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Comprehensive genome analysis of *Burkholderia contaminans* SK875, a quorum-sensing strain isolated from the swine

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Table S1. Genome features of *Burkholderia* species

#Organism Name	Strain	Size (Mb)	GC%	CDS	Assembly	Accession no.
<i>B. ambifaria</i>	MC40-6	7.64254	66.38	6,575	Complete	CP001025.1-CP001028.1
<i>B. ambifaria</i>	AMMD	7.52857	66.79	6,551	Complete	CP000440.1-CP000443.1
<i>B. ambifaria</i>	AMMD	7.52858	66.79	6,548	Complete	CP009797.1-CP009800.1
<i>B. cenocepacia</i>	J2315	8.05578	66.92	7,199	Complete	AM747720.1-AM747723.1
<i>B. cenocepacia</i>	AU 1054	7.27912	66.92	6,372	Complete	CP000378.1-CP000380.1
<i>B. cenocepacia</i>	MC0-3	7.97139	66.58	7,031	Complete	CP000958.1-CP000960.1
<i>B. cenocepacia</i>	HI2424	7.70284	66.80	6,867	Complete	CP000458.1-CP000461.1
<i>B. cenocepacia</i>	H111	7.71489	67.31	6,805	Complete	HG938370.1-HG938372.1
<i>B. cenocepacia</i>	DDS 22E-1	8.04525	66.97	7,038	Complete	CP007782.1-CP007784.1
<i>B. cenocepacia</i>	DWS 37E-2	6.61242	66.50	5,691	Complete	CP007779.1-CP007781.1
<i>B. cenocepacia</i>	ST32	8.09039	67.01	7,016	Complete	CP011917.1-CP011920.1
<i>B. cenocepacia</i>	842	8.1497	66.98	7,156	Complete	CP015032.1-CP015035.1
<i>B. cenocepacia</i>	895	8.73148	66.74	7,784	Complete	CP015036.1-CP015038.1
<i>B. cenocepacia</i>	FL-5-3-30-S1-D7	6.33075	67.04	5,624	Complete	CP013396.1-CP013397.1
<i>B. cenocepacia</i>	MSMB384WGS	7.7806	67.24	6,895	Complete	CP013450.1-CP013451.1
<i>B. cenocepacia</i>	VC7848	7.49946	66.90	6,631	Complete	CP019668.1
<i>B. cenocepacia</i>	VC12802	7.39491	67.03	6,508	Complete	CP019669.1-CP019670.1
<i>B. cenocepacia</i>	VC12308	7.6345	67.14	6,775	Complete	CP019671.1-CP019674.1
<i>B. cenocepacia</i>	CR318	7.66489	66.82	6,755	Complete	CP017238.1-CP017240.1
<i>B. cenocepacia</i>	PC184 Mulks	7.06705	66.83	6,177	Complete	CP021067.1-CP021069.1
<i>B. cenocepacia</i>	YG-3	8.03646	66.79	7,017	Complete	CP034545.1-CP034547.1
<i>B. cenocepacia</i>	PS27	7.60771	66.96	6,600	Complete	CP060039.1-CP060042.1
<i>B. cenocepacia</i>	K56-2	7.74192	67.02	6,851	Complete	CP053300.1-CP053303.1
<i>B. cepacia</i>	GG4	6.46732	66.71	5,724	Complete	CP003774.1-CP003775.1
<i>B. cepacia</i>	JBK9	8.48121	66.81	7,462	Complete	CP013730.1-CP013732.1
<i>B. cepacia</i>	DDS 7H-2	8.14711	67.06	7,280	Complete	CP007785.1-CP007787.1
<i>B. cepacia</i>	LO6	6.41938	67.00	5,542	Complete	CP011301.1
<i>B. cepacia</i>	UCB 717	8.60595	66.60	7,642	Complete	CP012981.1-CP012984.1
<i>B. cepacia</i>	INT3-BP177	7.33738	66.85	6,401	Complete	CP013375.1-CP013376.1
<i>B. cepacia</i>	MSMB1184WGS	8.00363	66.37	6,826	Complete	CP013442.1-CP013444.1
<i>B. cepacia</i>	FDAARGOS_3458.56985	66.58	7,655	Complete	CP022081.1-CP022084.2	
<i>B. cepacia</i>	FDAARGOS_3888.56982	66.58	7,615	Complete	CP023519.1-CP023521.1	
<i>B. cepacia</i>	ATCC 25416	8.56701	66.58	7,611	Complete	CP007745.1-CP007748.1
<i>B. cepacia</i>	ATCC 25416	8.57439	66.57	7,619	Complete	CP034553.1-CP034557.1
<i>B. cepacia</i>	BC16	8.36687	66.76	7,337	Complete	CP045235.1-CP045237.1
<i>B. cepacia</i>	39628	8.40391	66.79	7,194	Complete	CP032009.1-CP032011.1
<i>B. contaminans</i>	MS14	8.50925	66.40	7,494	Complete	CP009743.1-CP009745.1
<i>B. contaminans</i>	FL-1-2-30-S1-D0	8.17078	66.53	7,138	Complete	CP013390.1-CP013392.1
<i>B. contaminans</i>	ZCC	9.00224	66.06	7,724	Complete	CP042164.1-CP042168.1
<i>B. contaminans</i>	SK875	8.59605	66.30	7,564	Complete	CP028807.1-CP028810.1
<i>B. contaminans</i>	XL73	8.65686	66.27	7,565	Complete	CP046607.1-CP046611.1
<i>B. dolosa</i>	AU0158	6.40909	67.04	5,592	Complete	CP009793.1-CP009795.1
<i>B. dolosa</i>	FDAARGOS_5626.4091	67.04	5,612	Complete	CP033838.1-CP033840.1	
<i>B. lata</i>	383	8.67628	66.26	7,692	Complete	CP000150.1-CP000152.1
<i>B. lata</i>	FL-7-5-30-S1-D0	8.35484	66.50	7,345	Complete	CP013404.1-CP013406.1
<i>B. lata</i>	A05	8.78701	66.20	7,873	Complete	CP024943.1-CP024945.1
<i>B. multivorans</i>	ATCC 17616	7.00881	66.69	6,247	Complete	AP009385.1-AP009388.1
<i>B. multivorans</i>	ATCC 17616	7.00862	66.69	6,273	Complete	CP000868.1-CP000871.1
<i>B. multivorans</i>	DDS 15A-1	7.28187	66.60	6,460	Complete	CP008728.1-CP008730.1
<i>B. multivorans</i>	ATCC BAA-247	6.32275	67.20	5,584	Complete	CP009830.1-CP009832.1
<i>B. multivorans</i>	AU1185	6.62094	66.88	5,828	Complete	CP013430.1-CP013432.1

