Each group will have 12-minutes to present to the group. We will be collecting feedback for you from the consortia after your presentation. We recommend therefore that you focus your presentation time on areas in which you might like feedback and new thinking. There is a template for your report back [here](). Please place your report back presentation [here]().

This time is for each team to use as they need. You will have members from the Portal team joining your group. The below are suggestions only, please edit as you wish.

- Establish internal deadlines
  - Meeting within a month - at least one person attending per TMC
- Work towards finishing any joint work e.g., are the data levels the same across multiple assays? Work on defining QA/QC for each assay and harmonizing across, etc. Work on harmonizing file formats (consider embedded metadata in images and other assay-specific questions)? Are there minimum information standards in your community that you want to adopt?
  - TMCs provide QC metrics to "Minimum Data Release Deliverables" spreadsheet
    - Define minimum QC/assay metrics reported per assay per TMC (point person per TMC)
      - HIVE will run fastQC/scater appropriate QC tools and "flag" low QC data prior to release - define QC metrics (ENCODE???)
        - Library complexity (RNASeq), transcription start site consistency (ATAC), %mapping to exonic regions (exome), etc
      - Ambient/background extraction (soupex) for pooled samples - metadata inclusion
      - Doublet discrimination
      - Tissue type specific and assay specific - file type required for each tool
  - TMCs provide detailed analytic pipelines including file types (input and output)
    - Define minimum standards for custom code submitted to HIVE
    - Identify point people and upload to protocols.io
    - Provide references for any published tools (for workflow development)

  - TMC-defined workflows
    - Dockstore preferred, but all formats acceptable to deliver to HIVE to convert (have worked with Nextflow) contact Ben Paten
- Transferring data/metadata
  - Data curation (IEC contacts and help@hubmapconsortium.org)
  - Major metadata categories will be extracted
- Getting UUIDs and how to use these in the metadata files.
  - Contact Bill Shirey
- Transferring software
  - All formats acceptable
  - Private code registry for unpublished code

- How to execute your pipeline on the HIVE system - don't do that, HIVE responsibility
- Providing test data for pipeline development/prototyping on HIVE systems
  - Fastq and pipeline output
- How to know that the data is "ready for release"?
  - Pipelines tested w test data and confirmed
  - Agreement on HIVE pipeline output compared to individual TMC pipeline output (timeline - pre-March)
- What curation activities do you expect the HIVE will undertake?
  - Metadata
  - Consensus pipeline development (w test data)

Goal	% Done
Identify Assays & Centers & Reps	✓✓✓✓
Specific workflow for assay at each Center	
Definition of data levels	
File formats defined	
Assay metadata & file format defined	
Processing pipeline defined	
Identify potentially common processing steps & who/where it will run.	
Assay & data QA/QC criteria	
Understand how to upload data/metadata to HIVE	
Understand how to validate and transfer processing pipeline to HIVE.	