

**SupplementalTable S3.** Primers used for site-directed mutagenesis.

<i>GENE</i> ;	Mutation	Primer	Primer sequence <sup>a</sup>	Original Codon	Confirmation primer (5'-3') <sup>b</sup>
<i>ALT1</i>	K412A	alt1-K412A	CTTTGCATTCGACTTCTgctGGTGTTCCTGGTGAATG	AAG	ATCCAGGTAATCCTACAGGAGC
<i>ALT1</i>	K412N	alt1-K412N	CTTTGCATTCGACTTCTaatGGTGTTCCTGGTGAATG	AAG	ATCCAGGTAATCCTACAGGAGC
<i>ARG3</i>	C289A	arg3-C289A	ACTACAAATTTATGCATgctCTGCCAAGACATCAAGAAG	TGT	CGGTGCGACATTTGAATTAACACACG
<i>ARG3</i>	C289M	arg3-C289M	ACTACAAATTTATGCATatgCTGCCAAGACATCAAGAAG	TGT	CGGTGCGACATTTGAATTAACACACG
<i>ARG3</i>	H145A	arg3-H145A	CTATGTGACAAATTCgctCCTTTGCAAGCAATTTGTGATC	CAC	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>
<i>ARG3</i>	H145N	arg3-H145N	CTATGTGACAAATTCaatCCTTTGCAAGCAATTTGTGATC	CAC	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>
<i>ARG4</i>	H162A	arg4-H162A	TTAATGCCAGGCTACACAgctTTACAAAGGGCACAACCTA	CAT	CGTCATCCAAACGACGAGGATATCC
<i>ARG4</i>	H162N	arg4-H162N	TTAATGCCAGGCTACACAaacTTACAAAGGGCACAACCTA	CAT	CGTCATCCAAACGACGAGGATATCC
<i>ARO3</i>	H281A	aro3-H281A	ATTATGATCGATTGTTCCgccGGCAACAGTAATAAAGATT	CAC	CATCGACGCTATGAGAGC
<i>ARO3</i>	H281N	aro3-H281N	ATTATGATCGATTGTTCCaatGGCAACAGTAATAAAGATT	CAC	CATCGACGCTATGAGAGC
<i>ARO4</i>	H282A	aro4-H282A	TCTAATGATTGACTACTCTgcccGGTAACTCCAATAAGGAT	CAC	GCTGTGGATGCTTGTCAAGC
<i>ARO4</i>	H282N	aro4-H282N	TCTAATGATTGACTACTCTaatGGTAACTCCAATAAGGAT	CAC	GCTGTGGATGCTTGTCAAGC
<i>ARO7</i>	E246A	aro7_E246A	ATACCTATCACTAAGGAAGTTgcaGTGGAATACTTGCTAAG AAGGT	GAG	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>
<i>ARO7</i>	E246S	aro7-E246S	CCTATCACTAAGGAAGTTtctGTGGAATACTTGCTAAGA	GAG	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>
<i>ASN1</i>	C2A	asn1-C2A	GGACGTAACCTTAAGATGgcccGGTATTTTCGCCGCTTTCAG	TGT	TAGATTTCCCGTTAACACATAGCA
<i>ASN1</i>	C2M	asn1-C2M	GGACGTAACCTTAAGATGatgGGTATTTTCGCCGCTTTCAG	TGT	TAGATTTCCCGTTAACACATAGCA
<i>ASN2</i>	C2A	asn2-C2A	CTACAATACAATATGgcccGGTATCTTTGCAGCCTTCAAGC	TGT	TGCAGGAATGGTCTACATTTTCTAT <sup>(F)</sup>
<i>ASN2</i>	C2M	asn2-C2M	CTACAATACAATATGatgGGTATCTTTGCAGCCTTCAAGC	TGT	TGCAGGAATGGTCTACATTTTCTAT <sup>(F)</sup>
<i>BAT2</i>	K202H	bat2-K202H	GAGGCTGTGGTGACAAGcatCTAGGTGCAAACACTACGC	AAA	GAGTTGATTACCCTAATTGGGAAACTG
<i>BAT2</i>	K202M	bat2-K202M	GAGGCTGTGGTGACAAGatgCTAGGTGCAAACACTACGC	AAA	GAGTTGATTACCCTAATTGGGAAACTG
<i>HOM2</i>	C156A	hom2-C156A	CATTATCTGTATTTCCAATgcccTCCACTGCAGGTTTGGTTG CACC	TGT	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>
<i>HOM2</i>	C156M	hom2-C156M	CATTATCTGTATTTCCAATatgTCCACTGCAGGTTTGGTTG CACC	TGT	ATGTTACTTACCACATCACGATAGGTC <sup>(P)</sup>

