

Supplementary Information

Early clearance of Chikungunya virus in children is associated with a strong innate immune response

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Supplementary legends

Supplementary Figure S1. Forest plots of pro-inflammatory cytokines that were significantly elevated in different CHIKF cohorts ($P < 0.05$). Dotted line represents no differences in the mean of the healthy controls and CHIKF patients. Red diamond represents the combined effect size for each mediator.

Supplementary Figure S2. Forest plots of anti-inflammatory cytokines that were significantly elevated in different CHIKF cohorts ($P < 0.05$). Dotted line represents no differences in the mean of the healthy controls and CHIKF patients. Red diamond represents the combined effect size for each mediator.

Supplementary Figure S3. Forest plots of chemokines that were significantly elevated in different CHIKF cohorts ($P < 0.05$). Dotted line represents no differences in the mean of the healthy controls and CHIKF patients. Red diamond represents the combined effect size for each mediator.

Supplementary Figure S4. Forest plots of growth and other factors that were significantly elevated in different CHIKF cohorts ($P < 0.05$). Dotted line represents no differences in the mean of the healthy controls and CHIKF patients. Red diamond represents the combined effect size for each mediator.

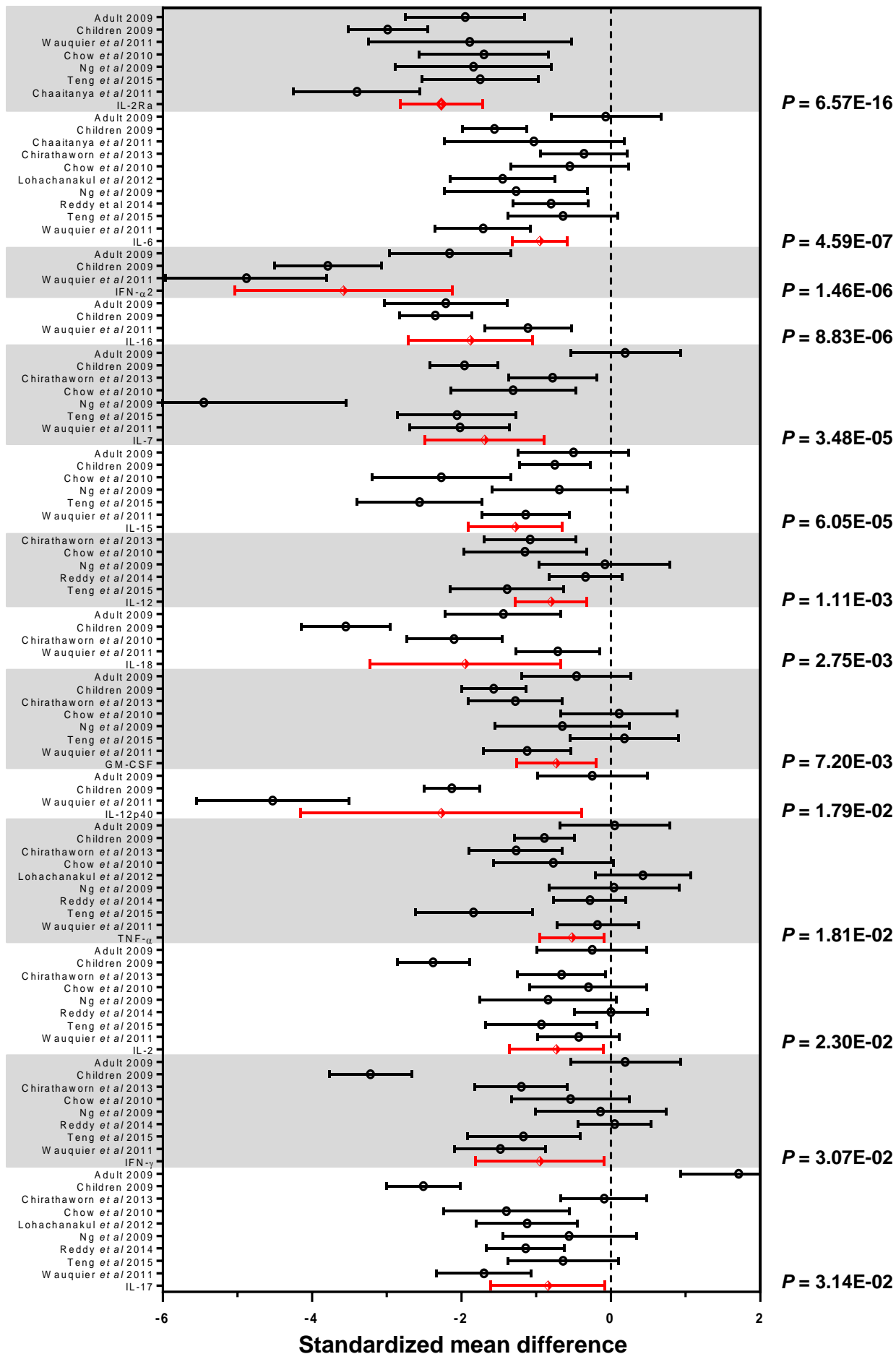
Supplementary Figure S5. Phylogeny of Sarawak CHIKV. A maximum likelihood tree was prepared from a 517 base-pair portion of the E1 gene. Results of this gene nucleotide sequencing work has been deposited at GenBank on 12 Nov 2015 with accession number (BS259-Sarawak-09: KU196260, BS260-Sarawak-09: KU196259, BS258-Sarawak-09: KU196261, BS239-Sarawak-09: KU196262, BS232-Sarawak-09: KU196263, BS200-Sarawak-09: KU196264, BS169-Sarawak-09: KU196265, BS166-Sarawak-09: KU196266, BS105-Sarawak-09: KU196267 and BS5-Sarawak-09: KU196268). Sequence from the closely related O'nyong-nyong virus (GenBank accession: AF192890) was used as an out-group to root the tree. CHIKV sequences from CHIKF outbreaks in Sarawak (2009) and Singapore (2007/08) are indicated with closed circle and open square labels respectively, and Indian Ocean lineage sequences are labelled with open circles. All GenBank reference sequences are identified by their accession numbers. Bootstrap values $>70\%$ are indicated at relevant branch nodes. All branch lengths are drawn to scale and a measurement of relative phylogenetic distance is provided by the scale at the bottom of the tree.

