

Figure S1. Relative abundance of secreted proteins in *L. plantarum* WCFS1 wild type and the *lgt* deletion strain (Δlgt ; NZ3565Cm). The relative abundance was the ratio taken from the label free quantitation (LFQ, \log_{10} value) of detected proteins in wild type and the deletion strain in tandem mass spectrometry (MS/MS) analysis. The Av iBAQ intensity represents average Intensity-based absolute quantification of the protein detected in WT and Δlgt . The red dots represent lipoproteins, whereas blue dots represent all other type of proteins, average LFQ ratio and LogAv-iBAQ values are indicated by vertical and horizontal green dashed lines, respectively.

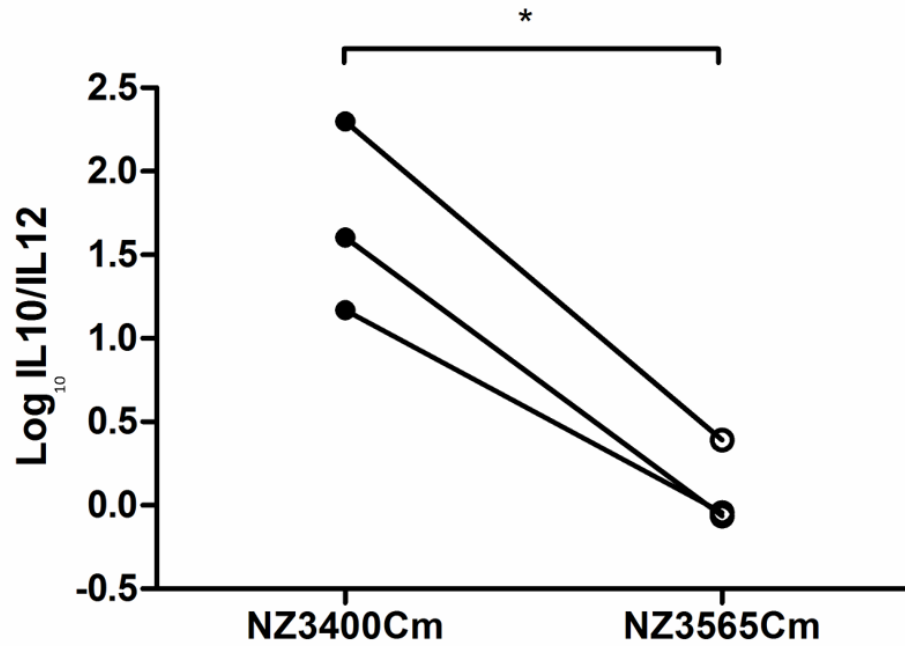


Figure S2. IL10/IL12 cytokine ratio (presented as \log_{10} values) elicited by *L. plantarum* NZ3400Cm and the *lgt* deletion strain NZ3565Cm (Δlgt ; NZ3565Cm) following co-incubation with PBMC. The cytokine levels for individual donors stimulated with the strains were connected by a line to focus the read-outs on intrapersonal changes elicited by the deletion. The differences of IL10/IL12 ratio between NZ3400Cm and NZ3565Cm were statistically analyzed using paired t test; *, $P \leq 0.05$.

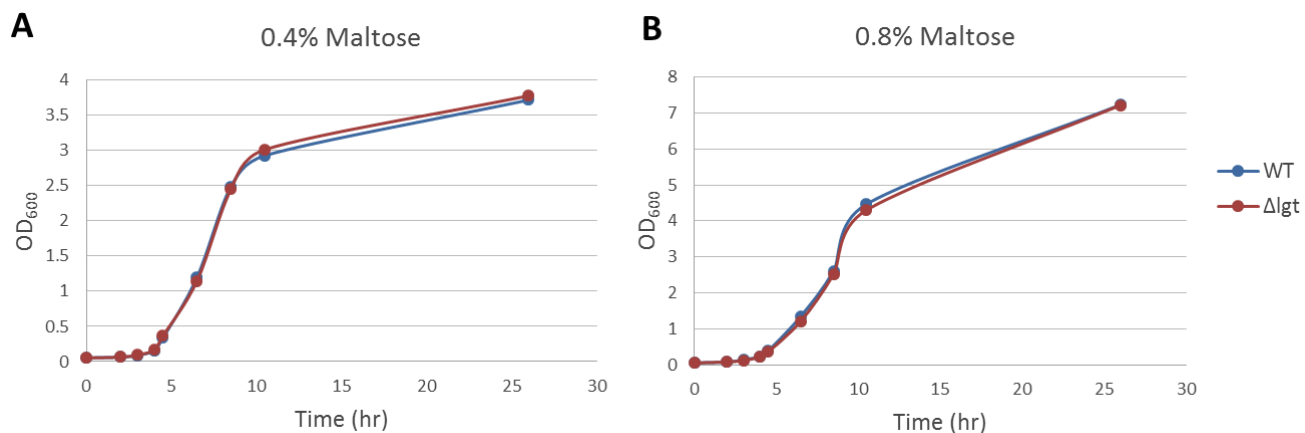


Figure S3. Comparison of the growth curves of *L. plantarum* NZ3400Cm and the *lgt* deletion strain (Δ*lgt*; NZ3565Cm). Bacteria were cultured in chemical defined medium with 0.4% (A) or 0.8% (B) maltose as a sole carbon source at 37° C. The growth was monitored for 26 hour by measuring the absorbance at 600 nm (OD₆₀₀).

