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Title	Comparative genomics reveals the regulatory complexity of Bifidobacterial arabinose and Arabino-oligosaccharide utilization
Authors	Arzamasov, Aleksandr A.;van Sinderen, Douwe;Rodionov, Dmitry A.
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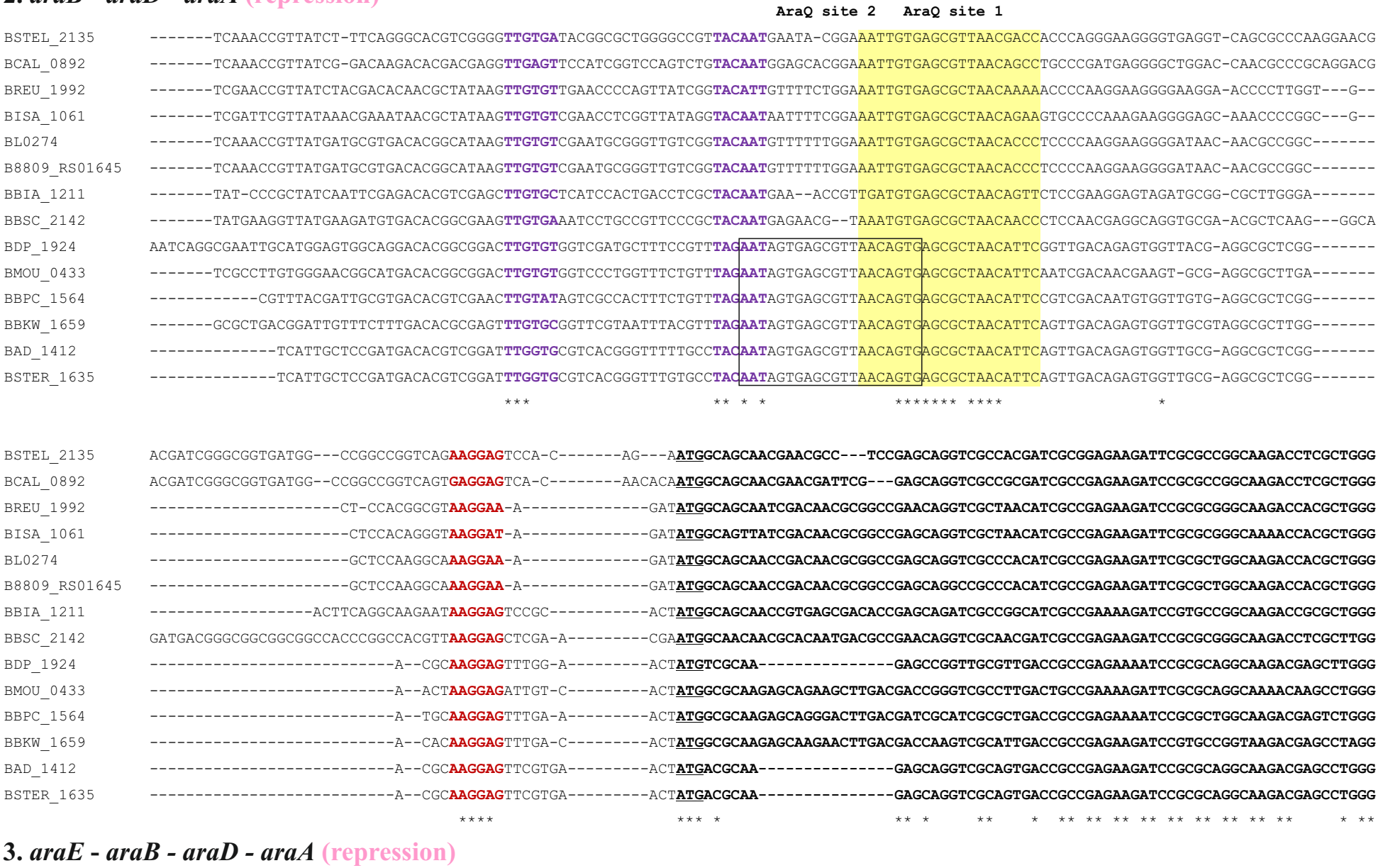
FIGURE S1. Multiple sequence alignments of gene upstream regions containing candidate AraQ-binding sites in *Bifidobacterium* spp. Predicted AraQ-binding sites are highlighted in mild yellow (when several overlapping sites are present the weaker one is marked with a rectangle box). Candidate binding sites for Crp, MalR and BfrR1 are in blue, green and orange, respectively. Predicted promoter elements (-35 and -10 boxes) and shown in bold purple. Known transcription start sites are marked in bold red. Putative ribosome binding sites are shown in bold dark red. Coding sequences are in bold, initiation codons are underlined. Conservative nucleotides are marked with asterisks.

1. *araQ* (repression)

