



## Supplementary Material

**Article Title:** Association of Common Variations in the Norepinephrine Transporter Gene With Response to Olanzapine-Fluoxetine Combination Versus Continued-Fluoxetine Treatment in Patients With Treatment-Resistant Depression: A Candidate Gene Analysis

**Author(s):** John P. Houston, MD, PhD; Kit Lau, PhD; Virginie Aris, PhD; Wenlei Liu, PhD; Bonnie A. Fijal, PhD; Alexandra N. Heinloth, MD; and Roy H. Perlis, MD, MSc

**Citation:** J Clin Psychiatry 2012;73

**DOI Number:** 10.4088/JCP.10m06744

### List of Supplementary Material for the article

1. [eTable 1](#) Candidate Genes Used in the Association Analyses
2. [eTable 2](#) Baseline Patient Characteristics
3. [eTable 3](#) Number of Patients in the OFC, OLZ, and FLX Groups from Visit 7 (Baseline) to Visit 16 (End of Trial)
4. [eTable 4](#) Tier 2 SNPs, Nominally Statistically Significantly Associated with Response to Continued-Fluoxetine During Study Period 3
5. [eTable 5](#) Candidate SNPs Statistically Significantly Associated with Response to Olanzapine
6. [eTable 6](#) Tier 2 SNPs, Nominally Statistically Significantly Associated with Response to Olanzapine
7. [eTable 7](#) Comparison of change of MADRS total score from baseline by genotype for OFC versus continued-FLX for selected SLC6A2 SNPs

### Disclaimer

This Supplementary Material has been provided by the author(s) as an enhancement to the published article. It has been approved by peer review; however, it has undergone neither editing nor formatting by in-house editorial staff. The material is presented in the manner supplied by the author.

**eTable 1. Candidate Genes Used in the Association Analyses.**

<b>Gene</b>	<b>Number of genetic variants analyzed</b>
<i>ABCB1</i>	2
<i>ADRA1A</i>	22
<i>ADRA2A</i>	4
<i>ANKK1</i>	6
<i>BDNF</i>	1
<i>COMT</i>	13
<i>CRH</i>	6
<i>CRHR1</i>	15
<i>CRHR2</i>	21
<i>CYP2D6</i>	12
<i>DBH</i>	2
<i>DRD1</i>	5
<i>DRD2</i>	59
<i>DRD3</i>	26
<i>DRD4</i>	1
<i>GNB3</i>	1
<i>GRIA4</i>	1
<i>GRIK1</i>	1
<i>GRM3</i>	6
<i>HFE</i>	1
<i>HRH1</i>	7
<i>HTR1A</i>	5
<i>HTR2A</i>	14
<i>HTR2B</i>	10
<i>HTR2C</i>	10
<i>HTR3A</i>	3
<i>HTR6</i>	9
<i>IL6</i>	1
<i>INS</i>	1
<i>KIAA0999</i>	1
<i>MC2R</i>	10
<i>MC3R</i>	5
<i>MTHFR</i>	2
<i>NR3C1</i>	13
<i>NUDT9P1</i>	1
<i>POMC</i>	5
<i>RGS4</i>	5
<i>SLC2A2</i>	1
<i>SLC6A2</i>	77
<i>SLC6A4</i>	14
<i>TNF</i>	1
<i>TPH1</i>	7
<i>TPH2</i>	3
<i>XKR4</i>	1

**eTable 2. Baseline Patient Characteristics.**

<b>Parameter</b>	<b>Study Period 3 atients (Non-responsive to FLX lead-in)</b>		
	<b>OFC-treated patients (N=71)</b>	<b>Continued-FLX-treated patients (N=78)</b>	<b>OLZ-treated patients (N=56)</b>
Female gender, n (%)	52 (73.2)	48 (61.5)	36 (64.3)
Country of origin, n (%)			
USA	56 (78.9)	68 (87.2)	48 (85.7)
Canada	15 (21.1)	10 (12.8)	8 (14.3)
Age (years), mean (SD)	43.8 (9.5)	45.0 (10.4)	44.9 (9.2)
BMI (kg/m <sup>2</sup> )	31.5 (7.8)	30.4 (8.3)	31.7 (6.3)
MADRS-total score, mean (SD)	30.8 (6.1)	30.8 (6.8)	30.7 (6.8)

