Supporting Information

Benes et al. 10.1073/pnas.0903066106

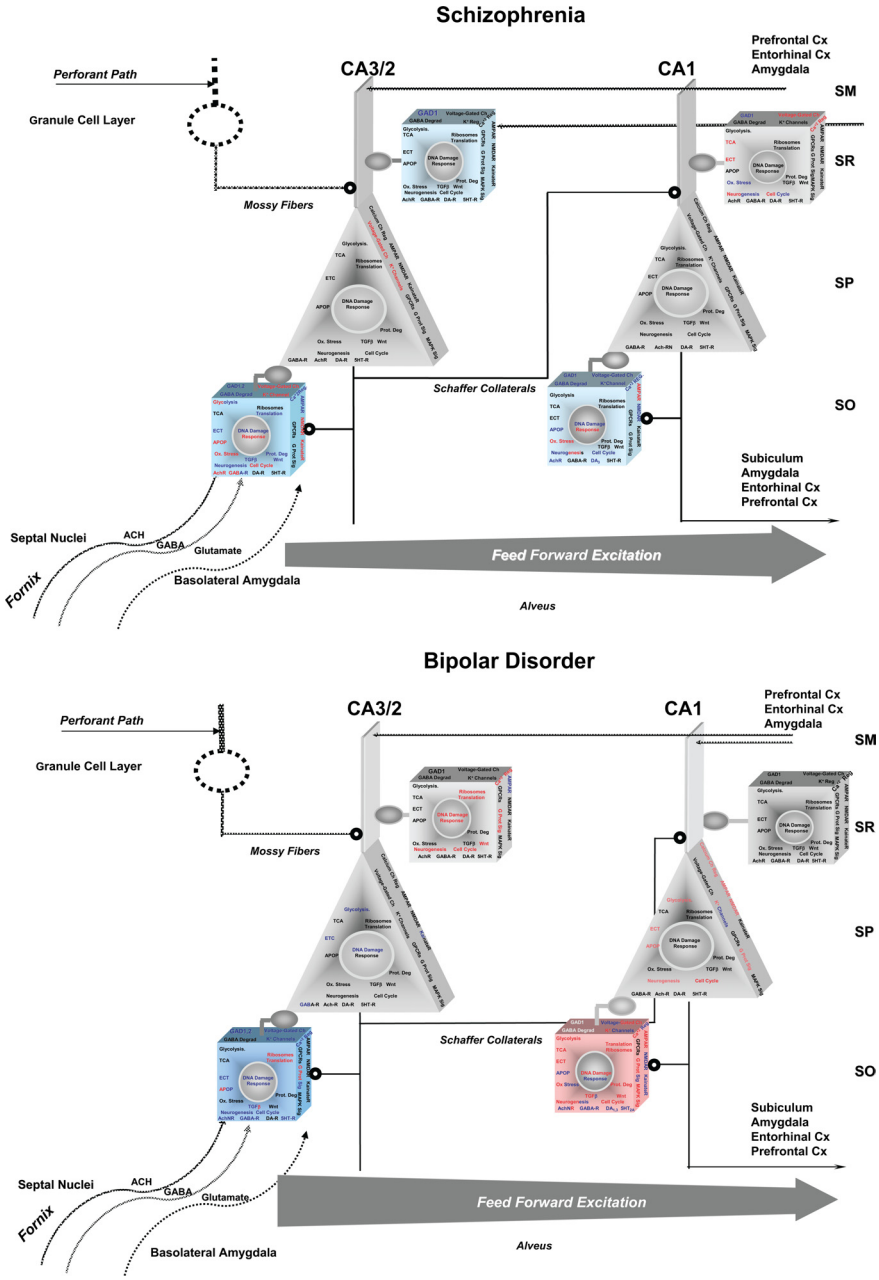


Fig. S1. Schematic diagrams of the trisynaptic pathway showing pyramidal neurons (triangular) and GABA cells (square) in stratum oriens (SO), stratum pyramidal (SP) and stratum radiatum (SR) of sectors CA3/2 and CA1. The perforant path projection from the entorhinal cortex project to the granule cells and these in turn send mossy fiber projections that synapse on the apical dendrites of pyramidal neurons in sector CA3/2. The latter cell sends projects axons into the SO where they travel as Schaffer collaterals that eventually form excitatory synapse with the apical dendrites of pyramidal neurons in sector CA1. Collateral branches of pyramidal neurons in CA3/2 and CA1 form synapses GABAergic interneurons on the SO. The arrows at the bottom of each diagram show the direction of feed forward excitation along the trisynaptic pathway and suggest that this may be increased in schizophrenics (*Upper*), because of diminished GABAergic tone in both CA3/2 and CA1. In BDs (*Lower*), however, feed forward excitation may be attenuated at the level of CA1, because of the heightened activity of GABA cells with in SO at this locus.

