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# **QBE<sub>max</sub> is a sequence-permuted and internally protected base editor**

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In the format provided by the  
authors and unedited

## **Supplementary Information**

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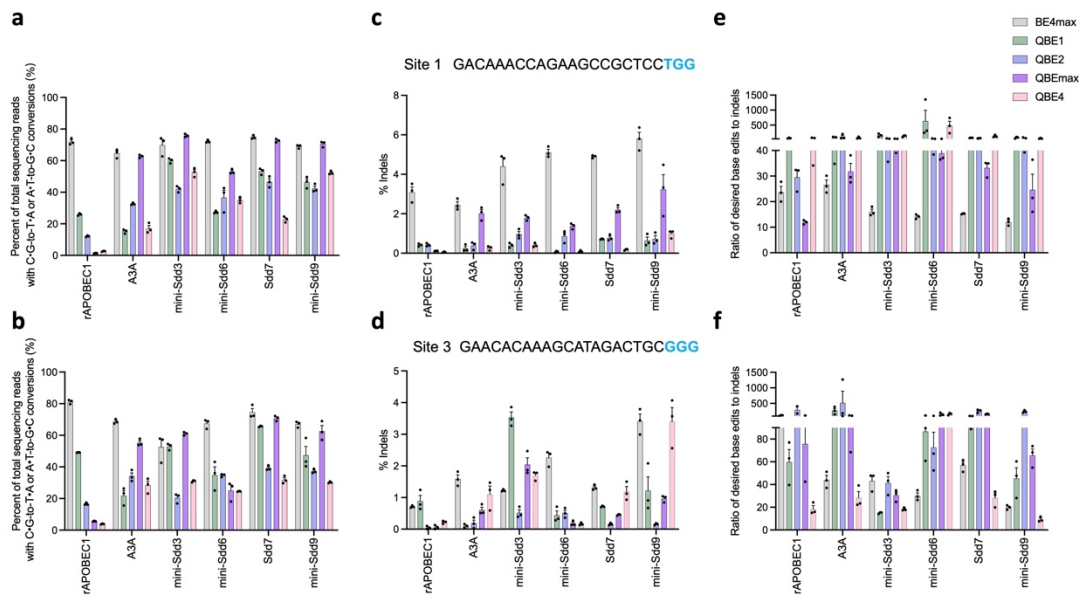
**Supplementary Table 1.** sgRNA list of the 5 CAR-T genes, provided as separate.xlsx. file

**Supplementary Table 2.** All sites used, NGS primers, amplicon sequences.

**Supplementary Table 3.** ipTM and pTM scores of the AlphaFold3 predicted structures.

**Supplementary Sequences**

**Supplementary Figure 1. Editing efficiencies, indels and edit/indel ratios of the QBE editors at site 1 and site 3.**



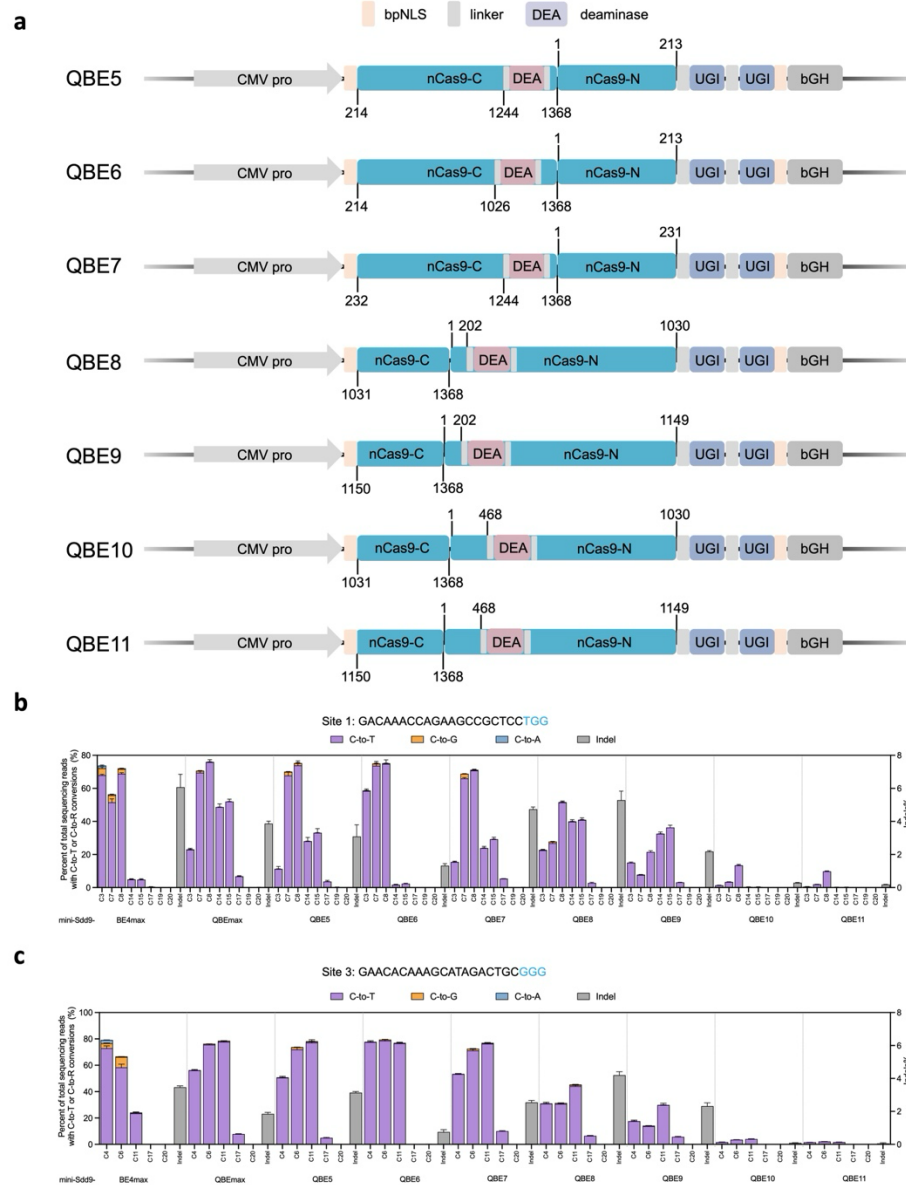
**Supplementary Figure 1. Editing efficiencies, indels and edit/indel ratios of the QBE editors at site 1 and site 3.**

**a-f**, Frequencies of C-to-T or A-to-G conversions (**a-b**), indels (**c-d**), and ratio of base edits to indels (**e-f**) induced by the BE4max, QBEs-based editors at site 1 (upper panel) and site 3 (bottom panel). Values and error bars represent the means and standard errors of the mean for three independent biological replicates.

[illegible]

**a-b**, Frequencies of C-to-T or C-to-R conversions using different QBE editors inlaid with the different deaminases at site 1 (**a**) and site 3 (**b**) at the specified positions in the HEK293T cells. Values and error bars represent the means and standard errors of the mean for three independent biological replicates.

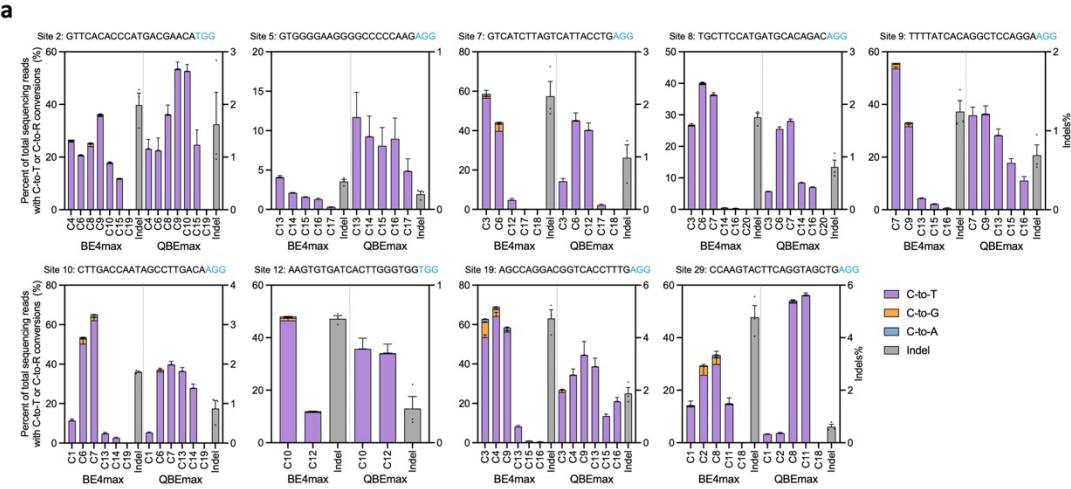
**Supplementary Figure 3. Schematic representations of QBE5 to QBE11 editors and their relative editing properties.**



**Supplementary Figure 3. Schematic representations of the QBE5 to QBE11 editors and their relative editing properties.**

**a**, Schematic representations of the QBE5-QBE11 editors. Numbers under and above nCas9(D10A) represent amino acid positions in reference to wild-type SpCas9. CMV pro, enhanced cytomegalovirus promoter; DEA, deaminase; NLS, nuclear localization signals; bGH, bovine growth hormone polyadenylation signal. **b-c**, Frequencies of C-to-T or C-to-R conversions (left Y axis) and indels (right Y axis) induced by different QBE editors at site 1 (**b**) and site 3 (**c**) at the specified positions in the HEK293T cells. Values and error bars represent the means and standard errors of the mean for three independent biological replicates.

