HTT (Huntington's Dx); SBMA/SMAX1/AR (Kennedy's Dx); FXN/X25 (Friedrich's Ataxia); ATX3 (Machado-Joseph's Dx); ATXN1 and ATXN2 (spinocerebellar ataxias); DMPK (myotonic dystrophy); Atrophin-1 and Atn1 (DRPLA Dx); CBP (Creb-BP - global instability); VLDLR (Alzheimer's); Atxn7; Atxn10
Fragile X Syndrome	FMR2; FXR1; FXR2; mGLUR5
Secretase Related Disorders	APH-1 (alpha and beta); Presenilin (Psen1); nicastrin (Ncstn); PEN-2

DISEASE / DISORDERS	GENE(S)
Others	Nos1; Parp1; Nat1; Nat2
Prion related disorders	Prp
ALS	SOD1; ALS2; STEX; FUS; TARDBP; VEGF (VEGF-a; VEGF-b; VEGF-c)
Addiction	Prkce (alcohol); Drd2; Drd4; ABAT (alcohol); GRIA2; Grm5; Grin1; Htr1b; Grin2a; Drd3; Pdyn; Gria1 (alcohol)
Autism	Mecp2; BZRAP1; MDGA2; Sema5A; Neurexin 1; Fragile X (FMR2 (AFF2); FXR1; FXR2; Mglur5)
Alzheimer's Disease	E1; CHIP; UCH; UBB; Tau; LRP; PICALM; Clusterin; PS1; SORL1; CR1; Vldlr; Uba1; Uba3; CHIP28 (Aqp1, Aquaporin 1); Uchl1; Uchl3; APP
Inflammation	IL-10; IL-1 (IL-1a; IL-1b); IL-13; IL-17 (IL-17a (CTLA8); IL-17b; IL-17c; IL-17d; IL-17f); IL-23; Cx3cr1; ptpn22; TNFa; NOD2/CARD15 for IBD; IL-6; IL-12 (IL-12a; IL-12b); CTLA4; Cx3cl1
Parkinson's Disease	x-Synuclein; DJ-1; LRRK2; Parkin; PINK1

Table B - Diseases, Disorders and their associated genes

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
Blood and coagulation diseases and disorders	Anemia (CDAN1, CDA1, RPS19, DBA, PKLR, PK1, NT5C3, UMPH1, PSN1, RHAG, RH50A, NRAMP2, SPTB, ALAS2, ANH1, ASB, ABCB7, ABC7, ASAT); Bare lymphocyte syndrome (TAPBP, TPSN, TAP2, ABCB3, PSF2, RING11, MHC2TA, C2TA, RFX5, RFXAP, RFX5), Bleeding disorders (TBXA2R, P2RX1, P2X1); Factor H and factor H-like 1 (HF1, CFH, HUS); Factor V and factor VIII (MCFD2); Factor VII deficiency (F7); Factor X deficiency (F10); Factor XI deficiency (F11); Factor XII deficiency (F12, HAF); Factor XIIIa deficiency (F13A1, F13A); Factor XIIIb deficiency (F13B); Fanconi anemia (FANCA, FACA, FA1, FA, FAA, FAAP95, FAAP90, FLJ34064, FANCB, FANCC, FACC, BRCA2,

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	FANCD1, FANCD2, FANCD, FACD, FAD, FANCE, FACE, FANCF, XRCC9, FANCG, BRIP1, BACH1, FANCI, PHF9, FANCL, FANCM, KIAA1596); Hemophagocytic lymphohistiocytosis disorders (PRF1, HPLH2, UNC13D, MUNC13-4, HPLH3, HLH3, FHL3); Hemophilia A (F8, F8C, HEMA); Hemophilia B (F9, HEMB), Hemorrhagic disorders (PI, ATT, F5); Leukocyte deficiencies and disorders (ITGB2, CD18, LCAMB, LAD, EIF2B1, EIF2BA, EIF2B2, EIF2B3, EIF2B5, LVWM, CACH, CLE, EIF2B4); Sickle cell anemia (HBB); Thalassemia (HBA2, HBB, HBD, LCRB, HBA1)
Cell dysregulation and oncology diseases and disorders	B-cell non-Hodgkin lymphoma (BCL7A, BCL7); Leukemia (TAL1, TCL5, SCL, TAL2, FLT3, NBS1, NBS, ZNFN1A1, IK1, LYF1, HOXD4, HOX4B, BCR, CML, PHL, ALL, ARNT, KRAS2, RASK2, GMPS, AF10, ARHGEF12, LARG, KIAA0382, CALM, CLTH, CEBPA, CEBP, CHIC2, BTL, FLT3, KIT, PBT, LPP, NPM1, NUP214, D9S46E, CAN, CAIN, RUNX1, CBFA2, AML1, WHSC1L1, NSD3, FLT3, AF1Q, NPM1, NUMA1, ZNF145, PLZF, PML, MYL, STAT5B, AF10, CALM, CLTH, ARL11, ARLTS1, P2RX7, P2X7, BCR, CML, PHL, ALL, GRAF, NF1, VRNF, WSS, NFNS, PTPN11, PTP2C, SHP2, NS1, BCL2, CCND1, PRAD1, BCL1, TCRA, GATA1, GF1, ERYF1, NFE1, ABL1, NQO1, DIA4, NMOR1, NUP214, D9S46E, CAN, CAIN)
Inflammation and immune related diseases and disorders	AIDS (KIR3DL1, NKAT3, NKB1, AMB11, KIR3DS1, IFNG, CXCL12, SDF1); Autoimmune lymphoproliferative syndrome (TNFRSF6, APT1, FAS, CD95, ALPS1A); Combined immunodeficiency, (IL2RG, SCIDX1, SCIDX, IMD4); HIV-1 (CCL5, SCYA5, D17S136E, TCP228), HIV susceptibility or infection (IL10, CSIF, CMKBR2, CCR2, CMKBR5, CCCR5 (CCR5)); Immunodeficiencies (CD3E, CD3G, AICDA, AID, HIGM2, TNFRSF5, CD40, UNG, DGU, HIGM4, TNFSF5, CD40LG, HIGM1, IGM, FOXP3, IPEX, AIID, XPID, PIDX, TNFRSF14B, TACI); Inflammation (IL-10, IL-1 (IL-1a, IL-1b), IL-13, IL-17 (IL-17a (CTLA8), IL-17b, IL-17c, IL-17d, IL-17f), IL-23, Cx3cr1, ptpn22, TNFa, NOD2/CARD15 for IBD, IL-6, IL-12 (IL-12a, IL-12b), CTLA4, Cx3cl1); Severe combined immunodeficiencies (SCIDs)(JAK3, JAKL, DCLRE1C, ARTEMIS, SCIDA, RAG1, RAG2, ADA, PTPRC, CD45, LCA, IL7R, CD3D, T3D, IL2RG, SCIDX1, SCIDX, IMD4)

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
Metabolic, liver, kidney and protein diseases and disorders	Amyloid neuropathy (TTR, PALB); Amyloidosis (APOA1, APP, AAA, CVAP, AD1, GSN, FGA, LYZ, TTR, PALB); Cirrhosis (KRT18, KRT8, CIRH1A, NAIC, TEX292, KIAA1988); Cystic fibrosis (CFTR, ABCC7, CF, MRP7); Glycogen storage diseases (SLC2A2, GLUT2, G6PC, G6PT, G6PT1, GAA, LAMP2, LAMPB, AGL, GDE, GBE1, GYS2, PYGL, PFKM); Hepatic adenoma, 142330 (TCF1, HNF1A, MODY3), Hepatic failure, early onset, and neurologic disorder (SCOD1, SCO1), Hepatic lipase deficiency (LIPC), Hepatoblastoma, cancer and carcinomas (CTNNB1, PDGFRL, PDGRL, PRLTS, AXIN1, AXIN, CTNNB1, TP53, P53, LFS1, IGF2R, MPRI, MET, CASP8, MCH5; Medullary cystic kidney disease (UMOD, HNFJ, FJHN, MCKD2, ADMCKD2); Phenylketonuria (PAH, PKU1, QDPR, DHPR, PTS); Polycystic kidney and hepatic disease (FCYT, PKHD1, ARPKD, PKD1, PKD2, PKD4, PKDTS, PRKCSH, G19P1, PCLD, SEC63)
Muscular / Skeletal diseases and disorders	Becker muscular dystrophy (DMD, BMD, MYF6), Duchenne Muscular Dystrophy (DMD, BMD); Emery-Dreifuss muscular dystrophy (LMNA, LMN1, EMD2, FPLD, CMD1A, HGPS, LGMD1B, LMNA, LMN1, EMD2, FPLD, CMD1A); Facioscapulohumeral muscular dystrophy (FSHMD1A, FSHD1A); Muscular dystrophy (FKRP, MDC1C, LGMD2I, LAMA2, LAMM, LARGE, KIAA0609, MDC1D, FCMD, TTID, MYOT, CAPN3, CANP3, DYSF, LGMD2B, SGCG, LGMD2C, DMDA1, SCG3, SGCA, ADL, DAG2, LGMD2D, DMDA2, SGCB, LGMD2E, SGCD, SGD, LGMD2F, CMD1L, TCAP, LGMD2G, CMD1N, TRIM32, HT2A, LGMD2H, FKRP, MDC1C, LGMD2I, TTN, CMD1G, TMD, LGMD2J, POMT1, CAV3, LGMD1C, SEPN1, SELN, RSMD1, PLEC1, PLTN, EBS1); Osteopetrosis (LRP5, BMND1, LRP7, LR3, OPPG, VBCH2, CLCN7, CLC7, OPTA2, OSTM1, GL, TCIRG1, TIRC7, OC116, OPTB1); Muscular atrophy (VAPB, VAPC, ALS8, SMN1, SMA1, SMA2, SMA3, SMA4, BSCL2, SPG17, GARS, SMAD1, CMT2D, HEXB, IGHMBP2, SMUBP2, CATF1, SMARD1)
Dermatological diseases and disorders	Albinism (TYR, OCA2, TYRP1, SLC45A2, LYST), Ectodermal dysplasias (EDAR, EDARADD, WNT10A), Ehlers-Danlos syndrome (COL5A1, COL5A2, COL1A1, COL1A2, COL3A1, TNXB, ADAMTS2, PLOD1, FKBP14), Ichthyosis-associated disorders (FLG, STS, TGM1, ALOXE3/ALOX12B, KRT1, KRT10, ABCA12, KRT2, GJB2, TGM1, ABCA12,

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	CYP4F22, ALOXE3, CERS3, NSHDL, EBP, MBTPS2, GJB2, SPINK5, AGHD5, PHYH, PEX7, ALDH3A2, ERCC2, ERCC3, GFT2H5, GBA), Incontinentia pigmenti (IKBKG, NEMO), Tuberous sclerosis (TSC1, TSC2), Premature aging syndromes (POLR3A, PYCR1, LMNA, POLD1, WRN, DMPK)
Neurological and Neuronal diseases and disorders	ALS (SOD1, ALS2, STEEX, FUS, TARDBP, VEGF (VEGF-a, VEGF-b, VEGF-c); Alzheimer disease (APP, AAA, CVAP, AD1, APOE, AD2, PSEN2, AD4, STM2, APBB2, FE65L1, NOS3, PLA1, URK, ACE, DCP1, ACE1, MPO, PACIP1, PAXIP1L, PTIP, A2M, BLMH, BMH, PSEN1, AD3); Autism (Mecp2, BZRAP1, MDGA2, Sema5A, Neurexin 1, GLO1, MECP2, RTT, PPMX, MRX16, MRX79, NLGN3, NLGN4, KIAA1260, AUTSX2); Fragile X Syndrome (FMR2, FXR1, FXR2, mGLUR5); Huntington's disease and disease like disorders (HD, IT15, PRNP, PRIP, JPH3, JP3, HDL2, TBP, SCA17); Parkinson disease (NR4A2, NURR1, NOT, TINUR, SNCAIP, TBP, SCA17, SNCA, NACP, PARK1, PARK4, DJ1, PARK7, LRRK2, PARK8, PINK1, PARK6, UCHL1, PARK5, SNCA, NACP, PARK1, PARK4, PRKN, PARK2, PDJ, DBH, NDUFV2); Rett syndrome (MECP2, RTT, PPMX, MRX16, MRX79, CDKL5, STK9, MECP2, RTT, PPMX, MRX16, MRX79, x-Synuclein, DJ-1); Schizophrenia (Neuregulin1 (Nrg1), Erb4 (receptor for Neuregulin), Complexin1 (Cplx1), Tph1 Tryptophan hydroxylase, Tph2, Tryptophan hydroxylase 2, Neurexin 1, GSK3, GSK3a, GSK3b, 5-HTT (Slc6a4), COMT, DRD (Drd1a), SLC6A3, DAOA, DTNBP1, Dao (Dao1)); Secretase Related Disorders (APH-1 (alpha and beta), Presenilin (Psen1), nicastrin, (Ncstn), PEN-2, Nos1, Parp1, Natl, Nat2); Trinucleotide Repeat Disorders (HTT (Huntington's Dx), SBMA/SMAX1/AR (Kennedy's Dx), FXN/X25 (Friedrich's Ataxia), ATX3 (Machado-Joseph's Dx), ATXN1 and ATXN2 (spinocerebellar ataxias), DMPK (myotonic dystrophy), Atrophin-1 and Atn1 (DRPLA Dx), CBP (Creb-BP - global instability), VLDLR (Alzheimer's), Atxn7, Atxn10)
Ocular diseases and disorders	Age-related macular degeneration (Abcr, Ccl2, Cc2, cp (ceruloplasmin), Timp3, cathepsinD, Vldlr, Ccr2); Cataract (CRYAA, CRYA1, CRYBB2, CRYB2, PITX3, BFSP2, CP49, CP47, CRYAA, CRYA1, PAX6, AN2, MGDA, CRYBA1, CRYB1, CRYGC, CRYG3, CCL, LIM2, MP19, CRYGD, CRYG4, BFSP2, CP49, CP47, HSF4, CTM, HSF4, CTM, MIP, AQP0, CRYAB, CRYA2, CTPP2, CRYBB1, CRYGD, CRYG4, CRYBB2, CRYB2, CRYGC, CRYG3, CCL, CRYAA, CRYA1,

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	GJA8, CX50, CAE1, GJA3, CX46, CZP3, CAE3, CCM1, CAM, KRIT1); Corneal clouding and dystrophy (APOA1, TGFBI, CSD2, CDGG1, CSD, BIGH3, CDG2, TACSTD2, TROP2, M1S1, VSX1, RINX, PPCD, PPD, KTCN, COL8A2, FECD, PPCD2, PIP5K3, CFD); Cornea plana congenital (KERA, CNA2); Glaucoma (MYOC, TIGR, GLC1A, JOAG, GPOA, OPTN, GLC1E, FIP2, HYPL, NRP, CYP1B1, GLC3A, OPA1, NTG, NPG, CYP1B1, GLC3A); Leber congenital amaurosis (CRB1, RP12, CRX, CORD2, CRD, RPGRIP1, LCA6, CORD9, RPE65, RP20, AIPL1, LCA4, GUCY2D, GUC2D, LCA1, CORD6, RDH12, LCA3); Macular dystrophy (ELOVL4, ADMD, STGD2, STGD3, RDS, RP7, PRPH2, PRPH, AVMD, AOFMD, VMD2)

[00652] Unless otherwise defined, all technical and/or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the invention, exemplary methods and/or materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be necessarily limiting.

[00653] In the discussion unless otherwise stated, adjectives such as “substantially” and “about” modifying a condition or relationship characteristic of a feature or features of an embodiment of the invention, are understood to mean that the condition or characteristic is defined to within tolerances that are acceptable for operation of the embodiment for an application for which it is intended. Unless otherwise indicated, the word “or” in the specification and claims is considered to be the inclusive “or” rather than the exclusive or, and indicates at least one of and any combination of items it conjoins.

[00654] It should be understood that the terms “a” and “an” as used above and elsewhere herein refer to “one or more” of the enumerated components. It will be clear to one of ordinary skill in the art that the use of the singular includes the plural unless specifically stated otherwise. Therefore, the terms “a,” “an” and “at least one” are used interchangeably in this application.

[00655] For purposes of better understanding the present teachings and in no way limiting the scope of the teachings, unless otherwise indicated, all numbers expressing quantities, percentages or proportions, and other numerical values used in the specification and claims, are to be understood as being modified in all instances by the term “about.” Accordingly, unless indicated to the contrary, the numerical parameters set forth in the following specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained. At the very least, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques.

[00656] It is understood that where a numerical range is recited herein, the present invention contemplates each integer between, and including, the upper and lower limits, unless otherwise stated.

[00657] In the description and claims of the present application, each of the verbs, “comprise,” “include” and “have” and conjugates thereof, are used to indicate that the object or objects of the verb are not necessarily a complete listing of components, elements or parts of the subject or subjects of the verb. Other terms as used herein are meant to be defined by their well-known meanings in the art.

[00658] The terms "polynucleotide", "nucleotide", "nucleotide sequence", "nucleic acid" and "oligonucleotide" are used interchangeably. They refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise one or more modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[00659] The term "nucleotide analog" or "modified nucleotide" refers to a nucleotide that contains one or more chemical modifications (e.g., substitutions), in or on the nitrogenous base of the nucleoside (e.g., cytosine (C), thymine (T) or uracil (U), adenine (A) or guanine (G)), in or on the sugar moiety of the nucleoside (e.g., ribose, deoxyribose, modified ribose, modified deoxyribose, six-membered sugar analog, or open-chain sugar analog), or the phosphate. Each of the RNA sequences described herein may comprise one or more nucleotide analogs.

[00660] As used herein, the following nucleotide identifiers are used to represent a referenced nucleotide base(s):

Nucleotide reference	Base(s) represented			
	A	C	G	T
A	A			
C		C		
G			G	
T				T
W	A			T
S		C	G	
M	A	C		
K			G	T
R	A		G	
Y		C		T
B		C	G	T
D	A		G	T
H	A	C		T
V	A	C	G	
N	A	C	G	T

[00661] As used herein, the term "targeting sequence" or "targeting molecule" refers a nucleotide sequence or molecule comprising a nucleotide sequence that is capable of hybridizing to a specific target sequence, e.g., the targeting sequence has a nucleotide sequence which is at least partially complementary to the sequence being targeted along the length of the targeting sequence. The targeting sequence or targeting molecule may be part of a targeting RNA molecule that can form a complex with a CRISPR nuclease with the targeting sequence serving as the targeting portion of

the CRISPR complex. When the molecule having the targeting sequence is present contemporaneously with the CRISPR molecule, the RNA molecule is capable of targeting the CRISPR nuclease to the specific target sequence. Each possibility represents a separate embodiment. A targeting RNA molecule can be custom designed to target any desired sequence.

[00662] The term “targets” as used herein, refers to preferential hybridization of a targeting sequence or a targeting molecule to a nucleic acid having a targeted nucleotide sequence. It is understood that the term “targets” encompasses variable hybridization efficiencies, such that there is preferential targeting of the nucleic acid having the targeted nucleotide sequence, but unintentional off-target hybridization in addition to on-target hybridization might also occur. It is understood that where an RNA molecule targets a sequence, a complex of the RNA molecule and a CRISPR nuclease molecule targets the sequence for nuclease activity.

[00663] In the context of targeting a DNA sequence that is present in a plurality of cells, it is understood that the targeting encompasses hybridization of the guide sequence portion of the RNA molecule with the sequence in one or more of the cells, and also encompasses hybridization of the RNA molecule with the target sequence in fewer than all of the cells in the plurality of cells. Accordingly, it is understood that where an RNA molecule targets a sequence in a plurality of cells, a complex of the RNA molecule and a CRISPR nuclease is understood to hybridize with the target sequence in one or more of the cells, and also may hybridize with the target sequence in fewer than all of the cells. Accordingly, it is understood that the complex of the RNA molecule and the CRISPR nuclease introduces a double strand break in relation to hybridization with the target sequence in one or more cells and may also introduce a double strand break in relation to hybridization with the target sequence in fewer than all of the cells. As used herein, the term “modified cells” refers to cells in which a double strand break is affected by a complex of an RNA molecule and the CRISPR nuclease as a result of hybridization with the target sequence, i.e. on-target hybridization.

[00664] As used herein the term "wild type" is a term of the art understood by skilled persons and means the typical form of an organism, strain, gene or characteristic as it occurs in nature as distinguished from mutant or variant forms. Accordingly, as used herein, where a sequence of amino acids or nucleotides refers to a wild type sequence, a variant refers to variant of that sequence, e.g., comprising substitutions, deletions, insertions. In embodiments of the present

invention, an engineered CRISPR nuclease is a variant CRISPR nuclease comprising at least one amino acid modification (e.g., substitution, deletion, and/or insertion) compared to the CRISPR nuclease of any of the CRISPR nucleases indicated in Table 1.

[00665] The terms "non-naturally occurring" or "engineered" are used interchangeably and indicate human manipulation. The terms, when referring to nucleic acid molecules or polypeptides may mean that the nucleic acid molecule or the polypeptide is at least substantially free from at least one other component with which they are naturally associated in nature and as found in nature.

[00666] As used herein the term "amino acid" includes natural and/or unnatural or synthetic amino acids, including glycine and both the D or L, optical isomers, and amino acid analogs and peptidomimetics.

[00667] As used herein, "genomic DNA" refers to linear and/or chromosomal DNA and/or to plasmid or other extrachromosomal DNA sequences present in the cell or cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments, the cell of interest is a prokaryotic cell. In some embodiments, the methods produce double-stranded breaks (DSBs) at pre-determined target sites in a genomic DNA sequence, resulting in mutation, insertion, and/or deletion of DNA sequences at the target site(s) in a genome.

[00668] "Eukaryotic" cells include, but are not limited to, fungal cells (such as yeast), plant cells, animal cells, mammalian cells and human cells.

[00669] The term "nuclease" as used herein refers to an enzyme capable of cleaving the phosphodiester bonds between the nucleotide subunits of nucleic acid. A nuclease may be isolated or derived from a natural source. The natural source may be any living organism. Alternatively, a nuclease may be a modified or a synthetic protein which retains the phosphodiester bond cleaving activity.

[00670] The term "PAM" as used herein refers to a nucleotide sequence of a target DNA located in proximity to the targeted DNA sequence and recognized by the CRISPR nuclease. The PAM sequence may differ depending on the nuclease identity.

[00671] The term "mutation disorder" or "mutation disease" as used herein refers to any disorder or disease that is related to dysfunction of a gene caused by a mutation. A dysfunctional gene

manifesting as a mutation disorder contains a mutation in at least one of its alleles and is referred to as a “disease-associated gene.” The mutation may be in any portion of the disease-associated gene, for example, in a regulatory, coding, or non-coding portion. The mutation may be any class of mutation, such as a substitution, insertion, or deletion. The mutation of the disease-associated gene may manifest as a disorder or disease according to the mechanism of any type of mutation, such as a recessive, dominant negative, gain-of-function, loss-of-function, or a mutation leading to haploinsufficiency of a gene product.

[00672] A skilled artisan will appreciate that embodiments of the present invention disclose RNA molecules capable of complexing with a nuclease, e.g. a CRISPR nuclease, such as to associate with a target genomic DNA sequence of interest next to a protospacer adjacent motif (PAM). The nuclease then mediates cleavage of target DNA to create a double-stranded break within the protospacer.

[00673] In embodiments of the present invention, a CRISPR nuclease and a targeting molecule form a CRISPR complex that binds to a target DNA sequence to effect cleavage of the target DNA sequence. A CRISPR nuclease may form a CRISPR complex comprising the CRISPR nuclease and RNA molecule without a further, separate tracrRNA molecule. Alternatively, CRISPR nucleases may form a CRISPR complex between the CRISPR nuclease, an RNA molecule, and a tracrRNA molecule.

[00674] The term “protein binding sequence” or “nuclease binding sequence” refers to a sequence capable of binding with a CRISPR nuclease to form a CRISPR complex. A skilled artisan will understand that a tracrRNA capable of binding with a CRISPR nuclease to form a CRISPR complex comprises a protein or nuclease binding sequence.

[00675] An “RNA binding portion” of a CRISPR nuclease refers to a portion of the CRISPR nuclease which may bind to an RNA molecule to form a CRISPR complex, e.g. the nuclease binding sequence of a tracrRNA molecule. An “activity portion” or “active portion” of a CRISPR nuclease refers to a portion of the CRISPR nuclease which effects a double strand break in a DNA molecule, for example when in complex with a DNA-targeting RNA molecule.

[00676] An RNA molecule may comprise a sequence sufficiently complementary to a tracrRNA molecule so as to hybridize to the tracrRNA via basepairing and promote the formation of a

CRISPR complex. (See U.S. Patent No. 8,906,616). In embodiments of the present invention, the RNA molecule may further comprise a portion having a tracr mate sequence.

[00677] In embodiments of the present invention, the targeting molecule may further comprise the sequence of a tracrRNA molecule. Such embodiments may be designed as a synthetic fusion of the guide portion of the RNA molecule (gRNA or crRNA) and the trans-activating crRNA (tracrRNA), together forming a single guide RNA (sgRNA). (See Jinek et al., Science (2012)). Embodiments of the present invention may also form CRISPR complexes utilizing a separate tracrRNA molecule and a separate RNA molecule comprising a guide sequence portion. In such embodiments the tracrRNA molecule may hybridize with the RNA molecule via base pairing and may be advantageous in certain applications of the invention described herein.

[00678] In embodiments of the present invention an RNA molecule may comprise a “nexus” region and/or “hairpin” regions which may further define the structure of the RNA molecule. (See Briner et al., Molecular Cell (2014)).

[00679] As used herein, the term “direct repeat sequence” refers to two or more repeats of a specific amino acid sequence of nucleotide sequence.

[00680] As used herein, an RNA sequence or molecule capable of “interacting with” or “binding” with a CRISPR nuclease refers to the RNA sequence or molecules ability to form a CRISPR complex with the CRISPR nuclease.

[00681] As used herein, the term “operably linked” refers to a relationship (i.e. fusion, hybridization) between two sequences or molecules permitting them to function in their intended manner. In embodiments of the present invention, when an RNA molecule is operably linked to a promoter, both the RNA molecule and the promoter are permitted to function in their intended manner.

[00682] As used herein, the term “heterologous promoter” refers to a promoter that does not naturally occur together with the molecule or pathway being promoted.

[00683] As used herein, a sequence or molecule has an X% “sequence identity” to another sequence or molecule if X% of bases or amino acids between the sequences of molecules are the same and in the same relative position. For example, a first nucleotide sequence having at least a

95% sequence identity with a second nucleotide sequence will have at least 95% of bases, in the same relative position, identical with the other sequence.

Nuclear Localization Sequences

[00684] The terms "nuclear localization sequence" and "NLS" are used interchangeably to indicate an amino acid sequence/peptide that directs the transport of a protein with which it is associated from the cytoplasm of a cell across the nuclear envelope barrier. The term "NLS" is intended to encompass not only the nuclear localization sequence of a particular peptide, but also derivatives thereof that are capable of directing translocation of a cytoplasmic polypeptide across the nuclear envelope barrier. NLSs are capable of directing nuclear translocation of a polypeptide when attached to the N-terminus, the C-terminus, or both the N- and C-termini of the polypeptide. In addition, a polypeptide having an NLS coupled by its N- or C-terminus to amino acid side chains located randomly along the amino acid sequence of the polypeptide will be translocated. Typically, an NLS consists of one or more short sequences of positively charged lysines or arginines exposed on the protein surface, but other types of NLS are known. Non-limiting examples of NLSs include an NLS sequence derived from: the SV40 virus large T-antigen, nucleoplasmin, c-myc, the hRNPA1 M9 NLS, the IBB domain from importin-alpha, myoma T protein, human p53, mouse c-abl IV, influenza vims NS1, Hepatitis virus delta antigen, mouse Mx1 protein, human poly(ADP-ribose) polymerase, and the steroid hormone receptors (human) glucocorticoid.

Delivery

[00685] The CRISPR nuclease or CRISPR compositions described herein may be delivered as a protein, DNA molecules, RNA molecules, Ribonucleoproteins (RNP), nucleic acid vectors, or any combination thereof. In some embodiments, the RNA molecule comprises a chemical modification. Non-limiting examples of suitable chemical modifications include 2'-O-methyl (M), 2'-O-methyl, 3'phosphorothioate (MS) or 2'-O-methyl, 3'thioPACE (MSP), pseudouridine, and 1-methyl pseudo-uridine. Each possibility represents a separate embodiment of the present invention.

[00686] The CRISPR nucleases and/or polynucleotides encoding same described herein, and optionally additional proteins (e.g., ZFPs, TALENs, transcription factors, restriction enzymes) and/or nucleotide molecules such as guide RNA may be delivered to a target cell by any suitable means. The target cell may be any type of cell e.g., eukaryotic or prokaryotic, in any environment e.g., isolated or not, maintained in culture, *in vitro*, *ex vivo*, *in vivo* or *in planta*.

[00687] In some embodiments, the composition to be delivered includes mRNA of the nuclease and RNA of the guide. In some embodiments, the composition to be delivered includes mRNA of the nuclease, RNA of the guide and a donor template. In some embodiments, the composition to be delivered includes the CRISPR nuclease and guide RNA. In some embodiments, the composition to be delivered includes the CRISPR nuclease, guide RNA and a donor template for gene editing via, for example, homology directed repair. In some embodiments, the composition to be delivered includes mRNA of the nuclease, DNA-targeting RNA and the tracrRNA. In some embodiments, the composition to be delivered includes mRNA of the nuclease, DNA-targeting RNA and the tracrRNA and a donor template. In some embodiments, the composition to be delivered includes the CRISPR nuclease DNA-targeting RNA and the tracrRNA. In some embodiments, the composition to be delivered includes the CRISPR nuclease, DNA-targeting RNA and the tracrRNA and a donor template for gene editing via, for example, homology directed repair.

[00688] Any suitable viral vector system may be used to deliver RNA compositions. Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids and/or CRISPR nuclease in cells (e.g., mammalian cells, plant cells, etc.) and target tissues. Such methods can also be used to administer nucleic acids encoding and/or CRISPR nuclease protein to cells in vitro. In certain embodiments, nucleic acids and/or CRISPR nuclease are administered for in vivo or ex vivo gene therapy uses. Non-viral vector delivery systems include naked nucleic acid, and nucleic acid complexed with a delivery vehicle such as a liposome or poloxamer. For a review of gene therapy procedures, see Anderson, *Science* (1992); Nabel and Felgner, *TIBTECH* (1993); Mitani and Caskey, *TIBTECH* (1993); Dillon, *TIBTECH* (1993); Miller, *Nature* (1992); Van Brunt, *Biotechnology* (1988); Vigne et al., *Restorative Neurology and Neuroscience* 8:35-36 (1995); Kremer and Perricaudet, *British Medical Bulletin* (1995); Haddada et al., *Current Topics in Microbiology and Immunology* (1995); and Yu et al., *Gene Therapy* 1:13-26 (1994).

[00689] Methods of non-viral delivery of nucleic acids and/or proteins include electroporation, lipofection, microinjection, biolistics, particle gun acceleration, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, artificial virions, and agent-enhanced uptake of nucleic acids or can be delivered to plant cells by bacteria or viruses (e.g., *Agrobacterium*, *Rhizobium* sp. NGR234, *Sinorhizobium meliloti*, *Mesorhizobium loti*, tobacco

mosaic virus, potato virus X, cauliflower mosaic virus and cassava vein mosaic virus. See, e.g., Chung et al. Trends Plant Sci. (2006). Sonoporation using, e.g., the Sonitron 2000 system (Rich-Mar) can also be used for delivery of nucleic acids. Cationic-lipid mediated delivery of proteins and/or nucleic acids is also contemplated as an in vivo or in vitro delivery method. See Zuris et al., Nat. Biotechnol. (2015), Coelho et al., N. Engl. J. Med. (2013); Judge et al., Mol. Ther. (2006); and Basha et al., Mol. Ther. (2011). Non-viral vectors, such as transposon-based systems e.g., recombinant Sleeping Beauty transposon systems or recombinant PiggyBac transposon systems, may also be delivered to a target cell and utilized for transposition of a polynucleotide sequence of a molecule of the composition or a polynucleotide sequence encoding a molecule of the composition in the target cell.

[00690] Additional exemplary nucleic acid delivery systems include those provided by Amaxa® Biosystems (Cologne, Germany), Maxcyte, Inc. (Rockville, Md.), BTX Molecular Delivery Systems (Holliston, Mass.) and Copernicus Therapeutics Inc., (see for example U.S. Patent No. 6,008,336). Lipofection is described in e.g., U.S. Patent No. 5,049,386, U.S. Patent No. 4,946,787; and U.S. Patent No. 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam.TM., Lipofectin.TM. and Lipofectamine.TM. RNAiMAX). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those disclosed in PCT International Publication Nos. WO/1991/017424 and WO/1991/016024. Delivery can be to cells (ex vivo administration) or target tissues (in vivo administration).

[00691] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science (1995); Blaese et al., Cancer Gene Ther. (1995); Behr et al., Bioconjugate Chem. (1994); Remy et al., Bioconjugate Chem. (1994); Gao and Huang, Gene Therapy (1995); Ahmad and Allen, Cancer Res., (1992); U.S. Patent Nos. 4,186,183; 4,217,344; 4,235,871; 4,261,975; 4,485,054; 4,501,728; 4,774,085; 4,837,028; and 4,946,787).

[00692] Additional methods of delivery include the use of packaging the nucleic acids to be delivered into EnGeneIC delivery vehicles (EDVs). These EDVs are specifically delivered to target tissues using bispecific antibodies where one arm of the antibody has specificity for the target tissue and the other has specificity for the EDV. The antibody brings the EDVs to the target

cell surface and then the EDV is brought into the cell by endocytosis. Once in the cell, the contents are released (see MacDiamid et al., Nature Biotechnology (2009)).

[00693] The use of RNA or DNA viral based systems for the delivery of nucleic acids take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (in vivo) or they can be used to treat cells in vitro and the modified cells are administered to patients (ex vivo). Conventional viral based systems for the delivery of nucleic acids include, but are not limited to, recombinant retroviral, lentivirus, adenoviral, adeno-associated, vaccinia and herpes simplex virus vectors for gene transfer. However, an RNA virus is preferred for delivery of the RNA compositions described herein. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues. Nucleic acid of the invention may be delivered by non-integrating lentivirus. Optionally, RNA delivery with Lentivirus is utilized. Optionally the lentivirus includes mRNA of the nuclease, RNA of the guide. Optionally the lentivirus includes mRNA of the nuclease, RNA of the guide and a donor template. Optionally, the lentivirus includes the nuclease protein, guide RNA. Optionally, the lentivirus includes the nuclease protein, guide RNA and/or a donor template for gene editing via, for example, homology directed repair. Optionally the lentivirus includes mRNA of the nuclease, DNA-targeting RNA, and the tracrRNA. Optionally the lentivirus includes mRNA of the nuclease, DNA-targeting RNA, and the tracrRNA, and a donor template. Optionally, the lentivirus includes the nuclease protein, DNA-targeting RNA, and the tracrRNA. Optionally, the lentivirus includes the nuclease protein, DNA-targeting RNA, and the tracrRNA, and a donor template for gene editing via, for example, homology directed repair.

[00694] As mentioned above, the compositions described herein may be delivered to a target cell using a non-integrating lentiviral particle method, e.g. a LentiFlash® system. Such a method may be used to deliver mRNA or other types of RNAs into the target cell, such that delivery of the RNAs to the target cell results in assembly of the compositions described herein inside of the target cell. See also PCT International Publication Nos. WO2013/014537, WO2014/016690, WO2016185125, WO2017194902, and WO2017194903.

[00695] The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors

capable of transducing or infecting non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system depends on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations thereof (see, e.g., Buchscher Panganiban, J. Virol. (1992); Johann et al., J. Virol. (1992); Sommerfelt et al., Virol. (1990); Wilson et al., J. Virol. (1989); Miller et al., J. Virol. (1991); PCT International Publication No. WO/1994/026877A1).

[00696] At least six viral vector approaches are currently available for gene transfer in clinical trials, which utilize approaches that involve complementation of defective vectors by genes inserted into helper cell lines to generate the transducing agent.

[00697] pLASN and MFG-S are examples of retroviral vectors that have been used in clinical trials (Dunbar et al., Blood (1995); Kohn et al., Nat. Med. (1995); Malech et al., PNAS (1997)). PA317/pLASN was the first therapeutic vector used in a gene therapy trial. (Blaese et al., Science (1995)). Transduction efficiencies of 50% or greater have been observed for MFG-S packaged vectors. (Ellem et al., Immunol Immunother. (1997); Dranoff et al., Hum. Gene Ther. (1997)).

[00698] Packaging cells are used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, AAV, and psi.2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by a producer cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host (if applicable), other viral sequences being replaced by an expression cassette encoding the protein to be expressed. The missing viral functions are supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess inverted terminal repeat (ITR) sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences. The cell line is also infected with

adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV. Additionally, AAV can be produced at clinical scale using baculovirus systems (see U.S. Patent No. 7,479,554).

[00699] In many gene therapy applications, it is desirable that the gene therapy vector be delivered with a high degree of specificity to a particular tissue type. Accordingly, a viral vector can be modified to have specificity for a given cell type by expressing a ligand as a fusion protein with a viral coat protein on the outer surface of the virus. The ligand is chosen to have affinity for a receptor known to be present on the cell type of interest. For example, Han et al., Proc. Natl. Acad. Sci. USA (1995), reported that Moloney murine leukemia virus can be modified to express human heregulin fused to gp70, and the recombinant virus infects certain human breast cancer cells expressing human epidermal growth factor receptor. This principle can be extended to other virus-target cell pairs, in which the target cell expresses a receptor and the virus expresses a fusion protein comprising a ligand for the cell-surface receptor. For example, filamentous phage can be engineered to display antibody fragments (e.g., FAB or Fv) having specific binding affinity for virtually any chosen cellular receptor. Although the above description applies primarily to viral vectors, the same principles can be applied to non-viral vectors. Such vectors can be engineered to contain specific uptake sequences which favor uptake by specific target cells.

[00700] Gene therapy vectors can be delivered *in vivo* by administration to an individual patient, typically by systemic administration (e.g., intravenous, intraperitoneal, intramuscular, subdermal, or intracranial infusion) or topical application, as described below. Alternatively, vectors can be delivered to cells *ex vivo*, such as cells explanted from an individual patient (e.g., lymphocytes, bone marrow aspirates, tissue biopsy) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector. In some embodiments, delivery of mRNA *in vivo* and *ex vivo*, and RNPs delivery may be utilized.

[00701] *Ex vivo* cell transfection for diagnostics, research, or for gene therapy (e.g., via re-infusion of the transfected cells into the host organism) is well known to those of skill in the art. In a preferred embodiment, cells are isolated from the subject organism, transfected with an RNA

composition, and re-infused back into the subject organism (e.g., patient). Various cell types suitable for ex vivo transfection are well known to those of skill in the art (see, e.g., Freshney, "Culture of Animal Cells, A Manual of Basic Technique and Specialized Applications (6th edition, 2010)) and the references cited therein for a discussion of how to isolate and culture cells from patients).

[00702] Suitable cells include but not limited to eukaryotic and prokaryotic cells and/or cell lines. Non-limiting examples of such cells or cell lines generated from such cells include COS, CHO (e.g., CHO--S, CHO-K1, CHO-DG44, CHO-DUXB11, CHO-DUKX, CHOK1SV), VERO, MDCK, WI38, V79, B14AF28-G3, BHK, HaK, NSO, SP2/0-Ag14, HeLa, HEK293 (e.g., HEK293-F, HEK293-H, HEK293-T), and perC6 cells, any plant cell (differentiated or undifferentiated) as well as insect cells such as *Spodoptera frugiperda* (Sf), or fungal cells such as *Saccharomyces*, *Pichia* and *Schizosaccharomyces*. In certain embodiments, the cell line is a CHO-K1, MDCK or HEK293 cell line. Additionally, primary cells may be isolated and used ex vivo for reintroduction into the subject to be treated following treatment with the nucleases (e.g. ZFNs or TALENs) or nuclease systems (e.g. CRISPR). Suitable primary cells include peripheral blood mononuclear cells (PBMC), and other blood cell subsets such as, but not limited to, CD4⁺ T cells or CD8⁺ T cells. Suitable cells also include stem cells such as, by way of example, embryonic stem cells, induced pluripotent stem cells, hematopoietic stem cells (CD34⁺), neuronal stem cells and mesenchymal stem cells.

[00703] In one embodiment, stem cells are used in ex vivo procedures for cell transfection and gene therapy. The advantage to using stem cells is that they can be differentiated into other cell types in-vitro or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34⁺ cells in vitro into clinically important immune cell types using cytokines such as GM-CSF, IFN-gamma, and TNF-alpha are known (as a non-limiting example see, Inaba et al., J. Exp. Med. (1992)).

[00704] Stem cells are isolated for transduction and differentiation using known methods. For example, stem cells are isolated from bone marrow cells by panning the bone marrow cells with antibodies which bind unwanted cells, such as CD4⁺ and CD8⁺ (T cells), CD45⁺ (panB cells), GR-1 (granulocytes), and Iad (differentiated antigen presenting cells) (as a non-limiting example

see Inaba et al., J. Exp. Med. (1992)). Stem cells that have been modified may also be used in some embodiments.

[00705] Notably, any one of the CRISPR nucleases described herein may be suitable for genome editing in post-mitotic cells or any cell which is not actively dividing, e.g., arrested cells. Examples of post-mitotic cells which may be edited using a CRISPR nuclease of the present invention include, but are not limited to, myocyte, a cardiomyocyte, a hepatocyte, an osteocyte and a neuron.

[00706] Vectors (e.g., retroviruses, liposomes, etc.) containing therapeutic RNA compositions can also be administered directly to an organism for transduction of cells in vivo. Alternatively, naked RNA or mRNA can be administered. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells including, but not limited to, injection, infusion, topical application and electroporation. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

[00707] Vectors suitable for introduction of transgenes into immune cells (e.g., T-cells) include non-integrating lentivirus vectors. See, for example, U.S. Patent Publication No. 2009/0117617.

[00708] Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions available, as described below (see, e.g., Remington's Pharmaceutical Sciences, 17th ed., 1989).

DNA Repair by Homologous Recombination

[00709] The term "homology-directed repair" or "HDR" refers to a mechanism for repairing DNA damage in cells, for example, during repair of double-stranded and single-stranded breaks in DNA. HDR requires nucleotide sequence homology and uses a "nucleic acid template" (nucleic acid template or donor template used interchangeably herein) to repair the sequence where the double-stranded or single break occurred (e.g., DNA target sequence). This results in the transfer of genetic information from, for example, the nucleic acid template to the DNA target sequence. HDR may result in alteration of the DNA target sequence (e.g., insertion, deletion, mutation) if the nucleic acid template sequence differs from the DNA target sequence and part or all of the nucleic

acid template polynucleotide or oligonucleotide is incorporated into the DNA target sequence. In some embodiments, an entire nucleic acid template polynucleotide, a portion of the nucleic acid template polynucleotide, or a copy of the nucleic acid template is integrated at the site of the DNA target sequence.

[00710] The terms "nucleic acid template" and "donor", refer to a nucleotide sequence that is inserted or copied into a genome. The nucleic acid template comprises a nucleotide sequence, e.g., of one or more nucleotides, that will be added to or will template a change in the target nucleic acid or may be used to modify the target sequence. A nucleic acid template sequence may be of any length, for example between 2 and 10,000 nucleotides in length (or any integer value there between or there above), preferably between about 100 and 1,000 nucleotides in length (or any integer there between), more preferably between about 200 and 500 nucleotides in length. A nucleic acid template may be a single stranded nucleic acid, a double stranded nucleic acid. In some embodiment, the nucleic acid template comprises a nucleotide sequence, e.g., of one or more nucleotides, that corresponds to wild type sequence of the target nucleic acid, e.g., of the target position. In some embodiment, the nucleic acid template comprises a ribonucleotide sequence, e.g., of one or more ribonucleotides, that corresponds to wild type sequence of the target nucleic acid, e.g., of the target position. In some embodiment, the nucleic acid template comprises modified ribonucleotides.

[00711] Insertion of an exogenous sequence (also called a "donor sequence," donor template" or "donor"), for example, for correction of a mutant gene or for increased expression of a wild-type gene can also be carried out. It will be readily apparent that the donor sequence is typically not identical to the genomic sequence where it is placed. A donor sequence can contain a non-homologous sequence flanked by two regions of homology to allow for efficient HDR at the location of interest. Additionally, donor sequences can comprise a vector molecule containing sequences that are not homologous to the region of interest in cellular chromatin. A donor molecule can contain several, discontinuous regions of homology to cellular chromatin. For example, for targeted insertion of sequences not normally present in a region of interest, said sequences can be present in a donor nucleic acid molecule and flanked by regions of homology to sequence in the region of interest.

[00712] The donor polynucleotide can be DNA or RNA, single-stranded and/or double-stranded and can be introduced into a cell in linear or circular form. See, e.g., U.S. Patent Publication Nos. 2010/0047805; 2011/0281361; 2011/0207221; and 2019/0330620. If introduced in linear form, the ends of the donor sequence can be protected (e.g., from exonucleolytic degradation) by methods known to those of skill in the art. For example, one or more dideoxynucleotide residues are added to the 3' terminus of a linear molecule and/or self-complementary oligonucleotides are ligated to one or both ends. See, for example, Chang and Wilson, Proc. Natl. Acad. Sci. USA (1987); Nehls et al., Science (1996). Additional methods for protecting exogenous polynucleotides from degradation include, but are not limited to, addition of terminal amino group(s) and the use of modified internucleotide linkages such as, for example, phosphorothioates, phosphoramidates, and O-methyl ribose or deoxyribose residues.

[00713] Accordingly, embodiments of the present invention using a donor template for repair may use a DNA or RNA, single-stranded and/or double-stranded donor template that can be introduced into a cell in linear or circular form. In embodiments of the present invention a gene-editing composition comprises: (1) an RNA molecule comprising a guide sequence to affect a double strand break in a gene prior to repair and (2) a donor RNA template for repair, the RNA molecule comprising the guide sequence is a first RNA molecule and the donor RNA template is a second RNA molecule. In some embodiments, the guide RNA molecule and template RNA molecule are connected as part of a single molecule.

[00714] A donor sequence may also be an oligonucleotide and be used for gene correction or targeted alteration of an endogenous sequence. The oligonucleotide may be introduced to the cell on a vector, may be electroporated into the cell, or may be introduced via other methods known in the art. The oligonucleotide can be used to 'correct' a mutated sequence in an endogenous gene (e.g., the sickle mutation in beta globin), or may be used to insert sequences with a desired purpose into an endogenous locus.

[00715] A polynucleotide can be introduced into a cell as part of a vector molecule having additional sequences such as, for example, replication origins, promoters and genes encoding antibiotic resistance. Moreover, donor polynucleotides can be introduced as naked nucleic acid, as nucleic acid complexed with an agent such as a liposome or poloxamer, or can be

delivered by recombinant viruses (e.g., adenovirus, AAV, herpesvirus, retrovirus, lentivirus and integrase defective lentivirus (IDLV)).

[00716] The donor is generally inserted so that its expression is driven by the endogenous promoter at the integration site, namely the promoter that drives expression of the endogenous gene into which the donor is inserted. However, it will be apparent that the donor may comprise a promoter and/or enhancer, for example a constitutive promoter or an inducible or tissue specific promoter.

[00717] The donor molecule may be inserted into an endogenous gene such that all, some or none of the endogenous gene is expressed. For example, a transgene as described herein may be inserted into an endogenous locus such that some (N-terminal and/or C-terminal to the transgene) or none of the endogenous sequences are expressed, for example as a fusion with the transgene. In other embodiments, the transgene (e.g., with or without additional coding sequences such as for the endogenous gene) is integrated into any endogenous locus, for example a safe-harbor locus, for example a CCR5 gene, a CXCR4 gene, a PPP1R12c (also known as AAVS1) gene, an albumin gene or a Rosa gene. See, e.g., U.S. Patent Nos. 7,951,925 and 8,110,379; U.S. Publication Nos. 2008/0159996; 20100/0218264; 2010/0291048; 2012/0017290; 2011/0265198; 2013/0137104; 2013/0122591; 2013/0177983 and 2013/0177960 and U.S. Provisional Application No. 61/823,689).

[00718] When endogenous sequences (endogenous or part of the transgene) are expressed with the transgene, the endogenous sequences may be full-length sequences (wild-type or mutant) or partial sequences. Preferably the endogenous sequences are functional. Non-limiting examples of the function of these full length or partial sequences include increasing the serum half-life of the polypeptide expressed by the transgene (e.g., therapeutic gene) and/or acting as a carrier.

[00719] Furthermore, although not required for expression, exogenous sequences may also include transcriptional or translational regulatory sequences, for example, promoters, enhancers, insulators, internal ribosome entry sites, sequences encoding 2A peptides and/or polyadenylation signals.

[00720] In certain embodiments, the donor molecule comprises a sequence selected from the group consisting of a gene encoding a protein (e.g., a coding sequence encoding a protein that is lacking in the cell or in the individual or an alternate version of a gene encoding a protein),

a regulatory sequence and/or a sequence that encodes a structural nucleic acid such as a microRNA or siRNA.

[00721] For the foregoing embodiments, each embodiment disclosed herein is contemplated as being applicable to each of the other disclosed embodiment. For example, it is understood that any of the RNA molecules or compositions of the present invention may be utilized in any of the methods of the present invention.

[00722] As used herein, all headings are simply for organization and are not intended to limit the disclosure in any manner. The content of any individual section may be equally applicable to all sections.

[00723] Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

[00724] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless the embodiment is inoperative without those elements.

[00725] Generally, the nomenclature used herein, and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, Sambrook et al., "Molecular Cloning: A laboratory Manual" (1989); Ausubel, R. M. (Ed.), "Current Protocols in Molecular Biology" Volumes I-III (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (Eds.), "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998);

Methodologies as set forth in U.S. Patent Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; Cellis, J. E. (Ed.), "Cell Biology: A Laboratory Handbook", Volumes I-III (1994); Freshney, "Culture of Animal Cells - A Manual of Basic Technique" Third Edition, Wiley-Liss, N. Y. (1994); Coligan J. E. (Ed.), "Current Protocols in Immunology" Volumes I-III (1994); Stites et al. (Eds.), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (Eds.), "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); Clokie and Kropinski (Eds.), "Bacteriophage Methods and Protocols", Volume 1: Isolation, Characterization, and Interactions (2009), all of which are incorporated by reference. Other general references are provided throughout this document.

[00726] Examples are provided below to facilitate a more complete understanding of the invention. The following examples illustrate the exemplary modes of making and practicing the invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only.

EXPERIMENTAL DETAILS

[00728] Examples are provided below to facilitate a more complete understanding of the invention. The following examples illustrate the exemplary modes of making and practicing the invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only.

[00729] CRISPR repeat (crRNA), trans-activating RNA (tracrRNA), nuclease polypeptide (OMNI), and protospacer adjacent motif (PAM) sequences were predicted from different metagenomic databases of sequences of environmental samples.

Construction of OMNI nuclease polypeptides

[00730] For construction of novel nuclease polypeptides (OMNIs), the open reading frame of several identified OMNIs were codon optimized for human cell line expression. The ORF was cloned into the bacterial expression plasmid pET9a and into the mammalian expression plasmid pmOMNI (**Table 4**).

Prediction and construction of sgRNA

[00731] For each OMNI the single guide RNA (sgRNA) was predicted by detection of the CRISPR repeat array sequence and a tracrRNA in the respective bacterial genome. The native pre-mature crRNA and tracrRNA sequences were connected *in silico* with a tetra-loop 'gaaa' sequence and the secondary structure elements of the duplex were predicted using an RNA secondary structure prediction tool.

[00732] The predicted secondary structures of the full duplex RNA elements (crRNA-tracrRNA chimera) were used for identification of possible tracrRNA sequences for the design of a sgRNA. Several possible sgRNA scaffolds versions were constructed by shortening the duplex at the upper stem at different locations (sgRNA designs of all OMNIs are listed in **Table 2**). Additionally, to overcome potential transcriptional and structural constraints and to assess the plasticity of the sgRNA scaffold in the human cellular environmental context, small changes in the nucleotide sequence of the possible sgRNA were made in some cases (**Fig. 1, Table 2**). Finally, up to four versions of possible designed scaffolds were synthesized for each OMNI and connected downstream to a 22-nucleotide universal unique spacer sequence (T2, SEQ ID NO: 268) and

cloned into a bacterial expressing plasmid under an inducible T7 promoter combined with a U6 promoter for mammalian expression (pShuttleGuide, **Table 4**).

T2 – GGAAGAGCAGAGCCTTGGTCTC (SEQ ID NO: 2782)

In-vitro Depletion assay by TXTL

[00733] Depletion of PAM sequences *in vitro* was followed as described by Maxwell *et al*, Methods. 2018. Briefly, linear DNA expressing the OMNI nucleases and an sgRNA under T7 promoter were added to a cell-free transcription-translation *in vitro* system (TXTL mix, Arbor Bioscience) together with a linear construct expressing T7 polymerase. RNA expression and protein translation by the TXTL mix result in the formation of a ribonucleoprotein (RNP) complex. Since linear DNA was used, Chi6 DNA sequences were added to the TXTL reaction mix to inhibit the exonuclease activity of RecBCD, thereby protecting the linear DNA from degradation. The sgRNA spacer is designed to target a library of plasmids containing the target protospacer (pbPOS T2 library, **Table 4**) flanked by an 8N randomized set of potential PAM sequences. Depletion of PAM sequences from the library was measured by high-throughput sequencing using PCR to add the necessary adapters and indices to both the cleaved library and to a control library expressing a non-targeting gRNA. Following deep sequencing, the *in vitro* activity was confirmed by the fraction of the depleted sequences having the same PAM sequence relative to their occurrence in the control, indicating functional DNA cleavage by the OMNI nuclease (**Figs. 2-109, Table 3**).

Activity in human cells on endogenous genomic targets

[00734] OMNIs were also assayed for their ability to promote editing on specific genomic locations in human cells. To this end, per each OMNI, a corresponding OMNI-P2A-mCherry expression vector (pmOMNI, **Table 4**) was transfected into HeLa cells together with an sgRNA designed to target a specific location in the human genome (pShuttle guide - **Table 4**, spacer sequence - **Table 5**). At 72h, cells were harvested, and their genomic DNA content was used in a PCR reaction, amplifying the corresponding putative genomic targets. Amplicons were subjected to next-generation sequence (NGS) and the resulting sequences were then used to calculate the percentage of editing events in each target site. Short insertions or deletions (indels) around the cut site are the typical outcome of DNA repair following nuclease induced DNA cleavage. The calculation of editing percent was therefore deduced from the fraction of indel-containing sequences within each amplicon.

[00735] Genomic activity of each ONMI was assessed using a panel of six (6) unique sgRNAs each designed to target a different genomic location. The results of these experiments are summarized in **Table 5**. As can be seen in the table (column 6, “% indels”), many OMNIIs exhibited high and significant editing levels compared to the negative control (not shown) in most or some of the target sites tested.

Table 1 - OMNI CRISPR nuclease sequences

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-263	1	109	217	(D9 or E513 or H733 or D736)	(D594* or H595 or N618)	(D9 or E513 or H733 or D736) and (D594* or H595 or N618)
OMNI-264	2	110	218	(D9 or E480 or H697 or D700)	(E562* or H563 or N586)	(D9 or E480 or H697 or D700) and (E562* or H563 or N586)
OMNI-266	3	111	219	(D9 or E533 or H756 or D759)	(D612* or H613 or N636)	(D9 or E533 or H756 or D759) and (D612* or H613 or N636)
OMNI-268	4	112	220	(D9 or E492 or H719 or D722)	(D571* or H572 or N595)	(D9 or E492 or H719 or D722) and (D571* or H572 or N595)
OMNI-269	5	113	221	(D8 or E491 or H702 or D705)	(D572* or H573 or N596)	(D8 or E491 or H702 or D705) and (D572* or H573 or N596)
OMNI-271	6	114	222	(D7 or E495 or H719 or D722)	(E576* or H577 or N600)	(D7 or E495 or H719 or D722) and (E576* or H577 or N600)
OMNI-274	7	115	223	(D8 or E498 or H709 or D712)	(D579* or H580 or N603)	(D8 or E498 or H709 or D712) and (D579* or H580 or N603)
OMNI-275	8	116	224	(D8 or E534 or H761 or D764)	(D609* or H610 or N635)	(D8 or E534 or H761 or D764) and (D609* or H610 or N635)
OMNI-276	9	117	225	(D16 or E518 or H748 or D751)	(D599* or H600 or N623)	(D16 or E518 or H748 or D751) and (D599* or H600 or N623)
OMNI-278	10	118	226	(D12 or E784 or H998 or D1001)	(D865* or H866 or N890)	(D12 or E784 or H998 or D1001) and (D865* or H866 or N890)
OMNI-279	11	119	227	(D8 or E742 or H1064 or D1067)	(E866* or H867 or N890)	(D8 or E742 or H1064 or D1067) and (E866* or H867 or N890)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-280	12	120	228	(D10 or E527 or H756 or D759)	(D609* or H610 or N633)	(D10 or E527 or H756 or D759) and (D609* or H610 or N633)
OMNI-281	13	121	229	(D9 or E479 or H703 or D706)	(D558* or H559 or N582)	(D9 or E479 or H703 or D706) and (D558* or H559 or N582)
OMNI-283	14	122	230	(D14 or E528 or H786 or D789)	(D611* or H612 or N635)	(D14 or E528 or H786 or D789) and (D611* or H612 or N635)
OMNI-284	15	123	231	(D9 or E515 or H735 or D738)	(D596* or H597 or N620)	(D9 or E515 or H735 or D738) and (D596* or H597 or N620)
OMNI-286	16	124	232	(D7 or E503 or H719 or D722)	(D584* or H585 or N608)	(D7 or E503 or H719 or D722) and (D584* or H585 or N608)
OMNI-287	17	125	233	(D8 or E508 or H727 or D730)	(D588* or H589 or N612)	(D8 or E508 or H727 or D730) and (D588* or H589 or N612)
OMNI-288	18	126	234	(D24 or E534 or H759 or D762)	(E614* or H615 or N638)	(D24 or E534 or H759 or D762) and (E614* or H615 or N638)
OMNI-290	19	127	235	(D10 or E506 or H725 or D728)	(D587* or H588 or N611)	(D10 or E506 or H725 or D728) and (D587* or H588 or N611)
OMNI-291	20	128	236	(D10 or E500 or H719 or D722)	(D581* or H582 or N605)	(D10 or E500 or H719 or D722) and (D581* or H582 or N605)
OMNI-293	21	129	237	(D8 or E509 or H728 or D731)	(D590* or H591 or N614)	(D8 or E509 or H728 or D731) and (D590* or H591 or N614)
OMNI-294	22	130	238	(D10 or E501 or H720 or D723)	(D582* or H583 or N606)	(D10 or E501 or H720 or D723) and

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
						(D582* or H583 or N606)
OMNI-295	23	131	239	(D7 or E521 or H780 or D783)	(D605* or H606 or N629)	(D7 or E521 or H780 or D783) and (D605* or H606 or N629)
OMNI-296	24	132	240	(D8 or E509 or H731 or D734)	(D590* or H591 or N614)	(D8 or E509 or H731 or D734) and (D590* or H591 or N614)
OMNI-297	25	133	241	(D9 or E505 or H722 or D725)	(D585* or H586 or N609)	(D9 or E505 or H722 or D725) and (D585* or H586 or N609)
OMNI-298	26	134	242	(D8 or E499 or H721 or D724)	(D581* or H582 or N605)	(D8 or E499 or H721 or D724) and (D581* or H582 or N605)
OMNI-299	27	135	243	(D10 or E504 or H723 or D726)	(D585* or H586 or N609)	(D10 or E504 or H723 or D726) and (D585* or H586 or N609)
OMNI-300	28	136	244	(D8 or E503 or H719 or D722)	(D583* or H584 or N607)	(D8 or E503 or H719 or D722) and (D583* or H584 or N607)
OMNI-301	29	137	245	(D9 or E507 or H726 or D729)	(D588* or H589 or N612)	(D9 or E507 or H726 or D729) and (D588* or H589 or N612)
OMNI-302	30	138	246	(D9 or E506 or H725 or D728)	(D587* or H588 or N611)	(D9 or E506 or H725 or D728) and (D587* or H588 or N611)
OMNI-303	31	139	247	(D8 or E505 or H720 or D723)	(D584* or H585 or N608)	(D8 or E505 or H720 or D723) and (D584* or H585 or N608)
OMNI-304	32	140	248	(D8 or E517 or H775 or D778)	(D613* or H614 or N637)	(D8 or E517 or H775 or D778) and (D613* or H614 or N637)
OMNI-305	33	141	249	(D8 or E510 or H729 or D732)	(D591* or H592 or N615)	(D8 or E510 or H729 or D732) and (D591* or H592 or N615)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-307	34	142	250	(D9 or E779 or H996 or D999)	(D863* or H864 or N887)	(D9 or E779 or H996 or D999) and (D863* or H864 or N887)
OMNI-308	35	143	251	(D8 or E504 or H727 or D730)	(D585* or H586 or N609)	(D8 or E504 or H727 or D730) and (D585* or H586 or N609)
OMNI-309	36	144	252	(D11 or E518 or H737 or D740)	(D598* or H599 or N622)	(D11 or E518 or H737 or D740) and (D598* or H599 or N622)
OMNI-310	37	145	253	(D9 or E506 or H741 or D744)	(D593* or H594 or N617)	(D9 or E506 or H741 or D744) and (D593* or H594 or N617)
OMNI-311	38	146	254	(D8 or E510 or H740 or D743)	(D597* or H598 or N621)	(D8 or E510 or H740 or D743) and (D597* or H598 or N621)
OMNI-312	39	147	255	(D11 or E583 or H836 or D839)	(E662* or H663 or N686)	(D11 or E583 or H836 or D839) and (E662* or H663 or N686)
OMNI-313	40	148	256	(D34 or E534 or H752 or D755)	(D615* or H616 or N639)	(D34 or E534 or H752 or D755) and (D615* or H616 or N639)
OMNI-314	41	149	257	(D8 or E505 or H725 or D728)	(D586* or H587 or N610)	(D8 or E505 or H725 or D728) and (D586* or H587 or N610)
OMNI-315	42	150	258	(D8 or E507 or H744 or D747)	(D593* or H594 or N617)	(D8 or E507 or H744 or D747) and (D593* or H594 or N617)
OMNI-316	43	151	259	(D8 or E498 or H730 or D733)	(D584* or H585 or N608)	(D8 or E498 or H730 or D733) and (D584* or H585 or N608)
OMNI-317	44	152	260	(D11 or E531 or H751 or D754)	(D612 or H613 or N636)	(D11 or E531 or H751 or D754) and (D612* or H613 or N636)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-318	45	153	261	(D17 or E516 or H753 or D756)	(D597* or H598 or N621)	(D17 or E516 or H753 or D756) and (D597* or H598 or N621)
OMNI-319	46	154	262	(D38 or E537 or H768 or D771)	(D624* or H625 or N648)	(D38 or E537 or H768 or D771) and (D624* or H625 or N648)
OMNI-320	47	155	263	(D12 or E533 or H755 or D758)	(D614* or H615 or N638)	(D12 or E533 or H755 or D758) and (D614* or H615 or N638)
OMNI-321	48	156	264	(D10 or E524 or H747 or D750)	(D605* or H606 or N629)	(D10 or E524 or H747 or D750) and (D605* or H606 or N629)
OMNI-322	49	157	265	(D10 or E530 or H751 or D754)	(D611* or H612 or N635)	(D10 or E530 or H751 or D754) and (D611* or H612 or N635)
OMNI-323	50	158	266	(D8 or E537 or H800 or D803)	(E613* or H614 or N637)	(D8 or E537 or H800 or D803) and (E613* or H614 or N637)
OMNI-324	51	159	267	(D8 or E508 or H753 or D756)	(D594* or H595 or N618)	(D8 or E508 or H753 or D756) and (D594* or H595 or N618)
OMNI-325	52	160	268	(D26 or E544 or H769 or D772)	(D624* or H625 or N648)	(D26 or E544 or H769 or D772) and (D624* or H625 or N648)
OMNI-326	53	161	269	(D26 or E541 or H766 or D769)	(D621* or H622 or N645)	(D26 or E541 or H766 or D769) and (D621* or H622 or N645)
OMNI-327	54	162	270	(D9 or E523 or M799 or S802)	(D606* or H607 or N632)	(D9 or E523 or M799 or S802) and (D606* or H607 or N632)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-329	55	163	271	(D9 or E760 or H974 or D977)	(D841* or H842 or N865)	(D9 or E760 or H974 or D977) and (D841* or H842 or N865)
OMNI-330	56	164	272	(D8 or E592 or H836 or D839)	(E671* or H672 or N695)	(D8 or E592 or H836 or D839) and (E671* or H672 or N695)
OMNI-331	57	165	273	(D8 or E594 or H843 or D846)	(E676* or H677 or N700)	(D8 or E594 or H843 or D846) and (E676* or H677 or N700)
OMNI-332	58	166	274	(D9 or E594 or H853 or D856)	(E680* or H681 or N704)	(D9 or E594 or H853 or D856) and (E680* or H681 or N704)
OMNI-333	59	167	275	(D8 or E541 or H777 or D780)	(D626* or H627 or N650)	(D8 or E541 or H777 or D780) and (D626* or H627 or N650)
OMNI-334	60	168	276	(D7 or E629 or H890 or D893)	(E707* or H708 or N731)	(D7 or E629 or H890 or D893) and (E707* or H708 or N731)
OMNI-336	61	169	277	(D12 or E746 or H964 or D967)	(D831* or H832 or N855)	(D12 or E746 or H964 or D967) and (D831* or H832 or N855)
OMNI-337	62	170	278	(D12 or E754 or H972 or D975)	(D839* or H840 or N863)	(D12 or E754 or H972 or D975) and (D839* or H840 or N863)
OMNI-338	63	171	279	(D12 or E756 or H967 or D970)	(D836* or H837 or N860)	(D12 or E756 or H967 or D970) and (D836* or H837 or N860)
OMNI-339	64	172	280	(D18 or E765 or H981 or D984)	(D848* or H849 or N872)	(D18 or E765 or H981 or D984) and (D848* or H849 or N872)
OMNI-340	65	173	281	(D13 or E794 or H1018 or D1021)	(D881* or H882 or N905)	(D13 or E794 or H1018 or D1021) and (D881* or H882 or N905)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-341	66	174	282	(D18 or E767 or H983 or D986)	(D851* or H852 or N875)	(D18 or E767 or H983 or D986) and (D851* or H852 or N875)
OMNI-342	67	175	283	(D10 or E763 or H976 or D979)	(D844* or H845 or N868)	(D10 or E763 or H976 or D979) and (D844* or H845 or N868)
OMNI-343	68	176	284	(D10 or E764 or H979 or D982)	(D847* or H848 or N871)	(D10 or E764 or H979 or D982) and (D847* or H848 or N871)
OMNI-344	69	177	285	(D18 or E775 or H991 or D994)	(D858* or H859 or N882)	(D18 or E775 or H991 or D994) and (D858* or H859 or N882)
OMNI-345	70	178	286	(D18 or E775 or H991 or D994)	(D858* or H859 or N882)	(D18 or E775 or H991 or D994) and (D858* or H859 or N882)
OMNI-346	71	179	287	(D18 or E780 or H996 or D999)	(D863* or H864 or N887)	(D18 or E780 or H996 or D999) and (D863* or H864 or N887)
OMNI-347	72	180	288	(D18 or E783 or H999 or D1002)	(D866* or H867 or N890)	(D18 or E783 or H999 or D1002) and (D866* or H867 or N890)
OMNI-348	73	181	289	(D9 or E776 or H985 or D988)	(D853* or H854 or N877)	(D9 or E776 or H985 or D988) and (D853* or H854 or N877)
OMNI-349	74	182	290	(D15 or E765 or H982 or D985)	(D850* or H851 or N874)	(D15 or E765 or H982 or D985) and (D850* or H851 or N874)
OMNI-350	75	183	291	(D15 or E773 or H986 or D989)	(D854* or H855 or N878)	(D15 or E773 or H986 or D989) and (D854* or H855 or N878)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-351	76	184	292	(D13 or E766 or H983 or D986)	(D850* or H851 or N874)	(D13 or E766 or H983 or D986) and (D850* or H851 or N874)
OMNI-352	77	185	293	(D12 or E774 or H984 or D987)	(D852* or H853 or N876)	(D12 or E774 or H984 or D987) and (D852* or H853 or N876)
OMNI-353	78	186	294	(D10 or E780 or H992 or D995)	(D860* or H861 or N884)	(D10 or E780 or H992 or D995) and (D860* or H861 or N884)
OMNI-354	79	187	295	(D15 or E764 or H1003 or D1006)	(D862* or H863 or N886)	(D15 or E764 or H1003 or D1006) and (D862* or H863 or N886)
OMNI-356	80	188	296	(D13 or E777 or H992 or D995)	(D859* or H860 or N883)	(D13 or E777 or H992 or D995) and (D859* or H860 or N883)
OMNI-357	81	189	297	(D10 or E773 or H998 or D1001)	(D857* or H858 or N881)	(D10 or E773 or H998 or D1001) and (D857* or H858 or N881)
OMNI-358	82	190	298	(D7 or E785 or H1000 or D1003)	(D867* or H868 or N892)	(D7 or E785 or H1000 or D1003) and (D867* or H868 or N892)
OMNI-359	83	191	299	(D12 or E778 or H995 or D998)	(D861* or H862 or N886)	(D12 or E778 or H995 or D998) and (D861* or H862 or N886)
OMNI-360	84	192	300	(D10 or E781 or H997 or D1000)	(D865* or H866 or N890)	(D10 or E781 or H997 or D1000) and (D865* or H866 or N890)
OMNI-361	85	193	301	(D11 or E778 or H995 or D998)	(E863* or H864 or N888)	(D11 or E778 or H995 or D998) and

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
						(E863 or H864 or N888)
OMNI-362	86	194	302	(D11 or E779 or H996 or D999)	(D863* or H864 or N888)	(D11 or E779 or H996 or D999) and (D863* or H864 or N888)
OMNI-363	87	195	303	(D10 or E788 or H1005 or D1008)	(D872* or H873 or N897)	(D10 or E788 or H1005 or D1008) and (D872* or H873 or N897)
OMNI-364	88	196	304	(D9 or E778 or H1000 or D1003)	(D867* or H868 or N892)	(D9 or E778 or H1000 or D1003) and (D867* or H868 or N892)
OMNI-365	89	197	305	(D10 or E778 or H997 or D1000)	(D864* or H865 or N889)	(D10 or E778 or H997 or D1000) and (D864* or H865 or N889)
OMNI-366	90	198	306	(D9 or E780 or H999 or D1002)	(E866* or H867 or N891)	(D9 or E780 or H999 or D1002) and (E866* or H867 or N891)
OMNI-367	91	199	307	(D14 or E776 or H992 or D995)	(D859* or H860 or N883)	(D14 or E776 or H992 or D995) and (D859* or H860 or N883)
OMNI-368	92	200	308	(D14 or E783 or H995 or D998)	(D863* or H864 or N887)	(D14 or E783 or H995 or D998) and (D863* or H864 or N887)
OMNI-369	93	201	309	(D11 or E787 or H1006 or D1009)	(D871* or H872 or N896)	(D11 or E787 or H1006 or D1009) and (D871* or H872 or N896)
OMNI-370	94	202	310	(D11 or E789 or H1006 or D1009)	(D873* or H874 or N898)	(D11 or E789 or H1006 or D1009) and (D873* or H874 or N898)

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-371	95	203	311	(D13 or E789 or H1014 or D1017)	(D881* or H882 or N905)	(D13 or E789 or H1014 or D1017) and (D881* or H882 or N905)
OMNI-372	96	204	312	(D8 or E746 or H1070 or D1073)	(E875* or H876 or N899)	(D8 or E746 or H1070 or D1073) and (E875* or H876 or N899)
OMNI-373	97	205	313	(D10 or E791 or H1007 or D1010)	(D873* or H874 or N898)	(D10 or E791 or H1007 or D1010) and (D873* or H874 or N898)
OMNI-375	98	206	314	(D10 or E801 or H1018 or D1021)	(D886* or H887 or N910)	(D10 or E801 or H1018 or D1021) and (D886* or H887 or N910)
OMNI-376	99	207	315	(D11 or E784 or H1000 or D1003)	(D868* or H869 or N892)	(D11 or E784 or H1000 or D1003) and (D868* or H869 or N892)
OMNI-377	100	208	316	(D8 or E793 or H1013 or D1016)	(D877* or H878 or N902)	(D8 or E793 or H1013 or D1016) and (D877* or H878 or N902)
OMNI-378	101	209	317	(D25 or E817 or H1035 or D1038)	(D901* or H902 or N925)	(D25 or E817 or H1035 or D1038) and (D901* or H902 or N925)
OMNI-380	102	210	318	(D10 or E733 or H1023 or D1026)	(E855* or H856 or N879)	(D10 or E733 or H1023 or D1026) and (E855* or H856 or N879)
OMNI-381	103	211	319	(D18 or E830 or H1045 or D1048)	(D912* or H913 or N936)	(D18 or E830 or H1045 or D1048) and (D912* or H913 or N936)
OMNI-382	104	212	320	(D8 or E700 or H1022 or D1025)	(E824* or H825 or N848)	(D8 or E700 or H1022 or D1025) and

“OMNI” Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
						(E824* or H825 or N848)
OMNI-383	105	213	321	(D8 or E738 or H1060 or D1063)	(E862* or H863 or N886)	(D8 or E738 or H1060 or D1063) and (E862* or H863 or N886)
OMNI-384	106	214	322	(D15 or E895 or H1122 or D1125)	(D976* or H977 or N1000)	(D15 or E895 or H1122 or D1125) and (D976* or H977 or N1000)
OMNI-385	107	215	323	(D8 or E731 or H1054 or D1057)	(E859* or H860 or N883)	(D8 or E731 or H1054 or D1057) and (E859* or H860 or N883)
OMNI-386	108	216	324	(D8 or E744 or H1068 or D1071)	(E870* or H871 or N894)	(D8 or E744 or H1068 or D1071) and (E870* or H871 or N894)

Table 1. OMNI nuclease sequences: Table 1 lists the OMNI name, its corresponding nuclease protein sequence, its native DNA sequence, its human optimized DNA sequence, alternative positions to be substituted to generate a nickase having an inactivated RuvC domain, alternative positions to be substituted to generate a nickase having an inactivated HNH domain, and alternative positions to be substituted to generate a catalytically dead nuclease having inactivated RuvC and HNH domains. Substitution to any other amino acid is permissible for each of the amino acid positions indicated in columns 5-7, except a substitution of aspartic acid (D) to glutamic acid (E) or glutamic acid (E) to aspartic acid (D) in the HNH domain, in order to achieve inactivation.

