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
- 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?
- Transferring data/metadata
- Getting UUIDs and how to use these in the metadata files.
- Transferring software
- How to execute your pipeline on the HIVE system
- How to know that the data is “ready for release”?
- What curation activities do you expect the HIVE will undertake?

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.	

Notes:

- How large will the data volume be
- What is the goal of this meeting...actionable items
    - How do we define QC/QA for our mass spec workflows
        - Especially imaging mass spec
    - What are some similarities and differences in how we process our data
- Absolute raw data coming off of the system is not useful
    - We propose that the raw data is converted into an open source format
    - We then do data reduction, going from full spectral profile to peak-picked
    - We then generate tifs
- TMC should send the data to the repository
- We should also have a reference system for all the organs
    - Take chunks from each organ, blend them all up
    - We should suggest a common reference that groups should have
        - Should be a mix of tissue from all the organs, or maybe cell lines
- LC main action item: find a common reference system
    - We should establish a reference group responsible for determining this reference system
- Need to have something deliverable in the short term
- Are we distinguishing between an individual group's QA/QC measurements, and the overall quality of data we are ingesting?
- Standard search parameters for metadata
- There is an MS Imaging Consortium, we should harmonize with them
- Jeff: you can do fragmentation-based imaging mass spec, but thats not usually how we do it
    - We do a separate LC experiment
    - Better than 5ppm mass accuracy
- How many imaging groups are there for mass spec?
    - 2
- Might be good for program managers to lay out a 1 page sheet of main hooks
- What can the HIVE do?
    - Peak alignment
    - Intensity normalization
    - Then a set of data reduction steps
    - These could all go up to the HIVE as a standard workflow
    - How much bandwidth does the HIVE have?
- Who from the HIVE is going to interfacing with us?
    - Who are we handing off the data to?
- There is a difference between individuals doing QA/QC in the lab vs people in the HIVE doing QA/QC
- Would the imaging be the same as the other LCs?
    - The QC parameters are a bit different
    - We could potentially come up with a list of parameters
- A single point of contact and a sandbox for two example data sets
    - We have a sandbox

- Nick (IEC): we should name Joel Welling as the single point of contact for all the groups here, and all the people doing mass spec in the future
- Where are the protocols going?
    - Mandatory that they need to go into protocols.io
- Timeline: within the next week, we share LC protocols
    - Within the next month: get a feel for the metadata
    - Use the Human Microbiome as a starting point
    - Format a reference subgroup
        - Try several references to see what works
- Actionable items
    - Share all parameters on the LC side so we all have standard footing
    - Compile all metadata
    - Establish a common standard for LC based data
    - Establish standards subgroup
    - Finalize our individual QC protocols on our assays (internally), and work with the HIVE
    - Define what a minimal set of quality characteristics are for what can be uploaded to the HIVE