cells

Supplementary data

Table S1. Primers for qRT-PCR.

Gene	Forward Primer (5′-3′)	Forward Primer (5′-3′)
Il-1 β	CAGGCAGGCAGTATCACTCA	AGCTCATATGGGTCCGACAG
Tnf-α	ACGTGGAACTGGCAGAAGAG	AGGGTCTGGGCCATAGAACT
Il-6	TACCACTTCACAAGTCG	CTGCAAGTGCATCATCG
Nr1h3 (coding LXR*α)*	CCCTAGCCTTTCCCCAAATTGC	CGGAAGAATCCCTTGCAACC
Abca1	AGTTTCGGTATGGCGGGTTT	AGCATGCCAGCCCTTGTTAT
Abcg1	ACCTACCACAACCCAGCAGACTTT	GGTGCCAAAGAAACGGGTTCACAT
Cyp27a1	GCCTTGCACAAGGAAGTGACT	CGCAGGGTCTCCTTAATCACA
Cyp46a1	CCCTAGCCTTTCCCCAAATTGC	CGGAAGAATCCCTTGCAACC
Tmem119	*CCTTCACCCAGAGCTGGTTC*	*GGCTACATCCTCCAGGAAGG*
Gapdh	GTCTCCTGCGACTTCAGC	TCATTGTCATACCAGGAAATGAGC

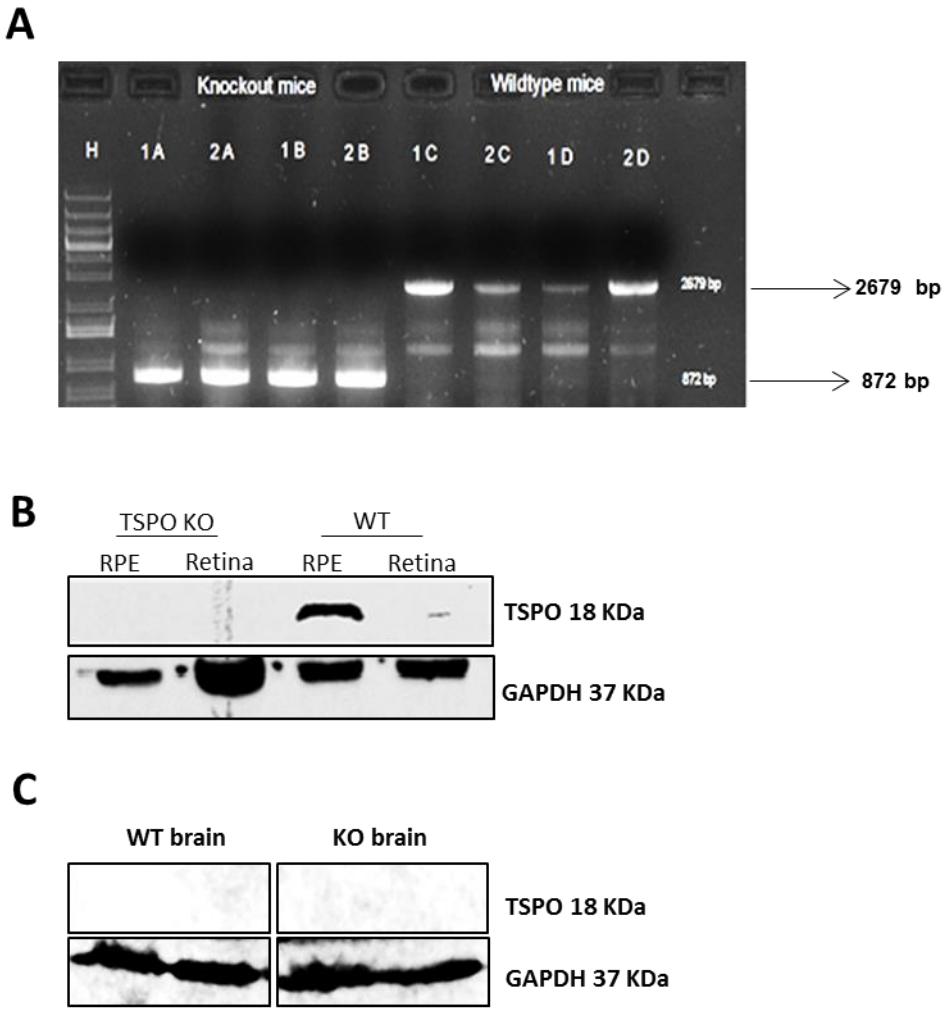

Figure S1. Genotyping of wildtype (flx) and TSPO KO (DD4X) mouse by PCR **(A).** Lane 1: 1kb plus DNA ladder; Lane 2-5: KO amplicon gave 872bp band; Lane 6-9: WT amplicon gave 2679bp band. WT and TSPO-KO mice **(B)** RPE, Retina and **(C)** Brain were screened for TSPO protein expression using a monoclonal TSPO antibody. The TSPO-deleted colonies in (RPE, Retina and Brain) were identified by Western blotting.

