Supplementary Table 1. Subjects and Phenotyping

	Entire Sample									Individuals with DNA						
Collections Used	Subjects with DNA	Subjects without DNA	Total Subjects	Total Families	Full Trios	Founders with DNA	EA	AA	Other Race	M	F	SZ	SA	UD	Average Age at Onset	Range of Ages at Onset
NIMH-IRP only	325	117	442	67	39	108	88%	4%	7%	180	145	136	24	165	20.4	6 to 45
NIMH-GI only	321	39	360	69	38	106	55%	32%	13%	159	162	137	22	162	18.5	5 to 38
All Collections	646	156	802	136	77	214	72%	18%	10%	339	307	273	46	327	19.5	5 to 45

Note: EA = European ancestry; AA = African American; SZ = schizophrenia; SA = schizoaffective disorder; UD = unknown diagnosis; M = male; F = female. Age at onset refers to overt psychosis onset. NIMH-IRP (Intramural Research Program, also known as the Clinical Neurogenetics – CNG – group) [34,35] and NIMH-GI (Genetics Initiative – Part I) [36] collections have been previously described. The sex distribution was approximately equal (males 52%, females 48%) for subjects with DNA, but more skewed for affected subjects with DNA (males 62%, females 38%).

Supplementary Table 2. FBAT Results for All 20 Markers of *DTNBP1*[a]

						All Families			EA Subset		
Markers[b]	LD bins	Distance[c]	Genotyping Completion Rate	SNP	Allele	Freq.	Z Score	*p*-value	Freq.	Z Score	*p*-value
rs742102		6,815	0.99	C/T	T	0.04	1.07	0.28	0.03	1.01	0.31
rs17470454		1,032	0.99	C/T	C	0.95	0.67	0.50	0.93	0.63	0.53
rs742106		13,956	0.98	C/T	T	0.31	0.26	0.79	0.33	0.64	0.52
rs875462	**A**	7,427	**0.99**	**A/G**	**A**	**0.80**	**2.65**	**0.008**	**0.75**	**2.30**	**0.021**
rs10949305	B	16,887	0.98	T/A	A	0.18	0.27	0.79	0.10	-0.07	0.95
rs2743553	B	10,324	0.99	C/T	T	0.14	1.53	0.13	0.09	1.06	0.29
rs742105	C	16,047	0.98	G/A	A	0.40	0.45	0.65	0.43	0.72	0.47
rs760666	**A**	4,119	**0.98**	**C/T**	**C**	**0.81**	**2.76**	**0.006**	**0.77**	**2.14**	**0.032**
rs7758659	**A**	27,615	**0.99**	**G/A**	**G**	**0.81**	**2.84**	**0.004**	**0.77**	**2.16**	**0.030**
rs2619539	C	5,448	0.99	C/G	G	0.40	0.55	0.58	0.44	0.43	0.67
rs2743865	B	1,799	0.99	C/T	T	0.17	0.87	0.38	0.10	0.47	0.64
rs3213207	D	5,330	0.98	A/G	A	0.90	0.55	0.58	0.87	0.64	0.52

rs1011313	E	16,397	0.98	G/A	A	0.09	0.14	0.89	0.10	-0.31	0.76
rs2619528	F	1,303	0.98	G/A	A	0.28	0.02	0.99	0.23	-0.54	0.59
rs760761	F	2,517	0.99	C/T	C	0.72	0.38	0.71	0.77	1.18	0.24
rs2619522	F	3,421	0.98	T/G	T	0.72	0.22	0.83	0.77	0.82	0.41
rs1018381	B	3,801	0.99	C/T	T	0.17	0.81	0.42	0.10	0.43	0.66
rs909706	G	4,338	0.98	A/G	G	0.31	1.33	0.18	0.32	1.43	0.15
rs2619538		3,452	0.99	A/T	T	0.43	0.58	0.56	0.42	1.09	0.27
rs742208		N/A	0.96	T/C	C	0.17	1.00	0.32	0.11	-0.12	0.90

[a] FBAT results for all 20 screening SNPs are shown in the whole current sample and EA subset. SNP = nucleotide changes listed as major allele / minor allele. Allele nucleotides were converted to a unified format by ensuring they were from the minus strand. Nominal *p*-value and associated allele are shown. Freq. = frequency of the more often transmitted allele. Significant SNP (rs7758659) row is bolded, as are the two rows with SNPs in high LD with rs7758659 (rs875462 and rs760666).

[b] rs numbers are in first column, and LD bins (see Figure 2b) if any in the second column. Markers are in the order from the 3' to the 5' flanking regions.

[c] Distance to next marker in base pairs (bp). The position for the first marker is nucleotide 15,624,612 in the UCSC May 2004 freeze of chromosome 6.