



US 20250257352A1

(19) **United States**(12) **Patent Application Publication**
MCNEILL et al.(10) **Pub. No.: US 2025/0257352 A1**(43) **Pub. Date: Aug. 14, 2025**(54) **METHODS FOR NOMINATION OF
NUCLEASE ON-/OFF-TARGET EDITING
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(US)(21) Appl. No.: **19/067,623**(22) Filed: **Feb. 28, 2025****Related U.S. Application Data**(63) Continuation of application No. 17/382,945, filed on
Jul. 22, 2021, now abandoned.(60) Provisional application No. 63/055,460, filed on Jul.
23, 2020.**Publication Classification**(51) **Int. Cl.****C12N 15/11** (2006.01)**C12N 9/22** (2006.01)**C12Q 1/6853** (2018.01)(52) **U.S. Cl.**CPC **C12N 15/111** (2013.01); **C12N 9/22**
(2013.01); **C12Q 1/6853** (2013.01); **C12N**
2310/20 (2017.05)

(57)

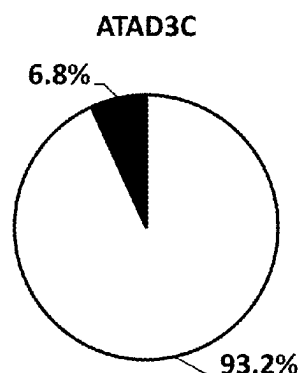
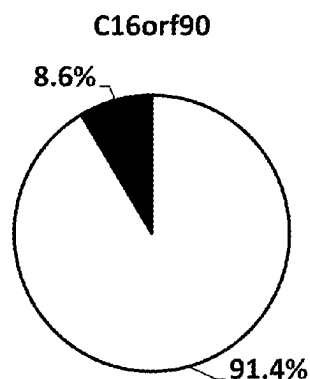
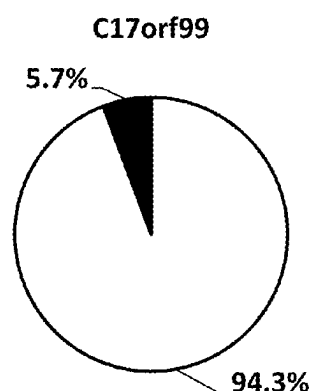
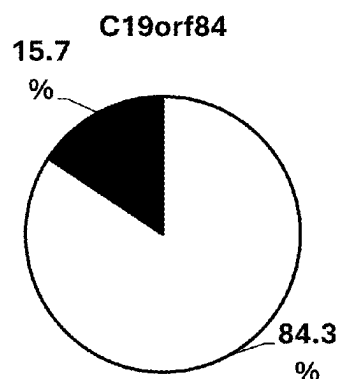
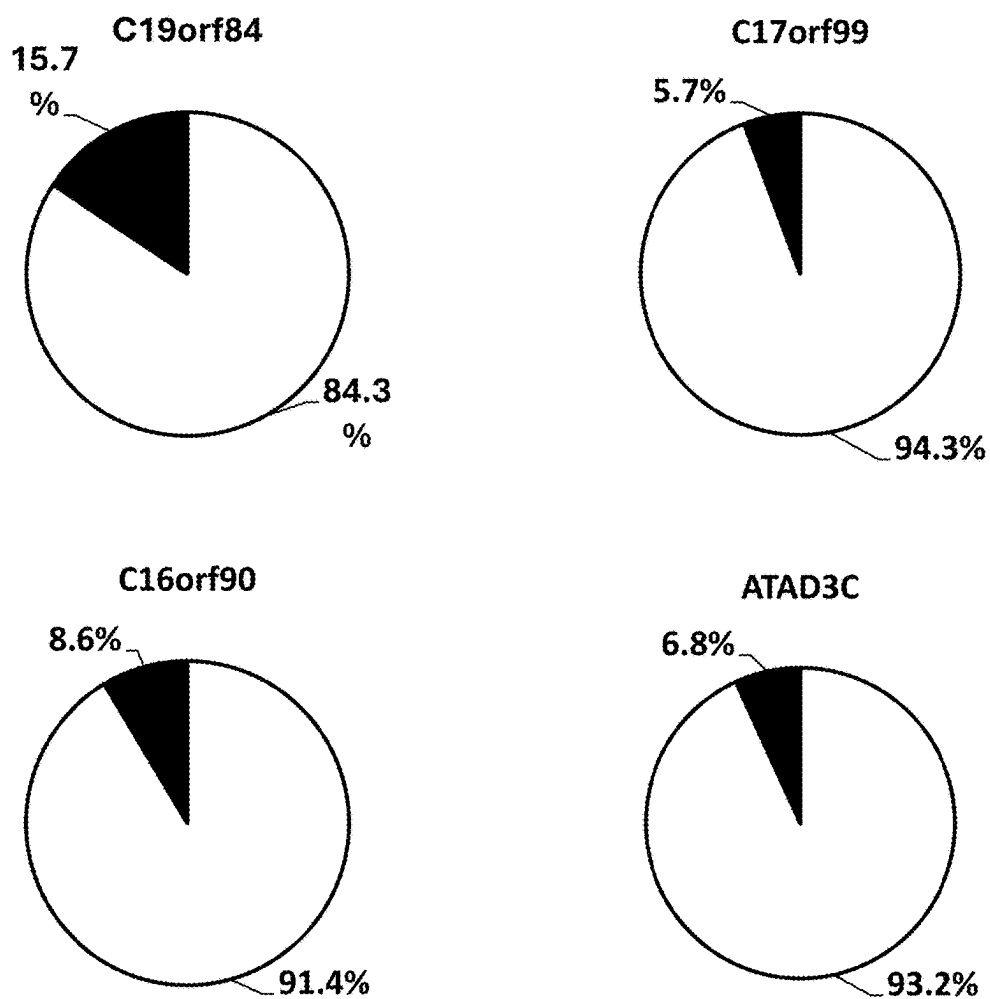
ABSTRACTDescribed herein are methods for identifying and nominat-
ing on- and off-target CRISPR editing sites with improved
accuracy and sensitivity.**Specification includes a Sequence Listing.****Average Percentage Reads Present in 3 Biological Replicates****Average Percentage Reads Present in 1 or 2 Biological Replicates**

FIG. 1



Average Percentage Reads Present in 3 Biological Replicates
 Average Percentage Reads Present in 1 or 2 Biological Replicates

FIG. 2

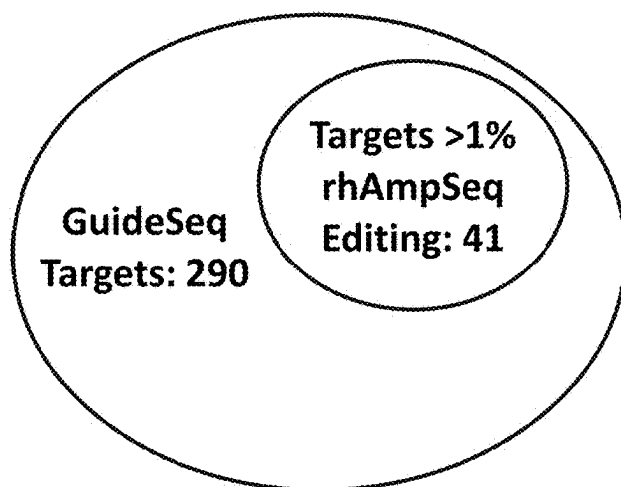


FIG. 3

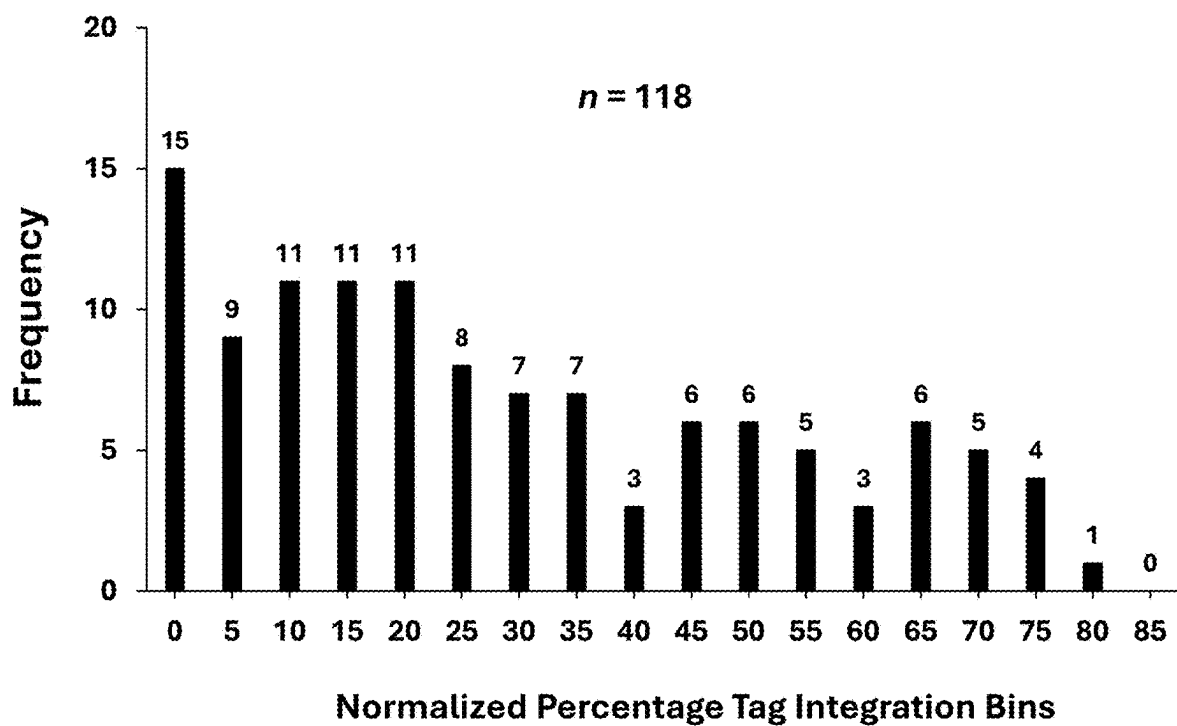


FIG. 4

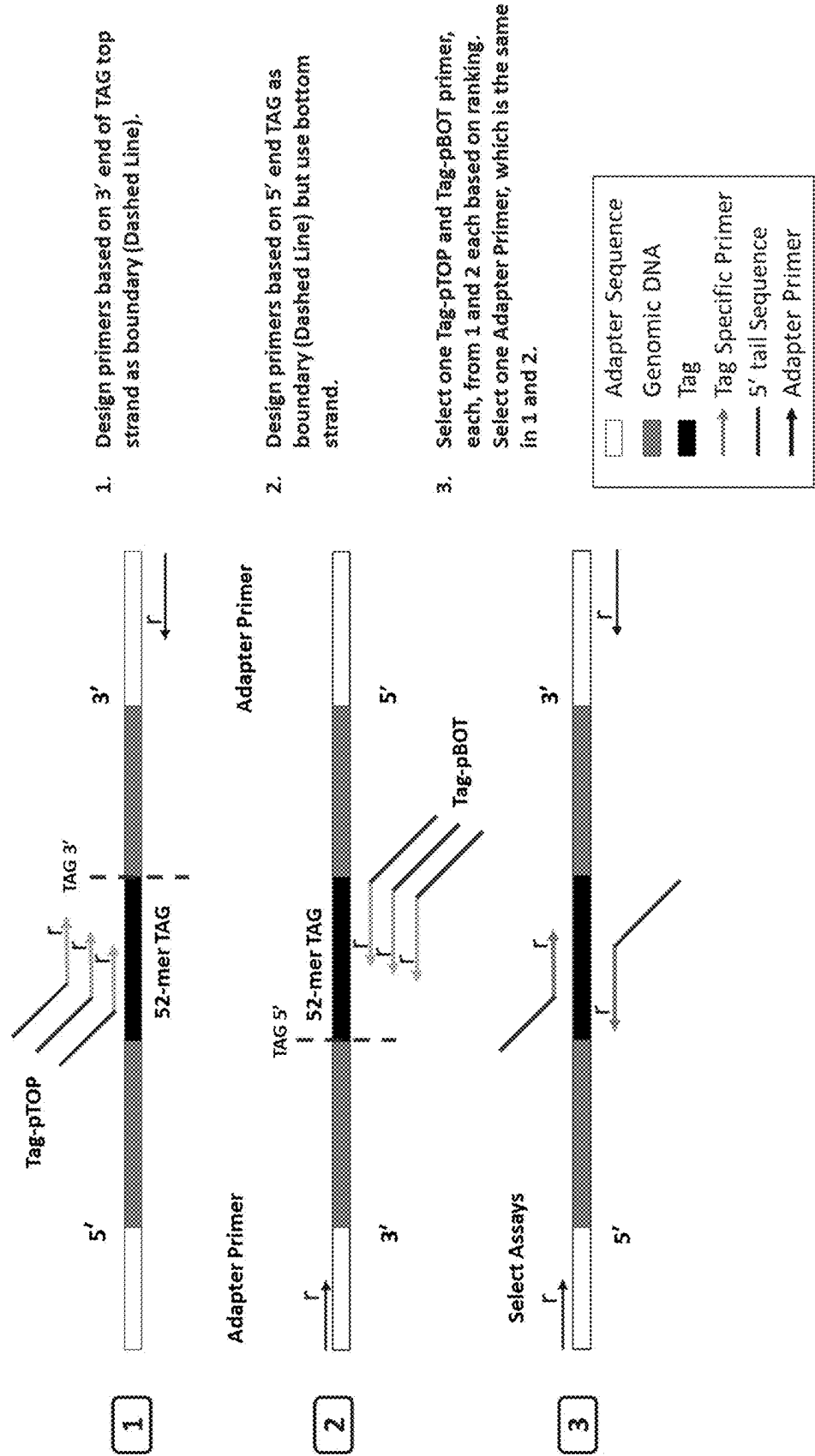


FIG. 5

Design pipeline overview

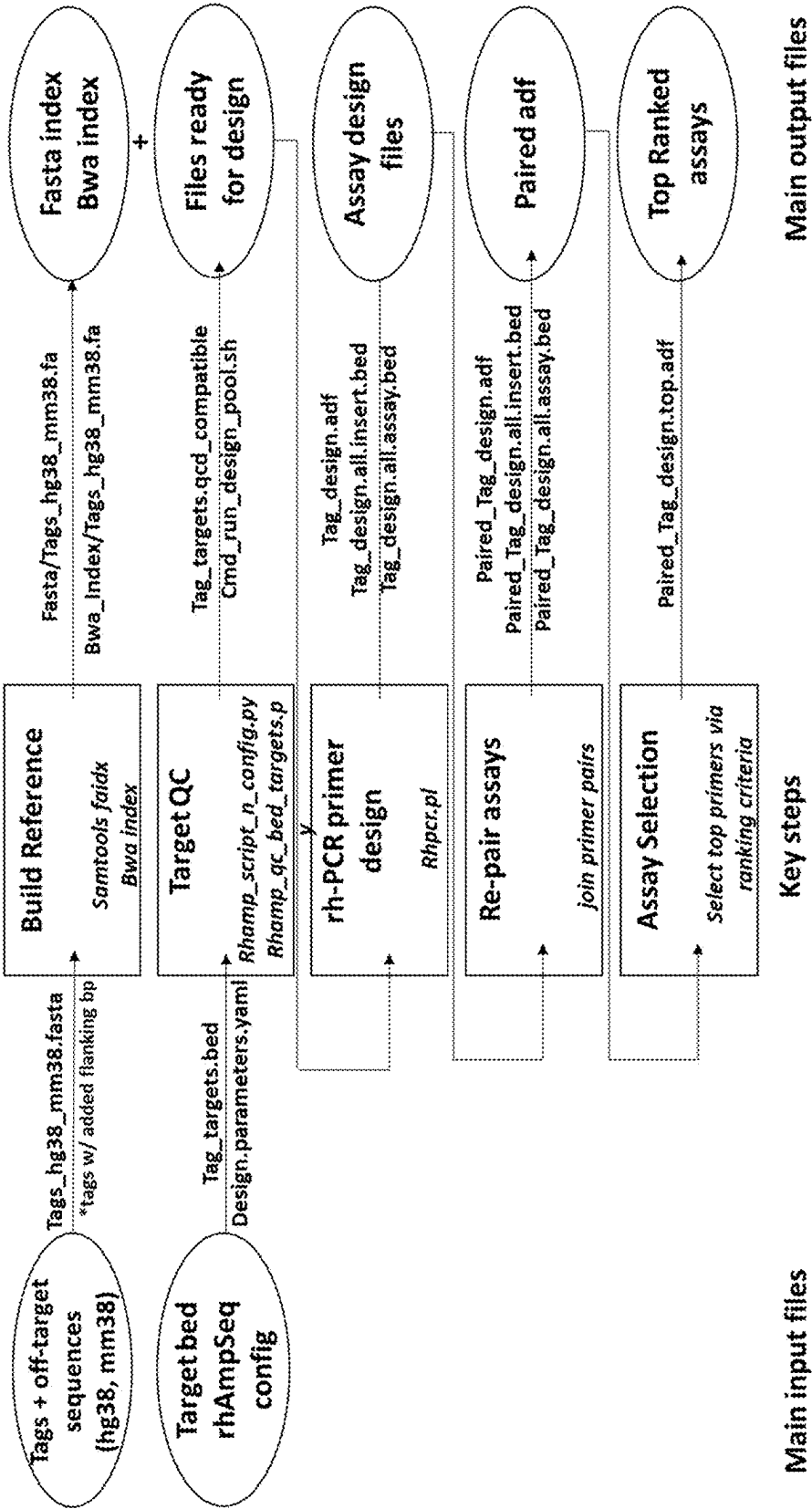


FIG. 6

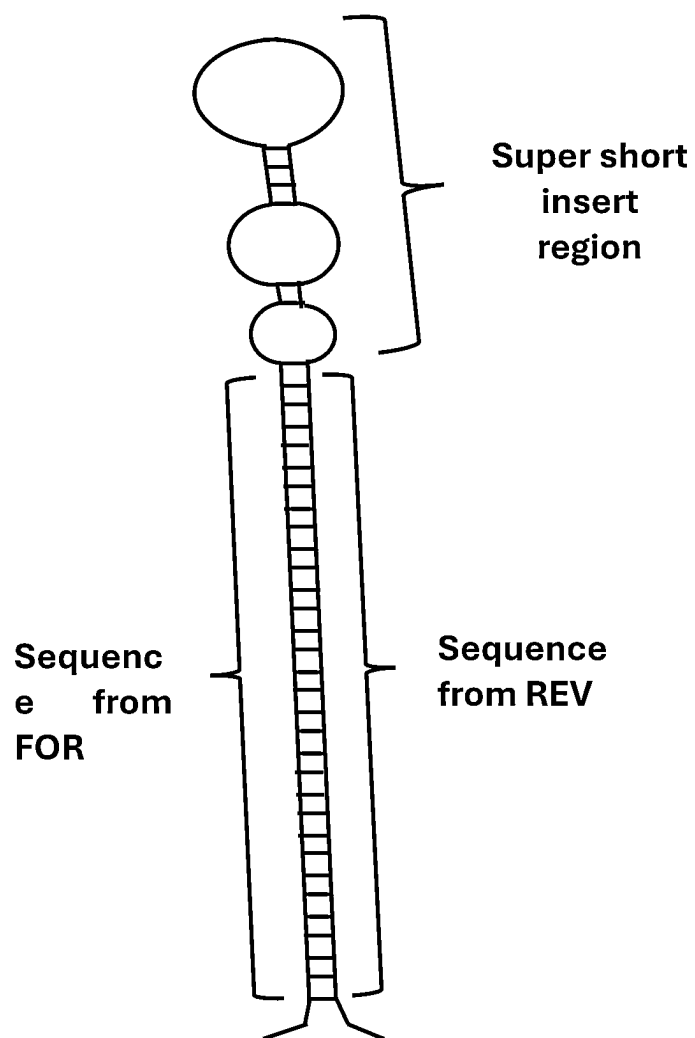


FIG. 7

EMX1 - Number of sites with integration (out of 32)

