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(71) Applicant: **THE GENERAL HOSPITAL CORPORATION** [US/US]; 55 Fruit Street, Boston, Massachusetts 02114 (US).

(72) Inventors: **JOUNG, J. Keith**; 1 Magnolia Way, Winchester, Massachusetts 01890 (US). **KLEINSTIVER, Benjamin**; 100 Rivers Edge Drive Unit 225, Medford, Massachusetts 02155 (US). **PATTANAYAK, Vikram**; 280 Linden Street, Wellesley, Massachusetts 02482 (US).

(74) Agents: **DEYOUNG, Janice Kugler** et al.; Fish & Richardson P.C., P.O. Box 1022, Minneapolis, Minnesota 55440-1022 (US).

[Continued on next page]

(54) Title: ENGINEERED CRISPR-CAS9 NUCLEASES

(57) Abstract: Engineered CRISPR-Cas9 nucleases with improved specificity and their use in genomic engineering, epigenomic engineering, genome targeting, and genome editing.

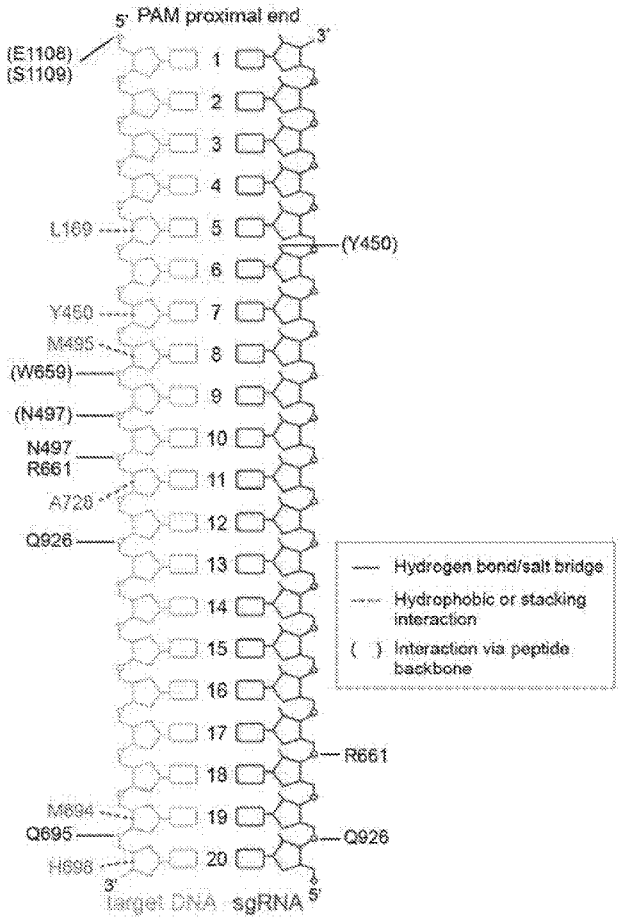

FIG. 1A

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Engineered CRISPR-Cas9 Nucleases

CLAIM OF PRIORITY

This application claims priority under 35 USC §119(e) to U.S. Patent Application Serial Nos. 62/211,553, filed on August 28, 2015; 62/216,033, filed on September 9, 2015; 62/258,280, filed on November 20, 2015; 62/271,938, filed on December 28, 2015; and 15/015,947, filed on February 4, 2016. The entire contents of the foregoing are hereby incorporated by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on August 26, 2016, is named SEQUENCE LISTING.txt and is 129,955 bytes in size.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with Government support under Grant Nos. DP1 GM105378 and R01 GM088040 awarded by the National Institutes of Health. The Government has certain rights in the invention.

TECHNICAL FIELD

The invention relates, at least in part, to engineered Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs)/CRISPR-associated protein 9 (Cas9) nucleases with altered and improved target specificity and their use in genomic engineering, epigenomic engineering, genome targeting, genome editing, and in vitro diagnostics.

BACKGROUND

CRISPR-Cas9 nucleases enable efficient genome editing in a wide variety of organisms and cell types (Sander & Joung, Nat Biotechnol 32, 347-355 (2014); Hsu et al., Cell 157, 1262-1278 (2014); Doudna & Charpentier, Science 346, 1258096 (2014); Barrangou & May, Expert Opin Biol Ther 15, 311-314 (2015)). Target site recognition by Cas9 is programmed by a chimeric single guide RNA (**sgRNA**) that encodes a sequence complementary to a target protospacer (Jinek et al., Science 337,

816-821 (2012)), but also requires recognition of a short neighboring PAM (Mojica et al., Microbiology 155, 733-740 (2009); Shah et al., RNA Biol 10, 891-899 (2013); Jiang et al., Nat Biotechnol 31, 233-239 (2013); Jinek et al., Science 337, 816-821 (2012); Sternberg et al., Nature 507, 62-67 (2014)).

SUMMARY

As described herein, Cas9 Proteins can be engineered to show increased specificity, theoretically by reducing the binding affinity of Cas9 for DNA. Thus, described herein are a number of Cas9 variants that have increased specificity (i.e., induce substantially fewer off target effects at imperfectly matched or mismatched DNA sites) as compared to the wild type protein, as well as methods of using them.

In a first aspect, the invention provides isolated *Streptococcus pyogenes* Cas9 (**SpCas9**) proteins with mutations at one, two, three, four, five, six or all seven of the following positions: L169A, Y450, N497, R661, Q695, Q926, and/or D1135E e.g., comprising a sequence that is at least 80% identical to the amino acid sequence of SEQ ID NO:1 with mutations at one, two, three, four, five, six, or seven of the following positions: L169, Y450, N497, R661, Q695, Q926, D1135E, and optionally one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag. A mutation alters the amino acid to an amino acid other than the native amino acid (e.g., 497 is anything but N). In preferred embodiments the mutation changes the amino acid to any amino acid other than the native one, arginine or lysine; in some embodiments, the amino acid is alanine.

In some embodiments, the variant SpCas9 proteins comprise mutations at one, two, three, or all four of the following: N497, R661, Q695, and Q926, e.g., one, two, three, or all four of the following mutations: N497A, R661A, Q695A, and Q926A.

In some embodiments, the variant SpCas9 proteins comprise mutations at Q695 and/or Q926, and optionally one, two, three, four or all five of L169, Y450, N497, R661 and D1135E, e.g., including but not limited to Y450A/Q695A, L169A/Q695A, Q695A/Q926A, Q695A/D1135E, Q926A/D1135E, Y450A/D1135E, L169A/Y450A/Q695A, L169A/Q695A/Q926A, Y450A/Q695A/Q926A, R661A/Q695A/Q926A, N497A/Q695A/Q926A, Y450A/Q695A/D1135E, Y450A/Q926A/D1135E, Q695A/Q926A/D1135E, L169A/Y450A/Q695A/Q926A, L169A/R661A/Q695A/Q926A,Y450A/R661A/Q695A/Q926A,

N497A/Q695A/Q926A/D1135E, R661A/Q695A/Q926A/D1135E, and Y450A/Q695A/Q926A/D1135E.

In some embodiments, the variant SpCas9 proteins comprise mutations at N14; S15; S55; R63; R78; H160; K163; R165; L169; R403; N407; Y450; M495; N497; K510; Y515; W659; R661; M694; Q695; H698; A728; S730; K775; S777; R778; R780; K782; R783; K789; K797; Q805; N808; K810; R832; Q844; S845; K848; S851; K855; R859; K862; K890; Q920; Q926; K961; S964; K968; K974; R976; N980; H982; K1003; K1014; S1040; N1041; N1044; K1047; K1059; R1060; K1107; E1108; S1109; K1113; R1114; S1116; K1118; D1135; S1136; K1153; K1155 ; K1158; K1200; Q1221; H1241; Q1254; Q1256; K1289; K1296; K1297; R1298; K1300; H1311; K1325; K1334; T1337 and/or S1216.

In some embodiments, the variant SpCas9 proteins also comprise one or more of the following mutations: N14A; S15A; S55A; R63A; R78A; R165A; R403A; N407A; N497A; Y450A; K510A; Y515A; R661A; Q695A; S730A; K775A; S777A; R778A; R780A; K782A; R783A; K789A; K797A; Q805A; N808A; K810A; R832A; Q844A; S845A; K848A; S851A; K855A; R859A; K862A; K890A; Q920A; Q926A; K961A; S964A; K968A; K974A; R976A; N980A; H982A; K1003A; K1014A; S1040A; N1041A; N1044A; K1047A; K1059A; R1060A; K1107A; E1108A; S1109A; K1113A; R1114A; S1116A; K1118A; D1135A; S1136A; K1153A; K1155A; K1158A; K1200A; Q1221A; H1241A; Q1254A; Q1256A; K1289A; K1296A; K1297A; R1298A; K1300A; H1311A; K1325A; K1334A; T1337A and/or S1216A. In some embodiments, the variant proteins include HF1(N497A/R661A/Q695A/Q926A)+K810A, HF1+K848A, HF1+K855A, HF1+H982A, HF1+K848A/K1003A, HF1+K848A/R1060A, HF1+K855A/K1003A, HF1+K855A/R1060A, HF1+H982A/K1003A, HF1+H982A/R1060A, HF1+K1003A/R1060A, HF1+K810A/K1003A/R1060A, HF1+K848A/K1003A/R1060A. In some embodiments, the variant proteins include HF1+K848A/K1003A, HF1+K848A/R1060A, HF1+K855A/K1003A, HF1+K855A/R1060A, HF1+K1003A/R1060A, HF1+K848A/K1003A/R1060A. In some embodiments, the variant proteins include Q695A/Q926A/R780A, Q695A/Q926A/R976A, Q695A/Q926A/H982A, Q695A/Q926A/K855A, Q695A/Q926A/K848A/K1003A, Q695A/Q926A/K848A/K855A, Q695A/Q926A/K848A/H982A, Q695A/Q926A/K1003A/R1060A,

Q695A/Q926A/K848A/R1060A, Q695A/Q926A/K855A/H982A,
Q695A/Q926A/K855A/K1003A, Q695A/Q926A/K855A/R1060A,
Q695A/Q926A/H982A/K1003A, Q695A/Q926A/H982A/R1060A,
Q695A/Q926A/K1003A/R1060A, Q695A/Q926A/K810A/K1003A/R1060A,
Q695A/Q926A/K848A/K1003A/R1060A. In some embodiments, the variants include N497A/R661A/Q695A/Q926A/K810A,
N497A/R661A/Q695A/Q926A/K848A, N497A/R661A/Q695A/Q926A/K855A,
N497A/R661A/Q695A/Q926A/R780A, N497A/R661A/Q695A/Q926A/K968A,
N497A/R661A/Q695A/Q926A/H982A, N497A/R661A/Q695A/Q926A/K1003A,
N497A/R661A/Q695A/Q926A/K1014A, N497A/R661A/Q695A/Q926A/K1047A,
N497A/R661A/Q695A/Q926A/R1060A,
N497A/R661A/Q695A/Q926A/K810A/K968A,
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N497A/R661A/Q695A/Q926A/K855A/K1003A,
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N497A/R661A/Q695A/Q926A/K810A/K1003A/R1060A,
N497A/R661A/Q695A/Q926A/K848A/K1003A/R1060A, Q695A/Q926A/R780A,
Q695A/Q926A/K810A, Q695A/Q926A/R832A, Q695A/Q926A/K848A,
Q695A/Q926A/K855A, Q695A/Q926A/K968A, Q695A/Q926A/R976A,
Q695A/Q926A/H982A, Q695A/Q926A/K1003A, Q695A/Q926A/K1014A,
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Q695A/Q926A/R832A/R1060A, Q695A/Q926A/K968A/K1003A,

Q695A/Q926A/K968A/R1060A, Q695A/Q926A/K848A/R1060A, Q695A/Q926A/K855A/H982A, Q695A/Q926A/K855A/K1003A, Q695A/Q926A/K855A/R1060A, Q695A/Q926A/H982A/K1003A, Q695A/Q926A/H982A/R1060A, Q695A/Q926A/K1003A/R1060A, Q695A/Q926A/K810A/K1003A/R1060A, Q695A/Q926A/K1003A/K1047A/R1060A, Q695A/Q926A/K968A/K1003A/R1060A, Q695A/Q926A/R832A/K1003A/R1060A, or Q695A/Q926A/K848A/K1003A/R1060A

Mutations to amino acids other than alanine are also included, and can be made and used in the present methods and compositions.

In some embodiments, variant SpCas9 proteins comprise one or more of the following additional mutations: R63A, R66A, R69A, R70A, R71A, Y72A, R74A, R75A, K76A, N77A, R78A, R115A, H160A, K163A, R165A, L169A, R403A, T404A, F405A, N407A, R447A, N497A, I448A, Y450A, S460A, M495A, K510A, Y515A, R661A, M694A, Q695A, H698A, Y1013A, V1015A, R1122A, K1123A, K1124A, K1158A, K1185A, K1200A, S1216A, Q1221A, K1289A, R1298A, K1300A, K1325A, R1333A, K1334A, R1335A, and T1337A.

In some embodiments, the variant SpCas9 proteins comprise multiple substitution mutations: N497/R661/Q695/Q926 (quadruple variant mutants); Q695/Q926 (double mutant); R661/Q695/Q926 and N497/Q695/Q926 (triple mutants). In some embodiments, additional substitution mutations at L169, Y450 and/or D1135 might be added to these double-, triple, and quadruple mutants or added to single mutants bearing substitutions at Q695 or Q926. In some embodiments, the mutants have alanine in place of the wild type amino acid. In some embodiments, the mutants have any amino acid other than arginine or lysine (or the native amino acid).

In some embodiments, the variant SpCas9 proteins also comprise one or more mutations that decrease nuclease activity selected from the group consisting of mutations at D10, E762, D839, H983, or D986; and at H840 or N863. In some embodiments, the mutations are: (i) D10A or D10N, and (ii) H840A, H840N, or H840Y.

In some embodiments, the SpCas9 variants can also include one of the following sets of mutations: D1135V/R1335Q/T1337R (VQR variant);

D1135E/R1335Q/T1337R (EQR variant); D1135V/G1218R/R1335Q/T1337R (VRQR variant); or D1135V/G1218R/R1335E/T1337R (VRER variant).

Also provided herein are isolated *Staphylococcus aureus* Cas9 (**SaCas9**) protein, with mutations at one, two, three, four, five, six, or more of the following positions: Y211, Y212, W229, Y230, R245, T392, N419, Y651, or R654, e.g., comprising a sequence that is at least 80% identical to the amino acid sequence of SEQ ID NO:1 with mutations at one, two, three, four, or five, or six of the following positions: Y211, Y212, W229, Y230, R245, T392, N419, Y651, or R654, and optionally one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag. In some embodiments, the SaCas9 variants described herein include the amino acid sequence of SEQ ID NO:2, with mutations at one, two, three, four, five, six, or more of the following positions: Y211, Y212, W229, Y230, R245, T392, N419, Y651and/or R654. In some embodiments the variants include one or more of the following mutations: Y211A, Y212A, W229, Y230A, R245A, T392A, N419A, Y651, and/or R654A.

In some embodiments, the variant SaCas9 proteins comprise mutations at N419 and/or R654, and optionally one, two, three, four or more of the additional mutations Y211, Y212, W229, Y230, R245 and T392, preferably N419A/R654A, Y211A/R654A, Y211A/Y212A, Y211A/Y230A, Y211A/R245A, Y212A/Y230A, Y212A/R245A, Y230A/R245A, W229A/R654A, Y211A/Y212A/Y230A, Y211A/Y212A/R245A, Y211A/Y212A/Y651A, Y211A/Y230A/R245A, Y211A/Y230A/Y651A, Y211A/R245A/Y651A, Y211A/R245A/R654A, Y211A/R245A/N419A, Y211A/N419A/R654A, Y212A/Y230A/R245A, Y212A/Y230A/Y651A, Y212A/R245A/Y651A, Y230A/R245A/Y651A, R245A/N419A/R654A, T392A/N419A/R654A, R245A/T392A/N419A/R654A, Y211A/R245A/N419A/R654A, W229A/R245A/N419A/R654A, Y211A/R245A/T392A/N419A/R654A, or Y211A/W229A/R245A/N419A/R654A.

In some embodiments, the variant SaCas9 proteins comprise mutations at Y211; Y212; W229; Y230; R245; T392; N419; L446; Q488; N492; Q495; R497; N498; R499; Q500; K518; K523; K525; H557; R561; K572; R634; Y651; R654; G655; N658; S662; N667; R686; K692; R694; H700; K751; D786; T787; Y789; T882; K886; N888; 889; L909; N985; N986; R991; R1015; N44; R45; R51; R55; R59; R60; R116; R165; N169; R208; R209; Y211; T238; Y239; K248; Y256; R314;

N394; Q414; K57; R61; H111; K114; V164; R165; L788; S790; R792; N804; Y868; K870; K878; K879; K881; Y897; R901; and/or K906.

In some embodiments, the variant SaCas9 proteins comprise one or more of the following mutations: Y211A; Y212A; W229A; Y230A; R245A; T392A; N419A; L446A; Q488A; N492A; Q495A; R497A; N498A; R499A; Q500A; K518A; K523A; K525A; H557A; R561A; K572A; R634A; Y651A; R654A; G655A; N658A; S662A; N667A; R686A; K692A; R694A; H700A; K751A; D786A; T787A; Y789A; T882A; K886A; N888A; A889A; L909A; N985A; N986A; R991A; R1015A; N44A; R45A; R51A; R55A; R59A; R60A; R116A; R165A; N169A; R208A; R209A; T238A; Y239A; K248A; Y256A; R314A; N394A; Q414A; K57A; R61A; H111A; K114A; V164A; R165A; L788A; S790A; R792A; N804A; Y868A; K870A; K878A; K879A; K881A; Y897A; R901A; K906A.

In some embodiments, variant SaCas9 proteins comprise one or more of the following additional mutations: Y211A, W229A, Y230A, R245A, T392A, N419A, L446A, Y651A, R654A, D786A, T787A, Y789A, T882A, K886A, N888A, A889A, L909A, N985A, N986A, R991A, R1015A, N44A, R45A, R51A, R55A, R59A, R60A, R116A, R165A, N169A, R208A, R209A, T238A, Y239A, K248A, Y256A, R314A, N394A, Q414A, K57A, R61A, H111A, K114A, V164A, R165A, L788A, S790A, R792A, N804A, Y868A, K870A, K878A, K879A, K881A, Y897A, R901A, K906A.

In some embodiments, the variant SaCas9 proteins comprise multiple substitution mutations: R245/T392/N419/R654 and Y221/R245/N419/R654 (quadruple variant mutants); N419/R654, R245/R654, Y221/R654, and Y221/N419 (double mutants); R245/N419/R654, Y211/N419/R654, and T392/N419/R654 (triple mutants). In some embodiments the mutants contain alanine in place of the wild type amino acid.

In some embodiments, the variant SaCas9 proteins also comprise one or more mutations that decrease nuclease activity selected from the group consisting of mutations at D10, E477, D556, H701, or D704; and at H557 or N580. In some embodiments, the mutations are: (i) D10A or D10N, (ii) H557A, H557N, or H557Y, (iii) N580A, and/or (iv) D556A.

In some embodiments, the variant SaCas9 proteins comprise one or more of the following mutations: E782K, K929R, N968K, or R1015H. Specifically,

E782K/N968K/R1015H (KKH variant); E782K/K929R/R1015H (KRH variant); or E782K/K929R/N968K/R1015H (KRKH variant).

In some embodiments, the variant Cas9 proteins include mutations to one or more of the following regions to increase specificity:

Functional Region	SpCas9	SaCas9
Residues contacting the DNA of the spacer region	L169; Y450; M495; N497; W659; R661; M694; Q695; H698; A728; Q926; E1108; V1015	Y211; W229; Y230; R245; T392; N419; L446; Y651; R654
Residues that potentially contact the DNA of the non-target strand	N14; S15; S55; S730; K775; S777; R778; R780; K782; R783; K789; K797; Q805; N808; K810; R832; Q844; S845; K848; S851; K855; R859; K862; K890; Q920; K961; S964; K968; K974; R976; N980; H982; K1003; K1014; S1040; N1041; N1044; K1047; K1059; R1060; K1200; H1241; Q1254; Q1256; K1289; K1296; K1297; K1300; H1311; K1325	Q488A; N492A; Q495A; R497A; N498A; R499; Q500; K518; K523; K525; H557; R561; K572; R634; R654; G655; N658; S662; N667; R686; K692; R694; H700; K751
Residues contacting the DNA of the PAM region (including direct PAM contacts)	R71; Y72; R78; R165; R403; T404; F405; K1107; S1109; R1114; S1116; K1118; D1135; S1136; K1200; S1216; E1219; R1333; R1335; T1337	D786; T787; Y789; T882; K886; N888; A889; L909; N985; N986; R991; R1015
Residues contacting the RNA of the spacer region	Y72; R75; K76; L101; S104; F105; R115; H116; I135; H160; K163; Y325; H328; R340; F351; D364; Q402; R403; I1110; K1113; R1122; Y1131	N44; R45; R51; R55; R59; R60; R116; R165; N169; R208; R209; Y211; T238; Y239; K248; Y256; R314; N394; Q414
Residues contacting the RNA of the repeat/anti-repeat region	R63; R66; R70; R71; R74; R78; R403; T404; N407; R447; I448; Y450; K510; Y515; R661; V1009; Y1013	K57; R61; H111; K114; V164; R165; L788; S790; R792; N804; Y868; K870; K878; K879; K881; Y897; R901; K906
Residues contacting the RNA stem loops	K30; K33; N46; R40; K44; E57; T62; R69; N77; L455; S460; R467; T472; I473; H721; K742; K1097; V1100; T1102; F1105; K1123; K1124; E1225; Q1272; H1349; S1351; Y1356	R47; K50; R54; R58; H62; R209; E213; S219; R452; K459; R774; N780; R781; L783

Also provided herein are fusion proteins comprising the isolated variant Cas9 proteins described herein fused to a heterologous functional domain, with an optional intervening linker, wherein the linker does not interfere with activity of the fusion protein. In some embodiments, the heterologous functional domain acts on DNA or protein, e.g., on chromatin. In some embodiments, the heterologous functional domain is a transcriptional activation domain. In some embodiments, the transcriptional activation domain is from VP64 or NF-κB p65. In some embodiments, the heterologous functional domain is a transcriptional silencer or transcriptional repression domain. In some embodiments, the transcriptional repression domain is a Kruppel-associated box (KRAB) domain, ERF repressor domain (ERD), or mSin3A interaction domain (SID). In some embodiments, the transcriptional silencer is Heterochromatin Protein 1 (HP1), e.g., HP1α or HP1β. In some embodiments, the heterologous functional domain is an enzyme that modifies the methylation state of DNA. In some embodiments, the enzyme that modifies the methylation state of DNA is a DNA methyltransferase (DNMT) or the entirety or the dioxygenase domain of a TET protein, e.g., a catalytic module comprising the cysteine-rich extension and the 2OGFeDO domain encoded by 7 highly conserved exons, e.g., the Tet1 catalytic domain comprising amino acids 1580-2052, Tet2 comprising amino acids 1290-1905 and Tet3 comprising amino acids 966-1678. In some embodiments, the TET protein or TET-derived dioxygenase domain is from TET1. In some embodiments, the heterologous functional domain is an enzyme that modifies a histone subunit. In some embodiments, the enzyme that modifies a histone subunit is a histone acetyltransferase (HAT), histone deacetylase (HDAC), histone methyltransferase (HMT), or histone demethylase. In some embodiments, the heterologous functional domain is a biological tether. In some embodiments, the biological tether is MS2, Csy4 or lambda N protein. In some embodiments, the heterologous functional domain is FokI.

Also provided herein are nucleic acids, isolated nucleic acids encoding the variant Cas9 proteins described herein, as well as vectors comprising the isolated nucleic acids, optionally operably linked to one or more regulatory domains for expressing the variant Cas9 proteins described herein. Also provided herein are host cells, e.g., bacterial, yeast, insect, or mammalian host cells or transgenic animals (e.g.,

mice), comprising the nucleic acids described herein, and optionally expressing the variant Cas9 proteins described herein.

Also provided herein are isolated nucleic acids encoding the Cas9variants, as well as vectors comprising the isolated nucleic acids, optionally operably linked to one or more regulatory domains for expressing the variants, and host cells, e.g., mammalian host cells, comprising the nucleic acids, and optionally expressing the variant proteins.

Also provided herein are methods of altering the genome or epigenome of a cell, by expressing in the cell or contacting the cell with variant Cas9 proteins or fusion proteins as described herein, and at least one guide RNA having a region complementary to a selected portion of the genome of the cell with optimal nucleotide spacing at the genomic target site. The methods can include contacting the cell with a nucleic acid encoding the Cas9 protein and the guide RNA, e.g., in a single vector; contacting the cell with a nucleic acid encoding the Cas9 protein and a nucleic acid encoding the guide RNA, e.g., in multiple vectors; and contacting the cell with a complex of purified Cas9 protein and synthetic or purified gRNA, *inter alia*. In some embodiments, the cell stably expresses one or both of the gRNA or the variant protein/fusion protein, and the other element is transfected or introduced into the cell. For example, the cell may stably express a variant protein or fusion protein as described herein, and the methods can include contacting the cell with a synthetic gRNA, a purified recombinantly produced gRNA, or a nucleic acid encoding the gRNA. In some embodiments, the variant protein or fusion protein comprises one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag.

Also provided herein are methods for altering, e.g., selectively altering, an isolated dsDNA molecule *in vitro* by contacting the dsDNA with a purified variant protein or fusion protein as described herein, and a guide RNA having a region complementary to a selected portion of the dsDNA molecule.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present invention; other, suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended

to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Other features and advantages of the invention will be apparent from the following detailed description and figures, and from the claims.

DESCRIPTION OF DRAWINGS

FIGs. 1A-E | Identification and characterization of SpCas9 variants bearing mutations in residues that form non-specific DNA contacts. A, Schematic depicting wild-type SpCas9 recognition of the target DNA:sgRNA duplex, based on PDB 4OOG and 4UN3 (adapted from refs. 31 and 32, respectively). B, Characterization of SpCas9 variants that contain alanine substitutions in positions that form hydrogen bonds to the DNA backbone. Wild-type SpCas9 and variants were assessed using the human cell EGFP disruption assay when programmed with a perfectly matched sgRNA or four other sgRNAs that encode mismatches to the target site. Error bars represent s.e.m. for n = 3; mean level of background EGFP loss represented by red dashed line (for this panel and panel C). C and D, On-target activities of wild-type SpCas9 and SpCas9-HF1 across 24 sites assessed by EGFP disruption assay (panel C) and 13 endogenous sites by T7E1 assay (panel D). Error bars represent s.e.m. for n = 3. E, Ratio of on-target activity of SpCas9-HF1 to wild-type SpCas9 (from panels C and D).

FIG. 2A-C | Genome-wide specificities of wild-type SpCas9 and SpCas9-HF1 with sgRNAs for standard target sites. A, Off-target sites of wild-type SpCas9 and SpCas9-HF1 with eight sgRNAs targeted to endogenous human genes, as determined by GUIDE-seq. Read counts represent a measure of cleavage frequency at a given site; mismatched positions within the spacer or PAM are highlighted in color. B, Summary of the total number of genome-wide off-target sites identified by GUIDE-seq for wild-type SpCas9 and SpCas9-HF1 from the eight sgRNAs used in panel A. C, Off-target sites identified for wild-type SpCas9 and SpCas9-HF1 for the eight sgRNAs, binned according to the total number of mismatches (within the protospacer and PAM) relative to the on-target site.

FIG. 3A-C | Validation of SpCas9-HF1 specificity improvements by targeted deep sequencing of off-target sites identified by GUIDE-seq. A, Mean

on-target percent modification determined by deep sequencing for wild-type SpCas9 and SpCas9-HF1 with six sgRNAs from Fig. 2. Error bars represent s.e.m. for n = 3. B, Percentage of deep sequenced on-target sites and GUIDE-seq detected off-target sites that contain indel mutations. Triplicate experiments are plotted for wild-type SpCas9, SpCas9-HF1, and control conditions. Filled circles below the x-axis represent replicates for which no insertion or deletion mutations were observed. Off-target sites that could not be amplified by PCR are shown in red text with an asterisk. Hypothesis testing using a one-sided Fisher exact test with pooled read counts found significant differences ($p < 0.05$ after adjusting for multiple comparisons using the Benjamini-Hochberg method) for comparisons between SpCas9-HF1 and the control condition only at EMX1-1 off-target 1 and FANCF-3 off-target 1. Significant differences were also found between wild-type SpCas9 and SpCas9-HF1 at all off-target sites, and between wild-type SpCas9 and the control condition at all off-target sites except RUNX1-1 off-target 2. C, Scatter plot of the correlation between GUIDE-seq read counts (from Fig. 2A) and mean percent modification determined by deep sequencing at on- and off-target cleavage sites with wild-type SpCas9.

FIG. 4A-C | Genome-wide specificities of wild-type SpCas9 and SpCas9-HF1 with sgRNAs for non-standard, repetitive sites. A, GUIDE-seq specificity profiles of wild-type SpCas9 and SpCas9-HF1 using two sgRNAs known to cleave large numbers of off-target sites (Fu et al., Nat Biotechnol 31, 822-826 (2013); Tsai et al., Nat Biotechnol 33, 187-197 (2015)). GUIDE-seq read counts represent a measure of cleavage efficiency at a given site; mismatched positions within the spacer or PAM are highlighted in color; red circles indicate sites likely to have the indicated bulge (Lin et al., Nucleic Acids Res 42, 7473-7485 (2014)) at the sgRNA-DNA interface; blue circles indicate sites that may have an alternative gapped alignment relative to the one shown (see Fig. 8). B, Summary of the total number of genome-wide off-target sites identified by GUIDE-seq for wild-type SpCas9 and SpCas9-HF1 from the two sgRNAs used in panel A. C, Off-target sites identified with wild-type SpCas9 or SpCas9-HF1 for VEGFA sites 2 and 3, binned according to the total number of mismatches (within the protospacer and PAM) relative to the on-target site. Off-target sites marked with red circles in panel A are not included in these counts; sites marked with blue circles in panel A are counted with the number of mismatches in the non-gapped alignment.

FIG. 5A-D| Activities of SpCas9-HF1 derivatives bearing additional substitutions. A, Human cell EGFP disruption activities of wild-type SpCas9, SpCas9-HF1, and SpCas9-HF1-derivative variants with eight sgRNAs. SpCas9-HF1 harbors N497A, R661A, Q695, and Q926A mutations; HF2 = HF1 + D1135E; HF3 = HF1 + L169A; HF4 = HF1 + Y450A. Error bars represent s.e.m. for n = 3; mean level of background EGFP loss represented by the red dashed line. B, Summary of the on-target activity when using SpCas9-HF variants compared to wild-type SpCas9 with the eight sgRNAs from panel a. The median and interquartile range are shown; the interval showing >70% of wild-type activity is highlighted in green. C, Mean percent modification by SpCas9 and HF variants at the FANCF site 2 and VEGFA site 3 on-target sites, as well as off-target sites from Figs. 2A and 4A resistant to the effects of SpCas9-HF1. Percent modification determined by T7E1 assay; background indel percentages were subtracted for all experiments. Error bars represent s.e.m. for n = 3. D, Specificity ratios of wild-type SpCas9 and HF variants with the FANCF site 2 or VEGFA site 3 sgRNAs, plotted as the ratio of on-target to off-target activity (from panel C).

FIGs. 5E-F | Genome-wide specificities of SpCas9-HF1, -HF2, and -HF4 with sgRNAs that have off-target sites resistant to the effects of SpCas9-HF1. E, Mean GUIDE-seq tag integration at the intended on-target site for GUIDE-seq experiments in panel F. SpCas9-HF1 = N497A/R661A/Q695A/Q926A; HF2 = HF1 + D1135E; HF4 = HF1 + Y450A. Error bars represent s.e.m. for n = 3. F, GUIDE-seq identified off-target sites of SpCas9-HF1, -HF2, or -HF4 with either the FANCF site 2 or VEGFA site 3 sgRNAs. Read counts represent a measure of cleavage frequency at a given site; mismatched positions within the spacer or PAM are highlighted in color. The fold-improvement in off-target discrimination was calculated by normalizing the off-target read counts for an SpCas9-HF variant to the read counts at the on-target site prior to comparison between SpCas9-HF variants.

FIG. 6A-B | SpCas9 interaction with the sgRNA and target DNA. A, Schematic illustrating the SpCas9:sgRNA complex, with base pairing between the sgRNA and target DNA. B, Structural representation of the SpCas9:sgRNA complex bound to the target DNA, from PDB: 4UN3 (ref. 32). The four residues that form hydrogen bond contacts to the target-strand DNA backbone are highlighted in blue; the HNH domain is hidden for visualization purposes.

FIG. 7A-D | On-target activity comparisons of wild-type and SpCas9-HF1 with various sgRNAs used for GUIDE-seq experiments. A and C, Mean GUIDE-seq tag integration at the intended on-target site for GUIDE-seq experiments shown in Figs. 2A and 4A (panels 7A and 7C, respectively), quantified by restriction fragment length polymorphism assay. Error bars represent s.e.m. for n = 3. b and d, Mean percent modification at the intended on-target site for GUIDE-seq experiments shown in Figs. 2A and 4A (panels 7B and 7D, respectively), detected by T7E1 assay. Error bars represent s.e.m. for n = 3.

FIG. 8 | Potential alternate alignments for VEGFA site 2 off-target sites. Ten VEGFA site 2 off-target sites identified by GUIDE-seq (left) that may potentially be recognized as off-target sites that contain single nucleotide gaps (Lin et al., Nucleic Acids Res 42, 7473-7485 (2014))) (right), aligned using Geneious (Kearse et al., Bioinformatics 28, 1647-1649 (2012)) version 8.1.6.

