

**A mutation in the methionine aminopeptidase gene provides phage resistance in  
*Streptococcus thermophilus***

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**Table S1. List of primers**

Primer	Sequence 5'-3'	Function	Ref
SJL128	TCAATCTACTCAAGGTATGAATCA	Natural transformation of <i>metAP</i>	This study
SJL130	GTCAGTAGTAGTGGTCAAGA	Natural transformation of <i>metAP</i>	This study
SJL150	AGTCCTGATAGGT CGCATT	Detection of the mutation in <i>metAP</i>	This study
SJL151	GAGTTGGACCAACAATGCAG	Detection of the mutation in <i>metAP</i>	This study
SJL154	<u>CAGCAGCGGCCTGGTGCCGCGCGCAGCCAATGAT</u> TACACTGAAATCAGCACGTG	Cloning <i>metAP</i> in pNZ123	This study
SJL155	<u>GCCGGATCTCAGTGGTGGTGGTGGTGGCTTAATAA</u> GTTCTTCTCCCCTTGAG	Cloning <i>metAP</i> in pNZ123	This study
SJL160	<u>ATTACAGCTCCAGATCCAGTACTGAATTCTTGAGCCT</u> GCTATGATTGACTCTGCA	Cloning the mutated <i>S. mutans metAP</i> in pNZ123	This study
SJL161	ATTGGGTTCTTCCTGCATGGTTGG	Cloning the mutated <i>S. mutans metAP</i> in pNZ123	This study
SJL162	CCAACCATGCAGGAAGAACCAAAT	Cloning the mutated <i>S. mutans metAP</i> in pNZ123	This study
SJL163	<u>GAAAATATGCACTCGAGAAGCTTGAGCTCTCCGAAG</u> GTGGACAAACATAATAGC	Cloning the mutated <i>S. mutans metAP</i> in pNZ123	This study
CM_145	<u>GAATTCGAATTCAAAGGCTGTTGTGACAGCAA</u>	Cloning the <i>S. mutans metAP</i> in pNZ123	This study
CM_146	<u>CTCGAGCTCGAGTTAATAAGTCCCTTGTGACACC</u>	Cloning the <i>S. mutans metAP</i> in pNZ123	This study
CR1-fwd	TGCTGAGACAACCTAGTCTCTC	CR1 locus screening	32
CR1-revLong	TAAACAGAGCCTCCCTATCC	CR1 locus screening	32
CR3-fwd	CTGAGATTAATAGT GCGATTACG	CR3 locus screening	32
CR3-rev	GCTGGATATT CGTATAACATGTC	CR3 locus screening	32

Underlined nucleotides correspond to either restriction sites or part of the primer sequence complementary to the cloning vector.

Table S2. Analysis of the post-translational processing of the N-terminal methionine