<i>B. multivorans</i>	MSMB1640WGS	6.84536	66.90	6,008	Complete	CP013466.1-CP013468.1
<i>B. multivorans</i>	FDAARGOS_2466	32286	67.20	5,828	Complete	CP020397.1-CP020399.1
<i>B. multivorans</i>	FDAARGOS_5476	39408	67.29	5,592	Complete	CP033748.1-CP033750.1
<i>B. multivorans</i>	FDAARGOS_5486	65386	66.99	5,837	Complete	CP033745.1-CP033747.1
<i>B. multivorans</i>	FDAARGOS_4967	79642	67.24	6,732	Complete	CP033854.1-CP033856.1
<i>B. multivorans</i>	FDAARGOS_6236	47862	67.12	5,918	Complete	CP044053.1-CP044055.1
<i>B. multivorans</i>	FDAARGOS_6226	47864	67.12	5,916	Complete	CP044056.1-CP044058.1
<i>B. multivorans</i>	FDAARGOS_7196	56565	67.25	5,785	Complete	CP046336.1-CP046340.1
<i>B. multivorans</i>	FDAARGOS_7266	51869	67.30	5,737	Complete	CP046341.1-CP046343.1
<i>B. multivorans</i>	FDAARGOS_7226	59044	67.08	5,873	Complete	CP046344.1-CP046346.1
<i>B. anthina</i>	BJQ0011	6.4565	66.39	5,759	Complete	CP066769.1-CP066770.1
<i>B. anthina</i>	1CH1	8.45737	66.27	7,654	Complete	CP071825.1-CP071829.1
<i>B. pyrrocinia</i>	DSM 10685	7.96135	66.47	6,924	Complete	CP011503.1-CP011506.1
<i>B. pyrrocinia</i>	mHSR5	8.0044	66.33	7,078	Complete	CP024902.1-CP024904.1
<i>B. stabilis</i>	ATCC BAA-67	8.52795	66.41	7,552	Complete	CP016442.1-CP016444.1
<i>B. stabilis</i>	FERMP-21014	7.7211	66.69	6,770	Complete	AP018111.1-AP018113.1
<i>B. ubonensis</i>	MSMB22	7.18907	67.31	6,206	Complete	CP009486.1-CP009488.1
<i>B. ubonensis</i>	RF23-BP41	7.9616	67.08	6,914	Complete	CP013368.1-CP013371.1
<i>B. ubonensis</i>	MSMB2035	7.23506	66.85	6,500	Complete	CP013414.1-CP013416.1
<i>B. ubonensis</i>	MSMB0783	6.68485	67.32	5,631	Complete	CP013420.1-CP013422.1
<i>B. ubonensis</i>	MSMB1189WGS	8.02876	66.79	6,968	Complete	CP013445.1-CP013447.1
<i>B. ubonensis</i>	MSMB1471WGS	7.46341	67.38	6,560	Complete	CP013462.1-CP013465.1
<i>B. vietnamiensis</i>	G4	8.39107	65.73	7,617	Complete	CP000614.1-CP000621.1
<i>B. vietnamiensis</i>	LMG 10929	6.9305	66.84	6,013	Complete	CP009629.1-CP009632.1
<i>B. vietnamiensis</i>	FL-2-3-30-S1-D0	6.81528	67.27	5,846	Complete	CP013393.1-CP013395.1
<i>B. vietnamiensis</i>	AU1233	6.83507	66.86	5,988	Complete	CP013433.1-CP013434.1
<i>B. vietnamiensis</i>	HI2297	6.76453	67.09	5,854	Complete	CP013439.1-CP013441.1
<i>B. vietnamiensis</i>	MSMB608WGS	6.89171	67.02	5,998	Complete	CP013453.1-CP013456.1
<i>B. vietnamiensis</i>	FDAARGOS_2396	93041	66.84	6,007	Complete	CP020393.1-CP020395.1

Table S2. COG distribution of the genes in *B. contaminans* SK875

Functional class	Category	Ratio (%)
Information storage and processing	J: Translation, ribosomal structure & biogenesis	3.02
	K: Transcription	10.87
	L: Replication, recombination & repair	2.55
Cellular processes and signaling	D: Cell cycle control, cell division, chromosome partitioning	0.54
	M: Cell wall/membrane/envelope biogenesis	5.96
	N: Cell motility	1.63
	O: Post-translational modification, protein turnover & chaperones	2.88
	T: Signal transduction mechanisms	4.30
	U: Intracellular trafficking, secretion & vesicular transport	2.67
	V: Defense mechanisms	0.97
Metabolism	P: Inorganic ion transport & metabolism	6.64
	F: Nucleotide transport & metabolism	1.49
	G: Carbohydrate transport & metabolism	6.45
	E: Amino acid transport & metabolism	11.06
	H: Coenzyme transport & metabolism	2.96
	I: Lipid transport & metabolism	4.78
	C: Energy production & conversion	5.91
	Q: Secondary metabolites biosynthesis, transport & catabolism	3.97
Poorly characterized	R: General function prediction only	14.15
	S: Function unknown	7.20

Table S3. KEGG distribution of the genes in *B. contaminans* SK875

KEGG pathway	Number of genes
Cell cycle [ko04110]	1
Cell cycle - yeast [ko04111]	1
Cell cycle - Caulobacter [ko04112]	9
Meiosis - yeast [ko04113]	1
Oocyte meiosis [ko04114]	1
p53 signaling pathway [ko04115]	3
Apoptosis [ko04210]	1
Bacterial chemotaxis [ko02030]	21
Flagellar assembly [ko02040]	15
Regulation of actin cytoskeleton [ko04810]	2
Adherens junction [ko04520]	1
Tight junction [ko04530]	2
Regulation of autophagy [ko04140]	1
Lysosome [ko04142]	7
Endocytosis [ko04144]	1
Peroxisome [ko04146]	36
ABC transporters [ko02010]	198
Phosphotransferase system (PTS) [ko02060]	5
Bacterial secretion system [ko03070]	18
Two-component system [ko02020]	95
Ras signaling pathway [ko04014]	1
cGMP - PKG signaling pathway [ko04022]	2
cAMP signaling pathway [ko04024]	4
HIF-1 signaling pathway [ko04066]	4
FoxO signaling pathway [ko04068]	5
Phosphatidylinositol signaling system [ko04070]	3
Sphingolipid signaling pathway [ko04071]	1
mTOR signaling pathway [ko04150]	1
PI3K-Akt signaling pathway [ko04151]	1
AMPK signaling pathway [ko04152]	5
Hippo signaling pathway [ko04390]	3
Hippo signaling pathway -fly [ko04391]	1
RNA degradation [ko03018]	14
Protein export [ko03060]	12
Ubiquitin mediated proteolysis [ko04120]	2
Sulfur relay system [ko04122]	8
Protein processing in endoplasmic reticulum [ko04141]	1
DNA replication [ko03030]	13
Base excision repair [ko03410]	10
Nucleotide excision repair [ko03420]	9
Mismatch repair [ko03430]	14
Homologous recombination [ko03440]	17
Fanconi anemia pathway [ko03460]	1
RNA polymerase [ko03020]	3
Basal transcription factors [ko03022]	3
Aminoacyl-tRNA biosynthesis [ko00970]	34

