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Poor replication of candidate genes for major depressive disorder using genome-wide association data

Fokko J Bosker PhD^{1*}, Catharina A Hartman PhD^{1*}, Ilja M Nolte PhD^{2*}, Bram P Prins MSc², Peter Terpstra PhD², Danielle Posthuma PhD^{3,4}, Tineke van Veen PhD⁵, Gonneke Willemsen PhD³, Roel H DeRijk PhD⁵, Eco J de Geus PhD³, Witte J Hoogendijk MD, PhD⁶, Patrick F Sullivan MD⁷, Brenda W Penninx PhD^{1,5,6}, Dorret I Boomsma PhD³, Harold Snieder PhD^{2*}, Willem A Nolen MD, PhD^{1*}

¹ Department of Psychiatry, University Medical Center Groningen, University of Groningen, The Netherlands

² Unit of Genetic Epidemiology & Bioinformatics, Department of Epidemiology, University Medical Center Groningen, University of Groningen, The Netherlands

³ Department of Biological Psychology, Vrije Universiteit Amsterdam, The Netherlands

⁴ Depts of Medical and Functional Genomics, VU University Medical Center, Amsterdam, The Netherlands

⁵ Department of Psychiatry, Leiden University Medical Center, Leiden, The Netherlands

⁶ Department of Psychiatry, VU University Medical Center, Amsterdam, The Netherlands

⁷ Department of Genetics, University of North Carolina, Chapel Hill, NC, USA

* These authors contributed equally

Corresponding author:

Fokko J Bosker: Department of Psychiatry, University Medical Center Groningen, University of Groningen, PO Box 30.001, 9700 RB Groningen, The Netherlands, email f.j.bosker@psy.umcg.nl

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Abstract

Data from the GAIN genome-wide association study (GWAS) in major depressive disorder (MDD) were used to explore previously reported candidate gene and SNP associations in MDD. A systematic literature search of candidate genes associated with MDD in case-control studies was performed before the results of the GAIN MDD study became available.

Measured and imputed candidate SNPs and genes were tested in the GAIN MDD study encompassing 1,738 cases and 1,802 controls. Imputation was used to increase the number of SNPs from the GWAS and to improve coverage of SNPs in the candidate genes selected. Tests were carried out for individual SNPs and the entire gene using different statistical approaches, with permutation analysis as the final arbiter.

Seventy-eight papers reporting on 57 genes were identified, from which 92 SNPs could be mapped. In the GAIN MDD study, two SNPs were associated with MDD: *C5orf20* (rs12520799; $p=0.038$; OR AT=1.10, 95% CI 0.95-1.29; OR TT=1.21, 95% CI 1.01-1.47), and *NPY* (rs16139; $p=0.034$; OR C allele=0.73, 95% CI 0.55-0.97) constituting a direct replication of previously identified SNPs. At the gene level, *TNF* (rs76917; OR T=1.35, 95%CI 1.13-1.63; $p=0.0034$) was identified as the only gene for which the association with MDD remained significant after correction for multiple testing. For *SLC6A2* (NET) significantly more SNPs (19 out of 100; $p=0.039$) than expected were associated while accounting for the linkage disequilibrium structure. Thus, we found support for involvement in MDD for only 4 genes. However, given the number of candidate SNPs and genes that were tested, even these significant may well be false positives.

The poor replication may point to publication bias and false-positive findings in previous candidate gene studies, but may also be related to heterogeneity of the MDD phenotype as well as contextual genetic or environmental factors.

Keywords: candidate genes, genome-wide association study, major depressive disorder, replication, single nucleotide polymorphisms

Introduction

Major depressive disorder (MDD) is a multi-factorial disease, with both genetic and environmental factors likely to play a role in its etiology. The Netherlands Study of Depression and Anxiety (NESDA; www.nesda.nl) and the Netherlands Twin Registry (NTR; www.tweelingenregister.org) took part in the Genetic Association Information Network (GAIN; <http://www.fnih.org/GAIN>) project to enable a genome-wide association study (GWAS) using a 600K Perlegen chip ¹. Within the GAIN MDD study ² 1862 participants with a diagnosis of MDD and 1860 controls at low liability for MDD were selected for genome-wide genotyping.

A GWAS approach allows a hypothesis-free search for potential new susceptibility genes. The downside of a GWAS is that a strict statistical adjustment for the large number of single nucleotide polymorphisms (SNPs; in the GAIN MDD study 435,291 SNPs) is required before associations can be considered significant on a genome-wide level ³ and replication of such findings in independent cohorts is mandatory to exclude false positive findings ⁴.

Another potential use of a GWAS is to use the results for a large-scale replication study of previous candidate gene studies. Application of such prior knowledge within the context of a GWAS allows less stringent significance thresholds than those for the hypothesis-free GWAS analysis ^{5,6}. So far, the role of candidate genes in MDD has been the subject of many association studies. Unfortunately, there is little consistency between candidate gene studies for multifactorial diseases such as MDD (e.g., ^{7,8}).

In the current study we attempted to replicate significant findings from previous candidate gene studies in MDD. To this end we conducted a systematic review of the literature and selected those genes that were reported to be significantly associated with MDD at least once. The GWAS data from the GAIN MDD study were used to screen all the identified candidate genes in two ways: 1) for association with the specific SNPs reported in the literature; and 2) for association with any of the SNPs (genotyped or imputed) from the Perlegen chip within the identified genes.

Materials and methods

Selection of studies reporting on candidate genes

In order to prevent any bias from the results of the GAIN MDD study, we identified candidate genes for MDD before the results from the GAIN MDD study became available. Therefore, a so called “enhanced search” was performed in Medline® via Pubmed on September 1, 2007 using the following search terms: (("genes"[TIAB] NOT Medline[SB]) OR "genes"[MeSH Terms] OR gene[Text Word]) OR ("genes"[MeSH Terms] OR genes[Text Word]) OR snp[All Fields] OR ("single nucleotide polymorphism"[Text Word] OR "polymorphism, single nucleotide"[MeSH Terms] OR snps[Text Word]) OR ("genetic polymorphism"[Text Word] OR "polymorphism, genetic"[MeSH Terms] OR polymorphism[Text Word]) OR polymorphisms[All Fields] AND ("major depressive disorder"[Text Word] OR "depressive disorder, major"[MeSH Terms] OR major depression[Text Word]) AND "humans"[MeSH Terms]. This resulted in 641 hits. We additionally scrutinized the reference list of the meta-analysis of genetic studies on MDD by Lopez-Leon and colleagues⁹ that appeared on-line on 16 October, 2007, shortly after the end date of our search, resulting in an additional 39 hits of possibly relevant papers. These authors used somewhat broader search terms than we did, and their search ran until June 2007; Therefore, as a final check, we searched the literature using their search terms for the period June 2007-September 2007 not covered in their paper. This yielded an additional 110 hits. Of all these papers we retrieved the abstracts, and if considered relevant, the full paper.

In the next step, we selected all papers fulfilling the following five inclusion criteria: 1) the study had to be a candidate gene case-control association study. Linkage and fine-mapping studies were excluded; 2) the primary diagnosis of the patients in the candidate gene study had to be MDD to enable comparison with the GAIN MDD study. Therefore, we excluded studies involving patients (i) with a depressive episode in the course of bipolar disorder, (ii) with a primary psychotic disorder such as schizophrenia and a secondary depression, (iii) with a seasonal affective disorder not being MDD with a seasonal pattern,

(iv) with a primary anxiety disorder (i.e. panic disorder, agoraphobia or social phobia) or obsessive compulsive disorder and a secondary depression, and (v) with MDD plus an additional specific comorbid disorder or condition, e.g. MDD plus alcoholism. However, we allowed subgroups within MDD, e.g. MDD in women or in men, recurrent MDD, or early onset MDD; 3) the sample of a specific study consisted of at least 30 patients with MDD and 30 healthy controls; 4) the findings on the association with MDD of any variant within the candidate gene (either a SNP, a microsatellite marker or a haplotype) had reached a statistical significance at the level of $p < 0.05$; and 5) the genetic association had to be with the diagnosis of MDD and not with other aspects such as associated personality features (e.g. neuroticism) or factors related to treatment response. This resulted in 78 papers.

In order not to miss potential true positive findings, we did not exclude candidate genes with associated markers that had low allele frequencies or that deviated from Hardy-Weinberg equilibrium. Two investigators (FB, CH) independently made a selection from the initial list of papers using the abovementioned criteria. When both reached consensus, the paper was included or excluded; in case of disagreement, consensus was obtained with assistance of two other authors (WN, HS). As a final step, one author (IN) double checked whether all selected papers fulfilled the aforementioned selection criteria 1 through 5. Figure 1 shows a flowchart of how we retrieved the 78 papers for the present study.

Bioinformatic tools

For many SNPs no reference SNP identification number (rs-id) was given in the original papers, but codes based on position (e.g., 677C/T in *MTHFR* or Tyr129Ser in *HTR3B*) or even own codes (e.g., s1-s5 in *AVPR1B*). In order to retrieve rs-ids for these SNPs, we used searches in PubMed or in NCBI's dbSNP database (<http://www.ncbi.nlm.nih.gov/SNP/>) using the "Geneview" option in conjunction with NCBI's MapViewer with the human genome assembly build 37.1 (<http://www.ncbi.nlm.nih.gov/projects/mapview/map>). Six SNPs remained that could not be easily found in this way. We contacted the corresponding authors of the papers and used NCBI's Primer-Blast and SNP-Blast

(<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) to map these SNPs using the provided primer sequences.

Sample

The 1,862 MDD cases included in the GAIN MDD study were mainly from NESDA, a longitudinal cohort study designed to be representative of individuals with depressive and/or anxiety disorders¹⁰ and were recruited from mental health care organizations (N=785), primary care (N=603), and community samples (N=314). Additional cases came from the NTR (N=160). Regardless of recruitment setting, similar inclusion and exclusion criteria were used to select MDD cases. Inclusion criteria were a lifetime diagnosis of MDD according to DSM-IV¹¹ as diagnosed via the Composite International Diagnostic Interview (CIDI Version 2.1.¹²), age 18-65 years, and self-reported western European ancestry. Persons who were not fluent in Dutch and those with a primary diagnosis of a psychotic disorder, obsessive compulsive disorder, bipolar disorder, or severe alcohol or substance use disorder were excluded.

Most of the 1,860 control subjects were from the NTR (N=1,703) and additional controls from NESDA (N=157). Longitudinal phenotyping in NTR includes assessment of depressive symptoms (via multiple instruments), anxiety and neuroticism. Inclusion required no report of MDD at any measurement occasion and never scoring high (>0.5 SD) on a general factor score based on combined measures of neuroticism, anxiety and depressive symptoms. Finally, controls and their parents were required to have been born in the Netherlands or Western Europe. Only one control per family was selected. NESDA controls had no lifetime diagnosis of MDD or an anxiety disorder as assessed by the CIDI and reported low depressive symptoms at baseline. For more details see².

Genotyping

Perlegen Sciences (Mountain View, CA, USA) performed all genotyping according to strict standard operating procedures. DNA samples from cases and controls were randomly

assigned to plates, shipped to Perlegen and identified only by barcode. High-density oligonucleotide arrays were used yielding 599,164 SNPs. Eight SNPs with duplicate numbers were deleted and 73 mitochondrial SNPs were removed for later analysis. From the remaining 599,083 SNPs on the Perlegen chip 435,291 passed quality control. Two hundred eighty subjects were excluded because of various quality control issues leaving 1,738 cases (93.4%) and 1,802 controls (96.9%) in the final analysis dataset. For more details see ^{2,4}.