FIG. 9 | Activities of wild-type SpCas9 and SpCas9-HF1 with truncated sgRNAs14. EGFP disruption activities of wild-type SpCas9 and SpCas9-HF1 using full-length or truncated sgRNAs targeted to four sites in EGFP. Error bars represent s.e.m. for n = 3; mean level of background EGFP loss in control experiments is represented by the red dashed line

FIG. 10 | Wild-type SpCas9 and SpCas9-HF1 activities with sgRNAs bearing 5'-mismatched guanine bases. EGFP disruption activities of wild-type SpCas9 and SpCas9-HF1 with sgRNAs targeted to four different sites. For each target site, sgRNAs either contain the matched non-guanine 5'-base or a 5'-guanine that is intentionally mismatched.

FIG. 11 | Titrating the amount of wild-type SpCas9 and SpCas9-HF1 expression plasmids. Human cell EGFP disruption activities from transfections with varying amounts of wild-type and SpCas9-HF1 expression plasmids. For all transfections, the amount of sgRNA-containing plasmid was fixed at 250 ng. Two sgRNAs targeting separate sites were used; Error bars represent s.e.m. for n = 3; mean level of background EGFP loss in negative controls is represented by the red dashed line.

FIG. 12A-D | Altering the PAM recognition specificity of SpCas9-HF1. A, Comparison of the mean percent modification of on-target endogenous human sites by SpCas9-VQR (ref. 15) and an improved SpCas9-VRQR using 8 sgRNAs,

quantified by T7E1 assay. Both variants are engineered to recognize an NGAN PAM. Error bars represent s.e.m. for n = 2 or 3. B, On-target EGFP disruption activities of SpCas9-VQR and SpCas9-VRQR compared to their -HF1 counterparts using eight sgRNAs. Error bars represent s.e.m. for n = 3; mean level of background EGFP loss in negative controls represented by the red dashed line. C, Comparison of the mean on-target percent modification by SpCas9-VQR and SpCas9-VRQR compared to their -HF1 variants at eight endogenous human gene sites, quantified by T7E1 assay. Error bars represent s.e.m. for n = 3; ND, not detectable. D, Summary of the fold-change in on-target activity when using SpCas9-VQR or SpCas9-VRQR compared to their corresponding -HF1 variants (from panels B and C). The median and interquartile range are shown; the interval showing >70% of wild-type activity is highlighted in green.

FIGs. 13A-B | Activities of wild-type SpCas9, SpCas9-HF1, and wild-type SpCas9 derivatives bearing one or more alanine substitutions at positions that can potentially contact the non-target DNA strand. A and B, Nucleases were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene as well as an sgRNA that is intentionally mismatched at positions 11 and 12 (panel A) or positions 9 and 10 (panel B). Mismatched positions are numbered with position 20 being the most PAM-distal position; the red dashed line represents background levels of EGFP disruption; HF1 = SpCas9 with N497A/R661A/Q695A/Q926A substitutions.

FIGs. 14A-B | Activity of wild-type SpCas9, SpCas9-HF1, and SpCas9-HF1 derivatives bearing one or more alanine substitutions at positions that can potentially contact the non-target DNA strand. A and B, Nucleases were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene as well as an sgRNA that is intentionally mismatched at positions 11 and 12 (panel A) or positions 9 and 10 (panel B). Mismatched positions are numbered with position 20 being the most PAM-distal position; the red dashed line represents background levels of EGFP disruption; HF1 = SpCas9 with N497A/R661A/Q695A/Q926A substitutions.

FIG. 15 | Activity of wild-type SpCas9, SpCas9-HF1, and SpCas9(Q695A/Q926A) derivatives bearing one or more alanine substitutions at positions that can potentially contact the non-target DNA strand. Nucleases were

assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene as well as an sgRNA that is intentionally mismatched at positions 11 and 12. Mismatched positions are numbered with position 20 being the most PAM-distal position; the red dashed line represents background levels of EGFP disruption; HF1 = SpCas9 with N497A/R661A/Q695A/Q926A substitutions; Dbl = SpCas9 with Q695A/Q926A substitutions.

FIG. 16 | Activities of wild-type SpCas9, SpCas9-HF1, and eSpCas9-1.1 using a matched sgRNA and sgRNAs with single mismatches at each position in the spacer. Nucleases were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene ("matched") as well as sgRNAs that are intentionally mismatched at the positions indicated. Mismatched positions are numbered with position 20 being the most PAM-distal position. SpCas9-HF1 = N497A/R661A/Q695A/Q926A, and eSP1.1 = K848A/K1003A/R1060A.

FIGs. 17A-B | Activities of wild-type SpCas9 and variants using a matched sgRNA and sgRNAs with single mismatches at various positions in the spacer. (**A**) The activities of SpCas9 nucleases containing combinations of alanine substitutions (directed to positions that may potentially contact the target or non-target DNA strands) were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene ("matched") as well as sgRNAs that are intentionally mismatched at the indicated spacer positions. (**B**) A subset of these nucleases from (a) were tested using the remainder of all possible singly mismatched sgRNAs for the matched on-target site. Mismatched positions are numbered with position 20 being the most PAM-distal position. mm = mismatch, WT = wild-type, Db = Q695A/Q926A, HF1 = N497A/R661A/Q695A/Q926A, 1.0 = K810A/K1003A/R1060A, and 1.1 = K848A/K1003A/R1060A.

FIG 18 | Activities of wild-type SpCas9 and variants using a matched sgRNA and sgRNAs with mismatches at various individual positions in the spacer. The activities of SpCas9 nucleases containing combinations of alanine substitutions (directed to positions that may potentially contact the target or non-target DNA strands), were assessed using the EGFP disruption assay with an sgRNA that is perfectly matched to a site in the *EGFP* gene ("matched") as well as sgRNAs that are intentionally mismatched at the indicated positions. Db = Q695A/Q926A, HF1 = N497A/R661A/Q695A/Q926A.

FIGs. 19A-B | Activities of wild-type SpCas9 and variants using a matched sgRNA and sgRNAs with mismatches at various individual positions in the spacer. **(A)** The on-target activities of SpCas9 nucleases containing combinations of alanine substitutions (directed to positions that may potentially contact the target or non-target DNA strands), were assessed using the EGFP disruption assay with two sgRNAs that are perfectly matched to a site in the *EGFP* gene. **(B)** A subset of these nucleases from (a) were tested with sgRNAs containing mismatches at positions 12, 14, 16, or 18 (of sgRNA 'site 1') in their spacer sequence to determine whether intolerance to mismatches was imparted by these substitutions. Db = Q695A/Q926A, HF1 = N497A/R661A/Q695A/Q926A.

FIG. 20 | Structural comparison of SpCas9 (top) and SaCas9 (bottom) illustrating the similarity between the positions of the mutations in the quadruple mutant constructs (shown in yellow sphere representation). Also, shown in pink sphere representation are other residues that contact the DNA backbone.

FIGs. 21A-B | Activity of wild-type SaCas9 and SaCas9 derivatives bearing one or more alanine substitutions. A and B, SaCas9 substitutions were directed to positions that may potentially contact the target DNA strand (panel A) or have previously been shown to influence PAM specificity (panel B). Nucleases were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene as well as an sgRNA that is intentionally mismatched at positions 11 and 12. Mismatched positions are numbered with position 20 being the most PAM-distal position; the red dashed line represents background levels of EGFP disruption.

FIGs. 22A-B | Activities of wild-type (WT) SaCas9 and SaCas9 derivatives bearing one or more alanine substitutions at residues that may potentially contact the target DNA strand. **A** and **B**, Nucleases were assessed using the EGFP disruption assay, with an sgRNA that is perfectly matched to a site in the *EGFP* gene ("matched") and with an sgRNA that is intentionally mismatched at positions 19 and 20. Mismatched positions are numbered with position 20 being the most PAM-distal position.

FIG. 23 | Activities of wild-type (WT) SaCas9 and SaCas9 variants bearing triple combinations of alanine substitutions at residues that may potentially contact the target DNA strand. Nucleases were assessed using the

EGFP disruption assay. Four different sgRNAs were used (matched #1-4), with each of the four target sites also being tested with mismatched sgRNAs known to be efficiently used by wild-type SaCas9. Mismatched sgRNAs for each site are shown to the right of each matched sgRNA (for example, the only mismatched sgRNA for matched site 3 is mm 11&12). Mismatched positions are numbered with position 21 being the most PAM-distal position; mm, mismatch.

FIGs. 24A-B | Activities of wild-type (WT) SaCas9 and SaCas9 derivatives bearing one or more alanine substitutions at residues that may potentially contact the target DNA strand. **A** and **B**, SaCas9 variants bearing double (**A**) or triple (**B**) combinations substitutions were assessed against matched and singly mismatched endogenous human gene target sites using the T7E1 assay. Matched 'on-target' sites are named according to their gene target site sgRNA number from Kleinstiver et al., *Nature* Biotechnology 2015. Mismatched sgRNAs are numbered with the mismatch occurring at position 21, the most PAM-distal position; mismatched sgRNAs are derived from the matched on-target site that is listed to the left of the mismatched sgRNA.

DETAILED DESCRIPTION

A limitation of the CRISPR-Cas9 nucleases is their potential to induce undesired "off-target" mutations at imperfectly matched target sites (see, for example, Tsai et al., Nat Biotechnol. 2015), in some cases with frequencies rivaling those observed at the intended on-target site (Fu et al., Nat Biotechnol. 2013). Previous work with CRISPR-Cas9 nucleases has suggested that reducing the number of sequence-specific interactions between the guide RNA (gRNA) and the spacer region of a target site can reduce mutagenic effects at off-target sites of cleavage in human cells (Fu et al., Nat Biotechnol. 2014).

This was earlier accomplished by truncating gRNAs at their 5' ends by 2 or 3 nts and it was hypothesized that the mechanism of this increased specificity was a decrease in the interaction energy of the gRNA/Cas9 complex so that it was poised with just enough energy to cleave the on-target site, making it less likely to have enough energy to cleave off-target sites where there would presumably be an energetic penalty due to mismatches in the target DNA site (WO2015/099850).

It was hypothesized that off-target effects (at DNA sites that are imperfect matches or mismatches with the intended target site for the guide RNA) of SpCas9

might be minimized by decreasing non-specific interactions with its target DNA site. SpCas9-sgRNA complexes cleave target sites composed of an NGG PAM sequence (recognized by SpCas9) (Deltcheva, E. et al. Nature 471, 602-607 (2011); Jinek, M. et al. Science 337, 816-821 (2012); Jiang, W., et al., Nat Biotechnol 31, 233-239 (2013); Sternberg, S.H., et al., Nature 507, 62-67 (2014)) and an adjacent 20 bp protospacer sequence (which is complementary to the 5' end of the sgRNA) (Jinek, M. et al. Science 337, 816-821 (2012); Jinek, M. et al. Elife 2, e00471 (2013); Mali, P. et al., Science 339, 823-826 (2013); Cong, L. et al., Science 339, 819-823 (2013)). It was previously theorized that the SpCas9-sgRNA complex may possess more energy than is needed for recognizing its intended target DNA site, thereby enabling cleavage of mismatched off-target sites (Fu, Y., et al., Nat Biotechnol 32, 279-284 (2014)). One can envision that this property might be advantageous for the intended role of Cas9 in adaptive bacterial immunity, giving it the capability to cleave foreign sequences that may become mutated. This excess energy model is also supported by previous studies demonstrating that off-target effects can be reduced (but not eliminated) by decreasing SpCas9 concentration (Hsu, P.D. et al. Nat Biotechnol 31, 827-832 (2013); Pattanayak, V. et al. Nat Biotechnol 31, 839-843 (2013)) or by reducing the complementarity length of the sgRNA (Fu, Y., et al., Nat Biotechnol 32, 279-284 (2014), although other interpretations for this effect have also been proposed (Josephs, E.A. et al. Nucleic Acids Res 43, 8924-8941 (2015); Sternberg, S.H., et al. Nature 527, 110-113 (2015); Kiani, S. et al. Nat Methods 12, 1051-1054 (2015))). Structural data suggests that the SpCas9-sgRNA-target DNA complex may be stabilized by several SpCas9-mediated DNA contacts, including direct hydrogen bonds made by four SpCas9 residues (N497, R661, Q695, Q926) to the phosphate backbone of the target DNA strand (Nishimasu, H. et al. Cell 156, 935–949 (2014); Anders, C., et al. Nature 513, 569-573 (2014)) (**Fig. 1a** and **Figs. 6a and 6b**). The present inventors envisioned that disruption of one or more of these contacts might energetically poise the SpCas9-sgRNA complex at a level just sufficient to retain robust on-target activity but with a diminished ability to cleave mismatched off-target sites.

As described herein, Cas9 proteins can be engineered to show increased specificity, theoretically by reducing the binding affinity of Cas9 for DNA. Several variants of the widely used *Streptococcus pyogenes* Cas9 (SpCas9) were engineered by introducing individual alanine substitutions into various residues in SpCas9 that

might be expected to interact with phosphates on the DNA backbone using structural information, bacterial selection-based directed evolution, and combinatorial design. The variants were further tested for cellular activity using a robust *E.coli*-based screening assay to assess the cellular activities of these variants; in this bacterial system, cell survival depended on cleavage and subsequent destruction of a selection plasmid containing a gene for the toxic gyrase poison ccdB and a 23 base pair sequence targeted by a gRNA and SpCas9, and led to identification of residues that were associated with retained or lost activity. In addition, another SpCas9 variant was identified and characterized, which exhibited improved target specificity in human cells.

Furthermore, activities of single alanine substitution mutants of SpCas9 as assessed in the bacterial cell-based system indicated that survival percentages between 50-100% usually indicated robust cleavage, whereas 0% survival indicated that the enzyme had been functionally compromised. Additional mutations of SpCas9 were then assayed in bacteria to include: R63A, R66A, R69A, R70A, R71A, Y72A, R74A, R75A, K76A, N77A, R78A, R115A, H160A, K163A, R165A, L169A, R403A,T404A, F405A, N407A, R447A, N497A, I448A, Y450A, S460A, M495A, K510A, Y515A, R661A, M694A, Q695A, H698A, Y1013A, V1015A, R1122A, K1123A, K1124A, K1158A, K1185A, K1200A, S1216A, Q1221A, K1289A, R1298A, K1300A, K1325A, R1333A, K1334A, R1335A, and T1337A. With the exception of 2 mutants (R69A and F405A) that had < 5% survival in bacteria, all of these additional single mutations appeared to have little effect on the on-target activity of SpCas9 (>70% survival in the bacterial screen).

To further determine whether the variants of Cas9 identified in the bacterial screen functioned efficiently in human cells, various alanine substitution Cas9 mutants were tested using a human U2OS cell-based EGFP-disruption assay. In this assay, successful cleavage of a target site in the coding sequence of a single integrated, constitutively expressed EGFP gene led to the induction of indel mutations and disruption of EGFP activity, which was quantitatively assessed by flow cytometry (see, for example, Reyon et al., Nat Biotechnol. 2012 May;30(5):460-5).

These experiments show that the results obtained in the bacterial cell-based assay correlate well with nuclease activities in human cells, suggesting that these engineering strategies could be extended to Cas9s from other species and different

cells. Thus these findings provide support for SpCas9 and SaCas9 variants, referred to collectively herein as "variants" or "the variants".

All of the variants described herein can be rapidly incorporated into existing and widely used vectors, e.g., by simple site-directed mutagenesis, and because they require only a small number of mutations, the variants should also work with other previously described improvements to the SpCas9 platform (e.g., truncated sgRNAs (Tsai et al., Nat Biotechnol 33, 187-197 (2015); Fu et al., Nat Biotechnol 32, 279-284 (2014)), nickase mutations (Mali et al., Nat Biotechnol 31, 833-838 (2013); Ran et al., Cell 154, 1380-1389 (2013)), FokI-dCas9 fusions (Guilinger et al., Nat Biotechnol 32, 577-582 (2014); Tsai et al., Nat Biotechnol 32, 569-576 (2014); WO2014144288); and engineered CRISPR-Cas9 nucleases with altered PAM specificities (Kleinstiver et al., Nature. 2015 Jul 23;523(7561):481-5).

Thus, provided herein are Cas9 variants, including SpCas9 variants. The SpCas9 wild type sequence is as follows:

```
         10         20         30         40         50         60
MDKKYSIGLD IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE

         70         80         90        100        110        120
ATRLKRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSFFHR LEESFLVEED KKHERHPIFG

        130        140        150        160        170        180
NIVDEVAYHE KYPTIYHLRK KLVDSTDKAD LRLIYLALAH MIKFRGHFLI EGDLNPDNSD

        190        200        210        220        230        240
VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN

        250        260        270        280        290        300
LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLDNLLA QIGDQYADLF LAAKNLSDAI

        310        320        330        340        350        360
LLSDILRVNT EITKAPLSAS MIKRYDEHHQ DLTLLKALVR QQLPEKYKEI FFDQSKNGYA

        370        380        390        400        410        420
GYIDGGASQE EFYKFIKPIL EKMDGTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH

        430        440        450        460        470        480
AILRRQEDFY PFLKDNREKI EKILTFRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE

        490        500        510        520        530        540
VVDKGASAQS FIERMTNFDK NLPNEKVLPK HSLLYEYFTV YNELTKVKYV TEGMRKPAFL

        550        560        570        580        590        600
SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLLKI

        610        620        630        640        650        660
IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKTYA HLFDDKVMKQ LKRRRYTGWG

        670        680        690        700        710        720
RLSRKLINGI RDKQSGKTIL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGDSL
```

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       730        740        750        760        770        780
HEHIANLAGS PAIKKGILQT VKVVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER

       790        800        810        820        830        840
MKRIEEGIKE LGSQILKEHP VENTQLQNEK LYLYYLQNGR DMYVDQELDI NRLSDYDVDH

       850        860        870        880        890        900
IVPQSFLKDD SIDNKVLTRS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL

       910        920        930        940        950        960
TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILDSRMN TKYDENDKLI REVKVITLKS

       970        980        990       1000       1010       1020
KLVSDFRKDF QFYKVREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK

      1030       1040       1050       1060       1070       1080
MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGRDF

      1090       1100       1110       1120       1130       1140
ATVRKVLSMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA

      1150       1160       1170       1180       1190       1200
YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDLIIKLPK

      1210       1220       1230       1240       1250       1260
YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLKGSPE DNEQKQLFVE

      1270       1280       1290       1300       1310       1320
QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA

      1330       1340       1350       1360
PAAFKYFDTT IDRKRYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD   (SEQ ID NO:1)
```

The SpCas9 variants described herein can include the amino acid sequence of SEQ ID NO:1, with mutations (i.e., replacement of the native amino acid with a different amino acid, e.g., alanine, glycine, or serine), at one or more of the following positions: N497, R661, Q695, Q926 (or at positions analogous thereto). In some embodiments, the SpCas9 variants are at least 80%, e.g., at least 85%, 90%, or 95% identical to the amino acid sequence of SEQ ID NO:1, e.g., have differences at up to 5%, 10%, 15%, or 20% of the residues of SEQ ID NO:1 replaced, e.g., with conservative mutations, in addition to the mutations described herein. In preferred embodiments, the variant retains desired activity of the parent, e.g., the nuclease activity (except where the parent is a nickase or a dead Cas9), and/or the ability to interact with a guide RNA and target DNA).

To determine the percent identity of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). The

length of a reference sequence aligned for comparison purposes is at least 80% of the length of the reference sequence, and in some embodiments is at least 90% or 100%. The nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein nucleic acid "identity" is equivalent to nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. Percent identity between two polypeptides or nucleic acid sequences is determined in various ways that are within the skill in the art, for instance, using publicly available computer software such as Smith Waterman Alignment (Smith, T. F. and M. S. Waterman (1981) J Mol Biol 147:195-7); "BestFit" (Smith and Waterman, Advances in Applied Mathematics, 482-489 (1981)) as incorporated into GeneMatcher Plus™, Schwarz and Dayhof (1979) Atlas of Protein Sequence and Structure, Dayhof, M.O., Ed, pp 353-358; BLAST program (Basic Local Alignment Search Tool; (Altschul, S. F., W. Gish, et al. (1990) J Mol Biol 215: 403-10), BLAST-2, BLAST-P, BLAST-N, BLAST-X, WU-BLAST-2, ALIGN, ALIGN-2, CLUSTAL, or Megalign (DNASTAR) software. In addition, those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the length of the sequences being compared. In general, for proteins or nucleic acids, the length of comparison can be any length, up to and including full length (e.g., 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100%). For purposes of the present compositions and methods, at least 80% of the full length of the sequence is aligned.

For purposes of the present invention, the comparison of sequences and determination of percent identity between two sequences can be accomplished using a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

In some embodiments, the SpCas9 variants include one of the following sets of mutations: N497A/R661A/Q695/Q926A (quadruple alanine mutant); Q695A/Q926A (double alanine mutant); R661A/Q695A/Q926A and N497A/Q695A/Q926A (triple alanine mutants). In some embodiments, the additional substitution mutations at L169 and/or Y450 might be added to these double-, triple, and quadruple mutants or added to single mutants bearing substitutions at Q695 or Q926. In some embodiments, the mutants have alanine in place of the wild type amino acid. In some embodiments, the mutants have any amino acid other than arginine or lysine (or the native amino acid).

In some embodiments, the SpCas9 variants also include one of the following mutations, which reduce or destroy the nuclease activity of the Cas9: D10, E762, D839, H983, or D986 and H840 or N863, e.g., D10A/D10N and H840A/H840N/H840Y, to render the nuclease portion of the protein catalytically inactive; substitutions at these positions could be alanine (as they are in Nishimasu al., Cell 156, 935–949 (2014)), or other residues, e.g., glutamine, asparagine, tyrosine, serine, or aspartate, e.g., E762Q, H983N, H983Y, D986N, N863D, N863S, or N863H (see WO 2014/152432). In some embodiments, the variant includes mutations at D10A or H840A (which creates a single-strand nickase), or mutations at D10A and H840A (which abrogates nuclease activity; this mutant is known as dead Cas9 or dCas9).

The SpCas9 N497A/R661A/Q695A/R926A mutations have analogous residues in Staphylococcus aureus Cas9 (SaCas9); see FIG. 20. Mutations to the residues contacting the DNA or RNA backbone are expected to increase the specificity of SaCas9 as we've observed for SpCas9. Thus, also provided herein are SaCas9 variants.

The SaCas9 wild type sequence is as follows:

```
          10         20         30         40         50
MKRNYILGLD IGITSVGYGI IDYETRDVID AGVRLFKEAN VENNEGRRSK
          60         70         80         90         100
RGARRLKRRR RHRIQRVKKL LFDYNLLTDH SELSGINPYE ARVKGLSQKL
          110        120        130        140        150
SEEEFSAALL HLAKRRGVHN VNEVEEDTGN ELSTKEQISR NSKALEEKYV
          160        170        180        190        200
AELQLERLKK DGEVRGSINR FKTSDYVKEA KQLLKVQKAY HQLDQSFIDT
          210        220        230        240        250
YIDLLETRRT YYEGPGEGSP FGWKDIKEWY EMLMGHCTYF PEELRSVKYA
          260        270        280        290        300
YNADLYNALN DLNNLVITRD ENEKLEYYEK FQIIENVFKQ KKKPTLKQIA
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       310        320        330        340        350
KEILVNEEDI KGYRVTSTGK PEFTNLKVYH DIKDITARKE IIENAELLDQ
       360        370        380        390        400
IAKILTIYQS SEDIQEELTN LNSELTQEEI EQISNLKGYT GTHNLSLKAI
       410        420        430        440        450
NLILDELWHT NDNQIAIFNR LKLVPKKVDL SQQKEIPTTL VDDFILSPVV
       460        470        480        490        500
KRSFIQSIKV INAIIKKYGL PNDIIIELAR EKNSKDAQKM INEMQKRNRQ
       510        520        530        540        550
TNERIEEIIR TTGKENAKYL IEKIKLHDMQ EGKCLYSLEA IPLEDLLNNP
       560        570        580        590        600
FNYEVDHIIP RSVSFDNSFN NKVLVKQEEN SKKGNRTPFQ YLSSSDSKIS
       610        620        630        640        650
YETFKKHILN LAKGKGRISK TKKEYLLEER DINRFSVQKD FINRNLVDTR
       660        670        680        690        700
YATRGLMNLL RSYFRVNNLD VKVKSINGGF TSFLRRKWKF KKERNKGYKH
       710        720        730        740        750
HAEDALIIAN ADFIFKEWKK LDKAKKVMEN QMFEEKQAES MPEIETEQEY
       760        770        780        790        800
KEIFITPHQI KHIKDFKDYK YSHRVDKKPN RELINDTLYS TRKDDKGNTL
       810        820        830        840        850
IVNNLNGLYD KDNDKLKKLI NKSPEKLLMY HHDPQTYQKL KLIMEQYGDE
       860        870        880        890        900
KNPLYKYYEE TGNYLTKYSK KDNGPVIKKI KYYGNKLNAH LDITDDYPNS
       910        920        930        940        950
RNKVVKLSLK PYRFDVYLDN GVYKFVTVKN LDVIKKENYY EVNSKCYEEA
       960        970        980        990       1000
KKLKKISNQA EFIASFYNND LIKINGELYR VIGVNNDLLN RIEVNMIDIT
      1010       1020       1030       1040       1050
YREYLENMND KRPPRIIKTI ASKTQSIKKY STDILGNLYE VKSKKHPQII
```

KKG (SEQ ID NO:2)

SaCas9 variants described herein include the amino acid sequence of SEQ ID NO:2, with mutations at one, two, three, four, five, or all six of the following positions: Y211, W229, R245, T392, N419, and/or R654, e.g., comprising a sequence that is at least 80% identical to the amino acid sequence of SEQ ID NO:2 with mutations at one, two, three, four five or six of the following positions: Y211, W229, R245, T392, N419, and/or R654.

In some embodiments, the variant SaCas9 proteins also comprise one or more of the following mutations: Y211A; W229A; Y230A; R245A; T392A; N419A; L446A; Y651A; R654A; D786A; T787A; Y789A; T882A; K886A; N888A; A889A; L909A; N985A; N986A; R991A; R1015A; N44A; R45A; R51A; R55A; R59A; R60A; R116A; R165A; N169A; R208A; R209A; Y211A; T238A; Y239A; K248A; Y256A; R314A; N394A; Q414A; K57A; R61A; H111A; K114A; V164A; R165A; L788A; S790A; R792A; N804A; Y868A; K870A; K878A; K879A; K881A; Y897A; R901A; K906A.

In some embodiments, variant SaCas9 proteins comprise one or more of the following additional mutations: Y211A, W229A, Y230A, R245A, T392A, N419A, L446A, Y651A, R654A, D786A, T787A, Y789A, T882A, K886A, N888A, A889A, L909A, N985A, N986A, R991A, R1015A, N44A, R45A, R51A, R55A, R59A, R60A, R116A, R165A, N169A, R208A, R209A, Y211A, T238A, Y239A, K248A, Y256A, R314A, N394A, Q414A, K57A, R61A, H111A, K114A, V164A, R165A, L788A, S790A, R792A, N804A, Y868A, K870A, K878A, K879A, K881A, Y897A, R901A, K906A.

In some embodiments, the variant SaCas9 proteins comprise multiple substitution mutations: R245/T392/N419/R654 and Y221/R245/N419/R654 (quadruple variant mutants); N419/R654, R245/R654, Y221/R654, and Y221/N419 (double mutants); R245/N419/R654, Y211/N419/R654, and T392/N419/R654 (triple mutants). In some embodiments the mutants contain alanine in place of the wild type amino acid.

In some embodiments, the variant SaCas9 proteins also comprise mutations at E782K, K929R, N968K, and/or R1015H. For example, the KKH variant (E782K/N968K/R1015H), the KRH variant (E782K/K929R/R1015H), or the KRKH variant (E782K/K929R/N968K/R1015H)]

In some embodiments, the variant SaCas9 proteins also comprise one or more mutations that decrease nuclease activity selected from the group consisting of mutations at D10, E477, D556, H701, or D704; and at H557 or N580.

In some embodiments, the mutations are: (i) D10A or D10N, (ii) H557A, H557N, or H557Y, (iii) N580A, and/or (iv) D556A.

Also provided herein are isolated nucleic acids encoding the Cas9 variants, vectors comprising the isolated nucleic acids, optionally operably linked to one or more regulatory domains for expressing the variant proteins, and host cells, e.g., mammalian host cells, comprising the nucleic acids, and optionally expressing the variant proteins.

The variants described herein can be used for altering the genome of a cell; the methods generally include expressing the variant proteins in the cells, along with a guide RNA having a region complementary to a selected portion of the genome of the cell. Methods for selectively altering the genome of a cell are known in the art, see, e.g., US 8,993,233; US 20140186958; US 9,023,649; WO/2014/099744; WO

2014/089290; WO2014/144592; WO144288; WO2014/204578; WO2014/152432; WO2115/099850; US8,697,359; US20160024529; US20160024524; US20160024523; US20160024510; US20160017366; US20160017301; US20150376652; US20150356239; US20150315576; US20150291965; US20150252358; US20150247150; US20150232883; US20150232882; US20150203872; US20150191744; US20150184139; US20150176064; US20150167000; US20150166969; US20150159175; US20150159174; US20150093473; US20150079681; US20150067922; US20150056629; US20150044772; US20150024500; US20150024499; US20150020223;; US20140356867; US20140295557; US20140273235; US20140273226; US20140273037; US20140189896; US20140113376; US20140093941; US20130330778; US20130288251; US20120088676; US20110300538; US20110236530; US20110217739; US20110002889; US20100076057; US20110189776; US20110223638; US20130130248; US20150050699; US20150071899; US20150050699; ; US20150045546; US20150031134; US20150024500; US20140377868; US20140357530; US20140349400; US20140335620; US20140335063; US20140315985; US20140310830; US20140310828; US20140309487; US20140304853; US20140298547; US20140295556; US20140294773; US20140287938; US20140273234; US20140273232; US20140273231; US20140273230; US20140271987; US20140256046; US20140248702; US20140242702; US20140242700; US20140242699; US20140242664; US20140234972; US20140227787; US20140212869; US20140201857; US20140199767; US20140189896; US20140186958; US20140186919; US20140186843; US20140179770; US20140179006; US20140170753; WO/2008/108989; WO/2010/054108; WO/2012/164565; WO/2013/098244; WO/2013/176772; US 20150071899; Makarova et al., "Evolution and classification of the CRISPR-Cas systems" 9(6) Nature Reviews Microbiology 467-477 (1-23) (Jun. 2011); Wiedenheft et al., "RNA-guided genetic silencing systems in bacteria and archaea" 482 Nature 331-338 (Feb. 16, 2012); Gasiunas et al., "Cas9-crRNA ribonucleoprotein complex mediates specific DNA cleavage for adaptive immunity in bacteria" 109(39) Proceedings of the National Academy of Sciences USA E2579-E2586 (Sep. 4, 2012); Jinek et al., "A Programmable Dual-RNA-Guided DNA Endonuclease in Adaptive Bacterial

Immunity" 337 Science 816-821 (Aug. 17, 2012); Carroll, "A CRISPR Approach to Gene Targeting" 20(9) Molecular Therapy 1658-1660 (Sep. 2012); U.S. Appl. No. 61/652,086, filed May 25, 2012; Al-Attar et al., Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs): The Hallmark of an Ingenious Antiviral Defense Mechanism in Prokaryotes, Biol Chem. (2011) vol. 392, Issue 4, pp. 277-289; Hale et al., Essential Features and Rational Design of CRISPR RNAs That Function With the Cas RAMP Module Complex to Cleave RNAs, Molecular Cell, (2012) vol. 45, Issue 3, 292-302.

The variant proteins described herein can be used in place of or in addition to any of the Cas9 proteins described in the foregoing references, or in combination with mutations described therein. In addition, the variants described herein can be used in fusion proteins in place of the wild-type Cas9 or other Cas9 mutations (such as the dCas9 or Cas9 nickase described above) as known in the art, e.g., a fusion protein with a heterologous functional domains as described in US 8,993,233; US 20140186958; US 9,023,649; WO/2014/099744; WO 2014/089290; WO2014/144592; WO144288; WO2014/204578; WO2014/152432; WO2115/099850; US8,697,359; US2010/0076057; US2011/0189776; US2011/0223638; US2013/0130248; WO/2008/108989; WO/2010/054108; WO/2012/164565; WO/2013/098244; WO/2013/176772; US20150050699; US 20150071899 and WO 2014/124284. For example, the variants, preferably comprising one or more nuclease-reducing, -altering, or -killing mutation, can be fused on the N or C terminus of the Cas9 to a transcriptional activation domain or other heterologous functional domains (e.g., transcriptional repressors (e.g., KRAB, ERD, SID, and others, e.g., amino acids 473–530 of the ets2 repressor factor (ERF) repressor domain (ERD), amino acids 1–97 of the KRAB domain of KOX1, or amino acids 1–36 of the Mad mSIN3 interaction domain (SID); see Beerli et al., PNAS USA 95:14628-14633 (1998)) or silencers such as Heterochromatin Protein 1 (HP1, also known as swi6), e.g., HP1α or HP1β; proteins or peptides that could recruit long non-coding RNAs (lncRNAs) fused to a fixed RNA binding sequence such as those bound by the MS2 coat protein, endoribonuclease Csy4, or the lambda N protein; enzymes that modify the methylation state of DNA (e.g., DNA methyltransferase (DNMT) or TET proteins); or enzymes that modify histone subunits (e.g., histone acetyltransferases (HAT), histone deacetylases (HDAC), histone methyltransferases

(e.g., for methylation of lysine or arginine residues) or histone demethylases (e.g., for demethylation of lysine or arginine residues)) as are known in the art can also be used. A number of sequences for such domains are known in the art, e.g., a domain that catalyzes hydroxylation of methylated cytosines in DNA. Exemplary proteins include the Ten-Eleven-Translocation (TET)1-3 family, enzymes that converts 5-methylcytosine (5-mC) to 5-hydroxymethylcytosine (5-hmC) in DNA.

Sequences for human TET1-3 are known in the art and are shown in the following table:

	GenBank Accession Nos.	
Gene	Amino Acid	Nucleic Acid
TET1	NP_085128.2	NM_030625.2
TET2*	NP_001120680.1 (var 1) NP_060098.3 (var 2)	NM_001127208.2 NM_017628.4
TET3	NP_659430.1	NM_144993.1

* Variant (1) represents the longer transcript and encodes the longer isoform (a). Variant (2) differs in the 5' UTR and in the 3' UTR and coding sequence compared to variant 1. The resulting isoform (b) is shorter and has a distinct C-terminus compared to isoform a.

In some embodiments, all or part of the full-length sequence of the catalytic domain can be included, e.g., a catalytic module comprising the cysteine-rich extension and the 2OGFeDO domain encoded by 7 highly conserved exons, e.g., the Tet1 catalytic domain comprising amino acids 1580-2052, Tet2 comprising amino acids 1290-1905 and Tet3 comprising amino acids 966-1678. See, e.g., Fig. 1 of Iyer et al., Cell Cycle. 2009 Jun 1;8(11):1698-710. Epub 2009 Jun 27, for an alignment illustrating the key catalytic residues in all three Tet proteins, and the supplementary materials thereof (available at ftp site ftp.ncbi.nih.gov/pub/aravind/DONS/supplementary_material_DONS.html) for full length sequences (see, e.g., seq 2c); in some embodiments, the sequence includes amino acids 1418-2136 of Tet1 or the corresponding region in Tet2/3.

Other catalytic modules can be from the proteins identified in Iyer et al., 2009.

In some embodiments, the heterologous functional domain is a biological tether, and comprises all or part of (e.g., DNA binding domain from) the MS2 coat protein, endoribonuclease Csy4, or the lambda N protein. These proteins can be used to recruit RNA molecules containing a specific stem-loop structure to a locale

specified by the dCas9 gRNA targeting sequences. For example, a dCas9 variant fused to MS2 coat protein, endoribonuclease Csy4, or lambda N can be used to recruit a long non-coding RNA (lncRNA) such as XIST or HOTAIR; see, e.g., Keryer-Bibens et al., Biol. Cell 100:125–138 (2008), that is linked to the Csy4, MS2 or lambda N binding sequence. Alternatively, the Csy4, MS2 or lambda N protein binding sequence can be linked to another protein, e.g., as described in Keryer-Bibens et al., supra, and the protein can be targeted to the dCas9 variant binding site using the methods and compositions described herein. In some embodiments, the Csy4 is catalytically inactive. In some embodiments, the Cas9 variant, preferably a dCas9 variant, is fused to FokI as described in US 8,993,233; US 20140186958; US 9,023,649; WO/2014/099744; WO 2014/089290; WO2014/144592; WO144288; WO2014/204578; WO2014/152432; WO2115/099850; US8,697,359; US2010/0076057; US2011/0189776; US2011/0223638; US2013/0130248; WO/2008/108989; WO/2010/054108; WO/2012/164565; WO/2013/098244; WO/2013/176772; US20150050699; US 20150071899 and WO 2014/204578.

In some embodiments, the fusion proteins include a linker between the dCas9 variant and the heterologous functional domains. Linkers that can be used in these fusion proteins (or between fusion proteins in a concatenated structure) can include any sequence that does not interfere with the function of the fusion proteins. In preferred embodiments, the linkers are short, e.g., 2-20 amino acids, and are typically flexible (i.e., comprising amino acids with a high degree of freedom such as glycine, alanine, and serine). In some embodiments, the linker comprises one or more units consisting of GGGS (SEQ ID NO:3) or GGGGS (SEQ ID NO:4), e.g., two, three, four, or more repeats of the GGGS (SEQ ID NO:5) or GGGGS (SEQ ID NO:6) unit. Other linker sequences can also be used.

In some embodiments, the variant protein includes a cell-penetrating peptide sequence that facilitates delivery to the intracellular space, e.g., HIV-derived TAT peptide, penetratins, transportans, or hCT derived cell-penetrating peptides, see, e.g., Caron et al., (2001) Mol Ther. 3(3):310-8; Langel, Cell-Penetrating Peptides: Processes and Applications (CRC Press, Boca Raton FL 2002); El-Andaloussi et al., (2005) Curr Pharm Des. 11(28):3597-611; and Deshayes et al., (2005) Cell Mol Life Sci. 62(16):1839-49.

Cell penetrating peptides (CPPs) are short peptides that facilitate the movement of a wide range of biomolecules across the cell membrane into the cytoplasm or other organelles, e.g. the mitochondria and the nucleus. Examples of molecules that can be delivered by CPPs include therapeutic drugs, plasmid DNA, oligonucleotides, siRNA, peptide-nucleic acid (PNA), proteins, peptides, nanoparticles, and liposomes. CPPs are generally 30 amino acids or less, are derived from naturally or non-naturally occurring protein or chimeric sequences, and contain either a high relative abundance of positively charged amino acids, e.g. lysine or arginine, or an alternating pattern of polar and non-polar amino acids. CPPs that are commonly used in the art include Tat (Frankel et al., (1988) Cell. 55:1189-1193, Vives et al., (1997) J. Biol. Chem. 272:16010-16017), penetratin (Derossi et al., (1994) J. Biol. Chem. 269:10444-10450), polyarginine peptide sequences (Wender et al., (2000) Proc. Natl. Acad. Sci. USA 97:13003-13008, Futaki et al., (2001) J. Biol. Chem. 276:5836-5840), and transportan (Pooga et al., (1998) Nat. Biotechnol. 16:857-861).

CPPs can be linked with their cargo through covalent or non-covalent strategies. Methods for covalently joining a CPP and its cargo are known in the art, e.g. chemical cross-linking (Stetsenko et al., (2000) J. Org. Chem. 65:4900-4909, Gait et al. (2003) Cell. Mol. Life. Sci. 60:844-853) or cloning a fusion protein (Nagahara et al., (1998) Nat. Med. 4:1449-1453). Non-covalent coupling between the cargo and short amphipathic CPPs comprising polar and non-polar domains is established through electrostatic and hydrophobic interactions.

CPPs have been utilized in the art to deliver potentially therapeutic biomolecules into cells. Examples include cyclosporine linked to polyarginine for immunosuppression (Rothbard et al., (2000) Nature Medicine 6(11):1253-1257), siRNA against cyclin B1 linked to a CPP called MPG for inhibiting tumorigenesis (Crombez et al., (2007) Biochem Soc. Trans. 35:44-46), tumor suppressor p53 peptides linked to CPPs to reduce cancer cell growth (Takenobu et al., (2002) Mol. Cancer Ther. 1(12):1043-1049, Snyder et al., (2004) PLoS Biol. 2:E36), and dominant negative forms of Ras or phosphoinositol 3 kinase (PI3K) fused to Tat to treat asthma (Myou et al., (2003) J. Immunol. 171:4399-4405).

CPPs have been utilized in the art to transport contrast agents into cells for imaging and biosensing applications. For example, green fluorescent protein (GFP)

attached to Tat has been used to label cancer cells (Shokolenko et al., (2005) DNA Repair 4(4):511-518). Tat conjugated to quantum dots have been used to successfully cross the blood-brain barrier for visualization of the rat brain (Santra et al., (2005) Chem. Commun. 3144-3146). CPPs have also been combined with magnetic resonance imaging techniques for cell imaging (Liu et al., (2006) Biochem. and Biophys. Res. Comm. 347(1):133-140). See also Ramsey and Flynn, Pharmacol Ther. 2015 Jul 22. pii: S0163-7258(15)00141-2.

Alternatively, or in addition, the variant proteins can include a nuclear localization sequence, e.g., SV40 large T antigen NLS (PKKKRRV (SEQ ID NO:7)) and nucleoplasmin NLS (KRPAATKKAGQAKKKK (SEQ ID NO:8)). Other NLSs are known in the art; see, e.g., Cokol et al., EMBO Rep. 2000 Nov 15; 1(5): 411–415; Freitas and Cunha, Curr Genomics. 2009 Dec; 10(8): 550–557.

In some embodiments, the variants include a moiety that has a high affinity for a ligand, for example GST, FLAG or hexahistidine sequences. Such affinity tags can facilitate the purification of recombinant variant proteins.

