**Supplementary Table 2.**  List of synthetic DNA oligonucleotides and primers.

|  |  |
| --- | --- |
| **Name** | **Sequence (5'-3')** |
| Cy5 601 10 nts. Sense | Cy5-CGCGCTGTCC |
| Cy5 601 20 nts. Sense | Cy5-ACGTACGCGCTGTCCCCCGC |
| Cy5 601 30 nts. Sense | Cy5‑AACGCACGTACGCGCTGTCCCCCGCGTTTT |
| Cy5 601 40 nts. Sense | Cy5‑GCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCG |
| 601 40 nts. Sense | GCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCG |
| Cy5 601 50 nts. Sense | Cy5‑GCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAG |
| Cy5 601 80 nts. Sense | Cy5‑GTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTA |
| 601 10 nts. Antisense | GGACAGCGCG |
| 601 20 nts. Antisense | GCGGGGGACAGCGCGTACGT |
| 601 30 nts. Antisense | AAAACGCGGGGGACAGCGCGTACGTGCGTT |
| 601 40 nts. Antisense | CGGTTAAAACGCGGGGGACAGCGCGTACGTGCGTTTAAGC |
| 601 50 nts. Antisense | CTTGGCGGTTAAAACGCGGGGGACAGCGCGTACGTGCGTTTAAGCGGTGC |
| 601 80 nts. Antisense | TAGGGAGTAATCCCCTTGGCGGTTAAAACGCGGGGGACAGCGCGTACGTGCGTTTAAGCGGTGCTAGAGCTGTCTACGAC |
| Cac1 ∆KER  Forward | GCACAATCCCGTATTGGTAACTTCTTTAAAAAACTAAGCG |
| Cac1 ∆KER  Reverse | TTACCAATACGGGATTGTGCCGATGAGGAAAGTTCTCTCTTAGAGCATGG |
| Cac1 ∆middle-A Forward | AGAAAAGAGGAGGAAAGATTGAAAAAGGAGGAGGAAATACG |
| Cac1 ∆middle-A Reverse | AATCTTTCCTCCTCTTTTCTTTTCTCTTCTGCACGTTGCTGCTTTTTTAGTTCC |
| Cac1 ∆WHD Forward | ATGCCAACCCCGTCTTTGTCAGGATGGAGCCACCCGCAGTTCGAAAAGTAG |
| Cac1 ∆WHD Reverse | GACAAAGACGGGGTTGGCATTTTCTTTTCGGGACTTTGAGATTGGCTAGCGG |
| Cac1 KER::Myosin7a SAH Forward | GCACAATCCCGTATTGGTAA |
| Cac1 KER::Myosin7a SAH Reverse | CGATGAGGAAAGTTCTCTCT |
| Cac1 KER::Myosin7a SAH dsDNA | AGAGAGAACTTTCCTCATCGCGCCTGGAAGCGGAACGCATGCGCCTGGCGGAAGAAGAAAAACTGCGCAAAGAAATGAGCGCGAAAAAAGCGAAAGAAGAAGCGGAACGCAAACATCAGGAACGCCTGGCGCAGCTGGCGCGCGAAGATGCGGAACGCGAACTGAAAGAAAAAGAAGAAGCGCGCCGCAAAAAAGAACTGCTGGAACAGATGGAAAAAGCGGCACAATCCCGTATTGGTAA |
| Cac1 ED::GSL  Forward | AACAGTGATTTGGATGGCCTACCCTGC |
| Cac1 ED::GSL  Reverse | TTCTTCTTCTTCATTAACCCATTCAACG |