Group	Accession Number	Putative function	TIGR Link	Role	SubRole	
A	DGCC7796_0001	DNA polymerase III beta subunit	TIGR0063	132 DNA metabolism	Degradation of DNA	DCLC7796 + D490
A	DGCC7796_0112	CGG139 protein in cluster with ribosomal protein L32p	TIGR0092	157 Unknown function	Conserved	DGCC7796,MetGp+H206Q +
A	DGCC7796_0406	1-phosphofructokinase				DGCC7796 + H206Q +
A	DGCC7796_0563	Mercuro ion reductase				DGCC7796 + M5876
A	DGCC7796_0581	Threonyl-tRNA synthetase	TIGR00745	83 Biosynthesis of cofactors, prosthetic groups, and carriers	Molybdopterin	DGCC7796 + D490
A	DGCC7796_0620	Catalytic contrahelix protein A	TIGR00115	95 Protein fate	Toxin production and resistance	DGCC7796 + D490
A	DGCC7796_0702	2-haloalkanolic acid dehalogenase				DGCC7796 + D490
A	DGCC7796_1159	LSU ribosomal protein L19p	TIGR01979	76 Biosynthesis of cofactors, prosthetic groups, and carriers	Serine family	DGCC7796 + D490
A	DGCC7796_11757	FIG13747B: Hypothetical protein Yglj				DGCC7796 + D490
A	DGCC7796_1250	Phenylalanyl-tRNA synthetase alpha chain				DGCC7796 + D490
A	DGCC7796_1295	Threonyl-tRNA synthetase				DGCC7796 + D490
A	DGCC7796_1361	Oxidoreductase of aldo/keto reductase family, subgroup 1				DGCC7796 + D490
A	DGCC7796_1424					DGCC7796 + D490
A	DGCC7796_1857	Thioredoxin reductase				DGCC7796 + D490
A	DGCC7796_1941	Surfact-5-phosphate hydrolase (EC 3.2.1.83)	TIGR00040	703 Unknown function	Conjugation	DGCC7796 + D490
A	DGCC7796_1957	Single-stranded DNA-binding protein	TIGR00232	117 Energy metabolism	Glycolysis/gluconeogenesis	DGCC7796 + D490
A	DGCC7796_1961	Pyrrole-5-carboxylate reductase				DGCC7796 + D490
A	DGCC7796_1980	Tyrosyl-tRNA synthetase				DGCC7796 + D490
A	DGCC7796_1995	Hypothetical protein ywlG				DGCC7796 + D490
A	DGCC7796_2192	Hypothetical protein	TIGR01136	75 Amino acid biosynthesis	Pyruvate family	DGCC7796 + D490
A	DGCC7796_2193					DGCC7796 + D490
A	DGCC7796_2196	Preprotein translocase secY subunit	TIGR03168			DGCC7796 + D490
A	DGCC7796_2046	ABC transporter ATP-binding protein upu				DGCC7796 + D490
A	DGCC7796_2082					DGCC7796 + D490
A	MS876_0033		TIGR00061	158 Protein synthesis	General	
A	MS876_0036		TIGR00496	169 Protein synthesis	tRNA and rRNA base modification	
A	DGCC7796_1173	GTP-binding and nucleic acid-binding protein YchF				
B	DGCC7796_0004		TIGR00962	111 Energy metabolism	Anaerobic	
B	DGCC7796_0072	2-dehydrodantoate 2-reductase	TIGR01216	111 Energy metabolism	Anaerobic	
B	DGCC7796_0093					
B	DGCC7796_0117					
B	DGCC7796_0129	Cell division trigger factor	TIGR00855	158 Protein synthesis	General	
B	DGCC7796_0229	Aminopeptidase C	TIGR01891	138 Protein fate	tRNA aminoylation	
B	DGCC7796_0242		TIGR01373	89 Cell envelope	Other	
B	DGCC7796_0367	Cysteine synthase	TIGR00418	137 Protein synthesis	Other	
B	DGCC7796_0371		TIGR01223	74 Amino acid biosynthesis	Glutamate family	
B	DGCC7796_0392					
B	DGCC7796_0460					
B	DGCC7796_0481					
B	DGCC7796_0486	ATP synthase alpha chain	TIGR01481	261 Regulatory functions	Chlorophyll and bacteriochlorophyll	
B	DGCC7796_0489	ATP synthase epsilon chain	TIGR01060	116 Energy metabolism	Fermentation	
B	DGCC7796_0539	Alpha subunit of ribosomal protein L7/L12 (P1/P2)	TIGR01549	137 Protein synthesis	Other	
B	DGCC7796_0646	Endopeptidase	TIGR00055	703 Unknown function	Conjugation	
B	DGCC7796_0747	Cell division protein FtsZ	TIGR01344	93 Cellular processes	Other	
B	DGCC7796_0752	Cell division initiation protein DivIVa				
B	DGCC7796_0837	Tripeptidyl aminopeptidase				
B	DGCC7796_0982	Orotate phos-phorusfranose transferase	TIGR00836	140 Protein fate	Degradation of proteins, peptides, and glycopeptides	
B	DGCC7796_1299	Alphaketoglutarate dehydrogenase	TIGR00892	139 Protein fate	tRNA amidinotranscarbamylase	
B	DGCC7796_1359	Uridyl diphosphate kinase	TIGR01886	138 Protein fate	tRNA amidylation	
B	DGCC7796_1399	UDP glucose 4-epimerase	TIGR01549	703 Unknown function	Pyrimidine ribonucleotide biosynthesis	
B	DGCC7796_1624	Nicotinate-nucleotide adenylyltransferase	TIGR01007	127 Purines, pyrimidines, nucleosides, and nucleotides		
B	DGCC7796_1782	Glutamine synthetase type I	TIGR00836	140 Protein fate		
B	DGCC7796_1797	SSU ribosomal protein S12p (S23e)	TIGR02093	105 Energy metabolism	Polyamine biosynthesis	
B	DGCC7796_1881	Ketol-acid reducto-isomerase	TIGR00972	143 Transport and binding proteins	Amino acids, peptides and amines	
B	DGCC7796_1940		TIGR00336	126 Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis	
B	DGCC7796_1941		TIGR01870	719		
B	DGCC7796_1944	SSU ribosomal protein S8p (S15A)e				
B	DGCC7796_0921 (+)					
B	DGCC7796_1890					
B	DGCC7796_1987					
