Supplemental Information

Methods and Materials

We conducted a confirmatory region of interest (ROI) analysis for prefrontal and limbic structures, using bilateral DLPFC (BA9/46), amygdala, and parahippocampal cortex as defined by the WFU PickAtlas software (PickAtlas2.4; Wake Forest University, Winston-Salem, North Carolina; http://fmri.wfubmc.edu/) (1). Correlations between genotype and mean ROI were calculated for each diagnostic group and then compared between groups using Fisher's Z transformation.

Results

In repeat analyses excluding the two non-Caucasian patients, results were unchanged, except the left precuneus finding (within schizophrenia group analysis) no longer met the cluster-level correction. In repeat analyses using sex as a nuisance covariate, results were unchanged, except both inferior frontal gyrus findings (within control group and between diagnostic group analyses) no longer met the cluster-level correction.

Region of interest analyses confirmed the reported findings, showing in patients statistically significant relationships between genotype and resting rCBF in the DLPFC (R^2=0.19, df=23) and amygdala (R^2=0.20, df=23) and a trend-level relationship in the parahippocampus (R^2=0.13, df=23). Healthy participants showed no significant relationship between genotype and rCBF in these same regions (R^2<0.002, df=45 for all

ROIs). Between-diagnostic-group differences in these correlations were significant ($p<0.05$) in the DLPFC and amygdala and trend-level ($p=0.07$) in the parahippocampus.

1. Maldjian JA, Laurienti PJ, Kraft RA, Burdette JH (2003): An automated method for neuroanatomic and cytoarchitectonic atlas-based interrogation of fMRI data sets. *Neuroimage* 19:1233-9.

Table S1. *COMT* Genotype-Resting rCBF Relationships in Patients and Healthy Volunteers

Parametric Analyses

Patients			Healthy Volunteers		
Region	**Peak Voxel Coordinates (x, y, z)**	**Association with COMT Met Alleles**	**Region**	**Peak Voxel Coordinates (x, y, z)**	**Association with COMT Met Alleles**
right middle frontal gyrus (BA9/46)	26, 44, 32	positive*	left orbital cortex (BA47)	-22, 14, -16	positive
right superior temporal gyrus (BA22)	56, -48, 16	positive*	left middle temporal gyrus (BA21)	-66, -30, -12	positive
precuneus (BA7)	-2, -70, 48	positive	right cingulate gyrus	14, 8, 28	negative
right amygdala	20, 2, -20	negative			
left para-hippocampal gyrus (BA28)	-16, 2, -32	negative*			

Regions of Interest Analyses

Patients			Healthy Volunteers		
Region	**R^2 (df)**	**Association with COMT Met Alleles**	**Region**	**R^2 (df)**	**Association with COMT Met Alleles**
bilateral dorsolateral prefrontal cortex (BA9/46)	0.19(23)	positive*	bilateral dorsolateral prefrontal cortex (BA9/46)	<0.001(45)	-
bilateral amygdala	0.20(23)	negative*	bilateral amygdala	0.002(45)	-
bilateral para-hippocampus	0.13(23)	negative	bilateral para-hippocampus	<0.001(45)	-

*statistically significant between-diagnostic-group difference