ERRATUM

Several typographical and nomenclature errors in Figure 1 and Table 1 have been identified in the September 15, 2006, issue of *Biological Psychiatry*, Volume 60, Issue 6, in the article "Novel, Replicated Associations Between Dopamine D3 Receptor Gene Polymorphisms and Schizophrenia in Two Independent Samples" by Talkowski *et al*. (Biol Psychiatry 2006;60:570-577). The authors note that the errors, detailed below, do not alter the statistical analyses or their interpretation of the data.

In Figure 1, rs7625287 should instead have read rs7625282. This single nucleotide polymorphism (SNP) was otherwise identified correctly in both Table 1 and throughout the manuscript. Also, rs7616367 is now indicated with an asterisk as an associated SNP, rather than rs2399504 as previously indicated. Additionally, the order of rs1800828 and rs324026 was reversed and has now been corrected. The corrected Figure 1 appears below.

In Table 1, the nucleotides were mismatched with their allele designations (1 or 2) and/or strand genotyped for eight SNPs. Nucleotide, strand designations, and/or allele codes (columns 4, 5, and 6) have been corrected so as to make them compatible with HapMap (2) while retaining the integrity of the dataset presented in the manuscript. Allele codes "1" or "2" listed in the manuscript for the associated haplotypes have been retained. Also, the data for rs2399504 and rs7616367 was previously transposed for the US sample. All information is now corrected in Table 1, below.

1. Anney RJ, Rees MI, Bryan E, Spurlock G, Williams N, Norton N, Williams H, Cardno A, Zammit S, Jones S, *et al.* (2002): Characterisation, mutation detection, and association analysis of alternative promoters and 5′ UTRs of the human dopamine D3 receptor gene in schizophrenia. *Mol Psychiatry,* 7, 493–502.
2. HapMap (2003): The International HapMap Project. *Nature,* 426, 789–96.

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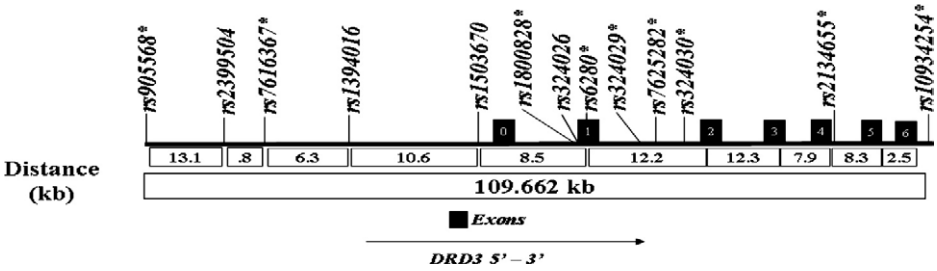

Figure 1. Dopamine D3 receptor (DRD3) genomic organization and SNPs investigated in the U.S. sample. Known exons are numbered, as well as an additional exon (numbered 0) suggested by Anney *et al.* (1). *Denotes associated SNP in U.S. analyses.

Table 1. SNP-Based Results Across Samples

						U.S. Samples					India Trios	
SNP #	SNP	Location	Nuc	Strand	Allele Code	[a]Freq. (Case/ Control)	[b]Case-Control *p*-value	GC Corrected *p*-value	[c]TDT (T/NT)	TDT *p*-value	TDT (T/NT)	TDT *p*-value
1	rs905568	5′	C	+	2	.48/.37	<.0001	.0008	78/72	.62	51/47	0.69
2	rs2399504	5′	C	+	1	.82/.81	.923	.933	49/36	.16	28/27	0.89
–	rs7616367	5′	A	+	2	.74/.74	.944	.95	66/43	.02	–	–
3	rs1394016	5′	T*	−	2	.37/.33	.145	.194	77/62	.2	64/46	0.07
4	rs1503670	5′	G	+	1	.63/.64	.72	.75	83/65	.14	74/64	0.39
5	rs1800828	5′	G	−	1	.80/.77	.175	.23	62/39	.02	59/45	0.17
6	rs324026	5′	T*	+	2	.69/.68	.62	.66	78/59	.1	70/56	0.21
7	rs6280	Exon	A*	−	1	.75/.67	.001	.004	71/54	.13	70/60	0.36
8	rs324029	Intron	C*	−	2	.73/.72	.855	.87	72/50	.04	60/42	0.07
–	rs7625282	Intron	T	−	2	.77/.76	.776	.806	71/45	.01	–	–
9	rs324030	Intron	C*	+	2	.72/.73	.813	.83	72/49	.04	59/44	0.14
10	rs2134655	Intron	G	−	2	.73/.67	.022	.075	65/53	.27	48/42	0.53
11	rs10934254	3′	C	−	1	.44/.39	.073	.12	80/57	.05	71/48	0.03

Single nucleotide polymorphism (SNP) # is given in sequential order according to DRD3 transcription (5′ to 3′) from the most upstream (telomeric) to downstream (centromeric) SNP. SNP# is only given for SNPs assayed in both samples. Nuc = nucleotide.

*Nucleotide provided is designated as "other" allele, not "reference" allele by HapMap (2).

[a]Frequency of the allele provided in cases and controls.

[b]Trends test p-values from genotype distributions.

[c]T = transmitted allele, NT = not transmitted allele (transmission disequilibrium test [TDT]).