

Supplementary material to: Transcriptomics analysis of *Psidium cattleianum* Sabine (Myrtaceae) unveil potential genes involved in fruit pigmentation

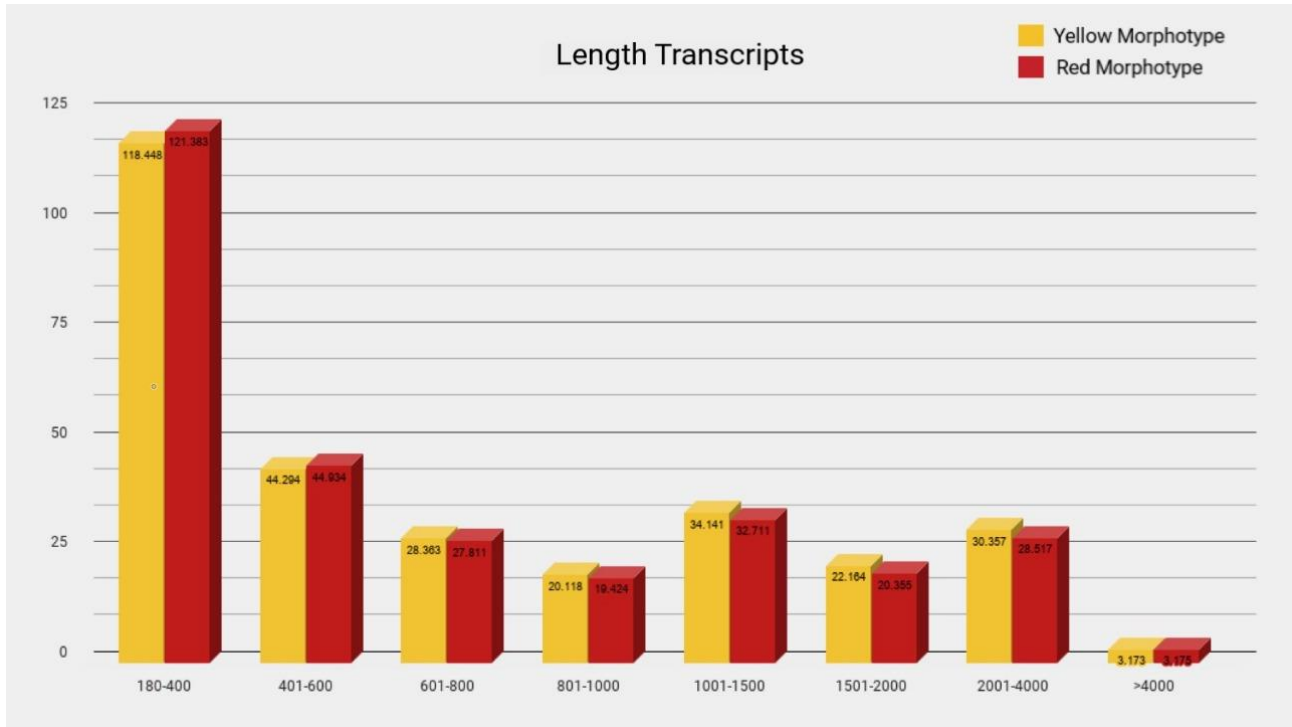


Figure S1 - Length distribution of *P. cattleianum* transcripts from the combined assembly. The yellow and red bars represent the transcript numbers for the yellow and red morphotypes, respectively.