Ribosome biogenesis in eukaryotes [ko03008]	2
Ribosome [ko03010]	50
RNA transport [ko03013]	1
Transcriptional misregulation in cancers [ko05202]	1
Viral carcinogenesis [ko05203]	5
Chemical carcinogenesis [ko05204]	15
Proteoglycans in cancer [ko05205]	3
MicroRNAs in cancer [ko05206]	2
Central carbon metabolism in cancer [ko05230]	7
Choline metabolism in cancer [ko05231]	2
Viral myocarditis [ko05416]	1
beta-Lactam resistance [ko01501]	16
Vancomycin resistance [ko01502]	6
Cationic antimicrobial peptide (CAMP) resistance [ko01503]	14
Type II diabetes mellitus [ko04930]	1
Non-alcoholic fatty liver disease (NAFLD) [ko04932]	16
Type I diabetes mellitus [ko04940]	1
Primary immunodeficiency [ko05340]	2
Bacterial invasion of epithelial cells [ko05100]	1
Vibrio cholerae pathogenic cycle [ko05111]	3
Pathogenic Escherichia coli infection [ko05130]	2
Shigellosis [ko05131]	1
Salmonella infection [ko05132]	1
Pertussis [ko05133]	1
Legionellosis [ko05134]	3
Staphylococcus aureus infection [ko05150]	1
Tuberculosis [ko05152]	4
Herpes simplex infection [ko05168]	2
Alzheimer's disease [ko05010]	21
Parkinson's disease [ko05012]	20
Amyotrophic lateral sclerosis (ALS) [ko05014]	3
Huntington's disease [ko05016]	22
Cocaine addiction [ko05030]	1
Amphetamine addiction [ko05031]	1
Alcoholism [ko05034]	5
Alanine, aspartate and glutamate metabolism [ko00250]	38
Glycine, serine and threonine metabolism [ko00260]	44
Cysteine and methionine metabolism [ko00270]	30
Valine, leucine and isoleucine degradation [ko00280]	60
Valine, leucine and isoleucine biosynthesis [ko00290]	24
Lysine biosynthesis [ko00300]	24
Lysine degradation [ko00310]	31
Arginine and proline metabolism [ko00330]	51
Histidine metabolism [ko00340]	30
Tyrosine metabolism [ko00350]	24
Phenylalanine metabolism [ko00360]	26
Tryptophan metabolism [ko00380]	35
Phenylalanine, tyrosine and tryptophan biosynthesis [ko00400]	21
Caffeine metabolism [ko00232]	3

Monobactam biosynthesis [ko00261]	12
Carbapenem biosynthesis [ko00332]	2
Novobiocin biosynthesis [ko00401]	3
Streptomycin biosynthesis [ko00521]	9
Phenylpropanoid biosynthesis [ko00940]	3
Isoquinoline alkaloid biosynthesis [ko00950]	4
Tropane, piperidine and pyridine alkaloid biosynthesis [ko00960]	5
Glycolysis / Gluconeogenesis [ko00010]	48
Citrate cycle (TCA cycle) [ko00020]	25
Pentose phosphate pathway [ko00030]	27
Pentose and glucuronate interconversions [ko00040]	31
Fructose and mannose metabolism [ko00051]	18
Galactose metabolism [ko00052]	13
Ascorbate and aldarate metabolism [ko00053]	20
Starch and sucrose metabolism [ko00500]	17
Amino sugar and nucleotide sugar metabolism [ko00520]	25
Inositol phosphate metabolism [ko00562]	8
Pyruvate metabolism [ko00620]	47
Glyoxylate and dicarboxylate metabolism [ko00630]	46
Propanoate metabolism [ko00640]	27
Butanoate metabolism [ko00650]	47
C5-Branched dibasic acid metabolism [ko00660]	10
Oxidative phosphorylation [ko00190]	45
Photosynthesis [ko00195]	3
Methane metabolism [ko00680]	22
Carbon fixation in photosynthetic organisms [ko00710]	15
Carbon fixation pathways in prokaryotes [ko00720]	26
Nitrogen metabolism [ko00910]	11
Sulfur metabolism [ko00920]	52
N-Glycan biosynthesis [ko00510]	3
Other glycan degradation [ko00511]	3
Various types of N-glycan biosynthesis [ko00513]	1
Other types of O-glycan biosynthesis [ko00514]	4
Glycosaminoglycan degradation [ko00531]	1
Lipopolysaccharide biosynthesis [ko00540]	12
Peptidoglycan biosynthesis [ko00550]	26
Glycosphingolipid biosynthesis - globo series [ko00603]	1
Glycosphingolipid biosynthesis - ganglio series [ko00604]	2
Fatty acid biosynthesis [ko00061]	39
Fatty acid elongation [ko00062]	4
Fatty acid degradation [ko00071]	52
Synthesis and degradation of ketone bodies [ko00072]	15
Steroid biosynthesis [ko00100]	2
Primary bile acid biosynthesis [ko00120]	3
Steroid hormone biosynthesis [ko00140]	6
Glycerolipid metabolism [ko00561]	20
Glycerophospholipid metabolism [ko00564]	13
Ether lipid metabolism [ko00565]	1
Arachidonic acid metabolism [ko00590]	10

