Table S1. Sanger sequencing of 16S rRNA genes and taxonomy assigned to genus level by BLASTn against the NCBI database.

Facility	Isolate	Query cover (%; F/R)	E-value	Identity (%; F/R)	Closest cultivated genus
F1	F1_1	100	0.0	99.32	*Tenacibaculum*
F1	F1_2	100/99	0.0	98.38/98.02	*Tenacibaculum*
F1	F1_3	99	0.0	97.21	*Tenacibaculum*
F1	F1_4	99	0.0	98.74	*Shewanella*
F1	F1_5	99	0.0	98.92	*Litoreibacter*
F1	F1_6	99/100	0.0	98.70/99.12	*Shewanella*
F1	F1_7	99/99	0.0	98.75/97.48	*Litoreibacter*
F1	F1_8	100/100	0.0	98.82/98.26	*Vibrio*
F1	F1_9	100/100	0.0	97.77/98.30	*Vibrio*
F1	F1_10	98/99	0.0	98.70/98.73	*Vibrio*
F1	F1_11	100	0.0	99.31	*Vibrio*
F1	F1_12	100/100	0.0	98.56/98.76	*Vibrio*
F1	F1_13	97/100	0.0	98.41/98.43	*Vibrio*
F2	F2_1	99/99	0.0	98.92/99.17	*Joostella*
F2	F2_2	100	0.0	99.70	*Joostella*
F2	F2_3	98/99	0.0	98.93/99.72	*Joostella*
F2	F2_4	100	0.0	99.85	*Joostella*
F2	F2_5	N/A	N/A	N/A	*N/A*
F2	F2_6	N/A	N/A	N/A	*N/A*
F2	F2_7	98/99	0.0	98.18/98.44	*Tenacibaculum*
F2	F2_8	N/A	N/A	N/A	*N/A*
F2	F2_9	100	0.0	99.18	*Tenacibaculum*
F2	F2_10	99/99	0.0	98.75/98.15	*Epibacterium*
F2	F2_11	99/100	0.0	97.89/97.79	*Tenacibaculum*

F2	F2_12	100	0.0	99.92	*Epibacterium*
F2	F2_13	99/100	0.0	98.06/99.07	*Tenacibaculum*
F2	F2_14	99/100	0.0	97.98/98.33	*Vibrio*
F2	F2_15	100	0.0	98.99	*Vibrio*
F2	F2_16	99/100	0.0	98.14/98.26	*Tenacibaculum*
F2	F2_17	97/100	0.0	99.12/99.58	*Pseudoalteromonas*
F2	F2_18	99	0.0	99.12	*Tenacibaculum*
F2	F2_19	100	0.0	99.05	*Pseudoalteromonas*
F2	F2_20	100	0.0	99.10	*Tenacibaculum*
F2	F2_21	100	0.0	99.65	*Vibrio*
F2	F2_22	97	0.0	99.17	*Tenacibaculum*
F2	F2_23	99	0.0	99.00	*Pseudoalteromonas*
F2	F2_24	100	0.0	99.07	*Vibrio*
F2	F2_25	100	0.0	99.10	*Tenacibaculum*
F2	F2_26	100	0.0	99.65	*Pseudoalteromonas*
F2	F2_27	100	0.0	99.79	*Tenacibaculum*
F2	F2_28	99	0.0	99.77	*Epibacterium*
F2	F2_29	100/99	0.0	98.22/99.62	*Tenacibaculum*
F2	F2_30	95/100	0.0	90.99/98.91	*Pseudoalteromonas*
F2	F2_31	96	0.0	99.10	*Pseudoalteromonas*
F2	F2_32	100	0.0	98.31	*Vibrio*
F2	F2_33	100	0.0	99.72	*Tenacibaculum*
F2	F2_34	98	0.0	99.33	*Pseudoalteromonas*
F2	F2_35	98	0.0	98.60	*Pseudoalteromonas*

F/R: Forward read/Reverse read
N/A: Taxonomy could not be assigned at the genus level

Table S2. Gene occurrence in the 19 flavobacterial isolates. Strains are arranged with increasing susceptibility from left to right.

