Supplementray Information

Genome analysis revealed a repertoire of oligosaccharide utilizing CAZymes in *Weissella confusa* CCK931 and *Weissella cibaria* YRK005

Table S1. Number of genes associated with general COG functional categories.

COG category distribution	**Description**	**Code**	***W. cibaria-YRK005***		***W. confusa-CCK931***	
			Value	%	*Value*	%
CELLULAR PROCESSES AND SIGNALING	Cell cycle control, cell division, chromosome partitioning	**D**	30	1.36%	30	1.36%
	Cell wall/membrane/envelope biogenesis	**M**	96	4.37%	111	5.05%
	Cell motility	**N**	9	0.41%	8	0.36%
	Posttranslational modification, protein turnover, chaperones	**O**	48	2.18%	46	2.09%
	Signal transduction mechanisms	**T**	38	1.73%	44	2.00%
	Intracellular trafficking, secretion, and vesicular transport	**U**	11	0.50%	11	0.50%
	Defense mechanisms	**V**	45	2.05%	43	1.96%
INFORMATION STORAGE AND PROCESSING	Translation, ribosomal structure and biogenesis	**J**	183	8.32%	182	8.28%
	Transcription	**K**	103	4.68%	105	4.78%
	Replication, recombination and repair	**L**	101	4.59%	93	4.23%
METABOLISM	Energy production and conversion	**C**	66	3.00%	66	3.00%
	Amino acid transport and metabolism	**E**	123	5.59%	138	6.28%
	Nucleotide transport and metabolism	**F**	96	4.37%	91	4.14%
	Carbohydrate transport and metabolism	**G**	148	6.73%	156	7.09%
	Coenzyme transport and metabolism	**H**	70	3.18%	71	3.23%
	Lipid transport and metabolism	**I**	67	3.05%	68	3.09%
	Inorganic ion transport and metabolism	**P**	83	3.77%	83	3.77%
	Secondary metabolites biosynthesis, transport and catabolism	**Q**	14	0.64%	17	0.77%
POORLY CHARACTERISED	General function prediction only	**R**	84	3.82%	86	3.91%
	Function unknown	**S**	119	5.41%	111	5.05%

Table S2: Number and types of CAZymes present in *W. cibaria* YRK005.

Sr. No.	Gene ID	Number of Tools	HMMER	DIAMOND	Hotpep
1.	NZ_JACGMM010000001.1_1	1	N	N	GH25+GH73
2.	NZ_JACGMM010000001.1_12	3	GH73(42-180)	GH73	GH73
3.	NZ_JACGMM010000001.1_14	3	GT2_Glycos_transf_2(5-152)	GT2	GT2
4.	NZ_JACGMM010000001.1_140	3	GH2(20-629)	GH2	GH2+CBM67
5.	NZ_JACGMM010000001.1_150	3	GH1(4-482)	GH1	GH1
6.	NZ_JACGMM010000001.1_151	1	N	N	GH25+GH73
7.	NZ_JACGMM010000001.1_16	2	GT2_Glycos_transf_2(4-171)	GT2	N
8.	NZ_JACGMM010000001.1_17	2	GT2_Glycos_transf_2(5-169)	GT2	N
9.	NZ_JACGMM010000001.1_18	1	N	N	GH73
10.	NZ_JACGMM010000001.1_192	3	GT51(84-257)	GT51	GT51
11.	NZ_JACGMM010000001.1_2	3	GH25(46-226)	GH25	GH25+GH73
12.	NZ_JACGMM010000001.1_208	2	GH73(119-253)	GH73	N
13.	NZ_JACGMM010000001.1_21	2	N	GH23	GH73
14.	NZ_JACGMM010000001.1_227	3	GH70(389-1182)	GH70	GH70
15.	NZ_JACGMM010000001.1_307	3	GH32(13-316)	GH32	GH32
16.	NZ_JACGMM010000001.1_38	1	N	N	GH25+GH73
17.	NZ_JACGMM010000001.1_51	3	GT4(204-342)	GT4	GT4
18.	NZ_JACGMM010000001.1_53	2	GT2_Glycos_transf_2(16-159)	GT2	N
19.	NZ_JACGMM010000001.1_58	2	GT2_Glycos_transf_2(26-123)	GT2	N
20.	NZ_JACGMM010000001.1_62	1	N	N	GH25+GH73
21.	NZ_JACGMM010000001.1_75	1	N	GH13_30	N
22.	NZ_JACGMM010000001.1_8	2	GT111(3-216)	GT111	N
23.	NZ_JACGMM010000002.1_103	3	GH13_31(29-380)	GH13_31	GH13

