|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene Name\_Strain** | **Sequence (5’-3’)** |
| **qPCR** |  |  |
| P96712 | *bmr3*\_ BCRC-16100 | Forward: TATCGGGAACCTAGTCGTGAA  Reverse: CGCCTGAATGCCAAGTAGAA |
| P71879 | *stp*\_ BCRC-16100 | Forward: CGCTGTTGGAGCTAGATCTTT  Reverse: GAATCAGACTCGGTGCTACTAAC |
| Q9CHL8 | *lmrA*\_ BCRC-16100 | Forward: CGTTGTGCCGCTTGTTATTC  Reverse: TAAACGCTGCCAGATTCTCTT |
| P52600 | *emrY*\_ BCRC-16100 | Forward: CTGTTTACTGGCGGGATGAT  Reverse: CCACCAGCAAGGATGAGAAA |
| O07550 | *yheI*\_ BCRC-16100 | Forward: GCCAACTGGTTTCCTTTGTG  Reverse: GTTCATCGACCCGATCATAACT |
| P71879 | *stp\_* ZFM54 | Forward: GGTCTGATCGGTTCCTTTGT  Reverse: GATCAAAGCGACAATCCCAATC |
| O07550 | *yheI\_* ZFM54 | Forward: GCCAACTGGTTTCCTTTGTG  Reverse: GTTCATCGACCCGATCATAACT |
|  | *yheH\_* ZFM54 | Forward: CGAAGCGACGAATGAGGAATA  Reverse: AACCGCAATCAACGCAAAG |
| P96712 | *bmr3\_* ZFM54 | Forward: CCGGGTTTCACGATTGGTAT  Reverse: GCACTCAAGCCTAATGTTTCTTC |
|  | *tetA\_1\_* ZFM54 | Forward: GCATAACGTCGGTCCCATTA  Reverse: GATCGCCGTAACGACCTAATC |
| Q9CHL8 | *lmrA\_* ZFM54 | Forward: CAACCTCACCAAAGTCGTTAGA  Reverse: GCTCTTCCGCATGGTGATAA |
|  | *tetA\_2\_* ZFM54 | Forward: GCATAACGTCGGTCCCATTA  Reverse: GATCGCCGTAACGACCTAATC |
|  | *tetO\_* ZFM54 | Forward: CACTGACGAAAGCCGTAGAA  Reverse: TCGGCGGCAAAGGTTAAT |
|  | *marR\_* ZFM54 | Forward: GCTCAGTGAGTGCCACAATTA  Reverse: CTCGCTTGTCAGTTGGATTAGG |
| **PCR** |  |  |
|  | *16s rRNA* | Forward: AGAGTTTGATCMTGGCTCAG  Reverse: GGTTACCTTGTTACGACTT |

**Supporting Table 1.** Primers for PCR and qPCR and sequencing *Lacticaseibacillus paracase*i BCRC-16100 and *Lacticaseibacillus paracase*i ZFM54.

**Supporting Table 2.** ANOVA for alcohol tolerance of *Lacticaseibacillus paracasei* BCRC-16100.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 0.309963 | 3 | 0.103321 | 0.585954 | 0.640971 | 4.066181 |
| Within Groups | 1.410637 | 8 | 0.176330 |  |  |  |
| Total | 1.7206 | 11 |  |  |  |  |

**Supporting Table 3.** ANOVA for alcohol tolerance of *Lacticaseibacillus paracasei* ZFM54.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 0.189667 | 3 | 0.066322 | 2.056680 | 0.184527 | 4.066181 |
| Within Groups | 0.257978 | 8 | 0.032247 |  |  |  |
| Total | 0.456944 | 11 |  |  |  |  |

**Supporting Table 4.** ANOVA for pH tolerance of *Lacticaseibacillus paracasei* BCRC-16100.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 4.733412 | 3 | 1.577804 | 246.822308 | 3.20 E-08 | 4.066181 |
| Within Groups | 0.051140 | 8 | 0.006392 |  |  |  |
| Total | 4.784551 | 11 |  |  |  |  |

**Supporting Table 5.** ANOVA for pH tolerance of *Lacticaseibacillus paracasei* ZFM54.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 6.803493 | 3 | 2.267831 | 504.4387402 | 1.87788 E-09 | 4.066181 |
| Within Groups | 0.035966 | 8 | 0.004495751 |  |  |  |
| Total | 6.839459 | 11 |  |  |  |  |

**Supporting Table 6.** ANOVA for inhibition zone of *Lacticaseibacillus paracasei* BCRC-16100 in five antibiotics (clindamycin, vancomycin, gentamycin, ofloxacin, erythromycin, and streptomycin).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 3023.50 | 5 | 604.699356 | 17.1633044 | 4.2317E-05 | 3.105875239 |
| Within Groups | 422.785 | 12 |  |  |  |  |
| Total | 3446.29 | 17 |  |  |  |  |

