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| Requests | Proposed solutions | Estimated time taken (# hours) |
| Identify somatic mutations in tumor vs normal samples: SNVs, INDELs + variant filtration and priorisation | Implement nf-core sarek in --wes mode.  Additional tasks include:   1. Prepping annotation samplesheet 2. Running pipeline on AWS via AGC 3. Taking consensus across variant callers 4. Determine appropriate variant filtration thresholds. | 50 |
| Identify MNVs | Assess tools that correct MNV misannotations (multiple SNVs in the same codon / on same chromosome called separately):  [VCFMNVChecker](https://github.com/kirovsa/VCFMNVcchecker)  [MAC](https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-015-1779-7) | 30 |
| Identify CNVs | Implement nfcore-sarek: cnvtools/ascat | 20 |
| Report microsateliite instabiliy | Implement nfcore-sarek: msisensor/msi | 20 |
| HLA-typing | Implement nfcore-hlatying (optitype) | 20 |
| Reporting tumor cellularity (purity/ploidiy) and LOH | Implement nfcore-sarek : control-freec | 20 |
| Reporting of tumor mutational burden | Assess tools that report TMB score:  [TMB](https://github.com/bioinfo-pf-curie/TMB)  [ecTMB](https://www.nature.com/articles/s41598-020-61575-1#about-the-journal) | 30 |
| Prediction of driver vs passenger mutations | Assess tools described in [Raimondi et al., (2021)](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7807764/#:~:text=Identifying%20variants%20that%20drive%20tumor,understanding%20tumorigenesis%20and%20precision%20oncology.) | 30 |
| Calculation of homologous recombination deficiency score (Clin Cancer Res 2016 Aug 1;22(15):3764-73.) using weighted sum of loss of heterozygosity (LOH), telomeric allelic imbalance (TAI), and large-scale state transitions (LST) | Implementation following Telli et al., (2016). Requires implementation of 3 other scores from Timms et al., (2014) | 50 |