

## Fig S3. Nucleotide sequence alignments suggesting recombination in the past

### Table of contents

#### **(A). Alignment suggesting recombination between MahEastAsia2 and undetected *Mycobacterium* lineage: the 53 kb region**

**(i)** Alignment for the *pntB* side of the 53.8-kb highly diverged region (4,758,973 to 4,812,752 in TH135 coordinate) in the MahEastAsia2 strains and three MahEastAsia1 strains is shown. The differentiated region in the three MahEastAsia1 strains, possibly imported from MahEastAsia2, are underlined. The border of the import in the tree MahEastAsia1 strains is unclear due to the absence of lineage-specific polymorphic sites around this region. **(ii)** Alignment for the MAH\_4513 side of the highly-diverged region.

#### **(B). Alignment of East Asia-type alleles in the *treS-maK* operon.**

**(i)** TreS. A nucleotide that differentiate East Asian alleles from *M. avium*-type alleles is indicated by blue or red background color. A nucleotide position that differentiate EA2-subtype from EA1-subtype were indicated by asterisk. Substitutions that affect product sequence are indicated by amino-acid sequence change below the alignment. The EA1-subtype contains a fragment possibly originating from *M. avium*-type allele. The possible import (216 bp) is underlined. Crossover regions are indicated by grey background. **(ii)** MalK. **(iii)** Membrane protein. Substitutions in the membrane-protein coding region does not affect product sequence.

#### **(C). Alignment suggesting recombination between MahEastAsia1 and SC2: the *treS-maK* operon**

The differentiated region containing the *treS-maK* operon in the genomes of MahEastAsia1. The 5,080 bp long diverged region was underlined. SNPs unique to the SC2 group are shown in green background, whereas SNPs unique to the MahEastAsia1 group is shown in red background. Alignment was generated using MAFFT software for 19,500 bp region spanning from MAV\_RS24815 (no original locus\_tag given) to MAV\_RS24905 (original locus\_tag: MAV\_5190). Alignment position on the sides indicate base position in the original alignment.

#### **(D). Alignment suggesting recombination between MahEastAsia1 and MahEastAsia2: the *treS-maK* operon**

An imported fragment containing the *treS-maK* operon in strain OCU404. SNPs derived from MahEastAsia1, and MahEastAsia1 were indicated by blue and red background colors, respectively. Possible crossover regions were indicated by grey background color. Alignment was generated using MAFFT software for 11,547 bp region spanning from *fbpC* to *sauT*. Alignment position on the sides indicate base position in the original alignment. Note that in strains 2344, OCU404, CAM57, DNA genomic regions around this region showed similarity to strains in MahEastAsia2, despite their overall chromosome similarity to strains in MahEastAsia1. Predicted length of the import in OCU404 (underlined) was 5,798 bp.

#### **(E). Alignment suggesting recombination between MahEastAsia1 and MahEastAsia2: MCE operon locus 3.**

**(i)** Left border of recent import predicted by fastGEAR. An alignment for 5,281 bp from *mmsB* to MAH\_0777-euivalent gene is shown. Crossover region is indicated by grey background. Imported region in OCU464 is underlined. **(ii)** Right border of recent import. An alignment for 1,159 bp from *pdC* (MAH\_0823) to MAH\_0824-equivalent gene is shown.

**Fig S3. A - i.**

TH135 coordinate 4,758,345

Alignment pos. .  
EA2\_HP17 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA2\_TH135 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA2\_OCU462 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA2\_5581 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA2\_P7 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA2\_S2 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_2344 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_OCU404 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_CAM57 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_CAM78 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_OCU466 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_CAM177 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690  
EA1\_OCU464 : 20601 acagcgacacccccgccgctgccgggatggggcgtgcagaccgatcaccaccgcggcgccacggcgccggccagcagcagcaggttgatcg 20690

TH135 coordinate 4,758,465

Alignment pos. .  
EA2\_HP17 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggcgggtcatcttggtca 20960  
EA2\_TH135 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA2\_OCU462 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA2\_5581 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA2\_P7 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA2\_S2 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_2344 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_OCU404 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_CAM57 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_CAM78 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_OCU466 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_CAM177 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960  
EA1\_OCU464 : 20691 gctgctgggccttgccgaagccgatcggggcgccggagatgatctcctgc (191 bp) ccagctgcgccatggccgtcatcttggtgt 20960

Fig S3. A-(i) continued

TH135 coordinate 4,758,735

Alignment pos.

```
EA2_HP17_ : 20961 ggcgggccgggtggcagccgagcaccgacgcccaccgaccaggccggcgatgatcagcaccaccgactcgggtgtgccggatcttgatcagcg 21050
EA2_TH135_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA2_OCU462 : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA2_5581_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA2_P7_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA2_S2_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_2344_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_OCU404 : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_CAM57_ : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_CAM78_ : 20961 agcgggcccggcgggacgccgagcaccacgccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_OCU466 : 20961 agcgggcccggcgggacgccgagcaccacaccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_CAM177 : 20961 agcgggcccggcgggacgccgagcaccacgccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
EA1_OCU464 : 20961 agcgggcccggcgggacgccgagcaccacgccaccaccaggccggcgatgatcagcaccaccattggtcgggtgtggcgaatcttgatcagcg 21050
pntB(<-) -ArgAlaProProValGlyLeuValValGlyValValLeuGlyAlaIleIleLeuValTrpGlnAspThrHisArgIleLysIleLeuThr
```

TH135 coordinate 4,758,825

Alignment pos.

```
EA2_HP17_ : 21051 tcgcccggcaccggcgagggccatgccgacggccggcgatcaggttccccggcaccggcgggtcttgggcccgggtgaggcccatcaaggccgtaga 21140
EA2_TH135_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA2_OCU462 : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA2_5581_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA2_P7_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA2_S2_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_2344_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_OCU404 : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_CAM57_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_CAM78_ : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_OCU466 : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_CAM177 : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
EA1_OCU464 : 21051 tcgcccggcaccggcgatggccatgcccaccggcgatcaggttgcccgcgaccggcgtcttgggcccgggtcagcccatcaggccgtaga 21140
pntB(<-) -AlaAlaValAlaIleAlaMetGlyValAlaAlaIleLeuAsnGlyArgValAlaThrLysProGlyThrLeuGlyMetLeuGlyTyrIle
in TH135
```

Fig S3. A-(i) continued

TH135 coordinate 4,758,914

Alignment pos.

```
.
EA2_HP17_ : 21141 atgaagagggcgaaacgagatgatgtagaggacggtagcagaggtagttcatttggccgcc-----agatcttccgtcttgacgggcacg 21230
EA2_TH135_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA2_OCU462 : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA2_5581_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA2_P7_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA2_S2_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA1_2344_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA1_OCU404 : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA1_CAM57_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgcc-----tcgtcagccttggcggg---- 21230
EA1_CAM78_ : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgccgcctcttgtgttcggcttcgccggg---- 21230
EA1_OCU466 : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgccgcctcttgtgttcggcttcgccggg---- 21230
EA1_CAM177 : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgccgcctcttgtgttcggcttcgccggg---- 21230
EA1_OCU464 : 21141 atgaacagcgcgaaggaacgatgtagaggccgatcaccaagtagttcatttggccgccgcctcttgtgttcggcttcgccggg---- 21230
pntB(<-)      IlePheLeuAlaPheSerValIleTyrLeuGlyIleValLeuTyrAsnMet
pntA(<-)      *LysAlaAla-          GluAspAlaLysAlaPro
```

TH135 coordinate 4,758,900

Alignment pos.

```
.
EA2_HP17_ : 21231 ctttcttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA2_TH135_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA2_OCU462 : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA2_5581_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA2_P7_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA2_S2_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_2344_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_OCU404 : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_CAM57_ : 21231 ----tttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_CAM78_ : 21231 --ctcttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_OCU466 : 21231 --ctcttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_CAM177 : 21231 --ctcttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
EA1_OCU464 : 21231 --ctcttcttgccttgaacatgccagcatccggtcggtgacgatgaaccgcgcatgacgttcagggttccgaacaccaccgcgacga 21320
pntA(<-)      LysLysSerLysPheMetGlyLeuMetArgAspThrValIlePheGlyGlyIleValAsnLeuThrGlyPheValValAlaValPhe
```

Fig S3. A-(i) continued



TH135 coordinate 4,759,256

Alignment pos. .

```
EA2_HP17_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA2_TH135_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA2_OCU462 : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA2_5581_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA2_P7_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA2_S2_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA1_2344_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA1_OCU404 : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA1_CAM57_ : 21681 tggccaatagctcgtcgtacatgtagtcctctcctaccgggtcactgggcccgggtcacgcacgccgccgcgacgacctcgtcgtcgaag 21770
EA1_CAM78_ : 21681 tggccaacagttcgtcgtacatctatgcactct-----cccggtcacacacgccgccgcacgacctcgtcgtcgaag 21770
EA1_OCU466 : 21681 tggccaacagttcgtcgtacatctatgcactct-----cccggtcacacacgccgccgcacgacctcgtcgtcgaag 21770
EA1_CAM177 : 21681 tggccaacagttcgtcgtacatctatgcactct-----cccggtcacacacgccgccgcacgacctcgtcgtcgaag 21770
EA1_OCU464 : 21681 tggccaacagttcgtcgtacatctatgcactct-----cccggtcacacacgccgccgcacgacctcgtcgtcgaag 21770
pntA(<-) -AlaLeuLeuGluAspTyrMet
pntAA(<-) *GlnAlaArgThrValCysAlaAlaAlaValVal
```

Fig. S3 A – ii.

