Table S1 Analysis of sequence similarity and upstream and downstream genes

The name of 5’ sequence

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Species | Represent the strain | Identities | Upstream genetic name | Downstream genetic name |
| *B. amyloliguefaciens* | *R8-25* | 100 | *ydaH* | *ydaG* |
| *B. tequilensis* | EA-*CB0015* | 84.06 | *ydaH* | *ydaG* |
| *B. subtilis* | *168* | 81.52 | *ydaH* | *ydaG* |
|  | *At3* | 81.52 | *ydaH* | *ydaG* |
|  | *NRS6167* | 81.52 | *ydaH* | *ydaG* |
|  | *TU-B-10* | 81.16 | *ydaH* | *ydaG* |
| *B. atrophaeus* | *CNY01* | 80.80 | *ydaH* | *ydaG* |
|  | *PENSV20* | 81.16 | *ydaH* | *ydaG* |
| *B. inaquosorum* | *KCTC 13429* | 81.88 | *ydaH* | *ydaG* |
|  | *DE111* | 81.52 | *ydaH* | *ydaG* |
| *B. cabrialesii* | *TE3* | 81.16 | *ydaH* | *ydaG* |
| *B. spizizenii* | *DN* | 81.16 | *ydaH* | *ydaG* |
| *B. rugosus* | *A78.1* | 81.16 | *ydaH* | *ydaG* |
| *B. glycinifermentans* | *SRCM103574* | 61.84 | *ydaH* | *ydaG* |
|  | *MGMM1* | 63.73 | *ydaH* | *ydaG* |
| *B. paralicheniformis*. | *NCTC8721* | 64.35 | *ydaH* | *ydaG* |
|  | *CBMAI 1303* | 64.75 | *ydaH* | *ydaG* |
|  | *TXO7B-1SG6* | 62.82 | *ydaH* | *ydaG* |
| *B. haynesii* | *P19* | 65.02 | *ydaH* | *ydaG* |
| *B. licheniformis* | *P8\_B2* | 65.45 | *ydaH* | *ydaG* |
|  | *SCDB 34* | 64.62 | *ydaH* | *ydaG* |
|  | *NWMCC0046* | 63.64 | *ydaH* | *ydaG* |
| *B. safensis* . | PgKB20 | 65.83 | *ydaH* | *ydaG* |
|  | KCTC 12796BP | 65.23 | *ydaH* | *ydaG* |
|  | PLA 1006 | 65.59 | *ydaH* | *ydaG* |
|  | U17-1 | 65.23 | *ydaH* | *ydaG* |
|  | FO-36b | 65.11 | *ydaH* | *ydaG* |
|  | BRM1 | 64.52 | *ydaH* | *ydaG* |
|  | LG01 | 64.52 | *ydaH* | *ydaG* |
|  | AHB11 | 64.87 | *ydaH* | *ydaG* |
|  | IDN1 | 64.18 | *ydaH* | *ydaG* |
| *B. pumilus* | SF-4 | 65.47 | *ydaH* | *ydaG* |
|  | NCTC10337 | 65.23 | *ydaH* | *ydaG* |
|  | ZB201701 | 66.55 | *ydaH* | *ydaG* |
|  | 3-19 | 66.55 | *ydaH* | *ydaG* |
|  | TUAT1 | 64.39 | *ydaH* | *ydaG* |
|  | C4 | 63.08 | *ydaH* | *ydaG* |
|  | MTCC B6033 | 63.08 | *ydaH* | *ydaG* |
| *B. cellulasensis* | NJ-V | 64.62 | *ydaH* | *ydaG* |
| *B. altitudinis* Cr2-1. | HQ-51-Ba | 64.62 | *ydaH* | *ydaG* |
|  | SCU11 | 63.08 | *ydaH* | *ydaG* |
|  | CHB19 | 64.64 | *ydaH* | *ydaG* |
|  | ZAP62 | 63.44 | *ydaH* | *ydaG* |
| *B. aerophilus* . | 232 | 64.03 | *ydaH* | *ydaG* |
| *B. zhangzhouensis* | *XN149* | 65.23 | *ydaH* | *ydaG* |
| *B. xiamenensis* | *VV3* | 63.44 | *ydaH* | *ydaG* |

Table S2 sRNA Bvs091 target prediction

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| [Target](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=id1&toolName=IntaRNA&jobID=9884241) | [Start](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start1&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start1&toolName=IntaRNA&jobID=9884241)  [(T)](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start1&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start1&toolName=IntaRNA&jobID=9884241) | [End](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end1&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end1&toolName=IntaRNA&jobID=9884241)  [(T)](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end1&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end1&toolName=IntaRNA&jobID=9884241) | [Start](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start2&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start2&toolName=IntaRNA&jobID=9884241)  [(Q)](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start2&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=start2&toolName=IntaRNA&jobID=9884241) | [End](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end2&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end2&toolName=IntaRNA&jobID=9884241)  [(Q)](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end2&toolName=IntaRNA&jobID=9884241" \o "http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=end2&toolName=IntaRNA&jobID=9884241) | [Energy](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=E&toolName=IntaRNA&jobID=2053476) | [gene](http://rna.informatik.uni-freiburg.de/IntaRNA/Result.jsp?t_top100_row=0&t_top100_rows=100&t_top100_srt=geneName&toolName=IntaRNA&jobID=9884241) |
| GKO36\_RS20010 | -51 | -28 | 178 | 203 | -26.1 | UDP-glucose--hexose-1-phosphate uridylyltransferase |
| GKO36\_RS16230 | -71 | -28 | 120 | 153 | -21.93 | nicotinate phosphoribosyltransferase |
| GKO36\_RS06350 | 7 | 41 | 182 | 199 | -20.18 | Protein Homology. |
| GKO36\_RS16695 | -42 | -10 | 22 | 53 | -19.54 | ketohydroxyglutarate aldolase |
| GKO36\_RS16205 | -73 | -19 | 27 | 47 | -19.36 | nitrite reductase (NAD(P)H) small subunit |
| GKO36\_RS20450 | -69 | -50 | 121 | 137 | -18.1 | sigma-54-dependent Fis family transcriptional regulator |
| GKO36\_RS10220 | -67 | -38 | 139 | 196 | -18.06 | aspartate-semialdehyde dehydrogenase |
| GKO36\_RS17755 | 8 | 46 | 56 | 82 | -18.01 | phosphopentomutase |
| GKO36\_RS01695 | 44 | 65 | 192 | 203 | -17.64 | Protein Homology. |
| GKO36\_RS12465 | 26 | 55 | 181 | 200 | -17.2 | uroporphyrinogen-III synthase |
| GKO36\_RS08535 | -1 | 49 | 54 | 149 | -17.1 | Protein Homology. |
| GKO36\_RS01840 | 27 | 70 | 120 | 134 | -16.92 | Protein Homology. |
| GKO36\_RS09825 | 47 | 58 | 171 | 203 | -16.89 | Protein Homology. |
| GKO36\_RS19900 | -8 | 5 | 182 | 203 | -16.87 | Protein Homology. |
| GKO36\_RS08560 | -73 | -46 | 45 | 136 | -16.73 | YqzL family protein |
| GKO36\_RS06165 | -12 | 14 | 61 | 88 | -16.69 | GeneMarkS+. |
| GKO36\_RS08075 | -25 | 57 | 67 | 88 | -16.6 | ABC transporter permease |
| GKO36\_RS12930 | -62 | -33 | 52 | 138 | -16.6 | 30S ribosomal protein S1 |
| GKO36\_RS07880 | 63 | 73 | 179 | 203 | -16.32 | membrane protein |
| GKO36\_RS13465 | -20 | 51 | 183 | 199 | -16.2 | helicase |
| GKO36\_RS16925 | -10 | 17 | 70 | 121 | -16.19 | protein liaI |
| GKO36\_RS16085 | 48 | 61 | 5 | 77 | -16.19 | antiholin |
| GKO36\_RS20505 | -21 | 43 | 114 | 138 | -16.15 | amino acid transporter |
