

Supplemental Information

Altered expression of synapse and glutamate related genes in postmortem hippocampus of depressed subjects

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Supplemental Table S1. Case Demographics for subjects with major depressive disorder (MDD).

| Experimental ID | Age | Sex/Race | Cause of Death | PMI | pH | Toxicology | Medications ¹ | Axis I Comorbidity |
|--------------------|--------------------|----------|---------------------------|-------------|-------------|--------------------------------|--|--|
| 14B | 30* | M/AAm | suicide, SIGSW | 18 | 6.91 | ETOH | none | Hx alcohol abuse |
| 6B | 34** | F/C | suicide, CO | 24 | 6.27 | ETOH, CO, alprazolam | alprazolam, valproic acid | none |
| 10B | 38* | F/C | suicide, OD | 12 | 6.41 | diazepam, temazepam | sertraline, temazepam | none |
| 7B | 40 ² ** | F/C | CVD, accidental OD | 25 | 6.32 | morphine, codeine, hydrocodone | fluoxetine, temazepam, hydrocodone | sedative, hypnotic and anxiolytic disorder NOS |
| 16B | 42** | M/C | suicide, SIGSW | 20 | 6.8 | ND | none | none |
| 9B | 43** | M/C | suicide, hanging | 21 | 6.73 | ND | none | none |
| 8B | 46 | M/AAm | homicide | 17 | 6.26 | ND | none | none |
| 12B | 47* | M/C | suicide, SIGSW | 11 | 6.84 | ETOH | none | none |
| 3B | 48 | M/C | suicide, SIGSW | 21 | 6.9 | flurazepam | flurazepam, lorazepam | Hx alcohol abuse |
| 4B | 54 | M/C | suicide, CO | 23 | 6.24 | CO, phenobarbital, phenytoin | sertraline | none |
| 5B | 62 | M/C | suicide, SIGSW | 20 | 6.47 | ND | buspirone ³ , lorazepam ³ | none |
| 13B | 63 | F/C | CVD | 18 | 6.3 | ND | fluoxetine | none |
| 11B | 67 | F/C | aneurysm | 17 | 6.68 | ND | doxepine | agoraphobia, Hx stroke |
| 23B | 68 | M/C | suicide, CO | 4 | 6.21 | CO | none | Parkinson's disease |
| 20B | 73* | M/C | suicide, SIGSW | 18 | 6.59 | diazepam, codeine | none | none |
| 17B | 74** | M/C | suicide, hanging | 24 | 6.96 | ND | nortriptyline, L-DOPA | Parkinson's disease |
| 18B | 77* | F/C | CVD | 32 | 6.79 | propoxyphene | trazodone, thioridazine, venlafaxine, clonazepam | none |
| 21B | 77* | M/C | suicide, hanging | 26 | 6.74 | sertraline | sertraline | none |
| 15B | 78** | F/C | suicide, fall from height | 25 | 6.94 | ND | none | pathological gambling, delusional disorder |
| 22B | 82 | M/C | suicide, CO | 12 | 6.46 | CO | risperidone, sertraline | benzodiazepine abuse |
| 19B | 87 | F/C | aortic aneurysm | 24 | 6.56 | ND | flurazepam | none |
| DG Average | 61.3 | | | 18.2 | 6.56 | | | |
| SD | 16.9 | | | 6.8 | 0.24 | | | |
| SEM | 4.4 | | | 1.8 | 0.06 | | | |
| CA1 Average | 59.2 | | | 19.7 | 6.54 | | | |
| SD | 16.7 | | | 5.7 | 0.27 | | | |
| SEM | 4.3 | | | 1.5 | 0.07 | | | |

AAm, African American; C, Caucasian; CO, carbon monoxide; CVD, cardiovascular disease; ETOH, ethanol; F, female; Hx, history of alcohol abuse but not currently active; M, male; ND, no psychotropic medication detected; OD, drug overdose; PMI, postmortem interval (hours); SIGSW, self-inflicted gunshot wound; ¹Psychotropic prescriptions within last month; ²MDD in remission; ³prescriptions for six days prior to death; *, samples present only in array sets for the dentate gyrus; **, samples present only in array sets for CA1. Table adopted from Duric *et al.* (2010).

Supplemental Table S2. Case Demographics of matched control subjects.

| Experimental ID | Age | Sex/race | Cause of death | PMI | pH | Toxicology |
|--------------------|-------------|----------|-----------------------------|-------------|-------------|--------------|
| 8D | 37 | M/C | hemorrhagic pancreatitis | 17 | 6.47 | ND |
| 9D | 43 | M/C | pulmonary thromboemboli | 23 | 6.49 | propoxyphene |
| 10D | 45* | F/AAm | CVD | 9 | 6.86 | ND |
| 3D | 46 | M/AAm | CVD | 19 | 6.95 | ND |
| 6D | 46 | F/C | homicide | 24 | 6.32 | ND |
| 16D | 47** | M/C | pulmonary embolism | 25 | 6.1 | propoxyphene |
| 7D | 49 | F/AAm | CVD | 29 | 6.57 | ND |
| 1D | 50** | F/C | CVD | 27 | 6.74 | ND |
| 5D | 54** | M/AAm | CVD | 19 | 6.52 | ND |
| 4D | 56 | M/C | hypertrophic cardiomyopathy | 25 | 6.14 | ND |
| 14D | 26 | M/AAm | homicide | 13 | 6.66 | ND |
| 15D | 83 | F/C | CVD | 25 | 6.67 | ND |
| 23D | 66 | M/C | CVD | 12 | 7.17 | ND |
| 13D | 67 | F/AAm | CVD | 28 | 6.4 | ND |
| 20D | 69* | M/C | aortic aneurysm | 18 | 6.7 | ND |
| 17D | 70 | M/C | CVD | 20 | 6.81 | ND |
| 21D | 77* | M/C | CVD | 24 | 6.56 | ND |
| 18D | 80 | F/C | CVD | 21 | 6.78 | ND |
| 22D | 82 | M/C | aneurysm | 16 | 6.72 | ND |
| 19D | 84 | F/C | CVD | 22 | 6.23 | ND |
| DG Average | 61.1 | | | 20.5 | 6.61 | |
| SD | 16.0 | | | 5.5 | 0.28 | |
| SEM | 4.1 | | | 1.4 | 0.07 | |
| CA1 Average | 58.5 | | | 21.8 | 6.56 | |
| SD | 15.3 | | | 4.8 | 0.30 | |
| SEM | 4.0 | | | 1.2 | 0.08 | |

AAm, African American; C, Caucasian; CVD, cardiovascular disease; F, female; M, male; ND, no psychotropic medication detected, PMI, postmortem interval (hours); *, samples present only in array sets for the dentate gyrus; **, samples present only in array sets for CA1. Table adopted from Duric *et al.* (2010).