Linoleic acid metabolism [ko00591]	1
alpha-Linolenic acid metabolism [ko00592]	2
Sphingolipid metabolism [ko00600]	3
Biosynthesis of unsaturated fatty acids [ko01040]	13
Ubiquinone and other terpenoid-quinone biosynthesis [ko00130]	15
One carbon pool by folate [ko00670]	18
Thiamine metabolism [ko00730]	10
Riboflavin metabolism [ko00740]	7
Vitamin B6 metabolism [ko00750]	10
Nicotinate and nicotinamide metabolism [ko00760]	19
Pantothenate and CoA biosynthesis [ko00770]	23
Biotin metabolism [ko00780]	24
Lipoic acid metabolism [ko00785]	2
Folate biosynthesis [ko00790]	13
Retinol metabolism [ko00830]	15
Porphyrin and chlorophyll metabolism [ko00860]	18
beta-Alanine metabolism [ko00410]	34
Taurine and hypotaurine metabolism [ko00430]	7
Phosphonate and phosphinate metabolism [ko00440]	3
Selenocompound metabolism [ko00450]	15
Cyanoamino acid metabolism [ko00460]	7
D-Glutamine and D-glutamate metabolism [ko00471]	4
D-Alanine metabolism [ko00473]	1
Glutathione metabolism [ko00480]	20
Tetracycline biosynthesis [ko00253]	2
Geraniol degradation [ko00281]	16
Polyketide sugar unit biosynthesis [ko00523]	6
Terpenoid backbone biosynthesis [ko00900]	15
Limonene and pinene degradation [ko00903]	12
Zeatin biosynthesis [ko00908]	1
Sesquiterpenoid and triterpenoid biosynthesis [ko00909]	1
Insect hormone biosynthesis [ko00981]	2
Biosynthesis of ansamycins [ko01051]	2
Biosynthesis of siderophore group nonribosomal peptides [ko01053]	4
Nonribosomal peptide structures [ko01054]	9
Biosynthesis of vancomycin group antibiotics [ko01055]	1
Purine metabolism [ko00230]	61
Pyrimidine metabolism [ko00240]	47
Carbon metabolism [ko01200]	111
2-Oxocarboxylic acid metabolism [ko01210]	40
Fatty acid metabolism [ko01212]	59
Degradation of aromatic compounds [ko01220]	15
Biosynthesis of amino acids [ko01230]	131
Chlorocyclohexane and chlorobenzene degradation [ko00361]	2
Benzoate degradation [ko00362]	20
Bisphenol degradation [ko00363]	1
Fluorobenzoate degradation [ko00364]	2
Dioxin degradation [ko00621]	5
Xylene degradation [ko00622]	5

Toluene degradation [ko00623]	2
Chloroalkane and chloroalkene degradation [ko00625]	24
Naphthalene degradation [ko00626]	7
Aminobenzoate degradation [ko00627]	8
Nitrotoluene degradation [ko00633]	4
Ethylbenzene degradation [ko00642]	2
Styrene degradation [ko00643]	7
Caprolactam degradation [ko00930]	4
Metabolism of xenobiotics by cytochrome P450 [ko00980]	16
Drug metabolism - cytochrome P450 [ko00982]	16
Drug metabolism - other enzymes [ko00983]	8
Cardiac muscle contraction [ko04260]	9
Adrenergic signaling in cardiomyocytes [ko04261]	2
Vascular smooth muscle contraction [ko04270]	2
Salivary secretion [ko04970]	3
Gastric acid secretion [ko04971]	1
Pancreatic secretion [ko04972]	3
Carbohydrate digestion and absorption [ko04973]	1
Protein digestion and absorption [ko04974]	1
Fat digestion and absorption [ko04975]	2
Bile secretion [ko04976]	5
Vitamin digestion and absorption [ko04977]	1
Mineral absorption [ko04978]	4
PPAR signaling pathway [ko03320]	20
Insulin signaling pathway [ko04910]	8
Insulin secretion [ko04911]	2
GnRH signaling pathway [ko04912]	1
Ovarian Steroidogenesis [ko04913]	1
Prolactin signaling pathway [ko04917]	1
Thyroid hormone synthesis [ko04918]	2
Thyroid hormone signaling pathway [ko04919]	1
Adipocytokine signaling pathway [ko04920]	11
Glucagon signaling pathway [ko04922]	5
Plant-pathogen interaction [ko04626]	2
Circadian rhythm [ko04710]	1
Proximal tubule bicarbonate reclamation [ko04964]	2
Chemokine signaling pathway [ko04062]	1
Fc gamma R-mediated phagocytosis [ko04666]	3
Retrograde endocannabinoid signaling [ko04723]	2
Glutamatergic synapse [ko04724]	3
GABAergic synapse [ko04727]	5
Dopaminergic synapse [ko04728]	1

Table S4. List of unique genes of *B. contaminans* SK875

Proteins	Accession no.
hypothetical protein SK875_A00077	QFR08313.1
hypothetical protein SK875_A00158	QFR08392.1
hypothetical protein SK875_A00159	QFR08393.1
hypothetical protein SK875_A00161	QFR08395.1
hypothetical protein SK875_A00201	QFR08430.1
hypothetical protein SK875_A00210	QFR08439.1
hypothetical protein SK875_A00336	QFR08563.1
hypothetical protein SK875_A00392	QFR08617.1
hypothetical protein SK875_A00407	QFR08632.1
hypothetical protein SK875_A00426	QFR08651.1
hypothetical protein SK875_A00449	QFR08674.1
hypothetical protein SK875_A00451	QFR08676.1
hypothetical protein SK875_A00452	QFR08677.1
hypothetical protein SK875_A00612	QFR08836.1
hypothetical protein SK875_A00670	QFR08889.1
hypothetical protein SK875_A00671	QFR08890.1
hypothetical protein SK875_A00735	QFR08953.1
hypothetical protein SK875_A00868	QFR09081.1
Toxin HigB-2	QFR09185.1
hypothetical protein SK875_A01146	QFR09347.1
hypothetical protein SK875_A01154	QFR09355.1
hypothetical protein SK875_A01208	QFR09407.1
hypothetical protein SK875_A01365	QFR09564.1
hypothetical protein SK875_A01611	QFR09809.1
hypothetical protein SK875_A01843	QFR10040.1
hypothetical protein SK875_A01877	QFR10073.1
hypothetical protein SK875_A02034	QFR10228.1
hypothetical protein SK875_A02257	QFR10441.1
hypothetical protein SK875_A02261	QFR10445.1
hypothetical protein SK875_A02264	QFR10448.1
hypothetical protein SK875_A02274	QFR10458.1
hypothetical protein SK875_A02286	QFR10470.1
hypothetical protein SK875_A02640	QFR10814.1
hypothetical protein SK875_A02718	QFR10892.1
hypothetical protein SK875_A02754	QFR10928.1
hypothetical protein SK875_A02784	QFR10958.1
hypothetical protein SK875_A02809	QFR10983.1
hypothetical protein SK875_A02838	QFR11012.1
hypothetical protein SK875_A02904	QFR11075.1
hypothetical protein SK875_A02941	QFR11110.1
hypothetical protein SK875_A02982	QFR11150.1
hypothetical protein SK875_A03014	QFR11181.1
hypothetical protein SK875_A03133	QFR11300.1
hypothetical protein SK875_A03138	QFR11304.1
hypothetical protein SK875_A03142	QFR11308.1
hypothetical protein SK875_A03268	QFR11433.1

