



Figure S1. Coverage for all individuals of *Bettongia lesueur* sampled (including founder individuals) represented as a box plot, where mean coverage (white) is the average coverage for primary reads and mean merged coverage (grey) is the coverage after merging alleles. Average is indicated by a red diamond. Middle horizontal line reflects the median, the boxes are bound by the 25th and 75th quartiles and the vertical lines show the minimum and maximum range of values.