

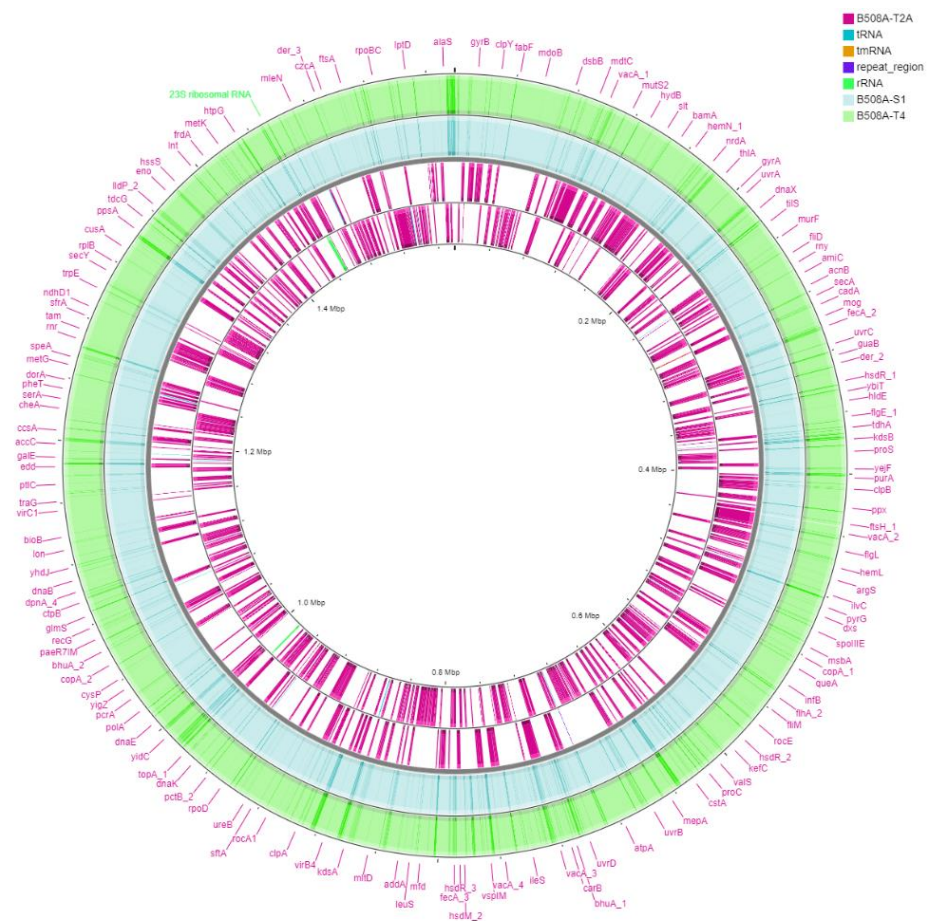


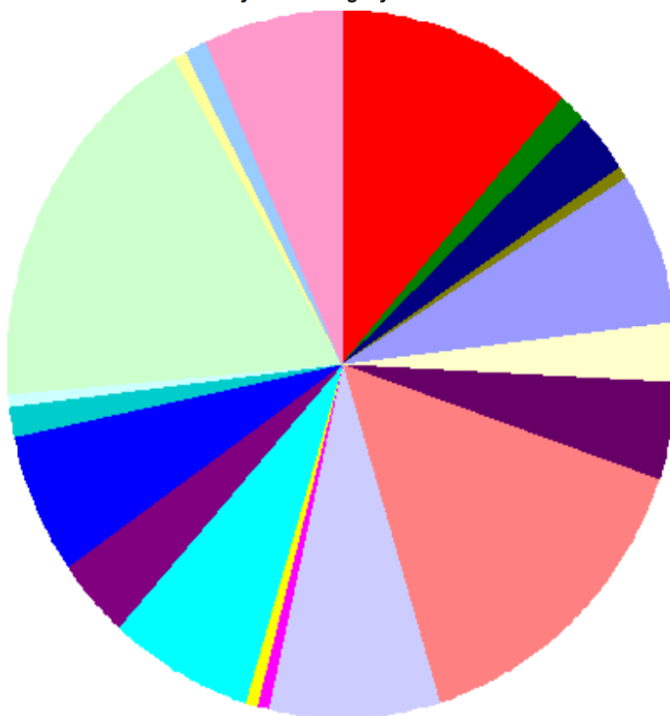
Figure S1. Circular comparative representation of the whole genomes using CGView. Inner circles represent the forward and reverse sequences of B508A-T2A.

