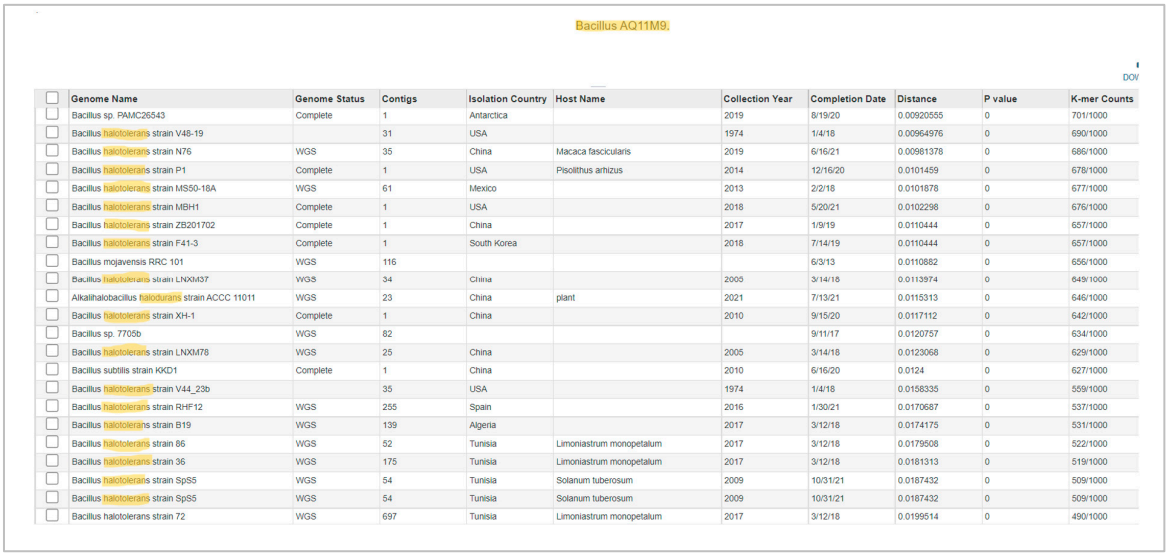
Supplementary figures and tables.



Genome Name	Genome Status	Contigs	Isolation Country	Host Name	Collection Year	Completion Date	Distance	P value	K-mer Counts
Bacillus sp. PAMC26543	Complete	1	Antarctica		2019	8/19/20	0.00920555	0	701/1000
Bacillus halotolerans strain V48-19		31	USA		1974	1/4/18	0.00964976	0	690/1000
Bacillus halotolerans strain N76	WGS	35	China	Macaca fascicularis	2019	6/16/21	0.00961378	0	686/1000
Bacillus halotolerans strain P1	Complete	1	USA	Pisolithus arhizus	2014	12/16/20	0.0101459	0	678/1000
Bacillus halotolerans strain MS50-18A	WGS	61	Mexico		2013	2/2/18	0.0101878	0	677/1000
Bacillus halotolerans strain MBH1	Complete	1	USA		2018	5/20/21	0.0102298	0	676/1000
Bacillus halotolerans strain ZB201702	Complete	1	China		2017	1/9/19	0.0110444	0	657/1000
Bacillus halotolerans strain F41-3	Complete	1	South Korea		2018	7/14/19	0.0110444	0	657/1000
Bacillus mojavensis RRC 101	WGS	116				6/3/13	0.0110882	0	656/1000
Bacillus halotolerans strain LNXM37	WGS	34	China		2005	3/14/18	0.0113974	0	649/1000
Alkalihalobacillus halodurans strain ACCC 11011	WGS	23	China	plant	2021	7/13/21	0.0115313	0	646/1000
Bacillus halotolerans strain XH-1	Complete	1	China		2010	9/15/20	0.0117112	0	642/1000
Bacillus sp. 7705b	WGS	82				9/11/17	0.0120757	0	634/1000
Bacillus halotolerans strain LNXM78	WGS	25	China		2005	3/14/18	0.0123068	0	629/1000
Bacillus subtilis strain KKD1	Complete	1	China		2010	6/16/20	0.0124	0	627/1000
Bacillus halotolerans strain V44_23b		35	USA		1974	1/4/18	0.0158335	0	559/1000
Bacillus halotolerans strain RHF12	WGS	255	Spain		2016	1/30/21	0.0170687	0	537/1000
Bacillus halotolerans strain B19	WGS	139	Algeria		2017	3/12/18	0.0174175	0	531/1000
Bacillus halotolerans strain 86	WGS	52	Tunisia	Limoniastrum monopetalum	2017	3/12/18	0.0179508	0	522/1000
Bacillus halotolerans strain 36	WGS	175	Tunisia	Limoniastrum monopetalum	2017	3/12/18	0.0181313	0	519/1000
Bacillus halotolerans strain SpS5	WGS	54	Tunisia	Solanum tuberosum	2009	10/31/21	0.0187432	0	509/1000
Bacillus halotolerans strain SpS5	WGS	54	Tunisia	Solanum tuberosum	2009	10/31/21	0.0187432	0	509/1000
Bacillus halotolerans strain 72	WGS	697	Tunisia	Limoniastrum monopetalum	2017	3/12/18	0.0199514	0	490/1000

Figure S1. Whole-genome sequence analysis in PATRIC for taxonomy of AQ11M9.

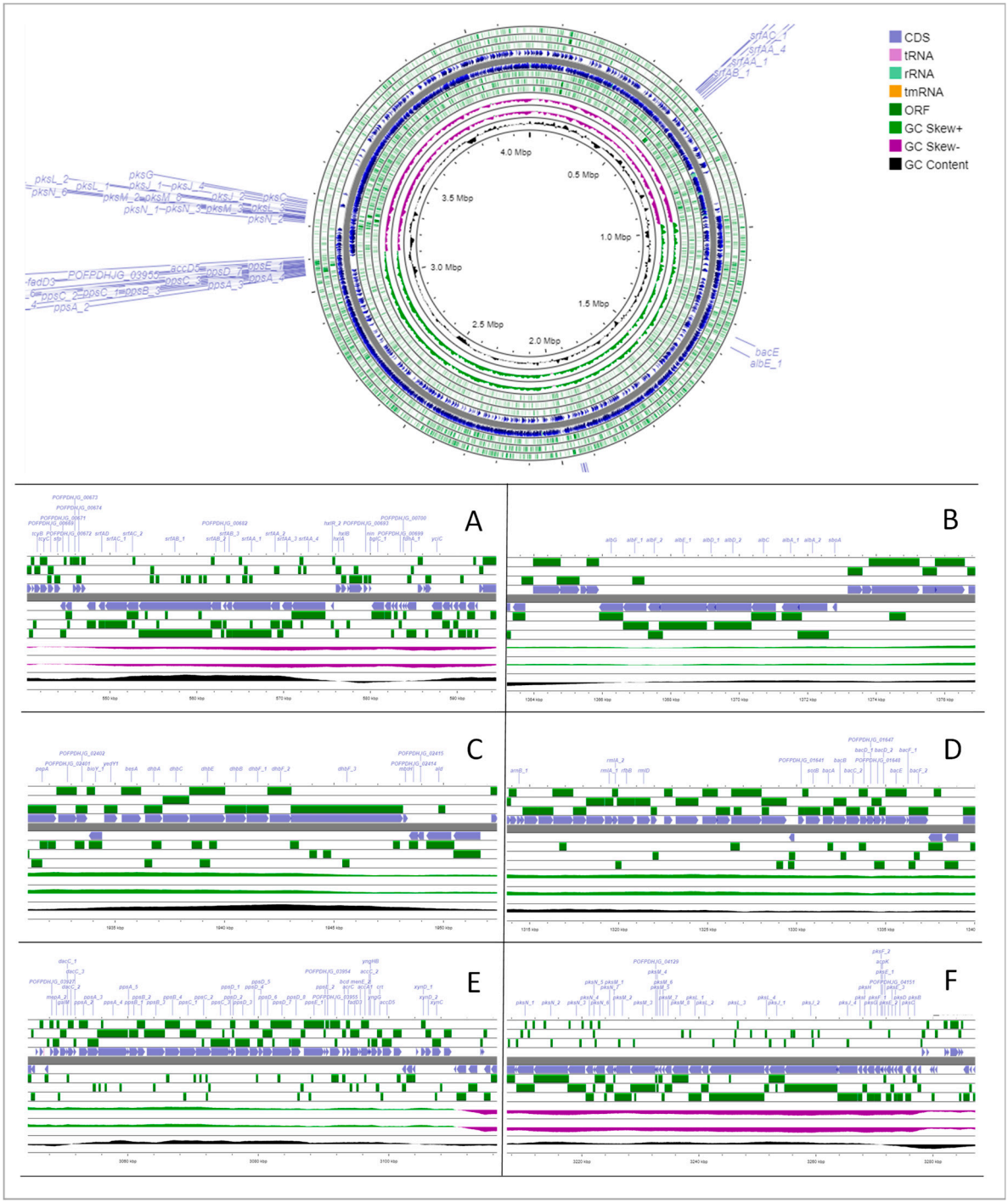


Figure S2. Top: Circular genome map for Bacillus halotolerans AQ11M9 strain represents all names of gene cluster. (A) Surfactin gene cluster; (B) subtilosin A gene cluster; (C) bacillibactin and paenibactin gene clusters; (D) bacilysin gene cluster; (E) fengycin, plipastatin and mycosubtilin gene clusters; (F) bacillaene and macrobrevin gene clusters.

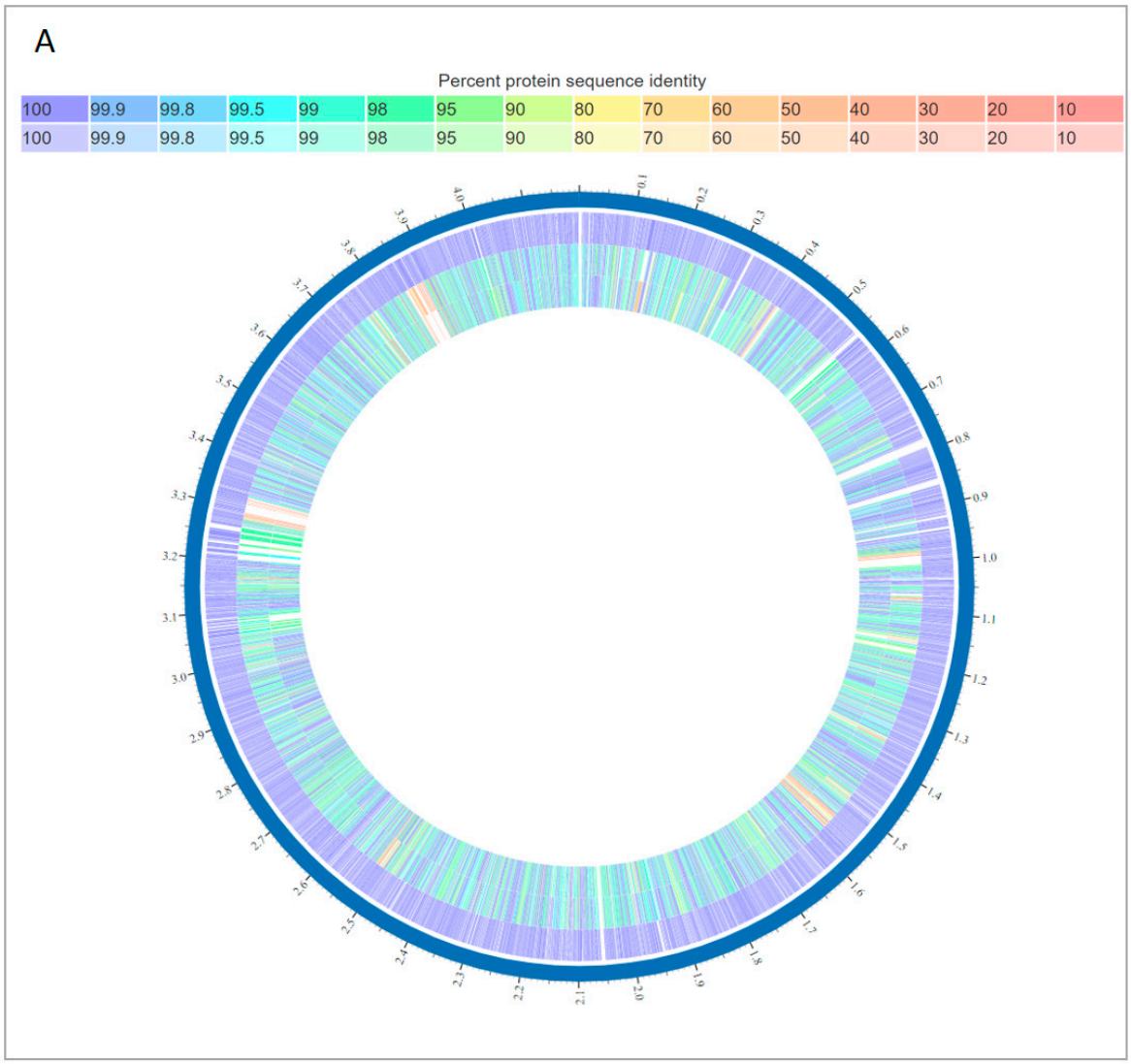


Figure S3. Proteome comparison from outside to inside AQ11M9, *B. halotolerans* strain V48-19 and PAMC26543.

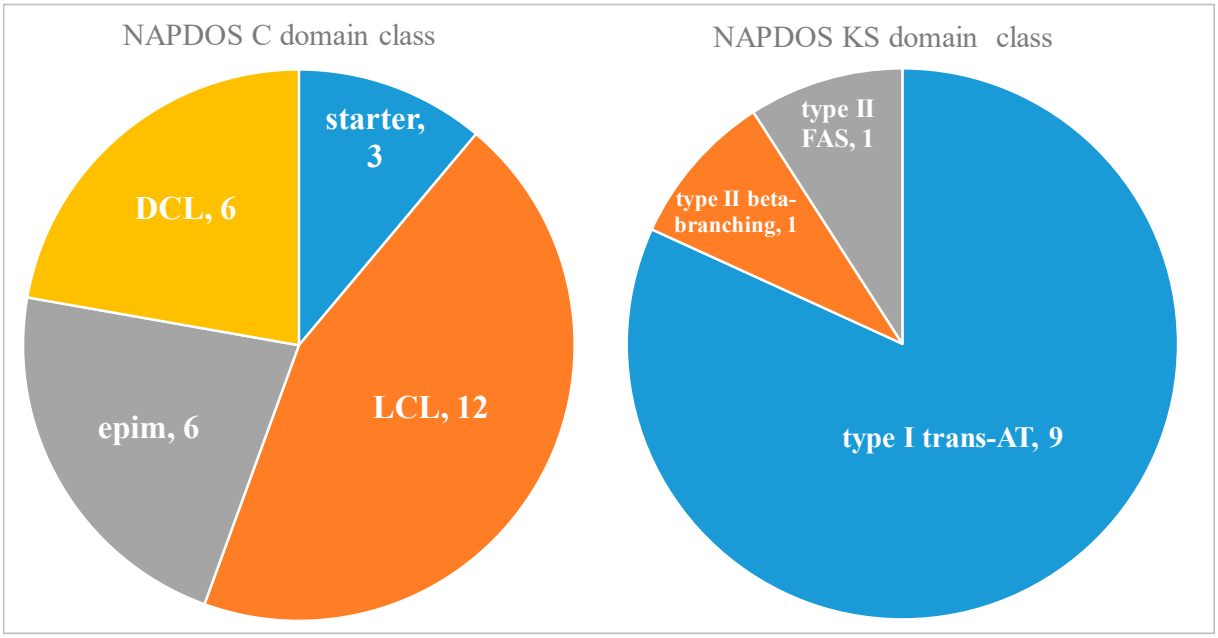


Figure S4. (A) NAPDOS organization of NRPS C domain in *B. halotolerans* AQ11M9 genome. Starter: first module of NRPS; Epim: epimerization domains which change the chirality from L- to D-amino acid in the last amino acid in the chain; LCL: catalyze establishment of a peptide bond between two L-amino acids; DCL: growing peptide linked with an L-amino acid ending with a D-amino acid. (B) NAPDOS arrangement of NRPS KS domain in *B. halotolerans* AQ11M9 genome. Type I trans AT is one of the Type I PKS classes; the acyltransferase (AT) activity is contributed via one or several independent proteins. Type II beta-branching is one of the Type II PKS classes responsible for the introduction of B-keto branches. Type II FAS, discrete, monofunctional proteins.

Table S1. Gene Family Statistics used for constructing whole genome phylogenetic tree of AQ11M9.

PGFam	Align. Score	Align. Length	Num Seqs	Mean Sqr Freq	Prop Gaps	Used In Analysis	Product
PGF_00060409	21.07	723	66	0.784	0.043	True	Translation elongation factor G
PGF_08675943	20.48	1281	66	0.572	0.088	True	Transcription-repair coupling factor
PGF_03272313	18.92	1040	66	0.587	0.199	True	DNA gyrase subunit A (EC 5.99.1.3)
PGF_00007041	18.17	663	66	0.706	0.076	True	GTP-binding protein TypA/BipA
PGF_05195027	17.52	498	66	0.785	0.054	True	ATP synthase beta chain (EC 3.6.3.14)
PGF_04569524	17.18	558	66	0.727	0.100	True	ATP synthase alpha chain (EC 3.6.3.14)
PGF_00016338	15.76	486	66	0.715	0.132	True	ATP-dependent Clp protease ATP-binding subunit ClpX
PGF_00052238	15.20	528	66	0.661	0.150	True	Signal recognition particle protein Ffh
PGF_04333086	15.10	859	66	0.515	0.218	True	DNA ligase (NAD(+)) (EC 6.5.1.2)
PGF_02226715	14.81	826	66	0.515	0.175	True	ATP-dependent DNA helicase RecG (EC 3.6.4.12)
PGF_10300474	13.92	1267	66	0.391	0.444	True	DNA topoisomerase I (EC 5.99.1.2)
PGF_00016393	13.77	282	66	0.820	0.020	True	LSU ribosomal protein L2p (L8e)
PGF_00422271	13.28	372	66	0.689	0.152	True	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)
PGF_00007024	13.19	576	66	0.550	0.237	True	GTP-binding protein EngA
PGF_02019462	12.38	404	66	0.616	0.147	True	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
PGF_02452671	11.98	533	66	0.519	0.195	True	Cell division trigger factor (EC 5.2.1.8)
PGF_03004613	11.79	542	66	0.506	0.213	True	Histidyl-tRNA synthetase (EC 6.1.1.21)
PGF_07063065	11.54	556	66	0.490	0.315	True	Transcription termination protein NusA
PGF_00016357	11.47	246	66	0.731	0.060	True	LSU ribosomal protein L1p (L10Ae)
PGF_00016443	10.78	185	66	0.792	0.035	True	LSU ribosomal protein L5p (L11e)
PGF_06162930	10.67	554	66	0.453	0.185	True	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase (EC 6.3.2.9)
PGF_00015259	10.26	329	66	0.566	0.129	True	ATP synthase gamma chain (EC 3.6.3.14)
PGF_04512522	10.00	216	66	0.680	0.052	True	LSU ribosomal protein L4p (L1e)
PGF_00016444	9.63	184	66	0.710	0.030	True	LSU ribosomal protein L6p (L9e)
PGF_00016343	9.62	146	66	0.796	0.045	True	LSU ribosomal protein L16p (L10e)
PGF_00423533	9.48	388	66	0.481	0.252	True	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
PGF_03215471	9.34	327	66	0.516	0.113	True	16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)
PGF_04807486	9.29	377	66	0.479	0.160	True	tRNA dimethylallyltransferase (EC 2.5.1.75)
PGF_00048926	9.28	188	66	0.676	0.016	True	Ribosome recycling factor
PGF_00049906	9.19	134	66	0.794	0.015	True	SSU ribosomal protein S8p (S15Ae)
PGF_00689961	8.99	243	66	0.577	0.159	True	Guanylate kinase (EC 2.7.4.8)
PGF_06180597	8.89	155	66	0.714	0.075	True	LSU ribosomal protein L13p (L13Ae)
PGF_08582746	8.89	342	66	0.481	0.269	True	23S rRNA (guanosine(2251)-2'-O)-methyltransferase (EC 2.1.1.185)
PGF_06626131	8.84	172	66	0.674	0.080	True	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
PGF_03790040	8.81	333	66	0.483	0.254	True	Ribonuclease III (EC 3.1.26.3)
PGF_00016445	8.35	129	66	0.736	0.060	True	LSU ribosomal protein L7p/L12p (P1/P2)
PGF_00413295	8.23	409	66	0.407	0.249	True	tRNA pseudouridine(55) synthase (EC 5.4.99.25)
PGF_00016358	8.20	129	66	0.722	0.085	True	LSU ribosomal protein L20p
PGF_00413554	7.99	198	66	0.568	0.210	True	tmRNA-binding protein SmpB

PGF_01213071	7.93	223	66	0.531	0.253	True	LSU ribosomal protein L10p (P0)
PGF_00060478	7.65	278	66	0.459	0.375	True	Translation initiation factor 3
PGF_08518355	7.65	330	66	0.421	0.268	True	ATP synthase F0 sector subunit a (EC 3.6.3.14)
PGF_04788810	7.58	224	66	0.506	0.152	True	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
PGF_06111020	7.45	251	66	0.470	0.159	True	Thymidylate kinase (EC 2.7.4.9)
PGF_03174068	7.27	326	66	0.403	0.448	True	Transcription antitermination protein NusG
PGF_00016377	6.69	140	66	0.566	0.256	True	LSU ribosomal protein L24p (L26e)
PGF_04978890	6.55	130	66	0.575	0.214	True	LSU ribosomal protein L21p
PGF_00020361	6.32	212	66	0.434	0.258	True	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly
PGF_00435430	5.75	164	66	0.449	0.278	True	Ribosomal silencing factor RsfA
PGF_03295678	5.72	466	66	0.265	0.580	True	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
PGF_00049901	5.14	141	66	0.433	0.315	True	SSU ribosomal protein S6p