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Variability in Working Memory Performance Explained by Epistasis versus Polygenic Scores in the *ZNF804A* Pathway

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Abstract

Importance—We investigated the variation in neuropsychological function explained by risk alleles at the psychosis susceptibility gene ZNF804A and its interacting partners using single nucleotide polymorphisms (SNPs), polygenic score and epistatic analyses. Of particular importance was the relative contribution of the polygenic score versus epistasis in variation explained.

Objective—The objectives were twofold: first, to assess the association between SNPs in ZNF804A and the ZNF804A polygenic score with measures of cognition in cases with psychosis. The second was to assess whether epistasis within the ZNF804A pathway could explain additional variation above and beyond that explained by the polygenic score.

Design, Setting and Participants—Patients with psychosis (N = 424) were assessed in areas of cognitive ability impaired in schizophrenia including IQ, memory, attention and social cognition. We used the Psychiatric GWAS Consortium (PGC1) schizophrenia GWAS to calculate a polygenic score based on identified risk variants within this genetic pathway. Cognitive measures significantly associated with the polygenic score were tested for an epistatic component using a training set (N = 170), which was used to develop linear regression models containing the polygenic score and two-SNP interactions. The best-fitting models were tested for replication in two independent test sets of cases: 1) 170 individuals with schizophrenia or schizoaffective

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Conflict of interest
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disorder and 2) 84 patients with broad psychosis (including bipolar disorder, major depressive disorder and other psychosis).

Results—Higher polygenic scores were associated with poorer performance amongst patients on IQ, memory and social cognition, explaining 1-3% of variation on these scores (*p*-values ranged from 0.012-0.034). Using a narrow psychosis training set and independent test sets of narrow phenotype psychosis (schizophrenia and schizoaffective disorder), broad psychosis, and controls (N = 89) respectively, the addition of two interaction terms containing two SNPs each increased the R^2 for spatial working memory (SWM) strategy in the independent psychosis test sets from 1.2% using the polygenic score only to 4.8% (*p*-values = 0.11 and 0.0012), but did not explain additional variation in controls.

Conclusions and Relevance—These data support a role for the ZNF804A pathway in IQ, memory and social cognition in cases. Further we show that epistasis increases variation explained above the contribution of the polygenic score.

Keywords

schizophrenia; working memory; epistasis; polygenic score; ZNF804A; cognition

Genome wide association studies (GWAS) have been at the forefront of identifying candidate genes for schizophrenia. One of the genetic variants achieving genome-wide significance for psychosis was rs1344706 in the zinc finger binding protein 804A (ZNF804A).[1] Several independent replication studies[2-3] and a recent meta-analysis[4] have supported an association between schizophrenia and the risk allele of this SNP. ZNF804A, which is expressed in the brain, is predicted to encode a protein with a C2H2 zinc finger domain. This suggests a role in the regulation of gene expression through DNA and/or RNA binding.[5] ZNF804A has been reported to show association with brain activity and structure[6-7]. A recent study by Hill and Bray[8] assessed the effects of its knockdown on the cellular transcriptome which linked ZNF804A to cell adhesion molecules, suggesting a role in neural migration, neurite outgrowth and synapse formation, which are hypothesized to be aberrant in schizophrenia.

Several studies have linked ZNF804A to cognition, based on imaging studies[6,9], traditional neuropsychological measures[10-12] and measures of social cognition.[13-14] The results of these studies deviate from what would be expected, in that whilst the rs1344706 risk allele appears to convey impairments in cognition in controls based on behavioural and imaging studies[11,15-17], the literature points to preserved cognition in patients.[10,12,18-19] Although some studies suggest that ZNF804A is associated with impaired social cognition in control subjects, it is uncertain if ZNF804A might also confer a disadvantage to patients as only one study[14] has assessed patients. If ZNF804A confers risk of psychosis, why does the risk-allele carrying patient population show preserved cognitive function? The answer may lie in the impact of ZNF804A embedded within its functional pathway. The development of complex traits, such as psychosis, is likely to involve the contribution of a large number of independent and/or interacting genetic variants, mostly of modest effect. [20-21] In case-control analyses, polygenic scores (a simple or weighted summation of the top sets of SNPs) have been shown to predict case status in related disorders and explain a significant

