Supplementary Methods

MRI acquisition

All subjects were scanned on a Siemens 3T Trio Tim using a 12-channel phased-array head coil. High resolution 3D T1-weighted magnetization prepared rapid gradient-echo (MPRAGE) sequence was used with the following parameters: 1mm isotropic voxels; 160 sagittal slices; acquisition matrix size=256×256; repetition time (TR)=2300 ms; echo time (TE)=2.98 ms; field of view (FOV)=256 mm. Changes in blood-oxygenation-level-dependent (BOLD) T2* signal were measured using 2 gradient echo-planar imaging sequences each with the following parameters: TR=5000 ms; TE=30 ms; flip angle 90; 256 mm FOV; 2mm isotropic voxels; sequence length=6 minutes, 40 seconds (76 time points/scan). Participants were instructed to stay awake and to remain as still as possible with eyes open. Bi-temporal foam pads restricted head motion and earplugs attenuated scanner noise.

MRI preprocessing

MRI data was preprocessed using FMRIB Software Library v5.0.7 (FSL) and MATLAB 2017a. The anatomical T1 preprocessing pipeline included: reorientation to right-posterior-inferior (RPI); alignment to anterior and posterior commissures; skull stripping; gray matter, white matter and cerebrospinal fluid segmentation; and computation of non-linear transformation between individual skull-stripped T1 and 2mm resolution MNI152 template images.

The functional MRI preprocessing pipeline included: slice time correction; reorientation to RPI; realigning functional volumes within runs with a rigid body transformations (6 parameters linear transformation); computation of the transformation between individual skull-stripped T1 and mean functional images; intensity normalization; removal of confounding factors from the data using linear regression - including 12 motion-related covariates (rigid motion parameters and its derivatives), linear and quadratic terms, and five components each from the lateral ventricles and white matter. Of note, global signal regression was not applied due to the spurious correlations this can introduce. Transformation of resting-state data to MNI space, concatenating the transformation from functional to structural and from structural to MNI, spatial smoothing with an isotropic Gaussian kernel of 6-mm FWHM, and band-pass filtering (0.01–0.08 Hz) to reduce low-frequency drift and high-frequency noise were also performed. Head motion was quantified using realignment parameters obtained during image preprocessing, which included 3 translation and 3 rotation estimates. Scrubbing of time points with excess head motion eliminated all time points with a frame displacement > 0.5mm. Finally, data was down-sampled to 6mm to perform voxel-level analyses. The two resting-state runs were concatenated and subjects with more than 25 time points exceeding the scrubbing head motion correction threshold were removed. To ensure that connectivity matrices included the same number of time points across subjects, we took 127 time points per subject. The distributions of the correlations across all time series were inspected for possible noise contamination; no outliers were observed from the whole-brain connectivity distributions across all participants. Note: of the original 35 subjects

with FND, five were excluded: excessive head motion (n=1); inability to tolerate scan (n=1); acquisition difficulties (n=3).

Data driven SFC alterations correlated with symptom severity (SOMS:CD-PHQ15 composite)

While the primary analyses in the main manuscript to assess within-group stepwise functional connectivity (SFC) profiles correlated with symptom severity were based on *a priori* hypothesized seeds (motor and amygdalar seeds), we also performed a secondary data-driven approach to identify all possible voxels that would show an alteration in their downstream propagation. For each voxel, we computed a single-class general linear model of the propagation in 1^{st}, 2^{nd} and 3^{rd} link step adjusting for age, gender and handedness. The results were corrected for multiple comparison using a Monte Carlo simulation (3dClustSim, afni.nimh.nih.gov) cluster-wise correction with 10,000 iterations to estimate the probability of false positive clusters with a p value<0.05. Supplementary Fig. 2 shows the map of seed regions that showed SFC correlations with SOMS:CD-PHQ15 composite in any of the 1^{st}, 2^{nd} and 3^{rd} link-steps.

Visualization

Cortical surfaces were visualized using the population-average landmark and surface-based projections of CARET software. Surface images were displayed using a color scale based on T-scores. In-volume images were added to show subcortical striatal-thalamic-limbic-midbrain findings when present.