Supplemental Table S3. Human subject pairs and corresponding sample RNA integrity numbers (RIN) that were used in microarray analysis.

Dentate Gyrus (n = 15)

| <i>Microarray Pairs:</i> | <u>Sample#</u> | <u>RIN</u> |
|--------------------------|----------------|------------|
| | 3B | 6.8 |
| | 3D | 6.1 |
| | 4B | 5.1 |
| | 4D | 5.6 |
| | 5B | 6.9 |
| | 23D | 7.5 |
| | 8B | 5.5 |
| | 8D | 5.4 |
| | 10B | 6.2 |
| | 10D | 7.4 |
| | 11B | 6.6 |
| | 13D | 7 |
| | 12B | 6.4 |
| | 9D | 5.6 |
| | 13B | 5.6 |
| | 6D | 6.1 |
| | 14B | 7.4 |
| | 7D | 6.4 |
| | 18B | 5.8 |
| | 18D | 5.8 |
| | 19B | 4.9 |
| | 19D | 5 |
| | 20B | 6.8 |
| | 20D | 7.3 |
| | 21B | 5.6 |
| | 21D | 5.5 |
| | 22B | 5.2 |
| | 22D | 6.2 |
| | 23B | 6.2 |
| | 17D | 7.7 |

Average RIN for all samples 6.2
 Average RIN for Control samples 6.3
 Average RIN for MDD samples 6.1

CA1 (n = 15)

| <i>Microarray Pairs:</i> | <u>Sample#</u> | <u>RIN</u> |
|--------------------------|----------------|------------|
| | 3B | 4.9 |
| | 3D | 4.7 |
| | 4B | 5 |
| | 4D | 4.8 |
| | 5B | 5 |
| | 5D | 4.6 |
| | 6B | 4.8 |
| | 7D | 6.6 |
| | 7B | 4.5 |
| | 1D | 4.6 |
| | 8B | 4.8 |
| | 8D | 6.4 |
| | 9B | 6.3 |
| | 9D | 5.8 |
| | 11B | 6 |
| | 13D | 6.5 |
| | 13B | 6.3 |
| | 6D | 5.2 |
| | 15B | 5.4 |
| | 18D | 6.8 |
| | 16B | 6.1 |
| | 16D | 5.9 |
| | 17B | 5.8 |
| | 23D | 6.2 |
| | 19B | 5.3 |
| | 19D | 5.4 |
| | 22B | 4.6 |
| | 22D | 4.4 |
| | 23B | 5.8 |
| | 17D | 4.8 |

Average RIN for all samples 5.4
 Average RIN for Control samples 5.5
 Average RIN for MDD samples 5.4

Supplemental Table S4. Cofactorial analysis of genes of interest found in DG microarray data.