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percentage of variability.[22] Limiting this polygenic risk score to include variants within genes shown to be altered by ZNF804A knockdown[8], we investigated whether more of the variance in patients' neuropsychological function can be explained than is explained by single variants. We used the *p*-values and odds ratios from the PGC1 schizophrenia case-control analysis[23] to rank SNPs for inclusion in the polygenic score. As variation in complex traits is thought to include both polygenic and epistatic components, we examined whether epistasis between SNPs within the ZNF804A pathway could explain variation above that explained by the polygenic score alone. We used half of the narrow psychosis (schizophrenia and schizoaffective disorder) set as a training set to test for pairwise epistasis among all SNPs included in the polygenic score, then assessed whether adding these interactions to the regression model containing the polygenic score increased the R^2 among three independent test sets including (1) additional narrow psychosis cases, (2) broad psychosis (bipolar disorder, major depressive disorder and psychosis NOS), and (3) healthy controls.

Materials and methods

Participants

Four hundred and twenty-four cases and 89 healthy participants who completed a full neuropsychological assessment battery and for whom GWAS data were available were included. Cases were clinically stable patients with a DSM-IV diagnosis of schizophrenia (SZ, N = 282), schizoaffective disorder (SZA, N = 58), bipolar disorder (BP, N = 61), major depressive disorder with psychotic features (MDD, N = 11) or psychosis not otherwise specified (PNOS, N = 12) (Table 1) recruited from five sites across Ireland. Inclusion criteria required that participants were clinically stable at neuropsychological assessment, aged 18 to 65 years, had no history of co-morbid psychiatric disorder, no substance abuse in the preceding six months, prior head injury with loss of consciousness or history of seizures. Diagnosis was confirmed by trained psychiatrists using the SCID.[24] Additional diagnostic details and clinical sample characteristics including symptom severity (SAPS/SANS)[25-26] and medication dosage are detailed elsewhere.[10] Healthy control participants were recruited via online and poster advertising. They were aged 18 to 65 years, with no history of substance abuse in the preceding six months, no prior head injury with loss of consciousness, history of seizures or personal history of psychosis or their first-degree relatives. All assessments were conducted in accordance with the relevant ethics committees' approval from each participating site. All participants had four grandparents born in Ireland and provided written informed consent.

Cognitive assessment

Participants completed a neuropsychological assessment battery designed to target the cognitive deficits of schizophrenia including general cognitive function, episodic memory, working memory, attentional control and social cognition. General cognitive functioning (IQ) was measured using selected subtests (Vocabulary, Similarities, Block Design and Matrix Reasoning) from the Wechsler Adult Intelligence Scale[27], yielding a full scale, verbal and performance IQ. Episodic memory was assessed using the logical memory subtest from the Wechsler Memory Scale (WMS-III).[28] Working memory was assessed

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using the spatial working memory task (SWM) from the Cambridge Automated Neuropsychological Test Battery (CANTAB)[29] and letter number sequencing (LNS) from WMS-III.[28] Attentional control was assessed using the continuous performance task identical pairs version (CPT-IP)[30], the intradimensional-extradimensional shift task (IDED) (CANTAB)[29] and the sustained attention to response task (SART).[31] Social cognition was assessed using the reading the mind in the eyes task[32] and the IPSAQ[33], which yields two bias scores; externalising bias (EB), which indicates a propensity to attribute positive events to oneself rather than to other people, and a personalising bias (PB), which indicates a propensity to attribute negative events to other people rather than to situational factors.

Genotyping

Genotyping was conducted on DNA extracted from blood in patients and saliva in controls. SNP data was obtained from a recent GWAS using the Affymetrix SNP Array 6.0 platform, conducted as part of the Wellcome Trust Case Control Consortium 2 (WTCCC2), described in detail elsewhere.[34]

Statistical analysis

Polygenic score calculation—Polygenic scores[22] for variants located within the ZNF804A pathway were calculated starting with all available SNPs within 20Kb of genes in the ZNF804A pathway[8] (Supplementary Table 1). Target alleles at these SNPs were identified as risk-associated based on the PGC1 GWAS. Two polygenic scores for each individual were calculated. The count polygenic score was based on the simple sum of the number of risk-associated alleles they carried averaged across the total number of valid genotypes for that individual. The weighted polygenic score was based on the count polygenic score, with the exception that each SNP was weighted by the log of the odds ratio from the PGC1. We used three *p*-value thresholds from the PGC1 case-control analysis as arbitrary thresholds as in previous polygenic analysis[22] (thresholds and N SNPs: $p < 1.0e^{-05}$, N = 10; $p < 0.05$, N = 218; $p < 0.50$, N = 1525). As individual ZNF804A SNPs have been associated with cognition, we examined whether association observed between the pathway-based polygenic score remained after removing all ZNF804A SNPs (N = 27). A subset of the WTCCC2 sample was included in the PGC1 schizophrenia case-control analysis, thus the samples are not entirely independent. However, the outcome of interest in the PGC1 was case status, whereas in the present study the outcome of interest is cognition in cases with psychosis. As suggested in Supplementary Materials of the original polygenic score report[22], we used all genotyped SNPs in genes within the ZNF804A pathway without pruning for linkage disequilibrium.