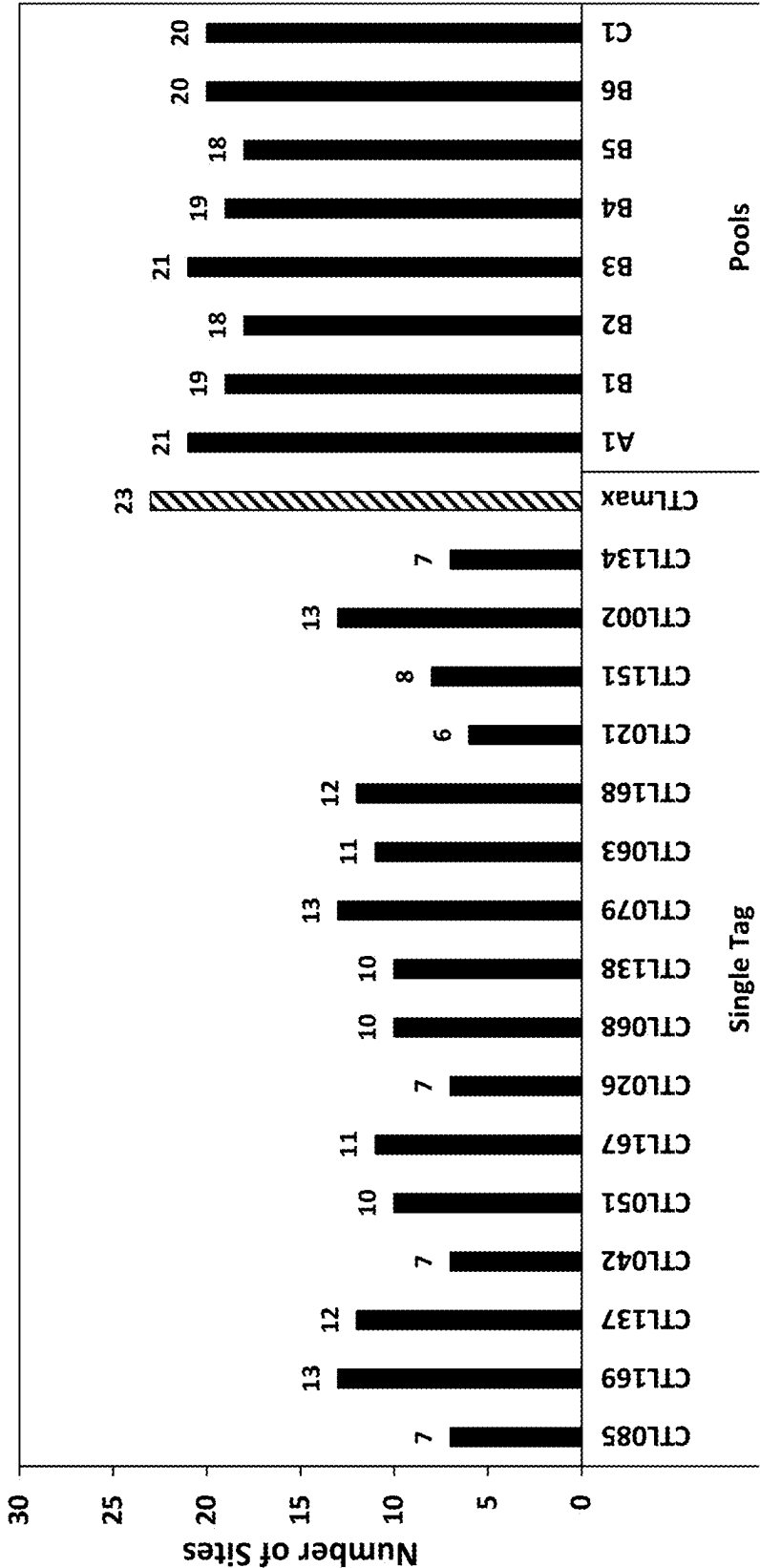
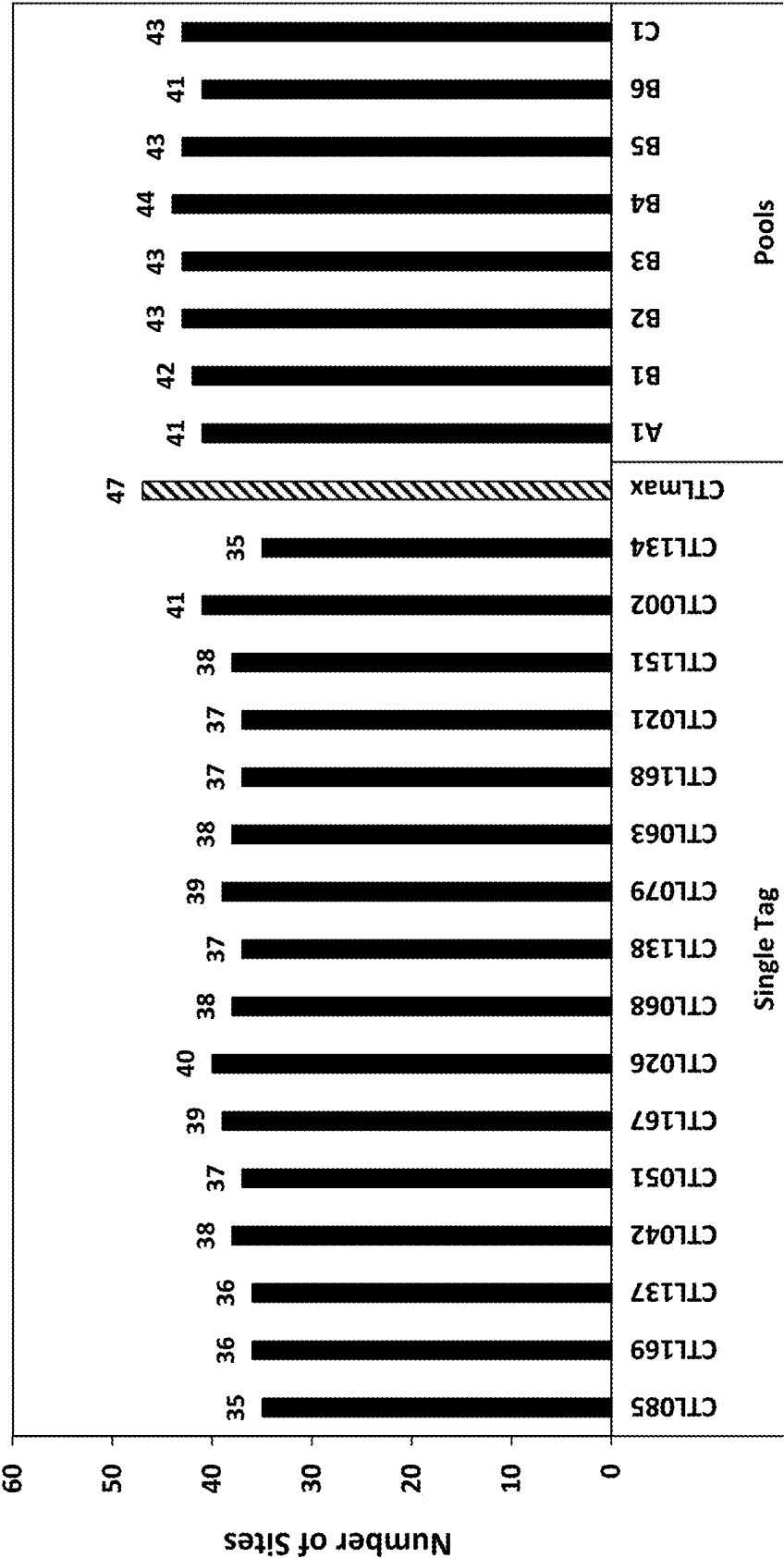


FIG. 8

AR - Number of sites with integration (out of 53)



**METHODS FOR NOMINATION OF
NUCLEASE ON-OFF-TARGET EDITING
LOCATIONS, DESIGNATED "CTL-SEQ"
(CRISPR TAG LINEAR-SEQ)**

**CROSS REFERENCE TO RELATED
APPLICATIONS**

[0001] This application is a continuation of U.S. patent application Ser. No. 17/382,945, filed on Jul. 22, 2021, which claims priority to U.S. Provisional Patent Application No. 63/055,460, filed on Jul. 23, 2020, which is incorporated by reference herein in its entirety.

REFERENCE TO SEQUENCE LISTING

[0002] This application was filed with a Sequence Listing XML in ST.26 XML format in accordance with 37 C.F.R. § 1.831. The Sequence Listing XML file submitted in the USPTO Patent Center, "013670-9056-US03_sequence_listing_xml_1 May 2025.xml," was created on May 1, 2025, contains 273 sequences, has a file size of 248.0 kilobytes (253,952 bytes), and is incorporated by reference in its entirety into the specification.

TECHNICAL FIELD

[0003] Described herein are methods for identifying and nominating on- and off-target CRISPR editing sites with improved accuracy and sensitivity.

BACKGROUND

[0004] CRISPR (clustered regularly interspaced short palindromic repeats) has revolutionized genomics by permitting the simple introduction of changes to the genetic code. CRISPR systems, such as Cas9 and Cas12a proteins, are guided to their target by RNA oligonucleotide sequences bound by the Cas proteins (forming ribonucleoprotein protein; RNP), where the enzyme creates double stranded breaks (DSBs) in DNA sequences. Native cellular machinery repairs DSBs, generally using non-homologous end joining (NHEJ) or homology directed repair (HDR) molecular pathways. DNA repaired through NHEJ, which occurs at on- and off-target locations, often contains indels (insertions/deletions), which can lead to mutations and change the function of encoded genes. Thus, identifying these locations is critical to deconvoluting the impact of on- and off-target editing on biological phenotypes.

[0005] To date, no "gold standard" method exists to identify or nominate off-target editing locations for CRISPR or other nucleases. Many methods have been developed. These methods use a variety of strategies, including the detection of endogenous repair machinery assembled at DSBs (Discover-Seq [1]), the integration of a DNA tag sequence into the host cell genome (GUIDE-Seq; see U.S. Pat. No. 9,822,407), iGUIDE [2, 3]), or by cutting DNA in vitro (BLISS [4], CIRCLE-Seq [5], SiteSeq [6]).

[0006] Cellular or cell based (sometimes referred to as in vivo) and biochemical (sometimes referred to as in vitro) off-target assay nomination systems each have their advantages. Proteins bound to the DNA and epigenetic marks modify the function of nuclease activity, suggesting that cellular or cell based methods may better identify actual editing targets [7]. However, biochemical methods have nominated sites not identified through cellular or cell based methods, suggesting biochemical methods may be more

comprehensive [5, 6]. Nevertheless, these current tools tend to have imperfect sensitivity [5, 6] (see FIG. 1).

[0007] What is needed is a method for detecting and nominating on- and off-target CRISPR editing sites with improved accuracy and sensitivity.

SUMMARY

[0008] One embodiment described herein is a method for identifying and nominating on- and off-target CRISPR edited sites with improved accuracy and sensitivity, the process comprising the steps of: (a) co-delivering a guide sequence RNA (sgRNA) or a two-part CRISPR RNA: trans-activating crRNA (crRNA: tracrRNA) duplex, one or more tag sequences, and an RNA-guided endonuclease to cells; (b) incubating the cells for a period of time sufficient for double strand breaks to occur; (c) isolating genomic DNA from the cells, fragmenting the genomic DNA, and ligating the fragmented genomic DNA to a unique molecular index containing a universal adapter sequence; (d) amplifying the ligated DNA fragments using primers targeting the tag and universal adapter sequences to produce a first set of amplified sequences; (e) amplifying the first set of amplified sequences using universal sequencing primers targeting the tails of Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences; (f) sequencing the pooled sequences and obtaining sequencing data; and (g) identifying on-/off-target CRISPR editing loci. In one aspect, the universal sequencing primers target SP1 or SP2 sequence (SEQ ID NO: 7, 8) tails on the Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences. In another aspect, the universal sequencing primers target predesigned non-homologous sequence (SEQ ID NO: 269-273) tails on the Tag-pTOP or Tag-pBot primers to produce a second set of amplified sequences. In another aspect, the universal sequencing primers target predesigned 13-mer tails on the Tag-pTOP or Tag-pBot primers to produce a second set of amplified sequences. In another aspect, step (g) comprises executing on a processor: (i) aligning the sequence data to a reference genome; (ii) identifying on-/off-target CRISPR editing loci; and (iii) outputting the alignment, analysis, and results data as custom-formatted files, tables or graphics. In another aspect, the method further comprises a step following step (e) comprising: (e1) normalizing the second set of amplified sequences to produce concentration normalized libraries, pooling the normalized libraries with other samples to produce pooled libraries; and continuing with steps (f)-(i). In another aspect, step (d) uses a suppression PCR method. In another aspect, the RNA-guided endonuclease comprises an endogenously-expressed Cas enzyme, a Cas expression vector, a Cas protein, or a Cas RNP complex. In another aspect, the RNA-guided endonuclease comprises an endogenously-expressed Cas9 enzyme, a Cas9 expression vector, a Cas9 protein, or a Cas9 RNP complex. In another aspect, the cells comprise human or mouse cells. In another aspect, the period of time is about 24 hours to about 96 hours. In another aspect, multiple tag sequences are co-delivered. In another aspect, the tag sequences comprise double-stranded deoxy-ribonucleotides (dsDNA) comprising 52-base pairs. In another aspect, the tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides. In another aspect, the tag sequences comprise a

double stranded DNA comprising the complementary top and bottom strand pairs of SEQ ID NO: 1-2 or 7-268.

[0009] Other embodiments described herein are on- and off-target CRISPR editing sites identified or nominated using the methods described herein.

[0010] Another embodiment described herein is a method for designing 52-base pair tag sequences, the method comprising, executing on a processor: (a) randomly generating 13-nucleotide sequences with 40-90% GC content, max homopolymer length A: 2, C: 3, G: 2, T: 2, weighted homopolymer rate <20, self-folding $T_m < 50^\circ \text{C}$., and self-dimer $T_m < 50^\circ \text{C}$.; (b) removing sequences that perfectly align to a particular genome or that are homopolymers or GG or CC dinucleotide motifs and obtaining a set of 13-mers; (c) selecting a subset of the 13-mer sequences that contain one or less CC or GG dinucleotide motifs; (d) concatenating four of the of 13-mer subset sequences to form random 52-mer sequences; (e) aligning the random 52-mer sequences to a genome; (f) removing the random 52-mer sequences that have similarity to the genome to produce a subset of 52-mer sequences; and (h) outputting the subset of 52-mer sequences and generating the complementary strands to produce double stranded 52-base pair tag sequences. In one aspect, the genome is human or mouse. In another aspect, the 52-base pair tag sequences are non-complementary to the genome. In another aspect, the method further comprises designing primers for the 52-base pair tag sequences. In another aspect, the 52-base pair tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides of the 52-base pair tag sequences. In another aspect, the method further comprises synthesizing oligonucleotides comprising the 52-base pair tag sequences, the complement of the 52-base pair tag sequences, or primers for the 52-base pair tag sequences.

[0011] Other embodiments described herein are one or more 52-base pair tag sequences designed using the methods described herein. In one aspect, the 52-base pair tag sequence comprises a double stranded DNA comprising the top and bottom strand pairs of SEQ ID NO: 1-2 or 7-268.

[0012] Another embodiment described herein is a method for designing primers partially complementary to the 52-base pair tag sequences of claim 23 and an adapter primer, the method comprising, executing on a processor: (a) designing tag primers that are partially complementary to the top and bottom strands of tag sequences; and (b) designing an adapter primer that is partially complementary to the top strand of the adapter sequence; wherein: the tag primers comprise a 5'-universal tail sequence; and the adapter primer comprises a sequence complementary to the tails of Tag-pTOP or Tag-pBOT primers. In one aspect, the 5'-universal tail sequence is complementary to an SP1 or SP2 sequence (SEQ ID NO: 7, 8), a locus specific segment, a ribonucleotide (rN) 6-nucleotides from the 3'-end, a 3'-end mismatch, a 3'-end block (3'-C₃ spacer), a predesigned non-homologous sequence (SEQ ID NO: 269-273), or a predesigned 13-mer sequence. In another aspect, the primers partially complementary to top and bottom strands of the tag sequences comprise a tail sequence complementary to the SP1 sequence (SEQ ID NO: 7) and the adapter primer comprises a sequence complementary to the SP2 sequence (SEQ ID NO: 8) tail on the Tag-pTOP or Tag-pBOT primers; or the primers partially complementary to top and bottom strands of the tag sequences comprise a tail sequence

complementary to the SP2 sequence (SEQ ID NO: 8) and the adapter primer comprises a sequence complementary to the SP1 sequence (SEQ ID NO: 7) tail on the Tag-pTOP or Tag-pBOT primers. In another aspect, the amplification of a nucleic acid molecule with the primers that are complementary to the top and bottom strands of tag sequences and primers that are complementary to the top strand of the adapter sequence produces a PCR product that comprises a portion of the tag sequence, a sgDNA sequence, and the adapter sequence. In another aspect, the method further comprises synthesizing oligonucleotides comprising the sequences of the forward and reverse tag primers and the adapter primer. In another aspect, the 52-base pair tag sequences and primers partially complementary to the 52-base pair tag sequences are designed and selected using an algorithm predicting whether the primers are likely to be partially complementary and have a propensity to form primer-dimers.

[0013] Other embodiments described herein are one or more primers partially complementary to the 52-base pair tag sequences and one or more adapter primers designed using the methods described herein. In one aspect, the primers comprise the sequences of SEQ ID NO: 3, 4; and the adapter primer, wherein the adapter primer comprises the sequence of SEQ ID NO: 5.

[0014] Another embodiment described herein is the use of one or more double-stranded 52-base pair tag sequences for identifying on- and off-target CRISPR editing sites.

DESCRIPTION OF THE DRAWINGS

[0015] FIG. 1 shows fraction of reads shared by three biological replicates are shown in white sectors; whereas reads shared by two replicates, or present in a single replicate, are shown in black sectors. Table 1 shows GUIDE-seq [3] based nomination for 4 different gRNAs in triplicate in a 96-well format. gRNA complexes were generated by mixing equimolar amounts of Alt-R crRNA-XT and Alt-R tracrRNA. HEK293 cells stably expressing Cas9 were transfected with 10 UM gRNA and 0.5 UM dsODN GUIDE-seq tag using the Nucleofector™ system (Lonza). After 72 hrs, genomic DNA (gDNA) was isolated. Genomic DNA was fragmented, and adapters were ligated using the Lotus DNA library preparation kit (IDT). Libraries were generated by amplification from the inserted tag to the ligated adapters [3]. Libraries were then sequenced in paired-end fashion on an Illumina® platform.

[0016] FIG. 2 shows that GUIDE-Seq finds more off-target locations than can be validated through rhAmpSeq targeted amplification. Presented results are an aggregate of 331 GUIDE-Seq nominated sites when delivering gRNA sequences (internally named: AR, CTNNB1, EMX1, GRHPR, HPRT38087, HPRT38285, VEGFA) into HEK293 cells stably expressing WT Cas9. GUIDE-seq nominated off-targets assigned >0.1% of the total reference genome aligned reads for each guide were designed and targeted by one rhAmpSeq panel all reference genome aligned. In subsequent experiments, gRNAs were again delivered to the same cells, and editing was assayed with rhAmpSeq. Targets were called "edited" if the treated condition had observed indels \geq the untreated control sample at $\geq 1\%$.

[0017] FIG. 3 illustrates that GUIDE-Seq tag integration rate varies. The graph shows the percentage of Tag integration (normalized to % Editing) for 118 unique Cas9 on/off-target sites that had InDel editing in rhAmpSeq panels

targeting GUIDE-Seq nominated on/off-target loci for guide sequences targeting the RAG1, RAG2, and EMX1 genes. Each guide was co-delivered with the 34-base pair GUIDE-Seq, dsODN tag into HEK293 cells stably expressing Cas9 by nucleofection. DNA was extracted 72 hrs later, amplified by rhAmpSeq multiplex PCR, sequenced on an Illumina® MiSeq, and analyzed through a custom pipeline. The normalized tag integration rate is calculated as the percentage of sequenced reads at each target containing the tag sequence divided by the total reads containing an allele divergent from the reference genome (indicating Cas9 editing).

[0018] FIG. 4 shows the design of rhAmpSeq primers against alien sequence tags. A cartoon diagram shows the steps of the design process using the rhAmpSeq design pipeline including design of forward primers against the top (1) and bottom (2) strands, discarding unneeded primers, and selecting tag-targeting primers that have 5'-overlapping, but not 3'-overlapping sequences, so that the top/bottom strand primer dimers would hairpin (3).

[0019] FIG. 5 shows an overview of the rhAmpSeq design pipeline used to construct the overlapping primer designs. In the pipeline, a known sequence is appended onto the 5'-end and 3'-end of each tag sequence, the inputs are quality-controlled and assays (shown in FIG. 4A) are designed against the top and bottom strand of each tag. Primers targeting each tag strand are paired such that at least 4-nucleotides 3' of the RNA nucleotide do not overlap between primers targeting the same tag, and primer pairs are ranked and selected. Hg38 and mm38 acronyms represent versions of the human and mouse genomes, respectively.

[0020] FIG. 6 illustrates hairpin formation if overlapping primers generate PCR amplicons. The diagram shows a representative target sequence and hairpin PCR product of undesired short amplicons from overlapping primer regions with complementary 5' primer tail ends at the 3'- and 5'-end of the PCR product.

[0021] FIG. 7 shows the number of target sites (black bars) with integration of the specified single tag (SEQ ID NO: 9-40) or pools of tags described in Table 5 (SEQ ID NO: 9-40, 45-268). The striped bar (CTLmax) shows the maximum number of target sites that theoretically can be found if a combination of the single tags (SEQ ID NO: 9-40) is used (23 sites out of a maximum of 32 sites). Pool A1 contains all the single tags (SEQ ID NO: 9-40). Pools B1-6 contain 16 different tags each (SEQ ID NO: 45-268). Pool C1 contains all tags tested (SEQ ID NO: 9-40, 45-268). Integration events were determined using an in-house data analysis tool.

[0022] FIG. 8 shows the number of target sites (black bars) with integration of the specified single tag (SEQ ID NO: 9-40) or pools of tags described in Table 5 (SEQ ID NO: 9-40, 45-268). The striped bar (CTLmax) shows the maximum number of target sites that theoretically can be found if a combination of the single tags (SEQ ID NO: 9-40) is used (47 sites out of a maximum of 53 sites). Pool A1 contains all the single tags (SEQ ID NO: 9-40). Pools B1-6 contain 16 different tags each (SEQ ID NO: 45-268). Pool C1 contains all tags tested (SEQ ID NO: 9-40, 45-268). Integration events were determined using an in-house data analysis tool.

DETAILED DESCRIPTION

[0023] Described herein are methods for detecting and nominating on- and off-target CRISPR editing sites with

improved accuracy and sensitivity. The intracellular context information is maintained by building upon prior in vivo nomination methods. The sensitivity is expanded by co-delivering a set of unique, predefined sequence tags. In one aspect, the co-delivered set of predefined unique tags may range from 13-80 base pairs. In another aspect, the co-delivered set of predefined tags may be comprised of 13 base pair tag sequence tags, 26 base pair tag sequence tags, 39 base pair tag sequence tags, 52 base pair tag sequence tags, 65 base pair tag sequence tags, or 78 base pair tag sequence tags. In another aspect, the unique predefined tags are a set of 52-base pair tag sequence tags (the increased length of the sequence tags improves the ability to find good primer landing sites for rhPrimers). This limitation is believed to be mitigated by using a diversity of tag sequences that are distinct from human and mouse genomes. The specificity is improved by building upon Integrated DNA Technologies (IDT)'s rhAmp technology that uses RNAaseH2 (*Pyrococcus abyssi*) to unblock primers that have correctly annealed to their target; this yields lower rates of false priming. Specificity can be further enhanced by only nominating targets using reads that contain an expected tag sequence at the 5'-end. The incorporation of suppression PCR into this method permits ease of use. The prior in vivo methods (e.g., GUIDE-seq and iGUIDE) require parallel PCR reactions (2 pool amplification) to amplify by annealing to and extending from the top and bottom strand of the tags. Here, suppression PCR is used to allow both pools to be amplified simultaneously without causing problematic dimer sequences.

