

**Association of *PCK1* with Body Mass Index and other metabolic features in patients with psychotropic treatments.**

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17

18 **ABSTRACT**

19 Weight gain is a major health problem among psychiatric populations. It implicates several receptors and  
20 hormones involved in energy balance and metabolism. Phosphoenolpyruvate carboxykinase 1 (PCK1) is  
21 a rate-controlling enzyme involved in gluconeogenesis, glyceroneogenesis and cataplerosis and has  
22 been related to obesity and diabetes phenotypes in animals and humans. The aim of this study was to  
23 investigate the association of *PCK1* polymorphisms with metabolic traits in psychiatric patients treated  
24 with psychotropic drugs inducing weight gain and in general population samples. One polymorphism  
25 (*rs11552145G>A*) significantly associated with Body Mass Index in the psychiatric discovery sample  
26 ( $n=478$ ) was replicated in 2 other psychiatric samples ( $n_1=168$ ,  $n_2=188$ ), with *AA*-genotype carriers having  
27 lower Body Mass Index as compared to *G*-allele carriers. Stronger associations were found among  
28 women younger than 45 years carrying *AA*-genotype as compared to *G*-allele carriers (-2.25 kg/m<sup>2</sup>,  
29  $n=151$ ,  $p=0.009$ ) and in the discovery sample (-2.20 kg/m<sup>2</sup>,  $n=423$ ,  $p=0.0004$ ). In the discovery sample for  
30 which metabolic parameters were available, *AA*-genotype showed lower waist circumference (-6.86 cm,  
31  $p=0.008$ ) and triglycerides levels (-5.58 mg/100mL,  $p<0.002$ ) when compared to *G*-allele carriers. Finally,  
32 waist to hip ratio was associated with *rs6070157* (proxy of *rs11552145*,  $r^2=0.99$ ) in a population-based  
33 sample ( $N=123'865$ ,  $p=0.022$ ). Our results suggest an association of *rs11552145G>A* polymorphism with  
34 metabolic-related traits, especially in psychiatric populations and in women younger than 45 years old.

## 35 INTRODUCTION

36 Weight gain is a known side-effect of psychotropic drugs such as antipsychotics, mood stabilizers and  
37 antidepressants.<sup>1</sup> Psychotropic-induced weight gain can lead to many metabolic complications (e.g.  
38 increase in triglycerides, cholesterol, waist circumference) and is related to comorbidities such as  
39 diabetes, hypertension and other cardiovascular diseases.<sup>2</sup> Psychiatric populations have a 10 to 25 year  
40 reduction in life expectancy due to comorbidities and to the psychiatric illness itself, corresponding to a 2-  
41 3 fold increased mortality rate when compared to healthy populations.<sup>3</sup> Obesity is attributed to the  
42 psychiatric illness, to behavioral and environmental factors (i.e. diet, exercise, smoking), as well as  
43 genetic factors.<sup>4</sup> Besides, an interaction between genetic factors and psychotropic drug inducing weight  
44 gain has been described implicating several receptors (e.g. serotonin and dopamine receptors) and  
45 hormones (e.g. leptin) involved in energy balance or metabolism pathways.<sup>5, 6</sup>

46 The *Phosphoenolpyruvate carboxykinase (PCK)* gene codes for an enzyme involved in the  
47 gluconeogenesis<sup>7</sup> and is found in two forms, PCK1 (cytosolic) and PCK2 (mitochondrial). Both enzymes  
48 are expressed equally in the liver but their expression may vary depending on the tissue.<sup>7, 8</sup> PCK  
49 catalyzes the conversion from oxalacetate into phosphoenolpyruvate (a rate-controlling step of  
50 gluconeogenesis) and is also involved in glyceroneogenesis and cataplerosis.<sup>7</sup> Of note, *PCK* is a  
51 downstream gene of the *CREB-regulated transcription coactivator 1 (CRTC1)* which is implicated in  
52 hypothalamic control of food intake<sup>9, 10</sup> and we recently found in general and psychiatric populations that

53 carriers of a variant allele of a *CRTC1* polymorphism appear to be protected against weight gain  
54 especially in women younger than 45 years old.<sup>11</sup>

55 Rodents who over-express *PCK1* and *PCK2* were obese, hyperglycemic and insulin resistant<sup>12, 13</sup>  
56 whereas mice that under-expressed *PCK1* and *PCK2* developed a lipodystrophy type of metabolic  
57 syndrome.<sup>14</sup> This is in line with the positive correlation found between *PCK1* mRNA expression levels and  
58 Body Mass Index (BMI), body fat percentage, triglycerides (TG) and cholesterol (CHOL) levels in  
59 subcutaneous adipose tissue of non-menopausal women.<sup>15</sup> In humans, regions near *PCK1* locus have  
60 been related to obesity or fat mass<sup>16, 17</sup> and several positive associations have been reported between  
61 *PCK1* polymorphisms and type 2 diabetes<sup>18-20</sup> although these results could not always be replicated.<sup>21</sup>  
62 Other studies conducted in the general population showed no significant association between *PCK1*  
63 polymorphisms and BMI, waist circumference (WC) or physical activity.<sup>22</sup> A case-control study in a  
64 diabetic versus non diabetic population also found that non diabetic homozygous for the minor allele of a  
65 *PCK1* polymorphism (+4824T>C) had increased levels of high density lipoproteins (HDL) and lower TG  
66 levels when compared to wild type.<sup>23</sup> Thus growing evidence supports that *PCK* contributes to obesity  
67 and metabolic syndrome in the general population but, to our knowledge, no studies have yet been  
68 conducted in psychiatric populations which are at high risk for developing obesity and metabolic  
69 syndrome. The aim of the present study was to analyze whether *PCK1* polymorphisms were associated  
70 with BMI and other metabolic traits (i.e. WC, blood glucose levels (BGL), low density lipoprotein (LDL),

71 HDL, CHOL and TG in three independent psychiatric populations treated with drugs inducing weight gain  
72 and in 3 large general population cohorts. As a secondary aim, we wanted to explore how *PCK1* and  
73 *CRTC1* polymorphisms are associated with BMI in a combined analysis.

## 74 **MATERIALS AND METHODS**

### 75 **Psychiatric sample description**

76 The first psychiatric sample (discovery sample) was recruited during a longitudinal follow-up study on  
77 metabolic syndrome at the Lausanne Psychiatric University Hospital (started in 2007, ongoing). 478  
78 Caucasian patients switching or starting a treatment with drugs known to potentially induce weight gain  
79 (aripiprazole, amisulpride, clozapine, olanzapine, quetiapine, risperidone, mirtazapine, lithium and/or  
80 valproate) were included. Weight, height and other clinical variables were reported at baseline and at 1, 2,  
81 3, 6, 9 and 12 months after starting the treatment according to published monitoring guidelines of weight  
82 and metabolic syndrome parameters.<sup>24</sup> Most patients had already received other psychotropic treatment  
83 before the current treatment. Fasting BGL and lipid levels (i.e. CHOL, TG, LDL, HDL) were analyzed on a  
84 routine basis on blood samples using a Modular P apparatus (Roche Diagnostics, Switzerland). For  
85 patients for whom drug plasma determinations were available, we conducted preliminary analysis on the  
86 influence of compliance on the observed associations. For this purpose, we defined an arbitrary threshold  
87 at 10% of the minimal therapeutic drug plasma concentration<sup>25</sup> (i.e. 2, 35, 10, 2, 15, 10, 2 ng/mL, 0.05  
88 mmol/L, 5 mg/L for olanzapine, clozapine, quetiapine, risperidone + hydroxy-risperidone, aripiprazole,

89 amisulpride, paliperidone, lithium, and valproate) to ensure psychotropic drug intake. Similar results to  
90 those described in the present paper were obtained (data not shown). Thus, to increase the power of  
91 the study, the whole cohort was used for statistical analysis. Two other psychiatric samples were used as  
92 replication samples. A retrospective study (replication sample 1) was conducted in an outpatient setting in  
93 Geneva University Hospital in 2007. 168 Caucasian patients treated for at least 3 months with  
94 olanzapine, clozapine, quetiapine, risperidone, lithium and/or valproate were recruited. Another  
95 retrospective outpatient study in Lausanne, replication sample 2 (started in 2010, ongoing) included 188  
96 Caucasian patients mostly treated for more than one year with aripiprazole, amisulpride, clozapine,  
97 olanzapine, quetiapine, risperidone, mirtazapine, lithium and/or valproate. For both replication samples,  
98 questionnaires were filled during one of the patient routine follow-ups and weight, height, WC and  
99 treatment duration were reported among other clinical variables. Weight before starting psychotropic  
100 treatment was self-reported or extracted from medical files. As shown previously,<sup>11</sup> self-reported weight  
101 was found to be a reliable estimate of the measured weight extracted from medical files.

