KSBi-BIML 2026

Bioinformatics & Machine Learning(BIML) Workshop for Life Scientists

생명정보학 & 머신러닝 워크샵 (온라인)

Introduction to Cancer Dependency Map

이해승 _ 부산대학교

KSBI KOREAN SOCIETY FOR BIOINFORMATICS | 한국생명정보학회

KSBi-BIML 2026

Bioinformatics & Machine Learning (BIML) Workshop for Life Scientists

한국생명정보학회가 주최하는 BIML-2026 동계 Bioinformatics &Machine Learning 교육 워크숍에 여러분을 초대합니다.

BIML 워크숍은 생명정보학 연구자들이 최신 AI바이오 분야의 인공지능 기반 분석 기술과 바이오 데이터 분석 기법을 이론과 실습을 통해 체계적으로 배울 수 있는 전문 교육 프로그램입니다. 2015년에 시작된 BIML 워크숍은 올해로 12년 차를 맞이하며, 국내 생명정보학 분야의 최초이자 최고 수준의 교육 프로그램으로 자리 잡았습니다. 이번 워크숍은 크게 인공지능바이오(AI바이오) 분야와 디지털바이오 분야, 두 분야로 구성됩니다.

AI바이오 분야에서는 생명정보 분석에 폭넓게 응용되고 있는 다양한 인공지능 기반 자료 모델링 기법을 다룰 예정입니다. 특히, 인공지능 심층학습을 활용한 단백질 구조 예측, 유전체 분석, 신약 개발에 대한 이론 및 실습 강의가 진행됩니다.

또한 디지털바이오 분야에서는 단일세포오믹스, 공간오믹스, 멀티오믹스, 메타오믹스에 대한 강의도 마련되어 있어, 연구자들의 분석 역량 강화에 실질적인 도움을 줄 것으로 기대됩니다.

또한 2024년부터 추가된 의료정보 자료 분석을 다루는 강의를 올해도 지속해서 운영하고자 합니다. 이는 최근 의료정보 자료 분석에 관한 연구 수요 증가를 반영한 것으로, 관련 연구를 수행하는 의과학자 및 의료정보 연구자들에게 유용한 지침을 제공할 것입니다.

또한, 올해도 생명정보학 기술의 다양화에 발맞춰 온라인 강좌를 대폭 확대했습니다. 올해는 무료 강좌 10개를 포함한 총 40개 이상의 강좌가 개설되며, 연구 주제에 맞는 강좌 추천과 강연료 할인 혜택도 제공합니다.

BIML-2026는 국내 주요 연구 중심 대학의 전임 교수 및 각 분야 최고 전문가들의 강의로 구성되어 있으며, 기초 이론부터 최신 연구 동향까지 아우르는 심도 있는 교육의 장이 될 것으로 확신합니다.

여러분의 많은 관심과 참여를 기대합니다!

2026년 2월

한국생명정보학회장 류 성 호

강의개요

Introduction to Cancer Dependency Map

암은 유전적, 분자적 이질성이 매우 큰 질환으로, 동일한 암종 내에서도 치료 반응과 예후가 크게 달라진다. 이러한 이질성 속에서 효과적인 항암 치료 표적을 발굴하기 위해서는 단순한 변이 정보나 발현 패턴을 넘어, 암 세포가 생존과 증식을 위해 실제로 의존하는 분자적 취약점에 대한 기능적 정보가 필수적이다. 최근 CRISPR 기반 gene knockdown/knockout screening과 다중 오믹스 기술의 발전으로 대규모 기능유전체 데이터가 축적되고 있으나, 이러한 데이터를 체계적으로 통합하여 암 연구와 신약개발로 연결하는 데에는 여전히 높은 진입 장벽이 존재한다.

본 강의에서는 대규모 암 세포주 기반 기능유전체 프로젝트인 Cancer Dependency Map (DepMap)을 중심으로, DepMap에 포함된 다양한 데이터세트의 구성과 의미를 설명하고, 이를 활용한 암 표적 발굴, 바이오마커 탐색, AI기반 신약개발 등 연구 사례를 소개한다.

강의는 다음의 내용을 포함한다:

- DepMap 프로젝트 개요 및 데이터 구조
- DepMap 데이터 기반 암 연구 및 신약개발 활용 사례

* 교육생준비물:

노트북 (메모리 8GB 이상, 디스크 여유공간 30GB 이상)

* 강의 난이도: 초급

* 강의: 이해승 교수 (부산대학교 약학과)

Curriculum Vitae

Speaker Name: Haeseung Lee, Ph.D.

▶ Personal Info

Name	Haeseung Lee
Title	Associate Professor
Affiliation	Pusan National University

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Address	2, Busandaehak-ro 63beon-gil, Geumjeong-gu, Busan, 46241, Republic of Korea
Email	haeseung@pusan.ac.kr

Research Interest

Systems Pharmacology, Pharmacogenomics, Drug Discovery, Machine learning

Educational Experience

2009	B.S. in Life Science, Ewha Womans University, Republic of Korea
2015	Ph.D. in Bioinformatics, Ewha Womans University, Republic of Korea

Professional Experience

2015–2017	Postdoctoral Fellow, Ewha Womans University
2017–2020	Research Professor, Ewha Womans University
2020–2021	Researcher, Korea Institute of Oriental Medicine
2021–2025	Assistant Professor, College of Pharmacy, Pusan National University
2025–present	Associate Professor, College of Pharmacy, Pusan National University

Selected Publications (3 maximum)

1. Park SY, Son K, Kim J, Kim K, Joo S, Kim B, Lee M, Kim W, Jung WJ, Choi BK, Jeon N, Chung WY, Hu Y, Lee H, Song NY. Cathepsin L as a dual-target to mitigate muscle wasting while enhancing anti-tumor efficacy of anti-PD-L1. Nature Communications, 2025, 16(1):10706.
2. Lee JE, Kim M, Ochiai S, Kim SH, Yeo H, Bok J, Kim J, Park M, Kim D, Lamiable O, Lee M, Kim MJ, Kim HY, Ronchese F, Kwon SW, Lee H, Kim TG, Chung Y. Tonic type 2 immunity is a critical tissue checkpoint controlling autoimmunity in the skin. Cell Reports, 2024, 43(7):114364.
3. Kwon EJ, Cha HJ, Lee H. Systematic omics analysis identifies CCR6 as a therapeutic target to overcome cancer resistance to EGFR inhibitors. iScience. 2024, 27(4):109448.

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KSBi-BIML 2026

Introduction to Cancer Dependency Map

DepMap 데이터 기반 암 취약점과 치료제 발굴

부산대학교 약학대학
이해승, Ph.D.

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1. **암정복을 위한 DepMap 프로젝트 소개**
2. DepMap 데이터 구성 및 구조
3. DepMap 데이터 활용 연구 사례

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Cancer Dependency Map (DepMap) portal (https://depmap.org/portal)

depmap portal | Search for a gene, cell line, compound, lineage, or file | Tools | Downloads | About | Forum

Welcome to the DepMap Portal

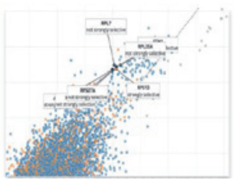
The goal of the Dependency Map (DepMap) portal is to empower the research community to make discoveries related to cancer vulnerabilities by providing open access to key cancer dependencies, analytical, and visualization tools.

Learn more about DepMap | Learn more about PedDep

DepMap is part of a public-private partnership called the DepMap Consortium. Learn more about becoming a member of the DepMap Consortium.

Featured Tools

Data Explorer



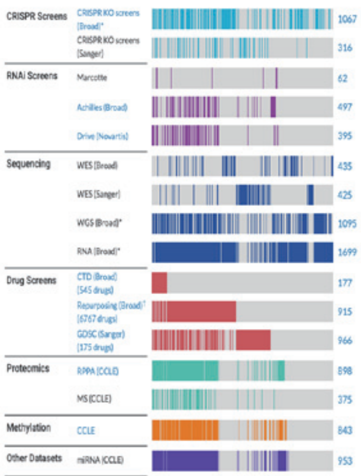
Cell Line Selector

Data Downloads

Tools

- Data Explorer
- Custom Analyses
- Celligner
- Target Discovery
- Context Explorer

Downloads



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What is DepMap ?

nature reviews cancer

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nature > nature reviews cancer > perspectives > article

Perspective | Published: 28 October 2024

The present and future of the Cancer Dependency Map

Rand Arafeh, Tsukasa Shibue, Joshua M. Dempster, William C. Hahn & Francisca Vazquez

Nature Reviews Cancer 25, 59–73 (2025) | Cite this article

Abstract

Despite tremendous progress in the past decade, the complex and heterogeneous nature of cancer complicates efforts to identify new therapies and therapeutic combinations that achieve durable responses in most patients. Further advances in cancer therapy will rely, in part, on the development of targeted therapeutics matched with the genetic and molecular characteristics of cancer. The Cancer Dependency Map (DepMap) is a large-scale data repository and research platform, aiming to systematically reveal the landscape of cancer
취약점! vulnerabilities in thousands of genetically and molecularly annotated cancer models. DepMap is used routinely by cancer researchers and translational scientists and has facilitated the identification of several novel and selective therapeutic strategies for multiple cancer types that are being tested in the clinic. However, it is also clear that the current version of DepMap is not yet comprehensive. In this Perspective, we review (1) the impact and current uses of DepMap, (2) the opportunities to enhance DepMap to overcome its current limitations, and (3) the ongoing efforts to further improve and expand DepMap.

