Figure S1. Sample distribution among three time points
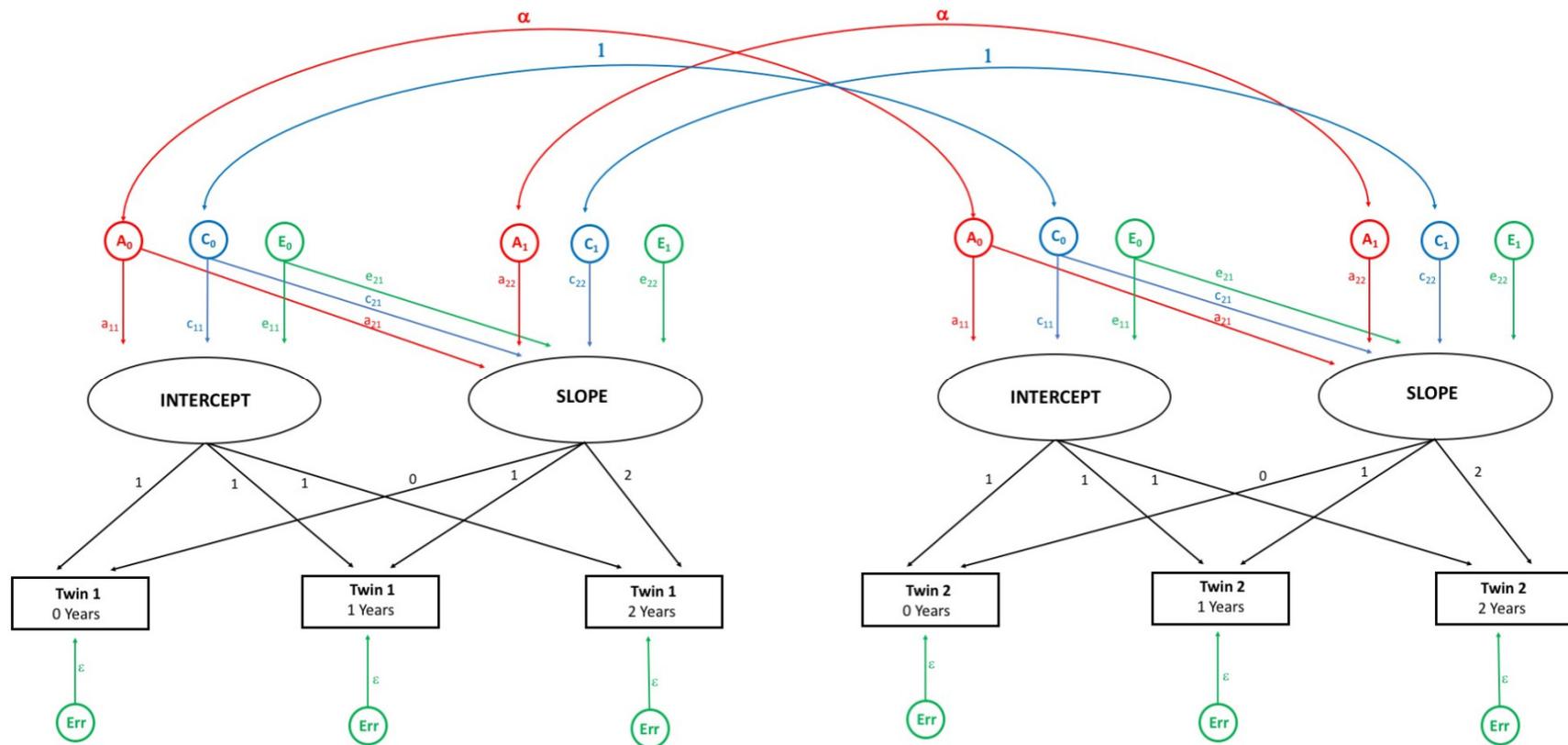
Figure S2: **Path diagram for a genetically-informative latent growth curve model (LGC).** Two latent factors (intercept, slope) describe the linear growth trajectory in surface area or cortical thickness over three timepoints. Given the availability of twin data, the variance in the latent factors can be further decomposed into additive genetic (A), shared environmental (C), and unique environmental (E) variance components via Cholesky decomposition. The longitudinal nature of the data also allow for estimation of measurement error (Err). The labeled paths (e.g. a_{11}) represent freely-estimated parameters determined by maximum