[0024] A GUIDE-Seq dsDNA tag was co-delivered with one guide RNA to HEK293 cells constitutively expressing Cas9 using nucleofection. See U.S. Pat. No. 9,822,407, which is incorporated by reference herein for such teachings. A total of four different guide RNAs were tested in this fashion. Ribonucleoprotein complexes (RNPs) between the expressed Cas9 and guide RNA form within the cells, introducing double stranded breaks. Repaired breaks can contain the co-delivered tags. After delivery, cells were incubated, and the resulting DNA was extracted. Target amplification was performed according to the GUIDE-Seq protocol and assayed with a modified version of the GUIDE-Seq analytical pipeline (github.com/aryeelab/guideseq). Nominated targets were compared between three biological replicates (unique guideRNA+Tag co-deliveries). Not all nominated targets were common to all biological replicates (commonly/total nominated targets: 7/31, 6/19, 2/4, 3/5 respectively; see Table 1). However, >90% of the total reads, attributed to any target, were attributed to common targets (on average; see FIG. 1).

TABLE 1

Identified off-target sites for four different gRNAs and relative level of editing at off-target sites compared to the on-target site			
Location	C19orf84_BR1	C19orf84_BR2	C19orf84_BR3
chr19_51389306	100.00%	100.00%	100.00%
chr9_20224748	38.55%	16.43%	29.00%
chr4_28036434	16.33%	13.05%	14.36%
chr15_74256506	14.30%	18.18%	25.17%
chr2_171312919	11.40%	8.51%	7.93%
chr8_65742269	10.82%	1.17%	10.40%
chr13_96554656	8.70%	0.00%	0.00%
chr4_86807920	8.50%	9.21%	1.92%
chr3_124485356	6.57%	0.00%	0.00%

TABLE 1-continued

Identified off-target sites for four different gRNAs and relative level of editing at off-target sites compared to the on-target site			
chr9_20330398	5.60%	0.00%	0.00%
chr11_71298123	5.12%	0.00%	0.00%
chr7_101729696	4.83%	0.00%	9.58%
chr19_10923882	3.67%	3.03%	0.00%
chr10_15548456	3.57%	15.38%	0.00%
chr12_117097457	2.80%	0.00%	2.60%
chr22_33493900	2.13%	0.00%	4.79%
chrX_149763439	2.13%	0.00%	3.83%
chr17_7435217	1.93%	0.00%	0.55%
chr12_26286721	1.74%	0.00%	5.06%
chr16_49704848	1.26%	5.01%	7.11%
chr12_51288216	1.06%	0.00%	0.00%
chr12_56010621	0.87%	0.00%	0.00%
chr13_29717148	0.48%	0.00%	0.00%
chr1_3088065	0.29%	0.00%	0.00%
chr15_73442915	0.19%	0.00%	0.55%
chr10_118045968	0.19%	0.00%	0.00%
chr14_102199972	0.00%	0.00%	0.68%
chr18_56334679	0.00%	0.00%	2.33%
chr21_36426137	0.00%	0.00%	2.19%
chr5_139002763	0.00%	0.00%	3.83%
chrX_58291642	0.00%	0.00%	3.83%
Location	C17orf99_BR1	C17orf99_BR2	C17orf99_BR3
chr17_78164110	100.00%	100.00%	100.00%
chr22_24471716	15.00%	13.24%	10.86%
chr10_101156881	6.22%	11.07%	9.79%
chr3_170476431	5.86%	3.97%	4.57%
chr17_17692965	4.94%	0.66%	8.62%
chr15_73400031	3.93%	4.63%	5.73%
chr19_15238775	0.00%	0.00%	2.56%
chr2_18362316	0.00%	0.00%	1.59%
chr2_171087784	0.00%	0.54%	0.84%
chr22_19959968	0.00%	1.26%	0.19%
chr22_32114104	0.00%	0.00%	4.06%
chr4_129034015	0.00%	0.00%	0.33%
chr5_61219030	0.00%	0.00%	0.33%
chr5_66209615	0.00%	0.00%	1.86%
chr7_69709389	0.00%	0.12%	2.75%
chr7_158662844	0.00%	1.44%	5.27%
chrX_9567397	0.00%	0.00%	0.23%
chr19_55657073	0.00%	0.66%	0.00%
chr22_43788032	0.00%	2.47%	0.00%
Location	C16orf90_BR1	C16orf90_BR2	C16orf90_BR3
chr16_3494817	100.00%	100.00%	100.00%
chr2_109189307	75.32%	4.27%	52.05%
chr22_24586001	45.45%	0.00%	0.00%
chr10_104736568	0.00%	0.00%	8.22%
Location	ATAD3C_BR1	ATAD3C_BR2	ATAD3C_BR3
chr1_1450685	100.00%	100.00%	100.00%
chr1_1503588	11.73%	10.07%	9.27%
chr1_1516015	2.47%	1.86%	5.14%
chr19_32167960	26.34%	0.93%	0.00%
chr2_111077960	0.00%	1.12%	0.00%

[0025] Additionally, nominated targets may not be replicable or detectable using orthogonal methods. Using the GUIDE-Seq method, the GUIDE-Seq DNA tag was co-delivered with each of 6 guides (each tag is delivered with one guide RNA) to HEK293 cells constitutively expressing Cas9 using nucleofection. rhAmpSeq multiplex amplicon panels were designed to amplify the nominated targets, and we quantified editing in biological replicates. Of the 331 targets nominated by GUIDE-Seq, only 41 (12%) could be verified with rhAmpSeq (see FIG. 2).

[0026] dsDNA tag sequences co-delivered with the guide RNAs into a stably expressing CRISPR cell line, which are

used in the NHEJ repair, are incorporated at varying rates. Here, the GUIDE-Seq dsDNA tag was co-delivered with each of 6 guides into HEK293 cells constitutively expressing Cas9. In another aspect, the dsDNA tag sequences co-delivered with CRISPR RNP, which are used in the NHEJ repair, are incorporated at varying rates. Here, the GUIDE-Seq dsDNA tag was co-delivered with each of 6 guides into HEK293 cells constitutively expressing Cas9. rhAmpSeq panels were developed to amplify nominated targets, and in biological replicates, the rates of tag integration were analyzed using a custom analytical pipeline. These results demonstrate that tags are incorporated at 0-85% of edited genomic copies, varying by target (see FIG. 3). Without being bound by any theory, it is hypothesized that the rate varies by sequence context.

[0027] Described herein are methods to improve the signal to noise ratio by combining Integrated DNA Technology's rhAmpSeq™ technology, suppression PCR, and novel alien DNA sequence designs to nominate nuclease off-target editing locations within a host genome.

[0028] In this method, Cas9, a sgRNA or a two-part CRISPR RNA: trans-activating crRNA (crRNA: tracrRNA) duplex, and one or more double stranded DNA (dsDNA) tag sequences are delivered to cells. Co-delivering multiple tags permits improved tag integration at off-target sites (see below). The tag sequences have sequence content significantly different (i.e., alien) to the host genome. After nuclease introduced DSBs, NHEJ repair will insert the tag sequence(s) into the target site, forming known primer landing sites. After cells have time to repair the DSBs and possibly further divide (such as after 72 hr), genomic DNA is isolated, fragmented (e.g., Covaris® shearing, enzyme-based shearing, Tn5, etc.), ligated a unique molecular index (UMI)-containing universal adapter sequence to the fragmented DNA, and the un-ligated material is removed. Next, the DNA fragments are amplified by targeting primers to the tag and universal adapter sequences (Round 1 PCR). Using universal primers, a sample index (PCR2) is added, the amplified material is concentration normalized, pooled with other samples, and the pooled material is sequenced on an Illumina® (or similar) machine. The sequenced reads are aligned to a reference genome, and loci where large numbers of reads map may nominate on/off-target locations.

[0029] Alien sequences were designed by generating >1 M random 13-mer sequences with 40-90% GC content, max homopolymer length A: 2, C: 3, G: 2, T: 2, weighted homopolymer rate <20, self-folding Tm<50° C., and self-dimer Tm<50° C. From the list of sequences, sequences that aligned perfectly against human (GRCh38.p2; hg38) or mouse (GRCh38.p4; mm38) reference genomes or had troubling motif sequences (homopolymers, most G-G or C-C dinucleotide motifs) were removed, resulting in 479 sequences.

[0030] To design the 52-base pair tag sequences described herein, 49 13-mer oligo sequences were selected that contain ≤1 C or G dinucleotide, and 10,000 unique combinations of four 13-mer sequences were generated. The length of each concatenated sequence (e.g., pasting four 13-mer sequences in a row using software) is 52-nucleotides. Next, each 52-nucleotide tag sequence was aligned against the human (GRCh38.p2) and mouse (GRCh38.p4) genomes using an internally modified version of bwa, called bwa-psm. Implementation of bwa-psm returns all possible secondary matches up to a defined threshold. A set of tag

sequences (SEQ ID NO:1-2) were designed that were intended to work as a group, that had no similarity to the human or mouse genomes (max seed size: 7, seed edit distance: 2, max edit distance: 21, max gap open: 2, max gap extension: 3, mismatch penalty: 1, gap open penalty: 1, gap extension penalty: 1).

[0031] Overlapping rhAmpSeq V1 primers (SEQ ID NO: 3-4) were designed complementary to the top and bottom strands of the tag and 5'-end of the adapter sequence (SEQ ID NO: 6) (FIG. 4). The tag-specific primers (SEQ ID NO: 3-4) contain a 5'-universal tail sequence matching the SP1 and SP2 primer sequences (SEQ ID NO: 7-8), a locus specific segment, a ribonucleotide (rN) 6-nucleotides from the 3'-end, a 3'-end mismatch, and a 3'-end block (3'-C3 spacer). The adapter-specific primer (SEQ ID NO: 5) targets the 5'-end of the 5'-P5 adapter sequence (SEQ ID NO: 6), and the adapter sequence contains unique molecular index (UMI) sequence (Table 2). The primers were designed to target the plus and minus strands of the annealed tag such that, if these primers unexpectedly form a dimer, the formed product will hairpin, removing the oligo from the available reaction templates (e.g., suppression PCR). (FIG. 6A-B). Primer sequences targeting the tags were chosen based on a proprietary design algorithm designed and implemented by IDT (internal copy of the algorithm with a public-facing UI: www.idtdna.com/site/account?ReturnURL=/site/order/designtool/index/RHAMPSEQ), which selects the most optimally performing primer pairs to amplify the intended template sequence. (FIG. 5). Primer sequences were assessed for non-specific binding to all other tag sequences and both human and mouse primary genome assemblies to verify they were unlikely to form off-target amplicons when combined with a universal adapter sequence and the presence of human or mouse genomic DNA.

[0032] The primers were desired to work in pairs where one tag-specific primer (top or bottom strand) pairs with the adapter-specific primer (SEQ ID NO:5). This results in the amplification of a molecule that contains a portion of the tag, gDNA, and the adapter sequence when amplified using suppression PCR methods (FIG. 4).

TABLE 2

Sequences Used for First Proof of Concept			
Type	Name	Sequence (5'→3')	SEQ ID NO
Tag	9022179029169042579 04625907201907281	T*C*GTTTCGTTTC	SEQ ID NO: 1
		CGCTCTAACC GG CGAATCTACCGC GCATATCTACGC CGCA*A*T	ID NO: 1
Tag	9022179029169042579 04625907201907281_r ev	A*T*TGCGGCGT	SEQ ID NO: 2
		AGATATGCGCGG TAGATTGCGCGG TTAGAGCGGAAC GAAC*G*A	ID NO: 2
Tag Primers	pFWD.ID_Target1: 9022179029169042579 04625907201907281.12 7.150.1.SP1	acactctttccc	SEQ ID NO: 3
		tacacgacgctc ttccgatctTCT ACCGCGCATATC TACrGCCGCT/ 3SpC3/	ID NO: 3

TABLE 2-continued

Sequences Used for First Proof of Concept			
Type	Name	Sequence (5'→3')	SEQ ID NO
Tag Primers	pFWD.ID_Target2: 9022179029169042579 04625907201907281.11 6.140.-1.SP1	acactctttccc	SEQ ID NO: 4
		tacacgacgctc ttccgatctATA TGCGCGGTAGAT TCGCrCGGTTT/ 3SpC3/	ID NO: 4
Adapter Primer	Adapter Primer	gtgactggagtt	SEQ ID NO: 5
		cagacgtgtgct cttccgatctAA TGATACGGCGAC CACCGAGATCTA CArCAAGGC/ 3SpC3/	ID NO: 5
P5 Adapter	Example Sequence	AATGATACGGCG	SEQ ID NO: 6
		ACCACCGAGATC TACACTAGATCG CNNWNNWNNACA CTCTTTCCTTAC ACGACGCTCTTC CGATC*T	ID NO: 6
SP1	Sequencing Primer 1	acactctttccc	SEQ ID NO: 7
		tacacgacgctc ttccgatct	ID NO: 7
SP2	Sequencing Primer 2	gtgactggagtt	SEQ ID NO: 8
		cagacgtgtgct cttccgatct	ID NO: 8

*** indicates a phosphorothioate linkage; "rN" indicates a ribonucleotide, where N is the nucleotide preceded by the "r"; "/3SpC3/" indicates a 3'-C₃ spacer.

[0033] One embodiment described herein is a method for identifying and identifying and nominating on- and off-target CRISPR editing sites with improved accuracy and sensitivity, the process comprising the steps of: (a) co-delivering a guide sequence RNA (sgRNA) or a two-part CRISPR RNA: trans-activating crRNA (crRNA: tracrRNA) duplex and one or more tag sequences to cells; (b) incubating the cells for a period of time; (c) isolating genomic DNA from the cells, fragmenting the genomic DNA, and ligating the fragmented genomic DNA to a unique molecular index containing a universal adapter sequence; (d) amplifying the ligated DNA fragments using primers targeting the tag and universal adapter sequences to produce a first set of amplified sequences; (e) amplifying the first set of amplified sequences using universal sequencing primers targeting the tails of Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences; (f) sequencing the pooled sequences and obtaining sequencing data; and (g) identifying on-/off-target CRISPR editing loci. In one embodiment, the universal sequencing primers target SP1 or SP2 sequence (SEQ ID NO: 7, 8) tails on the Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences. In another embodiment, the universal sequencing primers target pre-designed non-homologous sequence (Table 6; SEQ ID NO: 269-273) tails on the Tag-pTOP or Tag-pBot to produce a second set of amplified sequences. In yet another embodiment, the universal primers target pre-designed 13-mer tails on the Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences. In one

embodiment, step (g) comprises executing on a processor: (i) aligning the sequence data to a reference genome; (ii) identifying on-/off-target CRISPR editing loci; and (iii) outputting the alignment, analysis, and results data as tables or graphics. In another embodiment, the method further comprises a step following step (e) comprising: (e1) normalizing the second set of amplified sequences to produce concentration normalized libraries, pooling the normalized libraries with other samples to produce pooled libraries; and continuing with steps (f)-(i). In one aspect, step (d) uses a suppression PCR method. In another aspect, the cells constitutively express a Cas enzyme, are co-delivered with a Cas expression vector, are co-delivered with a Cas protein, or are co-delivered with a Cas RNP complex. In another aspect, the cells constitutively express a Cas9 enzyme, are co-delivered with a Cas9 expression vector, are co-delivered with a Cas9 protein, or are co-delivered with a Cas9 RNP complex. In another aspect, the cells comprise human or mouse cells. In another aspect, the period of time is about 24 hours to about 96 hours. In another aspect, multiple tag sequences are co-delivered. In another aspect, the tag sequences comprise double-stranded deoxyribonucleotides (dsDNA) comprising 52-base pairs. In another aspect, the tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides. In another aspect, the tag sequences comprise a double stranded DNA comprising the top and bottom strand pairs of SEQ ID NO: 9-40 or 45-268.

[0034] Another embodiment described herein is on- and off-target CRISPR editing sites identified or nominated using the methods described herein.

[0035] Another embodiment described herein is a method for designing 52-base pair tag sequences, the method comprising, executing on a processor: (a) randomly generating 13-nucleotide sequences with 40-90% GC content, max homopolymer length A: 2, C: 3, G: 2, T: 2, weighted homopolymer rate <20, self-folding Tm<50° C., and self-dimer Tm<50° C.; (b) removing sequences that perfectly align to a particular genome or that are homopolymers or GG or CC dinucleotide motifs and obtaining a set of 13-mers; (c) selecting a subset of the 13-mer sequences that contain one or less CC or GG dinucleotide motifs; (d) concatenating four of the of 13-mer subset sequences to form random 52-mer sequences; (e) aligning the random 52-mer sequences to a genome; (f) removing the random 52-mer sequences that have similarity to the genome to produce a subset of 52-mer sequences; and (h) outputting the subset of 52-mer sequences and generating the complementary strands to produce double stranded 52-base pair tag sequences. In one aspect, the genome is human or mouse. In one aspect, the 52-base pair tag sequences are not complementary to the genome. In another aspect, the method further comprises designing primers for the 52-base pair tag sequences. In another aspect, the 52-base pair tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides of the 52-base pair tag sequences. In another aspect, the method further comprises synthesising oligonucleotides comprising the 52-base pair tag sequences, the complement of the 52-base pair tag sequences, or primers for the 52-base pair tag sequences.

[0036] Another embodiment described herein is one or more 52-base pair tag sequences designed using the methods described herein. In one aspect, the 52-base pair tag

sequence comprises a double stranded DNA comprising the complementary top and bottom strand pairs of SEQ ID NO: 9-40 or 45-268.

[0037] Another embodiment described herein is a method for designing primers partially complementary to the 52-base pair tag sequences described herein and an adapter primer, the method comprising, executing on a processor: (a) designing tag primers that are partially complementary to the top and bottom strands of tag sequences; and (b) designing an adapter primer that is partially complementary to the top strand of the adapter sequence; wherein: the tag primers comprise a 5'-universal tail sequence complementary to an SP1 or SP2 sequence (SEQ ID NO: 7, 8), a locus specific segment, a ribonucleotide (rN) 6-nucleotides from the 3'-end, a 3'-end mismatch, and a 3'-end block (3'-C3 spacer); and the adapter primer comprises a sequence complementary to the SP1 or SP2 sequence (SEQ ID NO: 7, 8). In one aspect, the primers partially complementary to top and bottom strands of the tag sequences comprise a sequence complementary to the SP1 sequence and the adapter primer comprises a sequence complementary to the SP2 sequence; or the primers partially complementary to top and bottom strands of the tag sequences comprise a sequence complementary to the SP2 sequence and the adapter primer comprises a sequence complementary to the SP1 sequence. In another aspect, amplification of a nucleic acid molecule with the primers that are complementary to the top and bottom strands of tag sequences and primers that are complementary to the top strand of the adapter sequence produces a PCR product that comprises a portion of the tag sequence, a sgDNA sequence, and the adapter sequence. In another aspect, the method further comprises synthesising oligonucleotides comprising the sequences of the forward and reverse tag primers and the adapter primer.

[0038] In another embodiment described herein, the 52-base pair tag sequences and primers partially complementary to the 52-base pair tag sequences are designed and selected using an algorithm predicting whether the primers are likely to be partially complementary and have a propensity to form primer-dimers.

[0039] Another embodiment described herein is one or more primers partially complementary to the 52-base pair tag sequences and one or more adapter primers designed using the methods described herein. In one aspect, the primers partially complementary to the 52-base pair tag sequence comprise the sequences of SEQ ID NO: 3, 4; and the adapter primer comprises the sequence of SEQ ID NO:5.

[0040] Another embodiment described herein is the use of one or more double-stranded 52-base pair tag sequences for identifying on- and off-target CRISPR editing sites.

[0041] It will be apparent to one of ordinary skill in the relevant art that suitable modifications and adaptations to the compositions, formulations, methods, processes, and applications described herein can be made without departing from the scope of any embodiments or aspects thereof. The compositions and methods provided are exemplary and are not intended to limit the scope of any of the specified embodiments. All the various embodiments, aspects, and options disclosed herein can be combined in any variations or iterations. The scope of the methods and processes described herein include all actual or potential combinations of embodiments, aspects, options, examples, and preferences herein described. The methods described herein may omit any component or step, substitute any component or

step disclosed herein, or include any component or step disclosed elsewhere herein. It should also be understood that embodiments may include and otherwise be implemented by a combination of various hardware, software, and electronic components. For example, various microprocessors and application specific integrated circuits (“ASICs”) can be utilized, as can software of a variety of languages. Also, servers and various computing devices can be used and can include one or more processing units, one or more computer-readable mediums, one or more input/output interfaces, and various connections (e.g., a system bus) connecting the components. Should the meaning of any terms in any of the patents or publications incorporated by reference conflict with the meaning of the terms used in this disclosure, the meanings of the terms or phrases in this disclosure are controlling. Furthermore, the specification discloses and describes merely exemplary embodiments. All patents and publications cited herein are incorporated by reference herein for the specific teachings thereof.

[0042] Various embodiments and aspects of the inventions described herein are summarized by the following clauses:
[0043] Clause 1. A method for identifying and nominating on- and off-target CRISPR edited sites with improved accuracy and sensitivity, the process comprising the steps of:

[0044] (a) co-delivering a guide sequence RNA (sgRNA) or a two-part CRISPR RNA: trans-activating crRNA (crRNA: tracrRNA) duplex, one or more tag sequences, and an RNA-guided endonuclease to cells;

[0045] (b) incubating the cells for a period of time sufficient for double strand breaks to occur;

[0046] (c) isolating genomic DNA from the cells, fragmenting the genomic DNA, and ligating the fragmented genomic DNA to a unique molecular index containing a universal adapter sequence;

[0047] (d) amplifying the ligated DNA fragments using primers targeting the tag and universal adapter sequences to produce a first set of amplified sequences;

[0048] (e) amplifying the first set of amplified sequences using universal sequencing primers targeting the tails of Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences;

[0049] (f) sequencing the pooled sequences and obtaining sequencing data; and

[0050] (g) identifying on-/off-target CRISPR editing loci.