Supplementary References

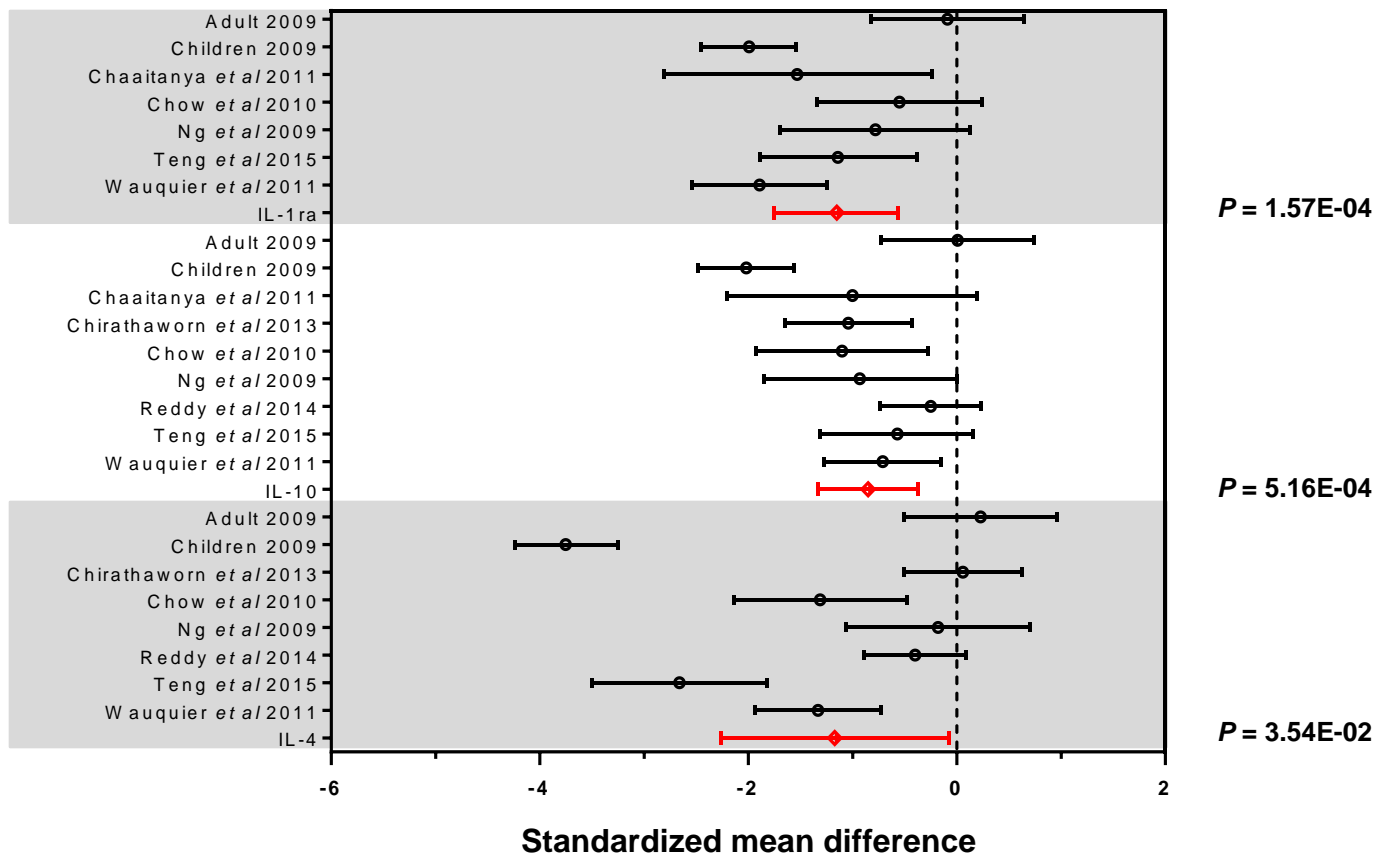
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