**Supplementary File 1a. Comparison in components in LBS and ASWT**

|  |  |  |
| --- | --- | --- |
|  | **LBS** | **ASWT** |
| Tryptone(%) | 1 | 1 |
| Yeast extract(%) | 0.5 | 0.5 |
| NaCl(mM) | 171 | 210 |
| MgSO4(mM) | 0 | 35 |
| KCl(mM) | 0 | 7 |
| CaCl2(mM) | 0 | 7 |

**Supplementary File 1b. Primes used in the present study**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| gene | 　 | KEGG entry | Sequences (5’-3’) | 　 | gene | 　 | KEGG entry | Sequences (5’-3’) |
| *accA* | Forward | N646\_1411 | AAAGGTCGTGAAACCAAAGA | 　 | *fadD* | Forward | N646\_4025 | CATTATTTACTGCGATCCTCG |
| Reverse | AGCCGTGTCGATAAATGTG | 　 | Reverse | CCATATTGAGATATTTGTCTGGG |
| *accB* | Forward | N646\_1967 | TCAAGCACCAATTCACTACG | 　 | *fadE* | Forward | N646\_1395 | TATCCCAACTGATGTCAAAGG |
| Reverse | ACTTTCTGACCCACTTCTACG | Reverse | CAACCGACAGACACTCAACC |
| *accC* | Forward | N646\_1968 | AGAAGTGACTGGTGCTGTGG | 　 | *fadB* | Forward | N646\_2210 | ATCACTAAAACGCCCAGAAAA |
| Reverse | GGATAGTGTCTGCCTTTGGAC | Reverse | GCTGAAGCCGCCAAAGTA |
| *accD* | Forward | N646\_1292 | CGAACTTGAGCCACAGGATA | 　 | *fadA* | Forward | N646\_1311 | CAGATTAGCGGCCAGTTTCT |
| Reverse | ACGACTGAACCCATTGAACC | 　 | Reverse | TCAAGCGGCGGTTAATGT |
| *accD* | Forward | N646\_4704 | AAGTTTGTCCGAGCAGTTGA | 　 | *fadA* | Forward | N646\_2209 | ATTGCGGGCTGCGATC |
| Reverse | GAGACGCCACCATAAGTTTG | 　 | Reverse | GCACACGGCAGAGACTGC |
| *fabD* | Forward | N646\_1131 | CTCGCCTGGTCAAGTCGT | 　 | *fadH* | Forward | N646\_1258 | AAGTGCTGCCCTGCTCG |
| Reverse | TGCTGGCTTCATAAGTGCA | 　 | Reverse | ATGATGGCGTCGAGTTAATG |
| *fabH* | Forward | N646\_1132 | GACCGTTCAACCATCATCCT | 　 | *fabR* | Forward | N646\_2038 | TTTGCTACTACGCCAACTGATGCGT |
| Reverse | GCCATTTATCCGCATCTTG | 　 | Reverse | CGCTCACGCAACAACAAACGAA |
| *fabH* | Forward | N646\_1439 | GACGCTCCAACATGGCTAG | 　 | *fadR* | Forward | N646\_1147 | AATGCTAGGCGCTGGAA |
| Reverse | AGTTCGCTGGTGACAATAAGA | Reverse | TGAATGCGGCTTCCTG |
| *fabH* | Forward | N646\_4350 | GGAAGACAACGGTTACTGGG | 　 | *arcA* | Forward | N646\_1744 | TGGGTTGAATGGTTTAGTGATG |
| Reverse | TGCGGAATCACAACATCG | 　 | Reverse | TGAAGCCAGTGACGGTGAA |
| *fabB* | Forward | N646\_1292 | TTGACAGTGCGCCCATC | 　 | *crp* | Forward | N646\_1004 | AAGGTTGCTGCTACTTGCTGA |
| Reverse | TGTCTTGCTACGCCATTTAAGA | Reverse | GCTTCGGATTGGTAATGGTT |
| *fabB* | Forward | N646\_3036 | CAACATTAATGCTGCGGCT | 　 | *crp* | Forward | N646\_1885 | CAAAACAACCAGACGCAATG |
| Reverse | TGAGCGGCCCACATTAC | 　 | Reverse | CTCACGAGAACAGCCAACAAT |
| *fabF* | Forward | N646\_1128 | GGTGTTGCTATCGGCTCA | 　 | *gpsA* | Forward | N646\_1922 | GTGCGGGTATGTCTGATGG |
| Reverse | ATGTTTACAATGGTCGAAGGA | 　 | Reverse | ATAAAGGTTTCTGGCTGTGC |
| *fabF* | Forward | N646\_3033 | AACTGCCAAAGCACTACAAGC | *plsB* | Forward | N646\_2043 | GCTTAGTTCGCTTTAGTCCC |
| Reverse | TGATGAGCCGTATGCGATAC | 　 | Reverse | CACTTGGCGTTGTGGC |
