

**Additional file 2: Table S2.** Information on microsatellite loci used for the genotyping of *Aedes albopictus* populations. *Abbreviations:* F, forward; R, reverse.

Marker	Sequence	Size range (bp)	Dye	Multiplex	Quantity ( $\mu$ M)	References
Aealbmic3	F: ACCATACAGCCTGGAGTTCG R: GGGGTTGTGTGAATTGTCGT	206-238	VIC	M1	2	[1]
Aealbmic6	F: GATGGTCCGTATTTGGGTTG R: ATCTTCACTCATCCGCCATC	248-269	PET	M1	4	[1]
Aealbmic8	F: TTGTTGTTCCGGTTGTTGTTT R: CGGGTTCCAACATGTACGA	225-235	6FAM	M1	6	[1]
Albtri3	F: AGATGTGTGCGCAATGCTTCC R: GATTCCGGTGATGTTGAGGCC	119-131	PET	M1	2	[2]
Albtri45	F: TTTCAGCTCGGTGTTATGGC R: TGATGTTGATGATGATGACTACGA	116-133	6FAM	M1	2	[2]
Aealbmic4	F: ATCGCGGGTTTTCTATTCCCT R: ATCAACGAAACCGAAAGCAT	172-187	NED	M2	1.6	[1]
Aealbmic5	F: AACCCATCGAACACAGAAGG R: GTACGGTTGACTCGCTGTGA	148-222	6FAM	M2	1.6	[1]
Aealbmic7	F: ATAGACGGGAGTCGGTTCCT R: TCCAACCGCTAGTGTCAATCA	200-215	PET	M2	1.6	[1]
Aealbmic13	F: TCACACCATGGTCAAAGCAT R: TGCTGAGTTGAATGGAAACG	142-155	VIC	M2	2.5	[1]
Albdi6	F: TCTTCATCTACGCTGTGCTC R: GACCCAATCCGACAAAGTC	259-276	VIC	M2	2.5	[2]
Aealbmic2	F: ACGATGCGTAACCATTCGAT R: AACACCGCCGAATATGAAAC	190-193	PET	M3	2.5	[1]
Aealbmic9	F: GCGATGACAGTGAACAAGA R: GCTTGGCAGGGAACAAATTA	133-147	VIC	M3	1.2	[1]
Aealbmic10	F: ATCGCCTTCACTCTTCTTCG R: CCAATCTGAGCCGTACATT	171-182	6FAM	M3	4	[1]
Aealbmic11	F: CTCTGCGTTCGGTTCTATC R: AGGCAACCTCTCGAATGAAA	213-234	VIC	M3	7	[1]
Aealbmic12	F: AGAGCCCTCGAAAAGAGAGC R: AGCACTCATTCTTGGCTTGG	158-184	NED	M3	3	[1]
Aealbmic16	F: CACAACAACGAGAGTGTCGAA R: CCGAGGGCAACACGATATAC	218-250	6FAM	M3	5.6	[1]

### References

1. Manni M, Gomulski LM, Aketarawong N, Tait G, Scolari F, Somboon P, et al. Molecular markers for analyses of intraspecific genetic diversity in the asian tiger mosquito, *Aedes albopictus*. *Parasit Vectors*. 2015;8:1–11.
2. Beebe NW, Ambrose L, Hill LA, Davis JB, Hapgood G, Cooper RD, et al. Tracing the tiger : Population genetics provides valuable insights into the *Aedes* (*Stegomyia*) *albopictus* invasion of the australasian region. *PLoS Negl Trop Dis*. 2013;7:e2361.
3. Peakall R, Smouse PE. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics*. 2012;28:2537–9.