

## SUPPLEMENTARY MATERIAL

**Table S1.** Functional annotation of genes in RI1 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_00857	1.2e-233	Bifidobacteriales	XK27_00240	Fic/DOC family
IAEJDAMG_00858	7.2e-59	Bifidobacteriales	yccF	Inner membrane component domain
IAEJDAMG_00859	2.3e-159	Bifidobacteriales	ksgA	Methyltransferase domain
IAEJDAMG_00860	4.2e-67	Bifidobacteriales	-	Cupin 2, conserved barrel domain protein
IAEJDAMG_00861	2e-52	Bifidobacteriales	-	PemK-like, MazF-like toxin of type II toxin-antitoxin system
IAEJDAMG_00862	1.8e-37	Bifidobacteriales	-	RelB antitoxin
IAEJDAMG_00863	2.1e-243	Bifidobacteriales	-	HipA-like C-terminal domain
IAEJDAMG_00864	2.2e-15	Bacteria	-	addiction module antidote protein HigA
IAEJDAMG_00865	4.4e-220	Bifidobacteriales	-	Transmembrane secretion effector
IAEJDAMG_00866	2.7e-118	Bifidobacteriales	-	Bacterial regulatory proteins, tetR family
IAEJDAMG_00867	1.3e-11	Bifidobacteriales	-	

**Table S2.** Functional annotation of genes in RI2 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_01133	1.1e-126	Bifidobacteriales	-	Major facilitator Superfamily
IAEJDAMG_01134	1.9e-186	Bifidobacteriales	-	VanZ-like family
IAEJDAMG_01135	1.8e-65	Bifidobacteriales	-	Aminoacyl-tRNA editing domain
IAEJDAMG_01136	4.9e-42	Bifidobacteriales	-	Toxic component of a toxin-antitoxin (TA) module
IAEJDAMG_01137	1.9e-18	Bifidobacteriales	relB	RelB antitoxin
IAEJDAMG_01138	8.5e-87	Bifidobacteriales	-	FR47-like protein
IAEJDAMG_01140	4e-26	Bifidobacteriales	-	Helix-turn-helix domain
IAEJDAMG_01141	7.8e-161	Bifidobacteriales	mocA	Aldo/keto reductase family
IAEJDAMG_01142	1.3e-13	Bifidobacteriales	-	Antitoxin component of a toxin-antitoxin (TA) module
IAEJDAMG_01143	1.3e-80	Bifidobacteriales	-	ABC transporter
IAEJDAMG_01144	6.5e-71	Bifidobacteriales	-	FtsX-like permease family
IAEJDAMG_01145	1.1e-53	Bifidobacteriales	-	Histidine kinase
IAEJDAMG_01146	3.8e-74	Bifidobacteriales	-	Bacterial regulatory proteins, luxR family
IAEJDAMG_01147	1.7e-19	Bifidobacteriales	-	
IAEJDAMG_01148	4.4e-86	Bifidobacteriales	-	Acetyltransferase (GNAT) domain
IAEJDAMG_01149	5.5e-50	Bifidobacteriales	-	
IAEJDAMG_01150	8.8e-121	Bifidobacteriales	-	
IAEJDAMG_01151	3.1e-161	Corynebacteriac eae	ksgA	Belongs to the class I-like SAM-binding methyltransferase superfamily. rRNA adenine N(6)-methyltransferase family
IAEJDAMG_01152	2e-111	Bacteria	-	
IAEJDAMG_01153	5.1e-228	Corynebacteriac eae	-	Transposase and inactivated derivatives
IAEJDAMG_01156	6.2e-214	Bifidobacteriales	-	Transposase, Mutator family
IAEJDAMG_01157	1.7e-16	Bifidobacteriales	-	Histidine kinase

**Table S3.** Functional annotation of genes in GI1 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_00028	4.1e-216	Bifidobacteriales	ytfL	Transporter associated domain
IAEJDAMG_00029	1.5e-195	Bifidobacteriales	-	AAA ATPase domain
IAEJDAMG_00030	2.2e-137	Bifidobacteriales	-	Helix-turn-helix lactose operon repressor
IAEJDAMG_00031	5.3e-210	Bifidobacteriales	msmE	Bacterial extracellular solute-binding protein
IAEJDAMG_00032	1.2e-147	Bifidobacteriales	amyD	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_00033	7.5e-131	Bifidobacteriales	amyC	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_00034	5e-293	Bifidobacteriales	-	Glycosyl hydrolase family 36 N-terminal domain

