S4 Table. Overview of primers used in this study. When relevant, primer attachment sites are indicated in bold, linker sequences in blue, spacer sequences in orange, artificial ribosome binding sites in purple and restriction sites in red.

|  |  |
| --- | --- |
| **Primer name** | **Sequence** |
| SG1 | TCGAACGCGTGATTCCGGAAGCGAAAAAACCGCGCCGTATCGAAATCAAC**AGCGGTGGCGGTGGC** |
| SG2 | CCTGACGGCGAGCATGGAGATGTCAGGCCGCGCCAGGCGGCCTTAGGGAATTAGTTGATT**ATTCCGGGGATCCGTCGACC** |
| SG3 | CCATCGCAGCGCAGCGTATCGCTATCAGCGAACGTCCCGCGTTAAATAGC**AGCGGTGGCGGTGGC** |
| SG4 | GTAAGACAAAAAAAGCCCCACCAGAATGGCGGGGCAAAGAGAATAGCTAG**ATTCCGGGGATCCGTCGACC** |
| SG5 | CTAACGTACCGGCATTTGTTTCTGGCAAGGCACTGAAAGACGCAGTTAAG**GGCAGCGGCAGCGGCA** |
| SG6 | AAAAGGGGTGAAACCACCCCTTCGTTAAAACTGTTCACTGCCACGCAATC**GTGTAGGCTGGAGCTGCTTC** |
| SG7 | AGAATTCGGCAGCGGCAGCGGCAGC**GTGAGCAAGGGCGAGGA** |
| SG8 | AGGATCCTTACTTGTACAGCTCGTCCA  |
| SG9 | AGAATTCGGCAGCGGCAGCGGCAGC**GCTAGCAAAGGAGAAGAACT** |
| SG10 | AGGATCCTTATTTGTAGAGCTCATCCATG |
| SG11 | GTCCATTGTGGAAGGTCTTACATTCTCGCTGATTTCAGGAGCTATTGATTATG**GTGAGCAAGGGCGAGGAG** |
| SG12 | CCTGACGGCGAGCATGGAGATGTCAGGCCGCGCCAGGCGGCCTTAGGGAATTAGTTGATT**GTGTAGGCTGGAGCTGCTTC** |
| SG13 | **GCAAAGTGCGTCGGGTGAT** |
| SG14 | **GCCGAATAAATACCTGTGACG** |
| SG15 | TGCCATGGCA**GTGAGCAAGGGCGAGGAG** |
| SG16 | AGGATCC**CTTGTACAGCTCGTCCATGC** |
| SG17 | AGGATCCGGCAGCGGCAGC**AGCCCTTCAATCGCCAGAGA** |
| SG18 | TGAGTCGAC**TCAGCCAAACGTCTCTTCAGGC** |
| SG19 | AAAGAGGAGAATACTAG**ATGCGTAACTTTGATTTATCCCCGCT** |
| SG20 | TTATTTGTAGAGTTCATCCATGCCGT |
| SG21 | CTCGGTACCCGGGGATCCTC |
| SG22 | CTCGAATTCGCTAGCCCAAA |
| SG23 | AAGATGACGATGTTGTCGACGCTGAATTTGAAGAAGTCAAAGACAAAAAA**AGCGGTGGCGGTGGC** |
| SG24 | AGGAAATTCCCCTTCGCCCGTGTCAGTATAATTACCCGTTTATAGGGCGA**ATTCCGGGGATCCGTCGACC** |
| SG25 | CAAAGAGCTTCTTTGATGGTGTGAAGAAGTTTTTTGACGACCTGACCCGC**AGCGGTGGCGGTGGC** |
| SG26 | ACGCACCCTATTTTTACCCAGGCCTGCCCACGGGCAGGCTTTTGGGGAGG**ATTCCGGGGATCCGTCGACC** |
| SG27 | GTAAAGTGATTCGCCTGGAAGTTAATGAAGACCGGATTGTCGCCGTCCAG**AGCGGTGGCGGTGGC** |
| SG28 | TCCGTCTAACTTATAGACAAAAACGAGCCCCGAAGGGCTCGTTTTATCAT**ATTCCGGGGATCCGTCGACC** |
| SG29 | CTGAAGCGGTGGAATACGGTCTGGTCGATTCGATTCTGACCCATCGTAAT**AGCGGTGGCGGTGGC** |
| SG30 | AGCGTTGTGCCGCCCTGGATAAGTATAGCGGCACAGTTGCGCCTCTGGCA**ATTCCGGGGATCCGTCGACC** |
