UNIVERSITY OF NAPLES FEDERICO II

MEDICAL SCHOOL

Department of Neuroscience, Reproductive Science, and Odontostomatology

Altered interactions between monoaminergic and glutamatergic neurotransmission in schizophrenia: insights from a bi-regional network analysis of postmortem tissues

PhD candidate: Dr. Giuseppe De Simone

PhD Program in Neuroscience, XXXVIII Cycle

Coordinator: Prof. Maurizio Taglialatela

Tutor: Prof. Andrea de Bartolomeis

Co-Tutor: Prof. Alessandro Usiello

Academic year 2024/2025

Summary

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Schizophrenia is a severe mental illness characterized by significant impairments in social and occupational functioning, whose neurobiology increasingly points to altered integration of glutamatergic and monoaminergic signaling across multiple spatial scales.

This thesis investigates microscale dysconnectivity between glutamatergic and monoaminergic pathways in schizophrenia by applying an intersubject network analysis to postmortem dorsolateral prefrontal cortex (DLPFC) and hippocampal tissues from 20 patients with schizophrenia and 20 non-psychiatric controls. Concentrations of 38 molecular effectors, including amino acids, monoamines, glutamate receptors and transporters, synaptic proteins, and catabolic enzymes, were quantified using high-performance liquid chromatography and Western blotting at the Neuroscience Lab of CEINGE - Advanced Biotechnologies. Missing data were handled through multiple imputation by chained equations, and molecular networks were estimated using conditional mutual information combined with autoencoder-based dimensionality reduction to capture both linear and non-linear associations while mitigating high-dimensional bias. Group differences in global strength, node strength, and pairwise edge weights were assessed via permutation testing with cluster-based correction for multiple comparisons.

Results revealed region- and hierarchy-specific patterns of molecular dysconnectivity in schizophrenia. Global connectivity was preserved in the DLPFC but significantly reduced in the hippocampus, where several nodes, including dopamine, GluA4, GLT-1, 5-HIAA, CaMKII, NR1, Synapsin I, and DOPAC, showed decreased degree in patients compared with controls. At the edge level, most alterations involved glutamatergic components across pre- and postsynaptic compartments, as well as cross-system interactions between monoamines and glutamatergic effectors, indicating disrupted integration of synaptic signaling across the cleft. Dopamine emerged as a central hub with

reduced weighted degree in both regions, suggesting a network-level impairment of dopaminergic modulation of glutamatergic plasticity.

Taken together, these findings extend the dysconnectivity hypothesis of schizophrenia to the molecular domain, showing that alterations in glutamate-monoamine interactions are reflected in reorganized synaptic networks within DLPFC and hippocampus. By leveraging an entropy- and autoencoder-based framework for network estimation, this work further provides a novel methodology for intersubject molecular network analysis.

1. Introduction

Schizophrenia is a severe mental illness that affects approximately 1% of the global population, significantly impacting both social and occupational functioning[1]. Despite extensive research, its neurobiological underpinning remains unknown[2]. However, growing evidence suggests that schizophrenia stems from neurodevelopmental disruptions, involving alterations in neurotransmitter pathways and postsynaptic architecture[2-5].

Several studies have highlighted the pivotal role of the glutamatergic pathway and postsynaptic density proteins (PSD), including PSD-95, Homer, N-methyl-D-aspartate receptor (NMDAR) subunits (NR1, NR2A, NR2B), AMPAR subunits (GluA1, GluA2/3, GluA4), and metabotropic receptors (mGluR1, mGluR2/3, mGluR5), in the pathophysiology of schizophrenia[6-10]. Beyond the glutamatergic system, monoaminergic neurotransmission, above all the dopaminergic pathway, has consistently been implicated in the onset and persistence of psychotic symptoms, especially under dynamic conditions, such as dopamine release triggered by amphetamine administration[11, 12].

Rather than considering their isolated effects, increasing evidence has shown that interactions between glutamatergic and monoaminergic neurotransmission may be critical for synaptogenesis and synaptic maturation, key processes in brain development[13]. Of interest, disruptions in this crosstalk, especially between glutamate and dopamine, have been detected in patients affected by psychotic disorders and have been proven to be susceptible to antipsychotic treatment, aligning with the neurodevelopmental hypothesis of schizophrenia[14, 15].

However, dysconnectivity patterns have usually been investigated at the circuit or system level, focusing on neurons that selectively release either monoamines or glutamate[14-16] . In this framework, the relationship between these systems has been conceptualized as hierarchical, with alterations in cortical glutamatergic pathways proposed to trigger secondary disturbances in subcortical

dopaminergic signaling, as traditionally described in the synaptic hypothesis of schizophrenia[9].

Indeed, recent studies have hypothesized and proved that alterations could also be detected at microscales, in co-culture models of dopaminergic and glutamatergic cells[2] as well as in neurons co-releasing both the neurotransmitters[5], therefore extending the concept of dysconnectivity to the molecular level. Furthermore, two recent studies have shown that antipsychotic drugs, which represent the treatment of choice for schizophrenia and primarily exert their effects through dopamine D2 receptor (D2R) occupancy, can induce adaptive changes in synaptic architecture and modulate the expression of multiple components of the glutamatergic pathway, supporting the hypothesis of an extended dysconnectivity at the molecular level in psychotic disorders[17, 18].

Despite these recent findings, a full characterization of microscale disruptions in the interaction patterns between monoaminergic and glutamatergic systems, including the precise contribution of individual molecular components, is still lacking. To fill this gap, we performed an intersubject network analysis of 38 molecules measured in the postmortem dorsolateral prefrontal cortex (DLPFC) and hippocampus from 20 patients affected by schizophrenia and 20 healthy controls, using data collected from previous experiments[19, 20]. A comprehensive representation of the molecules included in the present analysis, along with their structural and functional interactions, has been provided in Figure 1.

To our knowledge, this is the first study to estimate intraregional networks in schizophrenia based on actual levels of a diverse set of molecular effectors, including concentrations of monoamines, D- and L-amino acids, glutamatergic receptors, PSD proteins, and key catabolic enzymes (e.g., MAO, COMT). Further, by combining dimensionality reduction based on neural networks, such as autoencoders, with conditional mutual information (CMI), an entropy-derived measure of conditional dependence, we were able to detect both linear

and non-linear associations, capturing complex relationships that traditional correlation-based methods might not reveal.

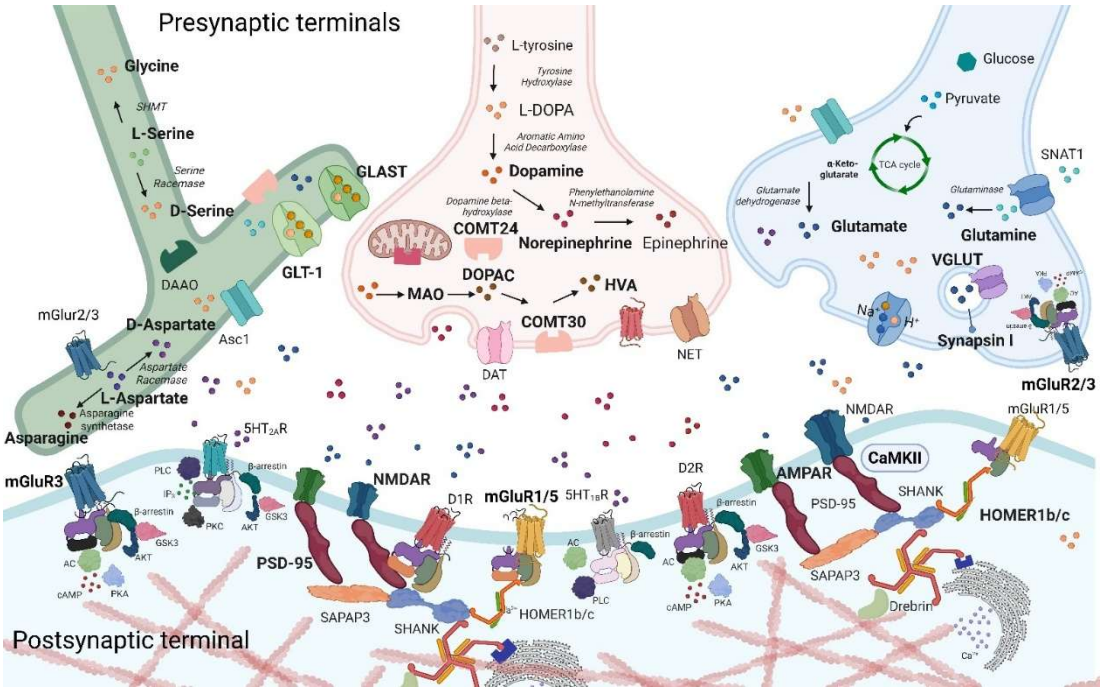

Figure 1. The molecules included in the network analysis are shown according to their cellular localization. Molecule names are highlighted in bold. On the presynaptic side, an astrocyte, a monoaminergic neuron, and a glutamatergic neuron are represented. On the postsynaptic side, the different receptors and their signaling apparatus are depicted. Molecular interactions occur both structurally and functionally, within the presynaptic and postsynaptic compartments, involving molecules of the same neurotransmitter pathway as well as across different pathways. Created in https://BioRender.com.

2. Methods

All the stages of the methodological process have been summarized in Figure 2.

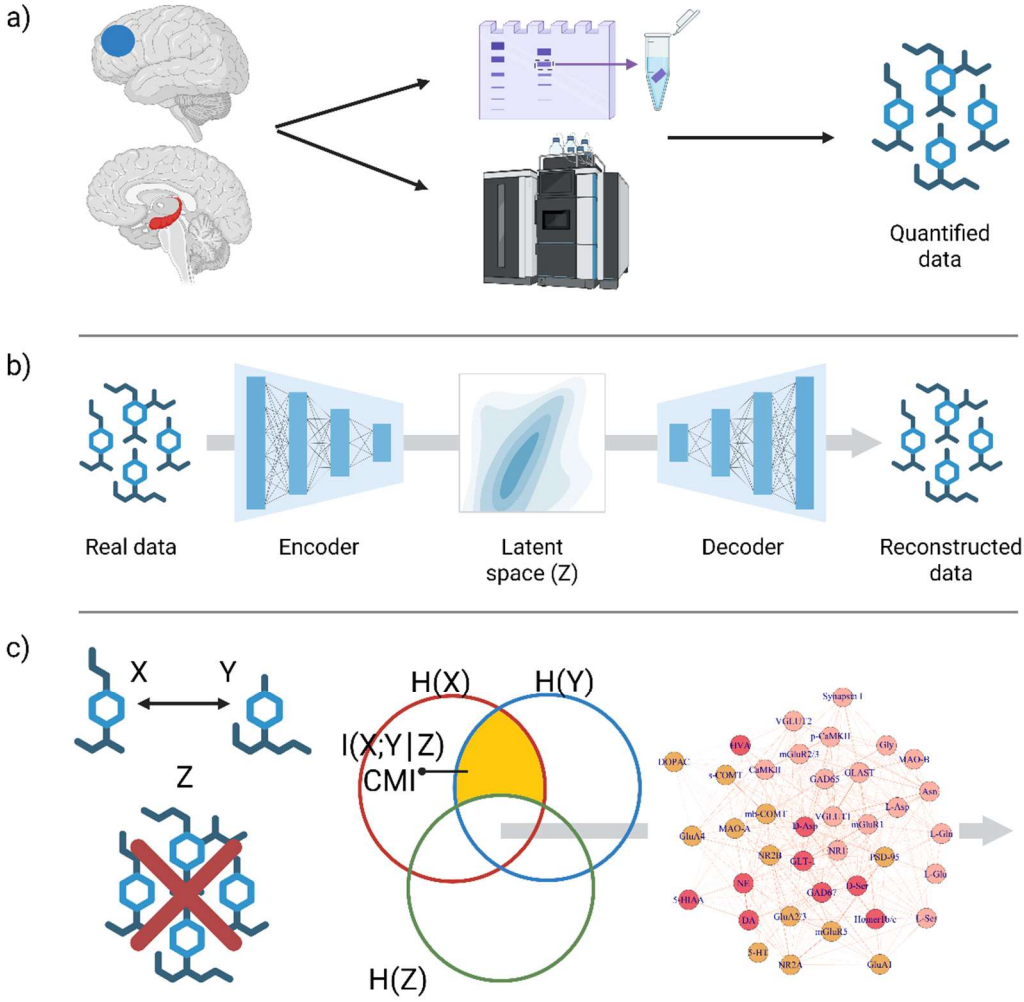

Figure 2. Methodological processes. (a) Human tissue samples from the DLPFC and hippocampus were obtained from the Human Brain and Spinal Fluid Resource Center, Los Angeles Healthcare Center. Proteins, amino acids, and monoamine levels were quantified by Western blot and HPLC. (b) For each pair of variables (*x* and *y*), an autoencoder was trained to compress the information from the remaining 36 molecules, age, and PMI into a single latent variable (*z*); the autoencoder can be conceived as an accordion with a compressing (encoding) and decompressing (decoding) step, where in this study only the compressed representation was used. (c) Each connection between molecules was then quantified through CMI, which corresponds to the information shared between *x* and *y* once *z* is taken into account. In the diagram, each circle represents the entropy of one variable (H(*x*), H(*y*), H(*z*)), the pairwise overlap represent the joint entropy, and the yellow area highlights the CMI value for the *x*-*y* pair. Networks were estimated as a matrix containing the CMI values of each pair of molecules.

2.1 Brain samples collection

Human tissue samples from the DLPFC and hippocampus were collected from postmortem brains of both non-psychiatric controls and schizophrenia patients ($n = 20$ per brain region per clinical condition). These samples were obtained from the Human Brain and Spinal Fluid Resource Center, located at the Los Angeles Healthcare Center in Los Angeles, CA, USA. All tissue collection and processing procedures were conducted in compliance with the regulations and licenses of the Human Tissue Authority and in accordance with the Human Tissue Act of 2004. The clinical diagnosis of schizophrenia was established based on DSMIII-R criteria. Frozen tissues were pulverized in liquid nitrogen and subsequently stored at −80 °C for further processing.

2.2 High-Performance Liquid Chromatography (HPLC) analysis

Samples of postmortem DLPFC and hippocampus were homogenized, sonicated, and centrifuged. The precipitated protein pellets, as well as the supernatants, were stored at −80 °C for protein quantification and HPLC, respectively. Identification and quantification of D-aspartate (D-Asp), L-aspartate (L-Asp), L-glutamate (L-Glu), L-asparagine (L-Asp), D-serine (D-Ser), L-serine (L-Ser), L-glutamine (L-Gln), glycine Gly), dopamine, norepinephrine, homovanillic acid (HVA), 3,4-dihydroxyphenylacetic acid (DOPAC), serotonin (5-HT), and 5-hydroxy indoleacetic acid (5-HIAA) were based on retention times and peak areas. Calibration curves were set using external standards. D-Asp peak specificity was also evaluated by selective degradation catalyzed by a recombinant human D-aspartate oxidase.

2.3 Western Blotting

Frozen, powdered samples of postmortem DLPFC and hippocampal tissues were sonicated in 1% SDS, boiled for 10 minutes, and then subjected to protein determination using a Bio-Rad Protein Assay kit. Equal amounts of total protein

(30 μg) were loaded onto a pre-cast 4-20% gradient gel and separated by SDS-PAGE. The proteins were transferred to PVDF membranes and immunoblotted overnight with primary antibodies against NR1, NR2A, NR2B, GluA1, GluA2/3, GluA4, mGluR2/3, mGluR5, Homer1b/c, PSD-95, glutamic acid decarboxylase 65 and 67 (GAD65 and GAD67), glutamate-aspartate transporter (GLAST or EAAT1), glial glutamate transporter-1 (GLT-1 or EAAT2), vesicular glutamate transporter 1 and 2 (VGLUT1 and VGLUT2), Ca2+/calmodulin-dependent protein kinase II (CaMKII), pThr^{286}-CaMKII (p-CaMKII), Synapsin I, mGluR1, the 30 (membrane-bound) and 24KDa (soluble) isoforms of the catechol-O-methyltransferase (mb-COMT and s-COMT), monoamine oxidase A (MAO-A) and B (MAO-B). Blots were then incubated with α-rabbit or α-mouse horseradish peroxidase conjugated secondary antibodies, visualized using enhanced chemiluminescence, and quantified by Quantity One software. Optical density values were normalized to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) to account for variations in loading and transfer efficiency. All blots were processed in parallel.

2.4 Imputation of missing data

To address missing data, the multiple imputation by chained equations (MICE) method was employed. MICE imputes missing values by creating a model for each incomplete variable using the observed values of the other variables in the database. Using random forest as the imputation method, the MICE algorithm generated 10 imputed datasets by iteratively updating the missing values over 50 iterations[19]. We performed the imputation separately on two databases: one containing variables collected from the DLPFC and another containing variables collected from the hippocampus. Imputations were performed via the "mice" package[21] in RStudio R version 4.1.2[22].

2.5 Estimation of molecular networks

To overcome the assumption of linearity in molecular associations, we employed CMI to estimate network connectivity. Mutual information (MI) can be considered as a generalization of correlation[23]. While correlation quantifies only linear dependence, MI measures the reduction in uncertainty of one variable when another is considered[23]. In information theory, this uncertainty is defined as entropy, which quantifies the unpredictability or disorder of a variable's distribution. When two variables share information, their joint entropy is lower than the sum of their individual entropies, and MI captures this reduction[24]. Specifically, MI is the sum of the individual entropy of the two variables minus their joint entropy[24] (Figure 2). Greater variability of one molecule explained by another molecule results in lower joint entropy and, therefore, higher MI[24].

CMI extends this framework by estimating the dependence between two variables (x and y) while conditioning on a third (z), thereby ruling out spurious associations (third-effect bias) that may stem from indirect relationships[24]. Here, CMI was estimated using a k-nearest neighbor (kNN) approach, in which the distances among the k closest data points are used to compute entropy[24]. Compared to classical binning methods for entropy estimation, the kNN approach provides greater robustness and efficiency in high-dimensional data[23]. As CMI is sensitive to variable scaling, all molecules were standardized prior to analysis by z-score normalization.

To evaluate the effect of all other molecules, as well as age and PMI, on the association between each pair of variables, we faced the challenge to compress this information into a single latent vector (z). For each pair of molecules, we trained an autoencoder neural network, which is designed to learn a compressed representation of multidimensional data[25]. The autoencoder works like an accordion, compressing (encoding) and decompressing (decoding) the input data through a low-dimensional bottleneck or latent space (Figure 2), and is

trained to reproduce its input as accurately as possible[25]. In our analysis, we used only the encoding part of the network to extract the latent representation (z), which compressed the information from the remaining 36 molecules, age, and PMI into a single latent value capturing the essential structure of the data.

While a multidimensional z vector could increase sparsity and inflate joint entropy, thus reducing CMI, the autoencoder produces a single, informative conditional variable for each pair of molecules in each subject and brain region. This reduces the complex multivariate structure, mitigating the curse of dimensionality, and providing more accurate estimation of conditional dependencies[26, 27]. The procedure was performed separately for both schizophrenia and control groups, and for the DLPFC and hippocampus. The autoencoder was trained prior to network estimation.

To assess the robustness of molecular network, we implemented a bootstrap procedure with 100 resamples[28]. At each bootstrap iteration, subjects were resampled with replacement, CMI values among pairs of variables were recalculated, and an edge was retained if it appeared in at least 70% of bootstrap samples[29]. This procedure resulted in stable estimates of molecular connectivity, reducing the influence of sampling variability.

Analyses were performed by the "knnmi"[30], "keras"[31], "purrr"[32], and "dplyr"[33] packages in RStudio R version 4.1.2[22].

2.6 Quantitative comparison of networks between schizophrenia and control groups

To statistically assess group differences in network connectivity, we performed permutation testing separately for the DLPFC and hippocampus.

Observed network metrics were extracted at three hierarchical levels: (i) global strength (sum of all unique edge weights)[34-36], (ii) node strength (sum of edge weights for each node)[34, 36], and (iii) pairwise edges (individual edge weights)[34, 36].

To determine the statistical significance of differences in these metrics between patient and control groups, we generated a null distribution by randomly shifting diagnostic labels (schizophrenia or control) across subjects (N = 1,000 permutations), recalculating CMI networks at each iteration, and computing the network metrics at each step. For each permutation, the differences in global strength, node strength, and pairwise edge weights between the permuted schizophrenia and control networks were calculated, yielding a null distribution against which the observed differences were compared to compute two-tailed p-values.

Given the large number of statistical comparisons, we applied a correction for multiple testing. However, classic Bonferroni correction assumes independent testing, which may not be valid in the context of interrelated variables[37, 38]. Here, to correct for multiple comparisons in the node- and edge-wise analyses, we applied a cluster-based correction. Specifically, the number of network modules was estimated using the Louvain algorithm on each network, and the maximum number of communities observed across conditions was used as the correction factor. Corrected p-values were obtained by multiplying uncorrected p-values by the number of detected clusters. In this way, multiple comparisons were not correct on the total number of tests, but on the actual number of independent information units, similarly to the method proposed by Gao[37].

Permutated p-values were deemed significant if they were below 0.05 after correction from multiple testing. Statistical analyses and graphical representations were obtained by the "knnmi"[30], "igraph"[39], and "ggplot2"[40] packages in RStudio R version 4.1.2[22].

3. Results

Demographic characteristics are represented in Table 1.

Characteristics	Control	Schizophrenia	Statistic	*p*-value
Subjects (total number)	20	20	-	-
Sex (M/F)	16/4	12/8	$\chi^2 = 1.071$ (df=1)	0.301 [a]
Age (years, median [IQR])	73.50 [66.00–80.25]	52.50 [39.50−61.25]	t = 4.819 (df = 38)	<0.001 [b]
PMI (hours, median [IQR])	12.90 [11.80 −16.32]	15.25 [12.52−24.58]	t = −2.426 (df = 38)	0.020 [c]
pH (median, [IQR])	6.54 [6.49–6.63]	6.50 [6.42−6.56]	t = 0.708 (df = 26)	0.485 [c]
Continuous variables are reported as median along with IQR.				
M/F = number of males/females, PMI = post-mortem interval, IQR = Interquartile Range (first-third quartiles), df = degrees of freedom. [a]p-value from Chi-Square test (with Yates's correction). [b]p-value from two sample t-test. [c]p-value from two sample t-test on log transformed values.				

Table 1. Demographic characteristics, presented as medians with interquartile ranges, were assessed for normality using the Shapiro-Wilk test. Non-normally distributed variables were log-transformed for statistical analyses. Variables that were significantly different between the two groups (i.e., age and PMI) were regarded as potential confounders in the subsequent analyses.

Estimated networks with CMI values for each pair of molecules are represented in Figure 3.