**Table S4.** Functional annotation of genes in GI2 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_00578	3.2e-169	Actinobacteria	ugpQ	Domain of unknown function
IAEJDAMG_00579	5.9e-239	Actinobacteria	ugpB	Bacterial extracellular solute-binding protein
IAEJDAMG_00580	6.8e-142	Bifidobacteriales	ugpE	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_00581	5e-163	Bifidobacteriales	ugpA	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_00582	7.6e-161	Actinobacteria	-	Phosphate transporter family
IAEJDAMG_00583	2.2e-190	Bifidobacteriales	-	Helix-turn-helix lactose operon repressor
IAEJDAMG_00584	2.3e-142	Bifidobacteriales	-	LysR substrate binding domain
IAEJDAMG_00585	9.9e-102	Bifidobacteriales	-	LysR substrate binding domain

**Table S5.** Functional annotation of genes in GI3 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_01653	1.9e-179	Bifidobacteriales	-	
IAEJDAMG_01654	5e-107	Bifidobacteriales	ytrE	ABC transporter
IAEJDAMG_01655	1.4e-179	Bifidobacteriales	-	Putative peptidoglycan binding domain
IAEJDAMG_01656	1.9e-105	Bifidobacteriales	-	
IAEJDAMG_01657	6.3e-56	Bifidobacteriales	-	
IAEJDAMG_01658	1.2e-117	Bifidobacteriales	-	Transcriptional regulatory protein, C terminal
IAEJDAMG_01659	4.2e-210	Bifidobacteriales	qseC	GHKL domain

**Table S6.** Functional annotation of genes in GI4 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_01906	9.4e-45	Ruminococcaceae	-	Sugar phosphate isomerase involved in capsule formation
IAEJDAMG_01907	2.2e-58	Lachnoclostridium	-	Branched-chain amino acid transport system / permease component
IAEJDAMG_01908	1.1e-72	Clostridia	-	Branched-chain amino acid ABC transporter, permease protein
IAEJDAMG_01909	6.2e-120	Lachnoclostridium	-	ATPases associated with a variety of cellular activities
IAEJDAMG_01910	3.6e-79	Alphaproteobacteria	-	ABC-type sugar transport system periplasmic component
IAEJDAMG_01911	3e-167	Actinobacteria	xylB	Belongs to the FGGY kinase family
IAEJDAMG_01912	1.8e-75	Actinobacteria	xylR	ROK family
IAEJDAMG_01913	1.1e-36	Bifidobacteriales	-	-

**Table S7.** Functional annotation of genes in GI5 of *B. breve* 110<sup>1A</sup>.

Locus tag	E-value	Taxonomy	Gene	Description
IAEJDAMG_01984	1.9e-296	Bifidobacteriales	rafA	Raffinose synthase or seed imbibition protein Sip1
IAEJDAMG_01985	0.0	Bifidobacteriales	-	Alpha-amylase domain
IAEJDAMG_01986	7.1e-147	Bifidobacteriales	-	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_01987	2.3e-190	Bifidobacteriales	malC	Binding-protein-dependent transport system inner membrane component
IAEJDAMG_01988	2.8e-249	Bifidobacteriales	msmE	Bacterial extracellular solute-binding protein
IAEJDAMG_01989	1.2e-232	Actinobacteria	-	Protein of unknown function (DUF2961)
IAEJDAMG_01990	8.9e-232	Bifidobacteriales	msmE	Bacterial extracellular solute-binding protein
IAEJDAMG_01991	1.5e-189	Bifidobacteriales	-	Helix-turn-helix lactose operon repressor
IAEJDAMG_01992	2.7e-188	Bifidobacteriales	-	Periplasmic binding protein-like domain

