Supplemental Material

Table S1. Discovery sample sizes, from the Psychiatric Genomics Consortium (Cross-Disorder Group of the Psychiatric Genomics Consortium, 2013; Ripke *et al.*, 2014), and the number of single nucleotide polymorphisms (SNPs) included for each polygenic risk score (PRS) at the p-value threshold (p_T) of $p < 0.1$.

Polygenic risk score (PRS)	**Discovery sample size**	**SNPs included ($p_T < 0.1$)**
Attention Deficit Hyperactivity Disorder (ADHD) PRS	1,947 trio cases; 1,947 trio pseudocontrols; 840 cases; 688 controls	13,372
Autism Spectrum Disorder PRS	4,788 trio cases; 4,788 trio pseudocontrols; 161 cases; 526 controls	14,161
Bipolar Disorder PRS	6,990 cases; 4,820 controls	14,367
Schizophrenia PRS	36,989 cases; 113,078 controls	37,894

Table S2. Polygenic Risk Scores (PRS) for the four disorders across the three participant groups.

	Healthy Controls (N=111)		**Patients with Major Depression** (N=69)		**Patients with Bipolar Disorder** (N=33)	
	mean	SD	mean	SD	mean	SD
ADHD PRS	9.7×10^{-4}	3.1×10^{-4}	1.00×10^{-3}	2.8×10^{-4}	1.00×10^{-3}	3.5×10^{-4}
Autism Spectrum Disorder PRS	-1.62×10^{-3}	2.1×10^{-4}	-1.61×10^{-3}	2.2×10^{-4}	-1.54×10^{-3}	1.9×10^{-4}
Bipolar Disorder PRS	6.27×10^{-3}	4.7×10^{-4}	6.46×10^{-3}	2.1×10^{-4}	6.63×10^{-4}	4.4×10^{-4}
Schizophrenia PRS	-2.49×10^{-3}	1.5×10^{-4}	-2.51×10^{-3}	6×10^{-5}	-2.48×10^{-3}	9×10^{-5}
ADHD = Attention Deficit Hyperactivity Disorder; SD = Standard Deviation						

Figure S1. Violin plots showing Polygenic Risk Scores (z scores) across clinical groups. ADHD = Attention Deficit Hyperactivity Disorder, BPD = Patients with Bipolar Disorder, CNT = Controls, MDD = Patients with major Depressive Disorder