Abbreviations: BMI = body mass index; FLX = fluoxetine; MADRS = Montgomery-Åsberg Depression Rating Scale; N = total number of patients in group; n = number of affected patients; OFC = olanzapine/fluoxetine combination; OLZ = olanzapine; SD = standard deviation.

**eTable 3. Number of Patients in the OFC, OLZ, and FLX Groups from Visit 7 (Baseline) to Visit 16 (End of Trial).**

<b>Visit</b>	<b>OFC</b>	<b>OLZ</b>	<b>FLX</b>
7	71	56	78
8	71	56	78
9	67	55	77
10	64	55	74
11	62	51	74
12	59	47	69
13	57	44	69
14	53	40	66
15	51	37	66
16	52	36	64

Abbreviations: FLX = fluoxetine; OFC = olanzapine/fluoxetine combination; OLZ = olanzapine.

**eTable 4. Tier 2 SNPs, Nominally Statistically Significantly Associated with Response to Continued-Fluoxetine During Study Period 3.**

Gene SNP	Gene region <sup>a</sup>	LS mean change (SE) MADRS-TS and n			Uncorrected p-value
		AA	AB	BB	
<i>ADRA1A</i>					
rs526302 (G/T)	Intron-1	-11.8 (1.6), n=40	-10.1 (2.0), n=25	-5.4 (3.5), n=6	.016
rs472865 (C/T)	Intron-1	-9.3 (1.5), n=54	-14.4 (2.1), n=18	-22.9 (8.2), n=1	.020
<i>DRD3</i>					
rs3732783 (A/G)	Exon-2	-10.3 (1.3), n=64	-20.8 (3.9), n=6	NA	.011
<i>GRM3</i>					
rs1989796 (C/T)	Intron-5	-11.4 (2.1), n=21	-8.7 (1.6), n=36	-13.6 (2.3), n=16	.041
<i>HTR2A</i>					
rs912127 (G/A)	Intron-2	-10.2 (1.6), n=34	-11.6 (1.8), n=36	-22.7 (6.8), n=2	.014
rs3742278 (A/G)	Intron-2	-9.6 (1.4), n=49	-14.9 (2.1), n=22	-5.5 (8.1), n=1	.015
<i>HTR1A</i>					
rs10042486 (G/A)	Upstream	-7.7 (2.1), n=21	-11.4 (1.6), n=40	-11.1 (2.6), n=12	.037
rs6295 (G/C)	Upstream	-8.1 (2.0), n=24	-11.4 (1.6), n=41	-11.9 (2.5), n=13	.037
rs878567 (T/C)	Downstream	-7.7 (2.1), n=21	-11.5 (1.6), n=41	-11.1 (2.6), n=12	.037
rs749099 (G/A)	Downstream	-8.2 (2.1), n=23	-12.0 (1.7), n=35	-11.7 (2.6), n=13	.035
<i>MC3R</i>					
rs6127698 (G/T)	Upstream	-11.4 (2.0), n=23	-12.0 (1.5), n=37	-3.3 (2.5), n=14	.013
<i>MTHFR</i>					
rs1801133 (G/A)	Exon-4	-14.1 (1.9), n=28	-9.1 (1.6), n=33	-8.4 (3.0), n=9	.016
rs1801131 (T/G)	Exon-7	-10.0 (1.6), n=43	-10.5 (1.9), n=26	-15.3 (4.1), n=4	.044
<i>POMC</i>					
rs7582597 (C/T)	Upstream	-15.7 (2.3), n=21	-8.6 (1.4), n=51	NA	.032
<i>SLC6A2</i>					
rs17306977 (A/T)	Intron-2 (LD1)	-10.5 (1.3), n=65	-16.7 (3.4), n=7	-17.6 (8.1), n=1	.0077
rs12932949 (G/C)	Intron-2 (LD1)	-10.0 (1.4), n=61	-16.5 (3.5), n=7	-17.7 (8.2), n=1	.0072
rs2062723 (T/C)	Intron-2 (LD1)	-9.8 (1.7), n=27	-10.4 (1.6), n=35	-14.6 (3.0), n=9	.042
rs6499771 (A/G)	Intron-2 (LD1)	-10.2 (1.3), n=63	-18.4 (3.0), n=9	-17.8 (8.0), n=1	.0020
rs734980 (A/G)	Intron-2 (LD1)	-10.5 (1.3), n=65	-16.7 (3.4), n=7	-17.6 (8.1), n=1	.0077
rs36023 (G/A)	Intron-4	-8.1 (1.8), n=29	-11.6 (1.7), n=33	-17.4 (2.9), n=11	.019