TH135 coordinate 4,811,022

Alignment pos. .

```
EA2_HP17_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA2_TH135_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA2_OCU462 : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA2_5581_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA2_P7_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA2_S2_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA1_2344_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA1_OCU404 : 7371 CGGGCGGCGCAAAACCACTCTGGTCGAAAGCGCTGCTGgtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA1_CAM57_ : 7371 cgggtgccggcaagaccaccctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA1_CAM78_ : 7371 cgggcggcggcaaaaccactctggtcgaaggcgtgctggtgcgccggcgggggtcctgaccagagcgggttcggtcaccgacggcagcagcgg 7460
EA1_OCU466 : 7371 cgggcggcggcaaaaccactctggtcgaaggcgtgctggtgcgccggcgggggtgtgaccgcccgggttcggtcggcgcagcagcagcgg 7460
EA1_CAM177 : 7371 cgggcggcggcaaaaccactctggtcgaaggcgtgctggtgcgccggcgggggtgtgaccgcccgggttcggtcggcgcagcagcagcgg 7460
EA1_OCU464 : 7371 cgggcggcggcaaaaccactctggtcgaaggcgtgctggtgcgccggcgggggtgtgaccgcccgggttcggtcggcgcagcagcagcgg 7460
MAH_4514 (->) SerGlyAlaGlyLysThrThrLeuValGluAlaLeuValAlaGlyGlyValLeuThrArgAlaGlySerValThrAspGlySerThr-
```

Fig S3. A-(ii) continued

TH135 coordinate 4,811,112

Alignment pos.

```
.
EA2_HP17_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA2_TH135_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA2_OCU462 : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA2_5581_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA2_P7_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA2_S2_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_2344_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_OCU404 : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_CAM57_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_CAM78_ : 7461 tatgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_OCU466 : 7461 tctgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_CAM177 : 7461 tctgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
EA1_OCU464 : 7461 tctgcgactacgacgagccgagatccgccaacagcgggtccgtcggcctcgccgtcgcgtccttggcgcacgacggcatcaagatcaacc 7550
MAH_4514 (->) ValCysAspTyrAspGluAlaGluIleArgGlnGlnArgSerValGLyLeuAlaValAlaSerLeuAlaHisAspGlyIleLysIleAsn-
```

TH135 coordinate 4,811,202

Alignment pos.

```
.
EA2_HP17_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA2_TH135_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA2_OCU462 : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA2_5581_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA2_P7_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA2_S2_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_2344_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_OCU404 : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_CAM57_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_CAM78_ : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_OCU466 : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_CAM177 : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
EA1_OCU464 : 7551 tggtagacacgcccgggtacgcccgatctcgtcggtagctgcgccggcctgcccgcgcggactgcccgttggttcgtgatcgccgcca 7640
MAH_4514 (->) LeuValAspThrProGlyTyrAlaAspPheValGlyGluLeuArgAlaGlyLeuArgAlaAlaAspCysAlaLeuPheValIleAlaAla-
```

Fig S3. A-(ii) continued

TH135 coordinate 4,812,692

```
Alignment pos.
EA2_HP17_ : 9041 gacattcgcgctcacctgctcgcacggcaaggccacacgctcgactcgtcggacttcggttccagatggcggggcgcgctggcgctgcgg 9130
EA2_TH135_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA2_OCU462 : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA2_5581_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA2_P7_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA2_S2_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA1_2344_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA1_OCU404 : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA1_CAM57_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA1_CAM78_ : 9041 gacatccgggtcacgctgctcgcacggcaaggccacacgctcgactcctcggatttcgctttccagatggcggggcgcgctggcgctgcgg 9130
EA1_OCU466 : 9041 gacattcgcgctcacctgctcgcacggcaaggccacacgctcgactcgtcggacttcggttccagatggcggggcgcgctggcgctgcgg 9130
EA1_CAM177 : 9041 gacattcgcgctcacctgctcgcacggcaaggccacacgctcgactcgtcggacttcggttccagatggcggggcgcgctggcgctgcgg 9130
EA1_OCU464 : 9041 gacattcgcgctcacctgctcgcacggcaaggccacacgctcgactcgtcggacttcggttccagatggcggggcgcgctggcgctgcgg 9130
MAH_4514 (->) AspIleArgValThrLeuLeuAspGlyLysAlaHisSerValAspSerSerAspPheAlaPheGlnMetAlaGlyAlaLeuAlaLeuArg
```

TH135 coordinate 4,759,256

```
Alignment pos.
EA2_HP17_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA2_TH135_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA2_OCU462 : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA2_5581_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA2_P7_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA2_S2_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_2344_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_OCU404 : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_CAM57_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_CAM78_ : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_OCU466 : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_CAM177 : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
EA1_OCU464 : 9131 gaggcgccgcgccaccaaggtggtggtgctcgcagcccatcgacgagatctcgggtgctggtgcccgcagatttcgctcgggtgcggtgatg 9220
MAH_4514 (->) GluAlaAlaAlaAlaThrLysValValLeuLeuGluProIleAspGluIleSerValLeuValProAspAspPheValGlyAlaValMet
```

Fig S3. A-(ii) continued



TH135 coordinate 4,759,256

```
Alignment pos. .
EA2_HP17_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA2_TH135_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA2_OCU462: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA2_5581_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA2_P7_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA2_S2_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_2344_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_OCU404: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_CAM57_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_CAM78_: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_OCU466: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_CAM177: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
EA1_OCU464: 9221 ggcgatctgtccggcggcgcgccgctgctcggcaccgacaccgcccggtcacgagcgcaccctgggtcaaggccgaggtgccgcaggtg 9310
MAH_4514 (->) GlyAspLeuSerGlyArgArgGlyArgValLeuGlyThrAspThrAlaGlyHisGluArgThrValValLysAlaGluValProGlnVal
```

TH135 coordinate 4,759,256

```
Alignment pos. .
EA2_HP17_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcgacggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA2_TH135_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA2_OCU462: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA2_5581_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA2_P7_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA2_S2_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_2344_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_OCU404: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_CAM57_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_CAM78_: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_OCU466: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_CAM177: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
EA1_OCU464: 9311 gagctgaccgctacgcatcgacctgcggtcgctggcaccggcgcgccctcgttcaccggctcggtcgcccgctacgagccgatgccg 9400
MAH_4514 (->) GluLeuThrArgTyrAlaIleAspLeuArgSerLeuAlaHisGlyAlaAlaSerPheThrArgSerPheAlaArgTyrGluProMetPro
```

Fig S3. A-(ii) continued

TH135 coordinate 4,759,256

```
Alignment pos.
EA2_HP17_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA2_TH135_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA2_OCU462 : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA2_5581_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA2_P7_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA2_S2_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_2344_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_OCU404 : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_CAM57_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_CAM78_ : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_OCU466 : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_CAM177 : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
EA1_OCU464 : 9401 gaatccgcgggcccccagtgggcaccgcccgggtctgaccggaatcacactgcccgtcaagcgctttcgccgaattgttcggccaccgc 9490
MAH_4514 (->) GluSerAlaAlaAlaArgValAlaThrAlaAlaVal*
SauT (<-) *AlaSerGluGlyPheGlnGluAlaValAla
```

TH135 coordinate 4,759,256

```
Alignment pos.
EA2_HP17_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA2_TH135_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA2_OCU462 : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA2_5581_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA2_P7_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA2_S2_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_2344_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_OCU404 : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_CAM57_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_CAM78_ : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_OCU466 : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_CAM177 : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
EA1_OCU464 : 9491 gcggcggtccagcgagcccttcgcggtgtgcggcagctcgggcgcccgcgggaactcggccggcacctcgaagggcgccaaccggttcccg
SauT (<-) ArgArgAspLeuSerGlyLysAlaThrHisProLeuGluAlaAlaArgArgPheGluAlaProValGluPheProAlaLeuArgGluArg
```

**(A). Alignment suggesting recombination between MahEastAsia2 and undetected *Mycobacterium* lineage: the 53 kb region**

**(i)** Alignment for the *pntB* side of the 53.8-kb highly diverged region (4,758,973 to 4,812,752 in TH135 coordinate) in the MahEastAsia2 strains and three MahEastAsia1 strains is shown. The differentiated region in the three MahEastAsia1 strains, possibly imported from MahEastAsia2, are underlined. The border of the import in the tree MahEastAsia1 strains is unclear due to the absence of lineage-specific polymorphic sites around this region. **(ii)** Alignment for the MAH\_4513 side of the highly diverged region.

