**Table S1.** Probiotic characteristic genes

| Function | gene | Description | SHY0006 locus |
|---|---|---|---|
| Temperature tolerance | *xylA* | xylose isomerase | ACWNPI_00990 |
| | *cspA* | cold shock protein | ACWNPI_00412 |
| | *cspB* | cold shock protein | ACWNPI_00412 |
| | *cspC* | cold shock protein | ACWNPI_00412 |
| | *dnaJ* | molecular chaperone DnaJ | ACWNPI_02040 |
| | *dnaK* | molecular chaperone DnaK | ACWNPI_02041 |
| | *hrcA* | heat-inducible transcriptional repressor | ACWNPI_02043 |
| | *clpC* | ATP-dependent Clp protease ATP-binding subunit ClpC | ACWNPI_02009 |
| | *groEL* | chaperonin GroEL | ACWNPI_02174 |
| | *groES* | chaperonin GroES | ACWNPI_02173 |
| | *lexA* | repressor LexA | ACWNPI_00752 |
| | *recA* | recombination protein RecA | ACWNPI_00098 |
| | *trxA* | thioredoxin | ACWNPI_00115 |
| | *trxB* | thioredoxin reductase (NADPH) | ACWNPI_00782 |
| | *feoB* | ferrous iron transport protein B | ACWNPI_00935 |
| | *cydA* | cytochrome bd ubiquinol oxidase subunit | ACWNPI_00588 |
| | *cydC* | ATP-binding cassette, subfamily C | ACWNPI_00591 |
| | *ndh* | NADH:quinone reductase (non-electrogenic) | ACWNPI_01963 |
| Oxidative Stress | *msrA* | peptide-methionine (S)-S-oxide reductase | ACWNPI_01576 |
| | *msrB* | peptide-methionine (R)-S-oxide reductase | ACWNPI_00914 |
| | *msrC* | L-methionine (R)-S-oxide reductase | ACWNPI_00917 |
| | *hslO* | molecular chaperone Hsp33 | ACWNPI_00131 |
| | *tpx* | thioredoxin-dependent peroxiredoxin | ACWNPI_00083 |
| | *mutT* | MTH2; 8-oxo-dGTP diphosphatase | ACWNPI_00730 |
| | *msrB* | peptide-methionine (R)-S-oxide reductase | ACWNPI_00914 |
| | *ahpC* | NADH-dependent peroxiredoxin subunit C | ACWNPI_00995 |
| osmotic shock tolerance | *opuA* | osmoprotectant transport system ATP-binding protein | ACWNPI_00220 |
| | *opuC* | osmoprotectant transport system substrate-binding protein | ACWNPI_00222 |
| | *opuCA* | osmoprotectant transport system ATP-binding protein | ACWNPI_00220 |

| | | | |
|---|---|---|---|
| | *opuCB* | osmoprotectant transport system permease protein | ACWNPI_00219 |
| | *opuCC* | osmoprotectant transport system substrate-binding protein | ACWNPI_00222 |
| | *grpE* | molecular chaperone GrpE | ACWNPI_02042 |
| | *opuCB* | osmoprotectant transport system permease protein | ACWNPI_00219 |
| | *osmV* | osmoprotectant transport system ATP-binding protein | ACWNPI_00220 |
| | *atpC* | F-type H+-transporting ATPase subunit epsilon | ACWNPI_01533 |
| | *atpD* | F-type H+/Na+-transporting ATPase subunit beta | ACWNPI_01532 |
| | *atpG* | F-type H+-transporting ATPase subunit gamma | ACWNPI_01531 |
| | *atpH* | F-type H+-transporting ATPase subunit delta | ACWNPI_01529 |
| | *atpF* | F-type H+-transporting ATPase subunit b | ACWNPI_01528 |
| | *atpB* | F-type H+-transporting ATPase subunit a | ACWNPI_01526 |
| | *atpE* | F-type H+-transporting ATPase subunit c | ACWNPI_01527 |
| | *recA* | recombination protein RecA | ACWNPI_00098 |
| | *aspS* | aspartyl-tRNA synthetase | ACWNPI_00840 |
| | *cspA* | cold shock protein | ACWNPI_00412 |
| acid stress | *gpmA* | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | ACWNPI_00016 |
| | *glmU* | UDP-N-acetylglucosamine pyrophosphorylase | ACWNPI_01321 |
| | *glmS* | glutamine---fructose-6-phosphate transaminase (isomerizing) | ACWNPI_00969 |
| | *glmM1* | Phosphoglucosamine mutase | ACWNPI_00968 |
| | *glmM2* | Phosphoglucosamine mutase | ACWNPI_00968 |
| | *yphJ* | 4-carboxymuconolactone decarboxylase | ACWNPI_00500 |
| | *grpE* | molecular chaperone GrpE | ACWNPI_02042 |
| | *atpA* | F-type H+/Na+-transporting ATPase subunit alpha | ACWNPI_01530 |
| | *clpE* | ATP-dependent Clp protease ATP-binding subunit ClpE | ACWNPI_01900 |
| | *clpP_1* | ATP-dependent Clp protease proteolytic subunit precursor | ACWNPI_01269 |