likelihood. The statistical significance of genetic effects on phenotypic variance were estimated by comparing this full model to submodels with genetic paths removed (i.e. removing a_{11}, a_{21}, and a_{22} to test for absolute genetic effects, or a_{21}, and a_{22} to assess genetically-mediated change). Other variance components were assessed similarly, as well as familial (A+C) and total phenotypic (A+C+E) changes in variance over time. The numeric paths from the latent factors to the observed variables (rectangles) represent fixed scalars. For simplicity, the means regression portion of the model is not shown.
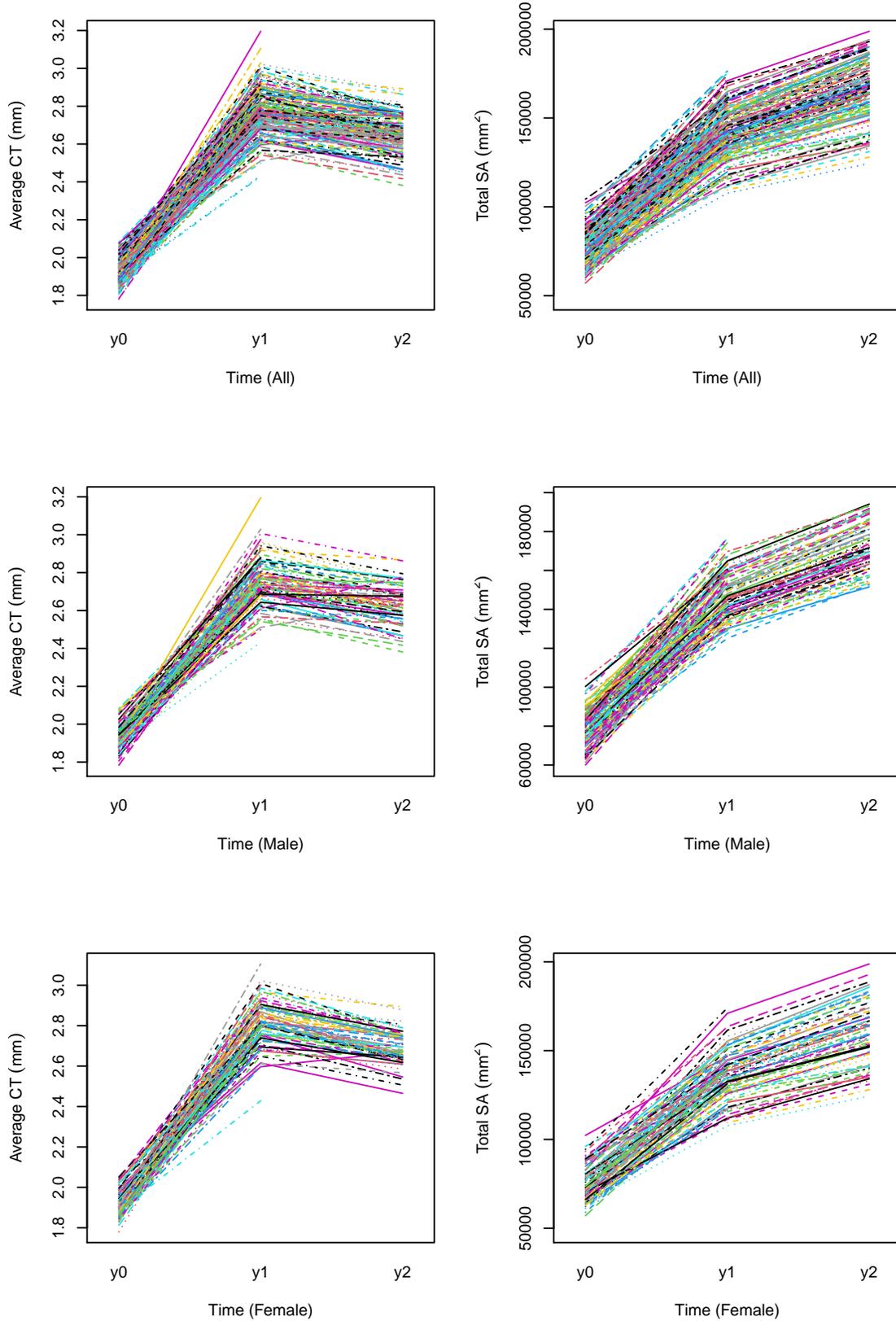
Figure S3. Trajectories of global CT and SA in first two years

