Supplementary Table 1

Demographics

			Age		Sex (%)		Ethnicity (%)		Race (%)						
Project	Group	N	M	SD	Male	Female	Not Hispanic	Hispanic	AA	AI	AS	CA	NH	MR	OT/UNK
B-SNIP1															
	HC	274	37.34	12.25	42	57	90	10	25	0	6	65	0	2	2
	B1	263	37.76	12.67	51	49	91	9	49	0	2	45	0	3	2
	B2	222	35.89	12.87	50	50	91	9	37	0	2	57	0	1	2
	B3	226	34.19	11.81	54	46	93	7	19	0	2	73	0	4	2
	SZ	312	35.84	12.78	68	32	93	7	45	0	3	46	0	3	3
	SAD	173	36.49	11.80	41	59	89	11	39	0	1	54	0	5	1
	BDP	226	35.98	12.80	37	63	92	8	19	0	2	75	0	1	2
Replication															
	HC	198	40.96	11.04	49	51	91	9	34	1	7	53	0	4	2
	B1	277	41.06	11.04	56	44	89	11	54	1	3	30	0	8	5
	B2	208	39.80	10.78	39	61	82	18	44	1	2	45	0	5	4
	B3	232	36.73	11.95	50	50	85	15	28	0	4	57	0	8	3
	SZ	263	40.16	11.48	60	40	89	11	56	1	4	28	0	6	5
	SAD	248	40.13	10.90	43	57	83	17	40	1	3	41	0	10	5
	BDP	206	37.19	11.73	42	58	84	16	27	0	1	65	0	4	3

Note. AA = African American or Black, AI = American Indian or First Nations, AS = Asian, CA = Caucasian, NH = Hawaiian or Pacific Islander, MR = Multiracial, OT/UNK = Other or Unknown

Supplementary Table 2.

Group Scores on Symptom/Sign Measures (These clinical data by Biotype are also plotted in Supplementary Figure 8)

Project	Group		GAF	SFS	Subject Hollingshead Score	Family Hollingshead Score	YMRS	MADRS	SBS	PANSS Positive	PANSS Negative	PANSS General	PANSS Total
B-SNIP1													
	HC	Mean	86.5	156.7	35.8	39.2	N/A	N/A	N/A	N/A	N/A	N/A	N/A
		SD	6.5	17.3	14.6	15.0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
		N	267	201	264	258	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	BT1	Mean	50.1	118.2	52.1	44.1	5.8	10.6	5.4	16.0	15.3	31.5	62.8
		SD	12.5	25.3	14.6	16.2	6.0	9.9	3.1	5.6	5.6	8.5	16.5
		N	261	210	240	217	255	251	252	257	257	257	257
	BT2	Mean	52.1	125.3	49.2	41.7	6.3	10.3	5.8	16.9	15.5	32.8	65.0
		SD	13.2	23.5	15.1	16.3	6.4	8.7	3.0	5.9	5.4	9.4	17.7
		N	220	180	206	200	217	219	217	216	216	216	214
	BT3	Mean	56.7	130.8	44.9	37.5	5.8	10.4	4.1	14.4	14.1	30.7	59.2
		SD	13.9	24.3	15.0	15.6	6.5	9.3	3.3	5.2	5.5	8.9	17.0
		N	225	179	216	208	219	220	221	221	221	221	221
	SZ	Mean	49.5	120.8	53.2	42.2	5.5	8.2	7.9	16.7	16.8	32.0	65.4
		SD	12.5	24.4	14.0	16.2	5.8	7.9	1.2	5.8	6.0	9.0	17.5
		N	311	250	283	262	301	299	303	302	302	303	301
	BDP	Mean	60.8	134.3	43.1	37.9	5.8	10.2	1.1	12.9	12.0	28.7	53.5
		SD	12.9	22.6	15.5	15.4	6.7	9.3	1.1	4.5	3.9	8.0	13.7
		N	224	177	218	212	222	221	219	222	222	222	222
	SAD	Mean	48.5	118.4	49.1	43.8	7.1	14.7	5.1	17.9	15.8	34.8	68.5
		SD	11.7	25.1	14.4	17.0	6.5	10.3	1.5	5.2	5.0	8.8	16.3
		N	171	142	161	151	168	170	168	170	170	169	169