24.	NZ_JACGMM010000002.1_126	2	N	CBM50	CBM50
25.	NZ_JACGMM010000002.1_152	1	N	CBM50	N
26.	NZ_JACGMM010000002.1_153	1	N	CBM50	N
27.	NZ_JACGMM010000002.1_154	1	N	CBM50	N
28.	NZ_JACGMM010000002.1_166	3	GH3(36-275)	GH3	GH3+CBM6
29.	NZ_JACGMM010000002.1_229	1	N	GT13	N
30.	NZ_JACGMM010000002.1_232	2	GT4(374-560)	GT4	N
31.	NZ_JACGMM010000002.1_233	1	N	GT4	N
32.	NZ_JACGMM010000002.1_271	1	N	GH28	N
33.	NZ_JACGMM010000003.1_159	1	N	N	GH73
34.	NZ_JACGMM010000003.1_175	3	GH65(317-694)	GH65	GH65
35.	NZ_JACGMM010000003.1_201	2	GT4(324-478)	GT4	N
36.	NZ_JACGMM010000003.1_203	2	GT4(323-436)	GT4	N
37.	NZ_JACGMM010000003.1_210	1	N	CBM50	N
38.	NZ_JACGMM010000003.1_219	3	GH1(9-483)	GH1	GH1
39.	NZ_JACGMM010000003.1_4	3	GT4(159-309)	GT4	GT4
40.	NZ_JACGMM010000003.1_5	3	GT4(202-331)	GT4	GT4
41.	NZ_JACGMM010000003.1_93	1	N	N	GH23
42.	NZ_JACGMM010000004.1_109	2	GT4(270-416)	GT4	N
43.	NZ_JACGMM010000004.1_134	2	N	CBM50	CBM50
44.	NZ_JACGMM010000004.1_152	3	GH1(4-482)	GH1	GH1
45.	NZ_JACGMM010000004.1_155	3	GH1(6-479)	GH1	GH1
46.	NZ_JACGMM010000004.1_19	1	N	N	GH23
47.	NZ_JACGMM010000004.1_60	1	N	GT2	N
48.	NZ_JACGMM010000004.1_73	3	GT28(188-352)	GT28	GT28
49.	NZ_JACGMM010000004.1_8	3	GH73(79-217)	GH73	GH73

50.	NZ_JACGMM010000005.1_144	1	N	GT2	N
51.	NZ_JACGMM010000005.1_190	3	GH43_26(5-313)	GH43_26	GH43+CBM13+CBM42
52.	NZ_JACGMM010000005.1_211	2	GT2_Glyco_tranf_2_3(49-279)	GT2	N
53.	NZ_JACGMM010000005.1_213	3	GH8(36-367)	GH8	GH8
54.	NZ_JACGMM010000005.1_214	2	N	GT0	GT0
55.	NZ_JACGMM010000005.1_224	2	GT2_Glycos_transf_2(5-90)	GT2	N
56.	NZ_JACGMM010000005.1_226	2	GT2_Glycos_transf_2(6-112)	GT2	N
57.	NZ_JACGMM010000005.1_227	1	N	GT2	N
58.	NZ_JACGMM010000005.1_228	1	GT2_Glycos_transf_2(5-135)	N	N
59.	NZ_JACGMM010000005.1_28	3	GH1(2-463)	GH1	GH1
60.	NZ_JACGMM010000005.1_45	2	GT51(31-203)	GT51	N
61.	NZ_JACGMM010000006.1_130	3	CE9(8-374)	CE9	CE9
62.	NZ_JACGMM010000006.1_140	1	N	CBM50	N
63.	NZ_JACGMM010000006.1_7	2	GT4(184-324)	GT4	N
64.	NZ_JACGMM010000007.1_19	2	GT2_Glycos_transf_2(9-123)	GT2	N
65.	NZ_JACGMM010000007.1_25	3	GH1(6-475)	GH1	GH1
66.	NZ_JACGMM010000007.1_26	3	GH1(5-456)	GH1	GH1
67.	NZ_JACGMM010000007.1_33	1	N	GH42	N
68.	NZ_JACGMM010000007.1_60	2	GT4(336-486)	GT4	N
69.	NZ_JACGMM010000007.1_61	2	GT4(328-477)	GT4	N
70.	NZ_JACGMM010000007.1_80	1	N	GH6	N
71.	NZ_JACGMM010000007.1_87	3	GH31(274-703)	GH31	GH31
72.	NZ_JACGMM010000008.1_22	1	N	N	GH73
73.	NZ_JACGMM010000008.1_3	3	GH25(36-211)	GH25	GH25
74.	NZ_JACGMM010000008.1_61	3	GT51(73-249)	GT51	GT51
75.	NZ_JACGMM010000008.1_81	1	N	N	GH23+CBM50