102 In all samples, patients with previous treatments were included after having switched medication. The  
103 latest introduced psychotropic medication was considered as the main psychotropic treatment. Weight  
104 (patients with light clothes and without shoes) was measured in kilograms to the nearest kg. Height was  
105 measured using a height gauge to the nearest cm. WC was measured to the nearest cm. BMI for all  
106 individuals was obtained by dividing weight (in kg) by squared height (in m<sup>2</sup>).



107 Written informed consent was provided by all individuals or by their legal representatives and the studies  
108 were approved by the ethics committee of the corresponding centers. Further details of the 3 psychiatric  
109 cohorts have already been described elsewhere.<sup>11, 26</sup> Of note, the present study refers to the same 3  
110 psychiatric populations than in our previous paper,<sup>11</sup> but with a larger number of patients included in the  
111 discovery cohort and in the replication sample 2 (inclusions ongoing).

### 112 **Population-based samples**

113 Significant results were tested for replication in three population based samples: Participants in CoLaus  
114 (n=5'338) were recruited between June 2003 and May 2006 in the Lausanne area as described  
115 previously.<sup>27</sup> The Genetic Investigation of Anthropometric Traits Consortium (GIANT) performed a meta-  
116 analysis of genome-wide association study data with a discovery set of 123'865 individuals of European  
117 ancestry from 46 studies for height,<sup>28</sup> BMI,<sup>4</sup> and waist-to-hip ratio (WHR).<sup>29</sup> Finally, the second set of  
118 association summary statistics for general populations (Global Lipids Genetics Consortium) was  
119 downloaded from "Genome Wide Associations Scans for Total Cholesterol, HDL-C, LDL-C and  
120 triglycerides" website<sup>30</sup> and contains data related to lipid traits (n=100'184). Of note, CoLaus is part of  
121 both GIANT and Global Lipids Genetics Consortium.

### 122 **SNP selection and Genotyping**

123 In a first step, the best replicated and studied *PCK1* polymorphism in the literature (i.e. *rs2071023*) was  
124 manually genotyped using TaqMan allelic discrimination assay (ABI PRISM 7000 Sequence Detection  
125 System; Applied Biosystems, Rotkreuz, Switzerland, TaqMan SNP genotyping assays ID: C\_2508731\_1).  
126 Additionally, three SNPS which were available in the CardioMetaboChip were also considered for  
127 analysis (i.e. *rs11552145*, *rs707555* and *rs8123020*). The CardioMetaboChip is a custom Illumina iSelect  
128 genotyping array designed to test DNA variation of 200'000 SNPs from regions identified by large scale  
129 meta-analyses of genome wide association studies (GWAS) for metabolic and cardiovascular traits.  
130 Quality control excluded samples from the analysis if gender was inconsistent with genetic data from X-  
131 linked markers, genotype call rate <0.96, Gene Call (GC) score <0.15. GenomeStudio Data Analysis  
132 Software was used to export results generated by Illumina CardioMetaboChip. In total, four SNPs were  
133 considered for analyses with minor allele frequency (MAF) higher than 0.10 (Table S-1). All of them were  
134 in Hardy Weinberg Equilibrium (HWE) (Table S-2). Finally, looking at HapMap Genome Browser (release  
135 27, MAF>0.10, cutoff of  $r^2$  set at 0.8),<sup>31</sup> we found that several *PCK1* tagging SNPs were in linkage  
136 disequilibrium (LD) with our four selected SNPs (see details in Figure S-1).

137 DNA was extracted from blood samples as described by the manufacturer's protocol using Flexigene  
138 DNA kit and QIAamp DNA Blood Mini QIAcube Kit (Qiagen AG, Switzerland) for 834 Caucasian patients  
139 from the three psychiatric cohorts. Genotyping of the *rs3746266A>G* SNP from *CRTC1* was performed  
140 using TaqMan allelic discrimination assay (ABI PRISM 7000 Sequence Detection System; Applied

141 Biosystems, Rotkreuz, Switzerland) and according to the manufacturers protocol as described  
142 elsewhere.<sup>11</sup> Genotyping of the CoLaus subjects was performed using the Affymetrix GeneChip Human  
143 Mapping 500K array set as previously described.<sup>27</sup>

#### 144 **Variables of the study**

145 The main outcome analyzed in the three psychiatric samples was the BMI [kg/m<sup>2</sup>] used as a continuous  
146 variable. Other outcomes studied were WC [cm], LDL, HDL, TG, CHOL and BGL [mg/100mL]. *PCK1*  
147 genotypes were grouped and analyzed in recessive (for *rs11552145*, *rs707555* and *rs8123020*) and  
148 dominant (for *rs2071023*) models according to their association with BMI showed in preliminary analyses.  
149 Other covariates were extracted from medical files or during the interview and included demographic data  
150 (i.e. sex, age and ethnicity) as well as history of treatment (type of psychotropic drug and treatment  
151 duration). In order to preserve homogeneity of the samples, only patients treated up to 24 months were  
152 taken into account in combined (i.e discovery plus replication) psychiatric sample analyses.

#### 153 **Statistical analysis**

##### 154 *Psychiatric Samples*

155 HWE was determined for each polymorphism by a chi-square test. Statistical analyses were done using  
156 STATA 12.1 (StataCorp, College Station TX, USA) and R version 2.11.1 software.<sup>32</sup> P-values less than  
157 0.05 were considered as statistically significant and when necessary, Bonferroni correction for multiple

158 tests was applied. Eventually, differences in sample size might be due to missing genotypes and/or  
159 covariates. First, exploratory analyses were conducted to explore differences in BMI between genetic  
160 groups in the three psychiatric samples using Mann–Whitney U non parametric test. To fit a longitudinal  
161 model on the BMI trend, due to complex and non-linear BMI evolution in time and presence of multiple  
162 observations per individual which introduces interdependence among observations, a Generalized  
163 Additive Mixed Model (GAMM) was used to assess the association of genetic polymorphism with BMI  
164 adjusted by sex, age, treatment and treatment duration. This allowed a smooth trend for the response in  
165 time based on multiple observations for each patient (using a thin plate regression spline basis). A  
166 random effect at the subject level was also introduced to take the dependence structure of observed data  
167 into account.<sup>33</sup> The GAMMs were fitted using the mgcv package of R (settings were fixed at package  
168 defaults). To be more conservative, the uncertainty of estimated parameters was assessed by 1'000  
169 bootstraps on individuals. For those p-values lower than 0.001, 10'000 bootstraps were performed  
170 whenever possible. Multivariate analysis used the same methodology as previously described for the  
171 upstream *CRTC1* gene:<sup>11</sup> It was first conducted in the discovery sample and the significant results were  
172 tested for replication in the two replication samples. In fitted longitudinal models, stratification by sex, and  
173 in some cases by age, was applied when analyzing all samples together. Also, analyzes on WC and on  
174 other metabolic traits (i.e. BGL and lipid levels) were conducted in the discovery sample (data available  
175 only in this sample) and only for *rs11552145* and *rs2071023* polymorphisms. Due to some missing data  
176 and the relatively low number of variant alleles of *rs707555* and *rs8123020*, analysis could not be

177 conducted for these polymorphisms. Finally it should be mentioned that preliminary analysis on *PCK1*  
178 haplotypes and BMI for the 3 SNPs that formed a haplotype block (i.e. *rs11552145*, *rs707555* and  
179 *rs8123020*) showed no significant results (results not shown).

