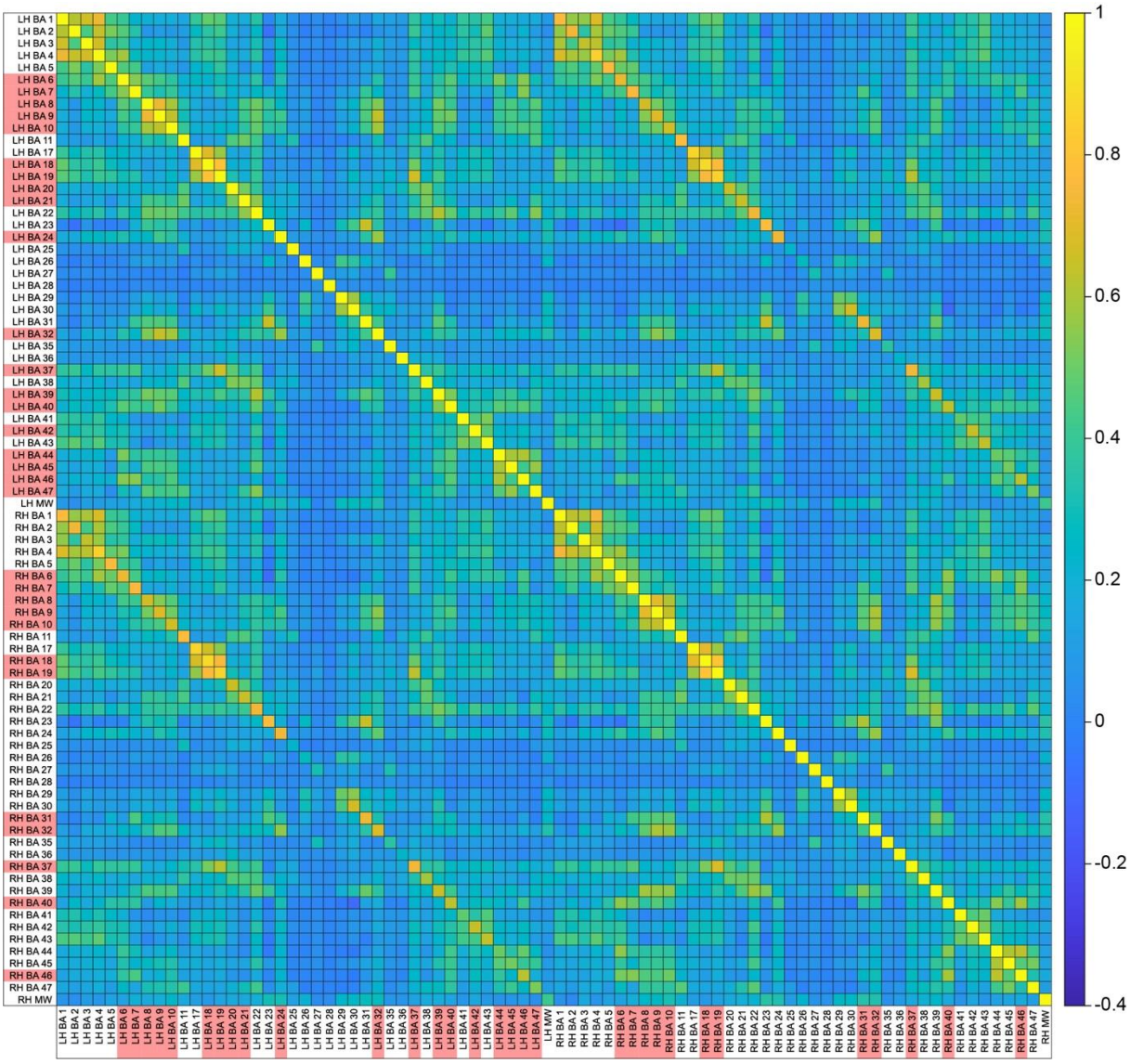
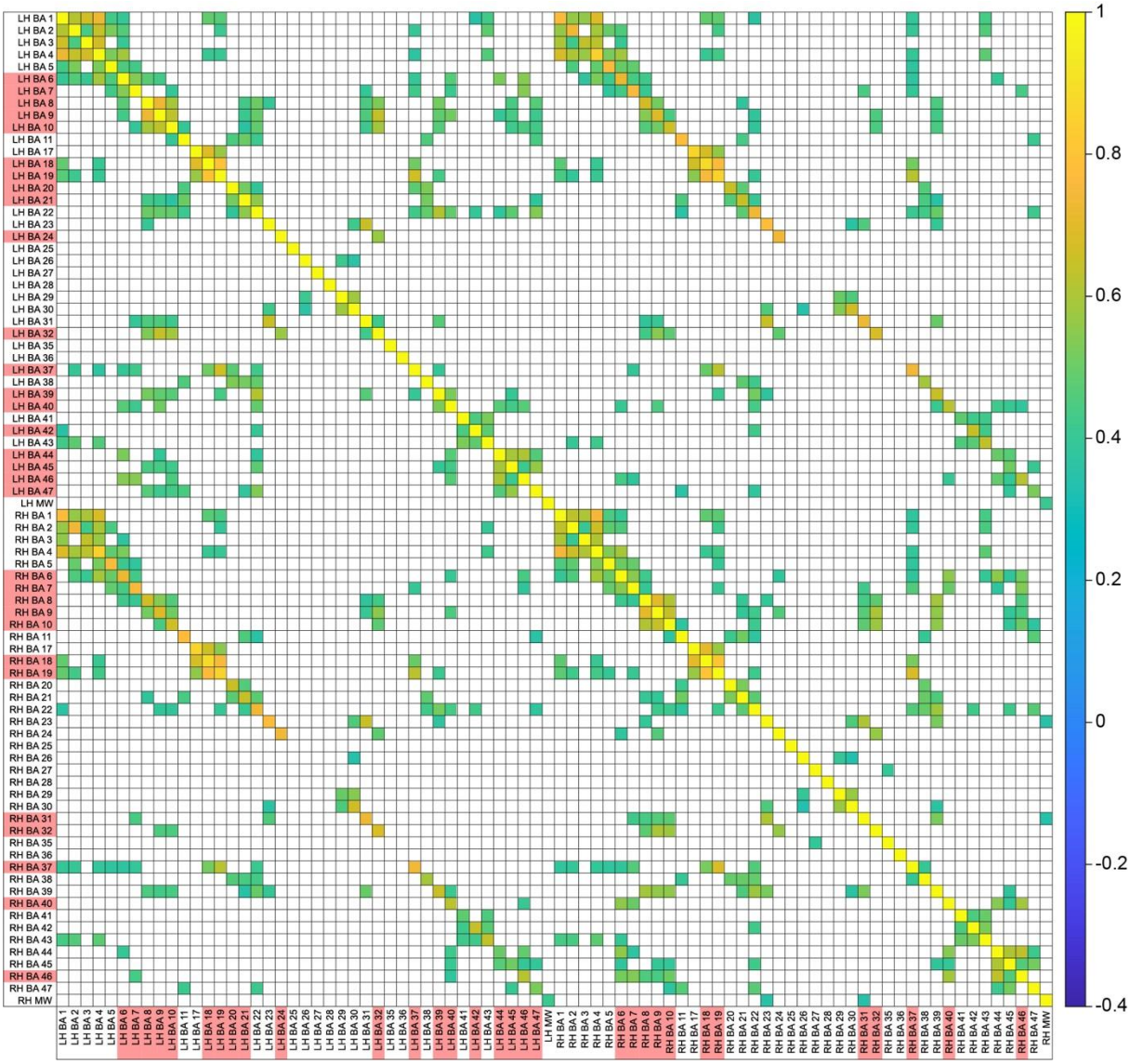
