

**Supplementary Table 4.** Comparison of gene content among *Psa* isolates based on aligning reads against the reference genome of *Psa* NCPPB3871 (GenBank:AFTF01000000).

Gene	Genomic coordinates	346	CFBP7285	CFBP7286	CFBP7287	PsaKN.2	Kw41	PA459	CH2010-5	CH2010-6	NCPPB2598
As predicted by RAST ( <a href="http://http://rast.nmpdr.org/">http://http://rast.nmpdr.org/</a> )	(GenBank accession: start-end)	Portugal	Italy	Italy	Italy	Korea	Japan	Japan	China	China	Japan (theae)
site-specific recombinase2C phage integrase family;Note=site-specific recombinase2C phage integrase family	AFTF01000284.1: 1160-2170	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Serine protease;Note=Serine protease	AFTF01000284.1: 2148-3203	○ 0.08	○ 0.07	○ 0.08	○ 0.08	● 1.00	● 1.00	● 1.00	○ 0.08	○ 0.08	○ 0.00
Long-chain-fatty-acid--CoA ligase;Ontology_term=KEGG_ENZYME:6.2.1.3;Note=Long-chain-fatty-acid--CoA ligase	AFTF01000280.1: 1865-4321	○ 0.01	○ 0.01	○ 0.01	○ 0.01	● 1.00	● 1.00	● 1.00	○ 0.01	○ 0.01	○ 0.01
Name=titin titin;Note=titin	AFTF01000278.1: 882-2111	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
DNA polymerase III alpha subunit;Ontology_term=KEGG_ENZYME:2.7.7.7;Note=DNA polymerase III alpha subunit	AFTF01000278.1: 2169-2933	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 0.99
DNA polymerase-like protein PA0670;Note=DNA polymerase-like protein PA0670	AFTF01000278.1: 2930-4345	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
RecA/RadA recombinase;Note=RecA/RadA recombinase	AFTF01000278.1: 4353-4976	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
SOS-response repressor and protease LexA;Ontology_term=KEGG_ENZYME:3.4.21.88;Note=SOS-response repressor	AFTF01000278.1: 4973-5590	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
FIG00961388: hypothetical protein;Note=FIG00961388: hypothetical protein	AFTF01000275.1: 1861-1980	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
FIG00961388: hypothetical protein;Note=FIG00961388: hypothetical protein	AFTF01000275.1: 2093-2437	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000432.1: 1709-2545	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
membrane protein2C putative;Note=membrane protein2C putative	AFTF01000432.1: 2671-3198	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000263.1: 1639-1782	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
hypothetical protein;Note=hypothetical protein	AFTF01000263.1: 1894-2364	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
NreA-like protein;Note=NreA-like protein	AFTF01000263.1: 2593-2886	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
Nickel and cobalt efflux transporter rcnA;Note=Nickel and cobalt efflux transporter rcnA	AFTF01000263.1: 2894-3766	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00
Protein with ParB-like nuclease domain in PFGI-1-like cluster;Note=Protein with ParB-like nuclease domain in PFGI-1-like cluster	AFTF01000262.1: 4586-5038	○ 0.10	○ 0.13	○ 0.13	○ 0.14	● 1.00	● 1.00	● 1.00	● 0.53	● 0.53	○ 0.00
Name=ORF2 ORF2;Note=ORF2	AFTF01000450.1: 58-1182	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	○ 0.19	● 1.00	● 1.00	● 1.00	○ 0.00
Protein with ParB-like nuclease domain in PFGI-1-like cluster;Note=Protein with ParB-like nuclease domain in PFGI-1-like cluster	AFTF01000259.1: 58-1359	○ 0.05	○ 0.05	○ 0.05	○ 0.05	● 1.00	● 1.00	● 1.00	● 0.86	● 0.86	○ 0.03