Table S1. Proteins detected in mass spectrometry with different abundances between wild type *L. plantarum* WCFS1 and Δlgt mutant

Gene ID	Relative abundance (WT/ Δlgt) ^a	Function	LocateP Subcellular Localization Prediction	Mol. weight [kDa]
Only detected in Δlgt				
<i>lp_0200</i>	-	ABC transporter, substrate binding protein	Lipid anchored	61.0
<i>lp_0929</i>	-	alkaline shock protein	Intracellular	15.8
<i>lp_0937</i>	-	membrane alanine aminopeptidase (aminopeptidase N)	Intracellular	93.9
<i>lp_1539</i>	-	lipoprotein precursor	Lipid anchored	21.1
<i>lp_2974</i>	-	ABC transporter, substrate binding protein	Lipid anchored	33.8
<i>lp_3018</i>	-	ABC transporter substrate binding protein	Lipid anchored	32.9
<i>lp_3302</i>	-	ABC transporter substrate binding protein	Lipid anchored	33.9
<i>lp_3352</i>	-	small heat shock protein	Intracellular	16.7
<i>lp_3642</i>	-	ABC transporter, substrate binding protein, mannose related oligosaccharides	Lipid anchored	54.1
At least 2x higher in Δlgt				
<i>lp_0018</i>	0.013	ABC transporter, substrate binding protein, oligopeptide	Lipid anchored	59.7
<i>lp_0175</i>	0.053	ABC transporter, substrate binding protein, maltodextrin	Lipid anchored	45.7
<i>lp_0200</i>	0.026	ABC transporter, substrate binding protein	Lipid anchored	61.0
<i>lp_0201</i>	0.008	ABC transporter, substrate binding proteins	Lipid anchored	61.1
<i>lp_0733</i>	0.033	phosphate ABC transporter, substrate binding protein	Lipid anchored	31.5
<i>lp_0783</i>	0.096	ABC transporter, substrate binding protein	Lipid anchored	61.1
<i>lp_1010</i>	0.281	serine-type D-Ala-D-Ala carboxypeptidase	Lipid anchored	33.0
<i>lp_1070</i>	0.013	lipoprotein precursor, FMN-binding protein	Lipid anchored	43.4
<i>lp_1146</i>	0.262	lipoprotein, pheromone precursor (putative)	Lipid anchored	108.0
<i>lp_1452</i>	0.015	peptidylprolyl isomerase	Lipid anchored	32.6
<i>lp_1473</i>	0.011	iron chelatin ABC transporter, substrate binding protein (putative)	Lipid anchored	21.1
<i>lp_2312</i>	0.195	ABC transporter, substrate binding protein, histidine	Lipid anchored	31.3
<i>lp_2350</i>	0.008	ABC transporter, substrate binding protein, D-Methionine -like precursor	Lipid anchored	29.9

