Correction to: Terpene synthase genes in *Melaleuca alternifolia*: comparative analysis of lineage-specific subfamily variation within Myrtaceae

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In the methods on page 112, we report a “cytological” estimate of 710 Mb based on flow cytometry for *Melaleuca alternifolia*. For clarity, this should have been qualified as a “2C” or diploid estimate of genome size.

Furthermore the last paragraph of the online resource 2 should read; “The 1 C genome size estimate from flow cytometry of 355 Mb was similar to the estimate of 356 Mb based on sequencing.”

The original article can be found online at <https://doi.org/10.1007/s00606-017-1454-3>.

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