Supplemental Figure S1: DENV1 Whole Genome ML Trees. (a) DENV1 Whole Genome ML tree, (b) Genotype 1-I, (c) Genotype 1-IV, (d) Genotype 1-V (isolates incorrectly classified as 1-III indicated by arrows) and sylvatic. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
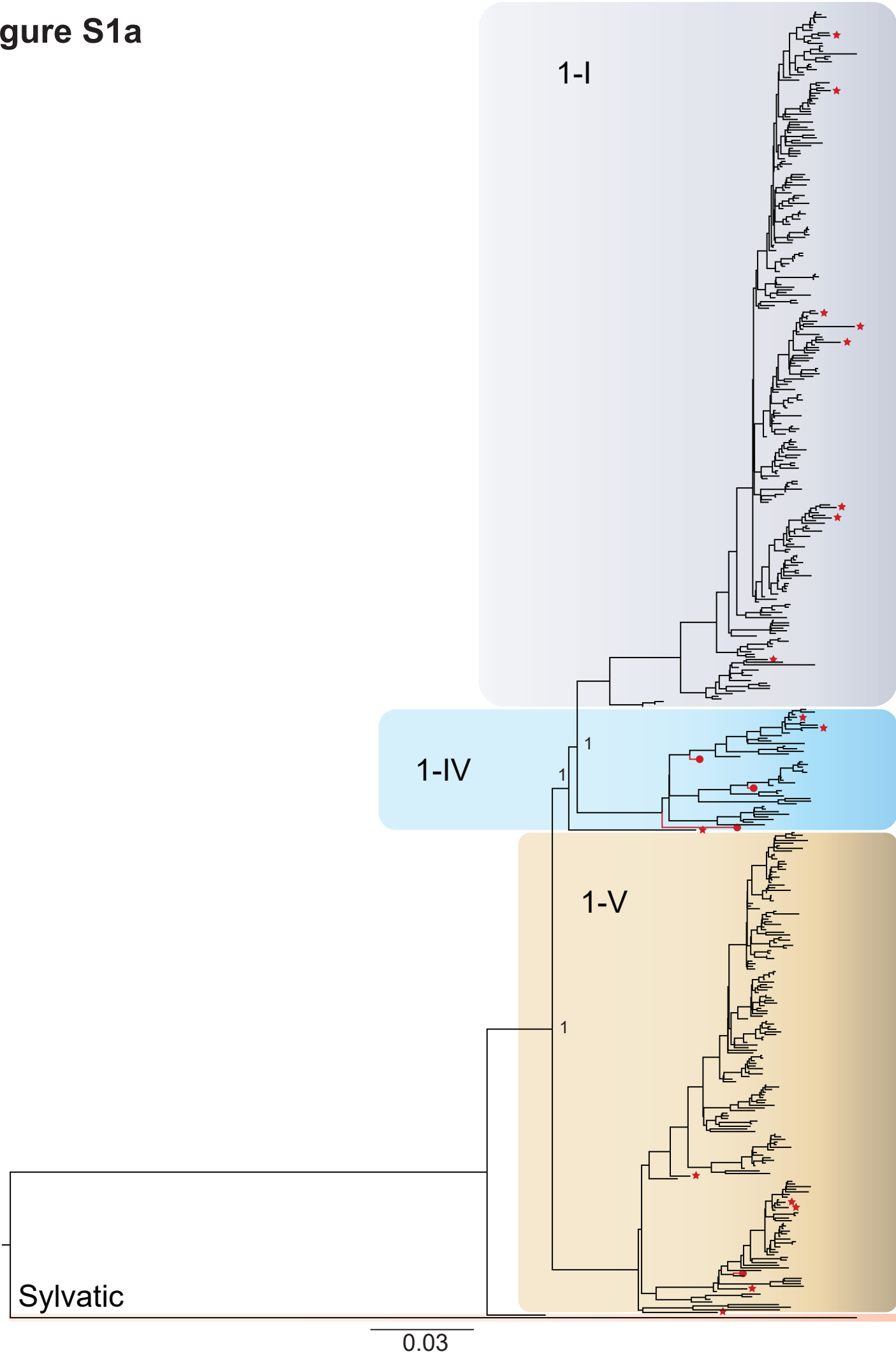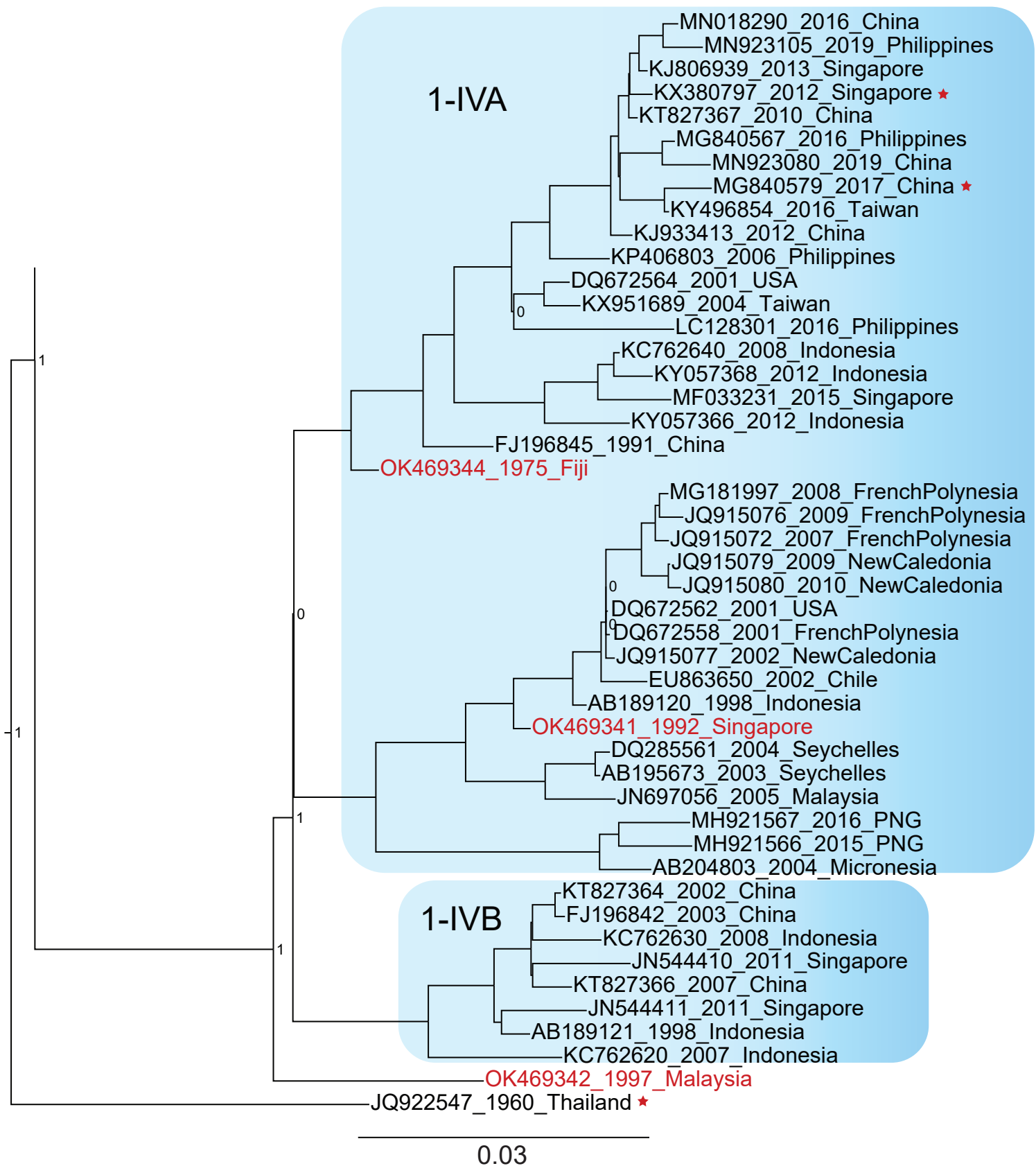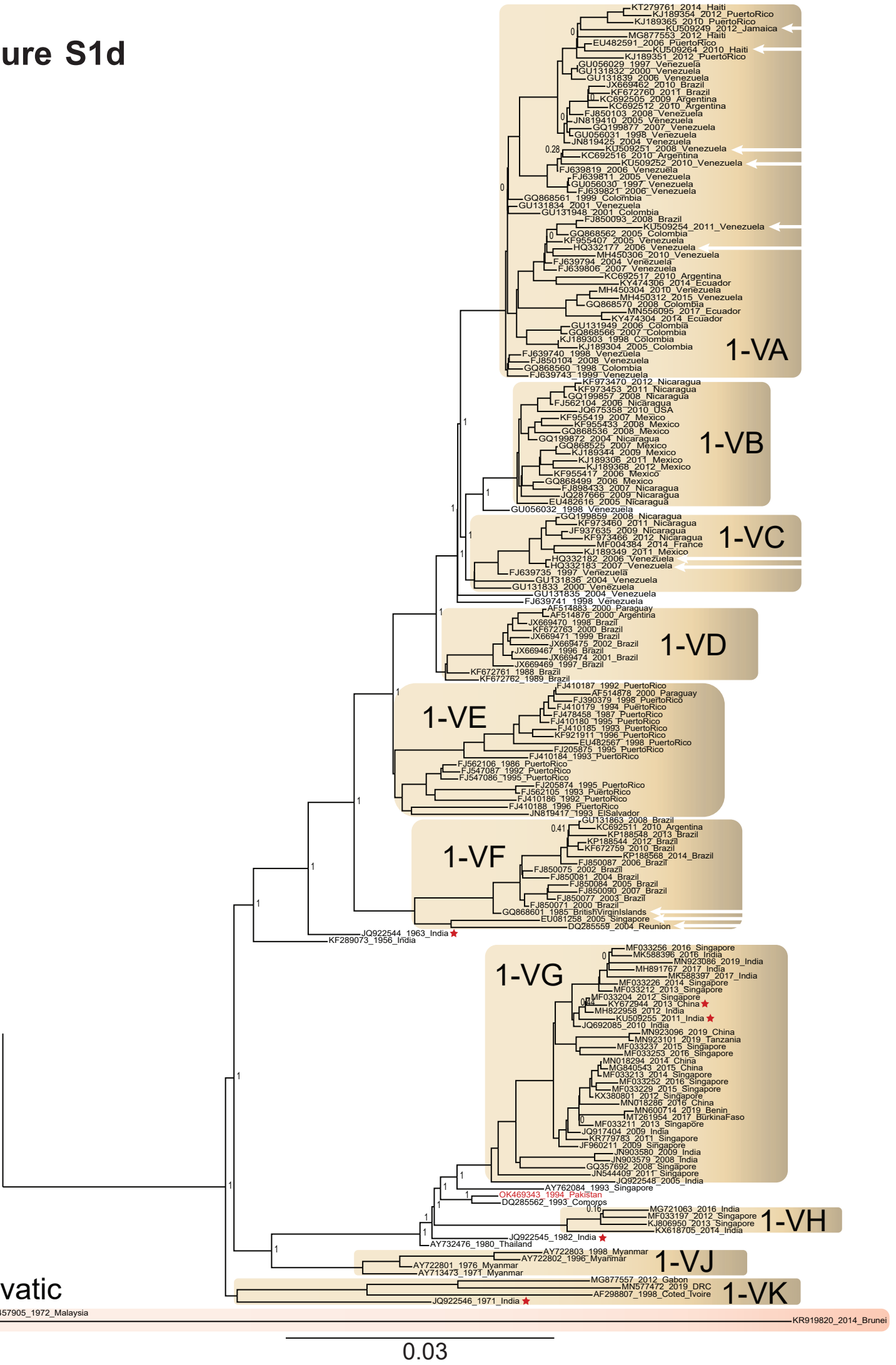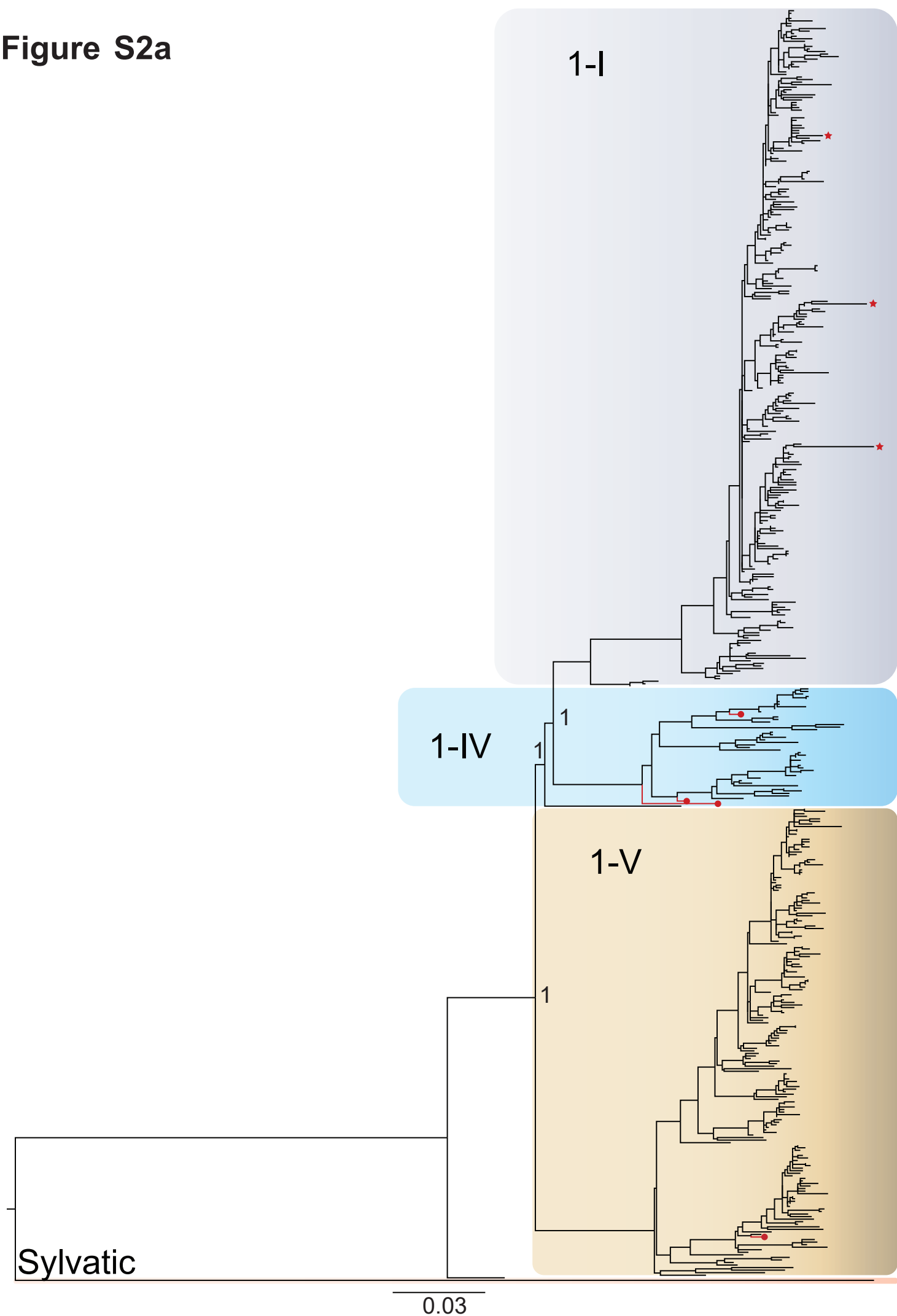
Figure S1a

1-I

1-IV

1-V

Sylvatic

0.03

Figure S1b

Figure S1c

1-IVA

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KY057366_2012_Indonesia
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1-IVB

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0.03

Figure S1d

Supplemental Figure S2: DENV1 E Gene ML Trees. (a) DENV1 E gene ML tree, (b) Genotype 1-I, (c) Genotype 1-IV, (d) Genotype 1-V (isolates incorrectly classified as 1-III indicated by arrows) and sylvatic. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
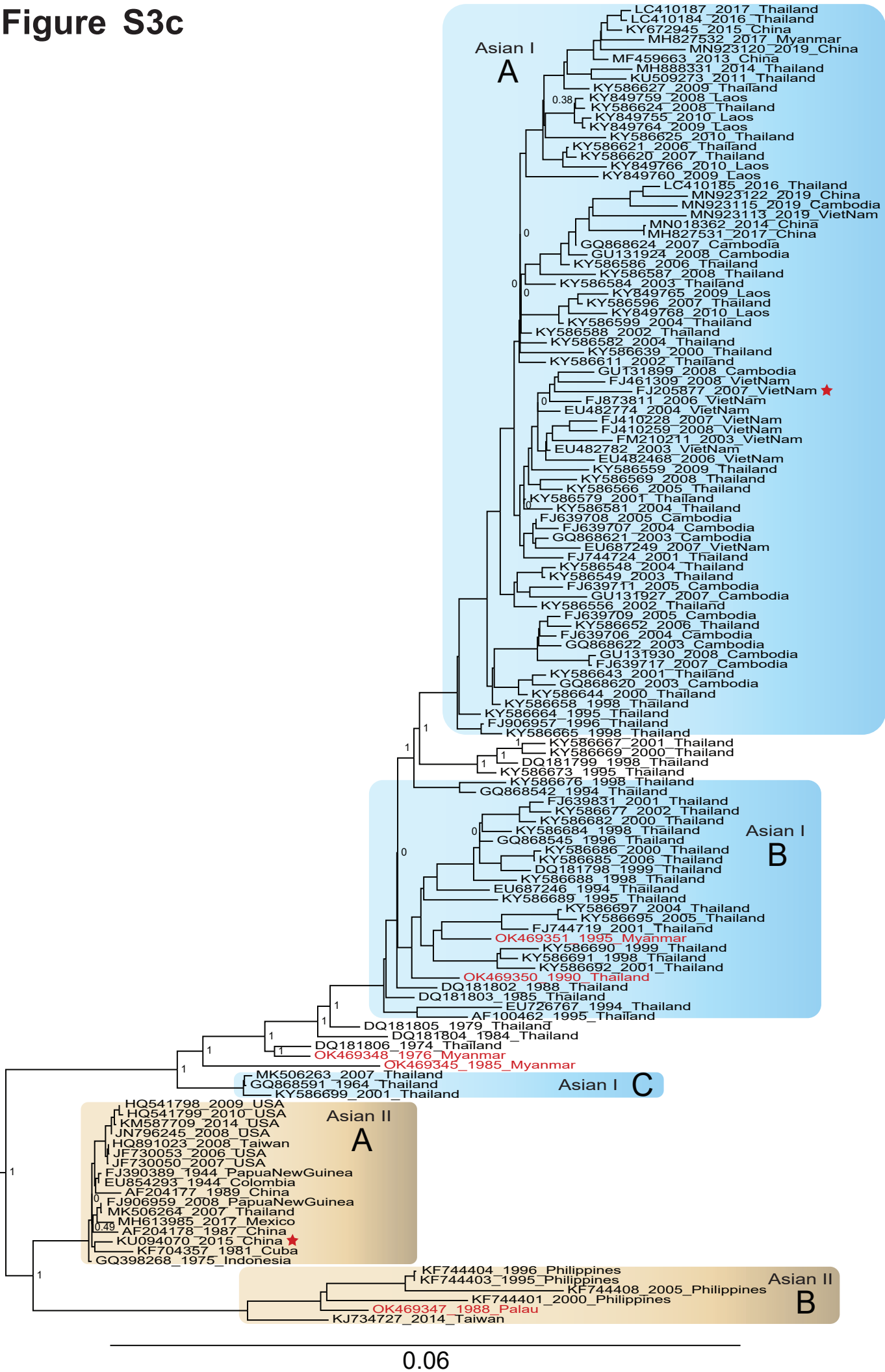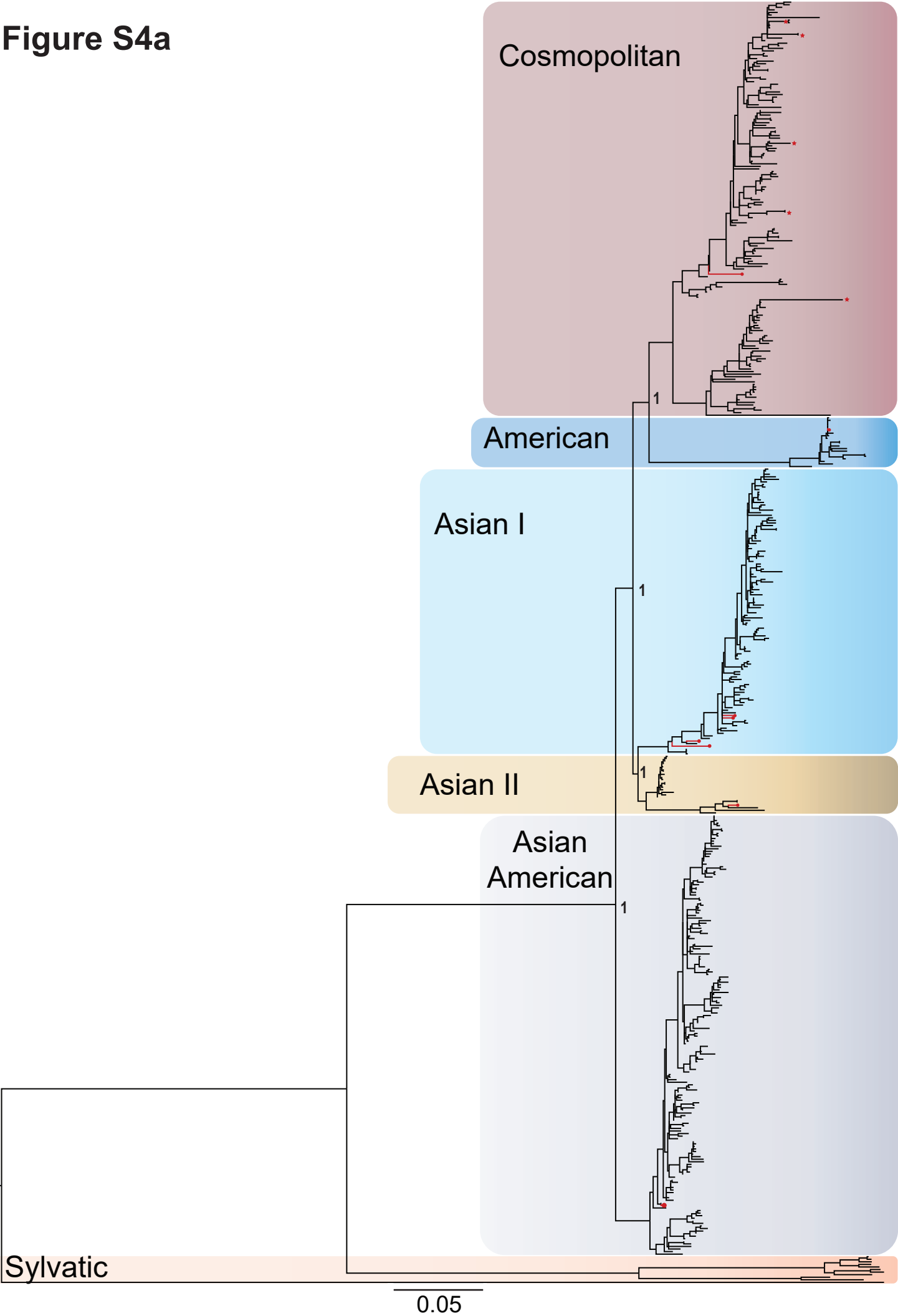
Figure S2a