| *fabG* | Forward | N646\_1130 | CAACCTAACGCCAATCTACC | 　 | *plsY* | Forward | N646\_2566 | CGCCAAGAATGATAGGGTC |
| Reverse | CCACGAGACGCAACTTCA | 　 | Reverse | TTATTAGGTTCGGTTTCCAGT |
| *fabG* | Forward | N646\_3034 | GACCGAAGAAGAATGGGATG | 　 | *plsC* | Forward | N646\_1749 | CGATTCGCTCGGTCAA |
| Reverse | TGCGCTGTAGTTAGTTTGACC | Reverse | TACTGTTTCTGCGGCTGT |
| *fabG* | Forward | N646\_3826 | AGTAAAGGCGGCGTCATC | 　 | *cdsA* | Forward | N646\_1423 | TTGCTGCCCTTGTGCC |
| Reverse | TCTGGCAGGTTCTTGGTCA | 　 | Reverse | GCCAAGATTTCGTCGTTTT |
| *fabG* | Forward | N646\_4505 | CCCAAGGCGTTATCATCA | 　 | *pgsA* | Forward | N646\_1026 | GTTTTGGCGCGTTTATT |
| Reverse | TTCGGGTTTCATTTGCTCT | 　 | Reverse | TTTCTCGCGCAATCATC |
| *fabZ* | Forward | N646\_1416 | GAGAAGTACCTTCACGCGAT | 　 | *pgpA* | Forward | N646\_2838 | ATGAGTTTGCGGGCTTT |
| Reverse | CTGTTGCCTGAGCCATTG | 　 | Reverse | TCCCGCCACGATATCAT |
| *fabV* | Forward | N646\_4267 | AGTAATGGGCGGCGAAG | 　 | *pgpB* | Forward | N646\_3562 | TTTCTTTGGCGGGTTGT |
| Reverse | TGGGTGCGTAATGTCAGG | 　 | Reverse | CTTCAGGGCGGTGCAT |
| *fabV* | Forward | N646\_0267 | GGTGGTTTACTCACTGGCATC | *pssA* | Forward | N646\_2008 | GATAAAACCGCCAACGA |
| Reverse | TCTTCACCGCCCATTACC | 　 | Reverse | TTACGTGCGGCGATATT |
| *tesA* | Forward | N646\_4268 | AGCATTTCTGGCGATACAAC | 　 | *psd* | Forward | N646\_1916 | CACTCTGCGCCAAATG |
| Reverse | GGAGGGAAACCTCTTAGGC | 　 | Reverse | ACGAGGCGGAGTGATC |
| *tesB* | Forward | N646\_0021 | CTTTGGATTCGTGCTAATGG | 　 | *pldA* | Forward | N646\_4183 | CTTTTTAGGTCGCCAGAAC |
| Reverse | ATAGAGTGGTCAATGGTGGC | 　 | Reverse | CATAACCCGCTGAGTATTGT |
| *yciA* | Forward | N646\_1052  | TGTCTCAGCTCGACTTAGCG | 　 | *pldB* | Forward | N646\_2069 | GATCTCTACCGCCAAGGT |
| Reverse | GGGTTTGACCCATACTTCCA | 　 | Reverse | AGTGCGCGATGATGAAG |
| *fadL* | Forward | N646\_1315  | CTAAGTATTGGCGCAACGTACG | *glpQ* | Forward | N646\_1500 | CTATCCAACCCGATTCCC |
| Reverse | GCCGCCGACTTGTTCTG | 　 | Reverse | ACCAAGGCGCTTTAATTT |
| *fadL* | Forward | N646\_1316 | CTGCCTTCGCCGATGAT | 　 | *glpQ* | Forward | N646\_3581 | AAAAGTCCAATGCCGCA |
| Reverse | GAAATTCGCGATTGGTTTG | 　 | Reverse | GTAACCGGCTTGTTGGAG |
| *fadL* | Forward | N646\_3657 | TTATCTGCGGGTGCCTCT | 　 | *glpQ* | Forward | N646\_3723 | CACAAATGGCGCTATCTG |
| Reverse | GTCACGCCCGTCACCAT | 　 | Reverse | CCATCGGCTTCTTCACTC |
| *fadD* | Forward | N646\_1045  | TGTTCTTGAGCTGGTGGAAA | 　 | *glpQ* | Forward | N646\_3724 | GACTTGTGAAGCCCGC |
| Reverse | AACACGCAATGACGAGGTAT | 　 | Reverse | AGATACTCAGGGCCAATAAAC |
| *fadD* | Forward | N646\_2540 | GCATCGGTCGATTCTTCC | 　 | *etuC* | Forward | N646\_3725 | CTTTTAAGCGCTGATGATGA |
| Reverse | CGCCAATCTTAACCTGTGC | 　 | Reverse | GTTAGACCGGGTCTCTCTC |
| *fadD* | Forward | N646\_3023 | CTCTGATGATGCCAAACCTAC | *adhE* | Forward | N646\_1240 | AGCGATGCTGCACGAA |
| Reverse | ACGAGGAGTGTAAAGTGGGTT | Reverse | CCTGTAACTAATATGGCTGAAC |