| Cac1 ED::GSL  dsDNA | GGGTTAATGAAGAAGAAGAAGGCTCACTGGGGTCCCTTGGAAGCTTAGGGTCTCTTGGGTCCCTGGGCTCTTTAGGAAGCCTTGGTTCACTTGGTTCATTAGGATCCCTAGGATCTTTGGGATCCAACAGTGATTTGGATGGCCT |
| Cac1 2xKER Forward | GCACAATCCCGTATTGGTAA |
| Cac1 2xKER Reverse | TCTTTCCTTGGCTTCTTCTTTCAAACG |
| Cac1 2xKER dsDNA -Fwd | AAGAAGAAGCCAAGGAAAGAAAAAAGGAAGAAGCTAAAAGAGAAAAGG |
| Cac1 2xKER dsDNA -Rev | TTACCAATACGGGATTGTGCTCTTTCCTTGGCTTCTTCTTTCAAACGTATTTCCTCC |
| Cac1 +N-half Forward | GCACAATCCCGTATTGGTAA |
| Cac1 +N-half Reverse | TCTTTCCTTGGCTTCTTCTTTCAAACG |
| Cac1 +N-half dsDNA | AAGAAGAAGCCAAGGAAAGAAAAAAGGAAGAAGCTAAAAGAGAAAAGGAACTAAAAAAGCAGCAACGTGCAGAAGAGAAACACAGAAAAGAGTTATTACGACAAGAAGAGAAAAAGAAAAAAGAGCTAAAGGCACAATCCCGTATTGGTAA |
| Cac1 KER::hKER Forward | GCACAATCCCGTATTGGTAA |
| Cac1 KER::hKER Reverse | CGATGAGGAAAGTTCTCTCT |
| Cac1 KER::hKER dsDNA -Fwd | AGAGAGAACTTTCCTCATCGGAAAAGAACAAACTGCGCCTGCAACGCGACC |
| Cac1 KER::hKER dsDNA -Rev | TTACCAATACGGGATTGTGCTTCCGCTTTGATACGCTTTTCTTC |
| Cac1 KER Forward | CTGTTCCAGGGGCCCCTGAAAAAGGAAGAAGCTAAAAGAGAAAAGG |
| Cac1 KER Reverse | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTACTATCTTTCCTTGGCTTCTTCTTTC |
| Cac1 KER Reverse +Y | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTACTAATATCTTTCCTTGGCTTCTTCTTT |
| Cac1 N-half Forward | CTGTTCCAGGGGCCCCTGAAAAAGGAAGAAGCTAAAAGAGAAAAGG |
| Cac1 N-half Reverse | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTACTAATACTTTAGCTCTTTTTTCTTTTT |
| Cac1 middle-A dsDNA | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTGGAAGTTCTGTTCCAGGGGCCCCTGAAACATCGTAAAGAATTACTTCGTCAAGAAGAAAAGAAAAAGAAGGAACTTAAAGTAGAGGAAGAACGGCAGCGGCGGGCTGAACTGAAAAAGCAGAAGGAAGAGGAAAAACGGCGTAAAGAGGAGGCGCGTTTGGAGGCCAAACGGCGCTAT  TAGTAGGACCCAGCTTTCTTGTACAAAGTGGTCCCC |
| Cac1 middle-B dsDNA | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTGGAAGTTCTGTTCCAGGGGCCCCTGGTAGAGGAAGAACGGCAGCGGCGGGCTGAACTGAAAAAGCAGAAGGAAGAGGAAAAACGGCGTAAAGAGGAGGCGCGTTTGGAGGCCAAACGGCGCTATTAGTAGGACCCAGCTTTCTTGTACAAAGTGGTCCCC |
| Cac1 C-half Forward | CTGTTCCAGGGGCCCCTGAGGCGTGCTGAGCTGAAAAAGC |