FIG004780: hypothetical protein in PFGI-1-like cluster;Note=FIG004780: hypothetical protein in PFGI-1-like cluster	AFTF01000259.1: 1396-2133	○ 0.05	○ 0.06	○ 0.07	○ 0.07	● 1.00	● 1.00	● 1.00	● 0.96	● 0.96	○ 0.00
DNA/RNA helicase in PFGI-1-like cluster;Note=DNA/RNA helicase in PFGI-1-like cluster	AFTF01000259.1: 8682-10466	○ 0.04	○ 0.04	○ 0.05	○ 0.05	● 1.00	● 1.00	● 1.00	● 0.91	● 0.90	● 0.79
Conjugative transfer protein PilL in PFGI-1-like cluster;Note=Conjugative transfer protein PilL in PFGI-1-like cluster	AFTF01000259.1: 12010-13155	○ 0.03	○ 0.04	○ 0.04	○ 0.17	● 1.00	● 1.00	● 1.00	● 0.34	● 0.28	● 1.00
ABC-type amino acid transport2C signal transduction systems2C periplasmic component/domain;Note=ABC-type amino acid transport2C signal transduction systems2C periplasmic component/domain	AFTF01000258.1: 1775-2530	○ 0.03	○ 0.03	○ 0.04	○ 0.04	● 1.00	● 1.00	● 1.00	○ 0.04	○ 0.04	● 1.00
FIG00962378: hypothetical protein;Note=FIG00962378: hypothetical protein	AFTF01000258.1: 13738-14688	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000448.1: 2842-2976	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
TnpA transposase;Note=TnpA transposase	AFTF01000240.1: 3415-4110	○ 0.03	○ 0.02	○ 0.03	○ 0.03	● 1.00	● 1.00	● 1.00	○ 0.14	○ 0.14	○ 0.02
DNA integration/recombination/inversion protein;Note=DNA integration/recombination/inversion protein	AFTF01000448.1: 3018-3158	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
FIG00960122: hypothetical protein;Note=FIG00960122: hypothetical protein	AFTF01000230.1: 718-2076	● 0.93	● 0.94	● 0.94	● 0.95	● 1.00	● 1.00	● 1.00	● 0.96	● 0.96	○ 0.00
Name=Integrase Integrase;Note=Integrase	AFTF01000230.1: 2348-3583	○ 0.05	○ 0.05	○ 0.04	○ 0.05	● 1.00	● 1.00	● 1.00	○ 0.11	○ 0.11	○ 0.00
Serine protease;Note=Serine protease	AFTF01000226.1: 414-2510	○ 0.04	○ 0.04	○ 0.06	○ 0.07	● 1.00	● 1.00	● 1.00	○ 0.08	○ 0.08	○ 0.07
FIG00958716: hypothetical protein;Note=FIG00958716: hypothetical protein	AFTF01000226.1: 4391-4999	● 0.47	● 0.48	● 0.52	● 0.54	● 1.00	● 1.00	● 1.00	● 0.62	● 0.62	○ 0.00
TonB-dependent receptor%3B Outer membrane receptor for ferrienterochelin and colicins;Note=TonB-dependent receptor	AFTF01000225.1: 51-2450	○ 0.02	○ 0.02	○ 0.02	○ 0.02	● 1.00	● 1.00	● 1.00	○ 0.09	○ 0.09	○ 0.02
Methyl-accepting chemotaxis protein;Note=Methyl-accepting chemotaxis protein	AFTF01000223.1: 3245-3619	● 0.82	● 0.96	● 1.00	● 0.97	○ 0.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00
hypothetical protein;Note=hypothetical protein	AFTF01000223.1: 3677-5083	● 0.98	● 0.98	● 1.00	● 1.00	○ 0.00	○ 0.00	● 1.00	● 1.00	● 1.00	● 1.00
Aconitase B;Note=Aconitase B	AFTF01000223.1: 5093-5422	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	○ 0.16	● 1.00	● 1.00	● 1.00	● 1.00
ATP-dependent helicase HrpB;Note=ATP-dependent helicase HrpB	AFTF01000222.1: 2218-4317	○ 0.03	○ 0.03	○ 0.03	○ 0.03	● 1.00	● 1.00	● 1.00	○ 0.03	○ 0.03	● 1.00
hypothetical protein;Note=hypothetical protein	AFTF01000218.1: 585-701	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000218.1: 1041-3584	● 0.86	● 0.86	● 0.86	● 0.86	● 1.00	● 1.00	● 1.00	● 0.86	● 0.86	○ 0.00
Protein involved in meta-pathway of phenol degradation;Note=Protein involved in meta-pathway of phenol degradation	AFTF01000216.1: 47276-48169	○ 0.04	○ 0.04	○ 0.05	○ 0.05	● 1.00	● 1.00	● 1.00	○ 0.05	○ 0.05	● 0.86
FIG045374: Type II restriction enzyme2C methylase subunit YeeA;Note=FIG045374: Type II restriction enzyme2C methylase subunit	AFTF01000216.1: 48154-50226	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000216.1: 51011-51142	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000211.1: 1067-1186	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
