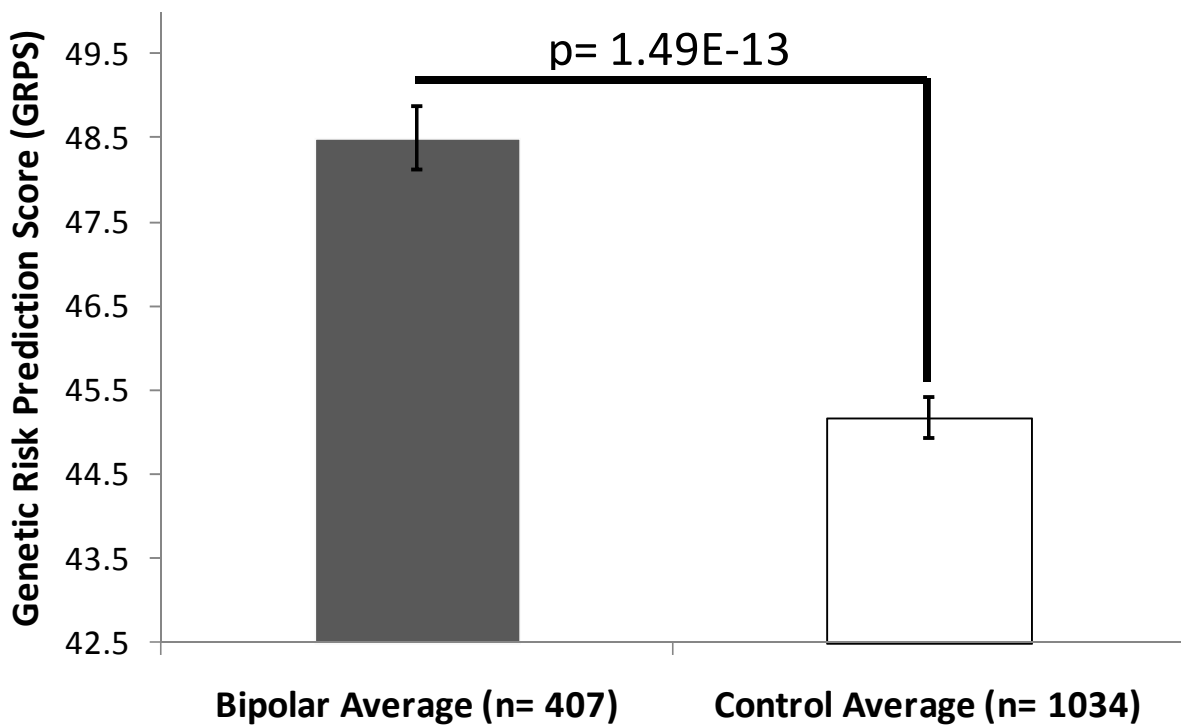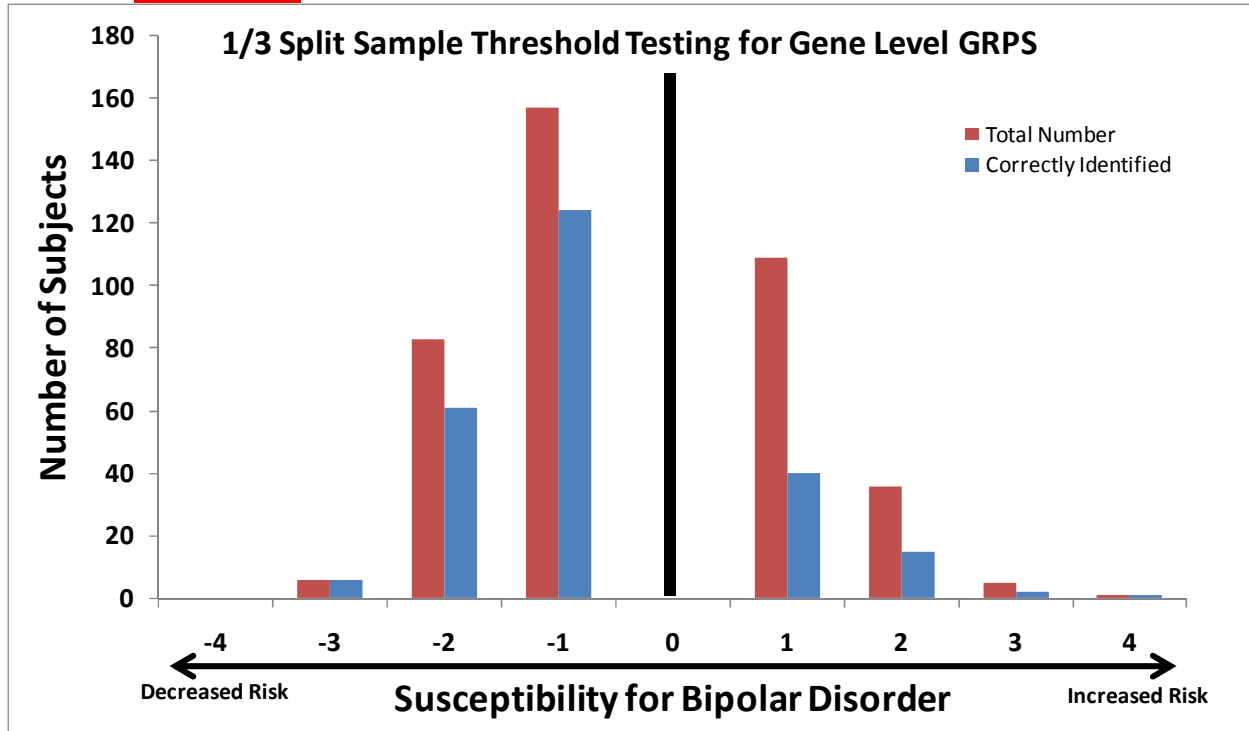**Gene Level GRPS for European American Data**

>75% affected alleles= 2; >60% affected alleles= 1; and <59% affected alleles= 0

p= 1.49E-13

This is a gene level analysis of the top 56 candidate genes for bipolar disorder from Patel et al. 2010. All significant SNPS for these top 56 genes were collected from the four discovery studies and were queried for overlap with the SNPs in the GAIN-BP study. Then we used thresholds to obtain scores for each gene. If more than 75% of the SNPs in a particular gene were affected in a particular subject, then that gene was given a score of 2 in that subject. If between 60% and 75% of the SNPs were affected, that gene was given a score of 1 in that subject. If below 60% of the genes were affected, then that gene was given a score of zero in that particular subject. Finally, the scores were averaged for all genes (n= 56) in a particular subject (combinations of 0, 1, and 2) and multiplied by 100 to obtain a Genetic Risk Prediction Score (GRPS). This figure shows that there greater separation if the analysis is performed at a gene level, as opposed to the SNP level analysis in Patel et al. 2010.

Risk Score	Total Number	Correctly Identified	Positive Predictive Value
-3	6	6	100.00%
-2	83	61	73.49%
-1	157	124	78.98%
0			
1	109	40	36.70%
2	36	15	41.67%
3	5	2	40.00%
4	1	1	100.00%

This figure shows the predictive power of the panel of top genes for bipolar disorder (n=56) using Gene-level GRPS. Overall the results are similar to the results published in the paper using SNP-level GRPS, showing better ability to predict who is at lower risk for the illness than ability to predict who is at higher risk.