Table 2 – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-263	OMNI-264
	sgRNA V1 sequence	GUUAUCGCUUCCUUUCgaaa GAAAGGAAGCGAUAAUAAU CGAUAAAUUUCGAGUGGGG CAACGGCGAUCCGGUCUUU UAUCGGGGUAGCCGUCCCC UAAUUUUUU (SEQ ID NO: 325)	GUUGUGACUUGCACUCgaaaGUG UGCUUGCCAUAACAAGCGCAAG UCGCGCAGGCACUGCCCCGGCG GGCAUCACCCGAUGCCCCGCCG GGUAUCUCCUUUUUU (SEQ ID NO: 339)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUAUCGCUUCCUUUC (SEQ ID NO: 326)	GUUGUGACUUGCACUC (SEQ ID NO: 340)
	Partial crRNA 1	GUUAUCGCUUCCUUU (SEQ ID NO: 327)	GUUGUGACUUGCACU (SEQ ID NO: 341)
	Partial crRNA 2	GUUAUCGCUUCC (SEQ ID NO: 328)	GUUGUGACUUGC (SEQ ID NO: 342)
	Partial crRNA 3	GUUAUCGCUU (SEQ ID NO: 329)	GUUGUGACUU (SEQ ID NO: 343)
	tracrRNA (Antirepeat)	GAAAGGAAGCGAUAAU (SEQ ID NO: 330)	GUGUGCUUGCCAUAAC (SEQ ID NO: 344)
	Partial tracrRNA 1	AAAGGAAGCGAUAAU (SEQ ID NO: 331)	GUGUGCUUGCCAUAAC (SEQ ID NO: 345)
	Partial tracrRNA 2	GGAAGCGAUAAU (SEQ ID NO: 332)	GCUUGCCAUAAC (SEQ ID NO: 346)
	Partial tracrRNA 3	AAGCGAUAAU (SEQ ID NO: 333)	UUGCCAUAAC (SEQ ID NO: 347)
tracrRNA V1 sequences	tracrRNA Portion 1	AAUCGAUAAAUUUCGAGU (SEQ ID NO: 334)	AAGCGCAAGUCGCGC (SEQ ID NO: 348)
	tracrRNA Portion 1 - partial	AAUCGAUAAAUUUCGA (SEQ ID NO: 335)	AAGCGCAAGUCGCGC (SEQ ID NO: 349)
	tracrRNA Portion 2	GGGGCAACGGCGAUCCGGU CUUGUAUCGGGGUAGCCGU CCCCUAAUUUUUU (SEQ ID NO: 336)	AGGCACUGCCCCGGCGGGCAUC ACCCGAUGCCCGCCGGGGUAUC UCCUUUUUU (SEQ ID NO: 350)
	tracrRNA Portion 2 - partial	GGGGCAACGGCGAUCCGGU CUUGUAUCGGGGUAGCCGU CCCC (SEQ ID NO: 337)	AGGCACUGCCCCGGCGGGCAUC ACCCGAUGCCCGCCGGGGUAUC UCCU (SEQ ID NO: 351)
	tracrRNA Portion 2 – without polyT	GGGGCAACGGCGAUCCGGU CUUGUAUCGGGGUAGCCGU CCCCUA (SEQ ID NO: 338)	AGGCACUGCCCCGGCGGGCAUC ACCCGAUGCCCGCCGGGGUAUC UCC (SEQ ID NO: 352)

		OMNI-266	OMNI-268
	sgRNA V1 sequence	GUUAUAGUUGCCUUUCgaaa GAAAGGCGACUAUAAUAAU CGAGAAAUUUCGAGUAAGG CUCUAACGUUUACACGUUA UCCGAAAAGCAGCCGGUUC GCCGGUUGCUUCUUUUUUU (SEQ ID NO: 353)	GUUUUGAUUUACUCUAAUgaaa GUUAAGAGUCCAAUCAGAAUUG ACAAGAGAAUAGUCGGUACCUC UGCUAAAGCACGUAAAGAUCUC AUUCUCUAAAACAUUUAAAAA UUUUUU (SEQ ID NO: 369)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUAUAGUUGCCUUUC (SEQ ID NO: 354)	GUUUUGAUUUACUCUAAU (SEQ ID NO: 370)
	Partial crRNA 1	GUUAUAGUUGCCUUU (SEQ ID NO: 355)	GUUUUGAUUUACUCU (SEQ ID NO: 371)
	Partial crRNA 2	GUUAUAGUUGCC (SEQ ID NO: 356)	GUUUUGAUUUAC (SEQ ID NO: 372)
	Partial crRNA 3	GUUAUAGUUG (SEQ ID NO: 357)	GUUUUGAUUU (SEQ ID NO: 373)
	tracrRNA (Antirepeat)	GAAAGGCGACUAUAAU (SEQ ID NO: 358)	GUUAAGAGUCCAAUCAGAAU (SEQ ID NO: 374)
	Partial tracrRNA 1	AAAGGCGACUAUAAU (SEQ ID NO: 359)	AGAGUCCAAUCAGAAU (SEQ ID NO: 375)
	Partial tracrRNA 2	GGCGACUAUAAU (SEQ ID NO: 360)	GUCCAAUCAGAAU (SEQ ID NO: 376)
	Partial tracrRNA 3	CGACUAUAAU (SEQ ID NO: 361)	CCAAUCAGAAU (SEQ ID NO: 377)
tracrRNA V1 sequences	tracrRNA Portion 1	AAUCGAGAAAUUUCGAGUA A (SEQ ID NO: 362)	UGACAAGAGAAUAGUCGGUACC UCUGCUAAAAGCACGUAAAGAUC UCAUUCUCUAAAACAUUUAAAA AAUUUUUU (SEQ ID NO: 378)
	tracrRNA Portion 1 - partial	AAUCGAGAAAUUUCGA (SEQ ID NO: 363)	AGAGAAUAGUCGGUACCUCUGC UAAAGCACGUAAAGAUCUCAUU CUCU (SEQ ID NO: 379)
	tracrRNA Portion 1 - without polyT	-	UGACAAGAGAAUAGUCGGUACC UCUGCUAAAAGCACGUAAAGAUC UCAUUCUCUAAAACAUUUAAAA AA (SEQ ID NO: 380)
	tracrRNA Portion 2	GGCUCUAACGUUUACACGU UAUCCGAA (SEQ ID NO: 364)	-
	tracrRNA Portion 2 - partial	GGCUCUAACGUUUACACGU UAUCC (SEQ ID NO: 365)	-
	tracrRNA Portion 3	AAGCAGCCGGUUCGCCGGU UGCUUCUUUUUUU (SEQ ID NO: 366)	-
	tracrRNA Portion 3 - partial	AAGCAGCCGGUUCGCCGGU UGCUU (SEQ ID NO: 367)	-

		OMNI-266	OMNI-268
	tracrRNA Portion 3 - without polyT	AAGCAGCCGGUUCGCCGGU UGCUUC (SEQ ID NO: 368)	-

		OMNI-269	OMNI-271
	sgRNA V1 sequence	GCUAUAGUUUCCUUUCGAA gaaaUUCGAAACGUUACU AGUAAGAAAUUUUCGAAAA GUUCUGCCUAAUACUUA UGUAUUAGGCAUCUUUUUU (SEQ ID NO: 381)	GCUGGGGCUUGUAGAGgaaaCUC UACAAGUCCUGGUAAGGAUUU GCUGGCUACUUUCUGCGGAAAG UCCAUUCGGGCGGCUUCAUAAG CCGUCUUUUUU (SEQ ID NO: 396)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GCUAUAGUUUCCUUUCGAA (SEQ ID NO: 382)	GCUGGGGCUUGUAGAG (SEQ ID NO: 397)
	Partial crRNA 1	GCUAUAGUUUCCUUU (SEQ ID NO: 383)	GCUGGGGCUUGUAGA (SEQ ID NO: 398)
	Partial crRNA 2	GCUAUAGUUUCC (SEQ ID NO: 384)	GCUGGGGCUUGU (SEQ ID NO: 399)
	Partial crRNA 3	GCUAUAGUUU (SEQ ID NO: 385)	GCUGGGGCUU (SEQ ID NO: 400)
	tracrRNA (Antirepeat)	UUCGAAACGUUACUUAUAGU (SEQ ID NO: 386)	CUCUACAAGUCCUGGU (SEQ ID NO: 401)
	Partial tracrRNA 1	AAACGUUACUUAUAGU (SEQ ID NO: 387)	UCUACAAGUCCUGGU (SEQ ID NO: 402)
	Partial tracrRNA 2	CGUUACUUAUAGU (SEQ ID NO: 388)	ACAAGUCCUGGU (SEQ ID NO: 403)
	Partial tracrRNA 3	UUACUUAUAGU (SEQ ID NO: 389)	AAGUCCUGGU (SEQ ID NO: 404)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGAAAUUUUCGAAAAGUU CUGCCUAAUACUUAUUAUGU AUUAGGCAUCUUUUUU (SEQ ID NO: 390)	AAAGGAUUUGCUGGCUACUUUC UGCGGAAAGUCCAUUC (SEQ ID NO: 405)
	tracrRNA Portion 1 - partial	GAAAAGUUCUGCCUAAUAC UAUUAUGUAUUAGGCAUCU UUUU (SEQ ID NO: 391)	AAAGGAUUUGCUGGCUACUUUC UGCGGAAAGUCC (SEQ ID NO: 406)
	tracrRNA Portion 1 - without polyT	AAGAAAUUUUCGAAAAGUU CUGCCUAAUACUUAUUAUGU AUUAGGCAUC (SEQ ID NO: 392)	-
	tracrRNA Portion 2	-	GGGCGGCUUCAUAAGCCGUCUU UUUU (SEQ ID NO: 407)

		OMNI-269	OMNI-271
	tracrRNA Portion 2 - partial	-	GGGCGGCUUCAUAAGCCGUCU (SEQ ID NO: 408)
	tracrRNA Portion 2 – without polyT	-	GGGCGGCUUCAUAAGCCGUC (SEQ ID NO: 409)
	sgRNA V2 sequence	GCUAUAGUUUCCUUUCGAA gaaaUUCGAAACGUUACUAU AGUAAGAAAUUCUCGAAAA GUUCUGCCUAAUACUAUUA UGUAUUAGGCAUCUUUUUU (SEQ ID NO: 393)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAGAAAUUCUCGAAAAGUU CUGCCUAAUACUAUUAUGU AUUAGGCAUCUUUUUU (SEQ ID NO: 394)	-
	tracrRNA Portion 1 - without polyT	AAGAAAUUCUCGAAAAGUU CUGCCUAAUACUAUUAUGU AUUAGGCAUC (SEQ ID NO: 395)	-

		OMNI-274	OMNI-275
	sgRNA V1 sequence	GUUAUAGUUUCCUUUCGAA gaaaUUUGAAACGUUACUAU AAUAAGAAAGUUUCGUGAA GUUCUGUCCGAUAAUUUUUA UCGGACAUCUUCUUUUUUGC GGCUUUUUU (SEQ ID NO: 410)	GUUUUGAUUUGAGUgaaaACUCA AAUCUUAACUGAUGAAUGCGGA UAUACAGCACCGAAACUUUAUU GUUUCGCCUGUAUAUCCGUUUU CGUUUUUU (SEQ ID NO: 434)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUAUAGUUUCCUUUCGAA (SEQ ID NO: 411)	GUUUUGAUUUGAGU (SEQ ID NO: 435)
	Partial crRNA 1	GUUAUAGUUUCCUUU (SEQ ID NO: 412)	-
	Partial crRNA 2	GUUAUAGUUUCC (SEQ ID NO: 413)	GUUUUGAUUUGA (SEQ ID NO: 436)
	Partial crRNA 3	GUUAUAGUUU (SEQ ID NO: 414)	GUUUUGAUUU (SEQ ID NO: 437)
	tracrRNA (Antirepeat)	UUUGAAACGUUACUAUAAU (SEQ ID NO: 415)	ACUCAAUCUUAAC (SEQ ID NO: 438)
	Partial tracrRNA 1	AAACGUUACUAUAAU (SEQ ID NO: 416)	-
	Partial tracrRNA 2	CGUUACUAUAAU (SEQ ID NO: 417)	UCAAUCUUAAC (SEQ ID NO: 439)

		OMNI-274	OMNI-275
	Partial tracrRNA 3	UUACUAUAAU (SEQ ID NO: 418)	AAAUCUUAAC (SEQ ID NO: 440)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUUUUAUCG GACAUUCUUCUUUUGCGGC UUUUUU (SEQ ID NO: 419)	UGAUGAAUGCGGAUUAACAGCA CCGAAACUUUAUUGUUUCGCCU GUAUAUCCGUUUUCGUUUUUU (SEQ ID NO: 441)
	tracrRNA Portion 1 - partial	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUUUUAUCG GACAUUCUUCUUUUGCGGC UUUUUU (SEQ ID NO: 420)	GAUGAAUGCGGAUUAACAGCAC CGAAACUUUAUUGUUUCGCCUG UAUAUCCGUUUUCGUU (SEQ ID NO: 442)
	tracrRNA Portion 1 - without polyT	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUUUUAUCG GACAUUCUUCUUUUGCGGC (SEQ ID NO: 421)	UGAUGAAUGCGGAUUAACAGCA CCGAAACUUUAUUGUUUCGCCU GUAUAUCCGUUUUCG (SEQ ID NO: 443)
	sgRNA V2 sequence	GUUAUAGUUUCCUUUCGAA gaaaUUUGAAACGUUACUAAU AAUAAGAAAGUUUCGUGAA GUUCUGUCCGAUAAUCUUA UCGGACAUCUUCUUUCUGC GGCUUUUUU (SEQ ID NO: 422)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUCUUAUCG GACAUUCUUCUUUCUGCGGC UUUUUU (SEQ ID NO: 423)	-
	tracrRNA Portion 1 - partial	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUCUUAUCG GACAUUCUUCUUUCUGCGGC UUUUUU (SEQ ID NO: 424)	-
	tracrRNA Portion 1 - without polyT	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUCUUAUCG GACAUUCUUCUUUCUGCGGC (SEQ ID NO: 425)	-
	sgRNA V3 sequence	GUUAUAGUUUCCUUUCGAA gaaaUUUGAAACGUUACUAAU AAUAAGAAAGUUUCGUGAA GUUCUGUCCGAUAAUUUUA UCGGACAUCUUCUUUUUU (SEQ ID NO: 426)	GUUUUGAUUUGAGUgaaaACUCA AAUCUUAACUGAUGAAUGCGGA UAUACAGCACCGAAACUUUAUU GUUUCGCCUGUAUAUCCGUUUU UU (SEQ ID NO: 444)
tracrRNA V3 sequences	tracrRNA Portion 1	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUUUUAUCG GACAUUCUUCUUUUUU (SEQ ID NO: 427)	UGAUGAAUGCGGAUUAACAGCA CCGAAACUUUAUUGUUUCGCCU GUAUAUCCGUUUUUU (SEQ ID NO: 445)
	tracrRNA Portion 1 - partial	GAAGUUCUGUCCGAUAAUU UUAUCGGACAUCUUC (SEQ ID NO: 428)	GAAUGCGGAUUAACAGCACCGA AACUUUAUUGUUUCGCCUGUAU AUCCGUUUUU (SEQ ID NO: 446)
	tracrRNA Portion 1 - without polyT	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUUUUAUCG GACAUUCUUC (SEQ ID NO: 429)	UGAUGAAUGCGGAUUAACAGCA CCGAAACUUUAUUGUUUCGCCU GUAUAUCCG (SEQ ID NO: 447)

		OMNI-274	OMNI-275
	sgRNA V4 sequence	GUUAUAGUUUCCUUUCGAA gaaaUUUGAAACGUUACU AAUAAGAAAGUUUCGUGAA GUUCUGUCCGAUAAUCUUA UCGGACAUCUUCUUUUUU (SEQ ID NO: 430)	-
tracrRNA V4 sequences	tracrRNA Portion 1	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUCUUAUCG GACAUCUUCUUUUUU (SEQ ID NO: 431)	-
	tracrRNA Portion 1 - partial	GAAGUUCUGUCCGAUAAUC UUAUCGGACAUCUUC (SEQ ID NO: 432)	-
	tracrRNA Portion 1 - without polyT	AAGAAAGUUUCGUGAAGUU CUGUCCGAUAAUCUUAUCG GACAUCUUC (SEQ ID NO: 433)	-

		OMNI-276	OMNI-278
	sgRNA V1 sequence	GUCAUGGGUUCUUUCgaaa GAAGGGAACCCAUGAUAAAC GCUGAAGGCAGAACCGUC UUCAGCGCCGCACAGCUCU GCUCCGGCCUCAUGGCCG GAGCAUCUGUUUUUUU (SEQ ID NO: 448)	GUUUGAGAACCUUGUAAgaaaUU ACAAGGUGAGUGCAAAUAAGGA UUUAUCCGAAAUAGUCGCCCCG CAUCGUGCGGCAAUUUUUU (SEQ ID NO: 462)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUCAUGGGUUCUUUC (SEQ ID NO: 449)	GUUUGAGAACCUUGUAA (SEQ ID NO: 463)
	Partial crRNA 1	GUCAUGGGUUCUU (SEQ ID NO: 450)	GUUUGAGAACCUUGU (SEQ ID NO: 464)
	Partial crRNA 2	GUCAUGGGUUC (SEQ ID NO: 451)	GUUUGAGAACCU (SEQ ID NO: 465)
	Partial crRNA 3	GUCAUGGGUU (SEQ ID NO: 452)	GUUUGAGAAC (SEQ ID NO: 466)
	tracrRNA (Antirepeat)	GAAGGGAACCCAUGAU (SEQ ID NO: 453)	UUACAAGGUGAGUGCAAAU (SEQ ID NO: 467)
	Partial tracrRNA 1	AAGGGAACCCAUGAU (SEQ ID NO: 454)	ACAAGGUGAGUGCAAAU (SEQ ID NO: 468)
	Partial tracrRNA 2	GGAACCCAUGAU (SEQ ID NO: 455)	AGGUGAGUGCAAAU (SEQ ID NO: 469)
	Partial tracrRNA 3	AACCCAUGAU (SEQ ID NO: 456)	GUGAGUGCAAAU (SEQ ID NO: 470)

		OMNI-276	OMNI-278
tracrRNA V1 sequences	tracrRNA Portion 1	AACGCUGAAGGCAGAACCU GUCUUCAGCGCCGC (SEQ ID NO: 457)	AAGGAUUUAUCC (SEQ ID NO: 471)
	tracrRNA Portion 1 - partial	AACGCUGAAGGCAGAACCU GUCUUCAGCG (SEQ ID NO: 458)	AAGGAUUUAUCC (SEQ ID NO: 472)
	tracrRNA Portion 2	ACAGCUCUGCUCCGGCCUC AAUGGCCGGAGCAUCUGUU UUUUU (SEQ ID NO: 459)	GAAAUAGUCUGCCCGCAUCGUG CGGCAAUCAUUUUUU (SEQ ID NO: 473)
	tracrRNA Portion 2 - partial	ACAGCUCUGCUCCGGCCUC AAUGGCCGGAGCAUCUGU (SEQ ID NO: 460)	GAAAUAGUCUGCCCGCAUCGUG CGGCAAUCAUUUU (SEQ ID NO: 474)
	tracrRNA Portion 2 – without polyT	ACAGCUCUGCUCCGGCCUC AAUGGCCGGAGCAUCUG (SEQ ID NO: 461)	GAAAUAGUCUGCCCGCAUCGUG CGGCAAUCA (SEQ ID NO: 475)

		OMNI-279	OMNI-280
	sgRNA V1 sequence	GUUGUGAAUUGCUUUCgaaa GAAAGCAAUUCACAAUAG GAUUAUCCGUUGUGAAAA CAUCCAGGGCGGGGCAACU CGCCCUUUUUU (SEQ ID NO: 476)	GUUUUAGUACUCUGUUGgaaaCA ACAAGAGUUCUAAGAUAGACC UUAUGUGUCGUAGGGUAGCG GUAUCCCGAAUAAUCCGCUCU UUGAAAUCAACGCCGUUGCAUU UGCGACGGCUUUUUU (SEQ ID NO: 492)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUGAAUUGCUUUC (SEQ ID NO: 477)	GUUUUAGUACUCUGUUG (SEQ ID NO: 493)
	Partial crRNA 1	GUUGUGAAUUGCUUU (SEQ ID NO: 478)	GUUUUAGUACUCUGU (SEQ ID NO: 494)
	Partial crRNA 2	GUUGUGAAUUGC (SEQ ID NO: 479)	GUUUUAGUACUC (SEQ ID NO: 495)
	Partial crRNA 3	GUUGUGAAUU (SEQ ID NO: 480)	GUUUUAGUAC (SEQ ID NO: 496)
	tracrRNA (Antirepeat)	GAAAGCAAUUCACAAU (SEQ ID NO: 481)	CAACAAGAGUUCUAAGAU (SEQ ID NO: 497)
	Partial tracrRNA 1	AAAGCAAUUCACAAU (SEQ ID NO: 482)	ACAAGAGUUCUAAGAU (SEQ ID NO: 498)
	Partial tracrRNA 2	GCAAUUCACAAU (SEQ ID NO: 483)	AGAGUUCUAAGAU (SEQ ID NO: 499)
	Partial tracrRNA 3	AAUUCACAAU (SEQ ID NO: 484)	GUUCUAAGAU (SEQ ID NO: 500)

		OMNI-279	OMNI-280
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGAUUAUCCGU (SEQ ID NO: 485)	AAGACCUUAUGUGUCGUAGGGU AU (SEQ ID NO: 501)
	tracrRNA Portion 1 - partial	AAGGAUUAUCC (SEQ ID NO: 486)	AAGACCUUAUGUGUCGUAGGGU (SEQ ID NO: 502)
	tracrRNA Portion 2	UGUGAAAACAUC (SEQ ID NO: 487)	AGCGGUAUCCCGAAUAAUCCG CUCUUUGAAAUCAAC (SEQ ID NO: 503)
	tracrRNA Portion 2 - partial	UGUGAAAACA (SEQ ID NO: 488)	AGCGGUAUCCCGAAUAAUCCG CU (SEQ ID NO: 504)
	tracrRNA Portion 3	AGGGCGGGGCAACUCGCCC UUUUUU (SEQ ID NO: 489)	GCCGUUGCAUUUGCGACGGCUU UUUU (SEQ ID NO: 505)
	tracrRNA Portion 3 - partial	AGGGCGGGGCAACUCGCCC U (SEQ ID NO: 490)	GCCGUUGCAUUUGCGACGGC (SEQ ID NO: 506)
	tracrRNA Portion 3 - without polyT	AGGGCGGGGCAACUCGCCC (SEQ ID NO: 491)	GCCGUUGCAUUUGCGACGGC (SEQ ID NO: 507)
	sgRNA V2 sequence	-	GUCUUAGUACUCUGUUGgaaaCA ACAAGAGUUCUAAGAUAAAGACC UUAUGUGUCGUAGGGUAUAGCG GUAUCCCGAAUAAUCCGCUCU UUGAAAUCAACGCCGUUGCAUU UGCGACGGCUUUUUU (SEQ ID NO: 508)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GUCUUAGUACUCUGUUG (SEQ ID NO: 509)
	Partial crRNA 1	-	GUCUUAGUACUCUGU (SEQ ID NO: 510)
	Partial crRNA 2	-	GUCUUAGUACUC (SEQ ID NO: 511)
	Partial crRNA 3	-	GUCUUAGUAC (SEQ ID NO: 512)

		OMNI-281	OMNI-283
	sgRNA V1 sequence	GUUUUAGUACUCUGUAAUUGaaaAAUUACAGAAUCUACU AAAACAAGACAAUUGUCG UGUUUAGCCCAUCAAUUUA UUGGUGGGCUUUUUU (SEQ ID NO: 513)	GCUUUGCCAUAGUUCAgaaaGAAC UAUGACAAAGUUAAGAUAAACGCA GACCGCGUCCCUAACCGCCAUGC GGUAACACCGUGUUA AAAAAGCG UUGUUUAAGAGGUGCGACUUCA CCGUUGCGCCUCUUUUUU (SEQ ID NO: 536)

		OMNI-281	OMNI-283
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGUACUCUGUAAUU (SEQ ID NO: 514)	GCUUUGCCAUAGUUCA (SEQ ID NO: 537)
	Partial crRNA 1	GUUUUAGUACUCUGU (SEQ ID NO: 515)	GCUUUGCCAUAGUUC (SEQ ID NO: 538)
	Partial crRNA 2	GUUUUAGUACUC (SEQ ID NO: 516)	GCUUUGCCAUAG (SEQ ID NO: 539)
	Partial crRNA 3	GUUUUAGUAC (SEQ ID NO: 517)	GCUUUGCCAU (SEQ ID NO: 540)
	tracrRNA (Antirepeat)	AAUUACAGAAUCUACUAAAAC (SEQ ID NO: 518)	GAACUAGACAAAGU (SEQ ID NO: 541)
	Partial tracrRNA 1	ACAGAAUCUACUAAAAC (SEQ ID NO: 519)	GAACUAGACAAAGU (SEQ ID NO: 542)
	Partial tracrRNA 2	GAAUCUACUAAAAC (SEQ ID NO: 520)	CUAUGACAAAGU (SEQ ID NO: 543)
	Partial tracrRNA 3	AUCUACUAAAAC (SEQ ID NO: 521)	AUGACAAAGU (SEQ ID NO: 544)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGACAAUAUGUCGUGUUU (SEQ ID NO: 522)	UAGAUACGCAGACCGCGUCCCC UAACCGCCAUGCGGUUACACCG UGUUAAAAAGCGUUGUUUA (SEQ ID NO: 545)
	tracrRNA Portion 1 - partial	AAGACAAUAUGUC (SEQ ID NO: 523)	UAGAUACGCAGACCGCGUCCCC UAACCGCCAUGCGGUUACACCG UGUUAAAAAGCGUUGUUUA (SEQ ID NO: 546)
	tracrRNA Portion 2	AGCCCAUCAUUUAUUGGU GGGCUUUUUU (SEQ ID NO: 524)	AGAGGUGCGACUUCACGGUUGC GCCUCUUUUUU (SEQ ID NO: 547)
	tracrRNA Portion 2 - partial	AGCCCAUCAUUUAUUGGU GGGCU (SEQ ID NO: 525)	AGAGGUGCGACUUCACGGUUGC GCCUCU (SEQ ID NO: 548)
	tracrRNA Portion 2 – without polyT	AGCCCAUCAUUUAUUGGU GGGC (SEQ ID NO: 526)	AGAGGUGCGACUUCACGGUUGC GCCUC (SEQ ID NO: 549)
	sgRNA V2 sequence	GUUCUAGUACUCUGUAAUU gaaaAAUUACAGAAUCUACU AGAACAAGACAAUAUGUCG UGUUUAGCCCAUCAUUUA UUGGUGGGCUUUUUU (SEQ ID NO: 527)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGUACUCUGUAAUU (SEQ ID NO: 528)	-
	Partial crRNA 1	GUUCUAGUACUCUGU (SEQ ID NO: 529)	-

		OMNI-281	OMNI-283
	Partial crRNA 2	GUUCUAGUACUC (SEQ ID NO: 530)	-
	Partial crRNA 3	GUUCUAGUAC (SEQ ID NO: 531)	-
	tracrRNA (Antirepeat)	AAUUACAGAAUCUACUAGAAC (SEQ ID NO: 532)	-
	Partial tracrRNA 1	ACAGAAUCUACUAGAAC (SEQ ID NO: 533)	-
	Partial tracrRNA 2	GAAUCUACUAGAAC (SEQ ID NO: 534)	-
	Partial tracrRNA 3	AUCUACUAGAAC (SEQ ID NO: 535)	-

		OMNI-284	OMNI-286
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUAUCGCUUCCUUUgaaaA AAGGAAGCCGAUAAUAAUC GAAACGAAAGUUUCCGAG UGGGGCUCCGGCGAUCCGG UCUUGUAUCGGGGUAGCCG UCCCCUCAGAAGAAAAGGG GGCUGACCGCGCGUCGCCC CCUUUUCAUUUUUU (SEQ ID NO: 550)	GUUGUAGUUCCCUAUUUUgaaa GUAAAUAGGUUACUACAAUAAAG GCCCUUGCGCAAGCAUGGUGCC GCAACUGGAAGGUGCUGUGCGA GUCACGGCACUUUUUU (SEQ ID NO: 576)
	crRNA (Repeat)	GUUAUCGCUUCCUUU (SEQ ID NO: 551)	GUUGUAGUUCCCUAUUUU (SEQ ID NO: 577)
	Partial crRNA 1	-	GUUGUAGUUCCCUAU (SEQ ID NO: 578)
	Partial crRNA 2	GUUAUCGCUUCC (SEQ ID NO: 552)	GUUGUAGUUCCC (SEQ ID NO: 579)
	Partial crRNA 3	GUUAUCGCUU (SEQ ID NO: 553)	GUUGUAGUUC (SEQ ID NO: 580)
	tracrRNA (Antirepeat)	AAAGGAAGCCGAUAAU (SEQ ID NO: 554)	GUAAAUAGGUUACUACAAU (SEQ ID NO: 581)
	Partial tracrRNA 1	-	AUAGGUUACUACAAU (SEQ ID NO: 582)
	Partial tracrRNA 2	GGAAGCCGAUAAU (SEQ ID NO: 555)	GGUUACUACAAU (SEQ ID NO: 583)
	Partial tracrRNA 3	AAGCCGAUAAU (SEQ ID NO: 556)	UUACUACAAU (SEQ ID NO: 584)

		OMNI-284	OMNI-286
tracrRNA V1 sequences	tracrRNA Portion 1	AAUCGAAACGAAAGUUUUC (SEQ ID NO: 557)	AAGGCCCUUGCGCAAGCAUGGU GCCGCAACU (SEQ ID NO: 585)
	tracrRNA Portion 1 - partial	AAUCGAAACGAAAGUUUU (SEQ ID NO: 558)	AAGGCCCUUGCGCAAGCAUGGU GCC (SEQ ID NO: 586)
	tracrRNA Portion 2	GAGUGGGGCUCCGGCGAUC CGGUCUUGUAUCGGGGUAG CCGUCCCCUCAGAA (SEQ ID NO: 559)	GGAAGGUGCUGUGCGAGUCACG GCACUUUUUU (SEQ ID NO: 587)
	tracrRNA Portion 2 - partial	GAGUGGGGCUCCGGCGAUC CGGUCUUGUAUCGGGGUAG CCGUCCCCUC (SEQ ID NO: 560)	GGAAGGUGCUGUGCGAGUCACG GCACUUUUUU (SEQ ID NO: 588)
	tracrRNA Portion 2 – without polyT	-	GGAAGGUGCUGUGCGAGUCACG GCAC (SEQ ID NO: 589)
	tracrRNA Portion 3	GAAAAGGGGGCUGACCGCG CGUCGCCCCCUUUCAUUU UUU (SEQ ID NO: 561)	-
	tracrRNA Portion 3 - partial	GAAAAGGGGGCUGACCGCG CGUCGCCCCCUUUUC (SEQ ID NO: 562)	-
	tracrRNA Portion 3 - without polyT	GAAAAGGGGGCUGACCGCG CGUCGCCCCCUUUUCA (SEQ ID NO: 563)	-
	sgRNA V2 sequence	GUUAUCGCUUCCUUUgaaaA AAGGAAGCCGAUAAUAAUC GAAACGAAAGUUUCCCGAG UGGGGCUCCGGCGAUCCGG UCUUGUAUCGGGGUAGCCG UCCCCUCAGAAGAGAAGGG GGCUGACCGCGCGUCGCCC CCUUCUCAUUUUUU (SEQ ID NO: 564)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAUCGAAACGAAAGUUUCC C (SEQ ID NO: 565)	-
	tracrRNA Portion 1 - partial	AAUCGAAACGAAAGUUUC (SEQ ID NO: 566)	-
	tracrRNA Portion 3	GAGAAGGGGGCUGACCGCG CGUCGCCCCCUUCUCAUUU UUU (SEQ ID NO: 567)	-
	tracrRNA Portion 3 - partial	GAGAAGGGGGCUGACCGCG CGUCGCCCCCUUCUC (SEQ ID NO: 568)	-
	tracrRNA Portion 3 - without polyT	GAGAAGGGGGCUGACCGCG CGUCGCCCCCUUCA (SEQ ID NO: 569)	-

		OMNI-284	OMNI-286
	sgRNA V3 sequence	GUUAUCGCUUCCUUUgaaaA AAGGAAGCCGAUAAUAAUC GAAACGAAAGUUUCCGAG UGGGGCUCCGGCGAUCCGG UCUUGUAUCGGGGUAGCCG UCCCCUCAGAAGAAAAGGG GGCUGACCGCGCGUCGCCC CCUUUUUU (SEQ ID NO: 570)	GUUGUAGUUCCCUAUUUUgaaa GUAAAUAGGUUACUACAAUAAAG GCCCUGCGCAAGCAUGGUGCC GCAACUGGAAGGUGCUGUGCGA GUCACGGCACUUUUGCUUUUUU (SEQ ID NO: 590)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGGCCCUUGCGCAAGCAUGGU GCC (SEQ ID NO: 591)
	tracrRNA Portion 2	GAGUGGGGCUCCGGCGAUC CGGUCUUGUAUCGGGGUAG CCGUCCCCUCAGA (SEQ ID NO: 571)	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACUUUUGCUUUUUU (SEQ ID NO: 592)
	tracrRNA Portion 2 - partial	-	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACUUUUGC (SEQ ID NO: 593)
	tracrRNA Portion 2 – without polyT	-	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACUUUUGC (SEQ ID NO: 594)
	tracrRNA Portion 3	AGAAAAGGGGGCUGACCGC GCGUCGCCCCCUUUUUU (SEQ ID NO: 572)	-
	tracrRNA Portion 3 - partial	AGAAAAGGGGGCUGACCGC GCGUCGCCCCCUUUUUU (SEQ ID NO: 573)	-
	tracrRNA Portion 3 - without polyT	AGAAAAGGGGGCUGACCGC GCGUCGCCCCC (SEQ ID NO: 574)	-
	sgRNA V4 sequence	GUUAUCGCUUCCUUUgaaaA AAGGAAGCCGAUAAUAAUC GAAACGAAAGUUUCCGAG UGGGGCUCCGGCGAUCCGG UCUUGUAUCGGGGUAGCCG UCCCCUCAGAAGAAAAGGG GGCUGACCGCGCGUCGCCC CCUUUUUU (SEQ ID NO: 575)	GUUGUAGUUCCCUAUUUUgaaa GUAAAUAGGUUACUACAAUAAAG GCCCUGCGCAAGCAUGGUGCC GCAACUGGAAGGUGCUGUGCGA GUCACGGCACCUUUGCUUUUUU (SEQ ID NO: 595)
	tracrRNA Portion 2	-	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACCUUUGCUUUUUU (SEQ ID NO: 596)
	tracrRNA Portion 2 - partial	-	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACCUUUGC (SEQ ID NO: 597)
	tracrRNA Portion 2 – without polyT	-	GCAACUGGAAGGUGCUGUGCGA GUCACGGCACCUUUGC (SEQ ID NO: 598)

		OMNI-287	OMNI-288
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUAUACUUUGCUACUAA gaaUUAAGUAGCUUAGUAU AAUAAGUGAAAAACGCGAA GUUUGCCCUAUACGUUAUU GUAUGGGGUAUCUUCUUUU UUU (SEQ ID NO: 599)	GCUAUGUUUUGAAGGGAAU gaa AUUUCUCUCUUAACAUAGUAAG GAGUUAUGCUCCGUGCGUGUAG CCGAUUAGGUGAAACGAAGCGC CUCCAGUGGGGCGCAUAAAUU UUUU (SEQ ID NO: 613)
	crRNA (Repeat)	GUUAUACUUUGCUACUAA (SEQ ID NO: 600)	GCUAUGUUUUGAAGGGAAU (SEQ ID NO: 614)
	Partial crRNA 1	GUUAUACUUUGCUAC (SEQ ID NO: 601)	GCUAUGUUUUGAAGG (SEQ ID NO: 615)
	Partial crRNA 2	GUUAUACUUUGC (SEQ ID NO: 602)	GCUAUGUUUUGA (SEQ ID NO: 616)
	Partial crRNA 3	GUUAUACUUU (SEQ ID NO: 603)	GCUAUGUUUU (SEQ ID NO: 617)
	tracrRNA (Antirepeat)	UUAAGUAGCUUAGUAUAAU (SEQ ID NO: 604)	AUUUCUCUCUUAACAUAGU (SEQ ID NO: 618)
	Partial tracrRNA 1	GUAGCUUAGUAUAAU (SEQ ID NO: 605)	UCUCUUAACAUAGU (SEQ ID NO: 619)
	Partial tracrRNA 2	GCUUAGUAUAAU (SEQ ID NO: 606)	CUUAACAUAGU (SEQ ID NO: 620)
	Partial tracrRNA 3	UUAGUAUAAU (SEQ ID NO: 607)	UUAACAUAGU (SEQ ID NO: 621)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGUGAAAAACGC (SEQ ID NO: 608)	AAGGAGUUAUGCUCCGUG (SEQ ID NO: 622)
	tracrRNA Portion 1 - partial	AAGUGAAAAACGC (SEQ ID NO: 609)	AAGGAGUUAUGCUCC (SEQ ID NO: 623)
	tracrRNA Portion 2	GAAGUUUGCCCUAUACGUU AUUGUAUGGGGUAUCUUCU UUUUUU (SEQ ID NO: 610)	CGUGUAGCCGAUUAGGUGAAAC GAA (SEQ ID NO: 624)
	tracrRNA Portion 2 - partial	GAAGUUUGCCCUAUACGUU AUUGUAUGGGGUAUCUUC (SEQ ID NO: 611)	CGUGUAGCCGAUUAGGUGAAAC G (SEQ ID NO: 625)
	tracrRNA Portion 2 – without polyT	GAAGUUUGCCCUAUACGUU AUUGUAUGGGGUAUCUUC (SEQ ID NO: 612)	-
	tracrRNA Portion 3	-	GCGCCUCCCAGUGGGGCGCAUA AAUUUUUU (SEQ ID NO: 626)
	tracrRNA Portion 3 - partial	-	GCGCCUCCCAGUGGGGCGC (SEQ ID NO: 627)

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	tracrRNA Portion 3 - without polyT	-	GCGCCUCCCAGUGGGGCGCAUAA (SEQ ID NO: 628)
	sgRNA V2 sequence	-	GCUAUGUUCUGAAGGGAAUgaaa AUUUCUCUCUUAACAUAAGUAAG GAGUUAUGCUCGUGCGUGUAG CCGAUUAGGUGAAACGAAGCGC CUCCCAGUGGGGCGCAUAAAUU UUUU (SEQ ID NO: 629)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GCUAUGUUCUGAAGGGAAU (SEQ ID NO: 630)
	Partial crRNA 1	-	GCUAUGUUCUGAAGG (SEQ ID NO: 631)
	Partial crRNA 2	-	GCUAUGUUCUGA (SEQ ID NO: 632)
	Partial crRNA 3	-	GCUAUGUUCU (SEQ ID NO: 633)

		OMNI-290	OMNI-291
	sgRNA V1 sequence	GUUGUAGUUCCCUUUCAGUgaaa ACUGCAAGGUUGCUACAAUAAGGUAGUAUACCGCA AAGCUCUGGCGCUCUGCUU UUGCAGGGCGCCAUCUUUU UU (SEQ ID NO: 634)	GUUGUAGCUCUCCUGACAGUgaaaA CUGUCAUGGUUGCUACAAUAG GUAGUAUACCGUAAAGCUCUGA CGCCUGCUUGCAGGGCGUCAU CUUUUUUU (SEQ ID NO: 652)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGUUCCCUUUCAGU (SEQ ID NO: 635)	GUUGUAGCUCUCCUGACAGU (SEQ ID NO: 653)
	Partial crRNA 1	GUUGUAGUUCCCUUU (SEQ ID NO: 636)	GUUGUAGCUCUCCUGA (SEQ ID NO: 654)
	Partial crRNA 2	GUUGUAGUUCCC (SEQ ID NO: 637)	GUUGUAGCUCUCCC (SEQ ID NO: 655)
	Partial crRNA 3	GUUGUAGUUC (SEQ ID NO: 638)	GUUGUAGCUC (SEQ ID NO: 656)
	tracrRNA (Antirepeat)	ACUGCAAGGUUGCUACAAU (SEQ ID NO: 639)	ACUGUCAUGGUUGCUACAAU (SEQ ID NO: 657)
	Partial tracrRNA 1	CAAGGUUGCUACAAU (SEQ ID NO: 640)	UCAUGGUUGCUACAAU (SEQ ID NO: 658)
	Partial tracrRNA 2	GGUUGCUACAAU (SEQ ID NO: 641)	UGGUUGCUACAAU (SEQ ID NO: 659)

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	Partial tracrRNA 3	UUGCUACAAU (SEQ ID NO: 642)	UUGCUACAAU (SEQ ID NO: 660)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUAGUAUACCGC (SEQ ID NO: 643)	AAGGUAGUAUACCGU (SEQ ID NO: 661)
	tracrRNA Portion 1 - partial	AAGGUAGUAUACC (SEQ ID NO: 644)	AAGGUAGUAUACC (SEQ ID NO: 662)
	tracrRNA Portion 2	AAAGCUCUGGGCGCUCUGCUUUUGCAGGGCGCCAUCUUUU (SEQ ID NO: 645)	AAAGCUCUGACGCCCUGCUUGCAGGGCGUCAUCUUUUUUU (SEQ ID NO: 663)
	tracrRNA Portion 2 - partial	AAAGCUCUGGGCGCUCUGCUUUUGCAGGGCGCCAUCUUU (SEQ ID NO: 646)	AAAGCUCUGACGCCCUGCUUGCAGGGCGUCAUCUUU (SEQ ID NO: 664)
	tracrRNA Portion 2 – without polyT	AAAGCUCUGGGCGCUCUGCUUUUGCAGGGCGCCAUC (SEQ ID NO: 647)	AAAGCUCUGACGCCCUGCUUGCAGGGCGUCAUC (SEQ ID NO: 665)
tracrRNA V2 sequences	sgRNA V2 sequence	GUUGUAGUUCCCUUUCAGUgaaaACUGCAAGGUUGCUACAAUAAGGUAGUAUACCGCAAAGCUCUGGGCGCUCUGCUUCUGCAGGGCGCCAUCUUUUU (SEQ ID NO: 648)	-
	tracrRNA Portion 2	AAAGCUCUGGGCGCUCUGCUUCUGCAGGGCGCCAUCUUUUU (SEQ ID NO: 649)	-
	tracrRNA Portion 2 - partial	AAAGCUCUGGGCGCUCUGCUUCUGCAGGGCGCCAUCUUU (SEQ ID NO: 650)	-
	tracrRNA Portion 2 – without polyT	AAAGCUCUGGGCGCUCUGCUUCUGCAGGGCGCCAUC (SEQ ID NO: 651)	-

		OMNI-293	OMNI-294
	sgRNA V1 sequence	AUUGUAGUUCCCUAAUUUUUgaaaACAAAUAAGGUUGCUACAAAAAGGUAGAAAACCGAAAGCUCUGACGGCUCCUUUUGGAGCCGUUAUCUUUUU (SEQ ID NO: 666)	GUUGUAGUUCCCUAGACAGUgaaaACUGUUAUGGUUACUACAAUAAAGGUAGUACACCGUAGAGCUCUGACGCCCUGCUCGCAGGGCGUCAUCUUUUUUU (SEQ ID NO: 684)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	AUUGUAGUUCCCUAAUUUUU (SEQ ID NO: 667)	GUUGUAGUUCCCUAGACAGU (SEQ ID NO: 685)
	Partial crRNA 1	AUUGUAGUUCCCUAA (SEQ ID NO: 668)	GUUGUAGUUCCCUGA (SEQ ID NO: 686)

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	Partial crRNA 2	AUUGUAGUCCCC (SEQ ID NO: 669)	GUUGUAGUCCCC (SEQ ID NO: 687)
	Partial crRNA 3	AUUGUAGUUC (SEQ ID NO: 670)	GUUGUAGUUC (SEQ ID NO: 688)
	tracrRNA (Antirepeat)	ACAAAUUAGGUUGCUACAA (SEQ ID NO: 671)	ACUGUUAUGGUUACUACAAU (SEQ ID NO: 689)
	Partial tracrRNA 1	UUAGGUUGCUACAA (SEQ ID NO: 672)	UUAUGGUUACUACAAU (SEQ ID NO: 690)
	Partial tracrRNA 2	GGUUGCUACAA (SEQ ID NO: 673)	UGGUUACUACAAU (SEQ ID NO: 691)
	Partial tracrRNA 3	UUGCUACAA	UUACUACAAU (SEQ ID NO: 692)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGGUAGAAAACC (SEQ ID NO: 674)	AAGGUAGUACACCGUAGAGCUC (SEQ ID NO: 693)
	tracrRNA Portion 1 - partial	AAAGGUAGAAAACC (SEQ ID NO: 675)	AAGGUAGUACACCGUAGAGCU (SEQ ID NO: 694)
	tracrRNA Portion 2	GAAAAGCUCUGACGGCUCC UUUUUGGAGCCGUUAUCUU UUUU (SEQ ID NO: 676)	UGACGCCCUGCUCGCAGGGCGU CAUCUUUUUUU (SEQ ID NO: 695)
	tracrRNA Portion 2 - partial	GAAAAGCUCUGACGGCUCC UUUUUGGAGCCGUUAUCUU UUU (SEQ ID NO: 677)	UGACGCCCUGCUCGCAGGGCGU CA (SEQ ID NO: 696)
	tracrRNA Portion 2 – without polyT	GAAAAGCUCUGACGGCUCC UUUUUGGAGCCGUUAUC (SEQ ID NO: 678)	UGACGCCCUGCUCGCAGGGCGU CAUC (SEQ ID NO: 697)
	sgRNA V2 sequence	AUUGUAGUCCCCUAAUUUC gaaaACAAAUUAGGUUGCUA CAAAAAGGUAGAAAACCGA AAAGCUCUGACGGCUCCUU CUUGGAGCCGUUAUCUUUU UU (SEQ ID NO: 679)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	AUUGUAGUCCCCUAAUUUC (SEQ ID NO: 680)	-
tracrRNA V2 sequences	tracrRNA Portion 2	GAAAAGCUCUGACGGCUCC UUCUUGGAGCCGUUAUCUU UUUU (SEQ ID NO: 681)	-
	tracrRNA Portion 2 - partial	GAAAAGCUCUGACGGCUCC UUCUUGGAGCCGUUAUCUU UUU (SEQ ID NO: 682)	-
	tracrRNA Portion 2 – without polyT	GAAAAGCUCUGACGGCUCC UUCUUGGAGCCGUUAUC (SEQ ID NO: 683)	-

		OMNI-293	OMNI-294
	sgRNA V3 sequence	-	GUUGUAGUCCCCUGACAGU _{gaaa} ACUGUUAUGGUUACUACAAUAA GGUAGUACACCGUAGAGCUCUG ACGCCCUGCUCGCAGGGCGUCA UCUUUUUUUACAGUAAUUUUUU (SEQ ID NO: 698)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGGUAGUACACC (SEQ ID NO: 699)
	tracrRNA Portion 1 - partial	-	AAGGUAGUACACC (SEQ ID NO: 700)
	tracrRNA Portion 2	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUUUUUAC AGUAAUUUUUU (SEQ ID NO: 701)
	tracrRNA Portion 2 - partial	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUUUUUAC (SEQ ID NO: 702)
	tracrRNA Portion 2 – without polyT	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUUUUUAC AGUAA (SEQ ID NO: 703)
	sgRNA V4 sequence	-	GUUGUAGUCCCCUGACAGU _{gaaa} ACUGUUAUGGUUACUACAAUAA GGUAGUACACCGUAGAGCUCUG ACGCCCUGCUCGCAGGGCGUCA UCUUUCUUUACAGUAAUUUUUU (SEQ ID NO: 704)
	tracrRNA Portion 2	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUCUUUAC AGUAAUUUUUU (SEQ ID NO: 705)
	tracrRNA Portion 2 - partial	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUCUUUAC (SEQ ID NO: 706)
	tracrRNA Portion 2 – without polyT	-	GUAGAGCUCUGACGCCCUGCUC GCAGGGCGUCAUCUUUCUUUAC AGUAA (SEQ ID NO: 707)

		OMNI-295	OMNI-296
	sgRNA V1 sequence	GUUUUAGUCCCUUGUU _{gaaa} AACAAGGGACUAAAAUAAG GGGAGUGGGCAUCCCGCAG GGUGAUGCUUGUGUCAAGG GGCAAGCUAGUCAAUCCC UAAGCCACCCGCAUUUUU U (SEQ ID NO: 708)	GUUAUAGUCCCCGAUUAU _{gaaa} AGUAAUUGGUUUCUAUAAUAAU CAUUGUUAUUGAUUGUAAGAAU CAAUGAAGAGUAAAGUAUCCCC CUUGUUCUUGGAGCAAGGGGUA UCUUUUUU (SEQ ID NO: 729)
	crRNA (Repeat)	GUUUUAGUCCCUUGUU (SEQ ID NO: 709)	GUUAUAGUCCCCGAUUAU (SEQ ID NO: 730)

		OMNI-295	OMNI-296
crRNA:tracrRNA duplex V1 sequences	Partial crRNA 1	GUUUUAGUCCCUUGU (SEQ ID NO: 710)	GUUAUAGUCCCCGAU (SEQ ID NO: 731)
	Partial crRNA 2	GUUUUAGUCCCU (SEQ ID NO: 711)	GUUAUAGUCCCC (SEQ ID NO: 732)
	Partial crRNA 3	GUUUUAGUCC (SEQ ID NO: 712)	GUUAUAGUUC (SEQ ID NO: 733)
	tracrRNA (Antirepeat)	AACAAGGGACUAAAAU (SEQ ID NO: 713)	AGUAAUUGGUUUCUAUAAU (SEQ ID NO: 734)
	Partial tracrRNA 1	ACAAGGGACUAAAAU (SEQ ID NO: 714)	AUUGGUUUCUAUAAU (SEQ ID NO: 735)
	Partial tracrRNA 2	AGGGACUAAAAU (SEQ ID NO: 715)	GGUUUCUAUAAU (SEQ ID NO: 736)
	Partial tracrRNA 3	GGACUAAAAU (SEQ ID NO: 716)	UUUCUAUAAU (SEQ ID NO: 737)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGGGAGUGGGCAUCCCG CAGGGUGAUGCUUGUGUCA AGGGGGCAAGCUAGUCAAU CCCUAAGCCCACCCGCAUU UUUU (SEQ ID NO: 717)	AAUCAUUGUUAUUGAUUGUAAG AAUCAAUGAAGAGU (SEQ ID NO: 738)
	tracrRNA Portion 1 - partial	GGGGAGUGGGCAUCCCGCA GGGUGAUGCUUGUGUCAAG GGGGCAAGCUAGUCAAUCC CUAAGCCCACCCGC (SEQ ID NO: 718)	AAUCAUUGUUAUUGAUUGUAAG AAUCAAUGA (SEQ ID NO: 739)
	tracrRNA Portion 1 - without polyT	AAGGGGAGUGGGCAUCCCG CAGGGUGAUGCUUGUGUCA AGGGGGCAAGCUAGUCAAU CCCUAAGCCCACCCGCA (SEQ ID NO: 719)	-
	tracrRNA Portion 2	-	AAAGUAUCCCCUUGUUCUUGG AGCAAGGGGU AUCUUUUU (SEQ ID NO: 740)
	tracrRNA Portion 2 - partial	-	AAAGUAUCCCCUUGUUCUUGG AGCAAGGGGU AUCUUU (SEQ ID NO: 741)
	tracrRNA Portion 2 – without polyT	-	AAAGUAUCCCCUUGUUCUUGG AGCAAGGGGU AUC (SEQ ID NO: 742)
	sgRNA V2 sequence	GUUCUAGUCCCUUGUUGaaa AACAAGGGACUAGAAUAAG GGGAGUGGGCAUCCCGCAG GGUGAUGCUUGUGUCAAGG GGGCAAGCUAGUCAAUCCC UAAGCCCACCCGCAUUUUU U (SEQ ID NO: 720)	-

		OMNI-295	OMNI-296
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGUCCCUUGUU (SEQ ID NO: 721)	-
	Partial crRNA 1	GUUCUAGUCCCUUGU (SEQ ID NO: 722)	-
	Partial crRNA 2	GUUCUAGUCCCU (SEQ ID NO: 723)	-
	Partial crRNA 3	GUUCUAGUCC (SEQ ID NO: 724)	-
	tracrRNA (Antirepeat)	AACAAGGGACUAGAAU (SEQ ID NO: 725)	-
	Partial tracrRNA 1	ACAAGGGACUAGAAU (SEQ ID NO: 726)	-
	Partial tracrRNA 2	AGGGACUAGAAU (SEQ ID NO: 727)	-
	Partial tracrRNA 3	GGACUAGAAU (SEQ ID NO: 728)	-

		OMNI-297	OMNI-298
	sgRNA V1 sequence	GUUGUAGUCCCUUGAUUGGUGAAAACUGCUCAGGUUACUAGAUAAAGGUAGUAAACCGAAGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUUAACAUUUUUU (SEQ ID NO: 743)	GUUGUAAUCCCUAAUAUUGAAA GAUAAUAGGUAAUACAAUAGGUCCAACAGGAGUGUUGGUACCGUAAGGCUCUGACGGUACGUCUAUUGGCGUACCGUCAUCCUUUUU (SEQ ID NO: 762)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGUCCCUUGAUUGGUG (SEQ ID NO: 744)	GUUGUAAUCCCUAAUAUUG (SEQ ID NO: 763)
	Partial crRNA 1	GUUGUAGUCCCUUGA (SEQ ID NO: 745)	GUUGUAAUCCCUAA (SEQ ID NO: 764)
	Partial crRNA 2	GUUGUAGUCCC (SEQ ID NO: 746)	GUUGUAAUCCC (SEQ ID NO: 765)
	Partial crRNA 3	GUUGUAGUUC (SEQ ID NO: 747)	GUUGUAAUUC (SEQ ID NO: 766)
	tracrRNA (Antirepeat)	ACUGCUCAGGUUACUAGAU (SEQ ID NO: 748)	GAUAAUAGGUAAUACAAU (SEQ ID NO: 767)
	Partial tracrRNA 1	CUCAGGUUACUAGAU (SEQ ID NO: 749)	UUAGGUAAUACAAU (SEQ ID NO: 768)

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	Partial tracrRNA 2	GGUUACUAUGAU (SEQ ID NO: 750)	GGUUAUUACAAU (SEQ ID NO: 769)
	Partial tracrRNA 3	UUACUAUGAU (SEQ ID NO: 751)	UUAUUACAAU (SEQ ID NO: 770)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUAGUAAACCGA (SEQ ID NO: 752)	AAGGUCCAACAGGAGUGUUGGUACCGU (SEQ ID NO: 771)
	tracrRNA Portion 1 - partial	AAGGUAGUAAACC (SEQ ID NO: 753)	AAGGUCCAACAGGAGUGUUGGUACC (SEQ ID NO: 772)
	tracrRNA Portion 2	AGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUCUAACA UUUUUU (SEQ ID NO: 754)	AAGGCUCUGACGGUACGUCUAUUGGCGUACCGUCAUCCUUUUU (SEQ ID NO: 773)
	tracrRNA Portion 2 - partial	AGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUCU (SEQ ID NO: 755)	AAGGCUCUGACGGUACGUCUAUUGGCGUACCGUCAUCCUU (SEQ ID NO: 774)
	tracrRNA Portion 2 – without polyT	AGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUCUAACA (SEQ ID NO: 756)	AAGGCUCUGACGGUACGUCUAUUGGCGUACCGUCAUCC (SEQ ID NO: 775)
tracrRNA V3 sequences	sgRNA V3 sequence	GUUGUAGUUCCUGAUGGUgaaaACUGCUCAGGUUACUAUGAUAAAGGUAGUAAACCGAAGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUCUAACAGCGAAAAGGCAAAU UUUUU (SEQ ID NO: 757)	-
	tracrRNA Portion 2	AGAGCUCUAAUGCCCCGUCUCGCACGGGGCAUUAUCUCUAACA (SEQ ID NO: 758)	-
	tracrRNA Portion 3	GCGAAAAGGCAAAUUUUUU (SEQ ID NO: 759)	-
	tracrRNA Portion 3 - partial	GCGAAAAGGC (SEQ ID NO: 760)	-
	tracrRNA Portion 3 - without polyT	GCGAAAAGGCAAA (SEQ ID NO: 761)	-

		OMNI-299	OMNI-300
	sgRNA V1 sequence	GUUGUAGCUCUCCUGUUAGUgaaaACUAAAUAGGUUGCUAUGAUAAAGGUCAUAGGACCGCAAAGCUCUGGCGCUCCGC UUCGGCGGAGCGCCAUCUU UUUU (SEQ ID NO: 776)	GUUGUAGCUCUCCUGGUAGUgaaaACUAUCAGGUUGCUAUGAUAAAGGUUACUUAUCGUAGUAUACCGCAGAGCUCUGACGAUCGGUUUACCGAUCGUCAUCUUUGUAU

		OMNI-299	OMNI-300
			CUCCACUUUUUU (SEQ ID NO: 799)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGCUCCUGUUAGU (SEQ ID NO: 777)	GUUGUAGCUCCUGGUAGU (SEQ ID NO: 800)
	Partial crRNA 1	GUUGUAGCUCCUGU (SEQ ID NO: 778)	GUUGUAGCUCCUGG (SEQ ID NO: 801)
	Partial crRNA 2	GUUGUAGCUCCC (SEQ ID NO: 779)	GUUGUAGCUCCC (SEQ ID NO: 802)
	Partial crRNA 3	GUUGUAGCUC (SEQ ID NO: 780)	GUUGUAGCUC (SEQ ID NO: 803)
	tracrRNA (Antirepeat)	ACUAAAUAGGUUGCUGAUGAU (SEQ ID NO: 781)	ACUAUCAGGUUGCUGAUGAU (SEQ ID NO: 804)
	Partial tracrRNA 1	AAUAGGUUGCUGAUGAU (SEQ ID NO: 782)	UCAGGUUGCUGAUGAU (SEQ ID NO: 805)
	Partial tracrRNA 2	GGUUGCUGAUGAU (SEQ ID NO: 783)	GGUUGCUGAUGAU (SEQ ID NO: 806)
	Partial tracrRNA 3	UUGCUGAUGAU (SEQ ID NO: 784)	UUGCUGAUGAU (SEQ ID NO: 807)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUCAUAGGACCGC (SEQ ID NO: 785)	AAGGUUACUACUUAUCGUAGUAUACC (SEQ ID NO: 808)
	tracrRNA Portion 1 - partial	AAGGUCAUAGGACC (SEQ ID NO: 786)	AAGGUUACUACUUAUCGUAGUAUACC (SEQ ID NO: 809)
	tracrRNA Portion 2	AAAGCUCUGGCGCUCCGCUUCGGCGGAGCGCCAUCUUUU (SEQ ID NO: 787)	GCAGAGCUCUGACGAUCGGUUUUUACCGAUCGUCAUCUUUGUAUCUCCACUUUUUU (SEQ ID NO: 810)
	tracrRNA Portion 2 - partial	AAAGCUCUGGCGCUCCGCUUCGGCGGAGCGCCAUCUUUU (SEQ ID NO: 788)	GCAGAGCUCUGACGAUCGGUUUUUACCGAUCGUCAUCUUUGU (SEQ ID NO: 811)
	tracrRNA Portion 2 – without polyT	AAAGCUCUGGCGCUCCGCUUCGGCGGAGCGCCAUC (SEQ ID NO: 789)	GCAGAGCUCUGACGAUCGGUUUUUACCGAUCGUCAUCUUUGUAUCUCCAC (SEQ ID NO: 812)
	sgRNA V2 sequence	-	GUUGUAGCUCCUGGUAGU ^{gaaa} ACUAUCAGGUUGCUGAUGAU ^{AAG} GUUACUACUUAUCGUAGUAU ^{AC} CGCAGAGCUCUGACGAUCGGUUCUACCGAUCGUCAUCUUUGUAUCUCCACUUUUUU (SEQ ID NO: 813)
tracrRNA V2 sequences	tracrRNA Portion 2	-	GCAGAGCUCUGACGAUCGGUUCUACCGAUCGUCAUCUUUGUAUCUCCACUUUUUU (SEQ ID NO: 814)

		OMNI-299	OMNI-300
	tracrRNA Portion 2 - partial	-	GCAGAGCUCUGACGAUCGGUUC UACCGAUCGUCAUCUUUGU (SEQ ID NO: 815)
	tracrRNA Portion 2 – without polyT	-	GCAGAGCUCUGACGAUCGGUUC UACCGAUCGUCAUCUUUGUAUC UCCAC (SEQ ID NO: 816)
	sgRNA V3 sequence	GUUGUAGCUCCUGUUAGU gaaaACUAAAUAGGUUGCUA UGAUAAGGUCAUAGGACCG CAAAGCUCUGGCGCUCCGC UUCGGCGGAGCGCCAUCUU UUUUGCUCAUUUUUU (SEQ ID NO: 790)	-
tracrRNA V3 sequences	tracrRNA Portion 1	AAGGUCAUAGGACC (SEQ ID NO: 791)	-
	tracrRNA Portion 2	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UUUUUGCUCAUUUUUU (SEQ ID NO: 792)	-
	tracrRNA Portion 2 - partial	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UUUUUGC (SEQ ID NO: 793)	-
	tracrRNA Portion 2 – without polyT	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UUUUUGCUCA (SEQ ID NO: 794)	-
	sgRNA V4 sequence	GUUGUAGCUCCUGUUAGU gaaaACUAAAUAGGUUGCUA UGAUAAGGUCAUAGGACCG CAAAGCUCUGGCGCUCCGC UUCGGCGGAGCGCCAUCUU CUUUGCUCAUUUUUU (SEQ ID NO: 795)	-
tracrRNA V4 sequences	tracrRNA Portion 2	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UCUUUGCUCAUUUUUU (SEQ ID NO: 796)	-
	tracrRNA Portion 2 - partial	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UCUUUGC (SEQ ID NO: 797)	-
	tracrRNA Portion 2 – without polyT	GCAAAGCUCUGGCGCUCCG CUUCGGCGGAGCGCCAUCU UCUUUGCUCA (SEQ ID NO: 798)	-

		OMNI-301	OMNI-302
	sgRNA V1 sequence	GUUGUAGUUCCCGACGGU gaaaACUGUUAGGUUACUAC GAUAAGGUUACUACCUUGU GUAGUAUACCGCAAAGCUC UAGCGCCUCGCUUUAUGCG GGGCGCUAUCUUUAUUUUU U (SEQ ID NO: 817)	GUUGUAGUUCCCCGGUAGUgaaa ACUAUCGGGUUACUAUGAUAAAG GUAGUAAACCGAAGAGCUCUGA CGCCUCGCAUUUCGUGGGGCGU UAUCUCUUUAUGGGGCGGUUUG CAUAACGAGAGAAUUGGUUCAG GAGGGAUCAAGAUUUUUU (SEQ ID NO: 831)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGUUCCCGACGGU (SEQ ID NO: 818)	GUUGUAGUUCCCCGGUAGU (SEQ ID NO: 832)
	Partial crRNA 1	GUUGUAGUUCCCGA (SEQ ID NO: 819)	GUUGUAGUUCCCCGG (SEQ ID NO: 833)
	Partial crRNA 2	GUUGUAGUUCCC (SEQ ID NO: 820)	GUUGUAGUUCCC (SEQ ID NO: 834)
	Partial crRNA 3	GUUGUAGUUC (SEQ ID NO: 821)	GUUGUAGUUC (SEQ ID NO: 835)
	tracrRNA (Antirepeat)	ACUGUUAGGUUACUACGAU (SEQ ID NO: 822)	ACUAUCGGGUUACUAUGAU (SEQ ID NO: 836)
	Partial tracrRNA 1	UUAGGUUACUACGAU (SEQ ID NO: 823)	UCGGGUUACUAUGAU (SEQ ID NO: 837)
	Partial tracrRNA 2	GGUUACUACGAU (SEQ ID NO: 824)	GGUUACUAUGAU (SEQ ID NO: 838)
	Partial tracrRNA 3	UUACUACGAU (SEQ ID NO: 825)	UUACUAUGAU (SEQ ID NO: 839)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUUACUACCUUGUGUA GUAUACCGC (SEQ ID NO: 826)	AAGGUAGUAAACCGAAGAGCUC UGACGCCUCGCAUUUCGUGGGG CGUUAUCUCUUUAUGGGGCGGU UUGCAUAAC (SEQ ID NO: 840)
	tracrRNA Portion 1 - partial	AAGGUUACUACCUUGUGUA GUAUACC (SEQ ID NO: 827)	AAGGUAGUAAACCGAAGAGCUC UGACGCCUCGCAUUUCGUGGGG CGUUAUCUCUUUAUGGGGCGGU UUGC (SEQ ID NO: 841)
	tracrRNA Portion 2	AAAGCUCUAGCGCCUCGCU UUAUGCGGGGCGCUAUCUU UAUUUUUU (SEQ ID NO: 828)	GAGAGAAUUGGUUCAGGAGGGA UCAAGAUUUUUU (SEQ ID NO: 842)
	tracrRNA Portion 2 - partial	AAAGCUCUAGCGCCUCGCU UUAUGCGGGGCGCUAUCUU U (SEQ ID NO: 829)	GAGAGAAUUGGUUCAGGAGGGA UCAAGAUUUUUU (SEQ ID NO: 843)
	tracrRNA Portion 2 – without polyT	AAAGCUCUAGCGCCUCGCU UUAUGCGGGGCGCUAUCUU UA (SEQ ID NO: 830)	GAGAGAAUUGGUUCAGGAGGGA UCAAGA (SEQ ID NO: 844)

		OMNI-303	OMNI-304
	sgRNA V1 sequence	GUUGUAGCUCCCUAACAGU gaaaACUAAUAGGUUGCUAU GAUAAGGUUACUGCUUUAU UGUAGUAUACCGCAAAGCU CUGACGAUCGAUUUUUAUCG GUCGUCAUCUUCAUUUUU UU (SEQ ID NO: 845)	GUUUUAGCUCUCUGAUGA gaaaU CAUCAGAGUUCUAAGACAAGGC AGAAUGCCGUAGGGUAGUGGAA ACCCAAAACACCACACUGAGCA AUCUAAACGAUUGCUCUUUUUU (SEQ ID NO: 863)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGCUCCCUAACAGU (SEQ ID NO: 846)	GUUUUAGCUCUCUGAUGA (SEQ ID NO: 864)
	Partial crRNA 1	GUUGUAGCUCCCUAA (SEQ ID NO: 847)	GUUUUAGCUCUCUGA (SEQ ID NO: 865)
	Partial crRNA 2	GUUGUAGCUCCC (SEQ ID NO: 848)	GUUUUAGCUCUC (SEQ ID NO: 866)
	Partial crRNA 3	GUUGUAGCUC (SEQ ID NO: 849)	GUUUUAGCUC (SEQ ID NO: 867)
	tracrRNA (Antirepeat)	ACUAAUAGGUUGCUAUGAU (SEQ ID NO: 850)	UCAUCAGAGUUCUAAGAC (SEQ ID NO: 868)
	Partial tracrRNA 1	ACUAAUAGGUUGCUAUGAU (SEQ ID NO: 851)	UCAGAGUUCUAAGAC (SEQ ID NO: 869)
	Partial tracrRNA 2	GGUUGCUAUGAU (SEQ ID NO: 852)	GAGUUCUAAGAC (SEQ ID NO: 870)
	Partial tracrRNA 3	UUGCUAUGAU (SEQ ID NO: 853)	GUUCUAAGAC (SEQ ID NO: 871)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUUACUGCUUUAAUUGU AGUAUACCGCAAAGCUC (SEQ ID NO: 854)	AAGGCAGAAUGCC (SEQ ID NO: 872)
	tracrRNA Portion 1 - partial	AAGGUUACUGCUUUAAUUGU AGUAUACC (SEQ ID NO: 855)	AAGGCAGAAUGCC (SEQ ID NO: 873)
	tracrRNA Portion 2	UGACGAUCGAUUUUUAUCGG UCGUCAUCUUCAUUUUUU U (SEQ ID NO: 856)	GUAGGGUAGUGGAAACCCAAA CACCACACU (SEQ ID NO: 874)
	tracrRNA Portion 2 - partial	UGACGAUCGAUUUUUAUCGG UCGUCA (SEQ ID NO: 857)	GUAGGGUAGUGGAAACCCAAA CACCAC (SEQ ID NO: 875)
	tracrRNA Portion 2 – without polyT	UGACGAUCGAUUUUUAUCGG UCGUCAUCUUCAU (SEQ ID NO: 858)	-
	tracrRNA Portion 3	-	GAGCAAUCUAAACGAUUGCUCUU UUUU (SEQ ID NO: 876)
	tracrRNA Portion 3 - partial	-	GAGCAAUCUAAACGAUUGCUC (SEQ ID NO: 877)

		OMNI-303	OMNI-304
	tracrRNA Portion 3 - without polyT	-	GAGCAAUCUAACGAUUGCUC (SEQ ID NO: 878)
	sgRNA V2 sequence	GUUGUAGCUCCCUAACAGU gaaaACUAUUAGGUUGCUAU GAUAAGGUUACUGCUUUAU UGUAGUAUACCGCAAAGCU CUGACGAUCGAUUCUAUCG GUCGUCAUCUUCUAUUUUU UU (SEQ ID NO: 859)	GUCUUAGCUCUCUGAUGA AUCAGAGUUCUAAGACAAGGCA GAAUGCCGUAGGUAGUGGAAA CCCAAAACACCACACUGAGCAA UCUAACGAUUGCUCUUUUUU (SEQ ID NO: 879)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GUCUUAGCUCUCUGAUGA (SEQ ID NO: 880)
	Partial crRNA 1	-	GUCUUAGCUCUCUGA (SEQ ID NO: 881)
	Partial crRNA 2	-	GUCUUAGCUCUC (SEQ ID NO: 882)
	Partial crRNA 3	-	GUCUUAGCUC (SEQ ID NO: 883)
tracrRNA V2 sequences	tracrRNA Portion 2	UGACGAUCGAUUCUAUCGG UCGUCAUCUUCUAUUUUU U (SEQ ID NO: 860)	-
	tracrRNA Portion 2 - partial	UGACGAUCGAUUCUAUCGG UCGUCA (SEQ ID NO: 861)	-
	tracrRNA Portion 2 – without polyT	UGACGAUCGAUUCUAUCGG UCGUCAUCUUCUAU (SEQ ID NO: 862)	-

		OMNI-305	OMNI-307
	sgRNA V1 sequence	AUUGUAGUCCCUAAUUUU gaaaACAAUUAGGUUACUAC AAACAAGGUAGAAAACCGAA AAGCUCUGACGGUUCACUU UUUUGGUGGGCCGUCAUCU UUUUU (SEQ ID NO: 884)	GUUUGAGAGUCUUGUU AACAAGACGAGUUCAAAUAAA AUUUAUUCUAACCACUUGUUCG CAUUGGCGACGCGCUCUCUUCG GAGAGCUUUUUU (SEQ ID NO: 902)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	AUUGUAGUCCCUAAUUUU (SEQ ID NO: 885)	GUUUGAGAGUCUUGUUA (SEQ ID NO: 903)
	Partial crRNA 1	AUUGUAGUCCCUAA (SEQ ID NO: 886)	GUUUGAGAGUCUUGU (SEQ ID NO: 904)
	Partial crRNA 2	AUUGUAGUCCC (SEQ ID NO: 887)	GUUUGAGAGUCU (SEQ ID NO: 905)

		OMNI-305	OMNI-307
	Partial crRNA 3	AUUGUAGUUC (SEQ ID NO: 888)	GUUUGAGAGU (SEQ ID NO: 906)
	tracrRNA (Antirepeat)	ACAAUUAGGUUACUACAA (SEQ ID NO: 889)	UAAACAAGACGAGUUCAAAU (SEQ ID NO: 907)
	Partial tracrRNA 1	UUAGGUUACUACAA (SEQ ID NO: 890)	ACAAGACGAGUUCAAAU (SEQ ID NO: 908)
	Partial tracrRNA 2	GGUUACUACAA (SEQ ID NO: 891)	AGACGAGUUCAAAU (SEQ ID NO: 909)
	Partial tracrRNA 3	UUACUACAA	ACGAGUUCAAAU (SEQ ID NO: 910)
tracrRNA V1 sequences	tracrRNA Portion 1	CAAGGUAGAAAACC (SEQ ID NO: 892)	AAAAAUUUUUAUUCUAACCACUUG UUCGCAUUGGCGACGC (SEQ ID NO: 911)
	tracrRNA Portion 1 - partial	CAAGGUAGAAAACC (SEQ ID NO: 893)	AAAAAUUUUUAUUCUAACCACUUG UUCGCAUUGGCGACGC (SEQ ID NO: 912)
	tracrRNA Portion 2	GAAAAGCUCUGACGGUUCA CUUUUUUGGUGGGCCGUCA UCUUUUUU (SEQ ID NO: 894)	GCUCUCUUCGGAGAGCUUUUUU (SEQ ID NO: 913)
	tracrRNA Portion 2 - partial	GAAAAGCUCUGACGGUUCA CUUUUUUGGUGGGCCGUCA UCUUUUUU (SEQ ID NO: 895)	GCUCUCUUCGGAGAGC (SEQ ID NO: 914)
	tracrRNA Portion 2 – without polyT	GAAAAGCUCUGACGGUUCA CUUUUUUGGUGGGCCGUCA UC (SEQ ID NO: 896)	GCUCUCUUCGGAGAGC (SEQ ID NO: 915)
	sgRNA V2 sequence	AUUGUAGUCCCCUAAUUUC gaaaACAAUUAGGUUACUAC AACAAGGUAGAAAACCGAA AAGCUCUGACGGUUCACUU UCUUGGUGGGCCGUCAUCU UUUUU (SEQ ID NO: 897)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	AUUGUAGUCCCCUAAUUUC (SEQ ID NO: 898)	-
tracrRNA V2 sequences	tracrRNA Portion 2	GAAAAGCUCUGACGGUUCA CUUUCUUGGUGGGCCGUCA UCUUUUUU (SEQ ID NO: 899)	-
	tracrRNA Portion 2 - partial	GAAAAGCUCUGACGGUUCA CUUUCUUGGUGGGCCGUCA UCUUUUUU (SEQ ID NO: 900)	-
	tracrRNA Portion 2 – without polyT	GAAAAGCUCUGACGGUUCA CUUUCUUGGUGGGCCGUCA UC (SEQ ID NO: 901)	-

		OMNI-308	OMNI-309
	sgRNA V1 sequence	GUUGUAGUCCCCUAAUUUUU gaaaAUUAAUAGGUUACUAAU GAUAAGGUAGUACACCGAA AAGCUCUAAACGCUCUGUCU UGGACAGAGCGUUAUCUUU UUU (SEQ ID NO: 916)	GUUGUGGUUCCCUGUUCUUgaaa GAGAACAUUGUGUUACCGCAAUA AGGUAAAACACCACAAAGCACU GCCCCAGCCUAAACGGCUGGGGC AUCUUUGUAGAUAAAUAUUAGG CAAAGGAGCUGACAUCAUUUUU U (SEQ ID NO: 932)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUAGUCCCCUAAUUUUU (SEQ ID NO: 917)	GUUGUGGUUCCCUGUUCUU (SEQ ID NO: 933)
	Partial crRNA 1	GUUGUAGUCCCCUAA (SEQ ID NO: 918)	GUUGUGGUUCCCUGU (SEQ ID NO: 934)
	Partial crRNA 2	GUUGUAGUCCC (SEQ ID NO: 919)	GUUGUGGUUCCC (SEQ ID NO: 935)
	Partial crRNA 3	GUUGUAGUUC (SEQ ID NO: 920)	GUUGUGGUUC (SEQ ID NO: 936)
	tracrRNA (Antirepeat)	AUUAAUAGGUUACUAGAU (SEQ ID NO: 921)	GAGAACAUUGUGUUACCGCAAU (SEQ ID NO: 937)
	Partial tracrRNA 1	UUAGGUUACUAGAU (SEQ ID NO: 922)	ACAUGUGUUACCGCAAU (SEQ ID NO: 938)
	Partial tracrRNA 2	GGUUACUAGAU (SEQ ID NO: 923)	UGUGUUACCGCAAU (SEQ ID NO: 939)
	Partial tracrRNA 3	UUACUAGAU (SEQ ID NO: 924)	UUACCGCAAU (SEQ ID NO: 940)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUAGUACACC (SEQ ID NO: 925)	AAGGUAAAACACC (SEQ ID NO: 941)
	tracrRNA Portion 1 - partial	AAGGUAGUACACC (SEQ ID NO: 926)	AAGGUAAAACACC (SEQ ID NO: 942)
	tracrRNA Portion 2	GAAAAGCUCUAAACGCUCUG UCUUGGACAGAGCGUUAUC UUUUUU (SEQ ID NO: 927)	ACAAAGCACUGCCCCAGCCUAA CGGCUGGGGCAUCUUUGUAGAU AAAUAAUA (SEQ ID NO: 943)
	tracrRNA Portion 2 - partial	GAAAAGCUCUAAACGCUCUG UCUUGGACAGAGCGUUAUC UUUUU (SEQ ID NO: 928)	ACAAAGCACUGCCCCAGCCUAA CGGCUGGGGCAUCUUUGU (SEQ ID NO: 944)
	tracrRNA Portion 2 – without polyT	GAAAAGCUCUAAACGCUCUG UCUUGGACAGAGCGUUAUC (SEQ ID NO: 929)	-
	tracrRNA Portion 3	-	GGCAAAGGAGCUGACAUCAUUU UUU (SEQ ID NO: 945)
	tracrRNA Portion 3 - partial	-	GGCAAAGGAGCU (SEQ ID NO: 946)

		OMNI-308	OMNI-309
	tracrRNA Portion 3 - without polyT	-	GGCAAAGGAGCUGACAUCA (SEQ ID NO: 947)
	sgRNA V2 sequence	GUUGUAGUUCCCUAAUUCU gaaaAUUAUUAGGUUACU GAUAAGGUAGUACACCGAA AAGCUCUACGCUCUGUCU UGGACAGAGCGUUAUCUUU UUU (SEQ ID NO: 930)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUGUAGUUCCCUAAUUCU (SEQ ID NO: 931)	-

		OMNI-310	OMNI-311
	sgRNA V1 sequence	AUUUUAGUACCCGGAGAAA gaaaUUUCUUCGGACCUAUU AAAACAAGGCUUUAUGCCG AAAGUUUACUUUGAAGAAA UUAACAAAAAAGGCACCGA CGGUGCCUUUUUU (SEQ ID NO: 948)	GUUUUAGUACCUGGAAAAA gaaaUUUUUUCAGAUACUAAAA UUAAGGCUUUAUGCCGAAACU AAAGGACACCGACGGGUGUCCU UUUUU (SEQ ID NO: 963)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	AUUUUAGUACCCGGAGAAA (SEQ ID NO: 949)	GUUUUAGUACCUGGAAAAA (SEQ ID NO: 964)
	Partial crRNA 1	AUUUUAGUACCCGGA (SEQ ID NO: 950)	GUUUUAGUACCUGGA (SEQ ID NO: 965)
	Partial crRNA 2	AUUUUAGUACCC (SEQ ID NO: 951)	GUUUUAGUACCU (SEQ ID NO: 966)
	Partial crRNA 3	AUUUUAGUAC (SEQ ID NO: 952)	GUUUUAGUAC (SEQ ID NO: 967)
	tracrRNA (Antirepeat)	UUUCUUCGGACCUAUUAAA A (SEQ ID NO: 953)	UUUUUUCAGAUACUAAAAU (SEQ ID NO: 968)
	Partial tracrRNA 1	UUCGGACCUAUUAAAA (SEQ ID NO: 954)	UUCAGAUACUAAAAU (SEQ ID NO: 969)
	Partial tracrRNA 2	GGACCUAUUAAAA (SEQ ID NO: 955)	AGAUCUACUAAAAU (SEQ ID NO: 970)
	Partial tracrRNA 3	ACCUAUUAAAA (SEQ ID NO: 956)	AUCUACUAAAAU (SEQ ID NO: 971)
tracrRNA V1 sequences	tracrRNA Portion 1	CAAGGCUUUAUGCCG (SEQ ID NO: 957)	AAGGCUUUAUGCCGAAACU (SEQ ID NO: 972)

		OMNI-310	OMNI-311
	tracrRNA Portion 1 - partial	CAAGGCUUUAUGCC (SEQ ID NO: 958)	AAGGCUUUAUGCC (SEQ ID NO: 973)
	tracrRNA Portion 2	AAAGUUUACUUUGAAGAAA UUAAC (SEQ ID NO: 959)	AAAGGACACCGACGGGUGUCCU UUUUU (SEQ ID NO: 974)
	tracrRNA Portion 2 - partial	AAAGUUUACUUU (SEQ ID NO: 960)	AAAGGACACCGACGGGUGUCCU UU (SEQ ID NO: 975)
	tracrRNA Portion 2 – without polyT	-	AAAGGACACCGACGGGUGUCC (SEQ ID NO: 976)
	tracrRNA Portion 3	AAAAAAGGCACCGACGGGU GCCUUUUUU (SEQ ID NO: 961)	-
	tracrRNA Portion 3 - without polyT	AAAAAAGGCACCGACGGGU GCC (SEQ ID NO: 962)	-
	sgRNA V2 sequence	-	GUUCUAGUACCUGGAAGAAgaaa UUCUUUCAGAUACUAGAAUA AGGCUUUAUGCCGAAACUAAAG GACACCGACGGGUGUCCUUUUU U (SEQ ID NO: 977)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GUUCUAGUACCUGGAAGAA (SEQ ID NO: 978)
	Partial crRNA 1	-	GUUCUAGUACCUGGA (SEQ ID NO: 979)
	Partial crRNA 2	-	GUUCUAGUACCU (SEQ ID NO: 980)
	Partial crRNA 3	-	GUUCUAGUAC (SEQ ID NO: 981)
	tracrRNA (Antirepeat)	-	UUCUUUCAGAUACUAGAAU (SEQ ID NO: 982)
	Partial tracrRNA 1	-	UUCAGAUACUAGAAU (SEQ ID NO: 983)
	Partial tracrRNA 2	-	AGAUCUACUAGAAU (SEQ ID NO: 984)
	Partial tracrRNA 3	-	AUCUACUAGAAU (SEQ ID NO: 985)

		OMNI-312	OMNI-313
	sgRNA V1 sequence	GUUUUGCCUUGAAUCCgaaa GGAUUCAAGACAAAAUUUG AGAUGCAAACCGAUUUUCC UGACUGCAAGCCAGUCACA CCGGUAACAAGAGCAUUUU UUAAGACUGUCUCACUGUA GAAGUGAGGCAGUCUUUUU U (SEQ ID NO: 986)	GUUUUAGUUCCCUGAUGUUgaaa ACCAUCAGGUUACUAAGAUAAAG GUCUUAGUACCGCAAAGCUCUA ACACCUUGUUUCGGCAGGGUGU UAUCUUUUUUU (SEQ ID NO: 1011)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUGCCUUGAAUCC (SEQ ID NO: 987)	GUUUUAGUUCCCUGAUGUU (SEQ ID NO: 1012)
	Partial crRNA 1	GUUUUGCCUUGAAUC (SEQ ID NO: 988)	GUUUUAGUUCCCUGA (SEQ ID NO: 1013)
	Partial crRNA 2	GUUUUGCCUUGA (SEQ ID NO: 989)	GUUUUAGUUCCC (SEQ ID NO: 1014)
	Partial crRNA 3	GUUUUGCCUU (SEQ ID NO: 990)	GUUUUAGUUC (SEQ ID NO: 1015)
	tracrRNA (Antirepeat)	GGAUUCAAGACAAAAU (SEQ ID NO: 991)	ACCAUCAGGUUACUAAGAU (SEQ ID NO: 1016)
	Partial tracrRNA 1	GAUUCAAGACAAAAU (SEQ ID NO: 992)	UCAGGUUACUAAGAU (SEQ ID NO: 1017)
	Partial tracrRNA 2	UCAAGACAAAAU (SEQ ID NO: 993)	GGUUACUAAGAU (SEQ ID NO: 1018)
	Partial tracrRNA 3	AAGACAAAAU (SEQ ID NO: 994)	UUACUAAGAU (SEQ ID NO: 1019)
tracrRNA V1 sequences	tracrRNA Portion 1	UUGAGAUGCAAACCGAUUU UCCUGACUGCAAGCCAGUC ACACCGGUAACAAGAGCAU UUUUU (SEQ ID NO: 995)	AAGGUCUUAGUACCGC (SEQ ID NO: 1020)
	tracrRNA Portion 1 - partial	UUGAGAUGCAAACCGAUUU UCCUGACUGCAAGCCAGUC ACACCGGUAACAAGAGCAU UUU (SEQ ID NO: 996)	AAGGUCUUAGUACC (SEQ ID NO: 1021)
	tracrRNA Portion 2	AAGACUGUCUCACUGUAGA AGUGAGGCAGUCUUUUUU (SEQ ID NO: 997)	AAAGCUCUAACACCUUGUUUCG GCAGGGUGUUUUCUUUUUUU (SEQ ID NO: 1022)
	tracrRNA Portion 2 - partial	AAGACUGUCUCACUGUAGA AGUGAGGCAGUCUU (SEQ ID NO: 998)	AAAGCUCUAACACCUUGUUUCG GCAGGGUGUUUUCUUU (SEQ ID NO: 1023)
	tracrRNA Portion 2 – without polyT	AAGACUGUCUCACUGUAGA AGUGAGGCAGUC (SEQ ID NO: 999)	AAAGCUCUAACACCUUGUUUCG GCAGGGUGUUAUC (SEQ ID NO: 1024)
	sgRNA V2 sequence	GUUCUGCCUUGAAUCCgaaa GGAUUCAAGACAGAAUUUG AGAUGCAAACCGAUUCUCC	GUCUUAGUUCCCUGAUGUUgaaa ACCAUCAGGUUACUAAGAUAAAG GUCUUAGUACCGCAAAGCUCUA

		OMNI-312	OMNI-313
		UGACUGCAAGCCAGUCACA CCGGUAACAAGAGCAUUUC UUAAGACUGUCUCACUGUA GAAGUGAGGCAGUCUUUUU U (SEQ ID NO: 1000)	ACACCUUGUUUCGGCAGGGUGU UAUCUUUUUUU (SEQ ID NO: 1025)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUGCCUUGAAUCC (SEQ ID NO: 1001)	GUCUUAGUUCCCUGAUGUU (SEQ ID NO: 1026)
	Partial crRNA 1	GUUCUGCCUUGAAUC (SEQ ID NO: 1002)	GUCUUAGUUCCCUGA (SEQ ID NO: 1027)
	Partial crRNA 2	GUUCUGCCUUGA (SEQ ID NO: 1003)	GUCUUAGUUCCC (SEQ ID NO: 1028)
	Partial crRNA 3	GUUCUGCCUU (SEQ ID NO: 1004)	GUCUUAGUUC (SEQ ID NO: 1029)
	tracrRNA (Antirepeat)	GGAUUCAAGACAGAAU (SEQ ID NO: 1005)	-
	Partial tracrRNA 1	GAUUCAAGACAGAAU (SEQ ID NO: 1006)	-
	Partial tracrRNA 2	UCAAGACAGAAU (SEQ ID NO: 1007)	-
	Partial tracrRNA 3	AAGACAGAAU (SEQ ID NO: 1008)	-
tracrRNA V2 sequences	tracrRNA Portion 1	UUGAGAUGCAAACCGAUUC UCCUGACUGCAAGCCAGUC ACACCGGUAACAAGAGCAU UUCUU (SEQ ID NO: 1009)	-
	tracrRNA Portion 1 - partial	UUGAGAUGCAAACCGAUUC UCCUGACUGCAAGCCAGUC ACACCGGUAACAAGAGCAU UUC (SEQ ID NO: 1010)	-

		OMNI-314	OMNI-315
	sgRNA V1 sequence	AUUUUAGUUCCCUUUUAUU gaaaAACAAAAGGUUACUAA AACAAGGGAUUUAUCCCCG CAAAGCUCUAAUCCGACAA UAAACGUUGUCGGAUUAUC UUUUUU (SEQ ID NO: 1030)	GUUUUAGUUCUCUGAUGGgaaC CAUCA AUGAGUUCUAAGAU AAG GCAUAUGCCGUGGGGUAUGGU GGUAACCUCAAAAGCGAUCCAC CUUUGAUAAACGUACCGUCUGG UGCGUUUUUCUUUUUU (SEQ ID NO: 1051)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	AUUUUAGUUCCCUUUUAUU (SEQ ID NO: 1031)	GUUUUAGUUCUCUGAUGG (SEQ ID NO: 1052)
	Partial crRNA 1	AUUUUAGUUCCCUUU (SEQ ID NO: 1032)	GUUUUAGUUCUCUGA (SEQ ID NO: 1053)

		OMNI-314	OMNI-315
	Partial crRNA 2	AUUUUAGUCCCC (SEQ ID NO: 1033)	GUUUUAGUUCUC (SEQ ID NO: 1054)
	Partial crRNA 3	AUUUUAGUUC (SEQ ID NO: 1034)	GUUUUAGUUC (SEQ ID NO: 1055)
	tracrRNA (Antirepeat)	AACAAAAGGUUACUAAAA (SEQ ID NO: 1035)	CCAUCAAGAGUUCUAAGAU (SEQ ID NO: 1056)
	Partial tracrRNA 1	AAAGGUUACUAAAA (SEQ ID NO: 1036)	UCAAUGAGUUCUAAGAU (SEQ ID NO: 1057)
	Partial tracrRNA 2	GGUUACUAAAA (SEQ ID NO: 1037)	AUGAGUUCUAAGAU (SEQ ID NO: 1058)
	Partial tracrRNA 3	UUACUAAAA	GUUCUAAGAU (SEQ ID NO: 1059)
tracrRNA V1 sequences	tracrRNA Portion 1	CAAGGGAUUUAUCCCCG (SEQ ID NO: 1038)	AAGGCAAUAUGCCGUGGGGUAU (SEQ ID NO: 1060)
	tracrRNA Portion 1 - partial	CAAGGGAUUUAUCCCC (SEQ ID NO: 1039)	AAGGCAAUAUGCCGUGGGGUAU (SEQ ID NO: 1061)
	tracrRNA Portion 2	AAAGCUCUAAUCCGACAAU AAACGUUGUCGGAUUAUCU UUUUU (SEQ ID NO: 1040)	GGUGGUAACCUCAAAAGCGAUC CACCUUU (SEQ ID NO: 1062)
	tracrRNA Portion 2 - partial	AAAGCUCUAAUCCGACAAU AAACGUUGUCGGAUUAUCU UU (SEQ ID NO: 1041)	GGUGGUAACCUCAAAAGCGAUC CACC (SEQ ID NO: 1063)
	tracrRNA Portion 2 – without polyT	AAAGCUCUAAUCCGACAAU AAACGUUGUCGGAUUAUC (SEQ ID NO: 1042)	-
	tracrRNA Portion 3	-	GAUAAACGUACCGUCUGGUGCG UUUUUCUUUUUU (SEQ ID NO: 1064)
	tracrRNA Portion 3 - partial	-	GAUAAACGUACCGUCUGGUGCG UUUUUC (SEQ ID NO: 1065)
	tracrRNA Portion 3 - without polyT	-	GAUAAACGUACCGUCUGGUGCG UUUUUC (SEQ ID NO: 1066)
	sgRNA V2 sequence	AUUCUAGUCCCCUUCUAUU gaaaAACAGAAGGUUACUAG AACAAGGGAUUUAUCCCCG CAAAGCUCUAAUCCGACAA UAAACGUUGUCGGAUUAUC UUUUUU (SEQ ID NO: 1043)	GUCUUAGUUCUCUGAUGGgaaaCC AUCAAUGAGUUCUAAGAUAAGG CAAUAUGCCGUGGGGUAUGGUG GUAACCUCAAAAGCGAUCCACC UUUGAUAAACGUACCGUCUGGU GCGUUUCUCUUUUUU (SEQ ID NO: 1067)
	crRNA (Repeat)	AUUCUAGUCCCCUUCUAUU (SEQ ID NO: 1044)	GUCUUAGUUCUCUGAUGG (SEQ ID NO: 1068)

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crRNA:tracrRNA duplex V2 sequences	Partial crRNA 1	AUUCUAGUCCCUUC (SEQ ID NO: 1045)	GUCUUAGUUCUCUGA (SEQ ID NO: 1069)
	Partial crRNA 2	AUUCUAGUUC (SEQ ID NO: 1046)	GUCUUAGUUC (SEQ ID NO: 1070)
	Partial crRNA 3	AUUCUAGUUC (SEQ ID NO: 1047)	GUCUUAGUUC (SEQ ID NO: 1071)
	tracrRNA (Antirepeat)	AACAGAAGGUACUAGAA (SEQ ID NO: 1048)	-
	Partial tracrRNA 1	GAAGGUACUAGAA (SEQ ID NO: 1049)	-
	Partial tracrRNA 2	GGUUACUAGAA (SEQ ID NO: 1050)	-
	Partial tracrRNA 3	UUACUAGAA	-
tracrRNA V2 sequences	tracrRNA Portion 3	-	GAUAAACGUACCGUCUGGUGCG UUUCUCUUUUU (SEQ ID NO: 1072)
	tracrRNA Portion 3 - partial	-	GAUAAACGUACCGUCUGGUGCG UUUCUC (SEQ ID NO: 1073)
	tracrRNA Portion 3 - without polyT	-	GAUAAACGUACCGUCUGGUGCG UUUCUC (SEQ ID NO: 1074)
	sgRNA V3 sequence	-	GUUUUAGUUCUCUGAUGGgaaC CAUCAAUGAGUUCUAAGAUAAAG GCAAUAGCCGUGGGGUAUGGU GGUAACCUCAAAAGCGAUCCAC CUUUGAUAAACGUACCGUCUGG UGCGUUUUU (SEQ ID NO: 1075)
tracrRNA V3 sequences	tracrRNA Portion 2	-	GGUGGUAACCUCAAAAGCGAUC CACCUUUGAU (SEQ ID NO: 1076)
	tracrRNA Portion 3	-	AAACGUACCGUCUGGUGCGUUU UUU (SEQ ID NO: 1077)
	tracrRNA Portion 3 - partial	-	AAACGUACCGUCUGGUGCGUUU (SEQ ID NO: 1078)
	tracrRNA Portion 3 - without polyT	-	AAACGUACCGUCUGGUGCG (SEQ ID NO: 1079)
	sgRNA V4 sequence	-	GUCUUAGUUCUCUGAUGGgaaCC AUCAAUGAGUUCUAAGAUAAAG CAAUAGCCGUGGGGUAUGGUG GUAACCUCAAAAGCGAUCCACC

