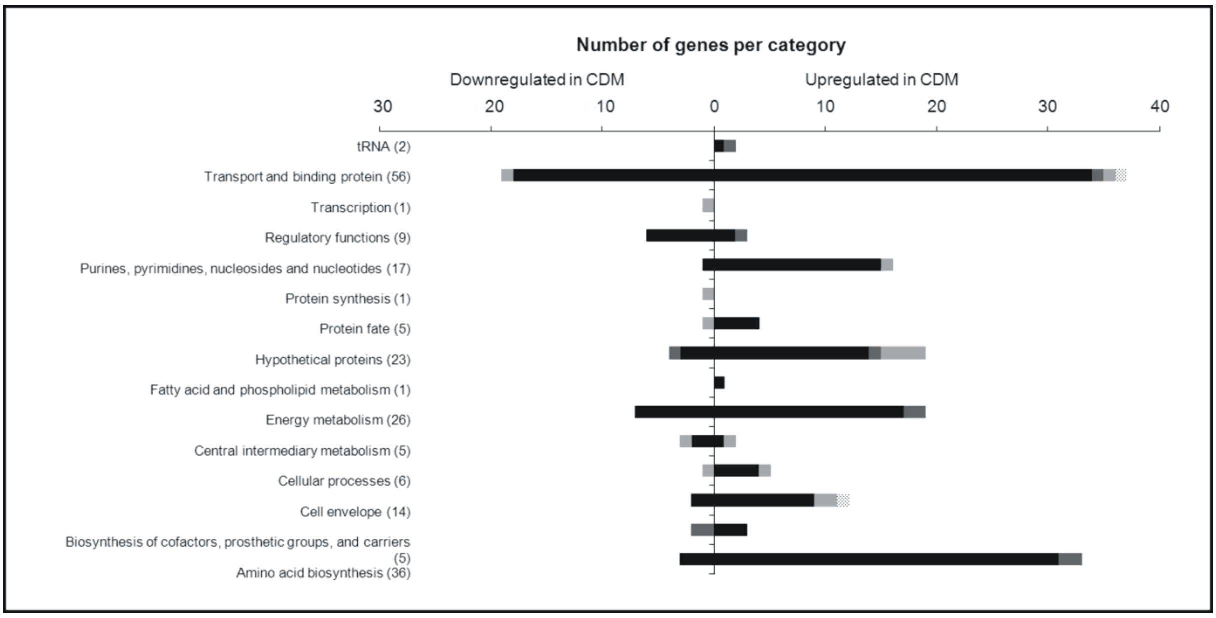

FIG S1 *L. plantarum* WCFS1 genes in functional groups that were up-regulated and down-regulated in CDM compared to MRS grown cells, using total RNA (dark grey), enriched mRNA (light grey) and both (black). Dotted grey bar represent genes with opposite transcript direction between total RNA and enriched mRNA.