For methods in which the variant proteins are delivered to cells, the proteins can be produced using any method known in the art, e.g., by in vitro translation, or expression in a suitable host cell from nucleic acid encoding the variant protein; a number of methods are known in the art for producing proteins. For example, the proteins can be produced in and purified from yeast, *E. coli*, insect cell lines, plants, transgenic animals, or cultured mammalian cells; see, e.g., Palomares et al., "Production of Recombinant Proteins: Challenges and Solutions," Methods Mol Biol. 2004;267:15-52. In addition, the variant proteins can be linked to a moiety that facilitates transfer into a cell, e.g., a lipid nanoparticle, optionally with a linker that is cleaved once the protein is inside the cell. See, e.g., LaFountaine et al., Int J Pharm. 2015 Aug 13;494(1):180-194.

Expression Systems

To use the Cas9 variants described herein, it may be desirable to express them from a nucleic acid that encodes them. This can be performed in a variety of ways. For example, the nucleic acid encoding the Cas9 variant can be cloned into an intermediate vector for transformation into prokaryotic or eukaryotic cells for replication and/or expression. Intermediate vectors are typically prokaryote vectors, e.g., plasmids, or shuttle vectors, or insect vectors, for storage or manipulation of the

nucleic acid encoding the Cas9 variant for production of the Cas9 variant. The nucleic acid encoding the Cas9 variant can also be cloned into an expression vector, for administration to a plant cell, animal cell, preferably a mammalian cell or a human cell, fungal cell, bacterial cell, or protozoan cell.

To obtain expression, a sequence encoding a Cas9 variant is typically subcloned into an expression vector that contains a promoter to direct transcription. Suitable bacterial and eukaryotic promoters are well known in the art and described, e.g., in Sambrook et al., Molecular Cloning, A Laboratory Manual (3d ed. 2001); Kriegler, Gene Transfer and Expression: A Laboratory Manual (1990); and Current Protocols in Molecular Biology (Ausubel et al., eds., 2010). Bacterial expression systems for expressing the engineered protein are available in, e.g., *E. coli*, *Bacillus* sp., and *Salmonella* (Palva et al., 1983, Gene 22:229-235). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially available.

The promoter used to direct expression of a nucleic acid depends on the particular application. For example, a strong constitutive promoter is typically used for expression and purification of fusion proteins. In contrast, when the Cas9 variant is to be administered in vivo for gene regulation, either a constitutive or an inducible promoter can be used, depending on the particular use of the Cas9 variant. In addition, a preferred promoter for administration of the Cas9 variant can be a weak promoter, such as HSV TK or a promoter having similar activity. The promoter can also include elements that are responsive to transactivation, e.g., hypoxia response elements, Gal4 response elements, lac repressor response element, and small molecule control systems such as tetracycline-regulated systems and the RU-486 system (see, e.g., Gossen & Bujard, 1992, Proc. Natl. Acad. Sci. USA, 89:5547; Oligino et al., 1998, Gene Ther., 5:491-496; Wang et al., 1997, Gene Ther., 4:432-441; Neering et al., 1996, Blood, 88:1147-55; and Rendahl et al., 1998, Nat. Biotechnol., 16:757-761).

In addition to the promoter, the expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the nucleic acid in host cells, either prokaryotic or eukaryotic. A typical expression cassette thus contains a promoter operably linked, e.g., to the nucleic acid sequence encoding the Cas9 variant, and any signals required,

e.g., for efficient polyadenylation of the transcript, transcriptional termination, ribosome binding sites, or translation termination. Additional elements of the cassette may include, e.g., enhancers, and heterologous spliced intronic signals.

The particular expression vector used to transport the genetic information into the cell is selected with regard to the intended use of the Cas9 variant, e.g., expression in plants, animals, bacteria, fungus, protozoa, etc. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and commercially available tag-fusion expression systems such as GST and LacZ.

Expression vectors containing regulatory elements from eukaryotic viruses are often used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, and vectors derived from Epstein-Barr virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A+, pMTO10/A+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the SV40 early promoter, SV40 late promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

The vectors for expressing the Cas9 variants can include RNA Pol III promoters to drive expression of the guide RNAs, e.g., the H1, U6 or 7SK promoters. These human promoters allow for expression of Cas9 variants in mammalian cells following plasmid transfection.

Some expression systems have markers for selection of stably transfected cell lines such as thymidine kinase, hygromycin B phosphotransferase, and dihydrofolate reductase. High yield expression systems are also suitable, such as using a baculovirus vector in insect cells, with the gRNA encoding sequence under the direction of the polyhedrin promoter or other strong baculovirus promoters.

The elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of recombinant sequences.

Standard transfection methods are used to produce bacterial, mammalian, yeast or insect cell lines that express large quantities of protein, which are then purified using standard techniques (see, e.g., Colley et al., 1989, J. Biol. Chem., 264:17619-22; Guide to Protein Purification, in Methods in Enzymology, vol. 182

(Deutscher, ed., 1990)). Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (see, e.g., Morrison, 1977, J. Bacteriol. 132:349-351; Clark-Curtiss & Curtiss, Methods in Enzymology 101:347-362 (Wu et al., eds, 1983).

Any of the known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, nucleofection, liposomes, microinjection, naked DNA, plasmid vectors, viral vectors, both episomal and integrative, and any of the other well-known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Sambrook et al., supra). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the Cas9 variant.

The present methods can also include modifying gDNA by introducing purified Cas9 protein with a gRNA into cells as a ribonuclear protein (RNP) complex, as well as introducing a gRNA plus mRNA encoding the Cas9 protein. The gRNA can be synthetic gRNA or a nucleic acid (e.g., in an expression vector) encoding the guide RNA.

The present invention also includes the vectors and cells comprising the vectors.

EXAMPLES

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

Methods

Bacterial-based positive selection assay for evolving SpCas9 variants

Competent *E.coli* BW25141(λDE3)[23] containing a positive selection plasmid (with embedded target site) were transformed with Cas9/sgRNA-encoding plasmids. Following a 60 minute recovery in SOB media, transformations were plated on LB plates containing either chloramphenicol (non-selective) or chloramphenicol + 10 mM arabinose (selective).

To identify additional positions that might be critical for genome wide target specificity, a bacterial selection system previously used to study properties of homing

endonucleases (hereafter referred to as the positive selection) (Chen & Zhao, Nucleic Acids Res 33, e154 (2005); Doyon et al., J Am Chem Soc 128, 2477-2484 (2006)) was adapted.

In the present adaptation of this system, Cas9-mediated cleavage of a positive selection plasmid encoding an inducible toxic gene enables cell survival, due to subsequent degradation and loss of the linearized plasmid. After establishing that SpCas9 can function in the positive selection system, both wild-type and the variants were tested for their ability to cleave a selection plasmid harboring a target site selected from the known human genome. These variants were introduced into bacteria with a positive selection plasmid containing a target site and plated on selective medium. Cleavage of the positive selection plasmid was estimated by calculating the survival frequency: colonies on selective plates / colonies on non-selective plates **(see FIG. 1, 5-6).**

A subset of plasmids used in this study (sequences shown below)

Name	Addgene ID	Description
JDS246	43861	CMV-T7-humanSpCas9-NLS-3xFLAG
VP12	pending	CMV-T7-humanSpCas9-HF1(N497A, R661A, Q695A, Q926A)-NLS-3xFLAG
MSP2135	pending	CMV-T7-humanSpCas9-HF2(N497A, R661A, Q695A, Q926A, D1135E)-NLS-3xFLAG
MSP2133	pending	CMV-T7-humanSpCas9-HF4(Y450A, N497A, R661A, Q695A, Q926A)-NLS-3xFLAG
MSP469	65771	CMV-T7-humanSpCas9-VQR(D1135V, R1335Q, T1337R)-NLS-3xFLAG
MSP2440	pending	CMV-T7-humanSpCas9-VQR-HF1(N497A, R661A, Q695A, Q926A, D1135V, R1335Q, T1337R)-NLS-3xFLAG
BPK2797	pending	CMV-T7-humanSpCas9-VRQR(D1135V, G1218R, R1335Q, T1337R)-NLS-3xFLAG
MSP2443	pending	CMV-T7-humanSpCas9-VRQR-HF1(N497A, R661A, Q695A, Q926A, D1135V, G1218R, R1335Q, T1337R)-NLS-3xFLAG
BPK1520	65777	U6-BsmBIcassette-Sp-sgRNA

Human cell culture and transfection

U2OS.EGFP cells harboring a single integrated copy of a constitutively expressed EGFP-PEST reporter gene[15] were cultured in Advanced DMEM media (Life Technologies) supplemented with 10% FBS, 2 mM GlutaMax (Life Technologies), penicillin/streptomycin, and 400 µg/ml of G418 at 37 °C with 5% CO_2. Cells were co-transfected with 750 ng of Cas9 plasmid and 250 ng of sgRNA plasmid (unless otherwise noted) using the DN-100 program of a Lonza 4D-nucleofector according to the manufacturer's protocols. Cas9 plasmid transfected

together with an empty U6 promoter plasmid was used as a negative control for all human cell experiments. (see **FIGs. 2, 7-10**).

Human cell EGFP disruption assay

EGFP disruption experiments were performed as previously described[16]. Transfected cells were analyzed for EGFP expression ~52 hours post-transfection using a Fortessa flow cytometer (BD Biosciences). Background EGFP loss was gated at approximately 2.5% for all experiments (see **FIGs. 2,** 7).

T7E1 assay, targeted deep-sequencing, and GUIDE-seq to quantify nuclease-induced mutation rates

T7E1 assays were performed as previously described for human cells (Kleinstiver, B.P. et al., Nature 523, 481-485 (2015)). For U2OS.EGFP human cells, genomic DNA was extracted from transfected cells ~72 hours post-transfection using the Agencourt DNAdvance Genomic DNA Isolation Kit (Beckman Coulter Genomics). Roughly 200 ng of purified PCR product was denatured, annealed, and digested with T7E1 (New England BioLabs). Mutagenesis frequencies were quantified using a Qiaxcel capillary electrophoresis instrument (Qlagen), as previously described for human cells (Kleinstiver et al., Nature 523, 481-485 (2015); Reyon et al,. Nat Biotechnol 30, 460-465 (2012)).

GUIDE-seq experiments were performed as previously described (Tsai et al., Nat Biotechnol 33, 187-197 (2015)). Briefly, phosphorylated, phosphorothioate-modified double-stranded oligodeoxynucleotides (dsODNs) were transfected into U2OS cells with Cas9 nuclease along with Cas9 and sgRNA expression plasmids, as described above. dsODN-specific amplification, high-throughput sequencing, and mapping were performed to identify genomic intervals containing DSB activity. For wild-type versus double or quadruple mutant variant experiments, off-target read counts were normalized to the on-target read counts to correct for sequencing depth differences between samples. The normalized ratios for wild-type and variant SpCas9 were then compared to calculate the fold-change in activity at off-target sites. To determine whether wild-type and SpCas9 variant samples for GUIDE-seq had similar oligo tag integration rates at the intended target site, restriction fragment length polymorphism (RFLP) assays were performed by amplifying the intended target loci

with Phusion Hot-Start Flex from 100 ng of genomic DNA (isolated as described above). Roughly 150 ng of PCR product was digested with 20 U of NdeI (New England BioLabs) for 3 hours at 37 °C prior to clean-up using the Agencourt Ampure XP kit. RFLP results were quantified using a Qiaxcel capillary electrophoresis instrument (Qiagen) to approximate oligo tag integration rates. T7E1 assays were performed for a similar purpose, as described above.

Example 1

One potential solution to address targeting specificity of CRISPR-Cas9 RNA guided gene editing would be to engineer Cas9 variants with novel mutations.

Based on these earlier results, it was hypothesized (without wishing to be bound by theory) that the specificity of CRISPR-Cas9 nucleases might be significantly increased by reducing the non-specific binding affinity of Cas9 for DNA, mediated by the binding to the phosphate groups on the DNA or hydrophobic or base stacking interactions with the DNA. This approach would have the advantage of not decreasing the length of the target site recognized by the gRNA/Cas9 complex, as in the previously described truncated gRNA approach. It was reasoned that non-specific binding affinity of Cas9 for DNA might be reduced by mutating amino acid residues that contact phosphate groups on the target DNA.

An analogous approach has been used to create variants of non-Cas9 nucleases such as TALENs (see, for example, Guilinger et al., Nat. Methods. 11: 429 (2014)).

In an initial test of the hypothesis, the present inventors attempted to engineer a reduced affinity variant of the widely used *S. pyogenes* Cas9 (SpCas9) by introducing individual alanine substitutions into various residues in SpCas9 that might be expected to interact with phosphates on the DNA backbone. An E.coli-based screening assay was used to assess the activities of these variants (Kleinstiver et al., Nature. 2015 Jul 23;523(7561):481-5). In this bacterial system, cell survival depended on cleavage (and subsequent destruction) of a selection plasmid containing a gene for the toxic gyrase poison ccdB and a 23 base pair sequence targeted by a gRNA and SpCas9. Results of this experiment identified residues that retained or lost activity (**Table 1**).

Table 1: Activities of single alanine substitution mutants of Cas9 as assessed in the bacterial cell-based system shown in FIG. 1.

mutation	% survival	mutation	% survival	mutation	% survival
R63A	84.2	Q926A	53.3	K1158A	46.5
R66A	0	K1107A	47.4	K1185A	19.3
R70A	0	E1108A	40.0	K1200A	24.5
R74A	0	S1109A	96.6	S1216A	100.4
R78A	56.4	K1113A	51.8	Q1221A	98.8
R165A	68.9	R1114A	47.3	K1289A	55.2
R403A	85.2	S1116A	73.8	R1298A	28.6
N407A	97.2	K1118A	48.7	K1300A	59.8
N497A	72.6	D1135A	67.2	K1325A	52.3
K510A	79.0	S1136A	69.2	R1333A	0
Y515A	34.1	K1151A	0	K1334A	87.5
R661A	75.0	K1153A	76.6	R1335A	0
Q695A	69.8	K1155A	44.6	T1337A	64.6

Survival percentages between 50-100% usually indicated robust cleavage, whereas 0% survival indicated that the enzyme has been functionally compromised. Additional mutations that were assayed in bacteria (but are not shown in the table above) include: R69A, R71A, Y72A, R75A, K76A, N77A, R115A, H160A, K163A, L169A, T404A, F405A, R447A, I448A, Y450A, S460A, M495A, M694A, H698A, Y1013A, V1015A, R1122A, K1123A, and K1124A. With the exception of R69A and F405A (which had < 5% survival in bacteria), all of these additional single mutations appeared to have little effect on the on-target activity of SpCas9 (>70% survival in the bacterial screen).

15 different SpCas9 variants bearing all possible single, double, triple and quadruple combinations of the N497A, R661A, Q695A, and Q926A mutations were constructed to test whether contacts made by these residues might be dispensable for on-target activity (**Fig. 1b**). For these experiments, a previously described human cell-based assay was used in which cleavage and induction of insertion or deletion mutations (**indels**) by non-homologous end-joining (**NHEJ**)-mediated repair within a single integrated EGFP reporter gene leads to loss of cell fluorescence (Reyon, D. et al., Nat Biotechnol. 30, 460-465, 2012). Using a EGFP-targeted sgRNA previously shown to efficiently disrupt EGFP expression in human cells when paired with wild-type SpCas9 (Fu, Y. et al., Nat Biotechnol 31, 822-826 (2013), all 15 SpCas9 variants possessed EGFP disruption activities comparable to that of wild-type SpCas9 (**Fig. 1b**, grey bars). Thus, substitution of one or all of these residues did not reduce on-target cleavage efficiency of SpCas9 with this EGFP-targeted sgRNA.

Next, experiments were performed to assess the relative activities of all 15 SpCas9 variants at mismatched target sites. To do this, the EGFP disruption assay was repeated with derivatives of the EGFP-targeted sgRNA used in the previous experiment that contain pairs of substituted bases at positions 13 and 14, 15 and 16, 17 and 18, and 18 and 19 (numbering starting with 1 for the most PAM-proximal base and ending with 20 for the most PAM-distal base; **Fig. 1b**). This analysis revealed that one of the triple mutants (R661A/Q695A/Q926A) and the quadruple mutant (N497A/R661A/Q695A/Q926A) both showed levels of EGFP disruption equivalent to that of background with all four of the mismatched sgRNAs (**Fig. 1b**, colored bars). Notably, among the 15 variants, those possessing the lowest activities with the mismatched sgRNAs all harbored the Q695A and Q926A mutations. Based on these results and similar data from an experiment using a sgRNA for another EGFP target site, the quadruple mutant (N497A/R661A/Q695A/Q926A) was chosen for additional analysis and designated it as **SpCas9-HF1** (for high-fidelity variant #1).

On-target activities of SpCas9-HF1

To determine how robustly SpCas9-HF1 functions at a larger number of on-target sites, direct comparisons were performed between this variant and wild-type SpCas9 using additional sgRNAs. In total, 37 different sgRNAs were tested: 24 targeted to EGFP (assayed with the EGFP disruption assay) and 13 targeted to endogenous human gene targets (assayed using the T7 Endonuclease I (**T7EI**) mismatch assay). 20 of the 24 sgRNAs tested with the EGFP disruption assay (**Fig. 1c**) and 12 of the 13 sgRNAs tested on endogenous human gene sites (**Fig. 1d**) showed activities with SpCas9-HF1 that were at least 70% as active as wild-type SpCas9 with the same sgRNA (**Fig. 1e**). Indeed, SpCas9-HF1 showed highly comparable activities (90-140%) to wild-type SpCas9 with the vast majority of sgRNAs (**Fig. 1e**). Three of the 37 sgRNAs tested showed essentially no activity with SpCas9-HF1 and examination of these target sites did not suggest any obvious differences in the characteristics of these sequences compared to those for which high activities were seen (**Table 3**). Overall, SpCas9-HF1 possessed comparable activities (greater than 70% of wild-type SpCas9 activities) for 86% (32/37) of the sgRNAs tested.

