Figure e-1. Number of patients in each study sub-group. The two sub-groups were 1) patients with available baseline plasma (n = 141) and 2) patients with available baseline CSF (n = 50). Of those, 11 patients had plasma only; 108 had plasma and baseline MRI; 3 had plasma and CSF; 19 had plasma, MRI and CSF; 27 had CSF and MRI; and 1 had CSF only.

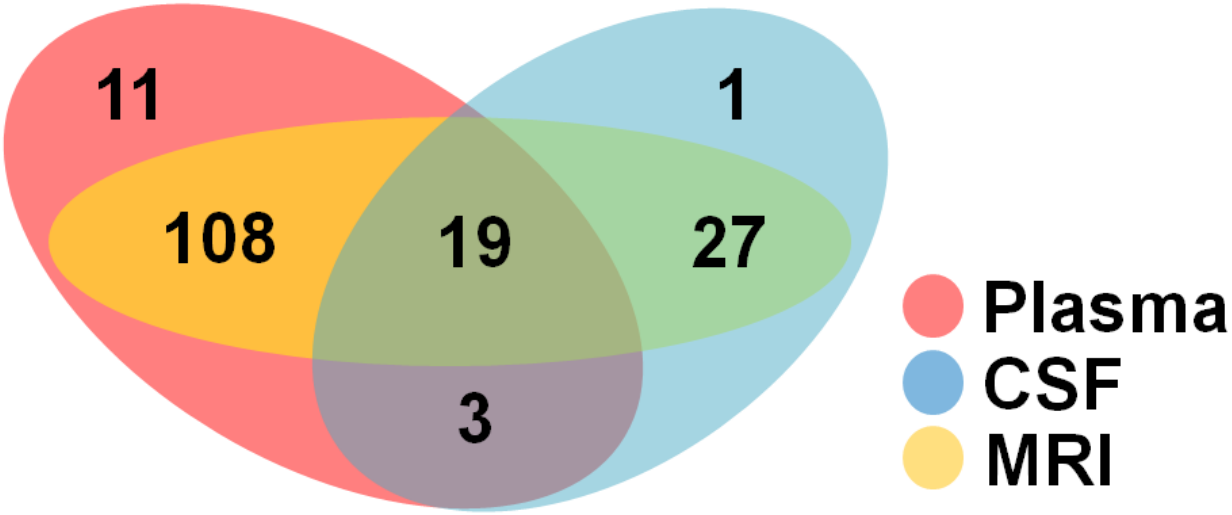

Figure e-2. Correlations between baseline biomarkers and clinical scales scores.

Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

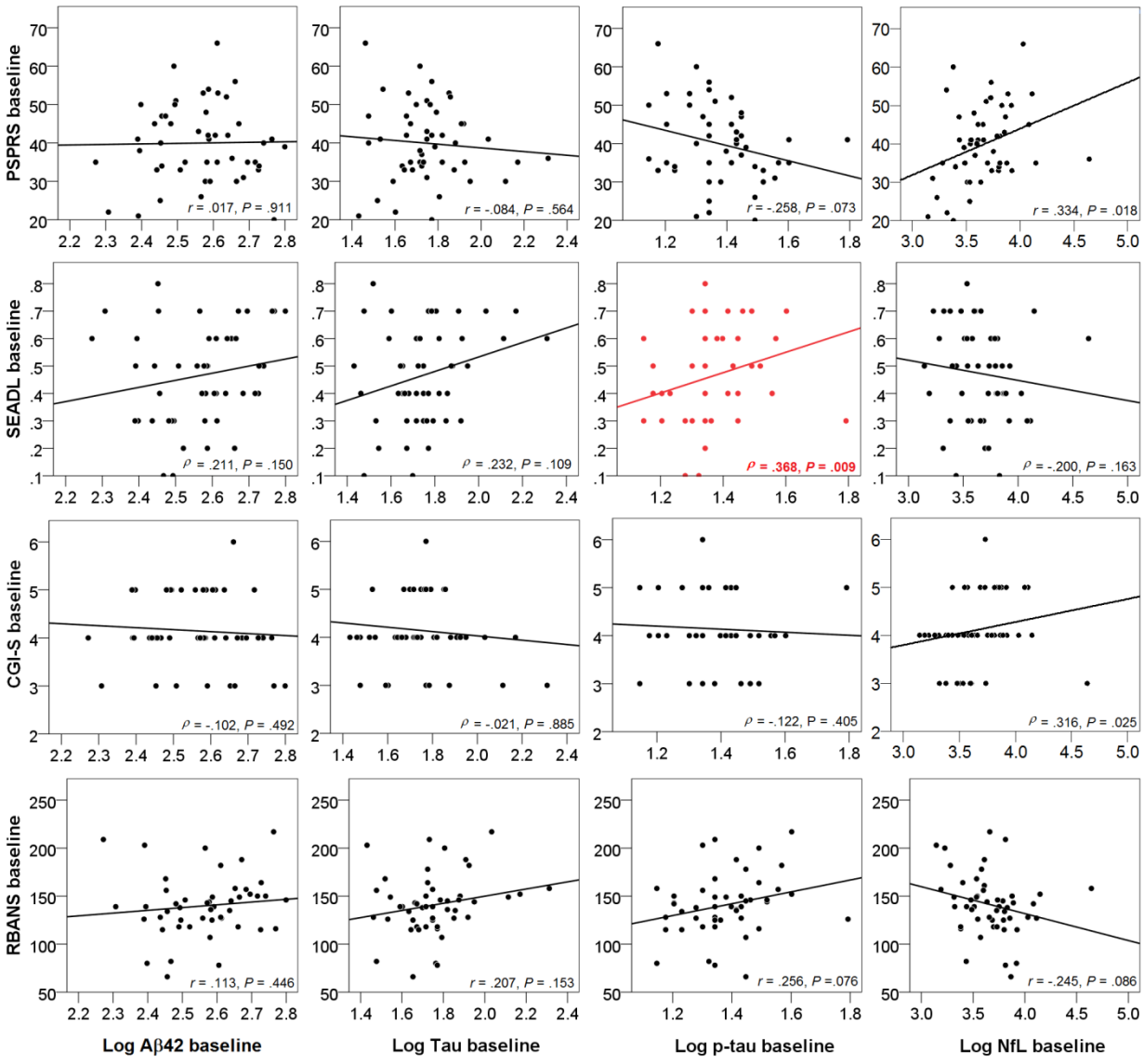

Figure e-3. Correlations between baseline biomarkers and executive function scores.

Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

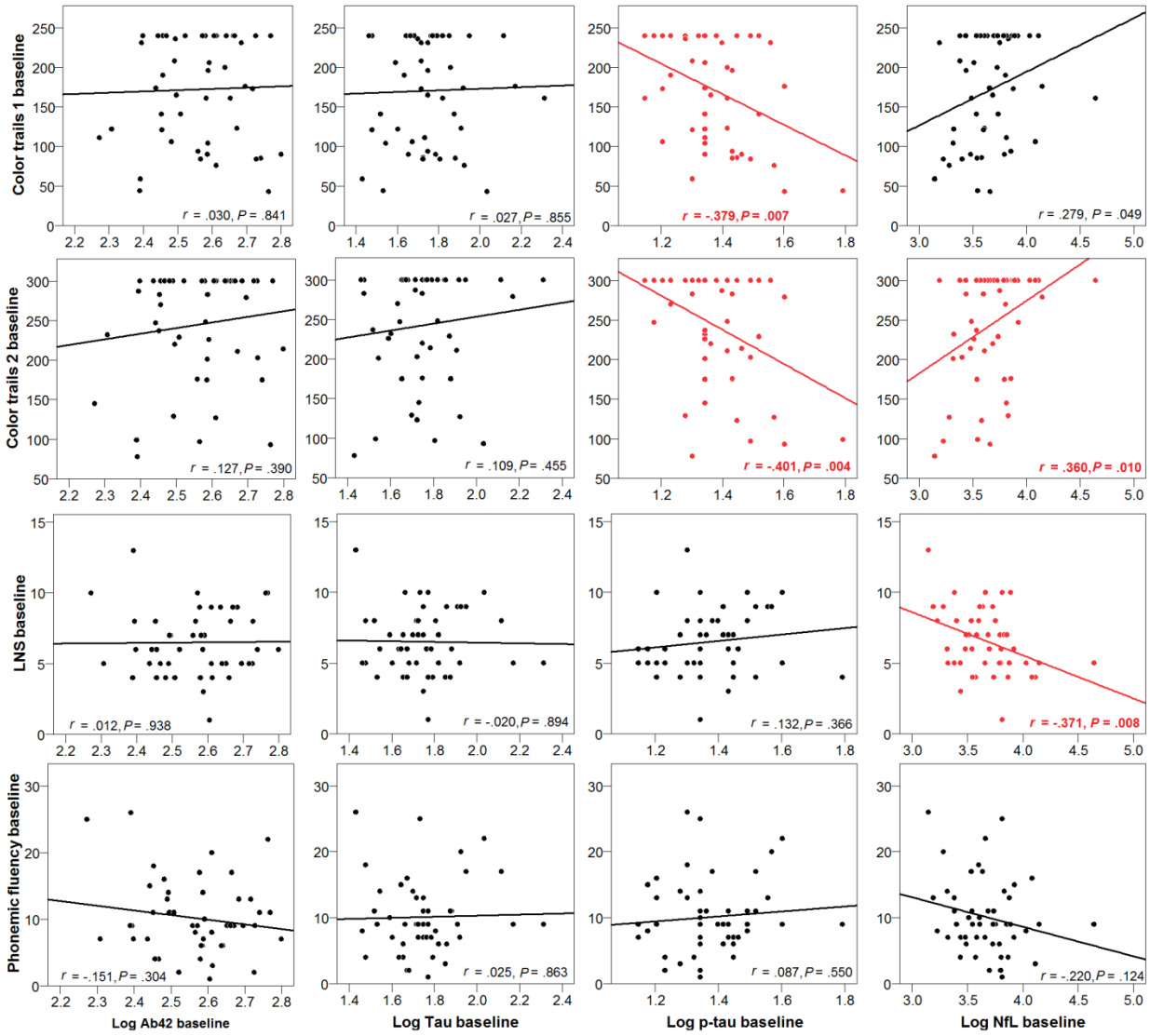

Figure e-4. Correlations between baseline biomarkers and brain volumes. Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