TnpA transposase;Note=TnpA transposase	AFTF01000210.1: 4484-4972	○ 0.05	○ 0.05	○ 0.05	○ 0.05	● 1.00	● 1.00	● 1.00	○ 0.05	○ 0.05	● 0.32
hypothetical protein;Note=hypothetical protein	AFTF01000206.1: 10136-10399	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Putative heat shock protein YegD;Note=Putative heat shock protein YegD	AFTF01000198.1: 26591-28156	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000198.1: 28706-28870	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 0.90	● 1.00	● 1.00	○ 0.00
Unknown pentose utilization regulator 22C DeoR family;Note=Unknown pentose utilization regulator 22C DeoR family	AFTF01000189.1: 30-983	● 0.99	● 0.99	● 0.99	● 0.99	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
3-oxoacyl-[acyl-carrier protein] reductase;Ontology_term=KEGG_ENZYME:1.1.1.100;Note=3-oxoacyl-[acyl-carrier protein] reductase	AFTF01000189.1: 1065-1865	● 1.00	● 0.99	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Short chain dehydrogenase;Note=Short chain dehydrogenase	AFTF01000189.1: 1896-2660	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
D-xylose transport ATP-binding protein XylG;Note=D-xylose transport ATP-binding protein XylG	AFTF01000189.1: 2692-4221	● 1.00	● 0.99	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Xylose ABC transporter2C periplasmic xylose-binding protein XylF;Note=Xylose ABC transporter2C periplasmic xylose-binding protein	AFTF01000189.1: 4237-5169	● 0.99	● 0.96	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
ribose ABC transporter2C permease protein;Note=ribose ABC transporter2C permease protein	AFTF01000189.1: 5236-5658	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
ribose ABC transporter2C permease protein;Note=ribose ABC transporter2C permease protein	AFTF01000189.1: 5659-6240	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Transketolase2C N-terminal section;Ontology_term=KEGG_ENZYME:2.2.1.1;Note=Transketolase2C N-terminal section	AFTF01000189.1: 6604-7440	● 1.00	● 0.98	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
Transketolase2C C-terminal section;Ontology_term=KEGG_ENZYME:2.2.1.1;Note=Transketolase2C C-terminal section	AFTF01000189.1: 7430-8362	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.05
Unknown pentose kinase TM0952;Note=Unknown pentose kinase TM0952	AFTF01000189.1: 8375-9868	● 0.93	● 0.96	● 0.92	● 0.93	● 1.00	● 1.00	● 1.00	● 0.95	● 0.95	○ 0.01
Glucans biosynthesis protein D precursor;Note=Glucans biosynthesis protein D precursor	AFTF01000187.1: 22766-23083	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
putative integrase protein;Note=putative integrase protein	AFTF01000444.1: 482-2140	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	○ 0.14	● 1.00	● 1.00	● 1.00	● 1.00
avirulence protein;Note=avirulence protein	AFTF01000184.1: 16557-17003	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00
hypothetical protein;Note=hypothetical protein	AFTF01000444.1: 2207-2347	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00	○ 0.43	● 1.00	● 1.00	● 1.00	● 1.00
FIG00635470: hypothetical protein;Note=FIG00635470: hypothetical protein	AFTF01000178.1: 21173-22069	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	● 1.00	○ 0.00

**Supplementary Table 4.** Comparison of gene content among *Psa* isolates based on aligning reads against the reference genome of *Psa* NCPPB3871 (GenBank:AFTF01000000).