(a) CT: a_{neo}^2

(b) a_{yr1}^2

(c) a_{yr2}^2

(d) CT: c_{neo}^2

(e) c_{yr1}^2

(f) c_{yr2}^2

(g) SA: a_{neo}^2

(h) a_{yr1}^2

(i) a_{yr2}^2

(j) SA: c_{neo}^2

(k) c_{yr1}^2

(l) c_{yr2}^2
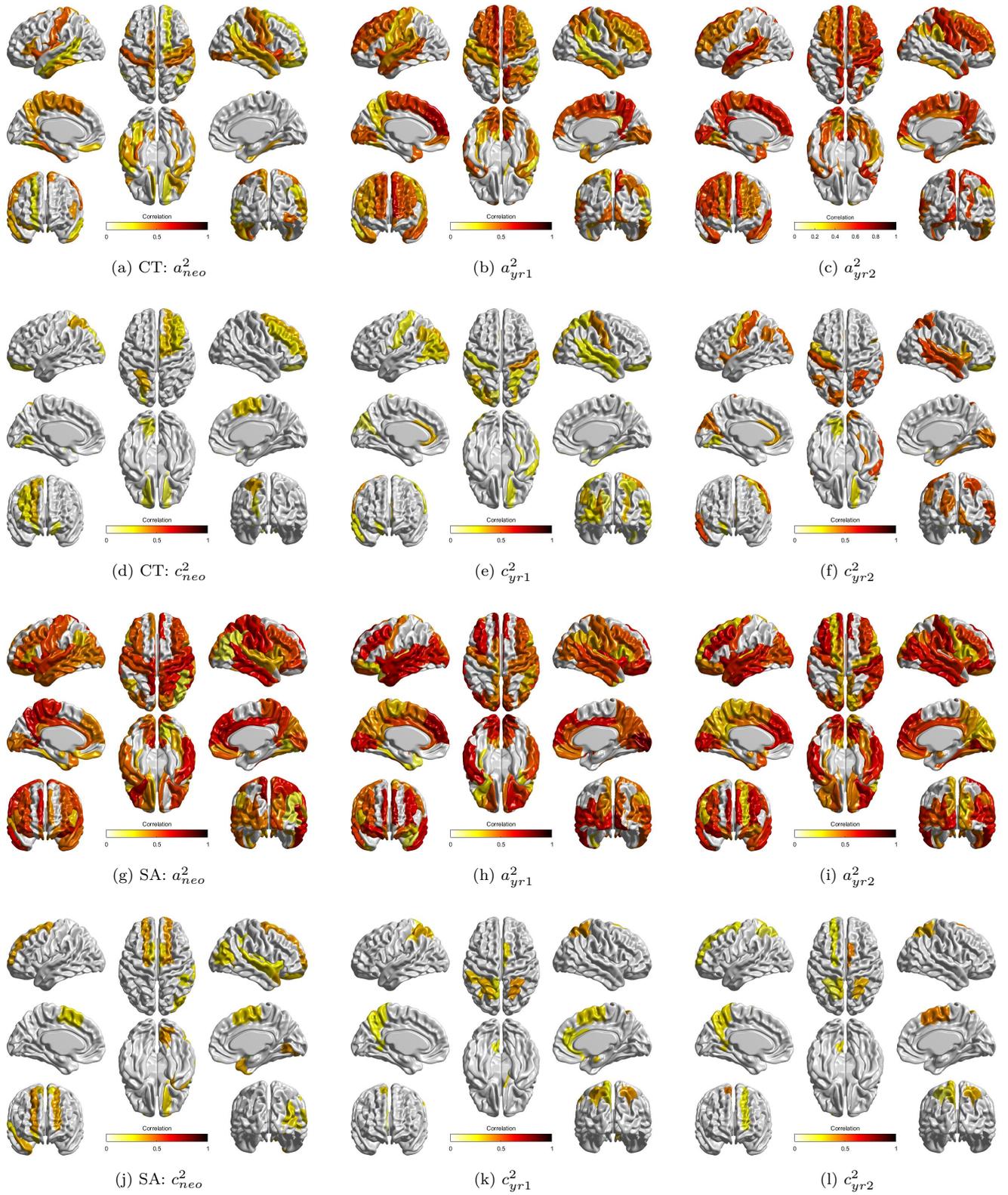
Figure S4. Significant Variance Component of CT and SA