rs10521329 (C/A)	Intron-5 (LD2)	-9.0 (1.5), n=51	-15.0 (1.9), n=21	NA	.017
rs1861646 (G/T)	Intron-5 (LD2)	-8.9 (1.5), n=52	-14.6 (2.0), n=20	NA	.024
rs880711 (G/A)	Intron-5 (LD2)	-8.4 (1.6), n=49	-15.5 (2.2), n=18	NA	.041
rs12924088 (A/G)	Intron-9 (LD2)	-14.4 (1.8), n=30	-9.4 (1.7), n=29	-8.0 (2.4), n=14	.031
rs12708954 (C/A)	Intron-9 (LD2)	-9.1 (1.5), n=52	-15.4 (2.0), n=20	NA	.014
rs8047672 (G/A)	Intron-9 (LD2)	-8.6 (1.5), n=52	-16.3 (2.0), n=19	NA	.005
rs5569 (G/A)	Exon-9 (LD2)	-14.3 (1.8), n=32	-8.8 (1.7), n=31	-8.1 (2.4), n=14	.023
rs998424 (G/A)	Intron-10 (LD2)	-14.4 (1.9), n=29	-9.3 (1.8), n=29	-9.5 (2.6), n=12	.049
rs1800887 (T/C)	Intron-12	-9.0 (1.6), n=44	-13.1 (1.8), n=28	NA	.036
rs8050050 (G/A)	Intron-13	-8.6 (1.4), n=51	-15.8 (2.1), n=17	NA	.040
rs9930182 (T/G)	Downstream	-8.7 (1.6), n=45	-13.5 (1.8), n=27	NA	.028
rs16955708 (T/C)	Downstream	-9.8 (1.5), n=55	-13.4 (2.0), n=18	NA	.043
<i>TNF</i>					
rs1800610 (C/T)	Intron-2	-11.6 (1.3), n=61	-1.7 (2.7), n=12	NA	.0042

Abbreviations: LS mean=least-squared mean; MADRS-TS = Montgomery-Åsberg Depression Rating Scale Total Score; n=number of patients; NA=not available; SE = standard error; SNP = single nucleotide polymorphism

<sup>a</sup> LD1 and LD2 are *SLC6A2* linkage disequilibrium blocks as described in Results.

Note: the alleles in parentheses following the SNP number represent A and B.

**eTable 5. Candidate SNPs Statistically Significantly Associated with Response to Olanzapine.**

Gene SNP (A/B)	Gene region	LS mean change (SE) MADRS-TS and n			Uncorrected p-value
		AA	AB	BB	
<i>RGS4</i> rs6678136 (G/A)	Upstream	-7 (2.7), n=11	-13 (1.8), n=28	-13 (2.2), n=14	.008
<i>HTR6</i> rs6693503 (G/A)	Upstream	-15 (1.9), n=24	-11 (1.8), n=28	-8 (5.0), n=4	.021
rs9659997 (T/C)	Intron-2	-15 (1.9), n=24	-11 (1.8), n=28	-8 (5.0), n=4	.021
<i>COMT</i> rs174696 (T/C)	Intron-6	-10 (1.8), n=31	-13 (2.2), n=18	-19 (4.3), n=3	.023

Abbreviations: LS mean=least-squared mean; MADRS-TS = Montgomery-Åsberg Depression Rating Scale Total Score; n=number of patients;SE = standard error; SNP = single nucleotide polymorphism.

