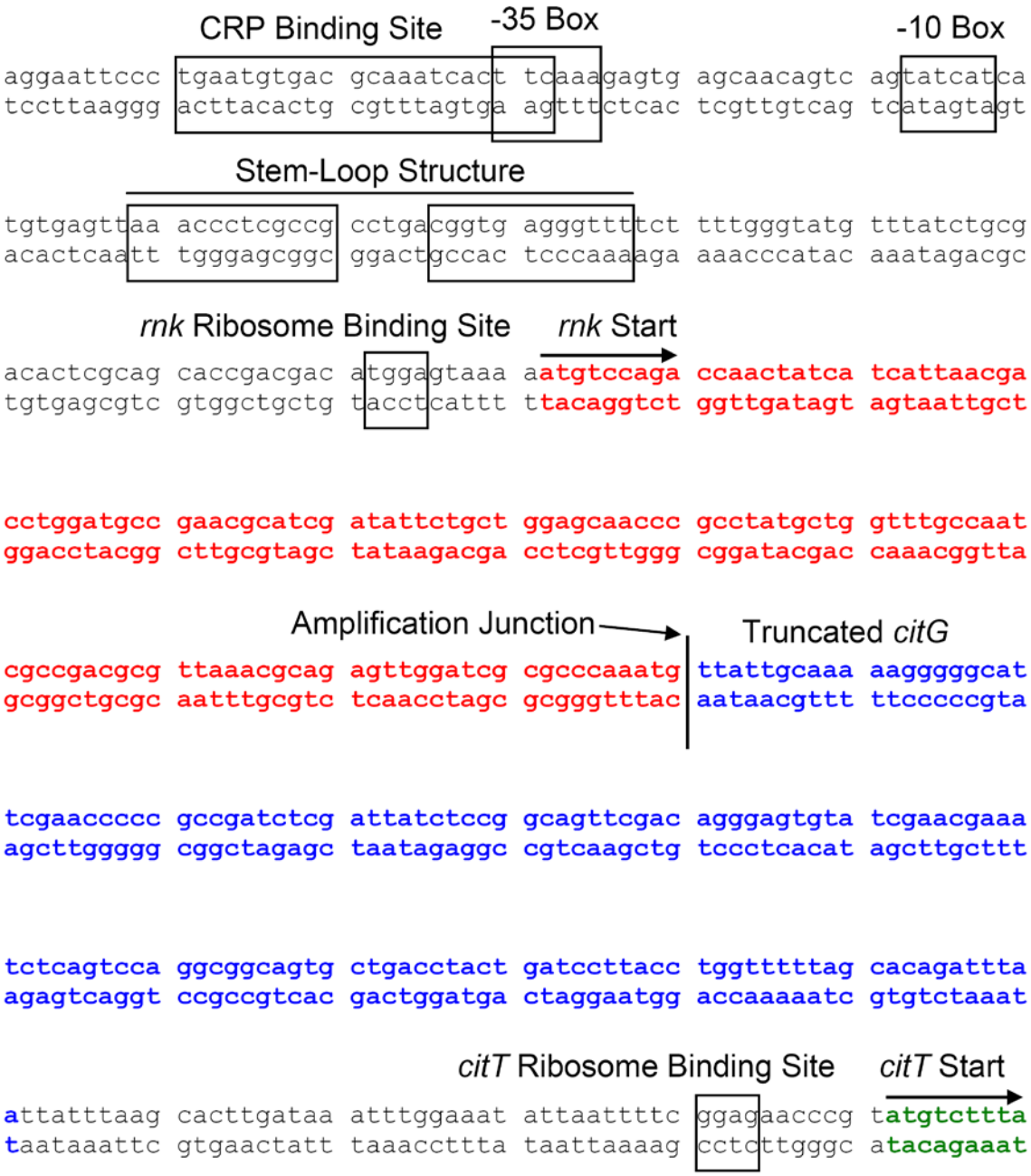
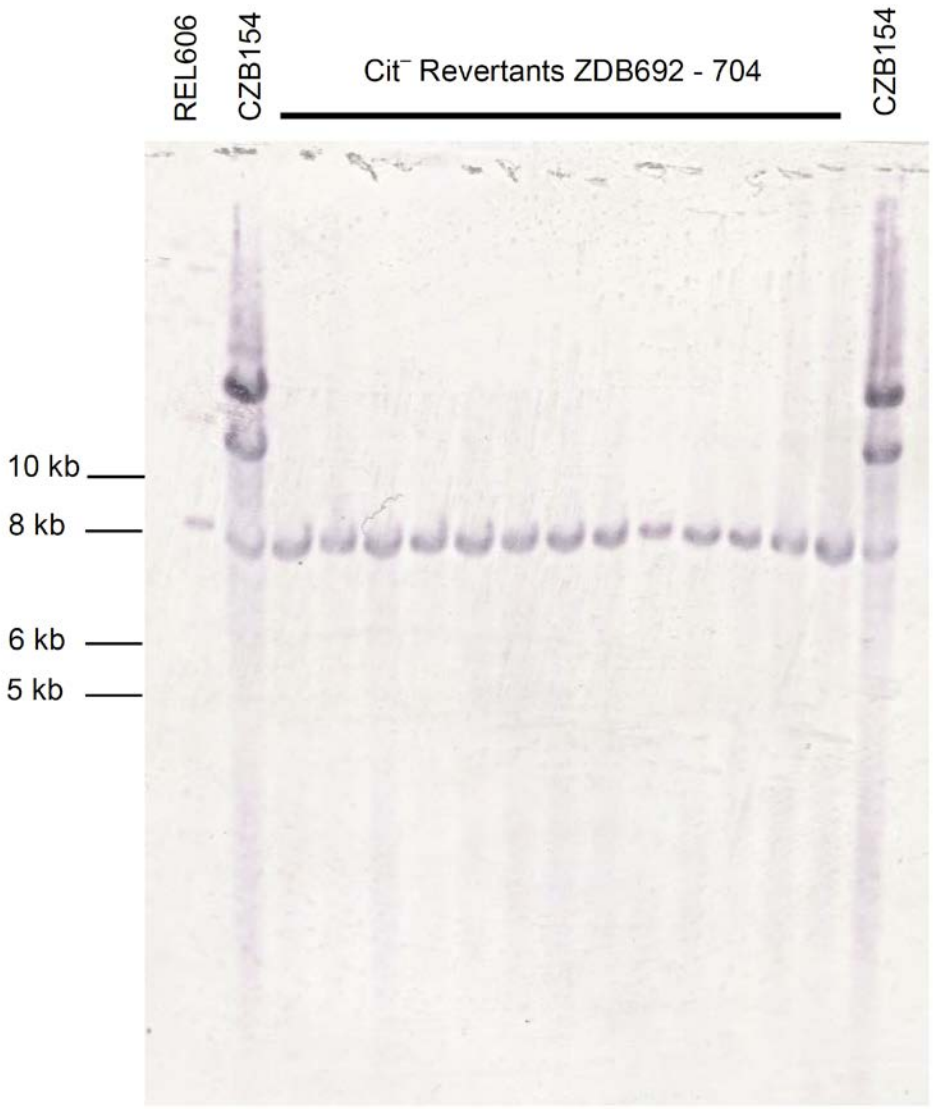
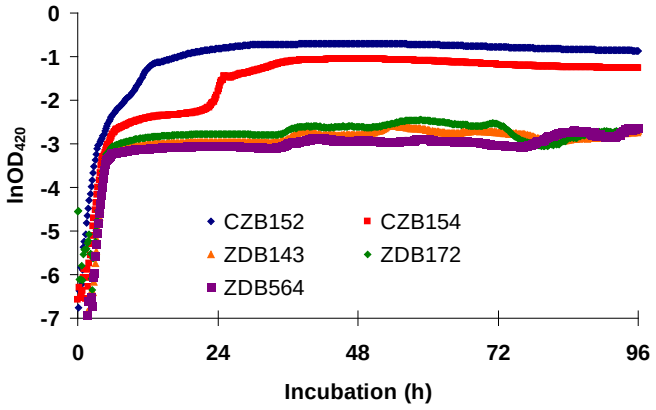


