**Supplementary Table 5.** List of unique genes found in the genome of *Ligilactobacillus salivarius* TUCO-L2 compared with the strains isolated from porcine intestine *L. salivarius* JCM1046 and ZLS006.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Annotation** | **TUCO-L2 ID** |
| *asp2* | Accessory Sec system protein Asp2 | SOPE01000100.1\_00759 |
| *casC* | CRISPR system Cascade subunit CasC | SOPE01000100.1\_00947 |
| *ygbT* | CRISPR-associated endonuclease Cas1 | SOPE01000100.1\_00950 |
| *bglH\_1* | Aryl-phospho-beta-D-glucosidase BglH | SOPE01000100.1\_00886 |
| *bglH\_2* | Aryl-phospho-beta-D-glucosidase BglH | SOPE01000100.1\_00995 |
| *celD* | PTS system cellobiose-specific EIIA component | SOPE01000100.1\_00793 |
| *csbB\_1* | Putative glycosyltransferase CsbB | SOPE01000100.1\_00536 |
| *epsE\_1* | Putative glycosyltransferase EpsE | SOPE01000100.1\_00264 |
| *epsE\_2* | Putative glycosyltransferase EpsE | SOPE01000100.1\_01201 |
| *cap8A* | Capsular polysaccharide type 8 biosynthesis protein cap8A | SOPE01000100.1\_00096 |
| *epsJ\_1* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00104 |
| *epsJ\_2* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00112 |
| *wbbI\_2* | Beta-1,6-galactofuranosyltransferase WbbI | SOPE01000100.1\_00811 |
| *epsJ\_3* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00812 |
| *epsJ\_4* | putative glycosyltransferase EpsJ | SOPE01000100.1\_00813 |
| *wbbI\_3* | Beta-1,6-galactofuranosyltransferase WbbI | SOPE01000100.1\_01116 |
| *epsJ\_5* | putative glycosyltransferase EpsJ | SOPE01000100.1\_01199 |
| *gtfC* | Glucosyltransferase-SI | SOPE01000100.1\_01094 |
| *tagE* | Poly(glycerol-phosphate) alpha-glucosyltransferase | SOPE01000100.1\_01200 |
| *yjaB* | putative N-acetyltransferase YjaB | SOPE01000100.1\_01372 |
| *wfgD* | UDP-Glc:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-glucosyltransferase WfgD | SOPE01000100.1\_00690 |
| *iolA* | Methylmalonate semialdehyde dehydrogenase [acylating] | 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 |
| *apbE* | FAD:protein FMN transferase | SOPE01000100.1\_00799 |
| *aroD* | 3-dehydroquinate dehydratase | SOPE01000100.1\_01172 |
| *aroE* | Shikimate dehydrogenase (NADP(+)) | SOPE01000100.1\_01173 |
| *arsC* | Glutaredoxin arsenate reductase | SOPE01000100.1\_00037 |
| *bacC\_3* | Dihydroanticapsin 7-dehydrogenase | SOPE01000100.1\_01175 |
| *cadA\_1* | putative cadmium-transporting ATPase | SOPE01000100.1\_00580 |
| *cdd* | Cytidine deaminase | SOPE01000100.1\_00791 |
| *copZ* | Copper chaperone CopZ | SOPE01000100.1\_00581 |
| *cynR* | HTH-type transcriptional regulator CynR | SOPE01000100.1\_00387 |
| *dacA\_2* | D-alanyl-D-alanine carboxypeptidase DacA | SOPE01000100.1\_01019 |
| *dps* | DNA protection during starvation protein | SOPE01000100.1\_00583 |
| *gerN\_3* | Na(+)/H(+)-K(+) antiporter GerN | SOPE01000100.1\_00795 |
| *gldA* | Glycerol dehydrogenase | SOPE01000100.1\_01300 |
| *gltC\_2* | HTH-type transcriptional regulator GltC | SOPE01000100.1\_01177 |
| *cysM* | Cysteine synthase | SOPE01000100.1\_00022 |