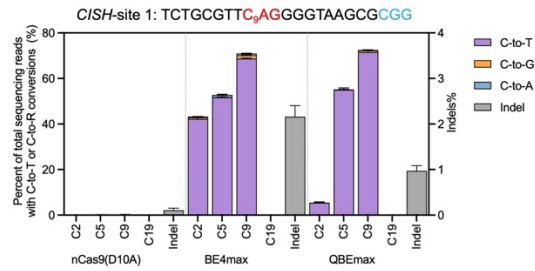
Supplementary Figure 4. Comparison of QBEmax and BE4max at multiple genomic sites.



Supplementary Figure 4. Comparison of QBEmax and BE4max at multiple genomic sites.

**a**, Frequencies of C-to-T or C-to-R conversions (left Y axis) and indels (right Y axis) induced by the mini-Sdd9-BE4max and mini-Sdd9-QBEmax. Values and error bars represent the means and standard errors of the mean for three independent biological replicates.

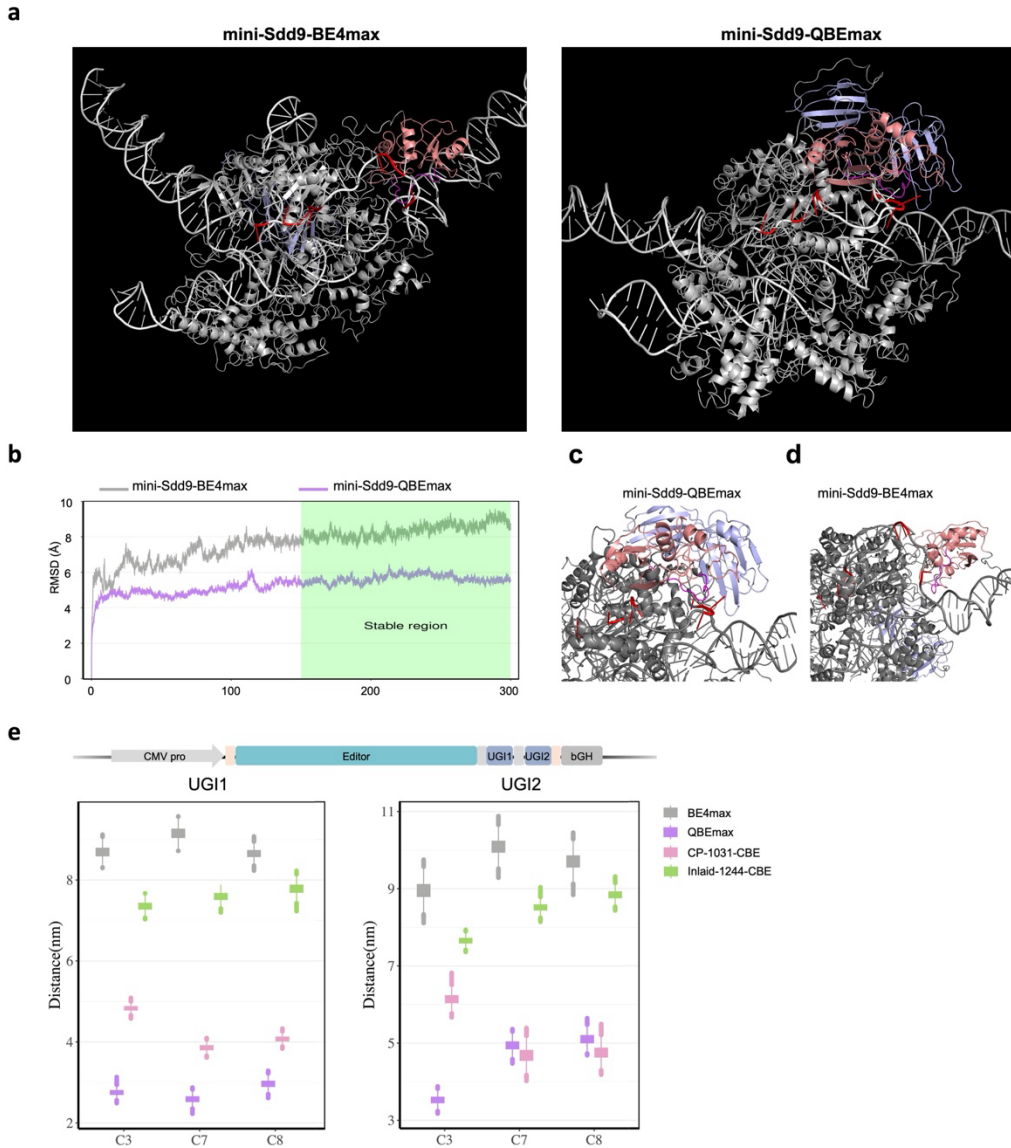
**Supplementary Figure 5. On-target DNA editing efficiencies during RNA-off target analyses.**



**Supplementary Figure 5. On-target DNA editing efficiencies during RNA-off target analyses.**

Frequencies of C-to-T or C-to-R conversions (left Y axis) and indels (right Y axis) induced by nCas9(D10A), BE4max and QBE4max transfected cells. Values and error bars represent the means and standard errors of the mean for two (nCas9(D10A)) or four (BE4max and QBE4max) independent biological replicates.

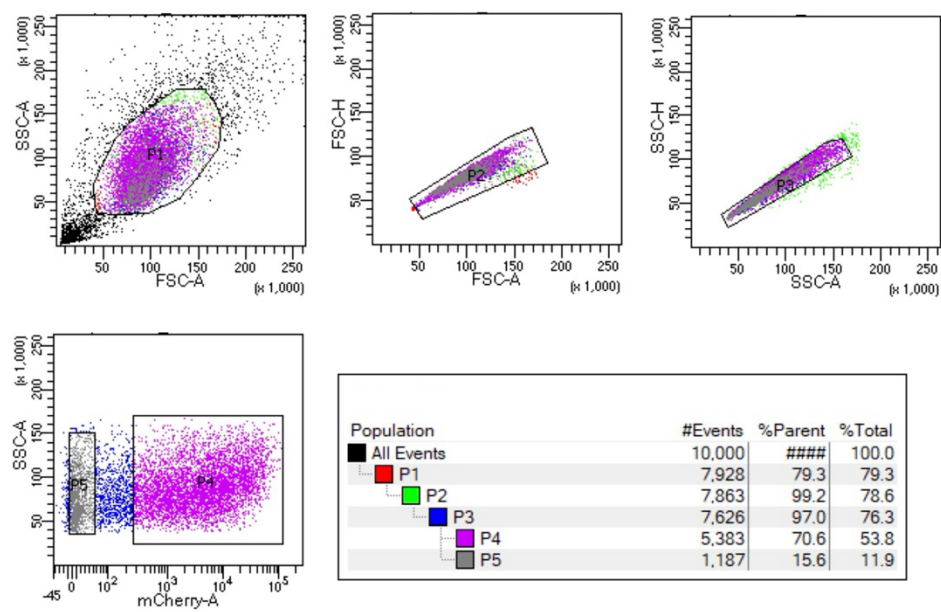
**Supplementary Figure 6. Molecular dynamic analysis of QBEmax.**



**Supplementary Figure 6. Molecular dynamic analysis of QBEmax.**

**a**, Snapshots for mini-Sdd9-BE4max and mini-Sdd9-QBEmax in the 300 ns MD simulations. **b**, RMSD plot for mini-Sdd9-BE4max and mini-Sdd9-QBEmax in the MD simulation, the systems equilibrated after 150 ns; gray, Cas9 domain; pink, mini-Sdd9; blue, UGI; red, catalytic region of mini-Sdd9. **c-d**, Snapshots for mini-Sdd9-QBEmax (**c**) and mini-Sdd9-BE4max (**d**) at the minimum energy state in the MD simulation; gray, Cas9 domain; pink, mini-Sdd9; blue, UGI; red, catalytic region of mini-Sdd9. **e**, Distance of UGI1 (left) and UGI2 (right) to the target Cs of site 1.

**Supplementary Figure 7. Representative examples of gates used to flow sort mScarlet-positive and mScarlet-negative cells for RNA off-target analysis.**



**Supplementary Figure 7. Representative examples of gates used to flow sort mScarlet-positive and mScarlet-negative cells for RNA off-target analysis.**

P4 for mScarlet-positive cells and P5 for mScarlet-negative cells.