Arafeh R et al. Nat Rev Cancer. 2025 doi: 10.1038/s41568-024-00763-x

depmap portal

Overview

The DepMap project, building off of the original Cancer Cell Line Encyclopedia (CCLE) project and Project Achilles, generates data and tools that can be used and shared by researchers. New DepMap data is released twice a year, in May and November.

DepMap has an ever-evolving data structure that allows for flexibility in incorporating and analyzing new types of data. To learn more about our data structure, read "How is DepMap data structured?" below.

DepMap also hosts datasets that are generated with or provided by collaborators and other institutions. These datasets may or may not be continuously updated, but are available for the community to use through the DepMap Portal.

Release Datasets

The DepMap Release dataset is continuously growing as new data are generated by DepMap. Data may be analyzed and visualized using our portal tools, including Data Explorer. To learn more about our releases, visit the Current Release page.

View Current Release

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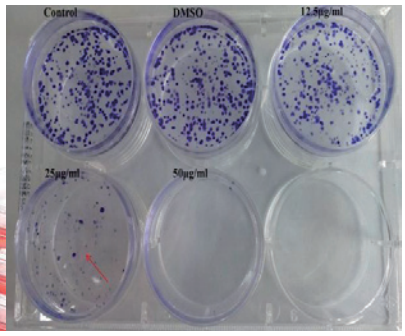
Cancer cell lines (암세포주)



정의
- 환자 종양 조직 유래, in vitro에서 장기간 증식하도록 확립된 세포 집단
- 동일한 유전적 배경에서 반복 실험이 가능한 모델

특징
- 텔로머레이스 활성 등으로 분열 한계 소실 → 무한 증식 가능
- 종양과정에서 축적된 돌연변이, 염색체 이상, CNV 보유

장점
- 표준화된 배양 조건 확립되어 실험 재현성 높음
- 고속·저비용 대규모 스크리닝(약물, 유전자) 적합
- 유전자 조작, 약물 처리 등 perturbation 용이
- 분자 오믹스 데이터와 스크리닝 결과 간 연계 용이

한계
- 장기 배양 시 분자적·표현형적 드리프트 발생 가능
  → 원래 종양 특성 소실 가능
- 단일 세포 기원 → 실제 종양 미세환경 (공간적·세포적 이질성) 반영 부족
- 약물 반응 과대평가 위험: *in vivo* 효능과 불일치 빈번

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암세포주 기반 대규모 연구의 시작, NCI-60 패널

nature reviews cancer

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nature > nature reviews cancer > timeline > article

Timeline | Published: 01 October 2006

The NCI60 human tumour cell line anticancer drug screen

Robert H. Shoemaker

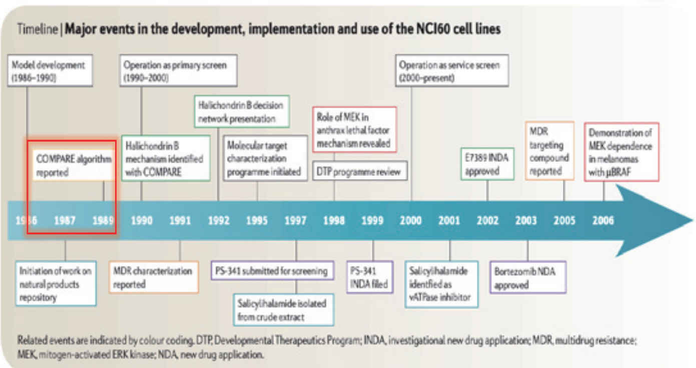
Nature Reviews Cancer 6, 813–823 (2006) | Cite this article

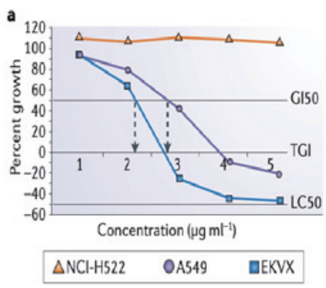
27k Accesses | 2421 Citations | 27 Altmetric | Metrics

Abstract

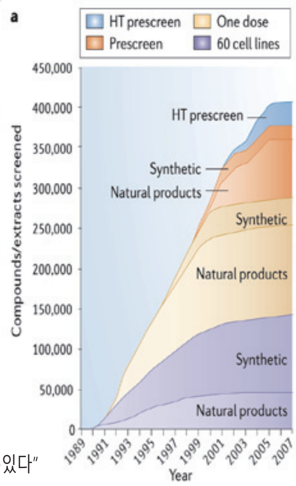
The US National Cancer Institute (NCI) 60 human tumour cell line anticancer drug screen (NCI60) was developed in the late 1980s as an *in vitro* drug-discovery tool intended to supplant the use of transplantable animal tumours in anticancer drug screening. This screening model was rapidly recognized as a rich source of information about the mechanisms of growth inhibition and tumour-cell killing. Recently, its role has changed to that of a service screen supporting the cancer research community. Here I review the development, use and productivity of the screen, highlighting several outcomes that have contributed to advances in cancer chemotherapy.

Shoemaker RH. Nature Reviews Cancer, 2006.
Weinstein JN et al. Science, 1997.





GI50 (50% growth inhibition)
LC50 (50% lethal concentration)
TGI (total growth inhibition)



COMPARE: "세포주 간 약물 반응 패턴을 비교하여 작용기전을 추론할수있다"

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Motivations for the Cancer Cell Line Encyclopedia (CCLE)
https://sites.broadinstitute.org/ccle/

DepMap Motivations

사례 1: A549-EGFR inhibitor

- NCI60에서 NSCLC연구는 A549(EGFR wild-type)가 표준으로 사용
- EGFR 활성화 변이 보유 환자의 뚜렷한 민감성이 확인
  → EGFR 변이암의 높은 EGFR inhibitor 감수성 신호 재현안됨
- 세포주 다양성 부족, 환자 집단의 분자적 이질성 반영 한계

사례2: BRAF변이-MEK inhibitor

- NC60 세포주 대상 SNP array – Mutation, CNV, Expression 측정
- NCI60 의 42,796 compounds 약물 감수성 데이터와 교차분석
  → BRAF 변이 흑색종이 MEK저해제에 선택적으로 민감함 포착
- 이후 임상시험에서 MEK 억제의 유효성 검증(Phase III로 이어짐)

결론: 세포주 다양성 확장 & 멀티오믹스 프로파일링

- TCGA가 환자 종양 유전학을 확장하던 시점, 세포주도 동급의 체계적 특성화 필요
- 대규모 세포주(≈1000)의 유전형6발현 등 멀티오믹스 표준화
- 화합물 스크리닝과의 통합으로 “유전형 <-> 약물 취약성” 체계적 연결
- 정밀의학을 위한 바이오마커6표적의 조기 탐지 및 검증 기반 마련

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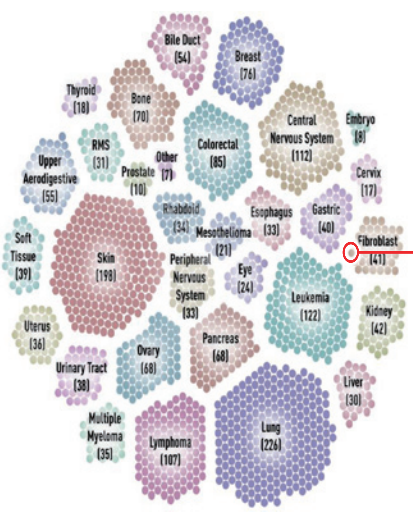
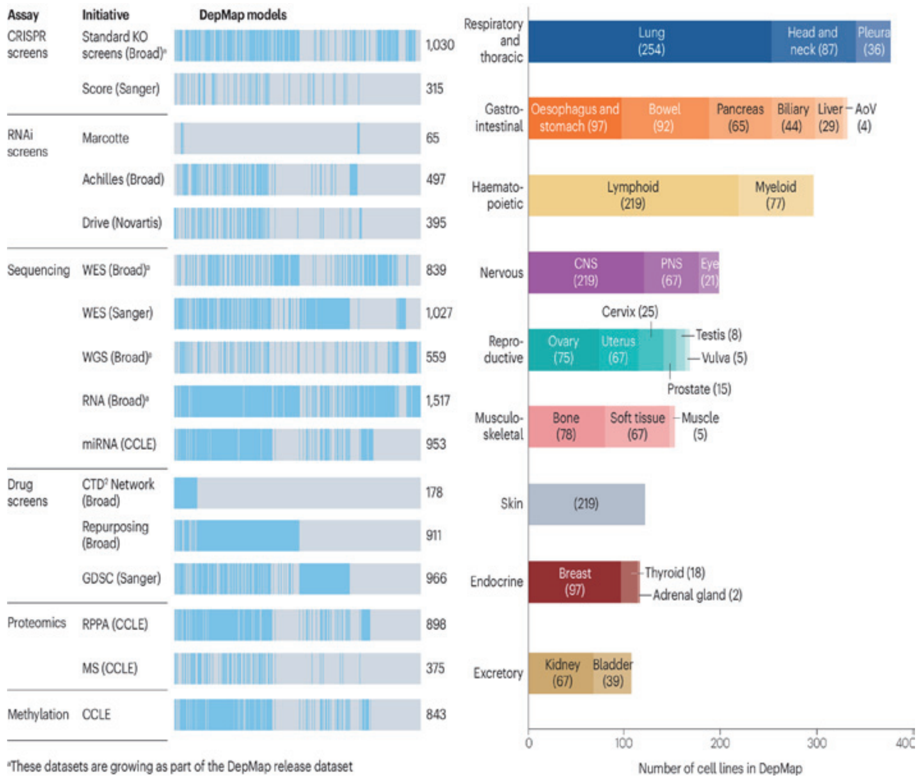
대규모 암세포주 패널 확장 (NCI60 → DepMap)





Arafeh R et al. Nat Rev Cancer. 2025 doi: 10.1038/s41568-024-00763-x

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BROAD INSTITUTE

DepMap founded by the Broad Institute

Broad Institute of MIT and Harvard.