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			UUUGAUAAACGUACCGUCUGGU GCGUUUUUU (SEQ ID NO: 1080)
		OMNI-316	OMNI-317
	sgRNA V1 sequence	AUUUUAGUCCCUAAUUUU gaaaAAAGUUAGGUUACUAA AACAAGGGUCCUACGAG GAGACCCGCAAAGCUCUAA GUUCGCUGGGUUUCACAGC GGACUUAUCUUUUUUU (SEQ ID NO: 1081)	GCUGUAGCCCCCUGUUAUUgaaaA GUAACACGUCGCUACAGUAAGG CUCCGUCGUGGACGGAUGCCGC AAAGCUCUAAACCAUUCUUCG GAAUGGGUUUAUCUUUUUU (SEQ ID NO: 1102)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	AUUUUAGUCCCUAAUUUU (SEQ ID NO: 1082)	GCUGUAGCCCCCUGUUAUU (SEQ ID NO: 1103)
	Partial crRNA 1	AUUUUAGUCCCUAA (SEQ ID NO: 1083)	GCUGUAGCCCCCUGU (SEQ ID NO: 1104)
	Partial crRNA 2	AUUUUAGUCCC (SEQ ID NO: 1084)	GCUGUAGCCCCC (SEQ ID NO: 1105)
	Partial crRNA 3	AUUUUAGUUC (SEQ ID NO: 1085)	GCUGUAGCCC (SEQ ID NO: 1106)
	tracrRNA (Antirepeat)	AAAGUUAGGUUACUAAAA (SEQ ID NO: 1086)	AGUAAACACGUCGCUACAGU (SEQ ID NO: 1107)
	Partial tracrRNA 1	UUAGGUUACUAAAA (SEQ ID NO: 1087)	ACACGUCGCUACAGU (SEQ ID NO: 1108)
	Partial tracrRNA 2	GGUUAUAAAA (SEQ ID NO: 1088)	CGUCGCUACAGU (SEQ ID NO: 1109)
	Partial tracrRNA 3	UUACUAAAA	UCGCUACAGU (SEQ ID NO: 1110)
tracrRNA V1 sequences	tracrRNA Portion 1	CAAGGGUCCUACGAGGA GACCCGC (SEQ ID NO: 1089)	AAGGCUCCGUCGUGGACGGAUG CCGC (SEQ ID NO: 1111)
	tracrRNA Portion 1 - partial	CAAGGGUCCUACGAGGA GACCC (SEQ ID NO: 1090)	AAGGCUCCGUCGUGGACGGAUG CC (SEQ ID NO: 1112)
	tracrRNA Portion 2	AAAGCUCUAAAGUUCGUGG GUUUCUCAGCGGACUUAUC UUUUUUU (SEQ ID NO: 1091)	AAAGCUCUAAACCAUUCUUCG GAAUGGGUUUAUCUUUUUU (SEQ ID NO: 1113)
	tracrRNA Portion 2 - partial	AAAGCUCUAAAGUUCGUGG GUUUCUCAGCGGACUUAUC UUU (SEQ ID NO: 1092)	AAAGCUCUAAACCAUUCUUCG GAAUGGGUUUAUCUUU (SEQ ID NO: 1114)
	tracrRNA Portion 2 –	AAAGCUCUAAAGUUCGUGG GUUUCUCAGCGGACUUAUC (SEQ ID NO: 1093)	AAAGCUCUAAACCAUUCUUCG GAAUGGGUUUAUC (SEQ ID NO: 1115)

		OMNI-316	OMNI-317
	without polyT		
	sgRNA V2 sequence	AUUCUAGUUCCCUAACUUU gaaaAAAGUUAGGUUACUAG AACAAGGGUCCCUACGAG GAGACCCGCAAAGCUCUAA GUUCGCUGGGUUUCUCAGC GGACUUAUCUUUUUUU (SEQ ID NO: 1094)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	AUUCUAGUUCCCUAACUUU (SEQ ID NO: 1095)	-
	Partial crRNA 1	AUUCUAGUUCCCUAA (SEQ ID NO: 1096)	-
	Partial crRNA 2	AUUCUAGUUCCC (SEQ ID NO: 1097)	-
	Partial crRNA 3	AUUCUAGUUC (SEQ ID NO: 1098)	-
	tracrRNA (Antirepeat)	AAAGUUAGGUUACUAGAA (SEQ ID NO: 1099)	-
	Partial tracrRNA 1	UUAGGUUACUAGAA (SEQ ID NO: 1100)	-
	Partial tracrRNA 2	GGUUACUAGAA (SEQ ID NO: 1101)	-
	Partial tracrRNA 3	UUACUAGAA	-

		OMNI-318	OMNI-319
	sgRNA V1 sequence	GUUAUAGUUCCCUAACAAU gaaaAUUGUUUUAGGUUUCU AUAUAUUUUAGCAACUUA GGGCGGCGAUUUUGGUCGU GCAGCUACGGUUGAGAAUU CUAUUGUGAAUCUAAAGCA AAGCUCUAAUCCGCUCACU AGUUGGGCGGAUUAUCUUU UUU (SEQ ID NO: 1116)	AUUUUAGUACCUGAAAAAAgaaa UUUUUUUCAGAAUCUACUAAAAC AAGGCUUUUAUGCCGAAAUCAAG GACAUCCGACGGAUGUCCUUUUU U (SEQ ID NO: 1136)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUAUAGUUCCCUAACAAU (SEQ ID NO: 1117)	AUUUUAGUACCUGAAAAAA (SEQ ID NO: 1137)
	Partial crRNA 1	GUUAUAGUUCCCUAA (SEQ ID NO: 1118)	AUUUUAGUACCUGAA (SEQ ID NO: 1138)

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	Partial crRNA 2	GUUAUAGUCCCC (SEQ ID NO: 1119)	AUUUUAGUACCU (SEQ ID NO: 1139)
	Partial crRNA 3	GUUAUAGUUC (SEQ ID NO: 1120)	AUUUUAGUAC (SEQ ID NO: 1140)
	tracrRNA (Antirepeat)	AUUGUUUUAGGUUUCUAUAU (SEQ ID NO: 1121)	UUUUUUCAGAAUCUACUAAAA (SEQ ID NO: 1141)
	Partial tracrRNA 1	UUUUAGGUUUCUAUAAU (SEQ ID NO: 1122)	UUCAGAAUCUACUAAAA (SEQ ID NO: 1142)
	Partial tracrRNA 2	GGUUUCUAUAAU (SEQ ID NO: 1123)	AGAAUCUACUAAAA (SEQ ID NO: 1143)
	Partial tracrRNA 3	UUUCUAUAAU (SEQ ID NO: 1124)	AAUCUACUAAAA (SEQ ID NO: 1144)
tracrRNA V1 sequences	tracrRNA Portion 1	AAUUUAGCAACUAGGGCG GCGAUUUUGGUCGUGC (SEQ ID NO: 1125)	CAAGGCUUUAUGCCGAAAUC (SEQ ID NO: 1145)
	tracrRNA Portion 1 - partial	-	CAAGGCUUUAUGCC (SEQ ID NO: 1146)
	tracrRNA Portion 2	AGCUACGGUUGAGAAUUCU AUUGUGAAUCUAAAGCAAA GCUC (SEQ ID NO: 1126)	AAGGACAUCGACGGAUGUCCUU UUUU (SEQ ID NO: 1147)
	tracrRNA Portion 2 - partial	AGCUACGGUUGAGAAUUCU AUUGUGAAUCUAAAGCAAA GCU (SEQ ID NO: 1127)	AAGGACAUCGACGGAUGUCCUU (SEQ ID NO: 1148)
	tracrRNA Portion 2 – without polyT	-	AAGGACAUCGACGGAUGUCC (SEQ ID NO: 1149)
	tracrRNA Portion 3	UAAUCCGCUCACUAGUUGG GCGGAUUAUCUUUUUU (SEQ ID NO: 1128)	-
	tracrRNA Portion 3 - partial	UAAUCCGCUCACUAGUUGG GCGGAUUA (SEQ ID NO: 1129)	-
	tracrRNA Portion 3 - without polyT	UAAUCCGCUCACUAGUUGG GCGGAUUAUC (SEQ ID NO: 1130)	-
	sgRNA V2 sequence	GUUAUAGUCCCCUAACAAU gaaaAUUGUUCUAGGUUUCU AUAUAUUUUAGCAACUUA GGGCGGCGAUCUUGGUCGU GCAGCUACGGUUGAGAAU CUAUUGUGAAUCUAAAGCA AAGCUCUAAUCCGCUCACU AGUUGGGCGGAUUAUCUUU UUU (SEQ ID NO: 1131)	AUUCUAGUACCUGAAAGAAgaaa UUCUUUCAGAAUCUACUAGAAC AAGGCUUUAUGCCGAAAUCAAG GACAUCGACGGAUGUCCUUUUU U (SEQ ID NO: 1150)

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crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	AUUCUAGUACCUGAAAGAA (SEQ ID NO: 1151)
	Partial crRNA 1	-	AUUCUAGUACCUGAA (SEQ ID NO: 1152)
	Partial crRNA 2	-	AUUCUAGUACCU (SEQ ID NO: 1153)
	Partial crRNA 3	-	AUUCUAGUAC (SEQ ID NO: 1154)
	tracrRNA (Antirepeat)	AUUGUUCUAGGUUUCUAUAU (SEQ ID NO: 1132)	UUCUUUCAGAAUCUACUAGAA (SEQ ID NO: 1155)
	Partial tracrRNA 1	UUCUAGGUUUCUAUAAU (SEQ ID NO: 1133)	UUCAGAAUCUACUAGAA (SEQ ID NO: 1156)
	Partial tracrRNA 2	-	AGAAUCUACUAGAA (SEQ ID NO: 1157)
	Partial tracrRNA 3	-	AAUCUACUAGAA (SEQ ID NO: 1158)
tracrRNA V2 sequences	tracrRNA Portion 1	AAUUUAGCAACUUAGGGCG GCGAUCUUGGUCGUGC (SEQ ID NO: 1134)	-
	tracrRNA Portion 2	AAUUUAGCAACUUAGGGCG GCGAUCUUGGUCGUGCAGC UACGGUUG (SEQ ID NO: 1135)	-
	sgRNA V3 sequence	-	AUUUUAGUACCUGAAAAAagaa UUUUUUCAGAAUCUACUAAAAC AAGGCUUUU AUGCCGAAAUCAAG GACAUCGACGGAUGUCCUUUUU UCUUUGCAUUUUU (SEQ ID NO: 1159)
tracrRNA V3 sequences	tracrRNA Portion 1	-	CAAGGCUUU AUGCC (SEQ ID NO: 1160)
	tracrRNA Portion 2	-	GAAAUCAAGGACAUCGACGGAU GUCCUUUUUUCUUUGCAUUUUU U (SEQ ID NO: 1161)
	tracrRNA Portion 2 - partial	-	GAAAUCAAGGACAUCGACGGAU GUCCUUUUUUC (SEQ ID NO: 1162)
	tracrRNA Portion 2 – without polyT	-	GAAAUCAAGGACAUCGACGGAU GUCCUUUUUUCUUUGCA (SEQ ID NO: 1163)
	sgRNA V4 sequence	-	AUUCUAGUACCUGAAAGAAgaa UUCUUUCAGAAUCUACUAGAAC AAGGCUUUU AUGCCGAAAUCAAG GACAUCGACGGAUGUCCUUUU

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			UCUUUGCAUUUUUU (SEQ ID NO: 1164)
tracrRNA V4 sequences	tracrRNA Portion 2	-	GAAAUCAAGGACAUCGACGGAU GUCCUUCUUUCUUUGCAUUUUU U (SEQ ID NO: 1165)
	tracrRNA Portion 2 - partial	-	GAAAUCAAGGACAUCGACGGAU GUCCUUCUUUC (SEQ ID NO: 1166)
	tracrRNA Portion 2 – without polyT	-	GAAAUCAAGGACAUCGACGGAU GUCCUUCUUUCUUUGCA (SEQ ID NO: 1167)

		OMNI-320	OMNI-321
	sgRNA V1 sequence	GCUGUAGUCCCCGGUUAUU gaaaAGUAACAGGUUUCUAC AGUAAGGUAGAACACCUAA AAGCUCUAAUCCCAUUCUU CGGAAUGGGAUUUUCUUUU UU (SEQ ID NO: 1168)	GUUUUAGUCCCCAUUUUG gaaa UAAAAUAGGUUACUAAAAUAAA GGUGGCAGUUUACUGCUACCUA UGGUAAUUCGUAAGAAUUAUCC AGUAAGUGGUUGCCGACGGGCA ACCUUUUUUU (SEQ ID NO: 1187)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GCUGUAGUCCCCGGUUAUU (SEQ ID NO: 1169)	GUUUUAGUCCCCAUUUUG (SEQ ID NO: 1188)
	Partial crRNA 1	GCUGUAGUCCCCGGU (SEQ ID NO: 1170)	GUUUUAGUCCCCAU (SEQ ID NO: 1189)
	Partial crRNA 2	GCUGUAGUCCCC (SEQ ID NO: 1171)	GUUUUAGUCCCC (SEQ ID NO: 1190)
	Partial crRNA 3	GCUGUAGUUC (SEQ ID NO: 1172)	GUUUUAGUUC (SEQ ID NO: 1191)
	tracrRNA (Antirepeat)	AGUAACAGGUUUCUACAGU (SEQ ID NO: 1173)	UAAAAUAGGUUACUAAAAU (SEQ ID NO: 1192)
	Partial tracrRNA 1	ACAGGUUUCUACAGU (SEQ ID NO: 1174)	AUAGGUUACUAAAAU (SEQ ID NO: 1193)
	Partial tracrRNA 2	AGUAACAGGUUUCUACAGU (SEQ ID NO: 1175)	GGUUACUAAAAU (SEQ ID NO: 1194)
	Partial tracrRNA 3	UUUCUACAGU (SEQ ID NO: 1176)	UUACUAAAAU (SEQ ID NO: 1195)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUAGAACACCU (SEQ ID NO: 1177)	AAAGGUGGCAGUUUACUGCUAC CUA (SEQ ID NO: 1196)
	tracrRNA Portion 1 - partial	AAGGUAGAACACCU (SEQ ID NO: 1178)	AAAGGUGGCAGUUUACUGCUAC CU (SEQ ID NO: 1197)

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	tracrRNA Portion 2	AAAAGCUCUAAUCCCAUUC UUCGGAAUGGGAUUAUCUU UUUU (SEQ ID NO: 1179)	UGGUAAUUCGUAAGAAUUAUCC AGUAAGU (SEQ ID NO: 1198)
	tracrRNA Portion 2 - partial	AAAAGCUCUAAUCCCAUUC UUCGGAAUGGGAUUAUCUU UU (SEQ ID NO: 1180)	UGGUAAUUCGUAAGAAUUAUCC A (SEQ ID NO: 1199)
	tracrRNA Portion 2 – without polyT	AAAAGCUCUAAUCCCAUUC UUCGGAAUGGGAUUAUC (SEQ ID NO: 1181)	-
	tracrRNA Portion 3	-	GGUUGCCGACGGGCAACCUUUU UUU (SEQ ID NO: 1200)
	tracrRNA Portion 3 - partial	-	GGUUGCCGACGGGCAACC (SEQ ID NO: 1201)
	tracrRNA Portion 3 - without polyT	-	GGUUGCCGACGGGCAACC (SEQ ID NO: 1202)
	sgRNA V2 sequence	-	GUUCUAGUUCCCUAUUCUGgaaaU AGAAUAGGUUACUAGAAUAAAG GUGGCAGUUUACUGCUACCUAU GGUAAUUCGUAAGAAUUAUCCA GUAAGUGGUUGCCGACGGGCAA CCUUUUUUU (SEQ ID NO: 1203)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GUUCUAGUUCCCUAUUCUG (SEQ ID NO: 1204)
	Partial crRNA 1	-	GUUCUAGUUCCCUAU (SEQ ID NO: 1205)
	Partial crRNA 2	-	GUUCUAGUUCCC (SEQ ID NO: 1206)
	Partial crRNA 3	-	GUUCUAGUUC (SEQ ID NO: 1207)
	tracrRNA (Antirepeat)	-	UAGAAUAGGUUACUAGAAU (SEQ ID NO: 1208)
	Partial tracrRNA 1	-	AUAGGUUACUAGAAU (SEQ ID NO: 1209)
	Partial tracrRNA 2	-	GGUUACUAGAAU (SEQ ID NO: 1210)
	Partial tracrRNA 3	-	UUACUAGAAU (SEQ ID NO: 1211)
	sgRNA V3 sequence	GCUGUAGUUCCCGGUUAUU gaaaAGUAAACAGGUUUCUAC AGUAAGGUAGAACCACUAA AAGCUCUAAUCCCAUUCUU	-

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		CGGAAUGGGAUUAUUUUUU (SEQ ID NO: 1182)	
tracrRNA V3 sequences	tracrRNA Portion 1	AAGGUAGAACACCUAAAAAG CUC (SEQ ID NO: 1183)	-
	tracrRNA Portion 2	UAAUCCCAUUCUUCGGAAU GGGAUUAUUUUUU (SEQ ID NO: 1184)	-
	tracrRNA Portion 2 - partial	UAAUCCCAUUCUUCGGAAU GGGAUUA (SEQ ID NO: 1185)	-
	tracrRNA Portion 2 – without polyT	UAAUCCCAUUCUUCGGAAU GGGAUUA (SEQ ID NO: 1186)	-

		OMNI-322	OMNI-323
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUUUAGUUUCUAAUUAU gaaaUUAUUAAAGCUACUAA AAUAAUGGCAGGCGAAAGC CUUGUCCAGUAAGUGACCA CCUUAUGGGUGGUCUUUUU UU (SEQ ID NO: 1212)	GUUAUAGUUGACCGUgaaaACGG UCAACACAUUAUAAUAAAGGCU GAAAAUGCCGUAGAUGAGGGG GCGAUGCGUUGCCCCCAUUAUU UUUU (SEQ ID NO: 1244)
	crRNA (Repeat)	GUUUUAGUUUCUAAUUAU (SEQ ID NO: 1213)	GUUAUAGUUGACCGU (SEQ ID NO: 1245)
	Partial crRNA 1	GUUUUAGUUUCUAA (SEQ ID NO: 1214)	-
	Partial crRNA 2	GUUUUAGUUUCU (SEQ ID NO: 1215)	GUUAUAGUUGAC (SEQ ID NO: 1246)
	Partial crRNA 3	GUUUUAGUUU (SEQ ID NO: 1216)	GUUAUAGUUG (SEQ ID NO: 1247)
	tracrRNA (Antirepeat)	UUAUUAAAGCUACUAAAAU (SEQ ID NO: 1217)	ACGGUCAACACAUUAUAAU (SEQ ID NO: 1248)
	Partial tracrRNA 1	UUAAGCUACUAAAAU (SEQ ID NO: 1218)	-
	Partial tracrRNA 2	AGCUACUAAAAU (SEQ ID NO: 1219)	GUCAACACAUUAUAAU (SEQ ID NO: 1249)
	Partial tracrRNA 3	CUACUAAAAU (SEQ ID NO: 1220)	CAACACAUUAUAAU (SEQ ID NO: 1250)
tracrRNA V1 sequences	tracrRNA Portion 1	AAUGGCAGGCGAAAGCCUU GUCCAGUAAGU (SEQ ID NO: 1221)	AAGGCUGAAAAUGCCGU (SEQ ID NO: 1251)
	tracrRNA Portion 1 - partial	AAUGGCAGGCGAAAGCCUU GUCCA (SEQ ID NO: 1222)	AAGGCUGAAAAUGCC (SEQ ID NO: 1252)
	tracrRNA Portion 2	GACCACCUUAUGGGUGGUC UUUUUUU (SEQ ID NO: 1223)	AAGAUGAGGGGGCGAUGCGUUG CCCCCAUUAUUUUU (SEQ ID NO: 1253)
	tracrRNA Portion 2 - partial	GACCACCUUAUGGGUGGUC (SEQ ID NO: 1224)	AAGAUGAGGGGGCGAUGCGUUG CCCCCAUUAUUUUU (SEQ ID NO: 1254)
	tracrRNA Portion 2 – without polyT	GACCACCUUAUGGGUGGUC (SEQ ID NO: 1225)	AAGAUGAGGGGGCGAUGCGUUG CCCCCAUUA (SEQ ID NO: 1255)
	sgRNA V2 sequence	GUUCUAGUUUCUAAUUAU gaaaUUAUUAAAGCUACUAG AAUAAUGGCAGGCGAAAGC CUUGUCCAGUAAGUGACCA CCUUAUGGGUGGUCUUUUU UU (SEQ ID NO: 1226)	-

		OMNI-322	OMNI-323
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGUUUCUAAUUAU (SEQ ID NO: 1227)	-
	Partial crRNA 1	GUUCUAGUUUCUAA (SEQ ID NO: 1228)	-
	Partial crRNA 2	GUUCUAGUUUCU (SEQ ID NO: 1229)	-
	Partial crRNA 3	GUUCUAGUUU (SEQ ID NO: 1230)	-
	tracrRNA (Antirepeat)	UUAUUUAAGCUACUAGAAU (SEQ ID NO: 1231)	-
	Partial tracrRNA 1	UUAAGCUACUAGAAU (SEQ ID NO: 1232)	-
	Partial tracrRNA 2	AGCUACUAGAAU (SEQ ID NO: 1233)	-
	Partial tracrRNA 3	CUACUAGAAU (SEQ ID NO: 1234)	-
	sgRNA V3 sequence	GUUUUAGUUUCUAAUUAU gaaaUUAUUUAAGCUACUAA AAUAAUGGCAGGCGAAAGC CUUGUCCAGUAAGUGACCA CCUUAUGGGUGGUCUUUUU UUGCGAACUUUUUU (SEQ ID NO: 1235)	-
tracrRNA V3 sequences	tracrRNA Portion 1	AAUGGCAGGCGAAAGCCUU GUCCA (SEQ ID NO: 1236)	-
	tracrRNA Portion 2	GUAAGUGACCACCUUAUGG GUGGUCUUUUUUUGCGAAC UUUUUU (SEQ ID NO: 1237)	-
	tracrRNA Portion 2 - partial	GUAAGUGACCACCUUAUGG GUGGUCUUUUUUUGC (SEQ ID NO: 1238)	-
	tracrRNA Portion 2 – without polyT	GUAAGUGACCACCUUAUGG GUGGUCUUUUUUUGCGAAC (SEQ ID NO: 1239)	-
	sgRNA V4 sequence	GUUCUAGUUUCUAAUUAU gaaaUUAUUUAAGCUACUAG AAUAAUGGCAGGCGAAAGC CUUGUCCAGUAAGUGACCA CCUUAUGGGUGGUCUUUCU UUGCGAACUUUUUU (SEQ ID NO: 1240)	-
tracrRNA V4 sequences	tracrRNA Portion 2	GUAAGUGACCACCUUAUGG GUGGUCUUUCUUUGCGAAC UUUUUU (SEQ ID NO: 1241)	-

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	tracrRNA Portion 2 - partial	GUAAGUGACCACCUUAUGG GUGGUCUUUCUUUGC (SEQ ID NO: 1242)	-
	tracrRNA Portion 2 – without polyT	GUAAGUGACCACCUUAUGG GUGGUCUUUCUUUGCGAAC (SEQ ID NO: 1243)	-

		OMNI-324	OMNI-325
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUUUAGUUCUCUGAUGAg aaaUCAUCAAGAGUUCUAAG AUAAGGCAUUAUGCCGUAG GGUAUAGCGGUAUCCCAAA ACACUCCGCUCAUUUUUU (SEQ ID NO: 1256)	GUUGUUGUUCGCUUAUCgaaa GAUAUACGGUACAACAUAAG ACCUCCAUCUUUUUGAUGGUGU GUCUCAGGCUCUGAUCCCAUCU AAAGUUAUUCUUUAGGUGGGA UUAUCCAUUUUUU (SEQ ID NO: 1285)
	crRNA (Repeat)	GUUUUAGUUCUCUGAUGA (SEQ ID NO: 1257)	GUUGUUGUUCGCUUAUC (SEQ ID NO: 1286)
	Partial crRNA 1	GUUUUAGUUCUCUGA (SEQ ID NO: 1258)	GUUGUUGUUCGCGU (SEQ ID NO: 1287)
	Partial crRNA 2	GUUUUAGUUCUC (SEQ ID NO: 1259)	GUUGUUGUUCG (SEQ ID NO: 1288)
	Partial crRNA 3	GUUUUAGUUC (SEQ ID NO: 1260)	GUUGUUGUUC (SEQ ID NO: 1289)
	tracrRNA (Antirepeat)	UCAUCAAGAGUUCUAAGAU (SEQ ID NO: 1261)	GAUAUACGGUACAACAUA (SEQ ID NO: 1290)
	Partial tracrRNA 1	UCAAGAGUUCUAAGAU (SEQ ID NO: 1262)	UACGGUACAACAUA (SEQ ID NO: 1291)
	Partial tracrRNA 2	AGAGUUCUAAGAU (SEQ ID NO: 1263)	GGUACAACAUA (SEQ ID NO: 1292)
	Partial tracrRNA 3	GUUCUAAGAU (SEQ ID NO: 1264)	UUACAACAUA (SEQ ID NO: 1293)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGCAUUAUGCCGUAGGG UAUA (SEQ ID NO: 1265)	AAGACCUCCAUCUUUUUGAUGG UGUGUCUCA (SEQ ID NO: 1294)
	tracrRNA Portion 1 - partial	AAGGCAUUAUGCCGUAGGG UAUA (SEQ ID NO: 1266)	AAGACCUCCAUCUUUUUGAUGG UGUGUCU (SEQ ID NO: 1295)
	tracrRNA Portion 2	GCGGUAUCCCAAAACACUC CGCUCAUUUUUU (SEQ ID NO: 1267)	GGCUCUGAUCCCAUCUAAAGUU AAUUCUUUAGGUGGGAUUAUCC AUUUUUU (SEQ ID NO: 1296)

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	tracrRNA Portion 2 - partial	GCGGUAUCCCAAAACACUC CGC (SEQ ID NO: 1268)	GGCUCUGAUCCCAUCUAAAGUU AAUUCUUUAGGUGGGAUUAUCC (SEQ ID NO: 1297)
	tracrRNA Portion 2 – without polyT	GCGGUAUCCCAAAACACUC CGCUCA (SEQ ID NO: 1269)	GGCUCUGAUCCCAUCUAAAGUU AAUUCUUUAGGUGGGAUUAUCC A (SEQ ID NO: 1298)
	sgRNA V2 sequence	GUCUUAGUUCUCUGAUGAg aaaUCAUCAAGAGUUCUAAG AUAAGGCAUUAUGCCGUAG GGUAUAGCGGUAUCCCAAA ACACUCCGCUCAUUUUUU (SEQ ID NO: 1270)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUCUUAGUUCUCUGAUGA (SEQ ID NO: 1271)	-
	Partial crRNA 1	GUCUUAGUUCUCUGA (SEQ ID NO: 1272)	-
	Partial crRNA 2	GUCUUAGUUCUC (SEQ ID NO: 1273)	-
	Partial crRNA 3	GUCUUAGUUC (SEQ ID NO: 1274)	-
	sgRNA V3 sequence	GUUUUAGUUCUCUGAUGAg aaaUCAUCAAGAGUUCUAAG AUAAGGCAUUAUGCCGUAG GGUAUAGCGGUAUCCCAAA ACACUCCGCUCAUUUUUGAU UGAUUAAGGUUGUUUCUUU AAUGGAACAACCUUUUUU (SEQ ID NO: 1275)	-
tracrRNA V3 sequences	tracrRNA Portion 2	GCGGUAUCCCAAAACACUC CGCUCAUUUUUGAUU (SEQ ID NO: 1276)	-
	tracrRNA Portion 3	GAUUAAGGUUGUUUCUUUA AUGGAACAACCUUUUUU (SEQ ID NO: 1277)	-
	tracrRNA Portion 3 - partial	GAUUAAGGUUGUUUCUUUA AUGGAACAACCUUUUUU (SEQ ID NO: 1278)	-
	tracrRNA Portion 3 - without polyT	GAUUAAGGUUGUUUCUUUA AUGGAACAACC (SEQ ID NO: 1279)	-
	sgRNA V4 sequence	GUCUUAGUUCUCUGAUGAg aaaUCAUCAAGAGUUCUAAG AUAAGGCAUUAUGCCGUAG GGUAUAGCGGUAUCCCAAA ACACUCCGCUCAUUCUGAU UGAUUAAGGUUGUUUCUUU AAUGGAACAACCUUUUUU (SEQ ID NO: 1280)	-

		OMNI-324	OMNI-325
tracrRNA V4 sequences	tracrRNA Portion 1	AAGGCAUUAUGCCG (SEQ ID NO: 1281)	-
	tracrRNA Portion 1 - partial	AAGGCAUUAUGCC (SEQ ID NO: 1282)	-
	tracrRNA Portion 2	UAGGGUAUAGCGGUAUCCC AAAACACUCCGCUCAUUCU GAUU (SEQ ID NO: 1283)	-
	tracrRNA Portion 2 - partial	UAGGGUAUAGCGGUAUCCC AAAACACUCCGCUCAUUCU G (SEQ ID NO: 1284)	-

		OMNI-326	OMNI-327
	sgRNA V1 sequence	GUUGUUGUCCCCGGUUAUC gaaGAUAAACGGUUAACAAC AAUAAGGUCCCCGCCGUGG CGGUGUACCUCAAAGCUCU AAUCCCACUUAAGUGAAU ACUUUAAGUGGGAUUAUCU AUUUUUU (SEQ ID NO: 1299)	GUUCCUAUUAGGgaaCCUCAACU UAGGUAACAAGGGCAUUAAGC CCACAAAGGGAUUUAUUCAC UUAAAUAUUUUUGAUUUGAUU GUAAAUAUUAAAAAUCCUCA AAAGUAUGAGUUGCUCGUGCUU UUUGGGGAUUUUUU (SEQ ID NO: 1313)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUGUUGUCCCCGGUUAUC (SEQ ID NO: 1300)	GUUCCUAUUAGG (SEQ ID NO: 1314)
	Partial crRNA 1	GUUGUUGUCCCCGGU (SEQ ID NO: 1301)	-
	Partial crRNA 2	GUUGUUGUCCCC (SEQ ID NO: 1302)	-
	Partial crRNA 3	GUUGUUGUUC (SEQ ID NO: 1303)	GUUCCUAUUA (SEQ ID NO: 1315)
	tracrRNA (Antirepeat)	GAUAAACGGUUAACAACAAU (SEQ ID NO: 1304)	CCUCAACUUAGGUAAC (SEQ ID NO: 1316)
	Partial tracrRNA 1	AACGGUUAACAACAAU (SEQ ID NO: 1305)	-
	Partial tracrRNA 2	GGUUAACAACAAU (SEQ ID NO: 1306)	-
	Partial tracrRNA 3	UUACAACAAU (SEQ ID NO: 1307)	UCAACUUAGGUAAC (SEQ ID NO: 1317)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUCCCCGCCGUGGCGG UGUACCUCAAAGCUC (SEQ ID NO: 1308)	AAGGGCAUUAAGCCCACAAA (SEQ ID NO: 1318)

		OMNI-326	OMNI-327
	tracrRNA Portion 1 - partial	AAGGUCCCGCCGCGGGCGG UGUACCU (SEQ ID NO: 1309)	AAGGGCAUUAAGCCC (SEQ ID NO: 1319)
	tracrRNA Portion 2	UAAUCCACUAAAAGUGAA UACUUUAAGUGGGAUUAUC UAUUUUUU (SEQ ID NO: 1310)	GGGAUUUAUCCAC (SEQ ID NO: 1320)
	tracrRNA Portion 2 - partial	UAAUCCACUAAAAGUGAA UACUUUAAGUGGGAUUA (SEQ ID NO: 1311)	GGGAUUUAUCC (SEQ ID NO: 1321)
	tracrRNA Portion 2 – without polyT	UAAUCCACUAAAAGUGAA UACUUUAAGUGGGAUUAUC UA (SEQ ID NO: 1312)	-
	tracrRNA Portion 3	-	UUAAAUUAGUUUUGAUUUGAUU GUAAAUAAUU (SEQ ID NO: 1322)
	tracrRNA Portion 3 - partial	-	UUAAAUUAGUUUUGAUUUGA (SEQ ID NO: 1323)
	tracrRNA Portion 4	-	AAAAAUCCUCAAAAAGUAUGAG UUGCUCGUGCUUUUUGGGGAUU UUUU (SEQ ID NO: 1324)
	tracrRNA Portion 4 - partial	-	AAAAAUCCUCAAAAAGUAUGAG UUGCUCGUGCUUUUUGGGGAUU UUU (SEQ ID NO: 1325)
	tracrRNA Portion 4 - without polyT	-	AAAAAUCCUCAAAAAGUAUGAG UUGCUCGUGCUUUUUGGGGA (SEQ ID NO: 1326)
	sgRNA V2 sequence	-	GUUCCUAUUAGGgaaaCCUCAACU UAGGUAACAAGGGCAUUAAGC CCACAAAGGAUUUAUCCAC UUAAAUUAGUCUUGAUUUGAUU GUAAAUAAUAAAAAUCCUCA GAAGUAUGAGUUGCUCGUGCUU CUUGGGGAUUUUUU (SEQ ID NO: 1327)
tracrRNA V2 sequences	tracrRNA Portion 3	-	UUAAAUUAGUCUUGAUUUGAUU GUAAAUAAUU (SEQ ID NO: 1328)
	tracrRNA Portion 3 - partial	-	UUAAAUUAGUCUUGAUUUGA (SEQ ID NO: 1329)
	tracrRNA Portion 4	-	AAAAAUCCUCAAGAAGUAUGAG UUGCUCGUGCUUCUUGGGGAUU UUUU (SEQ ID NO: 1330)
	tracrRNA Portion 4 - partial	-	AAAAAUCCUCAAGAAGUAUGAG UUGCUCGUGCUUCUUGGGGAUU UUU (SEQ ID NO: 1331)
	tracrRNA Portion 4 -	-	AAAAAUCCUCAAGAAGUAUGAG UUGCUCGUGCUUCUUGGGGA (SEQ ID NO: 1332)

		OMNI-326	OMNI-327
	without polyT		
	sgRNA V3 sequence	-	GUUCCUAUUAGGgaaaCCUCAACU UAGGUAACAAGGGCAUUAAGC CCACAAAGGGAUUUAUUCCCAC UUAAAUUAGUUUUUU (SEQ ID NO: 1333)
crRNA:tracrRNA duplex V3 sequences	crRNA (Repeat)	-	GUUCCUAUUAGG (SEQ ID NO: 1334)
	Partial crRNA 3	-	GUUCCUAUUA (SEQ ID NO: 1335)
	tracrRNA (Antirepeat)	-	CCUCAACUAGGUAAC (SEQ ID NO: 1336)
	Partial tracrRNA 3	-	UCAACUUAGGUAAC (SEQ ID NO: 1337)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGGGCAUUAAGCCCACAAA (SEQ ID NO: 1338)
	tracrRNA Portion 1 - partial	-	AAGGGCAUUAAGCCC (SEQ ID NO: 1339)
	tracrRNA Portion 2	-	GGGAUUUAUUCCCACUAAAUU AGUUUUUU (SEQ ID NO: 1340)
	tracrRNA Portion 2 - partial	-	GGGAUUUAUUCCC (SEQ ID NO: 1341)
	tracrRNA Portion 2 – without polyT	-	GGGAUUUAUUCCCACUAAAUU AG (SEQ ID NO: 1342)

		OMNI-329	OMNI-330
	sgRNA V1 sequence	GUUUGAGAGCCUUGUUAga aUAACAAGGCAAGUCAA UAAAACUUUUGUCUAAUCA CUUAUUCGCAUUGGCGAAC CGCUCUCCUUUUCGGAAG AGUUUUUU (SEQ ID NO: 1343)	GUUGUGGUUUGAUGUAGGAga aUCCUACAUCUUAUCACAAUAG GCCAUAAUGGCCGAAGGGUAAA ACCUAUACUCCCGCUUCGGUGG GAGUUUUUUU (SEQ ID NO: 1363)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGCCUUGUUA (SEQ ID NO: 1344)	GUUGUGGUUUGAUGUAGGA (SEQ ID NO: 1364)
	Partial crRNA 1	GUUUGAGAGCCUUGU (SEQ ID NO: 1345)	GUUGUGGUUUGAUGU (SEQ ID NO: 1365)

		OMNI-329	OMNI-330
	Partial crRNA 2	GUUUGAGAGCCU (SEQ ID NO: 1346)	GUUGUGGUUUGA (SEQ ID NO: 1366)
	Partial crRNA 3	GUUUGAGAGC (SEQ ID NO: 1347)	GUUGUGGUUU (SEQ ID NO: 1367)
	tracrRNA (Antirepeat)	UAACAAGGCAAGUUCAAAU (SEQ ID NO: 1348)	UCCUACAUCUUAUCACAAU (SEQ ID NO: 1368)
	Partial tracrRNA 1	ACAAGGCAAGUUCAAAU (SEQ ID NO: 1349)	ACAUCUUAUCACAAU (SEQ ID NO: 1369)
	Partial tracrRNA 2	AGGCAAGUUCAAAU (SEQ ID NO: 1350)	UCUUAUCACAAU (SEQ ID NO: 1370)
	Partial tracrRNA 3	GCAAGUUCAAAU (SEQ ID NO: 1351)	UUAUCACAAU (SEQ ID NO: 1371)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAACUUUUGUCUAAUCACUUAUUCGCAUUGGCGAACC (SEQ ID NO: 1352)	AAGGCCAUAAUGGCCGA (SEQ ID NO: 1372)
	tracrRNA Portion 1 - partial	AAAACUUUUGUCUAAUCACUUAUUCGCAUUGGCGAA (SEQ ID NO: 1353)	AAGGCCAUAAUGGCC (SEQ ID NO: 1373)
	tracrRNA Portion 2	GCUCUCCUUUUCGGAAGAGUUUUU (SEQ ID NO: 1354)	AGGGUAAAACCUAU (SEQ ID NO: 1374)
	tracrRNA Portion 2 - partial	GCUCUCCUUUUCGGAAGAGU (SEQ ID NO: 1355)	AGGGUAAAACCU (SEQ ID NO: 1375)
	tracrRNA Portion 2 – without polyT	GCUCUCCUUUUCGGAAGAG (SEQ ID NO: 1356)	-
	tracrRNA Portion 3	-	ACUCCCGCUUCGGUGGGAGUUUU (SEQ ID NO: 1376)
	tracrRNA Portion 3 - partial	-	ACUCCCGCUUCGGUGGGAGU (SEQ ID NO: 1377)
	tracrRNA Portion 3 - without polyT	-	ACUCCCGCUUCGGUGGGAG (SEQ ID NO: 1378)
	sgRNA V2 sequence	GUUUGAGAGCCUUGUUAgaaUAACAAGGCAAGUUCAAAUAAAACUUCUGUCUAAUCACUUAUUCGCAUUGGCGAACCGCUCUCCUUCUCGGAAGAGUUUUU (SEQ ID NO: 1357)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAAACUUCUGUCUAAUCACUUAUUCGCAUUGGCGAACC (SEQ ID NO: 1358)	-

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	tracrRNA Portion 1 - partial	AAAACUUCUGUCUAAUCAC UUAUUCGCAUUGGCGAA (SEQ ID NO: 1359)	-
	tracrRNA Portion 2	GCUCUCCUUCUCGGAAGA GUUUUUU (SEQ ID NO: 1360)	-
	tracrRNA Portion 2 - partial	GCUCUCCUUCUCGGAAGA GU (SEQ ID NO: 1361)	-
	tracrRNA Portion 2 – without polyT	GCUCUCCUUCUCGGAAGA G (SEQ ID NO: 1362)	-

		OMNI-331	OMNI-332
	sgRNA V1 sequence	GUUGUGAUUUGAUGUAGAA gaaaAUCUACAUCUUAUCAC AAUAAGGCUAUAUGCCGAA GGAUUUUUAUCCUAUAGUCC CGCGUACUCCGUGGGACUU UUUU (SEQ ID NO: 1379)	GUUGUGGUUUGAUGUAGAAgaaa UUCUACAUCUUAUCACAAUAAG GCUAU AUGCCGAAGGAUUUAUA UCCUAUGUGCCCUCUUCGGAGG GCAUUAUUUUUUU (SEQ ID NO: 1398)
	crRNA:tracrRNA duplex V1 sequences		
	crRNA (Repeat)	GUUGUGAUUUGAUGUAGAA (SEQ ID NO: 1380)	GUUGUGGUUUGAUGUAGAA (SEQ ID NO: 1399)
	Partial crRNA 1	GUUGUGAUUUGAUGU (SEQ ID NO: 1381)	GUUGUGGUUUGAUGU (SEQ ID NO: 1400)
	Partial crRNA 2	GUUGUGAUUUGA (SEQ ID NO: 1382)	GUUGUGGUUUGA (SEQ ID NO: 1401)
	Partial crRNA 3	GUUGUGAUUU (SEQ ID NO: 1383)	GUUGUGGUUU (SEQ ID NO: 1402)
	tracrRNA (Antirepeat)	AUCUACAUCUUAUCACAAU (SEQ ID NO: 1384)	UUCUACAUCUUAUCACAAU (SEQ ID NO: 1403)
	Partial tracrRNA 1	ACAUCUUAUCACAAU (SEQ ID NO: 1385)	ACAUCUUAUCACAAU (SEQ ID NO: 1404)
	Partial tracrRNA 2	UCUUAUCACAAU (SEQ ID NO: 1386)	UCUUAUCACAAU (SEQ ID NO: 1405)
	Partial tracrRNA 3	UUAUCACAAU (SEQ ID NO: 1387)	UUAUCACAAU (SEQ ID NO: 1406)
	tracrRNA V1 sequences		
	tracrRNA Portion 1	AAGGCUAUAUGCCGA (SEQ ID NO: 1388)	AAGGCUAUAUGCCGA (SEQ ID NO: 1407)
	tracrRNA Portion 1 - partial	AAGGCUAUAUGCC (SEQ ID NO: 1389)	AAGGCUAUAUGCC (SEQ ID NO: 1408)

		OMNI-331	OMNI-332
	tracrRNA Portion 2	AGGAUUUUUAUCCUAU (SEQ ID NO: 1390)	AGGAUUUUAUUAUCCUAU (SEQ ID NO: 1409)
	tracrRNA Portion 2 - partial	AGGAUUUUUAUCCU (SEQ ID NO: 1391)	AGGAUUUUAUUAUCCU (SEQ ID NO: 1410)
	tracrRNA Portion 3	AGUCCCCGCGUACUCCGUGG GACUUUUUUU (SEQ ID NO: 1392)	GUGCCCUCUUCGGAGGGCAUUA UUUUUUUU (SEQ ID NO: 1411)
	tracrRNA Portion 3 - partial	AGUCCCCGCGUACUCCGUGG GACU (SEQ ID NO: 1393)	GUGCCCUCUUCGGAGGGCAU (SEQ ID NO: 1412)
	tracrRNA Portion 3 - without polyT	AGUCCCCGCGUACUCCGUGG GAC (SEQ ID NO: 1394)	GUGCCCUCUUCGGAGGGCAUUA (SEQ ID NO: 1413)
	sgRNA V2 sequence	GUUGUGAUUUUGAUGUAGAA gaaaAUCUACAUCUUAUCAC AAUAAGGCUAU AUGCCGAA GGAUUCUAUCCUAUAGUCC CGCGUACUCCGUGGGACUU UUUU (SEQ ID NO: 1395)	-
tracrRNA V2 sequences	tracrRNA Portion 2	AGGAUUCUAUCCUAU (SEQ ID NO: 1396)	-
	tracrRNA Portion 2 - partial	AGGAUUCUAUCCU (SEQ ID NO: 1397)	-

		OMNI-333	OMNI-334
	sgRNA V1 sequence	GUUUUAGGUCUCGGACAgaa aUGUCCGAGGAUUCUAAGA UAAAGCUUU AUGCUGUGGG GUUGCGUAUCCCCUUAUCG AACGUACUAGACGAGCUCC GGCUCGUCUUUUUU (SEQ ID NO: 1414)	GUUGUGAAAAGACACCgaaaGAG CCGUCUUUUCACAACAAGGCUA UAUGCCGCAGUCGAAAUGACUC UCCCCGCACGUACGCCGUGUGG GGAUUUUUUU (SEQ ID NO: 1438)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGGUCUCGGACA (SEQ ID NO: 1415)	GUUGUGAAAAGACACC (SEQ ID NO: 1439)
	Partial crRNA 1	GUUUUAGGUCUCGGA (SEQ ID NO: 1416)	GUUGUGAAAAGACAC (SEQ ID NO: 1440)
	Partial crRNA 2	GUUUUAGGUCUC (SEQ ID NO: 1417)	GUUGUGAAAAGA (SEQ ID NO: 1441)
	Partial crRNA 3	GUUUUAGGUC (SEQ ID NO: 1418)	GUUGUGAAAA (SEQ ID NO: 1442)

		OMNI-333	OMNI-334
	tracrRNA (Antirepeat)	UGUCCGAGGAUUCUAAGAU (SEQ ID NO: 1419)	GAGCCGUCUUUUCACAAC (SEQ ID NO: 1443)
	Partial tracrRNA 1	UCCGAGGAUUCUAAGAU (SEQ ID NO: 1420)	GAGCCGUCUUUUCACAAC (SEQ ID NO: 1444)
	Partial tracrRNA 2	GAGGAUUCUAAGAU (SEQ ID NO: 1421)	UCUUUUCACAAC (SEQ ID NO: 1445)
	Partial tracrRNA 3	GGAUUCUAAGAU (SEQ ID NO: 1422)	UUUUCACAAC (SEQ ID NO: 1446)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGCUUUUAUGCUGU (SEQ ID NO: 1423)	AAGGCUAUAUGCCGC (SEQ ID NO: 1447)
	tracrRNA Portion 1 - partial	AAAGCUUUUAUGC (SEQ ID NO: 1424)	AAGGCUAUAUGCC (SEQ ID NO: 1448)
	tracrRNA Portion 2	GGGGUUGCGUAUCCCCUUA UCGAACGUACU (SEQ ID NO: 1425)	AGUCGAAAUGACUC (SEQ ID NO: 1449)
	tracrRNA Portion 2 - partial	GGGGUUGCGUAUCCCC (SEQ ID NO: 1426)	AGUCGAAAUGACU (SEQ ID NO: 1450)
	tracrRNA Portion 3	AGACGAGCUCCGGCUCGUC UUUUUU (SEQ ID NO: 1427)	UCCCCGCACGUACGCCGUGUGG GGAUUUUUU (SEQ ID NO: 1451)
	tracrRNA Portion 3 - partial	AGACGAGCUCCGGCUCGUC U (SEQ ID NO: 1428)	UCCCCGCACGUACGCCGUGUGG GGA (SEQ ID NO: 1452)
	tracrRNA Portion 3 - without polyT	AGACGAGCUCCGGCUCGUC (SEQ ID NO: 1429)	UCCCCGCACGUACGCCGUGUGG GGA (SEQ ID NO: 1453)
	sgRNA V2 sequence	GUCUUAGGUCUCGGACAgaa aUGUCCGAGGAUUCUAAGA UAAAGCUUUUAUGCUGUGGG GUUGCGUAUCCCCUUAUCG AACGUACUAGACGAGCUCC GGCUCGUCUUUUUU (SEQ ID NO: 1430)	GUUGUGAGAAGACACCgaaGAG CCGUCUUCUCACAACAAGGCUA UAUGCCGCAGUCGAAAUGACUC UCCCCGCACGUACGCCGUGUGG GGAUUUUUU (SEQ ID NO: 1454)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUCUUAGGUCUCGGACA (SEQ ID NO: 1431)	GUUGUGAGAAGACACC (SEQ ID NO: 1455)
	Partial crRNA 1	GUCUUAGGUCUCGGA (SEQ ID NO: 1432)	GUUGUGAGAAGACAC (SEQ ID NO: 1456)
	Partial crRNA 2	GUCUUAGGUCUC (SEQ ID NO: 1433)	GUUGUGAGAAGA (SEQ ID NO: 1457)
	Partial crRNA 3	GUCUUAGGUC (SEQ ID NO: 1434)	GUUGUGAGAA (SEQ ID NO: 1458)

		OMNI-333	OMNI-334
	tracrRNA (Antirepeat)	-	GAGCCGUCUUCUCACAAC (SEQ ID NO: 1459)
	Partial tracrRNA 1	-	GAGCCGUCUUCUCACAAC (SEQ ID NO: 1460)
	Partial tracrRNA 2	-	UCUUCUCACAAC (SEQ ID NO: 1461)
	Partial tracrRNA 3	-	UUCUCACAAC (SEQ ID NO: 1462)
	sgRNA V3 sequence	GUUUUAGGUCUCGGACAgaa aUGUCCGAGGAUUCUAAGA UAAAGCUUU AUGCUGUGGG GUUGCGUAUCCCCUUAUCU UUUUU (SEQ ID NO: 1435)	-
tracrRNA V3 sequences	tracrRNA Portion 2	GGGGUUGCGUAUCCCCUUA UCUUUUUU (SEQ ID NO: 1436)	-
	tracrRNA Portion 2 – without polyT	GGGGUUGCGUAUCCCCUUA UC (SEQ ID NO: 1437)	-

		OMNI-336	OMNI-337
	sgRNA V1 sequence	GUUUUAGAUAUUAUGUUGaaa AGCAUAAAUGAGUUA AAAAU AAGGUAAAACCUUAAAUGC CAAUUUAUAUUGGUUUUG CUUAGGCAAGUAAAGUCUU AGUUAUCUAAGGCUUUUUU U (SEQ ID NO: 1463)	GUUUUAGAAGUAUGUUAUUGaaa AAUAGCAUAAUGAGUUA AAAAU AGGUUUUUAACCUAUA AUGCCA AUUCAUUUGGUUUCGCUUAGGC GAAAAAUGAGAGUUCUAAUUUAU UUAGGACUUUUUAUUUUUUU (SEQ ID NO: 1496)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGAUAUUAUGUU (SEQ ID NO: 1464)	GUUUUAGAAGUAUGUUAU (SEQ ID NO: 1497)
	Partial crRNA 1	GUUUUAGAUAUUAUGU (SEQ ID NO: 1465)	GUUUUAGAAGUAUGU (SEQ ID NO: 1498)
	Partial crRNA 2	GUUUUAGAUAUUA (SEQ ID NO: 1466)	GUUUUAGAAGUA (SEQ ID NO: 1499)
	Partial crRNA 3	GUUUUAGAUU (SEQ ID NO: 1467)	GUUUUAGAAG (SEQ ID NO: 1500)
	tracrRNA (Antirepeat)	AGCAUAAAUGAGUUA AAAAU (SEQ ID NO: 1468)	AAUAGCAUAAUGAGUUA AAAAU (SEQ ID NO: 1501)
	Partial tracrRNA 1	AGCAUAAAUGAGUUA AAAAU (SEQ ID NO: 1469)	GCAUAAUGAGUUA AAAAU (SEQ ID NO: 1502)

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	Partial tracrRNA 2	UAAUGAGUUAAAAU (SEQ ID NO: 1470)	UAAUGAGUUAAAAU (SEQ ID NO: 1503)
	Partial tracrRNA 3	AAUGAGUUAAAAU (SEQ ID NO: 1471)	AUGAGUUAAAAU (SEQ ID NO: 1504)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUAAAACCUUAAAUGC CAAUUUAAUUAUUGGUUUUG CUUAGGCAAGU (SEQ ID NO: 1472)	AAGGUUUUUAACCUAUAAU (SEQ ID NO: 1505)
	tracrRNA Portion 1 - partial	AAGGUAAAACCUUAAAUGC CAAUUUAAUUAUUGGUUUUG CUU (SEQ ID NO: 1473)	AAGGUUUUUAACCU (SEQ ID NO: 1506)
	tracrRNA Portion 2	AAAGUCUUAGUUAUCUAAG GCUUUUUUU (SEQ ID NO: 1474)	GCCAAUUCAUUUUGGU (SEQ ID NO: 1507)
	tracrRNA Portion 2 - partial	AAAGUCUUAGUUAUCUAAG GCUUU (SEQ ID NO: 1475)	GCCAAUUCAUUUUGGU (SEQ ID NO: 1508)
	tracrRNA Portion 2 – without polyT	AAAGUCUUAGUUAUCUAAG GC (SEQ ID NO: 1476)	-
	tracrRNA Portion 3	-	UUCGCUUAGGCGAA (SEQ ID NO: 1509)
	tracrRNA Portion 3 - partial	-	UUCGCUUAGGCGAA (SEQ ID NO: 1510)
	tracrRNA Portion 4	-	AAAUGAGAGUUCUAAUUAUUUA GGACUUUUU (SEQ ID NO: 1511)
	tracrRNA Portion 4 - partial	-	AAAUGAGAGUUCUAAUUAUUUA GGACUUUUU (SEQ ID NO: 1512)
	tracrRNA Portion 4 - without polyT	-	AAAUGAGAGUUCUAAUUAUUUA GGACUUUUU (SEQ ID NO: 1513)
	sgRNA V2 sequence	GUUCUAGAUAUUUAUGUUGaaa AGCAUAAAUGAGUUAGAAU AAGGUAGAACCUUAAAUGC CAAUUUAAUUAUUGGUUCUG CUUAGGCAAGUAAAGUCUU AGUUAUCUAAGGCUUUUUU U (SEQ ID NO: 1477)	GUUCUAGAAGUAUGUUAUUgaaa AAUAGCAUAAUGAGUUAGAAU AGGUUUCUAAACCUAUAUAGCCA AUUCAUUUGGUUUCGCUUAGGC GAAAAAUGAGAGUUCUAAUUAU UUAGGACUCUUAUUUUUUU (SEQ ID NO: 1514)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGAUAUUUAUGUU (SEQ ID NO: 1478)	GUUCUAGAAGUAUGUUAUU (SEQ ID NO: 1515)
	Partial crRNA 1	GUUCUAGAUAUUUAUGU (SEQ ID NO: 1479)	GUUCUAGAAGUAUGU (SEQ ID NO: 1516)

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	Partial crRNA 2	GUUCUAGAUIUA (SEQ ID NO: 1480)	GUUCUAGAAGUA (SEQ ID NO: 1517)
	Partial crRNA 3	GUUCUAGAUI (SEQ ID NO: 1481)	GUUCUAGAAG (SEQ ID NO: 1518)
	tracrRNA (Antirepeat)	AGCAUAAAUGAGUUAGAAU (SEQ ID NO: 1482)	AAUAGCAUAAAUGAGUUAGAAU (SEQ ID NO: 1519)
	Partial tracrRNA 1	AGCAUAAAUGAGUUAGAAU (SEQ ID NO: 1483)	GCAUAAAUGAGUUAGAAU (SEQ ID NO: 1520)
	Partial tracrRNA 2	UAAAUGAGUUAGAAU (SEQ ID NO: 1484)	UAAUGAGUUAGAAU (SEQ ID NO: 1521)
	Partial tracrRNA 3	AAUGAGUUAGAAU (SEQ ID NO: 1485)	AUGAGUUAGAAU (SEQ ID NO: 1522)
tracrRNA V2 sequences	tracrRNA Portion 1	AAGGUAGAACCUUAAAUGC CAAUUAAUUAUUGGUUCUG CUUAGGCAAGU (SEQ ID NO: 1486)	AAGGUUUCUAACCUAUAAU (SEQ ID NO: 1523)
	tracrRNA Portion 1 - partial	AAGGUAGAACCUUAAAUGC CAAUUAAUUAUUGGUUCUG CUU (SEQ ID NO: 1487)	AAGGUUUCUAACCU (SEQ ID NO: 1524)
	tracrRNA Portion 2	AAAGUCUUAGUUAUCUAAG GCUUUUUUU (SEQ ID NO: 1488)	-
	tracrRNA Portion 2 - partial	AAAGUCUUAGUUAUCUAAG GCUUU (SEQ ID NO: 1489)	-
	tracrRNA Portion 2 – without polyT	AAAGUCUUAGUUAUCUAAG GC (SEQ ID NO: 1490)	-
	tracrRNA Portion 4	-	AAAUGAGAGUUCUAAUUAUUUA GGACUCUUAUUUUUUU (SEQ ID NO: 1525)
	tracrRNA Portion 4 - partial	-	AAAUGAGAGUUCUAAUUAUUUA GGACUCUUAUUU (SEQ ID NO: 1526)
	tracrRNA Portion 4 - without polyT	-	AAAUGAGAGUUCUAAUUAUUUA GGACUCUUA (SEQ ID NO: 1527)
	sgRNA V3 sequence	GUUUUAGAUIUAUGUUGaaa AGCAUAAAUGAGUUAUUUA AAGGUAAAACCUUAAAUGC CAAUUAAUUAUUGGUUUUG CUUAGGCAAGUAAAGUCUU AGUUAUCUAAGGCUUUUUU UAUUUUUU (SEQ ID NO: 1491)	GUUUUAGAAGUAUGUUAUUgaaa AAUAGCAUAAAUGAGUUAUUUA AGGUUUUUUAACCUAUAUAGCCA AUUCAUUUGGUUUCGCUUAGGC GAAAAAUGAGAGUUCUAAUUAU UUAGGACUUUUUU (SEQ ID NO: 1528)

		OMNI-336	OMNI-337
tracrRNA V3 sequences	tracrRNA Portion 1	AAGGUAAAACCUUAAAUGC CAAUUUAAUAUUGGUUUUG CUUAGGC (SEQ ID NO: 1492)	-
	tracrRNA Portion 2	AAGUAAAGUCUUAGUUAUC UAAGGCUUUUUUUUAUUUUU U (SEQ ID NO: 1493)	-
	tracrRNA Portion 2 - partial	AAGUAAAGUCUUAGUUAUC UAAGGCUUUUUUUU (SEQ ID NO: 1494)	-
	tracrRNA Portion 2 – without polyT	AAGUAAAGUCUUAGUUAUC UAAGGCUUUUUUUA (SEQ ID NO: 1495)	-
	tracrRNA Portion 3	-	UUCGCUUAGGCGAAAAAU (SEQ ID NO: 1529)
	tracrRNA Portion 4	-	GAGAGUUCUAAUUAUUUAGGAC UUUUUU (SEQ ID NO: 1530)
	tracrRNA Portion 4 - partial	-	GAGAGUUCUAAUUAUUUAGGAC UUUU (SEQ ID NO: 1531)
	tracrRNA Portion 4 - without polyT	-	GAGAGUUCUAAUUAUUUAGGAC (SEQ ID NO: 1532)
	sgRNA V4 sequence	-	GUUCUAGAAGUAUGUUAUUGaaa AAUAGCAUAAUGAGUUAGAAUA AGGUUUCUAACCUAUAAGCCA AUUCAUUUGGUUUCGCUUAGGC GAAAAAUGAGAGUUCUAAUUAU UUAGGACUUUUUU (SEQ ID NO: 1533)

		OMNI-338	OMNI-339
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACAAGUUCAAA UAAAAAUUUAUUCAACCCG UCGCUUUGCGACCUCACAG UGUGUGAGUUACGACCUGC UUUUAAGUAGGUCUUUUUU (SEQ ID NO: 1534)	GUUUGAGAGUAGUGUAAgaaaUU ACACUACAAGUUCAAAUAGCU UAUAGCGAAAUCAUCGCAUUGC GAACUCACAGUGGGUGAGCGAA AAAGACUCCUUCGGGAGUCUUU UUU (SEQ ID NO: 1557)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1535)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1558)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1536)	GUUUGAGAGUAGUGU (SEQ ID NO: 1559)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1537)	GUUUGAGAGUAG (SEQ ID NO: 1560)

		OMNI-338	OMNI-339
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1538)	GUUUGAGAGU (SEQ ID NO: 1561)
	tracrRNA (Antirepeat)	UUACACUACAAGUUCAAAU (SEQ ID NO: 1539)	UUACACUACAAGUUCAAAU (SEQ ID NO: 1562)
	Partial tracrRNA 1	ACACUACAAGUUCAAAU (SEQ ID NO: 1540)	ACACUACAAGUUCAAAU (SEQ ID NO: 1563)
	Partial tracrRNA 2	CUACAAGUUCAAAU (SEQ ID NO: 1541)	CUACAAGUUCAAAU (SEQ ID NO: 1564)
	Partial tracrRNA 3	ACAAGUUCAAAU (SEQ ID NO: 1542)	ACAAGUUCAAAU (SEQ ID NO: 1565)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAAAUUUUAUUAACCCGU CGCUUUGCGAC (SEQ ID NO: 1543)	AAGCUUAUAGCGAAAUCAUCGC AUU (SEQ ID NO: 1566)
	tracrRNA Portion 1 - partial	AAAAAUUUUAUUAACCCGU CGCUUUGCGAC (SEQ ID NO: 1544)	AAGCUUAUAGCGAAAUCAUCGC (SEQ ID NO: 1567)
	tracrRNA Portion 2	CUCACAGUGUGAGUUAC (SEQ ID NO: 1545)	GCGAACUCACAGUGGGUGAGC (SEQ ID NO: 1568)
	tracrRNA Portion 2 - partial	CUCACAGUGUGAG (SEQ ID NO: 1546)	GCGAACUCACAGUGGGUGAGC (SEQ ID NO: 1569)
	tracrRNA Portion 3	GACCUGCUUUUAAGUAGGU CUUUUUU (SEQ ID NO: 1547)	GAAAAAGACUCCUUCGGGAGUC UUUUUU (SEQ ID NO: 1570)
	tracrRNA Portion 3 - partial	GACCUGCUUUUAAGUAGGU C (SEQ ID NO: 1548)	GAAAAAGACUCCUUCGGGAGUC UUUUUU (SEQ ID NO: 1571)
	tracrRNA Portion 3 - without polyT	GACCUGCUUUUAAGUAGGU C (SEQ ID NO: 1549)	GAAAAAGACUCCUUCGGGAGUC (SEQ ID NO: 1572)
	sgRNA V2 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACAAGUUCAAA UAAAAAUUUUAUUAACCCG UCGCUUUGCGACCUCACAG UGUGUGAGUUACGACCUGC UUUCAAGUAGGUCUUUUUU (SEQ ID NO: 1550)	-
tracrRNA V2 sequences	tracrRNA Portion 3	GACCUGCUUUAAGUAGGU CUUUUUU (SEQ ID NO: 1551)	-
	tracrRNA Portion 3 - partial	GACCUGCUUUAAGUAGGU C (SEQ ID NO: 1552)	-
	tracrRNA Portion 3 - without polyT	GACCUGCUUUAAGUAGGU C (SEQ ID NO: 1553)	-

		OMNI-338	OMNI-339
	sgRNA V3 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACAAGUUCAAA UAAAAAUUUAUUCAACCCG UCGCUUUGCGACCUCACAG UGUGUGAGUUACGACCUGC UUUUUU (SEQ ID NO: 1554)	-
tracrRNA V3 sequences	tracrRNA Portion 2	CUCACAGUGUGAGUUAC GACCUGCUUUUUU (SEQ ID NO: 1555)	-
	tracrRNA Portion 2 – without polyT	CUCACAGUGUGAGUUAC GACCUGC (SEQ ID NO: 1556)	-

		OMNI-340	OMNI-341
	sgRNA V1 sequence	GUUUUAGGUCUAUGUAAgaa aUUACAUAGCAGUAAAAU AAAUGUUAACAAAAAGCC UUUUUAAUAAGGUGUUGCG UUGGCAACGAAUUUAGAGG ACCUUUUCGGUUCUCUUUU UUUGUUGUAAAAGCUUUGU AGAAAUGCUUUGCAUUUUU GCGGUAUUGCCCAUGCAAA CUUUUUU (SEQ ID NO: 1573)	GUUUGAGAGUAGUGUAgaaaUAC ACUACUAAGUUCAAAUAAGCUU UUAGCGAAAUCAUCGUUUAACG AAUUCACAGUGUGUGAACCUUU UUU (SEQ ID NO: 1618)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGGUCUAUGUAA (SEQ ID NO: 1574)	GUUUGAGAGUAGUGUA (SEQ ID NO: 1619)
	Partial crRNA 1	GUUUUAGGUCUAUGU (SEQ ID NO: 1575)	GUUUGAGAGUAGUGU (SEQ ID NO: 1620)
	Partial crRNA 2	GUUUUAGGUCUA (SEQ ID NO: 1576)	GUUUGAGAGUAG (SEQ ID NO: 1621)
	Partial crRNA 3	GUUUUAGGUC (SEQ ID NO: 1577)	GUUUGAGAGU (SEQ ID NO: 1622)
	tracrRNA (Antirepeat)	UUACAUAGCAGUAAAAU (SEQ ID NO: 1578)	UACACUACUAAGUUCAAAU (SEQ ID NO: 1623)
	Partial tracrRNA 1	ACAUAGCAGUAAAAU (SEQ ID NO: 1579)	ACACUACUAAGUUCAAAU (SEQ ID NO: 1624)
	Partial tracrRNA 2	UAGCAGUAAAAU (SEQ ID NO: 1580)	CUACUAAGUUCAAAU (SEQ ID NO: 1625)
	Partial tracrRNA 3	GCAGUAAAAU (SEQ ID NO: 1581)	ACUAAGUUCAAAU (SEQ ID NO: 1626)

		OMNI-340	OMNI-341
tracrRNA V1 sequences	tracrRNA Portion 1	AAAUGUUAACAAAAAGCC UUUUUAAUAAGGUGUU (SEQ ID NO: 1582)	AAGCUUUUAGCGAAAUCAUCGU UUAACGAA (SEQ ID NO: 1627)
	tracrRNA Portion 1 - partial	AAAUGUUAACAAAAAGCC UUUUUAAUAAGGU (SEQ ID NO: 1583)	AAGCUUUUAGCGAAAUCAUCGU U (SEQ ID NO: 1628)
	tracrRNA Portion 2	GCGUUGGCAACGAAUUUAG AGGACCUUUUCGGUUCUCU UUUUUUGUUGUAAAAGCUU U (SEQ ID NO: 1584)	UUCACAGUGUGUGAACC UUUUU U (SEQ ID NO: 1629)
	tracrRNA Portion 2 - partial	GCGUUGGCAACGAAUUUAG AGGACCUUUUCGGUUCUCU UUUUUUGUUGUAAAAGC (SEQ ID NO: 1585)	UUCACAGUGUGUGAA (SEQ ID NO: 1630)
	tracrRNA Portion 2 – without polyT	-	UUCACAGUGUGUGAACC (SEQ ID NO: 1631)
	tracrRNA Portion 3	GUAGAAAUGCUUUGCAUUU UUGC (SEQ ID NO: 1586)	-
	tracrRNA Portion 3 - partial	GUAGAAAUGCUUUGCAUUU UUGC (SEQ ID NO: 1587)	-
	tracrRNA Portion 4	GGUAUUGCCCAUGCAAACU UUUUU (SEQ ID NO: 1588)	-
	tracrRNA Portion 4 - partial	GGUAUUGCCCAUGCAAACU (SEQ ID NO: 1589)	-
	tracrRNA Portion 4 - without polyT	GGUAUUGCCCAUGCAAAC (SEQ ID NO: 1590)	-
	sgRNA V2 sequence	GUUCUAGGUCUAUGUAAgaa aUUACAUAGCAGUUAGAAU AAAUGUUAACAAAAAGCC UUUCUAAUAAGGUGUUGCG UUGGCAACGAAUUUAGAGG ACCUUCUCGGUUCUCUUUC UUUGUUGUAAAAGCUUUGU AGAAAUGCUUUGCAUUUCU GCGGUAUUGCCCAUGCAA CUUUUUU (SEQ ID NO: 1591)	GUUUGAGAGUAGUGUAgaaaUAC ACUACUAAGUUCAAAUAAGCUU CUAGCGAAAUCAUCGUUUAACG AAUUCACAGUGUGUGAACC UUU UUU (SEQ ID NO: 1632)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGGUCUAUGUAA (SEQ ID NO: 1592)	-
	Partial crRNA 1	GUUCUAGGUCUAUGU (SEQ ID NO: 1593)	-
	Partial crRNA 2	GUUCUAGGUCUA (SEQ ID NO: 1594)	-

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	Partial crRNA 3	GUUCUAGGUC (SEQ ID NO: 1595)	-
	tracrRNA (Antirepeat)	UUACAUAGCAGUUAGAAU (SEQ ID NO: 1596)	-
	Partial tracrRNA 1	ACAUAGCAGUUAGAAU (SEQ ID NO: 1597)	-
	Partial tracrRNA 2	UAGCAGUUAGAAU (SEQ ID NO: 1598)	-
	Partial tracrRNA 3	GCAGUUAGAAU (SEQ ID NO: 1599)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAAUGUUAAACAAAAAGCC UUUCUAAUAAGGUGUU (SEQ ID NO: 1600)	AAGCUUCUAGCGAAAUCAUCGU UUAACGAA (SEQ ID NO: 1633)
	tracrRNA Portion 1 - partial	AAAUGUUAAACAAAAAGCC UUUCUAAUAAGGU (SEQ ID NO: 1601)	AAGCUUCUAGCGAAAUCAUCGU U (SEQ ID NO: 1634)
	tracrRNA Portion 2	GCGUUGGCAACGAAUUUAG AGGACCUUCUCGGUUCUCU UUCUUUGUUGUAAAAGCUU U (SEQ ID NO: 1602)	-
	tracrRNA Portion 2 - partial	GCGUUGGCAACGAAUUUAG AGGACCUUCUCGGUUCUCU UUCUUUGUUGUAAAAGC (SEQ ID NO: 1603)	-
	tracrRNA Portion 3	GUAGAAUUGCUUUGCAUUU CUGC (SEQ ID NO: 1604)	-
	tracrRNA Portion 3 - partial	GUAGAAUUGCUUUGCAUUU CUGC (SEQ ID NO: 1605)	-
	sgRNA V3 sequence	GUUUUAGGUCUAUGUAAgaa aUUACAUAGCAGUUAAAAU AAAUGUUAAACAAAAAGCC UUUUUAAUAAGGUGUUGCG UUGGCAACGAAUUUAGAGG ACCUUUUCGGUUCUCUUUU UUU (SEQ ID NO: 1606)	-
tracrRNA V3 sequences	tracrRNA Portion 1	AAAUGUUAAACAAAAAGCC UUUUUAAUAAGGU (SEQ ID NO: 1607)	-
	tracrRNA Portion 2	GUUGCGUUGGCAACGAAUU U (SEQ ID NO: 1608)	-
	tracrRNA Portion 2 - partial	GUUGCGUUGGCAAC (SEQ ID NO: 1609)	-
	tracrRNA Portion 3	AGAGGACCUUUUCGGUUCU CUUUUUUU (SEQ ID NO: 1610)	-

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	tracrRNA Portion 3 - partial	AGAGGACCUUUUCGGUUCU CU (SEQ ID NO: 1611)	-
	tracrRNA Portion 3 - without polyT	AGAGGACCUUUUCGGUUCU C (SEQ ID NO: 1612)	-
	sgRNA V4 sequence	GUUCUAGGUCUAUGUAAgaa aUUACAUAGCAGUUAGAAU AAAUGUUAACAAAAAGCC UUUCUAAUAAGGUGUUGCG UUGGCAACGAAUUUAGAGG ACCUUCUCGGUUCUCUUUU UUU (SEQ ID NO: 1613)	-
tracrRNA V4 sequences	tracrRNA Portion 1	AAAUGUUAACAAAAAGCC UUUCUAAUAAGGU (SEQ ID NO: 1614)	-
	tracrRNA Portion 3	AGAGGACCUUCUCGGUUCU CUUUUUUU (SEQ ID NO: 1615)	-
	tracrRNA Portion 3 - partial	AGAGGACCUUCUCGGUUCU CU (SEQ ID NO: 1616)	-
	tracrRNA Portion 3 - without polyT	AGAGGACCUUCUCGGUUCU C (SEQ ID NO: 1617)	-
	tracrRNA Portion 4	-	-
	tracrRNA Portion 4 - partial	-	-
	tracrRNA Portion 4 - without polyT	-	-

		OMNI-342	OMNI-343
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUAUGCGUUCAAA UAACGAUUUAUCGAAACCG CUGCUUUGCAGCAUCACAG UGUGUGAUUAAAGACCGU UCACCAGGUCUUUUUU (SEQ ID NO: 1635)	GUUUGAGUAUGGUGUAAgaaaUU ACACCAUUAGUUCAAAUAAGAU UUUUUCAAACCGCCGUUAUUCG GUCGCACACGCUGUGGCAAUA GGAACUGUUGCGUUGCAGCAGU UCUUUUUU (SEQ ID NO: 1656)
	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1636)	GUUUGAGUAUGGUGUAA (SEQ ID NO: 1657)

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crRNA:tracrRNA duplex V1 sequences	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1637)	GUUUGAGUAUGGUGU (SEQ ID NO: 1658)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1638)	GUUUGAGUAUGG (SEQ ID NO: 1659)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1639)	GUUUGAGUAU (SEQ ID NO: 1660)
	tracrRNA (Antirepeat)	UUACACUAUGCGUUCAAAU (SEQ ID NO: 1640)	UUACACCAUUAGUUCAAAU (SEQ ID NO: 1661)
	Partial tracrRNA 1	ACACUAUGCGUUCAAAU (SEQ ID NO: 1641)	ACACCAUUAGUUCAAAU (SEQ ID NO: 1662)
	Partial tracrRNA 2	CUAUGCGUUCAAAU (SEQ ID NO: 1642)	CCAUUAGUUCAAAU (SEQ ID NO: 1663)
	Partial tracrRNA 3	AUGCGUUCAAAU (SEQ ID NO: 1643)	AUUAGUUCAAAU (SEQ ID NO: 1664)
tracrRNA V1 sequences	tracrRNA Portion 1	AACGAUUUAUCGAAACC (SEQ ID NO: 1644)	AAGAUUUUUUCAAACCGCCGUU AUUCGGUC (SEQ ID NO: 1665)
	tracrRNA Portion 1 - partial	AACGAUUUAUCG (SEQ ID NO: 1645)	AAGAUUUUUUCAAACCGCCGUU AUUCGGU (SEQ ID NO: 1666)
	tracrRNA Portion 2	GCUGCUUUGCAGC (SEQ ID NO: 1646)	GCACACGCUGUGUGCAAU (SEQ ID NO: 1667)
	tracrRNA Portion 2 - partial	GCUGCUUUGCAGC (SEQ ID NO: 1647)	GCACACGCUGUGUGC (SEQ ID NO: 1668)
	tracrRNA Portion 3	AUCACAGUGUGUGAUU (SEQ ID NO: 1648)	AGGAACUGUUGCGUUGCAGCAG UUCUUUUUU (SEQ ID NO: 1669)
	tracrRNA Portion 3 - partial	AUCACAGUGUGUGAU (SEQ ID NO: 1649)	AGGAACUGUUGCGUUGCAGCAG UUCUU (SEQ ID NO: 1670)
	tracrRNA Portion 3 - without polyT	-	AGGAACUGUUGCGUUGCAGCAG UUC (SEQ ID NO: 1671)
	tracrRNA Portion 4	AAAGACCUGUUCACCAGGU CUUUUUU (SEQ ID NO: 1650)	-
	tracrRNA Portion 4 - partial	AAAGACCUGUUCACCAGGU CUUU (SEQ ID NO: 1651)	-
	tracrRNA Portion 4 - without polyT	AAAGACCUGUUCACCAGGU C (SEQ ID NO: 1652)	-

		OMNI-342	OMNI-343
	sgRNA V2 sequence	-	GUUUGAGUAUGGUGUAAgaaUU ACACCAUUAGUUCAAAUAAGAU UCUUUCAAACCGCCGUUAUUCG GUCGCACACGCUGUGUGCAAUA GGAACUGUUGCGUUGCAGCAGU UCUUUUUU (SEQ ID NO: 1672)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AAGAUUCUUUCAAACCGCCGUU AUUCGGUC (SEQ ID NO: 1673)
	tracrRNA Portion 1 - partial	-	AAGAUUCUUUCAAACCGCCGUU AUUCGGU (SEQ ID NO: 1674)
	sgRNA V3 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUAUGCGUUCAAA UAACGAUUUAUCGAAACCG CUGCUUUGCAGCAUCACAG UGUGUGAUUUUUU (SEQ ID NO: 1653)	-
tracrRNA V3 sequences	tracrRNA Portion 3	AUCACAGUGUGUGAUUUUU U (SEQ ID NO: 1654)	-
	tracrRNA Portion 3 - without polyT	AUCACAGUGUGUGA (SEQ ID NO: 1655)	-

		OMNI-344	OMNI-345
	sgRNA V1 sequence	GUUUGAGAGUAGUGUUAga aUAACACUACAAGUUCAAA UAAGCUUCGUAGCGAAUCG AUCGCCUUUGGCGAACUCA CAGUGUGUGAGACAGCAGA CCCCGAAAGGGGUCUGUUU UUU (SEQ ID NO: 1675)	GUUUGAGAGUAGUGUAAgaaUU ACACUACAAGUUCAAAUAAGCU UUUAGCGAAAACAUCGCCUUCG GCGAAUUCACAGUGUGUGAACU AACAGACUCUUUCAAGGGUCUG UUUUUU (SEQ ID NO: 1702)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUUA (SEQ ID NO: 1676)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1703)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1677)	GUUUGAGAGUAGUGU (SEQ ID NO: 1704)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1678)	GUUUGAGAGUAG (SEQ ID NO: 1705)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1679)	GUUUGAGAGU (SEQ ID NO: 1706)
	tracrRNA (Antirepeat)	UAACACUACAAGUUCAAA (SEQ ID NO: 1680)	UUACACUACAAGUUCAAA (SEQ ID NO: 1707)

		OMNI-344	OMNI-345
	Partial tracrRNA 1	ACACUACAAGUUCAAAU (SEQ ID NO: 1681)	ACACUACAAGUUCAAAU (SEQ ID NO: 1708)
	Partial tracrRNA 2	CUACAAGUUCAAAU (SEQ ID NO: 1682)	CUACAAGUUCAAAU (SEQ ID NO: 1709)
	Partial tracrRNA 3	ACAAGUUCAAAU (SEQ ID NO: 1683)	ACAAGUUCAAAU (SEQ ID NO: 1710)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGCUUCGUAGCGAAUCGA (SEQ ID NO: 1684)	AAGCUUUUAGCGAAAACA (SEQ ID NO: 1711)
	tracrRNA Portion 1 - partial	AAGCUUCGUAGC (SEQ ID NO: 1685)	AAGCUUUUAGC (SEQ ID NO: 1712)
	tracrRNA Portion 2	UCGCCUUUGGCGAA (SEQ ID NO: 1686)	UCGCCUUCGGCGAA (SEQ ID NO: 1713)
	tracrRNA Portion 2 - partial	UCGCCUUUGGCGA (SEQ ID NO: 1687)	UCGCCUUCGGCGA (SEQ ID NO: 1714)
	tracrRNA Portion 3	CUCACAGUGUGAGAGAC (SEQ ID NO: 1688)	UUCACAGUGUGUGAACU (SEQ ID NO: 1715)
	tracrRNA Portion 3 - partial	CUCACAGUGUGAG (SEQ ID NO: 1689)	UUCACAGUGUGUGAA (SEQ ID NO: 1716)
	tracrRNA Portion 4	AGCAGACCCCGAAAGGGGU CUGUUUUUU (SEQ ID NO: 1690)	AACAGACUCUUUCAAGGGUCUG UUUUUU (SEQ ID NO: 1717)
	tracrRNA Portion 4 - partial	AGCAGACCCCGAAAGGGGU CUGUU (SEQ ID NO: 1691)	AACAGACUCUUUCAAGGGUCUG UU (SEQ ID NO: 1718)
	tracrRNA Portion 4 - without polyT	AGCAGACCCCGAAAGGGGU CUG (SEQ ID NO: 1692)	AACAGACUCUUUCAAGGGUCUG (SEQ ID NO: 1719)
	sgRNA V2 sequence	-	GUUUGAGAGUAGUGUAAgaaaUU ACACUACAAGUUCAAAUAAGCU UCUAGCGAAAACAUCGCCUUCG GCGAAUUCACAGUGUGUGAACU AACAGACUCUUUCAAGGGUCUG UUUUUU (SEQ ID NO: 1720)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AAGCUUCUAGCGAAAACA (SEQ ID NO: 1721)
	tracrRNA Portion 1 - partial	-	AAGCUUCUAGC (SEQ ID NO: 1722)
	sgRNA V3 sequence	GUUUGAGAGUAGUGUUAga aUAACACUACAAGUUCAAA UAAGCUUCGUAGCGAAUCG AUCGCCUUUGGCGAACUCA CAGUGUGUGAGACAGCAGA	GUUUGAGAGUAGUGUAAgaaaUU ACACUACAAGUUCAAAUAAGCU UUUAGCGAAAACAUCGCCUUCG GCGAAUUUUUU (SEQ ID NO: 1723)

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		CCCCGAAAGGGGUCUGUUU UUAUUUUUAUGCGCAUUUUU U (SEQ ID NO: 1693)	
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGCUUUUAGC (SEQ ID NO: 1724)
	tracrRNA Portion 2	UCGCCUUUGGCGAACUCAC A (SEQ ID NO: 1694)	GAAAACAUCGCCUUCGGCGAAU UUUUU (SEQ ID NO: 1725)
	tracrRNA Portion 2 - partial	-	GAAAACAUCGCCUUCGGCGAAU UUUUU (SEQ ID NO: 1726)
	tracrRNA Portion 2 – without polyT	-	GAAAACAUCGCCUUCGGCGAA (SEQ ID NO: 1727)
	tracrRNA Portion 3	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUUUU AUUUUAUGCGCAUUUUU (SEQ ID NO: 1695)	-
	tracrRNA Portion 3 - partial	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUUUU AUUUUAUGCGC (SEQ ID NO: 1696)	-
	tracrRNA Portion 3 - without polyT	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUUUU AUUUUAUGCGCA (SEQ ID NO: 1697)	-
	sgRNA V4 sequence	GUUUGAGAGUAGUGUUAga aUAACACUACAAGUUCAAA UAAGCUUCGUAGCGAAUCG AUCGCCUUUGGCGAACUCA CAGUGUGUGAGACAGCAGA CCCCGAAAGGGGUCUGUUC UUAUCUUAUGCGCAUUUUU U (SEQ ID NO: 1698)	GUUUGAGAGUAGUGUAAga aUAACACUACAAGUUCAAA UAAGCUUCGUAGCGAAUCG AUCGCCUUUGGCGAACUCA CAGUGUGUGAGACAGCAGA CCCCGAAAGGGGUCUGUUC UUAUCUUAUGCGCAUUUUU (SEQ ID NO: 1728)
tracrRNA V4 sequences	tracrRNA Portion 1	-	AAGCUUCUAGC (SEQ ID NO: 1729)
	tracrRNA Portion 3	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUCUU AUCUUAUGCGCAUUUUU (SEQ ID NO: 1699)	-
	tracrRNA Portion 3 - partial	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUCUU AUCUUAUGCGC (SEQ ID NO: 1700)	-
	tracrRNA Portion 3 - without polyT	GUGUGUGAGACAGCAGACC CCGAAAGGGGUCUGUUCUU AUCUUAUGCGCA (SEQ ID NO: 1701)	-

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	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAgaa aUCACACUACAAGUUCAAA UAAGCUUUUAGCGAAGACA UCGCCUCUGGCGAACUCAC AGUGUGAGAGACAACAGAC UCCGAAAGGGGUCUGUUUU UU (SEQ ID NO: 1730)	GUUUGAGAGUAGUGUAAgaaaUU ACACUACAAAGUUCAAAUAAGC UUGUAGCGAAACCAUCGCGUAA GCGAACUCACAGUGUGUGAGAU CAAAAAGCUCCGAAAGGAGCUU UUUU (SEQ ID NO: 1748)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1731)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1749)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1732)	GUUUGAGAGUAGUGU (SEQ ID NO: 1750)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1733)	GUUUGAGAGUAG (SEQ ID NO: 1751)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1734)	GUUUGAGAGU (SEQ ID NO: 1752)
	tracrRNA (Antirepeat)	UCACACUACAAGUUCAAAU (SEQ ID NO: 1735)	UUACACUACAAGUUCAAAU (SEQ ID NO: 1753)
	Partial tracrRNA 1	UCACACUACAAGUUCAAAU (SEQ ID NO: 1736)	ACACUACAAGUUCAAAU (SEQ ID NO: 1754)
	Partial tracrRNA 2	CUACAAGUUCAAAU (SEQ ID NO: 1737)	CUACAAGUUCAAAU (SEQ ID NO: 1755)
	Partial tracrRNA 3	ACAAGUUCAAAU (SEQ ID NO: 1738)	ACAAAGUUCAAAU (SEQ ID NO: 1756)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGCUUUUAGCGAAGACA (SEQ ID NO: 1739)	AAGCUUGUAGCGAAACCAUCGC GUAAGC (SEQ ID NO: 1757)
	tracrRNA Portion 1 - partial	AAGCUUUUAGC (SEQ ID NO: 1740)	AAGCUUGUAGCGAAACCAUCGC GUAAGC (SEQ ID NO: 1758)
	tracrRNA Portion 2	UCGCCUCUGGCGAA (SEQ ID NO: 1741)	GAACUCACAGUGUGUGAGAUC (SEQ ID NO: 1759)
	tracrRNA Portion 2 - partial	UCGCCUCUGGCGA (SEQ ID NO: 1742)	GAACUCACAGUGUGUGAGAUC (SEQ ID NO: 1760)
	tracrRNA Portion 3	CUCACAGUGUGUGAGAC (SEQ ID NO: 1743)	AAAAAGCUCCGAAAGGAGCUUU UUU (SEQ ID NO: 1761)
	tracrRNA Portion 3 - partial	CUCACAGUGUGUGAG (SEQ ID NO: 1744)	AAAAAGCUCCGAAAGGAGCUUU U (SEQ ID NO: 1762)
	tracrRNA Portion 3 - without polyT	-	AAAAAGCUCCGAAAGGAGC (SEQ ID NO: 1763)

		OMNI-346	OMNI-347
	tracrRNA Portion 4	AACAGACUCCGAAAGGGGU CUGUUUUUU (SEQ ID NO: 1745)	-
	tracrRNA Portion 4 - partial	AACAGACUCCGAAAGGGGU CUGUU (SEQ ID NO: 1746)	-
	tracrRNA Portion 4 - without polyT	AACAGACUCCGAAAGGGGU CUG (SEQ ID NO: 1747)	-
	sgRNA V3 sequence	-	GUUUGAGAGUAGUGUAAgaaUU ACACUACAAAGUUCAAAUAAGC UUGUAGCGAAACCAUCGCGUAA GCGAACUCACAGUGUGUGAGAU CAAAAAGCUCCGAAAGGAGCUU UUUGUUUUUU (SEQ ID NO: 1764)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGCUUGUAGCGAAACCAUCGC GUAAGCGAA (SEQ ID NO: 1765)
	tracrRNA Portion 2	-	CUCACAGUGUGUGAGAU (SEQ ID NO: 1766)
	tracrRNA Portion 2 - partial	-	CUCACAGUGUGUGAG (SEQ ID NO: 1767)
	tracrRNA Portion 3	-	CAAAAAGCUCCGAAAGGAGCUU UUUGUUUUUU (SEQ ID NO: 1768)
	tracrRNA Portion 3 - partial	-	CAAAAAGCUCCGAAAGGAGCUU UUUG (SEQ ID NO: 1769)
	tracrRNA Portion 3 - without polyT	-	CAAAAAGCUCCGAAAGGAGCUU UUUG (SEQ ID NO: 1770)
	sgRNA V4 sequence	-	GUUUGAGAGUAGUGUAAgaaUU ACACUACAAAGUUCAAAUAAGC UUGUAGCGAAACCAUCGCGUAA GCGAACUCACAGUGUGUGAGAU CAAGAAGCUCCGAAAGGAGCUU CUUGUUUUUU (SEQ ID NO: 1771)
tracrRNA V4 sequences	tracrRNA Portion 3	-	CAAGAAGCUCCGAAAGGAGCUU CUUGUUUUUU (SEQ ID NO: 1772)
	tracrRNA Portion 3 - partial	-	CAAGAAGCUCCGAAAGGAGCUU CUUG (SEQ ID NO: 1773)
	tracrRNA Portion 3 - without polyT	-	CAAGAAGCUCCGAAAGGAGCUU CUUG (SEQ ID NO: 1774)