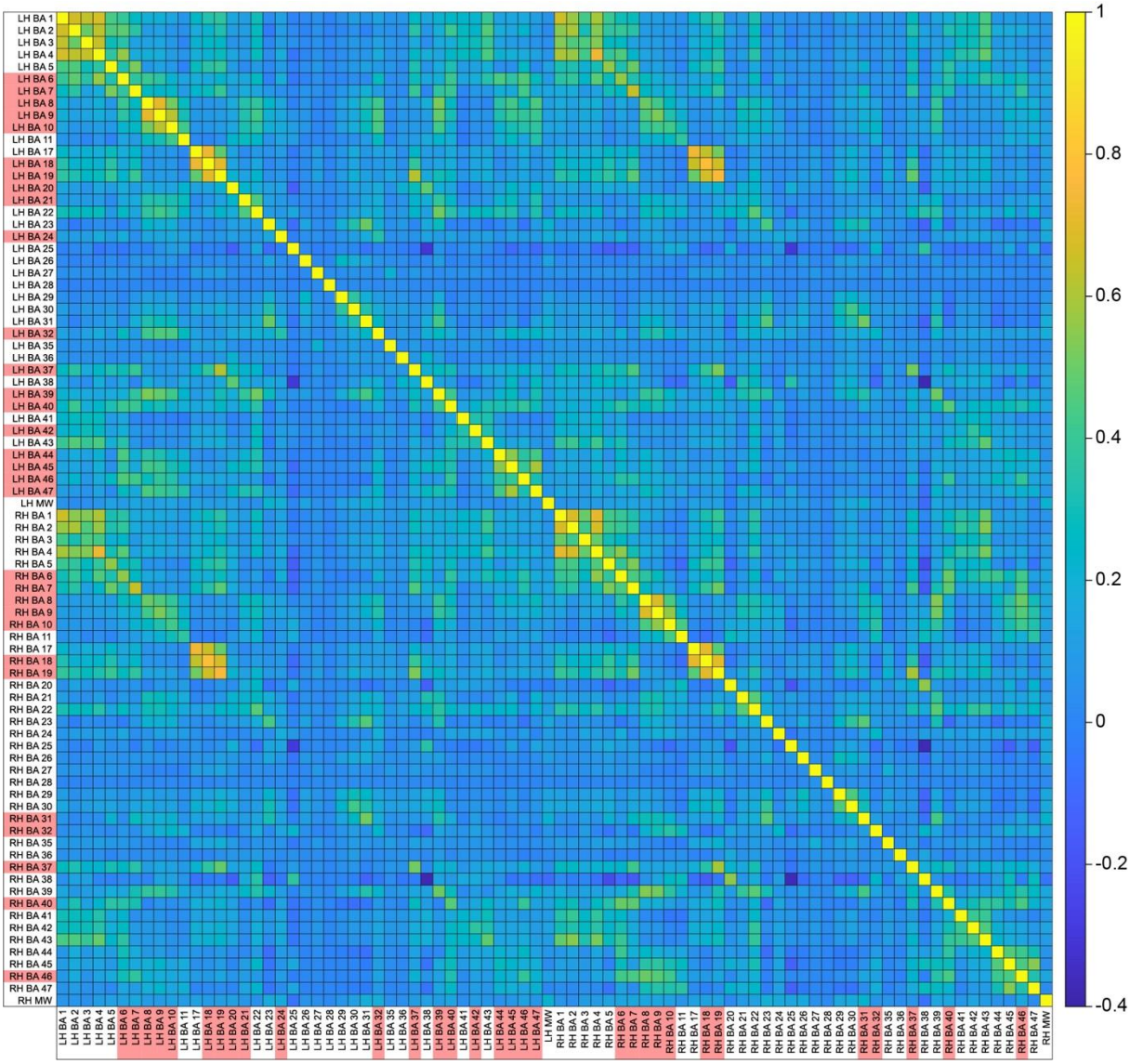
Supplementary Material