| | | | |
|---|---|---|---|
| | *clpP_2/clpP* | ATP-dependent Clp protease proteolytic subunit precursor | ACWNPI_01269 |
| | *copA* | P-type Cu+ transporter | ACWNPI_00244 |
| | *dltA* | D-alanine--poly(phosphoribitol) ligase subunit 1 | ACWNPI_01180 |
| | *dltD* | D-alanine transfer protein | ACWNPI_01177 |
| | *dnaJ* | molecular chaperone DnaJ | ACWNPI_02040 |
| | *dnaK* | molecular chaperone DnaK | ACWNPI_02041 |
| | *eno* | enolase 1/2/3 | ACWNPI_00953 |
| | *eno2* | enolase 1/2/3 | ACWNPI_00953 |
| | *gapA* | glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) | ACWNPI_00950 |
| | *groL/groEL* | chaperonin GroEL | ACWNPI_02174 |
| | *groS/groES* | chaperonin GroES | ACWNPI_02173 |
| | *grpE* | molecular chaperone GrpE | ACWNPI_02042 |
| | *guaA* | GMP synthase (glutamine-hydrolysing) | ACWNPI_01978 |
| | *ldh_1/ldh* | L-lactate dehydrogenase | ACWNPI_01097 |
| | *pgk* | phosphoglycerate kinase | ACWNPI_00951 |
| | *pyk* | pyruvate kinase | ACWNPI_00874 |
| | *recA* | recombination protein RecA | ACWNPI_00098 |
| | *tpiA* | triosephosphate isomerase | ACWNPI_00952 |
| | *uvrA/uvrA_1* | excinuclease ABC subunit A | ACWNPI_01355 |
| | *yjbM* | GTP pyrophosphokinase | ACWNPI_01662 |
| | *ywaC* | GTP pyrophosphokinase | ACWNPI_01662 |
| | *argS* | arginyl-tRNA synthetase | ACWNPI_00370 |
| | *clp* | ATP-dependent Clp protease | ACWNPI_01269 |
| | *dps* | starvation-inducible DNA-binding protein | ACWNPI_01023 |
| | *glf* | UDP-galactopyranose mutase | ACWNPI_01619 |
| | *glnA* | glutamine synthetase | ACWNPI_00310 |
| | *luxS* | S-ribosylhomocysteine lyase | ACWNPI_01468 |
| | *pdhD_2/lpdA* | dihydrolipoyl dehydrogenase | ACWNPI_00539 |
| Bile resistance | *pepO* | putative endopeptidase | ACWNPI_01801 |
| | *ponA/pbp1A* | penicillin-binding protein 1A | ACWNPI_02111 |
| | *pyrG* | CTP synthase | ACWNPI_01314 |
| | *rplD* | large subunit ribosomal protein L4 | ACWNPI_01257 |
| | *rplE* | large subunit ribosomal protein L5 | ACWNPI_01246 |
| | *rplF* | large subunit ribosomal protein L6 | ACWNPI_01243 |
| | *rpsC* | small subunit ribosomal protein S3 | ACWNPI_01252 |
| | *rpsE* | small subunit ribosomal protein S5 | ACWNPI_01241 |
| | *srtA* | sortase A | ACWNPI_00149 |

**Table S2.** CARD (RGI) result

| Analysis item | Description |
|---|---|
| Database | Comprehensive Antibiotic Resistance Database (CARD) |
| Tool | Resistance Gene Identifier (RGI) |
| Screening criteria | Strict and perfect hits |
| Result | No acquired antibiotic resistance genes detected |