Association analysis

Polygenic scores—Associations between ZNF804A polygenic score and the phenotypes of IQ, episodic memory, working memory, attention and social cognition were tested in multiple regression analyses implemented in SPSS 17[35] or the R Statistical Computing Environment.[36] In each case, scores for each neuropsychological phenotype were entered as dependent variables, controlling for age and gender as necessary.

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Polygenic scores plus epistatic effects—To test whether additional variation could be explained by epistasis beyond that explained by the polygenic score, we developed a novel approach within the context of the regression models described above. To reduce multiple testing, we restricted our search for epistasis to the models where the polygenic score accounted for a small but significant amount of variation in the neuropsychological phenotype in broad or narrow psychosis including SWM strategy, IPSAQ-EB, and performance IQ. First, we created equal-sized training and test sets from the narrow psychosis cases (N = 170). Second, to obtain a stable and consistent estimate of the *p*-value from two-SNP interactions, we took 100 bootstrap samples with replacement from the narrow psychosis training sample and performed linear regression analysis for all-possible pairs of SNPs falling under the threshold at hand (SWM threshold $p < = 0.05$, N SNPs = 218; IPSAQ-EB and performance IQ threshold $p < 1.0e^{-05}$, N SNPs = 10). For performance IQ and IPSAQ-EB, the 10 SNPs were all on chromosome 10 and in tight linkage disequilibrium (r^2 ranged from 0.6-1.0), which led to collinearity in the interactions and were not tested further. For SWM, the linear regression model in the training data contained the unweighted polygenic score plus an epistatic term which was the product of the risk-associated alleles at two SNPs. The unweighted polygenic score was used so the alleles comprising the score were on the same scale of measurement as those used in the interactions; however, the use of the weighted score did not change the results (discussed below). The average *p*-value from the 100 replicates was used to determine which interactions would be evaluated using the three independent test sets, using an uncorrected *p*-value < 0.05 threshold estimated from the training set. To account for linkage disequilibrium, a further condition was that only the interaction with the smallest *p*-value containing a particular SNP would be tested for replication in the independent test sets and all other interactions containing that SNP would not be considered for replication due to collinearity. This led to three significant two-SNP interaction terms, independent of one another, being brought forward for replication in the 3 test sets. R^2 values on the independent test sets were calculated as the square of the correlation between the fitted values for the test set based on the model estimated from the training data and the observed values from the test set.

Results

Demographic and clinical measures

Demographic and clinical characteristics for patients and healthy participants appear in Table 1. The characteristics of the broad psychosis group were compared to the narrow psychosis group and to the control group using *t*-tests. No significant differences were observed between the narrow and broad psychosis groups for age, gender, age at onset, full scale IQ, medication dosage as measured by chlorpromazine equivalents or positive and negative symptoms, with the exception of the ‘mania’ factor where the broad psychosis group scored significantly higher. The patient group contained significantly more males than the healthy group, was significantly older at the time of assessment and had a significantly lower full scale IQ.

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ZNF804A pathway polygenic score

ZNF804A weighted polygenic scores were associated (uncorrected *p*-value < 0.05) with measurements of both general and social cognition, including SWM, IPSAQ-EB and performance IQ, although the effect size was moderate (1.2%-3%) (Table 2; results for all phenotypes are in Supplemental Table 2). Larger ZNF804A polygenic scores were predictive of poorer performance on performance IQ in the broad psychosis group at the *p*-value threshold of $1.0e^{-05}$, but did not predict performance IQ in the narrow psychosis group (Table 2). The IPSAQ-EB demonstrated significant association with the ZNF804A polygenic score among broad and narrow psychosis at a *p*-value threshold of $1.0e^{-05}$. Patients with psychosis who had greater polygenic scores demonstrated a decreased IPSAQ-EB score suggesting that these patients were less likely to show what is known as a "self-serving" bias: the adaptive tendency to attribute causality for negative events to external factors and positive events to onself. Among both narrow and broad psychosis groups, a higher ZNF804A polygenic score led to significantly poorer performance on SWM strategy at a *p*-value threshold of 0.05.