hypothetical protein SK875_A03280	QFR11445.1
hypothetical protein SK875_A03323	QFR11488.1
hypothetical protein SK875_B00004	QFR11492.1
50S ribosomal protein L25	QFR11493.1
hypothetical protein SK875_B00006	QFR11494.1
50S ribosomal protein L25	QFR11495.1
hypothetical protein SK875_B00008	QFR11496.1
hypothetical protein SK875_B00009	QFR11497.1
hypothetical protein SK875_B00010	QFR11498.1
hypothetical protein SK875_B00011	QFR11499.1
KDP operon transcriptional regulatory protein KdpE	QFR11517.1
hypothetical protein SK875_B00037	QFR11525.1
hypothetical protein SK875_B00122	QFR11610.1
hypothetical protein SK875_B00211	QFR11699.1
hypothetical protein SK875_B00238	QFR11726.1
hypothetical protein SK875_B00409	QFR11894.1
hypothetical protein SK875_B00440	QFR11925.1
hypothetical protein SK875_B00450	QFR11935.1
hypothetical protein SK875_B00491	QFR11975.1
hypothetical protein SK875_B00515	QFR11999.1
Hca operon transcriptional activator	QFR12024.1
hypothetical protein SK875_B00637	QFR12121.1
hypothetical protein SK875_B00671	QFR12155.1
hypothetical protein SK875_B00704	QFR12188.1
hypothetical protein SK875_B00728	QFR12212.1
Sulfite exporter TauE/SafE	QFR12306.1
hypothetical protein SK875_B00967	QFR12450.1
hypothetical protein SK875_B00976	QFR12459.1
Serine/threonine-protein kinase HipA	QFR12476.1
hypothetical protein SK875_B01007	QFR12490.1
hypothetical protein SK875_B01199	QFR12682.1
hypothetical protein SK875_B01319	QFR12802.1
hypothetical protein SK875_B01334	QFR12817.1
hypothetical protein SK875_B01335	QFR12818.1
hypothetical protein SK875_B01364	QFR12847.1
hypothetical protein SK875_B01398	QFR12881.1
hypothetical protein SK875_B01422	QFR12904.1
hypothetical protein SK875_B01556	QFR13037.1
hypothetical protein SK875_B01683	QFR13164.1
hypothetical protein SK875_B01694	QFR13175.1
IgA FC receptor precursor	QFR13237.1
hypothetical protein SK875_B01773	QFR13253.1
hypothetical protein SK875_B01866	QFR13346.1
hypothetical protein SK875_B01949	QFR13428.1
hypothetical protein SK875_B01955	QFR13434.1
hypothetical protein SK875_B01976	QFR13455.1
hypothetical protein SK875_B02102	QFR13581.1
Oxygen-dependent choline dehydrogenase	QFR13624.1
hypothetical protein SK875_B02161	QFR13640.1

hypothetical protein SK875_B02162	QFR13641.1
hypothetical protein SK875_B02241	QFR13720.1
hypothetical protein SK875_B02256	QFR13735.1
hypothetical protein SK875_B02300	QFR13779.1
hypothetical protein SK875_B02313	QFR13792.1
Long-chain-fatty-acid--CoA ligase	QFR13825.1
hypothetical protein SK875_B02347	QFR13826.1
Serine/threonine-protein kinase PknB	QFR13857.1
hypothetical protein SK875_B02402	QFR13881.1
hypothetical protein SK875_B02504	QFR13983.1
hypothetical protein SK875_B02558	QFR14037.1
hypothetical protein SK875_B02573	QFR14052.1
hypothetical protein SK875_B02629	QFR14107.1
hypothetical protein SK875_B02697	QFR14175.1
hypothetical protein SK875_B02765	QFR14243.1
putative cobalt transporter subunit (CbtA)	QFR14263.1
hypothetical protein SK875_C00047	QFR14376.1
hypothetical protein SK875_C00052	QFR14381.1
hypothetical protein SK875_C00086	QFR14415.1
hypothetical protein SK875_C00170	QFR14499.1
hypothetical protein SK875_C00213	QFR14542.1
hypothetical protein SK875_C00217	QFR14546.1
hypothetical protein SK875_C00218	QFR14547.1
hypothetical protein SK875_C00242	QFR14571.1
hypothetical protein SK875_C00314	QFR14643.1
hypothetical protein SK875_C00324	QFR14653.1
hypothetical protein SK875_C00338	QFR14667.1
hypothetical protein SK875_C00354	QFR14683.1
hypothetical protein SK875_C00356	QFR14685.1
hypothetical protein SK875_C00357	QFR14686.1
hypothetical protein SK875_C00358	QFR14687.1
hypothetical protein SK875_C00410	QFR14738.1
hypothetical protein SK875_C00439	QFR14767.1
hypothetical protein SK875_C00444	QFR14772.1
hypothetical protein SK875_C00474	QFR14802.1
hypothetical protein SK875_C00475	QFR14803.1
hypothetical protein SK875_C00506	QFR14834.1
hypothetical protein SK875_C00516	QFR14844.1
hypothetical protein SK875_C00517	QFR14845.1
hypothetical protein SK875_C00578	QFR14906.1
hypothetical protein SK875_C00610	QFR14938.1
hypothetical protein SK875_C00666	QFR14994.1
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC	QFR15050.1
hypothetical protein SK875_C00821	QFR15149.1
N-acetyldiaminopimelate deacetylase	QFR15209.1
hypothetical protein SK875_C00949	QFR15276.1
hypothetical protein SK875_C00956	QFR15283.1
hypothetical protein SK875_C00966	QFR15293.1
hypothetical protein SK875_C01011	QFR15338.1