		OMNI-348	OMNI-349
	sgRNA V1 sequence	GUUUUAGUUCUAUGUCgaaa GACAUAGAGAGUUAAAAUA AAGGUUUUCGUUUCGAUUA CCCAAAAUGCCCAUUUAUU AUGUGGCCGACUACUUAGG UAGUCAUUUUUU (SEQ ID NO: 1775)	GUUUGAGAGUAGUGUAAgaaaUU ACACUAUGAGUUCAAAUAACU UUUUUCAAUCGCCGCUUAUGC GGUUCACGCUGUGUGAAUUAAG CUCUCAUCUGUGGGAGCUUUUU U (SEQ ID NO: 1802)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGUUCUAUGUC (SEQ ID NO: 1776)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1803)
	Partial crRNA 1	GUUUUAGUUCUAUGU (SEQ ID NO: 1777)	GUUUGAGAGUAGUGU (SEQ ID NO: 1804)
	Partial crRNA 2	GUUUUAGUUCUA (SEQ ID NO: 1778)	GUUUGAGAGUAG (SEQ ID NO: 1805)
	Partial crRNA 3	GUUUUAGUUC (SEQ ID NO: 1779)	GUUUGAGAGU (SEQ ID NO: 1806)
	tracrRNA (Antirepeat)	GACAUAGAGAGUUAAAAU (SEQ ID NO: 1780)	UUACACUAUGAGUUCAAAU (SEQ ID NO: 1807)
	Partial tracrRNA 1	ACAUAGAGAGUUAAAAU (SEQ ID NO: 1781)	ACACUAUGAGUUCAAAU (SEQ ID NO: 1808)
	Partial tracrRNA 2	UAGAGAGUUAAAAU (SEQ ID NO: 1782)	CUAUGAGUUCAAAU (SEQ ID NO: 1809)
	Partial tracrRNA 3	GAGAGUUAAAAU (SEQ ID NO: 1783)	AUGAGUUCAAAU (SEQ ID NO: 1810)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGGUUUUCGUUUCGAUU ACCCAAAAU (SEQ ID NO: 1784)	AAACUUUUUCAAUCGCCGCU UAUGCGGU (SEQ ID NO: 1811)
	tracrRNA Portion 1 - partial	AAAGGUUUUCGUUUCGAUU ACC (SEQ ID NO: 1785)	AAACUUUUUCAAUCGCCGCU UAUGCGGU (SEQ ID NO: 1812)
	tracrRNA Portion 2	GCCCAUUUAUUAUGUGGCC (SEQ ID NO: 1786)	UCACGCUGUGUGAAUU (SEQ ID NO: 1813)
	tracrRNA Portion 2 - partial	GCCCAUUUAUUAUGUGGCC (SEQ ID NO: 1787)	UCACGCUGUGUGA (SEQ ID NO: 1814)
	tracrRNA Portion 3	GACUACUUAGGUAGUCAUU UUUU (SEQ ID NO: 1788)	AAGCUCUCAUCUGUGGGAGCUU UUUU (SEQ ID NO: 1815)
	tracrRNA Portion 3 - partial	GACUACUUAGGUAGUC (SEQ ID NO: 1789)	AAGCUCUCAUCUGUGGGAGCUU (SEQ ID NO: 1816)
	tracrRNA Portion 3 - without polyT	GACUACUUAGGUAGUCA (SEQ ID NO: 1790)	AAGCUCUCAUCUGUGGGAGC (SEQ ID NO: 1817)

		OMNI-348	OMNI-349
	sgRNA V2 sequence	GUUCUAGUUCUAUGUCgaaa GACAUAGAGAGUUAGAAUA AAGGUUCUCGUUUCGAUUA CCCAAAUGCCCAUUUAUU AUGUGGCCGACUACUUAGG UAGUCAUUUUUU (SEQ ID NO: 1791)	GUUUGAGAGUAGUGUAAgaaaUU ACACUAGAGUUCAAUAAACU UCUUUCAAUUCGCCGCUUAUGC GGUUCACGCUGUGUGAAUUAAG CUCUCAUCUGUGGGAGCUUUUU U (SEQ ID NO: 1818)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGUUCUAUGUC (SEQ ID NO: 1792)	-
	Partial crRNA 1	GUUCUAGUUCUAUGU (SEQ ID NO: 1793)	-
	Partial crRNA 2	GUUCUAGUUCUA (SEQ ID NO: 1794)	-
	Partial crRNA 3	GUUCUAGUUC (SEQ ID NO: 1795)	-
	tracrRNA (Antirepeat)	GACAUAGAGAGUUAGAAU (SEQ ID NO: 1796)	-
	Partial tracrRNA 1	ACAUAGAGAGUUAGAAU (SEQ ID NO: 1797)	-
	Partial tracrRNA 2	UAGAGAGUUAGAAU (SEQ ID NO: 1798)	-
	Partial tracrRNA 3	GAGAGUUAGAAU (SEQ ID NO: 1799)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAAGGUUCUCGUUUCGAUU ACCCAAAUAU (SEQ ID NO: 1800)	AAACUUCUUUCAAUUCGCCGCU UAUGCGGU (SEQ ID NO: 1819)
	tracrRNA Portion 1 - partial	AAAGGUUCUCGUUUCGAUU ACC (SEQ ID NO: 1801)	AAACUUCUUUCAAUUCGCCGCU UAUGCGGU (SEQ ID NO: 1820)
	sgRNA V3 sequence	-	GUUUGAGAGUAGUGUAAgaaaUU ACACUAGAGUUCAAUAAACU UUUUUCAAUUCGCCGCUUAUGC GGUUCACGCUGUGUGAAUUAAG CUCUCAUCUGUGGGAGCUUUUU UAUUGCUUUUUU (SEQ ID NO: 1821)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAACUUUUUUCAAUUCGCCGCU UAUGCGGUUCAC (SEQ ID NO: 1822)
	tracrRNA Portion 2	-	GCUGUGUGAAUUAAGCUCUCAU CUGUGGGAGCUUUUUUAUUGCU UUUUU (SEQ ID NO: 1823)
	tracrRNA Portion 2 - partial	-	GCUGUGUGAAUUAAGCUCUCAU CUGUGGGAGCUUUUUUAUUGC (SEQ ID NO: 1824)

		OMNI-348	OMNI-349
	tracrRNA Portion 2 – without polyT	-	GCUGUGUGAAUUAAGCUCUCAU CUGUGGGAGCUUUUUUAUUGC (SEQ ID NO: 1825)
	sgRNA V4 sequence	-	GUUUGAGAGUAGUGUAAgaaaUU ACACUAUGAGUUCAAAUAACU UCUUUCAAUCGCCGCUUAUGC GGUUCACGUGUGGAAUUAAG CUCUCAUCUGUGGGAGCUUCU UAUUGCUUUUUU (SEQ ID NO: 1826)
tracrRNA V4 sequences	tracrRNA Portion 3	-	AAGCUCUCAUCUGUGGGAGCUU CUUUAUUGCUUUUUU (SEQ ID NO: 1827)
	tracrRNA Portion 3 - without polyT	-	AAGCUCUCAUCUGUGGGAGCUU CUUUAUUGC (SEQ ID NO: 1828)

		OMNI-350	OMNI-351
	sgRNA V1 sequence	GUUUGAGAGUAGUGUUGgaa aCGACACUACAAGUUCAAA UAAAGACUUGUCCAAUUCG UCUCUUUAAGAGGCUCGCG AUAGUGCGGAUAGAGAAUC UACGAAAGUAGAUUCUUUU UU (SEQ ID NO: 1829)	GUUUGAGUAUGGUGUAAgaaaUU ACACUAUUAGUUCAAAUAUU UUUUUCACUUCGCCGAAUUUU CGGUAACACACGUGUGUAC AUCUAUCCGCUUUUAUGUAAGCG GAUUUUUU (SEQ ID NO: 1845)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUUG (SEQ ID NO: 1830)	GUUUGAGUAUGGUGUAA (SEQ ID NO: 1846)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1831)	GUUUGAGUAUGGUGU (SEQ ID NO: 1847)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1832)	GUUUGAGUAUGG (SEQ ID NO: X) (SEQ ID NO: 1848)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1833)	GUUUGAGUAU (SEQ ID NO: 1849)
	tracrRNA (Antirepeat)	CGACACUACAAGUUCAAAU (SEQ ID NO: 1834)	UUACACUAUUAGUUCAAAU (SEQ ID NO: 1850)
	Partial tracrRNA 1	ACACUACAAGUUCAAAU (SEQ ID NO: 1835)	ACACUAUUAGUUCAAAU (SEQ ID NO: 1851)
	Partial tracrRNA 2	CUACAAGUUCAAAU (SEQ ID NO: 1836)	CUAUUAGUUCAAAU (SEQ ID NO: 1852)
	Partial tracrRNA 3	ACAAGUUCAAAU (SEQ ID NO: 1837)	AUUAGUUCAAAU (SEQ ID NO: 1853)

		OMNI-350	OMNI-351
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGACUUGUCCAAAUCGU CUCUUUAAGAGGC (SEQ ID NO: 1838)	AAAAUUUUUUCACAUCGCCGAA AUUUUCGGUA (SEQ ID NO: 1854)
	tracrRNA Portion 1 - partial	AAAGACUUGUCCAAAUCGU CUCUUUAAGAGGC (SEQ ID NO: 1839)	AAAAUUUUUUCACAUCGCCGAA AUUUUCGGU (SEQ ID NO: 1855)
	tracrRNA Portion 2	UCCGCAUAGUGCGGAU (SEQ ID NO: 1840)	ACACACGCUGUGUGUACAUCU (SEQ ID NO: 1856)
	tracrRNA Portion 2 - partial	UCCGCAUAGUGCGGA (SEQ ID NO: 1841)	ACACACGCUGUGUGU (SEQ ID NO: 1857)
	tracrRNA Portion 3	AGAGAAUCUACGAAAGUAG AUUCUUUUUU (SEQ ID NO: 1842)	AUCCGCUUUAUGUAAGCGGAUU UUUU (SEQ ID NO: 1858)
	tracrRNA Portion 3 - partial	AGAGAAUCUACGAAAGUAG AUUCUUU (SEQ ID NO: 1843)	AUCCGCUUUAUGUAAGCGGAU (SEQ ID NO: 1859)
	tracrRNA Portion 3 - without polyT	AGAGAAUCUACGAAAGUAG AUUC (SEQ ID NO: 1844)	AUCCGCUUUAUGUAAGCGGA (SEQ ID NO: 1860)
	sgRNA V2 sequence	-	GUUUGAGUAUGGUGUAAgaaaUU ACACUAUUAGUUCAAAUAAAAU UCUUUCACAUCGCCGAAACUUU CGGUAAACACACGCUGUGUGUAC AUCUAUCCGCUUUAUGUAAGCG GAUUUUUU (SEQ ID NO: 1861)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AAAAUUCUUUCACAUCGCCGAA ACUUUCGGUA (SEQ ID NO: 1862)
	tracrRNA Portion 1 - partial	-	AAAAUUCUUUCACAUCGCCGAA ACUUUCGGU (SEQ ID NO: 1863)
	sgRNA V3 sequence	-	GUUUGAGUAUGGUGUAAgaaaUU ACACUAUUAGUUCAAAUAAAAU UUUUUCACAUCGCCGAAAUUUU CGGUAAACACACGCUGUGUGUUU UUU (SEQ ID NO: 1864)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAAAUUUUUUCACAUCGCCGAA AUUUUCGGU (SEQ ID NO: 1865)
	tracrRNA Portion 2	-	AACACACGCUGUGUGUUUUUU (SEQ ID NO: 1866)
	tracrRNA Portion 2 - partial	-	AACACACGCUGUGUGUU (SEQ ID NO: 1867)
	tracrRNA Portion 2 – without polyT	-	AACACACGCUGUGUG (SEQ ID NO: 1868)

		OMNI-350	OMNI-351
	sgRNA V4 sequence	-	GUUUGAGUAUGGUGUAAgaaaUU ACACUAUUAGUUCAAAUA AAAU UCUUUCACAUCGCCGAAACUUU CGGUAACACACGCUGUGUGUUU UUU (SEQ ID NO: 1869)
tracrRNA V4 sequences	tracrRNA Portion 1	-	AAAAUUCUUUCACAUCGCCGAA ACUUUCGGU (SEQ ID NO: 1870)

		OMNI-352	OMNI-353
	sgRNA V1 sequence	GUUUUAGAUCUAUGUCAgaa aUGACAUAGAGAGUUAAAA UAAAGGUUUAACCCUAAA ACUCUAUUUGAGCGACUGC UUUGGCAGUCUUUUUUU (SEQ ID NO: 1871)	GUUUGAGAAUGAUGUAAgaaaUU ACAUCUAAGUUCAAAUAAGAA UUUAUUCAAAACGCCGUCUUAG AUGGCCCAUGUGUGGAACA AAAAGUCUGCUAUGCAGACUUU UUU (SEQ ID NO: 1896)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUAGAUCUAUGUCA (SEQ ID NO: 1872)	GUUUGAGAAUGAUGUAA (SEQ ID NO: 1897)
	Partial crRNA 1	GUUUUAGAUCUAUGU (SEQ ID NO: 1873)	GUUUGAGAAUGAUGU (SEQ ID NO: 1898)
	Partial crRNA 2	GUUUUAGAUCUA (SEQ ID NO: 1874)	GUUUGAGAAUGA (SEQ ID NO: 1899)
	Partial crRNA 3	GUUUUAGAUC (SEQ ID NO: 1875)	GUUUGAGAAU (SEQ ID NO: 1900)
	tracrRNA (Antirepeat)	UGACAUAGAGAGUUAAAAU (SEQ ID NO: 1876)	UUACAUCUAAGUUCAAAU (SEQ ID NO: 1901)
	Partial tracrRNA 1	ACAUCAGAGAGUUAAAAU (SEQ ID NO: 1877)	ACAUCUAAGUUCAAAU (SEQ ID NO: 1902)
	Partial tracrRNA 2	UAGAGAGUUAAAAU (SEQ ID NO: 1878)	UCAUAAGUUCAAAU (SEQ ID NO: 1903)
	Partial tracrRNA 3	GAGAGUUAAAAU (SEQ ID NO: 1879)	AUAAGUUCAAAU (SEQ ID NO: 1904)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGGUUUAACCCUAAAUA (SEQ ID NO: 1880)	AAGAAUUUAUUCAAAACGCCGU CUUAGAUGGC (SEQ ID NO: 1905)
	tracrRNA Portion 1 - partial	AAAGGUUUAACCCU (SEQ ID NO: 1881)	AAGAAUUUAUUCAAAACGCCGU CUUAGAUGGC (SEQ ID NO: 1906)
	tracrRNA Portion 2	CUCUAUUUGAGC (SEQ ID NO: 1882)	CCACAGUGUGUGGAAC (SEQ ID NO: 1907)
	tracrRNA Portion 2 - partial	CUCUAUUUGAG (SEQ ID NO: 1883)	CCACAGUGUGUGG (SEQ ID NO: 1908)

		OMNI-352	OMNI-353
	tracrRNA Portion 3	GACUGCUUUGGCAGUCUUU UUUU (SEQ ID NO: 1884)	AAAAAGUCUGCUAUGCAGACUU UUUU (SEQ ID NO: 1909)
	tracrRNA Portion 3 - partial	GACUGCUUUGGCAGUC (SEQ ID NO: 1885)	AAAAAGUCUGCUAUGCAGACUU UUU (SEQ ID NO: 1910)
	tracrRNA Portion 3 - without polyT	GACUGCUUUGGCAGUC (SEQ ID NO: 1886)	AAAAAGUCUGCUAUGCAGAC (SEQ ID NO: 1911)
	sgRNA V2 sequence	GUUCUAGAUCUAUGUCa aUGACAUAGAGAGUUAGAA UAAAGGUUUAACCCUAAAU ACUCUAUUUGAGCGACUGC UUUGGCAGUCUUUUUUU (SEQ ID NO: 1887)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGAUCUAUGUCA (SEQ ID NO: 1888)	-
	Partial crRNA 1	GUUCUAGAUCUAUGU (SEQ ID NO: 1889)	-
	Partial crRNA 2	GUUCUAGAUCUA (SEQ ID NO: 1890)	-
	Partial crRNA 3	GUUCUAGAUC (SEQ ID NO: 1891)	-
	tracrRNA (Antirepeat)	UGACAUAGAGAGUUAGAAU (SEQ ID NO: 1892)	-
	Partial tracrRNA 1	ACAUAGAGAGUUAGAAU (SEQ ID NO: 1893)	-
	Partial tracrRNA 2	UAGAGAGUUAGAAU (SEQ ID NO: 1894)	-
	Partial tracrRNA 3	GAGAGUUAGAAU (SEQ ID NO: 1895)	-

		OMNI-354	OMNI-356
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAg aUUACACUACAAAGUUCAA AUAAGCUUUUAGCGAAAUC AUCGCAAUGCGAAUGCACA GUGUGUGCUCAGUAAGACC UCAUUACGAGGUCUUUUUU (SEQ ID NO: 1912)	GUUUGGUAGCUGUGUg aaaACACAGCAUGUCCAAAU AAAAACAUGUCAA AAAUGCCCUAUAGAGGGU UAUAAACAUCUAAUUUAGUGGGU GUUUUUUU (SEQ ID NO: 1931)
	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 1913)	GUUUGGUAGCUGUGU (SEQ ID NO: 1932)

		OMNI-354	OMNI-356
crRNA:tracrRNA duplex V1 sequences	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 1914)	-
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 1915)	GUUUGGUAGCUG (SEQ ID NO: 1933)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 1916)	GUUUGGUAGC (SEQ ID NO: 1934)
	tracrRNA (Antirepeat)	UUACACUACAAAGUUCAAA U (SEQ ID NO: 1917)	ACACAGCAUGUCCAAAU (SEQ ID NO: 1935)
	Partial tracrRNA 1	ACACUACAAAGUUCAAAU (SEQ ID NO: 1918)	-
	Partial tracrRNA 2	CUACAAAGUUCAAAU (SEQ ID NO: 1919)	CAGCAUGUCCAAAU (SEQ ID NO: 1936)
	Partial tracrRNA 3	ACAAAGUUCAAAU (SEQ ID NO: 1920)	GCAUGUCCAAAU (SEQ ID NO: 1937)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGCUUUUAGCGAAAUCAU CGCAA (SEQ ID NO: 1921)	AAAAACAUGUUCAAAAGGCCU AUAGAGGGUUAU (SEQ ID NO: 1938)
	tracrRNA Portion 1 - partial	AAGCUUUUAGCGAAAUCAU CGC (SEQ ID NO: 1922)	AAAAACAUGUUCAAAAGGCCU AUAGAGGGU (SEQ ID NO: 1939)
	tracrRNA Portion 2	UGCGAAUGCACAGUGUGUG CUCAGUA (SEQ ID NO: 1923)	AAACAUCCAUUUAGUGGGUGUU UUUUU (SEQ ID NO: 1940)
	tracrRNA Portion 2 - partial	UGCGAAUGCACAGUGUGUG CUCAGUA (SEQ ID NO: 1924)	AAACAUCCAUUUAGUGGGUGUU U (SEQ ID NO: 1941)
	tracrRNA Portion 2 – without polyT	-	AAACAUCCAUUUAGUGGGUG (SEQ ID NO: 1942)
	tracrRNA Portion 3	AGACCUCAUUACGAGGUCU UUUUU (SEQ ID NO: 1925)	-
	tracrRNA Portion 3 - partial	AGACCUCAUUACGAGGUCU (SEQ ID NO: 1926)	-
	tracrRNA Portion 3 - without polyT	AGACCUCAUUACGAGGUC (SEQ ID NO: 1927)	-
	sgRNA V2 sequence	GUUUGAGAGUAGUGUAaagaaUUACACUACAAAGUUCAA AUAAGCUUCUAGCGAAAUCAUCGCAAUGCGAAUGCACA GUGUGUGCUCAGUAAGACC UCAUUACGAGGUCUUUUUU (SEQ ID NO: 1928)	-

		OMNI-354	OMNI-356
tracrRNA V2 sequences	tracrRNA Portion 1	AAGCUUCUAGCGAAAUCAU CGCAA (SEQ ID NO: 1929)	-
	tracrRNA Portion 1 - partial	AAGCUUCUAGCGAAAUCAU CGC (SEQ ID NO: 1930)	-

		OMNI-357	OMNI-358
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUUUAGAUGUAUGUAAgaa aUUACAUGCAAAGUUAAAA UAAAUGUUAUACUAAAUGC CUUUUUAUAGGUCCCGUUUU GACGGGGGAGAUGCCACUA UCGUGGCAUUUUUU (SEQ ID NO: 1943)	GUUUGAGAACCUUGUAAgaaaUU ACAAGGUGAGUGCAAUAAGGA UUUUUCCGAAAUCGCUCAUUUA UAUGAGUCCGCAUGGUGCGGUU AAAAGACCUAUUUUUUAGGUCUU UUUU (SEQ ID NO: 1972)
	crRNA (Repeat)	GUUUUAGAUGUAUGUAA (SEQ ID NO: 1944)	GUUUGAGAACCUUGUAA (SEQ ID NO: 1973)
	Partial crRNA 1	GUUUUAGAUGUAUGU (SEQ ID NO: 1945)	GUUUGAGAACCUUGU (SEQ ID NO: 1974)
	Partial crRNA 2	GUUUUAGAUGUA (SEQ ID NO: 1946)	GUUUGAGAACCU (SEQ ID NO: 1975)
	Partial crRNA 3	GUUUUAGAUG (SEQ ID NO: 1947)	GUUUGAGAAC (SEQ ID NO: 1976)
	tracrRNA (Antirepeat)	UUACAUGCAAAGUUAAAAU (SEQ ID NO: 1948)	UUACAAGGUGAGUGCAAUA (SEQ ID NO: 1977)
	Partial tracrRNA 1	ACAUGCAAAGUUAAAAU (SEQ ID NO: 1949)	ACAAGGUGAGUGCAAUA (SEQ ID NO: 1978)
	Partial tracrRNA 2	UGCAAAGUUAAAAU (SEQ ID NO: 1950)	AGGUGAGUGCAAUA (SEQ ID NO: 1979)
	Partial tracrRNA 3	CAAAGUUAAAAU (SEQ ID NO: 1951)	GUGAGUGCAAUA (SEQ ID NO: 1980)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAUGUUUAUACUAAAUGCC UUUUUAUAGGU (SEQ ID NO: 1952)	AAGGAUUUUUCCGAAAUC (SEQ ID NO: 1981)
	tracrRNA Portion 1 - partial	AAAUGUUUAUACUAAAUGCC UUUUUAUAGGU (SEQ ID NO: 1953)	AAGGAUUUUUCC (SEQ ID NO: 1982)
	tracrRNA Portion 2	CCCGUUUUGACGGG (SEQ ID NO: 1954)	GCUCAUUUAUAUGAGU (SEQ ID NO: 1983)
	tracrRNA Portion 2 - partial	CCCGUUUUGACGGG (SEQ ID NO: 1955)	GCUCAUUUAUAUGAGU (SEQ ID NO: 1984)

		OMNI-357	OMNI-358
	tracrRNA Portion 3	GGAGAUGCCACUAUCGUGG CAUUUUUU (SEQ ID NO: 1956)	CCGCAUGGUGCGGUU (SEQ ID NO: 1985)
	tracrRNA Portion 3 - partial	GGAGAUGCCACUAUCGUGG CAUUUUUU (SEQ ID NO: 1957)	CCGCAUGGUGCGG (SEQ ID NO: 1986)
	tracrRNA Portion 3 - without polyT	GGAGAUGCCACUAUCGUGG CA (SEQ ID NO: 1958)	-
	tracrRNA Portion 4	-	AAAAGACCUAUUUUUUAGGUCUU UUUU (SEQ ID NO: 1987)
	tracrRNA Portion 4 - partial	-	AAAAGACCUAUUUUUUAGGUCUU UU (SEQ ID NO: 1988)
	tracrRNA Portion 4 - without polyT	-	AAAAGACCUAUUUUUUAGGUC (SEQ ID NO: 1989)
	sgRNA V2 sequence	GUUCUAGAUGUAUGUAAgaa aUUACAUGCAAAGUUAGAA UAAAGUUUAUACUAAAGUC CUUUCAUAGGUCCCGUUUC GACGGGGGAGAUGCCACUA UCGUGGCAUUUUUU (SEQ ID NO: 1959)	GUUUGAGAACCUUGUAAgaaaUU ACAAGGUGAGUGCAAUAAGGA UUCUCCGAAAU CGCUCAUUUA UAUGAGUCCGCAUGGUGCGGUU AAAAGACCUAUUCUUAGGUCUU UUUU (SEQ ID NO: 1990)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUAGAUGUAUGUAA (SEQ ID NO: 1960)	-
	Partial crRNA 1	GUUCUAGAUGUAUGU (SEQ ID NO: 1961)	-
	Partial crRNA 2	GUUCUAGAUGUA (SEQ ID NO: 1962)	-
	Partial crRNA 3	GUUCUAGAUG (SEQ ID NO: 1963)	-
	tracrRNA (Antirepeat)	UUACAUGCAAAGUUAGAAU (SEQ ID NO: 1964)	-
	Partial tracrRNA 1	ACAUGCAAAGUUAGAAU (SEQ ID NO: 1965)	-
	Partial tracrRNA 2	UGCAAAGUUAGAAU (SEQ ID NO: 1966)	-
	Partial tracrRNA 3	CAAAGUUAGAAU (SEQ ID NO: 1967)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAAUGUUUAUACUAAAGGCC UUUCAUAGGU (SEQ ID NO: 1968)	AAGGAUUCUCCGAAAU (SEQ ID NO: 1991)

		OMNI-357	OMNI-358
	tracrRNA Portion 1 - partial	AAAUGUUAUACUAAAUGCCUUUCAUAGGU (SEQ ID NO: 1969)	AAGGAUUCUCC (SEQ ID NO: 1992)
	tracrRNA Portion 2	CCCGUUUCGACGGG (SEQ ID NO: 1970)	-
	tracrRNA Portion 2 - partial	CCCGUUUCGACGGG (SEQ ID NO: 1971)	-
	tracrRNA Portion 4	-	AAAAGACCUAUUCUUAGGUCUUUUU (SEQ ID NO: 1993)
	tracrRNA Portion 4 - partial	-	AAAAGACCUAUUCUUAGGUCUUU (SEQ ID NO: 1994)
	tracrRNA Portion 4 - without polyT	-	AAAAGACCUAUUCUUAGGUC (SEQ ID NO: 1995)
	sgRNA V3 sequence	-	GUUUGAGAACCUUGUAAgaaaUUAACAAGGUGAGUGCAAUAAGGAUUUUUCCGAAAUCGCUCAUUUAUAUGAGUCCGCAUGGUGCGGUUAAAAGACCUAUUUUUU (SEQ ID NO: 1996)
tracrRNA V3 sequences	tracrRNA Portion 3	-	CCGCAUGGUGCGGUUAAAAGACCUAUUUUUU (SEQ ID NO: 1997)
	tracrRNA Portion 3 - without polyT	-	CCGCAUGGUGCGGUUAAAAGACCUA (SEQ ID NO: 1998)
	sgRNA V4 sequence	-	GUUUGAGAACCUUGUAAgaaaUUAACAAGGUGAGUGCAAUAAGGAUUCUCCGAAAUCGCUCAUUUAUAUGAGUCCGCAUGGUGCGGUUAAAAGACCUAUUUUUU (SEQ ID NO: 1999)

		OMNI-359	OMNI-360
	sgRNA V1 sequence	GUUUGAGAGUAGUGUGAgaaaUCACACUACGAGUUCAAAUAAAGAUAUUUCCAAAUCGCCGGUUUGCCGGCCGCACAUUGGUGCUAAAAAAGAUCUUCGGGAUCUUUUUU (SEQ ID NO: 2000)	GUUUGAGAGCCUUGUUAgaaaUAACAAGGCGAGUGCAAUAAGGAUUAUCCGAAAUCGUCUAUUGACGCUACAUGGUGUAGCAUUUAAAGUCCGAAAGGACUUUUUU (SEQ ID NO: 2025)
	crRNA (Repeat)	GUUUGAGAGUAGUGUGA (SEQ ID NO: 2001)	GUUUGAGAGCCUUGUUA (SEQ ID NO: 2026)

		OMNI-359	OMNI-360
crRNA:tracrRNA duplex V1 sequences	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 2002)	GUUUGAGAGCCUUGU (SEQ ID NO: 2027)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 2003)	GUUUGAGAGCCU (SEQ ID NO: 2028)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2004)	GUUUGAGAGC (SEQ ID NO: 2029)
	tracrRNA (Antirepeat)	UCACACUACGAGUUCAAAU (SEQ ID NO: 2005)	UAACAAGGCGAGUGCAAAU (SEQ ID NO: 2030)
	Partial tracrRNA 1	ACACUACGAGUUCAAAU (SEQ ID NO: 2006)	ACAAGGCGAGUGCAAAU (SEQ ID NO: 2031)
	Partial tracrRNA 2	CUACGAGUUCAAAU (SEQ ID NO: 2007)	AGGCGAGUGCAAAU (SEQ ID NO: 2032)
	Partial tracrRNA 3	ACGAGUUCAAAU (SEQ ID NO: 2008)	GCGAGUGCAAAU (SEQ ID NO: 2033)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGAUUUUCCAAAUC (SEQ ID NO: 2009)	AAGGAUUAUUCCGAAAUC (SEQ ID NO: 2034)
	tracrRNA Portion 1 - partial	AAAGAUUUUCCAAAUC (SEQ ID NO: 2010)	AAGGAUUAUUCC (SEQ ID NO: 2035)
	tracrRNA Portion 2	GCCGGUUUGCCGGCC (SEQ ID NO: 2011)	GUCUAUUGAC (SEQ ID NO: 2036)
	tracrRNA Portion 2 - partial	GCCGGUUUGCCGGC (SEQ ID NO: 2012)	GUCUAUUGAC (SEQ ID NO: 2037)
	tracrRNA Portion 3	GCACAUUGGUGCU (SEQ ID NO: 2013)	GCUACAUGGUGUAGCAUUU (SEQ ID NO: 2038)
	tracrRNA Portion 3 - partial	GCACAUUGGUGC (SEQ ID NO: 2014)	GCUACAUGGUGUAGC (SEQ ID NO: 2039)
	tracrRNA Portion 4	AAAAAAGAUCUUCGGGAU CUUUUUU (SEQ ID NO: 2015)	AAAGUCCGAAAGGACUUUUUUU (SEQ ID NO: 2040)
	tracrRNA Portion 4 - partial	AAAAAAGAUCUUCGGGAU CUUUUUU (SEQ ID NO: 2016)	AAAGUCCGAAAGGACUUU (SEQ ID NO: 2041)
	tracrRNA Portion 4 - without polyT	AAAAAAGAUCUUCGGGAU C (SEQ ID NO: 2017)	AAAGUCCGAAAGGAC (SEQ ID NO: 2042)
	sgRNA V2 sequence	GUUUGAGAGUAGUGUGAaa aUCACACUACGAGUUCAAA UAAAGAUUUCUCCAAAUCG CCGGUUUGCCGGCCGCACA UUGGUGCUAAAAAAGAUC	-

		OMNI-359	OMNI-360
		UUCGGGAUCUUUUUU (SEQ ID NO: 2018)	
tracrRNA V2 sequences	tracrRNA Portion 1	AAAGAUUUCUCCAAAUC (SEQ ID NO: 2019)	-
	tracrRNA Portion 1 - partial	AAAGAUUUCUCCAAAUC (SEQ ID NO: 2020)	-
	sgRNA V3 sequence	GUUUGAGAGUAGUGUGAga aUCACACUACGAGUUCAAA UAAAGAUUUUCCAAAUCG CCGGUUUGCCGGCCUUUUU U (SEQ ID NO: 2021)	GUUUGAGAGCCUUGUUAga aUAACAAGGCGAGUGCAAAU AAGGAUUAUUCGAAAUUCG GUCUAUUGACGCUACAUGG UGUAGCAUUUUU (SEQ ID NO: 2043)
tracrRNA V3 sequences	tracrRNA Portion 2	GCCGGUUUGCCGGCCUUUU UU (SEQ ID NO: 2022)	-
	tracrRNA Portion 2 – without polyT	GCCGGUUUGCCGGCC (SEQ ID NO: 2023)	-
	tracrRNA Portion 3	-	GCUACAUGGUGUAGCAUUUUUU (SEQ ID NO: 2044)
	tracrRNA Portion 3 - without polyT	-	GCUACAUGGUGUAGCA (SEQ ID NO: 2045)
	sgRNA V4 sequence	GUUUGAGAGUAGUGUGAga aUCACACUACGAGUUCAAA UAAAGAUUUCUCCAAAUCG CCGGUUUGCCGGCCUUUUU U (SEQ ID NO: 2024)	-

		OMNI-361	OMNI-362
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAga aUUACACUACGCGUUCAAA UAAAGAUUUUCCAAAUCG CCGGGCAACCGGUUGCACA GUGUGUGCGAAAAAGGUCU CUUCGGAGGCCUUUUUU (SEQ ID NO: 2046)	GUUUGAGAGCUGUGUAAga aUUACACAGCAAGUUCAAA UAAGAUUUUUCGAAAUUCG CCCGCAUUCGCGGCGACAG GUGUGCGAUCUUGGAUGCC GUAAGGCAUCUUUUU (SEQ ID NO: 2064)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 2047)	GUUUGAGAGCUGUGUAA (SEQ ID NO: 2065)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 2048)	GUUUGAGAGCUGUGU (SEQ ID NO: 2066)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 2049)	GUUUGAGAGCUG (SEQ ID NO: 2067)

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	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2050)	GUUUGAGAGC (SEQ ID NO: 2068)
	tracrRNA (Antirepeat)	UUACACUACGCGUUCAAAU (SEQ ID NO: 2051)	UUACACAGCAAGUUCAAAU (SEQ ID NO: 2069)
	Partial tracrRNA 1	ACACUACGCGUUCAAAU (SEQ ID NO: 2052)	ACACAGCAAGUUCAAAU (SEQ ID NO: 2070)
	Partial tracrRNA 2	CUACGCGUUCAAAU (SEQ ID NO: 2053)	CAGCAAGUUCAAAU (SEQ ID NO: 2071)
	Partial tracrRNA 3	ACGCGUUCAAAU (SEQ ID NO: 2054)	GCAAGUUCAAAU (SEQ ID NO: 2072)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGAUUUUAUCCAAAUC (SEQ ID NO: 2055)	AAGAUUUUUCGAAAUC (SEQ ID NO: 2073)
	tracrRNA Portion 1 - partial	AAAGAUUUUAUCCAAAUC (SEQ ID NO: 2056)	AAGAUUUUUCGAAAUC (SEQ ID NO: 2074)
	tracrRNA Portion 2	GCCGGGCAACCGGUU (SEQ ID NO: 2057)	GCCGAUUCAUUCGGC (SEQ ID NO: 2075)
	tracrRNA Portion 2 - partial	GCCGGGCAACCGGU (SEQ ID NO: 2058)	GCCGAUUCAUUCGGC (SEQ ID NO: 2076)
	tracrRNA Portion 3	GCACAGUGUGUGC (SEQ ID NO: 2059)	CGCACAGGUGUGCGAUCUU (SEQ ID NO: 2077)
	tracrRNA Portion 3 - partial	GCACAGUGUGUGC (SEQ ID NO: 2060)	CGCACAGGUGUGCG (SEQ ID NO: 2078)
	tracrRNA Portion 4	GAAAAAGGUCUCUUCGGAG GCCUUUUUU (SEQ ID NO: 2061)	GGAUGCCGUAAGGCAUCUUUUU U (SEQ ID NO: 2079)
	tracrRNA Portion 4 - partial	GAAAAAGGUCUCUUCGGAG GCCUUUUUU (SEQ ID NO: 2062)	GGAUGCCGUAAGGCAUCU (SEQ ID NO: 2080)
	tracrRNA Portion 4 - without polyT	GAAAAAGGUCUCUUCGGAG GCC (SEQ ID NO: 2063)	GGAUGCCGUAAGGCAUC (SEQ ID NO: 2081)
	sgRNA V2 sequence	-	GUUUGAGAGCUGUGUAAgaaaUU ACACAGCAAGUUCAAAUAAGAU UUCUCGAAAUCGCCGAUUCAUU CGGCCGCACAGGUGUGCGAUCU UGGAUGCCGUAAGGCAUCUUUU UU (SEQ ID NO: 2082)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AAGAUUUCUCGAAAUC (SEQ ID NO: 2083)

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	tracrRNA Portion 1 - partial	-	AAGAUUUCUCGAAAUC (SEQ ID NO: 2084)
	sgRNA V3 sequence	-	GUUUGAGAGCUGUGUAAgaaaUU ACACAGCAAGUUCAAAUAAGAU UUUUCGAAAUCGCCGAUUCAUU CGGCUUUUUU (SEQ ID NO: 2085)
tracrRNA V3 sequences	tracrRNA Portion 2	-	GCCGAUUCAUUCGGCUUUUUU (SEQ ID NO: 2086)
	tracrRNA Portion 2 – without polyT	-	GCCGAUUCAUUCGGC (SEQ ID NO: 2087)
	sgRNA V4 sequence	-	GUUUGAGAGCUGUGUAAgaaaUU ACACAGCAAGUUCAAAUAAGAU UUCUCGAAAUCGCCGAUUCAUU CGGCUUUUUU (SEQ ID NO: 2088)

		OMNI-363	OMNI-364
	sgRNA V1 sequence	GUUUGAGAGUCUUGUAAgaa aUUACAAGACGAGUGCAAA UAAGGAUUUAUCCGAAACC GUCGUAAUGACGCCCCAUG GUGGGGCAUUUAAAAAGAU UACGCCUAGCGUAGUCUUU UUU (SEQ ID NO: 2089)	GUUUGAGAGCUUUGUUAaaaaUA ACAAAGCGAGUGCAAAUAAGGU UAAUCCGAAACCGCCAUUUAUG GCUCUGCAUGGUGCAGAAUUUU UUUAGCCCCUGAUAGGGGCUUU UUU (SEQ ID NO: 2110)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUCUUGUAA (SEQ ID NO: 2090)	GUUUGAGAGCUUUGUUA (SEQ ID NO: 2111)
	Partial crRNA 1	GUUUGAGAGUCUUGU (SEQ ID NO: 2091)	GUUUGAGAGCUUUGU (SEQ ID NO: 2112)
	Partial crRNA 2	GUUUGAGAGUCU (SEQ ID NO: 2092)	GUUUGAGAGCUU (SEQ ID NO: 2113)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2093)	GUUUGAGAGC (SEQ ID NO: 2114)
	tracrRNA (Antirepeat)	UUACAAGACGAGUGCAAAU (SEQ ID NO: 2094)	UAACAAAGCGAGUGCAAAU (SEQ ID NO: 2115)
	Partial tracrRNA 1	ACAAGACGAGUGCAAAU (SEQ ID NO: 2095)	ACAAAGCGAGUGCAAAU (SEQ ID NO: 2116)
	Partial tracrRNA 2	AGACGAGUGCAAAU (SEQ ID NO: 2096)	AAGCGAGUGCAAAU (SEQ ID NO: 2117)
	Partial tracrRNA 3	ACGAGUGCAAAU (SEQ ID NO: 2097)	GCGAGUGCAAAU (SEQ ID NO: 2118)

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tracrRNA V1 sequences	tracrRNA Portion 1	AAGGAUUUAUCCGAAACC (SEQ ID NO: 2098)	AAGGUUAAUCCGAAACC (SEQ ID NO: 2119)
	tracrRNA Portion 1 - partial	AAGGAUUUAUCC (SEQ ID NO: 2099)	AAGGUUAAUCCGAAACC (SEQ ID NO: 2120)
	tracrRNA Portion 2	GUCGUAAUGAC (SEQ ID NO: 2100)	GCCAUUUAUGGC (SEQ ID NO: 2121)
	tracrRNA Portion 2 - partial	GUCGUAAUGAC (SEQ ID NO: 2101)	GCCAUUUAUGGC (SEQ ID NO: 2122)
	tracrRNA Portion 3	GCCCCAUGGUGGGGCAUUU (SEQ ID NO: 2102)	UCUGCAUGGUGCAGAAUUUUUUU (SEQ ID NO: 2123)
	tracrRNA Portion 3 - partial	GCCCCAUGGUGGGGC (SEQ ID NO: 2103)	UCUGCAUGGUGCAGA (SEQ ID NO: 2124)
	tracrRNA Portion 4	AAAAAGAUUACGCCUAGCG UAGUCUUUUUU (SEQ ID NO: 2104)	AGCCCCUGAUAGGGGCUUUUUU (SEQ ID NO: 2125)
	tracrRNA Portion 4 - partial	AAAAAGAUUACGCCUAGCG UAGUCUUUUU (SEQ ID NO: 2105)	AGCCCCUGAUAGGGGCU (SEQ ID NO: 2126)
	tracrRNA Portion 4 - without polyT	AAAAAGAUUACGCCUAGCG UAGUC (SEQ ID NO: 2106)	AGCCCCUGAUAGGGGC (SEQ ID NO: 2127)
	sgRNA V2 sequence	-	GUUUGAGAGCUUUGUUAgaaaUAACAAAGCGAGUGCAAUAAGGUUAAUCCGAAACCGCCAUUUAUGGCUCUGCAUGGUGCAGAAUUUCUUUAGCCCCUGAUAGGGGCUUUUUU (SEQ ID NO: 2128)
tracrRNA V2 sequences	tracrRNA Portion 3	-	UCUGCAUGGUGCAGAAUUUCUUU (SEQ ID NO: 2129)
	sgRNA V3 sequence	GUUUGAGAGUCUUGUAAgaa aUUACAAGACGAGUGCAAAUAAGGAUUUAUCCGAAACC GUCGUAAUGACGCCCAUG GUGGGGCAUUUUUU (SEQ ID NO: 2107)	GUUUGAGAGCUUUGUUAgaaaUAACAAAGCGAGUGCAAUAAGGUUAAUCCGAAACCGCCAUUUAUGGCUCUGCAUGGUGCAGAAUUUUUUU (SEQ ID NO: 2130)
tracrRNA V3 sequences	tracrRNA Portion 3	GCCCCAUGGUGGGGCAUUU (SEQ ID NO: 2108)	-
	tracrRNA Portion 3 - without polyT	GCCCCAUGGUGGGGCA (SEQ ID NO: 2109)	UCUGCAUGGUGCAGAA (SEQ ID NO: 2131)

		OMNI-365	OMNI-366
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACGAGUUCAAA UAAAGAUUUUCCAAAUCG UCGGGUUUCUCCGACAGCA CAGUGUGUGCUUCAAAGA CCUCUUAUGAGGUCUUUUU U (SEQ ID NO: 2132)	GUUUGAGAGUAGUGUAAgaaaUU ACACUACGAGUUCAAAUAAAGA UUCUUCGAAAUCGCGGCUUGUC CGUCAGCACAGGUGUGCUUCCA AAAGACCUCUUCGGAGGUCUUU UUU (SEQ ID NO: 2157)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 2133)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 2158)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 2134)	GUUUGAGAGUAGUGU (SEQ ID NO: 2159)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 2135)	GUUUGAGAGUAG (SEQ ID NO: 2160)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2136)	GUUUGAGAGU (SEQ ID NO: 2161)
	tracrRNA (Antirepeat)	UUACACUACGAGUUCAAAU (SEQ ID NO: 2137)	UUACACUACGAGUUCAAAU (SEQ ID NO: 2162)
	Partial tracrRNA 1	ACACUACGAGUUCAAAU (SEQ ID NO: 2138)	ACACUACGAGUUCAAAU (SEQ ID NO: 2163)
	Partial tracrRNA 2	CUACGAGUUCAAAU (SEQ ID NO: 2139)	CUACGAGUUCAAAU (SEQ ID NO: 2164)
	Partial tracrRNA 3	ACGAGUUCAAAU (SEQ ID NO: 2140)	ACGAGUUCAAAU (SEQ ID NO: 2165)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGAUUUUCCAAAUC (SEQ ID NO: 2141)	AAAGAUUCUUCGAAAUC (SEQ ID NO: 2166)
	tracrRNA Portion 1 - partial	AAAGAUUUUCCAAAUC (SEQ ID NO: 2142)	AAAGAUUCUUCGAAAUC (SEQ ID NO: 2167)
	tracrRNA Portion 2	GUCGGGUUUCUCCGAC (SEQ ID NO: 2143)	GCGGCUUGUCCGUC (SEQ ID NO: 2168)
	tracrRNA Portion 2 - partial	GUCGGGUUUCUCCGAC (SEQ ID NO: 2144)	GCGGCUUGUCCGU (SEQ ID NO: 2169)
	tracrRNA Portion 3	AGCACAGUGUGUGCUUC (SEQ ID NO: 2145)	AGCACAGGUGUGCUUCC (SEQ ID NO: 2170)
	tracrRNA Portion 3 - partial	AGCACAGUGUGUGCU (SEQ ID NO: 2146)	AGCACAGGUGUGCU (SEQ ID NO: 2171)
	tracrRNA Portion 4	AAAAGACCUCUUAUGAGGU CUUUUUU (SEQ ID NO: 2147)	AAAAGACCUCUUCGGAGGUCUU UUUU (SEQ ID NO: 2172)
	tracrRNA Portion 4 - partial	AAAAGACCUCUUAUGAGGU CUUUU (SEQ ID NO: 2148)	AAAAGACCUCUUCGGAGGUCUU UU (SEQ ID NO: 2173)

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	tracrRNA Portion 4 - without polyT	AAAAGACCUCUUAUGAGGUC (SEQ ID NO: 2149)	AAAAGACCUCUUCGGAGGUC (SEQ ID NO: 2174)
	sgRNA V2 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACGAGUUCAAA UAAAGAUUUCUCCAAAUCG UCGGGUUUCUCCGACAGCA CAGUGUGUGCUUCAAAGA CCUCUUAUGAGGUCUUUUU U (SEQ ID NO: 2150)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAAGAUUUCUCCAAAUC (SEQ ID NO: 2151)	-
	tracrRNA Portion 1 - partial	AAAGAUUUCUCCAAAUC (SEQ ID NO: 2152)	-
	sgRNA V3 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACGAGUUCAAA UAAAGAUUUUCCAAAUCG UCGGGUUUCUCCGACAGCA CAGUGUGUGCUUCUUUUU (SEQ ID NO: 2153)	GUUUGAGAGUAGUGUAAgaaaUU ACACUACGAGUUCAAAUAAAGA UUCUUCGAAAUCGCGGCUUGUC CGUCUUUUUU (SEQ ID NO: 2175)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAAGAUUCUUCGAAAUCGCGGC UUGUCCGUCUUUUUU (SEQ ID NO: 2176)
	tracrRNA Portion 1 - partial	-	GAAAUCCGCGGCUUGUCCGUCUU UUU (SEQ ID NO: 2177)
	tracrRNA Portion 1 - without polyT	-	AAAGAUUCUUCGAAAUCGCGGC UUGUCCGUC (SEQ ID NO: 2178)
	tracrRNA Portion 3	AGCACAGUGUGUGCUUCUU UUU (SEQ ID NO: 2154)	-
	tracrRNA Portion 3 - without polyT	AGCACAGUGUGUGCUUC (SEQ ID NO: 2155)	-
	sgRNA V4 sequence	GUUUGAGAGUAGUGUAAgaa aUUACACUACGAGUUCAAA UAAAGAUUUCUCCAAAUCG UCGGGUUUCUCCGACAGCA CAGUGUGUGCUUCUUUUUU (SEQ ID NO: 2156)	-

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	sgRNA V1 sequence	GUUUGAGAGUGGUGUAAgaa aUUACACCGCAUGUUCAAA CAAAAACAUGUUCAAACCG	GUUUGAGAGUAAUGUAAgaaaUU ACAUCACGAGUUCAAAAUCAU GAUUUAUUCAAAUCGUCUUCU

		OMNI-367	OMNI-368
crRNA:tracrRNA duplex V1 sequences		UCCAAUAGGACUCCAUUG UGGAAACAAAGAAGCUUGC CCGUUUGGGUAGGCUUUUU UGUUUUUU (SEQ ID NO: 2179)	CGGAAGACCCACAGCGUGUGG ACUAAAAACUAGCUUCGGCUA GUUUUUU (SEQ ID NO: 2204)
	crRNA (Repeat)	GUUUGAGAGUGGUGUAA (SEQ ID NO: 2180)	GUUUGAGAGUAAUGUAA (SEQ ID NO: 2205)
	Partial crRNA 1	GUUUGAGAGUGGUGU (SEQ ID NO: 2181)	GUUUGAGAGUAAUGU (SEQ ID NO: 2206)
	Partial crRNA 2	GUUUGAGAGUGG (SEQ ID NO: 2182)	GUUUGAGAGUAA (SEQ ID NO: 2207)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2183)	GUUUGAGAGU (SEQ ID NO: 2208)
	tracrRNA (Antirepeat)	UUACACCGCAUGUCAAAC (SEQ ID NO: 2184)	UUACAUCACGAGUCAA (SEQ ID NO: 2209)
	Partial tracrRNA 1	ACACCGCAUGUCAAAC (SEQ ID NO: 2185)	ACAUCACGAGUCAA (SEQ ID NO: 2210)
	Partial tracrRNA 2	CCGCAUGUCAAAC (SEQ ID NO: 2186)	UCACGAGUCAA (SEQ ID NO: 2211)
tracrRNA V1 sequences	Partial tracrRNA 3	GCAUGUCAAAC (SEQ ID NO: 2187)	UUACAUCACGAGUCAA (SEQ ID NO: 2212)
	tracrRNA Portion 1	AAAAACAUGUCAAACCGU CCAUAAGGACUCCAUUGU (SEQ ID NO: 2188)	AAUCAUGAUUUUAUCAAUC (SEQ ID NO: 2213)
	tracrRNA Portion 1 - partial	AAAAACAUGUCAAACCGU CCAUAAGGAC (SEQ ID NO: 2189)	AAUCAUGAUUUUAUCAAUC (SEQ ID NO: 2214)
	tracrRNA Portion 2	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUUUUU GUUUUUU (SEQ ID NO: 2190)	GUCUUCUUCGGAAGACC (SEQ ID NO: 2215)
	tracrRNA Portion 2 - partial	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUUUUU GUUUUU (SEQ ID NO: 2191)	GUCUUCUUCGGAAGAC (SEQ ID NO: 2216)
	tracrRNA Portion 2 – without polyT	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUUUUU G (SEQ ID NO: 2192)	-
	tracrRNA Portion 3	-	CCACAGCGUGUGGACU (SEQ ID NO: 2217)
	tracrRNA Portion 3 - partial	-	CCACAGCGUGUGG (SEQ ID NO: 2218)
	tracrRNA Portion 4	-	AAAAAACUAGCUUCGGCUAGUU UUUU (SEQ ID NO: 2219)

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	tracrRNA Portion 4 - partial	-	AAAAAACUAGCUUCGGCUAGUUUUU (SEQ ID NO: 2220)
	tracrRNA Portion 4 - without polyT	-	AAAAAACUAGCUUCGGCUAG (SEQ ID NO: 2221)
	sgRNA V2 sequence	GUUUGAGAGUGGUGUAAgaa aUUACACCGCAUGUUCAAA CAAAAACAUGUUCAAACCG UCCAAUAGGACUCCAUUG UGGAAACAAAGAAGCUUGC CCGUUUGGGUAGGCUUCUU UGUUUUUU (SEQ ID NO: 2193)	-
tracrRNA V2 sequences	tracrRNA Portion 2	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUCUUU GUUUUUU (SEQ ID NO: 2194)	-
	tracrRNA Portion 2 - partial	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUCUUU GUUUUU (SEQ ID NO: 2195)	-
	tracrRNA Portion 2 – without polyT	GGAAACAAAGAAGCUUGCC CGUUUGGGUAGGCUUCUUU G (SEQ ID NO: 2196)	-
	sgRNA V3 sequence	GUUUGAGAGUGGUGUAAgaa aUUACACCGCAUGUUCAAA CAAAAACAUGUUCAAACCG UCCAAUAGGACUCCAUUG UGGAAACAAAGAAGCUUGC CCGUUUGGGUAGGCUUUUU U (SEQ ID NO: 2197)	GUUUGAGAGUAAUGUAAgaaaUU ACAUCACGAGUUCAAAAUCAU GAUUUAUUCAAAUCGUCUUCUU CGGAAGACCCACAGCGUGUGG ACUAAAAACUAGCUUCGGCUA GUUUUUUAUUUUUU (SEQ ID NO: 2222)
tracrRNA V3 sequences	tracrRNA Portion 1	AAAAACAUGUUCAAACCGU CCAAUAGGAC (SEQ ID NO: 2198)	-
	tracrRNA Portion 2	UCCAUUGUGGAAAC (SEQ ID NO: 2199)	-
	tracrRNA Portion 2 - partial	UCCAUUGUGGAA (SEQ ID NO: 2200)	-
	tracrRNA Portion 3	AAAGAAGCUUGCCCGUUUG GGUAGGCUUUUUU (SEQ ID NO: 2201)	CCACAGCGUGUGGAC (SEQ ID NO: 2223)
	tracrRNA Portion 3 - partial	AAAGAAGCUUGCCCGUUUG GGUAGGCUUUUUU (SEQ ID NO: 2202)	-
	tracrRNA Portion 3 - without polyT	AAAGAAGCUUGCCCGUUUG GGUAGGC (SEQ ID NO: 2203)	-

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	tracrRNA Portion 4	-	UAAAAAACUAGCUUCGGCUAGU UUUUUAUUUUUU (SEQ ID NO: 2224)
	tracrRNA Portion 4 - partial	-	UAAAAAACUAGCUUCGGCUAGU UUUUUA (SEQ ID NO: 2225)
	tracrRNA Portion 4 - without polyT	-	UAAAAAACUAGCUUCGGCUAGU UUUUUA (SEQ ID NO: 2226)
	sgRNA V4 sequence	-	GUUUGAGAGUAAUGUAAgaaUU ACAUCACGAGUUCAAAAUCAU GAUUUAUUCAAAUCGUCUUCUU CGGAAGACCCACAGCGUGUGG ACUAAAGAACUAGCUUCGGCUA GUUCUUUAUUUUUU (SEQ ID NO: 2227)
tracrRNA V4 sequences	tracrRNA Portion 4	-	UAAAGAACUAGCUUCGGCUAGU UCUUUAUUUUUU (SEQ ID NO: 2228)
	tracrRNA Portion 4 - partial	-	UAAAGAACUAGCUUCGGCUAGU UCUUUA (SEQ ID NO: 2229)
	tracrRNA Portion 4 - without polyT	-	UAAAGAACUAGCUUCGGCUAGU UCUUUA (SEQ ID NO: 2230)

		OMNI-369	OMNI-370
	sgRNA V1 sequence	GUUUGAGAGCCUUGUUAga aUAACAAGGCGGGUGCAAA UAAGGUUUUUACCGGAAUC GUCGUUAUGACUCUGCAUG GUGCAGAUUUUAAGACUUA GAAAUAGUCUUUUUUU (SEQ ID NO: 2231)	GUUUGAGAGCCUUGUUAga aUAACAAGGCGAGUGCAAAUAAGGU UAAUCCGUAAUCGUCUCUUCGG AGACUCCACAGGGUGUGGAUAA AAGUCAUGAGUAUUC AUGGCUU UUUU (SEQ ID NO: 2257)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGCCUUGUUA (SEQ ID NO: 2232)	GUUUGAGAGCCUUGUUA (SEQ ID NO: 2258)
	Partial crRNA 1	GUUUGAGAGCCUUGU (SEQ ID NO: 2233)	GUUUGAGAGCCUUGU (SEQ ID NO: 2259)
	Partial crRNA 2	GUUUGAGAGCCU (SEQ ID NO: 2234)	GUUUGAGAGCCU (SEQ ID NO: 2260)
	Partial crRNA 3	GUUUGAGAGC (SEQ ID NO: 2235)	GUUUGAGAGC (SEQ ID NO: 2261)

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	tracrRNA (Antirepeat)	UAACAAGGCGGGUGCAAAU (SEQ ID NO: 2236)	UAACAAGGCGAGUGCAAAU (SEQ ID NO: 2262)
	Partial tracrRNA 1	ACAAGGCGGGUGCAAAU (SEQ ID NO: 2237)	ACAAGGCGAGUGCAAAU (SEQ ID NO: 2263)
	Partial tracrRNA 2	AGGCGGGUGCAAAU (SEQ ID NO: 2238)	AGGCGAGUGCAAAU (SEQ ID NO: 2264)
	Partial tracrRNA 3	GCGGGUGCAAAU (SEQ ID NO: 2239)	GCGAGUGCAAAU (SEQ ID NO: 2265)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGUUUUUACCGGAAUC (SEQ ID NO: 2240)	AAGGUUAAUCCGUAAUC (SEQ ID NO: 2266)
	tracrRNA Portion 1 - partial	AAGGUUUUUACC (SEQ ID NO: 2241)	AAGGUUAAUCCGUAAUC (SEQ ID NO: 2267)
	tracrRNA Portion 2	GUCGUUAUGAC (SEQ ID NO: 2242)	GUCUCUUCGGAGAC (SEQ ID NO: 2268)
	tracrRNA Portion 2 - partial	GUCGUUAUGAC (SEQ ID NO: 2243)	GUCUCUUCGGAGAC (SEQ ID NO: 2269)
	tracrRNA Portion 3	UCUGCAUGGUGCAGAUUUU (SEQ ID NO: 2244)	UCCACAGGGUGUGGAU (SEQ ID NO: 2270)
	tracrRNA Portion 3 - partial	UCUGCAUGGUGCAGA (SEQ ID NO: 2245)	UCCACAGGGUGUGGA (SEQ ID NO: 2271)
	tracrRNA Portion 4	AAGACUUAGAAAUAGUCU UUUUUU (SEQ ID NO: 2246)	AAAAGUCAUGAGUAUUCAUGGC UUUUUU (SEQ ID NO: 2272)
	tracrRNA Portion 4 - partial	AAGACUUAGAAAUAGUCU U (SEQ ID NO: 2247)	AAAAGUCAUGAGUAUUCAUGGC UUUU (SEQ ID NO: 2273)
	tracrRNA Portion 4 - without polyT	AAGACUUAGAAAUAGUC (SEQ ID NO: 2248)	AAAAGUCAUGAGUAUUCAUGGC (SEQ ID NO: 2274)
	sgRNA V2 sequence	GUUUGAGAGCCUUGUUAga aUAACAAGGCGGGUGCAAA UAAGGUUUCUACCGGAAUC GUCGUUAUGACUCUGCAUG GUGCAGAUUCUAAGACUUA GAAUAAGUCUUUUUUU (SEQ ID NO: 2249)	-
tracrRNA V2 sequences	tracrRNA Portion 1	AAGGUUUCUACCGGAAUC (SEQ ID NO: 2250)	-
	tracrRNA Portion 1 - partial	AAGGUUUCUACCGGAAUC (SEQ ID NO: 2251)	-

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	tracrRNA Portion 3	UCUGCAUGGUGCAGAUUCU (SEQ ID NO: 2252)	-
	sgRNA V3 sequence	GUUUGAGAGCCUUGUUAga aUAACAAGGCGGGUGCAAA UAAGGUUUUUACCGGAAUC GUCGUUAUGACUCUGCAUG GUGCAGAUUUUUU (SEQ ID NO: 2253)	GUUUGAGAGCCUUGUUAga aUAACAAGGCGAGUGCAAAUAAGGU UAAUCCGUAAUCGUCUCUUCGG AGACUCCACAGGGUGUGGAUUU UUU (SEQ ID NO: 2275)
tracrRNA V3 sequences	tracrRNA Portion 3	UCUGCAUGGUGCAGAUUUU UU (SEQ ID NO: 2254)	UCCACAGGGUGUGGAUUUUUU (SEQ ID NO: 2276)
	tracrRNA Portion 3 - without polyT	UCUGCAUGGUGCAGA (SEQ ID NO: 2255)	UCCACAGGGUGUGGA (SEQ ID NO: 2277)
	sgRNA V4 sequence	GUUUGAGAGCCUUGUUAga aUAACAAGGCGGGUGCAAA UAAGGUUUCUACCGGAAUC GUCGUUAUGACUCUGCAUG GUGCAGAUUUUUU (SEQ ID NO: 2256)	-

		OMNI-371	OMNI-372
	sgRNA V1 sequence	GUUUGAGAGCAGUGUUGaa aCAACACUGCACGUUCAAA UAAGCAGAUUGCUACAAGG UCCCCGUAAGGGAAUGACC AUCUGGUCACAUGAAUAGC CCCCGGCAACGGUGGCUGU UUUUGUUUUUU (SEQ ID NO: 2278)	GUUGUGUAUUGCUUUCgaaaGAA GCAAUACACAAUAAGGAUUUU CCGUUGUGAAACUUUUAAAGGAG GGAGAAUAGAUUUUCUAUUCUC UCGCUUUCUUUUUU (SEQ ID NO: 2305)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGCAGUGUUG (SEQ ID NO: 2279)	GUUGUGUAUUGCUUUC (SEQ ID NO: 2306)
	Partial crRNA 1	GUUUGAGAGCAGUGU (SEQ ID NO: 2280)	GUUGUGUAUUGCUUU (SEQ ID NO: 2307)
	Partial crRNA 2	GUUUGAGAGCAG (SEQ ID NO: 2281)	GUUGUGUAUUGC (SEQ ID NO: 2308)
	Partial crRNA 3	GUUUGAGAGC (SEQ ID NO: 2282)	GUUGUGUAUU (SEQ ID NO: 2309)
	tracrRNA (Antirepeat)	CAACACUGCACGUUCAAAU (SEQ ID NO: 2283)	GAAGCAAUACACAAU (SEQ ID NO: 2310)
	Partial tracrRNA 1	ACACUGCACGUUCAAAU (SEQ ID NO: 2284)	GAAGCAAUACACAAU (SEQ ID NO: 2311)

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	Partial tracrRNA 2	CUGCACGUUCAAU (SEQ ID NO: 2285)	GCAAUACACAAU (SEQ ID NO: 2312)
	Partial tracrRNA 3	GCACGUUCAAU (SEQ ID NO: 2286)	AAUACACAAU (SEQ ID NO: 2313)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGCAGAUUGCACAAAG (SEQ ID NO: 2287)	AAGGAUUAUUC (SEQ ID NO: 2314)
	tracrRNA Portion 1 - partial	AAGCAGAUUGC (SEQ ID NO: 2288)	AAGGAUUAUUC (SEQ ID NO: 2315)
	tracrRNA Portion 2	GUUCCCGUAAGGGAAU (SEQ ID NO: 2289)	GUUGUGAAACUUU (SEQ ID NO: 2316)
	tracrRNA Portion 2 - partial	GUUCCCGUAAGGGAAU (SEQ ID NO: 2290)	GUUGUGAAAC (SEQ ID NO: 2317)
	tracrRNA Portion 3	GACCAUCUGGUC (SEQ ID NO: 2291)	AAGGAGGGAGAAUAGAUAUUUCU AUUCUCUCGCUUUUUUUU (SEQ ID NO: 2318)
	tracrRNA Portion 3 - partial	GACCAUCUGGUC (SEQ ID NO: 2292)	AAGGAGGGAGAAUAGAUAUUUCU AUUCUCUCGCUUU (SEQ ID NO: 2319)
	tracrRNA Portion 3 - without polyT	-	AAGGAGGGAGAAUAGAUAUUUCU AUUCUCUCGCUUUC (SEQ ID NO: 2320)
	tracrRNA Portion 4	ACAUGAAUAGCCCCGGCA ACGGUGGCUGUUUUUGUUU UUU (SEQ ID NO: 2293)	-
	tracrRNA Portion 4 - partial	ACAUGAAUAGCCCCGGCA ACGGUGGCUGUUUUUGU (SEQ ID NO: 2294)	-
	tracrRNA Portion 4 - without polyT	ACAUGAAUAGCCCCGGCA ACGGUGGCUGUUUUUG (SEQ ID NO: 2295)	-
	sgRNA V2 sequence	GUUUGAGAGCAGUGUUGgaa aCAACACUGCACGUUCAA UAAGCAGAUUGCACAAAGG UUCCCGUAAGGGAAUGACC AUCUGGUCACAUGAAUAGC CCCCAGCAACGGUGGCUGU UUCUGUUUUUU (SEQ ID NO: 2296)	GUUGUGUAUUGCUUUCgaaaGAA GCAAUACACAAUAAGGAUUAU CCGUUGUGAAACUUCUAAGGAG GGAGAAUAGAUCUUCUAUUCUC UCGCUUUCUUUUUU (SEQ ID NO: 2321)
tracrRNA V2 sequences	tracrRNA Portion 2	-	GUUGUGAAACUUCU (SEQ ID NO: 2322)
	tracrRNA Portion 3	-	AAGGAGGGAGAAUAGAUCUUCU AUUCUCUCGCUUUUUUUU (SEQ ID NO: 2323)

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	tracrRNA Portion 3 - partial	-	AAGGAGGGAGAAUAGAUCUUCU AUUCUCUCGCUUU (SEQ ID NO: 2324)
	tracrRNA Portion 3 - without polyT	-	AAGGAGGGAGAAUAGAUCUUCU AUUCUCUCGCUUUC (SEQ ID NO: 2325)
	tracrRNA Portion 4	ACAUGAAUAGCCCCCGGCA ACGGUGGCUGUUUCUGUUU (SEQ ID NO: 2297)	-
	tracrRNA Portion 4 - partial	ACAUGAAUAGCCCCCGGCA ACGGUGGCUGUUUCUGU (SEQ ID NO: 2298)	-
	tracrRNA Portion 4 - without polyT	ACAUGAAUAGCCCCCGGCA ACGGUGGCUGUUUCUG (SEQ ID NO: 2299)	-
	sgRNA V3 sequence	GUUUGAGAGCAGUGUUGgaa aCAACACUGCACGUUCAAA UAAGCAGAUUGCACAAAGG UUCCCGUAAGGGAAUGACC AUCUGGUCACAUGAAUAGC CCCC GGCAACGGUGGCUGU UUUUU (SEQ ID NO: 2300)	GUUGUGUAUUGCUUUCgaaaGAA GCAAUACACAAUAAGGAUUAU CCGUUGUGAAACUUUUAAGGAG GGAGAAUAGAUUUUCUAUUCUC UCGCUUUCUUUUAUUCACGUAG CAACACA UUUUUU (SEQ ID NO: 2326)
tracrRNA V3 sequences	tracrRNA Portion 2	-	GUUGUGAAACUUUUAAGGAGGG AGAAUAGAUUUUCUAUUCUCUC GCUUUCUUUUAUUCACGUAGCA ACACA UUUUUU (SEQ ID NO: 2327)
	tracrRNA Portion 2 - partial	-	GUUGUGAAACUUUUAAGGAGGG AGAAUAGAUUUUCUAUUCUCUC GCUUUCUUUUAUUCACGUAGC (SEQ ID NO: 2328)
	tracrRNA Portion 2 – without polyT	-	GUUGUGAAACUUUUAAGGAGGG AGAAUAGAUUUUCUAUUCUCUC GCUUUCUUUUAUUCACGUAGCA ACACA (SEQ ID NO: 2329)
	tracrRNA Portion 3	GACCAUCUGGUCACAU (SEQ ID NO: 2301)	-
	tracrRNA Portion 4	GAAUAGCCCCCGGCAACGG UGGCUGUUUUUU (SEQ ID NO: 2302)	-
	tracrRNA Portion 4 - partial	GAAUAGCCCCCGGCAACGG UGGCUGUUU (SEQ ID NO: 2303)	-
	tracrRNA Portion 4 - without polyT	GAAUAGCCCCCGGCAACGG UGGCUG (SEQ ID NO: 2304)	-
	sgRNA V4 sequence	-	GUUGUGUAUUGCUUUCgaaaGAA GCAAUACACAAUAAGGAUUAU CCGUUGUGAAACUUCUAAGGAG

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			GGAGAAUAGAUCUUCUAUUCUC UCGCUUUCUUCUAUUCACGUAG CAACACAUUUUUU (SEQ ID NO: 2330)
tracrRNA V4 sequences	tracrRNA Portion 2	-	GUUGUGAAACUUCUAAGGAGGG AGAAUAGAUCUUCUAUUCUCUC GCUUUCUUCUAUUCACGUAGCA ACACAUUUUUU (SEQ ID NO: 2331)
	tracrRNA Portion 2 - partial	-	GUUGUGAAACUUCUAAGGAGGG AGAAUAGAUCUUCUAUUCUCUC GCUUUCUUCUAUUCACGUAGC (SEQ ID NO: 2332)
	tracrRNA Portion 2 – without polyT	-	GUUGUGAAACUUCUAAGGAGGG AGAAUAGAUCUUCUAUUCUCUC GCUUUCUUCUAUUCACGUAGCA ACACA (SEQ ID NO: 2333)

		OMNI-373	OMNI-375
	sgRNA V1 sequence	GUUUGAGAACCUUGUAAgaa aUUACAAGGUGAGUGCAAA UAAGGAUUCAUCCGAAAUA GUUUACCCGCAUUGUGCGG UCAAAAAAGACUUGAAAAA GUCUUUUUUU (SEQ ID NO: 2334)	GUUUGAGAGUAGUGUAAgaaaUU ACACUACACGGUUCAAAUAAG AAUUUUCCUAAUCGCCCUAGG GGCCACGUUGAUGUGGAUGAA AACUCGCCAGCUAAAGCGAGU UUUUUU (SEQ ID NO: 2350)
crRNA:tracr RNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAACCUUGUAA (SEQ ID NO: 2335)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 2351)
	Partial crRNA 1	GUUUGAGAACCUUGU (SEQ ID NO: 2336)	GUUUGAGAGUAGUGU (SEQ ID NO: 2352)
	Partial crRNA 2	GUUUGAGAACCU (SEQ ID NO: 2337)	GUUUGAGAGUAG (SEQ ID NO: 2353)
	Partial crRNA 3	GUUUGAGAAC (SEQ ID NO: 2338)	GUUUGAGAGU (SEQ ID NO: 2354)
	tracrRNA (Antirepeat)	UUACAAGGUGAGUGCAAAU (SEQ ID NO: 2339)	UUACACUACACGGUUCAAAU (SEQ ID NO: 2355)
	Partial tracrRNA 1	ACAAGGUGAGUGCAAAU (SEQ ID NO: 2340)	ACACUACACGGUUCAAAU (SEQ ID NO: 2356)
	Partial tracrRNA 2	AGGUGAGUGCAAAU (SEQ ID NO: 2341)	CUACACGGUUCAAAU (SEQ ID NO: 2357)
	Partial tracrRNA 3	GUGAGUGCAAAU (SEQ ID NO: 2342)	ACACGGUUCAAAU (SEQ ID NO: 2358)

		OMNI-373	OMNI-375
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGAUUCAUCCGAAAUAGUUUAC (SEQ ID NO: 2343)	AAAGAAUUUCCUAAUCGCCCCUAGGGGC (SEQ ID NO: 2359)
	tracrRNA Portion 1 - partial	AAGGAUUCAUCC (SEQ ID NO: 2344)	AAAGAAUUUCCUAAUCGCCCCUAGGGGC (SEQ ID NO: 2360)
	tracrRNA Portion 2	CCGCAUUGUGCGGUC (SEQ ID NO: 2345)	CCACGUUGAUGUGGAU (SEQ ID NO: 2361)
	tracrRNA Portion 2 - partial	CCGCAUUGUGCGG (SEQ ID NO: 2346)	CCACGUUGAUGUGG (SEQ ID NO: 2362)
	tracrRNA Portion 3	AAAAAAGACUUGAAAAAGUCUUUUUUU (SEQ ID NO: 2347)	GAAAACUCGCCAGCUAUAAGCGAGUUUUUUU (SEQ ID NO: 2363)
	tracrRNA Portion 3 - partial	AAAAAAGACUUGAAAAAGUCUUUUUUU (SEQ ID NO: 2348)	GAAAACUCGCCAGCUAUAAGCGAGUUUUUUU (SEQ ID NO: 2364)
	tracrRNA Portion 3 - without polyT	AAAAAAGACUUGAAAAAGUC (SEQ ID NO: 2349)	GAAAACUCGCCAGCUAUAAGCGAG (SEQ ID NO: 2365)
	sgRNA V2 sequence	-	GUUUGAGAGUAGUGUAAgaaaUUAACACUACACGGUUCAAAUAAGAAUUCUCCUAAUCGCCCCUAGGGGCCACGUUGAUGUGGAUGAAACUCGCCAGCUAUAAGCGAGUUUUUUU (SEQ ID NO: 2366)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AAAGAAUUCUCCUAAUCGCCCCUAGGGGC (SEQ ID NO: 2367)
	tracrRNA Portion 1 - partial	-	AAAGAAUUCUCCUAAUCGCCCCUAGGGGC (SEQ ID NO: 2368)

		OMNI-376	OMNI-377
	sgRNA V1 sequence	GUUUGAGAGUAGUGUAAgaaaUUAACACUACGAGUUCAAAUA AAAAUCUUUUCAAAUCGUUCGGUUUGACCGUUCGCAAGUGUUGUGCAUUGAUCUUGCUUUUAAGCAAGGAUUUUUUU (SEQ ID NO: 2369)	GUUUGAGAGCCUUGUUAagaaaUAACAAGGCGAGUGCAAUAAGGUUUAUCCGAAAUUCGUCUUAUGACGCCACACGGUGUGGCAUGAAAAAGUCGCGUAUGCGGCUUUUUUU (SEQ ID NO: 2391)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUGAGAGUAGUGUAA (SEQ ID NO: 2370)	GUUUGAGAGCCUUGUUA (SEQ ID NO: 2392)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 2371)	GUUUGAGAGCCUUGU (SEQ ID NO: 2393)

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	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 2372)	GUUUGAGAGCCU (SEQ ID NO: 2394)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 2373)	GUUUGAGAGC (SEQ ID NO: 2395)
	tracrRNA (Antirepeat)	UUACACUACGAGUUCAAAU (SEQ ID NO: 2374)	UAACAAGGCGAGUGCAAAU (SEQ ID NO: 2396)
	Partial tracrRNA 1	ACACUACGAGUUCAAAU (SEQ ID NO: 2375)	ACAAGGCGAGUGCAAAU (SEQ ID NO: 2397)
	Partial tracrRNA 2	CUACGAGUUCAAAU (SEQ ID NO: 2376)	AGGCGAGUGCAAAU (SEQ ID NO: 2398)
	Partial tracrRNA 3	ACGAGUUCAAAU (SEQ ID NO: 2377)	GCGAGUGCAAAU (SEQ ID NO: 2399)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAAAUCUUUUCAAAUCGU UCGGUUUGACCGUUC (SEQ ID NO: 2378)	AAGGUUUAUCCGAAAUC (SEQ ID NO: 2400)
	tracrRNA Portion 1 - partial	AAAAAUCUUUUCAAAUCGU UCGGUUUGA (SEQ ID NO: 2379)	AAGGUUUAUCCGAAAUC (SEQ ID NO: 2401)
	tracrRNA Portion 2	GCACAAGUGUUGUGCAUU (SEQ ID NO: 2380)	GUCUAUUGAC (SEQ ID NO: 2402)
	tracrRNA Portion 2 - partial	GCACAAGUGUUGUGC (SEQ ID NO: 2381)	GUCUAUUGAC (SEQ ID NO: 2403)
	tracrRNA Portion 3	GAUCCUUGCUUUUAAGCAA GGAUUUUUUU (SEQ ID NO: 2382)	GCCACACGGUGUGGCAU (SEQ ID NO: 2404)
	tracrRNA Portion 3 - partial	GAUCCUUGCUUUUAAGCAA GGAUU (SEQ ID NO: 2383)	GCCACACGGUGUGGC (SEQ ID NO: 2405)
	tracrRNA Portion 3 - without polyT	GAUCCUUGCUUUUAAGCAA GGA (SEQ ID NO: 2384)	-
	tracrRNA Portion 4	-	GAAAAAGUCGCGUAUGCGGCUU UUUU (SEQ ID NO: 2406)
	tracrRNA Portion 4 - partial	-	GAAAAAGUCGCGUAUGCGGCUU UUUU (SEQ ID NO: 2407)
	tracrRNA Portion 4 - without polyT	-	GAAAAAGUCGCGUAUGCGGC (SEQ ID NO: 2408)
	sgRNA V2 sequence	GUUUGAGAGUAGUGUAaGaa aUUACACUACGAGUUCAAA UAAAAAUCUUCUCAAUUCG UUCGGUUUGACCGUUCGCA	-

		OMNI-376	OMNI-377
tracrRNA V2 sequences		CAAGUGUUGUGCAUUGAUC CUUGC UUUCAAGCAAGGAU UUUUUU (SEQ ID NO: 2385)	
	tracrRNA Portion 1	AAAAAUCUUCUCAAUCGU UCGGUUUGACCGUUC (SEQ ID NO: 2386)	-
	tracrRNA Portion 1 - partial	AAAAAUCUUCUCAAUCGU UCGGUUUGA (SEQ ID NO: 2387)	-
	tracrRNA Portion 3	GAUCCUUGCUUUCAAGCAA GGAUUUUUUU (SEQ ID NO: 2388)	-
	tracrRNA Portion 3 - partial	GAUCCUUGCUUUCAAGCAA GGAUU (SEQ ID NO: 2389)	-
	tracrRNA Portion 3 - without polyT	GAUCCUUGCUUUCAAGCAA GGA (SEQ ID NO: 2390)	-
	sgRNA V3 sequence	-	GUUUGAGAGCCUUGUUAgaaaUA ACAAGGCGAGUGCAAUAAGGU UUAUCCGAAAUCGUCUAUUGAC GCCACACGGUGUGGCAUUUUUU (SEQ ID NO: 2409)
tracrRNA V3 sequences	tracrRNA Portion 3	-	GCCACACGGUGUGGCAUUUUUU (SEQ ID NO: 2410)
	tracrRNA Portion 3 - without polyT	-	GCCACACGGUGUGGCA (SEQ ID NO: 2411)

		OMNI-378	OMNI-380
	sgRNA V1 sequence	GUUUUGGGGCAGCGUCAgaa aUGACGCUGCGAGUCAAAA UAAAGGUUUACCCUAAUUG CCCGUUUCGGGUUUCGCUU AAGCGAAAUUUUUU (SEQ ID NO: 2412)	GUUGGGAAUUGCUUUCAAA gaaGGAGAAAGACUUUCUCAA UAAAGGCUAUAAGCCGAAGAUG UCUAACAGCCUGCGUUGUCGUG GGGAAACUGUGGAAACCCUGCA UCUUAGAAGCAGGGUUUUUU (SEQ ID NO: 2437)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUUUUGGGGCAGCGUCA (SEQ ID NO: 2413)	GUUGGGAAUUGCUUUCAAA (SEQ ID NO: 2438)
	Partial crRNA 1	GUUUUGGGGCAGCGU (SEQ ID NO: 2414)	GUUGGGAAUUGCUUU (SEQ ID NO: 2439)
	Partial crRNA 2	GUUUUGGGGCAG (SEQ ID NO: 2415)	GUUGGGAAUUGC (SEQ ID NO: 2440)

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	Partial crRNA 3	GUUUUGGGGC (SEQ ID NO: 2416)	GUUGGGAAUU (SEQ ID NO: 2441)
	tracrRNA (Antirepeat)	UGACGCUGCGAGUCAAAAU (SEQ ID NO: 2417)	GGAGAAAGACUUUUCUCAAU (SEQ ID NO: 2442)
	Partial tracrRNA 1	ACGCUGCGAGUCAAAAU (SEQ ID NO: 2418)	AAAGACUUUUCUCAAU (SEQ ID NO: 2443)
	Partial tracrRNA 2	CUGCGAGUCAAAAU (SEQ ID NO: 2419)	GACUUUUCUCAAU (SEQ ID NO: 2444)
	Partial tracrRNA 3	GCGAGUCAAAAU (SEQ ID NO: 2420)	UUUUCUCAAU (SEQ ID NO: 2445)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAGGUUUACCCUAAUU (SEQ ID NO: 2421)	AAGGCUAUAAGCCGAAGAUGUCUA (SEQ ID NO: 2446)
	tracrRNA Portion 1 - partial	AAAGGUUUACCCU (SEQ ID NO: 2422)	AAGGCUAUAAGCC (SEQ ID NO: 2447)
	tracrRNA Portion 2	GCCCGUUUCGGGU (SEQ ID NO: 2423)	ACAGCCUGCGUUGUCGUGGGAA CUGU (SEQ ID NO: 2448)
	tracrRNA Portion 2 - partial	GCCCGUUUCGGGU (SEQ ID NO: 2424)	ACAGCCUGCGUUGUCGUGGGAA CUGU (SEQ ID NO: 2449)
	tracrRNA Portion 3	UUCGCUUAAGCGAAAUUUU (SEQ ID NO: 2425)	GGAAACCCUGCAUCUUUAGAAG CAGGGUUUUU (SEQ ID NO: 2450)
	tracrRNA Portion 3 - partial	UUCGCUUAAGCGAA (SEQ ID NO: 2426)	GGAAACCCUGCAUCUUUAGAAG CAGGGUUUUU (SEQ ID NO: 2451)
	tracrRNA Portion 3 - without polyT	UUCGCUUAAGCGAAA (SEQ ID NO: 2427)	GGAAACCCUGCAUCUUUAGAAG CAGGG (SEQ ID NO: 2452)
	sgRNA V2 sequence	GUUCUGGGGCAGCGUCAgaa aUGACGCUGCGAGUCAGAA UAAAGGUUUACCCUAAUUG CCCGUUUCGGGUUUCGCUU AAGCGAAAUUUUUU (SEQ ID NO: 2428)	-
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	GUUCUGGGGCAGCGUCA (SEQ ID NO: 2429)	-
	Partial crRNA 1	GUUCUGGGGCAGCGU (SEQ ID NO: 2430)	-
	Partial crRNA 2	GUUCUGGGGCAG (SEQ ID NO: 2431)	-
	Partial crRNA 3	GUUCUGGGGC (SEQ ID NO: 2432)	-

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	tracrRNA (Antirepeat)	UGACGCUGCGAGUCAGAAU (SEQ ID NO: 2433)	-
	Partial tracrRNA 1	ACGCUGCGAGUCAGAAU (SEQ ID NO: 2434)	-
	Partial tracrRNA 2	CUGCGAGUCAGAAU (SEQ ID NO: 2435)	-
	Partial tracrRNA 3	GCGAGUCAGAAU (SEQ ID NO: 2436)	-

		OMNI-381	OMNI-382
	sgRNA V1 sequence	GUCUAGGAGUAGUGCUgaa aCGGCACUACAAGUCUAGA UAAAAUUUAUUCAAAGCA CCGUUUAGGCGGUACCCCG UUGUGGGGACAUAAUUCAG CCCGAAUUAUUGGUUAUUC GGGCUGAAUUAUUUUUU (SEQ ID NO: 2453)	GUUGUGACUUGCUUGAgaaaUCA AGCAAGUCACAAUAAGGAUUUAU UCCGUUGUGAAAACAUUAGGGC GGGGCAACUCGCCUUUUUUU (SEQ ID NO: 2469)
crRNA:tracrRNA duplex V1 sequences	crRNA (Repeat)	GUCUAGGAGUAGUGCUG (SEQ ID NO: 2454)	GUUGUGACUUGCUUGA (SEQ ID NO: 2470)
	Partial crRNA 1	GUCUAGGAGUAGUGC (SEQ ID NO: 2455)	GUUGUGACUUGCUUG (SEQ ID NO: 2471)
	Partial crRNA 2	GUCUAGGAGUAG (SEQ ID NO: 2456)	GUUGUGACUUGC (SEQ ID NO: 2472)
	Partial crRNA 3	GUCUAGGAGU (SEQ ID NO: 2457)	GUUGUGACUU (SEQ ID NO: 2473)
	tracrRNA (Antirepeat)	CGGCACUACAAGUCUAGAU (SEQ ID NO: 2458)	UCAAGCAAGUCACAAU (SEQ ID NO: 2474)
	Partial tracrRNA 1	GCACUACAAGUCUAGAU (SEQ ID NO: 2459)	CAAGCAAGUCACAAU (SEQ ID NO: 2475)
	Partial tracrRNA 2	CUACAAGUCUAGAU (SEQ ID NO: 2460)	GCAAGUCACAAU (SEQ ID NO: 2476)
	Partial tracrRNA 3	ACAAGUCUAGAU (SEQ ID NO: 2461)	AAGUCACAAU (SEQ ID NO: 2477)
tracrRNA V1 sequences	tracrRNA Portion 1	AAAAAUUUUAUUCAAAGCAC CGUUUAGGCGGUA (SEQ ID NO: 2462)	AAGGAUUUAUCCGU (SEQ ID NO: 2478)
	tracrRNA Portion 1 - partial	AAAAAUUUUAUUCAAAGCAC CGUUUAGGCGGU (SEQ ID NO: 2463)	AAGGAUUUAUCC (SEQ ID NO: 2479)