The Broad Institute is an independent, non-profit research organization that aims to discover the root causes of all common and rare diseases, and to use this insight to help develop safe and effective therapeutic interventions.

Based primarily in Kendall Square in Cambridge, Massachusetts, the Broad Institute was founded in 2004 to fulfill the promise of genomic medicine — three years after completion of the Human Genome Project, which Broad scientists helped create and lead.

We tackle big scientific questions that no single lab can address alone. We empower cross-disciplinary teams to solve the most important challenges in biomedicine. We invent and openly share cutting-edge technologies and tools to accelerate research and catalyze improvements in human health throughout the United States and beyond.

The Broad has spearheaded flagship scientific projects that have benefited the entire country, such as:

- Human Genome Project (HGP)
- The Cancer Genome Atlas (TCGA)
- Human Cell Atlas (HCA)
- Cancer Dependency Map (DepMap)
- Covid testing to safely reopen K-12 schools, colleges, and universities

https://www.broadinstitute.org/about-us

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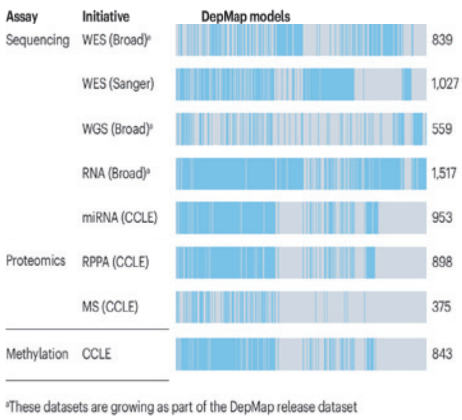
DepMap데이터 분류: 분자오믹스 vs 표현형스크리닝

분자 오믹스 (Molecular Omics)

세포의 분자 상태를 정량화하여 기전·바이오마커를 규명

CCLE GDSC

- 유전체(WES/WGS), 전사체(RNA-seq), 단백체(MS) 멀티오믹스
- 출력: 변이·복제수·mRNA·**miRNA**·단백질 수준

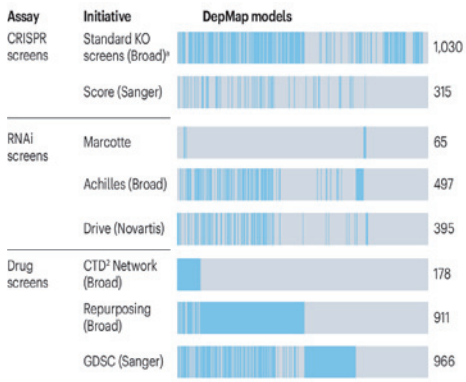


표현형 스크리닝 (Phenotypic Screening)

유전자 교란·약물 처리·in vivo 실험의 결과(표현형) 관찰

Achilles GDSC CTRP PRISM MetMap

- Achilles: CRISPR/RNAi 의존성(세포 생존/증식)
- GDSC/CTRP/PRISM: 약물 감수성(AUC/IC50, pooled 바코딩)
- MetMap: 전이 잠재력(in vivo, 장기 특이 패턴)



대규모 암세포주의 오믹스 정보

CCLE Cancer Cell Line Encyclopedia

nature

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> 8900 회 인용

Published: 28 March 2012

The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity

Jordi Barretina, Giordano Caponigro, Nicolas Stransky, Kavitha Venkatesan, Adam A. Margolin, Sungjoon Kim, Christopher J. Wilson, Joseph Lehár, Gregory V. Kryukov, Dmitriy Sonkin, Anupama Reddy, Manway Liu, Lauren Murray, Michael F. Berger, John E. Monahan, Paula Morais, Jodi Meltzer, Adam Korejwa, Judit Jané-Valbuena, Felipa A. Mapa, Joseph Thibault, Eva Bric-Furlong, Pichai Raman, Aaron Shipway, ... Levi A. Garraway + Show authors

Nature 483, 603–607 (2012) | Cite this article

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BROAD INSTITUTE

Barretina J, et al., Nature. 2012, https://doi.org/10.1038/nature11003

Mutation, gene expression, CNV data from **947 human cancer cell lines**
Pharmacological profiles for **24 anticancer drugs** across 479 of the cell line

GDSC² Genomics of Drug Sensitivity in Cancer

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> 2800 회 인용

Published: 28 March 2012

Systematic identification of genomic markers of drug sensitivity in cancer cells

Mathew J. Garnett, Elena J. Edelman, Sonja J. Heidorn, Chris D. Greenman, Anahita Dastur, King Wai Lau, Patricia Greninger, I. Richard Thompson, Xi Luo, Jorge Soares, Qingsong Liu, Francesco Iorio, Didier Surdez, Li Chen, Randy J. Milano, Graham R. Bignell, Ah T. Tam, Helen Davies, Jesse A. Stevenson, Syd Barthorpe, Stephen R. Lutz, Fiona Kogera, Karl Lawrence, Anne McLaren-Douglas, ... Cyril H. Benes + Show authors

Nature 483, 570–575 (2012) | Cite this article

62k Accesses | 1718 Citations | 124 Altmetric | Metrics

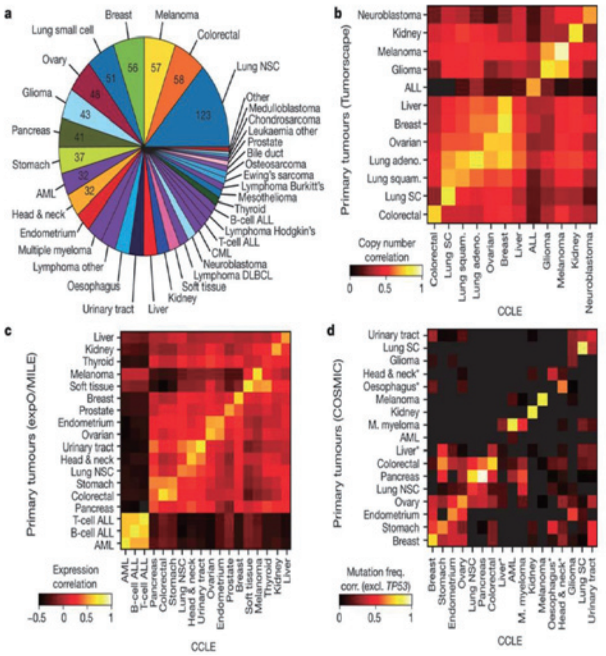
wellcome sanger institute MASSACHUSETTS GENERAL HOSPITAL CANCER CENTER

Garnett MJ et al., Nature. 2012, doi: 10.1038/nature11005

Mutation, gene expression, CNV data from **639 human cancer cell lines**
Pharmacological profiles for **130 anticancer drugs** across 507 of the cell line

Cancer Cell Line Encyclopedia (CCLE)

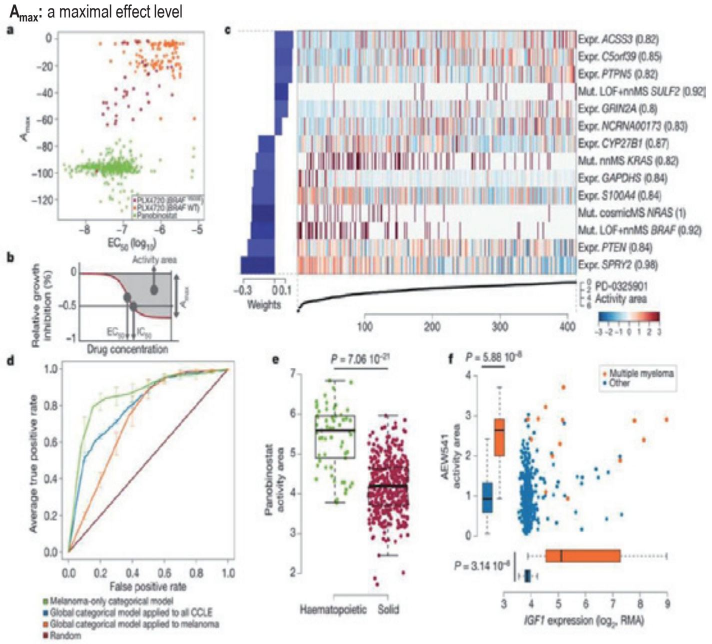
Molecular Omics



Drug Screening

EC50 : half-maximal effective concentration

A_{max}: a maximal effect level



Barretina J, et al., Nature. 2012, https://doi.org/10.1038/nature11003

Mutation, gene expression, CNV data from **947 human cancer cell lines**

Pharmacological profiles for **24 anticancer drugs** across 479 of the cell line

CCLE Updates (2019) + microRNA + Proteomics (RPPA)

ARTICLE

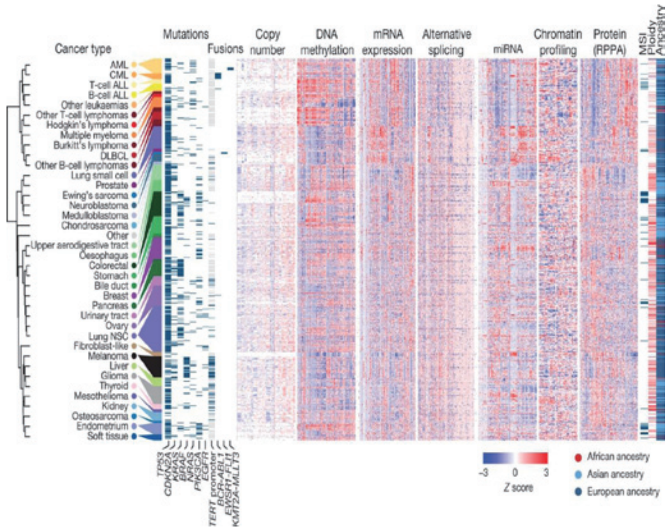
https://doi.org/10.1038/s41586-019-1186-3