Imputation

Not all SNPs selected from the literature were present on the genotyping array. Based on the linkage disequilibrium (LD) structure between SNPs we followed an imputation procedure to predict non-genotyped SNPs using the HapMap CEU data (release 22, build 36) as the reference database. The imputation was performed by IMPUTE version 0.3.2 using the default settings and the recommended number 11418 for the effective population size of Caucasians ¹³. In this way we extended the genome-wide autosomal SNP dataset from 427,049 to 2,467,430 SNPs. For our candidate genes this meant an extension from 851 to 4,955 SNPs. However, the quality of the imputation was low for 85 SNPs (SNPTEST proper_info <0.5). These SNPs were excluded leaving 4,870 SNPs for analysis. No SNP had a minor allele frequency <1%.

Association test

Association between MDD and the autosomal SNP data was tested by means of a frequentist case-control test provided in the software package SNPTEST version 1.1.4 using allele dosages with sex as a covariate in order to adjust for the slight imbalance in percentage of females between cases (69.6%) and controls (62%) ^{2,4} and the “proper” option to account for the uncertainty of the genotypes that were imputed ¹³. In addition, 7,988 genotyped SNPs on the X chromosome were analyzed in PLINK version 1.03 ¹⁴ by means of logistic regression with sex as a covariate. SNPs on the Y chromosome (n=15) and SNPs mapped to ambiguous locations (n=239) were not analyzed.

Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated for the significant candidate SNPs according to the disease model from the original article using counted or estimated numbers for genotyped or imputed SNPs, respectively. In order to establish true replication, we checked whether the effect was for the same allele and in the same direction.

Permutation procedure

In order to facilitate interpretation of the significance of our findings for each SNP we calculated three p-values by permutation: (i) a crude uncorrected significance; (ii) a gene-wide significance (corrected for all SNPs in the gene), and (iii) an overall significance (corrected for all SNPs in all selected genes). The crude uncorrected p-value was determined as the fraction of permutations that yielded a p-value that was smaller than the observed one. This p-value was determined in order to validate the permutation procedure since it should be similar to the p-value calculated by SNPTEST or PLINK. The gene-wide significance of a particular SNP was defined as the fraction of permutations that the p-value of any SNP in the candidate gene concerned was smaller than the one observed for that SNP. This procedure corrects the p-value for testing multiple SNPs within a gene. Based on the rationale that each selected gene is a candidate for MDD (hypothesis-driven) no correction for all SNPs in the entire gene set is necessary. Nonetheless, we also calculated an overall significance (i.e., corrected for all SNPs in all candidate genes) by determining an overall p-value for each SNP as the fraction of permutations for which any of the SNPs in any of the candidate genes had a p-value smaller than the observed one. For each of the three p-values we conducted 10,000 permutations. Case-control status was randomly permuted within males and females separately, hence leaving the number of affected males and females intact.

In addition to the three SNP specific p-values, we also determined whether the number of SNPs within a candidate gene with an original p-value <0.05 based on SNPTEST or PLINK (see above) was higher than expected. For each permutation the number of SNPs

in each candidate gene that was significant at 0.05 was recorded. The fraction of permutations with a higher number of significant SNPs than originally observed determined the significance of the number of significant SNPs of that candidate gene. By permuting case-control status the LD structure of the genes is preserved, that is, the resulting significance is corrected for possible high correlation between SNPs. The number of permutations for this test was 10,000 as well.

Results

Literature search

The 78 papers which resulted from our systematic literature search reported 115 statistically significant differences between MDD cases and healthy controls in 57 genes: for 96 SNPs, 7 microsatellite markers (i.e., length polymorphisms), 11 haplotypes, and one protein polymorphism in the haptoglobin gene¹⁵ (Table 1). Twenty-nine SNPs were identified by an rs-id, while 67 SNPs were only specified by a location code, restriction enzyme or author designed code. For 64 of these 67 SNPs, rs-ids could be obtained, while two rs-ids were not found (246G/A in *CCKAR*¹⁶ and -7054C/A in *DRD2*¹⁶). In addition, for SNP 1463G/A in *TPH2*, others have tried to replicate the association, but the SNP appeared to be non-existent^{17, 18}. Thus, we could map 93 SNPs.

For the 7 microsatellite markers no LD data with SNPs are known and hence we cannot determine whether these are covered by any of the available SNPs in the corresponding genes. Among them is the 5-HTTLPR 44 base pair deletion in the promoter region of the serotonin transporter gene *SLC6A4* (*SERT*), which has attracted considerable attention in various previous candidate gene studies for MDD.

Association in the GAIN MDD data with specific SNPs from the literature

Sixty one of the 93 selected SNPs in the 57 candidate genes were either present (n= 18) on the Perlegen array or could be imputed (n= 43). Four additional SNPs could be tagged by

other available SNPs (Table 2). Two of these were not genotyped in the CEU population of the HapMap Phase2 (release 22, build 36) project, but were available in the JPT and CHB populations in which they showed high LD ($r^2=0.97$ and 1.00 , respectively) with at least one other available SNP. The two other SNPs were genotyped in the CEU population and could be tagged by available SNPs with $r^2=1$, but were for unreported reasons not included in the HapMap reference file used for the imputation procedure as provided on the website of the imputation software package IMPUTE

(<http://www.stats.ox.ac.uk/~marchini/software/gwas/impure.html>). Twenty eight SNPs were neither genotyped directly nor imputed nor could be tagged, hence were not available for replication.

We investigated which of the 65 available or tagged SNPs could be confirmed in our data (Table 2). SNPs rs12520799 in *C5orf20* (*DCNP1*) ($p=0.038$; OR AT=1.10, 95% CI 0.95-1.29; OR TT=1.21, 95% CI 1.01-1.47) and rs16139 in *NPY* ($p=0.034$; OR C allele=0.73, 95% CI 0.55-0.97) replicated the reported effect in the literature. In addition, three SNPs in the *ACE* gene selected from the literature, which were in strong LD with each other ($r^2=0.78-1.00$), were also significant in the GAIN MDD sample (rs4333: $p=0.029$; rs4329: $p=0.030$; rs4461142: $p=0.036$). However these three SNPs showed effects in the opposite direction compared to previous results¹⁹ (Baghai, personal communication). Hence these SNPs do not represent a true replication.

Candidate genes from the literature in the GAIN MDD study

As in different populations different SNPs might play a role, we also studied all SNPs present on the genotyping array or available through imputation in an area from 5kb upstream to 5kb downstream of each selected candidate gene in order to cover the promoter and 3' untranslated region, respectively. Forty nine of the 57 genes were covered by one or more SNPs that were present on the Perlegen chip. For another six genes no genotyped SNPs were available but imputed ones were. Neither genotyped nor imputed SNPs were available for two genes (*AVPR1B* and *CHRFAM7A*). In total 4,870 SNPs, of which 820 were

genotyped and 4,019 were imputed, covered the 55 candidate genes ranging from 1 SNP for *AR* to 642 SNPs for *PDE11A* (Figure 2). We noted a significant correlation of 0.75 between gene size and the number of genotyped SNPs (including genes on the X chromosome) and a correlation of 0.96 between gene size and total number of SNPs (excluding genes on the X chromosome, since SNPs on the X chromosome were not imputed).

For 28 of the 55 genes one or more SNPs were found to be different between MDD cases and healthy controls in the GAIN MDD GWA scan at a significance level of $p < 0.05$ (Table 3). The remaining 27 genes were not associated with MDD as none of the SNPs reached $p < 0.05$. The smallest p-value was observed for SNP rs769178 in the *TNF* gene region ($p = 0.00029$; OR T allele = 1.35, 95%CI 1.13-1.63). The minor allele T was observed in 8.0% of the MDD cases and 6.1% of the controls.

With genes covered by a large number of SNP markers, the expected minimal p-value will decrease purely as a result of chance alone as a function of the number of SNPs. Thus, we used gene-wide p-values from the permutation procedure that corrects for the number of SNPs within a candidate gene and only SNP rs769178 in *TNF* remained significant ($p = 0.0034$) (Figure 3; Table 3). The second strongest associated SNP, which was observed in *DISC1* (rs7533169: p -value=0.0025), became non-significant after this correction (gene-wide p -value=0.28), because in this gene there were 491 SNPs and apparently the small p-value was observed purely based on chance. In addition to the gene-wide significance, we also determined overall significance per SNP accounting for testing 4,870 SNPs in 55 candidate genes. In that case none of the SNPs remained significant, not even the *TNF* SNP rs769178 (overall $p = 0.33$).

The significance levels per SNP are one way of testing the true value of the selected candidate genes. If many SNPs in a candidate gene are associated, this could also indicate potential involvement of a gene in the disorder under study²⁰. We noticed for instance that in the norepinephrine transporter *SLC6A2* (*NET*) 19 of the 100 SNPs were significant at a level of 0.05 (Table 3). The permutation procedure that tested whether the number of SNPs that were significant at 0.05 was larger than expected, revealed that this finding for *SLC6A2* was

indeed significant ($p=0.039$). Figure 4 shows that the 19 SNPs are scattered in the right half of the gene. Seventeen of them lie in three independent haplotype blocks and the other 2 SNPs are not in LD with the haplotype blocks or with each other. For none of the other candidate genes this permutation test revealed a significant result.

Discussion

Several genome-wide linkage studies of MDD have been published (reviewed in ²) but the GAIN MDD study is among the first genome-wide association studies (GWAS) in MDD ^{4,21}. We used these GWAS data as a large scale replication of previously reported significant findings from candidate gene studies in MDD. To this end, we first conducted a systematic review of the literature and identified a total of 57 genes for which a significant association with MDD has been reported at least once. Fifty-five of these genes could be included in our replication study, with either genotyped or imputed SNPs available from the GWAS data. With a sample size (1,738 cases and 1,802 controls) by far exceeding all previous candidate gene studies (with a mean sample size of 164 MDD cases and 252 controls, and only 1 study with > 1000 MDD cases and controls) ²², we found minimal support for involvement in MDD for only 4 out of 55 candidate genes: *C5orf20* ($p=0.038$), *NPY* ($p=0.034$), *TNF* ($p=0.0034$), and *SLC6A2* ($p=0.039$). Replication of these genes was based on three different statistical approaches. First, the involvement of *C5orf20* (rs12520799) and *NPY* (rs16139) constituted a direct replication at SNP level of previously identified SNPs associated with MDD. Second, studying the selected candidate genes for all SNPs present on the genotyping array, *TNF* (rs76917) was identified as the only gene for which the association with MDD remained gene-wide significant. Third, the potential involvement of *SLC6A2* (*NET*) in MDD was derived on the basis of a statistically significant number of SNPs (i.e., 19 out of 100) associated with MDD within this gene, which could not be explained solely by high LD between the SNPs. Note that the prior evidence in the selected studies for the involvement of *C5orf20*, *NPY*, *TNF*, and *SLC6A2* in MDD did not stand out as particularly strong, i.e. odds ratios were mostly in the moderate range (minimum OR = 0.33; maximum OR = 2.41), and

none of the p-values in these studies was smaller than $p < 0.001$, not even for the largest study on *C5orf20* with a total sample size of 864. *NPY* was the one exception where the allele was present in 6.3 % of the controls but not in the patients, thus suggesting a strong effect ($OR=0$). However, this was based on only 51 patients²³⁻²⁶.

An important question is why so few candidate genes were replicated by our GWAS, while the sample size of our study was so much larger than any of the 78 selected candidate gene studies. One possible - and in our opinion most likely - explanation is publication bias: positive results have a better chance of being published than negative results. This would also imply that many previously reported positive findings were actually false positive findings (type 1 errors), probably amplified by insufficient correction for multiple testing. Testing this, e.g. with funnel plots, is not appropriate for the approach followed here as our literature search strategy did not include negative candidate gene studies. Second, given that MDD is a rather heterogeneous disorder, and that it was diagnosed with different instruments across studies, previous and current study samples may have differed phenotypically (see²⁷ for a discussion of this point). A third explanation is that associations between genes and etiologically complex diseases may depend on genetic (gene*gene interactions or epistasis) and environmental (gene*environment interactions) contexts, which may differ in samples from different populations²⁸. Thus, previous and current samples may have been different genetically or in their contextual factors.