1-I

1-IV

1-V

Sylvatic

1

1

1

0.03
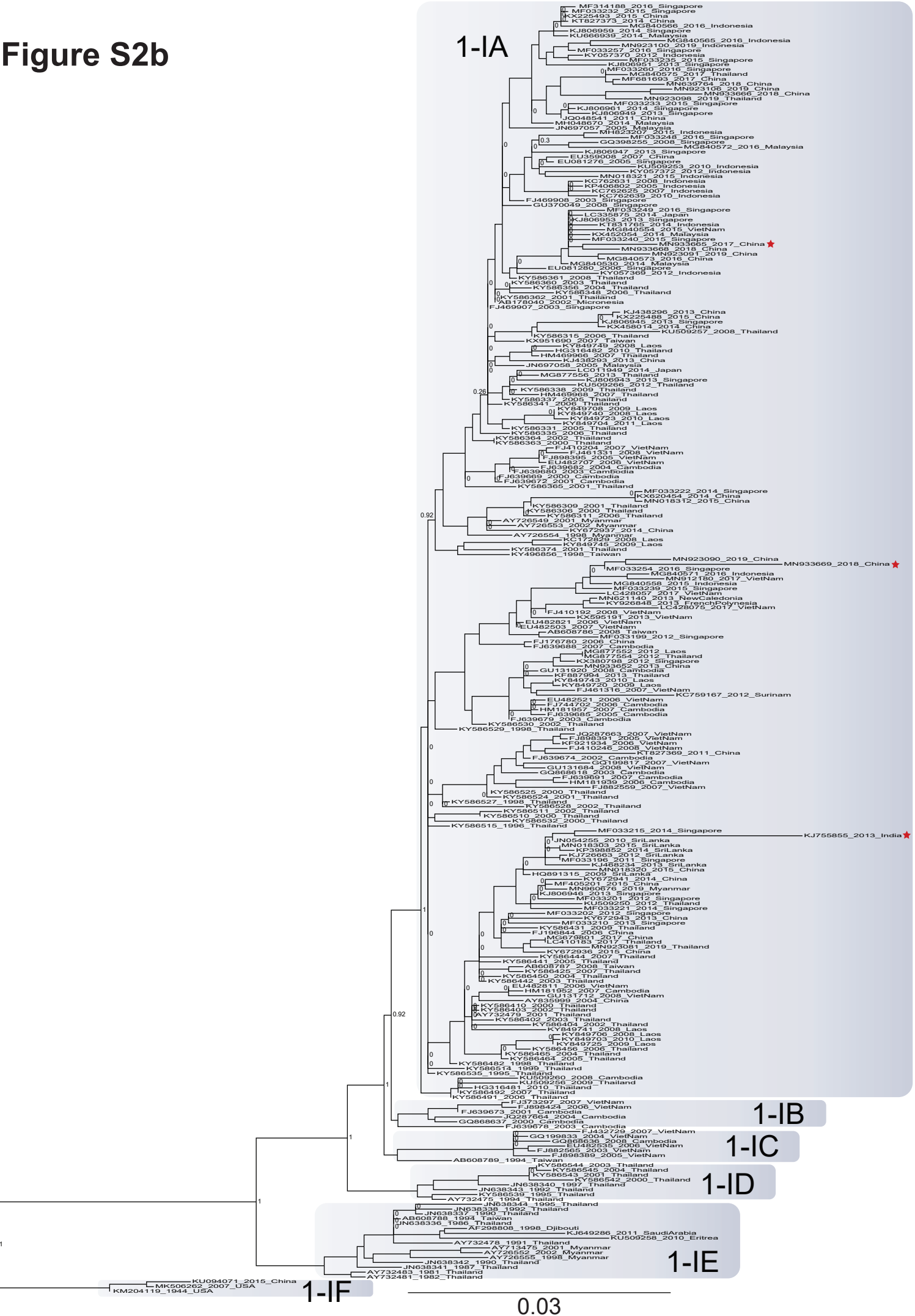
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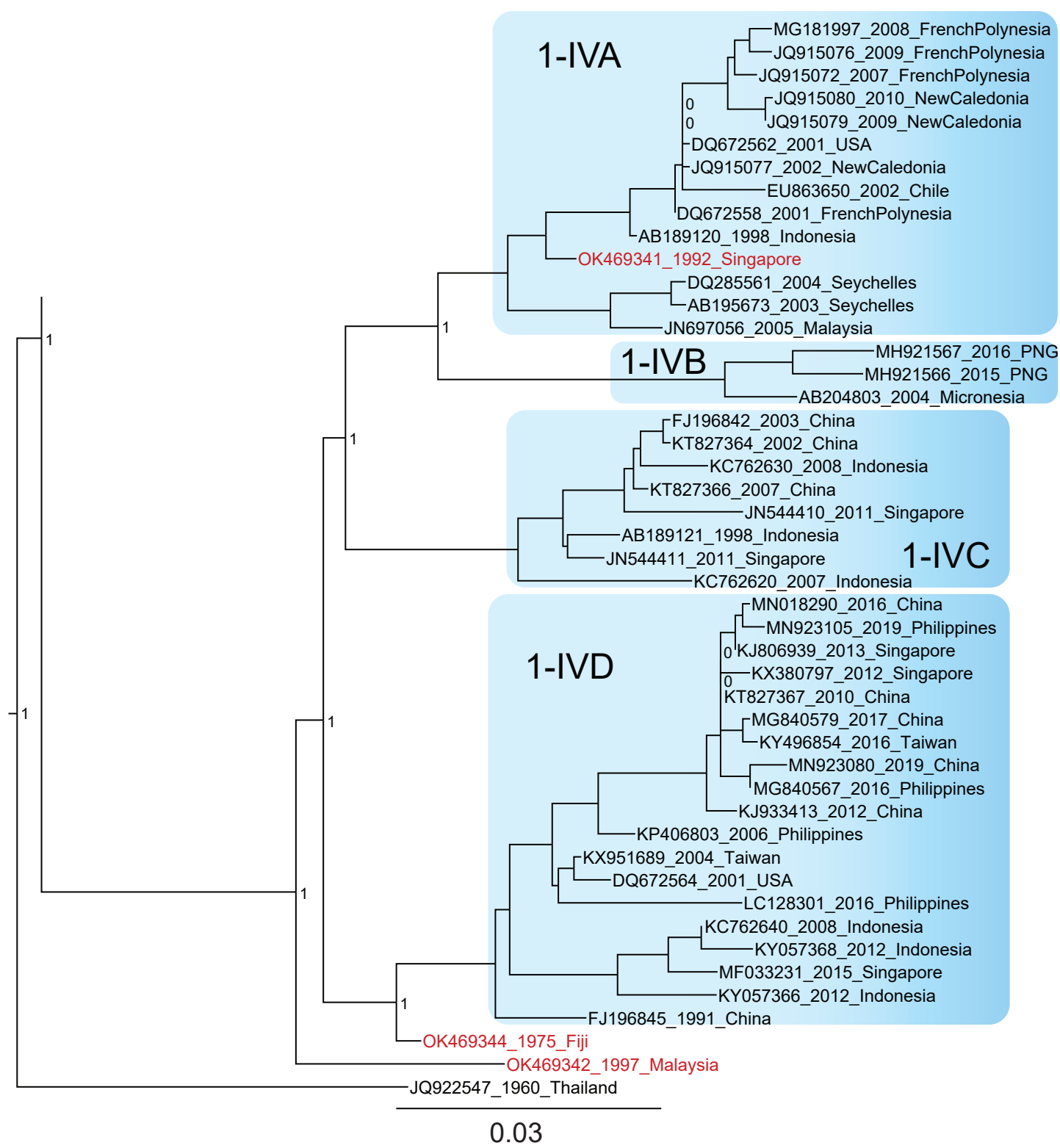
Figure S2c

Figure S2d
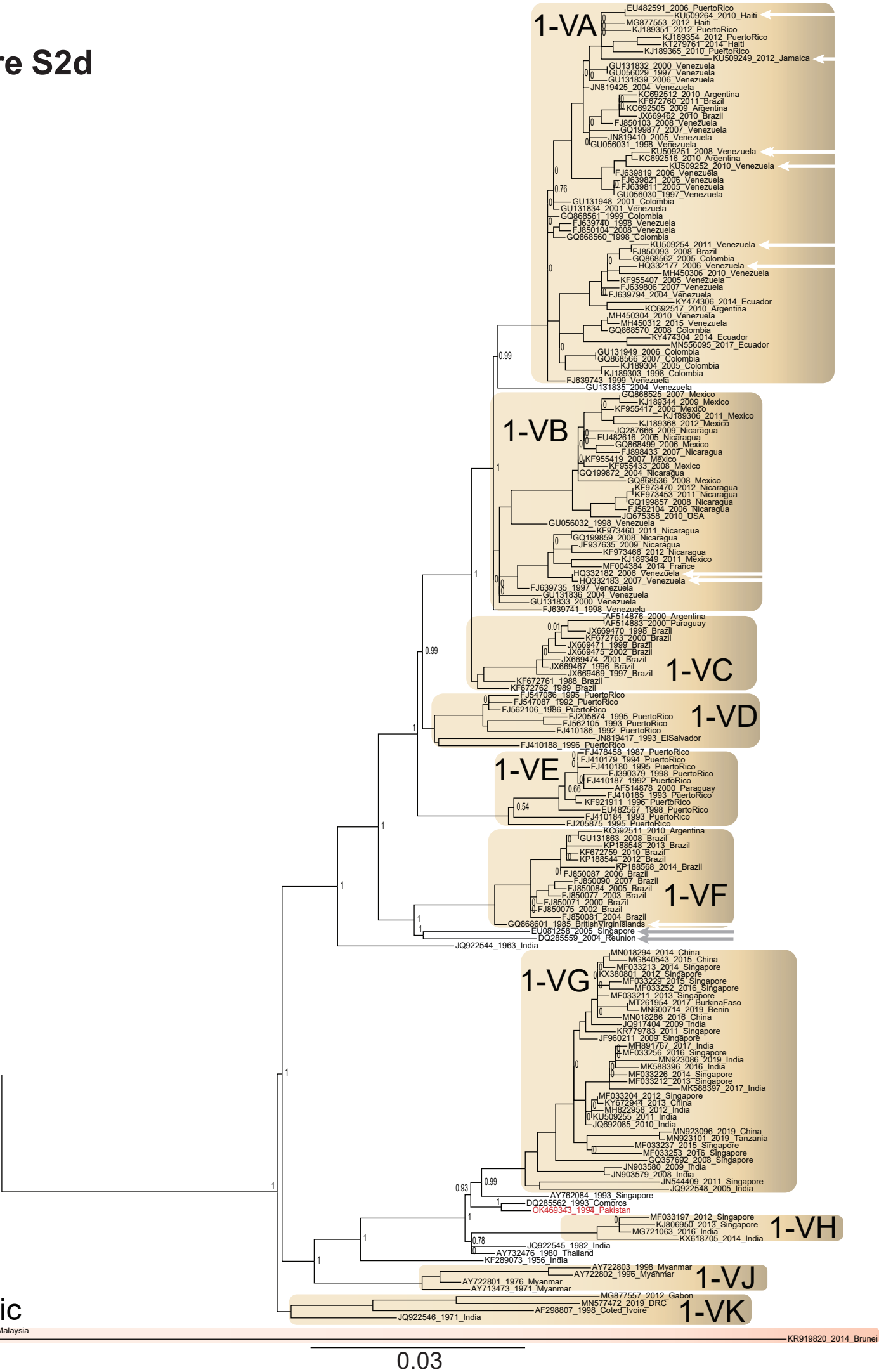
Supplemental Figure S3: DENV2 Whole Genome ML Trees. (a) DENV2 Whole Genome ML tree, (b) Asian American genotype, (c) Asian I and Asian II genotypes, (d) Cosmopolitan genotype, (e) American and sylvatic genotypes. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
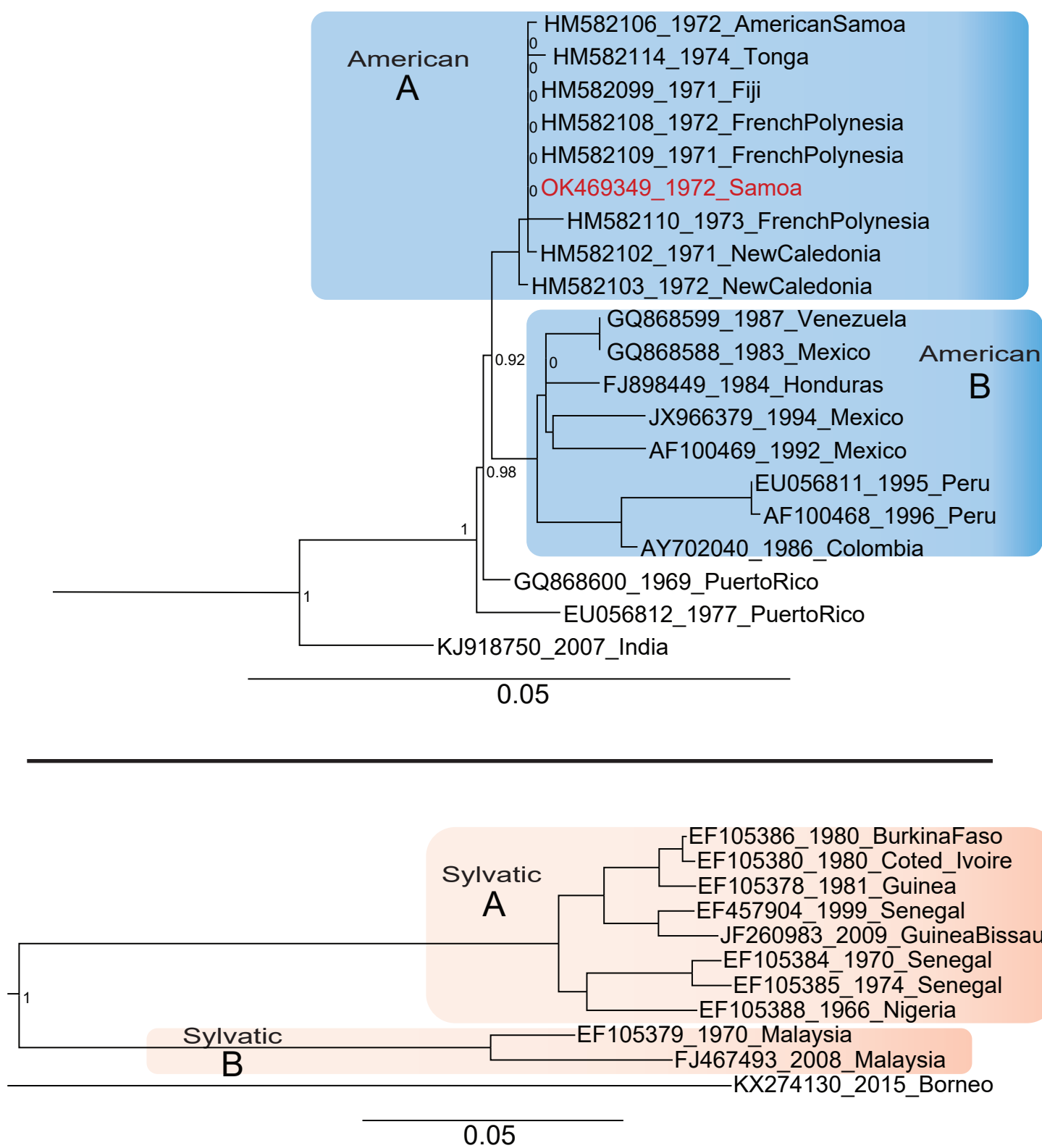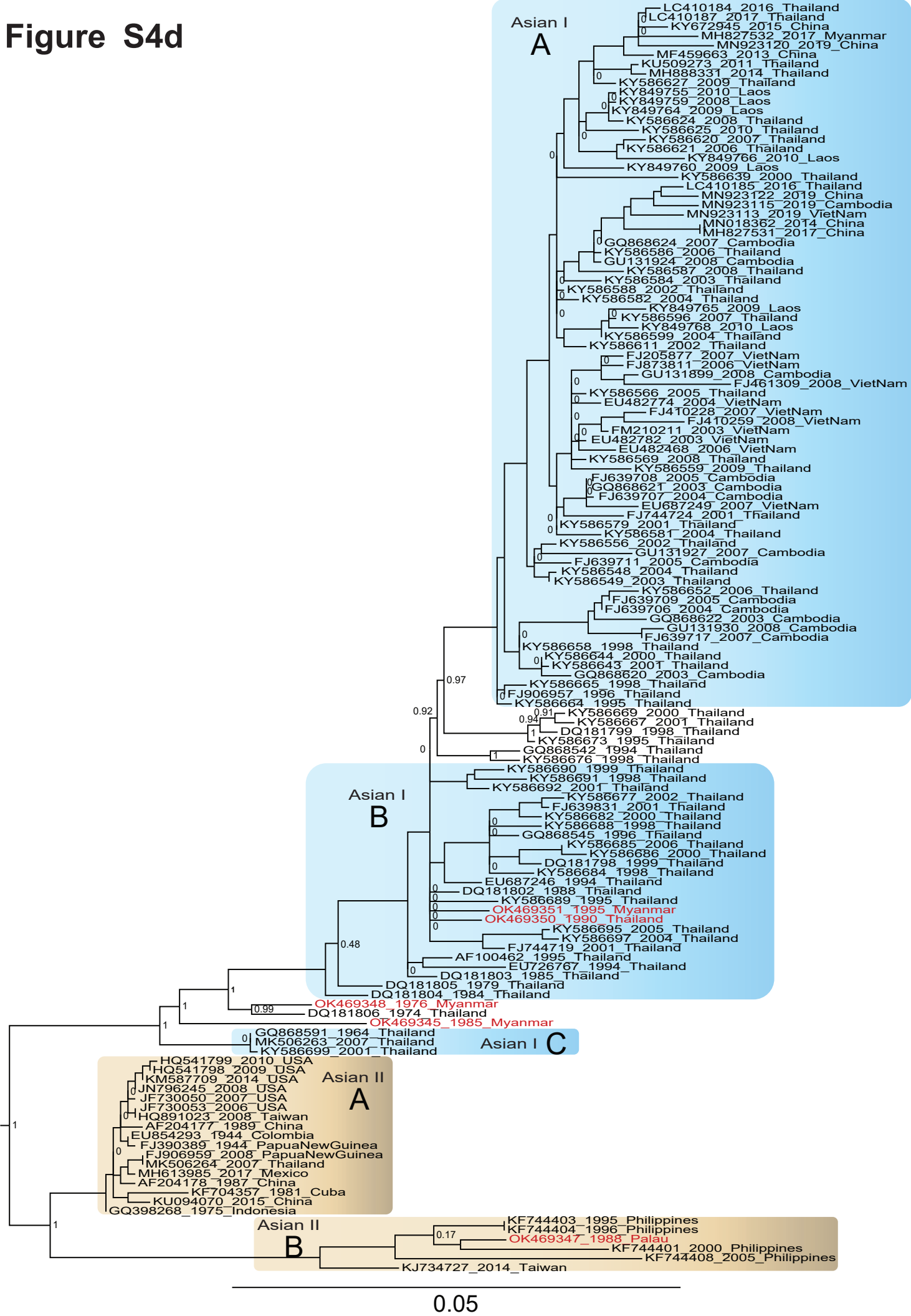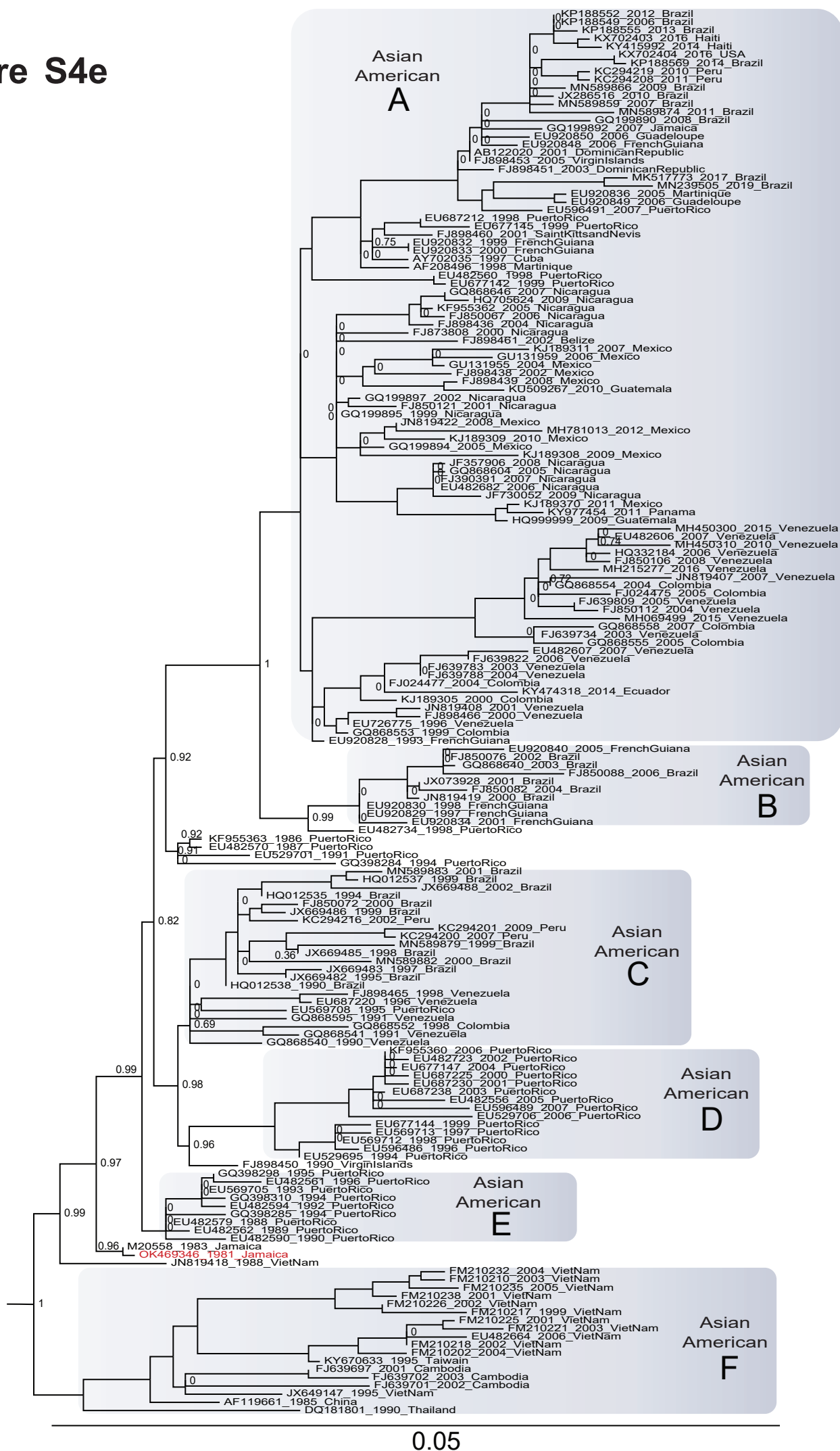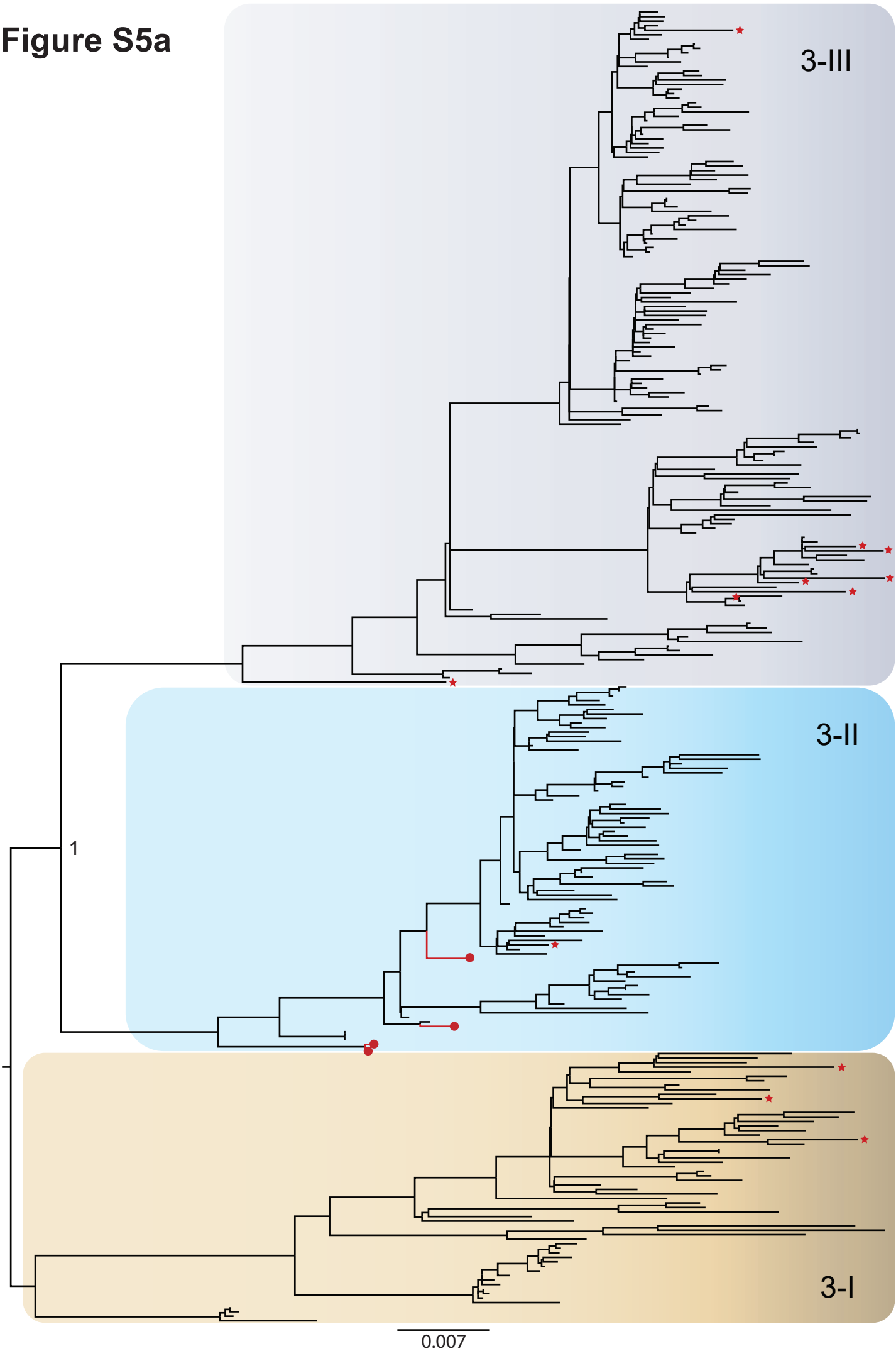
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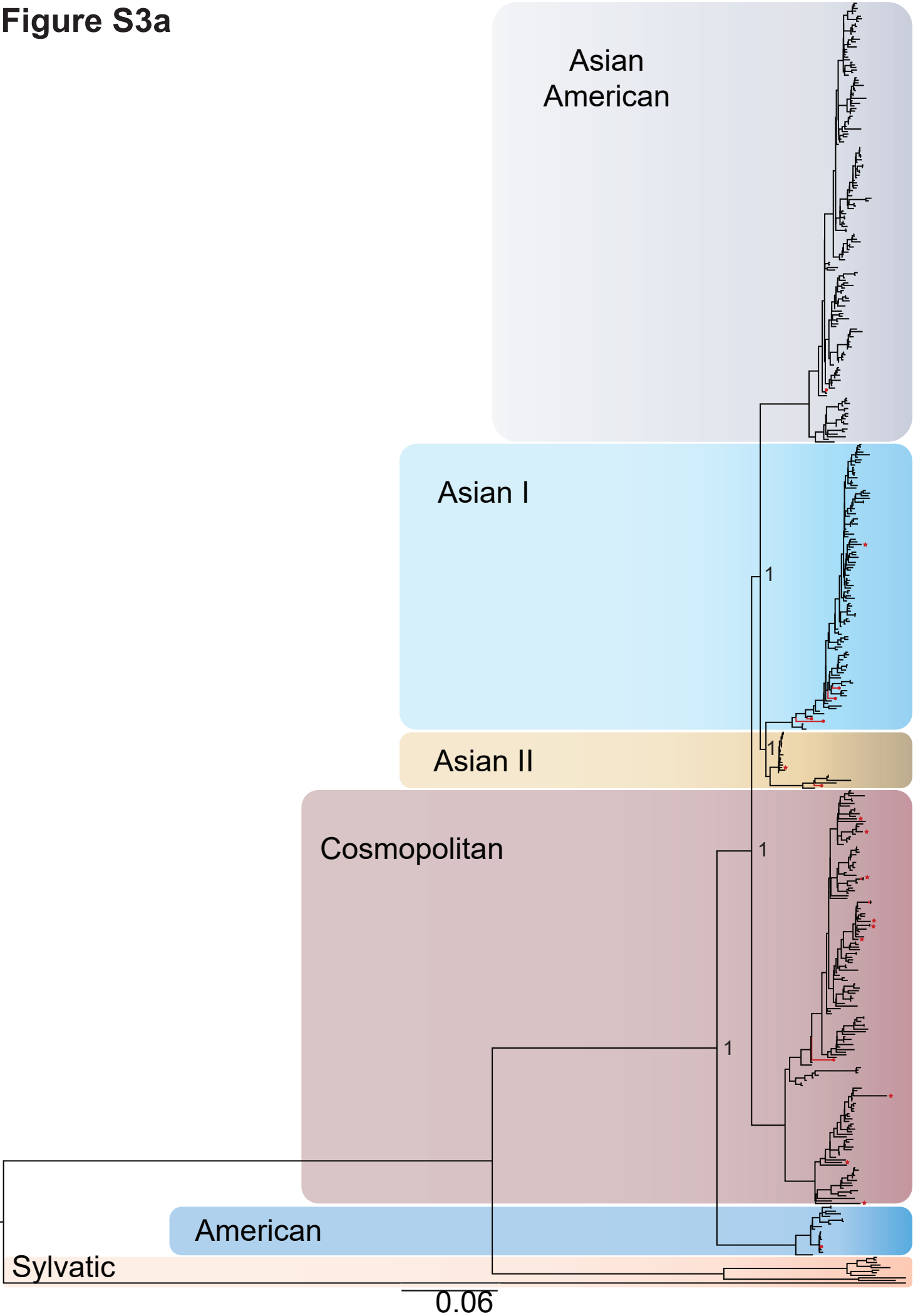
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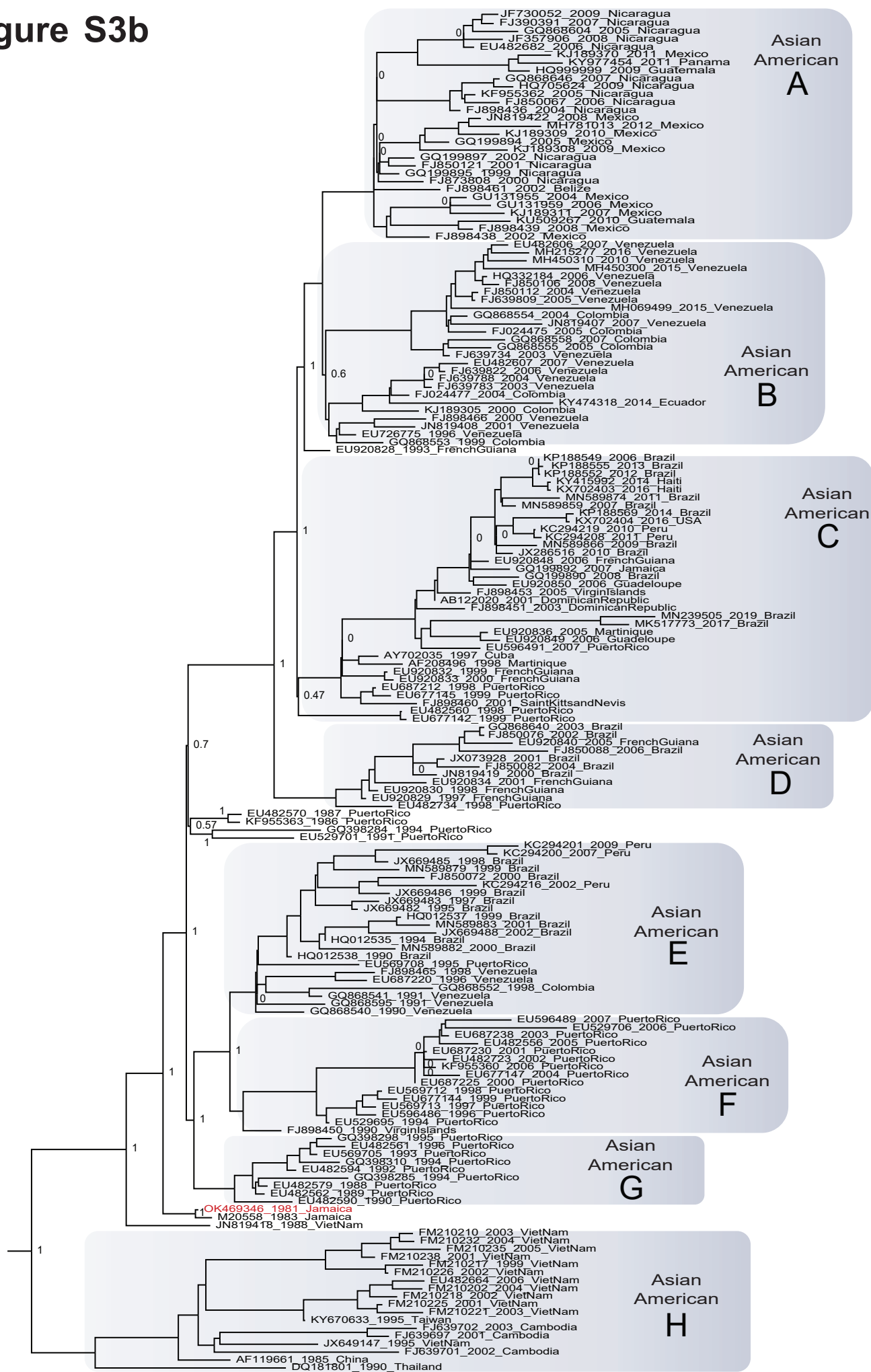
Figure S3c