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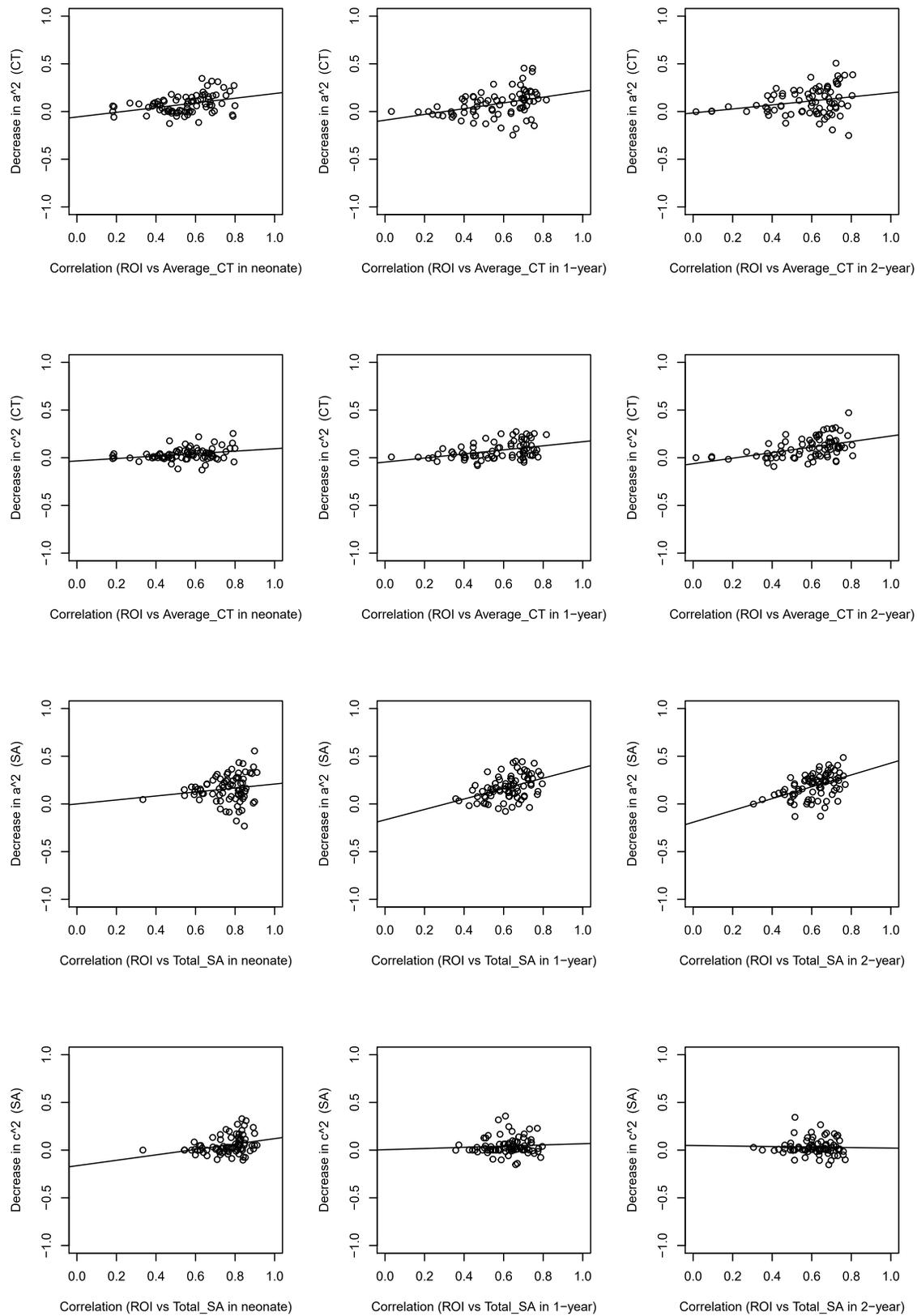
Figure S5. The correlation between global measures and decrease in point estimate
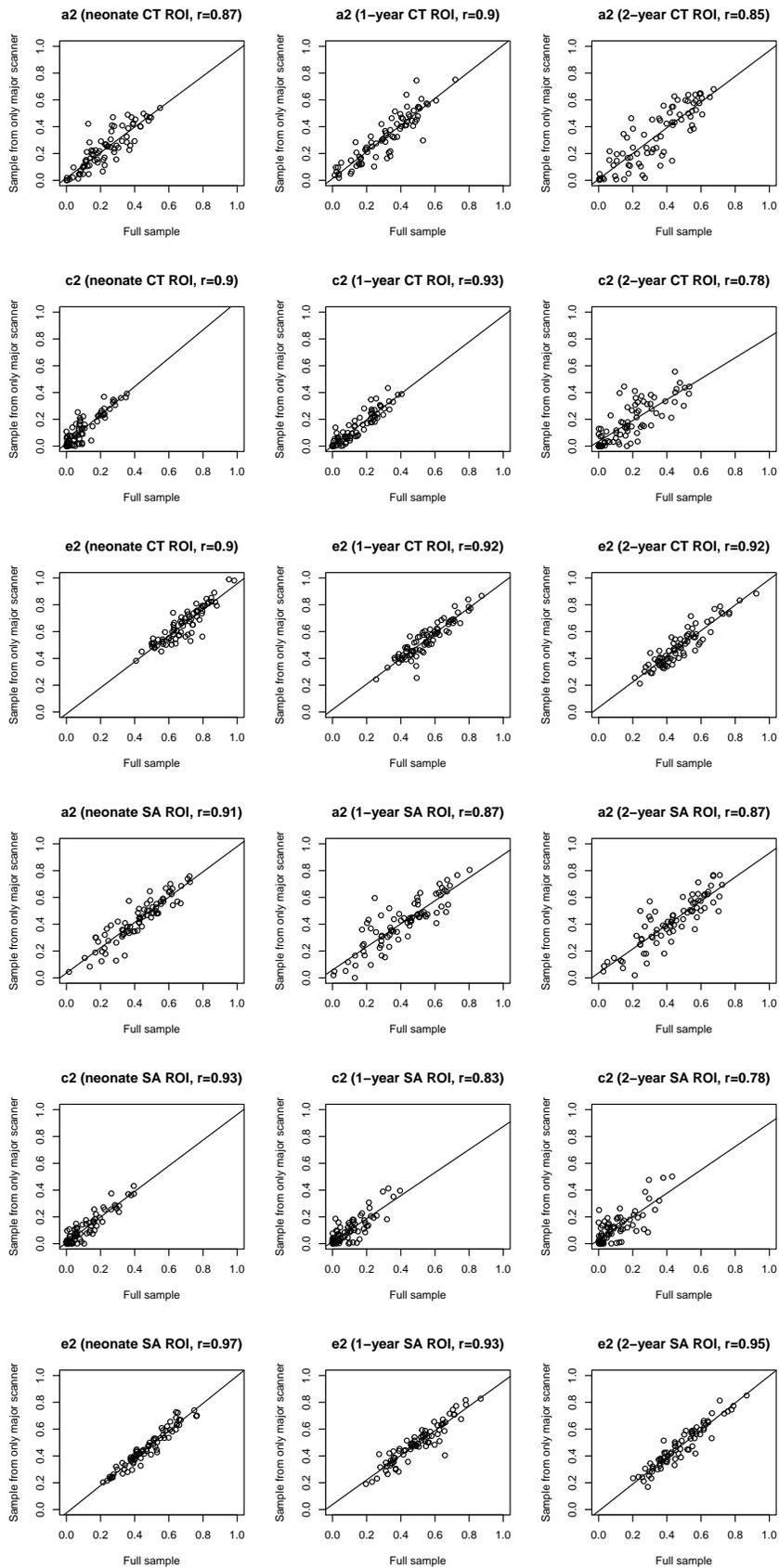
Figure S6. The correlation between estimates of variance components using full sample and subset with only majority scanner.