**Fig. S3 B – i**

Alignment pos. 1  
SC2\_104: ATGAACGACGCAAGAGAAGCTGTGCGAACACCCATCCCAGGAAAGGCAGTCCAGTCCAGGACGGTGTTCGTTCGAGCACCCCGAGGCCGAGGAC  
EA1\_OCU464: ATGAACGACGCACGAGACGCTGTGCGAGCACCATCCCAGAGGGGGCAGTCCAGTCCAGGACGGTGTTCGTTCGAGCACCCCGACTCCGACGAC  
EA2\_TH135: ATGAACGACGCACGAGACGCTGTGCGAGCACCATCCCAGAGGGGGCAGTCCAGTCCAGGACGGTGTTCGTTCGAGCACCCCGACTCCGACGAC  
\*

Alignment pos. 91  
SC2\_104: TTCGACAACGCCGCCGCGCTGCCACCCGACCCGACGTGGTTCAAGCAGCCCGTGTTCACGAGGTGCTGGTCCGGCGGTTCTTCGACGCC  
EA1\_OCU464: TTCGACAACGCCGCCGCGCTGCCACCCGATCCGACGTGGTTCAAGCAGCCCGTGTTCACGAGGTGCTGGTCCGGGCGTTCCTTCGACGCC  
EA2\_TH135: TTCGACAACGCCGCCGCGCTGCCACCCGATCCGACGTGGTTCAAGCAGCCCGTGTTCACGAGGTGCTGGTCCGGGCGTTCCTTCGACGCC

Alignment pos. 181  
SC2\_104: AACGCCGACGGCGCCGGCGACCTGCGCGGTCTGTGGCGCAGCTGGACTACCTGCAGTGGCTGGGCATCGACTGCATCTGGCTGCCCCCG  
EA1\_OCU464: AACGCCGACGGGGCGGGTGGACCTGCGCGGACTGTGGGGCGCTGGACTACCTGCAGTGGCTGGGCATCGACTGCATTTGGCTGCCGCC  
EA2\_TH135: AACGCCGACGGGGCGGGTGGACCTGCGCGGACTGTGGGGCGCTGGATACCTGCAGTGGCTGGGCATCGACTGCATTTGGCTGCCGCC  
\*

Alignment pos. 271  
SC2\_104: TTCTACGACTCGCCGCTGCGCGACGGCGGTTACGACATCCGGGATTTCTACAAGGTGCTGCCGGAGTTCGGCACCGTCGAGGATTTTCGTG  
EA1\_OCU464: TTCTACGATTCGCCGCTGCGCGACGGCGGATACGACATCCGGGATTTCTACAAGGTGCTGCCGGAGTTCGGCACCGTCGAGGATTTTCGTG  
EA2\_TH135: TTCTACGATTCGCCGCTGCGCGACGGCGGTTACGACATCCGGGATTTCTACAAGGTGCTGCCGGAGTTCGGCACCGTCGAGGATTTTCGTG

Alignment pos. 361  
SC2\_104: GCGTGCTCAACGCCGCGCACGAGCGGGGCATCCGGGTGATCACCGACCTGGTGTGATGAATCACACATCGGAGTCGCACCCCTGGTTCCAG  
EA1\_OCU464: GCGTGCTCAACGCCGCGCACGAGCGGGGCATTCGGGTGATCACCGACCTGGTGTGATGAATCACACATCGGATTCGCACCCCTGGTTCCAG  
EA2\_TH135: GCGTGCTCAACGCCGCGCACGAGCGGGGCATCCGGGTGATCACCGACCTGGTGTGATGAATCACACATCGGATTCGCACCCCTGGTTCCAG  
\*

451  
 Alignment pos. . . . .  
 SC2\_104: GAGTCCCAGGACGACCCCGACGGACCGTATGGCGACTTCTACGTGTGGAGCGACACCAGCGACCGCTACGCCGATGCCCGCATCATCTTC  
 EA1\_OCU464: GAGTCCGCGGCACGACCCCGACGGCCCGTACGGCGACTTCTACGTGTGGAGCGACACCAGCGAGCGCTACACCGACGCGAGGATCATCTTC  
 EA2\_TH135: GAGTCCGCGGCACGACCCCGACGGCCCGTACGGCGACTTCTACGTGTGGAGCGACACCAGCGAGCGCTACACCGACGCGAGGATCATCTTC

\*

541  
 Alignment pos. . . . .  
 SC2\_104: GTCGACACCGAGGAGTCCAACCTGGACGTTTCGACCCGGTGCGCCGCCAGTTCTACTGGCACCGGTTCTTCTCCACCAGCCCGACCTGAAC  
 EA1\_OCU464: GTCGACACCGAGGAGTCCAACCTGGACGTTTCGACCCGGTGCGCCAAAAGTTCTACTGGCACCGGTTCTTCTCCACCAGCCGGACCTCAAC  
 EA2\_TH135: GTCGACACCGAGGAGTCCAACCTGGACGTTTCGACCCGGTGCGCCAAAAGTTCTACTGGCACCGGTTCTTCTCCACCAGCCGGACCTCAAC

631  
 Alignment pos. . . . .  
 SC2\_104: TACGACAACCCGGCCGTGCAGGAAGCCATGATCGACGTGATCCGGTCTGGCTCGGGCTGGGAATCGACGGGTCCGGCTGGACGCGGTG  
 EA1\_OCU464: TACGACAACCCGGCCGTGCAGGACGCCATGATCGACGTGATCCGGTCTGGCTGGGCTGGGATCGACGGGTCCGGCTGGACGCGGTG  
 EA2\_TH135: TACGACAACCCGGCCGTGCAGGACGCCATGATCGACGTGATCCGGTCTGGCTGGGCTGGGATCGACGGGTCCGGCTGGACGCGGTG

721  
 Alignment pos. . . . .  
 SC2\_104: CCCTACCTGTTTCGAGCGGGAGGGCACCAACTGCGAGAACCTGCCGGAGACGCACGCCTTCTCAAGCGGGTCCGCAAGGTCGTGACGAC  
 EA1\_OCU464: CCCTACCTGTTTCGAGCGCGAGGGCACCAACTGCGAGAACCTGCCGGAGACGCACGCCTTCTGAGGCGCGTGCGCAAGGTCGTGACGAC  
 EA2\_TH135: CCCTACCTGTTTCGAGCGCGAGGGCACCAACTGCGAGAACCTGCCGGAGACGCACGCCTTCTGAGGCGCGTGCGCAAGGTCGTGACGAC

811  
 Alignment pos. . . . .  
 SC2\_104: GAGTTCGCGGCCGGGTGTTGCTGGCCGAGGCCAACCAAGTGGCCGGCCGACGTGGTTCGAGTATTTCCGGCGACCCAGCACCGGGCGGGCAG  
 EA1\_OCU464: GAAATTTCCCGGCCGGGTGCTGCTGGCCGAGGCCAACCAAGTGGCCGGCCGACGTGGTTCGAGTATTTCCGGCGACCCAGCACCGGGCGGGCAG  
 EA2\_TH135: GAAATTTCCCGGCCGGGTGCTGCTGGCCGAGGCCAACCAAGTGGCCGGCCGACGTGGTTCGAGTATTTCCGGCGACCCAGCACCGGGCGGGCAG

Fig S3. B-(i) continued



1351  
Alignment pos. . . . .  
SC2\_104: CCCGGCCGGCTGTATCTGCCACCCAGCCAGGACCCGGTGTACGGCTACCAGGCGGTCAACGTGGAGGCGCAGCGGACACCTCGACGTCCG  
EA1\_OCU464: CCCGGCCGGCTGTATTTGCCACCCAGCCAGGACCCGGTGTACGGCTACCAGGCGGTCAACGTGGAGGCGCAGCGGACACCTCGACGTCCG  
EA2\_TH135: CCCGGCCGGCTCTACCCTGCCGGCCAGCCAGGACTCCGTCTACGGGTATTCAGGCGGTCAACGTGGAGGCGCAGCGGACACCTTCACGTCCG  
\* \*\* \*\* \* \* \* \* \* \* \* \* \* \*  
^P->A (TH135) ^P->S (TH135)

1441  
Alignment pos. . . . .  
SC2\_104: CTGCTCAACTTCACCCGCACCATGCTGGCCGTGCGGCGCCGGCACGAGGCCCTTCGCGATCGGCACGTTTCGAGGAGCTCGGCGGGTCCAAC  
EA1\_OCU464: CTGCTCAACTTCACCCGCACCATGCTGACCGGTGCGGCGCCGGCACGAGGCCCTTCGCGGTCGCGCACGTTTCGAGGAACTGGGCGGATCCAAC  
EA2\_TH135: CTGCTCAACTTCACCCGCCTGATGCTGGCCGTGCGGCGCCGGCACGAGGCCCTTCGCGGTCGCGCACGTTTCGAGGAACTGGGCGGATCCAAC  
\* \*\*\*  
^T->V (TH135)  
^A->T (OCU464)

