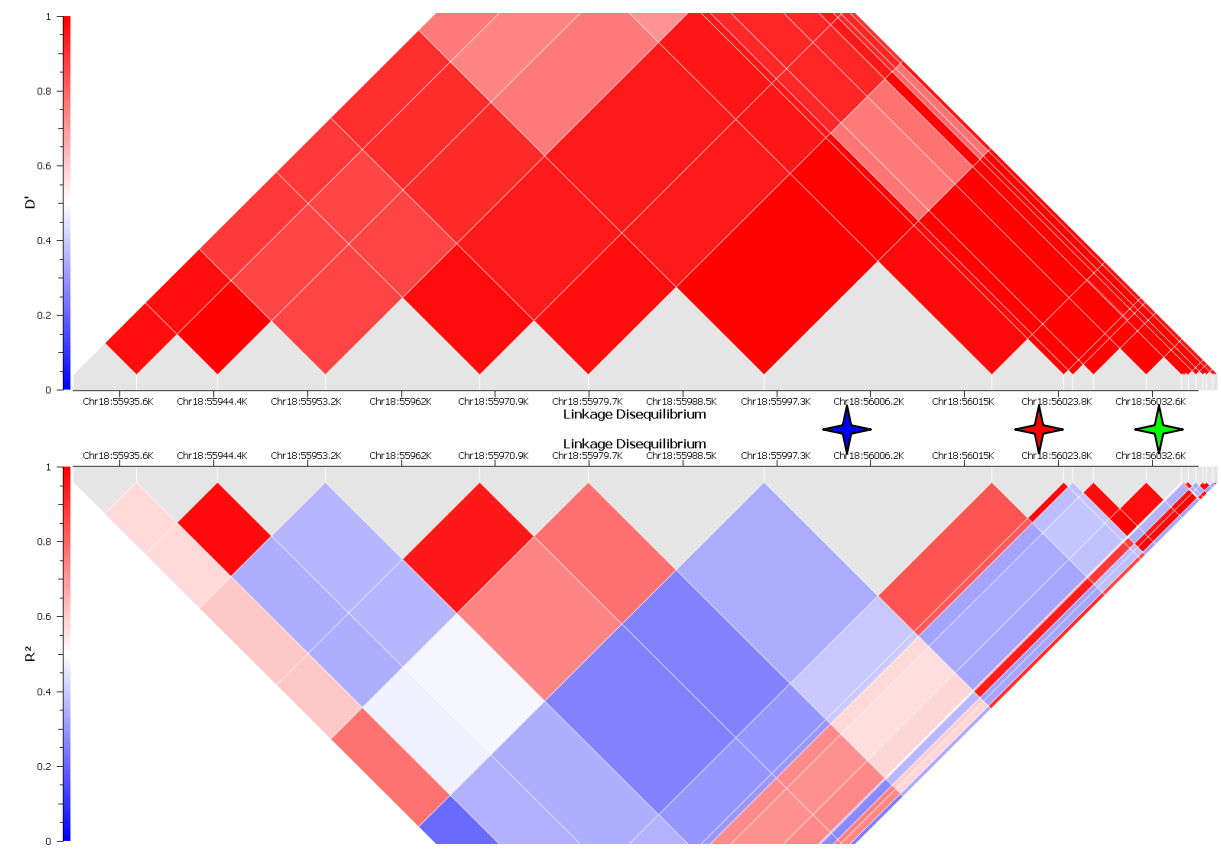


SUPPLEMENTAL TABLE 1. DEMOGRAPHIC AND CLINICAL CHARACTERISTICS OF FOUR COHORTS

	Discovery Cohort	Replication Cohort 1	Replication Cohort 2	Replication Cohort 3
Duration (wks)	12	6	6	12
Total N	139	73	40	92
Female N (%)	58 (41.7)	28 (38.4)	18 (45.0)	39 (42.4)
Male N (%)	81 (58.3)	45 (61.6)	22 (55.0)	53 (57.6)
Age (SD)	13.38 (3.75)	33.48 (8.33)	35.20 (11.33)	26.02 (5.17)
Age range	4 - 19	18 - 58	18 - 62	18-40
% Caucasian	77 (55.4)	51 (69.9)	40 (100)	92 (100)
% African American	22 (23.0)	22 (30.1)	0	0
% other	30 (21.6)	0	0	0
Clozapine N (%)	0	73 (100.0%)	0	0
Risperidone N (%)	84 (60.4)	0	20 (50.0)	0
Aripiprazole N (%)	30 (21.6)	0	15 (37.5)	0
Quetiapine N (%)	25 (18.0)	0	5 (12.5)	25 (33.7)
Haloperidol N (%)	0	0	0	31 (27.2)
Amisulpride N (%)	0	0	0	21 (22.8)
Ziprasidone N (%)	0	0	0	15 (16.3)
rs489693 CC N (%)	58 (41.7)	36 (49.3)	17 (49.3)	46(50.0)
rs489693 AC N (%)	66 (47.5)	26 (35.6)	17 (35.6)	39 (42.4)
rs489693 AA N (%)	15 (10.8)	11 (15.1)	5 (15.1)	7 (7.6)