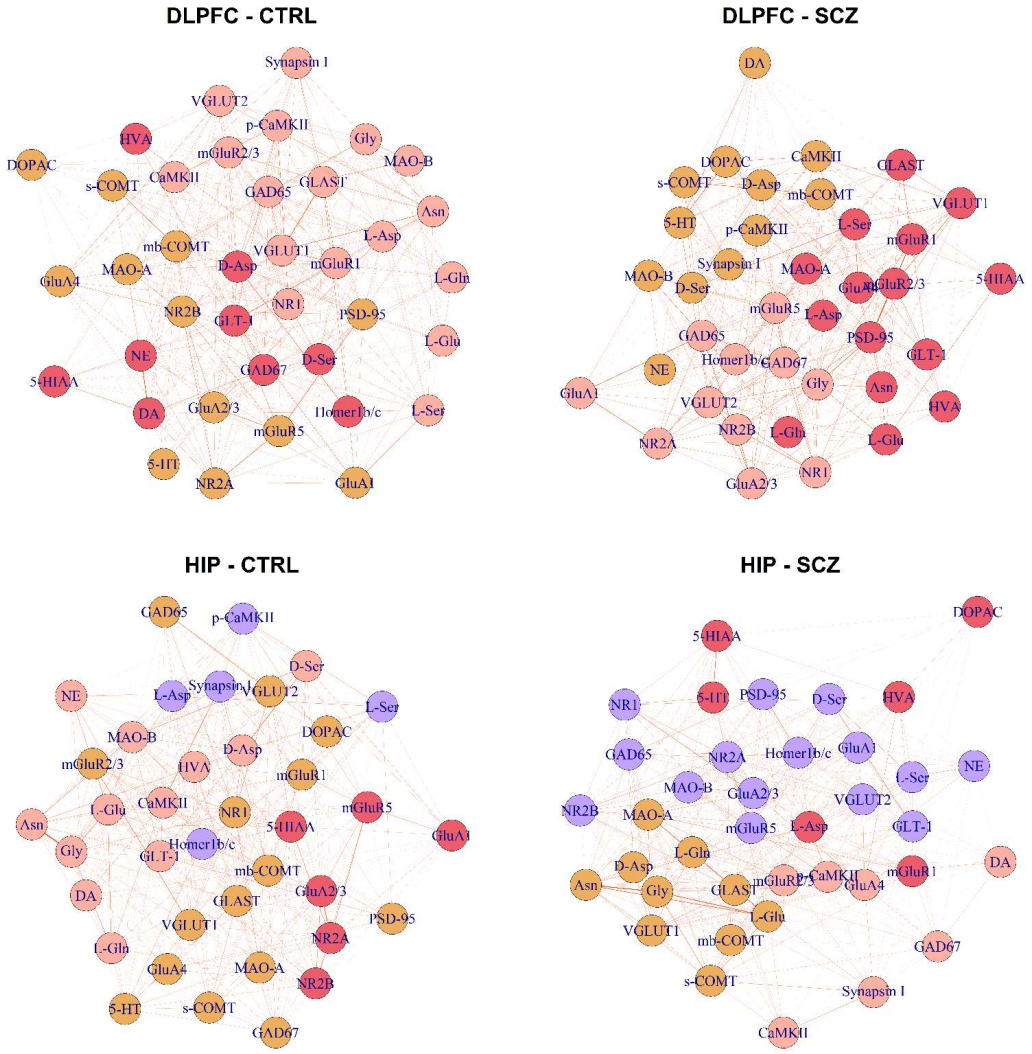

Figure 3. Estimated molecular networks. Nodes represent the different molecules while edges their pairwise connection. Nodes' colors identify molecules belonging to the same module or cluster, highlighting groups of variables with higher intra-connectivity. Node positions are determined by the Fruchterman-Reingold layout algorithm, that lead to closely connected nodes being closer to one another and loosely connected nodes pushed towards outside, without implying any anatomical or spatial localization. Edges' widths symbolize the strength of interactions and are correspondent to the CMI values.

3.1 Qualitative and quantitative appraisal of molecular networks at global and modular levels

In the DLPFC, global strength was comparable between groups (53.55 in schizophrenia subjects; 53.51 in controls; difference = 0.04; p-value = 0.99). In the hippocampus, controls showed a significant higher overall connectivity compared to patients (52.57 *vs* 57.95; difference = -5.38; p-value = 0.02). Permutation distributions of global strength for both DLPFC and hippocampus are provided in Figure 4.

The modular organization, identified using the Louvain community detection algorithm, was comparable between schizophrenia and control groups within each region, but differed across brain areas. Specifically, three molecular clusters were detected in the DLPFC for both groups, whereas four clusters emerged in the hippocampus (Figure 3).

Overall, these results highlight that while global connectivity is preserved in the DLPFC, schizophrenia is associated with a significant reduction of network strength in the hippocampus.

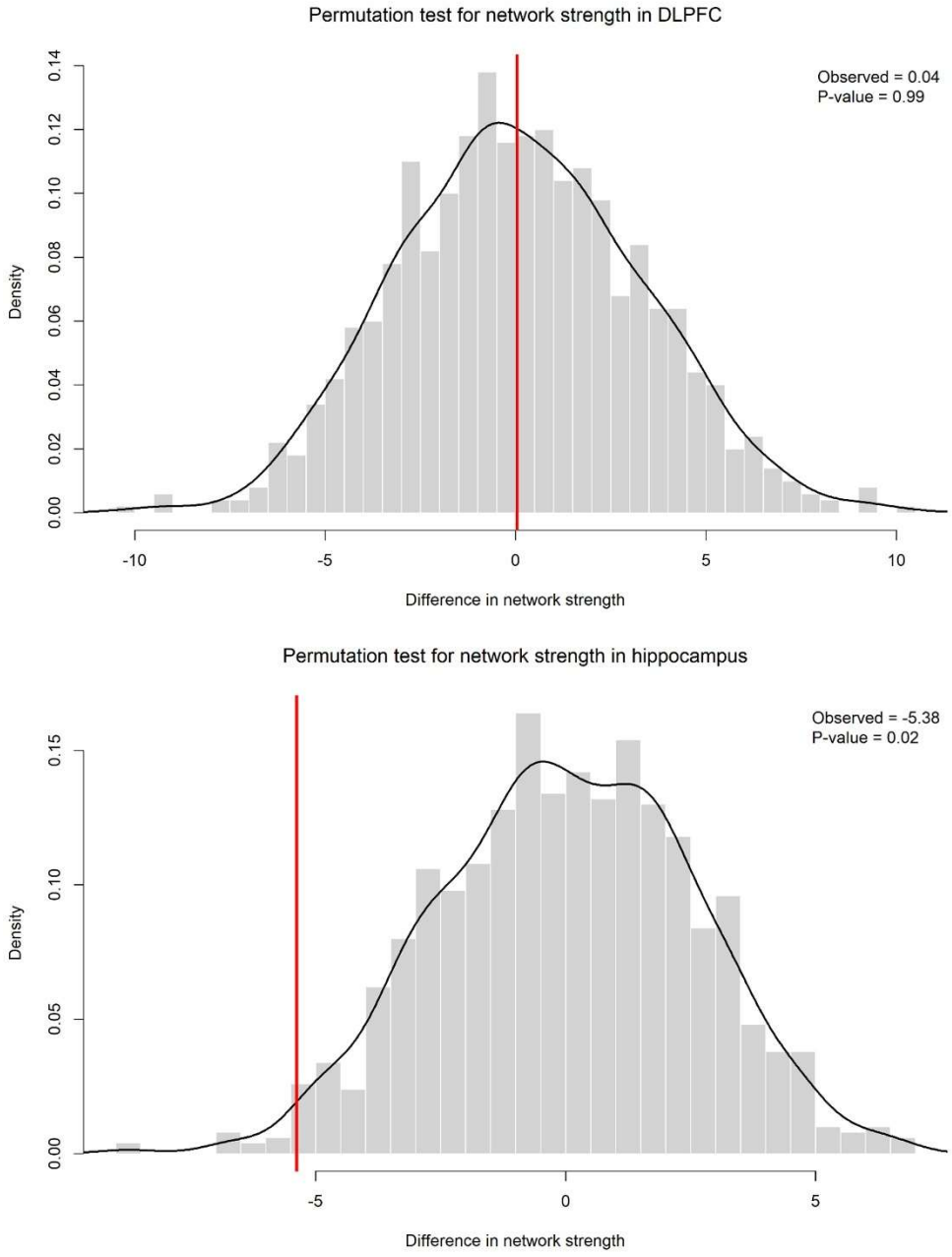

Figure 4. Permutation distribution of global strength in DLPFC and hippocampus. Each panel shows the distribution of global strength differences obtained from permutation testing (gray histogram) with the corresponding density overlaid (black line). The red vertical line indicates the position of the observed difference between schizophrenia patients and controls within the gray histogram.

3.2 Quantitative comparison of nodes' strength between schizophrenia and control groups

In the DLPFC, a significant higher node strength was retrieved for dopamine (1.47 *vs* 2.85; difference = -1.38; adjusted p-value = 0.03) and GLT-1 (2.71 *vs* 4.04; difference = -1.33; adjusted p-value = 0.045) in controls compared to schizophrenia patients. Conversely, GluA4 exhibited significantly higher node strength in schizophrenia than control group (3.75 *vs* 2.31; difference = 1.44; adjusted p-value = 0.03).

Dopamine weighted degree was significantly altered even in the hippocampus, with lower values detected in schizophrenia subjects than controls (1.4 *vs* 2.71; difference = -1.31; adjusted p-value = 0.008). Further, 5-HIAA (1.71 *vs* 3.83; difference = -2.13; adjusted p-value = 0.004), CaMKII (1.59 *vs* 4.07; difference = -2.48; adjusted p-value = 0.004), DOPAC (0.89 *vs* 2.31; difference = -1.42; adjusted p-value = 0.02), NR1 (2.39 *vs* 4.15; difference = -1.76; adjusted p-value = 0.02), and Synapsin I (1.88 *vs* 3.36; difference = -1.48; adjusted p-value = 0.004) showed a significant reduction of node weighted degree in the hippocampus of schizophrenia patients compared to controls.

A representation of permutation distribution for differences in node strength has been provided for the DLPFC and hippocampus in Figure 5. A qualitative and quantitative appraisal of nodes' degree values, adjusted and not adjusted p-values has been shown in Supplementary Information.

Globally, these findings suggest alterations at this hierarchical level of network organization in both brain regions, with prominent involvement of dopamine and molecules belonging to the glutamatergic pathway.

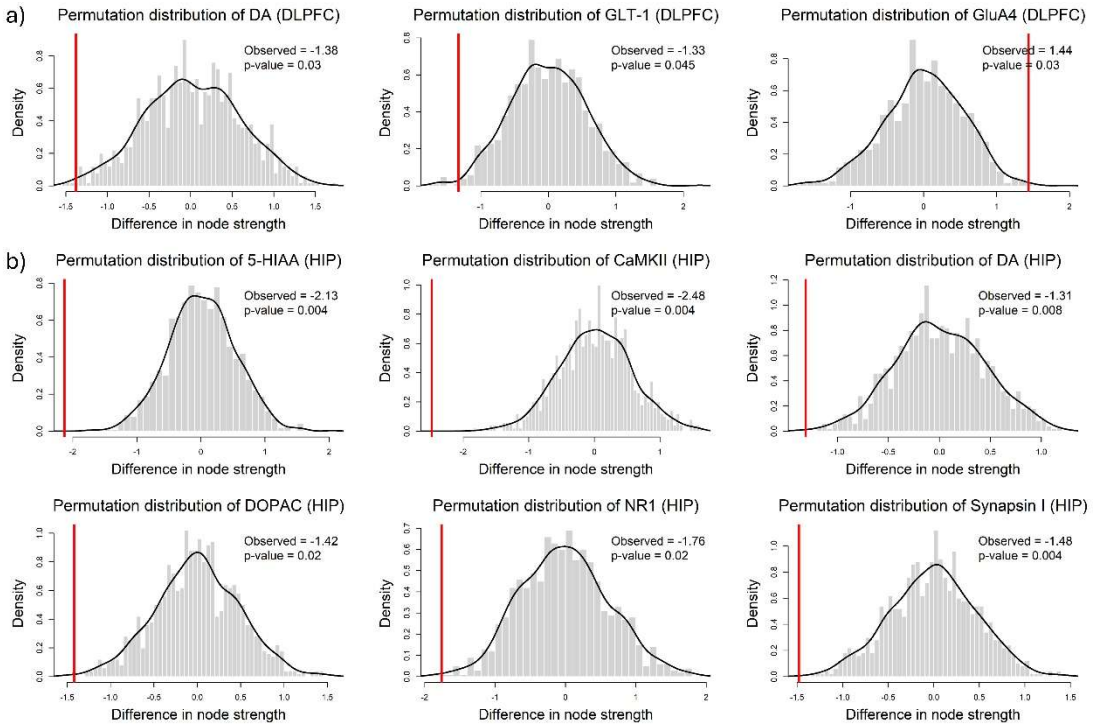

Figure 5. Permutation distributions of node strength differences in the DLPFC (a) and hippocampus (b) for nodes with significant results. Each panel shows the distribution of node strength differences obtained from permutation testing (gray histogram) with the corresponding density overlaid (black line). The red vertical line indicates the position of the observed difference between schizophrenia patients and controls within the gray histogram. Observed values and their associated p-values are shown in the legend. Nodes with significant differences ($p < 0.05$) include DA, GLT-1, GluA4 for the DLPFC, and 5-HIAA, CaMKII, DA, DOPAC, NR1, Synapsin I for the hippocampus.

3.3 Quantitative comparison of pairwise edge weights in the DLPFC

Several significant differences emerged by comparing the degree of edges connecting pairs of molecules across group conditions. Overall results have been shown in Figure 6, and, in a details, in Supplementary Information.

In the DLPFC, altered molecular connectivity within nodes belonging to the glutamatergic pathway was detected. The edges linking the excitatory transporter GLT-1 with both GAD67 (difference = -0.18; adjusted p-value = 0.039) and p-CaMKII (difference = -0.22; adjusted p-value = 0.006) showed reduced values in schizophrenia patients compared to controls. Also the other excitatory amino acid transporter, GLAST, exhibited alterations in its connectivity, showing a lower degree of interaction with Homer1b/c (difference = -0.21; adjusted p-value = 0.018) and a higher one with mGluR5 (difference = 0.15; adjusted p-value = 0.012) in the schizophrenia than control group. The AMPAR GluA2/3 subunit showed altered connections with GAD65 (difference = 0.27; adjusted p-value = 0.024), L-Asp (difference = -0.16; adjusted p-value = 0.033), and p-CaMKII (difference = 0.15; adjusted p-value = 0.048) while the linkage of GluA4 with GAD67 (difference = 0.16; adjusted p-value = 0.036) was significantly greater in patients than controls. Schizophrenia individuals exhibited a lower connection between glutamate vesicular transporters, VGLUT1 and VGLUT2 (difference = -0.12; adjusted p-value = 0.042). Further, VGLUT2 relationship with Synapsin I (difference = 0.17; adjusted p-value = 0.048) was significantly increased in schizophrenia subjects compared to controls. Other impairments were found in the connectivity of various amino acids with PSD proteins, including the association of L-Glu with the NMDAR subunit NR2A (difference = 0.12; adjusted p-value = 0.021), the linkage of Gly with PSD-95 (difference = 0.32; adjusted p-value = 0.042), and finally the edge linking L-Ser with mGluR5 (difference = 0.22; adjusted p-value = 0.039), which were greater in schizophrenia patients than controls.

Further alterations were found in connections across different pathways, especially between monoamines and components of the glutamatergic system. Dopamine interactions with GAD67 (difference = -0.21; adjusted p-value = 0.003) and NR2A (difference = -0.2; adjusted p-value = 0.009) were found to be significantly decreased in schizophrenia subjects. Conversely, 5-HT and 5-HIAA exhibited higher connectivity with CaMKII (difference = 0.16; adjusted p-value = 0.03) and L-Glu (difference = 0.23; adjusted p-value = 0.03), respectively, in individuals affected by schizophrenia compared to control subjects. Similarly, DOPAC showed an impaired association with p-CaMKII (difference = 0.17; adjusted p-value = 0.048). Network analyses also revealed alterations in the connectivity of catabolizing enzymes with molecules involved in the glutamatergic neurotransmission. Specifically, edges connecting mb-COMT to both Gly (difference = -0.15; adjusted p-value = 0.042) and NR2A (difference = -0.17; adjusted p-value = 0.033) showed reduced values in schizophrenia patients compared to controls. The connectivity of MAO-B with both GluA1 (difference = 0.16; adjusted p-value = 0.012) and L-Glu (difference = -0.16; adjusted p-value = 0.048) was impaired, as well as that of MAO-A with mGluR5 (difference = -0.16; adjusted p-value = 0.039).

Within the monoaminergic system, dopamine relationship with norepinephrine (difference = -0.36; adjusted p-value = 0.027) was significantly decreased in patients compared to controls.

Overall, most of the alterations were found in connectivity within the glutamatergic pathway, especially between pre- and postsynaptic molecules. Other impairments were identified between the glutamatergic and monoaminergic pathways, particularly the dopaminergic one. Finally, alterations within the monoaminergic pathway concerned the connection between dopamine and norepinephrine.

3.4 Quantitative comparison of pairwise edge weights in the DLPFC

In the hippocampus, multiple alterations were detected in the connectivity within molecules involved in the regulation of PSD. Specifically, Homer1b/c showed disrupted interactions with both NR1 (difference = -0.14; adjusted p-value = 0.036) and PSD-95 (difference = 0.28; adjusted p-value = 0.02). The metabotropic receptors, mGluR1 and mGluR5, exhibited reduced connections with L-Glu (difference = -0.16; adjusted p-value = 0.04) and NR1 (difference = -0.16; adjusted p-value = 0.044), respectively, in schizophrenia patients compared to controls. Other impairments involved amino acids, especially the relationship between Gly and CaMKII (difference = -0.19; adjusted p-value = 0.04), and the one between D-Asp and GluA1 (difference = 0.13; adjusted p-value = 0.032). Compared to controls, networks from patients revealed increased connectivity of vesicular glutamate transporters, VGLUT1 and VGLUT2, with GAD65 (difference = 0.13; adjusted p-value = 0.048) and GluA4 (difference = 0.2; adjusted p-value < 0.001), respectively.

Cross-systems disturbances between the monoaminergic and glutamatergic pathways were found. The catabolizing enzyme MAO-A showed higher associations with both mGluR1 (difference = 0.22; adjusted p-value = 0.036) and NR2B (difference = 0.17; adjusted p-value = 0.004) in patients affected by schizophrenia than controls. Conversely, mb-COMT exhibited a lower degree of connection with both mGluR1 (difference = -0.2; adjusted p-value = 0.032) and Synapsin I (difference = -0.23; adjusted p-value = 0.044) in the schizophrenia than control group. Finally, disrupted connectivity was found between monoamines and other molecules involved in the glutamatergic signaling, namely the association between dopamine and GLAST (difference = -0.12; adjusted p-value = 0.044), norepinephrine and L-Ser (difference = 0.21; adjusted p-value = 0.048), and the one between 5-HIAA and GluA1 (difference = -0.13; adjusted p-value = 0.028).

For a comprehensive assessment of results, please refer to Figure 6 and Supplementary Information.

Overall, network analyses revealed altered connectivity in the hippocampus within glutamatergic components, especially considering molecules that participate in shaping the postsynaptic architecture. Although no impairments were detected between molecules belonging to the monoaminergic neurotransmission, cross-systems disruptions were found, mainly involving catabolizing enzymes.

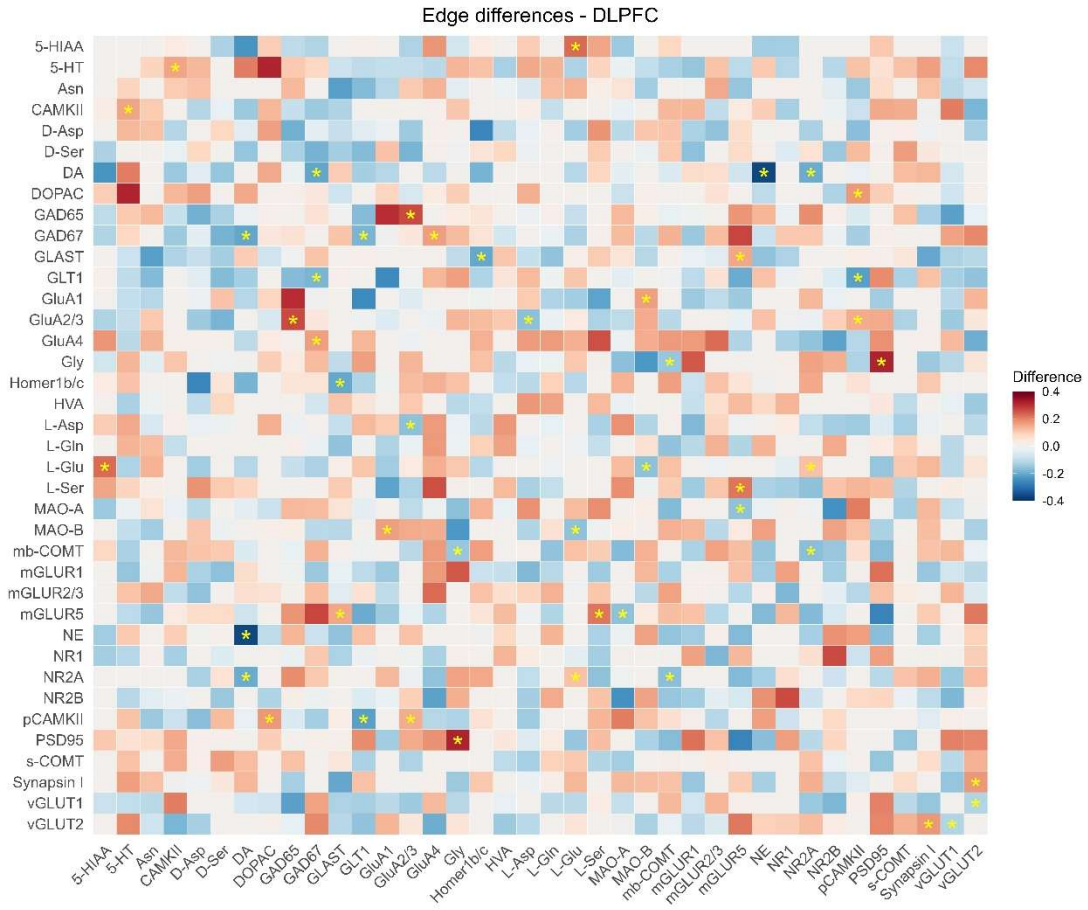

Figure 6. Heatmaps showing differences in pairwise edge weights in the DLPFC. Colors code for the observed difference in the pairwise edges among groups, with red pointing out increased values in schizophrenia and blue higher values in controls. Yellow asterisks (*) indicate significant

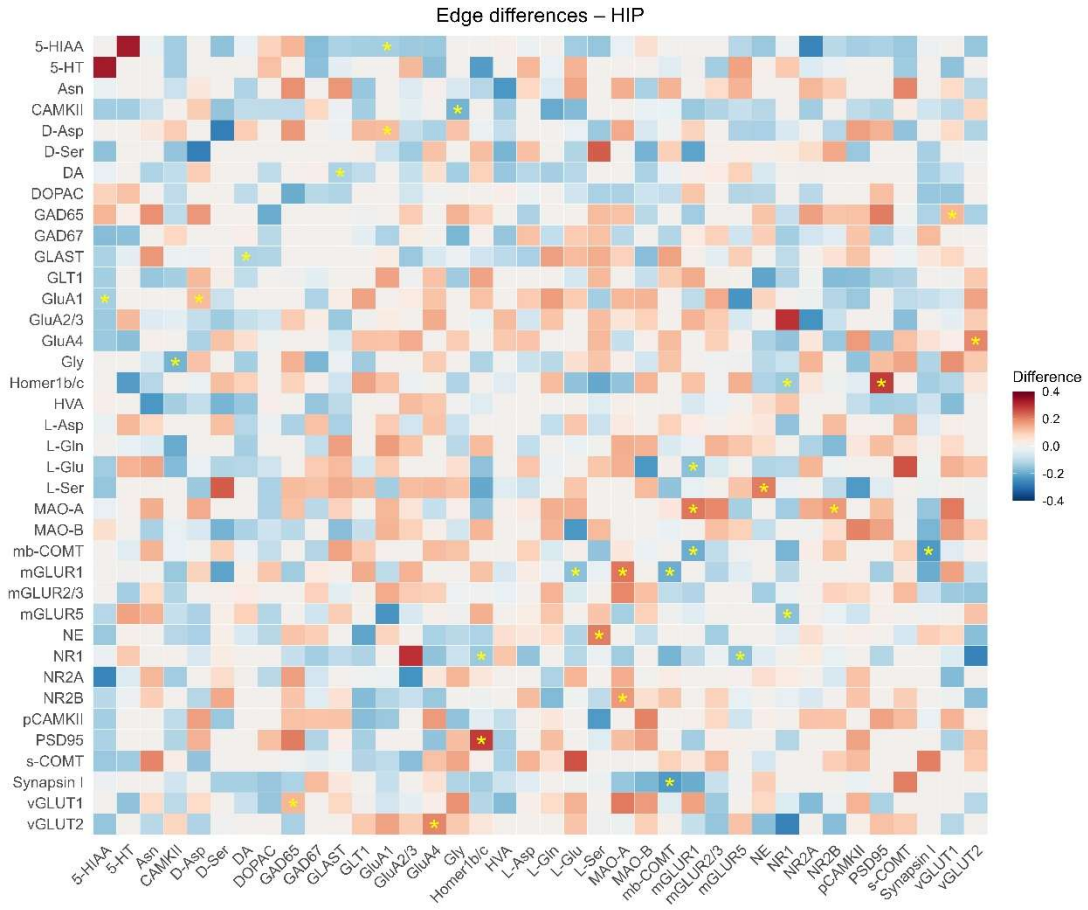

Figure 7. Heatmaps showing differences in pairwise edge weights in the hippocampus. Colors code for the observed difference in the pairwise edges among groups, with red pointing out increased values in schizophrenia and blue higher values in controls. Yellow asterisks (*) indicate significant

4. Discussion

In the present study, we computed networks from postmortem DLPFC and hippocampal tissues of schizophrenia patients and controls by applying CMI combined with autoencoder-based dimensionality reduction. This approach allowed us to move beyond traditional linear measures of associations and to quantify higher-order dependencies between and within amino acids, monoamines, receptors, transporters, enzymes, and synaptic proteins. Overall, our results revealed region-specific alterations in molecular connectivity in schizophrenia patients.

