Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

eAppendix 1. Missing Data

A total of 1415 participants were recruited between July 1, 2010, and January 31, 2014. Listwise deletion was used for analyses, resulting in missing data for at least one variable in 436 participants. To determine if those with and without missing data differed on demographic characteristics, we conduced independent samples *t*-tests and chi-square tests for age, age of illness onset, education, race, and sex. These results are presented in eTable 1.

eAppendix 2. Analysis of Network Robustness and Stability

We used a bootstrapping approach from the *bootnet* package¹ in R with 95% confidence intervals to examine edge stability for all network analyses (eFigure 1).² We also examined expected influence stability using a similar approach (eFigure 2). To measure stability, we repeatedly correlated expected influence values calculated from the complete data set with those calculated from a subsample with a percentage of participants missing. The correlation stability (CS) coefficient indicates the proportion of participants that can be dropped from the original sample while maintaining a correlation of 0.70 or above for centrality measures. A CS value of at least 0.25 is recommended to interpret centrality measures as stable.² All network analyses met this threshold and thus were deemed stable.

eAppendix 3. Analysis of an additional community structure

We used the R package *EGAnet*³ to conduct another community detection analysis with the positive symptom domains removed. Analyses showed that a 3-community structure represented the data in 97% of samples (eFigure 3). Independent living, family relationships, and social network formed the first community; avolition, anhedonia, and work functioning formed the second community; and flat affect and alogia formed the other community. All items and communities were highly stable (eTable 2), and anhedonia connected the three communities, showing associations with independent living, alogia, and flat affect (eTable 3).

eAppendix 4. Statistical Code Availability

Statistical code is available at https://osf.io/j7smc/

Complete and Missing Data							
	Complete data	Missing data	t or χ^2	P value			
	sample (<i>n</i> = 979)	sample (<i>n</i> = 436)					
Age (mean (<i>SD</i>))	46.50 (11.11)	46.00 (10.97)	-0.76	0.45			
Age of illness onset (mean	22.47 (7.05)	21.70 (6.46)	-2.00	0.05			
(SD))							
Education (mean (SD))	12.50 (2.05)	12.70 (2.15)	1.56	0.12			
Race (%)	-	-	6.49	0.37			
White	42.1	46.4	-	-			
African American	40	37.2	-	-			
More than one race	12.8	10.8	-	-			
Asian	3	3.7	-	-			
Pacific Islander	0.8	1.0	-	-			
Native American	0.7	0.6	-	-			
Did not identify	0.5	0.2	-	-			
Sex (%)	-	-	3.42	0.06			
Male	66.5	75	-	-			
Female	33.5	25	-	-			

eTable 1. Demographic Characteristic and Differences Between Participants with Complete and Missing Data



eFigure 1. Bootstrapped 95% Confidence Intervals of Edge Weights for All Network Analyses

Note. The top left figure corresponds to network model a; the top figure corresponds to network model b; and the bottom figure corresponds to network model c. Edge weights (x-axis) sorted in increasing order (red line). The grey areas are the 95% confidence intervals. y-axis-labels (i.e., edge-edge relationships) are omitted to limit unclear interpretation.



eFigure 2. Results of Case-Dropping Bootstrap Procedure to Assess Stability of Expected Influence in All Network Analyses

Note. The top left figure corresponds to network a; the top figure corresponds to network b; and the bottom figure corresponds to the network c. Correlations between the original expected influence values in the whole sample and those estimated in subgroups obtained by decreasing percentages of participants. Average correlations are reported in the y-axis and percentages of sampled participants in the x-axis. All networks had an average correlation with the original values of at least .75

eFigure 3. Bootstrapped exploratory graph analysis (EGA) for community detection of role functioning and negative symptoms



Note. F1 = Work functioning; F2 = Independent living; F3 = Family relationships; F4 = Social network; N1 = Flat affect; N2 = Avolition; N3 = Anhedonia; N4 = Alogia.

eTable 2. Item replicability corresponding to the EGA community structure					
	Community 1	Community 2	Community 3		
Anhedonia	-	0.99	-		
Avolition	-	0.99	-		
Flat affect	-	-	0.98		
Alogia	-	-	0.98		
Work functioning	-	0.99	-		
Family relationships	0.99	-	-		
Social network	0.99	-	-		
Independent living	0.98	-	-		

Abbreviations: EGA, Exploratory Graph Analysis. Note. Values equate to the proportion of times that an item was a part of the community in the bootstrapped EGA samples (e.g., 0.99 = 99%).

eTable 3. Network loadings corresponding to the EGA community structure					
	Community 1	Community 2	Community 3		
Flat affect	-0.017	0.233	0.338		
Alogia	0.000	0.138	0.338		
Avolition	0.000	0.446	0.112		
Anhedonia	0.336	0.294	0.360		
Work functioning	0.212	0.263	0.063		
Family relationships	0.265	0.029	0.000		
Social network	0.242	0.151	0.000		
Independent living	0.229	0.221	-0.018		

Abbreviations: EGA, Exploratory Graph Analysis.

eReferences

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