1551  
Alignment pos. . . . .  
SC2\_104: CCGTCGGTGCTGGCGTTCGTGCGGCAGGTGTCCAACGACGGGGACACCGTGTGTGCGTCAACAACCTGTTCGGGTTCCCGCAGCCGATC  
EA1\_OCU464: CCGTCGGTGCTGGCGTTCGTGCGGTACAGGCACCCGGTGGCGGCGACACCGTGTGTGCGTCAACAACCTGTTCGGGTTCCCGCAGCCGATC  
EA2\_TH135: CCGTCGGTGCTGGCGTTCGTGCGGTACAGGCACCCGGTGGCGGCGACACCGTGTGTGCGTCAACAACCTGTTCGGGTTCCCGCAGCCGATC

180+

1641  
Alignment pos. . . . .  
SC2\_104: GAGCTGAATCTGCAGCACTGGAGCGGGTGCATCCCGGTTCGAGCTGACCGGGCACGTGGAATTCCTCCCGCATCGGGCACCTGCCCTACCTG  
EA1\_OCU464: GAACTGAATCTGCAGCACTGGAGCGGGTGCACGCCGGTGGAACTGACCGGGCACGTGGAATTCCTCCCGCATCGGGCACCTGCCCTACCTG  
EA2\_TH135: GAACTGAATCTGCAGCACTGGAGCGGGTGCACGCCGGTGGAACTGACCGGGCACGTGGAATTCCTCCCGCATCGGGCACCTGCCCTACCTG

1731  
Alignment pos. . . . .  
SC2\_104: CTGACCTTGCCGGGGCACGGTTTCTATTGGTTCCAGCTGACCGCATGCGAGGAGGACACATGA  
EA1\_OCU464: CTGACCTTGCCGGGGCACGGTTTCTACTGGTTCCAGCTGACCGCATGTGAGGAGGACTCATGA  
EA2\_TH135: CTGACCTTGCCGGGGCACGGTTTCTACTGGTTCCAGCTGACCGCATGTGAGGAGGACTCATGA

**Fig. S3 B – ii**

```

1
Alignment pos. .
SC2_104: ATGACCGAACCCGCCAAGCTGCCGTGGTCCGATTGGCTTCCGCAGCAACGTTGGTACGCCGGCCGAACCCGGCTGACCGGCCGAA
EA1_OCU464: ATGACTGATCCAGCCAAGTTGCCCTGGTCCGACTGGCTCCCCAGCAGCGCTGGTACGCCGGAACGCAACCCGGAGCTCACCTCCGCCGAG
EA2_TH135: ATGACTGATCCAGCCAAGTTGCCCTGGTCCGACTGGCTCCCCAGCAGCGCTGGTACGCCGGAACGCAACCCGGAGCTCACCTCCGCCGAG

91
Alignment pos. .
SC2_104: CCGAGCGTGATCGTCGGGTTGCGCGACGATCTGGACCTGGTGTGGTTCGACGCCGACTACGCCGACGGCTCACGGGACCGCTACCAGGTC
EA1_OCU464: GCCGCGCTCGTGGTCCGCTGCGGGACGACCTCGACCTGGTCTGGTTCGACGCCCGGTACGCCGACGGCTCGTCCGAGCGCTACCAGGTC
EA2_TH135: GCCGCGCTCGTGGTCCGCTGCGGGACGACCTCGACCTGGTCTGGTTCGACGCCCGGTACGCCGACGGCGCGTCCGAGCGCTACCAGGTC
*
S->A (TH135)

181
Alignment pos. .
SC2_104: CTGGTCTGCTGGGATGCCGCACCGGTCTCCGAGTACAGCACGGTGGCCACCATCGGCGCCGCCGACGACCGGACCGGCTTCGACGCGTTG
EA1_OCU464: ATCGTCCGGTGGGACACCGCGCCGGTCTCCGAGTACAGCAACGTGGCCACCATCGGCGCCGCCGCGTACCGCACCGGCTTCGACGGCCTC
EA2_TH135: ATCGTCCGGTGGGACACCGCGCCGGTCTCCGAGTACAGCAACGTGGCCACCATCGGCGCCGCCGCGTACCGCACCGGCTTCGACGGCCTC

271
Alignment pos. .
SC2_104: TACGACGACGAGGCGCCGAGTTTTTGTCTCCCTGATCGACTCGTCGGCGGTGCGCAGCGCTCCGGGGCCGAGGTGAGATTGCGCAAG
EA1_OCU464: TACGACACCGACGCGCCGAGTTCTTGCTGTCCCTGATCGACGAGTCCGCCGTTTCGCGCGGCGTCGGGCACCGAGGTGAGTTTCGTTCCGG
EA2_TH135: TACGACACCGACGCGCCGAGTTCTTGCTGTCCCTGATCGACGAGTCCGCCGTTTCGCGCGGCGTCGGGCACCGAGGTGAGTTTCGTTCCGG

361
Alignment pos. .
SC2_104: GAGCCCAGCGCCAGCTGCCGCTCGAGGCGATGGCGCACGTGTGGACGCCGAGCAGTCCAACACCAGCGTGATCTTCGACCGCGACGCC
EA1_OCU464: GAGCCCAGCGTGGAGCTGCCGCTCGAGGCGCTGCCGCACGTCTCCGACGCCGAAACAGAGCAACACCAGCGTGATCTTCGACCGCGCCGCG
EA2_TH135: GAGCCCAGCGTGGACCTGCCGCTCGAGGCGCTGCCGCACGTCTCCGACGCCGAAACAGAGCAACACCAGCGTGATCTTCGACCGCGCCGCG

```

Fig S3. B-(ii) continued

451  
 Alignment pos. .  
 SC2\_104: ATCTTCAAGGTGTTCCGCCGGGTGAGCAGCGGCATCAACCCCGACATCGAGCTGAACCGGGTGTCTGGGCCGCCGGCAATCCGCACGTG  
 EA1\_OCU464: ATCTTCAAGGCGTTCCGCCGGGTGAGCAGCGGTATCAACCCCGACATCGAACTCAACCGGGTGTCTGGGTTCGCGCCGGCAACCCGCACGTG  
 EA2\_TH135: ATCTTCAAGGCGTTCCGCCGGGTGAGCAGCGGTATCAACCCCGACATCGAACTCAACCGGGTGTCTGGGTTCGCGCCGGCAACCCGCACGTG

541  
 Alignment pos. .  
 SC2\_104: GCCCGGCTGCTGGGCACCTACGAGATGGCGGGTGC GGACGGCACCCCGAGACGGCCTGGCCGCTGGGCATGGTGACCGAGTTCGCGGCC  
 EA1\_OCU464: GCCCGCTGCTGGGCACCTACGAGATGGCCGCCCGGACGGCACGGCCGACGGCCTGGCCGCTCGGCATGGTGACCGAGTTCGCGGCC  
 EA2\_TH135: GCCCGCTGCTGGGCACGTACGAGATGGCCGCCCGGACGGCACGGCCGACGGCCTGGCCGCTCGGCATGGTGACCGAGTTCGCGGCC  
 \*

631  
 Alignment pos. .  
 SC2\_104: AACGCCGGAGGGGTGGGCGATGGCCACCGCCAGCGTTCGCGACCTGTTCCGCCAGGGCGATCTGTACGCGCACGAGGTTCGGCGGCGAC  
 EA1\_OCU464: AACGCCGGAGGGGTGGGCGATGGCCACCGCCAGCGTCCGCGACCTGTTCCGCCAGGGCGACTGTACGCGCACGAAAGTTCGGCGGCGAC  
 EA2\_TH135: AACGCCGGAGGGGTGGGCGATGGCCACCGCCAGCGTCCGCGACCTGTTCCGCCAGGGCGACTGTACGCGCACGAAAGTTCGGCGGCGAC

721  
 Alignment pos. .  
 SC2\_104: TTCGCCGGTGAGTCTACCGCCTGGGCGAGGGCGTGGCGTCCGTGCACGCCACCCTGGCCGAGACGCTGGGCACCTCGCAAGCCGGTTC  
 EA1\_OCU464: TTCGCCGGTGAAATCTGCCGGCTGGGCGAGGGCGTGGCGTCCGTGCACGCCACCCTGGCCGAATCCCTCGGGACGGCACAGTCTCCTTC  
 EA2\_TH135: TTCGCCGGTGAAATCTGCCGGCTGGGCGAGGGCGTGGCGTCCGTGCACGCCACCCTGGCCGAATCCCTCGGGACGGCACAGTCTCCTTC

811  
 Alignment pos. .  
 SC2\_104: CCGGTGGACAACGTGCTGGCGGGTGTCTCTGACCGCGGCCCTGGTGCCCGAGCTGACCGAGTACGCGGCCACCATCGAGGAGCGGTTC  
 EA1\_OCU464: CCCGTCGAGACCGTGCTGTTCGCGGCTGGCGTGCACCGTGGC AAA GGTGCCCGAGCTGCAGGAGTACGCGGCCACCATCGAAAGAGCGATTTC  
 EA2\_TH135: CCCGTCGAGACCGTGCTGTTCGCGGCTGGCGTGCACCGTGGC AAA GGTGCCCGAGCTGCAGGAGTACGCGGCCACCATCGAAAGAGCGATTTC