C	DGCC7796_2201		TIGR00884	125 Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	
C	DGCC7796_2527	phosphotriesterase	TIGR00866	157 Unknown function	Conserved	
C	DGCC7796_2586	Transketolase	TIGR01135	89 Cell envelope	Other	
C	DGCC7796_0331					
C	DGCC7796_0409	FIGG115503: hypothetical protein				
C	DGCC7796_0602	Branched-chain amino acid aminotransferase	TIGR01024	158 Protein synthesis	General	
C	DGCC7796_0759	3'-to-5' oligoribonuclease 3'	TIGR02651	166 Transcription	Transcription factors	
C	DGCC7796_0848	Acetylcoenzyme A/acetyl-CoA acetyltransferase/Succinyl-diaminopimelate desuccinylase	TIGR00486	157 Unknown function	Conserved	
C	DGCC7796_0941	Maltodextrin phosphorylase				
C	DGCC7796_1064	Cystathione beta-lyase	TIGR00468	137 Protein synthesis	Other	
C	DGCC7796_1214	Glutathione biosynthesis bifunctional protein gshF	TIGR01296	71 Amino acid biosynthesis	Other	
C	DGCC7796_1410	Phosphoserine aminotransferase				
C	DGCC7796_1525	Universal stress protein family				
C	DGCC7796_1643	Gamma-glutamyl phosphate reductase	TIGR01179	119 Energy metabolism	Pyruvate dehydrogenase	
C	DGCC7796_1714	Alkaline shock protein	TIGR01435	86 Biosynthesis of cofactors, prosthetic groups, and carriers	Riboflavin, FMN, and FAD	
C	DGCC7796_1831	Alkaline shock protein				
C	DGCC7796_1839	Alkaline shock protein				
C	DGCC7796_1964	Adenylosuccinate synthetase	TIGR01214	90 Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	
C	DGCC7796_2024		TIGR01364	75 Amino acid biosynthesis	Pyruvate family	
C	DGCC7796_0760					
D	DGCC7796_0699	LysM-1 RNA synthetase (class II)	TIGR00125			
D	DGCC7796_1476	Carboxy anhydrase	TIGR0292	112 Energy metabolism	ATP-proton motive force interconversion	
D	DGCC7796_1505	DNA-directed RNA polymerase delta subunit	TIGR00407	137 Amino acid biosynthesis	Aspartate family	
D	DGCC7796_0130	DNA-directed RNA polymerase delta subunit	TIGR01322	105 Energy metabolism	Polyamine biosynthesis	
D	DGCC7796_0155	Amino acid transport ATP-binding protein				
D	DGCC7796_0162	Cysteine desulfurase, SufS subfamily	TIGR00621	132 DNA metabolism	Degradation of DNA	
D	DGCC7796_0202		TIGR00635	73 Amino acid biosynthesis	Aspartate family	
D	DGCC7796_0236					
D	DGCC7796_0300	Methionine ABC transporter permease protein	TIGR00581	158 Protein synthesis	General	
D	DGCC7796_0417	LSU ribosomal protein L21p				
D	DGCC7796_0440	Ribosome recycling factor				
D	DGCC7796_1337	Adenylyl kinase	TIGR00292	112 Energy metabolism		
D	DGCC7796_0130	DNA-directed RNA polymerase delta subunit	TIGR00407	137 Amino acid biosynthesis		
D	DGCC7796_0155	Amino acid transport ATP-binding protein	TIGR01322	105 Energy metabolism		
D	DGCC7796_0202	Cysteine desulfurase, SufS subfamily				
D	DGCC7796_0236					
D	DGCC7796_0300					
D	DGCC7796_0417					
D	DGCC7796_0440					
D	DGCC7796_0541	LSU ribosomal protein L19p (P0)				
D	DGCC7796_0560	Aminocycline/N-acyl-L-amino acid amidohydrolase/hippurate hydrolase	TIGR00112	73 Amino acid biosynthesis	Aspartate family	
D	DGCC7796_0570	Glucosamine-1-phosphate N-acetyltransferase	TIGR00234	137 Protein synthesis	Other	
D	DGCC7796_0674	Protein-(N)-glutamine methyltransferase PrmC	TIGR00440	156 Hypothetical proteins	Glutamate family	
D	DGCC7796_0681	Purine nucleotide phosphorylase	TIGR00465	74 Amino acid biosynthesis	Transposon functions	
D	DGCC7796_0921	Dihydrofolate acetyltransferase	TIGR00322	116 Energy metabolism		
D	DGCC7796_0948	Phosphate transport ATP-binding protein PstB	TIGR00167	70 Amino acid biosynthesis		
D	DGCC7796_0988	CRISPR-associated protein, Csm2 family	TIGR01351	124 Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism	
D	DGCC7796_1002	Fibronectin/fibrillin-binding protein				
D	DGCC7796_1032	FG0119309: hypothetical protein				
D	DGCC7796_1037					
D	DGCC7796_1063	mannose-containing polysaccharide translocation permease				
D	DGCC7796_1535	Putrescine transport ATP-binding protein PotA	TIGR00184	125 Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	
D	DGCC7796_1794					
D	DGCC7796_1917	hypothetical protein				
D	DGCC7796_1925	Fructose-bisphosphate aldolase class II				
D	DGCC7796_1942					
D	DGCC7796_1947					
D	DGCC7796_1953					
D	DGCC7796_1955					
D	DGCC7796_0031					
D	DGCC7796_0095					
D	DGCC7796_0330					
D	DGCC7796_0389					
D	DGCC7796_0636					
D	DGCC7796_0649					
D	DGCC7796_1461					
D	MS876_0027					

**Y** : processed

**N** : not processed  
Groups A-D refer to

Groups A-D refer to the classification of Figure 4.

**Figure S1. Frequency of the BIMs naturally transformed A) without DNA, B) with MetAP<sup>H206Q</sup> or C) with a MetAP obtain following an error prone PCR.**

