Abstract

To understand the contributions of copy number variations (CNVs) to the etiology of cocaine dependence (CD), we employ innovative analytic approaches, use our own and existing genome-wide association study (GWAS) and CNV data sets, and combine into meta-analyses to identify CD-associated CNVs. We have developed a novel CNV analytic pipeline specifically for the proposed study. This is the *first and largest* genome-wide CNV meta-analysis of CD.