Next-generation characterization of the Cancer Cell Line Encyclopedia

Mahmoud Ghandi[1,17], Franklin W. Huang[1,2,13,17], Judit Jané-Valbuena[1,2], Gregory V. Kryukov[1], Christopher C. Lo[1], E. Robert McDonald III[3], Jordi Barretina[3,16], Ellen T. Gelfand[1], Craig M. Bielski[1], Haoxin Li[1,2], Kevin Hu[1], Alexander Y. Andreev-Drakhlin[1], Jaegil Kim[1], Julian M. Hess[1], Brian J. Haas[1], François Aguet[1], Barbara A. Weir[1], Michael V. Rothberg[1], Brenton R. Paolella[1], Michael S. Lawrence[1,4,5,6], Rehan Akbani[7], Yiling Lu[7], Hong L. Tiv[8], Prafulla C. Gokhale[8], Antoine de Weck[9], Ali Amin Mansour[1], Coyin Oh[1], Juliann Shih[1], Kevin Hadi[10,11], Yanay Rosen[1], Jonathan Bistline[1], Kavitha Venkatesan[3], Anupama Reddy[3], Dmitriy Sonkin[3,14], Manway Liu[3], Joseph Lehar[3], Joshua M. Korn[3], Dale A. Porter[3], Michael D. Jones[3], Javad Golji[3], Giordano Caponigro[3], Jordan E. Taylor[1], Caitlin M. Dunning[1], Amanda L. Creech[1], Allison C. Warren[1], James M. McFarland[1], Mahdi Zamanighomi[1], Audrey Kauffmann[9], Nicolas Stransky[1], Marcin Imielinski[10,11], Yosef E. Maruvka[1,4], Andrew D. Cherniack[1,2], Aviad Tsherniak[1], Francisca Vazquez[1], Jacob D. Jaffe[1], Andrew A. Lane[2], David M. Weinstock[2], Cory M. Johannessen[1], Michael P. Morrissey[3], Frank Stegmeier[3], Robert Schlegel[3], William C. Hahn[1,2], Gad Getz[1,4,5,6], Gordon B. Mills[7], Jesse S. Boehm[1], Todd R. Golub[1,2,12], Levi A. Garraway[1,2,18] & William R. Sellers[3,15,18]*

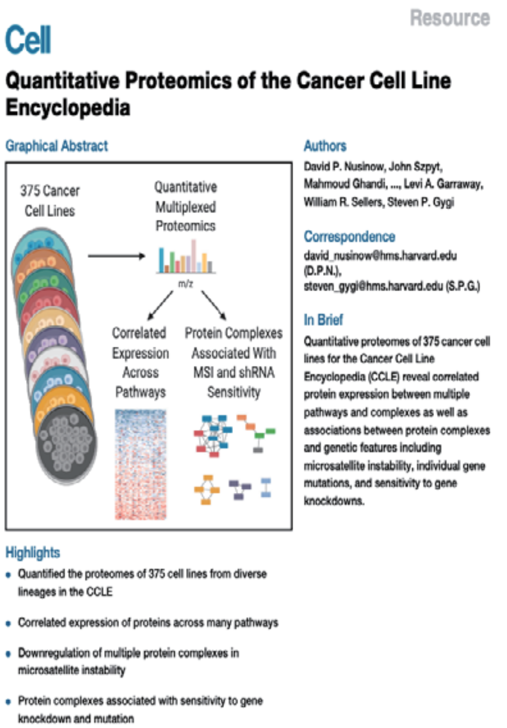
Large panels of comprehensively characterized human cancer models, including the Cancer Cell Line Encyclopedia (CCLE), have provided a rigorous framework with which to study genetic variants, candidate targets, and small-molecule and biological therapeutics and to identify new marker-driven cancer dependencies. To improve our understanding of the molecular features that contribute to cancer phenotypes, including drug responses, here we have expanded the characterizations of cancer cell lines to include genetic, RNA splicing, DNA methylation, histone H3 modification, microRNA expression and reverse-phase protein array data for 1,072 cell lines from individuals of various lineages and ethnicities. Integration of these data with functional characterizations such as drug-sensitivity, short hairpin RNA knockdown and CRISPR–Cas9 knockout data reveals potential targets for cancer drugs and associated biomarkers. Together, this dataset and an accompanying public data portal provide a resource for the acceleration of cancer research using model cancer cell lines.

Ghandi M et al. Nature. 2019, doi: 10.1038/s41586-019-1186-3



Genetic, RNA splicing, DNA methylation, histone H3 modification, microRNA expression, RPPA data for **1072 human cancer cell lines**

CCLE Updates (2020) + Proteomics (MS)



Resource

Cell

Quantitative Proteomics of the Cancer Cell Line Encyclopedia

Graphical Abstract

Authors

David P. Nusinow, John Szpyt, Mahmoud Ghandi, ..., Levi A. Garraway, William R. Sellers, Steven P. Gygi

Correspondence

david_nusinow@hms.harvard.edu (D.P.N.), steven_gygi@hms.harvard.edu (S.P.G.)

In Brief

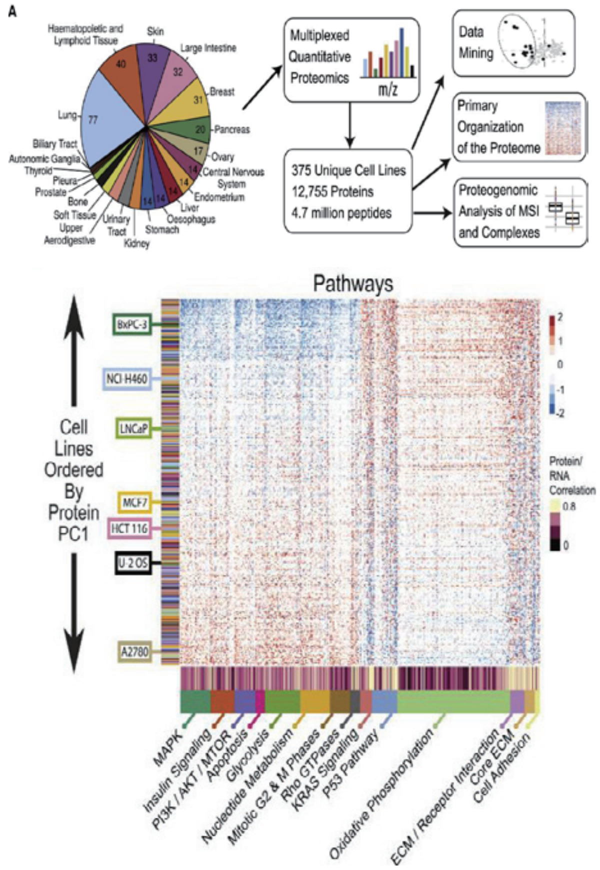
Quantitative proteomes of 375 cancer cell lines for the Cancer Cell Line Encyclopedia (CCLE) reveal correlated protein expression between multiple pathways and complexes as well as associations between protein complexes and genetic features including microsatellite instability, individual gene mutations, and sensitivity to gene knockdowns.

Highlights

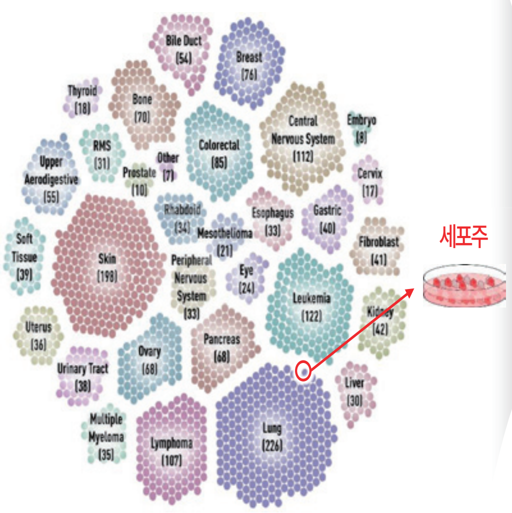
- Quantified the proteomes of 375 cell lines from diverse lineages in the CCLE
- Correlated expression of proteins across many pathways
- Downregulation of multiple protein complexes in microsatellite instability
- Protein complexes associated with sensitivity to gene knockdown and mutation

Nusinow DP, et al. Cell. 2020, doi: 10.1016/j.cell.2019.12.023

Mass spectrometry data for **375 human cancer cell lines**



CCLE Data 예시



세포주정보

샘플 (n=1,673)

