			NON-M	MUCOID	MUCOID	1	l No	ON-MUCOID		MUCOID		7		
	Lineage Time point	Ref	Ref1 Ref1 Ref2	Ref2 Ref3 Ref3	MUCCOID  MET A Ref A Ref A Ref Bef Bef Bef Bef Bef Bef Bef Bef Bef B	Mut Anc	Mut1 Mut1 N	Mut2 Mut2 Mut3 Mut3	Mut4 Mut4 Mut4	Mut5 Mut5 Mut5	Mut6 Mut6 Mut6	Ī		
	Identifier	EC32	EC01 EC13 EC02	EC14 EC03 EC15	EC04 EC25 EC16 EC05 EC26 EC17 EC06 EC27 EC16	8 EC31	EC07 EC19 E	C08 EC20 EC09 EC21	EC10 EC28 EC22	EC11 EC29 EC23	EC12 EC30 EC24	l		
Position	Mutation →G									SNP SNP SNP		intergenic (+64/-198)	Gene carB → / → caiF	Description Carbamoyi-phosphate synthase large subunit/cai operon transcriptional activator
5,753 T-	→A									0111 0111 0111	SNP	I150N (ATC→AAC)	ftsZ →	GTP-binding tubulin-like cell division protein
	→T →G							SNP	SNP SNP SNP			A215V (GCC→GTC)	$lpxC \rightarrow erpA \rightarrow / \leftarrow yadS$	UDP-3-O-acyl N-acetylglucosamine deacetylase iron-sulfur cluster insertion protein/UPF0126 family inner membrane protein
3.291 T-	→C								SNP SNP SNP			intergenic (+34/+13) F1056L (TTT→CTT)	dnaE →	DNA polymerase III alpha subunit
0,254 Δ3 7,188 A-	33,701 bp →G		Δ	Δ							SND SND SND	IS5-mediated R20R (CGT→CGC)	ivy–[ykfC] betA ←	42 genes choline dehydrogenase, a flavoprotein
1.843 IS	1 (-) +9 bp							IS			0141 0141 0141	intergenic (+347/-520)	$betT \rightarrow / \rightarrow yahA$	choline transporter of high affinity/c-di-GMP-specific phosphodiesterase
6,941 G- 0,014 A- 0,012 +0 0,892 +0	→A →G						SNP SNP		SNP SNP SNP			A257A (GCG→GCA) T468T (ACA→ACG)	codA →	cytosine/isoguanine deaminase
0,014 +0	à								SINF SINF SINF		INS INS INS	intergenic (-131/+57)	$mhpA \rightarrow frmR \leftarrow / \leftarrow yaiO$	3-(3-hydroxyphenyl)propionate hydroxylase regulator protein that represses frmRAB operon/outer membrane protein manno(fructo)kinase
0,892 +0 28,744 T-	a a →C										INS INS INS	intergenic (-131/+57) coding (749/909 nt) pseudogene (105/491 nt)	mak → ybbD →	manno(fructo)kinase losseudosene
33.709 IS	2 (+) +5 bp									IS	SINF SINF SINF	coding (29-33/750 nt)	appY →	global transcriptional activator: DLP12 prophage
58.080 A-	→Ġ´ →G						SNP SNP					pseudogene (50/788 nt) noncoding (55/77 nt)	ybeM → metT ←	pseudogene, C-N hydrolase superfamily homology;putative enzyme; Not classified; putative amidase IRNA-Met
97,909 G-	→T						SNP SNP SNP					C423* (TGC→TGA)	asnB ←	asparagine synthetase B
13,699 C- 12,930 T-	→T →C		SNP SNP						SNP SNP SNP			R48C (CGT→TGT) V35A (GTG→GCG)	pgm →	phosphoglucomutase MIC2 (amily mottal binding protein
6,995 C-	→T							SNP	SINF SINF SINF			intergenic (-348/-49)	ybhK ← / → moaA	NIF3 family metal-binding protein  NIF3 family metal-binding protein  putative Coff Superfamily transferase/molybdopterin biosynthesis protein A theconine and homoserine efflux system/outer membrane protein X  alkanesulfonate monoxygenase, FRMH(2)-dependent prohage e1 41 all protein homolog
6,995 C- 0,116 IS 5,392 T-	5 (–) +4 bp →C		IS							SNP SNP SNP		intergenic (-348/-49) intergenic (-19/-331) E199E (GAA→GAG)	rhtA ← / → ompX	threonine and homoserine efflux system/outer membrane protein X
207,085 T-	→Č						SNP SNP			SINF SINF SINF		L58P (CTG→CCG)	ymfQ →	analissundriae indroxygenae, i with (2)-dependent prohage e14 tail protein homolog
292,335 G- 689,096 A-	→A →G							SNP SNP SNP				W293* (TGG→TGA) Q174R (CAG→CGG)	galU → manA →	glucose-1-phosphate uridylyltransferase mannose-6-phosphate isomerase
695,738 T-	→C									SNP		T112A (ACG→GCG)	uidA ←	beta-D-glucuronidase