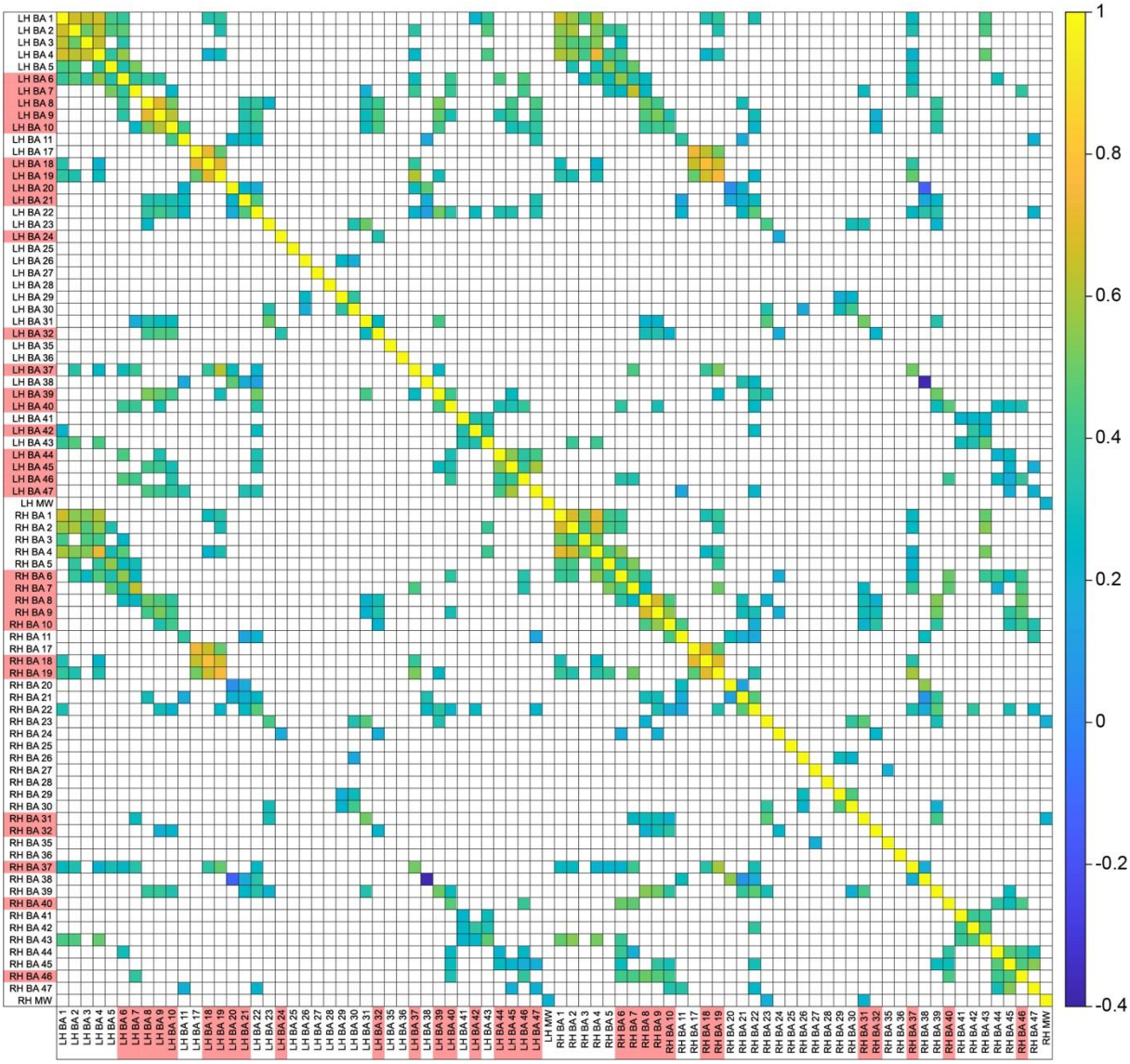
Supplementary Figure 1. Symmetrical 82-by-82 matrix visualizing mean functional connectivity for 3321 individual connections in sample S498. All cells represent BOLD signal correlations, which were controlled for the effects of in-scanner head motion and spurious BOLD signals exhibited by voxels representing white matter or cerebro-spinal fluid. Respective correlation coefficients were averaged across all subjects in sample S498. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



