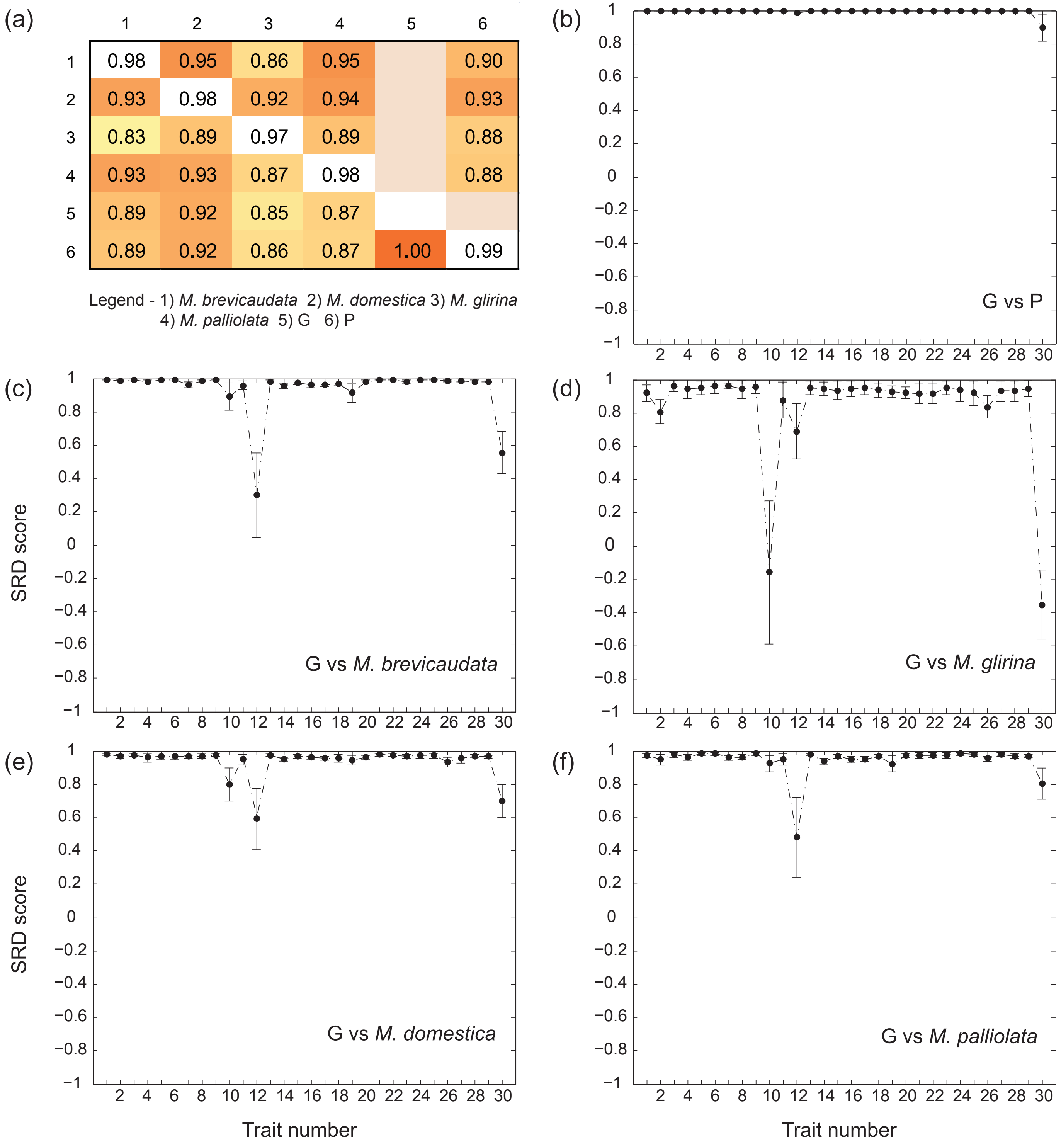

	1	2	3	4	5	6
1	0.98	0.95	0.86	0.95		0.90
2	0.93	0.98	0.92	0.94		0.93
3	0.83	0.89	0.97	0.89		0.88
4	0.93	0.93	0.87	0.98		0.88
5	0.89	0.92	0.85	0.87		
6	0.89	0.92	0.86	0.87	1.00	0.99

Figure S1– (a) Raw (lower triangle) and adjusted (upper triangle) vector correlations among the different Monodelphis V/CV matrices. Matrix repeatabilities are shown on the diagonal; (b-f) Profile plots illustrating the pairwise comparisons between G and different P-matrices. High values indicate high similarity among matrices, and vice-versa. P-matrices are identified on the lower right corner of the plot. SRD scores are illustrated in the Y axis and are measured in terms of average vector correlations. Morphological traits are depicted in the X-axis. The trait order corresponds to the one in Table S2.