**Supplementary Table 1.** sgRNA list of the 5 CAR-T genes, provided as separate xlsx. file

**Supplementary Table 2** (all sites used, NGS primers, amplicon sequences)

| Target site | Target sequence<br>(Without PAM, 5'-to-3') | NGS primers                                                                                                                                                                            | Amplicon sequence                                                                                                                                                                                                                                                                                             |
|-------------|--------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Site 1      | GACAAACCAGAAGCCGCTC<br>C                   | NGS-sitesite1-<br>F5:ACACTCTTTCCTACACGA<br>CGCTCTCCGATCTNNNTACC<br>TATCACAATCACAACCTGC<br>NGS-sitesite1-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGTAACTTAGTT<br>TTCTTGTAGCCC            | TACCTATCACAATCACAACCT<br>GCAATATTACATAAATAGTC<br>TGTTAGAGAAGGACAACCTG<br>AATCTGCAAATCAGTATCTT<br>CTCAATGAGAGTACAAGGA<br>GGCAATGGCTACATACGAT<br>GGACAAACCAGAAGCCGCT<br>CCTGGGCTATGTTTACTATT<br>TACTTTTATGGTATAAAAAAT<br>GTTCTCAGTCAAGCAGTTTC<br>AACAATAGATACCACAGTT<br>CCAATAAAAAGAGGGCTAC<br>AAGAAACTAAGTTAAC |
| Site 2      | GTTACACCCATGACGAAC<br>A                    | NGS-sitesite2-<br>F5:ACACTCTTTCCTACACGA<br>CGCTCTCCGATCTNNNNGGA<br>GCGTGTCCATAGGGTGC<br>NGS-sitesite2-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGACCCGGGTTC<br>ATAACTGTCTG               | GGAGCGTGTCCATAGGGTG<br>CCAGGCTGGCCGCTTCTCCA<br>CGGGCCCTGCCTTCTCACC<br>TGATGATCTTGAGGCTGTTG<br>TCATACTTCTCATGGTTCAC<br>ACCCATGACGAACATGGGG<br>GCATCAGCAGAGGGGGCAG<br>AGATGATGACCCTTTTGGCT<br>CCCCCTGCAAATGAGCCTA<br>CAGCAGAGAAGCAGACAGT<br>TATGAACCCGGGTC                                                      |
| Site 3      | GAACACAAAGCATAGACTG<br>C                   | NGS-sitesite3-250-<br>F:ACACTCTTTCCTACACGAC<br>GCTCTTCCGATCTNNNTAAC<br>AAGACCTGGCTGAGCTAA<br>NGS-sitesite3-250-<br>R:TGGAGTTCAGACGTGTGCTC<br>TTCCGATCTGTGCGTATGACAT<br>CATCAGATATTCTGC | TAACAAGACCTGGCTGAGC<br>TAACTGTGACAGCATGTGGT<br>AATTTTCCAGCCCGCTGGCC<br>CTGTAAAGGAACTGGAAC<br>ACAAAGCATAGACTGCGGG<br>GCGGGCCAGCCTGAATAGC<br>TGCAAACAAGTGCAGAATA<br>TCTGATGATGTCATACGCAC                                                                                                                        |
| Site 5      | GTGGGGAAGGGGCCCCAA<br>G                    | NGS-sitesite5-<br>F6:ACACTCTTTCCTACACGA<br>CGCTCTCCGATCTNNNNCAA<br>GGCTGGCCAACCCATGG<br>NGS-sitesite5-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGTCCTGGTATCC                             | CAAGGCTGGCCAACCCATG<br>GGTGGAGTTTAGCCAGGGA<br>CCGTTTCAGACAGATATTTG<br>CATTGAGATAGTGTGGGGA<br>AGGGGCCCCAAGAGGATA<br>CTGCTAATTTTTTTATAGC<br>CTTTCCTTGTTCGGATTCA                                                                                                                                                 |

|         |                      |                                                                                                                                                                                   |                                                                                                                                                                                                                                                                              |
|---------|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|         |                      | TCTATGATGGG                                                                                                                                                                       | GTCATTCCAGTTTTTCTCTA<br>ATTTATTCTTCCCTTTAGCTA<br>GTTTCCTTCTCCCATCATAG<br>AGGATACCAGGAC                                                                                                                                                                                       |
| Site 7  | GTCATCTTAGTCATTACCTG | NGS-site7-250-<br>F2:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTN<br>NNNAACGGAAGTCAACCATTA<br>AGCA<br>NGS-site7-250-<br>R2:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCCAACATACAGA<br>AGTCAGGAATGC | CAACATACAGAAAGTCAGGA<br>ATGCTTGAATATAAAATTTAT<br>TATTACTCTATGTTCTATTTA<br>AGTTTTCATGTTCTAAAAAT<br>GTATCCCAGTTTACACGTCT<br>CATATGCCCCCTTGGCAGTCA<br>TCTTAGTCATTACCTGAGGT<br>GTTTCGTTGTAATCATATAA<br>ACTGAGTTCCTCATGTTTGC<br>TTAATGGTTGAGTTCCGTT                               |
| Site 8  | TGCTTCCATGATGCACAGAC | NGS-sitesite8-<br>F6:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNAATA<br>TTTGATGAAGTCAGGGAC<br>NGS-sitesite8-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGTCTGTCAAAT<br>CTACCTCCCC       | AATATTTGATGAAGTCAGG<br>GACATTATTATACTTAGTGT<br>GTTTTAAATATTCTCAATTA<br>AGTTACTTTTTCTCCTCTTCT<br>TCTAGCAACGTTTCTACTGTT<br>GCTTCCATGATGCACAGACA<br>GGAGACTGTAGACTGCTTG<br>AAGAAATTTAATGCTAGAA<br>GAAAAGTAAAGGTAAGAAA<br>TTTTACATTTTATGGGGAG<br>GTAGATTGACAGACT                 |
| Site 9  | TTTTATCACAGGCTCCAGGA | NGS-sitesite9-<br>F6:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNTAG<br>GCCAGAAAAGAGATATGGC<br>NGS-sitesite9-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCCAAGAGAGCC<br>TTCCGAAAGA        | TAGGCCAGAAAAGAGATAT<br>GGCATCTACTCTTAGACATA<br>ACACACCAGGGTCAATACA<br>ACTTTGAAGCTAGTCTAGTG<br>CAAGCTAACAGTTGCTTTTA<br>TCACAGGCTCCAGGAAGGG<br>TTTGGCCTCTGATTAGGGTG<br>GGGGCGTGGGTGGGGTAGA<br>AGAGGACTGGCAGACCTCT<br>CCATCGGTGGCCGTTTGCCC<br>AGGGGGGCCTCTTTCGGAA<br>GGCTCTCTTG |
| Site 10 | CTTGACCAATAGCCTTGACA | NGS-sitesite10-<br>F5:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNCAG<br>CAGTATCCTCTTGGGGG<br>NGS-sitesite10-<br>R5:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGAACTGCTGAA                      | CAGCAGTATCCTCTTGGGGG<br>CCCCTTCCCCACACTATCTC<br>AATGCAAATATCTGTCTGAA<br>ACGGTCCCTGGCTAAACTCC<br>ACCCATGGGTTGGCCAGCCT<br>TGCCTTGACCAATAGCCTTG<br>ACAAGGCAAACCTTGACCAA                                                                                                         |

|         |                          |                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                    |
|---------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|         |                          | GGGTGCTTCC                                                                                                                                                             | TAGTCTTAGAGTATCCAGTG<br>AGGCCAGGGGCCGGCGGCT<br>GGCTAGGGATGAAGAATAA<br>AAGGAAGCACCCCTCAGCA<br>GTTC                                                                                                                                                                                                  |
| Site 11 | CGGAGTTCGCCCTGGAGAG<br>G | NGS-Site11-F :<br>ACACTCTTTCCTACACGACG<br>CTCTCCGATCTNNNNCTGTC<br>TCAGTTCTCAGTCCGG<br>NGS-Site11-R :<br>GACTGGAGTTCAGACGTGTGC<br>TCTTCCGATCTTAGCTCTGCCT<br>TATGGGGAGG  | CTGTCTCAGTTCTCAGTCCG<br>GTTTCTTCGTATCTTGAGAG<br>TTTATCCAGGCACCTCCAGC<br>CCAGCAGTGACAGGCTGT<br>GTGTCGGAGTTCGCCCTGGA<br>GAGGTGGGTACTCTGCAGA<br>CCACGTGTGAAAGGCTTCCG<br>AACATCAGCTCTTGTGCCTG<br>CCTCTCCTCCCCATAAAGCA<br>GAGCTA                                                                        |
| Site 12 | AAGTGTGATCACTTGGGTGG     | NGS-Site12-F :<br>GACTGGAGTTCAGACGTGTGC<br>TCTTCCGATCTTAGCTCTGCCT<br>TATGGGGAGG<br>NGS-Site12-R :<br>GACTGGAGTTCAGACGTGTGC<br>TCTTCCGATCTGAGCTGCAGG<br>TGTAATGAAGACC   | AATGTGTCAACTCTTGACAG<br>GGCTCTATTTTATAGGCTTC<br>TTCTCTGGAATCTTCTTCAT<br>CATCCTCCTGACAATCGATA<br>GGTACCTGGCTGTCTGCCAT<br>GCTGTGTTTGCTTTAAAAGC<br>CAGGACGGTCACCTTTGGG<br>GTGGTGACAAGTGTGATCA<br>CTTGGGTGGTGGCTGTGTTT<br>GCGTCTCTCCCAGGAATCAT<br>CTTACCAGATCTCAAAAAG<br>AAGGTCTTCATTACACCTGC<br>AGCTC |
| Site 13 | CAGGACGGTCACCTTTGGG<br>G | NGS-Site13-F :<br>ACACTCTTTCCTACACGACG<br>CTCTCCGATCTNNNNAATGT<br>GTCAACTCTTGACAGGG<br>NGS-Site13-<br>R:GACTGGAGTTCAGACGTGT<br>GCTCTTCCGATCTGAGCTGCA<br>GGTGAATGAAGACC | AATGTGTCAACTCTTGACAG<br>GGCTCTATTTTATAGGCTTC<br>TTCTCTGGAATCTTCTTCAT<br>CATCCTCCTGACAATCGATA<br>GGTACCTGGCTGTCTGCCAT<br>GCTGTGTTTGCTTTAAAAGC<br>CAGGACGGTCACCTTTGGG<br>GTGGTGACAAGTGTGATCA<br>CTTGGGTGGTGGCTGTGTTT<br>GCGTCTCTCCCAGGAATCAT<br>CTTACCAGATCTCAAAAAG<br>AAGGTCTTCATTACACCTGC<br>AGCTC |
| Site 15 | GGTACCTATCGATTGTCAGG     | NGS-Site15-<br>F:ACACTCTTTCCTACACGAC<br>GCTCTTCCGATCTNNNNAATG                                                                                                          | GAGCTGCAGGTGTAATGAA<br>GACCTTCTTTTGAGATCTG<br>GTAAAGATGATTCTGGGA                                                                                                                                                                                                                                   |

