# Data supplement

Table DS1 Sociodemographic, clinical and cell-related features of the first-episode psychosis and control groups[a]

	Control group (n = 14)	First-episode psychosis group (n = 11)	t (d.f.)	χ²	U	P
Sociodemographic features						
Age, years: mean (s.d.)						
All	25.26 (5.23)	24.53 (6.02)	0.321 (23)			0.751
Men	23.99 (5.04)	21.48 (1.80)	1.055 (11)			0.314
Women	26.95 (5.44)	27.08 (7.27)	0.034 (10)			0.973
Women, n (%)	6 (42.9)	6 (54.5)		0.34 (1)		0.561
College education, n (%)	7 (50.0)	3 (27.3)		4.57 (1)		0.032
Clinical features, mean (s.d.)						
Duration of illness, days	N/A	84.27 (56)			N/A	N/A
Daily dosage antipsychotics,[b] mg	N/A	324.2 (172)			N/A	N/A
Positive and Negative Syndrome Scale, total score	N/A	76.5 (10.9)			N/A	N/A
Calgary Depression Scale for Schizophrenia (CDSS), total score	0.4 (1.3)	4.6 (5.2)			28	0.0016
Young Mania Rating Scale (YMRS), total score	11.5 (1.2)	14.7 (2.5)			16.5	<0.001
Cell-related feature, mean (s.d.)						
RNA integrity number (RIN)	9.07 (0.46)	9.05 (0.35)[c]			57.5	0.657

N/A, not applicable.
a. We found significant differences regarding the educational level where the first-episode psychosis group had received less formal education. This group also showed higher scores on the YMRS and CDSS. Between-group comparisons were performed with Student's *t* and χ² test for quantitative and qualitative variables, respectively. Nevertheless, in quantitative comparisons, when normality distribution was not confirmed (according to the Kolmogorov–Smirnov test), we used the non-parametric Mann–Whitney's *U*-test.
b. Chlorpromazine equivalents.
c. One patient sample was excluded from the analysis because of the low quality of the RNA as detected by RIN (n = 10).
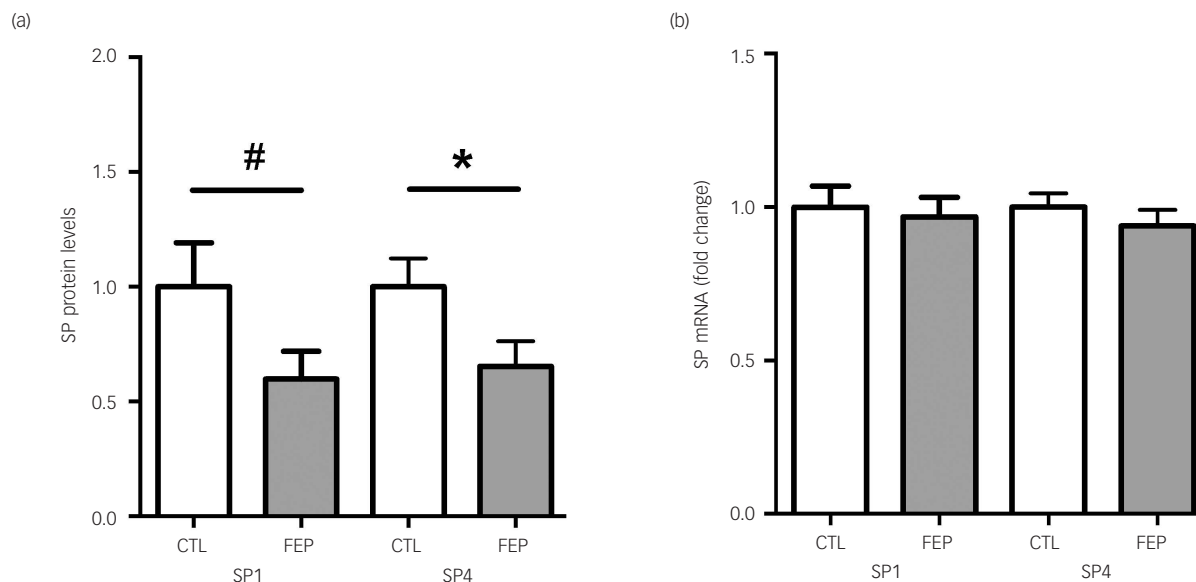
Fig. DS1 Protein levels of specificity protein 4 (SP4) protein levels are reduced in peripheral blood mononuclear cells (PBMC) of the first-episode psychosis group and SP1 shows a downward trend (#).