(a)

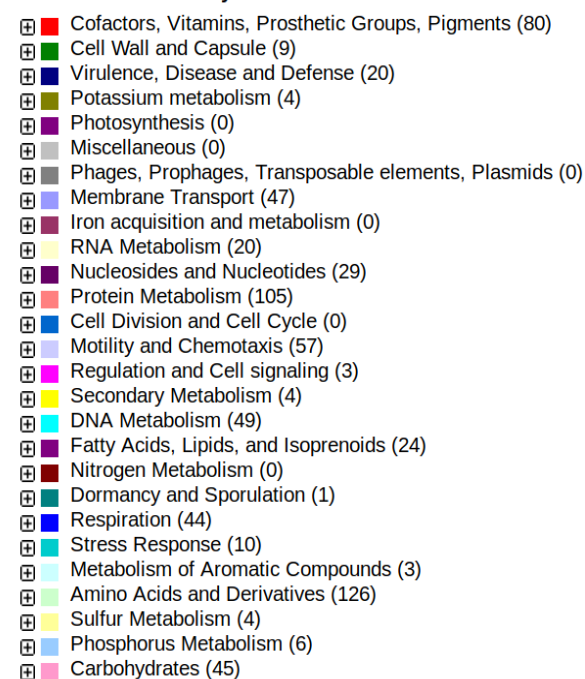
Subsystem Coverage



Subsystem Category Distribution



Subsystem Feature Counts

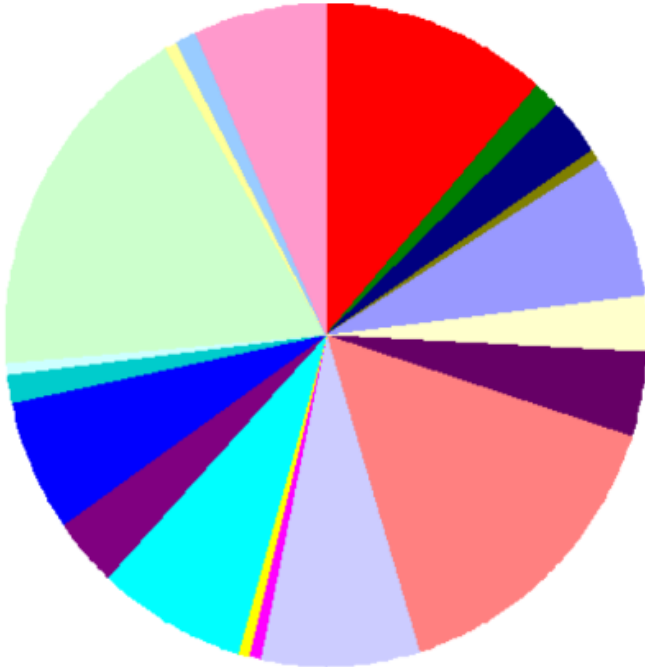


(b)

