**Cell Line Models of Cytotoxic Response - Integration of Statistical Methods Development
and Genetic Association Mapping
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The investigation and discovery of genetic factors that determine differential drug response is the fundamental goals of pharmacogenomics.  Lymphoblastoid cell lines (LCLs) have become a well-established model for understanding dose response, including exploring the genetic etiology of such drug response.  Here We present the results of genome-wide association mapping studies (GWAS) for a large number of commonly used anti-cancer drugs, along with the methods development studies behind the high throughput mapping.  This GWAS screen produced interesting potential candidate genes, and we present initial results of functional/clinical follow-up of these candidates.  We will also present the initial results of clinical validation results from top candidates.  Additionally, we present topical challenges and new directions related to drug combinations.  These results demonstrate an integrated approach to bioinformatics methods development and application.