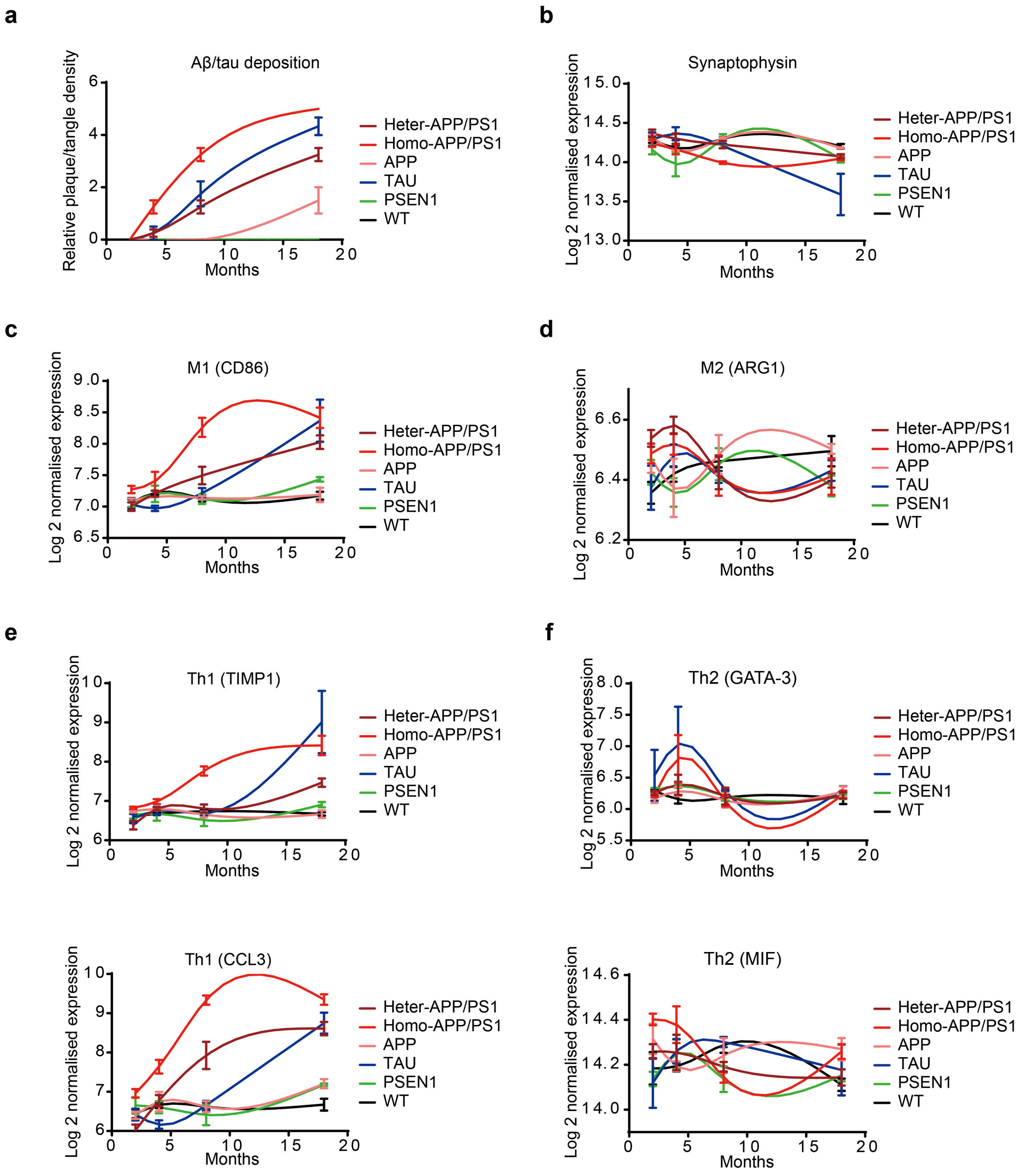

Figure S2. Changes in the hallmarks of AD in five animal models and wild-type (WT) mice at 2-, 4-, 8- and 18-month-old from the Mouseac database.

(**a**) Changes in relative densities of Aβ plaque or tau neurofibrillary tangle (n = 4 for each group). The data are presented as the mean ± standard error of the mean (mean ± sem). Colours indicate different models; lines are fitted using a polynomial algorithm.

(**b**) Changes in $\log_2$ normalized expression levels of synaptophysin (n = 4 for each group). The data are presented as the mean ± standard error of the mean (mean ± sem). Colours indicate different models; lines are fitted using a polynomial algorithm.

(**c-d**) Changes in $\log_2$ normalized expression levels of CD86 and ARG1, representing changes in M1 and M2 cell counts (n = 4 for each group). The data are presented as the mean ± standard error of the mean (mean ± sem). Colours indicate different models; lines are fitted using a polynomial algorithm.

(**e-f**) Changes in $\log_2$ normalized expression levels of TIPM, CCL3, GATA-3 and MIF, representing changes in Th1 and Th2 counts (n = 4 for each group). The data are presented as the mean ± standard error of the mean (mean ± sem). Colours indicate different models; lines are fitted using a polynomial algorithm.