To determine whether the polygenic score results were powered by ZNF804A SNPs, we excluded all variants in ZNF804A and reassessed association with the polygenic score; the results were virtually unchanged (Table 2) with the exception of SWM strategy, which showed a slightly reduced R^2 and larger *p*-value in the narrow psychosis set (results for all phenotypes are in Supplemental Table 3).

Epistasis within the ZNF804A pathway

As described above, we tested for additional variation in SWM explained by two-SNP epistasis in the narrow psychosis training set. Because of linkage disequilibrium, 112 average *p*-values across 100 bootstrap samples of the training set were less than 0.05, but of these, only three were completely independent of the other sets and thus only these three interaction terms were brought forward for replication in the three independent test sets. Beginning with SWM strategy, adding the most significant interaction (rs17186340:rs140512) to the model containing the polygenic count score led to an increase of 1.4% in the narrow psychosis test set (*p*-value = 0.050), 3.7% (*p*-value = 0.035) in the broad psychosis test set, and a combined case test set increase of 2.3% (*p*-value = 0.0064) (Table 3). Although adding this interaction increased the variation explained in two independent sets of cases, it did not increase variation explained in controls (R^2 = 0.0069, *p*-value = 0.45). Adding a second interaction term to the model (rs2295984:rs34138673) further increased the variation explained in cases: in the narrow psychosis test set the R^2 increased by 1.3% (*p*-value = 0.016) to a total of 4.0%, in the broad psychosis test set the R^2 increased further by 1.2% (*p*-value = 0.036) for a total variation explained of 6.2%, and in the combined set of cases the R^2 increase was 1.3% (*p*-value = 0.0012) for a total of 4.8%. In controls, the adding the second interaction did not increase the variation explained (R^2 = 0.001, *p*-value = 0.77). The third epistatic term did not increase the R^2 values in any independent test set and thus was not considered further.

To test whether the increase in R^2 was attributable to strongly associated SNPs contained in the interactions themselves, interaction SNPs were tested individually for association with

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SWM strategy in a model containing the polygenic count score. Two SNPs were associated with SWM strategy at an uncorrected *p*-value of < 0.05 and both were in the second interaction term: rs17186340:rs34138673. The improvement in R^2 values from the narrow psychosis training set model containing the polygenic count score plus rs17186340 on the narrow psychosis, broad psychosis and total test cases set were $5.89e^{-06}$, $9.1e^{-04}$ and $8.0e^{-05}$, respectively. Results for the same analysis using rs34138673 were 0.0056, 0.013 and 0.0079, indicating that the interaction term explained more variation than either single SNP.

To see whether the type of polygenic score influenced the amount of variation explained, the weighted polygenic score was substituted for the count polygenic score and R^2 values were calculated for the case test sets. In the narrow psychosis test set, the use of the weighted polygenic score in the three models (polygenic-only, one and two interactions) increased the R^2 value by $9.1e^{-04}$ - 0.001 versus models containing the count polygenic score, whereas the use of the weighted polygenic score in broad psychosis reduced the R^2 value by $4.7e^{-04}$ - 0.0061 versus the count polygenic score, suggesting the choice of polygenic score was trivial in this instance. When strongly-associated SNPs with very large or very small effect sizes (ORs) are present we would expect to see differences between using the count or weighted score.

Discussion

We used polygenic scores to investigate whether ZNF804A pathway schizophrenia risk-associated alleles were associated with neuropsychological function amongst 424 psychosis patients. Higher ZNF804A polygenic scores were significantly associated with poorer performance in IQ, working memory, and biased social cognition, and explained 1-3% of the variation in these measures, consistent with estimates previously reported in general intelligence in controls.[37] Removal of the SNPs within ZNF804A reduced the R^2 values only slightly, suggesting the combined contribution of genes within the pathway was driving the association. Further, we showed that considering epistasis along with the polygenic score resulted in over three times the amount of variation explained in two independent test sets of cases (total R^2 ranged from 4.0-6.2%). Since the SNPs participating in interactions were not in ZNF804A, we provide further evidence that this gene was not the key contributor to our pathway-based results. Thus, our findings are not inconsistent with previous studies showing preserved cognitive function in cases is associated with ZNF804A. Although the polygenic score explained a similar amount of variation in controls, improvements due to epistasis were specific to psychosis cases.

