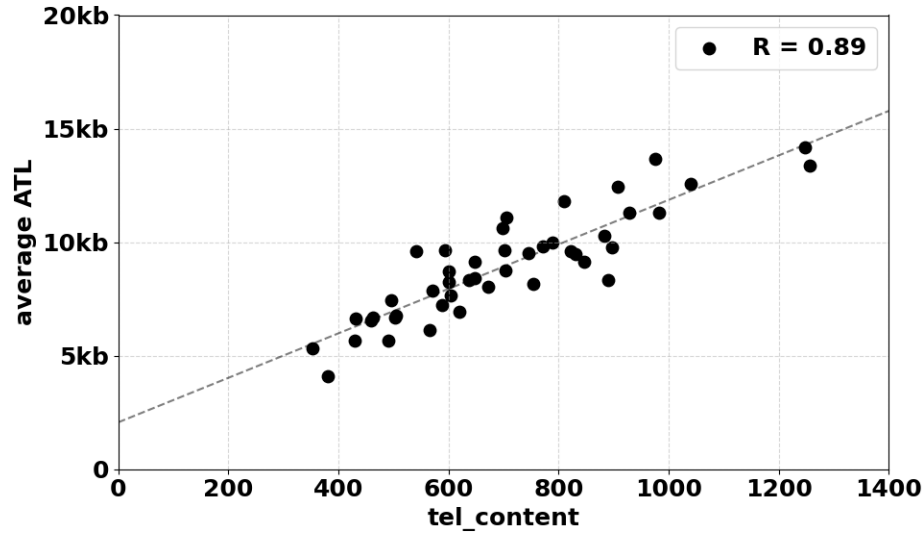




Supplemental Fig S6. Correlation of average ATL computed by Telogator2 from long reads vs. tel_content computed by TelomereHunter from short reads. Short read BAMs (aligned to GRChg38) for the 45 pangenome samples were downloaded from SRA. These BAMs were processed by TelomereHunter, yielding a report of telomere length statistics for each sample. For each sample we then compared the “tel_content” metric produced by TelomereHunter to the average of the ATL values reported by our method. The average telomere length estimates from short reads are correlated ($R = 0.89$) with the average ATL observed in long reads, indicating that average telomere length measurements are largely unaffected by the variability of TVR regions. Average ATL in base pairs can be approximated from the tel_content value produced by TelomereHunter via: $ATL_{avg} \approx 10 \times tel_content + 2000$.