804,803 +A 841,779 A	\ →C							INS				pseudogene (1710/1900 nt) E97A (GAA→GCA)	$arpB \rightarrow nudG \rightarrow$	pseudogene, ankyrin repeats CTP pyrophosphohydrolase; also hydrolyzes 2-hydroxy-dATP, 8-hydroxy-dGTP, 5-hydroxy-CTP, dCTP and 5-methyl-dCTP
864,110 G-	→A									SNP		A87A (GCG→GCA)	yeaD →	D-havosa-6-nhosphate enimerase-like protein
904,376 +0 915,284 T-	a →C			INS INS					SNP SNP SNP			coding (482/852 nt) D84G (GAC→GGC)	yeaD → manZ → proQ ← yebK →	mannose-specific enzyme IID component of PTS RNA charenne, nutstive Prop translation regulator
937.034 +	\								SINI SINF SINF	INS INS INS		coding (383/870 nt)	yebK →	mannose-specific enzyme IID component of PTS RNA chaperone, putative ProP translation regulator putative DNA-binding transreptional regulator
,979,486 IS ,989,693 A-	5 (+) +4 bp →G		IS	IS				SNP SNP				intergenic (-271/-264) T5A (ACC→GCC)	insA ← / → uspC tyrP →	IS1 repressor TnpA/universal stress protein tyrosine transporter
023,656 IS	5 (-) +4 bp		IS					SINF SINF				coding (764-767/786 nt)	fliR →	flagallar ayport para protoin
	→A →C									SNP SNP SNP	SNP	A18A (GCC→GCT) G166G (GGT→GGC)	wcaG ←	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase/ GDP-4-dehydro-6-L-deoxygalactose reductase dibudronymidine dehydronenase. NADH-denoprient sulpunit C
284,907 91	op x 2			DUP								duplication	preA → yejM →	inagenal export port protein britancia (DP-4-dehydro-6-deoxy-D-mannose epimerase/ GDP-4-dehydro-6-L-deoxygalactose reductase dihydropyrimidine dehydrogenase, ADH-dependen, subunit C sessential inner membrane DUF3413 domain-containing protein; lipid A production and membrane permeability factor
311.931 C-	23,972 bp →T						SNP SNP	Δ Δ				IS5-mediated W273* (TGG→TGA)	[yejO]-[rcsD] ompC ← ompC ← ompC ←	
312,534 81	op x 2		DUP DUP					DEL DEL				duplication	ompC ←	outer membrane porin protein C
312,771 G-	bp →T		SNP	SNP			'	DEL DEL				coding (186/1104 nt) intergenic (-22/-717)	ompC ← / → rcsD	act get res under membrane porin protein C outer membrane porin protein C) outer membrane porin protein C
312,582 Δ1 ,313,002 Δ1	13,109 bp 14,218 bp				Δ						Δ		[ompC]-[atoE]	[ompC], rosD, rosB, rosC, atoS, atoC, atoD, atoA, [atoE] rosD, rosB, rosC, atoS, atoC, atoD, atoA, atoE, [atoB]
313,540 Δ2	2 :: IS186 (+) +6 bp	0			IS						Δ	coding (53-58/2673 nt)	rcsD-[atoB] rcsD →	rcsu, rcss, rcss, alos, atios,
315,677 IS 316,207 IS	2 :: IS186 (+) +6 bp 1 (−) +9 bp 1 (−) +9 bp →A				IS				IS			coding (2190-2198/2673 nt) coding (31-39/651 nt) R160H (CGC→CAC)	rcsD →	phosphotransfer intermediate protein in two-component regulatory system with RcsBC resonose regulator in two-component regulatory system with RcsBC NIN NIN NIN NIN NIN NIN NIN NIN NIN NI
316,655 G	→A									SNP SNP	•	R160H (CGC→CAC)	rcsB → rcsB →	response regulator in two-component regulatory system with RcsC and YojN
317,103 T- 317,386 C-	→G →T				SNP SNP SNF	<b>'</b>			SNP SNP SNP			K925T (AAG→ACG) D831N (GAT→AAT)	rcsC ← rcsC ←	hybrid sensory kinase in two-component regulatory system with RcsB and YojN hybrid sensory kinase in two-component regulatory system with RcsB and YojN hybrid sensory kinase in two-component regulatory system with RcsB and YojN
318.226 \D4	1,019 bp 64 bp				Δ							coding (705-768/2850 nt)	[rcsC]-[atoC]	[rcsC], atoS, [atoC]
319,266 Δ1	182 bp								Δ		Δ	coding (430-611/2850 nt)	[rcsC]–[atoC] rcsC ← rcsC ←	Injoria sensory kinase in two-component regulatory system with RcsB and YojiN hybrid sensory kinase in two-component regulatory system with RcsB and YojiN
