|  |  |
| --- | --- |
| **Name** | **Sequence (‘5 to ’3)** |
| **TpiA insertions** |
| TpiAE55.1-fw | GGCGGTTCTGGTGAAAACCTGTATTTTCAGGGCTCTGGTGGCTCTGGCAGCCACATCATGCTGGG |
| TpiAE55.2-fw | GGGTGTCTGGGGGAATCTGAAAACCTGTATTTTCAGGGCGATGAAAGAAAGAACAAAGGCAGCCACATCATGCTG |
| TpiAE55.3-fw | GGCTGCCTGCCGACAACCGAAAACCTGTATTTTCAGAGCGGCACAGTGAAAAACAAAGGCAGCCACATCATGCTG |
| TpiAE55-rv | TTC AGC TTC GCG CTT CGC CAT ATC |
| TpiAN69-fw | GAGAATCTTTACTTCCAAGGTCTGTCCGGCGCATTCACCG |
| TpiAN69-rv | GTT CAG GTC CAC GTT TTG CGC AC |
| TpiAT130-fw | GAAAACCTGTACTTCCAGGGTGGTTCTGGTAAAACTGAAGAAGTTTGCGCACGTC |
| TpiAT130.1-rv | GGTTTCACCGATGCACAGAACCG |
| TpiAT130.2-rv | AGAACCACCGGTTTCACCGATGCACAGAACCG |
| TpiAT152-fw | GACTATGACATCCCGACAACCGAAAACCTGTATTTTCAGAGCGGCACAGTGGACGCCGGCGCCGACCAGGGTGCTGCGGCATTCGAAG |
| TpiAT152-rv | AGTTTTCAGTACCGCGTCGATCTG |
| TpiAL70-fw | GACTCACCTTGGAAGTACAGATTTTCATTTTTCGGTGGCAGGTTCAGGTCCACGTTTTGC |
| TpiAL70-rv | tgAAAATCTGTACTTCCAAGGTGAGTCcCTGtttaaaggTccaTCCGGCGCATTCACCGG |
| **Adk insertions** |
| *adk*-forward | GGATCCCGGGCCGCAAATTATCTCGCCATTAACCG |
| *adk*-reverse | CGGAGCTCTTAATTAACGGCCGGCTTAGTGGTGGTGGTGGTG |
| D76-fw | GAAAACCTGTATTTTCAGGGCAATGGTTTCCTGTTGGACGGCTTC |
| D76-rv | GTCTTCCTGAGCAATGCGCTC |
| PSII-library1-fw | GAAAACCTGTATTTTCAGGGGGAAGGGCATCAATGTTGATTACGTTTAATAATTCG |
| PSII-library2-fw | GAAAACCTGTATTTTCAGGGGGAAGCGGGCATCAATGTTGATTAC |
| PSII-library3-fw | GAAAACCTGTATTTTCAGGGG AAAGAAGCGGGCATCAATGTTGATTACG |
| PSII-library4-fw | GAAAACCTGTATTTTCAGGGGGAAGATGAAAGAAGCGGGCATCAATGTTGATTAC |
| PSII-library5-fw | GAAAACCTGTATTTTCAGGGGGCGATGAAAGAAGCGGGCATCAATG |
| PSII-library6-fw | GAAAACCTGTATTTTCAGGGGGAAGGACGCGATGAAAGAAGCGGGCATCAATG |
| PSII-library1-rv | CGCTTCTTTCATCGCGTCTGCCTG |
| PSII-library2-rv | TTTCATCGCGTCTGCCTGCG |
| PSII-library3-rv | CATCGCGTCTGCCTGCGGAATGG |
| PSII-library4-rv | CGCGTCTGCCTGCGGAATG |
| PSII-library5-rv | GTCTGCCTGCGGAATGGTACGCGG |
| PSII-library6-rv | TGCCTGCGGAATGGTACGCGGGAAGCCG |
| AdkP140-fw | GAAAACCTGTATTTTCAGGGGGACGACGTTACCGGTGAAGAAC |
| AdkP140-rv | CGGCGGATTGAATTTAACGTGAT |
| AdkA186-fw | GAAAACCTGTATTTTCAGGGGAATACCAAATACGCGAAAGTTGAC |
| AdkA186-rv | TTCTGCTTCTTTGGAGTAGTAGCC |
| **GpsA insertions** |
| secBgpsA-forward | CGCCCGGGCCATGGGTGTGAACGTTGGCATTACATTGCG |