Subsystem Coverage



Subsystem Category Distribution



Subsystem Feature Counts

- ⊕ Cofactors, Vitamins, Prosthetic Groups, Pigments (80)
- ⊕ Cell Wall and Capsule (9)
- ⊕ Virulence, Disease and Defense (20)
- ⊕ Potassium metabolism (4)
- ⊕ Photosynthesis (0)
- ⊕ Miscellaneous (0)
- ⊕ Phages, Prophages, Transposable elements, Plasmids (0)
- ⊕ Membrane Transport (47)
- ⊕ Iron acquisition and metabolism (0)
- ⊕ RNA Metabolism (20)
- ⊕ Nucleosides and Nucleotides (29)
- ⊕ Protein Metabolism (105)
- ⊕ Cell Division and Cell Cycle (0)
- ⊕ Motility and Chemotaxis (57)
- ⊕ Regulation and Cell signaling (3)
- ⊕ Secondary Metabolism (4)
- ⊕ DNA Metabolism (52)
- ⊕ Fatty Acids, Lipids, and Isoprenoids (24)
- ⊕ Nitrogen Metabolism (0)
- ⊕ Dormancy and Sporulation (1)
- ⊕ Respiration (44)
- ⊕ Stress Response (10)
- ⊕ Metabolism of Aromatic Compounds (3)
- ⊕ Amino Acids and Derivatives (126)
- ⊕ Sulfur Metabolism (4)
- ⊕ Phosphorus Metabolism (6)
- ⊕ Carbohydrates (45)

(c)

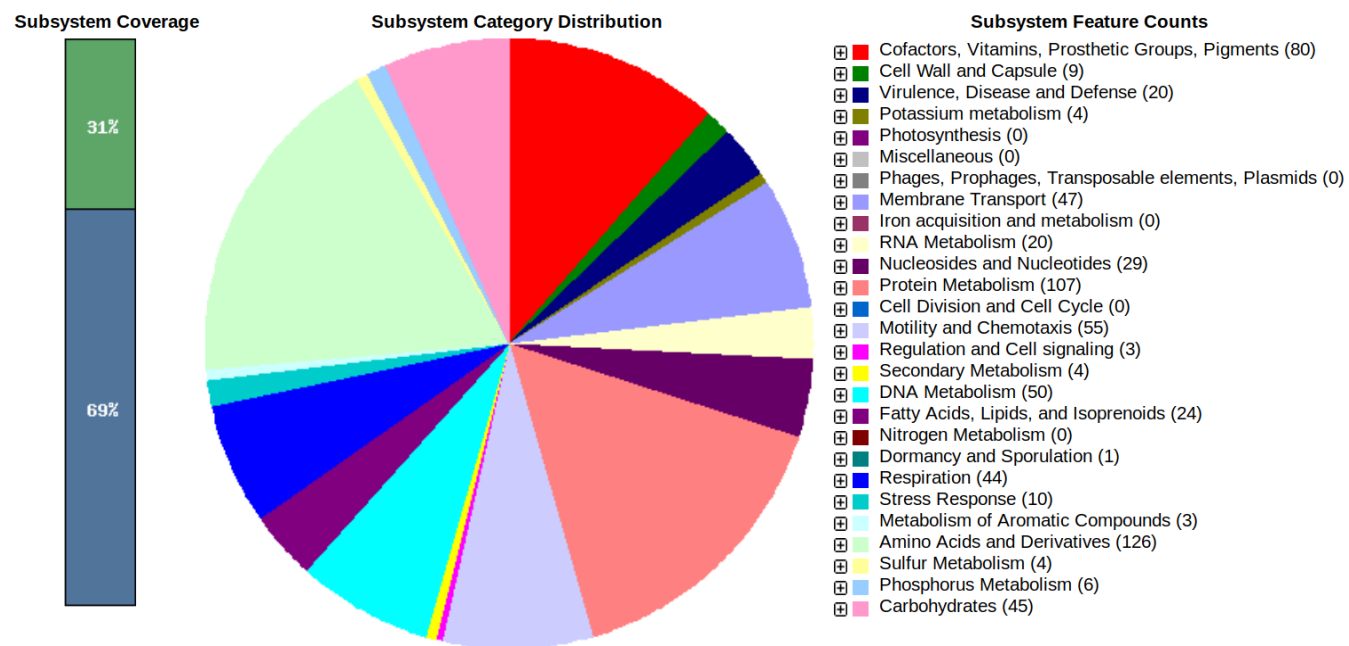


Figure S2. Pie charts representing RAST functional subsystems in the B508A-S1 (a), B508A-T2A (b), and B508A-T4 (c) genomes. The pie chart shows the % distribution of 19 most abundant subsystems on the “category” level, each of which is represented by a particular colour indicated in the right column showing the counts of features.