Given the modest support for the replicated candidate genes (one p-value < 0.01 , three p-values < 0.05) it is possible that even the four replications of our analysis are false positive results. With the number of SNPs ($n=65$) been tested and under the null hypothesis of no true associations of any of the candidate SNPs in previous studies, one would expect three significant findings. Thus, it is possible that our two significant findings in *C5orf20* and *NPY* are false positive results. In addition, under a similar null hypothesis for the 55 candidate genes, two significant findings were expected implying that the single gene-wide significant result of *TNF* might also be a false positive result. This is supported by the lack of overall significance for the *TNF* SNP ($p=0.33$). And finally, also the significant finding for

SLC6A2, the only gene showing a larger number of significant SNPs than expected, might be a chance finding.

On the other hand, the above calculations may be too conservative when assuming that at least some of the previously found associations of candidate genes with MDD were true findings. In that case, our approach of replicating candidate genes is more or less hypothesis-driven, thus not requiring the same multiple testing penalty as the genome-wide approach⁴. Nonetheless, the few replications in our study are rather sobering and in order to uncover whether the replicated SNPs and genes are truly associated to MDD confirmation in independent samples is crucial. As such, meta-analytical results from the Psychiatric GWAS Consortium are also eagerly awaited²⁹.

From the most recent meta-analysis of genetic studies on MDD, Lopez-Leon et al.⁹ concluded that statistically significant evidence exists for six MDD susceptibility genes, i.e., *APOE*, *DRD4*, *GNB3*, *MTHFR*, *SLC6A3*, and *SLC6A4*. Our study offers little support for these genes. Given our sample size we had 80% power to detect odds ratios of >1.15 for allele frequencies >5% under an additive disease model. All of the above genes meet these criteria. The association of *GNB3* and *MTHFR* with MDD was directly tested but could not be replicated in the GAIN MDD sample, although the effect of *MTHFR* showed a trend in the expected direction ($p=0.074$; OR TT versus CC=1.14). In addition, *APOE*, *DRD4*, and *SLC6A4* were not associated with MDD in our study, but the previously identified genetic variants were length polymorphisms instead of SNPs. Hence these could not directly be tested and since it is unsure whether these variants are tagged by the SNPs in the corresponding genes we cannot refute the associations. *SLC6A3* was not identified in our literature search as a candidate gene for MDD, because individual studies did not report significant effects for this gene^{30, 31} and it only reached significance in the pooled meta-analysis. Post-hoc we also tested for significance in our sample and we did not find any association (59 SNPs, most significant SNP: rs27072, $P=0.096$).

In the context of the non-replication of many of the selected candidate genes as discussed earlier, two limitations of our study need to be noted. First, we did not have direct

or indirect information on one third of the candidate SNPs as these were not present on the genotyping chip and could not be imputed using the HapMap CEU data. Second, we were unable to test candidate length polymorphisms previously associated with MDD. Among these was the 44 base pair insertion/deletion polymorphism (or 5-HTTLPR) in the promoter region of the serotonin transporter gene *SLC6A4* (*SERT*). Length polymorphisms are often difficult to tag with single SNPs because LD information between SNPs and length polymorphisms is either unavailable or LD with SNPs is insufficiently strong³². However, a recent study by Wray and colleagues³³ identified a two-SNP haplotype proxy for 5HTTLPR.

In conclusion, the GWAS data of the GAIN MDD study failed to replicate all but four of the previously reported candidate gene associations with MDD. However, given the number of candidate SNPs and genes that were tested, even these significant may well be false positives, implying that we found no replication at all. This might point to publication bias and false-positive findings in previous studies, but also to heterogeneity of the MDD phenotype as well as variations in contextual genetic or environmental factors.

Conflict of interest: None

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Table 1: Candidate genes and associated polymorphisms or haplotypes based on the systematic literature search. Sample sizes (N cases/N controls) as well as p-values for allelic (P allele), genotypic (P genotype) and/or multimarker tests (P multimarker) are shown. Odds ratios (ORs) are given whenever possible.

Gene	HUGO name	Chromosome position	Gene size (kb)	Variant	rs-id	Refs	N cases	N controls	P allele	OR allele	P genot.	OR genot.	P multi-marker	OR
MTHFR	MTHFR	1p36.3	20.3	677C/T	rs1801133	34	32	419	0.005	2.8				
						35	100	89			0.03	1.90		
5-HT1A	HTR1A	5q11.2-q13	1.3	-1019C/G	rs6295	36	129	134	0.0006	1.84 ^b	0.0017	het:1.54 hom:3.75 ^b		
5-HT2A	HTR2A	13q14-q21	62.7	-1438A/G	rs6311	37	71	157	0.018	0.62	0.039	0.47		
						38	189	148	0.007	1.52	0.005			
						39	120	131	0.03		0.01	2.4		
5-HT2C	HTR2C	Xq24	326.1	68G/C = Cys23Ser	rs6318	16	177	160	0.02	1.84 ^b				
						40	513	901	0.006	n.a.				
5-HT3B	HTR3B	11q23.1	41.7	Tyr129Ser (3B06)	rs1176744	41	47	90			0.027	n.a.		
						41	47	90	0.015	2.27	0.011	n.a.		
						41	47	90			0.023	n.a.		
						41	47	90			0.031	n.a.		
						41	47	90						0.002
ACE	ACE	17q23.3	20.5	dbSNP4295	rs4295	19	642	608			0.0011	rec:1.87 ^b		
						42	92	92	<0.0001		0.001		0.0001	n.a.
						42	92	92	0.03	1.59				
				dbSNP4309	rs4309									

				rs2286572 ^a	rs2286572	19	642	608			p<0.05	n.a.
				rs4968779 ^a	rs4968779	19	642	608			p<0.05	n.a.
				rs4291	rs4291	19	642	608			0.00076	rec:1.91 ^b
				rs4277405	rs4277405	19	642	608			p<0.05	n.a.
				rs4305	rs4305	19	642	608			p<0.01	n.a.
				rs4311	rs4311	19	642	608			p<0.05	n.a.
				rs4329	rs4329	19	642	608			p=0.05	n.a.
				rs4333	rs4333	19	642	608			p<0.05	n.a.
				rs4461142	rs4461142	19	642	608			p<0.05	n.a.
				rs867640	rs867640	19	642	608			p<0.05	n.a.
FACL4	ACSL4	Xq22.3-q23	92.1	C/T in intron 1	rs1324805	43	198	229	0.003	1.5 (F) 1.9 (M)		
AR	AR	Xq11.2-q12	180.2	microsatellite	NA	44	71	83	0.003	0.41 ^b		
AT1R	AGTR1	3q21-q25	45.1	1166A/C	rs5186	45	132	132			0.036	het:0.66 hom:1.61 ^b
APOE	APOE	19q13.2	3.6	epsilon2	rs429358+rs7412	46	42	73	0.04	0.36 ^b		
						47	273	429			<0.0005	het:0.17 hom:0.03 ^b
AVPR1B	AVPR1B	1q32	7.7	AVPR1b-s3	rs33976516	48	89	88	0.026	n.a.	0.014	n.a.
				AVPR1b-s5	rs33933482	48	89	89	0.043	n.a.		
				AVPR1b-s1+s2+s3+s4+s5	rs33976516+rs33933482	48	89	88				0.002 0.52
						48	89	89				0.0003 0.28
BDNF	BDNF	11p13	66.9	Val66Met	rs6265	49	110	171	0.001		0.003	2.49
						50	284	331	0.005	1.7		
				(GT)n (microsatellite)	NA	51	465	1097	0.028	n.a.		
BCR	BCR	22q11.23	137.7	rs2267012	rs2267012	52	329	351	0.0097	1.33		

				rs3761418	rs3761418	52	329	351	0.012	1.32		
				rs2267013	rs2267013	52	329	351	0.044	1.27		
				rs2267015	rs2267015	52	329	351	0.023	1.30		
				rs2156921	rs2156921	52	329	351	0.031	1.29		
				rs2213172	rs2213172	52	329	351	0.031	1.28		
COMT	COMT	22q11.21	27.2	Val158Met -287A>G	rs4680 rs2075507	53 54	120 30	628 467	0.009 0.046	1.44 1.79		
				-287A>G+rs737865 +Val158Met+rs165599	rs2075507+rs737865	54	30	467			0.0378	2.12
MCP1	CCL2	17q11.2-q12	1.9	-2518G/A	rs1024611	55	90	114	0.004	1.83	0.027	1.87
CCKAR	CCKAR	4p15.1-p15.2	9.0	246G/A -128G/T-246G/A- -608G/A-1266T/C	rs number unknown rs1799723-rs?- -rs1800856-rs1800857	16 16	177 177	160 160	0.006	2.58 ^b		0.002 6.68 ^b
CHRM2	CHRM2	7q31-q35	148.4	1890A/T	rs8191992	56	126	304			0.001	het:0.44 hom:0.47 ^b
a7nAChR	CHRFAM7A	15q13.1	32.4	2 bp deletion	rs10581632	57	72	103	0.037	n.a.	0.027	2.14
CRH-BP	CRHBP	5q11.2-q13.3	16.6	CRH-BPs02 CRH-BPs11	rs7728378 rs1875999	58 58	89 89	88 88	0.042 0.048		0.031 0.043	
				CRH-BPs17+s02 +s14+s11	rs3811939+rs7728378	58	89	88				0.00014 2.21
CRHR1	CRHR1	17q12-q22	51.5	rs242939	rs242939	59	206	195	0.0008	2.07 ^b	0.0002	het:2.45 hom:1.18 ^b
CRHR2	CRHR2	7p15.1	29.3	1047G/A	rs2240403	60	89	89	0.04	2.14 ^b	0.03	het:1.21 hom:2.06 ^b
CYP2C9	CYP2C9	10q24	50.7	CYP2C9*3	rs1057910	61 62	70 70	142 138	<0.05 <0.01	2.03 2.61		