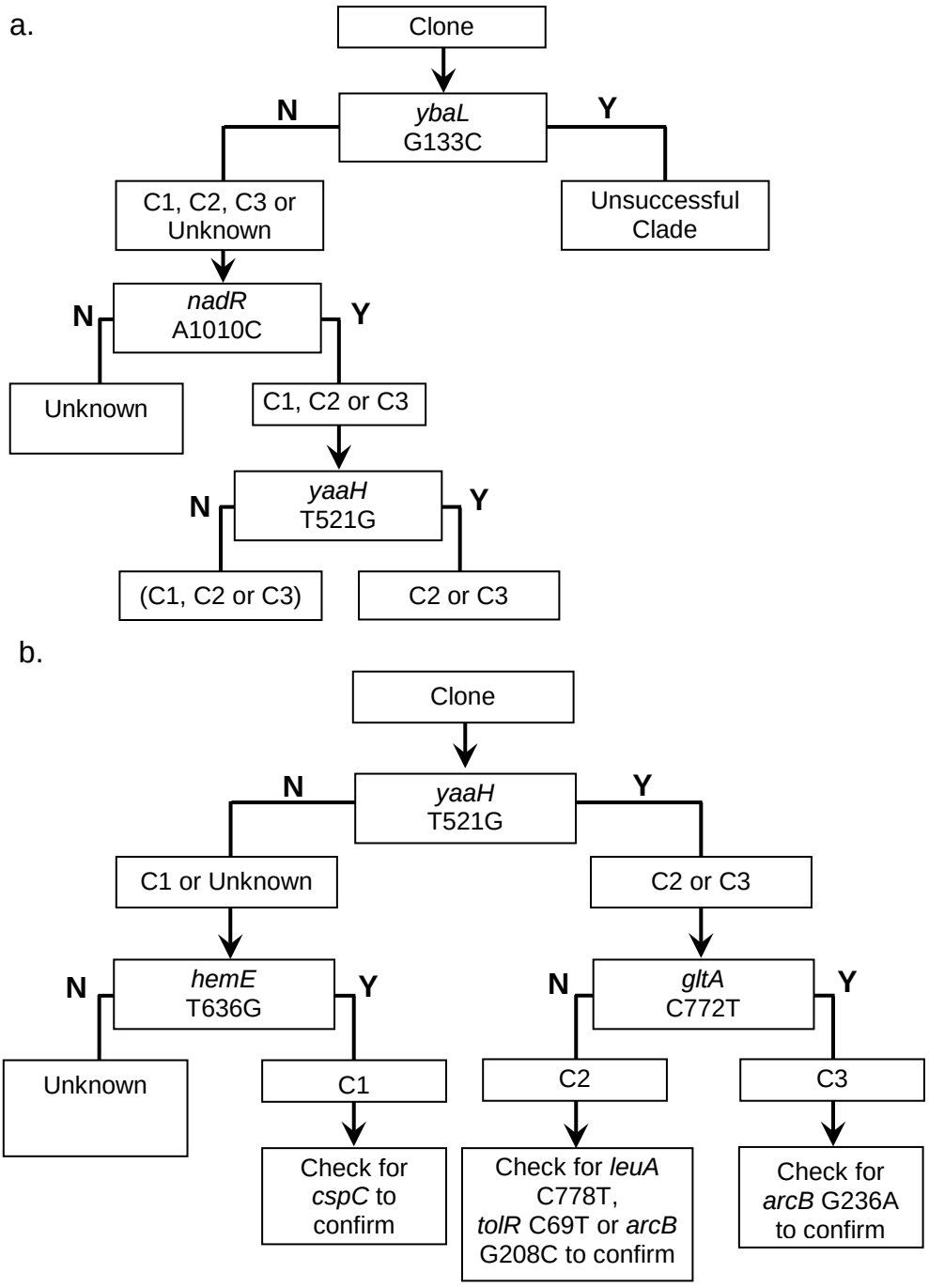
Supplementary Figure 1 | Annotation of sequence adjacent to the *cit* amplification boundary found in Cit$^+$ genomes.



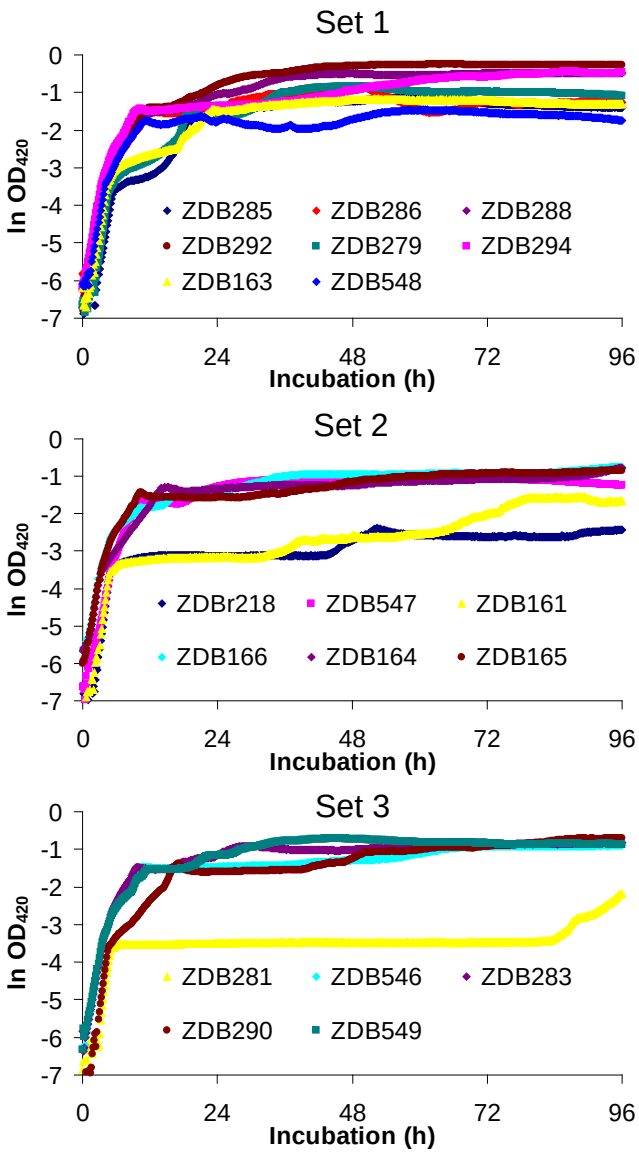
Supplementary Figure 2 | Reversion to Cit⁻ phenotype is associated with loss of *cit* amplification.
The 33,000-generation Cit$^+$ clone, CZB154, has an increased *citT* band size relative to the ancestral strain, REL606, as a consequence of the *cit* amplification. By contrast, all 13 independent Cit$^-$ revertants of CZB154 have reduced *citT* band sizes, consistent with the loss of the *cit* amplification.