76.	NZ_JACGMM010000009.1_73	1	N	N	CE11
77.	NZ_JACGMM010000010.1_18	1	AA4(10-244)	N	N
78.	NZ_JACGMM010000011.1_11	3	GH13_39(182-488)	GH13_39	GH13+GH77+CBM20+CBM34+CBM48
79.	NZ_JACGMM010000011.1_12	3	GT35(95-792)	GT35	GT35
80.	NZ_JACGMM010000011.1_13	3	GT5(3-475)	GT5	GT5
81.	NZ_JACGMM010000011.1_15	1	N	GH13_9	N
82.	NZ_JACGMM010000011.1_16	3	CBM48(29-111)+GH13_9(177-473)	CBM48+GH13_9	GH13+CBM48
83.	NZ_JACGMM010000011.1_3	1	N	AA1	N
84.	NZ_JACGMM010000011.1_31	3	GH43_11(3-304)	GH43_11	GH43
85.	NZ_JACGMM010000011.1_43	1	N	CBM50	N
86.	NZ_JACGMM010000011.1_48	3	GH1(3-277)	GH1	GH1
87.	NZ_JACGMM010000011.1_49	3	GH1(5-177)	GH1	GH1
88.	NZ_JACGMM010000012.1_21	1	N	GH6	N
89.	NZ_JACGMM010000012.1_38	1	N	GH13_11	N
90.	NZ_JACGMM010000014.1_1	1	N	GT4	N
91.	NZ_JACGMM010000016.1_6	1	AA7(35-241)	N	N
92.	NZ_JACGMM010000018.1_7	1	N	GH32	N

Table S2: Number and types of CAZymes present in *W. confusa* CCK931.

Sr. No.	Gene ID	Number of Tools	HMMER	DIAMOND	Hotpep
1.	NZ_JACGMJ010000001.1_100	3	GT51(75-249)	GT51	GT51
2.	NZ_JACGMJ010000001.1_119	1	N	N	GH23
3.	NZ_JACGMJ010000001.1_135	1	GT111(3-215)	N	N
4.	NZ_JACGMJ010000001.1_142	2	GH73(43-180)	N	GH73
5.	NZ_JACGMJ010000001.1_143	2	GH25(5-135)	N	GH25
6.	NZ_JACGMJ010000001.1_145	3	GT2_Glycos_transf_2(5-170)	GT2	GT2
7.	NZ_JACGMJ010000001.1_149	1	GT2_Glycos_transf_2(7-141)	N	N
8.	NZ_JACGMJ010000001.1_150	2	GT2_Glycos_transf_2(4-170)	GT2	N
9.	NZ_JACGMJ010000001.1_153	2	GT2_Glycos_transf_2(7-125)	GT2	N
10.	NZ_JACGMJ010000001.1_180	1	N	CBM50	N
11.	NZ_JACGMJ010000001.1_197	1	N	GH13_30	N
12.	NZ_JACGMJ010000001.1_261	3	GH2(26-628)	GH2	GH2+CBM51+CBM67
13.	NZ_JACGMJ010000001.1_34	3	CBM34(6-131)+GH13_20(181-484)	CBM34+GH13_20	GH13+CBM20+CBM34
14.	NZ_JACGMJ010000001.1_35	3	GH65(317-695)	GH65	GH65
15.	NZ_JACGMJ010000001.1_42	2	GT4(213-359)	GT4	N
16.	NZ_JACGMJ010000002.1_13	3	GH120(310-400)	GH120	GH120+CBM6
17.	NZ_JACGMJ010000002.1_154	2	N	CBM50	CBM50
18.	NZ_JACGMJ010000002.1_178	3	GH43_11(4-315)	GH43_11	GH43
19.	NZ_JACGMJ010000002.1_187	1	N	N	CBM2
20.	NZ_JACGMJ010000002.1_219	3	GT28(188-352)	GT28	GT28
21.	NZ_JACGMJ010000002.1_270	1	N	N	GH23
22.	NZ_JACGMJ010000002.1_285	3	GH73(79-217)	GH73	GH73
23.	NZ_JACGMJ010000002.1_70	3	GH1(6-479)	GH1	GH1