Although previous studies have shown that the risk allele of ZNF804A rs1344706 shows differential effects in cases and controls[10-19], we show that, at the pathway level, the effect of the combination of schizophrenia risk alleles leads to poorer performance in patients with psychosis on measures of intelligence, working memory and social cognition. The 4 SNPs participating in epistasis that increased the R^2 values in our test sets were near STAC (rs17186340), MAPK8IP2 (rs140512) and flanking either side of FAM46A (rs2295984 and rs34138673). In mice, Stac is expressed in brain, neurons and postsynaptic densities and within the brain the expression is highest in the hippocampus and cerebellum.[38-39] A Stac

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knockout mouse model showed reduced social interaction, impaired learning, and deficits in exploration of novel environments.[39] MAPK8IP2 is located within the Chr22q13.3 deletion region associated with autism spectrum disorders and Phelan-McDermid syndrome, which is characterised by developmental delay. Also known as JIP2, it is a scaffold protein that is necessary for N-methyl-D-aspartic acid (NDMA) receptor function and modulates signal transduction.[40] FAM46A is expressed in adult human brain and shows higher expression in human fetal brain.[41] The SNPs participating in the second interaction term, rs2295984 and rs34138673, are located on either side of FAM46A, approximately 19.5K bp apart, possibly indicating a promoter and/or enhancer role.

How can we reconcile previous research that has shown the risk allele at ZNF804A rs1344706 is associated with less impaired cognition in psychosis patients with the results of the present study, which showed that the polygenic score from the ZNF804A pathway was associated with poorer performance IQ, working memory, and social cognition? The *p*-values from the PGC1 were used to select SNPs for inclusion in the polygenic score, and the smallest ZNF804A *p*-value was 0.0015 for rs1344706. Therefore, the set with the most stringent threshold did not include any ZNF804A SNPs, and this set was negatively associated with IQ and social cognition. For working memory, the removal of the ZNF804A SNPs at a *p*-value threshold of 0.05 would have included 12 of the 27 SNPs with p-values ranging between 0.002-0.05. We have shown that the removal of these SNPs did not lead to significant differences in the magnitude of association between the polygenic score and working memory. The use of the weighted polygenic score would have ensured a weak contribution of these SNPs as they were not strongly associated with schizophrenia in the PGC1 and they comprised only 5.5% of the total number of SNPs at that threshold. Interestingly, the PGC *p*-values for the 4 SNPs participating in epistasis ranged between 0.007 (rs2295984) to 0.043 (rs17186340), showing that although they are marginally associated with schizophrenia they would not have been considered for follow-up. As was the case with the previous use of the polygenic score[22], we showed that the polygenic score and epistatic models based on a narrow psychosis training sample was able to significantly account for variation in working memory in two independent psychosis samples, but not able to predict variation in controls. Although the control sample size was modest (N = 89) the broad psychosis sample was of a similar size (N = 84) so a lack of statistical power cannot fully explain the inability to account for additional variation in controls.

Interestingly, the 10 SNPs in linkage disequilibrium that comprised the most strongly associated polygenic score for IPSAQ-EB and performance IQ included 5 SNPs in CNNM2 and 5 SNPs either 3′ or 5′ of the gene. This gene is strongly associated with schizophrenia[23,42-43] and we and other groups have shown variation within the gene is associated with gray matter volume in schizophrenia patients[44-45] and with attributional style.[45] Our results support a polygenic contribution of variation within and around this gene weakly contributing to attributional style and performance IQ.

We have introduced a novel method to evaluate the combined effect of the polygenic score and epistasis which is both simple and computationally tractable. The addition of the epistatic terms also increased the interpretability of the model, as it is difficult to determine which genes were contributing signal to the polygenic score. We show the results estimated

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on the training sample were generalizable to two independent test sets of patients – one with narrow psychosis and the other with non-schizophrenia psychosis – similar to previous studies' use of the polygenic score.[22] In both instances the variation explained by our epistatic terms was much larger than that explained by the polygenic score itself: the polygenic score explained between 1.2-1.3% of variation whereas increases in R^2 using our novel approach in the test sets were between 2.7-4.9%. Epistasis is thought to be a key element in complex phenotypes[20-21] and has been shown to influence risk for schizophrenia and inefficient dorsolateral prefrontal cortex processing during a working memory task in healthy controls.[20-21,46-47] The potential limitations of our study include modest sample sizes and the fact that we may not have captured all variation (especially rare variation) in the genes in the ZNF804A pathway due to our reliance on SNPs from a GWAS.