Replication												
	HC	Mean	82.4	153.2	34.4	37.7	N/A	N/A	N/A	N/A	N/A	N/A	N/A
		SD	7.1	18.0	13.4	15.0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
		N	161	191	193	187	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	BT1	Mean	51.3	118.8	49.2	46.0	10.4	12.1	5.6	17.5	16.2	32.3	66.1
		SD	10.8	23.4	12.8	16.5	8.1	10.8	2.6	6.8	6.8	10.3	21.1
		N	260	259	268	251	244	245	265	247	246	247	246
	BT2	Mean	51.1	115.5	49.1	44.6	9.8	12.5	5.7	17.5	17.0	33.5	68.0
		SD	11.9	24.7	14.2	15.3	8.1	11.1	2.6	6.4	7.1	10.0	20.6
		N	197	196	199	186	184	185	195	186	186	186	186
	BT3	Mean	56.9	129.2	42.0	37.5	8.7	12.4	4.3	14.2	13.5	29.8	57.5
		SD	12.9	23.3	14.0	15.9	7.6	9.9	2.6	5.6	5.9	9.0	18.3
		N	220	219	227	214	219	220	229	216	216	215	215
	SZ	Mean	50.5	116.6	50.9	46.3	9.3	9.3	7.7	17.4	17.0	31.8	66.3
		SD	11.3	21.3	13.3	16.2	7.4	9.2	1.2	6.3	6.7	10.1	20.4
		N	245	244	251	230	230	231	247	232	231	232	231
	BDP	Mean	56.4	131.3	41.2	38.4	8.9	14.2	2.0	13.7	13.5	30.7	57.9
		SD	12.8	24.4	13.4	16.3	8.4	11.5	1.4	5.6	6.4	10.1	20.1
		N	198	196	205	196	189	189	198	189	189	188	188
	SAD	Mean	52.9	117.6	47.2	43.1	10.7	13.7	5.2	17.7	15.6	32.8	66.1
		SD	11.8	25.0	13.7	15.8	8.0	10.4	1.4	6.7	6.8	9.4	20.1
		N	234	234	238	225	228	230	244	228	228	228	228

Note. HC=healthy persons, BT1=Biotype-1, BT2=Biotype-2, BT3=Biotype-3, SZ=schizophrenia, SAD=schizoaffective disorder, BDP=bipolar disorder with psychosis, GAF = Global Assessment of Function (DSM); SFS = Birchwood Social Functioning Scale; YMRS = Young Mania Ratings Scale; MADRS = Montgomery-Asberg Depression Rating Scale; SBS = Schizobipolar Scale; PANSS = Positive and Negative Syndrome Scale for Schizophrenia