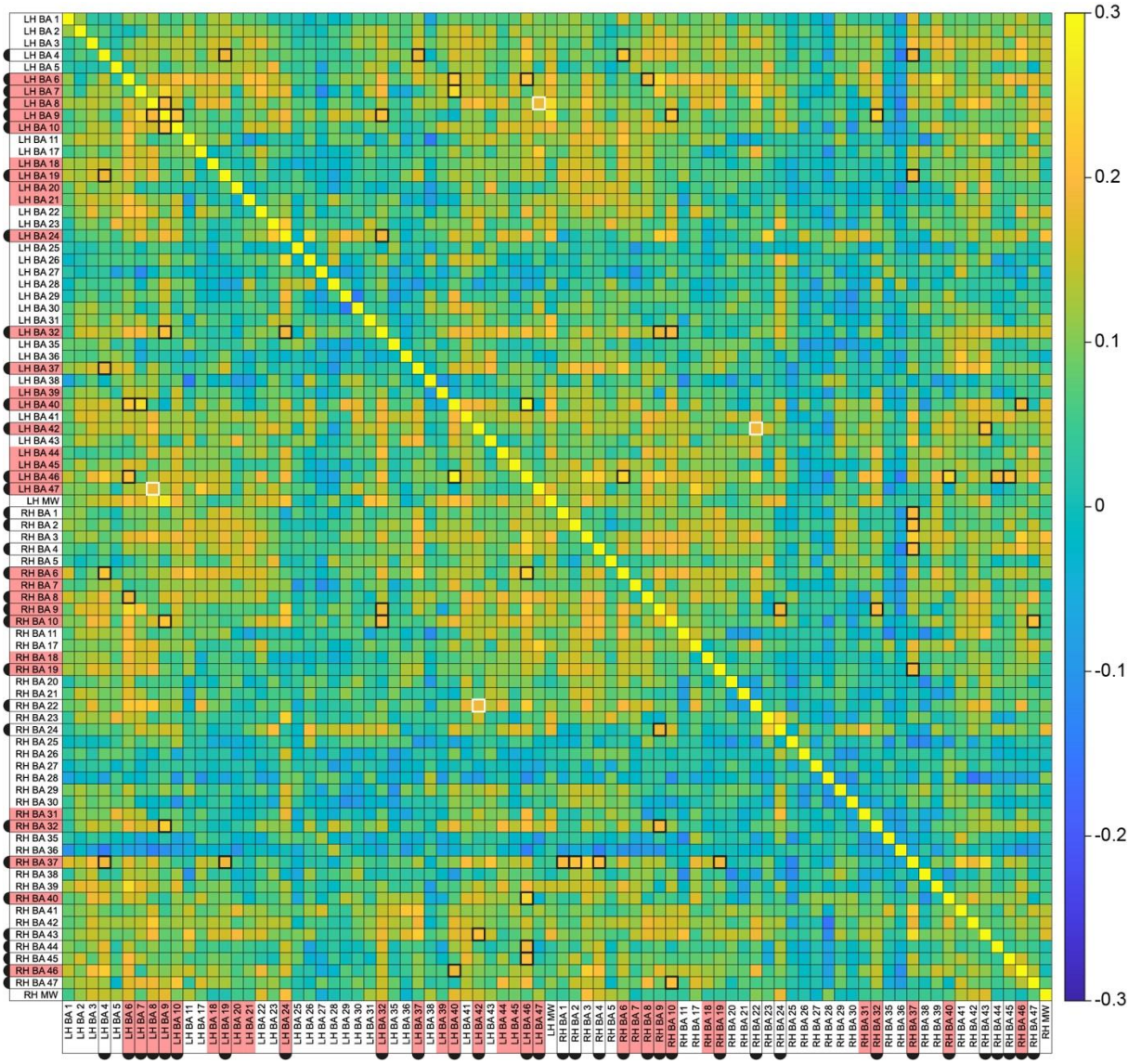
Supplementary Figure 2. Symmetrical 82-by-82 matrix visualizing the pruned version of the mean functional connectivity matrix computed for sample S498. In contrast to the original matrix comprising the total set of 3321 individual connections, this matrix only displays those 401 individual connections for which functional connectivity, i.e. BOLD signal correlations, was found to reach statistical significance ($p < .05$) in 90% of subjects across both samples. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



