**R code for Pokhilko, et.al. 2022.**

To simulate kinetics of mTOR pathway (Fig. S1, Fig. S2), run

mTOR\_ode\_kinetics\_insulin.R; mTOR\_ode\_kinetics\_PDGF.R; mTOR\_ode\_kinetics\_NRG.R

For **Fig. 2**, Fig. S4,S5 run

correlation\_plots.R

For **Fig. 3B-E**,run

S6Ka\_EC50\_plots.R

For **Fig. 3A** run

dose\_response\_plots.R

For **Fig. 4** run

S6Ka\_EC50\_ADplots.R

For **Fig.5** run

summary\_Fig.R

normalized expression values for mTOR components in brain cell types are stored in

snRNAseq\_grouped\_upquant\_0422.csv; snRNAseq\_grouped\_upquant\_AD\_0422.csv (for AD)

these files were generated using mTOR\_expression.R (also used for Fig. S3, S6)

results on S6Ka and EC50 are stored in files

S6Ka\_max\_EC50\_all.csv; S6Ka\_max\_EC50\_all\_AD.csv (for AD)

these files were generated using S6Ka\_EC50\_calculate.R