|         |                          |                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                    |
|---------|--------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|         |                          | TGTCAACTCTTGACAGGG<br>NGS-Site15-<br>R:GACTGGAGTTCAGACGTGT<br>GCTCTTCCGATCTGAGCTGCA<br>GGTGTAATGAAGACC                                                                   | GAGACGCAAACACAGCCAC<br>CACCCAAGTGATCACACTTG<br>TCACCACCCCAAGGTGAC<br>CGTCCTGGCTTTTAAAGCAA<br>ACACAGCATGGACGACAGC<br>CAGGTACCTATCGATTGTCA<br>GGAGGATGATGAAGAAGAT<br>TCCAGAGAAGAAGCCTATA<br>AAATAGAGCCCTGTCAAGA<br>GTTGACACATT                                                                       |
| Site 17 | GGATTGACCCAGGCCAGGG<br>C | NGS-Site17-<br>F:ACACTCTTTCCCTACACGAC<br>GCTCTTCCGATCTNNNNAGCA<br>TGCATTTGTAGGCTTGAT<br>NGS-Site17-R:<br>TGGAGTTCAGACGTGTGCTCT<br>TCCGATCTCCAGCCAACTT<br>GTCAACC         | CCCAGCCAAACTTGTCAACC<br>AGTATCCCGGTGCAGGAGC<br>TGCACATACTAGCCCCCTGTC<br>TAGGAAAAGCTGTCCTGCG<br>ACGCCCTCTGGAGGAAGCA<br>GGGCTTCCTTTCCTCTGCCA<br>TCACGTGCTCAGTCTGGGCC<br>CCAAGGATTGACCCAGGCC<br>AGGGCTGGAGAAGCAGAAA<br>AAAAGCATCAAGCCTACAA<br>ATGCATGCT                                               |
| Site 19 | AGCCAGGACGGTCACCTTTG     | NGS-Site19-<br>F:ACACTCTTTCCCTACACGAC<br>GCTCTTCCGATCTNNNNAATG<br>TGTCAACTCTTGACAGGG<br>NGS-Site19-<br>R:GACTGGAGTTCAGACGTGT<br>GCTCTTCCGATCTGAGCTGCA<br>GGTGTAATGAAGACC | AATGTGTCAACTCTTGACAG<br>GGCTCTATTTTATAGGCTTC<br>TTCTCTGGAATCTTCTTCAT<br>CATCCTCCTGACAATCGATA<br>GGTACCTGGCTGTCGTCCAT<br>GCTGTGTTTGCTTTAAAAGC<br>CAGGACGGTCACCTTTGGG<br>GTGGTGACAAGTGTGATCA<br>CTTGGGTGGTGGCTGTGTTT<br>GCGTCTCTCCAGGAATCAT<br>CTTTACCAGATCTCAAAAAG<br>AAGGTCTTCATTACACCTGC<br>AGCTC |
| Site 21 | CCAAGGATTGACCCAGGCC<br>A | NGS-Site21-<br>F:ACACTCTTTCCCTACACGAC<br>GCTCTTCCGATCTNNNNAGCA<br>TGCATTTGTAGGCTTGAT<br>NGS-Site21-<br>R:TGGAGTTCAGACGTGTGCTC<br>TTCCGA<br>TCTCCAGCCAACTTGTCAA<br>CC     | CCCAGCCAAACTTGTCAACC<br>AGTATCCCGGTGCAGGAGC<br>TGCACATACTAGCCCCCTGTC<br>TAGGAAAAGCTGTCCTGCG<br>ACGCCCTCTGGAGGAAGCA<br>GGGCTTCCTTTCCTCTGCCA<br>TCACGTGCTCAGTCTGGGCC<br>CCAAGGATTGACCCAGGCC<br>AGGGCTGGAGAAGCAGAAA                                                                                   |

|            |                          |                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                 |
|------------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|            |                          |                                                                                                                                                                        | AAAAGCATCAAGCCTACAA<br>ATGCATGCT                                                                                                                                                                                                                                                                                                |
| Site 22    | CCACCGCTGCGCCAAGGTG<br>C | NGS-Site22-<br>F:ACACTCTTTCCCTACACGAC<br>GCTCTTCCGATCTNNNNCTAG<br>CCTTGCGTTCCGAGG<br>NGS-Site22-<br>R:TGGAGTTCAGACGTGTGCTC<br>TTCCGATCTCCTGCAGTCCCCA<br>AGA            | CTAGCCTTGCGTTCCGAGGA<br>GGACGGCCTGGCCGAAGCA<br>CCCGAGCACGGAACACAG<br>CCACCTTCCACCGCTGCGCC<br>AAGGTGCGGGTGTAGGGGT<br>GGGAGGCCGGGGCGAACCC<br>GCAGCCGGGACGGTGCGGT<br>GCTGTTTCTCTCGGGCCTC<br>AGTTTCCCCCATGTAAGAG<br>AGGAAGTGGAGTGCAGGTC<br>GCCGAGGGCTCTTCGCTTGG<br>CACGATCTTGGGGACTGCA<br>GG                                        |
| Site 29    | CCAAGTACTTCAGGTAGCTG     | NGS-Site29-<br>F:ACACTCTTTCCCTACACGAC<br>GCTCTTCCGATCTNNNNGGCT<br>TATGAAGGCAGAGACTGA<br>NGS-Site29-<br>R:TGGAGTTCAGACGTGTGCTC<br>TTCCGATCTGTACCTCTCCTT<br>TCCAAGGCAC   | GGCTTATGAAGGCAGAGAC<br>TGAGAATGAGTTGAAAAGT<br>CAGTAGTAAAAAGAATTG<br>AGAGCATGGGGTAAGGAGA<br>GATTCAACTCTGGGCAATCC<br>CAAGTACTTCAGGTAGCTGA<br>GGTCAAGTTTAGTCTGGTAT<br>TGAAATAATTCAAATAATGT<br>TCACTGTTGGATTGTGAATT<br>AGGTAAAAATAGTCTCAAG<br>TGCCCATCCACATGCCCTA<br>ACAAATTCAGGACTCCTCCT<br>AACACACCAAAGTGCCTTG<br>GAAAGGAGAGGTAAC |
| PD1-site 1 | ACGACTGGCCAGGGCGCCT<br>G | NGS-PD1site1-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site1-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCAGTT<br>GTAGCACCGCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT                                                                                                        |
| PD1-site 2 | CGACTGGCCAGGGCGCCTG<br>T | NGS-PD1site2-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site2-                                                                 | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCAGTT                                                                                                                                                                                                               |

|            |                          |                                                                                                                                                                        |                                                                                                                                                                                                                            |
|------------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|            |                          | 2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT                                                                                                           | GTAGCACCGCCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT                                                                                                                       |
| PD1-site 3 | TGTAGCACCGCCCAGACGA<br>C | NGS-PD1site3-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site3-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCCAGTT<br>GTAGCACCGCCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT |
| PD1-site 4 | CACCGCCCAGACGACTGGC<br>C | NGS-PD1site4-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site4-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCCAGTT<br>GTAGCACCGCCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT |
| PD1-site 5 | ACCGCCCAGACGACTGGCC<br>A | NGS-PD1site5-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site5-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCCAGTT<br>GTAGCACCGCCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT |
|            |                          |                                                                                                                                                                        |                                                                                                                                                                                                                            |
| PD1-site 7 | GGGCGGTGCTACAACTGGG<br>C | NGS-PD1site7-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site7-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AGTGGAGAAGGCGGCACTC<br>TGGTGGGGCTGCTCCAGGC<br>ATGCAGATCCCACAGGCGC<br>CCTGGCCAGTCGTCTGGGCG<br>GTGCTACAACTGGGCTGGC<br>GGCCAGGATGGTTCTTAGGT<br>AGGTGGGGTCGGCGGTCAG<br>GTGTCCCAGAGCCAGGGGT                                     |

|             |                          |                                                                                                                                                                          |                                                                                                                                                                                                                                      |
|-------------|--------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             |                          |                                                                                                                                                                          | CTGGAGGGACCTTCCACCCT<br>CAGTCCCT                                                                                                                                                                                                     |
| PD1-site 8  | CGGTGCTACAACTGGGCTG<br>G | NGS-PD1site8-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site8-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT   | AGTGGAGAAGGCGGCACTC<br>TGGTGGGGGTGCTCCAGGC<br>ATGCAGATCCCACAGGCGC<br>CCTGGCCAGTCGTCTGGGCG<br>GTGCTACAACTGGGCTGGC<br>GGCCAGGATGGTTCTTAGGT<br>AGGTGGGGTCGGCGGTGAG<br>GTGTCCCAGAGCCAGGGGT<br>CTGGAGGGACCTTCCACCCT<br>CAGTCCCT           |
| PD1-site 9  | CTACAACTGGGCTGGCGGC<br>C | NGS-PD1site9-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site9-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT   | AGTGGAGAAGGCGGCACTC<br>TGGTGGGGGTGCTCCAGGC<br>ATGCAGATCCCACAGGCGC<br>CCTGGCCAGTCGTCTGGGCG<br>GTGCTACAACTGGGCTGGC<br>GGCCAGGATGGTTCTTAGGT<br>AGGTGGGGTCGGCGGTGAG<br>GTGTCCCAGAGCCAGGGGT<br>CTGGAGGGACCTTCCACCCT<br>CAGTCCCT           |
| PD1-site 10 | CAGCAACCAGACGGACAAG<br>C | NGS-PD1site10-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACTCTNGS-<br>PD1site10-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT | AACACATCGGAGAGCTTCG<br>TGCTAAACTGGTACCGCATG<br>AGCCCCAGCAACCAGACGG<br>ACAAGCTGGCCGCCTTCCCC<br>GAGGACCGCAGCCAGCCCG<br>GCCAGGACTGCCGCTTCCGT<br>GTCACACAACTGCCAACG<br>GGCGTGACTTCCACATGAGC<br>GTGGTCAGGGCCCGGCGCA<br>ATGACAGCGGCACCTACC |
| PD1-site 11 | CGTGTCACACAACTGCCAA<br>A | NGS-PD1site11-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNACC<br>TGCAGCTTCTCCAAC<br>NGS-PD1site11-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGGTAGGTGCCG<br>CTGTATTG    | AACACATCGGAGAGCTTCG<br>TGCTAAACTGGTACCGCATG<br>AGCCCCAGCAACCAGACGG<br>ACAAGCTGGCCGCCTTCCCC<br>GAGGACCGCAGCCAGCCCG<br>GCCAGGACTGCCGCTTCCGT<br>GTCACACAACTGCCAACG<br>GGCGTGACTTCCACATGAGC<br>GTGGTCAGGGCCCGGCGCA<br>ATGACAGCGGCACCTACC |
| PD1-site 12 | GTGTCACACAACTGCCAA<br>A  | NGS-PD1site12-<br>2F:ACACTCTTTCCCTACACGA                                                                                                                                 | AACACATCGGAGAGCTTCG<br>TGCTAAACTGGTACCGCATG                                                                                                                                                                                          |

