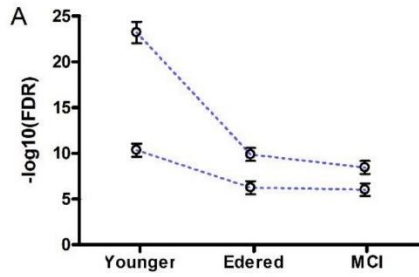
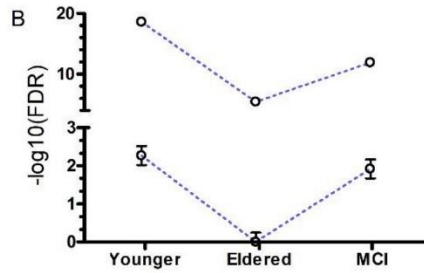


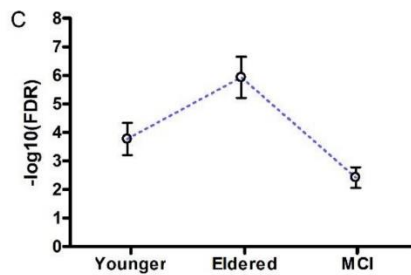
Supplementary Materials



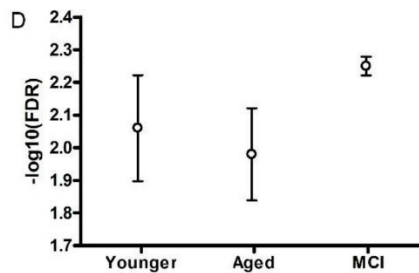
Group 1. Decreased in aging, but falling was kept in the MCI. The upper curve represents the evolution of the “somato-dendritic compartment”, “dendritic tree”, “axon”, “synapses”, and “post-synapses”. The lower curve represents the evolution of ontologies categories as “pre-synapses”, “dendritic shafts”, and “dendritic spines”.



Group 2. Decreased in aging, but compensated in the MCI. The upper curve represents the evolution of “glutamatergic synapses”, whereas the lower curve represents the evolution of ontology classes as “CA3 pyramidal cell dendrites”, “Schaffer collateral synapses”, “guanylate complex soluble”, and “Calcium channel complex”.



Group 3. Up-regulated in aging, but decreased in the MCI. This group includes ontology classes as “synaptic vesicles”, “exocytic vesicles”, and “secretory vesicles”.



Group 4. Ontology classes only significant in a given stage. **Younger Group:** “astrocyte projection”, “Ranvier nodes”, “caveola”, “voltage-gated Na⁺ channels”, “rough endoplasmic reticulum”, “synaptobrevin2-SNAP25-syntaxin 1a-complexin II complex”, “PML body”, “Golgi apparatus”; **Elderled Group:** “dense core granule”, “voltage-gated K⁺ channel”, “death-inducing signal complex”, “Bim-Bcl2 complex”, “caspase complex”, “pore complex”, “amyloidβ complex”, “γ-secretase complex”, “cAMP-dependent complex”, “NURF complex”, “neuronal ribonucleoprotein complex”; **MCI Group:** “heterotrimeric G protein complex”, “GTPase complex”, “excitatory synapses”, “ionotropic selective glutamate receptors”, “AMPA selective glutamate receptors”.

Figure S1. Main profiles across the three stages analyzed (Younger, Elderled, and MCI) as derived from the cell-component ontology analysis. The ontologies found significant were grouped by hierarchical cluster analysis using $(1-R_{\text{Spearman}})$ as metric of correlation distance, and “average” as criterium of linkage function. The error bars cover the confidence intervals for a level $(1-\alpha) = 0.95$. The significances in the y-axis are quantified as $-\log_{10}(\text{FDR})$, where FDR is the false discovery rate. For details about the gene composition corresponding to each ontology class, see the Supplementary Tables S1–S3.