DCNP1	C5orf20	5q31.1	3.1	rs12520799	rs12520799	23	431	433	0.003	2.01 ^b		
DISC1	DISC1	1q42.1	414.5	Ser704Cys (SNP12) SNP1	rs821616	63	373	717	0.005	1.46		
					rs6541281	63	373	717	0.048	0.75		
DRD1	DRD1	5q35.1	3.5	-2102C/A	rs10063995	16	177	160	0.008	3.69 ^b		
DRD2	DRD2	11q23	65.6	-7054C/A	rs number unknown	16	177	160	0.03	0.53 ^b		
DRD3	DRD3	3q13.3	50.3	Bal I	rs6280	64	36	38	0.014	2.32 ^b	0.027	3.00 ^b
DRD4	DRD4	11p15.5	3.4	48bp polymorphism	NA		49	100	0.011 (4)	0.43 ^b	0.007 (4/4)	0.36 ^b
									0.041 (5)	2.79 ^b	0.035 (4/5)	2.99 ^b
						31	126	471			0.004	2.09
ER-alpha	ESR1	6q25.1	295.7	PvuII XbaI	rs2234693	66	89	126	0.004	1.76 ^b	0.01	het:1.63 hom:3.83 ^b
					rs9340799	66	89	126	0.02	n.a.		
ER-beta	ESR2	14q23.2	111.5	microsatellite	NA	67	102	150	<0.005	0.30 ^b	<0.0005	het:0.40 hom:0.14 ^b
GPR50	GPR50	Xq28	4.9	Val606Ile	rs13440581	68	226	562	0.040	1.30 ^b		
						68	136	260	0.0096	1.49 ^b		
						68	226	562	0.011	1.39 ^b		
						68	136	260	0.0064	1.51 ^b		
				Δ502-505	in complete LD with rs561077							
GABA3	GABRA3	Xq28	284.2	microsatellite	NA	69	128	81	<0.0001	0.14		
GMIP	GMIP	19p11-p12	14.2	-525G/A (SNP1)	rs3794996	70	164	164	0.039	1.66		
				rs2043293 (SNP2)	rs2043293	70	59	59	0.0086	1.46		

				rs2304129 (SNP3)	rs2304129	70	59	59	0.0086	1.50				
				rs880090 (SNP4)	rs880090	70	59	59	0.015	1.46				
Gbeta3	GNB3	12p13	7.2	825C/T	rs5443	71	184	158			0.001	2.21		
						72	106	133	0.012	2.14				
						73	78	111	0.004	1.67	0.008	n.a.		
HP	HP	16q22.1	6.4	genotyping based on phenotypes	NA	15	72	200	0.04	0.68 ^b	0.01	rec:0.45 ^b		
cPLA2-α	PLA2G4A	1q25	160.1	BanI	rs10798059	74	62	117	0.007	1.83	0.017	3.40		
CD-MPR	M6PR	12p13	9.3	C/T in 3'UTR of exon 7	rs3318	75	193	259	0.014	1.96				
MAOA	MAOA	Xp11.3	90.7	uVNTR1 (microsatellite)	NA	76	73	68			0.029	dom:0.47 ^b		
						77	228	213	<0.001					
						77	133	110	0.009	2.39	0.008	n.a.		
						77	95	103	0.015	1.97				
				EcoRV2	rs1137070	78	78	104	0.01	2.3				
				uVNTR1+EcoRV2	NA	78	78	104					0.008	2.5
p75NTR	NGFR	17q21-q22	19.7	S205L	rs2072446	79	164	164	<0.05	0.54				
NPY	NPY	7p15.1	7.7	-399T/C	rs16147	24	48	140	0.03	1.69 ^b				
				1128T/C (Leu7Pro)	rs16139	24	51	140	0.009	0.00 ^{b,c}				
GR	NR3C1	5q31.3	157.6	BclI	rs41423247	80	170	374			0.03	1.8		
				ER22/23EK	rs6189+rs6190	80	183	497	0.043	1.98				
				R23K	rs6190	81	134	181	0.02	n.a.	0.02	n.a.		
				-3211T/C (NR3C1-1)	rs10482605	81	180	173	0.02	n.a.	0.02	n.a.		
				-3211T/C+R23K	rs10482605+rs6190	81	134	181					0.01	4.58
						81	180	173					0.02	n.a.

PAM	PAM	5q14-q21	163.9	dbSNP13340364 G>A	rs13340364	42	92	92	0.04	0.31	0.03			
PDE10A	PDE10A	6q26	331.1	rs717602	rs717602	82	284	331	0.009	n.a.				
				rs220818	rs220818	82	284	331	0.01	n.a.				
				rs676389	rs676389	82	284	331	0.03	n.a.				
PDE11A	PDE11A	2q31.2	485.1	rs3770018	rs3770018	82	284	331	0.0005	2.1				
PDE2A	PDE2A	11q13.4	98.2	rs370013	rs370013	82	284	331	0.01					
PDE5A	PDE5A	4q25-q27	134.4	rs3775845	rs3775845	82	284	331	0.007					
PDE6C	PDE6C	10q24	53.1	rs650058	rs650058	82	284	331	0.01					
				rs701865	rs701865	82	284	331	0.03					
PDE9A	PDE9A	21q22.3	121.8	rs729861	rs729861	82	284	331	0.0006	0.6				
P2RX7	P2RX7	12q24	53.2	rs2230912	rs2230912	22	1000	1029	0.0019	1.30				
										1.40				
NET	SLC6A2	16q12.2	47.1	-182T/C	rs2242446	25	145	164				0.02	het:0.99	hom:0.33 ^b
						83	112	136				0.019	1.86	
SERT	SLC6A4	17q11.1-q12	37.5	5-HTTLPR (44 bp del/ins)	NA	61	70	142	p<0.05	2.03				
						71	184	158	0.01	1.82				
						84	68	68	0.021	1.81	0.025	n.a.		
						85	466	836	0.007	1.26	0.015	1.5		
						86	262	475	0.05	1.24				
						87	184	360	0.01	1.40 ^b	0.009	1.39 ^b		
						88	95	156			0.04	2.6		
						89	53	103			0.008	het:2.75	hom:0.87 ^b	

				VNTR STin2	rs57098334	90	39	193	<0.02	6.51 ^b	<0.004	6.95 ^b		
						91	33	362	0.011	3.73 ^b				
						92	71	99			p<0.05	rec:2.50 ^b		
						93	114	120	0.04	0.68				
						94	119	346	0.005	4.44	0.001	n.a.		
				5-HTTLPR+VNTR STin2	NA	95	74	84					0.0069	2.53
NK1R	TACR1	2p13.1	150.0	dbSNP13013430 C>T	rs13013430	42	92	92	0.04	0.64				
LBP-1C	TFCP2	12q13	78.0	2236G/A	rs13463	96	180	225	0.016	0.43				
TPH	TPH1	11p15.3-p14	19.8	IVS7+218A/C	rs1800532	97	91	139			0.032	het:2.43 hom:1.39 ^b		
				SNP1	rs4537731	98	228	253			0.019	het:0.59 hom:1.01 ^b		
				SNP2	rs684302	98	228	253			0.0119	het:0.78 hom:1.54 ^b		
				SNP5	rs1799913	98	228	253	0.0013	1.52 ^b	0.0035	het:1.39 hom:2.50 ^b		
				SNP1+SNP2+SNP3+ SNP4+SNP5+SNP6	rs4537731+rs684302+ +rs211105+rs1800532+ rs1799913+rs7933505	98	228	253					<0.00001	2.11 ^b
TPH2	TPH2	12q21.1	93.6	SNPB	rs1843809	99	300	265	0.0496	1.38				
				SNPE	rs1386494	99	300	265	0.0012	0.6				
				SNPB+SNPE+SNPD	rs1843809+rs1386494+ +rs1386495	99	300	265					<0.0001	n.a
				SNP4 = C_245410	rs10784941	100	135	315	0.01	0.62 ^b				
				SNP7 = C_15836061	rs2171363	100	135	315	0.001	0.51 ^b				
				SNP12 = C_8376042	rs1386486	100	135	315	0.01	0.67 ^b				
				1463G/A	unconfirmed variant	17	87	219	<0.001	8.31 ^b				
TNF-alpha	TNF	6p21.3	2.8	308G/A	rs1800629	26	108	125	0.0125	2.24	0.024			
WFS1	WFS1	4p16	33.4	684C/G = R228R	rs7672995	101	177	160	0.007	1.56 ^b				
				1023C/T = F341F	rs56072215	101	177	160	0.02	0.55 ^b				

	1185C/T = V395V	rs1801206	¹⁰¹	177	160	0.01	1.56 ^b				
	2206G/A = G736S	rs number unknown	¹⁰¹	177	160	0.04	0.57 ^b				
	2565G/A = S855S	rs1046316	¹⁰¹	177	160	0.04	0.71 ^b				

NA: not applicable; n.a.: not available; het: heterozygotes; hom: homozygotes; rec: recessive; dom: dominant; F: female; M: male

^a SNP is located more than 5kb away from gene and is not included in our analyses

^b OR was not reported in corresponding article, but could be estimated from genotype counts or frequencies

^c allele was not observed in cases, which resulted in OR = 0.00

Table 2: Significance of candidate SNPs for MDD identified from the literature within the GAIN MDD GWAS

gene	SNP	p-value	genotyped or imputed
ACE	rs4295	0.36	genotyped
ACE	rs4305	0.11	imputed
ACE	rs4309	0.057	imputed
ACE	rs4311	0.21	imputed
ACE	rs4329	0.030	imputed
ACE	rs4333	0.029	imputed
ACE	rs4461142	0.036	imputed
ACE	rs867640	0.39	imputed
BCR	rs2156921	0.76	imputed
BCR	rs2213172 ¹	0.73	genotyped
BCR	rs2267012 ²	0.92	imputed
BCR	rs2267013	0.68	imputed
BCR	rs2267015	0.89	imputed
BCR	rs3761418	0.96	imputed
BDNF	rs6265	0.22	genotyped
C5orf20	rs12520799	0.038	genotyped
CCL2	rs1024611	0.50	imputed
CHRM2	rs8191992	0.13	imputed
COMT	rs4680	0.55	genotyped
CRHBP	rs1875999	0.68	imputed
CRHBP	rs7728378	0.40	imputed
CRHR1	rs242939	0.22	imputed
CRHR2	rs2240403	0.86	genotyped
CYP2C9	rs1057910	0.46	genotyped
DISC1	rs6541281	0.93	imputed
DISC1	rs821616	0.58	genotyped
DRD3	rs6280	0.87	genotyped
ESR1	rs2234693	0.75	imputed
ESR1	rs9340799	0.82	imputed
GMIP	rs2043293	1.00	imputed
GMIP	rs2304129	0.46	imputed
GMIP	rs3794996	0.23	imputed
GMIP	rs880090	0.58	imputed
GNB3	rs5443 ³	0.70	imputed
HTR2A	rs6311	0.57	imputed
HTR2A	rs6313	0.52	genotyped
HTR2C	rs6318	0.092	genotyped
HTR3B	rs1176744	0.50	genotyped
HTR3B	rs2276307	0.62	imputed
HTR3B	rs2276308 ⁴	0.65	imputed
MAOA	rs1137070	0.72	genotyped
MTHFR	rs1801133	0.074	genotyped
NGFR	rs2072446	0.52	imputed
NPY	rs16139	0.034	genotyped
NPY	rs16147	0.82	imputed
P2RX7	rs2230912	0.42	genotyped
PAM	rs13340364	0.78	imputed
PDE10A	rs220818	0.60	imputed
PDE10A	rs676389	0.48	imputed
PDE10A	rs717602	0.78	imputed

PDE11A	rs3770018	0.58	imputed
PDE5A	rs3775845	0.41	imputed
PDE6C	rs650058	0.36	genotyped
PDE6C	rs701865	0.84	genotyped
SLC6A2	rs2242446	0.37	imputed
TACR1	rs13013430	0.056	genotyped
TNF	rs1800629	0.29	imputed
TPH1	rs1800532	0.066	imputed
TPH1	rs4537731	0.11	imputed
TPH1	rs684302	0.071	imputed
TPH2	rs1386486	0.26	imputed
TPH2	rs1386494	0.61	imputed
TPH2	rs1843809	0.69	imputed
TPH2	rs2171363	0.58	imputed
WFS1	rs1801206	0.18	imputed

Notes: ¹tagged by rs877590 ($r^2=0.97$); ²tagged by rs2267010 ($r^2=1$); ³tagged by rs2301339 ($r^2=1$)
⁴tagged by rs12270070 ($r^2=1$)