Note: the alleles in parentheses following the SNP number represent A and B.

**eTable 6. Tier 2 SNPs, Nominally Statistically Significantly Associated with Response to Olanzapine.**

Gene SNP (A/B)	Gene region	LS mean change (SE) MADRS-TS and n			Uncorrected p-value
		AA	AB	BB	
<i>ADRA1A</i>					
rs2291775 (A/G)	Intron-2	-10.3 (1.6), n=46	-20.3 (4.1), n=4	NA	.032
rs10503799 (G/A)	Downstream	-10.2 (1.5), n=48	-20.4 (4.1), n=4	NA	.024
<i>ANKK1</i>					
rs2734848 (A/G)	Exon-8	-14.2 (1.8), n=29	-10.8 (1.9), n=22	-7.1 (3.9), n=5	.0059
rs1800497 (G/A)	Exon-8	-9.3 (1.7), n=37	-15.6 (1.9), n=16	NA	.0061
rs11214601 (C/T)	Downstream	-10.0 (1.6), n=43	-16.0 (2.1), n=13	NA	.0030
<i>COMT</i>					
rs174696 (T/C)	Intron-6	-9.8 (1.8), n=31	-13.2 (2.2), n=18	-19.5 (4.3), n=3	.023
rs165774 (G/A)	Intron-6	-12.2 (1.8), n=24	-12.2 (1.9), n=25	-6.4 (5.2), n=4	.049
<i>CRHR1</i>					
rs242924 (C/A)	Intron-3	-17.0 (2.5), n=18	-11.3 (1.7), n=25	-7.2 (2.7), n=10	.011
rs242940 (T/C)	Intron-3	-16.1 (2.7), n=16	-12.1 (1.8), n=21	-7.7 (2.4), n=14	.037
rs171440 (C/T)	Intron-3	-16.1 (2.7), n=16	-12.1 (1.8), n=22	-8.3 (2.3), n=15	.049
<i>CRHR2</i>					
rs255121 (C/T)	Upstream	-13.2 (1.3), n=44	-7.3 (3.5), n=8	NA	.0058
rs255099 (A/G)	Upstream	-14.0 (2.0), n=16	-12.0 (2.1), n=24	-7.4 (3.5), n=10	.011
rs255100 (T/A)	Upstream	-13.5 (1.9), n=17	-12.0 (2.0), n=26	-7.1 (3.4), n=10	.014
rs2267716 (T/C)	Intron-2	-13.4 (1.7), n=26	-11.7 (2.2), n=17	-8.1 (4.6), n=7	.026
rs975537 (A/T)	Intron-8	-13.4 (1.5), n=34	-7.8 (2.3), n=19	NA	.031
<i>CYP2D6</i>					
<b>rs9623531 (T/C)<sup>a</sup></b>	<b>Upstream</b>	<b>-15.2 (1.8), n=24</b>	<b>-9.1 (1.8), n=24</b>	<b>1.3 (3.9), n=4</b>	<b>&lt;.00001</b>
rs2267448 (A/G)	Exon-4	-6.7 (2.2), n=17	-11.7 (2.4), n=23	-15.4 (2.5), n=12	.012
<b>rs16947 (G/A)<sup>b</sup></b>	<b>Exon-6</b>	<b>-15.2 (1.8), n=25</b>	<b>-9.7 (2.2), n=20</b>	<b>-3.2 (3.7), n=5</b>	<b>.00008</b>
rs1135840 (C/G)	Exon-9	-10.1 (2.0), n=20	-10.6 (2.5), n=19	-15.9 (2.5), n=13	.0158
rs5758589 (G/A)	Downstream	-6.4 (2.3), n=14	-11.2 (2.3), n=24	-15.7 (2.5), n=13	.0014
rs6002626 (G/C)	Downstream	-6.6 (2.2), n=15	-11.1 (2.3), n=24	-15.6 (2.5), n=13	.0017
<i>DRD2</i>					
<b>rs1125393 (G/A)<sup>c</sup></b>	<b>Intron-1</b>	<b>-9.7 (1.6), n=41</b>	<b>-15.8 (2.1), n=12</b>	<b>NA</b>	<b>.0062</b>