Supplementary Table 3.
Group Comparisons of Symptom/Sign Measures

	By Biotype			By DSM		
	F(df1,df2)	*p*	Tukey's B Homogenous Subsets	F(df1,df2)	*p*	Tukey's B Homogenous Subsets
B-SNIP1						
GAF (with HC)	F(3,969) = 546.9	<.001	BT1/BT2 < BT3 < HC	F(3,969) = 661.6	<.001	SZ/SAD < BDP < HC
GAF	F(2,703) = 15.8	<.001	BT1/BT2 < BT3	F(2,703) = 69.2	<.001	SZ/SAD < BDP
SFS (with HC)	F(3,766) = 109.4	<.001	BT1 < BT2 < BT3 < HC	F(3,766) = 119.1	<.001	SZ/SAD < BDP < HC
SFS	F(2,566) = 13.0	<.001	BT1 < BT2 < BT3	F(2,566) = 22.3	<.001	SZ/SAD < BDP
Subject Hollingshead Score	F(2,659) = 13.6	<.001	BT3 < BT1/BT2	F(2,659) = 29.1	<.001	BDP < SAD < SZ
Family Hollingshead Score	F(2,622) = 9.1	<.001	BT3 < BT1/BT2	F(2,622) = 7.0	0.001	BDP < SAD/SZ
YMRS	F(2,688) = 0.5	0.61	N/A	F(2,688) = 3.6	0.03	SZ/BDP < BDP/SAD
MADRS	F(2,687) = 0.1	0.95	N/A	F(2,687) = 28.7	<.001	SZ < BDP < SAD
SBS	F(2,687) = 18.1	<.001	BT3 < BT1/BT2	F(2,687) = 1943.6	<.001	BDP < SAD < SZ
PANSS Positive	F(2,691) = 11.4	<.001	BT3 < BT1/BT2	F(2,691) = 51.5	<.001	BDP < SZ < SAD
PANSS Negative	F(2,691) = 3.7	0.03	BT3/BT1 < BT1/BT2	F(2,691) = 57.9	<.001	BDP < SAD/SZ
PANSS General	F(2,691) = 3.1	0.048	BT3/BT1 < BT1/BT2	F(2,691) = 24.6	<.001	BDP < SZ < SAD
PANSS Total	F(2,689) = 6.5	<.01	BT3 < BT1/BT2	F(2,689) = 51.1	<.001	BDP < SAD/SZ
Replication						
GAF (with HC)	F(3,834) = 315.1	<.001	BT1/BT2 < BT3 < HC	F(3,834) = 310.1	<.001	SZ/SAD < BDP < HC
GAF	F(2,674) = 16.8	<.001	BT1/BT2 < BT3	F(2,674) = 13.6	<.001	SZ/SAD < BDP
SFS (with HC)	F(3,861) = 113.6	<.001	BT1/BT2 < BT3 < HC	F(3,861) = 119.6	<.001	SZ/SAD < BDP < HC
SFS	F(2,671) = 19.3	<.001	BT1/BT2 < BT3	F(2,671) = 25.4	<.001	SZ/SAD < BDP
Subject Hollingshead Score	F(2,691) = 21.2	<.001	BT3 < BT1/BT2	F(2,691) = 29.7	<.001	BDP < SAD < SZ
Family Hollingshead Score	F(2,648) = 17.8	<.001	BT3 < BT1/BT2	F(2,648) = 13.0	<.001	BDP < SAD/SZ
YMRS	F(2,644) = 2.6	0.07	N/A	F(2,644) = 3.1	0.046	no subsets
MADRS	F(2,647) = 0.1	0.91	N/A	F(2,647) = 14.7	<.001	SZ < SAD/BDP
SBS	F(2,686) = 20.2	<.001	BT3 < BT1/BT2	F(2,686) = 991.2	<.001	BDP < SAD < SZ
PANSS Positive	F(2,646) = 20.6	<.001	BT3 < BT1/BT2	F(2,646) = 25.6	<.001	BDP < SAD/SZ
PANSS Negative	F(2,645) = 15.8	<.001	BT3 < BT1/BT2	F(2,645) = 14.4	<.001	BDP < SAD/SZ
PANSS General	F(2,645) = 7.8	<.001	BT3 < BT1/BT2	F(2,645) = 2.5	0.09	N/A
PANSS Total	F(2,644) = 16.4	<.001	BT3 < BT1/BT2	F(2,644) = 11.2	<.001	BDP < SAD/SZ

Supplementary Table 4.

Medications

	B-SNIP1						
	HC n = 274	B1 n = 263	B2 n = 222	B3 n = 226	SZ n = 312	SAD n = 173	BDP n = 226
Unknown Med History, n (%)	1 (.4)	5 (1.9)	2 (.9)	0 (0)	5 (1.6)	0 (0)	2 (.9)
N with data	273	258	220	226	307	173	224
No Medication taken, n (%)	143 (52.2)	0 (0)	8 (3.6)	11 (4.9)	5 (1.6)	4 (2.3)	10 (4.4)
Not on Psychotropic Medications, n (%)	264 (96.7)	5 (1.9)	15 (6.8)	19 (8.4)	14 (4.6)	9 (5.2)	16 (7.1)
Antipsychotic (Any), n (%)	0 (0)	235 (91.1)	191 (86.8)	175 (77.4)	282 (91.9)	153 (88.4)	166 (74.1)
A. 1st Generation	0 (0)	32 (12.4)	20 (9.1)	18 (8)	37 (12.1)	19 (11)	14 (6.3)
B. 2nd Generation	0 (0)	203 (78.7)	170 (77.3)	157 (69.5)	245 (79.8)	133 (76.9)	152 (67.9)
Mood Stabilizers (Any), n (%)	0 (0)	122 (47.3)	85 (38.6)	112 (49.6)	66 (21.5)	94 (54.3)	159 (71)
A. Lithium	0 (0)	31 (12)	30 (13.6)	30 (13.3)	17 (5.5)	18 (10.4)	56 (25)
B. Anticonvulsants	0 (0)	91 (35.3)	55 (25)	82 (36.3)	49 (16)	76 (43.9)	103 (46)
Antidepressants (Any), n (%)	3 (1.1)	118 (45.7)	93 (42.3)	107 (47.3)	118 (38.4)	100 (57.8)	100 (44.6)
A. SSRIs/SNRIs	3 (1.1)	72 (27.9)	55 (25)	62 (27.4)	79 (25.7)	61 (35.3)	49 (21.9)
B. Tricyclics	0 (0)	2 (.8)	6 (2.7)	4 (1.8)	3 (1)	2 (1.2)	7 (3.1)
C. MAO Inhibitors	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
D. Miscellaneous	0 (0)	44 (17.1)	32 (14.5)	41 (18.1)	36 (11.7)	37 (21.4)	44 (19.6)
Anxiolytics/Sedatives/ Hypnotics, n (%)	6 (2.2)	67 (26)	61 (27.7)	62 (27.4)	68 (22.1)	50 (28.9)	72 (32.1)
Anticholinergics/ Antiparkinsonians, n (%)	0 (0)	52 (20.2)	30 (13.6)	20 (8.8)	57 (18.6)	25 (14.5)	20 (8.9)
Stimulants, n (%)	1 (.4)	14 (5.4)	10 (4.5)	23 (10.2)	14 (4.6)	8 (4.6)	25 (11.2)
Miscellaneous, Psychotropic/ Centrally Active, n (%)	0 (0)	8 (3.1)	2 (.9)	7 (3.1)	7 (2.3)	5 (2.9)	5 (2.2)

