

# Supplementary Figures and Tables - A new genetic locus for antipsychotic-induced weight gain: a genome-wide study of first-episode psychosis patients using amisulpride (from the OPTiMiSE cohort)

Running Title: GWAS of amisulpride-induced weight gain

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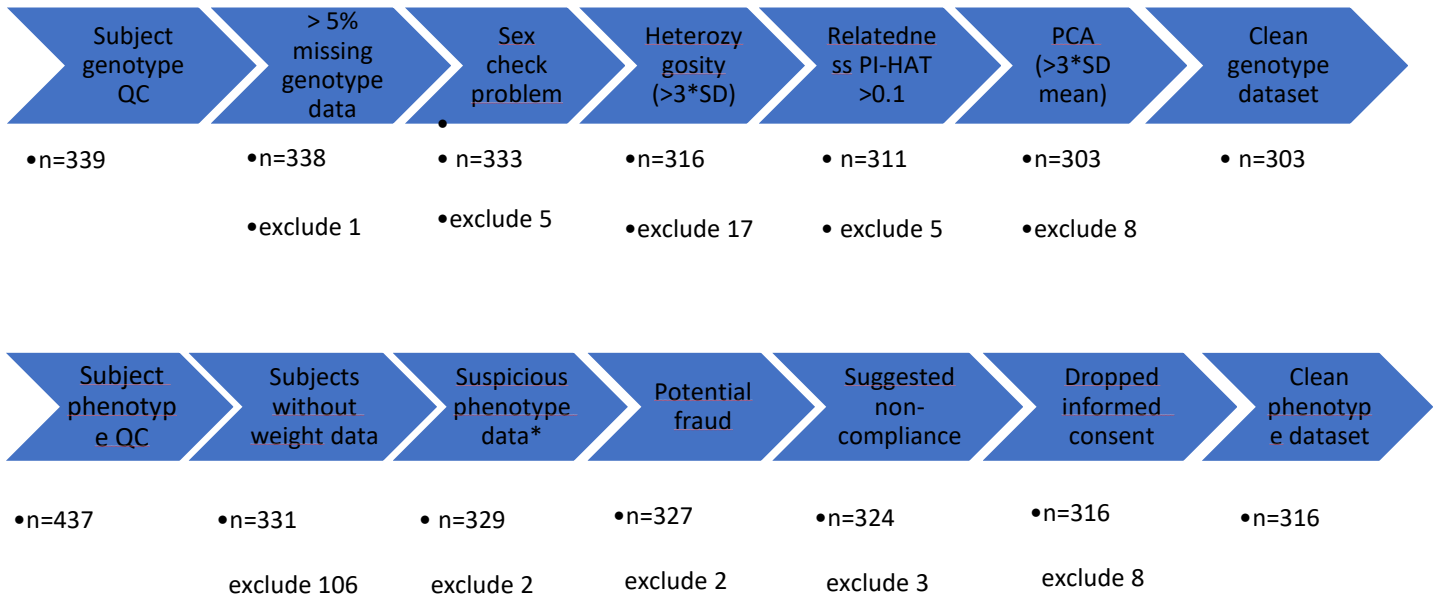
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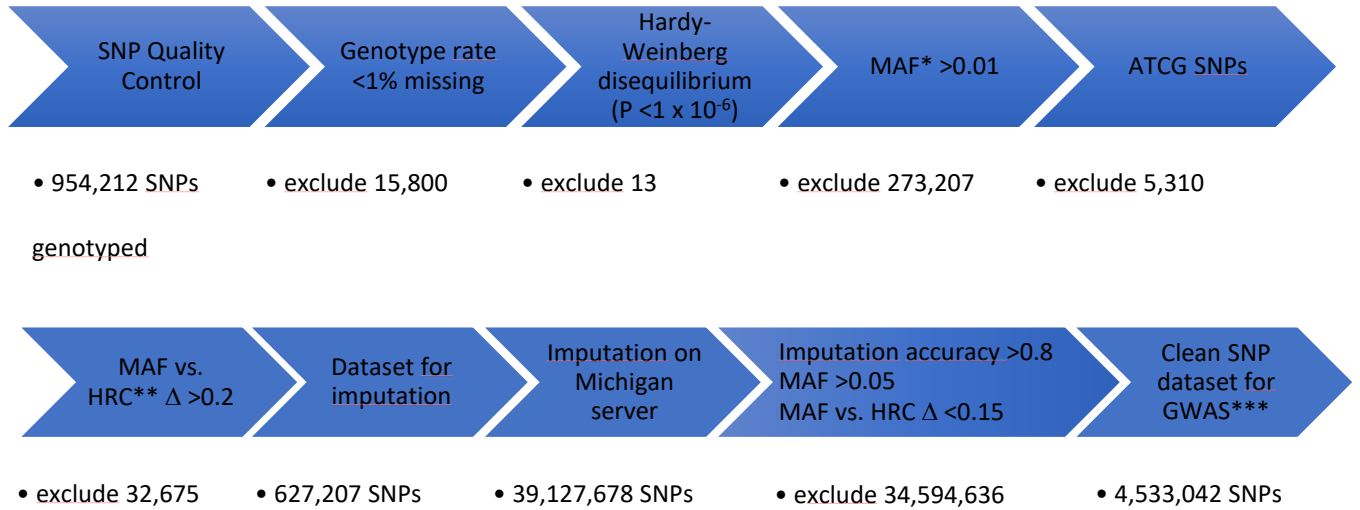
**Supplementary figure 1.** Subject-level Quality Control (QC) steps: genotype and phenotype QC steps. Merging

