Aim and deliverables for the functional impact paper

Provide comprehensive functional annotations and decipher over all functional burdening of cancer genomes in the PCAWG project.

- Overall variation burden observed in various genomic elements (coding & non-coding) in different PCAWG cohorts.
  - Comparison between real and simulated data to highlight genomic elements with significant burden in different cohorts

- Coding and non-coding functional impact score distribution across pan-cancer cohorts.
  - Enrichment/depletion of high impact variants (other than drivers) in gene block/neighborhood
  - Correlating high impact variants with downstream gene expression changes
  - Framework to evaluate structural variation impact score

- Comparison between somatic and germline variation burdening
  - Investigate influence of germline mutational burden on the somatic genome variation profile

- Decipher the underlying mechanism driving differential functional burdening in various cohorts
  - Signature, Ageing, sub-clonality & other clinical information
  - Any other suggestions ?