Supplementary Figure 3 | Growth of early Cit$^+$ clones in DM25.
Early Cit$^+$ clones from population Ara–3 improved greatly in their capacity to grow on the citrate in DM25 over time. Cit$^+$ clones from generations 31,500 (ZDB564), 32,000 (ZDB172), and 32,500 (ZDB143) showed little growth on citrate even after 96 h, while two clones from generation 33,000 (CZB152 and CZB154) achieved substantial growth on citrate within 24 h. This improvement in citrate utilization allowed Cit$^+$ clones to rise from a minority of the population to numerical dominance.



Supplementary Figure 4 | Keys for placement of clones used in replay experiments. The phylogenetic placement of each clone used in the replay experiments was determined by scoring the presence or absence of informative mutations according to the keys above. Clones sampled before generation 20,000 were placed using according to **a**, while those from generation 20,000 and later were placed using **b**. The lower resolution for earlier clones reflects the lesser divergence in earlier generations.



Supplementary Figure 5 | Growth of Cit$^+$ mutants derived in replay experiments. The 19 spontaneous Cit$^+$ mutants isolated during the course of replay experiments vary in how quickly they transition from the glucose to the citrate and how well they grow on the citrate in DM25. Here mutants are grouped according to the mutations responsible for the Cit$^+$ phenotype. The eight mutants in Set 1 have tandem *citT* duplications similar to that which evolved in the original population. The six mutants in Set 2 mutants have IS*3* insertions in *citG*. The five mutants in Set 3 have a variety of mutations, as described in the main text and Supplementary Table 12.

Supplementary Table 1 | Historical Ara–3 Clones Subjected to Whole Genome Sequencing		
Generation	**Clones**	**Clade**
0	REL606	N/A
2,000	REL1166A	?
5,000	ZDB409	?
10,000	ZDB429	UC
15,000	ZDB446	UC
20,000	ZDB458	(C1,C2)
	ZDB464*	(C1,C2)
	ZDB467	(C1,C2)
25,000	ZDB477	C1
	ZDB483	C3
30,000	ZDB16	C1
	ZDB357	C2
31,500	ZDB199*	C1
	ZDB200	C2
	ZDB564	Cit^+
32,000	ZDB30*	C3
	ZDB172	Cit^+
32,500	ZDB158	C2
	ZDB143	Cit^+
33,000	CZB199	C1
	CZB152	Cit^+
	CZB154	Cit^+
34,000	ZDB83	Cit^+
	ZDB87	C2
36,000	ZDB96	Cit^+
	ZDB99	C1
38,000	ZDB107	Cit^+
	ZDB111	C2
40,000	REL10979	Cit^+
	REL10988	C2

*Known potentiated clone

Supplementary Table 2 │ Mutations in Population Ara–3 Clones Subjected to Whole Genome Sequencing

This table shows all of the mutations found in the 29 genomes from population Ara–3 that were sequenced for this study. Owing to its large size, this table is provided in a separate zip file. When opened, this zip file generates a summary table showing all of the mutations in html format; separate tables that show the mutations for each individual genome in html format; and machine-readable data files for each individual genome.

Supplementary Table 3 | Results of PCR screens on whole-population samples for *cit* amplification		
Generation	**Replicate**	***cit* Amplification Detected?**
25,000	A	–
	B	–
	C	–
30,000	A	–
	B	–
	C	–
31,500	A	–
	B	–
	C	–
32,000	A	–
	B	–
	C	+
32,500	A	–
	B	–
	C	–
33,000	A	+
	B	+
	C	+
33,500	A	+
	B	+
	C	+
34,000	A	+
	B	+
	C	+
36,000	A	+
	B	+
	C	+

Supplementary Table 4 | PCR screens for *cit* amplification in Ara–3 clones

Generation	Clone	Cit Phenotype	Amplification Detected?	Generation	Clone	Cit Phenotype	Amplification Detected?
31,500	ZDB25	-	No	35,000	ZDB89	+	Yes
	ZDB26	-	No		ZDB90	+	Yes
	ZDB27	-	No		ZDB91	+	Yes
	ZDB564	+	Yes		ZDB92	-	No
	ZDB565	+	Yes		ZDB93	+	Yes
	ZDB566	+	Yes		ZDB94	+	Yes
32,000	ZDB28	-	No	36,000	ZDB95	+	Yes
	ZDB29	-	No		ZDB96	+	Yes
	ZDB30	-	No		ZDB97	+	Yes
	ZDB172	+	Yes		ZDB98	+	Yes
	ZDB173	+	Yes		ZDB99	-	No
	ZDB179	+	Yes		ZDB100	-	No
32,500	ZDB31	-	No	37,000	ZDB101	+	Yes
	ZDB32	-	No		ZDB102	+	Yes
	ZDB33	-	No		ZDB103	-	No
	ZDB143	+	Yes		ZDB104	-	No
	ZDB144	+	Yes		ZDB105	-	No
	ZDB145	+	Yes		ZDB106	-	No
33,000	CZB199	-	No	38,000	ZDB107	+	Yes
	CZB204	-	No		ZDB108	+	Yes
	CZB205	-	No		ZDB109	+	Yes
	CZB151	+	Yes		ZDB110	-	No
	CZB152	+	Yes		ZDB111	-	No
	CZB154	+	Yes		ZDB112	+	Yes
34,000	ZDB83	-	No	40,000	REL10979	+	Yes
	ZDB84	-	No		REL10980	+	Yes
	ZDB85	-	No		REL10981	+	Yes
	ZDB86	+	Yes		REL10988	-	No
	ZDB87	+	Yes		REL10989	-	No
	ZDB88	+	Yes		REL10990	-	No

Supplementary Table 5 | Point mutations in early Cit$^+$ genomes

Genome Position	Nucleotide Change	Type	Amino-acid Change	Gene	Product	Clone (generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
447290	T → C	NC	N/A	*tesB/ybaY*	Acyl-CoA thioesterase II / predicted outer membrane lipoprotein						
1399744	T → C	NS	I228V	*abgB*	Predicted peptidase / aminobenoyl-glutamate utilization protein						
2241625	C → A	NS	A259S	*ccmH*	Heme lyase subunit						
2443160	C → A	S	N/A	*glk*	Glucokinase						
3612959	C→ T	NC	N/A	*dctA/yhjK*	C4-dicarboxylate transporter / Predicted diguanylate cyclase						

Mutations shown are those that were not uniformly found in all five Cit$^+$ clones under study. Red fill indicates presence of mutation. Crosshatching further indicates mutation was also present in Cit$^+$ clones from generations 34,000, 36,000, and 38,000. Gray fill indicates absence of mutation.

Supplementary Table 6 | IS-element insertions in early Cit$^+$ genomes									
Genome Position	Element	Gene	Product	Clone (generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
595335	IS*150*	*fepA/fes*	Outer membrane transporter/Ferric enterobactin esterase						
620126	IS*150*	*dsbG*	Periplasmic disulfide isomerase/Thiol-disulphide oxidase						
1028311	IS*150*	*uup*	Fused predicted transporter subunits of ABC superfamily: ATP-binding components						
2322345	IS*186*	*menC*	O-succinylbenzoate						
2877315	IS*150*	*kduD*	2-deoxy-D-fluconate/3-dehydrogenase						
4252526	IS*150*	*uvrA*	Excinuclease ABC subunit A						

Mutations shown are those that were not uniformly found in all five Cit$^+$ clones under study. Red fill indicates presence of mutation. Crosshatching further indicates mutation was also present in Cit$^+$ clones from generations 34,000, 36,000, and 38,000. Gray fill indicates absence of mutation.

