**Supplementary Table 6.** List of unique genes found in the genome of *Ligilactobacillus salivarius* TUCO-L2 compared with the strains isolated from chicken intestine *L. salivarius* DJ-sa-01 and CICC23174.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Annotation** | **TUCO-L2** |
| *cbh\_1* | Choloylglycine hydrolase | SOPE01000100.1\_00308 |
| *bglF\_2* | PTS system beta-glucoside-specific EIIBCA component | SOPE01000100.1\_00996 |
| *bglH\_1* | Aryl-phospho-beta-D-glucosidase BglH | SOPE01000100.1\_00886 |
| *bglH\_2* | Aryl-phospho-beta-D-glucosidase BglH | SOPE01000100.1\_00995 |
| *bglK* | Beta-glucoside kinase | SOPE01000100.1\_01167 |
| *cap8A* | Capsular polysaccharide type 8 biosynthesis protein cap8A | SOPE01000100.1\_00096 |
| *celD* | PTS system cellobiose-specific EIIA component | SOPE01000100.1\_00793 |
| *epsE\_1* | Putative glycosyltransferase EpsE | SOPE01000100.1\_00264 |
| *epsE\_2* | Putative glycosyltransferase EpsE | SOPE01000100.1\_01201 |
| *epsJ\_1* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00104 |
| *epsJ\_2* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00112 |
| *epsJ\_4* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00813 |
| *epsJ\_5* | putative glycosyltransferase EpsJ | SOPE01000100.1\_01199 |
| *fsaA* | Fructose-6-phosphate aldolase 1 | SOPE01000100.1\_00144 |
| *epsJ\_3* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00812 |
| *gtfC* | Glucosyltransferase-SI | SOPE01000100.1\_01094 |
| *rhaA* | L-rhamnose isomerase | SOPE01000100.1\_01090 |
| *rhaB* | Rhamnulokinase | SOPE01000100.1\_01089 |
| *rhaD* | Rhamnulose-1-phosphate aldolase | SOPE01000100.1\_00693 |
| *srlA* | PTS system glucitol/sorbitol-specific EIIC component | SOPE01000100.1\_00124 |
| *srlE* | PTS system glucitol/sorbitol-specific EIIB component | SOPE01000100.1\_00123 |
| *wbbI\_2* | Beta-1,6-galactofuranosyltransferase WbbI | SOPE01000100.1\_00811 |
| *wbbI\_3* | Beta-1,6-galactofuranosyltransferase WbbI | SOPE01000100.1\_01116 |
| *iolA* | Methylmalonate semialdehyde dehydrogenase | SOPE01000100.1\_00635 |
| *iolB* | 5-deoxy-glucuronate isomerase | SOPE01000100.1\_00920 |
| *iolD* | 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase | SOPE01000100.1\_00981 |
| *iolE* | Inosose dehydratase | SOPE01000100.1\_01209 |
| *iolG* | Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase | SOPE01000100.1\_00982 |
| *iolI* | Inosose isomerase | SOPE01000100.1\_01176 |
| *adhE* | Aldehyde-alcohol dehydrogenase | SOPE01000100.1\_01245 |
| *aroD* | 3-dehydroquinate dehydratase | SOPE01000100.1\_01172 |
| *aroE* | Shikimate dehydrogenase (NADP(+)) | SOPE01000100.1\_01173 |
| *bacC\_1* | Dihydroanticapsin 7-dehydrogenase | SOPE01000100.1\_00993 |
| *bacC\_3* | Dihydroanticapsin 7-dehydrogenase | SOPE01000100.1\_01175 |
| *cadA\_1* | putative cadmium-transporting ATPase | SOPE01000100.1\_00580 |
| *copZ* | Copper chaperone CopZ | SOPE01000100.1\_00581 |
| *csbB\_1* | Putative glycosyltransferase CsbB | SOPE01000100.1\_00536 |
| *csbC* | putative metabolite transport protein CsbC | SOPE01000100.1\_00266 |
| *cysM* | Cysteine synthase | SOPE01000100.1\_00022 |
| *dapL* | LL-diaminopimelate aminotransferase | SOPE01000100.1\_00772 |
| *desK\_1* | Sensor histidine kinase DesK | SOPE01000100.1\_00311 |
| *desR* | Transcriptional regulatory protein DesR | SOPE01000100.1\_00310 |
| *dosC* | Diguanylate cyclase DosC | SOPE01000100.1\_00849 |
| *dps* | DNA protection during starvation protein | SOPE01000100.1\_00583 |
| *fixK* | Nitrogen fixation regulation protein FixK | SOPE01000100.1\_00582 |
| *gerN\_2* | Na(+)/H(+)-K(+) antiporter GerN | SOPE01000100.1\_00572 |
| *gerN\_3* | Na(+)/H(+)-K(+) antiporter GerN | SOPE01000100.1\_00795 |
| *gltC\_2* | HTH-type transcriptional regulator GltC | SOPE01000100.1\_01177 |
| *rsmF* | Ribosomal RNA small subunit methyltransferase F | SOPE01000100.1\_00066 |
|  | putative HTH-type transcriptional regulator | SOPE01000100.1\_00164 |
| *iphP* | Tyrosine-protein phosphatase | SOPE01000100.1\_00309 |
| *yhdG\_1* | putative amino acid permease YhdG | SOPE01000100.1\_00566 |
| *toxA\_1* | Toxin A | SOPE01000100.1\_00599 |