암세포주	Cancer Type	Cancer Subtype	Age	Sex	Race	Cell Line Origin	Sample Collection Site
ACH-000007	Bowel	Colon Adenocarcinoma	63	Male	Caucasian	Primary	Large Intestine
ACH-000008	Skin	Melanoma	56	Male	Caucasian	Primary	Skin
ACH-000011	Bladder or Urinary Tract	Bladder Urothelial Carcinoma	53	Male	-	Metastatic	Lymph Node
ACH-000012	Lung	Lung Adenocarcinoma	39	Female	Caucasian	Primary	Lung
ACH-000013	Ovary or Fallopian Tube	High-Grade Serous Ovarian Cancer	60	Female	Caucasian	Metastatic	Ascites
ACH-000014	Skin	Melanoma	56	Male	Caucasian	Metastatic	Lymph Node
ACH-000015	Lung	Large Cell Lung Carcinoma	44	Male	Caucasian	Primary	Lung
ACH-000018	Bladder or Urinary Tract	Bladder Urothelial Carcinoma	82	Female	Caucasian	Primary	Urinary Tract
ACH-000019	Breast	Invasive Breast Carcinoma	69	Female	Caucasian	Metastatic	Pleural Effusion
ACH-000021	Lung	Lung Adenocarcinoma	55	Female	Caucasian	Metastatic	Lymph Node
ACH-000022	Pancreas	Pancreatic Adenocarcinoma	64	Female	-	Metastatic	Liver

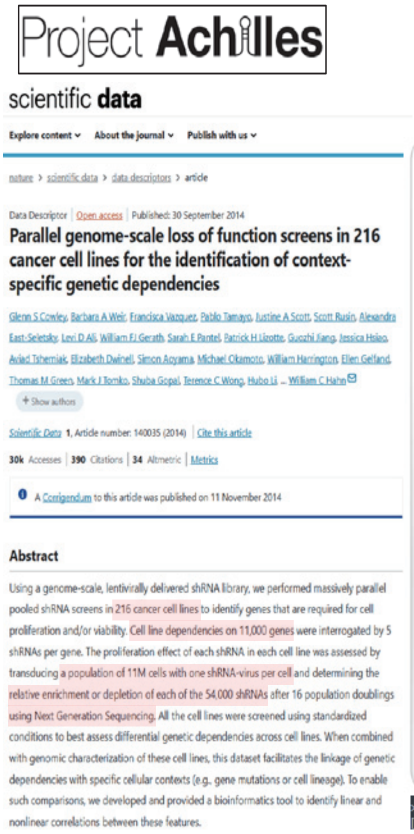
전사체발현값

유전자(n=19,197)

샘플 (n=1,673)

암세포주	TSPAN6	TNMD	DPM1	SCYL3	C1orf112	FGR	CFH	FUCA2
ACH-000007	3.350497	0	5.957218	3.129283	3.716991	0.028569	0.014355	5.630231
ACH-000008	2.887525	0	7.188638	2.198494	4.116864	0	0.097611	6.474274
ACH-000011	3.925999	0	5.638074	2.117695	2.584963	0	0.378512	5.575312
ACH-000012	5.15866	0	6.132577	1.974529	3.77926	0.028569	2.746313	6.27538
ACH-000013	4.917432	0.056584	7.639232	1.914565	3.566815	0.028569	2.056584	5.455163
ACH-000014	2.967169	0	7.575993	2.381283	3.639232	0.056584	0.263034	6.350674
ACH-000015	4.180307	0	6.990501	2.950468	3.697107	0.014355	3.548437	6.185074
ACH-000018	3.785551	0	7.348286	1.87578	3.545968	0.070389	2.077243	5.932392
ACH-000019	2.403268	0	7.49049	2.606442	3.177918	0.014355	0.056584	6.759822
ACH-000021	4.209453	0	6.615299	2.419539	4.520422	0	2.130931	6.102028
ACH-000022	3.527321	0	6.454834	2.735522	3.040892	0.014355	0.097611	5.822475

Genetic Perturbation Data (Project Achilles, RNAi)


Project Achilles

scientific data

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Data Descriptor | Open access | Published: 30 September 2014

Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific dependencies

Glenn S Cowley, Barbara A Weir, Francisca Vazquez, Pablo Tamayo, Justine A Scott, Scott Rusin, Alexandra East-Seletsky, Levi D Ali, William FJ Gerath, Sarah E Pantel, Patrick H Lizotte, Guozhi Jiang, Jessica Hsiao, Aviad Tsherniak, Elizabeth Dwinell, Simon Aoyama, Michael Okamoto, William Harrington, Ellen Gelfand, Thomas M Green, Mark J Tomko, Shuba Gopal, Terence C Wong, Hubo Li ... William C Hahn

+ Show authors

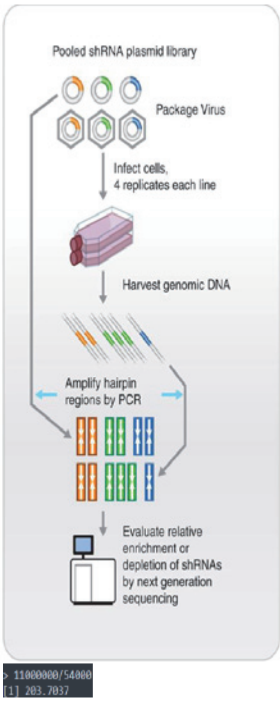
Scientific Data 1, Article number: 140035 (2014) | Cite this article

30k Accesses | 390 Citations | 34 Altmetric | Metrics

A Corrigendum to this article was published on 11 November 2014

Abstract

Using a genome-scale, lentivirally delivered shRNA library, we performed massively parallel pooled shRNA screens in 216 cancer cell lines to identify genes that are required for cell proliferation and/or viability. Cell line dependencies on 11,000 genes were interrogated by 5 shRNAs per gene. The proliferation effect of each shRNA in each cell line was assessed by transducing a population of 11M cells with one shRNA-virus per cell and determining the relative enrichment or depletion of each of the 54,000 shRNAs after 16 population doublings using Next Generation Sequencing. All the cell lines were screened using standardized conditions to best assess differential genetic dependencies across cell lines. When combined with genomic characterization of these cell lines, this dataset facilitates the linkage of genetic dependencies with specific cellular contexts (e.g. gene mutations or cell lineage). To enable such comparisons, we developed and provided a bioinformatics tool to identify linear and nonlinear correlations between these features.



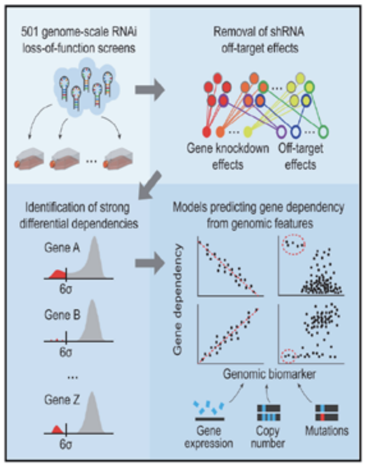
Cowley, G., et al., Sci Data 2014, https://doi.org/10.1038/sdata.2014.35

Resource

Cell

Defining a Cancer Dependency Map

Graphical Abstract



Authors

Aviad Tsherniak, Francisca Vazquez, Phil G. Montgomery, ..., Todd R. Golub, Jesse S. Boehm, William C. Hahn

Correspondence

william_hahn@dfci.harvard.edu

In Brief

A large-scale analysis of 501 cancer cell lines reveals new vulnerabilities that will help prioritize therapeutic targets

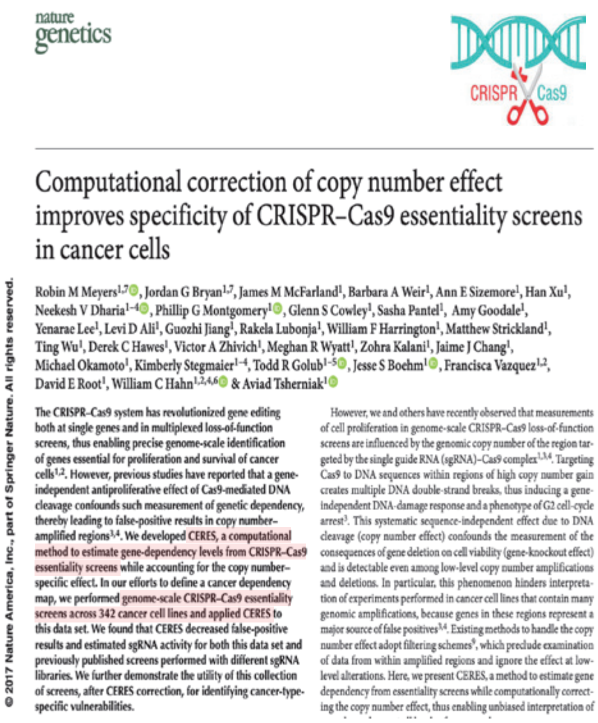
DEMETER computational model segregates on- from off-target effects of RNAi.

