Supplementary materials

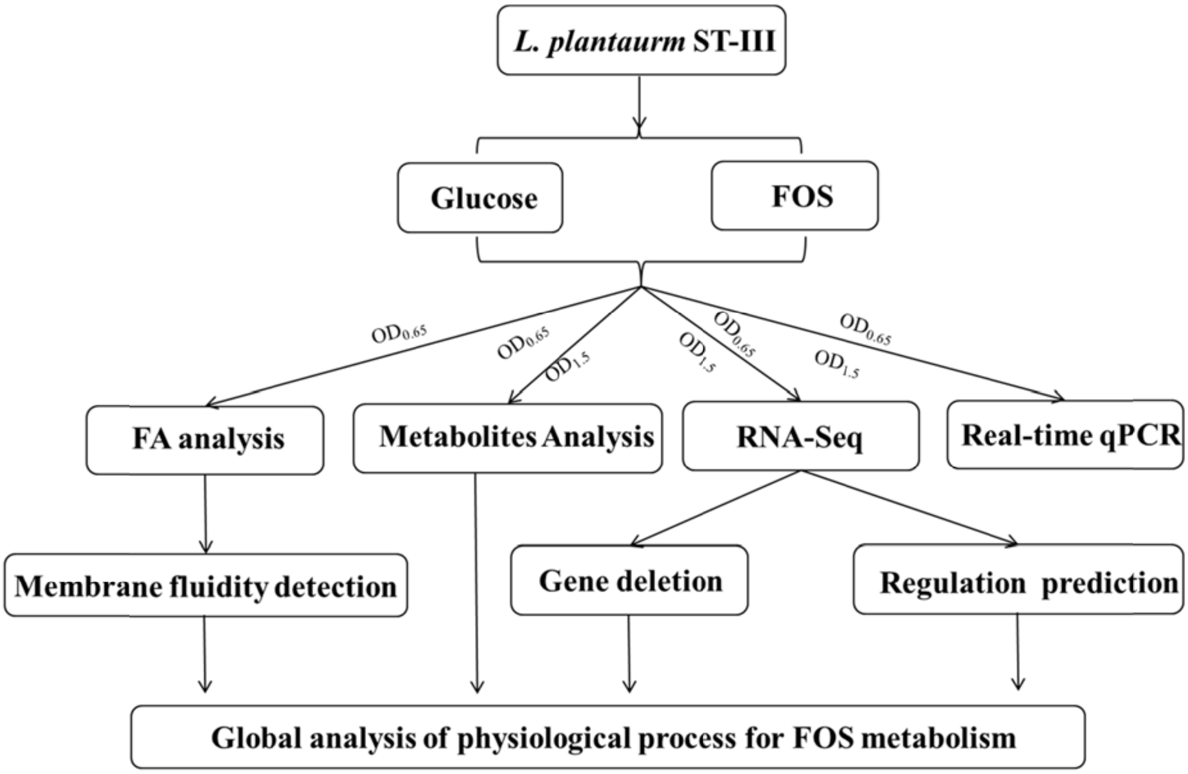

Fig. S1 Work flow of the transcriptomic and physiological analysis of FOS metabolism in *Lactobacillus plantarum* ST-III

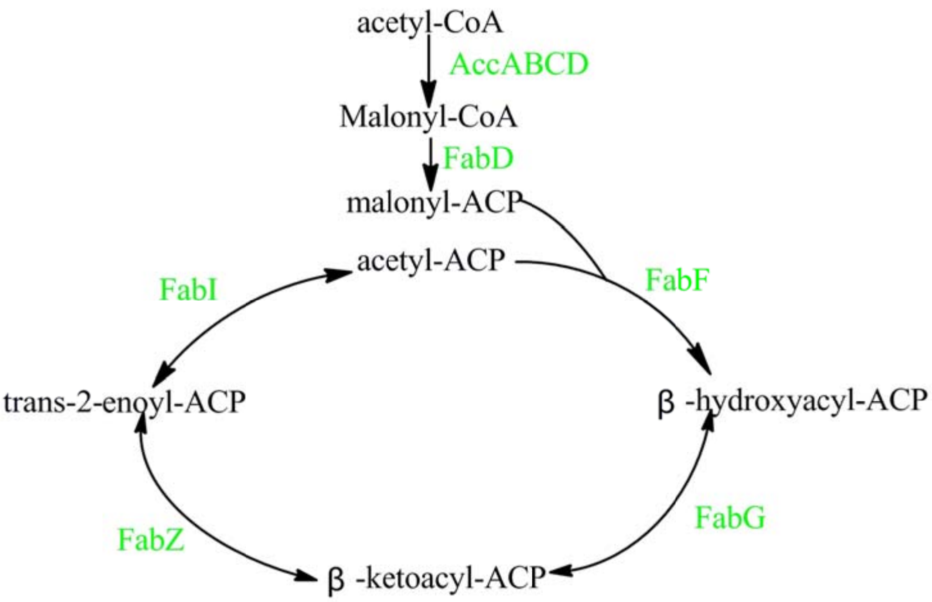

Fig. S2 The down-regulated genes related to fatty acids biosynthesis for *L. plantarum* ST-III grown in the presence of FOS versus glucose. Genes that are up-regulated are in green color. CoA, coenzyme A; ACP, acyl carrier protein; AccABCD, Acetyl-CoA carboxylase; FabD, ACP-S-malonyltransferase; FabI, enoyl-ACP reductase; FabF, 3-oxoacyl-ACP synthase II; FabZ, (3R)-hydroxymyristoyl-ACP dehydratase; FabG, 3-oxoacyl-ACP reductase.

