

Supplemental Table 4 - Unique mutations identified in sMGAg populations

Time Point	Position	Mutation	sMGAG1	sMGAG2	sMGAG3	sMGAG4	Annotation	Gene	Description
21-days	989,185	C→T				0.248	A80V (GCT→GTT)	<i>DQM59_RS05150</i> →	response regulator transcription factor (<i>ciaR</i>)
	990,017	T→G			0.713		I136S (ATT→AGT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	990,700	G→T		0.060			V364F (GTT→TTT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	867,786	G→T	0.356	0.261	0.158	0.310	L253F (TTG→TTT)	<i>DQM59_RS04495</i> →	ATP phosphoribosyltransferase regulatory subunit
	1,615,368	G→T	0.170				S67I (AGT→ATT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,616,220	G→T	0.257				G351V (GGT→GTT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
42-days	989,185	C→T				0.088	A80V (GCT→GTT)	<i>DQM59_RS05150</i> →	response regulator transcription factor (<i>ciaR</i>)
	990,017	T→G			0.088		I136S (ATT→AGT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	867,786	G→T	0.907	0.947	0.883	0.073	L253F (TTG→TTT)	<i>DQM59_RS04495</i> →	ATP phosphoribosyltransferase regulatory subunit
	1,615,232	G→A		0.869			G22R (GGA→AGA)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,615,349	G→T			0.867		G61C (GGT→TGT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,615,368	G→T	0.887				S67I (AGT→ATT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,615,953	A→G	0.064				Y262C (TAT→TGT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,616,526	T→G				0.578	M453R (ATG→AGG)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
63-days	989,185	C→T				0.495	A80V (GCT→GTT)	<i>DQM59_RS05150</i> →	response regulator transcription factor (<i>ciaR</i>)
	990,017	T→G			1.000		I136S (ATT→AGT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	1,615,368	G→T	0.846				S67I (AGT→ATT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	990,700	G→T		0.906			V364F (GTT→TTT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	867,786	G→T	0.920	0.101			L253F (TTG→TTT)	<i>DQM59_RS04495</i> →	ATP phosphoribosyltransferase regulatory subunit
100-days	989,185	C→T				1.000	A80V (GCT→GTT)	<i>DQM59_RS05150</i> →	response regulator transcription factor (<i>ciaR</i>)
	990017.000	T→G			1.000		I136S (ATT→AGT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	990,700	G→T		1.000			V364F (GTT→TTT)	<i>DQM59_RS05155</i> →	HAMP domain-containing histidine kinase (<i>ciaH</i>)
	1,616,549	A→G				0.153	S461G (AGT→GGT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1,615,368	G→T	0.846				S67I (AGT→ATT)	<i>DQM59_RS08180</i> →	PBP1A family penicillin-binding protein
	1260160.000	G→T			0.214		A260E (GCA→GAA)	<i>gorA</i> ←	glutathione-disulfide reductase
	1260412.000	C→T		1.000			G176D (GGT→GAT)	<i>gorA</i> ←	glutathione-disulfide reductase
	1336077.000	C→T	1.000				intergenic (-28/+102)	<i>ahpC</i> ← / ← <i>DQM59_RS06790</i>	peroxiredoxin/U32 family peptidase
	645,126:1	+A	1.000				intergenic (+197/-110)	<i>DQM59_RS03470</i> → / → <i>laca</i>	DeoR/GlpR transcriptional regulator/galactose-6-phosphate isomerase subunit LacA
	883506.000	G→T		1.000			A327S (GCT→TCT)	<i>DQM59_RS04610</i> →	phosphopyruvate hydratase
	1338612.000	C→A		1.000			E18* (GAA→TAA)	<i>DQM59_RS06795</i> ←	U32 family peptidase
	1977533.000	C→T			0.833		P117S (CCT→TCT)	<i>DQM59_RS10135</i> →	hypothetical protein
	1979894.000	C→T			0.888		Q261* (CAA→TAA)	<i>DQM59_RS10150</i> →	NAD-dependent succinate-semialdehyde dehydrogenase
	850,047:1	+T				0.943	coding (103/678 nt)	<i>DQM59_RS04410</i> →	TVP38/TMEM64 family protein
	850,047:2	+G				1.000	coding (103/678 nt)	<i>DQM59_RS04410</i> →	TVP38/TMEM64 family protein
	850,045	A→T				0.943	Y34F (TAT→TTT)	<i>DQM59_RS04410</i> →	TVP38/TMEM64 family protein
	1,781,472	G→A				0.911	I469I (ATC→ATT)	<i>DQM59_RS09050</i> ←	peptide cleavage/export ABC transporter
	1,962,559:1	+T				1.000	coding (527/1845 nt)	<i>DQM59_RS10040</i> →	APC family permease
	2,000,078	A→C				0.928	L52W (TTG→TGG)	<i>DQM59_RS10245</i> ←	energy-coupling factor transporter ATPase
								<i>DQM59_RS03180</i> → / → <i>DQM59_RS03185</i>	
	580855.000	G→T	0.059				intergenic (+27/-10)	<i>DQM59_RS03185</i> →	cation-transporting P-type ATPase/potassium uptake protein TrkA
	581059.000	Δ1 bp			0.112		coding (195/654 nt)	<i>DQM59_RS03185</i> →	potassium uptake protein TrkA
	581517.000	G→T	0.241				*218L (TGA→TTA)	<i>DQM59_RS03185</i> →	potassium uptake protein TrkA
								<i>DQM59_RS03185</i> → / → <i>DQM59_RS03190</i>	
	581523.000	G→T		0.074			intergenic (+5/-9)	<i>DQM59_RS03190</i> →	potassium uptake protein TrkA/potassium transporter TrkB
	581537.000	+ATT		0.157			coding (6/660 nt)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581538.000	Δ3 bp		0.079			coding (7-9/660 nt)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581565.000	G→T			0.114		G12* (GGA→TGA)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581578.000	C→A	0.086				A16D (GCT→GAT)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581619.000	G→T			0.340		E30* (GAG→TAG)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581688.000	G→A			0.111		G53R (GGG→AGG)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581760.000	G→C		0.081			D77H (GAT→CAT)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	581871.000	G→T		0.069			G114W (GGG→TGG)	<i>DQM59_RS03190</i> →	potassium transporter TrkB
	582156.000	C→T	0.223				Q209* (CAA→TAA)	<i>DQM59_RS03190</i> →	potassium transporter TrkB