Glenn S. Cowley et. al, Nature Scientific Data (2014)
Andrew J. Aguirre et. al. Cancer Discovery (2016)
Tsherniak, A. et. al. Cell (2017)

Genome-scale **RNAi** loss-of-function screens (**17K genes x 707 cell lines**)

17

Genetic Perturbation Data (Project Achilles, CRISPR-Cas9)


nature genetics

CRISPR Cas9

Computational correction of copy number effect improves specificity of CRISPR–Cas9 essentiality screens in cancer cells

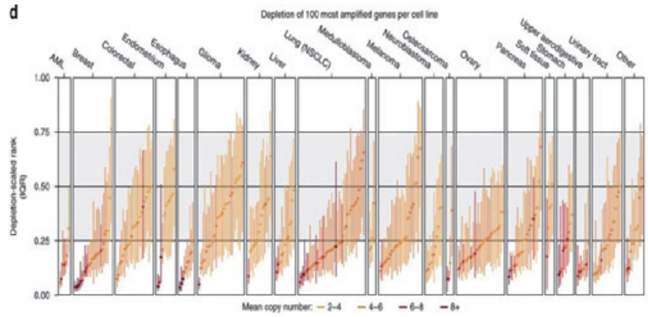
Robin M Meyers[1,7], Jordan G Bryan[1,7], James M McFarland[1], Barbara A Weir[1], Ann E Sizemore[1], Han Xu[1], Neekesh V Dharia[1–4], Phillip G Montgomery[1], Glenn S Cowley[1], Sasha Pantel[1], Amy Goodale[1], Yenarae Lee[1], Levi D Ali[1], Guozhi Jiang[1], Rakela Lubonja[1], William F Harrington[1], Matthew Strickland[1], Ting Wu[1], Derek C Hawes[1], Victor A Zhivich[1], Meghan R Wyatt[1], Zohra Kalani[1], Jaime J Chang[1], Michael Okamoto[1], Kimberly Stegmaier[1–4], Todd R Golub[1–5], Jesse S Boehm[1], Francisca Vazquez[1,2], David E Root[1], William C Hahn[1,2,4,6] & Aviad Tsherniak[1]

The CRISPR-Cas9 system has revolutionized gene editing both at single genes and in multiplexed loss-of-function screens, thus enabling precise genome-scale identification of genes essential for proliferation and survival of cancer cells[1,2]. However, previous studies have reported that a gene-independent antiproliferative effect of Cas9-mediated DNA cleavage confounds such measurement of genetic dependency, thereby leading to false-positive results in copy number–amplified regions[3,4]. We developed CERES, a computational method to estimate gene-dependency levels from CRISPR–Cas9 essentiality screens while accounting for the copy number–specific effect. In our efforts to define a cancer dependency map, we performed genome-scale CRISPR-Cas9 essentiality screens across 342 cancer cell lines and applied CERES to this data set. We found that CERES decreased false-positive results and estimated sgRNA activity for both this data set and previously published screens performed with different sgRNA libraries. We further demonstrate the utility of this collection of screens, after CERES correction, for identifying cancer-type-specific vulnerabilities.

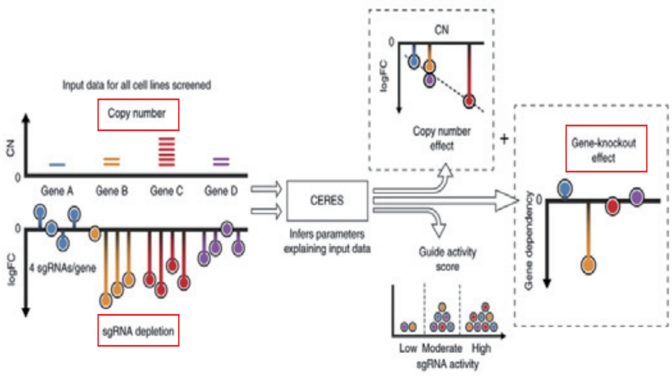
However, we and others have recently observed that measurements of cell proliferation in genome-scale CRISPR-Cas9 loss-of-function screens are influenced by the genomic copy number of the region targeted by the single guide RNA (sgRNA)–Cas9 complex[1,3,4]. Targeting Cas9 to DNA sequences within regions of high copy number gain creates multiple DNA double-strand breaks, thus inducing a gene-independent DNA-damage response and a phenotype of G2 cell-cycle arrest[3]. This systematic sequence-independent effect due to DNA cleavage (copy number effect) confounds the measurement of the gene-knockout effect on cell viability (gene-knockout effect) and is detectable even among low-level copy number amplifications and deletions. In particular, this phenomenon hinders interpretation of experiments performed in cancer cell lines that contain many genomic amplifications, because genes in these regions represent a major source of false positives[3,4]. Existing methods to handle the copy number effect adopt filtering schemes[5], which preclude examination of data from within amplified regions and ignore the effect at low-level alterations. Here, we present CERES, a method to estimate gene dependency from essentiality screens while computationally correcting the copy number effect, thus enabling unbiased interpretation of

Meyers RM, et al., Nat Genet. 2017, https://doi.org/10.1038/ng.3984

Genomic copy number confounds CRISPR–Cas9 loss-of-function screening results.



Schematic of the **CERES** computational model:



Genome-scale **CRISPR-Cas9** screening data (**18K genes x 1078 cell lines**)

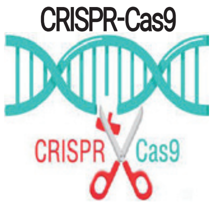
18

Project Achilles Data 예시

Gene effect score

Dempster JM, et al., Genome Biol. 2021, doi: 10.1186/s13059-021-02540-7

Chronos: a cell population dynamics model of CRISPR experiments that improves inference of gene fitness effects.



Gene (n=17453)

	A1BG (1)	A1CF (29974)	A2M (2)	A2ML1 (144568)	A3GALT2 (127550)	A4GALT (53947)	A4GNT (51146)	AAAS (8086)	AACS (65985)	AADAC (13)	AADACL2 (34475
ACH-000004	0.014633313	-0.032776881	-0.151299335	-0.071388055	0.046511348	-0.162850264	0.29069796	-0.240990578	0.176709618	0.159418272	-0.0337576
ACH-000005	-0.261566013	0.174832966	0.106526178	0.135634859	-0.07675266	-0.278640387	0.239278911	-0.325966623	-0.116848091	0.022227046	0.196319
ACH-000007	-0.028717259	-0.117016695	0.030970917	0.083795472	0.03266787	-0.035708844	0.012354577	-0.192435733	-0.077173848	0.164876538	0.022104
ACH-000009	0.000225193	-0.283123657	0.051248458	0.120321302	0.022834458	-0.077521593	0.028013228	-0.190494584	0.031588999	0.043242185	0.130025
ACH-000011	0.095790835	-0.09962218	0.0222039	0.199771439	-0.048125726	-0.290811843	-0.013276809	-0.095840138	0.090306588	0.029378859	-0.000738
ACH-000012	-0.108980039	0.058619973	0.172384329	0.22333558	0.119961004	-0.212956371	0.24949426	-0.186590778	0.019211123	0.233628909	0.014815
ACH-000013	-0.077777425	-0.078709387	0.026442403	0.100745776	-0.069464547	-0.103456242	-0.018182221	-0.246801117	-0.055118181	0.150498766	0.073710
ACH-000014	-0.05374029	-0.157497516	0.038028005	0.05747727	0.026941614	-0.139086887	-0.27422737	-0.114681587	-0.148565521	0.05385278	-0.058643
ACH-000015	-0.189235489	-0.035973688	-0.08122651	0.040641109	0.073001869	-0.036026227	0.145735018	-0.215469094	0.006971712	0.076011901	0.076131
ACH-000017	-0.009788805	-0.028755467	-0.003560714	0.022337554	-0.271078441	-0.13156375	0.139689059	-0.135385331	-0.056921675	0.131126809	-0.115684
ACH-000018	-0.132354658	0.00373113	-0.241208774	0.08067838	0.08757853	0.060882308	0.153020561	-0.129359938	0.094829653	-0.238871343	0.014186
ACH-000019	-0.035709147	0.065842266	0.071567865	0.085402581	-0.09803548	0.079596074	0.024516003	-0.391174984	-0.055396738	-0.132411528	-0.059595
ACH-000021	-0.105938293	-0.128982525	-0.031954757	-0.037816921	-0.0084916	-0.142512117	0.015930934	-0.339397891	-0.0047865	0.038653282	-0.006190
ACH-000022	-0.066232694	0.082552379	0.10526581	-0.076127482	-0.135723189	-0.069813265	0.068649629	-0.0930021	-0.026797883	0.08262064	-0.003441
ACH-000024	-0.064594325	-0.010429737	0.006144276	0.020655644	0.070508525	-0.151402344	0.046927159	-0.329979703	-0.003031012	0.075533718	0.003783
ACH-000025	-0.146706645	-0.202706494	0.015312183	0.144106709	0.017333282	-0.084314155	-0.119422164	-0.410011055	-0.156415687	0.088010479	-0.074597
ACH-000028	-0.1390997	-0.165146792	0.117512932	0.167261975	-0.041199177	-0.024998519	-0.104082333	-0.296743293	0.085726357	0.047016718	-0.060661

cell line(n=1078)

Drug Response Data (CTRP)

Cancer Therapeutics Response Portal v2

CTD²

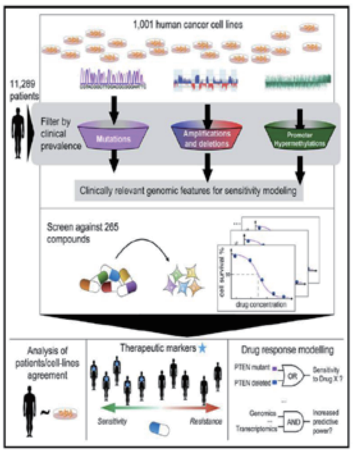
Cell

Resource

July 28, 2016

A Landscape of Pharmacogenomic Interactions in Cancer

Graphical Abstract



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Francesco Iorio, Theo A. Knijnenburg, Daniel J. Vis, ..., Julio Saez-Rodriguez, Ultan McDermott, Mathew J. Garnett

Correspondence

um1@sanger.ac.uk (U.M.), mg12@sanger.ac.uk (M.J.G.)