| GKO36\_RS04040 | -70 | -47 | 120 | 130 | -16.02 | Protein Homology. |
| GKO36\_RS16445 | -29 | -6 | 121 | 131 | -15.99 | sensor histidine kinase |
| GKO36\_RS12175 | 2 | 68 | 183 | 199 | -15.9 | Protein Homology. |
| GKO36\_RS16330 | -14 | 20 | 186 | 204 | -15.83 | NAD-dependent malic enzyme |
| GKO36\_RS04780 | -55 | -43 | 183 | 204 | -15.82 | Protein Homology. |
| GKO36\_RS17420 | 28 | 72 | 185 | 203 | -15.73 | Protein Homology. |
| GKO36\_RS16150 | -58 | -28 | 185 | 210 | -15.71 | DUF3907 domain-containing protein |
| GKO36\_RS14735 | -3 | 64 | 187 | 205 | -15.59 | XkdX family protein |
| GKO36\_RS06630 | -14 | 9 | 184 | 200 | -15.58 | HNH endonuclease |
| GKO36\_RS06540 | 43 | 72 | 122 | 130 | -15.48 | DNA-binding protein |
| GKO36\_RS17605 | 17 | 32 | 183 | 202 | -15.48 | chorismate synthase |
| GKO36\_RS05495 | -22 | -2 | 159 | 192 | -15.42 | DsbA family oxidoreductase |
| GKO36\_RS09505 | -13 | -2 | 119 | 149 | -15.37 | acyl-CoA carboxylase subunit beta |
| GKO36\_RS18125 | -73 | -51 | 183 | 200 | -15.37 | Protein Homology. |
| GKO36\_RS12910 | -66 | -38 | 191 | 202 | -15.27 | SMC family ATPase |
| GKO36\_RS12185 | -68 | -49 | 175 | 209 | -15.22 | cytochrome aa3 quinol oxidase subunit I |
| GKO36\_RS00065 | -64 | -35 | 183 | 202 | -14.98 | Protein Homology. |
| GKO36\_RS01850 | -24 | -9 | 120 | 128 | -14.97 | fosfomycin resistance protein FosB |
| GKO36\_RS15300 | 17 | 34 | 182 | 198 | -14.94 | metal ABC transporter permease |
| GKO36\_RS20680 | -73 | -35 | 119 | 136 | -14.94 | sensor histidine kinase |
| GKO36\_RS03240 | -16 | 10 | 182 | 201 | -14.91 | SsrA-binding protein |
| GKO36\_RS09340 | 14 | 37 | 192 | 218 | -14.85 | stage II sporulation protein M |
| GKO36\_RS02515 | -7 | 10 | 125 | 142 | -14.83 | aspartate--tRNA ligase |
| GKO36\_RS10395 | 19 | 56 | 185 | 199 | -14.77 | membrane protein |
| GKO36\_RS09470 | 46 | 65 | 186 | 216 | -14.75 | tRNA 2-thiouridine synthase MnmA |
| GKO36\_RS19295 | -14 | 15 | 118 | 137 | -14.72 | D-alanyl-lipoteichoic acid biosynthesis protein DltB |
| GKO36\_RS20920 | -22 | -7 | 183 | 202 | -14.72 | LLM class flavin-dependent oxidoreductase |
| GKO36\_RS15100 | -5 | 11 | 184 | 203 | -14.69 | division/cell wall cluster transcriptional repressor MraZ |
| GKO36\_RS20045 | -15 | 9 | 49 | 61 | -14.68 | AbrB family transcriptional regulator |
| GKO36\_RS12325 | -40 | -10 | 120 | 130 | -14.67 | amino acid permease |
| GKO36\_RS12090 | -18 | -1 | 189 | 209 | -14.63 | Protein Homology. |
| GKO36\_RS05590 | 10 | 18 | 120 | 137 | -14.57 | 23-dihydro-23-dihydroxybenzoate dehydrogenase |
| GKO36\_RS09235 | 55 | 74 | 116 | 129 | -14.48 | carbamoyl phosphate synthase small subunit |
| GKO36\_RS01355 | -71 | -34 | 181 | 199 | -14.43 | Protein Homology. |
| GKO36\_RS05625 | -14 | -2 | 122 | 145 | -14.4 | TIGR04086 family membrane protein |
| GKO36\_RS15465 | -54 | -33 | 183 | 202 | -14.4 | LysR family transcriptional regulator |
| GKO36\_RS01925 | -18 | -8 | 56 | 129 | -14.37 | phenylalanine--tRNA ligase subunit alpha |
