

Supplemental Figures for “Process-based allometry describes the influence of management on orchard tree aboveground architecture”

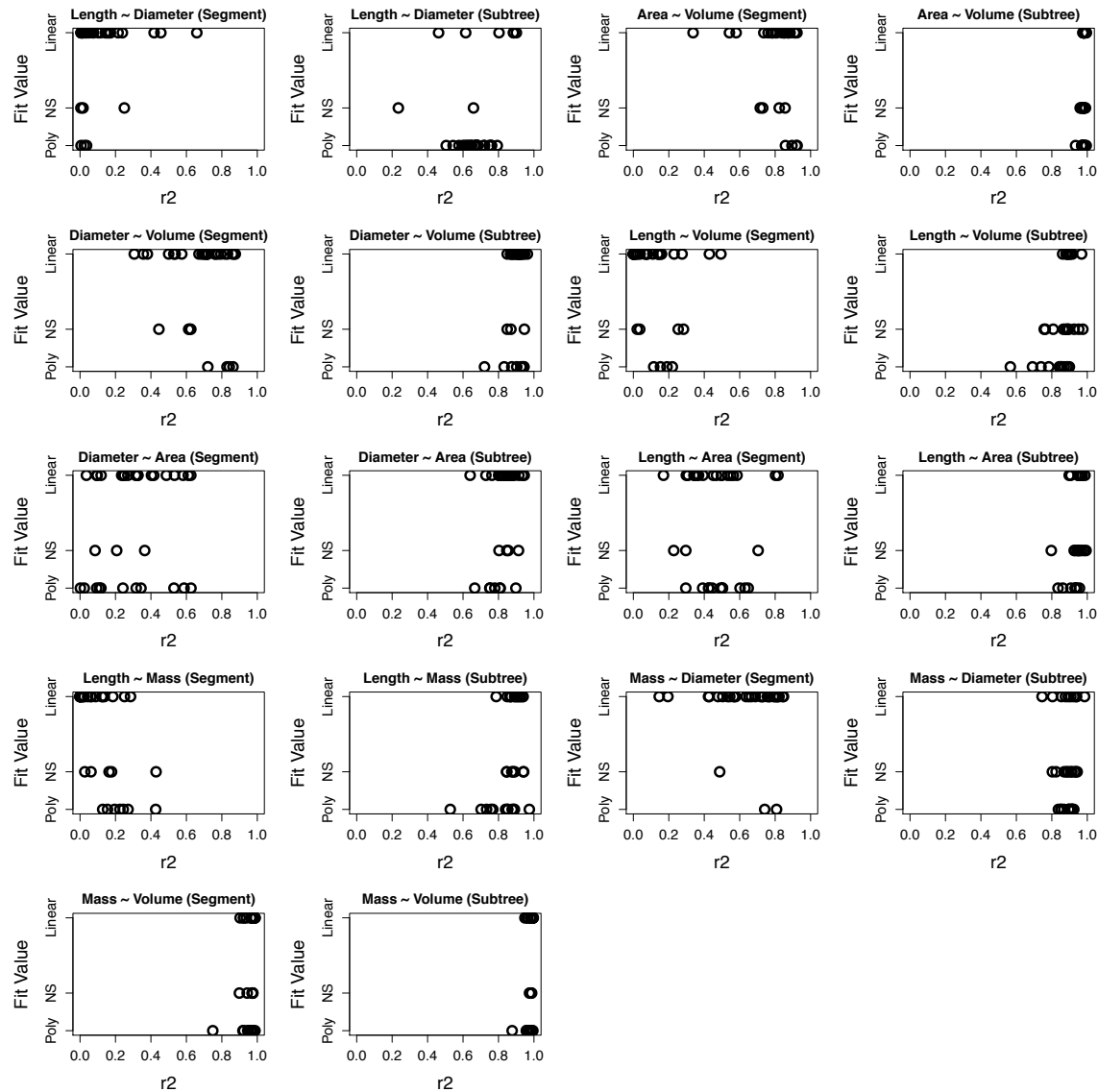


Figure S1-1. Strongest model fitted in relation to the r^2 of the linear model. The strongest model fitted was determined by comparing AIC of linear or polynomial (Poly) models with the lower AIC identifying the strongest model. The polynomial model was reported as not significant (NS) if expressing the lower AIC but the 2*standard error of the polynomial term overlapped with 0.

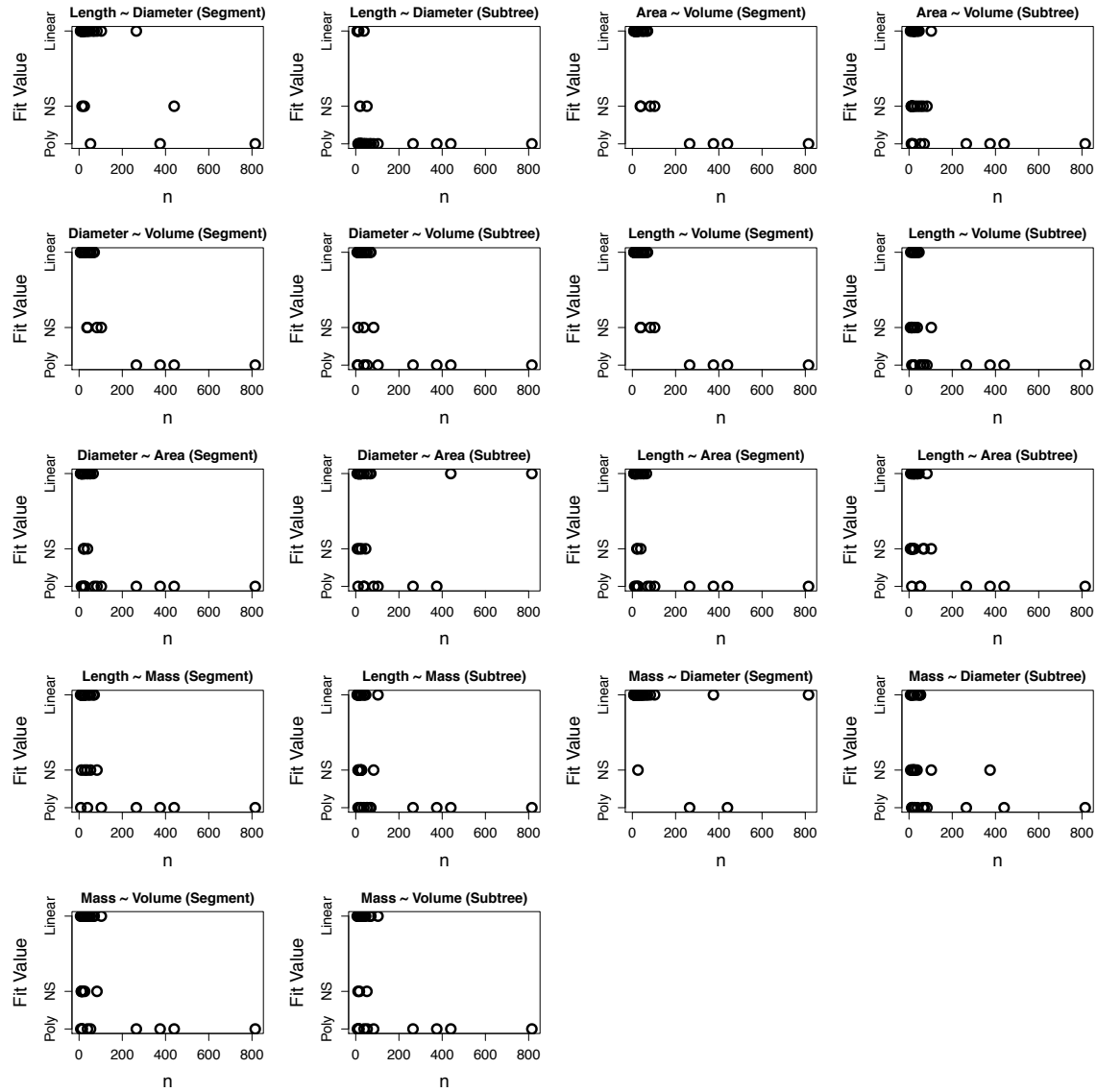


Figure S1-2. Strongest model fitted in relation to the branch sample size (n). The strongest model fitted was determined by comparing AIC of linear or polynomial (Poly) models with the lower AIC identifying the strongest model. The polynomial model was reported as not significant (NS) if expressing the lower AIC but the 2*standard error of the polynomial term overlapped with 0.

