

Figure S3. Quantitative RT-PCR of genes up regulated at P3 and P5 corroborate the RNA-seq data. (A) Quantitative RT-PCR results of several up regulated genes at P3 and P5 (*p <0.05, **p <0.01, by t test; values are mean \pm s.e.m.). (B) Analysis using the Ingenuity Pathway Analysis software shows that networks associated with *Cellular Growth, Proliferation* and *Cell Cycle* are represented with the up regulated genes at P3 and P5. Red: up regulated genes at P5; Green: up regulated genes at P3. The color degree on (B) reflects gene expression level differences between P5 and P3. Light colors denote small changes. White: no changes between P5 and P3.