Table 3: Gene-wide results for the 57 candidate genes identified by the systematic literature search

gene	#genotyped	#imputed	#total	minimal p (analytical)	minimal p (permuted)	gene-wide p	overall p	rs-id	#SNPs at p<0.05	p-value #SNPs
<i>TNF</i>	2	18	20	0.00029	0.00094	0.0034	0.34	rs769178	1	0.32
<i>DISC1</i>	105	386	491	0.0025	0.0015	0.29	0.95	rs7533169	18	0.56
<i>SLC6A2</i>	25	75	100	0.0061	0.0058	0.19	1.00	rs5564	19	0.039
<i>DRD2</i>	12	68	80	0.0079	0.0077	0.15	1.00	rs7131056	3	0.32
<i>HTR3B</i>	6	33	39	0.0081	0.0077	0.11	1.00	rs7945926	3	0.21
<i>CHRM2</i>	43	157	200	0.0097	0.0081	0.32	1.00	rs6944132	3	0.54
<i>MTHFR</i>	6	37	43	0.0098	0.0080	0.11	1.00	rs3737967	4	0.18
<i>PDE10A</i>	107	392	499	0.013	0.014	0.74	1.00	rs7741623	8	0.80
<i>APOE</i>	0	5	5	0.015	0.012	0.057	1.00	rs10119	1	0.11
<i>TACR1</i>	31	141	172	0.016	0.019	0.50	1.00	rs1012686	24	0.10
<i>TPH2</i>	21	134	155	0.017	0.016	0.29	1.00	rs17722134	6	0.29
<i>PDE11A</i>	66	576	642	0.018	0.016	0.63	1.00	rs6433706	11	0.57
<i>DRD3</i>	13	41	54	0.018	0.021	0.23	1.00	rs1800827	3	0.27
<i>PDE5A</i>	7	108	115	0.019	0.020	0.20	1.00	rs13104219	21	0.08
<i>NR3C1</i>	14	60	74	0.024	0.025	0.37	1.00	rs4607376	12	0.11
<i>MAOA</i>	5	0	5	0.026	0.028	0.078	1.00	rs5906883	1	0.11
<i>ESR1</i>	50	272	322	0.027	0.025	0.84	1.00	rs17081749	1	0.93
<i>ACE</i>	3	28	31	0.028	0.031	0.21	1.00	rs4344	8	0.08
<i>NPY</i>	6	38	44	0.030	0.031	0.29	1.00	rs1073317	6	0.15
<i>PDE9A</i>	25	133	158	0.033	0.031	0.69	1.00	rs13046735	1	0.75
<i>HTR2A</i>	35	100	135	0.037	0.037	0.72	1.00	rs2770292	3	0.56
<i>C5orf20</i>	10	35	45	0.038	0.038	0.36	1.00	rs12520799	5	0.13
<i>TPH1</i>	6	24	30	0.040	0.038	0.25	1.00	rs10741734	2	0.19
<i>PLA2G4A</i>	26	92	118	0.040	0.042	0.68	1.00	rs7555140	1	0.68
<i>BCR</i>	14	110	124	0.041	0.045	0.69	1.00	rs11090231	1	0.67
<i>ESR2</i>	43	155	198	0.042	0.040	0.80	1.00	rs1255949	2	0.68
<i>P2RX7</i>	21	87	108	0.047	0.049	0.62	1.00	rs11065464	1	0.57
<i>AGTR1</i>	8	44	52	0.054	0.049	0.58	1.00	rs12721331	0	0.77
<i>PDE6C</i>	18	52	70	0.055	0.056	0.71	1.00	rs10882288	0	0.84
<i>CYP2C9</i>	8	47	55	0.057	0.056	0.48	1.00	rs1799853	0	0.72
<i>CCKAR</i>	4	17	21	0.060	0.058	0.33	1.00	rs11726159	0	0.64

<i>NGFR</i>	4	16	20	0.065	0.064	0.55	1.00	rs741073	0	0.73
<i>TFCP2</i>	4	59	63	0.066	0.064	0.53	1.00	rs2029686	0	0.72
<i>CRHR2</i>	12	35	47	0.083	0.085	0.70	1.00	rs2267717	0	0.77
<i>GPR50</i>	3	0	3	0.090	0.092	0.24	1.00	rs5969987	0	0.57
<i>HTR2C</i>	10	0	10	0.092	0.091	0.39	1.00	rs6318	0	0.62
<i>CRHBP</i>	3	9	12	0.093	0.092	0.43	1.00	rs7721799	0	0.63
<i>PAM</i>	7	92	99	0.096	0.090	0.81	1.00	rs1650500	0	0.79
<i>SLC6A4</i>	6	26	32	0.11	0.11	0.72	1.00	rs12150465	0	0.72
<i>M6PR</i>	3	21	24	0.11	0.10	0.54	1.00	rs1805729	0	0.65
<i>BDNF</i>	7	29	36	0.11	0.11	0.60	1.00	rs11030104	0	0.68
<i>GABRA3</i>	10	0	10	0.11	0.10	0.50	1.00	rs994423	0	0.63
<i>WFS1</i>	3	55	58	0.12	0.13	0.51	1.00	rs4689393	0	0.63
<i>COMT</i>	5	31	36	0.13	0.13	0.78	1.00	rs2871047	0	0.72
<i>CCL2</i>	0	9	9	0.14	0.14	0.55	1.00	rs2857655	0	0.62
<i>DRD1</i>	5	16	21	0.17	0.17	0.79	1.00	rs5326	0	0.69
<i>PDE2A</i>	16	62	78	0.20	0.19	0.97	1.00	rs11604811	0	0.81
<i>CRHR1</i>	4	42	46	0.22	0.22	0.86	1.00	rs242939	0	0.69
<i>AR</i>	1	0	1	0.23	0.23	0.23	1.00	rs2207040	0	0.52
<i>GMIP</i>	0	10	10	0.23	0.23	0.83	1.00	rs12003	0	0.66
<i>DRD4</i>	0	6	6	0.29	0.30	0.74	1.00	rs3758653	0	0.59
<i>ACSL4</i>	2	0	2	0.31	0.30	0.50	1.00	rs7887981	0	0.55
<i>HP</i>	1	5	6	0.32	0.32	0.77	1.00	rs5475	0	0.59
<i>GNB3</i>	3	10	13	0.39	0.39	0.96	1.00	rs3759348	0	0.23
<i>HTR1A</i>	0	5	5	0.54	0.55	0.79	1.00	rs10042486	0	0.55
<i>AVPR1B</i>	0	0	0	NA	NA	NA	NA	NA	NA	NA
<i>CHRFAM7A</i>	0	0	0	NA	NA	NA	NA	NA	NA	NA

Note Analytical p-values were determined using SNPTTest for the autosomes and logistic regression in PLINK for the X chromosome.

Permutations (N=10,000) were performed to determine uncorrected SNP p-values, gene-wide corrected p-values, overall corrected p-values and p-values for number of SNPs with p<0.05. All p-values were calculated assuming an additive model. P-values <0.05 are shown in bold.

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Figure 1: Selection procedure of studies reporting on candidate genes. PM, PUBMED; LL, Lopez-Leon.

Figure 2: Coverage by genotyped (black bar) and imputed (grey bar) SNPs and size (white circles) of the 57 selected candidate genes (above: genes with 50 or less SNPs, below: genes with more than 50 SNPs)

Figure 3: Observed minimal p-value versus the expected minimal p-value based on the number of SNPs in the gene

Figure 4: Association of SLC6A2 (NET) with MDD. Along the x-axis the location of all 100 SNPs within 5 kb of SLC6A2 is shown and the $-\log^{10}(\text{p-value})$ on the y-axis. Nineteen SNPs have a p-value <0.05 , which is significantly more than expected ($p=0.039$). Seventeen of them lie in three haplotype blocks (squares, upward triangles [light grey], and downward triangles [dark grey]) (r^2 values HapMap CEU: squares-upward triangles: 0.020, squares-downward triangles: 0.661, and upward triangles-downward triangles: 0.013). The other 2 (black diamonds) are not in LD with the haplotype blocks or with each other. The light grey line shows the recombination rate in this area (axis on the right).

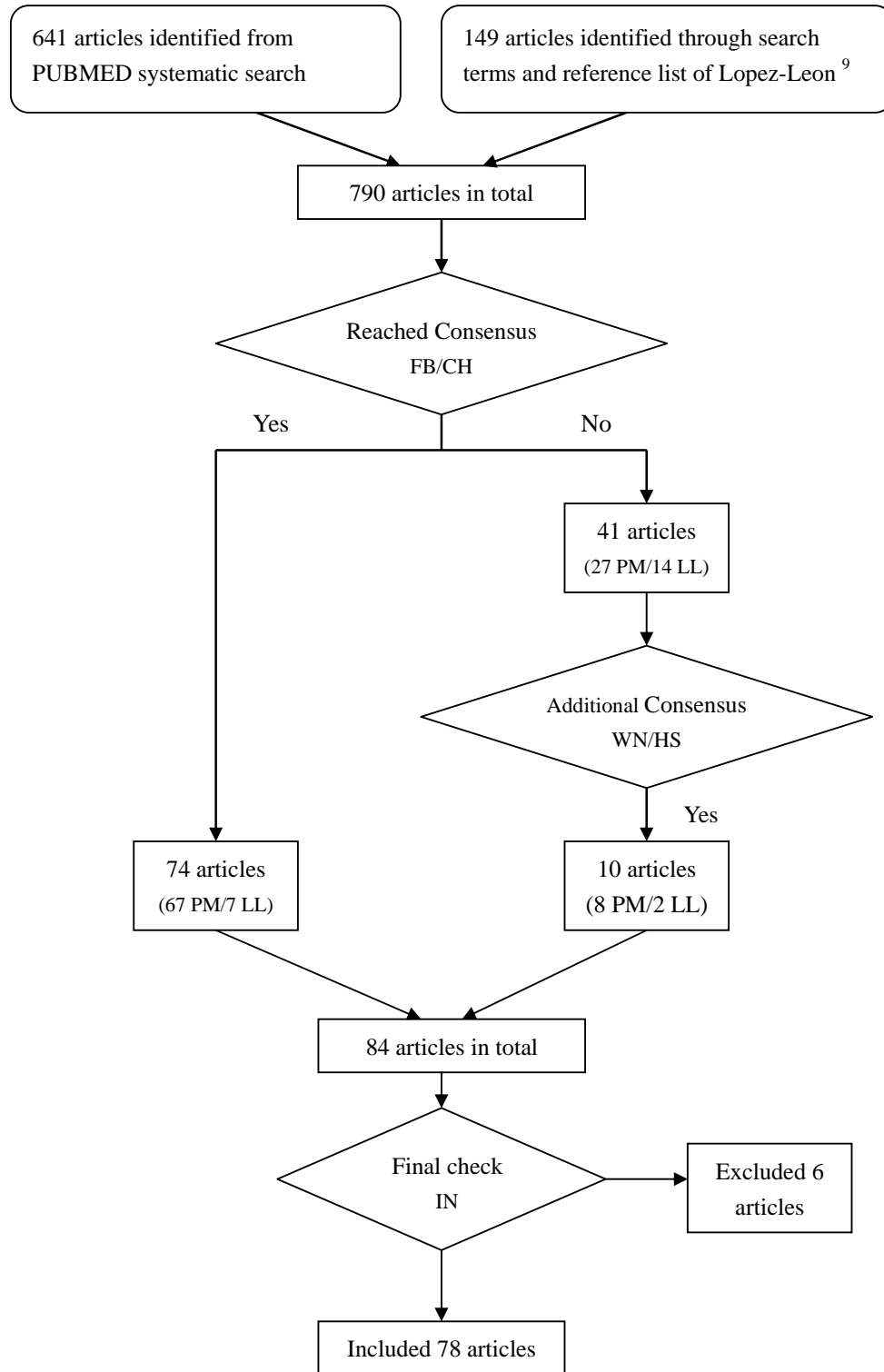


Figure 1 Selection procedure of studies reporting on candidate genes. PM, PUBMED; LL, Lopez-Leon.