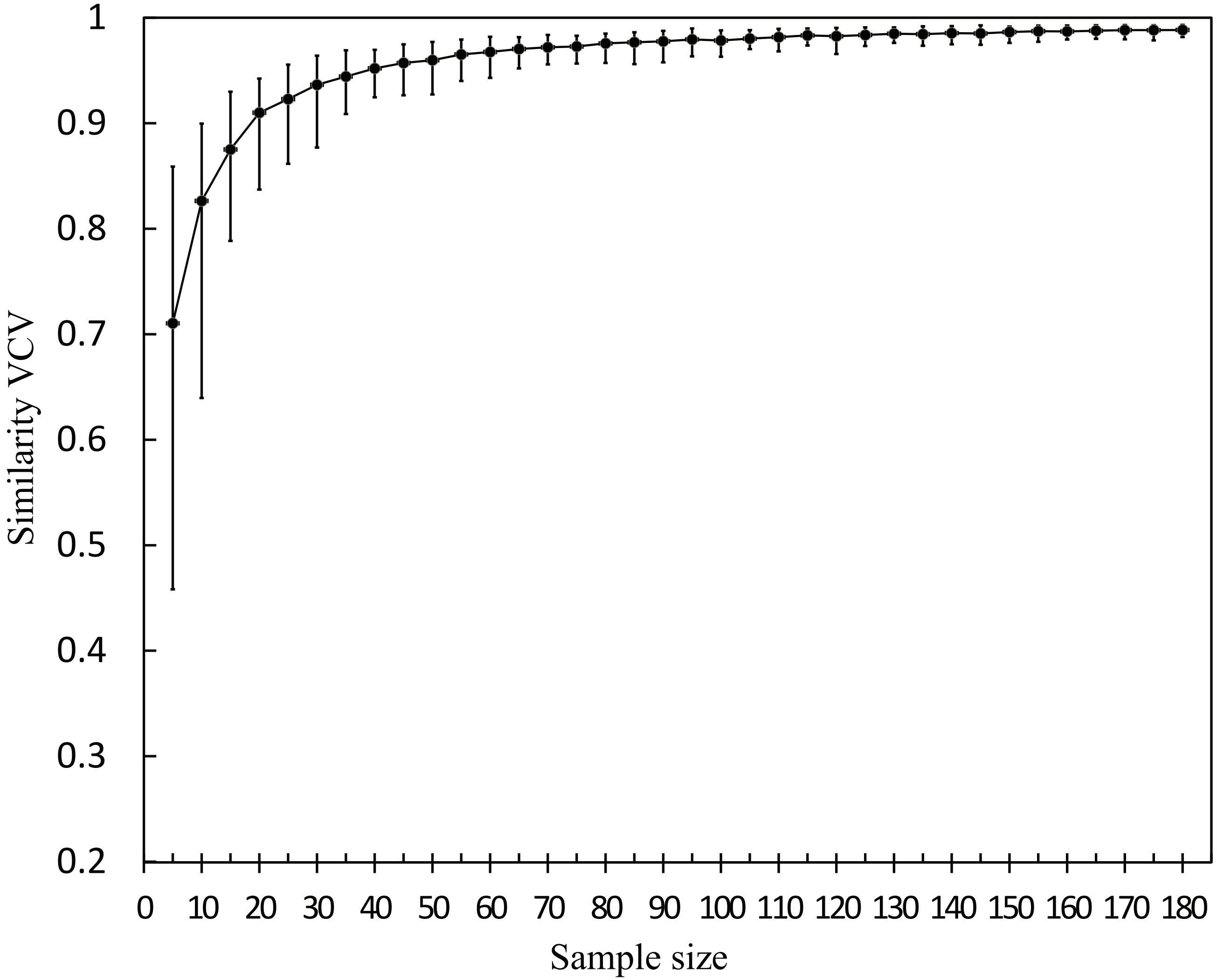

Figure S2- Mean vector correlation (Y-axis) between the original P-matrix and its undersampled counterparts. The number of individuals sampled is shown in the X-axis. 95% confidence intervals calculated based on the bootstrap resamples are shown for each sample size.