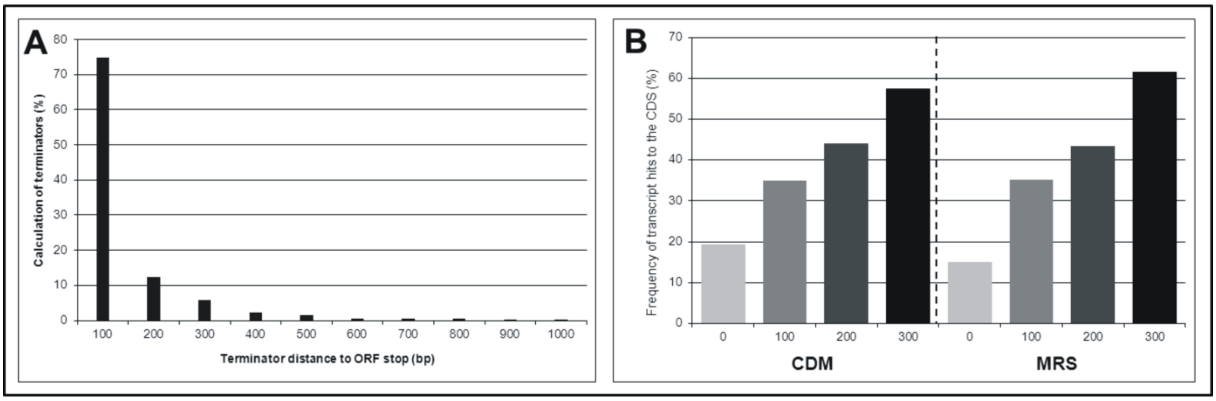

FIG S2 Distance of predicted terminators downstream of protein encoding genes employed for the prediction for 3’-UTR length of *L. plantarum* WCFS1 (panel A) and increase of 3’-UTR sequencing transcripts mapping percentage to the CDS based on 100bp, 200bp and 300bp extension (panel B)

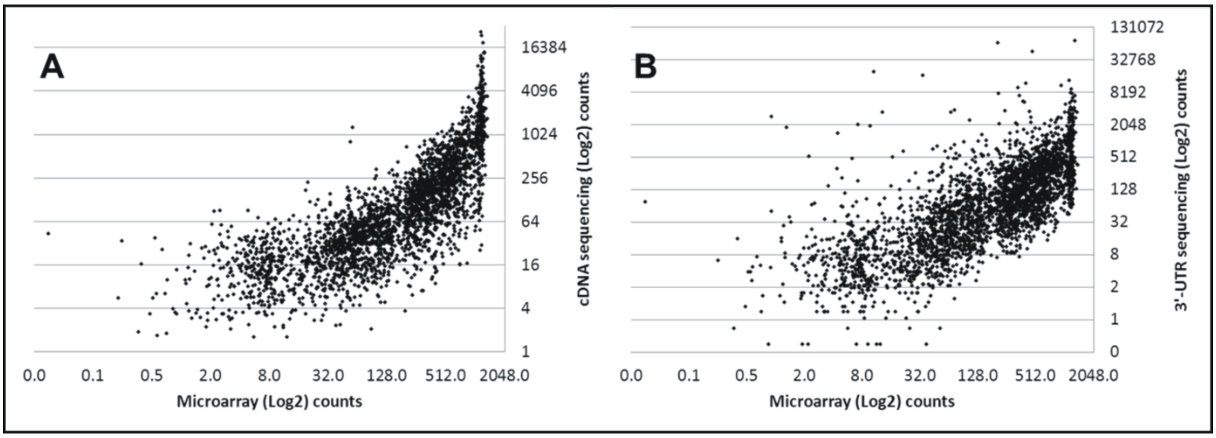

FIG S3 Comparison of mean-normalized values between signal intensity of microarray (X axis) and number of read counts (Y-axis) of direct cDNA sequencing (panel A) and 3'-UTR sequencing (panel B) in CDM. A saturation range was observed for the highest expression values obtained by microarray analysis, while the read counts of direct cDNA and 3'-UTR sequencings still appeared to be within the dynamic range of the technology.

TABLE S1 RNA-sequencing analysis summary of direct cDNA sequencing and 3'-UTR sequencing of *L. plantarum* WCFS1 grown in CDM or MRS

	Direct cDNA sequencing				**3'-UTR sequencing**			
	CDM		**MRS**		**CDM**		**MRS**	
	Reads	**%**	*Reads*	**%**	*Reads*	**%**	*Reads*	**%**
Total no. of reads	25,980,870	99.65	28,117,544	99.79	17,542,374	94.58	27,268,505	95.49
No. of reads mapped to the genome	25,112,191	96.66	27,488,120	97.76	16,628,389	94.79	25,392,216	93.12
No. of reads mapped to CDS	14,616,459	56.26	18,547,758	65.97	3,388,642	19.32	4,106,265	15.06
No of reads mapped to non-CDS	10,495,732	40.40	8,940,362	31.80	13,239,747	75.47	21,285,951	78.06

TABLE S2 An example of operon predictions which show increase in the frequency of mapped sequence reads at the last gene or the gene next to the 3'-UTR after mapping extension of 100bp (highlighted in grey).

