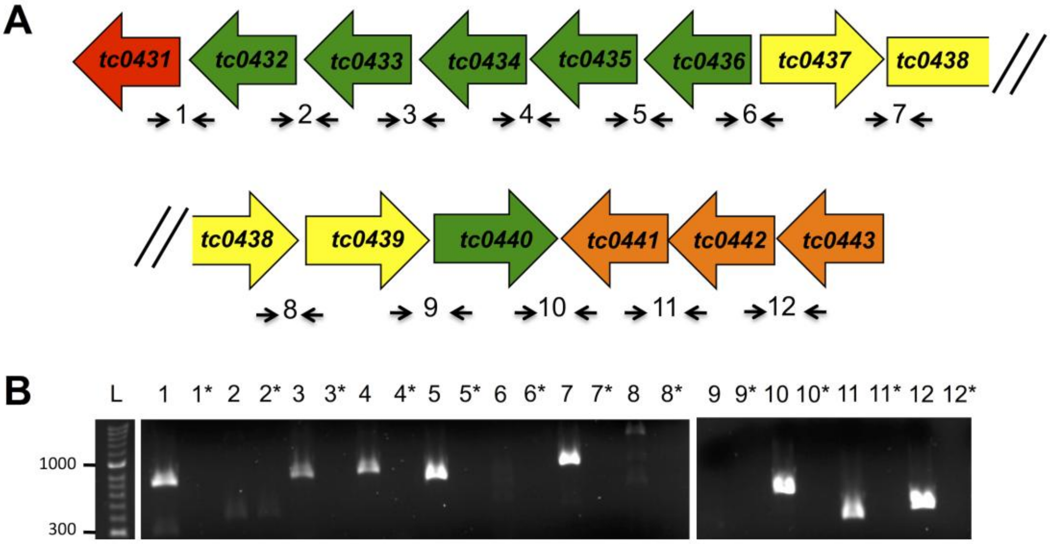
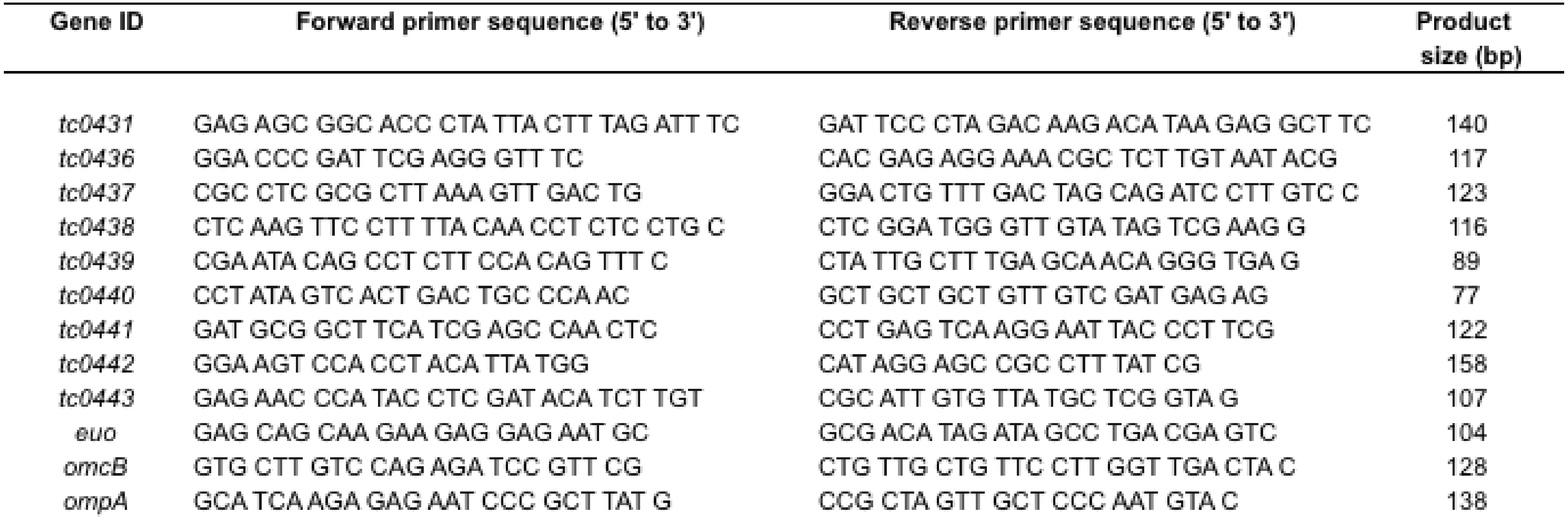


Fig. S1. Several *C. muridarum* PZ genes are encoded in operons. (A) Diagram of the *C. muridarum* PZ from *tc0431(MACPF)* to *tc0443 (guaB)* with locations of primers. (B) Agarose gel of RT-PCR amplification products and RT-negative control samples (*).