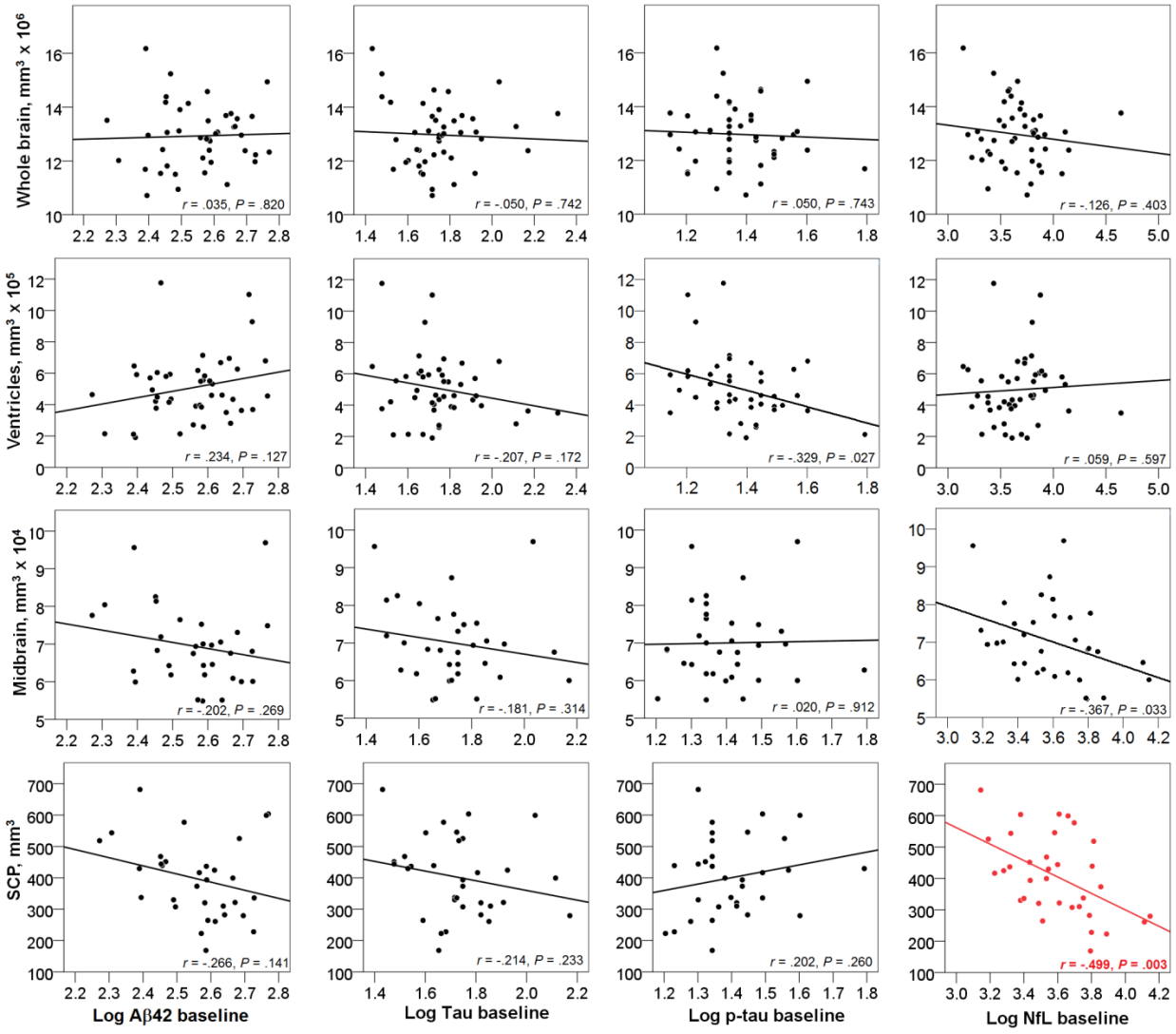

Figure e-5. Correlations between baseline biomarker ratios and clinical scales.

Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

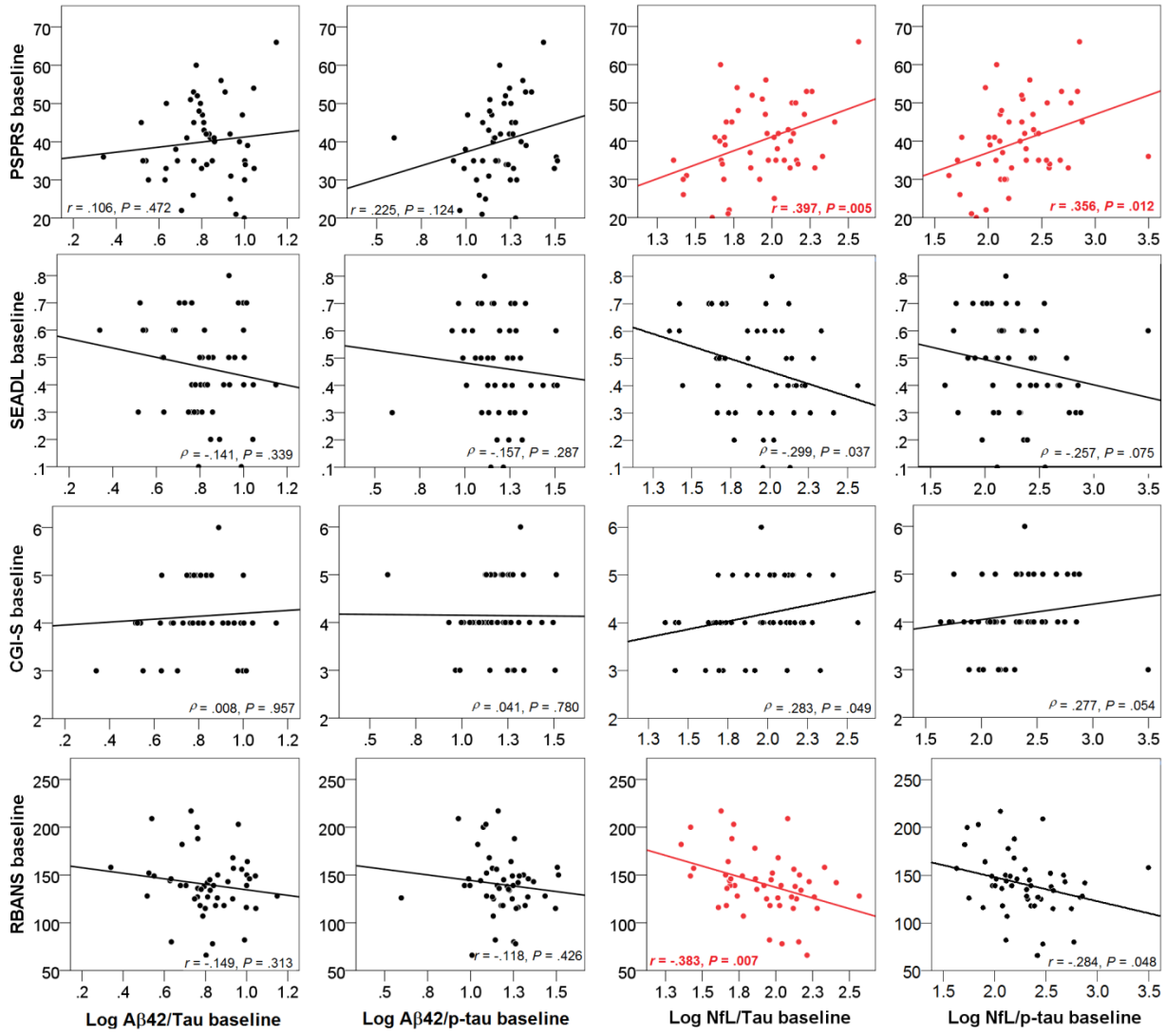

Figure e-6. Correlations between baseline biomarker ratios and executive function scores. Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

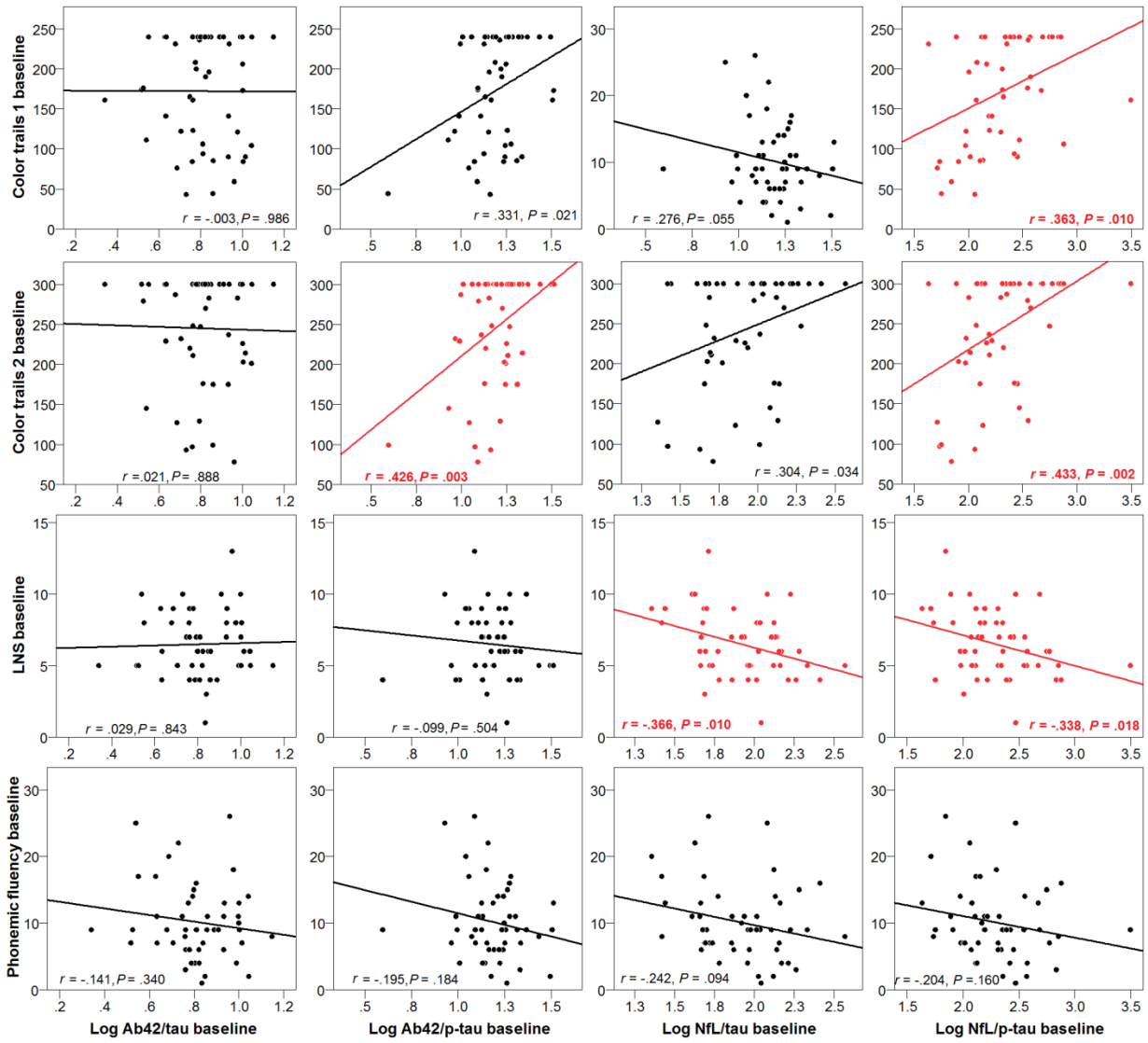

Figure e-7. Correlations between baseline biomarker ratios and brain volumes.