|  |  |
| Cac1 C-half Reverse | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTACTAATACTCTTTTCTTCTTTT GGC |
| Myosin 7a SAH dsDNA | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTGGAAGTTCTGTTCCAGGGGCCCCTGCGCCTGGAAGCGGAACGCATGCGCCTGGCGGAAGAAGAAAAACTGCGCAAAGAAATGAGCGCGAAAAAAGCGAAAGAAGAAGCGGAACGCAAACATCAGGAACGCCTGGCGCAGCTGGCGCGCGAAGATGCGGAACGCGAACTGAAAGAAAAAGAAGAAGCGCGCCGCAAAAAAGAACTGCTGGAACAGATGGAAAAAGCG  TATTAGTAGGACCCAGCTTTCTTGTACAAAGTGGTCCCC |
| CHAF1A dsDNA for cloning in pGEX-6P-1 | GGGGCCCCTGGGATCCATGGATTGCAAAGATCGCCCGGCGTTTCCGGTGAAAAAACTGATTCAGGCGCGCCTGCCGTTCAAGCGCCTGAACCTGGTGCCGAAAGGCAAAGCGGATGATATGAGCGACGATCAAGGTACGAGCGTTCAGAGCAAATCGCCGGATCTGGAAGCCAGCCTGGATACGCTGGAAAACAACTGTCACGTGGGTAGCGATATTGACTTTCGCCCGAAACTGGTTAATGGTAAAGGCCCGCTGGATAATTTTCTGCGCAACCGCATTGAAACCAGCATCGGCCAGAGCACCGTTATCATTGATCTGACCGAGGATAGCAACGAGCAGCCGGATAGCCTGGTGGATCATAACAAACTGAACAGCGAGGCGAGCCCGTCGCGCGAGGCGATCAATGGCCAGCGCGAAGACACCGGTGATCAACAGGGTTTACTGAAGGCGATTCAAAATGACAAACTGGCCTTCCCGGGTGAAACCCTGAGCGACATTCCGTGTAAGACCGAGGAAGAAGGTGTGGGTTGTGGTGGCGCGGGCCGCCGTGGCGATAGCCAGGAATGCAGCCCGCGCAGCTGTCCGGAACTGACGAGCGGTCCGCGCATGTGTCCGCGCAAGGAACAAGATAGCTGGAGCGAGGCCGGCGGCATTCTGTTCAAGGGAAAAGTTCCGATGGTTGTTCTGCAGGACATTCTGGCGGTGCGCCCTCCGCAGATCAAAAGCCTGCCGGCCACGCCGCAAGGCAAAAACATGACGCCGGAAAGCGAAGTGCTGGAAAGCTTTCCGGAAGAGGACAGCGTTCTGAGCCATTCGAGCCTGTCGAGCCCGAGCAGCACCTCGAGCCCGGAAGGTCCTCCGGCCCCGCCGAAGCAGCATTCGAGCACGAGCCCGTTTCCGACGAGCACCCCGCTGCGTCGCATTACCAAGAAATTTGTGAAAGGTAGCACGGAAAAGAACAAACTGCGCCTGCAACGCGACCAAGAACGCCTGGGTAAGCAACTGAAACTGCGCGCCGAGCGCGAGGAAAAGGAAAAGCTGAAAGAGGAAGCCAAACGCGCCAAGGAGGAGGCGAAGAAAAAAAAGGAGGAAGAAAAGGAACTGAAGGAGAAAGAGCGCCGTGAAAAGCGCGAAAAGGATGAGAAGGAAAAAGCGGAAAAACAACGCCTGAAGGAGGAACGCCGTAAAGAACGCCAGGAAGCCCTGGAAGCCAAACTGGAAGAAAAACGCAAAAAGGAGGAAGAAAAGCGTCTGCGCGAGGAAGAAAAGCGTATCAAAGCGGAAAAGGCGGAAATTACCCGCTTCTTCCAGAAGCCGAAGACGCCTCAGGCCCCGAAGACGCTGGCGGGTAGCTGTGGTAAATTTGCCCCGTTCGAGATTAAGGAACATATGGTGCTGGCCCCGCGTCGCCGCACGGCGTTTCATCCGGACCTGTGCAGCCAGCTGGACCAGCTGCTGCAGCAGCAGAGCGGTGAGTTCTCGTTCCTGAAGGATTTAAAGGGCCGCCAACCGCTGCGCAGCGGTCCGACCCACGTTAGCACGCGCAACGCCGATATCTTCAATAGCGACGTTGTGATCGTGGAGCGCGGCAAAGGCGACGGTGTTCCGGAGCGTCGCAAGTTTGGACGCATGAAGTTACTGCAATTCTGCGAGAACCATCGCCCGGCCTATTGGGGCACGTGGAACAAGAAAACTGCGCTGATTCGCGCGCGTGATCCGTGGGCCCAGGATACGAAGTTACTGGACTACGAAGTTGATAGCGATGAAGAGTGGGAAGAAGAGGAACCGGGTGAGAGCCTGTCGCACAGCGAGGGCGACGATGATGACGACATGGGTGAGGATGAGGACGAAGACGATGGTTTCTTTGTGCCTCATGGTTACCTGAGCGAAGACGAGGGTGTTACCGAAGAGTGTGCGGACCCGGAAAACCATAAGGTGCGCCAGAAGCTGAAGGCCAAAGAGTGGGACGAGTTCCTGGCGAAGGGCAAACGTTTTCGCGTTCTGCAGCCGGTTAAAATTGGCTGTGTTTGGGCCGCGGATCGCGACTGCGCGGGTGATGACCTGAAAGTTCTGCAGCAATTCGCGGCCTGCTTCCTGGAGACCCTGCCGGCGCAGGAGGAACAAACCCCGAAAGCCAGCAAACGCGAACGTCGCGATGAGCAGATTCTGGCGCAGTTACTGCCGTTACTGCATGGCAACGTTAACGGTAGCAAAGTGATCATTCGCGAATTCCAGGAGCACTGCCGTCGCGGTTTACTGAGCAATCATACCGGTAGCCCGCGCACGCCGAGCACCACCTACCTGCATACGCCGACCCCGAGCGAGGATGCCGCGATTCCGAGCAAGTCGCGCCTGAAGCGCCTGATTAGCGAAAATAGCGTTTACGAAAAGCGCCCGGACTTTCGCATGTGTTGGTACGTGCATCCGCAGGTGCTGCAGAGCTTTCAGCAGGAACATCTGCCGGTTCCGTGCCAATGGAGCTACGTTACGAGCGTGCCGAGCGCCCCGAAAGAGGATAGCGGTAGCGTGCCGAGCACGGGTCCGAGCCAAGGTACCCCGATCAGCCTGAAGCGCAAGAGCGCCGGTAGCATGTGCATTACCCAATTTATGAAGAAACGTCGCCATGACGGCCAGATCGGTGCGGAGGACATGGACGGTTTTCAAGCGGATACCGAGGAAGAGGAAGAAGAAGAGGGCGACTGCATGATTGTTGATGTTCCGGACGCCGTGGAAGTTCAGGCCCCGTGTGGTGCCGCGAGCGGGGCCGGTGGCGGCGTTGGCGTGGATACCGGAAAAGCGACCCTGACGGCCAGCCCGCTGGGTGCGAGCTAAGGATCCCCGGAATTCC |
| CHAF1A KER (hKER) Forward | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCTGGAAGTTCTGTTCCAGGGGCCCCTGGAAAAGAACAAACTGCGCCTGCAACGCGACC |
| CHAF1A KER (hKER) Reverse | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTACTAATATTCCGCTTTGATACGCTTTTCTTC |
| CAC1\_FLAG\_gRNA\_F | CTTTCCGTTCAAGTTACAAAGACG |
| CAC1\_FLAG\_gRNA\_R | AAACCGTCTTTGTAACTTGAACGG |
| mPIP\_∆225-226\_gRNA\_F | CTTTACGTTTGAAAGAAGAAGCCA |
| mPIP\_∆225-226\_gRNA\_R | AAACTGGCTTCTTCTTTCAAACGT |
| mWHD\_gRNA\_F | CTTTAACAATTAAAAACACCATAA |
| mWHD\_gRNA\_R | AAACTTATGGTGTTTTTAATTGTT |
| ∆KER\_gRNA\_F | CTTTAGGTAGAAGAGGAAAGACAA |
| ∆KER\_gRNA\_F | AAACTTGTCTTTCCTCTTCTACCT |