Figure S3d

Figure S3e
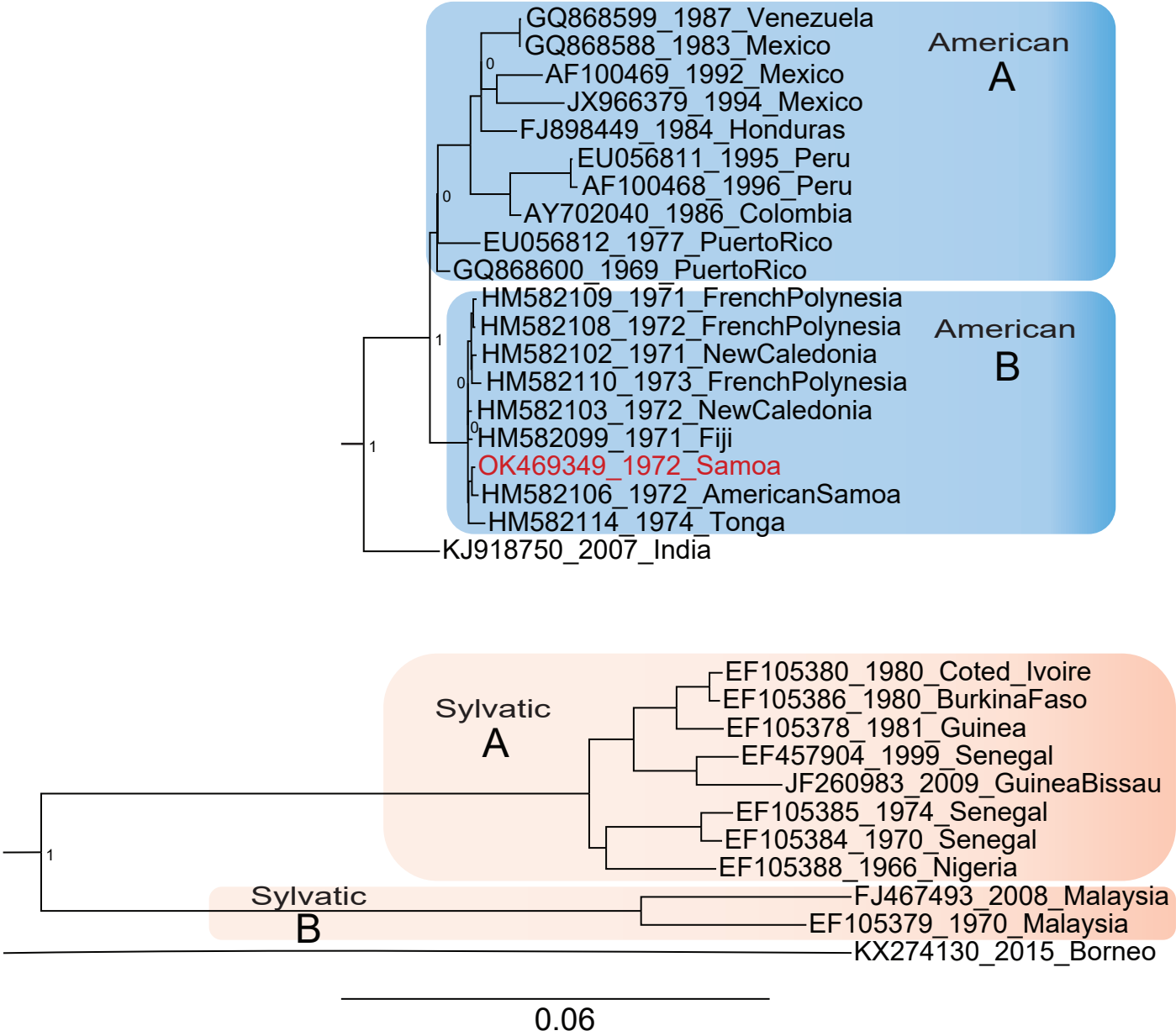
Supplemental Figure S4: DENV2 E Gene ML Trees. (a) DENV2 E gene ML tree, (b) Cosmopolitan genotype, (c) American and sylvatic genotypes, (d) Asian I and Asian II genotypes, (e) Asian American genotype. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
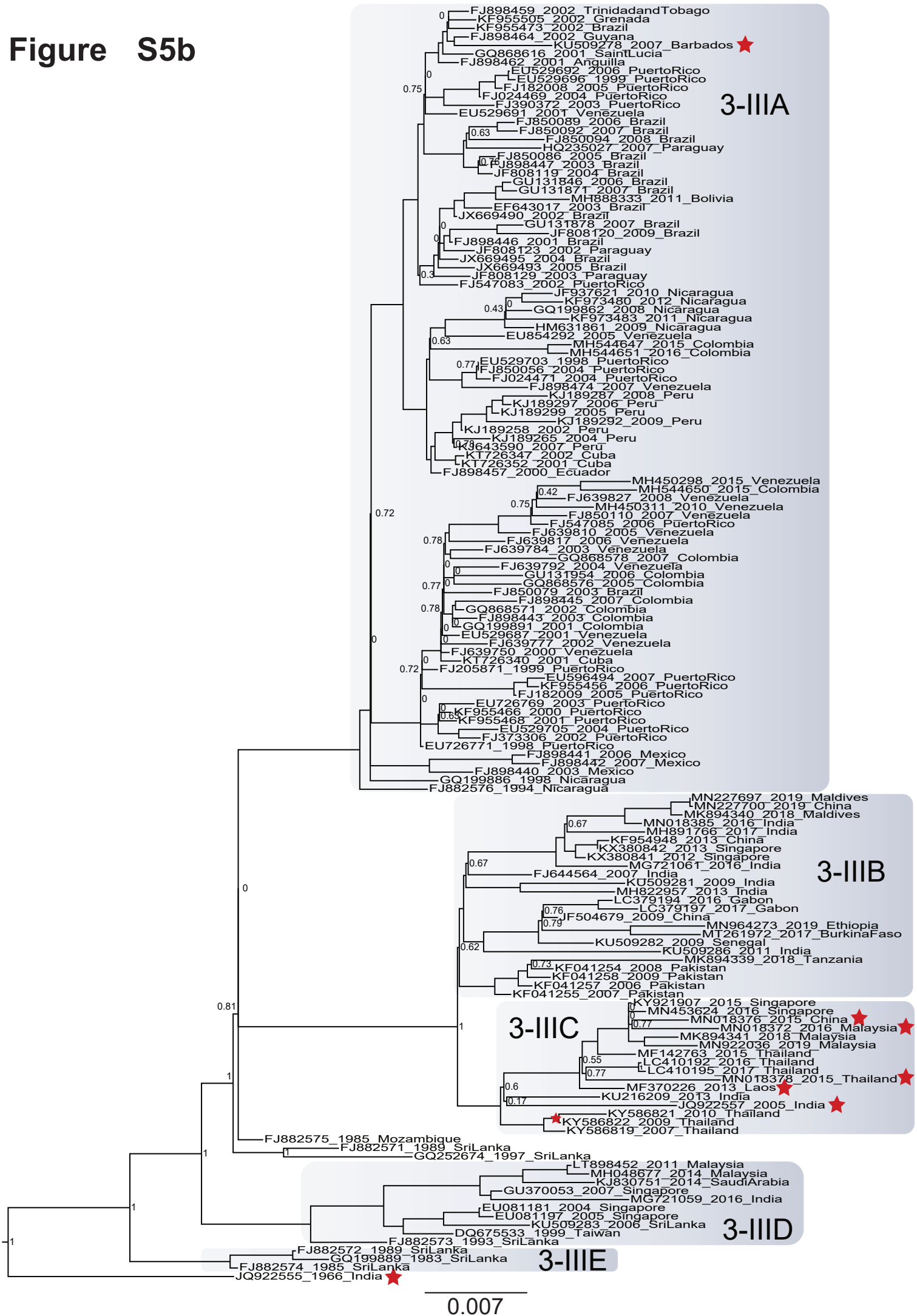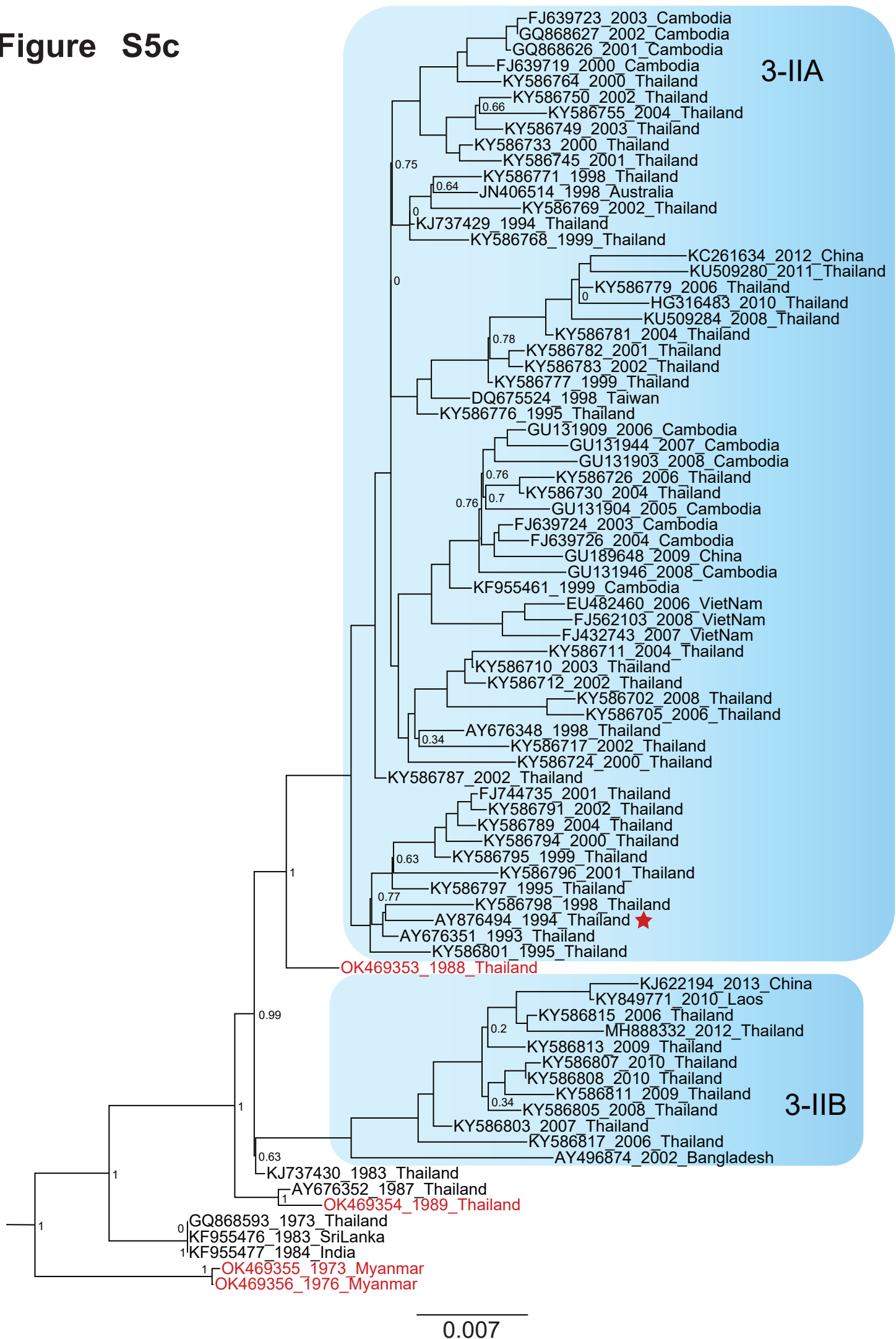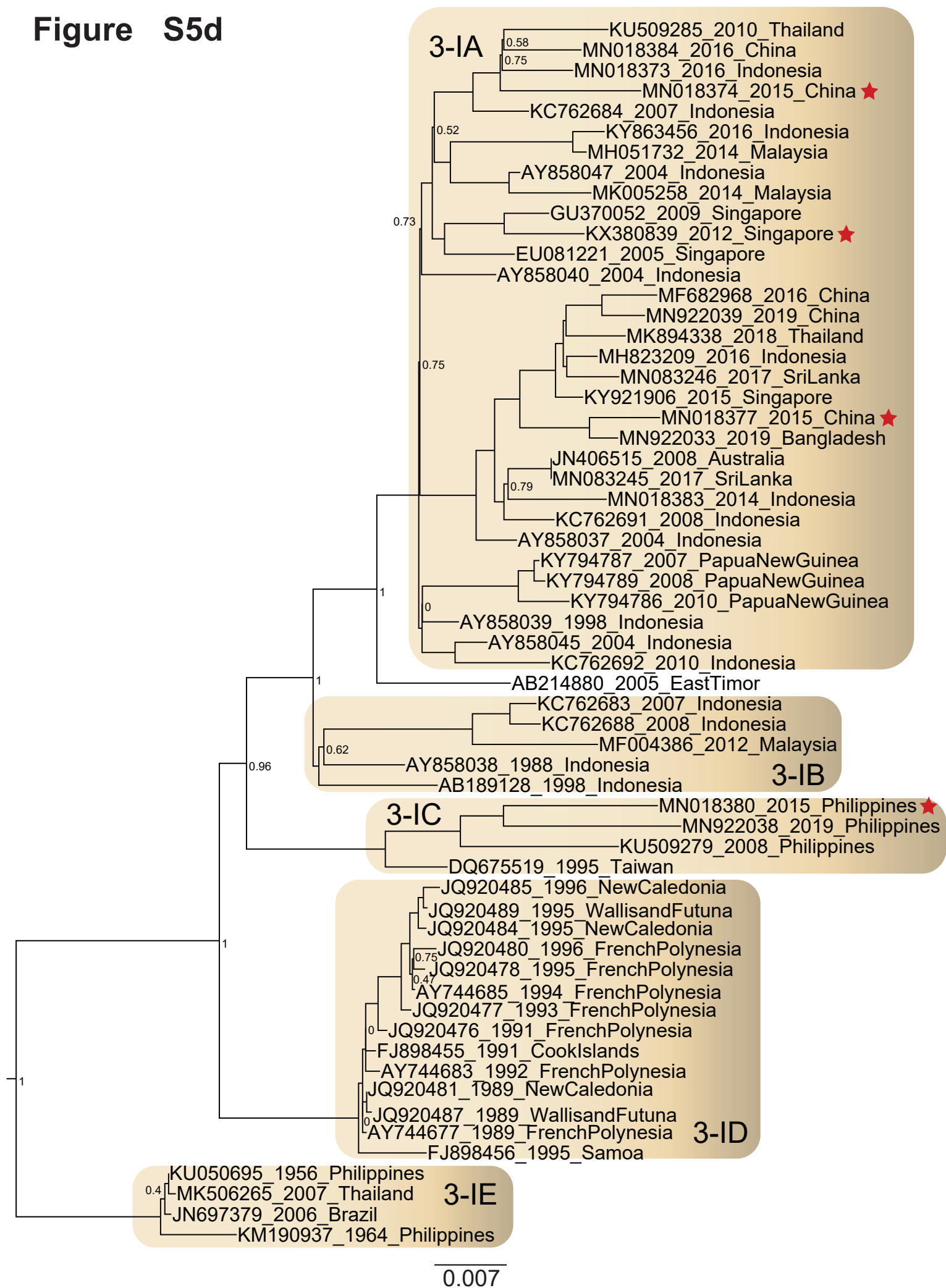
Figure S4a