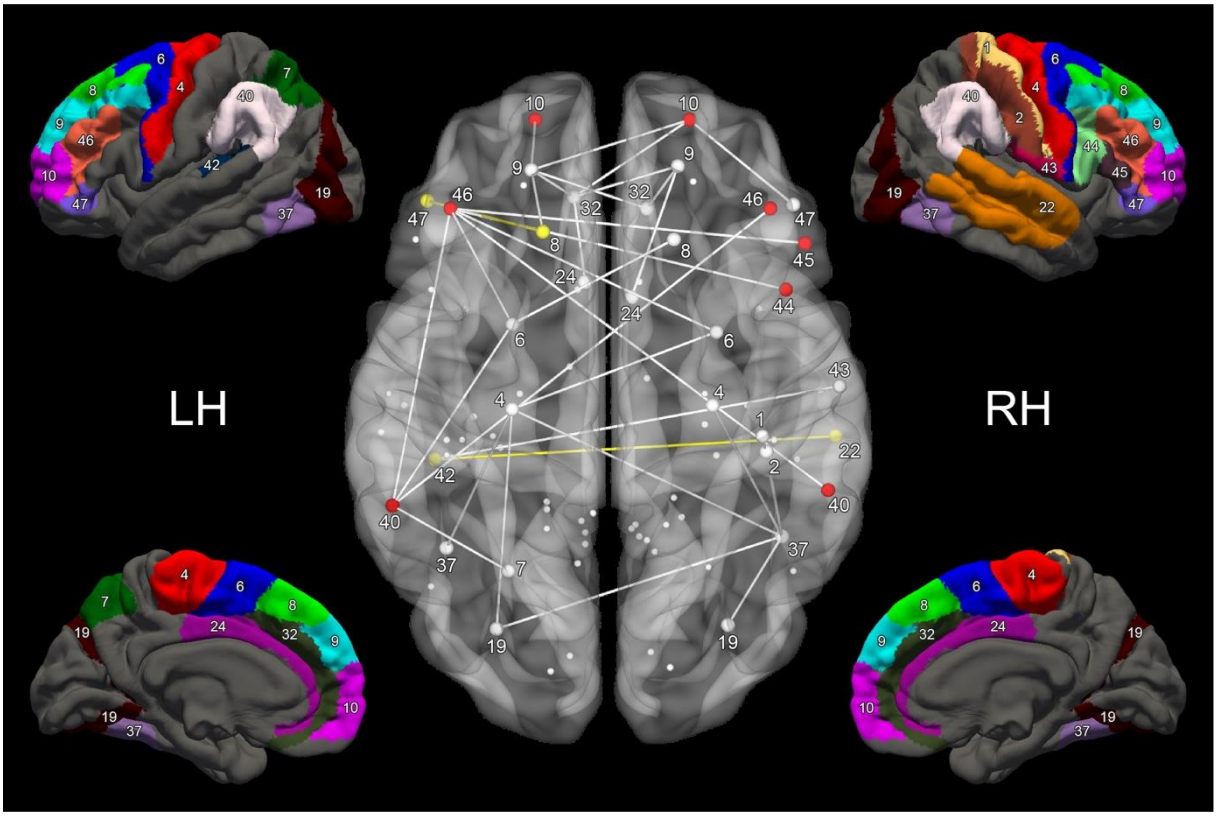
Supplementary Figure 3. Symmetrical 82-by-82 matrix visualizing mean functional connectivity for 3321 individual connections in sample S991. All cells represent BOLD signal correlations, which were controlled for the effects of in-scanner head motion and spurious BOLD signals exhibited by voxels representing white matter or cerebro-spinal fluid. Respective correlation coefficients were averaged across all subjects in sample S991. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