TABLE S1. Primers for RT-PCR

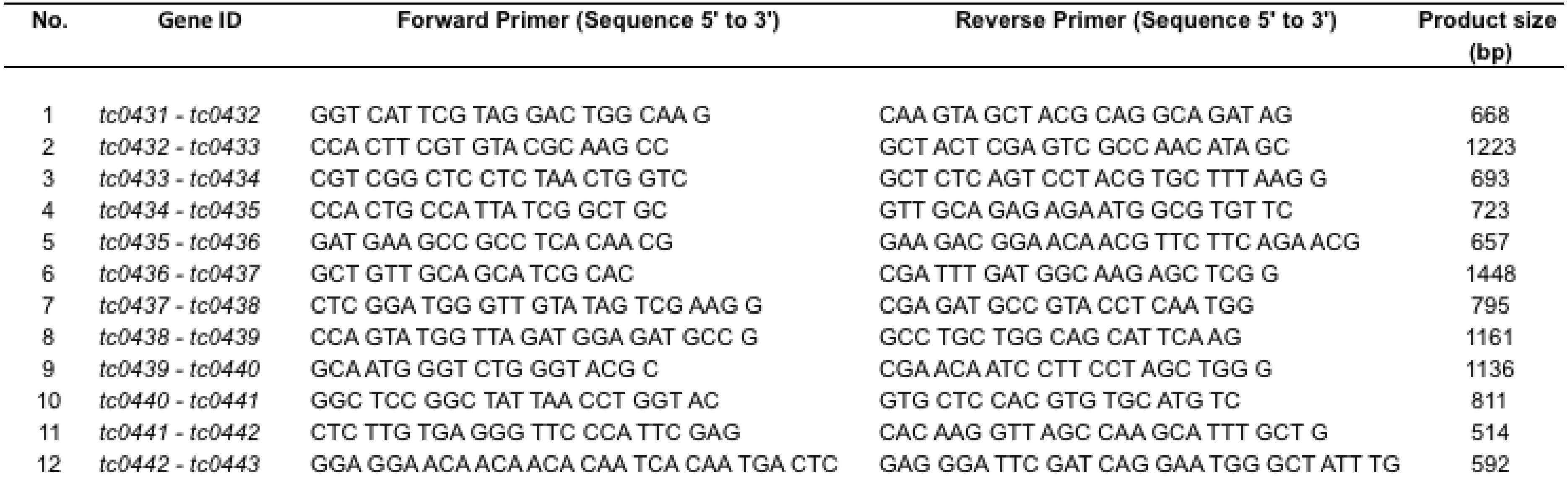
Gene ID	Forward primer sequence (5' to 3')	Reverse primer sequence (5' to 3')	Product size (bp)
tc0431	ATG CCC CAC TCT CCT TTT TTA TAT GTT	CAA GTA GCT ACG CAG GCA GAT AG	272
tc0432	GTC AGT CAT TTG TAA GCT TAT GAA CCA GG	GCT ACT CGA GTC GCC AAC ATA GC	342
tc0433	GTG CTC TCC TTG TTC ACG TCA TAT C	GCT CTC AGT CCT ACG TGC TTT AAG G	292
tc0434	ATG ACC GCA CCT TTA ATA ACT ACC AC	GTT GCA GAG AGA ATG GCG TGT TC	317
tc0435	GGT CTC TCC TTT AAT AAC TAC CAC CTC	GAA GAC GGA ACA ACG TTC TTC AGA ACG	291
tc0436	CGA TAC AAG GTG TGT CCG TAA GC	CTC CAT TAA ACT AGC GAG ATG CAT G	251
tc0437	CCC CCT TCA GCA ATT TCA	TCT GAA GAA ACT GTA GGC TGT TTA C	399
tc0438	CCT GTT TCC GGT TCA ATT GTT GCA T	CGT ATC TTT AGA AGT GAA GCG A	406
tc0439	GTT AGG CAA GCC AAA ATT CTA G	CTA CTC CTT TGA GCT GGC AGT AG	550
tc0440	GTC ACT GAC TGC CCA ACT TG	GAT AGT GCG AAC TGC TAA TCG G	816
tc0441	GAA GCT CGC TTA CGA TTG TAC GAT C	CGC TGA GCT TAT GGT CTC TAA ATA ATG C	574
tc0442	GAA CTC GGA CTC CTA AAC CAG G	GCG CTT ATT CCC ACT CAA TAG TTG C	339
tc0443	ATG CGC GAA GCT CTG ACT TTT GAT G	GAG AAC CCA TAC CTC GAT ACA TCT TGT	781
tc0444	ATG GGC GCC AAT AAG ATA C	TTA TTC GAT TTT TGG AGA AAA AAT GTT C	363
tc0445	ATG GGC GCC AAT AAG ATA CAC GC	CCC TGT AAC CTC TGC ATT CGG ATT C	153
tc0446	GGC TTA ACG TCT TGT CAC CAG AAA G	GAT GTA CAA AAC TGG TAG CAA TGC	269
tc0447	CAG CTG CTT CAT CCT ATC TCC GC	CTG TGA CAA CGG ATT AGT TCT G	400
euo	ATG GAA TGC TTA CAA CAA GAT AC	CTA AGA AAC AAA ATC CTC TGA GTC	345
omcB	ATG CGA ATA GGA GAT CCT ATG AAC	GCA CGA TTT CTA CAT TAC GAT CAT C	340
ompA	ATG AAA AAA CTC TTG AAA TCG GTA TTA GC	CTT GCA TAT GCT TGC CAT AAG C	340

TABLE S2. Primers for qRT-PCR



Gene ID	Forward primer sequence (5' to 3')	Reverse primer sequence (5' to 3')	Product size (bp)
tc0431	GAG AGC GGC ACC CTA TTA CTT TAG ATT TC	GAT TCC CTA GAC AAG ACA TAA GAG GCT TC	140
tc0436	GGA CCC GAT TCG AGG GTT TC	CAC GAG AGG AAA CGC TCT TGT AAT ACG	117
tc0437	CGC CTC GCG CTT AAA GTT GAC TG	GGA CTG TTT GAC TAG CAG ATC CTT GTC C	123
tc0438	CTC AAG TTC CTT TTA CAA CCT CTC CTG C	CTC GGA TGG GTT GTA TAG TCG AAG G	116
tc0439	CGA ATA CAG CCT CTT CCA CAG TTT C	CTA TTG CTT TGA GCA ACA GGG TGA G	89
tc0440	CCT ATA GTC ACT GAC TGC CCA AC	GCT GCT GCT GTT GTC GAT GAG AG	77
tc0441	GAT GCG GCT TCA TCG AGC CAA CTC	CCT GAG TCA AGG AAT TAC CCT TCG	122
tc0442	GGA AGT CCA CCT ACA TTA TGG	CAT AGG AGC CGC CTT TAT CG	158
tc0443	GAG AAC CCA TAC CTC GAT ACA TCT TGT	CGC ATT GTG TTA TGC TCG GTA G	107
euo	GAG CAG CAA GAA GAG GAG AAT GC	GCG ACA TAG ATA GCC TGA CGA GTC	104
omcB	GTG CTT GTC CAG AGA TCC GTT CG	CTG TTG CTG TTC CTT GGT TGA CTA C	128
ompA	GCA TCA AGA GAG AAT CCC GCT TAT G	CCG CTA GTT GCT CCC AAT GTA C	138