**Table S8.** Functional annotation information about the 63 unique genes of *B. breve* 110<sup>1A</sup>.

Locus tag	Length	Product	Completeness	Gene Ontology
IAEJDAMG_00028	393	Transporter associated domain-containing protein	86.18% [393/456]	GO:0016021 - integral component of membrane  GO:0050660 - flavin adenine dinucleotide binding
IAEJDAMG_00029	355	AAA family ATPase	92.21% [355/385]	-
IAEJDAMG_00030	243	Transcriptional regulator LacI family	71.47% [243/340]	GO:0003677 - DNA binding  GO:0006355 - regulation of transcription DNA-templated
IAEJDAMG_00031	361	ABC transporter substrate-binding protein	85.34% [361/423]	GO:0055085 - transmembrane transport GO:0005886 - plasma membrane
IAEJDAMG_00032	275	ABC transporter permease protein, probably xylobiose porter	89.00% [275/309]	GO:0016021 - integral component of membrane  GO:0055085 - transmembrane transport GO:0005886 - plasma membrane
IAEJDAMG_00033	248	Maltose ABC transporter permease	84.64% [248/293]	GO:0016021 - integral component of membrane  GO:0055085 - transmembrane transport
IAEJDAMG_00034	491	Alpha-galactosidase	67.35% [491/729]	GO:0016052 - carbohydrate catabolic process  GO:0052692 - raffinose alpha-galactosidase activity GO:0003677 - DNA binding
IAEJDAMG_00208	50	Uncharacterized protein	68.49% [50/73]	GO:0006310 - DNA recombination  GO:0015074 - DNA integration GO:0004565 - beta-galactosidase activity
IAEJDAMG_00403	705	Beta-galactosidase	96.71% [705/729]	GO:0006012 - galactose metabolic process  GO:0009341 - beta-galactosidase complex
IAEJDAMG_00416	226	Acyltransferase	96.17% [226/235]	GO:0016746 - transferase activity transferring acyl groups
IAEJDAMG_00417	327	Glyco-trans-2-like domain-containing protein	97.03% [327/337]	-
IAEJDAMG_00418	399	Uncharacterized protein	98.28% [399/406]	GO:0016021 - integral component of membrane

IAEJDAMG_00424	482	dTDP-4-dehydrorhamnose reductase	97.57% [482/494]	GO:0008830 - dTDP-4-dehydrorhamnose 35-epimerase activity  GO:0008831 - dTDP-4-dehydrorhamnose reductase activity  GO:0019305 - dTDP-rhamnose biosynthetic process
IAEJDAMG_00437	439	Uncharacterized protein	91.84% [439/478]	GO:0016021 - integral component of membrane
IAEJDAMG_00549	46	Uncharacterized protein	47.92% [46/96]	-
IAEJDAMG_00642	177	Uncharacterized protein	98.33% [177/180]	-
IAEJDAMG_00643	108	Uncharacterized protein	98.18% [108/110]	-
IAEJDAMG_00644	437	Uncharacterized protein	98.20% [437/445]	-
IAEJDAMG_00649	56	Uncharacterized protein	98.25% [56/57]	-
IAEJDAMG_00650	206	HTH IS21-type domain-containing protein	98.10% [206/210]	-
IAEJDAMG_00651	206	Uncharacterized protein	98.10% [206/210]	-
IAEJDAMG_00652	569	DUF4091 domain-containing protein	98.27% [569/579]	-
IAEJDAMG_00653	130	Uncharacterized protein	97.74% [130/133]	GO:0043565 - sequence-specific DNA binding GO:0015074 - DNA integration  GO:0032196 – transposition
IAEJDAMG_00654	200	Integrase catalytic domain-containing protein	98.04% [200/204]	GO:0003677 - DNA binding  GO:0006310 - DNA recombination  GO:0015074 - DNA integration
IAEJDAMG_00723	400	Site-specific recombinase phage integrase family	98.28% [400/407]	GO:0000155 - phosphorelay sensor kinase activity  GO:0016021 - integral component of membrane  GO:0046983 - protein dimerization activity
IAEJDAMG_00849	721	Two-component system sensor histidine kinase	85.33% [721/845]	-
IAEJDAMG_00920	87	PadR family transcriptional regulator	63.97% [87/136]	GO:0016021 - integral component of membrane
IAEJDAMG_00921	123	Uncharacterized protein	54.91% [123/224]	GO:0003677 - DNA binding  GO:0015074 - DNA integration
IAEJDAMG_00922	175	Integrase	41.87% [175/418]	GO:0016021 - integral component of membrane  GO:0022857 - transmembrane transporter activity
IAEJDAMG_00986	387	MFS transporter	97.97% [387/395]	