| ∆145-149\_gRNA\_R | CTTTGGAAGAAGCTAAAAGAGAAA |
| ∆145-149\_gRNA\_R | TTTCTCTTTTAGCTTCTTCC |
| CAC1\_FLAG\_HR\_F | CCAATGCAAATATGCCAACCCCGTCTTTGGGATCCGCTGGCTCCGCTGCTGGTTCTGGCG |
| CAC1\_FLAG\_HR\_M | GGTTCTGGCGATTACAAGGATGACGACGATAAGGACTATAAGGACGATGATGACAAGGACTACAAAGATGATGACGATAAATAACTTGAA |
| CAC1\_FLAG\_HR\_R | TACCAATAAATAATCAGTTTATCTGTATGTTTCTATATACTAAAGATCCGTTCAAGTTAT |
| CAC1\_mPIP\_HR\_F | AAATACGTTTGAAAGAAGAAGCCAAAGAAAGAGCACAATCCCGTATTGGTAACGC |
| CAC1\_mPIP\_HR\_M | TTGGTAACGCCGCGAAAAAACTAAGCGATTCTAATACGCCTGTGGTTGAAAAGTCGGATT |
| CAC1\_mPIP\_HR\_R | CTCTAACTCCATCTTTAGCATAGAAAGGTAGAAAAAATTTTTCATAATCCGACTT |
| CAC1\_mWHD\_HR\_F | CAGCACGTTTTCTTTGGGTACTGTGACTGAAATAGCACAGAAAAATTTGCCGCAATACAA |
| CAC1\_mWHD\_HR\_M | CGCAATACAACAAACAAACAATTGAAAACACCATAGAGGAATATGCCATAAGAAGTTCTG |
| CAC1\_mWHD\_HR\_R | CCAGTTTTGTGCGTCTTTGATTACCCATTTGCGGGGCAAATCACCCTTTCCAGAACTTCT |
| CAC1\_∆KER\_HR\_F | TACCCAATGGAAATATAATAGCTATCGAGACAAAAAGCAGAAGCTCTTCTCCATGCTCTA |
| CAC1\_∆KER\_HR\_M | TCTCCATGCTCTAAGAGAGAACTTTCCTCATCGGCACAATCCCGTATTGGTAACTTCTTT |
| CAC1\_∆KER\_HR\_R | TCATAATCCGACTTTTCAACCACAGGCGTATTAGAATCGCTTAGTTTTTTAAAGAAGTTA |
| CAC1\_∆KERmPIP\_HR\_M | TCTCCATGCTCTAAGAGAGAACTTTCCTCATCGGCACAATCCCGTATTGGTAACGCCGCG |
| CAC1\_∆KERmPIP\_HR\_R | TCATAATCCGACTTTTCAACCACAGGCGTATTAGAATCGCTTAGTTTTTTCGCGGCGTTA |
| CAC1\_∆1-2KER\_HR\_F | CTAAGAGAGAACTTTCCTCATCGAAAAAGGAAGAAGCTAAAAGAGAAAAGGAACTAAAAA |
| CAC1\_∆1-2KER\_HR\_M | GAACTAAAAAAGCAGCAACGTGCAGAAGAGAAAGAGGAGGAAAGATTGAAAAAGGAGGAG |
| CAC1\_∆1-2KER\_HR\_R | CCAATACGGGATTGTGCTCTTTCCTTGGCTTCTTCTTTCAAACGTATTTCCTCCTCCTTT |
| CAC1\_2xandHumanKER\_HR\_F | GCTATCGAGACAAAAAGCAGAAGCTCTTCTCCATGCTCTAAGAGAGAACTTTCCTCATCG |
| CAC1\_2xandHumanKER\_HR\_R | AACCACAGGCGTATTAGAATCGCTTAGTTTTTTAAAGAAGTTACCAATACGGGATTGTGC |
| CAC1\_∆225-226\_HR\_F | GATTAGAAGCCAAAAGAAGAAAAGAGGAGGAAAGATTGAAAAAGGAAGAGGAAATACGTT |
| CAC1\_∆225-22\_HR\_M | GAAATACGTTTGAAAGAAGAAGCCAAAGAACAATCCCGTATTGGTAACTTCTTTAAAAAA |
| CAC1\_∆225-226\_HR\_R | AATTTTTCATAATCCGACTTTTCAACCACAGGCGTATTAGAATCGCTTAGTTTTTTAAAG |