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	tracrRNA Portion 2	CCCCGUUGUGGGGAC (SEQ ID NO: 2464)	UGUGAAAACAUU (SEQ ID NO: 2480)
	tracrRNA Portion 2 - partial	CCCCGUUGUGGGG (SEQ ID NO: 2465)	UGUGAAAACA (SEQ ID NO: 2481)
	tracrRNA Portion 3	AUAAUUCAGCCCGAAUAUU UGGUUAUUCGGGCUGAAUU AUUUUUU (SEQ ID NO: 2466)	AGGGCGGGGCAACUCGCCUUUU (SEQ ID NO: 2482)
	tracrRNA Portion 3 - partial	AUAAUUCAGCCCGAAUAUU UGGUUAUUCGGGCUGAAUU AU (SEQ ID NO: 2467)	AGGGCGGGGCAACUCGCCUU (SEQ ID NO: 2483)
	tracrRNA Portion 3 - without polyT	AUAAUUCAGCCCGAAUAUU UGGUUAUUCGGGCUGAAUU A (SEQ ID NO: 2468)	AGGGCGGGGCAACUCGCC (SEQ ID NO: 2484)

		OMNI-383	OMNI-384
crRNA:tracrRNA duplex V1 sequences	sgRNA V1 sequence	GUUGUGAUUUUGCUUACgaaa UAAGCAAAUCACAAUAAGG AUUAUUCGUGUGAAAAAC AUUCAAGGCGGGGCAACUC GCCUUUUUUU (SEQ ID NO: 2485)	GUUUUGGCGCAGUGUCGgaaaCG AUACUGCGAGUCAAAAUAACGG CUUUUGCCUAAAAUGUCUGAU UCAAUCGAGACGCUCCGGAGGG AGCUAUCUGACUUGCAUAAGGC AUCCAAGCGUUCUUGGAUGCCU UUUUU (SEQ ID NO: 2501)
	crRNA (Repeat)	GUUGUGAUUUUGCUUAC (SEQ ID NO: 2486)	GUUUUGGCGCAGUGUCG (SEQ ID NO: 2502)
	Partial crRNA 1	GUUGUGAUUUUGCUUA (SEQ ID NO: 2487)	GUUUUGGCGCAGUGU (SEQ ID NO: 2503)
	Partial crRNA 2	GUUGUGAUUUUGC (SEQ ID NO: 2488)	GUUUUGGCGCAG (SEQ ID NO: 2504)
	Partial crRNA 3	GUUGUGAUUU (SEQ ID NO: 2489)	GUUUUGGCGC (SEQ ID NO: 2505)
	tracrRNA (Antirepeat)	UAAGCAAAUCACAAU (SEQ ID NO: 2490)	CGAUACUGCGAGUCAAAAU (SEQ ID NO: 2506)
	Partial tracrRNA 1	UAAGCAAAUCACAAU (SEQ ID NO: 2491)	AUACUGCGAGUCAAAAU (SEQ ID NO: 2507)
	Partial tracrRNA 2	GCAAAUCACAAU (SEQ ID NO: 2492)	CUGCGAGUCAAAAU (SEQ ID NO: 2508)
	Partial tracrRNA 3	AAAUACAAU (SEQ ID NO: 2493)	GCGAGUCAAAAU (SEQ ID NO: 2509)

		OMNI-383	OMNI-384
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGAUUAUCCGU (SEQ ID NO: 2494)	AACGGCUUUUGCCUAAAAU (SEQ ID NO: 2510)
	tracrRNA Portion 1 - partial	AAGGAUUAUCC (SEQ ID NO: 2495)	AACGGCUUUUGCC (SEQ ID NO: 2511)
	tracrRNA Portion 2	UGUGAAAACAUUC (SEQ ID NO: 2496)	GUCUCGAUUCAAUCGAGAC (SEQ ID NO: 2512)
	tracrRNA Portion 2 - partial	UGUGAAAACA (SEQ ID NO: 2497)	GUCUCGAUUCAAUCGAGAC (SEQ ID NO: 2513)
	tracrRNA Portion 3	AAGGCGGGGCAACUCGCCU UUUUUU (SEQ ID NO: 2498)	GCUCCGGAGGGAGCUAUCUGAC UUGCAU (SEQ ID NO: 2514)
	tracrRNA Portion 3 - partial	AAGGCGGGGCAACUCGCCU U (SEQ ID NO: 2499)	GCUCCGGAGGGAGC (SEQ ID NO: 2515)
	tracrRNA Portion 3 - without polyT	AAGGCGGGGCAACUCGCC (SEQ ID NO: 2500)	-
	tracrRNA Portion 4	-	AAGGCAUCCAAGCGUUCUUGGA UGCCUUUUUU (SEQ ID NO: 2516)
	tracrRNA Portion 4 - partial	-	AAGGCAUCCAAGCGUUCUUGGA UGCCUU (SEQ ID NO: 2517)
	tracrRNA Portion 4 - without polyT	-	AAGGCAUCCAAGCGUUCUUGGA UGCC (SEQ ID NO: 2518)
	sgRNA V2 sequence	-	GUUCUGGCGCAGUGUCGaaaCGA UACUGCGAGUCAGAAUACGGC UUCUGCCUAAAUGUCUGAUU CAAUCGAGACGCUCGGAGGGA GCUAUCUGACUUGCAUAAGGCA UCCAAGCGUUCUUGGAUGCCUU UUUU (SEQ ID NO: 2519)
crRNA:tracrRNA duplex V2 sequences	crRNA (Repeat)	-	GUUCUGGCGCAGUGUCG (SEQ ID NO: 2520)
	Partial crRNA 1	-	GUUCUGGCGCAGUGU (SEQ ID NO: 2521)
	Partial crRNA 2	-	GUUCUGGCGCAG (SEQ ID NO: 2522)
	Partial crRNA 3	-	GUUCUGGCGC (SEQ ID NO: 2523)
	tracrRNA (Antirepeat)	-	CGAUACUGCGAGUCAGAAU (SEQ ID NO: 2524)

		OMNI-383	OMNI-384
	Partial tracrRNA 1	-	AUACUGCGAGUCAGAAU (SEQ ID NO: 2525)
	Partial tracrRNA 2	-	CUGCGAGUCAGAAU (SEQ ID NO: 2526)
	Partial tracrRNA 3	-	GCGAGUCAGAAU (SEQ ID NO: 2527)
tracrRNA V2 sequences	tracrRNA Portion 1	-	AACGGCUUCUGCCUAAAAU (SEQ ID NO: 2528)
	tracrRNA Portion 1 - partial	-	AACGGCUUCUGCC (SEQ ID NO: 2529)
	sgRNA V3 sequence	-	GUUUUGGCGCAGUGUCGgaaaCG AUACUGCGAGUCAAAUAACGG CUUUUGCCUAAAAUGUCUCGAU UCAAUCGAGACUUUUUU (SEQ ID NO: 2530)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AACGGCUUUUGCCU (SEQ ID NO: 2531)
	tracrRNA Portion 2	-	AAAAUGUCUCGAUUCAAUCGAG ACUUUUUU (SEQ ID NO: 2532)
	tracrRNA Portion 2 - partial	-	AAAAUGUCUCGAUUCAAUCGAG ACUUUUUU (SEQ ID NO: 2533)
	tracrRNA Portion 2 – without polyT	-	AAAAUGUCUCGAUUCAAUCGAG AC (SEQ ID NO: 2534)
	sgRNA V4 sequence	-	GUUCUGGCGCAGUGUCGgaaaCGA UACUGCGAGUCAGAAUAACGGC UUCUGCCUAAAAUGUCUCGAUU CAAUCGAGACUUUUUU (SEQ ID NO: 2535)
tracrRNA V4 sequences	tracrRNA Portion 1	-	AACGGCUUCUGCCU (SEQ ID NO: 2536)

		OMNI-385	OMNI-386
	sgRNA V1 sequence	GUUGUGAUUAGCUAGAgaaa UCUAGCUAAUCACAAUAAG GAUUAUCCGUUGUGAAAA CAUUAACGGGUGGGGUGACU CACCCUUUUUU (SEQ ID NO: 2537)	GUUGUGAUUUGCUUUCgaaaGAA GCAAAUCACAAUAAGGAUUAUU CCGUUGUGAAAACAUUAAGGUUG CUCUCGUCCUUUAACGGGAGCA UUUUUUUGUUUUUU (SEQ ID NO: 2553)
	crRNA (Repeat)	GUUGUGAUUAGCUAGA (SEQ ID NO: 2538)	GUUGUGAUUUGCUUUC (SEQ ID NO: 2554)

		OMNI-385	OMNI-386
crRNA:tracrRNA duplex V1 sequences	Partial crRNA 1	GUUGUGAUUAGCUAG (SEQ ID NO: 2539)	GUUGUGAUUUGCUUU (SEQ ID NO: 2555)
	Partial crRNA 2	GUUGUGAUUAGC (SEQ ID NO: 2540)	GUUGUGAUUUGC (SEQ ID NO: 2556)
	Partial crRNA 3	GUUGUGAUUA (SEQ ID NO: 2541)	GUUGUGAUUU (SEQ ID NO: 2557)
	tracrRNA (Antirepeat)	UCUAGCUAAUCACAAU (SEQ ID NO: 2542)	GAAGCAAAUCACAAU (SEQ ID NO: 2558)
	Partial tracrRNA 1	CUAGCUAAUCACAAU (SEQ ID NO: 2543)	GAAGCAAAUCACAAU (SEQ ID NO: 2559)
	Partial tracrRNA 2	GCUAAUCACAAU (SEQ ID NO: 2544)	GCAAAUCACAAU (SEQ ID NO: 2560)
	Partial tracrRNA 3	UAAUCACAAU (SEQ ID NO: 2545)	AAAUCACAAU (SEQ ID NO: 2561)
tracrRNA V1 sequences	tracrRNA Portion 1	AAGGAUUAUUC (SEQ ID NO: 2546)	AAGGAUUAUUCGUUGU (SEQ ID NO: 2562)
	tracrRNA Portion 1 - partial	AAGGAUUAUUC (SEQ ID NO: 2547)	AAGGAUUAUUC (SEQ ID NO: 2563)
	tracrRNA Portion 2	GUUGUGAAAACAUUAC (SEQ ID NO: 2548)	GAAAACAUUAGGUUGCUCUCGU CCUUUAACGGGAGCAUUUUUUU GUUUUUU (SEQ ID NO: 2564)
	tracrRNA Portion 2 - partial	GUUGUGAAAACAUUAC (SEQ ID NO: 2549)	GAAAACAUUAGGUUGCUCUCGU CCUUUAACGGGAGCAUUUUUUU GUUUUUU (SEQ ID NO: 2565)
	tracrRNA Portion 2 – without polyT	-	GAAAACAUUAGGUUGCUCUCGU CCUUUAACGGGAGCAUUUUUUU G (SEQ ID NO: 2566)
	tracrRNA Portion 3	GGGUGGGGUGACUCACCCU UUUUU (SEQ ID NO: 2550)	-
	tracrRNA Portion 3 - partial	GGGUGGGGUGACUCACCC (SEQ ID NO: 2551)	-
	tracrRNA Portion 3 - without polyT	GGGUGGGGUGACUCACCC (SEQ ID NO: 2552)	-
	sgRNA V2 sequence	-	GUUGUGAUUUGCUUUCgaaaGAA GCAAAUCACAAUAAGGAUUAU CCUUGUGAAAACAUUGGGUUG CUCUCGUCCUUUAACGGGAGCA UUUCUUUGUUUUUU (SEQ ID NO: 2567)

		OMNI-385	OMNI-386
tracrRNA V2 sequences	tracrRNA Portion 1	-	GAAAACAUUGGGUUGCUCUCGU CCUUUAACGGGAGCAUUUCUUU GUUUUUU (SEQ ID NO: 2568)
	tracrRNA Portion 1 - partial	-	GAAAACAUUGGGUUGCUCUCGU CCUUUAACGGGAGCAUUUCUUU GUUUUUU (SEQ ID NO: 2569)
	tracrRNA Portion 1 - without polyT	-	GAAAACAUUGGGUUGCUCUCGU CCUUUAACGGGAGCAUUUCUUU G (SEQ ID NO: 2570)
	sgRNA V3 sequence	-	GUUGUGAUUUGCUUUCgaaaGAA GCAAAUCACAAUAAGGAUUAUU CCGUUGUGAAAACAUUAGGUUG CUCUCGUCCUUUAACGGGAGCA UUUUUUUGUUUUUUGGGAUUAG UUUUUU (SEQ ID NO: 2571)
tracrRNA V3 sequences	tracrRNA Portion 1	-	AAGGAUUAUCCGUUGUGAAAA CAUUAGGUUGCUCUCGUCCUUU AACGGGAGCAUUUUUUUGUUUU AUGGGAUUAGUUUUUU (SEQ ID NO: 2572)
	tracrRNA Portion 1 - partial	-	AAGGAUUAUCCGUUGUGAAAA CAUUAGGUUGCUCUCGUCCUUU AACGGGAGCAUUUUUUUGUUUU AUGGGAUUAGUUUUUU (SEQ ID NO: 2573)
	tracrRNA Portion 1 - without polyT	-	AAGGAUUAUCCGUUGUGAAAA CAUUAGGUUGCUCUCGUCCUUU AACGGGAGCAUUUUUUUGUUUU AUGGGAUUAG (SEQ ID NO: 2574)

Table 3 – OMNI PAM Sequences showing activity for each tested sgRNA

Name	Relaxed PAM	Strict PAM	Additional PAM # 1	Additional PAM # 2	Additional PAM # 3	Additional PAM # 4
OMNI-263	NNNVCCNR	NNNRCCNR	NNNRCMNN	Not listed	Not listed	Not listed
OMNI-264	NRRNANNN	NRRNAANN	NGGYANNN	NRRYANNN	Not listed	Not listed
OMNI-266	NNNNCDMA	NNNNCTAA	NNNCCTMA	NNNNCWMA	Not listed	Not listed
OMNI-268	NNNNNCNN	NVRMNCNN	NNRAACNN	NNRNNCNN	Not listed	Not listed
OMNI-269	NNNNCMDN	NDDNCMAN	NNNNCMNN	Not listed	Not listed	Not listed
OMNI-271	NDNCHTNN	NNNCHTNN	Not listed	Not listed	Not listed	Not listed
OMNI-274	NNRDGNMN	NNRKGNMN	NNRKGHNN	Not listed	Not listed	Not listed
OMNI-275	NNRCAANN	BRRCAAGN	CNVCAANN	CNRCAAGN	Not listed	Not listed
OMNI-276	NNDGCHNN	NNRGCYNR	NNRKCHNN	KNRGCCNN	NNGGCHNN	Not listed
OMNI-278	NDHAANNN	NAYAAWNN	NDYANNNN	NRYANNNN	Not listed	Not listed
OMNI-279	NNAANNNN	NNAARGNN	NNAAVNNN	Not listed	Not listed	Not listed

Name	Relaxed PAM	Strict PAM	Additional PAM # 1	Additional PAM # 2	Additional PAM # 3	Additional PAM # 4
OMNI-280	NNVGGNNN	NNRGGGNN	NNRGNNNN	NNGGGNNN	Not listed	Not listed
OMNI-281	NNGRVNNN	NNGRVNNN	NNGAVNNN	Not listed	Not listed	Not listed
OMNI-283	NNNRTMNN	CNNRTMNN	NNNRTANN	Not listed	Not listed	Not listed
OMNI-284	NNNNRTWN	NNRMATWN	NNNNATAN	NNNNATWN	Not listed	Not listed
OMNI-286	NNNNCNAN	NNNNCMAA	NNNNCNNN	Not listed	Not listed	Not listed
OMNI-287	NNNNRTAA	NNNNRTAN	Not listed	Not listed	Not listed	Not listed
OMNI-288	NNNYMAAN	NNNTAAAN	NNNYAAAN	Not listed	Not listed	Not listed
OMNI-290	NNNNGHNN	NNNNGMAA	NNNNGMDN	Not listed	Not listed	Not listed
OMNI-291	NNNNCVKA	NNNNCVTA	NNNNCNKN	NNNNCNTA	Not listed	Not listed
OMNI-293	NNNNCNAN	NNWNCNAC	NNNNCNNN	Not listed	Not listed	Not listed
OMNI-294	NNNNGYDA	NNNNGYRA	NNNNGYDN	Not listed	Not listed	Not listed
OMNI-295	NNRNCDNN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-296	NNNNGNHN	NNNNGHAA	NNNNGNAN	Not listed	Not listed	Not listed
OMNI-297	NNNNAYRN	NNNNAYRA	NNNNVYAN	NNNNAYAN	Not listed	Not listed
OMNI-298	NNRNGCNN	NNRGGCNA	NNNNGYNN	NNNNGCNN	Not listed	Not listed
OMNI-299	NNNNRYAA	NNNVGTAA	NNNNRYHN	NNNNRYAN	Not listed	Not listed
OMNI-300	NNNNGMAA	NNASGMAA	NNNNGNAN	NNNNGVAN	Not listed	Not listed
OMNI-301	NNNNGYKW	NNNNGTTA	NNNNGYNN	Not listed	Not listed	Not listed
OMNI-302	NNNNCHWA	NNNNCMWA	NNNNCDNN	NNNNCNNN	Not listed	Not listed
OMNI-303	NNNNCATR	NNNHcata	NNNNCATA	NNNCCATA	NNNNCAYA	Not listed
OMNI-304	NNNGVGNN	NNRGGGNN	NNRGRGNN	Not listed	Not listed	Not listed
OMNI-305	NNNNGRAN	NNNNGRAA	NNNNGRDN	Not listed	Not listed	Not listed
OMNI-307	NRDAATNN	NRGAATNN	NNGAATNN	Not listed	Not listed	Not listed
OMNI-308	NNNNRYAT	NNNNRYAN	Not listed	Not listed	Not listed	Not listed
OMNI-309	NNNNGHAA	NNNNGAAA	NNNNRNDN	NNNNRWDN	Not listed	Not listed
OMNI-310	NNGYAARN	NNGCAARN	NNGCAANN	Not listed	Not listed	Not listed
OMNI-311	NNANGNNN	NNAMGMNN	Not listed	Not listed	Not listed	Not listed
OMNI-312	NNVNRYNN	NNRNRTNN	NNNRTANN	Not listed	Not listed	Not listed
OMNI-313	NNRNRYNN	NNRNRTKN	NNRNRTNN	Not listed	Not listed	Not listed
OMNI-314	NNNNCABN	NNNNCABA	NNNNCANN	NNNNCATN	Not listed	Not listed
OMNI-315	NNSCGNHN	NNSCGNCN	NNCCNNNN	Not listed	Not listed	Not listed
OMNI-316	NNNNCNYN	NNNNCMYN	NNNNCHYN	NNNNCHCN	Not listed	Not listed
OMNI-317	NNNNGAAD	NNNGGAAA	NNNNGRAD	Not listed	Not listed	Not listed
OMNI-318	NNNCCYNN	NNNCCCNN	NNNNMCNN	NNNNCCNN	Not listed	Not listed
OMNI-319	NNAARAAN	NYAARAAN	NNANVDNN	NNAARDNN	Not listed	Not listed
OMNI-320	NNNNCMAW	NNANCAAW	NNNNCHAY	NNNNCAAY	NNNNCNAN	Not listed
OMNI-321	NNNNRYAR	NNNSGTAA	NNNNVTAN	NNNNRTAA	NNNVRTAR	NNNVGTAR
OMNI-322	NNNNGNNC	NNNSGMAC	NNNNRNNC	Not listed	Not listed	Not listed

Name	Relaxed PAM	Strict PAM	Additional PAM # 1	Additional PAM # 2	Additional PAM # 3	Additional PAM # 4
OMNI-323	NRRNGGNN	NGGNGGNN	Not listed	Not listed	Not listed	Not listed
OMNI-324	NNRCMNNN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-325	NNBCRNNN	NNNRCAGW	NNNNCAAC	Not listed	Not listed	Not listed
OMNI-326	NNNNCAGN	NNNRCAGA	NNNNCMRN	NNNRCAGW	Not listed	Not listed
OMNI-327	NRVWWGNN	NRCAWGDN	NNVWWGN	NNSAWGNN	Not listed	Not listed
OMNI-329	NVRATTNN	NRAATTAN	NVRAYTNN	NRRATTNN	NNRATTNN	Not listed
OMNI-330	NNNNNHAA	NNNNNYAA	Not listed	Not listed	Not listed	Not listed
OMNI-331	NNNNGWDA	NNNSGTKA	NNNSGWDA	NNNNGNDA	Not listed	Not listed
OMNI-332	NRRNNCVN	NRRNMCVN	NRGCMCRN	NRRNNCRN	NNGYACRN	Not listed
OMNI-333	NNRCVCNN	NRRCACYN	NNRCRCNN	NRRCACNN	Not listed	Not listed
OMNI-334	NNANANNN	NSAMANNN	NNAMANNN	Not listed	Not listed	Not listed
OMNI-336	NVTAYTNN	NGGNNNNN	NGGNGNNN	Not listed	Not listed	Not listed
OMNI-337	NNGWMRNN	NNGAAANN	NNGAANNN	NNGAMANN	Not listed	Not listed
OMNI-338	NRNRNCNN	NRWANCNN	NRTAYNNN	Not listed	Not listed	Not listed
OMNI-339	NAGBNNNN	NAGYNNNN	NRNAHCNN	Not listed	Not listed	Not listed
OMNI-340	NAGBNNNN	NAGYNNNN	Not listed	Not listed	Not listed	Not listed
OMNI-341	NRNAANNN	NVYAATTN	Not listed	Not listed	Not listed	Not listed
OMNI-342	NVMADCNN	NRYAANNN	Not listed	Not listed	Not listed	Not listed
OMNI-343	NNHADCNN	NNNCCCNN	Not listed	Not listed	Not listed	Not listed
OMNI-344	NVTAACNN	NRTAACNN	NNNCCCNN	Not listed	Not listed	Not listed
OMNI-345	NVTAAYNN	NRTAAYNN	NRTANYNN	NRTAACNN	Not listed	Not listed
OMNI-346	NRTANNNN	YGTANNNN	NCCNNSMN	NCCNNNVN	BCSMCSSB	BNSMNSSB
OMNI-347	NNTANNNN	NVTANNNN	Not listed	Not listed	Not listed	Not listed
OMNI-348	NNGNNNNN	NNGNMANN	NNGHNNHN	NCGHVANN	Not listed	Not listed
OMNI-349	NRNAAANN	NRMAAANN	NVNMAANN	NACAAANN	Not listed	Not listed
OMNI-350	NNTANNNN	NNTAHNNN	Not listed	Not listed	Not listed	Not listed
OMNI-351	NNGRYNNN	NNGRCANN	NNGRYANN	NNGGYANN	Not listed	Not listed
OMNI-352	NGGNNNNN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-353	NRHAATTN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-354	NVNACNNN	NVWACANN	NRHACANN	Not listed	Not listed	Not listed
OMNI-356	NNNRAANN	NNYRAANN	NNYAAANN	NNNNANNN	NNNRANNN	
OMNI-357	NGGNNNNN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-358	NNRACYNN	NNRACTNN	Not listed	Not listed	Not listed	Not listed
OMNI-359	NRHRAANN	NRMAAANN	NRHAAANN	Not listed	Not listed	Not listed
OMNI-360	NNNAACNN	NRNAACNN	Not listed	Not listed	Not listed	Not listed
OMNI-361	NRTAYNNN	NGTACNNN	NGTAYNNN	Not listed	Not listed	Not listed
OMNI-362	NVHARKNN	NRYARKNN	NRYARTNN	Not listed	Not listed	Not listed
OMNI-363	NRNARWNN	NRNAAWNN	NRNAATNN	Not listed	Not listed	Not listed

Name	Relaxed PAM	Strict PAM	Additional PAM # 1	Additional PAM # 2	Additional PAM # 3	Additional PAM # 4
OMNI-364	NRNACBNN	NRNACTNN	Not listed	Not listed	Not listed	Not listed
OMNI-365	NNNACNNN	NRHACNNN	NNHACNNN	Not listed	Not listed	Not listed
OMNI-366	NVTAMNNN	NVTAMMNN	NVTACNNN	Not listed	Not listed	Not listed
OMNI-367	NRTADMNN	NGTADCCN	NRTANMNN	NRTARNNN	Not listed	Not listed
OMNI-368	NNRACYNN	NNRACTTN	NNNACTNN	Not listed	Not listed	Not listed
OMNI-369	NNNAACNN	NRNAACNN	NNNADCNN	Not listed	Not listed	Not listed
OMNI-370	NRNRAANN	NRNAAANN	NNNAAANN	Not listed	Not listed	Not listed
OMNI-371	NRWRTARN	NGWATAGN	NRNRTANN	NRYATARN	NNNATANN	Not listed
OMNI-372	NNAAATNN	NNAAANNN	Not listed	Not listed	Not listed	Not listed
OMNI-373	NDRACNNN	NNRACNNN	NRRACNNN	Not listed	Not listed	Not listed
OMNI-375	NNAAYNYN	NNAACNY	Not listed	Not listed	Not listed	Not listed
OMNI-376	NNYAANNN	Not listed	Not listed	Not listed	Not listed	Not listed
OMNI-377	NRNVCCNN	NRNACCNN	NRDACCNN	Not listed	Not listed	Not listed
OMNI-378	NNGNNNNN	NNGNMRNN	NNGNNANN	Not listed	Not listed	Not listed
OMNI-380	NRGCCCN	NRGCCRN	NNGCCCN	Not listed	Not listed	Not listed
OMNI-381	NNNGMTTN	NNTGATTN	NNNGATDN	Not listed	Not listed	Not listed
OMNI-382	NVAYAANN	NAATAANN	NRAYAANN	NNAYAANN	Not listed	Not listed
OMNI-383	NNRRVCNN	NNRRACNN	Not listed	Not listed	Not listed	Not listed
OMNI-384	NRRCNNNN	NAGCNNNN	Not listed	Not listed	Not listed	Not listed
OMNI-385	NNAAMGNN	NNAAAGNN	Not listed	Not listed	Not listed	Not listed
OMNI-386	NRRYAANN	NRAYAANN	NRACAANN	Not listed	Not listed	Not listed

Table 4 - Plasmids used in assays

Plasmid	Purpose	Elements	Example
pET9a	Expressing OMNI polypeptide in the bacterial system	T7 promoter HA Tag-Linker-OMNI ORF (Human optimized) -SV40 NLS-8XHisTag -T7 terminator	pET9a-OMNI-263 (SEQ ID NO: 2575)
pbShuttle Guide T2	Expressing OMNI sgRNA in the bacterial system	U6 promotor - T7promoter - T2 spacer sgRNA scaffold - T7 terminator	pShuttle Guide-T2-OMNI-264 V1 (SEQ ID NO: 2576)
pbPOS T2 library	Bacterial/TXTL depletion assay	T2 protospacer - 8N PAM library - chloramphenicol acetyltransferase	pbPOS T2 library (SEQ ID NO: 2577)
pmOMNI	Expressing OMNI polypeptide in the human cell system	CMV promoter - Kozak - SV40 NLS - OMNI ORF (human optimized) - HA - SV40 NLS - P2A - mCherry - bGH poly(A) signal	pmOMNI-OMNI-263 (SEQ ID NO: 2578)

Table 4 Appendix - Details of construct elements

Element	Protein Sequence	DNA sequence
HA Tag	SEQ ID NO: 2579	SEQ ID NO: 2583
NLS	SEQ ID NO: 2580	SEQ ID NO: 2584
P2A	SEQ ID NO: 2581	SEQ ID NO: 2585
mCherry	SEQ ID NO: 2582	SEQ ID NO: 2586

Table 5 - Nuclease activity in endogenous context in mammalian cells

Nuclease	Gene target	Corresponding spacer name	Spacer sequence	Max Activity Mean	PAM
OMNI-266	hTRAC	hTRAC_s160_2 2bp_II	CCCUGCCGUGUA CCAGCUGAGA (SEQ ID NO: 2588)	51%	GACTCTAA
OMNI-268	hSAMD9	hSAMD9L_g83 _alt_22bp_II	AAAACAGAACAC CAAAAAAUC (SEQ ID NO: 2590)	1%	CAAAACAC
	hCXCR4	hCXCR4_S40_2 2bp_II	GAUAAGGCCAAC CAUGAUGUGC (SEQ ID NO: 2589)	1%	TGAAACTG
OMNI-269	hTGFBi	hTGFBi_g20_22 bp_II	CAGCACGGGUAA GCCGAGCCGC (SEQ ID NO: 2783)	11%	CTGGCCAG
	hELANE	hELANE_g145_22 bp_II	CCCCUCGGAGUC UACCCCGCU (SEQ ID NO: 2593)	12%	GTGACCAT
	hELANE	hELANE_g146_22 bp_II	UGUUAUGGUCAC AGCGGGUGUA (SEQ ID NO: 2594)	19%	GACTCCGA
	hELANE	hELANE_g62_2 2bp_II	GUGUCAAGCCCC AGAGGCCACA (SEQ ID NO: 2595)	21%	GGGACAGA
	hSAMD9	hSAMD9L_g14 7_alt_22bp_II	UUCCAAGGAACA AAGAGCCUUU (SEQ ID NO: 2601)	29%	GGTGCCAA
	hTRAC	hTRAC_S72_22 bp_II	UUC CAGAAGACA CCUUCUCCCC (SEQ ID NO: 2598)	43%	CAGCCCAG
	hLRRK2	hLRRK2_g13_al t_22bp_II	AUAUCACUUUCU UCAUCCAGUA (SEQ ID NO: 2597)	44%	TCAGCAAG
	hELANE	hELANE_g136_22 bp_II	CCACCCGCUC AGCCCGGACU (SEQ ID NO: 2592)	54%	GCAGCAAC
OMNI-274	hLRRK2	hLRRK2_g11_al t_22bp_II	UCUAGGGAGGUA ACGUAAAAG (SEQ ID NO: 2596)	73%	AAAACAAG
	hTRAC	hTRAC_S25_22 bp_II	CUCAGCUGGUAC ACGGCAGGGU (SEQ ID NO: 2603)	26%	CAGGGTTC
OMNI-278	hPDCD1	hPDCD1_S6_22 bp_II	CAUGAGCGUGGU CAGGGCCCCG (SEQ ID NO: 2606)	1%	CGCAATGA
	hCXCR4	hCXCR4_S55_2 2bp_II	CACGAGGAUGGC AAGAGACCCA (SEQ ID NO: 2605)	2%	CACACCGG
	hTRAC	hTRAC_S88_22 bp_II	GCUGAGAGACUC UAAAUCCAGU (SEQ ID NO: 2607)	3%	GACAAGTC

OMNI-279	hCXCR4	hCXCR4_s79_2 2bp_II	GGCUUCAAGCAA CUUGUAGUGG (SEQ ID NO: 2608)	13%	GTAAAGAG
OMNI-280	hTRAC	hTRAC_S25_22 bp_II	CUCAGCUGGUAC ACGGCAGGGU (SEQ ID NO: 2603)	2%	CAGGGTTC
	hTRAC	hTRAC_s119_2 2bp_II	ACCAAAGCUGCC CUUACCUGGG (SEQ ID NO: 2611)	3%	CTGGGGAA
	hPDCD1	hPDCD1_S30_2 2bp_II	UUCCGUGUCACA CAACUGCCCA (SEQ ID NO: 2610)	4%	ACGGGCGT
	hPDCD1	hPDCD1_S29_2 2bp_II	AAGAGAGCCUGC GGGCAGAGCU (SEQ ID NO: 2609)	4%	CAGGGTGA
OMNI-281	hELANE	hELANE_g145_22 bp_II	CCCCUCGGAGUC UACACCCGCU (SEQ ID NO: 2593)	15%	GTGACCAT
	hELANE	hELANE_g147_22 bp_II	CAGUCCGGGCUG GGAGCGGGUG (SEQ ID NO: 2621)	19%	GGGAGCAG
	hLRRK2	hLRRK2_g16_al t_22bp_II	AUCACCUUGCUG AUACUGGAUG (SEQ ID NO: 2625)	24%	AAGAAAGT
	hLRRK2	hLRRK2_g10_al t_22bp_II	AAAAUCACCUUG CUGAUACUGG (SEQ ID NO: 2624)	24%	ATGAAGAA
	hSERP	hSERP_g147_22 bp_II	CUGACCAUCGAC GAGAAAGGGA (SEQ ID NO: 2628)	29%	CTGAAGCT
	hELANE	hELANE_g62_2 2bp_II	GUGUCAAGCCCC AGAGGCCACA (SEQ ID NO: 2595)	57%	GGGACAGA
	hTRAC	hTRAC_S35_22 bp_II	GACCCUGCCGUG UACCAGCUGA (SEQ ID NO: 2617)	63%	GAGACTCT
	hLRRK2	hLRRK2_g18_al t_22bp_II	GGUUCUAGGGAG GUAACGUAA (SEQ ID NO: 2627)	63%	AAGAAAAC
	hCXCR4	hCXCR4_s89_2 2bp_II	AAGAAAGCUAGG GCCUCGGUGA (SEQ ID NO: 2613)	65%	TGGAATC
	hTRAC	hTRAC_S41_22 bp_II	GCCUUCACAAC AGCAUUAUUC (SEQ ID NO: 2618)	86%	CAGAAGAC
OMNI-286	hSAMD9	hSAMD9L_g14 7_alt_22bp_II	UUCCAAGGAACA AAGAGCCUUU (SEQ ID NO: 2601)	44%	GGTGCCAA
	hCXCR4	hCXCR4_S36_2 2bp_II	GUAAGGCAGCCA ACAGGCGAAG (SEQ ID NO: 2599)	55%	AAAGCCAG

OMNI-290	hCXCR4	hCXCR4_S113_22bp_II	GGAAGAAAGCUA GGGCCUCGGU (SEQ ID NO: 2633)	48%	GATGGAAA
OMNI-291	hSERP	hSERP_g115_22bp_II	CCUUUCUCGUCG AUGGUCAGCA (SEQ ID NO: 2645)	25%	CAGCCTTA
	hLRRK2	hLRRK2_g22_al t_22bp_II	CAUCCAGUAUCA GCAAGGUGAU (SEQ ID NO: 2643)	30%	TTTACCTA
	hCXCR4	hCXCR4_S117_22bp_II	ACGGAAACAGGG UUCUUCUAUG (SEQ ID NO: 2635)	30%	GAGTCATA
	hELANE	hELANE_g124_22bp_II	UGCAGCAACAGG CACCGUGGCU (SEQ ID NO: 2641)	46%	AGACCCTA
	hB2M	hB2M_S25_22bp_II	UUUCAUCCAUC GACAUUGAAG (SEQ ID NO: 2639)	46%	TTGACTTA
	hTIGIT	hTIGIT_S28_22bp_II	CAGCUGUCUGAU GCCUCCUGUC (SEQ ID NO: 2646)	58%	TCTGCCTA
	hB2M	hB2M_s89_22bp_II	CAAAGUCACAUG GUUCACACGG (SEQ ID NO: 2640)	83%	CAGGCATA
	hPDCD1	hPDCD1_S123_22bp_II	CAUUCCGCUAGG AAAGACAAUG (SEQ ID NO: 2637)	91%	GTGGCATA
OMNI-293	hELANE	hELANE_g149_22bp_II	GAGUCCCAGCUG CGGGAAUGGG (SEQ ID NO: 2654)	35%	ATTCCCAG
	hCXCR4	hCXCR4_S36_22bp_II	GUAAGGCAGCCA ACAGGCGAAG (SEQ ID NO: 2599)	38%	AAAGCCAG
	hELANE	hELANE_g122_22bp_II	AGCUGCGGGAAU GGGAUUCCCA (SEQ ID NO: 2651)	50%	GGACCCAG
	hTRAC	hTRAC_S56_22bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	82%	TGTACCAG
OMNI-294	hPDCD1	hPDCD1_S121_22bp_II	ACCCUCCACCAU GAGCCCGGGU (SEQ ID NO: 2657)	43%	CAGCGCAT
OMNI-295	hCXCR4	hCXCR4_S38_22bp_II	AUCCACUUGUGC ACAGUGUUCU (SEQ ID NO: 2658)	1%	CAAACCTCA
	hTRAC	hTRAC_S20_22bp_II	AGCGUCAUGAGC AGAUUAAACC (SEQ ID NO: 2659)	8%	CGGCCACT
OMNI-296	hCXCR4	hCXCR4_S113_22bp_II	GGAAGAAAGCUA GGGCCUCGGU (SEQ ID NO: 2633)	1%	GATGGAAA

OMNI-297	hCXCR4	hCXCR4_S122_22bp_II	AUAAACACGAGG AUGGCAAGAG (SEQ ID NO: 2660)	32%	ACCCACAC
OMNI-298	hELANE	hELANE_g147_22bp_II	CAGUCCGGGCUG GGAGCGGGUG (SEQ ID NO: 2621)	10%	GGGAGCAG
	hELANE	hELANE_g148_alt_22bp_II	GGCUGGGUCCUG GGAAUCCCAU (SEQ ID NO: 2669)	12%	TCCCGCAG
	hCXCR4	hCXCR4_S69_22bp_II	AGGAUGACCAAU CCAUUGCCCA (SEQ ID NO: 2664)	13%	CAATGCCA
	hPDCD1	hPDCD1_S88_22bp_II	UUCUCCAACACA UCGGAGAGCU (SEQ ID NO: 2666)	38%	TCGTGCTA
	hCXCR4	hCXCR4_S22_22bp_II	UUCCCUUCUGGG CAGUUGAUGC (SEQ ID NO: 2663)	47%	CGTGGCAA
	hPDCD1	hPDCD1_S79_22bp_II	UGCUCGUGGUGA CCGAAGGGGA (SEQ ID NO: 2665)	53%	CAACGCCA
OMNI-299	hPDCD1	hPDCD1_S121_22bp_II	ACCCUCCACCAU GAGCCCGGU (SEQ ID NO: 2657)	10%	CAGCGCAT
OMNI-300	hCXCR4	hCXCR4_S113_22bp_II	GGAAGAAAGCUA GGGCCUCGGU (SEQ ID NO: 2633)	45%	GATGGAAA
OMNI-302	hCXCR4	hCXCR4_S36_22bp_II	GUAAGGCAGCCA ACAGGCGAAG (SEQ ID NO: 2599)	1%	AAAGCCAG
	hTRAC	hTRAC_S56_22bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	5%	TGTACCAG
OMNI-303	hCXCR4	hCXCR4_S117_22bp_II	ACGGAAACAGGG UUCUUCAUG (SEQ ID NO: 2635)	27%	GAGTCATA
OMNI-304	hTRAC	hTRAC_s139_22bp_II	UCUCAGCUGGUA CACGGCAGGG (SEQ ID NO: 2681)	1%	TCAGGGTT
	hTRAC	hTRAC_s140_22bp_II	ACACCUUCUUC CCAGCCCAGG (SEQ ID NO: 2682)	2%	TAAGGGCA
	hPDCD1	hPDCD1_S124_22bp_II	CACCUGCAGCUU CUCCAACACA (SEQ ID NO: 2680)	2%	TCGGAGAG
	hCXCR4	hCXCR4_S118_22bp_II	UUCAGACAACAG UGGAAGAAAG (SEQ ID NO: 2679)	2%	CTAGGGCC
OMNI-308	hCXCR4	hCXCR4_S120_22bp_II	AGUUCCAAAGU ACCAGUUUGC (SEQ ID NO: 2683)	14%	CACGGCAT

	hTIGIT	hTIGIT_S27_22 bp_II	GGCUACUUUCAG UGGCAGAAGA (SEQ ID NO: 2693)	15%	GGCCACAT
	hTRAC	hTRAC_s136_2 2bp_II	UGGCCUGGAGCA ACAAUUCUGA (SEQ ID NO: 2686)	35%	CTTTGCAT
	hLRRK2	hLRRK2_g15_2 2bp_II	UACCAUUACCUC CCUAGAACCA (SEQ ID NO: 2784)	69%	TAAAGTAT
	hCTLA4	hCTLA4_S17_2 2bp_II	UGCUGUGGUACU GGCCAGCAGC (SEQ ID NO: 2689)	74%	CGAGGCAT
	hCXCR4	hCXCR4_S121_2 2bp_II	CAUGGGUUACCA GAAGAAACUG (SEQ ID NO: 2684)	83%	AGAAGCAT
	hTIGIT	hTIGIT_S26_22 bp_II	CCCUUGAUUCUA GGCAGAGACA (SEQ ID NO: 2692)	84%	GGAGGCAT
	hCTLA4	hCTLA4_S16_2 2bp_II	CAGUACCACAGC AGGCUGGGCC (SEQ ID NO: 2688)	86%	ACGTGCAT
	hTRAC	hTRAC_s135_2 2bp_II	GUGUCACAAAGU AAGGAUUCUG (SEQ ID NO: 2673)	92%	ATGTGTAT
OMNI-309	hTRAC	hTRAC_s95_22 bp_II	GAUAUCCAGAAC CCUGACCCUG (SEQ ID NO: 2695)	7%	CCGTGTAC
OMNI-312	hCXCR4	hCXCR4_S107_2 2bp_II	CUGCCUUGCAUA GGAAGUCCCC (SEQ ID NO: 2785)	1%	AAAGTACC
OMNI-313	hCXCR4	hCXCR4_S123_2 2bp_II	GACUCAGACUCA GUGGAAACAG (SEQ ID NO: 2696)	14%	ATGAATGT
OMNI-314	hCXCR4	hCXCR4_S116_2 2bp_II	CUGUGUAGAUGA CAUGGACUGC (SEQ ID NO: 2634)	12%	CTTGCATA
	hPDCD1	hPDCD1_S123_2 2bp_II	CAUUCGCUAGG AAAGACAAUG (SEQ ID NO: 2637)	20%	GTGGCATA
OMNI-316	hCISH	hCISH_S15_22b p_II	GGAAAAGGCCUG CCUCCCCCU (SEQ ID NO: 2786)	10%	CAGACTCA
	hCIITA	hCIITA_S1_22b p_II	UGAGGGCACGAG GAGGGGCGUC (SEQ ID NO: 2787)	11%	CAGACTCC
	hTIGIT	hTIGIT_S31_22 bp_II	GCCCUGUGAAAG UCCGGGCCA (SEQ ID NO: 2788)	13%	GCCGCACT
	hTRAC	hTRAC_s92_22 bp_II	UCCUCUUGUCCC ACAGAUAUCC (SEQ ID NO: 2705)	33%	AGAACCCT

	hCXCR4	hCXCR4_S38_2 2bp_II	AUCCACUUGUGC ACAGUGUUCU (SEQ ID NO: 2658)	33%	CAAACCTCA
	hCXCR4	hCXCR4_S49_2 2bp_II	CAGGGGACUAUG ACUCCAUGAA (SEQ ID NO: 2701)	36%	GGAACCCT
	hELANE	hELANE_g155_2 2bp_II	CUGUCCCUGUGG CCUCUGGGGC (SEQ ID NO: 2789)	74%	TTGACACC
OMNI-317	hSAMD9	hSAMD9L_g13 1_alt_22bp_II	CACCAAAGGCUC UUUGUCCUU (SEQ ID NO: 2708)	2%	GGAAGAAA
	hCXCR4	hCXCR4_S113_2 2bp_II	GGAAGAAAGCUA GGGCCUCGGU (SEQ ID NO: 2633)	3%	GATGGAAA
OMNI-318	hCXCR4	hCXCR4_s86_2 2bp_II	UACCAGUUUGCC ACGGCAUCAA (SEQ ID NO: 2648)	40%	CTGCCCAG
OMNI-319	hCXCR4	hCXCR4_s81_2 2bp_II	GGUAUAUUGGGC GGGAGUGUCA (SEQ ID NO: 2711)	30%	GAAAATGA
OMNI-320	hTRAC	hTRAC_S56_22 bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	1%	TGTACCAG
	hCXCR4	hCXCR4_s86_2 2bp_II	UACCAGUUUGCC ACGGCAUCAA (SEQ ID NO: 2648)	2%	CTGCCCAG
OMNI-321	hCXCR4	hCXCR4_s127_2 2bp_II	AAGGAGUCGAUG CUGAUCCCAA (SEQ ID NO: 2790)	1%	TGTAGTAA
OMNI-322	hTRAC	hTRAC_s95_22 bp_II	GAUAUCCAGAAC CCUGACCCUG (SEQ ID NO: 2695)	12%	CCGTGTAC
OMNI-323	hCXCR4	hCXCR4_S15_2 2bp_II	GGAUGGCAAGAG ACCCACACAC (SEQ ID NO: 2715)	55%	CGGAGGAG
OMNI-324	hPDCD1	hPDCD1_S90_2 2bp_II	ACUGGUACCGCA UGAGCCCCAG (SEQ ID NO: 2791)	1%	CAACCAGA
	hCXCR4	hCXCR4_s85_2 2bp_II	CCUCGGUGAUGG AAAUCCACUU (SEQ ID NO: 2792)	1%	GTGCACAG
OMNI-327	hTRAC	hTRAC_S88_22 bp_II	GCUGAGAGACUC UAAAUCCAGU (SEQ ID NO: 2607)	1%	GACAAGTC
OMNI-336	hPDCD1	hPDCD1_S45_2 2bp_II	CAGGGCUGGGGA GAAGGUGGGG (SEQ ID NO: 2793)	1%	GGGTTCCA
OMNI-338	hCXCR4	hCXCR4_s142_2 2bp_II	ACGAAGGCCUUU CGGUGCUUGG (SEQ ID NO: 2794)	1%	GGTATATT

	hCXCR4	hCXCR4_s141_22bp_II	UCGGCCACUGAC AGGUGCAGCC (SEQ ID NO: 2722)	3%	TGTACTTG
OMNI-339	hTRAC	hTRAC_S56_22bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	18%	TGTACCAG
	hPDCD1	hPDCD1_S147_22bp_II	CCUGCUCGUGGU GACCGAAGGG (SEQ ID NO: 2719)	19%	GACAACGC
OMNI-340	hCXCR4	hCXCR4_s144_22bp_II	GGGUUCAGACAA CAGUGGAAGA (SEQ ID NO: 2716)	3%	AAGCTAGG
	hCXCR4	hCXCR4_S27_22bp_II	CGGCAUCAACUG CCCAGAAGGG (SEQ ID NO: 2717)	3%	AAGCGTGA
	hPDCD1	hPDCD1_S9_22bp_II	GCAGCUUCUCCA ACACAUCGGA (SEQ ID NO: 2718)	4%	GAGCTTCG
OMNI-341	hPDCD1	hPDCD1_S147_22bp_II	CCUGCUCGUGGU GACCGAAGGG (SEQ ID NO: 2719)	1%	GACAACGC
OMNI-342	hCXCR4	hCXCR4_s146_22bp_II	CCAGGAUGACCA AUCCAUGCC (SEQ ID NO: 2723)	13%	CACAATGC
OMNI-343	hCXCR4	hCXCR4_s148_22bp_II	UGGUAACCCAUG ACCAGGAUGA (SEQ ID NO: 2795)	1%	CCAATCCA
OMNI-344	hTRAC	hTRAC_S19_22bp_II	CCACUUUCAGGA GGAGGAUUCG (SEQ ID NO: 2725)	3%	GAACCCAA
	hTRAC	hTRAC_S71_22bp_II	GUCCACAGAUUA UCCAGAACCC (SEQ ID NO: 2726)	5%	TGACCCTG
OMNI-349	hCXCR4	hCXCR4_s156_22bp_II	UGGGCGGGAGUG UCAGAAAAUG (SEQ ID NO: 2796)	1%	AACAAACG
OMNI-352	hPDCD1	hPDCD1_S45_22bp_II	CAGGGCUGGGGA GAAGGUGGGG (SEQ ID NO: 2793)	1%	GGGTTCCA
	hPDCD1	hPDCD1_S21_22bp_II	UCCGUGUCACAC AACUGCCCAA (SEQ ID NO: 2797)	1%	CGGGCGTG
OMNI-353	hCXCR4	hCXCR4_s81_22bp_II	GGUAUAUUGGGC GGGAGUGUCA (SEQ ID NO: 2711)	25%	GAAAATGA
OMNI-354	hCXCR4	hCXCR4_s159_22bp_II	AACACGAGGAUG GCAAGAGACC (SEQ ID NO: 2727)	14%	CACACACC
OMNI-357	hPDCD1	hPDCD1_S45_22bp_II	CAGGGCUGGGGA GAAGGUGGGG (SEQ ID NO: 2793)	1%	GGGTTCCA

OMNI-358	hTRAC	hTRAC_S35_22 bp_II	GACCCUGCCGUG UACCAGCUGA (SEQ ID NO: 2617)	20%	GAGACTCT
OMNI-359	hSAMD9	hSAMD9L_g97 _22bp_II	UUGACCACUUCA AUGUAAUGAU (SEQ ID NO: 2739)	2%	CAAAAAGT
	hSAMD9	hSAMD9L_g17 2_alt_22bp_II	ACCAAAAAAUC CAAAACACAC (SEQ ID NO: 2738)	2%	CAAAAAGG
	hCXCR4	hCXCR4_s164_ 22bp_II	CCUUCUGGGCAG UUGAUGCCGU (SEQ ID NO: 2737)	2%	GGCAAACCT
OMNI-360	hCXCR4	hCXCR4_S39_2 2bp_II	AUCCUGGUCAUG GGUUACCAGA (SEQ ID NO: 2798)	1%	AGAAACTG
OMNI-362	hCXCR4	hCXCR4_s167_ 22bp_II	AAACAGGGUUC UUCAUGGAGU (SEQ ID NO: 2740)	11%	CATAGTCC
	hCXCR4	hCXCR4_s167_ 22bp_II	AAACAGGGUUC UUCAUGGAGU (SEQ ID NO: 2740)	11%	CATAGTCC
OMNI-365	hCXCR4	hCXCR4_S55_2 2bp_II	CACGAGGAUGGC AAGAGACCCA (SEQ ID NO: 2605)	16%	CACACCGG
OMNI-366	hTIGIT	hTIGIT_S34_22 bp_II	GCUGUGACAGCC AUGGAGCUCC (SEQ ID NO: 2799)	16%	CCTACCAC
	hPDCD1	hPDCD1_S145_ 22bp_II	UCGGAGAGCUUC GUGCUAAACU (SEQ ID NO: 2746)	23%	GGTACCGC
	hCXCR4	hCXCR4_s154_ 22bp_II	GCCUUGCAUAGG AAGUCCCAA (SEQ ID NO: 2744)	50%	AGTACCAG
	hCXCR4	hCXCR4_s169_ 22bp_II	UUCUUCGCCUGU UGGCUGCCUU (SEQ ID NO: 2745)	53%	ACTACATT
	hB2M	hB2M_S42_22b p_II	CCGUGGCCUUAG CUGUGCUCGC (SEQ ID NO: 2800)	55%	GCTACTCT
	hPDCD1	hPDCD1_S146_ 22bp_II	GUCUGGUUGCUG GGGCUAUGC (SEQ ID NO: 2747)	56%	GGTACCAG
	hTRAC	hTRAC_S56_22 bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	59%	TGTACCAG
	hTRAC	hTRAC_s184_2 2bp_II	CUGGAUUUAGAG UCUCUCAGCU (SEQ ID NO: 2748)	62%	GGTACACG
OMNI-368	hCIITA	hCIITA_S2_22b p_II	AGGUAGCCACCU UCUAGGGGCC (SEQ ID NO: 2801)	14%	CCAACTCC

	hPDCD1	hPDCD1_S40_2 2bp_II	AACACAUCGGAG AGCUUCGUGC (SEQ ID NO: 2735)	17%	TAAACTGG
	hTRAC	hTRAC_S36_22 bp_II	UCAAAAUCGGUG AAUAGGCAGA (SEQ ID NO: 2802)	21%	CAGACTTG
	hTRAC	hTRAC_S35_22 bp_II	GACCCUGCCGUG UACCAGCUGA (SEQ ID NO: 2617)	24%	GAGACTCT
	hCXCR4	hCXCR4_s168_22bp_II	UACACCGAGGAA AUGGGCUCAG (SEQ ID NO: 2803)	51%	GGGACTAT
	hTRAC	hTRAC_S35_22 bp_II	GACCCUGCCGUG UACCAGCUGA (SEQ ID NO: 2617)	66%	GAGACTCT
OMNI-369	hCXCR4	hCXCR4_s176_22bp_II	CUGAUCCCAAUG UAGUAAGGCA (SEQ ID NO: 2750)	11%	GCCAACAG
	hTRAC	hTRAC_S89_22 bp_II	CAUGAGGUCUAU GGACUUCAAG (SEQ ID NO: 2754)	16%	AGCAACAG
	hPDCD1	hPDCD1_S147_22bp_II	CCUGCUCGUGGU GACCGAAGGG (SEQ ID NO: 2719)	32%	GACAACGC
OMNI-370	hTRAC	hTRAC_S69_22 bp_II	UCCUGUGAUGUC AAGCUGGUCG (SEQ ID NO: 2758)	11%	AGAAAAGC
	hCXCR4	hCXCR4_s164_22bp_II	CCUUCUGGGCAG UUGAUGCCGU (SEQ ID NO: 2737)	15%	GGCAAACCT
OMNI-373	hPDCD1	hPDCD1_S40_2 2bp_II	AACACAUCGGAG AGCUUCGUGC (SEQ ID NO: 2735)	4%	TAAACTGG
	hTRAC	hTRAC_S35_22 bp_II	GACCCUGCCGUG UACCAGCUGA (SEQ ID NO: 2617)	5%	GAGACTCT
OMNI-375	hTRAC	hTRAC_s92_22 bp_II	UCCUCUUGUCCC ACAGAUAUCC (SEQ ID NO: 2705)	47%	AGAACCCT
OMNI-376	hPDCD1	hPDCD1_S147_22bp_II	CCUGCUCGUGGU GACCGAAGGG (SEQ ID NO: 2719)	12%	GACAACGC
	hTIGIT	hTIGIT_S33_22 bp_II	CACCACGGCACA AGUGACCCAG (SEQ ID NO: 2804)	18%	GTCAACTG
	hB2M	hB2M_g93_22bp_II	GAUGGAUGAAAC CCAGACACAU (SEQ ID NO: 2805)	22%	AGCAATTC
	hPDCD1	hPDCD1_S6_22 bp_II	CAUGAGCGUGGU CAGGGCCCCG (SEQ ID NO: 2606)	23%	CGCAATGA

	hCIITA	hCIITA_S19_22 bp_II	UGCUGCCUGGCU GGGAUCCUA (SEQ ID NO: 2806)	47%	CACAATGC
	hTRAC	hTRAC_s180_2 2bp_II	CCUCCUCCUGAA AGUGGCCGGG (SEQ ID NO: 2765)	55%	TTTAATCT
OMNI-377	hPDCD1	hPDCD1_S56_2 2bp_II	GACAAGCUGGCC GCCUCCCCCG (SEQ ID NO: 2768)	24%	AGGACCGC
	hTRAC	hTRAC_S56_22 bp_II	AUCCAGAACCCU GACCCUGCCG (SEQ ID NO: 2650)	30%	TGTACCAG
OMNI-378	hPDCD1	hPDCD1_S33_2 2bp_II	ACAUGAGCGUGG UCAGGGCCCG (SEQ ID NO: 2772)	1%	GCGCAATG
	hCXCR4	hCXCR4_S33_2 2bp_II	GGAGUCGAUGCU GAUCCCAAUG (SEQ ID NO: 2771)	1%	TAGTAAGG
	hTRAC	hTRAC_s115_2 2bp_II	UGUGUAUAUCAC AGACAAAACU (SEQ ID NO: 2773)	9%	GTGCTAGA
OMNI-381	hTRAC_	hTRAC_S15_22 bp_II	UAAACCCGGCCA CUUUCAGGAG (SEQ ID NO: 2775)	18%	GAGGATTC
OMNI-382	hCXCR4	hCXCR4_s192_2 2bp_II	ACUGCCCAGAAG GGAAGCGUGA (SEQ ID NO: 2807)	1%	TGACAAAG
	hCXCR4	hCXCR4_s191_2 2bp_II	GAAAGCAUAGAG GAUGGGGUUC (SEQ ID NO: 2776)	1%	AGACAACA
OMNI-385	hCXCR4	hCXCR4_s80_2 2bp_II	AUGGGGUUCAGA CAACAGUGGA (SEQ ID NO: 2778)	13%	AGAAAGCT
OMNI-386	hPDCD1	hPDCD1_S174_2 2bp_II	CCCUGCUCGUGG UGACCGAAGG (SEQ ID NO: 2780)	15%	GGACAACG

Table 5. Nuclease activity in endogenous context in mammalian cells: OMNI nucleases were expressed in mammalian cell system (HeLa) by DNA transfection together with an sgRNA expressing plasmid. Cell lysates were used for site specific genomic DNA amplification and NGS. The percentage of indels was measured and analyzed to determine the editing level. Each sgRNA is composed of the tracrRNA (see **Table 2**) and the spacer detailed here. The spacer 3' genomic sequence contains the expected PAM relevant for each OMNI nuclease. All tests were performed in triplicates. OMNI nuclease only (no guide) transfected cells served as a negative control.

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CLAIMS

What is claimed is:

1. A non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 90% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 1-12, and 14-108, or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.
2. The composition of claim 1, further comprising one or more RNA molecules, or a DNA polynucleotide encoding any one of the one or more RNA molecules, wherein the one or more RNA molecules and the CRISPR nuclease do not naturally occur together and the one or more RNA molecules are configured to form a complex with the CRISPR nuclease and/or target the complex to a target site.
3. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 513-535.
4. The composition of claim 3, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 514-517 and 528-531.
5. The composition of claim 4, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 518-526 and 532-535.
6. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 513-535.
7. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 325-338,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 339-352,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 353-368,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 369-380,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 381-395,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 396-409,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 410-433,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 434-447,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 448-461,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 462-475,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 476-491,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 492-512,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 536-549,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 550-575,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 576-598,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 599-612,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 613-633

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 634-651,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 652-665,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 666-683 and UUGCUCACAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 684-707,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 708-728,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 729-742,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 743-761,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 762-775,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 776-798,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 799-816,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 817-830,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 831-844,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 845-862,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 863-883,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 884-901 and UUACUACAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 902-915,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 916-931,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 932-947,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 948-962,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 963-985,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 986-1010,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1011-1029,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1030-1050, UUACUAAAA, and UUACUAGAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1051-1080,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1081-1101, UUACUAAAA, and UUACUAGAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1102-1115,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1116-1135,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1136-1167,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1168-1186,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1187-1211,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1212-1243,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1244-1255,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1256-1284,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1285-1298,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1299-1312,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1313-1342,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1343-1362,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1363-1378,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1379-1397,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1398-1413,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1437,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1438-1462,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1463-1495,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1496-1533,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1534-1556,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1557-1572,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1573-1617,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1618-1634,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1635-1655,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1656-1674,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1675-1701,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1702-1729,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1730-1747,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1748-1774,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1775-1801,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1802-1828,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1829-1844,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1845-1870,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1871-1895,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1896-1911,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1912-1930,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1931-1942,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1943-1971,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 1972-1999,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2000-2024,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2025-2045,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2046-2063,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2064-2088,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2089-2109,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2110-2131,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2132-2156,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2157-2178,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2179-2203,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2204-2230,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2231-2256,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2257-2277,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2278-2304,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2305-2333,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2334-2349,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2350-2368,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2369-2390,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2391-2411,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2412-2436,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2437-2452,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 24523-2468,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2469-2484,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2485-2500,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2501-2536,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2537-2552, or

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 2553-2574.

8. The composition of claim 7, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 326-329,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 340-343,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a CRISPR

RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 354-357,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 370-373 and 114,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 382-385,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 397-400,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 411-414,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 435-437,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 449-452,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 463-466,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 477-480,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 493-496 and 509-512,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 537-540,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 551-553,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 577-580,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 600-603 and 201,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 614-617 and 630,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 635-638,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 653-656,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 667-670 and 680,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 685-688,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 709-712 and 721-724,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 730-733,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 744-747,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 763-766,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 777-780,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 800-803,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 818-821,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 832-835,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 846-849,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 864-867 and 880-883,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 885-888 and 898,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 903-906,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 917-920 and 931,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 933-936,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 949-952,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 964-967 and 978-981,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 987-990 and 1001-1004,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1012-1015 and 1026-1029,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1031-1034 and 1044-1047,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1052-1055 and 1068-1071,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1082-1085 and 1095-1098,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1103-1106,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1117-1120,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1137-1140 and 1151-1154,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1169-1172,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1188-1191 and 1204-1207,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1213-1216 and 1227-1230,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1245-1247,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1257-1260 and 1271-1274,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1286-1289,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1300-1303,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177 and 178,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1344-1347,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1364-1367,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1380-1383,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1399-1402,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1415-1418 and 1431-1434,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1439-1442 and 1455-1458,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1464-1467 and 1478-1481,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1497-1500 and 1515-1518,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1535-1538,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1558-1561,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1574-1577 and 1592-1595,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1619-1622,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1636-1639,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1657-1660,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1676-1679,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1703-1706,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1731-1734,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1749-1752,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1776-1779 and 1792-1795,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1803-1806,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1830-1833,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1846-1849,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1872-1875 and 1888-1891,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1897-1900,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1913-1916,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1932-1934,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1944-1947 and 1960-1963,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1973-1976,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2001-2004,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2026-2029,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2047-2050,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2065-2068,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2090-2093,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2111-2114,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2133-2136,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2158-2161,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2180-2183,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2205-2208,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2232-2235,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94 and at least one RNA molecule is a

CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2258-2261,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2279-2282,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2306-2309,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2335-2338,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2351-2354,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2370-2373,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2392-2395,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2413-2416 and 2429-2432,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2438-2441,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2454-2457,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2470-2473,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2486-2489,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2502-2505 and 2520-2523,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2538-2541, or

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2554-2557.

9. The composition of claim 8, further comprising

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 330-338,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 344-352,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 358-368,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 374-380,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 386-395,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 401-409

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 415-433,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 438-447,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 453-461,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 467-475,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 481-491,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 497-507,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 541-549,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 554-563, 565-569, and 571-575,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 581-589 and 591-598,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 604-612,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 618-628 and 631-633,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 639-647 and 649-651,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 657-665,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 671-678, 681-683, and UUGCUACAA,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 689-697, 699-703, and 705-707,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 713-719 and 725-728,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 734-742,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 748-756 and 758-761,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 767-775,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 781-789, 791-794, and 796-798,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 804-812 and 814-816,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 822-830,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 836-844,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 850-858 and 860-862,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 868-878,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 889-896, 899-901, and UUACUACAA,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 907-915,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 921-929,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 937-947,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 953-962,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 968-976 and 982-985,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 991-999 and 1005-1010,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1016-1024,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1035-1042, 1048-1050, UUACUAAAA, and UUACUAGAA,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1056-1066, 1072-1074, and 1076-1079,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1086-1093, 1099-1101, UUACUAAAA, and UUACUAGAA,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1107-1115,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1121-1130 and 1132-1135,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1141-1149, 1155-1158, 1160-1163, and 1167-1167,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1173-1181 and 1183-1186,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1192-1202 and 1208-1211,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1217-1225, 1231-1234, 1236-1239, and 1241-1243,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1248-1255,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1261-1269, 1276-1279, and 1281-1284,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1290-1298,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1304-1312,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1314-1315 and 1334-1335,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1348-1356 and 1358-1362,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1368-1378,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1384-1394 and 1396-1397,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1403-1413,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1419-1429 and 1436-1437,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1443-1453 and 1459-1462,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1468-1476, 1482-1490, and 1492-1495,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1501-1513, 1519-1527, and 1529-1532,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1539-1549, 1551-1553, and 1555-1556,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1562-1572,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1578-1590, 1596-1605, 1607-1612, and 1614-1617,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1623-1631 and 1633-1634,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1640-1652 and 1654-1655,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1661-1671 and 1673-1674,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1680-1692, 1694-1697, and 1699-1701,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1707-1719, 1721-1722, 1724-1727, and 1729,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1735-1747,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1753-1763, 1765-1770, and 1772-1774,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1780-1790 and 1796-1801,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1807-1817, 1819-1820, 1822-1825, and 1827-1828,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1834-1844,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1850-1860, 1862-1863, 1685-1868, and 1870,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1876-1886 and 1892-1895,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1901-1911,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1917-1927 and 1929-1930,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1935-1942,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1948-1958 and 1964-1971,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 1977-1989, 1991-1995, and 1997-1998,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2030-2042 and 2044-2045,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2051-2063,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2069-2081, 2083-2084, and 2086-2087,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2094-2106 and 2108-2109,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2115-2127, 2129, and 2131,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2137-2149, 2151-2152, and 2154-2155,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2162-2174 and 2176-2178,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2184-2192, 2194-2196, and 2198-2203,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2209-2221, 2223-2226, and 2228-2230,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2236-2248, 2250-2252, and 2254-2255,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2262-2274 and 2276-2277,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2283-2295, 2297-2299, and 2301-2304,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2310-2320, 2322-2325, 2327-2329, and 2331-2333,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2339-2349,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2355-2365 and 2367-2368,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2374-2384 and 2386-2390,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2396-2408 and 2410-2411,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2417-2427 and 2433-2436,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2442-2452,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2458-2468,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2474-2484,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2490-2500,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2506-2518, 2524-2529, 2531-2534, and 2536,

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2542-2552, or

a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 2558-2566, 2568-2570, and 2572-2574.

10. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 325-338, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 339-352,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 353-368,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 4 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 369-380,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 5 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 381-395,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 6 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 396-409,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 7 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 410-433,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 8 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 434-447,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 9 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 448-461,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 462-475,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 476-491,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 492-512,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 14 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 536-549,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 15 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 550-575,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 576-598,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 599-612,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 18 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 613-633,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 19 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 634-651,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 20 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 652-665,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 21 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 666-683 and UUGCUACAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 22 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 684-707,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 23 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 708-728,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 24 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 729-742,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 25 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 743-761,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 26 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 762-775,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 27 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 776-798,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 28 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 799-816,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 29 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 817-830,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 30 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 831-844,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 31 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 845-862,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 32 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 863-883,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 33 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 884-901 and UUACUACAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 34 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 902-915,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 35 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 916-931,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 36 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 932-947,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 37 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 948-962,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 38 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 963-985,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 39 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 986-1010,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 40 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1011-1029,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 41 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1030-1050, UUACUAAAA, and UUACUAGAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 42 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1051-1080,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 43 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1081-1101, UUACUAAAA, and UUACUAGAA,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 44 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1102-1115,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 45 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1116-1135,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 46 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1136-1167,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 47 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1168-1186,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 48 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1187-1211,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 49 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1212-1243,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 50 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1244-1255,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 51 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1256-1284,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 52 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1285-1298,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 53 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1299-1312,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 54 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1316-1326, 1328-1332, and 1336-1342,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 55 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1343-1362,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 56 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1363-1378,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 57 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1379-1397,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 58 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1398-1413,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 59 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1414-1437,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 60 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1438-1462,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 61 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1463-1495,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 62 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1496-1533,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 63 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1534-1556,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 64 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1557-1572,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 65 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1573-1617,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 66 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1618-1634,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 67 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1635-1655,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 68 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1656-1674,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 69 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1675-1701,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 70 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1702-1729,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 71 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1730-1747,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 72 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1748-1774,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 73 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1775-1801,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 74 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1802-1828,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 75 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1829-1844,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 76 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1845-1870,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 77 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1871-1895,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 78 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1896-1911,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 79 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1912-1930,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 80 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1931-1942,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 81 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1943-1971,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 82 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 1972-1999,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 83 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2000-2024,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 84 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2025-2045,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 85 and at least one RNA molecule is a single-

guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2046-2063,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 86 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2064-2088,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 87 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2089-2109,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 88 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2110-2131,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 89 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2132-2156,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 90 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2157-2178,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 91 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2179-2203,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 92 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2204-2230,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 93 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2231-2256,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 94 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2257-2277,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 95 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2278-2304,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 96 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2305-2333,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 97 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2334-2349,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 98 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2350-2368,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 99 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2369-2390,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 100 and at least one RNA molecule is a

single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2391-2411,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 101 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2412-2436,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 102 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2437-2452,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 103 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 24523-2468,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 104 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2469-2484,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 105 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2485-2500,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 106 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2501-2536,

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 107 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2537-2552, or

wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 108 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 2553-2574.

11. The composition of any one of claims 1-10, wherein the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1.
12. The composition of any one of claims 1-10, wherein the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1.
13. The composition of any one of claims 1-10, wherein the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1.
14. The composition of any one of claims 1-10, wherein the CRISPR nuclease utilizes a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in any one of columns 2-7 of Table 3.
15. A method of modifying a nucleotide sequence at a DNA target site in a cell-free system or the genome of a cell comprising introducing into the cell the composition of any one of claims 2-14.
16. The method of claim 15, wherein the CRISPR nuclease effects a DNA break in a DNA strand adjacent to a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in any one of columns 2-7 of Table 3, and/or effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.
17. The method of claim 15, wherein the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.
18. The method of claim 15, wherein the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

19. The method of any one of claims 15-18, wherein the cell is a eukaryotic cell or a prokaryotic cell.
20. The method of claim 19, wherein the cell is a mammalian cell or a human cell.
21. A composition, method, process, or use as disclosed herein.

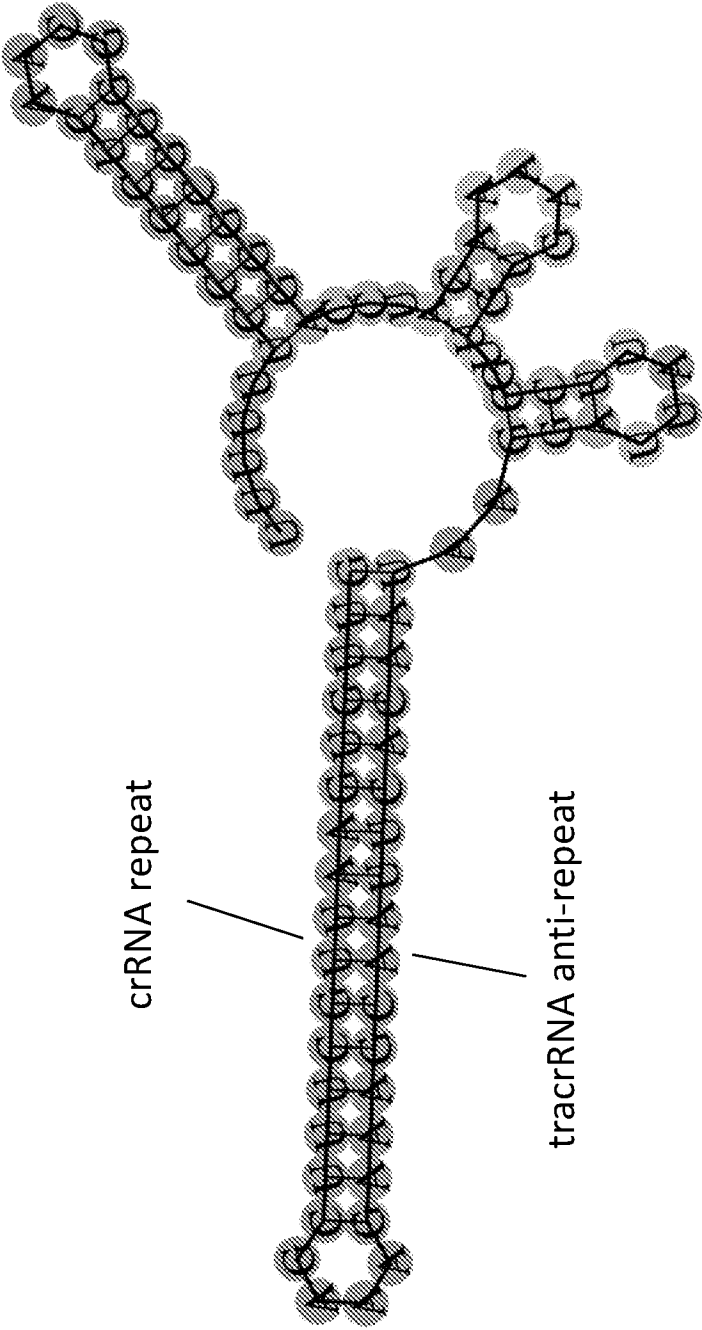
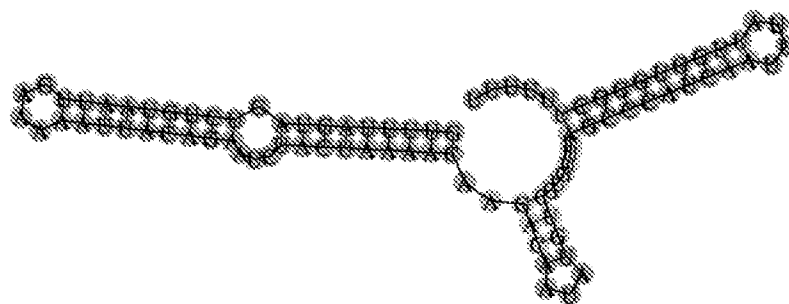


