Supplementary Table 14A: qPCR-based fold change analysis of selected genes in the hippocampus of APP/PS1 mice that were previously identified in the 5XFAD AD model (Siwek et al, 2015).

(i) FCs and related p-values in female APP/PS1 mice versus controls.

Gene	**Fold-change**	**p-value**
Cacna1c	1.1047	1.000
Cacna1d	1.1681	0.114
Plcd4	-1.0829	0.485
Casp8	**1.3674**	**0.028**
Chrm1	1.1682	0.8857
Chrm3	1.1711	0.3428
Chrm5	-1.0344	0.485

(ii) FCs and related p-values in male APP/PS1 mice versus controls.

Gene	**Fold-change**	**p-value**
Cacna1c	-2.2217	0.114
Cacna1d	**-1.2122**	**0.0285**
Plcd4	1.0201	0.885
Casp8	1.0892	0.685
Chrm1	-1.0418	0.685
Chrm3	-1.1810	0.485
Chrm5	-1.1284	0.885

Supplementary Table 14B: qPCR-based fold change analysis of selected DEGs (from our transcriptome study) in the RS cortex of APP/PS1 mice vs. WT control animals. Fold changes from qPCR studies are listed first, those from microarrays are given in brackets.

(i) FCs and related p-values in female APP/PS1 mice versus controls.

Gene	Fold-change (Microarrays)	p-value
Siglech	**1.39 (+2.046)**	**0.032**
Ptpn6	**1.744 (+1.853)**	**0.032**
Laptm5	**2.376 (+1.646)**	**0.016**
Plek	**1.609 (+1.651)**	**0.016**
Arpp21	**-1.591 (- 1.464)**	**0.016**
Shisa9	**-1.427 (-1.048)**	**0.016**

(ii) FCs and related p-values in male APP/PS1 mice versus controls.

Gene	Fold-change (Microarrays)	p-value
Siglech	**1.523 (+1.720)**	**0.051**
Ptpn6	**1.877 (+1.538)**	**0.023**
Laptm5	**2.391 (+1.583)**	**0.009**
Plek	**1.738 (+1.309)**	**0.039**
Arpp21	**-1.395 (-1.413)**	**0.039**
Shisa9	-1.194 (-1.107)	0.437