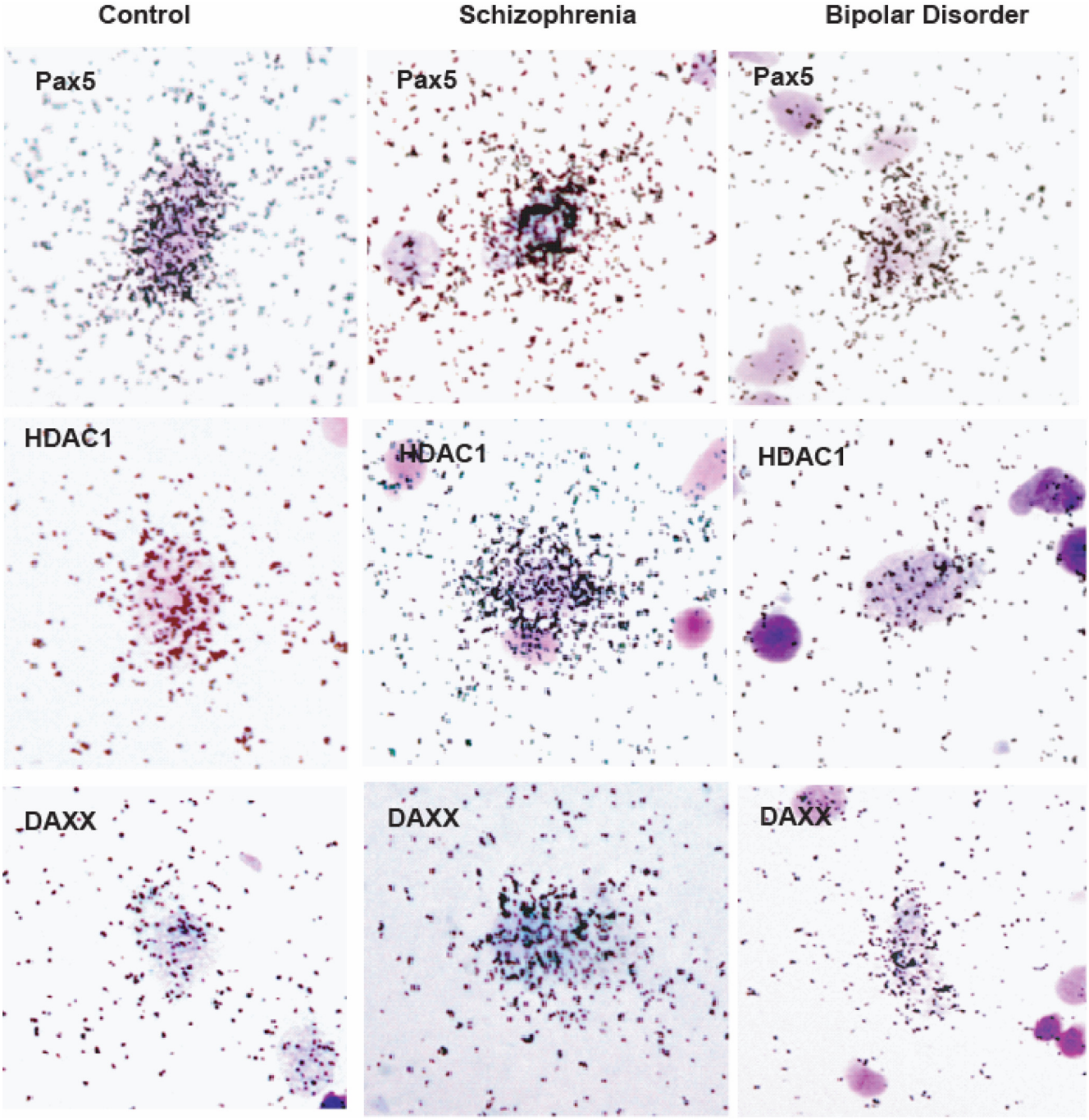


Fig. S2. Photomicrographs showing in situ hybridization studies of HDAC1, DAXX and PAX5 in the stratum oriens of sector CA3/2 of normal controls, schizophrenics and bipolars. The density of autoradiographic grains representing antisense RNA labeled with [^{35}S] for HDAC1 and DAXX is greater in schizophrenic patients, whereas that for PAX5 is lower in bipolars.