Fig. 1A

V1 – 2 hairpins



V2 – 2 hairpins

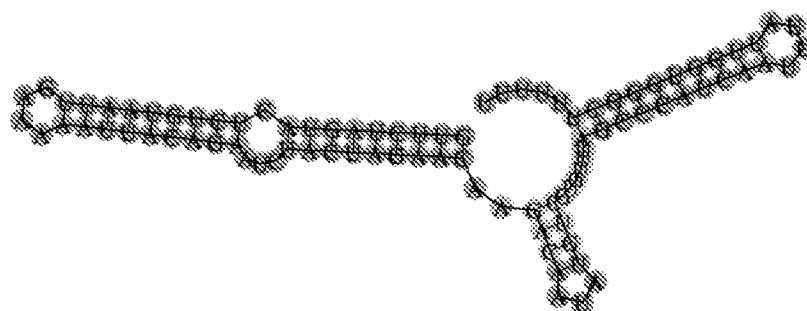


Fig. 1B

V1 – 3 hairpins

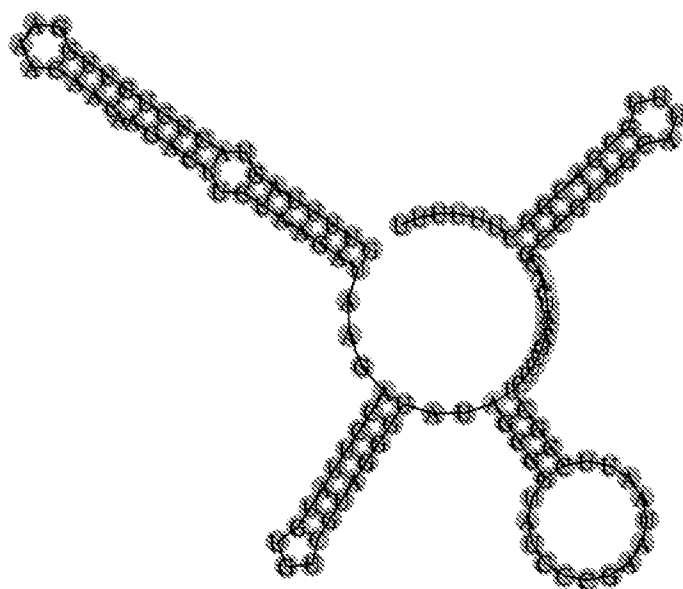


Fig. 1C

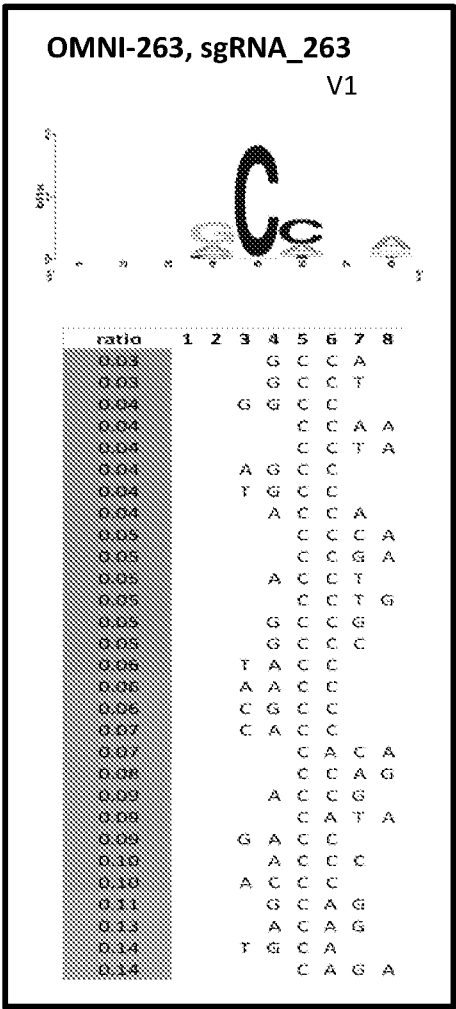


Fig. 2

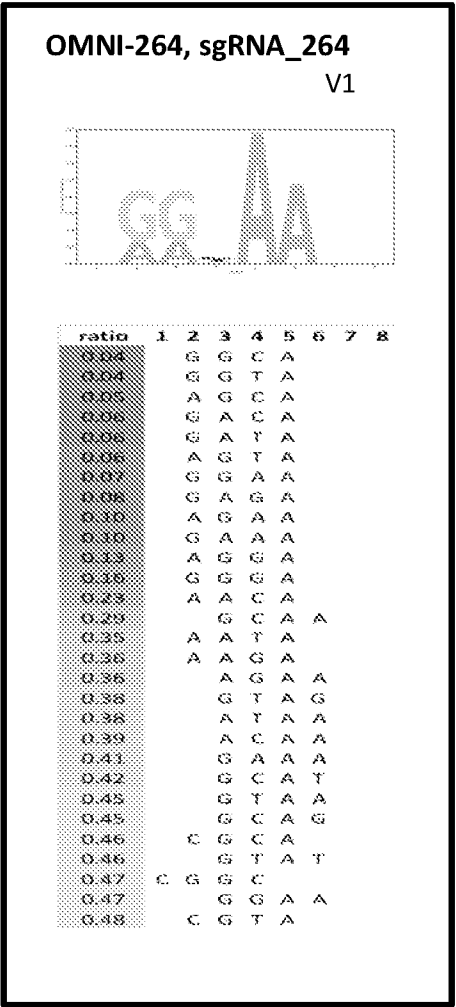


Fig. 3

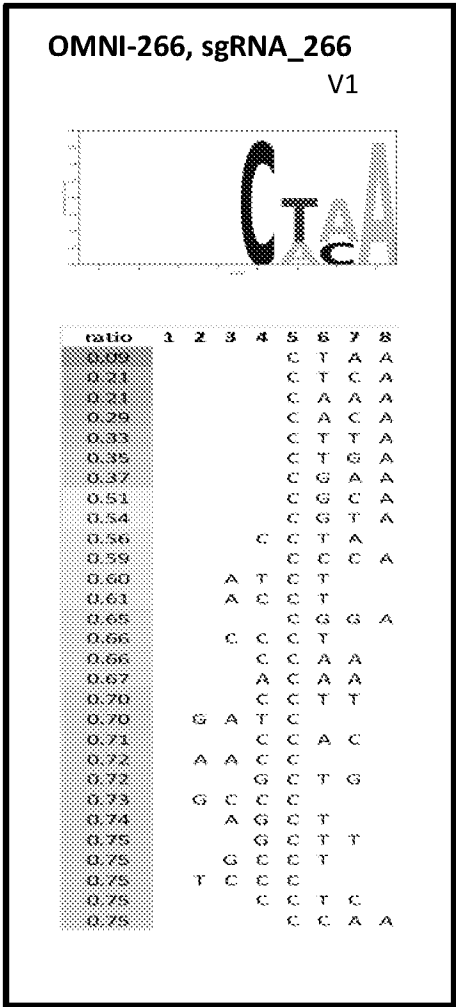


Fig. 4

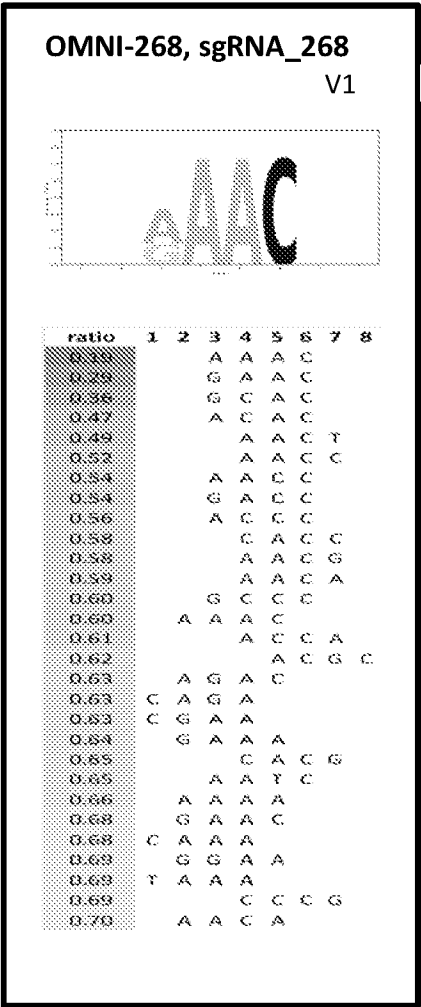


Fig. 5

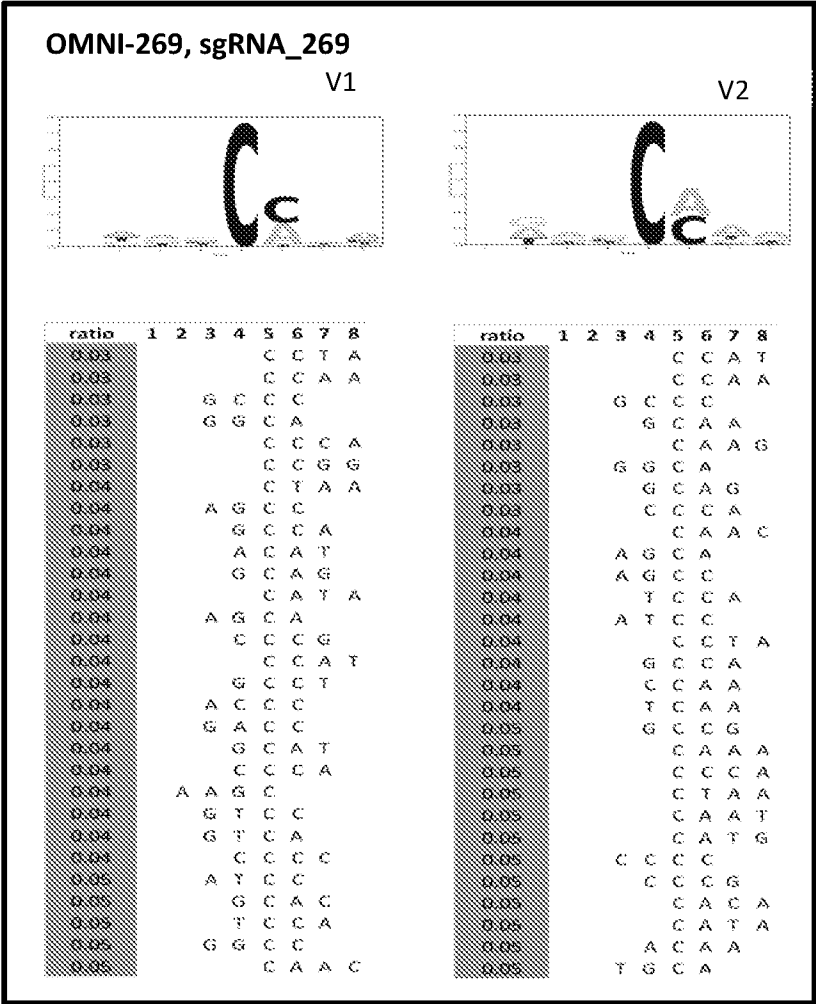


Fig. 6

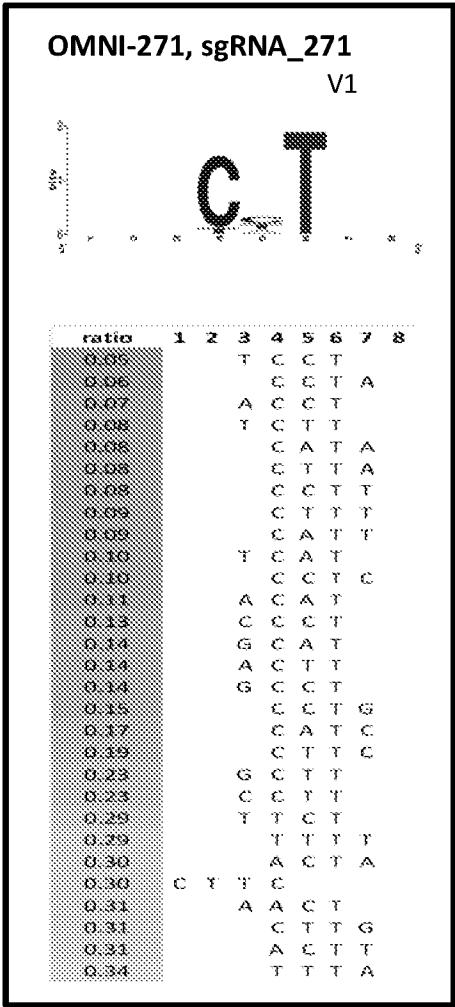


Fig. 7

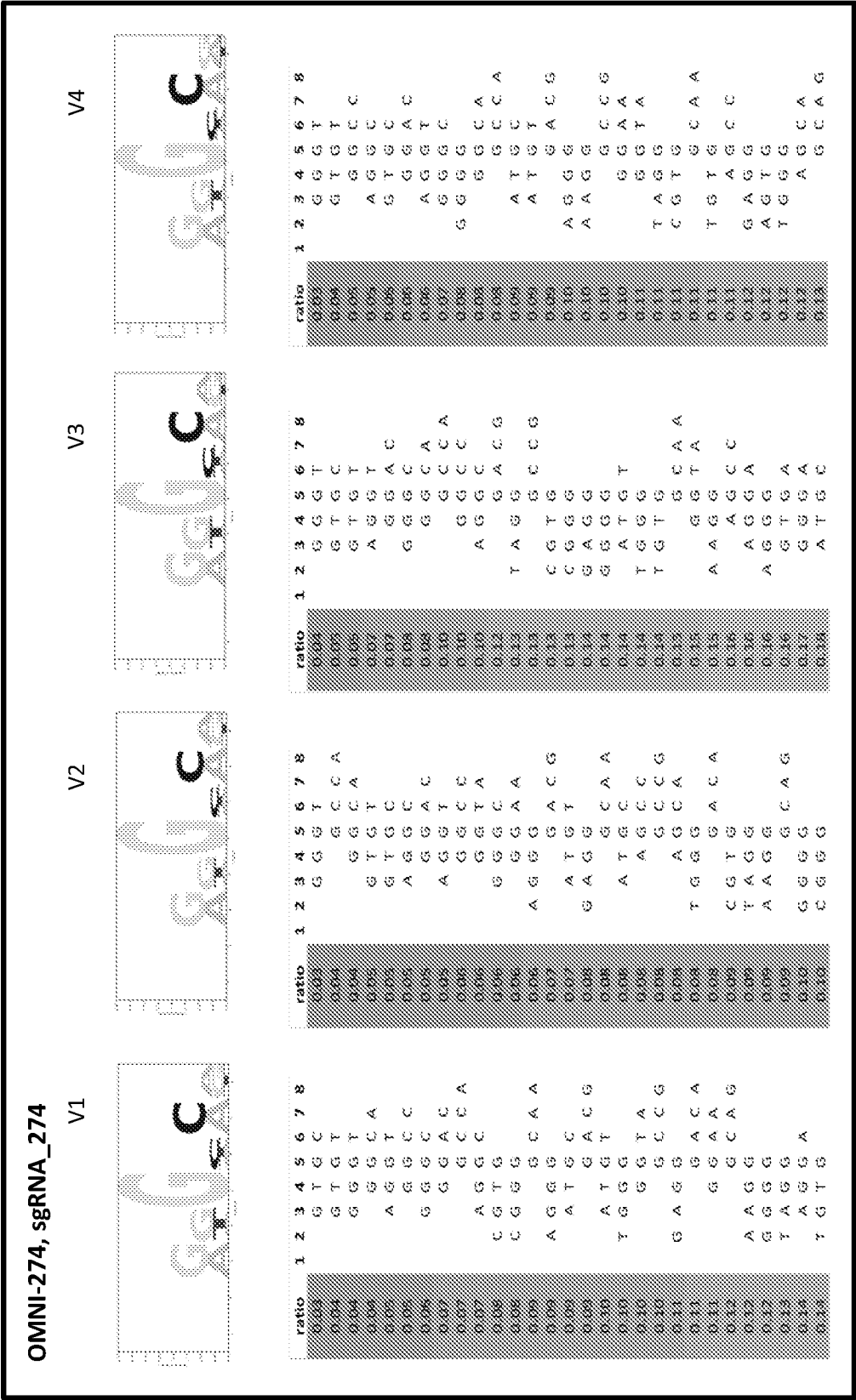


Fig. 8

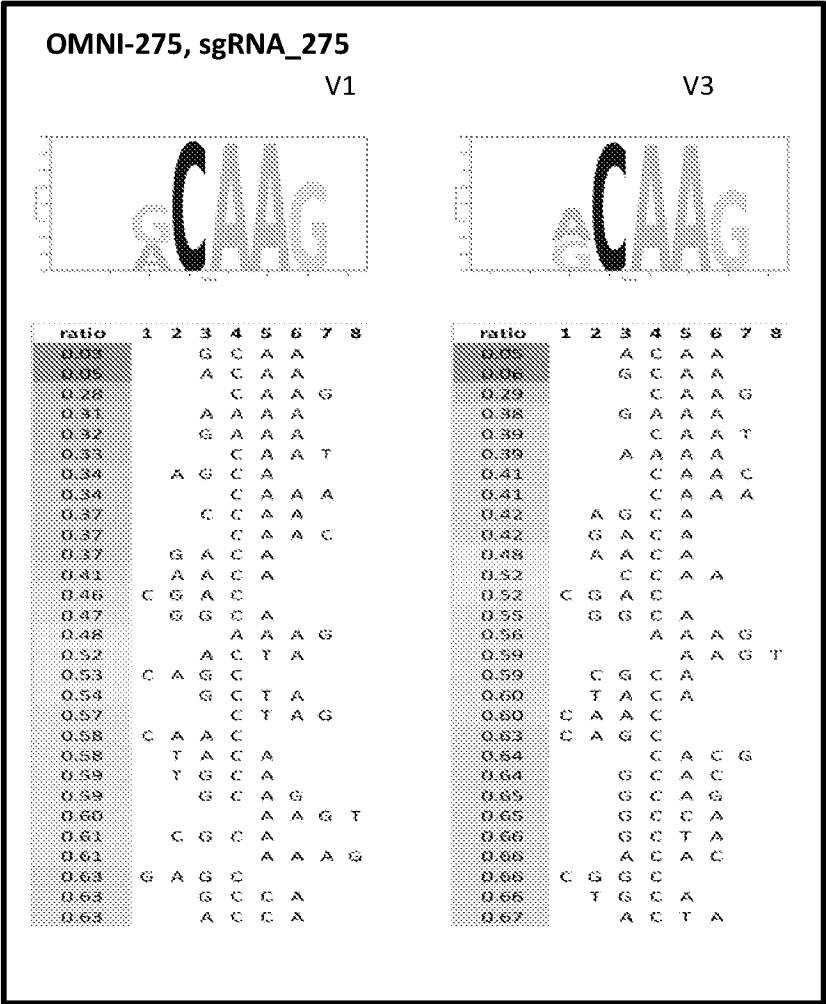


Fig. 9

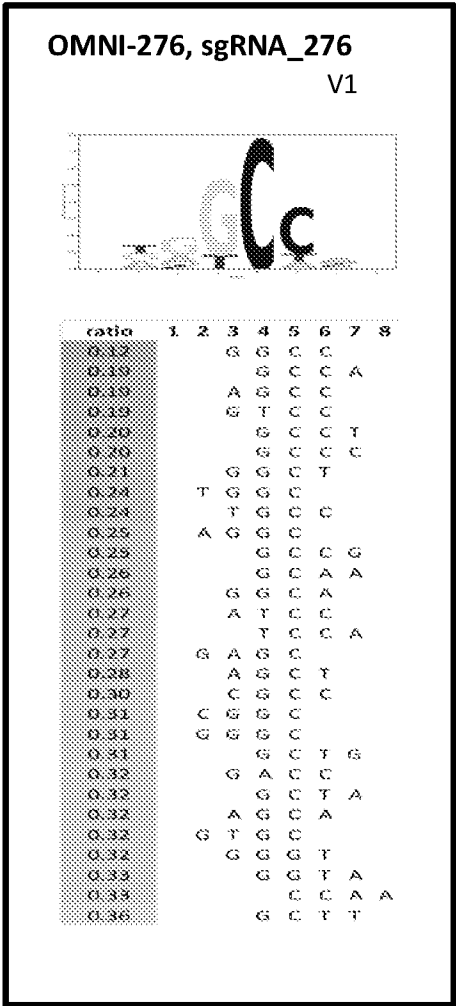


Fig. 10

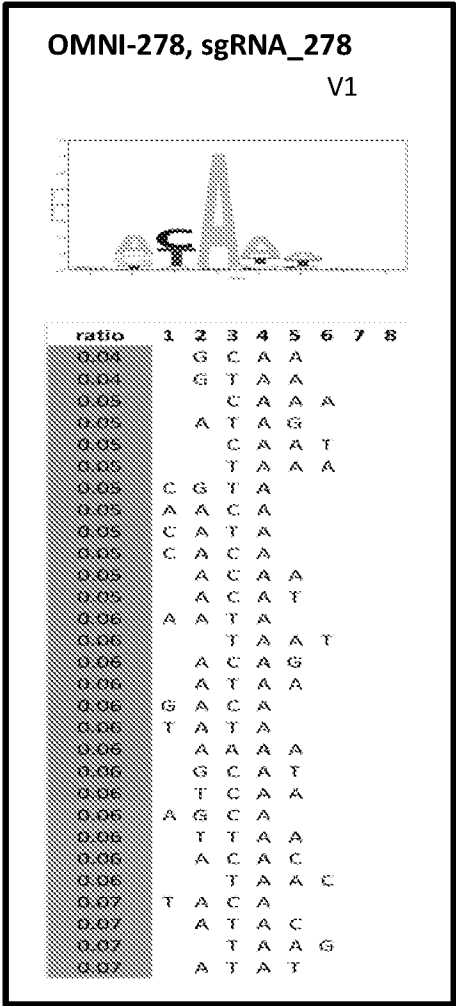


Fig. 11

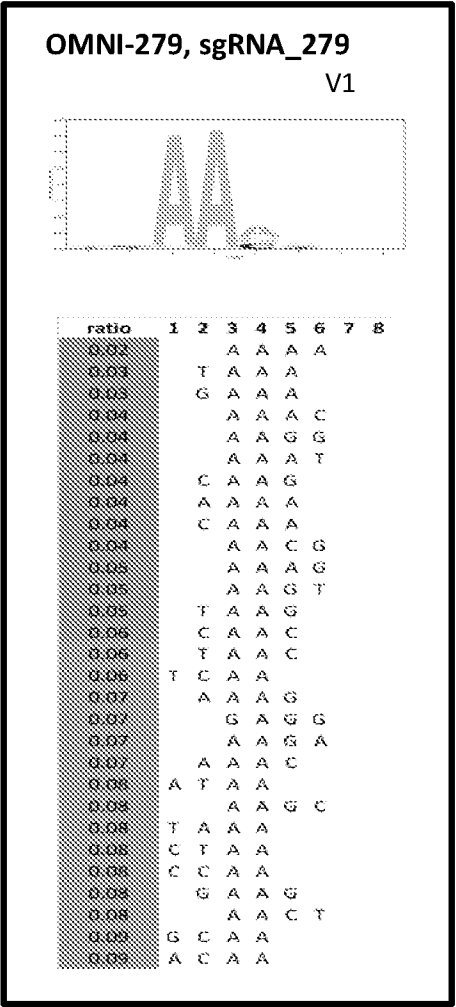


Fig. 12

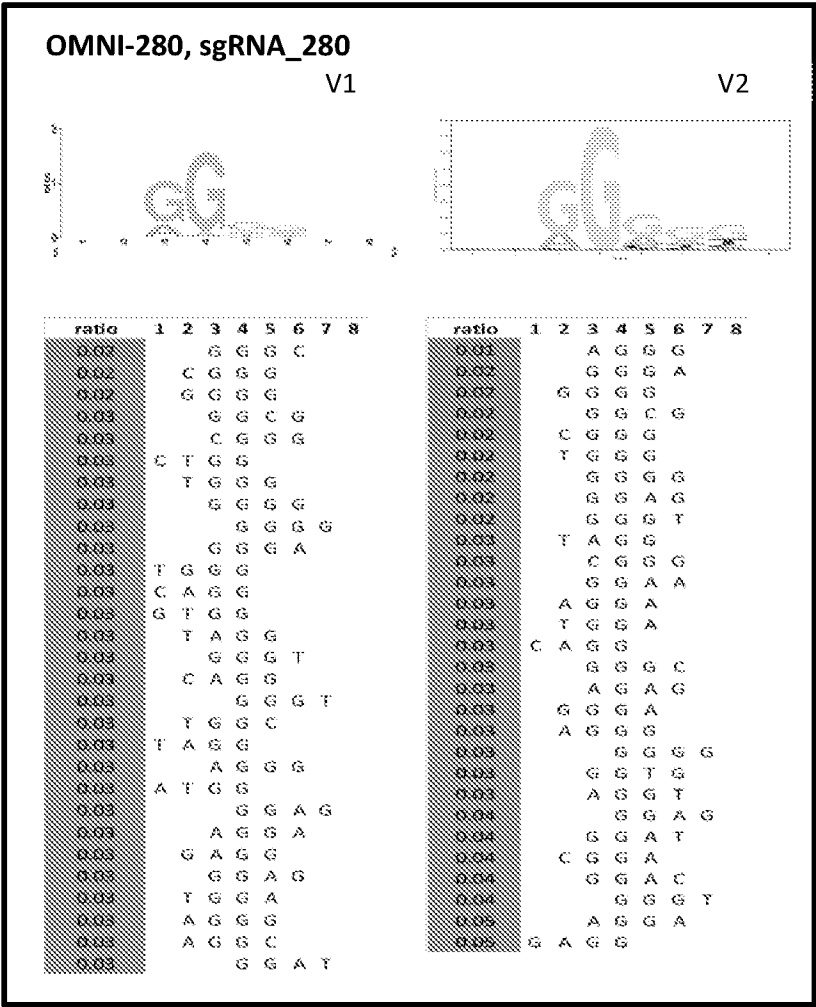


Fig. 13

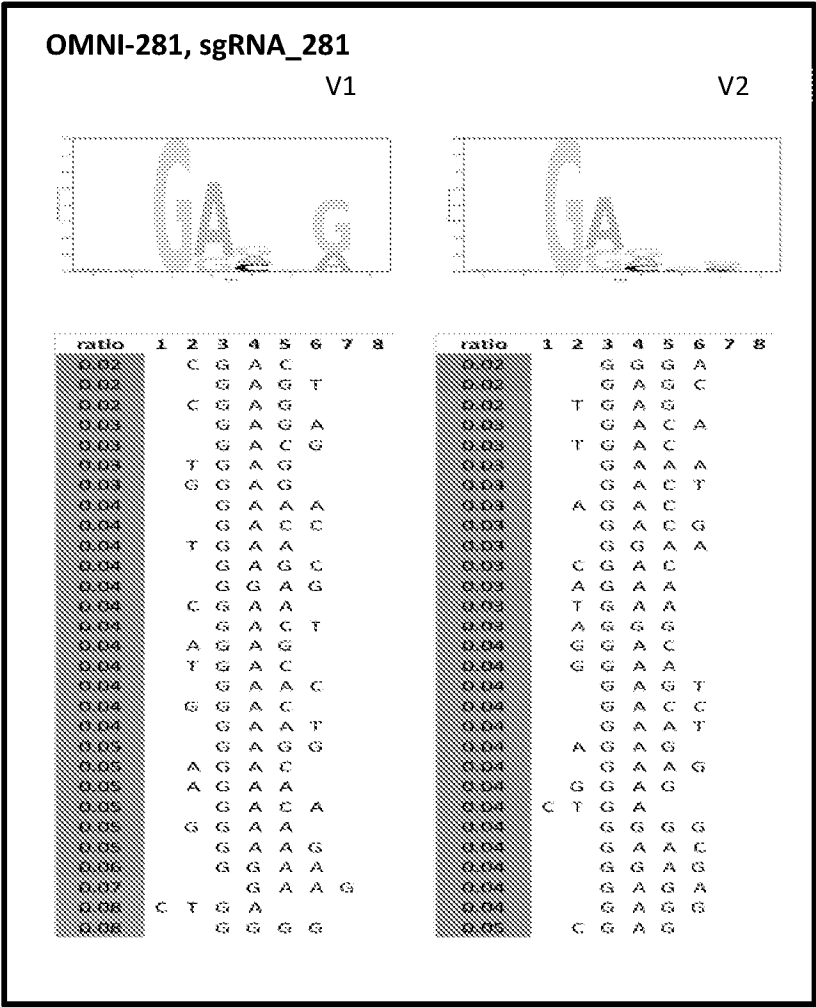


Fig. 14

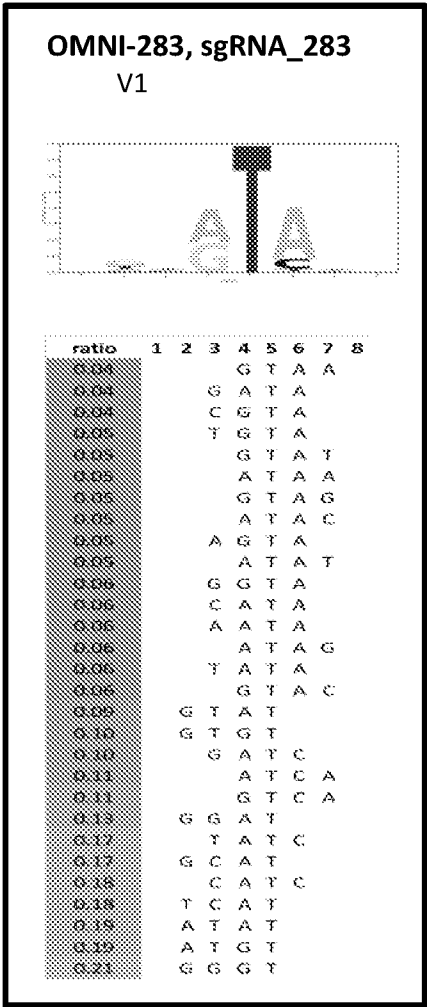


Fig. 15

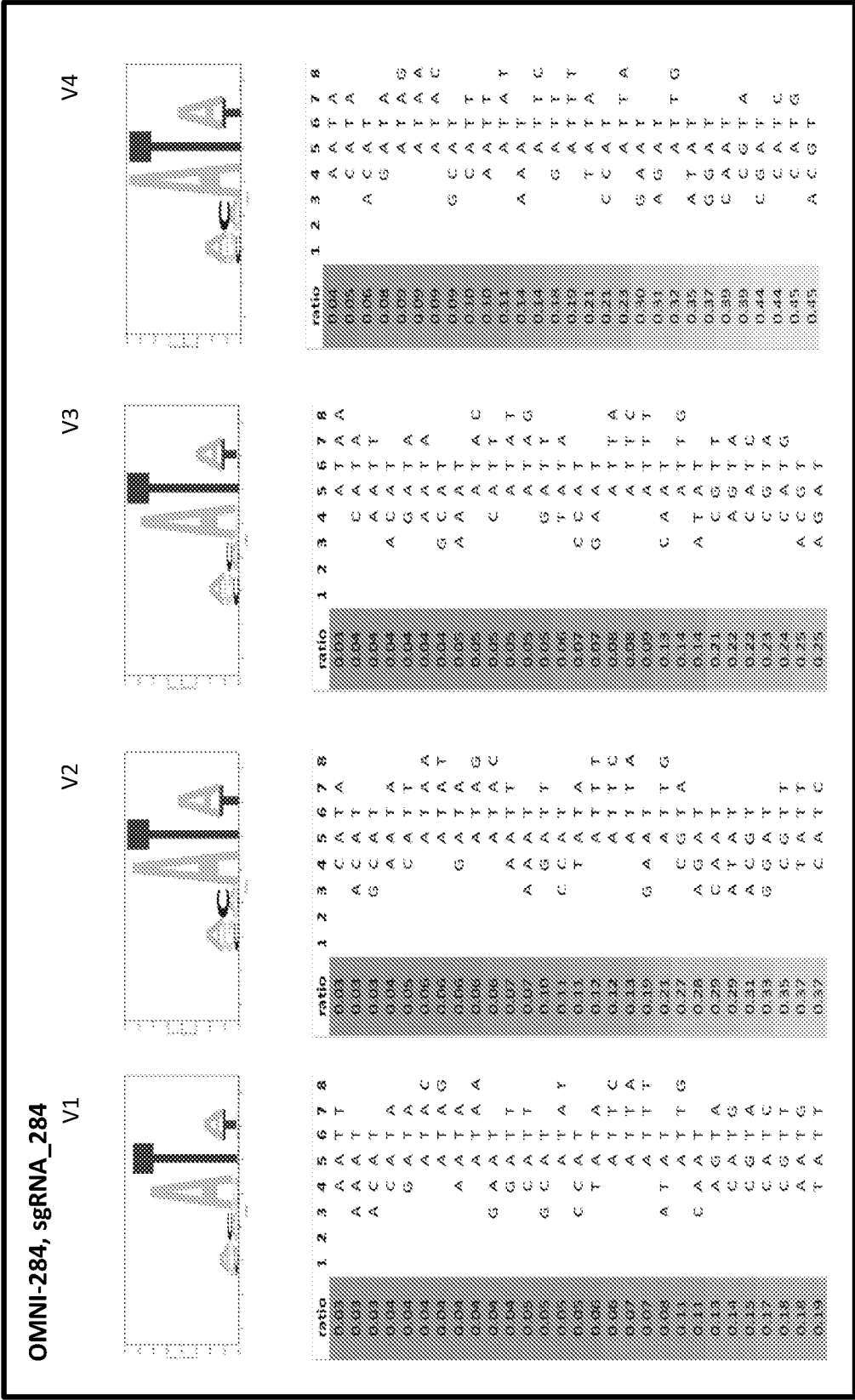


Fig. 16



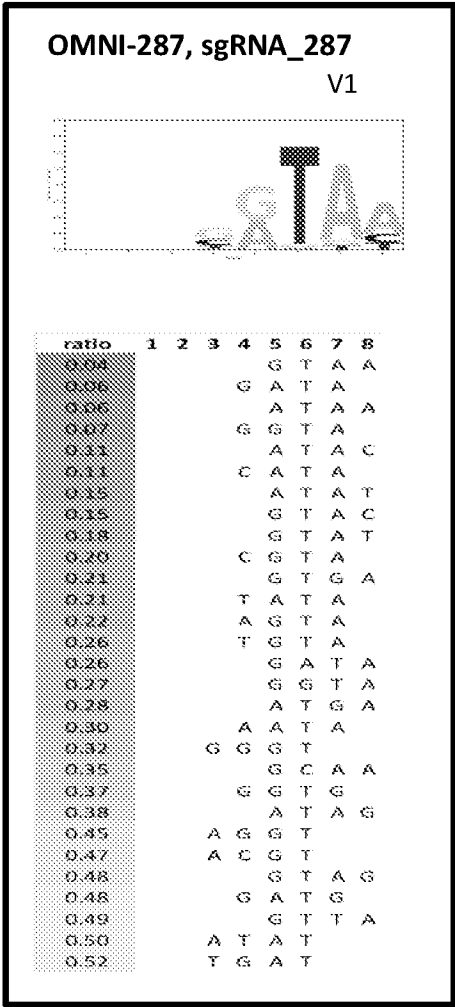


Fig. 18

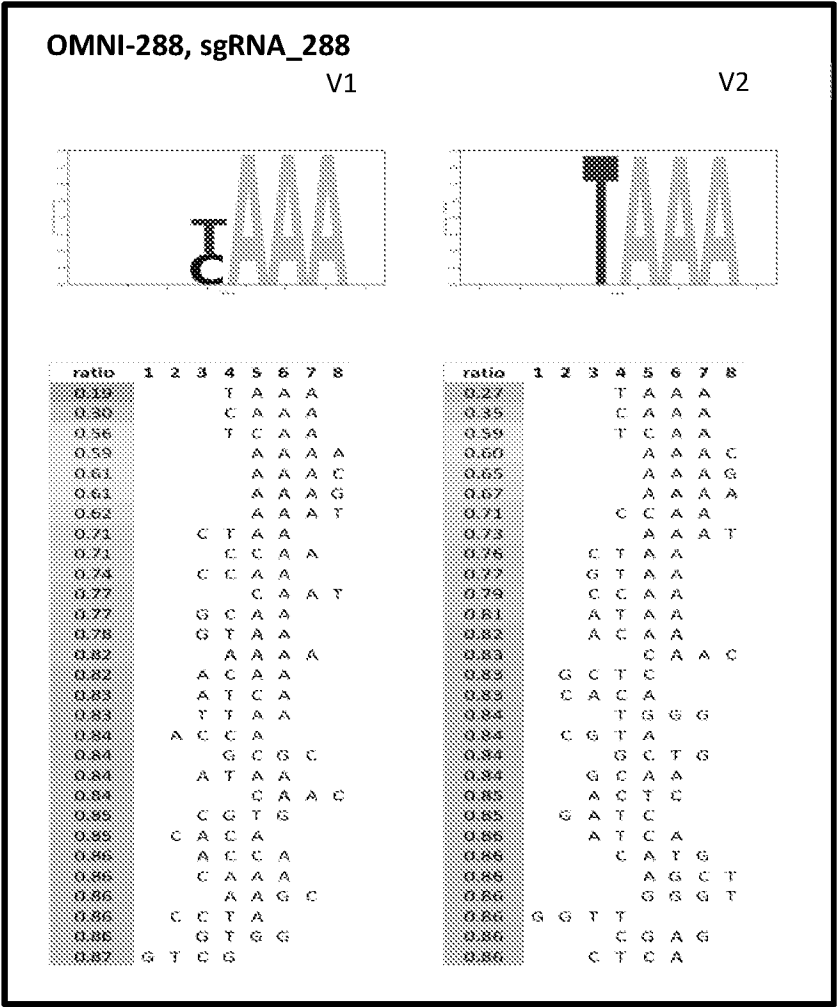


Fig. 19

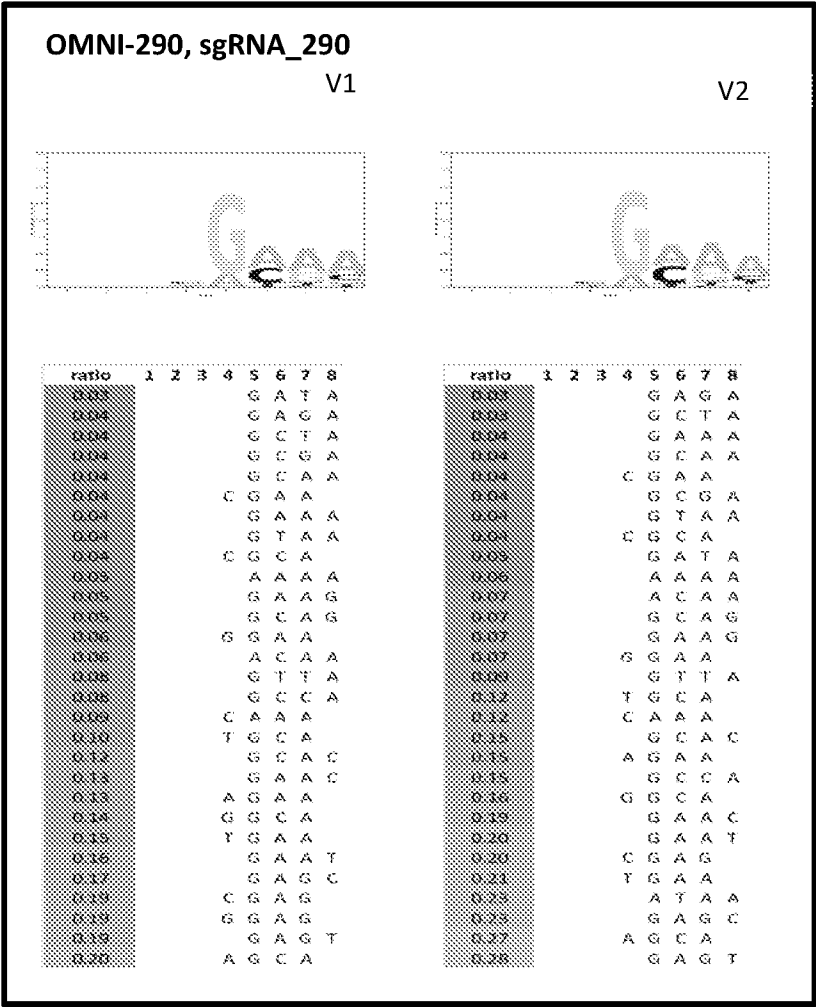


Fig. 20

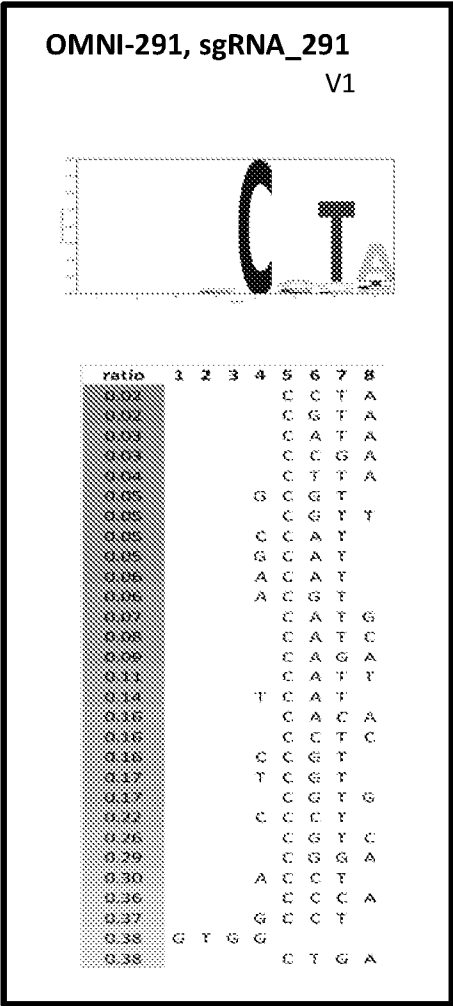


Fig. 21

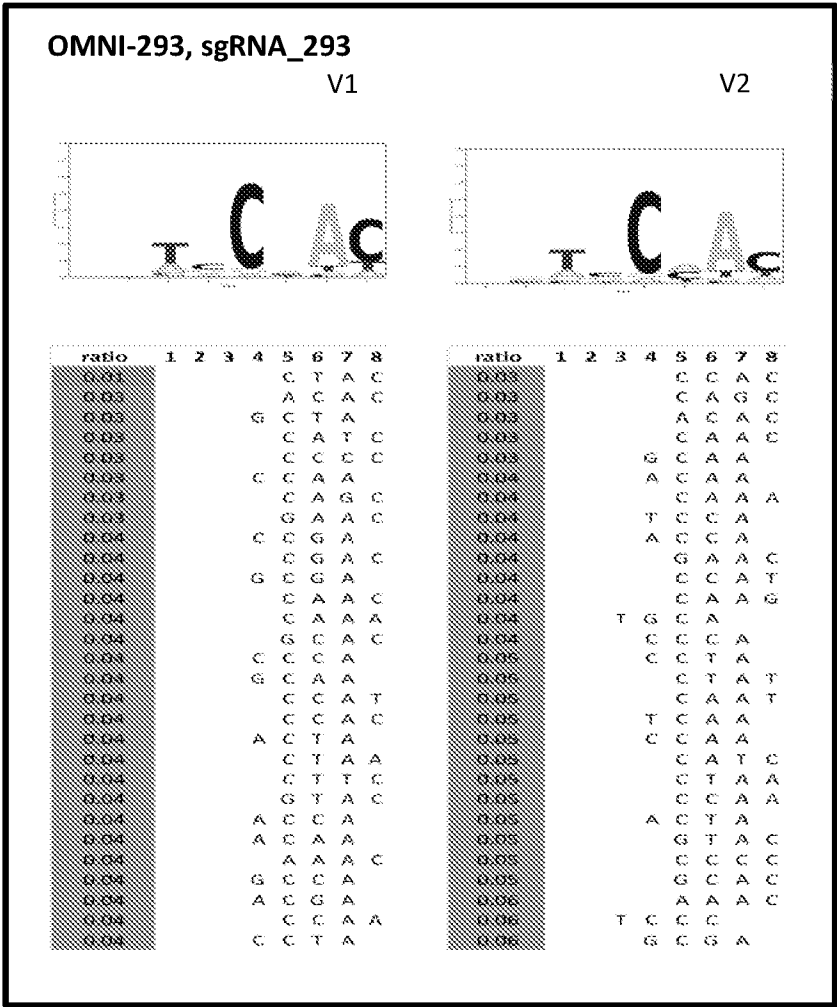


Fig. 22

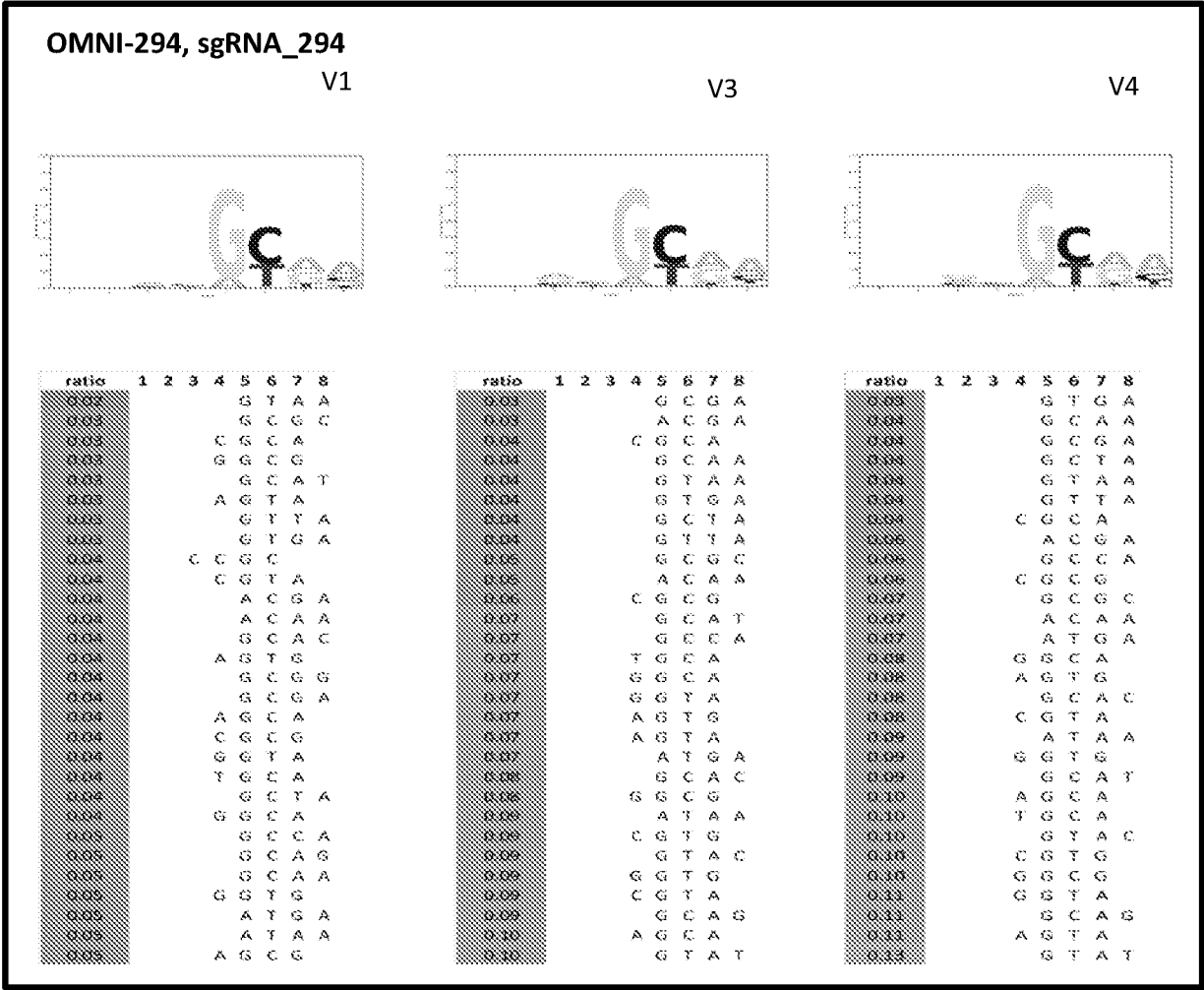


Fig. 23

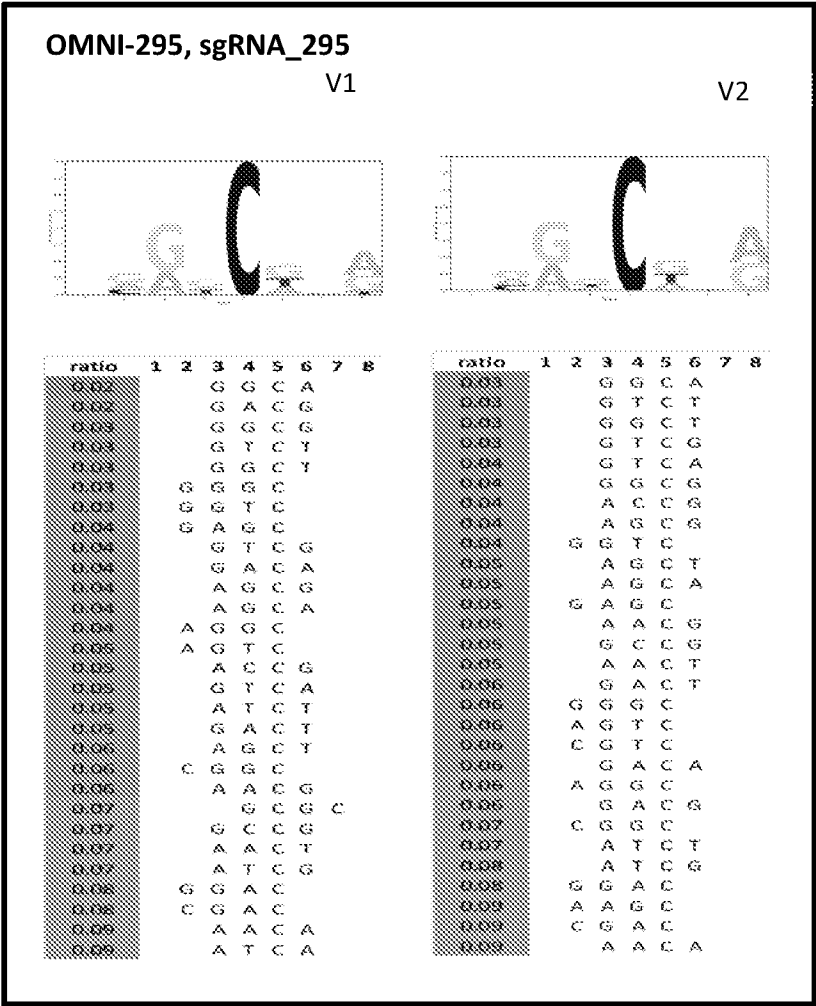


Fig. 24

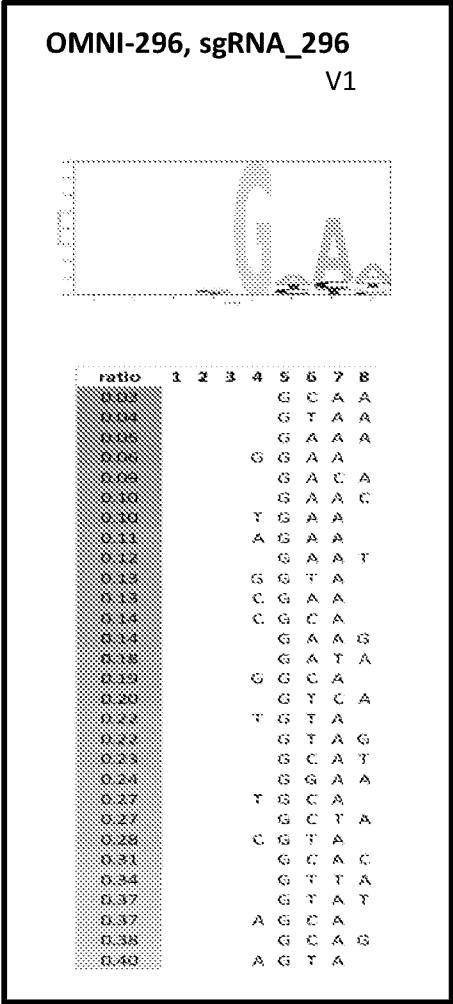


Fig. 25

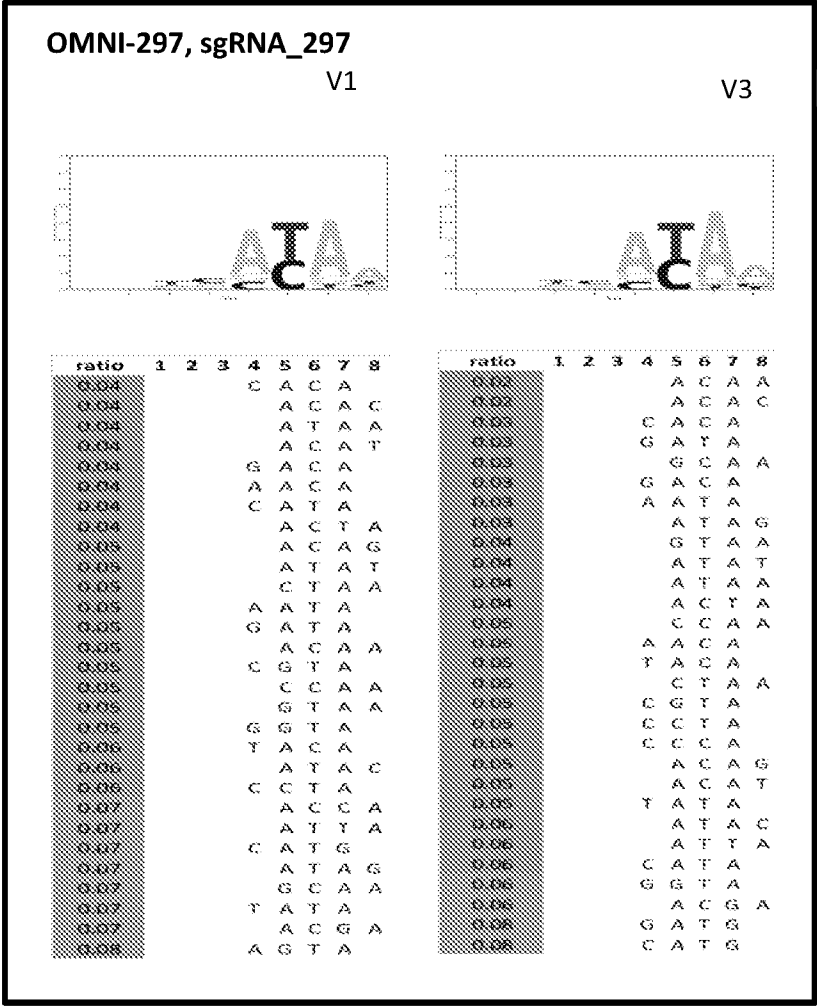


Fig. 26

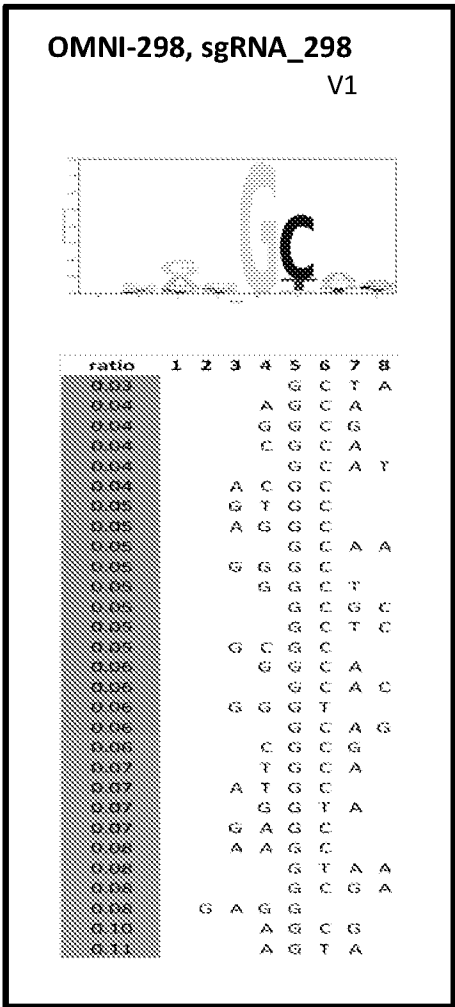


Fig. 27

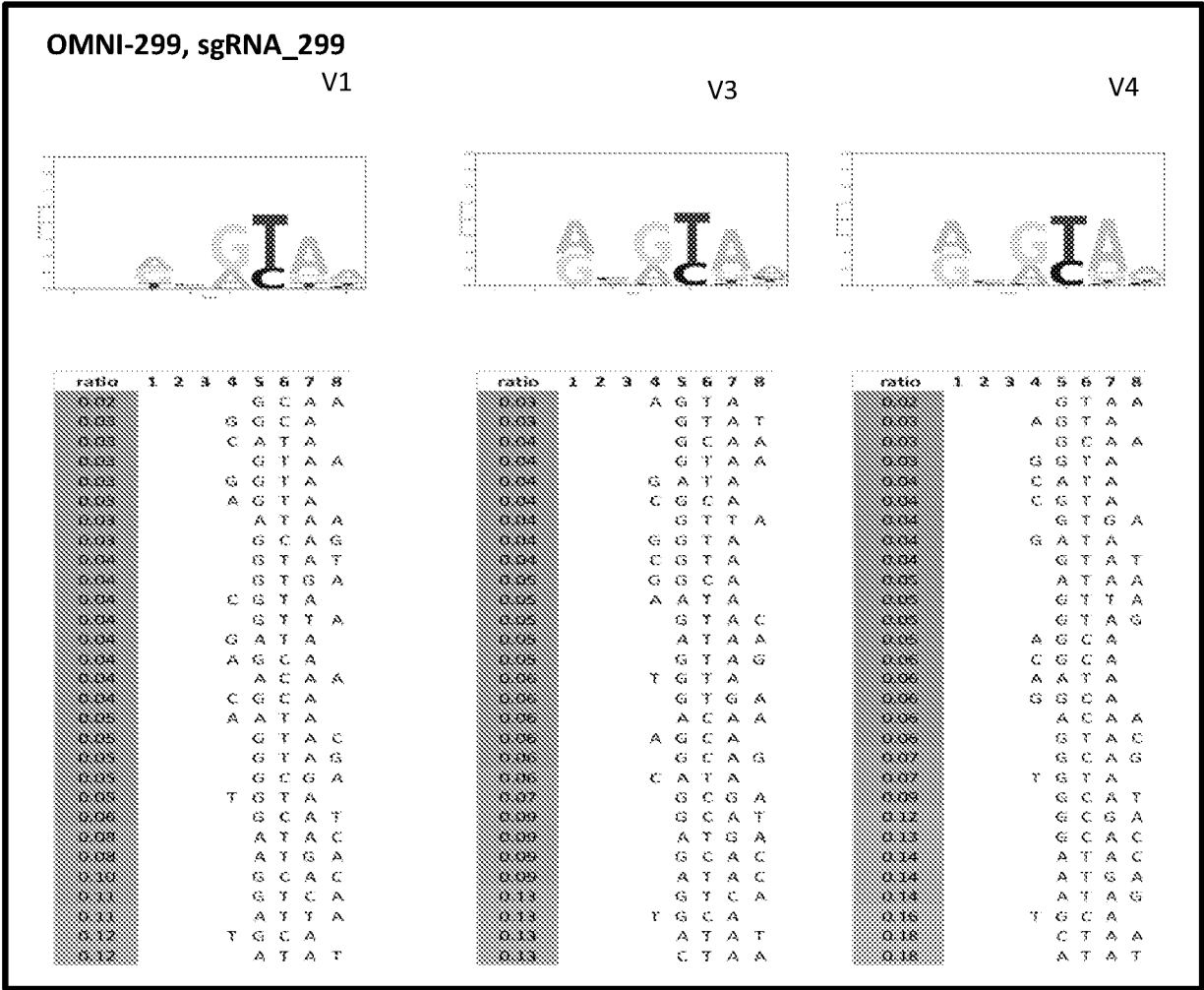


Fig. 28

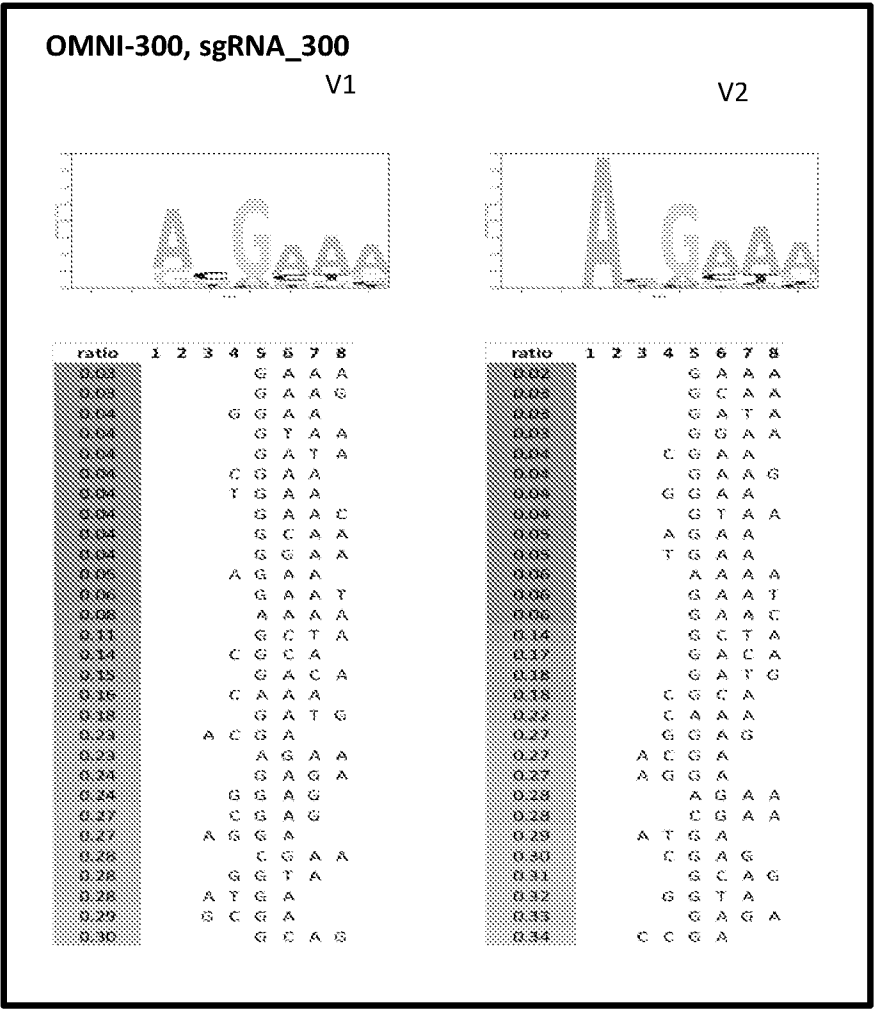


Fig. 29

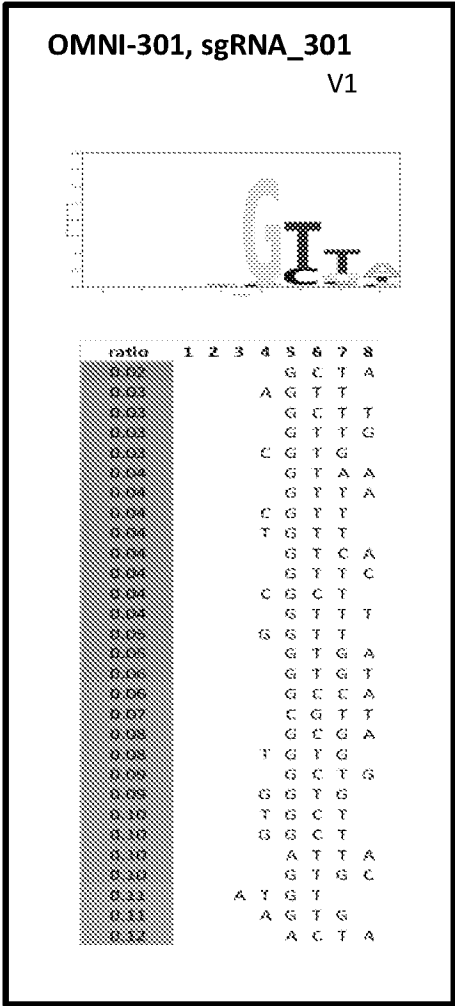


Fig. 30

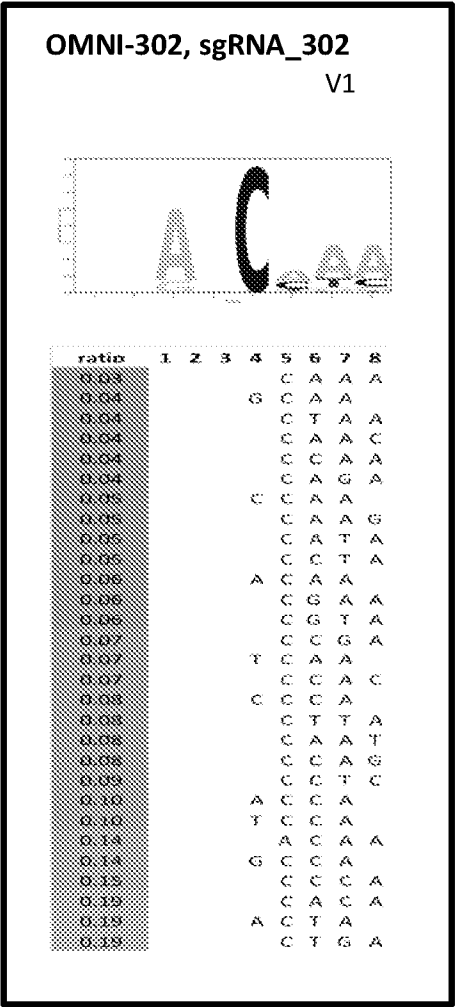


Fig. 31

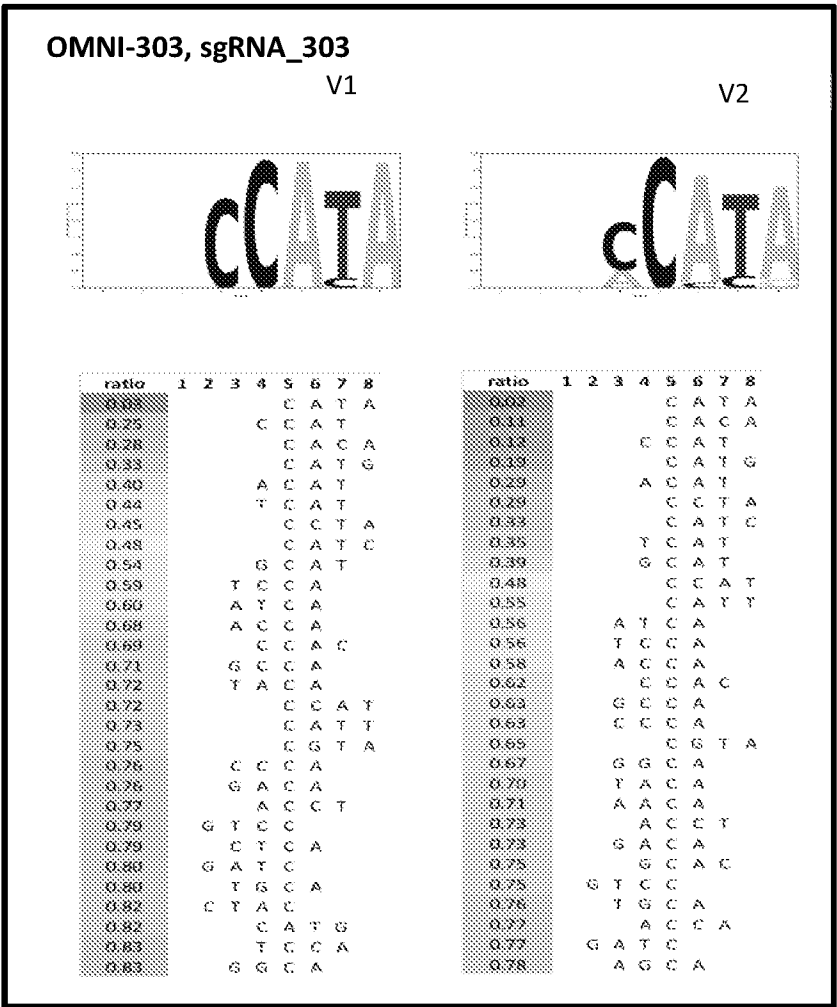


Fig. 32

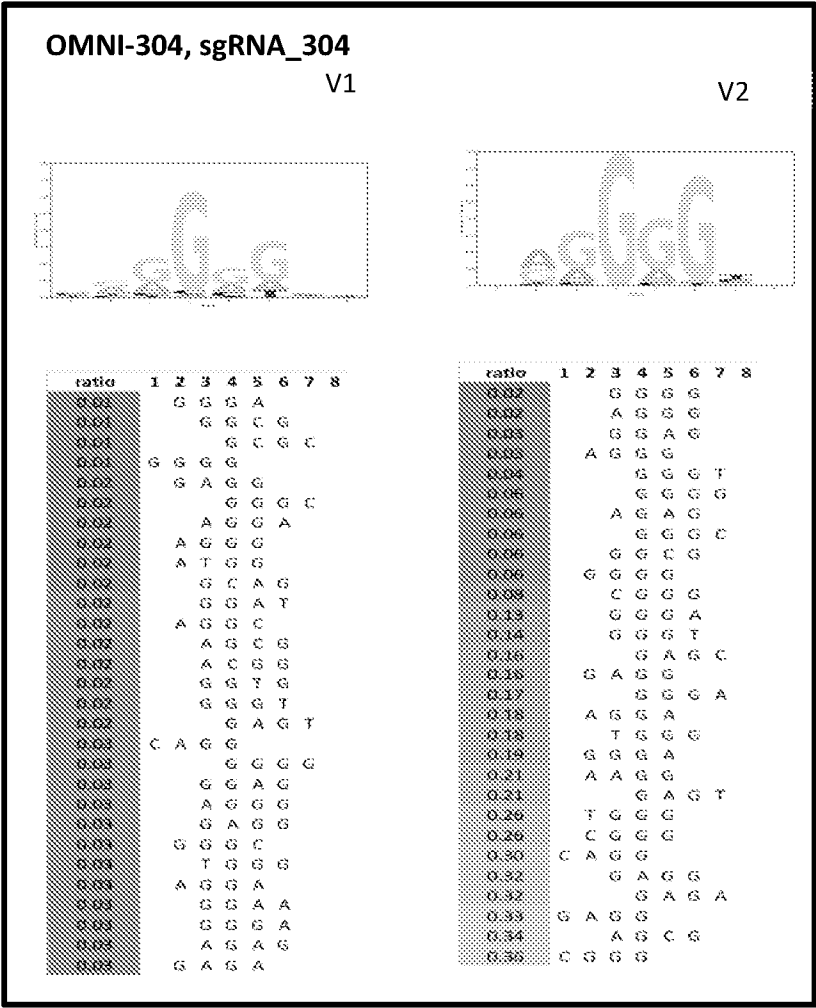


Fig. 33

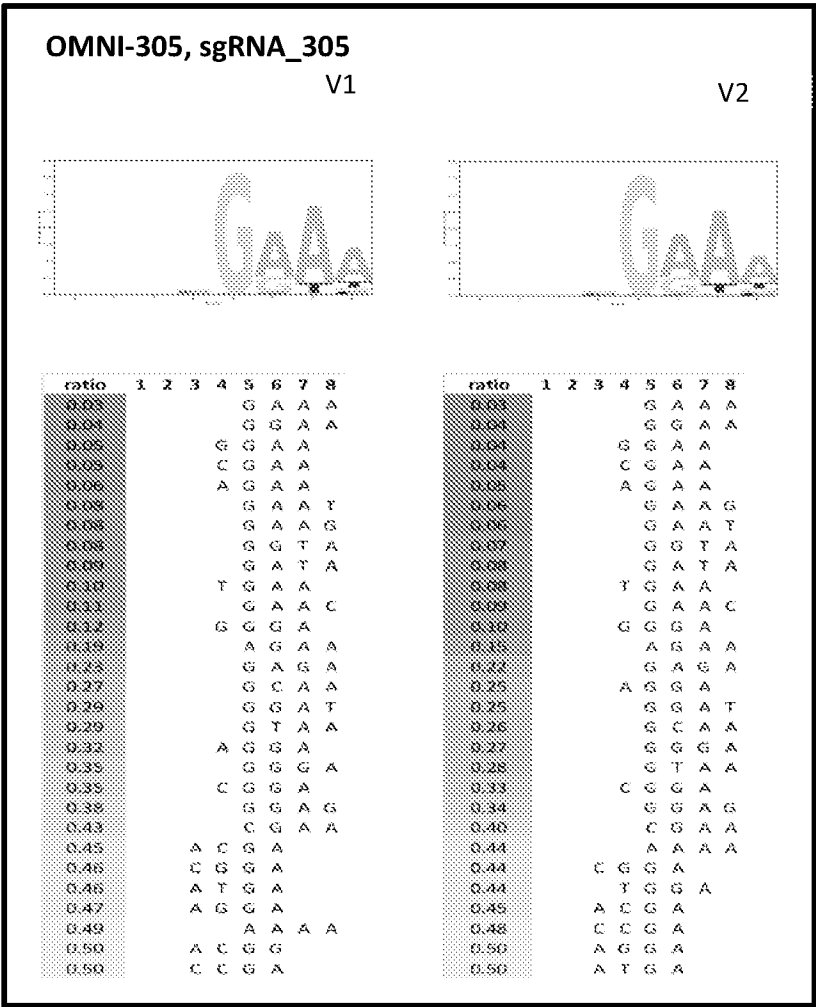


Fig. 34

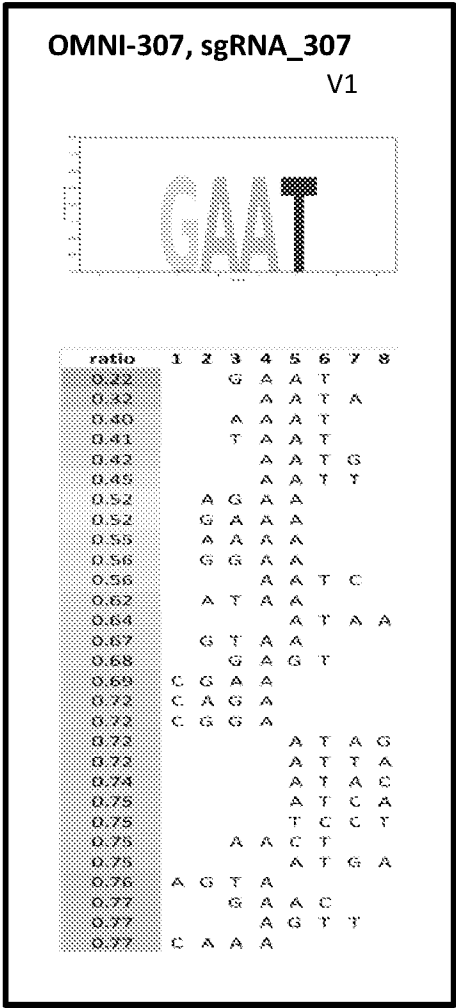


Fig. 35

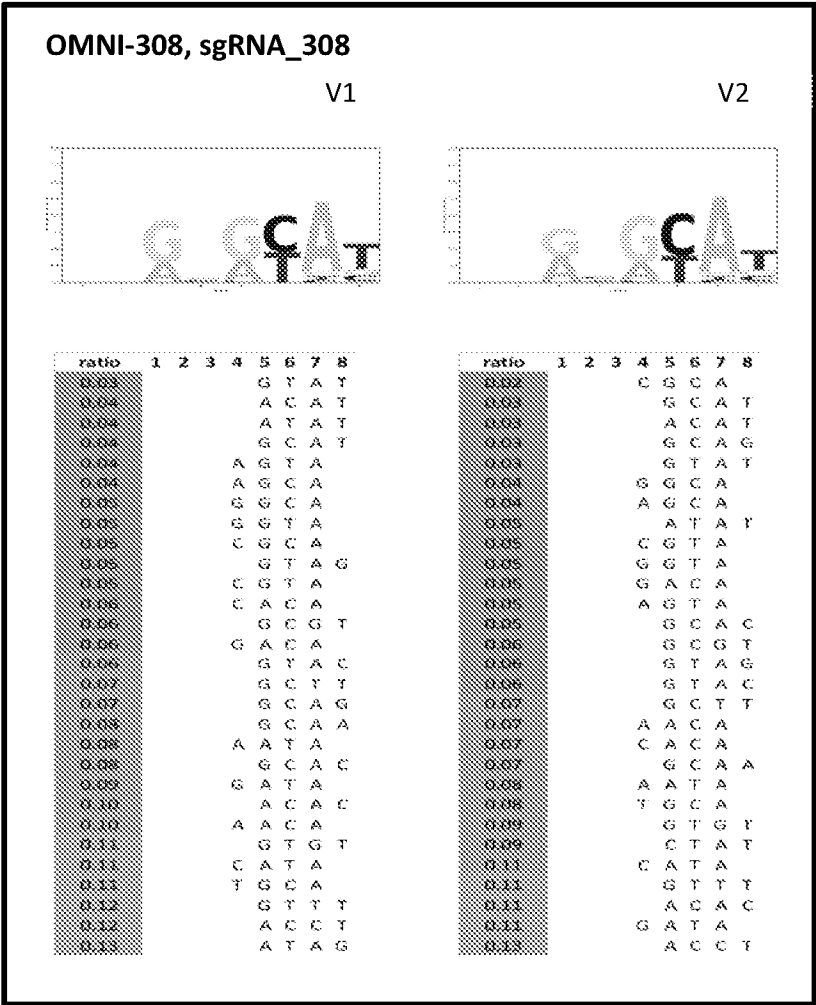


Fig. 36

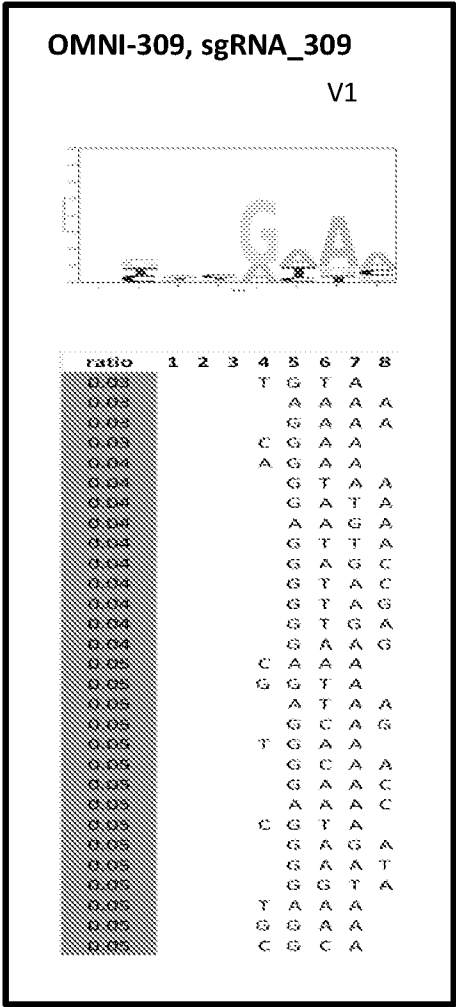


Fig. 37

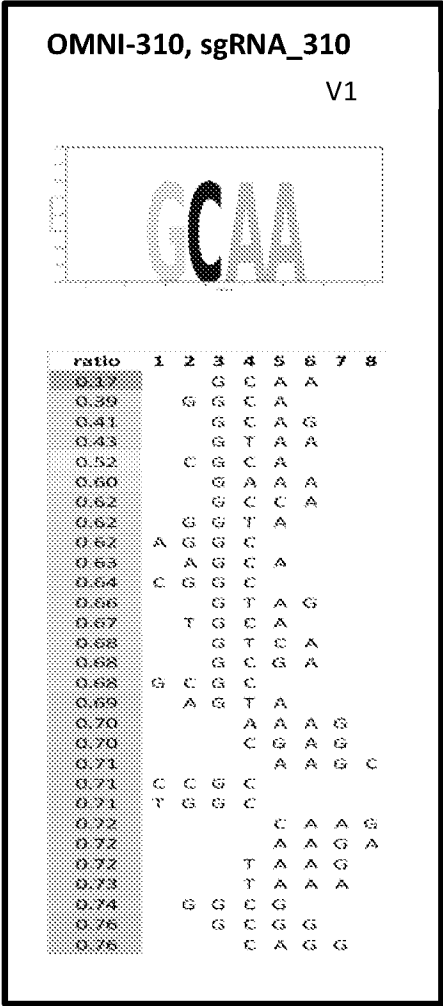


Fig. 38

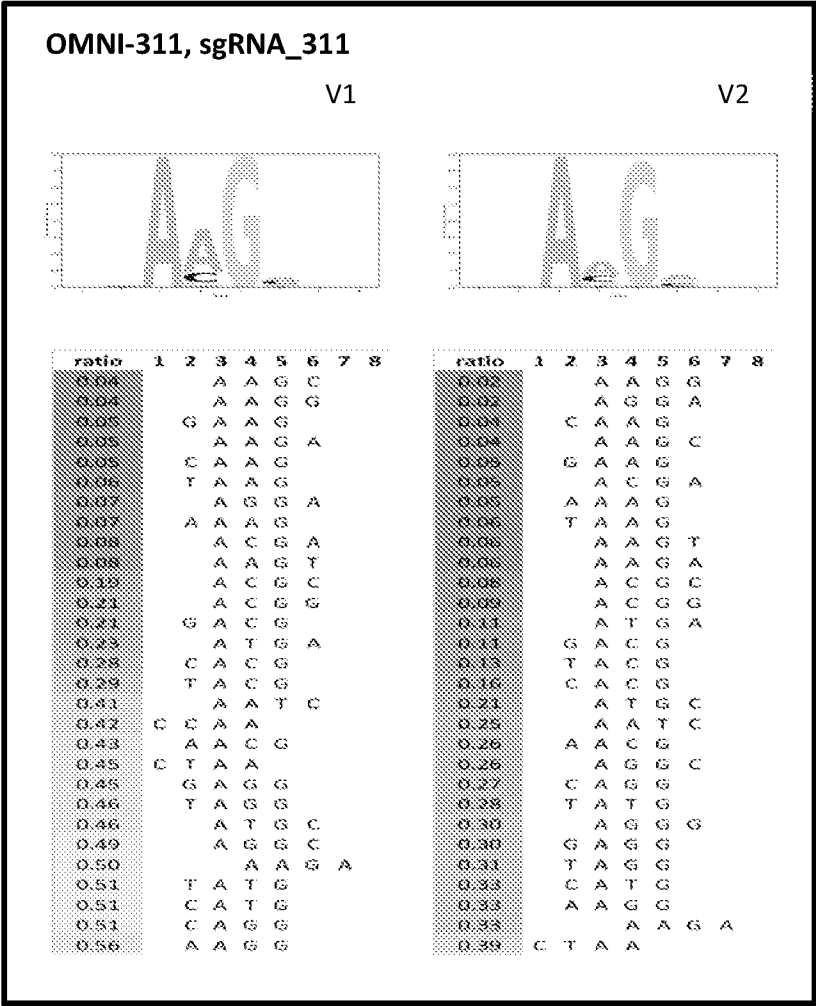


Fig. 39

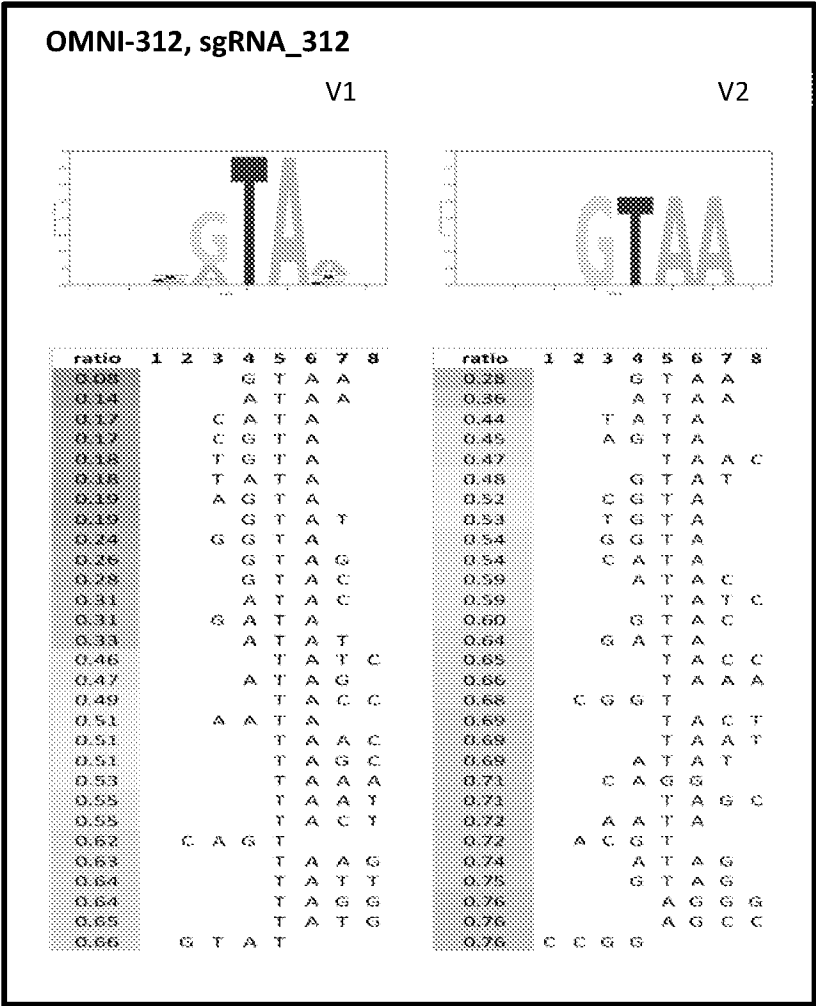


Fig. 40

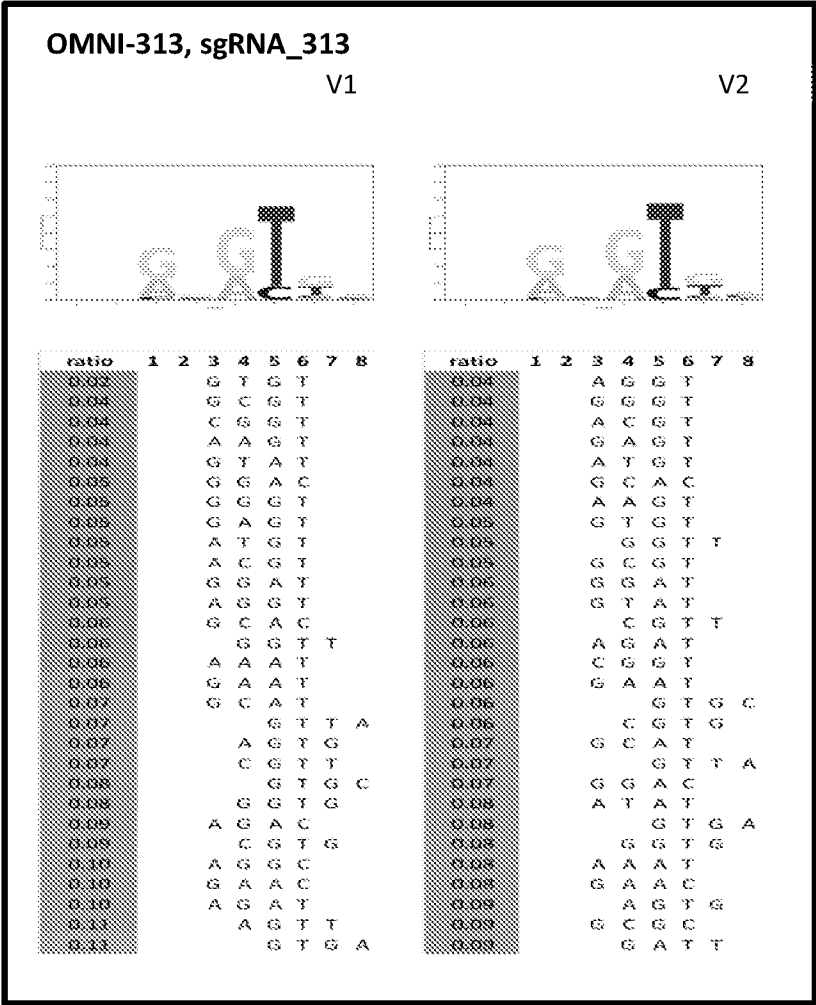


Fig. 41

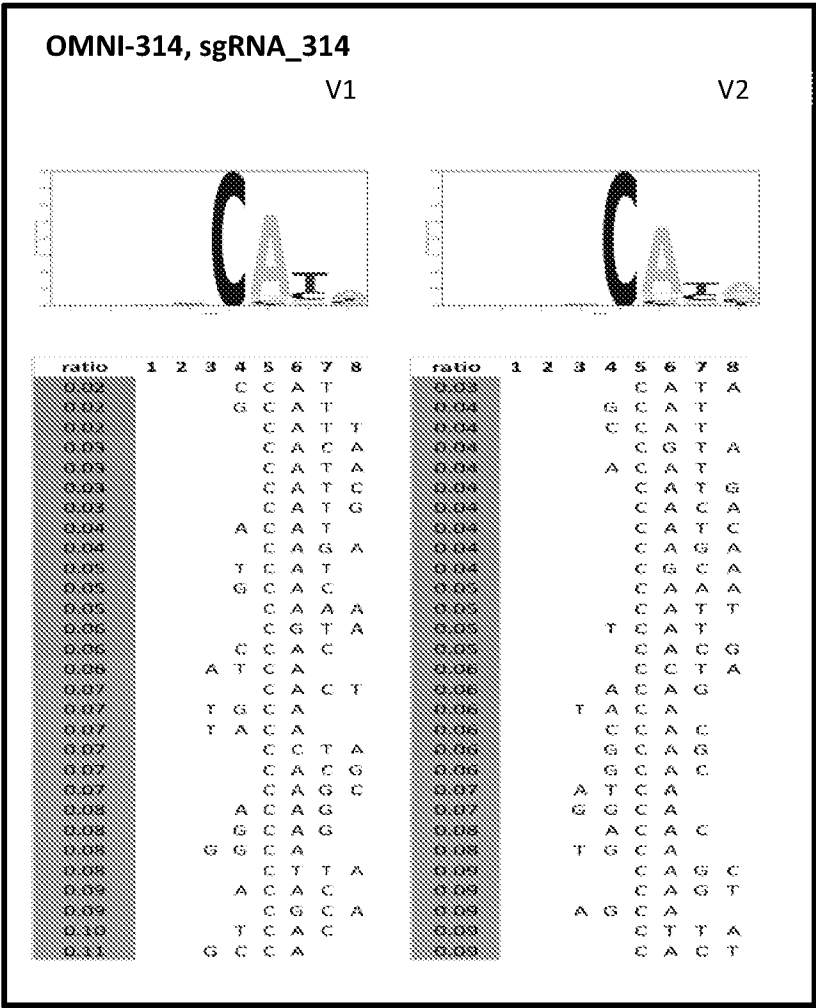


Fig. 42

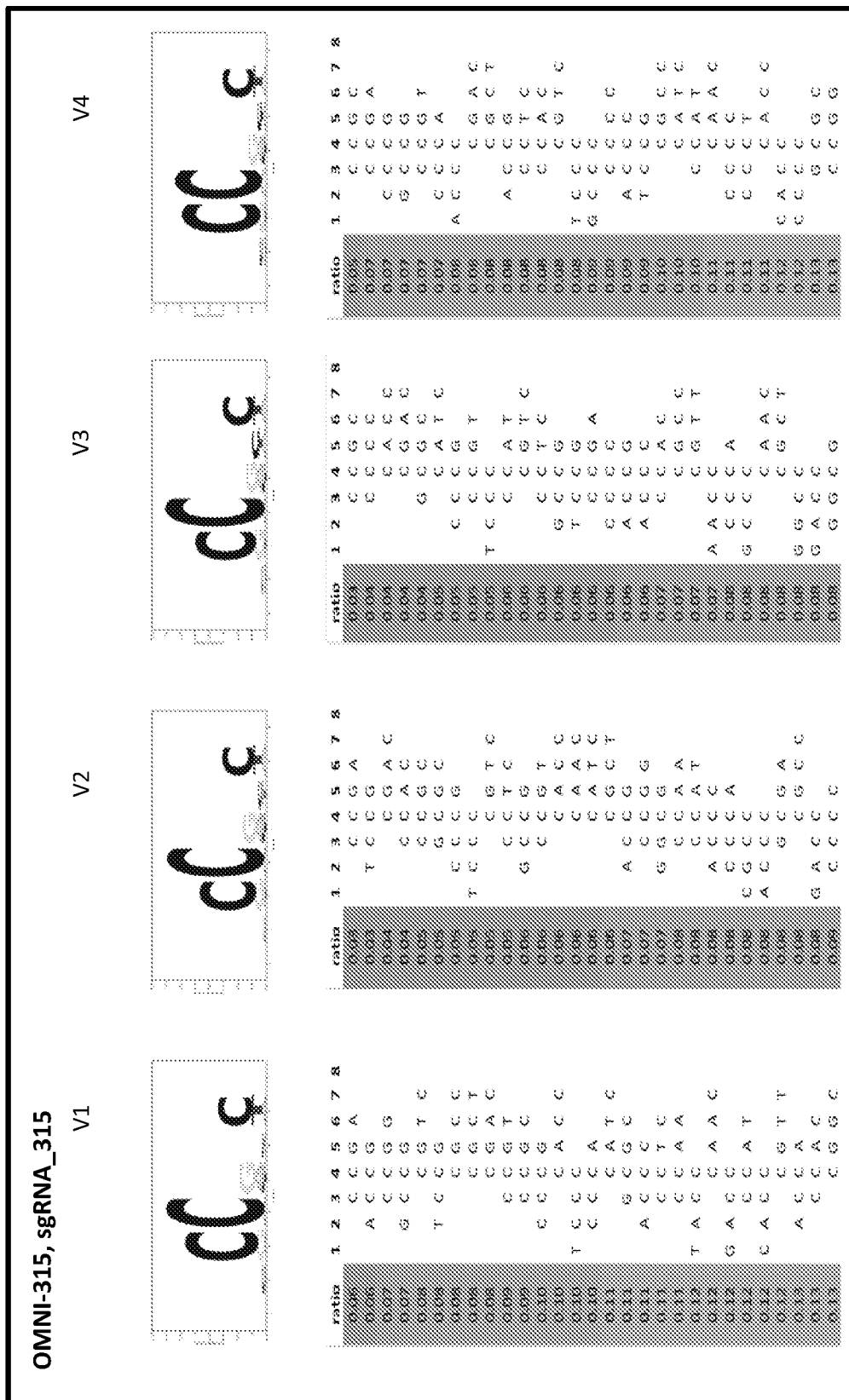


Fig. 43

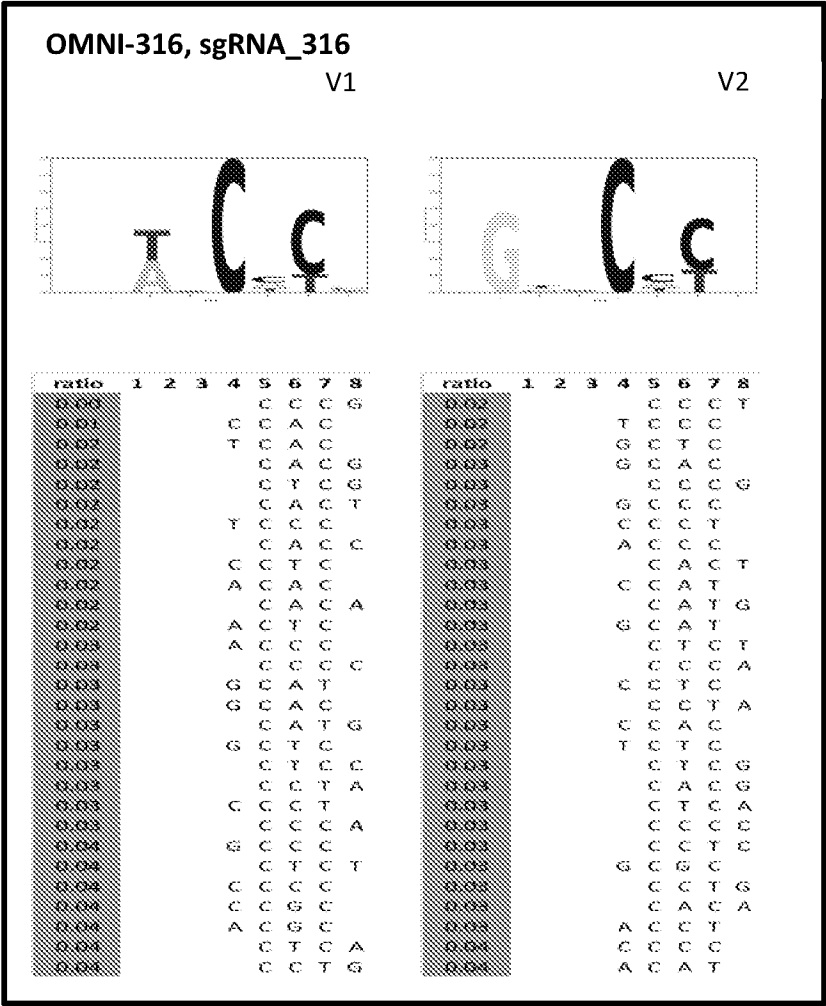


Fig. 44

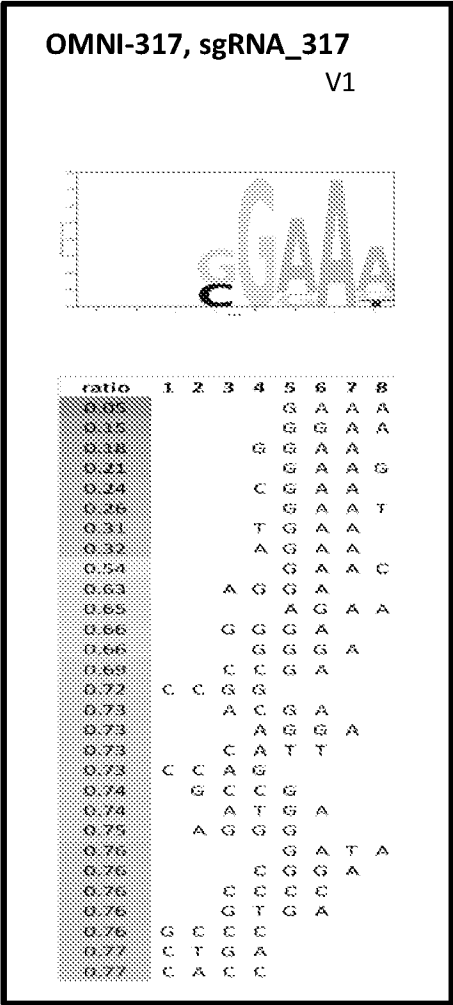


Fig. 45

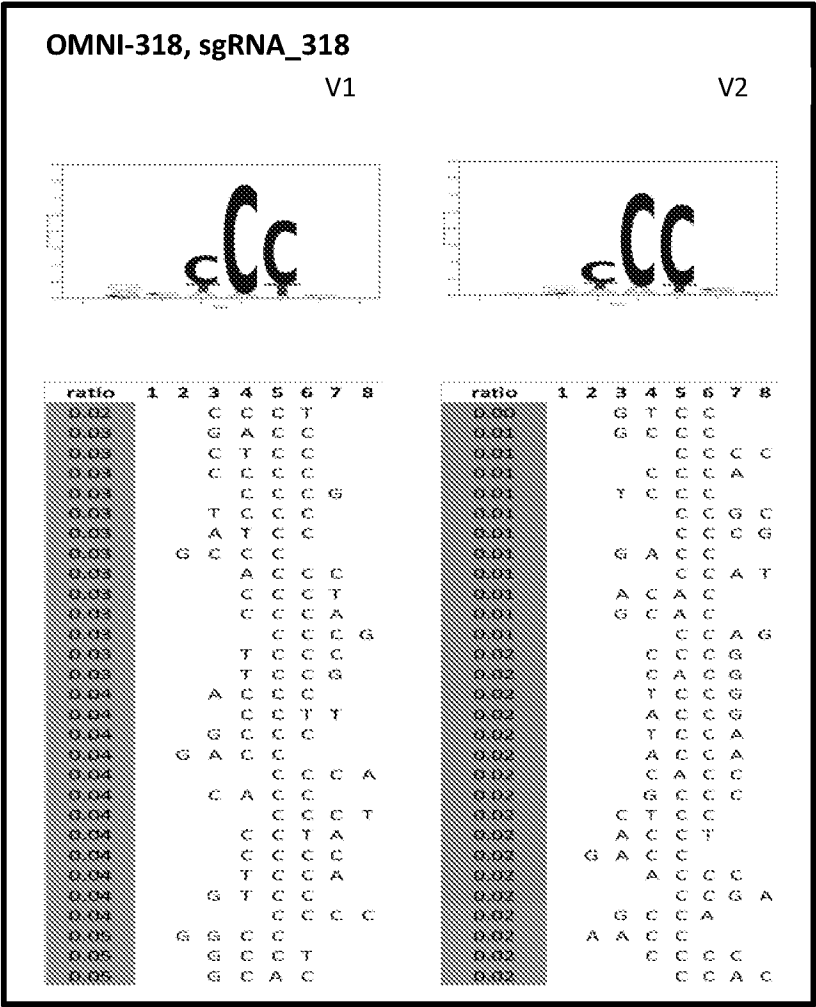


Fig. 46

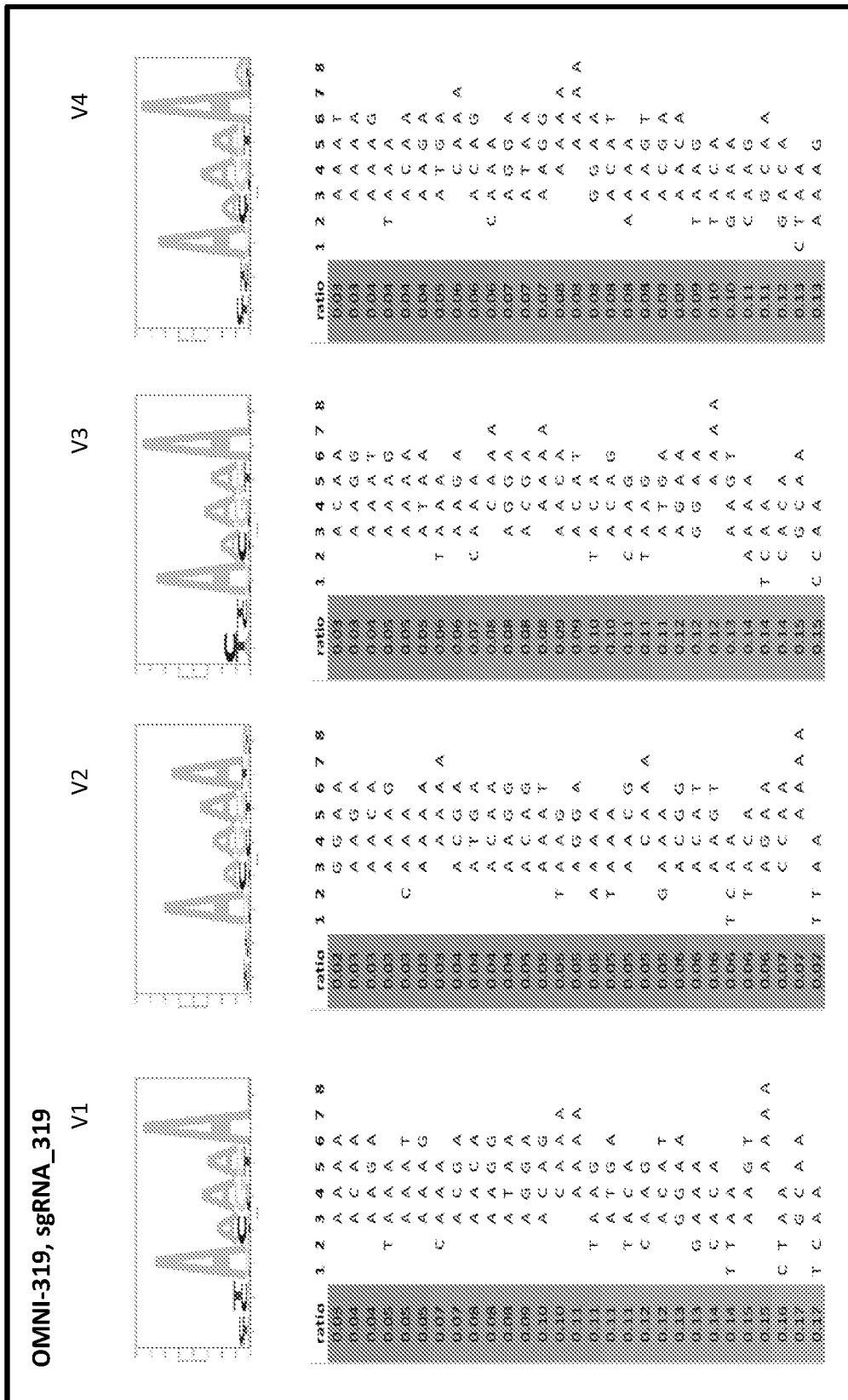


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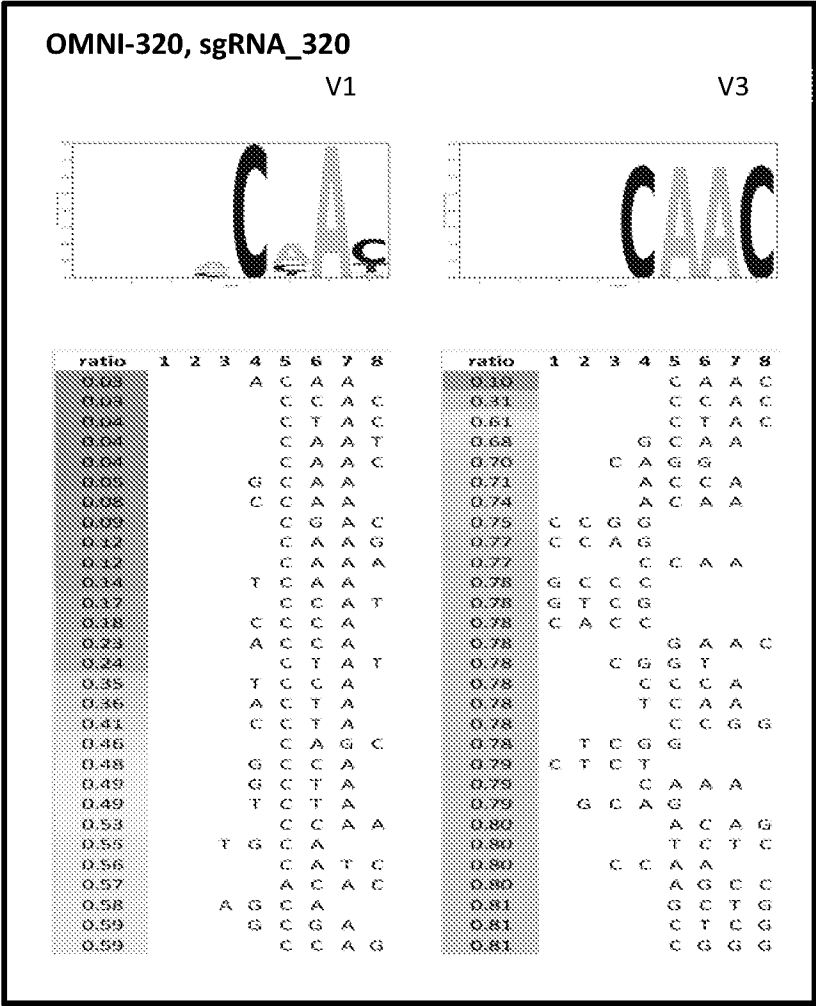


