

## Supplementary Information

### **DNA methylation landscape of the genes regulating D-serine and D-aspartate metabolism in post-mortem brain from controls and subjects with schizophrenia**

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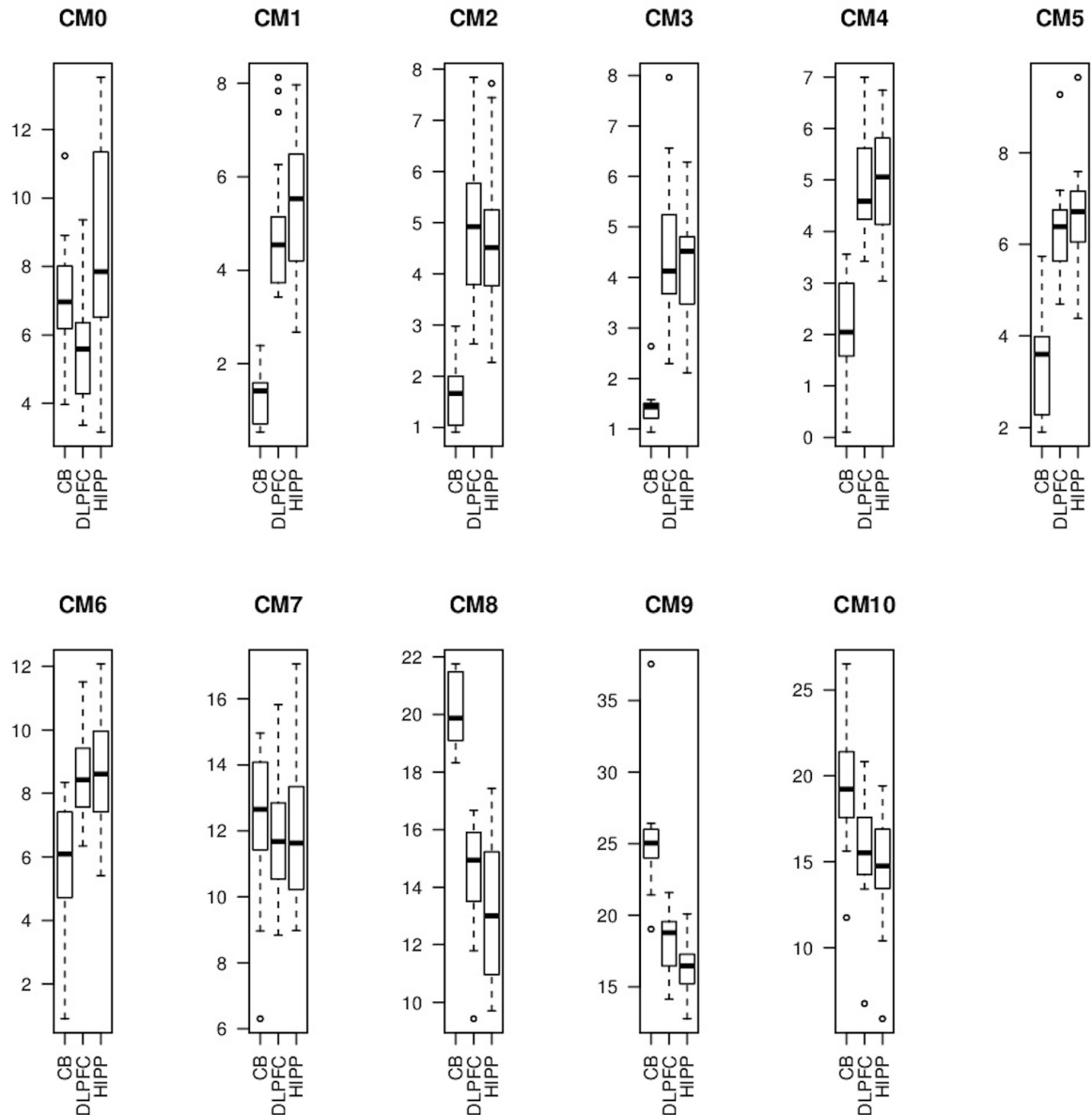
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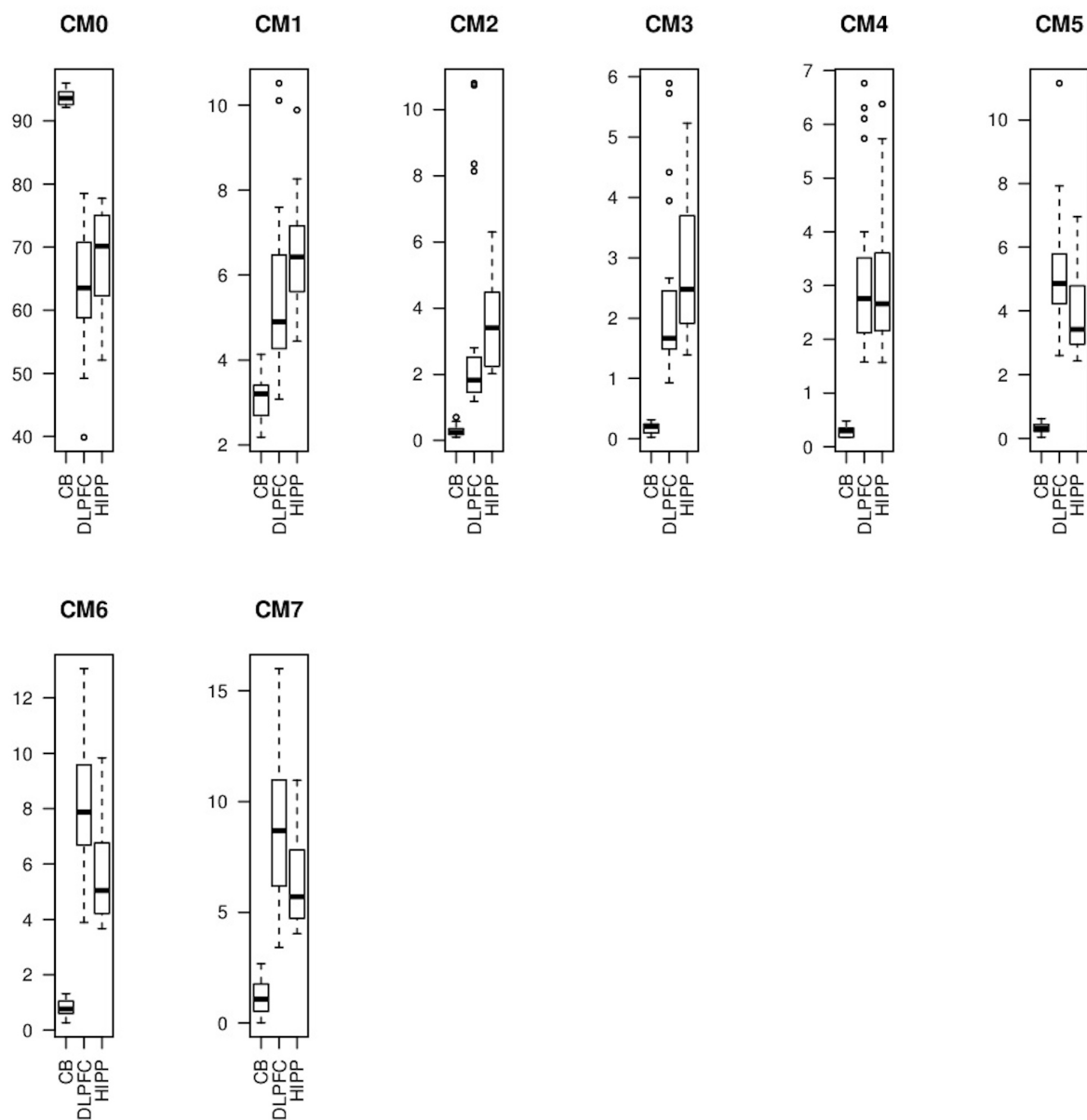
## Supplementary Figures