TABLE S3. Primers for PZ operon analysis



No.	Gene ID	Forward Primer (Sequence 5' to 3')	Reverse Primer (Sequence 5' to 3')	Product size (bp)
1	*tc0431 - tc0432*	GGT CAT TCG TAG GAC TGG CAA G	CAA GTA GCT ACG CAG GCA GAT AG	668
2	*tc0432 - tc0433*	CCA CTT CGT GTA CGC AAG CC	GCT ACT CGA GTC GCC AAC ATA GC	1223
3	*tc0433 - tc0434*	CGT CGG CTC CTC TAA CTG GTC	GCT CTC AGT CCT ACG TGC TTT AAG G	693
4	*tc0434 - tc0435*	CCA CTG CCA TTA TCG GCT GC	GTT GCA GAG AGA ATG GCG TGT TC	723
5	*tc0435 - tc0436*	GAT GAA GCC GCC TCA CAA CG	GAA GAC GGA ACA ACG TTC TTC AGA ACG	657
6	*tc0436 - tc0437*	GCT GTT GCA GCA TCG CAC	CGA TTT GAT GGC AAG AGC TCG G	1448
7	*tc0437 - tc0438*	CTC GGA TGG GTT GTA TAG TCG AAG G	CGA GAT GCC GTA CCT CAA TGG	795
8	*tc0438 - tc0439*	CCA GTA TGG TTA GAT GGA GAT GCC G	GCC TGC TGG CAG CAT TCA AG	1161
9	*tc0439 - tc0440*	GCA ATG GGT CTG GGT ACG C	CGA ACA ATC CTT CCT AGC TGG G	1136
10	*tc0440 - tc0441*	GGC TCC GGC TAT TAA CCT GGT AC	GTG CTC CAC GTG TGC ATG TC	811
11	*tc0441 - tc0442*	CTC TTG TGA GGG TTC CCA TTC GAG	CAC AAG GTT AGC CAA GCA TTT GCT G	514
12	*tc0442 - tc0443*	GGA GGA ACA ACA ACA CAA TCA CAA TGA CTC	GAG GGA TTC GAT CAG GAA TGG GCT ATT TG	592

TABLE S4. Primers for cloning PZ fragments into the pAC-lacZ vector

Construct	Forward primer sequence (5' to 3')	Reverse primer sequence (5' to 3')	Genbank Coordinates flanking Construct
1	ATA ATA TCG CGA ACC AAT GCG AAC AAC ATC TTC TGT	GCT CTT CGG CCG GTA ATA CGA AAA GGT GTG TTT C	506506-505406
2	TAA TAA TCG CGA ATG GAC CCG ATT CGA GGG TTT CAC CAG	AAG TGC CGG CCG CAC CAA GTG CAC AAA TC	505479-504381
3	ATC ATA TCG CGA AAA CTG TTA TCA TCG GCT CCG CTA ATT GGT CCG	GAT TAG CGG CCG CAT TTT GTC TGC GGG TAG GCC	504505-503381
4	ACA AAC TCG CGA AAT ACA CCC TTG AAA AGC TAT CCT CTC AC	CAG CGA CGG CCG GTT CTG GGC TAT TTA CTC GC	503476-502487
5	CGT TCA TCG CGA CTA TTT CAC AAA AAA ACT CTT ATC ATT GAT AAA C	GTT TTG CGG CCG CTA GAA GTC TCT AAC GAA TGA	502509-501488
6	GAA GAT TCG CGA TTG TTT ATC GTT CGA AAT CTA ACA GCA C	AGA GAT CGG CCG GGT TGT TGT TGC AGG ATA ATC	500724-499715
7	ACA ACC TCG CGA ATC TCT ATT CCA CAG AAA ATC GCT GG	GGC AGA CGG CCG TAG TTT GGG TTC TAG AAC GG	499715-498724
8	TTT ATT TCG CGA GAA AAC CTA CCT TTA GAA ATT TTT GGA GCC	GGC TTG CGG CCG CTG AAA ACG CTG CTG	498833-497707
9	ATA ATA TCG CGA GTT CCA ATG TAG TTT GGA TGA CC	ATA ATA CGG CCG CAA CAA TCC ATC CAC AAC GTT C	497801-496846
10	CAT AGG TCG CGA TTC TTT ACC TAT TCG ACA AAA GAT TTT TGG C	GCT GAG CGG CCG TAG AAT TAT GGG AAT TCT TAT TG	496910-495810
11	CCT GAA TCG CGA GCT CCG GTA ATC GCA ACC TCT CC	GAG CCT CGG CCG CGC TCT CTG TCT CAG TAC ATT	495919-494389
12	ATC ATA TCG CGA GTG CTC TTG AAC ATC TGG AG	ATC ATA CGG CCG GTT GTG TAA TAG TGC GTG G	505999-504971
13	ATCATA TCGCGA GTC CAA AAC AAC TAT AGA GCT AAT CCA G	ATC ATA CGG CCG GTC TTA TGA GGG CAA TGT ATG	504984-503936
14	ATC ATA TCG CGA GAA CGT TGT TCC GTC TTC TAA ATC	ATC ATA CGG CCG GTG GTA GTT ATT AAA GGT GC	503977-503108
15	CTG ATA TCG CGA GTA AGT TAG ATA GGC TGC G	ATA ATA CGG CCG GAA GAG TCA GCG TTT TCG	503120-501964
16	GTG GTC TCG CGA GTG AGA ATA GTA CTG CTA TAA C	ATA ATA CGG CCG GAT GGA AGA CAA TGG AGA G	501974-501177
17	ATA ATA TCG CGA CGC TGG TTG TTG ATC ACA GAA TG	ATA ATA CGG CCG GTC TCT AAC GAA TGA CGA TTG C	501231-500093
18	GTG GTA TCG CGA GAT CTC TCC CAT CGA GTT ATT TAT G	ATA GTA CGG CCG CTG ATA AGG ATT GGC ATT GAG	500098-499295
19	ATA GTA TCG CGA GGA TCT TCT AAT TGG TCA TTC GTA GG	ATA ATA CGG CCG GTC ACA AGA ATT TCC TGC TGT C	499340-498170
20	GTA GTA TCG CGA CTT TTT GTG TAC CAC CTC TTA CC	ATA ATA CGG CCG GAC ACT TTC AGA CCA ATC TTT AAA ATC	498229-497370
21	ATA ATA TCG CGA CAG CAC GGA ATC TGG CTA CTC TAC	ATA ATA CGG CCG GAT GAA CCT TCT GGG AAC CTG	497473-496327
22	ATA ATA TCG CGA CAG CTA ACT CTC GAT CAT GAG TTA CG	ATA ATA CGG CCG GCT TGT TCC AAT ATT GTG ACC	497415-495248
23	GTA CGA TCG CGA TTC CTG CTT GAT TTT TC	GAT ATA CGG CCG GTG TTT ACT TGA TCT AG	504810-505810
24	ATA CAG TCG CGA GAA CCT TAA TTG GGC	TAA ATA CGG CCG GTT CCA AGA GAA AAC GGC TTA	525699-526699
25	CTC ACG TCG CGA ATA AAA GCT TAT CAA TTG	ATA TTA CGG CCG GAA CAA TGC TTG GC	525199-526199
26	ATA CGA TCG CGA ATG CAA CAA CAC TAA AAT T	ATA TTA CGG CCG CTT GTC TTT AGA TGT GC	524699-525699
27	ATA TAA TCG CGA ACC CAA GAA TAG CGA AG	ATC CGA CGG CCG TGT TTT TTA TTT TAA CAA AG	535815-536815
28	ATT TAT TCG CGA CTA GCA ACC CAT CGG C	ATA CTA CGG CCG CGT TCT TCT TCT GTT GTC	535315-536315
29	TAT TCG CGG CCG TGC TCT TTC TAA ACC TTG	CGC AGG CGG CCG TAA ATC CCT TAA AAT AAG	541942-542942
30	TAT TCG CGG CCG TGC TCT TTC TAA ACC TTG	CGC AGG CGG CCG TAA ATC CCT TAA AAT AAG	542942-541942