(a) rP_{neo}

(b) rP_{yr1}

(c) rP_{yr2}

(d) rG_{neo}

(e) rG_{yr1}

(f) rG_{yr2}

(g) rC_{neo}

(h) rC_{yr1}

(i) rC_{yr2}

(j) rE_{neo}

(k) rE_{yr1}

(l) rE_{yr2}
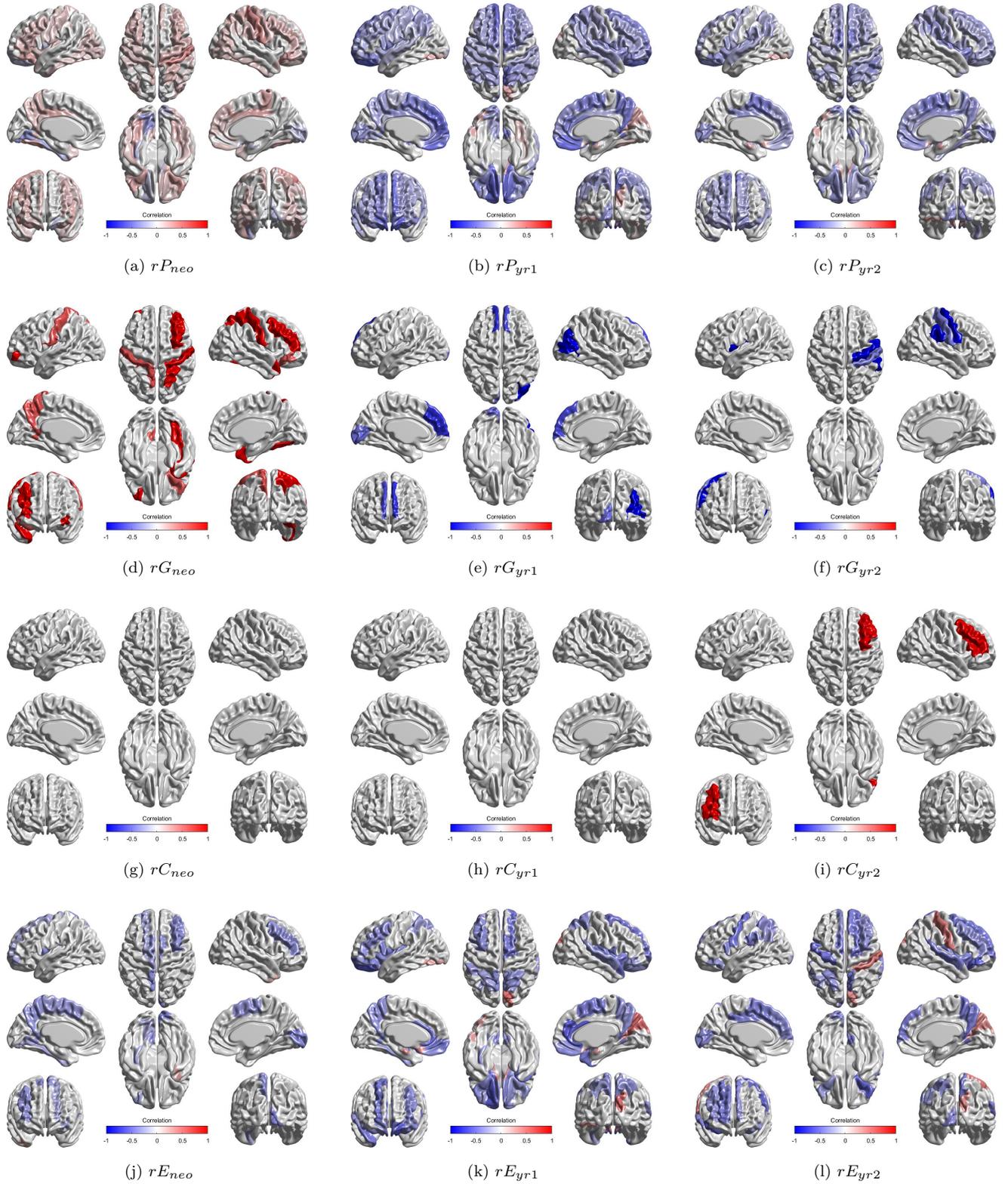
Figure S7. Significant Correlation of regional CT vs regional SA
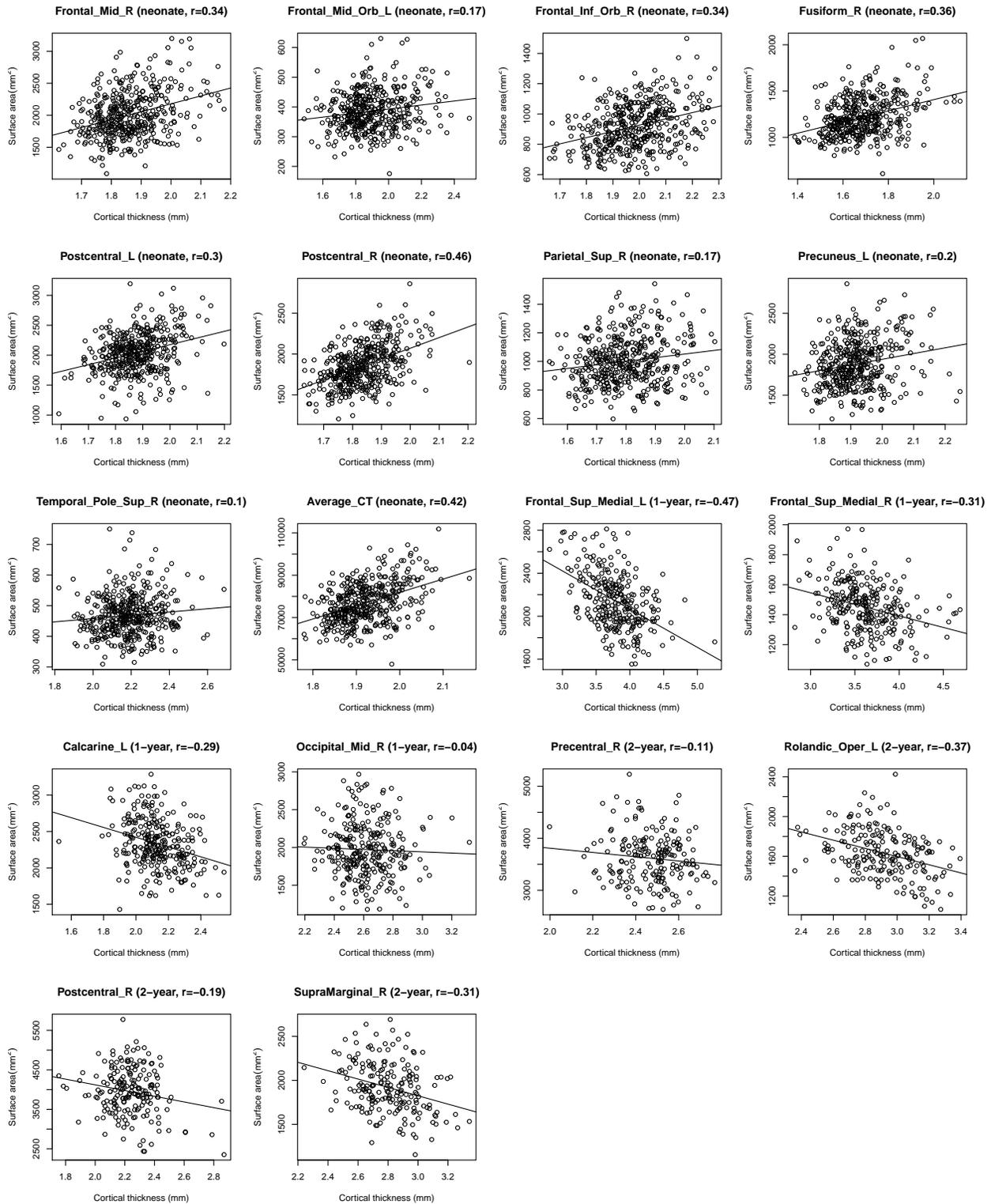
Figure S8. Scatter plots of key ROIs with strong bivariate rG between CT and SA