### 180 *Population-Based Samples*

181 Significant results from *PCK1* polymorphisms in the discovery sample (i.e. *rs6070157*, proxy of  
182 *rs11552145*,  $r^2=0.99$  and *rs2071023*) were further tested for replication in the three population samples  
183 (CoLaus, GIANT and Global Lipids Genetics Consortium).

184 The associations of *PCK1* polymorphisms with adiposity markers such as BMI, WC, fat mass and lipid  
185 factors were analyzed using multiple linear regression with additive model in which potential confounding  
186 factors such as age, sex, and smoking status were added as covariates in the CoLaus study. For  
187 anthropometric traits (BMI, WHR) we performed lookups from the summary statistics of the GIANT  
188 consortium. For lipid traits (i.e. TG, HDL, CHOL), we looked up association results from the Global Lipid  
189 Consortium.<sup>30</sup>

## 190 **RESULTS**

191 Table S-3 shows the characteristics of the three psychiatric samples. The discovery sample included  
192 patients with the shortest treatment duration (median of 6 months versus 27.4 and 36 months in the  
193 replication 1 and 2, respectively,  $p=0.0001$ ), as well as the lowest BMI (current median BMI of 25 versus

194 28 and 27 kg/m<sup>2</sup> for replication 1 and 2, respectively, p=0.0001) and the lowest prevalence of obesity  
195 (BMI≥30 kg/m<sup>2</sup>) (18% versus 40% and 27%, respectively, p<0.001).

#### 196 **Association of *PCK1* polymorphisms with BMI in psychiatric populations**

197 Table S-2 shows *PCK1* genotype distribution among the three psychiatric samples. No significant  
198 associations were found between *PCK1* polymorphisms and baseline BMI when exploratory analyses  
199 were conducted (Table S-4). However, a trend and a significant association was found between  
200 *rs11552145* and *rs2071023* and current BMI (BMI at the last follow-up assessment) in the discovery (p-  
201 corrected 0.08 and 0.018, respectively) and in the combined sample (p-corrected 0.01 and 0.003,  
202 respectively). Figure 1 shows the association of *PCK1 rs11552145* polymorphism with BMI.

203 Multivariate analyses were first conducted in the discovery sample for the four SNPs (Table 1). Carriers of  
204 *rs11552145-AA* genotype had, on average, 2.20 lower BMI units when compared to carriers of *G-allele*  
205 (p= 0.0004). Similar results were found for *rs2071023-CC* genotype which had 1.27 lower BMI units when  
206 compared to *G-allele* carriers (p= 0.004). Significant results were replicated for *rs11552145* and BMI  
207 when combining the 2 replication samples. *AA* carriers had 1.42 lower BMI units when compared to *G-*  
208 *allele* carriers (p= 0.009). When combining the three samples similar results were found for both  
209 *rs11552145* and *rs2071023* (estimates -1.89 and -1.11 kg/m<sup>2</sup> and p<0.001 and p<0.001, respectively).  
210 Explained variances in the combined sample for *rs11552145* and *rs2071023* were 0.65% and 0.85%,  
211 respectively. For both *rs11552145* and *rs2071023*, further analyses stratified by sex and age were

212 conducted in the three samples combined. *rs2071023* was associated with BMI only in women whereas  
213 for *rs11552145* an association was found in both genders, but a stronger association was found among  
214 women younger than 45 years, where *rs11552145* AA-carriers had 2.25 lower BMI units when compared  
215 to *G-allele* carriers (p-value 0.009, explained variance 0.77%). No significant results were found for the  
216 other two SNPs *rs8123020* and *rs707555*.

### 217 ***PCK1* polymorphisms and metabolic parameters in psychiatric populations**

218 The association of *rs11552145* and *rs2071023* with other metabolic parameters (i.e. WC, BGL, CHOL,  
219 HDL, LDL and TG) was analyzed in the discovery sample (Table 2). In agreement with results on BMI,  
220 both carriers of *rs11552145-AA* genotype and *rs2071023-CC* genotype had significantly lower WC (-6.86  
221 and -3.45 cm, p-values 0.008 and 0.004, respectively). In addition, *rs11552145-AA* genotype carriers had  
222 lower TG levels when compared to *G-allele* carriers (-27.59 mg/100mL, p-value <0.002).

### 223 **Association of *CRTC1* and *PCK1* with BMI**

224 Since *PCK1* is a downstream gene of *CRTC1*, we wanted to further analyze the association of both  
225 *CRTC1 rs3746266A>G* previously associated with BMI<sup>11</sup> and *PCK1 rs11552145G>A* with BMI over  
226 treatment duration (Figure 2). In the combined analysis, *CRTC1 G-allele* and *PCK1 AA* genotype were  
227 pooled together since carriers of these alleles showed lower BMI units when compared to others when  
228 analyzed individually. Thus, in the multivariate analysis adjusted by age, sex, treatment and treatment

229 duration (n=610), those carriers of *AA* genotype for *CRTC1* and *PCK1* or carriers of *G-allele* of *CRTC1*  
230 and *PCK1* had 0.79 less units of BMI when compared to the reference group (p 0.009). Similarly, carriers  
231 of *PCK1 AA* genotype and *CRTC1 G-allele* had 2.43 less units of BMI compared to the reference group  
232 (p<0.001).

### 233 **Functional relevance of *PCK1* polymorphisms**

234 We explored further the functional relevance of *PCK1* polymorphisms. For *rs11552145* and *rs707555*, the  
235 two variants in coding regions, PolyPhen-2<sup>34</sup> predicted both mutations to be benign. Further analysis on  
236 gene expression platform (GTEx portal<sup>35</sup>) showed significant differences in *rs11552145* expression in  
237 subcutaneous adipose tissue with homozygous carriers of the variant allele having lower expression (p  
238 0.03). No differences were found for *rs707555*, *rs8123020* or *rs2071023*.

### 239 ***PCK1* polymorphisms in population-based samples**

240 The association of *rs6070157* (proxy of *rs11552145*,  $r^2=0.97$ ) and *rs2071023* with BMI and other  
241 metabolic features was further analyzed for replication in three population-based samples (GIANT,  
242 CoLaus and Global Lipids Genetics Consortium). Significant associations were found between the two  
243 *PCK1* polymorphisms and the WHR in the GIANT cohort (N=123'865) for women and for both genders  
244 combined. In addition, significant associations were found for *rs2071023* with HDL and TGL in the Global  
245 Lipids Genetics Consortium (N=100'184; p-values: 0.003 and 0.03, respectively) (Table 3).



246 **DISCUSSION**

247 Growing evidence supports that *PCK* can contribute to obesity and metabolic syndrome both in animal  
248 models and in the general population.<sup>12-14, 16, 17</sup> The main results from this study suggest that carriers of  
249 *PCK1 rs11552145-AA* genotype have lower BMI when compared to *G-allele* carriers in psychiatric  
250 patients treated with weight gain inducing drugs, this association being found in the discovery sample and  
251 in the replication samples analyzed together. Moreover, low WC and TG levels were associated with  
252 *rs11552145-AA* in the discovery sample and low BMI and WC were found as well for *rs2071023-CC*  
253 genotype. To our knowledge, this is the first study carried out in psychiatric patients and the first one to  
254 find a positive association between *PCK1* polymorphisms and BMI.