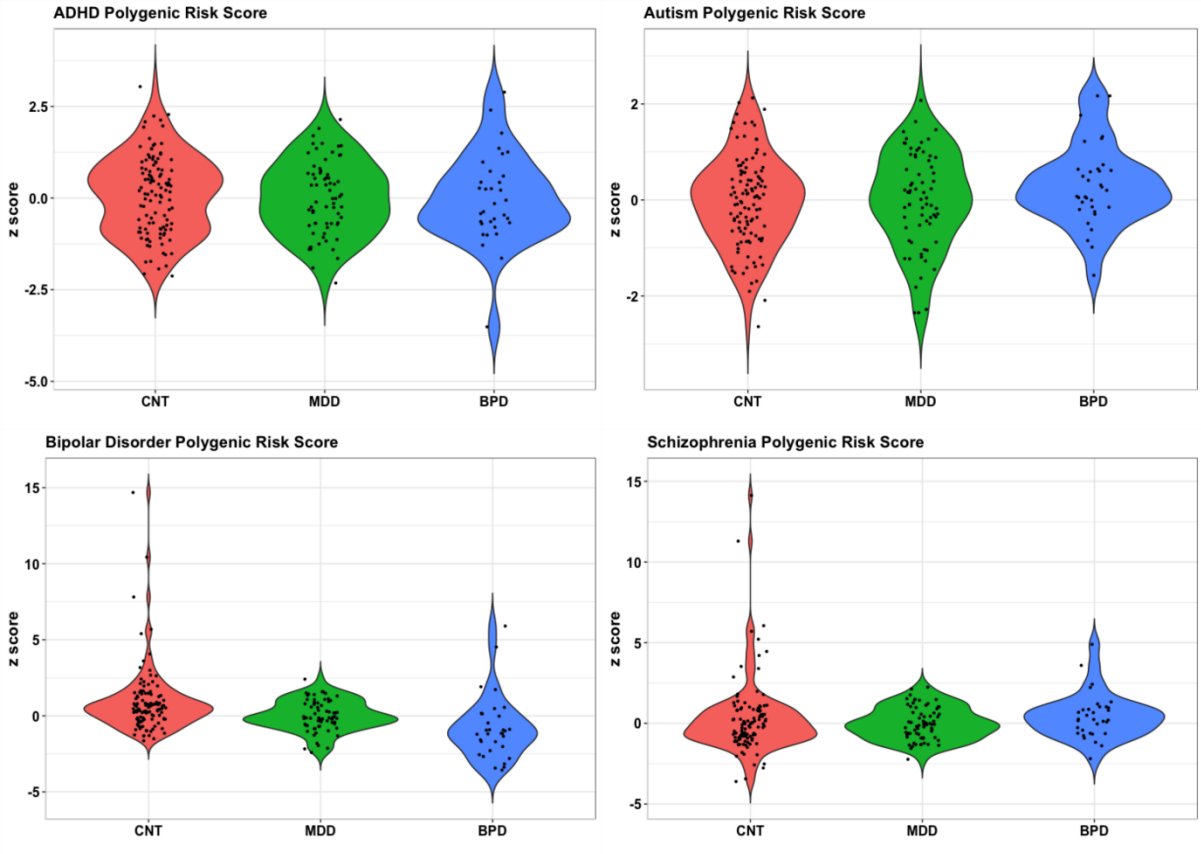

Table S3. Correlations between the four polygenic risk scores (PRS). Shown are pairwise Pearson's correlations (r) and p-values.

	ADHD PRS	**Autism Spectrum Disorder PRS**	**Bipolar Disorder PRS**
Autism Spectrum Disorder PRS	r = -0.001, p_{unc} = 0.992 p_{FDR} = 0.992		
Bipolar Disorder PRS	*r = 0.230,* *p_{unc} = 0.001* *p_{FDR} = 0.004*	r = 0.054, p_{unc} = 0.437 p_{FDR} = 0.624	
Schizophrenia PRS	*r = 0.201,* *p_{unc} = 0.003* *p_{FDR} = 0.010*	r = 0.064, p_{unc} = 0.355 p_{FDR} = 0.592	*r = 0.604,* *$p_{unc} = 2.2x10^{-16}$* *$p_{FDR} = 2.2x10^{-15}$*

Figure S2. A scatterplot between the Schizophrenia PRS and the Bipolar Disorder PRS. We also performed a Spearman's correlation between the Schizophrenia and Bipolar Disorder PRS. The results showed that the correlation remained significant: rs = 0.139, p-value = 0.043.

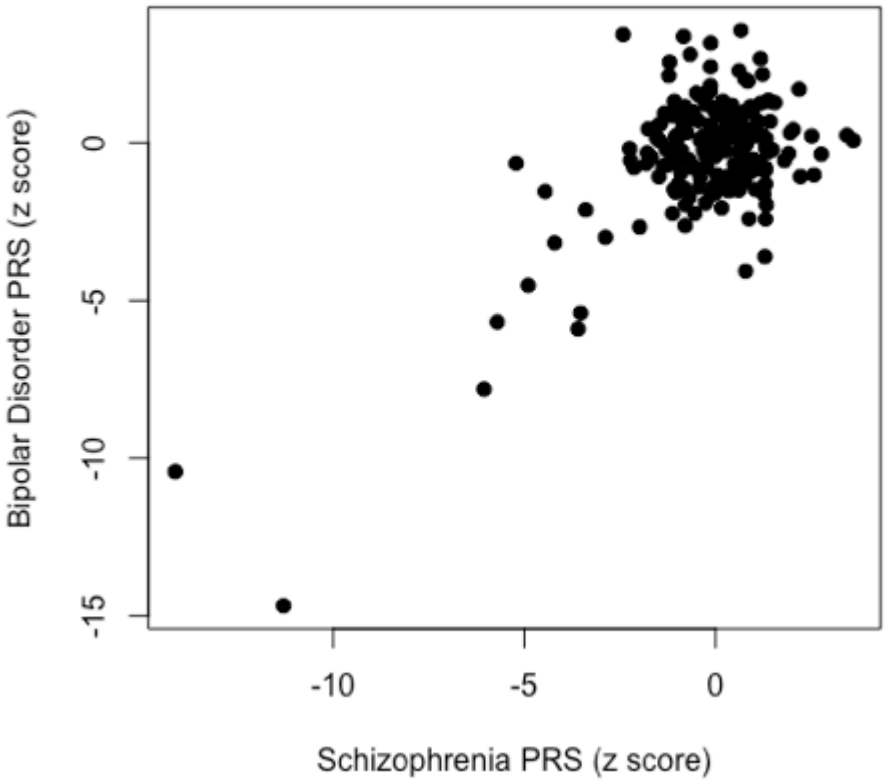

Figure S3. Un-thresholded t-maps of univariate regression results across the four Polygenic Risk Scores (PRS). ADHD = Attention Deficit Hyperactivity Disorder.