(a) rP_{neo}

(b) rP_{yr1}

(c) rP_{yr2}

(d) rG_{neo}

(e) rG_{yr1}

(f) rG_{yr2}

(g) rC_{neo}

(h) rC_{yr1}

(i) rC_{yr2}
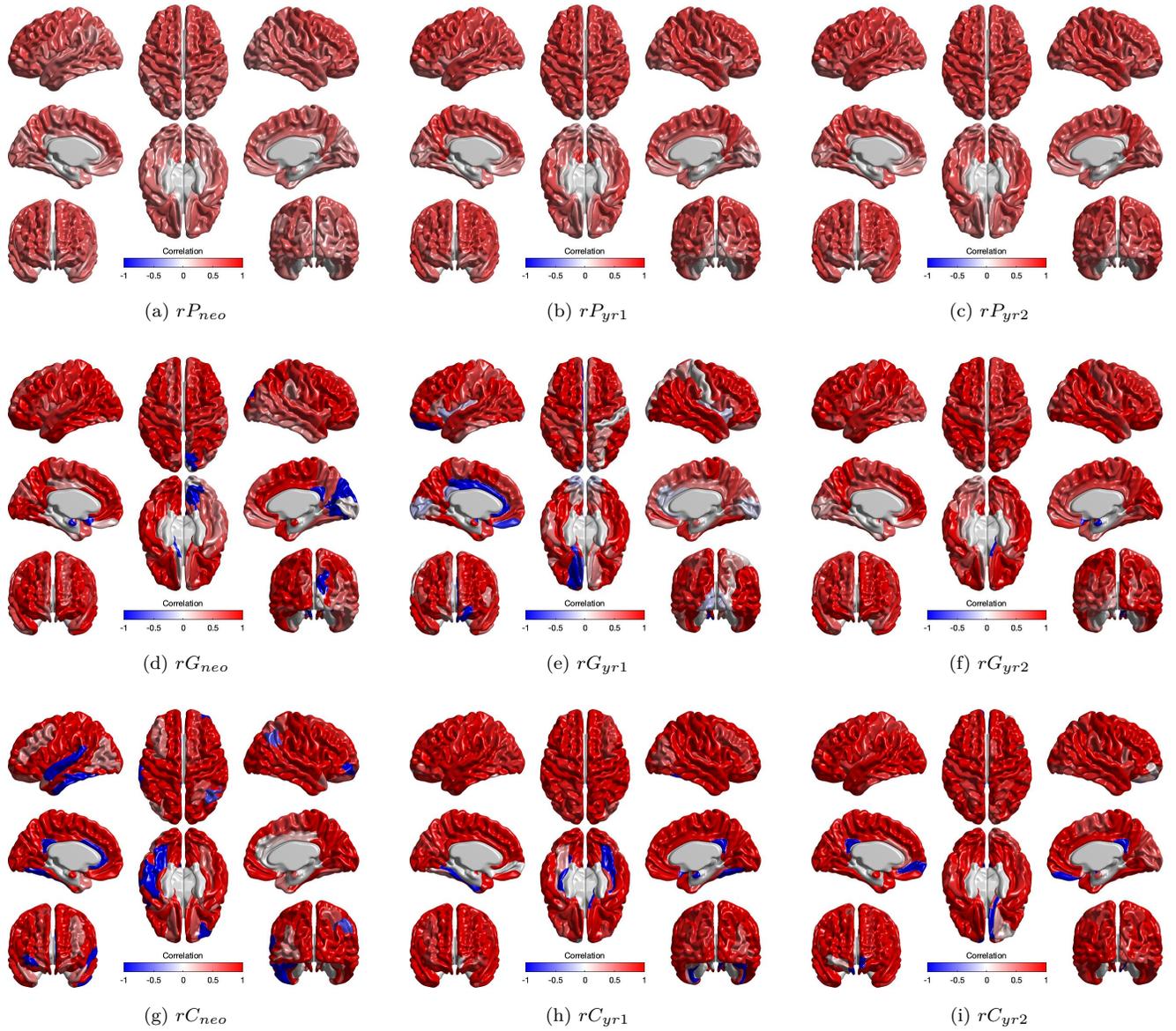
Figure S9. Correlation of Global CT vs ROI

(a) rP_{neo}

(b) rP_{yr1}

(c) rP_{yr2}

(d) rG_{neo}

(e) rG_{yr1}

(f) rG_{yr2}

(g) rC_{neo}

(h) rC_{yr1}

(i) rC_{yr2}
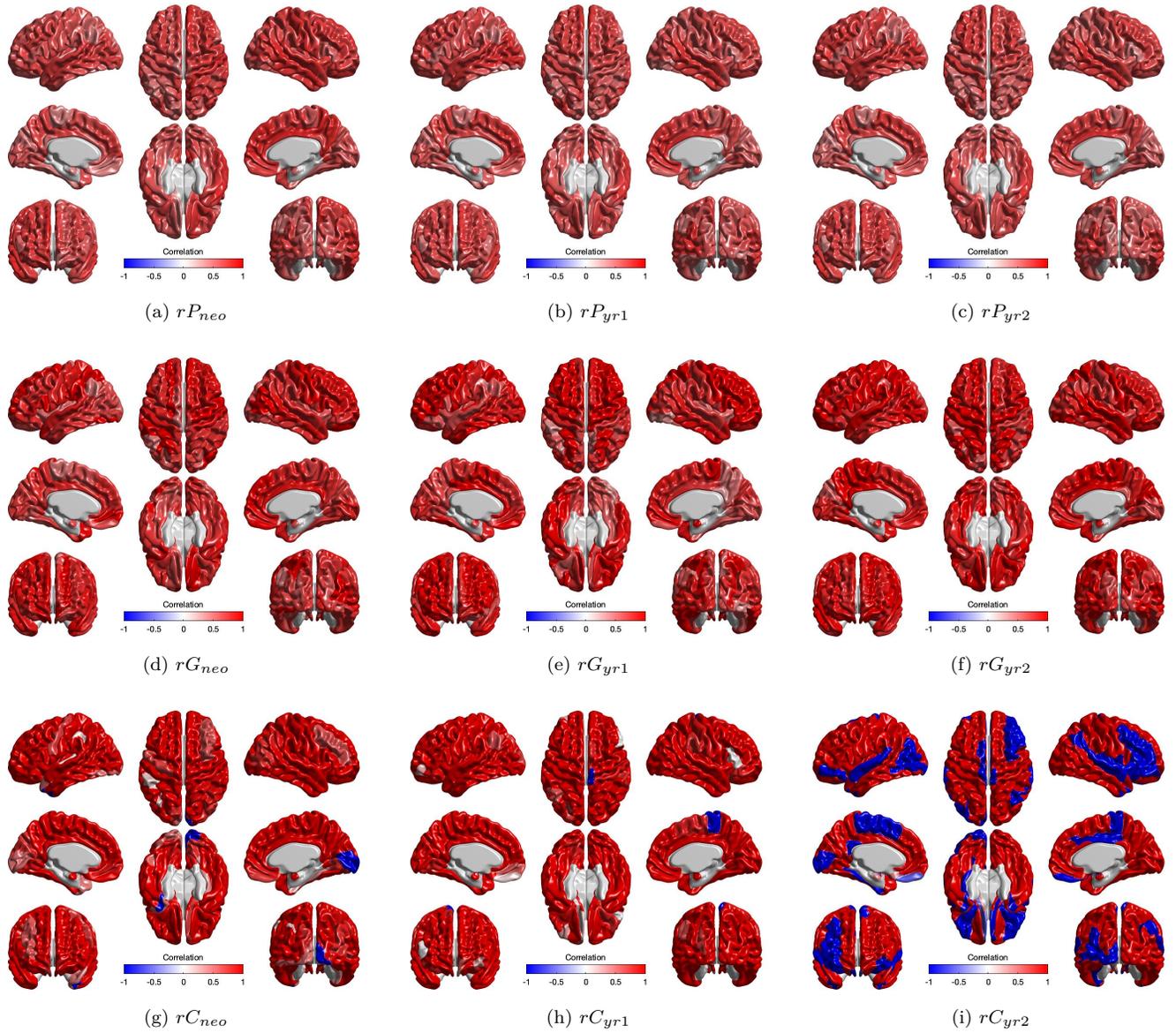
Figure S10. Correlation of Global SA vs ROI