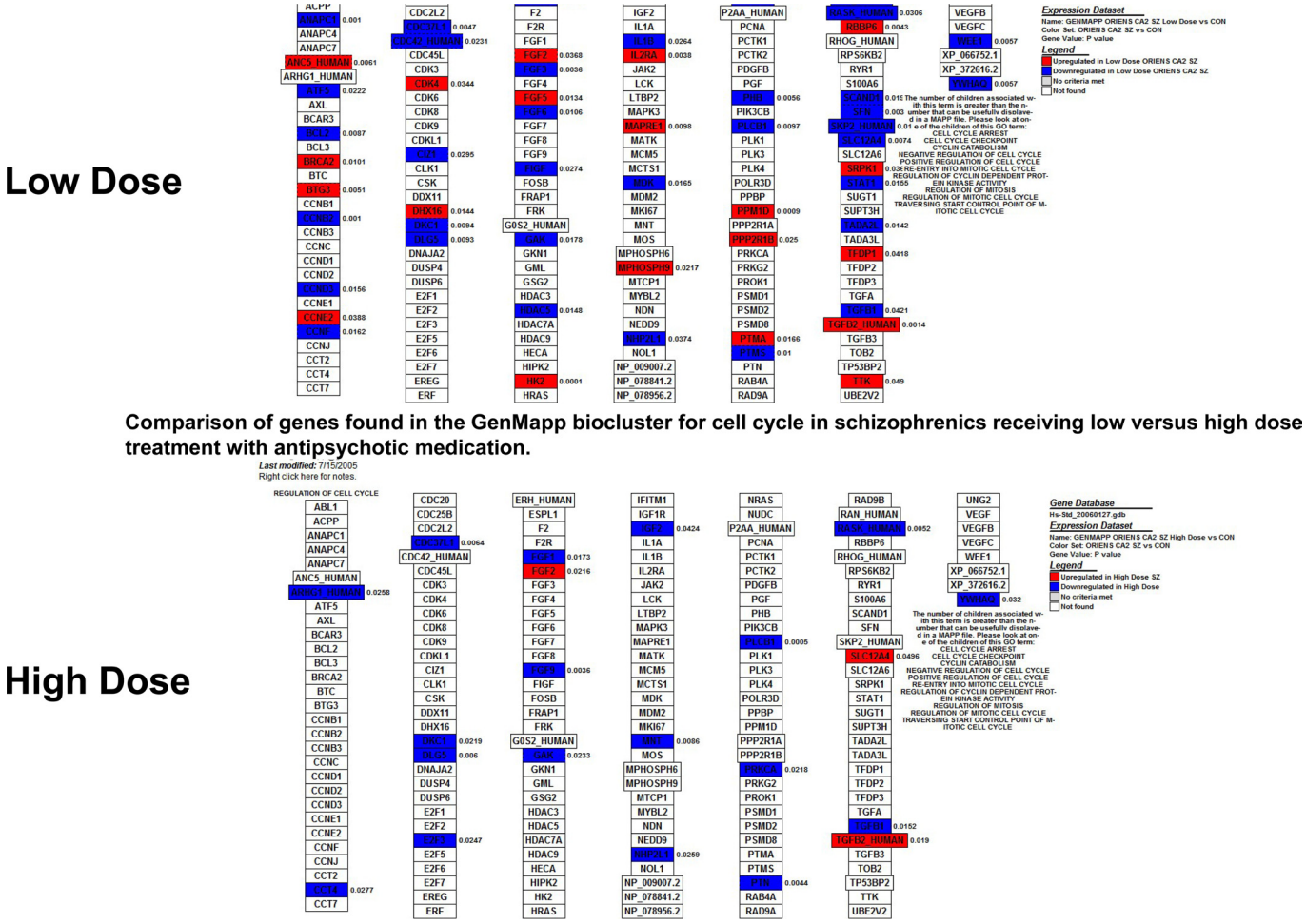
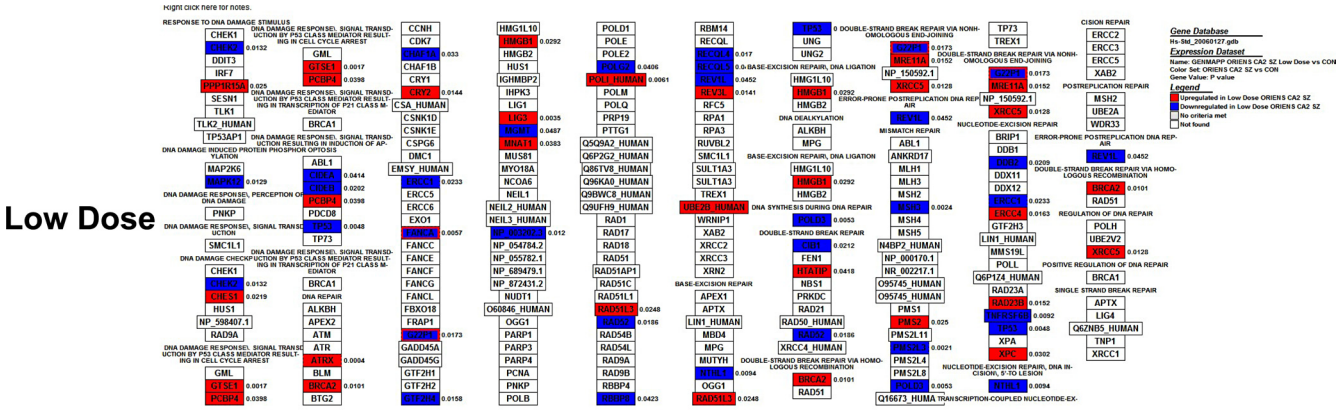