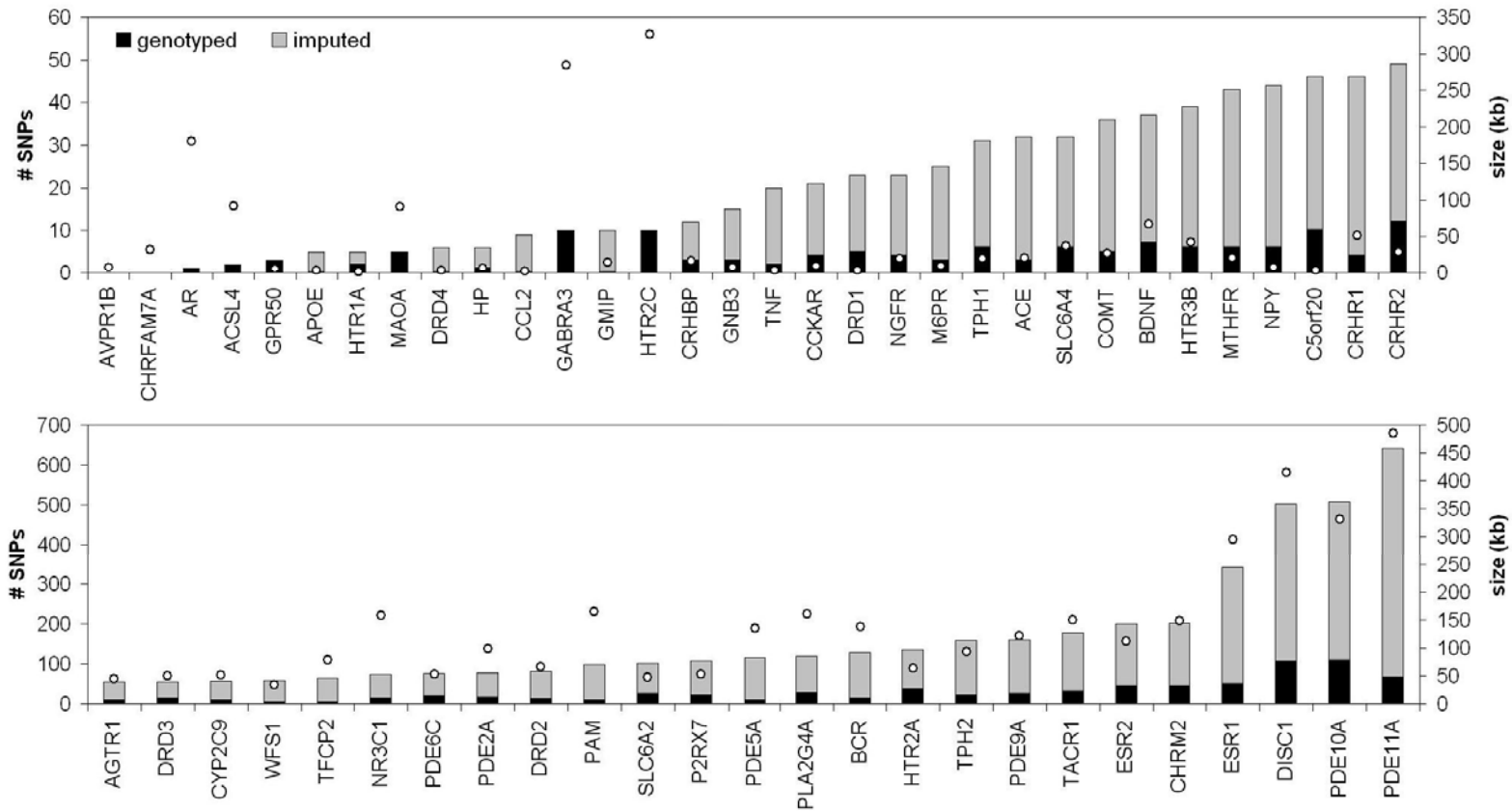


Figure 2: Coverage by genotyped (black bar) and imputed (grey bar) SNPs and size (white circles) of the 57 selected candidate genes (above: genes with 50 or less SNPs, below: genes with more than 50 SNPs)

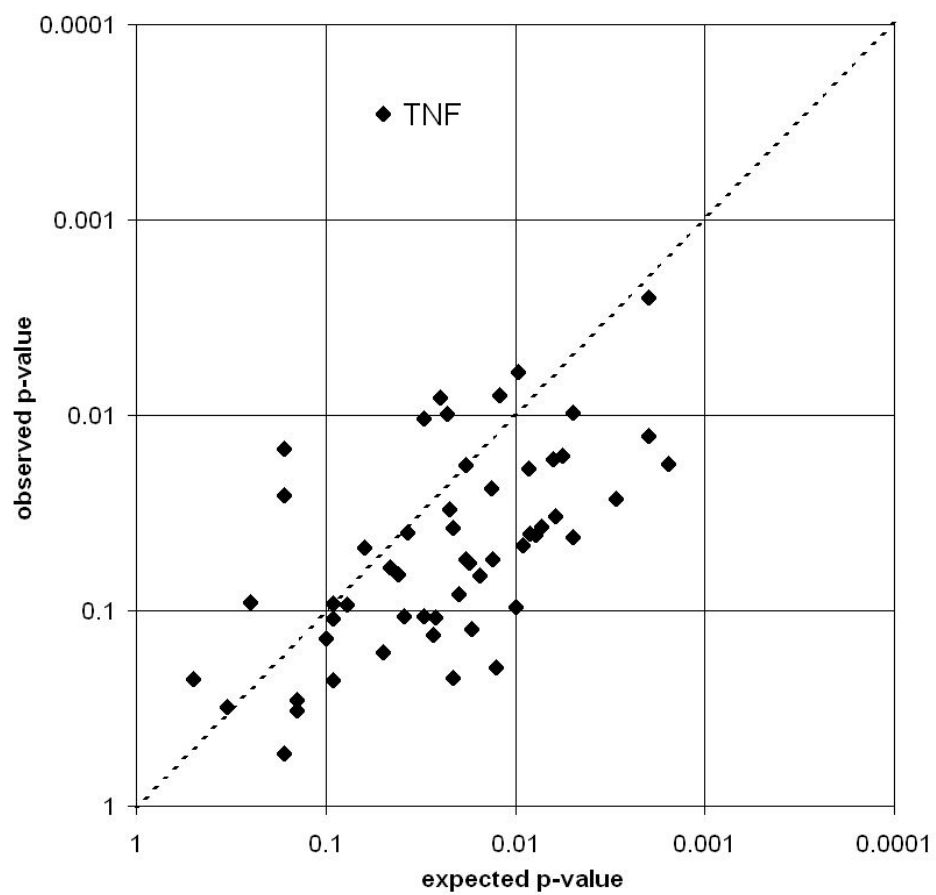


Figure 3: Observed minimal p-value versus the expected minimal p-value based on the number of SNPs in the gene

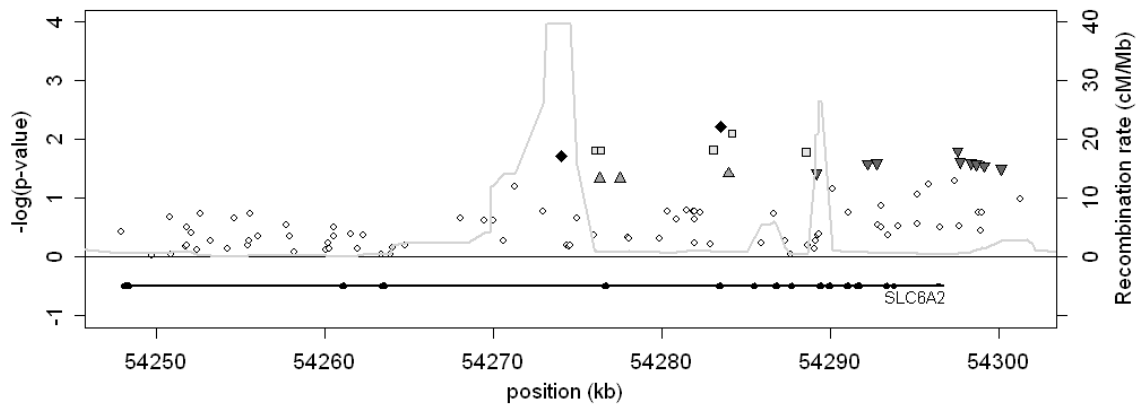


Figure 4: Association of SLC6A2 (NET) with MDD. Along the x-axis the location of all 100 SNPs within 5 kb of SLC6A2 is shown and the $-\log_{10}(p\text{-value})$ on the y-axis. Nineteen SNPs have a p-value <0.05 , which is significantly more than expected ($p=0.039$). Seventeen of them lie in three haplotype blocks (light grey squares, middle grey upward triangles and dark grey downward triangles) (r^2 values HapMap CEU: light-middle grey 0.020, light-dark grey 0.661, and middle-dark grey 0.013). The other two (black diamonds) are not in LD with the haplotype blocks or with each other. The light grey line shows the recombination rate in this area (axis on the right).

Table 1: Candidate genes and associated polymorphisms or haplotypes based on the systematic literature search. Sample sizes (N cases/N controls) as well as p-values for allelic (P allele), genotypic (P genotype) and/or multimarker tests (P multimarker) are shown. Odds ratios (ORs) are given whenever possible.

Gene	HUGO name	Chromosome position	Gene size (kb)	Variant	rs-id	Refs	N cases	N controls	P allele	OR allele	P genot.	OR genot.	P multi-marker	OR
MTHFR	MTHFR	1p36.3	20.3	677C/T	rs1801133	34	32	419	0.005	2.8				
						35	100	89			0.03	1.90		
5-HT1A	HTR1A	5q11.2-q13	1.3	-1019C/G	rs6295	36	129	134	0.0006	1.84 ^b	0.0017	het:1.54 hom:3.75 ^b		
5-HT2A	HTR2A	13q14-q21	62.7	-1438A/G	rs6311	37	71	157	0.018	0.62	0.039	0.47		
						38	189	148	0.007	1.52	0.005			
						39	120	131	0.03		0.01	2.4		
5-HT2C	HTR2C	Xq24	326.1	68G/C = Cys23Ser	rs6318	16	177	160	0.02	1.84 ^b				
						40	513	901	0.006	n.a.				
5-HT3B	HTR3B	11q23.1	41.7	Tyr129Ser (3B06)	rs1176744	41	47	90			0.027	n.a.		
				Ala154Ala (3B08)	rs2276305	41	47	90	0.015	2.27	0.011	n.a.		
				IVS6+72A>G (3B10)	rs2276307	41	47	90			0.023	n.a.		
				IVS6+161C>G (3B11)	rs2276308	41	47	90			0.031	n.a.		
				3B04+3B06+3B08+3B09+3B10+3B11+3B12	rs1176746+rs1176744+rs2276305+rs3782025	41	47	90						0.002
ACE	ACE	17q23.3	20.5	dbSNP4295	rs4295	19	642	608			0.0011	rec:1.87 ^b		
						42	92	92	<0.0001		0.001		0.0001	n.a.
				dbSNP4309	rs4309	42	92	92	0.03	1.59				