255 In addition, as a proof of concept, a positive association was found in the general population (GIANT  
256 cohort) with WHR and *rs6070157* (proxy of *rs11552145*,  $r^2=0.99$ ) and *rs2071023*, again suggesting an  
257 association of the polymorphisms with obesity traits, although the value was much weaker than in  
258 psychiatric samples and being of no clinical significance in the general population. This goes in the same  
259 line of what we found in previous results,<sup>11</sup> since psychiatric populations are at high risk of obesity and/or  
260 metabolic syndrome. *PCK1* function has been previously associated in animal models with glucose and  
261 lipid homeostasis and also with weight gain.<sup>36</sup> In humans, the main investigated polymorphism is the -  
262 *232C/G (rs2071023)* which is located in the promoter region of *PCK1*. This polymorphism has been  
263 previously associated with type 2 diabetes (T2DM) and gestational diabetes mellitus (GDM) but with

264 conflicting results in different ethnicities. Positive associations were found among South Asian and  
265 Japanese populations<sup>20, 37</sup> concluding that carriers of the minor allele (*GG*) were at risk of developing  
266 T2DM, whereas no significant findings were found in German or Danish Caucasian populations.<sup>18, 21</sup>  
267 Finally, a case series study conducted in 3 Maltese women found that those who developed GDM carried  
268 the homozygous variant allele, but these results must be replicated in larger cohorts.<sup>38</sup> In the present  
269 study, no association was found between *rs2071023* and BGL, although the diabetes phenotype was not  
270 assessed. Additionally, and consistent with our results, another *PCK1* polymorphism (*rs707555*) showed  
271 no significant association with anthropometric traits such as WC, weight and fat mass or BMI.<sup>22, 39</sup>  
272 Analyses were conducted in the combined discovery and replication samples for treatment duration up to  
273 24 months. Different effect sizes, detected in the discovery versus the replication samples, could be  
274 explained by lower prevalence of obesity at baseline and shorter treatment durations in the discovery  
275 sample (Table S-3), since both baseline BMI and treatment duration are moderators of weight gain.<sup>40</sup>  
276 However, to exclude a winner's curse event, these results need to be replicated in other short treatment  
277 duration samples.

278 Of note, in the present study as in previous genetic studies, genetically explained variances of BMI are  
279 quite low suggesting that BMI and metabolic features are influenced by multiple genetic factors as  
280 previously described in the literature.<sup>4</sup> However, in the present study, *rs11552145* was strongly  
281 associated with BMI in the subgroup of women younger than 45 years and the observed difference in BMI

282 between genotypes is of clinical significance. This result is in agreement with our previous study showing  
283 that the association between a polymorphism of *CRTC1* (an upstream gene of *PCK1*) and BMI was  
284 higher in women younger than 45 years as compared to non-gender stratified sample.<sup>11</sup> In addition, a  
285 positive correlation was found between *PCK1* mRNA expression levels and BMI in a study conducted  
286 with non-menopausal women.<sup>15</sup> Other pharmacogenetic studies also highlighted the importance of  
287 stratifying by sex.<sup>41, 42</sup> This finding could be tentatively explained by the influence of estrogen circulating  
288 levels on energy balance.<sup>43</sup> Thus, a lack of estrogen in mice was related to obesity, decreasing fasting  
289 blood glucose levels, activating AMPK and reducing the expression of gluconeogenic genes, such as  
290 *PCK* in the liver.<sup>44, 45</sup> However, this hypothesis could not be tested in our samples as estrogen circulating  
291 levels were not measured.

292 In order to assess the contribution of *PCK1* and *CRTC1* polymorphisms on BMI, analyses combining both  
293 SNPs were conducted. An additive association with BMI was observed over treatment duration among  
294 carriers of *CRTC1 rs3746266 G-allele* and *PCK1 rs11552145 AA* genotype which had lower BMI when  
295 compared to the reference group. As described elsewhere,<sup>46</sup> *PCK* family genes contain in their promoter  
296 region a CREB-regulated element binding site where *CRTC1* binds, enhancing *PCK* expression. In the  
297 present study, the strongest associations were found among psychiatric population under psychotropic  
298 treatment which could be explained by the additive effect between *PCK1* and *CRTC1* genes and  
299 psychotropic drugs. In particular, *CRTC1* is modulated, among other mechanisms, by adenosine

300 monophosphate protein kinase (AMPK) which is increased by antipsychotics.<sup>47</sup> Besides, several  
301 polymorphisms on the *AMPK* gene, showed an association with weight gain induced by antipsychotics.<sup>48</sup>  
302 *AMPK* has also been related to gluconeogenesis modulation.<sup>49</sup> Another study conducted in rats showed  
303 that olanzapine increased the mRNA levels of glucose-6-phosphatase in the liver.<sup>47</sup> Although little is  
304 known about *PCK* family genes and psychotropic drugs, *PCK* expression is inhibited by lithium in isolated  
305 hepatocytes from fasted rats<sup>50</sup>. In addition, chronic clozapine administration upregulates *PCK* expression  
306 in rat liver.<sup>51</sup> Therefore, several genes coding for enzymes implicated in the gluconeogenic pathway have  
307 been associated with antipsychotics.

308 Finally, in our sample, higher associations were found among psychiatric patients rather than in general  
309 population possibly explained by the high prevalence of overweight or obesity in psychiatric patients  
310 induced by the illness, the lifestyle (diet, physical activity), in addition to the direct effect of drug inducing  
311 weight gain.

312 Some limitations of the present study must be mentioned. Firstly, patients were not drug naive, therefore,  
313 we could not assess whether the association between the polymorphisms and BMI or other phenotypes  
314 was influenced by the psychiatric illness itself and/or by the psychotropic treatment. Secondly, although  
315 the main inclusion criteria for patients in the present study was that they were receiving psychotropic  
316 drugs known to induce weight gain (i.e aripiprazole, amisulpride, clozapine, olanzapine, quetiapine,  
317 risperidone, mirtazapine, lithium and/or valproate), other drugs possibly inducing weight (psychotropic

318 and/or somatic drugs) were prescribed, the influence of which could not be evaluated. This study was  
319 conducted in Caucasians, thus results cannot be extrapolated to other ethnicities. Not all tagging SNPs  
320 could be tested due to limited availability of the genotypes. In addition, no significant associations with  
321 BMI were found for the two other tested SNPs (*rs707555* and *rs8123020*), either because of a lack of  
322 effect or a lack of power due to the low MAF. Further replications of this study should increase sample  
323 size in order to test low MAF polymorphisms and to increase the coverage of *PCK1* gene by including  
324 other tagging SNPs. Finally, variants obtained through GWAS should be also considered in further  
325 analysis, in particular those on gluconeogenic pathway. It has thus been recently shown that *PCK1*  
326 expression is regulated by *CAMK1D*,<sup>52</sup> a gene previously related to diabetes in GWAS.<sup>53</sup>

327 In conclusion, this is the first study investigating the association of *PCK1* polymorphisms with BMI and  
328 other metabolic traits in psychiatric populations. Higher associations were found in psychiatric patients  
329 treated with psychotropic drugs over short periods, and in women younger than 45 years. In addition, the  
330 present study supports research on pathway related genes such as *CRTC1* and *PCK1*, which may have  
331 an additive association with BMI. Further studies on the same and other pathways are therefore  
332 warranted, to increase our knowledge on the multiple genetic risk factors influencing obesity, lipid  
333 disturbances or metabolic syndrome in psychiatric population. This could ultimately help, by the  
334 determination and the combination of multiple genetic and clinical risk factors, to better adapt  
335 pharmacological treatments among particular populations at risk.

