**Minutes**

**MoTrPAC Data Working Group Conference Call**

**Wednesday, April 01, 2020**

Chair: David Amar

Attendees

BIC: Terra Coakley, David Jimenez Morales, David Amar, Malene Lindholm, Karen Dalton, Steve Hershman, Archana Raja, Jimmy Zhen, Young Kim

CAS: Josh Adkins, Yongchao Ge, Matthew Monroe, Stephen Montgomery, Karan Uppal, Nicole Gay, Charles Evans, Marty Walsh, Kevin Smith, Pierre Jean-Beltran, Bingqing Zhao, Si Wu, Mike Snyder, Jim Sanford, Steve Carr, Julian Avila, Greg Smith

CC: Jon Gelfond, Catherine Jankowski, Lindsay Page, Tuomo Rankinen, Vanessa Richardson

CCC: Jane Lu, Heather Kiesel, Joseph Rigdon, Shannon Suggs, Eric Reynolds

NIH: Rebecca Lenzi, Ashley Xia, Marie Nierras, Padma Maruveda

PASS: Michael Hirshman

Minutes were approved at 12:02pm ET.

Nicole Gay presented on: Acute endurance exercise induces widespread transcriptional changes across tissues (PASS1A data). A simple differential analysis for each time point vs the controls identifies ~180 genes shared across all tissues (with the same direction and time point). Pulse-fitting analysis (Chechik and Koller 2009 JMB) identifies different dynamics. Genes were compared by their time to half peak and the peak's slope. See slides attached.

Zoom Cloud recording:   
<https://stanford.zoom.us/rec/share/ppJwI47BqlxJErfx4k_bRPR5E7aieaa8hilIrvtZzUcQYg0F5IJcFkX9itn6XT5d>

GET updates

Sinai are still working on ATAC-Seq and comparison of the controls groups (different assays).

Metabolomics updates

The teams are still working on comparing  the targeted and untargeted platforms while focusing on specific metabolite groups.

Proteomics updates

Broad uploaded PASS1B data to the BIC. David JM gave an update on the pipeline development.

Data analysis plan

David Amar shared screen of the plan with some edits. He will work on this over the next few days.

Group discussion:

(1) David P from Joslin + David Amar suggested focusing on specific PASS1A group pairs that match (e.g., 0h-c vs 24h-ex, 7h-c vs. 7h-ex, and maybe 1h-ex vs. 4h-ex) as a way to both develop methods and obtain initial results.

(2) Pierre: Proteomics groups have reached a consensus re normalization analysis (batch effect removal using custom code and median normalization), we still need to reach a consensus for metabolomics data

(3) Mike Snyder: suggests that we have presentations focusing on testing and comparing new analysis tools, similar to Nicole's pulse-fitting presentation

Google doc link below:

<https://docs.google.com/document/d/1p1VQQp6pj_j4p_D_80-5mpoHO4tTFfDCmWgUdqf97d8/edit#heading=h.1tdthom78o0a>

Next Data WG call is Wednesday, April 22, 2020.

Next DQAR call is Wednesday, April 15, 2020.

Meeting adjourned at 12:54pm ET.