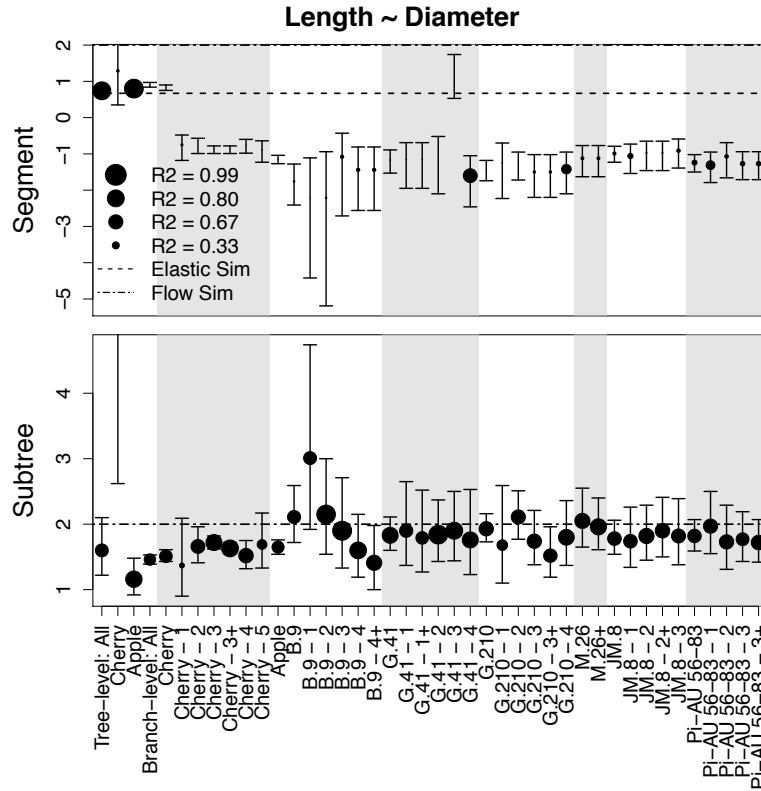


Figure S2-1. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

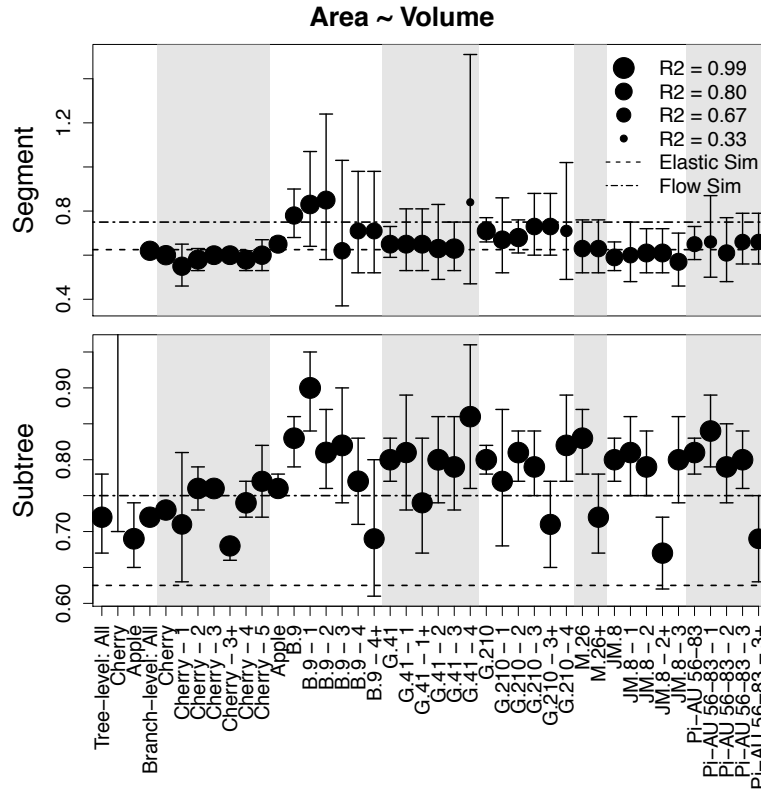


Figure S2-2. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

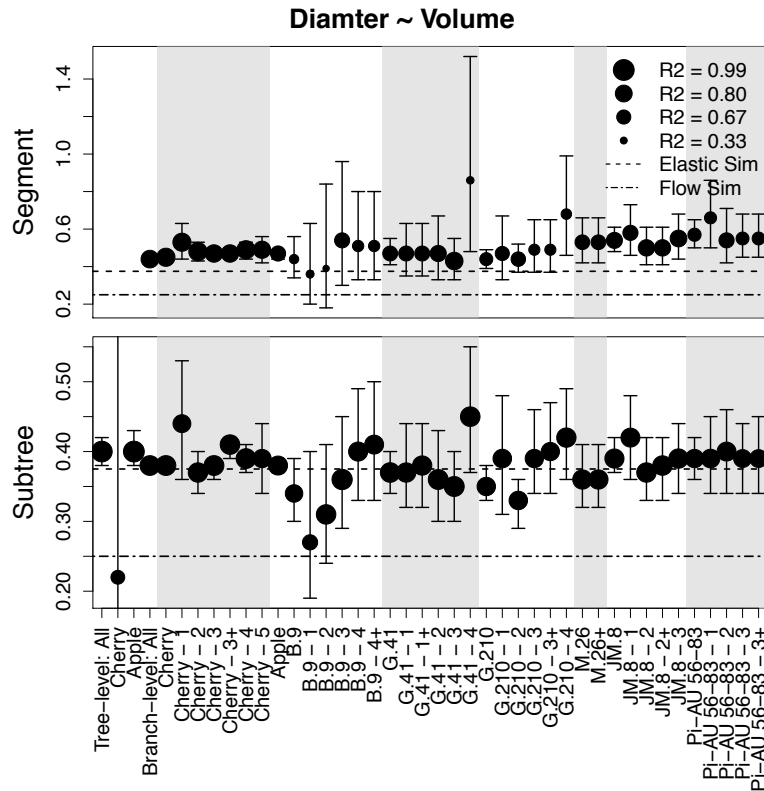


Figure S2-3. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

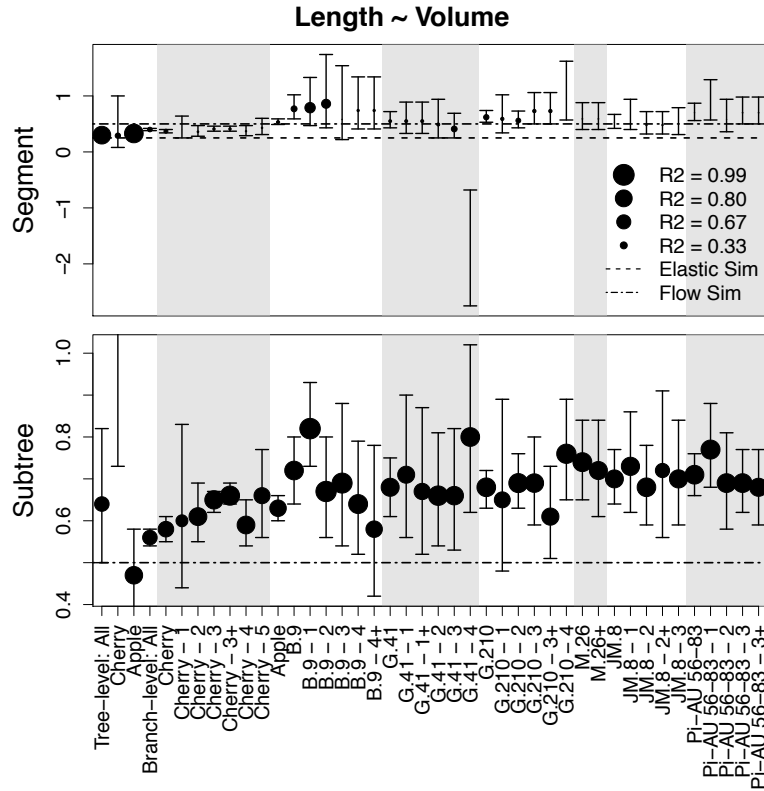


Figure S2-4. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

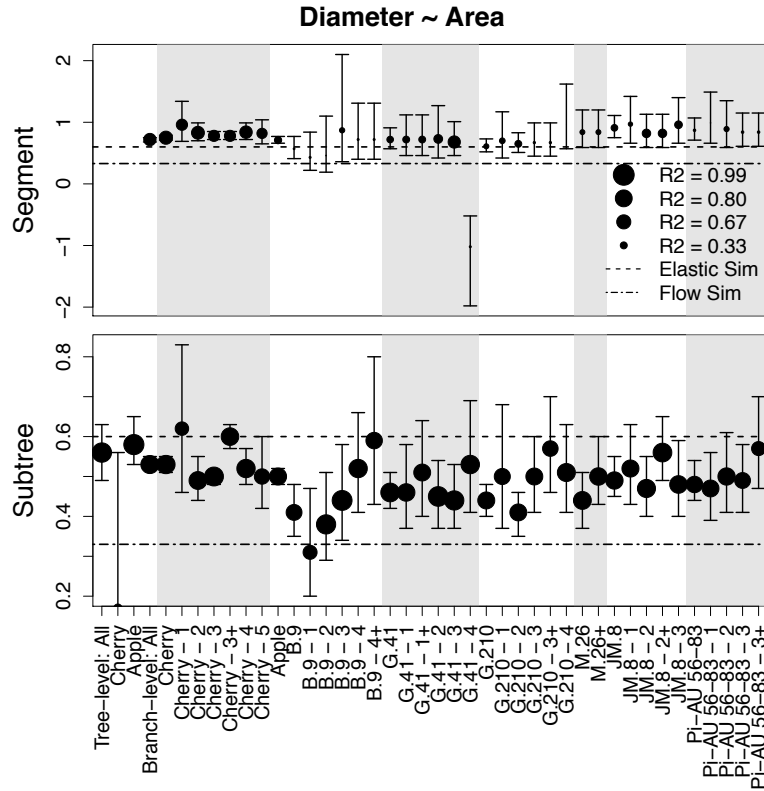


Figure S2-5. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

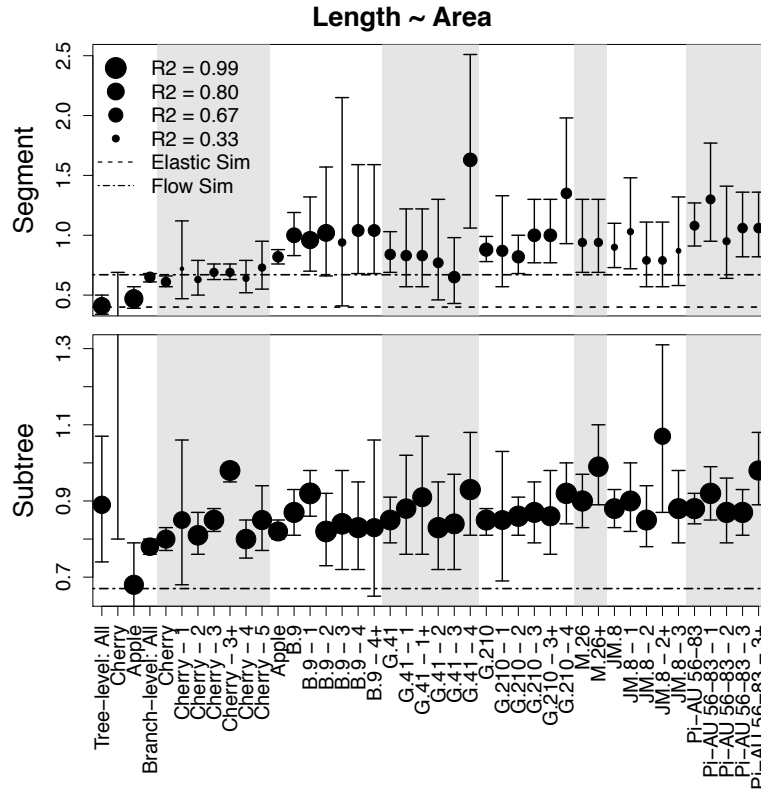


Figure S2-6. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-bases models are marked as horizontal lines. The predicted a from the FS model: elastic similarity is marked by a dashed line and flow similarity by a dot-dash line. R^2 is shown by scaled dot size.

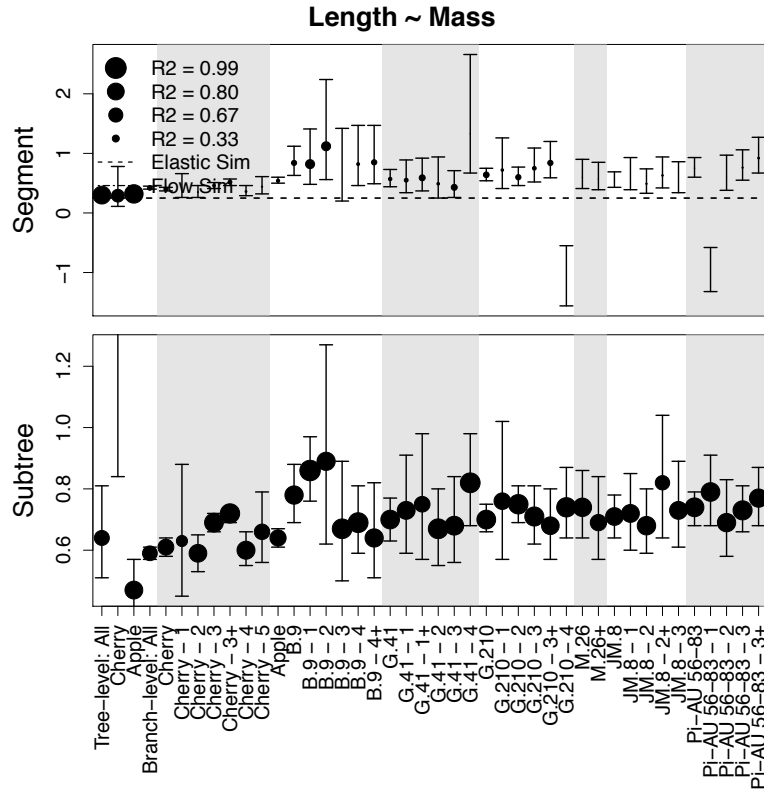
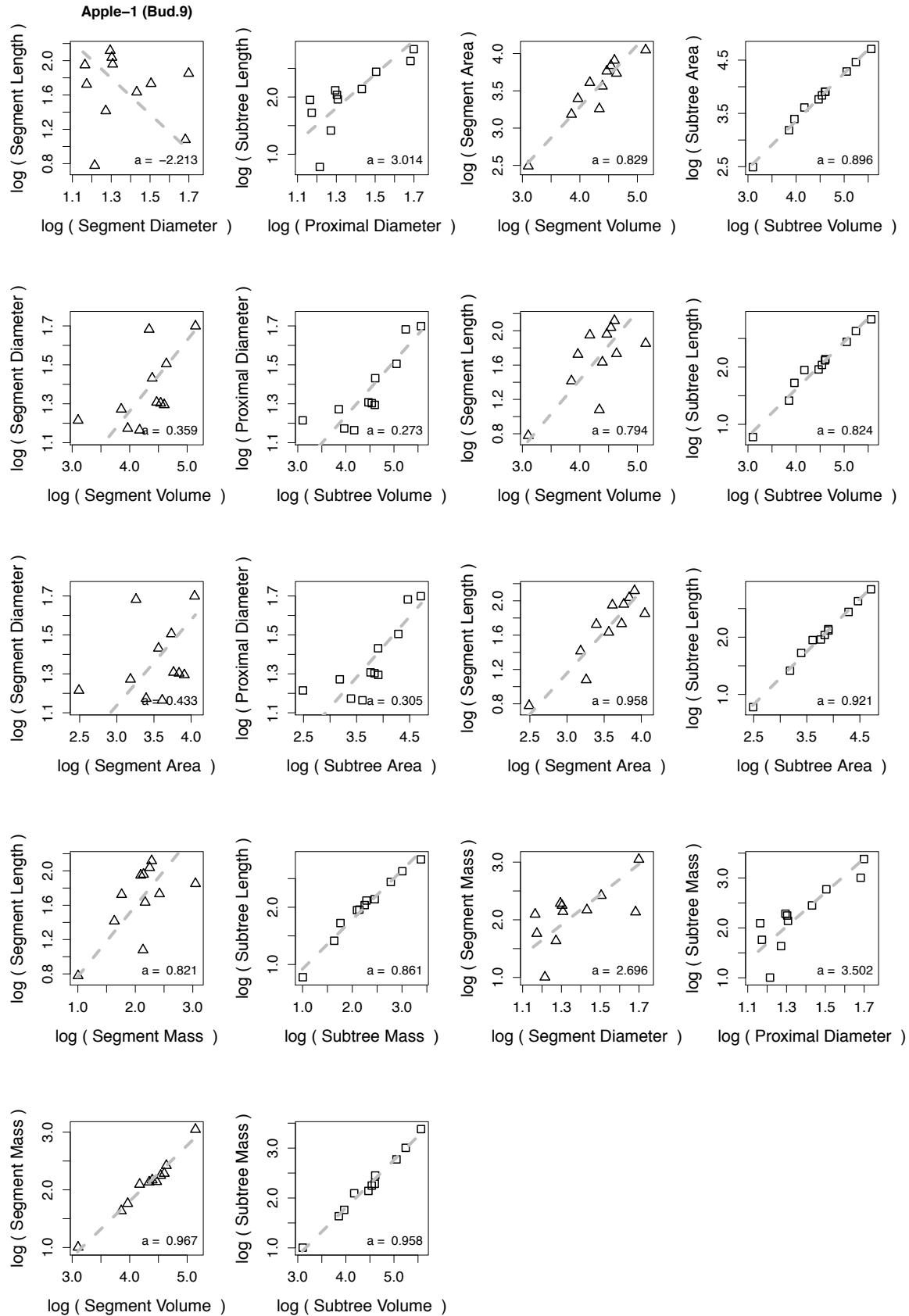
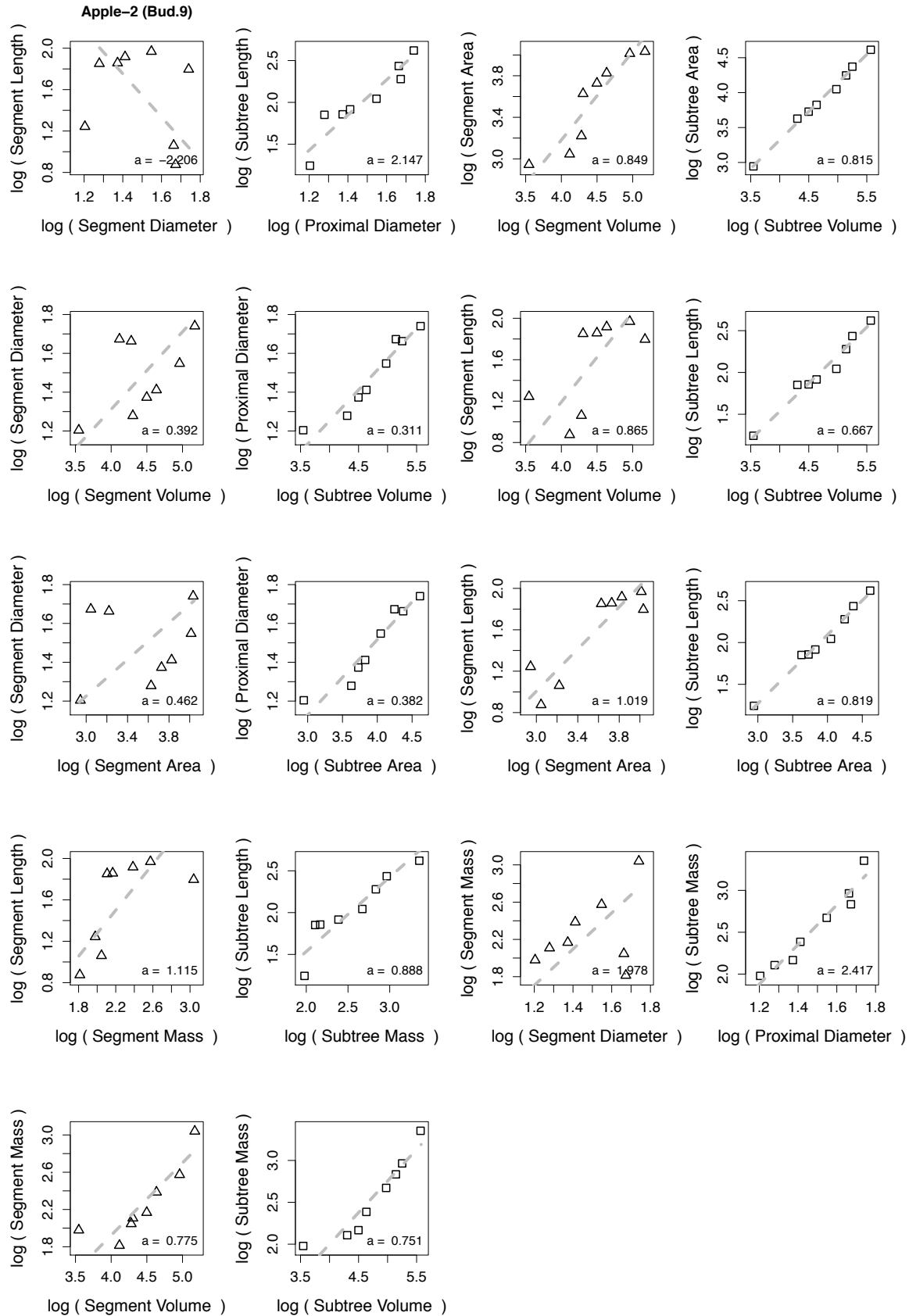
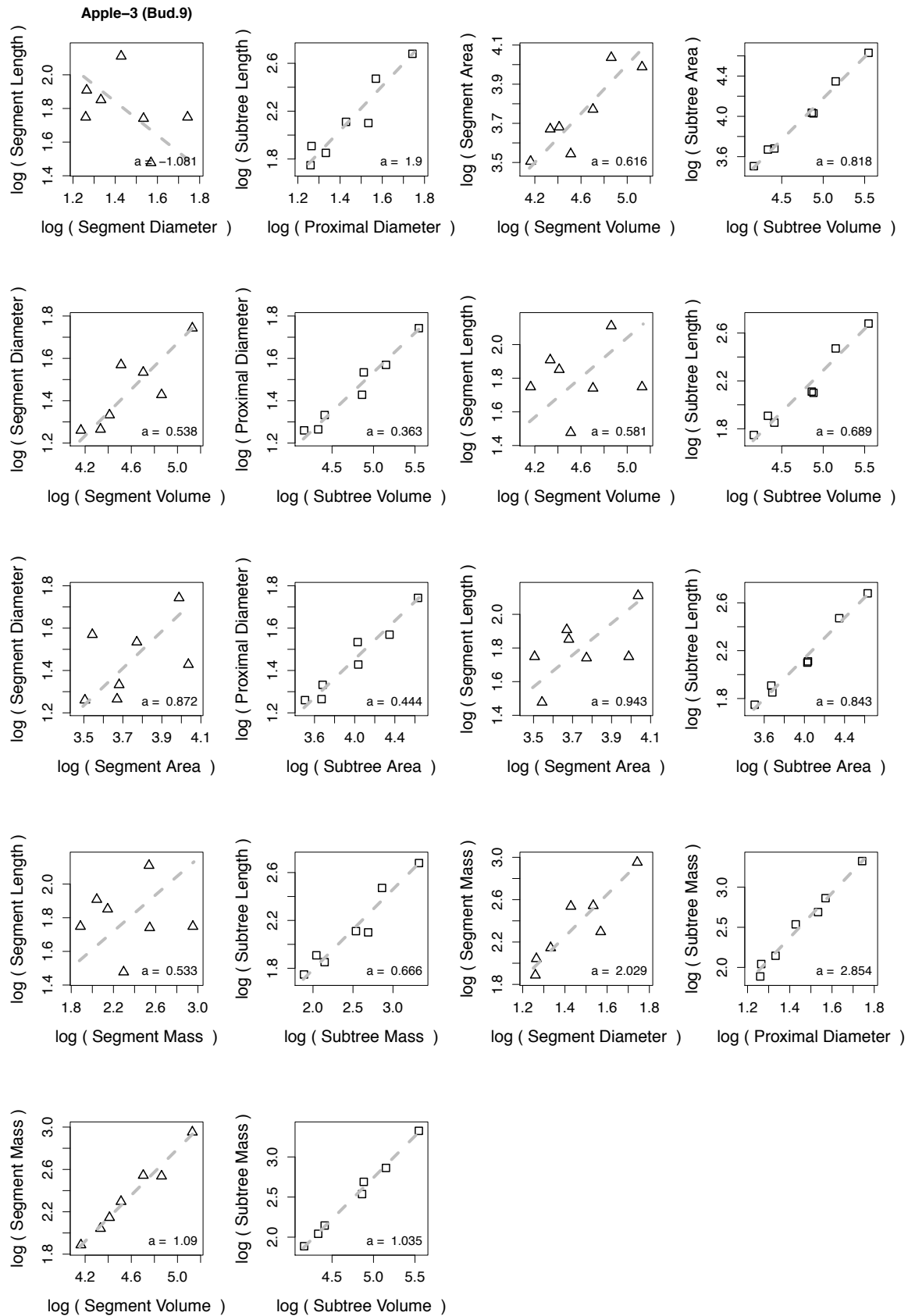