| Gene | Fold Change (log2) | Fold Change | Q-value (No Adjust) | Q (ADT) | Q (CNS Dis) | Q (pH) | Q (PMI) | Q (Suicide) | Q (Age) | Q (Sex) | A0S0 | A1S0 | A1S1 | Error Variance |
|---------------|--------------------|-------------|---------------------|---------|--------------|--------|---------|-------------|---------|---------|---------|---------|---------|----------------|
| DLG1 | -0.21 | 0.86 | 0.2247 | 0.7648 | 0.3942 | 0.2353 | 0.3336 | 0.5624 | 0.2677 | 0.2634 | 0.2298 | 0.4454 | 0.4435 | 0.1109 |
| DLG2 | -1.30 | 0.41 | 0.0065 | 0.0181 | 0.0185 | 0.0027 | 0.0170 | 0.1165 | 0.0070 | 0.0069 | -0.6819 | 0.4799 | 0.7107 | 0.8926 |
| DLG3 | -0.30 | 0.81 | 0.0140 | 0.0564 | 0.0199 | 0.0190 | 0.0261 | 0.0679 | 0.0202 | 0.0163 | -0.3780 | 0.0041 | -0.1391 | 0.0399 |
| DLG4 | 0.08 | 1.05 | 0.7728 | 0.8872 | 0.7635 | 0.7978 | 0.7239 | 0.8953 | 0.7647 | 0.7682 | 0.4626 | 0.3882 | 0.3869 | 0.1966 |
| GRIA1 | -1.94 | 0.26 | 0.0005 | 0.0029 | 0.0011 | 0.0005 | 0.0011 | 0.0153 | 0.0007 | 0.0005 | -0.9499 | 0.8580 | 1.0841 | 0.8897 |
| GRIA1.1 | -0.65 | 0.64 | 0.0570 | 0.1143 | 0.0917 | 0.0328 | 0.0900 | 0.2511 | 0.0567 | 0.0537 | 0.2547 | 0.8787 | 0.9143 | 0.4730 |
| GRIA2 | 0.26 | 1.20 | 0.0979 | 0.4018 | 0.0277 | 0.1049 | 0.0473 | 0.4048 | 0.1215 | 0.1012 | 1.3868 | 1.1191 | 1.1241 | 0.0884 |
| GRIA2.1 | 0.23 | 1.17 | 0.1153 | 0.3654 | 0.0245 | 0.1233 | 0.0789 | 0.5149 | 0.1489 | 0.1184 | 1.6684 | 1.4721 | 1.4187 | 0.0698 |
| GRIA3 | 0.07 | 1.05 | 0.2991 | 0.6719 | 0.2403 | 0.3014 | 0.4608 | 0.5183 | 0.0862 | 0.3124 | -0.1589 | -0.2558 | -0.2163 | 0.0130 |
| GRIA3.1 | -2.90 | 0.13 | 0.0003 | 0.0024 | 0.0007 | 0.0004 | 0.0007 | 0.0064 | 0.0004 | 0.0004 | -1.0682 | 1.9845 | 1.7270 | 1.8434 |
| GRIA3.2 | 0.10 | 1.07 | 0.4272 | 0.6309 | 0.6178 | 0.4410 | 0.5537 | 0.8816 | 0.4475 | 0.5116 | -0.1664 | -0.2099 | -0.3029 | 0.0499 |
| GRIA3.3 | 0.00 | 1.00 | 0.9750 | 0.9959 | 0.9881 | 0.9863 | 0.9974 | 0.8694 | 0.9692 | 0.9429 | -0.2128 | -0.2458 | -0.1858 | 0.0169 |
| GRIA3.4 | -0.49 | 0.71 | 0.0046 | 0.0128 | 0.0076 | 0.0061 | 0.0090 | 0.0500 | 0.0063 | 0.0051 | -0.4803 | 0.0392 | -0.0167 | 0.0814 |
| GRIA4 | -0.28 | 0.82 | 0.0066 | 0.0533 | 0.0163 | 0.0061 | 0.0163 | 0.0950 | 0.0092 | 0.0085 | -0.3500 | -0.0523 | -0.0827 | 0.0266 |
| GRIN1 | 0.38 | 1.30 | 0.1020 | 0.4842 | 0.0567 | 0.0986 | 0.0675 | 0.6503 | 0.1196 | 0.1134 | 0.8146 | 0.5876 | 0.3310 | 0.1975 |
| GRIN1.1 | 0.08 | 1.06 | 0.8396 | 0.8688 | 0.5107 | 0.8766 | 0.6473 | 0.7954 | 0.8738 | 0.8569 | 0.5112 | 0.3159 | 0.5077 | 0.4820 |
| GRIN1.2 | 0.20 | 1.15 | 0.5785 | 0.9790 | 0.4483 | 0.5931 | 0.5917 | 0.6076 | 0.5961 | 0.6301 | 0.3615 | -0.0055 | 0.2649 | 0.5214 |
| GRIN2A | -0.28 | 0.82 | 0.2796 | 0.2625 | 0.5533 | 0.2922 | 0.3287 | 0.7748 | 0.3051 | 0.2774 | -0.2149 | -0.0537 | 0.1404 | 0.2610 |
| GRIN2B | -0.07 | 0.95 | 0.5306 | 0.2962 | 0.4357 | 0.5829 | 0.4261 | 0.8942 | 0.6141 | 0.4690 | -0.2835 | -0.2488 | -0.1846 | 0.0353 |
| GRIN2C | -0.09 | 0.94 | 0.7761 | 0.7940 | 0.6451 | 0.7426 | 0.9993 | 0.7798 | 0.7926 | 0.8740 | 0.1129 | 0.2829 | 0.1513 | 0.3055 |
| GRIN2D | 0.12 | 1.09 | 0.7205 | 0.5947 | 0.7130 | 0.5973 | 0.8152 | 0.8301 | 0.6179 | 0.6667 | 0.1942 | 0.0415 | 0.0957 | 0.3711 |
| HTR1A | -0.28 | 0.82 | 0.0024 | 0.0438 | 0.0063 | 0.0021 | 0.0032 | 0.0455 | 0.0034 | 0.0038 | -0.3585 | -0.0491 | -0.0966 | 0.0186 |
| HTR1B | -0.13 | 0.91 | 0.0239 | 0.1792 | 0.0355 | 0.0338 | 0.0346 | 0.0226 | 0.0333 | 0.0327 | -0.2488 | -0.0318 | -0.1773 | 0.0054 |
| HTR2A | -0.12 | 0.92 | 0.2014 | 0.4612 | 0.2419 | 0.2251 | 0.3047 | 0.3432 | 0.2154 | 0.1939 | -0.2604 | -0.0935 | -0.1750 | 0.0259 |
| HTR2B | -0.16 | 0.90 | 0.3446 | 0.6849 | 0.3635 | 0.3382 | 0.4626 | 0.3011 | 0.3233 | 0.3171 | -0.2934 | 0.0073 | -0.2288 | 0.0863 |
| HTR2C | 0.83 | 1.78 | 0.0206 | 0.1465 | 0.0489 | 0.0255 | 0.0361 | 0.0743 | 0.0229 | 0.0233 | 0.5046 | -0.5921 | -0.1556 | 0.4975 |
| HTR3A | 0.27 | 1.20 | 0.2495 | 0.6780 | 0.3757 | 0.2767 | 0.4043 | 0.4247 | 0.2610 | 0.3085 | -0.0283 | -0.3676 | -0.2488 | 0.1958 |
| HTR3A.1 | 0.03 | 1.02 | 0.8687 | 0.7193 | 0.8875 | 0.8038 | 0.9783 | 0.9101 | 0.7955 | 0.9410 | 1.0120 | 1.0505 | 0.9437 | 0.0533 |
