Supplementary Online Content

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

eMethods. Detailed Methods

Details of Counties from Which we Obtained Primary Care Data:

Blekinge (2009-2016), Värmland (2005-2015), Kalmar (2007-2016), Sörmland (1997-2017), Uppsala (2005-2015), Västernorrland (2008-2015), Norrbotten (2009-2016), Gävleborg (2010-2016), Halland (2007-2014), Jönköping (2008-2014), Kronoberg (2006-2016), Skåne (1998-2013), Östergötland (1997-2014), Stockholm (2003-2016), and Västergötland (2000-2013). The time periods differ because of the timing of a structured digitalizing of patient records.

Definition of Hierarchy of Diagnoses:

To separate individuals with both registration for BP and NAP/SZ we calculated the number of registrations for BP and NAP/SZ. The table below illustrates how individuals were categorized as either registered for BP or NAP/SZ. We then applied the same algorithm to categorized individuals as either registered for NAP or SZ. Individuals with MD could not have a registration for BP, NAP or SZ.

		Number of lifetime NAP diagnoses in the registers				
		1	2	3-5	6-10	More than 10
Number of lifetime BP diagnoses in the registers	1	Last diagnosis	Last diagnosis	Most common diagnosis	Most common diagnosis	Most common diagnosis
	2	Last diagnosis	Majority of last 3 diagnoses	Majority of last 3 diagnoses	Most common diagnosis	Most common diagnosis
	3-5	Most common diagnosis	Majority of last 3 diagnoses	Majority of last 3 diagnoses	Majority of last 3 diagnoses	Majority of last 5 diagnoses
	6-10	Most common diagnosis	Most common diagnosis	Majority of last 3 diagnoses	Majority of last 5 diagnoses	Majority of last 5 diagnoses
	More than 10	Most common diagnosis	Most common diagnosis	Majority of last 5 diagnoses	Majority of last 5 diagnoses	Majority of last 5 diagnoses

Calculation of the Genetic Correlations

The genetic correlation between two disorders were calculated as follows: $rG = Cov(AB) /sqrt(VA*VB)$ where $Cov(AB)$ equals tow times the weighted average of the correlation between A and B from biological father to offspring and offspring to biological fathers from Not-lived with fathers families, and from Biological Fathers to offspring, Biological Mothers to offspring, Offspring to Biological Fathers and Offspring to Biological Mothers in adopted families. VA equals two times the weighted correlation between A and A from biological father to offspring from Not-lived with father's families, and from Biological Fathers to offspring, Biological Mothers to offspring, in adopted families. VB equals two times the weighted correlation between B and B from biological father to offspring from Not-lived with father's families, and from Biological Fathers to offspring, Biological Mothers to offspring, in adopted families. The 95% CI was created using bootstrapping; i.e., we created three samples (1,000,000 each) of correlations (VA, VB, Cov(AB)) based on their mean and SE. Thereafter we calculated the r_G and used the 2.5 and 97.5th percentile for our confidence intervals.

Analyses for Narrowly Defined Schizophrenia

eTable 1 – Cross-Design Weighted Estimates from Weighted Estimates from Parent to Offspring and Offspring to Parent Designs					
Disorders		Bipolar Disorder in Parents	Bipolar Disorder in Offspring	Weighted Estimate	P-value for test of heterogeneity
Bipolar Disorder and Major Depression	Genes and Rearing	0.07 (0.06; 0.08)	0.10 (0.08; 0.11)	0.09 (0.07; 0.10)	0.005
	Genes Only	0.03 (-0.01; 0.07)	0.05 (0.01; 0.09)	0.04 (0.01; 0.07)	0.48
	Rearing Only	0.04 (-0.01; 0.08)	0.05 (0.01; 0.09)	0.05 (0.01; 0.08)	0.77
Bipolar Disorder and Broad Schizophrenia	Genes and Rearing	0.13 (0.12; 0.15)	0.10 (0.09; 0.11)	0.12 (0.11; 0.13)	0.005
	Genes Only	0.13 (0.09; 0.17)	0.10 (0.06; 0.14)	0.12 (0.09; 0.14)	0.29
	Rearing Only	-0.03 (-0.13; 0.06)	-0.04 (-0.16; 0.07)	-0.03 (-0.11; 0.04)	0.90