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- 472

Table 1. Multivariate analysis of *PCK1* polymorphisms and BMI.

	n	<i>rs11552145</i>			<i>rs2071023</i>			<i>rs707555</i>			<i>rs8123020</i>		
		BMI difference [kg/m <sup>2</sup> ] between AA and G-allele carriers (95% CI)	p-value	E var (%)	BMI difference [kg/m <sup>2</sup> ] between CC and G-allele carriers (95% CI)	p-value	E var (%)	BMI difference [kg/m <sup>2</sup> ] between GG and C-allele carriers (95% CI)	p-value	E var (%)	BMI difference [kg/m <sup>2</sup> ] between TT and C-allele carriers (95% CI)	p-value	E var (%)
Discovery Sample#	423	-2.20 (-3.35 – (-)1.12)	<b>0.0004</b> <sup>§</sup>	0.84	-1.27 (-2.09 – (-)0.49)	<b>0.004</b> <sup>§</sup>	1.24	-0.38 (-3.26 – 2.21)	1.00 <sup>§</sup>		-0.83 (-2.46 – 0.82)	0.5 <sup>§</sup>	
Replication 1	168	-1.82 (-4.24 – 0.45)	0.07		-0.73 (-1.97 – 0.61)	0.1							
Replication 2	183	-0.64 (-2.72 – 1.22)	0.2		-0.18 (-1.40 – 1.04)	0.4							
Replication 1 and Replication 2*	337	-1.42 (-2.69 – (-)0.25)	<b>0.009</b>	0.49	-0.53 (-1.40 – 0.41)	0.1							
Combined sample*	760	-1.89 (-2.67 – (-)1.09)	<b>&lt;0.001</b>	0.65	-1.11 (-1.71 – (-)0.52)	<b>&lt;0.001</b>	0.85						
Combined sample men*	377	-1.98 (-3.18 – (-)0.85)	<b>0.001</b>	1.01	-0.63 (-1.49 – 0.23)	0.08							
Combined sample women*	383	-1.70 (-2.79 – (-)0.62)	<b>0.002</b>	0.35	-1.58 (-2.41 – (-)0.72)	<b>0.0001</b>	1.55						
Combined sample women <45 years*	151	-2.25 (-4.18 – (-)0.45)	<b>0.009</b>	0.77	-1.48 (-2.74 – (-)0.11)	<b>0.01</b>	0.57						
Combined sample women ≥ 45 years*	235	-1.54 (-3.59 – 0.86)	0.06		-1.68 (-2.74 – (-)0.60)	<b>0.002</b>	1.63						

#bootstrap at 10 000. Only significant results in discovery sample were further tested for replication.

<sup>§</sup>p-corrected value for discovery sample.

\*Patients treated for up to 24 months.

E var (%): explained variance by the polymorphism, only calculated for significant tests.

Adjusted by: age, sex, treatment (antipsychotic or mood stabilizer) and treatment duration. Bootstrap at 1000.

**Table 2. Association of *PCK1* polymorphisms with other metabolic phenotypes in the discovery sample.**

<i>rs11552145</i>	n	Difference between AA and G-allele carriers (95% CI)	p-value <sup>§</sup>	E.var (%)
WC [cm]	408	-6.86 (-11.07 – (-)2.59)	<b>0.008</b>	1.04
HDL** [mg /100 mL]	305	5.85 (-1.95 – 14.04)	0.13	
TG** [mg /100 mL]	305	-27.59 (-39.16 – (-)14.24)	<b>&lt;0.002</b>	0.90
LDL** [mg /100 mL]	299	-10.14 (-19.89 – 2.34)	0.12	
CHOL** [mg /100 mL]	307	-10.53 (-28.08 – 8.19)	0.28	
BGL** [mg /100 mL]	289	-3.6 (-8.28 – 0.36)	0.09	
<i>rs2071023</i>	n	Difference between CC and G-allele carriers (95% CI)	p-value <sup>§</sup>	E.var (%)
WC [cm]	409	-3.45 (-5.74 – (-)1.18)	<b>0.004</b>	1.14
HDL** [mg /100 mL]	305	1.95 (-0.39 - 4.29)	0.12	
TG** [mg /100 mL]	305	-8.01 (-19.58 – 3.56)	0.64	
LDL** [mg /100 mL]	299	-2.34 (-10.14 – 5.07)	0.54	
CHOL** [mg /100 mL]	307	-3.12 (-11.7 – 5.07)	0.32	
BGL** [mg /100 mL]	289	2.52(-2.16 - 5.94)	0.42	

\*\*Fasting patients

<sup>§</sup>p-corrected value for discovery sample.

E. var (%): explained variance by the polymorphism (%) calculated only for significant tests.

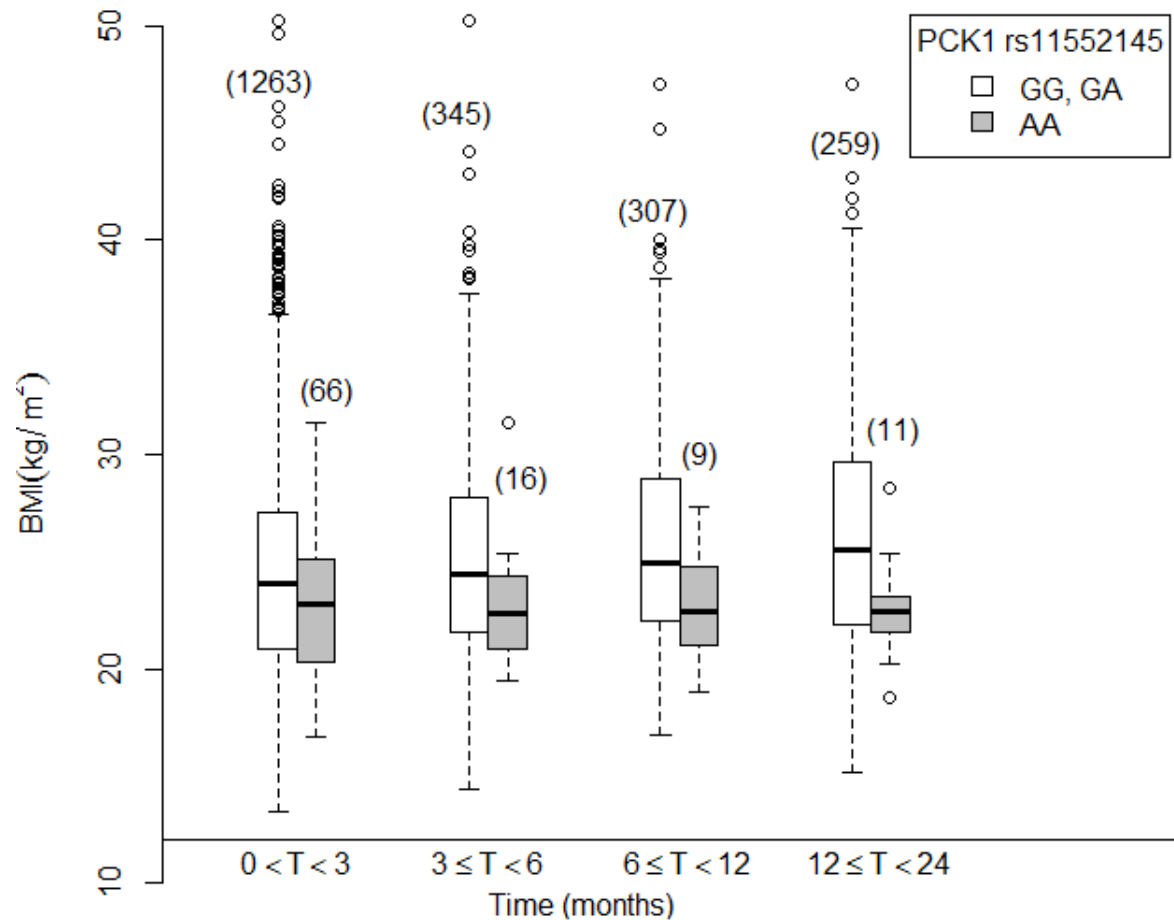
Adjusted by: BMI, age, sex, treatment (antipsychotic or mood stabilizer) and treatment duration. Bootstrap at 1000. WC: waist circumference, HDL: high lipoprotein, TG: triglycerides, CHOL: cholesterol, BGL: blood glucose levels