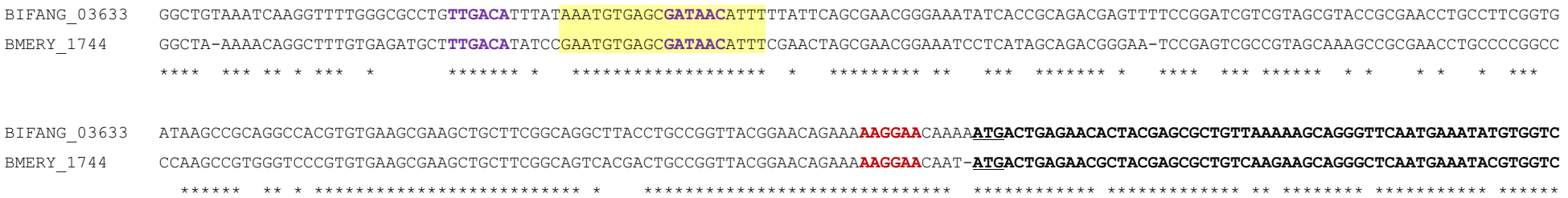
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BBPC_1565    CGCTGCGCGACTCGCTCAAATGGCT----------------------------------------GAAAAAT--------------------AGCGTCTGTTAGCGCTAACCGAAGTTGCGTGTAGAATAGTCGAAA
BBKW_1660    CGCAGCACGACTTGCTCAAATGGCT----------------------------------------GAAAAAT--------------------AGCGTCTGTTAGCGCTAACCGAGGCTGCGTGTAGAATAGTCGAAA
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BSTER_1634   CGCGGCGCGTCTGCGTGCTTTGGCGGCC----GTGCGGTAGCCTGCGCGCAGTGTGCCGCATCCTTGGAACAT--------------------GACGGCTGTTAGCGCTAACTGAAGTTGCGTGTACAATAGGCGAAC
              ** ** ** **       ****                                    * *   *                     *  ************ ** * ******** *** * ** *
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BBKW_1660    GTAACAACGGTAGTGTGCGGGAGGCGACGGGGCATGGCAGGCAGGCGTAATGCAGGCAAAAAACGTCCTTCGATGTTCGAAGTGGCAAAATTCGCGGGAGTG
BAD_1413     GTACCAACAGTTGTGTGCGAAAGGCGACGGGGCATGGCAGGCAAACGCGATGCGGGCAATAAGCGTCCTTCGATGTTCGAAGTGGCGAAGCTGGCTGGTGTG
BSTER_1634   GTACCAACAGTTGTGTGCGAAAGGCGACGGGGCATGGCAGGCAAACGCAATGCGGGCAATAAGCGTCCTTCGATGTTCGAAGTGGCGAAGCTGGCTGGTGTG
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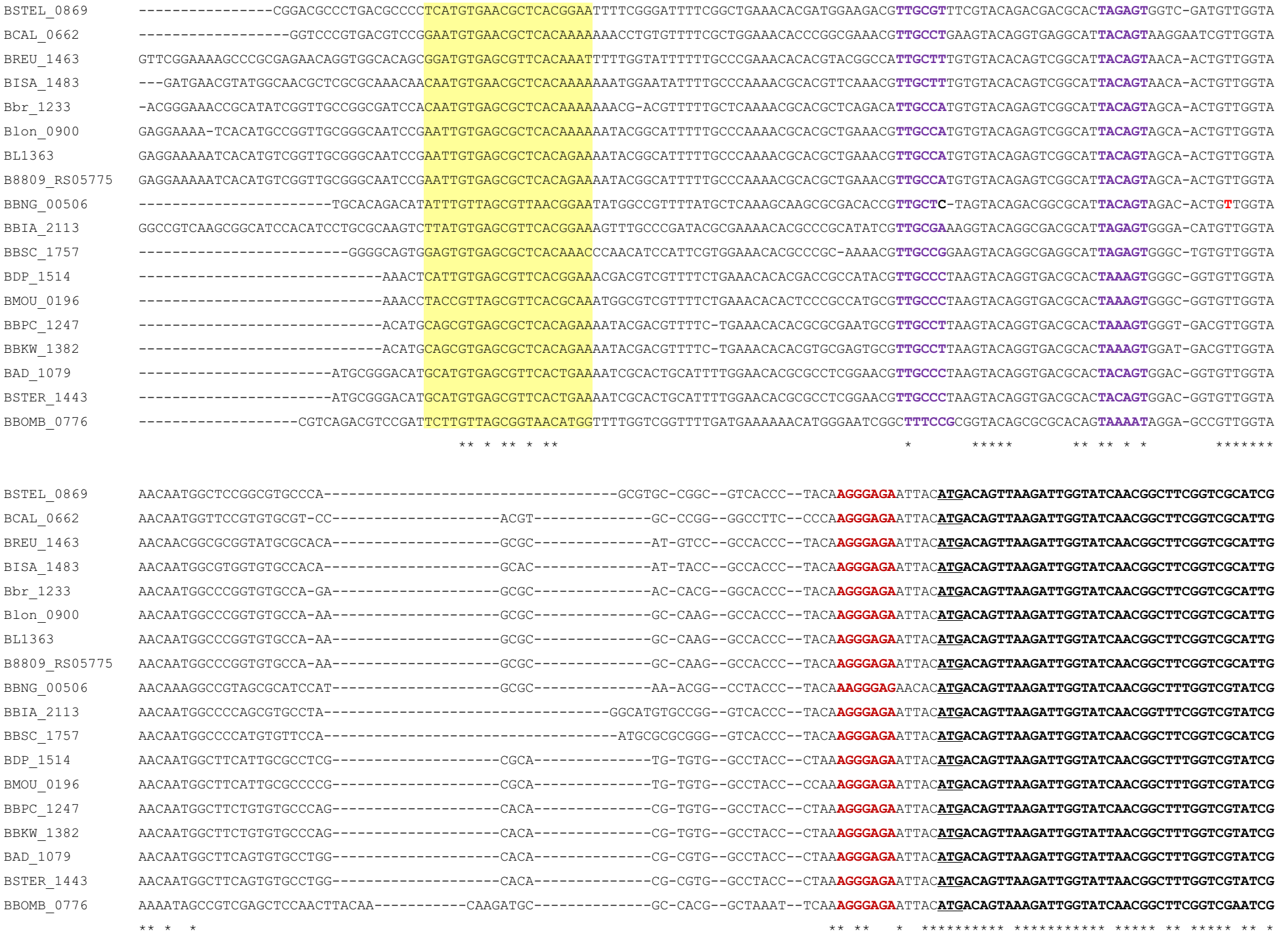
2. *araB - araD - araA* (repression)



3. *araE - araB - araD - araA* (repression)



4. *gap* (activation)



5. *eno* (activation)

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D805_0822        -TGAAGCGCACGCGGCTGTGAACGCTCACAGGAAACAGTGAGTGAAATCG-GCGATATCGTCCAACAATTCCACTATCCTTGACA-GTGTCATCACA--A-CCTGA---G-CAAAAGGAGTAGTTGTGGCAGCAA
BITS_1198        --ATGGCGTCGAAAACTGTGAACGCTCACACACGCCATGCAGCACAATCA-CAGTTATCGTCCACAAAGCCCACTATTCTTGGAA-ACGTCAACACA--A-CCTAA--TT-GCTAAGGAGTAGTTGTGGCAGCTA
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BDP_0870         -ATGTCCGCAGATGTATGTGAGCGTTCACATGATTCGTGTCGGAAAAGTT-TGCGCTACGTCCACAAAACGCACTATTCTAGGCA-TTGTCATCACA---ACCTAACGTT-TATAAGGAGTAGTTGTGGCAGTAA
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BSAE_0901        --AGGGGATTCGCCGATGTGAGCGCTAACGAAAGTTCTTCCGCG-TGTCTTCGCCCAACGTCCATCAAACCCACTATCCTTAACA-GTGTCATCACA--A-CCCAACGT--CGTAAGGAGTAGTTGTGGCAGTAA
BPSY_1734        GGATAGGCATCCGACTTGTTAGCGCTAACATAAAAATTGGCCCC-ACTCAG-CGCCATCGTCCAACAAACGCACTACTCTTATGA-GTGTCAGCACA--A-CATACATGT-CTTAAGGAGAAGTTGTGGCAGCAA
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BBOMB_0226       GGTTTCCCACGTTCTATGTTAACGCTAATATAAATTATGAT-T--TCCTT-GCACGCTCGTCCAACTTTGCAACTAAACTGGTAG-CTGTTAGTACA---AA-CA--AGC-TCGAAGGAGTAATTGTGTCTGCAA
                              **  * ** *                                  ****          **   *        *  *                     ******   ***** * *  *
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6. *pyk* (activation)