Table 3: List of sgRNA targets

S. pyogenes sgRNAs

EGFP						
Prep Name	**Name**	**Spacer length (nt)**	**Spacer Sequence**	**SEQ ID NO:**	**Sequence with extended PAM**	**SEQ ID NO:**
FYF1320	NGG site 1	20	GGGCACGGGCAGCTTGCCGG	9.	GGGCACGGGCAGCTTGCCGGTGGT	10.
FYF1641	NGG site 1	18	GCACGGGCAGCTTGCCGG	11.	GCACGGGCAGCTTGCCGGTGGT	12.
CK1012	NGG site 1-13&14	20	GGGCACccGCAGCTTGCCGG	13.	GGGCACccGCAGCTTGCCGGTGGT	14.
FYF1429	NGG site 1-15&16	20	GGGCtgGGGCAGCTTGCCGG	15.	GGGCtgGGGCAGCTTGCCGGTGGT	16.
FYF1430	NGG site 1-17&18	20	GGcgACGGGCAGCTTGCCGG	17.	GGcgACGGGCAGCTTGCCGGTGGT	18.
FYF1347	NGG site 1-18&19	20	GccCACGGGCAGCTTGCCGG	19.	GccCACGGGCAGCTTGCCGGTGGT	20.
BPK1345	NGG site 2	20	GTCGCCCTCGAACTTCACCT	21.	GTCGCCCTCGAACTTCACCTCGGC	22.
BPK1350	NGG site 3	20	GTAGGTCAGGGTGGTCACGA	23.	GTAGGTCAGGGTGGTCACGAGGGT	24.
BPK1353	NGG site 4	20	GGCGAGGGCGATGCCACCTA	25.	GGCGAGGGCGATGCCACCTACGGC	26.
MSP792	NGG site 5	20	GGTCGCCACCATGGTGAGCA	27.	GGTCGCCACCATGGTGAGCAAGGG	28.
MSP795	NGG site 6	20	GGTCAGGGTGGTCACGAGGG	29.	GGTCAGGGTGGTCACGAGGGTGGG	30.
FYF1328	NGG site 7	20	GGTGGTGCAGATGAACTTCA	31.	GGTGGTGCAGATGAACTTCAGGGT	32.
JAF1001	NGG site 7	17	GGTGCAGATGAACTTCA	33.	GGTGCAGATGAACTTCAGGGT	34.
BPK1365	NGG site 8	20	GTTGGGGTCTTTGCTCAGGG	35.	GTTGGGGTCTTTGCTCAGGGCGGA	36.
MSP794	NGG site 9	20	GGTGGTCACGAGGGTGGGCC	37.	GGTGGTCACGAGGGTGGGCCAGGG	38.
FYF1327	NGG site 10	20	GATGCCGTTCTTCTGCTTGT	39.	GATGCCGTTCTTCTGCTTGTCGGC	40.
JAF997	NGG site 10	17	GCCGTTCTTCTGCTTGT	41.	GCCGTTCTTCTGCTTGTCGGC	42.
BPK1347	NGG site 11	20	GTCGCCACCATGGTGAGCAA	43.	GTCGCCACCATGGTGAGCAAGGGC	44.
BPK1369	NGG site 12	20	GCACTGCACGCCGTAGGTCA	45.	GCACTGCACGCCGTAGGTCAGGGT	46.
MSP2545	NGG site 13	20	GTGAACCGCATCGAGCTGAA	47.	GTGAACCGCATCGAGCTGAAGGGC	48.

MSP2 546	NGG site 14	20	GAAGGGCATC GACTTCAAGG	49.	GAAGGGCATCGACTTCA AGGAGGA	50.
MSP2 547	NGG site 15	20	GCTTCATGTGG TCGGGGTAG	51.	GCTTCATGTGGTCGGGG TAGCGGC	52.
MSP2 548	NGG site 16	20	GCTGAAGCAC TGCACGCCGT	53.	GCTGAAGCACTGCACGC CGTAGGT	54.
MSP2 549	NGG site 17	20	GCCGTCGTCCT TGAAGAAGA	55.	GCCGTCGTCCTTGAAGA AGATGGT	56.
MSP2 550	NGG site 18	20	GACCAGGATG GGCACCACCC	57.	GACCAGGATGGGCACC ACCCCGGT	58.
MSP2 551	NGG site 19	20	GACGTAGCCT TCGGGCATGG	59.	GACGTAGCCTTCGGGCA TGGCGGA	60.
MSP2 553	NGG site 20	20	GAAGTTCGAG GGCGACACCC	61.	GAAGTTCGAGGGCGAC ACCCTGGT	62.
MSP2 554	NGG site 21	20	GAGCTGGACG GCGACGTAAA	63.	GAGCTGGACGGCGACGT AAACGGC	64.
MSP2 555	NGG site 22	20	GGCATCGCCC TCGCCCTCGC	65.	GGCATCGCCCTCGCCCT CGCCGGA	66.
MSP2 556	NGG site 23	20	GGCCACAAGT TCAGCGTGTC	67.	GGCCACAAGTTCAGCGT GTCCGGC	68.
FYF1 331	NGG site 24	20	GGGCGAGGAG CTGTTCACCG	69.	GGGCGAGGAGCTGTTCA CCGGGGT	70.
FYF1 560	NGG site 24	18	GCGAGGAGCT GTTCACCG	71.	GCGAGGAGCTGTTCACC GGGGT	72.
BPK1 348	NGG site 25-no 5' G	20	CCTCGAACTTC ACCTCGGCG	73.	CCTCGAACTTCACCTCG GCGCGGG	74.
BPK1 349	NGG site 25-mm 5' G	20	GCTCGAACTTC ACCTCGGCG	75.	GCTCGAACTTCACCTCG GCGCGGG	76.
BPK1 351	NGG site 26-no 5' G	20	CAACTACAAG ACCCGCGCCG	77.	CAACTACAAGACCCGCG CCGAGGT	78.
BPK1 352	NGG site 26-mm 5' G	20	GAACTACAAG ACCCGCGCCG	79.	GAACTACAAGACCCGCG CCGAGGT	80.
BPK1 373	NGG site 27-no 5' G	20	CGCTCCTGGA CGTAGCCTTC	81.	CGCTCCTGGACGTAGCC TTCGGGC	82.
BPK1 375	NGG site 27-mm 5' G	20	GGCTCCTGGA CGTAGCCTTC	83.	CGCTCCTGGACGTAGCC TTCGGGC	84.
BPK1 377	NGG site 28-no 5' G	20	AGGGCGAGGA GCTGTTCACC	85.	AGGGCGAGGAGCTGTTC ACCGGGG	86.
BPK1 361	NGG site 28-mm 5' G	20	GGGGCGAGGA GCTGTTCACC	87.	GGGGCGAGGAGCTGTTC ACCGGGG	88.
BPK1 468	NGAA site 1	20	GTTCGAGGGC GACACCCTGG	89.	GTTCGAGGGCGACACCC TGGTGAA	90.

MSP807	NGAA site 2	20	GTTCACCAGGGTGTCGCCCT	91.	GTTCACCAGGGTGTCGCCCTCGAA	92.
MSP170	NGAC site 1	20	GCCCACCCTCGTGACCACCC	93.	GCCCACCCTCGTGACCACCCTGAC	94.
MSP790	NGAC site 2	20	GCCCTTGCTCACCATGGTGG	95.	GCCCTTGCTCACCATGGTGGCGAC	96.
MSP171	NGAT site 1	20	GTCGCCGTCCAGCTCGACCA	97.	GTCGCCGTCCAGCTCGACCAGGAT	98.
MSP169	NGAT site 2	20	GTGTCCGGCGAGGGCGAGGG	99.	GTGTCCGGCGAGGGCGAGGGCGAT	100.
MSP168	NGAG site 1	20	GGGGTGGTGCCCATCCTGGT	101.	GGGGTGGTGCCCATCCTGGTCGAG	102.
MSP366	NGAG site 2	20	GCCACCATGGTGAGCAAGGG	103.	GCCACCATGGTGAGCAAGGGCGAG	104.

Endogenous genes

EMX1

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
FYF1548	NGG site 1	20	GAGTCCGAGCAGAAGAAGAA	105.	GAGTCCGAGCAGAAGAAGAAGGGC	106.
MSP809	NGG site 2	20	GTCACCTCCAATGACTAGGG	107.	GTCACCTCCAATGACTAGGGTGGG	108.
VC475	NGG site 3	20	GGGAAGACTGAGGCTACATA	109.	GGGAAGACTGAGGCTACATAGGGT	110.
MSP814 *1	NGA site 1	20	GCCACGAAGCAGGCCAATGG	111.	GCCACGAAGCAGGCCAATGGGGAG	112.

FANCF

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
DR348	NGG site 1	20	GGAATCCCTTCTGCAGCACC	113.	GGAATCCCTTCTGCAGCACCTGGA	114.
MSP815	NGG site 2	20	GCTGCAGAAGGGATTCCATG	115.	GCTGCAGAAGGGATTCCATGAGGT	116.
MSP816	NGG site 3	20	GGCGGCTGCACAACCAGTGG	117.	GGCGGCTGCACAACCAGTGGAGGC	118.
MSP817	NGG site 4	20	GCTCCAGAGCCGTGCGAATG	119.	GCTCCAGAGCCGTGCGAATGGGGC	120.
MSP818 *2	NGA site 1	20	GAATCCCTTCTGCAGCACCT	121.	GAATCCCTTCTGCAGCACCTGGAT	122.
MSP820 *3	NGA site 2	20	GCGGCGGCTGCACAACCAGT	123.	GCGGCGGCTGCACAACCAGTGGAG	124.
MSP885 *4	NGA site 3	20	GGTTGTGCAGCCGCCGCTCC	125.	GGTTGTGCAGCCGCCGCTCCAGAG	126.

RUNX1

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
MSP822	NGG site 1	20	GCATTTTCAGGAGGAAGCGA	127.	GCATTTTCAGGAGGAAGCGATGGC	128.
MSP825	NGG site 2	20	GGGAGAAGAAAGAGATGT	129.	GGGAGAAGAAAGAGAGATGTAGGG	130.
MSP826 *5	NGA site 1	20	GGTGCATTTTCAGGAGGAAG	131.	GGTGCATTTTCAGGAGGAAGCGAT	132.
MSP828 *6	NGA site 2	20	GAGATGTAGGGCTAGAGGGG	133.	GAGATGTAGGGCTAGAGGGGTGAG	134.
MSP1725	NGAA site 1	20	GGTATCCAGCAGAGGGGAGA	135.	GGTATCCAGCAGAGGGGAGAAGAA	136.
MSP1726	NGAA site 2	20	GAGGCATCTCTGCACCGAGG	137.	GAGGCATCTCTGCACCGAGGTGAA	138.
MSP1728	NGAC site 1	20	GAGGGGTGAGGCTGAAACAG	139.	GAGGGGTGAGGCTGAAACAGTGAC	140.
MSP1730	NGAC site 2	20	GAGCAAAAGTAGATATTACA	141.	GAGCAAAAGTAGATATTACAAGAC	142.
MSP1732	NGAT site 1	20	GGAATTCAAACTGAGGCATA	143.	GGAATTCAAACTGAGGCATATGAT	144.
MSP829	NGAT site 2	20	GCAGAGGGGAGAAGAAAGAG	145.	GCAGAGGGGAGAAGAAAGAGAGAT	146.
MSP1734	NGAG site 1	20	GCACCGAGGCATCTCTGCAC	147.	GCACCGAGGCATCTCTGCACCGAG	148.
MSP828	NGAG site 2	20	GAGATGTAGGGCTAGAGGGG	149.	GAGATGTAGGGCTAGAGGGGTGAG	150.

ZSCAN2

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
NN675	NGG site	20	GTGCGGCAAGAGCTTCAGCC	151.	GTGCGGCAAGAGCTTCAGCCGGGG	152.

VEGFA

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
VC297	NGG site 1	20	GGGTGGGGGGAGTTTGCTCC	153.	GGGTGGGGGGAGTTTGCTCCTGGA	154.
VC299	NGG site 2	20	GACCCCCTCCACCCCGCCTC	155.	GACCCCCTCCACCCCGCCTCCGGG	156.
VC228	NGG site 3	20	GGTGAGTGAGTGTGTGCGTG	157.	GGTGAGTGAGTGTGTGCGTGTGGG	158.
BPK1846 *7	NGA site 1	20	GCGAGCAGCGTCTTCGAGAG	159.	GCGAGCAGCGTCTTCGAGAGTGAG	160.

ZNF629

Prep Name	Name	Spacer length (nt)	Spacer Sequence	SEQ ID NO:	Sequence with extended PAM	SEQ ID NO:
NN675 *8	NGA site	20	GTGCGGCAAGAGCTTCAGCC	161.	GTGCGGCAAGAGCTTCAGCCAGAG	162.

*1, NGA EMX1 site 4 from Kleinstiver et al., Nature 2015

*2, NGA FANCF site 1 from Kleinstiver et al., Nature 2015

*3, NGA FANCF site 3 from Kleinstiver et al., Nature 2015

*4, NGA FANCF site 4 from Kleinstiver et al., Nature 2015

*5, NGA RUNX1 site 1 from Kleinstiver et al., Nature 2015

*6, NGA RUNX1 site 3 from Kleinstiver et al., Nature 2015

*7, NGA VEGFA site 1 from Kleinstiver et al., Nature 2015

*8, NGA ZNF629 site from Kleinstiver et al., Nature 2015

Genome-wide specificity of SpCas9-HF1

To test whether SpCas9-HF1 exhibited reduced off-target effects in human cells, the genome-wide unbiased identification of double-stranded breaks enabled by sequencing (**GUIDE-seq**) method was used. GUIDE-seq uses integration of a short double-stranded oligodeoxynucleotide (**dsODN**) tag into double-strand breaks to enable amplification and sequencing of adjacent genomic sequence, with the number of tag integrations at any given site providing a quantitative measure of cleavage efficiency (Tsai, S.Q. et al,Nat Biotechnol 33, 187-197 (2015)). GUIDE-seq was used to compare the spectrum of off-target effects induced by wild-type SpCas9 and SpCas9-HF1 using eight different sgRNAs targeted to various sites in the endogenous human *EMX1*, *FANCF*, *RUNX1*, and *ZSCAN2* genes. The sequences targeted by these sgRNAs are unique and have variable numbers of predicted mismatched sites in the reference human genome (**Table 2**). Assessment of on-target dsODN tag integration (by restriction fragment length polymorphism (**RFLP**) assay) and indel formation (by T7EI assay) for the eight sgRNAs revealed comparable on-target activities with wild-type SpCas9 and SpCas9-HF1 (**Figs. 7a** and **7b**, respectively). GUIDE-seq experiments showed that seven of the eight sgRNAs induced cleavage at multiple genome-wide off-target sites (ranging from 2 to 25 per sgRNA) with wild-type SpCas9, whereas the eighth sgRNA (for FANCF site 4) did not produce any detectable off-target sites (**Figs. 2a** and **2b**). However, six of the seven sgRNAs that

induced indels with wild-type SpCas9 showed a strikingly complete absence of GUIDE-seq detectable off-target events with SpCas9-HF1 (**Figs. 2a** and **2b**); and the remaining seventh sgRNA (for FANCF site 2) induced only a single detectable genome-wide off-target cleavage event, at a site harboring one mismatch within the protospacer seed sequence (**Fig. 2a**). Collectively, the off-target sites that were not detected when using SpCas9-HF1 harbored one to six mismatches in the protospacer and/or PAM sequence (**Fig. 2c**). As with wild-type SpCas9, the eighth sgRNA (for FANCF site 4) did not yield any detectable off-target cleavage events when tested with SpCas9-HF1 (**Fig. 2a**).

To confirm the GUIDE-seq findings, targeted amplicon sequencing was used to more directly measure the frequencies of NHEJ-mediated indel mutations induced by wild-type SpCas9 and SpCas9-HF1. For these experiments, human cells were transfected only with sgRNA- and Cas9-encoding plasmids (i.e., without the GUIDE-seq tag). Next-generation sequencing was then used to examine 36 of the 40 off-target sites that had been identified with wild-type SpCas9 for six sgRNAs in the GUIDE-seq experiments (four of the 40 sites could not be examined because they could not be specifically amplified from genomic DNA). These deep sequencing experiments showed that: (1) wild-type SpCas9 and SpCas9-HF1 induced comparable frequencies of indels at each of the six sgRNA on-target sites (**Figs. 3a** and **3b**); (2) wild-type SpCas9, as expected showed statistically significant evidence of indel mutations at 35 of the 36 off-target sites (**Fig. 3b**) at frequencies that correlated well with GUIDE-seq read counts for these same sites (**Fig. 3c**); and (3) the frequencies of indels induced by SpCas9-HF1 at 34 of the 36 off-target sites were indistinguishable from the background level of indels observed in samples from control transfections (**Fig. 3b**). For the two off-target sites that appeared to have statistically significant mutation frequencies with SpCas9-HF1 relative to the negative control, the mean frequencies of indels were 0.049% and 0.037%, levels at which it is difficult to determine whether these are due to sequencing/PCR error or are *bona fide* nuclease-induced indels. Based on these results, it was concluded that SpCas9-HF1 can completely or nearly completely reduce off-target mutations that occur across a range of different frequencies with wild-type SpCas9 to undetectable levels.

Next the capability of SpCas9-HF1 to reduce genome-wide off-target effects of sgRNAs that target atypical homopolymeric or repetitive sequences was assessed.

Although many now try to avoid on-target sites with these characteristics due to their relative lack of orthogonality to the genome, it was desirable to explore whether SpCas9-HF1 might reduce off-target indels even for these challenging targets. Therefore, previously characterized sgRNAs (Fu, Y. et al., Nat Biotechnol 31,Tsai, S.Q. et al., Nat Biotechnol 33, 187-197 (2015) were used that target either a cytosine-rich homopolymeric sequence or a sequence containing multiple TG repeats in the human *VEGFA* gene (VEGFA site 2 and VEGFA site 3, respectively) (**Table 2**). In control experiments, each of these sgRNAs induced comparable levels of GUIDE-seq ds ODN tag incorporation (**Fig. 7c**) and indel mutations (**Fig. 7d**) with both wild-type SpCas9 and SpCas9-HF1, demonstrating that SpCas9-HF1 was not impaired in on-target activity with either of these sgRNAs. Importantly, GUIDE-seq experiments revealed that SpCas9-HF1 was highly effective at reducing off-target sites of these sgRNAs, with 123/144 sites for VEGFA site 2 and 31/32 sites for VEGFA site 3 not detected (**Figs. 4a** and **4b**). Examination of these off-target sites not detected with SpCas9-HF1 showed that they each possessed a range of total mismatches within their protospacer and PAM sequences: 2 to 7 mismatches for the VEGFA site 2 sgRNA and 1 to 4 mismatches for the VEGFA site 3 sgRNA (**Fig. 4c**); also, nine of these off-targets for VEGFA site 2 may have a potential bulged base (Lin, Y. et al,. Nucleic Acids Res 42, 7473-7485 (2014).at the sgRNA-DNA interface (**Fig. 4a** and **Fig. 8**). The sites that were not detected with SpCas9-HF1 possessed 2 to 6 mismatches for the VEGFA site 2 sgRNA and 2 mismatches in the single site for the VEGFA site 3 sgRNA (**Fig. 4c**), with three off-target sites for VEGFA site 2 sgRNA again having a potential bulge (**Fig. 8**). Collectively, these results demonstrated that SpCas9-HF1 can be highly effective at reducing off-target effects of sgRNAs targeted to simple repeat sequences and can also have substantial impacts on sgRNAs targeted to homopolymeric sequences.

Table 2| Summary of potential mismatched sites in the reference human genome for the ten sgRNAs examined by GUIDE-seq

		mismatches to on-target site*						
site	spacer with PAM	1	2	3	4	5	6	total
EMX1-1	GAGTCCGAGCAGAAGAAGAAGGG (SEQ ID NO:163)	0	1	18	273	2318	15831	18441
EMX1-2	GTCACCTCCAATGACTAGGGTGG (SEQ ID NO:164)	0	0	3	68	780	6102	6953
FANCF-1	GGAATCCCTTCTGCAGCACCTGG (SEQ ID NO:165)	0	1	18	288	1475	9611	11393
FANCF-2	GCTGCAGAAGGGATTCCATGAGG (SEQ ID NO:166)	1	1	29	235	2000	13047	15313
FANCF-3	GGCGGCTGCACAACCAGTGGAGG (SEQ ID NO:167)	0	0	11	79	874	6651	7615
FANCF-4	GCTCCAGAGCCGTGCGAATGGGG (SEQ ID NO:168)	0	0	6	59	639	5078	5782
RUNX1-1	GCATTTTCAGGAGGAAGCGATGG(SEQ ID NO:169)	0	2	6	189	1644	11546	13387
ZSCAN2	GTGCGGCAAGAGCTTCAGCCGGG(SEQ ID NO:170)	0	3	12	127	1146	10687	11975
VEGFA2	GACCCCCTCCACCCCGCCTCCGG(SEQ ID NO:171)	0	2	35	456	3905	17576	21974
VEGFA3	GGTGAGTGAGTGTGTGCGTGTGG (SEQ ID NO:172)	1	17	383	6089	13536	35901	55927

* determined using Cas-OFFinder (Bae et al., Bioinformatics 30, 1473-1475 (2014))

Table 4: Oligonucleotides used in the study

description of T7E1 primers	sequence	SEQ ID NO:
forward primer to amplify EMX1 in U2OS human cells	GGAGCAGCTGGTCAGAGGGG	173.
reverse primer to amplify EMX1 in U2OS human cells	CCATAGGGAAGGGGGACACTGG	174.
forward primer to amplify FANCF in U2OS human cells	GGGCCGGGAAAGAGTTGCTG	175.
reverse primer to amplify FANCF in U2OS human cells	GCCCTACATCTGCTCTCCCTCC	176.
forward primer to amplify RUNX1 in U2OS human cells	CCAGCACAACTTACTCGCACTTGAC	177.
reverse primer to amplify RUNX1 in U2OS human cells	CATCACCAACCCACAGCCAAGG	178.
forward primer to amplify VEGFA in U2OS human cells	TCCAGATGGCACATTGTCAG	179.
reverse primer to amplify VEGFA in U2OS human cells	AGGGAGCAGGAAAGTGAGGT	180.
forward primer to amplify VEGFA (NGG site 2) in U2OS human cells	CGAGGAAGAGAGAGACGGGGTC	181.
reverse primer to amplify VEGFA (NGG site 2) in U2OS human cells	CTCCAATGCACCCAAGACAGCAG	182.
forward primer to amplify ZSCAN2 in U2OS human cells	AGTGTGGGGTGTGTGGGAAG	183.
reverse primer to amplify ZSCAN2 in U2OS human cells	GCAAGGGGAAGACTCTGGCA	184.

forward primer to amplify ZNF629 in U2OS human cells	TACGAGTGCCTAGAGT GCG	185.
reverse primer to amplify ZNF629 in U2OS human cells	GCAGATGTAGGTCTTG GAGGAC	186.

description of deep sequencing primers	sequence	SEQ ID NO:
forward primer to amplify EMX1-1 on-target	GGAGCAGCTGGTCAG AGGGG	187.
reverse primer to amplify EMX1-1 on-target	CGATGTCCTCCCCATT GGCCTG	188.
forward primer to amplify EMX1-1-GUIDE_seq-OT#1	GTGGGGAGATTTGCAT CTGTGGAGG	189.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#1	GCTTTTATACCATCTT GGGGTTACAG	190.
forward primer to amplify EMX1-1-GUIDE_seq-OT#2	CAATGTGCTTCAACCC ATCACGGC	191.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#2	CCATGAATTTGTGATG GATGCAGTCTG	192.
forward primer to amplify EMX1-1-GUIDE_seq-OT#3	GAGAAGGAGGTGCAG GAGCTAGAC	193.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#3	CATCCCGACCTTCATC CCTCCTGG	194.
forward primer to amplify EMX1-1-GUIDE_seq-OT#4	GTAGTTCTGACATTCC TCCTGAGGG	195.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#4	TCAAACAAGGTGCAG ATACAGCA	196.
forward primer to amplify EMX1-1-GUIDE_seq-OT#5	CAGGGTCGCTCAGTCT GTGTGG	197.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#5	CCAGCGCACCATTCAC TCCACCTG	198.
forward primer to amplify EMX1-1-GUIDE_seq-OT#6	GGCTGAAGAGGAAGA CCAGACTCAG	199.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#6	GGCCCCTCTGAATTCA ATTCTCTGC	200.
forward primer to amplify EMX1-1-GUIDE_seq-OT#7	CCACAGCGAGGAGTG ACAGCC	201.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#7	CCAAGTCTTTCCTAAC TCGACCTTGG	202.
forward primer to amplify EMX1-1-GUIDE_seq-OT#8	CCCTAGGCCCACACCA GCAATG	203.
reverse primer to amplify EMX1-1-GUIDE_seq-OT#8	GGGATGGGAATGGGA ATGTGAGGC	204.
forward primer to amplify EMX1-2 on-target	GCCCAGGTGAAGGTGT GGTTCC	205.
reverse primer to amplify EMX1-2 on-target	CCAAAGCCTGGCCAGG GAGTG	206.
forward primer to amplify EMX1-2-GUIDE_seq-OT#1	AGGCAAAGATCTAGG ACCTGGATGG	207.

reverse primer to amplify EMX1-2-GUIDE_seq-OT#1	CCATCTGAGTCAGCCAGCCTTGTC	208.
forward primer to amplify EMX1-2-GUIDE_seq-OT#2	GGTTCCCTCCCTTCTGAGCCC	209.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#2	GGATAGGAATGAAGACCCCCTCTCC	210.
forward primer to amplify EMX1-2-GUIDE_seq-OT#3	GGACTGGCTGGCTGTGTGTTTTGAG	211.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#3	CTTATCCAGGGCTACCTCATTGCC	212.
forward primer to amplify EMX1-2-GUIDE_seq-OT#4	GCTGCTGCTGCTTTGATCACTCCTG	213.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#4	CTCCTTAAACCCTCAGAAGCTGGC	214.
forward primer to amplify EMX1-2-GUIDE_seq-OT#5	GCACTGTCAGCTGATCCTACAGG	215.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#5	ACGTTGGAACAGTCGAGCTGTAGC	216.
forward primer to amplify EMX1-2-GUIDE_seq-OT#6	TGTGCATAACTCATGTTGGCAAACT	217.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#6	TCCACAACTACCCTCAGCTGGAG	218.
forward primer to amplify EMX1-2-GUIDE_seq-OT#7	CCACTGACAATTCACTCAACCCTGC	219.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#7	AGGCAGACCAGTTATTTGGCAGTC	220.
