



Fig. S2 (A,B) UMAP embedding of single nuclei RNA sequencing data from CA3 of hippocampus of 24M *MAPT* KI, S305N and P301S mice (N=4, sex matched). Each dot represents a cell that is coloured according to the genotype (**A**) or broad cell-type annotation (**B**). OPC: oligodendrocyte progenitor cells. (**C**) Relative proportion of broad cell-types between lines (info in A,B). (**D,E**) Density plots per cell-types of gene counts (**D**) and fraction of mitochondrial reads (**E**). Note that x-axes are displayed in log scale. (F) UMAP embedding of neuronal cells. Each cell is coloured according to its fine-grained identity (Supplementary table 6 for a full description). (**G,H**) Volcano plots displaying differentially expressed genes (in red, $|\text{Log}_2\text{FC}| > 0.5$ and adjusted p-value < 0.05) between S305N and *MAPT* KI (**G**) and P301S and *MAPT* KI (**H**). (**I**) Upset plot highlighting the fraction of shared or unique differentially expressed genes for each comparison.