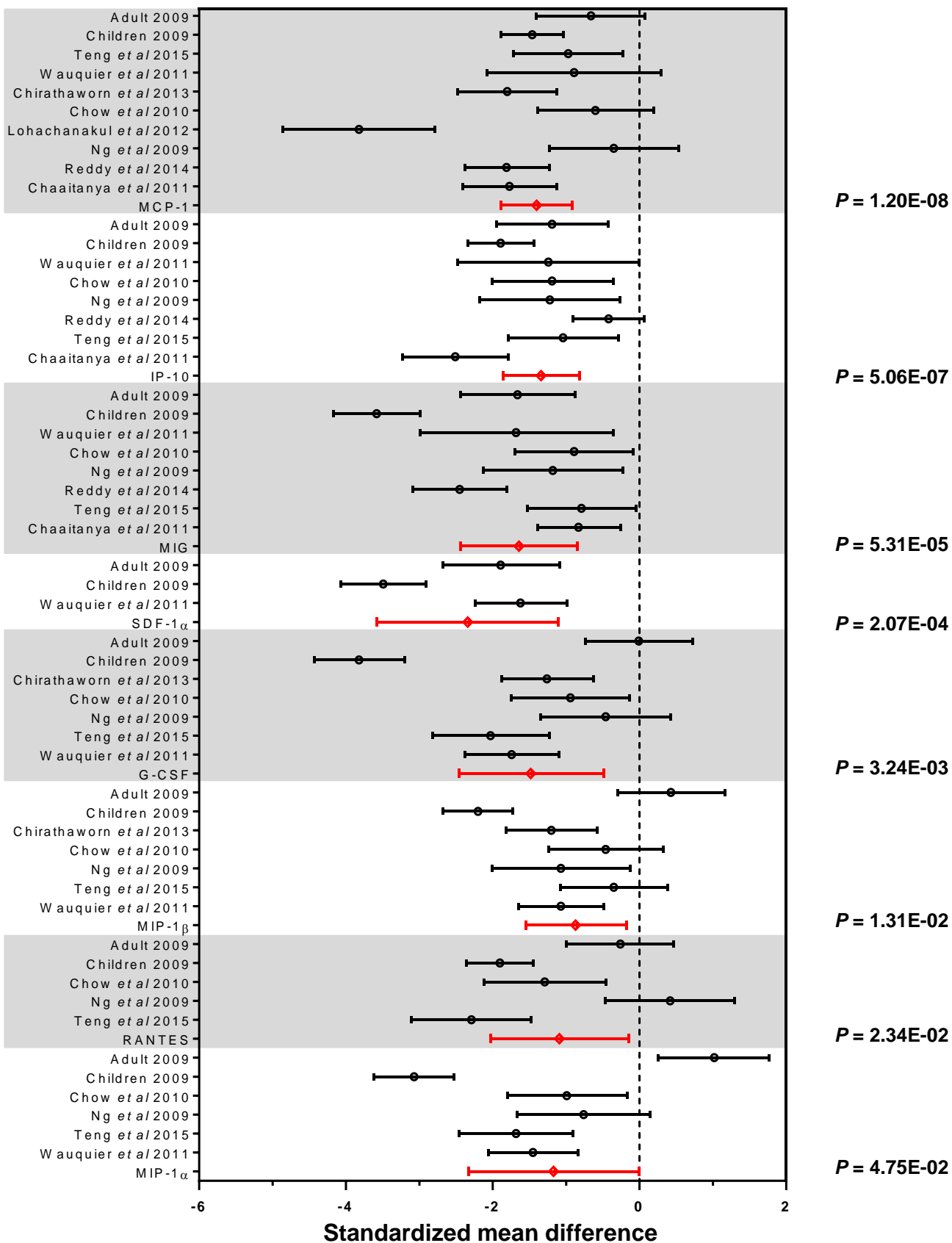
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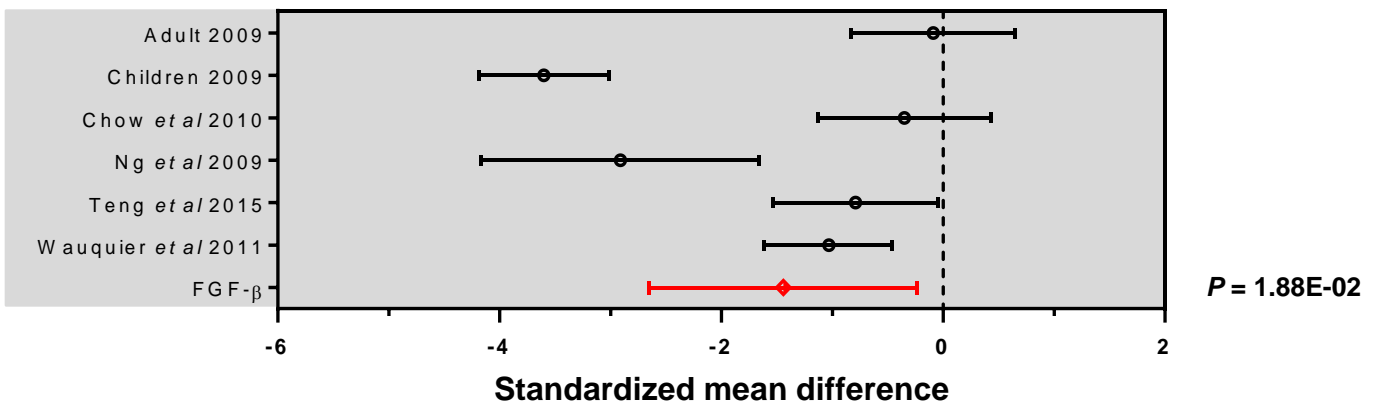


