

## Supplementary Table Legends

**Supplementary Table 1. Detailed information and RNA-seq quality metrics for each rTg4510 sample included in this study.**

**Supplementary Table 2. Detailed information and RNA-seq quality metrics for each J20 sample included in this study.**

**Supplementary Table 3. Differentially expressed genes associated with rTg4510 genotype (FDR < 0.05).** Results for all transcripts are available to download at [www.epigenomicslab.com/ADmice](http://www.epigenomicslab.com/ADmice).

**Supplementary Table 4. Differentially expressed genes associated with J20 genotype (FDR < 0.05).** Results for all transcripts are available to download at [www.epigenomicslab.com/ADmice](http://www.epigenomicslab.com/ADmice).

**Supplementary Table 5. Differentially expressed genes associated with the progression of tau pathology in rTg4510 mice (FDR < 0.05).** Results for all transcripts are available to download at [www.epigenomicslab.com/ADmice](http://www.epigenomicslab.com/ADmice).

**Supplementary Table 6. Gene ontology categories enriched amongst genes characterized by progressively-altered gene expression in rTg4510 mice.**

**Supplementary Table 7. Differentially expressed genes associated with the progression of amyloid pathology in J20 mice (FDR < 0.05).** Results for all transcripts are available to download at [www.epigenomicslab.com/ADmice](http://www.epigenomicslab.com/ADmice).

**Supplementary Table 8. Association statistics for genes associated with rTg4510 genotype in the TAU model from the Mouseac dataset.**

**Supplementary Table 9. Association statistics for genes associated with the progression of rTg4510 pathology in the TAU model from the Mouseac dataset.**

**Supplementary Table 10. Association statistics for genes associated with the progression of rTg4510 pathology in the TAS10 model from the Mouseac dataset.**

**Supplementary Table 11. Six gene co-expression modules were significantly associated with rTg4510 genotype (Bonferroni corrected,  $P < 0.0028$ ).**

**Supplementary Table 12. Gene ontology categories enriched amongst genes within the red WGCNA module in rTg4510 mice.**

**Supplementary Table 13. Gene ontology categories enriched amongst genes within the turquoise WGCNA module in rTg4510 mice.**

**Supplementary Table 14. Gene ontology categories enriched amongst genes within the salmon WGCNA module in rTg4510 mice.**

**Supplementary Table 15. Gene ontology categories enriched amongst genes within the purple WGCNA module in rTg4510 mice.**

**Supplementary Table 16. Gene ontology categories enriched amongst genes within the yellow WGCNA module in rTg4510 mice.**

**Supplementary Table 17. Intra-modular connectivity for genes in the turquoise WGCNA module.**

**Supplementary Table 18. Intra-modular connectivity for genes in the yellow WGCNA module.**

**Supplementary Table 19. Intra-modular connectivity for genes in the red WGCNA module.**

**Supplementary Table 20. Overlaps between rTg4510 co-expression modules and AD-associated modules in the human dorsolateral prefrontal cortex (DLPFC).**

**Supplementary Table 21. Overlaps between rTg4510 co-expression modules and AD-associated modules in the human temporal cortex (TCX).**

**Supplementary Table 22. Gene ontology categories enriched amongst genes within the rTg4510 turquoise module overlapping with those in both the “DLPFC-blue” module.**

**Supplementary Table 23. Gene ontology categories enriched amongst genes within the rTg4510 turquoise module overlapping with those in both the “TCX-turquoise” module.**

**Supplementary Table 24. Results from Enrichr for functional biological terms for annotated genes from common DMPs associated with genotype in both rTg4510 and J20 mouse model.**

**Supplementary Table 25. Results from Enrichr for molecular function terms for annotated genes from common DMPs associated with genotype in both rTg4510 and J20 mouse models.**

**Supplementary Table 26. Results from Enrichr for functional biological terms for common annotated genes associated with genotype in both rTg4510 and J20 mouse models.**

**Supplementary Table 27. Results from Enrichr molecular function terms for common annotated genes associated with genotype in both rTg4510 and J20 mouse models.**