[0051] Clause 2. The method of clause 1, wherein the universal sequencing primers target SP1 or SP2 sequence (SEQ ID NO: 7, 8) tails on the Tag-pTOP or Tag-pBOT primers to produce a second set of amplified sequences.

[0052] Clause 3. The method of clause 1 or 2, wherein the universal sequencing primers target predesigned non-homologous sequence (SEQ ID NO: 269-273) tails on the Tag-pTOP or Tag-pBot primers to produce a second set of amplified sequences.

[0053] Clause 4. The method of any one of clauses 1-3, wherein the universal sequencing primers target predesigned 13-mer tails on the Tag-pTOP or Tag-pBot primers to produce a second set of amplified sequences.

[0054] Clause 5. The method of any one of clauses 1-4, wherein step (g) comprises executing on a processor:

[0055] Clause 6. aligning the sequence data to a reference genome;

[0056] (a) (ii) identifying on-/off-target CRISPR editing loci; and

[0057] (b) (iii) outputting the alignment, analysis, and results data as custom-formatted files, tables or graphics.

[0058] Clause 7. The method of any one of clauses 1-5, further comprising a step following step (e) comprising:

[0059] (a) (e1) normalizing the second set of amplified sequences to produce concentration normalized libraries, pooling the normalized libraries with other samples to produce pooled libraries; and continuing with steps (f)-(i).

[0060] Clause 8. The method of any one of clauses 1-6, wherein step (d) uses a suppression PCR method.

[0061] Clause 9. The method of any one of clauses 1-7, wherein the RNA-guided endonuclease comprises an endogenously-expressed Cas enzyme, a Cas expression vector, a Cas protein, or a Cas RNP complex.

[0062] Clause 10. The method of any one of clauses 1-8, wherein the RNA-guided endonuclease comprises an endogenously-expressed Cas9 enzyme, a Cas9 expression vector, a Cas9 protein, or a Cas9 RNP complex.

[0063] Clause 11. The method of any one of clauses 1-9, wherein the cells comprise human or mouse cells.

[0064] Clause 12. The method of any one of clauses 1-10, wherein the period of time is about 24 hours to about 96 hours.

[0065] Clause 13. The method of any one of clauses 1-11, wherein multiple tag sequences are co-delivered.

[0066] Clause 14. The method of any one of clauses 1-12, wherein the tag sequences comprise double-stranded deoxy-ribonucleotides (dsDNA) comprising 52-base pairs.

[0067] Clause 15. The method of any one of clauses 1-13, wherein the tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides.

[0068] Clause 16. The method of any one of clauses 1-14, wherein the tag sequences comprise a double stranded DNA comprising the complementary top and bottom strand pairs of SEQ ID NO: 1-2 or 7-268.

[0069] Clause 17. On- and off-target CRISPR editing sites identified or nominated using the method of any one of clauses 1-15.

[0070] Clause 18. A method for designing 52-base pair tag sequences, the method comprising, executing on a processor:

[0071] (a) randomly generating 13-nucleotide sequences with 40-90% GC content, max homopolymer length A: 2, C: 3, G: 2, T: 2, weighted homopolymer rate <20, self-folding Tm<50° C., and self-dimer Tm<50° C.;

[0072] (b) removing sequences that perfectly align to a particular genome or that are homopolymers or GG or CC dinucleotide motifs and obtaining a set of 13-mers;

[0073] (c) selecting a subset of the 13-mer sequences that contain one or less CC or GG dinucleotide motifs;

[0074] (d) concatenating four of the of 13-mer subset sequences to form random 52-mer sequences;

[0075] (e) aligning the random 52-mer sequences to a genome;

[0076] (f) removing the random 52-mer sequences that have similarity to the genome to produce a subset of 52-mer sequences; and

[0077] (g) outputting the subset of 52-mer sequences and generating the complementary strands to produce double stranded 52-base pair tag sequences.

[0078] Clause 19. The method of clause 17, wherein the genome is human or mouse.

[0079] Clause 20. The method of clause 17 or 18, wherein the 52-base pair tag sequences are non-complementary to the genome.

[0080] Clause 21. The method of any one of clauses 17-19, further comprising designing primers for the 52-base pair tag sequences.

[0081] Clause 22. The method of any one of clauses 17-20, wherein the 52-base pair tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides of the 52-base pair tag sequences.

[0082] Clause 23. The method of any one of clauses 17-21, further comprising synthesizing oligonucleotides comprising the 52-base pair tag sequences, the complement of the 52-base pair tag sequences, or primers for the 52-base pair tag sequences.

[0083] Clause 24. One or more 52-base pair tag sequences designed using the methods of clauses 17-22.

[0084] Clause 25. The 52-base pair tag sequences of clause 23, wherein the 52-base pair tag sequence comprises a double-stranded DNA comprising the top and bottom strand pairs of SEQ ID NO: 1-2 or 7-268.

[0085] Clause 26. A method for designing primers partially complementary to the 52-base pair tag sequences of clause 23 and an adapter primer, the method comprising, executing on a processor:

[0086] (a) designing tag primers that are partially complementary to the top and bottom strands of tag sequences; and

[0087] (b) designing an adapter primer that is partially complementary to the top strand of the adapter sequence;

[0088] (c) wherein:

[0089] (d) the tag primers comprise a 5'-universal tail sequence; and

[0090] (e) the adapter primer comprises a sequence complementary to the tails of Tag-pTOP or Tag-pBOT primers.

[0091] Clause 27. The method of clause 25, wherein the 5'-universal tail sequence is complementary to an SP1 or SP2 sequence (SEQ ID NO: 7, 8), a locus specific segment, a ribonucleotide (rN) 6-nucleotides from the 3'-end, a 3'-end mismatch, a 3'-end block (3'-C3 spacer), a pre-designed non-homologous sequence (SEQ ID NO: 269-273), or a pre-designed 13-mer sequence.

[0092] Clause 28. The method of clause 25 or 26, wherein the primers partially complementary to top and bottom strands of the tag sequences comprise a tail sequence complementary to the SP1 sequence (SEQ ID NO: 7) and the adapter primer comprises a sequence complementary to the SP2 sequence (SEQ ID NO: 8) tail on the Tag-pTOP or Tag-pBOT primers; or the primers partially complementary to top and bottom strands of the tag sequences comprise a tail sequence complementary to the SP2 sequence (SEQ ID NO: 8) and the adapter primer comprises a sequence complementary to the SP1 sequence (SEQ ID NO: 7) tail on the Tag-pTOP or Tag-pBOT primers.

[0093] Clause 29. The method of any one of clauses 25-27, wherein the amplification of a nucleic acid molecule with the primers that are complementary to the top and bottom strands of tag sequences and primers that are complementary to the top strand of the adapter sequence produces a PCR

product that comprises a portion of the tag sequence, a sgDNA sequence, and the adapter sequence.

[0094] Clause 30. The method of any one of clauses 25-28, further comprising synthesizing oligonucleotides comprising the sequences of the forward and reverse tag primers and the adapter primer.

[0095] Clause 31. The method of any one of clauses 17-21 and 25-29, wherein the 52-base pair tag sequences and primers partially complementary to the 52-base pair tag sequences are designed and selected using an algorithm predicting whether the primers are likely to be partially complementary and have a propensity to form primer-dimers.

[0096] Clause 32. One or more primers partially complementary to the 52-base pair tag sequences and one or more adapter primers designed using the method of clauses 22-25.

[0097] Clause 33. The primers of clause 32, wherein the primers comprise the sequences of SEQ ID NO: 3, 4; and the adapter primer, wherein the adapter primer comprises the sequence of SEQ ID NO: 5.

[0098] Clause 34. Use of one or more double-stranded 52-base pair tag sequences for identifying on- and off-target CRISPR editing sites.

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EXAMPLES

Example 1

[0107] This experiment demonstrates the increased efficiency in tag integration when using double-stranded DNA tags with a length of 52-base pairs and varying genetic sequence. The sequences used are shown in Tables 3-5. Double-stranded tags were generated by hybridization of a top strand and a complementary bottom strand (Tables 3-4; SEQ ID NO: 9-40 or 45-268). Sixteen different tag designs were introduced separately into HEK293 cells constitutively expressing Cas9 together with a guideRNA which targets the

EMX1 locus. Alternatively, either pools of 16 tags or one pool of 112 tags were introduced into HEK293 cells constitutively expressing Cas9 together with a guideRNA which targets the EMX1 locus. GuideRNAs were electroporated at a concentration of 10 U μ M, whereas the single Tag or pooled Tags were delivered at a final concentration of 0.5 μ M. Tag integration levels were determined by targeted amplification using rhAmpSeq primers (SEQ ID NO: 3-4), enriching for known on- and off-target sites of the EMX1 guideRNA. The rhAmpSeq pool for EMX1 consists of 32 sites, which represent empirically determined ON and OFF target loci. Amplified products were sequenced on an Illumina® MiSeq, and tag integration levels were determined using custom software. This example shows that tag integration efficiency varies among single tag constructs individually with a range between 6 (CTL021) and 13 (CTL169, CTL079, CTL002) sites out of a maximum of 32 sites, and is therefore sequence dependent (Single Tags, FIG. 7). By taking the mathematical union of the single tag results, a hypothetical number of 23 sites was calculated (CTLmax, FIG. 7). The hypothesis that combining a pool of tags would increase the likelihood of tag integration was tested and was demonstrated (Pooled Tags, Table, FIG. 7). Pool A1 consists of the tags represented in the Single Tags (see Table 5) and demonstrated that 21 tag integration events were detected out of a maximum of 32 sites, which is higher than achieved with any of the single tags. Similarly, Pool B3 demonstrated integration of a tag at 21 sites out of a maximum of 32 sites. Again, variability between pools was shown (Pooled Tags, FIG. 7), indicating optimization of tag designs can potentially maximize tag integration.

TABLE 3

Sequences Used for Second Proof of Concept		
Name	Sequence (5'→3')	SEQ ID NO
CTL085_ TOP_tag	/5Phos/A*C*GAGCGGTAGTCACCTA GTCGTCGTACCAATTCGACGCACACTA CTCGC*G*C	SEQ ID NO: 9
CTL085_ BOT_tag	/5Phos/G*C*GCGAGTAGTGCGTC GAATTGGTACGACGACTAGGTGACTAC CGCTC*G*T	SEQ ID NO: 10
CTL169_ TOP_tag	/5Phos/T*A*GCGCGAGTAGTCGGAC GAGCGGTTACCAATACGCCGCACCTTA ATCCG*C*G	SEQ ID NO: 11
CTL169_ BOT_tag	/5Phos/C*G*CGGATTAAGGTGCGGC GTATTGGTAACCGCTCGTCCGACTACT CGCGC*T*A	SEQ ID NO: 12
CTL137_ TOP_tag	/5Phos/T*C*GCGACAGTAGTCGTTT GGCTAGGTACCTATTACCGCGTAGTTA GCGGC*G*T	SEQ ID NO: 13
CTL137_ BOT_tag	/5Phos/A*C*GCCGCTAAGTACGCGG TAATAGGTACCTAGCCGAACGACTACT GTCGC*G*A	SEQ ID NO: 14

TABLE 3-continued

Sequences Used for Second Proof of Concept		
Name	Sequence (5'→3')	SEQ ID NO
CTL042_ TOP_tag	/5Phos/C*G*CGCTACTAGGTGCGTC GAATTGGTACCGATCCGCAATACACTA CTCGC*G*C	SEQ ID NO: 15
CTL042_ BOT_tag	/5Phos/G*C*GCGAGTAGTGATTGC GGATCGGTACCAATTCGACGCACCTAG TAGCG*C*G	SEQ ID NO: 16
CTL051_ TOP_tag	/5Phos/G*G*TAACGAGCGGTGCGTC GAATTGGTAACCGCTCGTCCGACCTTA ATCGC*G*C	SEQ ID NO: 17
CTL051_ BOT_tag	/5Phos/G*C*GCGATTAGGTGCGAC GAGCGGTTACCAATTCGACGCACCGCT CGTTA*C*C	SEQ ID NO: 18
CTL167_ TOP_tag	/5Phos/T*T*CGGCGCTAGGTGCGGC GTATTGGTAACCGCTCGTCCGTTGCGC GCTAG*G*T	SEQ ID NO: 19
CTL167_ BOT_tag	/5Phos/A*C*CTAGCGCCGAACGGAC GAGCGGTTACCAATACGCCGCACCTAG CGCCG*A*A	SEQ ID NO: 20
CTL026_ TOP_tag	/5Phos/T*A*CGCGACTAGGTGCGCG ATTAAGGTACCTATTACCGCGCGACTA TGTGC*G*C	SEQ ID NO: 21
CTL026_ BOT_tag	/5Phos/G*C*GCACATAGTCGCGCGG TAATAGGTACCTTAATCGCGCACCTAG TCGCG*T*A	SEQ ID NO: 22
CTL068_ TOP_tag	/5Phos/G*T*CGCGCAGTGTAGCGCG ATTAAGGTACCTATTACCGCGTCGCGA CAGTA*G*T	SEQ ID NO: 23
CTL068_ BOT_tag	/5Phos/A*C*TACTGTGCGGACGCGG TAATAGGTACCTTAATCGCGCTACACT GCGCG*A*C	SEQ ID NO: 24
CTL138_ TOP_tag	/5Phos/A*A*CCGTGATCCGCGCGT AGTATGGTACCGATCCGCAATACCTAGC GCGAC*A*A	SEQ ID NO: 25
CTL138_ BOT_tag	/5Phos/T*T*GTGCGCTAGTATTGC GGATCGGTACCACTACGCGCGGATC GACGG*T*T	SEQ ID NO: 26
CTL079_ TOP_tag	/5Phos/T*C*GCTCGATTGGTTACGC GCACTACTATGCGCTCGACTCGTTTCG GCTAG*G*T	SEQ ID NO: 27
CTL079_ BOT_tag	/5Phos/A*C*CTAGCCGAACGAGTCG AGCGCATAAGTAGTGCGCGTAACCAAT CGAGC*G*A	SEQ ID NO: 28

TABLE 3-continued

Sequences Used for Second Proof of Concept		
Name	Sequence (5'→3')	SEQ ID NO
CTL063_ TOP_tag	/5Phos/A*C*TCGAGCGTACTTGTC GCGCTAGTACCAATTCGACGCAACCGC TCGTC*C*G	SEQ ID NO: 29
CTL063_ BOT_tag	/5Phos/C*G*GACGAGCGTTGCGTC GAATTGGTACTAGCGCGACAAGTACGC TCGCA*G*T	SEQ ID NO: 30
CTL168_ TOP_tag	/5Phos/C*G*CATTAGTCGGTGCGGC GTATTGGTAACCGCTCGTCCGACGCGC TACCT*A*T	SEQ ID NO: 31
CTL168_ BOT_tag	/5Phos/A*T*AGGTAGCGGTCGGAC GAGCGGTTACCAATACGCCGACCGAC TAATG*C*G	SEQ ID NO: 32
CTL021_ TOP_tag	/5Phos/A*T*TCGCGATCGGTGCGTC GAATTGGTAACCGCTCGTCCGTACGCG CACTA*C*T	SEQ ID NO: 33
CTL021_ BOT_tag	/5Phos/A*G*TAGTGC CGGTACGGAC GAAGCGGTTACCAATTCCGCGACCGAT CCGCA*A*T	SEQ ID NO: 34
CTL151_ TOP_tag	/5Phos/T*C*GGCGAGTAGTTGCGCG GTTATGGTACCATAACCGCGCAGTAGT ACGCG*G*T	SEQ ID NO: 35
CTL151_ BOT_tag	/5Phos/A*C*CGCGTACTACTGCGCG GTTATGGTACCATAACCGCGCAACTAC TCGCC*G*A	SEQ ID NO: 36
CTL002_ TOP_tag	/5Phos/A*C*TAGCGATCGGTACCTA GCGCCGAAACCTATTACCGCGACCTAG CGTTG*C*G	SEQ ID NO: 37
CTL002_ BOT_tag	/5Phos/C*G*CAACGCTAGGTCGCGG TAATAGGTTTCGGCGCTAGGTACCGAT CGCTA*G*T	SEQ ID NO: 38
CTL134_ TOP_tag	/5Phos/T*A*GCGCGTCAAGAGCGCG GTTATGGTTTCGGCGCTAGGTTAACAG CGCGT*C*G	SEQ ID NO: 39
CTL134_ BOT_tag	/5Phos/C*G*ACGCGCTGTTAACCTA GCGCCGAAACCTAACC CGCTCTTGA CGCGC*T*A	SEQ ID NO: 40
GuideSeq_ TOP_tag	/5Phos/G*T*TTAATTGAGTTGTCAT ATGTTAATAACGGT*A*T	SEQ ID NO: 41
GuideSeq_ BOT_tag	/5Phos/A*T*ACCGTTATTAACATAT GACAACTCAATTAA*A*C	SEQ ID NO: 42

TABLE 3-continued

Sequences Used for Second Proof of Concept		
Name	Sequence (5'→3')	SEQ ID NO
EMX1 protospacer	GAGTCCGAGCAGAAGAAGAA	SEQ ID NO: 43
AR protospacer	GTTGGAGCATCTGAGTCCAG	SEQ ID NO: 44

"/5Phos/" indicates a 5'-phosphate moiety; "*" indicates a phosphorothioate linkage.

Example 2

[0108] This experiment demonstrates the increased efficiency in tag integration when using double-stranded DNA tags with a length of 52-base pairs and varying genetic sequence. The sequences used are shown in Tables 3-5. Double-stranded tags were generated by hybridization of a top strand and a complementary bottom strand (SEQ ID NO: 9-40 or 45-268). Sixteen different tag designs were introduced separately into HEK293 cells constitutively expressing Cas9 together with a guideRNA which targets the AR locus. Alternatively, either pools of 16 tags or one pool of 112 tags were introduced into HEK293 cells constitutively expressing Cas9 together with a guideRNA which targets the AR locus. GuideRNAs were electroporated at a concentration of 10 μ M, whereas the single Tag or pooled Tags were delivered at a final concentration of 0.5 μ M. Tag integration levels were determined by targeted amplification using rhAmpSeq primers (SEQ ID NO: 3-4), enriching for known on- and off-target sites of the AR guideRNA. The rhAmpSeq pool for AR consists of 53 sites which represent empirically determined ON and OFF target loci. Amplified products were sequenced on an Illumina® MiSeq, and tag integration levels were determined using custom software. This example shows that tag integration efficiency varies among single tag constructs individually with a range between 35 (CTL085, CTL134) and 41 sites (CTL002) out of a maximum of 53 sites, and is therefore sequence dependent (Single Tags, Table 5, FIG. 8).

[0109] By taking the mathematical union of the single tag results, a hypothetical number of 47 sites was calculated (CTLmax, FIG. 8). The hypothesis that combining a pool of tags would increase the likelihood of tag integration was tested and was demonstrated (Pooled Tags, Table 5, FIG. 8). Pool B4 (see Table 5) demonstrated that 44 tag integration events were detected out of a maximum of 53 sites, which is higher than achieved with any of the single tags. Again, variability between pools was shown (Pooled Tags, Table 5, FIG. 8), indicating optimization of tag designs can potentially maximize tag integration.