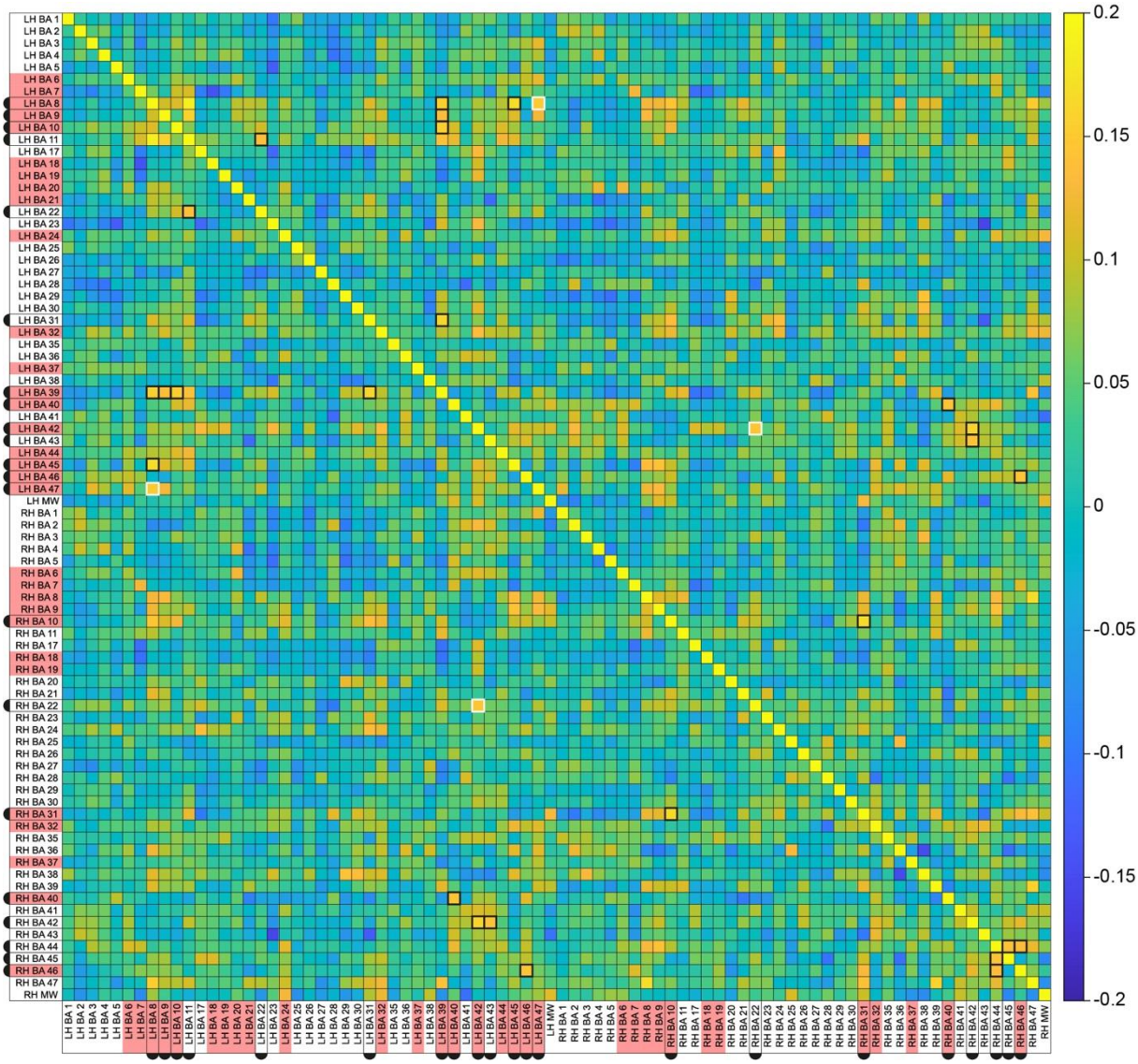
Supplementary Figure 4. Symmetrical 82-by-82 matrix visualizing the pruned version of the mean functional connectivity matrix computed for sample S991. In contrast to the original matrix comprising the total set of 3321 individual connections, this matrix only displays those 401 individual connections for which functional connectivity, i.e. BOLD signal correlations, was found to reach statistical significance ($p < .05$) in 90% of subjects across both samples. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