| *xerC\_2* | Tyrosine recombinase XerC | SOPE01000100.1\_00640 |
| *lexA\_1* | LexA repressor | SOPE01000100.1\_00645 |
|  | putative ABC transporter ATP-binding protein | SOPE01000100.1\_00665 |
|  | putative membrane protein | SOPE01000100.1\_00668 |
|  | 2-oxoglutaramate amidase | SOPE01000100.1\_00771 |
| *Int-Tn\_1* | Transposase from transposon Tn916 | SOPE01000100.1\_00951 |
| *Int-Tn\_2* | Transposase from transposon Tn916 | SOPE01000100.1\_00963 |
|  | DegV domain-containing protein | SOPE01000100.1\_01003 |
| *dacA\_2* | D-alanyl-D-alanine carboxypeptidase DacA | SOPE01000100.1\_01019 |
| *crcB\_1* | Putative fluoride ion transporter CrcB | SOPE01000100.1\_01078 |
| *toxA\_3* | Toxin A | SOPE01000100.1\_01117 |
|  | Nitronate monooxygenase | SOPE01000100.1\_01244 |
| *smc\_4* | Chromosome partition protein Smc | SOPE01000100.1\_01299 |
| *immR\_2* | HTH-type transcriptional regulator ImmR | SOPE01000100.1\_01374 |
| *gspA* | General stress protein A | SOPE01000100.1\_00356 |
| *hexR* | HTH-type transcriptional regulator HexR | SOPE01000100.1\_01015 |
| *immR\_1* | HTH-type transcriptional regulator ImmR | SOPE01000100.1\_00643 |
| *ldhD* | D-lactate dehydrogenase | SOPE01000100.1\_00143 |
| *licB* | Lichenan-specific phosphotransferase enzyme IIB component | SOPE01000100.1\_01211 |
| *licT* | Transcription antiterminator LicT | SOPE01000100.1\_00997 |
| *lyc* | Autolytic lysozyme | SOPE01000100.1\_01122 |
| *mrp* | Iron-sulfur cluster carrier protein | SOPE01000100.1\_00568 |
| *nanE* | Putative N-acetylmannosamine-6-phosphate 2-epimerase | SOPE01000100.1\_01014 |
| *ndkA* | Nucleoside diphosphate kinase | SOPE01000100.1\_01168 |
| *oppA* | Oligopeptide-binding protein OppA | SOPE01000100.1\_00666 |
| *parA* | Chromosome partitioning protein ParA | SOPE01000100.1\_00846 |
| *pepQ\_2* | Xaa-Pro dipeptidase | SOPE01000100.1\_00714 |
| *pflA* | Pyruvate formate-lyase-activating enzyme | SOPE01000100.1\_00080 |
| *pflB* | Formate acetyltransferase | SOPE01000100.1\_00079 |
| *prtP* | PII-type proteinase | SOPE01000100.1\_00631 |
| *radD* | Putative DNA repair helicase RadD | SOPE01000100.1\_01381 |
| *rhaR* | HTH-type transcriptional activator RhaR | SOPE01000100.1\_01005 |
| *rluD\_3* | Ribosomal large subunit pseudouridine synthase D | SOPE01000100.1\_01326 |
| *rpe* | Ribulose-phosphate 3-epimerase | SOPE01000100.1\_00084 |
| *rpiA* | Ribose-5-phosphate isomerase A | SOPE01000100.1\_00085 |
| *rpsN2* | Alternate 30S ribosomal protein S14 | SOPE01000100.1\_00682 |
| *sdhA* | L-serine dehydratase, alpha chain | SOPE01000100.1\_00569 |
| *sdhB* | L-serine dehydratase, beta chain | SOPE01000100.1\_00570 |
| *sglT* | Sodium/glucose cotransporter | SOPE01000100.1\_00571 |
| *smc\_3* | Chromosome partition protein Smc | SOPE01000100.1\_00881 |
| *sufB\_1* | FeS cluster assembly protein SufB | SOPE01000100.1\_00661 |
| *sufB\_2* | FeS cluster assembly protein SufB | SOPE01000100.1\_00664 |
| *sufS* | Cysteine desulfurase SufS | SOPE01000100.1\_00663 |
| *sufU* | Zinc-dependent sulfurtransferase SufU | SOPE01000100.1\_00662 |
| *tetO* | Tetracycline resistance protein TetO | SOPE01000100.1\_00683 |
| *tphA1I* | Terephthalate 1,2-dioxygenase, reductase component 1 | SOPE01000100.1\_00585 |
| *tuaB* | Teichuronic acid biosynthesis protein TuaB | SOPE01000100.1\_00360 |
| *ugd* | UDP-glucose 6-dehydrogenase | SOPE01000100.1\_00676 |
| *urdA* | Urocanate reductase | SOPE01000100.1\_01174 |
| *wfgD* | UDP-Glc:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-glucosyltransferase WfgD | SOPE01000100.1\_00690 |
| *xerS* | Tyrosine recombinase XerS | SOPE01000100.1\_01171 |
| *xre* | HTH-type transcriptional regulator Xre | SOPE01000100.1\_00644 |
| *ydiM\_1* | Inner membrane transport protein YdiM | SOPE01000100.1\_00122 |
| *ydiM\_2* | Inner membrane transport protein YdiM | SOPE01000100.1\_01178 |
| *yhdG\_2* | putative amino acid permease YhdG | SOPE01000100.1\_00567 |
| *yidK* | putative symporter YidK | SOPE01000100.1\_01210 |
| *yjaB* | putative N-acetyltransferase YjaB | SOPE01000100.1\_01372 |
| *ykfC* | Gamma-D-glutamyl-L-lysine endopeptidase | SOPE01000100.1\_01126 |