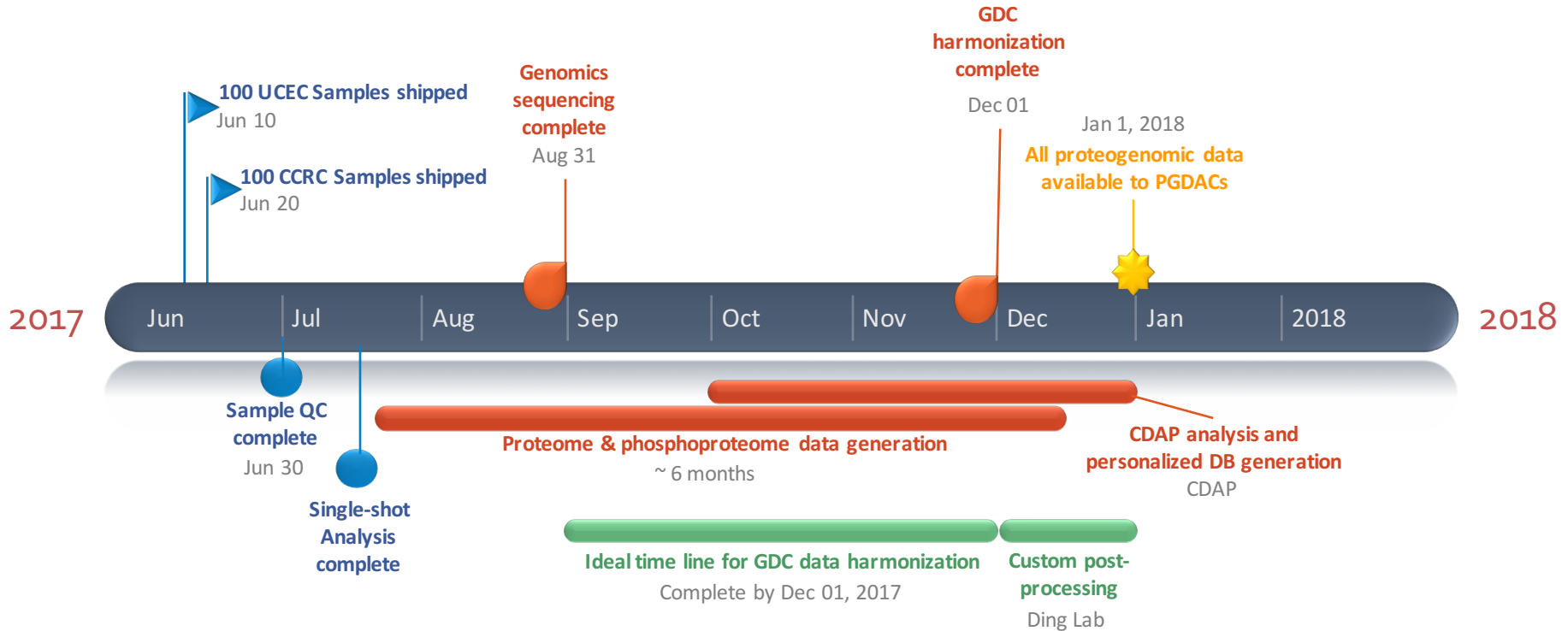


# PCC-CDAP-GDC Timelines for UCEC and CCRC

Update from 2017\_12\_06 Call

miRNA data by Jan/Feb 2018  
methylation data by Jan 2018  
(both deposited to Georgetown DCC)



# Basic Genomics Analysis (@ GDC)

- Harmonized alignment and mutation calling on WES and WGS
- Harmonized alignment and expression quantification on RNA-seq sequences
- miRNA harmonization pipeline
- Germline variant calling
- Indel calling
- Variant calling using 4 different callers

# Additional Genomics Analysis (@ GDC, under development)

- Copy number variation analysis from both WGS and WES data
- Methylation array harmonization pipeline
- Fusion calling and alternative splicing detection using integrated WGS and WES data
- Transcriptome sequencing - RSEM quantification and isoform abundance/expression apart from FPKM

# Genomics Custom Post-processing (@ Ding Lab)

- Evaluation of multiple variant calls with information about specificity and sensitivity of the calls, to filter mutations and assess quality.
- Compare calls from adjacent normal, tumor samples and germline blood.
- Structural variant calling.
- Microsatellite (MSI) status from WES and WGS data for colorectal cancer.

# CDAP Processing (@ DCC/P-CDAP)

- Convert raw data to standard formats
  - mzML, mzXML
- Peptide identification (peptide / PSM tables)
- Protein identification (with specified FDR)
- Peptide and protein relative quantification
  - TMT-10
- Phosphosite relative quantification
- QC and consistency reports
- Personalized DB generation (@ multiple PGDACs)