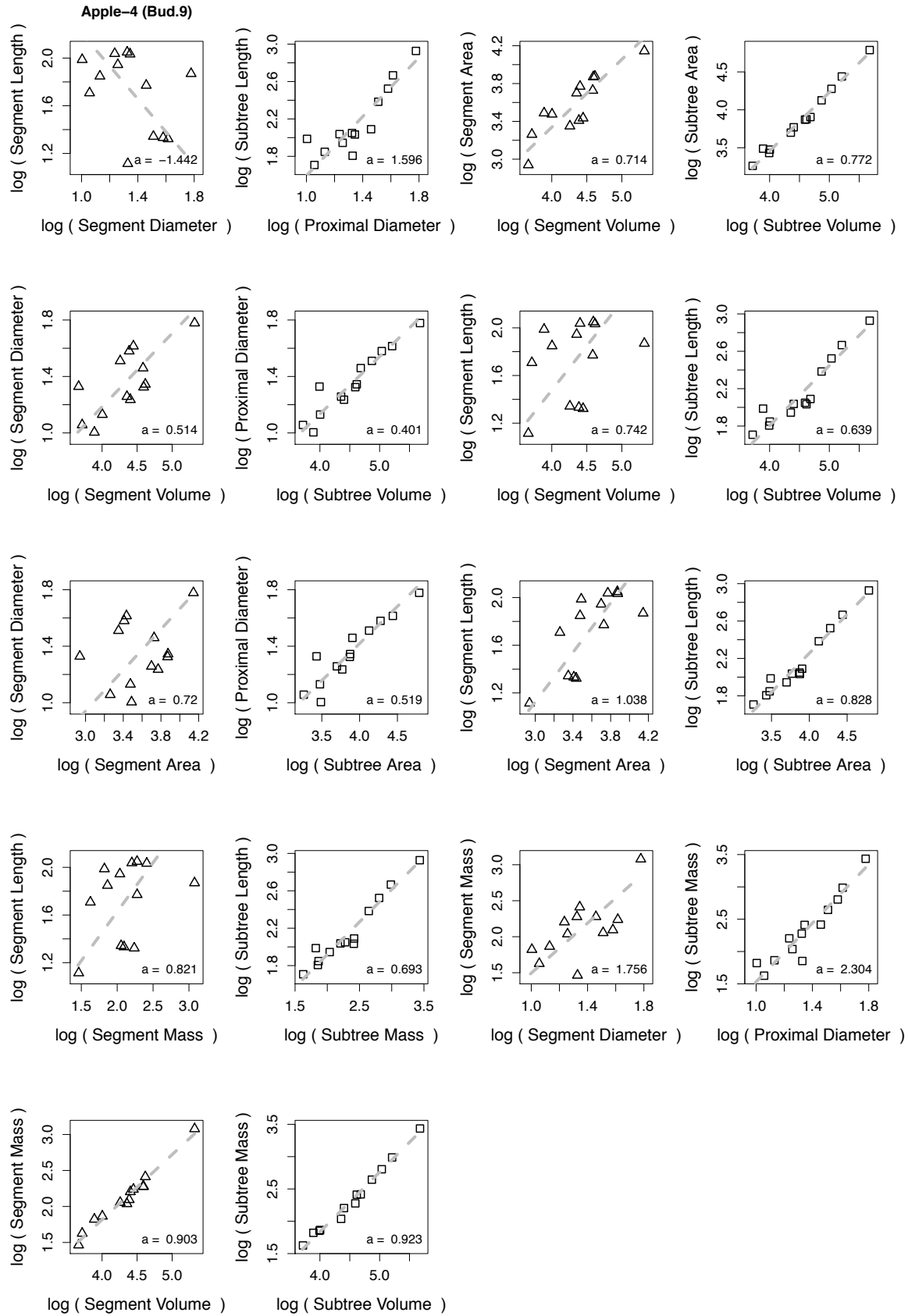
Figure S2-7. Estimates of allometric exponent (a) and 95% confidence intervals for five 24-year-old tart cherry (*Prunus cerasus*; *P. mahaleb*) and nineteen 10-year-old ‘Golden Delicious’ apple (*Malus spp.*; various rootstocks) at an individual and group level for each branch-level classification: segment and subtree. The groups are organized roughly by shaded region. The first group (white space) are the tree-level data, except for the ‘all-branch’ group for all branches collected in the dataset. The remaining groups are branch-level data broken down by species (tart cherry, apple) and the rootstock abbreviations for apples. Individuals are identified by a hyphen and an individual number. The addition of the ‘+’ indicates the individuals that were sampled in more detail and include twig length and mass data noted by a ‘+’. The predicted a from the process-based models are marked as horizontal lines. The predicted a from the WBE model is marked by a dashed line. R^2 is shown by scaled dot size.

Figure S3. Data visualization for each allometric relationship at an individual level. Each individual in the data set (19 apple; 5 tart cherry) are depicted in order of trunk diameter per page. Each apple is identified by its rootstock noted in parentheses. Data points correspond to branches at each branch-level classification. Segment level estimates are marked by triangles and subtree by squares. Dashed lines mark the estimated exponent (a) displayed on the figure.