TABLE 4

Tag Sequences			
Name	Sequence (5'→3')	SEQ	ID NO
CTL085_TOP_tag	/5Phos/A*C*GAGCGGTAGTCACCTAGTCGTCGTACCAATTCGASEQ CGCACACTACTCGC*G*C	ID NO:	45
CTL169_TOP_tag	/5Phos/T*A*GCGCGAGTAGTCGGACGAGCGGTTACCAATACGCSEQ CGCACCTTAATCCG*C*G	ID NO:	46
CTL137_TOP_tag	/5Phos/T*C*GCGACGAGTAGTCGTTCCGGCTAGGTACCTATTACCSEQ GCGTAGTTAGCGGC*G*T	ID NO:	47
CTL042_TOP_tag	/5Phos/C*G*CGCTACTAGGTGCGTCGAATTGGTACCGATCCGCSEQ AATACACTACTCGC*G*C	ID NO:	48
CTL051_TOP_tag	/5Phos/G*G*TAACGAGCGGTGCGTCGAATTGGTAACCGCTCGTSEQ CCGACCTTAATCGC*G*C	ID NO:	49
CTL167_TOP_tag	/5Phos/T*T*CGGCGCTAGGTGCGGCGTATTGGTAACCGCTCGTSEQ CCGTTCCGGCGCTAG*G*T	ID NO:	50
CTL026_TOP_tag	/5Phos/T*A*CGCGACTAGGTGCGCGATTAAGGTACCTATTACCSEQ GCGCGACTATGTGC*G*C	ID NO:	51
CTL068_TOP_tag	/5Phos/G*T*CGGCGAGTGTAGCGCGATTAAGGTACCTATTACCSEQ GCGTCGCGACAGTA*G*T	ID NO:	52
CTL138_TOP_tag	/5Phos/A*A*CCGTCGATCCGCGCGTAGTATGGTACCGATCCGCSEQ AATACTAGCGCGAC*A*A	ID NO:	53
CTL079_TOP_tag	/5Phos/T*C*GCTCGATTGGTTACGCGCACTACTTATGCGCTCGSEQ ACTCGTTCGGCTAG*G*T	ID NO:	54
CTL063_TOP_tag	/5Phos/A*C*TGCGAGCGTACTTGTGCGGCTAGTACCAATTCGASEQ CGCAACCGCTCGTC*C*G	ID NO:	55
CTL168_TOP_tag	/5Phos/C*G*CATTAGTCGGTGCGGCGTATTGGTAACCGCTCGTSEQ CCGACGCGCTACCT*A*T	ID NO:	56
CTL021_TOP_tag	/5Phos/A*T*TGCGGATCGGTGCGTCGAATTGGTAACCGCTCGTSEQ CCGTACGCGCACTA*C*T	ID NO:	57
CTL151_TOP_tag	/5Phos/T*C*GGCGAGTAGTTGCGCGGTTATGGTACCATAACCGSEQ CGCAGTAGTACGCG*G*T	ID NO:	58
CTL002_TOP_tag	/5Phos/A*C*TAGCGATCGGTACCTAGCGCCGAAACCTATTACCSEQ GCGACCTAGCGTTG*C*G	ID NO:	59
CTL134_TOP_tag	/5Phos/T*A*GCGCGTCAAGAGCGCGGTTATGGTTCCGGCGCTASEQ GGTTAACAGCGGT*C*G	ID NO:	60
CTL085_BOT_tag	/5Phos/G*C*GCGAGTAGTGTGCGTCGAATTGGTACGACGACTASEQ GGTGACTACCGCTC*G*T	ID NO:	61
CTL169_BOT_tag	/5Phos/C*G*CGGATTAAGGTGCGGCGTATTGGTAACCGCTCGTSEQ CCGACTACTCGCGC*T*A	ID NO:	62
CTL137_BOT_tag	/5Phos/A*C*GCCGCTAACTACGCGGTAATAGGTACCTAGCCGASEQ ACGACTACTGTCGC*G*A	ID NO:	63
CTL042_BOT_tag	/5Phos/G*C*GCGAGTAGTGATTGCGGATCGGTACCAATTCGASEQ CGCACCTAGTAGCG*C*G	ID NO:	64
CTL051_BOT_tag	/5Phos/G*C*GCGATTAAGGTGCGACGAGCGGTTACCAATTCGASEQ CGCACCGCTCGTTA*C*C	ID NO:	65
CTL167_BOT_tag	/5Phos/A*C*CTAGCGCCGAACGGACGAGCGGTTACCAATACGCSEQ CGCACCTAGCGCCG*A*A	ID NO:	66
CTL026_BOT_tag	/5Phos/G*C*GCACATAGTCGCGCGGTAATAGGTACCTTAATCGSEQ CGCACCTAGTCGCG*T*A	ID NO:	67
CTL068_BOT_tag	/5Phos/A*C*TACTGTGCGGACGCGGTAATAGGTACCTTAATCGSEQ CGCTACACTGCGCG*A*C	ID NO:	68

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL138_BOt_tag	/5Phos/T*T*GTCGCGCTAGTATTGCGGATCGGTACCATACTACSEQ GCCGCGATCGACGG*T*T	ID NO: 69	
CTL079_BOt_tag	/5Phos/A*C*CTAGCCGAACGAGTCGAGCGCATAAGTAGTGCGCSEQ GTAACCAATCGAGC*A*A	ID NO: 70	
CTL063_BOt_tag	/5Phos/C*G*GACGAGCGGTTGCGTCGAATTGGTACTAGCGCGASEQ CAAGTACGCTCGCA*A*T	ID NO: 71	
CTL168_BOt_tag	/5Phos/A*T*AGGTAGCGGTCGGACGAGCGGTTACCAATACGCSEQ CGCACCAGCTAATG*C*G	ID NO: 72	
CTL021_BOt_tag	/5Phos/A*G*TAGTGCGCGTACGGACGAGCGGTTACCAATTCGASEQ CGCACCAGATCCGCA*A*T	ID NO: 73	
CTL151_BOt_tag	/5Phos/A*C*CGCGTACTACTGCGCGGTTATGGTACCATAACCGSEQ CGCAACTACTCGCC*A*A	ID NO: 74	
CTL002_BOt_tag	/5Phos/C*G*CAACGCTAGGTGCGGTAATAGGTTTCGGCGCTASEQ GGTACCGATCGCTA*A*T	ID NO: 75	
CTL134_BOt_tag	/5Phos/C*G*ACGCGCTGTTAACCTAGCGCCGAAACCATAACCGSEQ CGCTCTTGACGCGC*T*A	ID NO: 76	
CTL161_TOP_tag	/5Phos/T*A*CACTGCGCGACACTGCGAGCGTACACCTTAATCGSEQ CGCTAGTTAGCGGC*A*T	ID NO: 77	
CTL164_TOP_tag	/5Phos/A*A*CCGTCGAGTGCACCGCGTACTACTAATGTCGAACSEQ CGCTACGCGCACTA*C*T	ID NO: 78	
CTL030_TOP_tag	/5Phos/C*G*CGGACTAAGGTGCGCGAGTAGTGTTACGCGCACTSEQ ACTAATCTAGCCGC*A*A	ID NO: 79	
CTL088_TOP_tag	/5Phos/A*C*TAGTGCGACGAACCTACTCGCGCTAACCAATTCGASEQ CGCACCAGATCGCTA*A*T	ID NO: 80	
CTL148_TOP_tag	/5Phos/A*A*TGTGGAACCGCGCGGAGTAGTGTTACCATAACCGSEQ CGCACCTTAGTCCG*C*G	ID NO: 81	
CTL152_TOP_tag	/5Phos/G*C*GTCGAATTGGTACCGCCGACTTATACCAATACGCSEQ CGCATAGGTAGCGC*A*T	ID NO: 82	
CTL007_TOP_tag	/5Phos/A*C*CTAGTAGCGCGGCGTCGAATTGGTACTAGCGCGASEQ CAACGCGTAGTATG*A*T	ID NO: 83	
CTL141_TOP_tag	/5Phos/A*C*CGCTCGTTACCGCGGATTAAGGTACGCCGCTAASEQ CTACGGTACGGTCG*A*T	ID NO: 84	
CTL064_TOP_tag	/5Phos/A*C*CGCCGACTTATCGTTCCGGCTAGGTACCAATTCGASEQ CGCACTGCGAGCGT*A*C	ID NO: 85	
CTL158_TOP_tag	/5Phos/A*C*CTTAATCCGCGACTGCGAGCGTACACCTATTACCSEQ GCGCGACGCGCTGT*T*A	ID NO: 86	
CTL066_TOP_tag	/5Phos/A*C*GACGACTAGGTACCGCTCGTTACCTCTTGACGCGSEQ CTAACCAATTTCGAC*A*C	ID NO: 87	
CTL144_TOP_tag	/5Phos/A*C*CATACTACGCGGCGGTTTCGACATTACCATAACCGSEQ CGCTAGTGCGAGCG*T*A	ID NO: 88	
CTL107_TOP_tag	/5Phos/C*T*TGTACGGCGGTGCGGCGTATTGGTACCAATACGCSEQ CGTCTGTCGCACTA*A*T	ID NO: 89	
CTL149_TOP_tag	/5Phos/G*T*ACGCTCGCAGTACCGCCGACTTATACCTTAATCGSEQ CGCACTAGCGCGAC*A*A	ID NO: 90	
CTL008_TOP_tag	/5Phos/A*C*GACGACTAGGTTATGGTACGGCGTTAGCGCGAGTSEQ AGTACCTTAGTCCG*C*G	ID NO: 91	
CTL099_TOP_tag	/5Phos/A*C*GAGCGGTAGTCATAGGTAGCGCGTTCTTGACGCGSEQ CTAACCGATCGCTA*A*T	ID NO: 92	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL089_TOP_tag	/5Phos/A*C*CGATCCGCAATGCGTCGAATTGGTACCATAACCGSEQ CGCACCGCCGTACA*A*G	ID NO: 93	
CTL081_TOP_tag	/5Phos/A*C*TAGTGCACGAACTACTGTGCGAACCTATTACCSEQ GCGACCAATCGAGC*G*A	ID NO: 94	
CTL075_TOP_tag	/5Phos/A*C*CGCCGTACAAGTCGCGACAGTAGTAACCGCTCGTSEQ CCGTTCGGCGCTAG*G*T	ID NO: 95	
CTL160_TOP_tag	/5Phos/T*C*GTGCGACTAGTCGCATTAGTCGGTAGTAGACGCSEQ GGTATAGGTAGCGC*G*T	ID NO: 96	
CTL133_TOP_tag	/5Phos/A*C*CAATTCGACGCTAGTTAGCGCGGTACACTACTCGSEQ CGCGCACTCGACGG*T*T	ID NO: 97	
CTL076_TOP_tag	/5Phos/C*G*CGGTAATAGGTCGCGGTAATAGGTACGAGCGGTASEQ GTCACACTACTCGC*G*C	ID NO: 98	
CTL024_TOP_tag	/5Phos/T*C*GGCGAGTAGTTTAGTGCAGCGTAAGTAGTGCGCSEQ GTAACCAATCGAGC*G*A	ID NO: 99	
CTL045_TOP_tag	/5Phos/G*T*CGCGCAGTGTAGCGCGTTATGGTACCATAACCGSEQ CGCACTAGTGCAC*G*A	ID NO: 100	
CTL009_TOP_tag	/5Phos/T*A*TGCGCTCGACTGCGCGATTAAGGTAATGTCGAACSEQ CGCAGTAGTACGCG*G*T	ID NO: 101	
CTL055_TOP_tag	/5Phos/A*C*TAGCGCGACAACGACTATGTGCGCACCAATTCGASEQ CGCTACGCGCACTA*C*T	ID NO: 102	
CTL101_TOP_tag	/5Phos/A*A*CTACTCGCGACTTGTACGGCGGTACCAATTCGASEQ CGCAACTAATCCGC*G*C	ID NO: 103	
CTL135_TOP_tag	/5Phos/C*G*CGGATTAAGGTCTTGTACGGCGGTACCTAGCCGASEQ ACGTACGCGCACTA*C*T	ID NO: 104	
CTL155_TOP_tag	/5Phos/T*A*GCGCGTCAAGACTTGTACGGCGGTACCGATCCGCSEQ AATGCACTCGACGG*T*T	ID NO: 105	
CTL122_TOP_tag	/5Phos/C*G*CATTAGTCGGTGCGGCGTATTGGTACGACGACTASEQ GGTACCAATACGCC*G*C	ID NO: 106	
CTL080_TOP_tag	/5Phos/A*C*CTAGTAGCGCGCGCGTTATGGTACCGACTAATSEQ GCGACTAGCGATCG*G*T	ID NO: 107	
CTL126_TOP_tag	/5Phos/A*C*TACTCGCGCTAACCTAGTCGTGTAATCTAGCCGSEQ CGATACGCTCGCAC*T*A	ID NO: 108	
CTL098_TOP_tag	/5Phos/A*C*CGCCGTATACGCGGATTAAGGTGTACGCTCGCSEQ AGTCGCGGACTAAG*G*T	ID NO: 109	
CTL038_TOP_tag	/5Phos/T*A*CGCGCACTACTAACCGTCGAGTGCGTACGCTCGCSEQ AGTACCGATCGCTA*G*T	ID NO: 110	
CTL139_TOP_tag	/5Phos/G*T*CGCGCAGTGTATAACAGCGCGTCGTTAGTGCGCSEQ AGAACGACGACTAG*G*T	ID NO: 111	
CTL010_TOP_tag	/5Phos/G*C*GTCGAATTGGTCGCGTAGTATGGTACCGCCGCTASEQ TACACCAATACGCC*G*C	ID NO: 112	
CTL034_TOP_tag	/5Phos/T*A*CGCGCACTACTTACGCGACTAGGTACCGATCGCTSEQ AGTCGACGCGCTGT*T*A	ID NO: 113	
CTL117_TOP_tag	/5Phos/A*C*GCCGCTAACTATAGTTAGCGCGGTACCAATTCGASEQ CGCAACTAATCCGC*G*C	ID NO: 114	
CTL035_TOP_tag	/5Phos/C*G*CGGACTAAGGTTAGTTAGCGCGGTTACGCGCACTSEQ ACTACCGATCCGA*A*T	ID NO: 115	
CTL121_TOP_tag	/5Phos/A*C*GACGACTAGGTACCGCGGCTTATACGCGCTAASEQ CTAATAGGTAGCGC*G*T	ID NO: 116	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL106_TOP_tag	/5Phos/C*G*GATCGACGGTTGCGCGAGTAGTGTAGTAGTACGCSEQ GGTTACACTGCGCG*A*C	ID NO: 117	
CTL059_TOP_tag	/5Phos/A*T*TGCGGATCGGTACCGCCGACTTATACCGATCCGCSEQ AATTCGCTCGATTG*G*T	ID NO: 118	
CTL157_TOP_tag	/5Phos/A*C*TGCGAGCGTACACTGCGAGCGTACACCTTAATCGSEQ CGCACCGCTCGTTA*C*C	ID NO: 119	
CTL015_TOP_tag	/5Phos/A*C*TACTGTGCGGATCGTGCCTAGTTACGCTCGCASEQ CTAATTGCGGATCG*G*T	ID NO: 120	
CTL110_TOP_tag	/5Phos/G*G*TAACGAGCGGTTCTCGCGCACTAATTAGTGCGCGSEQ AGAACCATACTACG*C*G	ID NO: 121	
CTL123_TOP_tag	/5Phos/A*C*TACTCGCGCTAGCGGATTAAGGTACCTTAATCGSEQ CGCAACTACTCGCC*G*A	ID NO: 122	
CTL014_TOP_tag	/5Phos/T*A*CGCGCACTACTCTTGACGGCGGTACCAATTCGASEQ CGCAACCGTCGAGT*G*C	ID NO: 123	
CTL131_TOP_tag	/5Phos/A*A*CCGTCGATCCGATTGCGGATCGGTACCTTAATCGSEQ CGCACTAGTGCAC*G*A	ID NO: 124	
CTL062_TOP_tag	/5Phos/A*G*TAGTGCGCGTATACACTGCGCGACACACTACTCGSEQ CGCACCTTAATCCG*C*G	ID NO: 125	
CTL044_TOP_tag	/5Phos/A*C*GCCGTACCATACGCGTAATAGGTAGTAGTGCGCSEQ GTATTGCGCGCTAG*G*T	ID NO: 126	
CTL043_TOP_tag	/5Phos/T*A*GCGCGTCAAGAACCTAGCGTTGCGATAAGTCGGCSEQ GGTAGTAGTACGCG*G*T	ID NO: 127	
CTL118_TOP_tag	/5Phos/C*G*CATTAGTCGGTAATCTAGCCGGAACCATAACCGSEQ CGCACCGATCGCTA*G*T	ID NO: 128	
CTL128_TOP_tag	/5Phos/T*A*TGGTACGGCGTGCGCGTATTGGTACGCCGCTAASEQ CTAATAAGTCGGCG*G*T	ID NO: 129	
CTL067_TOP_tag	/5Phos/G*C*GCGGTTATGGTGCGCGTATTGGTACGAGCGGTASEQ GTCAACCGCTCGTC*C*G	ID NO: 130	
CTL020_TOP_tag	/5Phos/C*G*ACTATGTGCGCAACTACTCGCCGAACCATAACCGSEQ CGCTATGCGCTCGA*C*T	ID NO: 131	
CTL006_TOP_tag	/5Phos/T*A*GTTAGCGGCGTACCGCTCGTTACCACCTTAATCGSEQ CGCACCATACTACG*C*G	ID NO: 132	
CTL017_TOP_tag	/5Phos/C*G*CATTAGTCGGTAGTAGTGCGCGTAAACCGCTCGTSEQ CCGTTAGTGCGGA*G*A	ID NO: 133	
CTL057_TOP_tag	/5Phos/T*A*GCGCGAGTAGTACCGACTAATGCGTCTCGCGCACSEQ TAAGACTACCGTC*G*T	ID NO: 134	
CTL078_TOP_tag	/5Phos/T*A*CGCTCGCACTATCGCTCGATTGGTACGCCGCTASEQ TACACCATAACCGC*G*C	ID NO: 135	
CTL031_TOP_tag	/5Phos/A*C*CAATCGAGCGAAGTCGAGCGCATAACGCGCTACCSEQ TATACGCGCTAAC*T*A	ID NO: 136	
CTL136_TOP_tag	/5Phos/A*C*CTTAATCCGCGACTGCGAGCGTACACCGACTAATSEQ GCGACTACTGTCGC*G*A	ID NO: 137	
CTL165_TOP_tag	/5Phos/A*G*TAGTGCGCGTATCGCTCGATTGGTTCTTGACGCGSEQ CTAGTATAGCGCG*G*T	ID NO: 138	
CTL039_TOP_tag	/5Phos/T*C*GTCGCACTAGTCGGTACGGTCGGTGCGCACATAGSEQ TCGTATGGTACGGC*G*T	ID NO: 139	
CTL036_TOP_tag	/5Phos/C*G*CGGATTAAGGTAGTCGAGCGCATAACCGCTACTSEQ ACTACGACGACTAG*G*T	ID NO: 140	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL048_TOP_tag	/5Phos/C*G*ACTATGTGCGCTACGCTCGCACTAACACTACTCGSEQ CGCACCTAGCGCCG*A*A	ID NO: 141	
CTL053_TOP_tag	/5Phos/A*C*CGCCGACTTATTCTCGCGCACTAATCGTCGCACTSEQ AGTAACCGTCGATC*C*G	ID NO: 142	
CTL072_TOP_tag	/5Phos/A*C*CTAGCGTTGCGACCGACTAATGCGGGTAACGAGCSEQ GGTTATGGTACGGC*G*T	ID NO: 143	
CTL096_TOP_tag	/5Phos/C*G*CGCTACTAGGTCGCGGTAATAGGTACCTAGCGTTSEQ GCGACCTAGTCGCG*T*A	ID NO: 144	
CTL150_TOP_tag	/5Phos/C*G*TTGCGCTAGGTACTACTCGCGCTACGCATTAGTCSEQ GGTTCGCGACAGTA*G*T	ID NO: 145	
CTL084_TOP_tag	/5Phos/C*G*GACGAGCGGTTTCGCGGTAATAGGTACGACGACTASEQ GGTTAGTTAGCGGC*G*T	ID NO: 146	
CTL142_TOP_tag	/5Phos/T*A*CGCTCGCACTAATTGCGGATCGGTACCGACTAATSEQ GCGACCGCGTACTA*C*T	ID NO: 147	
CTL102_TOP_tag	/5Phos/A*C*CGACCGTACCGTATGGTACGGCGTTCTTGACGCGSEQ CTAACCTAGCGCCG*A*A	ID NO: 148	
CTL154_TOP_tag	/5Phos/G*C*GCGGATTAGTTAACCGTCGAGTGCACACTACTCGSEQ CGCACTGCGAGCGT*A*C	ID NO: 149	
CTL112_TOP_tag	/5Phos/A*C*CTTAATCCGCGACCGACTAATGCGTACGCGCACTSEQ ACTATAAGTCGGCG*G*T	ID NO: 150	
CTL145_TOP_tag	/5Phos/A*C*CTTAATCCGCGCGCGTTATGGTACCGACTAATSEQ GCGAACCCTCGTC*C*G	ID NO: 151	
CTL060_TOP_tag	/5Phos/A*C*TGCGAGCGTACCTTGTACGGCGGTACCTAGTAGCSEQ GCGATAAGTCGGCG*G*T	ID NO: 152	
CTL016_TOP_tag	/5Phos/T*T*CGGCGCTAGGTACCTTAGTCCGCGTTCGGCGCTASEQ GGTACCTAGCGTTG*C*G	ID NO: 153	
CTL159_TOP_tag	/5Phos/A*C*CTAGTCGCGTACTTGTACGGCGGTACCTAGCCGASEQ ACGAACCGTCGAGT*G*C	ID NO: 154	
CTL056_TOP_tag	/5Phos/A*C*CATAACCGCGCTACACTGCGCGACCAATACGCSEQ CGCTATGGTACGGC*G*T	ID NO: 155	
CTL162_TOP_tag	/5Phos/A*C*ACTACTCGCGCTACGCGACTAGGTAATGTGCAACSEQ CGCACGCCGCTAAC*T*A	ID NO: 156	
CTL018_TOP_tag	/5Phos/A*C*CGACTAATGCGTAACAGCGCGTCGTTAGTGCAGSEQ AGAACCTTAATCGC*G*C	ID NO: 157	
CTL115_TOP_tag	/5Phos/A*C*GCCGTACCATAACCGACTAATGCGATAAGTCGGCSEQ GGTACCAATACGCC*G*C	ID NO: 158	
CTL033_TOP_tag	/5Phos/G*T*ACGCTCGCAGTCGCGGTAATAGGTTTCGGCGAGTASEQ GTTACCATAACCGC*G*C	ID NO: 159	
CTL047_TOP_tag	/5Phos/C*G*GACGAGCGGTTGCGCGGTTATGGTACTAGTGCAGSEQ CGAGCGCACATAGT*C*G	ID NO: 160	
CTL108_TOP_tag	/5Phos/A*C*TACTCGCGCTAGCGGATTAAGGTACGCGCTAASEQ CTATCGCGGCTAGA*T*T	ID NO: 161	
CTL041_TOP_tag	/5Phos/A*C*CAATTCGACGCAACTAATCCGCGCACCAATTCGASEQ CGCAGTAGTGCAGG*T*A	ID NO: 162	
CTL061_TOP_tag	/5Phos/A*C*CGCCGCTATACCTAGCGCCGAAGTACGCTCGCSEQ AGTGATAGCGGCG*G*T	ID NO: 163	
CTL166_TOP_tag	/5Phos/A*C*ACTACTCGCGCCGACGAGCGGTTACCAATACGCSEQ CGCTAGCGGAGTA*G*T	ID NO: 164	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL012_TOP_tag	/5Phos/T*C*GTGCGACTAGTACCTTAATCCGCGCGCAACGCTASEQ GGTACACTACTCGC*G*C	ID NO: 165	
CTL052_TOP_tag	/5Phos/C*G*CGCTACTAGGTACCGACTAATGCGCGCAACGCTASEQ GGTAATGTGGAACC*G*C	ID NO: 166	
CTL153_TOP_tag	/5Phos/A*C*GAGCGGTAGTCACTACTGTGCGGACGCAACGCTASEQ GGTTACACTGCGCG*A*C	ID NO: 167	
CTL094_TOP_tag	/5Phos/A*C*CTAGTCGCGTACGCGTAGTATGGTACCGATCGCTSEQ AGTGGTAACGAGCG*G*T	ID NO: 168	
CTL095_TOP_tag	/5Phos/G*C*GGTTCGACATTACCGACTAATGCGTATGCGCTCGSEQ ACTACCTAGCGTTG*C*G	ID NO: 169	
CTL105_TOP_tag	/5Phos/A*C*TGCGAGCGTACTCTCGCGCACTAAACGCCGCTAASEQ CTACGCGCTACTAG*G*T	ID NO: 170	
CTL109_TOP_tag	/5Phos/C*G*GTACGGTCGGTAATCTAGCCGCGAACCTTAGTCCSEQ GCGACCGCGGTACA*A*G	ID NO: 171	
CTL032_TOP_tag	/5Phos/T*C*GGCGAGTAGTTACGCGCTACCTATTCGCGGCTAGSEQ ATTACGCGCTAAC*T*A	ID NO: 172	
CTL161_BOT_tag	/5Phos/A*C*GCCGCTAACTAGCGGATTAAGGTGTACGCTCGCSEQ AGTGTGCGCGAGTG*T*A	ID NO: 173	
CTL164_BOT_tag	/5Phos/A*G*TAGTGCCTAGCGGTTGACATTAGTAGTACGCGSEQ GGTGCACTCGACGG*T*T	ID NO: 174	
CTL030_BOT_tag	/5Phos/T*C*GCGGCTAGATTAGTAGTGCCTGAACACTACTCGSEQ CGCACCTTAGTCCG*C*G	ID NO: 175	
CTL088_BOT_tag	/5Phos/A*C*TAGCGATCGGTGCGTGAATTGGTTAGCGCGAGTSEQ AGTTCGTGCGACTA*G*T	ID NO: 176	
CTL148_BOT_tag	/5Phos/C*G*CGGACTAAGGTGCGCGTTATGGTACACTACTCGSEQ CGCGCGTTGACACA*T*T	ID NO: 177	
CTL152_BOT_tag	/5Phos/A*C*GCGCTACCTATGCGCGTATTGGTATAAGTCGGCSEQ GGTACCAATTCGAC*G*C	ID NO: 178	
CTL007_BOT_tag	/5Phos/A*C*CATACTACGCGTTGTCGCGCTAGTACCAATTCGASEQ CGCCGCGCTACTAG*G*T	ID NO: 179	
CTL141_BOT_tag	/5Phos/A*C*CGACCGTACCGTAGTTAGCGCGGTACCTTAATCGSEQ CGCGGTAAAGAGCG*G*T	ID NO: 180	
CTL064_BOT_tag	/5Phos/G*T*ACGCTCGCAGTGCCTGAATTGGTACCTAGCCGASEQ ACGATAAGTCGCG*G*T	ID NO: 181	
CTL158_BOT_tag	/5Phos/T*A*ACAGCGGTGCGCGGTAATAGGTGTACGCTCGCSEQ AGTCGCGGATTAG*G*T	ID NO: 182	
CTL066_BOT_tag	/5Phos/G*C*GTGCAATTGGTTAGCGCGTCAAGAGGTAACGAGCSEQ GGTACCTAGTCGTC*G*T	ID NO: 183	
CTL144_BOT_tag	/5Phos/T*A*CGCTCGCACTAGCGCGTTATGGTAATGTCGAACSEQ CGCCGCGTAGTATG*G*T	ID NO: 184	
CTL107_BOT_tag	/5Phos/A*C*TAGTGCACGAGCGCGTATTGGTACCAATACGCGSEQ CGCACCGCGGTACA*A*G	ID NO: 185	
CTL149_BOT_tag	/5Phos/T*T*GTCGCGCTAGTGCCTGATTAAGGTATAAGTCGGCSEQ GGTACTGCGAGCGT*A*C	ID NO: 186	
CTL008_BOT_tag	/5Phos/C*G*CGGACTAAGGTACTACTCGCGCTAACGCCGTACCSEQ ATAACCTAGTCGTC*G*T	ID NO: 187	
CTL099_BOT_tag	/5Phos/A*C*TAGCGATCGGTAGCGCGTCAAGAACGCGCTACCSEQ TATGACTACCGCTC*G*T	ID NO: 188	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL089_BOT_tag	/5Phos/C*T*GTACGGCGGTGCGCGTTATGGTACCAATTCGASEQ CGCATTGCGGATCG*G*T	ID NO: 189	
CTL081_BOT_tag	/5Phos/T*C*GCTCGATTGGTCGCGGTAATAGGTTGCGCACAGTSEQ AGTTCGTCGCACTA*G*T	ID NO: 190	
CTL075_BOT_tag	/5Phos/A*C*CTAGCGCCGAACGGACGAGCGGTTACTACTGTCGSEQ CGACTTGTACGGCG*G*T	ID NO: 191	
CTL160_BOT_tag	/5Phos/A*C*GCGCTACCTATACCGCGTACTACTACCGACTAATSEQ GCGACTAGTGCAC*G*A	ID NO: 192	
CTL133_BOT_tag	/5Phos/A*A*CCGTCGAGTGCAGCGAGTAGTGTACGCCGCTAASEQ CTAGCGTCGAATTG*G*T	ID NO: 193	
CTL076_BOT_tag	/5Phos/G*C*GCGAGTAGTGTGACTACCGCTCGTACCTATTACCSEQ GCGACCTATTACCG*C*G	ID NO: 194	
CTL024_BOT_tag	/5Phos/T*C*GCTCGATTGGTTACGCGCACTACTTACGCTCGCASEQ CTAAACTACTCGCC*G*A	ID NO: 195	
CTL045_BOT_tag	/5Phos/T*C*GTCGCACTAGTGCAGCGTTATGGTACCATAACCGSEQ CGCTACACTGCGCG*A*C	ID NO: 196	
CTL009_BOT_tag	/5Phos/A*C*CGCGTACTACTGCGGTTTCGACATTACCTTAATCGSEQ CGCAGTCGAGCGCA*T*A	ID NO: 197	
CTL055_BOT_tag	/5Phos/A*G*TAGTGCAGCTAGCGTCGAATTGGTGCACACATAGSEQ TCGTTGTCGCGCTA*G*T	ID NO: 198	
CTL101_BOT_tag	/5Phos/G*C*GCGGATTAGTTGCGTCGAATTGGTACCGCCGTACSEQ AAGTCGGCGAGTAG*T*T	ID NO: 199	
CTL135_BOT_tag	/5Phos/A*G*TAGTGCAGCTACGTTCCGGCTAGGTACCGCCGTACSEQ AAGACCTTAATCCG*C*G	ID NO: 200	
CTL155_BOT_tag	/5Phos/A*A*CCGTCGAGTGCATTGCGGATCGGTACCGCCGTACSEQ AAGTCTTGACGCGC*T*A	ID NO: 201	
CTL122_BOT_tag	/5Phos/G*C*GGCGTATTGGTACCTAGTCGTCGTACCAATACGSEQ CGCACCAGCTAATG*C*G	ID NO: 202	
CTL080_BOT_tag	/5Phos/A*C*CGATCGCTAGTCGCATTAGTCGGTACCATAACCGSEQ CGCCGCGCTACTAG*G*T	ID NO: 203	
CTL126_BOT_tag	/5Phos/T*A*GTGCGAGCGTATCGCGGCTAGATTACGACGACTASEQ GGTTAGCGCGAGTA*G*T	ID NO: 204	
CTL098_BOT_tag	/5Phos/A*C*CTTAGTCCGCGACTGCGAGCGTACACCTTAATCGSEQ CGCGTATAGCGGCG*G*T	ID NO: 205	
CTL038_BOT_tag	/5Phos/A*C*TAGCGATCGGTACTGCGAGCGTACGCACTCGACGSEQ GTTAGTAGTGCGCG*T*A	ID NO: 206	
CTL139_BOT_tag	/5Phos/A*C*CTAGTCGTCGTTCTCGCGCACTAACGACGCGCTGSEQ TTATACACTGCGCG*A*C	ID NO: 207	
CTL010_BOT_tag	/5Phos/G*C*GGCGTATTGGTGTATAGCGGCGGTACCATACTACSEQ GCGACCAATTCGAC*G*C	ID NO: 208	
CTL034_BOT_tag	/5Phos/T*A*ACAGCGCGTCGACTAGCGATCGGTACCTAGTCGSEQ GTAAGTAGTGCGCG*T*A	ID NO: 209	
CTL117_BOT_tag	/5Phos/G*C*GCGGATTAGTTGCGTCGAATTGGTACGCCGCTAASEQ CTATAGTTAGCGCG*G*T	ID NO: 210	
CTL035_BOT_tag	/5Phos/A*T*TGCGGATCGGTAGTAGTGCAGTAACGCCGCTAASEQ CTAACCTTAGTCCG*C*G	ID NO: 211	
CTL121_BOT_tag	/5Phos/A*C*GCGCTACCTATTAGTTAGCGGCGTATAAGTCGCGSEQ GGTACCTAGTCGTC*G*T	ID NO: 212	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL106_BOT_tag	/5Phos/G*T*CGCGCAGTGTAAACCGCTACTACTACACTACTCGSEQ CGCAACCGTCGATC*C*G	ID NO: 213	
CTL059_BOT_tag	/5Phos/A*C*CAATCGAGCGAATTGCGGATCGGTATAAGTCGGCSEQ GGTACCGATCCGCA*A*T	ID NO: 214	
CTL157_BOT_tag	/5Phos/G*G*TAAACGAGCGGTGCGCGATTAAAGGTGTACGCTCGCSEQ AGTGTACGCTCGCA*G*T	ID NO: 215	
CTL015_BOT_tag	/5Phos/A*C*CGATCCGCAATTAGTGCAGCGTAACTAGTGCAGSEQ CGATCGGACAGTA*G*T	ID NO: 216	
CTL110_BOT_tag	/5Phos/C*G*CGTAGTATGGTTCTCGCGCACTAATTAGTGCAGSEQ AGAACCGCTCGTTA*C*C	ID NO: 217	
CTL123_BOT_tag	/5Phos/T*C*GGCGAGTAGTTGCGCGATTAAAGGTACCTTAATCGSEQ CGCTAGCGGAGTA*G*T	ID NO: 218	
CTL014_BOT_tag	/5Phos/G*C*ACTCGACGGTTGCGTCGAATTGGTACCGCCGTACSEQ AAGAGTAGTGCGCGT*A	ID NO: 219	
CTL131_BOT_tag	/5Phos/T*C*GTCGCACTAGTGCAGGATTAAAGGTACCGATCCGSEQ AATCGGATCGACGGT*A	ID NO: 220	
CTL062_BOT_tag	/5Phos/C*G*CGGATTAAGGTGCGCGAGTAGTGTGTCGCGCAGTSEQ GTATACGCGCACTA*C*T	ID NO: 221	
CTL044_BOT_tag	/5Phos/A*C*CTAGCGCCGAATACGCGCACTACTACCTATTACCSEQ GCGTATGGTACGCGC*G*T	ID NO: 222	
CTL043_BOT_tag	/5Phos/A*C*CGCGTACTACTACCGCCGACTTATCGCAACGCTASEQ GGTTCTTGACGCGC*T*A	ID NO: 223	
CTL118_BOT_tag	/5Phos/A*C*TAGCGATCGGTGCGCGTTATGGTTCGCGGCTAGSEQ ATTACCGACTAATG*C*G	ID NO: 224	
CTL128_BOT_tag	/5Phos/A*C*CGCCGACTTATTAGTTAGCGGCGTACCAATACGSEQ CGCAGCGGTACCA*T*A	ID NO: 225	
CTL067_BOT_tag	/5Phos/C*G*GACGAGCGGTTGACTACCGCTCGTACCAATACGSEQ CGCACCATAACCGC*G*C	ID NO: 226	
CTL020_BOT_tag	/5Phos/A*G*TCGAGCGCATAGCGCGTTATGGTTCGGCGAGTASEQ GTTGCGCACATAGT*C*G	ID NO: 227	
CTL006_BOT_tag	/5Phos/C*G*CGTAGTATGGTGCAGGATTAAAGGTGGTAACGAGCSEQ GGTACGCGGCTAAC*T*A	ID NO: 228	
CTL017_BOT_tag	/5Phos/T*C*TCGCGCACTAACGGACGAGCGGTTACGCGCACTSEQ ACTACCGACTAATG*C*G	ID NO: 229	
CTL057_BOT_tag	/5Phos/A*C*GAGCGGTAGTCTTAGTGCAGGAGACGATTAGTCSEQ GGTACTACTCGCGC*T*A	ID NO: 230	
CTL078_BOT_tag	/5Phos/G*G*GCGGTTATGGTGTATAGCGGCGGTACCAATCGAGSEQ CGATAGTGCGAGCGT*A	ID NO: 231	
CTL031_BOT_tag	/5Phos/T*A*GTTAGCGGCGTATAGGTAGCGGTTATGCGCTCGSEQ ACTTCGCTCGATTG*G*T	ID NO: 232	
CTL136_BOT_tag	/5Phos/T*C*GCGACAGTAGTCGCATTAGTCGGTGTACGCTCGCSEQ AGTCGCGGATTAA*G*T	ID NO: 233	
CTL165_BOT_tag	/5Phos/A*C*CGCCGCTATACTAGCGCGTCAAGAACCAATCGAGSEQ CGATACGCGCACTA*C*T	ID NO: 234	
CTL039_BOT_tag	/5Phos/A*C*GCCGTACCATACGACTATGTGCGCACCGACGTASEQ CCGACTAGTGCGAC*G*A	ID NO: 235	
CTL036_BOT_tag	/5Phos/A*C*CTAGTCGTCGTAGTAGTACGCGGTTATGCGCTCGSEQ ACTACCTTAATCCG*C*G	ID NO: 236	