	Replication						
	HC n = 198	B1 n = 277	B2 n = 208	B3 n = 232	SZ n = 263	SAD n = 248	BDP n = 206
Unknown Med History, n (%)	1 (.5)	1 (.4)	3 (1.4)	1 (.4)	4 (1.5)	1 (.4)	0 (0)
N with data	197	277	206	231	259	247	206
No Medication taken, n (%)	99 (50)	15 (5.4)	11 (5.4)	21 (9.1)	19 (7.2)	14 (5.60	14 (6.8)
Not on Psychotropic Medications, n (%)	189 (95.5)	23 (8.3)	19 (9.2)	39 (16.9)	35 (13.5)	26 (10.5)	20 (9.7)
Antipsychotic (Any), n (%)	0 (0)	230 (83)	167 (81.1)	145 (62.8)	213 (81.9)	192 (77.4)	137 (66.5)
A. 1st Generation	0 (0)	36 (13)	38 (18.4)	12 (5.2)	49 (18.8)	32 (12.9)	5 (2.4)
B. 2nd Generation	0 (0)	212 (76.5)	144 (69.9)	140 (60.6)	188 (72.3)	174 (70.2)	134 (65)
Mood Stabilizers (Any), n (%)	2 (1)	114 (41.2)	78 (37.9)	103 (44.6)	56 (21.5)	108 (43.5)	131 (63.6)
A. Lithium	0 (0)	34 (12.3)	26 (12.6)	23 (10)	11 (4.2)	26 (10.5)	46 (22.3)
B. Anticonvulsants	2 (1)	97 (35)	59 (28.6)	87 (37.7)	45 (17.3)	97 (39.1)	101 (49)
Antidepressants (Any), n (%)	4 (2)	141 (50.9)	94 (45.6)	94 (40.7)	108 (41.5)	129 (52)	92 (44.7)
A. SSRIs/SNRIs	2 (1)	107(38.6)	64 (31.1)	69 (29.9)	82 (31.5)	101 (40.7)	57 (27.7)
B. Tricyclics	1 (.5)	5 (1.8)	3 (1.5)	3 (1.3)	3 (1.2)	4 (1.6)	4 (1.9)
C. MAO Inhibitors	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
D. Miscellaneous	1 (.5)	64 (23.1)	49 (23.8)	43 (18.6)	46 (17.7)	54 (21.8)	56 (27.2)
Anxiolytics/Sedatives/ Hypnotics, n (%)	2 (1)	63 (22.7)	41 (19.9)	46 (19.9)	38 (14.6)	52 (21)	60 (29.1)
Anticholinergics/ Antiparkinsonians, n (%)	0 (0)	44 (15.9)	34 (16.5)	13 (5.6)	53 (20.4)	33 (13.3)	5 (2.4)
Stimulants, n (%)	3 (1.5)	7 (2.5)	9 (4.4)	13 (5.6)	4 (1.5)	10 (4)	15 (7.3)
Miscellaneous, Psychotropic/ Centrally Active, n (%)	0 (0)	14 (5.1)	16 (7.8)	14 (6.1)	14 (5.4)	15 (6)	15 (7.3)

Supplementary Table 5.