Figure S4b

Figure S4c

Figure S4d

Figure S4e

Supplemental Figure S5: DENV3 Whole Genome ML Trees. (a) DENV3 Whole Genome ML tree, (b) Genotype 3-III, (c) Genotype 3-II, (d) Genotype 3-I. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
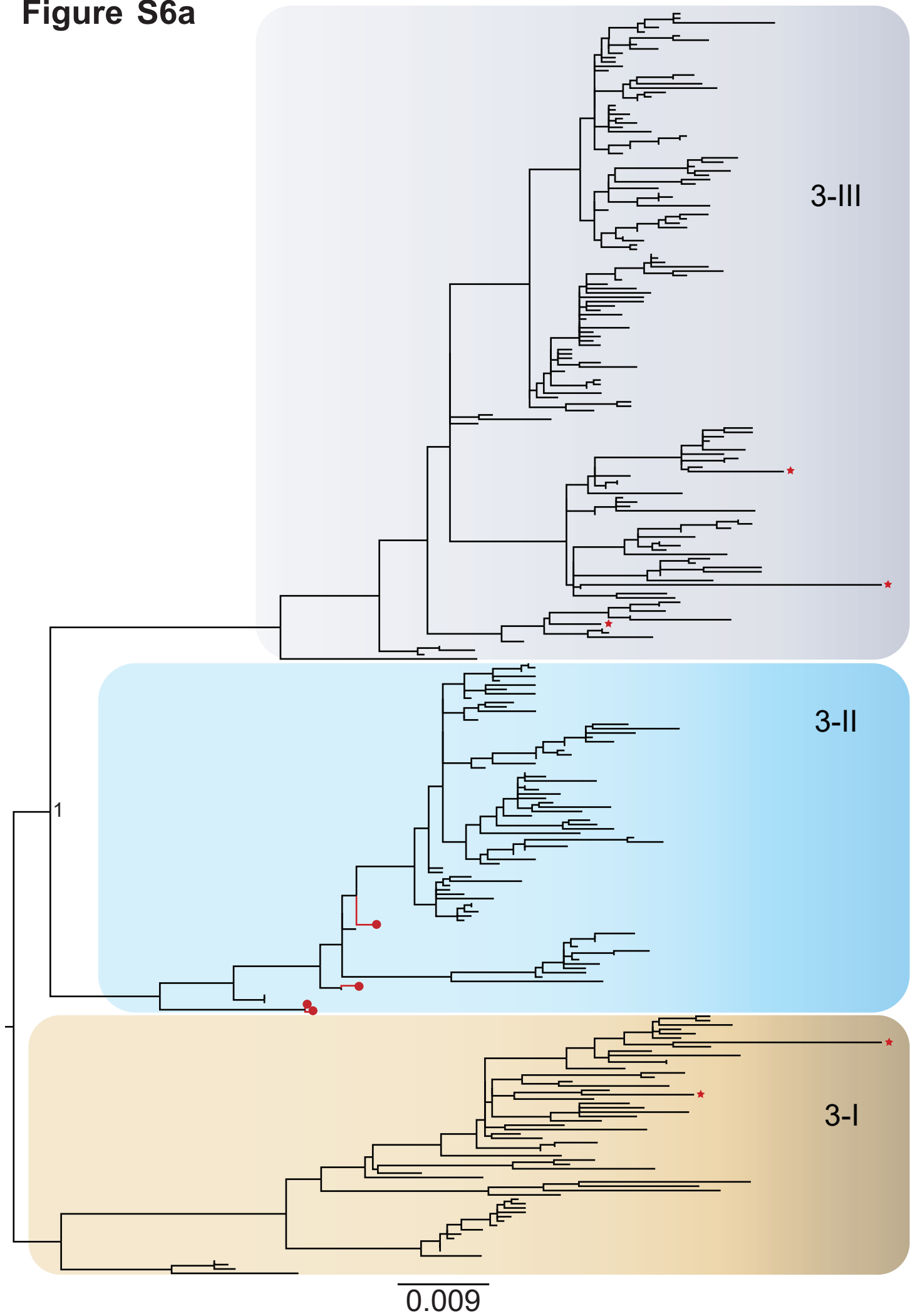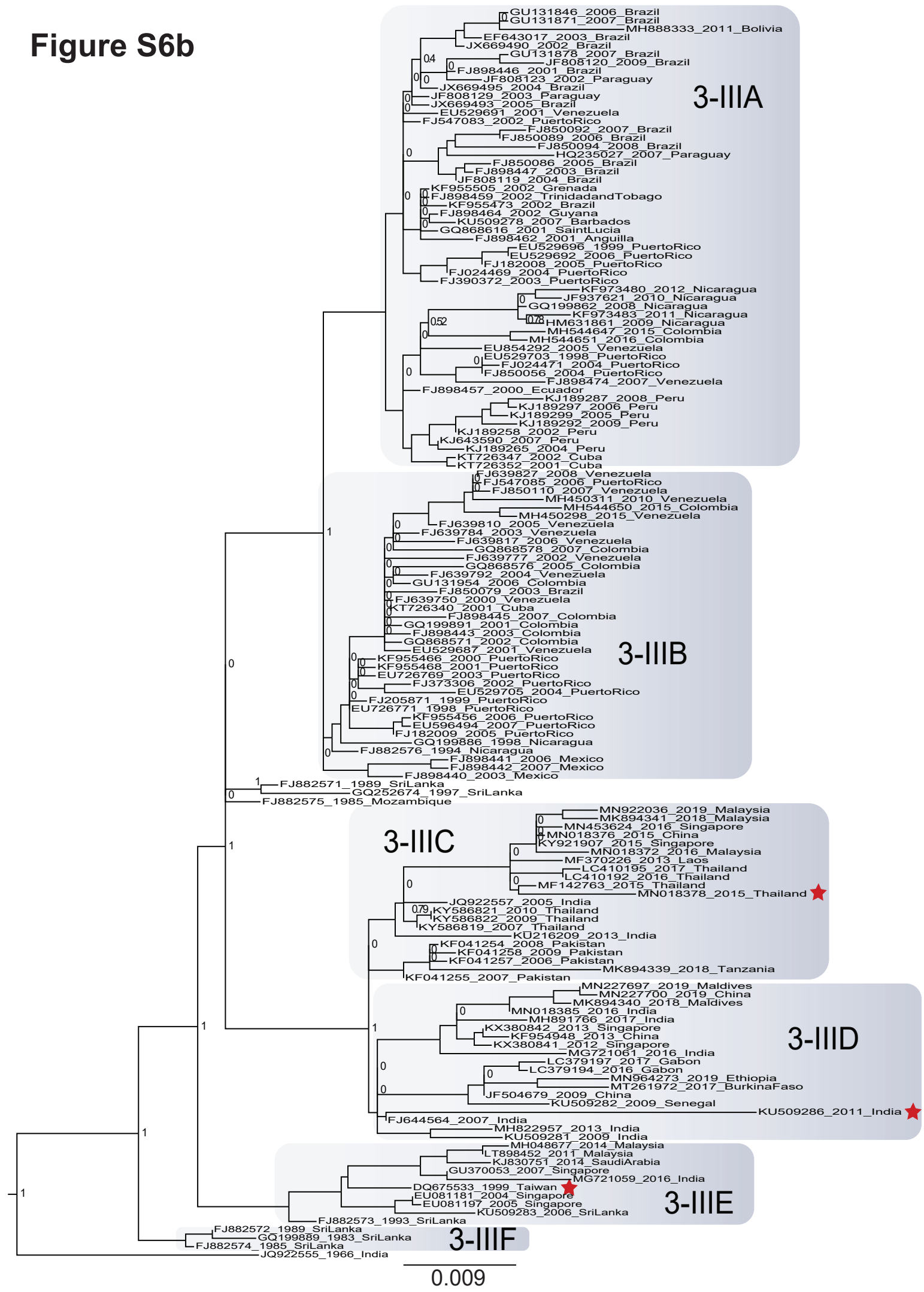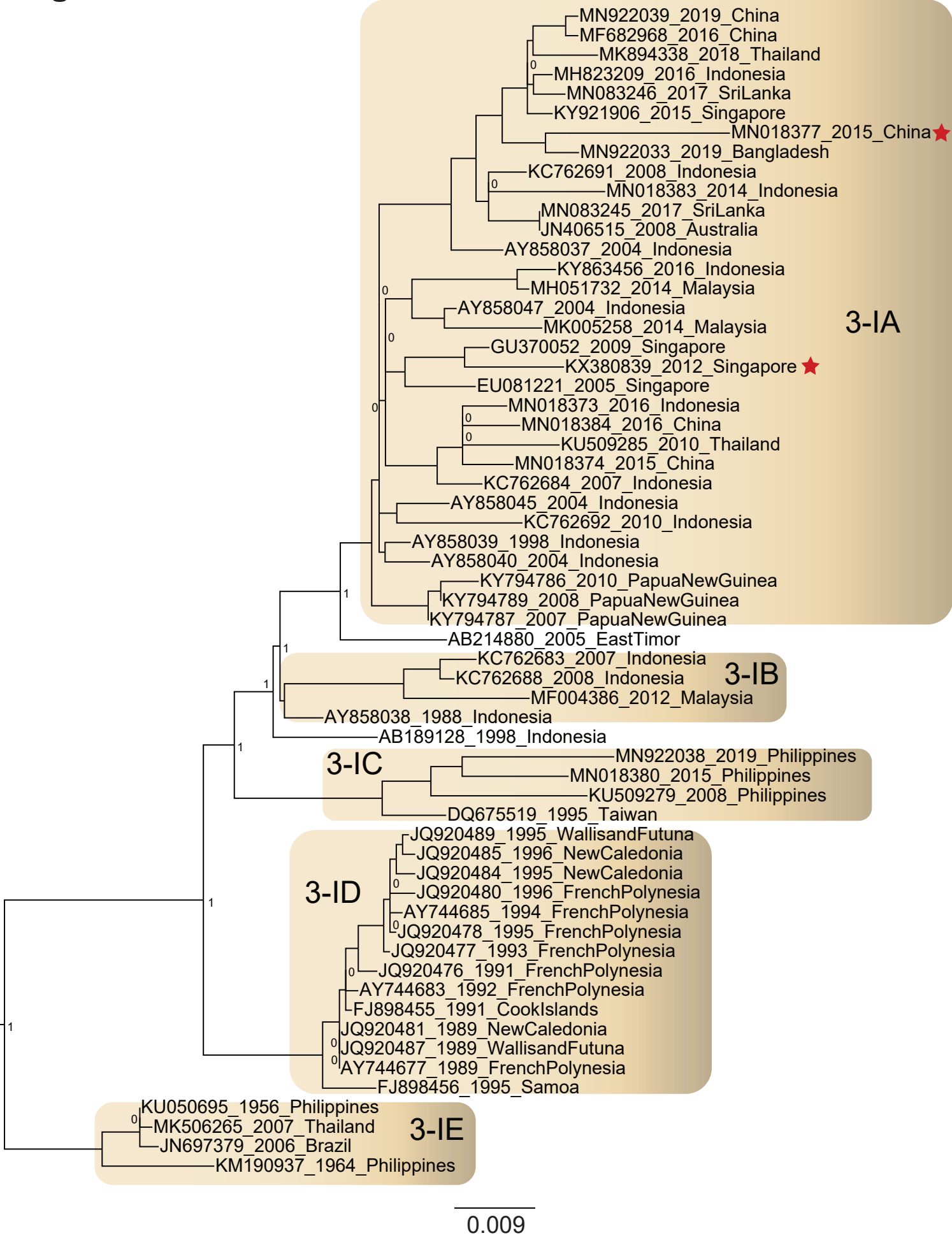
Figure S5a

Figure S5b

Figure S5c

Figure S5d

Supplemental Figure S6: DENV3 E Gene ML Trees. (a) DENV3 E gene ML tree, (b) Genotype 3-III, (c) Genotype 3-II, (d) Genotype 3-I. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
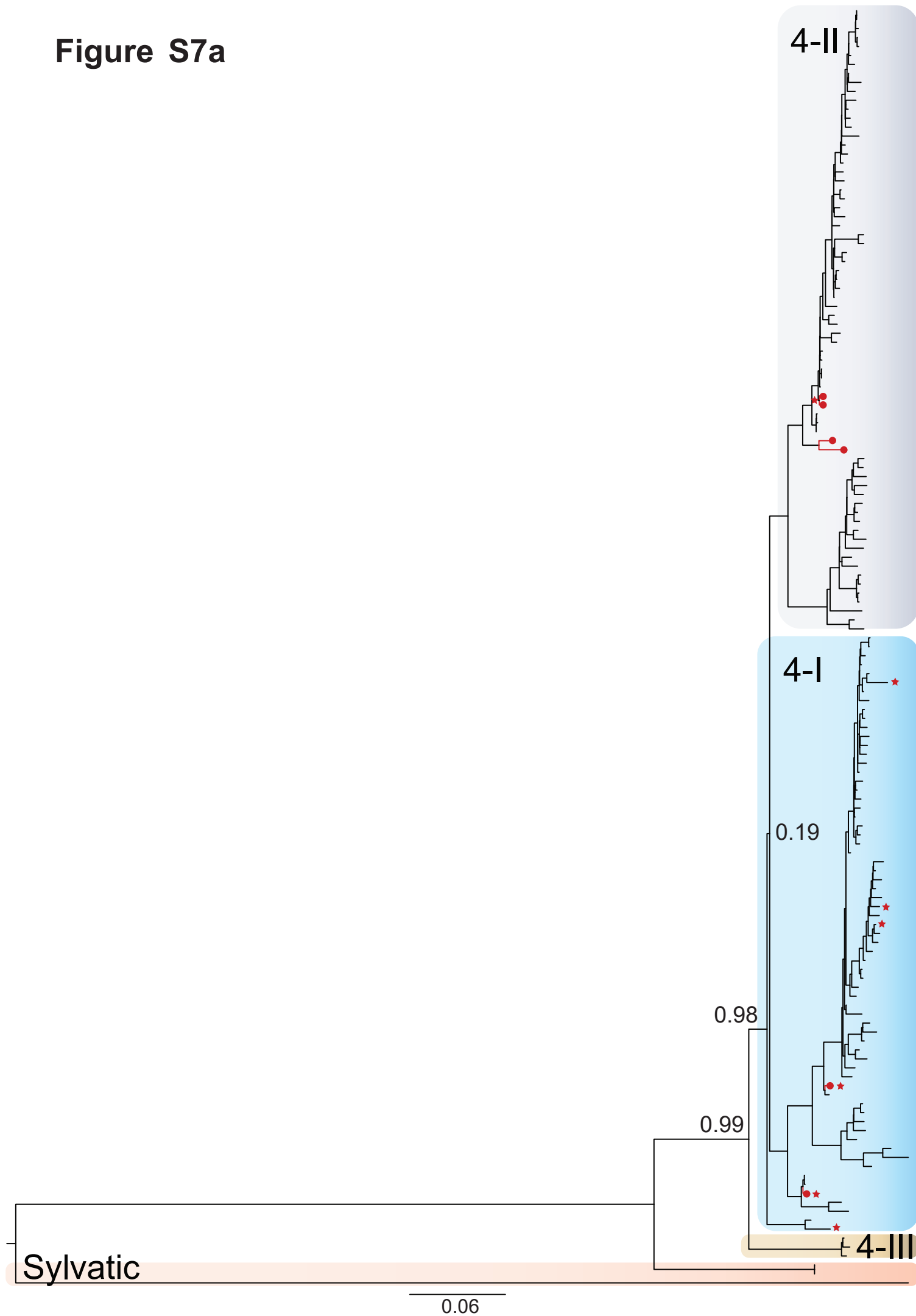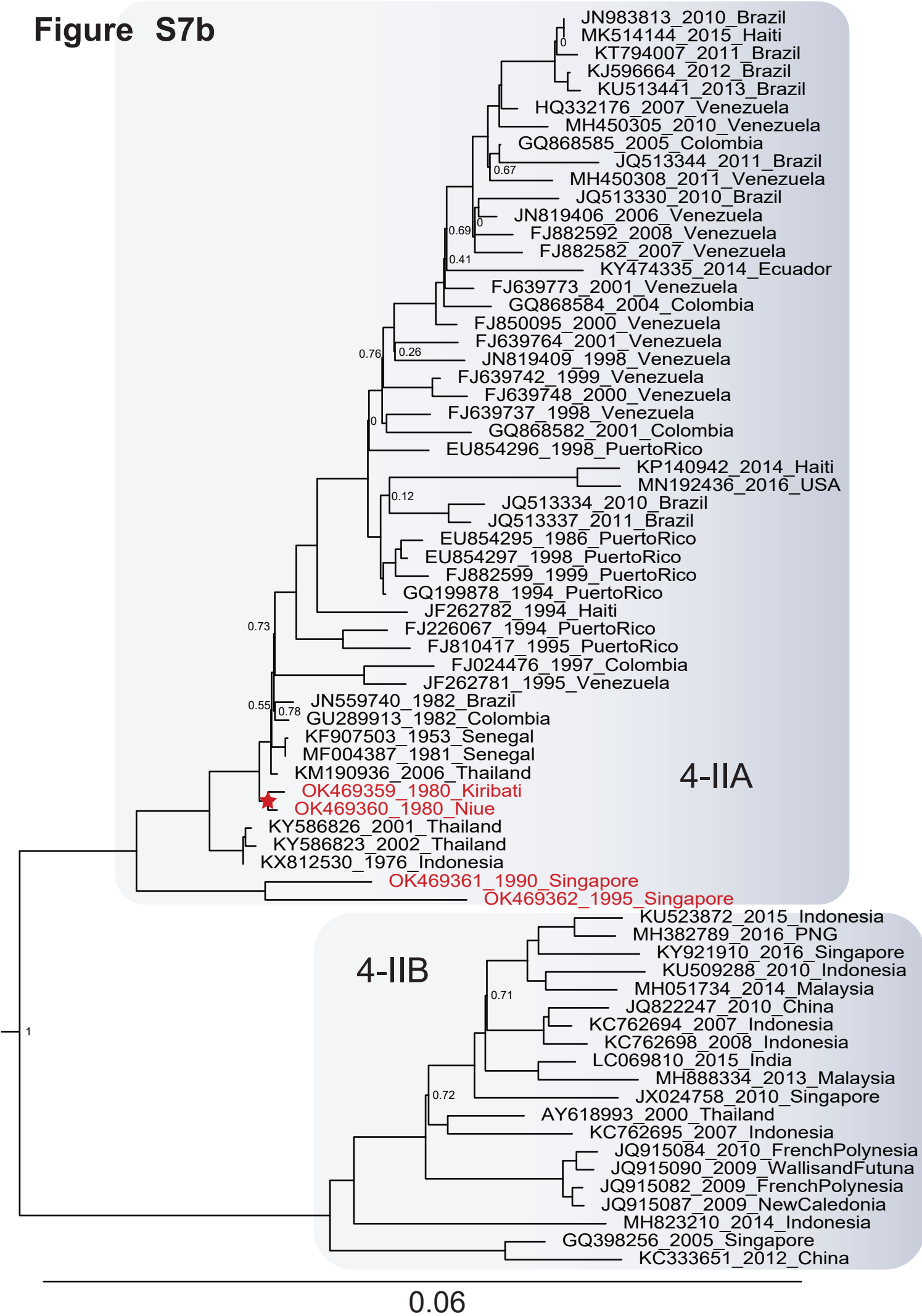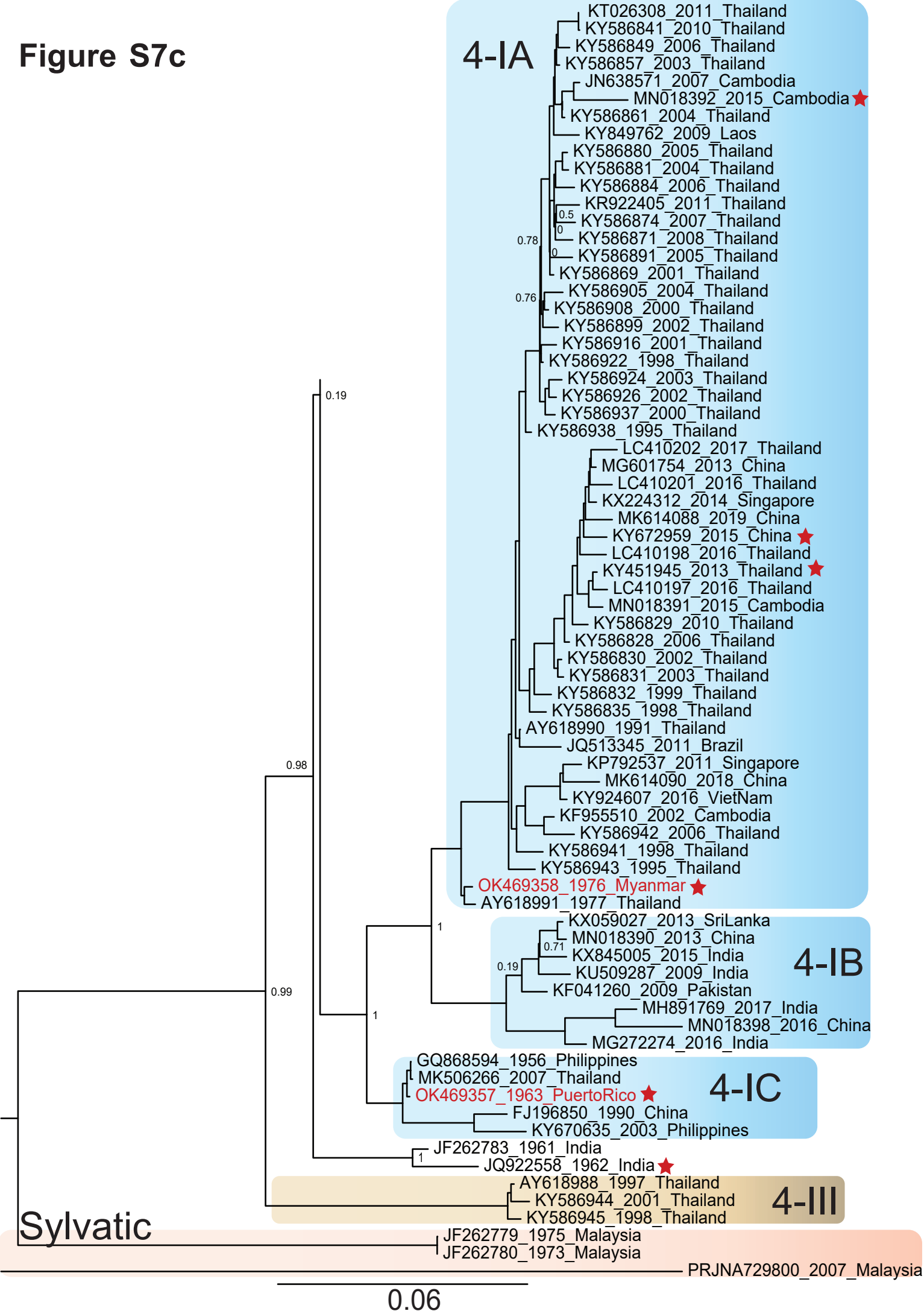
Figure S6a