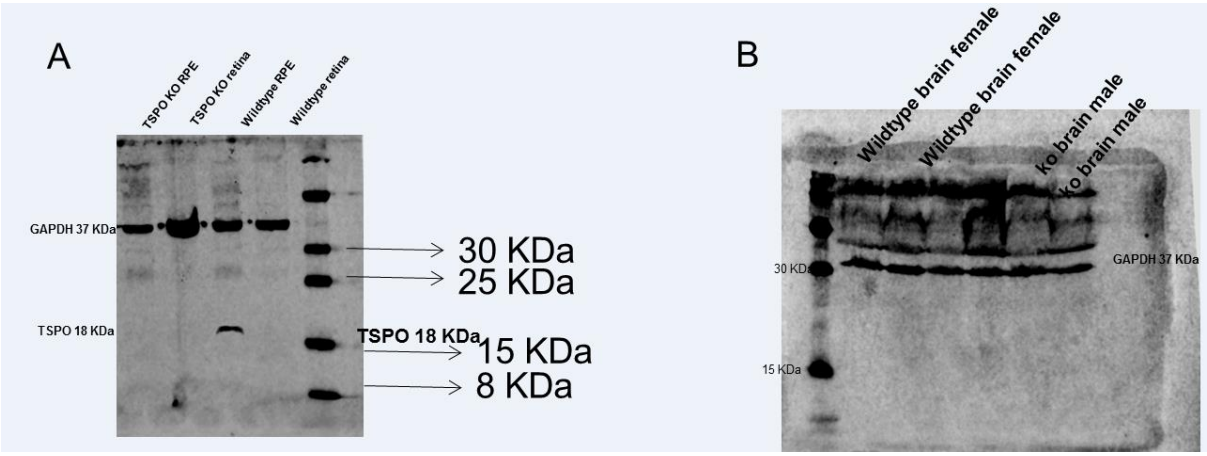

Figure S2. The original gel images for data presented in Figure S1B and C.

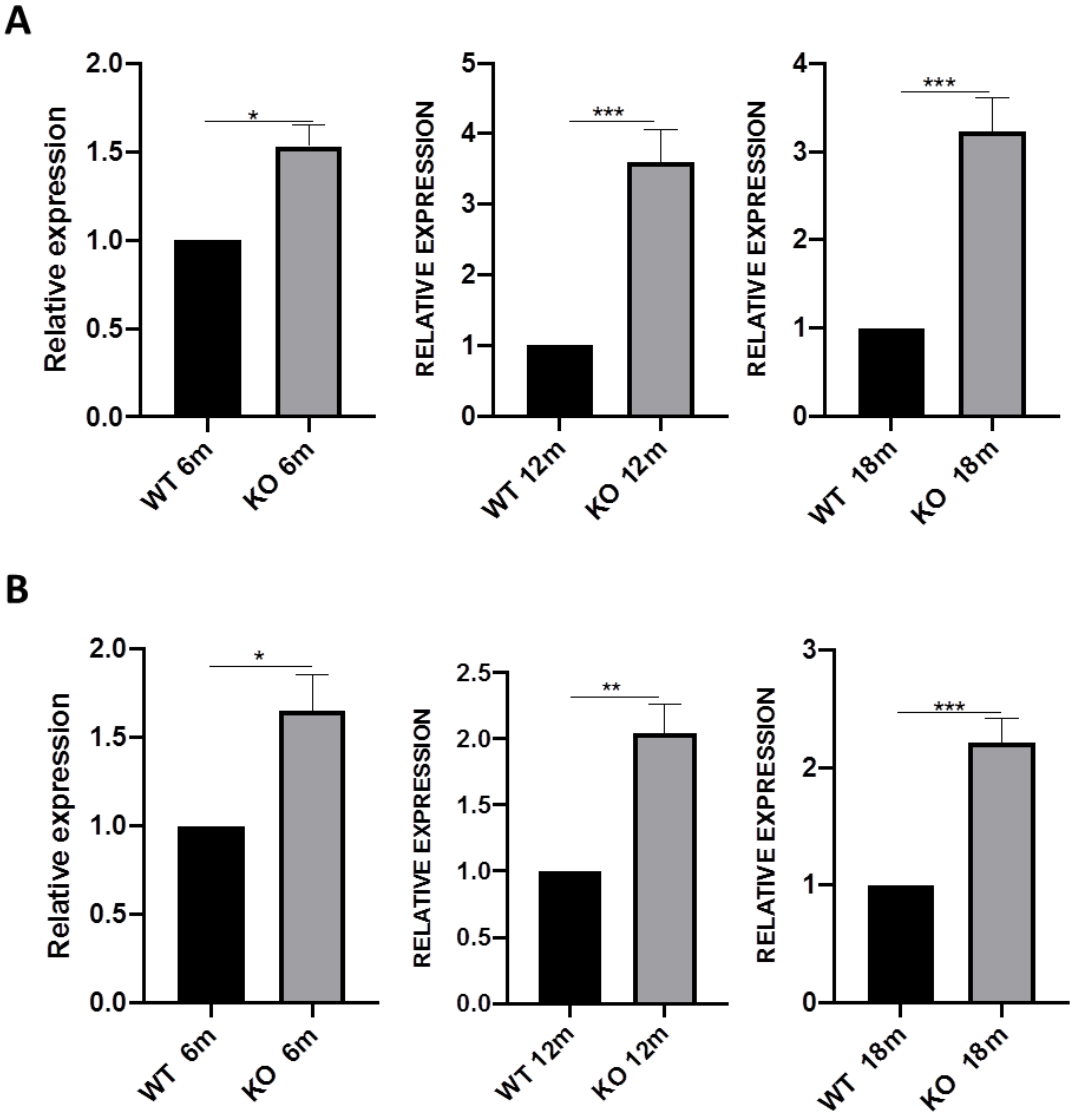

Figure S3. The expression of microglial biomarker, *Tmem119* gene, in RPE/choroid/sclera **(A)** and retinas **(B)** of wildtype and Tspo KO mice at age of 6, 12 and 18 months. The qRT-PCR data was collected as ct (Cycle threshold) values and normalised to *Gapdh* then analysed by $2^{-\Delta\Delta CT}$ formula. The data were presented as means ± SD and analysed using a t-test with the appropriate post hoc test Bonferroni multiple comparisons tests. *p<0.05, **P<0.01, ***P<0.001.