| secBgpsA-reverse | GTCTCTAGATTACTTAGTGGTGGTGGTGGTGGTGGTGGCTGCTGCGCTCGTCC |
| GpsAC49-fw | GAGAATCTGTACTTCCAAGGCTTTCCCGATACGCTCCATCTTG |
| GpsAC49-rv | ACAGCGGTCGCGTTCAAGC |
| GpsAP60-fw | GAGAATCTGTACTTCCAAGGCGTGCCTTTTCCCGATACGCTCC |
| GpsAP60-rv | GGG AAA AGG CAC ATC GGG GAG AAA C |
| GpsAM99-fw | CCAACCACCGAAAACCTGTATTTTCAGGGGTGTCTGGGGCGTCCTGATGCGCGTCTGG |
| GpsAM99-rv | CATCAGTGGTTTAATCTGGCGCAG |
| GpsAI132-fw | CCAACCACCGAAAACCTGTATTTTCAGGGGTGTCTGGGGCCGCTGGCGGTTATCTCTGG |
| GpsAI132-rv | AATTTGATCGCCTAAGGCCTCACG |
| GpsAQ269-fw | CCGACCACAGAGAATCTGTACTTCCAAGGCGGCACCGTTGGCATGGATGTACAAAGCGCG |
| GpsAQ269-rv | CTGACCGAGCATCATGCCAAAAC |
| GpsAD56.1-fw | CCGATgaaaacctgtattttcagggtGTGCCTTTTCCCGATACGCTC |
| GpsAD56.1-rv | TATCGGGAAAAGGCACACCCTGAAAATACAGGTTTTCATCGGGGAGAAACGCGGCGTTAC |
| GpsAD56.2-fw | ctgtattttcagggtgaaagcctgtttaaaggcccgGTGCCTTTTCCCGATACGCTC |
| GpsAD56.2-rv | ACAGGCTTTCACCCTGAAAATACAGGTTTTCGTTTTTCGGCGGATCGGGGAGAAACGCGG |
| **pKTS adk**  |  |
| Adk\_wt\_fw | GCGCATTGCTCA |
| Adk\_wt\_rv | AGGAAACCATTACGGCAGTCTTCCTGAGCAATGCGC |
| Adk76-1-rv | TTTAAACAGGCTTTCCCCCTGGAAGTACAGATTCTCGTCTTCCTGAGCAATGCGCTC |
| Adk76-1-fw | GAGAATCTGTACTTCCAGGGGGAAAGCCTGTTTAAATGCCGTAATGGTTTCCTGTTG |
| Adk76-2-fw | GGTCCATGCCGTAATGGTTTCCTGTTGGACGGCTTCCCG |
| Adk76-2-rv | GAAACCATTACGGCATGGACCTTTAAACAGGCTTTCCCC |
| **Colony PCR and sequencing for MAGE** |
| MutS(mut)-fw[1] | AACCGGACATAA |
| MutS(wt)-fw [1]  | AACCGGACATAACCCCATG  |
| MutS-rv[1] | CGGGATCGGCTCTCC  |
| MutS-seq [1]  | GCTGCAAAACAGCATCTTTCC  |
| TEV-rv |  CCCCTGAAAATACAGGTTTTC |
| TEV-2-rv | ACCTTGAAAGTACAAATTCTC |
| TEV-3-rv | CCCCTGAAAATACAGATTCTC |
| TEV-4-rv | CCCCTGGAAGTACAGATTCTC |
| Adk-fw | AAAGGGACTCAGGCTC |
| Adk-ins2-rv | ACGGCATTTAAACAGGCTTTC |
| AtpD-fw | GGCATGGGGGATAAC |
| AtpA-fw | ATGAAGCTGCTAACAGC |
| AtpA-seq\_rv | ACCTTGCCGAAGGCATGAAAG |
| AtpD-seq\_rv | GGATGTAAAAGACCTCGAACAC |
| Adk-seq-rv | TTAGCCGAGGATTTTTTCC |
| TpiA-rv | CTGCTCTTTCAGCACCGCG |
| TpiA-ins1-fw | ATGCGACATCCTTTAGTGATGG |
| TpiA-ins2-fw | CGGACCCCTGGAAGTACAGATT |
| TpiA-ins3-fw | ACCTTTAAACAGGGACTC |
| TpiA-STOP-fw | CATCCTTTAGTGATGGGTtAgTGat |
| TpiA-STOP-rv | ATAACCGCACCTTCGAATGCCGCAG |
| Amn-seq-rv | TTTGCCGGGAACTGGCATAG |
| Amn-STOP-rv  | GCTCGGAATAGGAATATCGG  |