rs1079596 (G/A)	Intron-1	-9.7 (1.6), n=41	-15.8 (2.1), n=12	NA	.0062
rs1125394 (A/G)	Intron-1	-9.9 (1.7), n=39	-16.3 (2.4), n=10	NA	.0075
rs4648319 (C/T)	Intron-1	-9.8 (1.6), n=40	-15.8 (2.1), n=13	NA	.0093
rs7103679 (G/A)	Intron-1	-9.8 (1.7), n=41	-15.6 (2.5), n=9	NA	.036
rs2734836 (G/A)	Intron-2	-9.5 (1.7), n=41	-15.7 (2.5), n=10	NA	.0020
rs2075654 (G/A)	Intron-2	-9.7 (1.6), n=41	-15.8 (2.1), n=12	NA	.0062
rs1076560 (G/T)	Intron-6	-9.5 (1.7), n=41	-15.2 (2.4), n=11	NA	.0021
rs1124491 (G/A)	Intron-7	-9.4 (1.8), n=38	-16.9 (2.7), n=9	NA	.00032
rs1079594 (T/G)	Intron-7	-9.5 (1.7), n=40	-15.2 (2.4), n=11	NA	.0026
rs6278 (G/T)	3Prime_UTR	-10.0 (1.6), n=43	-16.0 (2.1), n=13	NA	.0030
rs2242591 (G/A)	Downstream	-9.7 (1.6), n=41	-15.8 (2.1), n=12	NA	.0062
rs2242593 (A/G)	Downstream	10.0 (1.6), n=43	-16.0 (2.1), n=13	NA	.0030
rs2234689 (G/C)	Downstream	-14.2 (1.8), n=28	-10.3 (1.9), n=20	-7.3 (3.9), n=5	.0067
<i>HRHI</i>					
rs346070 (C/T)	3Prime_UTR	-14.1 (1.6), n=39	-9.4 (2.3), n=14	-5.4 (4.8), n=3	.029
<i>HTR2A</i>					
rs3125 (G/C)	3Prime_UTR	-10.8 (1.6), n=41	-12.8 (2.7), n=11	NA	.0079
<i>HTR2C</i>					
rs518147 (G/C)	5Prime_UTR	-15.1 (1.8), n=27	-9.7 (2.0), n=19	-7.9 (3.3), n=8	.010
rs569959 (T/C)	Intron-2	-14.5 (1.8), n=28	-10.0 (2.1), n=17	-8.0 (3.3), n=8	.010
rs2192372 (G/A)	Intron-3	-14.2 (1.7), n=29	-10.2 (2.2), n=16	-8.0 (3.3), n=8	.013
rs6318 (G/C)	Exon-5	-12.7 (1.4), n=45	-8.6 (7.4), n=3	-5.5 (5.1), n=4	.049
<i>HTR6</i>					
rs6693503 (G/A)	Upstream	-14.6 (1.9), n=24	-10.6 (1.8), n=28	-8.2 (5.0), n=4	.021
rs4912138 (G/A)	Intron-2	-14.4 (1.6), n=36	-9.7 (2.1), n=19	NA	.0031
rs9659997 (T/C)	Intron-2	-14.6 (1.9), n=24	-10.6 (1.8), n=28	-8.2 (5.0), n=4	.021
LLY12 (T/C)	NA	-15 (2.05), n=21	-12 (1.92), n=23	-6 (2.94), n=9	.019
<i>MC3R</i>					
rs6014649 (G/A)	Upstream	-12.3 (1.4), n=46	-11.1 (4.2), n=6	NA	.047
rs3746619 (C/A)	5Prime_UTR	-12.0 (1.4), n=47	-10.8 (4.2), n=6	NA	.041
rs3827103 (G/A)	Exon-1	-12.0 (1.4), n=46	-10.6 (4.2), n=6	NA	.042
<i>NR3C1</i>					
rs13186836 (T/C)	Upstream	-11.7 (1.5), n=37	-13.6 (2.7), n=13	-10.9 (4.3), n=3	.048
rs852983 (G/A)	Intron-2	-15.2 (2.4), n=13	-10.7 (1.5), n=39	NA	.0073
rs33388 (A/T)	Intron-2	-15.1 (2.5), n=13	-12.1 (2.2), n=20	-8.3 (2.4), n=13	.020