Chi-Square Tests of Group X Medication Status

	Biotype		DSM	
	Chi-Square (df=2)	p	Chi-Square (df=2)	p
Antipsychotic (Any)	49.6	<.001	45.0	<.001
A. 1st Generation	13.8	.001	N/A*	N/A*
B. 2nd Generation	20.1	<.001	12.0	0.003
Mood Stabilizers (Any)	7.2	0.03	215.4	<.001
A. Lithium	0.5	0.78	N/A*	N/A*
B. Anticonvulsants	11.8	.003	121.8	<.001
Antidepressants (Any)	2.7	0.26	20.8	<.001
A. SSRIs/SNRIs	4.2	0.12	20.8	<.001
B. Tricyclics	N/A*	N/A*	N/A*	N/A*
C. MAO Inhibitors	N/A*	N/A*	N/A*	N/A*
D. Miscellaneous	0.5	0.76	14.3	0.001
Anxiolytics/Sedatives/Hypnotics	0.1	0.97	19.4	<.001
Anticholinergics/Antiparkinsonians	25.1	<.001	N/A*	N/A*
Stimulants	N/A*	N/A*	N/A*	N/A*
Miscellaneous, Psychotropic/Centrally Active	N/A*	N/A*	N/A*	N/A*

Note. *Chi-Square test only performed for medication categories with n>30 in each cell

Supplementary Table 6

B-SNIP1 Two-Step Solution

Number of Clusters	Schwarz's Bayesian Criterion (BIC)	BIC Change[a]	Ratio of BIC Changes[b]	Ratio of Distance Measures[c]
1	2278.063			
2	2166.284	-111.780	1.000	1.597
3	2135.718	-30.566	.273	1.462
4	2148.107	12.390	-.111	1.348
5	2184.522	36.414	-.326	1.164
6	2230.648	46.126	-.413	1.111
7	2282.697	52.049	-.466	1.386
8	2349.608	66.912	-.599	1.018
9	2417.202	67.594	-.605	1.055
10	2486.763	69.561	-.622	1.015

a. The changes are from the previous number of clusters in the table.

b. The ratios of changes are relative to the change for the two cluster solution.

c. The ratios of distance measures are based on the current number of clusters against the previous number of clusters.

Replication Sample Two-Step Solution

Number of Clusters	Schwarz's Bayesian Criterion (BIC)	BIC Change[a]	Ratio of BIC Changes[b]	Ratio of Distance Measures[c]
1	2749.442			
2	2655.405	-94.037	1.000	1.121
3	2583.292	-72.113	.767	1.897
4	2596.756	13.464	-.143	1.024
5	2612.478	15.722	-.167	1.395
6	2654.603	42.125	-.448	1.031
7	2698.724	44.121	-.469	1.202
8	2753.743	55.019	-.585	1.139
9	2815.342	61.599	-.655	1.215
10	2885.314	69.971	-.744	1.033

a. The changes are from the previous number of clusters in the table.

b. The ratios of changes are relative to the change for the two cluster solution.

c. The ratios of distance measures are based on the current number of clusters against the previous number of clusters.