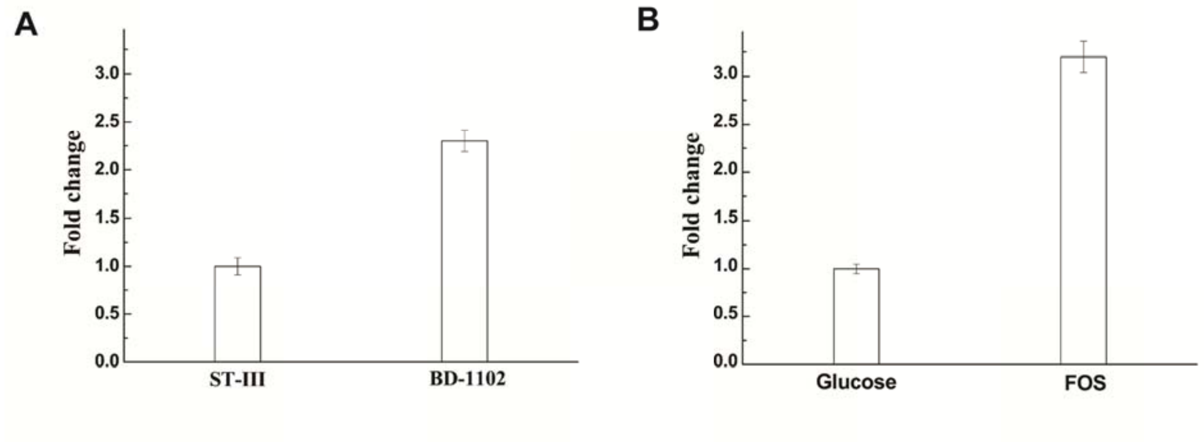

Fig. S3 The relative gene expression of *pts26* in BD1102 mutant grown on FOS compared with ST-III grown on FOS (A) and the value obtained in BD1102 mutant grown on FOS compared with glucose (B).

Table S1 Primers used in the mutants construction

ID	Primer	Sequence (5’ to 3’)	Reference
A	*sacA* upstream F	GTGAACGTAAAGTCAAATGCACC	This work
B	*sacA* upstream R	TACGATTCCATATCATGACGATGAG	This work
C	*sacA* downstream F	ATACTGGAGTCGATAACAATGAAACC	This work
D	*sacA* downstream R	CGGTTGTTCTACTGTTGTTAATTCAG	This work
E	*pts1* upstream F	GATGATTCATAATAATTCACTCCCTGAG	This work
F	*pts1* upstream R	TGGTCAGATCCTTTGAGAAATAAAC	This work
G	*pts1* downstream F	TTAAAGCAGCCTGAGCTAACAATAG	This work
H	*pts1* downstream R	CTGCTACAGCGATATAAAACGATCT	This work
I	*pts26* upstream F	CAATAATTTTTTTCGCAAGTACCTG	This work
J	*pts26* upstream R	ATGACCAACTTGGACAATTTATTGG	This work
K	*pts26* downstream F	TTCACATTGTTCGCCATAAGACTC	This work
L	*pts26* downstream R	CTGCAACAGCATCCTAAACGTAAG	This work
M	*sacA*-outI	CGACTGGGAAGATAAAAGAACCT	This work
N	*sacA*-outII	TAAGGCCCTTGATGAGCTTAACT	This work
O	*pts1*-outI	GTTTGTGATAACCCTTGGGGAC	This work
P	*pts1*-outII	TCATTAACCGAATGACAAATTGACT	This work
Q	*pts26*-outI	CGACCTGGTATTGAAAAGTTCTTAG	This work
R	*pts26*-outII	AAACCTATACCACCGATTTGTTAAG	This work
S	85	GTTTTTTTCTAGTCCAAGCTCACA	(1)
T	87	GCCGACTGTACTTTCGGATCCT	(1)

Table S2 Primers and the results of RT-qPCR

Gene	Locus	Primer	Sequence (5’ to 3’)	Products (bp)	Fold Change	
					OD=0.65	OD=1.5
sacK1	LPST_C0151	F	TTTAATGGTCGCACTCATACTGAAC	116	28.74	20.75
		R	CCAGCAGCTAAACCTTCTAAACAG			
pts1	LPST_C0152	F	CGGAATTACGGAACCTGCTAT	187	24.15	15.32
		R	CATGAATGCTGGAATCGACTT			
sacA	LPST_C0153	F	GGATGGACACGGATAATCACATT	177	4.04	2.56
		R	TTGAGAAATAAACCAAGATAGCACC			
sacR	LPST_C0154	F	ACGGTCTTCCGATTATTTCATT	196	6.11	5.42
		R	AAGTAGGCTTCATATCCTTCACG			
agl2	LPST_C0155	F	CTATCAGGTCTATCCACGGAGTT	143	4.36	5.23
		R	CGTTGGGTGAACGATAAATGG			
ack2	LPST_C0255	F	GTCAGGGTTACTTGGTATTTCAGG	156	6.12	8.24
		R	TCAATCCCGTTCATTTCAGCA			
pta	LPST_C0630	F	TTTTGAAGCGGTGGGTCCTGT	120	3.32	4.23
		R	GCTAATCCTTGGGCTGCTGTAAT			
pox2	LPST_C0667	F	ATCGGCGTTTCATTTGGTTCT	130	2.23	2.17
		R	TCGTGTTCATCGTCGCTTGTG			
IdhL1	LPST_C1774	F	TACGCCCAGACACCGTTTATC	133	2.95	4.14
		R	ATAGCACCATATCCGCCATTC			
pdhD	LPST_C1775	F	TCTTGAAGGGACACCGCAAAT	153	25.21	24.22
		R	GCGTAGGTAACCGTAACACCACTATC			
pdhC	LPST_C1776	F	TGCCAAAGAAATTACTGACAATACG	173	45.21	20.12
		R	TACCGATACGCCCAACACCT			
pdhB	LPST_C1777	F	TGCGATTCAAGAAGCACAACG	132	30.19	25.84
		R	CCGAATGGGTAGACCGTATCTG			
pdhA	LPST_C1778	F	TTAATGCCTGCTTACCGTGAT	145	22.55	21.23
		R	CGCCGATAATAATCTGTGGTG			
pox3	LPST_C2161	F	GCACCATCATTTGGATTTCGG	130	5.73	15.63
		R	TTTCCAGTCAGCCATATCTGCT			
pgb6	LPST_C2478	F	TCCTGCGACAGCAACCACTTC	166	2.40	1.97
		R	CCCAGCGGCATTAAACTCACC			