Figure S6b

Figure S6c

Figure S6d

Supplemental Figure S7: DENV4 Whole Genome ML Trees. (a) DENV4 Whole Genome ML tree, (b) Genotype 4-II, (c) Genotypes 4-I, 4-III, and sylvatic. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.
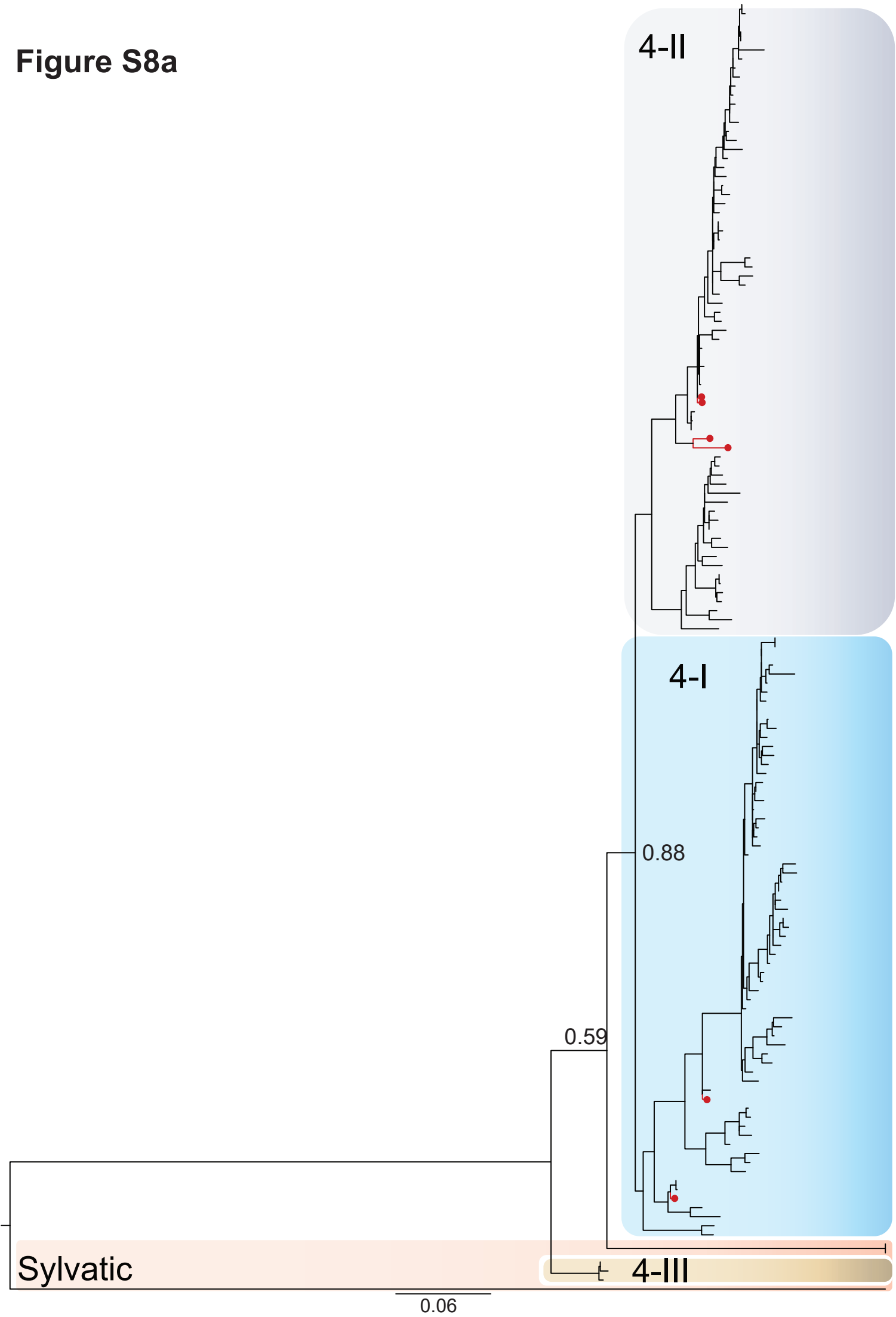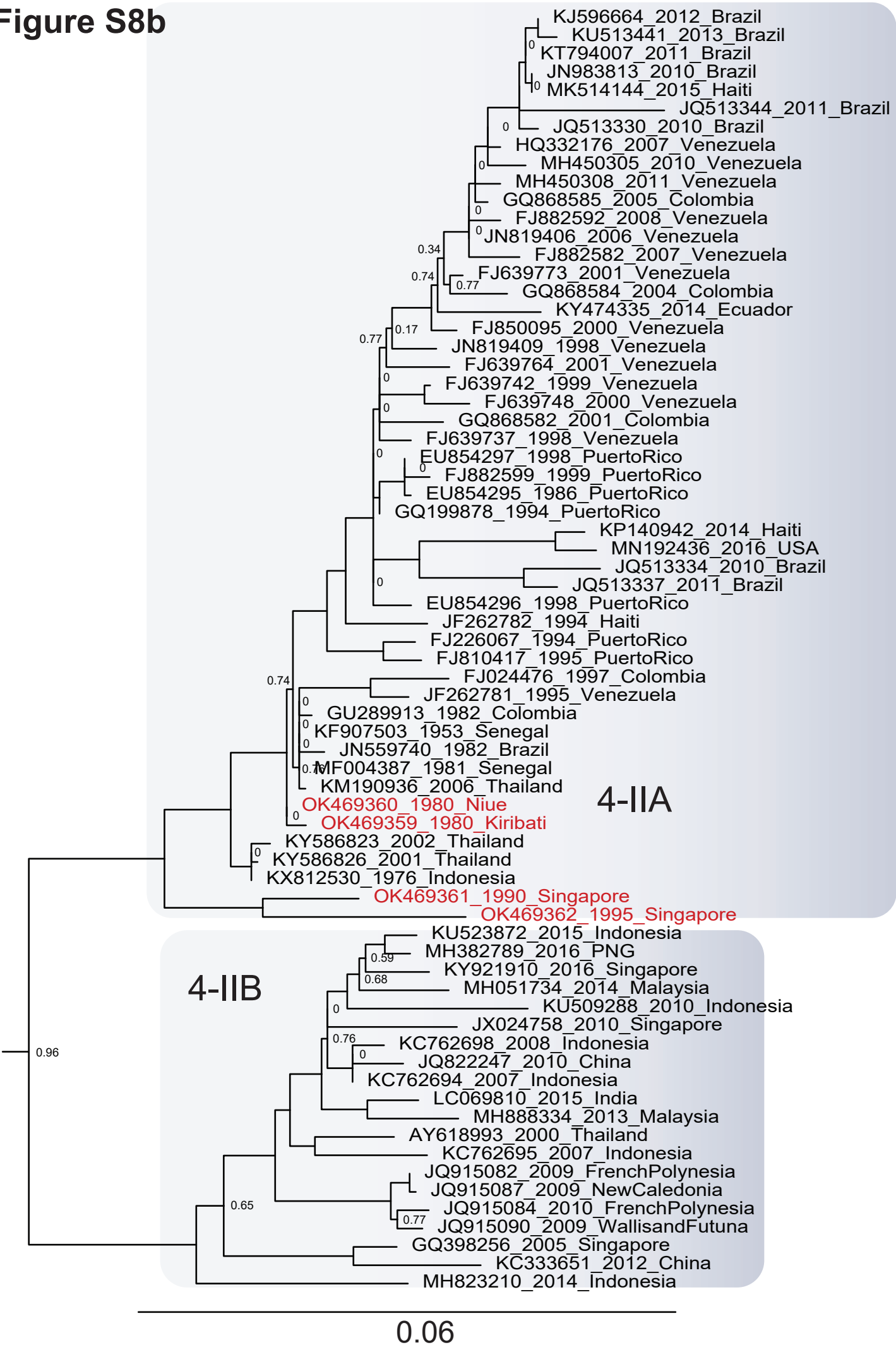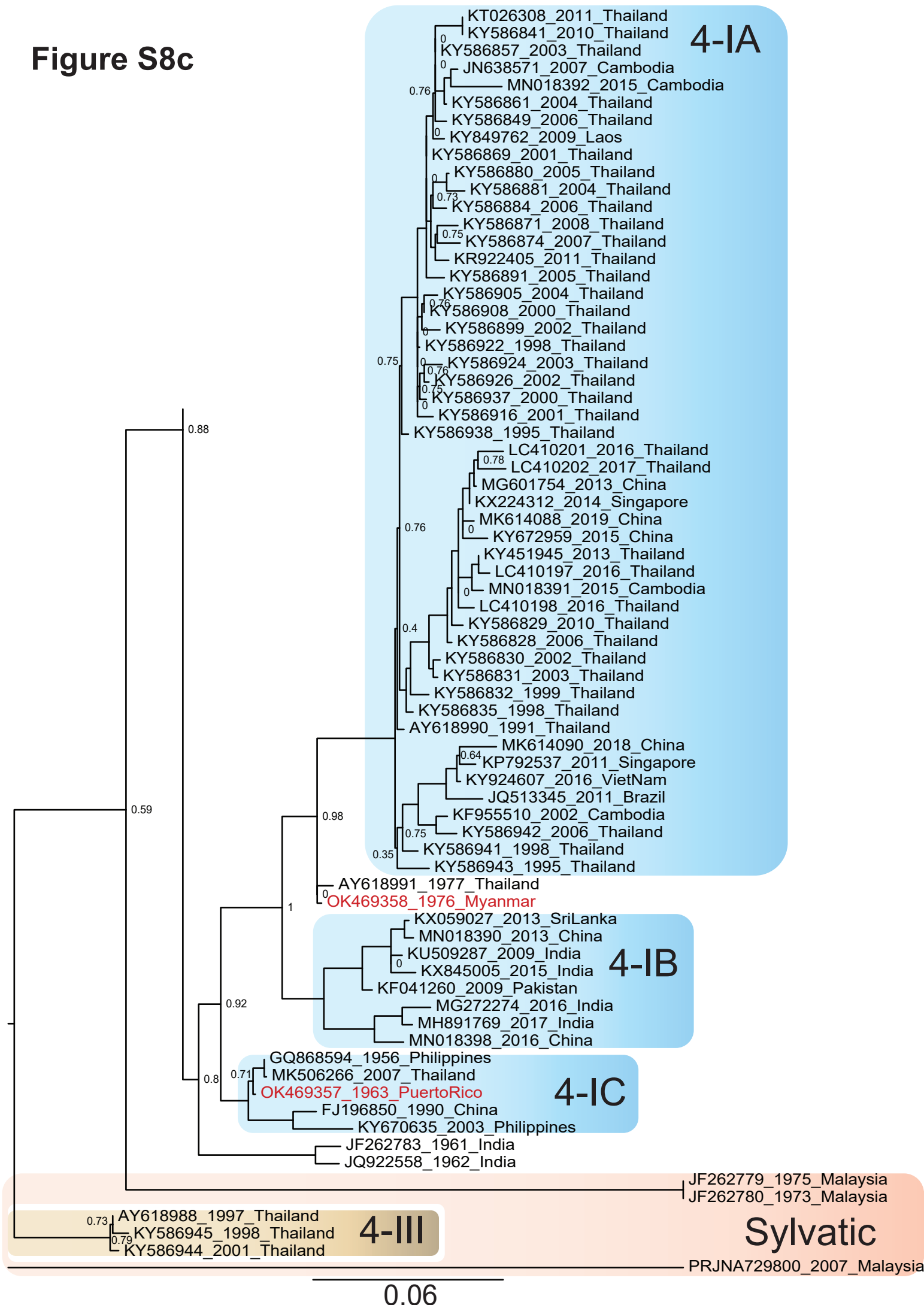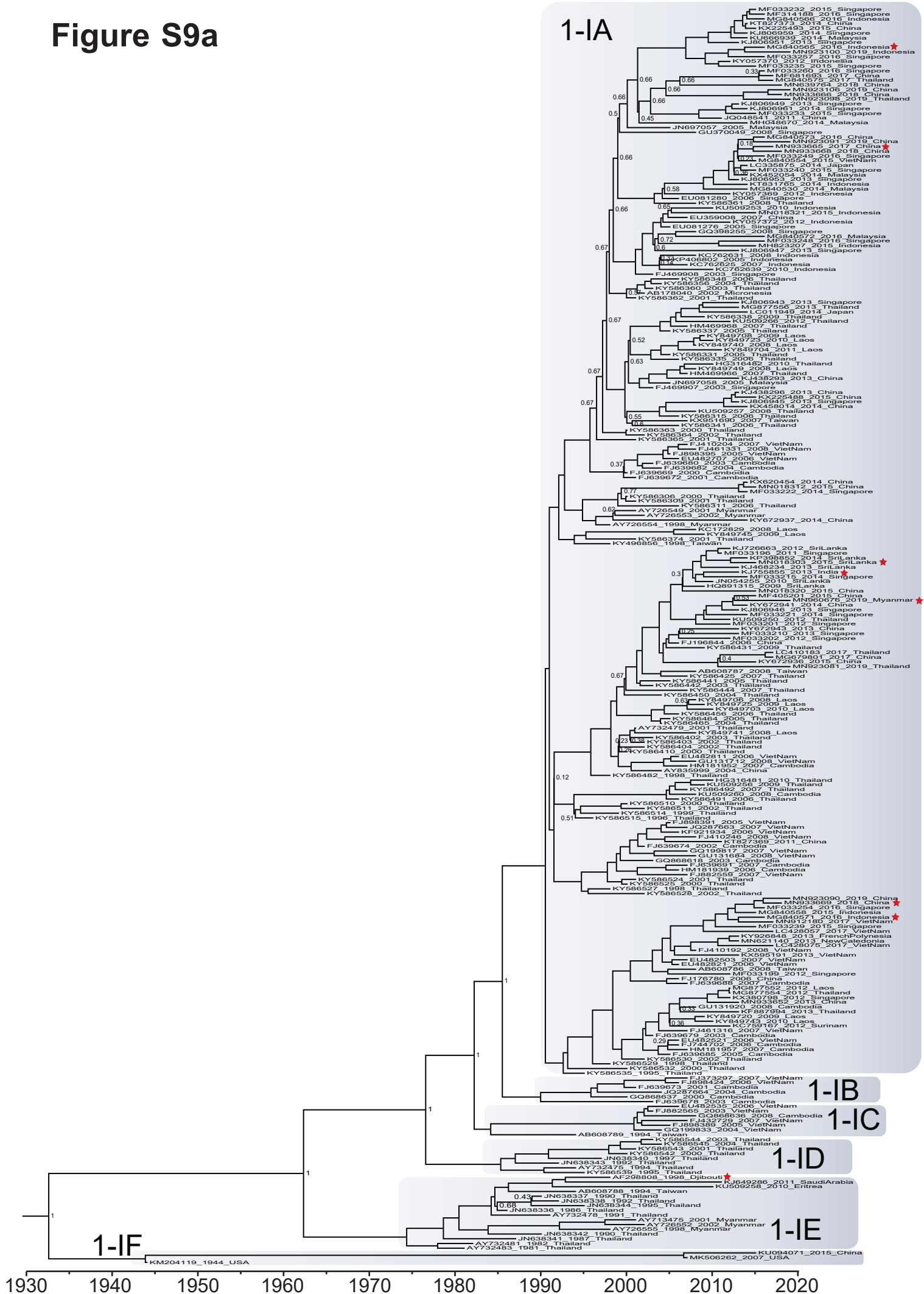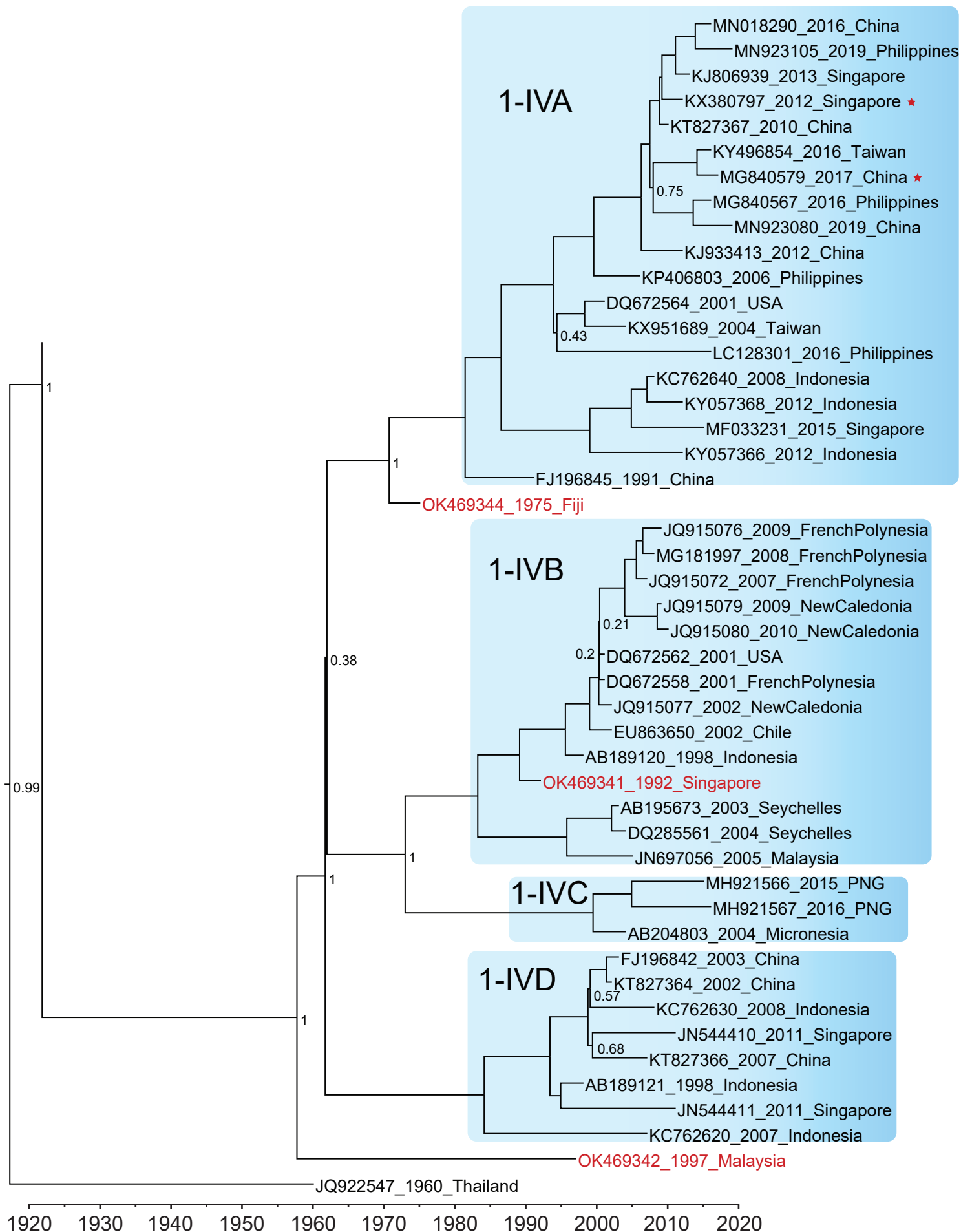
Figure S7a

Figure S7b

Figure S7c

Supplemental Figure S8: DENV4 E Gene ML Trees. (a) DENV4 E gene ML tree, (b) Genotype 4-II, (c) Genotypes 4-I, 4-III, and sylvatic. aLRT SH-like branch support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicate newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star.

Figure S8a

Figure S8b

Figure S8c

Supplemental Figure S9: DENV1 Whole Genome Genotypes MCMC Trees. (a) Genotype 1-I, (b) Genotype 1-IV, (c) Genotypes 1-V (isolates incorrectly classified as 1-III indicated by arrows) and sylvatic. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
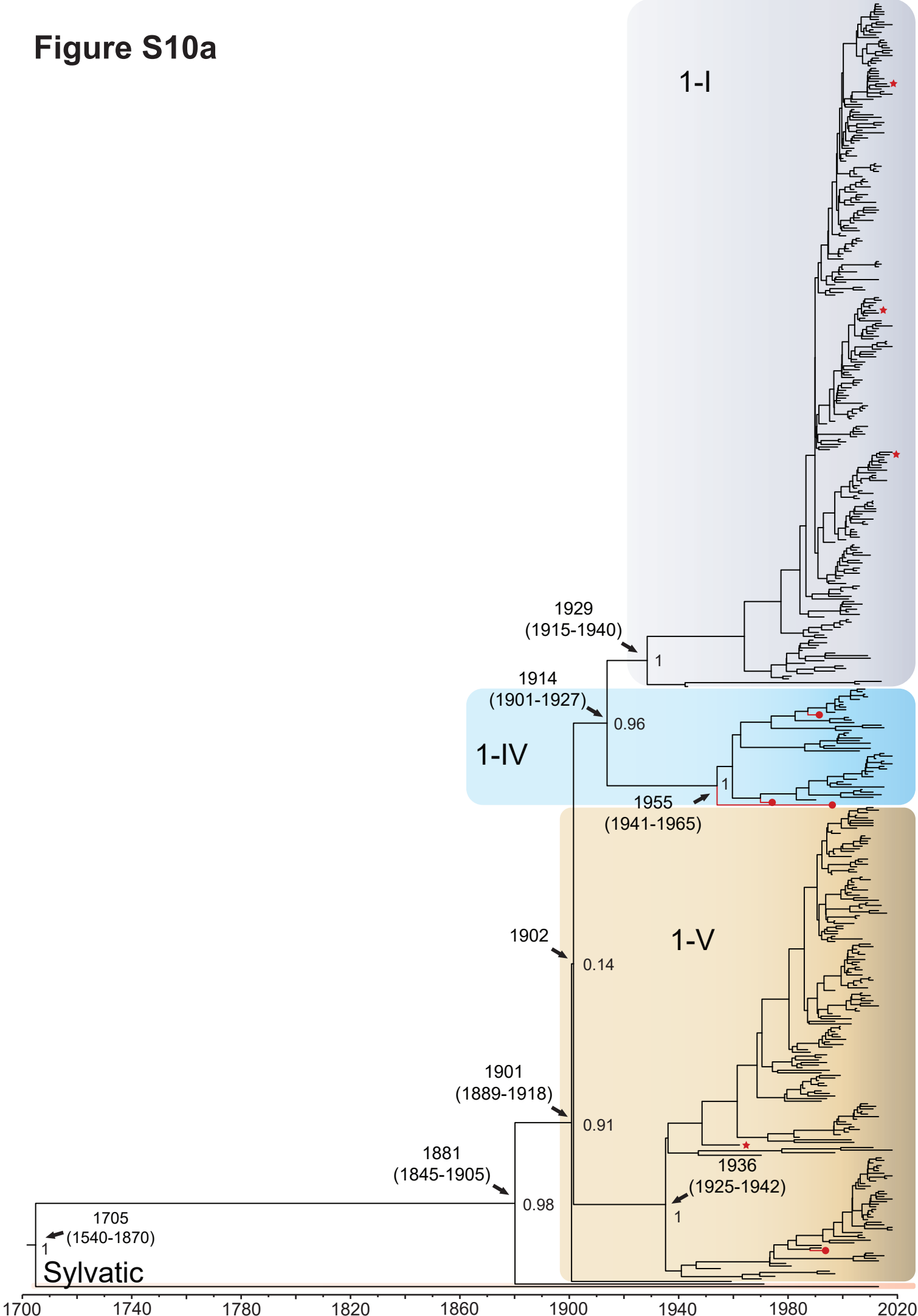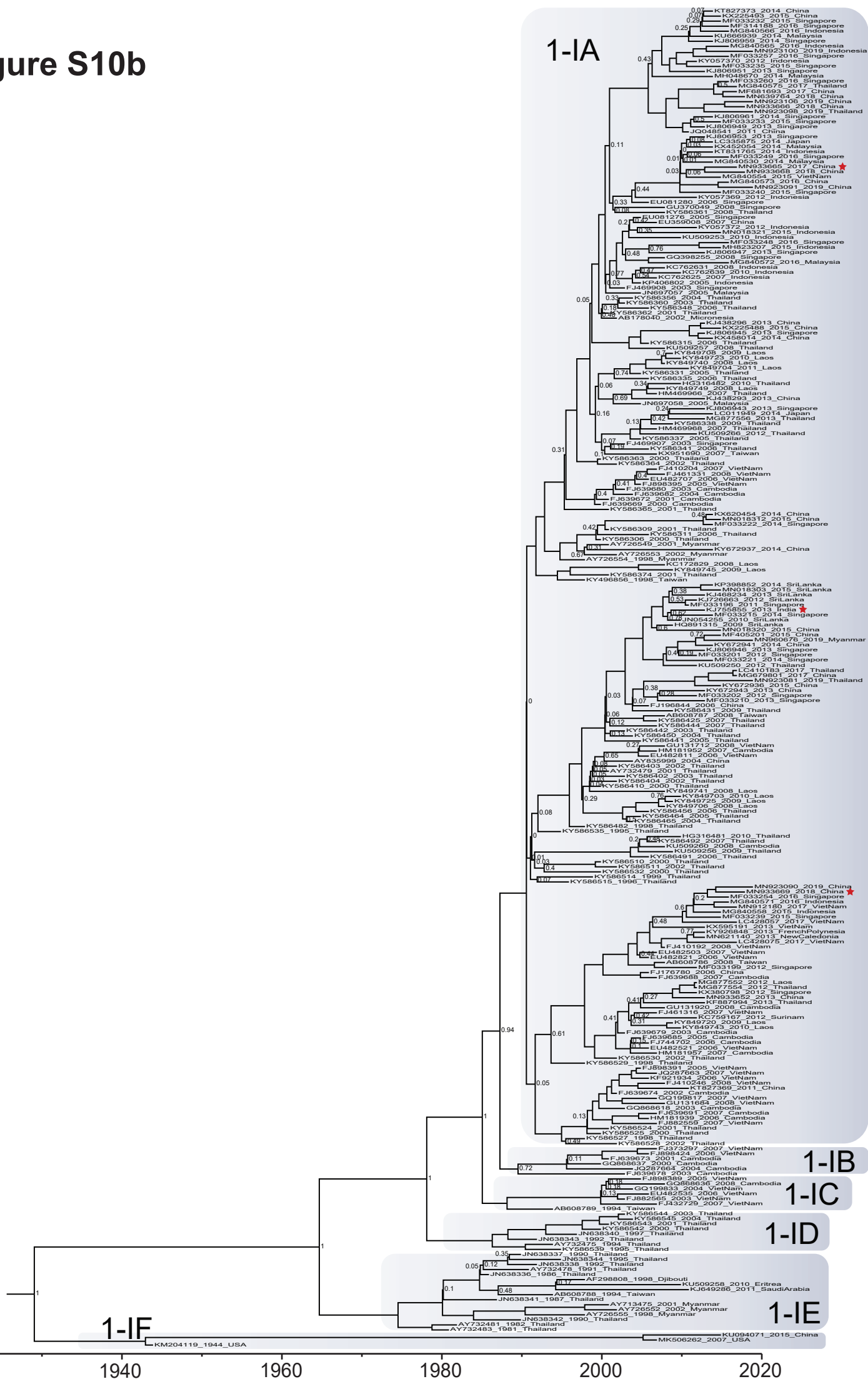
Figure S9a

Figure S9b

Figure S9c
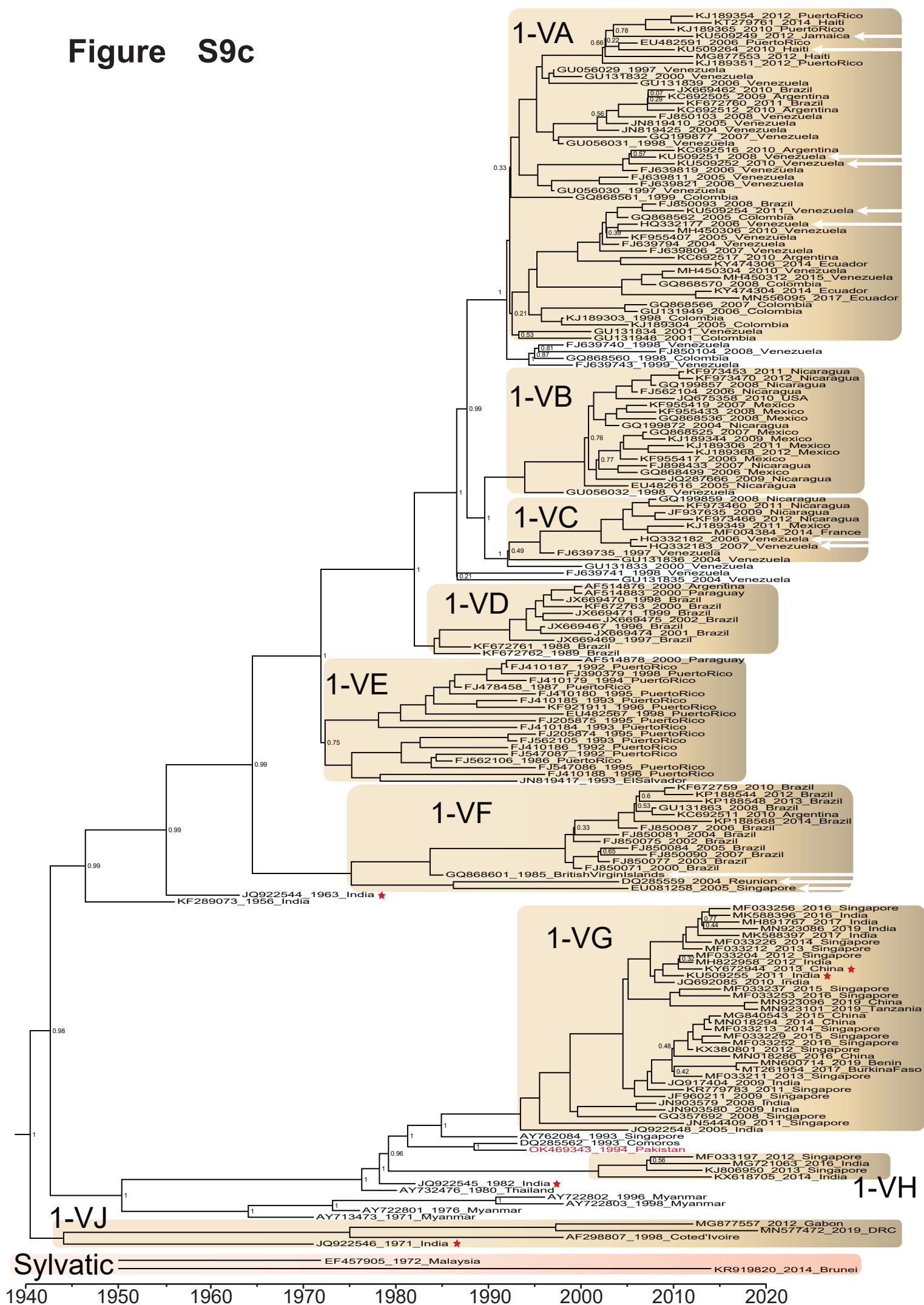
Supplemental Figure S10: DENV1 E Gene MCMC Trees. (a) DENV1 E gene MCMC tree, (b) Genotype 1-I, (c) Genotype 1-IV, (d) Genotypes 1-V (isolates incorrectly classified as 1-III indicated by arrows) and sylvatic. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
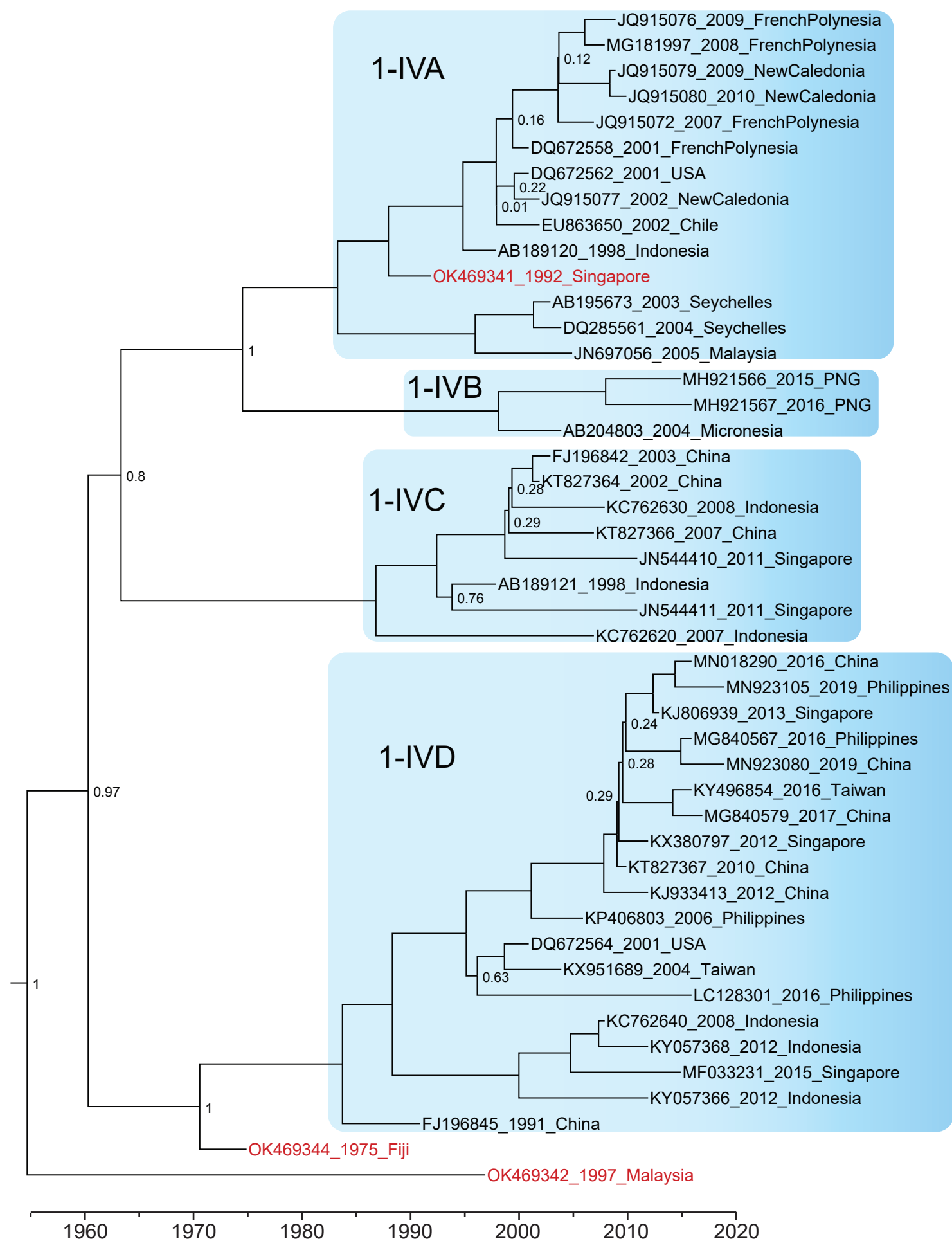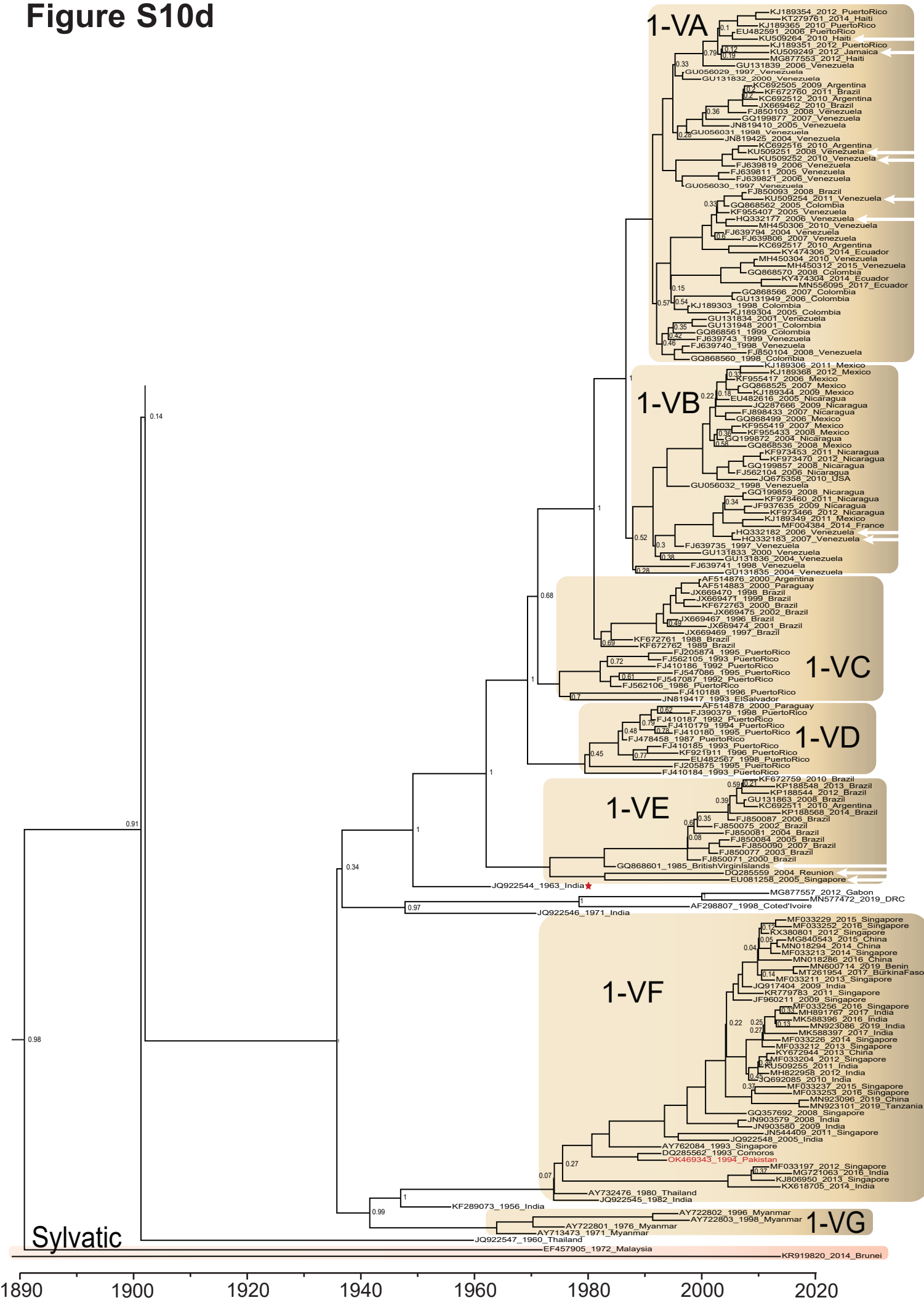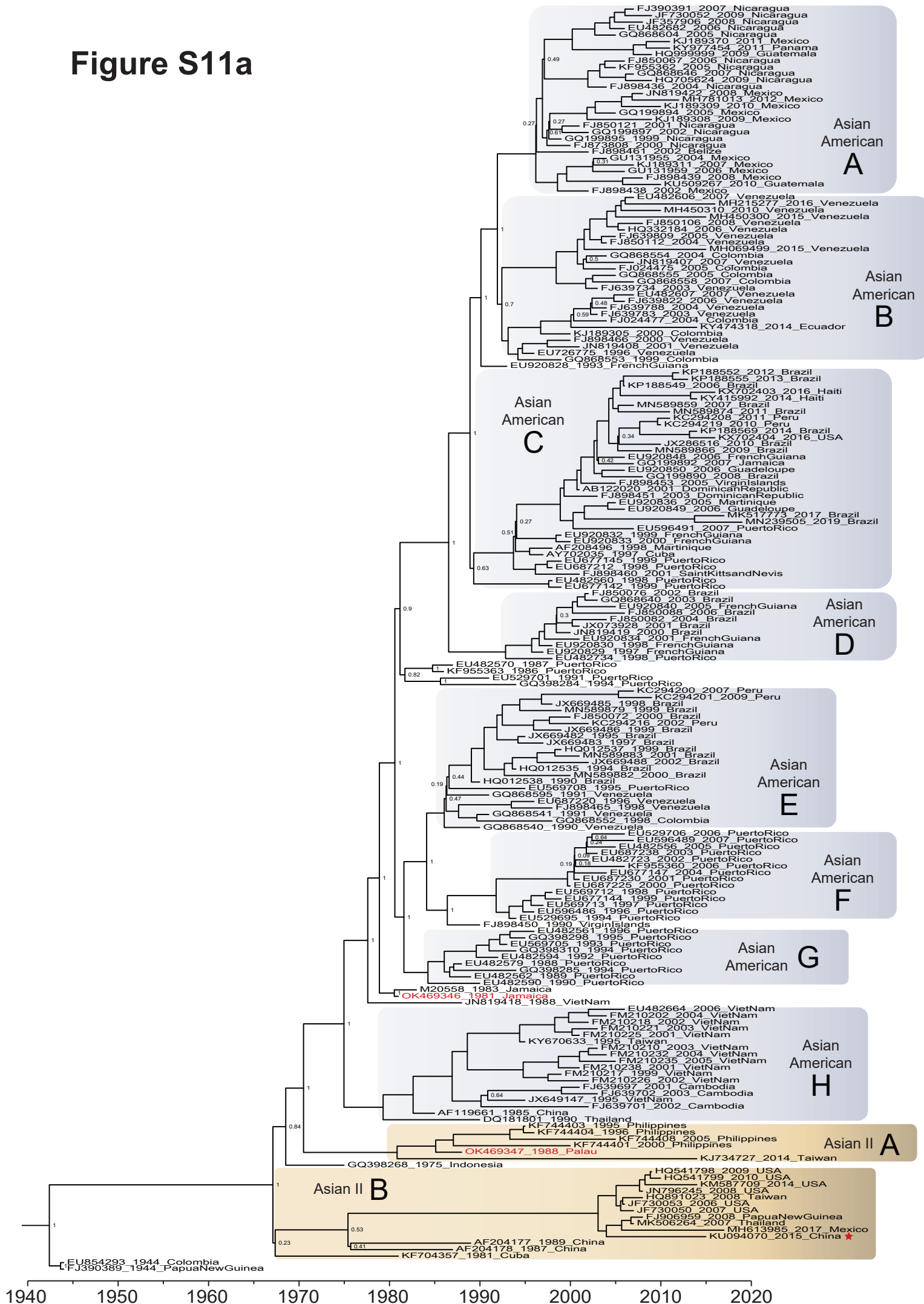
Figure S10a