Supplementary Table 7 - Medication-biomarkers partial variance

Biomarker	Risperidone	Aripiprazole	Quetiapine	Olanzapine
BACS Verbal Memory	0.76	0.29	0.34	0.30
BACS Digit Sequence	0.44	0.30	0.14	0.00
BACS Token Motor	0.66	0.44	0.00	0.02
BACS Verbal Fluency	0.53	**1.19**	0.02	0.02
BACS Symbol Coding	0.64	**1.14**	0.00	0.36
BACS Tower	0.09	0.16	0.38	0.02
Antisaccade Error Rate	0.06	0.34	0.19	0.62
Antisaccade Error Latency	0.42	0.04	0.00	0.02
Prosaccade Latency - No Gap	0.04	0.10	0.10	0.08
Prosaccade Latency - Gap	0.14	0.02	0.27	0.14
Prosaccade Latency - Overlap	0.00	0.01	0.00	0.35
SSTGoDiff	0.00	0.53	0.01	0.03
SSTProportionError.stop	0.01	0.25	0.03	0.06
GATE_S1_N100_70_130	0.35	0.30	0.64	0.31
TGT2_N100_70_130	0.06	0.03	0.40	0.02
STD_N100_50_130	0.32	0.10	0.05	0.08
GATE_S1_Low_early_40_160	0.38	0.01	**1.30**	0.66
TGT1_LOW_20_100_F	0.00	0.02	0.50	0.01
STD_BETA_20_100	0.06	0.04	0.29	0.01
STD_LOW_30_480	0.19	0.00	0.04	0.01
TGT2_LOW_140_280_P	0.52	0.00	0.02	0.01
TGT2_LOW_280_400_P	0.52	0.00	0.02	0.01
TGT1_p300a_330_540	0.07	0.02	0.11	0.01
TGT1_LOW_190_440_F	0.04	0.25	0.03	0.01
TGT2_BETA_180_240_P	0.01	0.18	0.13	0.00
TGT1_BETA_140_230_F	0.01	0.20	0.06	0.00
GATE_S2_late_770_850	0.14	0.32	0.18	0.08
GATE_preS2_420_510	0.03	0.25	0.06	0.01
GATE_S2_P50_530_600	0.07	0.44	0.10	0.07
GATE_S2_P200_660_710	0.03	0.34	0.00	0.01
GATE_S2_N100_600_660	0.15	0.28	0.00	0.00
GATE_S1_N200_290_310	0.74	0.05	0.10	0.16
STD_GAMMA_480_520	0.26	0.24	0.14	0.18
GATE_S2_Beta_Late_760_780	0.19	0.04	0.02	0.03
GATE_preS1_Gamma_n100_n70	0.02	0.01	0.62	0.01
TGT2_GAMMA_20_70	0.21	0.03	0.20	0.16
STD_GAMMA_30_70	0.09	0.05	0.01	0.45
STD_BETA_230_270	0.04	0.04	0.46	0.07
GATE_S1_Beta_Early_40_90	0.11	0.12	0.18	0.55
STD_P200_140_250	0.12	0.34	0.10	0.01
TGT2_P200_140_240	0.10	0.52	0.11	0.12
GATE_S1_P200_200_260	0.01	0.31	0.14	0.00
TGT1_n200_160_230	0.77	0.17	0.08	0.52
GATE_S1_Low_midlatency_260_310	0.02	0.00	0.01	0.00

* For each biomarker, multiple regression was calculated using the above medications as predictors. Report

*** Associations accounting for at least 1% of variance are highlighted**

Supplementary Table 6 - Medication-biomarkers partial variance (cont)

Clozapine	Haloperidol	Lithium	Valproic Acid	Gabapentin	Lamotrigine	Fluoxetine
0.71	0.28	0.35	0.07	0.03	0.49	0.03
0.04	0.72	0.18	0.01	0.41	**1.06**	0.12
0.71	0.04	0.04	0.00	0.03	0.08	0.20
0.10	**1.59**	0.01	0.01	0.00	**2.07**	0.29
0.77	0.41	0.01	0.32	0.04	0.34	0.01
0.00	0.34	0.69	0.01	0.08	**1.21**	0.00
2.37	0.90	0.81	0.28	0.04	0.46	0.01
0.04	0.90	0.17	0.35	0.02	0.76	0.04
0.25	0.40	0.14	**1.30**	0.01	0.08	0.08
0.38	0.41	0.28	**1.35**	0.00	0.01	0.00
0.04	0.76	0.00	0.44	0.03	0.01	0.00
0.55	0.07	0.01	0.00	0.53	**1.54**	0.02
0.56	0.00	0.41	0.10	0.04	0.00	0.00
2.69	0.62	0.09	0.18	0.20	0.34	0.00
0.81	0.18	0.13	0.03	0.05	0.20	0.07
0.92	0.18	0.36	0.38	0.02	0.29	0.06
1.39	0.29	0.12	0.22	0.13	0.12	0.00
0.28	0.00	0.01	0.21	0.12	0.35	0.31
0.38	0.07	0.24	0.03	0.12	0.11	0.20
1.02	0.04	0.44	0.01	0.06	0.31	0.18
0.13	0.10	0.05	0.00	0.08	0.09	0.06
0.13	0.10	0.05	0.00	0.08	0.09	0.06
0.00	0.02	0.12	0.00	0.16	0.05	0.04
0.16	0.02	0.02	0.02	0.16	0.05	0.04
0.00	0.01	0.14	0.40	0.00	0.00	0.01
0.00	0.00	0.27	0.31	0.02	0.00	0.04
0.37	0.06	0.08	**1.51**	0.06	**2.86**	0.00
0.00	0.62	0.66	0.04	0.00	**1.08**	0.10
1.56	0.71	0.00	0.31	0.03	0.14	0.01
0.56	0.28	0.02	0.64	0.00	1.21	0.00
0.19	0.44	0.05	**1.10**	0.00	**1.25**	0.16
0.49	0.00	0.06	0.69	0.29	1.69	0.56
0.14	0.10	0.00	0.26	0.59	0.06	0.32
0.22	0.53	0.14	0.35	0.03	0.06	0.03
0.07	0.00	0.30	0.10	0.19	0.04	0.28
0.01	0.00	0.01	0.01	0.00	0.04	0.62
0.01	0.00	0.03	0.92	0.00	0.17	0.10
0.14	0.86	0.44	0.42	0.00	0.08	0.02
0.76	0.00	0.66	0.59	0.00	0.04	0.11
0.23	0.00	0.81	**1.93**	0.07	**3.88**	0.07
1.14	0.23	**1.02**	0.44	0.12	**2.16**	0.14
0.00	0.17	0.13	**1.00**	0.00	0.86	0.03
0.49	0.05	0.62	0.00	0.36	0.27	0.17
0.05	0.07	0.03	0.26	0.18	0.28	0.19