(a)

B508A-S1 s2m2i2 scaffold_15 (s= 286bp, m= 642bp, i= 432bp)

1 TGCTAAATTT AGCGTTTTGT GCGCTTAATT CTAAATTTTT ACTAAAATCG CTTATTGAGT
61 GGCTTCGCTC TAACGCTCTT TTTAGGTGAT ACTTTAAAGC CGCGCCTGCG GTGGCTTCGT
121 TTAAAGCGTA GCCGCTAAAC TAAAACTTTT TTTAAGAGCG CAGTTGTTGT AAGGCTTCTT
...
5641 ACTTTTAAAT CCTATGGGTT TTATATTCAT TTATCTTAAC TTAATAAAAA TTGAACATTG
5701 GTTGTAGATA CTGCATATTT ATAACCTTAA TCGTAAATGC AACAGAAATT TTCTAGTCTA
5761 AAGTCGCACC CTTTGTGCAA AAATCGTTTT AAAAAAGAA AGGAAAAAA A TGGAAATACA
5821 ACAAACACAC CGCAAAATCA ATCGCCCAT TATCTCTCTC GCTCTAGTGG GGGTGTTAAT
5881 GGGCACCAGT CTAGGGGCTA ATACGCCAAA TGATCCATA CACAGCGAGA GTCGCGCCTT
5941 TTTTACAACC GTGATCATT CAGCCATTGT TGGGGGTATC GCTACAGGCG CTGCTGTAGG
6001 AACGGTCTCA GGGCTTCTTA GCTGGGGGCT CAAACAAGCC GAACAAGCCA ATAAAGCCCC
6061 AGACAAACCC GATAAA GTTT GCGCATTCA AGCAG GAAGA GGCTTTGATA ATTTCCCCCA
6121 CAAGCAATAC GACTTATACA AATCCCTACT ATCTAGCAAA ATTGATGGAG GTTGGGA CTG
6181 GGGGAATGCC GCTAGGCATT ATTGGGTCAA AGACGGGCAG TGAACAAAC TTGAAGTGGA
6241 TATGCAAAAC GCTGTAGGGA CTTATAACCT TTCAGGCCTT ATCAACTTTA CTGGTGGGGA
6301 TTTGGACATC AATATGCAAA AAGCCACTTT GCGTTTGGGC CAATTCAATG GCAATCTTT
6361 CACAAGCTAT AAGGATAGCG CCGATCGCAC CACGAGGGTG AATTTTGACG CTAAAAATAT
6421 CTTAATTGAT AATTTTGTAG AAATCAACAA TCGTGTGGT TCTGGAGCCG GAAGAAAAGC
6481 CAGCTCTACG GTTTTGACCT TGAAAAGTTC AGAAAAAATT ACAAGCCGTG AAAACGCGGA
6541 AATCTCTCTT TATGATGGCG CCACGCTCAA TTTGGTTTCA AGC TCAAATC AGAGCGTTGA