Figure S10b

Figure S10c

Figure S10d

Supplemental Figure S11: DENV2 Whole Genome Genotypes MCMC Trees. (a) Asian American and Asian II genotypes, (b) Asian I genotype, (c) Cosmopolitan genotype, (d) American and sylvatic genotypes. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
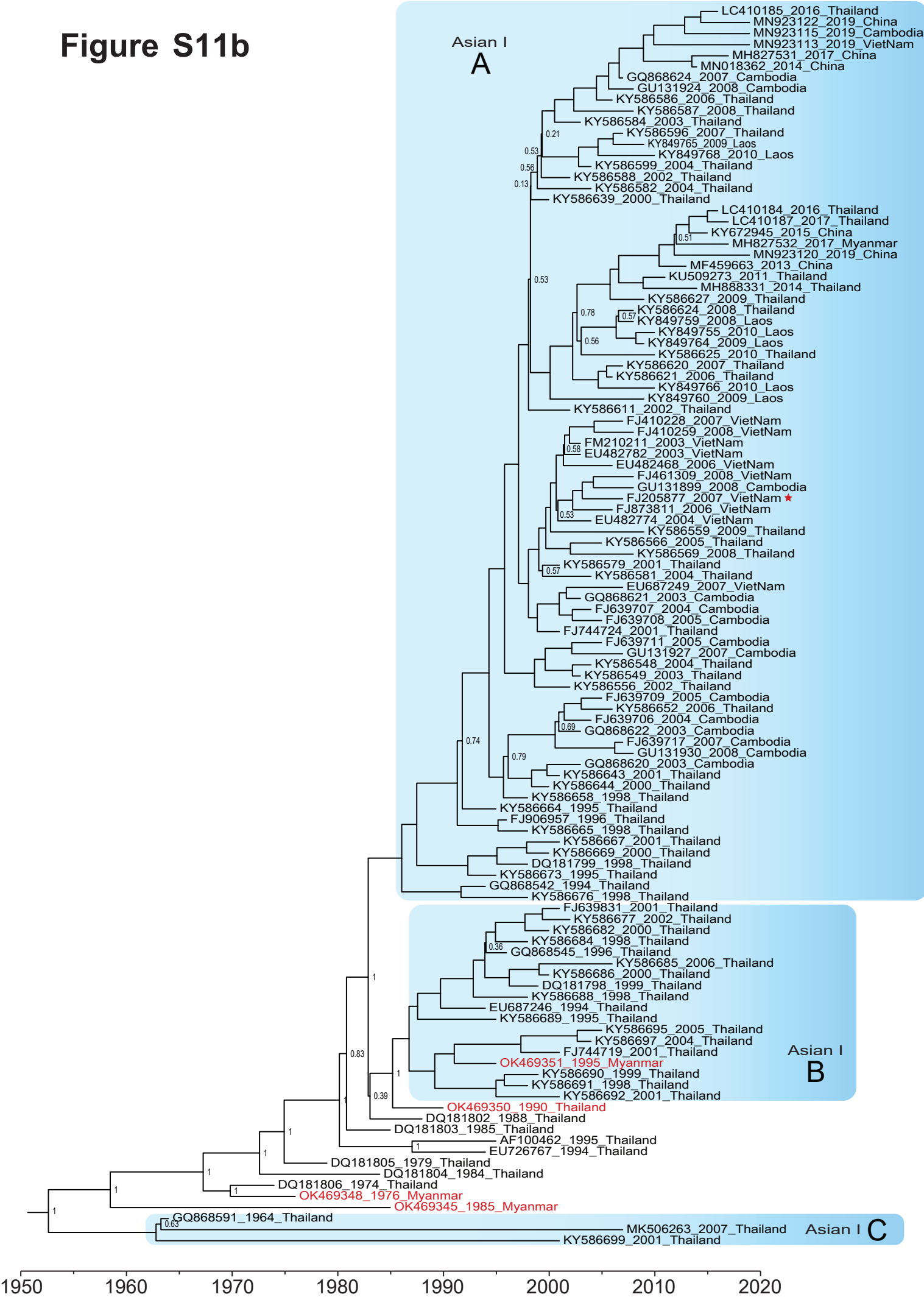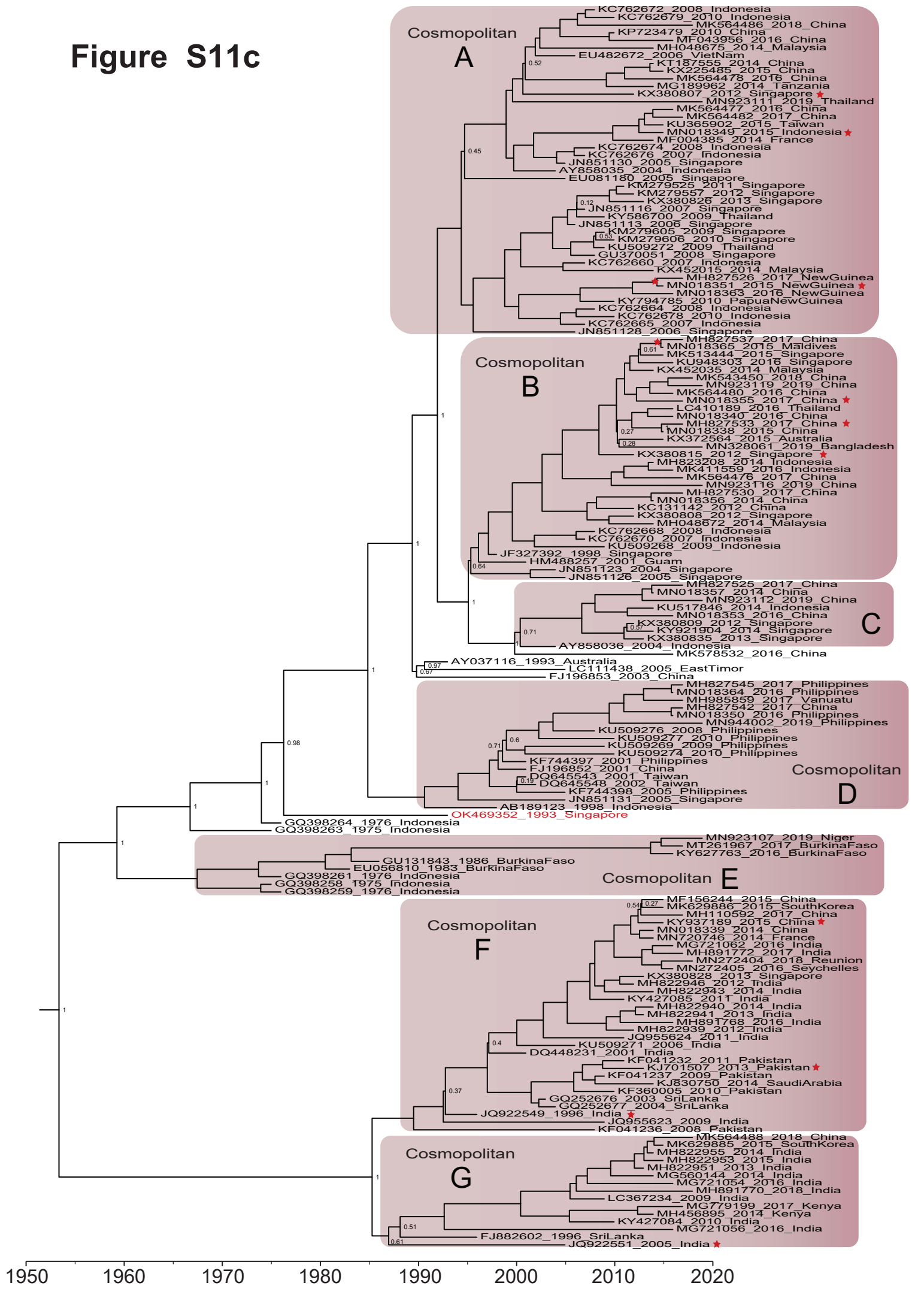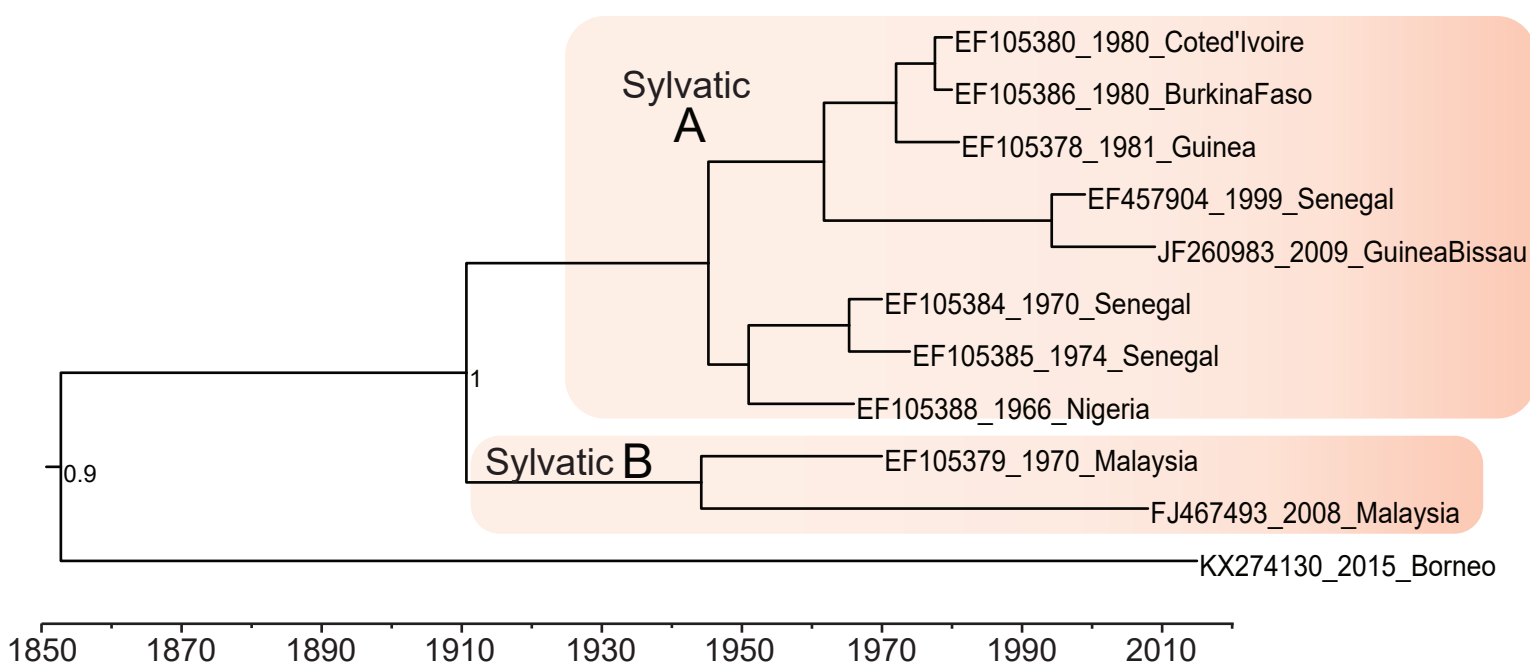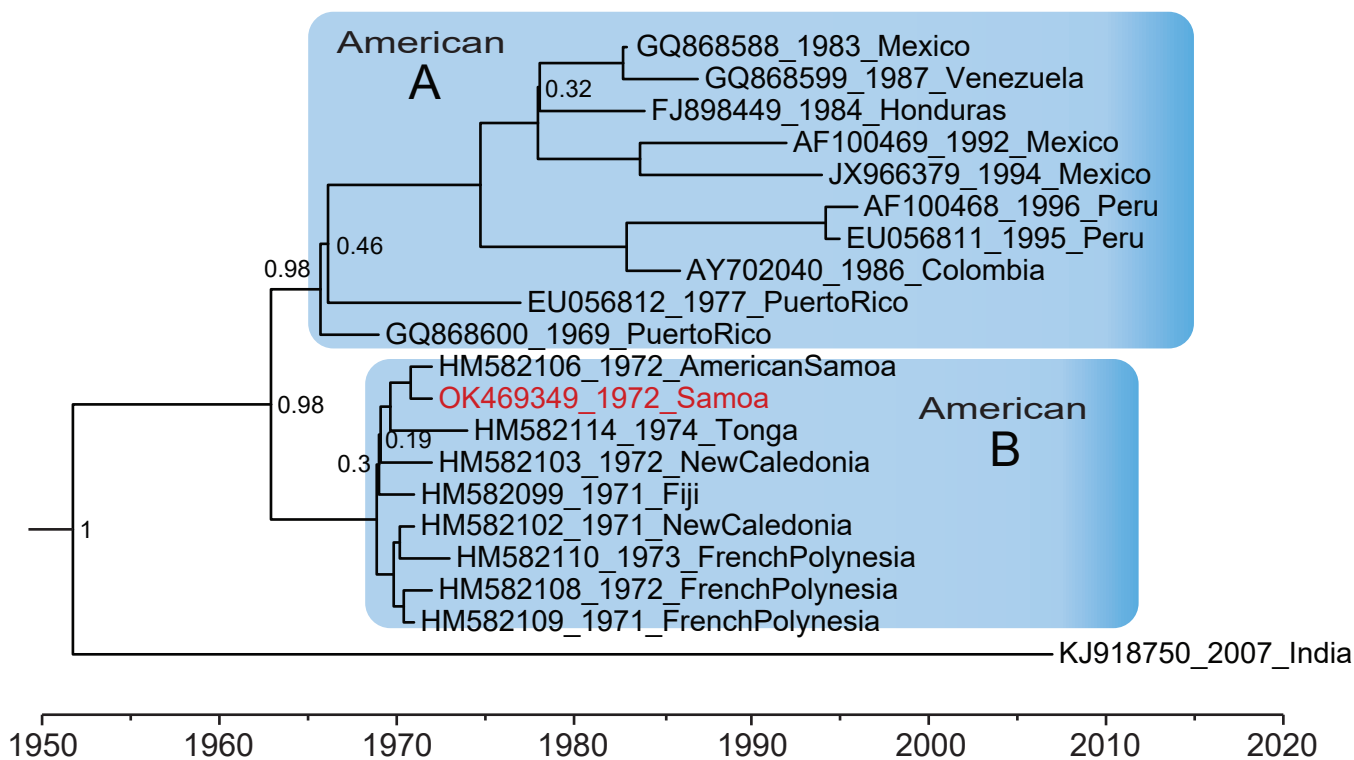
Figure S11a