|             |                          |                                                                                                                                                                             |                                                                                                                                                                                                                                                       |
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|             |                          | CGCTCTCCGATCTNNNNACC<br>TGCAGCTTCTCCAAC<br>NGS-PD1site12-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGGTAGGTGCCG<br>CTGTCATTG                                                   | AGCCCCAGCAACCAGACGG<br>ACAAGCTGGCCGCCTTCCCC<br>GAGGACCGCAGCCAGCCCG<br>GCCAGGACTGCCGCTTCCGT<br>GTCACAACTGCCCAACG<br>GGCGTGAATTCCACATGAGC<br>GTGGTCAGGGCCCCGGCGCA<br>ATGACAGCGGCACCTACC                                                                 |
| PD1-site 13 | CACCTACCTAAGAACCATCC     | NGS-PD1site13-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>GGAGAAGGCGGCACT<br>NGS-PD1site13-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGGACTGAGG<br>GTGGAAGGT       | AGGGACTGAGGGTGGAAGG<br>TCCCTCCAGACCCCTGGCTC<br>TGGGACACCTGACCGCCGA<br>CCCCACCTACCTAAGAACCA<br>TCCTGGCCGCCAGCCCAGTT<br>GTAGCACCGCCAGACGAC<br>TGGCCAGGGCGCCTGTGGG<br>ATCTGCATGCCTGGAGCAGC<br>CCCACCAGAGTGCCGCCTTC<br>TCCACT                             |
| PD1-site 14 | CGCAGATCAAAGAGAGCCT<br>G | NGS-PD1site14-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNCGT<br>GACTTCCACATGAGCGTGG<br>NGS-PD1site14-<br>3R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTGATCCTGTGCA<br>GGAGGGGACA | CGTGAATTCCACATGAGCGT<br>GGTCAGGGCCCCGGCGCAAT<br>GACAGCGGCACCTACCTCTG<br>TGGGGCCATCTCCCTGGCCC<br>CCAAGGCGCAGATCAAAGA<br>GAGCCTGCGGGCAGAGCTC<br>AGGGTGACAGGTGCGGCCT<br>CGGAGGCCCCGGGGCAGGG<br>GTGAGCTGAGCCGGTCTCTG<br>GGGTGGGTGTCCCCTCCTGC<br>ACAGGATCA |
| PD1-site 15 | CGGCCAGTTCCAAACCCTGG     | NGS-PD1site15-<br>4F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNTAA<br>CCCCTGACCTTTGTGCCC<br>NGS-PD1site15-<br>3R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGACCCAGAC<br>TAGCAGCACCA  | TAACCCCTGACCTTTGTGCC<br>CTTCCAGAGAGAAGGGCAG<br>AAGTGCCACAGCCCACCC<br>CAGCCCCTACCCAGGCCA<br>GCCGGCCAGTTCCAAACCCT<br>GGTGGTTGGTGTCTGGGGCG<br>GCCTGCTGGGCAGCCTGGTG<br>CTGCTAGTCTGGGTCCT                                                                  |
| PD1-site 16 | AGCCGGCCAGTTCCAAACC<br>C | NGS-PD1site16-<br>4F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNTAA<br>CCCCTGACCTTTGTGCCC<br>NGS-PD1site16-<br>3R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGACCCAGAC                 | TAACCCCTGACCTTTGTGCC<br>CTTCCAGAGAGAAGGGCAG<br>AAGTGCCACAGCCCACCC<br>CAGCCCCTACCCAGGCCA<br>GCCGGCCAGTTCCAAACCCT<br>GGTGGTTGGTGTCTGGGGCG                                                                                                               |

|             |                            |                                                                                                                                                                          |                                                                                                                                                                                                                                                    |
|-------------|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             |                            | TAGCAGACCA                                                                                                                                                               | GCCTGCTGGGCAGCCTGGTG<br>CTGCTAGTCTGGGTCCT                                                                                                                                                                                                          |
| PD1-site 17 | CAGTTCCAAACCCTGGTGGT       | NGS-PD1site17-<br>4F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNTAA<br>CCCCTGACCTTTGTGCCC<br>NGS-PD1site17-<br>3R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAGGACCCAGAC<br>TAGCAGACCA | TAACCCCTGACCTTTGTGCC<br>CTTCCAGAGAGAAGGGCAG<br>AAGTGCCACAGCCCACCC<br>CAGCCCCACCCAGGCCA<br>GCCGGCCAGTTCCAAACCCT<br>GGTGGTTGGTGTCTGGGCG<br>GCCTGCTGGGCAGCCTGGTG<br>CTGCTAGTCTGGGTCCT                                                                 |
| CISH-site 1 | TCTGCGTTCAGGGTAAGCG        | NGS-CISHsite1-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNACT<br>GGTTCCTCCAGCCG<br>NGS-CISHsite1-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCTGCGCTCAGT<br>CACCTCTG      | ACTGGTTCCTCCAGCCGCC<br>GCCGTCCAGCCGAGTCCCCA<br>CTCCGAGTCGCCGCTGCCG<br>CGGGGACATGGTCTCTGCC<br>TTCAGGGTAAGCGCGGCT<br>CTCTGCCCCCTTCCGGCCA<br>CCACGAGGGGCGCACGGGA<br>GAACAGGGGCTTCGTGCTA<br>GCTGCCGGGCATTGGGAGG<br>GCTTGACGGGCCAGAGGTG<br>ACTGAGCGCAGA |
| CISH-site 2 | GGACTGGGCAGCGGCCCT<br>GTGG | NGS-CISHsite2-2F:ACA<br>CTCTTTCCTACACGACGCTC<br>TTCCGATCTNNNACTCACTG<br>CTCATCCACTGCC<br>NGS-CISHsite2-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCCAGCACCTT<br>GGCTCACTCT | ACTCACTGCTCATCCACTGC<br>CTTCTAGACCTCGTCCTTTG<br>CTGGCTGTGGAGCGGACTG<br>GGCAGCGGCCCTGTGGGC<br>CCCGTCCCTGGAAGTCCCCA<br>AGCCAGTCATGCAGCCCTTG<br>CCTGCTGGGGCCTTCCTCGA<br>GGAGGTGGCAGAGGGTACC<br>CCAGCCCAGACAGAGAGTG<br>AGCCAAAGGTGCTGGA                |
| CISH-site 3 | GACTGGGCAGCGGCCCTG<br>T    | NGS-CISHsite3-2F:ACA<br>CTCTTTCCTACACGACGCTC<br>TTCCGATCTNNNACTCACTG<br>CTCATCCACTGCC<br>NGS-CISHsite3-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCCAGCACCTT<br>GGCTCACTCT | ACTCACTGCTCATCCACTGC<br>CTTCTAGACCTCGTCCTTTG<br>CTGGCTGTGGAGCGGACTG<br>GGCAGCGGCCCTGTGGGC<br>CCCGTCCCTGGAAGTCCCCA<br>AGCCAGTCATGCAGCCCTTG<br>CCTGCTGGGGCCTTCCTCGA<br>GGAGGTGGCAGAGGGTACC<br>CCAGCCCAGACAGAGAGTG<br>AGCCAAAGGTGCTGGA                |
| CISH-site 4 | GTTCCAGGGACGGGGCCCA<br>C   | NGS-CISHsite4-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNACT                                                                                                          | ACTCACTGCTCATCCACTGC<br>CTTCTAGACCTCGTCCTTTG<br>CTGGCTGTGGAGCGGACTG                                                                                                                                                                                |