| HTR3C | 0.17 | 1.13 | 0.3250 | 0.8951 | 0.5727 | 0.3696 | 0.3547 | 0.1386 | 0.3354 | 0.2688 | 0.1949 | -0.2170 | 0.1822 | 0.0722 |
| HTR4 | 0.39 | 1.31 | 0.1763 | 0.3203 | 0.2851 | 0.1836 | 0.2283 | 0.7589 | 0.2236 | 0.1780 | 0.2979 | 0.1136 | -0.2338 | 0.3472 |
| HTR4.1 | 0.21 | 1.16 | 0.0766 | 0.3614 | 0.1428 | 0.0669 | 0.1483 | 0.2454 | 0.0848 | 0.1273 | -0.0729 | -0.3207 | -0.2651 | 0.0427 |
| HTR4.2 | -2.22 | 0.21 | 0.0000 | 0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0002 | 0.0000 | 0.0000 | -1.3025 | 1.0974 | 0.8029 | 0.1980 |
| HTR4.3 | -0.11 | 0.93 | 0.7767 | 0.8735 | 0.8288 | 0.7852 | 0.9659 | 0.9851 | 0.8300 | 0.8195 | 0.3718 | 0.3885 | 0.5401 | 0.4748 |
| HTR4.4 | -0.75 | 0.60 | 0.0003 | 0.0037 | 0.0010 | 0.0005 | 0.0009 | 0.0048 | 0.0006 | 0.0006 | -0.5470 | 0.4061 | 0.0628 | 0.0702 |
| HTR6 | 0.32 | 1.25 | 0.0471 | 0.1259 | 0.0116 | 0.0529 | 0.0340 | 0.5760 | 0.0567 | 0.0553 | 0.0971 | 0.0780 | -0.3158 | 0.0802 |
| HTR7 | -0.71 | 0.61 | 0.0001 | 0.0029 | 0.0005 | 0.0002 | 0.0004 | 0.0056 | 0.0002 | 0.0002 | -0.5816 | 0.2146 | 0.0719 | 0.0572 |
| HTR7.1 | 0.13 | 1.10 | 0.2350 | 0.2900 | 0.4020 | 0.2567 | 0.3366 | 0.6374 | 0.2574 | 0.2205 | -0.1161 | -0.2346 | -0.2617 | 0.0399 |
| HTR7.2 | 0.02 | 1.02 | 0.8028 | 0.4896 | 0.8150 | 0.7896 | 0.6376 | 0.8081 | 0.7008 | 0.8396 | -0.1707 | -0.1264 | -0.2375 | 0.0149 |
| HTR7.3 | -0.05 | 0.97 | 0.8130 | 0.7878 | 0.8868 | 0.8277 | 0.8387 | 0.8293 | 0.8063 | 0.8426 | -0.0769 | -0.1586 | 0.0590 | 0.1127 |
| MAP1A | -0.04 | 0.97 | 0.9455 | 0.8273 | 0.7735 | 0.9698 | 0.9304 | 0.8180 | 0.9417 | 0.9267 | 0.2778 | 0.0484 | 0.4934 | 0.9345 |
| MAP1A.1 | 0.46 | 1.37 | 0.0005 | 0.0109 | 0.0008 | 0.0008 | 0.0005 | 0.0145 | 0.0011 | 0.0002 | 1.9867 | 1.4715 | 1.5660 | 0.0316 |
| MAP1A.2 | -0.41 | 0.75 | 0.1266 | 0.2219 | 0.2620 | 0.0987 | 0.2322 | 0.4940 | 0.1214 | 0.1458 | 1.0567 | 1.4276 | 1.4862 | 0.2830 |
| MAP1B | 0.07 | 1.05 | 0.1429 | 0.3385 | 0.3201 | 0.1672 | 0.2664 | 0.1587 | 0.1540 | 0.2138 | -0.2204 | -0.3424 | -0.2595 | 0.0047 |
| MAP1B.1 | -0.21 | 0.87 | 0.0064 | 0.0450 | 0.0105 | 0.0051 | 0.0135 | 0.0534 | 0.0106 | 0.0069 | -0.3467 | -0.0890 | -0.1702 | 0.0134 |
| MAP1B.2 | -0.33 | 0.80 | 0.3117 | 0.2684 | 0.4734 | 0.3221 | 0.3988 | 0.8497 | 0.3313 | 0.2449 | -0.1613 | -0.0254 | 0.2951 | 0.4222 |
| MAP1B.3 | -0.55 | 0.68 | 0.1296 | 0.3958 | 0.3047 | 0.1242 | 0.2628 | 0.7175 | 0.1317 | 0.1292 | 0.2000 | 0.4851 | 0.9336 | 0.5733 |
| MAP2 | 0.04 | 1.03 | 0.7373 | 0.8042 | 0.9984 | 0.7092 | 0.9337 | 0.8202 | 0.6591 | 0.8497 | -0.1874 | -0.2444 | -0.2179 | 0.0353 |
| MAP2.1 | -0.03 | 0.98 | 0.6126 | 0.7762 | 0.6057 | 0.6207 | 0.6558 | 0.8560 | 0.5864 | 0.5280 | -0.2538 | -0.2279 | -0.2197 | 0.0079 |
| MAP2.5 | -0.26 | 0.83 | 0.0026 | 0.0296 | 0.0031 | 0.0032 | 0.0035 | 0.0615 | 0.0039 | 0.0025 | -0.3017 | -0.0268 | -0.0462 | 0.0167 |
| MAPT | -1.80 | 0.29 | 0.0002 | 0.0022 | 0.0006 | 0.0004 | 0.0006 | 0.0140 | 0.0004 | 0.0003 | -0.6305 | 1.0288 | 1.2646 | 0.6144 |
| MAPT.1 | 0.29 | 1.22 | 0.1655 | 0.4186 | 0.3368 | 0.1287 | 0.2818 | 0.4638 | 0.1844 | 0.2248 | -0.0756 | -0.3671 | -0.3621 | 0.1607 |
| SNAP25 | -0.24 | 0.85 | 0.7019 | 0.9686 | 0.9252 | 0.7179 | 0.8269 | 0.8820 | 0.6900 | 0.7035 | 0.9861 | 0.7850 | 1.5221 | 1.5746 |
| SNAP25.1 | 0.07 | 1.05 | 0.4919 | 0.9805 | 0.4233 | 0.4224 | 0.5790 | 0.8694 | 0.4833 | 0.5362 | -0.1943 | -0.2332 | -0.2840 | 0.0269 |
| SNAP25.2 | -1.32 | 0.40 | 0.0359 | 0.0522 | 0.0646 | 0.0389 | 0.0527 | 0.1071 | 0.0367 | 0.0242 | -0.3878 | 1.1541 | 0.7833 | 1.8628 |
| SYN1 | -0.04 | 0.97 | 0.9360 | 0.8488 | 0.9160 | 0.9981 | 0.9892 | 0.8622 | 0.9308 | 0.9039 | 0.4711 | 0.2847 | 0.6683 | 0.9535 |
| SYN1.1 | -0.25 | 0.84 | 0.1935 | 0.6310 | 0.2162 | 0.2138 | 0.2500 | 0.3104 | 0.1817 | 0.1521 | 1.0630 | 1.4405 | 1.2279 | 0.1277 |
| SYN3 | -0.11 | 0.93 | 0.6733 | 0.8110 | 0.5482 | 0.6787 | 0.3977 | 0.8624 | 0.7163 | 0.6593 | 0.4123 | 0.5110 | 0.5282 | 0.2093 |
| N.Significant | NA | NA | 6665 | 3510 | 5801 | 6518 | 5678 | 2504 | 6194 | 6583 | NA | NA | NA | NA |