TABLE 4-continued

Tag Sequences			
Name	Sequence (5'→3')	SEQ ID NO	
CTL048_BOT_tag	/5Phos/T*T*CGGCGCTAGGTGCGCGAGTAGTGTAGTGCAGCSEQ GTAGCGCACATAGT*C*G	ID NO: 237	
CTL053_BOT_tag	/5Phos/C*G*GATCGACGGTTACTAGTGCAGCATTAGTGCAGCSEQ AGAATAAGTCGGCG*G*T	ID NO: 238	
CTL072_BOT_tag	/5Phos/A*C*GCCGTACCATAACCGCTCGTTACCCGCATTAGTCSEQ GGTCGCAACGCTAG*G*T	ID NO: 239	
CTL096_BOT_tag	/5Phos/T*A*CGCGACTAGGTGCAACGCTAGGTACCTATTACCSEQ GCGACCTAGTAGCG*C*G	ID NO: 240	
CTL150_BOT_tag	/5Phos/A*C*TACTGTCGCGAACCGACTAATGCGTAGCGCGAGTSEQ AGTACCTAGCCGAA*C*G	ID NO: 241	
CTL084_BOT_tag	/5Phos/A*C*GCCGCTAACTAACCTAGTCGTCTACCTATTACCSEQ GCGAACCGCTCGTC*C*G	ID NO: 242	
CTL142_BOT_tag	/5Phos/A*G*TAGTACGCGGTTCGATTAGTCGGTACCGATCCGCSEQ AATTAGTGCAGCG*T*A	ID NO: 243	
CTL102_BOT_tag	/5Phos/T*T*CGGCGCTAGGTAGCGCGTCAAGAACGCCGTACCSEQ ATACGGTACGGTCG*G*T	ID NO: 244	
CTL154_BOT_tag	/5Phos/G*T*ACGCTCGCAGTGCAGCGAGTAGTGTGCACTCGACGSEQ GTTAACTAATCCGC*G*C	ID NO: 245	
CTL112_BOT_tag	/5Phos/A*C*CGCCGACTTATAGTAGTGCAGCTACGCATTAGTCSEQ GGTCGCGGATTAAG*G*T	ID NO: 246	
CTL145_BOT_tag	/5Phos/C*G*GACGAGCGGTTTCGATTAGTCGGTACCATAACCGSEQ CGCCGCGGATTAAG*G*T	ID NO: 247	
CTL060_BOT_tag	/5Phos/A*C*CGCCGACTTATCGCGCTACTAGGTACCGCCGTACSEQ AAGGTACGCTCGCA*G*T	ID NO: 248	
CTL016_BOT_tag	/5Phos/C*G*CAACGCTAGGTACCTAGCGCCGAACGCGACTAASEQ GGTACCTAGCGCCG*A*A	ID NO: 249	
CTL159_BOT_tag	/5Phos/G*C*ACTCGACGGTTTCGTTTCGGCTAGGTACCGCCGTACSEQ AAGTACGCGACTAG*G*T	ID NO: 250	
CTL056_BOT_tag	/5Phos/A*C*GCCGTACCATAGCGGCGTATTGGTGTGCGCAGTSEQ GTAGCGCGGTTATG*G*T	ID NO: 251	
CTL162_BOT_tag	/5Phos/T*A*GTTAGCGGCGTGCAGTTTCGACATTACCTAGTCGSEQ GTAGCGCGAGTAGT*G*T	ID NO: 252	
CTL018_BOT_tag	/5Phos/G*C*GCGATTAAAGTTCTCGCGCACTAACGACGCGCTGSEQ TTACGCATTAGTCG*G*T	ID NO: 253	
CTL115_BOT_tag	/5Phos/G*C*GGCGTATTGGTACCGCCGACTTATCGCATTAGTCSEQ GGTTATGGTACGGC*G*T	ID NO: 254	
CTL033_BOT_tag	/5Phos/G*C*GCGGTTATGGTAACTACTCGCCGAACCTATTACCSEQ GCGACTGCGAGCGT*A*C	ID NO: 255	
CTL047_BOT_tag	/5Phos/C*G*ACTATGTGCGCTCGTCGCACTAGTACCATAACCGSEQ CGCAACCGCTCGTC*C*G	ID NO: 256	
CTL108_BOT_tag	/5Phos/A*A*TCTAGCCGCGATAGTTAGCGGCGTACCTTAATCGSEQ CGCTAGCGCGAGTA*G*T	ID NO: 257	
CTL041_BOT_tag	/5Phos/T*A*CGCGCACTACTGCGTCGAATTGGTGCAGGATTASEQ GTTGCGTCGAATTG*G*T	ID NO: 258	
CTL061_BOT_tag	/5Phos/A*C*CGCCGCTATACACTGCGAGCGTACTTCGGCGCTASEQ GGTGATAGCGGCG*G*T	ID NO: 259	
CTL166_BOT_tag	/5Phos/A*C*TACTCGCGCTAGCGGCGTATTGGTAACCGCTCGTSEQ CCGGCGCGAGTAGT*G*T	ID NO: 260	

TABLE 4-continued

Tag Sequences		
Name	Sequence (5'→3')	SEQ ID NO
CTL012_BOT_tag	/5Phos/G*C*GCGAGTAGTGCTACCTAGCGTTGCGCGCGGATTAASEQ GGTACTAGTGCAC*G*A	261
CTL052_BOT_tag	/5Phos/G*C*GGTTCGACATTACCTAGCGTTGCGCGCATTAGTCSEQ GGTACCTAGTAGCG*C*G	262
CTL153_BOT_tag	/5Phos/G*T*CGCGCAGTGTAACCTAGCGTTGCGTCGCGACAGTSEQ AGTGACTACCGCTC*G*T	263
CTL094_BOT_tag	/5Phos/A*C*CGCTCGTTACCACTAGCGATCGGTACCATACTACSEQ GCGTACGCGACTAG*G*T	264
CTL095_BOT_tag	/5Phos/C*G*CAACGCTAGGTAGTCGAGCGCATACGCATTAGTCSEQ GGTAATGTGCAACC*G*C	265
CTL105_BOT_tag	/5Phos/A*C*CTAGTAGCGCGTAGTTAGCGGCGTTTAGTGCGGSEQ AGAGTACGCT CGCA*G*T	266
CTL109_BOT_tag	/5Phos/C*T*GTACGGCGGTGCGGACTAAGGTTGCGGCTAGSEQ ATTACCGACCGTAC*C*G	267
CTL032_BOT_tag	/5Phos/T*A*GTTAGCGCGTAATCTAGCCGGAATAGGTAGCGSEQ CGTAACTACTGCC*G*A	268

"/5Phos/" indicates a 5'-phosphate moiety; "*" indicates a phosphorothioate linkage.