FIG00962025: hypothetical protein;Note=FIG00962025: hypothetical protein	AFTF01000174.1: 669-830	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Glutamate transport membrane-spanning protein;Note=Glutamate transport membrane-spanning protein	AFTF01000174.1: 1135-1800	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Glutamate transport membrane-spanning protein;Note=Glutamate transport membrane-spanning protein	AFTF01000174.1: 1781-2440	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ABC-type amino acid transport/signal transduction systems2C periplasmic component/domain;Note=ABC-type	AFTF01000174.1: 3195-3761	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ABC-type amino acid transport/signal transduction systems2C periplasmic component/domain;Note=ABC-type	AFTF01000174.1: 3816-4067	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
NADH:flavin oxidoreductases2C Old Yellow Enzyme family;Note=NADH:flavin oxidoreductases2C Old Yellow En	AFTF01000174.1: 5172-6269	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000174.1: 6247-6942	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Permeases of the major facilitator superfamily;Note=Permeases of the major facilitator superfamily	AFTF01000174.1: 7003-7389	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
NADH:flavin oxidoreductases2C Old Yellow Enzyme family;Note=NADH:flavin oxidoreductases2C Old Yellow En	AFTF01000174.1: 7447-8115	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
NADH:flavin oxidoreductases2C Old Yellow Enzyme family;Note=NADH:flavin oxidoreductases2C Old Yellow En	AFTF01000174.1: 8156-8557	●	0.65	●	0.64	●	0.65	●	0.65	●	1.00	●	1.00	●	0.66	○	0.66
Transcriptional regulator2C TetR family;Note=Transcriptional regulator2C TetR family	AFTF01000174.1: 8613-9194	●	0.99	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000174.1: 10309-10488	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
transcriptional regulator2C AraC family;Note=transcriptional regulator2C AraC family	AFTF01000174.1: 10698-11681	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.01
ABC-type polar amino acid transport system2C ATPase component;Note=ABC-type polar amino acid transport	AFTF01000169.1: 50794-51591	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.01
ABC-type amino acid transport/signal transduction systems2C periplasmic component/domain;Note=ABC-type	AFTF01000169.1: 52973-53326	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ABC-type amino acid transport/signal transduction systems2C periplasmic component/domain;Note=ABC-type	AFTF01000169.1: 53545-53844	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
avirulence protein;Note=avirulence protein	AFTF01000442.1: 1060-2079	●	1.00	●	1.00	●	1.00	○	0.00	○	0.08	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000442.1: 2764-2886	●	1.00	●	1.00	●	1.00	○	0.00	○	0.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000442.1: 3287-3445	●	1.00	●	1.00	●	1.00	○	0.00	○	0.00	●	1.00	●	1.00	○	0.00
Putative large exoprotein involved in heme utilization or adhesion of ShlA/HecA/FhaA family;Note=Putative larg	AFTF01000159.1: 28-11799	●	0.99	●	0.99	●	0.99	○	0.00	○	1.00	●	1.00	●	1.00	●	0.99
Cellulose synthase operon protein C;Note=Cellulose synthase operon protein C	AFTF01000158.1: 38043-41858	●	0.57	●	0.57	●	0.57	●	1.00	●	1.00	●	1.00	●	0.57	○	0.57
Name=transposase transposase;Note=transposase	AFTF01000442.1: 3435-3845	●	1.00	●	1.00	●	1.00	○	0.00	○	0.00	●	1.00	●	1.00	○	0.00
YoeB toxin protein;Note=YoeB toxin protein	AFTF01000154.1: 15016-15318	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Endoglucanase precursor;Ontology_term=KEGG_ENZYME:3.2.1.4;Note=Endoglucanase precursor;Ontology_ter	AFTF01000137.1: 44172-45206	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.05