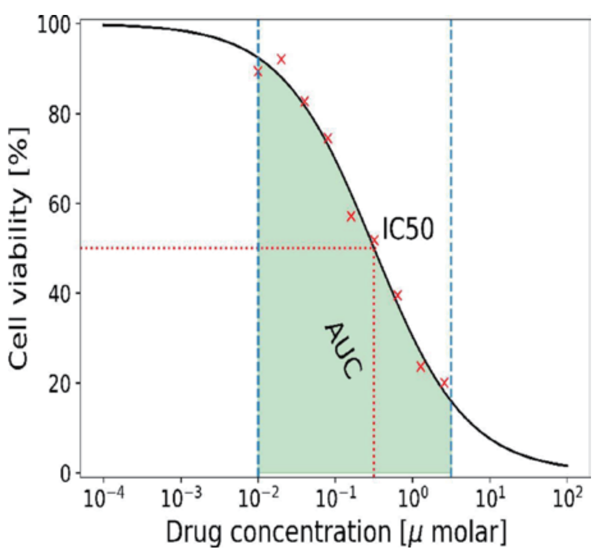
In Brief

A look at the pharmacogenomic landscape of 1,001 human cancer cell lines points to new treatment applications for hundreds of known anti-cancer drugs.

Cheah, et al., Cell, 154, 1151-1161 (2013)
Seashore-Ludlow et al., Cancer Discovery, 5, 1210-1223 (2015)
Rees et al., Nat Chem Biol, 12, 109-116 (2016)

Drug sensitivity screens (**545 drugs x 860 cell lines**)

Dose-dependent viability screening for all drugs & cells



IC50: drug concentration that reduces viability by 50% (특정 지점)

AUC: area under the dose-response curve (전체 반응)

Drug Response Data (PRISM)

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Resource | Published: 20 January 2020

Discovering the anticancer potential of non-oncology drugs by systematic viability profiling

Steven M. Corsello, Rohith T. Nagari, Ryan D. Spangler, Jordan Rossen, Mustafa Kocak, Jordan G. Bryan, Ranad Humeidi, David Peck, Xiaoyun Wu, Andrew A. Tang, Vickie M. Wang, Samantha A. Bender, Evan Lemire, Rajiv Narayan, Philip Montgomery, Uri Ben-David, Colin W. Garvie, Yejia Chen, Matthew G. Rees, Nicholas J. Lyons, James M. McFarland, Bang T. Wong, Li Wang, Nancy Dumont, … Todd R. Golub

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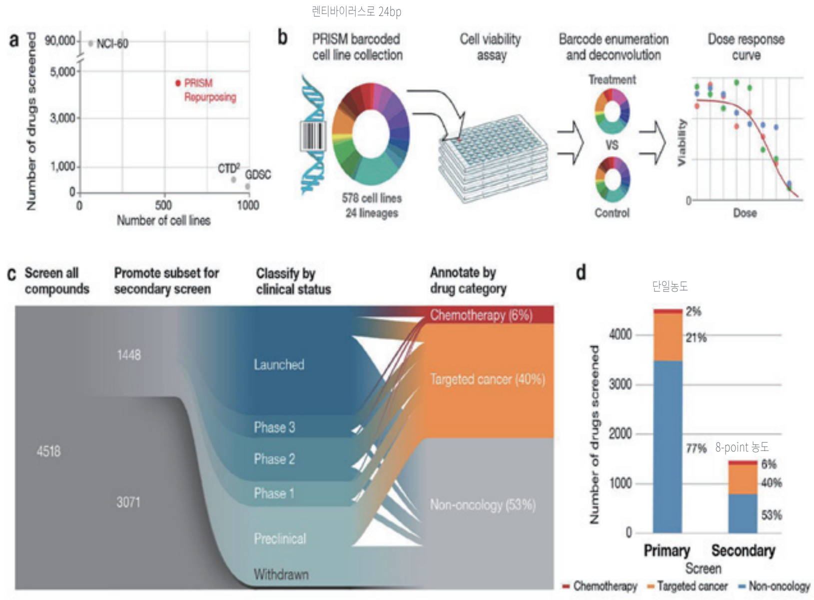
Nature Cancer 1, 235–248 (2020) | Cite this article

Abstract

Anticancer uses of non-oncology drugs have occasionally been found, but such discoveries have been serendipitous. We sought to create a public resource containing the growth-inhibitory activity of 4,518 drugs tested across 578 human cancer cell lines. We used PRISM (profiling relative inhibition simultaneously in mixtures), a molecular barcoding method, to screen drugs against cell lines in pools. An unexpectedly large number of non-oncology drugs selectively inhibited subsets of cancer cell lines in a manner predictable from the molecular features of the cell lines. Our findings include compounds that killed by inducing phosphodiesterase 3A-Schlafen 12 complex formation, vanadium-containing compounds whose killing depended on the sulfate transporter SLC26A2, the alcohol dependence drug disulfiram, which killed cells with low expression of metallothioneins, and the anti-inflammatory drug tepoxalin, which killed via the multidrug resistance protein ATP-binding cassette subfamily B member 1 (ABCB1). The PRISM drug repurposing resource (https://depmap.org/repurposing) is a starting point to develop new oncology therapeutics, and more rarely, for potential direct clinical translation.

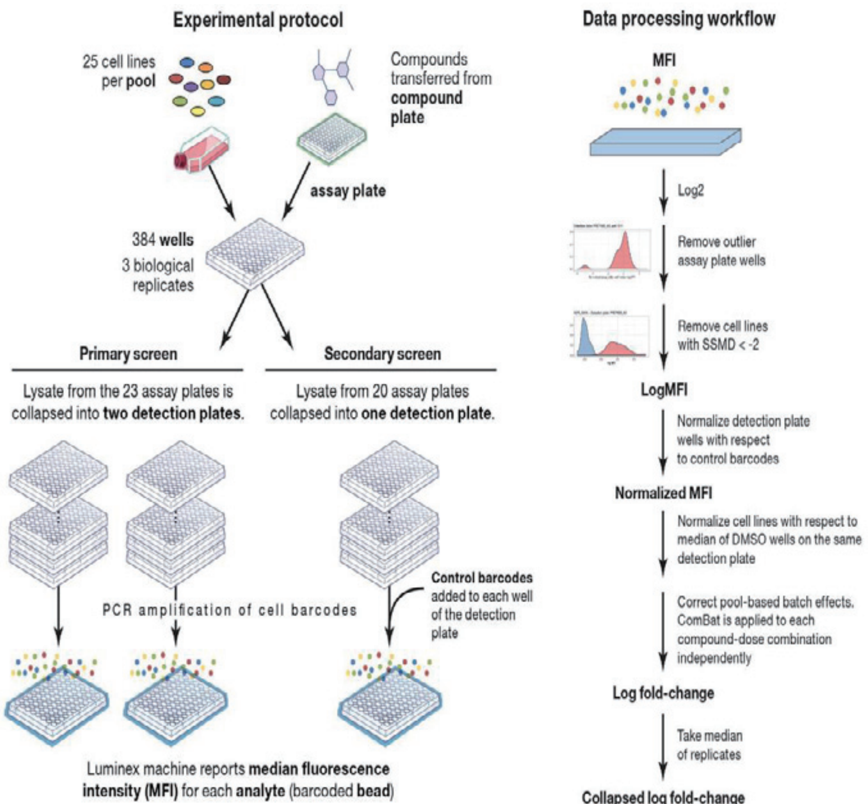
PRISM
MULTIPLEXED CELL LINE SCREENING



Corsello SM, et al. Nat Cancer. 2020

Drug sensitivity screens (**6,767 drugs x 915 cell lines**)

Drug Response Data (PRISM)



Corsello SM, et al. Nat Cancer. 2020

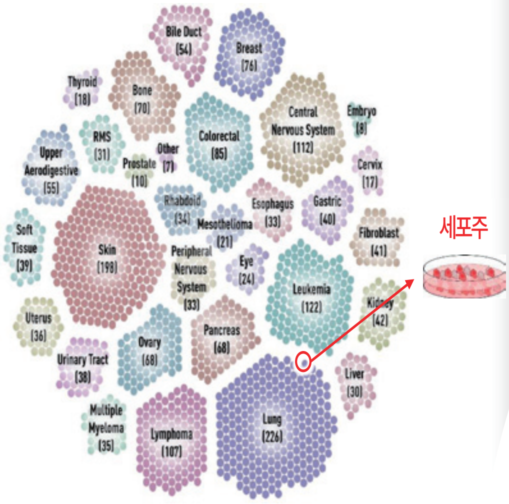
DNA 추출 후 바코드 영역을 MFI로 측정
Intensity → 생존도

Drug sensitivity screens (**6,767 drugs x 915 cell lines**)

CTRP, PRISM Data 예시

> 30 Lineages

1,673 Cell lines



CTRP (AUC값) 약물(n=545)

샘플 (n=825)

암세포주	CIL56 (CTRP:100490)	FQI-1 (CTRP:102193)	ML050 (CTRP:153820)	ML162 (CTRP:154846)	CIL41 (CTRP:176181)
ACH-000002			14.709	10.467	
ACH-000004	11.733	10.825	15.689	7.0524	14.78
ACH-000005			14.662	6.7487	
ACH-000006				9.8786	
ACH-000007	14.562	11.469	15.638	8.565	15.313
ACH-000008			14.62	10.455	
ACH-000009			14.447	10.157	
ACH-000011	14.75	11.391	14.736		14.017
ACH-000012	11.715	12.065	14.878	7.5232	14.609
ACH-000013	13.11	11.578	14.688	7.3517	14.055
ACH-000014			14.616	7.2436	
ACH-000015	11.534	11.537	14.162	6.8405	12.159

PRISM (logFC값) 약물(n=6,767)

샘플 (n=915)