hypothetical protein SK875_C01024	QFR15351.1
hypothetical protein SK875_C01025	QFR15352.1
Putative cyclase	QFR15355.1
hypothetical protein SK875_C01035	QFR15362.1
hypothetical protein SK875_C01043	QFR15370.1
hypothetical protein SK875_C01081	QFR15408.1
hypothetical protein SK875_C01082	QFR15409.1
Integrase core domain protein	QFR15434.1
short chain dehydrogenase	QFR15557.1
hypothetical protein SK875_C01288	QFR15608.1
hypothetical protein SK875_C01293	QFR15613.1
hypothetical protein SK875_p00004 (plasmid)	QFR15644.1
hypothetical protein SK875_p00007 (plasmid)	QFR15647.1
hypothetical protein SK875_p00018 (plasmid)	QFR15658.1
hypothetical protein SK875_p00019 (plasmid)	QFR15659.1
hypothetical protein SK875_p00020 (plasmid)	QFR15660.1
hypothetical protein SK875_p00033 (plasmid)	QFR15673.1
hypothetical protein SK875_p00035 (plasmid)	QFR15675.1
hypothetical protein SK875_p00041 (plasmid)	QFR15681.1
hypothetical protein SK875_p00044 (plasmid)	QFR15684.1
hypothetical protein SK875_p00056 (plasmid)	QFR15696.1
hypothetical protein SK875_p00063 (plasmid)	QFR15703.1
hypothetical protein SK875_p00065 (plasmid)	QFR15705.1
hypothetical protein SK875_p00067 (plasmid)	QFR15707.1
hypothetical protein SK875_p00089 (plasmid)	QFR15729.1
hypothetical protein SK875_p00099 (plasmid)	QFR15739.1
Error-prone DNA polymerase (plasmid)	QFR15767.1
hypothetical protein SK875_p00145 (plasmid)	QFR15785.1
hypothetical protein SK875_p00153 (plasmid)	QFR15793.1
hypothetical protein SK875_p00157 (plasmid)	QFR15797.1
hypothetical protein SK875_p00168 (plasmid)	QFR15807.1
hypothetical protein SK875_p00171 (plasmid)	QFR15810.1
IS2 repressor TnpA (plasmid)	QFR15818.1
Thiol:disulfide interchange protein DsbD precursor (plasmid)	QFR15821.1
hypothetical protein SK875_p00193 (plasmid)	QFR15832.1
hypothetical protein SK875_p00195 (plasmid)	QFR15834.1
hypothetical protein SK875_p00196 (plasmid)	QFR15835.1
hypothetical protein SK875_p00216 (plasmid)	QFR15855.1
Integrase core domain protein (plasmid)	QFR15857.1
RNA polymerase sigma factor (plasmid)	QFR15862.1
hypothetical protein SK875_p00227 (plasmid)	QFR15866.1
hypothetical protein SK875_p00228 (plasmid)	QFR15867.1

Table S5. COG distribution of the unique genes in *B. contaminans* SK875

Functional class	Category	Ratio (%)
Information storage and processing	J: Translation, ribosomal structure & biogenesis	2.22
	K: Transcription	6.65
	L: Replication, recombination & repair	17.74
Cellular processes and signaling	D: Cell cycle control, cell division, chromosome partitioning	4.43
	M: Cell wall/membrane/envelope biogenesis	0.00
	N: Cell motility	0.00
	O: Post-translational modification, protein turnover & chaperones	2.22
	T: Signal transduction mechanisms	2.22
	U: Intracellular trafficking, secretion & vesicular transport	0.00
	V: Defense mechanisms	0.00
Metabolism	P: Inorganic ion transport & metabolism	4.43
	F: Nucleotide transport & metabolism	0.00
	G: Carbohydrate transport & metabolism	4.43
	E: Amino acid transport & metabolism	6.65
	H: Coenzyme transport & metabolism	0.00
	I: Lipid transport & metabolism	4.43
	C: Energy production & conversion	6.65
	Q: Secondary metabolites biosynthesis, transport & catabolism	6.65
Poorly characterized	R: General function prediction only	22.17
	S: Function unknown	8.87

Table S6. Prophage regions of the *B. contaminans* genomes

Strains	Location	Completeness	Start (bp)	End (bp)	GC %	Most Common Phage
MS14	Chromosome 1	incomplete	2,451,943	2,471,894	59.71	Burkho_AP3 (NC_047752(1))
	Chromosome 2	intact	3,157,388	3,187,151	61.42	Salmon_118970_sal3 (NC_031940(13))
	Chromosome 3	incomplete	953,153	960,936	67.74	Burkho_phi1026b (NC_005284(2))
FL-1-2-30-S1-D0	Chromosome 1	questionable	2,105,046	2,149,176	60.58	Escher_vB_EcoM_ECOO78 (NC_041926(9))
	Chromosome 2	incomplete	2,884,643	2,895,876	63.97	Acinet_vB_AbaM_ME3 (NC_041884(3))
	Chromosome 3	incomplete	450,919	458,702	67.74	Burkho_phi1026b (NC_005284(2))
ZCC	Chromosome 1	incomplete	3,655,141	3,668,410	61.76	Gordon_Bowser (NC_030930(2))
	Chromosome 1	incomplete	3,712,981	3,721,713	61.98	Bacill_SP_15 (NC_031245(1))
	Plasmid 2	incomplete	45,760	53,972	59.32	Burkho_BcepIL02 (NC_012743(2))
SK875	Chromosome 1	incomplete	270,930	279,358	61.69	Entero_phi92 (NC_023693(4))
	Chromosome 1	incomplete	2,586,105	2,592,869	66.03	Ralsto_RP12 (NC_041911(2))
XL73	Chromosome 3	incomplete	2,410,143	2,418,703	62.41	Entero_fiAA91_ss (NC_022750(2))
	Plasmid 1	questionable	66,247	88,331	62.81	Stx2_c_Stx2a_F451 (NC_049924(3))
	Plasmid 2	incomplete	58,918	67,148	59.41	Pseudo_JG004 (NC_019450(1))

Table S7. The CRISPR loci of the five *B. contaminans* genomes

Strain	Location	Start	End	DR No.	Repeat consensus/Cas genes	DR length (bp)
MS14	Chromosome 1	27,879	27,977	1	GCTGCACCGCACGTCAATCTGGC	98
FL-1-2-30-S1-D0	Chromosome 2	2,802,389	2,802,487	1	GCCAGATTGACGTGCGGTGCAGC	98
FL-1-2-30-S1-D0	Chromosome 2	3,166,134	3,166,234	1	CGCCGGCCGTGCCGGGGCTGCCG	100
ZCC	Chromosome 1	932,298	932,390	1	CACTCGGCAACCTCGGCGGCTCGA	92
SK875	Chromosome 2	2,456,771	2,457,221	5	AGCAATGTCGGCGGCCTCGTCGGCA	450
SK875	Chromosome 2	2,981,872	2,982,191	4	ATCGGCGGCGCCATCGGCGGCGGCGC	319
XL73	Chromosome 2	302,358	302,551	2	GCCGACGAGGCCGCCGACCAGGCTG	193
XL73	Chromosome 2	302,622	302,877	3	GCCGACGAGGCCGCCGACCAGGCTG	255
XL73	Chromosome 2	305,476	305,839	4	TGCCGACGAGGCCGCCGACATAGCT	363
XL73	Chromosome 2	3,029,591	3,029,796	3	GCGCCGCCGCCGAGGGCGCCGCCGAT	205

Table S8. Putative virulence genes in five *B. contaminans* genomes predicted by VFDB