				rs2286572 ^a	rs2286572	19	642	608			p<0.05	n.a.
				rs4968779 ^a	rs4968779	19	642	608			p<0.05	n.a.
				rs4291	rs4291	19	642	608			0.00076	rec:1.91 ^b
				rs4277405	rs4277405	19	642	608			p<0.05	n.a.
				rs4305	rs4305	19	642	608			p<0.01	n.a.
				rs4311	rs4311	19	642	608			p<0.05	n.a.
				rs4329	rs4329	19	642	608			p=0.05	n.a.
				rs4333	rs4333	19	642	608			p<0.05	n.a.
				rs4461142	rs4461142	19	642	608			p<0.05	n.a.
				rs867640	rs867640	19	642	608			p<0.05	n.a.
FACL4	ACSL4	Xq22.3-q23	92.1	C/T in intron 1	rs1324805	43	198	229	0.003	1.5 (F) 1.9 (M)		
AR	AR	Xq11.2-q12	180.2	microsatellite	NA	44	71	83	0.003	0.41 ^b		
AT1R	AGTR1	3q21-q25	45.1	1166A/C	rs5186	45	132	132			0.036	het:0.66 hom:1.61 ^b
APOE	APOE	19q13.2	3.6	epsilon2	rs429358+rs7412	46	42	73	0.04	0.36 ^b		
						47	273	429			<0.0005	het:0.17 hom:0.03 ^b
AVPR1B	AVPR1B	1q32	7.7	AVPR1b-s3	rs33976516	48	89	88	0.026	n.a.	0.014	n.a.
				AVPR1b-s5	rs33933482	48	89	89	0.043	n.a.		
				AVPR1b-s1+s2+s3+s4+s5	rs33976516+rs33933482	48	89	88				0.002 0.52
						48	89	89				0.0003 0.28
BDNF	BDNF	11p13	66.9	Val66Met	rs6265	49	110	171	0.001		0.003	2.49
						50	284	331	0.005	1.7		
				(GT)n (microsatellite)	NA	51	465	1097	0.028	n.a.		
BCR	BCR	22q11.23	137.7	rs2267012	rs2267012	52	329	351	0.0097	1.33		

				rs3761418	rs3761418	52	329	351	0.012	1.32		
				rs2267013	rs2267013	52	329	351	0.044	1.27		
				rs2267015	rs2267015	52	329	351	0.023	1.30		
				rs2156921	rs2156921	52	329	351	0.031	1.29		
				rs2213172	rs2213172	52	329	351	0.031	1.28		
COMT	COMT	22q11.21	27.2	Val158Met -287A>G	rs4680 rs2075507	53 54	120 30	628 467	0.009 0.046	1.44 1.79		
				-287A>G+rs737865 +Val158Met+rs165599	rs2075507+rs737865	54	30	467			0.0378	2.12
MCP1	CCL2	17q11.2-q12	1.9	-2518G/A	rs1024611	55	90	114	0.004	1.83	0.027	1.87
CCKAR	CCKAR	4p15.1-p15.2	9.0	246G/A -128G/T-246G/A- -608G/A-1266T/C	rs number unknown rs1799723-rs?- -rs1800856-rs1800857	16 16	177 177	160 160	0.006	2.58 ^b		0.002 6.68 ^b
CHRM2	CHRM2	7q31-q35	148.4	1890A/T	rs8191992	56	126	304			0.001	het:0.44 hom:0.47 ^b
a7nAChR	CHRFAM7A	15q13.1	32.4	2 bp deletion	rs10581632	57	72	103	0.037	n.a.	0.027	2.14
CRH-BP	CRHBP	5q11.2-q13.3	16.6	CRH-BPs02 CRH-BPs11 CRH-BPs17+s02 +s14+s11	rs7728378 rs1875999 rs3811939+rs7728378	58 58 58	89 89 89	88 88 88	0.042 0.048		0.031 0.043	
												0.00014 2.21
CRHR1	CRHR1	17q12-q22	51.5	rs242939	rs242939	59	206	195	0.0008	2.07 ^b	0.0002	het:2.45 hom:1.18 ^b
CRHR2	CRHR2	7p15.1	29.3	1047G/A	rs2240403	60	89	89	0.04	2.14 ^b	0.03	het:1.21 hom:2.06 ^b
CYP2C9	CYP2C9	10q24	50.7	CYP2C9*3	rs1057910	61 62	70 70	142 138	<0.05 <0.01	2.03 2.61		

DCNP1	C5orf20	5q31.1	3.1	rs12520799	rs12520799	23	431	433	0.003	2.01 ^b		
DISC1	DISC1	1q42.1	414.5	Ser704Cys (SNP12) SNP1	rs821616	63	373	717	0.005	1.46		
					rs6541281	63	373	717	0.048	0.75		
DRD1	DRD1	5q35.1	3.5	-2102C/A	rs10063995	16	177	160	0.008	3.69 ^b		
DRD2	DRD2	11q23	65.6	-7054C/A	rs number unknown	16	177	160	0.03	0.53 ^b		
DRD3	DRD3	3q13.3	50.3	Bal I	rs6280	64	36	38	0.014	2.32 ^b	0.027	3.00 ^b
DRD4	DRD4	11p15.5	3.4	48bp polymorphism	NA		49	100	0.011 (4)	0.43 ^b	0.007 (4/4)	0.36 ^b
									0.041 (5)	2.79 ^b	0.035 (4/5)	2.99 ^b
						31	126	471			0.004	2.09
ER-alpha	ESR1	6q25.1	295.7	PvuII XbaI	rs2234693	66	89	126	0.004	1.76 ^b	0.01	het:1.63 hom:3.83 ^b
					rs9340799	66	89	126	0.02	n.a.		
ER-beta	ESR2	14q23.2	111.5	microsatellite	NA	67	102	150	<0.005	0.30 ^b	<0.0005	het:0.40 hom:0.14 ^b
GPR50	GPR50	Xq28	4.9	Val606Ile	rs13440581	68	226	562	0.040	1.30 ^b		
						68	136	260	0.0096	1.49 ^b		
						68	226	562	0.011	1.39 ^b		
						68	136	260	0.0064	1.51 ^b		
				Δ502-505	in complete LD with rs561077							
GABA3	GABRA3	Xq28	284.2	microsatellite	NA	69	128	81	<0.0001	0.14		
GMIP	GMIP	19p11-p12	14.2	-525G/A (SNP1)	rs3794996	70	164	164	0.039	1.66		
				rs2043293 (SNP2)	rs2043293	70	59	59	0.0086	1.46		

				rs2304129 (SNP3)	rs2304129	70	59	59	0.0086	1.50				
				rs880090 (SNP4)	rs880090	70	59	59	0.015	1.46				
Gbeta3	GNB3	12p13	7.2	825C/T	rs5443	71	184	158			0.001	2.21		
						72	106	133	0.012	2.14				
						73	78	111	0.004	1.67	0.008	n.a.		
HP	HP	16q22.1	6.4	genotyping based on phenotypes	NA	15	72	200	0.04	0.68 ^b	0.01	rec:0.45 ^b		
cPLA2-α	PLA2G4A	1q25	160.1	BanI	rs10798059	74	62	117	0.007	1.83	0.017	3.40		
CD-MPR	M6PR	12p13	9.3	C/T in 3'UTR of exon 7	rs3318	75	193	259	0.014	1.96				
MAOA	MAOA	Xp11.3	90.7	uVNTR1 (microsatellite)	NA	76	73	68			0.029	dom:0.47 ^b		
						77	228	213	<0.001					
						77	133	110	0.009	2.39	0.008	n.a.		
						77	95	103	0.015	1.97				
				EcoRV2	rs1137070	78	78	104	0.01	2.3				
				uVNTR1+EcoRV2	NA	78	78	104					0.008	2.5
p75NTR	NGFR	17q21-q22	19.7	S205L	rs2072446	79	164	164	<0.05	0.54				
NPY	NPY	7p15.1	7.7	-399T/C	rs16147	24	48	140	0.03	1.69 ^b				
				1128T/C (Leu7Pro)	rs16139	24	51	140	0.009	0.00 ^{b,c}				
GR	NR3C1	5q31.3	157.6	BclI	rs41423247	80	170	374			0.03	1.8		
				ER22/23EK	rs6189+rs6190	80	183	497	0.043	1.98				
				R23K	rs6190	81	134	181	0.02	n.a.	0.02	n.a.		
				-3211T/C (NR3C1-1)	rs10482605	81	180	173	0.02	n.a.	0.02	n.a.		
				-3211T/C+R23K	rs10482605+rs6190	81	134	181					0.01	4.58
						81	180	173					0.02	n.a.

PAM	PAM	5q14-q21	163.9	dbSNP13340364 G>A	rs13340364	42	92	92	0.04	0.31	0.03			
PDE10A	PDE10A	6q26	331.1	rs717602	rs717602	82	284	331	0.009	n.a.				
				rs220818	rs220818	82	284	331	0.01	n.a.				
				rs676389	rs676389	82	284	331	0.03	n.a.				
PDE11A	PDE11A	2q31.2	485.1	rs3770018	rs3770018	82	284	331	0.0005	2.1				
PDE2A	PDE2A	11q13.4	98.2	rs370013	rs370013	82	284	331	0.01					
PDE5A	PDE5A	4q25-q27	134.4	rs3775845	rs3775845	82	284	331	0.007					
PDE6C	PDE6C	10q24	53.1	rs650058	rs650058	82	284	331	0.01					
				rs701865	rs701865	82	284	331	0.03					
PDE9A	PDE9A	21q22.3	121.8	rs729861	rs729861	82	284	331	0.0006	0.6				
P2RX7	P2RX7	12q24	53.2	rs2230912	rs2230912	22	1000	1029	0.0019	1.30				
										1.40				
NET	SLC6A2	16q12.2	47.1	-182T/C	rs2242446	25	145	164			0.02		het:0.99	
						83	112	136			0.019		hom:0.33 ^b	1.86
SERT	SLC6A4	17q11.1-q12	37.5	5-HTTLPR (44 bp del/ins)	NA	61	70	142	p<0.05	2.03				
						71	184	158	0.01	1.82				
						84	68	68	0.021	1.81	0.025		n.a.	
						85	466	836	0.007	1.26	0.015		1.5	
						86	262	475	0.05	1.24				
						87	184	360	0.01	1.40 ^b	0.009		1.39 ^b	
						88	95	156			0.04		2.6	
						89	53	103			0.008		het:2.75	hom:0.87 ^b

				VNTR STin2	rs57098334	90	39	193	<0.02	6.51 ^b	<0.004	6.95 ^b		
						91	33	362	0.011	3.73 ^b				
						92	71	99			p<0.05	rec:2.50 ^b		
						93	114	120	0.04	0.68				
						94	119	346	0.005	4.44	0.001	n.a.		
				5-HTTLPR+VNTR STin2	NA	95	74	84					0.0069	2.53
NK1R	TACR1	2p13.1	150.0	dbSNP13013430 C>T	rs13013430	42	92	92	0.04	0.64				
LBP-1C	TFCP2	12q13	78.0	2236G/A	rs13463	96	180	225	0.016	0.43				
TPH	TPH1	11p15.3-p14	19.8	IVS7+218A/C	rs1800532	97	91	139			0.032	het:2.43 hom:1.39 ^b		
				SNP1	rs4537731	98	228	253			0.019	het:0.59 hom:1.01 ^b		
				SNP2	rs684302	98	228	253			0.0119	het:0.78 hom:1.54 ^b		
				SNP5	rs1799913	98	228	253	0.0013	1.52 ^b	0.0035	het:1.39 hom:2.50 ^b		
				SNP1+SNP2+SNP3+ SNP4+SNP5+SNP6	rs4537731+rs684302+ +rs211105+rs1800532+ rs1799913+rs7933505	98	228	253					<0.00001	2.11 ^b
TPH2	TPH2	12q21.1	93.6	SNPB	rs1843809	99	300	265	0.0496	1.38				
				SNPE	rs1386494	99	300	265	0.0012	0.6				
				SNPB+SNPE+SNPD	rs1843809+rs1386494+ +rs1386495	99	300	265					<0.0001	n.a
				SNP4 = C_245410	rs10784941	100	135	315	0.01	0.62 ^b				
				SNP7 = C_15836061	rs2171363	100	135	315	0.001	0.51 ^b				
				SNP12 = C_8376042	rs1386486	100	135	315	0.01	0.67 ^b				
				1463G/A	unconfirmed variant	17	87	219	<0.001	8.31 ^b				
TNF-alpha	TNF	6p21.3	2.8	308G/A	rs1800629	26	108	125	0.0125	2.24	0.024			
WFS1	WFS1	4p16	33.4	684C/G = R228R	rs7672995	101	177	160	0.007	1.56 ^b				
				1023C/T = F341F	rs56072215	101	177	160	0.02	0.55 ^b				