,319,566 IS ,420,984 +C	2 (–) +5 bp				IS IS					INS INS INS		coding (307-311/2850 nt) coding (364/648 nt)	rcsC ← yfcG →	hybrid sensory kinase in two-component regulatory system with RcsB and YojN (SSL despendent distlike) board system with RcsB and YojN
484,027 T-	, →C						SNP SNP			1140 1140 1140		C91C (TGT→TGC)	evgA → pbpC ←	response regulator in two-component regulatory system with EvgS
646,684 Δ1 686.214 T-	I2 bp →C			Δ					SNP SNP SNP			coding (631-642/2313 nt) L127P (CTG→CCG)	pbpC ← hmp →	penicillin-insensitive murein repair transglycosylase; inactive transpeptidase domain protein tused nitro oxide diovenense/distronteridine reductase 2
764.853 A-	→G									SNP SNP SNP	1	S101P (TCC→CCC)	yfjL ← yfjL ← / ← yfjM	CP4-57 putative defective prophage, DUF4297/DUF1837 polymorphic toxin family protein
	op x 2 →A										SNP SNP SNP	duplication A224A (GCG→GCA)	yfjL ← / ← yfjM ascF →	hýbrid sensorý kinase in two-component regulatorý sýstem with RcsB and YojN [rcsC], atoS, [atoC] hybrid sensory kinase in two-component regulatory system with RcsB and YojN hybrid sensory kinase in two-component regulatory system with RcsB and YojN hybrid sensory kinase in two-component regulatory system with RcsB and YojN GSH-dependent disulfide bord oxidoreductase response regulator in two-component regulatory system with EvgS periodillin-insensitive murein repair transglycosylase; inactive transpeptidase domain protein lused nitric oxide dioxygenase/dihydropteridine reductase 2 CP4-57 putative defective prophage, DUF4297/DUF1837 polymorphic toxin family protein CP4-57 putative defective prophage, DUF4297/DUF1837 polymorphic toxin family protein/CP4-57 prophage; uncharacterized protein celiobiose/arbutin/salicin-specific PTS enzymes, IIB and IC components cysteine sulfinate desuffinase.
943,707 T-	→C						OND SUB				SNP SNP SNP	V124A (GTC→GCC)		
	→C Ibp						SNP SNP		DEL DEL DEL			T312A (ACC→GCC) intergenic (-290/-295)	ptrA ← aas ← / → galR	protease III fused 2-acylglycerophospho-ethanolamine acyl transferase/acyl-acyl carrier protein synthetase/galactose-inducible d-galactose regulon transcriptional repressor; autorepressor
166,819 A8	33 bp →T						] .	SNP SNP				coding (818-900/1608 nt) D22E (GAT→GAA)	ygiS ← hldE ←	putative ARG transporter permease heptose 7-phosphate kinase and heptose 1-phosphate adenyltransferase
381.705 AS	90 bp		Δ	Δ				DINE DINE				coding (963-1052/1368 nt)	nidE ← degQ → frIB →	serine endonrotease, perinlasmic
	→G . 5 (+) +4 bp				IS IS IS		SNP SNP					H33R (CAC→CGC)	frIB →	Tructosely/sine-6-P-deglycase adenosine nucleotide hydrolase; Ap3A/Ap2A/ADP-ribose/NADH hydrolase/putative RcsCDB-response attenuator, inner membrane protein
527.155 G-	→A									SNP SNP SNP		intergenic (-210/-107) W229* (TGG→TGA)	nudE ← / → yrfF yrfF → yrfF →	Iputative RcsCDB-response attenuator, inner memprane protein
528,036 T- 528,396 T-	→C →C				SNP SNP SNP						SNP SNP SNP	L523P (CTG→CCG) L643P (CTT→CCT)	yrfF → yrfF →	putative RcsCDB-response attenuator, inner membrane protein putative RcsCDB-response attenuator, inner membrane protein
535,001 T-	→A			SNP SNP							5141 5141	T290S (ACC→TCC)	envZ ←	sensory histidine kinase in two-component regulatory system with OmpR
627,833 A-	→T →G							SNP SNP			SNP SNP SNP	Q189* (CAG→TAG) V569A (GTG→GCG)	malT → rbbA ←	mal regulon transcriptional activator ribosome-associated ATPase: ATP-binding protein/ATP-binding membrane protein