Supplementary Table 7 | Deletions in early Cit$^+$ genomes									
Genome Start	Genome End	Size (bp)	Genes Deleted	Clone (generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
590472	599560	9088	*hokE, insL-3, entD, fepA, fes, ybdZ*						
590472	595335	4863	*hokE, insL-3, entD, fepA*						
1345210	1345211	1	*yciR/rnb*						
3786737	3786738	1	Noncoding						

Mutations shown are those that were not uniformly found in all five Cit$^+$ clones under study. Red fill indicates presence of mutation. Crosshatching further indicates mutation was also present in Cit$^+$ clones from generations 34,000, 36,000, and 38,000. Gray fill indicates absence of mutation.

Supplementary Table 8 | Amplifications in early Cit$^+$ genomes									
Genome Start	Genome End	Size (bp)	Genes Duplicated	Clone (Generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
12452	12455	3 (x2)	dnaK (internal fragment)						
599561	666130	66569 (x2)	*[entF], fepE, fepC, fepG, fepD, ybdA, fepB, entC, entE, entB, entA, ybdB, cstA, cstA, ybdD, ybdH, ybdL, ybdM, ybdN, insB-8, insA-8, dsbG, ahpC, ahpF, ybdQ,ybdR, rnk, rna, citT, citG, citX, citF, citE,citD, citC, insB-9, insA-9, citA, citB, dcuC, crcA, cspE, ccrB, ybeM, tatE, lipA,ybeF, lipB, ybeD, dacA, rlpA, mrdB, mrdA, ybeA, ybeB, phpB, nadD, holA, rlpB, leuS, ybeL, ybeQ, ybeQ, ybeR, ybeV, hscC, rihA, gltL, insJ-2, insK-2, [gltL]*						
619885	634746	14861 (x3)	*[dsbG], ahpC, ahpF, ybdQ, ybdR, rnk, rna, citT, citG, citX, citF, citE, citD, citC, insB-9, insA-9*						
1729052	1995783	266731 (x3)	*[ydhV], ydhY, ydhZ, pykF, lpp, ynhG, sufE, sufS, sufD, sufC, sufB, sufA, ydiH, ydiI, ydiJ, ydiK, ydiL, ydiM, ydiM, ydiN, ydiB, aroD, ydiF, ydiO, ydiP, ydiQ, ydiR, ydiS, ydiT, ydiD, ppsA, ydiA, aroH, ydiE, ydiU, ydiV, nlpC, btuD, btuE, btuC, himA, pheT, pheS, pheM, rplT, rpmI, infC, thrS, arpB, arpB, ECB_01690, ydiY, pfkB, ydiZ ,yniA, yniB, yniC, ydjM, ydjN, ydjO, cedA, katE, ydjC, celF, celD, celC, celB, celA, osmE, nadE, ydjQ, ydjR, spy, astE, astB, astD, astA, astC, xthA, ydjX, ydjY, ydjY, ydjZ, ynjA, ynjB, ynjC, ynjD, ynjE, ynjF, nudG, ynjH, gdhA, ynjI, topB, selD, ydjA, sppA, ansA, pncA, ydjE, ydjF, ydjG, ydjH ,ydjI, ydjJ, ydjK, ydjL, yeaC, yeaA, gapA, yeaD, yeaE, mipA, yeaG, yeaH, yeaI, yeaJ, yeaK, ECB_01757, yeaL, yeaM, yeaN, yeaO, yoaF, yeaP, yeaQ, yoaG, yeaR, insL-4, yeaS, yeaT, yeaU, yeaV, yeaW, yeaX, rnd, fadD, yeaY, yeaZ, yoaA, yoaB, yoaC, yoaH, pabB, yeaB,sdaA, yoaD, yoaE, manX, manY, manZ,yobD, yebN, rrmA, cspC, yobF, yebO,yobG, ECB_01797, kdgR, yebQ, htpX,prc, proQ, yebR, yebS, yebT, yebU, yebV, yebW, pphA, yebY, yebZ, yobA, holE, yobB, exoX, ptrB, yebE, yebF,*						

Supplementary Table 8 | Amplifications in early Cit$^+$ genomes									
Genome Start	Genome End	Size (bp)	Genes Duplicated	Clone (Generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
			yebG, purT, eda, edd, zwf, yebK, pykA, msbB, yebA, znuA, znuC, znuB, ruvB ,ruvA, yebB, ruvC, yebC, ntpA, aspS, yecD, yecE, yecN, yecO, yecP, torZ,torY, cutC, yecM, argS, yecT, flhE, flhA,flhB, cheZ ,cheY, cheB, cheR, tap, tar, cheW, cheA, motB, motA, flhC, flhD,yecG, otsA, otsB, araH, araG, araF, yecI, yecJ, yecR, ftn, yecH, tyrP, yecA, leuZ, cysT, glyW, pgsA, uvrC, yvrY, insA-13, insB-13, yedU, yedV, yedW, yedX, yedY, yedZ, yodA, yodB, serU, yeeI, asnT, yeeJ, yeeL, yeeL, shiA, amn, yeeN						
3268052	2086894	1181158 (x2)	*rpmA, rplU, ispB, nlp, murA, yrbA, yrbB, yrbC, yrbD, yrbE, yrbF, yrbG, yrbH, yrbI, yrbK, yhbN, yhbG, rpoN, yhbH, ptsN, yhbJ, ptsO, yrbL, mtgA, yhbL, arcB,yhcC gltB, gltD, yhcG, ECB_03080,yhcH, nanK, nanE, nanT, nanA, nanR,dcuD, sspB, sspA, rpsI, rplM, yhcM,yhcB, degQ degS, mdh, argR, yhcN,yhcO, yhcP, yhcQ, yhcR, yhcS, tldD, yhdP, rng, maf, mreD, mreC, mreB,yhdA, yhdH, accB, accC, yhdT, panF,prmA, yhdG, fis, yhdJ, yhdU, envR, acrE,acrF, yhdV, yhdW, yhdX, yhdY, yhdZ,rrfF, thrV, rrfD, rrlD, alaU, ileU, rrsD,yrdA, yrdB, aroE, yrdC, yrdD, smg, smf,def, fmt, rrmB, trkA, mscL, yhdL, zntR,yhdN, rplQ, rpoA, rpsD, rpsK, rpsM,rpmJ, prlA, rplO, rpmD, rpsE, rplR, rplF,rpsH, rpsN, rplE, rplX, rplN, rpsQ, rpmC,rplP, rpsC, rplV, rpsS, rplB, rplW, rplD, rplC, rpsJ, pioO, gspA, gspC, gspD,gspE, gspF, gspG, gspH, gspI, gspJ,gspK, gspL, gspM, gspO, bfr, bfd, chiA,tuf, fusA, rpsG, rpsL, yheL, yheM, yheN,yheO, fkpA, slyX, slyD, kefB, yheR,yheS, yheT, yheU, prkB, yhfA, crp, yhfK,argD, pabA, fic, yhfG, ppiA, yhfC, nirB,nirD, nirC, cysG, yhfL, yhfM, yhfN, frlC,yhfQ, yhfR, yhfS, insB-23, insA-23, yhfS, yhfT, yhfU, yhfV, yhfW, yhfX, yhfY, yhfZ,trpS, gph, rpe, dam, damX, aroB, aroK,hofQ, yrfA, yrfB, yrfC, yrfD, mrcA, yrfE,yrfF, yrfG, hslR, hslO, yhgE, pckA, envZ,ompR, greB, yhgF, feoA, feoB, yhgG,yhgA, bioH, yhgH, yhgI, gntT, malQ,malP, malT, rtcA, rtcB, rtcR, glpR, glpG,glpE, glpD, yzgL, ECB_03279, yzgL,glgP, glgA, glgC, glgX, glgB, asd, yhgN,*						