Figure S11b

Figure S11c

Figure S11d

Supplemental Figure S12: DENV2 E Gene MCMC Trees. (a) DENV2 E gene MCMC tree, (b) Asian American genotype, (c) Asian I and Asian II genotypes, (d) Cosmopolitan genotype, (e) American and sylvatic genotypes. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
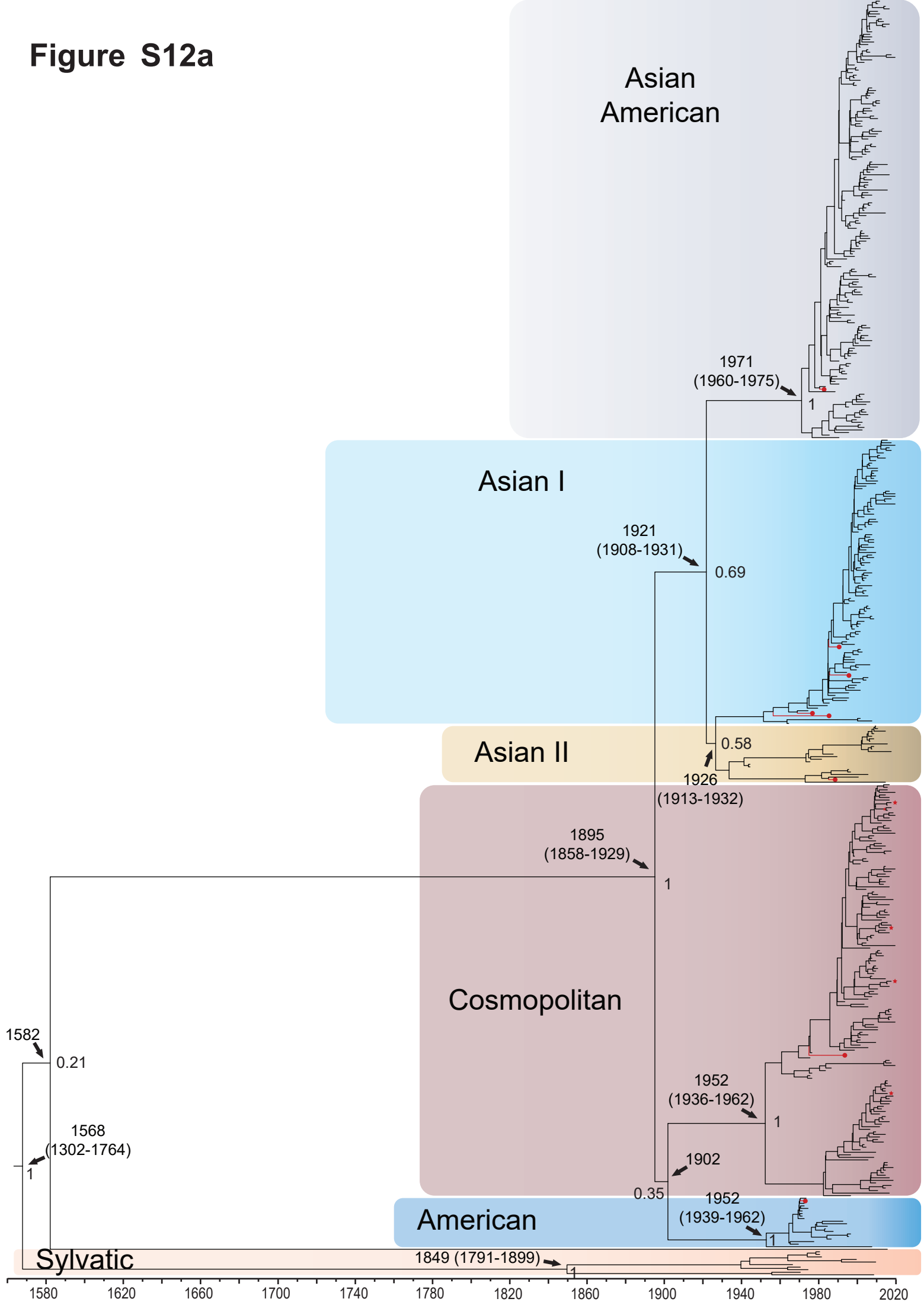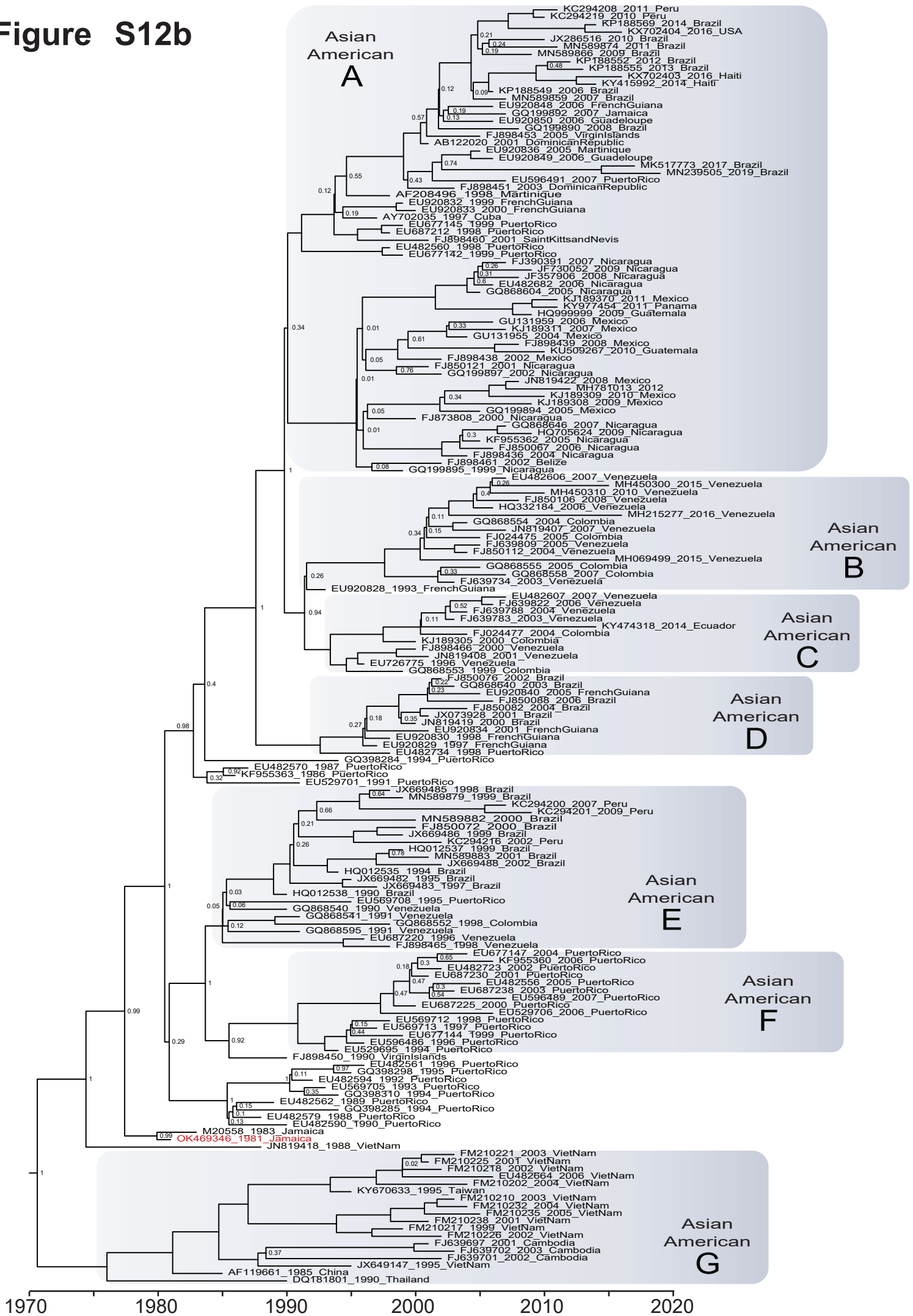
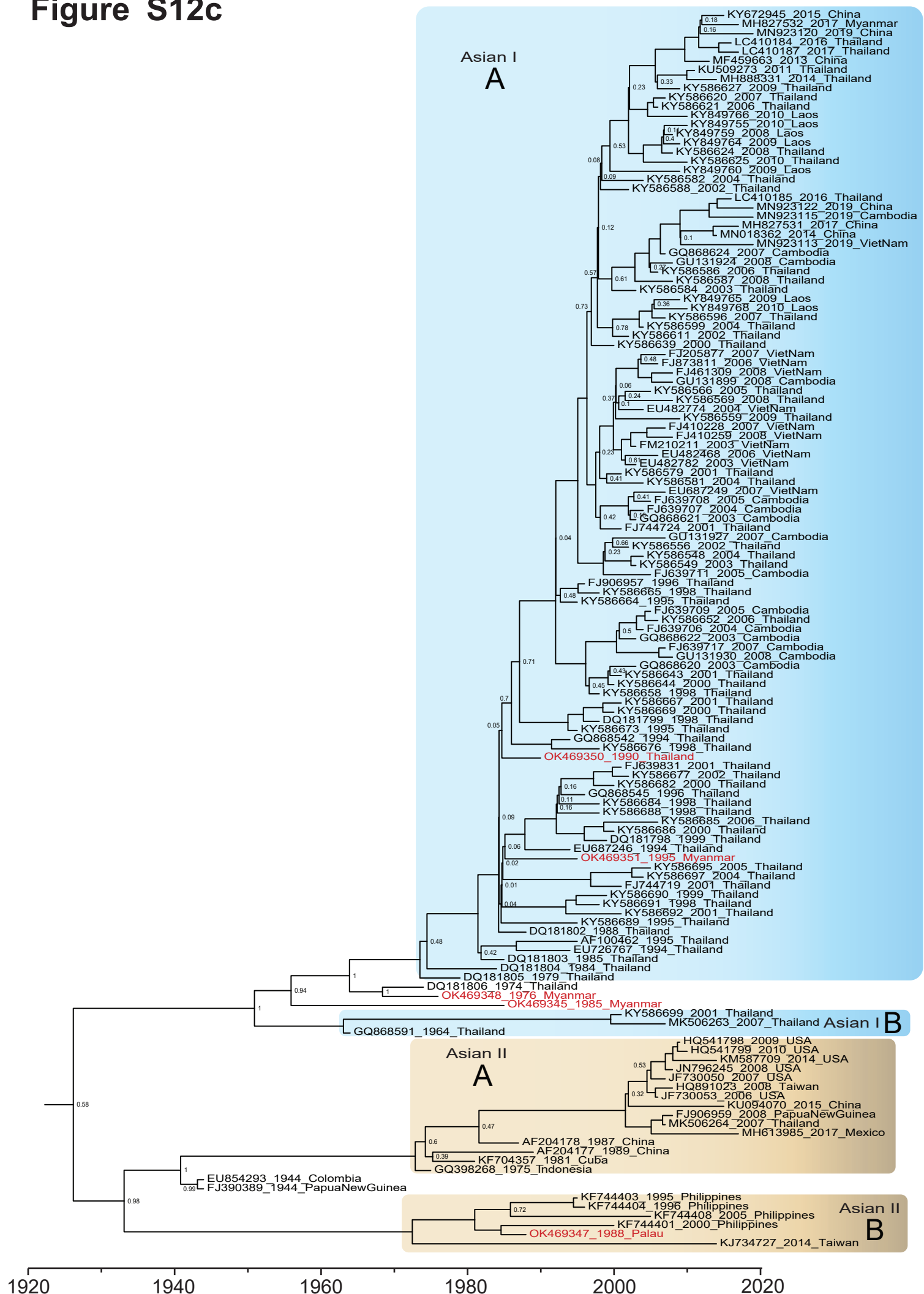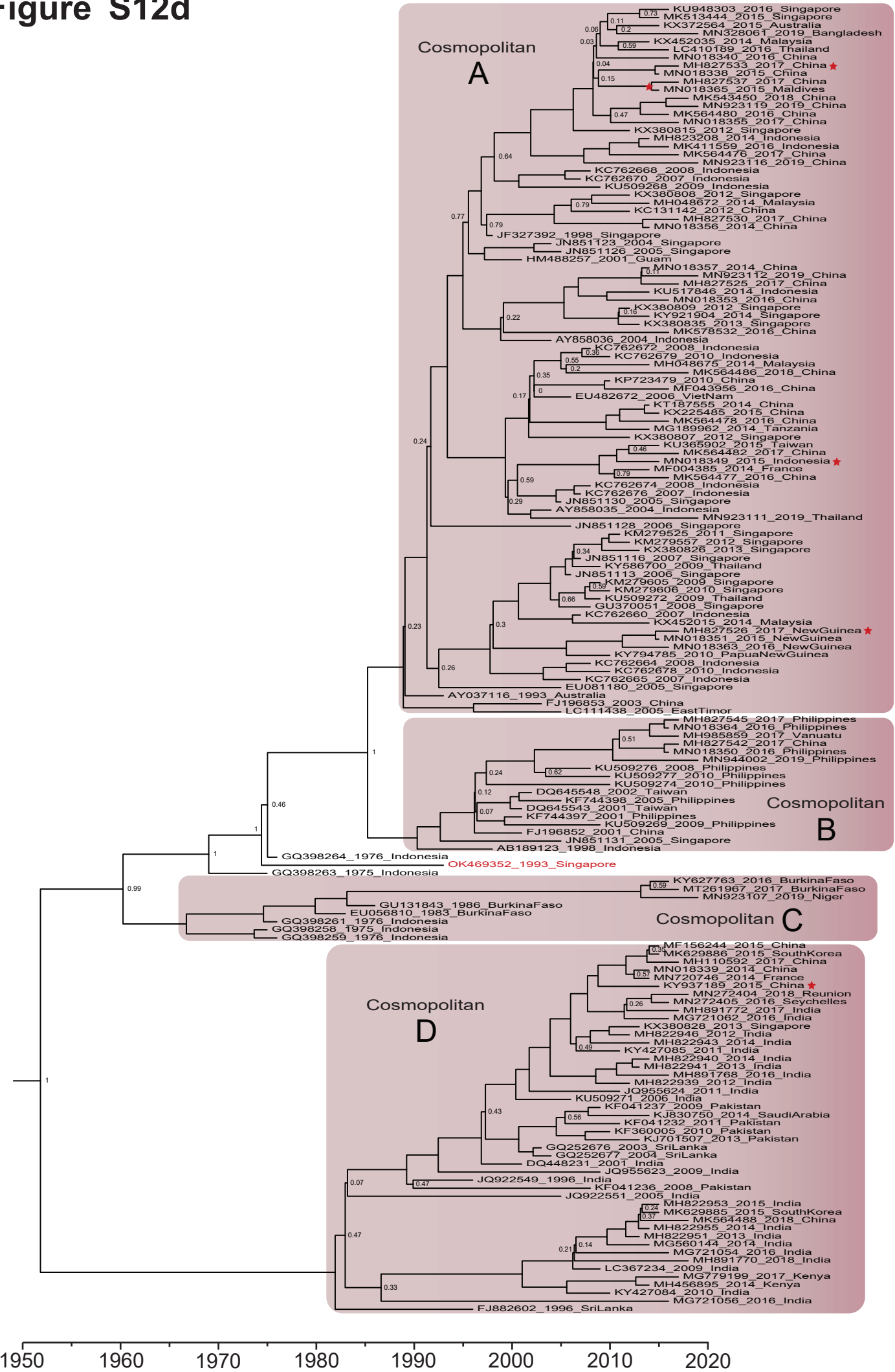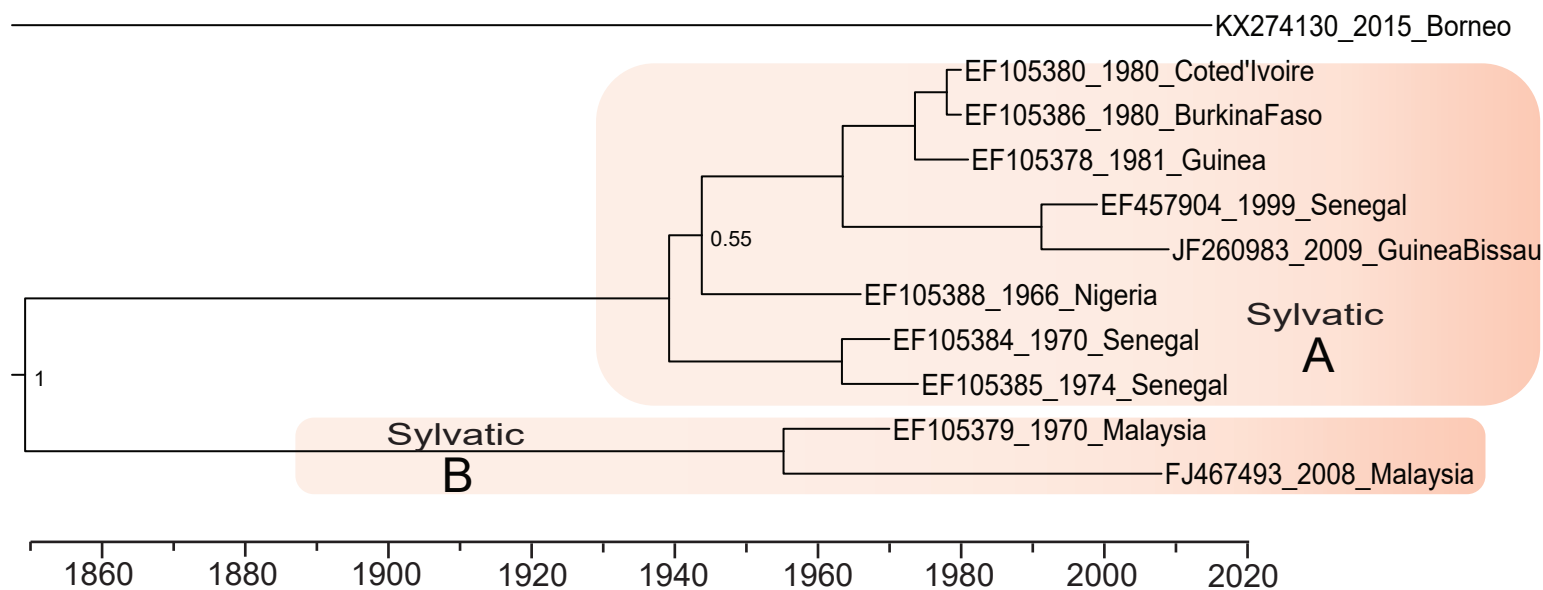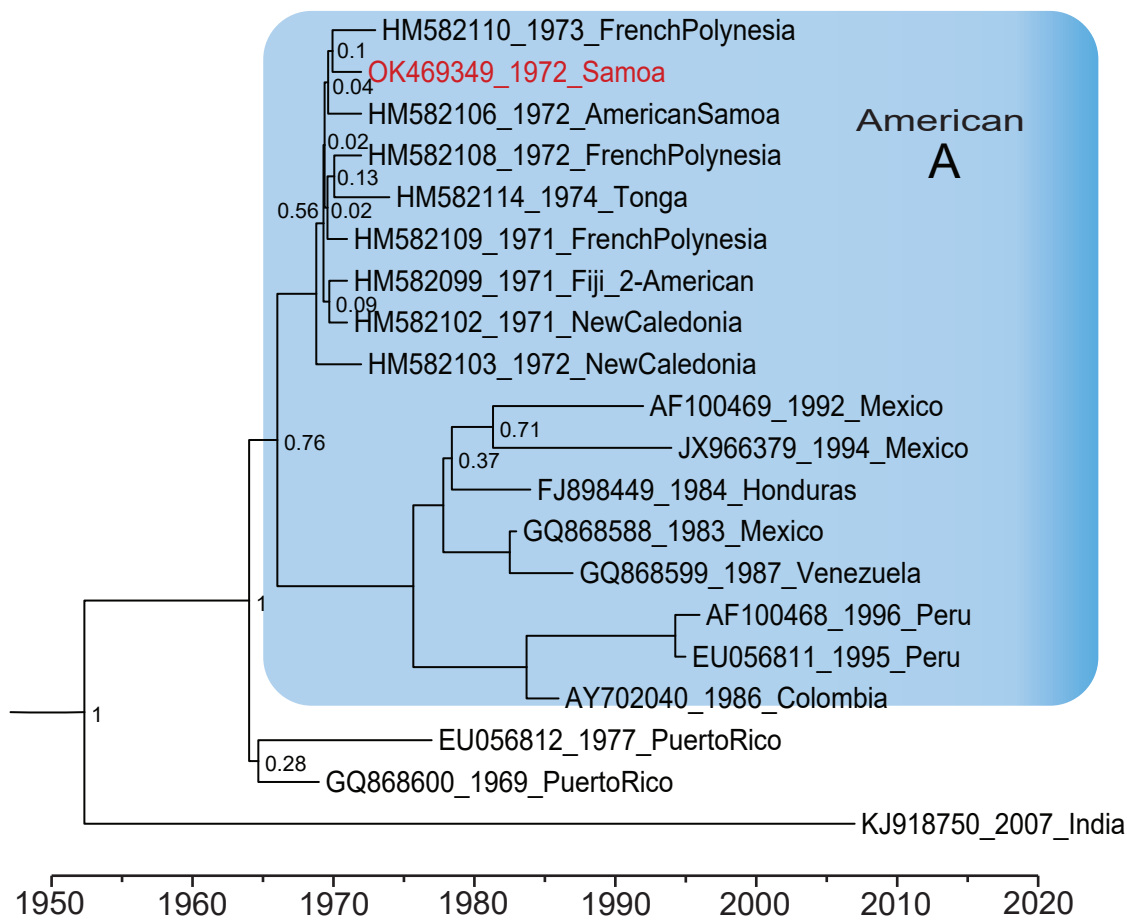**Figure S12a**

Figure S12b

Figure S12c

Figure S12d

Figure S12e

Supplemental Figure S13: DENV3 Whole Genome Genotypes MCMC Trees. (a) Genotype 3-III, (b) Genotype 3-II and 3-I. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
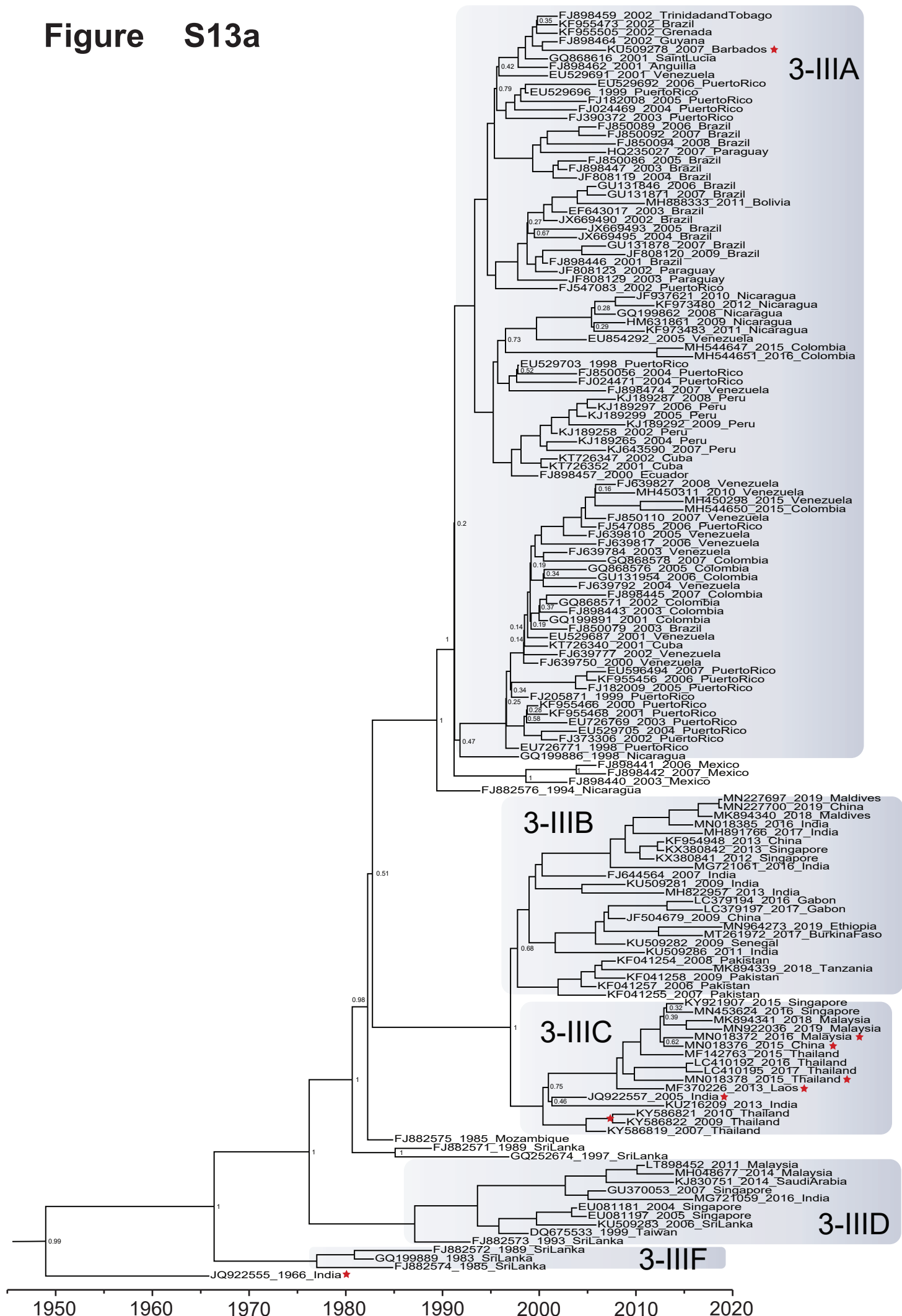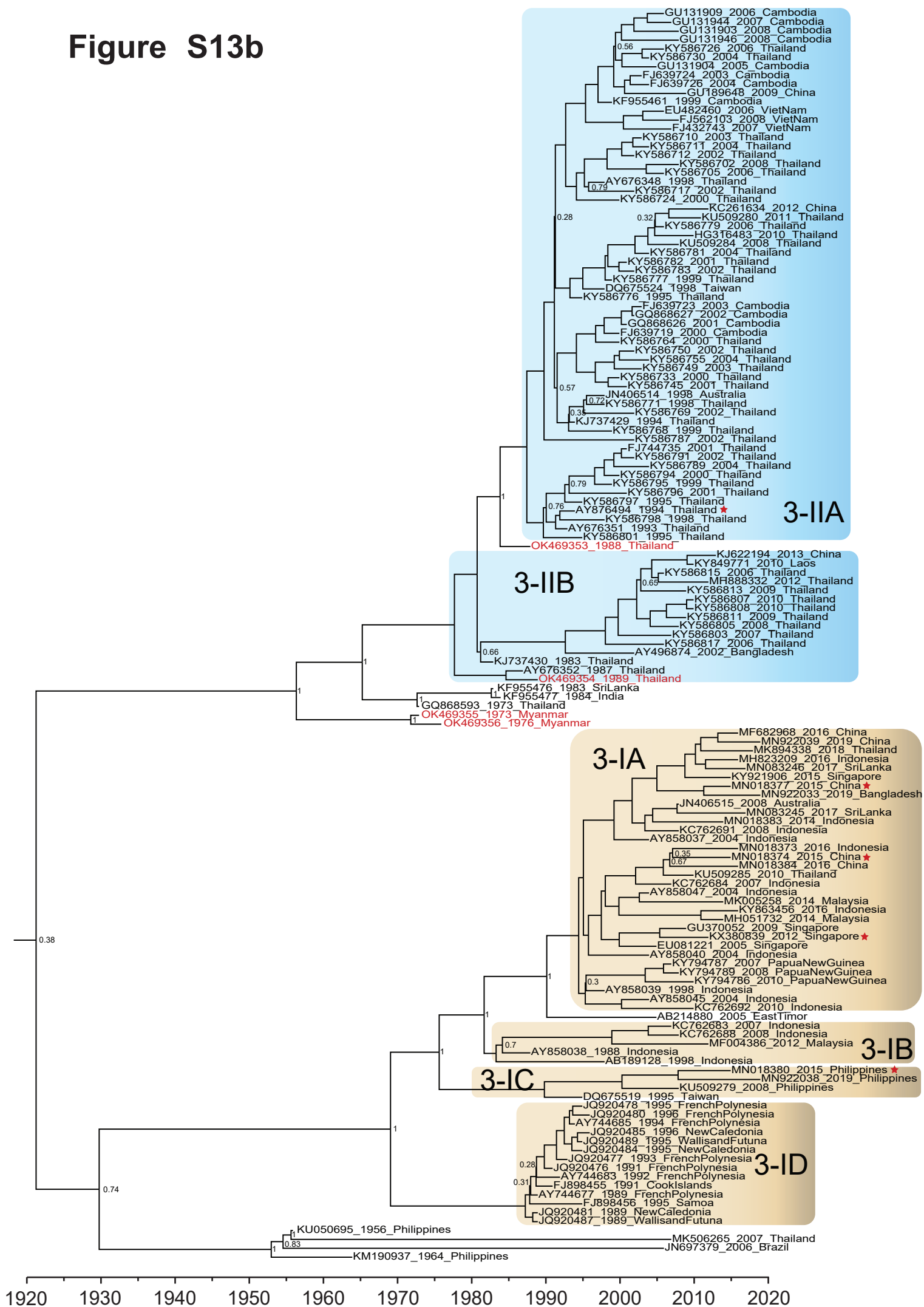
Figure S13a