TABLE 5

Pools of Tag Sequences								
Pools								
Tags Present in Pools	Pool A1	Pool B1	Pool B2	Pool B3	Pool B4	Pool B5	Pool B6	Pool C1
CTL085	CTL161	CTL089	CTL098	CTL062	CTL048	CTL018	Pool A1	
CTL169	CTL164	CTL081	CTL038	CTL044	CTL053	CTL115	Pool B1	
CTL137	CTL030	CTL075	CTL139	CTL043	CTL072	CTL033	Pool B2	
CTL042	CTL088	CTL160	CTL010	CTL118	CTL096	CTL047	Pool B3	
CTL051	CTL148	CTL133	CTL034	CTL128	CTL150	CTL108	Pool B4	
CTL167	CTL152	CTL076	CTL117	CTL067	CTL084	CTL041	Pool B5	
CTL026	CTL007	CTL024	CTL035	CTL020	CTL142	CTL061	Pool B6	
CTL068	CTL141	CTL045	CTL121	CTL006	CTL102	CTL166		
CTL138	CTL064	CTL009	CTL106	CTL017	CTL154	CTL012		
CTL079	CTL158	CTL055	CTL059	CTL057	CTL112	CTL052		
CTL063	CTL066	CTL101	CTL157	CTL078	CTL145	CTL153		
CTL168	CTL144	CTL135	CTL015	CTL031	CTL060	CTL094		
CTL021	CTL107	CTL155	CTL110	CTL136	CTL016	CTL095		
CTL151	CTL149	CTL122	CTL123	CTL165	CTL159	CTL105		
CTL002	CTL008	CTL080	CTL014	CTL039	CTL056	CTL109		
CTL134	CTL099	CTL126	CTL131	CTL036	CTL162	CTL032		

TABLE 6

Non-homologous tails		
Name	Sequence (5'→3')	SEQ ID NO:
H1	ACGCGACTATACGCGCAATATGGT	SEQ ID NO: 269
H2	CTAGCGATACTACGCGATACGAGAT	SEQ ID NO: 270
H3	CATAGCGGTATTACGCGAGATTACGA	SEQ ID NO: 271

TABLE 6-continued

Non-homologous tails		
Name	Sequence (5'→3')	SEQ ID NO:
H4	CGCGAGTACGTACGATTACCG	SEQ ID NO: 272
H5	ACGCGCGACTATACGCGCCTC	SEQ ID NO: 273

SEQUENCE LISTING

Sequence total quantity: 273

SEQ ID NO: 1 moltype = DNA length = 52

FEATURE Location/Qualifiers

source 1..52

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 1

tcgttcgttc cgctctaacc ggcgaaatcta ccgcgcatat ctacgccgca at 52

SEQ ID NO: 2 moltype = DNA length = 52

FEATURE Location/Qualifiers

source 1..52

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 2

attgcggcgt agatatgcgc ggtagattcg ccggttagag cggaacgaac ga 52

SEQ ID NO: 3 moltype = DNA length = 57

FEATURE Location/Qualifiers

source 1..57

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 3

acactctttc cctacacgac gctcttccga tcttctaccg cgcatatcta cgccgct 57

SEQ ID NO: 4 moltype = DNA length = 58

FEATURE Location/Qualifiers

source 1..58

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 4

acactctttc cctacacgac gctcttccga tctatatgcg cggtagattc gccgggtt 58

SEQ ID NO: 5 moltype = DNA length = 68

FEATURE Location/Qualifiers

source 1..68

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 5

gtgactggag ttcagacgtg tgctcttccg atctaagtat acggcgacca ccgagatcta 60
cacaaggc 68

SEQ ID NO: 6 moltype = DNA length = 78

FEATURE Location/Qualifiers

source 1..78

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 6

aatgatacgg cgaccaccga gatctacact agatcgcnw nnwnnacact ctttccctac 60
acgacgtct tccgatct 78

SEQ ID NO: 7 moltype = DNA length = 33

FEATURE Location/Qualifiers

source 1..33

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 7

acactctttc cctacacgac gctcttccga tct 33

SEQ ID NO: 8 moltype = DNA length = 34

FEATURE Location/Qualifiers

-continued

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source                1..34
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 8
gtgactggag ttcagacgtg tgctcttccg atct                               34

SEQ ID NO: 9          moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 9
acgagcggta gtcacctagt cgctgtacca attcgacgca cactactcgc gc          52

SEQ ID NO: 10         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 10
gcgcgagtag tgtgcgtcga attggtacga cgactagggtg actaccgctc gt        52

SEQ ID NO: 11         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 11
tagcgcgagt agtcggacga gcggttacca atacgccga ccttaatccg cg          52

SEQ ID NO: 12         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 12
cgcggattaa ggtgcggcgt attggtaacg gctcgtccga ctactcgcgc ta        52

SEQ ID NO: 13         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 13
tcgcgacagt agtcgttcgg ctaggtacct attaccgctg agttagcggc gt        52

SEQ ID NO: 14         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 14
acgccgctaa ctacgcggta ataggtacct agccgaacga ctactgtcgc ga          52

SEQ ID NO: 15         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 15
cgcgctacta ggtgcgtcga attggtaccg atccgcaata cactactcgc gc          52

SEQ ID NO: 16         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 16
gcgcgagtag tgtattgcgg atcggtacca attcgacgca cctagtagcg cg          52

SEQ ID NO: 17         moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 17

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ggtaacgagc ggtgcgtcga attggttaacc gctcgctccga ccttaatcgc gc	52
SEQ ID NO: 18	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 18	
gcgcgattaa ggtcggacga gcggttacca attcgacgca ccgctcgta cc	52
SEQ ID NO: 19	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 19	
ttcggcgcta ggtgcgcggt attggttaacc gctcgctccgt tcggcgctag gt	52
SEQ ID NO: 20	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 20	
acctagcgcc gaacggacga gcggttacca atacgccgca cctagcgccg aa	52
SEQ ID NO: 21	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 21	
tacgcgacta ggtgcgcgat taaggtacct attacgcgc gactatgtgc gc	52
SEQ ID NO: 22	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 22	
gcgcacatag tcgcgcggta ataggtacct taatcgcgca cctagtcgcg ta	52
SEQ ID NO: 23	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 23	
gtcgcgcagt gtagcgcgat taaggtacct attacgcgct cgcgacagta gt	52
SEQ ID NO: 24	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 24	
actactgtcg cgacgcggta ataggtacct taatcgcgct acactgcgcg ac	52
SEQ ID NO: 25	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 25	
aaccgtcgat ccgcgcgtag tatggtaccg atccgcaata ctacgcgcgac aa	52
SEQ ID NO: 26	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 26	
ttgtcgcgct agtattgcgg atcggtacca tactacgcgc ggatcgacgg tt	52
SEQ ID NO: 27	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 27
tcgctcgatt ggttacgcgc actacttatg cgctcgactc gtcggctag gt      52

SEQ ID NO: 28          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 28
acctagccga acgagtcgag cgcataagta gtgcgcgtaa ccaatcgagc ga      52

SEQ ID NO: 29          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 29
actgcgagcg tacttgctgc gctagtagca attcgacgca accgctcgtc cg      52

SEQ ID NO: 30          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 30
cggacgagcg gttgcgtcga attggtacta gcgcgacaag tacgctcgca gt      52

SEQ ID NO: 31          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 31
cgcattagtc ggtgcggcgt attggtacc gctcgtccga cgcgtacct at      52

SEQ ID NO: 32          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 32
ataggtagcg cgtcggacga gcggttacca atacgccga ccgactaatg cg      52

SEQ ID NO: 33          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 33
attgcggatc ggtgcgtcga attggtacc gctcgtccgt acgcgcacta ct      52

SEQ ID NO: 34          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 34
agtagtgccg gtacggacga gcggttacca attcgacgca ccgatccgca at      52

SEQ ID NO: 35          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 35
tcggcgagta gttgcgcggt tatggtacca taaccgcgca gtagtacgcg gt      52

SEQ ID NO: 36          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 36

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accgcgtact actgcgcggt tatggtacca taaccgcgca actactcgcc ga	52
SEQ ID NO: 37	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 37	
actagcgatc ggtacctagc gccgaaacct attaccgcga ctagcggtg cg	52
SEQ ID NO: 38	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 38	
cgcaacgcta ggtcgcggtata taggttttcg gcgctaggta ccgacgcgta gt	52
SEQ ID NO: 39	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 39	
tagcgcgtca agagcgcggt tatggttttcg gcgctaggta aacagcgcgt cg	52
SEQ ID NO: 40	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 40	
cgacgcgctg ttaacctagc gccgaaacca taaccgcgct cttgacgcgc ta	52
SEQ ID NO: 41	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 41	
gtttaattga gttgtcatat gtttaataacg gtat	34
SEQ ID NO: 42	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 42	
ataccgttat taacatatga caactcaatt aaac	34
SEQ ID NO: 43	moltype = DNA length = 20
FEATURE	Location/Qualifiers
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 43	
gagtccgagc agaagaagaa	20
SEQ ID NO: 44	moltype = DNA length = 20
FEATURE	Location/Qualifiers
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 44	
gttgagcat ctgagtcag	20
SEQ ID NO: 45	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 45	
acgagcggta gtcacctagt cgtcgtagca attcgacgca cactactcgc gc	52
SEQ ID NO: 46	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 46
tagcgcgagt agtcggacga gcggttacca atacgccga ccttaatccg cg          52

SEQ ID NO: 47          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 47
tcgcgacagt agtcgttcgg ctaggtacct attaccgcgt agttagcggc gt          52

SEQ ID NO: 48          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 48
cgcgctacta ggtgcgtcga attggtaccg atccgcaata cactactcgc gc          52

SEQ ID NO: 49          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 49
ggtaacgagc ggtgcgtcga attggtaacg gctcgtccga ccttaatcgc gc          52

SEQ ID NO: 50          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 50
ttcggcgcta ggtgcggcgt attggtaacg gctcgtccgt tcggcgctag gt          52

SEQ ID NO: 51          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 51
tacgcgacta ggtgcgcgat taaggtacct attaccgcgc gactatgtgc gc          52

SEQ ID NO: 52          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 52
gtcgcgcagt gtagcgcgat taaggtacct attaccgcgt cgcgacagta gt          52

SEQ ID NO: 53          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 53
aaccgtcgat ccgcgcgtag tatggtaccg atccgcaata ctacgcgcac aa          52

SEQ ID NO: 54          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 54
tcgctcgatt gggtacgcgc actacttatg cgctcgactc gttcggctag gt          52

SEQ ID NO: 55          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 55

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actgcgagcg tacttgctgc gctagtagca attcgacgca accgctcgtc cg	52
SEQ ID NO: 56	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 56	
cgcattagtc ggtgcgcgct attggttaacc gctcgtagca cgcgctacct at	52
SEQ ID NO: 57	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 57	
attgcggatc ggtgcgtagc attggttaacc gctcgtagct acgcgtagca ct	52
SEQ ID NO: 58	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 58	
tcggcgagta gttgcgcggt tatggttagca taaccgcgca gtagtagcgc gt	52
SEQ ID NO: 59	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 59	
actagcgatc ggtacctagc gccgaacact attaccgcga ctagcgtagt cg	52
SEQ ID NO: 60	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 60	
tagcgcgtagc agagcgcggt tatggtttcg gcgtagtagt aacagcgcggt cg	52
SEQ ID NO: 61	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 61	
gcgcgagtag tgtgcgtagc attggttagc cgactagtag actaccgctc gt	52
SEQ ID NO: 62	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 62	
cgcggattaa ggtgcgcggt attggttaacc gctcgtagca ctactcgtag ta	52
SEQ ID NO: 63	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 63	
acgcgtagta ctacgcgtag ataggtacct agccgaacga ctactgtagc ga	52
SEQ ID NO: 64	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 64	
gcgcgagtag tgtagtcggt atcggttagca attcgacgca ctagtagcgc cg	52
SEQ ID NO: 65	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 65
gcgcgattaa ggtcggacga gcggttacca attcgacgca ccgctcgtaa cc          52

SEQ ID NO: 66          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 66
acctagcgcc gaacggacga gcggttacca atacgccga cctagcgccg aa          52

SEQ ID NO: 67          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 67
gcgcacatag tcgcgcggta ataggtagct taatcgcgca cctagtcgag ta          52

SEQ ID NO: 68          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 68
actactgtcg cgacgcggta ataggtagct taatcgcgct aactgcgag ac          52

SEQ ID NO: 69          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 69
ttgtcgcgct agtattgcgg atcggtacca tactacgcgc ggatcgacgg tt          52

SEQ ID NO: 70          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 70
acctagccga acgagtcgag cgcataagta gtgcgcgtaa ccaatcgagc ga          52

SEQ ID NO: 71          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 71
cggacgagcg gttgcgtcga attggtacta gcgcgacaag tacgctcgca gt          52

SEQ ID NO: 72          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 72
ataggtagcg cgctcggacga gcggttacca atacgccga ccgactaatg cg          52

SEQ ID NO: 73          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 73
agtagtgcgc gtacggacga gcggttacca attcgacgca ccgatccgca at          52

SEQ ID NO: 74          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 74

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accgcgtact actgcgcggt tatggtacca taaccgcgca actactcgcc ga	52
SEQ ID NO: 75	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 75	
cgcaacgcta ggtcgcggtata taggtttcg gcgctaggta ccgacgcta gt	52
SEQ ID NO: 76	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 76	
cgacgcgctg ttaacctagc gccgaaacca taaccgcgct cttgacgcgc ta	52
SEQ ID NO: 77	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 77	
tacctgcgc gacctgcga gcgtacacct taatcgcgct agttagcggc gt	52
SEQ ID NO: 78	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 78	
aaccgtcgag tgcaccgct actactaatg tcgaaccgct acgcgcacta ct	52
SEQ ID NO: 79	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 79	
cgcggactaa ggtgcgcgag tagtgttacg cgcactacta atctagccgc ga	52
SEQ ID NO: 80	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 80	
actagtgcga cgaactactc gcgctaacca attcgacgca ccgacgcta gt	52
SEQ ID NO: 81	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 81	
aatgtcgaac cgcgcgcgag taggtacca taaccgcgca ccttagtcgc cg	52
SEQ ID NO: 82	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 82	
gcgtcgaatt ggtaccgcgc acttatacca atacgccga taggtagcgc gt	52
SEQ ID NO: 83	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 83	
acctagtagc gcggcgctga attggtacta gcgcgacaac gcgtagtatg gt	52
SEQ ID NO: 84	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 84
accgctcggt accgcgcgat taaggtacgc cgctaactac ggtacggtcg gt      52

SEQ ID NO: 85          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 85
accgccgact tatcggttcg ctaggtacca attcgacgca ctgcgagcgt ac      52

SEQ ID NO: 86          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 86
accttaatcc gcgactgcga gcgtacacct attaccgcgc gacgcgctgt ta      52

SEQ ID NO: 87          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 87
acgacgacta ggtaccgctc gttacctctt gacgcgctaa ccaattcgac gc      52

SEQ ID NO: 88          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 88
accatactac gcggcggttc gacattacca taaccgcgct agtgcgagcg ta      52

SEQ ID NO: 89          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 89
cttgtagcgc ggtgcggcgt attggtacca ataccgcgct cgtcgcacta gt      52

SEQ ID NO: 90          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 90
gtacgctcgc agtaccgcgc acctatacct taatcgcgca ctacgcgcgac aa      52

SEQ ID NO: 91          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 91
acgacgacta gggtatggta cggcgtagc gcgagtagta ccttagtcg cg      52

SEQ ID NO: 92          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 92
acgagcggta gtcataggta gcgcggtctt gacgcgctaa ccgatcgcta gt      52

SEQ ID NO: 93          moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 93

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accgatccgc aatgcgctcga attggtacca taaccgcgca ccgccgtaca ag	52
SEQ ID NO: 94	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 94	
actagtgcga cgaactactg tcgcgaacct attaccgcga ccaatcgagc ga	52
SEQ ID NO: 95	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 95	
accgccgtac aagtcgcgac agtagtaacc gctcgctccg tcggcgctag gt	52
SEQ ID NO: 96	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 96	
tcgtcgact agtcgcatta gtcggtagta gtacgcggta taggtagcgc gt	52
SEQ ID NO: 97	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 97	
accaattcga cgctagttag cggcgtagac tactcgcgcg cactcgacgg tt	52
SEQ ID NO: 98	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 98	
cgcggtaata ggtcgcggta ataggtacga gcggtagtca cactactcgc gc	52
SEQ ID NO: 99	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 99	
tcggcgagta gtttagtgcg agcgtaagta gtgcgcgtaa ccaatcgagc ga	52
SEQ ID NO: 100	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 100	
gtcgcgcagt gtagcgcggt tatggtacca taaccgcgca ctagtgcgac ga	52
SEQ ID NO: 101	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 101	
tatgcgctcg actcgcgcat taaggtaatg tcgaaccgca gtagtacgcg gt	52
SEQ ID NO: 102	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 102	
actagcgcga caacgactat gtgcgcacca attcgacgct acgcgcacta ct	52
SEQ ID NO: 103	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 103
aactactcgc cgacttgtag ggcggtagca attcgacgca actaatccgc gc      52

SEQ ID NO: 104        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 104
cgcggaataa ggtcttgtag ggcggtagct agccgaacgt acgcgcacta ct      52

SEQ ID NO: 105        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 105
tagcgcgtag agacttgtag ggcggtagccg atccgcaatg cactcgacgg tt      52

SEQ ID NO: 106        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 106
cgcattagtc ggtcgcgtag attggtacga cgactagtag ccaatacgcc gc      52

SEQ ID NO: 107        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 107
acctagtagc ggcgcgcggt tatggtaccg actaatgcga ctagegatcg gt      52

SEQ ID NO: 108        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 108
actactcgcg ctaacctagt cgctcgtaac tagccgcgat acgctcgcac ta      52

SEQ ID NO: 109        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 109
accgccccta tacgcgcgat taagggtgtag gctcgcagtc gcggactaag gt      52

SEQ ID NO: 110        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 110
tacgcgcact actaacgcgc gagtgcgtac gctcgcagta ccgatcgcta gt      52

SEQ ID NO: 111        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 111
gtcgcgcagt gtataacagc gcgtcgtagg tgcgcgagaa cgacgactag gt      52

SEQ ID NO: 112        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 112

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gcgtcgaatt ggtcgcgtag tatggtagcg ccgtatata ccaatacgcc gc 52

SEQ ID NO: 113 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 113
 tacgcgcact acttacgcga ctaggtaccg atcgctagtc gacgcgctgt ta 52

SEQ ID NO: 114 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 114
 acgcgcgctaa ctatagttag cggcgtagca attcgacgca actaatccgc gc 52

SEQ ID NO: 115 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 115
 cgcgactaa ggtagtttag cggcggttacg cgcactacta ccgatccgca at 52

SEQ ID NO: 116 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 116
 acgacgacta ggtaccgcgc acttataccg cgctaactaa taggtagcgc gt 52

SEQ ID NO: 117 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 117
 cggatcgacg gttgcgcgag tagttagta gtacgcggtt aactgcgcgc ac 52

SEQ ID NO: 118 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 118
 attgcggatc ggtaccgcgc acttataccg atccgcaatt cgctcgattg gt 52

SEQ ID NO: 119 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 119
 actgcgagcg tacactgcga gcgtacacct taatcgcgca ccgctcgtta cc 52

SEQ ID NO: 120 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 120
 actactgtcg cgatcgctgc actagttacg ctgcactaa ttgcggatcg gt 52

SEQ ID NO: 121 moltype = DNA length = 52
 FEATURE Location/Qualifiers
 source 1..52
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 121
 ggtaacgagc ggttctcgcg cactaattag tgccgcgagaa ccatactacg cg 52

SEQ ID NO: 122 moltype = DNA length = 52
 FEATURE Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 122
actactcgcg ctagcgcgat taaggtagct taatcgcgca actactcgcc ga      52

SEQ ID NO: 123        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 123
tacgcgcact actcttgtag gccggtagca attcgacgca accgtcgagt gc      52

SEQ ID NO: 124        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 124
aaccgtcgat ccgattgcgg atcggtacct taatcgcgca ctagtgcgac ga      52

SEQ ID NO: 125        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 125
agtagtgcgc gtatacactg cgcgacacac tactcgcgca ccttaatccg cg      52

SEQ ID NO: 126        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 126
acgccgtacc atacgcggta ataggtagta gtgcgcgtat tcggcgctag gt      52

SEQ ID NO: 127        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 127
tagcgcgta agaacctagc gttgcgataa gtccggcgta gtagtacgcg gt      52

SEQ ID NO: 128        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 128
cgcattagtc ggtaacttag ccgcgaacca taaccgcgca ccgacgcta gt      52

SEQ ID NO: 129        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 129
tatggtacgg cgtgcggcgt attggtacgc cgctaactaa taagtcggcg gt      52

SEQ ID NO: 130        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 130
gcgcggttat ggtgcggcgt attggtacga gcggtagtca accgctcgtc cg      52

SEQ ID NO: 131        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 131

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cgactatgtg cgcaactact cgccgaacca taaccgcgct atgcgctcga ct	52
SEQ ID NO: 132	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 132	
tagttagcgg cgtaccgctc gttaccacct taatcgcgca ccatactacg cg	52
SEQ ID NO: 133	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 133	
cgcattagtc ggtagtagtg cgcgtaaacc gctcgctcgt tagtgcgcga ga	52
SEQ ID NO: 134	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 134	
tagcgcgagt agtaccgact aatgcgtctc gcgcactaag actaccgctc gt	52
SEQ ID NO: 135	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 135	
tacgctcgca ctatcgctcg attggtaccg ccgctataca ccataaccgc gc	52
SEQ ID NO: 136	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 136	
accaatcgag cgaagtcgag cgcataacgc gctacctata cgccgctaac ta	52
SEQ ID NO: 137	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 137	
accttaatcc gcgactgcga gcgtacaccg actaatgcga ctactgtcgc ga	52
SEQ ID NO: 138	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 138	
agtagtgcgc gtatcgctcg attggttctt gacgcgctag tatagcggcg gt	52
SEQ ID NO: 139	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 139	
tcgtcgact agtcggtacg gtcggtgcgc acatagtcgt atggtacggc gt	52
SEQ ID NO: 140	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 140	
cgcgattaa ggtagtcgag cgcataaccg cgtactacta cgacgactag gt	52
SEQ ID NO: 141	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 141
cgactatgtg cgctacgctc gcactaacac tactcgcgca cctagcgccg aa          52

SEQ ID NO: 142         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 142
accgccgact tattctcgcg cactaatcgt cgcactagta accgtcgatc cg          52

SEQ ID NO: 143         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 143
acctagcggt gcgaccgact aatgcgggta acgagcggtt atggtagcgc gt          52

SEQ ID NO: 144         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 144
cgcgctacta ggtcgcggtg ataggtacct agcggtgcga cctagtcgcg ta          52

SEQ ID NO: 145         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 145
cgttcggcta ggtactactc gcgctacgca ttagtcggtt cgcgacagta gt          52

SEQ ID NO: 146         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 146
cggacgagcg gttcgcggta ataggtacga cgactaggtt agttagcggc gt          52

SEQ ID NO: 147         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 147
tacgctcgca ctaattgcgg atcggtagcg actaatgcga ccgcgtacta ct          52