rs852979 (T/C)	Intron-3	-10.4 (1.7), n=27	-11.2 (2.4), n=15	-18.5 (3.2), n=8	.017
rs860457 (T/C)	Intron-4	-10.5 (1.7), n=28	-11.7 (2.2), n=17	-18.5 (3.2), n=8	.011
rs852977 (A/G)	Intron-4	-10.5 (1.7), n=28	-11.5 (2.3), n=16	-18.6 (3.2), n=8	.014
rs258750 (T/C)	Intron-8	-10.5 (1.7), n=28	-11.7 (2.2), n=17	-18.5 (3.2), n=8	.011
rs6191 (T/G)	3Prime_UTR	-15.0 (2.4), n=15	-13.7 (1.9), n=26	-7.5 (2.2), n=15	.020
<i>POMC</i>					
rs934778 (T/C)	Intron-1	-10.3 (2.1), n=19	-12.6 (1.8), n=28	-15.7 (3.2), n=6	.0014
rs1009388 (C/G)	Intron-1	-10.2 (1.8), n=27	-11.7 (2.3), n=17	-18.4 (5.1), n=2	.018
rs1042571 (C/T)	3Prime_UTR	-11.5 (1.7), n=30	-11.2 (2.2), n=19	-12.4 (5.2), n=3	.033
<i>RGS4</i>					
rs6678136 (G/A)	Upstream	-7.4 (2.7), n=11	-13.4 (1.8), n=28	-12.8 (2.2), n=14	.0075
rs6427711 (G/A)	Upstream	-10.5 (1.8), n=28	-15.0 (2.4), n=17	-15.2 (3.8), n=5	.032
<i>SLC6A4</i>					
rs1872924 (T/C)	Intron-2	-9.8 (1.8), n=33	-14.0 (2.5), n=13	-15.9 (4.5), n=3	.047
rs3794808 (G/A)	Intron-12	-11.2 (2.4), n=16	-12.6 (1.9), n=27	-6.3 (3.1), n=9	.034
<i>SLC6A2</i>					
rs36021 (A/T)	Intron-4	-12.8 (1.9), n=22	-11.2 (2.5), n=20	-6.3 (3.0), n=10	.035
rs42460 (A/G)	3Prime_UTR	-12.0 (1.6), n=45	-5.6 (3.7), n=6	-2.5 (7.4), n=1	.010
<i>TNF</i>					
rs1800610 (C/T)	Intron-2	-13.9 (1.4), n=41	-6.5 (2.8), n=11	NA	.0071
<i>TPH2</i>					
<b>rs7305115 (G/A)<sup>d</sup></b>	<b>Exon-7 end region</b>	<b>-12.2 (2.4), n=19</b>	<b>-12.0 (1.8), n=25</b>	<b>-11.9 (2.9), n=8</b>	<b>.020</b>

Abbreviations: continued-FLX = continued-fluoxetine; LS mean=least-squared mean; MADRS-TS = Montgomery-Åsberg Depression Rating Scale Total Score; NA = not available; SE = standard error; SNP = single nucleotide polymorphism; UTR = untranslated region.