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BCAL_0786     ----------------------TTGTTGCGGCCATTGGGTTGTGAGCGCTAACAACACGCCTTGTGAAAAAC-TGGATTCACC-GGAGGGAACCTAGTACACTGCTGTAGTGGAAAACGGA-----GCCATTCCG-GTT
BREU_1094     ----------------------CC-CAATGGCCACAACAATGTGAGCGCTCACAACACACCGGCGAAAAAAT-TTGTCTTGCGTCGGTGAGCGCTAGTAGACTGAAACA-CGGCAAGTGAG-----GCTTTCCGCCTCG
BISA_1328     ----------------------CC-CAATGGGCAGAACAATGTGAGCGCTCACAACACACCGAGTAAAAAAC-TTGTCATGCGTCGGTGAGCGCTAGTAGACTATTGCA-CGGCAAGTGAG-----GCTTCAAGCCTCG
Bbr_0757      ----------------------CC-CAATCGGCGCAACAGTGTGAGCGCTCACAACACACCGGGGAATAAAC-TTGTCATGAGCCGGTCTGCGCTAGTAGACTGGGCTG-CGGCAAGTGAG-----GCAATCGCGCCTC
Blon_1745     ----------------------CC-CAGTCAACACAACAATGTGAGCGCTCACAACACACCGTGAAGAAAAC-TTGTCATGAGTCGGCTCGCGCTAGTAGACTGAGTTT-CGGCAAGTGAG-----GCGATCGCGCCTC
BBSC_1400     ----------------------CC-TTTTCCCGACATAATTGTTAGCGCTCACAACACACCCCGTTCCGTAC-TGGAGAAGT-TGGGGCCAAGCTAGTAGACTATGCCG-TGGAAGCCGGG-----CCGTCAGGTCCGG
THER5_1025    ----------------------AACGCGACATGAAGCTGATGTGAGCGTTCACAACACAGTTGCCTGAATGG-TTGGCGCATGGTGGGGGAACCGAGTAGACTAGCACA-CGGAAACAGGA-----TTCTCACCTGTTC
BDP_0904      ----------------------TCGTTCTCCCGACAAAAATGTGAGCGCTCACAACACGCCTCTGTCCGGAG-TGGAAGTGAG-CGCTTTTTGCTAGTAAACTATGCCATTGGAAACAGGG-----TCGTCAGATCCAA
BMOU_0847     ----------------------TCATTCTCCCGAAAGAAATGTGAGCGCTCACAACACACCTCGGTCCGGGG-TGGAAGTGAG-CGCTATTTGCTAGTAGACTATGCCATTGGAAACAGGG-----TCGTCAGATCCAA
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BPSY_1700     ----------------------CATTGGGCTCACATCAATTGTGAGCGCTAACAACACACCGGGCCGATTCGCTGTCTTCCGT-CGCCGATTGCTAGTAGACTCGGTTT-TGGAAGACGAG-----GGGATATCTACCC
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BCAL_0786     CC---GTC---CG-TTGCAAAGTTAGGAATAGGCAACATGCGCAAAGCCAAGATCGTCGACACCATCGGCCCCGCCAGCGAGTCCCTTGAAGGCATCACCAGCCTCGTTGAGGCCGGCAT
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BSTER_1676    AATCA--A---TA-TCAACAAGAATAGGCAGGCATTCATGCGTAAAGCCAAGATCGTAGATACCATCGGTCCCGCCACCGAGTCCCTGGAAGGCATCACCAGCCTTGTCGAAGCAGGTAT
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BSAE_0869     ACACG---------TCAAGAAGGATAGGCAGCCAT--ATGCGTAAAGCCAAGATCGTAGATACCATCGGTCCCGCCACCGAATCGCTCGAGAACCTCACCAAGCTCGTCGAAGCGGGTAT
BPSY_1700     CCCAACCA---TC-AAATAGGAAATAGGCAGGCATTCATGCGCAAAGCCAAGATTGTAGACACCATCGGACCAGCCACAGAATCGTTGGAGAACCTCACCAAGCTCGTCGAAGCGGGTAT
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7. *tkt - tal* (activation)

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BREU_0025    ---------------GATGTGAATTGTGAACGCTAACAGCACACAAACTACCAAA-ACACGCCAAATATGCACCACAAACGTCGTCTTGCGACGCTAGCATGGAAAACGCAATGTGAGGGCGTCATGCGCCCGGCACA
BISA_0603    ---------------CATGTTAATTGTGAACGCTAACAGAACACAACTTACCAAA-ACACGCCAAATATGCACCACAAACGTCTTCTTGCGACGTTAACATGGGAAACGCAATGTGAGGGCGTCGTGCGCCCGGCACA
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BDP_1145     GTGCAAATGCACGGAAATGTTCATTGTGAACGCTAACAGAACACAACTTACCAAA-ACACGCCAAAATATCACTGCTACGTCATCGCGCA-TCGCTACTATGGGATACGCAATGTGAGGGCGTCAAGCGCTCGGCACA
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BSTER_1013   TCTGAAGTTCACGCGAATGTTAATTGTGAGCGCTAACAGCACACAAACTACCAAA-ACACGCCAAAATTTCACCACAAACGTCACCTCACA-TCGCTACTATGGGAAACGCAATGTGAGGGCGTCGAGCGCTCGGCACA
BSAE_1261    --------------GCGGCTGAATTGTGAGCGTTAACATCGCGAAATGGCCGAAA-ACACGCGAACAATGCCTTGTCAGGTCGGTCTTGA-AAGTTAGGATG-TAAGAGCAATGTGAGGACGTTCATGGCCCGGCACA
BISU_1589    ---------AAA-TATGCGGATTCTGTGAACGCTCACGAACCGTAAACCGGCCGA-ACACGCCAACGCCGCGGCGTCAAGTCGTCTGCGA-AAGCTACCATGA-AGGGGCAATGTGAGGGCATATATGGCGCGGCATA
                                 ***** ** * **    *  **        * ****** **                          * **  **       ***********         **  **** *

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BCAL_0272    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAACTGGACGAACGCGCCATCAAGATGGCGAAGGTC
BREU_0025    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA---ATC-CATGACCGAATTCAAGGAGACCGAGCTCGACGAGCGTGCCATCAAGATGGCAAAGGTC
BISA_0603    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA---ATC-CATGACCGAATTCAAGGAGACCGAGCTCGACGAGCGCGCCATCAAGATGGCAAAGGTC
Bbr_1003     AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTCGACGAGCGCGCCATCAAGATGGCGAAGGCC
Blon_1096    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTCGACGAGCGCGCCATCAAGATGGCGAAGGTC
BL0716       AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTCGACGAGCGCGCCATCAAGATGGCGAAGGTC
BBNG_00949   AGCC--GAAATGCGTGGT--G--CCCGAAG-TATTGGAAGGAAA---GTA-C--ATC-CATGACCGAATTCAAGGAGACCGAGCTGGACGAGCGCGCCATCAACATGGCCAAGGTC
BBIA_1485    AGCC--ATGCG-CG--TG--GTGTCCGAAG-TATTGGAAGGAAA---ACTAC--AGA-CATGACCGAATTCAAGGAAACCGAACTGGACGAGCGCGCCATCAAGATGGCCAAGGTC
BBSC_1462    AGCC--GGACG-CG--TG--GTACCCGAAG-TATTGGAAGGAAA---ATTAC--AGA-CATGACCGAATTCAAGGAAACCGAACTGGACGAACGCGCCATCAAGATGGCCAAGGTC
BDP_1145     AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TCCTATGACCGAATTCAAGGAGACCGAGCTGGACGAGCGCGCCATCAAGATGGCCAAGGTC
BMOU_1044    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TCCTATGACCGAATTCAAGGAGACCGAGCTGGACGAGCGCGCCATCAAGATGGCCAAGGTC
BBPC_0945    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTGGACGAGCGCGCCATCAAGATGGCCAAGGTC
BBKW_1047    AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTGGACGAGCGCGCCATCAAGATGGCCAAGGTC
BAD_0829     AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTGGACGAACGCGCCATCAAGATGGCCAAGGTC
BSTER_1013   AGCC--GGATA-CG--CG--G--CCCGACC-AATTGGAAGGAAA---GTAA----TC-CATGACCGAATTCAAGGAGACCGAGCTGGACGAACGCGCCATCAAGATGGCCAAGGTC
BSAE_1261    AGCC--GAAGG-CG--TG--GCGTTCGACG-TATTGGAAGGAAA---GTAGA--ATC-TATGACCGATAACACGTGGTCTGAATTGGACGAGCGCGCCATCAAGATGGCGAAGGTG
BISU_1589    AGCC--GTATG-CG--TGATG--CTCGCAG-TATTGGAAGGAAA---GTAGATCACC-TATGACCGATTTCACTTGGTCTGACTTGGACGAGCGCGCTGTGAAGATGGCGAAGGCC
             ****        **      *    **     *  *********              ********   **      * **  * ***** ** **  * ** ***** ** *
```

8. *ldh* (activation)

Crp site **AraQ site** **Crp site** (not conserved in all strains)

