**Table S1 Nucleotide sequences of oligonucleotides harbouring the putative TFBSand mutated sites used for EMSA.**

|  |  |  |  |
| --- | --- | --- | --- |
| TFBS | Sequence | Mutated TFBS | Mutated sequencea |
| TFBSsacA TFBSpts1 | AATGTCAAACGATTGA TGTAAAGCGCTTGCAT | TFBSsacAMUT TFBSpts1MUT | **CTG**G**AT**A**GTTTGC**T**AG AAGATTTGACGGGAGG** |
| TFBSagl4 | AAGTGGAATCGATTCC | TFBSagl4MUT | **TCA**T**AT**A**GAAT**A**GGAA** |
| TFBSsacR2S26 | TGGAAACGATTCCAAA | TFBSsacR2MUT | **AATGTGTC**A**G**TC**GGGG** |

a Mutated nucleotide are marked with bold.

**Table S2 Primers used in this study.**

|  |  |
| --- | --- |
| Primer | Sequence (5’ to 3’) |
| **Primers for gene cloning** |
| sacR1F | GGAATTCCATATGATACTGGAGTCGATAACAATGAAACCCC |
| sacR1R | CCGCTCGAGTTACGCGGTAAGGCCCTTG |
| sacR2F | GGAATTCCATATGGCCTAAATGACAACGATTAGTGAAAT |
| sacR2R | CCGCTCGAGGGCTTAAGCACTTTTTCTTTTGAT |
| **Primers for gene mutation** |
| sacR1UpF | AGGACCGATAACGCGCTCGAGACGACTACTGAGATCGGTGCTATCT |
| sacR1UpR | CGGTAGATTTAAATTGTTTAAACGCCGCGAAAACTTTTTCTTTAG |
| sacR2UpF | CCGCTCGAGTGACGATTTATCAATTCAATTGGCC |
| sacR2UpF | GCGTTTAAACAATCGCTGCCTGAATCTGTTTCTTC |
| sacR1DownF | GCGAATTGTACACTGGAATCAAA |
| sacR1DownR | GGAAGATCTTAGCGCCACTAACGGTGTCTT |
| sacR2DownF | CATTTGCGGCAGTGGCCC |
| sacR2DownR | GGAAGATCTAAGTTGGTCATAACTAACCCCCGAA |
| sacR1-85 | GGTATACGAGTTCGTTTCGTGAT |
| sacR1-87 | AGGAATCATTACCGAAGTAATCGT |
| sacR1-108 | TAATGCCGACTGTACTTTCGG |
| sacR1-109 | CATCATATCTGCCGGTGATAGTAG |
| sacR2-85 | GTTTTTTTCTAGTCCAAGCTCACA |
| sacR2-87 | TAATGCCGACTGTACTTTCGG |
| sacR2-108 | TGGTTAGTACCACTCATATTTGGAA |
| sacR2-109 | TAACTAACCCCCGAAGCCTC |
| 120 | AGAACAATCAAAGCGAGAATAAGG |
| 20 | AATAGTTATCTATTATTTAACGGGAGG |
| CmF | TCTTAGTGACAAGGGTGATAAACTC |
| CmR | CCGAACCATTATATTTCTCTACATC |
| EmF | CGATACCGTTTACGAAATTGG |
| EmR | CTTGCTCATAAGTAACGGTAC |
| sacK1F | TTTAATGGTCGCACTCATACTGAAC |
| sacK1R | CCAGCAGCTAAACCTTCTAAACAG |
| sacAF | GGATGGACACGGATAATCACATT |
| sacAR | TTGAGAAATAAACCAAGATAGCACC |
| sacPTS2F | TTAACCAGTGGGATAGGTGCTG |
| sacPTS2R | CGAGACGACCGTATAAATCAGC |
| 16SF | CGCAAGGCTGAAACTCAAAGG |
| 16SR | CTGACGACAACCATGCACCAC |
| **Primers for target analysis and EMSA** |
| pts1F | AACGACTCAAAGTCACAAATGTCC |
| sacAR | CAATCAGAGCATACTGGAGTCGAT |
| agl4F | CAACCGGGGTAACATTTGGAT |
| agl4R | GGCGGTCGATCAGCTATTACAT |
| sacR2F | GTGGACTAAATGTTTTAAGGGCAAAC |
| sacR2R | TGCCTGAATCTGTTTCTTCTTAGCA |
| pts1mutF | CTGTTTGTGATGGTTATCATGCAGG |
| sacAmutR | GGGCTGTACCGTTCGTATAGCATAC |
| pts1mut2F | TAGGAAAGGAGAACAGCTGAATG |
| sacAmut2R | TACCTGGCTTGGTAGTGATTGAG |
| agl4mutF | GTTTTAGAAACGCCAGTCTATGTG |
| agl4mutR | ATTACACGTTAGATCAACTGGCAA |
| sacR2mutF | GGTATACTACTGACAGCTTCCAAGG |
| sacR2mutR | GCTGTTGCGAGTTTATTTTGTCT |
| M13F-47 (FAM) | CGCCAGGGTTTTCCCAGTCACGAC |
| M13R-48 | AGCGGATAACAATTTCACACAGGA |
| **Primers for ChIP** |
| Flag- sacR1F | ACAAGGAGATTTTAGCCATGGGATTACAAGGATGACGACGATAAGA |
| Flag- sacR1R | CGGGGTACCGAATTCCTCGAGTTACGCGGTAAGGCCCTTG |
| Flag- sacR2F | CATGCCATGGACGATTACAAGGATGACGACGATAAGACAATGAAACCAAAATTAAATGA |
| Flag- sacR2R | CCGCTCGAGTACGATTAACTCCTTAGTTACGC |
| 403F | GAAATACCCGTCTAAGGAATTG |
| 403R | TGGTCATGAATTAGTCTCGGA |
| ChIP-pts1F | GTTTCGAAGGTCCCCTTAACG |
| ChIP-pts1R | TTGTTATTATTGGGTCTGTAAAGCG |
| ChIP-sacAF | ATTTAATAATGCAAGCGCTTTACAG |
| ChIP-sacAR | CATATCATGACGATGAGCTCCTTT |
| ChIP-agl4F | GGTTACAACGACCTGAGTTAGCG |
| ChIP-agl4R | CAATGCCATCGTTATTAGCATCTT |
| ChIP-sacR2F | AATGGTGGACTAAATGTTTTAAGGG |
| ChIP-sacR2R | TCTTAGCAACTGAAACACTAGGCC |