Transposase and inactivated derivatives;Note=Transposase and inactivated derivatives	AFTF01000128.1: 74-1123	○	0.03	○	0.03	○	0.03	○	0.03	○	0.03	○	0.03	○	0.03	○	0.03
FIG00965780: hypothetical protein;Note=FIG00965780: hypothetical protein	AFTF01000085.1: 19-573	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00965780: hypothetical protein;Note=FIG00965780: hypothetical protein	AFTF01000077.1: 195-1148	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
VgrG protein;Note=VgrG protein	AFTF01000077.1: 1112-4426	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.02
VgrG protein;Note=VgrG protein	AFTF01000077.1: 5271-7298	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.04
Yersinia/Haemophilus virulence surface antigen family;Note=Yersinia/Haemophilus virulence surface antigen fa	AFTF01000074.1: 446-1519	●	1.00	●	1.00	●	1.00	○	0.00	○	0.09	●	1.00	●	1.00	●	1.00
hypothetical protein;Note=hypothetical protein	AFTF01000074.1: 1742-1936	●	1.00	●	1.00	●	1.00	○	0.00	○	0.00	●	1.00	●	1.00	○	0.00
type III effector AvrB4-2;Note=type III effector AvrB4-2	AFTF01000074.1: 2464-3426	●	1.00	●	1.00	●	1.00	○	0.00	○	0.15	●	1.00	●	1.00	○	0.14
Name=transposase transposase;Note=transposase	AFTF01000072.1: 324-548	●	0.36	●	0.35	●	0.36	●	1.00	●	1.00	●	1.00	●	0.37	○	0.37
Dipeptide-binding ABC transporter2C periplasmic substrate-binding component (TC 3.A.1.5.2);Note=Dipeptide-	AFTF01000072.1: 571-789	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000072.1: 2423-2698	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
MFS general substrate transporter;Note=MFS general substrate transporter	AFTF01000072.1: 2721-3983	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00967211: hypothetical protein;Note=FIG00967211: hypothetical protein	AFTF01000069.1: 12758-13327	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ATP binding protein;Note=ATP binding protein	AFTF01000069.1: 13477-14832	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Sucrose specific transcriptional regulator CscR2C LacI family;Note=Sucrose specific transcriptional regulator Csc	AFTF01000068.1: 209-1156	●	1.00	●	1.00	●	1.00	○	0.00	○	1.00	●	1.00	●	1.00	●	1.00
Transducer protein car;Note=Transducer protein car	AFTF01000068.1: 1275-6983	●	1.00	●	1.00	●	1.00	○	0.00	○	1.00	●	1.00	●	1.00	●	1.00
hypothetical protein;Note=hypothetical protein	AFTF01000060.1: 1225-1575	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000060.1: 1526-1666	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00963107: hypothetical protein;Note=FIG00963107: hypothetical protein	AFTF01000409.1: 37033-38406	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
candidate type III effector HolPtoQ;Note=candidate type III effector HolPtoQ	AFTF01000060.1: 3106-4449	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
IS1294 orf;Note=IS1294 orf	AFTF01000060.1: 4796-5923	○	0.20	○	0.18	○	0.20	○	0.20	○	0.20	○	0.20	○	0.20	○	0.20
Transcriptional regulator2C LysR family;Note=Transcriptional regulator2C LysR family	AFTF01000059.1: 38238-39137	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00966512: hypothetical protein;Note=FIG00966512: hypothetical protein	AFTF01000050.1: 2748-3461	○	0.02	○	0.03	○	0.02	○	0.03	○	0.03	○	0.03	○	0.03	○	0.96