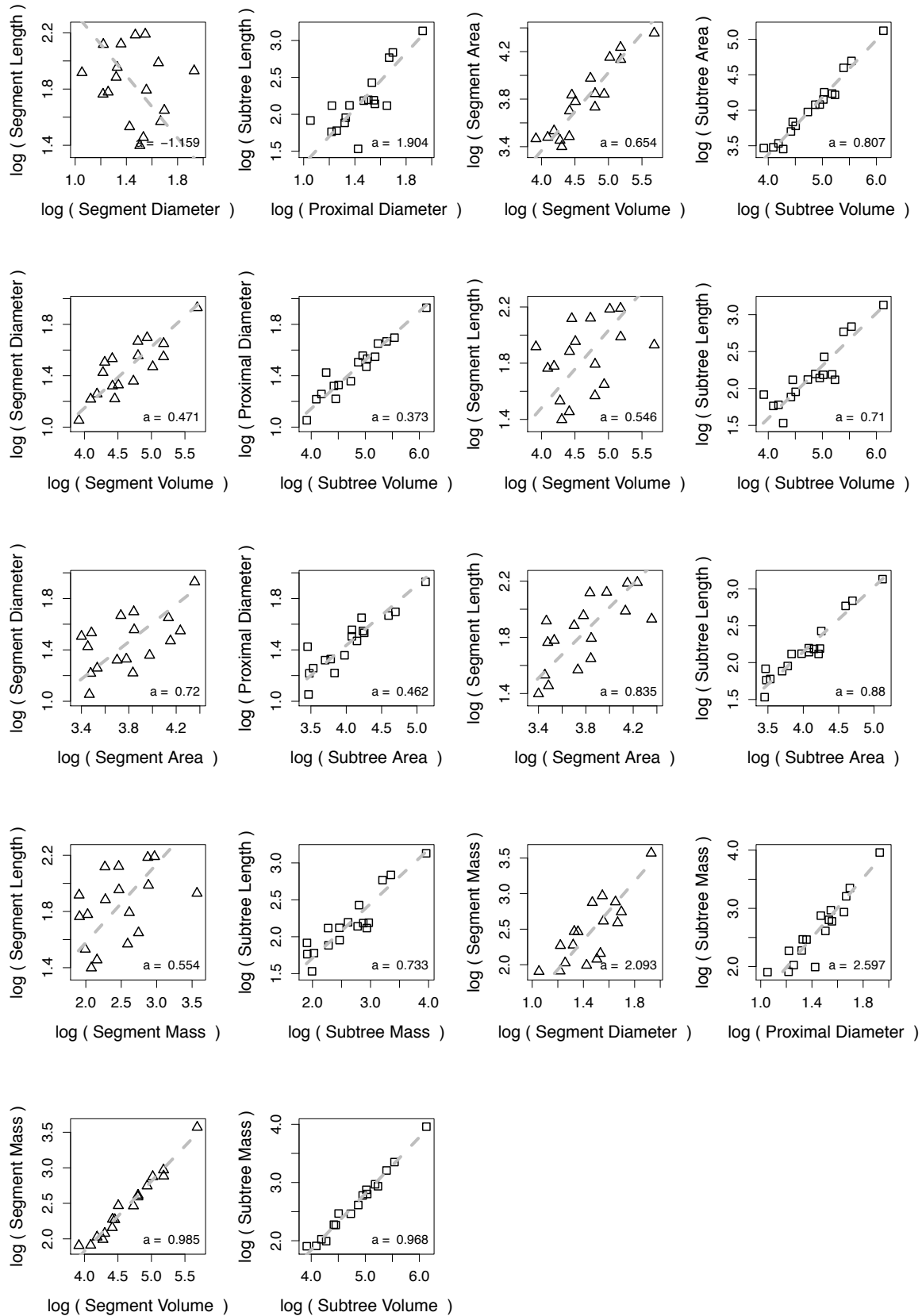


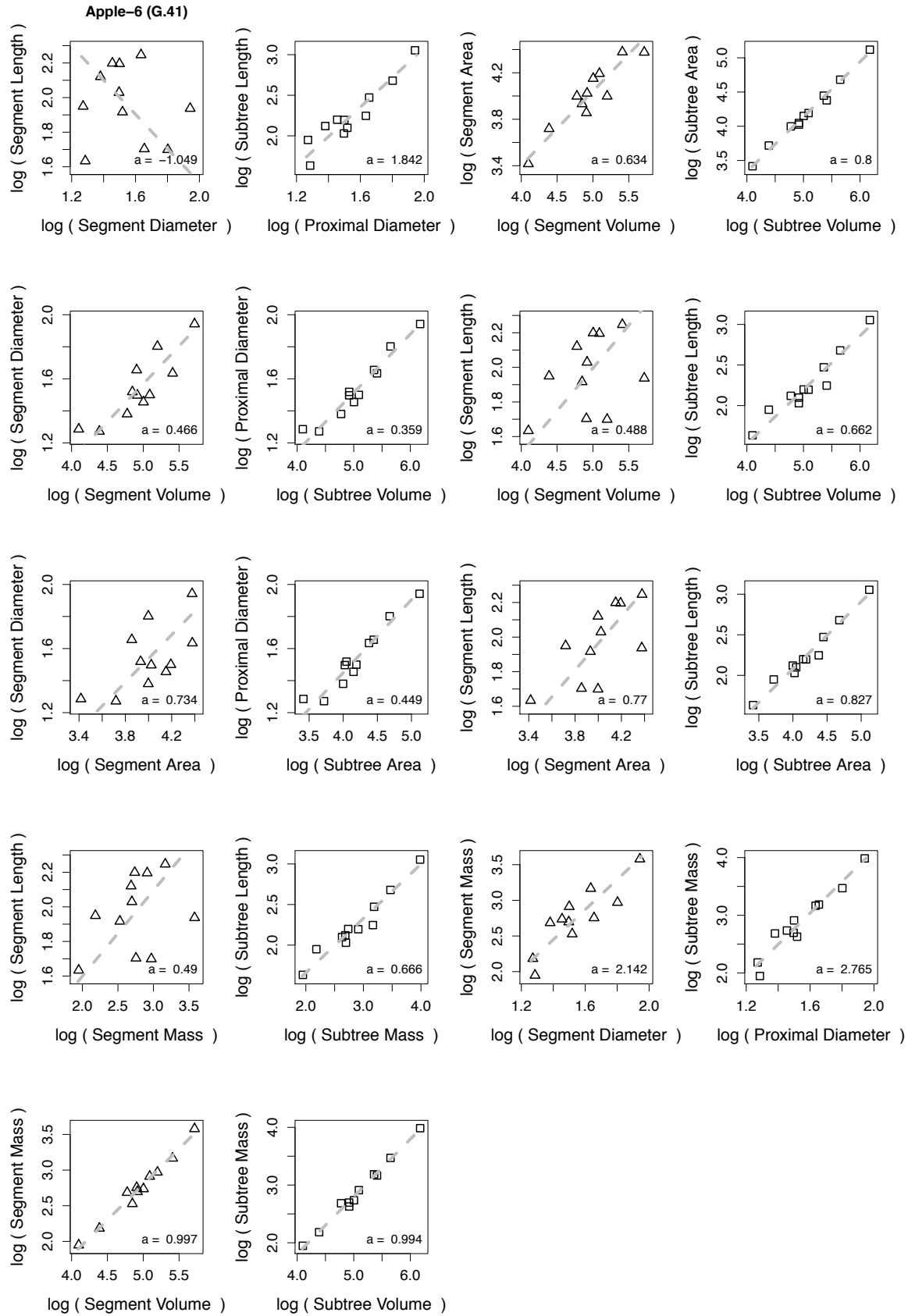


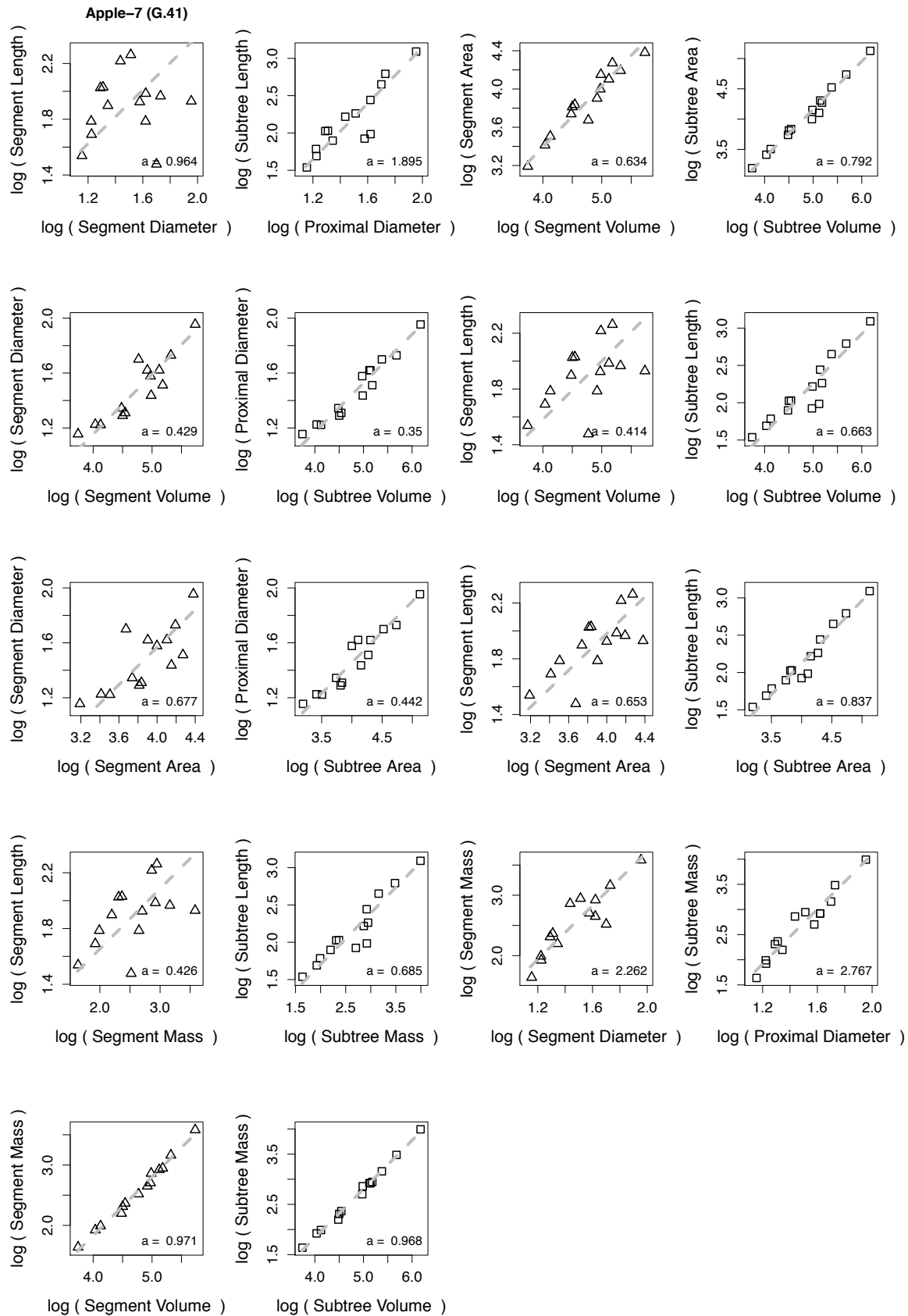




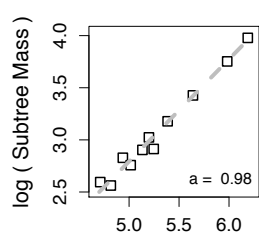
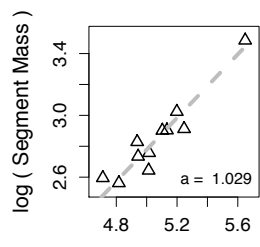
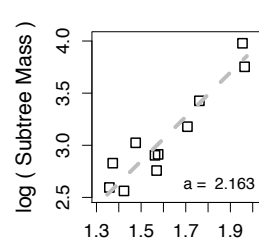
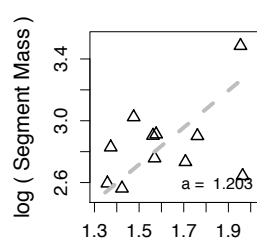
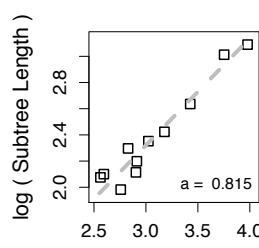
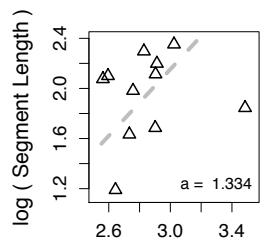
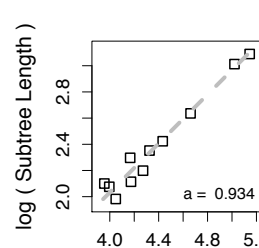
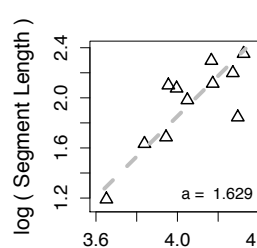
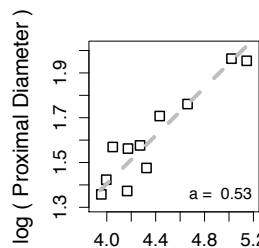
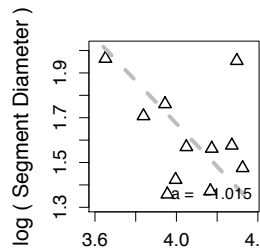
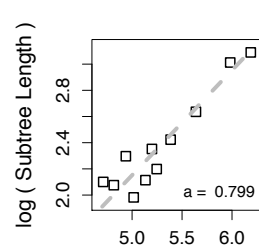
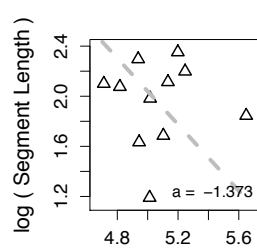
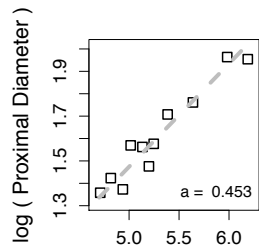
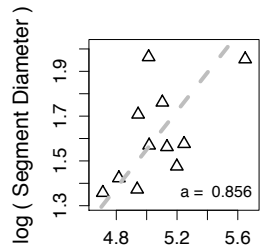
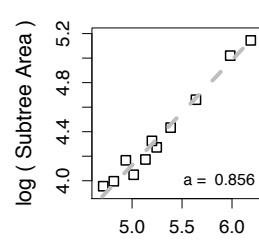
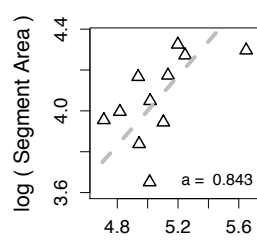
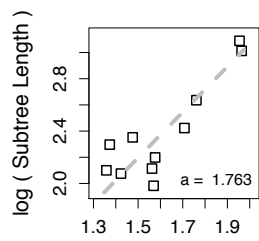
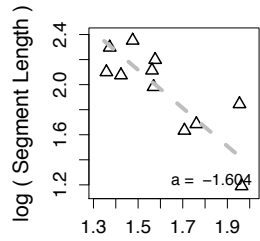
Apple-5 (G.41)