:ed values represent partial variance.

Supplementary Table 6 - Medication-biomarkers partial variance (cont)

(Es)Citalopram	Bupropion	Sertraline	Trazodone	Benztropine	Clonazepam	Lorazepam
0.04	0.18	0.14	0.07	**1.56**	0.00	0.06
0.12	**1.12**	0.20	0.17	0.17	0.04	0.00
0.14	0.37	0.01	0.17	0.20	**1.08**	0.46
0.07	0.14	0.10	0.02	0.00	0.01	0.22
0.00	**1.28**	0.04	0.10	0.44	0.04	0.04
0.04	0.37	0.01	0.03	0.03	0.31	0.00
0.00	**1.08**	0.00	0.15	0.61	0.01	0.06
0.00	0.08	0.00	0.18	0.23	0.92	0.01
0.04	0.01	0.02	**1.19**	0.06	0.41	0.55
0.00	0.06	0.02	**1.19**	0.14	0.12	0.08
0.01	0.06	0.04	0.36	0.08	0.59	0.12
0.00	0.08	0.13	0.35	0.00	0.15	0.00
0.00	0.04	0.00	0.04	0.18	0.06	0.01
0.18	0.14	0.32	0.01	0.06	0.22	0.11
0.11	0.04	0.29	0.01	0.08	0.02	0.67
0.01	0.01	0.00	0.07	0.01	0.01	0.02
0.08	0.26	0.12	0.02	0.36	0.55	0.05
0.08	0.00	0.20	0.37	0.21	0.07	0.71
0.13	0.25	0.01	0.06	0.07	0.88	0.37
0.06	0.34	0.02	0.03	0.00	0.41	0.71
0.03	0.64	0.01	0.21	0.17	0.08	0.10
0.03	0.64	0.01	0.21	0.17	0.08	0.10
0.03	0.90	0.14	0.06	0.79	0.00	0.02
0.00	0.98	0.00	0.00	0.48	0.48	0.20
0.10	0.58	0.00	0.01	0.22	0.06	0.77
0.08	0.55	0.00	0.00	0.12	0.12	0.98
0.01	0.46	0.71	0.10	0.02	0.50	0.00
0.02	0.50	0.04	0.00	0.45	0.37	0.00
0.08	0.12	0.01	0.03	0.25	0.06	0.08
0.34	0.36	0.26	0.00	0.03	0.41	0.03
0.06	0.08	0.02	0.00	0.00	0.00	0.01
0.01	0.05	0.12	0.40	0.15	0.00	0.13
0.12	0.01	0.00	0.07	0.10	0.08	0.00
0.03	0.03	0.00	0.12	0.01	0.42	0.16
0.01	0.06	0.12	0.02	0.07	0.23	0.00
0.03	0.08	0.20	0.01	0.30	0.03	0.74
0.05	0.29	0.03	0.01	0.00	0.00	0.17
0.00	0.01	0.38	0.01	0.25	0.01	1.96
0.04	0.08	0.00	0.00	0.30	0.02	0.38
0.00	0.09	0.77	0.00	0.00	**1.08**	0.00
0.02	0.01	0.00	0.00	0.17	0.00	0.06
0.07	0.00	0.35	0.06	0.41	0.71	0.00
0.00	0.04	0.13	0.00	0.04	0.04	0.13
0.13	0.17	0.03	0.14	0.18	0.30	0.25