hypothetical protein;Note=hypothetical protein	AFTF01000041.1: 40721-41539	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Dipeptide-binding ABC transporter2C periplasmic substrate-binding component (TC 3.A.1.5.2);Note=Dipeptide-	AFTF01000034.1: 561-2138	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Dipeptide transport system permease protein DppB (TC 3.A.1.5.2)%3B putative hemin permease;Note=Dipeptid	AFTF01000034.1: 2159-3169	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Dipeptide transport system permease protein DppC (TC 3.A.1.5.2);Note=Dipeptide transport system permease	AFTF01000034.1: 3166-4017	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Dipeptide transport ATP-binding protein DppD (TC 3.A.1.5.2);Note=Dipeptide transport ATP-binding protein Dp	AFTF01000034.1: 4010-4858	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
dipeptide ABC transporter2C ATP binding protein;Note=dipeptide ABC transporter2C ATP binding protein	AFTF01000034.1: 4855-5568	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Cytochrome B561;Note=Cytochrome B561	AFTF01000034.1: 5673-6230	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
transmembrane sensor2C putative;Note=transmembrane sensor2C putative	AFTF01000034.1: 8365-9330	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
TonB-dependent ferric achromobactin receptor protein;Note=TonB-dependent ferric achromobactin receptor	AFTF01000034.1: 9400-11802	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Shufflon-specific DNA recombinase;Note=Shufflon-specific DNA recombinase	AFTF01000033.1: 33940-34917	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000033.1: 34914-35159	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000032.1: 13190-13327	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000032.1: 37506-37766	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Name=Levansucrase;Ontology_term=KEGG_ENZYME:2.4.1.10;Note=Levansucrase Levansucrase;Ontology_term	AFTF01000031.1: 2809-4104	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ParA family protein;Note=ParA family protein	AFTF01000031.1: 17825-18412	●	1.00	●	1.00	●	1.00	●	1.00	●							

**Supplementary Table 4.** Comparison of gene content among *Psa* isolates based on aligning reads against the reference genome of *Psa* NCPPB3871 (GenBank:AFTF01000000).

conserved effector locus protein;Note=conserved effector locus protein	AFTF01000028.1: 53076-53414	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
type III effector HopN1;Note=type III effector HopN1	AFTF01000028.1: 53428-54480	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00955995: hypothetical protein;Note=FIG00955995: hypothetical protein	AFTF01000026.1: 10075-10281	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
3-oxoacyl-[acyl-carrier protein] reductase;Ontology_term=KEGG_ENZYME:1.1.1.100;Note=3-oxoacyl-[acyl-carri	AFTF01000026.1: 10336-11097	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
bacterial transferase2C hexapeptide repeat protein;Note=bacterial transferase2C hexapeptide repeat protein	AFTF01000026.1: 11109-11735	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
3-oxoacyl-[acyl-carrier-protein] synthase2C KASIII;Ontology_term=KEGG_ENZYME:2.3.1.41;Note=3-oxoacyl-[ac	AFTF01000026.1: 11762-12757	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
major facilitator family transporter;Note=major facilitator family transporter	AFTF01000026.1: 12800-13771	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
hypothetical protein;Note=hypothetical protein	AFTF01000008.1: 1289-1480	○	0.28	○	0.27	○	0.28	○	0.28	○	1.00	○	1.00	○	0.67	○	0.67
NAD-dependent protein deacetylase of SIR2 family;Note=NAD-dependent protein deacetylase of SIR2 family	AFTF01000397.1: 335-553	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
Hemolysin activator protein precursor;Note=Hemolysin activator protein precursor	AFTF01000397.1: 1944-3524	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.05