eTable 2 Transmission from Bipolar Illness in Parents to Schizophrenia in the Offspring and from Schizophrenia in the Parents to Bipolar illness in the Offspring								
Relationship	Phenotype	Sources of Resemblance	Intact Families	Not-lived-with Father Families	Step-Father Families	Adoptive Families	Weighted Estimate Across Families	P-value for test of heterogeneity
Mother – Offspring	BP to SZ	Genes+ Rearing	0.11 (0.08; 0.14)	0.09 (0.02; 0.16)	0.10 (-0.02; 0.23)		0.11 (0.08; 0.13)	0.85
	BP to SZ	Genes only		-	-	0.11 (-0.06; 0.28)	0.11 (-0.06; 0.28)	-
	BP to SZ	Rearing only		-		0.02 (-0.24; 0.28)	0.02 (-0.24; 0.28)	-
Father– Offspring	BP to SZ	Genes+ Rearing	0.09 (0.06; 0.12)	-	-		0.09 (0.06; 0.12)	-
	BP to SZ	Genes only	-	0.09 (0.02; 0.17)	-	0.21 (0.01; 0.42)	0.10 (0.04; 0.18)	0.25
	BP to SZ	Rearing only	-	-	-0.03 (-0.25; 0.18)		-0.03 (-0.25; 0.18)	-
Mother – Offspring	SZ to BPI	Genes+ Rearing	0.06 (0.02; 0.10)	0.09 (0.01; 0.17)	0.07 (-0.11; 0.25)		0.07 (0.03; 0.10)	0.80
	SZ to BPI	Genes only				0.10 (-0.02; 0.22)	0.11 (-0.01; 0.22)	
	SZ to BPI	Rearing only				Zero Cell	-	
Father– Offspring	SZ to BPI	Genes+ Rearing	0.14 (0.10; 0.18)			Zero Cell	0.14 (0.10; 0.18)	
	SZ to BPI	Genes only		0.08 (0.01; 0.14)		0.15 (-0.05; 0.35)	0.09 (0.02; 0.15)	0.51
	SZ to BPI	Rearing only			Zero Cell	Zero Cell	-	-

eTable 3. Cross-Parent Weighted Estimates from Weighted Estimates for Mothers and Fathers					
Disorders and Nature of Parent to Child Analyses		Mothers	Fathers	Weighted Estimate	Uncorrected P-value for test of heterogeneity
BP to SZ	Genes and Rearing	0.11 (0.08; 0.13)	0.09 (0.06; 0.12)	0.10 (0.08; 0.12)	0.34
	Genes Only	0.11 (-0.06; 0.28)	0.10 (0.04; 0.18)	0.10 (0.04; 0.16)	0.91
	Rearing Only	0.02 (-0.24; 0.28)	-0.03 (-0.25; 0.18)	-0.01 (-0.17; 0.16)	0.76
SZ to BP	Genes and Rearing	0.07 (0.03; 0.10)	0.14 (0.10; 0.18)	0.11 (0.08; 0.13)	0.006
	Genes Only	0.11 (-0.01; 0.22)	0.09 (0.02; 0.15)	0.10 (0.04; 0.15)	0.78
	Rearing Only	-	-	-	

eTable 4. Cross-Design Weighted Estimates from Weighted Estimates from Parent to Offspring and Offspring to Parent Designs					
Disorders		Parent to Offspring	Offspring to Parent	Weighted Estimate	Uncorrected P-value for test of heterogeneity
BP and SZ	Genes and Rearing	0.10 (0.08; 0.12)	0.11 (0.08; 0.13)	0.10 (0.08; 0.12)	0.63
	Genes Only	0.10 (0.04; 0.16)	0.10 (0.04; 0.15)	0.10 (0.06; 0.14)	1
	Rearing Only	-0.01 (-0.17; 0.16)		-0.01 (-0.17; 0.16)	-