TABLE S4. Cont.

Construct	Forward primer sequence (5' -> 3')	Reverse primer sequence (5' -> 3')	Genbank Coordinates flanking Construct
31	TTA TTA CGG CCG TAG CGT TCA GCA CTA CC	ATA TGC CGG CCG GTC GAT TTA ATT TCC	541442-542442
32	TTA TTA CGG CCG TAG CGT TCA GCA CTA CC	ATA TGC CGG CCG GTC GAT TTA ATT TCC	542442-541442
33	GTG CTA CGG CCG CGA AAA TAA AAG TTA ATA A	ATT CGA CGG CCG AAA CTT TTT TTT AGG CAT AAA G	543885-542868
34	TTA ATA CGG CCG TAG GTT GGA GGG ATT GTA ATG	CGC AGA CGG CCG ACT TTA GTA AAA AAA AGG	542368-543368
35	TTA ATA CGG CCG TAG GTT GGA GGG ATT GTA ATG	CGC AGA CGG CCG ACT TTA GTA AAA AAA AGG	543368-542368
36	GTA CGA TCG CGA GTT GTA GGG TTT GAT AAT GG	ATT CGA CGG CCG AAA CTT TTT TTT AGG CAT AAA G	542868-542368
37	GCA TGA TCG CGA ATC CAA GAA AAT AGT GAT GAA	GCA TGA CGG CCG ATT ATC TCC TAT TTC CCT CG	505347-506310
38	GCA TGA TCG CGA GAG ATA ATA TGC CCC CTT CA	GCA TGA CGG CCG CTA CCC AAA ATA AAA AAT CAA AC	506322-507296
39	GCA TGA TCG CGA GAG TAA AAA TTG ACA GTC	GCA TGA CGG CCG ACT TGA TTT TTG TTT ATT CTC	507174-508174
40	GCA TGA TCG CGA GGT TTC AGA TGG GGT TTT GAG	GCA TGA CGG CCG CAC ACA CTT GAT TAC GAA GAA	508021-509021
41	GCA TGA TCG CGA CGA GTT GCT AGA TCG ATT	GCA TGA CGG CCG CTA ATC TAG CAG ATG GAG	508915-509906
42	GCA TGA TCG CGA TTT AAC AGA GAT CAC TCG GTA	GCA TGA CGG CCG CCT CAT CTT CTA TGG ACA TAT	509812-510803
43	AAG TAT TCG CGA ACT TTG TTA TCT TGG CCA GAA	TGC CTC CCG CCG AAG AAA TTG AAA TAG AGA TGC	510635-511648
44	AAA CAT TCG CGA GTT TTA GAT TCT GAA ACG GTA	ATA ATT CGG CCG TAA AAG AAA ATT TCC TAA AAC	511514-512566
45	CTT TAC TCG CGA CCT CTT TGA TGC TAG CTG TGG	TTC CTC CGG CCG TTC CTT TAC CTG AAT AAA TAG	512355-513353
46	GTA GAA TCG CGA CAA GAT GTT CCG CTG ATA AGG	CCA TAA CGG CCG GAT TCC AAT AAC TTG GGT TTC	513179-514220
47	TAA GTT TCG CGA CCA TTC TAC CAA CTC TTA TAT	CTT GTC CGG CCG AAC TAA AAT CGC TAA ATT GAG	514008-514987
48	ATG GGA TCG CGA TTA ATT AAT CCT GCA TAT AGA	TCC TAA CGG CCG AGG TTT CAA GAA TGC GTC TAA	514913-515896
49	ATG GGA TCG CGA TTA ATT AAT CCT GCA TAT AGA	GTA CTA CGG CCG GAT TCA CCA ACA CTA TG	514913-515353
50	GTA CTA TCG CGA CTT CAC ATA GTG TTG GTG	TCC TAA CGG CCG AGG TTT CAA GAA TGC GTC TAA	515330-515896
51	GCA TGA TCG CGA GTA TTC CTA TAG CTT TAA	GCA TGA CGG CCG ATT GTA ATT AGT AAT AGC	515787-516852
52	CTC AAT TCG CGA CAG CCT CGG TCT TAG TC	GCC CAT CGG CCG TCC TGA TCG AAT CCC	542301-541321
53	CTG AAA TCG CGA TTG GTG TGG ACG CTG	CTT TGG CGG CCG GCA TTC TAT AGC GGC	541784-540688
54	CAC TGT TCG CGA CCC ATT GCC GCT ATA G	GGA GTG CGG CCG TCA TCG CTC AAC TCA G	540720-539541
55	GGT AAA TCG CGA GTT CTG GGT TTG CCG	CAA CTC CGG CCG GCA GCC TCT TCA G	540044-538928
56	CGT ACA TCG CGA GGG GCA TAG ACA TCC	CGA GTG CGG CCG GAA TAA GTA GCG CAG G	539248-538082
57	GCT CCG TCG CGA GCT ATT AAC CTG GTA C	GGA CTT CGG CCG CCG ATT AGC AGT TCG C	538633-537603
58	GTC TTG TCG CGA CGA GCA GTT GTT CAA G	GAT CCT CGG CCG GGA CAA TGG GTT CAG	545014-545939