<i>HOM2</i>	S41A	hom2-S41A	TTGGTGCCTCTTCTAGAgctGCTGGCAAGAAATACGT	TCA	CAGATCCAAATATCACCGGCAGC
<i>HOM2</i>	S41G	hom2-S41G	TTGGTGCCTCTTCTAGAggtGCTGGCAAGAAATACGT	TCA	CAGATCCAAATATCACCGGCAGC
<i>HOM6</i>	K223A	hom6-K223A	GGTTGGATGTTGCTAGA gctGTTACCATTGTTGGTAG	AAG	CTTATTTTCAGTGGCAGCTTC
<i>HOM6</i>	K223V	hom6-K223N	GGTTGGATGTTGCTAGAgtgGTTACCATTGTTGGTAG	AAG	CTTATTTTCAGTGGCAGCTTC
<i>ILV1</i>	K109A	ilv1-K109A	ATTGCCTGTTTTCTCTTTcgtCTTCGTGGTGCCTATAAC	AAG	GACTTGAGACCCTAATCTCG
<i>ILV1</i>	K109N	ilv1-K109N	ATTGCCTGTTTTCTCTTTCaacCTTCGTGGTGCCTATAAC	AAG	GACTTGAGACCCTAATCTCG
<i>ILV2</i>	E139A	ilv2-E139A	CTTCGTTCTTCCAAAACAgctCAAGGTGCCGGTCACATG	GAA	CCAGAGCCTGCTCCAAGTTTCAATG
<i>ILV2</i>	E139S	ilv2-E139S	CTTCGTTCTTCCAAAACActctCAAGGTGCCGGTCACATG	GAA	CCAGAGCCTGCTCCAAGTTTCAATG
<i>MET2</i>	S168A	met2-S168A	TATGGGGGGATGCTGgctTTGGAATGGGCTGCCA	AGT	GGGTAACGACTTAGCATTCGACC
<i>MET2</i>	S168T	met2-S168T	TATGGGGGGATGCTGactTTGGAATGGGCTGCCA	AGT	GGGTAACGACTTAGCATTCGACC
<i>MET2</i>	H430A	met2-H430A	GAATCTCCGAAGGCgccGATGCCTTCCTATTGGAG	CAC	ATGTTACTTACCACATCAGATAGGTC <sup>(P)</sup>
<i>MET2</i>	H430N	met2-H430N	GAATCTCCGAAGGCaatGATGCCTTCCTATTGGAG	CAC	ATGTTACTTACCACATCAGATAGGTC <sup>(P)</sup>
<i>THR4</i>	K124A	thr4-K124A	GTCCTACCTACGCTTTcgtGACGTTGCTTTACAATTG	AAA	GGTCAAAGCTCTCCTTCCAAGACT
<i>THR4</i>	K124N	thr4-K124N	GTCCTACCTACGCTTTCaacGACGTTGCTTTACAATTG	AAA	GGTCAAAGCTCTCCTTCCAAGACT
<i>TKL1</i>	E418A	tkl1-E418A	CATTAGGTACGGTATTAGAgctCACGCTATGGGTGCCAT	GAA	GGAATCTAAGTTGCCAACTTACACC
<i>TKL1</i>	E418S	tkl1-E418S	CATTAGGTACGGTATTAGAgctCACGCTATGGGTGCCAT	GAA	GGAATCTAAGTTGCCAACTTACACC
<i>TKL2</i>	E418A	tkl2-E418A	TTAGATACGGTGTGAGGgctCACGGAATGGGTGCCA	GAA	GGAAAAGCATTTACCGAAGTTTACTCC
<i>TKL2</i>	E418S	tkl2-E418S	TTAGATACGGTGTGAGGagtCACGGAATGGGTGCCA	GAA	GGAAAAGCATTTACCGAAGTTTACTCC
<i>TRP1</i>	C17A	trp1-C17A	GTCCATTGGTGAAAGTTgccGGCTTGACAGACACAG	TGC	GCTTGTCACCTTACGTACAATCTTG
<i>TRP1</i>	C17M	trp1-C17M	GTCCATTGGTGAAAGTTatgGGCTTGACAGACACAG	TGC	GCTTGTCACCTTACGTACAATCTTG

<sup>a</sup> Primer used to insert direct-mutation in catalytic mutants. Sequence shown is of the forward primer; the reverse primers were the reverse complement of the sequence shown. Replaced codons are shown in lowercase.

<sup>b</sup> Confirmation primers used to verify the insertion of site-mutation into the plasmids by sequencing. Most primers amplify in reverse orientation from within the *GENE* ORF; exceptions are forward primers (F) and primers that amplify from the plasmid backbone (P).