Genome-wide Association Analysis of Eye Movement Dysfunction in Schizophrenia

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Figure S1. QTL analysis of HPG in schizophrenia (SZ), healthy control (HC) and ALL groups. Manhattan plots in 60 SZ individuals (A), 166 HC individuals (B) and all 226 individuals (C). Red line and blue line indicate a genome-wide significant p-value ($p=5\times10^{-8}$) and a suggestive p-value ($p=1\times10^{-5}$), respectively.



Figure S2. QTL analysis of SPL in schizophrenia (SZ), healthy control (HC) and ALL groups. Manhattan plots in 60 SZ individuals (A), 166 HC individuals (B) and all 226 individuals (C). Red line and blue line indicate a genome-wide significant p-value ($p=5\times10^{-8}$) and a suggestive p-value ($p=1\times10^{-5}$), respectively.



Figure S3. QTL analysis of DF in schizophrenia (SZ), healthy control (HC) and ALL groups. Manhattan plots in 60 SZ individuals (A), 166 HC individuals (B) and all 226 individuals (C). Red line and blue line indicate a genome-wide significant p-value ($p=5\times10^{-8}$) and a suggestive p-value ($p=1\times10^{-5}$), respectively.



Figure S4. QTL analysis of EMS in schizophrenia (SZ), healthy control (HC) and ALL groups. Manhattan plots in 60 SZ individuals (A), 166 HC individuals (B) and all 226 individuals (C). Red line and blue line indicate a genome-wide significant p-value ($p=5\times10^{-8}$) and a suggestive p-value ($p=1\times10^{-5}$), respectively.



Figure S5. The state model of chromatin in 7p12.1 (A) and 2p23.1 (B). The chromatin was segmented into 25 states (i.e. promoter, enhancer, etc.) by ChromHMM algorithm (Ernst et al.) using data provided by NIH Roadmap Epigenomics Consortium (http://www.roadmapepigenomics.org), and was visualized by the WashU Epigenome Browser (<u>http://epigenomegateway.wustl.edu/browser/</u>). Here, 25 states were summarized to 9 states as shown a color legend. The gray shaded stripe represents active/weak enhancer regions.