

Table S1. The carbohydrate-active enzymes genes related of exopolysaccharides (EPS) of 14 strains of *Fructilactobacillus sanfranciscensis*.

Carbohydrate-active enzymes family	GH68 (levansucrase; EC 2.4.1.10)	GH70 (dextransucrase; EC 2.4.1.5)	GT5 (α -1,3-glucan synthase; EC 2.4.1.183)
	Cleaves sucrose into fructose and glucose and use the cleavage energy to form levan out of fructose.	Transfer a D-glucosyl residue from sucrose to a glucan chain.	A glucan primer is needed to begin the reaction, which brings about elongation of the glucan chains.
Strains			
Fs_1001	+	-	-
Fs_1002	-	-	-
Fs_1003	+	+	+
Fs_1004	-	+	-
Fs_1005	-	+	-
Fs_1006	-	-	-
Fs_1007	+	-	-
Fs_1008	-	+	-
Fs_1009	+	-	-
Fs_1010	-	+	-
Fs_1011	-	-	-
Fs_1012	-	-	-
Fs_1013	-	-	-
Fs_1014	-	-	-

–: No carbohydrate-active enzymes genes related of EPS.

+: Containing the carbohydrate-active enzymes genes related of EPS.

Table S2. CRISPR-Cas system in *Fructilactobacillus sanfranciscensis*.

Strains	DR sequence	DR length	CAS Type	CAS enzyme type
DSM20				
541/ TMW 1.53	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
TMW1. 54	GTATTCCCCACGCATGTGGGGGTG ATCCT	29	IE	cas3, cas5, cas6, cas7
TMW 1.392	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAG	35	IIA	cas9, cas1, cas2, csn2
TMW 1.640	GTTTTAGAAGTATGTCATTCTAATG AGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
TMW 1.726	GTATTCCCCACGCATGTGGGGGTG ATCC	28	IE	cas5, cas6, cas7
TMW 1.897	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	csn2
TMW 1.907	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	cas2, cas1, cas9, csn2
TMW 1.936	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
TMW 1.1150	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
TMW 1.1152	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
TMW 1.1154	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
TMW 1.1221	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, csn2
TMW 1.1304	AGGATCACCCCCACATGCGTGGGG AATAC	29	IE	cas5, cas6, cas7
TMW 1.1470	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
TMW 1.1730	GTATTCCCCACGCATGTGGGGGTG ATCCT	29	IE	cas3, cas5, cas6, cas7
TMW 1.2137	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
TMW 1.2138	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	cas2, cas1, cas9, csn2

TMW 1.2139	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
TMW 1.2140	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
TMW 1.2142	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
LS451	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
JCM 5668	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
Ls-1001	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	cas2, cas1, csn2
Ah4	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	cas2, cas1, cas9, csn2
Gs2	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2, cas2, cas1, cas9
Gs9	GTATTCCCCACGCATGTGGGGGTG ATCC	28	IE	cas1, cas2, cas3, cas5, cas6, cas7
Ts9	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	36	IIA	csn2
Sd1_3	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1001	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
Fs_1002	GTATTCCCCACGCATGTGGGGGTG ATCC	29	IE	cas1, cas2, cas3, cas5, cas6, cas7
Fs_1003	GCTCTTAATCTCATTAGAATGACG TACTTCTAAAAC	37	IIA	csn2
Fs_1004	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	38	IIA	cas2, cas1, cas9, csn2
Fs_1005	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	37	IIA	cas2, cas1, cas9, csn2
Fs_1006	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	37	IIA	cas9, cas1, cas2, csn2
Fs_1007	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1008	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2
Fs_1009	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1009	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas9, cas1, cas2, csn2

Fs_1010	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	csn2, cas3
Fs_1011	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1012	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1013	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2
Fs_1014	GTTTTAGAAGTACGTCATTCTAAT GAGATTAAGAGC	36	IIA	cas2, cas1, cas9, csn2

Table S3. Prediction of intact prophage regions of *Fructilactobacillus sanfranciscensis*.