**Supplementary File 1c. Primers used in the present study for construction of gene-deleted mutants**

|  |  |  |
| --- | --- | --- |
| *gene* | 　 | primer (5'-3') |
| *fadR* | P1 |  aaaaaggatcgatcct TACTTCCCCTGAACTCAAGCAC |
| P2 | TGTCAGCGCTTATCTACTTTTTATCCAATATTGATTTCTG |
| P3 | ATAAAAAGTAGATAAGCGCTGACAAGTTGGATAAAC |
| P4 |  atcgcatgcggtacc GCAAAGAGATGACTTGCATAATGAGTA |
| P5 | ATGGTCATAAAGGCGAAAAGCC |
| P6 | TTAGCTGTCGTCTTCCGTGAAGTT |
| P7 | AATAGTGCTTAAGTATCTGTTTGT |
| P8 | ATGACCATAGTGTTGCAAGA |
| *arcA*  | P1 | aaaaaggatcgatcct GACCTCAAGTTACTGTATGGGTTCC |
| P2 | TAGCGGTTAAATTGGCGGTACCTAAATTTGTGACA |
| P3 | TAGGTACCGCCATAGATTTAACCGCTAATATGCAAAGGG |
| P4 | atcgcatgcggtacc ATTGATGGCAGGCTGTAGTTCC |
| P5 | ATGCAAACCCCGCAGATTCT |
| P6 | TGGCGATGATTTCTGGCGT |
| P7 | CGACGGCAAAGCTTTCCTC |
| P8 | AAAAGTTGGTTGGAACAAAGGAA |
| *plsB* | P1 | aaaaaggatcgatcct TTAGGTGTTCCTCTGCGGCAT |
| P2 | AAGGTAAAACGGAAAGTTCACAGCCTCAATAGGTATTC |
| P3 | GCTGTGAACTTTTAACCGTTTTACCTTCTTCCAATAAGA |
| P4 | atcgcatgcggtacc AGCTATTTTTAGGCTTGGCTTTTA |
| P5 | ACAACGATAATGATGTCCCAACC |
| P6 | GAACGACCACCCTCACTGAAGTA |
| P7 | GCTCATCATTGGCTGCGTCT |
| P8 | TGCTGACCATGAACCCGC |
| *waaf* | P1 | aaaaaggatcgatcct AGTTGTGGGTTCGCTGTGTTGA |
| P2 | GAACTAACATGAGCTTTGTTTTTCCAGTATAGGAATT |
| P3 | GAAAAACAAAGCTCATGTTAGTTCGTATTGTTTATACCTT |
| P4 | atcgcatgcggtacc TTGGCGTAGTTCTGACACGATT |
| P5 | AACGCCATCCAGATAGCCAAAT |
| P6 | AGGTTTCAAGCCCGCCAAGA |
| P7 | ATATGTGGGTACTACAGTTGCTGCA |
| P8 | CATCTAATACCTGTTCGTCCTC |
| *lpxA* | P1 | aaaaaggatcgatcct TACGACCTGTTGCCACGTTTG |
| P2 | ATTCGCCAATTAATTAAAACTCTCGACGAGCACAC |
| P3 | GAGAGTTTTAATTAATTGGCGAATGAACCAATAAATAA |
| P4 | atcgcatgcggtacc ATTTTAAAGATGCGCTTCTGACG |
| P5 | GGCAGCGGTGGTAGAAGAGG |
| P6 | AACGGGTGAATCGCAGACAG |
| P7 | ATTGATGAGATGAATAAGCGCCT |
| P8 | TAACTCGCTACCACGACTGCCT |
| *lpxC* | P1 | aaaaaggatcgatcct AGACGGTTGGTAATACAGTGAAG |
| P2 | GCCAAGTATTTACTGCTTGCCTCTCAAAAATTTGC |
| P3 | AGAGGCAAGCAGTAAATACTTGGCATTAGAATTAATAA |
| P4 | atcgcatgcggtacc CTGGAGAAATCTTACAGCTTAAC |
| P5 | ATTGAATCAGACGAGCAACG |
| P6 | CGAATGTAGTCCACTCCCAC |
| P7 | AGAATGCCGTTCAAGGTATTGC |
| P8 | TTTACTTAAAGTGGTGACTGATT |
| *pgpA* | P1 | aaaaaggatcgatcct AAGCACTAGAGCGAGCTCATTAC |
| P2 | GTTCATGGTTTAATCCTTAAACCTATACTGCTAGTTT |
| P3 | AGGTTTAAGGATTAAACCATGAACTAAACACTGGACGT |
| P4 | atcgcatgcggtacc ATACCCTCGTGGTAGCGGCAT |
| P5 | GGCACAATTACCATTTACGG |
| P6 | TAGAAACAGGGCAACACCAG |
| P7 | CATTTTTCGAACTGGCTGATT |
| P8 | GCAACGTGGTTATGACCAATT |

Small letters are homologous recombination sequences with pDS132 plasmid.