4.1 Different hierarchical and regional patterns of network re-organization in schizophrenia

Schizophrenia patients exhibited several alterations at different hierarchical levels of network organization.

In the hippocampus, alterations emerged at higher hierarchical levels, with a significant reduction in global strength and decreases in node degree across six different molecules. Conversely, in the DLPFC, global strength was preserved and node degree was significantly altered only for three molecules. A more detailed analysis at the elementary level of network organization (i.e., examining differences in individual connections between pairs of molecules) revealed a greater number of altered edges in the DLPFC than in the hippocampus (24 *vs* 15) of schizophrenia patients.

This apparent discrepancy between different hierarchical and regional patterns can be explained by the directionality of the observed changes. Specifically, hippocampal alterations in schizophrenia primarily reflected reductions in connectivity, with decreased global strength and node degree for all six significantly affected molecules, implying an overall reduction in edge weights. In contrast, the DLPFC exhibited a more complex pattern, with both increases

and decreases in edge weights. Consequently, overall connectivity remained unchanged, and significant differences were observed only for nodes showing more consistent reductions (dopamine and GLT-1) or increases (GluA4) in node degree.

From a pathophysiological perspective, decreased molecular connectivity can be interpreted as a loss of function with reduced association between two molecules[41]. Network hypoconnectivity is a common evidence in schizophrenia studies and has been related to multiple symptomatic dimensions, although it usually refers to interregional patterns of functional decoupling measured by multiple neuroimaging modalities[36, 42-45]. Here, we extended the concept of connectivity across different spatial scales, suggesting that a hypoconnectivity pattern can be traced in schizophrenia subjects not only in large-scale networks but also at a molecular level, within synaptic effectors involved in neuronal communication.

The interpretation of increased connectivity, however, remains more controversial. One possible explanation of hyperconnectivity stems from its paradoxical observation at the system-level after disruption of neural networks secondary to brain injury or disease[46]. In this case, adaptive hyperconnectivity represents an early response, which operates to re-establish a network topology that maintains efficient communication through network nodes, followed by connectivity decline at later phases[46]. Extending this concept to the molecular level, hyperconnectivity may similarly reflect an adaptive mechanism, compensating for reduced function in specific molecular components.

4.2 Network-level impairments of glutamatergic pre- and postsynaptic signaling

In both the brain regions analyzed, network-level alterations were mainly detected among molecules belonging to the glutamatergic pathway (Figures 6-7). In the DLPFC of schizophrenia subjects, most changes affected the connectivity between pre- and postsynaptic components, particularly the associations of both transmembrane glutamate transporters, such as GLT-1 and GLAST, and amino acids, including L-Glu, L-Ser, and Gly, with PSD-enriched proteins[47]. Similarly, an impaired connectivity between presynaptic molecules, such as D-Asp, Gly, L-Glu, VGLUT2, and proteins involved in shaping the postsynaptic architecture was observed in the hippocampus of schizophrenia patients. Here, altered associations across PSD proteins were even more pronounced, especially those involving Homer1b/c, mGluR5, NR1, and PSD-95. Overall, these results suggest poor integration of the glutamatergic signaling through the synaptic cleft and postsynaptic structures, which operate a well-coordinate signal transduction and facilitate neuronal plasticity phenomena, in the schizophrenia group[48, 49].

These observed findings may provide a further molecular explanation for disruptions in glutamatergic-based synaptic plasticity and meta-plasticity processes, which have been often pointed out in schizophrenia and other psychotic disorders. Specifically, multiple lines of evidence have shown a putative link between schizophrenia and impaired synaptic plasticity, which could also underlie cognitive dysfunctions and clinical symptoms, as proven by postmortem[50-52], transcranial magnetic stimulation (TMS)[53-55], and electroencephalography (EEG)[56] studies.

Somehow, a disrupted communication across the synaptic cleft and a reduced capability to process postsynaptic signals, as observed in the present study, are not dissimilar in neurobiological terms to what happen in clinical and preclinical experimentations by the administration of NMDAR blockers, including

ketamine and phencyclidine, which disentangle glutamate release from postsynaptic activation. These substances yield to the precipitation of psychotic symptoms when administered in individuals affected by schizophrenia and replicate positive, negative, and cognitive manifestations of psychosis in healthy volunteers and rodents[57-59].

Globally, these results may represent a point of convergence in schizophrenia neurobiology by integrating previous evidence proving impairments in either presynaptic or postsynaptic glutamatergic components[7, 60-63], suggesting that their alterations may disrupt molecular homeostasis and, therefore, impact the whole pattern of connections, with consequences on clinical symptoms.

4.3 Cross-system neurotransmitter alterations and dopamine involvement in schizophrenia patients

In the present study, multiple alterations have been observed between monoaminergic and glutamatergic systems in both the DLPFC and hippocampal tissues of the schizophrenia group (Figures 6-7). The relationship among these two neurotransmitter pathways has been widely recognized as pivotal in neurodevelopmental processes by shaping synaptogenesis and modulating synaptic assembly, maturation, and maintenance[13, 64, 65]. The integration between different pathways may occur at different neuronal levels, with both pre- and postsynaptic sides involved. Specifically, the existence of dual neurons, which attend multiplexed neurotransmission and co-release both glutamate and monoamines, has been proven, providing evidence of a presynaptic mechanism of inter-signaling communication[66-68]. On the postsynaptic side, receptors belonging to different neurotransmitter pathways, including the glutamatergic, dopaminergic, noradrenergic, and serotonergic ones, have been found to be co-expressed at the PSD level, which may be responsible for the intra-cellular integration of their signaling cascades[65, 69, 70].

Regardless of the microanatomical location of their interplay, monoaminergic receptor activity may fail to induce synaptic plasticity and meta-plasticity processes, thus preventing the formation of a long-term molecular imprint and continuing to trigger acute and short-term molecular responses. In this scenario, our findings could be included within a broader framework, suggesting that impairments of glutamatergic synaptic plasticity, dependent on modulatory transmitters such as monoamines, may be responsible for large-scale dysconnectivity and the onset of clinical symptoms in individuals with schizophrenia[71].

Dopamine was the sole molecule to exhibit a significant reduction of weighted degree in both the DLPFC and hippocampus of schizophrenia subjects compared to controls (Figure 5). This observation confirms a large amount of

previous findings pointing to dopamine as a core molecule in the pathophysiology of schizophrenia and other related disorders, extending its impairment at the network level[11, 12, 72-79]. Our results showed an overall reduced signal integration between dopamine and all the other molecules included in the network, especially those involved in the glutamatergic pathway (Figures 5-7). Of interest, an altered dopamine-glutamate interplay has been widely investigated in the schizophrenia framework, and associated with clinical manifestations and drug responsiveness[5, 14, 80].

Within the monoaminergic system, a reduced association between dopamine and norepinephrine in the DLPFC of individuals with schizophrenia emerged whereas no other significant differences were observed among groups. A tight coordination between dopamine and norepinephrine signaling in prefrontal cortex neurons is considered essential for normal cognitive functions, such as working memory and attentional control[81]; therefore, its disruption may contribute to the well-documented cognitive deficits observed in schizophrenia. Overall, the absence of additional alterations within the monoaminergic pathway, together with the detection of cross-system disruptions, suggests that in schizophrenia the core deficit may lie in an impaired ability of monoamines to modulate long-term glutamatergic synaptic plasticity processes.

4.4 Limitations and conclusion

Multiple limitations within the present study should be acknowledged. First, although the sample size is comparable to other previous postmortem studies[82], the high number of variables could introduce bias. To reduce this risk, a specific statistical framework was adopted, such as bootstrapping procedures for a more robust and sparser network estimation, autoencoder to mitigate the curse of dimensionality, and permutation-based comparisons to create null distributions tailored to the data.

Second, we did not have detailed information on pharmacological treatments received by patients prior to death. So, we could not provide a clarified characterization of possible drug-related biases. Nevertheless, even though we knew details on the treatment, it would still represent a limitation since the impossibility to rule out their effects on the results, as commonly detected in previous postmortem studies[82]. Interestingly, evidence from in vitro and animal models supports the presence of molecular dysconnectivity in schizophrenia[2, 5], indicating that at least part of the observed alterations is likely related to disease etiology rather than to pharmacological treatment.

Last, analyses were limited to the brain regions available, such as DLPFC and hippocampus, whereas schizophrenia involves a broader pattern of areas. Future research should extend results to other brain regions, especially subcortical areas.

Despite these limitations, our findings support the dysconnectivity hypothesis of schizophrenia from a novel perspective, by assessing direct interactions between quantitatively measured synaptic effectors and providing a comprehensive characterization of the molecules involved. In addition, we implemented a novel statistical framework for network estimation aimed at minimizing potential biases, which may be useful for future intersubject network analyses.

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6. Supplementary Information

6.1 Qualitative and quantitative comparison of nodes' strength in the DLPFC

Node	SCZ	CTRL	Difference	p-value	p-value adjusted
5-HIAA	1.455	1.715	-0.26	0.546	1
5-HT	2.66	1.664	0.996	0.095	0.285
Asn	2.904	2.825	0.079	0.91	1
CAMKII	2.868	2.693	0.175	0.754	1
D-Asp	2.555	3.583	-1.028	0.021	0.063
D-Ser	2.73	3.211	-0.481	0.401	1
DA	1.473	2.85	-1.377	0.01	0.03
DOPAC	2.549	1.426	1.123	0.051	0.153
GAD65	3.874	3.427	0.447	0.546	1
GAD67	3.697	3.346	0.351	0.587	1
GLAST	2.323	3.752	-1.429	0.031	0.093
GLT-1	2.714	4.04	-1.326	0.015	0.045
GluA1	1.796	2.561	-0.765	0.211	0.633
GluA2/3	3.154	3.172	-0.018	0.981	1
GluA4	3.754	2.311	1.443	0.01	0.03
Gly	3.475	2.817	0.658	0.319	0.957
Homer1b/c	2.829	2.451	0.378	0.528	1
HVA	2.311	1.965	0.346	0.464	1
L-Asp	2.714	3.064	-0.35	0.553	1
L-Gln	2.801	2.535	0.266	0.674	1
L-Glu	2.341	2.223	0.118	0.801	1
L-Ser	3.19	2.264	0.926	0.092	0.276
MAO-A	3.117	3.351	-0.234	0.68	1
MAO-B	2.59	2.375	0.215	0.625	1
mb-COMT	2.996	2.707	0.289	0.508	1
mGluR1	2.689	3.628	-0.939	0.117	0.351
mGluR2/3	3.239	2.47	0.769	0.225	0.675
mGluR5	3.271	3.267	0.004	0.994	1
NE	2.158	2.636	-0.478	0.308	0.924
NR1	3.121	3.09	0.031	0.965	1
NR2A	2.599	2.814	-0.215	0.796	1
NR2B	3.292	3.882	-0.59	0.416	1
p-CaMKII	2.946	2.952	-0.006	0.998	1
PSD-9595	4.153	2.914	1.239	0.067	0.201
s-COMT	2.527	2.215	0.312	0.56	1
Synapsin I	2.721	2.122	0.599	0.233	0.699
VGLUT1	2.371	3.733	-1.362	0.062	0.186
VGLUT2	3.143	2.975	0.168	0.816	1

6.2 Qualitative and quantitative comparison of nodes' strength in the hippocampus

Node	SCZ	CTRL	Difference	p-value	p-value adjusted
5-HIAA	1.707	3.834	-2.127	0.001	0.004
5-HT	2.512	2.65	-0.138	0.798	1
Asn	3.706	3.182	0.524	0.522	1
CAMKII	1.587	4.067	-2.48	0.001	0.004
D-Asp	2.757	2.937	-0.18	0.768	1
D-Ser	2.444	3.207	-0.763	0.135	0.54
DA	1.401	2.708	-1.307	0.002	0.008
DOPAC	0.889	2.305	-1.416	0.005	0.02
GAD65	2.769	1.859	0.91	0.034	0.136
GAD67	2.032	2.83	-0.798	0.124	0.496
GLAST	3.811	3.768	0.043	0.954	1
GLT-1	2.742	3.461	-0.719	0.241	0.964
GluA1	2.322	2.058	0.264	0.684	1
GluA2/3	3.401	3.298	0.103	0.894	1
GluA4	3.306	2.609	0.697	0.181	0.724
Gly	3.549	3.792	-0.243	0.767	1
Homer1b/c	3.28	3.508	-0.228	0.712	1
HVA	2.003	3.392	-1.389	0.022	0.088
L-Asp	3.298	2.941	0.357	0.561	1
L-Gln	3.139	2.76	0.379	0.526	1
L-Glu	3.733	3.628	0.105	0.881	1
L-Ser	2.688	2.515	0.173	0.781	1
MAO-A	3.723	2.514	1.209	0.013	0.052
MAO-B	3.315	3.293	0.022	0.963	1
mb-COMT	3.08	3.259	-0.179	0.753	1
mGluR1	2.524	3.16	-0.636	0.184	0.736
mGluR2/3	3.421	3.229	0.192	0.704	1
mGluR5	3.187	3.327	-0.14	0.833	1
NE	1.668	2.451	-0.783	0.106	0.424
NR1	2.386	4.145	-1.759	0.005	0.02
NR2A	3.391	3.545	-0.154	0.799	1
NR2B	2.786	3.003	-0.217	0.709	1
p-CaMKII	2.886	2.482	0.404	0.436	1
PSD-9595	2.358	1.947	0.411	0.433	1
s-COMT	3.232	2.559	0.673	0.273	1
Synapsin I	1.884	3.363	-1.479	0.001	0.004
VGLUT1	3.432	3.437	-0.005	0.991	1
VGLUT2	2.789	2.881	-0.092	0.875	1

6.3 Comparison of pairwise edge weights in the DLPFC

mol1	mol2	difference	Adj p-value
5-HIAA	5-HIAA	0	1
5-HIAA	5-HT	0	1
5-HIAA	Asn	0	1
5-HIAA	CAMKII	0.032	1
5-HIAA	D-Asp	0	1
5-HIAA	D-Ser	-0.125	0.393
5-HIAA	DA	-0.236	0.087
5-HIAA	DOPAC	0.098	0.252
5-HIAA	GAD65	-0.103	0.441
5-HIAA	GAD67	-0.119	0.378
5-HIAA	GLAST	0	1
5-HIAA	GLT-1	0.014	1
5-HIAA	GluA1	0	1
5-HIAA	GluA2/3	-0.124	0.384
5-HIAA	GluA4	0.177	0.234
5-HIAA	Gly	-0.077	0.492
5-HIAA	Homer1 b/c	0.034	1
5-HIAA	HVA	0	1
5-HIAA	L-Asp	0.1	0.336
5-HIAA	L-Gln	0	1
5-HIAA	L-Glu	0.228	0.03
5-HIAA	L-Ser	0.155	0.12
5-HIAA	MAO-A	-0.144	0.129
5-HIAA	MAO-B	0	1
5-HIAA	mb-COMT	0.085	0.093
5-HIAA	mGluR1	0	1
5-HIAA	mGluR2/3	0	1
5-HIAA	mGluR5	0	1
5-HIAA	NE	-0.138	0.174
5-HIAA	NR1	-0.135	0.3
5-HIAA	NR2A	0	1
5-HIAA	NR2B	0	1
5-HIAA	p-CaMKII	0	1
5-HIAA	PSD-9595	0.106	0.222
5-HIAA	s-COMT	0	1
5-HIAA	Synapsin I	0	1
5-HIAA	VGLUT1	-0.088	0.189
5-HIAA	VGLUT2	0	1
5-HT	5-HIAA	0	1
5-HT	5-HT	0	1
5-HT	Asn	0.088	0.27
5-HT	CAMKII	0.156	0.03
5-HT	D-Asp	0.131	0.222
5-HT	D-Ser	0	1
5-HT	DA	0.205	0.252
5-HT	DOPAC	0.313	0.096
5-HT	GAD65	0.105	0.126
5-HT	GAD67	0.085	0.48
5-HT	GLAST	-0.085	0.363
5-HT	GLT-1	-0.101	0.21
5-HT	GluA1	-0.098	0.105
5-HT	GluA2/3	-0.097	0.477
5-HT	GluA4	-0.108	0.132
5-HT	Gly	0.135	0.297
5-HT	Homer1 b/c	0.115	0.261
5-HT	HVA	-0.13	0.699
5-HT	L-Asp	0.15	0.12
5-HT	L-Gln	0.136	0.135
5-HT	L-Glu	-0.123	0.411
5-HT	L-Ser	0.087	0.777
5-HT	MAO-A	-0.024	1
5-HT	MAO-B	-0.098	0.3
5-HT	mb-COMT	-0.129	0.306
5-HT	mGluR1	-0.152	0.054
5-HT	mGluR2/3	0.114	0.672
5-HT	mGluR5	-0.105	0.204
5-HT	NE	0.105	0.162
5-HT	NR1	-0.115	0.432
5-HT	NR2A	0	1
5-HT	NR2B	-0.112	0.861
5-HT	p-CaMKII	0.116	0.267
5-HT	PSD-9595	0.058	0.54
5-HT	s-COMT	0.117	0.246
5-HT	Synapsin I	0.164	0.177

5-HT	VGLUT 1	-0.099	0.246
5-HT	VGLUT 2	0.192	0.279
Asn	5-HIAA	0	1
Asn	5-HT	0.088	0.27
Asn	Asn	0	1
Asn	CAMKII	0.104	0.144
Asn	D-Asp	0.118	0.096
Asn	D-Ser	0	1
Asn	DA	0	1
Asn	DOPAC	0	1
Asn	GAD65	0.13	0.738
Asn	GAD67	0	1
Asn	GLAST	-0.22	0.147
Asn	GLT-1	-0.172	0.219
Asn	GluA1	-0.114	0.27
Asn	GluA2/3	0.105	0.078
Asn	GluA4	0.137	0.174
Asn	Gly	-0.041	1
Asn	Homer1 b/c	0	1
Asn	HVA	-0.02	1
Asn	L-Asp	-0.061	1
Asn	L-Gln	0.123	0.933
Asn	L-Glu	0.139	0.87
Asn	L-Ser	0.027	1
Asn	MAO-A	0.055	1
Asn	MAO-B	-0.138	0.708
Asn	mb-COMT	0	1
Asn	mGluR1	-0.01	1
Asn	mGluR2/3	0.15	0.342
Asn	mGluR5	-0.151	0.324
Asn	NE	0	1
Asn	NR1	0.012	1
Asn	NR2A	0	1
Asn	NR2B	-0.041	1
Asn	p-CaMKII	-0.145	0.324
Asn	PSD-9595	0.071	1
Asn	s-COMT	0	1
Asn	Synapsin I	0.119	0.408

Asn	VGLUT 1	-0.107	0.552
Asn	VGLUT 2	-0.079	1
CAMKII	5-HIAA	0.032	1
CAMKII	5-HT	0.156	0.03
CAMKII	Asn	0.104	0.144
CAMKII	CAMKII	0	1
CAMKII	D-Asp	-0.116	0.36
CAMKII	D-Ser	-0.031	1
CAMKII	DA	-0.146	0.546
CAMKII	DOPAC	0.132	0.84
CAMKII	GAD65	-0.092	0.294
CAMKII	GAD67	-0.142	0.354
CAMKII	GLAST	-0.121	0.42
CAMKII	GLT-1	0	1
CAMKII	GluA1	0	1
CAMKII	GluA2/3	0	1
CAMKII	GluA4	0.015	1
CAMKII	Gly	0.109	0.672
CAMKII	Homer1 b/c	0	1
CAMKII	HVA	0	1
CAMKII	L-Asp	0.022	1
CAMKII	L-Gln	-0.094	0.315
CAMKII	L-Glu	0	1
CAMKII	L-Ser	0	1
CAMKII	MAO-A	-0.028	1
CAMKII	MAO-B	0.005	1
CAMKII	mb-COMT	0.131	0.423
CAMKII	mGluR1	0.134	0.705
CAMKII	mGluR2/3	-0.1	0.339
CAMKII	mGluR5	0.035	1
CAMKII	NE	0.097	0.381
CAMKII	NR1	-0.131	0.528
CAMKII	NR2A	0	1
CAMKII	NR2B	-0.023	1
CAMKII	p-CaMKII	-0.088	1
CAMKII	PSD-9595	0.152	0.6
CAMKII	s-COMT	0.146	0.381
CAMKII	Synapsin I	-0.006	1

CAMKII	VGLUT 1	0.206	0.054
CAMKII	VGLUT 2	-0.183	0.177
D-Asp	5-HIAA	0	1
D-Asp	5-HT	0.131	0.222
D-Asp	Asn	0.118	0.096
D-Asp	CAMKII	-0.116	0.36
D-Asp	D-Asp	0	1
D-Asp	D-Ser	0.084	1
D-Asp	DA	-0.045	1
D-Asp	DOPAC	0.163	0.186
D-Asp	GAD65	-0.192	0.12
D-Asp	GAD67	-0.04	1
D-Asp	GLAST	-0.091	0.354
D-Asp	GLT-1	-0.044	1
D-Asp	GluA1	-0.019	1
D-Asp	GluA2/3	-0.142	0.072
D-Asp	GluA4	0.012	1
D-Asp	Gly	0	1
D-Asp	Homer1 b/c	-0.261	0.105
D-Asp	HVA	-0.1	0.189
D-Asp	L-Asp	-0.03	1
D-Asp	L-Gln	0.007	1
D-Asp	L-Glu	-0.137	0.165
D-Asp	L-Ser	0.179	0.144
D-Asp	MAO-A	-0.107	0.513
D-Asp	MAO-B	0.109	0.387
D-Asp	mb-COMT	0.113	0.396
D-Asp	mGluR1	-0.126	0.261
D-Asp	mGluR2 /3	-0.157	0.12
D-Asp	mGluR5	0.074	0.693
D-Asp	NE	-0.007	1
D-Asp	NR1	0	1
D-Asp	NR2A	-0.128	0.51
D-Asp	NR2B	0	1
D-Asp	p-CaMKII	-0.166	0.075
D-Asp	PSD-9595	0.011	1
D-Asp	s-COMT	0.023	1
D-Asp	Synapsin I	-0.013	1

D-Asp	VGLUT 1	0	1
D-Asp	VGLUT 2	-0.131	0.183
D-Ser	5-HIAA	-0.125	0.393
D-Ser	5-HT	0	1
D-Ser	Asn	0	1
D-Ser	CAMKII	-0.031	1
D-Ser	D-Asp	0.084	1
D-Ser	D-Ser	0	1
D-Ser	DA	-0.152	0.132
D-Ser	DOPAC	0	1
D-Ser	GAD65	-0.129	0.321
D-Ser	GAD67	-0.187	0.261
D-Ser	GLAST	-0.133	0.282
D-Ser	GLT-1	-0.171	0.096
D-Ser	GluA1	0.115	0.507
D-Ser	GluA2/3	-0.185	0.225
D-Ser	GluA4	0.015	1
D-Ser	Gly	-0.014	1
D-Ser	Homer1 b/c	0.051	1
D-Ser	HVA	0.084	0.981
D-Ser	L-Asp	-0.015	1
D-Ser	L-Gln	0	1
D-Ser	L-Glu	0	1
D-Ser	L-Ser	0.104	1
D-Ser	MAO-A	0	1
D-Ser	MAO-B	-0.022	1
D-Ser	mb-COMT	0.105	0.399
D-Ser	mGluR1	-0.161	0.057
D-Ser	mGluR2 /3	0	1
D-Ser	mGluR5	0.075	0.624
D-Ser	NE	0.011	1
D-Ser	NR1	-0.054	1
D-Ser	NR2A	0.057	1
D-Ser	NR2B	-0.148	0.504
D-Ser	p-CaMKII	0.126	0.171
D-Ser	PSD-9595	0.013	1
D-Ser	s-COMT	0.166	0.144
D-Ser	Synapsin I	0.04	1