Strain	Region	Region Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage	GC %
DSM20541								
/	-	-	-	-	-	-	-	-
TMW 1.53								
TMW1.54	1	8.5Kb	incomplete	30	14	2220-10785 info_outline	PHAGE_Bacill_G_NC_023719 (3)	40.01 %
TMW 1.392	-	-	-	-	-	-	-	-
	1	8.5Kb	incomplete	10	9	134128-142642 info_outline	PHAGE_Prochl_P_SSM2_NC_006883 (4)	38.18 %
TMW 1.640	1	8.3Kb	incomplete	40	10	25184-33578 info_outline	PHAGE_Lactob_3_521_NC_048753 (1)	35.32 %
TMW 1.726	-	-	-	-	-	-	-	-
TMW 1.897	-	-	-	-	-	-	-	-
TMW 1.907	1	43.1Kb	intact	130	55	69802-112961 info_outline	PHAGE_Lactob_LfeSau_NC_029068 (11)	36.64 %
TMW 1.936	1	8.1Kb	incomplete	40	9	33562-41719 info_outline	PHAGE_Brevib_Davies_NC_022980 (1)	35.85 %
TMW 1.1150	-	-	-	-	-	-	-	-
TMW 1.1152	1	8.4Kb	incomplete	40	10	9498-17923 info_outline	PHAGE_Brevib_Davies_NC_022980 (1)	35.30 %
TMW 1.1154	1	8.4Kb	incomplete	40	10	68950-77375 info_outline	PHAGE_Brevib_Jimmer2_NC_041976 (1)	35.30 %

TMW 1.1221	1	8.4Kb	incomplete	40	10	9403-17821 info_outline	PHAGE_Entero_phiEF24 C_NC_009904 (1)	35.31 %
TMW 1.1304	1	9Kb	incomplete	40	10	60527-69621 info_outline	PHAGE_Lactob_3_521_NC_048753 (1)	35.23 %
	1	6.1Kb	incomplete	10	9	82435-88554 info_outline	PHAGE_Bacill_vB_BtS_BMBtp14_NC_048640 (2)	31.83 %
TMW 1.1470	1	7.7Kb	incomplete	40	8	88429-96216 info_outline	PHAGE_Lactob_Lb338_1_NC_012530 (1)	35.41 %
	1	32.7Kb	questionable	70	21	45696-78484 info_outline	PHAGE_Shigel_Sf6_NC_005344 (2)	37.40 %
TMW 1.1730	1	9Kb	incomplete	40	10	25818-34912 info_outline	PHAGE_Yersin_fHe_Yen9_04_NC_042116 (1)	35.22 %
TMW 1.2137	-	-	-	-	-	-	-	-
TMW 1.2138	-	-	-	-	-	-	-	-
	1	8.4Kb	incomplete	40	13	3949-12392 info_outline	PHAGE_Bacill_G_NC_023719 (3)	43.02 %
TMW 1.2139	1	5.7Kb	incomplete	40	7	36-5832 info_outline	PHAGE_Brevib_Abouo_NC_029029 (1)	34.17 %
TMW 1.2140	-	-	-	-	-	-	-	-
TMW 1.2141	1	5.7Kb	incomplete	50	9	15541-21290 info_outline	PHAGE_Lactob_phiAT3_NC_005893 (2)	41.39 %
TMW 1.2142	-	-	-	-	-	-	-	-
TMW	1	9Kb	incompl	40	10	60527-69621	PHAGE_La	35.22