Putative large exoprotein involved in heme utilization or adhesion of ShlA/HecA/FhaA family;Note=Putative larg	AFTF01000397.1: 3549-12383	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.02
Error-prone2C lesion bypass DNA polymerase V (UmuC);Note=Error-prone2C lesion bypass DNA polymerase V	AFTF01000396.1: 3594-3842	○	0.01	○	0.00	○	0.02	○	0.02	●	1.00	●	1.00	●	1.00	○	0.31
Uncharacterized protein ImpA;Note=Uncharacterized protein ImpA	AFTF01000359.1: 434-1765	○	0.04	○	0.04	○	0.05	○	0.05	●	1.00	●	1.00	●	1.00	○	0.10
hypothetical protein;Note=hypothetical protein	AFTF01000358.1: 20-145	○	0.55	○	0.60	○	0.56	○	0.72	●	1.00	●	1.00	●	1.00	○	0.72
transcriptional regulator2C LysR family;Note=transcriptional regulator2C LysR family	AFTF01000356.1: 252-1076	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00	●	1.00	●	1.00	●	1.00
FIG00954449: hypothetical protein;Note=FIG00954449: hypothetical protein	AFTF01000356.1: 1216-3966	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00	●	1.00	●	1.00	●	1.00
hypothetical protein;Note=hypothetical protein	AFTF01000353.1: 446-619	○	0.59	○	0.58	○	0.59	○	0.60	●	1.00	●	1.00	●	1.00	○	0.59
hypothetical protein;Note=hypothetical protein	AFTF01000352.1: 84-566	○	0.06	○	0.05	○	0.06	○	0.06	●	1.00	●	1.00	●	1.00	○	0.05
hypothetical protein;Note=hypothetical protein	AFTF01000348.1: 24-437	○	0.53	○	0.61	○	0.70	○	0.72	○	0.20	●	1.00	○	0.20	○	0.82
TRAP-type C4-dicarboxylate transport system2C periplasmic component;Note=TRAP-type C4-dicarboxylate trar	AFTF01000344.1: 1185-1697	○	0.04	○	0.05	○	0.05	○	0.05	●	1.00	●	1.00	●	1.00	○	0.14
hypothetical protein;Note=hypothetical protein	AFTF01000343.1: 1524-2936	○	0.01	○	0.01	○	0.02	○	0.02	●	1.00	●	1.00	●	1.00	○	0.12
hypothetical protein;Note=hypothetical protein	AFTF01000340.1: 77-262	○	0.02	○	0.13	○	0.10	○	0.12	○	0.24	●	1.00	●	1.00	○	0.18
Two-component response regulator;Note=Two-component response regulator	AFTF01000336.1: 150-1655	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
ATP-dependent helicase HrpB;Note=ATP-dependent helicase HrpB	AFTF01000330.1: 1092-2456	○	0.62	○	0.62	○	0.62	○	0.62	●	1.00	●	1.00	●	1.00	○	0.68
FIG00953710: hypothetical protein;Note=FIG00953710: hypothetical protein	AFTF01000329.1: 1083-1343	○	0.07	○	0.04	○	0.07	○	0.10	○	0.10	●	1.00	●	1.00	○	0.11
hypothetical protein;Note=hypothetical protein	AFTF01000322.1: 2533-3027	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.03
FIG00454553: hypothetical protein;Note=FIG00454553: hypothetical protein	AFTF01000316.1: 113-3364	○	0.01	○	0.01	○	0.01	○	0.01	●	1.00	●	1.00	●	1.00	○	0.05
hypothetical protein;Note=hypothetical protein	AFTF01000313.1: 1289-1501	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00	○	0.00	●	1.00	○	0.00
FIG00955572: hypothetical protein;Note=FIG00955572: hypothetical protein	AFTF01000307.1: 760-2493	○	0.01	○	0.01	○	0.05	○	0.01	●	1.00	●	1.00	●	1.00	○	0.02
Name=Integrase Integrase;Note=Integrase	AFTF01000305.1: 109-1419	○	0.00	○	0.00	○	0.01	○	0.01	●	0.87	●	1.00	○	0.00	○	0.01
SanC2C putative;Note=SanC2C putative	AFTF01000299.1: 665-1036	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
FIG00959382: hypothetical protein;Note=FIG00959382: hypothetical protein	AFTF01000299.1: 3653-4573	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
plasmid stability protein StbB;Note=plasmid stability protein StbB	AFTF01000299.1: 6937-7083	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00
plasmid stability protein StbC;Note=plasmid stability protein StbC	AFTF01000299.1: 7080-7202	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	●	1.00	○	0.00