TABLE S5. Identification of promoter elements in the *C. muridarum* PZ

Construct	Genbank Coordinates flanking Construct	Average β-galactosidase activity (Miller Units)	± SD
1	506506-505406	0	0
2	505479-504381	31.28	1.04
3	504505-503381	30.78	0.74
4	503476-502487	8.66	0.99
5	502509-501488	14.21	0.67
6	500724-499715	0	0
7	499715-498724	52.49	2.06
8	498833-497707	0	0
9	497801-496846	2.79	0.15
10	496910-495810	12.3	0.7
11	495919-494389	0	0
12	505999-504971	0	0
13	504984-503936	0	0
14	503977-503108	0	0
15	503120-501964	39.46	1.44
16	501974-501177	0	0
17	501231-500093	0	0
18	500098-499295	0	0
19	499340-498170	0	0
20	498229-497370	105.1	2.23
21	497473-496327	150.83	9.75
22	497415-495248	0	0
23	504810-505810	7.3	7.3
24	525699-526699	0	0
25	525199-526199	8.3	0.26
26	524699-525699	88.64	2.82
27	535815-536815	27.63	0.58
28	535315-536315	157.17	7.64
29	541942-542942	82.87	2.42
30	542942-541942	89.2	2.32
31	541442-542442	156.1	13
32	542442-541442	0	0
33	543885-542868	188.76	27.14
34	542368-543368	95.77	2.3
35	543368-542368	3175.467	995.4
36	542868-542368	3470.29	115.87
37	505347-506310	5.1	2.33
38	506322-507296	8.57	3.43
39	507174-508174	49.13	1.17
40	508021-509021	103.7	4.68
41	508915-509906	10.37	1.3
42	509812-510803	12.96	2.84
43	510635-511648	4.88	1.53
44	511514-512566	185.98	24.8
45	512355-513353	3.69	1.2
46	513179-514220	7.87	0.96
47	514008-514987	27.6	2.32

TABLE S5. Cont.

Construct	Genbank Coordinates flanking Construct	Average β-galactosidase activity (Miller Units)	± SD
48	514913-515896	1320.84	459.73
49	514913-515353	59.03	6.59
50	515330-515896	1172.97	132.06
51	515787-516852	86.12	1
52	542301-541321	6.75	0.27
53	541784-540688	19.85	3.77
54	540720-539541	70.37	4.96
55	540044-538928	32.84	1.04
56	539248-538082	9.36	0.87
57	538633-537603	19.56	0.71
58	545014-545939	9.43	1.06
lacZ vector (-) control	-	111.04	39.65
dnaK (+) control	-	518.9	82.39

TABLE S6. Primers for TILLING

Gene ID	Forward primer Sequence (5' to 3')	GenBank Coordinates	Reverse primer sequence (5' to 3')	GenBank Coordinates
tc0431	ATG CCC CAC TCT CCT TTT TTA TAT GTT	498629	ATC AAT TAA CAC GGC TGC AAT TGT ATG	497607
tc0437	TCT ACG ACG CCT CAA GTC A	506363	AAT TTA GCC GCT CCA AAA GC	507325
tc0438	CCT GTT TCC GGT TCA ATT GTT GCA T	516121	GGC TCA TAT ACT GTT CTA TGC CCT C	517124
tc0439	GAA CAA GCA TTG TGT ACT ATG ACT C	526702	GCT GCA TCA AAA GCA ATT CG	527714
tc0440	ATG TGT TCC CCC TGT CCA CGT C	536815	GTG GAG CAC CAG GCT TGC G	537841
tc0441	GTT AGA GGT GAA GAT GTC ACA TGA G	538405	CCA CCG GCA ACT ATT GAG TG	539652
tc0442	GCG CTT ATT CCC ACT CAA TAG TTG C	539628	GCG TGA AGC ATA TTT GCC AGA C	540609
tc0443	GCA AGT TAT GGA TGT GGC TTT CAG	541225	CTC AAT CAG CCT CGG TCT TAG TCA	542301

TABLE S7. Summary of TILLING screen size and isolated mutants

Gene ID	Estimated Screen Size (N)	Total no. of mutants	No. of silent mutants	No. of missense mutants	No. of nonsense mutants
tc0431 (MACPF)	64	68	13	55	0
tc0437	33	20	4	14	2
tc0438	55	30	9	20	1
tc0439	36	47	8	37	2
tc0440 (PLD)	48	43	11	28	4
tc0441(add)	42	13	3	9	1
tc0442(guaA)	94	12	0	10	2
tc0443(guaB)	94	8	1	6	1

TABLE S8. SNPs in *C. muridarum tc0437* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc008	exodeoxyribonuclease V, gamma subunit	13703	G → A	Thr → Ile
tc0019	recA	26275	G → A	Glu → Lys
tc0035	hypothetical protein	40681	G → A	Leu → Leu
tc0069	endonuclease III	80096	C → T	Pro → Ser
tc0074	preprotein translocase SecA subunit; secA	85403	C → T	Arg → Cys
tc0096	ribosomal large subunit pseudouridine synthase B; rluB	115068	G → A	Gly → Gly
tc0120	hypothetical protein	144193	C → T	Arg → Cys
tc0125	alanyl-tRNA synthetase	153963	G → A	Ala → Val
tc0137	murF	168334	C → T	Leu → Leu
tc0159	primosomal protein N	193263	G → A	Arg → Arg
tc0172	conserved hypothetical protein	202909	G → A	Gly → Glu
tc0213	CDP-diacylglycerol--serine O-phosphatidyltransferase	252676	C → T	Met → Ile
tc0218	UDP-N-acetylenolpyruvoylglucosamine reductase; murB	260165	G → A	Ser → Phe
tc0237	hypothetical protein	277523	G → A	Arg → Cys
tc0283	PhoH-related protein	338843	C → T	Gly → Arg
tc0290	hypothetical protein	349249	C → T	Arg → Lys
tc0330	protein export protein, FHIPEP family protein	391857	C → T	Arg → Trp
tc0383	A/G-specific adenine glycosylase	444982	A → G	Thr → Ala
tc0412	conserved hypothetical protein	473585	C → T	Gln → STOP
tc0424	conserved hypothetical protein	487908	C → T	Ala → Val
tc0437	adherence factor	506777	C → T	Gln → STOP
tc0438	adherence factor	520769	G → A	Arg → Gln
tc0453	hypothetical protein	551457	G → A	Arg → Arg
tc0460	thymidylate kinase	558168	C → T	Glu → Lys
tc0469	hypothetical protein	569879	C → T	Ala → Val
tc0471	peptide ABC transporter, periplasmic peptide-binding protein	572022	C → T	Thr → Ile
tc0479	pfkA-2, beta subunit	581345	G → A	Glu → Lys
tc0490	Rep helicase family protein; uvrD	596078	G → A	Ser → Ser
tc0501	sodium:dicarboxylate symporter family protein	607577	C → T	Ser → Phe
tc0544	hypothetical protein	654353	G → A	Ile → Ile
tc0575	serine/threonine kinase protein	684627	G → A	Ala → Ala
tc0588	DNA-directed RNA polymerase, beta subunit; rpoC	702107	G → A	Leu → Phe
tc0635	hypothetical protein	761471	C → T	Glu → Gln
tc0645	3-phosphoshikimate 1-carboxyvinyltransferase; aroA	772383	G → A	Lys → Phe
tc0694	polymorphic membrane protein B/C family protein; pmpB/C-1	829608	C → T	Asn → Asn
tc0694	polymorphic membrane protein B/C family protein; pmpB/C-1	831869	C → T	Ser → Phe
tc0733	secDF protein	872206	G → A	Asp → Asp
tc0810	ribosomal protein, L22; rplV	945533	C → T	Gly → Arg
tc0816	hypothetical protein	949915	C → T	Thr → Thr
tc0833	uracil phosphoribosyltransferase; upp	969350	G → A	Gly → Arg
tc0842	branched-chain amino acid transport system carrier protein	977030	G → A	Gly → Glu
tc0864	DNA mismatch repair protein MutL	1001277	G → A	Leu → Phe
tc0877	regulatory protein	1016507	C → T	His → Tyr
tc0917	geranylgeranyl pyrophosphate synthase	1069215	G → A	Leu → Leu