Figure S13b

Supplemental Figure S14: DENV3 E Gene MCMC Trees. (a) DENV3 E gene MCMC tree, (b) Genotype 3-I, (c) Genotypes 3-III and 3-II. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
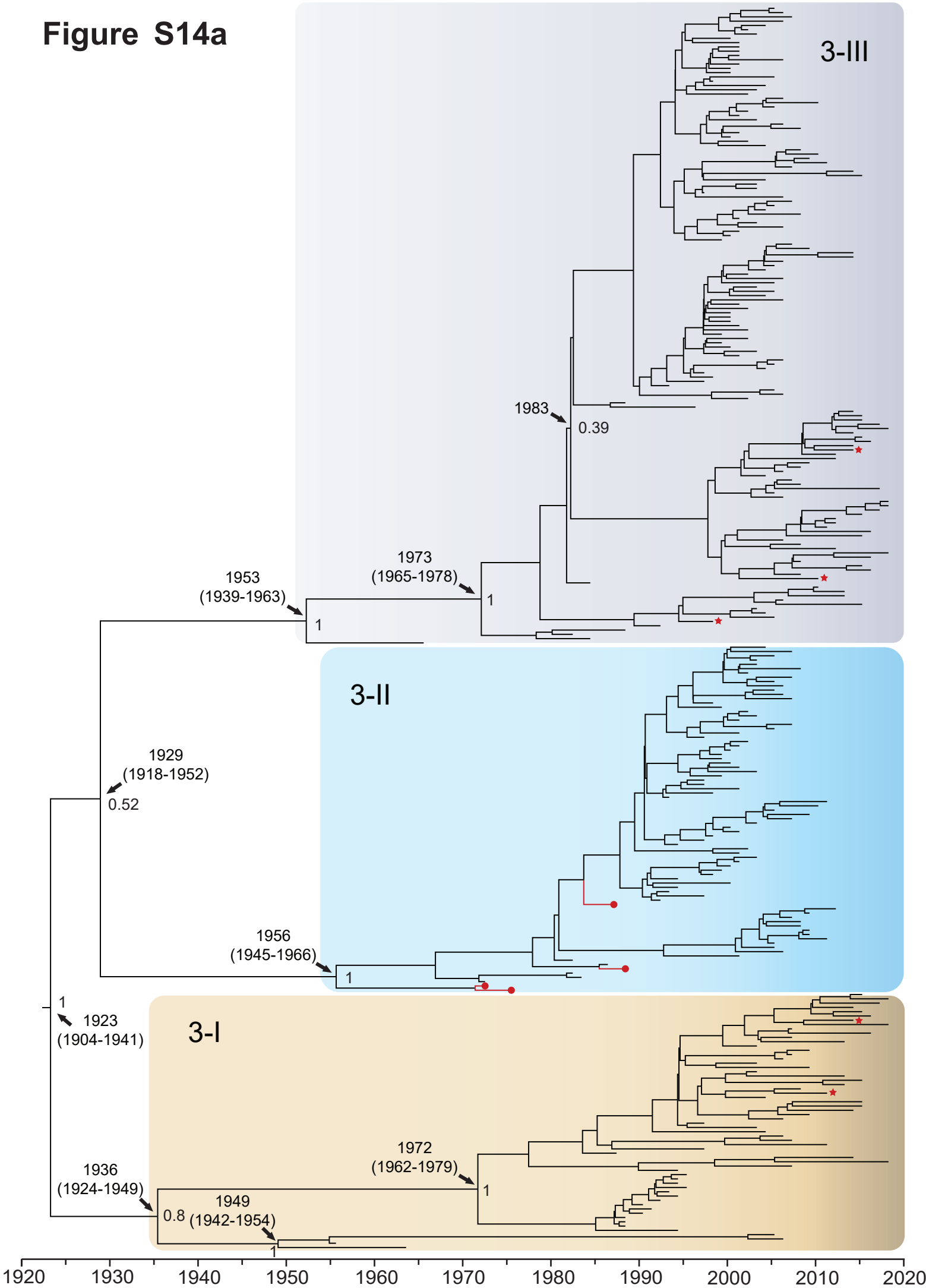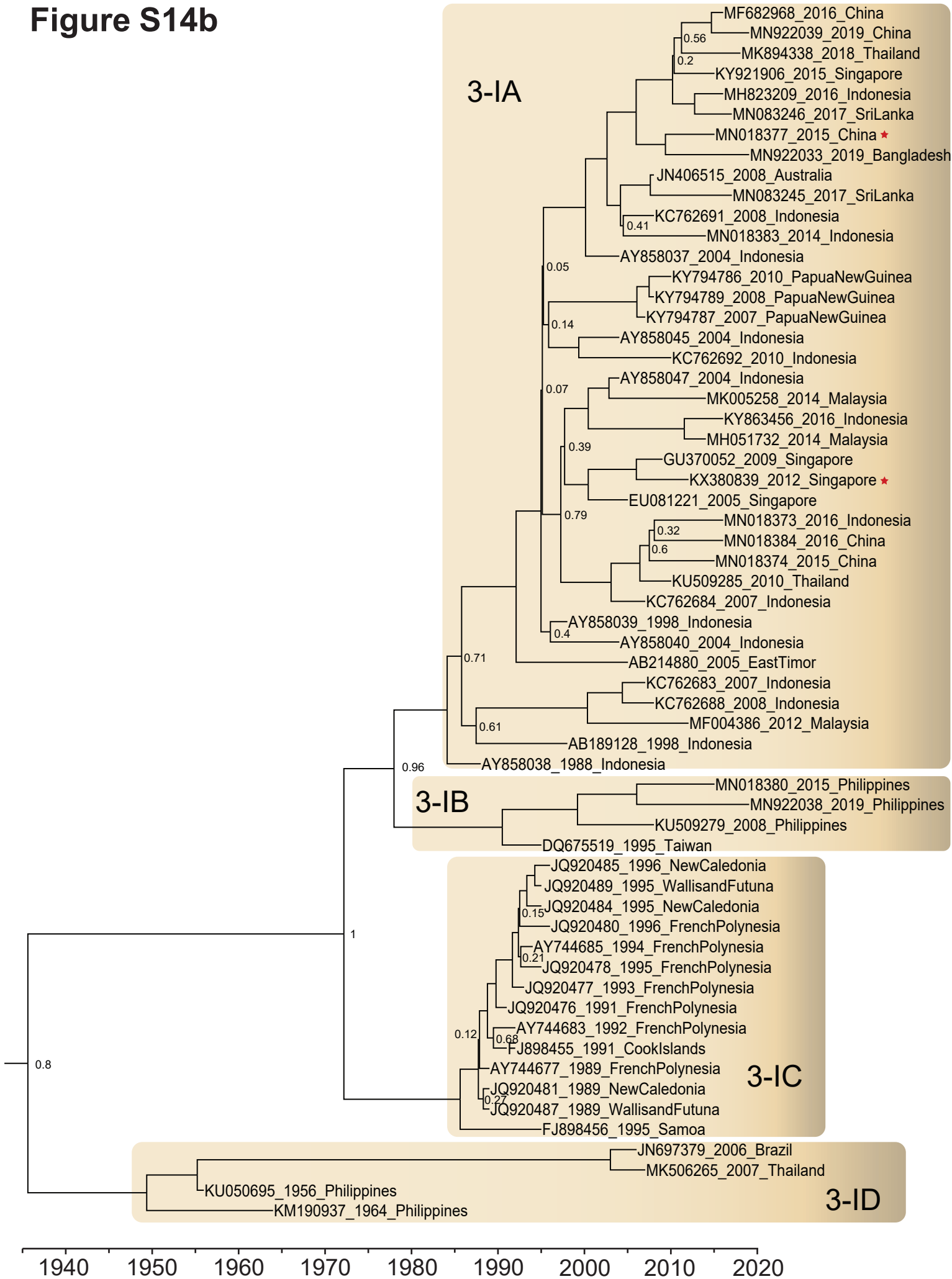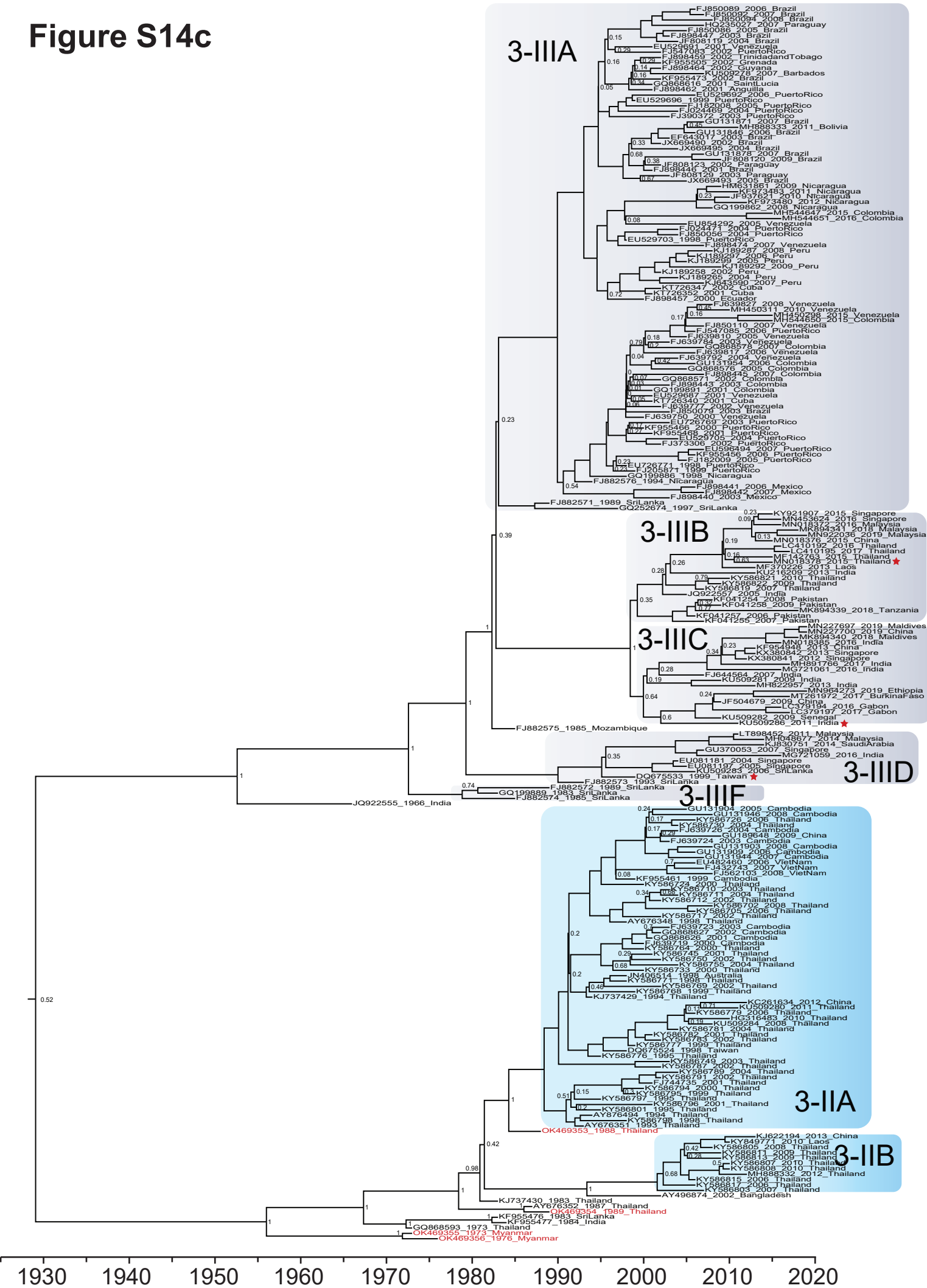
Figure S14a

Figure S14b

Figure S14c

Supplemental Figure S15: DENV4 Whole Genome Genotypes MCMC Trees. (a) Genotype 4-II, (b) Genotypes 4-I, 4-III, and sylvatic. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
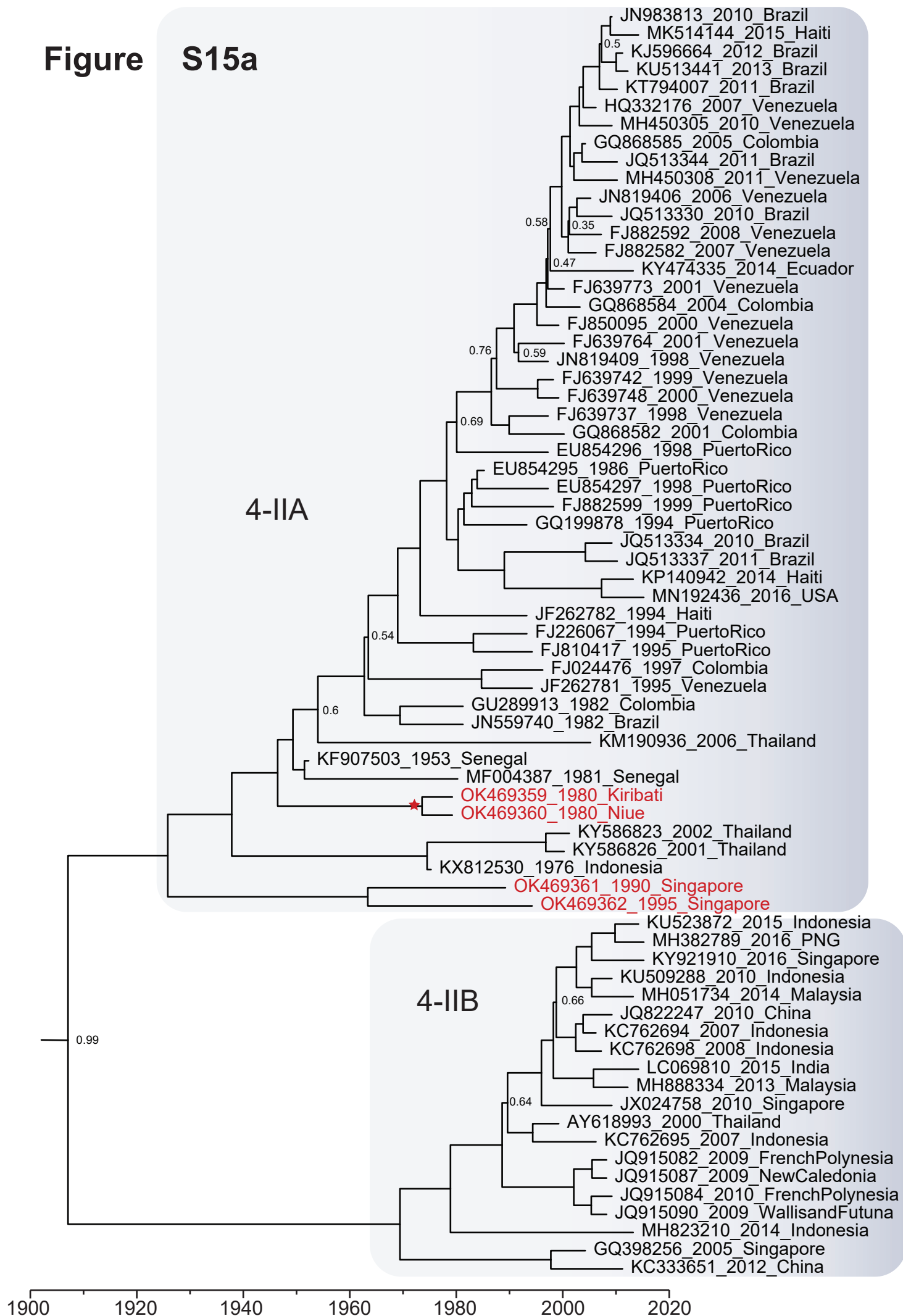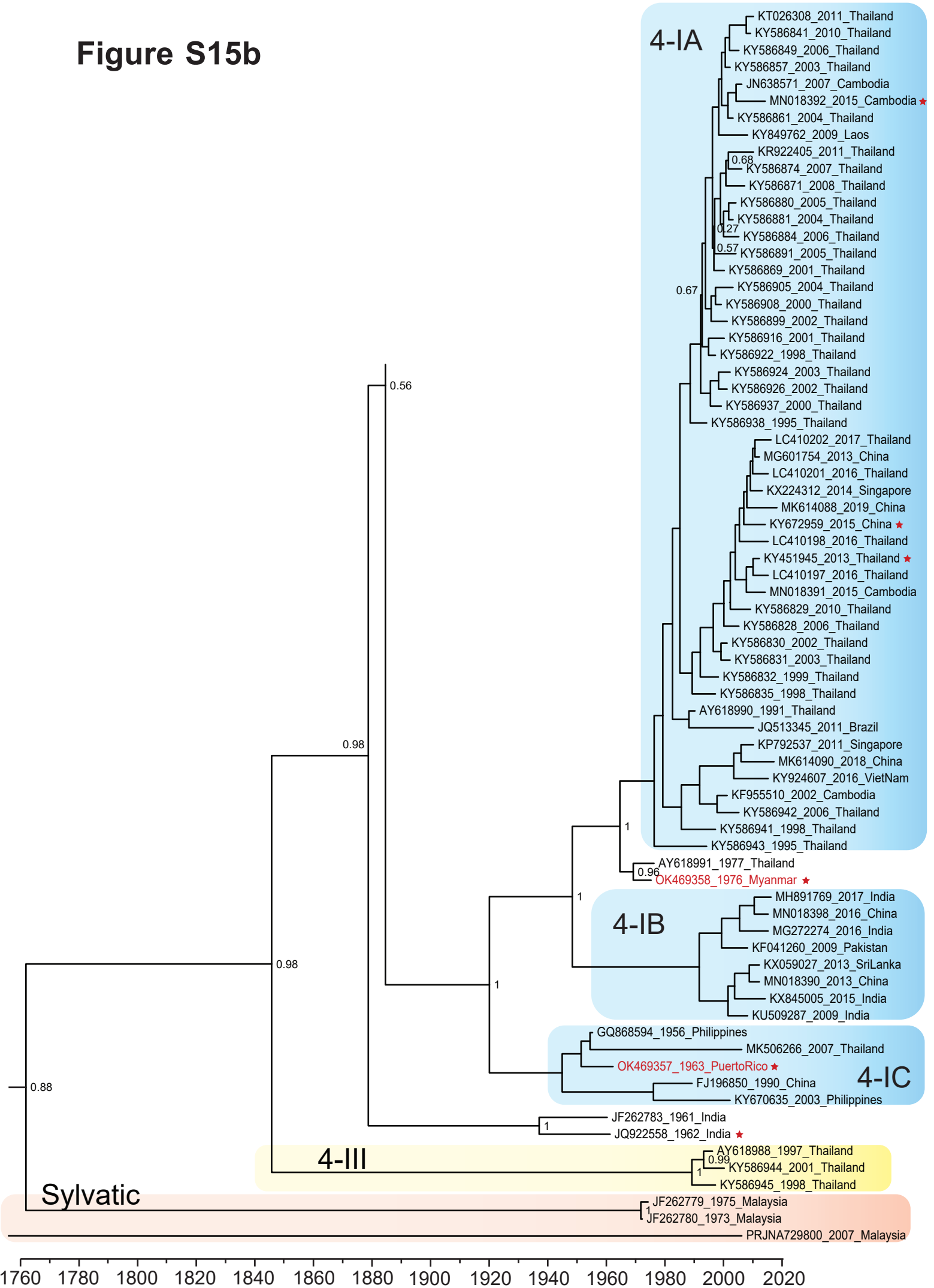
Figure S15a

Figure S15b

Supplemental Figure S16: DENV4 E Gene MCMC Trees. (a) DENV4 E gene MCMC tree, (b) Genotype 4-II, (c) Genotypes 4-I, 4-III, and sylvatic. Posterior node support indicated for the major branches. Support values >0.8 have been eliminated in most instances for clarity. Red circles/font indicates newly sequenced isolates from the QUT Arbovirus collection. Branches under positive selection (see section 3.2.2) are indicated by a red star. Scale axis is representative of calendar years.
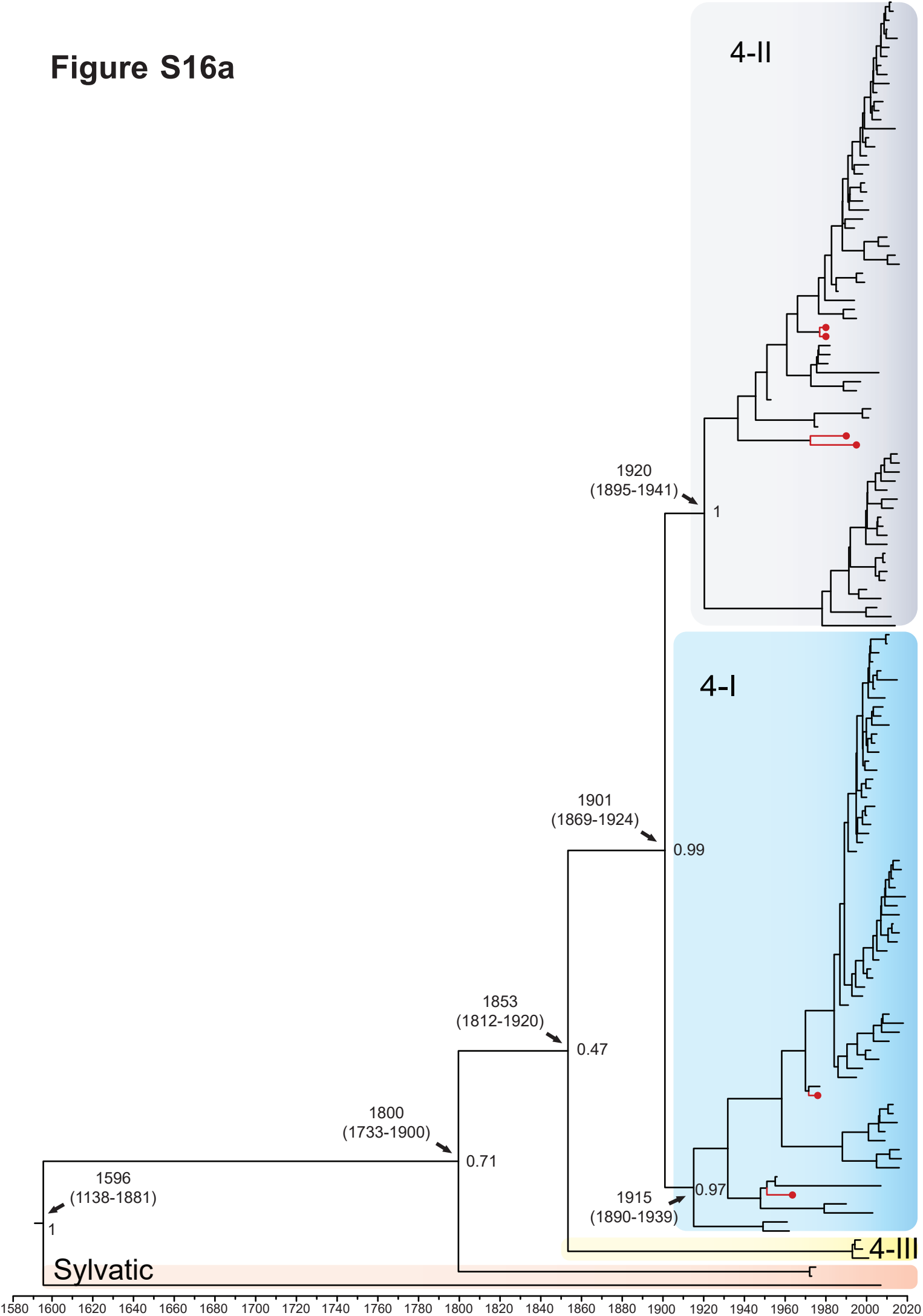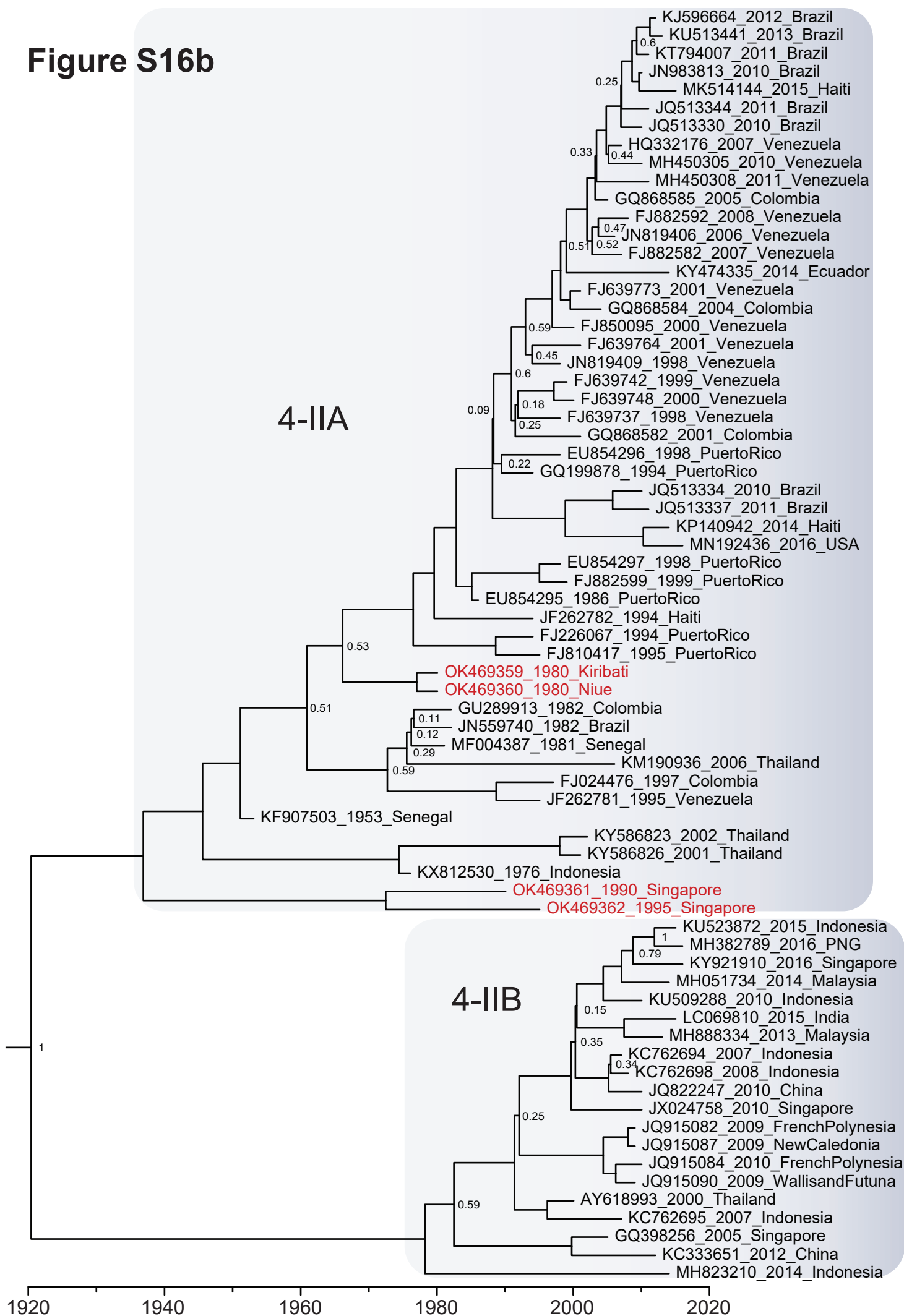
Figure S16a

Figure S16b

Figure S16c