Fig S3. B-(ii) continued



1001  
Alignment pos. . . . .  
SC2\_104: GCCAAGCTGGCCACCGAGACCATCACCGTGCAGCGGGTGCACGGCGACCTGCACCTGGGCCAGGTGCTGCGCACCCCGGAGAGCTGGCTG  
EA1\_OCU464: CAGAAGTTGTCGGGCGAGTCGATCACGGTGCAGCGCGTGCACGGTGACCTGCACCTCGGTTCAGGTGCTGCGGACCCCGAGAGCTGGTTG  
EA2\_TH135: CAGAAGTTGTCGGGCGAGTCGATCACGGTGCAGCGCGTGCACGGTGACCTGCACCTCGGTTCAGGTGCTGCGGACCCCGAGAGCTGGTTG

1091  
Alignment pos. . . . .  
SC2\_104: CTCATCGACTTCGAGGGCGAACCGGGCCAGCCGCTCGAGGAACGCCGCGCCCGACTCACCGCTGCGCGACGTGGCCGGCGTGCTGCGG  
EA1\_OCU464: CTGATCGACTTCGAGGGCGAACCGGGCCAGCCGTCGACCGAGCGCGCGGCGCCCGACTCACCGTTGCGCGACGTGGCCGGCGTGCTGCGG  
EA2\_TH135: CTGATCGACTTCGAGGGCGAACCGGGCCAGCCGTCGACCGAGCGCGCGGCGCCCGACTCACCGTTGCGCGACGTGGCCGGCGTGCTGCGG

1181  
Alignment pos. . . . .  
SC2\_104: TCGTTCGAGTACGCCGCTACGGGCCGCTGGTGGAGCAGGGCTCGCAAACACGACAAGCAGCTGGCCGGCCCGGCCGGGAATGGGTG  
EA1\_OCU464: TCCTTCGAATACGCCGCGTACGGGCCGCTGGTGGATCAGGC-----GACCGACAAGCAGCTGGCCGCCCGCGCCCGGAATGGGTG  
EA2\_TH135: TCCTTCGAATACGCCGCGTACGGGCCGCTGGTGGATCAGGC-----GACCGACAAGCAGCTGGCCGCCCGCGCCCGGAATGGGTG

1271  
Alignment pos. . . . .  
SC2\_104: GAGCGCAACCGCACCGGTTCTGTGACGGCTACGCGGCCGCTCCGGCATCGACCCGCGGATTCGGCGCCGCTGCTGGCCGCCTACGAA  
EA1\_OCU464: GAGCGCAACCGGACCGGTTCTGTGAGGGCTACGCGGCCGCTCGGGCATCGACCCGCGGATTCGGCCGAGCTGCTGGCCGCCTACGAG  
EA2\_TH135: GAGCGCAACCGGACCGGTTCTGTGAGGGCTACGCGGCCGCTCGGGCATCGACCCGCGGATTCGGCCGAGCTGCTGGCCGCCTACGAG

1361  
Alignment pos. . . . .  
SC2\_104: TTGGACAAGGCGGTCTACGAGGCCGGTACGAGGCGGGCACCGGCCCGGCTGGCTGCCGATCCCGCTGCGCTCCATCGCCCGGTTGACC  
EA1\_OCU464: CTCGACAAGGCGGTCTACGAGGCCGGTACGAGGCGGGCACCGGCCGAGCTGGCTGCCATTCCGCTGCGTTCATCGCCCGGCTCACC  
EA2\_TH135: CTCGACAAGGCGGTCTACGAGGCCGGTACGAGGCGGGCACCGGCCGAGCTGGCTGCCATTCCGCTGCGTTCATCGCCCGGCTCACC

Fig S3. B-(ii) continued

1451  
 Alignment pos. . . . .  
 SC2\_104: GCGGCCTGA  
 EA1\_OCU464: GCAGGATAG  
 EA2\_TH135: GCAGGATAG

**Fig. S3 B – iii**

1  
 Alignment pos. . . . .  
 SC2\_104: GTGCGTGTGCCGAGTGAGATCAACAACAGCGAAACCAGGTTGTCGTGGGTGCTGGCGGTGCTGGCCGGGGTGTGGGAGCCACCGCCTTC  
 EA1\_OCU464: -----GTGGCGAGCGAAACCTTCAATAGCGAAGCGCGGTTGTCGTGGGTCTGGCGCGCTGGCCGGTGTGGTGGGCGCGATCTCCTTC  
 EA2\_TH135: -----GTGGCGAGCGAAACCTTCAATAGCGAAGCGCGGTTGTCGTGGGTCTGGCGCGCTGGCCGGTGTGGTGGGCGCGATCTCCTTC

91  
 Alignment pos. . . . .  
 SC2\_104: ACGCACTCCGCCGGCTACTTTCGTGACCTTCATGACCGGCAACGCCAGCGCGCGATGCTCGGCTACTTCCGGGGCAGCTGGTGTGTTGTCG  
 EA1\_OCU464: ACCCACTCCGCCGGCTACTTTCGTGTTTTCATCACCGGTAACGCCAGCGCGCGTGTGCTCGGTTATTTCCAGGGGAAGGGTGGCTGGCC  
 EA2\_TH135: ACCCACTCCGCCGGCTACTTTCGTGTTTTCATCACCGGTAACGCCAGCGCGCGTGTGCTCGGTTATTTCCAGGGGAAGGGTGGCTGGCC

181  
 Alignment pos. . . . .  
 SC2\_104: GTGACGGCGGGGTGCTGATCGTGTGCTTCGTGCGCGGCGTGGTGATCGCCTCGGTATGCCGGCGGCATTTCTGGGTGGACCACCGCAC  
 EA1\_OCU464: GTGAGTGCCGGGCTGCTCATCGTGGCGTTCGTGCGCGGTGTGGTGGTGGCGTCACTGTGCCGCCGATTTTCTGGGTGGACCATCCGCAC  
 EA2\_TH135: GTGAGTGCCGGGCTGCTCATCGTGGCGTTCGTGCGCGGTGTGGTGGTGGCGTCACTGTGCCGCCGATTTTCTGGGTGGACCATCCGCAC

271  
 Alignment pos. . . . .  
 SC2\_104: GGGCCACCGTGCTGACGACGTTACGCTGGTGGCGGCCACCCTGGTGGACGTCATCGACGAGGGCTGGGAGGAGAACCTGCTCGACTTC  
 EA1\_OCU464: GGCCCGACAGTGCTGACCACCTTCAGTTTGGCGGCCGCCACCCTGGTGGACGTCATCGATGTGGGATGGACGCAGAACTCTCGTCGATTTTC  
 EA2\_TH135: GGCCCGACAGTGCTGACCACCTTCAGTTTGGCGGCCGCCACCCTGGTGGACGTCATCGATGTGGGATGGACGCAGAACTCTGGTTCGATTTTC

\*

Fig S3. B-(iii) continued

361  
 Alignment pos. . . . .  
 SC2\_104 : GCGCCGATCATGTTGGTGACGTTTCGGCATCGGGCGGTTGAACACGTCGTTTCGTC AAGGACGGCGAGGTGTCGGTTCGGCTGAGCTACGTG  
 EA1\_OCU464: GCGCCGATGATGCTGCTGGCGTTTGGCACCGGGGCGTTGAACACCTCTTTTCGTC AAGAACGGCGAGGTTCGGTCCCGTTGAGCTACGTG  
 EA2\_TH135\_ : GCGCCGATGATGCTGCTGGCGTTTGGCACCGGGGCGTTGAACACCTCTTTTCGTC AAGAACGGCGAGGTTCGGTCCCGTTGAGCTACGTG

451  
 Alignment pos. . . . .  
 SC2\_104 : ACCGGAACCCCTGGTCAAGATGGGGCAGGGCATCGAACGCCACATCGCCGGTGG---GACGGCGGGCGGACTGGCTGGGCTATTTTCTGCTG  
 EA1\_OCU464: ACCGGCACGACCGTCAAGATGGGGCAGGGCATCGAGCGCCACATCGCCGGTGGCGGAAACATCGGGGACTGGCTCGGTTACTTTCTGCTG  
 EA2\_TH135\_ : ACCGGCACGACCGTCAAGATGGGGCAGGGCATCGAGCGCCACATCGCCGGTGGCGGAAACATCGGGGACTGGCTCGGTTACTTTCTGCTG