Supplementary Table 8 | Amplifications in early Cit$^+$ genomes									
Genome Start	Genome End	Size (bp)	Genes Duplicated	Clone (Generation)	ZDB564 (31,500)	ZDB172 (32,000)	ZDB143 (32,500)	CZB152 (33,000)	CZB154 (33,000)
			*gntU, gntK, gntR, yhhW, yhhX, yhhY,yhhZ, yrhA, yrhB, ggt, yhhA, ugpQ, ugpC,ugpE, ugpA, ugpB, livF, livG, livM, livH,livK, yhhK, livJ, rpoH, ftsX, ftsE, ftsY,yhhF, yhhL, yhhM, yhhN, zntA, sirA,yhhQ, dcrB, yhhS, yhhT, acpT, nikA,nikB, nikC, nikD, nikE, nikR, rhsB, yhhH,yrhC, yhhI, yhhJ, yhiH, yhiI, yhiJ, yhiKL,yhiM, yhiN, pitA, yhiO, uspA, yhiP, yhiQ,prlC, yhiR, gor, arsR, arsB, arsC, yhiS,slp, yhiF, yhiD, hdeB, hdeA, hdeD, yhiE,yhiU, yhiV, yhiW, gadX, gadA, yhjA, treF,yhjB, yhjC, yhjD, yhjE, yhjG, yhjH, kdgK,yhjJ, dctA, yhjK, bcsC, bcsZ, yhjN, yhjO,yhjQ, yhjR, yhjS, yhjT, yhjU, ldrD, ldrD,ldrD, yhjV, dppF, dppD, dppC, dppB, dppA, proK, yhjW, yhjX, yhjY, tag, yiaC, bisC, yiaD, tkrA, yiaF, yiaG, cspA, hokA, insJ-4, insK-4***					

Mutations shown are those that were not uniformly found in all five Cit$^+$ clones under study. Red fill indicates presence of mutation. Crosshatching further indicates mutation was also present in Cit$^+$ clones from generations 34,000, 36,000, and 38,000. Gray fill indicates absence of mutation.

Supplementary Table 9 | Estimated *citT* copy number										
Gen (k)	Clone	Junction Number				Coverage			Predicted Configuration	Predicted *rnk-citT* Modules
		Anc *rnk*	Anc *citT*	*rnk-citT*	Relative *rnk-citT*	*citT*	Reference Regions	Relative *citT*		
31.5	ZDB564	52	49	42	0.83	120.8	64.9	1.86	2×	1
32	ZDB172	45	39	82	1.95	139.3	23.8	5.86	2× (3×)	4
32.5	ZDB143	116	76	301	3.14	457.2	112.8	4.05	4×	3
33	CZB152	22	23	192	8.53	267.4	32.7	8.18	9×	8
	CZB154	398	252	345	1.06	797.6	130.0	6.14	3× (2×)	3
34	ZDB83	57	43	125	2.50	214.7	62.9	3.42	4×	3
36	ZDB96	26	22	87	3.63	97.4	28.8	3.39	4×	3
38	ZDB107	51	32	133	3.20	204.7	60.0	3.41	4×	3
40	REL10979	36	32	73	2.15	115.6	32.5	3.56	4×	3

For each Cit$^+$ genome, the number of new junctions per genome was estimated from the relative number of reads supporting the new *rnk-citT* junction produced by the amplification versus the number of reads supporting the ancestral *rnk* and *citT* junctions. The total number of *citT* copies per genome was estimated by comparing read-depth coverage of the amplified *citT* region to coverage of regions that appear to be single copy in all genomes (comprising ~20 kb total including the *ara* operon and *tufB* gene). Together these data can be used to predict the likely configuration of *citT* amplification copies in each genome. Examination of read-depth coverage over a larger area supports the observation that there are nested amplifications in CZB154 and ZDB172. For example, the CZB154 genome contains three copies of a larger region, and each copy of that region contains two tandem copies with the usual *rnk-citT* junction.

Supplementary Table 10 | Phylogenetically informative mutations						
Gene	**Gene Product**	**Genome Position**	**Gene Position**	**Ancestral Nucleotide**	**Evolved Nucleotide**	**Associated Clades**
ybaL	Predicted transporter with NAD(P)-binding Rossmann-fold domain	475173	133	G	C	UC
nadR	Nicotinamide-nucleotide adenyltransferase	4616538	1010	A	C	C1,C2,C3
hemE	Uroporphyrinogen decarboxylase	4177963	636	T	G	C1
cspC	Stress protein, member of the CspA-family	1886011	4	C	A	C1
yaaH	Conserved inner membrane protein associated with acetate transport	9972	521	T	G	C2,C3
leuA	2-isopropylmalate synthase	85556	778	C	T	C2
tolR	Membrane spanning protein in TolA-TolQ-TolR complex	756799	69	C	T	C2
arcB	Hybrid sensory histidine kinase in two-component regulatory system with ArcA. Aerobic respiration control sensor	3288053	208	G	C	C2
		3288026	236	T	A	C3
gltA	Citrate synthase	734488	772	G	A	C3

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations										Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
0	REL606*												Ancestor
5,000	ZDB400												n.d.
5,000	ZDB401												n.d.
5,000	ZDB402												n.d.
5,000	ZDB403												n.d.
5,000	ZDB404												n.d.
5,000	ZDB405												n.d.
5,000	ZDB406												n.d.
5,000	ZDB407												n.d.
5,000	ZDB408												n.d.
5,000	ZDB409*												n.d.
5,000	ZDB410												n.d.
5,000	ZDB411												n.d.
5,000	ZDB412												n.d.
5,000	ZDB413												n.d.
5,000	ZDB414												n.d.
5,000	ZDB415												n.d.
5,000	ZDB416												n.d.
5,000	ZDB417												n.d.
5,000	ZDB418												n.d.
5,000	ZDB419												n.d.
10,000	ZDB1												(C1,C2,C3)
10,000	ZDB2												(C1,C2,C3)
10,000	ZDB3												(C1,C2,C3)
10,000	ZDB420												n.d.
10,000	ZDB421												UC
10,000	ZDB422												UC
10,000	ZDB423												n.d.
10,000	ZDB424												(C1,C2,C3)
10,000	ZDB425												(C1,C2,C3)
10,000	ZDB426												UC

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations										Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
10,000	ZDB427												n.d.
10,000	ZDB428												UC
10,000	ZDB429*												UC
10,000	ZDB430												UC
10,000	ZDB431												UC
10,000	ZDB432												n.d.
10,000	ZDB433												n.d.
10,000	ZDB434												UC
10,000	ZDB435												n.d.
10,000	ZDB436												UC
15,000	ZDB437												n.d.
15,000	ZDB438												(C1,C2,C3)
15,000	ZDB439												n.d.
15,000	ZDB440												UC
15,000	ZDB441												UC
15,000	ZDB442												n.d.
15,000	ZDB443												UC
15,000	ZDB444												n.d.
15,000	ZDB445												(C2,C3)
15,000	ZDB446*												UC
15,000	ZDB447												UC
15,000	ZDB448												(C2,C3)
15,000	ZDB449												n.d.
15,000	ZDB450												UC
15,000	ZDB451												n.d.
15,000	ZDB452												UC
15,000	ZDB453												n.d.
15,000	ZDB454												n.d.
15,000	ZDB455												(C2,C3)
15,000	ZDB456												n.d.
20,000	ZDB4												(C2,C3)
20,000	ZDB5												(C2,C3)
20,000	ZDB6												C1