Uncorrected *r* and ρ values are presented. Significant correlations that survived false discovery rate adjustment are in red.

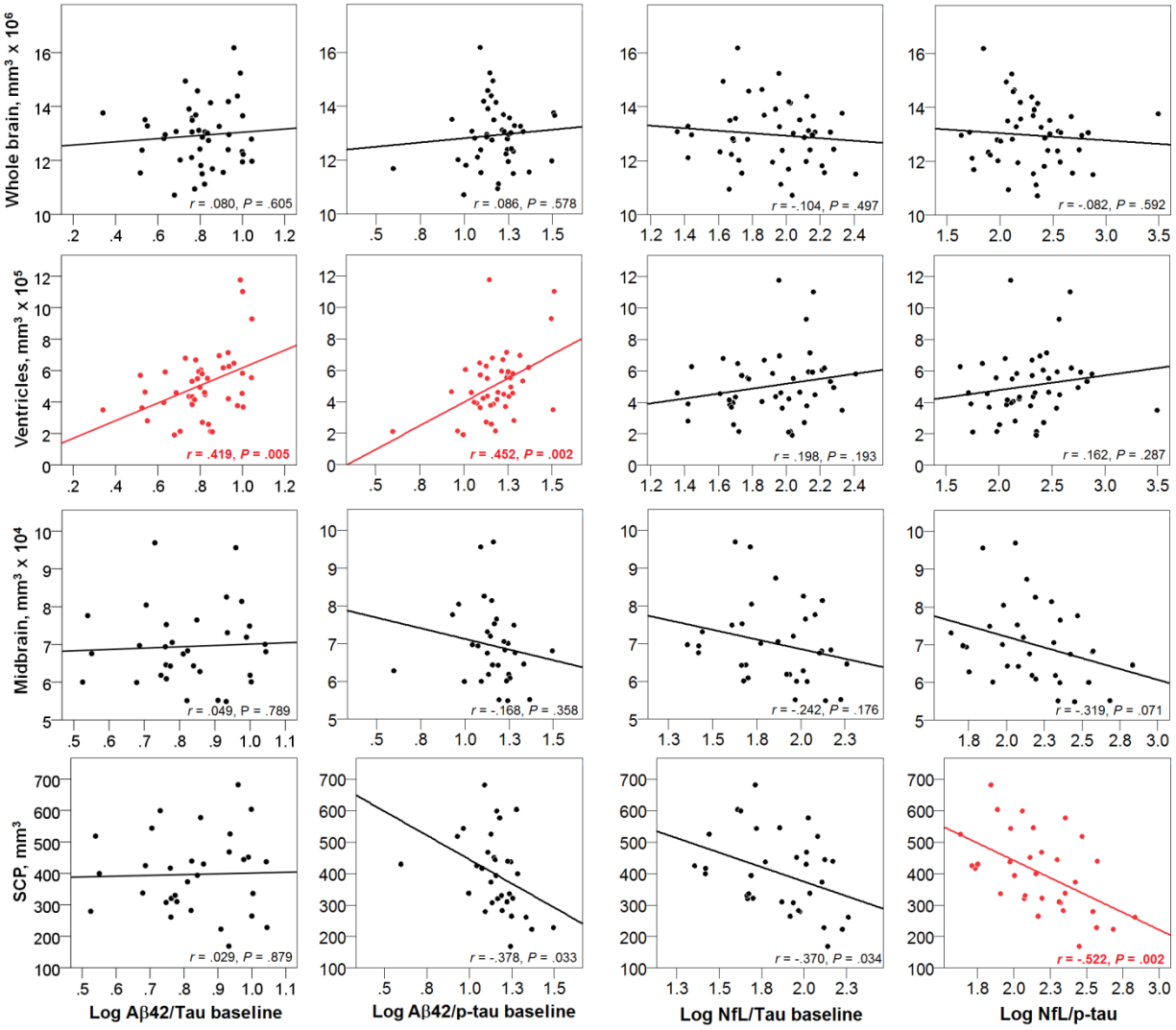

Figure e-8. Prediction of PSP disease progression measured by clinical by CSF biomarkers. Predicted scores corrected for age, sex and baseline MMSE are presented as a function of baseline biomarker levels, per mixed effects linear models. No fixed effects or biomarker by time interactions were observed after False Discovery Rate adjustment. Unadjusted *p* values are presented in table e-1. Longitudinal data for each individual are represented as arrays of dots of increasing intensity. Dotted lines represent 95% confidence intervals. CGI = clinical global impression of severity. RBANS = Repeatable Battery for the Assessment of Neuropsychological Disease Severity