(a) Protein levels for SP4 and SP1 normalised to actin levels in extracts from isolated PBMC were analysed by immunoblotting. The resultant bands were quantified by densitometry using Quantity One software version 4 for Windows. The graph represents the differences in protein levels between the control (CTL) and first-episode psychosis (FEP) groups. Values of SP1 and SP4 were normalised to actin and referred to a standard sample. Values represent the mean and the standard error of the mean for each group. Statistical analysis was performed using one-tail unpaired *t*-test (*P<0.05). (b) SP4 and SP1 messenger RNA (mRNA) levels in the PBMC of the control (n = 14) and first-episode psychosis (n = 10) groups. One sample was excluded in the first-episode psychosis group in gene expression analysis (RNA integrity number (RIN) = 3.3). Gene expression levels were determined by retrotranscriptase inverse reaction followed by real-time polymerase chain reaction and normalised to the geometric mean of *IPO8* and *TBP* expression levels, and a control reference sample. Values represent the mean and the standard error of the mean for each group. Statistical analysis was performed using unpaired *t*-test that was not significant. To plot the graph we used GraphPad Prism version 5.00 for Windows.
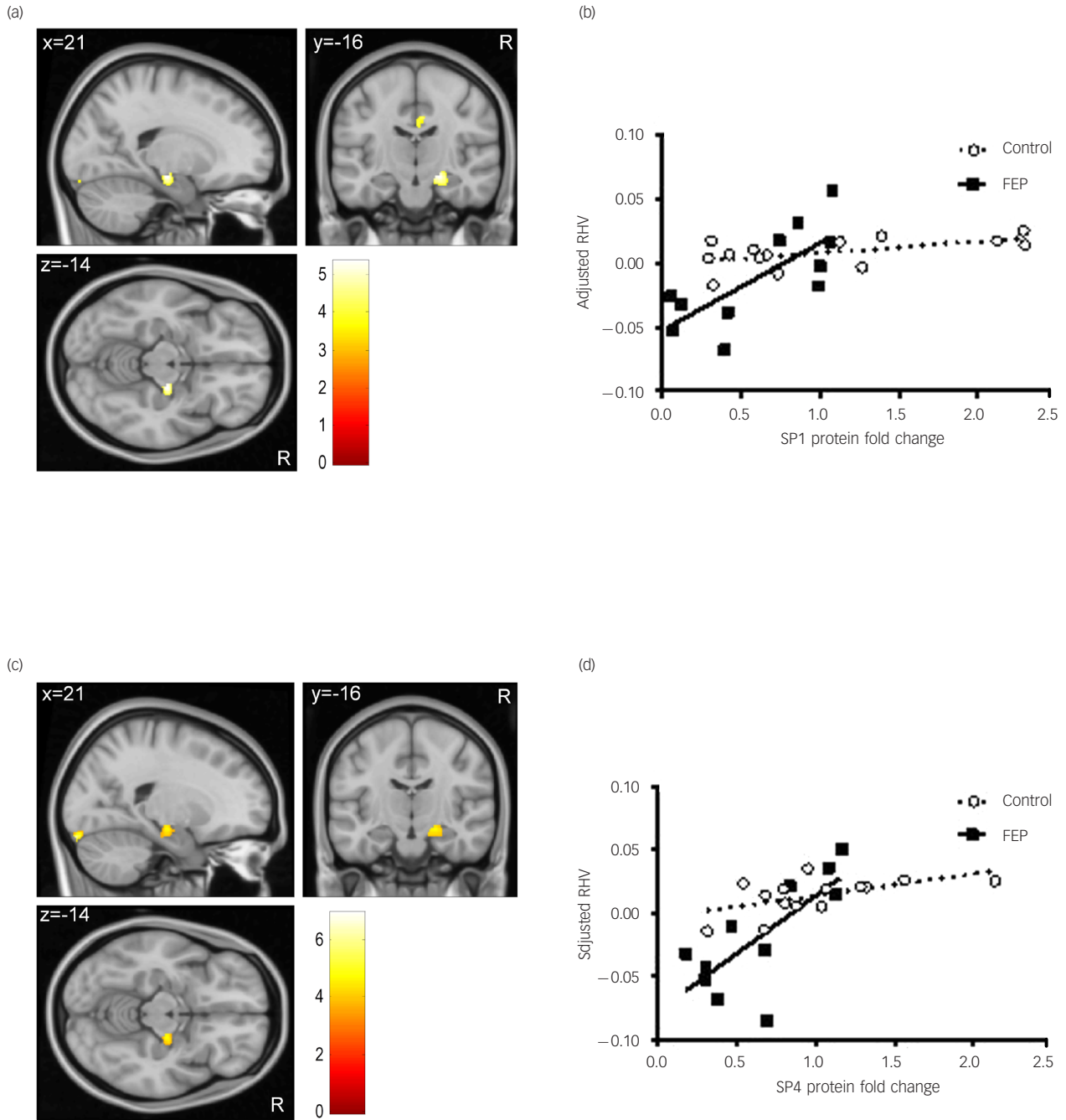
Fig. DS2 Reduced specificity protein (SP1) and SP4 protein levels are correlated with smaller right hippocampal volume (RHV).

(a) and (c) Voxel-based morphometry analysis depicting voxel-wise correlations in participants with first-episode psychosis between regional right hippocampal grey matter volumes and SP1 (a) and SP4 (c) protein levels in peripheral blood mononuclear cells (PBMC). At a more liberal significance threshold, such correlations were also observed in the left hippocampus (not shown). (b) and (d) graph of partial correlations between SP1 (b) and SP4 (d) protein levels and RHV for each group (control and first-episode psychosis) controlled for by gender, total global brain volume and age. As described in the text, correlations were only significant in the first-episode psychosis group, with $r = 0.79$ (SP1) and $r = 0.83$ (SP4). The values in (b) and (d) are the residual values of the hippocampal volume estimated after taking into account the effect of all the confounding variables. All variables were normally distributed according to a Kolmogorov–Smirnov test. To run the analysis we used IBM SPSS package version 21 for Windows. To plot the graph we used GraphPad Prism version 5.00 for Windows.