```
BBOU_0652           CGTTTGCCCCGCACACAGTGTGAACGCTCTCAAATTCATC------------TCGTACCGGTTCGCCCG--CAAAGCGTTT-T--CCCCGGAGAAACGTCACGGAGAACCACTAGAGTAGAAGTGTT
D805_0597           TACTTAATACGACTTCATTGTGAACGCTCTCATATTTTTC------------CTTCCCTTGGCCCCGCGT-CAAGGCGTTT-T--CCCTGCGTAAACGTCACGGAGAGCCACTAGAGTGGAGATGTT
BSTEL_0697          TGTGTCGCGCGATGTGCGTGTGAGCGGTAACAACGTTGACGTTGCAAGGAAATCGTCAACCA--TCGTTC-GACGCGT------------------CGTCACGTAATGCGAGTACATTGGTAGCCGT
BISA_1443     TAACGTGATGAAAGTCACATATAGATTGTGAGCGCTAACAACCATTGGGA---ATACAAGGTTTTCTGAT--TTTCGT-AGCAAATTTT---TGGGAGCGCAAACGTCTAACCGGGTTTATAAAGTAAAACCGTT
Bbr_1273      TAACGTGACGAAAATCACATAATGGCTGTGAGCGCTAACAACTGCTGAAA---ACATTAGGGTTATGGCA--TCATTGGATATGCATTG---TGGCCCGCGAAACGTCTTAGCGGGTTTATAAAGTGAAACCGTT
Blon_0840     TAACGTGATAAACATCACAGTTTGTTTGGGAGCGCTAACAACCGTTGAGA---ACATTACCATACCGTTA--TCAAACAGGGTGGTGCG---CTGGTAGCAAAACGTCTTAGCGGGTTTATAGAGTGAAGACGTT
BL1308        TAACGTGATAAACATCACAGTATATTCGTGAGCGCTAACAACCGTTGAAA---ACATTACCATACGGTTA--TCAAACAGGGTGGTGTG---CTGGTAGCAAAACGTCTTAGCGGGTTTATAGAGTGAAGACGTT
B8809_RS06070 TAACGTGATAAACATCACAGTATATTCGTGAGCGCTAACAACCGTTGAAA---ACATTACCATACGGTTG--TCAAACAGGGTGGTGTG---CCGGTAGCAAAACGTCTTAGCGGGTTTATAGAGTGAAGACGTT
BBNG_00458          TGCCGCTGACGCAATGTCTGTGAGCGTTCACAACAATGTGACGCAAATCACCTTGCCTTCG---GGGCGA-TAATGACTACGGCAATCAGCGCAAACGTCATCATGTGTAGATACAGTAAGTGTGTT
BIFANG_03283        TGGTAGACACGTGACCGATGTGAGCGCTGCCAGT-----------------------------------------------------------------GTCAGGTTATGTGAGTACTGTTGAAGTGAT
BMERY_0024          ACGTGGCACGCGGTGATATGTGAGCGCTGCCAGT-----------------------------------------------------------------GTCAGGTTATGTGAGTACAGTTGAAGTGAT
THER5_1329          TTCTTGATACGACTTCATTGTGAACGCTCTCATATTTTTC------------CTTCCCTTGGCCCCGCGT-CAAGGCGTTT-T--CCCTGCGTAAACGTCACGGAGAGCCACTAGAGTGGAGATGTT
BDP_1558            GTGAGTGCCCGCCATGTTTGTGAGCGCTCACATCAAGTGTGGCGCAAATCACGTTTCAGCCA--TGTCAG-GGCGTGCTAC---ACAAGCCTGAAACGTCATGCTGTGTGGATACAGTAAAAGTGTT
BMOU_0293           TGGTGGTCCCCACGGTTTTGTGAACGTTCACACCAATTGTGATGCAAATCACGTTTCAGTCA--TGACGG-GCTGTGCTAG---ACGGGTCCGAAACGTCATACTGTGTGGATACAGTAAAAGTGTT
BBPC_1284           CGCAACGAACACAGCGTTTGTGAGCGCTCACATCTTTTGTGATGCATATCACTTTTCATTAT--TTGCAA-GTCGTGTTAT---AACGCCTTGAAACGTCATGCTGTGTGGATAAAGTAAAGATGAA
BBKW_1423           CGCAACGGGCACAGCATTTGTGAGCGCTCACATGCTTTGTGAGGCATATCACTTTTCAGTAC--CTGCAA-GTCGTGTTAC---AACGCATCAAAACGTCATGCTGTATGGATAGAGTAAAGATGAA
BSTER_1405          TTCAACGGGCGCAGTGTATGTGAGCGCTCACAAAAGCTGTGACGAAAATCACTTTTCAGTGG--TTGCAA-ATCATGCGGA---TTCACGGCGAAACGTCATGCTGTATGGATAAAGTAGGGTTGAA
                                  * ** ** *  **                                                                  ***           **   *
```