6601 TCTATATGGG AAAGTGTGGA TGGGCCGTTT GCAATACGTG GGAGCGTATT TAGCCCTTC
6661 ATACAGCACA ATAGACACTT CAAAAGTGCA AGGGGAAATG AATTTTCGCC ATCTCGCTGT
6721 GGGTGATCAA AACGCCGCTC AAGCGGGCAT TATCGCTAAT AAAAAGACTA ATATTGGCAC
6781 ACTGGATTG TGGCAAAGTG CGGGGTAAAG CATCATCACC CCTCCGAAG GCGGTTATGA
6841 GAGTAAACT AAAGATAACC CTTCTCAAAA CAACCTAAA AATGACACGC AAAAAACAGA
6901 AATCAACCC ACGCAAGTCA TTGACGGGCC TTTTGCAGGC GGCAAAGACA CGGTTGTGAA
6961 TATTTTCCAC TAAACACTA AAGCCGATGG CACGCTTAAA GCGGGAGGGT TTAAAGCTTC
7021 TCTAGCACG AATGCGGCTC ATTTGAATAT CGGCGAAGGC GGTGT CAATC TGTCCAATCA
7081 AGCGAG CGGG CGCTCTCTT TAGTGAAAA CTAACCGGG AATATCACCG TTGAGGGGAC
7141 TTTAAGAGTG AATAATCAAG TGGGCGGTGC TGCTGTGGCA GGCTCAAGCG CGAATTTTGA
7201 GTTTAAGGCT GGTGAAGACA CCAACAACGC CACAGCCACT TTTAATAACG ATATCCATCT
7261 AGGAAAAGCG GTGAATTTAA GAGTGGATGC TCATACAGCT TATTTTAATG GCAATATTTA
7321 TCTGGGAAAA TCCACGAATT TAAGAGTGAA TGGCCATAGC GCTCATTTTA AAAATATTGA
7381 TGCCAGTAAG AGCGATAACG GGCTAAACAC TAGCGCTTTG GATTTTAGCG GCGTTACAGA
7441 CAAAGTCAAT ATCAACAAGC TCACTACATC TGCCACTAAT GTGAACGTTA AAACTTTGA
7501 CATTAAGGAA TTGGTGGTTA CAACCCGAGT TCAAAGTTTT GGGCAATACA CTATTTTGG
7561 CGAAAATATA GGCATAAGT CTCGCATTGG TGTCGTGAGT TTGCAAACGG GATATAGCCC
7621 GGCTTATTCT GGGGGCGTTA CTTTAAAAAG CGTAAGAAA CTCGTTATAG ATGAAATTTA
7681 CCATGCC CCT TGGAAATTATT TTGACGCTAG GAATGTTACC GATGTTGAAA TCAACAAAA

