Supplementary Material

## Supplementary Tables

**Supplementary Table S1** Premiers used in this study

|  |  |  |
| --- | --- | --- |
| **Primers** | **Sequence (5’ – 3’)** | **Purpose** |
| 16S | F: ATTCCTGGTGTAGCGGTG | qRT-PCR |
| R: CATCGTTTAGGGTGTGGAC |
| Dsr11 | F: GAGGACGCAGAAGAACAGC |
| R: GAGCAGTTCTCTTCAGACCTGAC |
| DR\_2376 | F: GTTCGACGAGGCGCTGTTC |
| R: GGCTCGGCGGAAAGGTGCTTC |
| DR\_2377 | F: GAATGGACCAGAGCCGCCTGATGAG |
| R: GTCTTTGCCGGTCGCGGCCTTGTAG |
| Dsr11-U | F: GCAACCTGATTCTGTCTGCCGTG | Dsr11 mutant construction |
| R: GCTCGGTCTCCATGCTCTGCCCCCACTTCGATAAC |
| Dsr11-M | F: GTGGGGGCAGAGCATGGAGACCGAGGGCCCTTG |
| R: GCAGTTCTCTTCTTAGAAAAACTCATCGAGCATC |
| Dsr11-D | F: CGAGTTTTTCTAAGAAGAGAACTGCTCAGGCGC |
| R: CGCGCAGCAGGTGTACGACTAC |

**Supplementary table S2** Synthesized ssRNA oligonucleotide derivatives for MST

|  |  |  |
| --- | --- | --- |
| Name | Sequence (5’ – 3’) | Relevant characteristics |
| dsr11-wt（5'FAM） | GCGCCCAGGUCAAGGAAGAAA | interaction with and trmE-wt |
| dsr11-wt（5'FAM） | AGGAAGUCCAGGCGGUGCA | interaction with and dr\_0651-wt |
| dsr11-mut（5'FAM） | GCCGCCACCAGUUCGUUCUUU | Dismatch mutation, no interaction with trmE-wt |
| dsr11-mut（5'FAM） | ACCAACAGGUCCGCCACCU | Dismatch mutation, no interaction with dr0651-wt |
| dr0651-wt | UCACCUGCCUGGAACGCCC | interaction with dsr11-wt |
| trmE-wt | UUUCUUUCUUGACCCGC | interaction with dsr11-wt |

**Supplememtary Table S4** The possible targets of *dsr11* predicted by TargetRNA2

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Rank** | **Gene ID** | **Description** | **Energy** | **Pvalue** |
| 1 | DR\_1576 | hypothetical protein | -17.09 | 0.000 |
| 2 | DR\_2456 | hypothetical protein | -15.08 | 0.001 |
| 3 | DR\_1016 (trmE) | tRNA modification GTPase TrmE | -14.99 | 0.001 |
| 4 | DR\_0697 | v-type ATP synthase subunit E | -14.3 | 0.001 |
| 5 | DR\_1902 | exodeoxyribonuclease V subunit RecD | -14.23 | 0.001 |
| 6 | DR\_1312 | hypothetical protein | -14.18 | 0.001 |
| 7 | DR\_0599 | aminoglycoside N3-acetyltransferase | -14.07 | 0.002 |
| 8 | DR\_0520 | hypothetical protein | -14.03 | 0.002 |
| 9 | DR\_1639 | hypothetical protein | -13.8 | 0.002 |
| 10 | DR\_0818 | hypothetical protein | -13.55 | 0.002 |
| 11 | DR\_2498 | GGDEF family protein | -13.51 | 0.003 |
| 12 | DR\_1821 | hypothetical protein | -13.03 | 0.004 |
| 13 | DR\_0552 | hypothetical protein | -12.5 | 0.005 |
| 14 | DR\_0650 | hypothetical protein | -12.46 | 0.005 |
| 15 | DR\_0651 | arginase | -11.49 | 0.010 |
| 16 | DR\_0348 | cytochrome c-type biogenesis heme exporter protein C | -11.28 | 0.012 |
| 17 | DR\_0895 | hypothetical protein | -11.18 | 0.012 |
| 18 | DR\_1852 | hypothetical protein | -10.7 | 0.016 |
| 19 | DR\_0456 | biopolymer transport protein | -10.61 | 0.017 |
| 20 | DR\_2545 | hypothetical protein | -10.51 | 0.018 |
| 21 | DR\_1692 | long-chain fatty acid--CoA ligase | -10.48 | 0.018 |
| 22 | DR\_2390 | homoserine kinase | -10.32 | 0.020 |
| 23 | DR\_1155 | malate synthase | -9.91 | 0.024 |
| 24 | DR\_2635 | pyruvate kinase | -9.83 | 0.025 |
| 25 | DR\_0935 | phosphatase | -9.55 | 0.029 |
| 26 | DR\_2102 | plasmid stability protein | -9.51 | 0.030 |
| 27 | DR\_1897 | hypothetical protein | -9.39 | 0.031 |
| 28 | DR\_1529 | hypothetical protein | -9.26 | 0.033 |
| 29 | DR\_0538 | hypothetical protein | -9.15 | 0.035 |
| 30 | DR\_2571 (moaC) | molybdenum cofactor biosynthesis protein MoaC | -9.03 | 0.037 |
| 31 | DR\_1587 | hypothetical protein | -8.79 | 0.041 |
| 32 | DR\_1994 | hypothetical protein | -8.76 | 0.041 |
| 33 | DR\_1753 | septum site-determining protein | -8.75 | 0.041 |
| 34 | DR\_1688 | hypothetical protein | -8.64 | 0.043 |
| 35 | DR\_1729 | hypothetical protein | -8.29 | 0.050 |