both cleaned datasets (genotype and phenotype) into one led to the current study population (n=206). \*Suspicious phenotype data is classified as either BMI change >5 (n=1) or height <1.40 meters (n=1).

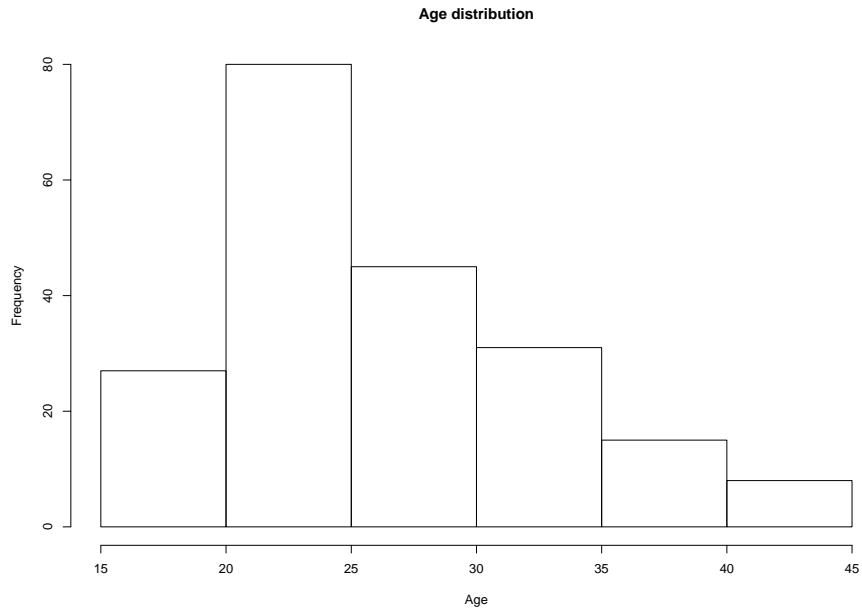


**Supplementary figure 2.** SNP Quality Control (QC). \*Minor allele frequency \*\*Haplotype reference

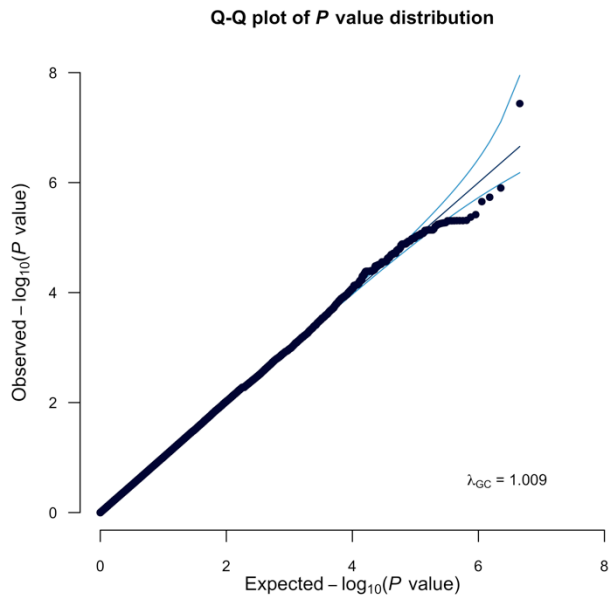
consortium.\*\*\*Genome-wide association study



**Supplementary figure 3.** Age distribution in this GWAS, mean age=26.4 years (SD=6.3). The Y-axis showing frequency and age (years) on the x-axis.



