Data Supplement for Burdick et al., Association of Genetic Variation in the *MET* Proto-Oncogene With Schizophrenia and General Cognitive Ability, American Journal of Psychiatry (doi: 10.1176/appi.ajp.2009.09050615)

### **Supplemental Methods**

#### Subjects

The initial sample was analyzed and reported on in Lencz et al. 2007. Subsequent to this, genotyping procedures were repeated for the second phase using an independent cohort of patients with schizophrenia and healthy controls collected at the Zucker Hillside Hospital-NSLIJHS. The timing of the second phase of genotyping allowed for the natural division of our cohort into the initial and replication samples used in the current study but methods were identical across all subjects.

#### Genotyping

Genotyping methods were identical for both initial and replication samples; however, genotyping was completed first for the initial sample and subsequently for the replication sample. The genotyping was done using an Affymetrix 500K array for genome wide association study. Genomic DNA was extracted from whole blood and hybridized to two chips as per Affymetrix specifications. Patient and control samples were equally distributed on each 96-well plate to avoid plate artifacts. Quality control analyses resulted in the exclusion of any sample with a mean call rate of <90% across both chips and SNPs that failed Hardy Weinberg equilibrium testing were also excluded from final analyses. The linkage disequilibrium structure from the initial sample was imposed upon the replication cohort, such that linkage disequilibrium blocks and haplotype structure were identical between samples.

## Population Structure Analyses

A principal components method was utilized to assess population structure, with primary results presented in the manuscript. In addition, the genomic inflation factor after correction for principal components analysis was  $\lambda$ =1.02. Figure S1 further illustrates the principal components analysis-corrected Q-Q plot derived from these analyses.

# Figure S1. Q-Q Plot of p-values after Adjustment for Principal Components Analysis<sup>a</sup>



a Trend test/additive model, -log10 scale. From genome-wide association study of the full sample. Green line is the diagonal.