Gene ID	Gene name	Function	Category	CDM normal	MRS normal	CDM + 100bp	MRS + 100bp
lp_0643	lp_0643	prophage P1 protein 20	Phage and prophage related functions	14	14	16	13
lp_0644	lp_0644	prophage P1 protein 21		1	0	1	1
lp_0645	lp_0645	prophage P1 protein 23		11	18	5	11
lp_0646	lp_0646	prophage P1 protein 24		18	13	19	15
lp_0647	lp_0647	prophage P1 protein 25		19	13	19	10
lp_0648	lp_0648	prophage P1 protein 26		7	3	7	4
lp_0649	lp_0649	prophage P1 protein 27		1	10	1	10
lp_0650	lp_0650	prophage P1 protein 28		10	3	12	3
lp_0651	lp_0651	prophage P1 protein 29		7	1	7	7
lp_0652	lp_0652	prophage P1 protein 30		3	9	5	17
lp_0653	lp_0653	prophage P1 protein 31		9	15	11	20
lp_0654	lp_0654	prophage P1 protein 32		19	32	22	35
lp_0655	lp_0655	prophage P1 protein 33, phage transcriptional regulator, ArpU family		18	40	11760	13765
lp_2719	purD	phosphoribosylamine--glycine ligase	Purine ribonucleotide biosynthesis	1694	49	6436	14373
lp_2720	purH	bifunctional protein: phosphoribosylaminoimidazolecarboxamide formyltransferase; IMP cyclohydrolase		753	47	742	48
lp_2721	purN	phosphoribosylglycinamide formyltransferase		233	18	260	18
lp_2722	purM	phosphoribosylformylglycinamidine cyclo-ligase		517	38	517	38
lp_2723	purF	amidophosphoribosyltransferase precursor		886	100	885	96
lp_2724	purI	phosphoribosylformylglycinamidine synthase II		710	87	730	88
lp_2725	purQ	phosphoribosylformylglycinamidine synthase I		98	26	111	29
lp_2726	purS	phosphoribosylformylglycinamidine synthase, PurS component		48	7	51	3
lp_2727	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase		90	14	104	19
lp_2728	purK1	phosphoribosylaminoimidazole carboxylase, ATPase subunit		159	40	153	41
lp_2729	pure	phosphoribosylaminoimidazole carboxylase, catalytic subunit		94	22	109	24
lp_1672	acpA2	acyl carrier protein	Fatty acid biosynthesis	433	1318	476	1401
lp_1673	fabD	(acyl-carrier protein) S-malonyltransferase		949	1698	949	1690
lp_1674	fabG1	3-oxoacyl-(acyl-carrier protein) reductase		500	1067	566	1209
lp_1675	fabF	3-oxoacyl-(acyl-carrier protein) synthase II		1454	2194	1455	2211
lp_1676	accB2	acetyl-CoA carboxylase, biotin carboxyl carrier protein		392	970	381	965
lp_1677	fabZ2	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase		374	746	431	839
lp_1678	accC2	acetyl-CoA carboxylase, biotin carboxylase subunit		1974	2518	2000	2558
lp_1679	accD2	acetyl-CoA carboxylase, carboxyl transferase subunit beta		724	1012	758	1074
lp_1680	accA2	acetyl-CoA carboxylase, carboxyl transferase subunit alpha		925	1523	976	1606
lp_1681	fabI	enoyl-(acyl-carrier protein) reductase (NADH)		572	806	528	760
lp_1682	lp_1682	Phosphopantetheinyltransferase		3475	4049	5079	7654