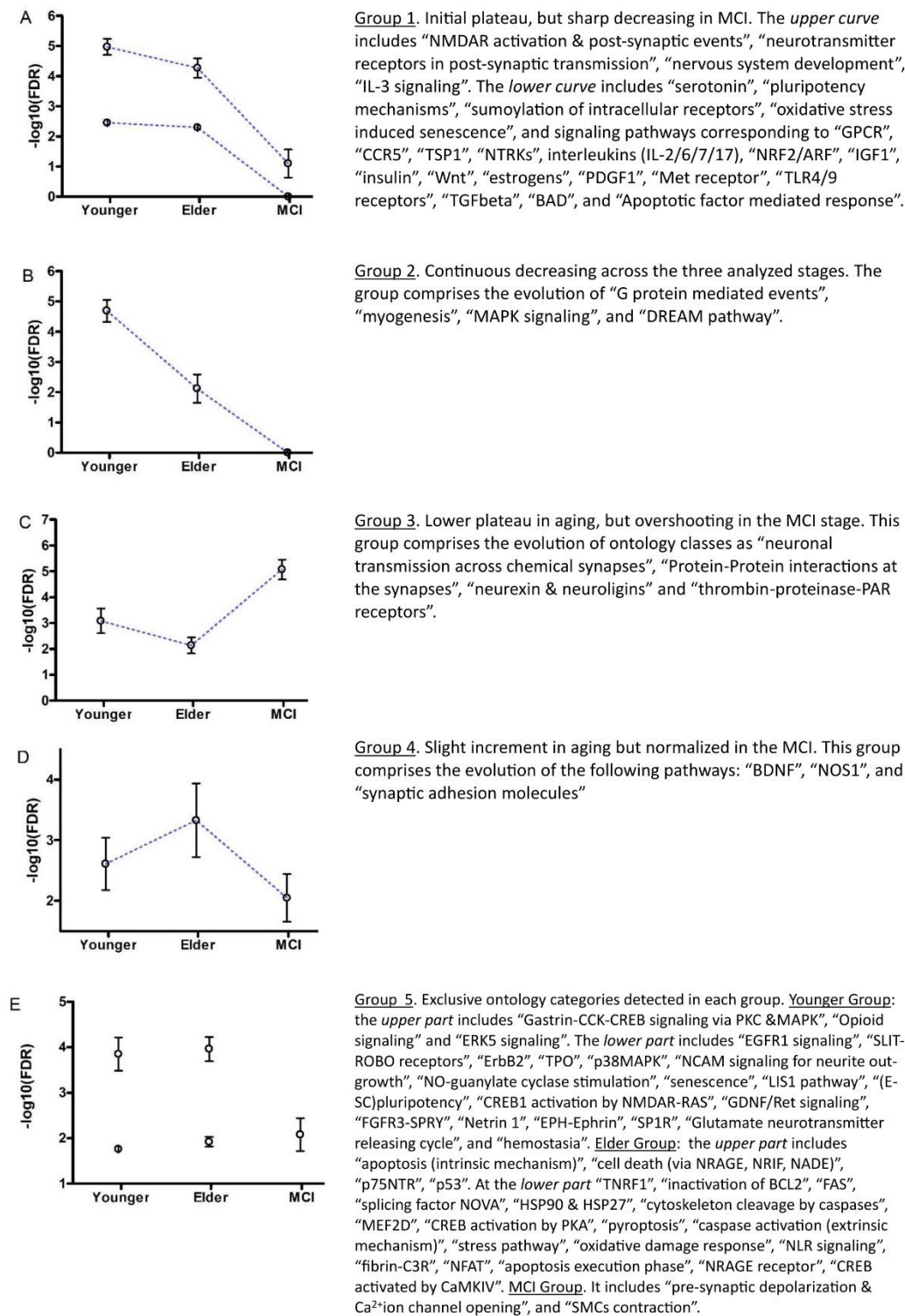


Figure S2. Main profiles across the three stages analyzed (Younger, Elder, and MCI) as derived from the pathway analysis. The ontologies found significant were grouped by hierarchical cluster analysis using (1- R_{Spearman}) as metric of correlation distance, and “average” as criterium of linkage function. The error bars cover the confidence intervals for a level $(1-\alpha) = 0.95$. The significances in the y-axis are quantified as $-\log_{10}(\text{FDR})$, where FDR is the false discovery rate. For details about the genes involved in each pathway, see the Supplementary Tables S1–S3.