In conclusion, this study is the first, to our knowledge, to investigate the role of the ZNF804A pathway in the cognitive decline commonly observed amongst psychotic patients. We have identified three new candidate genes for working memory in the ZNF804A pathway: STAC, MAPK8IP2 and FAM46A. Perhaps more critically, we introduced an improvement in the use of polygenic scores by adding an epistatic component which explained additional variation in working memory that was specific to cases with psychosis.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Table 1
Participant demographics, neurocognitive and clinical measures

	Patients		Healthy participants
	Psychosis narrow	Psychosis broad	
	N=340	N=424	N=89
Psychosis subtype			
SZ	N = 282	N = 282	N/A
SZA	N = 58	N = 58	
BP		N = 61	
MDD		N = 11	
PNOS		N = 12	
Gender (ratio; M:F)	2.6:1	2.2:1	1.4:1
Age (years; mean (SD))	41.3 (12.2)	41.3 (12.4)	36.27 (12.8)
Age at onset (years; mean(SD))	22.8 (7.2)	23.2 (7.5)	N/A
Chlorpromazine equivalent (mg/day; mean(SD))	589.8 (562.4)	555.5 (540.7)	N/A
SAPS/SANS:			N/A
Manic (mean (SD))	−0.18 (0.95)	0.04 (1.09)	
Depression (mean (SD))	0.16 (1.07)	0.23 (1.06)	
Positive (mean (SD))	−0.02 (0.99)	−0.12 (0.95)	
Disorganised (mean (SD))	−0.22 (0.76)	−0.31 (0.78)	
Negative (mean (SD))	0.39 (0.9)	0.32 (0.87)	
Cognition: full scale IQ (mean (SD))	89.6 (17.8)	90.3 (18.3)	124.6 (13.3)

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Table 2

Significant variance explained (R^2) and associated *p*-value for ZNF804A polygenic score regression on neuropsychological phenotypes[a]

Phenotype	Narrow Psychosis			Broad Psychosis		
***p*-value threshold**	**0.00001**	**0.05**	**0.5**	**0.00001**	**0.05**	**0.5**
Including ZNF804A: Performance IQ (R^2, (*p*-value))	0.009 (0.26)	0.001 (0.51)	0.002 (0.41)	**0.012 (0.028)**	< 0.001 (0.78)	0.004 (0.21)
Including ZNF804A: IPSAQ EB (R^2, (*p*-value))	**0.030 (0.012)**	0.0070 (0.21)	0.0030 (0.43)	**0.025 (0.010)**	0.0040 (0.28)	0.0030 (0.39)
Including ZNF804A: SWM Strategy (R^2, (*p*-value))	0.010 (0.09)	**0.017 (0.028)**	0.003 (0.35)	0.0040 (0.23)	**0.013 (0.034)**	0.0020 (0.41)
Excluding ZNF804A: SWM Strategy (R^2, (*p*-value)) [b]	0.010 (0.11)	**0.017 (0.028)**	0.003 (0.36)	0.0040 (0.23)	0.011 (0.052)	0.0010 (0.47)

[a] Bolded items indicate P < 0.05, uncorrected.

[b] Only the significant *p*-value threshold for SWM strategy (*p*-value < 0.05) included ZNF804A SNPs.

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Table 3

Increase in R^2 values using epistasis in conjunction with ZNF804A polygenic scores across the narrow psychosis test set and broad psychosis set

Model	Narrow Train R^2	Narrow Train p-value	Narrow Test R^2	Narrow Test *p*-value	Broad R^2	Broad *p*-value	Total Test Cases R^2	Total Test Cases *p*-value	Control R^2	Control *p*-value
Polygene Count Score	0.017	0.12	0.013	0.17	0.013	0.34	0.012	0.11	0.03	0.11
Polygene Count Score + rs17186340T:rs140512A	0.13	6.70E-005	0.027	0.05	0.05	0.06	**0.035**	**0.0064**	0.0069	0.45
Polygene Count Score + rs17186340T: rs140512A + rs2295984T:rs34138673G	0.16	2.70E-005	**0.04**	**0.016**	**0.062**	**0.036**	**0.048**	**0.0012**	0.001	0.77