			Strain																		
Gene	**Non-unique Gene name**	**Annotation**	**F2_16**	**F2_27**	**F2_33**	**F2_9**	**F2_11**	**F2_13**	**F2_18**	**F2_29**	**F2_20**	**F2_22**	**F2_25**	**F1_2**	**F1_3**	**F2_1**	**F2_7**	**F1_1**	**F2_2**	**F2_3**	**F2_4**
cusA		Cation efflux system protein CusA	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
parD1_1		Antitoxin ParD1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
gltD		Glutamate synthase [NADPH] small chain	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
parE1_1		Toxin ParE1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
lemA		Protein LemA	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
nosZ		Nitrous-oxide reductase	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
metF		5,10-methylenetetrahydrofolate reductase	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
bepE_1		Efflux pump membrane transporter BepE	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
gltB_2		Ferredoxin-dependent glutamate synthase 1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
ypdB_3		Transcriptional regulatory protein YpdB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mnmE		tRNA modification GTPase MnmE	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_142	cusA	Cation efflux system protein CusA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_1565		L-proline cis-4-hydroxylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rpsU		30S ribosomal protein S21	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
copZ		Copper chaperone CopZ	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
cusB		Cation efflux system protein CusB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
trpF		N-(5'-phosphoribosyl)anthranilate isomerase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_1641		oxidoreductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
dapL		LL-diaminopimelate aminotransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
chuR		Anaerobic sulfatase-maturating enzyme	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
hipO		Hippurate hydrolase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mobA		Molybdenum cofactor guanylyltransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nreB_4		Sensor histidine kinase LiaS	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

moeZ_1		adenylyltransferase/sulfurtransferase MoeZ	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
metC		Cystathionine beta-lyase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
endo I		Chitodextrinase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_1806		L-gulono-1,4-lactone dehydrogenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_1837		protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
iucC_1		Aerobactin synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
iucB		N(6)-hydroxylysine O-acetyltransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nlhH		Carboxylesterase NlhH	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yccM		electron transport protein YccM	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
sasA		Adaptive-response sensory-kinase SasA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
fieF		Ferrous-iron efflux pump FieF	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ccp_3		Cytochrome c551 peroxidase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nreB_2		Oxygen sensor histidine kinase NreB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pucA_1		xanthine dehydrogenase subunit A	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rsh		GTP pyrophosphokinase rsh	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_1993		Outer membrane lipoprotein Omp16	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rluA		Ribosomal large subunit pseudouridine synthase A	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
qmcA_2		Protein QmcA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rlmB_2		23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
kstR2_1		HTH-type transcriptional repressor KstR2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
arcB		Aerobic respiration control sensor protein ArcB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
comEC		ComE operon protein 3	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yrrB		TPR repeat-containing protein YrrB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
fnr		Fumarate and nitrate reduction regulatory protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
amnD		2-aminomuconate deaminase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
birA		Bifunctional ligase/repressor BirA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
chrR		Quinone reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
argB		Acetylglutamate kinase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
proC		Pyrroline-5-carboxylate reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
msrA		Peptide methionine sulfoxide reductase MsrA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2323	yfkO_1	NAD(P)H nitroreductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

ppiB_1		peptidyl-prolyl cis-trans isomerase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
fkpA		FKBP-type peptidyl-prolyl cis-trans isomerase FkpA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
phoD		Alkaline phosphatase D	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
comP_2		Sensor histidine kinase ComP	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yjjG		Pyrimidine 5'-nucleotidase YjjG	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2465	cirA_1	Colicin I receptor	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
btsR_1		Transcriptional regulatory protein BtsR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pphA		Serine/threonine-protein phosphatase 1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
inlJ_1		Internalin-J	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
araC_2		Transposon Tn10 TetD protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
dapA_1		4-hydroxy-tetrahydrodipicolinate synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2557		Alpha-ketoglutaric semialdehyde dehydrogenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pucB		Purine catabolism protein PucB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ypdA_7		Sensor histidine kinase YpdA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pld		Phospholipase D	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2570	lemA	Protein LemA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2591		Outer membrane lipoprotein Omp16	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
acuR		Transcriptional regulator AcuR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ideR		Iron-dependent repressor IdeR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
uspF		Universal stress protein F	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
secE2		Calcium dodecin	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
bepC		Outer membrane efflux protein BepC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ypmQ_2		SCO1 protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2684	susC_3	TonB-dependent receptor SusC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
bsn_2		Extracellular ribonuclease	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
doeB_1		N-alpha-acetyl-L-2,4-diaminobutyric acid deacetylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rimK_2		Ribosomal protein S6--L-glutamate ligase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2716	sigW_1	ECF RNA polymerase sigma factor SigE	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nprS		Thermolysin	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
cbhB		Exoglucanase B	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
katG_1		Catalase-peroxidase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ypdA_1		Sensor histidine kinase YpdA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