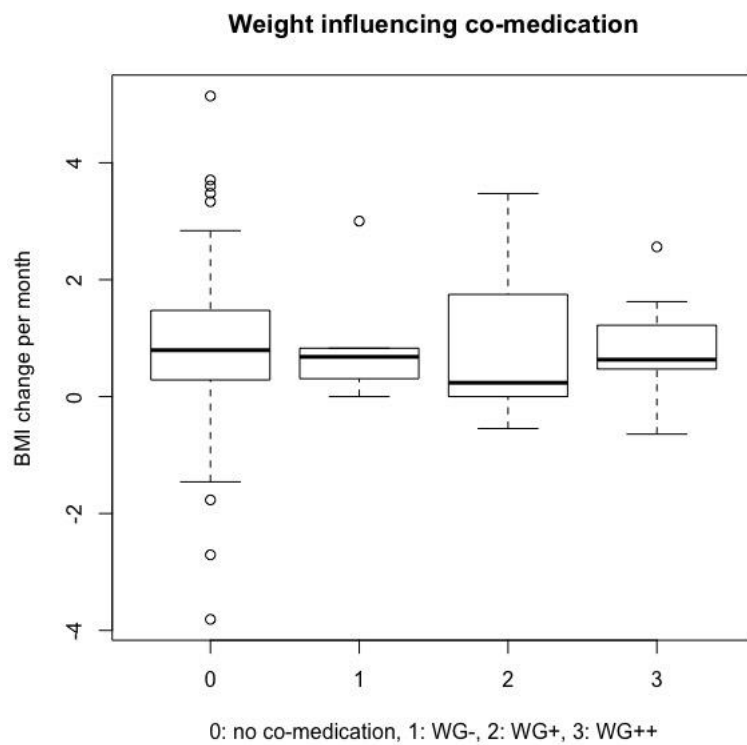
**Supplementary figure 4.** The QQ (Quantile-Quantile) plot of the OPTiMISE GWAS ( $n=206$ ), suggesting minimal inflation of the test statistic.



**Supplementary table 1.** *Ethnic origin of subjects.*

Race	Number of participants	Percentage (%)
European(EUR)	184	89,3%
African (AFR)	9	4,4%
Ad Mixed American (AMR)	6	2,9%
South Asian (SAS)	3	1,5%
East Asian (EAS)	2	0,9%
Unknown	2	0,9%

**Supplementary figure 5.** The effect of potentially weight influencing co-medication (this did not include antipsychotics as antipsychotic co-medication was not allowed) on BMI change per month in OPTiMISE. WG-: co-medication commonly associated with weight loss (methylphenidate or dextroamphetamine), WG+: co-medication commonly associated with weight gain (mirtazapine, carbamazepine, amitriptyline, clomipramine or SSRIs), WG++: co-medication commonly associated with substantial weight gain (lithium or valproate). Mean±SD BMI changes per month: group 0 (no co-medication): mean=0.90±1.13 (n=176), group 1 (WG-): mean=0.96±1.18 (n=5), group 2 (WG+): mean=0.95±1.61 (n=7) group 3 (WG++): mean=0.71±0.73 (n=18). ( $F_{ANOVA}=0.165$ ,  $P=0.92$ )





**Supplementary table 2.** *Sensitivity analyses*

	<b>GWAS Model</b>	<b>Number of subjects</b>	<b>Top SNP</b>	<b><math>\beta^a</math></b>	<b>P-value</b>
1	A dominant GWAS model	206	rs78310016	1.04	$2.817 \times 10^{-07}$
2	An additive GWAS model correcting for phenotypic variables associated with amisulpride-induced weight gain (MDD diagnosis, employment status)	195	rs78310016	1.033	$1.696 \times 10^{-07}$

<sup>a</sup> $\beta$  is the regression coefficient of the linear regression analysis

**Supplementary table 3.** Top 3 SNPs on HMGCS1 associated with AiWG (MAF >0.01). Nominally significant

associations ( $P < 0.05$ ) in are in bold.