**Table 3. Association of *PCK1* polymorphisms with metabolic traits in population based samples.**

	CoLaus (n=5'338)		GIANT (n= 123'865)		Global Lipids Genetics Consortium (n= 100'184)	
<i>rs6070157</i> (proxy of <i>rs11552145</i> , $r^2 = 0.99$ )	$\beta$ (SE)	p-value	$\beta$ (SE)	p-value	$\beta$ (SE)	p-value
<b>Anthropometric traits</b>						
BMI [kg/m <sup>2</sup> ]	-0.0016 (0.0258)	0.95	0.0025 (0.0053)	0.63	N.A	N.A
WC [cm]	-0.0026 (0.0258)	0.92	N.A	N.A	N.A	N.A
WHR	-0.0123 (0.0258)	0.63	-0.0163 (0.0071)	<b>0.02</b>	N.A	N.A
Men	0.0086 (0.038)	0.82	0.0151 (0.0096)	0.11	N.A	N.A
Women	-0.0308 (0.035)	0.39	-0.0202 (0.0089)	<b>0.02</b>	N.A	N.A
<b>Lipids</b>						
HDL [mg /100 mL]	0.38 (0.37)	0.30	N.A	N.A	0.16 (0.12)	0.20
CHOL [mg /100 mL]	-0.14 (1.02)	0.89	N.A	N.A	0.05 (0.12)	0.69
TG [mg /100 mL]	-3.25 (2.57)	0.21	N.A	N.A	-0.10 (-0.28)	0.73
LDL [mg /100 mL]	-0.41 (0.90)	0.65	N.A	N.A	N.A	N.A
<b>BGL [mg /100 mL]</b>	<b>0.85 (0.55)</b>	<b>0.12</b>	<b>N.A</b>	<b>N.A</b>	<b>-0.06 (-0.08)</b>	<b>0.50</b>
<i>rs2071023</i>	$\beta$ (SE)	p-value	$\beta$ (SE)	p-value	$\beta$ (SE)	p-value
<b>Anthropometric traits</b>						
BMI [kg/m <sup>2</sup> ]	-0.0196 (0.0198)	0.32	-0.0028 (0.0043)	0.2	N.A	N.A
WC [cm]	-0.0087 (0.0198)	0.66	N.A	N.A	N.A	N.A
WHR	0.0026 (0.0198)	0.90	-0.0195 (0.0057)	<b>0.001</b>	N.A	N.A
Men	-0.0145 (0.029)	0.61	-0.0013 (0.0077)	0.87	N.A	N.A
Women	0.0184 (0.028)	0.50	-0.0154 (0.0071)	<b>0.03</b>	N.A	N.A
<b>Lipids</b>						
HDL [mg /100 mL]	-0.54 (0.28)	0.06	N.A	N.A	0.28 (0.12)	<b>0.003</b>
CHOL [mg /100 mL]	-0.99 (0.78)	0.20	N.A	N.A	0.078 (0.12)	0.54
TG [mg /100 mL]	1.11 (1.98)	0.57	N.A	N.A	-0.61 (-0.28)	<b>0.03</b>
LDL [mg /100 mL]	-0.58 (0.69)	0.41	N.A	N.A	N.A	N.A
<b>BGL [mg /100 mL]</b>	<b>-0.35 (0.42)</b>	<b>0.41</b>	<b>N.A</b>	<b>N.A</b>	<b>-0.09 (-0.07)</b>	<b>0.16</b>

N.A: Data not available. BMI: Body Mass Index, WC: waist circumference, WHR: waist-to-hip ratio, HDL: high lipoprotein cholesterol, CHOL: cholesterol, TG: triglycerides, LDL: low lipoprotein cholesterol, BGL: blood glucose levels.

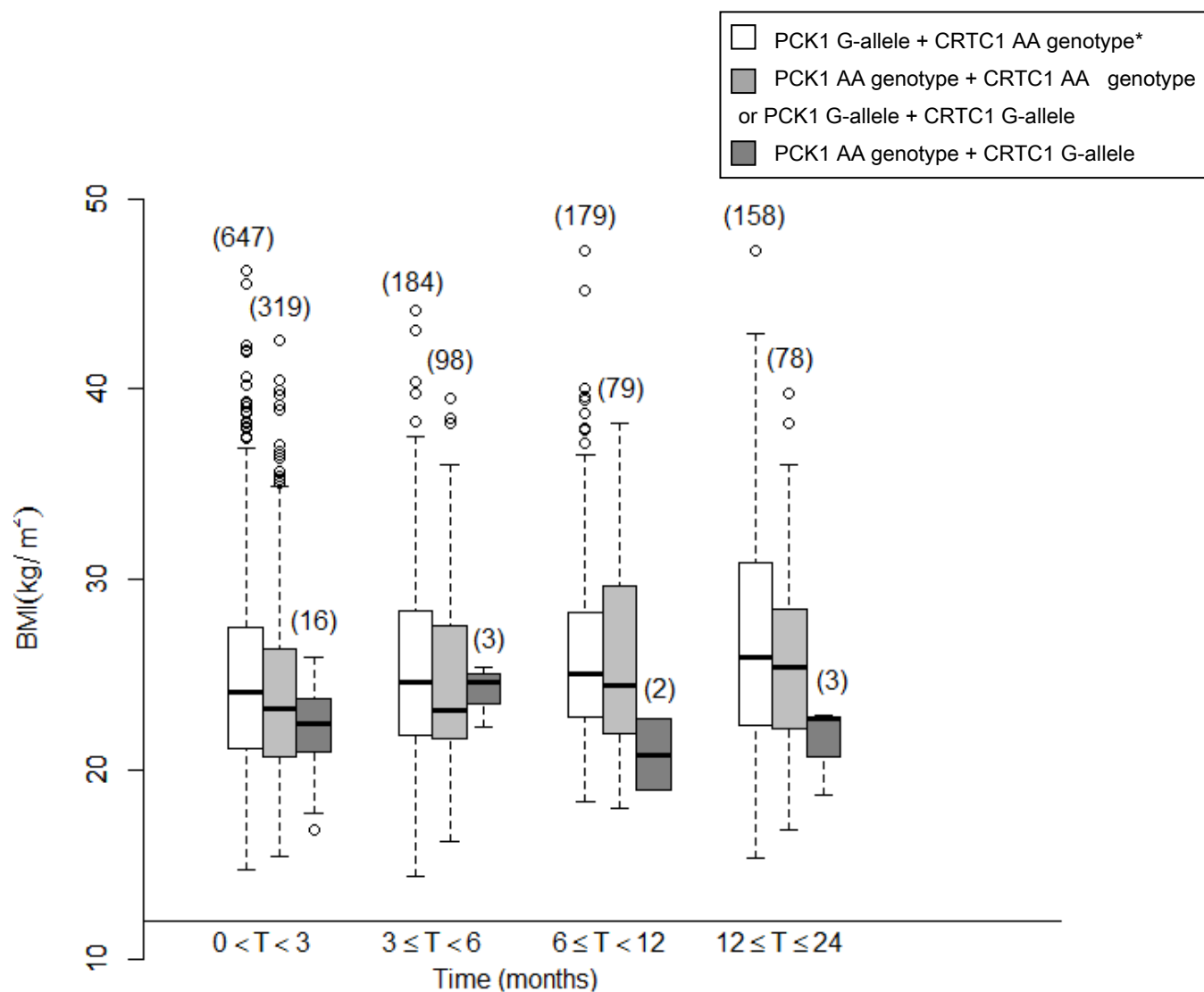
**Figure 1. BMI in relation to *rs11552145* G>A genotypes in the combined sample presented at different time periods of the current psychotropic treatment.**



Boxplots show median values of BMI for each time of the treatment duration (solid horizontal line), 25<sup>th</sup> and 75<sup>th</sup> percentile values (box outline), the lowest and upper value within 1.5 Interquartile range (whiskers) and outlier values (open circles).



