

10:00a-10:15a	Welcome (Francisca Vazquez & Kelly Sullivan)
10:15a–10:45a	Session A: The Cancer Dependency Map Project
10:15a	A1: DepMap: What are we learning and what are we missing? (Francisca Vazquez)
10:30a	A2: Advances and new directions in DepMap data science (James McFarland)
10:45a-11:00a	Coffee break
11:00a-12:20p	Session B: Towards a comprehensive Dependency Map: New models, Perturbations, and Computional Strategies (Co-chairs: Yuen-Yi "Moony" Tseng & James McFarland)
11:00a	B1: Broad model derivation update (Moony Tseng)
11:20a	B2: Towards representing all tumor types in DepMap: CRISPR screening 3D organoid models (James Neiswender)
11:40a	B3: Identifying vulnerabilities in resistant cell states (Liza Leshchiner)
12:00p	B4: Building a brain dependency map (Keith Ligon)
12:20p-12:30p	Coffee break
12:30p-1:30p	Session B continued:
12:30p	B5: Efficient CRISPR screens using Cas12a (Dave Root)
12:50p	B6: Advancing and optimizing dual knockout screens (Bill Sellers)
1:10p	B7: Sparse dictionary learning recovers pleiotropy from human cell fitness screens (Josh Pan)
1:30p-2:15p	Lunch break
2:15p-3:00p	Session C: DMC Partner Presentations (Chair: Francisca Vazquez)
2:15p	C1: Exploiting a mitotic spindle vulnerability in CIN cancers: Utilizing the PRISM platform to profile small molecule inhibitors of kinesin KIF18A motor protein (Marc Payton, Amgen)
2:35p	C2: CLIFF, a bioinformatics software tool to explore molecular differences between
	two sets of cancer cell lines (Andreas Wernitznig, Boehringer-Ingelheim)
3:00p-3:45p	Session D: Partner-Interactive Breakout Sessions (4 simultaneous sessions)
	D1: PRISM R&D: a year in review and a preview of 2022
	D2: DepMap omics data generation and analysis plans
	D3: DepMap portal updates
	D4: Target discovery strategies
3:45p-4:00p	Coffee break
4:00p-4:15p	DMC 2.0 Logistics (Kelly Sullivan)
4:15p-4:50p	Session E: Partner-Interactive Panel Discussion (Moderator: Bill Hahn) The Future of the Cancer Dependency Map: The opportunities of ex-vivo profiling short-term cultures
4:50p-5:00p	Closing Remarks (Bill Sellers & Francisca Vazquez)





SESSION D: PARTNER-INTERACTIVE BREAKOUT SESSIONS

Session D1: PRISM R&D: a year in review and a preview of 2022

The PRISM team will be sharing results from the past year as well as a brief preview of the projects we have prioritized for 2022. Highlights include initial results from our HPLM screen, updates to our combination analytics pipeline, and vignettes from the Rep1M dataset. We will also be sharing preliminary plans for repooling our cell lines, R&D toward an extended day assay, and the potential of screening additional biologics in the PRISM platform.

Broad Participants: Mustafa Kocak, Matthew Rees, Andrew Boghossian, Brienne Engel, and Jennifer Roth

DMC Partner Participants: Weilong Zhao, Marc Payton, Andrew Bloecher, Daniel Gerlach, Meredith Kuo, Marc Hafner, Susan Wee, Jon Oyer, Rami Rahal

Session D2: DepMap Omics data generation and analysis plans

In this session we will discuss some of the new datasets, improvements and features that the DepMap omics team is working on. Discussion topics will include: 1) Extracting new omics features from existing data, 2) Producing new data modalities, and 3) (if time permits) Tumor/cell-line alignment: finding gaps in the cell line models.

Broad Participants: Javad Noorbakhsh, Tsukasa Shibue, David Wu, and James McFarland

DMC Partner Participants: Zoltan Dezso, Pablo Hollstein, Steven Criscione, Alexandra Popa, Eugene Lurie, Matthew Grimmer, Mike Schaffer, Justin Huang, Gregory Kryukov, Philip Jonsson

Session D3: DepMap Portal updates

The DepMap portal continues to grow and expand and we'll be sharing our future directions for the portal. This includes details about running the DepMap portal on-premises, as well as our plans to generalize our genomic associations tool to support additional use cases. We would also like to hear from everyone about the portal features that would be most useful to you.

Broad Participants: Aviad Tsherniak and Phil Montgomery

DMC Partner Participants: Matt Barnes, Dane Mohl, Kathleen Burke, Angela Van, Scott Martin, Bruce Wolliston, Darrin Stuart

Session D4: Target Discovery strategies

There are many ways to define a 'good' target, making it challenging to develop a one size fits all prioritization scheme. Here we focus on new strategies to identify 1) targets with interpretable biomarkers or 2) targets within a given disease type. The discussion will include an overview of available tools and pre-computed resources to assist in implementing these strategies.

Broad Participants: Mike Burger, Brent Paolella, and Francisca Vazquez

DMC Partner Participants: Michael J Flister, Mali Potts, Ultan McDermott, Venu Thatikonda, Sacha Holland, Bob Yauch, Sandy Geeganage, Fred Derheimer, Alejandro Alvarez Quilon, Erica Jackson, Sunny Kuo

SESSION E: PARTNER-INTERACTIVE PANEL DISCUSSION

Session E: Partner-interactive Panel Discussion: The Future of the Cancer Dependency Map

Topic: The opportunities of ex-vivo profiling short-term cultures

Panel discussion on ex-vivo profiling using short-term cultures - what is happening in the field, the value of this approach, and how this might or might not align with the cancer dependency map research in the future.

Moderator: Bill Hahn

DMC Partner Panelists: Michael J Flister, Paul Hughes, Ultan McDermott, Alex Asiimwe, Andreas Wernitznig, Frank Parlati, Scott Martin, Bob Yauch, Benjamin Schwartz, Elsa Beyer Krall, Artur Veloso, Erica Jackson