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations										Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
20,000	ZDB457												(C2,C3)
20,000	ZDB458*												(C2,C3)
20,000	ZDB459												C1
20,000	ZDB460												(C2,C3)
20,000	ZDB461												(C2,C3)
20,000	ZDB462												(C2,C3)
20,000	ZDB463												(C2,C3)
20,000	ZDB464*												(C2,C3)
20,000	ZDB465												(C2,C3)
20,000	ZDB466												C1
20,000	ZDB467*												(C2,C3)
20,000	ZDB468												C1
20,000	ZDB469												(C2,C3)
20,000	ZDB470												(C2,C3)
20,000	ZDB471												(C2,C3)
20,000	ZDB472												(C2,C3)
20,000	ZDB473												(C2,C3)
25,000	ZDB7												(C2,C3)
25,000	ZDB8												C2
25,000	ZDB9												C1
25,000	ZDB474												C2
25,000	ZDB475												C1
25,000	ZDB476												C3
25,000	ZDB477												C1
25,000	ZDB478												C3
25,000	ZDB479												C3
25,000	ZDB480												(C2,C3)
25,000	ZDB481												C3
25,000	ZDB482												(C2,C3)
25,000	ZDB483												C3
25,000	ZDB484												(C2,C3)
25,000	ZDB485												C3
25,000	ZDB486												C3

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
25,000	ZDB487												C3
25,000	ZDB488												C3
25,000	ZDB489												C3
25,000	ZDB490												C3
27,000	ZDB300												C3
27,000	ZDB301												C2
27,000	ZDB302												C1
27,000	ZDB303												C1
27,000	ZDB304												C2
27,000	ZDB305												C2
27,000	ZDB306												C2
27,000	ZDB307												C2
27,000	ZDB308												C2
27,000	ZDB309												C3
27,000	ZDB310												C3
27,000	ZDB311												C3
27,000	ZDB312												C3
27,000	ZDB313												C1
27,000	ZDB314												C3
27,000	ZDB315												C2
27,000	ZDB316												C2
27,000	ZDB317												C3
27,000	ZDB318												C3
27,000	ZDB319												C2
27,500	ZDB10												C2
27,500	ZDB11												C1
27,500	ZDB12												C2
28,000	ZDB320												C2
28,000	ZDB321												C2
28,000	ZDB322												C1
28,000	ZDB323												C2
28,000	ZDB324												C2
28,000	ZDB325												C2

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
28,000	ZDB326												C2
28,000	ZDB327												C2
28,000	ZDB328												C2
28,000	ZDB329												C1
28,000	ZDB330												C2
28,000	ZDB331												C2
28,000	ZDB332												C2
28,000	ZDB333												C2
28,000	ZDB334												C3
28,000	ZDB335												C2
28,000	ZDB336												C2
28,000	ZDB337												C2
28,000	ZDB338												C2
28,000	ZDB339												C3
29,000	ZDB13												C3
29,000	ZDB14												C3
29,000	ZDB15												C2
29,000	ZDB340												C2
29,000	ZDB341												C2
29,000	ZDB342												C1
29,000	ZDB343												C2
29,000	ZDB344												C2
29,000	ZDB345												C2
29,000	ZDB346												C1
29,000	ZDB347												C1
29,000	ZDB348												C2
29,000	ZDB349												C1
29,000	ZDB350												C1
29,000	ZDB351												C2
29,000	ZDB352												C1
29,000	ZDB353												C2
29,000	ZDB354												C2
29,000	ZDB355												C1

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
29,000	ZDB356												C2
30,000	ZDB16*												C1
30,000	ZDB17												C3
30,000	ZDB18												C3
30,000	ZDB357*												C2
30,000	ZDB358												C2
30,000	ZDB359												C2
30,000	ZDB360												C1
30,000	ZDB361												C2
30,000	ZDB362												C2
30,000	ZDB363												C2
30,000	ZDB364												C2
30,000	ZDB365												C2
30,000	ZDB366												C2
30,000	ZDB367												C2
30,000	ZDB368												C2
30,000	ZDB369												C2
30,000	ZDB370												C1
30,000	ZDB371												C2
30,000	ZDB372												C2
30,000	ZDB373												C2
30,500	ZDB19												C3
30,500	ZDB20												C3
30,500	ZDB21												C2
31,000	ZDB22												C2
31,000	ZDB23												C3
31,000	ZDB24												C1
31,000	ZDB374												C2
31,000	ZDB375												C2
31,000	ZDB376												C2
31,000	ZDB377												C1
31,000	ZDB378												C2
31,000	ZDB379												C2

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
31,000	ZDB380												C2
31,000	ZDB381												C1
31,000	ZDB382												C2
31,000	ZDB383												C2
31,000	ZDB384												C2
31,000	ZDB385												C1
31,000	ZDB386												C2
31,000	ZDB387												C2
31,000	ZDB388												C2
31,000	ZDB389												C2
31,000	ZDB390												C1
31,500	ZDB25												C3
31,500	ZDB26												C1
31,500	ZDB27												C3
31,500	ZDB197												C2
31,500	ZDB198												C1
31,500	ZDB199*												C1
31,500	ZDB200*												C2
31,500	ZDB201												C1
31,500	ZDB202												C2
31,500	ZDB203												C2
31,500	ZDB204												C1
31,500	ZDB205												C1
31,500	ZDB206												C2
31,500	ZDB207												C2
31,500	ZDB208												C2
31,500	ZDB209												C2
31,500	ZDB210												C2
31,500	ZDB211												C2
31,500	ZDB212												C2
31,500	ZDB213												C2
31,500	ZDB214												C2
31,500	ZDB215												C1

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones

Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
31,500	ZDB216												C2
32,000	ZDB28												C3
32,000	ZDB29												C2
32,000	ZDB30*												C3
32,000	ZDB183												C3
32,000	ZDB184												C1
32,000	ZDB185												C3
32,000	ZDB186												C1
32,000	ZDB187												C1
32,000	ZDB188												C2
32,000	ZDB189												C1
32,000	ZDB190												C2
32,000	ZDB191												C3
32,000	ZDB192												C2
32,000	ZDB391												C2
32,000	ZDB392												C2
32,000	ZDB393												C2
32,000	ZDB394												C1
32,000	ZDB395												C2
32,000	ZDB396												C2
32,000	ZDB397												C1
32,500	ZDB31												C3
32,500	ZDB32												C2
32,500	ZDB33												C1
32,500	ZDB146												C1
32,500	ZDB147												C1
32,500	ZDB148												C1
32,500	ZDB149												C1
32,500	ZDB150												C1
32,500	ZDB151												C1
32,500	ZDB152												C1
32,500	ZDB153												C1
32,500	ZDB154												C1

Supplementary Table 11 | Phylogenetic placement of Cit⁻ replay clones													
Generation	Clone	Phylogenetically Informative Mutations											Clade
		Gene	*ybaL*	*nadR*	*hemE*	*cspC*	*yaaH*	*leuA*	*tolR*	*arcB*	*arcB*	*gltA*	
		Gene Position	133	1010	636	4	521	778	69	208	236	772	
		Ancestral Nucleotide	G	A	T	C	T	C	C	G	T	G	
		Evolved Nucleotide	C	C	G	A	G	T	T	C	A	A	
32,500	ZDB155												C1
32,500	ZDB156												C1
32,500	ZDB157												C3
32,500	ZDB158*												C2
32,500	ZDB159												C2
32,500	ZDB160												C1
32,500	ZDB398												C1
32,500	ZDB399												C2

*Genome has been sequenced.