```
BBOU_0652           ACTGAAT-----GAAACCCGTCACAATCGGGTCAT-----TGC------CAAGGAGAAGTAGCAA----ATGGTGAATTCAGCTGTAAAGCCCACGAAGCTCGCTATCATCGGTGCCGGCGCTGTCG
D805_0597           ACTGAAT-----GAAGCCCGTCACAATCGGGTCAT-----TGC------CAAGGAGAAGTAGCAA----ATGGTGAATTCAGCTGTAAAGCCCACGAAGCTCGCTATCATCGGTGCCGGCGCTGTCG
BSTEL_0697          TGGTTG---AATGATGCCCGG---CAACGGGCATT-----GAC----TCT-AAGAGAGGTTCATTAAC-ATGGCTGAATTGGTCAACAAGCCCACGAAGCTCGCTGTCATCGGCGCCGGCGCCGTCG
BISA_1443           AGTTACATGG--CCTGCCATTCT---GCAGACCGC------CT-----TTGAAGAGAGGTTAATCCATCATGGCGGAAACTACCGTTAAGCCCACGAAGCTTGCAATCATCGGTGCTGGTGCTGTTG
Bbr_1273            AGTTACAAGG--CCTGCCATTCATCAGCAGACCGC------CT-----TTGAAGAGAGGTTTATCCATCATGGCGGAAACTACCGTTAAGCCCACGAAGCTTGCTGTTATTGGTGCCGGTGCCGTTG
Blon_0840           AGTTACAAGG--CCTGCCATTCATCAGCAGACCGC------CT-----TTGAAGAGAGGTTCATCCATCATGGCGGAAACTACCGTTAAGCCCACGAAGCTTGCTGTTATTGGTGCCGGTGCCGTTG
BL1308              AGTTACAAGG--CCTGCCATTCATCAGCAGACCGC------CT-----TTGAAGAGAGGTTCATCCATCATGGCGGAAACTACCGTTAAGCCCACGAAGCTTGCTGTTATTGGTGCCGGTGCCGTTG
B8809_RS06070       AGTTACAAGG--CCTGCCATTCATCAGCAGACCGC------CT-----TTGAAGAGAGGTTCATCCATCATGGCGGAAACTACCGTTAAGCCCACGAAGCTTGCTGTTATTGGTGCCGGTGCCGTTG
BBNG_00458          GTCAAA-AT---GAACCCCGCCAAACACGGGGCAC-----TGT----GCT-AAGAGAGGTCTAGCAAACATGGTGGATTCACCCATTAAGCCCACAAAGCTCGCCATCGTCGGTGCCGGCGCAGTCG
BIFANG_03283        GTTGTGAGAAATGATGCGCCC---AACCGGCGCAT-----CTC--TC--T-AAGAGAGGTATAAAC---ATGGCAGAATCGCTTATCAAGCCCACGAAGCTTGCTGTTATCGGTGCCGGCGCAGTCG
BMERY_0024          GTTTTGAGGAACGATGCGCCC---AAACGGCGCAT-----CTC--TC--T-AAGAGAGGTATAGCC---ATGGCAGAATCGCTTATCAAGCCCACGAAGCTTGCTGTTATCGGTGCCGGCGCAGTCG
THER5_1329          ACTGAAT-----GAAGCCCGTCACAATCGGGTCAT-----TGC------CAAGGAGAAGTAGCAA----ATGGTGAATTCAGCTGTAAAGCCCACGAAGCTCGCTATCATCGGTGCCGGCGCTGTCG
BDP_1558            ATTGAAGAT---GAAGCCCGTCACCAACGGGACAT-----TCG--TTGCCAAAGAGAGGTAAGCAC---ATGGTGGATTCACCAATCAAGCCCACAAAGCTCGCTATCATCGGTGCCGGCGCAGTCG
BMOU_0293           ATTGAAGAT---GAAGCCCGTCACCAACGGGACAT-----TCGT-TTGCCAAAGAGAGGTAAGCAC---ATGGTGGATTCACCAATCAAGCCCACAAAGCTCGCTATCATCGGTGCCGGCGCAGTCG
BBPC_1284           ATTCTAAGAG--AAAACCTGCTACCAGCGGGACAT----TCTT-TCTTAT-AAGAGAGGTAAGCAC---ATGGTGGATTCACCAATCAAGCCCACAAAGCTCGCTATCATCGGTGCCGGTGCAGTCG
BBKW_1423           ATCCTAAGGA--GAAACCTGCTACCAGCGGGACAT----TCTTTTCTTGT-AAGAGAGGTAAGCAC---ATGGTGGATTCACCAATCAAGCCCACAAAGCTCGCTATCATCGGTGCCGGTGCAGTCG
BSTER_1405          ATCGAAAGAA--AATACCCTGCCACAACGCGGGACGTTCTTCTT-GCT-CAAAGAGAGGTAAAGCAC--ATGGTGGATTCACCAATCAAGCCCACAAAGCTCGCTATCATCGGTGCCGGCGCAGTCG
                              *         *                     * **** **         ****   *          ******** ***** **  *  * ** ** ** ** ** *
```

9. *galM* (repression)

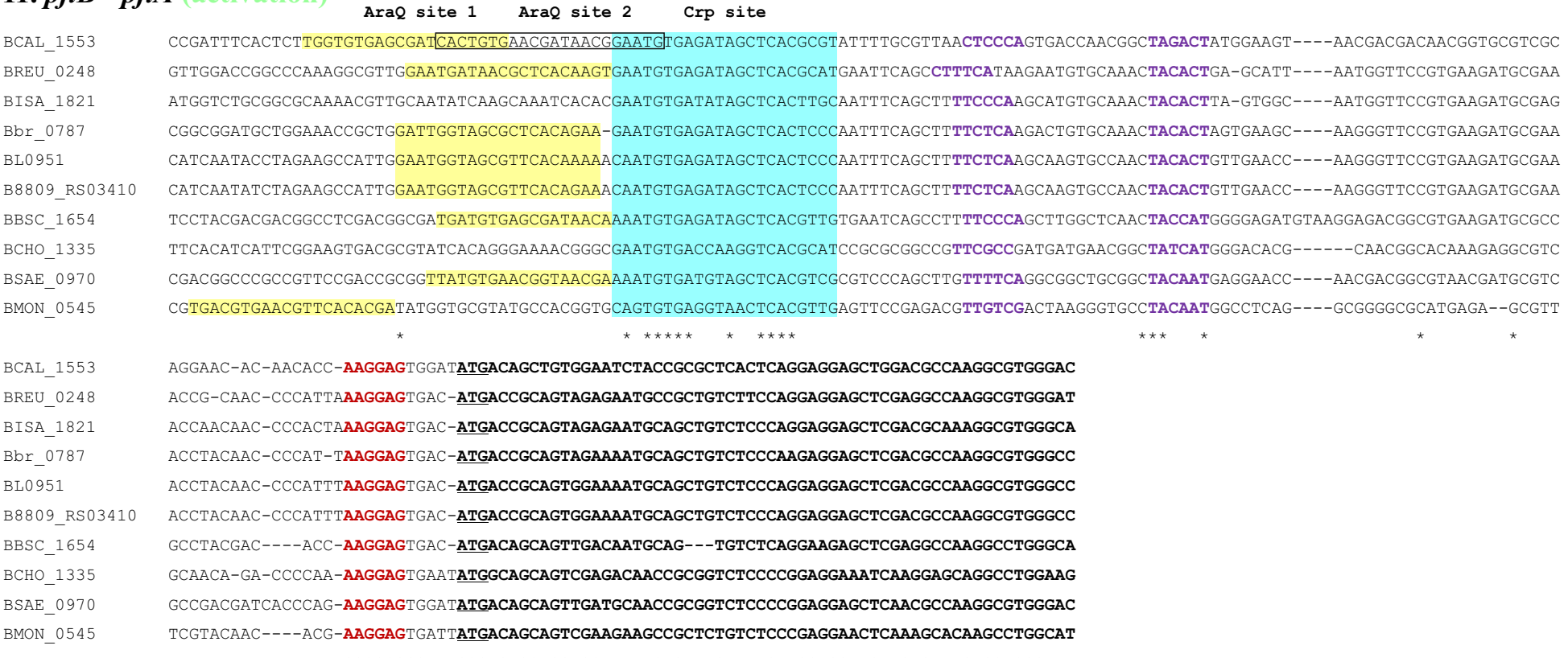
```
BCAL_0666       TTGCCTACAAACAGCTCCGCTGTTTGCTTCACGG----------CAACGTCCCATCAGAGGGGA-------------CCAAGGGTGCGGCAGTCCTCGCACTGAGGTGAGGTATCATTGTGAGCGATAACAATAC
Bbr_1237        GTTATGAAGTAGCCCAGAAGTAATCCAGAAATAGCCCTATGAATTGGCTCTCCTCATTGAGGAGAGCCAATTCTGTTATCTATATA-CGCCGCGTCCCAACGCTGATGCGGTACGATTGCGAGCGGTAACAATAC
Blon_0896       GCTACGAAGTAGCCCAGAAGTAGTTCCGTTACGT----------TGGCTCCCCGCCAGAGGGGAGCCAATTATTTATCCTTATGTGCCGCCGCGTCTTGGGACTTGTGCGATACGATTGTGAGCGGTAACAATCT
BL1359          GCTACGAAGTAGTCCAGAAGTAGTTCTGTTACGC----------TGGCTCCCCTCCAGAGGGGAGCCAATTTTTTATCCTTATGTGCCGCCGCGTCTTGGGACTTATGCGATACGATTGTGAGCGATAACAATTT
B8809_RS05795   GCTACGAAGTAGTCCAGAAGTAGTTCTGTTACGC----------TGGCTCCCCTCCAGAGGGGAGCCAATTTTTTATCCTTATGTGCCGCCGCGTCTTGGGACTTATGCGATACGATTGTGAGCGATAACAATTT
                      *   *   *     *  *      *               *   **       **                    *   ** *             ** * **  **** ***** *******