Factors	Related genes	SK875	MS14	FL-1-2-30-S1-D0	ZCC	XL73
BoaA	boaA	SK875_C00706	NL30_34935, NL30_35080	WI95_32125, WI95_32270	ND	GON15_05295
BoaB	boaB	SK875_B02235, SK875_p00121	NL30_15910	WI95_15970, WI95_17360, WI95_28155	FPQ37_40715	GON15_37945
Type IV pili	pilA	SK875_A01681	NL30_26290	WI95_13650	ND	GON15_35135
	pilB	SK875_A00593	NL30_21195	WI95_02555	FPQ37_02915	GON15_23885
	pilC	SK875_A00594	ND	WI95_02550	FPQ37_02910	GON15_23880
	pilD	SK875_A00595	NL30_21205	WI95_02545	FPQ37_02905	GON15_23875
Capsule I	Undetermined	SK875_A00382	ND	ND	FPQ37_04010	GON15_24975
	Undetermined	SK875_A00276, SK875_A00390, SK875_B01430	NL30_07355, NL30_11345	WI95_04035, WI95_20950	FPQ37_23705, FPQ37_03970, FPQ37_04560	GON15_24915, GON15_25510, GON15_11735
	gmhA	ND	ND	ND	ND	ND
	manC	ND	NL30_08080 NL30_21540	WI95_20230	ND	ND
	wcbA	SK875_A00404	ND	ND	FPQ37_03905	GON15_24850
	wcbB	SK875_A00403	ND	ND	FPQ37_03910	GON15_24855
	wcbC	SK875_A00402	ND	ND	FPQ37_03915	GON15_24860
	wcbD	SK875_A00401	ND	ND	FPQ37_03920	GON15_24865
	wcbO	SK875_A00388	ND	ND	FPQ37_03980	GON15_24925
	wcbP	SK875_A00387	ND	ND	FPQ37_03985	GON15_24950
	wcbQ	SK875_A00386	ND	ND	FPQ37_03990	GON15_24955
	wcbR	SK875_A00385, SK875_C00826	NL30_34420, NL30_35045, NL30_36200, NL30_36225	WI95_32160, WI95_32860	FPQ37_39430, FPQ37_03995	GON15_24960, GON15_05910
	wcbS	SK875_A00384	ND	ND	FPQ37_04000	GON15_24965
	wcbT	SK875_A00383	ND	ND	FPQ37_04005	GON15_24970
	wzm	SK875_A00400	ND	ND	FPQ37_03925	GON15_24870
	wzt2	SK875_A00399	ND	ND	FPQ37_03930	GON15_24875
Flagella	cheA	SK875_A00951	NL30_18600	WI95_00915	FPQ37_01020	GON15_22060

cheB	SK875_A00946	NL30_18575	WI95_00940	FPQ37_01045	GON15_22085
cheD	SK875_A00947	NL30_18580	WI95_00935	FPQ37_01040	GON15_22080
cheR	SK875_A00948	NL30_18585	WI95_00930	FPQ37_01035	GON15_22075
cheW	SK875_A00950	NL30_18595	WI95_00920	FPQ37_01025	GON15_22065
cheY1	SK875_A00952	NL30_18605	WI95_00910	FPQ37_01015	GON15_22055
cheY	SK875_A00945	NL30_18570	WI95_00945	FPQ37_01050	GON15_22090
cheZ	SK875_A00944	NL30_18565	WI95_00950	FPQ37_01055	GON15_22095
flgA	SK875_A01286	NL30_28210	WI95_15570	FPQ37_16635	GON15_37155
flgB	SK875_A01287	NL30_28205	WI95_15565	FPQ37_16630	GON15_37150
flgC	SK875_A01288	NL30_28200	WI95_15560	FPQ37_16625	GON15_37145
flgD	SK875_A01289	NL30_28195	WI95_15555	FPQ37_16620	GON15_37140
flgE	SK875_A01290, SK875_B01443	NL30_07420, NL30_28190	WI95_15550, WI95_20885	FPQ37_23770, FPQ37_16615	GON15_37135, GON15_11670
flgF	SK875_A01291	NL30_28185	WI95_15545	FPQ37_16610	GON15_37130
flgG	SK875_A01292	NL30_28180	WI95_15540	FPQ37_16605	GON15_37125
flgH	SK875_A01293	NL30_28175	WI95_15535	FPQ37_16600	GON15_37120
flgI	SK875_A01294	NL30_28170	WI95_15530	FPQ37_16595	GON15_37115
flgJ	SK875_A01295	NL30_28165	WI95_15525	FPQ37_16590	GON15_37110
flgK	SK875_A01297	NL30_28155	WI95_15515	FPQ37_16580	GON15_37100
flgL	SK875_A01298	NL30_28150	WI95_15510	FPQ37_16575	GON15_37095
flgM	SK875_A01285	NL30_28215	WI95_15575	FPQ37_16640	GON15_37160
flgN	SK875_A01284	NL30_28220	WI95_15580	FPQ37_16645	GON15_37165
flhA	SK875_A00937	NL30_18530	WI95_00985	FPQ37_01090	GON15_22130
flhB	SK875_A00938	NL30_18535	WI95_00980	FPQ37_01085	GON15_22125
flhF	SK875_A00936	NL30_18525	WI95_00990	FPQ37_01095	GON15_22135
flhG	SK875_A00935	NL30_18520	WI95_00995	FPQ37_01100	GON15_22140
fliA	SK875_A00934	NL30_18515	WI95_01000	FPQ37_01105	GON15_22145
fliC	ND	NL30_18665	ND	ND	ND
fliD	SK875_A00965, SK875_C00910	NL30_34040, NL30_18670	WI95_00845, WI95_33285	FPQ37_39870, FPQ37_00945	GON15_21990, GON15_06340
fliE	SK875_A01248	NL30_28410	WI95_15765	FPQ37_16835	GON15_37345
fliF	SK875_A01247	NL30_28415	WI95_15770	FPQ37_16845	GON15_37350
fliG	SK875_A01246	NL30_28420	WI95_15775	FPQ37_16850	GON15_37355
fliH	SK875_A01245	NL30_28425	WI95_15780	FPQ37_16855	GON15_37360
fliI	SK875_A01244	NL30_28430	WI95_15785	FPQ37_16860	GON15_37365