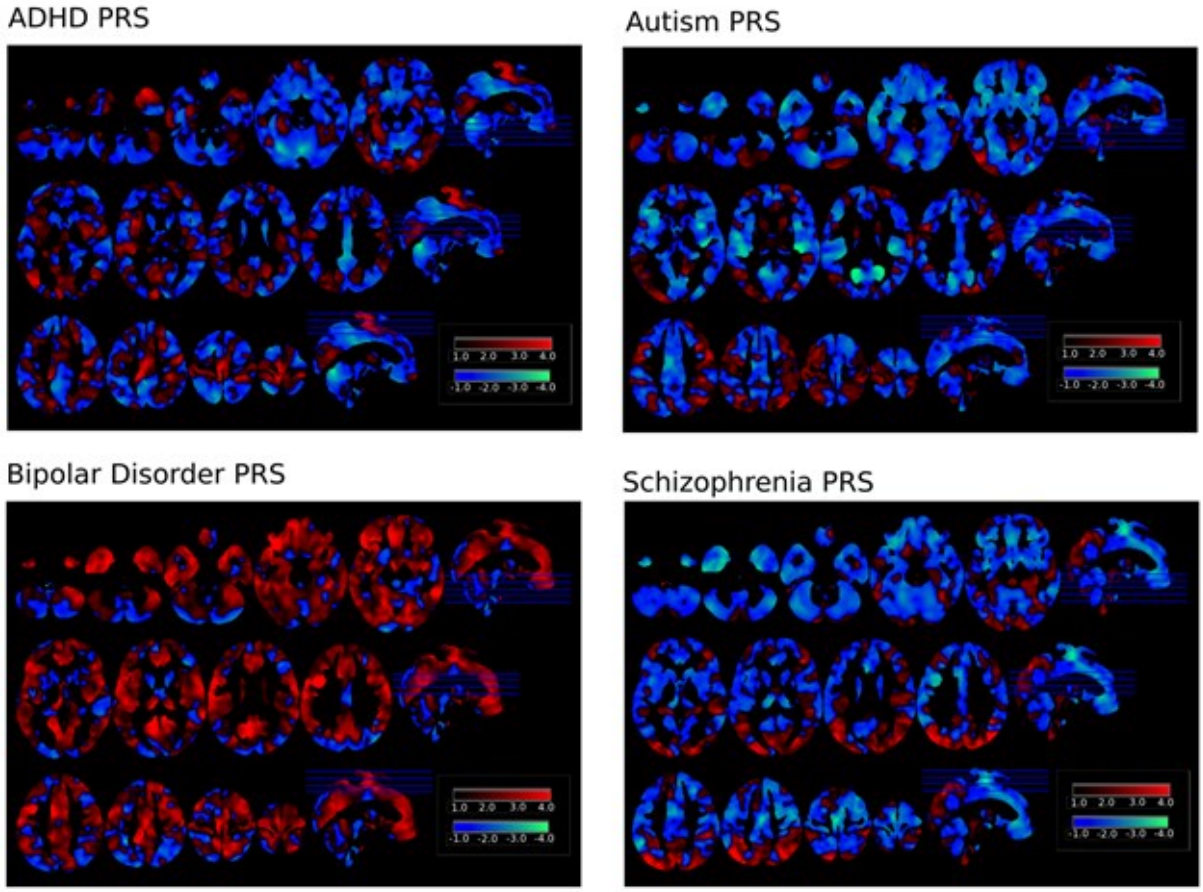

Figure S4. Weight maps for brain areas contributing the most to predictions of (a) autism and (b) schizophrenia polygenic risk scores. Brain areas were identified using the Automatic Anatomical Labelling (AAL) atlas. Note that all voxels contribute to the predictions and we show the top regions only for visualization purposes.