**Supporting Table 7.** ANOVA for inhibition zone of *Lacticaseibacillus paracasei* ZFM54 in five antibiotics (clindamycin, vancomycin, gentamycin, ofloxacin, erythromycin, and streptomycin).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 2613.37 | 5 | 522.6732 | 163.932176 | 1.2988E-10 | 3.105875 |
| Within Groups | 38.2602 | 12 | 3.18835 |  |  |  |
| Total | 2651.63 | 17 |  |  |  |  |

**Supporting Table 8.** ANOVA for CFU/ml of *Lacticaseibacillus paracasei* BCRC-16100 in five antibiotics (clindamycin, vancomycin, gentamycin, ofloxacin, erythromycin, and streptomycin).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 78112.3 | 5 | 15622.456 | 3159.5978 | 2.8009E-18 | 3.105875 |
| Within Groups | 59.3333 | 12 | 4.9444444 |  |  |  |
| Total | 78171.6 | 17 |  |  |  |  |

**Supporting Table 9.** ANOVA for CFU/ml of *Lacticaseibacillus paracasei* ZFM54 in five antibiotics (clindamycin, vancomycin, gentamycin, ofloxacin, erythromycin, and streptomycin).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **SS** | **df** | **MS** | **F** | **P-value** | **F crit** |
| Between Groups | 45516.7 | 5 | 9103.3333 | 3091.6981 | 3.1905E-18 | 3.10587 |
| Within Groups | 35.3333 | 12 | 2.9444444 |  |  |  |
| Total | 45552.0 | 17 |  |  |  |  |

**Supporting Table 10.** Antibiotic Resistant (AbR) Genes identified in the genome sequences of *Lacticaseibacillus paracasei* BCRC-16100 and *Lacticaseibacillus paracasei* ZFM54, associated with their corresponding transcription factors (TF) and respective binding site scores. Core score signifies the primary score indicating the strength of the binding interaction, while relative score represents the score normalized relative to other binding interactions.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antibiotic Resistant  (AbR) Genes | Transcription Factors | Binding Site | Score  (Core score) | Relative  score |
| *stp* | phoB | CTTTCATCAATTATATTCAGTC | 4.91  (3.35) | 0.79 |
| *yhel* | araC | TATGAATTGATCTGC | 3.21  (2.92) | 0.79 |
|  | fnr | TTGATATAAATCAA | 3.21  (2.92) | 0.79 |
|  | fis | GTAGACGATGTAGAC | 3.21  (2.92) | 0.93 |
| *yheH* | arcA | TGTTAAACAA | 3.62  (2.59) | 0.88 |
|  | purR | AAATTCGAACATTA | 3.21  (2.92) | 0.79 |
| *bmr3* | fnr | TTGAGGACAAACAA | 10.54  (7.72) | 0.87 |
|  | ihf | CAATAGTT | 4.69  (4.07) | 0.97 |
|  | lrp | CCCATTTTAA | 7.19  (6.58) | 0.98 |
|  | nagC | GTTAATTGATTTTGCGAAATAGG | 3.21  (2.92) | 0.79 |
| *tetA\_1* | fis | GCGGAAAAAATGACC | 3.41  (2.92) | 0.99 |
|  | arcA | TGTTATTTAA | 3.99  (3.04) | 0.97 |
|  | purR | AAATTCGAACATTA | 3.21  (2.92) | 0.79 |
|  | cpxR | GTAAAGGTGTCTAA | 11.14  (8.91) | 0.93 |
|  | crp | TGAGCGGTATAACCGC | 6.86  (5.57) | 0.90 |
|  | metR | TGAAAATTTTTCA | 3.21  (2.92) | 0.79 |
| *lmrA* | ihf | CAATTGTT | 4.69  (4.07) | 0.97 |
|  | lrp | CAGCCTTTTATC | 2.10  (1.63) | 0.91 |
|  | cpxR | GTAATTTAGGTAA | 3.21  (2.92) | 0.79 |
|  | fhlA | GTAATGGTCCAAAGTC | 3.21  (2.92) | 0.79 |
|  | ompR | TTTAACACTAAA | 8.58  (7.07) | 0.99 |
| *tetA-2* | purR | ATTTAAACGGTTGCGT | 3.21  (2.92) | 0.79 |
|  | argR | CGAATTACCATACT | 7.92  (5.32) | 0.80 |
| *tetO* | purR | ATTTAAACGGTTGCGT | 3.21  (2.92) | 0.79 |
|  | lrp | CGTTTTTTAG | 7.27  (6.58) | 0.99 |
|  | argR | CTAATTTCTATCCA | 7.99  (6.21) | 0.80 |
|  | dnaA | TTATCCACA | 3.21  (2.92) | 0.79 |
| *marR* | fnr | TTGTTGTCGAACAC | 10.46  (7.72) | 0.86 |
| *emrY* | Ihf | CAAGGGTT | 4.69  (4.07) | 0.97 |
|  | glpR | GTTCGGTTAAAAACAGA | 8.72  (6.52) | 0.85 |
|  | phoB | ATAACATACTTAAGTTACTAAT | 5.07  (3.28) | 0.81 |