	1185C/T = V395V	rs1801206	¹⁰¹	177	160	0.01	1.56 ^b				
	2206G/A = G736S	rs number unknown	¹⁰¹	177	160	0.04	0.57 ^b				
	2565G/A = S855S	rs1046316	¹⁰¹	177	160	0.04	0.71 ^b				

NA: not applicable; n.a.: not available; het: heterozygotes; hom: homozygotes; rec: recessive; dom: dominant; F: female; M: male

^a SNP is located more than 5kb away from gene and is not included in our analyses

^b OR was not reported in corresponding article, but could be estimated from genotype counts or frequencies

^c allele was not observed in cases, which resulted in OR = 0.00

Table 2: Significance of candidate SNPs for MDD identified from the literature within the GAIN MDD GWAS

gene	SNP	p-value	genotyped or imputed
ACE	rs4295	0.36	genotyped
ACE	rs4305	0.11	imputed
ACE	rs4309	0.057	imputed
ACE	rs4311	0.21	imputed
ACE	rs4329	0.030	imputed
ACE	rs4333	0.029	imputed
ACE	rs4461142	0.036	imputed
ACE	rs867640	0.39	imputed
BCR	rs2156921	0.76	imputed
BCR	rs2213172 ¹	0.73	genotyped
BCR	rs2267012 ²	0.92	imputed
BCR	rs2267013	0.68	imputed
BCR	rs2267015	0.89	imputed
BCR	rs3761418	0.96	imputed
BDNF	rs6265	0.22	genotyped
C5orf20	rs12520799	0.038	genotyped
CCL2	rs1024611	0.50	imputed
CHRM2	rs8191992	0.13	imputed
COMT	rs4680	0.55	genotyped
CRHBP	rs1875999	0.68	imputed
CRHBP	rs7728378	0.40	imputed
CRHR1	rs242939	0.22	imputed
CRHR2	rs2240403	0.86	genotyped
CYP2C9	rs1057910	0.46	genotyped
DISC1	rs6541281	0.93	imputed
DISC1	rs821616	0.58	genotyped
DRD3	rs6280	0.87	genotyped
ESR1	rs2234693	0.75	imputed
ESR1	rs9340799	0.82	imputed
GMIP	rs2043293	1.00	imputed
GMIP	rs2304129	0.46	imputed
GMIP	rs3794996	0.23	imputed
GMIP	rs880090	0.58	imputed
GNB3	rs5443 ³	0.70	imputed
HTR2A	rs6311	0.57	imputed
HTR2A	rs6313	0.52	genotyped
HTR2C	rs6318	0.092	genotyped
HTR3B	rs1176744	0.50	genotyped
HTR3B	rs2276307	0.62	imputed
HTR3B	rs2276308 ⁴	0.65	imputed
MAOA	rs1137070	0.72	genotyped
MTHFR	rs1801133	0.074	genotyped
NGFR	rs2072446	0.52	imputed
NPY	rs16139	0.034	genotyped
NPY	rs16147	0.82	imputed
P2RX7	rs2230912	0.42	genotyped
PAM	rs13340364	0.78	imputed
PDE10A	rs220818	0.60	imputed
PDE10A	rs676389	0.48	imputed

PDE10A	rs717602	0.78	imputed
PDE11A	rs3770018	0.58	imputed
PDE5A	rs3775845	0.41	imputed
PDE6C	rs650058	0.36	genotyped
PDE6C	rs701865	0.84	genotyped
SLC6A2	rs2242446	0.37	imputed
TACR1	rs13013430	0.056	genotyped
TNF	rs1800629	0.29	imputed
TPH1	rs1800532	0.066	imputed
TPH1	rs4537731	0.11	imputed
TPH1	rs684302	0.071	imputed
TPH2	rs1386486	0.26	imputed
TPH2	rs1386494	0.61	imputed
TPH2	rs1843809	0.69	imputed
TPH2	rs2171363	0.58	imputed
WFS1	rs1801206	0.18	imputed

Note ¹tagged by rs877590 ($r^2=0.97$); ²tagged by rs2267010 ($r^2=1$); ³tagged by rs2301339 ($r^2=1$)
⁴tagged by rs12270070 ($r^2=1$)

Table 3: Gene-wide results for the 57 candidate genes identified by the systematic literature search

gene	#genotyped	#imputed	#total	minimal p (analytical)	minimal p (permuted)	gene-wide p	overall p	rs-id	#SNPs at p<0.05	p-value #SNPs
<i>TNF</i>	2	18	20	0.00029	0.00094	0.0034	0.34	rs769178	1	0.32
<i>DISC1</i>	105	386	491	0.0025	0.0015	0.29	0.95	rs7533169	18	0.56
<i>SLC6A2</i>	25	75	100	0.0061	0.0058	0.19	1.00	rs5564	19	0.039
<i>DRD2</i>	12	68	80	0.0079	0.0077	0.15	1.00	rs7131056	3	0.32
<i>HTR3B</i>	6	33	39	0.0081	0.0077	0.11	1.00	rs7945926	3	0.21
<i>CHRM2</i>	43	157	200	0.0097	0.0081	0.32	1.00	rs6944132	3	0.54
<i>MTHFR</i>	6	37	43	0.0098	0.0080	0.11	1.00	rs3737967	4	0.18
<i>PDE10A</i>	107	392	499	0.013	0.014	0.74	1.00	rs7741623	8	0.80
<i>APOE</i>	0	5	5	0.015	0.012	0.057	1.00	rs10119	1	0.11
<i>TACR1</i>	31	141	172	0.016	0.019	0.50	1.00	rs1012686	24	0.10
<i>TPH2</i>	21	134	155	0.017	0.016	0.29	1.00	rs17722134	6	0.29
<i>PDE11A</i>	66	576	642	0.018	0.016	0.63	1.00	rs6433706	11	0.57
<i>DRD3</i>	13	41	54	0.018	0.021	0.23	1.00	rs1800827	3	0.27
<i>PDE5A</i>	7	108	115	0.019	0.020	0.20	1.00	rs13104219	21	0.08
<i>NR3C1</i>	14	60	74	0.024	0.025	0.37	1.00	rs4607376	12	0.11
<i>MAOA</i>	5	0	5	0.026	0.028	0.078	1.00	rs5906883	1	0.11
<i>ESR1</i>	50	272	322	0.027	0.025	0.84	1.00	rs17081749	1	0.93
<i>ACE</i>	3	28	31	0.028	0.031	0.21	1.00	rs4344	8	0.08
<i>NPY</i>	6	38	44	0.030	0.031	0.29	1.00	rs1073317	6	0.15
<i>PDE9A</i>	25	133	158	0.033	0.031	0.69	1.00	rs13046735	1	0.75
<i>HTR2A</i>	35	100	135	0.037	0.037	0.72	1.00	rs2770292	3	0.56
<i>C5orf20</i>	10	35	45	0.038	0.038	0.36	1.00	rs12520799	5	0.13
<i>TPH1</i>	6	24	30	0.040	0.038	0.25	1.00	rs10741734	2	0.19
<i>PLA2G4A</i>	26	92	118	0.040	0.042	0.68	1.00	rs7555140	1	0.68
<i>BCR</i>	14	110	124	0.041	0.045	0.69	1.00	rs11090231	1	0.67
<i>ESR2</i>	43	155	198	0.042	0.040	0.80	1.00	rs1255949	2	0.68
<i>P2RX7</i>	21	87	108	0.047	0.049	0.62	1.00	rs11065464	1	0.57
<i>AGTR1</i>	8	44	52	0.054	0.049	0.58	1.00	rs12721331	0	0.77
<i>PDE6C</i>	18	52	70	0.055	0.056	0.71	1.00	rs10882288	0	0.84
<i>CYP2C9</i>	8	47	55	0.057	0.056	0.48	1.00	rs1799853	0	0.72
<i>CCKAR</i>	4	17	21	0.060	0.058	0.33	1.00	rs11726159	0	0.64

<i>NGFR</i>	4	16	20	0.065	0.064	0.55	1.00	rs741073	0	0.73
<i>TFCP2</i>	4	59	63	0.066	0.064	0.53	1.00	rs2029686	0	0.72
<i>CRHR2</i>	12	35	47	0.083	0.085	0.70	1.00	rs2267717	0	0.77
<i>GPR50</i>	3	0	3	0.090	0.092	0.24	1.00	rs5969987	0	0.57
<i>HTR2C</i>	10	0	10	0.092	0.091	0.39	1.00	rs6318	0	0.62
<i>CRHBP</i>	3	9	12	0.093	0.092	0.43	1.00	rs7721799	0	0.63
<i>PAM</i>	7	92	99	0.096	0.090	0.81	1.00	rs1650500	0	0.79
<i>SLC6A4</i>	6	26	32	0.11	0.11	0.72	1.00	rs12150465	0	0.72
<i>M6PR</i>	3	21	24	0.11	0.10	0.54	1.00	rs1805729	0	0.65
<i>BDNF</i>	7	29	36	0.11	0.11	0.60	1.00	rs11030104	0	0.68
<i>GABRA3</i>	10	0	10	0.11	0.10	0.50	1.00	rs994423	0	0.63
<i>WFS1</i>	3	55	58	0.12	0.13	0.51	1.00	rs4689393	0	0.63
<i>COMT</i>	5	31	36	0.13	0.13	0.78	1.00	rs2871047	0	0.72
<i>CCL2</i>	0	9	9	0.14	0.14	0.55	1.00	rs2857655	0	0.62
<i>DRD1</i>	5	16	21	0.17	0.17	0.79	1.00	rs5326	0	0.69
<i>PDE2A</i>	16	62	78	0.20	0.19	0.97	1.00	rs11604811	0	0.81
<i>CRHR1</i>	4	42	46	0.22	0.22	0.86	1.00	rs242939	0	0.69
<i>AR</i>	1	0	1	0.23	0.23	0.23	1.00	rs2207040	0	0.52
<i>GMIP</i>	0	10	10	0.23	0.23	0.83	1.00	rs12003	0	0.66
<i>DRD4</i>	0	6	6	0.29	0.30	0.74	1.00	rs3758653	0	0.59
<i>ACSL4</i>	2	0	2	0.31	0.30	0.50	1.00	rs7887981	0	0.55
<i>HP</i>	1	5	6	0.32	0.32	0.77	1.00	rs5475	0	0.59
<i>GNB3</i>	3	10	13	0.39	0.39	0.96	1.00	rs3759348	0	0.23
<i>HTR1A</i>	0	5	5	0.54	0.55	0.79	1.00	rs10042486	0	0.55
<i>AVPR1B</i>	0	0	0	NA	NA	NA	NA	NA	NA	NA
<i>CHRFAM7A</i>	0	0	0	NA	NA	NA	NA	NA	NA	NA

Note Analytical p-values were determined using SNPTTest for the autosomes and logistic regression in PLINK for the X chromosome.

Permutations (N=10,000) were performed to determine uncorrected SNP p-values, gene-wide corrected p-values, overall corrected p-values and p-values for number of SNPs with $p < 0.05$. All p-values were calculated assuming an additive model. P-values < 0.05 are shown in bold.