Gene	Locus	Primer	Sequence (5’ to 3’)	Products (bp)	Fold Change	
					OD=0.65	OD=1.5
pgb1	LPST_C2580	F	CTGCTCATCAGTTTGAGGGTG	143	7.15	4.46
		R	CGCCTCGTGATTTGGATAGTT			
pts26	LPST_C2650	F	TTTTAACCAGTGGGATAGGTGC	137	2.33	3.32
		R	CGAGACGACCGTATAAATCAGC			
agl4	LPST_C2651	F	GGCTCTAAGGAAACGAATCTATC	142	2.40	2.93
		R	ACCTAACCCATCAACACCATC			
sacR2	LPST_C2652	F	AAACGGATACGGGTTTCAAGT	162	4.41	4.99
		R	TTAGCATACGTCGCCGACAAT			
pflB2	LPST_C2728	F	CCCACATTGGTGATGGTGAAT	132	7.06	4.21
		R	TTGCAGGCTTGCTAATATCGT			
pflA2	LPST_C2729	F	GGATTCGTCACGTCCTGGTTC	130	27.78	21.25
		R	CCCAAAGTATGGTACGGCAAT			
pox5	LPST_C2933	F	GACGCATTATCAGCAGAAAGG	189	11.39	24.31
		R	AACAGGGACATGGTCTTCACG			
srlR2	LPST_C2986	F	AATCATTGGCTGTGAGTCGTG	194	3.38	4.73
		R	ATCCCAGGTTGCTTCCAGTTC			
srlD2	LPST_C2987	F	AGTGTTTATTCAGCAACTAAGGGAG	166	2.03	1.98
		R	TATGCCGGGTATAAGCTAACG			
fabZ1	LPST_C1327	F	TGTCCGTCCCGGTGATGTCTT	113	0.11	0.23
		R	CAGTTGTGCAGGCTGCCTTGT			
fabH2	LPST_C1328	F	AATCATTGGCTGTGAGTCGTG	194	0.15	0.08
		R	ATCCCAGGTTGCTTCCAGTTC			
acpA2	LPST_C1329	F	GATGATCGTGGAACAATTAGACGT	175	0.15	0.20
		R	AACTAAATCACCAACCGTGGC			
fabD	LPST_C1330	F	ACTTTGCGGCCTGCTTACAAC	185	0.07	0.10
		R	TCCACGCTCACGTACCTCCTC			
fabG1	LPST_C1331	F	CACTGGAGCTGCTAAGGGTATTG	153	0.06	0.16
		R	TCACCAACTAATTGCGTCAACC			
fabF	LPST_C1332	F	TAGTAACGCCAGCAACTCAACATC	101	0.13	0.21
		R	CACCCACTTCTTAAAGGCAACC			
accB2	LPST_C1333	F	ACTTAGCTGCCGACCCGAAAC	125	0.07	0.15
		R	CCCACTAACTGGGCTAGGGACTT			

Gene	Locus	Primer	Sequence (5’ to 3’)	Products (bp)	Fold Change	
					OD=0.65	OD=1.5
fabZ2	LPST_C1334	F	CCGTATCGTAGCGGTCCAACC	154	0.08	0.16
		R	TAAAGCCACAACTCCCGTTTG			
accC2	LPST_C1335	F	CCGTATCGTAGCGGTCCAACC	154	0.13	0.21
		R	TAAAGCCACAACTCCCGTTTG			
accD2	LPST_C1336	F	TTTCAAGCACCCACTGAACGG	159	0.09	0.10
		R	AGCAGGCAAGCGAAACCCAT			
accA2	LPST_C1337	F	ATGCGGAATATGAGGGACAAGG	116	0.11	0.12
		R	TAATGCACCACCACTGCCACC			
fabI	LPST_C1338	F	AAGTTTACAGCGGTTTGTTGCG	200	0.11	0.13
		R	CCAAATCATATCCAGCTTTCGTG			
-	LPST_C1339	F	TGGACGGCTAAAGAAGCGGTAT	148	0.12	0.19
		R	GAGTCGCAGGCAATTCTAACG			
-	LPST_C1340	F	CACGGTTTGTCAAAGCACCAG	179	0.23	0.18
		R	TACCGCAGCAAAGAAGTCCAG			
-	LPST_C1341	F	TGCTGAATCAGGGTGATGGTG	183	0.18	0.17
		R	GGCTATACTTCGTCGCAAACG			
-	LPST_C1342	F	GCTGATTTGAATGAGCACGACA	104	0.24	0.25
		R	ACCGTCTCAATTCGAGCCACT			

Table S3 Summary of the RNA-seq data

	FOS	Glucose
Average read length	101 bp	101 bp
Number of reads	27,107,812	17,145,874
Number of mappable reads	26,497,608	16,941,988
Sequencing depth	524 fold	827 fold
Map-rate	0.97749	0.988109

Table S4 The up-regulated genes for *L.plantarum* ST-III grown in the presence of FOS versus glucose