TABLE S9. SNPs in *C. muridarum tc0438* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0019	recA	26275	G → A	Glu → Lys
tc0064	phosphate permease family protein	74467	G → A	Arg → Lys
tc0121	protoporphyrinogen oxidase; hemY	146183	G → A	Ser → Phe
tc0125	alanyl-tRNA synthetase	153963	G → A	Ala → Val
tc0137	murF	168503	G → A	Gly → Arg
tc0147	tRNA delta-2-isopentenylpyrophosphate transferase	179316	G → A	Glu → Lys
tc0186	ribosomal protein L9	218818	G → A	Glu → Lys
tc0214	ribonucleoside-diphosphate reductase, alpha subunit	255549	C → T	His → His
tc0218	UDP-N-acetylenolpyruvoylglucosamine reductase; murB	260165	G → A	Ser → Phe
tc0237	hypothetical protein	277523	G → A	Arg → Cys
tc0283	PhoH-related protein	338843	C → T	Gly → Arg
tc0294	signal recognition particle protein	352693	G → A	Asp → Asn
tc0330	protein export protein, FHIPEP family protein	391857	C → T	Arg → Trp
tc0404	adenylate kinase; adk	464247	G → A	Thr → Thr
tc0412	hypothetical protein	473585	C → T	Gln → STOP
tc0425	monooxygenase-related protein	491242	G → A	Ser → Phe
tc0438	adherence factor	516403	C → T	Gln → STOP
tc0438	adherence factor	519122	C → T	Ser → Phe
tc0438	adherence factor	520769	G → A	Arg → Gln
tc0438	adherence factor	525326	G → A	Arg → Lys
tc0450	hypothetical protein	549083	C → T	Arg → STOP
tc0471	peptide ABC transporter, periplasmic peptide-binding protein	572022	C → T	Thr → Ile
tc0575	serine/threonine kinase protein	684627	G → A	Ala → Ala
tc0580	ATP synthase subunit D; atpD	693778	G → A	Leu → Phe
tc0588	DNA-directed RNA polymerase, beta subunit; rpoC	702107	G → A	Leu → Phe
tc0635	hypothetical protein	761916	C → T	Glu → Lys
tc0644	hypothetical protein	771460	C → T	Asp → Asn
tc0645	3-phosphoshikimate 1-carboxyvinyltransferase; aroA	772383	G → A	Lys → Phe
tc0666	hypothetical protein	795149	G → A	Arg → Gln
tc0671	hypothetical protein	800641	C → A	Gly → Asp
tc0681	sodium:dicarboxylate symporter family protein	813777	G → A	Pro → Ser
tc0694	polymorphic membrane protein B/C family; pmpB/C-1	828687	C → T	Ser → Ser
tc0694	polymorphic membrane protein B/C family; pmpB/C-1	828944	G → A	Gly → Asp
tc0833	uracil phosphoribosyltransferase, upp	969350	G → A	Gly → Arg
tc0877	regulatory protein, putative	1016507	C → T	His → Tyr

TABLE S10. SNPs in *C. muridarum tc0439* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0044	serine/threonine protein kinase	50222	G → A	Val → Val
tc0054	penicillin-binding protein	62823	G → A	Gly → Glu
TC0084	hypothetical protein	101889	G → A	Asp → Asn
-	intergenic	126188	C → T	-
tc0191	hypothetical protein	224779	G → A	Gly → Gly
tc0197	polymorphic membrane protein; pmpD	233168	G → A	Glu → Lys
tc0226	hypothetical protein	265848	G → A	Cys → Cys
tc0230	polyribonucleotide nucleotidyltransferase; pnpA	273825	G → A	Ser → Ser
tc0244	fumarate hydratase; fumC	284699	G → A	Glu → Lys
tc0249	penicillin tolerance protein; lytB	291424	C → T	Arg → Trp
tc0250	hypothetical protein	292616	C → T	Val → Ile
tc0290	hypothetical protein	349120	G → A	Ser → Phe
tc0312	glycosyl hydrolase	369812	G → A	Ser → Phe
tc0390	hypothetical protein	455441	G → A	Glu → Lys
tc0414	hypothetical protein	474899	C → T	Ser → Leu
tc0439	adherence factor	527311	C → T	Gln → STOP
tc0472	peptide ABC transporter, permease protein	573799	C → T	Pro → Leu
tc0521	chromosomal replication initiator protein; dnaA	630193	C → T	Val → Val
tc0521	chromosomal replication initiator protein; dnaA	630703	G → A	Phe → Phe
tc0576	valyl-tRNA synthetase	687755	C → T	Lys → Lys
tc0588	DNA-directed RNA polymerase, beta subunit; rpoC	702342	G → A	Asn → Asn
tc0600	hypothetical protein	716734	G → A	Ser → Phe
tc0600	hypothetical protein	717761	G → A	Gln → STOP
tc0695	polymorphic membrane protein B/C family; pmpB/C-2	837382	G → A	Thr → Thr
tc0716	serine hydroxymethyltransferase; glyA	853750	C → T	Val → Val
-	intergenic	869958	C → T	-
tc0732	ssDNA-specific exonuclease; recJ	870022	C → T	Gln → His
-	intergenic	920321	C → T	-