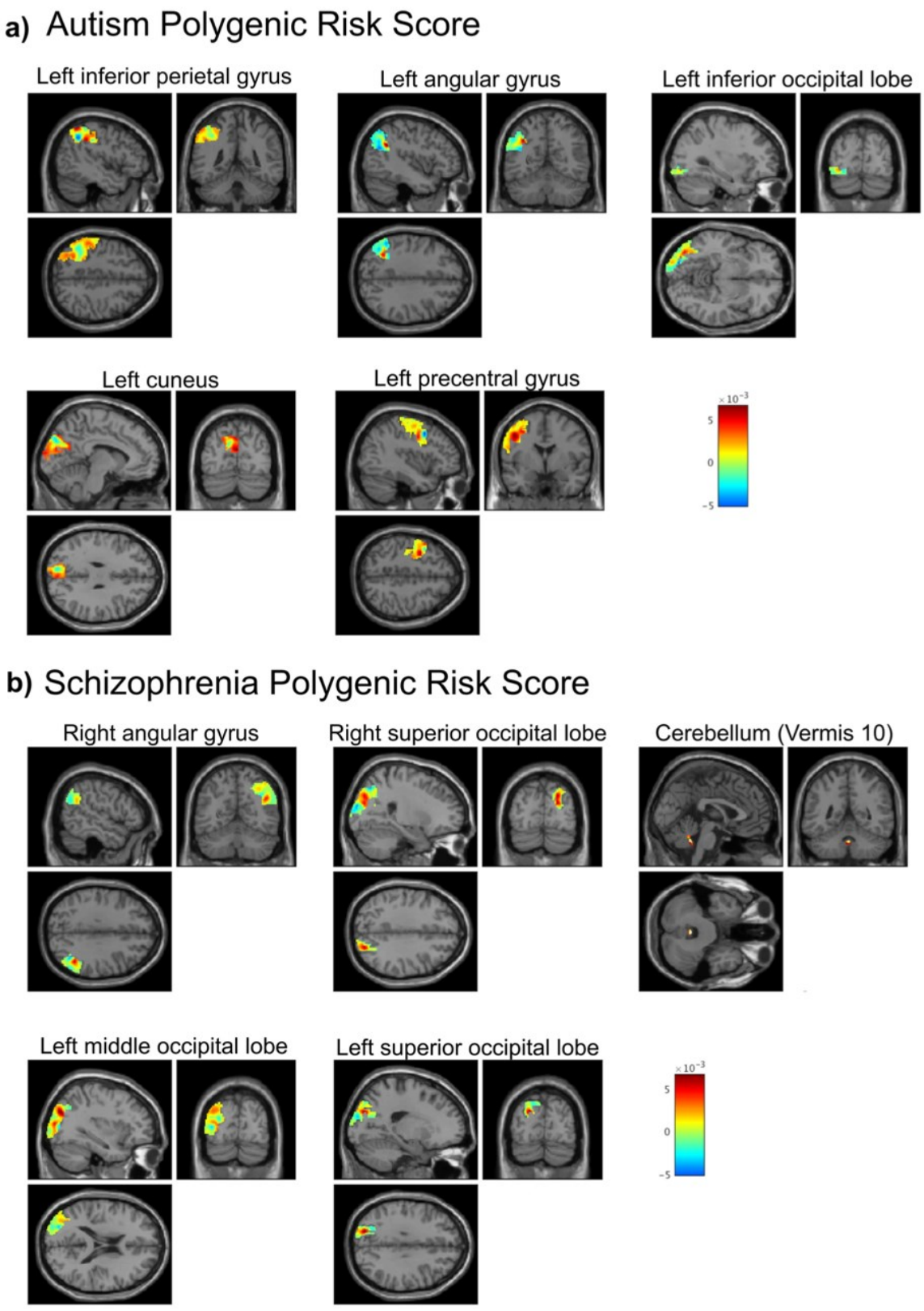

Table S4. The top 5 most predictive regions for the two significant models in the whole sample (N=213) showing the close proximity of expected to actual ranking. Brain areas were identified using the Automatic Anatomical Labelling (AAL) atlas. Shown is the contribution (weight, in %) and the size (in voxels) of the regions, as well as the expected ranking. The expected ranking indicates how consistent the ranking is across cross-validation folds; if the expected ranking is close to the actual ranking of a region (by weight) then the result is considered stable across the folds. Note that all voxels contribute to the predictions in a multivariate analysis, in the tables and figures we present only the top regions.