COG	Locus	Gene	Products	Fold Change
[G]	LPST_C0019	glgC	glucose-1-phosphate adenylyltransferase	2.00
[G]	LPST_C0021	glgA	starch synthase	2.12
[K]	LPST_C0037	-	transcription regulator	2.20
[TQ]	LPST_C0052	-	hypothetical protein	2.60
[CR]	LPST_C0068	-	oxidoreductase	2.22
	LPST_C0077	-	hypothetical protein	3.03
[R]	LPST_C0086	-	phosphoribosylaminoimidazole carboxylase catalytic subunit	3.15
[H]	LPST_C0092	thiM	hydroxyethylthiazole kinase	4.29
[H]	LPST_C0093	thiD	phosphomethylpyrimidine kinase	3.19
[H]	LPST_C0094	thiE	thiamine-phosphate diphosphorylase	3.46
[F]	LPST_C0095	-	purine-cytosine transport protein	2.75
[KT]	LPST_C0108	-	hypothetical protein	3.01
[S]	LPST_C0115	-	hypothetical protein	2.51
	LPST_C0116	-	extracellular protein	2.04
[K]	LPST_C0123	-	hypothetical protein	5.57
	LPST_C0124	-	hypothetical protein	4.04
	LPST_C0125	-	hypothetical protein	6.15
[S]	LPST_C0137	-	hypothetical protein	2.98
[G]	LPST_C0138	gplF2	glycerol uptake facilitator protein	2.13
[K]	LPST_C0140	-	transcription regulator	2.51
[G]	LPST_C0143	malF	maltose/maltodextrin ABC transporter, permease protein	2.63
[G]	LPST_C0146	amy2	alpha-amylase	2.13
[G]	LPST_C0148	map2	maltose phosphorylase	2.01
[KG]	LPST_C0151	sacK1	fructokinase	34.90
[G]	LPST_C0152	pts1	sucrose PTS, EIIBCA	26.29
[G]	LPST_C0153	sacA	beta-fructofuranosidase	4.05
[K]	LPST_C0154	sacR	sucrose operon repressor	6.99
[G]	LPST_C0155	agl2	alpha-glucosidase	7.60

COG	Locus	Gene	Products	Fold Change
[G]	LPST_C0157	agl3	alpha-glucosidase	4.94
[P]	LPST_C0177	-	ABC transporter, permease protein	2.44
[P]	LPST_C0178	-	ABC transporter, ATP-binding protein	3.78
[S]	LPST_C0179	-	ABC transporter subunit (putative)	3.04
[K]	LPST_C0188	mtlR	transcription regulator	2.05
[G]	LPST_C0189	pts2A	mannitol PTS, EIIA	3.30
[G]	LPST_C0190	mtlD	mannitol-1-phosphate 5-dehydrogenase	3.08
	LPST_C0195	-	hypothetical protein	19.20
[F]	LPST_C0196	ndk	nucleoside-diphosphate kinase	3.51
[S]	LPST_C0202	-	hypothetical protein	2.79
[E]	LPST_C0209	cysK	cysteine synthase	2.12
[G]	LPST_C0217	-	beta-glucosides PTS, EIIABC	2.07
[G]	LPST_C0218	-	beta-glucosides PTS, EIIABC	2.02
	LPST_C0221	-	hypothetical protein	5.76
[G]	LPST_C0234	pts6C	cellobiose PTS, EIIC	5.26
	LPST_C0247	-	CAAX family protease	2.17
[C]	LPST_C0255	ack2	acetate kinase	6.36
[R]	LPST_C0282	-	integral membrane protein	2.90
[Q]	LPST_C0299	sufI	cell division protein SufI	3.29
[IQR]	LPST_C0307	-	short chain dehydrogenase/reductase family oxidoreductase	2.01
[C]	LPST_C0312	glpK	glycerol kinase	16.95
[C]	LPST_C0313	glpD	glycerol-3-phosphate dehydrogenase	44.55
[G]	LPST_C0314	glpF3	glycerol uptake facilitator protein	33.70
[R]	LPST_C0327	thgA1	galactoside O-acetyltransferase	2.37
[GEPR]	LPST_C0328	-	transport protein	2.60
[R]	LPST_C0329	-	HAD superfamily hydrolase	2.50
[R]	LPST_C0331	-	HAD superfamily hydrolase	2.12
[G]	LPST_C0363	pts7C	cellobiose PTS, EIIC	2.98
	LPST_C0364	-	hypothetical protein	9.17
	LPST_C0365	-	hypothetical protein	4.39
[G]	LPST_C0366	pts8C	cellobiose PTS, EIIC	2.09
	LPST_C0393	-	integral membrane protein	2.69
[J]	LPST_C0408	serS1	serine--tRNA ligase	3.78