IAEJDAMG_01087	174	Uncharacterized protein	97.75% [174/178]	-
IAEJDAMG_01088	155	Uncharacterized protein	96.88% [155/160]	GO:0016021 - integral component of membrane
IAEJDAMG_01093	164	Uncharacterized protein	86.32% [164/190]	GO:0016021 - integral component of membrane
IAEJDAMG_01094	107	Uncharacterized protein	86.99% [107/123]	-
IAEJDAMG_01095	162	Uncharacterized protein	87.10% [162/186]	GO:0004222 - metalloendopeptidase activity  GO:0005524 - ATP binding
IAEJDAMG_01096	19	Uncharacterized protein	16.96% [19/112]	GO:0016021 - integral component of membrane
IAEJDAMG_01098	135	Uncharacterized protein	75.84% [135/178]	-
IAEJDAMG_01099	108	Uncharacterized protein	96.43% [108/112]	-
IAEJDAMG_01100	96	Putative transcriptional regulator XRE family	92.31% [96/104]	GO:0003677 - DNA binding
IAEJDAMG_01102	129	Uncharacterized protein	81.13% [129/159]	GO:0016021 - integral component of membrane
IAEJDAMG_01103	42	Uncharacterized protein	47.73% [42/88]	GO:0016021 - integral component of membrane GO:0003677 - DNA binding
IAEJDAMG_01104	391	Integrase catalytic domain-containing protein	84.45% [391/463]	GO:0015074 - DNA integration  GO:0032196 – transposition
IAEJDAMG_01105	437	Uncharacterized protein	98.20% [437/445]	-
IAEJDAMG_01106	108	Uncharacterized protein	98.18% [108/110]	-
IAEJDAMG_01107	18	IS3 family transposase	18.56% [18/97]	GO:0015074 - DNA integration
IAEJDAMG_01108	68	Uncharacterized protein	49.28% [68/138]	-
IAEJDAMG_01109	133	Sortase family protein	40.92% [133/325]	GO:0016021 - integral component of membrane
IAEJDAMG_01110	165	LPXTG-motif cell wall anchor domain protein	30.22% [165/546]	GO:0016021 - integral component of membrane
IAEJDAMG_01111	194	Uncharacterized protein	23.57% [194/823]	GO:0016021 - integral component of membrane
IAEJDAMG_01112	21	Transposase	63.64% [21/33]	-
IAEJDAMG_01113	74	Uncharacterized protein	53.24% [74/139]	-
IAEJDAMG_01114	173	DnaJ-like protein	60.70% [173/285]	-
IAEJDAMG_01115	54	Uncharacterized protein	72.97% [54/74]	-
IAEJDAMG_01116	190	Hydrolase	95.48% [190/199]	GO:0006807 - nitrogen compound metabolic process

				GO:0016787 - hydrolase activity
IAEJDAMG_01222	652	Putative membrane protein	96.45% [652/676]	GO:0016021 - integral component of membrane
IAEJDAMG_01227	2161	Cell surface protein	91.65% [2161/2358]	-
IAEJDAMG_01229	315	Uncharacterized protein	92.11% [315/342]	GO:0016021 - integral component of membrane
IAEJDAMG_01235	108	Uncharacterized protein	98.18% [108/110]	-
IAEJDAMG_01243	69	Helix-turn-helix domain-containing protein	97.18% [69/71]	-
IAEJDAMG_01654	229	Lipoprotein-releasing system ATP-binding protein LolD	90.51% [229/253]	GO:0005524 - ATP binding  GO:0016887 - ATPase activity
IAEJDAMG_01659	432	Histidine kinase	98.18% [432/440]	GO:0000155 - phosphorelay sensor kinase activity  GO:0016021 - integral component of membrane
IAEJDAMG_01984	609	Alpha-galactosidase	98.23% [609/620]	GO:0003824 - catalytic activity
IAEJDAMG_01985	556	Glycosidase	98.23% [556/566]	GO:0005975 - carbohydrate metabolic process  GO:0008788 - alphaalpha-phosphotrehalase activity