(b)

B508A-T2A s1m2i2 scaffold_17 (s = 259 bp, m= 642bp, i = 432bp)

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1 TGCTAAATTT AGCGTTTTGT GCGCTTAATT CTAAATTTTT ACTAAAATCG CTTATTGAGT
61 GGCTTCGCTC TAACGCTCTT TTAGGTGAT ACTTTAAAGC CGCGCCTGCG GTGGCTTCGT
121 TTAAAGCGTA GCCGCTAAAC TAAACTTTT TTAAAGAGCG CAGTTGTTGT AAGGCTTCTT
...
5461 TTTACAACAA AAAATCGCTT TGATGGACAC CCCACAAGGC ACGATTGGG AGAAGCTTTT
5521 TTAAACGCCT CCAATTTTAC CTTTTTACAC GCTCTAGCCA CAAATTCTAG CAATATTGCT
5581 TTTTAATCTT GTTGAGTTTT ATGTTCAATT ACCTTAATTT GATAAAAATT GAATATTGGT
5641 TGTAGATACT ATATATTAT AGCCTTAATC GTAAATGCAA CAGAAATTTT CTAGTCTAAA
5701 GTCGTACCCT TTGTGCAAAA ATCGTTTTAC AAGAAAAGAA GAAAGGAAAG AAATGGGAAAT
5761 ACAACAAACA CACCGCAAAA TGAATCGCCC TTAGTTTCT CTTGTTTTAG CAGGAGCGTT
5821 GATTAGCTCC ATACCGCAAG AGAGTCATGC TGCCTTTTTC ACAACCGTGA TCATTCCAGC
5881 CATTGTTGGG GGTATCGCTA CAGGCACCGC TGTAGGAACG GTATCAGGGC TTCTTAGCTG
5941 GGGACTCAAA CAAGCCGAAG AAGCGAATAA AACCCAGAT AAACCCGATA AAGTTGGCG
6001 CATTCAAGCA GGAAGAGGCT TTGATAATTT CCCCCACAAG CAATACGACT TATACAAATC
6061 CCTACTATCT AGCAAAATTG ATGGAGGTTG GGAAGTGGGG AATGCCGCTA GGCATTATTG
6121 GGTCAAAGAC GGGCAGTGGA ACAAATCTGA AGTGGATATG CAAAACGCTG TAGGGACTTA
6181 TAACCTTTCA GGCCTTATCA ACTTTACTGG TGGGGATTG GACATCAATA TGCAAAAAGC
6241 CACTTTGCGT TTGGGCCAAT TCAATGGCAA TTCTTTCACA AGCTATAAGG ATAGCGCCGA
6301 TCGCACACAG AGGGTGAATT TTGACGCTAA AAATATCTTA ATTGATAATT TTGTAGAAAT
6361 CAACAATCGT GTGGGTTCTG GAGCCGGAAG AAAAGCCAGC TCTACGTTT TGACCTTGAA
6421 AAGTTCAGAA AAAATTACAA GCCGTGAAAA CGCGGAAATC TCTCTTATG ATGGCGCCAC
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6541 CCGTTTGCAA TACGTGGGAG CGTATTAGC CCCTTCATAC AGCACAATAG ACACTTCAAA
6601 AGTGCAAGGG GAAATGAATT TTCGCCATCT CGCTGTGGGT GATCAAAACG CCGCTCAAGC
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6841 CGGGCCTTTT GCAGGCGGCA AAGACACGGT TGTGAATATT TTCCACTTAA AACTAAAGC
6901 CGATGGCACG CTAAAGCGG GAGGGTTTAA AGCTTCTCTT AGCACGAATG CGGCTCATT
6961 GAATATCGGC GAAGCGGTG TCAATCTGTC CAATCAAGCG AGCGGCGCT CTCTTTAGT
7021 GGAAACCTA ACCGGAATA TCACCGTTGA GGGGACTTTA AGAGTAATA ATCAAGTGGG
7081 CGGTGCTGCT GTGGCAGGCT CAAGCGCGAA TTTGAGTTT AAGGCTGGT AAGACACCAA
7141 CAACGCCACA GCCACTTTTA ATAACGATAT CCATCTAGGA AAAGCGGTGA ATTTAAGAGT
7201 GGATGCTCAT ACAGCTTATT TTAATGGCAA TATTATCTG GGAAATCCA CGAATTTAAG
7261 AGTGAATGGC CATAGCGCTC ATTTAAAAA TATTGATGCC AGTAAGAGCG ATAACGGGCT
7321 AAACACTAGC GCTTTGATT TTAGCGGCGT TACAGACAAA GTCAATATCA ACAAGCTCAC
7381 TACATCTGCC ACTAATGTGA ACGTTAAAAA CTTTGACATT AAGGAATTGG TGGTTACAAC
7441 CCGAGTTCAA AGTTTGGGC AATACACTAT TTTTGGCGAA AATATAGGCG ATAAGTCTCG
7501 CATTGGTGTC GTGAGTTTGC AAACGGGATA TAGCCCGGCT TATTCTGGGG GCGTTACTTT
7561 TAAAGCGGT AAGAACTCG TTATAGATGA AATTACCAT GCCCCTTGGGA ATTATTGGA
7621 CGCTAGGAAT GTTACCGATG TTGAAATCAA CAAAAGAATT CTTTTTGGAG CCCAGGAAA
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(c)

B508A-T4 s2m2i2 scaffold_15 (s= 286 bp, m= 642 bp, i= 432 bp)