COG	Locus	Gene	Products	Fold Change
[P]	LPST_C0543	phnE1	phosphonates ABC transporter, permease protein	2.43
[L]	LPST_C0562	comFA	ATP-dependent DNA helicase/translocase (putative)	2.01
[R]	LPST_C0563	-	late competence protein	2.56
	LPST_C0620	secG	preprotein translocase subunit SecG	2.55
	LPST_C0624	-	cell surface protein	2.03
[L]	LPST_C0629	ung	uracil-DNA glycosylase	2.42
[C]	LPST_C0630	pta	phosphotransacetylase	2.90
[EH]	LPST_C0667	pox2	putative pyruvate oxidase	2.63
	LPST_C0672	-	probable organic hydroperoxide resistance protein	3.19
	LPST_C0673	-	transposase	2.18
[G]	LPST_C0691	-	PTS, EIIA (putative)	9.18
[K]	LPST_C0692	bglG1	transcription antiterminator	12.27
[G]	LPST_C0693	-	beta-glucosides PTS, EIIBC	5.41
[S]	LPST_C0694	-	hypothetical protein	7.43
[G]	LPST_C0712	pbg2	6-phospho-beta-glucosidase	2.42
[K]	LPST_C0726	-	transcription regulator	5.62
[C]	LPST_C0763	-	fumarate reductase, flavoprotein subunit precursor	2.51
[EH]	LPST_C0807	als	acetolactate synthase	2.81
[C]	LPST_C0855	ndh2	NADH dehydrogenase	2.32
	LPST_C0866	-	hypothetical protein	3.05
[C]	LPST_C0897	mleS	malate dehydrogenase	2.35
[R]	LPST_C0898	mleP2	malate transport protein	3.14
[C]	LPST_C0903	cydA	cytochrome D ubiquinol oxidase, subunit I	2.25
	LPST_C0907	-	hypothetical protein	2.12
	LPST_C0939	-	hypothetical protein	3.93
[V]	LPST_C0942	pbpX1	serine-type D-Ala-D-Ala carboxypeptidase	3.86
[D]	LPST_C0960	cps2B	exopolysaccharide biosynthesis protein; chain length determinator Wzz	3.15
[GM]	LPST_C0961	cps2C	exopolysaccharide biosynthesis protein	8.66
[MG]	LPST_C0962	galE2	UDP-glucose 4-epimerase	2.47
	LPST_C0976	-	hypothetical protein	2.46
	LPST_C0981	-	hypothetical protein	2.60
[R]	LPST_C0983	cps3A	glycosyltransferase	2.01
[GE]	LPST_C1013	gntP	gluconate transport protein	3.09

COG	Locus	Gene	Products	Fold Change
[G]	LPST_C1014	gntK	gluconokinase	2.74
[G]	LPST_C1015	gnd1	6-phosphogluconate dehydrogenase-like protein	2.17
	LPST_C1056	sdr	cell surface SD repeat-containing protein	2.66
[G]	LPST_C1070	-	ABC superfamily ATP binding cassette transporter, membrane protein	2.70
[V]	LPST_C1078	-	ABC superfamily ATP binding cassette transporter, ABC protein	2.36
[R]	LPST_C1085	-	cof family hydrolase	3.25
	LPST_C1090	-	extracellular protein, membrane-anchored	3.11
[P]	LPST_C1111	-	sodium/sulfate symport protein (putative)	3.13
[KT]	LPST_C1119	-	transcription regulator levR	2.30
	LPST_C1138	-	hypothetical protein	2.58
[K]	LPST_C1140	-	transcription regulator	2.06
[S]	LPST_C1147	-	DedA protein (DSG-1 protein)	2.02
	LPST_C1161	-	extracellular protein	2.03
	LPST_C1163	-	cell surface protein precursor	3.03
	LPST_C1164	-	extracellular protein	2.50
[L]	LPST_C1199	cshA1	crossover junction endodeoxyribonuclease	2.39
[M]	LPST_C1201	racD	aspartate racemase	2.10
[M]	LPST_C1202	ica1	glycosyltransferase	2.30
[H]	LPST_C1220	-	prenyltransferase	2.02
[C]	LPST_C1225	-	acylphosphatase	2.93
[S]	LPST_C1237	-	hypothetical protein	6.88
[E]	LPST_C1250	glnA	glutamate--ammonia ligase	2.04
[K]	LPST_C1257	-	transcription regulator	2.07
[E]	LPST_C1315	trpF	phosphoribosylanthranilate isomerase	5.06
[GEPR]	LPST_C1345	-	EmrB/QacA family drug resistance transporter	2.22
[G]	LPST_C1383	map3	maltose phosphorylase	2.61
[G]	LPST_C1384	galM2	aldose 1-epimerase	2.32
[P]	LPST_C1399	-	ABC transporter, permease protein	2.30
	LPST_C1408	-	hypothetical protein	9.60
	LPST_C1409	-	glycosyltransferase	4.12
[G]	LPST_C1429	pgm5	phosphoglycerate mutase (putative)	2.27
[R]	LPST_C1437	-	ABC transporter, permease protein	2.25

COG	Locus	Gene	Products	Fold Change
[S]	LPST_C1442	-	integral membrane protein	2.17
	LPST_C1448	-	hypothetical protein	3.24
[C]	LPST_C1464	gshR3	glutathione reductase	2.17
	LPST_C1465	-	integral membrane protein	4.26
[M]	LPST_C1466	-	glycosyltransferase (putative)	2.55
[E]	LPST_C1488	-	hypothetical protein	2.18
[K]	LPST_C1489	-	transcription regulator	2.16
	LPST_C1502	-	hypothetical protein	3.24
[R]	LPST_C1506	-	possible sugar-phosphatase	2.91
[G]	LPST_C1535	pps	phosphoenolpyruvate synthase	2.29
[K]	LPST_C1537	-	transcription regulator	2.06
[P]	LPST_C1542	mntA	cadmium-/manganese-transporting P-type ATPase	2.02
[G]	LPST_C1543	eno	phosphopyruvate hydratase	2.02
[KG]	LPST_C1548	-	transcription regulator	2.25
	LPST_C1551	-	hypothetical protein	11.22
[K]	LPST_C1556	-	transcription regulator	2.18
[MG]	LPST_C1558	-	NAD-dependent epimerase/dehydratase	3.16
[K]	LPST_C1560	-	transcription regulator	2.45
[TK]	LPST_C1564	rrp6	response regulator	2.37
	LPST_C1570	-	transcription regulator	3.59
[IQ]	LPST_C1611	dltC1	D-alanine--poly(phosphoribitol) ligase subunit 2	2.18
[V]	LPST_C1615	pbpX2	serine-type D-Ala-D-Ala carboxypeptidase	2.35
	LPST_C1650	-	hypothetical protein	2.33
[GEPR]	LPST_C1717	-	integral membrane protein	2.23
	LPST_C1733	cps4H	polysaccharide polymerase	2.30
[M]	LPST_C1735	cps4F	glycosyltransferase	2.30
[M]	LPST_C1736	cps4E	priming glycosyltransferase	7.10
[GEPR]	LPST_C1754	-	multidrug transport protein	2.72
[G]	LPST_C1772	suhB	myo-inositol-1(or 4)-monophosphatase	2.64
[S]	LPST_C1773	-	hypothetical protein	2.08
	LPST_C1774	ldhL1	possible malate/lactate dehydrogenase	2.81
[C]	LPST_C1775	pdhD	dihydrolipoamide dehydrogenase	33.46
[C]	LPST_C1776	pdhC	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase	47.18

