

S2 Table. Single nucleotide polymorphisms between the chromosomes of *L. lactis* NCDO712 and its plasmids-free derivative MG1363 (72).

Predicted mutations					
Position [§]	Mutation	Annotation [*]	Gene	Description	SNP type [#]
26455	T→C	Intergenic (+111/-39)	<i>llmg_tRNA_07</i> → / → <i>mtlA</i>	tRNA-Asn/PTS system mannitol-specific transporter subunit IIBC	Intergenic, predicted to change promoter at position -39; the -10 box is altered from an optimal TATAAT into TACAAT
522850	G→T	S214S (TCG→TCT)	<i>glpT</i> →	glycerol-3-phosphatase transporter	Synonymous
668056	A→C	D155E (GAT→GAG)	<i>tnp1297</i> ←	transposase for insertion sequence element IS1297	Non-synonymous; SIFT score - 1
671366	G→T	Q2K (CAA→AAA)	<i>llmg_0678</i> ←	transposase helper protein for IS981	Non-synonymous; SIFT score - 1
671428	T→C	intergenic (-59/-71)	<i>llmg_0678</i> ← / → <i>llmg_0679</i>	transposase helper protein for IS981/hypothetical protein	Intergenic
1167414	T→G	Intergenic (+64/-55)	<i>llmg_1198</i> → / → <i>llmg_1200</i>	hypothetical protein/hypothetical protein	Intergenic
1272351	C→T	L84L (TTG→TTA)	<i>llmg_1303</i> ←	hypothetical protein	Synonymous
1529872	A→C	I36M (ATT→ATG)	<i>llmg_1557</i> ←	hypothetical protein	Non-synonymous; SIFT score - 0.79
2143208	T→G	S244S (TCT→TCG)	<i>tnp904</i> →	transposase for insertion sequence element IS904I	Synonymous
2380149	C→T	G118D (GGC→GAC)	<i>tsf</i> ←	elongation factor Ts	Non-synonymous; predicted to affect protein function; SIFT score - 0.01
2492669	A→C	V284G (GTT→GGT)	<i>gapB</i> ←	glyceraldehyde 3-phosphate dehydrogenase	Non-synonymous; predicted to affect protein function; SIFT score - 0.02

[§] Indicates nucleotide position in the genome sequence of *L. lactis* MG1363 (RefSeq: [NC_009004.1](#))

^{*} For mutations in intergenic regions the numbers indicates the relative position to the neighboring genes. For mutations in genes the amino acid (top) and nucleotide (bottom) changes are given.

[#] The amino acid substitution is predicted to be deleterious if the SIFT score is ≤ 0.05, and tolerated if the SIFT score is > 0.05. If intergenic mutations effect either the -10 or -35 box of the promoter it is indicated