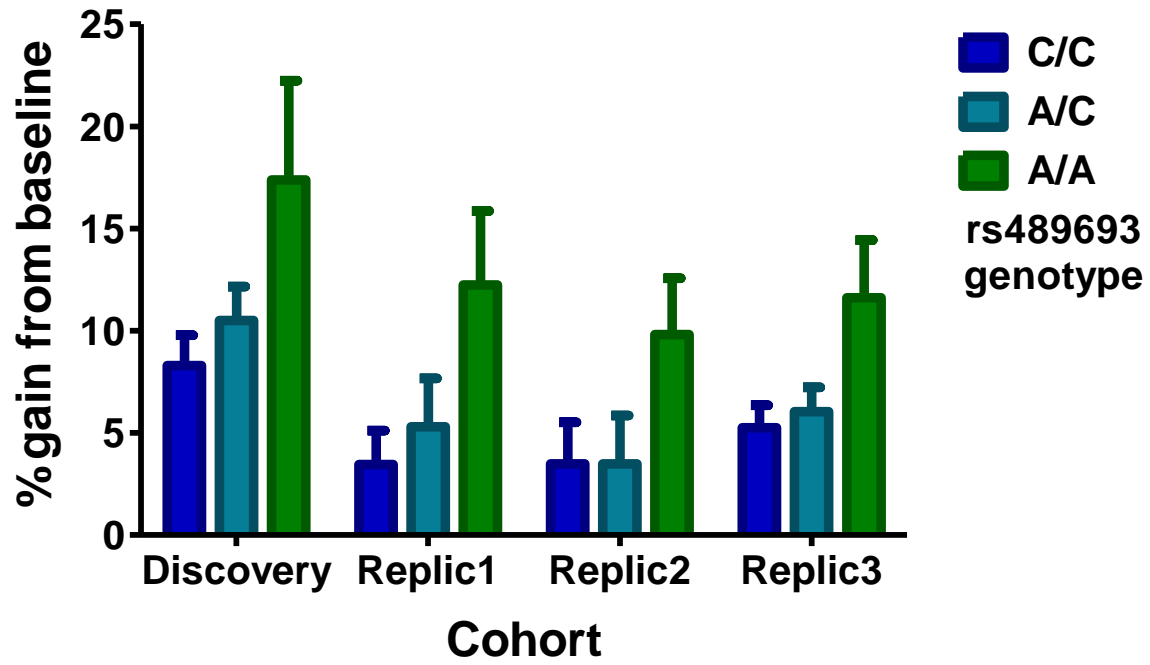
Supplemental Table 2. Diagnoses of Discovery Cohort.

<i>Dx</i>	<i>n</i>	<i>%</i>
Asperger's Disorder	3	2.2
Autistic Disorder	3	2.2
Bipolar Disorder	20	14.4
Brief Psychotic Disorder	1	0.7
Depressive Disorder NOS	5	3.6
Major Depressive Disorder	21	15.1
Mood Disorder NOS	18	12.9
Oppositional Defiant Disorder	20	14.4
Pervasive Developmental Disorder NOS	9	6.5
Psychotic Disorder NOS	30	21.6
Schizophrenia	7	5.0
Schizophreniform Disorder	1	0.7
Tourette's Disorder	1	0.7



Supplemental Figure 1. Linkage Disequilibrium Plot.

Linkage disequilibrium for the SNPs listed in Table 1A. Top half displays D' values, which are at or near 1 across the region, demonstrating that alleles tend to travel upon the same haplotypes. Bottom half displays r^2 values, which vary based on differing minor allele frequencies as listed in Table 2. Green star indicates location of best-replicated SNP in the present study (rs489693); red star indicates location of top SNP emerging from GWAS in the discovery cohort (rs1942876); blue star indicates location of top SNP emerging from large-scale GWAS of BMI in the general population (rs17782313; Loos et al. 2008)



Supplemental Figure 2. rs489693 genotype and percent change in weight from baseline for four cohorts.