541  
 Alignment pos. . . . .  
 SC2\_104 : TTGCCAGCTTCGTGGTGGGGCCACCGTCGGCGGCTTCATCAGTCTGTTTCGTC AACGGCACGTCGATGTTGGTGGCGGCCACCGTGATG  
 EA1\_OCU464: TTGCCAGCTTTATGGTGGGCGCGCGGTTGGGGCGGCTTCATCAGCGTTGTCGTC AACGGGACCTGGATGCTGGTGATGGCCACGTCTGTA  
 EA2\_TH135\_ : TTGCCAGCTTTATGGTGGGCGCGCGGTTGGGGCGGCTTCATCAGCGTTGTCGTC AACGGGACCTGGATGCTGGTGATGGCCACGTCTGTA  
 \*

631  
 Alignment pos. . . . .  
 SC2\_104 : TGCGCGTTGACCACCGGCTACACCTATTTCCATTCCGATCGCCGGGCGCTGCTCGACGAGGCG-----  
 EA1\_OCU464: TGCGCGGTGACGACCGGGTACACCTACTTCCACCAGGACCGGCGCGCCCTGTTGATGGAACGGTCCGAGAAAAAGCATCGGCAGCAGCGC  
 EA2\_TH135\_ : TGCGCGGTGACGACCGGGTACACCTACTTCCACCAGGACCGGCGCGCCCTGTTGATGGAACGGTCCGAGAAAAAGCATCGGCAGCAGCGC

721  
 Alignment pos. . . . .  
 SC2\_104 : TGA  
 EA1\_OCU464: TGA  
 EA2\_TH135\_ : TGA

**(B). Alignment of East Asia-type alleles in the *treS-maK* operon.**

(i) TreS. A nucleotide that differentiate East Asian alleles from *M. avium*-type alleles is indicated by blue or red background color. A nucleotide position that differentiate EA2-subtype from EA1-subtype were indicated by asterisk. Substitutions that affect product sequence are indicated by amino-acid sequence change below the alignment. The EA1-subtype contains a fragment possibly originating from *M. avium*-type allele. The possible import (216 bp) is underlined. Crossover regions are indicated by grey background. (ii) MalK. (iii) Membrane protein. Substitutions in the membrane-protein coding region does not affect product sequence.



104 coordinate 5,328,160

Alignment pos.

```
SC2_Mah104: 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
SC2_4293_ : 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
SC2_OCU556: 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
SC2_2285R_ : 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
SC2_XTB13_ : 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
SC2_27_1_ : 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccagttccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
EA1_OCU466: 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccaattccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
EA1_OCU464: 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccaattccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
EA1_CAM78_ : 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccaattccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
EA1_CAM177: 8931 tgccgtcgccgtcgatgggcccgaacatcaaggtccaattccagggcggcggcgcacgcggtctacctgctggacggcctgcgcgcg 9020
MAV_5183 (->) ValProSerProSerMetGlyArgAsnIleLysValGlnPheGlnGlyGlyGlyProHisAlaValTyrLeuLeuAspGlyLeuArgAla-
```

104 coordinate 5,328,250

Alignment pos.

```
SC2_Mah104: 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
SC2_4293_ : 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
SC2_OCU556: 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
SC2_2285R_ : 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
SC2_XTB13_ : 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
SC2_27_1_ : 9021 aggacgactacaacggttgggacatcaacaccccggcgttcgaggagttctaccagtccggtcttccggtgatcatgcccgtcggcggc 9110
EA1_OCU466: 9021 aggacgactacaacggttgggacatcaacaccccggccttcgaggagttctaccaatccggtctgctcggtggtgatgcccgtcggcggc 9110
EA1_OCU464: 9021 aggacgactacaacggttgggacatcaacaccccggccttcgaggagttctaccaatccggtctgctcggtggtgatgcccgtcggcggc 9110
EA1_CAM78_ : 9021 aggacgactacaacggttgggacatcaacaccccggccttcgaggagttctaccaatccggtctgctcggtggtgatgcccgtcggcggc 9110
EA1_CAM177: 9021 aggacgactacaacggttgggacatcaacaccccggccttcgaggagttctaccaatccggtctgctcggtggtgatgcccgtcggcggc 9110
MAV_5183 (->) GlnAspAspTyrAsnGlyTrpAspIleAsnThrProAlaPheGluGluPheTyrGlnSerGlyLeuSerValIleMetProValGlyGly-
```

104 coordinate 5,328,340

Alignment pos.

```
SC2_Mah104: 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
SC2_4293_ : 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
SC2_OCU556: 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
SC2_2285R_ : 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
SC2_XTB13_ : 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
SC2_27_1_ : 9111 agtccagcttctacagcaactggatcagccgtcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaga 9200
EA1_OCU466: 9111 agtccagcttctacagcaactggatccaaccctcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaaa 9200
EA1_OCU464: 9111 agtccagcttctacagcaactggatccaaccctcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaaa 9200
EA1_CAM78_ : 9111 agtccagcttctacagcaactggatccaaccctcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaaa 9200
EA1_CAM177: 9111 agtccagcttctacagcaactggatccaaccctcgtcgggcaacgggcagaactacacctacaagtgggagacgttcctgaccaggaaa 9200
MAV_5183 (->) GlnSerSerPheTyrSerAsnTrpTyrGlnProSerSerGlyAsnGlyGlnAsnTyrThrTyrLysTrpGluThrPheLeuThrGlnGlu-
```

Fig S3. C continued



TH135 coordinate 5,331,384

Alignment pos.

```
SC2_Mah104:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
SC2_4293_:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
SC2_OCU556:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
SC2_2285R_:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
SC2_XTB13_:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
SC2_27_1_:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacagcacggtgtcccgctcgttggacacctgocgcacg 12274
EA1_OCU466:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacacacggtgtcccgccaccgggtgcctgacgcacg 12274
EA1_OCU464:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacacacggtgtcccgccaccgggtgcctgacgcacg 12274
EA1_CAM78_:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacacacggtgtcccgccaccgggtgcctgacgcacg 12274
EA1_CAM177:12185 tgctgcagattcagctcgatcggctgcgggaaccgcgacaggtggtgacgcacacacggtgtcccgccaccgggtgcctgacgcacg 12274
MAV_5186 (<-) HisGlnLeuAsnLeuGluIleProGlnProPheArgSerLeuAsnAsnValCysLeuValThrAspGlyAspAsnSerValGlnArgVal-
```

104 coordinate 5,331,474

Alignment pos.

```
SC2_Mah104:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
SC2_4293_:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
SC2_OCU556:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
SC2_2285R_:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
SC2_XTB13_:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
SC2_27_1_:12275 aacgccagcaccgacgggttggacccgccagctcctcgaacgtgcccgaacgcgaaggcct (1692 bp) gtcgacggaccggaag 14009
EA1_OCU466:12275 aacgccagcaccgacgggttggatccgccagttcctcgaacgtgcccgaacgcgaaggcct (1692 bp) ccccgaggagcggtag 14009
EA1_OCU464:12275 aacgccagcaccgacgggttggatccgccagttcctcgaacgtgcccgaacgcgaaggcct (1692 bp) ccccgaggagcggtag 14009
EA1_CAM78_:12275 aacgccagcaccgacgggttggatccgccagttcctcgaacgtgcccgaacgcgaaggcct (1692 bp) ccccgaggagcggtag 14009
EA1_CAM177:12275 aacgccagcaccgacgggttggatccgccagttcctcgaacgtgcccgaacgcgaaggcct (1692 bp) ccccgaggagcggtag 14009
MAV_5186 (<-) PheAlaLeuValSerProAsnSerGlyGlyLeuGluGluPheThrGlyIleAlaPheAlaGlu
MAV_5187 (<-) AspValSerArgPhe-
```

104 coordinate 5,333,209

Alignment pos.

```
SC2_Mah104:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
SC2_4293_:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
SC2_OCU556:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
SC2_2285R_:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
SC2_XTB13_:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
SC2_27_1_:14010 tgcaccgcgatggtgtcaccgggatggtgcgggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
EA1_OCU466:14010 tgcaccgcgatggtgtcaccgggatggtgggggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
EA1_OCU464:14010 tgcaccgcgatggtgtcaccgggatggtgggggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
EA1_CAM78_:14010 tgcaccgcgatggtgtcaccgggatggtgggggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
EA1_CAM177:14010 tgcaccgcgatggtgtcaccgggatggtgggggacgagcacctcggtcacgcaggtcgccccgttgatcgggacggtgtcgacgcccgggtg 14009
MAV_5187 (<-) HisValAlaIleThrAspGlyProHisHisProValLeuValGluThrMetSerThrAlaGlyAsnIleProValThrAspValGlyThr-
```

Fig S3. C continued

```

104 coordinate      5,333,299
.
Alignment pos.
SC2_Mah104:14010  atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
SC2_4293_:14010  atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
SC2_OCU556:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
SC2_2285R_:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
SC2_XTB13_:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
SC2_27_1_:14010  atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
EA1_OCU466:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
EA1_OCU464:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
EA1_CAM78_:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
EA1_CAM177:14010 atgacgtcgccgggcgcgatgcccgggccgcgccggggccggtggtgaccaccgctgcaccgcgcgccgttgccgttgtgtccgtc 14189
MAV_5187 (<-)    IleValAspGlyProAlaIleGlyAlaAlaAlaAlaProGlyThrAsnValValArgGlnValArgAlaGlyAsnGlyAsnAsnAspThr-

