**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 |