Supplemental Table S5. Cofactorial analysis of genes of interest found in CA1 microarray data.

| Gene | Fold Change (log2) | Fold Change | Q-value (No Adjust) | Q (ADT) | Q (CNS Dis) | Q (pH) | Q (PMI) | Q (Suicide) | Q (Age) | Q (Sex) | A0S0 | A1S0 | A1S1 | Error Variance |
|---------------|--------------------|-------------|---------------------|---------|--------------|---------|---------|-------------|---------|---------|---------|---------|---------|----------------|
| DLG1 | -0.25 | 0.84 | 0.2476 | 0.8790 | 0.3488 | 0.1577 | 0.2378 | 0.6013 | 0.2604 | 0.2476 | 0.1795 | 0.4332 | 0.4234 | 0.1758 |
| DLG2 | -1.00 | 0.50 | 0.0076 | 0.1173 | 0.0065 | 0.0084 | 0.0099 | 0.0212 | 0.0115 | 0.0076 | -0.7665 | 0.7571 | -0.0287 | 0.4137 |
| DLG3 | -0.30 | 0.81 | 0.0025 | 0.0200 | 0.0055 | 0.0038 | 0.0023 | 0.0863 | 0.0038 | 0.0025 | -0.3947 | -0.0529 | -0.1118 | 0.0205 |
| DLG4 | -0.22 | 0.86 | 0.5703 | 0.4394 | 0.4459 | 0.5936 | 0.5594 | 0.9740 | 0.5636 | 0.5703 | -0.0041 | -0.0355 | 0.3467 | 0.6278 |
| GRIA1 | -1.20 | 0.44 | 0.0010 | 0.0130 | 0.0027 | 0.0013 | 0.0020 | 0.0234 | 0.0010 | 0.0010 | -0.7051 | 0.7668 | 0.3564 | 0.3517 |
| GRIA1.1 | -1.16 | 0.45 | 0.0004 | 0.0019 | 0.0017 | 0.0004 | 0.0006 | 0.0278 | 0.0006 | 0.0004 | -0.4895 | 0.7826 | 0.6131 | 0.2443 |
| GRIA2 | -0.08 | 0.95 | 0.8188 | 0.9806 | 0.5223 | 0.8696 | 0.8561 | 0.4293 | 0.8227 | 0.8188 | 0.7986 | 1.2971 | 0.6682 | 0.3495 |
| GRIA2.1 | 0.00 | 1.00 | 0.9940 | 0.9186 | 0.9699 | 0.8877 | 0.9853 | 0.8206 | 0.9939 | 0.9940 | 1.1719 | 1.3164 | 1.1034 | 0.2520 |
| GRIA3 | -1.25 | 0.42 | 0.0014 | 0.0714 | 0.0033 | 0.0020 | 0.0021 | 0.3433 | 0.0022 | 0.0014 | -0.2737 | 0.3441 | 1.2933 | 0.3974 |
| GRIA3.1 | -3.55 | 0.09 | 0.00001 | 0.0003 | 0.00004 | 0.00002 | 0.00002 | 0.0016 | 0.00001 | 0.00001 | -1.5570 | 2.1285 | 1.9230 | 0.7211 |
| GRIA3.2 | 0.20 | 1.15 | 0.3462 | 0.8663 | 0.3784 | 0.2345 | 0.3973 | 0.3472 | 0.3577 | 0.3462 | -0.0535 | -0.4153 | -0.1695 | 0.1350 |
| GRIA3.3 | -0.43 | 0.74 | 0.0227 | 0.2381 | 0.0538 | 0.0317 | 0.0283 | 0.5903 | 0.0280 | 0.0227 | -0.1362 | 0.0788 | 0.3999 | 0.1113 |
| GRIA3.4 | -0.29 | 0.82 | 0.0092 | 0.0187 | 0.0023 | 0.0125 | 0.0075 | 0.1300 | 0.0120 | 0.0092 | -0.3993 | -0.0551 | -0.1316 | 0.0327 |
| GRIA4 | -0.01 | 0.99 | 0.9323 | 0.5427 | 0.9151 | 0.9703 | 0.9228 | 0.8107 | 0.9341 | 0.9323 | -0.2485 | -0.1787 | -0.2649 | 0.0424 |
| GRIN1 | 0.13 | 1.10 | 0.7300 | 0.8584 | 0.9038 | 0.7556 | 0.7234 | 0.9983 | 0.7337 | 0.7300 | 0.2590 | 0.2570 | 0.0615 | 0.5147 |
| GRIN1.1 | 0.34 | 1.27 | 0.1700 | 0.5027 | 0.2004 | 0.1520 | 0.1827 | 0.3489 | 0.1757 | 0.1700 | 0.5298 | 0.0657 | 0.2522 | 0.2528 |
| GRIN1.2 | 0.19 | 1.14 | 0.2382 | 0.8246 | 0.4498 | 0.2595 | 0.2599 | 0.5808 | 0.2632 | 0.2382 | 0.0759 | -0.1173 | -0.1093 | 0.0878 |
| GRIN2A | -0.09 | 0.94 | 0.6069 | 0.7814 | 0.5782 | 0.4825 | 0.6151 | 0.6154 | 0.6168 | 0.6069 | 0.0137 | 0.1918 | 0.0548 | 0.0789 |
| GRIN2B | 0.16 | 1.12 | 0.1007 | 0.6349 | 0.1772 | 0.1165 | 0.1213 | 0.5733 | 0.0738 | 0.1007 | -0.1454 | -0.2717 | -0.3240 | 0.0287 |
| GRIN2C | 0.01 | 1.01 | 0.9734 | 0.9394 | 0.8364 | 0.9086 | 0.9751 | 0.9622 | 0.9737 | 0.9734 | 0.1580 | 0.1337 | 0.1580 | 0.1330 |
| GRIN2D | -0.04 | 0.97 | 0.9147 | 0.4722 | 0.9087 | 0.9171 | 0.8670 | 0.8001 | 0.9185 | 0.9147 | 0.0083 | 0.1835 | -0.0161 | 0.4198 |
| HTR1A | -0.07 | 0.95 | 0.5089 | 0.3129 | 0.6483 | 0.5491 | 0.5298 | 0.3076 | 0.5391 | 0.5089 | -0.2053 | -0.0063 | -0.2008 | 0.0233 |
| HTR1B | 0.06 | 1.04 | 0.7395 | 0.9038 | 0.5128 | 0.6605 | 0.7471 | 0.9984 | 0.7368 | 0.7395 | -0.0817 | -0.0826 | -0.1723 | 0.0884 |
| HTR2A | -0.29 | 0.82 | 0.1561 | 0.3844 | 0.2174 | 0.1573 | 0.1647 | 0.3811 | 0.1567 | 0.1561 | -0.3068 | 0.0130 | -0.0391 | 0.1465 |
| HTR2B | -0.20 | 0.87 | 0.0578 | 0.1065 | 0.0456 | 0.0686 | 0.0693 | 0.4677 | 0.0647 | 0.0578 | -0.3168 | -0.1530 | -0.1057 | 0.0300 |
| HTR2C | 0.09 | 1.06 | 0.6376 | 0.9474 | 0.6557 | 0.6318 | 0.6693 | 0.6033 | 0.6400 | 0.6376 | -0.1202 | -0.3000 | -0.1589 | 0.0963 |
| HTR3A | 0.28 | 1.21 | 0.0153 | 0.2099 | 0.0203 | 0.0105 | 0.0204 | 0.3741 | 0.0195 | 0.0153 | -0.0366 | -0.2403 | -0.3505 | 0.0338 |