	fliJ	SK875_A01243	NL30_28435	WI95_15790	FPQ37_16865	GON15_37370
	fliK	SK875_A01242	NL30_28440	WI95_15795	FPQ37_16870	GON15_37375
	fliL	SK875_A01091	NL30_19290	WI95_00255	FPQ37_00275	GON15_21350
	fliM	SK875_A01092	NL30_19295	WI95_00250	FPQ37_00270	GON15_21345
	fliN	SK875_A01093	NL30_19300	WI95_00245	FPQ37_00265	GON15_21340
	fliO	SK875_A01094	NL30_19305	WI95_00240	FPQ37_00260	GON15_21335
	fliP	SK875_A01095	NL30_19310	WI95_00235	FPQ37_00255	GON15_21330
	fliQ	SK875_A01096	NL30_19315	WI95_00230	FPQ37_00250	GON15_21325
	fliR	SK875_A01097	NL30_19320	WI95_00225	FPQ37_00245	GON15_21320
	fliS	SK875_A01249	NL30_28405	WI95_15760	FPQ37_16830	GON15_37340
	motA	SK875_A00954,	NL30_18615,	WI95_00900,	FPQ37_27215,	GON15_22045,
		SK875_B02110	NL30_23870	WI95_17885	FPQ37_01005	GON15_08320
	motB	SK875_A00953	NL30_18610	WI95_00905	FPQ37_01010	GON15_22050
	tsr	SK875_A00194,	NL30_32435,	WI95_00925,	FPQ37_35400,	GON15_22070,
		SK875_A00949,	NL30_32595,	WI95_04460,	FPQ37_35550,	GON15_25915,
		SK875_A02839,	NL30_34460	WI95_07700,	FPQ37_37565,	GON15_29285,
		SK875_B00449,	NL30_02170,	WI95_32820,	FPQ37_39390,	GON15_14215,
		SK875_B00666,	NL30_03040,	WI95_34725,	FPQ37_19755,	GON15_15590,
		SK875_B00938,	NL30_04420,	WI95_34785,	FPQ37_21160,	GON15_16675,
		SK875_C00037,	NL30_10920,	WI95_34870,	FPQ37_33410,	GON15_01930,
		SK875_C00067,	NL30_15080	WI95_18720,	FPQ37_01030,	GON15_02075,
		SK875_C00461,	NL30_18590,	WI95_23835,	FPQ37_04980,	GON15_04050,
		SK875_C00818	NL30_23055	WI95_25215,	FPQ37_08490	GON15_05870
				WI95_26120		
Quorum sensing system	bspI2	ND	ND	ND	ND	ND
	bspI3	ND	ND	ND	FPQ37_18040	ND
	bspR4	ND	NL30_36195	ND	ND	ND
	pmlI/bspI1	SK875_B00567	NL30_02710	WI95_25580	FPQ37_19250	GON15_16090
	pmlR/bspR1	SK875_B00569	NL30_02720	WI95_25570	FPQ37_19260	GON15_16080
Bsa T3SS	bapA	ND	ND	ND	ND	ND
	bicA	ND	NL30_37140	ND	ND	ND
	bprA	ND	ND	WI95_22305	FPQ37_34000,	ND
					FPQ37_38855,	

					FPQ37_39170, FPQ37_40335, FPQ37_17425	
	bsaQ	SK875_B00413	NL30_37190	ND	ND	GON15_16865
	bsaS	ND	NL30_37180	ND	ND	ND
	bsaX	ND	NL30_37155	ND	ND	ND
	spaP	ND	NL30_37160	ND	ND	ND
T6SS-1	Undetermined	ND	ND	WI95_32775	ND	ND
	Undetermined	ND	NL30_34485	ND	ND	ND
Pyochelin receptor	fptA	SK875_B00268	ND	ND	FPQ37_32455	GON15_17585
Pyochelin	pchB	SK875_B00259	ND	ND	FPQ37_32410	GON15_17630
	pchC	SK875_B00260	ND	ND	FPQ37_32415	GON15_17625
	pchD	SK875_B00261	ND	ND	FPQ37_32420	GON15_17620
	pchE	SK875_B00263	ND	ND	FPQ37_32430	GON15_17610
	pchF	SK875_B00264	ND	ND	FPQ37_32435	GON15_17605
	pchG	SK875_B00265	ND	ND	FPQ37_32440	GON15_17600
	pchH	SK875_B00266	ND	ND	ND	GON15_17595
	pchR	SK875_B00262	ND	ND	FPQ37_32425	GON15_17615
Catalase	katA	SK875_B02015	NL30_00985	WI95_27395	FPQ37_26715	GON15_08820

Table S9. Antibiotic resistance genes in five *B. contaminans* genomes

Product	Identified strains
Catalase-peroxidase KatG (EC 1.11.1.21)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Aminoglycoside 6-phosphotransferase, putative	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Class A beta-lactamase (EC 3.5.2.6)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Class C beta-lactamase (EC 3.5.2.6)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Class D beta-lactamase (EC 3.5.2.6)	MS14, FL-1-2-30-S1-D0
Alanine racemase (EC 5.1.1.1)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
D-alanine--D-alanine ligase (EC 6.3.2.4)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Translation elongation factor G	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Translation elongation factor Tu	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Dihydrofolate reductase (EC 1.5.1.3)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Dihydropteroate synthase (EC 2.5.1.15)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
DNA gyrase subunit A (EC 5.99.1.3)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
DNA gyrase subunit B (EC 5.99.1.3)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Isoleucyl-tRNA synthetase (EC 6.1.1.5)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Transcription termination factor Rho	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
SSU ribosomal protein S10p (S20e)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Undecaprenyl-diphosphatase BcrC (EC 3.6.1.27), conveys bacitracin resistance	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9), FabV => refractory to triclosan	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Tetracycline resistance, MFS efflux pump => unclassified	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Outer membrane factor (OMF) lipoprotein associated with EmrAB-OMF efflux system	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system EmrAB-OMF, inner-membrane proton/drug antiporter EmrB (MFS type)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system EmrAB-OMF, membrane fusion component EmrA	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Macrolide-specific efflux protein MacA	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Macrolide export ATP-binding/permease protein MacB	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Outer membrane factor (OMF) lipoprotein associated with MdtABC efflux system	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system MdtABC-TolC, inner-membrane proton/drug antiporter MdtB (RND type)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73

Multidrug efflux system MdtABC-TolC, inner-membrane proton/drug antiporter MdtC (RND type)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system MdtABC-TolC, membrane fusion component MdtA	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system, inner membrane proton/drug antiporter (RND type) => MexY of MexXY/AxyXY	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system, membrane fusion component => MexX of MexXY/AxyXY	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Multidrug efflux system, outer membrane factor associated with MexXY/AxyXY system	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Outer membrane low permeability porin, OprB family	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Outer membrane low permeability porin, OprD family	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
DNA-binding protein H-NS	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
Hydrogen peroxide-inducible genes activator => OxyR	MS14, FL-1-2-30-S1-D0, ZCC, SK875, XL73