(a) $h^2_{neo->yr1}$

(b) $h^2_{yr1->yr2}$

(c) $c^2_{neo->yr1}$

(d) $c^2_{yr1->yr2}$
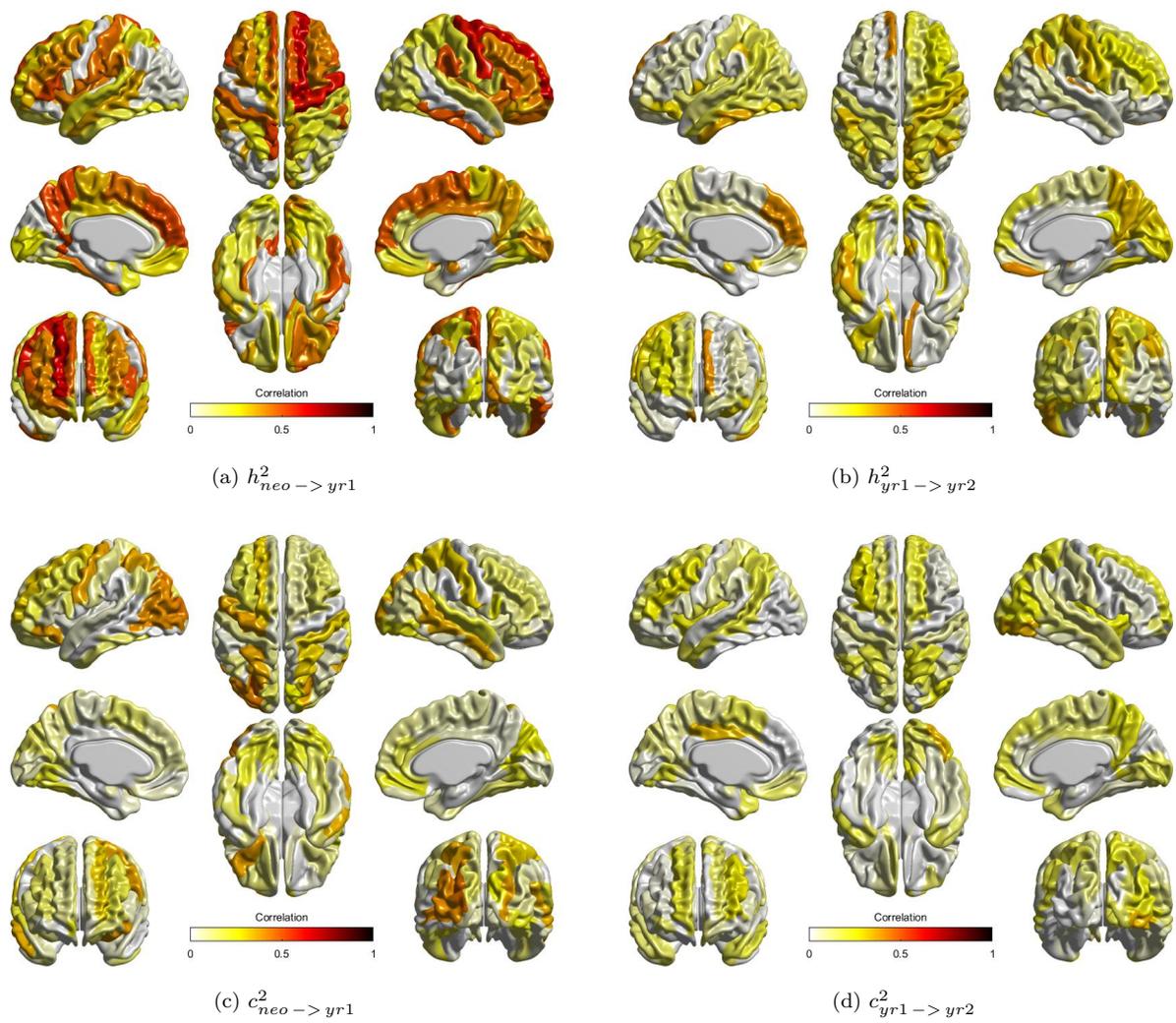
Figure S11. Heritability of Change in regional CT