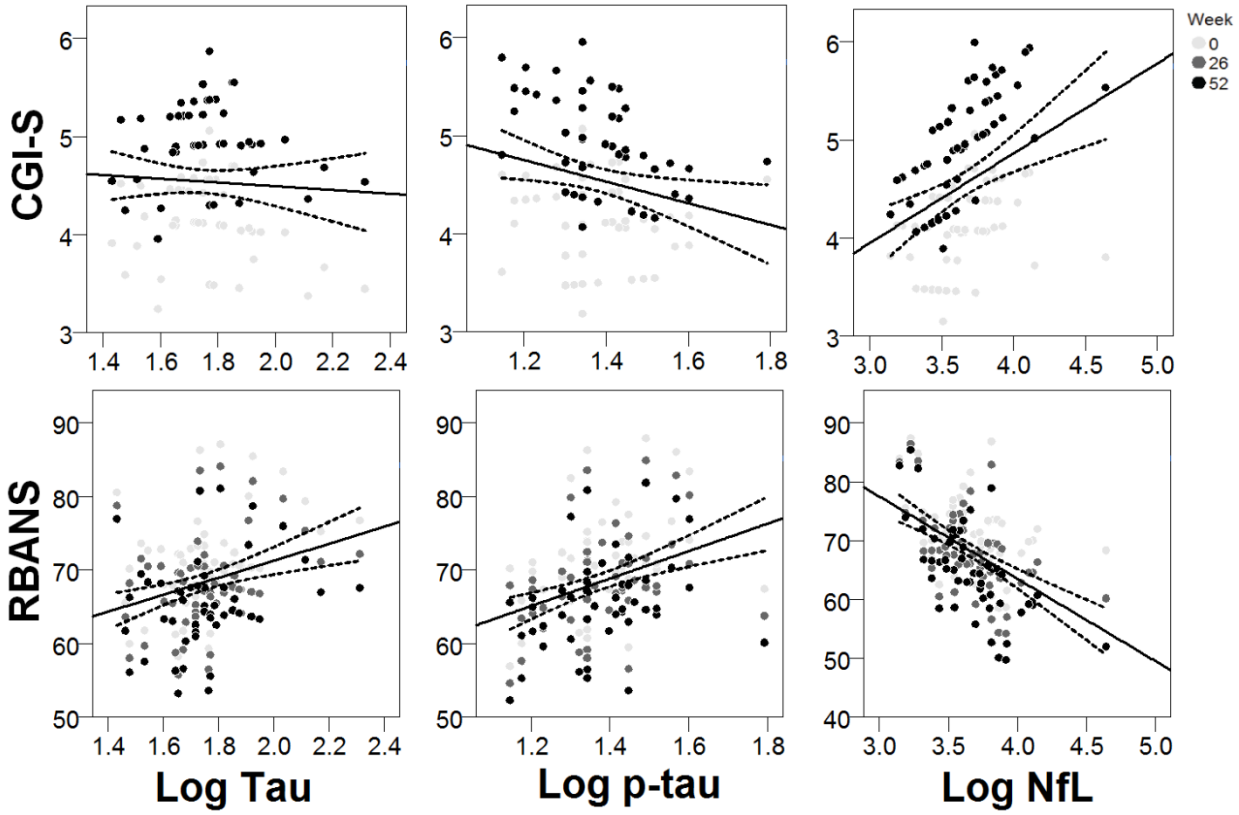

Figure e-9. Prediction of executive dysfunction by CSF biomarkers. Predicted scores corrected for age, sex and baseline MMSE are presented as a function of baseline biomarker levels, per mixed effects linear models. No fixed effects or interactions were observed after multiple comparisons correction (False Discovery Rate). Unadjusted *p* values are presented in table e-1. Longitudinal data for each individual are represented as arrays of dots of increasing intensity. Dotted lines represent 95% confidence intervals. LNS = letter-number sequencing.