D-Ser	VGLUT 1	0	1
D-Ser	VGLUT 2	0	1
DA	5-HIAA	-0.236	0.087
DA	5-HT	0.205	0.252
DA	Asn	0	1
DA	CAMKII	-0.146	0.546
DA	D-Asp	-0.045	1
DA	D-Ser	-0.152	0.132
DA	DA	0	1
DA	DOPAC	0.151	0.708
DA	GAD65	-0.024	1
DA	GAD67	-0.208	0.003
DA	GLAST	0.1	0.534
DA	GLT-1	-0.134	0.411
DA	GluA1	-0.115	0.246
DA	GluA2/3	0	1
DA	GluA4	-0.106	0.237
DA	Gly	-0.004	1
DA	Homer1 b/c	-0.186	0.138
DA	HVA	0	1
DA	L-Asp	0	1
DA	L-Gln	0	1
DA	L-Glu	-0.114	0.258
DA	L-Ser	0.086	0.555
DA	MAO-A	-0.038	1
DA	MAO-B	0	1
DA	mb-COMT	-0.057	1
DA	mGluR1	0.07	0.654
DA	mGluR2/3	0.066	1
DA	mGluR5	-0.08	1
DA	NE	-0.364	0.027
DA	NR1	0	1
DA	NR2A	-0.199	0.009
DA	NR2B	0	1
DA	p-CaMKII	-0.031	1
DA	PSD-9595	0	1
DA	s-COMT	0.123	0.174
DA	Synapsin I	0.133	0.165

DA	VGLUT 1	-0.072	0.411
DA	VGLUT 2	0	1
DOPAC	5-HIAA	0.098	0.252
DOPAC	5-HT	0.313	0.096
DOPAC	Asn	0	1
DOPAC	CAMKII	0.132	0.84
DOPAC	D-Asp	0.163	0.186
DOPAC	D-Ser	0	1
DOPAC	DA	0.151	0.708
DOPAC	DOPAC	0	1
DOPAC	GAD65	0.015	1
DOPAC	GAD67	0.044	1
DOPAC	GLAST	-0.079	0.432
DOPAC	GLT-1	0	1
DOPAC	GluA1	0.086	0.951
DOPAC	GluA2/3	-0.066	0.291
DOPAC	GluA4	0.033	1
DOPAC	Gly	0.097	0.597
DOPAC	Homer1 b/c	0	1
DOPAC	HVA	0	1
DOPAC	L-Asp	0.143	0.132
DOPAC	L-Gln	0	1
DOPAC	L-Glu	0	1
DOPAC	L-Ser	0	1
DOPAC	MAO-A	-0.088	0.639
DOPAC	MAO-B	0.02	1
DOPAC	mb-COMT	0	1
DOPAC	mGluR1	0	1
DOPAC	mGluR2/3	0.058	1
DOPAC	mGluR5	0	1
DOPAC	NE	-0.104	0.591
DOPAC	NR1	0	1
DOPAC	NR2A	0.007	1
DOPAC	NR2B	-0.122	0.144
DOPAC	p-CaMKII	0.173	0.048
DOPAC	PSD-9595	0.097	0.186
DOPAC	s-COMT	0.019	1
DOPAC	Synapsin I	0	1

DOPAC	VGLUT 1	-0.079	0.291
DOPAC	VGLUT 2	0.012	1
GAD65	5-HIAA	-0.103	0.441
GAD65	5-HT	0.105	0.126
GAD65	Asn	0.13	0.738
GAD65	CAMKII	-0.092	0.294
GAD65	D-Asp	-0.192	0.12
GAD65	D-Ser	-0.129	0.321
GAD65	DA	-0.024	1
GAD65	DOPAC	0.015	1
GAD65	GAD65	0	1
GAD65	GAD67	0.058	1
GAD65	GLAST	-0.008	1
GAD65	GLT-1	-0.17	0.162
GAD65	GluA1	0.3	0.3
GAD65	GluA2/3	0.267	0.024
GAD65	GluA4	0	1
GAD65	Gly	0.036	1
GAD65	Homer1 b/c	0.05	1
GAD65	HVA	0	1
GAD65	L-Asp	-0.018	1
GAD65	L-Gln	0.02	1
GAD65	L-Glu	-0.091	0.273
GAD65	L-Ser	0	1
GAD65	MAO-A	0.13	0.153
GAD65	MAO-B	0.025	1
GAD65	mb-COMT	-0.031	1
GAD65	mGluR1	-0.01	1
GAD65	mGluR2/3	0	1
GAD65	mGluR5	0.178	0.897
GAD65	NE	0.134	0.288
GAD65	NR1	-0.022	1
GAD65	NR2A	0.187	0.252
GAD65	NR2B	0.02	1
GAD65	p-CaMKII	-0.056	1
GAD65	PSD-9595	0	1
GAD65	s-COMT	0.119	0.315
GAD65	Synapsin I	-0.131	0.381

GAD65	VGLUT 1	-0.217	0.081
GAD65	VGLUT 2	-0.033	1
GAD67	5-HIAA	-0.119	0.378
GAD67	5-HT	0.085	0.48
GAD67	Asn	0	1
GAD67	CAMKII	-0.142	0.354
GAD67	D-Asp	-0.04	1
GAD67	D-Ser	-0.187	0.261
GAD67	DA	-0.208	0.003
GAD67	DOPAC	0.044	1
GAD67	GAD65	0.058	1
GAD67	GAD67	0	1
GAD67	GLAST	0.113	0.099
GAD67	GLT-1	-0.182	0.039
GAD67	GluA1	-0.005	1
GAD67	GluA2/3	0.043	1
GAD67	GluA4	0.163	0.036
GAD67	Gly	0.125	0.084
GAD67	Homer1 b/c	0.055	1
GAD67	HVA	-0.074	1
GAD67	L-Asp	0	1
GAD67	L-Gln	-0.022	1
GAD67	L-Glu	-0.125	0.06
GAD67	L-Ser	0.013	1
GAD67	MAO-A	0.126	0.585
GAD67	MAO-B	-0.107	0.375
GAD67	mb-COMT	0.14	0.156
GAD67	mGluR1	-0.145	0.075
GAD67	mGluR2/3	0.121	0.06
GAD67	mGluR5	0.271	0.054
GAD67	NE	-0.087	0.273
GAD67	NR1	0.106	1
GAD67	NR2A	0.106	0.996
GAD67	NR2B	-0.015	1
GAD67	p-CaMKII	-0.133	0.705
GAD67	PSD-9595	0.02	1
GAD67	s-COMT	0	1
GAD67	Synapsin I	0	1

GAD67	VGLUT 1	0.16	0.216
GAD67	VGLUT 2	0.193	0.426
GLAST	5-HIAA	0	1
GLAST	5-HT	-0.085	0.363
GLAST	Asn	-0.22	0.147
GLAST	CAMKII	-0.121	0.42
GLAST	D-Asp	-0.091	0.354
GLAST	D-Ser	-0.133	0.282
GLAST	DA	0.1	0.534
GLAST	DOPAC	-0.079	0.432
GLAST	GAD65	-0.008	1
GLAST	GAD67	0.113	0.099
GLAST	GLAST	0	1
GLAST	GLT-1	0.02	1
GLAST	GluA1	0	1
GLAST	GluA2/3	0	1
GLAST	GluA4	0	1
GLAST	Gly	-0.102	0.453
GLAST	Homer1 b/c	-0.206	0.018
GLAST	HVA	0.109	0.18
GLAST	L-Asp	-0.093	0.492
GLAST	L-Gln	-0.154	0.222
GLAST	L-Glu	0.02	1
GLAST	L-Ser	0.102	0.651
GLAST	MAO-A	0.055	1
GLAST	MAO-B	-0.111	1
GLAST	mb-COMT	0.012	1
GLAST	mGluR1	-0.03	1
GLAST	mGluR2 /3	-0.049	1
GLAST	mGluR5	0.153	0.012
GLAST	NE	-0.157	0.354
GLAST	NR1	-0.123	0.057
GLAST	NR2A	0	1
GLAST	NR2B	0	1
GLAST	p-CaMKII	0.028	1
GLAST	PSD-9595	0.016	1
GLAST	s-COMT	0.047	1
GLAST	Synapsin I	-0.207	0.066

GLAST	VGLUT 1	-0.124	1
GLAST	VGLUT 2	-0.111	0.36
GLT-1	5-HIAA	0.014	1
GLT-1	5-HT	-0.101	0.21
GLT-1	Asn	-0.172	0.219
GLT-1	CAMKII	0	1
GLT-1	D-Asp	-0.044	1
GLT-1	D-Ser	-0.171	0.096
GLT-1	DA	-0.134	0.411
GLT-1	DOPAC	0	1
GLT-1	GAD65	-0.17	0.162
GLT-1	GAD67	-0.182	0.039
GLT-1	GLAST	0.02	1
GLT-1	GLT-1	0	1
GLT-1	GluA1	-0.253	0.117
GLT-1	GluA2/3	-0.01	1
GLT-1	GluA4	0.133	0.189
GLT-1	Gly	0.164	0.339
GLT-1	Homer1 b/c	-0.122	0.57
GLT-1	HVA	0.049	1
GLT-1	L-Asp	0.128	0.21
GLT-1	L-Gln	-0.011	1
GLT-1	L-Glu	0.111	0.381
GLT-1	L-Ser	0	1
GLT-1	MAO-A	-0.038	0.834
GLT-1	MAO-B	0	1
GLT-1	mb-COMT	-0.014	1
GLT-1	mGluR1	-0.105	0.435
GLT-1	mGluR2 /3	0.059	1
GLT-1	mGluR5	-0.2	0.123
GLT-1	NE	0.118	0.273
GLT-1	NR1	-0.017	1
GLT-1	NR2A	0	1
GLT-1	NR2B	-0.054	1
GLT-1	p-CaMKII	-0.219	0.006
GLT-1	PSD-9595	0.188	0.684
GLT-1	s-COMT	-0.127	0.462
GLT-1	Synapsin I	0.119	0.747

GLT-1	VGLUT 1	-0.131	0.303
GLT-1	VGLUT 2	-0.154	0.111
GluA1	5-HIAA	0	1
GluA1	5-HT	-0.098	0.105
GluA1	Asn	-0.114	0.27
GluA1	CAMKII	0	1
GluA1	D-Asp	-0.019	1
GluA1	D-Ser	0.115	0.507
GluA1	DA	-0.115	0.246
GluA1	DOPAC	0.086	0.951
GluA1	GAD65	0.3	0.3
GluA1	GAD67	-0.005	1
GluA1	GLAST	0	1
GluA1	GLT-1	-0.253	0.117
GluA1	GluA1	0	1
GluA1	GluA2/3	-0.052	1
GluA1	GluA4	0	1
GluA1	Gly	0	1
GluA1	Homer1 b/c	-0.011	1
GluA1	HVA	0	1
GluA1	L-Asp	0.104	0.318
GluA1	L-Gln	-0.121	0.864
GluA1	L-Glu	-0.138	0.06
GluA1	L-Ser	-0.214	0.381
GluA1	MAO-A	0	1
GluA1	MAO-B	0.163	0.012
GluA1	mb-COMT	0	1
GluA1	mGluR1	-0.144	0.309
GluA1	mGluR2/3	-0.101	0.279
GluA1	mGluR5	-0.142	0.795
GluA1	NE	0	1
GluA1	NR1	0	1
GluA1	NR2A	0.131	1
GluA1	NR2B	-0.025	1
GluA1	p-CaMKII	0	1
GluA1	PSD-9595	-0.138	0.177
GluA1	s-COMT	0	1
GluA1	Synapsin I	0	1

GluA1	VGLUT 1	-0.108	0.417
GluA1	VGLUT 2	0.134	0.327
GluA2/3	5-HIAA	-0.124	0.384
GluA2/3	5-HT	-0.097	0.477
GluA2/3	Asn	0.105	0.078
GluA2/3	CAMKII	0	1
GluA2/3	D-Asp	-0.142	0.072
GluA2/3	D-Ser	-0.185	0.225
GluA2/3	DA	0	1
GluA2/3	DOPAC	-0.066	0.291
GluA2/3	GAD65	0.267	0.024
GluA2/3	GAD67	0.043	1
GluA2/3	GLAST	0	1
GluA2/3	GLT-1	-0.01	1
GluA2/3	GluA1	-0.052	1
GluA2/3	GluA2/3	0	1
GluA2/3	GluA4	-0.018	1
GluA2/3	Gly	0.134	0.087
GluA2/3	Homer1 b/c	0.126	0.513
GluA2/3	HVA	0.105	0.123
GluA2/3	L-Asp	-0.161	0.033
GluA2/3	L-Gln	-0.023	1
GluA2/3	L-Glu	0.037	1
GluA2/3	L-Ser	-0.123	0.129
GluA2/3	MAO-A	-0.104	0.111
GluA2/3	MAO-B	0.149	0.459
GluA2/3	mb-COMT	-0.108	0.297
GluA2/3	mGluR1	0	1
GluA2/3	mGluR2/3	0	1
GluA2/3	mGluR5	-0.028	1
GluA2/3	NE	0.115	0.345
GluA2/3	NR1	-0.011	1
GluA2/3	NR2A	-0.018	1
GluA2/3	NR2B	0.096	1
GluA2/3	p-CaMKII	0.147	0.048
GluA2/3	PSD-9595	0.149	0.051
GluA2/3	s-COMT	-0.124	0.393
GluA2/3	Synapsin I	0	1

GluA2/3	VGLUT 1	-0.142	0.465
GluA2/3	VGLUT 2	0.045	1
GluA4	5-HIAA	0.177	0.234
GluA4	5-HT	-0.108	0.132
GluA4	Asn	0.137	0.174
GluA4	CAMKII	0.015	1
GluA4	D-Asp	0.012	1
GluA4	D-Ser	0.015	1
GluA4	DA	-0.106	0.237
GluA4	DOPAC	0.033	1
GluA4	GAD65	0	1
GluA4	GAD67	0.163	0.036
GluA4	GLAST	0	1
GluA4	GLT-1	0.133	0.189
GluA4	GluA1	0	1
GluA4	GluA2/3	-0.018	1
GluA4	GluA4	0	1
GluA4	Gly	0	1
GluA4	Homer1 b/c	0.141	0.174
GluA4	HVA	0.016	1
GluA4	L-Asp	0.17	0.135
GluA4	L-Gln	0.17	0.192
GluA4	L-Glu	0.144	0.072
GluA4	L-Ser	0.259	0.078
GluA4	MAO-A	-0.016	1
GluA4	MAO-B	0.147	0.18
GluA4	mb-COMT	0.17	0.153
GluA4	mGluR1	0.171	0.369
GluA4	mGluR2 /3	0.228	0.078
GluA4	mGluR5	-0.12	0.081
GluA4	NE	0	1
GluA4	NR1	-0.128	0.102
GluA4	NR2A	-0.157	0.111
GluA4	NR2B	-0.216	0.477
GluA4	p-CaMKII	-0.115	0.237
GluA4	PSD-9595	0.182	0.114
GluA4	s-COMT	0	1
GluA4	Synapsin I	0.011	1

GluA4	VGLUT 1	0.129	0.672
GluA4	VGLUT 2	-0.196	0.057
Gly	5-HIAA	-0.077	0.492
Gly	5-HT	0.135	0.297
Gly	Asn	-0.041	1
Gly	CAMKII	0.109	0.672
Gly	D-Asp	0	1
Gly	D-Ser	-0.014	1
Gly	DA	-0.004	1
Gly	DOPAC	0.097	0.597
Gly	GAD65	0.036	1
Gly	GAD67	0.125	0.084
Gly	GLAST	-0.102	0.453
Gly	GLT-1	0.164	0.339
Gly	GluA1	0	1
Gly	GluA2/3	0.134	0.087
Gly	GluA4	0	1
Gly	Gly	0	1
Gly	Homer1 b/c	0.117	1
Gly	HVA	-0.109	0.06
Gly	L-Asp	-0.026	1
Gly	L-Gln	-0.02	1
Gly	L-Glu	0.108	1
Gly	L-Ser	0.01	1
Gly	MAO-A	-0.163	0.123
Gly	MAO-B	-0.232	0.201
Gly	mb-COMT	-0.149	0.042
Gly	mGluR1	0.248	0.09
Gly	mGluR2 /3	0	1
Gly	mGluR5	0	1
Gly	NE	0	1
Gly	NR1	0.016	1
Gly	NR2A	0.16	0.162
Gly	NR2B	0.143	0.225
Gly	p-CaMKII	-0.122	0.495
Gly	PSD-9595	0.317	0.042
Gly	s-COMT	0	1
Gly	Synapsin I	-0.143	0.075

Gly	VGLUT 1	-0.111	0.057
Gly	VGLUT 2	0.052	1
Homer1 b/c	5-HIAA	0.034	1
Homer1 b/c	5-HT	0.115	0.261
Homer1 b/c	Asn	0	1
Homer1 b/c	CAMKII	0	1
Homer1 b/c	D-Asp	-0.261	0.105
Homer1 b/c	D-Ser	0.051	1
Homer1 b/c	DA	-0.186	0.138
Homer1 b/c	DOPAC	0	1
Homer1 b/c	GAD65	0.05	1
Homer1 b/c	GAD67	0.055	1
Homer1 b/c	GLAST	-0.206	0.018
Homer1 b/c	GLT-1	-0.122	0.57
Homer1 b/c	GluA1	-0.011	1
Homer1 b/c	GluA2/3	0.126	0.513
Homer1 b/c	GluA4	0.141	0.174
Homer1 b/c	Gly	0.117	1
Homer1 b/c	Homer1 b/c	0	1
Homer1 b/c	HVA	-0.098	0.183
Homer1 b/c	L-Asp	-0.108	0.975
Homer1 b/c	L-Gln	0.094	0.252
Homer1 b/c	L-Glu	-0.112	0.138
Homer1 b/c	L-Ser	0.004	1
Homer1 b/c	MAO-A	0.139	0.288
Homer1 b/c	MAO-B	0	1
Homer1 b/c	mb-COMT	0.165	0.078
Homer1 b/c	mGluR1	-0.087	0.645
Homer1 b/c	mGluR2/3	0.115	0.117
Homer1 b/c	mGluR5	0.052	1
Homer1 b/c	NE	-0.006	1
Homer1 b/c	NR1	0	1
Homer1 b/c	NR2A	0.152	0.723
Homer1 b/c	NR2B	0	1
Homer1 b/c	p-CaMKII	0.058	1
Homer1 b/c	PSD-9595	0	1
Homer1 b/c	s-COMT	0	1
Homer1 b/c	Synapsin I	0.107	0.618
Homer1 b/c	VGLUT 1	0	1
Homer1 b/c	VGLUT 2	0	1
HVA	5-HIAA	0	1
HVA	5-HT	-0.13	0.699
HVA	Asn	-0.02	1
HVA	CAMKII	0	1
HVA	D-Asp	-0.1	0.189
HVA	D-Ser	0.084	0.981
HVA	DA	0	1
HVA	DOPAC	0	1
HVA	GAD65	0	1
HVA	GAD67	-0.074	1
HVA	GLAST	0.109	0.18
HVA	GLT-1	0.049	1
HVA	GluA1	0	1
HVA	GluA2/3	0.105	0.123
HVA	GluA4	0.016	1
HVA	Gly	-0.109	0.06
HVA	Homer1 b/c	-0.098	0.183
HVA	HVA	0	1
HVA	L-Asp	0.174	0.246
HVA	L-Gln	0.159	0.141

HVA	L-Glu	0	1
HVA	L-Ser	0.128	0.369
HVA	MAO-A	-0.026	1
HVA	MAO-B	0	1
HVA	mb-COMT	0	1
HVA	mGluR1	-0.093	0.345
HVA	mGluR2/3	0.065	1
HVA	mGluR5	0.124	0.336
HVA	NE	0.081	0.177
HVA	NR1	0.135	0.36
HVA	NR2A	0	1
HVA	NR2B	0	1
HVA	p-CaMKII	0	1
HVA	PSD-9595	0.044	1
HVA	s-COMT	-0.105	0.396
HVA	Synapsin I	0	1
HVA	VGLUT 1	-0.03	1
HVA	VGLUT 2	-0.142	0.195
L-Asp	5-HIAA	0.1	0.336
L-Asp	5-HT	0.15	0.12
L-Asp	Asn	-0.061	1
L-Asp	CAMKII	0.022	1
L-Asp	D-Asp	-0.03	1
L-Asp	D-Ser	-0.015	1
L-Asp	DA	0	1
L-Asp	DOPAC	0.143	0.132
L-Asp	GAD65	-0.018	1
L-Asp	GAD67	0	1
L-Asp	GLAST	-0.093	0.492
L-Asp	GLT-1	0.128	0.21
L-Asp	GluA1	0.104	0.318
L-Asp	GluA2/3	-0.161	0.033
L-Asp	GluA4	0.17	0.135
L-Asp	Gly	-0.026	1
L-Asp	Homer1 b/c	-0.108	0.975
L-Asp	HVA	0.174	0.246
L-Asp	L-Asp	0	1
L-Asp	L-Gln	-0.033	1
L-Asp	L-Glu	0	1

L-Asp	L-Ser	-0.128	0.447
L-Asp	MAO-A	0.184	0.138
L-Asp	MAO-B	-0.117	0.354
L-Asp	mb-COMT	0.014	1
L-Asp	mGluR1	-0.176	0.198
L-Asp	mGluR2/3	0.088	0.552
L-Asp	mGluR5	-0.013	1
L-Asp	NE	0	1
L-Asp	NR1	0.033	1
L-Asp	NR2A	-0.099	0.9
L-Asp	NR2B	-0.135	0.186
L-Asp	p-CaMKII	-0.14	0.516
L-Asp	PSD-9595	-0.052	1
L-Asp	s-COMT	-0.131	0.477
L-Asp	Synapsin I	-0.017	1
L-Asp	VGLUT 1	0	1
L-Asp	VGLUT 2	-0.107	0.426
L-Gln	5-HIAA	0	1
L-Gln	5-HT	0.136	0.135
L-Gln	Asn	0.123	0.933
L-Gln	CAMKII	-0.094	0.315
L-Gln	D-Asp	0.007	1
L-Gln	D-Ser	0	1
L-Gln	DA	0	1
L-Gln	DOPAC	0	1
L-Gln	GAD65	0.02	1
L-Gln	GAD67	-0.022	1
L-Gln	GLAST	-0.154	0.222
L-Gln	GLT-1	-0.011	1
L-Gln	GluA1	-0.121	0.864
L-Gln	GluA2/3	-0.023	1
L-Gln	GluA4	0.17	0.192
L-Gln	Gly	-0.02	1
L-Gln	Homer1 b/c	0.094	0.252
L-Gln	HVA	0.159	0.141
L-Gln	L-Asp	-0.033	1
L-Gln	L-Gln	0	1
L-Gln	L-Glu	-0.013	1
L-Gln	L-Ser	-0.095	0.384