SUPPLEMENTARY TABLE 8A: REPLICATION SAMPLE CROSS VALIDATION

Replication Sample K-means Clustering Cross-Validation					
		Biotype Membership Derived from Replication Sample			
		BT1	BT2	BT3	Total
Biotype Membership Derived from B-SNIP1 Sample (89.0% Accuracy)	BT1	249	11	7	267
	BT2	23	179	15	217
	BT3	5	18	210	233
	Total	277	208	232	717
		Accuracy of Biotype Membership Identification			
	BT1	**89.9%**	5.3%	3.0%	
	BT2	8.3%	**86.1%**	6.5%	
	BT3	1.8%	8.7%	**90.5%**	

SUPPLEMENTARY TABLE 8B: B-SNIP1 SAMPLE CROSS VALIDATION

B-SNIP1 Sample K-means Clustering Cross-Validation					
		Biotype Membership Derived from B-SNIP1 Sample			
		BT1	BT2	BT3	Total
Biotype Membership Derived from Replication Sample (88.5% Accuracy)	BT1	237	16	10	263
	BT2	22	183	17	222
	BT3	3	14	209	226
	Total	262	213	236	711
		Accuracy of Biotype Membership Identification			
	BT1	**90.11%**	7.21%	4.42%	
	BT2	8.37%	**82.43%**	7.52%	
	BT3	1.14%	6.31%	**92.48%**	

SUPPLEMENTARY TABLE 9A: BIOTYPE CDA CROSS-VALIDATION (JACKNIFE PROCEDURE)

Biotype Canonical Discriminant Analysis Classification					
		Predicted Biotype Membership			
		BT1	BT2	BT3	Total
Biotype Membership (90.9% Accuracy)	BT1	480	33	27	540
	BT2	22	396	12	430
	BT3	9	27	422	458
		Accuracy of Predicted Biotype Membership Classification			
	BT1	**88.9%**	6.1%	5.0%	
	BT2	5.1%	**92.1%**	2.8%	
	BT3	2.0%	5.9%	**92.1%**	

SUPPLEMENTARY TABLE 9B: DSM CDA CROSS-VALIDATION (JACKNIFE PROCEDURE)

DSM Canonical Discriminant Analysis Classification					
		Predicted DSM Diagnosis			
		SZ	SAD	BDP	Total
DSM Diagnosis (44.1% Accuracy)	SZ	313	130	132	575
	SAD	181	113	127	421
	BDP	125	103	204	432
		Accuracy of Predicted DSM Diagnosis Classification			
	SZ	**54.4%**	22.6%	23.0%	
	SAD	43.0%	**26.8%**	30.2%	
	BDP	28.9%	23.8%	**47.2%**	

Supplementary Table 10.

B-SNIP1 and Replication Cluster Centroids for Euclidian Distance Calculations

		BACS	Antisaccade	SST	Latency	N100	P300	P200	Ongoing Neural Activity	PS S2
B-SNIP1 Sample Cluster Centroids	**BT1**	-0.628	0.108	-0.337	0.357	-0.836	-0.893	-0.625	-0.798	0.506
	BT2	-0.571	1.059	-0.681	-0.441	-0.018	0.199	0.435	0.550	-0.040
	BT3	0.439	-0.512	0.519	-0.040	0.501	0.388	-0.100	0.269	-0.305
	Total Mean:	-0.268	0.192	-0.151	-0.022	-0.154	-0.142	-0.123	-0.033	0.077
	Total STD:	0.950	1.039	0.959	1.046	0.994	0.965	0.987	0.984	0.994

		BACS	Antisaccade	SST	Latency	N100	P300	P200	Ongoing Neural Activity	PS S2
Replication Sample Cluster Centroids	**BT1**	-0.467	0.324	-0.227	0.309	-0.660	-0.871	-0.550	-0.587	0.431
	BT2	-0.598	0.730	-0.727	-0.050	0.045	0.383	0.736	0.775	0.210
	BT3	0.510	-0.484	0.468	-0.197	0.339	0.276	-0.210	-0.024	-0.531
	Total Mean:	-0.189	0.162	-0.113	0.040	-0.127	-0.132	-0.069	-0.010	0.049
	Total STD:	0.951	0.985	0.994	1.038	0.928	0.957	0.959	0.928	0.996

Steps to determine Biotype membership for a single subject with standardized data: a) Standardize 9 Biofactor values based on the Total Mean and Standard Deviation from all Psychosis Probands. B) Calculate the Euclidian distance from each Biotype. C) Assign Biotype membership based on the smallest distance (i.e. closest to that Biotype).