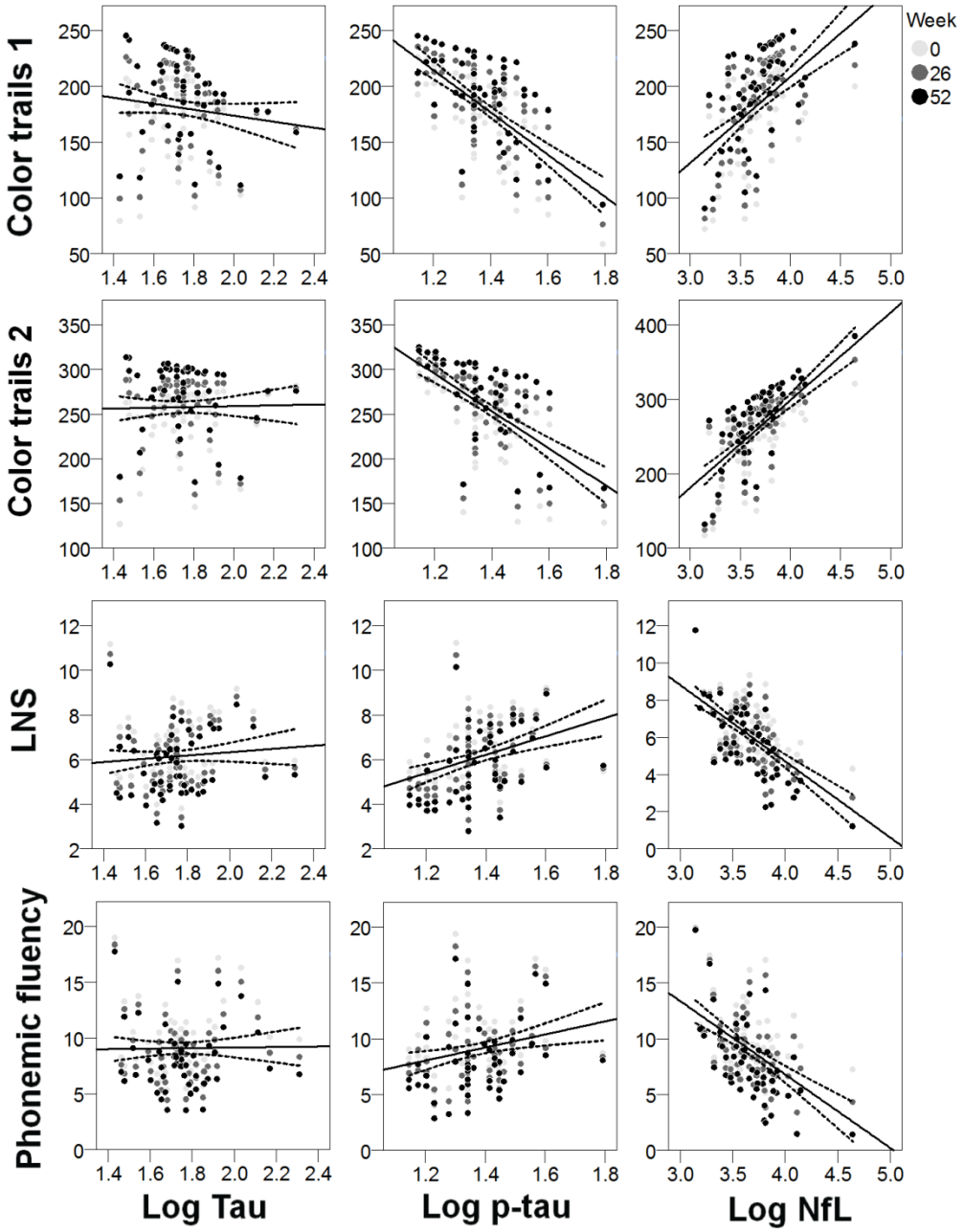

Figure e-10. Prediction of brain atrophy by CSF biomarkers. Predicted volumes corrected for age, sex and baseline total intracranial volume are presented as a function of baseline biomarker levels, per mixed effects linear models. No fixed effects or interactions were observed, after multiple comparisons correction (False Discovery Rate). Unadjusted *p* values are presented in table e-1. Longitudinal data for each individual are represented as arrays of dots of increasing intensity. Dotted lines represent 95% confidence intervals.