633,206 A-	→T →C								SNP SNP SNP			pseudogene (1253/1607 nt) R9R (CGT→CGC)	yhiL ← yhiD →	mai reguiori transcripitorial activator in filosome associated ATPase ATP-binding protein/ATP-binding membrane protein pseudogene, DUF-4094 family protein inner membrane putative Brits family protein inner membrane putative Brits family alternate lipid exporter UDP-D-galactose: (glucosy)/lipopolysaccharide- alpha-1,3-D-galactosyltransferase UDP-D-galactose: (glucosy)/lipopolysaccharide- alpha-1,3-D-galactosyltransferase
302.499 Δ1	l bp						DEL DEL		JINF JINF SINF			coding (560/1020 nt)	waaO ←	IUDP-D-galactose:(glucosy)lipopolysaccharide-alpha-1,3-D-galactosyltransferase
302,542 IS	5 (–) +4 bp →G			IS IS			SNP					coding (514-517/1020 nt) noncoding (27/77 nt)	waaO ←	UDP-D-galactose (glucosyl)lipopolysaccharide- alpha-1,3-D-galactosyltransferase IRNA-Asp
952,867 A-	→G						JINF	SNP				G128G (ĞĞA→GGĞ)	aspT → iIvE →	branched-chain amino acid aminotransferase
101,721 +0 213,581 T-	a →G							INS				coding (32/984 nt) S116R (AGT→AGG)	kdgT → yjaA →	2-keto-3-deoxy-D-gluconate transporter stress-induced protein
239,240 +0	à						1				INS INS INS	coding (1607/2097 nt)	lyihH →	DLIE940 family extracellular polysaccharide protein
248,502 T- 348,815 A-	→C →C →T						SNP SNP					S178P (TCC→CCC) intergenic (-71/+500)	lamB → dcuB ← / ← dcuB	Imallose outer membrane portin (maltoportin) C4-dicarboxydate transporter anaerobic: DouS co-sensor/response regulator in two-component regulatory system with DouS
522,404 C-	→T						SNP SNP					intergenic (-71/+500) G564E (GGG→GAG)	yjhG ←	maltose outer membrane porin (maltoporin) C4-dicarboxylate transporter, anaerobic; DcuS co-sensor/response regulator in two-component regulatory system with DcuS putative dehydratase lyrosine recombinase/inversion of on/off regulator of firmA/tyrosine recombinase/inversion of on/off regulator of firmA
542,161 IS	5 (–) +4 bp 5 (–) +4 bp				IS IS		IS	15				intergenic (+461/-14) coding (125-128/597 nt)	fimE →	Ityrosine recombinase/inversion of on/off regulator of fimA
542,308 IS	5 (-) +4 bp							IS			IS	coding (272-275/597 nt)	fim⊏ .	tyraning recombinated inversion of an left regulator of fim A
542.811 IS	1 (+) +9 bp 1 (+) +9 bp				IS			IS				coding (421-429/597 nt) intergenic (+178/-296)	$fimE \rightarrow / \rightarrow fimA$	tyrosine recombinase/inversion of on/off regulator of fimA tyrosine recombinase/inversion of on/off regulator of fimA/major type 1 subunit fimbrin (pilin)
.542,831 IS	5 (+) +4 bp →G			IS						IS	QNIP	intergenic (+198/-281) L507P (CTG→CCG)	$fimE \rightarrow fimA$ $fimE \rightarrow / \rightarrow fimA$ $fimE \rightarrow / \rightarrow fimA$ $hsdM \leftarrow$	tyrosine recombinase/inversion of on/off regulator of fimA/major type 1 subunit fimbrin (pilin) tyrosine recombinase/inversion of on/off regulator of fimA/major type 1 subunit fimbrin (pilin) DNA methyltransferase M
606,207 +0										INS	SINF	noncoding (80/87 nt)	leuP ←	DIV ineurynatiolerase w [RNA-Leu

Position gives the genomic location of each change in minutes.

Changes are denoted '\Delta' for big deletions (>50 bp), 'SNP' for single nucleotide polymorphism, 'IS' for insertion sequence, 'DUP' for duplications, 'DEL' for deletions and 'INS' for insertions. Mut and Ref refer to the mutator and reference genetic backgrounds as described in the main text.

'Mucoid' and 'Non-mucoid' refer to phage-resistant mutants at Time point=0; note that 'mucoid' genotypes at later time points had reverted to non-mucoid phenotypes but were derived from mucoid ancestors. Regions with significant parallelism are shaded grey.