L-Gln	MAO-A	0	1
L-Gln	MAO-B	0.059	1
L-Gln	mb-COMT	-0.154	0.255
L-Gln	mGluR1	-0.11	0.372
L-Gln	mGluR2/3	0.141	0.174
L-Gln	mGluR5	-0.117	0.867
L-Gln	NE	0.136	0.156
L-Gln	NR1	0.001	1
L-Gln	NR2A	0	1
L-Gln	NR2B	0.149	0.597
L-Gln	p-CaMKII	0	1
L-Gln	PSD-9595	0.034	0.855
L-Gln	s-COMT	0.094	0.378
L-Gln	Synapsin I	0.018	1
L-Gln	VGLUT 1	-0.108	0.702
L-Gln	VGLUT 2	0	1
L-Glu	5-HIAA	0.228	0.03
L-Glu	5-HT	-0.123	0.411
L-Glu	Asn	0.139	0.87
L-Glu	CAMKII	0	1
L-Glu	D-Asp	-0.137	0.165
L-Glu	D-Ser	0	1
L-Glu	DA	-0.114	0.258
L-Glu	DOPAC	0	1
L-Glu	GAD65	-0.091	0.273
L-Glu	GAD67	-0.125	0.06
L-Glu	GLAST	0.02	1
L-Glu	GLT-1	0.111	0.381
L-Glu	GluA1	-0.138	0.06
L-Glu	GluA2/3	0.037	1
L-Glu	GluA4	0.144	0.072
L-Glu	Gly	0.108	1
L-Glu	Homer1 b/c	-0.112	0.138
L-Glu	HVA	0	1
L-Glu	L-Asp	0	1
L-Glu	L-Gln	-0.013	1
L-Glu	L-Glu	0	1
L-Glu	L-Ser	0	1
L-Glu	MAO-A	0.126	0.072
L-Glu	MAO-B	-0.159	0.048
L-Glu	mb-COMT	0.118	0.276
L-Glu	mGluR1	0	1
L-Glu	mGluR2/3	-0.013	1
L-Glu	mGluR5	0	1
L-Glu	NE	0	1
L-Glu	NR1	-0.037	1
L-Glu	NR2A	0.117	0.021
L-Glu	NR2B	0	1
L-Glu	p-CaMKII	0	1
L-Glu	PSD-9595	-0.151	0.21
L-Glu	s-COMT	0.106	0.111
L-Glu	Synapsin I	0.133	0.111
L-Glu	VGLUT 1	-0.108	0.126
L-Glu	VGLUT 2	0.052	1
L-Ser	5-HIAA	0.155	0.12
L-Ser	5-HT	0.087	0.777
L-Ser	Asn	0.027	1
L-Ser	CAMKII	0	1
L-Ser	D-Asp	0.179	0.144
L-Ser	D-Ser	0.104	1
L-Ser	DA	0.086	0.555
L-Ser	DOPAC	0	1
L-Ser	GAD65	0	1
L-Ser	GAD67	0.013	1
L-Ser	GLAST	0.102	0.651
L-Ser	GLT-1	0	1
L-Ser	GluA1	-0.214	0.381
L-Ser	GluA2/3	-0.123	0.129
L-Ser	GluA4	0.259	0.078
L-Ser	Gly	0.01	1
L-Ser	Homer1 b/c	0.004	1
L-Ser	HVA	0.128	0.369
L-Ser	L-Asp	-0.128	0.447
L-Ser	L-Gln	-0.095	0.384
L-Ser	L-Glu	0	1
L-Ser	L-Ser	0	1
L-Ser	MAO-A	0.186	0.492
L-Ser	MAO-B	-0.009	1

L-Ser	mb-COMT	0.101	0.351
L-Ser	mGluR1	-0.14	0.069
L-Ser	mGluR2/3	0.11	0.516
L-Ser	mGluR5	0.215	0.039
L-Ser	NE	-0.125	0.399
L-Ser	NR1	-0.133	0.261
L-Ser	NR2A	-0.158	0.582
L-Ser	NR2B	0.114	0.42
L-Ser	p-CaMKII	0.135	0.108
L-Ser	PSD-9595	0.122	1
L-Ser	s-COMT	-0.117	0.429
L-Ser	Synapsin I	0	1
L-Ser	VGLUT 1	0.031	1
L-Ser	VGLUT 2	0	1
MAO-A	5-HIAA	-0.144	0.129
MAO-A	5-HT	-0.024	1
MAO-A	Asn	0.055	1
MAO-A	CAMKII	-0.028	1
MAO-A	D-Asp	-0.107	0.513
MAO-A	D-Ser	0	1
MAO-A	DA	-0.038	1
MAO-A	DOPAC	-0.088	0.639
MAO-A	GAD65	0.13	0.153
MAO-A	GAD67	0.126	0.585
MAO-A	GLAST	0.055	1
MAO-A	GLT-1	-0.038	0.834
MAO-A	GluA1	0	1
MAO-A	GluA2/3	-0.104	0.111
MAO-A	GluA4	-0.016	1
MAO-A	Gly	-0.163	0.123
MAO-A	Homer1 b/c	0.139	0.288
MAO-A	HVA	-0.026	1
MAO-A	L-Asp	0.184	0.138
MAO-A	L-Gln	0	1
MAO-A	L-Glu	0.126	0.072
MAO-A	L-Ser	0.186	0.492
MAO-A	MAO-A	0	1
MAO-A	MAO-B	0.025	1

MAO-A	mb-COMT	-0.173	0.291
MAO-A	mGluR1	0.008	1
MAO-A	mGluR2/3	0	1
MAO-A	mGluR5	-0.158	0.039
MAO-A	NE	-0.022	1
MAO-A	NR1	0.009	1
MAO-A	NR2A	-0.01	1
MAO-A	NR2B	-0.241	0.102
MAO-A	p-CaMKII	0.206	0.054
MAO-A	PSD-9595	0	1
MAO-A	s-COMT	-0.136	0.105
MAO-A	Synapsin I	0.131	0.093
MAO-A	VGLUT 1	-0.094	0.414
MAO-A	VGLUT 2	-0.004	1
MAO-B	5-HIAA	0	1
MAO-B	5-HT	-0.098	0.3
MAO-B	Asn	-0.138	0.708
MAO-B	CAMKII	0.005	1
MAO-B	D-Asp	0.109	0.387
MAO-B	D-Ser	-0.022	1
MAO-B	DA	0	1
MAO-B	DOPAC	0.02	1
MAO-B	GAD65	0.025	1
MAO-B	GAD67	-0.107	0.375
MAO-B	GLAST	-0.111	1
MAO-B	GLT-1	0	1
MAO-B	GluA1	0.163	0.012
MAO-B	GluA2/3	0.149	0.459
MAO-B	GluA4	0.147	0.18
MAO-B	Gly	-0.232	0.201
MAO-B	Homer1 b/c	0	1
MAO-B	HVA	0	1
MAO-B	L-Asp	-0.117	0.354
MAO-B	L-Gln	0.059	1
MAO-B	L-Glu	-0.159	0.048
MAO-B	L-Ser	-0.009	1
MAO-B	MAO-A	0.025	1
MAO-B	MAO-B	0	1

MAO-B	mb-COMT	0.141	0.084
MAO-B	mGluR1	0.133	0.369
MAO-B	mGluR2/3	-0.108	0.15
MAO-B	mGluR5	0.035	0.723
MAO-B	NE	0.162	0.216
MAO-B	NR1	0	1
MAO-B	NR2A	0	1
MAO-B	NR2B	0.159	0.12
MAO-B	p-CaMKII	0.117	0.363
MAO-B	PSD-9595	-0.127	0.291
MAO-B	s-COMT	0	1
MAO-B	Synapsin I	0.122	0.189
MAO-B	VGLUT 1	0	1
MAO-B	VGLUT 2	-0.128	0.177
mb-COMT	5-HIAA	0.085	0.093
mb-COMT	5-HT	-0.129	0.306
mb-COMT	Asn	0	1
mb-COMT	CAMKII	0.131	0.423
mb-COMT	D-Asp	0.113	0.396
mb-COMT	D-Ser	0.105	0.399
mb-COMT	DA	-0.057	1
mb-COMT	DOPAC	0	1
mb-COMT	GAD65	-0.031	1
mb-COMT	GAD67	0.14	0.156
mb-COMT	GLAST	0.012	1
mb-COMT	GLT-1	-0.014	1
mb-COMT	GluA1	0	1
mb-COMT	GluA2/3	-0.108	0.297
mb-COMT	GluA4	0.17	0.153
mb-COMT	Gly	-0.149	0.042
mb-COMT	Homer1 b/c	0.165	0.078
mb-COMT	HVA	0	1
mb-COMT	L-Asp	0.014	1
mb-COMT	L-Gln	-0.154	0.255
mb-COMT	L-Glu	0.118	0.276
mb-COMT	L-Ser	0.101	0.351
mb-COMT	MAO-A	-0.173	0.291
mb-COMT	MAO-B	0.141	0.084
mb-COMT	mb-COMT	0	1
mb-COMT	mGluR1	-0.127	0.162
mb-COMT	mGluR2/3	0.16	0.093
mb-COMT	mGluR5	0.122	0.147
mb-COMT	NE	-0.153	0.099
mb-COMT	NR1	0	1
mb-COMT	NR2A	-0.165	0.033
mb-COMT	NR2B	-0.149	0.528
mb-COMT	p-CaMKII	0.062	0.948
mb-COMT	PSD-9595	-0.168	0.519
mb-COMT	s-COMT	0.01	1
mb-COMT	Synapsin I	0.115	0.156
mb-COMT	VGLUT 1	0.131	0.399
mb-COMT	VGLUT 2	-0.029	1
mGluR1	5-HIAA	0	1
mGluR1	5-HT	-0.152	0.054
mGluR1	Asn	-0.01	1

mGluR1	CAMKII	0.134	0.705
mGluR1	D-Asp	-0.126	0.261
mGluR1	D-Ser	-0.161	0.057
mGluR1	DA	0.07	0.654
mGluR1	DOPAC	0	1
mGluR1	GAD65	-0.01	1
mGluR1	GAD67	-0.145	0.075
mGluR1	GLAST	-0.03	1
mGluR1	GLT-1	-0.105	0.435
mGluR1	GluA1	-0.144	0.309
mGluR1	GluA2/3	0	1
mGluR1	GluA4	0.171	0.369
mGluR1	Gly	0.248	0.09
mGluR1	Homer1 b/c	-0.087	0.645
mGluR1	HVA	-0.093	0.345
mGluR1	L-Asp	-0.176	0.198
mGluR1	L-Gln	-0.11	0.372
mGluR1	L-Glu	0	1
mGluR1	L-Ser	-0.14	0.069
mGluR1	MAO-A	0.008	1
mGluR1	MAO-B	0.133	0.369
mGluR1	mb-COMT	-0.127	0.162
mGluR1	mGluR1	0	1
mGluR1	mGluR2/3	0.015	1
mGluR1	mGluR5	0.115	0.102
mGluR1	NE	-0.139	0.081
mGluR1	NR1	0.161	0.111
mGluR1	NR2A	0	1
mGluR1	NR2B	-0.136	0.072
mGluR1	p-CaMKII	0.01	1
mGluR1	PSD-9595	0.221	0.885
mGluR1	s-COMT	0	1
mGluR1	Synapsin I	-0.149	0.06
mGluR1	VGLUT 1	-0.077	1
mGluR1	VGLUT 2	-0.108	0.813
mGluR2/3	5-HIAA	0	1
mGluR2/3	5-HT	0.114	0.672
mGluR2/3	Asn	0.15	0.342
mGluR2/3	CAMKII	-0.1	0.339
mGluR2/3	D-Asp	-0.157	0.12
mGluR2/3	D-Ser	0	1
mGluR2/3	DA	0.066	1
mGluR2/3	DOPAC	0.058	1
mGluR2/3	GAD65	0	1
mGluR2/3	GAD67	0.121	0.06
mGluR2/3	GLAST	-0.049	1
mGluR2/3	GLT-1	0.059	1
mGluR2/3	GluA1	-0.101	0.279
mGluR2/3	GluA2/3	0	1
mGluR2/3	GluA4	0.228	0.078
mGluR2/3	Gly	0	1
mGluR2/3	Homer1 b/c	0.115	0.117
mGluR2/3	HVA	0.065	1
mGluR2/3	L-Asp	0.088	0.552
mGluR2/3	L-Gln	0.141	0.174
mGluR2/3	L-Glu	-0.013	1
mGluR2/3	L-Ser	0.11	0.516
mGluR2/3	MAO-A	0	1
mGluR2/3	MAO-B	-0.108	0.15
mGluR2/3	mb-COMT	0.16	0.093
mGluR2/3	mGluR1	0.015	1
mGluR2/3	mGluR2/3	0	1
mGluR2/3	mGluR5	-0.112	0.096

mGluR2/3	NE	0.019	1
mGluR2/3	NR1	-0.178	0.309
mGluR2/3	NR2A	0	1
mGluR2/3	NR2B	-0.037	1
mGluR2/3	p-CaMKII	-0.112	0.699
mGluR2/3	PSD-9595	0.118	1
mGluR2/3	s-COMT	0.031	1
mGluR2/3	Synapsin I	0	1
mGluR2/3	VGLUT 1	0.135	1
mGluR2/3	VGLUT 2	-0.057	1
mGluR5	5-HIAA	0	1
mGluR5	5-HT	-0.105	0.204
mGluR5	Asn	-0.151	0.324
mGluR5	CAMKII	0.035	1
mGluR5	D-Asp	0.074	0.693
mGluR5	D-Ser	0.075	0.624
mGluR5	DA	-0.08	1
mGluR5	DOPAC	0	1
mGluR5	GAD65	0.178	0.897
mGluR5	GAD67	0.271	0.054
mGluR5	GLAST	0.153	0.012
mGluR5	GLT-1	-0.2	0.123
mGluR5	GluA1	-0.142	0.795
mGluR5	GluA2/3	-0.028	1
mGluR5	GluA4	-0.12	0.081
mGluR5	Gly	0	1
mGluR5	Homer1 b/c	0.052	1
mGluR5	HVA	0.124	0.336
mGluR5	L-Asp	-0.013	1
mGluR5	L-Gln	-0.117	0.867
mGluR5	L-Glu	0	1
mGluR5	L-Ser	0.215	0.039
mGluR5	MAO-A	-0.158	0.039
mGluR5	MAO-B	0.035	0.723
mGluR5	mb-COMT	0.122	0.147
mGluR5	mGluR1	0.115	0.102
mGluR5	mGluR2/3	-0.112	0.096
mGluR5	mGluR5	0	1
mGluR5	NE	-0.175	0.129
mGluR5	NR1	0.131	0.132
mGluR5	NR2A	-0.172	1
mGluR5	NR2B	-0.065	1
mGluR5	p-CaMKII	0	1
mGluR5	PSD-9595	-0.266	0.057
mGluR5	s-COMT	0	1
mGluR5	Synapsin I	0.101	0.411
mGluR5	VGLUT 1	0.016	1
mGluR5	VGLUT 2	0.211	0.327
NE	5-HIAA	-0.138	0.174
NE	5-HT	0.105	0.162
NE	Asn	0	1
NE	CAMKII	0.097	0.381
NE	D-Asp	-0.007	1
NE	D-Ser	0.011	1
NE	DA	-0.364	0.027
NE	DOPAC	-0.104	0.591
NE	GAD65	0.134	0.288
NE	GAD67	-0.087	0.273
NE	GLAST	-0.157	0.354
NE	GLT-1	0.118	0.273
NE	GluA1	0	1
NE	GluA2/3	0.115	0.345
NE	GluA4	0	1
NE	Gly	0	1
NE	Homer1 b/c	-0.006	1
NE	HVA	0.081	0.177
NE	L-Asp	0	1
NE	L-Gln	0.136	0.156
NE	L-Glu	0	1
NE	L-Ser	-0.125	0.399
NE	MAO-A	-0.022	1
NE	MAO-B	0.162	0.216
NE	mb-COMT	-0.153	0.099
NE	mGluR1	-0.139	0.081

NE	mGluR2/3	0.019	1
NE	mGluR5	-0.175	0.129
NE	NE	0	1
NE	NR1	0.006	1
NE	NR2A	-0.131	0.192
NE	NR2B	0.181	0.156
NE	p-CaMKII	0.165	0.096
NE	PSD-9595	-0.166	0.219
NE	s-COMT	0.004	1
NE	Synapsin I	-0.132	0.408
NE	VGLUT 1	0	1
NE	VGLUT 2	0.094	0.675
NR1	5-HIAA	-0.135	0.3
NR1	5-HT	-0.115	0.432
NR1	Asn	0.012	1
NR1	CAMKII	-0.131	0.528
NR1	D-Asp	0	1
NR1	D-Ser	-0.054	1
NR1	DA	0	1
NR1	DOPAC	0	1
NR1	GAD65	-0.022	1
NR1	GAD67	0.106	1
NR1	GLAST	-0.123	0.057
NR1	GLT-1	-0.017	1
NR1	GluA1	0	1
NR1	GluA2/3	-0.011	1
NR1	GluA4	-0.128	0.102
NR1	Gly	0.016	1
NR1	Homer1 b/c	0	1
NR1	HVA	0.135	0.36
NR1	L-Asp	0.033	1
NR1	L-Gln	0.001	1
NR1	L-Glu	-0.037	1
NR1	L-Ser	-0.133	0.261
NR1	MAO-A	0.009	1
NR1	MAO-B	0	1
NR1	mb-COMT	0	1
NR1	mGluR1	0.161	0.111

NR1	mGluR2/3	-0.178	0.309
NR1	mGluR5	0.131	0.132
NR1	NE	0.006	1
NR1	NR1	0	1
NR1	NR2A	0.061	1
NR1	NR2B	0.265	0.297
NR1	p-CaMKII	-0.084	0.48
NR1	PSD-9595	0.165	0.234
NR1	s-COMT	0	1
NR1	Synapsin I	0	1
NR1	VGLUT 1	0	1
NR1	VGLUT 2	0.098	1
NR2A	5-HIAA	0	1
NR2A	5-HT	0	1
NR2A	Asn	0	1
NR2A	CAMKII	0	1
NR2A	D-Asp	-0.128	0.51
NR2A	D-Ser	0.057	1
NR2A	DA	-0.199	0.009
NR2A	DOPAC	0.007	1
NR2A	GAD65	0.187	0.252
NR2A	GAD67	0.106	0.996
NR2A	GLAST	0	1
NR2A	GLT-1	0	1
NR2A	GluA1	0.131	1
NR2A	GluA2/3	-0.018	1
NR2A	GluA4	-0.157	0.111
NR2A	Gly	0.16	0.162
NR2A	Homer1 b/c	0.152	0.723
NR2A	HVA	0	1
NR2A	L-Asp	-0.099	0.9
NR2A	L-Gln	0	1
NR2A	L-Glu	0.117	0.021
NR2A	L-Ser	-0.158	0.582
NR2A	MAO-A	-0.01	1
NR2A	MAO-B	0	1
NR2A	mb-COMT	-0.165	0.033
NR2A	mGluR1	0	1

NR2A	mGluR2/3	0	1
NR2A	mGluR5	-0.172	1
NR2A	NE	-0.131	0.192
NR2A	NR1	0.061	1
NR2A	NR2A	0	1
NR2A	NR2B	-0.082	1
NR2A	p-CaMKII	0	1
NR2A	PSD-9595	-0.109	0.198
NR2A	s-COMT	0.115	0.177
NR2A	Synapsin I	0.143	0.198
NR2A	VGLUT 1	-0.146	0.087
NR2A	VGLUT 2	0.123	0.429
NR2B	5-HIAA	0	1
NR2B	5-HT	-0.112	0.861
NR2B	Asn	-0.041	1
NR2B	CAMKII	-0.023	1
NR2B	D-Asp	0	1
NR2B	D-Ser	-0.148	0.504
NR2B	DA	0	1
NR2B	DOPAC	-0.122	0.144
NR2B	GAD65	0.02	1
NR2B	GAD67	-0.015	1
NR2B	GLAST	0	1
NR2B	GLT-1	-0.054	1
NR2B	GluA1	-0.025	1
NR2B	GluA2/3	0.096	1
NR2B	GluA4	-0.216	0.477
NR2B	Gly	0.143	0.225
NR2B	Homer1 b/c	0	1
NR2B	HVA	0	1
NR2B	L-Asp	-0.135	0.186
NR2B	L-Gln	0.149	0.597
NR2B	L-Glu	0	1
NR2B	L-Ser	0.114	0.42
NR2B	MAO-A	-0.241	0.102
NR2B	MAO-B	0.159	0.12
NR2B	mb-COMT	-0.149	0.528
NR2B	mGluR1	-0.136	0.072

NR2B	mGluR2/3	-0.037	1
NR2B	mGluR5	-0.065	1
NR2B	NE	0.181	0.156
NR2B	NR1	0.265	0.297
NR2B	NR2A	-0.082	1
NR2B	NR2B	0	1
NR2B	p-CaMKII	0.079	1
NR2B	PSD-9595	0.086	1
NR2B	s-COMT	-0.029	1
NR2B	Synapsin I	-0.103	0.669
NR2B	VGLUT 1	-0.179	0.147
NR2B	VGLUT 2	0.03	1
p-CaMKII	5-HIAA	0	1
p-CaMKII	5-HT	0.116	0.267
p-CaMKII	Asn	-0.145	0.324
p-CaMKII	CAMKII	-0.088	1
p-CaMKII	D-Asp	-0.166	0.075
p-CaMKII	D-Ser	0.126	0.171
p-CaMKII	DA	-0.031	1
p-CaMKII	DOPAC	0.173	0.048
p-CaMKII	GAD65	-0.056	1
p-CaMKII	GAD67	-0.133	0.705
p-CaMKII	GLAST	0.028	1
p-CaMKII	GLT-1	-0.219	0.006
p-CaMKII	GluA1	0	1
p-CaMKII	GluA2/3	0.147	0.048
p-CaMKII	GluA4	-0.115	0.237
p-CaMKII	Gly	-0.122	0.495

p-CaMKII	Homer1 b/c	0.058	1
p-CaMKII	HVA	0	1
p-CaMKII	L-Asp	-0.14	0.516
p-CaMKII	L-Gln	0	1
p-CaMKII	L-Glu	0	1
p-CaMKII	L-Ser	0.135	0.108
p-CaMKII	MAO-A	0.206	0.054
p-CaMKII	MAO-B	0.117	0.363
p-CaMKII	mb-COMT	0.062	0.948
p-CaMKII	mGluR1	0.01	1
p-CaMKII	mGluR2/3	-0.112	0.699
p-CaMKII	mGluR5	0	1
p-CaMKII	NE	0.165	0.096
p-CaMKII	NR1	-0.084	0.48
p-CaMKII	NR2A	0	1
p-CaMKII	NR2B	0.079	1
p-CaMKII	p-CaMKII	0	1
p-CaMKII	PSD-9595	0	1
p-CaMKII	s-COMT	0.008	1
p-CaMKII	Synapsin I	-0.049	1
p-CaMKII	VGLUT 1	0.024	1
p-CaMKII	VGLUT 2	0	1
PSD-9595	5-HIAA	0.106	0.222
PSD-9595	5-HT	0.058	0.54
PSD-9595	Asn	0.071	1
PSD-9595	CAMKII	0.152	0.6
PSD-9595	D-Asp	0.011	1
PSD-9595	D-Ser	0.013	1
PSD-9595	DA	0	1
PSD-9595	DOPAC	0.097	0.186
PSD-9595	GAD65	0	1
PSD-9595	GAD67	0.02	1
PSD-9595	GLAST	0.016	1
PSD-9595	GLT-1	0.188	0.684
PSD-9595	GluA1	-0.138	0.177
PSD-9595	GluA2/3	0.149	0.051
PSD-9595	GluA4	0.182	0.114
PSD-9595	Gly	0.317	0.042
PSD-9595	Homer1 b/c	0	1
PSD-9595	HVA	0.044	1
PSD-9595	L-Asp	-0.052	1
PSD-9595	L-Gln	0.034	0.855
PSD-9595	L-Glu	-0.151	0.21
PSD-9595	L-Ser	0.122	1
PSD-9595	MAO-A	0	1
PSD-9595	MAO-B	-0.127	0.291
PSD-9595	mb-COMT	-0.168	0.519
PSD-9595	mGluR1	0.221	0.885
PSD-9595	mGluR2/3	0.118	1
PSD-9595	mGluR5	-0.266	0.057
PSD-9595	NE	-0.166	0.219
PSD-9595	NR1	0.165	0.234