|             |                          |                                                                                                                                                                             |                                                                                                                                                                                                                                                           |
|-------------|--------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|             |                          | CACTGCTCATCCACTGCC<br>NGS-CISHsite4-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCCAGCACCTTT<br>GGCTCACTCT                                                                      | GGCAGCGGCCCTGTGGGC<br>CCCGTCCCTGGAAGTGCCCA<br>AGCCAGTCATGCAGCCCTTG<br>CCTGCTGGGGCCTTCCTCGA<br>GGAGGTGGCAGAGGGTACC<br>CCAGCCCAGACAGAGAGTG<br>AGCCAAAGGTGCTGGA                                                                                              |
| CISH-site 5 | GTCATGCAGCCCTGCCTGC      | NGS-CISHsite5-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNACT<br>CACTGCTCATCCACTGCC<br>NGS-CISHsite5-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCCAGCACCTTT<br>GGCTCACTCT  | TCCAGCACCTTTGGCTCACT<br>CTCTGTCTGGGCTGGGGTAC<br>CCTCTGCCACCTCCTCGAGG<br>AAGGCCCCAGCAGGCAAGG<br>GCTGCATGACTGGCTTGGGC<br>AGTTCCAGGGACGGGGCCC<br>ACAGGGGCCGCTGCCCAGT<br>CCGCTCCACAGCCAGCAAA<br>GGACGAGGTCTAGAAGGCA<br>GTGGATGAGCAGTGAGT                      |
| CISH-site 6 | TGGAACCCCAATACCAGCT      | NGS-CISHsite6-<br>1F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNGAA<br>GCTGGAGGCACTGCCTTGA<br>NGS-CISHsite6-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCACTGACAGCG<br>TGAACAGGTAG | CACTGACAGCGTGAACAGG<br>TAGCTGGGGTGCGTGCTGTC<br>ACGTACTAAGAACGTGCCTT<br>CTGGCATCTTCTGCAGGTGT<br>TGTGGGGCCTCGCTGGCCGT<br>AATGGAACCCCAATACCAG<br>CCTAGGCAAGTGACAGAGGG<br>GGCCAAGGGACATAGTGGA<br>AATTAGCTGGGGTAACCAA<br>TCCAGTGCAAGTCAAGGCA<br>GTGCCTCCAGCTTC |
| CISH-site 7 | TCATGCAGCCCTGCCTGCT      | NGS-CISHsite5-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNACT<br>CACTGCTCATCCACTGCC<br>NGS-CISHsite5-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTCCAGCACCTTT<br>GGCTCACTCT  | TCCAGCACCTTTGGCTCACT<br>CTCTGTCTGGGCTGGGGTAC<br>CCTCTGCCACCTCCTCGAGG<br>AAGGCCCCAGCAGGCAAGG<br>GCTGCATGACTGGCTTGGGC<br>AGTTCCAGGGACGGGGCCC<br>ACAGGGGCCGCTGCCCAGT<br>CCGCTCCACAGCCAGCAAA<br>GGACGAGGTCTAGAAGGCA<br>GTGGATGAGCAGTGAGT                      |
| CISH-site 8 | CACCTGCAGAAGATGCCAG<br>A | NGS-CISHsite8-<br>1F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNGAA<br>GCTGGAGGCACTGCCTTGA<br>NGS-CISHsite8-<br>1R:TGGAGTTCAGACGTGTGCT                                         | GAAGCTGGAGGCACTGCCT<br>TGAAGTGCAGTGGATTGGTT<br>ACCCCAGCTAATTCCACTA<br>TGTCCCTTGGCCCCCTCTGC<br>ACTTGCTAGGCTGGTATTG<br>GGGTTCCATTACGGCCAGCG                                                                                                                 |

|                 |                          |                                                                                                                                                                                 |                                                                                                                                                                                                                                                                |
|-----------------|--------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                 |                          | CTTCGATCTCACTGACAGCG<br>TGAACAGGTAG                                                                                                                                             | AGGCCCCGACAAACACCTGCA<br>GAAGATGCCAGAAGGCACG<br>TTCTTAGTACGTGACAGCAC<br>GCACCCCAGCTACCTGTTCA<br>CGCTGTCAGTG                                                                                                                                                    |
| CISH-site 9     | CAGCCTTGTGCAGCACTATG     | NGS-CISHsite9-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNACT<br>CCAGCTTCCGTCTGGACTC<br>NGS-CISHsite9-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCGATCTGTACAGCAGTG<br>GCTGGTGGA       | ACTCCAGCTTCCGTCTGGAC<br>TCCAAGTCTTGTCCAGGCC<br>ACGCATCCTGGCCTTTCCGG<br>ATGTGGTCAGCCTTGTGCAG<br>CACTATGTGGCCTCCTGCAC<br>TGCTGATACCCGAAGCGAC<br>AGCCCCGATCCTGCTCCAC<br>CCCGGCCCTGCCTATGCCTA<br>AGGAGGATGCGCCTAGTGA<br>CCCAGCACTGCCTGCTCCTC<br>CACCAGCCACTGCTGTAC |
| CISH-site<br>10 | CTCACCAGATTCCCGAAGGT     | NGS-CISHsite10-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNACT<br>CCAGCTTCCGTCTGGACTC<br>NGS-CISHsite10-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCGATCTGTACAGCAGTG<br>GCTGGTGGA     | TCAAGGCAGTGCTCCAGCT<br>TCACGCTTCCCTAGAGAGGG<br>CTGTGCCTCTCCCATCAGAC<br>TCTCTGGGCGGGCTATGC<br>CTCCCAAATCAGACTCAA<br>GGCAGAACTAAGCTTCTCCC<br>ACCAGACTACTCAGGAAAA<br>GGCCTGCCTCCCCCTCAGA<br>CTCACCAGATTCCCGAAGGT<br>AGGAGAAGGTCTTGGCTAT<br>GCACAGCAGATCCTCC       |
| FAS-site 1      | GACTGCGTGCCCTGCCAAG<br>A | NGS-FASsite1-<br>10F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGGA<br>AAGCTAGGGACTGCACAGT<br>NGS-FASsite1-<br>7R:TGGAGTTCAGACGTGTGCT<br>CTTCGATCTCCAATTCTAAGC<br>CATGTCCTTCATCAC | GGAAAGCTAGGGACTGCAC<br>AGTCAATGGGGATGAACCA<br>GACTGCGTGCCCTGCCAAG<br>AAGGGAAGGAGTACACAGA<br>CAAAGCCCATTTTCTTCCA<br>AATGCAGAAGATGTAGATT<br>GTGTGATGAAGGACATGGC<br>TTAGAAGTGG                                                                                    |
| FAS-site 2      | ACTGCGTGCCCTGCCAAGA<br>A | NGS-FASsite2-<br>10F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGGA<br>AAGCTAGGGACTGCACAGT<br>NGS-FASsite2-<br>7R:TGGAGTTCAGACGTGTGCT<br>CTTCGATCTCCAATTCTAAGC<br>CATGTCCTTCATCAC | GGAAAGCTAGGGACTGCAC<br>AGTCAATGGGGATGAACCA<br>GACTGCGTGCCCTGCCAAG<br>AAGGGAAGGAGTACACAGA<br>CAAAGCCCATTTTCTTCCA<br>AATGCAGAAGATGTAGATT<br>GTGTGATGAAGGACATGGC<br>TTAGAAGTGG                                                                                    |

|            |                          |                                                                                                                                                                                  |                                                                                                                                                                                     |
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| FAS-site 3 | CGTGCCCTGCCAAGAAGGG<br>A | NGS-FASsite3-<br>10F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGGA<br>AAGCTAGGGACTGCACAGT<br>NGS-FASsite3-<br>7R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCCACTTCTAAGC<br>CATGTCCTTCATCAC | GGAAAGCTAGGGACTGCAC<br>AGTCAATGGGGATGAACCA<br>GACTGCGTGCCCTGCCAAG<br>AAGGGAAGGAGTACACAGA<br>CAAAGCCCATTTTTCTTCCA<br>AATGCAGAAGATGTAGATT<br>GTGTGATGAAGGACATGGC<br>TTAGAAGTGG        |
| FAS-site 4 | GAGGGTCCAGATGCCCAGC<br>A | NGS-FASsite4-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGT<br>ACGGAGTTGGGGAAGCTCT<br>NGS-FASsite4-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTACTTTGCCTATC<br>CCCGGGACT        | ACTTTGCCTATCCCCGGGAC<br>TAAGACGGGGTAAGCCTCC<br>ACCCGGGCAGGAGAGGGCT<br>CACCAGAGGTAGGAGGGTC<br>CAGATGCCCAGCATGGTTGT<br>TGAGCAATCCTCCGAAGTG<br>AAAGAGCTTCCCCAACTCCG<br>TACT            |
| FAS-site 5 | TACAGTTGAGACTCAGAACT     | NGS-FASsite5-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGAC<br>TGACATCAACTCCAAGGGA<br>NGS-FASsite5-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCACCTGGAGGA<br>CAGGGCTTA         | GACTGACATCAACTCCAAG<br>GGATTGGAATTGAGGAAGA<br>CTGTTACTACAGTTGAGACT<br>CAGAACTTGGAAGGCCTGC<br>ATCATGATGGCCAATTCTGC<br>CATAAGCCCTGTCCTCCAGG<br>TG                                     |
| FAS-site 6 | GTTGAGACTCAGAACTTGG<br>A | NGS-FASsite6-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGAC<br>TGACATCAACTCCAAGGGA<br>NGS-FASsite6-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCACCTGGAGGA<br>CAGGGCTTA         | GACTGACATCAACTCCAAG<br>GGATTGGAATTGAGGAAGA<br>CTGTTACTACAGTTGAGACT<br>CAGAACTTGGAAGGCCTGC<br>ATCATGATGGCCAATTCTGC<br>CATAAGCCCTGTCCTCCAGG<br>TG                                     |
| FAS-site 7 | AAGCCACCCCAAGTTAGAT<br>C | NGS-FASsite7-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGTC<br>CAATGTTCCAACCTACAGG<br>NGS-FASsite7-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGAGGCAAATCTT<br>TGTGAACTAC       | GAGGCAAATCTTTGTGAACT<br>ACTTCCCAAGTTATTTCAAT<br>CTGCAGTTTGAACAAAGCA<br>AGAACTTACCCCAACAATT<br>AGTGGAATTGGCAAAAGAA<br>GAAGACAAAGCCACCCCAA<br>GTTAGATCTGGATCCTGTAG<br>GTTGGAACATTGGAC |
| FAS-site 8 | CCCCAAACAATTAGTGGA<br>T  | NGS-FASsite8-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGTC<br>CAATGTTCCAACCTACAGG                                                                                          | GAGGCAAATCTTTGTGAACT<br>ACTTCCCAAGTTATTTCAAT<br>CTGCAGTTTGAACAAAGCA<br>AGAACTTACCCCAACAATT                                                                                          |