**Table S9.** Identified genes potentially involved in adhesion mechanisms in *B. breve* 110<sup>1A</sup>.

Locus tag	Name	Accession number	Identity	Length	E-value
IAEJDAMG_00064	Sortase srtA2	ACD98830.1	75.714	420	0
IAEJDAMG_00138	TadZ-like protein	ABE94843.1	99.123	228	6.18E-164
IAEJDAMG_00139	TadA-like protein	ABE94844.1	98.82	339	0
IAEJDAMG_00140	TadB-like protein	ABE94845.1	98.958	192	1.42E-136
IAEJDAMG_00141	TadC-like protein	ABE94846.1	99.083	218	3.13E-157
IAEJDAMG_00142	tadE	ABE94847.1	98.947	95	2.67E-66
IAEJDAMG_00143	tadF	ABE94848.1	98.413	126	9.80E-88
	Conserved hypothetical secreted protein				
IAEJDAMG_00144		ABE94849.1	100	112	4.70E-80
IAEJDAMG_00149	srtA1	ACD98732.1	76.35	389	0
IAEJDAMG_00304		VUX38545.1	98.969	97	4.83E-70
	LPXTG-type cell surface-anchoring secretion proteins (BLD_1637)				
IAEJDAMG_00343		ACD99082.1	76.471	34	1.06E-08
	LPXTG-type cell surface-anchoring secretion proteins (BLD_1638c)				
IAEJDAMG_00344		ACD99083.1	100	23	6.43E-09
IAEJDAMG_00565		-	92.732	399	0
IAEJDAMG_00714	Sortase	ACD98225.1	89.091	165	4.10E-111
	TadV type IV secretion peptidase				
IAEJDAMG_00939		ABE95585.1	98.485	132	4.64E-88
IAEJDAMG_01041		ACS47779.1	77.528	267	1.15E-160
IAEJDAMG_02029	srtA3	ACD98903.1	91.15	226	1.94E-160
IAEJDAMG_00502	luxS	VUX37541.1	97.561	164	1.99E-121

**Table S10.** Identified genes potentially involved in resistance mechanisms to stress in *B. breve* 110<sup>1A</sup>.

Locus tag	Name	Accession number	Identity	Length	E-value
IAEJDAMG_00075	hsp20	ABL75149.1	97.605	167	4.51E-127
IAEJDAMG_00129	dnaK	AAT90384.1	99.521	626	0.00E+00
IAEJDAMG_00130	dnaJ	AAT90385.1	99.559	227	5.36E-166
IAEJDAMG_00130		EEB21092.1	72.727	231	1.08E-113
IAEJDAMG_00131	grpE	AAT90386.1	100	337	0.00E+00
IAEJDAMG_00166		WP_109057771.1	86.667	270	4.22E-175
IAEJDAMG_00297	F1F0-ATPase a	KXS24185.1	98.885	269	0
IAEJDAMG_00299	F1F0-ATPase b	WP_101673713.1	100	172	9.79E-123
IAEJDAMG_00300	F1F0-ATPase delta	KXS24188.1	99.64	278	0
IAEJDAMG_00301	F1F0-ATPase alpha	QFZ79728.1	100	543	0
IAEJDAMG_00302	F1F0-ATPase gamma	KXS24190.1	99.349	307	0
IAEJDAMG_00303	F1F0-ATPase beta	QFZ79730.1	100	490	0
IAEJDAMG_00304	F1F0-ATPase epsilon	KXS24192.1	98.969	97	4.78E-70
IAEJDAMG_00388		WP_100496451.1	96.29	566	0
IAEJDAMG_00458	mutY	VUX33106.1	98.438	320	0
IAEJDAMG_00778		WP_044088523.1	96.875	480	0
IAEJDAMG_00830	clpP	RDX30841.1	100	227	4.30E-173
IAEJDAMG_00830		WP_026502573.1	83.26	227	4.78E-138
IAEJDAMG_00831	clpX	VUX37037.1	99.779	453	0
IAEJDAMG_00835		AUD86824.1	99.784	462	0
IAEJDAMG_00872	-	WP_109057771.1	85.926	270	8.79E-171
IAEJDAMG_00944	-	WP_044088362.1	97.649	553	0
IAEJDAMG_01015	-	AAT11512.1	91.083	314	0
IAEJDAMG_01051	-	ABA33885.1	99.213	381	0
IAEJDAMG_01051	-	ADQ03125.1	96.063	381	0
IAEJDAMG_01064	ruvA	WP_052789507.1	99.038	208	2.74E-151
IAEJDAMG_01306	recA	VEG21919.1	100	392	0
IAEJDAMG_01308	clgR	VUX34072.1	100	172	1.82E-124
IAEJDAMG_01315	-	WP_015450243.1	84.211	228	7.87E-147
IAEJDAMG_01373	-	WP_109057771.1	89.63	270	0
IAEJDAMG_01398	lexA	WP_052789257.1	99.156	237	3.26E-178
IAEJDAMG_01485	-	AAW49584.1	99.885	869	0
IAEJDAMG_01486	AAW49585.1	AAW49585.1	99.688	321	0
IAEJDAMG_01493	groEL	AAT95329.1	95.396	543	0
IAEJDAMG_01672		WP_033505167.1	85.088	342	0
IAEJDAMG_01680	-	KRN79975.1	48.165	218	7.70E-75