TABLE S11. SNPs in *C. muridarum tc0440* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0076	GTP-binding protein EngA; yfgk	88283	C → T	Gly → Ser
tc0108	sodium/alanine symporter family protein	127881	G → A	Val → Val
tc0124	transcription-repair coupling factor; trcF	150150	G → A	Asp → Asp
tc0192	glycerol-3-phosphate acyltransferase	225336	G → A	Asp → Asp
tc0212	hypothetical protein	251161	C → T	Met → Ile
tc0286	hypothetical protein	342465	G → A	Thr → Ile
tc0322	coproporphyrinogen III oxidase	380857	G → A	Leu → Phe
tc0355	hypothetical protein	415946	C → T	Pro → Leu
tc0408	hypothetical protein	469557	G → A	Arg → Cys
tc0437	adherence factor/cytotoxin	508662	C → T	Ser → Leu
tc0440	putative phospholipase D	537373	C → T	Gln → STOP
tc0464	hypothetical protein	564839	G → A	Ser → Leu
tc0477	diphosphate-fructose-6-phospahte 1-phosphotransferase; pfkA-1	580008	G → A	Arg → Gln
tc0532	DNA polymerase III subunit epsilon	643156	G → A	Val → Ile
tc0535	ABC transporter ATP-binding protein	645392	C → T	Leu → Leu
tc0554	glycine cleavage system protein H; gcvH	663397	C → T	Gly → Asp
tc0561	hypothetical protein	672063	C → T	Ile → Ile
tc0575	serine/threonine-protein kinase; pknD	686396	G → A	Pro → Ser
tc0579	V-type ATP synthase subunit I	692340	G → A	Thr → Thr
tc0579	V-type ATP synthase subunit I	692683	C → T	Arg → Gln
tc0588	DNA-directed RNA polymerase subunit beta; rpoC	701622	C → T	Arg → Arg
tc0602	helicase	721695	G → A	Thr → Ile
tc0605	exodeoxyribonuclease VII large subunit; xseA	724506	G → A	Gly → Glu
tc0610	excinuclease ABC subunit A; uvrA	735281	C → T	Leu → Phe
tc0617	hypothetical protein	740043	C → T	Ser → Ser
tc0635	hypothetical protein	762982	G → A	Arg → Arg
tc0650	hypothetical protein	777433	C → T	Ala → Val
tc0676	VacB/Rnb family exoribonuclease	809172	C → T	Ser → Ser
tc0690	sodium/alanine symporter family protein	820643	C → T	Ser → Ser
tc0697	ABC transporter ATP-binding protein	839505	C → T	Asp → Asp
tc0706	hemolysin	845268	C → T	Arg → Arg
tc0733	preprotein translocase subunit SecD/SecF	875842	G → A	Arg → Arg
-	intergenic	876181	C → T	-
tc0737	cytidylate kinase; cmk	879394	C → T	Ser → Ser
tc0814	50S ribosomal protein L4; rplD	947444	C → T	Arg → Lys
-	intergenic	953298	C → T	-
tc0864	DNA mismatch repair protein; mutL	1000005	G → A	Gln → STOP
tc0873	hypothetical protein	1011011	C → T	Leu → Phe
tc0886	ExbD/TolR family protein	1030795	C → T	Ser → Phe
tc0911	hypothetical protein	1057937	C → T	Val → Ile

TABLE S12. SNPs in *C. muridarum add* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0019	recA protein	26275	G → A	Glu → Lys
tc0035	hypothetical protein	40681	G → A	Leu → Leu
tc0069	endonuclease III; nth	80096	C → T	Ala → Thr
tc0098	BirA-related protein	116059	C → T	Leu → Phe
tc0120	hypothetical protein	144193	C → T	Arg → Cys
tc0125	alanyl-tRNA synthetase; alaS	153963	G → A	Ala → Val
-	intergenic	183496	T → C	-
-	intergenic	227658	C → T	-
tc0218	UDP-N-acetylenolpyruvoylglucosamine reductase; murB	260165	G → A	Ser → Phe
tc0226	hypothetical protein	266168	G → A	Pro → Ser
tc0237	hypothetical protein	277523	G → A	Arg → Cys
tc0252	type III secretion chaperone	295119	G → A	Leu → Leu
tc0283	PhoH-related protein	338843	C → T	Gly → Arg
tc0306	hypothetical protein	364225	G → A	Phe → Phe
tc0330	protein export protein, FHIPEP family	391857	C → T	Arg → Trp
tc0409	hypothetical protein	470580	G → A	Ile → Ile
tc0412	hypothetical protein	473585	C → T	Gln → STOP
tc0413	serine esterase	474570	C → T	Ser → Phe
tc0424	hypothetical protein	487580	C → T	Leu → Phe
tc0438	adherence factor	520769	G → A	Arg → Gln
tc0440	phospholipase D family protein	538075	G → A	Gly → Arg
tc0441	adenosine deaminase; add	539413	G → A	Gln → STOP
tc0466	magnesium transporter; mgtE	567943	G → A	Ser → Ser
tc0471	peptide ABC transporter, periplasmic peptide-binding protein	572022	C → T	Thr → Ile
tc0477	pfkA-1, beta subunit	579586	G → A	Glu → Glu
tc0479	pfkA-2, beta subunit	581345	G → A	Glu → Lys
tc0490	UvrD/REP helicase family protein	596078	G → A	Ser → Ser
tc0490	UvrD/REP helicase family protein	596953	C → T	Asp → Asn
tc0492	4-hydroxybenzoate octaprenyltransferase; ubiA	599868	C → T	Pro → Leu
tc0575	serine/threonine protein kinase	684627	G → A	Ala → Ala
tc0588	DNA-directed RNA polymerase, beta` subunit; rpoC	702107	G → A	Leu → Phe
tc0603	N-(5'-phosphoribosyl)-anthranilate isomerase; trpF	723235	C → T	Gly → Ser
tc0629	hypothetical protein	753985	G → A	Glu → Lys
tc0645	3-phosphoshikimate 1-carboxyvinyltransferase; aroA	772383	G → A	Lys → Lys
tc0649	3-dehydroquinate dehydratase/shikimate 5-dehydrogenase	776683	C → T	Gly → Ser
tc0674	grpE protein	804884	C → T	Pro → Leu
tc0699	GTP-binding protein, GTP1/Obg family	841076	C → T	Ala → Ala
tc0715	ATP-dependent Clp protease, proteolytic subunit; clpP-2	853202	C → T	Leu → Leu
tc0828	peptidyl-prolyl cis-trans isomerase; mip	959089	C → T	Glu → Lys
tc0833	uracil phosphoribosyltransferase; upp	969350	G → A	Gly → Arg
tc0877	regulatory protein	1016507	C → T	His → Tyr
tc0917	geranylgeranyl pyrophosphate synthase	1069215	G → A	Leu → Leu