COG	Locus	Gene	Products	Fold Change
[C]	LPST_C1777	pdhB	pyruvate dehydrogenase complex, E1 component, beta subunit	33.23
[C]	LPST_C1778	pdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit	24.46
	LPST_C1784	-	hypothetical protein	2.01
[G]	LPST_C1834	-	hypothetical protein	2.42
[R]	LPST_C1841	coiA	competence protein	2.19
[P]	LPST_C1843	nrpR3	negative regulator of proteolysis	2.29
	LPST_C1847	-	hypothetical protein	2.67
[NU]	LPST_C1863	comGB	ComG operon protein 2	3.34
[G]	LPST_C1936	treC	oligo-1,6-glucosidase (oligosaccharide alpha-1,6-glucosidase)	2.12
[G]	LPST_C1940	-	PTS family mannose/fructose/sorbose porter component IIB	5.84
[J]	LPST_C1961	-	ribosomal protein acetylating enzyme	2.08
[M]	LPST_C1962	murA2	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	2.33
[G]	LPST_C1982	pmi	mannose-6-phosphate isomerase	2.22
	LPST_C1990	-	hypothetical protein	2.14
	LPST_C2004	-	prophage major tail protein	2.48
	LPST_C2025	-	prophage Lp2 protein 24	3.90
	LPST_C2026	-	prophage Lp2 protein 23	2.14
	LPST_C2027	-	prophage Lp1 protein 22	3.96
	LPST_C2029	-	prophage Lp2 protein 20	2.39
[E]	LPST_C2041	-	hypothetical protein	2.20
	LPST_C2051	-	hypothetical protein	3.27
[V]	LPST_C2059	-	ABC superfamily ATP binding cassette transporter, ATP-binding and permease protein	2.13
	LPST_C2085	-	hypothetical protein	2.52
[R]	LPST_C2097	npr2	NADH peroxidase	3.71
[E]	LPST_C2103	hisE	phosphoribosyl-ATP pyrophosphatase	5.40
	LPST_C2129	-	cell surface protein precursor	2.26
[G]	LPST_C2134	-	sugar transport protein	2.75
[G]	LPST_C2139	tal1	fructose-6-phosphate aldolase	2.61
[R]	LPST_C2140	-	HAD superfamily hydrolase	2.33

COG	Locus	Gene	Products	Fold Change
[K]	LPST_C2153	-	transcription regulator	3.04
	LPST_C2157	-	transcription regulator	3.42
	LPST_C2159	-	hypothetical protein	2.62
	LPST_C2160	-	acetyltransferase (putative)	2.43
[EH]	LPST_C2161	pox3	pyruvate oxidase	6.35
[H]	LPST_C2172	lplA1	lipoate-protein ligase	2.03
[G]	LPST_C2174	-	N-acetylglucosamine/galactosamine PTS, EIIA	5.41
[G]	LPST_C2175	-	N-acetylgalactosamine-specific PTS system transporter subunit IID	4.96
[G]	LPST_C2176	-	N-acetylgalactosamine PTS, EIIC	3.74
[G]	LPST_C2177	-	N-acetylgalactosamine-specific PTS system transporter subunit IIB	3.10
[E]	LPST_C2206	araT2	aromatic amino acid specific aminotransferase	2.07
[EF]	LPST_C2221	pyrAA	carbamoyl phosphate synthase small subunit	2.55
[E]	LPST_C2232	-	hypothetical protein	2.44
[R]	LPST_C2242	-	NADPH-dependent FMN reductase domain protein	3.43
[T]	LPST_C2255	-	universal stress protein UspA	2.05
[G]	LPST_C2265	-	glucan 1,4-alpha-maltohydrolase	4.08
[R]	LPST_C2275	-	acetyltransferase (putative)	2.64
[E]	LPST_C2282	dsdA	D-serine ammonia-lyase	2.50
[G]	LPST_C2283	pbg4	6-phospho-beta-glucosidase	8.87
[G]	LPST_C2284	pbg5	6-phospho-beta-glucosidase	7.19
[G]	LPST_C2286	-	cellobiose PTS, EIIA	2.75
[K]	LPST_C2288	-	transcription regulator	3.79
[R]	LPST_C2291	-	HAD superfamily hydrolase	3.91
[E]	LPST_C2300	aroC1	3-dehydroquinate dehydratase	2.58
[E]	LPST_C2301	-	amino acid transport protein	5.26
[S]	LPST_C2311	-	hypothetical protein	2.10
	LPST_C2322	-	integral membrane protein	2.94
[J]	LPST_C2329	-	ribosomal protein acetylating enzyme	2.30
[MG]	LPST_C2375	-	oxidoreductase	2.24
[P]	LPST_C2424	-	transport protein	2.59
[S]	LPST_C2427	-	hypothetical protein	2.05
[K]	LPST_C2439	-	transcription regulator	3.56