PSD-9595	NR2A	-0.109	0.198
PSD-9595	NR2B	0.086	1
PSD-9595	p-CaMKII	0	1
PSD-9595	PSD-9595	0	1
PSD-9595	s-COMT	-0.152	0.396
PSD-9595	Synapsin I	0	1
PSD-9595	VGLUT 1	0.202	0.504
PSD-9595	VGLUT 2	0.196	0.096
s-COMT	5-HIAA	0	1
s-COMT	5-HT	0.117	0.246
s-COMT	Asn	0	1
s-COMT	CAMKII	0.146	0.381
s-COMT	D-Asp	0.023	1
s-COMT	D-Ser	0.166	0.144
s-COMT	DA	0.123	0.174
s-COMT	DOPAC	0.019	1
s-COMT	GAD65	0.119	0.315
s-COMT	GAD67	0	1
s-COMT	GLAST	0.047	1
s-COMT	GLT-1	-0.127	0.462
s-COMT	GluA1	0	1
s-COMT	GluA2/3	-0.124	0.393
s-COMT	GluA4	0	1
s-COMT	Gly	0	1
s-COMT	Homer1 b/c	0	1
s-COMT	HVA	-0.105	0.396
s-COMT	L-Asp	-0.131	0.477
s-COMT	L-Gln	0.094	0.378
s-COMT	L-Glu	0.106	0.111
s-COMT	L-Ser	-0.117	0.429
s-COMT	MAO-A	-0.136	0.105
s-COMT	MAO-B	0	1
s-COMT	mb-COMT	0.01	1
s-COMT	mGluR1	0	1
s-COMT	mGluR2/3	0.031	1
s-COMT	mGluR5	0	1
s-COMT	NE	0.004	1
s-COMT	NR1	0	1
s-COMT	NR2A	0.115	0.177
s-COMT	NR2B	-0.029	1
s-COMT	p-CaMKII	0.008	1
s-COMT	PSD-9595	-0.152	0.396
s-COMT	s-COMT	0	1
s-COMT	Synapsin I	0.071	1
s-COMT	VGLUT 1	-0.107	0.306
s-COMT	VGLUT 2	0.141	0.348
Synapsin I	5-HIAA	0	1
Synapsin I	5-HT	0.164	0.177
Synapsin I	Asn	0.119	0.408
Synapsin I	CAMKII	-0.006	1
Synapsin I	D-Asp	-0.013	1
Synapsin I	D-Ser	0.04	1
Synapsin I	DA	0.133	0.165
Synapsin I	DOPAC	0	1
Synapsin I	GAD65	-0.131	0.381
Synapsin I	GAD67	0	1
Synapsin I	GLAST	-0.207	0.066
Synapsin I	GLT-1	0.119	0.747
Synapsin I	GluA1	0	1
Synapsin I	GluA2/3	0	1
Synapsin I	GluA4	0.011	1
Synapsin I	Gly	-0.143	0.075
Synapsin I	Homer1 b/c	0.107	0.618
Synapsin I	HVA	0	1

Synapsin I	L-Asp	-0.017	1
Synapsin I	L-Gln	0.018	1
Synapsin I	L-Glu	0.133	0.111
Synapsin I	L-Ser	0	1
Synapsin I	MAO-A	0.131	0.093
Synapsin I	MAO-B	0.122	0.189
Synapsin I	mb-COMT	0.115	0.156
Synapsin I	mGluR1	-0.149	0.06
Synapsin I	mGluR2/3	0	1
Synapsin I	mGluR5	0.101	0.411
Synapsin I	NE	-0.132	0.408
Synapsin I	NR1	0	1
Synapsin I	NR2A	0.143	0.198
Synapsin I	NR2B	-0.103	0.669
Synapsin I	p-CaMKII	-0.049	1
Synapsin I	PSD-9595	0	1
Synapsin I	s-COMT	0.071	1
Synapsin I	Synapsin I	0	1
Synapsin I	VGLUT1	-0.152	0.132
Synapsin I	VGLUT2	0.174	0.048
VGLUT1	5-HIAA	-0.088	0.189
VGLUT1	5-HT	-0.099	0.246
VGLUT1	Asn	-0.107	0.552
VGLUT1	CAMKII	0.206	0.054
VGLUT1	D-Asp	0	1
VGLUT1	D-Ser	0	1

VGLUT1	DA	-0.072	0.411
VGLUT1	DOPAC	-0.079	0.291
VGLUT1	GAD65	-0.217	0.081
VGLUT1	GAD67	0.16	0.216
VGLUT1	GLAST	-0.124	1
VGLUT1	GLT-1	-0.131	0.303
VGLUT1	GluA1	-0.108	0.417
VGLUT1	GluA2/3	-0.142	0.465
VGLUT1	GluA4	0.129	0.672
VGLUT1	Gly	-0.111	0.057
VGLUT1	Homer1 b/c	0	1
VGLUT1	HVA	-0.03	1
VGLUT1	L-Asp	0	1
VGLUT1	L-Gln	-0.108	0.702
VGLUT1	L-Glu	-0.108	0.126
VGLUT1	L-Ser	0.031	1
VGLUT1	MAO-A	-0.094	0.414
VGLUT1	MAO-B	0	1
VGLUT1	mb-COMT	0.131	0.399
VGLUT1	mGluR1	-0.077	1
VGLUT1	mGluR2/3	0.135	1
VGLUT1	mGluR5	0.016	1
VGLUT1	NE	0	1
VGLUT1	NR1	0	1
VGLUT1	NR2A	-0.146	0.087
VGLUT1	NR2B	-0.179	0.147

VGLUT 1	p-CaMKII	0.024	1
VGLUT 1	PSD-9595	0.202	0.504
VGLUT 1	s-COMT	-0.107	0.306
VGLUT 1	Synapsin I	-0.152	0.132
VGLUT 1	VGLUT 1	0	1
VGLUT 1	VGLUT 2	-0.117	0.042
VGLUT 2	5-HIAA	0	1
VGLUT 2	5-HT	0.192	0.279
VGLUT 2	Asn	-0.079	1
VGLUT 2	CAMKII	-0.183	0.177
VGLUT 2	D-Asp	-0.131	0.183
VGLUT 2	D-Ser	0	1
VGLUT 2	DA	0	1
VGLUT 2	DOPAC	0.012	1
VGLUT 2	GAD65	-0.033	1
VGLUT 2	GAD67	0.193	0.426
VGLUT 2	GLAST	-0.111	0.36
VGLUT 2	GLT-1	-0.154	0.111
VGLUT 2	GluA1	0.134	0.327
VGLUT 2	GluA2/3	0.045	1
VGLUT 2	GluA4	-0.196	0.057
VGLUT 2	Gly	0.052	1

VGLUT 2	Homer1 b/c	0	1
VGLUT 2	HVA	-0.142	0.195
VGLUT 2	L-Asp	-0.107	0.426
VGLUT 2	L-Gln	0	1
VGLUT 2	L-Glu	0.052	1
VGLUT 2	L-Ser	0	1
VGLUT 2	MAO-A	-0.004	1
VGLUT 2	MAO-B	-0.128	0.177
VGLUT 2	mb-COMT	-0.029	1
VGLUT 2	mGluR1	-0.108	0.813
VGLUT 2	mGluR2 /3	-0.057	1
VGLUT 2	mGluR5	0.211	0.327
VGLUT 2	NE	0.094	0.675
VGLUT 2	NR1	0.098	1
VGLUT 2	NR2A	0.123	0.429
VGLUT 2	NR2B	0.03	1
VGLUT 2	p-CaMKII	0	1
VGLUT 2	PSD-9595	0.196	0.096
VGLUT 2	s-COMT	0.141	0.348
VGLUT 2	Synapsin I	0.174	0.048
VGLUT 2	VGLUT 1	-0.117	0.042
VGLUT 2	VGLUT 2	0	1

6.4 Comparison of pairwise edge weights in the hippocampus

mol1	mol2	difference	Adj p-value
5-HIAA	5-HIAA	0	1
5-HIAA	5-HT	0.332	0.076
5-HIAA	Asn	-0.022	1
5-HIAA	CAMKII	-0.138	0.244
5-HIAA	D-Asp	0	1
5-HIAA	D-Ser	-0.158	0.664
5-HIAA	DA	-0.025	1
5-HIAA	DOPAC	0.092	0.444
5-HIAA	GAD65	0.134	0.188
5-HIAA	GAD67	-0.169	0.172
5-HIAA	GLAST	-0.126	0.652
5-HIAA	GLT-1	-0.134	0.44
5-HIAA	GluA1	-0.133	0.028
5-HIAA	GluA2/3	-0.143	0.684
5-HIAA	GluA4	-0.146	0.084
5-HIAA	Gly	0	1
5-HIAA	Homer1 b/c	0.002	1
5-HIAA	HVA	0.018	1
5-HIAA	L-Asp	-0.024	1
5-HIAA	L-Gln	0	1
5-HIAA	L-Glu	-0.139	0.152
5-HIAA	L-Ser	-0.152	0.888
5-HIAA	MAO-A	-0.032	1
5-HIAA	MAO-B	0.062	1
5-HIAA	mb-COMT	0	1
5-HIAA	mGluR1	0	1
5-HIAA	mGluR2/3	0	1
5-HIAA	mGluR5	-0.113	0.488
5-HIAA	NE	-0.147	0.188
5-HIAA	NR1	-0.019	1
5-HIAA	NR2A	-0.265	0.36
5-HIAA	NR2B	-0.107	0.96
5-HIAA	p-CaMKII	-0.133	1
5-HIAA	PSD-9595	-0.126	0.288
5-HIAA	s-COMT	-0.147	0.34
5-HIAA	Synapsin I	-0.017	1
5-HIAA	VGLUT1	0	1
5-HIAA	VGLUT2	-0.152	0.056
5-HT	5-HIAA	0.332	0.076
5-HT	5-HT	0	1
5-HT	Asn	0	1
5-HT	CAMKII	-0.138	0.572
5-HT	D-Asp	0	1
5-HT	D-Ser	0	1
5-HT	DA	0.003	1
5-HT	DOPAC	0.118	0.14
5-HT	GAD65	0.025	1
5-HT	GAD67	-0.163	0.632
5-HT	GLAST	-0.038	1
5-HT	GLT-1	0	1
5-HT	GluA1	0	1
5-HT	GluA2/3	0.131	0.216
5-HT	GluA4	-0.165	0.252
5-HT	Gly	0	1
5-HT	Homer1 b/c	-0.223	0.136
5-HT	HVA	0	1
5-HT	L-Asp	0.132	0.704
5-HT	L-Gln	-0.025	1
5-HT	L-Glu	0.138	0.42
5-HT	L-Ser	0	1
5-HT	MAO-A	0.008	1
5-HT	MAO-B	0.005	1
5-HT	mb-COMT	-0.044	1
5-HT	mGluR1	-0.002	1
5-HT	mGluR2/3	-0.136	0.092
5-HT	mGluR5	0.16	0.4
5-HT	NE	0.011	1
5-HT	NR1	0.105	0.952
5-HT	NR2A	-0.055	1
5-HT	NR2B	-0.019	1
5-HT	p-CaMKII	0	1
5-HT	PSD-9595	0	1
5-HT	s-COMT	-0.14	0.328
5-HT	Synapsin I	0	1

5-HT	VGLUT 1	-0.158	0.332
5-HT	VGLUT 2	0	1
Asn	5-HIAA	-0.022	1
Asn	5-HT	0	1
Asn	Asn	0	1
Asn	CAMKII	-0.088	1
Asn	D-Asp	0.041	1
Asn	D-Ser	0	1
Asn	DA	-0.122	0.896
Asn	DOPAC	0	1
Asn	GAD65	0.184	0.06
Asn	GAD67	0	1
Asn	GLAST	0.175	0.288
Asn	GLT-1	-0.149	0.276
Asn	GluA1	0	1
Asn	GluA2/3	-0.052	1
Asn	GluA4	0.015	1
Asn	Gly	-0.062	1
Asn	Homer1 b/c	-0.113	0.772
Asn	HVA	-0.233	0.228
Asn	L-Asp	0.085	1
Asn	L-Gln	-0.053	1
Asn	L-Glu	0.156	1
Asn	L-Ser	0	1
Asn	MAO-A	0.145	0.152
Asn	MAO-B	-0.129	1
Asn	mb-COMT	0.137	0.3
Asn	mGluR1	0	1
Asn	mGluR2/3	0.076	1
Asn	mGluR5	0.138	0.264
Asn	NE	0	1
Asn	NR1	0.003	1
Asn	NR2A	0.133	0.532
Asn	NR2B	0.097	0.516
Asn	p-CaMKII	0	1
Asn	PSD-9595	0	1
Asn	s-COMT	0.197	0.468
Asn	Synapsin I	0	1

Asn	VGLUT 1	0.075	1
Asn	VGLUT 2	-0.11	0.236
CAMKII	5-HIAA	-0.138	0.244
CAMKII	5-HT	-0.138	0.572
CAMKII	Asn	-0.088	1
CAMKII	CAMKII	0	1
CAMKII	D-Asp	0.101	0.24
CAMKII	D-Ser	-0.153	0.112
CAMKII	DA	-0.1	1
CAMKII	DOPAC	-0.102	0.54
CAMKII	GAD65	-0.105	0.492
CAMKII	GAD67	0.083	1
CAMKII	GLAST	-0.019	1
CAMKII	GLT-1	-0.133	0.228
CAMKII	GluA1	0	1
CAMKII	GluA2/3	-0.038	1
CAMKII	GluA4	0	1
CAMKII	Gly	-0.188	0.04
CAMKII	Homer1 b/c	0	1
CAMKII	HVA	-0.133	0.404
CAMKII	L-Asp	0	1
CAMKII	L-Gln	-0.202	0.144
CAMKII	L-Glu	-0.173	0.216
CAMKII	L-Ser	0	1
CAMKII	MAO-A	0	1
CAMKII	MAO-B	-0.03	1
CAMKII	mb-COMT	-0.027	1
CAMKII	mGluR1	-0.148	0.08
CAMKII	mGluR2/3	-0.117	0.808
CAMKII	mGluR5	-0.092	0.332
CAMKII	NE	-0.113	0.384
CAMKII	NR1	0	1
CAMKII	NR2A	-0.137	0.136
CAMKII	NR2B	0	1
CAMKII	p-CaMKII	-0.102	0.376
CAMKII	PSD-9595	-0.117	0.256
CAMKII	s-COMT	0.029	1
CAMKII	Synapsin I	-0.08	1

CAMKII	VGLUT 1	-0.106	0.708
CAMKII	VGLUT 2	0.086	0.836
D-Asp	5-HIAA	0	1
D-Asp	5-HT	0	1
D-Asp	Asn	0.041	1
D-Asp	CAMKII	0.101	0.24
D-Asp	D-Asp	0	1
D-Asp	D-Ser	-0.275	0.26
D-Asp	DA	0.099	0.548
D-Asp	DOPAC	0	1
D-Asp	GAD65	0.174	0.204
D-Asp	GAD67	0	1
D-Asp	GLAST	-0.016	1
D-Asp	GLT-1	0.129	0.492
D-Asp	GluA1	0.125	0.032
D-Asp	GluA2/3	-0.097	1
D-Asp	GluA4	-0.127	0.292
D-Asp	Gly	0.115	0.124
D-Asp	Homer1 b/c	-0.024	1
D-Asp	HVA	-0.097	0.348
D-Asp	L-Asp	0	1
D-Asp	L-Gln	0.006	1
D-Asp	L-Glu	-0.031	1
D-Asp	L-Ser	-0.146	0.132
D-Asp	MAO-A	0.149	0.408
D-Asp	MAO-B	-0.062	1
D-Asp	mb-COMT	-0.011	1
D-Asp	mGluR1	0.09	0.296
D-Asp	mGluR2 /3	0	1
D-Asp	mGluR5	-0.125	0.52
D-Asp	NE	-0.13	0.124
D-Asp	NR1	-0.061	1
D-Asp	NR2A	0	1
D-Asp	NR2B	-0.113	0.332
D-Asp	p-CaMKII	0.164	0.592
D-Asp	PSD-9595	0.141	0.632
D-Asp	s-COMT	-0.156	0.244
D-Asp	Synapsin I	0.002	1

D-Asp	VGLUT 1	0.076	1
D-Asp	VGLUT 2	-0.121	0.748
D-Ser	5-HIAA	-0.158	0.664
D-Ser	5-HT	0	1
D-Ser	Asn	0	1
D-Ser	CAMKII	-0.153	0.112
D-Ser	D-Asp	-0.275	0.26
D-Ser	D-Ser	0	1
D-Ser	DA	0	1
D-Ser	DOPAC	0	1
D-Ser	GAD65	0	1
D-Ser	GAD67	0	1
D-Ser	GLAST	0.007	1
D-Ser	GLT-1	0.021	1
D-Ser	GluA1	-0.088	1
D-Ser	GluA2/3	-0.14	0.428
D-Ser	GluA4	0.116	0.136
D-Ser	Gly	0	1
D-Ser	Homer1 b/c	0.122	0.096
D-Ser	HVA	-0.184	0.108
D-Ser	L-Asp	0.12	0.192
D-Ser	L-Gln	0	1
D-Ser	L-Glu	-0.117	0.604
D-Ser	L-Ser	0.244	0.08
D-Ser	MAO-A	0	1
D-Ser	MAO-B	-0.188	0.148
D-Ser	mb-COMT	0.096	0.376
D-Ser	mGluR1	-0.213	0.068
D-Ser	mGluR2 /3	0.015	1
D-Ser	mGluR5	0.027	1
D-Ser	NE	0.02	1
D-Ser	NR1	0.03	1
D-Ser	NR2A	0.07	1
D-Ser	NR2B	0.152	0.064
D-Ser	p-CaMKII	-0.148	0.344
D-Ser	PSD-9595	0	1
D-Ser	s-COMT	0	1
D-Ser	Synapsin I	-0.131	0.224

D-Ser	VGLUT 1	0	1
D-Ser	VGLUT 2	-0.008	1
DA	5-HIAA	-0.025	1
DA	5-HT	0.003	1
DA	Asn	-0.122	0.896
DA	CAMKII	-0.1	1
DA	D-Asp	0.099	0.548
DA	D-Ser	0	1
DA	DA	0	1
DA	DOPAC	-0.102	0.164
DA	GAD65	0	1
DA	GAD67	0.022	1
DA	GLAST	-0.123	0.044
DA	GLT-1	-0.1	0.464
DA	GluA1	0	1
DA	GluA2/3	-0.092	0.632
DA	GluA4	0.065	0.968
DA	Gly	-0.134	0.248
DA	Homer1 b/c	0.094	0.564
DA	HVA	-0.149	0.544
DA	L-Asp	-0.115	0.144
DA	L-Gln	-0.133	0.32
DA	L-Glu	-0.115	0.54
DA	L-Ser	0	1
DA	MAO-A	0	1
DA	MAO-B	-0.126	0.612
DA	mb-COMT	-0.018	1
DA	mGluR1	0.019	1
DA	mGluR2/3	0.032	1
DA	mGluR5	0.094	0.808
DA	NE	-0.062	1
DA	NR1	0	1
DA	NR2A	-0.002	1
DA	NR2B	0	1
DA	p-CaMKII	0.004	1
DA	PSD-9595	0	1
DA	s-COMT	0	1
DA	Synapsin I	-0.131	0.136

DA	VGLUT 1	-0.09	0.292
DA	VGLUT 2	0	1
DOPAC	5-HIAA	0.092	0.444
DOPAC	5-HT	0.118	0.14
DOPAC	Asn	0	1
DOPAC	CAMKII	-0.102	0.54
DOPAC	D-Asp	0	1
DOPAC	D-Ser	0	1
DOPAC	DA	-0.102	0.164
DOPAC	DOPAC	0	1
DOPAC	GAD65	-0.198	0.076
DOPAC	GAD67	-0.109	0.14
DOPAC	GLAST	-0.117	0.072
DOPAC	GLT-1	0	1
DOPAC	GluA1	0	1
DOPAC	GluA2/3	-0.077	1
DOPAC	GluA4	-0.009	1
DOPAC	Gly	0	1
DOPAC	Homer1 b/c	0	1
DOPAC	HVA	0.024	1
DOPAC	L-Asp	-0.024	1
DOPAC	L-Gln	0	1
DOPAC	L-Glu	-0.081	0.62
DOPAC	L-Ser	-0.127	0.54
DOPAC	MAO-A	-0.125	0.324
DOPAC	MAO-B	-0.085	0.296
DOPAC	mb-COMT	-0.097	0.104
DOPAC	mGluR1	0.11	0.364
DOPAC	mGluR2/3	0	1
DOPAC	mGluR5	-0.116	0.516
DOPAC	NE	-0.111	0.324
DOPAC	NR1	0	1
DOPAC	NR2A	-0.108	0.54
DOPAC	NR2B	0	1
DOPAC	p-CaMKII	0	1
DOPAC	PSD-9595	0.12	0.136
DOPAC	s-COMT	0	1
DOPAC	Synapsin I	-0.149	0.148

DOPAC	VGLUT 1	-0.15	0.12
DOPAC	VGLUT 2	0.007	1
GAD65	5-HIAA	0.134	0.188
GAD65	5-HT	0.025	1
GAD65	Asn	0.184	0.06
GAD65	CAMKII	-0.105	0.492
GAD65	D-Asp	0.174	0.204
GAD65	D-Ser	0	1
GAD65	DA	0	1
GAD65	DOPAC	-0.198	0.076
GAD65	GAD65	0	1
GAD65	GAD67	0	1
GAD65	GLAST	0	1
GAD65	GLT-1	-0.005	1
GAD65	GluA1	0	1
GAD65	GluA2/3	0.103	0.544
GAD65	GluA4	0	1
GAD65	Gly	0.14	0.36
GAD65	Homer1 b/c	0.092	1
GAD65	HVA	0	1
GAD65	L-Asp	-0.125	0.388
GAD65	L-Gln	0	1
GAD65	L-Glu	0	1
GAD65	L-Ser	0.126	0.192
GAD65	MAO-A	0.117	0.292
GAD65	MAO-B	-0.107	0.26
GAD65	mb-COMT	0	1
GAD65	mGluR1	-0.139	0.304
GAD65	mGluR2/3	0	1
GAD65	mGluR5	0.001	1
GAD65	NE	0.112	0.62
GAD65	NR1	-0.091	1
GAD65	NR2A	0.163	0.228
GAD65	NR2B	0.113	0.372
GAD65	p-CaMKII	0.118	0.252
GAD65	PSD-9595	0.208	0.256
GAD65	s-COMT	-0.009	1
GAD65	Synapsin I	-0.123	0.292

GAD65	VGLUT 1	0.132	0.048
GAD65	VGLUT 2	-0.13	1
GAD67	5-HIAA	-0.169	0.172
GAD67	5-HT	-0.163	0.632
GAD67	Asn	0	1
GAD67	CAMKII	0.083	1
GAD67	D-Asp	0	1
GAD67	D-Ser	0	1
GAD67	DA	0.022	1
GAD67	DOPAC	-0.109	0.14
GAD67	GAD65	0	1
GAD67	GAD67	0	1
GAD67	GLAST	0.003	1
GAD67	GLT-1	-0.037	1
GAD67	GluA1	-0.123	0.376
GAD67	GluA2/3	0.031	1
GAD67	GluA4	0	1
GAD67	Gly	-0.181	0.344
GAD67	Homer1 b/c	0.012	1
GAD67	HVA	-0.15	0.272
GAD67	L-Asp	0.119	0.16
GAD67	L-Gln	-0.098	0.648
GAD67	L-Glu	0.103	0.828
GAD67	L-Ser	0.118	0.996
GAD67	MAO-A	-0.108	0.484
GAD67	MAO-B	0	1
GAD67	mb-COMT	-0.116	1
GAD67	mGluR1	0.036	1
GAD67	mGluR2/3	0.093	1
GAD67	mGluR5	-0.081	0.484
GAD67	NE	0.097	0.572
GAD67	NR1	-0.134	0.524
GAD67	NR2A	-0.078	0.54
GAD67	NR2B	-0.047	1
GAD67	p-CaMKII	0.112	0.28
GAD67	PSD-9595	-0.12	0.188
GAD67	s-COMT	-0.04	1
GAD67	Synapsin I	0.127	0.288