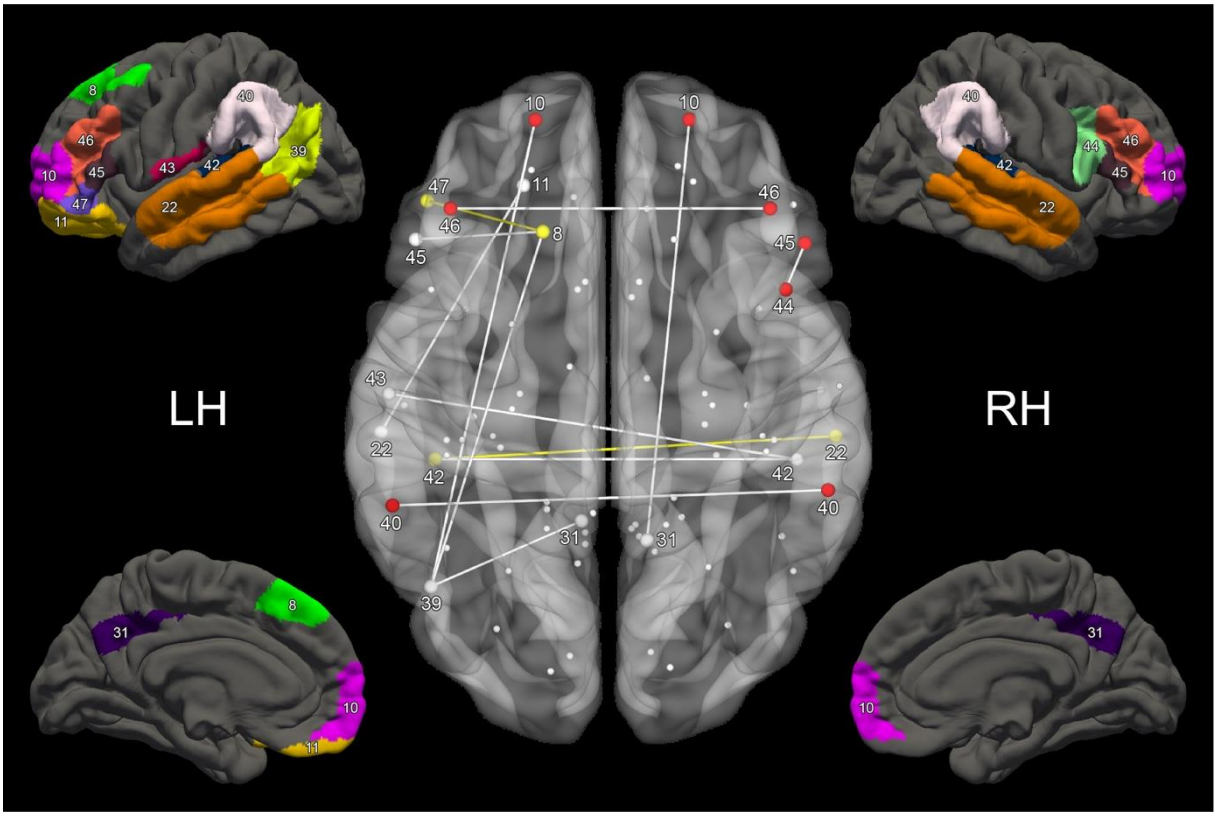
Supplementary Figure 5. Symmetrical 82-by-82 matrix visualizing mean functional connectivity for 3321 individual connections in the female subsample of S498. All cells represent BOLD signal correlations, which were controlled for the effects of in-scanner head motion and spurious BOLD signals exhibited by voxels representing white matter or cerebro-spinal fluid. Respective correlation coefficients were averaged across all female subjects in sample S498. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