| GKO36\_RS05395 | -60 | -49 | 32 | 57 | -14.33 | catalase HPII |
| GKO36\_RS14065 | -20 | -6 | 119 | 138 | -14.31 | EamA family transporter |
| GKO36\_RS05955 | 29 | 41 | 121 | 131 | -14.3 | membrane protein |
| GKO36\_RS01510 | -18 | -2 | 182 | 203 | -14.28 | transcriptional regulator |
| GKO36\_RS20800 | -21 | -11 | 118 | 128 | -14.28 | resolvase |
| GKO36\_RS01540 | -21 | -2 | 176 | 232 | -14.28 | cysteine ligase CoaBC |
| GKO36\_RS20155 | 57 | 74 | 119 | 132 | -14.27 | allophanate hydrolase |
| GKO36\_RS19995 | -5 | 29 | 31 | 68 | -14.24 | SGNH/GDSL hydrolase family protein |
| GKO36\_RS14620 | -68 | 6 | 126 | 149 | -14.21 | acetylornithine deacetylase |
| GKO36\_RS17730 | -19 | 0 | 190 | 203 | -14.2 | RNA-binding transcriptional accessory protein |
| GKO36\_RS20385 | -69 | -43 | 192 | 203 | -14.19 | RNA polymerase sporulation sigma factor SigG |
| GKO36\_RS13005 | 13 | 34 | 134 | 161 | -14.16 | 3-isopropylmalate dehydrogenase |
| GKO36\_RS07575 | -13 | -3 | 181 | 211 | -14.16 | GntR family transcriptional regulator |
| GKO36\_RS03835 | -13 | 1 | 194 | 212 | -14.12 | stage V sporulation protein AA |
| GKO36\_RS02365 | -14 | -4 | 120 | 137 | -14.12 | spore coat protein CotJB |
| GKO36\_RS19590 | -18 | 7 | 182 | 199 | -14.1 | anion permease |
| GKO36\_RS16810 | 4 | 24 | 53 | 74 | -14.1 | glutathione-dependent formaldehyde dehydrogenase |
| GKO36\_RS14135 | -25 | -6 | 182 | 196 | -14.09 | Protein Homology. |
| GKO36\_RS17660 | -24 | -2 | 37 | 130 | -14.08 | LacI family transcriptional regulator |
| GKO36\_RS09225 | -15 | 15 | 183 | 206 | -14.07 | Protein Homology. |
| GKO36\_RS21230 | 41 | 59 | 166 | 202 | -14.07 | GeneMarkS+. |
| GKO36\_RS13685 | 27 | 60 | 182 | 200 | -14.06 | ATP-binding protein |
| GKO36\_RS07730 | -64 | -45 | 182 | 204 | -14.01 | lipoyl synthase |
| GKO36\_RS14035 | -28 | 9 | 186 | 208 | -13.99 | ABC transporter ATP-binding protein |
| GKO36\_RS03800 | -19 | -2 | 21 | 36 | -13.96 | chromosome partitioning protein ParB |
| GKO36\_RS03600 | -71 | -36 | 53 | 136 | -13.94 | ribonuclease *yfkH* |
| GKO36\_RS01635 | 18 | 28 | 114 | 124 | -13.93 | tunicamycin resistance protein |
| GKO36\_RS13840 | -23 | -4 | 192 | 203 | -13.93 | FbpB family small basic protein |
| GKO36\_RS04625 | -50 | -30 | 182 | 203 | -13.91 | site-specific tyrosine recombinase XerD |
| GKO36\_RS01725 | -28 | -7 | 95 | 149 | -13.9 | competence protein ComE |
| GKO36\_RS14400 | 26 | 54 | 187 | 202 | -13.9 | DUF188 domain-containing protein |
| GKO36\_RS20000 | -68 | -26 | 52 | 148 | -13.88 | oligoendopeptidase |
| GKO36\_RS18205 | -9 | 74 | 120 | 131 | -13.88 | stage V sporulation protein R |
| GKO36\_RS14205 | 12 | 37 | 54 | 70 | -13.85 | NarK family nitrate/nitrite MFS transporter |
| GKO36\_RS17385 | 27 | 55 | 190 | 202 | -13.84 | fructose-bisphosphatase class II |
| GKO36\_RS06710 | 32 | 59 | 50 | 89 | -13.83 | homoserine dehydrogenase |
| GKO36\_RS21320 | -3 | 16 | 51 | 88 | -13.83 | cell division suppressor protein YneA |