GAD67	VGLUT 1	0	1
GAD67	VGLUT 2	0	1
GLAST	5-HIAA	-0.126	0.652
GLAST	5-HT	-0.038	1
GLAST	Asn	0.175	0.288
GLAST	CAMKII	-0.019	1
GLAST	D-Asp	-0.016	1
GLAST	D-Ser	0.007	1
GLAST	DA	-0.123	0.044
GLAST	DOPAC	-0.117	0.072
GLAST	GAD65	0	1
GLAST	GAD67	0.003	1
GLAST	GLAST	0	1
GLAST	GLT-1	0	1
GLAST	GluA1	0.03	1
GLAST	GluA2/3	-0.148	0.428
GLAST	GluA4	-0.063	1
GLAST	Gly	-0.017	1
GLAST	Homer1 b/c	-0.079	1
GLAST	HVA	-0.106	0.688
GLAST	L-Asp	-0.13	0.516
GLAST	L-Gln	0.163	0.088
GLAST	L-Glu	0.128	0.096
GLAST	L-Ser	0.147	0.476
GLAST	MAO-A	0.093	1
GLAST	MAO-B	-0.166	0.084
GLAST	mb-COMT	0.16	0.228
GLAST	mGluR1	0.013	1
GLAST	mGluR2 /3	-0.039	1
GLAST	mGluR5	0.098	0.824
GLAST	NE	0	1
GLAST	NR1	-0.103	0.368
GLAST	NR2A	0	1
GLAST	NR2B	0.059	1
GLAST	p-CaMKII	0.116	0.056
GLAST	PSD-9595	0.022	1
GLAST	s-COMT	-0.02	1
GLAST	Synapsin I	0.044	1

GLAST	VGLUT 1	0.083	1
GLAST	VGLUT 2	0.012	1
GLT-1	5-HIAA	-0.134	0.44
GLT-1	5-HT	0	1
GLT-1	Asn	-0.149	0.276
GLT-1	CAMKII	-0.133	0.228
GLT-1	D-Asp	0.129	0.492
GLT-1	D-Ser	0.021	1
GLT-1	DA	-0.1	0.464
GLT-1	DOPAC	0	1
GLT-1	GAD65	-0.005	1
GLT-1	GAD67	-0.037	1
GLT-1	GLAST	0	1
GLT-1	GLT-1	0	1
GLT-1	GluA1	0.159	0.488
GLT-1	GluA2/3	-0.005	1
GLT-1	GluA4	0.115	0.34
GLT-1	Gly	-0.141	0.104
GLT-1	Homer1 b/c	0.159	0.372
GLT-1	HVA	0.001	1
GLT-1	L-Asp	0.002	1
GLT-1	L-Gln	0	1
GLT-1	L-Glu	-0.071	1
GLT-1	L-Ser	0.129	0.104
GLT-1	MAO-A	0	1
GLT-1	MAO-B	-0.091	0.532
GLT-1	mb-COMT	0.101	0.348
GLT-1	mGluR1	0.148	0.652
GLT-1	mGluR2 /3	0.01	1
GLT-1	mGluR5	0	1
GLT-1	NE	-0.211	0.26
GLT-1	NR1	-0.121	0.5
GLT-1	NR2A	-0.009	1
GLT-1	NR2B	-0.171	0.448
GLT-1	p-CaMKII	-0.167	0.108
GLT-1	PSD-9595	-0.132	1
GLT-1	s-COMT	-0.118	0.808
GLT-1	Synapsin I	0	1

GLT-1	VGLUT 1	-0.003	1
GLT-1	VGLUT 2	0.105	0.784
GluA1	5-HIAA	-0.133	0.028
GluA1	5-HT	0	1
GluA1	Asn	0	1
GluA1	CAMKII	0	1
GluA1	D-Asp	0.125	0.032
GluA1	D-Ser	-0.088	1
GluA1	DA	0	1
GluA1	DOPAC	0	1
GluA1	GAD65	0	1
GluA1	GAD67	-0.123	0.376
GluA1	GLAST	0.03	1
GluA1	GLT-1	0.159	0.488
GluA1	GluA1	0	1
GluA1	GluA2/3	0.034	1
GluA1	GluA4	0.114	0.624
GluA1	Gly	0	1
GluA1	Homer1 b/c	0.117	0.452
GluA1	HVA	0	1
GluA1	L-Asp	0.103	0.412
GluA1	L-Gln	0.167	0.74
GluA1	L-Glu	0.104	0.412
GluA1	L-Ser	-0.134	0.436
GluA1	MAO-A	0.132	0.168
GluA1	MAO-B	0.136	0.516
GluA1	mb-COMT	0.008	1
GluA1	mGluR1	-0.104	0.356
GluA1	mGluR2 /3	0.149	0.264
GluA1	mGluR5	-0.235	0.18
GluA1	NE	0.087	0.672
GluA1	NR1	0	1
GluA1	NR2A	-0.016	1
GluA1	NR2B	-0.116	0.792
GluA1	p-CaMKII	-0.147	0.172
GluA1	PSD-9595	0.008	1
GluA1	s-COMT	-0.105	0.488
GluA1	Synapsin I	-0.092	0.28

GluA1	VGLUT 1	-0.075	0.824
GluA1	VGLUT 2	0.159	0.472
GluA2/3	5-HIAA	-0.143	0.684
GluA2/3	5-HT	0.131	0.216
GluA2/3	Asn	-0.052	1
GluA2/3	CAMKII	-0.038	1
GluA2/3	D-Asp	-0.097	1
GluA2/3	D-Ser	-0.14	0.428
GluA2/3	DA	-0.092	0.632
GluA2/3	DOPAC	-0.077	1
GluA2/3	GAD65	0.103	0.544
GluA2/3	GAD67	0.031	1
GluA2/3	GLAST	-0.148	0.428
GluA2/3	GLT-1	-0.005	1
GluA2/3	GluA1	0.034	1
GluA2/3	GluA2/3	0	1
GluA2/3	GluA4	0.148	0.236
GluA2/3	Gly	0	1
GluA2/3	Homer1 b/c	-0.022	1
GluA2/3	HVA	0.125	0.748
GluA2/3	L-Asp	-0.076	0.988
GluA2/3	L-Gln	0.114	0.292
GluA2/3	L-Glu	0	1
GluA2/3	L-Ser	0.123	0.324
GluA2/3	MAO-A	0.051	1
GluA2/3	MAO-B	0.094	1
GluA2/3	mb-COMT	0	1
GluA2/3	mGluR1	0.138	0.096
GluA2/3	mGluR2 /3	0.103	0.172
GluA2/3	mGluR5	-0.064	1
GluA2/3	NE	0	1
GluA2/3	NR1	0.294	0.36
GluA2/3	NR2A	-0.239	1
GluA2/3	NR2B	-0.09	1
GluA2/3	p-CaMKII	0	1
GluA2/3	PSD-9595	0	1
GluA2/3	s-COMT	-0.166	0.152
GluA2/3	Synapsin I	0	1

GluA2/3	VGLUT 1	-0.038	1
GluA2/3	VGLUT 2	0.101	0.18
GluA4	5-HIAA	-0.146	0.084
GluA4	5-HT	-0.165	0.252
GluA4	Asn	0.015	1
GluA4	CAMKII	0	1
GluA4	D-Asp	-0.127	0.292
GluA4	D-Ser	0.116	0.136
GluA4	DA	0.065	0.968
GluA4	DOPAC	-0.009	1
GluA4	GAD65	0	1
GluA4	GAD67	0	1
GluA4	GLAST	-0.063	1
GluA4	GLT-1	0.115	0.34
GluA4	GluA1	0.114	0.624
GluA4	GluA2/3	0.148	0.236
GluA4	GluA4	0	1
GluA4	Gly	0.101	1
GluA4	Homer1 b/c	0	1
GluA4	HVA	0.106	0.628
GluA4	L-Asp	0.113	0.944
GluA4	L-Gln	0.004	1
GluA4	L-Glu	0	1
GluA4	L-Ser	0.129	1
GluA4	MAO-A	-0.093	0.196
GluA4	MAO-B	0.019	1
GluA4	mb-COMT	0.125	0.636
GluA4	mGluR1	0	1
GluA4	mGluR2 /3	0.095	1
GluA4	mGluR5	0.013	1
GluA4	NE	-0.127	0.232
GluA4	NR1	-0.156	0.136
GluA4	NR2A	0.044	1
GluA4	NR2B	-0.148	0.084
GluA4	p-CaMKII	0.17	0.172
GluA4	PSD-9595	-0.156	0.312
GluA4	s-COMT	0.118	0.388
GluA4	Synapsin I	0.059	1

GluA4	VGLUT 1	0.022	1
GluA4	VGLUT 2	0.196	0
Gly	5-HIAA	0	1
Gly	5-HT	0	1
Gly	Asn	-0.062	1
Gly	CAMKII	-0.188	0.04
Gly	D-Asp	0.115	0.124
Gly	D-Ser	0	1
Gly	DA	-0.134	0.248
Gly	DOPAC	0	1
Gly	GAD65	0.14	0.36
Gly	GAD67	-0.181	0.344
Gly	GLAST	-0.017	1
Gly	GLT-1	-0.141	0.104
Gly	GluA1	0	1
Gly	GluA2/3	0	1
Gly	GluA4	0.101	1
Gly	Gly	0	1
Gly	Homer1 b/c	-0.121	0.596
Gly	HVA	-0.008	1
Gly	L-Asp	-0.086	1
Gly	L-Gln	-0.107	1
Gly	L-Glu	0.064	1
Gly	L-Ser	0.112	0.472
Gly	MAO-A	0.023	1
Gly	MAO-B	-0.073	1
Gly	mb-COMT	0.114	0.328
Gly	mGluR1	0	1
Gly	mGluR2 /3	-0.014	1
Gly	mGluR5	-0.006	1
Gly	NE	-0.107	0.18
Gly	NR1	-0.089	0.648
Gly	NR2A	0.134	0.204
Gly	NR2B	0	1
Gly	p-CaMKII	-0.155	0.4
Gly	PSD-9595	0.121	0.728
Gly	s-COMT	0.155	1
Gly	Synapsin I	-0.12	0.232

Gly	VGLUT 1	0.181	0.088
Gly	VGLUT 2	0.106	0.472
Homer1 b/c	5-HIAA	0.002	1
Homer1 b/c	5-HT	-0.223	0.136
Homer1 b/c	Asn	-0.113	0.772
Homer1 b/c	CAMKII	0	1
Homer1 b/c	D-Asp	-0.024	1
Homer1 b/c	D-Ser	0.122	0.096
Homer1 b/c	DA	0.094	0.564
Homer1 b/c	DOPAC	0	1
Homer1 b/c	GAD65	0.092	1
Homer1 b/c	GAD67	0.012	1
Homer1 b/c	GLAST	-0.079	1
Homer1 b/c	GLT-1	0.159	0.372
Homer1 b/c	GluA1	0.117	0.452
Homer1 b/c	GluA2/3	-0.022	1
Homer1 b/c	GluA4	0	1
Homer1 b/c	Gly	-0.121	0.596
Homer1 b/c	Homer1 b/c	0	1
Homer1 b/c	HVA	-0.049	1
Homer1 b/c	L-Asp	0	1
Homer1 b/c	L-Gln	0.126	0.496
Homer1 b/c	L-Glu	-0.159	0.152
Homer1 b/c	L-Ser	-0.206	0.144
Homer1 b/c	MAO-A	-0.155	0.16
Homer1 b/c	MAO-B	0.134	0.656
Homer1 b/c	mb-COMT	0	1
Homer1 b/c	mGluR1	0.116	0.472
Homer1 b/c	mGluR2/3	-0.008	1
Homer1 b/c	mGluR5	0.142	1
Homer1 b/c	NE	-0.123	0.14
Homer1 b/c	NR1	-0.143	0.036
Homer1 b/c	NR2A	0.047	1
Homer1 b/c	NR2B	-0.012	1
Homer1 b/c	p-CaMKII	-0.046	1
Homer1 b/c	PSD-9595	0.282	0.02
Homer1 b/c	s-COMT	0.016	1
Homer1 b/c	Synapsin I	-0.136	0.288
Homer1 b/c	VGLUT 1	-0.116	0.688
Homer1 b/c	VGLUT 2	0.046	1
HVA	5-HIAA	0.018	1
HVA	5-HT	0	1
HVA	Asn	-0.233	0.228
HVA	CAMKII	-0.133	0.404
HVA	D-Asp	-0.097	0.348
HVA	D-Ser	-0.184	0.108
HVA	DA	-0.149	0.544
HVA	DOPAC	0.024	1
HVA	GAD65	0	1
HVA	GAD67	-0.15	0.272
HVA	GLAST	-0.106	0.688
HVA	GLT-1	0.001	1
HVA	GluA1	0	1
HVA	GluA2/3	0.125	0.748
HVA	GluA4	0.106	0.628
HVA	Gly	-0.008	1
HVA	Homer1 b/c	-0.049	1
HVA	HVA	0	1
HVA	L-Asp	0	1
HVA	L-Gln	0	1

HVA	L-Glu	0.002	1
HVA	L-Ser	-0.051	1
HVA	MAO-A	0.014	1
HVA	MAO-B	0	1
HVA	mb-COMT	0	1
HVA	mGluR1	-0.061	1
HVA	mGluR2/3	-0.026	1
HVA	mGluR5	0	1
HVA	NE	0.062	1
HVA	NR1	0.111	0.36
HVA	NR2A	0	1
HVA	NR2B	0	1
HVA	p-CaMKII	-0.097	0.32
HVA	PSD-9595	-0.131	0.148
HVA	s-COMT	-0.127	0.932
HVA	Synapsin I	-0.085	0.604
HVA	VGLUT 1	-0.171	0.264
HVA	VGLUT 2	0.006	1
L-Asp	5-HIAA	-0.024	1
L-Asp	5-HT	0.132	0.704
L-Asp	Asn	0.085	1
L-Asp	CAMKII	0	1
L-Asp	D-Asp	0	1
L-Asp	D-Ser	0.12	0.192
L-Asp	DA	-0.115	0.144
L-Asp	DOPAC	-0.024	1
L-Asp	GAD65	-0.125	0.388
L-Asp	GAD67	0.119	0.16
L-Asp	GLAST	-0.13	0.516
L-Asp	GLT-1	0.002	1
L-Asp	GluA1	0.103	0.412
L-Asp	GluA2/3	-0.076	0.988
L-Asp	GluA4	0.113	0.944
L-Asp	Gly	-0.086	1
L-Asp	Homer1 b/c	0	1
L-Asp	HVA	0	1
L-Asp	L-Asp	0	1
L-Asp	L-Gln	-0.098	0.6
L-Asp	L-Glu	0.109	0.216
L-Asp	L-Ser	-0.087	1
L-Asp	MAO-A	0.038	1
L-Asp	MAO-B	0	1
L-Asp	mb-COMT	0.094	0.768
L-Asp	mGluR1	0.032	1
L-Asp	mGluR2/3	0	1
L-Asp	mGluR5	0.028	1
L-Asp	NE	0.043	1
L-Asp	NR1	-0.156	0.14
L-Asp	NR2A	0	1
L-Asp	NR2B	0.125	0.424
L-Asp	p-CaMKII	0.016	1
L-Asp	PSD-9595	0	1
L-Asp	s-COMT	0.138	0.428
L-Asp	Synapsin I	-0.043	1
L-Asp	VGLUT 1	0.024	1
L-Asp	VGLUT 2	0	1
L-Gln	5-HIAA	0	1
L-Gln	5-HT	-0.025	1
L-Gln	Asn	-0.053	1
L-Gln	CAMKII	-0.202	0.144
L-Gln	D-Asp	0.006	1
L-Gln	D-Ser	0	1
L-Gln	DA	-0.133	0.32
L-Gln	DOPAC	0	1
L-Gln	GAD65	0	1
L-Gln	GAD67	-0.098	0.648
L-Gln	GLAST	0.163	0.088
L-Gln	GLT-1	0	1
L-Gln	GluA1	0.167	0.74
L-Gln	GluA2/3	0.114	0.292
L-Gln	GluA4	0.004	1
L-Gln	Gly	-0.107	1
L-Gln	Homer1 b/c	0.126	0.496
L-Gln	HVA	0	1
L-Gln	L-Asp	-0.098	0.6
L-Gln	L-Gln	0	1
L-Gln	L-Glu	-0.022	1
L-Gln	L-Ser	-0.007	1

L-Gln	MAO-A	0.145	0.216
L-Gln	MAO-B	0.139	1
L-Gln	mb-COMT	-0.057	1
L-Gln	mGluR1	-0.018	1
L-Gln	mGluR2/3	0.139	0.152
L-Gln	mGluR5	0.111	0.248
L-Gln	NE	0.073	0.508
L-Gln	NR1	0	1
L-Gln	NR2A	-0.124	0.828
L-Gln	NR2B	-0.174	0.176
L-Gln	p-CaMKII	0.044	1
L-Gln	PSD-9595	0.121	0.964
L-Gln	s-COMT	0.068	1
L-Gln	Synapsin I	0	1
L-Gln	VGLUT 1	0.077	0.9
L-Gln	VGLUT 2	0	1
L-Glu	5-HIAA	-0.139	0.152
L-Glu	5-HT	0.138	0.42
L-Glu	Asn	0.156	1
L-Glu	CAMKII	-0.173	0.216
L-Glu	D-Asp	-0.031	1
L-Glu	D-Ser	-0.117	0.604
L-Glu	DA	-0.115	0.54
L-Glu	DOPAC	-0.081	0.62
L-Glu	GAD65	0	1
L-Glu	GAD67	0.103	0.828
L-Glu	GLAST	0.128	0.096
L-Glu	GLT-1	-0.071	1
L-Glu	GluA1	0.104	0.412
L-Glu	GluA2/3	0	1
L-Glu	GluA4	0	1
L-Glu	Gly	0.064	1
L-Glu	Homer1 b/c	-0.159	0.152
L-Glu	HVA	0.002	1
L-Glu	L-Asp	0.109	0.216
L-Glu	L-Gln	-0.022	1
L-Glu	L-Glu	0	1
L-Glu	L-Ser	0.111	0.808
L-Glu	MAO-A	0.144	0.244

L-Glu	MAO-B	-0.232	0.552
L-Glu	mb-COMT	0.009	1
L-Glu	mGluR1	-0.162	0.04
L-Glu	mGluR2/3	-0.056	1
L-Glu	mGluR5	0.003	1
L-Glu	NE	-0.117	0.608
L-Glu	NR1	-0.115	0.652
L-Glu	NR2A	0.134	0.108
L-Glu	NR2B	-0.011	1
L-Glu	p-CaMKII	0	1
L-Glu	PSD-9595	0	1
L-Glu	s-COMT	0.257	0.096
L-Glu	Synapsin I	-0.009	1
L-Glu	VGLUT 1	0.141	0.324
L-Glu	VGLUT 2	0.112	0.64
L-Ser	5-HIAA	-0.152	0.888
L-Ser	5-HT	0	1
L-Ser	Asn	0	1
L-Ser	CAMKII	0	1
L-Ser	D-Asp	-0.146	0.132
L-Ser	D-Ser	0.244	0.08
L-Ser	DA	0	1
L-Ser	DOPAC	-0.127	0.54
L-Ser	GAD65	0.126	0.192
L-Ser	GAD67	0.118	0.996
L-Ser	GLAST	0.147	0.476
L-Ser	GLT-1	0.129	0.104
L-Ser	GluA1	-0.134	0.436
L-Ser	GluA2/3	0.123	0.324
L-Ser	GluA4	0.129	1
L-Ser	Gly	0.112	0.472
L-Ser	Homer1 b/c	-0.206	0.144
L-Ser	HVA	-0.051	1
L-Ser	L-Asp	-0.087	1
L-Ser	L-Gln	-0.007	1
L-Ser	L-Glu	0.111	0.808
L-Ser	L-Ser	0	1
L-Ser	MAO-A	0	1
L-Ser	MAO-B	0.127	0.548

L-Ser	mb-COMT	-0.154	0.272
L-Ser	mGluR1	-0.03	1
L-Ser	mGluR2/3	0	1
L-Ser	mGluR5	0.113	0.224
L-Ser	NE	0.205	0.048
L-Ser	NR1	-0.017	1
L-Ser	NR2A	0	1
L-Ser	NR2B	-0.103	0.432
L-Ser	p-CaMKII	-0.229	0.496
L-Ser	PSD-9595	-0.047	1
L-Ser	s-COMT	0	1
L-Ser	Synapsin I	-0.015	1
L-Ser	VGLUT 1	0	1
L-Ser	VGLUT 2	-0.006	1
MAO-A	5-HIAA	-0.032	1
MAO-A	5-HT	0.008	1
MAO-A	Asn	0.145	0.152
MAO-A	CAMKII	0	1
MAO-A	D-Asp	0.149	0.408
MAO-A	D-Ser	0	1
MAO-A	DA	0	1
MAO-A	DOPAC	-0.125	0.324
MAO-A	GAD65	0.117	0.292
MAO-A	GAD67	-0.108	0.484
MAO-A	GLAST	0.093	1
MAO-A	GLT-1	0	1
MAO-A	GluA1	0.132	0.168
MAO-A	GluA2/3	0.051	1
MAO-A	GluA4	-0.093	0.196
MAO-A	Gly	0.023	1
MAO-A	Homer1 b/c	-0.155	0.16
MAO-A	HVA	0.014	1
MAO-A	L-Asp	0.038	1
MAO-A	L-Gln	0.145	0.216
MAO-A	L-Glu	0.144	0.244
MAO-A	L-Ser	0	1
MAO-A	MAO-A	0	1
MAO-A	MAO-B	0	1

MAO-A	mb-COMT	0.043	1
MAO-A	mGluR1	0.215	0.036
MAO-A	mGluR2/3	0.193	0.316
MAO-A	mGluR5	-0.132	0.08
MAO-A	NE	0	1
MAO-A	NR1	-0.139	1
MAO-A	NR2A	0.146	0.148
MAO-A	NR2B	0.173	0.004
MAO-A	p-CaMKII	0	1
MAO-A	PSD-9595	0.122	0.556
MAO-A	s-COMT	-0.002	1
MAO-A	Synapsin I	-0.15	0.068
MAO-A	VGLUT 1	0.21	0.056
MAO-A	VGLUT 2	-0.016	1
MAO-B	5-HIAA	0.062	1
MAO-B	5-HT	0.005	1
MAO-B	Asn	-0.129	1
MAO-B	CAMKII	-0.03	1
MAO-B	D-Asp	-0.062	1
MAO-B	D-Ser	-0.188	0.148
MAO-B	DA	-0.126	0.612
MAO-B	DOPAC	-0.085	0.296
MAO-B	GAD65	-0.107	0.26
MAO-B	GAD67	0	1
MAO-B	GLAST	-0.166	0.084
MAO-B	GLT-1	-0.091	0.532
MAO-B	GluA1	0.136	0.516
MAO-B	GluA2/3	0.094	1
MAO-B	GluA4	0.019	1
MAO-B	Gly	-0.073	1
MAO-B	Homer1 b/c	0.134	0.656
MAO-B	HVA	0	1
MAO-B	L-Asp	0	1
MAO-B	L-Gln	0.139	1
MAO-B	L-Glu	-0.232	0.552
MAO-B	L-Ser	0.127	0.548
MAO-B	MAO-A	0	1
MAO-B	MAO-B	0	1