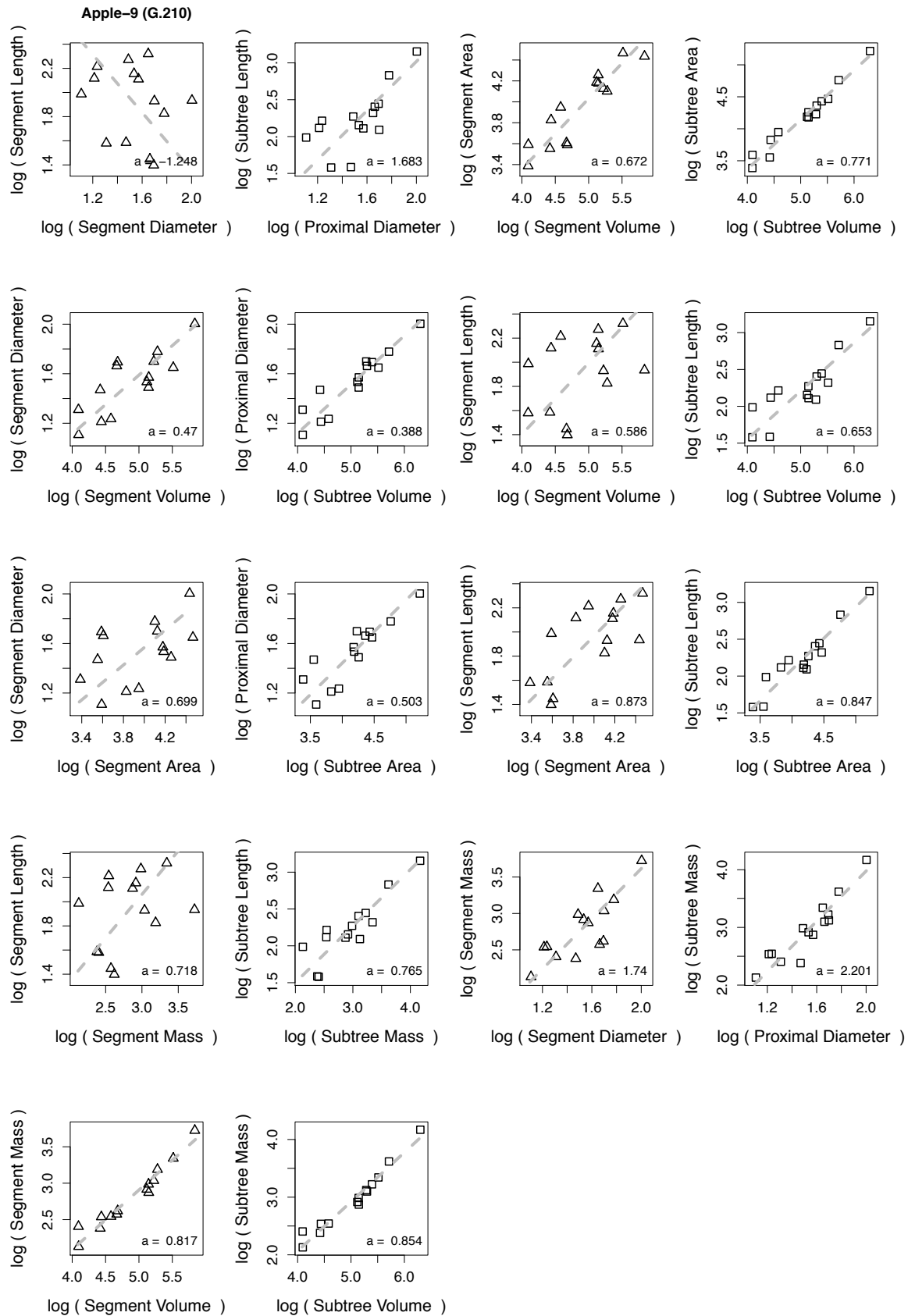


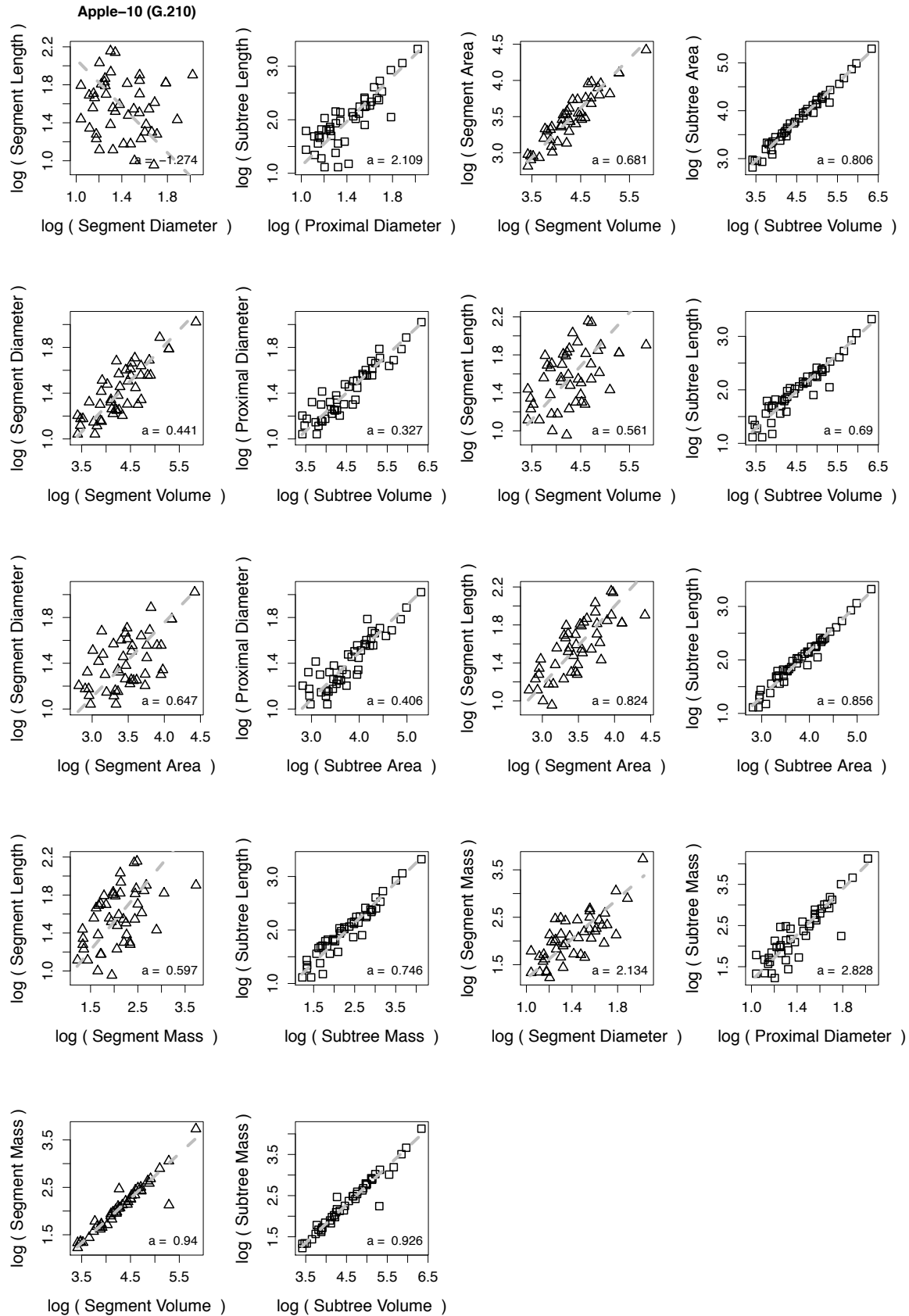




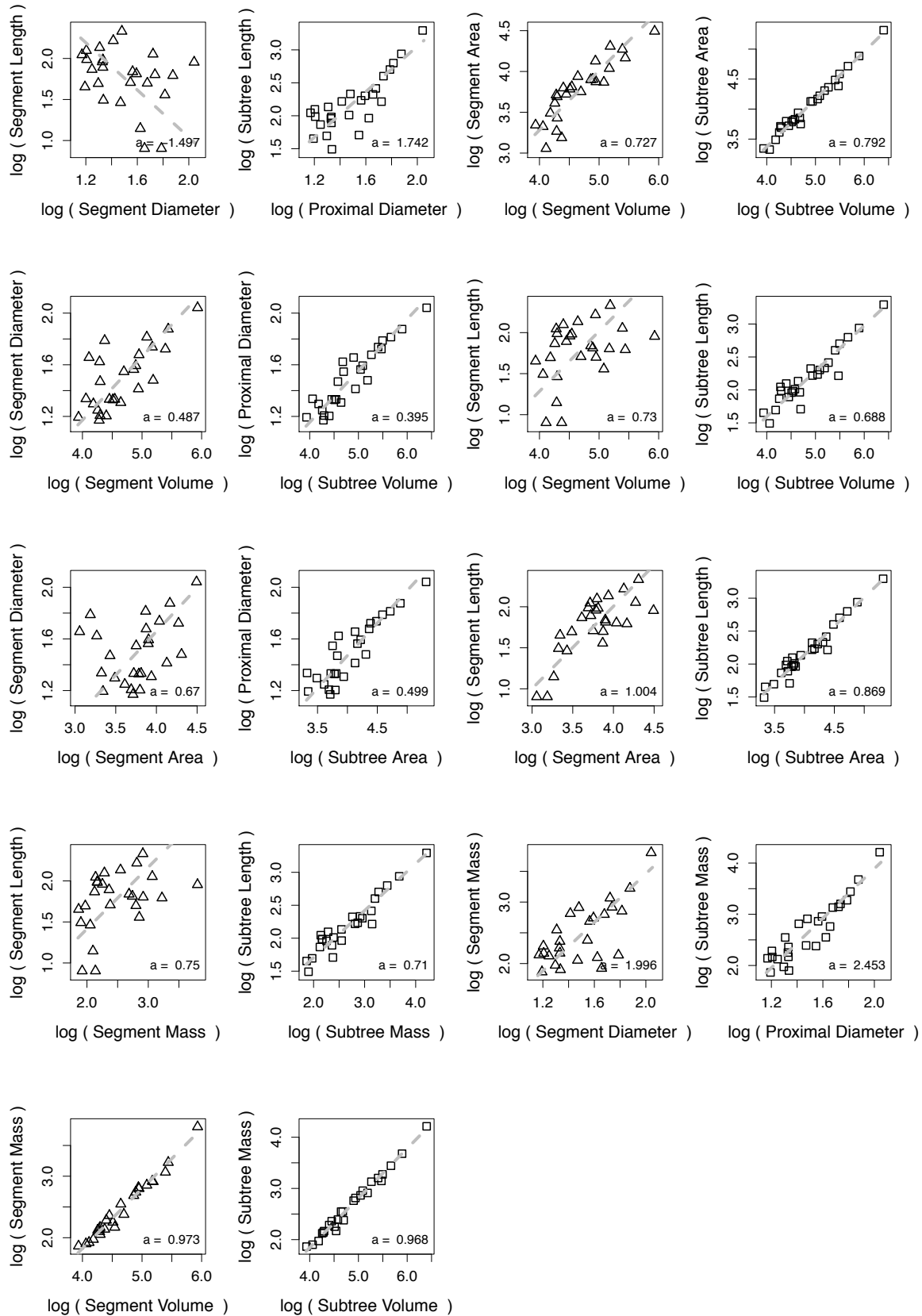
Apple-8 (G.41)



