



Figure S2. Statistical analyses for the size of clones analyzed in figure 1. (A) Control (Co), Rheb overexpressing (Rheb⁺), *PTEN* mutant (PTEN⁻) and combined (PTEN⁻; Rheb⁺) clones were analyzed in a wild type background. **(B)** MARCM control clones labelled by GFP (green) generated in a *Minute* background; these clones are slightly bigger than the surrounding cells, likely, because the latter are heterozygous for the *Minute* mutation, whereas control clones are homozygous wild type for *Minute*. **(C)** Co, Rheb⁺ and PTEN⁻ clones combined with the *Tor*^{2L1}(2L1), *Tor*^{ΔP}(ΔP) and *Tor*^{2L19}(2L19) mutations were analyzed in a *Minute* background. Note that the size ratio (clonal/surrounding cells) of *Tor*^{2L1},PTEN^{-/-} clones tends to be higher than the control clone ratio, although not significantly.