Red fill indicates presence of mutation has been established by sequencing. Gray fill indicates absence of mutation has been established by sequencing. No fill indicates that the presence or absence of mutation was not examined.

Clade refers to UC, C1, C2, or C3 as shown in Fig. 1 of the main text. When two or more clades are grouped by parentheses, either the clone belongs to the basal group or the clone's placement could not be resolved further based on the available data. n.d. indicates that the clone belongs to some other early clade or its placement could not be resolved based on the available data.

Supplementary Table 12 | Mutations affecting *cit* region in Cit$^+$ replay mutants				
Generation	**Cit$^-$ Parent**	**Clade**	**Cit$^+$ Mutant**	**Mutation affecting *cit* Region**
20,000	ZDB464*****	C3	ZDB285*****	2978-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
			ZDB286	2656-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
27,000	ZDB309	C3	ZDB288	2070-bp tandem *cit* duplication that creates *rna-citT* regulatory module.
	ZDB310	C3	ZDB290*****	~5,000-bp tandem duplication. Basis of *citT* activation unknown.
30,500	ZDB20	C3	ZDB547	IS*3* insertion in *citG.*
31,000	ZDB390	C1	ZDB292	2706-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
31,500	ZDB25	C3	ZDBr218	IS*3* insertion in *citG*
	ZDB199	C1	ZDB279	2745-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
32,000	ZDB28	C3	ZDB161	IS*3* insertion in *citG.*
	ZDB29	C2	ZDB166	IS*3* insertion in *citG.*
	ZDB30*****	C3	ZDB164	IS*3* insertion in *citG.*
			ZDB165*****	IS*3* insertion in *citG.*
			ZDB283*****	~568-kbp inversion that places much of the *cit* operon under control of the *fimB* promoter.
			ZDB294*****	2663-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
	ZDB183	C3	ZDB281*****	~14.3-kbp duplication. Basis of *citT* activation unresolved.
32,500	ZDB31	C3	ZDB163	2990-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.
			ZDB546	Unknown rearrangement or duplication affecting *citT*.
			ZDB549	422-bp deletion in *citG*. Basis of *citT* activation unresolved.
	ZDB32	C2	ZDB548	3144-bp tandem *cit* duplication that creates *rnk-citT* regulatory module.

*Genome has been sequenced.

Supplementary Table 13 | Annotated differences between genomes of four Cit$^+$ mutants and their Cit$^-$ parent clones

Supplementary Table 13a | Pair 1: ZDB464 (Generation 20,000) and Cit$^+$ Mutant ZDB285					Cit$^-$ Parent	Cit$^+$ Mutant
Position	**Mutation**	**Description**	**Gene or Genes Involved**	**Product(s)**	**ZDB464**	**ZDB285**
626102	2794 bp duplication	Tandem duplication with one junction in *citG* and the other between *rna* and *rnk*; presumed Cit$^+$ actualizing mutation	*citG*	Triphosphoribosul–dephospho–CoA transferase		
			citT	Citrate transporter		
			rna	Ribonuclease I		
848202	IS*150* Insertion	Insertion in a coding region	*ybiS*	Hypothetical protein		
1360374	IS*150* Insertion	Insertion in a coding region	*ycjC*	DNA–binding transcriptional repressor		
3270443	IS*150* Insertion	Insertion in a non–coding, intergenic region; promoters not disrupted	Site between *nlp/murA*	DNA–binding transcriptional activator of maltose metabolism/UDP–N–acetylglucosamine 1–carboxyvinyltransferase		

Supplementary Table 13b | Pair 2: ZDB30 (Generation 32,000) and Cit$^+$ Mutant ZDB165					Cit$^-$ Parent	Cit$^+$ Mutant
Position	**Mutation**	**Description**	**Gene or Genes Involved**	**Product(s)**	**ZDB30**	**ZDB165**
628716	IS*3* Insertion	Insertion in a coding region; presumed Cit$^+$ actualizing mutation	*citG*	Triphosphoribosul–dephospho–CoA transferase		
1651966	Δ795 bp	Deletion of multiple coding regions	*ydgG*	Transporter of quorum signal AI–2		
			pntB	Pyridine nucleotide transhydrogenase, β subunit		

Supplementary Table 13c | Pair 3: ZDB30 (Generation 32,000) and Cit$^+$ ZDB293					Cit$^-$ Parent	Cit$^+$ Mutant
Position	**Mutation**	**Description**	**Gene or Genes Involved**	**Gene Product(s)**	**ZDB30**	**ZDB293**
632864	568476 bp inversion	Most of *cit* operon structural genes placed downstream of *fimB* promoter; new junctions in *citC* and between *yjhA* and *fimB*; presumed Cit$^+$ actualizing mutation	*citC*	Citrate lyase synthetase		
			fimB	Regulator of *fimA* pili subunit		
687047	IS*150* Insertion	Insertion in a coding region	*nagE*	Fused N–acetyl glucosamine specific PTS enzyme: IIC, IIB, and IIA components		

Supplementary Table 13d | Pair 4: ZDB30 (Generation 32,000) and Cit$^+$ Mutant ZDB294					Cit$^-$ Parent	Cit$^+$ Mutant
Position	**Mutation**	**Description**	**Gene or Genes Involved**	**Gene Product(s)**	**ZDB30**	**ZDB294**
626107	2661 bp duplication	Tandem duplication with junctions in *citG* and between *rna* and *rnk*; presumed Cit$^+$ actualizing mutation	*citG*	Triphosphoribosul–dephospho–CoA transferase		
			citT	Citrate transporter		
			rna	Ribonuclease I		
1607917	Δ1 bp	Single nucleotide deletion in a coding region	*ECB_1510*	Putative tail component of prophage		
1729055	Δ2462 bp	IS*150*–mediated deletion of multiple coding regions	*ydhV*	Predicted oxidoreductase		
			ydhY	Predicted 4Fe–4S ferredoxin–type protein		
2157881	Δ12781 bp	IS*150*–mediated deletion of multiple coding regions.	*yehM*	Conserved protein		
			yehP	Conserved protein		
			yehQ	Possible pseudogene		
			yehR	Conserved protein		
			yehS	Conserved protein		
			yehT	Predicted sensory kinase in two–component system with YehU		
			yehU	Predicted sensory kinase in two–component system with YehT		
			yehV	MerR–like regulator		
			ECB 02057	Unknown function		
			yehW	Membrane component of an ABC transporter involved in osmoprotection		
			yehX	Membrane component of an ABC transporter involved in osmoprotection		
			yehY	Membrane component of an ABC transporter involved in osmoprotection		
			yehZ	Periplasmic component of an ABC transporter involved in osmoprotection		

Red fill indicates presence of mutation. Gray fill indicates absence of corresponding mutation.