24.	NZ_JACGMJ010000002.1_73	3	GH1(4-482)	GH1	GH1
25.	NZ_JACGMJ010000002.1_81	3	GH25(33-210)	GH25	GH25+CBM50
26.	NZ_JACGMJ010000002.1_93	1	N	CBM50	N
27.	NZ_JACGMJ010000003.1_22	2	GT2_Glycos_transf_2(9-135)	GT2	N
28.	NZ_JACGMJ010000003.1_33	2	GT4(336-486)	GT4	N
29.	NZ_JACGMJ010000003.1_34	2	GT4(329-478)	GT4	N
30.	NZ_JACGMJ010000003.1_57	1	N	CBM50	N
31.	NZ_JACGMJ010000003.1_77	2	GT4(182-324)	GT4	N
32.	NZ_JACGMJ010000003.1_84	1	N	GT30	N
33.	NZ_JACGMJ010000004.1_18	3	GH25(33-210)	GH25	GH25+CBM50
34.	NZ_JACGMJ010000004.1_22	3	GT51(78-256)	GT51	GT51
35.	NZ_JACGMJ010000004.1_38	3	GH1(4-482)	GH1	GH1
36.	NZ_JACGMJ010000005.1_4	3	GT4(159-310)	GT4	GT4
37.	NZ_JACGMJ010000005.1_5	3	GT4(198-330)	GT4	GT4
38.	NZ_JACGMJ010000006.1_21	2	GT2_Glyco_trans_2_3(89-306)	GT2	N
39.	NZ_JACGMJ010000006.1_29	1	N	GH13_11	N
40.	NZ_JACGMJ010000006.1_46	1	N	GH6	N
41.	NZ_JACGMJ010000007.1_3	3	GH31(274-703)	GH31	GH31
42.	NZ_JACGMJ010000007.1_5	3	GH8(36-366)	GH8	GH8+CBM36+CBM6
43.	NZ_JACGMJ010000007.1_87	2	N	CBM50	GH23
44.	NZ_JACGMJ010000007.1_90	2	GT51(59-230)	GT51	N
45.	NZ_JACGMJ010000008.1_47	3	GH1(3-463)	GH1	GH1
46.	NZ_JACGMJ010000008.1_57	1	N	GH42	N
47.	NZ_JACGMJ010000008.1_58	3	GH36(16-715)	GH36	GH36
48.	NZ_JACGMJ010000009.1_23	1	N	GH28	N
49.	NZ_JACGMJ010000009.1_47	1	N	GT4	N

