

Description of Additional Supplementary Files

Supplementary Data 1. Mouse models used in this study

Supplementary Data 2. Summary of mouse samples for profiling whole proteome, phosphoproteome, and proteome turnover in this study

Supplementary Data 3. Whole proteome profiling of mouse brain tissues

Supplementary Data 4. A β levels in mouse models

Supplementary Data 5. Age-related protein changes in mice

Supplementary Data 6. GO Enrichment analysis of proteins altered in aging

Supplementary Data 7. DE analysis of whole proteome of mouse brain tissues

Supplementary Data 8. A β levels correlate to the numbers of DEP in AD mice

Supplementary Data 9. GO analysis of shared 597 DE proteins in 5xFAD and NLGF

Supplementary Data 10. Complete list of identified phosphopeptides in the mouse analysis

Supplementary Data 11. Profiling of shared phosphopeptides in the mouse analysis

Supplementary Data 12. DE analysis of phosphoproteome of mouse brain tissues

Supplementary Data 13. GO Enrichment analysis of changed phosphoproteins

Supplementary Data 14. Consensus 866 DE proteins in AD and the conserved DE proteins in mice

Supplementary Data 15. Derived activity of key pathways in AD and mouse models

Supplementary Data 16. Whole proteome profiling of WT and 3xTG mice by TMT-LC/LC-MS/MS

Supplementary Data 17. Whole proteome profiling of WT, BiG and N40K mice by TMT-LC/LC-MS/MS

Supplementary Data 18. GO Enrichment analysis of changed DEPs in AD that are not changed in all test mouse models

Supplementary Data 19. Multiomic ranking of genes/proteins in AD and mouse models and their AD-related PUBMED publication counts

Supplementary Data 20. Transcriptome-proteome consistency analysis in human and mouse

Supplementary Data 21. Plaque proteome profiling in 5xFAD mice by LCM-TMT-LC/LC-MS/MS

Supplementary Data 22. The PSM numbers and T50 of human specific APP and Abeta peptides identified in TMT-LC/LC-MS/MS

Supplementary Data 23. Proteome turnover analysis by pulse SILAC-TMT profiling of WT and 5xFAD mice

Supplementary Data 24. Explanation of inconsistency between protein and mRNA abundance by the relative half-life change of proteins