IAEJDAMG_01786	groES	WP_106629637.1	98.969	97	5.93E-68
IAEJDAMG_01786	-	WP_007053011.1	95.876	97	1.65E-66
IAEJDAMG_01875	NADH oxidase	VUX32225.1	99.107	448	0
IAEJDAMG_01875	NADH peroxidase	AFJ17563.1	71.652	448	0
IAEJDAMG_01900	-	AAX52929.1	99.438	889	0
IAEJDAMG_02044	Thioredoxin reductase	VUX33397.1	100	339	0
IAEJDAMG_00830	Bile salt hydrolase	RDX30841.1	100	227	2.46E-173
IAEJDAMG_00041	bshA	VUW79572.1	99.153	472	0.00E+00

**Table S11.** Identified genes potentially involved in repair and protection of DNA and protein mechanisms in *B. breve* 110<sup>1A</sup>.

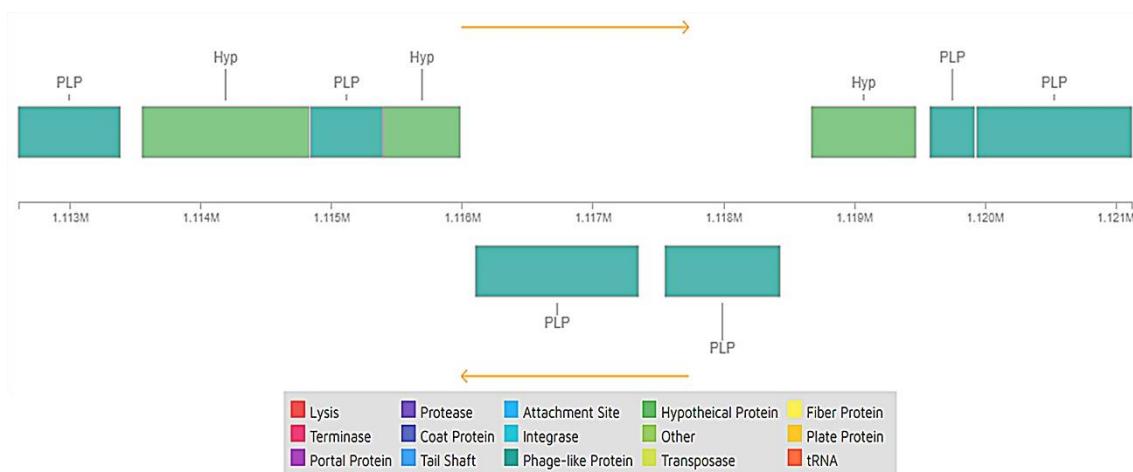
Locus tag	Name	Accession number	Identity	Length	E-value
IAEJDAMG_00027	DNA-binding ferritin-like protein (dps)	VEG20761.1	99.371	159	2.30E-118
IAEJDAMG_00087	mutT	AUE19745.1	100	137	4.10E-103
IAEJDAMG_00027	-	ADQ02354.1	98.742	159	5.91E-118
IAEJDAMG_00080	msr	BAQ99105.1	99.704	338	0
IAEJDAMG_00262	copA	VUX34953.1	99.297	853	0.00E+00
IAEJDAMG_00502	-	VEG23308.1	87.342	158	5.04E-108
IAEJDAMG_01035	uvrA	WP_103619798.1	99.491	982	0.00E+00
IAEJDAMG_01035	-	WP_044088239.1	96.036	1009	0.00E+00