Fig. 48

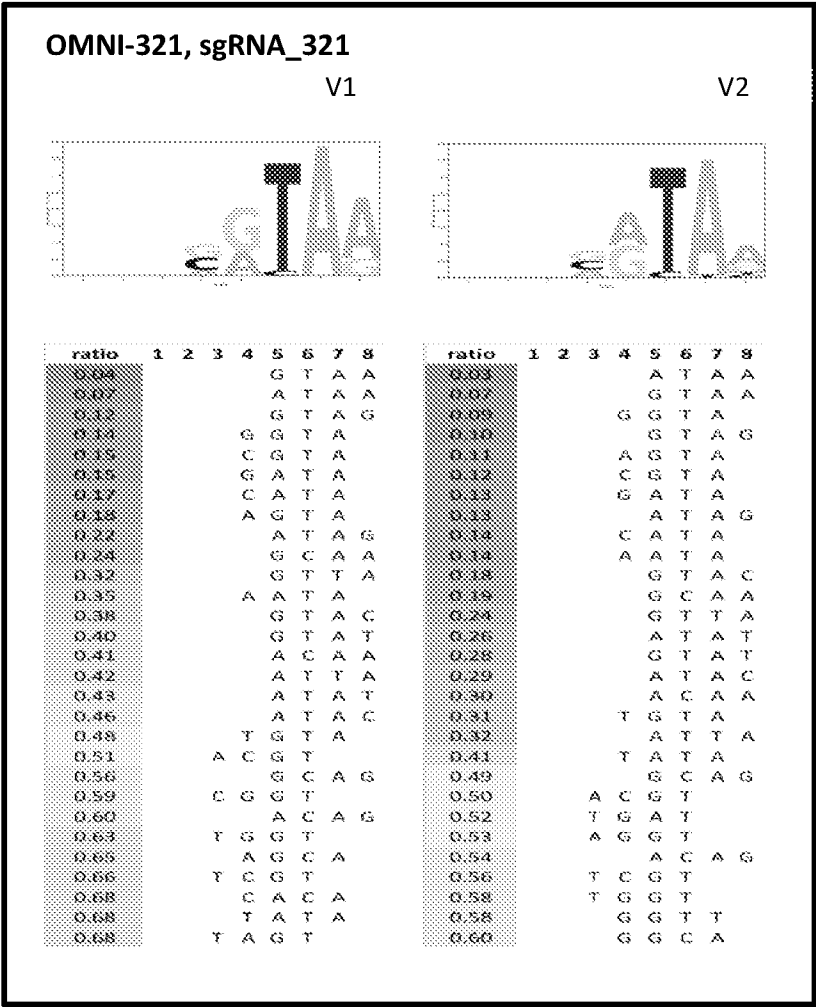


Fig. 49

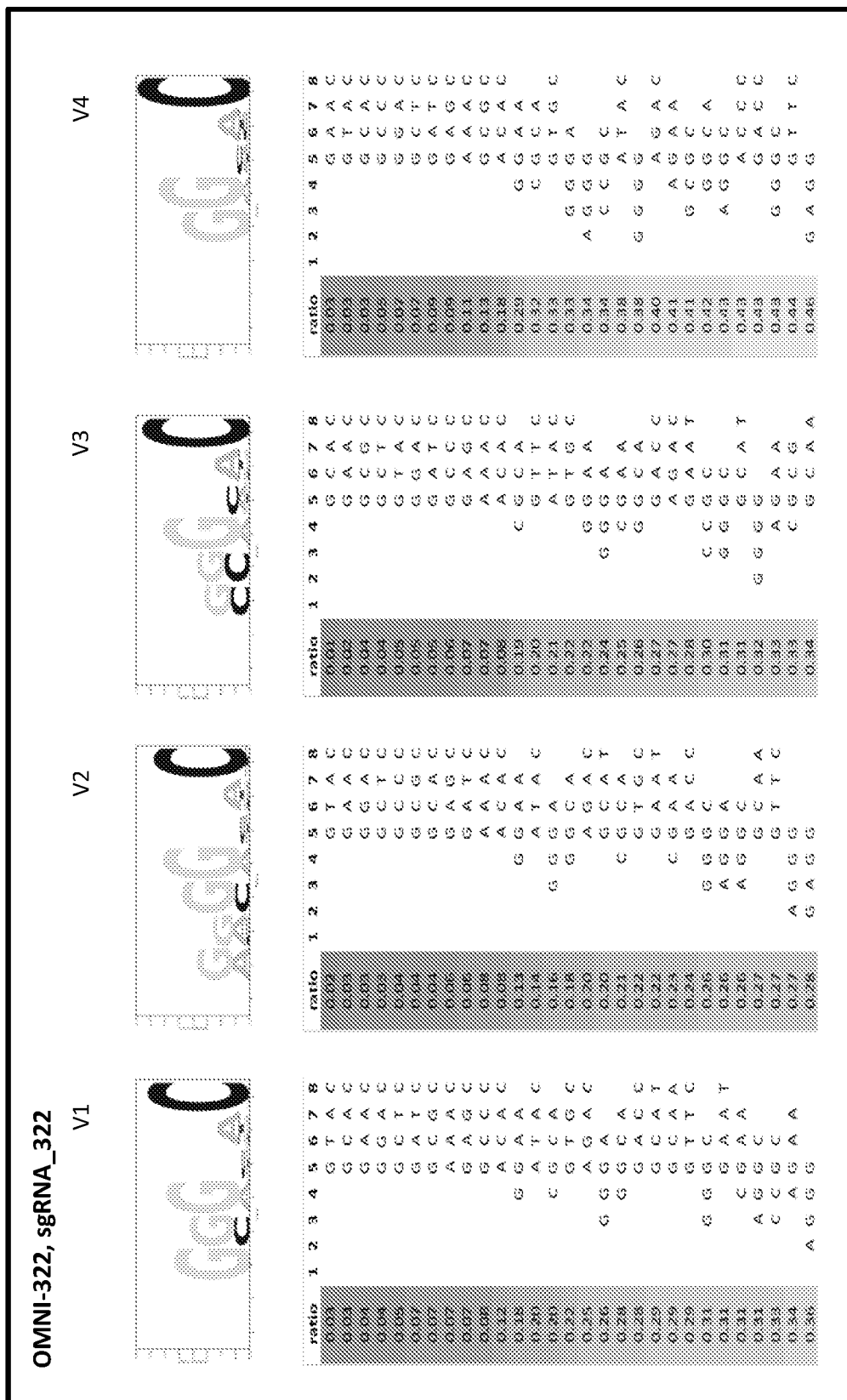


Fig. 50

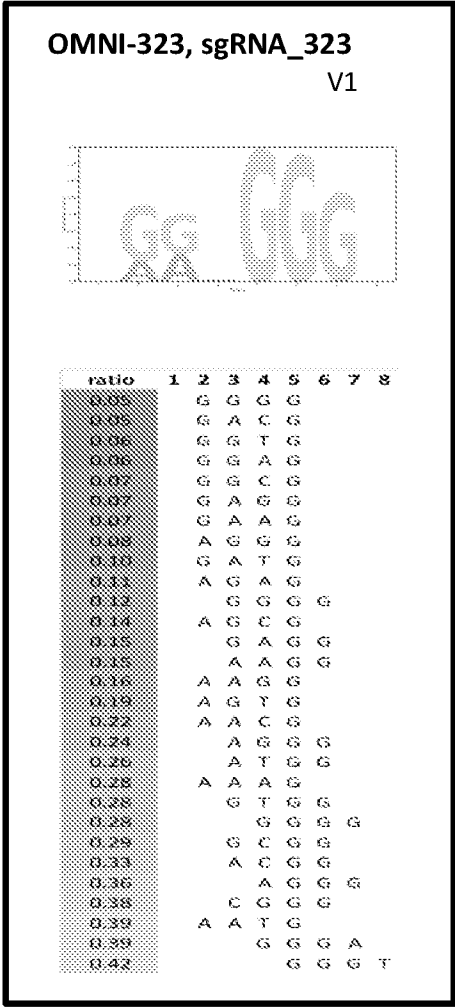


Fig. 51

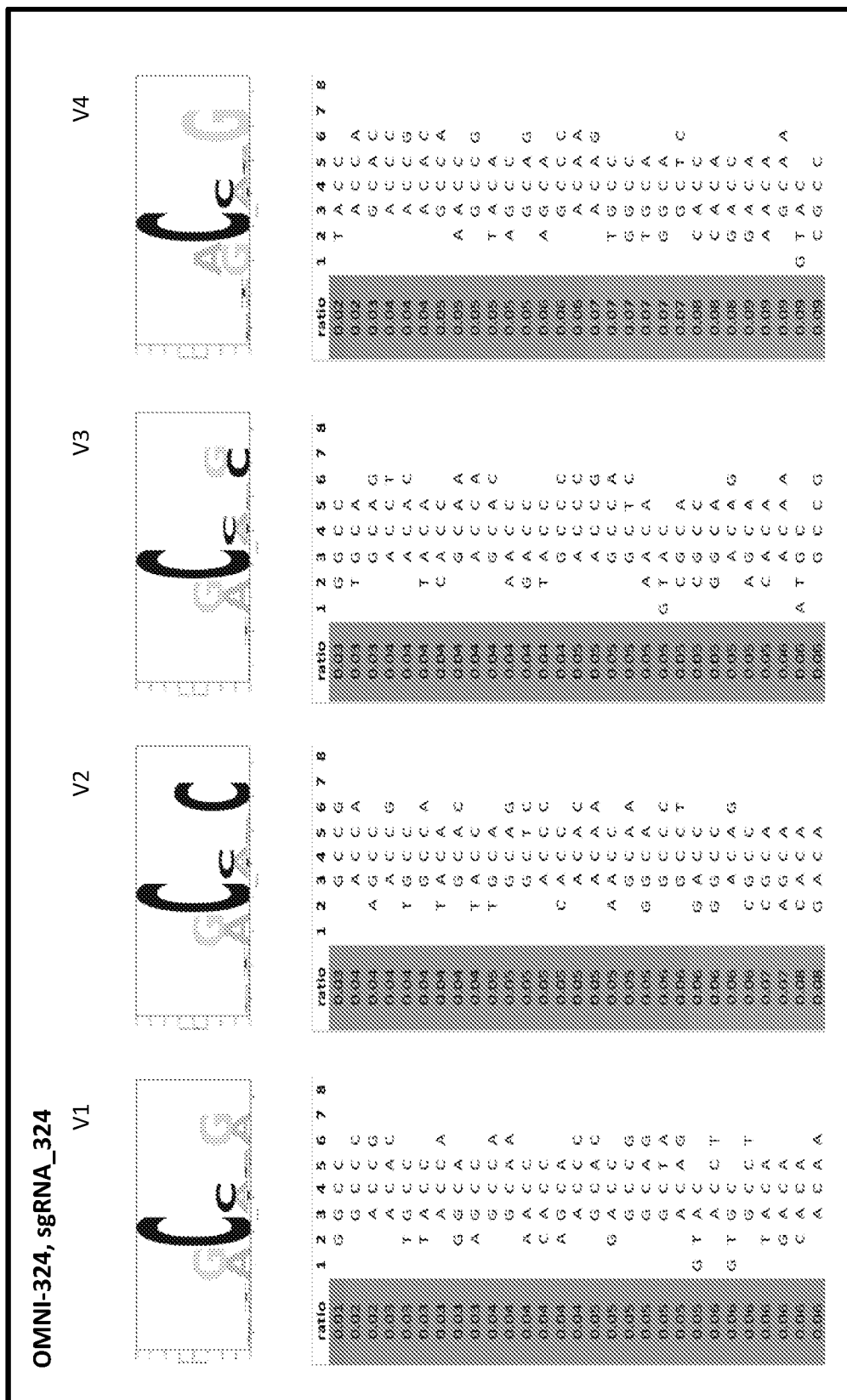


Fig. 52

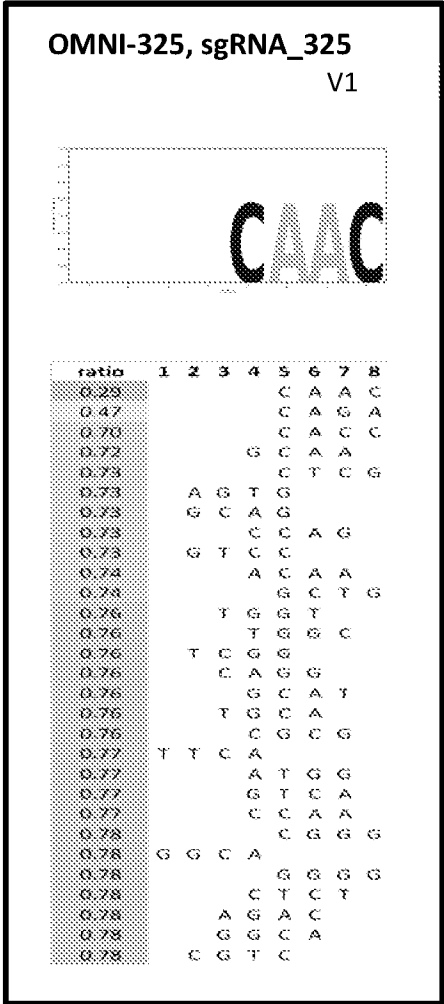


Fig. 53

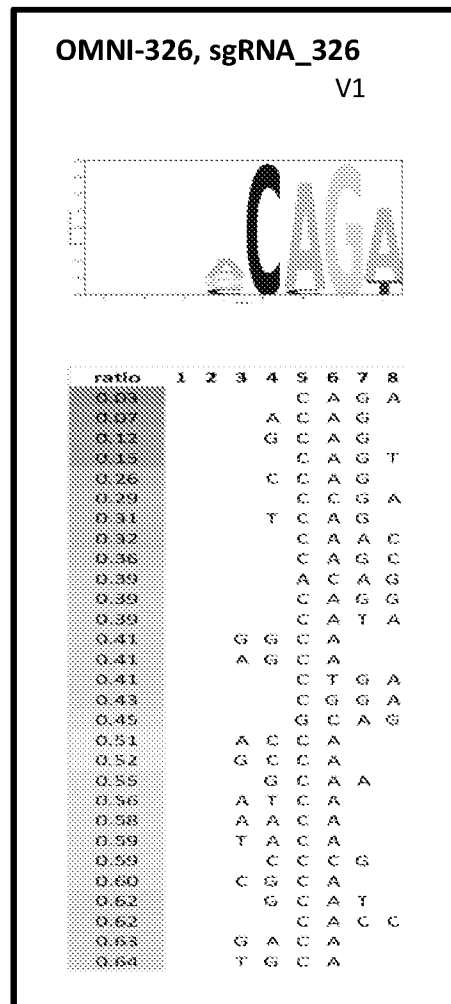


Fig. 54

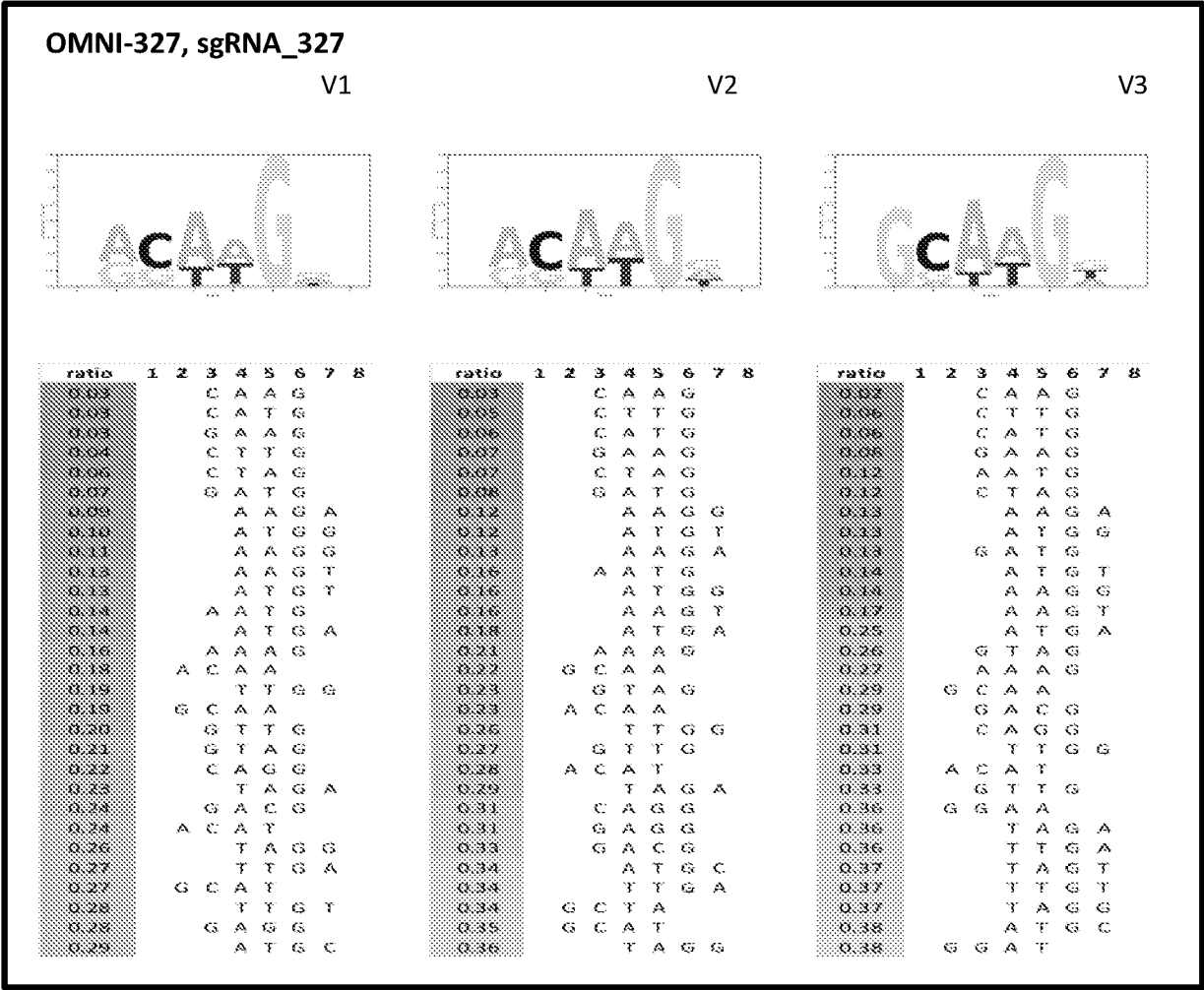


Fig. 55

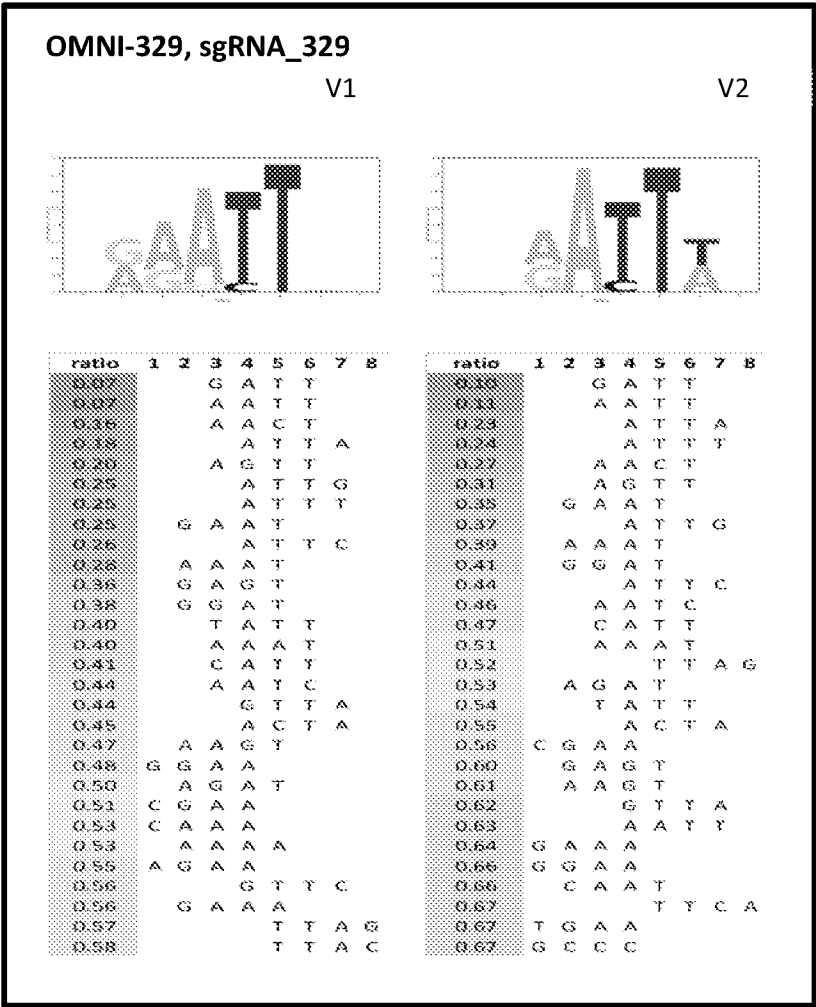


Fig. 56

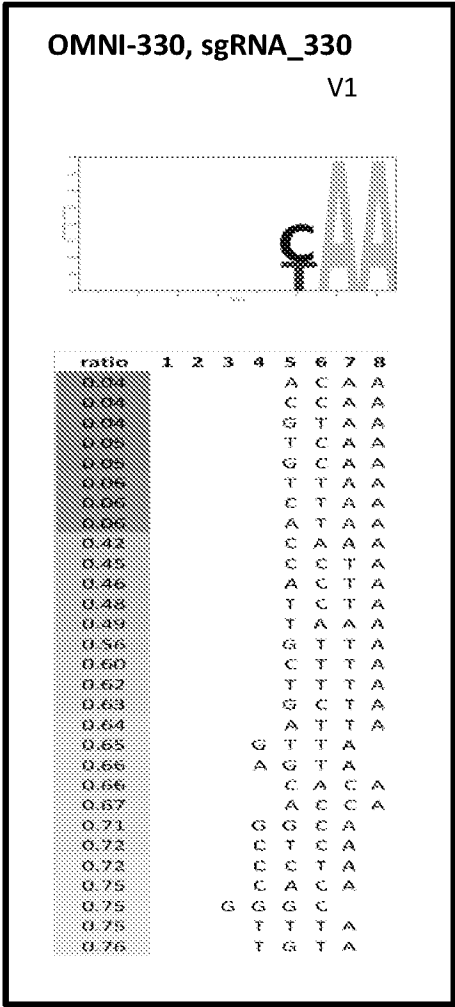


Fig. 57

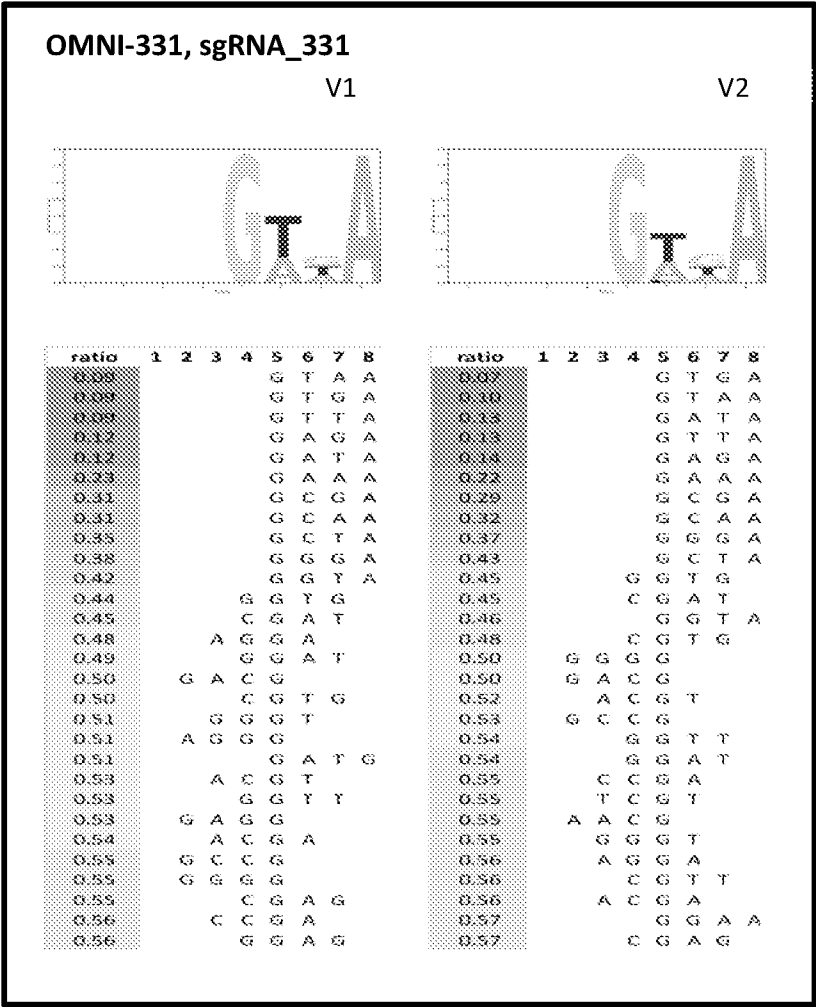


Fig. 58

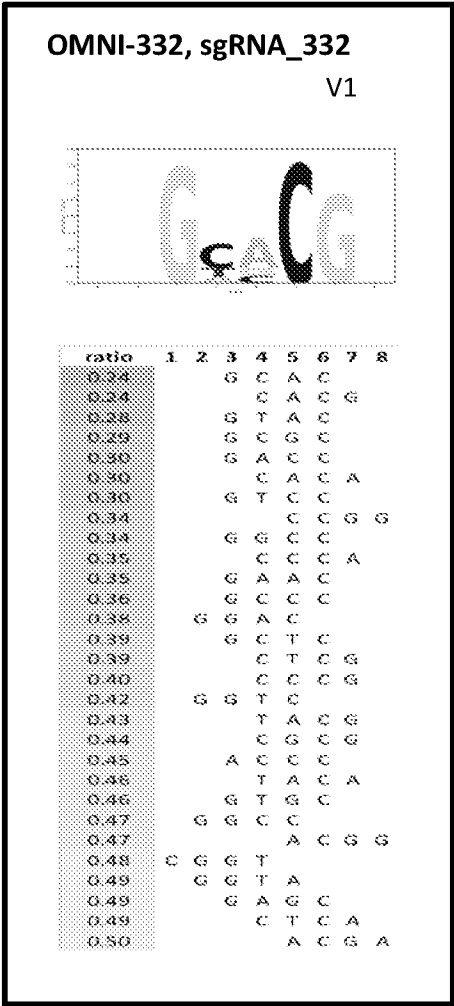


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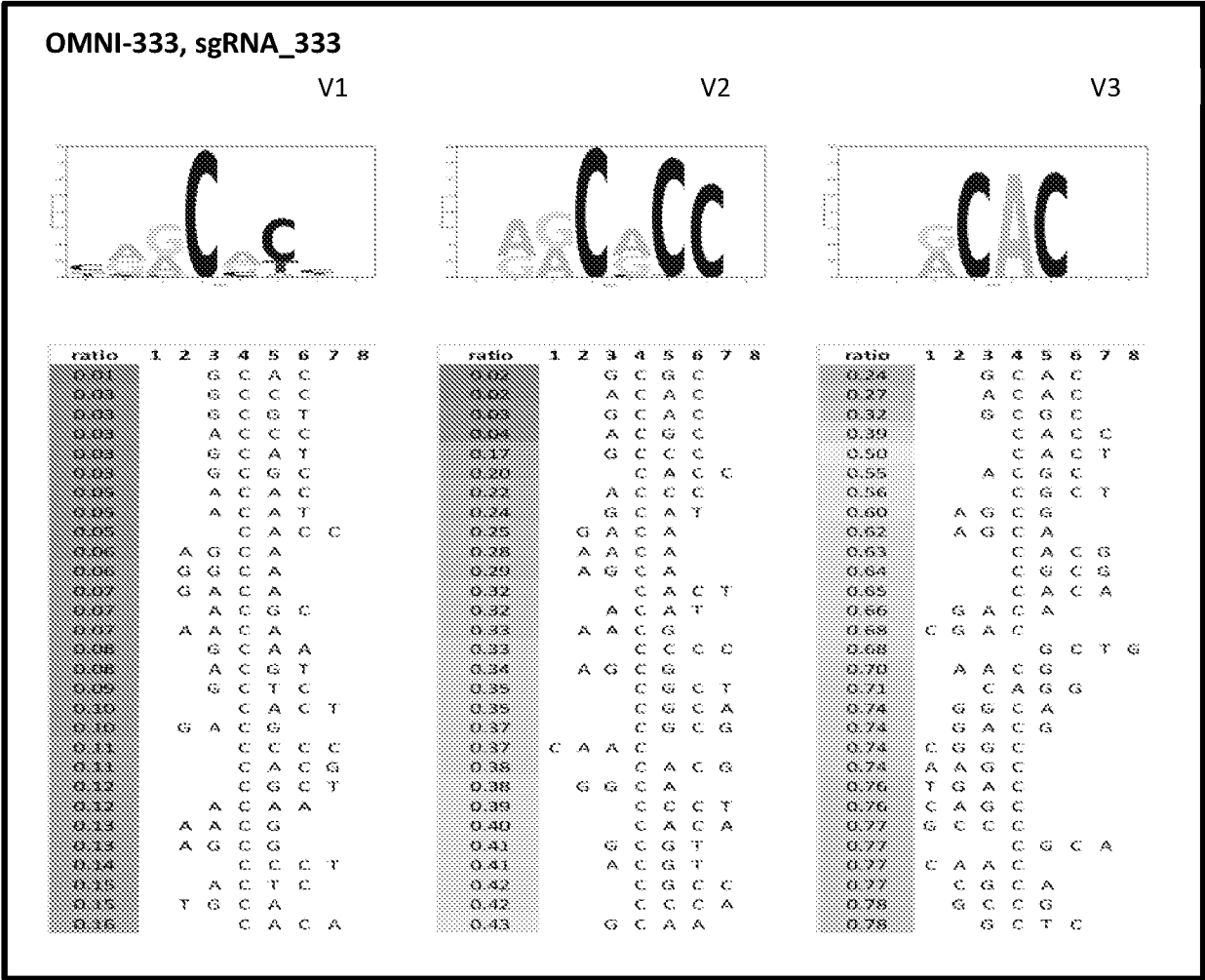


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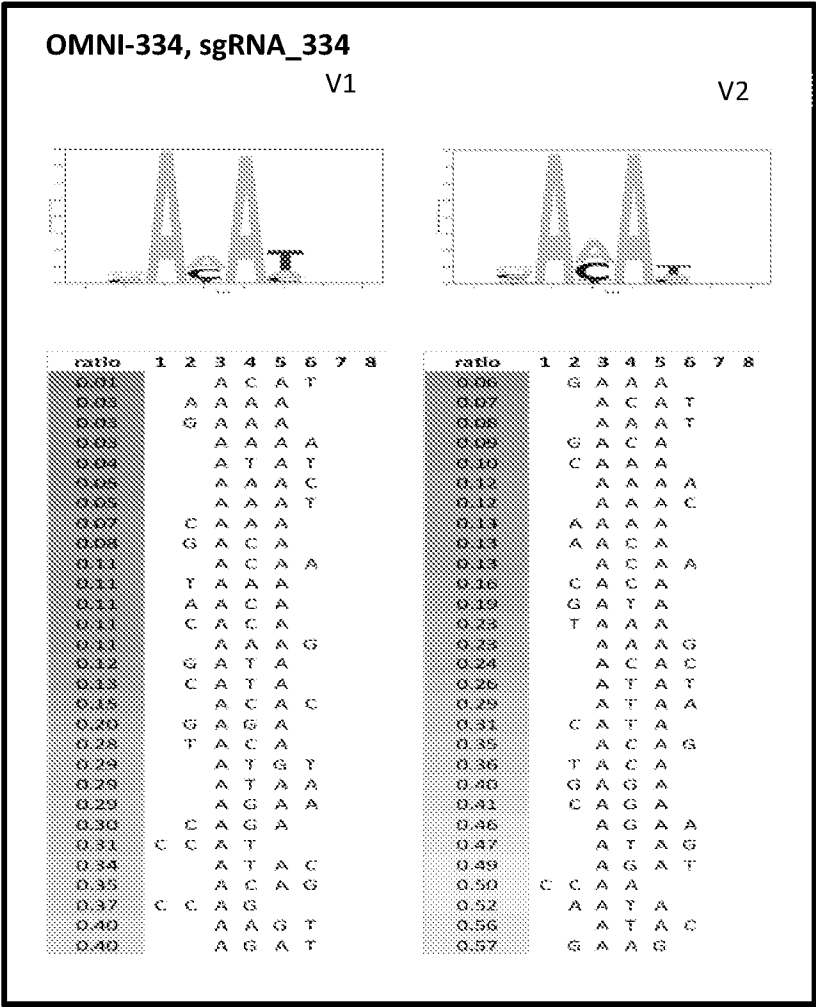


Fig. 61

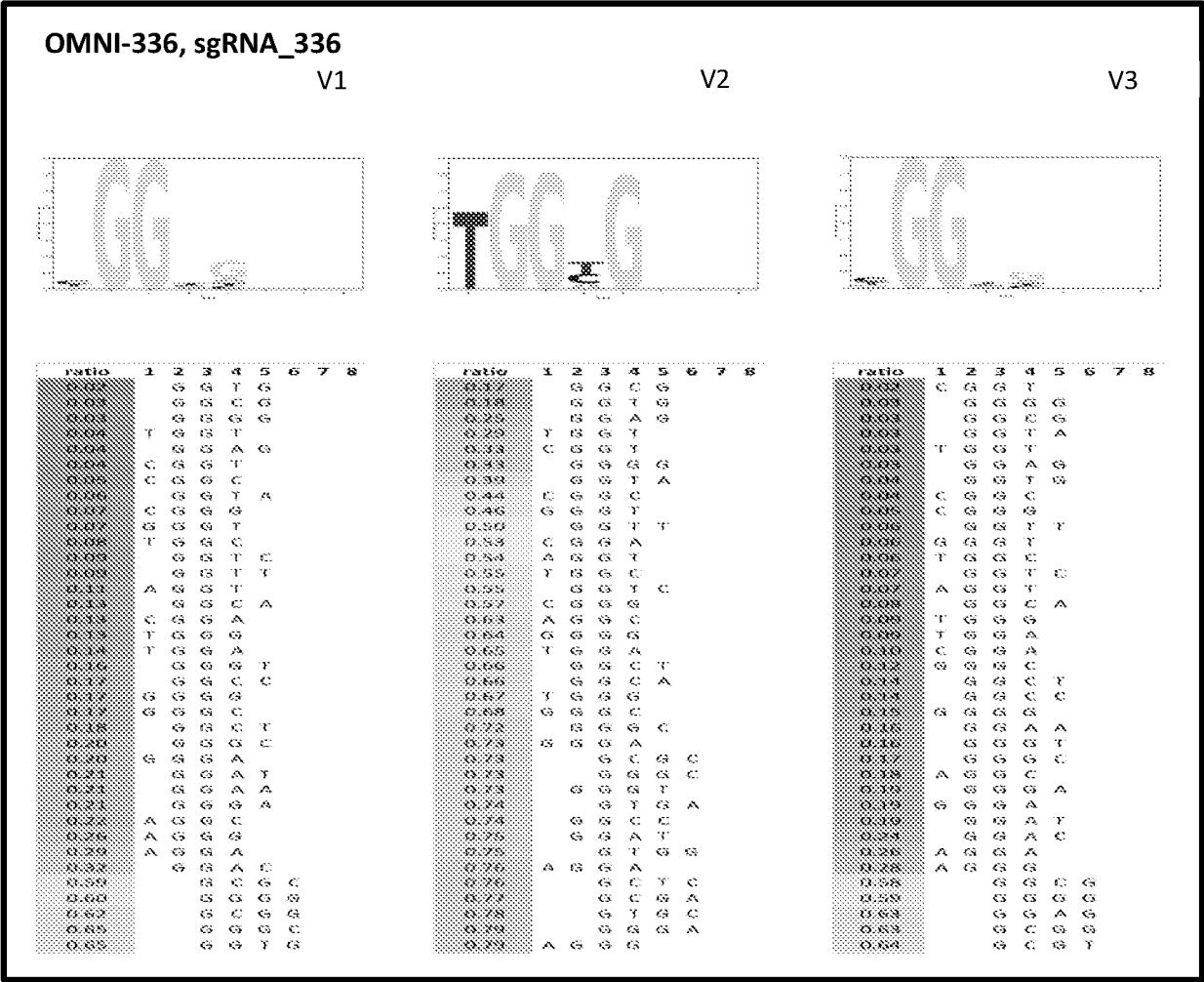


Fig. 62



Fig. 63

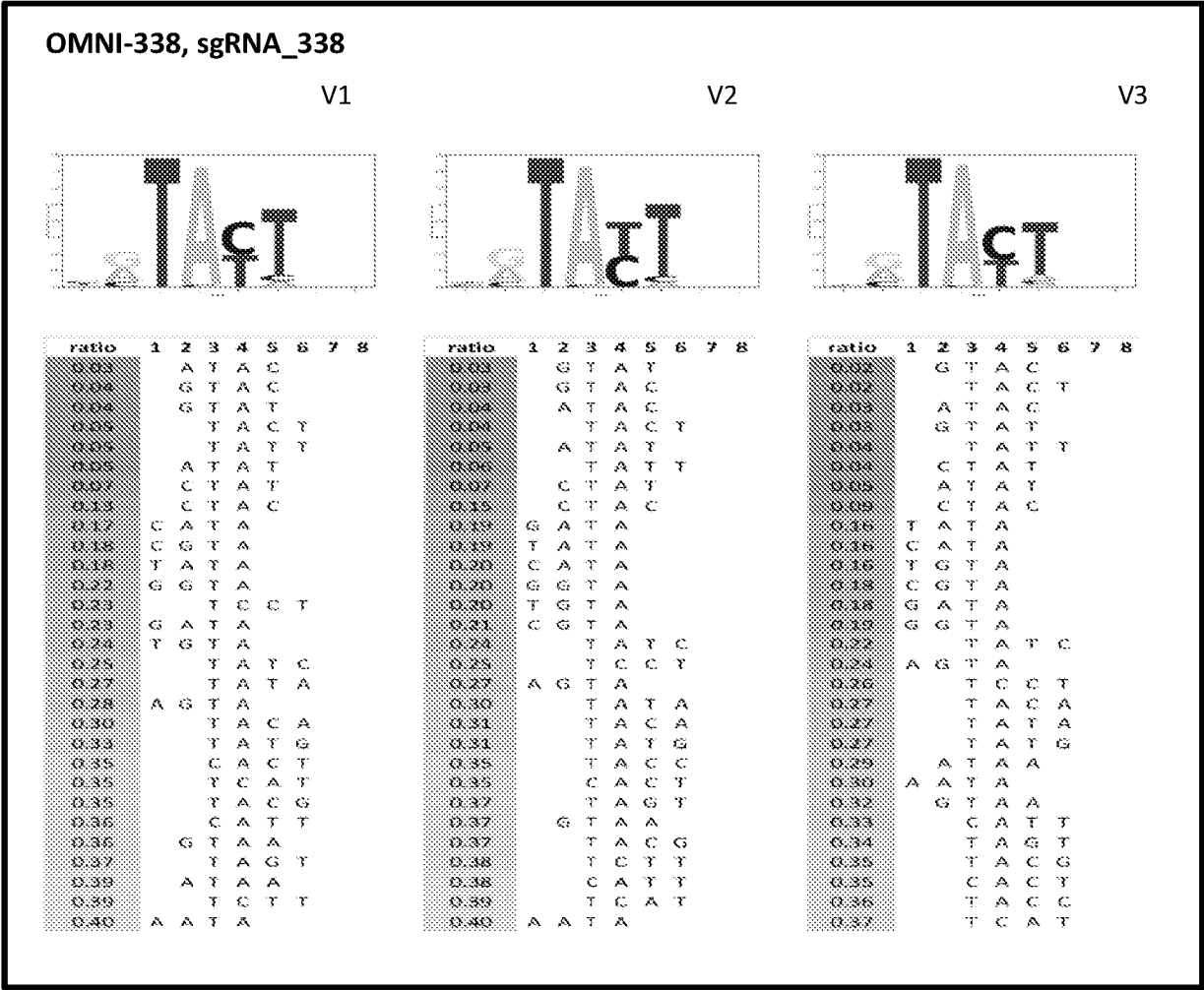


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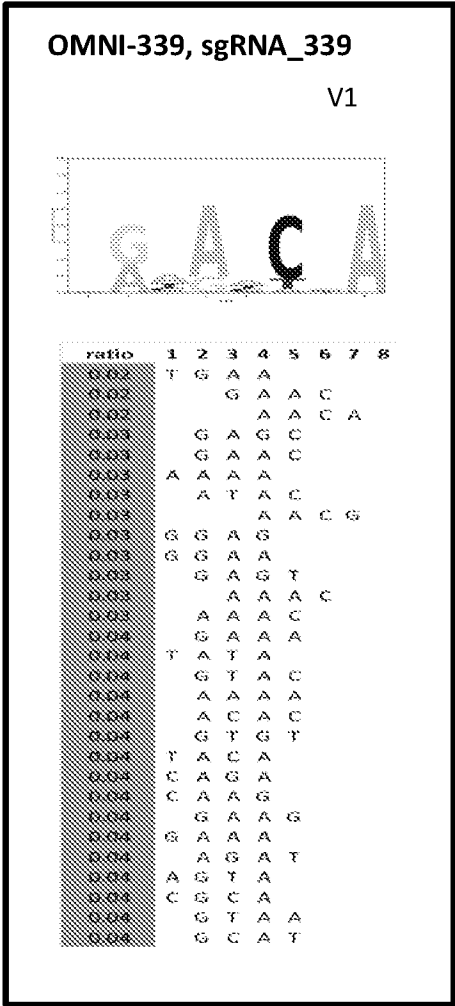


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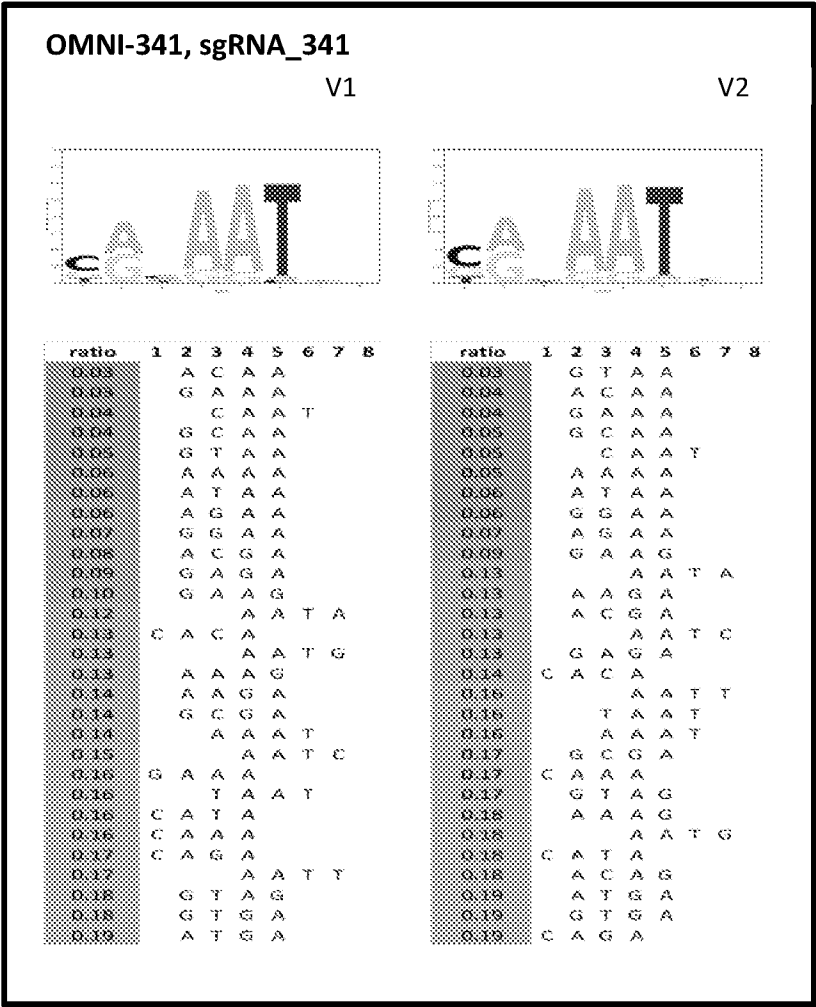


Fig. 67

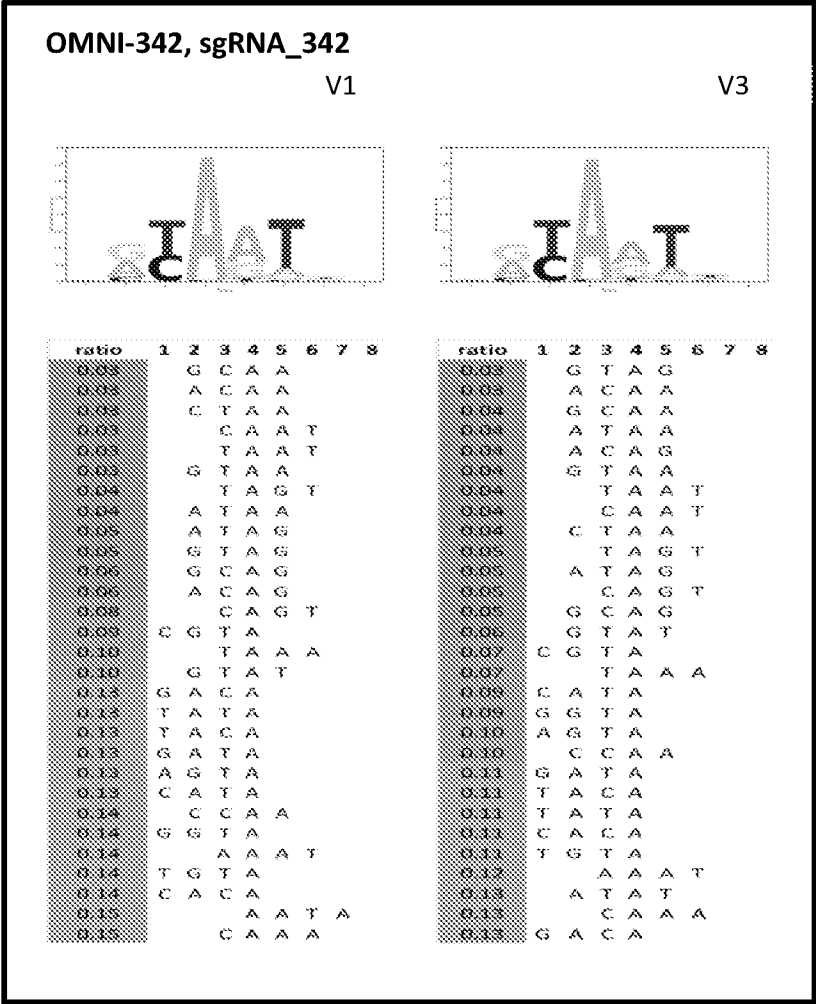


Fig. 68

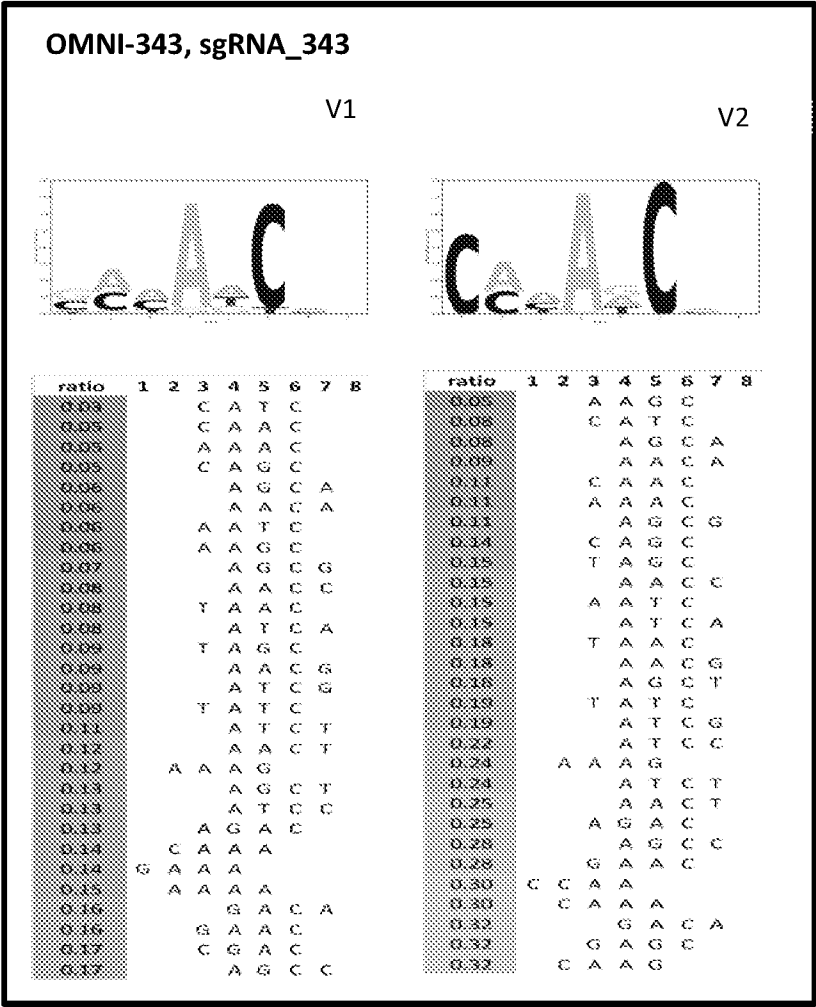


Fig. 69

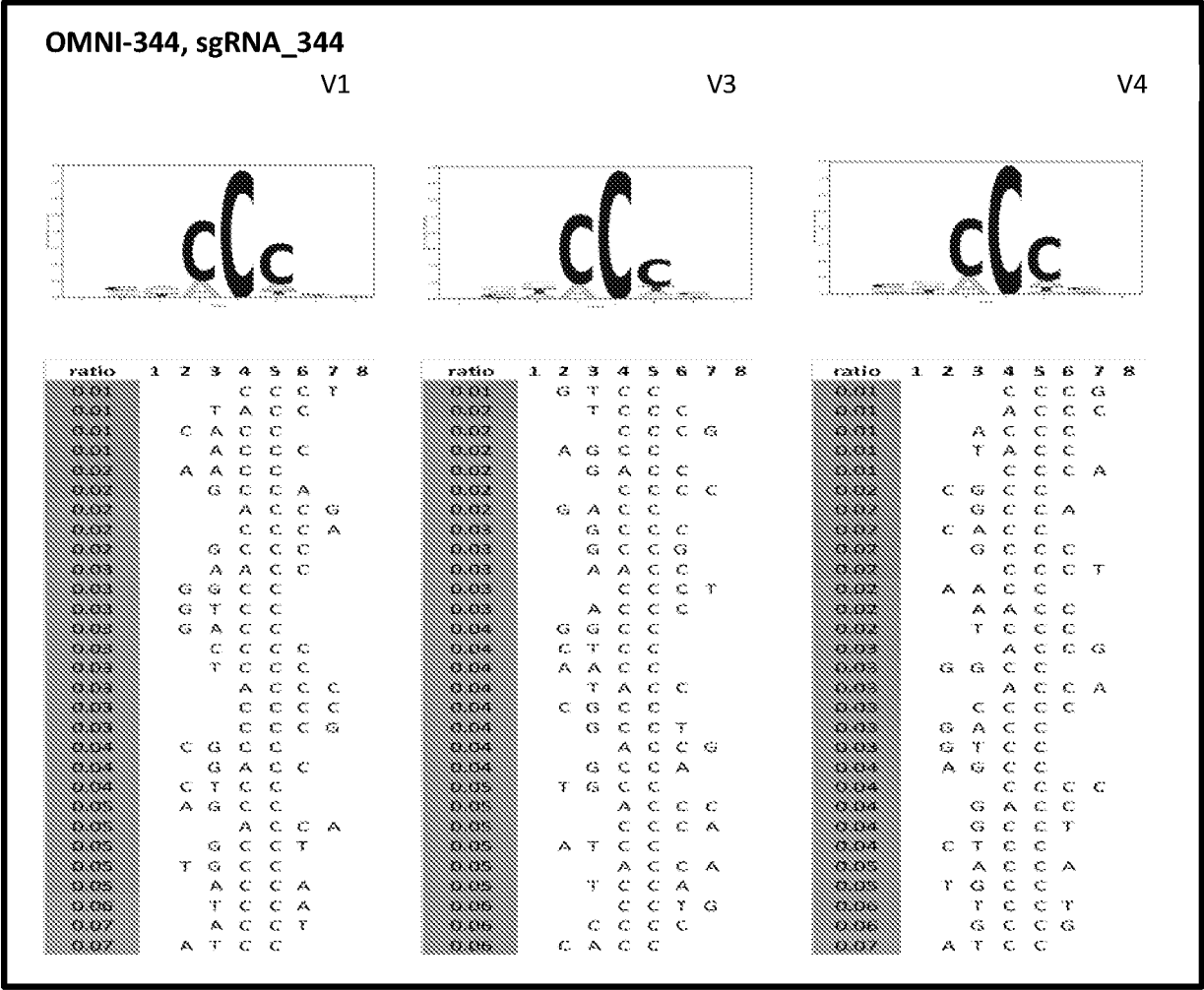


Fig. 70

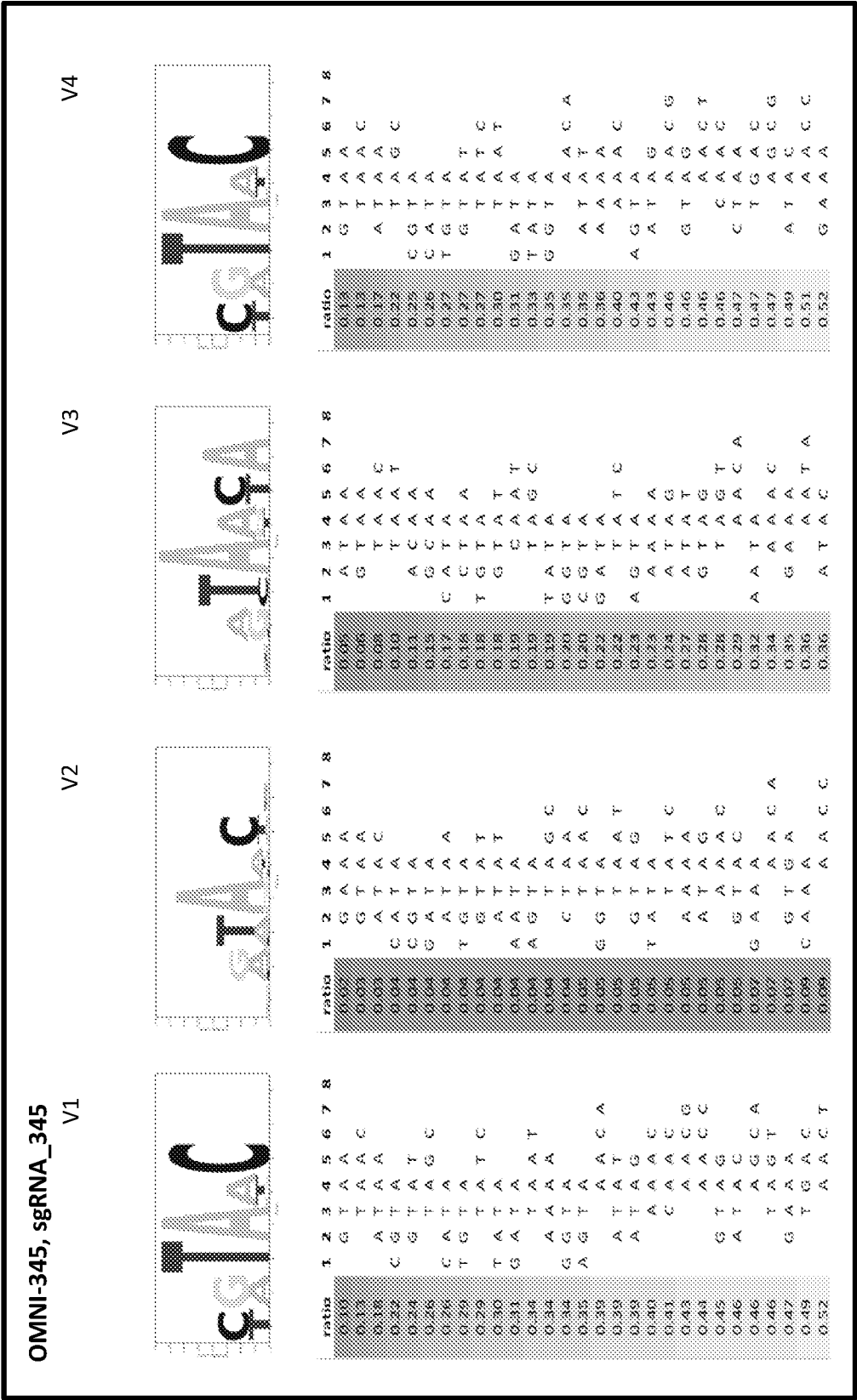


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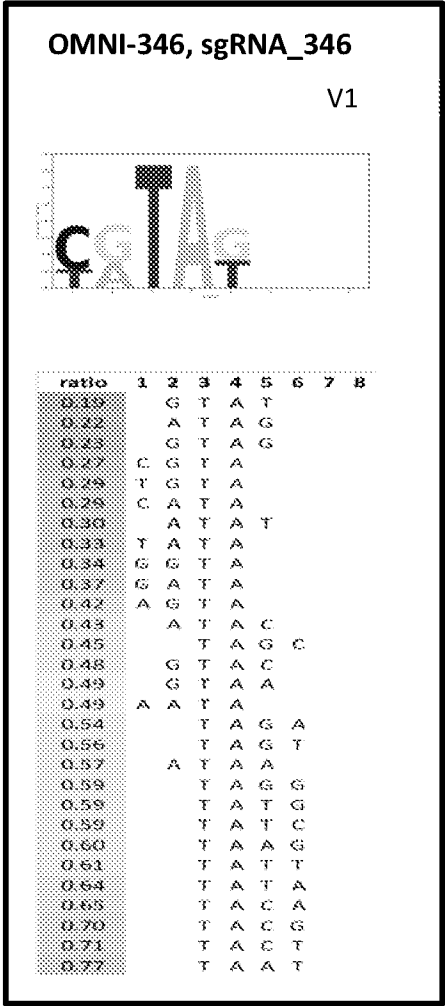


Fig. 72

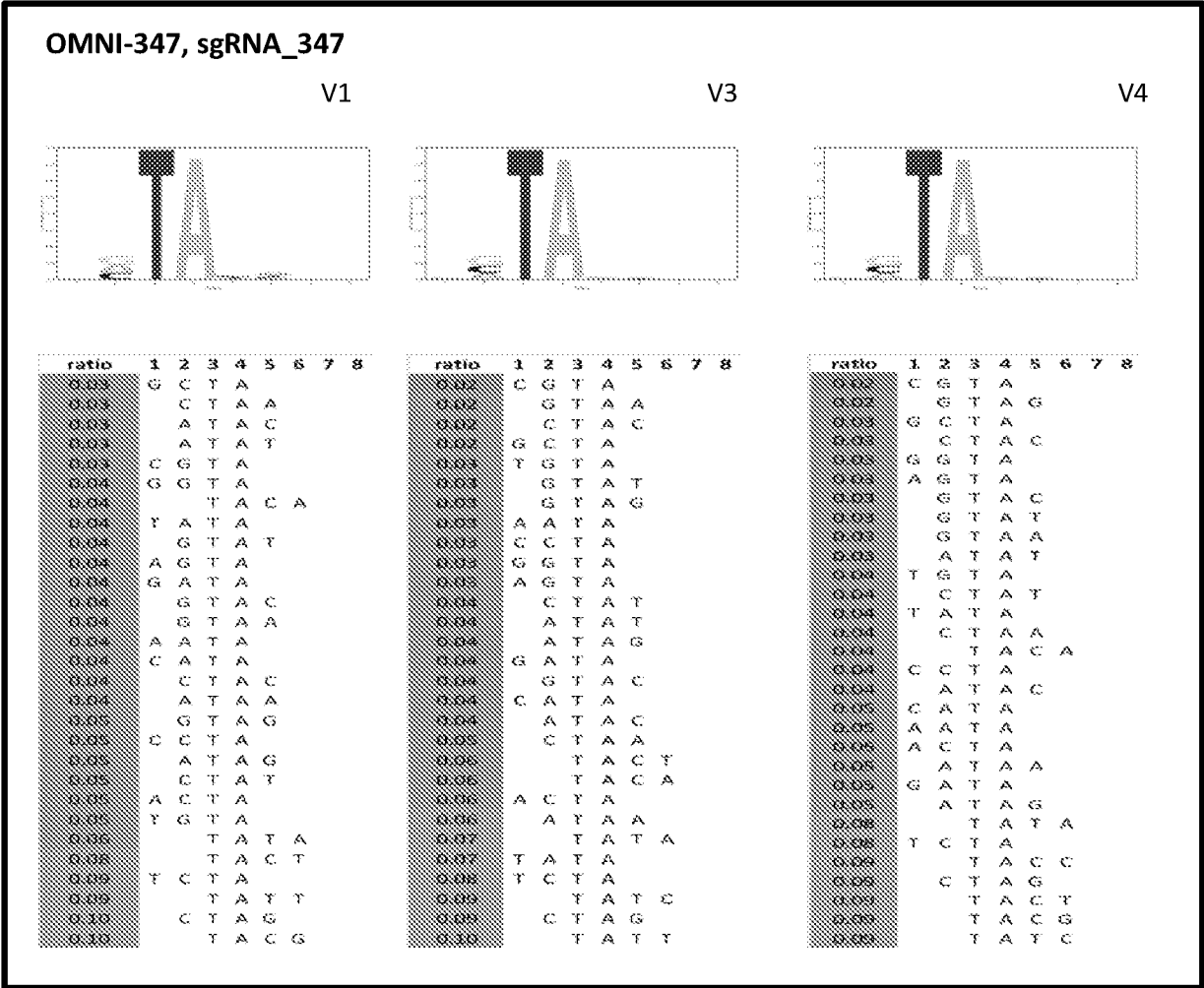


Fig. 73

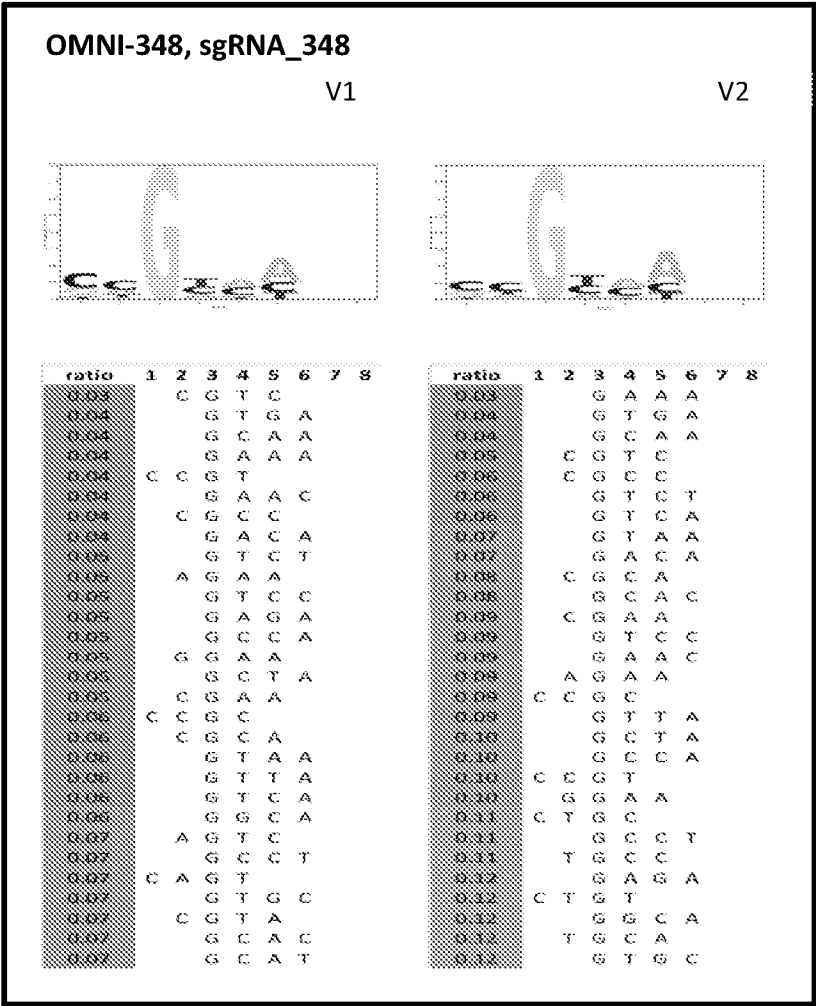


Fig. 74

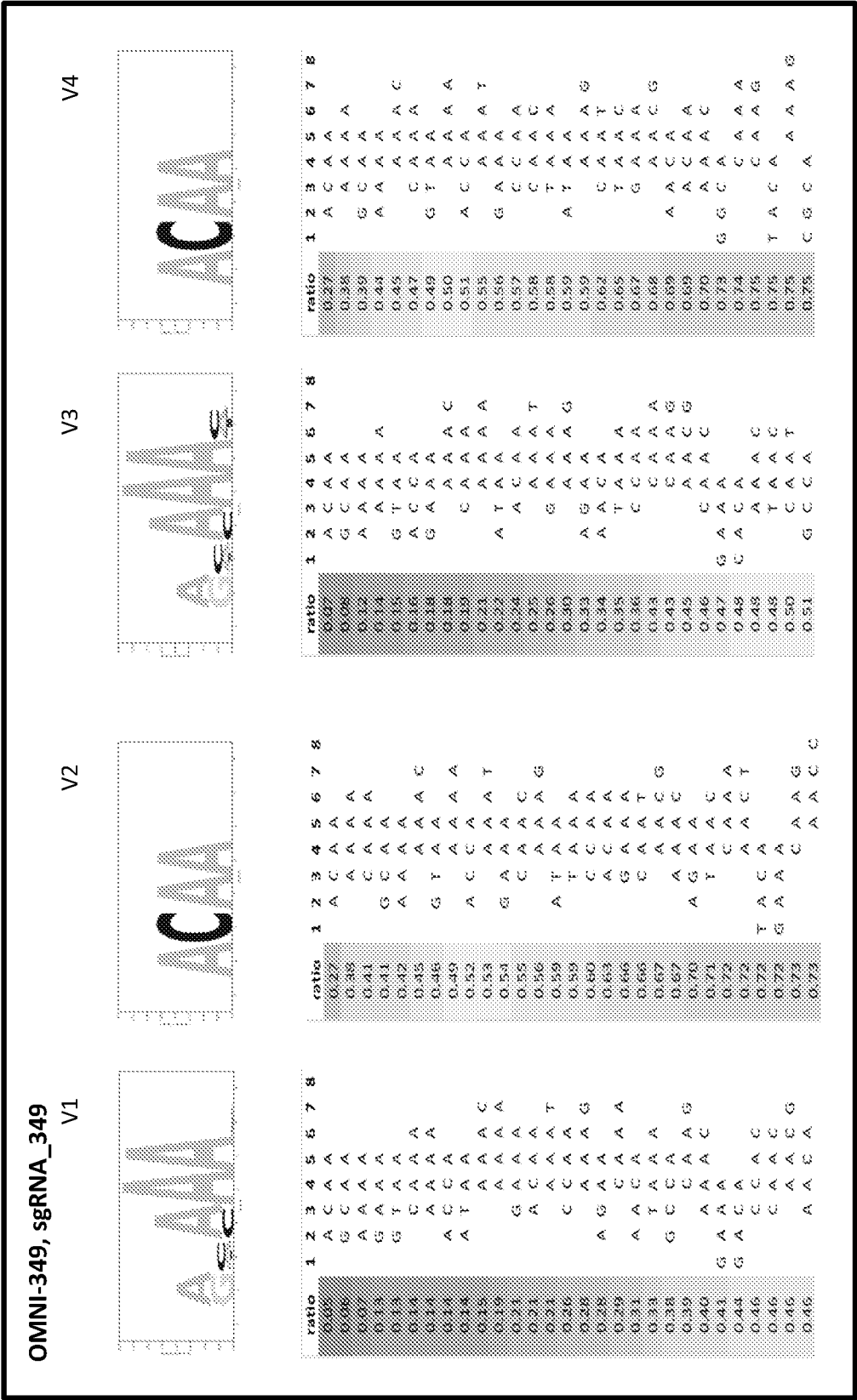


Fig. 75

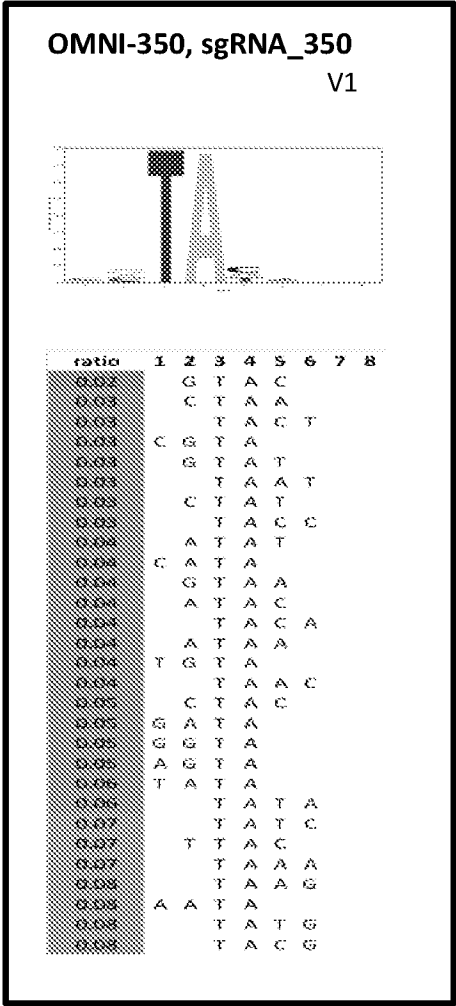


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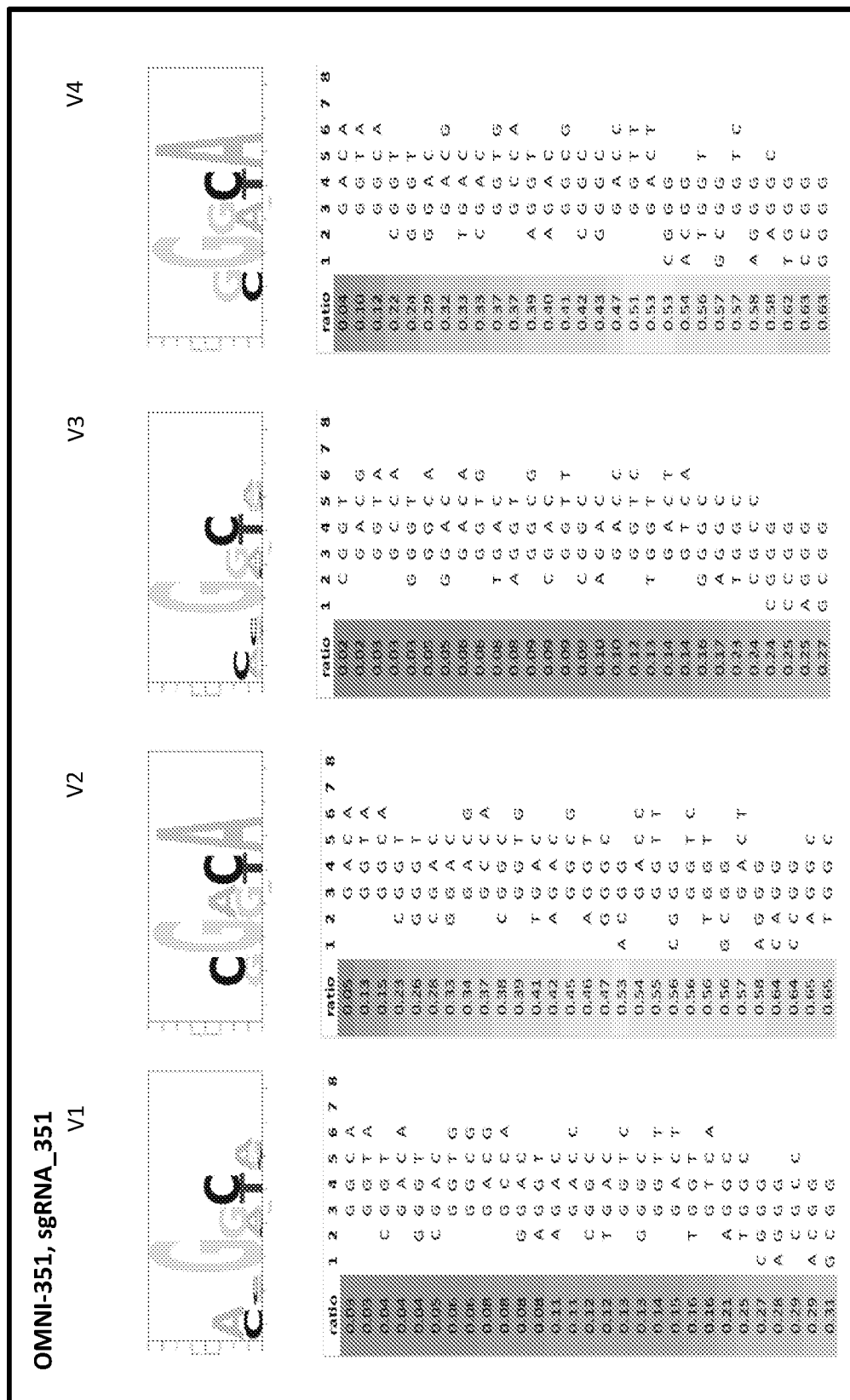


