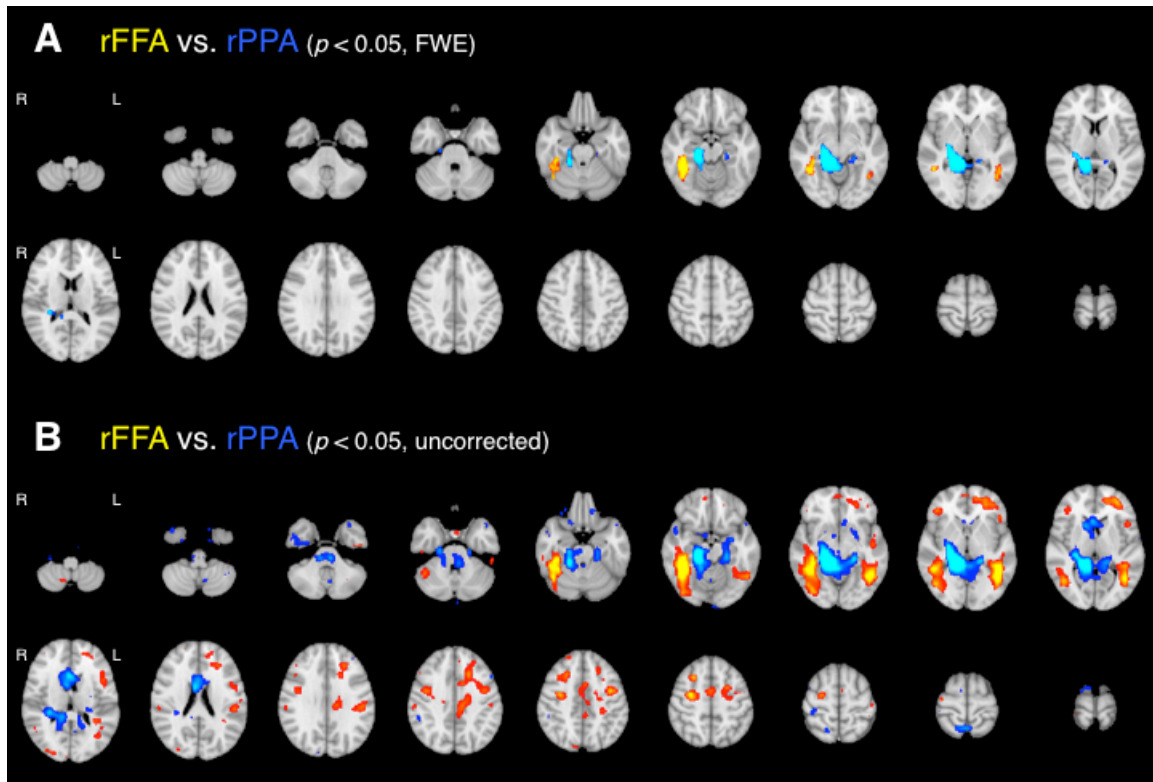
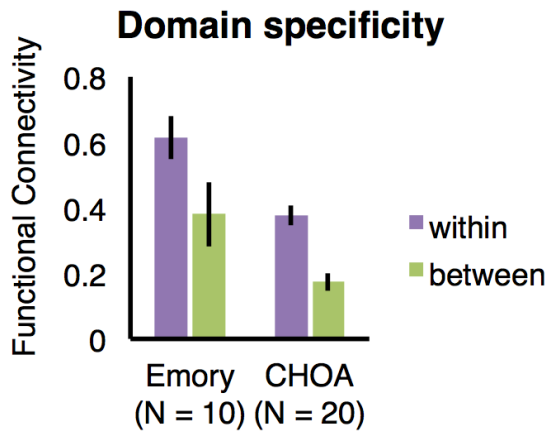
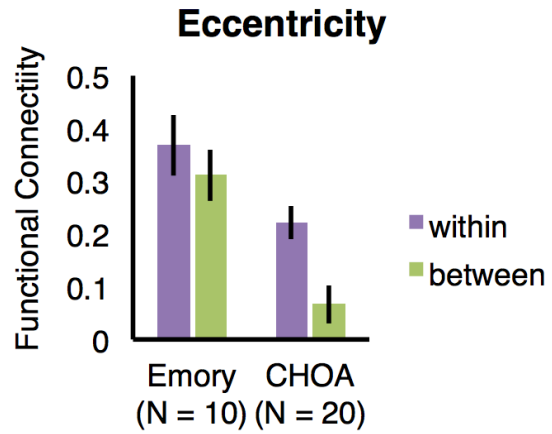


Supplemental Figure 1. Data from individual neonates (N = 30). A) Within- (dark gray) and between-domain (light gray) functional connectivity for each individual neonate. B) Within- (dark gray) and between-eccentricity (light gray) functional connectivity for each individual neonate. For both A) and B), Participants 1-10 were collected at Emory, while the remaining neonate data were collected at CHOA.



Supplemental Figure 2. Whole-brain functional connectivity in neonates. Seed-based analysis was performed using the same parameters as the primary ROI analyses, except that time courses from each ROI were now regressed on voxels across the whole brain, and the resultant data from each subject were registered to MNI space. To explore whole-brain functional connectivity that differed between the face and place networks, we computed a contrast of rFFA > rPPA. For this contrast, we conducted a nonparametric one-sample *t*-test using the FSL randomize program (Winkler, Ridgway, Webster, Smith, & Nichols, 2014), which tests the *t* value at each voxel against a null distribution generated from 5000 random permutations of group membership. The resultant statistical maps were then corrected for multiple comparisons ($p < .05$, FWE) using threshold-free cluster enhancement, a method that retains the power of cluster-wise inference without the dependence on an arbitrary cluster-forming threshold (Smith & Nichols, 2009). A) At corrected thresholds ($p < 0.05$, FWE), only seed regions and their homotopic regions, which receive direct colossal inputs, survived. B) To further explore the data, we also examined whole brain functional connectivity at uncorrected thresholds ($p < 0.05$). At uncorrected thresholds, we found patterns of functional connectivity consistent with the ROI analysis, with rFFA showing functional connectivity to regions of the fusiform gyrus (potentially including FFA and OFA) and with rPPA showing functional connectivity with regions of the parahippocampal gyrus and retrosplenial cortex (potentially including PPA and RSC). This analysis shows that functional connectivity effects are relatively specific to the networks tested here, and suggest that ROI analyses were more powerful than seed-based group analysis for detecting domain-specific functional connectivity.

A**B**

Supplemental Figure 3. Cohort effects. A) Average within- and between-domain functional connectivity for neonate data collected at Emory (N = 10, TR = 2, 300 volumes / run, 1-4 runs) and CHOA (N = 20, TR = 1, 130 volumes / run, 1 run). B) Average within- and between-eccentricity functional connectivity in the Emory and CHOA cohorts.