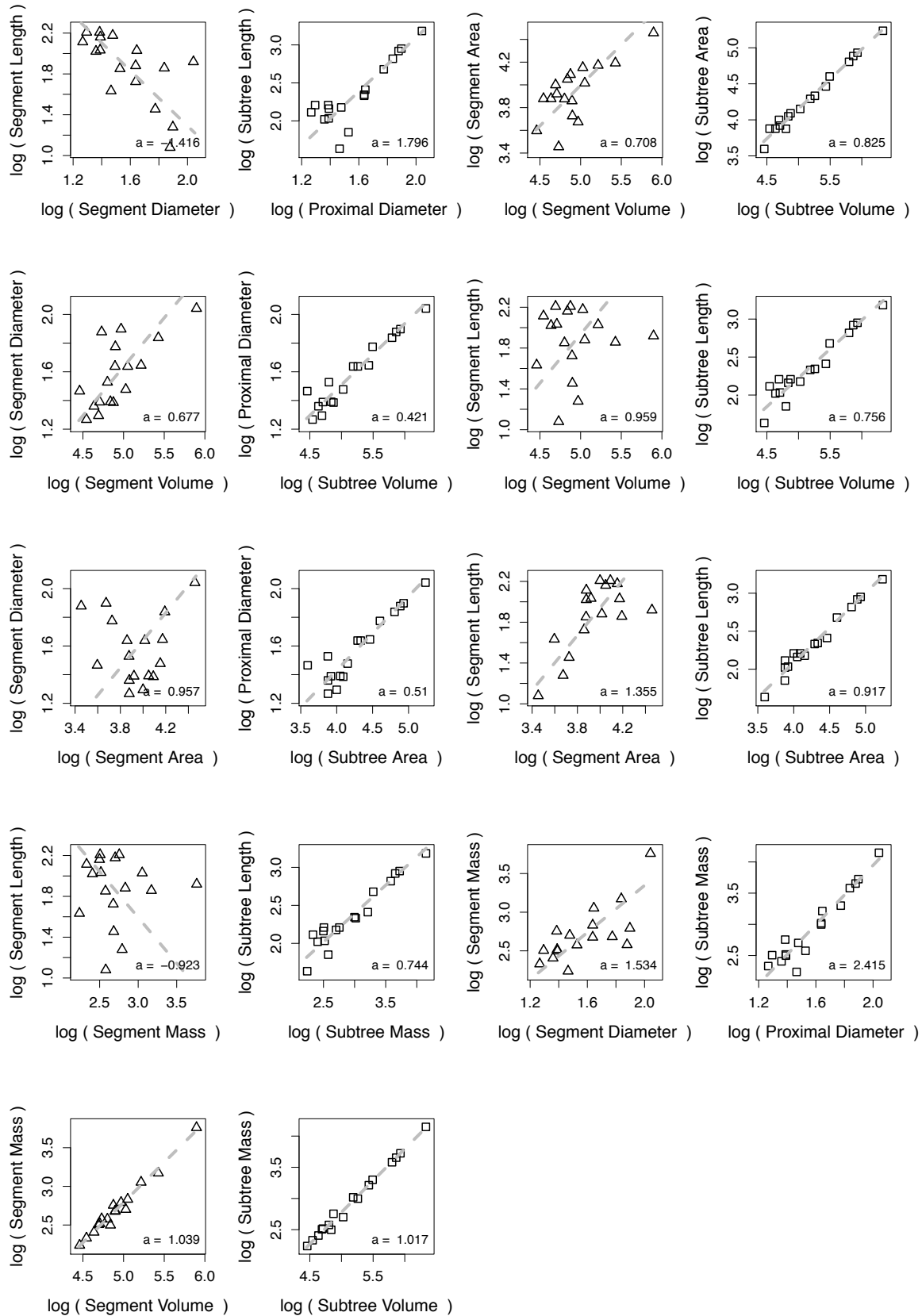


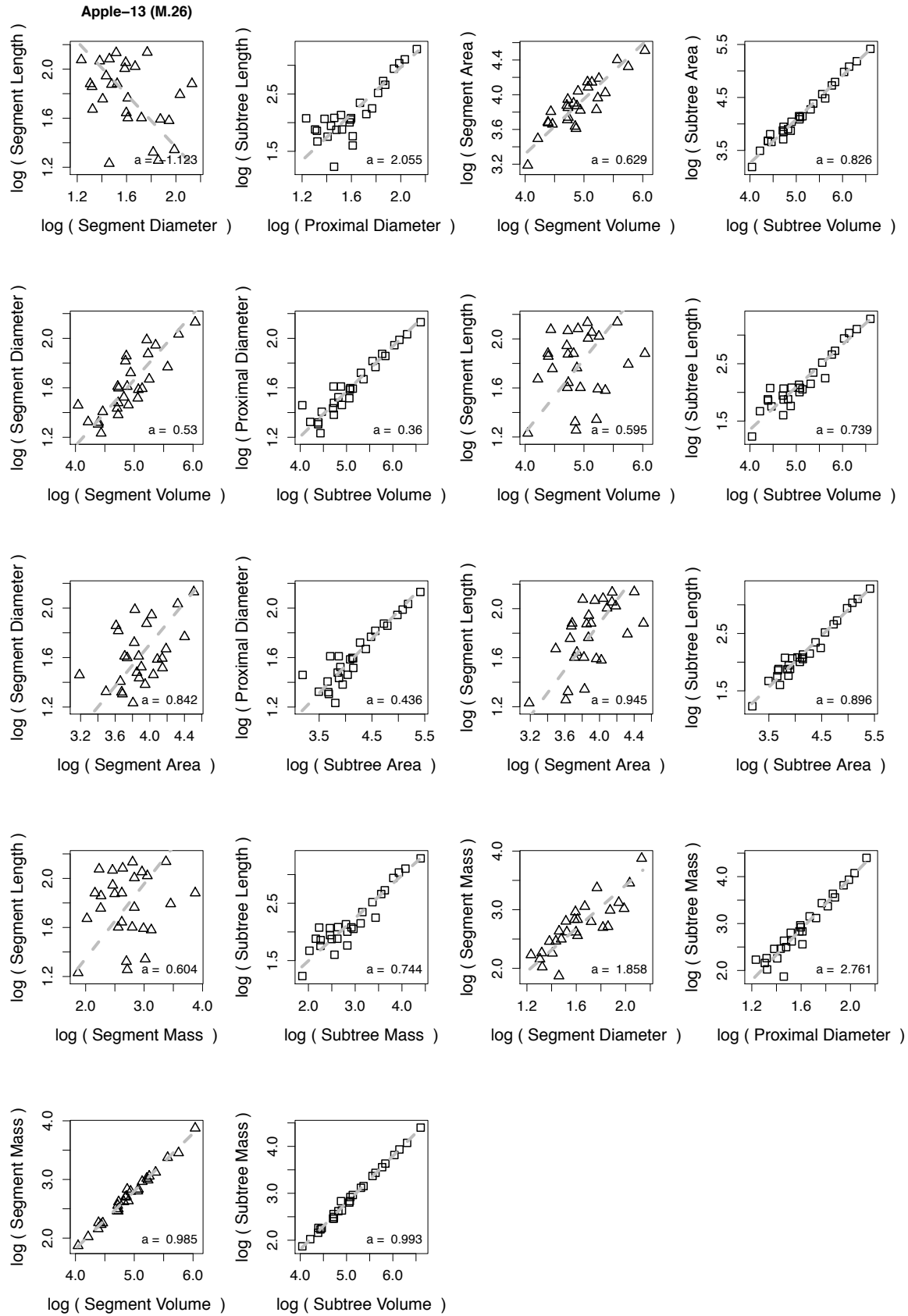


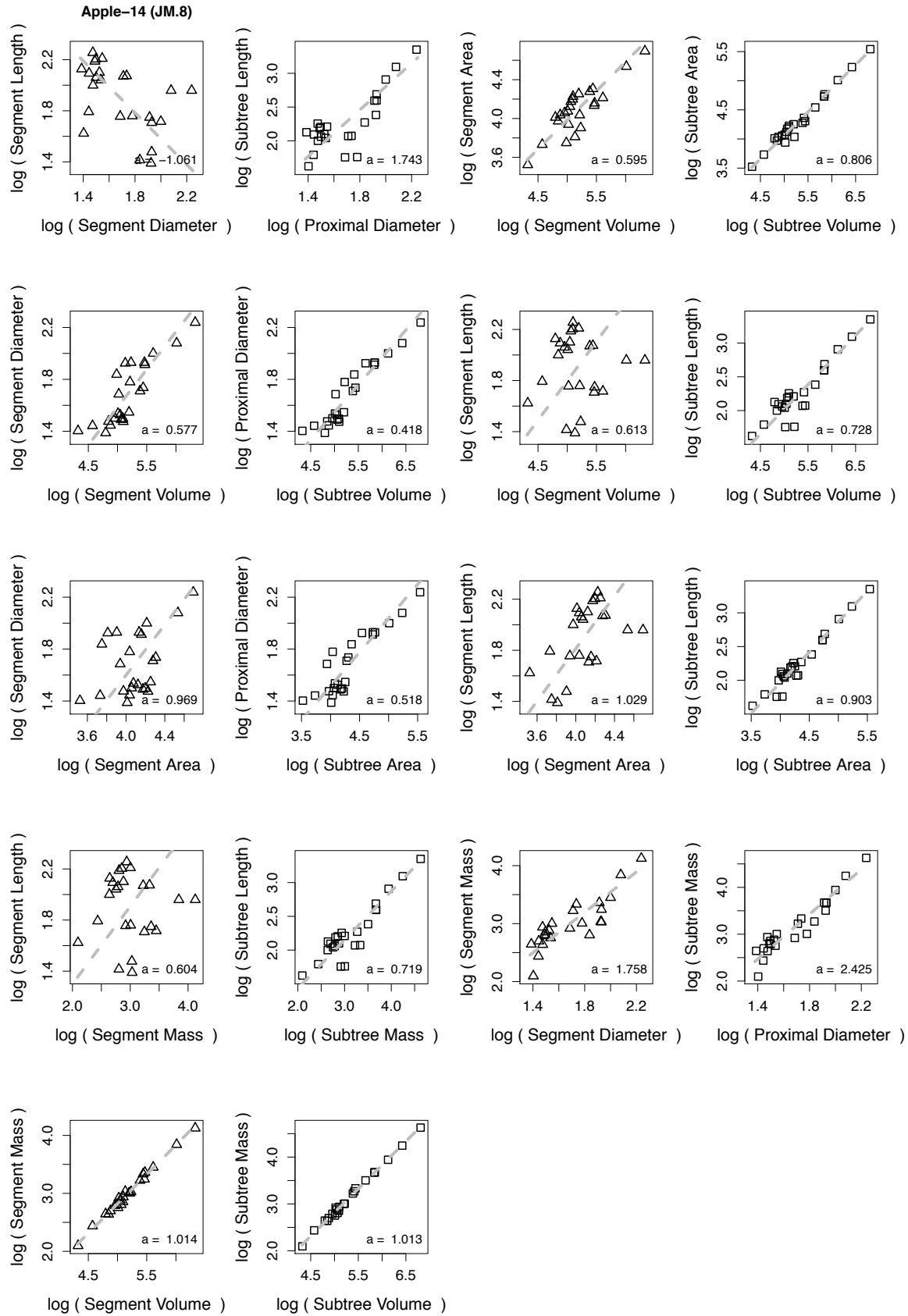
Apple-11 (G.210)

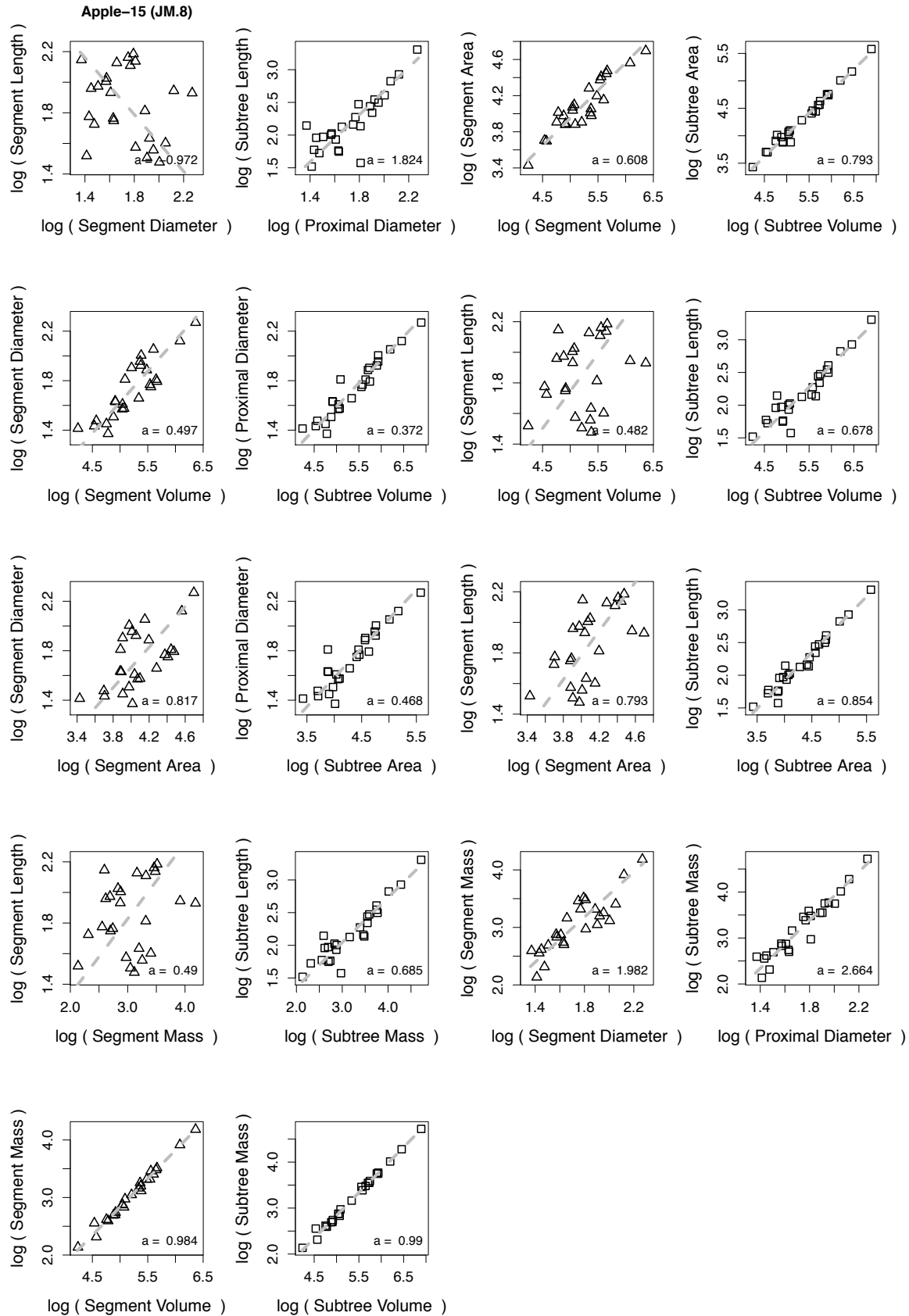


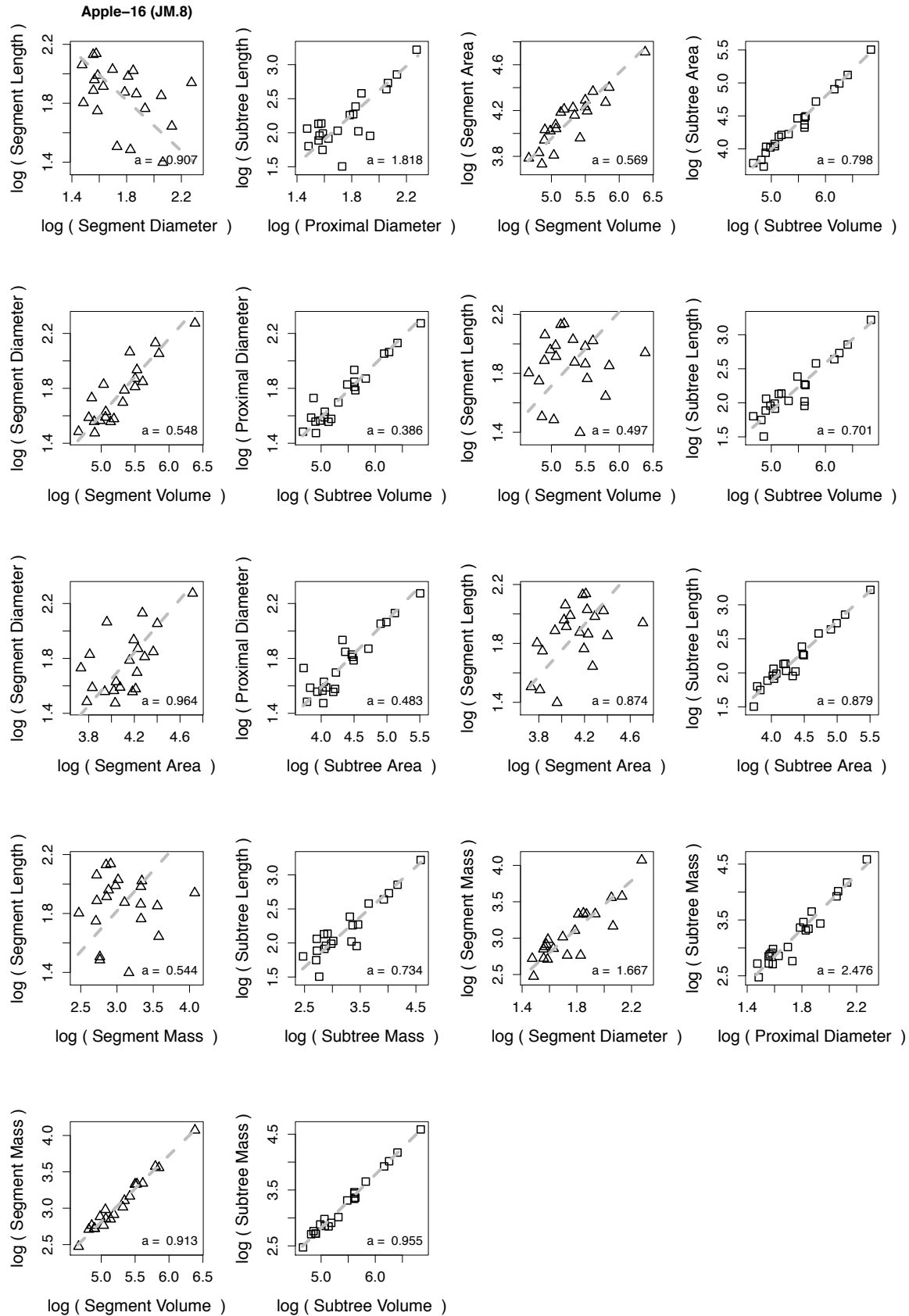
Apple-12 (G.210)



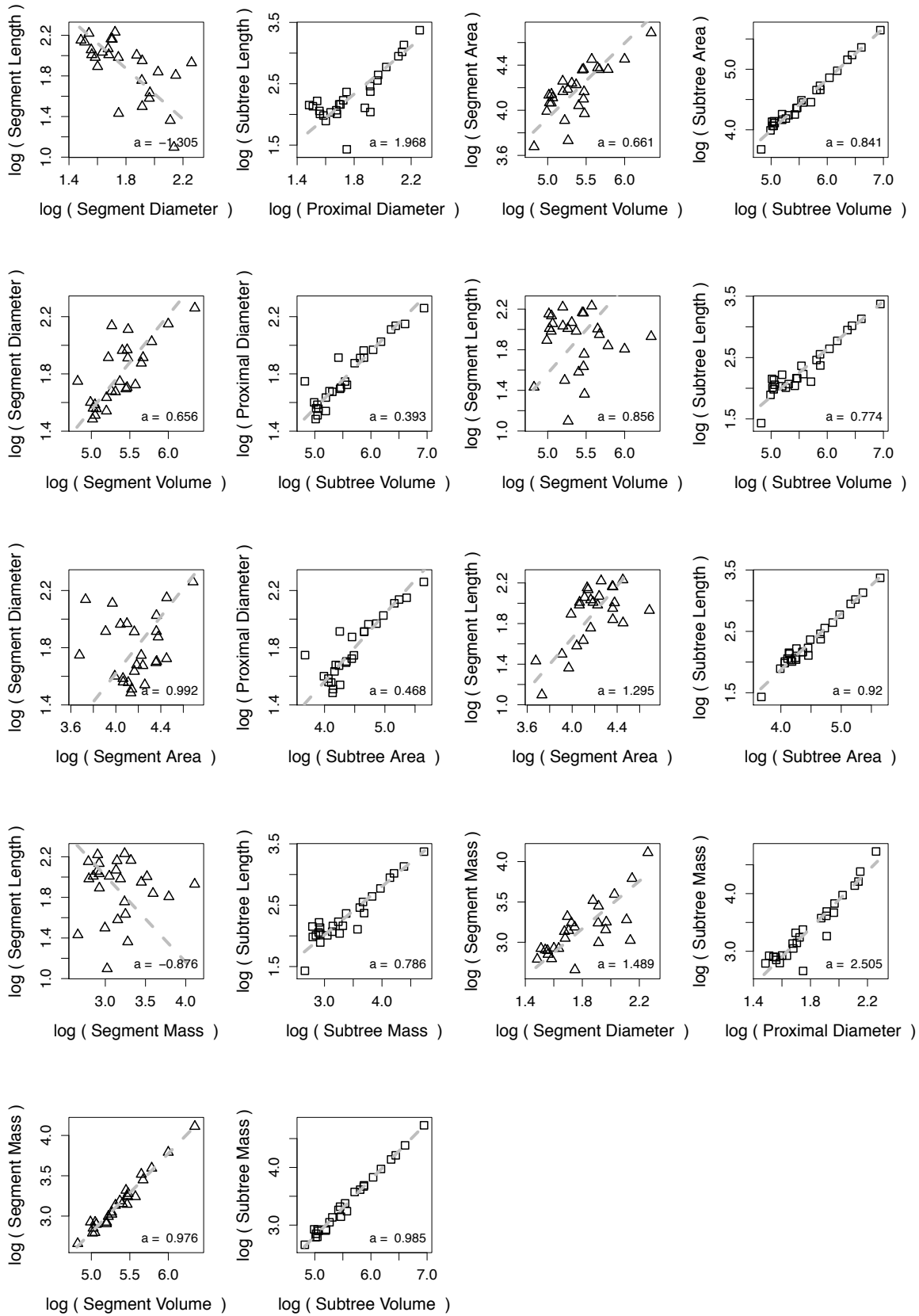




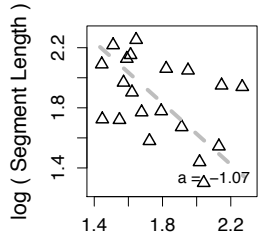




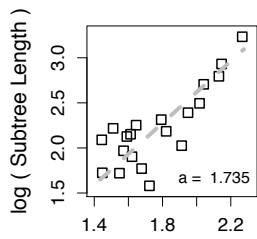
Apple-17 (PiAu.5683)