### Figure S1



**Figure S1.** Distribution of the DAO epiallelic classes frequencies in the three analyzed brain regions for CTRL samples. Each boxplot represents a methylation class from unmethylated (CM0) to fully methylated (CM10). The black central line indicates the median of the distribution. White circles represent samples with an outlier value. Statistical significant differences among areas were assessed by Cramer test: HIPP vs CB  $p < 0.001$ ; DLPFC vs CB  $p < 0.001$ ; HIPP vs DLPFC  $p = 0.03$ .

**Figure S2**



**Figure S2.** Distribution of the DDO epiallelic classes frequencies in the three analyzed brain regions for CTRL samples. Each boxplot represents a methylation class from unmethylated (CM0) to fully methylated (CM7). The black central line indicates the median of the distribution. White circles represent samples with an outlier value. Statistical significant differences among areas were assessed by Cramer test: HIPP vs CB  $p < 0.001$ ; DLPFC vs CB  $p < 0.001$ ; HIPP vs DLPFC  $p = 0.01$ ).

**Table S2**

	Hippocampus		Dorso-lateral prefrontal cortex		Cerebellum	
	Non-psychiatric controls	Schizophrenia patients	Non-psychiatric controls	Schizophrenia patients	Non-psychiatric controls	Schizophrenia patients
DAO	1.12 ± 0.04	1.66 ± 0.17	1.71 ± 0.05	1.73 ± 0.10	1.25 ± 0.03	1.31 ± 0.05
DAOA	24.47 ± 2.11	34.81 ± 4.23	18.48 ± 1.03	21.87 ± 2.82	16.70 ± 2.77	14.6 ± 1.28
SRR	0.29 ± 0.04	0.53 ± 0.09	0.31 ± 0.02	0.35 ± 0.30	0.27 ± 0.02	0.24 ± 0.02
DDO	0.77 ± 0.06	0.69 ± 0.06	1.08 ± 0.07	1.15 ± 0.06	0.30 ± 0.03	0.25 ± 0.01

**Table S2.** Average methylation at non-CpG sites. For all genes considered in our analysis, average of mCpH for both CTRL and SCZ groups and in each brain region was assessed and indicated as mean ± SEM. Percentage of average methylation at non-CpG sites was calculated in each sample as (amount of mCpH / total number of CpH sites)\*100.