**Table S12.** Identified genes potentially involved in the biosynthesis of vitamins in *B. breve* 110<sup>1A</sup>.

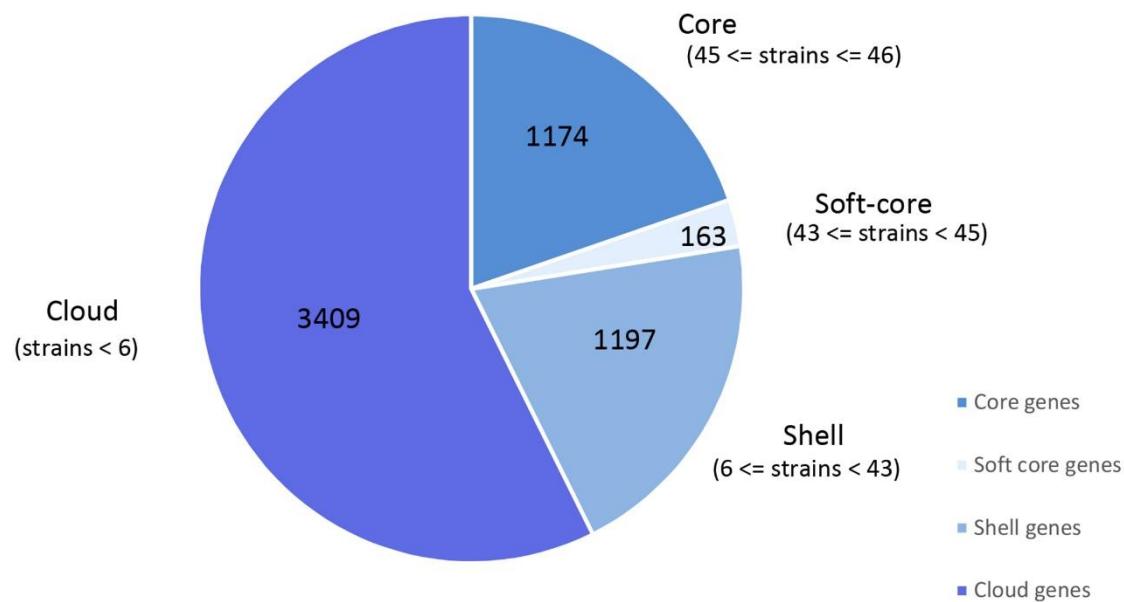
Locus tag	Name	Accession number	Identity	Length	E-value
IAEJDAMG_00138	Cobalamin, B12 (cobQ)	KXS24078.1	99.627	268	0
IAEJDAMG_00868	Riboflavin, B2 (ribZ)	VUW80559.1	99.268	683	0.00E+00
IAEJDAMG_00957	-	RDX31668.1	99.492	394	0
IAEJDAMG_01369	Folic Acid, B9 (folC)	VEG21982.1	99.25	533	0.00E+00
IAEJDAMG_01400	-	WP_003810784.1	92.5	320	0.00E+00
IAEJDAMG_01456	Riboflavin, B2 (ribU)	VUX35278.1	98.165	218	4.44E-156
IAEJDAMG_01631	Folic Acid, B9 (folK)	QFV12943.1	99.254	536	0.00E+00
IAEJDAMG_01632	Folic Acid, B9 (folP)	QHP50922.1	95.862	290	0
IAEJDAMG_01633	Folic Acid, B9 (folE)	QHP52232.1	99.515	206	4.01E-153
IAEJDAMG_01712	Riboflavin, B2 (ribF)	VUX29772.1	99.198	374	0.00E+00



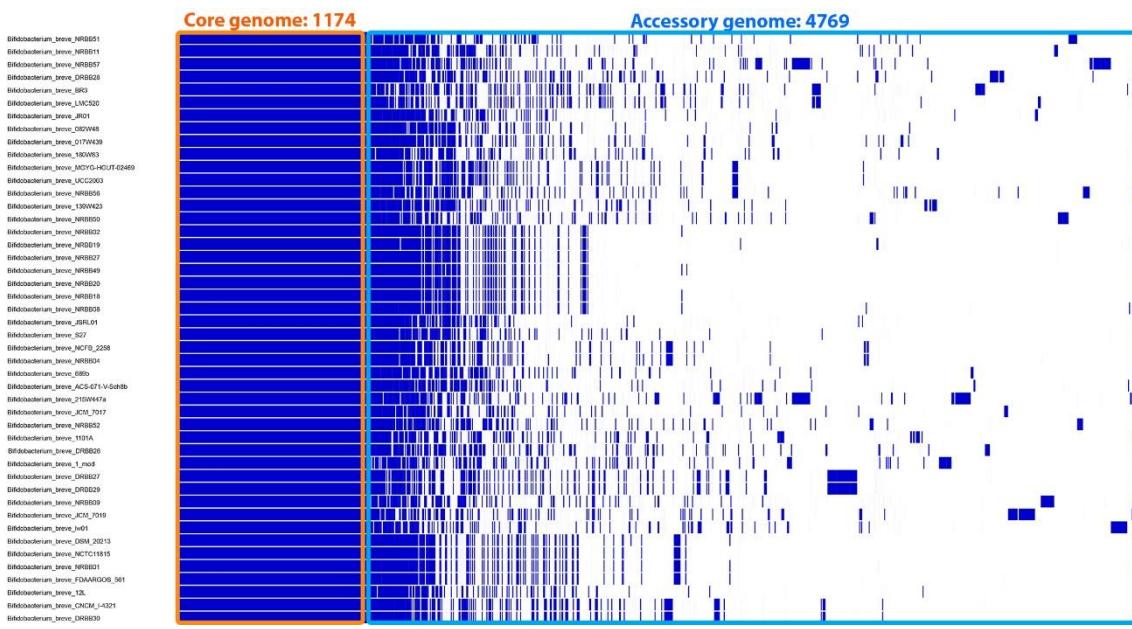
**Figure S1.** Representation of multiple sequence alignments of whole genomes of 46 *Bifidobacterium breve* strains shows conserved synteny and collinearity among gene blocks.



