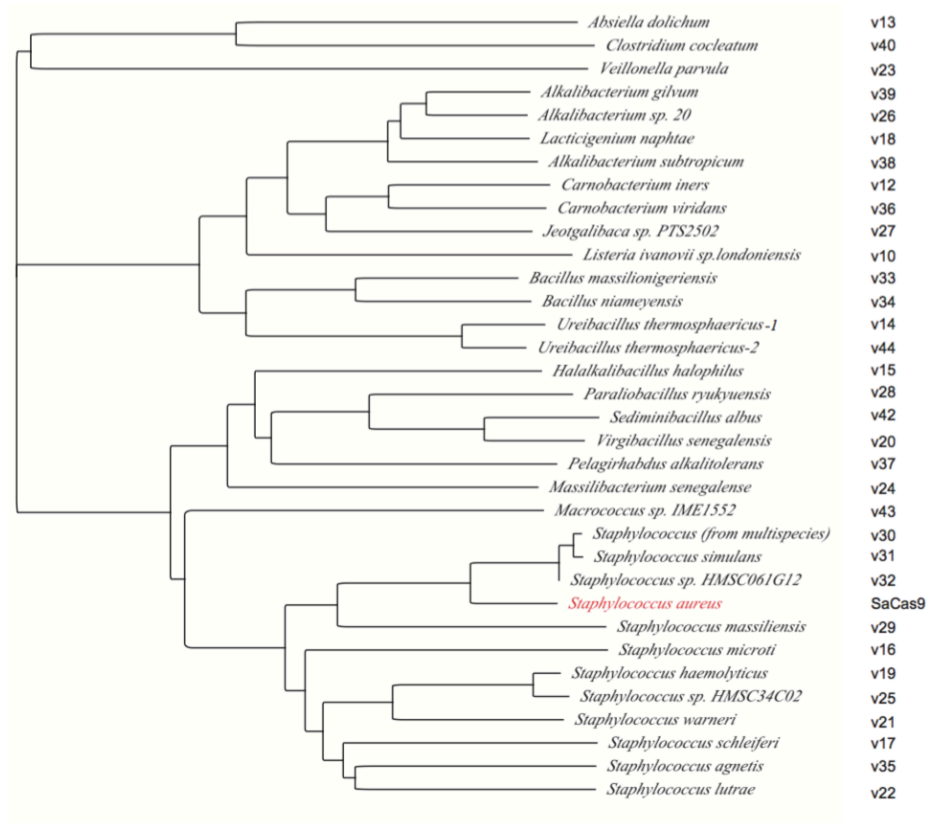


Engineer chimeric Cas9 to expand PAM recognition based on evolutionary information
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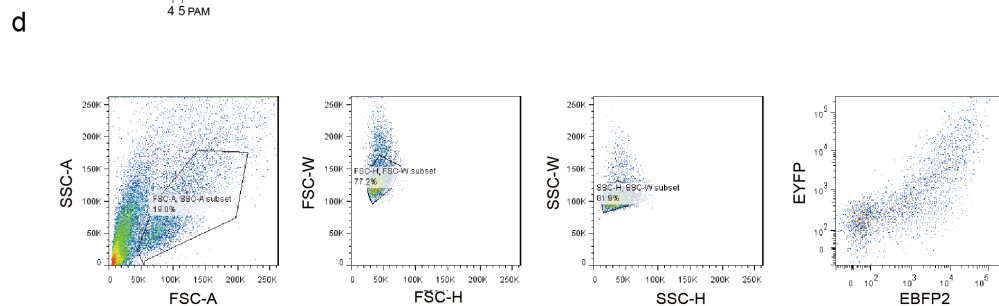
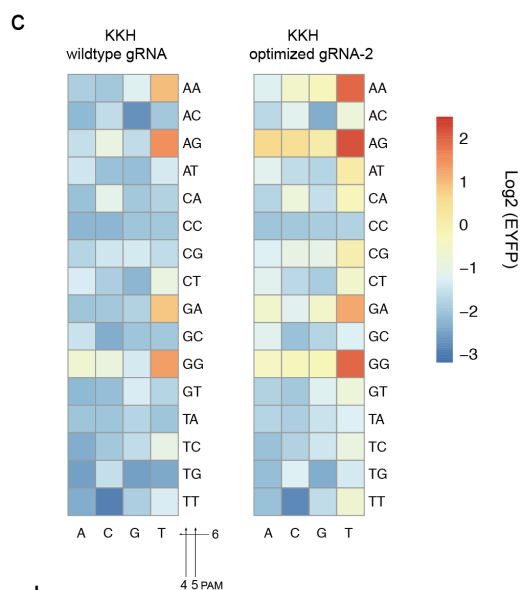
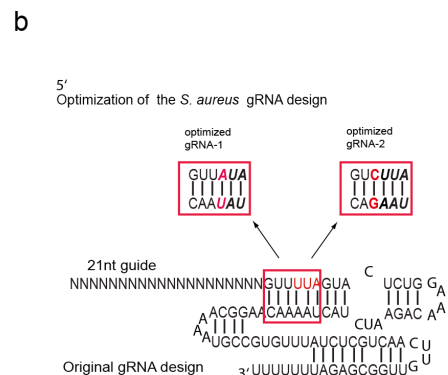
Supplementary Information

Supplementary Figures



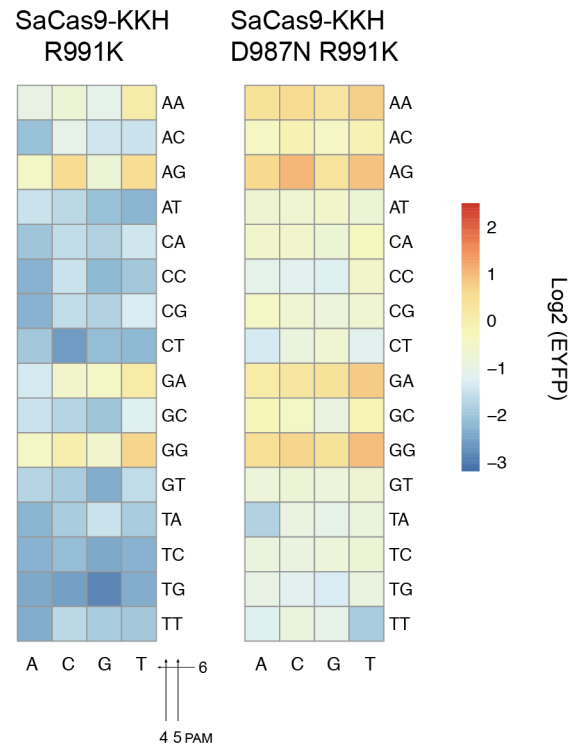
Supplementary Figure 1 | Phylogenetic tree of Cas9 orthologs.

The species names and numbers of the corresponding chimeric variants are listed. The phylogenetic tree was constructed by using Software Geneious R8.



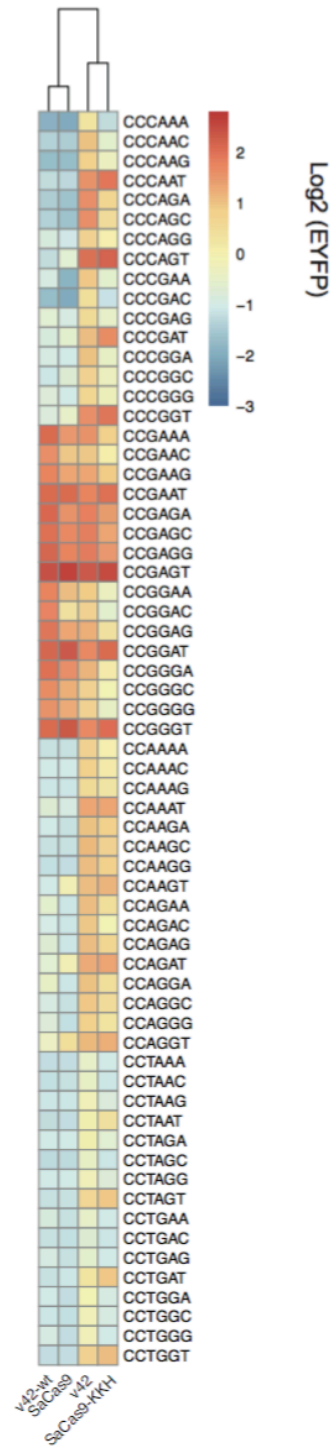
Supplementary Figure 2 | Optimization of gRNA scaffold for SaCas9 and its variants.

a. Sequence alignment of crRNA direct repeats in the corresponding species genome. **b.** The wildtype and two optimized gRNA scaffolds for SaCas9 variants. The optimized gRNA-1 was developed previously^{1,2}. **c.** Cleavage activities of SaCas9-KKH (KKH) at CCCNNN PAMs with the wildtype gRNA scaffold or the optimized gRNA-2 scaffold were evaluated. **d.** Illustration of gates strategy of EYFP reconstitution assay. **e.** Comparison of SaCas9 and SaCas9-KKH with the wildtype gRNA or optimized gRNA-2 at sites with CCCRRN and CCGRRN PAMs. **c.** and **e.** Experiments were performed by using the EYFP reconstitution assay 3 days after transfection into HEK293FT cells. Data indicated the mean of three independent biological replicates. Source data are provided as a Source Data file.



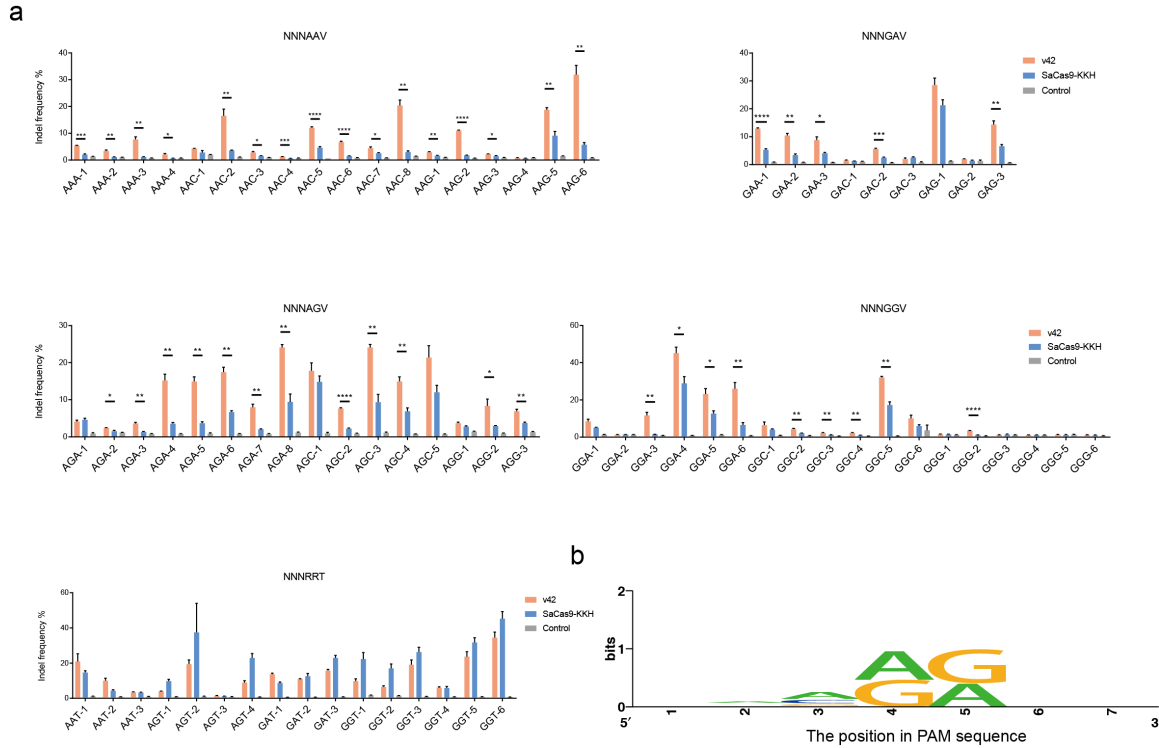
Supplementary Figure 3 | PAM preference of SaCas9-KKH based variants.