|               |                          |                                                                                                                                                                                  |                                                                                                                                                                                                                                                                             |
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|               |                          | NGS-FASsite8-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTCCGATCTGAGGCAAATCTT<br>TGTGAACTAC                                                                                                   | AGTGGAATTGGCAAAAGAA<br>GAAGACAAAGCCACCCCAA<br>GTTAGATCTGGATCCTGTAG<br>GTTGGAACATTGGAC                                                                                                                                                                                       |
| FAS-site 9    | AACTTACCCCAAACAATTAG     | NGS-FASsite9-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNGTC<br>CAATGTTCCAACCTACAGG<br>NGS-FASsite9-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTCCGATCTGAGGCAAATCTT<br>TGTGAACTAC         | GAGGCAAATCTTTGTGAACT<br>ACTTCCCAAGTTATTTCAAT<br>CTGCAGTTTGAACAAAGCA<br>AGAACTTACCCCAAACAATT<br>AGTGGAATTGGCAAAAGAA<br>GAAGACAAAGCCACCCCAA<br>GTTAGATCTGGATCCTGTAG<br>GTTGGAACATTGGAC                                                                                        |
| FAS-site 10   | AAGTTCAACTGCTTCGTAAT     | NGS-FASsite10-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNCAC<br>CACTATTGCTGGAGTCATG<br>NGS-FASsite10-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTCCGATCTCTGCAAGAGTA<br>CAAAGATTGGC      | CACCACTATTGCTGGAGTCA<br>TGACACTAAGTCAAGTTAA<br>AGGCTTTGTTGAAAGAATG<br>GTGTCAATGAAGCCAAAAT<br>AGATGAGATCAAGAATGAC<br>AATGTCCAAGACACAGCAG<br>AACAGAAAGTTCAACTGCTT<br>CGTAATTGGCATCAACTTCA<br>TGGAAAGAAAGAAGCGTAT<br>GACACATTGATTAAAGATCT<br>CAAAAAAGCCAATCTTTGTA<br>CTCTTGCAG |
| TGFBR2-site 1 | TTCAGAGCAGTTTGAGACA<br>G | NGS-TGFBR2Ssite1-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNGCT<br>GAGGTCTATAAGGCCAAGC<br>NGS-TGFBR2Ssite1-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTCCGATCTAACTCCGTCTTC<br>CGCTCCTCAG | GCTGAGGTCTATAAGGCCA<br>AGCTGAAGCAGAACACTTC<br>AGAGCAGTTTGAGACAGTG<br>GCAGTCAAGATCTTCCCTA<br>TGAGGAGTATGCCTCTTGGA<br>AGACAGAGAAGGACATCTT<br>CTCAGACATCAATCTGAAGC<br>ATGAGAACATACTCCAGTTC<br>CTGACGGCTGAGGAGCGGA<br>AGACGGAGTT                                                |
| TGFBR2-site 2 | GAACATACTCCAGTTCCTGA     | NGS-TGFBR2Ssite2-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNGCC<br>TCTTGGAAGACAGAGAAGG<br>NGS-TGFBR2Ssite2-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTCCGATCTGCTGATGACATG<br>CCGCGTCA   | GCCTCTTGGAAGACAGAGA<br>AGGACATCTTCTCAGACATC<br>AATCTGAAGCATGAGAACA<br>TACTCCAGTTCCTGACGGCT<br>GAGGAGCGGAAGACGGAGT<br>TGGGGAAACAATACTGGCT<br>GATCACCGCCTTCCACGCCA<br>AGGGCAACCTACAGGAGTA<br>CCTGACGCGCATGTCATCA<br>GC                                                        |

|                   |                          |                                                                                                                                                                                    |                                                                                                                                                                                                                                                      |
|-------------------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| TGFBR2-<br>site 3 | CGGAGTTGGGGAAACAATA<br>C | NGS-TGFBR2Ssite3-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNCATA<br>CTCCAGTTCCTGACGGCT<br>NGS-TGFBR2Ssite3-<br>1F:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTGTGGAGGTGA<br>GCAATCCCC   | CATACTCCAGTTCCTGACGG<br>CTGAGGAGCGGAAGACGGA<br>GTTGGGGAAACAATACTGG<br>CTGATCACCGCCTTCCACGC<br>CAAGGGCAACCTACAGGAG<br>TACCTGACGCGGCATGTCAT<br>CAGCTGGGAGGACCTGCGC<br>AAGCTGGGCAGCTCCCTCGC<br>CCGGGGGATTGCTCACCTCC<br>ACA                              |
| TGFBR2-<br>site 4 | ACCTACAGGAGTACCTGAC<br>G | NGS-TGFBR2Ssite4-<br>1F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNCATA<br>CTCCAGTTCCTGACGGCT<br>NGS-TGFBR2Ssite4-<br>1F:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTTGTGGAGGTGA<br>GCAATCCCC   | CATACTCCAGTTCCTGACGG<br>CTGAGGAGCGGAAGACGGA<br>GTTGGGGAAACAATACTGG<br>CTGATCACCGCCTTCCACGC<br>CAAGGGCAACCTACAGGAG<br>TACCTGACGCGGCATGTCAT<br>CAGCTGGGAGGACCTGCGC<br>AAGCTGGGCAGCTCCCTCGC<br>CCGGGGGATTGCTCACCTCC<br>ACA                              |
| TGFBR2-<br>site 5 | CCGTCTCACAGCCCAGTGTG     | NGS-TGFBR2Ssite5-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNAGC<br>CCACCAACTCATGGTG<br>NGS-TGFBR2Ssite5-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGGGAGCCGTCT<br>TCAGGAATCTT    | AGCCCACTCATGGTGC<br>CCTTTGGATCTCTTTCCCGC<br>TACAGGGCATCCAGATGGT<br>GTGTGAGACGTTGACTGAGT<br>GCTGGGACCACGACCCAGA<br>GGCCCGTCTCACAGCCCAGT<br>GTGTGGCAGAACGCTTCAGT<br>GAGCTGGAGCATCTGGACA<br>GGCTCTCGGGGAGGAGCTG<br>CTCGGAGGAGAAGATTCTT<br>GAAGACGGCTCCC |
| TGFBR2-<br>site 6 | GTCTTCTCTGTCTTCCAAG      | NGS-TGFBR2Ssite1-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGCT<br>GAGGTCTATAAGGCCAAGC<br>NGS-TGFBR2Ssite1-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTAACTCCGTCTTC<br>CGCTCCTCAG | AACTCCGTCTTCCGCTCCTC<br>AGCCGTCAGGAAGTGGAGT<br>ATGTTCTCATGCTTCAGATT<br>GATGTCTGAGAAGATGTCCT<br>TCTCTGTCTTCCAAGAGGCA<br>TACTCCTCATAGGGAAAGAT<br>CTTGACTGCCACTGTCTCAA<br>ACTGCTCTGAAGTGTTCTGC<br>TTCAGCTTGGCCTTATAGAC<br>CTCAGC                        |
| TGFBR2-<br>site 7 | ACTCCAGTTCCTGACGGCTG     | NGS-TGFBR2Ssite7-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNNGCC                                                                                                               | GCCTCTTGAAGACAGAGA<br>AGGACATCTTCTCAGACATC<br>AATCTGAAGCATGAGAACA                                                                                                                                                                                    |

|                |                          |                                                                                                                                                                                    |                                                                                                                                                                                                                                                                 |
|----------------|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                |                          | TCTTGGAAGACAGAGAAGG<br>NGS-TGFBR2Ssite7-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTGCTGATGACATG<br>CCGCGTCA                                                                           | TACTCCAGTTCCTGACGGCT<br>GAGGAGCGGAAGACGGAGT<br>TGGGGAAACAATACTGGCT<br>GATCACCGCCTTCCACGCCA<br>AGGGCAACCTACAGGAGTA<br>CCTGACGCGGCATGTCATCA<br>GC                                                                                                                 |
| TGFBR2-site 8  | TTCCCAGAGCACCAGAGCC<br>A | NGS-TGFBR2Ssite8-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNTGG<br>GAACTGCAAGATACATGGC<br>NGS-TGFBR2Ssite8-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCACAATGATGCT<br>GGTCCACACC   | CACAATGATGCTGGTCCACA<br>CCTACCTCCCACTGCATTAC<br>AGCGAGATGTCATTTCCAG<br>AGCACCAGAGCCATGGAGT<br>AGACATCGGTCTGCTTGAAG<br>GACTCAACATTCTCCAAATT<br>CATCCTGGATTCTAGGACTT<br>CTGGAGCCATGTATCTTGCA<br>GTTCCCA                                                           |
| TGFBR2-site 9  | CTGGTGGTTGAGCCAGAAG<br>C | NGS-TGFBR2Ssite9-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNATT<br>GGTTCCAAGGTGCGGGAG<br>NGS-TGFBR2Ssite9-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTACACAATGGGA<br>CCTTCCCTCAG   | ACACAATGGGACCTTCCCTC<br>AGATTTAAGCTCAATATTCC<br>AGAATTCTCTGCCACCTAAG<br>AGGCAACTTGGTTGAATCTT<br>ACTGACCTTTGTAAACACTC<br>ACTCCTTACCTGGTGGTTGA<br>GCCAGAAGCTGGGAATTTCT<br>GGTCGCCCTCGATCTCTCAA<br>CACGTTGTCCTTCATGCTTT<br>CGACACAGGGGTGCTCCCG<br>CACCTTGGAACCAAAT |
| TGFBR2-site 10 | TGGTGGTTGAGCCAGAAGC<br>T | NGS-TGFBR2Ssite10-<br>2F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNATT<br>GGTTCCAAGGTGCGGGAG<br>NGS-TGFBR2Ssite10-<br>2R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTACACAATGGGA<br>CCTTCCCTCAG | ACACAATGGGACCTTCCCTC<br>AGATTTAAGCTCAATATTCC<br>AGAATTCTCTGCCACCTAAG<br>AGGCAACTTGGTTGAATCTT<br>ACTGACCTTTGTAAACACTC<br>ACTCCTTACCTGGTGGTTGA<br>GCCAGAAGCTGGGAATTTCT<br>GGTCGCCCTCGATCTCTCAA<br>CACGTTGTCCTTCATGCTTT<br>CGACACAGGGGTGCTCCCG<br>CACCTTGGAACCAAAT |
| TRAC-site 1    | AACAAATGTGTCACAAAGT<br>A | NGS-TRACSsite1-<br>1F:ACACTCTTTCCTACACGA<br>CGCTCTTCCGATCTNNNNAGA<br>ACCCTGACCCTGCCGTGTA<br>NGS-TRACSsite1-<br>1R:TGGAGTTCAGACGTGTGCT                                              | AGAACCCTGACCCTGCCGTG<br>TACCAGCTGAGAGACTCTA<br>AATCCAGTGACAAGTCTGTC<br>TGCCTATTCACCGATTTTGA<br>TTCTCAAACAAATGTGTCAC<br>AAAGTAAGGATTCTGATGT                                                                                                                      |