SEQ ID NO: 148         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 148
accgaccgta ccgtatggta cggcggttctt gacgcgctaa cctagcgccg aa          52

SEQ ID NO: 149         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 149
gcgcggatta gttaacgctc gagtgcacac tactcgcgca ctgcgagcgt ac          52

SEQ ID NO: 150         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 150

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accttaatcc gcgaccgact aatgcgtacg cgcactacta taagtcggcg gt	52
SEQ ID NO: 151	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 151	
accttaatcc gcggcgcggt tatggtaccg actaatgcga accgctcgtc cg	52
SEQ ID NO: 152	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 152	
actgcgagcg taccttgtag ggcggtacct agtagcgca taagtcggcg gt	52
SEQ ID NO: 153	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 153	
ttcggcgcta ggtaccttag tccgcgttcg gcgctaggta cctagcgttg cg	52
SEQ ID NO: 154	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 154	
acctagtcgc gtacttgtag ggcggtacct agccgaacga accgctcgagt gc	52
SEQ ID NO: 155	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 155	
accataaccg cgctacactg cgcgacacca atacgccgt atggtacggc gt	52
SEQ ID NO: 156	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 156	
acactactcg cgctacgca ctaggtaatg tcgaaccgca cgccgctaac ta	52
SEQ ID NO: 157	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 157	
accgactaat gcgtaacagc gcgtcgtagg tcgcgagaa ccttaatcgc gc	52
SEQ ID NO: 158	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 158	
acgccgtacc ataaccgact aatgcgataa gtcgcggtta ccaatacggc gc	52
SEQ ID NO: 159	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 159	
gtacgctcgc agtcgcggtta ataggttcgg cgagtagtta ccataaccgc gc	52
SEQ ID NO: 160	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 160
cggacgagcg gttgcgcggt tatggtacta gtgcgacgag cgcacatagt cg          52

SEQ ID NO: 161        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 161
actactcgcg ctagcgcgat taaggtacgc cgctaactat cgcggctaga tt          52

SEQ ID NO: 162        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 162
accaattcga cgcaactaat ccgcgcacca attcgacgca gtagtgcgcg ta          52

SEQ ID NO: 163        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 163
accgccccta tacacctagc gccgaagtac gctcgcagtg tatagcggcg gt          52

SEQ ID NO: 164        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 164
acactactcg cgccggacga gcggttacca atacgccgct agcgcgagta gt          52

SEQ ID NO: 165        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 165
tcgtcgcact agtaccttaa tccgcgcgca acgctaggta cactactcgc gc          52

SEQ ID NO: 166        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 166
cgcgctacta ggtaccgact aatgcgcgca acgctaggta atgtcgaacc gc          52

SEQ ID NO: 167        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 167
acgagcggta gtcactactg tcgcgacgca acgctaggtt acactgcgcg ac          52

SEQ ID NO: 168        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 168
acctagtccg gtacgcgtag tatggtaccg atcgctagtg gtaacgagcg gt          52

SEQ ID NO: 169        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 169

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gcggttcgac attaccgact aatgcgtatg cgetcgacta cctagcggtg cg	52
SEQ ID NO: 170	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 170	
actgcgagcg tactctcgcg cactaaacgc cgctaactac gcgctactag gt	52
SEQ ID NO: 171	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 171	
cggtacggtc ggtaatctag ccgcgaacct tagtcgcga ccgccgtaca ag	52
SEQ ID NO: 172	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 172	
tcggcgagta gttacgcgct acctattcgc ggctagatta cgccgctaac ta	52
SEQ ID NO: 173	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 173	
acgccgctaa ctagcgcgat taagggtgac gctcgcagtg tcgcgcagtg ta	52
SEQ ID NO: 174	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 174	
agtagtgcgc gtagcgggtc gacattagta gtacgcggtg cactcgacgg tt	52
SEQ ID NO: 175	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 175	
tcgcggtag attagtagtg cgcgtaacac tactcgcgca ccttagtcg cg	52
SEQ ID NO: 176	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 176	
actagcgatc ggtgcgctga attgggtagc gcgagtagtt cgtcgcacta gt	52
SEQ ID NO: 177	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 177	
cgcgactaa ggtgcgcggt tatggtacac tactcgcgcg cggttcgaca tt	52
SEQ ID NO: 178	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 178	
acgcgtacc tatgcggcgt attggtataa gtcggcggtg ccaattcgac gc	52
SEQ ID NO: 179	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 179
accatactac gcgttgctgc gctagtagca attcgacgcc gcgctactag gt      52

SEQ ID NO: 180         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 180
accgaccgta ccgtagttag cggcgtagct taatcgcgcg gtaacgagcg gt      52

SEQ ID NO: 181         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 181
gtacgctcgc agtgcgctga attggtacct agccgaacga taagtcggcg gt      52

SEQ ID NO: 182         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 182
taacagcgcg tcgcgcggtg ataggtgtac gctcgcagtc gcggattaag gt      52

SEQ ID NO: 183         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 183
gcgtcgaatt ggtagcgcg tcaagaggta acgagcggtg cctagtcgct gt      52

SEQ ID NO: 184         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 184
tacgctcgca ctagcgcggt tatggtaatg tcgaaccgcc gcgtagtatg gt      52

SEQ ID NO: 185         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 185
actagtgcga cgagcgcggt attggtacca atacccgca cgcgcgtaca ag      52

SEQ ID NO: 186         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 186
ttgtcgcgct agtcgcgcat taaggataaa gtcggcggtg ctgcgagcgt ac      52

SEQ ID NO: 187         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 187
cgcggactaa ggtactactc gcgctaacgc cgtaccataa cctagtcgct gt      52

SEQ ID NO: 188         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                        mol_type = other DNA
                        organism = synthetic construct

SEQUENCE: 188

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actagcgatc ggttagcgcg tcaagaacgc gctacctatg actaccgctc gt	52
SEQ ID NO: 189	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 189	
cttgtacggc ggtgcgcggt tatggtacca attcgacgca ttgcggatcg gt	52
SEQ ID NO: 190	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 190	
tcgctcgatt ggtcgcggtata taggttcgc gacagtagtt cgctgcacta gt	52
SEQ ID NO: 191	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 191	
acctagcgcc gaacggacga gcggttacta ctgtcgcgac ttgtacggcg gt	52
SEQ ID NO: 192	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 192	
acgcgctacc tatacccggt actactaccg actaatgcga ctagtgcgac ga	52
SEQ ID NO: 193	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 193	
aaccgtcgag tgcgcgcgag tagtgtacgc cgctaactag cgtcgaattg gt	52
SEQ ID NO: 194	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 194	
gcgcgagtag tgtgactacc gctcgctacct attaccgcga cctattaccg cg	52
SEQ ID NO: 195	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 195	
tcgctcgatt ggttacgcgc actacttacg ctgcactaa actactcgcc ga	52
SEQ ID NO: 196	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 196	
tcgtcgact agtgcgcggt tatggtacca taaccgcgct acactgcgac ac	52
SEQ ID NO: 197	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 197	
accgcgtact actgcggttc gacattacct taatcgcgca gtcgagcgca ta	52
SEQ ID NO: 198	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 198
agtagtgcgcg gtagcgtcga attggtgcgcg acatagtcgt tgtcgcgcta gt      52

SEQ ID NO: 199        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 199
gcgcgggatta gttgcgtcga attggtaccg ccgtacaagt cggcgagtag tt      52

SEQ ID NO: 200        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 200
agtagtgcgcg gtagcggtcgg ctaggtaccg ccgtacaaga ccttaatccg cg      52

SEQ ID NO: 201        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 201
aaccgtcgag tgcatcgcg atcggtaccg ccgtacaagt cttgacgcgc ta      52

SEQ ID NO: 202        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 202
gcggcggtatt ggtacctagt cgtcgtagca atacgccgca ccgactaatg cg      52

SEQ ID NO: 203        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 203
accgatcgct agtcgcatta gtcggtacca taaccgcgcc gcgctactag gt      52

SEQ ID NO: 204        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 204
tagtgcgagc gtatcgcgcg tagattacga cgactagggt agcgcgagta gt      52

SEQ ID NO: 205        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 205
accttagtcc gcgactgcga gcgtacacct taatcgcgcg tatagcggcg gt      52

SEQ ID NO: 206        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 206
actagcgatc ggtactgcga gcgtacgcac tcgacggtta gtagtgcgcg ta      52

SEQ ID NO: 207        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 207

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acctagtcgt cgttctcgcg cactaacgac gcgctgttat acactgcgcg ac	52
SEQ ID NO: 208	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 208	
gcggcggtatt ggtgtatagc ggcggtacca tactacgcga ccaattcgac gc	52
SEQ ID NO: 209	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 209	
taacagcgcg tcgactagcg atcggtacct agtcgcgtaa gtagtcgcg ta	52
SEQ ID NO: 210	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 210	
gcgcggatta gttgcgtcga attggtacgc cgctaactat agttagcggc gt	52
SEQ ID NO: 211	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 211	
attgcggatc ggtagtagtg cgcgtaacgc cgctaactaa ccttagtcgc cg	52
SEQ ID NO: 212	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 212	
acgcgctacc tattagttag cggcgataaa gtcggcggtta cctagtcgct gt	52
SEQ ID NO: 213	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 213	
gtcgcgcagt gtaaccgcgt actactacac tactcgcgca accgtcgatc cg	52
SEQ ID NO: 214	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 214	
accaatcgag cgaattcggg atcggtataa gtcggcggtta ccgatccgca at	52
SEQ ID NO: 215	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 215	
ggtaacgagc ggtgcgcgat taagggtgac gtcgcgagt tacgctcgca gt	52
SEQ ID NO: 216	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 216	
accgatccgc aattagtgcg agcgtaacta gtgcgacgat cgcgacagta gt	52
SEQ ID NO: 217	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 217
cgcgtagtat ggttctcgcg cactaattag tgcgcgagaa cgcctcgta cc      52

SEQ ID NO: 218        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 218
tcggcgagta gttgcgcgat taaggtaacct taatcgcgct agcgcgagta gt      52

SEQ ID NO: 219        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 219
gcactcgacg gttgcgcga attggtaccg ccgtacaaga gtagtgcgcg ta      52

SEQ ID NO: 220        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 220
tcgtcgcaact agtgcgcgat taaggtaacct atccgcaatc ggatcgacgg tt      52

SEQ ID NO: 221        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 221
cgcggaattaa ggtgcgcgag tagtgtgtcg cgcagtgtat acgcgcacta ct      52

SEQ ID NO: 222        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 222
acctagcgcc gaatacgcgc actactacct attaccgcgt atggtacggc gt      52

SEQ ID NO: 223        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 223
accgcgtact actaccgcgc acttatcgca acgctagggt cttgacgcgc ta      52

SEQ ID NO: 224        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 224
actagcgatc ggtgcgcggt tatggttcgc ggctagatta ccgactaatg cg      52

SEQ ID NO: 225        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 225
accgccgact tattagttag cggcgtacca atacgccga cgccgtacca ta      52

SEQ ID NO: 226        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 226

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cggacgagcg gttgactacc gctcgtacca atacgccgca ccataaccgc gc	52
SEQ ID NO: 227	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 227	
agtcgagcgc atagcgcggt tatgggtcgg cgagtagttg cgcacatagt cg	52
SEQ ID NO: 228	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 228	
cgcgtagtat ggtgcgcgat taagggtgga acgagcggta cgccgctaac ta	52
SEQ ID NO: 229	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 229	
tctcgcgcac taacggacga gcgggttacg cgcactacta ccgactaatg cg	52
SEQ ID NO: 230	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 230	
acgagcggta gtcttagtgc gcgagacgca ttagtcggta ctactcgcgc ta	52
SEQ ID NO: 231	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 231	
gcgcgggttat ggtgtatagc ggcgggtacca atcgagcgat agtcgcgagcg ta	52
SEQ ID NO: 232	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 232	
tagttagcgg cgtataggta gcgcggtatg cgctcgactt cgctcgattg gt	52
SEQ ID NO: 233	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 233	
tcgcgacagt agtcgcatta gtcgggtgtac gctcgcagtc gcggattaag gt	52
SEQ ID NO: 234	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 234	
accgcgcgcta tactagcgcg tcaagaacca atcgagcgat acgcgcacta ct	52
SEQ ID NO: 235	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 235	
acgccgtacc atacgactat gtgcgcaccg accgtaccga ctagtgcgac ga	52
SEQ ID NO: 236	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 236
acctagtcgt cgtagtagta cgcgggttatg cgctcgacta ccttaatccg cg          52

SEQ ID NO: 237         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 237
ttcggcgcta ggtgcgcgag tagtgttagt gcgagcgtag cgcacatagt cg          52

SEQ ID NO: 238         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 238
cggatcgacg gttactagtg cgacgattag tgcgcgagaa taagtcggcg gt          52

SEQ ID NO: 239         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 239
acgccgtacc ataaccgctc gttaccgcga ttagtcggtc gcaacgctag gt          52

SEQ ID NO: 240         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 240
tacgcgacta ggtcgcaacg ctaggtagct attaccgcga cctagtagcg cg          52

SEQ ID NO: 241         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 241
actactgtcg cgaaccgact aatgcgtagc gcgagtagta cctagccgaa cg          52

SEQ ID NO: 242         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 242
acgccgctaa ctaacctagt cgctgtacct attaccgcga accgctcgtc cg          52

SEQ ID NO: 243         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 243
agtagtacgc ggtcgcata gtcggtaccg atccgcaatt agtgcgagcg ta          52

SEQ ID NO: 244         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 244
ttcggcgcta ggtagcgcg tcaagaacgc cgtaccatac ggtacggtcg gt          52

SEQ ID NO: 245         moltype = DNA length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 245

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gtacgctcgc agtgcgcgag tagtgtgcac tcgacggtta actaatccgc gc	52
SEQ ID NO: 246	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 246	
accgccgact tatagtagtg cgcgtaacgca ttagtcggtc gcggattaag gt	52
SEQ ID NO: 247	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 247	
cggacgagcg gttcgcatga gtcggtacca taaccgcgcc gcggattaag gt	52
SEQ ID NO: 248	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 248	
accgccgact tatcgcgcta ctaggtaccg ccgtacaagg tacgctcgca gt	52
SEQ ID NO: 249	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 249	
cgcaacgcta ggtacctagc gccgaacgcg gactaaggta cctagcgccg aa	52
SEQ ID NO: 250	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 250	
gcactcgacg gttcggttcg ctaggtaccg ccgtacaagt acgcgactag gt	52
SEQ ID NO: 251	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 251	
acgccgtacc atagcggcgt attggtgtcg cgcagtgtag cgcggttatg gt	52
SEQ ID NO: 252	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 252	
tagttagcgg cgtgcggttc gacattacct agtcgcgtag cgcgagtagt gt	52
SEQ ID NO: 253	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 253	
gcgcgattaa ggttctcgcg cactaacgac gcgctgttac gcattagtcg gt	52
SEQ ID NO: 254	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 254	
gcggcgattt ggtaccgcgg acttatcgca ttagtcggtt atggtaacggc gt	52
SEQ ID NO: 255	moltype = DNA length = 52
FEATURE	Location/Qualifiers

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source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 255
gcgcgggttat ggtaactact cgccgaacct attaccgcga ctgcgagcgt ac          52

SEQ ID NO: 256        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 256
cgactatgtg cgctcgtcgc actagtagca taaccgcgca accgctcgtc cg          52

SEQ ID NO: 257        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 257
aatctagcgc cgatagttag cggcgtagct taatcgcgct agcgcgagta gt          52

SEQ ID NO: 258        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 258
tacgcgcact actgcgtcga attggtgcgc ggattagttg cgtcgaattg gt          52

SEQ ID NO: 259        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 259
accgccgcta tacactgcga gcgtacttcg gcgctagggtg tatagcggcg gt          52

SEQ ID NO: 260        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 260
actactcgcg ctagcggcgt attggtaacc gctcgtccgg cgcgagtagt gt          52

SEQ ID NO: 261        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 261
gcgcgagtag tgtacctagc gttgcgcgcg gattaaggta ctagtgcgac ga          52

SEQ ID NO: 262        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 262
gcggttcgac attacctagc gttgcgcgca ttagtcggta cctagtagcg cg          52

SEQ ID NO: 263        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 263
gtcgcgcagt gtaacctagc gttgcgtcgc gacagtagtg actaccgctc gt          52

SEQ ID NO: 264        moltype = DNA length = 52
FEATURE              Location/Qualifiers
source                1..52
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 264

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accgctcgtt accactagcg atcggtagca tactacgcgt acgcgactag gt	52
SEQ ID NO: 265	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 265	
cgcaacgcta ggtagtcgag cgcatacgca ttagtcggtat atgtcgaacc gc	52
SEQ ID NO: 266	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 266	
acctagtagc gcgtagttag cggcggtttag tgcgcgagag tacgctcgca gt	52
SEQ ID NO: 267	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 267	
ctgtgtacggc ggtagcggac taagggttcgc ggtagatga cgcacgcgtac cg	52
SEQ ID NO: 268	moltype = DNA length = 52
FEATURE	Location/Qualifiers
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 268	
tagttagcgg cgtaattctag ccgcgaatag gtagcgcgta actactcgcc ga	52
SEQ ID NO: 269	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 269	
acgcgactat acgcgcaata tggc	24
SEQ ID NO: 270	moltype = DNA length = 25
FEATURE	Location/Qualifiers
source	1..25
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 270	
ctagcgatag tacgcgatac gagat	25
SEQ ID NO: 271	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 271	
catagcggta ttacgcgaga ttacga	26
SEQ ID NO: 272	moltype = DNA length = 21
FEATURE	Location/Qualifiers
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 272	
cgcgagtacg tacgattacc g	21
SEQ ID NO: 273	moltype = DNA length = 21
FEATURE	Location/Qualifiers
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 273	
acgcgcgact atacgcgcct c	21

1. A method for identifying and nominating on- and off-target CRISPR edited sites with improved accuracy and sensitivity, the process comprising the steps of:

- (a) isolating genomic DNA from a cell having one or more tag sequences incorporated into a target site within a genome of the cell;
- (b) integrating a universal adapter sequence comprising a unique molecular index (UMI) into the isolated genomic DNA;
- (c) providing a multiplex PCR reaction mixture comprising:
 - (i) one or more on-target oligonucleotide primers, each having a cleavage region comprising a ribonucleotide (rN) positioned 5' of a blocking group and a complementary region flanking the on-target genome edited locus, wherein the blocking group prevents primer extension and/or inhibits the oligonucleotide primer from serving as a template for DNA synthesis;
 - (ii) one or more adapter-specific oligonucleotide primers, each having a cleavage region comprising a ribonucleotide (rN) positioned 5' of a blocking group and a complementary region flanking the 5' of the universal adapter sequence; and
 - (iii) a cleaving enzyme, wherein the cleaving enzyme is an RNase H2 enzyme;
- (d) hybridizing the on-target oligonucleotide primer to the on-target genome edited locus to form an on-target double stranded substrate and hybridizing the one or more adapter-specific oligonucleotide primers to the 5' of the universal adapter sequence;
- (e) cleaving at a point within or adjacent to the cleavage region to remove the blocking group from the one or more on-target oligonucleotide primers and the one or more adapter-specific oligonucleotide primers; and
- (f) simultaneously amplifying a portion of the isolated genomic DNA comprising the one or more tag sequences and the universal adapter sequence; and
- (g) sequencing the amplified portion of the isolated genomic DNA, thereby identifying on- and off-target CRISPR edited sites.

2. The method of claim 1, wherein the one or more adapter-specific oligonucleotide primers target SP1 or SP2 sequence (SEQ ID NO: 7, 8) tails on a top strand of the one or more on-target oligonucleotide primers or a bottom strand of the one or more on-target oligonucleotide primers.

3. The method of claim 1, wherein the one or more adapter-specific oligonucleotide primers target predesigned non-homologous sequence (SEQ ID NO: 269-273) tails on a top strand of the one or more on-target oligonucleotide primers or a bottom strand of the one or more on-target oligonucleotide primers.

4. The method of claim 1, wherein the one or more adapter-specific oligonucleotide primers target predesigned 13-mer tails on a top strand of the one or more on-target oligonucleotide primers or a bottom strand of the one or more on-target oligonucleotide primers.

5. The method of claim 1, wherein the sequencing of step (g) further comprises executing on a processor:

- (i) aligning the sequence data to a reference genome; and
- (ii) outputting the alignment, analysis, and results data as custom-formatted files, tables or graphics.

6. (canceled)

7. The method of claim 1, wherein step (d) uses a suppression PCR method.

8. The method of claim 1, wherein the one or more on-target oligonucleotide primers comprise a first on-target oligonucleotide primer targeting a top strand of the isolated genomic DNA and a second on-target oligonucleotide primer targeting a bottom strand of the isolated genomic DNA.

9. The method of claim 1, wherein the one or more adapter-specific oligonucleotide primers comprise a first adapter-specific oligonucleotide primer targeting a top strand of the isolated genomic DNA and a second adapter-specific oligonucleotide primer targeting a bottom strand of the isolated genomic DNA.

10. The method of claim 1, wherein the cells comprise human or mouse cells.

11-12. (canceled)

13. The method of claim 1, wherein the one or more tag sequences comprise double-stranded deoxyribooligonucleotides (dsDNA) comprising 52-base pairs.

14. The method of claim 1, wherein the one or more tag sequences comprise a 5'-terminal phosphate, and phosphorothioate linkages between the 1st and 2nd, 2nd and 3rd, 50th and 51st, and 51st and 52nd nucleotides.

15. The method of claim 1, wherein the one or more tag sequences comprise a double stranded DNA comprising the complementary top and bottom strand pairs of SEQ ID NO: 1-2 or 7-268.

16. On- and off-target CRISPR editing sites identified or nominated using the method of claim 1.

17-33. (canceled)

34. The method of claim 1, wherein the one or more tag sequences alien sequence content containing no sequence identity to a mouse or human genome.

35. The method of claim 1, wherein the cleavage region comprises a ribonucleotide (rN) that is positioned 6-nucleotides from the 3'-end.

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