<i>lp_2397</i>	0.497	prophage P2a protein 59; extracellular polysaccharide deacetylase, lipid-anchored (putative)	Lipid anchored	31.6
<i>lp_2450</i>	0.013	prophage P2a protein 7; extracellular protein with lipoprotein anchor	Lipid anchored	12.0
<i>lp_2519</i>	0.009	cell surface hydrolase, DUF915 family, membrane-bound (putative)	Lipid anchored	31.7
<i>lp_2906</i>	0.407	DNA-entry nuclease	Lipid anchored	34.3
<i>lp_2974</i>	0.016	ABC transporter, substrate binding protein	Lipid anchored	33.8
<i>lp_2985</i>	0.026	branched-chain amino acid ABC transporter, substrate binding protein	Lipid anchored	41.9
<i>lp_3018</i>	0.013	ABC transporter substrate binding protein	Lipid anchored	32.9
<i>lp_3103</i>	0.033	iron chelatin ABC transporter, substrate binding protein	Lipid anchored	34.1
<i>lp_3209</i>	0.011	ABC transporter, substrate binding protein, cystine	Lipid anchored	29.0
<i>lp_3214</i>	0.007	ABC transporter, substrate binding protein, cystathionine (putative)	Lipid anchored	29.3
<i>lp_3302</i>	0.068	ABC transporter substrate binding protein	Lipid anchored	33.9
<i>lp_3642</i>	0.053	ABC transporter, substrate binding protein, mannose related oligosaccharides	Lipid anchored	54.1
<i>lp_0076</i>	0.246	elongation factor G	Intracellular	77.0
<i>lp_0764</i>	0.336	Phosphoglucomutase	Intracellular	63.5
<i>lp_0929</i>	0.053	alkaline shock protein	Intracellular	93.9
<i>lp_1046</i>	0.472	ribosomal protein L24	Intracellular	11.4
<i>lp_1879</i>	0.246	DNA-binding protein	Intracellular	62.9
<i>lp_3352</i>	0.350	small heat shock protein	Intracellular	16.7
<i>lp_1229</i>	0.039	mannose-specific adhesion	LPxTG Cell-wall anchored	60.3
<i>lp_0295</i>	0.160	transport protein, MMPL family	Multi-transmembrane	143.3
<i>lp_0925</i>	0.149	Acyltransferase	Multi-transmembrane	15.8
<i>lp_1000</i>	0.014	transcriptional attenuator, cell envelope-related, LytR family	N-terminally anchored	28.2
<i>lp_1097</i>	0.269	manganese/zinc ABC transporter, substrate binding protein	Secretory(released)	42.6
<i>lp_1278</i>	0.058	serine-type D-Ala-D-Ala carboxypeptidase	Secretory(released)	38.6

Only detected in WT				
<i>lp_0542</i>	-	septum formation initiator	N-terminally anchored	15.2
<i>lp_0575</i>	-	mannose PTS, EIIAB	Intracellular	35.3
<i>lp_1043</i>	-	ribosomal protein L29	Intracellular	7.5
<i>lp_1050</i>	-	ribosomal protein S8	Intracellular	14.6
<i>lp_1097</i>	-	manganese/zinc ABC transporter, substrate binding protein	Secretory(released)	34.6
<i>lp_3614</i>	-	Oxidoreductase	Intracellular	33.4
<i>lp_3686</i>	-	ABC transporter, substrate binding protein	Lipid anchored	60.5
At least 2x higher in WT				
<i>lp_2145</i>	3.775	extracellular protein, DC-SIGN ligand	C-terminally anchored	45.8
<i>lp_3678</i>	3.872	cell surface protein precursor, DUF916 family	C-terminally anchored	39.6
<i>lp_0355</i>	3.309	multicopper oxidase (putative)	Intracellular	56.8
<i>lp_0575</i>	13.299	mannose PTS, EIIAB	Intracellular	35.3
<i>lp_0578</i>	2.867	non-ribosomal peptide synthetase NpsA	Intracellular	602.6
<i>lp_0728</i>	13.425	GroEL chaperonin	Intracellular	57.4
<i>lp_0937</i>	3.414	membrane alanine aminopeptidase (aminopeptidase N)	Intracellular	128.2
<i>lp_1043</i>	79.973	ribosomal protein L29	Intracellular	7.5
<i>lp_1050</i>	19.487	ribosomal protein S8	Intracellular	14.6
<i>lp_1053</i>	5.335	ribosomal protein S5	Intracellular	17.3
<i>lp_1054</i>	2.682	ribosomal protein L30	Intracellular	6.7
<i>lp_1635</i>	5.452	signal recognition particle protein Ffh	Intracellular	236.1
<i>lp_1897</i>	6.808	pyruvate kinase	Intracellular	43.3
<i>lp_2055</i>	3.094	ribosomal protein S2	Intracellular	30.2
<i>lp_2118</i>	12.661	trigger factor; peptidylprolyl isomerase	Intracellular	49.4
<i>lp_2417</i>	2.485	prophage P2a protein 40; major capsid protein	Intracellular	38.1
<i>lp_2793</i>	3.150	Unknown	Intracellular	76.3
<i>lp_2988</i>	7.437	extracellular zinc metalloproteinase, M10 family (putative)	Intracellular	28.1
<i>lp_3170</i>	2.172	phosphoglycerate mutase family protein	Intracellular	26.1