Fig. S3. Comparison of expression changes in GenMapp functional gene clusters for schizophrenic patients receiving low (≤500 mg of chlorpromazine equivalents) versus high (≥500 mg of chlorpromazine equivalent) dose of antipsychotic medications. (*A*) Cell cycle cluster. (*B*) DNA damage repair.



Comparison of genes found in the GenMapp biocluster for the DNA damage response in schizophrenics receiving low versus high dose treatment with antipsychotic medication.

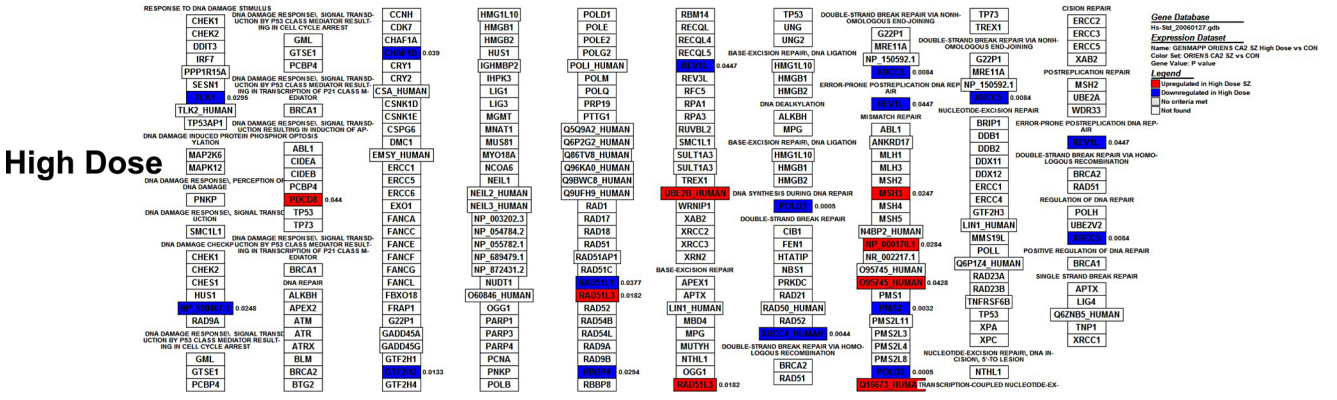


Fig. S3 (continued).