Cleavage activities of SaCas9-KKH with the R991K mutation and SaCas9-KKH with D987N and R991K double mutations at CCRRN PAMs by using the EYFP reconstitution assay (n=1). Source data are provided as a Source Data file.



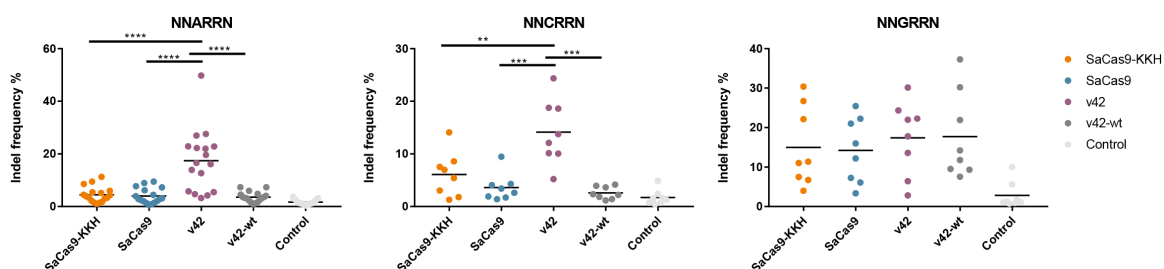
Supplementary Figure 4 | Comparison of variants at CCNRRN PAMs.

Cleavage activities of by SaCas9-KKH, SaCas9, cCas9 v42 and v42-wildtype (v42-wt) at CCNRRN PAMs using the EYFP reconstitution assay. Data represents the mean (n = 3 independent biologic replicates). Source data are provided as a Source Data file.



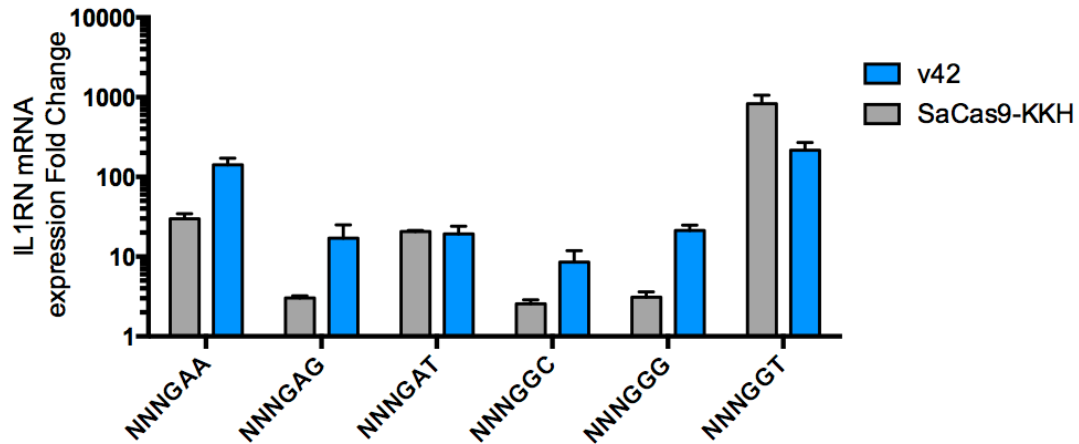
Supplementary Figure 5 | Indel frequency at NNNRRN PAMs.

a. Indel frequencies at sites generated by each gRNA measured by using the next generation sequencing. The information of gRNA sequences and primers used in this figure were listed in Supplementary Table 1. Error bar, s.e.m.; * $p < 0.05$ (paired t-test, two-tailed); ** $p < 0.01$ (paired t-test, two-tailed); *** $p < 0.001$ (paired t-test, two-tailed); **** $p < 0.0001$ (paired t-test, two-tailed). (n = 3 independent biologic replicates). **b.** Sequence logo shows the sequence preference in different PAM positions. The endogenous target sites with more than 5% mutation frequency generated by cCas9 v42 shown in Fig. 2d were used in the sequence logo analysis. Sequence logo was generated by using Web logo³. Source data are provided as a Source Data file.



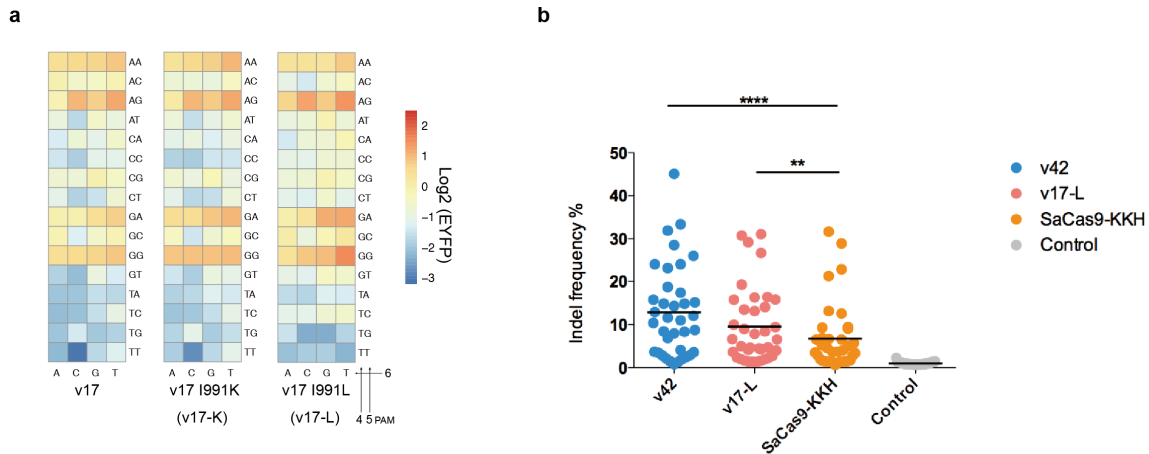
Supplementary Figure 6 | Indel frequency at NNVRN PAMs.

SaCas9, SaCas9-KKH, cCas9 v42 and v42-wildtype (v42-wt) were transfected along with different gRNAs targeting endogenous sites with indicated NNVRN PAMs (V=A, C or G). Indel frequencies were measured by using next generation sequencing as described in Methods. Each point represents the mean of one endogenous site. Black line indicates the mean indel frequency of all of the targets. The mean indel frequency of each endogenous site is listed in Supplementary Table 2. ** $P < 0.01$ (paired t-test, two-tailed); *** $P < 0.001$ (paired t-test, two-tailed); **** $P < 0.0001$ (paired t-test, two-tailed). Source data are provided as a Source Data file.



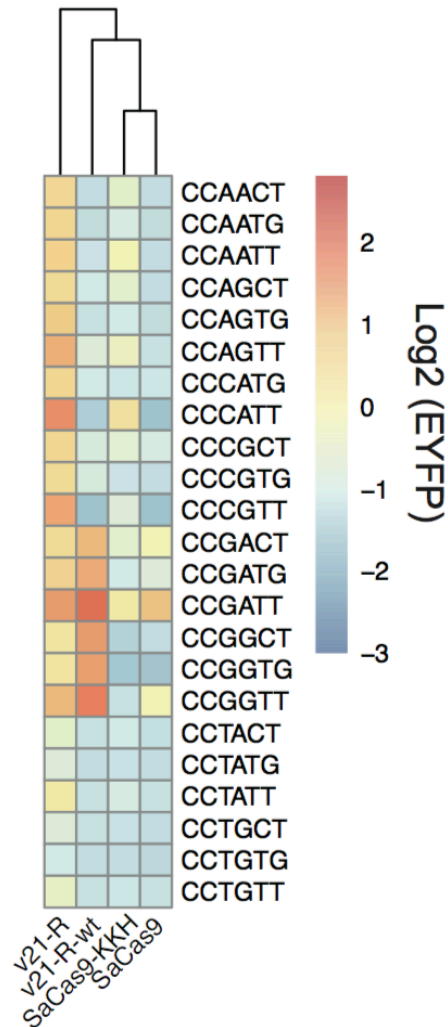
Supplementary Figure 7 | Transactivation efficiency of SaCas9 variants.

The *IL1RN* expression level was assayed using RT-PCR 4 days after transfecting dSaCas9-KKH:VPR or deactivated cCas9-v42:VPR in HEK293FT cells along with the corresponding gRNAs targeting at varying sites with indicated NNNRRN PAMs in the *IL1RN* promoter region. Data indicated the mean $\pm$ s.e.m. (n=2 or 3 independent replicates). Source data are provided as a Source Data file.



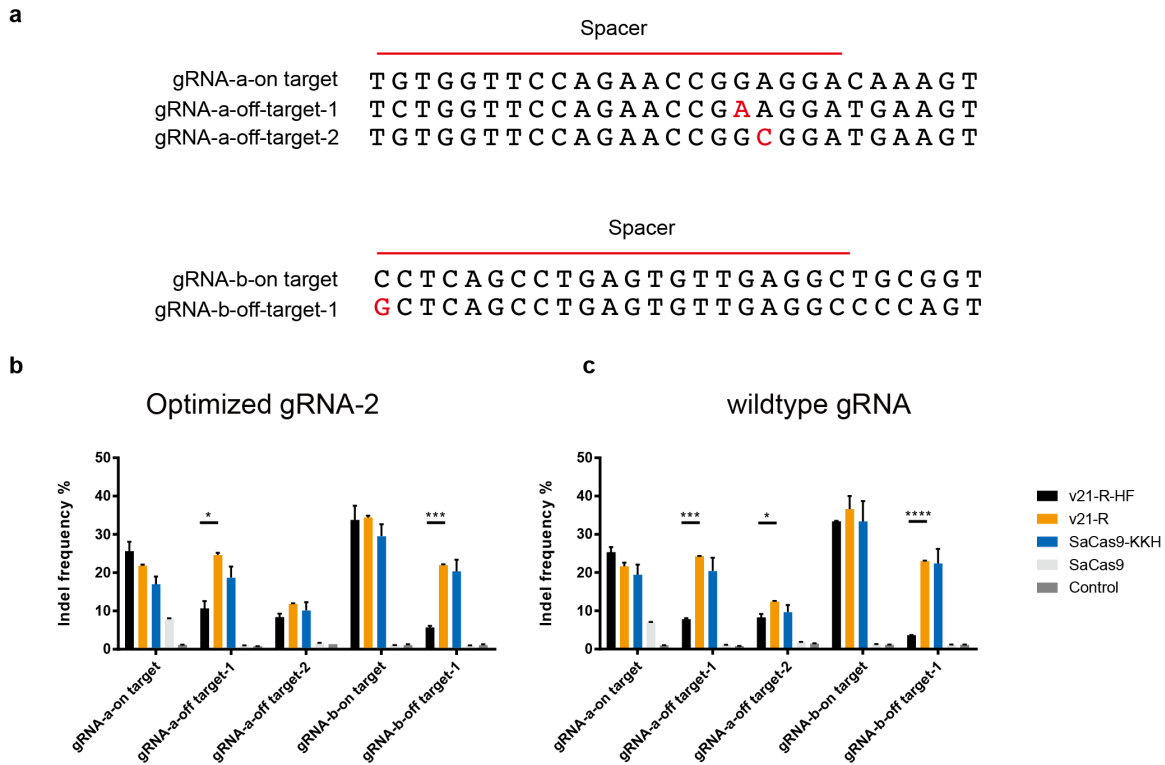
Supplementary Figure 8 | PAM preference of cCas9 v17 variants.

a. Cleavage activities of cCas9 v17, v17 with the I991K mutation (v17-K) and v17 with the I991L mutation (v17-L) at CCCRRN PAMs by using the EYFP reconstitution assay as shown in Fig. 1c (n=1). **b.** Indel frequencies generated by SaCas9-KKH, cCas9 v17-L and v42 at 37 different endogenous target sites with NNNRRV PAMs. Each point represents the mean of three independent biologic replicates targeting at one endogenous site. The black line indicates the mean value of all targets. The mean indel frequency of each endogenous site is listed in Supplementary Table 3. **** P<0.0001 (paired t-test, two-tailed); ** P<0.01 (paired t-test, two-tailed). Source data are provided as a Source Data file.



