



Supplementary Figure 1: Illustration of the correlation between five different tools to estimate telomere length from the whole-genome sequence data. The tools were as follows: (1) Computel (in kb) (2) Telseq (in kb) (2) Motif_counter (telomere reads per 1x genome coverage) (3) qMotif (telomere reads per 1x genome coverage) (4) Telomerecat (in kb).