Autism Polygenic Risk Score			
Region (in order of weight ranking)	**Weight**	**Size (voxels)**	**Expected ranking**
Left inferior parietal gyrus	1.60%	5052	1.00
Left angular gyrus	1.43%	2481	2.08
Left inferior occipital lobe	1.38%	1979	3.15
Left cuneus	1.32%	3029	4.18
Left precentral gyrus	1.30%	5523	5.10
Schizophrenia Polygenic Risk Score			
Region (in order of weight ranking)	**Weight**	**Size (voxels)**	**Expected ranking**
Right angular gyrus	1.53%	3364	1.11
Right superior occipital lobe	1.48%	2439	2.40
Cerebellum (Vermis 10)	1.45%	40	3.09
Left middle occipital lobe	1.34%	6784	4.37
Left superior occipital lobe	1.33%	2200	4.83

Table S5. Multivariate Relevance Vector regression results in subgroups of participants; correlations (r) between the actual and predicted polygenic risk scores and (normalised) mean squared errors (MSE). P-values uncorrected for multiple testing.

Polygenic Risk Score (PRS)	**All patients (N=102)**	**Patients with Bipolar Disorder (N=33)**	**Patients with Depression (N=69)**	**Healthy controls (N=111)**
ADHD PRS	r=-0.22, p=0.903, MSE=6.61×10^{-5}, p=0.970	r=-0.61, p=0.984 MSE=9.92×10^{-5}, p=0.993	r=-0.15, p=0.694, MSE=7.89×10^{-5}, p=0.900	r=-0.06, p=0.594, MSE=7.77×10^{-5}, p=0.839
Autism PRS	r=0.08, p=0.209 MSE=4.71×10^{-5}, p=0.153	r=0.13, p=0.155 MSE=4.14×10^{-5}, p=0.155	r=-0.01, p=0.420 MSE=5.40×10^{-5}, p=0.317	r=0.06, p=0.240, MSE=4.57×10^{-5}, p=0.266
Bipolar Disorder PRS	r=-0.16, p=0.824 MSE=5.67×10^{-5}, p=0.508	r=-0.46, p=0.954 MSE=1.26×10^{-4}, p=0.870	r=-0.33, p=0.930 MSE=5.53×10^{-5}, p=0.862	r=0.0001, p=0.410, MSE=7.17×10^{-5}, p=0.386
Schizophrenia PRS	r=0.01, p=0.392 MSE=1.34×10^{-5}, p=0.533	r=0.12, p=0.190 MSE=1.77×10^{-5}, p=0.229	r=-0.08, p=0.541 MSE=1.59×10^{-5}, p=0.560	r=0.10, p=0.151, MSE=2.06×10^{-5}, p=0.088
ADHD = Attention Deficit Hyperactivity Disorder				

Table S6. Multivariate Relevance Vector regression results using a ten-fold cross-validation method, i.e. leaving 10% of the sample out. Correlations (r) between the actual and predicted polygenic risk scores (PRS) – from grey matter volumes – and (normalised) mean squared errors (MSE) in the whole sample (N=213).

ADHD PRS	Autism PRS	Bipolar Disorder PRS	Schizophrenia PRS
r = -0.07 p_{unc} = 0.717 p_{FDR} = 0.794	r = 0.21 p_{unc} = 0.014 p_{FDR} = 0.056	r = -0.10 p_{unc} = 0.794 p_{FDR} = 0.794	r = 0.16 p_{unc} = 0.083 p_{FDR} = 0.166
MSE = $6.07x10^{-5}$ p_{unc} = 0.910 p_{FDR} = 0.910	MSE = $4.17x10^{-5}$ p_{unc} = 0.010 p_{FDR} = 0.038	MSE = $5.46x10^{-5}$ p_{unc} = 0.485 p_{FDR} = 0.646	MSE = $1.37x10^{-5}$ p_{unc} = 0.019 p_{FDR} = 0.038

Table S7. Multivariate Relevance Vector regression results using a randomly selected subsample of 100 individuals. Correlations (r) between the actual and predicted polygenic risk scores (PRS) – from grey matter volumes – and (normalised) mean squared errors (MSE). P-values uncorrected for multiple testing.

ADHD PRS	Autism PRS	Bipolar Disorder PRS	Schizophrenia PRS
r = -0.086 p_{unc} = 0.610 p_{FDR} = 0.610	r = -0.002 p_{unc} = 0.422 p_{FDR} = 0.562	r = 0.114 p_{unc} = 0.129 p_{FDR} = 0.258	r = 0.196 p_{unc} = 0.137 p_{FDR} = 0.148
MSE = $6.780x10^{-5}$ p_{unc} = 0.846 p_{FDR} = 0.846	MSE = $4.492x10^{-5}$ p_{unc} = 0.544 p_{FDR} = 0.726	MSE = $6.904x10^{-5}$ p_{unc} = 0.122 p_{FDR} = 0.244	MSE = $1.582x10^{-5}$ p_{unc} = 0.034 p_{FDR} = 0.136