| HTR3A.1 | -0.03 | 0.98 | 0.9166 | 0.8631 | 0.9504 | 0.9196 | 0.9671 | 0.6280 | 0.9163 | 0.9166 | 1.0783 | 1.3107 | 1.0040 | 0.1603 |
| HTR3C | 0.40 | 1.32 | 0.0760 | 0.7493 | 0.1277 | 0.0685 | 0.0873 | 0.1320 | 0.0794 | 0.0760 | 0.1989 | -0.4515 | -0.0757 | 0.1755 |
| HTR4 | 0.36 | 1.28 | 0.1672 | 0.9306 | 0.1996 | 0.1077 | 0.1892 | 0.2490 | 0.1747 | 0.1672 | 0.2343 | -0.3687 | -0.0052 | 0.2573 |
| HTR4.1 | -0.02 | 0.99 | 0.8846 | 0.8283 | 0.8911 | 0.9108 | 0.9141 | 0.7835 | 0.8886 | 0.8846 | -0.2317 | -0.1669 | -0.2385 | 0.0266 |
| HTR4.2 | -0.90 | 0.54 | 0.0003 | 0.0014 | 0.0013 | 0.0002 | 0.0006 | 0.0515 | 0.0005 | 0.0003 | -0.6110 | 0.2206 | 0.3260 | 0.1306 |
| HTR4.3 | 0.12 | 1.08 | 0.7326 | 0.9185 | 0.7622 | 0.7667 | 0.7285 | 0.7318 | 0.7345 | 0.7326 | 0.3656 | 0.1271 | 0.3086 | 0.4001 |
| HTR4.4 | -0.58 | 0.67 | 0.0022 | 0.0295 | 0.0049 | 0.0032 | 0.0032 | 0.0883 | 0.0031 | 0.0022 | -0.4643 | 0.1339 | 0.1002 | 0.0897 |
| HTR6 | 0.06 | 1.04 | 0.7832 | 0.8290 | 0.9285 | 0.8071 | 0.7798 | 0.8730 | 0.7900 | 0.7832 | 0.0478 | 0.1205 | 0.0747 | 0.1118 |
| HTR7 | -0.55 | 0.68 | 0.0003 | 0.0018 | 0.0008 | 0.0006 | 0.0006 | 0.0297 | 0.0006 | 0.0003 | -0.5262 | 0.0750 | -0.0015 | 0.0399 |
| HTR7.1 | 0.19 | 1.14 | 0.2649 | 0.4640 | 0.5384 | 0.2578 | 0.1812 | 0.3986 | 0.2820 | 0.2649 | 0.3085 | -0.0049 | 0.1803 | 0.0978 |
| HTR7.2 | 0.05 | 1.03 | 0.6141 | 0.9952 | 0.5378 | 0.6253 | 0.6552 | 0.7522 | 0.6220 | 0.6141 | -0.1432 | -0.2057 | -0.1802 | 0.0189 |
| HTR7.3 | 0.02 | 1.02 | 0.9217 | 0.9859 | 0.8870 | 0.9765 | 0.9579 | 0.7319 | 0.9229 | 0.9217 | -0.0002 | -0.1467 | 0.0394 | 0.1228 |
| MAP1A | -0.02 | 0.98 | 0.9532 | 0.9973 | 0.8880 | 0.9385 | 0.9643 | 0.7748 | 0.9513 | 0.9532 | 0.1015 | 0.3124 | 0.0308 | 0.4167 |
| MAP1A.1 | 0.18 | 1.14 | 0.3669 | 0.5131 | 0.7830 | 0.2782 | 0.3617 | 0.8884 | 0.3514 | 0.3669 | 1.6159 | 1.6890 | 1.3028 | 0.1447 |
| MAP1A.2 | -0.93 | 0.53 | 0.0250 | 0.1480 | 0.0158 | 0.0314 | 0.0293 | 0.1705 | 0.0278 | 0.0250 | 0.4402 | 1.5712 | 1.2671 | 0.7618 |
| MAP1B | 0.06 | 1.04 | 0.8229 | 0.9725 | 0.7972 | 0.8221 | 0.8421 | 0.8580 | 0.8266 | 0.8229 | -0.1339 | -0.2326 | -0.1695 | 0.1859 |
| MAP1B.1 | 0.10 | 1.08 | 0.5731 | 0.6040 | 0.5378 | 0.5028 | 0.5286 | 0.3501 | 0.5796 | 0.5731 | 0.0079 | -0.2957 | 0.0027 | 0.0923 |
| MAP1B.2 | -0.19 | 0.88 | 0.2042 | 0.5752 | 0.2404 | 0.2165 | 0.2268 | 0.2681 | 0.2164 | 0.2042 | -0.2238 | 0.1109 | -0.1066 | 0.0645 |
| MAP1B.3 | -0.85 | 0.56 | 0.0044 | 0.0744 | 0.0028 | 0.0056 | 0.0065 | 0.0392 | 0.0051 | 0.0044 | -0.3417 | 0.8674 | 0.3238 | 0.2498 |
| MAP2 | -0.05 | 0.97 | 0.6325 | 0.8044 | 0.7468 | 0.6292 | 0.6469 | 0.6785 | 0.6306 | 0.6325 | -0.2400 | -0.3188 | -0.1317 | 0.0167 |
| MAP2.1 | 0.16 | 1.12 | 0.1699 | 0.6219 | 0.2361 | 0.1443 | 0.1887 | 0.8576 | 0.1813 | 0.1699 | -0.1448 | -0.1948 | -0.3558 | 0.0356 |
| MAP2.5 | -0.32 | 0.80 | 0.0108 | 0.0275 | 0.0301 | 0.0141 | 0.0126 | 0.3020 | 0.0129 | 0.0108 | -0.3197 | -0.0767 | 0.0418 | 0.0400 |
| MAPT | -0.70 | 0.61 | 0.0052 | 0.0255 | 0.0155 | 0.0078 | 0.0079 | 0.0524 | 0.0072 | 0.0052 | -0.0618 | 0.9404 | 0.4935 | 0.1810 |
| MAPT.1 | 0.01 | 1.01 | 0.9718 | 0.6283 | 0.9787 | 0.9433 | 0.9910 | 0.9776 | 0.9702 | 0.9718 | -0.1519 | -0.1653 | -0.1569 | 0.1095 |
| SNAP25 | -0.65 | 0.64 | 0.2142 | 0.9454 | 0.2180 | 0.1155 | 0.2195 | 0.3465 | 0.2277 | 0.2142 | 0.4781 | 1.4697 | 0.9560 | 1.3413 |
| SNAP25.1 | 0.37 | 1.29 | 0.0470 | 0.1910 | 0.0698 | 0.0532 | 0.0551 | 0.2985 | 0.0534 | 0.0470 | 0.1213 | -0.2882 | -0.2308 | 0.1256 |
| SNAP25.2 | -1.36 | 0.39 | 0.0039 | 0.0523 | 0.0098 | 0.0055 | 0.0053 | 0.1273 | 0.0026 | 0.0039 | -0.5574 | 0.7627 | 0.8152 | 0.8465 |
| SYN1 | -0.21 | 0.86 | 0.6279 | 0.8295 | 0.4184 | 0.5270 | 0.6222 | 0.8309 | 0.6291 | 0.6279 | 0.0644 | 0.2518 | 0.2909 | 0.7812 |
| SYN1.1 | -0.35 | 0.78 | 0.3506 | 0.4182 | 0.4165 | 0.3512 | 0.3573 | 0.7899 | 0.3664 | 0.3506 | 1.0264 | 1.2650 | 1.4369 | 0.6631 |
| SYN3 | -0.82 | 0.57 | 0.0005 | 0.0138 | 0.0015 | 0.0009 | 0.0009 | 0.0071 | 0.0009 | 0.0005 | -0.2005 | 0.9943 | 0.4249 | 0.0728 |
| N.Significant | NA | NA | 7050 | 3343 | 5482 | 7043 | 6646 | 904 | 6711 | 7050 | NA | NA | NA | NA |