BCAL_0666       G-TCTCATCATCCACGAAGGAGTGTGCTCAAGACCATGGTTCTCAAACCCCGTACCGGCAACCAGTATTCGATTCGCAAGGGCGAGTGGAGCGCCGTCGTCACCGAGCTCGGCGCCAGCCTGCGCGAGCTCAAGT
Bbr_1237        GCTTTCAC-------AAAGGAGTGTGC-----ACTATGGCTTTGAAGCCTCGCACCGGTAACCAATACGCCATCTCATCCGGCGAATGGAGTGCCGTTGTCACTGAGCTGGGCGCCAGCTTGCGCGAACTGAAAT
Blon_0896       G-TTTCAC-------CAAGGAGTGTGC-----ACTATGGCTTTGAAGCCTCGCACTGGTAACCAATATGTCATCTCGGCCGGCGAATGGGGTGCCGTCGTCACCGAAATGGGTGCCAGCCTGCGCGAGCTGAAGT
BL1359          G-TTCCAC-------AAAGGAGTGTGC-----ACTATGGCTTTGAAGCCTCGCACTGGTAACCAATATGTCATCTCGTCCGGCGAATGGAGTGCCGTCGTCACCGAACTGGGTGCCAGCCTGCGCGAGCTGAAGT
B8809_RS05795   G-TTCCAC-------AAAGGAGTGTGC-----ACTATGGCTTTGAAGCCTCGCACTGGTAACCAATATGTCATCTCGTCCGGCGAATGGAGTGCCGTCGTCACCGAACTGGGTGCCAGCCTGCGCGAGCTGAAGT
                * *  **         ***********     ** **** * * ** ** ** ** ** ***** **    **       ***** *** * ***** ***** **  * ** ****** ******* ** ** *
```

10. *pta - ackA* (repression)

```
BSTEL_0445      CTTTCCGCGTTTTT----------------------CCCGGCAACACGGACGTGAGCGATAACAAGC---GCCGCTACAATAAGGGGTGGTACATCCGCACTGAATCATCAAAGGAGACTGACAC-CAGTGACC
BISA_1342       TCTTCCCGCAATTA----------------------CTCCGCGTCTTAAGCGTGAACGGTAACAATG---GTCAGTACAATGATGTGTGGTCCTAATTATGTTGATCATCAAAGGAGACAGAC-CAAAGTGACC
Bbr_0772        TCGATGGCAATGCTGAGCCTTGTCTTCGGGCATCCCGCCGCGACACAACACCGTGAACGATAACAACG---ACCACTACAATGAGATATGGTCCCACATATGTTGCACATCAAAGGAGACAGACACA--GTGACC
BL0968          AGCGTCGCAAAGGGGACGC--TTC---------CGATTGGCGCGACACCGGCGTGAGCGATAACAGTAATCGCCACTACAATGAGGTGTGGTCCCTATCGTGTTGATCATCAAAGGAGACAAAAACATCGTGACC
B8809_RS03270   AGCGTCGCCAAGGGGACGCTCTTC---------CGATTGGCGCGACACCGGCGTGAGCGATAACAGTAATCGCCACTACAATGAGGTGTGGTCCCTATCGTGTTGATTATCAAAGGAGACAAAAACATCGTGACC
                                              *   *     ***** ** *****  *     *  ****** *    **** *        *     ************  *  *   ******
```

11. *pflB - pflA* (activation)



12. BL1113 (repression)



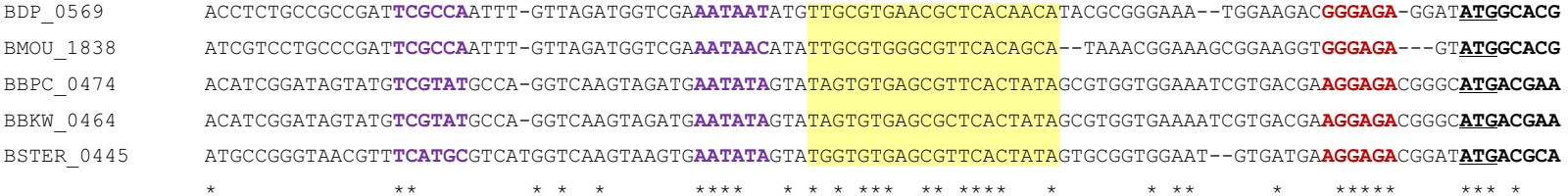
13. *malE* (activation), MalR represses the *malE* gene by binding to tandem sites (forms a tetramer)



14. *malQ1* (activation)



15. *maa* (repression)



16. *glgB* - Blon_1762 - Blon_1763 (repression)

```
BREU_1083       CGTGGATAAACGACCATATCGCCGACTTTATAAGACATGAATCCTCCGAGAACTGACGGCTCACACACAAAAACTCGAATAATTGTGCCATCTGGCATGGACTG-CGACGCTGATAGCGTTCACAATATGTACGA
BISA_1317       CGTGGATAGACGACCATATCGCCGACTTGATAAGACATGAATCCTCCGAGAACTGACGGCTCACACACAAAAACTCGAATAATTGTGCCACTTGGCATGGACCGGCCCCAATGAGAACGCTCACATTACCTAAGG
Bbr_0746        CGTGGGTAGACGACCATATCGCCGACTTGATAAGACATGTATCCTCCGAGAACTGACGGATTACTCACAAAAACTCGAATAATTGTGCCATATGGTCTGGACTG-GGACAATGAGAGCGCTCACAATCAAGCGAC
Blon_1761       CGCGGATAGACGACCATATCGCCGACTTTGTAAGACATGTACCCTCCGAGAACTGACGGCTTACACACAAAAACTCGAATAATTATGCCATGCGGTCTGGACCG-CCCCTATGAGAGCGCTCACAACCACGAAGA
B8809_RS03065   CGCGGATAGACGACCATATCGCCGACTTTGTAAGACATGTACCCTCCGAGAACTGACGGCTTACACACGAAAACTCGAATAATTATGCCATGCGGTCTGGACCA-CCCCTATGAGAGCGCTCACAACCACGGAAA
                ** ** ** ******************  ********* * ***************** * ** *** *************** *****   **  *****      *  *** * ** *****