Fig. 77

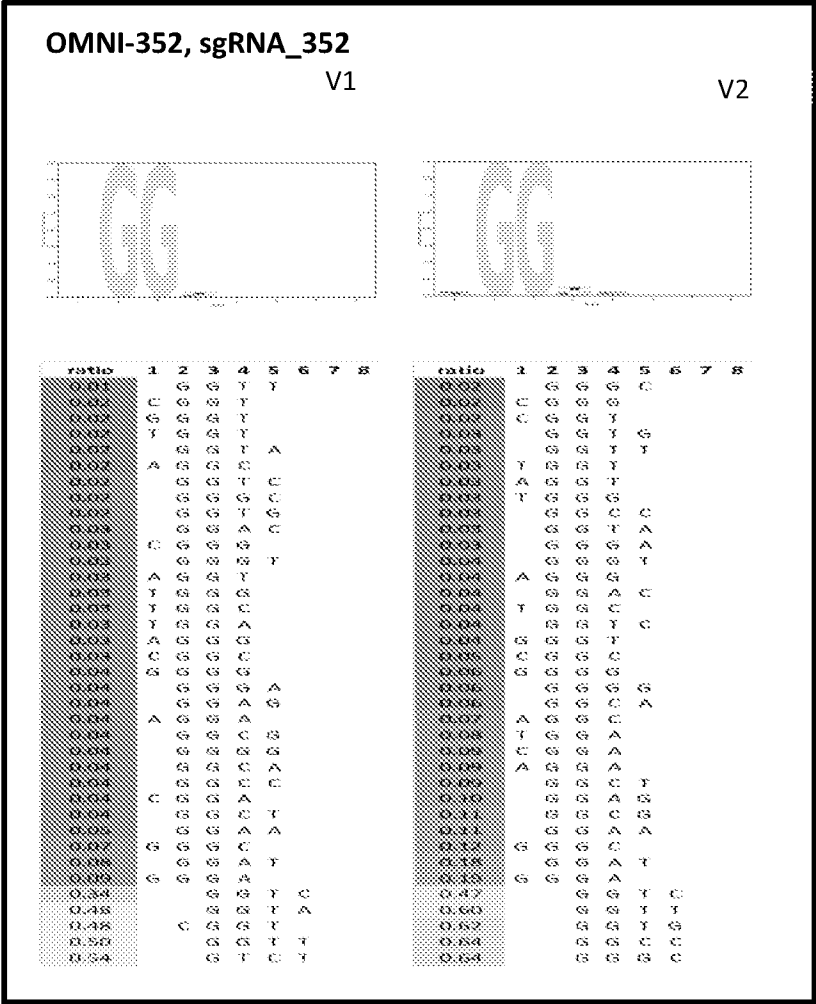


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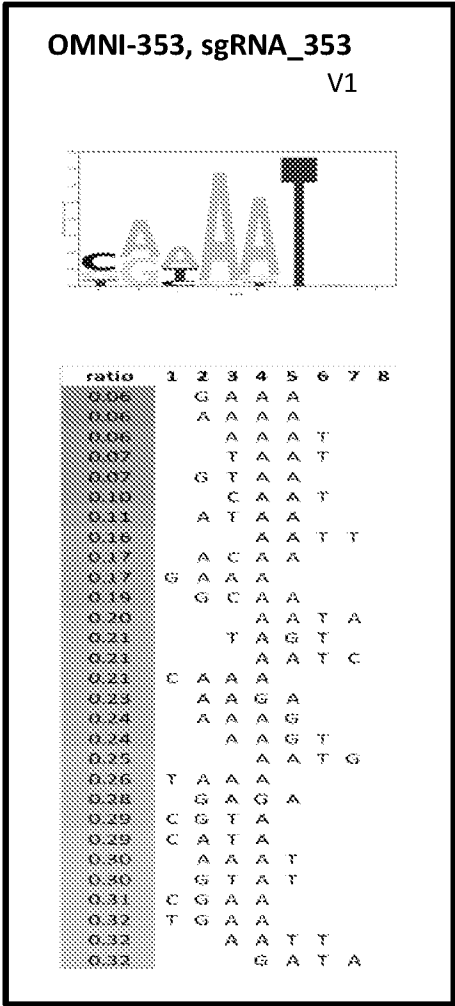


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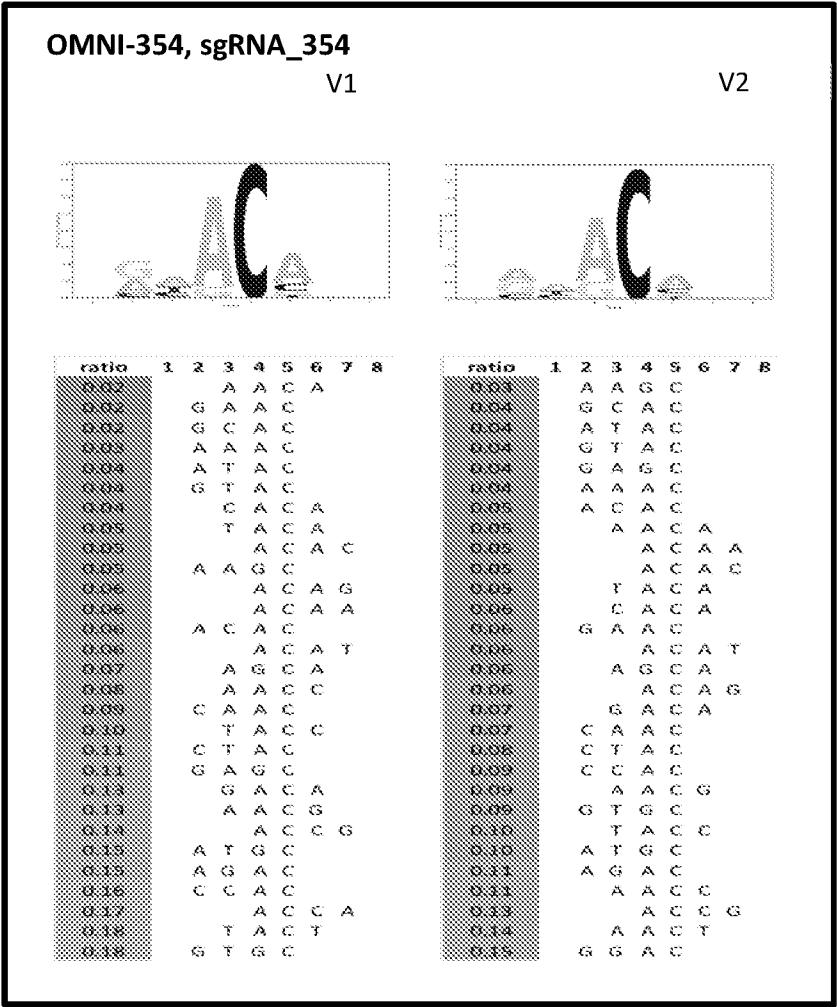


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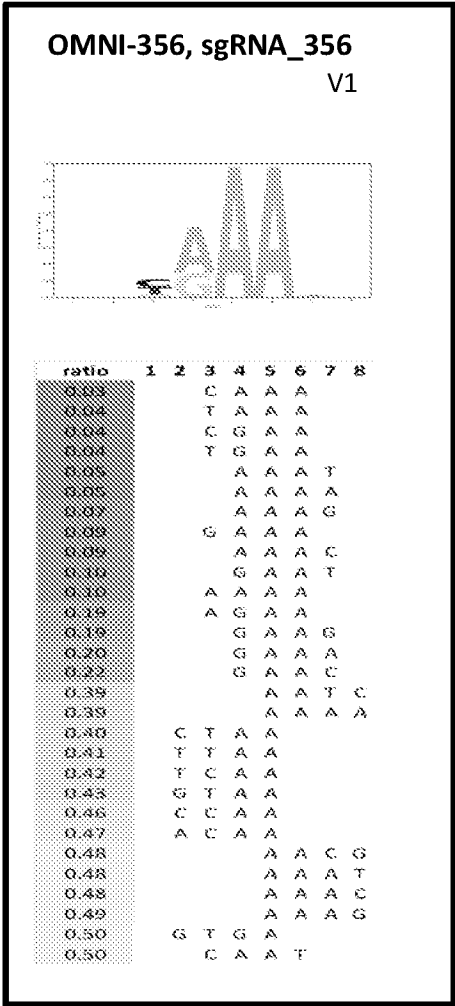


Fig. 81

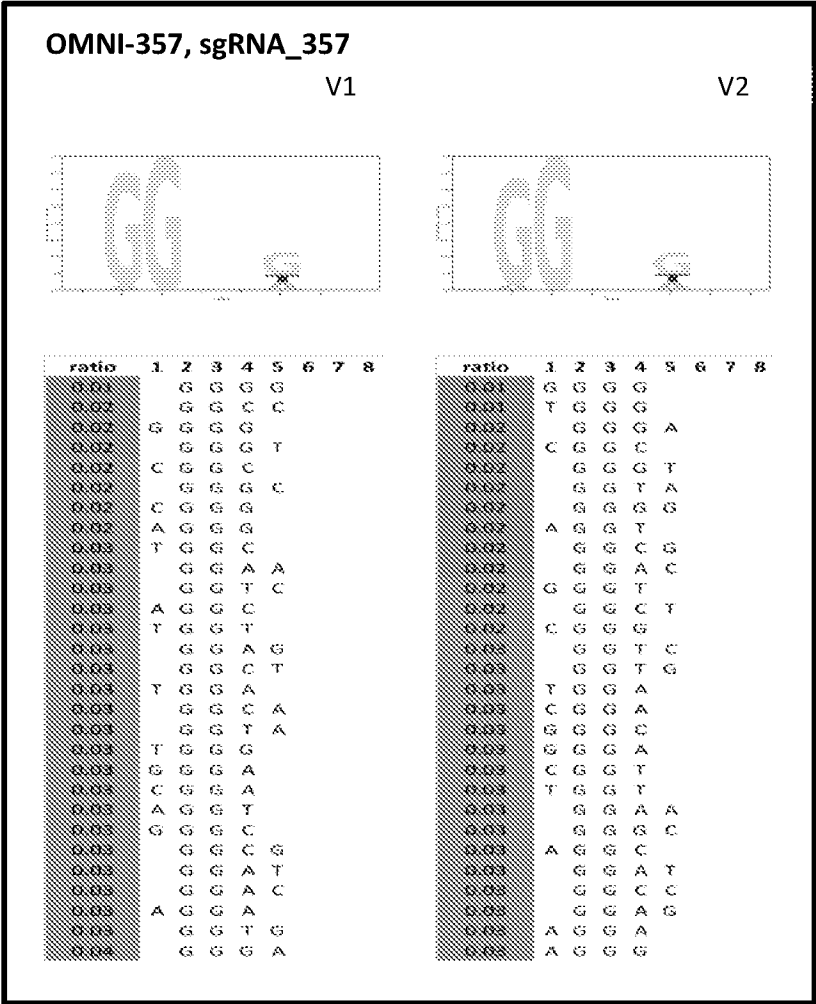


Fig. 82

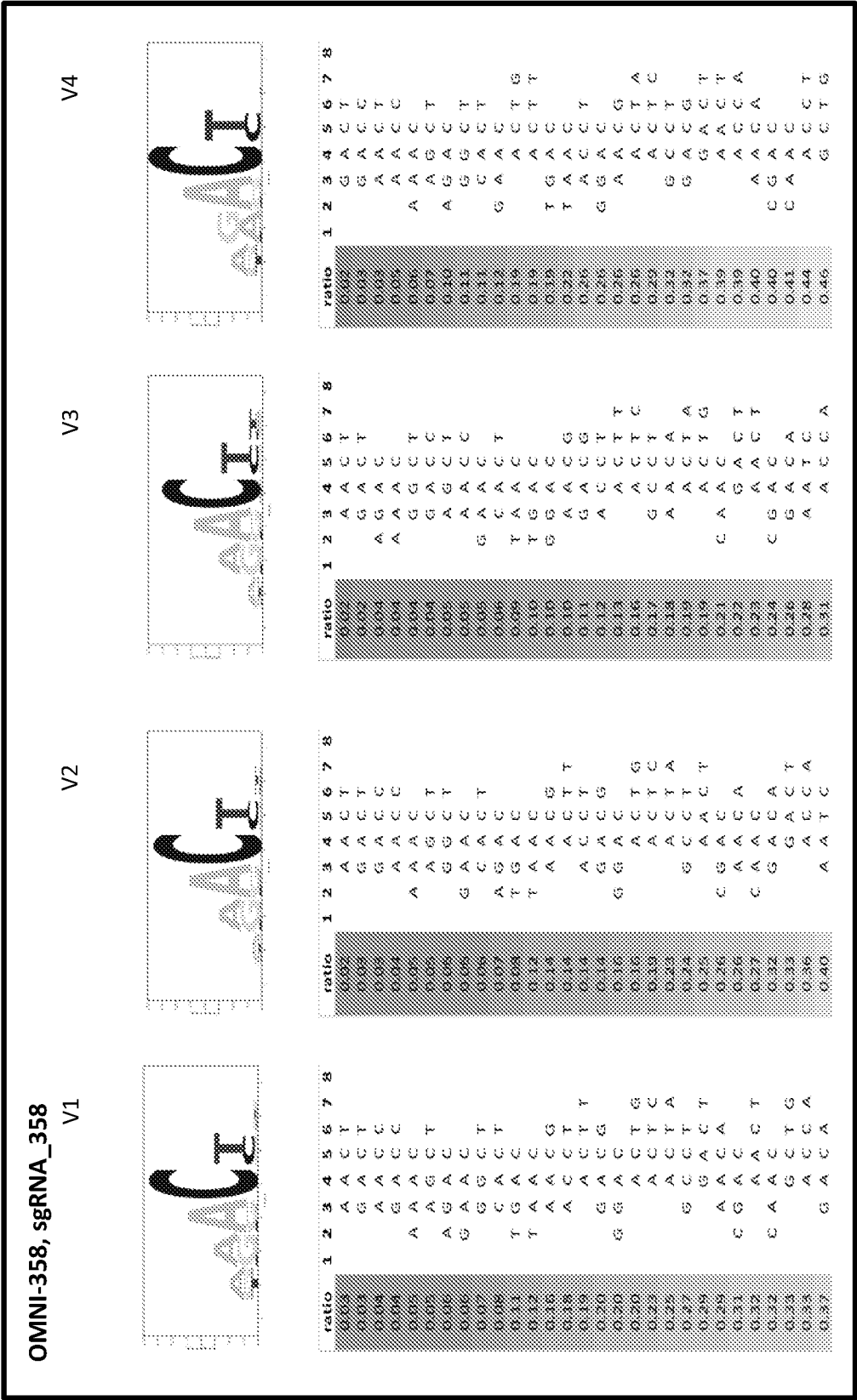


Fig. 83

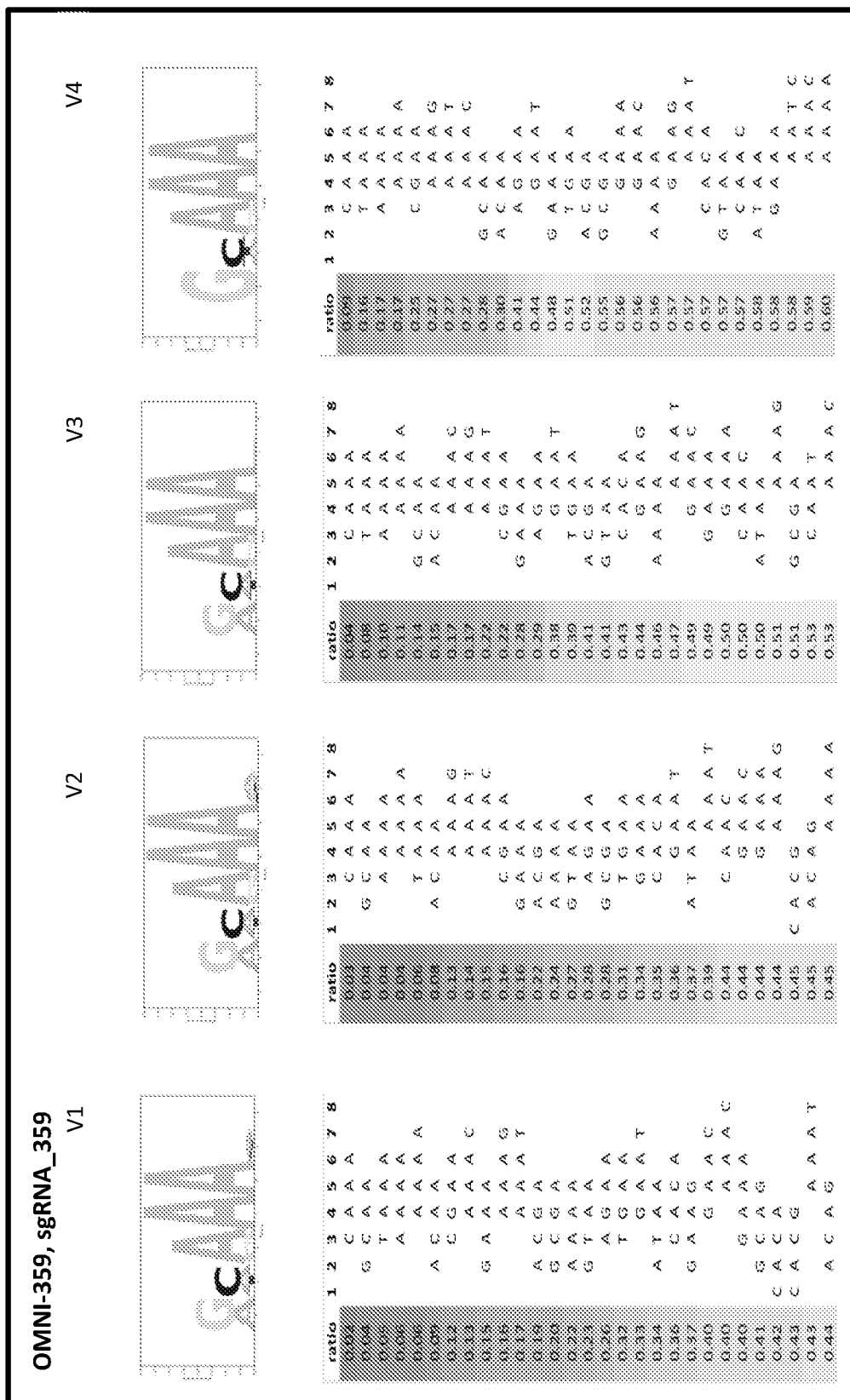


Fig. 84

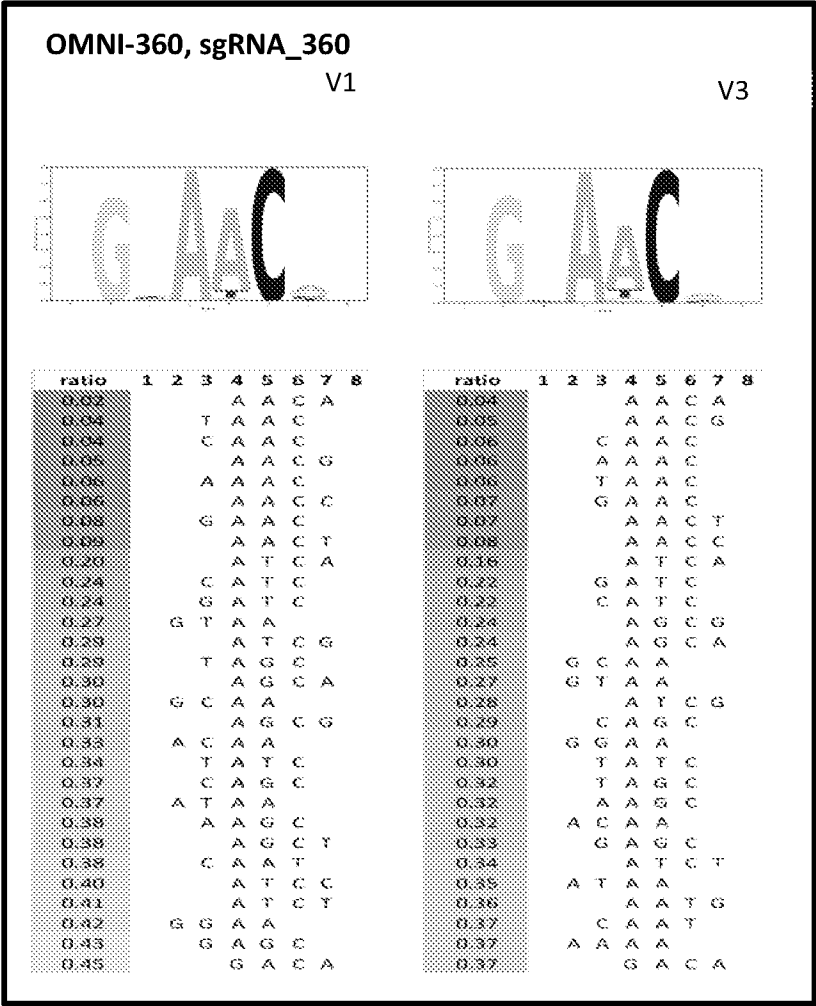


Fig. 85

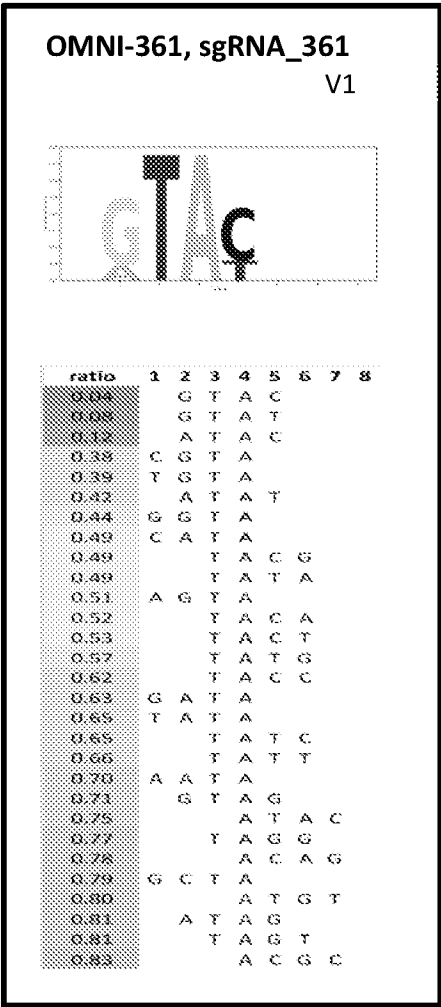


Fig. 86

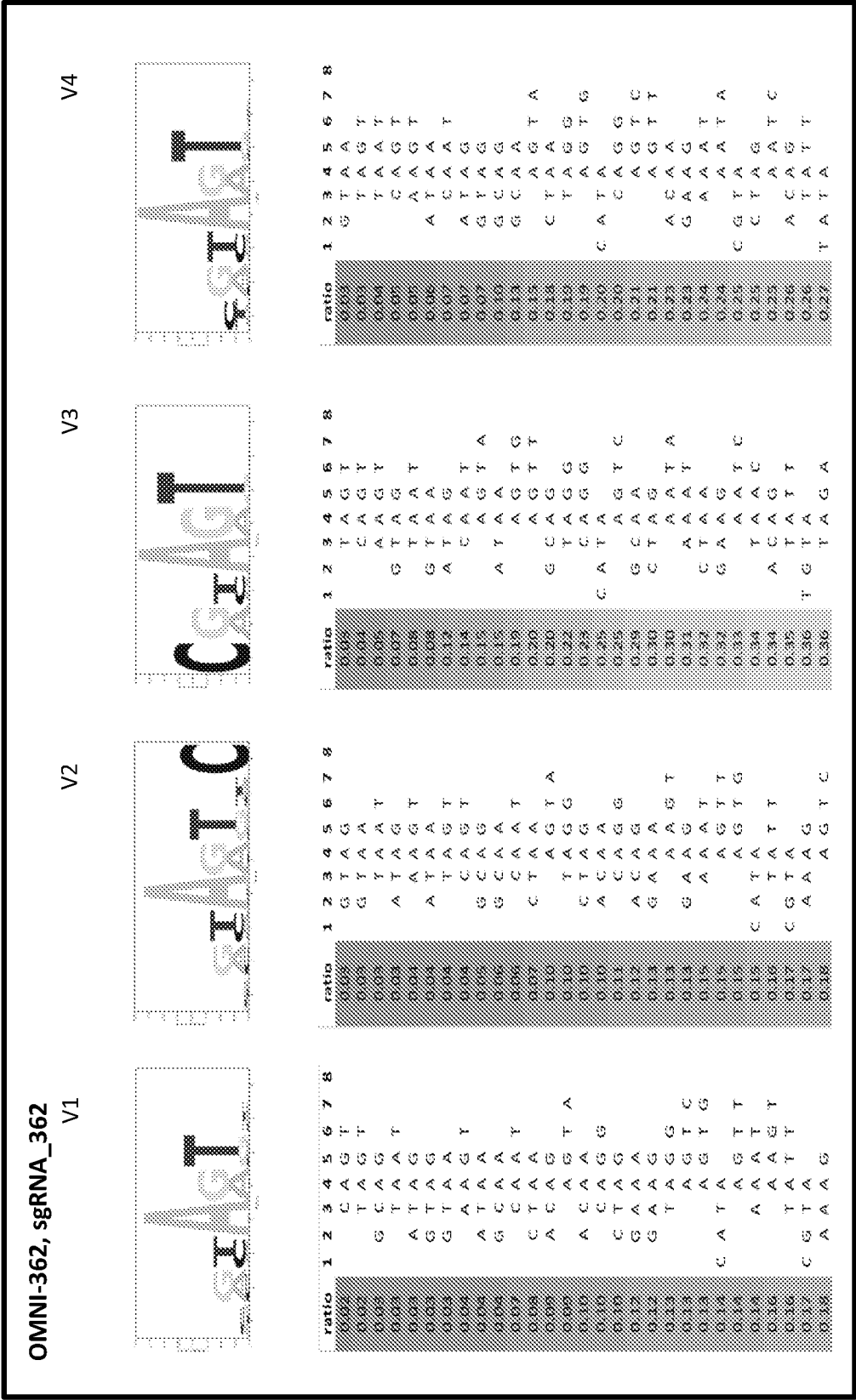


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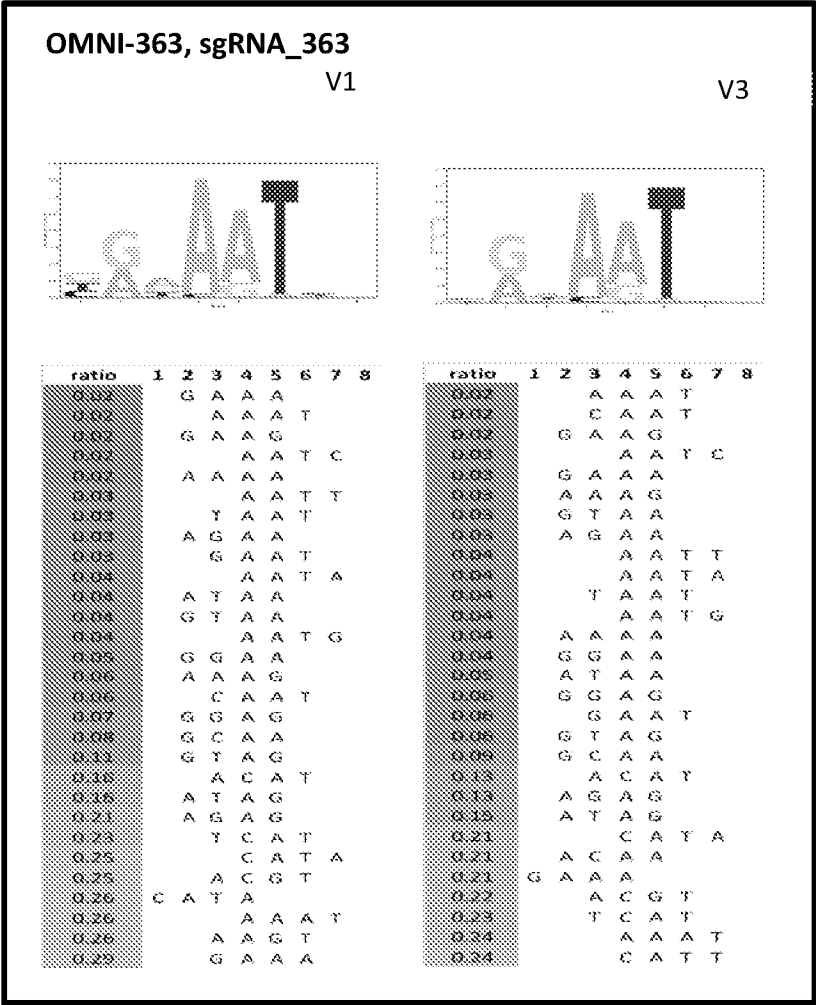


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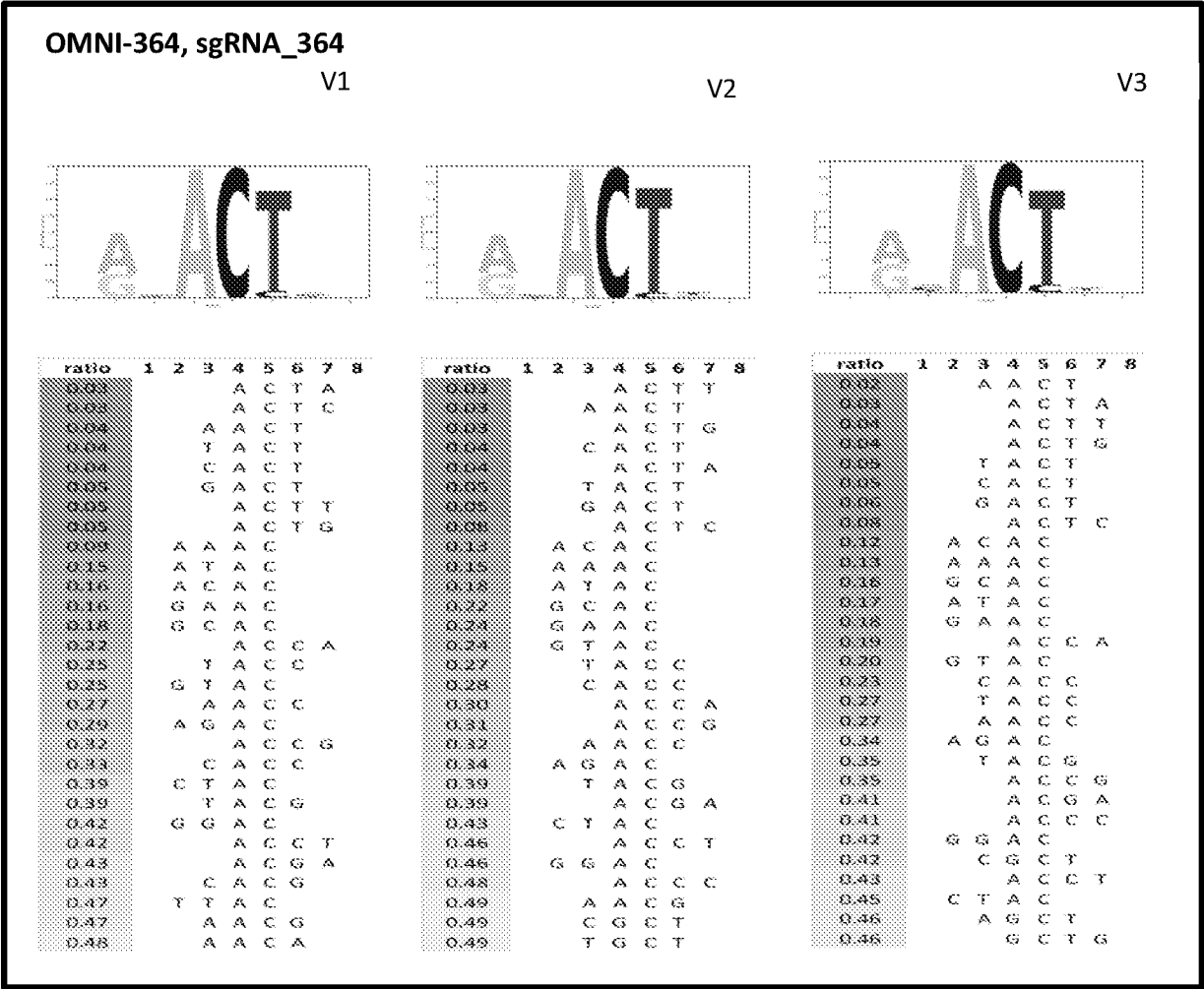


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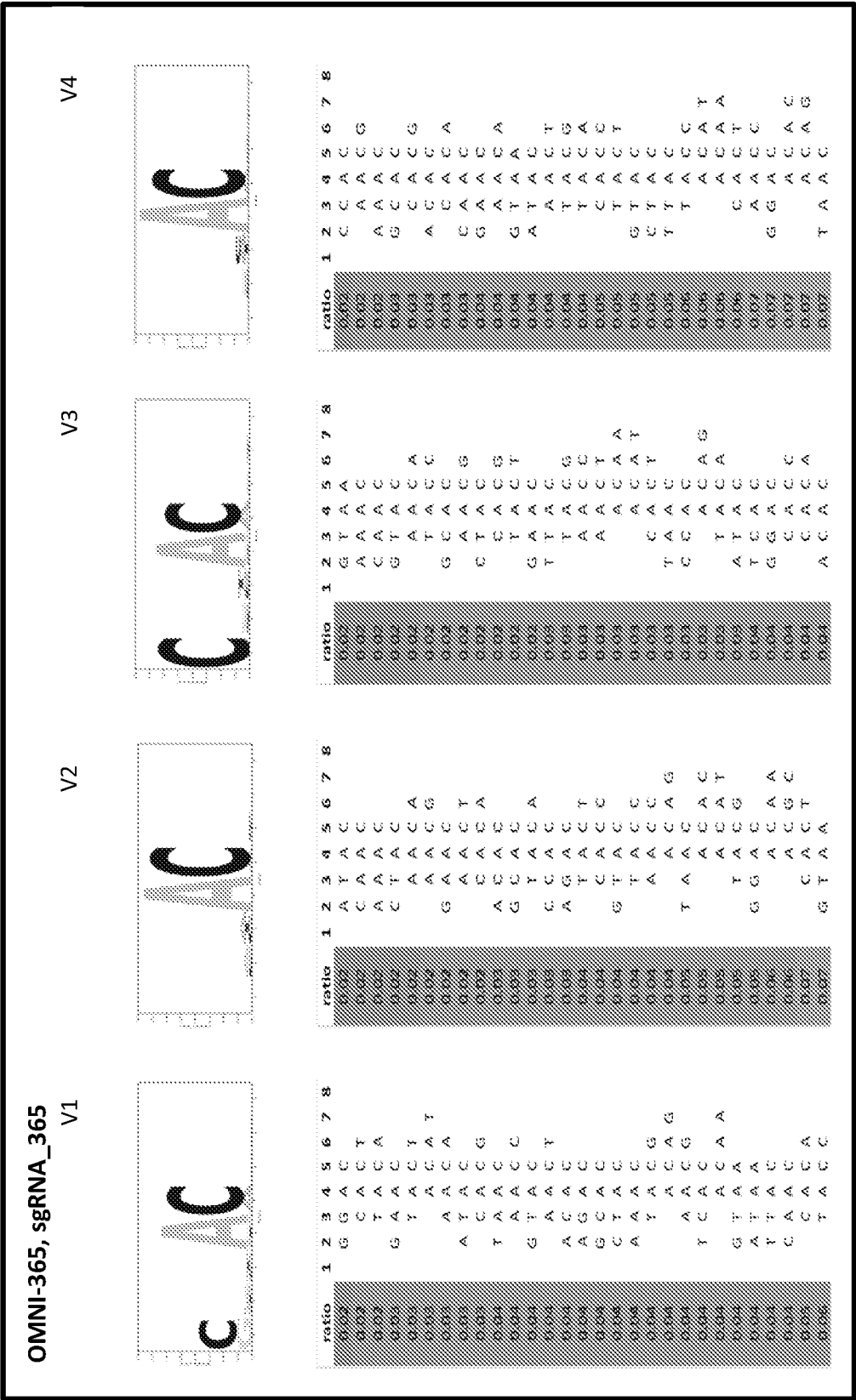


Fig. 90

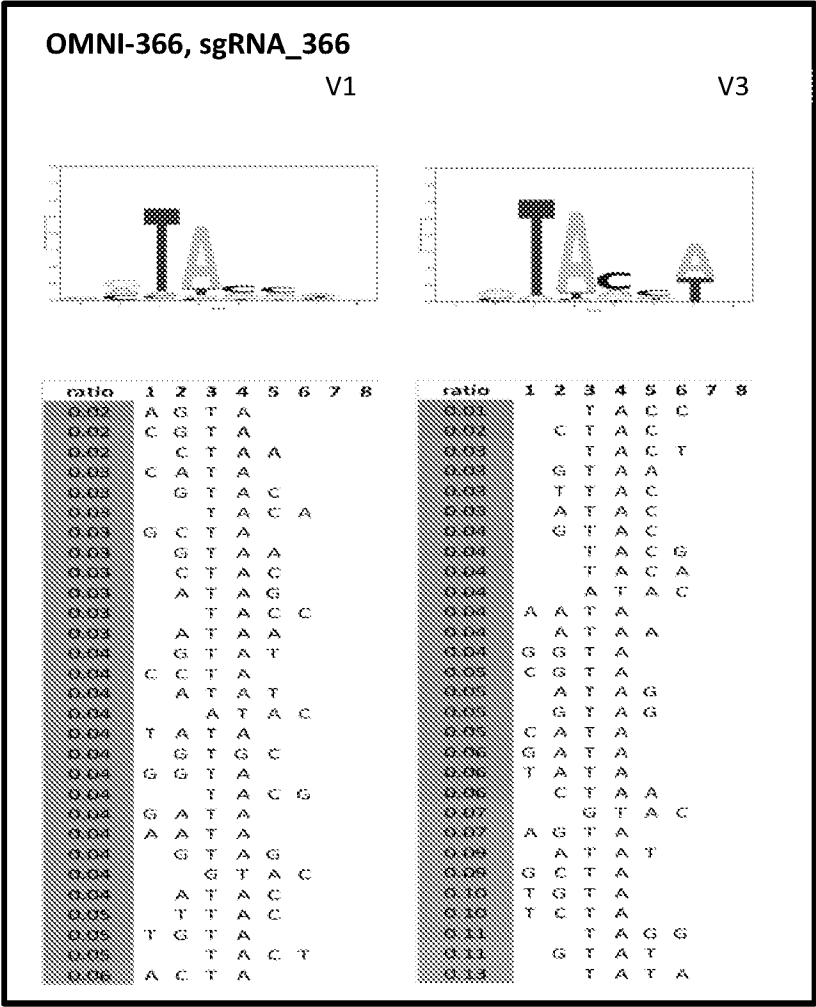


Fig. 91

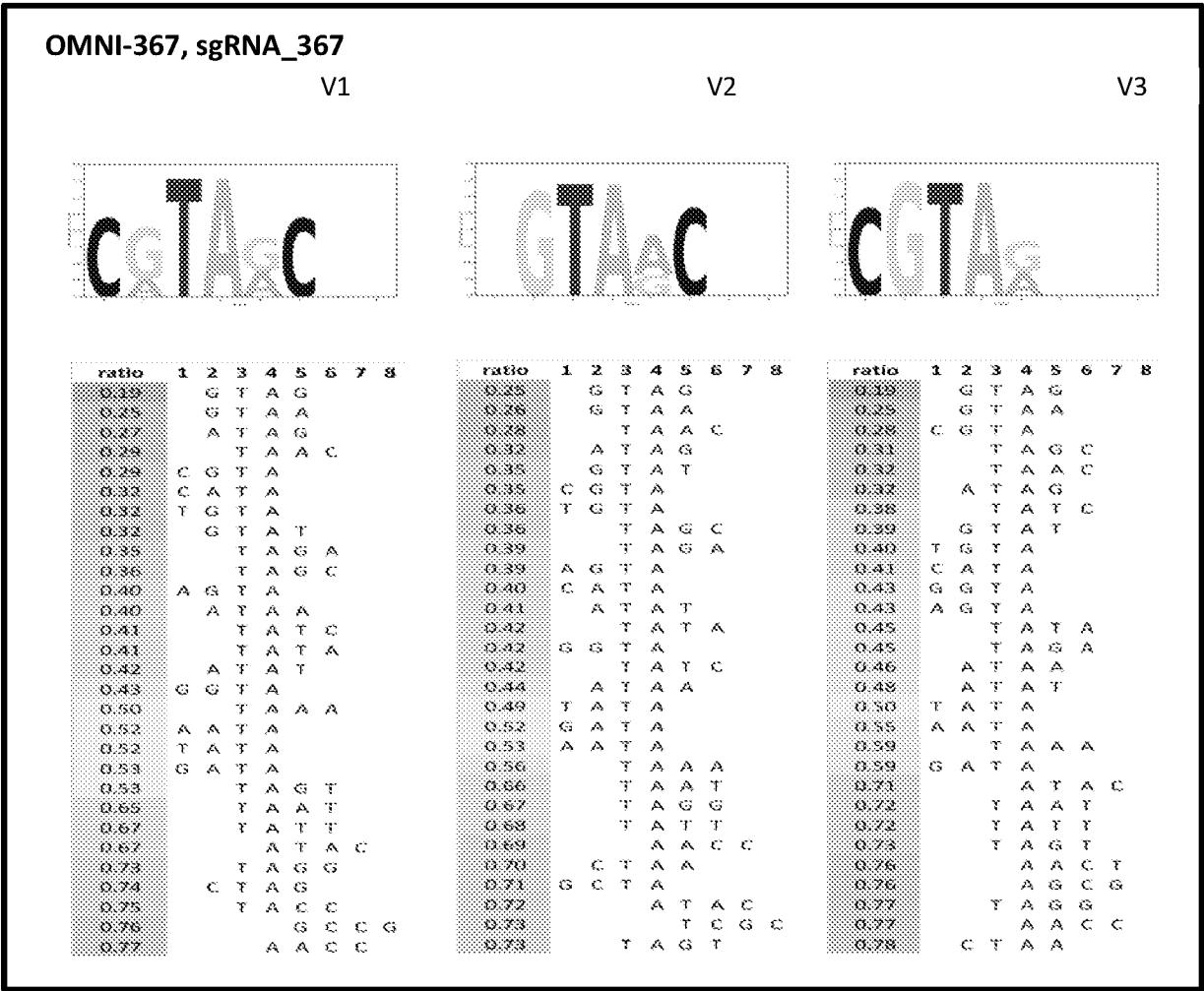


Fig. 92

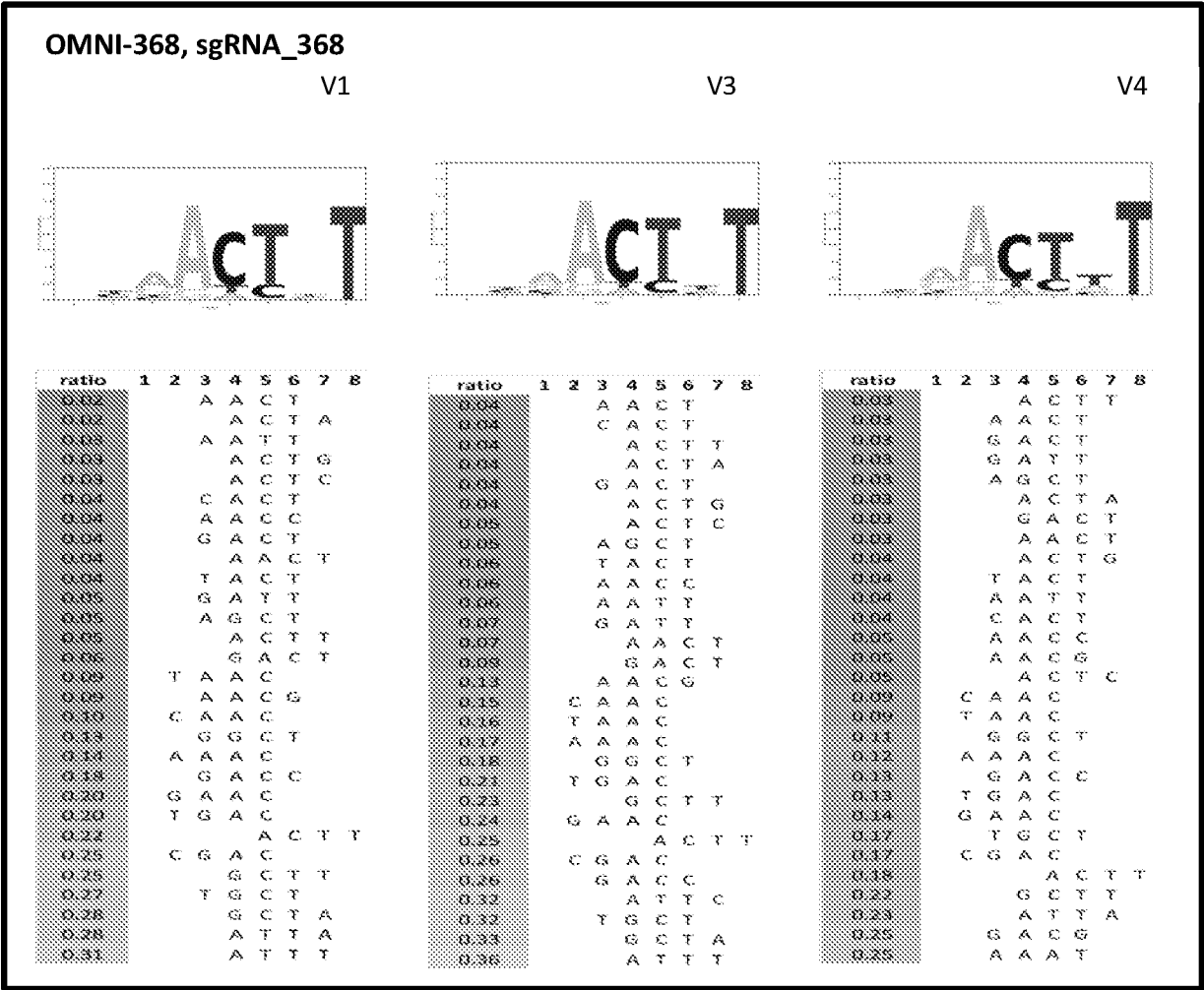


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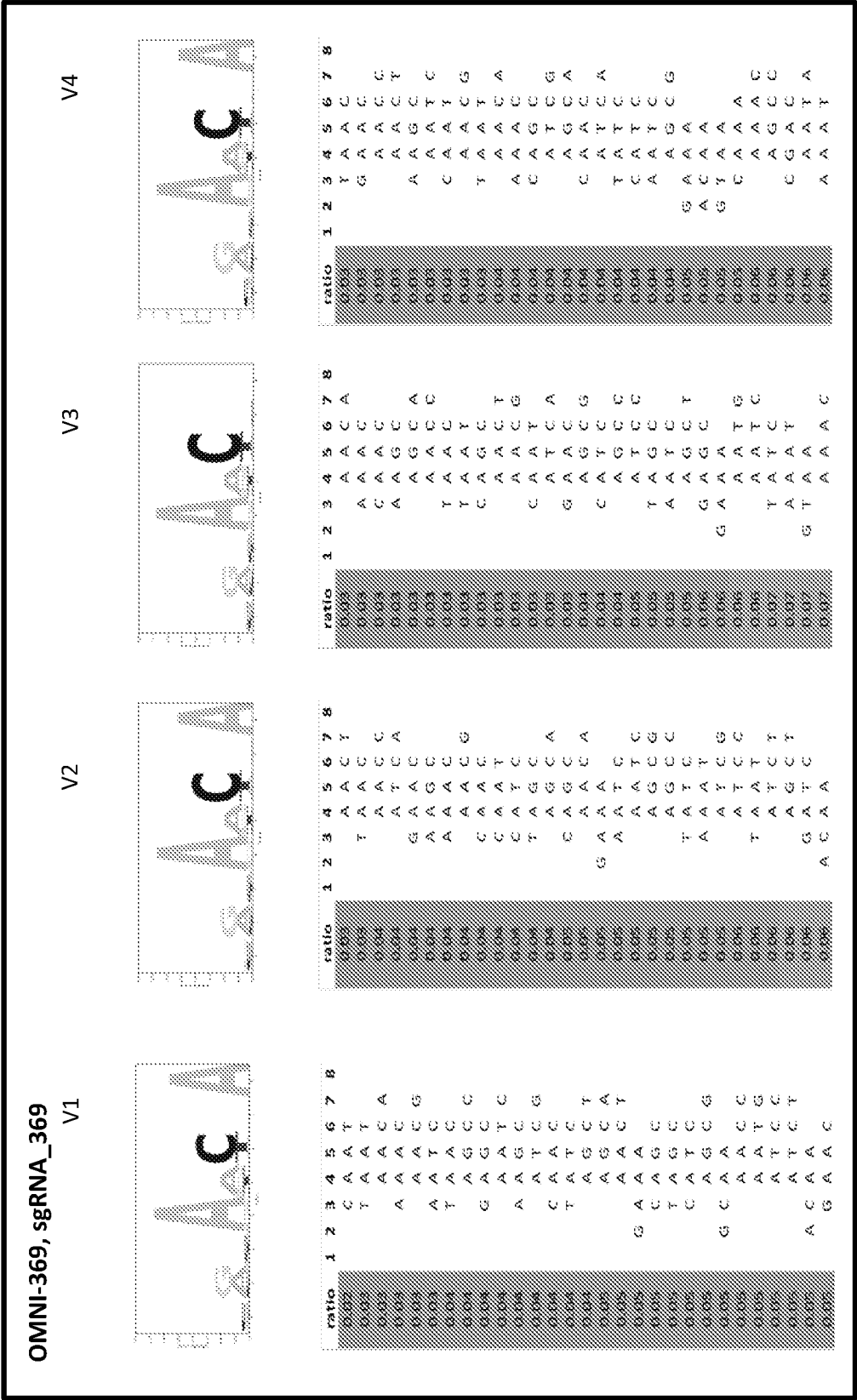


Fig. 94

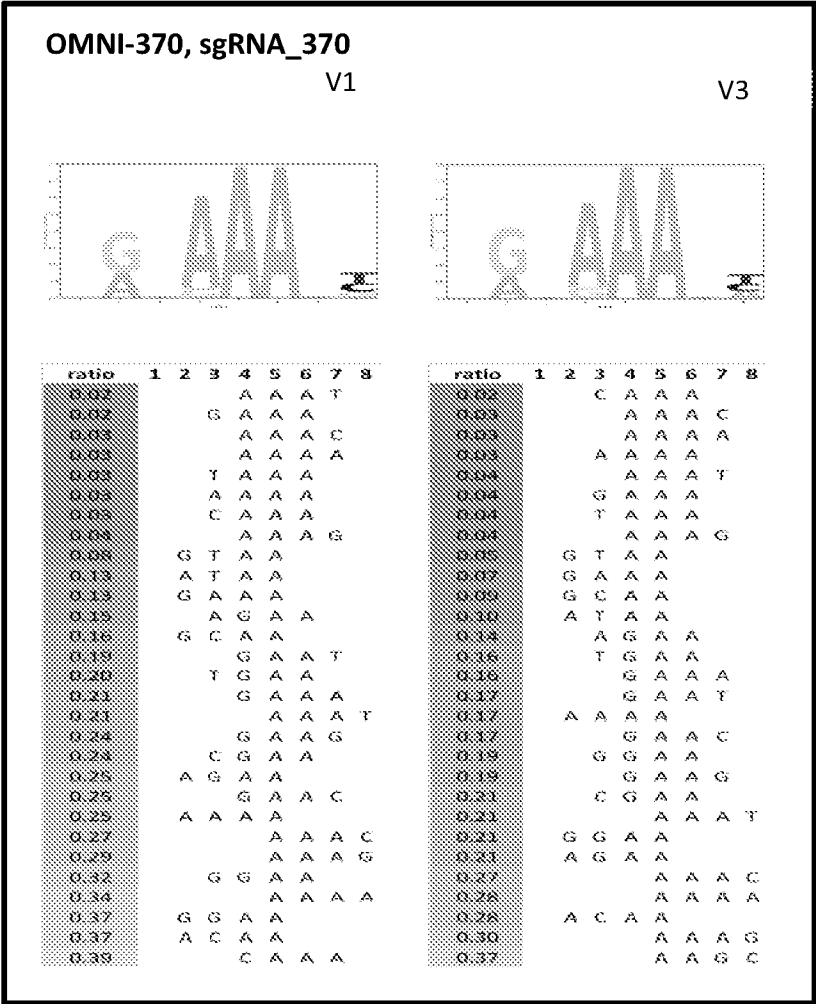


Fig. 95

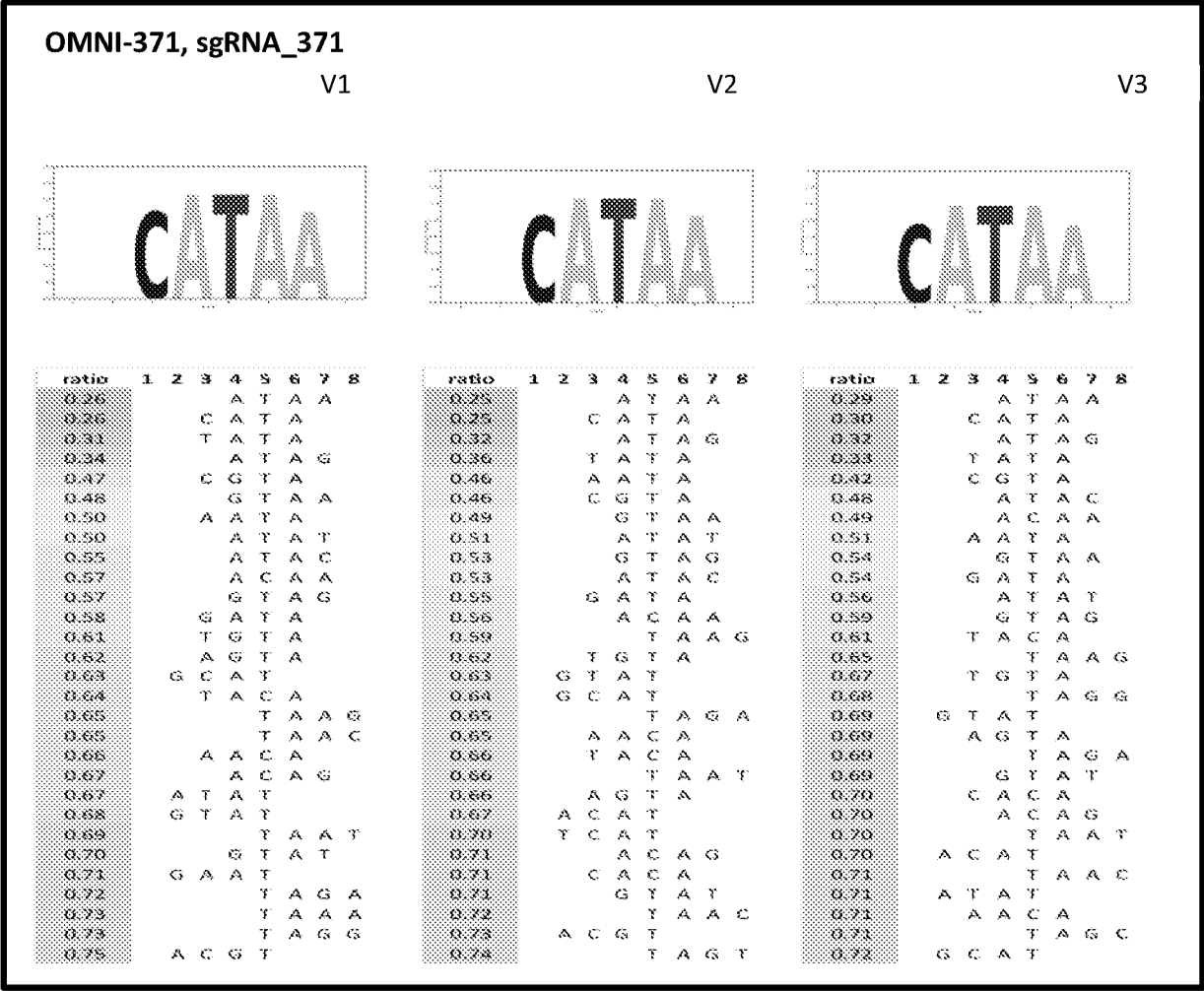


Fig. 96

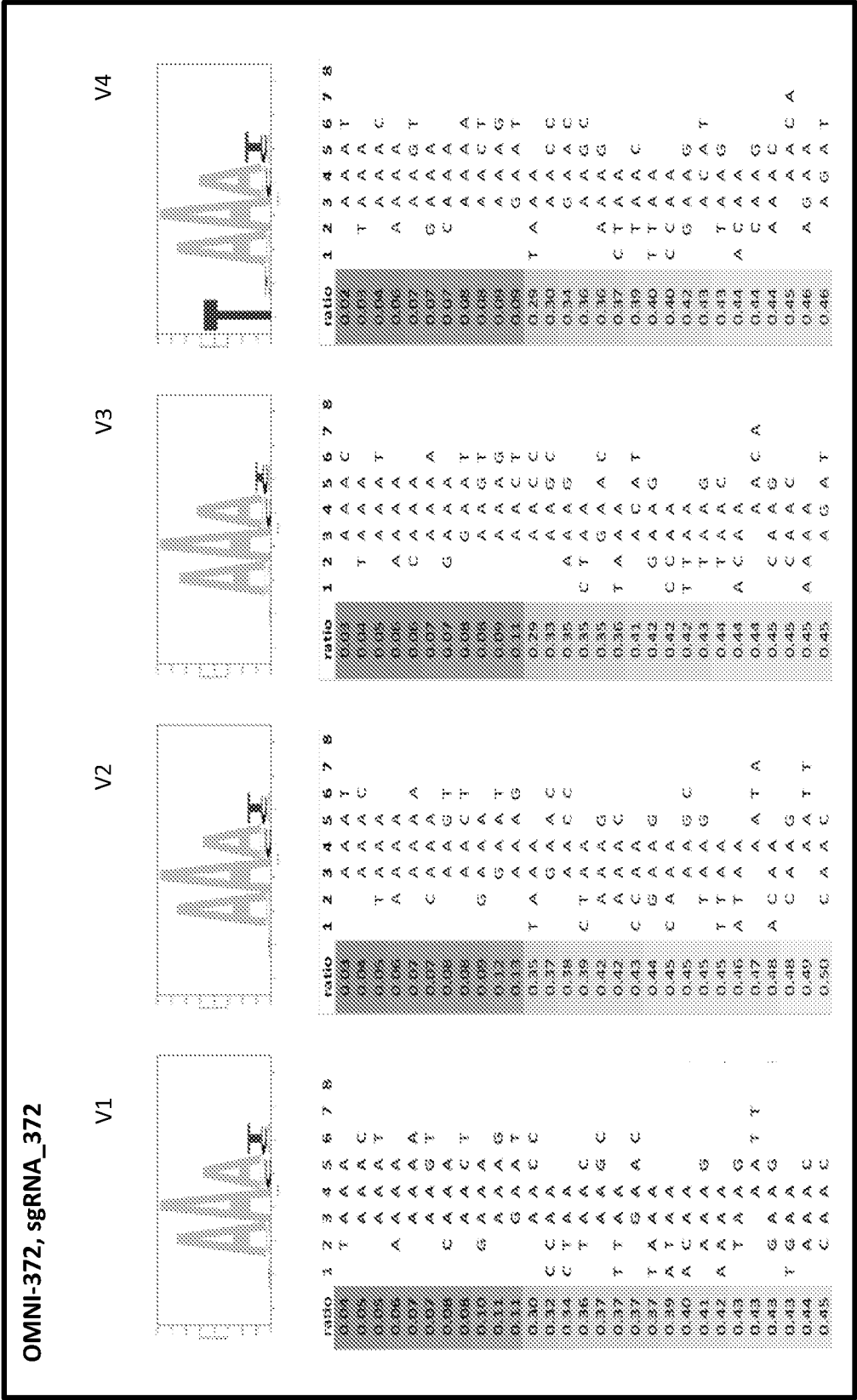


Fig. 97

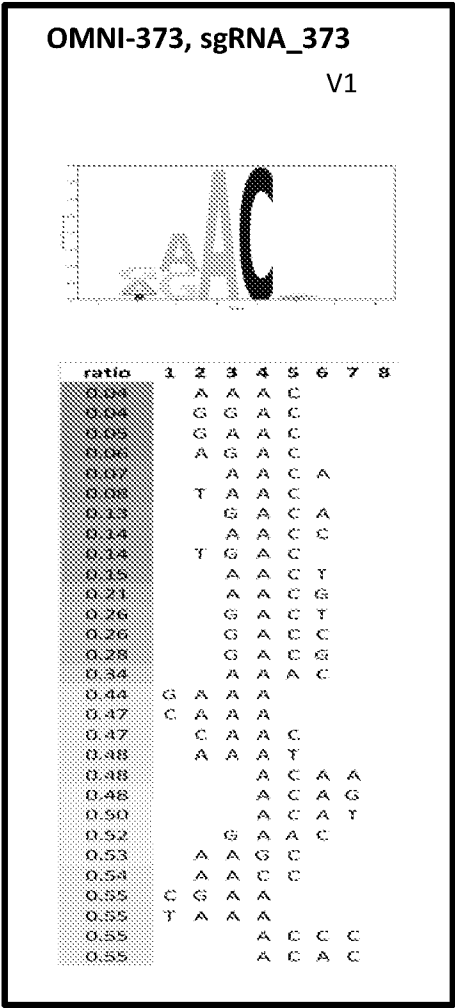


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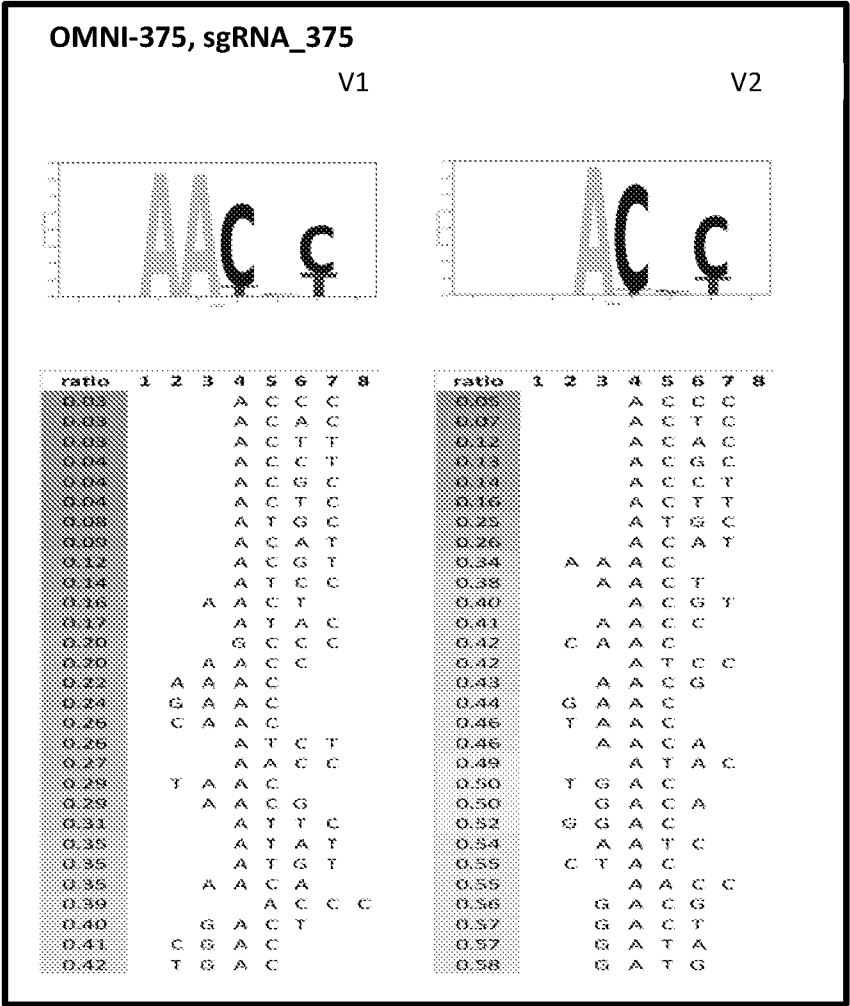


Fig. 99

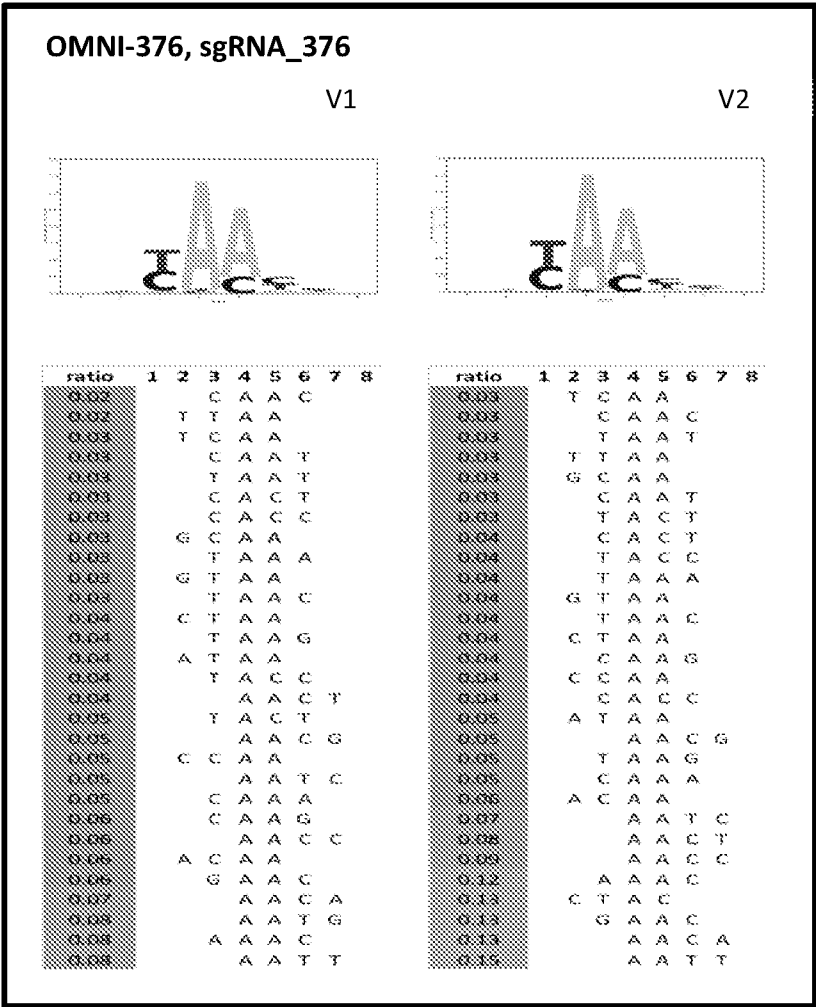


Fig. 100

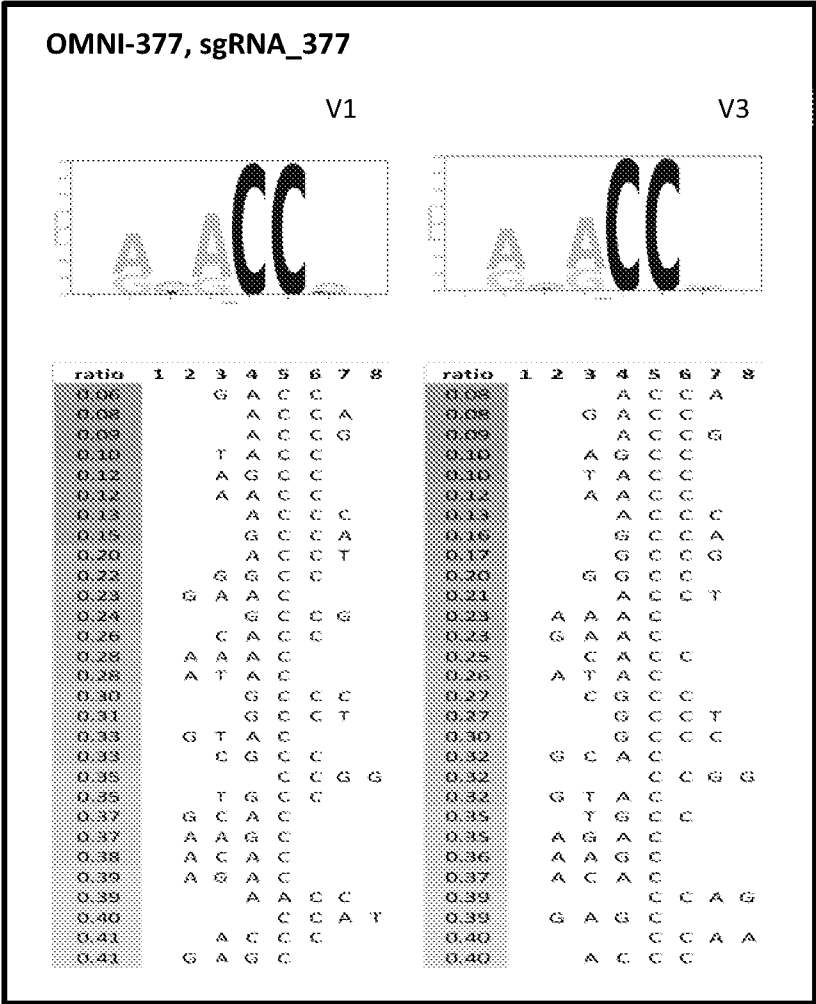


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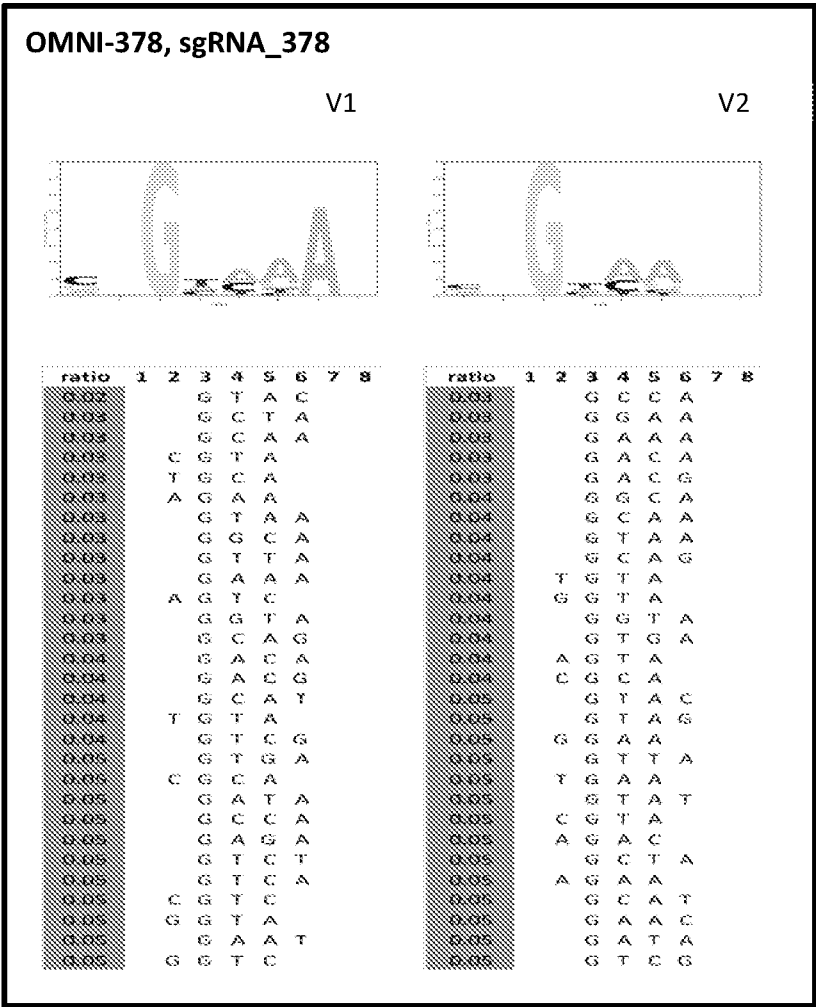


Fig. 102

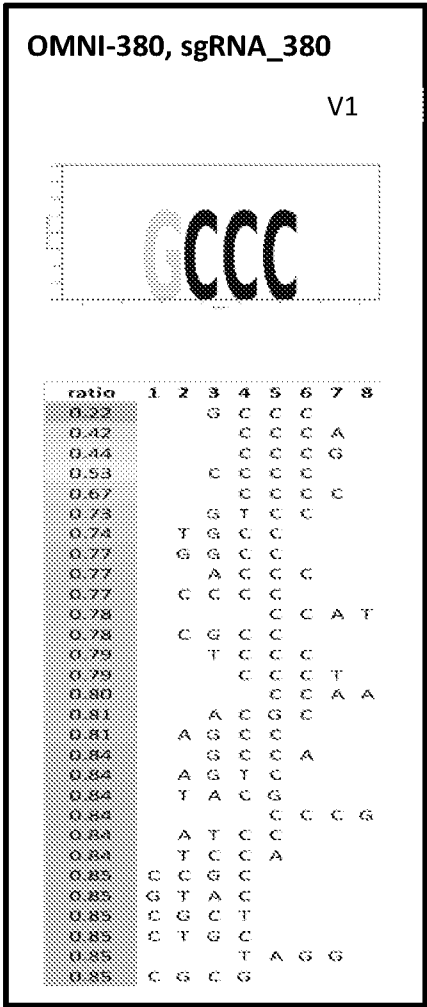


Fig. 103

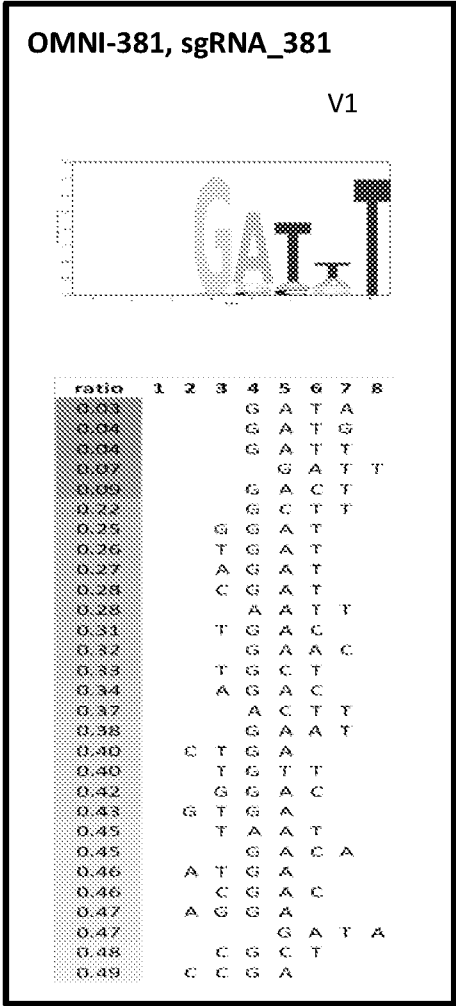


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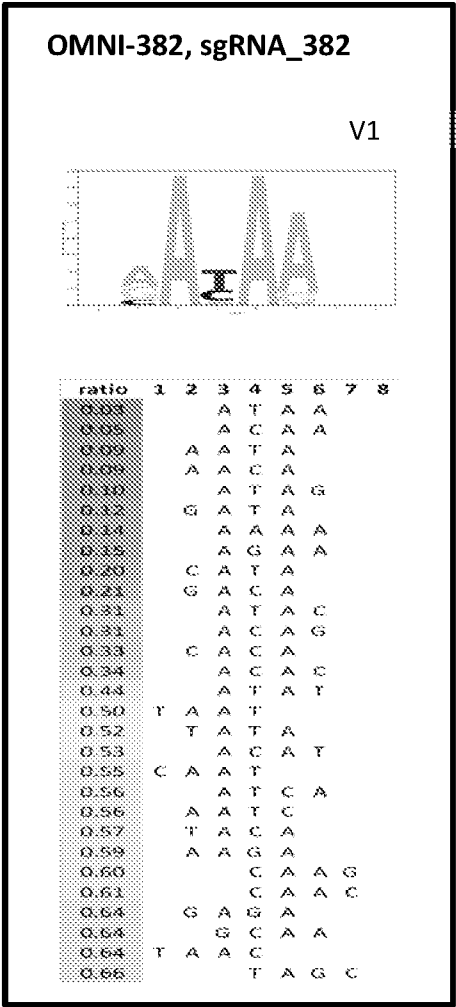


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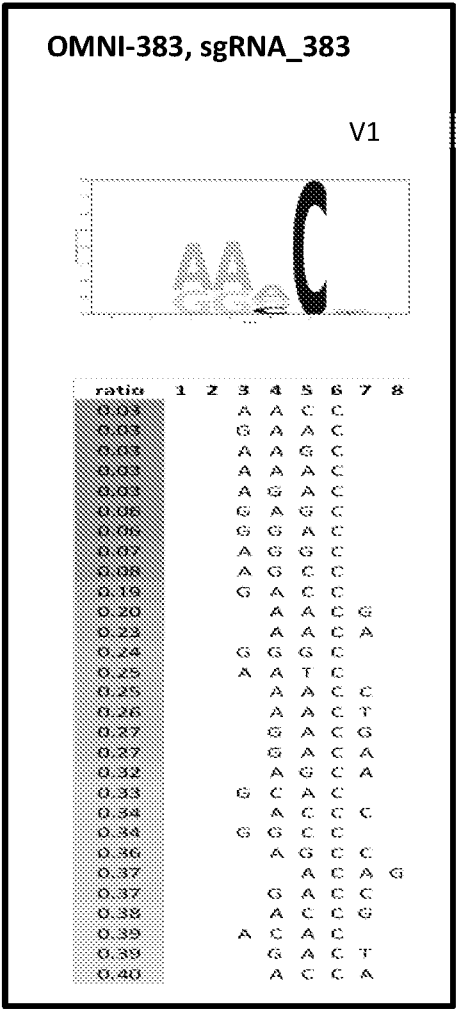


Fig. 106

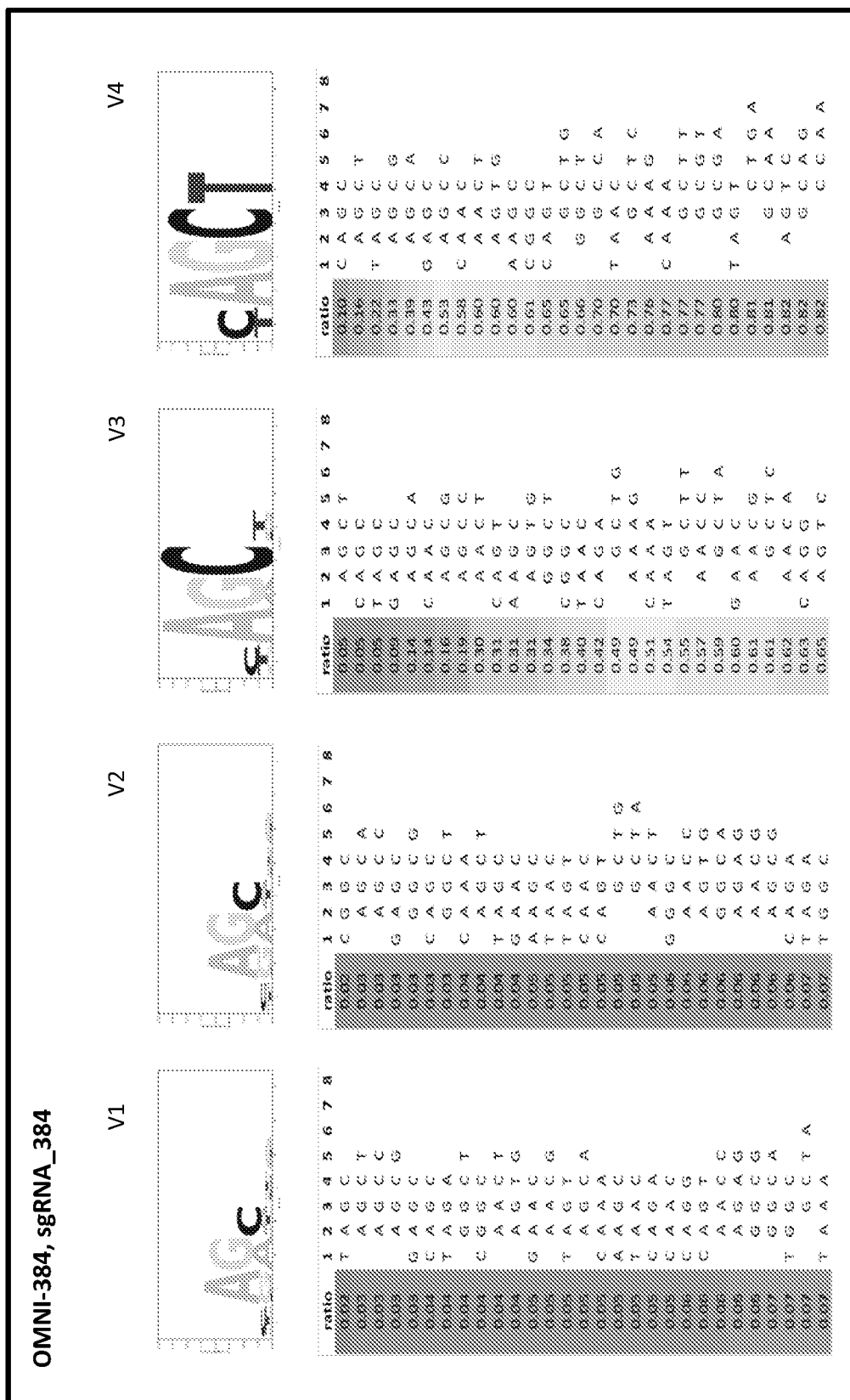


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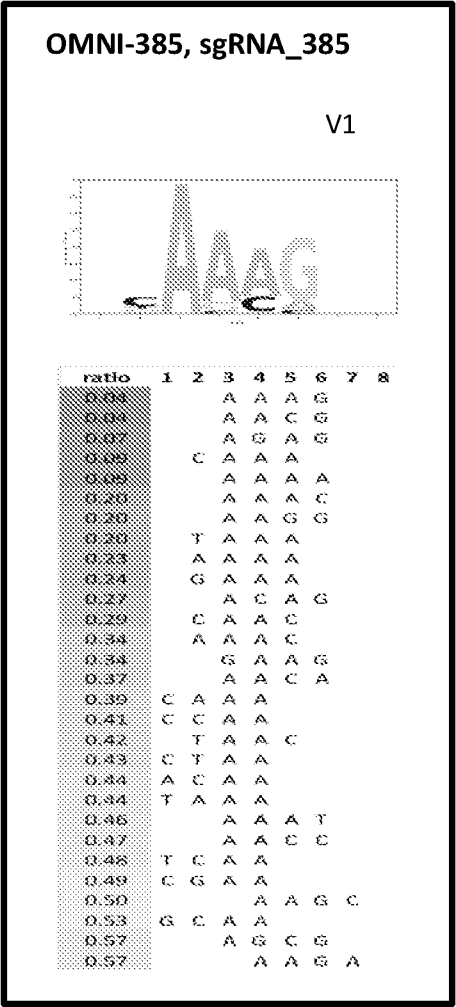


Fig. 108

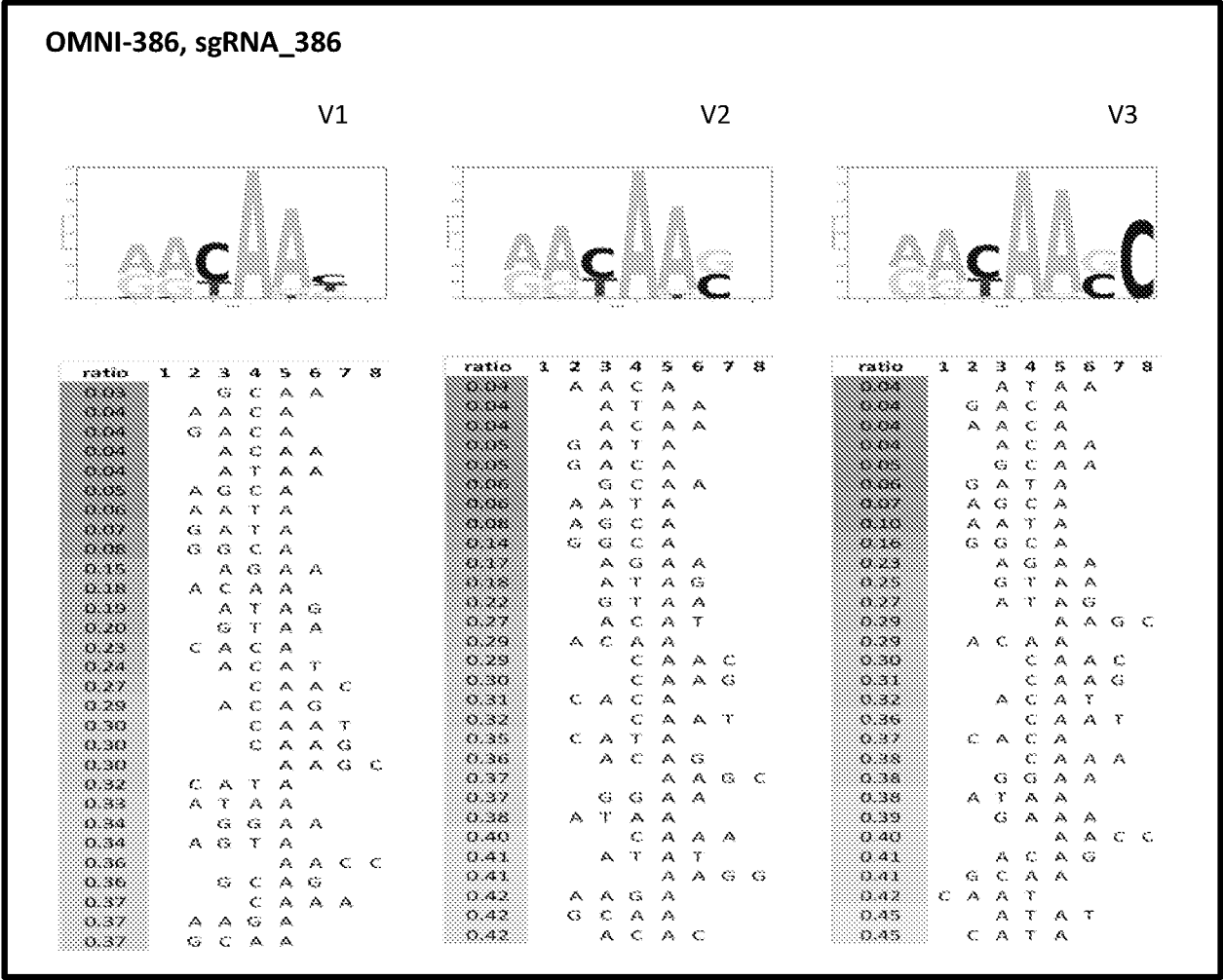


Fig. 109