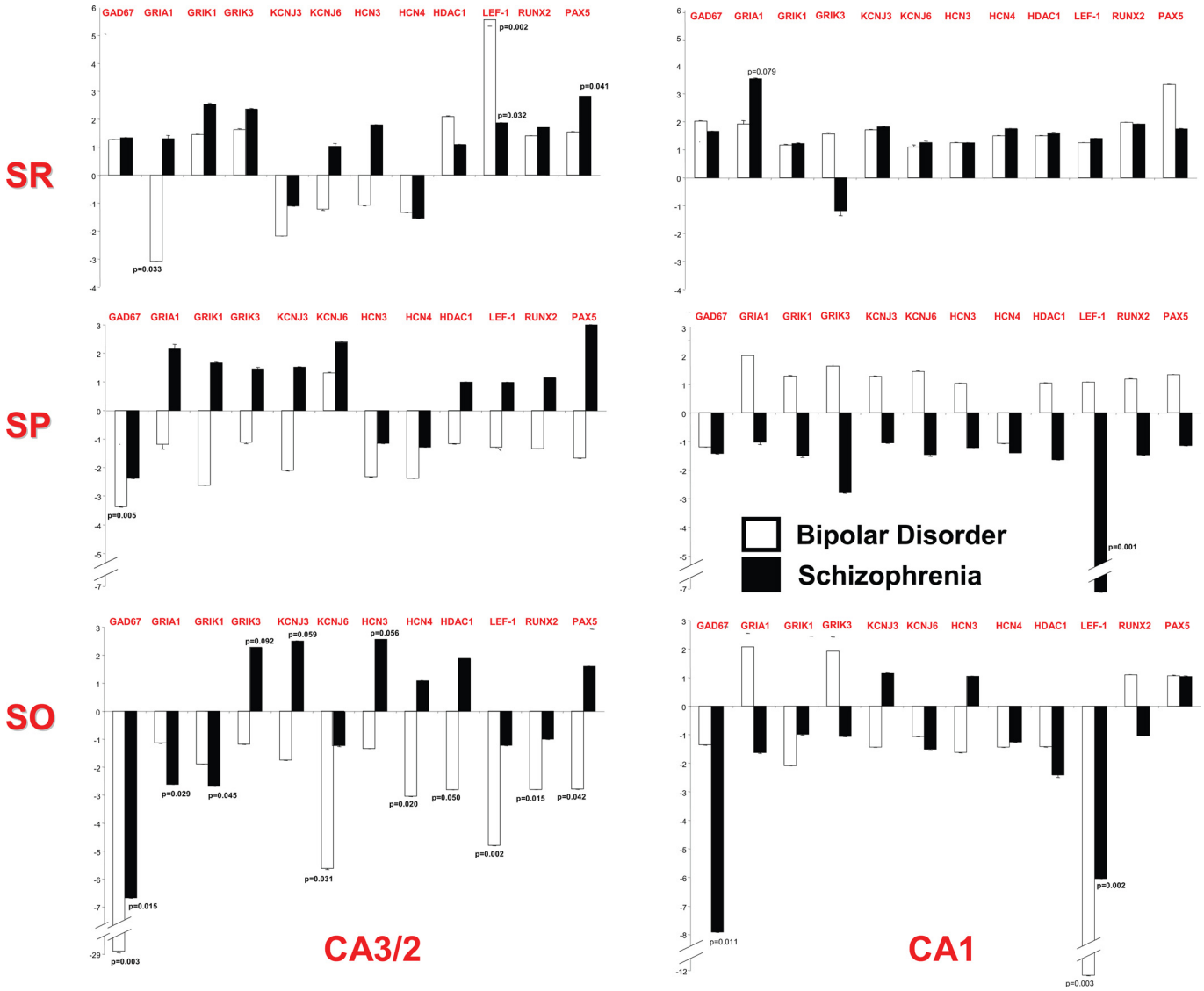


Fig. S4. Quantitative RT-PCR validation of microarray-based gene expression profiling data in the stratum radiatum, stratum pyramidale and stratum oriens of sectors CA3/2 and CA1 of schizophrenic and bipolar patients. The results for GAD_{67}, GRIA1, GRIK1, GRIK3, KCNJ3, KCNJ6, HCN3, HCN4, HDAC1, LEF1, Runx2 and PAX5 show changes in the same direction as those observed with microarray. The error bars are very small and in some cases are not visible. The *P* values for the REST analyses are quite robust, particularly in the stratum oriens of CA3/2 where almost all of the target genes show significant changes. The error bars for GAD_{67} appear to be larger than those of the other genes, because of the proportions of the graph needed to accommodate the data for all of the genes. On a percentage basis, the error bars for GAD_{67} when expressed as a percentage of the mean, are relatively similar to those for the other genes.

Other Supporting Information Files

Table S1
Table S2
Table S3
Table S4
Table S5
Table S6