BREU_1083       CACGCGAGCAACAGCAGAATTTCGCCGCATTTGCCGCGTTAATACGGCGTTTTACGCGCTGACACACGTAGACTTTGGGGCATGGATACTGAAACCAAGATCAACGAAGATACCATCACCGTGCCTGTCGCCGAA
BISA_1317       CAGGACAAATTTGACAGAAATTCGATATATTTACCGCGTTAATACGGCGTTTTCAACTTCTACACACGTAGACTTTGGGGCATGGATACTGAAAAGCAGATCAAAGAAGATACCATCACCGTGCCTGTTGCTCAG
Bbr_0746        AACACTCTAAGCGGCATAAATTCGCCATTTTCGACGCGCCAATGTAGCGTTTCCGACACCAACGCACGTAGACTTTGGGGCATGGCTAATGAAACGAAGATCAAGGAAGATACCGTCACCGTGCCTGTTGCCCAA
Blon_1761       CACACCGAAAAGGGCAAGAATTCGCCATTTTCGACGCGCCAATGTAGCGTTTTCGACTCCAACGCACGTAAACTTTGGGTCATGGCTAAAGAAACGAAGATCAAGGAAGATACCGTCACCGTGCCTGTCGCCCAA
B8809_RS03065   CACAACGAAAAGGGCAAGAATTCGCCATTTTCAACGCGCCAATGTAGCGTTTTCGACTTCAACGCACGTAGACTTTGGGACATGGCTAAAGAAACGAAGATCAAGGAAGATACCGTCACCGTGCCTGTCGCCCAA
                 *           **  * ****     **   ****  ***   ******    *    ** ****** ******** ***** **  ****   ******* ********* ************* **  *

BREU_1084       TTCTGCTGTTGCTCGCGTGTCGTACATATTGTGAACGCTATCAGCGTCGC-AGTCCATGCCAGATGGCACAATTATTCGAGTTTTTGTGTGTGAGCCGTCAGTTCTCGGAGGATTCATGTCTTATAAAGTCGGCG
BISA_1318       TTCTGTCAAATTTGTCCTGCCTTAGGTAATGTGAGCGTTCTCATTGGGGCCGGTCCATGCCAAGTGGCACAATTATTCGAGTTTTTGTGTGTGAGCCGTCAGTTCTCGGAGGATTCATGTCTTATCAAGTCGGCG
Blon_1760       TCTTGCCCTTTTCGGTGTGTCTTCGTGGTTGTGAGCGCTCTCATAGGGGC-GGTCCAGACCGCATGGCATAATTATTCGAGTTTTTGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
BL0998          TCTTGCCCTTTTCGTTGTGTTTCCGTGGTTGTGAGCGCTCTCATAGGGGT-GGTCCAGACCGCATGGCATAATCATTCGAGTTTTCGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
B8809_RS03070   TCTTGCCCTTTTCGTTGTGTTTCCGTGGTTGTGAGCGCTCTCATAGGGGT-GGTCCAGACCGCATGGCATAATTATTCGAGTTTTCGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
                *  **           **         ***** ** * ***  *  *   *****  **   ***** *** *********** ****** ****************** * *********  *********

BISA_1131       GGATGGATATGG-----------ATGGTGGGAGCCTTCTAGGGTGTGTGCGAGCGGCTGTGACTTTGCTCACCTGTGAACGTTCACATGGTCGCGGTATGTAGAAAAGCGGATTTTTGGGTTTGGAACCGTGAGA
Bbr_1723        ATTGCAGACGCAGGCAAGGCCGCTATGACTGCAATCGTATGCGGGCCATCTGCATGGTGTGACTTTGCTCACGTGTGAGCGTTCACACCGAGGTATTGGCCGAAAAATGGAGACAT-CGGGAATCTGGTCGCGCAA
Blon_2288       ATTGCCATTGTTCGCAAGCCAATACGACGGCCGGGTGCATGCGTGGGTTCGGCGAATGCGGAATTTTCGAAGTTGTGAACGTTAACACGGGCTATGTGGGTGAAAGTGGGAATATCGCGGGTAAAAAACGGCGCA
B8809_RS08755   ATCGCCATTGTTCGCAAGCCAATATGACGGCCGGGTGCATGCGTGGGGTCGGCGAATGCGGAATTTCCGAAGTTGTGAACGTTAACATGGGCTATGTGGGTGAAAATAGGAATAACGCGGGCATATCGCGCCAAA
                                                 * * *   *          ** *** *  *  ***** **** ***  *      *      **      *      **       **    *

BISA_1131       AATGCGGTAACGTTTTGCCCATGATGCTTGCACTACAGACCACGACGCCT
Bbr_1723        ATCGGGGTAACGTAGTTCCCATGATGATTGCTTTGCAAGCTGCAACGCCG
Blon_2288       ACCGAGGTAACGTAGTGTCCATGATGATTGCATTGAAAGCTGCAACGCCG
B8809_RS08755   ATCGAGGTAACGTAGTGCCCATGATGATTGCGTTGAAAGCTGCAACGCCG
                *  * ********  *  ******** ****  *  *  *  * *****
```

17. *carD - ispF* (repression?)

```
BREU_1084       TTCTGCTGTTGCTCGCGTGTCGTACATATTGTGAACGCTATCAGCGTCGC-AGTCCATGCCAGATGGCACAATTATTCGAGTTTTTGTGTGTGAGCCGTCAGTTCTCGGAGGATTCATGTCTTATAAAGTCGGCG
BISA_1318       TTCTGTCAAATTTGTCCTGCCTTAGGTAATGTGAGCGTTCTCATTGGGGCCGGTCCATGCCAAGTGGCACAATTATTCGAGTTTTTGTGTGTGAGCCGTCAGTTCTCGGAGGATTCATGTCTTATCAAGTCGGCG
Blon_1760       TCTTGCCCTTTTCGGTGTGTCTTCGTGGTTGTGAGCGCTCTCATAGGGGC-GGTCCAGACCGCATGGCATAATTATTCGAGTTTTTGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
BL0998          TCTTGCCCTTTTCGTTGTGTTTCCGTGGTTGTGAGCGCTCTCATAGGGGT-GGTCCAGACCGCATGGCATAATCATTCGAGTTTTCGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
B8809_RS03070   TCTTGCCCTTTTCGTTGTGTTTCCGTGGTTGTGAGCGCTCTCATAGGGGT-GGTCCAGACCGCATGGCATAATTATTCGAGTTTTCGTGTGTAAGCCGTCAGTTCTCGGAGGGTACATGTCTTACAAAGTCGGCG
                *  **           **         ***** ** * ***  *  *   *****  **   ***** *** *********** ****** ****************** * *********  *********
```

18. *birA* (repression)

```
BISA_1131       GGATGGATATGG-----------ATGGTGGGAGCCTTCTAGGGTGTGTGCGAGCGGCTGTGACTTTGCTCACCTGTGAACGTTCACATGGTCGCGGTATGTAGAAAAGCGGATTTTTGGGTTTGGAACCGTGAGA
Bbr_1723        ATTGCAGACGCAGGCAAGGCCGCTATGACTGCAATCGTATGCGGGCCATCTGCATGGTGTGACTTTGCTCACGTGTGAGCGTTCACACCGAGGTATTGGCCGAAAAATGGAGACAT-CGGGAATCTGGTCGCGCAA
Blon_2288       ATTGCCATTGTTCGCAAGCCAATACGACGGCCGGGTGCATGCGTGGGTTCGGCGAATGCGGAATTTTCGAAGTTGTGAACGTTAACACGGGCTATGTGGGTGAAAGTGGGAATATCGCGGGTAAAAAACGGCGCA
B8809_RS08755   ATCGCCATTGTTCGCAAGCCAATATGACGGCCGGGTGCATGCGTGGGGTCGGCGAATGCGGAATTTCCGAAGTTGTGAACGTTAACATGGGCTATGTGGGTGAAAATAGGAATAACGCGGGCATATCGCGCCAAA
                                                 * * *   *          ** *** *  *  ***** **** ***  *      *      **      *      **       **    *