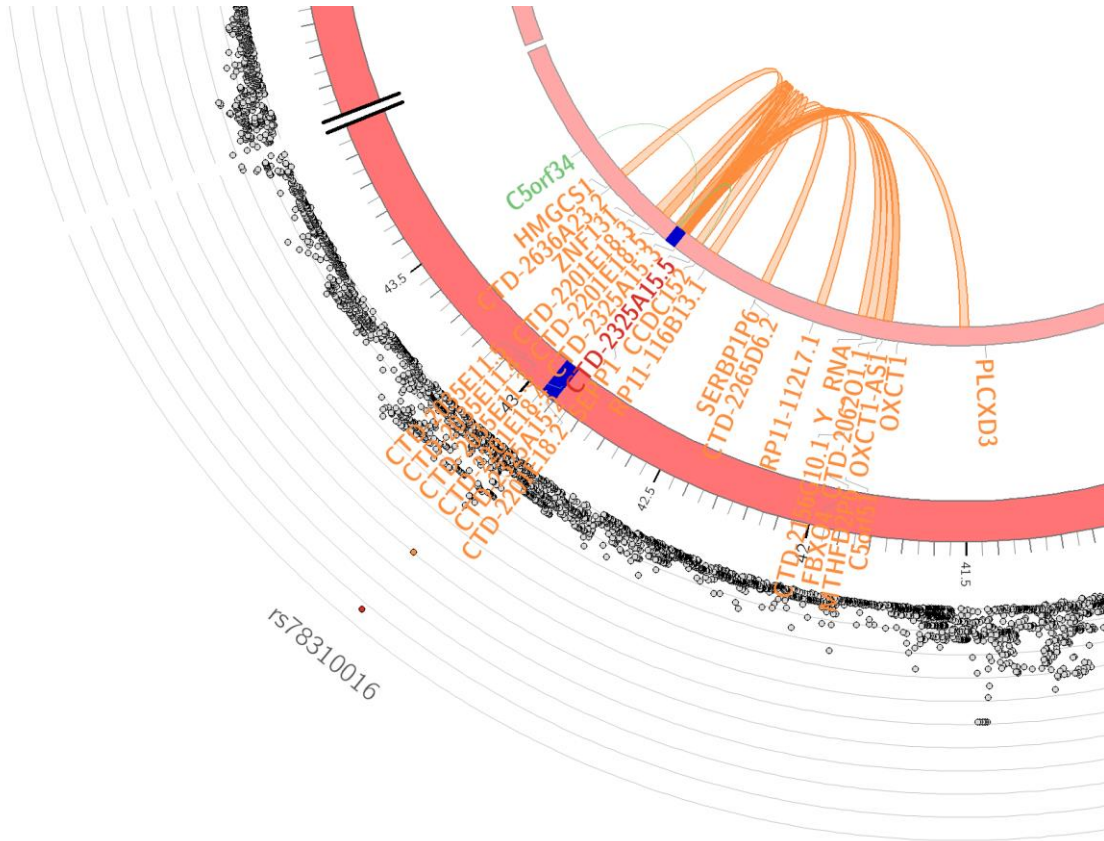
SNP	Location (GChr37)	A1	$\beta^a$	STAT <sup>b</sup>	P-value
rs9292869	5:43292808	G	0.8105	2.641	<b>0.008962</b>
rs6894240	5:43291532	T	0.0120	2.328	<b>0.02097</b>
rs10069507	5:43301801	A	0.0203	1.854	0.06531

<sup>a</sup> $\beta$  is the regression coefficient of the linear regression analysis

<sup>b</sup>STAT is the coefficient t-statistic

**Supplementary figure 6.** Circos plot showing eQTL interactions (green) and chromatin interactions (orange) of

rs78310016 (created in FUMA (Watanabe et al. 2017)).



**Supplementary table 4.** (Independent) SNPs associated with amisulpride-induced weight gain at  $P < 1 \times 10^{-05}$ .