|  | Putative phosphatase | SOPE01000100.1\_00044 |
| *rsmF* | Ribosomal RNA small subunit methyltransferase F | SOPE01000100.1\_00066 |
| *paiA* | Spermidine/spermine N(1)-acetyltransferase | SOPE01000100.1\_00067 |
| *ybaN* | Inner membrane protein YbaN | SOPE01000100.1\_00355 |
| *yhdG\_2* | putative amino acid permease YhdG | SOPE01000100.1\_00567 |
| *sdhB* | L-serine dehydratase, beta chain | SOPE01000100.1\_00570 |
| *toxA\_1* | Toxin A | SOPE01000100.1\_00599 |
| *xerC\_2* | Tyrosine recombinase XerC | SOPE01000100.1\_00640 |
| *xre* | HTH-type transcriptional regulator Xre | SOPE01000100.1\_00644 |
| *lexA\_1* | LexA repressor | SOPE01000100.1\_00645 |
| *gapA1* | Glyceraldehyde-3-phosphate dehydrogenase 1 | SOPE01000100.1\_00891 |
| *toxA\_2* | Toxin A | SOPE01000100.1\_00971 |
| *bglF\_2* | PTS system beta-glucoside-specific EIIBCA component | SOPE01000100.1\_00996 |
| *toxA\_3* | Toxin A | SOPE01000100.1\_01117 |
| *mvaA* | 3-hydroxy-3-methylglutaryl-coenzyme A reductase | SOPE01000100.1\_00534 |
| *smc\_4* | Chromosome partition protein Smc | SOPE01000100.1\_01299 |
| *adhR\_2* | HTH-type transcriptional regulator AdhR | SOPE01000100.1\_01330 |
| *radD* | Putative DNA repair helicase RadD | SOPE01000100.1\_01381 |
| *gspA* | General stress protein A | SOPE01000100.1\_00356 |
| *hmo* | 4-hydroxymandelate oxidase | SOPE01000100.1\_01152 |
| *immR\_1* | HTH-type transcriptional regulator ImmR | SOPE01000100.1\_00643 |
| *Int-Tn\_1* | Transposase from transposon Tn916 | SOPE01000100.1\_00951 |
| *licB* | Lichenan-specific phosphotransferase enzyme IIB component | SOPE01000100.1\_01211 |
| *licT* | Transcription antiterminator LicT | SOPE01000100.1\_00997 |
| *lyc* | Autolytic lysozyme | SOPE01000100.1\_01122 |
| *nudG\_2* | CTP pyrophosphohydrolase | SOPE01000100.1\_00884 |
| *pepQ\_2* | Xaa-Pro dipeptidase | SOPE01000100.1\_00714 |
| *qacA* | Antiseptic resistance protein | SOPE01000100.1\_00389 |
| *qorB\_2* | Quinone oxidoreductase 2 | SOPE01000100.1\_00390 |
| *rclA* | putative pyridine nucleotide-disulfide oxidoreductase RclA | SOPE01000100.1\_00354 |
| *rluD\_3* | Ribosomal large subunit pseudouridine synthase D | SOPE01000100.1\_01326 |
| *tuaB* | Teichuronic acid biosynthesis protein TuaB | SOPE01000100.1\_00360 |
| *ugd* | UDP-glucose 6-dehydrogenase | SOPE01000100.1\_00676 |
| *urdA* | Urocanate reductase | SOPE01000100.1\_01174 |
| *xynY* | Endo-1,4-beta-xylanase Y | SOPE01000100.1\_00391 |
| *ydiM\_1* | Inner membrane transport protein YdiM | SOPE01000100.1\_00122 |
| *ydiM\_2* | Inner membrane transport protein YdiM | SOPE01000100.1\_01178 |
| *yhdG\_1* | putative amino acid permease YhdG | SOPE01000100.1\_00566 |
| *yhjE* | Inner membrane metabolite transport protein YhjE | SOPE01000100.1\_00168 |
| *yidK* | putative symporter YidK | SOPE01000100.1\_01210 |
| *ykfC* | Gamma-D-glutamyl-L-lysine endopeptidase | SOPE01000100.1\_01126 |
| *yvdT\_1* | putative HTH-type transcriptional regulator YvdT | SOPE01000100.1\_00167 |
| *yvgN* | Glyoxal reductase | SOPE01000100.1\_00388 |