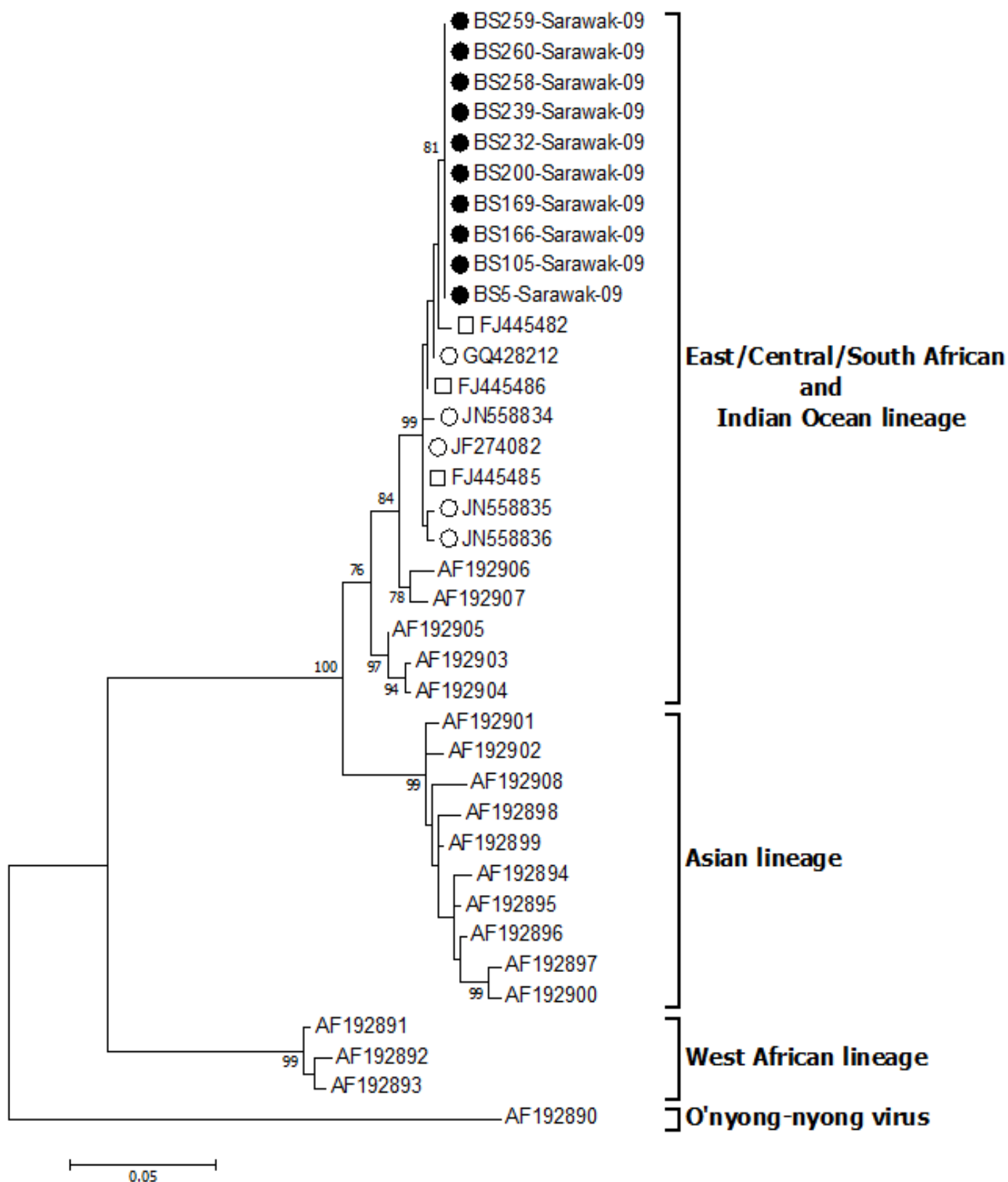
Supplementary Figure S1 Simarmata *et al.*, 2016





Supplementary Figure S3 Simarmata *et al.*, 2016





Supplementary Figure S5 Simarmata *et al.*, 2016