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1 TTTTCGGCGT TGGCTTGTTT TAATGGGCTT AAATTGGTAG CGTTTTGTGG GGTTCGTTT
61 AAATTTCTG TATTTTTTAA TAAATCCTCT TGATCTATTA AATCTTTTGG TGAGTATTC
121 TCTGTAGCAC CGCTATAGGA ACTCAACCTA TGGTTCACCT TTGCATCAGC ATTGAGTGTA
...
6481 TTAACCTAAT AAAAATTGAA CATTGGTTGT AGATACTGCA TATTTATAAC CTTAATCGTA
6541 AATGCAACAG AAATTTTCTA GTCTAAAGTC GCACCCTTTG TGCAAAAATC GTTTTACAAA
6601 AAGAAAGGAA AAAAATGGAA ATACAACAAA CACACGCGAA AATCAATCGC CCCATTATCT
6661 CTCTCGCTCT AGTGGGGGTG TTAATGGGCA CCGAACTAGG GGCTAATACG CCAAATGATC
6721 CCATACACAG CGAGAGTCGC GCCTTTTTTA CAACCGTGAT CATTCCAGCC ATTGTTGGGG
6781 GTATCGCTAC AGGCGCTGCT GTAGGAACGG TCTCAGGGCT TCTAGCTGG GGGCTCAAAC
6841 AAGCCGAACA AGCCAATAAA GCCCCAGACA AACCCGATAA AGTTGGCGC ATTCAAGCAG
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7081 GCCTTATCAA CTTTACTGGT GGGGATTGGG ACATCAATAT GCAAAAAGCC ACTTTCGCTT
7141 TGGGCCAATT CAATGGCAAT TCTTTCACAA GCTATAAGGA TAGCGCCGAT CGCACCACGA
7201 GGGTGAATTT TGACGCTAAA AATATCTTAA TTGATAATTT TGAGAAAATC AACAATCGTG
7261 TGGGTTCTGG AGCCGGAAGA AAAGCCAGCT CTACGGTTTT GACCTTGAAA AGTTCAGAAA
7321 AAATTACAAG CCGTGAAAAC GCGGAAATCT CTCTTATGA TGGCGCCACG CTCAATTTGG
7381 TTTCAAGC TC AAATCAGAGC GTTGATCTAT ATGGGAAAGT GTGGATGGGC CGTTTGCAAT
7441 ACGTGGGAGC GTATTAGCC CCTTCATACA GCACAATAGA CACTTCAAAA GTGCAAGGGG
7501 AAATGAATTT TCGCCATCTC GCTGTGGGTG ATCAAAACGC CGCTCAAGCG GGCATTATCG
7561 CTAATAAAAA GACTAATATT GGCACACTGG ATTTGTGGCA AAGTGCGGGG TTAAGCATCA
7621 TCACCCCTCC CGAAGGCGGT TATGAGAGTA AAATAAAGA TAACCCTTCT CAAAACAACC
7681 CTAATAATGA CACGCAAAAA ACAGAAATTC AACCCACGCA AGTCATTGAC GGGCCTTTTG
7741 CAGGCGGCAA AGACACGGTT GTGAATATTT TCCACTTAAA CACTAAAGCC GATGGCACGC
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7861 AAGGCGGTGT CAATCTGTCC AATCAAGCGA GCGGGCGCTC TCTTTAGTG GAAAACCTAA
7921 CCGGGAATAT CACCGTTGAG GGGACTTTAA GAGTGAATAA TCAAGTGGGC GGTGCTGCTG
7981 TGGCAGGCTC AAGCGCGAAT TTTGAGTTTA AGGCTGGTGA AGACACCAAC AACGCCACAG
8041 CCACTTTTAA TAACGATATC CATCTAGGAA AAGCGGTGAA TTAAAGAGTG GATGCTCATA
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8341 GTTTTGGGCA ATACACTATT TTTGGCGAAA ATATAGCGCA TAAGTCTCGC ATTGGTGTGC
8401 TGAGTTTGCA AACGGGATAT AGCCCGGCTT ATTCTGGGGG CGTTACTTTT AAAAGCGGTA
8461 AGAACTCGT TATAGATGAA ATTTACCATG CCTTGGAA TTATTTTGAC GCTAGGAATG
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Figure S3. *vacA* genomic sequences extracted from the whole genomes of strains B508A-S1 (a), B508A-T2A (b) and B508A-T4 (c). Primers used for the detection of *s*, *i* and *m* regions are highlighted.