(a) $h^2_{neo -> yr1}$

(b) $h^2_{yr1 -> yr2}$

(c) $c^2_{neo -> yr1}$

(d) $c^2_{yr1 -> yr2}$
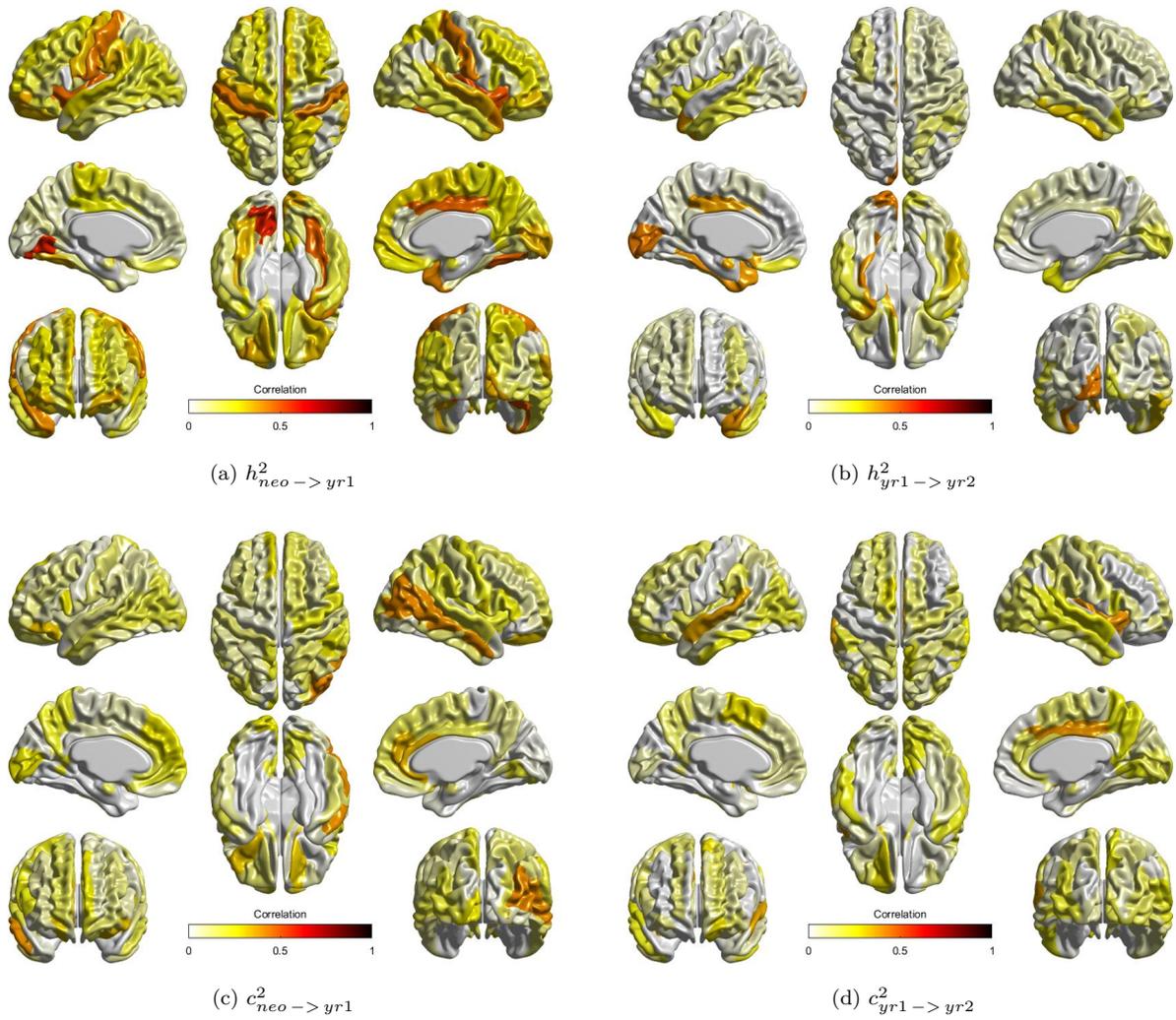
Figure S12. Heritability of Change in regional SA

Figure S13. LGC analysis for CT
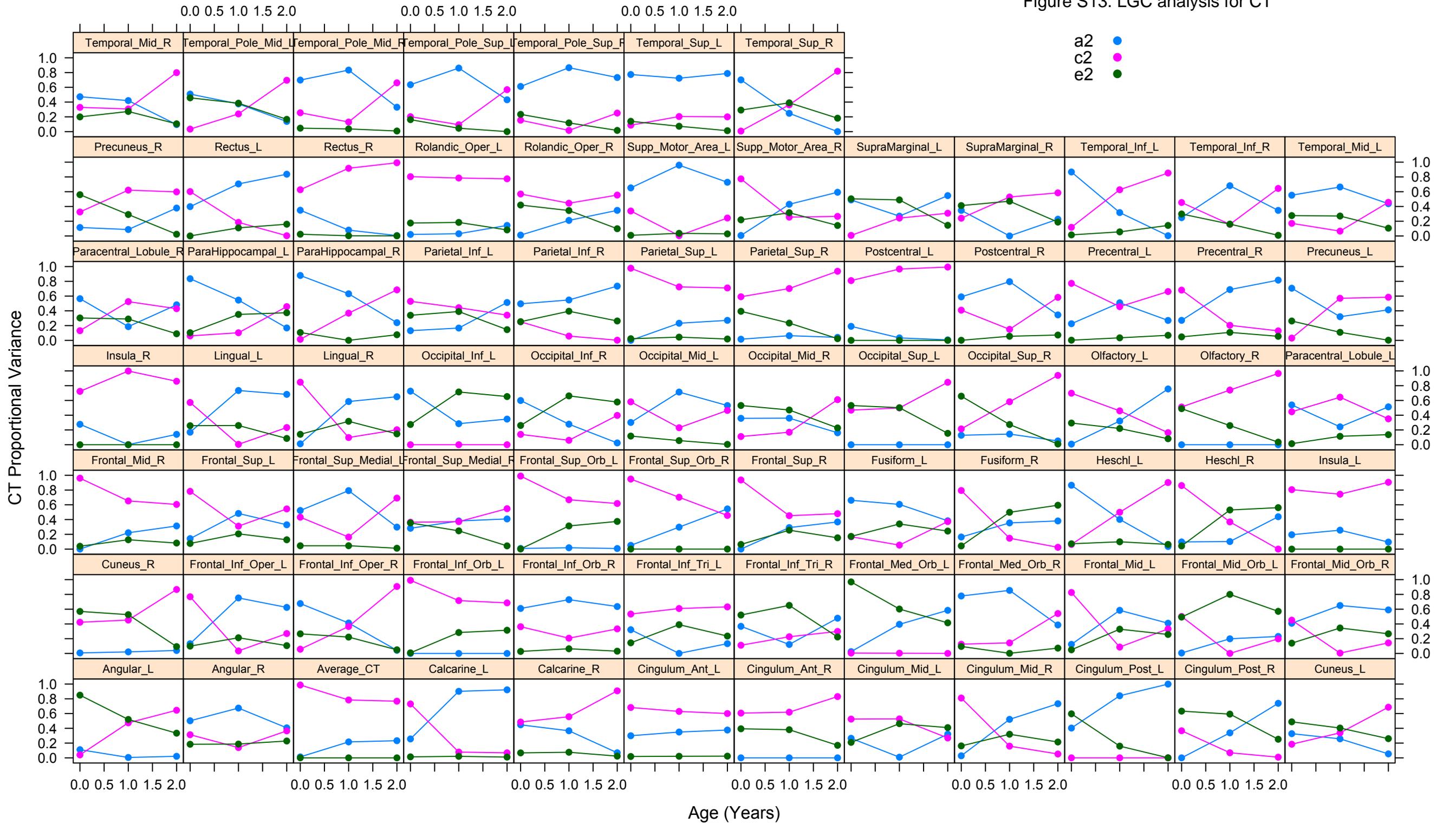
Figure S14. LGC analysis for SA