1.2134			ete			info_outline	ctob_Lb338 _1_NC_012 530 (1) PHAGE_Te	%
	1	8.7Kb	incompl ete	60	6	6003-14729 info_outline	naci_PTm1_ NC_049340 (2) PHAGE_Ba	30.56 %
	1	10.8Kb	incompl ete	10	9	50303-61195 info_outline	cill_G_NC_ 023719 (2) PHAGE_La	31.98 %
TMW 1.1597	1	26.9Kb	intact	120	31	279-27210 info_outline	ctob_LF1_N C_019486 (8) PHAGE_La	44.01 %
	1	5.7Kb	incompl ete	20	13	105-5890 info_outline	ctob_Lv_1_ NC_011801 (3) PHAGE_La	35.00 %
	1	6.6Kb	incompl ete	50	11	180297-1869 35 info_outline	ctob_521B_ NC_048752 (2) PHAGE_Ba	35.94 %
LS451	2	8Kb	incompl ete	40	8	242757-2508 47 info_outline	cill_Shanette _NC_02898 3 (1) PHAGE_La	35.83 %
	3	4.9Kb	incompl ete	40	8	1143165-114 8088 info_outline	ctob_Lb338 _1_NC_012 530 (1) PHAGE_No	34.26 %
JCM 5668	-	-	-	-	-	-	-	-
Ls-1001	1	8.8Kb	incompl ete	30	10	12550-21414 info_outline	dula_vB_Ns pS_kac65v1 51_NC_048 756 (2) PHAGE_Bu	36.25 %
Ah4	1	8.4Kb	incompl ete	40	10	38578-46999 info_outline	rkho_BcepS auron_NC_0 49851 (1) PHAGE_No	35.31 %
	1	8.8Kb	incompl ete	40	11	34145-42963 info_outline	dula_vB_Ns pS_kac65v1	36.67 %

Gs2	1	8.4Kb	incomplete	40	10	25806-34228 info_outline	51_NC_048756 (2) PHAGE_Achrom_Motura_NC_049849 (1)	35.33%
Gs9	1	8.8Kb	incomplete	30	10	30074-38912 info_outline	PHAGE_Nodula_vB_NspS_kac68v161_NC_048757 (2)	36.35%
Ts9	1	8.4Kb	incomplete	40	10	19322-27743 info_outline	PHAGE_Enterophi92_NC_023693 (1)	35.34%
Sd1_3	1	8.4Kb	incomplete	40	10	26439-34862 info_outline	PHAGE_Brevib_Abouo_NC_029029 (1)	35.34%
Fs_1001	1	15.7Kb	incomplete	40	10	115688-131483 info_outline	PHAGE_Bacill_Shanette_NC_028983 (1)	0.3509
Fs_1002	1	8.4Kb	incomplete	40	10	9432-17854 info_outline	PHAGE_Brevib_Jimmer1_NC_029104 (1)	0.3526
Fs_1003	1	8.4Kb	incomplete	40	10	38659-47080 info_outline	PHAGE_Brevib_Jimmer2_NC_041976 (1)	0.3538
Fs_1004	1	8.4Kb	incomplete	40	10	9933-18354 info_outline	PHAGE_Brevib_Jimmer2_NC_041976 (1)	0.3535
Fs_1005	1	15.7Kb	incomplete	40	10	115683-131478 info_outline	PHAGE_Brevib_Osiris_NC_028969 (1)	0.3509
Fs_1006	1	8.5Kb	incomplete	40	10	37588-46110 info_outline	PHAGE_Burkho_BcepSaruman_NC_049850 (1)	0.3523

Fs_1007	1	8.3Kb	incomplete	40	11	37360-45752 info_outline	PHAGE_Entero_EFLK1_NC_029026 (1)	0.354
Fs_1008	1	8.4Kb	incomplete	40	10	9933-18354 info_outline	PHAGE_Entero_EFLK1_NC_029026 (1)	0.3535
Fs_1009	1	8.4Kb	incomplete	40	10	9432-17854 info_outline	PHAGE_Entero_EfV12_phi1_NC_048087 (1)	0.3527
Fs_1010	1	8.4Kb	incomplete	40	10	29104-37564 info_outline	PHAGE_Entero_phi92_NC_023693 (1)	0.3537
Fs_1011	1	8.4Kb	incomplete	40	10	38659-47080 info_outline	PHAGE_Staphy_vB_SscM_1_NC_047767 (1)	0.3538
Fs_1012	1	15.7Kb	incomplete	40	10	115683-131478 info_outline	PHAGE_Strept_BRock_NC_048650 (1)	0.3509
Fs_1013	1	8.4Kb	incomplete	40	10	119712-128135 info_outline	PHAGE_Halovi_HGTV_1_NC_021328 (1)	0.3534
Fs_1014	1	8.4Kb	incomplete	40	10	119716-128139 info_outline	PHAGE_Brevib_Abouo_NC_029029 (1)	0.3534
