Supplementary Table S1. Genomes of *Bifidobacterium* strains available in the GenBank database (http://www.ncbi.nih.gov/genbank) used for the *in silico* analysis of *eps* clusters. Strains marked with an asterisk were selected to represent physical maps of their *eps* clusters.

		Genome	***eps* cluster**			**G+C content (%)**		**Priming-GTF[c]**		
Species	**Strain**	**Accession No.**	**Length (bp)[a]**	**No. genes**	**No. ME[b]**	**Genome**	***eps***	***cpsD***	***rfbP***	**Reference**
B. adolescentis	ATCC15703*	AP009256	19,467	17	0	59.2	55.3	BAD_1389	-	DS[d]
B. animalis subsp. *lactis*	DSM10140*	CP001606	54,249	42	1	60.5	53.5	Balat_1392	Balat_1371	(1)
	B1-04	CP001515	54,249	42	1	60.5	53.5	Balac_1392	Balac_1371	(1)
	AD011	CP001213	54,248	34	1	60.5	53.5	BLA_0595	BLA_0576	(2)
	BB-12	CP001853	54,215	41	1	60.5	53.5	BIF_00944	BIF_00983	(3)
	V9	CP001892	54,249	42	1	60.5	53.5	BalV_1349	BalV_1328	(4)
	BLC1	CP003039	54,250	41	1	60.5	53.5	BLC1_1349	BLC1_1328	(5)
	CNCM I-2494	CP002915	54,236	41	1	60.5	53.5	BALAC2494_01344	BALAC2494_01362	(6)
	Bi-07	CP003498	54,249	36	1	60.5	53.5	W91_1429	W91_1409	(7)
	B420	CP003497	54,248	37	1	60.5	53.5	W7Y_1394	W7Y_1374	(7)
B. animalis subsp. *animalis*	ATCC25527*	CP002567	54,307	32	8	60.5	56.1	BANAN_06765	-	(8)
B. asteroides	PRL2011*	CP003325	13,454	12	0	60.1	49.1	-	BAST_1667	(9)
B. bifidum	PRL2010	CP001840	-	-	-	62.7	-	-	-	(10)
	S17	CP002220	1,116	1	-	62.8	-	-	BBIF_0393	(11)
	BGN4	CP001361	-	-	-	62.4	-	-	-	(12)
B. breve	ACS-071-V-Sch8b	CP002743	15,174	10	1	58.7	51.5	-	HMPREF9228_0447	DS
	UCC2003*	CP000303	31,430	20	6	58.7	52.5	-	Bbr_0430	(13)
B. dentium	Bd1*	CP001750	58,993	49	0	58.5	52.0	-	BDP_1857	(14)
B. longum subsp. *infantis*	ATCC15697*	CP001095	19,310	13	5	59.9	51.4	-	Blon_2114	(15)
	157F	AP010890	1,719	1	-	60.1	57.7	-	BLIF_0362	(16)
B. longum subsp. *longum*	NCC2705*	AE014295	34,379	15	6	60.1	55.4	BL0237	BL0249	(17)

	DJ010A	CP000605	-	-	-	60.1	-	-	-	(18)
	F8	FP929034	17,580	10	3	59.9	50.8	-	BIL_15040	DS
	JDM301	CP002010	-	-	-	59.8	-	-	-	(19)
	JCM 1217	AP010888	10,265	6	1	60.3	56.3	BLLJ_0364	-	(16)
	KACC 91563	CP002794	20,193	14	4	59.8	50.7	-	BLNIAS_02272	(20)
	BBMN68	CP002286	14,316	11	0	59.9	45.9	BBMN68_1012	-	(21)
B. thermophilum	RBL67*	CP004346	27,116	20	3	60.1	52.9	-	D805_0348	DS

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[a] The hyphen (-) indicates the absence of the *priming-GTF* and therefore the absence of *eps*-cluster

[b] ME, Mobile Elements (transposase)

[c] Location of the priming-glycosyltransferase in the corresponding bifidobacterial genome

[d] DS, Direct Submission

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Supplementary Fig. S1. Physical maps of the putative exopolysaccharide (*eps*)-gene clusters from five *Bifidobacterium longum* subsp. *longum* strains. The genes were categorised according to their potential function as indicated in box-legend.