MAO-B	mb-COMT	-0.028	1
MAO-B	mGluR1	0	1
MAO-B	mGluR2/3	0.12	0.68
MAO-B	mGluR5	0.094	0.4
MAO-B	NE	-0.095	0.544
MAO-B	NR1	0	1
MAO-B	NR2A	-0.007	1
MAO-B	NR2B	0.069	1
MAO-B	p-CaMKII	0.199	0.096
MAO-B	PSD-9595	0.159	0.292
MAO-B	s-COMT	0	1
MAO-B	Synapsin I	-0.182	0.14
MAO-B	VGLUT 1	0.17	0.72
MAO-B	VGLUT 2	0.096	0.428
mb-COMT	5-HIAA	0	1
mb-COMT	5-HT	-0.044	1
mb-COMT	Asn	0.137	0.3
mb-COMT	CAMKII	-0.027	1
mb-COMT	D-Asp	-0.011	1
mb-COMT	D-Ser	0.096	0.376
mb-COMT	DA	-0.018	1
mb-COMT	DOPAC	-0.097	0.104
mb-COMT	GAD65	0	1
mb-COMT	GAD67	-0.116	1
mb-COMT	GLAST	0.16	0.228
mb-COMT	GLT-1	0.101	0.348
mb-COMT	GluA1	0.008	1
mb-COMT	GluA2/3	0	1
mb-COMT	GluA4	0.125	0.636
mb-COMT	Gly	0.114	0.328
mb-COMT	Homer1 b/c	0	1
mb-COMT	HVA	0	1
mb-COMT	L-Asp	0.094	0.768
mb-COMT	L-Gln	-0.057	1
mb-COMT	L-Glu	0.009	1
mb-COMT	L-Ser	-0.154	0.272
mb-COMT	MAO-A	0.043	1
mb-COMT	MAO-B	-0.028	1
mb-COMT	mb-COMT	0	1
mb-COMT	mGluR1	-0.196	0.032
mb-COMT	mGluR2/3	-0.1	1
mb-COMT	mGluR5	-0.006	1
mb-COMT	NE	0	1
mb-COMT	NR1	-0.185	0.428
mb-COMT	NR2A	0.029	1
mb-COMT	NR2B	0.111	0.408
mb-COMT	p-CaMKII	0	1
mb-COMT	PSD-9595	0	1
mb-COMT	s-COMT	0.094	1
mb-COMT	Synapsin I	-0.228	0.044
mb-COMT	VGLUT 1	-0.048	1
mb-COMT	VGLUT 2	0.015	1
mGluR1	5-HIAA	0	1
mGluR1	5-HT	-0.002	1
mGluR1	Asn	0	1

mGluR1	CAMKII	-0.148	0.08
mGluR1	D-Asp	0.09	0.296
mGluR1	D-Ser	-0.213	0.068
mGluR1	DA	0.019	1
mGluR1	DOPAC	0.11	0.364
mGluR1	GAD65	-0.139	0.304
mGluR1	GAD67	0.036	1
mGluR1	GLAST	0.013	1
mGluR1	GLT-1	0.148	0.652
mGluR1	GluA1	-0.104	0.356
mGluR1	GluA2/3	0.138	0.096
mGluR1	GluA4	0	1
mGluR1	Gly	0	1
mGluR1	Homer1 b/c	0.116	0.472
mGluR1	HVA	-0.061	1
mGluR1	L-Asp	0.032	1
mGluR1	L-Gln	-0.018	1
mGluR1	L-Glu	-0.162	0.04
mGluR1	L-Ser	-0.03	1
mGluR1	MAO-A	0.215	0.036
mGluR1	MAO-B	0	1
mGluR1	mb-COMT	-0.196	0.032
mGluR1	mGluR1	0	1
mGluR1	mGluR2/3	-0.118	0.472
mGluR1	mGluR5	-0.043	1
mGluR1	NE	0	1
mGluR1	NR1	-0.108	0.52
mGluR1	NR2A	0	1
mGluR1	NR2B	0	1
mGluR1	p-CaMKII	0.012	1
mGluR1	PSD-9595	-0.135	0.36
mGluR1	s-COMT	0.042	1
mGluR1	Synapsin I	-0.198	0.052
mGluR1	VGLUT 1	0.161	0.112
mGluR1	VGLUT 2	-0.093	1
mGluR2/3	5-HIAA	0	1
mGluR2/3	5-HT	-0.136	0.092
mGluR2/3	Asn	0.076	1
mGluR2/3	CAMKII	-0.117	0.808
mGluR2/3	D-Asp	0	1
mGluR2/3	D-Ser	0.015	1
mGluR2/3	DA	0.032	1
mGluR2/3	DOPAC	0	1
mGluR2/3	GAD65	0	1
mGluR2/3	GAD67	0.093	1
mGluR2/3	GLAST	-0.039	1
mGluR2/3	GLT-1	0.01	1
mGluR2/3	GluA1	0.149	0.264
mGluR2/3	GluA2/3	0.103	0.172
mGluR2/3	GluA4	0.095	1
mGluR2/3	Gly	-0.014	1
mGluR2/3	Homer1 b/c	-0.008	1
mGluR2/3	HVA	-0.026	1
mGluR2/3	L-Asp	0	1
mGluR2/3	L-Gln	0.139	0.152
mGluR2/3	L-Glu	-0.056	1
mGluR2/3	L-Ser	0	1
mGluR2/3	MAO-A	0.193	0.316
mGluR2/3	MAO-B	0.12	0.68
mGluR2/3	mb-COMT	-0.1	1
mGluR2/3	mGluR1	-0.118	0.472
mGluR2/3	mGluR2/3	0	1
mGluR2/3	mGluR5	0	1

mGluR2/3	NE	-0.136	0.312
mGluR2/3	NR1	-0.024	1
mGluR2/3	NR2A	0	1
mGluR2/3	NR2B	0.092	0.752
mGluR2/3	p-CaMKII	0.081	1
mGluR2/3	PSD-9595	0.024	1
mGluR2/3	s-COMT	0.128	0.388
mGluR2/3	Synapsin I	-0.09	1
mGluR2/3	VGLUT 1	-0.142	1
mGluR2/3	VGLUT 2	-0.152	0.66
mGluR5	5-HIAA	-0.113	0.488
mGluR5	5-HT	0.16	0.4
mGluR5	Asn	0.138	0.264
mGluR5	CAMKII	-0.092	0.332
mGluR5	D-Asp	-0.125	0.52
mGluR5	D-Ser	0.027	1
mGluR5	DA	0.094	0.808
mGluR5	DOPAC	-0.116	0.516
mGluR5	GAD65	0.001	1
mGluR5	GAD67	-0.081	0.484
mGluR5	GLAST	0.098	0.824
mGluR5	GLT-1	0	1
mGluR5	GluA1	-0.235	0.18
mGluR5	GluA2/3	-0.064	1
mGluR5	GluA4	0.013	1
mGluR5	Gly	-0.006	1
mGluR5	Homer1 b/c	0.142	1
mGluR5	HVA	0	1
mGluR5	L-Asp	0.028	1
mGluR5	L-Gln	0.111	0.248
mGluR5	L-Glu	0.003	1
mGluR5	L-Ser	0.113	0.224
mGluR5	MAO-A	-0.132	0.08
mGluR5	MAO-B	0.094	0.4
mGluR5	mb-COMT	-0.006	1
mGluR5	mGluR1	-0.043	1
mGluR5	mGluR2/3	0	1
mGluR5	mGluR5	0	1
mGluR5	NE	0	1
mGluR5	NR1	-0.163	0.044
mGluR5	NR2A	0.007	1
mGluR5	NR2B	-0.032	1
mGluR5	p-CaMKII	-0.08	1
mGluR5	PSD-9595	0.012	1
mGluR5	s-COMT	0	1
mGluR5	Synapsin I	-0.008	1
mGluR5	VGLUT 1	0	1
mGluR5	VGLUT 2	0.115	0.436
NE	5-HIAA	-0.147	0.188
NE	5-HT	0.011	1
NE	Asn	0	1
NE	CAMKII	-0.113	0.384
NE	D-Asp	-0.13	0.124
NE	D-Ser	0.02	1
NE	DA	-0.062	1
NE	DOPAC	-0.111	0.324
NE	GAD65	0.112	0.62
NE	GAD67	0.097	0.572
NE	GLAST	0	1
NE	GLT-1	-0.211	0.26
NE	GluA1	0.087	0.672
NE	GluA2/3	0	1
NE	GluA4	-0.127	0.232
NE	Gly	-0.107	0.18
NE	Homer1 b/c	-0.123	0.14
NE	HVA	0.062	1
NE	L-Asp	0.043	1
NE	L-Gln	0.073	0.508
NE	L-Glu	-0.117	0.608
NE	L-Ser	0.205	0.048
NE	MAO-A	0	1
NE	MAO-B	-0.095	0.544
NE	mb-COMT	0	1
NE	mGluR1	0	1

NE	mGluR2/3	-0.136	0.312
NE	mGluR5	0	1
NE	NE	0	1
NE	NR1	-0.043	1
NE	NR2A	0.064	0.616
NE	NR2B	0	1
NE	p-CaMKII	0.022	1
NE	PSD-9595	0	1
NE	s-COMT	-0.072	1
NE	Synapsin I	0.097	0.964
NE	VGLUT 1	0.083	0.16
NE	VGLUT 2	-0.165	0.252
NR1	5-HIAA	-0.019	1
NR1	5-HT	0.105	0.952
NR1	Asn	0.003	1
NR1	CAMKII	0	1
NR1	D-Asp	-0.061	1
NR1	D-Ser	0.03	1
NR1	DA	0	1
NR1	DOPAC	0	1
NR1	GAD65	-0.091	1
NR1	GAD67	-0.134	0.524
NR1	GLAST	-0.103	0.368
NR1	GLT-1	-0.121	0.5
NR1	GluA1	0	1
NR1	GluA2/3	0.294	0.36
NR1	GluA4	-0.156	0.136
NR1	Gly	-0.089	0.648
NR1	Homer1 b/c	-0.143	0.036
NR1	HVA	0.111	0.36
NR1	L-Asp	-0.156	0.14
NR1	L-Gln	0	1
NR1	L-Glu	-0.115	0.652
NR1	L-Ser	-0.017	1
NR1	MAO-A	-0.139	1
NR1	MAO-B	0	1
NR1	mb-COMT	-0.185	0.428
NR1	mGluR1	-0.108	0.52

NR1	mGluR2/3	-0.024	1
NR1	mGluR5	-0.163	0.044
NR1	NE	-0.043	1
NR1	NR1	0	1
NR1	NR2A	0.034	1
NR1	NR2B	-0.029	1
NR1	p-CaMKII	0	1
NR1	PSD-9595	-0.116	0.4
NR1	s-COMT	0	1
NR1	Synapsin I	0	1
NR1	VGLUT 1	-0.055	1
NR1	VGLUT 2	-0.269	0.312
NR2A	5-HIAA	-0.265	0.36
NR2A	5-HT	-0.055	1
NR2A	Asn	0.133	0.532
NR2A	CAMKII	-0.137	0.136
NR2A	D-Asp	0	1
NR2A	D-Ser	0.07	1
NR2A	DA	-0.002	1
NR2A	DOPAC	-0.108	0.54
NR2A	GAD65	0.163	0.228
NR2A	GAD67	-0.078	0.54
NR2A	GLAST	0	1
NR2A	GLT-1	-0.009	1
NR2A	GluA1	-0.016	1
NR2A	GluA2/3	-0.239	1
NR2A	GluA4	0.044	1
NR2A	Gly	0.134	0.204
NR2A	Homer1 b/c	0.047	1
NR2A	HVA	0	1
NR2A	L-Asp	0	1
NR2A	L-Gln	-0.124	0.828
NR2A	L-Glu	0.134	0.108
NR2A	L-Ser	0	1
NR2A	MAO-A	0.146	0.148
NR2A	MAO-B	-0.007	1
NR2A	mb-COMT	0.029	1
NR2A	mGluR1	0	1

NR2A	mGluR2/3	0	1
NR2A	mGluR5	0.007	1
NR2A	NE	0.064	0.616
NR2A	NR1	0.034	1
NR2A	NR2A	0	1
NR2A	NR2B	-0.062	1
NR2A	p-CaMKII	0.115	0.232
NR2A	PSD-9595	0	1
NR2A	s-COMT	0	1
NR2A	Synapsin I	0	1
NR2A	VGLUT 1	-0.173	0.748
NR2A	VGLUT 2	0.001	1
NR2B	5-HIAA	-0.107	0.96
NR2B	5-HT	-0.019	1
NR2B	Asn	0.097	0.516
NR2B	CAMKII	0	1
NR2B	D-Asp	-0.113	0.332
NR2B	D-Ser	0.152	0.064
NR2B	DA	0	1
NR2B	DOPAC	0	1
NR2B	GAD65	0.113	0.372
NR2B	GAD67	-0.047	1
NR2B	GLAST	0.059	1
NR2B	GLT-1	-0.171	0.448
NR2B	GluA1	-0.116	0.792
NR2B	GluA2/3	-0.09	1
NR2B	GluA4	-0.148	0.084
NR2B	Gly	0	1
NR2B	Homer1 b/c	-0.012	1
NR2B	HVA	0	1
NR2B	L-Asp	0.125	0.424
NR2B	L-Gln	-0.174	0.176
NR2B	L-Glu	-0.011	1
NR2B	L-Ser	-0.103	0.432
NR2B	MAO-A	0.173	0.004
NR2B	MAO-B	0.069	1
NR2B	mb-COMT	0.111	0.408
NR2B	mGluR1	0	1

NR2B	mGluR2/3	0.092	0.752
NR2B	mGluR5	-0.032	1
NR2B	NE	0	1
NR2B	NR1	-0.029	1
NR2B	NR2A	-0.062	1
NR2B	NR2B	0	1
NR2B	p-CaMKII	0.112	1
NR2B	PSD-9595	0	1
NR2B	s-COMT	0.097	0.692
NR2B	Synapsin I	0	1
NR2B	VGLUT 1	-0.016	1
NR2B	VGLUT 2	-0.167	0.164
p-CaMKII	5-HIAA	-0.133	1
p-CaMKII	5-HT	0	1
p-CaMKII	Asn	0	1
p-CaMKII	CAMKII	-0.102	0.376
p-CaMKII	D-Asp	0.164	0.592
p-CaMKII	D-Ser	-0.148	0.344
p-CaMKII	DA	0.004	1
p-CaMKII	DOPAC	0	1
p-CaMKII	GAD65	0.118	0.252
p-CaMKII	GAD67	0.112	0.28
p-CaMKII	GLAST	0.116	0.056
p-CaMKII	GLT-1	-0.167	0.108
p-CaMKII	GluA1	-0.147	0.172
p-CaMKII	GluA2/3	0	1
p-CaMKII	GluA4	0.17	0.172
p-CaMKII	Gly	-0.155	0.4

p-CaMKII	Homer1 b/c	-0.046	1
p-CaMKII	HVA	-0.097	0.32
p-CaMKII	L-Asp	0.016	1
p-CaMKII	L-Gln	0.044	1
p-CaMKII	L-Glu	0	1
p-CaMKII	L-Ser	-0.229	0.496
p-CaMKII	MAO-A	0	1
p-CaMKII	MAO-B	0.199	0.096
p-CaMKII	mb-COMT	0	1
p-CaMKII	mGluR1	0.012	1
p-CaMKII	mGluR2/3	0.081	1
p-CaMKII	mGluR5	-0.08	1
p-CaMKII	NE	0.022	1
p-CaMKII	NR1	0	1
p-CaMKII	NR2A	0.115	0.232
p-CaMKII	NR2B	0.112	1
p-CaMKII	p-CaMKII	0	1
p-CaMKII	PSD-9595	0.159	0.332
p-CaMKII	s-COMT	0.124	0.288
p-CaMKII	Synapsin I	-0.025	1
p-CaMKII	VGLUT 1	0.138	0.156
p-CaMKII	VGLUT 2	0.027	1
PSD-9595	5-HIAA	-0.126	0.288
PSD-9595	5-HT	0	1
PSD-9595	Asn	0	1
PSD-9595	CAMKII	-0.117	0.256
PSD-9595	D-Asp	0.141	0.632
PSD-9595	D-Ser	0	1
PSD-9595	DA	0	1
PSD-9595	DOPAC	0.12	0.136
PSD-9595	GAD65	0.208	0.256
PSD-9595	GAD67	-0.12	0.188
PSD-9595	GLAST	0.022	1
PSD-9595	GLT-1	-0.132	1
PSD-9595	GluA1	0.008	1
PSD-9595	GluA2/3	0	1
PSD-9595	GluA4	-0.156	0.312
PSD-9595	Gly	0.121	0.728
PSD-9595	Homer1 b/c	0.282	0.02
PSD-9595	HVA	-0.131	0.148
PSD-9595	L-Asp	0	1
PSD-9595	L-Gln	0.121	0.964
PSD-9595	L-Glu	0	1
PSD-9595	L-Ser	-0.047	1
PSD-9595	MAO-A	0.122	0.556
PSD-9595	MAO-B	0.159	0.292
PSD-9595	mb-COMT	0	1
PSD-9595	mGluR1	-0.135	0.36
PSD-9595	mGluR2/3	0.024	1
PSD-9595	mGluR5	0.012	1
PSD-9595	NE	0	1
PSD-9595	NR1	-0.116	0.4

PSD-9595	NR2A	0	1
PSD-9595	NR2B	0	1
PSD-9595	p-CaMKII	0.159	0.332
PSD-9595	PSD-9595	0	1
PSD-9595	s-COMT	0	1
PSD-9595	Synapsin I	0	1
PSD-9595	VGLUT 1	-0.126	0.204
PSD-9595	VGLUT 2	0.118	0.3
s-COMT	5-HIAA	-0.147	0.34
s-COMT	5-HT	-0.14	0.328
s-COMT	Asn	0.197	0.468
s-COMT	CAMKII	0.029	1
s-COMT	D-Asp	-0.156	0.244
s-COMT	D-Ser	0	1
s-COMT	DA	0	1
s-COMT	DOPAC	0	1
s-COMT	GAD65	-0.009	1
s-COMT	GAD67	-0.04	1
s-COMT	GLAST	-0.02	1
s-COMT	GLT-1	-0.118	0.808
s-COMT	GluA1	-0.105	0.488
s-COMT	GluA2/3	-0.166	0.152
s-COMT	GluA4	0.118	0.388
s-COMT	Gly	0.155	1
s-COMT	Homer1 b/c	0.016	1
s-COMT	HVA	-0.127	0.932
s-COMT	L-Asp	0.138	0.428
s-COMT	L-Gln	0.068	1
s-COMT	L-Glu	0.257	0.096
s-COMT	L-Ser	0	1
s-COMT	MAO-A	-0.002	1
s-COMT	MAO-B	0	1
s-COMT	mb-COMT	0.094	1
s-COMT	mGluR1	0.042	1
s-COMT	mGluR2/3	0.128	0.388
s-COMT	mGluR5	0	1
s-COMT	NE	-0.072	1
s-COMT	NR1	0	1
s-COMT	NR2A	0	1
s-COMT	NR2B	0.097	0.692
s-COMT	p-CaMKII	0.124	0.288
s-COMT	PSD-9595	0	1
s-COMT	s-COMT	0	1
s-COMT	Synapsin I	0.204	0.112
s-COMT	VGLUT 1	0.004	1
s-COMT	VGLUT 2	0.104	0.14
Synapsin I	5-HIAA	-0.017	1
Synapsin I	5-HT	0	1
Synapsin I	Asn	0	1
Synapsin I	CAMKII	-0.08	1
Synapsin I	D-Asp	0.002	1
Synapsin I	D-Ser	-0.131	0.224
Synapsin I	DA	-0.131	0.136
Synapsin I	DOPAC	-0.149	0.148
Synapsin I	GAD65	-0.123	0.292
Synapsin I	GAD67	0.127	0.288
Synapsin I	GLAST	0.044	1
Synapsin I	GLT-1	0	1
Synapsin I	GluA1	-0.092	0.28
Synapsin I	GluA2/3	0	1
Synapsin I	GluA4	0.059	1
Synapsin I	Gly	-0.12	0.232
Synapsin I	Homer1 b/c	-0.136	0.288
Synapsin I	HVA	-0.085	0.604

Synapsin I	L-Asp	-0.043	1
Synapsin I	L-Gln	0	1
Synapsin I	L-Glu	-0.009	1
Synapsin I	L-Ser	-0.015	1
Synapsin I	MAO-A	-0.15	0.068
Synapsin I	MAO-B	-0.182	0.14
Synapsin I	mb-COMT	-0.228	0.044
Synapsin I	mGluR1	-0.198	0.052
Synapsin I	mGluR2/3	-0.09	1
Synapsin I	mGluR5	-0.008	1
Synapsin I	NE	0.097	0.964
Synapsin I	NR1	0	1
Synapsin I	NR2A	0	1
Synapsin I	NR2B	0	1
Synapsin I	p-CaMKII	-0.025	1
Synapsin I	PSD-9595	0	1
Synapsin I	s-COMT	0.204	0.112
Synapsin I	Synapsin I	0	1
Synapsin I	VGLUT1	0	1
Synapsin I	VGLUT2	0	1
VGLUT1	5-HIAA	0	1
VGLUT1	5-HT	-0.158	0.332
VGLUT1	Asn	0.075	1
VGLUT1	CAMKII	-0.106	0.708
VGLUT1	D-Asp	0.076	1
VGLUT1	D-Ser	0	1

VGLUT1	DA	-0.09	0.292
VGLUT1	DOPAC	-0.15	0.12
VGLUT1	GAD65	0.132	0.048
VGLUT1	GAD67	0	1
VGLUT1	GLAST	0.083	1
VGLUT1	GLT-1	-0.003	1
VGLUT1	GluA1	-0.075	0.824
VGLUT1	GluA2/3	-0.038	1
VGLUT1	GluA4	0.022	1
VGLUT1	Gly	0.181	0.088
VGLUT1	Homer1 b/c	-0.116	0.688
VGLUT1	HVA	-0.171	0.264
VGLUT1	L-Asp	0.024	1
VGLUT1	L-Gln	0.077	0.9
VGLUT1	L-Glu	0.141	0.324
VGLUT1	L-Ser	0	1
VGLUT1	MAO-A	0.21	0.056
VGLUT1	MAO-B	0.17	0.72
VGLUT1	mb-COMT	-0.048	1
VGLUT1	mGluR1	0.161	0.112
VGLUT1	mGluR2/3	-0.142	1
VGLUT1	mGluR5	0	1
VGLUT1	NE	0.083	0.16
VGLUT1	NR1	-0.055	1
VGLUT1	NR2A	-0.173	0.748
VGLUT1	NR2B	-0.016	1

VGLUT 1	p-CaMKII	0.138	0.156
VGLUT 1	PSD-9595	-0.126	0.204
VGLUT 1	s-COMT	0.004	1
VGLUT 1	Synapsin I	0	1
VGLUT 1	VGLUT 1	0	1
VGLUT 1	VGLUT 2	-0.115	0.704
VGLUT 2	5-HIAA	-0.152	0.056
VGLUT 2	5-HT	0	1
VGLUT 2	Asn	-0.11	0.236
VGLUT 2	CAMKII	0.086	0.836
VGLUT 2	D-Asp	-0.121	0.748
VGLUT 2	D-Ser	-0.008	1
VGLUT 2	DA	0	1
VGLUT 2	DOPAC	0.007	1
VGLUT 2	GAD65	-0.13	1
VGLUT 2	GAD67	0	1
VGLUT 2	GLAST	0.012	1
VGLUT 2	GLT-1	0.105	0.784
VGLUT 2	GluA1	0.159	0.472
VGLUT 2	GluA2/3	0.101	0.18
VGLUT 2	GluA4	0.196	0
VGLUT 2	Gly	0.106	0.472

VGLUT 2	Homer1 b/c	0.046	1
VGLUT 2	HVA	0.006	1
VGLUT 2	L-Asp	0	1
VGLUT 2	L-Gln	0	1
VGLUT 2	L-Glu	0.112	0.64
VGLUT 2	L-Ser	-0.006	1
VGLUT 2	MAO-A	-0.016	1
VGLUT 2	MAO-B	0.096	0.428
VGLUT 2	mb-COMT	0.015	1
VGLUT 2	mGluR1	-0.093	1
VGLUT 2	mGluR2 /3	-0.152	0.66
VGLUT 2	mGluR5	0.115	0.436
VGLUT 2	NE	-0.165	0.252
VGLUT 2	NR1	-0.269	0.312
VGLUT 2	NR2A	0.001	1
VGLUT 2	NR2B	-0.167	0.164
VGLUT 2	p-CaMKII	0.027	1
VGLUT 2	PSD-9595	0.118	0.3
VGLUT 2	s-COMT	0.104	0.14
VGLUT 2	Synapsin I	0	1
VGLUT 2	VGLUT 1	-0.115	0.704
VGLUT 2	VGLUT 2	0	1