BISA_1131       AATGCGGTAACGTTTTGCCCATGATGCTTGCACTACAGACCACGACGCCT
Bbr_1723        ATCGGGGTAACGTAGTTCCCATGATGATTGCTTTGCAAGCTGCAACGCCG
Blon_2288       ACCGAGGTAACGTAGTGTCCATGATGATTGCATTGAAAGCTGCAACGCCG
B8809_RS08755   ATCGAGGTAACGTAGTGCCCATGATGATTGCGTTGAAAGCTGCAACGCCG
                *  * ********  *  ******** ****  *  *  *  * *****
```

19. *sixA* (repression)

```
BISA_0671       TGGATGCATGCCGATGAATATGTGAACGCTCACAACGGGCTATACTGGAATGACT--------TTGTGTTGTTCGTTGTGAGCTGTGCAAAACCTTGAAG-AGAGGGAGCCTCGAAGTGGGCATCAAGCTGAACA
BREU_0084       CGAGGCTGCCTGAACGATTATGTGAACGCTCACATCAAGCGTATAAT--AGTTTT--------TCTCAATGTTTGTTGTGAGCTACGCATATCC----GG-AAGGGGAGCATAACAATGGGCATCAAGCTGAGCA
Blon_1456       TAACCGCCAAACGATGAGTTTGTGAGCGCTCACACACCTCTATACTGGAAGCAAC--------GCCACACCGCCACACCGGGCAGG-------C-GGTTCGTGAAGGGAGCCACGGATGGGCATCAAGCTGAGCA
B8809_RS04185   TAACCGCCAAACGATGAGTTTGTGAACGCTCACACACCTCTATACTGGAAGCAATACCACACCGCCACACCGCCACACCGGGCAGA-------C-GGTTCGTGAAGGGAGCCACGGATGGGCATCAAGCTGAGTA
                          ** * ***** ********     *     *   *                              * **          *           **          ***************  *
```

20. *glk* (activation)

```
BISA_1968       TAGAACGATTGACGCGATGGAGCTGCGAATGCCAACGTTTGCGCTAACAATCCTTGTTTTGATTGGTTATGGCATGACAACGATTGCTGTGCAAAATATGTTCCGCGGTGAACAAGTTATGTACCTAGTGGTAAT
BREU_2338       -GCCGTCTTGCGAGCGGTTGGGAAACGAATGCTAACGTTTGCGCTAACAATCGTTGTTTTGCAAGGAAGCCGCTGATGGTGATGTATGAGACAGTATATGCCGCCAATCGTGCAGCTTATGTACCTGATGGTAGT
B8809_RS07595   TAGTCTGAATGACAACGTTTGCTATTGAATGACAACGTTAGCGTTAACAGTGCTTATAAATGGTGAAAAACGTGTGCAGGGTCACATTGGCAGAACGTGCGCGAGATATGACAAATCATGAAAAATACGCTATGG
BL1691          TAGTCTGAATGACAACGTTTGCTATTGAATGACAACGTTAGCGTTAACAGTGCTTATAAATGGTGAAAAACGTGTGCAGGGTCACATTGGCAGAACGTGCGCGAGATATGACAAATCATGAAAAATACGCTATGG
                          *        *****  ****** *** ***** *  ** *       *      *                                    *   *        *  *


BISA_1968       TAAGTCATCACGTTTCGTTATCATCTCAAGTATCTCAACTGATATCTCATAC-TCAAGGAGCGAGTCATGACCAC
BREU_2338       TGGGTCACCCCTCTTCGTTACTATTTCA-GTAGTTCCATAGGAATCCCATAC-TCAAGGAGCGAGTCATGACTAC
B8809_RS07595   GAGGTCATGGCAACTCGTTACTATTTTCGCTGTCTCGTACGCCACACAAGCCTTCAAGGAGTAAGCCATGACCAC
BL1691          GAGGTCATGGCAACTCGTTACTATTTTCGCTGTCTCGTACGTCACACAAGCCTTCAAGGAGTAAGCCATGACCAC
                   ****   *   ******  ** *    *   **    *  *    *  * ********  ** ****** **
```

21. Fructosides utilization operon (activation)

```
                                                                                                                AraQ site          BfrR site 1          BfrR site 2
BIFANG_03432    AATTGAGGGCGGAAATGGCGGG-GCGGTGCCGATGCCTACGTTTGCATGATGTGGCGGAAATGACGTTATGAGAGCGCTAACAGTTGGAATAATCGTTTAACGTTTGACATTAAACGATTAACGATTTACGGTGTT
BMERY_1312      AATTGAGGGCGGGAATGGCGGGGGGTGGTGCCGATGCCTACGTTTGCATGATGTGGCGGAAATGACGTTATGAGAGCGCTAACAGTTGGAATAATCGTTTAACGTTTGACATTAAACGATTAACGATTTACGGTGTT
BAD_1330        GGTGTTCTGCAAGAACGGCAGT-ATGGAGCCGAAGTTTACGTTTGC--GACGCTGGGGGGACTGGTTGATGAGAGCGCTAACTATTGAGATAAACGATTAACGTTTGACATTAAACGATTAACGATTTATAGTGTT
BSTER_1333      GGTGTTCTGCAAGAACGGCAGT-ATGGAGCCGAAGTTTACGTTTGCGACGCTGGGGGGACTGGT--CGATGAGAGCGTTAACTATTGAGATAAACGATTAACGTTTGACATTAAACGATTAACGATTTATAGTGTT
cons              *     **   ** *** *    ** ***** *  *********        * **          ********* ****  ***  **** ** ********************************  *****

BIFANG_03432    AACCACAGCAAGAGCACAACGCACGTGATCTTGAGGTTCGCGTCGGGGCGTACCCGAT------GCGGGAGGAATATTAAGGAAGAAGGAAT---ATCATGGCACGAAGGAGTGTACGCCTGATCGCAGCC
BMERY_1312      AACCACAACAAGAGCACAACGCACGTGATCTTGAGGTTCGCGTCGGGGCGTACCCGAT------GCGGGAGGAATATTAAGGAAGAAGGAAC---ATCATGGCACGAAGGAGTGTACGCCTGATCGCAGCT
BAD_1330        AATCAC---------CGCAAAGCAAGCGGCTGATGAGGTCGTACCGGTGCGTCTTACATCGGTACGAGGAGGAAACATCAAGGAAGAAGGAGCCTAATCATGGCACGAAGAAGTGTTCGCCTGTTGGCATCA
BSTER_1333      AACCAC---------CGCAAAGCAAGCGGCTGATGAGGTCGTACCGGTGCGTCTTACATCGGTACGAGGAGGAAACATCAAGGAAGAAGGAGCCTAATCATGGCACGAAGAAGTGTTCGCCTGTTGGCATCA
cons            ** ***        * *** *** * *        * ***   *** ****     **      * **  * ** ** ************     ************** ***** ****** * *** *
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