Legend for Supplemental Tables 4 and 5:

| | |
|----------------------------|---|
| Gene | Gene Symbol |
| Q-value (No Adjust) | Unadjusted model (Q value) |
| Q (ADT) | Controlling for antidepressant prescription (Q value) |
| Q (CNS Dis) | Controlling for neurological disease (Q value) |
| Q (pH) | Controlling for pH (Q value) |
| Q (PMI) | Controlling for PMI (Q value) |
| Q (Suicide) | Controlling for mode of death (Q value) |
| Q (Age) | Controlling for age (Q value) |
| Q (Sex) | Controlling for gender (Q value) |
| A0S0 | Control – non-suicidal (model-based mean estimate) |
| A1S0 | Depressed – non-suicidal (model-based mean estimate) |
| A1S1 | Depressed – suicidal (model-based mean estimate) |
| Error Variance | Error variance of the model |
| N. Significant | Number of significant ($Q < .05$) genes across entire array |

Supplemental Table S6. Human subject samples used in qPCR analysis and names of the genes that were assessed in each subpopulation of DG and CA1 cohorts (n=5-6).

Denate Gyrus

qPCR Experiment #1 (n=6)

| <i>Control</i> | <i>MDD</i> | <i>Gene(s) assessed</i> |
|----------------|------------|-------------------------|
| 23D | 5B | DLG2/SAP93 |
| 13D | 11B | MAP1a |
| 20D | 20B | MAP1b |
| 21D | 21B | AMPA1 |
| 22D | 22B | |
| 17D | 23B | |

qPCR Experiment #2 (n=6)

| <i>Control</i> | <i>MDD</i> | <i>Gene(s) assessed</i> |
|----------------|------------|-------------------------|
| 4D | 4B | SNAP25 |
| 23D | 5B | AMPA3 |
| 13D | 11B | HTR4 |
| 18D | 18B | HTR7 |
| 22D | 22B | |
| 17D | 23B | |

qPCR Experiment #3 (n=5)

| <i>Control</i> | <i>MDD</i> | <i>Gene(s) assessed</i> |
|----------------|------------|-------------------------|
| 3D | 3B | HTR2c |
| 4D | 4B | |
| 13D | 11B | |
| 7D | 14B | |
| 18D | 18B | |

CA1

qPCR Experiment #4 (n=6)

| <i>Control</i> | <i>MDD</i> | <i>Gene(s) assessed</i> |
|----------------|------------|-------------------------|
| 8D | 8B | DLG2/SAP93 |
| 6D | 13B | SNAP25 |
| 16D | 16B | MAP1a |
| 23D | 17B | MAP1b |
| 19D | 19B | HTR2c |
| 4D | 23B | |

qPCR Experiment #5 (n=6)

| <i>Control</i> | <i>MDD</i> | <i>Gene(s) assessed</i> |
|----------------|------------|-------------------------|
| 6D | 13B | AMPA1 |
| 14D | 14B | AMPA3 |
| 23D | 17B | HTR4 |
| 15D | 18B | HTR7 |
| 22D | 22B | |
| 4D | 23B | |