TABLE S13. SNPs in *C. muridarum guaA* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0001	delta-aminolevulinic acid dehydratase; hemB	576	G → A	Cys → Tyr
tc0024	hypothetical protein	31399	G → A	Pro → Ser
tc0032	DNA gyrase, subunit B; gyrB-1	36506	G → A	Pro → Leu
tc0059	aminotransferase, class V	69061	G → A	Val → Ile
tc0089	hypothetical protein	108562	G → A	Leu → Leu
tc0108	sodium/alanine symporter family protein	128662	G → A	Ala → Pro
tc0112	cell division protein FtsK, putative	131865	G → A	Ile → Ile
tc0123	uroporphyrinogen decarboxylase; hemE	148454	G → A	Pro → Pro
tc0124	transcription-repair coupling factor; trcF	151261	C → T	Gly → Glu
-	intergenic	182756	G → A	-
tc0193	ribonuclease G; cafA	226211	G → A	His → Tyr
tc0196	fatty acid/phospholipid synthesis protein; plsX	229357	G → A	Val → Met
-	intergenic	239576	G → A	-
tc0284	hypothetical protein	340204	C → T	Leu → Phe
tc0322	oxygen-independent coproporphyrinogen III oxidase; HemN	380626	G → A	Pro → Ser
tc0333	6-phosphogluconate dehydrogenase, decarboxylatin; pgd	395612	G → A	Thr → Thr
tc0383	A/G-specific adenine glycosylase; mutY	445590	G → A	Asp → Asn
tc0442	GMP synthase; guaA	540375	G → A	Gln → STOP
tc0527	hypothetical protein	637749	G → A	Val → Ile
tc0550	NADH:ubiquinone oxidoreductase, subunit B	659443	C → T	Pro → Pro
-	intergenic	667975	G → A	-
tc_t24	tRNA	712252	C → T	-
tc0610	excinuclease ABC, subunit A; uvrA	734634	C → T	Ser → Ser
tc0623	protease, Lon family	747850	C → T	Ser → Ser
tc0651	hypothetical protein	778747	C → T	Ser → Phe
-	intergenic	816010	G → A	
tc0694	polymorphic membrane protein B/C family; pmpB/C-1	830732	C → T	Ser → Phe
tc0721	translation elongation factor G; fusA	859591	G → A	Pro → Ser
tc0733	secDF protein, putative	874619	G → A	Pro → Leu
tc0759	hypothetical protein	899994	C → T	Asp → Asp
tc0764	peptide ABC transporter, permease protein	907437	C → A	Val → Val
tc0791	hypothetical protein	934794	C → T	Asp → Asn
tc0823	DNA polymerase III, epsilon subunit	955910	C → T	Gly → Glu
tc0842	branched-chain amino acid transport system carrier protein	976805	C → T	Pro → Leu
tc0843	helicase, Snf2 family	981172	T → G	Ser → Ala
tc0903	folK/P	1046666	G → A	His → Tyr
tc0906	hypothetical protein	1049784	G → A	Ser → Leu
tc0916	hypothetical protein	1067874	C → T	Ala → Val

TABLE S14. SNPs in *C. muridarum guaB* mutant

Gene ID	Description	Nucleotide Position	Nucleotide Change	Amino acid Change
tc0054	penicillin-binding protein	62823	G → A	Gly → Glu
tc0092	hypothetical protein	110539	C → T	Glu → Lys
-	intergenic	126188	C → T	-
tc0125	alanyl-tRNA synthetase; alaS	152652	C → T	Gly → Glu
tc0181	glycogen synthase; glgA	214991	G → A	Ala → Val
tc0191	hypothetical protein	224779	G → A	Gly → Gly
tc0197	polymorphic membrane protein D family; pmpD	233168	G → A	Glu → Lys
tc0228	MesJ/Ycf62 family protein	268437	G → A	Glu → Lys
tc0250	hypothetical protein	292616	C → T	Val → Ile
tc0263	polymorphic membrane protein G family; pmpG-1	312471	G → A	Asp → Asn
tc0285	hypothetical protein	341031	C → T	Ser → Phe
tc0290	hypothetical protein	349120	G → A	Ser → Phe
tc0312	glycosyl hydrolase family protein	369812	G → A	Ser → Phe
tc0319	hypothetical protein	376782	C → T	Ser → Phe
tc0331	RNA polymerase sigma factor, sigma-70 family	392203	C → T	His → His
tc0410	hypothetical protein	471306	C → T	Thr → Thr
tc0415	dipeptidase	475870	C → T	Val → Val
tc0439	adherence factor	536039	G → A	Gly → Asp
tc0443	inosine-5`-monophosphate dehydrogenase	541698	G → A	Gln → STOP
tc0473	peptide ABC transporter, permease protein	573799	C → T	Pro → Leu
tc0504	hypothetical protein	610197	C → T	Pro → Leu
tc0511	recombination protein RecR	617540	C → T	Phe → Phe
tcC0553	NADH:ubiquinone oxidoreductase, subunit E	662309	C → T	Ser → Phe
tc0600	hypothetical protein	717761	G → A	Gln → STOP
tc0610	excinuclease ABC, subunit A; uvrA	732712	G → A	Pro → Pro
tc0676	exoribonuclease, VacB/Rnb family	808732	G → A	Ile → Ile
-	intergenic	866802	G → A	-
tc0777	hypothetical protein	918927	G → A	Gly → Glu
tc0909	hypothetical protein	1052698	C → T	Gly → Gly