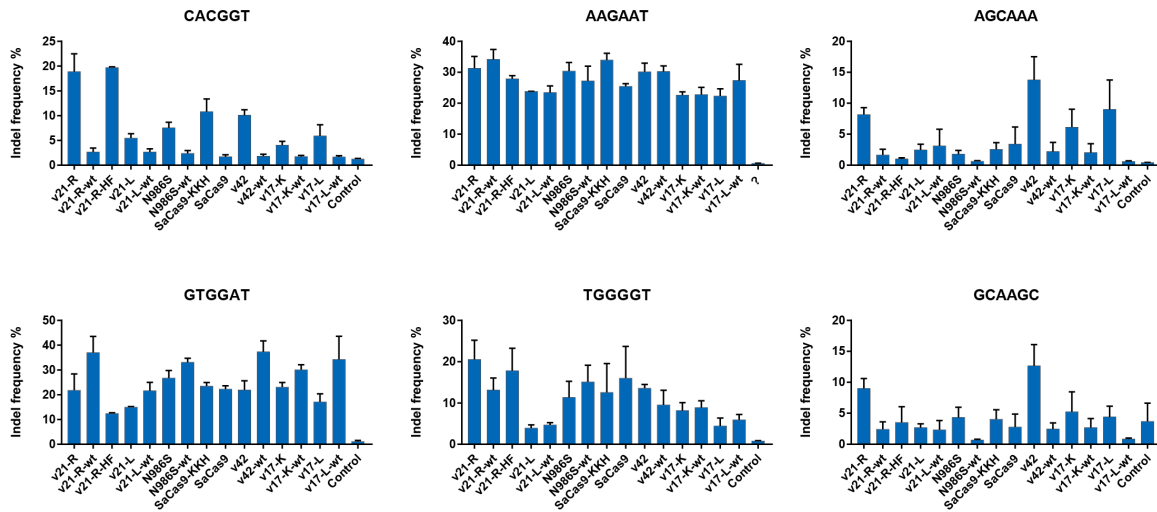
Supplementary Figure 9 | The preference in the third position of non-NNRRN PAMs.

SaCas9, SaCas9-KKH, cCas9 v21 with the I991R mutation (v21-R), and v21 with the I991R mutation and the wildtype SaCas9 scaffold instead of SaCas9-KKH scaffold (v21-R-wt) were used to target the fluorescent reporter gene containing sites with indicated PAMs. The scheme of the fluorescent reporter assay is shown in Fig. 1c. Cleavage activities were measured by using FACS 3 days after transfection into HEK293FT cells. Data indicated the mean $\pm$ s.e.m. (n = 3 independent biologic replicates). Source data are provided as a Source Data file.



Supplementary Figure 10 | Off-target effect of cCas9 variants at endogenous target sites.

a. Sequence alignment of on-target sites and off-target sites of gRNA-a and gRNA-b. Letter in red indicates the mismatch. **b.** and **c.** Indel frequencies induced by SaCas9 and SaCas9-KKH, cCas9 v21-R and v21-R-HF were measured by using the next generation sequencing 5 days after transfection into HEK293FT cells. Data indicate the mean $\pm$ s.e.m. (n =2 independent replicates). **** P<0.0001 (paired t-test, two-tailed); *** P<0.001 (paired t-test, two-tailed); * P<0.05 (paired t-test, two-tailed). Source data are provided as a Source Data file.



Supplementary Figure 11 | Genome editing efficiency of cCas9 variants at NNVRN PAMs.

Indel frequencies induced by indicated SaCas9 variants at indicated NNVRN PAMs were measured by the next generation sequencing 5 days after transfection into HEK293FT cells. Data indicated the mean $\pm$ s.e.m. (n =2 or 3 independent replicates). Source data are provided as a Source Data file.

Supplementary Tables

Supplementary Table 1| Indel frequency in Figure 2d and Supplementary Figure 5a

	v42	SaCas9-KKH	control
AAA-1	5.383788024	2.042248374	1.306799072
AAA-2	3.402756079	1.103170088	1.027052134
AAC-1	4.271990248	2.792671465	2.0112527
AAC-2	16.5550538	3.593279363	1.063740334
AAC-3	2.858080793	1.50079683	0.95394032
AAG-1	2.888478533	1.610489024	0.991765865
AAG-2	11.04153992	1.737134286	0.721921162
AAG-3	2.164166165	1.407361008	0.831974428
AAA-3	7.646681348	1.160600529	0.726599157
AAA-4	2.08220826	0.622104403	0.744622592
AAC-4	1.253566953	0.610897471	0.710144354
AAC-5	12.07589716	4.613157822	0.599518509
AAC-6	6.689099919	1.476474698	0.752239181
AAC-7	4.407234206	2.501331312	0.833189306
AAG-4	0.821875965	0.651561184	0.864294274
AAC-8	20.38138467	3.013375756	1.418486471
AAG-5	18.78359357	9.09596145	1.47857725
AAG-6	31.89745773	5.746877037	0.797583875
AAT-1	20.931038	14.64144917	1.163325043
AAT-2	10.04609089	4.283145261	0.852164045

AAT-3	3.399007223	3.254339049	0.936628732
AGA-1	4.11374284	4.589615638	0.853137062
AGA-2	2.423622466	1.503846807	1.165914836
AGC-1	17.82130348	14.82628023	0.963633002
AGC-2	7.626287989	2.211829938	0.862938518
AGG-1	3.683916248	2.799976128	1.378198967
AGG-2	8.347843498	2.903644571	0.923207805
AGT-1	3.981853808	9.769893369	0.863823287
AGT-2	19.36347817	37.49031066	1.013554984
AGA-3	3.602851554	1.304889034	0.780621408
AGA-4	15.19148426	3.535942727	0.761950958
AGA-5	14.91016734	3.688871135	0.854394237
AGA-6	17.43110729	6.689995764	0.838420507
AGA-7	7.975098005	2.022329368	0.763789016
AGT-3	1.453164233	1.160365415	0.775428699
AGT-4	8.912037516	22.94868291	0.720953644
AGA-8	24.08273229	9.442338254	1.115207821
AGG-3	6.888752331	3.703195595	1.288876399
AGC-3	24.08228367	9.33199372	1.078183362
AGC-4	14.90734792	6.895976845	0.794934783
AGC-5	21.35668053	12.01111414	0.675935126
GAA-1	12.93239191	5.288538631	0.877617219
GAA-2	10.38491926	3.390964915	0.766748453
GAG-1	28.52423813	21.29483955	1.277041971
GAG-2	1.963827355	1.381378736	1.362724879
GAA-3	8.752800468	4.046433489	0.76779198

GAG-3	14.34419176	6.571537047	0.654213655
GAT-2	11.02295959	12.59662582	0.644545319
GAT-3	15.77323106	22.9031055	0.819612298
GGA-1	8.451971395	5.084459189	1.318072034
GGC-1	6.378535503	4.026995258	0.897903612
GGT-1	9.73412833	22.26454243	1.808341393
GGT-2	6.580516174	16.97028217	1.406861519
GGT-3	19.07269305	26.2626449	0.987593676
GGA-2	1.332907671	1.350199474	1.306612487
GGC-2	4.302749423	2.102587518	0.807619368
GGG-1	1.463655043	1.391939008	1.252187458
GGT-4	6.074172152	5.759364608	0.801227704
GGA-3	11.63898719	1.450814542	0.876868468
GGA-4	45.10998651	28.89823637	0.859321826
GGC-3	2.282198285	1.159030711	0.598950081
GGC-4	2.28305406	0.940329907	0.614186307
GGC-5	32.07802121	17.22334605	0.622279078
GGG-2	3.460026689	1.082039826	0.631354085
GGA-5	23.17855202	12.62233624	1.122246355
GGA-6	26.00796462	6.545421396	0.75392965
GGC-6	10.01478885	5.987295983	3.618514981
GGT-5	23.64573915	31.71033343	0.868477208
GGT-6	34.4610265	45.2568938	0.742474882
GGG-3	1.228524418	1.371821451	1.245512197
GGG-4	1.119018655	1.125621074	1.120380982
GGG-5	1.29327884	1.109342438	1.407867728

GGG-6	1.234109603	0.916988899	0.730228194
GAC-1	1.50436264	1.276958779	1.080334222
GAC-2	5.584904789	2.488250127	0.647524559
GAC-3	1.966552459	2.524068701	0.82347796
GAT-1	13.6977706	8.746506016	0.522733219

Supplementary Table 2| Indel frequency in Supplementary Figure 6

gRNA sequence	SaCas9-KKH	SaCas9	v42	v42-wt	Control
GAGAACCACTTATAACTAACT	5.964977	6.152133	16.5705	7.345974	3.165357
GTTTTCGGGAAAACCAATGTG	6.72571	6.079152	2.826565	7.550714	0.949535
GGGATGGACCCTGTTATTCCT	2.192817	2.405336	13.91332	3.070477	2.865084
TCTGCATTCTGCCATCAGGGA	1.442926	1.423455	4.241936	1.23404	0.87536
TTATGAGCCCTTCTGCAAATG	3.306913	9.499751	26.96876	4.084066	1.567112
CTGGACCACTTGTCATTCCT	1.788048	1.981701	5.470734	3.560038	1.365287
GAAAGGACATTTGGAGGGTGC	7.468291	7.244384	6.404399	11.79585	1.062878
AGTGAATGACAAGTGGTCCAG	2.964778	2.032142	5.752632	3.160144	2.144033
GGAGCGGTCCCACTGCCACCC	3.037881	1.917354	12.09837	1.1653	1.629258
GCTTCCAGCCCCGCGAACAGC	3.979848	3.360766	17.7736	9.322766	1.725451
GAACCTGGATCCGAGCGGAGG	26.72098	22.26309	21.96992	37.29956	1.073405
TCTGTAGCTCACTGAAGGCTT	30.39664	25.44946	30.15816	30.21288	10.02323
TGGGCTTTATGGGCAAGCCAG	22.15709	21.03269	24.34252	21.91652	5.616783
TGCCGTGATCACAGGATAGCC	5.423019	4.289522	18.76475	3.641419	1.512041
GCATCATTTGGCTTGATCTTA	5.431097	4.404801	19.64185	3.593341	1.259107
ATTCTTAAGCCTTCAGTGAGC	1.296368	4.054265	5.215076	1.403914	0.764745