Table S1. Shared clusters between strains found using OrthoVenn2. **(a)** Strains B508A-T2A and B508A-T4. **(b)** Strains B508A-S1 and B508A-T2A. **(c)** Strains B508A-S1 and B508A-T4.

(a)

clusterID	Number of proteins	Swiss-Prot Hit
cluster 6	3	DUF874 family protein
cluster1409	2	hypothetical protein

(b)

clusterID	Number of proteins	Swiss-Prot Hit
cluster3	4	DUF874 family protein
cluster4	4	Outer membrane beta-barrel protein
cluster1405	2	Glycosyltransferase family 8 protein
cluster1406	2	hypothetical protein
cluster1407	2	Glycosyltransferase family 8 protein
cluster1408	2	DUF3519 domain-containing protein
cluster1410	2	DUF3519 domain-containing protein
cluster1411	2	Outer membrane protein family
cluster1412	2	Acetyl-coenzyme A synthetase
cluster1413	2	Alpha-1,2-fucosyltransferase
cluster1414	2	Flagellar biosynthesis protein FlhF
cluster1415	2	Modification methylase HinfI

(c)

clusterID	Number of proteins	Swiss-Prot Hit
cluster5	4	DUF874 family protein
cluster1416	2	Modification methylase VspI
cluster1417	2	hypothetical protein
cluster1418	2	DUF697 domain-containing protein
cluster1419	2	Uncharacterized chromosomal cassette SCCmec type IVc protein CR006
cluster1420	2	hypothetical protein
cluster1421	2	outer membrane protein OipA
cluster1422	2	LPS heptosyltransferase family protein
cluster1423	2	Lipooligosaccharide biosynthesis protein lic2B
cluster1424	2	hypothetical protein
cluster1425	2	Flagellar biosynthesis protein FlhA
cluster1426	2	Type III restriction-modification system
cluster1427	2	hypothetical protein
cluster1428	2	ATP-binding protein
cluster1429	2	SAM-dependent methyltransferase
cluster1430	2	Uncharacterized protein HI_1472
cluster1431	2	Inner membrane ABC transporter permease protein YejE
cluster1432	2	Proline/betaine transporter
cluster1433	2	ATP-binding protein
cluster1434	2	cysteine desulfurase
cluster1435	2	Trigger factor

Table S2. Description of the unique genes found with Roary.

Unique genes	Description name
<i>vacA</i>	Vacuolating cytotoxin autotransporter (<i>vacA_4</i>)
<i>flhA</i>	Flagellar biosynthesis protein FlhA (<i>flhA_1</i>)
<i>fucT_1</i>	Alpha-(1,3)-fucosyltransferase FucT (<i>fucT_1</i>)
<i>fucT_2</i>	Alpha-(1,3)-fucosyltransferase FucT (<i>fucT_2</i>)
type-1 restriction enzyme	Putative type-1 restriction enzyme specificity protein MG438
<i>hsdM</i>	Type I restriction enzyme EcoKI M protein (<i>hsdM_2</i>)
<i>rocC</i>	Amino-acid permease RocC (<i>rocC_1</i>)
<i>xerH</i>	Tyrosine recombinase XerH (<i>xerH_3</i>)
<i>hydB</i>	Quinone-reactive Ni/Fe-hydrogenase large chain (<i>hydB</i>)
<i>era</i>	GTPase Era (<i>era_3</i>)
<i>cpdA</i>	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA
<i>era</i>	GTPase Era (<i>era_2</i>)
<i>der</i>	GTPase Der (<i>der_3</i>)
<i>msrAB</i>	Peptide methionine sulfoxide reductase <i>msrA/msrB</i> (<i>msrAB</i>)
<i>yjeE</i>	Inner membrane ABC transporter permease protein YjeE (<i>yjeE_1</i>)