50.	NZ_JACGMJ010000009.1_48	2	GT4(374-560)	GT4	N
51.	NZ_JACGMJ010000009.1_50	1	N	GT13	N
52.	NZ_JACGMJ010000010.1_45	3	GH70(342-1133)	GH70	GH70
53.	NZ_JACGMJ010000010.1_51	3	GH13_31(29-380)	GH13_31	GH13
54.	NZ_JACGMJ010000011.1_41	1	N	GT2	N
55.	NZ_JACGMJ010000012.1_34	1	N	CBM50	N
56.	NZ_JACGMJ010000012.1_39	2	N	GT0	GT0
57.	NZ_JACGMJ010000012.1_40	3	GH8(37-364)	GH8	GH8
58.	NZ_JACGMJ010000012.1_41	2	GT2_Glyco_tranf_2_3(49-279)	GT2	N
59.	NZ_JACGMJ010000012.1_8	3	GH32(13-318)	GH32	GH32
60.	NZ_JACGMJ010000013.1_16	2	N	CBM50	GH73+CBM50
61.	NZ_JACGMJ010000013.1_51	1	N	CBM50	N
62.	NZ_JACGMJ010000013.1_52	1	N	CBM50	N
63.	NZ_JACGMJ010000013.1_64	3	GH3(37-275)	GH3	GH3+CBM6
64.	NZ_JACGMJ010000013.1_8	2	GT2_Glycos_transf_2(59-230)	GT2	N
65.	NZ_JACGMJ010000014.1_12	3	GH13_39(182-487)	GH13_39	GH13+GH77+CBM20+CBM34+CBM48
66.	NZ_JACGMJ010000014.1_13	3	GT35(95-792)	GT35	GT35
67.	NZ_JACGMJ010000014.1_14	3	GT5(2-475)	GT5	GT5
68.	NZ_JACGMJ010000014.1_16	1	N	GH13_9	N
69.	NZ_JACGMJ010000014.1_17	3	CBM48(29-111)+GH13_9(177-473)	CBM48+GH13_9	GH13+CBM48
70.	NZ_JACGMJ010000014.1_29	3	GH43_11(3-304)	GH43_11	GH43
71.	NZ_JACGMJ010000014.1_3	1	N	AA1	N
72.	NZ_JACGMJ010000016.1_28	1	N	GT47	N
73.	NZ_JACGMJ010000016.1_29	1	N	CBM50	N
74.	NZ_JACGMJ010000016.1_40	3	CE9(6-375)	CE9	CE9
75.	NZ_JACGMJ010000017.1_28	1	N	GH13_3	N

76.	NZ_JACGMJ010000018.1_17	3	GH1(3-473)	GH1	GH1
77.	NZ_JACGMJ010000018.1_7	1	N	CBM50	N
78.	NZ_JACGMJ010000019.1_9	1	N	GT4	N
79.	NZ_JACGMJ010000020.1_14	3	GH1(5-214)	GH1	GH1
80.	NZ_JACGMJ010000020.1_15	3	GH1(9-264)	GH1	GH1
81.	NZ_JACGMJ010000022.1_5	1	N	CBM50	N
82.	NZ_JACGMJ010000022.1_8	1	N	GH32	N
83.	NZ_JACGMJ010000024.1_2	3	GH70(442-1238)	GH70	GH70

Table S3: Protein list observed in 2 *Weisella* spp. but not in 4 *Leuconostoc* spp.

Sr No.	Representative functions
1.	hypothetical protein
2.	hypothetical protein
3.	Secreted antigen GbpB/SagA/PcsB, putative peptidoglycan hydrolase
4.	Probable tautomerase yrdN (EC 5.3.2.-)
5.	hypothetical protein
6.	Substrate-specific component BioY of biotin ECF transporter
7.	Transcriptional regulator in cluster with unspecified monosaccharide ABC transport system
8.	Cell division protein FtsL
9.	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
10.	chromate reductase
11.	hypothetical protein
12.	Probable low-affinity inorganic phosphate transporter
13.	Glucosamine-6-phosphate deaminase (EC 3.5.99.6)
14.	Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)
15.	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)
16.	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
17.	hypothetical protein
18.	hypothetical protein
19.	hypothetical protein
20.	Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)
21.	Methionine ABC transporter substrate-binding protein
22.	NADH dehydrogenase (EC 1.6.99.3)
23.	hypothetical protein
24.	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
25.	FIG01073890: hypothetical protein
26.	hypothetical protein
27.	hypothetical protein
28.	Glyoxalase family protein
29.	DUF124 domain-containing protein
30.	hypothetical protein
31.	Glycosyltransferase
32.	hypothetical protein
33.	hypothetical protein
34.	hypothetical protein
35.	Methionine ABC transporter substrate-binding protein
36.	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1)
37.	Alanine racemase (EC 5.1.1.1)
38.	hypothetical protein
39.	Hypothetical secreted protein
40.	Purine nucleoside ABC transporter, substrate-binding protein
41.	hypothetical protein
42.	D-alanine aminotransferase (EC 2.6.1.21)
43.	hypothetical protein
44.	NADH dehydrogenase (EC 1.6.99.3)
45.	Purine nucleoside ABC transporter, substrate-binding protein
46.	Predicted hydrolase of the HAD superfamily

47.	HAD phosphatase YigL
48.	hypothetical protein
49.	Putative oxidoreductase
50.	hypothetical protein
51.	hypothetical protein
52.	Zinc-type alcohol dehydrogenase-like protein
53.	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
54.	hypothetical protein
55.	hypothetical protein
56.	oxidoreductase of aldo/keto reductase family, subgroup 1
57.	hypothetical protein
58.	Thymidine kinase (EC 2.7.1.21)
59.	Broad-specificity multidrug efflux pump YkkC
60.	hypothetical protein
61.	Uncharacterized MFS-type transporter
62.	hypothetical protein
63.	hypothetical protein
64.	Neopullulanase (EC 3.2.1.135)
65.	Glycogen phosphorylase (EC 2.4.1.1)
66.	Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)
67.	hypothetical protein
68.	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
69.	1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)
70.	hypothetical protein
71.	hypothetical protein
72.	hypothetical protein
73.	hypothetical protein
74.	COG5039: Exopolysaccharide biosynthesis protein
75.	hypothetical protein
76.	Immunoreactive protein Se23.5 (Fragment)
77.	Inner membrane protein YbiR, putative anion permease
78.	hypothetical protein
79.	Nicotinamidase/isochorismatase family protein
80.	Efflux ABC transporter, ATP-binding protein
81.	Efflux ABC transporter, permease protein
82.	6-phospho-beta-glucosidase (EC 3.2.1.86)
83.	FIG00749917: hypothetical protein
84.	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
85.	hypothetical protein
86.	DedA protein
87.	Transcriptional regulator, AcrR family
88.	hypothetical protein
89.	ABC-type amino acid transport/signal transduction system, periplasmic component/domain
90.	NAD-dependent protein deacetylase of SIR2 family
91.	hypothetical protein
92.	hypothetical protein
93.	hypothetical protein

94.	Coenzyme A transferase
95.	Enoyl-[acyl-carrier-protein] reductase [FMN, NADH] (EC 1.3.1.9), FabK => refractory to triclosan
96.	hypothetical protein
97.	Aryldialkylphosphatase related protein
98.	hypothetical protein
99.	hypothetical protein
100.	Uncharacterized MFS-type transporter
101.	Permease of the drug/metabolite transporter (DMT) superfamily
102.	bacterial seryl-tRNA synthetase related
103.	hypothetical protein
104.	hypothetical protein
105.	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
106.	hypothetical protein
107.	FIG01032596: hypothetical protein
108.	hypothetical protein
109.	hypothetical protein
110.	Shikimate kinase I (EC 2.7.1.71)
111.	Sugar:proton symporter
112.	hypothetical protein
113.	hypothetical protein
114.	hypothetical protein
115.	hypothetical protein
116.	hypothetical protein
117.	probable RNA methyltransferase
118.	hypothetical protein
119.	hypothetical protein
120.	hypothetical protein
121.	hypothetical protein
122.	hypothetical protein
123.	probable RNA methyltransferase
124.	Broad-specificity multidrug efflux pump YkkC
125.	hypothetical protein
126.	small multidrug resistance family (SMR) protein
127.	PTS system, trehalose-specific IIB component (EC 2.7.1.69) / PTS system, trehalose-specific IIC component (EC 2.7.1.69)
128.	hypothetical protein
129.	Uncharacterized oxidoreductase YhhX
130.	Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
131.	hypothetical protein
132.	hypothetical protein
133.	hypothetical protein
134.	Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52)
135.	DNA-binding protein HBsu
136.	hypothetical protein
137.	hypothetical protein
138.	hypothetical protein
139.	hypothetical protein

140.	RecD-like DNA helicase YrrC
141.	Serine hydroxymethyltransferase (EC 2.1.2.1)
142.	UPF0473 protein YrzB
143.	hypothetical protein
144.	hypothetical protein
145.	hypothetical protein
146.	Oligopeptide ABC transporter, ATP-binding protein OppF (TC 3.A.1.5.1)
147.	Oligopeptide ABC transporter, ATP-binding protein OppD (TC 3.A.1.5.1)
148.	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
149.	Dipeptide ABC transporter, permease protein DppB (TC 3.A.1.5.2)
150.	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
151.	RecD-like DNA helicase YrrC
152.	hypothetical protein
153.	Oxidoreductase, short-chain dehydrogenase/reductase family
154.	hypothetical protein
155.	hypothetical protein
156.	hypothetical protein
157.	hypothetical protein
158.	Predicted acyltransferase
159.	Hydrolase, HAD superfamily
160.	Acylamino-acid-releasing enzyme (EC 3.4.19.1)
161.	Transcriptional regulator, PadR family
162.	Methionine ABC transporter substrate-binding protein
163.	hypothetical protein
164.	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)
165.	hypothetical protein
166.	hypothetical protein
167.	hypothetical protein
168.	hypothetical protein
169.	oxidoreductase of aldo/keto reductase family, subgroup 1
170.	hypothetical protein
171.	hypothetical protein
172.	Zinc-type alcohol dehydrogenase-like protein
173.	hypothetical protein
174.	L-lactate permease
175.	hypothetical protein
176.	FIG00627713: hypothetical protein
177.	alpha-xylosidase (EC 3.2.1.177)
178.	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
179.	Two-component transcriptional response regulator, OmpR family
180.	hypothetical protein
181.	hypothetical protein
182.	D-serine/D-alanine/glycine transporter
183.	hypothetical protein
184.	hypothetical protein
185.	Transcriptional regulator, LacI family

186.	hypothetical protein
187.	Mn-dependent transcriptional regulator MntR
188.	hypothetical protein
189.	YoeB toxin protein
190.	Short-chain dehydrogenase
191.	hypothetical protein
192.	hypothetical protein
193.	hypothetical protein
194.	hypothetical protein
195.	hypothetical protein
196.	hypothetical protein
197.	hypothetical protein
198.	hypothetical protein
199.	hypothetical protein
200.	hypothetical protein
201.	Uncharacterized protein YaaN
202.	hypothetical protein
203.	Uncharacterized MFS-type transporter
204.	hypothetical protein
205.	hypothetical protein
206.	hypothetical protein
207.	Immunodominant staphylococcal antigen A precursor
208.	hypothetical protein
209.	Integral membrane protein TerC
210.	hypothetical protein
211.	hypothetical protein
212.	Exonuclease SbcD
213.	Exonuclease SbcC
214.	NUDIX hydrolase
215.	hypothetical protein
216.	hypothetical protein
217.	hypothetical protein
218.	hypothetical protein
219.	hypothetical protein
220.	hypothetical protein

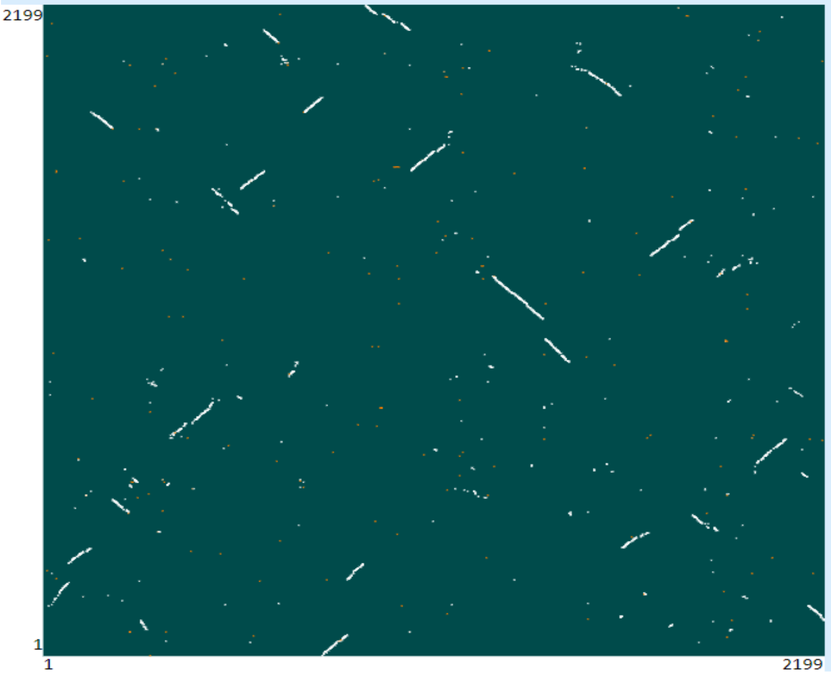

Fig. S1. Dot plot matrix of *W. confusa* CCK931 and *W. cibaria* YRK005.

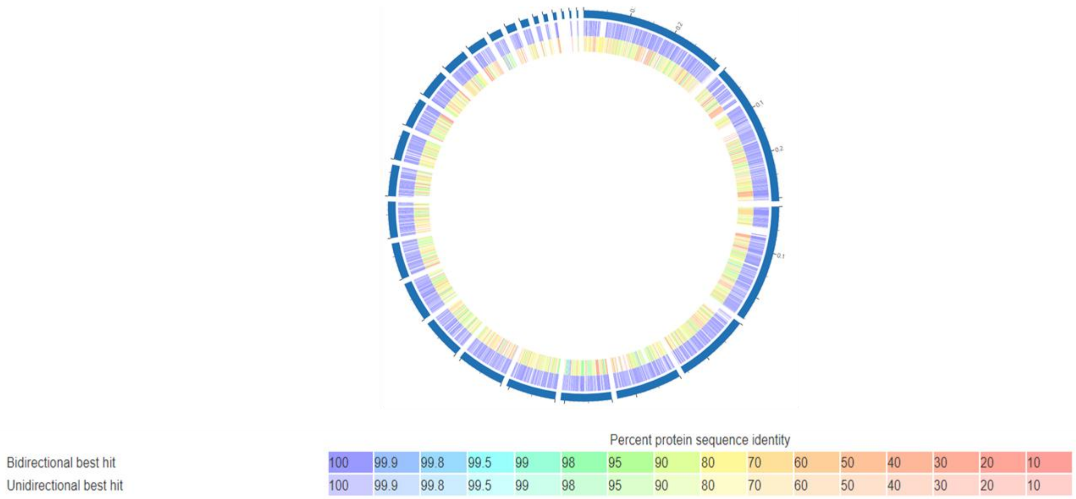

Fig. S2. Circular map based on protein sequence identity of *W. confusa* CCK931 and *W. cibaria* YRK005. CCK931 was used as a reference. Protein sequence identity (in percent) is depicted by different color codes as shown in the figure.

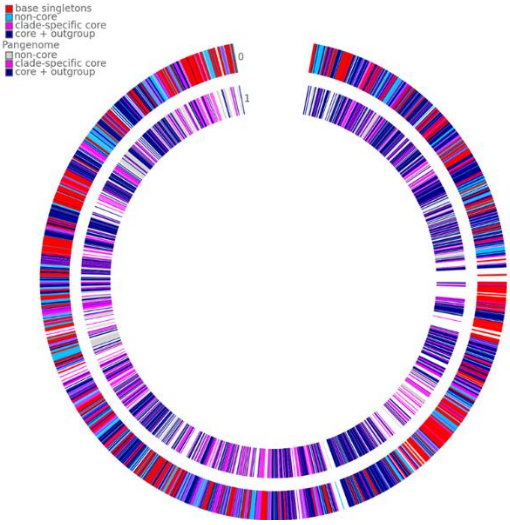

Fig. S3. Circle plot depicting the clade specific genes. *W. confusa* CCK931 was used as reference genome and *E. coli* MG1655 as an outgroup. 0 depicts *W. confusa* CCK931 and 1 depicts *W. cibaria* YRK005. Genes in pink are unique to *Weissella* spp.

Singleton: The genes in the reference genome with no sequence homology to genes in other genome. Clade-specific Core: Core gene orthologue clusters contain functions that are universal to all life. Nonspecific Core is present in all genomes, whereas Clade-specific Core is present in all but the outgroup genome. That means Clade-specific Core is present only in *Weisella* and not in *E. coli*. Other than these are non-core genes.