TCATTTGGCTTGATCTTATAA	4.470264	8.934931	22.84034	4.831125	1.495558
TTAAGAATTTGGGCTTTATGG	4.338785	2.775468	12.66736	2.467407	3.689073
GAATTTGGGCTTTATGGGCAA	8.584318	1.398834	18.62165	4.158306	4.898106
GCCGTGATCACAGGATAGCCT	9.493395	7.265513	22.87406	7.346522	2.652068
GGGGTTTTAAGGTAGTTCTCT	8.585745	1.309775	21.97974	1.614806	0.752924
GAAGCAGCTCCAGTGCCCAGA	7.525579	1.717651	10.06656	1.825731	1.242133
TCCGAGCGGAGGGTGGATGTT	11.33366	15.98731	13.57282	9.521295	0.779616
AGGCCCCGCCGTCCTGGTCCAA	6.982134	2.601923	10.14279	2.325242	2.41301
TGGGTGAGTGGGAGAGTCCCG	11.02806	12.18742	22.26803	14.20093	1.233051
GGGCAGAGAGCTGGTTTTTCGG	3.3531	0.54997	16.14013	0.955752	1.098554
GTTAAGAATTTGGGCTTTATG	14.08216	9.472067	24.35499	3.937848	0.742292
TGGCTTCCACGTAGTGCTCAA	1.066766	3.136055	4.675585	1.399205	0.703354
TAACTATGTGAAGTGTTACAC	5.184519	7.733171	49.75165	5.987027	2.387023
TGGAGGGTGCGTGGGGAGCTT	1.477927	0.921965	3.200313	2.291762	1.218692
CCTGATCTTCAAAGGTACAAA	3.857911	2.828971	22.22985	3.254008	0.441176
TTCAGGGCAAATAAGAGTAGA	11.28103	3.918283	27.56659	4.51224	1.068767
AGGTGTGTATTCCAGAATTGA	1.796273	3.411279	13.75203	2.204196	0.408876

Supplementary Table 3| Indel frequency in Supplementary Figure 8b

gRNA sequence	v42	SaCas9-KKH	v17-L	Control
GCGGAGGGTGGATGTTTGGGG	2.858081	1.500797	2.282631	0.95394
AACATCCACCCTCCGCTCGGA	2.888479	1.610489	6.546633	0.991766
GAGCAGACAAC TCACAAATGC	11.04154	1.737134	15.83583	0.721921
GCGGGATGGACCCTGTTATTC	2.164166	1.407361	4.019905	0.831974

AATTATTTATAATTCAGGGCA	0.821876	0.651561	1.945215	0.864294
GGACCACAGGGAAGGCTGCCA	18.78359	9.095961	19.32154	1.478577
GTTAAGAATTTGGGCTTTATG	31.89746	5.746877	26.68633	0.797584
GGAGGCCGATGGTGGGTGAGT	4.113743	4.589616	2.030864	0.853137
GGGCTGGAAGCAGCTCCAGTG	2.423622	1.503847	1.62053	1.165915
ACGGTGCCGCGACCGGCTTGG	3.683916	2.799976	2.712772	1.378199
TGGCTTCCACGTAGTGCTCAA	8.347843	2.903645	3.630279	0.923208
ATTATTTATAATTCAGGGCAA	3.602852	1.304889	1.634604	0.780621
GCAACTATCATAGGTGTGTAT	15.19148	3.535943	6.630174	0.761951
CCTGATCTTCAAAGGTACAAA	14.91017	3.688871	4.316389	0.854394
TGCCGTGATCACAGGATAGCC	17.43111	6.689996	15.80242	0.838421
ATTCTTAAGCCTTCAGTGAGC	7.975098	2.022329	4.1961	0.763789
GACCACAGGGAAGGCTGCCAT	12.05179	13.19317	4.464219	2.267423
TTAAGAATTTGGGCTTTATGG	33.35647	31.65914	29.1707	0.787909
GCATCATTTGGCTTGATCTTA	24.08273	9.442338	16.4371	1.115208
TGCCATAAAAGCTGCCGTGAT	6.888752	3.703196	9.039727	1.288876
TCATTTGGCTTGATCTTATAA	24.08228	9.331994	16.36372	1.078183
TGCAGGCTATCCTGTGATCAC	14.90735	6.895977	4.646831	0.794935
CCAGGAGGGTGACTCAGGCTA	12.93239	5.288539	13.20753	0.877617
CATCATTTGGCTTGATCTTAT	10.38492	3.390965	9.431238	0.766748
GCCGTGATCACAGGATAGCCT	28.52424	21.29484	30.71284	1.277042
CAGTGGAATTCTTAAGCCTTC	1.963827	1.381379	1.364419	1.362725
CTGATCTTCAAAGGTACAAAG	8.7528	4.046433	7.839242	0.767792
TTATTTATAATTCAGGGCAAA	14.34419	6.571537	9.996689	0.654214
ATCTTCAAAGGTACAAAGTAA	15.79986	22.89803	13.50426	0.820129
GTCGCAGCTTCAGACCGCGGC	8.451971	5.084459	4.988769	1.318072

CACCCCTCCTCCTTTTTGCCG	1.332908	1.350199	1.348846	1.306612
ACACCCCTCCTCCTTTTTGCC	1.463655	1.391939	1.376424	1.252187
CTTACTTTGTACCTTTGAAGA	11.63899	1.450815	2.354955	0.876868
GGTACAAAGTAAGAAGAGAAA	45.10999	28.89824	31.06465	0.859322
ATTTGCCCTGAATTATAAATA	3.460027	1.08204	8.421338	0.631354
GCCATAAAAGCTGCCGTGATC	23.17855	12.62234	4.74802	1.122246
TTTGGGCTTTATGGGCAAGCC	26.00796	6.545421	14.08938	0.75393

Supplementary Table 4| Indel frequency in Figure 4b

gRNA sequence	v21-R	v21-L	v21-R-HF	SaCas9-KKH	N986S	v21-L-wt	N986S-wt	SaCas9	Control
AGACAGGAGGAGGAGGTCA CC	11.1129 9	49.2441 9	22.8605 9	2.69769 2	13.0741 6	1.17611 5	1.12685 1	1.12073 1	1.03295 7
ATGTTAACCATGCTGCCAAA G	25.6427 2	14.9414 9	5.19863	9.47555 4	47.2314 9	1.11486 9	1.59437 6	1.32314 7	1.18996 3
AGTAGGGTGTGGCAGCTGA GA	16.8717 9	19.8111 7	9.85780 7	3.91529 3	14.4237 5	1.39426 4	1.12085 9	0.96202 2	1.17548 8
CCAAGGGGCATGGAAGGAA GC	26.3486 7	12.0567 2	24.6115 8	3.66344 7	18.8551 2	1.44885	1.60462 7	1.29303 9	1.43876 1
ATGATGGCTGCAGACATCCC G	35.7503	27.7749 6	33.7527 6	4.41166 9	17.9158 8	4.11542 7	2.95495 4	3.7021	1.24066 2
ACCTGGACCAAGGAGCTCA GC	16.2259 3	31.6195 6	19.6178 7	2.58184 1	9.98428 4	2.43705 1	1.55960 9	1.41845 8	1.46140 6

Supplementary Table 5| Indel frequency in Figure 4c

gRNA sequence	v21R	v21L	v21R-HF	SaCas9-KKH	N986S	v21L-wt	N986S-wt	SaCas9	control
CCTGCATGGTGGTTTCTAGG T	12.0265 4	5.26266 3	15.1369 2	3.24181 5	8.78513 1	9.02582 9	14.9120 7	5.12585 6	1.68582
AGGTCACCACCATGATCCT GG	48.2183 8	63.5283 3	61.5629 4	7.96017 8	46.4308 2	69.1956 4	45.3250 3	6.21872 5	1.17299 8
TCACCACCATGATCCTGGA GG	28.2238 9	6.92707 7	17.9042 9	5.48293 1	10.8245 4	40.5881	47.6117 2	21.9044 1	1.06018 1
TGCCTCCTCACTGCTTTCAG G	90.6808 5	88.7893	31.3198 8	31.4191 4	66.5268 2	85.5689 9	93.9679 4	71.8873 7	6.17489 1
AACTTGGATCCGAGCGGAG GG	17.8666 7	36.9402 5	54.4581 2	6.75221 6	26.2511 7	52.4269 8	52.8712	8.82245 7	1.23432 1

Supplementary Table 6| Information in Figure 2d and Supplementary Figure 5a

gRNA name	gRNA sequence	PAM position 1-7	Forward primer		Reverse primer	
AAA-1	GGGGGCAGAG AGCTGGTTTTTC	gggaaaa	AAA-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTCAGACCGGGCCAG GA	AAA-1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCTCAGAGAACTTGGATCCGA
AAA-2	GGGTCCAACA CATTGGTTTTTC	ccgaaaa	AAA-2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCCGATGGTGGGTGAGT GGG	AAA-2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGTCCCGGGATGTCGTTTCAG

AAC-1	ACTGGAGCTG CTTCCAGCCC C	gcgaaca	AAC-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTATCTCCCAGTGCCG	AAC-1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGCACTGCGCGGGA
AAC-2	GGGCAGAGAG CTGGTTTTCGG	gaaaacc	AAC-2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCTTCAGACCGCGGCCCA GGA	AAC-2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCTCAGAGAACTTGGATCCGA
AAC-3	GCGGAGGGTG GATGTTTGGG G	tccaaca	AAC-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGGAGAGTCCCGGAGAGC AGG	AAC-3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTAGCCTAACTCTCCCATTCGT
AAG-1	AACATCCACC CTCCGCTCGG A	tccaagt	AAG-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGGAGAGTCCCGGAGAGC AGG	AAG-1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTAGCTCAGCCTAACTCTCCCA
AAG-2	GAGCAGACAA CTCACAAATG C	ttaaagc	AAG-2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGGGGTCTCTTGCCA	AAG-2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCTCCTTTTTGCCGTTGGG
AAG-3	GCGGGATGGA CCCTGTTATTC	cctaaga	AAG-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGAGAGTATCTGGCCTTGT GG	AAG-3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGGTGGAGGGAACAGCAAGGG
AAA-3	AGGTGTGTAT TCCAGAATTG A	agcaaag	AAA-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCCCTTCAGCACAAAGTT ACCA	AAA-3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTATTGTTTATTGATGATTACA
AAA-4	AATTTAGCCT GTTTTCAAAC	tagaaat	AAA-4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCATATCCATCTTTCTCTT CT	AAA-4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCAAATAATATTTAAATCA

AAC-4	CACCTATGAT AGTTGCCTAA G	tgtaaca	AAC- 4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCAAGTTACCAGTTTTGAC AA	AAC- 4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTGATCTTGTATTGTTTATTG
AAC-5	TTCAGGGCAA ATAAGAGTAG A	agaaacc	AAC- 5F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTGGCAGCTCTCCACTTC TG	AAC- 5R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTCTATCTTTCCTGATCTTC
AAC-6	CTATGTGAAG TGTTACACTTA	ggcaact	AAC- 6F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCAAACTCCCGGAATTTT GG	AAC- 6R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTAAATTCTAATCTTTCCTGA
AAC-7	AAAGATGGGA GCAGGGAAGT T	gggaacc	AAC- 7F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTCTGTTAAGTCAGGATT TC	AAC- 7R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTAAGAGAAAGATGGATATGGT
AAG-4	AATTATTTATA ATTCAGGGCA	aataaga	AAG- 4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTAGAGTCAGATTGGCAG CTC	AAG- 4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTGATCTTCAAAGGTACAAAG
AAC-8	GTGATCACAG GATAGCCTGC A	gagaact	AAC- 8F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGGTGACCCAGATGCCAT GAG	AAC- 8R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCCCCTCTAGATGACCTTCC
AAG-5	GGACCACAGG GAAGGCTGCC A	taaaagc	AAG- 5F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGTTGATGCAGCTTGGGG AAT	AAG- 5R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTCTAGGTGGGGTTTTAAGG
AAG-6	GTTAAGAATT TGGGCTTTAT G	ggcaagc	AAG- 6F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAAAGTGAGGTTTCAGCAA	AAG- 6R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGGGCTTCCTACTGTC

AAT-1	TCTGTAGCTC ACTGAAGGCT T	agaatt	AAT- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAAAGAAGCTCTCATTAT	AAT- 1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCAGGTTGTAAAATGAAG
AAT-2	TGGGCTTTAT GGGCAAGCCA G	tggaatt	AAT- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCCCATTTTACAGAAGAG G	AAT- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCCTACTGTCCCCAAAAGC
AAT-3	AGAGAGCTGG TTTTCGGGAA A	accaatg	AAT- 3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGACCGCGGCCAGGA	AAT- 3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCGTTTCAGTTCTCAGA
AGA-1	GGAGGCCGAT GGTGGGTGAG T	gggagag	AGA- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCGTGACATCCAGAAAAC GCG	AGA- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTGACCAAGGGTGGATGTTTGGGGTC C
AGA-2	GGGCTGGAAG CAGCTCCAGT G	cccagac	AGA- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCCGTCCTGGTCCAAGC CGG	AGA- 2R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTAGCTTACGCTCACTCCCTTCACAAG
AGC-1	TGGGTGAGTG GGAGAGTCCC G	gagagca	AGC- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAAAACGCGAAACCTCAG GAA	AGC- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTACATGTAGGGTGGATGTTTGGGGTC C
AGC-2	AACACATTGG TTTTCCCGAA A	accagct	AGC- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCAGGAGGCCGATGGTGG GTG	AGC- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGGATGTCGTTTCAGTTCTCA
AGG-1	ACGGTGCCGC GACCGGCTTG G	accagga	AGG- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCCCAGAGCCTCAGAGAA GGC	AGG- 1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCGGTCCCACTGCCACCCTCC

AGG-2	TGGCTTCCAC GTAGTGCTCA A	acaaggc	AGG- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCAGGTATAGGGCATGGG GGT	AGG- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCAATGTCAAGGAAGGGGAAG
AGT-1	TTCCCTAAGA CATGGCTTCC A	cgtagtg	AGT- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCAGAGGCCAGGTATAG GG	AGT- 1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCAAGGAAGGGGAAGAATATT
AGT-2	GCTGACTTGA TGCCAAGCAG G	cccagtt	AGT- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTACGCAGATAAGAACC AGT	AGT- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGCCTCCCCTCCCACACACTC
AGA-3	ATTATTTATAA TTCAGGGCAA	ataagag	AGA- 3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGAGTCAGATTGGCAGC TCT	AGA- 3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCTGATCTTCAAAGGTACAAA
AGA-4	GCAACTATCA TAGGTGTGTA T	tccagaa	AGA- 4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCAGCACAAGTTACCAGT TTT	AGA- 4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTGTATTGTTTATTGATGAT
AGA-5	CCTGATCTTCA AAGGTACAAA	gtaagaa	AGA- 5F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTATTTATAATTGAGGGC AA	AGA- 5R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTAAAAATATAGACAGAATGAT
AGA-6	TGCCGTGATC ACAGGATAGC C	tgcagag	AGA- 6F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAAGGTGACCCAGATGCC ATG	AGA- 6R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCTCTAGATGACCTTCCCTGC
AGA-7	ATTCTTAAGC CTTCAGTGAG C	tacagag	AGA- 7F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGCTCTCATTATTATCCC CA	AGA- 7R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGGAGGTCAGGTTGTAAAATG

AGT-3	TATCCCCATTT TACAGAAGAG	gaaagtg	AGT-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCCTGACATTGTTTAAACT AT	AGT-3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCACAAAATCTATGCTGGGC
AGT-4	GAATTTGGGC TTTATGGGCA A	gccagtg	AGT-4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGAGGAAAGTGAGGTTCA GCA	AGT-4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTCCTACTGTCCCCAAAAGC
AGA-8	GCATCATTTG GCTTGATCTTA	taaagaa	AGA-8F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGGGATGAAAGCAGGGA TGC	AGA-8R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCAGATCGCCTTGCTGAACCTCACTTT
AGG-3	TGCCATAAAA GCTGCCGTGA T	cacagga	AGG-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTGCAGCTTGGGGAATGG TTC	AGG-3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTCCTGCATGGTGGTTTCT
AGC-3	TCATTTGGCTT GATCTTATAA	agaagct	AGC-3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGGGATGAAAGCAGGGA TGC	AGC-3R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTACTTGAGCCTTGCTGAACCTCACTTT
AGC-4	TGCAGGCTAT CCTGTGATCA C	ggcagct	AGC-4F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGGTGACCCAGATGCCAT GAG	AGC-4R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTCCCCTCTAGATGACCTTCC
AGC-5	TTAAGAATTT GGGCTTTATG G	gcaagcc	AGC-5F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCCCTTCAACACAAGTT ACCA	AGC-5R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCAGATCATTGTTTATTGATGATTACA
GAA-1	CCAGGAGGGT GACTCAGGCT A	gcagaaa	GAA-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAAGGCCAGCTCAGTTC TCT	GAA-1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTTGGCCAGCATGAGGAGATGG

GAA-2	CATCATTTGG CTTGATCTTAT	aaagaag	GAA- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGGGATGAAAGCAGGGA TGC	GAA- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGCCTTGCTGAACCTCACTTT
GAG-1	GCCGTGATCA CAGGATAGCC T	gcagaga	GAG- 1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAGGTGACCCAGATGCCA TGA	GAG- 1R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCCTCTAGATGACCTTCCCTG
GAG-2	CAGTGGAATT CTTAAGCCTTC	agtgagc	GAG- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTATTATTATCCCCATTTTA CA	GAG- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTGATGCAGGGAGGTCAGGTTG
GAA-3	CTGATCTTCA AAGGTACAAA G	taagaag	GAA- 3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTATTATTTATAATTCAGGG CA	GAA- 3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTAAAATATAGACAGAATGATT
GAG-3	TTATTTATAAT TCAGGGCAAA	taagagt	GAG- 3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGAGTCAGATTGGCAGCT CTC	GAG- 3R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTCCTGATCTTCAAAGGTACAA
GAT-2	TTCAATTCTGG AATACACACC	tatgata	GAT- 2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTGCCCTTCAGCACAAAGTT ACCA	GAT- 2R	GTGACTGGAGTTCAGACGTGTGCTCTTC CGATCTATTGTTTATTGATGATTACA
GAT-1	GAGAACCACT TATACTAAC T	ccagata	GAT- 1F	CTTTCCCTACACGACGCTCTTCCGATC TTTGCTGAGAGATAGGGCGGGGATTG C	GAT- 1R	GAGTTCAGACGTGTGCTCTTCCGATCTG TGTCGCCTCCAAATGTCTTTCCAT
GAT-3	CTCTTCTTACT TTGTACCTTT	gaagatc	GAT- 3F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTCTTTCCCAATTATTTAT AA	GAT- 3R	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTTCTTTCCCAATTATTTATAA

GAC-1	AGACAAACTC AGCTCCTGCC A	ggagaca	GAC- 1F	CTTTCCCTACACGACGCTCTTCCGATC TTCAGAGCCCTGTGTATAATTCTTCTA	GAC- 1R	GAGTTCAGACGTGTGCTCTTCCGATCTC GAGTACGTGGTTTGCTAAGGACTCT
GAC-2	GCTTACAGTTT AAAGAATGGA	aaggaca	GAC- 2F	CTTTCCCTACACGACGCTCTTCCGATC TTAGTAGTCCTAATGAAATGGAGAAC C	GAC- 2R	GAGTTCAGACGTGTGCTCTTCCGATCTG CCTAAAAAGGAGAGCTTTCAGTCTC
GAC-3	TGGAGGGTGC GTGGGGAGCT T	agagacc	GAC- 3F	CTTTCCCTACACGACGCTCTTCCGATC TAGTAATACTCCAGATACAAATTGTG G	GAC- 3R	CTTTCCCTACACGACGCTCTTCCGATCTA GTAATACTCCAGATACAAATTGTGG
GGA-1	GTCGCAGCTT CAGACCGCGG C	ccaggag	GGA- 1F	TCTTTCCCTACACGACGCTCTTCCGAT CTCGTCCCCTTTCAGAGCTGT	GGA- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTTCCCGAAAACCAGCTCTCT
GGC-1	GGACTCTCCC ACTCACCCAC C	atcggcc	GGC- 1F	TCTTTCCCTACACGACGCTCTTCCGAT CTAGAAAACGCGAAACCTCAGG	GGC- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGCCAATAGGGTGGATGTTTGGGGTC C
GGT-1	AGGCCCCGCCG TCCTGGTCCA A	gccggtc	GGT- 1F	TCTTTCCCTACACGACGCTCTTCCGAT CTCGCCGACACTTGAGCCCCCA	GGT- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGATCAGTGCCACCCTCCAGCTGTTC G
GGT-2	GAAGCAGCTC CAGTGCCAG A	cacggtg	GGT- 2F	TCTTTCCCTACACGACGCTCTTCCGAT CTCGATGTAAGGCGAGGGGGTGGATC TC	GGT- 2R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTACTTGACTTCACAAGGGGCCAGGCG G
GGT-3	TCCGAGCGGA GGGTGGATGT T	tggggtc	GGT- 3F	TCTTTCCCTACACGACGCTCTTCCGAT CTCGATGTGGAGAGTCCCGGAGAGCA GG	GGT- 3R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTTAGGCGCCTAACTCTCCCATTCGTC

GGA-2	CACCCCTCTC CTTTTGGCCG	ttgggag	GGA- 2F	TCTTTCCTACACGACGCTCTTCCGAT CTTTGTCTGCTCCCTGATGGCA	GGA- 2R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCTGCCGTGACATTGTCCACA
GGC-2	CCATCCAAGT TGATGGGGAG C	agtggca	GGC- 2F	TCTTTCCTACACGACGCTCTTCCGAT CTTGGCTGCAGACCTGGGGACT	GGC- 2R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGTAGCTTCATGTCTCTGCA
GGG-1	ACACCCCTCC TCCTTTTGGC	gttggga	GGG- 1F	TCTTTCCTACACGACGCTCTTCCGAT CTCATTGTGAGTTGTCTGCTC	GGG- 1R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCCACAAGGCCAGATACTCTC
GGT-4	ACCCCTGGGC AGGACGAAGT C	ccgggtc	GGT- 4F	TCTTTCCTACACGACGCTCTTCCGAT CTTGCCACACACACAACACTG	GGT- 4R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCTTCATGTCTCTGCATTCTG
GGA-3	CTTACTTTGTA CCTTTGAAGA	tcaggaa	GGA- 3F	TCTTTCCTACACGACGCTCTTCCGAT CTCTTGATCTTTCCCAATTATTATA A	GGA- 3R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGAATGATTCTAATTTAGCCT
GGA-4	GGTACAAAGT AAGAAGAGAA A	gatggat	GGA- 4F	TCTTTCCTACACGACGCTCTTCCGAT CTCCATCTTTCCCAATTATTTA	GGA- 4R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTAATGATTCTAATTTAGCCTG
GGC-3	GTGTAACACT TCACATAGTT A	tatggct	GGC- 3F	TCTTTCCTACACGACGCTCTTCCGAT CTTGACCACACTCCCGGAATTTTGGC TT	GGC- 3R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTAATAAATTCTAATCTTTCTT
GGC-4	CTTTCCCAATT ATTTATAATT	cagggca	GGC- 4F	TCTTTCCTACACGACGCTCTTCCGAT CTACATGTCACTCCCGGAATTTTGGCT T	GGC- 4R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCAAAGGTACAAAGTAAGAAG

GGC-5	TAACTATGTG AAGTGTTACA C	ttaggca	GGC-5F	TCTTTCCCTACACGACGCTCTTCCGAT CTGAAACCATAGAGTCAGATTG	GGC-5R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTAAATAAATTCTAATCTTTCT
GGG-2	ATTTGCCCTG AATTATAAAT A	attggga	GGG-2F	TCTTTCCCTACACGACGCTCTTCCGAT CTGCCAATCACTCCCAGGAATTTTGGC TT	GGG-2R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGATCAGTCCTGATCTTCAAAGGTAC A
GGA-5	GCCATAAAAG CTGCCGTGAT C	acaggat	GGA-5F	TCTTTCCCTACACGACGCTCTTCCGAT CTGCCAATTGCAGCTTGGGGAATGGT TC	GGA-5R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTGGTTTCTAGGTGGGGTTTT
GGA-6	TTTGGGCTTTA TGGGCAAGCC	agtggaa	GGA-6F	TCTTTCCCTACACGACGCTCTTCCGAT CTGAAGAGGAAAGTGAGGTTCA	GGA-6R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTACTGTCCCCAAAAGCCAAG
GGC-6	GAAGAGGAAA GTGAGGTTCA G	caaggct	GGC-6F	TCTTTCCCTACACGACGCTCTTCCGAT CTACATGTCACACAGCATCATTTGGC TT	GGC-6R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTTGACCAATTTGGGCTTTATGGGCAA G
GGT-5	CCATTTTACA GAAGAGGAAA G	tgaggtt	GGT-5F	TCTTTCCCTACACGACGCTCTTCCGAT CTTTAGGCGCCTTCATTCTCTGCATCA G	GGT-5R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCGATGTGTGGAATTCTTAAGCCTTC A
GGT-6	CCCTGCATGG TGGTTTCTAG G	tggggtt	GGT-6F	TCTTTCCCTACACGACGCTCTTCCGAT CTTTAGGCCTGCCATAAAAGCTGCCG TG	GGT-6R	ACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCGATGTAATGTTAGTGATCCCCAGT A
GGG-6	GATCCGAGCG GAGGGTGGAT G	tttgggg	GGG-6F	CTTTCCCTACACGACGCTCTTCCGATC TCGAAGTGTAGCTCAGCCTAACTCTC C	GGG-6R	GAGTTCAGACGTGTGCTCTTCCGATCTC CTTCAGGAGAGTCCCGGAGAGCAGG

GGG-3	CAAGCCGGTC GCGGCACCGT G	tctgggc	GGG-3F	CTTTCCTACACGACGCTCTTCCGATC TGCTATCCGGTCCCCTGCCACCCTCC	GGG-3R	GAGTTCAGACGTGTGCTCTTCCGATCTTT TCGCCCCCAGAGCCTCAGAGAAG
GGG-4	ACCGCGGCCC AGGAGGCCGA T	ggtgggt	GGG-4F	CTTTCCTACACGACGCTCTTCCGATC TTTTTGAACACATTGGTTTTCCCGAA	GGG-4R	GAGTTCAGACGTGTGCTCTTCCGATCTT GTCACGAGCTGTCCCCCGTGACATC
GGG-5	CACTGCCACC CTCCAGCTGTT	cgcgggg	GGG-5F	CTTTCCTACACGACGCTCTTCCGATC TACGGGGACGCTCACTCCCTTCACAA G	GGG-5R	GAGTTCAGACGTGTGCTCTTCCGATCTA GCGCGGTCCTGGTCCAAGCCGGTCG

Supplementary Table 7| Information in Supplementary Figure 6

gRNA sequence	PAM position 1-7	Forward primer		Reverse primer	
GAGAACCACTTA TAACTAACT	ccagata	SF6-1F	CTTTCCTACACGACGCTCTTCCGATCTT TGCTGAGAGATAGGGCGGGGATTGC	SF6-1R	GAGTTCAGACGTGTGCTCTTCCGATCTGTGTC GCCTCCAAATGTCCTTTCCAT
GTTTTCGGGAAA ACCAATGTG	ttggacc	SF6-2F	CTTTCCTACACGACGCTCTTCCGATCTC ACAAAATGTCGTTTCAGTTCTCAGA	SF6-2R	GAGTTCAGACGTGTGCTCTTCCGATCTGTGTG GCCCAGGAGGCCGATGGTGGG
TCTGCATTCTGCC ATCAGGGA	gcagaca	SF6-3F	CTTTCCTACACGACGCTCTTCCGATCTT CGCAGGTTCTGAACACCCCTCCTCC	SF6-3R	GAGTTCAGACGTGTGCTCTTCCGATCTATTAGT CCCAGGGGTCTCTTGCCACT

GGGATGGACCCT GTTATTCCC	taagaca	SF6- 4F	CTTTCCCTACACGACGCTCTTCCGATCTG ATATAGTGGAGGGAACAGCAAGGG	SF6- 4R	GAGTTCAGACGTGTGCTCTTCCGATCTTGGCCT GAGAGTATCTGGCCTTGTGG
TTATGAGCCCTTC TGCAAATG	agagggt	SF6- 5F	CTTTCCCTACACGACGCTCTTCCGATCTG GGGGCAGAGGAAGGAGCAGACCAGC	SF6- 5R	GAGTTCAGACGTGTGCTCTTCCGATCTACCTC GTGCAGGGTTAGAGGAAATTG
CTGGACCACTTGT CATTCACT	tgagacc	SF6- 6F	CTTTCCCTACACGACGCTCTTCCGATCTT CCGGAATAGATGGGTGTGGCGGGAG	SF6- 6R	GAGTTCAGACGTGTGCTCTTCCGATCTGGGCC GCTGCTTTCTCTGCTGGGACA
GAAAGGACATTT GGAGGGTGC	gtgggga	SF6- 7F	CTTTCCCTACACGACGCTCTTCCGATCTG TTACTCTTATAACTAACTCCAGATA	SF6- 7R	GAGTTCAGACGTGTGCTCTTCCGATCTCGCTAT CCTGGCGCTGCTTGAAAGGA
AGTGAATGACAA GTGGTCCAG	ggagacc	SF6- 8F	CTTTCCCTACACGACGCTCTTCCGATCTA AATGGATAGATGGGTGTGGCGGGAG	SF6- 8R	GAGTTCAGACGTGTGCTCTTCCGATCTATACA CCTGCTTTCTCTGCTGGGACA
GGAGCGGTCCCA CTGCCACCC	tccagct	SF6- 9F	CTTTCCCTACACGACGCTCTTCCGATCTA GTCTTTCTGGTCCAAGCCGGTCGC	SF6- 9R	GAGTTCAGACGTGTGCTCTTCCGATCTCGGCA GGGAAAGGGGACGCTCACTCC
GCTTCCAGCCCCG CGAACAGC	tggaggg	SF6- 10F	CTTTCCCTACACGACGCTCTTCCGATCTG CATCAGGATCTCCCAGTGCCGAGGC	SF6- 10R	GAGTTCAGACGTGTGCTCTTCCGATCTCGGCC CCTTCACAAGGGGCCAGGCGG
GAACTTGGATCC GAGCGGAGG	gtggatg	SF6- 11F	CTTTCCCTACACGACGCTCTTCCGATCTT CACACCCGGTGTGTAGCTCAGCCTA	SF6- 11R	GAGTTCAGACGTGTGCTCTTCCGATCTTGTCTT GGAGAGTCCCGGAGAGCAGG

TCTGTAGCTCACT GAAGGCTT	aagaatt	SF6- 12F	CTTTCCCTACACGACGCTCTTCCGATCTC AGAAGCAGGTTGTAAATGAAGTGG	SF6- 12R	GAGTTCAGACGTGTGCTCTTCCGATCTATGAT ATAAAGAAGCTCTCATTATTA
TGGGCTTTATGGG CAAGCCAG	tggaatt	SF6- 13F	CTTTCCCTACACGACGCTCTTCCGATCTC GACACACTGTCCCCAAAAGCCAAGA	SF6- 13R	GAGTTCAGACGTGTGCTCTTCCGATCTTAAGT GCAGAAGAGGAAAGTGAGGTT
TGCCGTGATCAC AGGATAGCC	tgcaag	SF6- 14F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAAGGTGACCCAGATGCCATG	SF6- 14R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTCTCTAGATGACCTCCCTGC
GCATCATTTGGCT TGATCTTA	taaagaa	SF6- 15F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTCAGAGGGATGAAAGCAGGGA TGC	SF6- 15R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTCTGAGCCTTGCTGAACCTCACTTT
ATTCTTAAGCCTT CAGTGAGC	tacagag	SF6- 16F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAGCTCTCATTATTATCCCCA	SF6- 16R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTGGAGGTCAGGTTGTAAATG
TCATTTGGCTTGA TCTTATAA	agaagct	SF6- 17F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAGGGATGAAAGCAGGGATGC	SF6- 17R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTGCCTTGCTGAACCTCACTTT
TTAAGAATTTGG GCTTTATGG	gcaagcc	SF6- 18F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAAAGTGAGGTTTCAGCAA	SF6- 18R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTGGGCTTCCTACTGTC
TGGCTTCCACGTA GTGCTCAA	acaaggc	SF6- 19F	TACACTCTTTCCCTACACGACGCTCTTCC GATCTTTGCAGCAGGTATAGGGCATGGG G	SF6- 19R	TGACTGGAGTTCAGACGTGTGCTCTTCCGATC TGGCTATCAATGTCAAGGAAGGGGAA

GAATTTGGGCTTT ATGGGCAA	gccagtg	SF6- 20F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTGAGGAAAGTGAGGTTTCAGCA	SF6- 20R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTTCTCTACTGTCCCCAAAAGC
GCCGTGATCACA GGATAGCCT	gcagaga	SF6- 21F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAGGTGACCCAGATGCCATGA	SF6- 21R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTCCTCTAGATGACCTTCCCTG
GGGGTTTTAAGG TAGTTCTCT	gcaggct	SF6- 22F	TCTTTCCCTACACGACGCTCTTCCGATCT ACTTGATGAGGTTGTGGCCAGGACCA	SF6- 22R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTT GACCAGCTTTCATCCCTGGCTACTG
GAAGCAGCTCCA GTGCCAGA	cacggtg	SF6- 23F	TCTTTCCCTACACGACGCTCTTCCGATCT CGATGTAAGGCGAGGGGGTGGATCTC	SF6- 23R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTA CTTGACTTCACAAGGGGCCAGGCGG
TCCGAGCGGAGG GTGGATGTT	tggggtc	SF6- 24F	TCTTTCCCTACACGACGCTCTTCCGATCT CGATGTGGAGAGTCCCGAGAGCAGG	SF6- 24R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTTT AGGCGCCTAACTCTCCCATTCGTC
AGGCCCCGCGTC CTGGTCCAA	gccggtc	SF6- 25F	TCTTTCCCTACACGACGCTCTTCCGATCT CGCCGACACTTGAGCCCCCA	SF6- 25R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTG ATCAGTGCCACCCTCCAGCTGTTCG
TGGGTGAGTGGG AGAGTCCCC	gagagca	SF6- 26F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTAAAACGCGAAACCTCAGGAA	SF6- 26R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTAGGGTGGATGTTTGGGGTCC
GGGCAGAGAGCT GGTTTTCGG	gaaaacc	SF6- 27F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTCTTCAGACCGCGGCCAGGA	SF6- 27R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTTCTCAGAGAACTTGATCCGA

TGGAGGGTGCCT GGGGAGCTT	agagacc	SF6- 28F	CTTTCCCTACACGACGCTCTTCCGATCTA GTAATACTCCAGATACAAATTGTGG	SF6- 28R	GAGTTCAGACGTGTGCTCTTCCGATCTGCCAC TGGATATACACATGCCTGGCG
GTTAAGAATTTG GGCTTTATG	ggcaagc	SF6- 29F	TCTACACTCTTTCCCTACACGACGCTCTT CCGATCTGGTCTAAAAGTGAGGTTCAGC AA	SF6- 29R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGAT CTTAAGCTGGGCTCCTACTGTC
TAACTATGTGAA GTGTTACAC	ttaggca	SF6- 30F	TTTCCCTACACGACGCTCTTCCGATCTGT TCACGCCAATCACTCCCGGAATTTTGGC	SF6- 30R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCTA CCTAGAAATAAATTCTAATCTTTCT
CCTGATCTTCAAA GGTACAAA	gtaagaa	SF6- 31F	TCTTTCCCTACACGACGCTCTTCCGATCT TACCGTTTATTTATAATTCAGGGCAA	SF6- 31R	TGACTGGAGTTCAGACGTGTGCTCTTCCGATC TCACTGAAAAAATATAGACAGAATGA
TTCAGGGCAAAT AAGAGTAGA	agaaacc	SF6- 32F	TACACTCTTTCCCTACACGACGCTCTTCC GATCTAGGCAATTGGCAGCTCTCCACTT C	SF6- 32R	TGACTGGAGTTCAGACGTGTGCTCTTCCGATC TAATCGCTTCTATCTTTCCTGATCTT
AGGTGTGTATTCC AGAATTGA	agcaaag	SF6- 33F	TACACTCTTTCCCTACACGACGCTCTTCC GATCTAGTCATGCCCTTCAGCACAAGTT AC	SF6- 33R	GACTGGAGTTCAGACGTGTGCTCTTCCGATCT TCCGAGATTGTTTATTGATGATTA

Supplementary Table 8| Information in Supplementary Figure 8

gRNA sequence	PAM position 1-7	Forward primer		Reverse primer	
CCAGGAGGGTGA CTCAGGCTA	gcagaaa	SF8-1F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAAGGCCCAGCTCAGTTCTCT	SF8-1R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTGGCCAGCATGAGGAGATGG
CATCATTTGGCTT GATCTTAT	aaagaag	SF8-2F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGGGATGAAAGCAGGGATGC	SF8-2R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGCCTTGCTGAACCTCACTTT
GCCGTGATCACA GGATAGCCT	gcagaga	SF8-3F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGGTGACCCAGATGCCATGA	SF8-3R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCCTCTAGATGACCTTCCCTG
CAGTGAATTCTT AAGCCTTC	agtgagc	SF8-4F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTATTATTATCCCCATTTTACA	SF8-4R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGATGCAGGGAGGTCAGGTTG
CTGATCTTCAAAG GTACAAAG	taagaag	SF8-5F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTATTATTTATAATTCAGGGCA	SF8-5R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTAAAATATAGACAGAATGATT
TTATTTATAATTC AGGGCAAA	taagagt	SF8-6F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGAGTCAGATTGGCAGCTCTC	SF8-6R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCCTGATCTTCAAAGGTACAA
ATCTTCAAAGGT ACAAAGTAA	gaagaga	SF8-7F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTTCTTTCCCAATTATTATATAA	SF8-7R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTAAATATAGACAGAATGATTC

GTCGCAGCTTCA GACCGCGGC	ccaggag	SF8- 8F	TCTTTCCCTACACGACGCTCTTCCGATCTCG TCCCTTTCCAGAGCTGT	SF8- 8R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TTTCCCGAAAACCAGCTCTCT
CACCCCTCCTCCT TTTTGCCG	ttgggag	SF8- 9F	TCTTTCCCTACACGACGCTCTTCCGATCTTT GTCTGCTCCCTGATGGCA	SF8- 9R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TCTGCCGTGACATTGTCCACA
ACACCCCTCCTCC TTTTTGCC	gttggga	SF8- 10F	TCTTTCCCTACACGACGCTCTTCCGATCTCA TTTGTGAGTTGTCTGCTC	SF8- 10R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TCCACAAGGCCAGATACTCTC
CTTACTTTGTACC TTTGAAGA	tcaggaa	SF8- 11F	TCTTTCCCTACACGACGCTCTTCCGATCTCT TGTATCTTTCCCAATTATTTATAA	SF8- 11R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TGAATGATTCTAATTTAGCCT
GGTACAAAGTAA GAAGAGAAA	gatggat	SF8- 12F	TCTTTCCCTACACGACGCTCTTCCGATCTCC ATCTTTCCCAATTATTTA	SF8- 12R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TAATGATTCTAATTTAGCCTG
ATTTGCCCTGAAT TATAAATA	attggga	SF8- 13F	TCTTTCCCTACACGACGCTCTTCCGATCTGC CAATCACTCCCGGAATTTTGGCTT	SF8- 13R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TGATCAGTCCTGATCTTCAAAGGTACA
GCCATAAAAGCT GCCGTGATC	acaggat	SF8- 14F	TCTTTCCCTACACGACGCTCTTCCGATCTGC CAATTGCAGCTTGGGGAATGGTTC	SF8- 14R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TTGGTTTCTAGGTGGGGTTTT
TTTGGGCTTTATG GGCAAGCC	agtggaa	SF8- 15F	TCTTTCCCTACACGACGCTCTTCCGATCTGA AGAGGAAAGTGAGGTTCA	SF8- 15R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TACTGTCCCCAAAAGCCAAG

GGAGGCCGATGG TGGGTGAGT	gggagag	SF8- 16F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTCGTGACATCCAGAAAACGCG	SF8- 16R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TTGACCAAGGGTGGATGTTGGGGTCC
GGGCTGGAAGCA GCTCCAGTG	cccagac	SF8- 17F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGCCGTCTGGTCCAAGCCGG	SF8- 17R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TTAGCTTACGCTCACTCCCTTCACAAG
ACGGTGCCGCGA CCGGCTTGG	accagga	SF8- 18F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTCCCAGAGCCTCAGAGAAGGC	SF8- 18R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCGGTCCCCTGCCACCCTCC
TGGCTTCCACGTA GTGCTCAA	acaaggc	SF8- 19F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTCAGGTATAGGGCATGGGGGT	SF8- 19R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCAATGTCAAGGAAGGGGAAG
ATTATTTATAATT CAGGGCAA	ataagag	SF8- 20F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGAGTCAGATTGGCAGCTCT	SF8- 20R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCTGATCTTCAAAGGTACAAA
GCAACTATCATA GGTGTGTAT	tccagaa	SF8- 21F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTCAGCACAAAGTTACCAGTTTT	SF8- 21R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTTGTATTGTTTATTGATGAT
CCTGATCTTCAAA GGTACAAA	gtaagaa	SF8- 22F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTTTATTTATAATTCAGGGCAA	SF8- 22R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTAAAAATATAGACAGAATGAT
TGCCGTGATCAC AGGATAGCC	tgcagag	SF8- 23F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAAGGTGACCCAGATGCCATG	SF8- 23R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCTCTAGATGACCTTCCCTGC

ATTCTTAAGCCTT CAGTGAGC	tacagag	SF8- 24F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGCTCTCATTATTATCCCCA	SF8- 24R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGGAGGTCAGGTTGTAAAATG
GACCACAGGGAA GGCTGCCAT	aaaagct	SF8- 25F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTTTGATGCAGCTTGGGGAATG	SF8- 25R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTTTCTAGGTGGGGTTTTAAG
TTAAGAATTTGG GCTTTATGG	gcaagcc	SF8- 26F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAAAGTGAGGTTTCAGCAA	SF8- 26R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGGGCTTCCTACTGTC
GCATCATTTGGCT TGATCTTA	taaagaa	SF8- 27F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGGGATGAAAGCAGGGATGC	SF8- 27R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TCAGATCGCCTTGCTGAACCTCACTTT
TGCCATAAAAGC TGCCGTGAT	cacagga	SF8- 28F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTTGCAGCTTGGGGAATGGTTC	SF8- 28R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTCCCTGCATGGTGTTTCT
TCATTTGGCTTGA TCTTATAA	agaagct	SF8- 29F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAGGGATGAAAGCAGGGATGC	SF8- 29R	ACTGGAGTTCAGACGTGTGCTCTTCCGATC TACTTGAGCCTTGCTGAACCTCACTTT
TGCAGGCTATCCT GTGATCAC	ggcagct	SF8- 30F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGGTGACCCAGATGCCATGAG	SF8- 30R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTCCCCCTCTAGATGACCTTCC
GCGGAGGGTGGAA TGTTTGGGG	tccaaca	SF8- 31F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGGAGAGTCCCGGAGAGCAGG	SF8- 31R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTAGCCTAACTCTCCCATTTCGT

AACATCCACCCTC CGCTCGGA	tccaagt	SF8- 32F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGGAGAGTCCCGGAGAGCAGG	SF8- 32R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTAGCTCAGCCTAACTCTCCCA
GAGCAGACAACT CACAAATGC	ttaaagc	SF8- 33F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGGGGTCTCTTGCCA	SF8- 33R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTCCTCCTTTTTGCCGTTGGG
GCGGGATGGACC CTGTTATTC	cctaaga	SF8- 34F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGAGAGTATCTGGCCTTGTGG	SF8- 34R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGGTGGAGGGAACAGCAAGGG
AATTATTTATAAT TCAGGGCA	aataaga	SF8- 35F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTTAGAGTCAGATTGGCAGCTC	SF8- 35R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTGATCTTCAAAGGTACAAAG
GGACCACAGGGA AGGCTGCCA	taaaagc	SF8- 36F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTGTTGATGCAGCTTGGGGAAT	SF8- 36R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTTTCTAGGTGGGGTTTTAAGG
GTTAAGAATTTG GGCTTTATG	ggcaagc	SF8- 37F	TCTACACTCTTTCCCTACACGACGCTCTTCC GATCTAAAGTGAGGTTTCAGCAA	SF8- 37R	GTGACTGGAGTTCAGACGTGTGCTCTTCCG ATCTGGGCTTCCTACTGTC

Supplementary Table 9| Information in Figure 4b and 4c

gRNA sequence	PAM position 1-7	Forward primer		Reverse primer	
AGACAGGAGGAG GAGGTCACC	accatga	F4bc-1F	TCTTTCCCTACACGACGCTCTTCCGATCT ATCACGGACATCCCGAGAGTGACCAC	F4bc-1R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GCTCAGACTCAGGGCCATCC
TGCCTCCTCACTG CTTTCAGG	ccgatgc	F4bc-2F	TCTTTCCCTACACGACGCTCTTCCGATCT CAAGGAGCAGATGTTAACCA	F4bc-2R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GAGGTTCTGCGTCTCACCAC
ATGTTAACCATGC TGCCAAAG	gaaattc	F4bc-3F	TCTTTCCCTACACGACGCTCTTCCGATCT ATCAGGGGAGGAGGTGACCAGGGGAC	F4bc-3R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT CAGATCCTGCCTCCTCACTGCTTTCAGG
AACTTGGATCCG AGCGGAGGG	tggatgt	F4bc-4F	TCTTTCCCTACACGACGCTCTTCCGATCT TTAGGCGGAGAGTCCCGGAGAGCAGG	F4bc-4R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GACGAATGGGAGAGTTAGGC
CCTGCATGGTGGT TTCTAGGT	ggggttt	F4bc-5F	TCTTTCCCTACACGACGCTCTTCCGATCT GATCAGCTGCCATAAAAGCTGCCGTG	F4bc-5R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT ACTTGAAATGTTAGTGATCCCCAGTA
AGTAGGGTGTGG CAGCTGAGA	ggagctg	F4bc-6F	TCTTTCCCTACACGACGCTCTTCCGATCT CAGATCTCAGGTCAGAGAAGGCTTCC	F4bc-6R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT TTAGGCAGCTCTCCTGTCACCCAAAG
CCAAGGGGCATG GAAGGAAGC	ggagttt	F4bc-7F	TCTTTCCCTACACGACGCTCTTCCGATCT GAAGGGTGGGTGAGGGCTTG	F4bc-7R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GCTTCCTGGCTGCTCTCCTG