| Amn-STOP-fw | AACTCGACGCGCTGTAATAGTG |
| **MAGE Oligosa** |
| mutS\_off [1]  | A\*T\*C \*A\*CACCCCATTTAATATCAGGGAACCGGACATAACCCCATCAGTGCAATAGAAAATTTCGA CGCCCATACGCCCATGAT  |
| mutS\_on [1]  | A\*T\*C \*A\*CACCCCATTTAATATCAGGGAACCGGACATAACCCCATGAGTGCAATAGAAAATTTCGA CGCCCATACGCCCATGAT |
| rpsL\_off [2] | G\*T\*C \*A\*GACGAACACGGCATACTTTACGCAGCGCGGAGTTCGGTTTTTTAGGAGTGGTAGTATA TACACGAGTACATACGCCACGTTTTTGC |
| rpsL\_on [2] | G\*T\*C \*A\*GACGAACACGGCATACTTTACGCAGCGCGGAGTTCGGTTTTCTAGGAGTGGTAGTATA TACACGAGTACATACGCCACGTTTTTGC |
| bla\_off [1] | G\*C\*C \*A\*CATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTATTAGGGGCGAAAACTCT CAAGGATCTTACCGCTGTTGAGATCCAG |
| bla\_on [1] | G\*C\*C\*A\*CATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAG |
| malk\_off [2] | C\*C\*AAATGACATGTTTTCTGCTACTGACAGGTGGGGATAGAGCGCCTAAGACTGAAACACCATACCAACGCCGCGTTCTGCTGGCGGAG\*T\*G |
| malK on [2] | C\*C\*A\*A\*ATGACATGTTTTCTGCTACTGACAGGTGGGGATAGAGCGCGTAAGACTGAAACACCATACCAACGCCGCGTTCTGCTGGCGGAGTG |
| atpA\_H123 | C\*C\*G\*G\*AGCGATTGCTTCTACAGCAGAGAAGCCGTCCCCCTGAAAATACAGGTTTTCGTGATCCAGCGGACCTTTACCGTCGATTGGTGCAC |
|  atpD\_E101 | C\*G\*C\*G\*GTGAATCGCCCAACGCTCTTCTTCACCGATCCCCTGAAAATACAGGTTTTCCTCGCCTTTCATGTCGACCGGTTCACCCAGTACGT |
| tpiA\_l70\_1 | A\*C\*A\*T\*CATGCTGGGTGCGCAAAACGTGGACCTGAACCTGCCaCCGAAAAAtGAGGGGTCCGGCGCATTCACCGGTGAAACCTCTGCTGCTA |
| tpiA\_l70\_2 | G\*C\*T\*G\*GGTGCGCAAAACGTGGACCTGAACCTGCCACCGAAAAATGAGAATCTGTACTTCGGGTCCGGCGCATTCACCGGTGAAACCTCTGC |
| tpiA\_I70\_3 | G\*C\*C\*A\*CCGAAAAAtGAGAATCTGTACTTCCAGGGGGAGTCcCTGtttaaaggTccaTCCGGCGCATTCACCGGTGAAACCTCTGCTGCTAT |
| adk\_D76 | G\*G\*A\*A\*GCCGTCCAACAGGAAACCATTACGGCACCCCTGAAAATACAGATTCTCGTCTTCCTGAGCAATGCGCTCTTTAACCAGCGCGATCA |
| adk\_D76\_2 | C\*G\*C\*G\*GGAAGCCGTCCAACAGGAAACCATTACGGCATTTAAACAGGCTTTCCCCCTGAAAATACAGATTCTCGTCTTCCTGAGCAATGCGC |

1. Carr PA, Wang HH, Sterling B, Isaacs FJ, Lajoie MJ, Xu G, Church GM, Jacobson JM: **Enhanced multiplex genome engineering through co-operative oligonucleotide co-selection**. *Nucleic acids research* 2012, **40**(17).

2. Nyerges A, Csorgo B, Nagy I, Latinovics D, Szamecz B, Posfai G, Pal C: **Conditional DNA repair mutants enable highly precise genome engineering**. *Nucleic acids research* 2014, **42**(8).