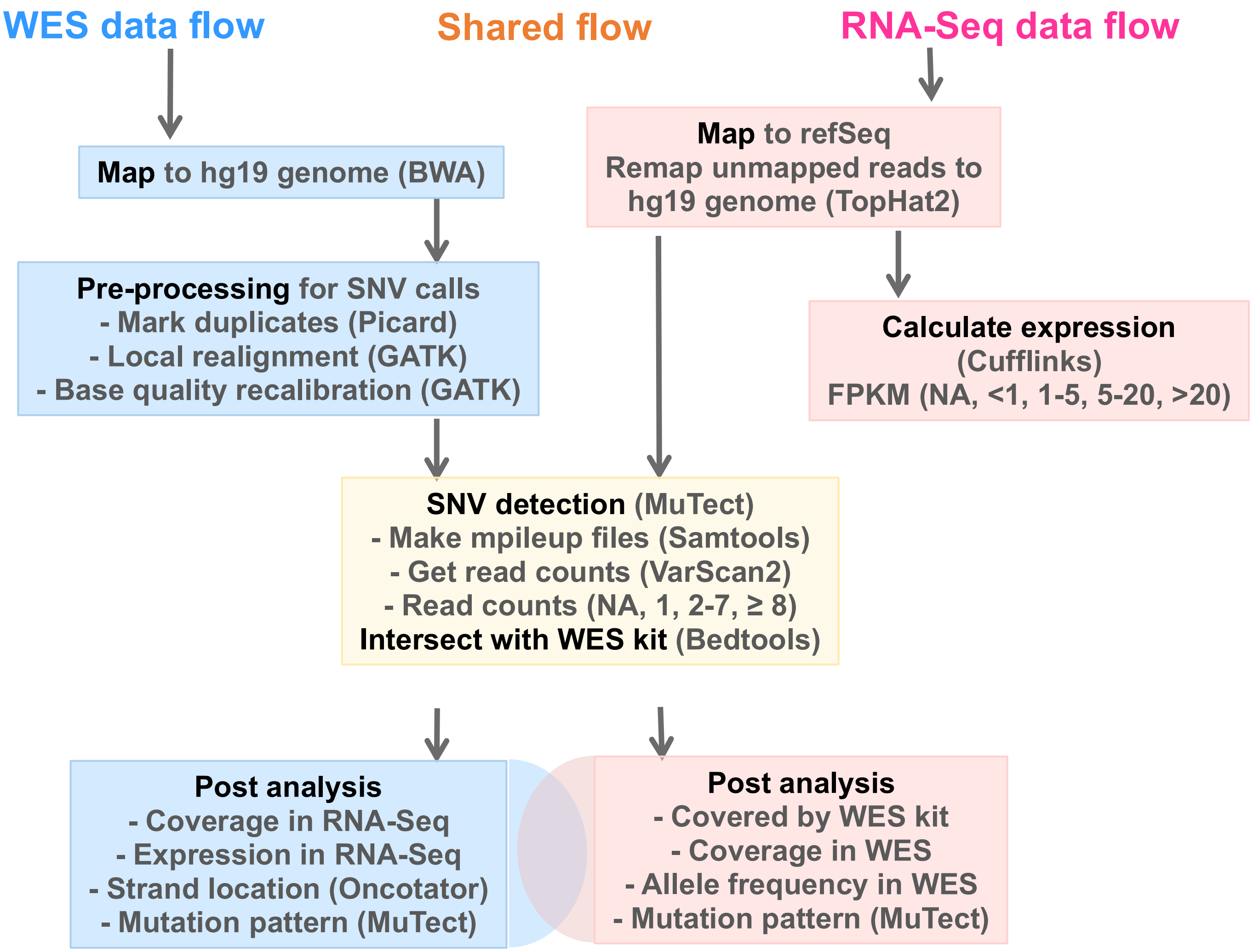
Supplemental File 2



Supplemental Fig. 1. Work flow for the overall analysis. The blue color scheme is for the WES work flow, the pink color scheme is for the RNA-Seq work flow. Typical pipelines for WES data and for RNA-Seq data were done. From the SNVs called using MuTect, we performed several comparisons. For the WES data sets, we compared SNV lists from RNA-Seq, analyzed gene expression patterns and explored the strand location of the SNVs. For the RNA-Seq data sets, we compared SNV lists from WES, analyzed the allele frequency and the mutation patterns.