Supplementary Table 14 | Primer pairs used in this study			
Gene or Region Amplified	**Primer Name**	**Primer Sequence**	**PCR Product Size**
ybaL mutation	*ybaL*mut F	5' CATCGCCCTGTTCCATCATTCCT 3'	503 bp
	*ybaL*mut R	5' ACCCCGCTTATCACCACCATTGTT 3'	
nadR mutation	*nadR*mut F	5' ATGGTCGCGATTATGTCTTTTCAC 3'	459 bp
	*nadR*mut R	5' CGTTTCATCGCGGTTATCTCTG 3'	
hemE mutation	*hemE*mut F	5' GTGCCGGACGCGATGGGGTTAG 3'	524 bp
	*hemE*mut R	5' CACTGTCCGCCGCCTTTGGTA 3'	
cspC mutation	*cspC*mut F	5' GGGCAAATATCCGAACG 3'	412 bp
	*cspC*mut R	5' AGCCTTATATTGGTGCCTCAT 3'	
yaaH mutation	*yaaH*mut F	5' CTTTCGCGTCAGGTTGGTGTG 3'	1030 bp
	*yaaH*mut R	5' CCTGCCTGCGCCGGATGGTTAG 3'	
leuA mutation	*leuA*mut F	5' GAATGCGCCGCTGCCAACA 3'	497 bp
	*leuA*mut R	5' GCCTCAACCAGCGCGTAAACAAA 3'	
tolR mutation	*tolR*mut F	5' GCCTCAACCAGCGCGTAAACAAA 3'	400 bp
	*tolR*mut R	5' ACTTCCGCCACCACCTGCTCTG 3'	
arcB mutation	*arcB*mut F	5' TGTCGCGACCAAAGCCCATCA 3'	709 bp
	*arcB*mut R	5' GCCCTCGTCGTTCTTGCCATTGT 3'	
gltA mutation	*gltA*mut F	5' TGTGTTTAACGGAGCTGATTTCTT 3'	626 bp
	*gltA*mut R	5' GCTGGCGACCGATTCTAACTACCT 3'	
cit amplification	*citT*out F	5' GTCCTGGGGTGATTATTTACGGCT 3'	1807 bp
	*citT*out R	5' CAATAACGCAAATAGTAACCGCAA 3'	
*cit*AmpJ fragment	*cit*AmpJ F	5' TTTTTTGGATCCGGTTCGAATGCCCCCTTTTT 3'	529 bp
	*cit*AmpJ R	5' TTTTTTGTCGACGGTAACCCTGCGTATTTGACTGAA 3'	
rnk promoter region of *rnk-citT* module for expression studies	nctForward	5' AAAAAAGGATCCGACACCCATCACCACCAGT 3'	707 bp
	nctReverse	5' AAAAAACTCGAGACGCCATCAACGCTCCGCTTTCT 3'	
citT-citG fragment for gene-gorging	*citT–citG* F	5' AACCAGCCAGGCCCCATTTCAGC 3'	648 bp
	citT–citG R	5' AAAAAAGGATCCCACGCCTTGCCGCATTACCTCACT 3'	
*citG*frag fragment for gene-gorging	*citG*frag F	5' TTTTTTGGATCCGGGGGTTCGAATGCCCCCTTTTT 3'	694 bp
	*citG*frag R	5' GCACAAAGATATGGCGCTGGAAGA 3'	
rnk promoter and *cit* amplification junction construct for gene-gorging	*citT–citG* Gorge F	5' TAGGGATAACAGGGTAATAACCAGCCAGGCCCCATTTCAGC 3'	1889 bp*
	*citG*frag R	5' GCACAAAGATATGGCGCTGGAAGA 3'	
rnk-citT module for cloning into pUC19	*citT*AmpX F	5' AAAAAAGGATCCGGGCAGCAACCGATTTAGG 3'	2490 bp
	*citT*AmpX R	5' AAAAAAGTCGACAACGCTCCGCTTTCTGC 3'	
citT internal fragment for Southern hybridizations	*citT*probe F	5' AGCCGTAAATAATCACCCCAGGAC 3'	1173 bp
	*citT*probe R	5' TTGCGGTTACTATTTGCGTTATTG 3'	
Amplification of genomic region immediately upstream of *citT*	*citT*upstrm R	5' CTCTCCCGCCGCGACTATTCA 3'	1264 bp†
	*citT*upstrm F	5' CAATAACGCAAATAGTAACCGCAA 3'	

*Length for fully assembled construct.

†Length without deletions or insertions.

Supplementary Table 15 | Clones used in growth-trajectory experiments			
Clone	**Generation**	**Description**	**Growth Curve Locations**
REL606	0	Ancestor	Fig. 6
CZB152	33,000	Cit$^+$ clone from main population	Fig. 5, Supplementary Fig. 3
CZB154	33,000	Cit$^+$ clone from main population	Supplementary Fig. 3
ZDB30	32,000	Potentiated Cit$^-$ clone from Clade 3	Fig. 4, 5, 6
ZDB143	32,500	Cit$^+$ clone from main population	Supplementary Fig. 3
ZDB161	32,000	Cit$^+$ mutant of ZDB28	Supplementary Fig. 5
ZDB163	32,500	Cit$^+$ mutant of ZDB31	Supplementary Fig. 5
ZDB164	32,000	Cit$^+$ mutant of ZDB30	Supplementary Fig. 5
ZDB165	32,000	Cit$^+$ mutant of ZDB30	Supplementary Fig. 5
ZDB166	32,000	Cit$^+$ mutant of ZDB29	Supplementary Fig. 5
ZDB172	32,000	Cit$^+$ clone from main population	Fig. 4, Supplementary Fig. 3
ZDB199	31,500	Potentiated Cit$^-$ clone from Clade 1	Fig. 6
ZDB200	31,500	Cit$^-$ clone from Clade 2	Fig. 6
ZDB279	31,500	Cit$^+$ mutant of ZDB199	Supplementary Fig. 5
ZDB281	32,000	Cit$^+$ mutant of ZDB183	Supplementary Fig. 5
ZDB283	32,000	Cit$^+$ mutant of ZDB30	Supplementary Fig. 5
ZDB285	20,000	Cit$^+$ mutant of ZDB464	Supplementary Fig. 5
ZDB286	20,000	Cit$^+$ mutant of ZDB464	Supplementary Fig. 5
ZDB288	27,000	Cit$^+$ mutant of ZDB309	Supplementary Fig. 5
ZDB290	27,000	Cit$^+$ mutant of ZDB310	Supplementary Fig. 5
ZDB292	31,000	Cit$^+$ mutant of ZDB390	Supplementary Fig. 5
ZDB294	32,000	Cit$^+$ mutant of ZDB30	Supplementary Fig. 5
ZDB546	32,500	Cit$^+$ mutant of ZDB31	Supplementary Fig. 5
ZDB547	30,500	Cit$^+$ mutant of ZDB20	Supplementary Fig. 5
ZDB548	32,500	Cit$^+$ mutant of ZDB32	Supplementary Fig. 5
ZDB549	32,500	Cit$^+$ mutant of ZDB31	Supplementary Fig. 5
ZDB564	31,500	Cit$^+$ clone from main population	Fig. 4, 5, Supplementary Fig. 3
ZDB595	32,000	Cit$^+$ isogenic construct of ZDB30 in which *rnk-citT* module promoter was inserted into the chromosome	Fig. 4
ZDB611	0	pUC19::*rnk-citT* transformant of REL606	Fig. 6
ZDB612	32,000	pUC19::*rnk-citT* transformant of ZDB30	Fig. 5, 6
ZDB614	31,500	pUC19::*rnk-citT* transformant of ZDB199	Fig. 6
ZDB615	31,500	pUC19::*rnk-citT* transformant of ZDB200	Fig. 6
ZDBr218	31,500	Cit$^+$ mutant of ZDB25	Supplementary Fig. 5