|                |                      |                                                                                                                                                                           |                                                                                                                                                                                     |
|----------------|----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                |                      | CTCCGATCTTTGCTCCAGGCC<br>ACAGCACT                                                                                                                                         | GTATATCACAGACAAAACCT<br>GTGCTAGACATGAGGTCTAT<br>GGACTTCAAGAGCAACAGT<br>GCTGTGGCCTGGAGCAA                                                                                            |
| TRAC-site<br>2 | TTTCAAAACCTGTCAGTGAT | NGS-TRACSite2-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNTGT<br>GTCCTGCAGGCCATGCA<br>NGS-TRACSite2-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCATGAGCAGATT<br>AAACCCGGCC | TGTGTCCTGCAGGCCATGCA<br>GGCCTGGGACATGCAAGCC<br>CATAACCGCTGTGGCCTCTT<br>GGTTTTACAGATACGAACCT<br>AAACTTTCAAAACCTGTCAG<br>TGATTGGGTTCGAATCCTC<br>CTCCTGAAAGTGGCCGGGTT<br>TAATCTGCTCATG |
| TRAC-site<br>3 | TTCAAAACCTGTCAGTGATT | NGS-TRACSite3-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNTGT<br>GTCCTGCAGGCCATGCA<br>NGS-TRACSite3-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCATGAGCAGATT<br>AAACCCGGCC | TGTGTCCTGCAGGCCATGCA<br>GGCCTGGGACATGCAAGCC<br>CATAACCGCTGTGGCCTCTT<br>GGTTTTACAGATACGAACCT<br>AAACTTTCAAAACCTGTCAG<br>TGATTGGGTTCGAATCCTC<br>CTCCTGAAAGTGGCCGGGTT<br>TAATCTGCTCATG |
| TRAC-site<br>4 | TTCGTATCTGTAAAACCAAG | NGS-TRACSite4-<br>2F:ACACTCTTTCCCTACACGA<br>CGCTCTTCCGATCTNNNTGT<br>GTCCTGCAGGCCATGCA<br>NGS-TRACSite4-<br>1R:TGGAGTTCAGACGTGTGCT<br>CTTCCGATCTCATGAGCAGATT<br>AAACCCGGCC | CATGAGCAGATTAAACCCG<br>GCCACTTTCAGGAGGAGGA<br>TTCGGAACCAATCACTGAC<br>AGGTTTTGAAAAGTTAGGTT<br>CGTATCTGTAAAACCAAGA<br>GGCCACAGCGTTATGGGC<br>TTGCATGTCCAGGCCTGCA<br>TGGCCTGCAGGACACA   |

**Supplementary Table 3:** ipTM and pTM scores of the AlphaFold3 predicted structures.

| AlphaFold3 predicted structures | pTM  | ipTM |
|---------------------------------|------|------|
| mini-Sdd9-BE4max-sgRNA-DNA      | 0.71 | 0.75 |
| mini-Sdd9-QBEmax-sgRNA-DNA      | 0.7  | 0.72 |
| mini-Sdd9-CP-1031-sgRNA-DNA     | 0.72 | 0.74 |
| mini-Sdd9-inlaid-1244-sgRNA-DNA | 0.75 | 0.77 |

**Supplementary Sequences**

mini-Sdd9-BE4max:

MKRTADGSEFESPKKKRKVCPIWVKNALQELVGRKETSGKVFDVDGKPIGPDIQSGYKDR  
ELRRGVYETLRKSPFFQKHFPSTATWYVSLHVEAQYAVWMLRNRIKHATVVINNTYVCSD  
MNLRLHDNCMTAVPHILPEGYTMTVWKADRTEVTLRGKAPKESGGSSGGSSGSETPGTSES  
ATPESSGGSSGSDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG  
ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLLEESFLVEED  
KKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIE

GDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLLENLIAQLPGE  
KKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLNLLAQIGDQYADLFLA  
AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQPEKYKEIFFDQ  
SKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIH  
LGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWN  
FEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKP  
AFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDL  
LKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTG  
WGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDS  
LHEHIANLAGSPAIKKILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRE  
RMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVD  
HIVPQSFLKDDSIDNKVLTRSDKNRGKSDNPSEEVVKMKKNYWRQLLNAKLITQRKFD  
NLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLK  
SKLVSDFRKDFQFYKVBREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDV  
RKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF  
ATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVA  
YSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKKDLIIKLPKYS  
LFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGGSPEDNEQKQLFVEQ  
HKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAF  
KYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDSGGSGGGSGGSTNLSDIIEK  
ETGKQLVIQESILMLPEEVVEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVI  
QDSNGENKIKMLSGGSGGGSGGSTNLSDIIEKETGKQLVIQESILMLPEEVVEVIGNKPESDIL  
VHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSKRTADGSEFEPKKK  
RKV\*

mini-Sdd9-QBEmax:

MKRTADGSEFESPKKRKVKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIV  
WDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYG  
GFDSP TVAYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKKD  
LIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKSGGSSGGSSG  
SETPGTSESATPESSGGSSGGSCPIWVKNALQELVGRKETSGKVFDVDGKPIGPDIQSGYK  
DRELRRGVYETLRKSPFFQKHFPSTATWYVSLHVEAQYAVWMLNRNRIKHATVVINNTYV  
CSDMNRLHDNCMTAVPHILPEGYTMTVWKADRTEVTLRGKAPKESGGSSGGSSGSETPG  
TSESATPESSGGSSGGSLKGGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDK  
VL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI  
TGLYETRIDLSQLGGDGGSGGSGGSGGSGGSGGMDKKYSIGLAIGTNSVGWAVITDE  
YKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI  
FSNEMAKVDDSFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDST  
DKADLRILIYALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDA  
KAILSARLSKSRRLLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSK  
DTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHH  
QDLTLLKALVRQQPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELL  
VKLNREDLLRKQRTFDNGSIPHQIH LGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYV

mini-Sdd9-QBEn:

MKRRTADGSEFESPKKKRKVARLSKSRLENLIAQLPGEEKNGLFGNLIASLSGLTPNFKSN  
 FDLAEDAKLQLSKDTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAP  
 LSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIK  
 PILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDNRE  
 KIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFD  
 KNLPNKVLPKHSLLEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKV  
 TVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDIEDIVL  
 TLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILD  
 FLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIAKKGILQTVK  
 VVDELVKVMGRHKPENIVIEAMARENQTTQKGQKNSRERMKRIEEGKELGSQILKEHPVE  
 NTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDK  
 NRGKSDNPVSEEVVKMKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQL  
 VETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVBREINNYH  
 HAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRKMAKSESSEGGSSGGSSGSETPGT  
 SESATPESSGGSSGGSCPIWVKNALQELVGRKETSGKVFDVDGKPIGPDIQSGYKDRELRR  
 GVEYETLRKSPFFQKHFPSTATWYVSLHVEAQYAVWMLRNRIKHATVVINNTYVCSDMNR  
 LHDNCMTAVPHILPEGYTMTVWKADRTEVTLRGKAPKESGGSSGGSSGSETPGTSESATP  
 ESSGGSSGGSQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGR  
 DFATVRKVLSPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT  
 VAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSEKPNIDFLEAKGYKEVKKDLIIKLPK  
 YSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFV  
 EQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKHARDKPIREQAENIIHLFTLTNLGAPA  
 AFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGSGGSGGSGGSGGS  
 GSGSGDKKYSIGLAIGTNSVGWAVITDEYKVP SKKFKVLGNTDRHSIKKNLIGALLFDSGE  
 TAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERHPIF  
 GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADRLIYLALAHMIKFRGHFLIEGDLNPDNSD  
 VDKLFIQLVQTYNQLFEENPINASGVDAKAILSSGGSGGSGGSTNLSDIIEKETGKQLVIEQ  
 SILMLPEEVVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIK  
 MLSSGGSGGSGGSTNLSDIIEKETGKOLVIOESILMLPEEVVEEVIGNKPESDILVHTAYDESTD

ENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSKRTADGSEFEPKKRKV