Identifying basal ganglia divisions in individuals using resting-state functional connectivity MRI

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FIGURE S1 | Analyses were conducted using an eta² threshold of 0.85 (black arrows, A–C) where there is strong community structure in the network (A, green bar at Q=0.3), the network is sparse (B, green bar at Edge Density ~0.05) but fully connected (C, green bar at Graph Connectedness ~1.0).
Figure S2 | Rows 1–3. From Cohort two, three subjects’ basal ganglia voxels colored with respect to modularity optimization groupings (shown on each subject’s MP-RAGE; coloring for each hemisphere and each subject is arbitrary). Arrows indicate modules labeled as Dorsal Caudate (Red Arrows, $z = 16$), Dorsal Caudal Putamen (Blue Arrows, $z = 10$), and Ventral Striatum (Purple Arrows, $z = -8$). Row 4. Conjunction of modules ascribed the same label across Cohort Two subjects. Color bar depicts number of subjects with a module assignment at each voxel.
Figure S3 | Z-transformed rs-fcMRI maps from modularity assignments are statistically reliable within each cohort for the right hemisphere divisions (first and second rows, $z \geq 3.00$, $k = 21$, corresponding to $p < 0.05$, Monte Carlo corrected) and yield common regions of correlation across cohorts (conjunction analysis, third row). Positive correlations are depicted in warm colors (first two rows) and their overlap is depicted in red in the conjunction analysis (third row). Negative correlations are depicted in cool colors (first two rows) and their overlap is depicted in green in the conjunction analysis (third row).