forward primer to amplify EMX1-2-GUIDE_seq-OT#9	ACAGGCGCAGTTCACTGAGAAG	221.
reverse primer to amplify EMX1-2-GUIDE_seq-OT#9	GGGTAGGCTGACTTTGGGCTCC	222.
forward primer to amplify FANCF-1 on-target	GCCCTCTTGCCTCCACTGGTTG	223.
reverse primer to amplify FANCF-1 on-target	CGCGGATGTTCCAATCAGTACGC	224.
forward primer to amplify FANCF-1-GUIDE_seq-OT#1	GCGGGCAGTGGCGTCTTAGTCG	225.
reverse primer to amplify FANCF-1-GUIDE_seq-OT#1	CCCTGGGTTTGGTTGGCTGCTC	226.
forward primer to amplify FANCF-1-GUIDE_seq-OT#2	CTCCTTGCCGCCCAGCCGGTC	227.
reverse primer to amplify FANCF-1-GUIDE_seq-OT#2	CACTGGGGAAGAGGCGAGGACAC	228.
forward primer to amplify FANCF-1-GUIDE_seq-OT#3	CCAGTGTTTCCCATCCCCAACAC	229.
reverse primer to amplify FANCF-1-GUIDE_seq-OT#3	GAATGGATCCCCCCCTAGAGCTC	230.
forward primer to amplify FANCF-1-GUIDE_seq-OT#4	CAGGCCCACAGGTCCTTCTGGA	231.
reverse primer to amplify FANCF-1-GUIDE_seq-OT#4	CCACACGGAAGGCTGACCACG	232.

forward primer to amplify FANCF-3 on-target	GCGCAGAGAGAGCAG GACGTC	233.
reverse primer to amplify FANCF-3 on-target	GCACCTCATGGAATCC CTTCTGC	234.
forward primer to amplify FANCF-3-GUIDE_seq-OT#1	CAAGTGATGCGACTTC CAACCTC	235.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#1	CCCTCAGAGTTCAGCT TAAAAAGACC	236.
forward primer to amplify FANCF-3-GUIDE_seq-OT#2	TGCTTCTCATCCACTCT AGACTGCT	237.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#2	CACCAACCAGCCATGT GCCATG	238.
forward primer to amplify FANCF-3-GUIDE_seq-OT#3	CTGCCTGTGCTCCTCG ATGGTG	239.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#3	GGGTTCAAAGCTCATC TGCCCC	240.
forward primer to amplify FANCF-3-GUIDE_seq-OT#4	GCATGTGCCTTGAGAT TGCCTGG	241.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#4	GACATTCAGAGAAGC GACCATGTGG	242.
forward primer to amplify FANCF-3-GUIDE_seq-OT#5	CCATCTTCCCCTTTGG CCCACAG	243.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#5	CCCCAAAAGTGGCCAA GAGCCTGAG	244.
forward primer to amplify FANCF-3-GUIDE_seq-OT#6	GTTCTCCAAAGGAAGA GAGGGGAATG	245.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#6	GGTGCTGTGTCCTCAT GCATCC	246.
forward primer to amplify FANCF-3-GUIDE_seq-OT#7	CGGCTTGCCTAGGGTC GTTGAG	247.
reverse primer to amplify FANCF-3-GUIDE_seq-OT#7	CCTTCAGGGGCTCTTC CAGGTC	248.
forward primer to amplify RUNX1-1 on-target	GGGAACTGGCAGGCA CCGAGG	249.
reverse primer to amplify RUNX1-1 on-target	GGGTGAGGCTGAAAC AGTGACC	250.
forward primer to amplify RUNX1-1-GUIDE_seq-OT#1	GGGAGGATGTTGGTTT TAGGGAACTG	251.
reverse primer to amplify RUNX1-1-GUIDE_seq-OT#1	TCCAATCACTACATGC CATTTTGAAGA	252.
forward primer to amplify RUNX1-1-GUIDE_seq-OT#2	CCACCCTCTTCCTTTG ATCCTCCC	253.
reverse primer to amplify RUNX1-1-GUIDE_seq-OT#2	TCCTCCCTACTCCTTCA CCCAGG	254.
forward primer to amplify ZSCAN2 on-target	GAGTGCCTGACATGTG GGGAGAG	255.
reverse primer to amplify ZSCAN2 on-target	TCCAGCTAAAGCCTTT CCCACAC	256.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#1	GAACTCTCTGATGCAC CTGAAGGCTG	257.

reverse primer to amplify ZSCAN2-GUIDE_seq-OT#1	ACCGTATCAGTGTGAT GCATGTGGT	258.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#2	TGGGTTTAATCATGTG TTCTGCACTATG	259.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#2	CCCATCTTCCATTCTG CCCTCCAC	260.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#3	CAGCTAGTCCATTTGT TCTCAGACTGTG	261.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#3	GGCCAACATTGTGAAA CCCTGTCTC	262.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#4	CCAGGGACCTGTGCTT GGGTTC	263.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#4	CACCCCATGACCTGGC ACAAGTG	264.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#5	AAGTGTTCCTCAGAAT GCCAGCCC	265.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#5	CAGGAGTGCAGTTGTG TTGGGAG	266.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#6	CTGATGAAGCACCAGA GAACCCACC	267.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#6	CACACCTGGCACCCAT ATGGC	268.
forward primer to amplify ZSCAN2-GUIDE_seq-OT#7	GATCCACACTGGTGAG AAGCCTTAC	269.
reverse primer to amplify ZSCAN2-GUIDE_seq-OT#7	CTTCCCACACTCACAG CAGATGTAGG	270.

Refining the specificity of SpCas9-HF1

Previously described methods such as truncated gRNAs (Fu, Y. et al., Nat Biotechnol 32, 279-284 (2014)) and the SpCas9-D1135E variant (Kleinstiver, B.P. et al., Nature 523, 481-485 (2015)) can partially reduce SpCas9 off-target effects, and the present inventors wondered whether these might be combined with SpCas9-HF1 to further improve its genome-wide specificity. Testing of SpCas9-HF1 with matched full-length and truncated sgRNAs targeted to four sites in the human cell-based EGFP disruption assay revealed that shortening sgRNA complementarity length substantially impaired on-target activities (**Fig. 9**). By contrast, SpCas9-HF1 with an additional D1135E mutation (a variant referred to herein as SpCas9-HF2) retained 70% or more activity of wild-type SpCas9 with six of eight sgRNAs tested using a human cell-based EGFP disruption assay (**Figs. 5a** and **5b**). SpCas9-HF3 and SpCas9-HF4 variants were also created harboring L169A or Y450A mutations, respectively, at positions whose side chains mediated hydrophobic non-specific interactions with the target DNA on its PAM proximal end (Nishimasu, H. et al., Cell

156, 935–949 (2014); Jiang, F., et al., Science 348, 1477-1481 (2015)). SpCas9-HF3 and SpCas9-HF4 retained 70% or more of the activities observed with wild-type SpCas9 with the same six out of eight EGFP-targeted sgRNAs (**Figs. 5a** and **5b**).

To determine whether SpCas9-HF2, -HF3, and -HF4 could reduce indel frequencies at two off-target sites (for the FANCF site 2 and VEGFA site 3 sgRNAs) that were resistant to SpCas9-HF1, further experiments were performed. For the FANCF site 2 off-target, which bears a single mismatch in the seed sequence of the protospacer, SpCas9-HF4 reduced indel mutation frequencies to near background level as judged by T7EI assay while also beneficially increasing on-target activity (**Fig. 5c**), resulting in the greatest increase in specificity among the three variants (**Fig. 5d**). For the VEGFA site 3 off-target site, which bears two protospacer mismatches (one in the seed sequence and one at the nucleotide most distal from the PAM sequence), SpCas9-HF2 showed the greatest reduction in indel formation while showing only modest effects on on-target mutation efficiency (**Fig. 5c**), leading to the greatest increase in specificity among the three variants tested (**Fig. 5d**). Taken together, these results demonstrate the potential for reducing off-target effects that are resistant to SpCas9-HF1 by introducing additional mutations at other residues that mediate non-specific DNA contacts or that may alter PAM recognition.

To generalize the T7E1 assay findings described above that show SpCas9-HF4 and SpCas9-HF2 have improved discrimination relative to SpCas9-HF1 against off-targets of the FANCF site 2 and VEGFA site 3 sgRNAs, respectively, the genome-wide specificities of these variants were examined using GUIDE-seq. Using an RFLP assay, it was determined that SpCas9-HF4 and SpCas9-HF2 had similar on-target activities to SpCas9-HF1, as assayed by GUIDE-seq tag integration rates (FIG. 5E). When analyzing the GUIDE-seq data, no new off-target sites were identified for SpCas9-HF2 or SpCas9-HF4 (FIG. 5F). Compared to SpCas9-HF1, off-target activities at all sites were either rendered undetectable by GUIDE-seq or substantially decreased. Relative to SpCas9-HF1, SpCas9-HF4 had nearly 26-fold better specificity against the single FANCF site 2 off-target site that remained recalcitrant to the specificity improvements of SpCas9-HF1 (FIG. 5F). SpCas9-HF2 had nearly 4-fold improved specificity relative to SpCas9-HF1 for the high-frequency VEGFA site 3 off-target, while also dramatically reducing (>38-fold) or eliminating GUIDE-seq detectable events at other low-frequency off-target sites. Of note, the genomic

position of 3 of these low frequency sites identified for SpCas9-HF1 are adjacent to previously characterized background U2OS cell breakpoint hotspots. Collectively, these results suggest that the SpCas9-HF2 and SpCas9-HF4 variants can improve the genome-wide specificity of SpCas9-HF1.

SpCas9-HF1 robustly and consistently reduced off-target mutations when using sgRNAs designed against standard, non-repetitive target sequences. The two off-target sites that were most resistant to SpCas9-HF1 have only one and two mismatches in the protospacer. Together, these observations suggest that off-target mutations might be minimized to undetectable levels by using SpCas9-HF1 and targeting non-repetitive sequences that do not have closely related sites bearing one or two mismatches elsewhere in the genome (something that can be easily accomplished using existing publicly available software programs (Bae, S., et al, Bioinformatics 30, 1473-1475 (2014)). One parameter that users should keep in mind is that SpCas9-HF1 may not be compatible with the common practice of using a G at the 5' end of the gRNA that is mismatched to the protospacer sequence. Testing of four sgRNAs bearing a 5' G mismatched to its target site showed three of the four had diminished activities with SpCas9-HF1 compared to wild-type SpCas9 (**Fig. 10**), perhaps reflecting the ability of SpCas9-HF1 to better discriminate a partially matched site.

Further biochemical work can confirm or clarify the precise mechanism by which SpCas9-HF1 achieves its high genome-wide specificity. It does not appear that the four mutations introduced alter the stability or steady-state expression level of SpCas9 in the cell, because titration experiments with decreasing concentrations of expression plasmids suggested that wild-type SpCas9 and SpCas9-HF1 behaved comparably as their concentrations are lowered (**Fig. 11**). Instead, the simplest mechanistic explanation is that these mutations decreased the energetics of interaction between the Cas9-sgRNA and the target DNA, with the energy of the complex at a level just sufficient to retain on-target activity but lowered it enough to make off-target site cleavage inefficient or non-existent. This mechanism is consistent with the non-specific interactions observed between the residues mutated and the target DNA phosphate backbone in structural data (Nishimasu, H. et al., Cell 156, 935–949 (2014); Anders, C et. Al., Nature 513, 569-573 (2014)). A somewhat similar mechanism has been proposed to explain the increased specificities of transcription

activator-like effector nucleases bearing substitutions at positively charged residues (Guilinger, J.P. et al., Nat Methods 11, 429-435 (2014)).

It was possible that SpCas9-HF1 might also be combined with other mutations that have been shown to alter Cas9 function. For example, an SpCas9 mutant bearing three amino acid substitutions (D1135V/R1335Q/T1337R, also known as the SpCas9-VQR variant), recognizes sites with NGAN PAMs (with relative efficiencies for NGAG>NGAT=NGAA>NGAC) (Kleinstiver, B.P. et al, Nature 523, 481-485 (2015)) and a recently identified quadruple SpCas9 mutant (D1135V/G1218R/R1335Q/T1337R, referred to as the SpCas9-VRQR variant) has improved activities relative to the VQR variant on sites with NGAH (H = A, C, or T) PAMs (**Fig. 12a**). Introduction of the four mutations (N497A/R661A/Q695A/Q926A) from SpCas9-HF1 into SpCas9-VQR and SpCas9-VRQR created SpCas9-VQR-HF1 and SpCas9-VRQR-HF1, respectively. Both HF versions of these nucleases showed on-target activities comparable (i.e., 70% or more) to their non-HF counterparts with five of eight sgRNAs targeted to the EGFP reporter gene and with seven of eight sgRNAs targeted to endogenous human gene sites (**Figs. 12b-12d**).

More broadly, these results illuminate a general strategy for the engineering of additional high-fidelity variants of CRISPR-associated nucleases. Adding additional mutations at non-specific DNA contacting residues further reduced some of the very small number of residual off-target sites that persist with SpCas9-HF1. Thus, variants such as SpCas9-HF2, SpCas9-HF3, SpCas9-HF4, and others can be utilized in a customized fashion depending on the nature of the off-target sequences. Furthermore, success with engineering high-fidelity variants of SpCas9 suggests that the approach of mutating non-specific DNA contacts can be extended to other naturally occurring and engineered Cas9 orthologues (Ran, F.A. et al., Nature 520, 186-191 (2015), Esvelt, K.M. et al., Nat Methods 10, 1116-1121 (2013); Hou, Z. et al., Proc Natl Acad Sci U S A (2013); Fonfara, I. et al., Nucleic Acids Res 42, 2577-2590 (2014); Kleinstiver, B.P. et al, Nat Biotechnol (2015) as well as newer CRISPR-associated nucleases (Zetsche, B. et al., Cell 163, 759-771 (2015); Shmakov, S. et al., Molecular Cell 60, 385-397) that are being discovered and characterized with increasing frequency.

Example 2

Described herein are SpCas9 variants with alanine substitutions in residues that contact the target strand DNA, including N497A, Q695A, R661A, and Q926A. Beyond these residues, the present inventors sought to determine whether the specificity of these variants, e.g., the SpCas9-HF1 variant (N497A/R661A/Q695A/Q926A), might be further improved by adding substitutions in positively-charged SpCas9 residues that appear to make contacts with the non-target DNA strand: R780, K810, R832, K848, K855, K968, R976, H982, K1003, K1014, K1047, and/or R1060 (see Slaymaker et al., Science. 2016 Jan 1;351(6268):84-8).

The activities of wild-type SpCas9 derivatives bearing single alanine substitutions at these positions and combinations thereof were initially tested using the EGFP disruption assay with a perfectly matched sgRNA designed to a site in the *EGFP* gene (to assess on-target activities) and the same sgRNA bearing intentional mismatches at positions 11 and 12 with position 1 being the most PAM-proximal base (to assess activities at mismatched sites, as would be found at off-target sites) (**Figure 13A**). (Note that the derivatives bearing the triple substitutions K810A/K1003A/R1060A or K848A/K1003A/R1060A are the same as recently described variants known as eSpCas9(1.0) and eSpCas9(1.1), respectively; see ref. 1). As expected, wild-type SpCas9 had robust on-target and mismatched-target activities. As a control, we also tested SpCas9-HF1 in this experiment and found that it maintained on-target activity while reducing mismatched-target activity as expected (**Figure 13A**). All of the wild-type SpCas9 derivatives bearing one or more alanine substitutions at positions that might potentially contact the non-target DNA strand showed on-target activities comparable to wild-type SpCas9 (**Figure 13A**). Interestingly, some of these derivatives also showed reduced cleavage with the mismatched 11/12 sgRNA relative to the activity observed with wild-type SpCas9, suggesting that a subset of the substitutions in these derivatives confer enhanced specificity against this mismatched site relative to wild-type SpCas9 (**Figure 13A**). However, none of these single substitutions or combinations of substitutions were sufficient to completely eliminate activities observed the 11/12 mismatched sgRNA. When we tested wild-type SpCas9, SpCas9-HF1, and these same wild-type SpCas9 derivatives using an additional sgRNA bearing mismatches at positions 9 and 10

(**Figure 13B**), only minimal changes in mismatched-target activities were observed for most derivatives. Again, this demonstrated that single, double, or even triple substitutions (equivalent to the previously described eSpCas9(1.0) and (1.1) variants) at these potential non-target strand contacting residues are insufficient to eliminate activities at imperfectly matched DNA sites. Collectively, these data demonstrate that the wild-type SpCas9 variants retain on-target activity with a matched sgRNA and that the substitutions contained in these derivatives on their own (in the context of wild-type SpCas9) are not sufficient to eliminate nuclease activities on two different mismatched DNA sites (**Figures 13A** and **13B**).

Given these results, it was hypothesized that SpCas9-HF1 derivatives bearing one or more additional amino acid substitutions at residues that might contact the non-target DNA strand might further improve specificity relative to the parental SpCas9-HF1 protein. Therefore, various SpCas9-HF1-derviatives bearing combinations of single, double, or triple alanine substitutions were tested in the human cell-based EGFP disruption assay using a perfectly matched sgRNA (to test on-target activities) and the same sgRNA bearing mismatches at positions 11 and 12 (to assess activities at a mismatched target site, as would be found for off-target sites). These sgRNAs are the same ones that were used for **Figures 13A-B**. This experiment revealed most of the SpCas9-HF1-derivative variants we tested showed comparable on-target activities to those observed with both wild-type SpCas9 and SpCas9-HF1 (**Figure 14A**). With the 11/12 mismatched sgRNA, some of the SpCas9-HF1 derivatives tested (such as SpCas9-HF1 + R832A and SpCas9-HF1 + K1014A) did not show an appreciable change in cleavage with the mismatched sgRNA. However, importantly, most of the SpCas9-HF1 derivatives had substantially lower activity with the 11/12 mismatched sgRNA than what was observed with SpCas9-HF1, eSpCas9(1.0), or eSpCas9(1.1), suggesting that certain combinations of these new variants have reduced mismatched-target activities and thus improved specificities (**Figure 14A**). Of the 16 SpCas9-HF1 derivatives that reduced mismatched-target activities with the 11/12 mismatched sgRNA to near background levels, 9 appeared to have only minimal effects on on-target activity (assessed using the perfectly matched sgRNA; **Figure 14A**). Additional testing of a subset of these SpCas9-HF1 derivatives in the EGFP disruption assay using an sgRNA intentionally mismatched at positions 9 and 10 (**Figure 14B**) also revealed that these variants possessed lower activities with this mismatched sgRNA

than what was observed either with SpCas9-HF1 (**Figure 14b**), with eSpCas9(1.1) (**Figure 13A**), or with the same substitutions added to wild-type SpCas9 nuclease (**Figure 13B**). Importantly, five variants showed background level off-target activity in this assay with the 9/10 mismatched sgRNA.