<i>lp_3614</i>	462.380	Oxidoreductase	Intracellular	33.4
<i>lp_0625</i>	2.397	prophage P1 protein 2, mitogenic factor, cell surface lipoprotein	Lipid anchored	41.8
<i>lp_0689</i>	2.187	cell surface protein, lipoprotein precursor	Lipid anchored	23.1
<i>lp_1072</i>	43.973	thiamin biosynthesis lipoprotein ApbE	Lipid anchored	34.6
<i>lp_1609</i>	4.847	glycine betaine/carnitine/choline ABC transporter, substrate binding protein	Lipid anchored	53.9
<i>lp_3686</i>	69.772	ABC transporter, substrate binding protein	Lipid anchored	60.5
<i>lp_0197</i>	3.233	cell surface protein precursor	LPxTG Cell-wall anchored	105.2
<i>lp_0800</i>	10.941	cell surface protein precursor	LPxTG Cell-wall anchored	226.4
<i>lp_0923</i>	3.653	cell surface protein precursor	LPxTG Cell-wall anchored	83.3
<i>lp_0946</i>	2.707	mucus-binding protein (putative)	LPxTG Cell-wall anchored	37.7
<i>lp_1643</i>	4.321	mucus binding protein precursor	LPxTG Cell-wall anchored	22.2
<i>lp_2925</i>	9.621	cell surface protein precursor	LPxTG Cell-wall anchored	89.5
<i>lp_2940</i>	11.259	cell surface protein precursor	LPxTG Cell-wall anchored	44.3
<i>lp_3114</i>	8.059	mucus-binding protein (putative)	LPxTG Cell-wall anchored	214.8
<i>lp_0802</i>	4.387	polar amino acid ABC transporter, substrate binding and permease protein	Multi-transmembrane	52.3
<i>lp_0856</i>	3.466	acyltransferase (putative)	Multi-transmembrane	74.4
<i>lp_2914</i>	2.922	integral membrane protein	Multi-transmembrane	66.8
<i>lp_0043</i>	2.774	serine protease HtrA	N-terminally anchored	43.1
<i>lp_0542</i>	40.886	septum formation initiator	N-terminally anchored	15.2
<i>lp_0593</i>	2.916	transcriptional attenuator, cell envelope-related, LytR family	N-terminally anchored	43.6
<i>lp_0600</i>	4.196	extracellular zinc metalloproteinase, M10 family (putative)	N-terminally anchored	26.5
<i>lp_0628</i>	4.558	prophage P1 protein 5, superinfection exclusion (cell surface N-anchored)	N-terminally anchored	37.9
<i>lp_0688</i>	2.626	DNA entry nuclease	N-terminally anchored	36.2
<i>lp_0746</i>	20.051	phosphate ABC transporter, substrate binding protein	N-terminally anchored	31.5
<i>lp_1568</i>	4.064	transpeptidase (penicillin binding protein 2B)	N-terminally anchored	34.8
<i>lp_1751</i>	31.422	transpeptidase-transglycosylase (penicillin binding protein 1A)	N-terminally anchored	50.0
<i>lp_2737</i>	16.042	cell surface hydrolase, DUF915 family, membrane-bound (putative)	N-terminally anchored	29.7
<i>lp_2809</i>	9.599	extracellular protein (putative)	N-terminally anchored	23.2

<i>lp_2812</i>	4.905	extracellular protein, membrane-anchored (putative)	N-terminally anchored	28.5
<i>lp_2845</i>	13.153	extracellular transglycosylase (putative)	N-terminally anchored	30.7
<i>lp_3014</i>	3.529	extracellular transglycosylase (putative)	N-terminally anchored	21.3
<i>lp_3093</i>	4.562	muramidase (putative)	N-terminally anchored	89.6
<i>lp_3411</i>	9.962	extracellular protein, DUF1002 family	N-terminally anchored	34.2
<i>lp_3421</i>	3.818	extracellular protein, gamma-D-glutamate-meso-diaminopimelate muropeptidase (putative)	N-terminally anchored	36.8
<i>lp_0092</i>	29.929	ABC transporter, substrate binding protein, oligopeptide	Secretory(released)	59.8
<i>lp_0141</i>	6.321	extracellular protein	Secretory(released)	28.6
<i>lp_0302</i>	3.404	extracellular transglycosylase (putative)	Secretory(released)	26.3
<i>lp_0304</i>	5.058	extracellular transglycosylase (putative)	Secretory(released)	22.1
<i>lp_0924</i>	4.442	extracellular protein	Secretory(released)	68.6
<i>lp_1697</i>	19.569	adherence protein, chitin-binding domain	Secretory(released)	31.6
<i>lp_2541</i>	2.890	ABC transporter, substrate binding protein	Secretory(released)	35.0
<i>lp_2978</i>	2.253	extracellular protein	Secretory(released)	25.5
<i>lp_3189</i>	3.826	serine-type D-Ala-D-Ala carboxypeptidase	Secretory(released)	47.0
<i>lp_3412</i>	4.978	extracellular protein	Secretory(released)	118.7
<i>lp_3414</i>	3.493	extracellular protein	Secretory(released)	27.4
<i>lp_3676</i>	12.665	extracellular protein	Secretory(released)	56.8
<i>lp_2960</i>	4.815	lipase/esterase, subfamily of SGNH-hydrolases	transmembrane	25.5

^a FDR Relative abundances were calculated by the ratio of Label-free quantitation (LFQ) of detected peptides in wild type and *lgt* mutant.