COG	Locus	Gene	Products	Fold Change
[G]	LPST_C2445	-	PTS family N-acetylglucosamine porter, IIABC component	4.98
[E]	LPST_C2455	livD	branched-chain amino acid ABC transporter, ATP-binding protein	2.29
[E]	LPST_C2456	livC	branched-chain amino acid ABC superfamily ATP binding cassette transporter, permease protein	2.20
[G]	LPST_C2476	-	cellobiose PTS, EIIB	4.86
[G]	LPST_C2477	-	cellobiose PTS, EIIC	4.49
[G]	LPST_C2478	pbg6	6-phospho-beta-glucosidase	2.51
	LPST_C2483	-	integral membrane protein	2.31
	LPST_C2499	-	hypothetical protein	2.95
[P]	LPST_C2514	copA	P-ATPase superfamily P-type ATPase copper transporter	2.23
[R]	LPST_C2533	-	HAD superfamily hydrolase	2.14
[C]	LPST_C2541	gabD	succinate-semialdehyde dehydrogenase (NAD(P)+)	2.48
[R]	LPST_C2542	-	muramidase (putative)	2.02
[S]	LPST_C2549	-	integral membrane protein	2.71
[R]	LPST_C2562	-	hypothetical protein	3.50
[IQR]	LPST_C2563	-	short-chain dehydrogenase/oxidoreductase	2.41
[M]	LPST_C2570	lepA2	GTP-binding protein LepA	2.10
[K]	LPST_C2574	-	transcription regulator	2.29
[G]	LPST_C2580	pbg1	6-phospho-beta-glucosidase	7.75
[G]	LPST_C2581	celD	cellobiose PTS, EIIC	6.57
	LPST_C2582	-	hypothetical protein	5.65
[KE]	LPST_C2641	-	aminotransferase	2.33
[K]	LPST_C2647	-	transcription regulator (putative)	3.65
[G]	LPST_C2650	pts26	sucrose PTS, EIIBCA	2.17
[G]	LPST_C2651	agl4	alpha-glucosidase	2.08
[K]	LPST_C2652	sacR2	transcription regulator	4.80
[G]	LPST_C2663	-	phosphotransferase system fructose-specific component IIA	2.13
[GT]	LPST_C2666	mtlR	transcription regulator, mannitol operon	3.01
[MG]	LPST_C2668	-	oxidoreductase	2.90
	LPST_C2678	-	hypothetical protein	4.98

COG	Locus	Gene	Products	Fold Change
	LPST_C2712	-	hypothetical protein	5.16
[C]	LPST_C2728	pflB2	formate C-acetyltransferase	7.90
[O]	LPST_C2729	pflA2	formate acetyltransferase activating enzyme	27.23
[R]	LPST_C2731	-	hypothetical protein	2.39
[R]	LPST_C2732	-	oxidoreductase	3.60
[S]	LPST_C2762	-	integral membrane protein	5.33
[S]	LPST_C2763	-	integral membrane protein	3.82
	LPST_C2796	-	transcription regulator (putative)	2.26
[C]	LPST_C2797	pck	phosphoenolpyruvate carboxykinase (ATP)	3.68
[G]	LPST_C2814	glpF5	glycerol uptake facilitator protein	2.99
[OC]	LPST_C2815	-	thioredoxin	2.23
	LPST_C2826	-	extracellular protein	2.67
	LPST_C2827	-	cell surface protein precursor	5.03
[GEPR]	LPST_C2843	-	sugar transport protein	3.21
	LPST_C2844	ram2	alpha-L-rhamnosidase (putative)	2.32
[M]	LPST_C2851	galE4	UDP-glucose 4-epimerase	2.06
[G]	LPST_C2852	galK	galactokinase	2.53
[G]	LPST_C2853	lacL	beta-galactosidase large subunit	3.84
[G]	LPST_C2854	lacM	beta-galactosidase, small subunit	2.88
[G]	LPST_C2857	galM3	aldose 1-epimerase	3.58
[C]	LPST_C2859	-	oxidoreductase	2.18
[R]	LPST_C2868	est2	acetylesterase	2.40
[G]	LPST_C2870	-	cellobiose PTS, EIIC	2.06
[R]	LPST_C2871	-	N-acetylmuramic acid 6-phosphate etherase	2.08
[G]	LPST_C2872	-	N-acetylglucosamine kinase (putative)	2.08
[G]	LPST_C2875	-	beta-glucosides PTS, EIIBCA	2.13
[K]	LPST_C2876	bglG4	transcription antiterminator	2.42
[G]	LPST_C2877	pbg9	6-phospho-beta-glucosidase	4.26
[G]	LPST_C2878	pbg10	6-phospho-beta-glucosidase	3.04
[G]	LPST_C2879	-	beta-glucosides PTS, EIIBCA	2.49
[K]	LPST_C2880	bglG5	transcription antiterminator	2.77
[G]	LPST_C2884	agl5	alpha-glucosidase	2.02
[R]	LPST_C2887	-	HAD superfamily hydrolase	4.20
[G]	LPST_C2888	tkt4	transketolase	2.15