| GKO36\_RS03585 | -73 | -58 | 164 | 199 | -13.79 | cytochrome aa3 quinol oxidase subunit II |
| GKO36\_RS03995 | -21 | 69 | 137 | 195 | -13.76 | Protein Homology. |
| GKO36\_RS07815 | 61 | 72 | 183 | 201 | -13.73 | DegV family protein |

Table S3 Strains and plasmid used in this study

|  |  |  |
| --- | --- | --- |
| **Strain/Plasmid** | **Description** | **Reference** |
| PEBA20 | *Bacillus velezensis* wild type | Our lab collection |
| *E. coli* DH5*α* | an *E. coli* strain used for molecular cloning | Vazyme Biotech Co., Ltd |
| pHT01 | Cloning Vector; *AmpR*; *KanR* | Miaoling Biotech Co., Ltd |
| pMAD | pMAD containing *cheA*: *AmpR*; *KanR* | Miaoling Biotech Co., Ltd |
| ∆*bvs091* | ∆*bvs091* mutant strain in PEBA20 | This study |
| *obvs091* | *obvs091*mutant strain in PEBA20 | This study |
| ∆*galT2* | ∆*galT2* mutant strain in PEBA20 | This study |
| ∆*bvs091*-∆*amyE*-*galT2*-*sfGFP* | *galT2*-*sfGFP* mutant strain in *∆bvs091* | This study |
| *obvs091*-∆*amyE*-*galT2*-*sfGFP* | *galT2*-*sfGFP* mutant strain in *obvs091* | This study |

Table S4 Primers used in this study

|  |  |  |
| --- | --- | --- |
| Primer Name | DNA sequence of PCR primer |  |
| *bvs091*-F-F | 5'-atctatcgatgcatgccatggGTGATCATCCCCGAATGGC -3' | Deletion of *bvs091* mutant  consturction |
| *bvs091*-F-R | 5'-attcttttcttacgCGGCCGGCGTTTTTTCAC-3' |
| *bvs091*-B-F | 5'-cggccgCGTAAGAAAAGAATAAGACAAGACCG-3' |
| *bvs091*-B-R | 5'-gcgtcgggcgatatcggatccTTATGATCGCGGCCTGAGAC-3' |
| *pHT01-bvs091*-F | 5'-agacgcgtcgggcgatatcCAAATAAATAATATATGGTTGCCCG-3' | *pHT01-bvs091* plasmid consturction |
| *pHT01-bvs09*-R | 5'- gcgggctgccccggggacgtcGCTTCAGGCTTCAACGGACA-3' |
| *galT2*-F-F | 5'-atctatcgatgcatgccatggCTTTCAAACGTGAATGGAAAGAGTG-3' | Deletion of *galT2* mutant  consturction |
| *galT2*-F-R | 5'-gctcaattgccatTGTGCAGTTTCAGCGTTTGC-3' |
| *galT2*-B-F | 5'-gacgagctgtacaagtaaTCATTGGCTATCAAAATCCGG-3' |
| *galT2*-B-R | 5'-agacgcgtcgggcgatatcCTTCCAACAAAACCTGCTCCG-3' |
| *pMAD-amyE-*F-F | 5'-atctatcgatgcatgccatggCTTCATGATTCCGCTGGCG-3' | Dual Plasmid Fluorescent Reporter System |
| *pMAD-amyE-*F-R | 5'-ccgcctccatTTTTTGACACTCCTTATTTGATTTTTG-3' |
| *amyE-galT*-F | 5'-gtgtcaaaaaATGGAGGCGGCGGTCATT-3' |
| *amyE-galT*-R | 5'-ctttgctcatTCAGCTGCCATTCTCCAATAACG-3' |
| *galT-sfGFP*-F | 5'-tggcagctgaATGAGCAAAGGAGAAGAACTTTTCA-3' |
| *galT-sfGFP*-R | 5'-ccacccatgtgactaacttTTTGTAGAGCTCATCCATGCCA-3' |
| *pMAD-amyE*-B-F | 5'-aAAGTTAGTCACATGGGTGGAATCA-3' |
| *pMAD-amyE*-B-R | 5'-agacgcgtcgggcgatatcTCATGGCTTTCCCCGGCC-3' |
| *galT-mRNA* | 5'-GAAGACAGGGAGAAAAGCUGACUUUUACACGGCGGAUGUCGGA  GCCGGAGCGAGAGAACUAAAGGG-3' | MST |
| T7*bvs091*-F | 5'-TAATACGACTCACTATAGGGCAAATAAATAATATATGGTTGCCC-3' |
| *bvs091-mut-1R* | 5'-AACTGTGCCCGCCGGCTAGCCTCGGCCAGTGACGATTGAGAGGTA  GGG-3' |
| *bvs091-mut-2F* | 5'-GCCGAGGCTAGCCGGCGGGCACAGTTTTGTAAAACAAAAAGTCT  TTTTTCC-3' |
| *bvs091-com-R* | 5'-TTTACACCGGCGGATGTTCGGAGCCGCAGTGACGATTGAGAGG  TAGGG-3' |
| *bvs091-com-2F* | 5'-CGGCTCCGAACATCCGCCGGTGTAAATTGTAAAACAAAAAGTCT  TTTTTCC-3' |