Supplementary Figure 6. Schematic depiction of functional connections showing statistically significant associations with matrix reasoning performance in the female subsample of S498. Brodmann areas included in the parcellation scheme used for this study are shown as white spheres within the semi-transparent MNI brain in the center. Functional connections exerting statistically significant correlations between their connectivity strength and matrix reasoning performance are shown as white lines. Spheres constituting statistically significant connections are slightly bigger than the rest and carry labels with the numbers of their corresponding Brodmann areas. Spheres and lines representing functional connections which replicated across both female subsamples (S498 and S991) are depicted in yellow. Brodmann areas which were involved in statistically significant connections in both samples are represented by red spheres. All Brodmann areas constituting statistically significant connections are also shown as colored labels on four brain surfaces in the corners (lateral and medial views of the left and right hemispheres).



Supplementary Figure 7. Symmetrical 82-by-82 matrix visualizing mean functional connectivity for 3321 individual connections in the female subsample of S498. All cells represent BOLD signal correlations, which were controlled for the effects of in-scanner head motion and spurious BOLD signals exhibited by voxels representing white matter or cerebro-spinal fluid. Respective correlation coefficients were averaged across all female subjects in sample S498. Brodmann areas that belong to the extended P-FIT network are highlighted in red. LH = left hemisphere, RH = right hemisphere, BA = Brodmann area, MW = medial wall.



Supplementary Figure 8. Schematic depiction of functional connections showing statistically significant associations with matrix reasoning performance in the female subsample of S991. Brodmann areas included in the parcellation scheme used for this study are shown as white spheres within the semi-transparent MNI brain in the center. Functional connections exerting statistically significant correlations between their connectivity strength and matrix reasoning performance are shown as white lines. Spheres constituting statistically significant connections are slightly bigger than the rest and carry labels with the numbers of their corresponding Brodmann areas. Spheres and lines representing functional connections which replicated across both female subsamples (S498 and S991) are depicted in yellow. Brodmann areas which were involved in statistically significant connections in both samples are represented by red spheres. All Brodmann areas constituting statistically significant connections are also shown as colored labels on four brain surfaces in the corners (lateral and medial views of the left and right hemispheres).

Supplementary Table 1. Results of multiple regression analysis for five functional connections from sample S498. Matrix reasoning performance, quantified as BOMAT test scores, was regressed on functional connectivity strength, quantified as BOLD signal correlations. β-coefficients reaching statistical significance ($p < 0.05$, two-tailed) are marked in bold.

	B	SE	β	T	$p_{predictor}$	R^2_{adj}	p_{model}
Constant	12.638	0.670		18.870	< .001	0.046	< .001
LH 8 to LH 47	1.647	0.906	0.086	1.819	.070		
LH 10 to LH 22	1.520	1.105	0.031	1.376	.170		
LH 10 to LH 39	0.656	1.023	0.029	0.642	.521		
LH 46 to RH 44	2.508	1.157	**0.116**	2.168	.031		
LH 46 to RH 45	0.342	1.078	0.002	0.317	.751		

Supplementary Table 2. Results of multiple regression analysis for five functional connections from sample S991. Matrix reasoning performance, quantified as PMAT24 test scores, was regressed on functional connectivity strength, quantified as BOLD signal correlations. β-coefficients reaching statistical significance ($p < 0.05$, two-tailed) are marked in bold.

	B	SE	β	T	$p_{predictor}$	R^2_{adj}	p_{model}
Constant	14.180	0.497		28.551	< .001	0.034	< .001
LH 8 to LH 47	1.788	0.715	**0.105**	2.499	.013		
LH 10 to LH 22	1.506	0.677	**0.071**	2.223	.026		
LH 10 to LH 39	1.417	0.707	**0.061**	2.004	.045		
LH 46 to RH 44	2.045	0.993	**0.164**	2.059	.040		
LH 46 to RH 45	0.718	0.790	0.024	0.909	.363		

Supplementary Table 3. Results of multiple regression analyses computed for the complete S498 and S991 samples as well as their male and female subsamples.

Matrix reasoning performance, quantified as BOMAT or PMAT24 test scores, was regressed on the connectivity strength, quantified as BOLD signal correlations, of five functional connections (see Supplementary Tables 1 and 2). Regression models were computed in iterative fashion (10000 analyses per group) with randomly picked subsamples (75% of subjects).

	$R^2_{adj\_mean}$	$R^2_{adj\_min}$	$R^2_{adj\_max}$	percentage of significant iterations
$S498_{complete}$	0.046	0.008	0.093	99.76
$S498_{male}$	0.022	-0.022	0.094	23.14
$S498_{female}$	0.072	-0.003	0.160	97.24
$S991_{complete}$	0.034	0.011	0.067	100.00
$S991_{male}$	0.020	-0.010	0.066	52.79
$S991_{female}$	0.040	0.007	0.088	99.56