**Figure 2. Association of *PCK1* rs11552145 and *CRTC1* rs3746266 genotypes with BMI over the time in all samples.**



\* Reference group.

Boxplots show median values of BMI for each time of the treatment duration (solid horizontal line), 25<sup>th</sup> and 75<sup>th</sup> percentile values (box outline), the lowest and upper value within 1.5 Interquartile range (whiskers) and outlier values (open circles).

**Table S-1. Selected descriptions of polymorphisms and Minor Allele Frequencies (MAF).**

<b>variant</b>	<b>position in gene</b>	<b>type of variation</b>	<b>major / minor allele</b>	<b>MAF in combined psychiatric sample</b>	<b>MAF in Caucasians*</b>
<i>rs11552145</i>	chr 20:56138648	missense Glu>Lys	G/A	0.17	0.16
<i>rs707555</i>	chr 20:56137895	missense Leu>Val	G/C	0.12	0.14
<i>rs8123020</i>	chr 20:56137061	intron variant	C/T	0.12	0.12
<i>rs2071023</i>	chr 20:56135934	5' near gene	C/G	0.46	0.48

\*Source: 1000 Genomes project (<http://www.ensembl.org/index.html>)

**Table S-2. HWE and *PCK1* genotypes distribution among three psychiatric cohorts.**

<b><i>rs11552145</i></b>	<b>Discovery sample</b>	<b>Replication 1</b>	<b>Replication 2</b>	<b>Combined Sample</b>
GG	478	141	173	792
GA	197	49	72	318
AA	30	8	11	49
HWE (p <sup>§</sup> -value)	0.40	0.68	1.00	0.08
<b><i>rs707555</i></b>	<b>Discovery sample</b>	<b>Replication 1</b>	<b>Replication 2</b>	<b>Combined Sample</b>
CC	547	166	190	903
CG	142	29	61	232
GG	16	3	6	25
HWE (p <sup>§</sup> -value)	0.28	0.80	1.00	0.12
<b><i>rs8123020</i></b>	<b>Discovery sample</b>	<b>Replication 1</b>	<b>Replication 2</b>	<b>Combined Sample</b>
CC	546	140	193	879
CT	149	55	62	266
TT	11	3	2	16
HWE (p <sup>§</sup> -value)	1.00	1.00	0.84	1.00
<b><i>rs2071023</i></b>	<b>Discovery sample</b>	<b>Replication 1</b>	<b>Replication 2</b>	<b>Combined Sample</b>
CC	217	52	69	338
CG	333	103	122	558
GG	153	41	53	247
HWE (p <sup>§</sup> -value)	0.96	1.00	1.00	1.00

<sup>§</sup>p-corrected value

**Table S-3. Description of demographic and clinical psychiatric Caucasian samples.**

<b>Characteristics</b>	<b>Discovery Sample n = 478</b>	<b>Replication Sample 1 n = 168</b>	<b>Replication Sample 2 n = 188</b>	<b>Combined sample n= 834</b>
Male,%	44	53	62	50
Age, median (range), years	50 (12-96)	42 (19-64)	42 (19-69)	45 (12-96)
<b>Diagnosis</b>				
Psychotic disorders,%	33.3	27.5	43.4	34.5
Schizo-affective disorders,%	6.5	15.6	12.1	10
Bipolar disorders,%	19.9	32.9	17	22.2
Depression disorders,%	20.4	16.8	13.7	17.9
Others diagnosis,%	19.9	7.2	13.7	15.4
<b>Initial BMI status<sup>†</sup></b>				
BMI, median (range), kg/m <sup>2</sup>	24 (13-44)	25 (15-46)	25 (16-46)	24 (13-46)
Overweight (25≥ Initial BMI<30), %	23	36	32	28
Obese (Initial BMI≥ 30), %	14	15	15	14
<b>Current BMI status<sup>#</sup></b>				
BMI, median (range), kg/m <sup>2</sup>	25 (15-50)	28 (16-42)	27 (17-44)	25 (15-50)
Overweight (25≥ Current BMI<30), %	26	30	34	27
Obese (Current BMI≥ 30), %	18	40	27	24
<b>Initial waist circumference<sup>†</sup></b>				
WC, median (range), cm	90 (54-138)	--	--	87 (54-138)
High WC ≥ 94cm (male), 88cm (female), %	43 (n=315)	--	--	43 (n=315)
<b>Current waist circumference<sup>#</sup></b>				
WC, median (range), cm	93 (48 – 162)	--	98 (51-148)	95 (48-162)
High WC ≥ 94 (male), 88 (female), %	54 (n=592)	--	64 (n=182)	57 (n=774)
<b>Initial Lipid status<sup>†</sup></b>				
High LDL, % (n) <sup>a</sup>	9 (n=224)	--	--	9 (n=224)
High TG, % (n) <sup>b</sup>	19 (n=234)	--	--	19 (n=234)
Low HDL, % (n) <sup>c</sup>	25 (n=222)	--	--	25 (n=222)
<b>Current Lipid status<sup>#</sup></b>				
High LDL, % (n) <sup>a</sup>	14 (n=383)	--	--	15 (n=363)
High TG, % (n) <sup>b</sup>	28 (n=402)	--	--	28 (n=402)
Low HDL, % (n) <sup>c</sup>	27 (n=359)	28 (n=164)	19 (n=160)	26 (n=665)
Smoker, %	41	60	75	50

	Discovery Sample n = 478	Replication Sample 1 n = 168	Replication Sample 2 n = 188	Combined sample n= 834
<b>Prescribed psychotropic drug</b>				
Amisulpride, %	8	-	10	7
Aripirazole, %	10	-	8	8
Clozapine, %	8	14	9	9
Olanzapine, %	10	16	12	11
Quetiapine, %	31	18	23	28
Risperidone, %	16	17	16	16
Lithium, %	7	20	12	10
Valproate, %	4	14	8	6
Treatment duration, median (range), months	6 (1-12)	27.4 (3-333)	36 (1-390)	9 (1-390)

‡ Before the current psychotropic treatment

# For replication Sample 1, 2 : current observation ; for discovery cohort : last follow-up

-- Missing clinical values or obtained in non fasting conditions

- a. High LDL cholesterol : equal or higher than 160 mg/100 mL
- b. High triglycerides : equal or higher than 196 mg/100 mL
- c. Low HDL cholesterol : lower than 39 mg/100 mL

BMI: body mass index, WC: waist circumference, LDL: low density lipoprotein, TG: triglycerides, HDL: high density lipoprotein

Table S-4. Exploratory analysis of the association of *PCK1* polymorphisms with BMI in the three psychiatric samples.