COG	Locus	Gene	Products	Fold Change
[GT]	LPST_C2892	-	hypothetical protein	4.78
[ER]	LPST_C2895	gutB	L-iditol 2-dehydrogenase	2.57
[G]	LPST_C2896	-	galacitol PTS, EIIC	2.26
[GT]	LPST_C2898	-	galacitol PTS, EIIA	4.77
[KG]	LPST_C2899	-	transcription regulator	2.40
[G]	LPST_C2900	xpk2	putative phosphoketolase	2.69
[G]	LPST_C2903	araA	L-arabinose isomerase	2.31
[G]	LPST_C2905	araB	L-ribulokinase	2.40
[GEPR]	LPST_C2906	araT	arabinose transport protein	2.33
[S]	LPST_C2909	-	hypothetical protein	2.13
[I]	LPST_C2911	-	lipase/esterase (putative)	2.04
[P]	LPST_C2913	napA4	Na(+)/H(+) antiporter	2.07
[KG]	LPST_C2915	-	sugar kinase and transcription regulator	2.42
[G]	LPST_C2917	-	N-acetylmannosamine-6-phosphate 2-epimerase	2.82
[K]	LPST_C2932	-	transcription regulator (putative)	5.16
[EH]	LPST_C2933	pox5	pyruvate oxidase	12.37
[G]	LPST_C2936	rhaD	Rhamnulose-1-phosphate aldolase	2.47
[G]	LPST_C2940	rhaB	rhamnulokinase	2.17
[GEPR]	LPST_C2941	-	MFS family rhamnose tranport protein	2.38
[G]	LPST_C2961	bgl	beta-glucosidase	3.02
[KG]	LPST_C2962	-	ROK family protein	2.90
[G]	LPST_C2963	-	family 38 glycosyl hydrolase	3.22
[S]	LPST_C2964	-	hypothetical protein	2.12
[G]	LPST_C2966	-	alpha-1,2-mannosidase (putative)	3.55
[G]	LPST_C2967	msmK2	multiple sugar ABC transporter, ATP-binding protein	3.43
[T]	LPST_C2969	rrp12	response regulator	2.15
[T]	LPST_C2970	hpk12	histidine protein kinase; sensor protein	2.25
[G]	LPST_C2973	-	sugar ABC transporter, substrate binding protein	2.27
[G]	LPST_C2974	-	sugar ABC transporter, permease protein	2.59
[G]	LPST_C2975	-	sugar ABC transporter, permease protein	2.91
	LPST_C2976	-	hypothetical protein	2.39
[K]	LPST_C2977	-	AraC family transcriptional regulator	2.80
[V]	LPST_C2978	-	multidrug ABC superfamily ATP binding cassette transporter, ABC protein	2.04

COG	Locus	Gene	Products	Fold Change
[G]	LPST_C2982	-	sorbitol PTS, EIIA	4.67
[G]	LPST_C2983	-	sorbitol PTS, EIIBC	4.56
[G]	LPST_C2984	-	sorbitol PTS, EIIC	5.00
	LPST_C2985	srlM2	sorbitol operon activator	3.46
[K]	LPST_C2986	srlR2	sorbitol operon transcription regulator	3.35
[IQR]	LPST_C2987	srlD2	sorbitol-6-phosphate 2-dehydrogenase	2.58
[G]	LPST_C2988	rbsU	ribose transport protein	2.11
[G]	LPST_C2989	rbsD	D-ribose pyranase	11.21

Table S5 The down-regulated genes for *L.plantarum* ST-III grown in the presence of FOS versus glucose

COG	Locus	Gene	Products	Fold Change
	LPST_C0150	-	integral membrane protein	0.44
[C]	LPST_C0172	ack1	acetate kinase	0.38
[D]	LPST_C0174	-	integral membrane protein	0.29
[D]	LPST_C0175	-	integral membrane protein	0.48
[R]	LPST_C0198	-	NADPH-dependent FMN reductase	0.41
[C]	LPST_C0274	acdH	acetaldehyde dehydrogenase	0.50
[H]	LPST_C0466	-	transport protein	0.50
[G]	LPST_C0484	-	mannose PTS, EIIAB	0.03
[G]	LPST_C0485	pts9C	mannose PTS, EIIC	0.04
[G]	LPST_C0486	pts9D	PTS family mannose/fructose/sorbose porter component IID	0.03
[C]	LPST_C0651	-	nitro/flavin reductase	0.49
	LPST_C0658	-	integral membrane protein	0.48
[R]	LPST_C0873	-	hypothetical protein	0.23
[P]	LPST_C0883	-	cation transport protein	0.49
[I]	LPST_C1327	fabZ1	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	0.09
[I]	LPST_C1328	fabH2	beta-ketoacyl-acyl-carrier-protein synthase III	0.11
[IQ]	LPST_C1329	acpA2	acyl carrier protein	0.12
[I]	LPST_C1330	fabD	(acyl-carrier protein) S-malonyltransferase	0.09
[IQR]	LPST_C1331	fabG1	3-oxoacyl-[acyl-carrier protein] reductase	0.09
[IQ]	LPST_C1332	fabF	3-oxoacyl-[acyl-carrier protein] synthase II	0.08
[I]	LPST_C1333	accB2	acetyl-CoA carboxylase, biotin carboxyl carrier protein	0.08
[I]	LPST_C1334	fabZ2	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	0.09
[I]	LPST_C1335	accC2	acetyl-CoA carboxylase, biotin carboxylase subunit	0.08
[I]	LPST_C1336	accD2	acetyl-CoA carboxylase, carboxyl transferase subunit beta	0.08
[I]	LPST_C1337	accA2	acetyl-CoA carboxylase, carboxyl transferase subunit alpha	0.08

COG	Locus	Gene	Products	Fold Change
[I]	LPST_C1338	fabI	enoyl-(acyl carrier protein) reductase	0.07
[H]	LPST_C1339	-	phosphopantetheinyltransferase	0.07
[R]	LPST_C1340	-	integral membrane protein	0.16
[K]	LPST_C1341	-	transcription regulator	0.16
[I]	LPST_C1342	-	cytosolic long-chain acyl-CoA thioester hydrolase	0.13
[L]	LPST_C1453	-	transposase	0.33
[G]	LPST_C2062	-	sugar transport protein	0.44
[G]	LPST_C2086	-	N-acetylglucosamine and glucose PTS, EIICBA	0.23
[F]	LPST_C2226	pucK	xanthine / uracil transport protein	0.50
[MG]	LPST_C2357	-	NAD-dependent epimerase/dehydratase	0.40
[R]	LPST_C2373	-	2,5-diketo-D-gluconate reductase	0.38
[R]	LPST_C2432	-	possible toxin regulator	0.29
	LPST_C2519	-	hypothetical protein	0.41
[S]	LPST_C2683	-	DegV family protein	0.35

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