```

```

104 coordinate      5,333,389
.
Alignment pos.
SC2_Mah104:14190  acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
SC2_4293_:14190  acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
SC2_OCU556:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
SC2_2285R_:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
SC2_XTB13_:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
SC2_27_1_:14190  acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
EA1_OCU466:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
EA1_OCU464:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
EA1_CAM78_:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
EA1_CAM177:14190 acgcccagcccaggaatgcggtgggcccgatgtgcacggtggtggagccggcgccggagcggatctggttggcgacggccatggcgcg 14279
MAV_5187 (<-)    ValGlyLeuGlyLeuPheAlaThrProGlyIleHisValThrAsnSerGlyAlaGlySerArgIleGlnAsnAlaValAlaMetAlaArg-

```

**(C). Alignment suggesting recombination between MahEastAsia1 and SC2: the *treS-maK* operon**

The differentiated region containing the *treS-maK* operon in the genomes of MahEastAsia1. The 5,080 bp long diverged region was underlined. SNPs unique to the SC2 group are shown in green background, whereas SNPs unique to the MahEastAsia1 group is shown in red background. Alignment was generated using MAFFT software for 19,500 bp region spanning from MAV\_RS24815 (no original locus\_tag given) to MAV\_RS24905 (original locus\_tag: MAV\_5190). Alignment position on the sides indicate base position in the original alignment.





TH135 coordinate 4,805,398

Alignment pos.

```
EA2_TH135_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA2_OCU462_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA2_HP17_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA2_5581_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA2_P7_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA2_S2_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA1_2344_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA1_OCU404_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA1_CAM57_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) accgtcgggccgtgcggatggtccaccag 1800
EA1_CAM78_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) actgtcgggccgtgcggatggtccaccag 1800
EA1_OCU466_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) actgtcgggccgtgcggatggtccaccag 1800
EA1_OCU464_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) actgtcgggccgtgcggatggtccaccag 1800
EA1_CAM177_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) actgtcgggccgtgcggatggtccaccag 1800
SC3_2495_ : 1661 cggtgccaaacgccagcagcatcatcggcgcgaaatcgaccagattctgc (60 bp) actgtcgggccgtgcggatggtccaccag 1800
Memb. Prot. (<-) -ThrGlyPheAlaLeuLeuMetMetProAlaPheAspValLeuAsnGln --ThrProGlyHrHisProHisAspValTrp-
```

TH135 coordinate 4,805,538

Alignment pos.

```
EA2_TH135_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA2_OCU462_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA2_HP17_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA2_5581_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA2_P7_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA2_S2_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA1_2344_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA1_OCU404_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
EA1_CAM57_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgatacccgtagacggagtcctggctggcc 3920
EA1_CAM78_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
EA1_OCU466_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
EA1_OCU464_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
EA1_CAM177_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
SC3_2495_ : 1801 aaaaatcggcggcacagtga (2042 bp) tgtcgcgctgggcctccacgttgaccgctgtagccgtaaccgggtcctggctgggt 3920
Memb. Prot. (<-) -PheArgArgCysLeuSer- (M.P.) -AspArgGlnAlaGluValAsnValAlaGlnTyrGlyTyrValSerAspGlnSerAla-
TreS (<-)
```

Fig S3. D continued

TH135 coordinate 4,807,649

Alignment pos.

```
EA2_TH135 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA2_OCU462 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA2_HP17 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA2_5581 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA2_P7 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA2_S2 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA1_2344 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA1_OCU404 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
EA1_CAM57 : 3921 ggcaggtag (3282 bp) ccctgtgagctaggacacaccgcgcggcgcccccgcgatgccggagacaactggaggaaacctcatgg 7280
EA1_CAM78 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
EA1_OCU466 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
EA1_OCU464 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
EA1_CAM177 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
SC3_2495 : 3921 ggcagatag (3282 bp) aggtgctagccgggccc-----gcaacgggtgcgccccgg-----gcaacctggaggaaagtcatgg 7280
TreS (<-) --LeuTyr-
MAH_4513 (->) Met-
```

TH135 coordinate 4,810,932

Alignment pos.

```
EA2_TH135 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA2_OCU462 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA2_HP17 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA2_5581 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA2_P7 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA2_S2 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA1_2344 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA1_OCU404 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
EA1_CAM57 : 7281 cggacaaggcgaatgcttcccagggcgcggcgccaccaccgcccggcgccggggcgaggtgcgcaacatcgctctggtcggaccgt 7370
EA1_CAM78 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
EA1_OCU466 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
EA1_OCU464 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
EA1_CAM177 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
SC3_2495 : 7281 cggacaagacaactacttcccagggcgcgggaaacgctccgaccgccaagagtcggggcgaggttcgcaacgctcgtgctggtgggaccgt 7370
MAH_4513 (->) AlaAspLysAlaAsnAlaSerGlnGlyAlaAlaAlaAlaProThrProAlaGlyProGlyGluValArgAsnIleValLeuValGlyPro-
```

Fig S3. D continued

TH135 coordinate 4,811,022

Alignment pos.

```
EA2_TH135 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA2_OCU462 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA2_HP17 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA2_5581 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA2_P7 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA2_S2 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA1_2344 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA1_OCU404 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA1_CAM57 : 7371 cgggtgccggcaagaccaccctgggtcgaggcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA1_CAM78 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtcctgaccagagcgggttcgggtcaccgacggcagcacgg 7460
EA1_OCU466 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtgttgaaccgcccgggtcgggtcggcggacggcagcacgg 7460
EA1_OCU464 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtgttgaaccgcccgggtcgggtcggcggacggcagcacgg 7460
EA1_CAM177 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtgttgaaccgcccgggtcgggtcggcggacggcagcacgg 7460
SC3_2495 : 7371 cgggcggcggcaaaaccactctgggtcgaagcgtgctgggtcgccggcgggggtgttgaaccgcccgggtcgggtcggcggacggcagcacgg 7460
MAH_4513 (->) SerGlyAlaGlyLysThrThrLeuValGluAlaLeuLeuValAlaGlyGlyValLeuThrArgAlaGlySerValThrAspGlySerThr-
In TH135
```

#### (D). Alignment suggesting recombination between MahEastAsia1 and MahEastAsia2: the *treS-maK* operon

An imported fragment containing the *treS-maK* operon in strain OCU404. SNPs derived from MahEastAsia1, and MahEastAsia2 were indicated by blue and red background colors, respectively. Possible crossover regions were indicated by grey background color. Alignment was generated using MAFFT software for 11,547 bp region spanning from *fbpC* to *sauT*. Alignment position on the sides indicate base position in the original alignment. Note that in strains 2344, OCU404, CAM57, DNA genomic regions around this region showed similarity to strains in MahEastAsia2, despite their overall chromosome similarity to strains in MahEastAsia1. Predicted length of the import in OCU404 (underlined) was 5,798 bp.

### Fig S3 E

TH135 coordinate 773,856

```
Alignment pos. .
EA2_OCU462: 1401 ccgcggtgccggtggccacctcgagtgacgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA2_HP17 : 1401 ccgcggtgccggtggccacctcgagtgacgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA2_TH135 : 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA2_5581 : 1401 ccgcggtgccggtggccacctcgagtgacgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA2_P7 : 1401 ccgcggtgccggtggccacctcgagtgacgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA2_S2 : 1401 ccgcggtgccggtggccacctcgagtgacgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_CAM177: 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_CAM57 : 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_2344 : 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_OCU404: 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_OCU464: 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_OCU466: 1401 ccgcggtgccggtggccacctcgagtgatgcgcccggggtgggaaggctggccagcaccgtttcggcgcggtcggccaccctcttttggcg 1490
EA1_CAM78 : 1401 ----- 1490
mmsB (<-) -AlaThrGlyThrAlaValGluLeuSerAlaGlyProThrProLeuSerAlaLeuValThrGluAlaGlyAspAlaValAlaLysProSer
```

TH135 coordinate 773,946

774,031

```
Alignment pos. .
EA2_OCU462: 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA2_HP17 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA2_TH135 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA2_5581 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA2_P7 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA2_S2 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_CAM177: 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_CAM57 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_2344 : 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_OCU404: 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_OCU464: 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_OCU466: 1491 acgagggcggggcgcgccccggcgggcgacgagggcgttcgagggcctcgcgggcggtgtcgaaggcgacgacgtcgtgctgttcgccaatga 1580
EA1_CAM78 : 1491 ----- 1580
mmsB (<-) -SerAlaProArgAlaGlyAlaAlaValAlaLeuArgGluLeuAlaGluArgArgSerAspPheAlaValValAspHisGlnGluArgIle-
```

Fig S3. E-(i) continued

TH135 coordinate 774,036

```
Alignment pos. .
EA2_OCU462: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA2_HP17_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA2_TH135_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA2_5581_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA2_P7_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA2_S2_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_CAM177: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_CAM57_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_2344_: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_OCU404: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_OCU464: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_OCU466: 1581 gccgagatgccatgggaaatcccatgtttcccagcccgatgaagccgatcgatgagttctcccgatcgagttcggcgaaacgcctcgcg 1670
EA1_CAM78_: 1581 ----- 1670
mmsB (<-) LeuArgSerAlaMetProPheGlyMetAsnGlyLeuGlyIlePheGlyIleThrMet
```

TH135 coordinate 774,126

```
Alignment pos. .
EA2_OCU462: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA2_HP17_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA2_TH135_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA2_5581_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA2_P7_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA2_S2_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_CAM177: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_CAM57_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_2344_: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_OCU404: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_OCU464: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_OCU466: 1671 ggcgatgcggaagctgtcaaccgcccggcacaccggcgtagatggccacctgcaggaacacctcgcggatctcctcgcggggtcacacc 1760
EA1_CAM78_: 1671 ----- 1760
^ OCU464 import start position (prediction based on comparisons of selected genomes)
```

Fig S3. E-(i) continued



TH135 coordinate 776,236

Alignment pos. . . . .