AGGTCACCACCA TGATCCTGG	aggatga	F4bc- 8F	TCTTTCCCTACACGACGCTCTTCCGATCT GACATCCCGAGAGTGACCAC	F4bc- 8R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT AGGGCTCAGACTCAGGGCCA
TCACCACCATGAT CCTGGAGG	atgactc	F4bc- 9F	TCTTTCCCTACACGACGCTCTTCCGATCT AGACATCCCGAGAGTGACCA	F4bc- 9R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GAAAGGGCTCAGACTCAGGG
ATGATGGCTGCA GACATCCCG	agagtga	F4bc- 10F	TCTTTCCCTACACGACGCTCTTCCGATCT GTGTCTTACCTGAGAGCCTG	F4bc- 10R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT CTCCTGTCTATCTTCCTCTT
ACCTGGACCAAG GAGCTCAGC	ggagtgg	F4bc- 11F	TCTTTCCCTACACGACGCTCTTCCGATCT CTAAGTGATTGCCCCAGGAC	F4bc- 11R	ACTGGAGTTCAGACGTGTGCTCTTCCGATCT GGCTAGTCTTGACCCAGGAGTCATC

Supplementary Table 10| Information in Supplementary Figure 7

spacer sequence	PAM position 1-7	IL1RN forward primer	IL1RN reverse primer	β -ACTIN forward primer	β -ACTIN reverse primer	gene name
AGGCCCTTACC AGATCCCTGT	tgagaag	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
TGCCCTTGCTGT TCCCTCCAC	ctggaat	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CTCCTCCTTTTT GCCGTTGGG	agcgaac	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN

CCAGGAGGGTG ACTCAGGCTA	gcagaaa	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
GAAGGCCCTTA CCAGATCCCT	gttgaga	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CTCCACTCTTAT GTCACCCTC	tcagaga	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ACCCCTCCTCCT TTTTGCCGT	tgggagc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ATGCCAAGCAG GCCAGTTTC	caggagg	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
AGAGGAAATTG AAGGCCCTTA	ccagatc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CCCTCAAAGC ATATCCTGCT	tgggatt	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CAAATGCTTAA AGCCATCCAA	gttgatg	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ACAGAGGGTTG GCCAGCATGA	ggagatg	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
TGTCAGGAGGG ACAGATTGTA	ggtggca	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
GGACCCTGTTAT TCCCTAAGA	catggct	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN

CCATCCAAGTT GATGGGGAGC	agtggca	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
AGGGTTGGCCA GCATGAGGAG	atgggcc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
TTATGAGCCCTT CTGCAAATG	agagggt	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ACTCTTATGTCA CCCTCTCAG	agagggc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ACACCCCTCCTC CTTTTTGCC	gttggga	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
GAGGGTTGGCC AGCATGAGGA	gatgggc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
TATGAGCCCTTC TGCAAATGA	gagggtt	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CTTCCCCTTCCT TGACATTGC	tcaggtc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
ACCCCTGGGCA GGACGAAGTC	ccgggtc	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN
CCAAGCAGGCC CAGTTTCCAG	gagggtg	GGAATCCATGGAG GGAAGAT	TGTTCTCGCTCAGG TCAGTG	CATGTACGTTGCTA TCCAGGC	CTCCTTAATGTCAC GCACGAT	IL1RN

Supplementary Table 11| Information in Supplementary Figure 10

gRNA name	Forward primer		Reverse primer	
gRNA-a-off target-1	aoff-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTTATTTGACACGAAAACG TC	aoff-1R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCTCCACCTTCTCCTCATCTC
gRNA-a-off target-2	aoff-2F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTAACCTGGGTCTCATCTCG GT	aoff-2R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGCTTCTCGCCAGCCTCCTTG
gRNA-a-on site	aon-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTGGCTGCTCTGGGGGCCT CC	aon-1R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGA TCTGGGAGCCCTTCTTCTTCTGC
gRNA-b-off target-1	boff-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTCCCAGTTGTTGATGGGTT TG	boff-1R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCTGGTGTAAACTGATCTATC
gRNA-b-on site	bon-1F	TCTACACTCTTTCCCTACACGACGCTC TTCCGATCTTGTGAATGTTAGACCCAT GG	bon-1R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGA TCTCCAGGGAGGGAGGGGCACAG

Supplementary Table 12| Information in Supplementary Figure 11

gRNA sequence	PAM position 1-7	Forward primer		Reverse primer	
GAACTTGG ATCCGAGC GGAGG	gtggatg	SF11-1F	CTTTCCTACACGACGCTCTTCCGA TCTTCACACCCGGTGTGTAGCTCAG CCTA	SF11-1R	GAGTTCAGACGTGTGCTCTTCCGAT CTTGTCTTGGAGAGTCCCGGAGAG CAGG
TCTGTAGCT CACTGAAG GCTT	aagaatt	SF11-2F	CTTTCCTACACGACGCTCTTCCGA TCTCAGAAGCAGGTTGTAAAATGA AGTGG	SF11-2R	GAGTTCAGACGTGTGCTCTTCCGAT CTATGATATAAAGAAGCTCTCATTA TTA
TTAAGAATT TGGGCTTTA TGG	gcaagcc	SF11-3F	TCTACACTCTTTCCTACACGACGC TCTTCCGATCTAAAGTGAGGTTTCAG CAA	SF11-3R	GTGACTGGAGTTCAGACGTGTGCTC TTCGATCTGGGCTTCCTACTGTC
GAAGCAGC TCCAGTGCC CAGA	cacggtg	SF11-4F	TCTTTCCTACACGACGCTCTTCCG ATCTCGATGTAAGGCGAGGGGGTG GATCTC	SF11-4R	ACTGGAGTTCAGACGTGTGCTCTTC CGATCTACTTGACTTCACAAGGGGC CAGGCGG
TCCGAGCG GAGGGTGG ATGTT	tggggtc	SF11-5F	TCTTTCCTACACGACGCTCTTCCG ATCTCGATGTGGAGAGTCCCGGAG AGCAGG	SF11-5R	ACTGGAGTTCAGACGTGTGCTCTTC CGATCTTTAGGCGCCTAACTCTCCC ATTCGTC
AGGTGTGTA TTCCAGAAT TGA	agcaaag	SF11-6F	TACACTCTTTCCTACACGACGCTC TTCGATCTAGTCATGCCCTTCAGC ACAAGTTAC	SF11-6R	GACTGGAGTTCAGACGTGTGCTCTT CCGATCTTCGAGATTGTTTATTGA TGATTA

Supplementary Table 13 | DNA/protein sequences

Name	DNA/protein sequence	Description
SaCas9-KKH	MPKKKKKVGGGSPGGGGSKRNYILGLDIGITSVGYGIIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRRHRIQR VKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYV AELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRYYEGPGEGSPFGWKDIKEWYEML MGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDEL WHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINE MQKRNRTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIIPRSVSFDNSFNKVLVKQE ENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAGKGRISKTKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYF RVNNLDVKVKSINGGFTSFLRRKWFKKERNKGYKHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEKQAESMPEIET EQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYH HDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNLYTKYSKKNPVIKKIKYYGNKLNALDITDDYPNSRNKVVKLKPYRF DVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVMIDI TYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKGTSGGGSKRPAATKKAGQAKKKKSR	Green:NLS

inactive EYFP reporter gene	ATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGC CACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA CCGGCAAGCTGCCCCTGCCCTGGCCACCCCTCGTGACCACCTTCGGCTACGGCCTGCAGTGCTTCGCCCCGCTACCCC GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAA GGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAA GGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTAT ATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCACAACCACTACCTGAG CTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATTAACCTAGATACGTTCTCTATCACTGATACCCNNN NGCCTGTGCTTCGCCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACC CTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACA ACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCA CAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCT GCTGCCCCGACAACCACTACCTGAGCTACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTC CTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAG	Blue:gRNA spacer sequence Red:3th-6th PAM sequence
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dSaCas9-KKH:VPR	MPKKRKVGGGSPGGGSKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQR VKKLLFDYNLLTDHSELGINPYEARVKGLSQKLEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYV AELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEML MGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDEL WHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINE MQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNPFNYEVDHIIIPRSVSFDNSFNKVLVKQE EASKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYF RVNNLDVKVKSINGGFTSFLRRKWFKKERNKGYKHAEDALIINANADFIFKEWKKLDKAKKVMENQMFEKQAESMPEIET EQEYKEIFITPHQIKHIKDFDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKLINKSPEKLLMYH HDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKNNGPVIKKIKYYGNKLNALHDITDDYPNSRNKVVKLSLKPYRF DVYLDNGVYKFVTVKNLDVIKENYYEVNSKCYEEAKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVMIDI TYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGTSRADPKKKRKVEASGSGRADALDDFDLDM GSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLINRSQYLPDTPDRHRIEEKRKRTYETFKSIMKKSPFSGPTDP RPPPRRIAVPSRSSASVPKPAPQPYPFTSSLSTINYDEFPTMVFPSSGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAP APVPVLAPGPPQAVAPPAPKPTQAGEGTLSEALLQLQFDDDELGALLGNSTDPVFTDLASVDNSEFQQLLNQGIPVAPHT TEPMLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFALLGSGSGSRDSREGMFLPKPEAGSAIS DVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAV KALREMADTVIPQKEEAICGQMDLSHPPPRGHDELTTTLESMTEDLNLDSPLTPELNEILDFTLNDECLHAMHISTGFSIF DTSLF	NLS VPR
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dV42:VPR	MPKKRKVGGGSPGGGSKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQR VKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYV AELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEML MGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDEL WHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINE MQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIIPRSVSFDNSFNKVLVKQE EASKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRIKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYF RVNNLDVKVKSINGGFTSFLRRKWFKKERNKGYKHAEDALIANADFIKEWKKLDKAKKVMENQMFEKQAESMPEIET EQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKLINKSPEKLLMYH HDPQTYQKLKLIMEQYGDENPLYKYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNALHDITDDYPNSRNKVVKLSLKPYRF DVYLDNGVYKFVTVKNLDVIKENYYEVNSKCYEEAKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNNRLNKIENMIDI TYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGTSRADPKKKRKVEASGSGRADALDDFDLDM GSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLINRSQYLPDTPDRHRIEEKRKRTYETFKSIMKKSPFSGPTDP RPPPRRIAVPSRSSASVPKPAPQPYPFTSSLTINYDEFPTMVFPSSQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAP APVPVLAPGPPQAVAPPAPKPTQAGEGTLSEALLQLQFDDDELGALLGNSTDPVFTDLASVDNSEFQQLLNQGIPVAPHT TEPMLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDFSALLGSGSGSRDSREGMFLPKPEAGSAIS DVFEGREVCQPKRIRPFHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDPEETSQAV KALREMADTVIPQKEEAICGQMDLSHPPPRGHDELTTTLESMTEDLNLDSPLTPELNEILDTFLNDECLHAMHISTGFSIF DTSLF	NLS VPR
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Supplementary Table 14 | primers used in quantitative PCR

β -actin-F	CATGTACGTTGCTATCCAGGC
β -actin-R	CTCCTTAATGTCACGCACGAT
IL1RN-F	GGAATCCATGGAGGGAAGAT
IL1RN-R	TGTTCTCGCTCAGGTCAGTG

Supplementary References

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