Next, whether these alanine substitutions of the non-target strand could be combined with the SpCas9 variant that contains only the Q695A and Q926A substitutions from our SpCas9-HF1 variant (here "double" variant) was tested. Because many of the HF1 derivatives tested above showed an observable (and undesirable) decrease in on-target activity, it was hypothesized that combining only the two most important substitutions from SpCas9-HF1 (Q695A and Q926A; see **Figure 1B**) with one or more non-target strand contacting substitutions might rescue on-target activity but still maintain the gains in specificity observed when these substitutions were added to the SpCas9-HF1 variant. Therefore, various SpCas9(Q695A/Q926A) derivatives bearing combinations of single, double, or triple alanine substitutions at potential non-target DNA strand interacting positions were tested in the human cell-based EGFP disruption assay using the same perfectly matched sgRNA targeted to EGFP described above (to test on-target activities) and the same sgRNA bearing mismatches at positions 11 and 12 (to assess activities at a mismatched target site, as would be found for off-target sites) that were used for **Figures 13A-B**. This experiment revealed most of the SpCas9(Q695A/Q926A) derivative variants tested showed comparable on-target activities to those observed with both wild-type SpCas9 and SpCas9-HF1 (**Figure 15**). Importantly, many of the SpCas9-HF1 derivatives had substantially lower activity with the 11/12 mismatched sgRNA compared with what was observed with SpCas9-HF1, eSpCas9(1.0), or eSpCas9(1.1) suggesting that certain combinations of these new variants have reduced mismatched-target activities and thus improved specificities (**Figure 15**). Of the 13 SpCas9(Q695A/Q926A) derivatives that reduced mismatched-target activities with the 11/12 mismatched sgRNA to near background levels, only 1 appeared to have a substantial effect on on-target activity (assessed using the perfectly matched sgRNA; **Figure 15**).

Overall, these data demonstrate that the addition of one, two, or three alanine substitutions to SpCas9-HF1 or SpCas9(Q695A/Q926A) at positions that might contact the non-target DNA strand can lead to new variants with improved abilities to

discriminate against mismatched off-target sites (relative to to their parental clones or the recently described eSpCas9(1.0) or (1.1). Importantly, these same substitutions in the context of wild-type SpCas9 do not appear to provide any substantial specificity benefit.

To better define and compare the tolerances of SpCas9-HF1 and eSpCas9-1.1 to mismatches at the sgRNA-target DNA complementarity interface, their activities were examined using sgRNAs containing single mismatches at all possible positions in the spacer complementarity region. Both the SpCas9-HF1 and eSPCas9-1.1 variants had similar activities on most singly mismatched sgRNAs when compared to wild-type SpCas9, with a few exceptions where SpCas9-HF1 outperformed eSpCas9-1.1 (**Figure 16**).

Next we tested the single nucleotide mismatch tolerance of some variants containing combinations of amino acid substitutions from either the double mutant (Db = Q695A/Q926A), SpCas9-HF1 (N497A/R661A/Q695A/Q926A), eSpCas9-1.0 (1.0 = K810A/K1003A/R1060A), or eSpCas9-1.1(1.1 = K848A/K1003A/R1060A) with additional alanine substitutions in residues that contact the target strand DNA or that potentially contact the non-target strand DNA (**Figures 17A-B**). On-target activity was assessed using a perfectly matched sgRNA, while single nucleotide mismatch tolerance was assessed using sgRNAs bearing such mismatches at positions 4, 8, 12, or 16 in the spacer sequence (**Figure 17A**). A number of these variants maintained on-target activity with substantial reductions in activities observed with the mismatched sgRNAs. Three of these variants (Q695A/K848A/Q926A/K1003A/R1060A, N497A/R661A/Q695A/K855A/Q926A/R1060A, and N497A/R661A/Q695A/Q926A/H982A/R1060A) were further tested with the remaining single mismatch sgRNAs (containing mismatches at positions 1-3, 5-7, 9-11, 13-15, and 17-20). These variants demonstrated a more robust intolerance to single nucleotide substitutions in the sgRNA compared with eSpCas9-1.1, demonstrating the improved specificity profile of these new variants (**Figure 17B**).

Additional variant nucleases containing alternative combinations of amino acid substitutions were tested using sgRNAs containing mismatches at positions 5, 7, and 9 in the spacer (these particular mismatched sgRNAs were used because earlier variants appeared to tolerate mismatches at these positions) (**Figure 18**). A number of these

nucleases had improved specificities against the mismatched sites, with only marginal reductions in on-target activities (**Figure 18**).

To further determine whether additional combinations of mutations could convey specificity improvements, a greatly expanded panel of nuclease variants with two additional matched sgRNAs was tested to examine on-target activity in our EGFP disruption activity (**Figure 19A**). A number of these variants maintained robust on-target activities, suggesting that they may be useful for generating further mprovements to specificity (**Figure 19B**). A number of these variants were tested with sgRNAs containing single substitutions at positions 12, 14, 16, or 18 to determine whether specificity improvements were observed and were found to exhibit greater intolerance to single nucleotide mismatches at these positions (**Figure 19B**).

Example 3

Taking an analogous strategy with *Staphylococcus aureus* Cas9 (SaCas9) as we had done with SpCas9, experiments were performed to improve the specificity of SaCas9 by introducing alanine substitutions in residues that are known to contact the target DNA strand (**Figure 20** and **Figure 21A**), residues that may contact the non-target DNA (ongoing experiments), and residues that we have previously shown can influence PAM specificity (**Figure 21B**). Residues that may contact the target strand DNA backbone include: Y211, Y212, W229, Y230, R245, T392, N419, L446, Y651, and R654; residues that may contact the non-target strand DNA include: Q848, N492, Q495, R497, N498, R499, Q500, K518, K523, K525, H557, R561, K572, R634, R654, G655, N658, S662, N668, R686, K692, R694, H700, K751; and residues that contact the PAM include: E782, D786, T787, Y789, T882, K886, N888, A889, L909, K929, N985, N986, R991, and R1015. In a preliminary experiment, single alanine substitutions (or some combinations thereof) in either target strand DNA contacting residues or PAM contacting residues (**Figures 21A and B**, respectively) had variable effects on on-target EGFP disruption activity (using a perfectly matched sgRNA) and were unable to eliminate off-target cleavage (when using an sgRNA mismatched at positions 11 and 12). Interestingly, SpCas9 mutations in the HF1 were unable to completely abolish off-target activity with a similarly mismatched target/sgRNA pair, suggesting that variants containing combinations of target strand/non-target strand substitutions may be necessary to improve specificity at such sites (as we observed with SpCas9).

To further assess the strategy of mutating potential target strand DNA contacts to improve SaCas9 specificity, the potential of single, double, triple, and quadruple combinations of mutations to tolerate mismatches at positions 19 and 20 in an sgRNA was examined (**Figures 22A and B**). These combinations revealed that alanine substitutions at Y230 and R245, when combined with other substitutions, can increase specificity as judged by the capability to better discriminate against mismatched sites.

Next the on-target gene disruption activities of two of these triple alanine substitution variants (Y211A/Y230A/R245A and Y212A/Y230A/R245A) were examined at 4 on-target sites in EGFP (matched sites #1-4; **Figure 23**). These variants maintained robust on-target activities for matched sites 1 and 2 but showed approximately 60-70% loss of on-target activity with matched sites 3 and 4. Both of these triple alanine substitution variants dramatically improved specificity relative to wild-type SaCas9 as judged by using sgRNAs bearing double mismatches at various positions in the spacers of target sites 1-4 (**Figure 23**).

SaCas9 variants bearing double and triple combinations (**Figures 24A and B, respectively**) of these alanine substitutions were tested on six endogenous sites for on target activities and improvements in specificity assessed using an sgRNA containing a single mismatch at position 21 (the most PAM distal position expected to be a challenging mismatch to discriminate against). In some cases, on-target activities with the matched sgRNA were maintained with the variants while 'off-target' activities with the sgRNA mismatched at position 21 were eliminated (**Figures 24A and B**). In other cases, marginal to complete loss of activity was observed with the matched sgRNA.

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Sequences

SEQ ID NO:271 - JDS246: CMV-T7-humanSpCas9-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, NLS double underlined, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
GAATACAAAGTACCTTCAAAGAAATTTAAGGTGTTGGGGAACACAGACCGTCATTCGATTAAAAAGAAT
CTTATCGGTGCCCTCCTATTCGATAGTGGCGAAACGGCAGAGGCGACTCGCCTGAAACGAACCGCTCGG
AGAAGGTATACACGTCGCAAGAACCGAATATGTTACTTACAAGAAATTTTTAGCAATGAGATGGCCAAA
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CACCCCATCTTTGGAAACATAGTAGATGAGGTGGCATATCATGAAAAGTACCCAACGATTTATCACCTC
AGAAAAAAGCTAGTTGACTCAACTGATAAAGCGGACCTGAGGTTAATCTACTTGGCTCTTGCCCATATG
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GGAGAGAAGAAAAATGGGTTGTTCGGTAACCTTATAGCGCTCTCACTAGGCCTGACACCAAATTTTAAG
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ATCCTCCTATCTGACATACTGAGAGTTAATACTGAGATTACCAAGGCGCCGTTATCCGCTTCAATGATC
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CGGTTCGCATGGATGACAAGAAAGTCCGAAGAAACGATTACTCCATGGAATTTTGAGGAAGTTGTCGAT
AAAGGTGCGTCAGCTCAATCGTTCATCGAGAGGATGACCAACTTTGACAAGAATTTACCGAACGAAAAA
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GATTCTGTCGAGATCTCCGGGGTAGAAGATCGATTTAATGCGTCACTTGGTACGTATCATGACCTCCTA
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ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:272 - VP12: CMV-T7-humanSpCas9-HF1(N497A, R661A, Q695A, Q926A)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
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CGATACACTTCTACCAAGGAGGTGCTAGACGCGACACTGATTCACCAATCCATCACGGGATTATATGAA
ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:273 - MSP2135: CMV-T7-humanSpCas9-HF2(N497A, R661A, Q695A, Q926A, D1135E)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold:**

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
GAATACAAAGTACCTTCAAAGAAATTTAAGGTGTTGGGGAACACAGACCGTCATTCGATTAAAAAGAAT
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CGATACACTTCTACCAAGGAGGTGCTAGACGCGACACTGATTCACCAATCCATCACGGGATTATATGAA
ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:274 - MSP2133: CMV-T7-humanSpCas9-HF4(Y450A, N497A, R661A, Q695A, Q926A)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
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ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:275 - MSP469: CMV-T7-humanSpCas9-VQR(D1135V, R1335Q, T1337R)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold**:

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cagTACagaTCTACCAAGGAGGTGCTAGACGCGACACTGATTCACCAATCCATCACGGGATTATATGAA
ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:276 - MSP2440: CMV-T7-humanSpCas9-VQR-HF1(N497A, R661A, Q695A, Q926A, D1135V, R1335Q, T1337R)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
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cagTACagaTCTACCAAGGAGGTGCTAGACGCGACACTGATTCACCAATCCATCACGGGATTATATGAA
ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:277 - BPK2797: CMV-T7-humanSpCas9-VRQR(D1135V, G1218R, R1335Q, T1337R)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS double underlined, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
GAATACAAAGTACCTTCAAAGAAATTTAAGGTGTTGGGGAACACAGACCGTCATTCGATTAAAAAGAAT
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ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCC<u>CCCAAGAAGAAGAGGAAAGTC</u>TCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:278 - MSP2443: CMV-T7-humanSpCas9-VRQR-HF1(N497A, R661A, Q695A, Q926A, D1135V, G1218R, R1335Q, T1337R)-NLS-3xFLAG

Human codon optimized *S. pyogenes* Cas9 in normal font, modified codons in lower case, NLS <u>double underlined</u>, 3xFLAG tag in **bold**:

ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCACTAATTCCGTTGGATGGGCTGTCATAACCGAT
GAATACAAAGTACCTTCAAAGAAATTTAAGGTGTTGGGGAACACAGACCGTCATTCGATTAAAAAGAAT
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ACTCGGATAGATTTGTCACAGCTTGGGGGTGACGGATCCCCCAAGAAGAAGAGGAAAGTCTCGAGC**GAC**
TACAAAGACCATGACGGTGATTATAAAGATCATGACATCGATTACAAGGATGACGATGACAAGTGA

SEQ ID NO:279 - BPK1520: U6-BsmBIcassette-Sp-sgRNA

U6 promoter in normal font, BsmBI sites *italicised*, *S. pyogenes* sgRNA in lower case, U6 terminator double underlined:

TGTACAAAAAAGCAGGCTTTAAAGGAACCAATTCAGTCGACTGGATCCGGTACCAAGGTCGGGCAGGAA
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GATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACCG*GAGACG*ATTAATG*CGTCTC*Cgtttta
gagctagaaatagcaagttaaaataaggctagtccgttatcaacttgaaaaagtggcaccgagtcggtg
ctttttt

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An isolated *Streptococcus pyogenes* Cas9 (SpCas9) protein, with mutations at one, two, three, four, five, six, or all seven of the following positions: L169, Y450, N497, R661, Q695, Q926, and/or D1135, preferably comprising a sequence that is at least 80% identical to the amino acid sequence of SEQ ID NO:1 with mutations at one, two, three, four, five, six, or seven of the following positions: L169, Y450, N497, R661, Q695, Q926, D1135 and optionally one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag.

2. The isolated protein of claim 1, comprising mutations at one, two, three, or all four of the following: N497, R661, Q695, and Q926, preferably one, two, three, or all four of the following mutations: N497A, R661A, Q695A, and Q926A.

3. The isolated protein of claim 1, comprising mutations at one or both of Q695 and/or Q926, and optionally one, two, three, four, or all five of L169, Y450, N497, R661, and D1135, preferably Y450A/Q695A, L169A/Q695A, Q695A/Q926A, Q695A/D1135E, Q926A/D1135E, Y450A/D1135E, L169A/Y450A/Q695A, L169A/Q695A/Q926A, Y450A/Q695A/Q926A, R661A/Q695A/Q926A, N497A/Q695A/Q926A, Y450A/Q695A/D1135E, Y450A/Q926A/D1135E, Q695A/Q926A/D1135E, L169A/Y450A/Q695A/Q926A, L169A/R661A/Q695A/Q926A,Y450A/R661A/Q695A/Q926A, N497A/Q695A/Q926A/D1135E, R661A/Q695A/Q926A/D1135E, or Y450A/Q695A/Q926A/D1135E.

4. The isolated proteins of claim 1 further comprising mutations at N14; S15; S55; R63; R78; H160; K163; R165; L169; R403; N407; Y450; M495; N497; K510; Y515; W659; R661; M694; Q695; H698; A728; S730; K775; S777; R778; R780; K782; R783; K789; K797; Q805; N808; K810; R832; Q844; S845; K848; S851; K855; R859; K862; K890; Q920; Q926; K961; S964; K968; K974; R976; N980; H982; K1003; Y1013; K1014; V1015; S1040; N1041; N1044; K1047; K1059; R1060; K1107; E1108; S1109; K1113; R1114; S1116; K1118; R1122; K1123; K1124; D1135; S1136; K1153; K1155 ; K1158; K1200; Q1221; H1241; Q1254; Q1256; K1289; K1296; K1297; R1298; K1300; H1311; K1325; K1334; T1337 and/or S1216, preferably N497A/R661A/Q695A/Q926A/K810A,

N497A/R661A/Q695A/Q926A/K848A, N497A/R661A/Q695A/Q926A/K855A, N497A/R661A/Q695A/Q926A/R780A, N497A/R661A/Q695A/Q926A/K968A, N497A/R661A/Q695A/Q926A/H982A, N497A/R661A/Q695A/Q926A/K1003A, N497A/R661A/Q695A/Q926A/K1014A,
N497A/R661A/Q695A/Q926A/K1047A,
N497A/R661A/Q695A/Q926A/R1060A,
N497A/R661A/Q695A/Q926A/K810A/K968A,
N497A/R661A/Q695A/Q926A/K810A/K848A,
N497A/R661A/Q695A/Q926A/K810A/K1003A,
N497A/R661A/Q695A/Q926A/K810A/R1060A,
N497A/R661A/Q695A/Q926A/K848A/K1003A,
N497A/R661A/Q695A/Q926A/K848A/R1060A,
N497A/R661A/Q695A/Q926A/K855A/K1003A,
N497A/R661A/Q695A/Q926A/K855A/R1060A,
N497A/R661A/Q695A/Q926A/K968A/K1003A,
N497A/R661A/Q695A/Q926A/H982A/K1003A,
N497A/R661A/Q695A/Q926A/H982A/R1060A,
N497A/R661A/Q695A/Q926A/K1003A/R1060A,
N497A/R661A/Q695A/Q926A/K810A/K1003A/R1060A,
N497A/R661A/Q695A/Q926A/K848A/K1003A/R1060A,
Q695A/Q926A/R780A, Q695A/Q926A/K810A, Q695A/Q926A/R832A, Q695A/Q926A/K848A, Q695A/Q926A/K855A, Q695A/Q926A/K968A, Q695A/Q926A/R976A, Q695A/Q926A/H982A, Q695A/Q926A/K1003A, Q695A/Q926A/K1014A, Q695A/Q926A/K1047A, Q695A/Q926A/R1060A, Q695A/Q926A/K848A/K968A, Q695A/Q926A/K848A/K1003A, Q695A/Q926A/K848A/K855A, Q695A/Q926A/K848A/H982A, Q695A/Q926A/K1003A/R1060A, Q695A/Q926A/R832A/R1060A, Q695A/Q926A/K968A/K1003A, Q695A/Q926A/K968A/R1060A, Q695A/Q926A/K848A/R1060A, Q695A/Q926A/K855A/H982A, Q695A/Q926A/K855A/K1003A, Q695A/Q926A/K855A/R1060A, Q695A/Q926A/H982A/K1003A, Q695A/Q926A/H982A/R1060A, Q695A/Q926A/K1003A/R1060A, Q695A/Q926A/K810A/K1003A/R1060A, Q695A/Q926A/K1003A/K1047A/R1060A,

Q695A/Q926A/K968A/K1003A/R1060A,
Q695A/Q926A/R832A/K1003A/R1060A, or
Q695A/Q926A/K848A/K1003A/R1060A.

5. The isolated protein of claim 1, further comprising one or more of the following mutations: D1135E; D1135V; D1135V/R1335Q/T1337R (VQR variant); D1135E/R1335Q/T1337R (EQR variant); D1135V/G1218R/R1335Q/T1337R (VRQR variant); or D1135V/G1218R/R1335E/T1337R (VRER variant).

6. The isolated protein of claim 1, further comprising one or more mutations that decrease nuclease activity selected from the group consisting of mutations at D10, E762, D839, H983, or D986; and at H840 or N863.

7. The isolated protein of claim 6, wherein the mutations that decrease nuclease activity are:
(i) D10A or D10N, and
(ii) H840A, H840N, or H840Y.

8. An isolated *Staphylococcus aureus* Cas9 (SaCas9) protein, with mutations at one, two, three, four, five, six, or more of the following positions: Y211, Y212, W229, Y230, R245, T392, N419, Y651, R654, preferably comprising a sequence that is at least 80% identical to the amino acid sequence of SEQ ID NO:1 with mutations at one, two, three, four, or five, six or more of the following positions: Y211, Y212, W229, Y230, R245, T392, N419, Y651, R654, and optionally one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag.

9. The isolated protein of claim 8, comprising one or more of the following mutations: Y211A, Y212A, W229, Y230A, R245A, T392A, N419A, Y651, and/or R654A.

10. The isolated protein of claim 8, comprising mutations at N419 and/or R654, and optionally one, two, three, four or more of the additional mutations Y211, Y212, W229, Y230, R245 and T392, preferably N419A/R654A, Y211A/R654A, Y211A/Y212A, Y211A/Y230A, Y211A/R245A, Y212A/Y230A, Y212A/R245A, Y230A/R245A, W229A/R654A, Y211A/Y212A/Y230A, Y211A/Y212A/R245A,

Y211A/Y212A/Y651A, Y211A/Y230A/R245A, Y211A/Y230A/Y651A, Y211A/R245A/Y651A, Y211A/R245A/R654A, Y211A/R245A/N419A, Y211A/N419A/R654A, Y212A/Y230A/R245A, Y212A/Y230A/Y651A, Y212A/R245A/Y651A, Y230A/R245A/Y651A, R245A/N419A/R654A, T392A/N419A/R654A, R245A/T392A/N419A/R654A, Y211A/R245A/N419A/R654A, W229A/R245A/N419A/R654A, Y211A/R245A/T392A/N419A/R654A, or Y211A/W229A/R245A/N419A/R654A.