SNP	BP	A1	$\beta$	P
rs927899	1:201428553	C	0.7423	$9.334 \times 10^{-06}$
rs2129108	2:179674929	A	0.7948	$8.466 \times 10^{-06}$
rs9836481	3:41189723	A	0.9768	$8.359 \times 10^{-06}$
rs57818938	5:2278069	T	0.9321	$1.254 \times 10^{-06}$
rs41501	5:9663859	A	0.5127	$7.933 \times 10^{-06}$
rs28800	5:9666545	A	0.5223	$5.541 \times 10^{-06}$
rs78310016	5:42949635	G	1.052	$3.656 \times 10^{-08}$
rs10070777	5:87424765	A	0.8786	$3.824 \times 10^{-06}$
rs28716841	5:132733467	C	0.8716	$9.452 \times 10^{-06}$
rs1107257	6:52229298	C	0.4668	$9.623 \times 10^{-06}$
rs11979775	7:5342413	C	0.5007	$5.351 \times 10^{-06}$
rs13230004	7:5345350	A	0.5336	$4.244 \times 10^{-06}$
rs7024062	9:71745073	A	-0.5885	$2.217 \times 10^{-06}$
rs112045010	12:64725714	C	0.9056	$5.404 \times 10^{-06}$
rs17834779	14:63122799	A	0.4471	$6.936 \times 10^{-06}$
rs1048164	15:40543104	A	0.4365	$8.966 \times 10^{-06}$
rs76356591	16:4187065	T	0.5878	$5.662 \times 10^{-06}$
rs17546654	17:42995095	A	0.5526	$7.292 \times 10^{-06}$
rs8092589	18:43229254	A	0.4724	$9.061 \times 10^{-06}$
rs10426669	19:4564781	G	0.7649	$6.304 \times 10^{-06}$

**Supplementary table 5.** Group difference in baseline characteristics between rs78310016 risk alleles carriers

(i.e. 1 or more G alleles) and non-carriers.

<b>Characteristic</b>	<b>Mean risk allele carriers</b>	<b>Mean risk allele non-carriers</b>	<b>Group difference (test performed)</b>
<b>Age (years)</b>	28.55	26.00	t=1.896, P=0.0664 (independent t-test)
<b>Average daily dose (mg/day)</b>	437.1	442.6	t=-0.1597, P=0.874 (independent t-test)
<b>Days of study participation (days)</b>	33.89	34.66	t=-0.7648, P=0.4491 (independent t-test)
<b>PANSS change (%)</b>	-24.72	-26.42	t=0.4044, P=0.6883 (independent t-test)
<b>Sex (male/female)</b>	18/10	121/57	$\chi^2=0.29119$ , P=0.865 (Pearson's Chi-squared Yates)

**Supplementary table 6.** Top 5 tissues from the MAGMA tissue expression analysis. Nominally significant

associations ( $P < 0.05$ ) in are in bold.

Tissue	Number of genes	$\beta^a$	SE <sup>b</sup>	P-value
Small intestine	15884	0.0175	0.00966	<b>0.035</b>
Liver	15884	0.0120	0.00674	<b>0.038</b>
Stomach	15884	0.0203	0.01420	0.076
Colon	15884	0.0212	0.0165	0.100
Bladder	15884	0.0125	0.0150	0.202

<sup>a</sup> $\beta$  is the regression coefficient of the linear regression analysis

<sup>b</sup>SE is the standard error

**Supplementary table 7.** Look-up of previously significantly associated SNPs with AiWG in GWASs.

Gene	Location (GChr37)	Outcome	Study information	Original AiWG association	OPTiMiSe
<i>MC4R</i>	rs489693A (18:57882787)	BMI change after 6 or 12 weeks of treatment	<u>Discovery cohort (n=139):</u>  • quetiapine  • risperidone  • aripiprazole	P=2.8 x 10 <sup>-7</sup>	β <sup>a</sup> =-0.033  STAT <sup>b</sup> =0.307  P=0.759 (NS)
			<u>First replication cohort (n=73):</u>  • clozapine	P=1.40 x 10 <sup>-4</sup>	
			<u>Second replication cohort (n=40):</u>  • quetiapine  • risperidone  • aripiprazole	P=0.007	
			<u>Third replication cohort (n=92):</u>  • haloperidol,  • amisulpride  • quetiapine  • ziprasidone	P=0.042	