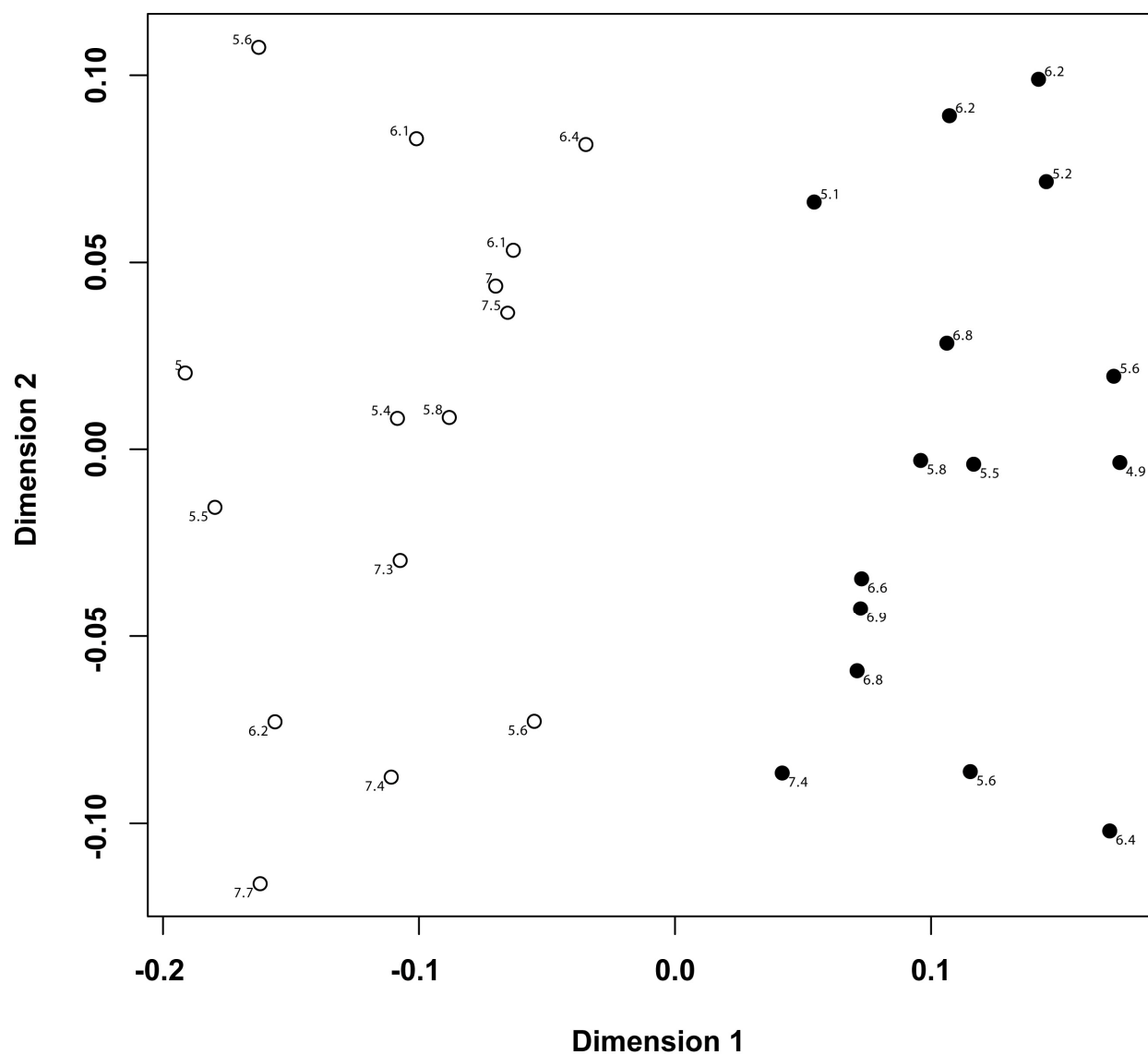
Supplemental Table S7. Human primers used in qPCR analysis.

| Gene | Forward Primer | Reverse Primer |
|-------------|----------------------------------|--------------------------------|
| GAPDH | 5'-cgggaaactgtggcgtgatgg-3' | 5'-gccagtgagctcccgttcagc-3' |
| Cyclophilin | 5'-caaatcagaatgggacaggtggag-3' | 5'-gtttgtgtgcggcctgcatttg-3' |
| HMBS | 5'-gcttcctcctggcttcacccatcg-3' | 5'-ctttctctgcagctgggctgctc-3' |
| B-Tubulin | 5'-cagggcttcagctgacccactc-3' | 5'-gtgagggcatgacgctgaagggtg-3' |
| GLUR1 | 5'-cggaaaccctgtgacaccatgaag-3' | 5'-cgccctgtctgaccaccatttg-3' |
| GLUR3 | 5'-catgaaatcagcggagccatctg-3' | 5'-catggtgactccagcaggaagg-3' |
| GLUR4 | 5'-cactgggagtggtggagagaatgg-3' | 5'-cgatgcaatgacagccaatctg-3' |
| HTR2C | 5'-caacacgacgtgctgctcaac-3' | 5'-ctcgggtggccgtgcagtaac-3' |
| HTR4 | 5'-ctgggcagggtggactgcttc-3' | 5'-cttcggtagcgtcatcatcacagc-3' |
| HTR7 | 5'-ctgtgctgatcagcattgacagg-3' | 5'-gctggagagaagccagacggagag-3' |
| SNAP25 | 5'-gccagcctgctcgtgtagtggac-3' | 5'-gtgacggaggtcccgatgatgc-3' |
| ITGB1 | 5'-gcctctgggctttacggaggaag-3' | 5'-caacacgcccttcattgcacctg-3' |
| DLG2 | 5'-cagtgggctgccaagtcaaggac-3' | 5'-cgggcacgttcctttctttccac-3' |
| MAP1A | 5'-cagtgccaccacacacccttc-3' | 5'-gcagcatctctttgcccacacc-3' |
| MAP1B | 5'-gtgtgaacttctctctgacgccaatg-3' | 5'-gccagtcacggactgagatggtg-3' |

Supplemental Table S8. Rat primers used in *in situ* hybridization experiments. T7 polymerase-binding promoter sequence was added to the 5' end of the reverse primer (5'CCAAGCCTTCTAATACGACTCACTATAGGGAGA3').

| Gene | Forward Primer | Reverse Primer |
|-------------|-------------------------------|-------------------------------|
| SNAP25 | 5'-cgaacaactggaacgcattgag-3' | 5'-gtttgtaccctgcggatgaagc-3' |
| GLUR1 | 5'-cgaaggtttgacaggaaatgtgc-3' | 5'-gtagccctcatagcggtcattgc-3' |
| GLUR3 | 5'-gcagaagccttccgatacctgag-3' | 5'-cggttctctgaggatgagctgac-3' |
| HTR4 | 5'-ctctgctgcattccctggatag-3' | 5'-gtgatggcatagggcttgtgac-3' |

Supplemental Figure S1. Two-dimensional non-metric multi-dimensional scaling analysis from the DG samples on the basis of the genes in Supplemental Table 4.



Supplemental Figure S2. Two-dimensional non-metric multi-dimensional scaling analysis from the CA1 samples on the basis of the genes in Supplemental Table 5.