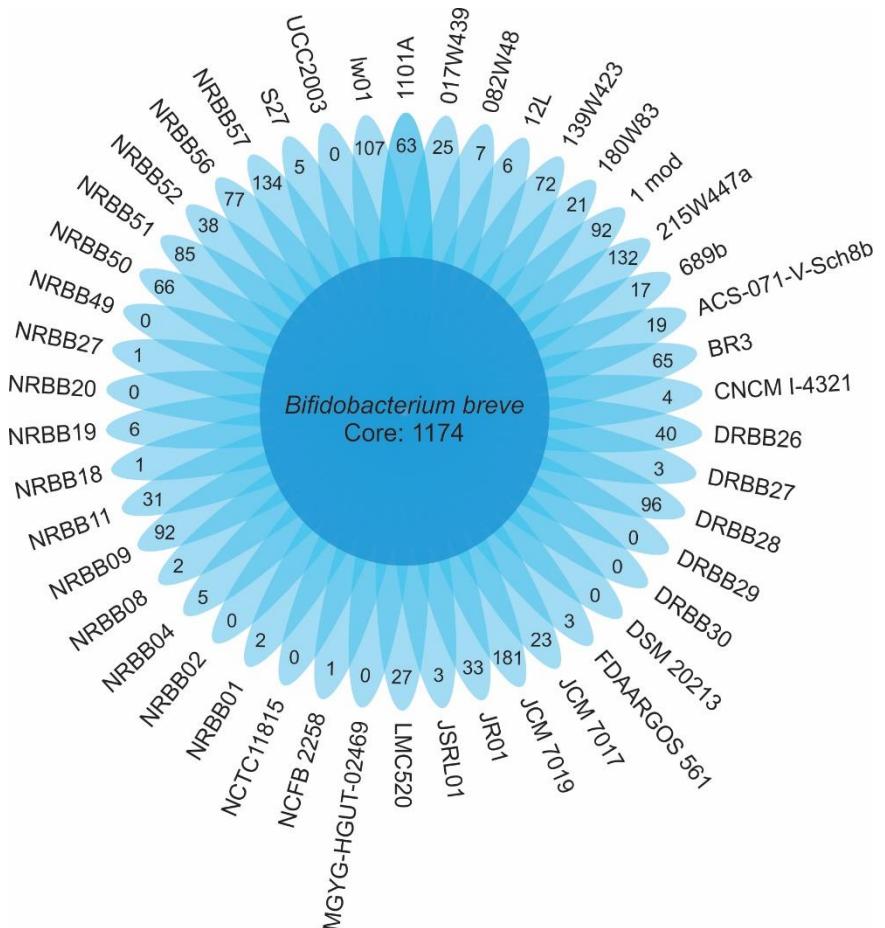
**Figure S2.** Representation of the incomplete prophage region in *Bifidobacterium breve* 110<sup>1A</sup>. The prophage showed 9 CDS: 6 CDS in dark turquoise identified as phage-like protein and 3 CDS in light green as a hypothetical protein



**Figure S3.** Pie chart representing the number of genes shared in the core, softcore, shell and cloud genome for the 46 *Bifidobacterium breve*



**Figure S4.** Matrix representation of the pangenome based on the presence-absence of genes of the pan-genome



**Figure S5.** Plot diagram showing the core-genome size of all 46 genomes of *Bifidobacterium breve* (central area) and unique genes for each strain