dependency map Consortium

Mapping cancers' dependencies

The last decade of oncology drug development has shown that some of the most exciting targets are not themselve mutated but rather represent unique "dependencies" in specific patient populations. But, a systematic approach to find such dependencies and discover ideal patient populations for oncology programs underway has been lacking.

The goal of the Cancer Dependency Map initiative at the Broad Institute of MIT and Harvard is to create a comprehensive preclinical reference map that connects tumor features with tumor dependencies to accelerate the development of precision treatments.

Introducing the Dependency Map (DepMap) Consortium

To support systematic discovery of novel dependencies and efficient identification of patient populations for target discovery programs in oncology, the Broad has launched the DepMap Consortium, an opportunity for partners to generate novel data for internal discovery programs, and gain access to know-how, data, and computational tools.

By joining the consortium, partners will be able to identify novel targets for treatment development, as well as biomarkers for revealing patient populations most likely to benefit from ongoing discovery efforts.

Primary components of the DepMap Consortium

- Genomically-characterized, patient-derived cell line models, curated, and in many instances generated, by the Broad Institute's Cancer Cell Line Factory.
- Massively-parallel compound screens in molecularly-barcoded cell lines using the PRISM method.
- Genome-wide CRISPR loss-of-function screens in genomically-characterized cell lines.
- Computational methods and biologist-friendly tools and portals for exploring data, discovering extraordinary dependencies, and finding patient populations with molecular features inducing such dependencies.
- Access to the expertise of the Broad's 50-member DepMap team.

Key offerings for Consortium partners

Consortium partners will have the opportunity to run specific experiments at the Broad, including the following per three-year contract period:

- **Fifteen** PRISM-based viability screening of partner-nominated small molecules in more than 550 genomically-characterized cell lines.
- **Five** genome-wide CRISPR loss-of-function viability screening of partner-nominated cell lines.
- **Five** attempts at generation of partner-nominated, patient-derived cell line or organoid models for large-scale dependency screening.

For more information about the DepMap project, visit depmap.org

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Relevant publications

Yu C, et al. High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. *Nat Biotechnol*. 2016. DOI: 10.1038/nbt.3460.

Meyers RM, Bryan JG, et al. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. *Nat Genet*. 2017. DOI: 10.1038/ng.3984

Tsherniak A, Vazquez F, et al. Defining a cancer dependency map. *Cell*. 2017. DOI: 10.1016/j.cell.2017.06.010

Boehm JS, Golub TR. An ecosystem of cell line factories to support a cancer dependency map. *Nat Rev Gen*. (2015) doi: 10.1038/nrg3967