EA2\_OCU462: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA2\_HP17\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA2\_TH135\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA2\_5581\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA2\_P7\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA2\_S2\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_CAM177: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_CAM57\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_2344\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_OCU404: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_OCU464: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_OCU466: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870  
EA1\_CAM78\_: 3781 cggcgccggctggccgcccgaatggccaaggcgtcggcgggggagtgccagtcgctggccttcgggcacggcctgcagctgcacggcgcc 3870

^ OCU464 recent import start position (fastGEAR prediction)

TH135 coordinate 776,325

Alignment pos. . . . .

EA2\_OCU462: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA2\_HP17\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA2\_TH135\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961 (776416)  
EA2\_5581\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA2\_P7\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA2\_S2\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_CAM177: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_CAM57\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_2344\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_OCU404: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_OCU464: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_OCU466: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961  
EA1\_CAM78\_: 3871 atgggattcacctgggagaacgacctgcagttcgcgctcaagcggggccaaggcgggtgagctgatgctggcgccgcccgggagcaccggg 3961

Fig S3. E-(i) continued



TH135 coordinate 776,417

Alignment pos. . . . .

EA2\_OCU462: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA2\_HP17\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA2\_TH135\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA2\_5581\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA2\_P7\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA2\_S2\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_CAM177: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_CAM57\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_2344\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_OCU404: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_OCU464: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_OCU466: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680  
EA1\_CAM78\_: 3962 cgcggat (638 bp) ttcgatcgcacgacaaggacttcaacgaggtggttcttcaccgacgtgcgggtgccggccgagAACCTGGTCGGTGA 4680

TH135 coordinate 777,135

Alignment pos. . . . .

EA2\_OCU462: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA2\_HP17\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA2\_TH135\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA2\_5581\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA2\_P7\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA2\_S2\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_CAM177: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_CAM57\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_2344\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_OCU404: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_OCU464: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_OCU466: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770  
EA1\_CAM78\_: 4681 actcaatcaagggtggctggtggccaacggttcgctgggtcacgagcgcaccatgatgtggtctgggggttcgCGGACCGCCTCGAGAACAT 4770

Fig S3. E-(i) continued

TH135 coordinate 777,226

```
Alignment pos. .
EA2_OCU462: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA2_HP17_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA2_TH135_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA2_5581_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA2_P7_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA2_S2_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_CAM177: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_CAM57_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_2344_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_OCU404: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_OCU464: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_OCU466: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggagatccagcgcaacatcatcgcccagcgggtgctc 5140
EA1_CAM78_: 4771 gatcgccgac (73 bp) ctcggctcggcagcgcctgg (227 bp) cacctcggaggtccagcgcaacatcatcgcccagcgggtgctc 5140
```

TH135 coordinate 777,595

```
Alignment pos. .
EA2_OCU462: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA2_HP17_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA2_TH135_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA2_5581_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA2_P7_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA2_S2_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_CAM177: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_CAM57_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_2344_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_OCU404: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_OCU464: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_OCU466: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
EA1_CAM78_: 5141 ggcctgcc (1300 bp) caggctcagcgttatcccggccacggcctggatcgccaccggcagccaacctatgcatcagcgaaatgtggttg 6520
```

Fig S3. E-(i) continued



**Fig. S3 E – ii.**

TH135 coordinate 826,143

```
Alignment pos. .
EA2_OCU462: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA2_HP17: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA2_TH135: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA2_5581: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA2_P7: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA2_S2: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA1_CAM177: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
EA1_CAM57: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
EA1_2344: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
EA1_OCU404: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
EA1_OCU464: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacatcagcgtggcgtgcgg 960
EA1_OCU466: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
EA1_CAM78: 871 cggcgcgctggccgagcccgcgtagatgcccaggaagttcggtagagctctcgtcgagcagactcttgccccacattagcgtggcgtgcgg 960
pdc(<-) ProAlaSerAlaSerGlyAlaTyrIleGlyLeuPheAsnProSerSerGluAspLeuLeuSerLysGlyTrpMetLeuThrAlaHisPro
```

TH135 coordinate 826,233

```
Alignment pos. .
EA2_OCU462: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA2_HP17: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA2_TH135: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA2_5581: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA2_P7: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA2_S2: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_CAM177: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_CAM57: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_2344: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_OCU404: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_OCU464: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_OCU466: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
EA1_CAM78: 961 caccacgtcggccgcccagcagcgcctcgagctccttgatcgctgcagtcggtgcaccagcaggtcggccagcagcgtgatccggtgctc 1050
pdc(<-) ValValAspAlaAlaLeuLeuAlaGluLeuGluLysIleAlaGlnLeuArgHisValLeuLeuAspAlaLeuValThrIleArgHisGlu
```

Fig S3. E-(ii) continued

TH135 coordinate 826,323 826,377

Alignment pos. . . . .

EA2\_OCU462: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtgccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA2\_HP17: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtgccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA2\_TH135: 1051 gccgatcagtgccgcgggcggcctcgggtgaacaacgccagcgcgcgggggctggtgccgccggtgtagcggggcagcggagcctcgggtgg 1140

EA2\_5581: 1051 gccgatcagtgccgcgggcggcctcgggtgaacaacgccagcgcgcgggggctggtgccgccggtgtagcggggcagcggagcctcgggtgg 1140

EA2\_P7: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtgccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA2\_S2: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtgccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_CAM177: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_CAM57: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_2344: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_OCU404: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_OCU464: 1051 gccgatcagtgccgcgggcggcctcgggtgaacaacgccagcgcgcgggggctggtgccgccggtgtagcggggcagcggagcctcgggtgg 1140

EA1\_OCU466: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

EA1\_CAM78: 1051 gccgatcagtgccgcgggcggcctcgggtgaacatcgccagcgcgcgggggctggtaccgccggtgtagcggggcagcgcagcctcgggtgg 1140

pdC(<-) glyIleLeuAlaAlaAlaAlaGluThrPheLeuAlaLeuAlaArgProSerThrGlyGlyThrTyrArgProLeuProAlaGluProPro

TH135 coordinate 826,413 826,427 827,156

Alignment pos. . . . .

EA2\_OCU462: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA2\_HP17: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA2\_TH135: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA2\_5581: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA2\_P7: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA2\_S2: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_CAM177: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_CAM57: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_2344: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_OCU404: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_OCU464: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_OCU466: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

EA1\_CAM78: 1141 ctcggtggggaagcggg(705 bp, no substitution detected)cgccgaggtcctggcgaccggccacgacgggcgggcccag 1890

^OCU464 recent import end pos. (prediction by fastGEAR)

pdC(<-) GluThrProPheArgAla

MAV\_0824 (->) --AlaGluValLeuAlaThrGlyAspAspGlyArgPro-

Fig S3. E-(ii) continued

TH135 coordinate 827,123

827,246

```
Alignment pos. .
EA2_OCU462: 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcgggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA2_HP17__ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA2_TH135_ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA2_5581__ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA2_P7____ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA2_S2____ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_CAM177: 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_CAM57_ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_2344__ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_OCU404: 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_OCU464: 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_OCU466: 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
EA1_CAM78_ : 1891 ccaggtcaggat ( 51 bp) gggcggacaacgcggtgagctggacgctggtcagctcgtcgcagcagaaggcgcaggacgggaagtac 2030
MAV_0824 (->) SerGlnValArgMet
```

**(E). Alignment suggesting recombination between MahEastAsia1 and MahEastAsia2: MCE locus 3.**

**(i)** Left border of recent import predicted by fastGEAR. An alignment for 5,281 bp from *mmsB* to MAH\_0777-euivalent gene is shown. Crossover region is indicated by grey background. Imported region in OCU464 is underlined. **(ii)** Right border of recent import. An alignment for 1,159 bp from *pdC* (MAH\_0823) to MAH\_0824-equivalent gene is shown.