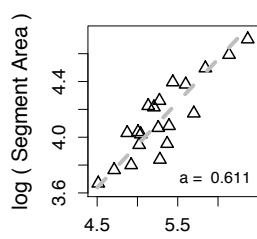
Apple-18 (PiAu.5683)



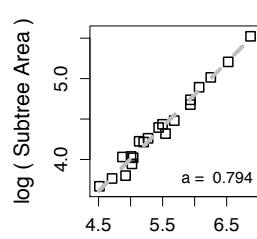
log (Segment Diameter)



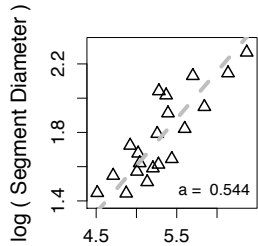
log (Proximal Diameter)



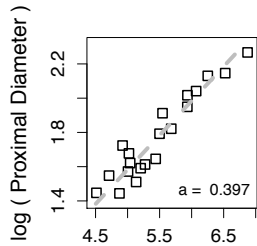
log (Segment Volume)



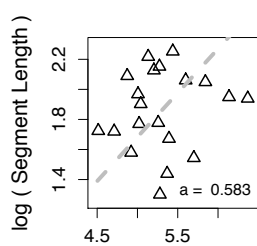
log (Subtree Volume)



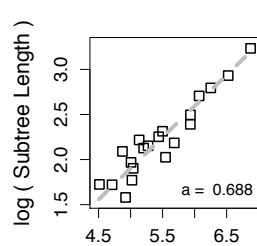
log (Segment Volume)



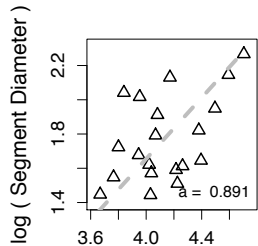
log (Subtree Volume)



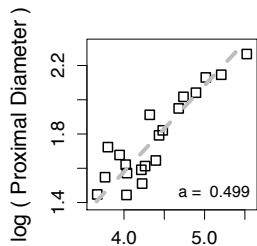
log (Segment Volume)



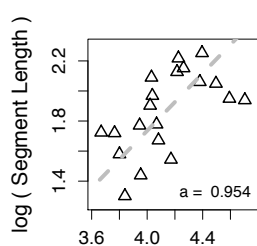
log (Subtree Volume)



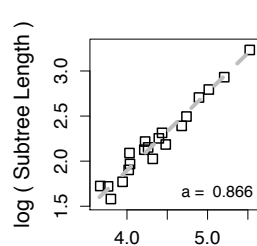
log (Segment Area)



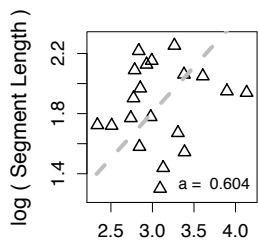
log (Subtree Area)



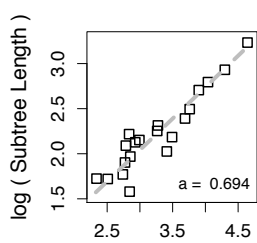
log (Segment Area)



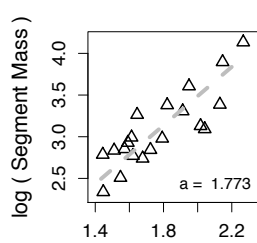
log (Subtree Area)



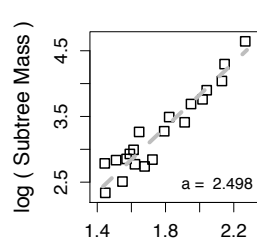
log (Segment Mass)



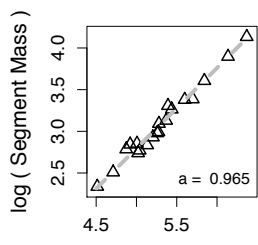
log (Subtree Mass)



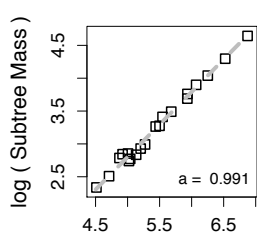
log (Segment Diameter)



log (Proximal Diameter)

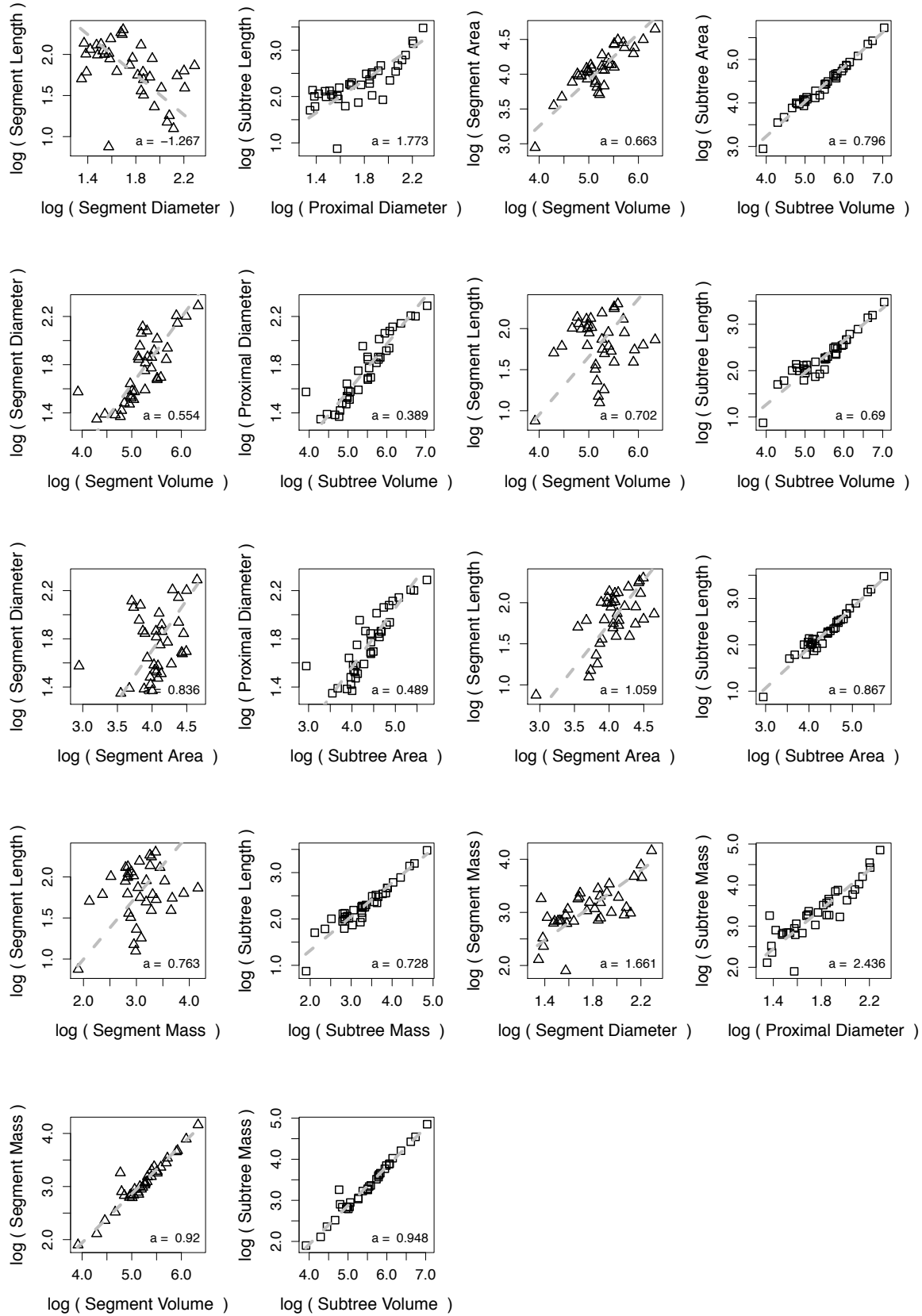


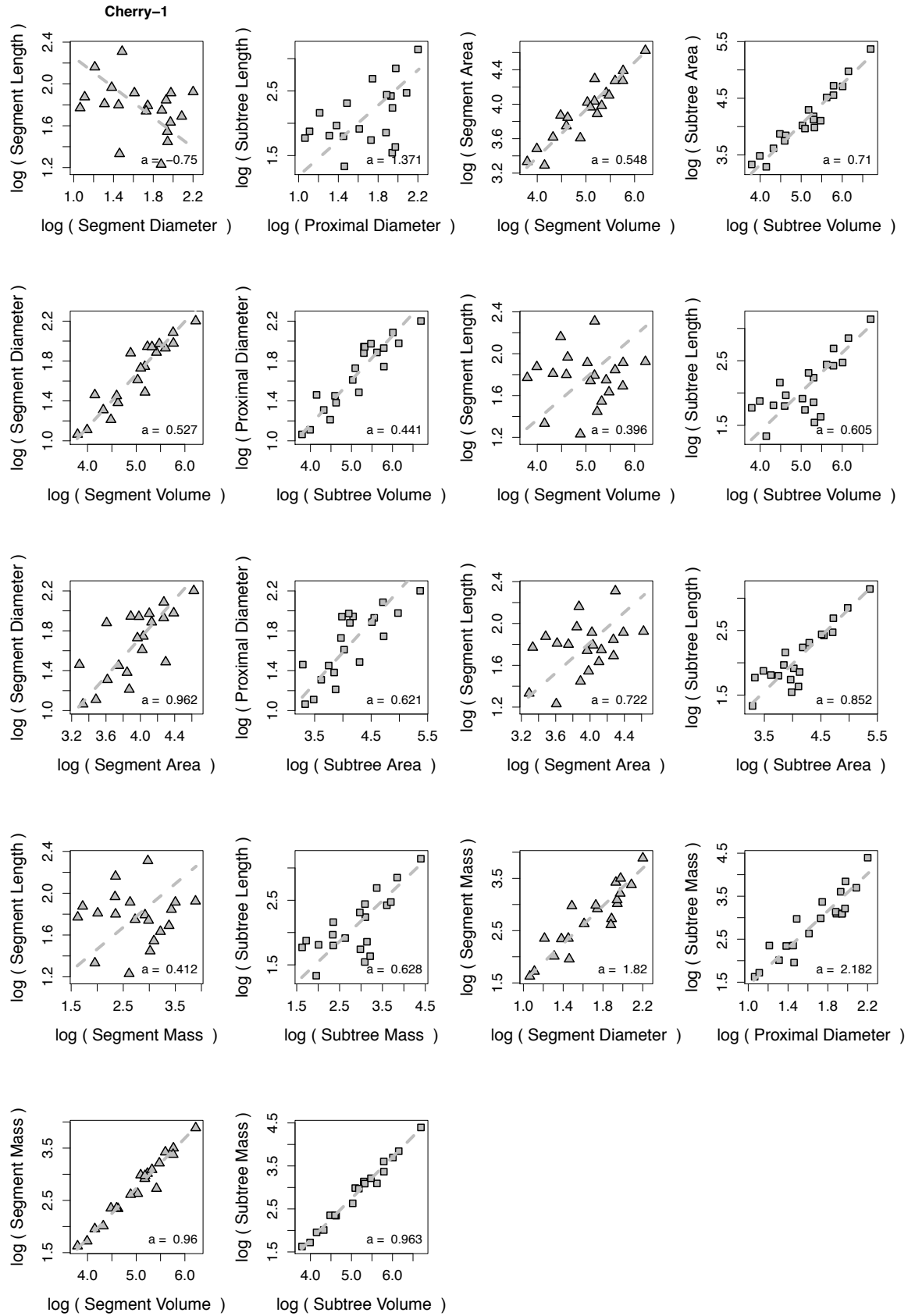
log (Segment Volume)