| CAC1\_∆225-226mPIP\_HR\_M | GAAATACGTTTGAAAGAAGAAGCCAAAGAACAATCCCGTATTGGTAACGCCGCGAAAAAA |
| CAC1\_∆225-226mPIP\_HR\_R | AATTTTTCATAATCCGACTTTTCAACCACAGGCGTATTAGAATCGCTTAGTTTTTTCGCG |
| CAC1\_∆145-149\_HR\_F | AAAAGCAGAAGCTCTTCTCCATGCTCTAAGAGAGAACTTTCCTCATCGAAAAAGGAAGAA |
| CAC1\_∆145-149\_HR\_M | AAAGGAAGAAGCTAAAAGAGAAAAGCAACGTGCAGAAGAGAAACACAGAA |
| CAC1\_∆145-149\_HR\_R | TTCTACCTTTAGCTCTTTTTTCTTTTTCTCTTCTTGTCGTAATAACTCTTTTCTGTGTTT |
| Yeast::Human KER | AAGAGAGAACTTTCCTCATCGGAAAAAAATAAGCTGAGATTACAACGTGACCAAGAGAGGCTGGGAAAGCAACTTAAACTTAGAGCCGAGCGTGAAGAAAAGGAGAAGCTAAAAGAAGAAGCTAAGAGGGCTAAGGAAGAGGCTAAAAAAAAGAAAGAAGAAGAGAAAGAGTTGAAAGAGAAAGAAAGGAGGGAAAAACGTGAAAAGGATGAAAAGGAGAAGGCAGAAAAGCAGCGTTTAAAAGAAGAGAGAAGAAAGGAACGTCAAGAAGCATTAGAAGCAAAGCTGGAGGAAAAGAGGAAGAAAGAAGAGGAAAAGAGGTTACGTGAAGAAGAAAAAAGAATAAAGGCTGAGGCACAATCCCGTATTGGTAAC |
| 2xKER | AAGAGAGAACTTTCCTCATCGAAAAAAGAAGAAGCAAAGAGGGAAAAGGAGCTTAAAAAGCAACAACGTGCTGAAGAGAAGCATAGGAAAGAATTGTTGAGACAGGAAGAAAAAAAGAAGAAAGAACTGAAGGTGGAGGAAGAGAGACAAAGGAGGGCCGAACTAAAAAAGCAGAAGGAGGAGGAAAAACGTCGTAAAGAAGAGGCGAGACTAGAGGCGAAAAGGAGAAAAGAAGAAGAAAGGTTGAAAAAGGAGGAGGAAATTAGGTTAAAAGAAGAAGCGAAGGAAAGGAAAAAGGAGGAGGCAAAGCGTGAGAAGGAGCTAAAGAAACAGCAACGTGCAGAAGAGAAACACAGAAAGGAGTTGTTGAGGCAGGAAGAAAAAAAAAAAAAGGAACTAAAAGTCGAAGAAGAAAGACAGAGACGTGCCGAACTAAAAAAACAAAAAGAAGAAGAGAAGCGTAGAAAGGAAGAAGCAAGGCTTGAAGCAAAACGTAGGAAGGAAGAGGAACGTCTGAAGAAAGAGGAGGAGATCAGACTAAAGGAAGAGGCTAAAGAGAGAGCACAATCCCGTATTGGTAAC |
| rtt106\_HIS\_F | TGTAGTAATAACTATGATGTAAAGGTGCTGGAAACGCTGACAGCTGAAGCTTCGTACGC |
| rtt106\_HIS\_R | TATTCTTCAGGATAAAAAAAGTGGTATTTATGAACTCTTACATAGGCCACTAGTGGATCTG |
| cac1\_KAN\_F | ACATTCTGTTATTGCTGTTACAGAGAATTATATGTTTTAGCAGCTGAAGCTTCGTACGC |
| cac1\_KAN\_R | TAGTGTTGTCGCCTTTTTCATGTATACCAATAAATAATCACATAGGCCACTAGTGGATCTG |
| sir2\_KAN\_F | CCCATCTCAGAGAAAAAACGAGG |
| sir2\_KAN\_R | AGCTATTTGTGAGAGCCTTGCGTC |
| bar1\_LEU2\_F | GCCAGCTATTCTGAAACACACCAC |
| bar1\_LEU2\_R | GCTACTTGTTCAAAATTGTGATGGCTGC |
| bar1\_LEU2\_R | GCTACTTGTTCAAAATTGTGATGGCTGC |