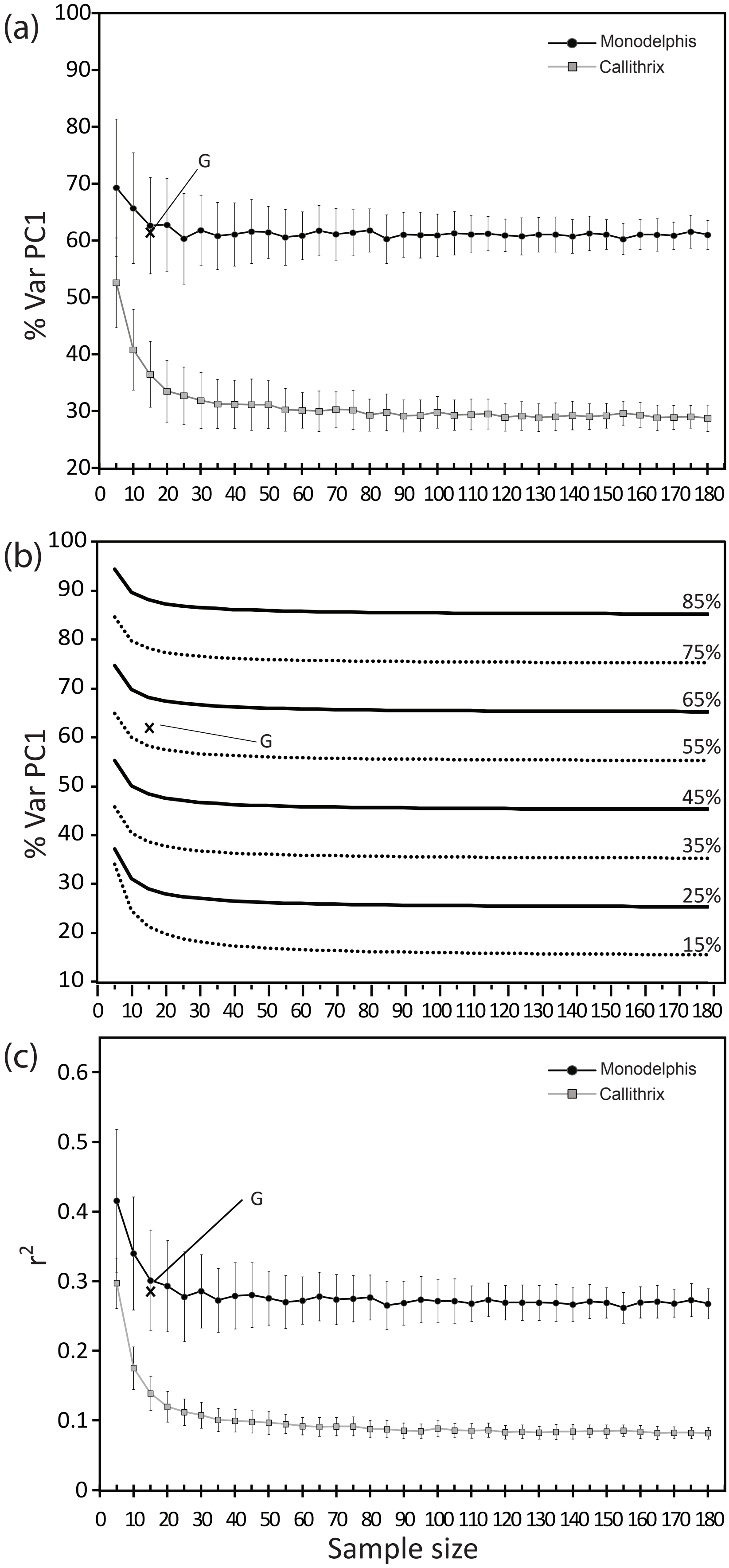

Figure S3- (a) Percent variance explained by the leading eigenvalue of phenotypic V/CV matrices calculated under different sampling conditions (N varying from 5 to 180). Values were calculated based on bootstrap resamples of a database of 30 cranial traits measured in two different mammal genera (Monodelphis and Callithrix). The Monodelphis G-matrix is indicated with an 'X' ; (b) Theoretical expectations for the percent variance explained by the leading eigenvalue of the Monodelphis G-matrix, given different initial true parameter values (true values varying from 15% to 85%; see text for formula). The observed value for G is indicated with an 'X'; (c) Magnitude of morphological integration (r^2) of phenotypic V/CV matrices calculated under different sampling conditions (N varying from 5 to 180). Values were calculated based on bootstrap resamples of a database of 30 cranial traits measured in two different mammal genera (Monodelphis and Callithrix). The Monodelphis G-matrix is indicated with an 'X'. Error bars represent the 95% CI.