| SG31 | AACCGTTGCTGATTTATGGCAAGCCGGAAGCGCAACAGGCATCTGGTGAA**AGCGGTGGCGGTGGC** |
| SG32 | GGAGATAAAATCCCCCCTTTTTGGTTAACTAATTGTATGGGAATGGTTAA**ATTCCGGGGATCCGTCGACC** |
| SG33 | TGGAAGATCCGAACCTGTTTATTCGTCGTATGAACCAGCTGCTGGTTTCC**AGCGGTGGCGGTGGC** |
| SG34 | GATGATGAAAAGAAAAATGCCGGATGACACGAAGGTCATCCGGCATTACA**ATTCCGGGGATCCGTCGACC** |
| SG35 | AACATCTGGATGCGTTGGTGGCAGATGAAGATCTGAGCCGTTTTATCCTA**AGCGGTGGCGGTGGC** |
| SG36 | AATGGGGCCTTTCAGCCCCATCAAACAATGATGAAAATGATTGAACGCGA**ATTCCGGGGATCCGTCGACC** |
| SG37 | CTCTGGCGCTGCAAAATGAACCGTCTGGTATGCAGGTTGTGACTGCAAAA**AGCGGTGGCGGTGGC** |
| SG38 | CGAATTAGCCTGCCAGCCCTGTTTTTATTAGTGCATTTTGCGCGAGGTCA**ATTCCGGGGATCCGTCGACC** |
| SG39 | GATGTTGTCGACGCTGAATTTGAAGAAGTCAAAGACAAAAAATAATCGCCAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG40 | CGGAGAGGAAATTCCCCTTCGCCCGTGTCAGTATAATTACCCGTTTATAG**ATTCCGGGGATCCGTCGACC** |
| SG41 | TTCTTTGATGGTGTGAAGAAGTTTTTTGACGACCTGACCCGCTAACCTCCAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG42 | CTTCAACGCACCCTATTTTTACCCAGGCCTGCCCACGGGCAGGCTTTTGG**ATTCCGGGGATCCGTCGACC** |
| SG43 | ATTCGCCTGGAAGTTAATGAAGACCGGATTGTCGCCGTCCAGTAAATGATAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG44 | TCTTTTCCGTCTAACTTATAGACAAAAACGAGCCCCGAAGGGCTCGTTTT**ATTCCGGGGATCCGTCGACC** |
| SG45 | GTGGAATACGGTCTGGTCGATTCGATTCTGACCCATCGTAATTGATGCCAAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG46 | CTTACAGCGTTGTGCCGCCCTGGATAAGTATAGCGGCACAGTTGCGCCTC**ATTCCGGGGATCCGTCGACC** |
| SG47 | CTGATTTATGGCAAGCCGGAAGCGCAACAGGCATCTGGTGAATAATTAACAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG48 | AAAGGGGAGATAAAATCCCCCCTTTTTGGTTAACTAATTGTATGGGAATG**ATTCCGGGGATCCGTCGACC** |
| SG49 | CCGAACCTGTTTATTCGTCGTATGAACCAGCTGCTGGTTTCCTGATGTAAAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG50 | GTGCAGATGATGAAAAGAAAAATGCCGGATGACACGAAGGTCATCCGGCA**ATTCCGGGGATCCGTCGACC** |
| SG51 | GATGCGTTGGTGGCAGATGAAGATCTGAGCCGTTTTATCCTATAATCGCGAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG52 | ATAAAAATGGGGCCTTTCAGCCCCATCAAACAATGATGAAAATGATTGAA**ATTCCGGGGATCCGTCGACC** |
| SG53 | CTGCAAAATGAACCGTCTGGTATGCAGGTTGTGACTGCAAAATAGTGACCAAAGAGGAGAATACTAGATG**AGTAAAGGTGAAGAACTGTTCACCGG** |
| SG54 | AAGCCCGAATTAGCCTGCCAGCCCTGTTTTTATTAGTGCATTTTGCGCGA**ATTCCGGGGATCCGTCGACC** |
| SG55 | **AATAAATTCATCTGTTGATCGTGGGT** |
| SG56 | **TTACTTGTACAGCTCGTCCATGCC** |