ddc_1		L-2,4-diaminobutyrate decarboxylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
iucD		L-lysine N6-monooxygenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
iucC_2		Aerobactin synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pchR_1		Regulatory protein PchR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ntcA_1		Global nitrogen regulator	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
sseA		3-mercaptopyruvate sulfurtransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
cbs_1		cystathionine beta-synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rluF		23S rRNA pseudouridine(2604) synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nnr		Bifunctional NAD(P)H-hydrate repair enzyme Nnr	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2842		Epimerase family protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ggt		Glutathione hydrolase proenzyme	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rlmG		Ribosomal RNA large subunit methyltransferase G	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
kdhB		6-hydroxypseudooxynicotine dehydrogenase complex subunit beta	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
steT		Serine/threonine exchanger SteT	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
bshC		cysteine ligase BshC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2885	ypdA_4	Sensor histidine kinase BtsS	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_2889		Acetyltransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
scdA		Iron-sulfur cluster repair protein ScdA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ygiD		4,5-DOPA dioxygenase extradiol	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ywrO		General stress protein 14	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ybiT_2		ABC transporter ATP-binding protein YbiT	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
entC		Isochorismate synthase EntC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
idi_1		Isopentenyl-diphosphate Delta-isomerase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ypdA_6		Sensor histidine kinase YpdA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
oar		Protein oar	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
hisD		Histidinol dehydrogenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nhaA		Na(+)/H(+) antiporter NhaA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
prmC		Release factor glutamine methyltransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
prfB_1		Peptide chain release factor RF2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rtcB		RNA-splicing ligase RtcB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yhhW		Quercetin 2,3-dioxygenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

aroK		Shikimate kinase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ply		Pneumolysin	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yueD		Benzil reductase ((S)-benzoin forming)	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rhaS_1		HTH-type transcriptional activator RhaS	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pgdA_2		Peptidoglycan deacetylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nemA		N-ethylmaleimide reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3023		Sulfurtransferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
gcdC		Glutaconyl-CoA decarboxylase subunit gamma	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ftnA		bacterial non-heme ferritin	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3029	resA_1	Thiol-disulfide oxidoreductase ResA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
tilS		tRNA(Ile)-lysidine synthase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ftsH_1		ATP-dependent zinc metalloprotease FtsH	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
clsA		Major cardiolipin synthase ClsA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mdtE		Multidrug resistance protein MdtE	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ybdG		Miniconductance mechanosensitive channel YbdG	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3057	zraR_1	Transcriptional regulatory protein ZraR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
alkB		Alkane 1-monooxygenase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
appB		Cytochrome bd-II ubiquinol oxidase subunit 2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3073		Thioredoxin-like protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3098		Major NAD(P)H-flavin oxidoreductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
gatA		Glutamyl-tRNA(Gln) amidotransferase subunit A	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
besA_1		Ferri-bacillibactin esterase BesA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ung		Uracil-DNA glycosylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3128		membrane protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
anmK		Anhydro-N-acetylmuramic acid kinase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3162	zraS_2	Sensor protein ZraS	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rnk		Regulator of nucleoside diphosphate kinase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
btr_5		HTH-type transcriptional activator Btr	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
katG_2		Catalase-peroxidase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
rhtB_2		Homoserine/homoserine lactone efflux protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ccoP2		Cbb3-type cytochrome c oxidase subunit CcoP2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

tlpA_2		Thiol:disulfide interchange protein TlpA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
resA_4		Thiol-disulfide oxidoreductase ResA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ohrA		Organic hydroperoxide resistance protein OhrA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ohrR		Organic hydroperoxide resistance transcriptional regulator	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3212		Outer membrane lipoprotein Omp16	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
manA		Mannose-6-phosphate isomerase ManA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ucpA		Oxidoreductase UcpA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3249		oxidoreductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
hutG_2		Formimidoylglutamase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
uvrY_2		Response regulator UvrY	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
corA		Cobalt/magnesium transport protein CorA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
atoE		short-chain fatty acid transporter	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3521		NADH dehydrogenase-like protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
alr1_2		Alanine racemase 1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3532	sglT_1	Sodium/glucose cotransporter	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
bepA_2		Beta-barrel assembly-enhancing protease	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
csgG		Curli production assembly/transport component CsgG	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yxlF_3		ABC transporter ATP-binding protein YxlF	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mtcA2		Carbonic anhydrase 2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
envC		Murein hydrolase activator EnvC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
moaD		Molybdopterin synthase sulfur carrier subunit	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3640		Asp/Glu-specific dipeptidyl-peptidase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3642		Bacterial leucyl aminopeptidase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yiaD		lipoprotein YiaD	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
xdhA		xanthine dehydrogenase molybdenum-binding subunit XdhA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yeeO		FMN/FAD exporter YeeO	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3705	cymR	HTH-type transcriptional regulator CymR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ytcD		HTH-type transcriptional regulator YtcD	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mtfA_1		Protein MtfA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3736		Cyclic nucleotide-gated potassium channel	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3737		Hydroxypyruvate reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

ompW		Outer membrane protein W	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
macB_1		Macrolide export ATP-binding/permease protein MacB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
susC_2		TonB-dependent receptor SusC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
fecR		Protein FecR	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
arfB		Peptidyl-tRNA hydrolase ArfB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
vgrG1_1		Actin cross-linking toxin VgrG1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3784	bepE_1	Efflux pump membrane transporter BepE	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
bepF		Efflux pump periplasmic linker BepF	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
clpC_1		ATP-dependent Clp protease ATP-binding subunit ClpC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
ndx1		Diadenosine hexaphosphate hydrolase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
dapF		Diaminopimelate epimerase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
atoC		Regulatory protein AtoC	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
nemR		HTH-type transcriptional regulator YxaF	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
benM_2		HTH-type transcriptional regulator BenM	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
uspG		Universal stress protein UP12	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
dapb3		Dipeptidyl aminopeptidase BIII	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yfkO_2		NAD(P)H nitroreductase YfkO	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
yjdJ		protein YjdJ	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3890		tautomerase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3891	crp	cAMP-activated global transcriptional regulator CRP	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3903		Butanoate coenzyme A-transferase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_3905	metF	5,10-methylenetetrahydrofolate reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
norB		Nitric oxide reductase subunit B	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
mfpA		Pentapeptide repeat protein MfpA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_4336		PKHD-type hydroxylase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
aprE		Subtilisin E	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
betS		Glycine betaine/proline betaine transporter BetS	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
glsA2		Glutaminase 2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
acoD		Acetaldehyde dehydrogenase 2	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
araC		Arabinose operon regulatory protein	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
phy		3-phytase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
macB_2		Macrolide export ATP-binding/permease protein MacB	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0

cydA	Cytochrome bd ubiquinol oxidase subunit 1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
deoD_2	Purine nucleoside phosphorylase DeoD-type	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
group_5479	Bifunctional NMN adenylyltransferase/Nudix hydrolase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
accA1	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
pccB	Propionyl-CoA carboxylase beta chain	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
topB	DNA topoisomerase 3	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
msrC	Free methionine-R-sulfoxide reductase	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
vgrG1_2	Actin cross-linking toxin VgrG1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
tri1_1	Tricorn protease	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
sigA_1	RNA polymerase sigma factor SigA	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
clpB	Chaperone protein ClpB	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
nrdG	Anaerobic ribonucleoside-triphosphate reductase-activating protein	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
spkD	Serine/threonine-protein kinase D	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
fpvA_1	Ferripyoverdine receptor	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
mecI	Methicillin resistance regulatory protein MecI	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
nuc	Thermonuclease	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
alsT_2	Amino-acid carrier protein AlsT	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0

1: Gene present
0: Gene absent

Table S3. Chrome Azurol S (CAS) assay for detection of siderophore excretion under various growth conditions.

	CAS assay					
	Growth conditions					
	1.5% $SS_{CAS+GLU}$		1.5% $SS_{CAS+MAN}$		½YTSS	
	15˚ C	25˚ C	15˚ C	25˚ C	15˚ C	25˚ C
DSM 17995 (*T. maritimum*)	-	-	-	-	-	-
F2_1 (*J. atrarenae*)	-	-	-	-	-	-
F1_2 (*T. soleae*)	-	-	-	-	-	-
F2_9 (*T. mesophilum*)	-	-	-	-	-	-
F2_11 (*T. discolor*)	-	-	-	-	-	-
Positive control (P*seudoalteromonas piscicidae* S2040)	+	+	+	+	+	+
Negative control	-	-	-	-	-	-

+/- denotes a positive or negative reaction in the assay.