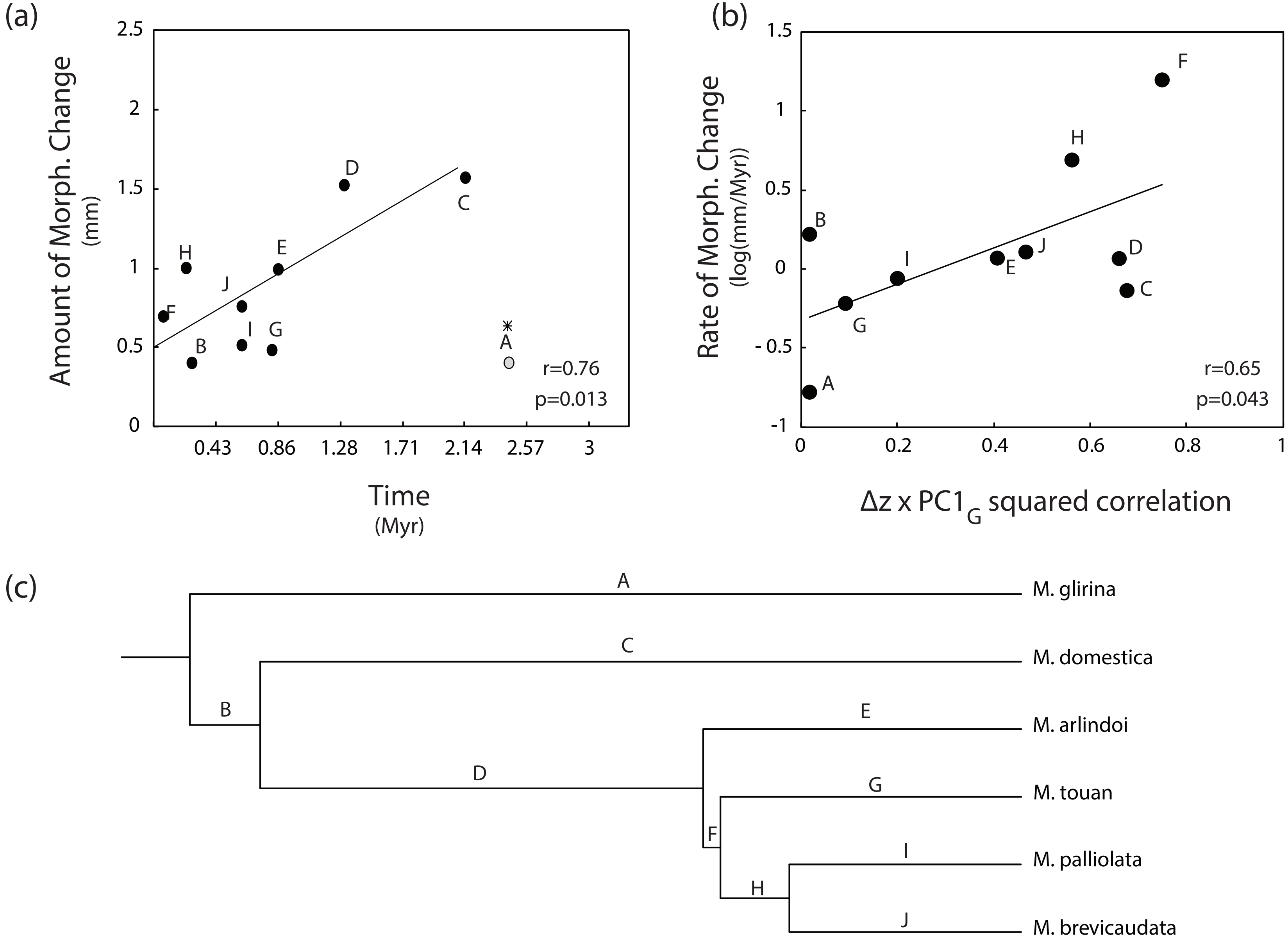

Figure S4 - Maximum parsimony reconstruction of Figure 4– (a) Plot of the amount of morphological change on each branch of the brevicaudata group's phylogeny against the corresponding branch length; (b) Plot of the rate of morphological change on each branch of the brevicaudata group's phylogeny against the direction of evolutionary change. Direction of evolutionary change is measured in terms of its alignment with an allometric size vector (Δz x PC1G squared correlation); (c) Most recently published phylogeny of the Monodelphis brevicaudata species group (Pavan et al., 2014).