Bolded entries indicate adjusted  $p < .05$ .

<sup>a</sup> FDR  $p = .000123$

<sup>b</sup> FDR  $p = .016$

<sup>c</sup> FDR  $p = .043$

<sup>d</sup> Li/Nyholt  $p = .04$

Note: the alleles in parentheses following the SNP number represent A and B.

**eTable 7. Comparison of change of MADRS total score from baseline by genotype for OFC versus continued-FLX for selected<sup>a</sup> *SLC6A2* SNPs.**

SNP (A/B) <sup>b</sup> region	Treatment	MMRM (SE) MADRS total score change from baseline and n by genotype			p-value <sup>c</sup>
		AA	AB	BB	
rs3785143 (C/T) Intron-2	OFC	-14.2 (1.7), n=48	-20.9 (3.3), n=11	N/A, n=0	.071
	FLX	-11.5 (1.4), n=57	-7.0 (2.5), n=14	N/A, n=0	.059
rs36024 (G/A) Intron-4	OFC	-9.2 (2.4), n=21	-16.7 (2.0), n=31	-21.9 (2.8), n=11	.00034
	FLX	-12.2 (2.2), n=19	-9.7 (1.6), n=38	-12.5 (2.4), n=16	.582
rs36023 (G/A) Intron-4	OFC	-12.7 (2.2), n=24	-16.5 (2.2), n=27	-22.5 (3.5), n=10	.067
	FLX	-8.1 (1.8), n=29	-11.6 (1.7), n=33	-17.4 (2.9), n=11	.019
rs2397772 (C/G) Intron-5	OFC	-14.9 (2.1), n=29	-13.8 (2.2), n=25	-21.7 (3.8), n=9	.048
	FLX	-14.2 (2.0), n=27	-10.0 (1.7), n=32	-8.1 (2.5), n=14	.092
rs12920735 (A/T) Intron-5	OFC	-14.7 (2.0), n=29	-14.6 (2.2), n=24	-21.1 (3.7), n=9	.036
	FLX	-14.4 (2.0), n=26	-9.6 (1.7), n=32	-8.1 (2.5), n=14	.089
rs12924088 (A/G) Intron-9	OFC	-14.8 (1.9), n=33	-14.5 (2.4), n=22	-21.7 (3.9), n=8	.066
	FLX	-14.4 (1.8), n=30	-9.4 (1.7), n=29	-8.0 (2.4), n=14	.031
rs5569 (G/A) Exon-9	OFC	-14.8 (1.9), n=35	-14.8 (2.1), n=28	-21.7 (3.8), n=8	.087
	FLX	-14.3 (1.8), n=32	-8.8 (1.7), n=31	-8.1 (2.4), n=14	.023
rs998424 (G/A) Intron-10	OFC	-15.3 (1.9), n=33	-15.2 (2.3), n=22	-27.5 (4.2), n=7	.0099
	FLX	-14.4 (1.9), n=29	-9.3 (1.8), n=29	-9.5 (2.6), n=12	.049

<sup>a</sup>SNPs had additive model p-values less than 0.1 for MMRM MADRS total score change from baseline for both OFC and continued-FLX treatment arms and rs36024.

<sup>b</sup>Note: the alleles in parentheses following the SNP number represent A and B.

<sup>c</sup>Uncorrected p-value for MMRM change in MADRS total score from baseline using additive model of genotypes.

Abbreviations: FLX = fluoxetine; MADRS = Montgomery-Åsberg Depression Rating Scale; MMRM = mixed model repeated measure; n = number of patients; OFC = olanzapine/fluoxetine combination; SE = standard error; SNP = single nucleotide polymorphism.