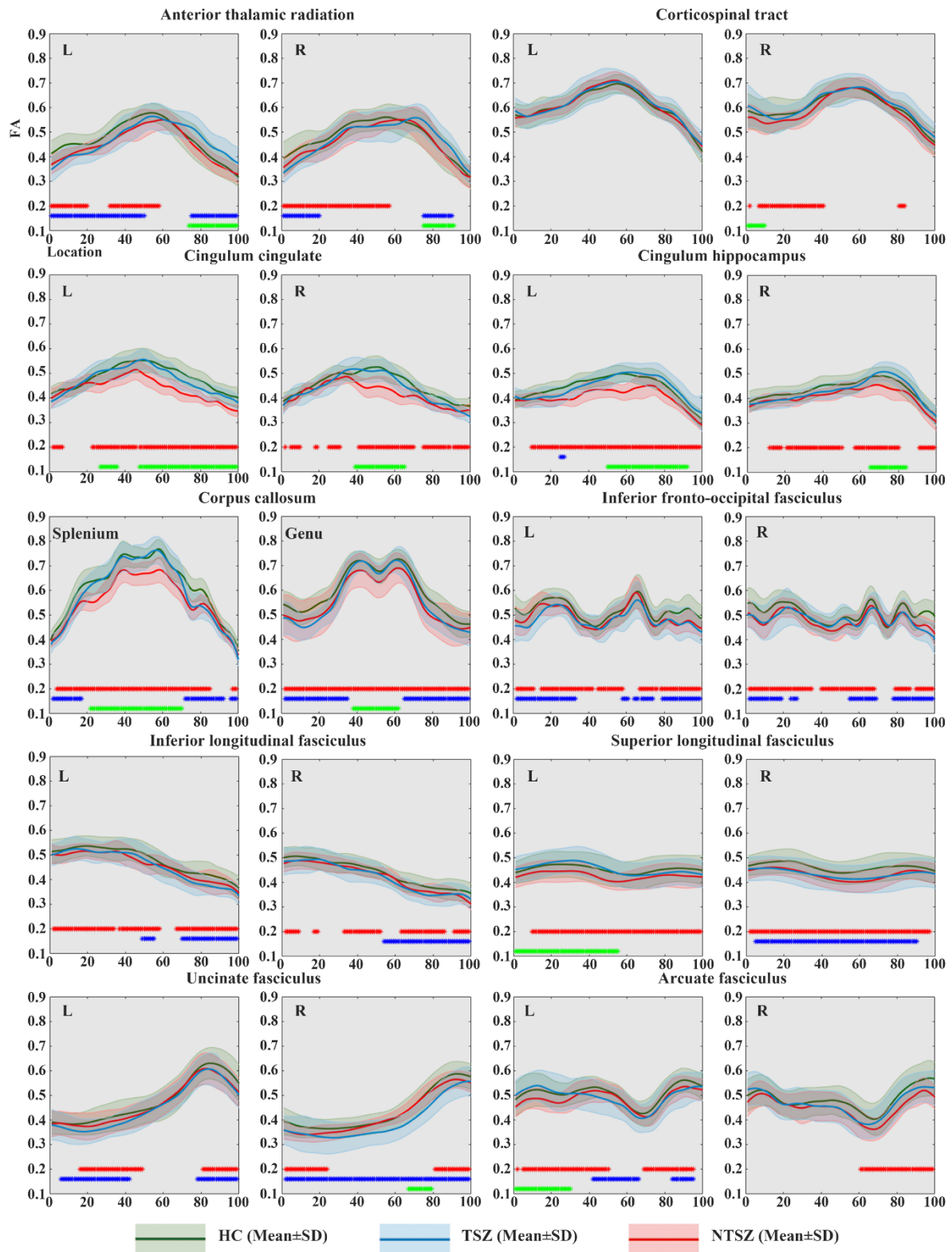


Besides the ANOVA testing for group differences in average fractional anisotropy (FA) across fiber tracts, in exploratory analyses, we examined each tract separately divided into 100 equal segments to characterize group differences along fiber tracts using point-wise comparisons. Briefly, the tract profiles from a participant were arranged in a single matrix. All these matrices were fed into permutation-based statistical analysis with 10,000 permutations using the FSL Randomize program, with age and illness duration as covariates. The statistical results were subject to family wise error correction for multiple comparisons following threshold-free cluster enhancement and thresholded at $p < 0.05$.

We used AFQ software which is based on an algorithm that automatically identifies 20 major white matter tracts and makes measurements at anatomically equivalent locations along their trajectories to quantify diffusion measurements at multiple locations along the trajectory of a white matter tract, creating a ‘‘Tract Profile’’ of diffusion measurements. Tract Profiles contain more information than mean diffusion measures. Second, changes in FA can occur at specific positions within the Tract Profile, rather than along the entire tract. These analyses provided an opportunity in an exploratory way to test for and visualize such effects. Third, Tract Profiles can be used to compare white matter properties of individual patients to standardized Tract Profiles of a healthy population to elucidate unique features of a patient’s white matter pathology (PLoS One. 2012; 7 (11): e49790).

Figure S1. Point-wise comparison of fractional anisotropy (FA) profiles among never-treated long-term schizophrenia patients, antipsychotic-treated patients of similar illness duration, and healthy controls.



Each tract was divided into 100 equal segments (X axis) and FA measurements (Y axis) and scaled in the same way across tracts. Tract profiles are color coded (green for healthy

comparison subjects (HC), red for never-treated (NTSZ) and blue for treated patients (TSZ); solid lines for means, shaded areas for SDs). The bars under the fiber tracts indicate tract regions with pairwise FA differences observed via permutation testing. Red bars indicate differences between never-treated patients and healthy controls, blue bars indicate differences between treated patients and healthy controls, and green bars indicate differences between the two patient groups. The x-axis represents the location between the beginning and termination waypoint regions of interest following the JHU white matter template convention. L: left: R: right. NTSZ: never-treated long-term schizophrenia patients; TSZ: antipsychotic-treated schizophrenia patients of similar illness duration; HC: healthy controls