**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.