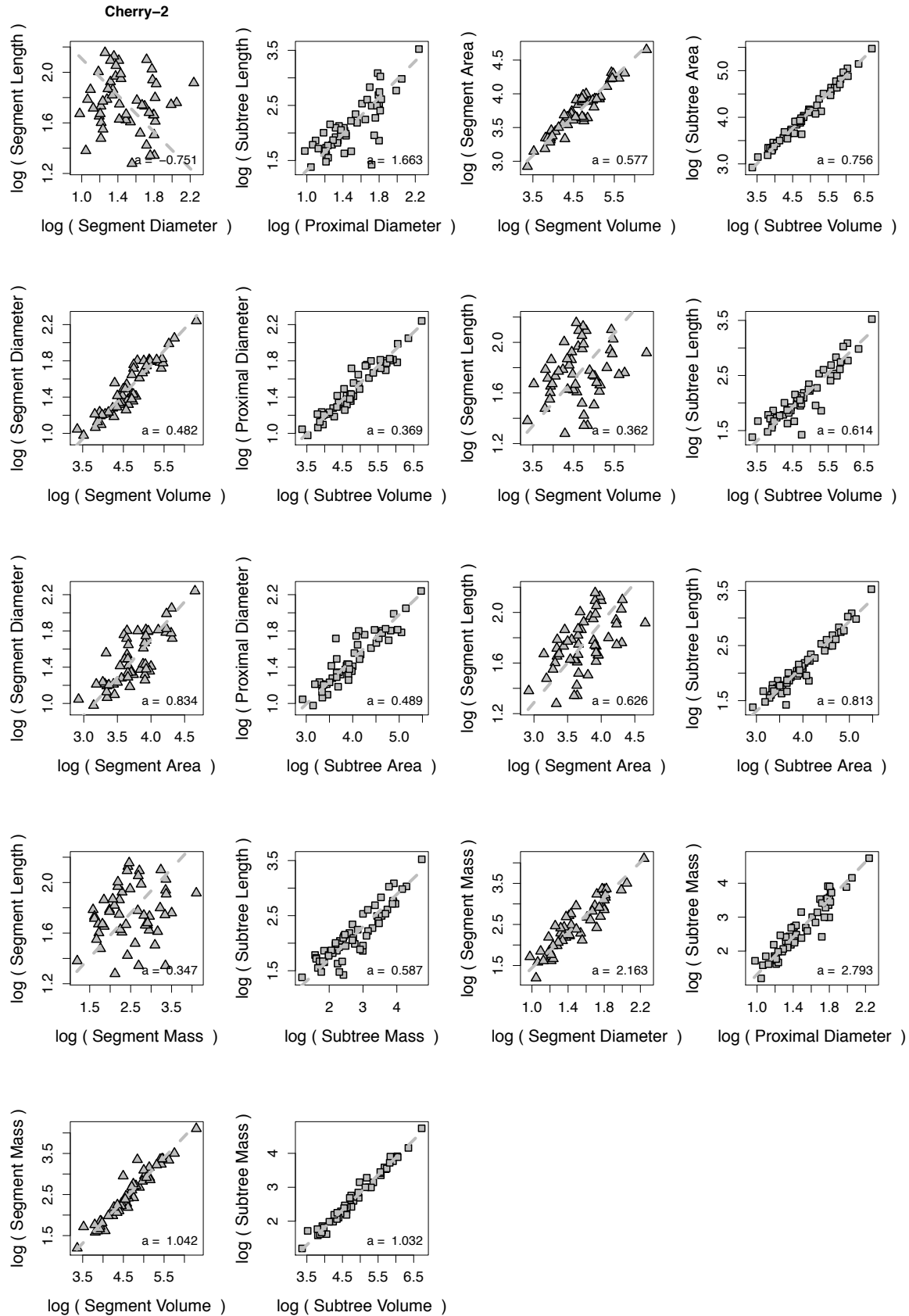


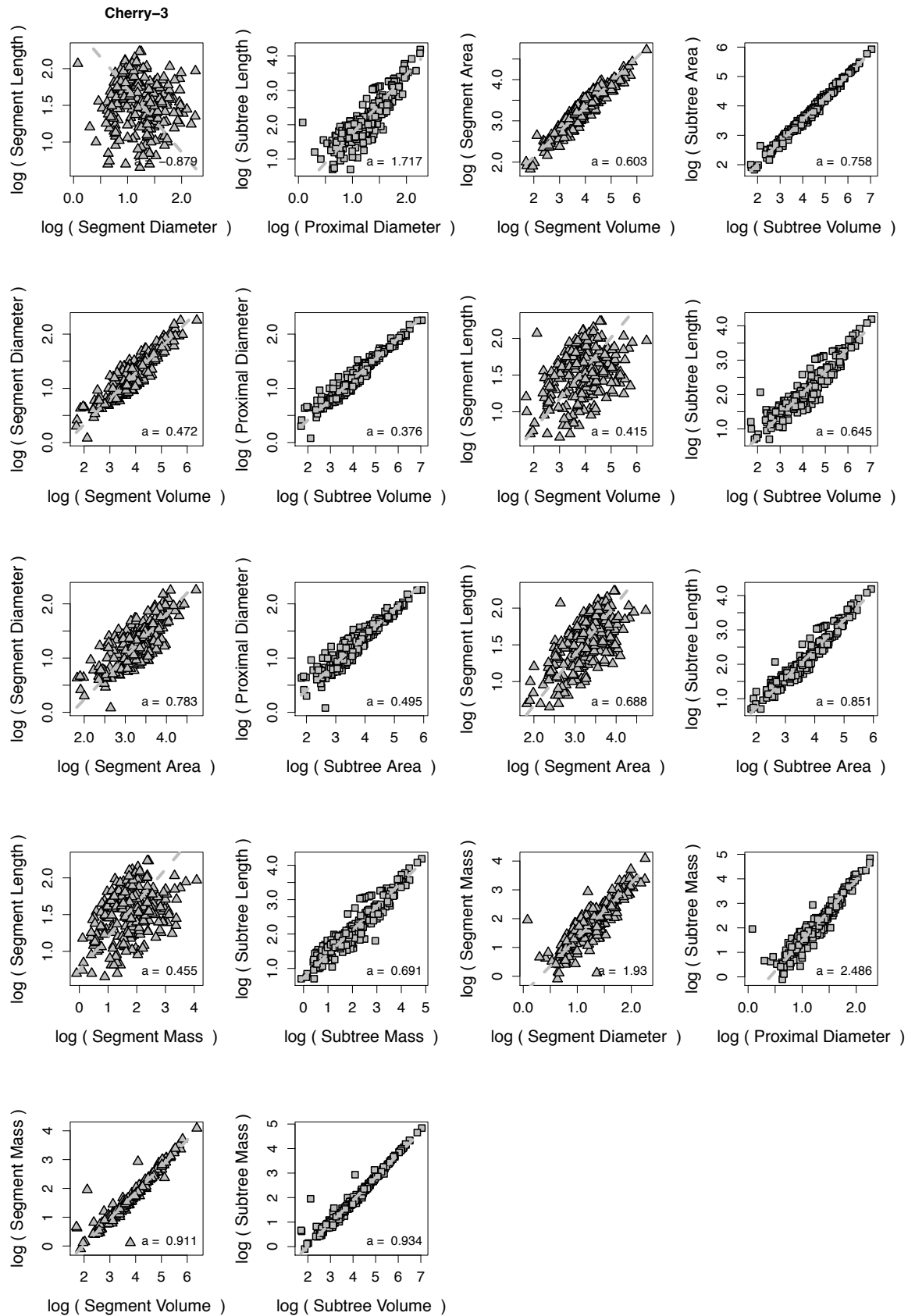
log (Subtree Volume)

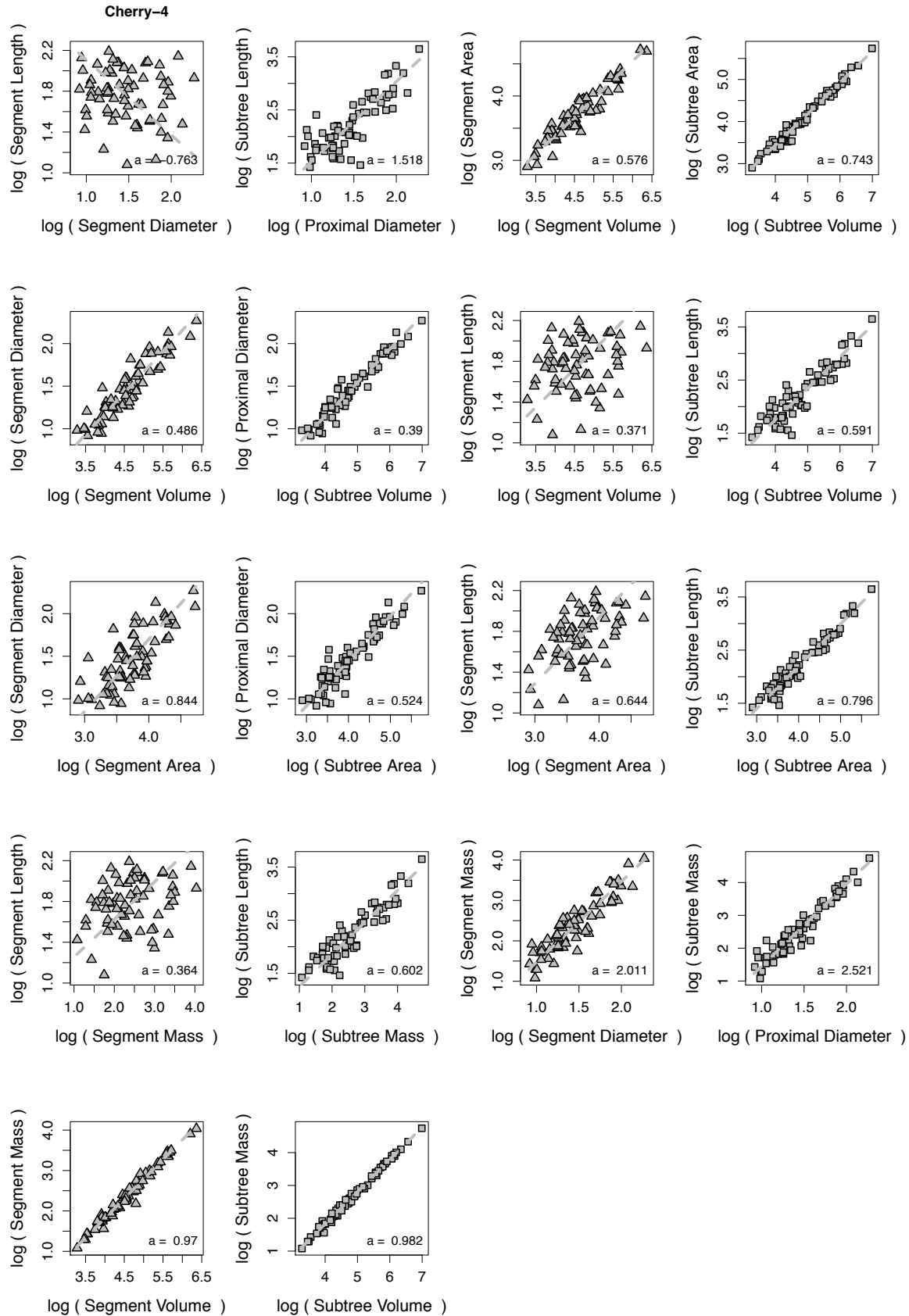
Apple-19 (PiAu.5683)











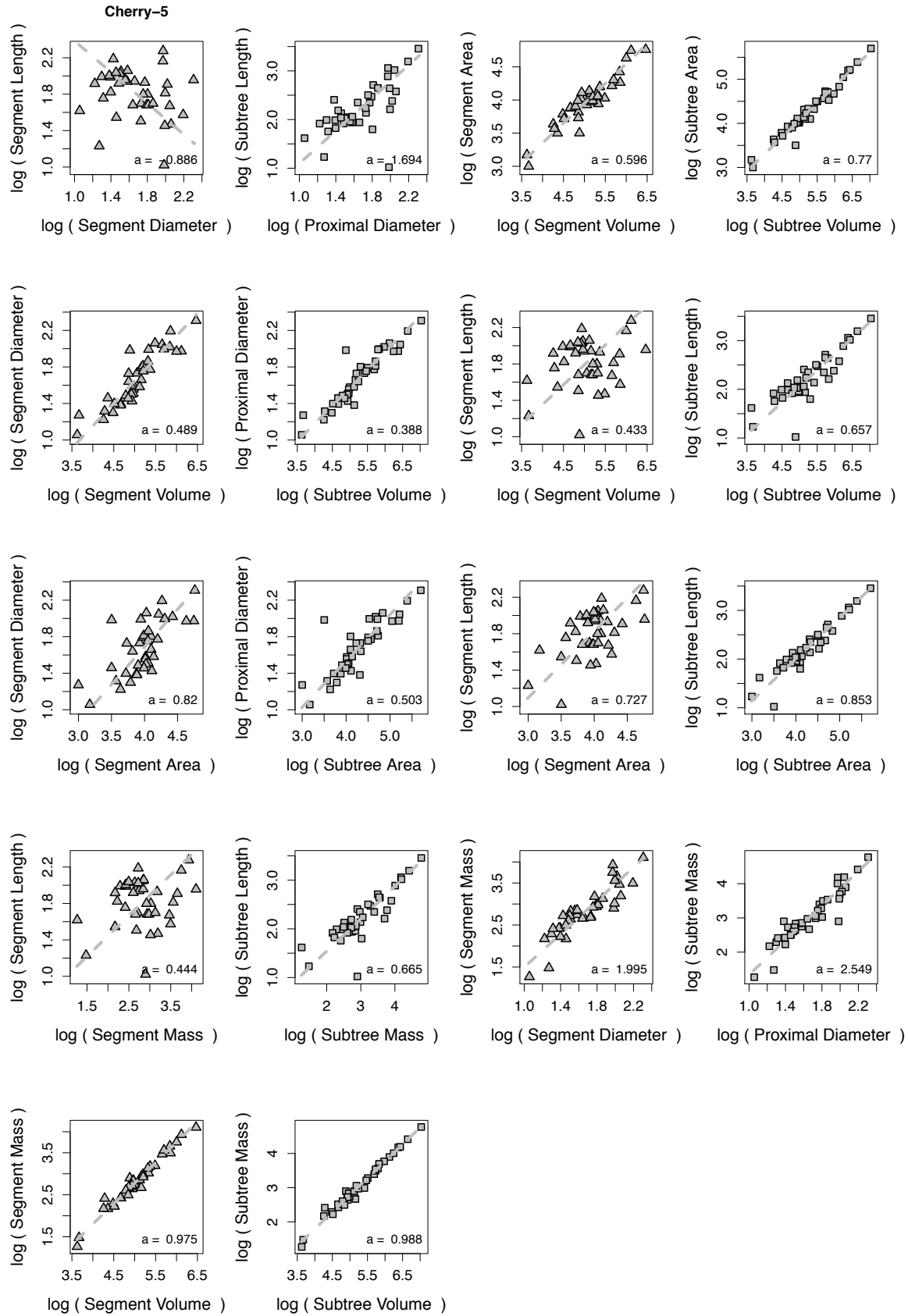


Figure S4. Data visualization for each allometric relationship at a species level. Data points correspond to branches at each branch-level classification. Segment level estimates are marked by triangles and subtree by squares with tart cherry shaded and apple open symbol. Dashed lines mark the estimated exponent (a) of the group. Dotted lines mark the estimated a of the species.