11. The isolated proteins of claim 8, further comprising mutations at Y211; Y212; W229; Y230; R245; T392; N419; L446; Q488A; N492A; Q495A; R497A; N498A; R499; Q500; K518; K523; K525; H557; R561; K572; R634; Y651; R654; G655; N658; S662; N667; R686; K692; R694; H700; K751; D786; T787; Y789; T882; K886; N888; 889; L909; N985; N986; R991; R1015; N44; R45; R51; R55; R59; R60; R116; R165; N169; R208; R209; Y211; T238; Y239; K248; Y256; R314; N394; Q414; K57; R61; H111; K114; V164; R165; L788; S790; R792; N804; Y868; K870; K878; K879; K881; Y897; R901; and/or K906.

12. The isolated protein of claim 8, further comprising one or more of the following mutations: E782K, K929R, N968K, or R1015H. Specifically, E782K/N968K/R1015H (KKH variant); E782K/K929R/R1015H (KRH variant); or E782K/K929R/N968K/R1015H (KRKH variant).

13. The isolated protein of claim 8, further comprising one or more mutations that decrease nuclease activity selected from the group consisting of mutations at D10, E477, D556, H701, or D704; and at H557 or N580.

14. The isolated protein of claim 13, wherein the mutations are:
(i) D10A or D10N, and /or
(ii) H557A, H557N, or H557Y, and/or
(iii) N580A, and/or
(iv) D556A.

15. A fusion protein comprising the isolated protein of claims 1-14, fused to a heterologous functional domain, with an optional intervening linker, wherein the linker does not interfere with activity of the fusion protein.

16. The fusion protein of claim 15, wherein the heterologous functional domain is a transcriptional activation domain.

17. The fusion protein of claim 16, wherein the transcriptional activation domain is from VP64 or NF-κB p65.

18. The fusion protein of claim 15, wherein the heterologous functional domain is a transcriptional silencer or transcriptional repression domain.

19. The fusion protein of claim 18, wherein the transcriptional repression domain is a Krueppel-associated box (KRAB) domain, ERF repressor domain (ERD), or mSin3A interaction domain (SID).

20. The fusion protein of claim 18, wherein the transcriptional silencer is Heterochromatin Protein 1 (HP1), preferably HP1α or HP1β.

21. The fusion protein of claim 15, wherein the heterologous functional domain is an enzyme that modifies the methylation state of DNA.

22. The fusion protein of claim 21, wherein the enzyme that modifies the methylation state of DNA is a DNA methyltransferase (DNMT) or a TET protein.

23. The fusion protein of claim 22, wherein the TET protein is TET1.

24. The fusion protein of claim 15, wherein the heterologous functional domain is an enzyme that modifies a histone subunit.

25. The fusion protein of claim 15, wherein the enzyme that modifies a histone subunit is a histone acetyltransferase (HAT), histone deacetylase (HDAC), histone methyltransferase (HMT), or histone demethylase.

26. The fusion protein of claim 15, wherein the heterologous functional domain is a biological tether.

27. The fusion protein of claim 26, wherein the biological tether is MS2, Csy4 or lambda N protein.

28. The fusion protein of claim 26, wherein the heterologous functional domain is FokI.

29. An isolated nucleic acid encoding the protein of claims 1-14.

30. A vector comprising the isolated nucleic acid of claim 29, optionally operably linked to one or more regulatory domains for expressing the protein of claims 1-24.

31. A host cell, preferably a mammalian host cell, comprising the nucleic acid of claim 29, and optionally expressing the protein of claims 1-14.

32. A method of altering the genome or epigenome of a cell, the method comprising expressing in the cell or contacting the cell with the isolated protein of claims 1-14, and a guide RNA having a region complementary to a selected portion of the genome of the cell.

33. An isolated nucleic acid encoding the protein of claim 15.

34. A vector comprising the isolated nucleic acid of claim 33, optionally operably linked to one or more regulatory domains for expressing the protein of claim 15.

35. A host cell, preferably a mammalian host cell, comprising the nucleic acid of claim 33, and optionally expressing the protein of claim 15.

36. A method of altering the genome or epigenome of a cell, the method comprising expressing in the cell or contacting the cell with the isolated protein of claims 1-14, and a guide RNA having a region complementary to a selected portion of the genome of the cell.

37. A method of altering the genome or epigenome of a cell, the method comprising expressing in the cell or contacting the cell with the isolated fusion protein of claims 15-28, and a guide RNA having a region complementary to a selected portion of the genome of the cell.

38. The method of claims 36 or 37, wherein the isolated protein or fusion protein comprises one or more of a nuclear localization sequence, cell penetrating peptide sequence, and/or affinity tag.

39. The method of claims 36 or 37, wherein the cell is a stem cell, preferably an embryonic stem cell, mesenchymal stem cell, or induced pluripotent stem cell; is in a living animal; or is in an embryo.

40. A method of altering a double stranded DNA D (dsDNA) molecule, the method comprising contacting the dsDNA molecule with the isolated protein of claims 1-14, and a guide RNA having a region complementary to a selected portion of the dsDNA molecule.

41. The method of claim 40, wherein the dsDNA molecule is *in vitro*.

42. A method of altering a double stranded DNA D (dsDNA) molecule, the method comprising contacting the dsDNA molecule with the fusion protein of claim 15, and a guide RNA having a region complementary to a selected portion of the dsDNA molecule.

43. The method of claim 42, wherein the dsDNA molecule is *in vitro*.

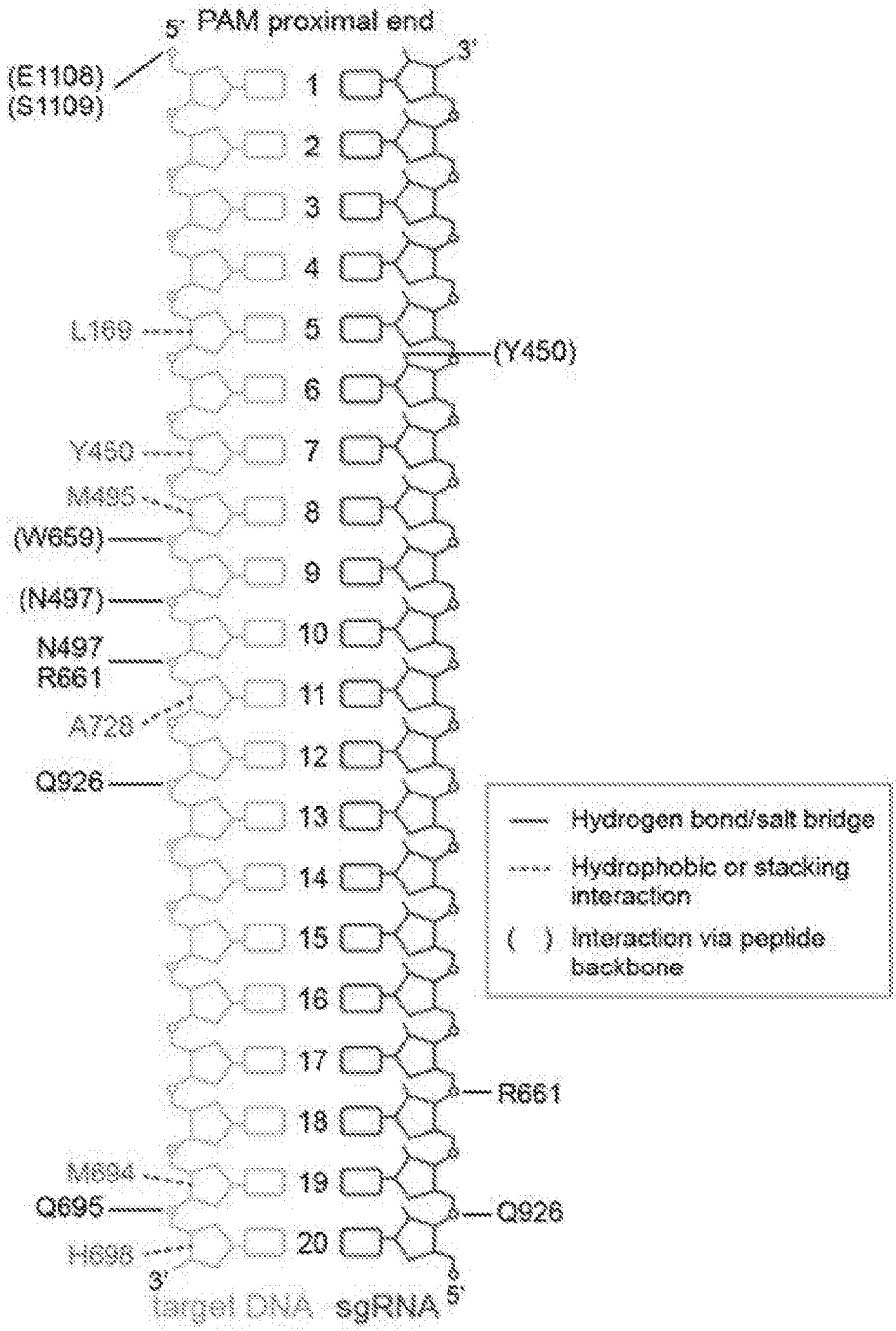

5' PAM proximal end
3'
(E1108)
(S1109)
1
2
3
4
L169
5
(Y450)
6
Y450
7
M495
8
(W659)
9
(N497)
10
N497
R661
11
A728
12
Q926
13
14
15
16
17
R661
18
19
M694
Q695
19
Q926
H698
20
3'
target DNA
sgRNA
5'
Hydrogen bond/salt bridge
Hydrophobic or stacking interaction
( ) Interaction via peptide backbone

FIG. 1A

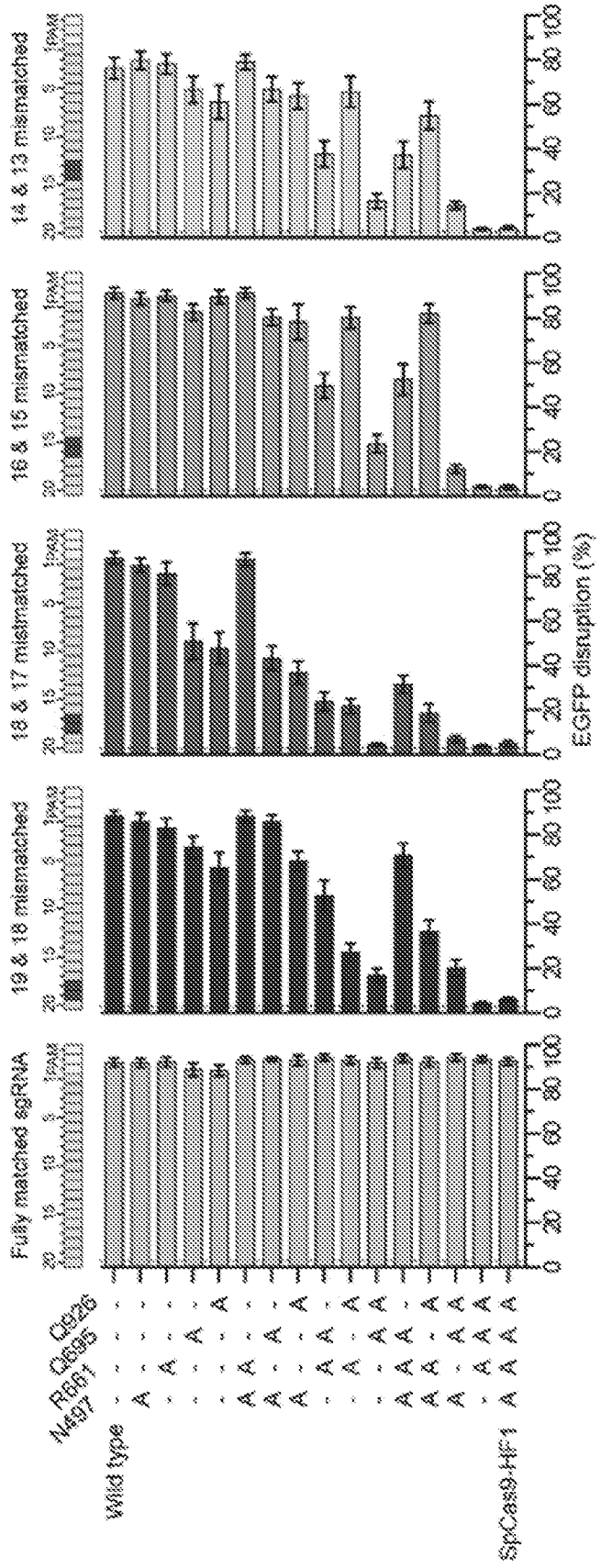

Fully matched sgRNA
19 & 18 mismatched
18 & 17 mismatched
16 & 15 mismatched
14 & 13 mismatched
PAM
Wild type
SpCas9-HF1
R661
Q695
Q926
N497
EGFP disruption (%)

FIG. 1B

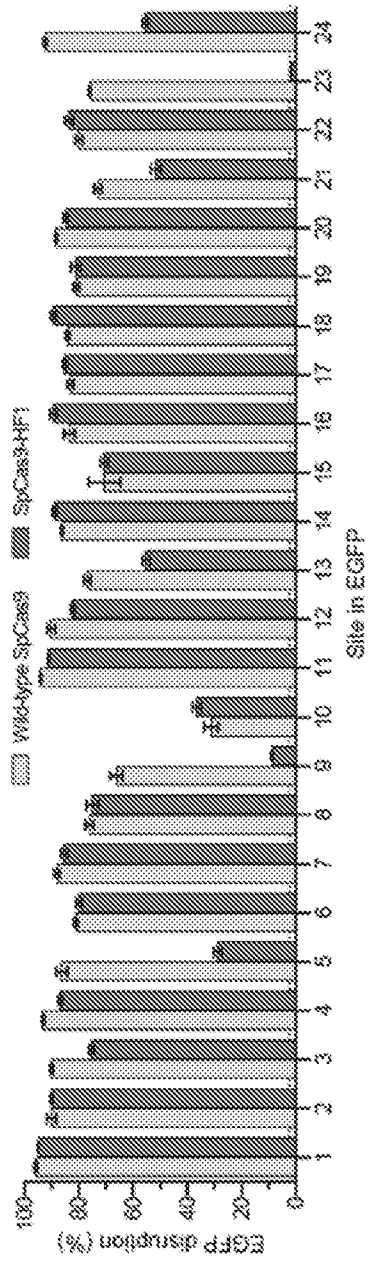

Wild-type SpCas9
SpCas9-HF1
EGFP disruption (%)
Site in EGFP

FIG. 1C

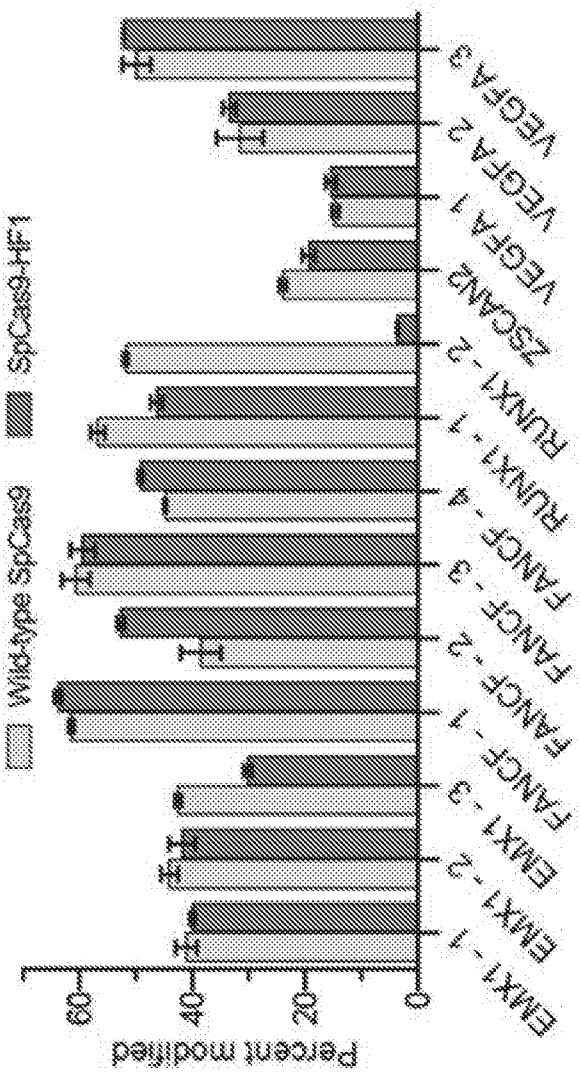

Wild-type SpCas9
SpCas9-HF1
Percent modified
0
20
40
60
EMX1 - 1
EMX1 - 2
EMX1 - 3
FANCF - 1
FANCF - 2
FANCF - 3
FANCF - 4
RUNX1 - 1
RUNX1 - 2
ZSCAN2
VEGFA 1
VEGFA 2
VEGFA 3

FIG. 1D

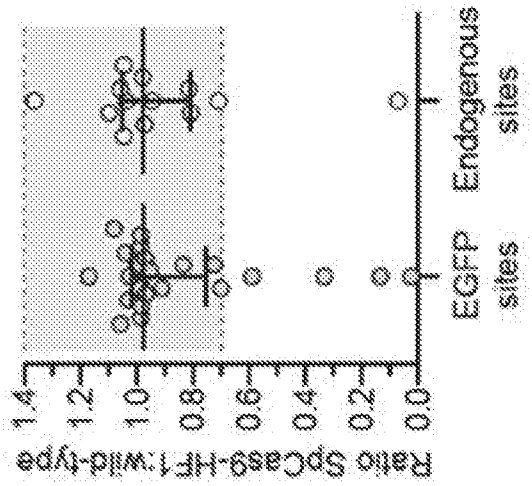

Ratio SpCas9-HF1:wild-type
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
EGFP sites
Endogenous sites

FIG. 1E

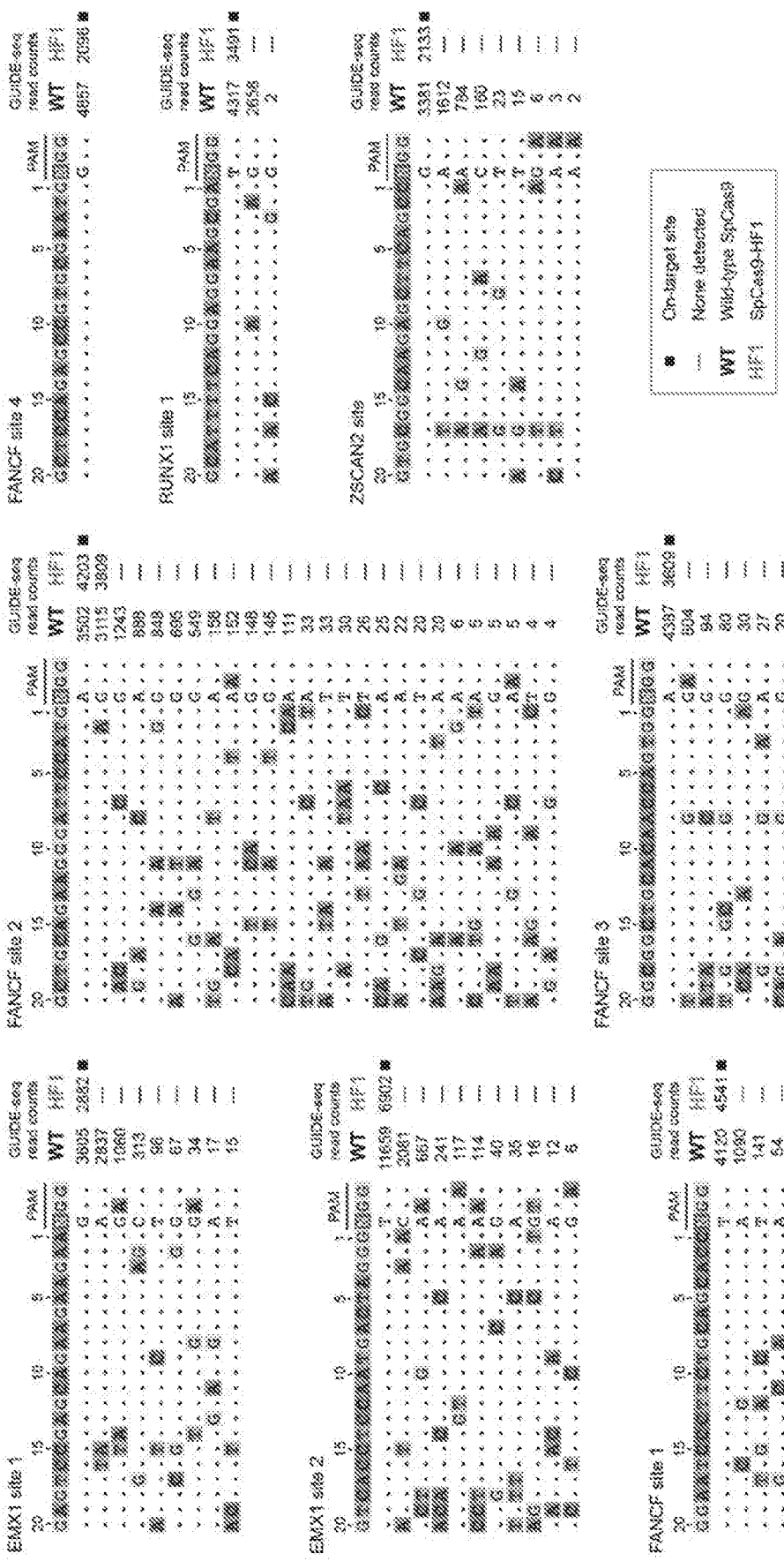

EMX1 site 1
FANCF site 2
FANCF site 4
RUNX1 site 1
EMX1 site 2
FANCF site 3
ZSCAN2 site
FANCF site 1
GUIDE-seq read counts
WT
HF1
PAM
* On-target site
— None detected
WT Wild-type SpCas9
HF1 SpCas9-HF1

FIG. 2A

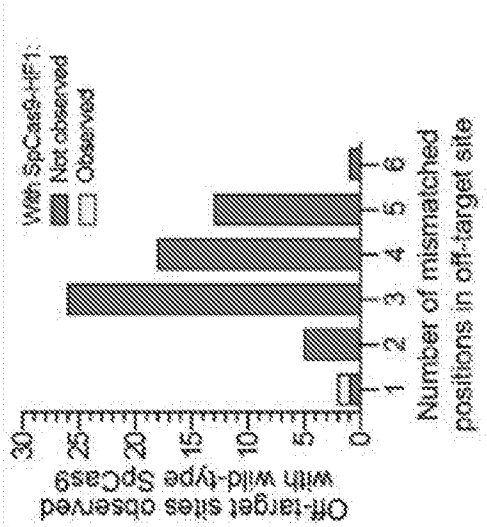


FIG. 2C

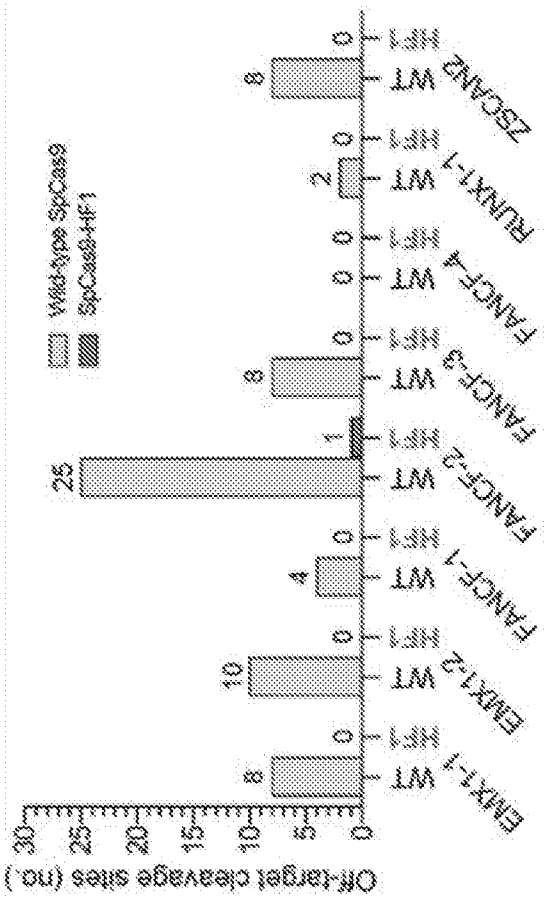


FIG. 2B

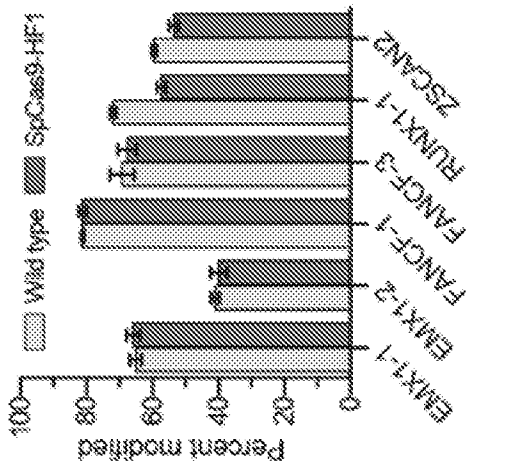


FIG. 3A

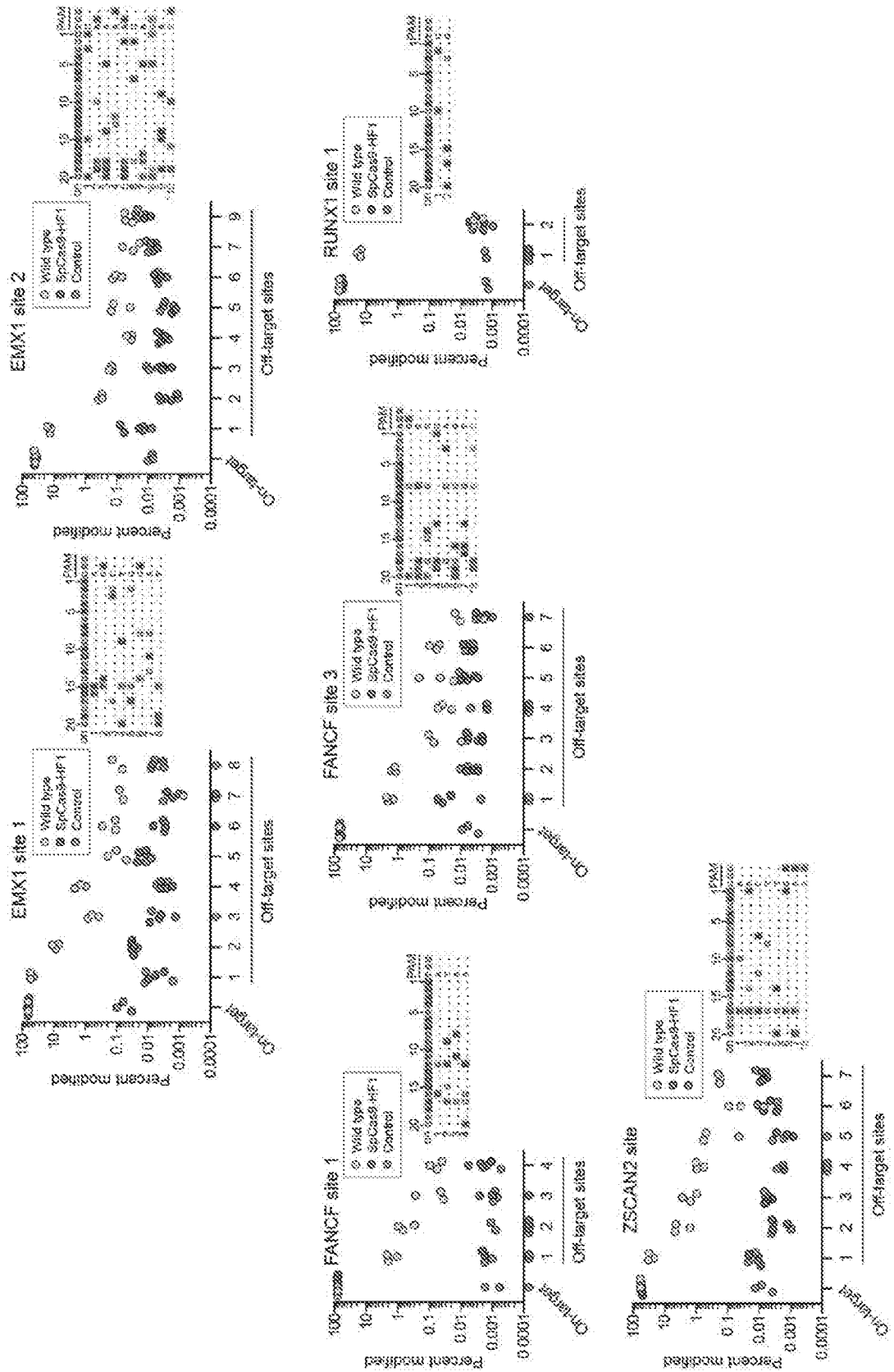

EMX1 site 1
EMX1 site 2
FANCF site 1
FANCF site 3
RUNX1 site 1
ZSCAN2 site
Wild type
SpCas9-HF1
Control
Percent modified
Off-target
Off-target sites
PAM

FIG. 3B

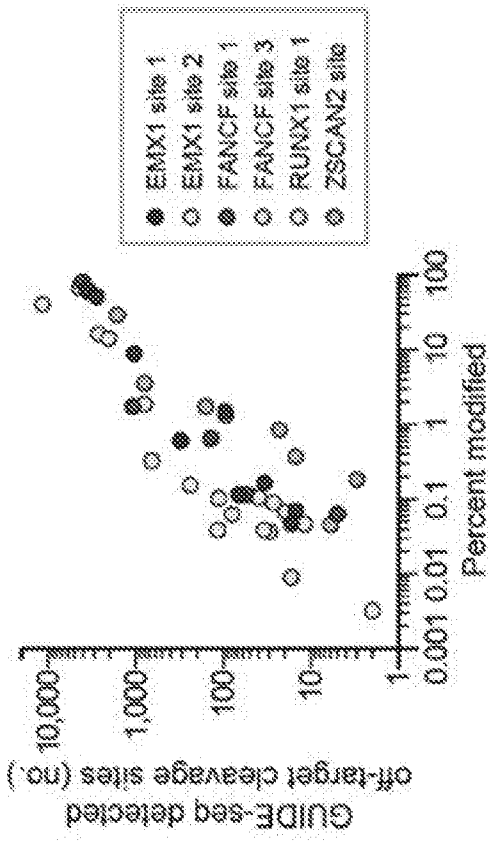

EMX1 site 1
EMX1 site 2
FANCF site 1
FANCF site 3
RUNX1 site 1
ZSCAN2 site
GUIDE-seq detected
off-target cleavage sites (no.)
10,000
1,000
100
10
1
0.001 0.01 0.1 1 10 100
Percent modified

FIG. 3C

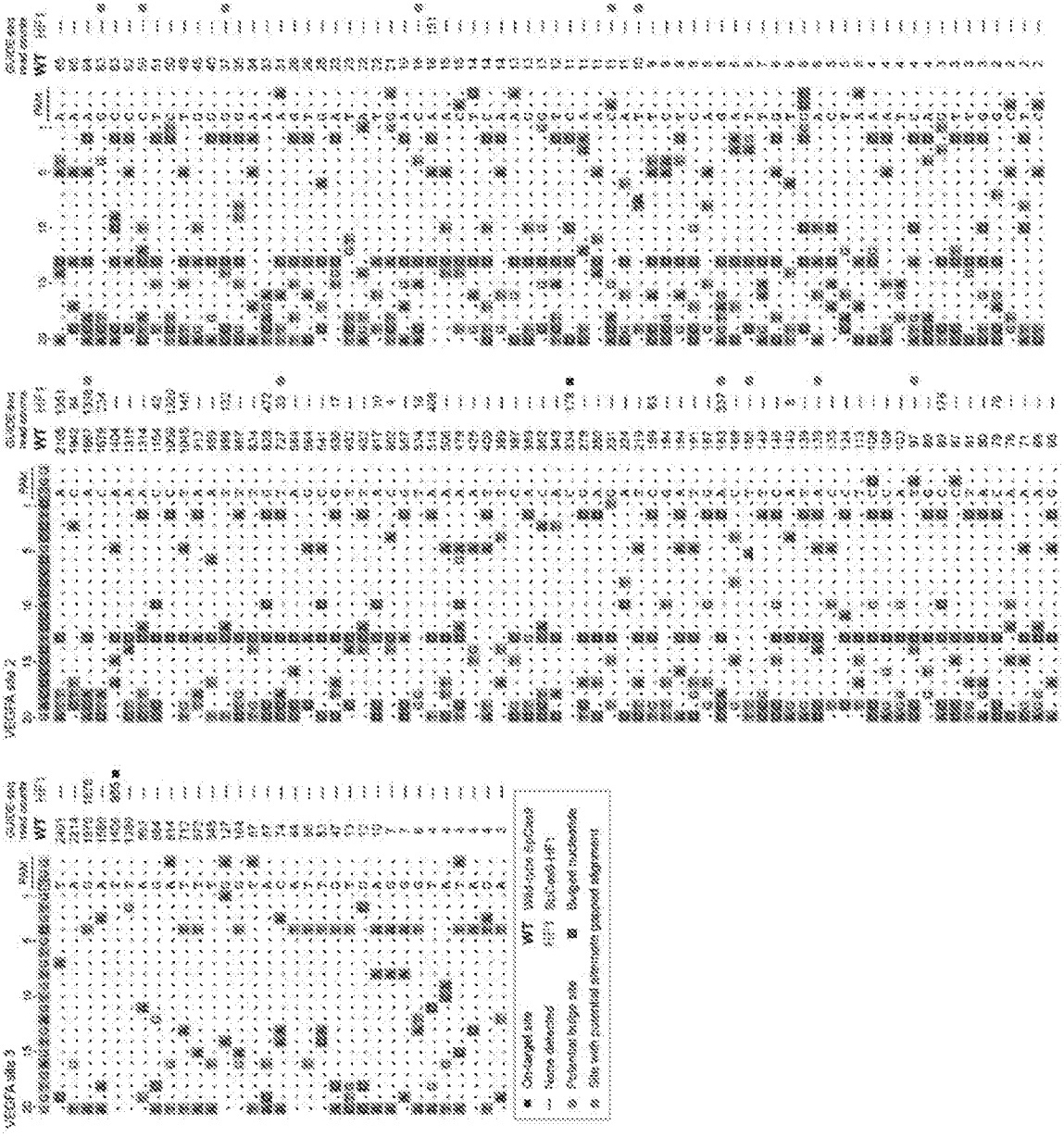


FIG. 4A

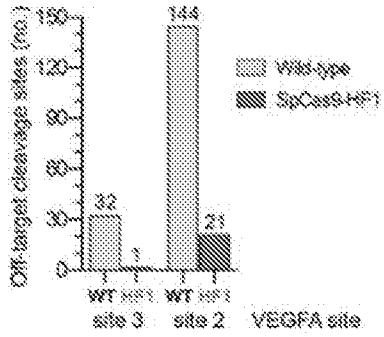


FIG. 4B

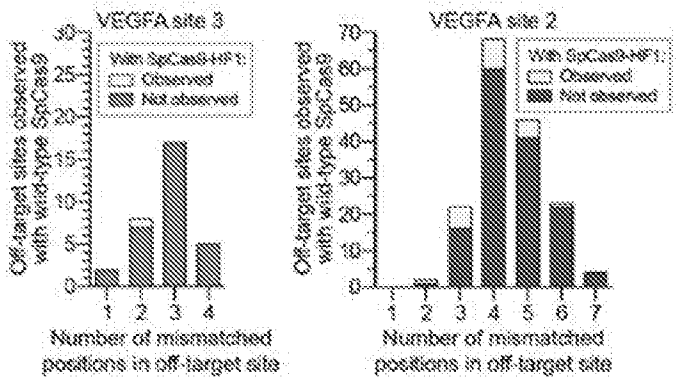


FIG. 4C

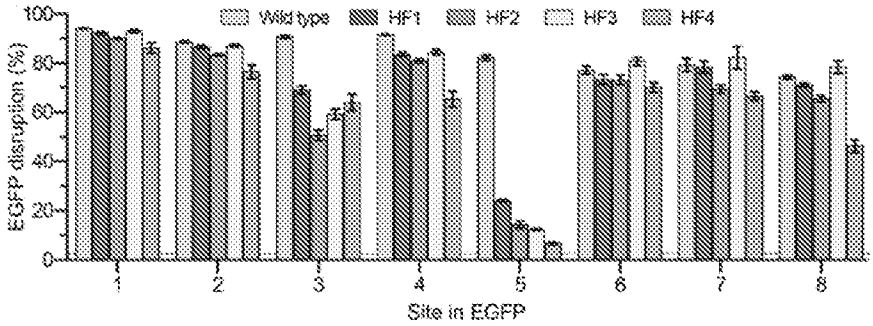


FIG. 5A

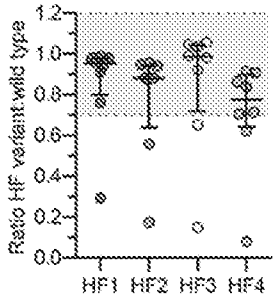


FIG. 5B

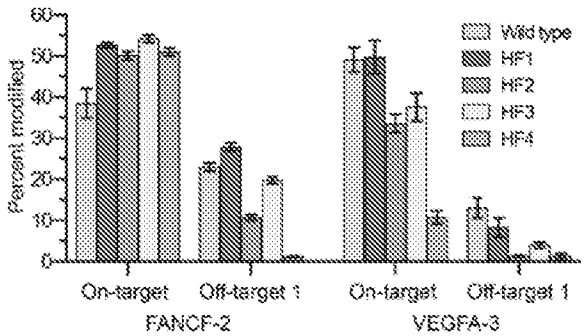


FIG. 5C

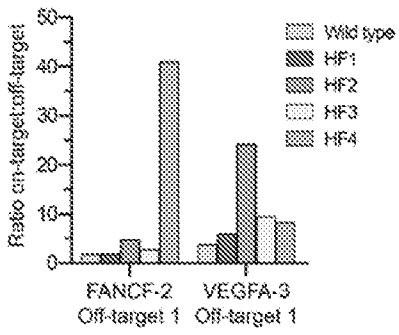


FIG. 5D

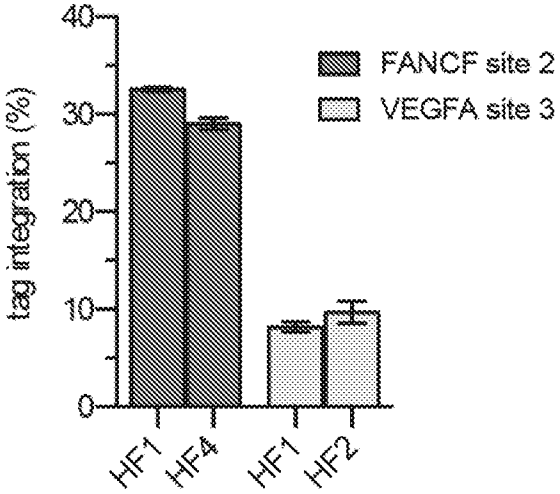

40
30
20
10
0
tag integration (%)
FANCF site 2
VEGFA site 3
HF1
HF4
HF1
HF2

FIG. 5E

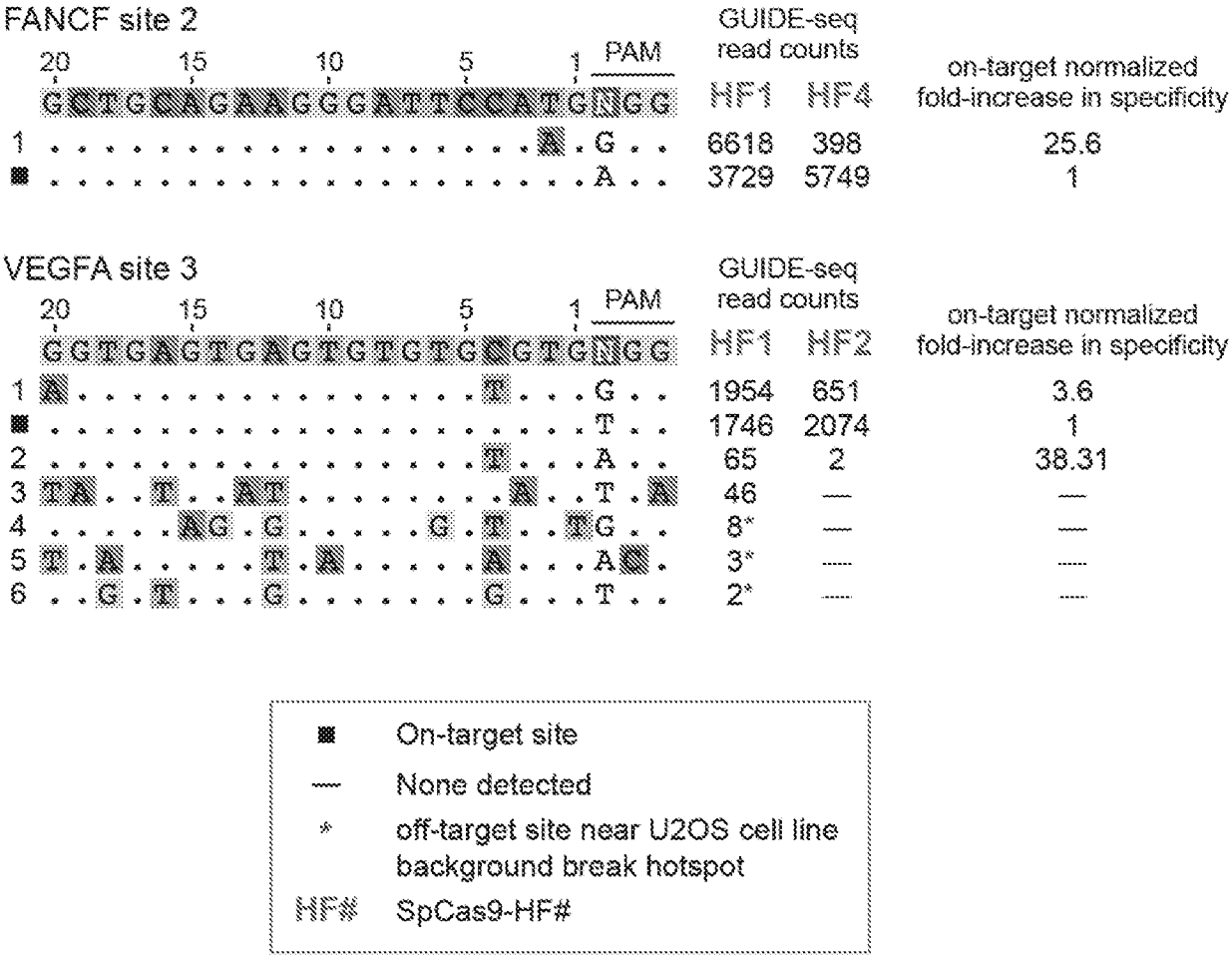

FANCF site 2
20 15 10 5 1 PAM
GCTGCAGAAGGGATTCCATGNGG
GUIDE-seq read counts
HF1 HF4
on-target normalized fold-increase in specificity
1 6618 398 25.6
■ 3729 5749 1
VEGFA site 3
20 15 10 5 1 PAM
GGTGAGTGAGTGTGTGCGTGNGG
GUIDE-seq read counts
HF1 HF2
on-target normalized fold-increase in specificity
1 1954 651 3.6
■ 1746 2074 1
2 65 2 38.31
3 46 — —
4 8* — —
5 3* — —
6 2* — —
■ On-target site
— None detected
* off-target site near U2OS cell line background break hotspot
HF# SpCas9-HF#

FIG. 5F

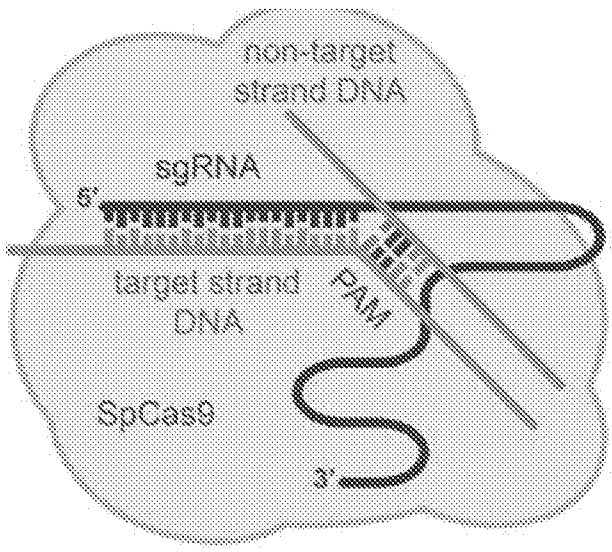

non-target strand DNA
sgRNA
5'
target strand DNA
PAM
SpCas9
3'

FIG. 6A

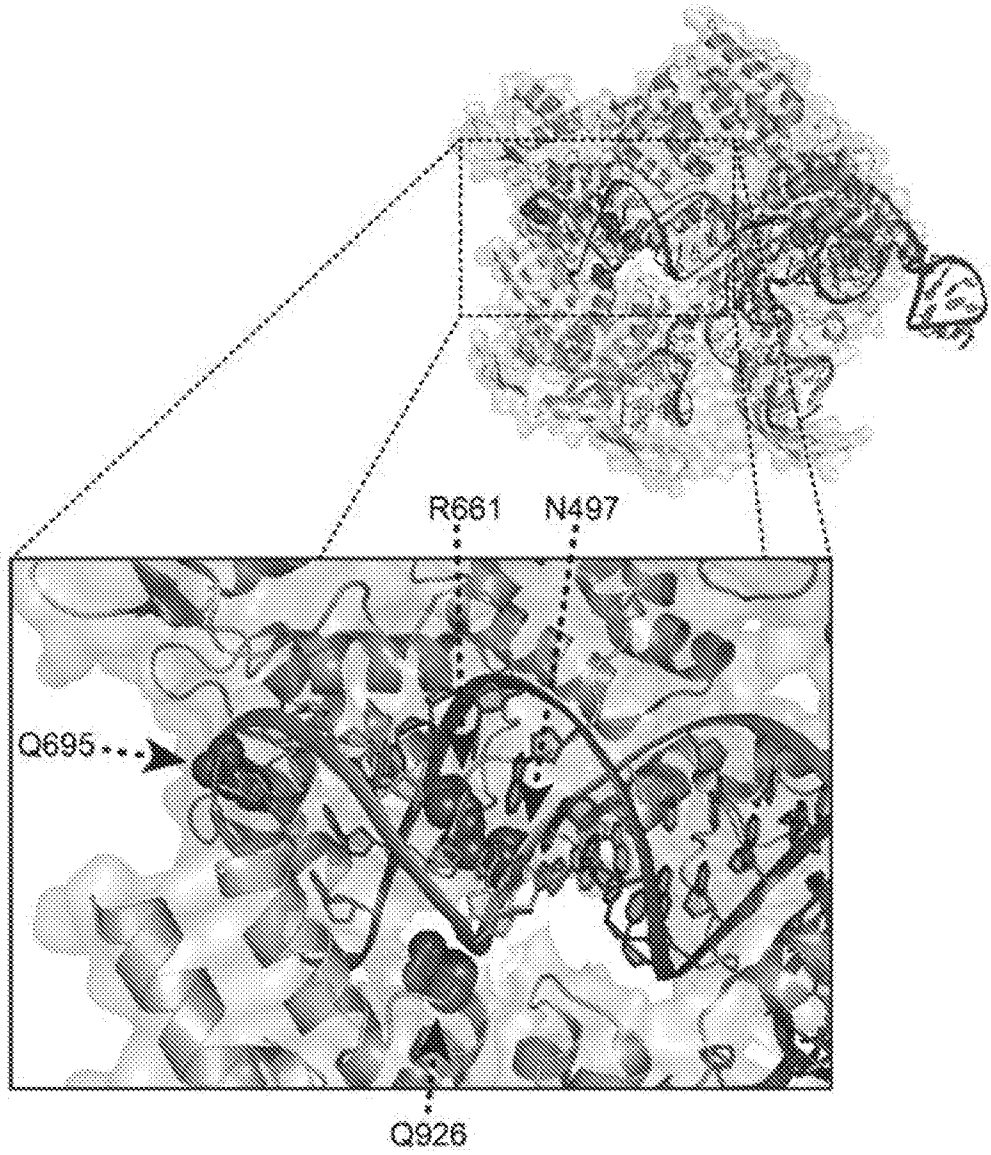


FIG. 6B

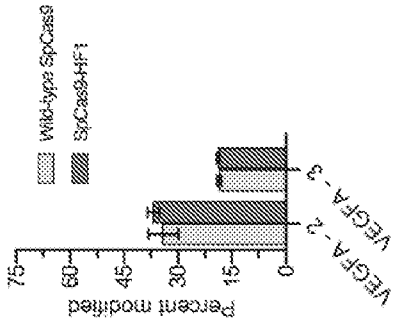


FIG. 7D

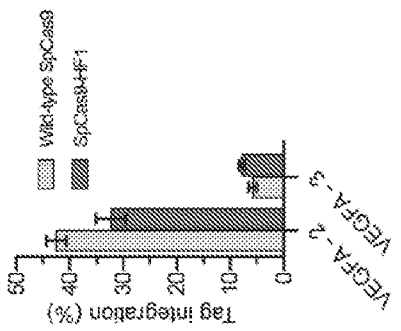


FIG. 7C

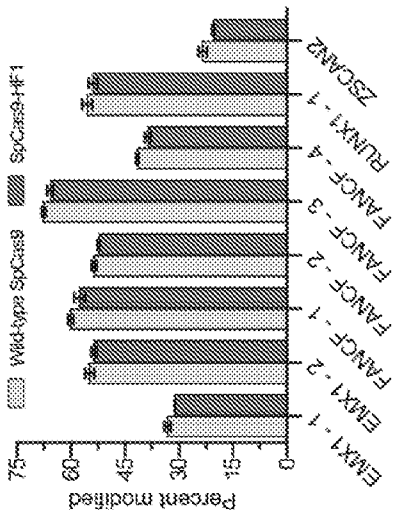


FIG. 7B

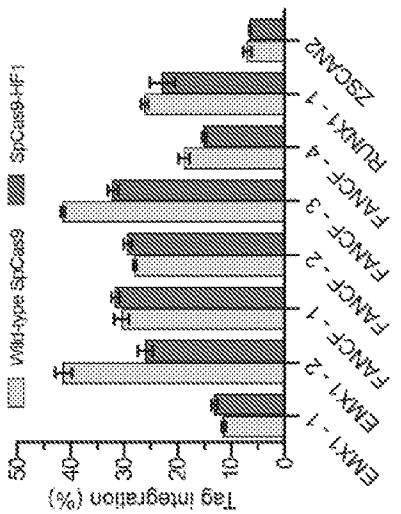


FIG. 7A

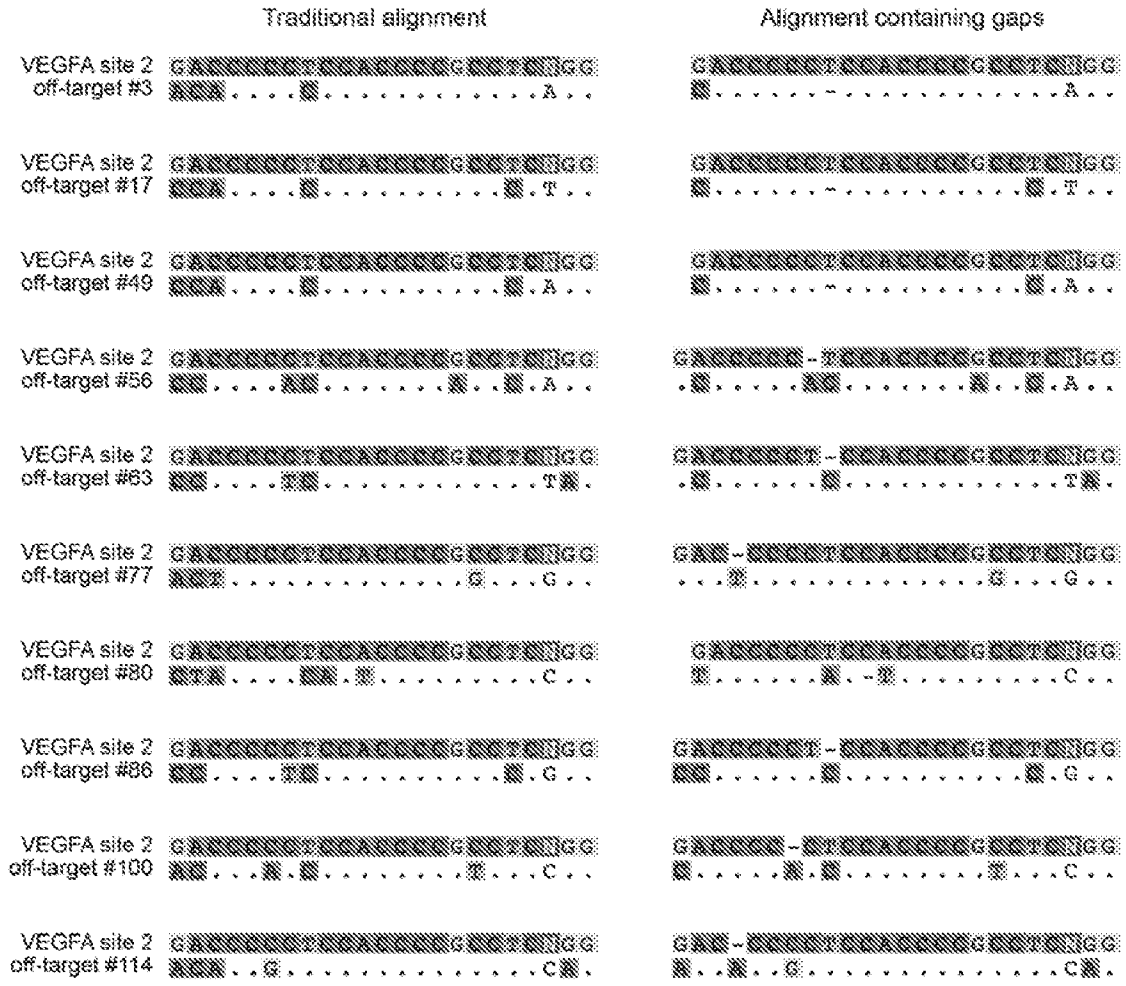

Traditional alignment
Alignment containing gaps
VEGFA site 2 off-target #3
VEGFA site 2 off-target #17
VEGFA site 2 off-target #49
VEGFA site 2 off-target #56
VEGFA site 2 off-target #63
VEGFA site 2 off-target #77
VEGFA site 2 off-target #80
VEGFA site 2 off-target #86
VEGFA site 2 off-target #100
VEGFA site 2 off-target #114

FIG. 8

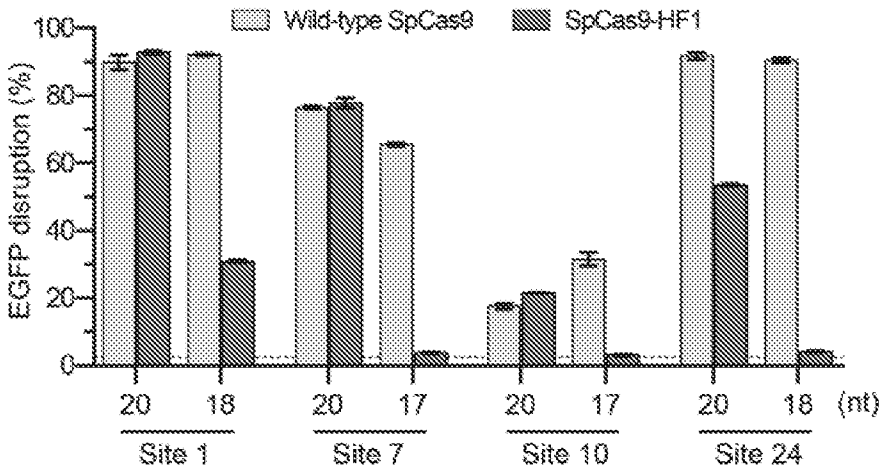

Wild-type SpCas9
SpCas9-HF1
EGFP disruption (%)
100
80
60
40
20
0
20
18
20
17
20
17
20
18
(nt)
Site 1
Site 7
Site 10
Site 24

FIG. 9

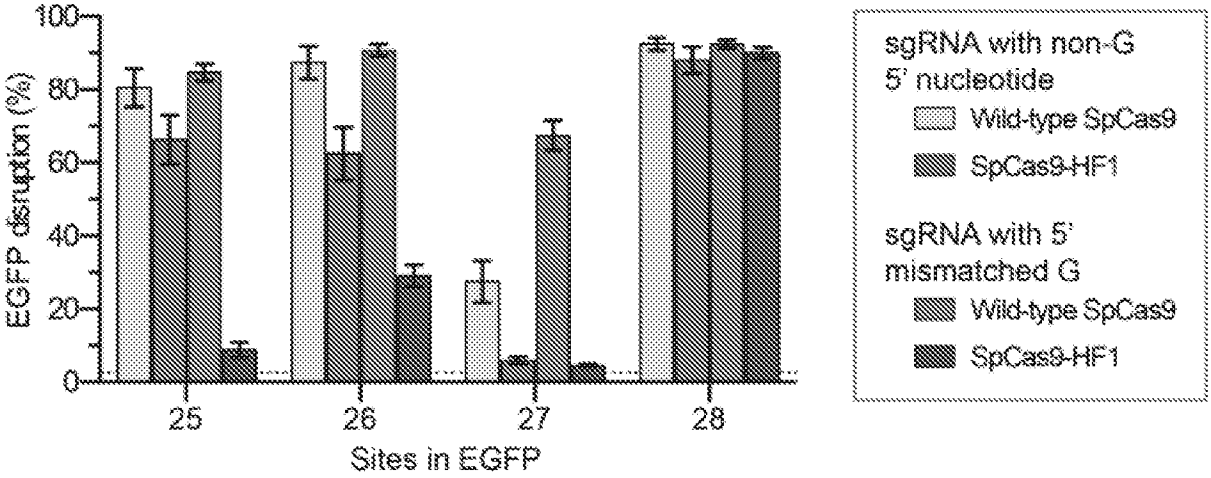


FIG. 10

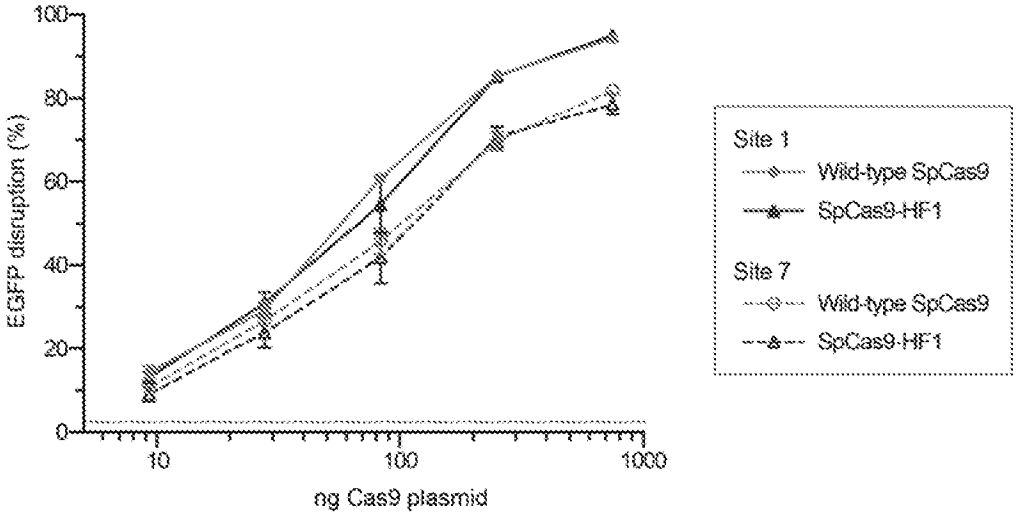


FIG. 11

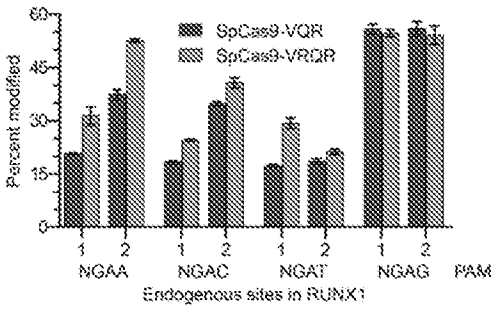


FIG. 12A

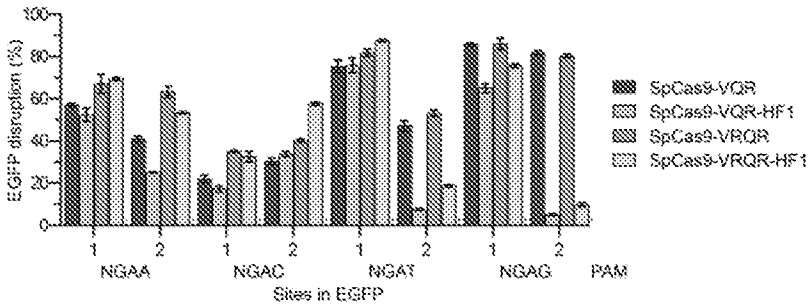


FIG. 12B

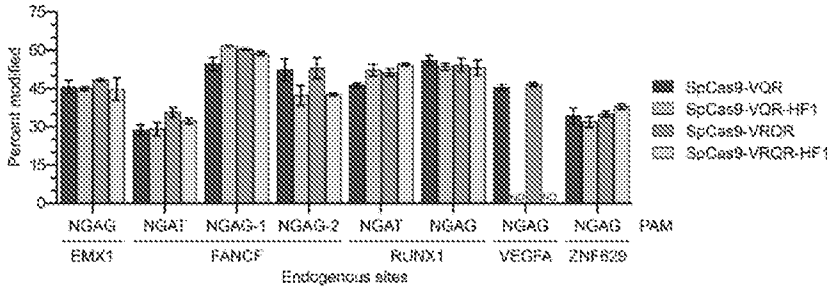


FIG. 12C

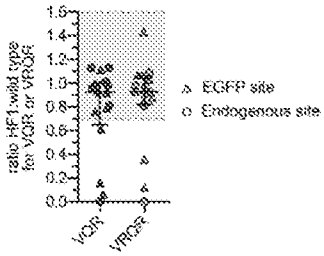
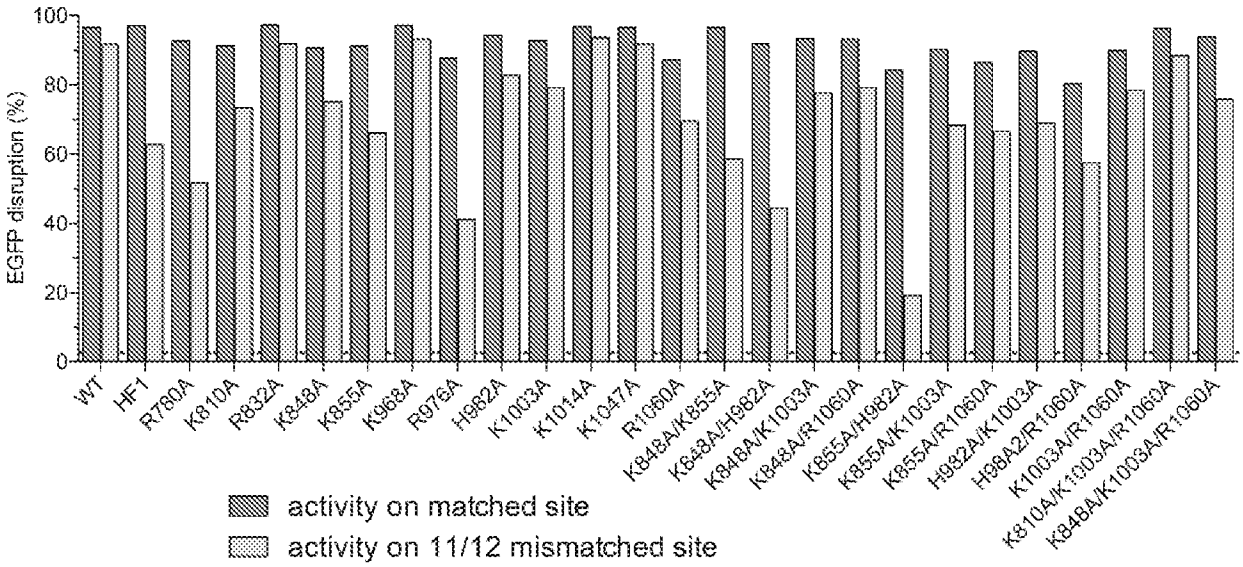


FIG. 12D

FIG. 13A



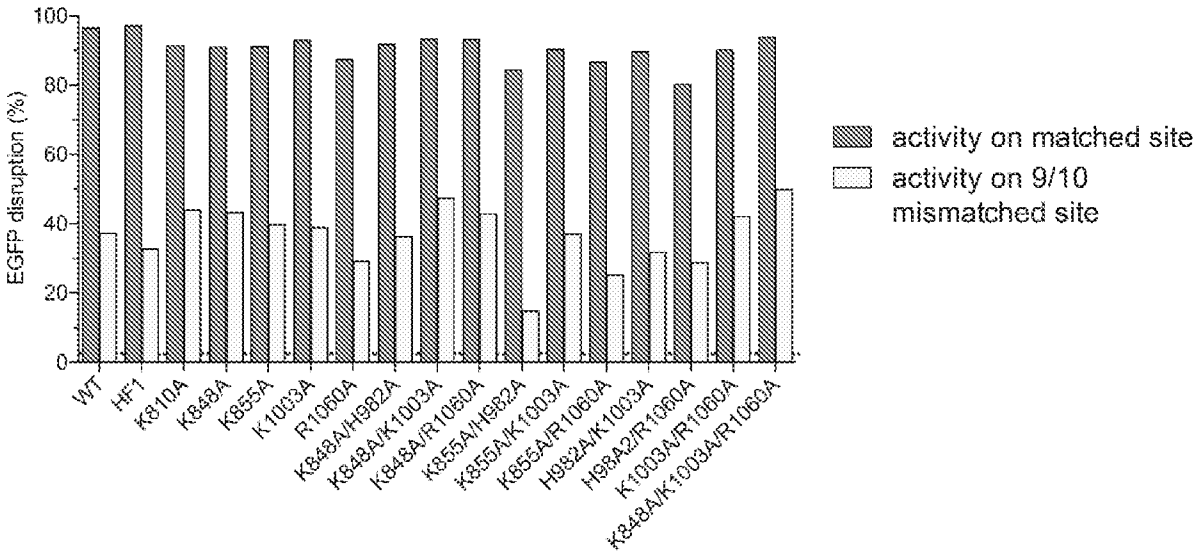
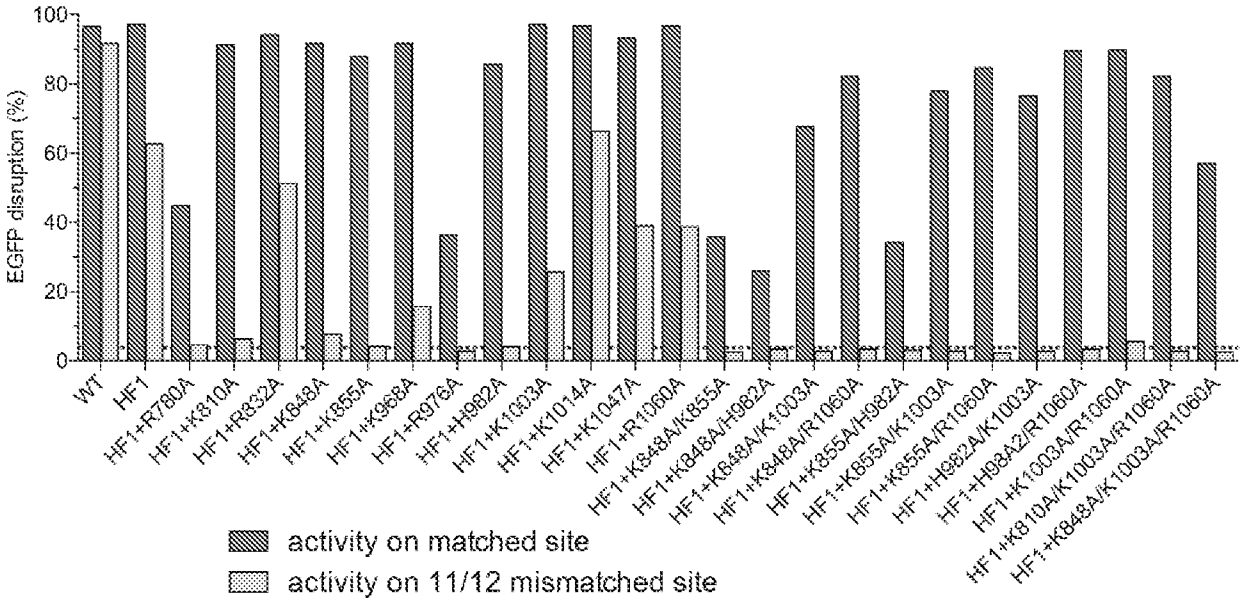


FIG. 13B

FIG. 14A



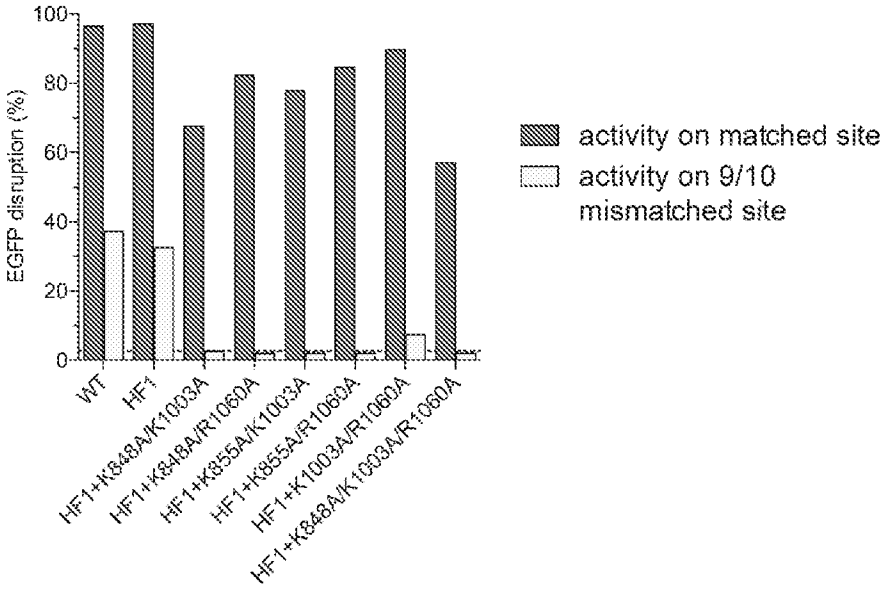


FIG. 14B

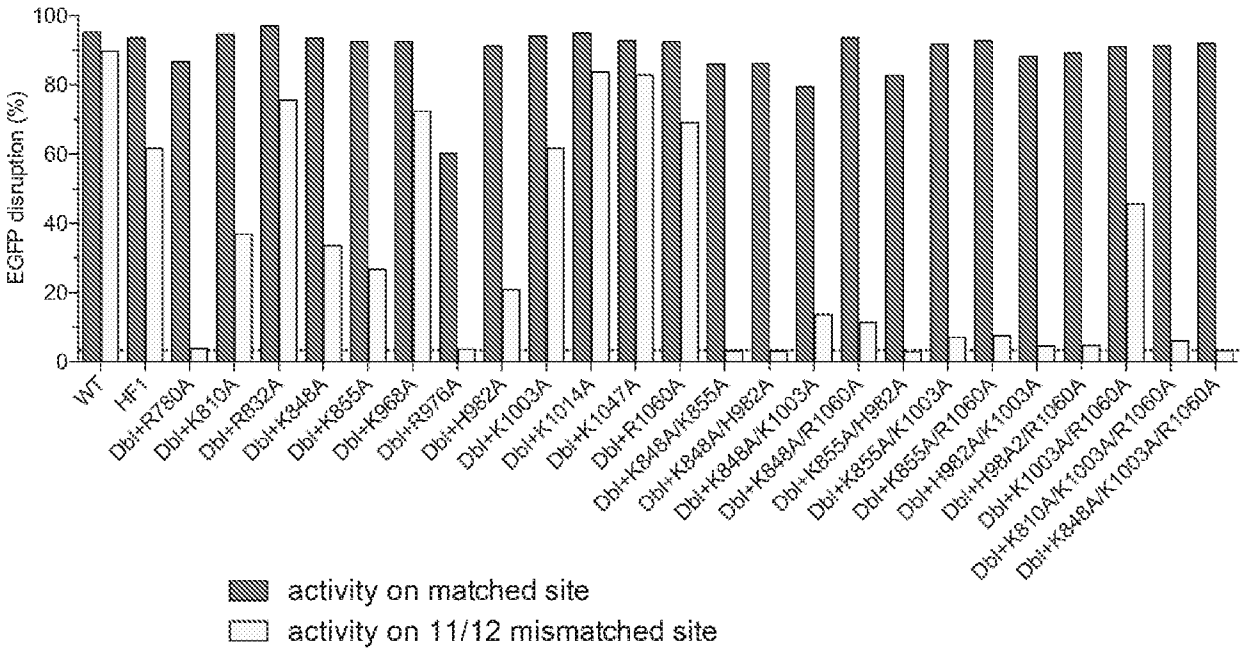

EGFP disruption (%)
100
80
60
40
20
0
WT
HF1
Dbl+R780A
Dbl+K810A
Dbl+R832A
Dbl+K948A
Dbl+K855A
Dbl+K968A
Dbl+R976A
Dbl+H982A
Dbl+K1003A
Dbl+K1014A
Dbl+K1047A
Dbl+R1060A
Dbl+K848A/K855A
Dbl+K848A/H982A
Dbl+K848A/K1003A
Dbl+K848A/R1060A
Dbl+K855A/H982A
Dbl+K855A/K1003A
Dbl+K855A/R1060A
Dbl+H982A/K1003A
Dbl+H982A2/R1060A
Dbl+K1003A/R1060A
Dbl+K810A/K1003A/R1060A
Dbl+K848A/K1003A/R1060A
activity on matched site
activity on 11/12 mismatched site

FIG. 15

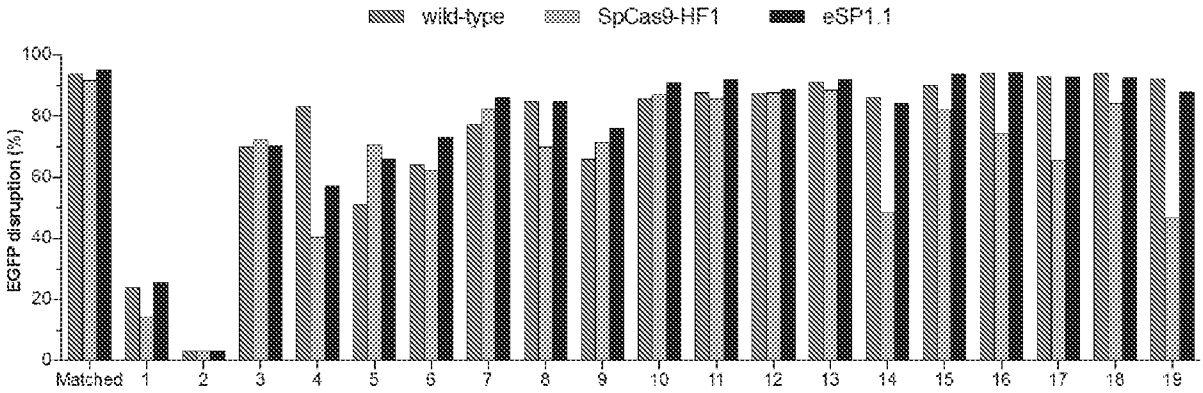

wild-type
SpCas9-HF1
eSP1.1
EGFP disruption (%)
100
80
60
40
20
0
Matched
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19

FIG. 16

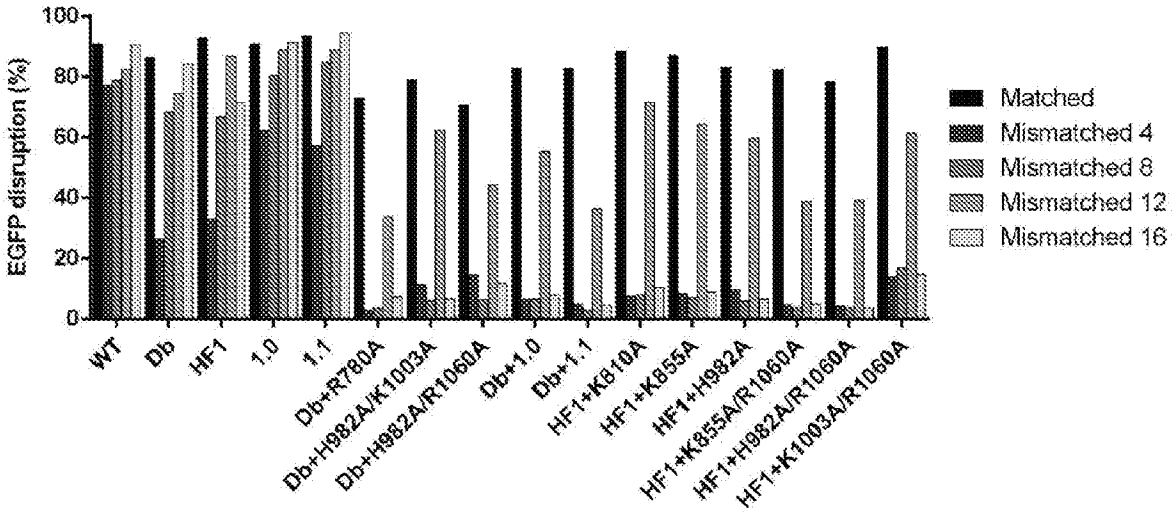


FIG. 17A

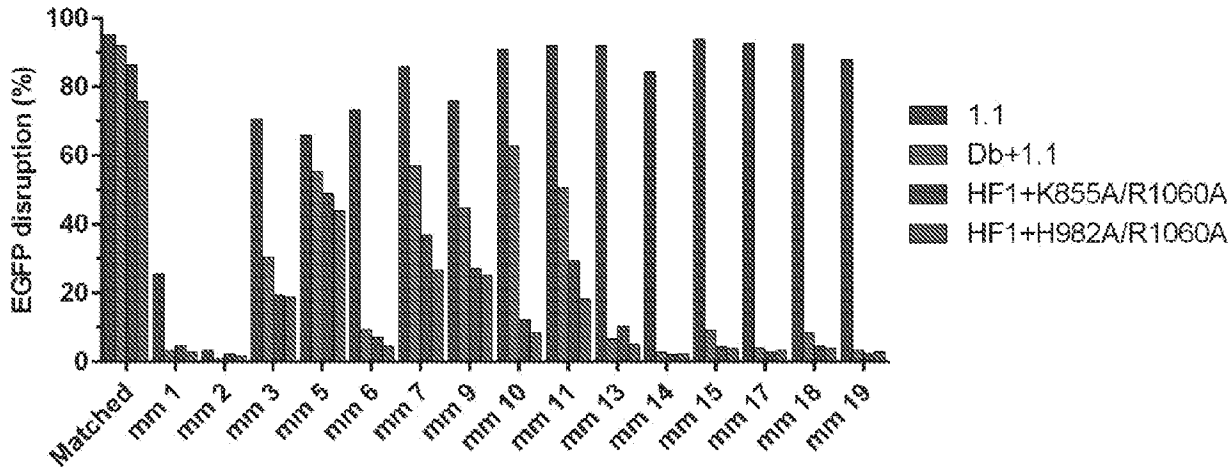


FIG. 17B

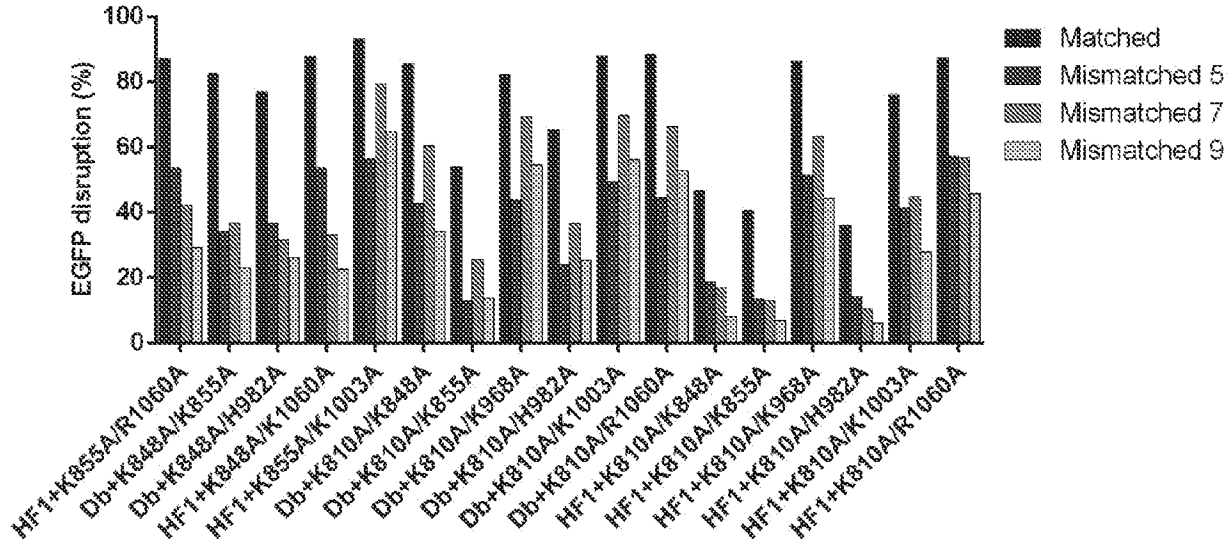


FIG. 18

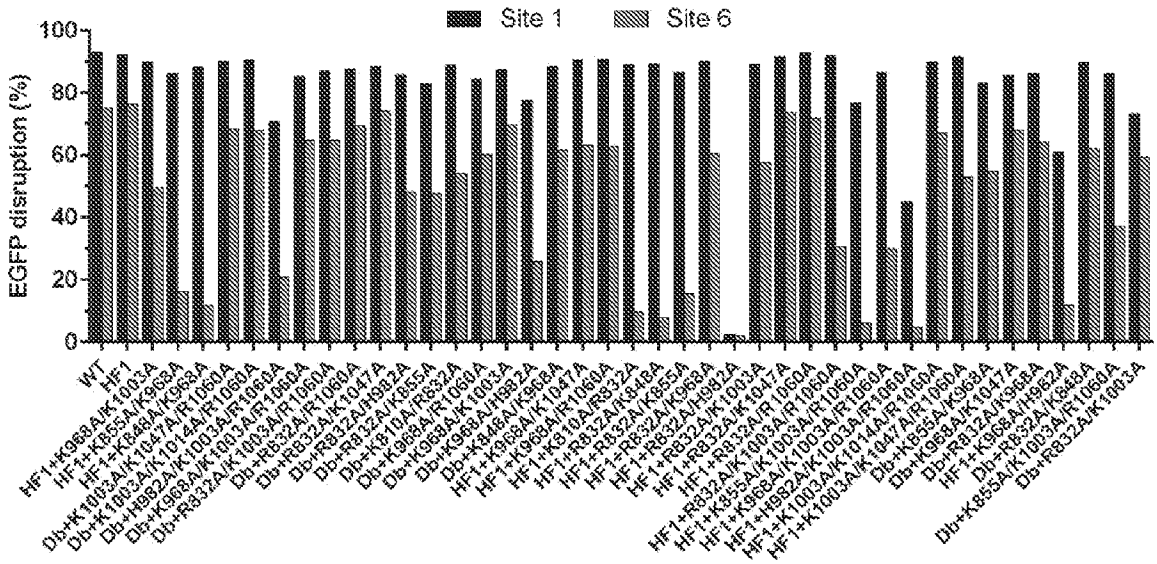


FIG. 19A

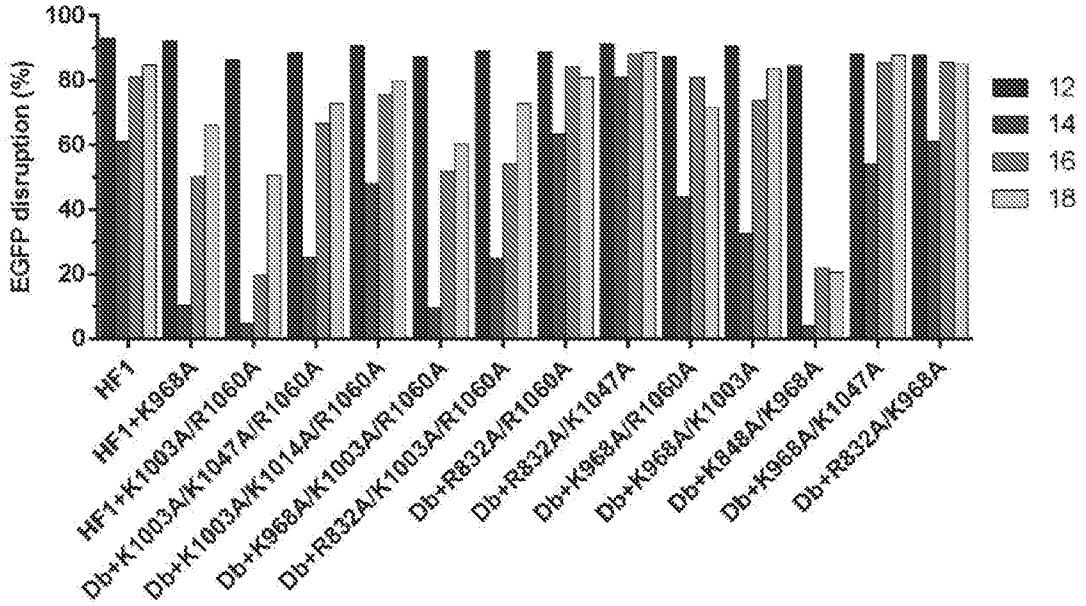

EGFP disruption (%)
100
80
60
40
20
0
12
14
16
18
HF1
HF1+K968A
HF1+K1003A/R1060A
Db+K1003A/K1047A/R1060A
Db+K1003A/K1014A/R1060A
Db+K968A/K1003A/R1060A
Db+R832A/K1003A/R1060A
Db+R832A/R1060A
Db+R832A/K1047A
Db+K968A/R1060A
Db+K968A/K1003A
Db+K848A/K968A
Db+K968A/K1047A
Db+R832A/K968A

FIG. 19B

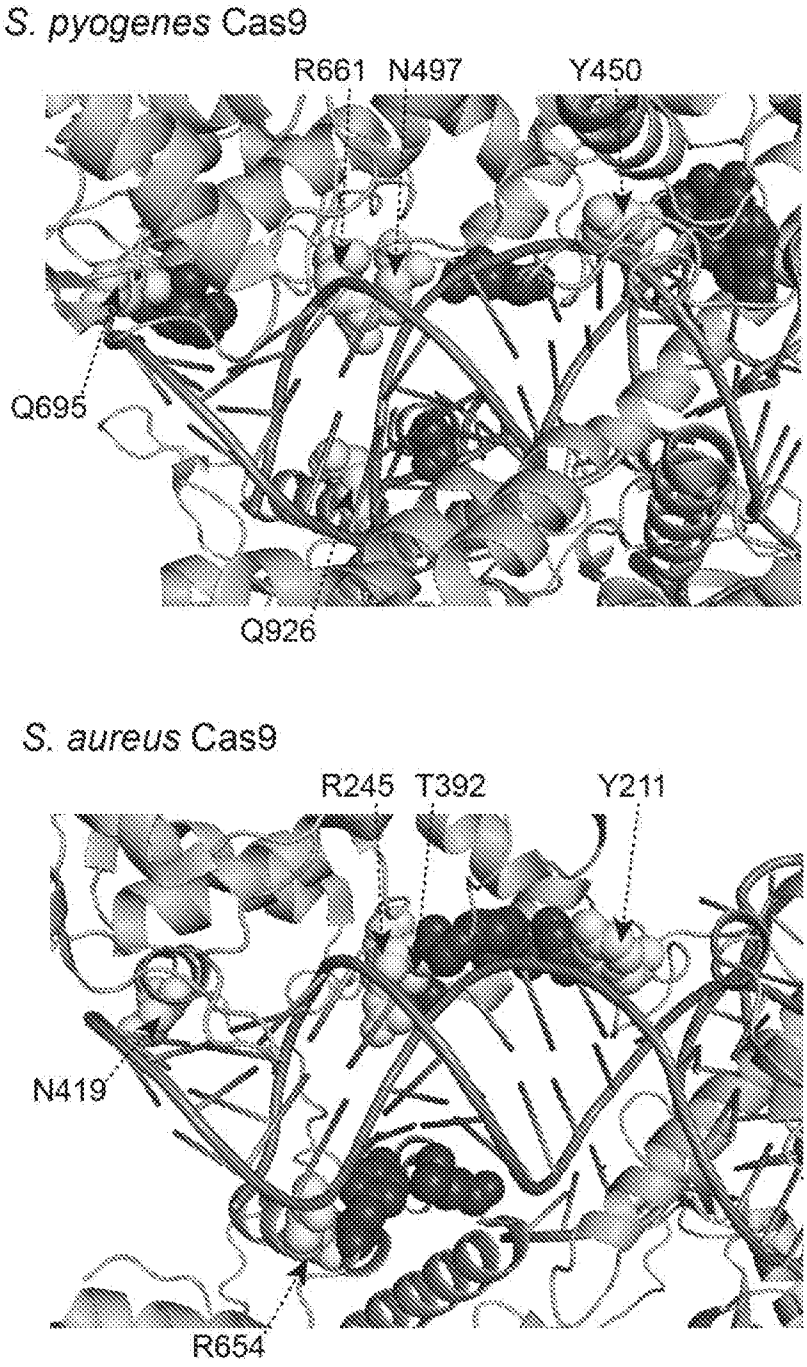

S. pyogenes Cas9
R661
N497
Y450
Q695
Q926
S. aureus Cas9
R245
T392
Y211
N419
R654

FIG. 20

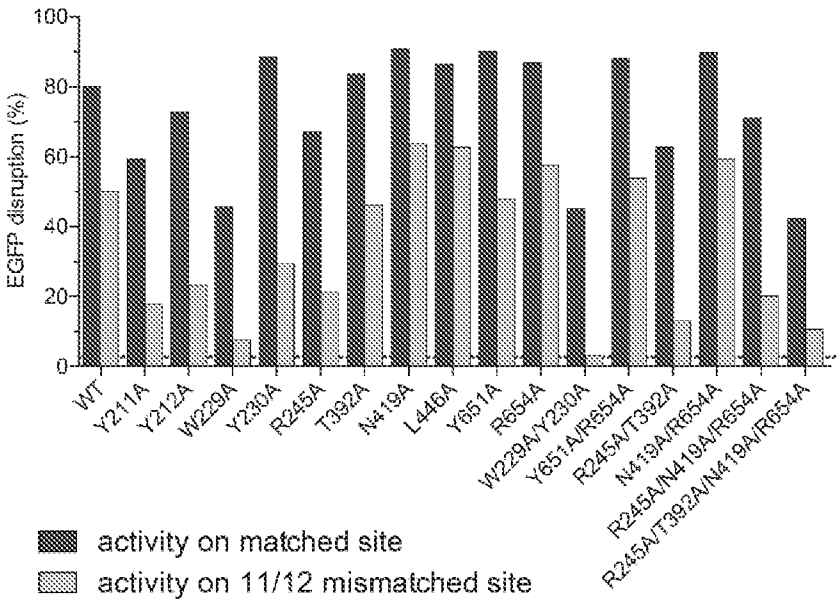


FIG. 21A

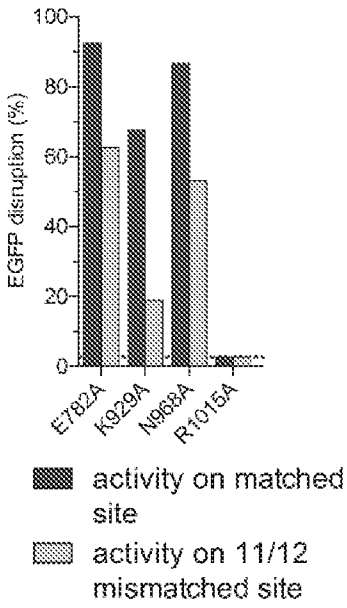


FIG. 21B

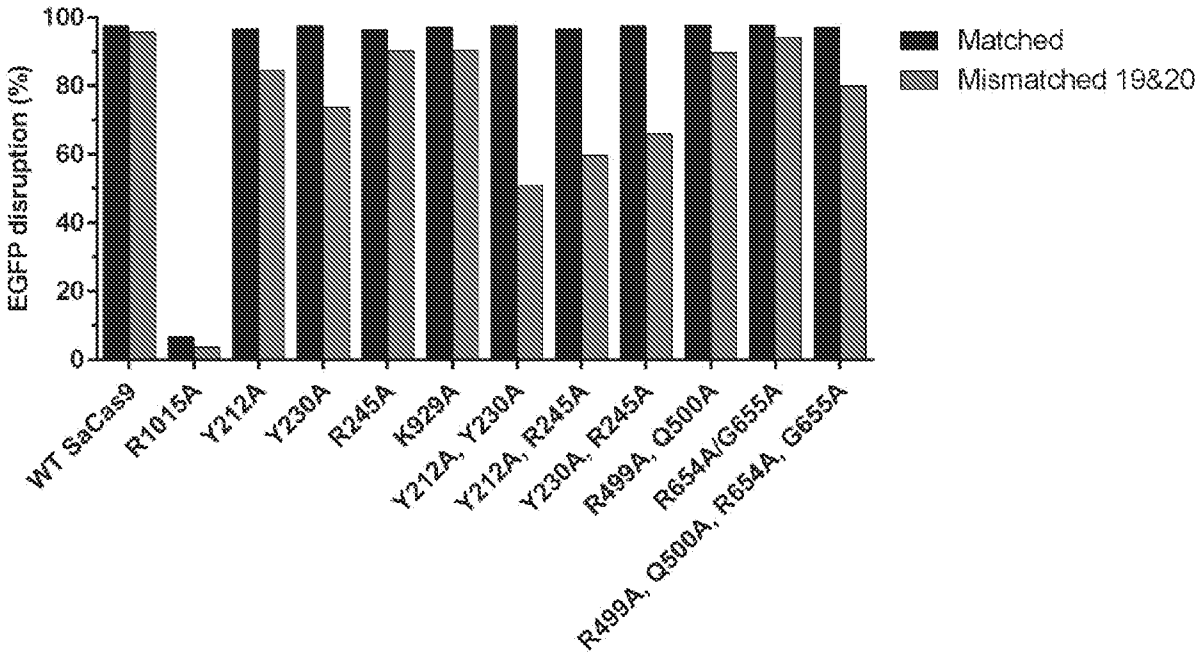


FIG. 22A

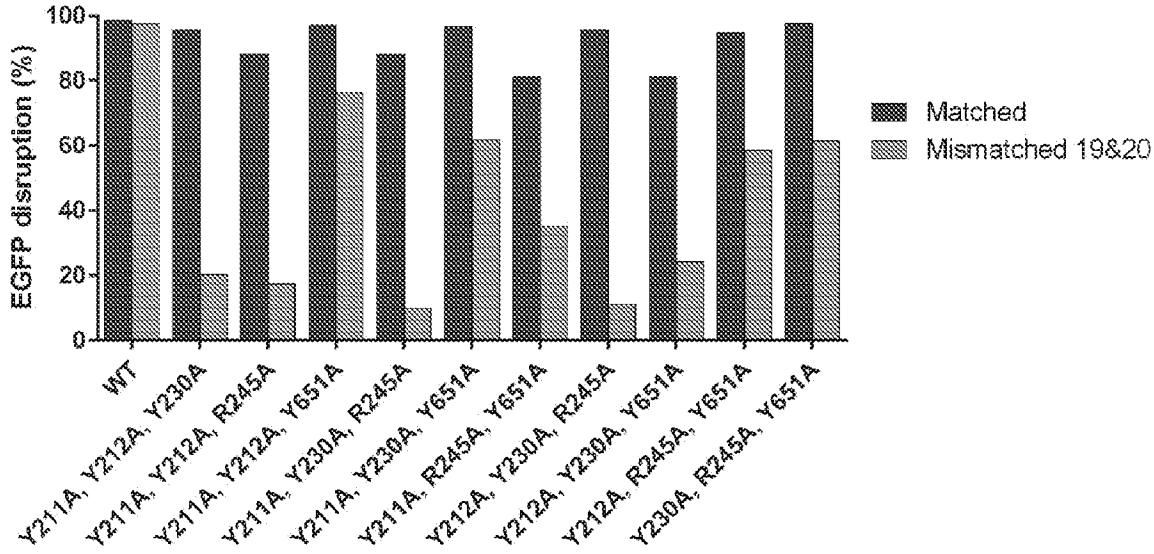


FIG. 22B

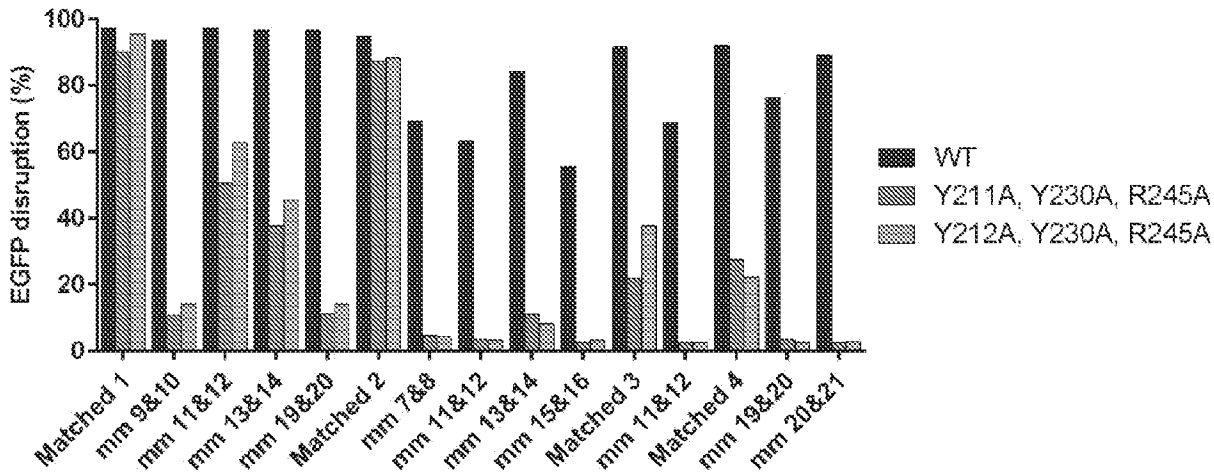


FIG. 23

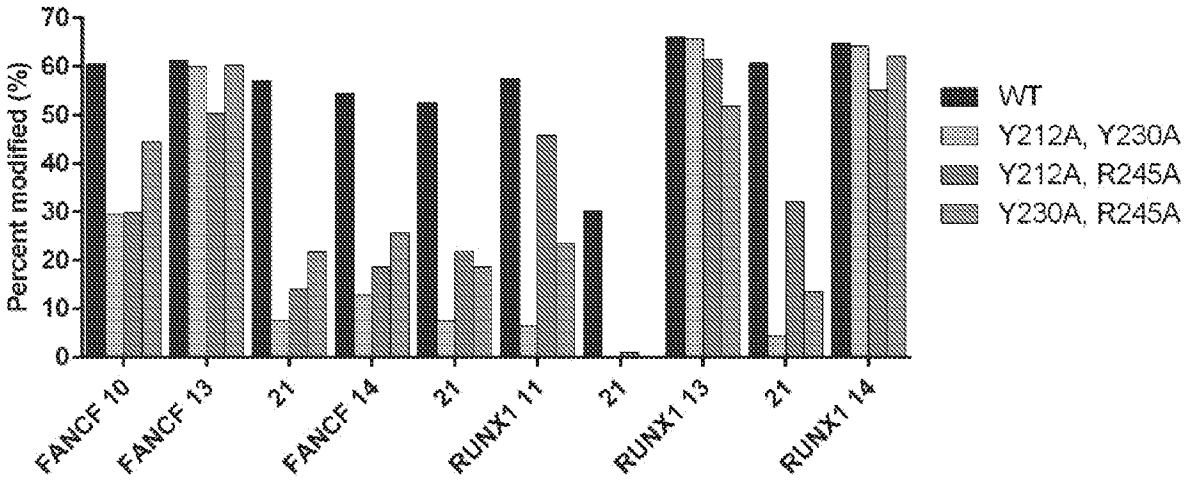


FIG. 24A

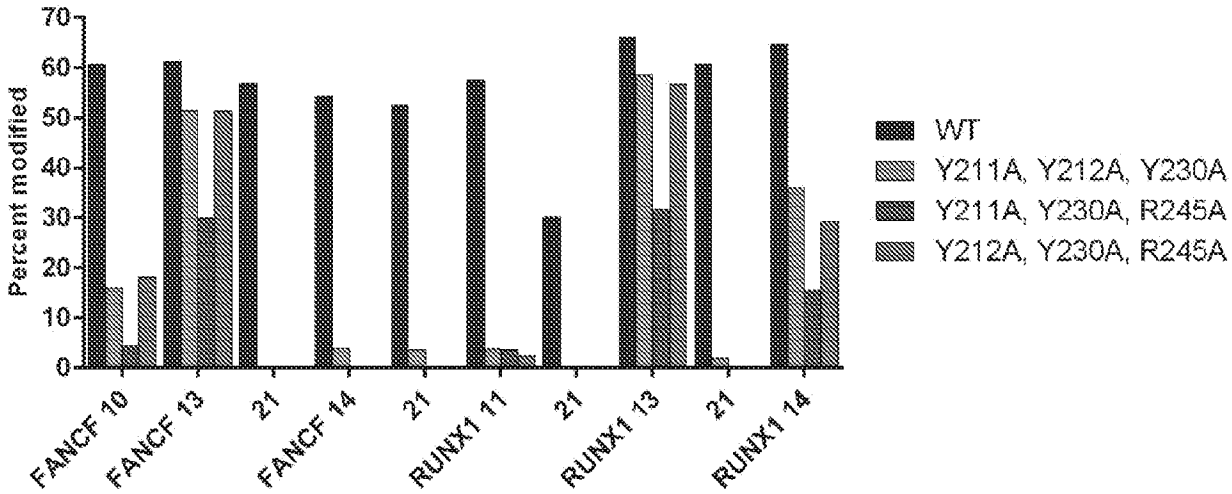


FIG. 24B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/49147

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C12N 15/00, 15/63, 15/113, 9/22; G06F 19/16 (2016.01)
CPC - C12N 15/63,15/113, 9/22; G06F 19/16
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8): C12N 15/87, 15/63,15/113, 9/22; G06F 19/16 (2016.01)
CPC: C12N 15/63,15/113, 9/22; G06F 19/16

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC: C12N 15/63,15/113, 9/22; G06F 19/16
USPC: 435/455, 375, 320.1, 195; 536/23.2, 23.7

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Electronic data bases: PatBase; Google Patents; Google Scholar
Search terms: Streptococcus pyogenes Cas9 (SpCas9), protein engineering, mutation or substitution or variant (e.g., L169*, Y450*, N497*, R661*, Q695*, Q926*, D1135*), genome engineering, genome targeting or editing, Staphylococcus aureus Cas9 (SaCas9)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2014/0068797 A1 (DOUDNA et al.) 06 March 2014 (06.03.2014) Especially SEQ ID NO: 2	1
A	KLEINSTIVER et al. Engineered CRISPR-Cas9 nucleases with altered PAM specificities. NATURE 23 July 2015 Vol 523 No 7561 Pages 481-485. Available as NCBI PMC Author Manuscript. Especially pg 2 paras 2,3 ; pg 4 paras 1, 4	1
A	WO 2015/089364 A1 (The Broad Institute, Inc.) 18 June 2015 (18.06.2015). Especially para [0069].	1
X,P	Kleinstiver et al. High-fidelity CRISPR-Cas9 nucleases with no detectable genome-wide off-target effects. Nature 28 January 2016 Vol 529 No 7587 Pages 490-495. Available as NCBI PMC Author Manuscript. Especially pg 5 para 2, pg 24 fig 5.	1
X,P	WO 2016/115355 A1 (Temple University of the Commonwealth System of Higher Education) 21 June 2016 (21.06.2016). Especially pg 3 ln 15-20, claim 3.	1

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 October 2016	23 DEC 2016
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer: Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/49147

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:
GenCore ver 6.4.1 SEQ ID NO: 1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/49147

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 15-43
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
-----Go to Extra Sheet for continuation-----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Claim 1 limited to SpCas9 with mutated L169.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 16/49147

------continuation of Box III (Lack of Unity of Invention)------

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I+: Claims 1-14, drawn to an isolated Cas9 protein having at least one amino acid substitution/mutation.
The Cas9 protein will be searched to the extent that it encompasses the first name species, Streptococcus pyogenes (claim 1) (SpCas9) comprising the first named mutation at L169 (claim 1). It is believed that claim 1 reads on this first named invention and thus this claim will be searched without fee to the extent that it encompass SpCas9 with mutated L169. Additional Cas9 proteins comprising one or more mutations will be searched upon payment of additional fees. Applicant must specify the claims that encompass any additional elected Cas9 proteins and mutations. Applicants must further indicate, if applicable, the claims which read on the first named invention if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined. An exemplary election would be: Staphylococcus aureus Cas9 (SaCas9) with mutation at W229 (claims 8, 9).

The inventions listed as Group I+ do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features:

The inventions of Group I+ each include the special technical feature of a Cas9 protein comprising amino acid substituions or mutations, recited therein. Each amino acid substitution is considered a distinct technical feature, because the changes in the structure-activity relationship induced by said amino acid substitution cannot readily be ascertained among these amino acid substitutions

Common Technical Feature:

Group I+: claims share the common technical feature of claims 1 and 8.

However, said common technical features do not represent a contribution over the prior art, and is obvious over the publication titled "Engineered CRISPR-Cas9 nucleases with altered PAM specificities" by KLEINSTIVER et al. (hereinafter "Kleinstiver") [published 23 July 2015 in Nature Vol 523 No 7561 Pages 481-485], in view of WO 2015/089364 A1 to The Broad Institute, Inc. (hereinafter "Broad Institute")[published 18 June 2015], and US 2014/0068797 A1 to DOUDNA et al. (hereinafter "Doudna").

As to claim 1, Kleinstiver teaches an isolated Streptococcus pyogenes Cas9 (SpCas9) protein, with mutations at one, two, three, four, five, six, or all seven of the following positions: LI69, Y450, N497, R661, Q695, Q926, and/or DI135 (abstract; "Here we show that the commonly used Streptococcus pyogenes Cas9 (SpCas9) can be modified to recognize alternative PAM sequences using structural information, bacterial selection-based directed evolution, and combinatorial design"; pg 2 para 4; To identify such mutations, we adapted a bacterial selection system (hereafter referred to as the positive selection) previously used to study properties of homing endonucleases. In our adaptation of this system, survival is enabled by Cas9-mediated cleavage of a selection plasmid encoding an inducible toxic gene.....Sequences of surviving clones from both libraries revealed the most frequent substitutions were D1135V/Y/N/E").

As to claim 8, Broad Institute teaches isolated Staphylococcus aureus Cas9 (SaCas9) protein, with mutations at one, two, three, four, five, six, or more positions (para [0069];" In an aspect the invention provides as to any or each or all embodiments herein-discussed wherein the CRISPR enzyme comprises at least one or more, or at least two or more mutations, wherein the at least one or more mutation.....N580 according to SaCas9 [i.e. Staphylococcus aureus Cas9], e.g., N580A as to SaCas9").

As to SEQ ID NO: 1, the sequence was well-known in the art to be the commonly isolated Streptococcus pyogenes Cas9 (SpCas9), as taught by Doudna (SEQ ID NO: 2; 1368 AA 100% sequence identity).

As the common technical features were known in the art at the time of the invention, they cannot be considered common special technical features that would otherwise unify the groups. The inventions lack unity with one another.

Therefore, Group I+ lack unity of invention under PCT Rule 13 because they do not share a same or corresponding special technical feature.

Note concerning item 4: Claims 15-43 are multiple dependent claims and are not drafted according to the second and third sentences of PCT Rule 6.4(a).