



Supplementary Figure 1. Expression of candidate miRNAs in a validation cohort of 5 MEN1 patients. Quantitative reverse transcription-PCR (qRT-PCR) was undertaken on the serum of an additional 5 MEN1 patients, with data shown relative to that of a sex matched unaffected relative. The two most highly upregulated miRNAs in the profiling experiment (miR-125a-3p and miR-582-3p) are indicated in red, and the second most highly downregulated miRNA (miR-3168) is indicated in green. A significant alteration in expression in these miRNAs was not observed. All experiments were undertaken with n=4 technical replicates.