PTPRD(Yu et al. 2016)	rs10977144T (9:8474233)	BMI change after 8 weeks of treatment	<u>Discovery cohort (n=534):</u>	P=9.26 x 10 <sup>-9</sup>	β <sup>a</sup> =-0.270
			<ul style="list-style-type: none"> <li>• risperidone</li> <li>• quetiapine</li> <li>• clozapine</li> <li>• aripiprazole</li> <li>• ziprasidone</li> </ul>		STAT <sup>b</sup> = -1.277 P=0.203 (NS)
			<u>Replication cohort (n=236)</u>	P=4.30 x 10 <sup>-3</sup>	
			<ul style="list-style-type: none"> <li>• risperidone</li> <li>• quetiapine</li> </ul>		

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<sup>a</sup>β is the regression coefficient of the linear regression analysis

<sup>b</sup>STAT is the coefficient t-statistic



**Supplementary table 8.** Look-up of previously significantly associated SNPs from (Zhang et al. 2016).

Nominally significant associations ( $P < 0.05$ ) in are in bold.

Gene	SNP	Location (GChr37)	Region	Major allele/minor allele	Proxy SNP ( $r^2$ )	OPTiMiSE (n=206)
<i>ADRA2A</i>	rs1800544	10:112836503		C/G	rs2484515G (1.0)	$\beta^a = 0.1052$ , P=0.3516
<i>ADRB3</i>	rs4994	8:37966280	(Missense)	T/C	rs2071493C (1.0)	$\beta = 0.1946$ , P=0.2942
<i>BDNF</i>	rs6265	11:27658369	(Missense)	G/A	rs4923464T (1.0)	$\beta = -0.03956$ , P=0.7602
<i>DRD2</i>	rs1799732	11:113475529	Intron	C/-	rs11214613A (1.0)	$\beta = 0.2779$ , P=0.08309
<i>DRD2</i>	rs6275A	11:113283477	Exon (synon)	A/G		$\beta = 0.0406$ , P=0.7074
<b><i>DRD2</i></b>	<b>rs7131056A</b>	<b>11:113329774</b>		<b>C/A</b>		<b><math>\beta = 0.2079</math>,</b> <b>P=0.04099</b>
<i>GNB3</i>	rs5443T	12:6954875	Exon (synon)	C/T		$\beta = -0.02676$ , P=0.8048
<i>HTR2C</i>	rs3813929	X: 113871991	Exon 5	G/C		NA <sup>b</sup>
<i>HTR2C</i>	rs518147	X:113818582	5'UTR	G/C		NA <sup>b</sup>

<i>INSIG2</i>	rs17047764	2:118868582		G/C	rs3849327C	$\beta=0.1282,$ P=0.3112
					(1.0)	
<i>MC4R</i>	rs489693A	18:57882787		C/A		$\beta=-0.03292,$ P=0.759
<i>SNAP25</i>	rs1051312C	20:10287088	3'UTR	T/C		$\beta=0.169,$ P=0.1554

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<sup>a</sup>  $\beta$  is the regression coefficient of the linear regression analysis

<sup>b</sup> NA not available

## References

Malhotra AK, Correll CU, Chowdhury NI, et al (2012) Association between common variants near the melanocortin 4 receptor gene and severe antipsychotic drug-induced weight gain. *Arch Gen Psychiatry* 69:904–912. doi: 10.1001/archgenpsychiatry.2012.191

Watanabe K, Taskesen E, van Bochoven A, Posthuma D (2017) Functional mapping and annotation of genetic associations with FUMA. *Nat Commun* 8:1826. doi: 10.1038/s41467-017-01261-5

Yu H, Wang L, Lv L, et al (2016) Genome-Wide Association Study Suggested the PTPRD Polymorphisms Were Associated With Weight Gain Effects of Atypical Antipsychotic Medications. *Schizophr Bull* 42:814–823. doi: 10.1093/schbul/sbv179

Zhang J-P, Lencz T, Zhang RX, et al (2016) Pharmacogenetic Associations of Antipsychotic Drug-Related Weight Gain: A Systematic Review and Meta-analysis. *Schizophr Bull* 42:1418–1437. doi: 10.1093/schbul/sbw058