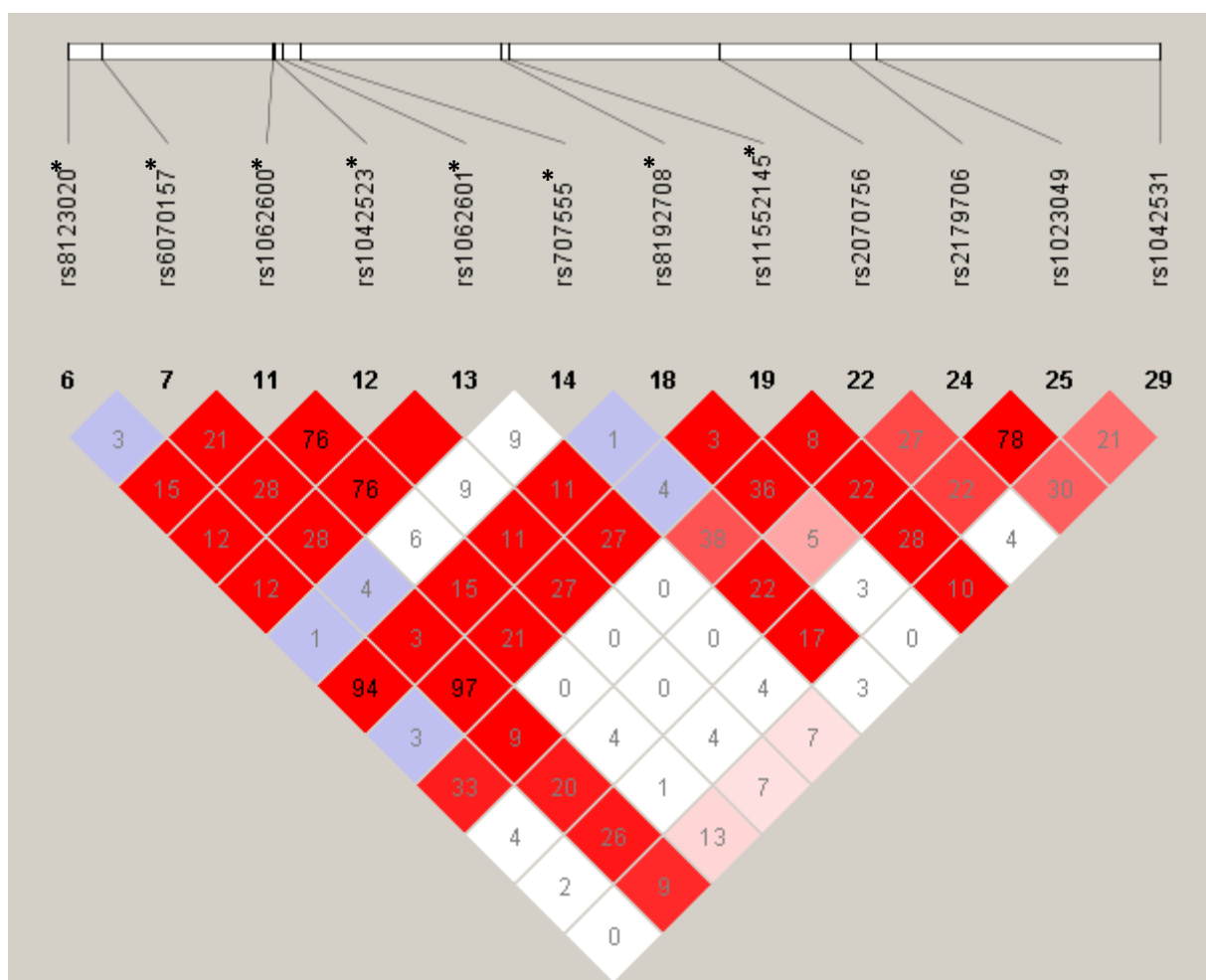
	Discovery Sample <sup>#</sup>				Replication 1			Replication 2			Combined Sample*		
	rs11552145	AA	G-allele	p-value <sup>§</sup>	AA	G-allele	p-value	AA	G-allele	p-value	AA	G-allele	p-value
<b>Baseline BMI</b>	n	22	354		8	131		10	169		40	654	
	BMI [kg/m <sup>2</sup> ] (SE)	22.4 (0.7)	24.3 (0.3)	0.36	24.3 (1.4)	25.5 (0.4)	0.49	23.8 (0.7)	25 (0.4)	0.46	23.1 (0.5)	24.7 (0.2)	0.05
	<b>rs707555</b>	<b>GG</b>	<b>C-allele</b>	<b>p-value<sup>§</sup></b>									
	n	10	366										
	BMI [kg/m <sup>2</sup> ] (SE)	23.6 (6.7)	24.2 (5.1)	1.00									
	<b>rs8123020</b>	<b>TT</b>	<b>C-allele</b>	<b>p-value<sup>§</sup></b>									
n	10	366											
BMI [kg/m <sup>2</sup> ] (SE)	23.4 (3.1)	24.2 (5.2)	1.00										
<b>rs2071023</b>	<b>CC</b>	<b>G-allele</b>	<b>p-value<sup>§</sup></b>										
n	122	277		33	106		46	130		194	496		
BMI [kg/m <sup>2</sup> ] (SE)	23.6 (0.5)	24.4 (0.3)	0.28	24.8 (0.6)	25.6 (0.5)	0.66	24.5 (0.7)	25.0 (0.5)	0.58	24.0 (0.4)	24.8 (0.2)	0.048	
<b>Current BMI</b>	<b>rs11552145</b>	<b>AA</b>	<b>G-allele</b>	<b>p-value<sup>§</sup></b>	<b>AA</b>	<b>G-allele</b>	<b>p-value</b>	<b>AA</b>	<b>G-allele</b>	<b>p-value</b>	<b>AA</b>	<b>G-allele</b>	<b>p-value</b>
	n	12	421		8	160		11	170		30	742	
	BMI [kg/m <sup>2</sup> ] (SE)	22.8 (2.9)	25.4 (5.4)	0.08	27.1 (1.3)	28.2 (0.4)	0.57	26.9 (1.6)	27.3 (0.4)	0.80	23.3 (0.6)	25.7 (0.2)	0.01
	<b>rs707555</b>	<b>CC</b>	<b>G-allele</b>	<b>p-value<sup>§</sup></b>									
	n	12	421	1.00									
	BMI [kg/m <sup>2</sup> ] (SE)	25.1 (6.1)	25.3 (5.4)										
<b>rs8123020</b>	<b>TT</b>	<b>C-allele</b>	<b>p-value<sup>§</sup></b>										
n	10	423											
BMI [kg/m <sup>2</sup> ] (SE)	25.8 (2.6)	25.3 (5.4)	1.00										
<b>rs2071023</b>	<b>CC</b>	<b>G-allele</b>	<b>p-value<sup>§</sup></b>										
n	143	333		39	128		49	132		287	722		
BMI [kg/m <sup>2</sup> ] (SE)	24.5 (0.5)	25.7 (0.3)	0.018	27.5 (0.7)	28.3 (0.5)	0.41	26.9 (0.7)	27.3 (0.5)	0.88	25.3 (0.3)	26.4 (0.2)	0.003	

# For current BMI, only significant findings in the discovery sample were further tested for replication. The same SNPs were also tested for replication at the baseline BMI.

\*Only patients treated for up to 24 months.

§ p-corrected value for the discovery sample.

**Figure S-1: Pairwise linkage disequilibrium (LD) in CEU HapMap samples for *PCK1* polymorphisms. LD expressed as  $r^2$ .**



\* SNPs tested in the present study, including SNPs in LD with one of the four analyzed SNPs. rs2071023 (not present in the figure) is in LD with rs1062600 ( $r^2=1$ ), rs1062601 ( $r^2=0.81$ ) and rs1042523 ( $r^2=0.82$ ). rs11552145 is in LD with rs6070157 ( $r^2=0.97$ ). rs8123020 is in LD with rs8192708 ( $r^2=0.94$ ).