



Supplementary Figure 1 Quantification of the protein amounts expressed by different transgenic lines.

To directly compare the vigorousness of the phenotypes induced by the different members of the APP family during PNS development, the protein expression levels had to be equilibrated. This is difficult as not all the constructs have a *myc*-tag which would allow the usage of an identical antibody for the detection of all the proteins. We bypassed this disadvantage by using a fly line expressing a Myc-tagged form of APLP1 and by using the Myc-tagged APP/APLP2 chimera. The different transgenic lines were crossed with GMR-GAL4 resulting in a robust expression of the proteins in the *Drosophila* compound eye. Shortly after hatching flies were frozen in liquid nitrogen, the heads removed from the body, homogenized in 3 μ l SDS sample buffer + 0.2 μ l Benzonase (Merck) per head and incubated for 10min at 94°C. Debris was pelleted for 5min by centrifugation and 30 μ l supernatant (= 10 heads) loaded per lane on 4-12% Tris-Bis gels (Invitrogen). Displayed are the corresponding western blots which allowed a direct comparison of the expression levels of the different transgenic lines even between different family members by choosing the 1xAPP/APLP2 transgene as reference. The expression of all other transgenes is given as a relative value of this transgenic line. The results of the densitometric analysis (ImageGauge, Fuji) were standardized against the amount of protein loaded.