암세포주	ARV-825	RS-0481	8-BROMO-CGMP	DOCUSATE
ACH-000001	-1.207281459	0.515743393	-0.01557664	-0.395122526
ACH-000002	-4.2315633			-0.538375593
ACH-000004	-3.860671666			0.306971335
ACH-000005	-2.271410721			0.035096029
ACH-000006	0.277832784			-0.12489917
ACH-000007	-4.011285013	0.196877764	-0.095730328	-0.86186002
ACH-000008	-0.615104645	0.347820872	0.379480425	-0.137544119
ACH-000011	-1.827661242	-0.001030595	0.145346065	0.159798233

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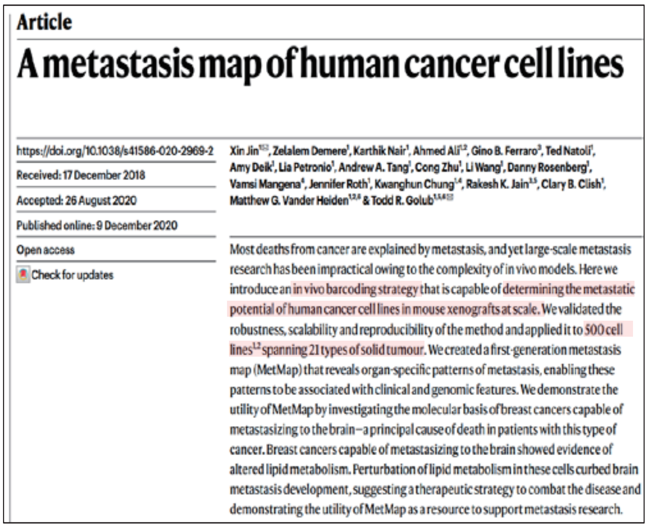
MetMap: 전이 잠재력 프로파일링



Article

A metastasis map of human cancer cell lines

https://doi.org/10.1038/s41586-020-2969-2
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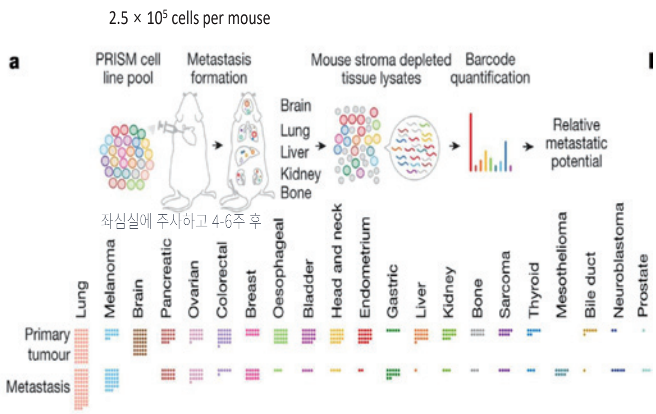
Accepted: 26 August 2020
Published online: 9 December 2020
Open access
Check for updates

Xin Jin[1,5], Zelalem Demere[1], Karthik Nair[1], Ahmed Ali[1,2], Gino B. Ferraro[3], Ted Natoli[1], Amy Deik[1], Lia Petronio[1], Andrew A. Tang[1], Cong Zhu[1], Li Wang[1], Danny Rosenberg[1], Vamsi Mangena[4], Jennifer Roth[1], Kwanghun Chung[1,4], Rakesh K. Jain[3,5], Clary B. Clish[1], Matthew G. Vander Heiden[1,2,6] & Todd R. Golub[1,5,6,8]

Most deaths from cancer are explained by metastasis, and yet large-scale metastasis research has been impractical owing to the complexity of in vivo models. Here we introduce an in vivo barcoding strategy that is capable of determining the metastatic potential of human cancer cell lines in mouse xenografts at scale. We validated the robustness, scalability and reproducibility of the method and applied it to 500 cell lines[1,2] spanning 21 types of solid tumour. We created a first-generation metastasis map (MetMap) that reveals organ-specific patterns of metastasis, enabling these patterns to be associated with clinical and genomic features. We demonstrate the utility of MetMap by investigating the molecular basis of breast cancers capable of metastasizing to the brain—a principal cause of death in patients with this type of cancer. Breast cancers capable of metastasizing to the brain showed evidence of altered lipid metabolism. Perturbation of lipid metabolism in these cells curbed brain metastasis development, suggesting a therapeutic strategy to combat the disease and demonstrating the utility of MetMap as a resource to support metastasis research.

Jin, X., et al., Nature, 2020



PRISM 세포 pool 일부의 'Metastasis Potential score (전이잠재력점수)'을 측정한 데이터

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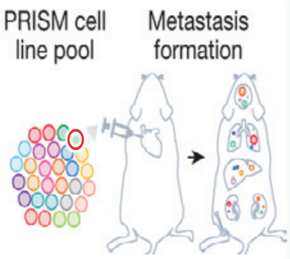
MetMap Data 예시

2.5 × 10^5 cells per mouse

498 lines in 1 pool
~500 cells per line
15 mice
8–10 weeks old, female
5 organs



샘플 (n=480)

5개장기

암세포주	all5	bone	brain	kidney	liver	lung
ACH-000824	-0.3990943	-0.41509247	-3.5884657	-2.7012691	-2.8143728	-1.9600358
ACH-001307	0.70043534	0.3598184	-3.08772	0.3406231	-1.0269101	-0.35483155
ACH-000756	-3.6238341	-3.6238341	-3.6238341	-3.6238341	-3.6238341	-3.6238341
ACH-000681	0.72302413	0.4708827	-1.3184494	0.06815637	-0.26031306	-0.2511465
ACH-000444	1.4668136	-0.38812956	1.1447339	-0.32549992	1.1296722	-0.008543288
ACH-000142	-3.9475245	-3.9475245	-3.9475245	-3.9475245	-3.9475245	-3.9475245
ACH-000905	-3.751187	-3.751187	-3.751187	-3.751187	-3.751187	-3.751187
ACH-000680	-3.5815332	-4.3031235	-4.3031235	-3.7536607	-4.095439	-3.9787605
ACH-000954	-0.35865268	-1.0332105	-1.8379211	-0.7988067	-0.81892747	-1.6904793
ACH-000280	-0.6313329	-3.5819612	-1.0898384	-0.83641493	-3.8443756	-2.166436
ACH-000012	-1.6870533	-1.7376165	-3.7329085	-3.7329085	-3.7329085	-2.6118636
ACH-000098	-3.2588358	-3.9414883	-3.9414883	-3.2588358	-3.9414883	-3.9414883
ACH-000589	-1.5956706	-3.6115925	-1.7836795	-3.6037877	-2.0683491	-4.3882265
ACH-000738	-1.2002637	-2.8095977	-4.055034	-1.2119788	-3.5168688	-4.055034
ACH-000837	-1.1058818	-3.98758	-1.151784	-2.1213114	-3.98758	-3.2985935
ACH-000967	-1.256578	-3.550686	-4.087905	-2.770807	-1.3833243	-1.920528
ACH-000662	-0.03221303	-2.5257874	-3.5254264	-2.2099063	-0.0955768	-0.9315127
ACH-000537	-2.117738	-3.8424711	-3.8424711	-2.138294	-3.304306	-3.8424711
ACH-000427	-3.158853	-3.5846462	-3.5846462	-3.5846462	-3.5846462	-3.158853

< = -4	non-metastatic
-4 ~ -2	(weakly) metastatic, but with low confidence
> = -2	metastatic, with higher confidence

→ *score* 높을수록 전이율 높음

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Summary: DepMap 역사 타임라인

2008
CCLE 시작

2015
CTRP v2 공개

2015–2017
Achilles (CRISPR 스크린)

2020
MetMap 공개

2012
CCLE · GDSC (Nature)

2016
PRISM 바코딩

2019
차세대 CCLE

2024
2세대
DepMap

리소스: CCLE · GDSC · CTRP · PRISM

기능유전체: Achilles (2015–2017)

확장: MetMap · 2세대 DepMap

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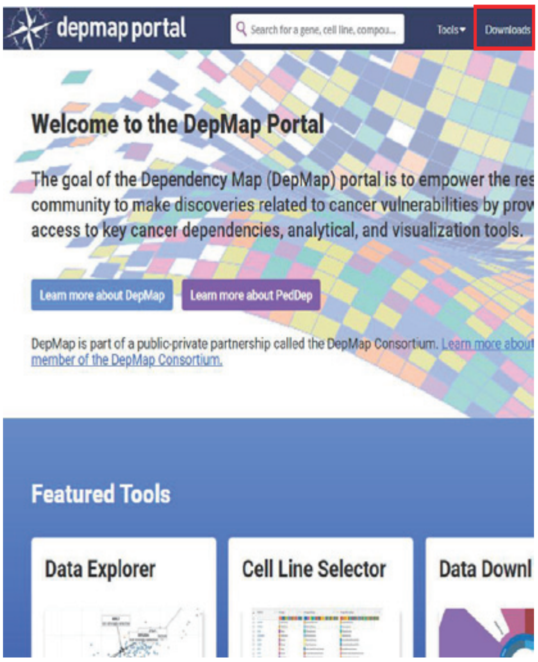
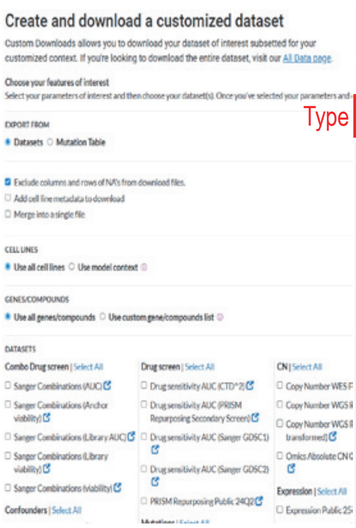
DepMap 데이터 얻기

How to get data

https://depmap.org/portal/



Custom Downloads



All Data Downloads

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Contents

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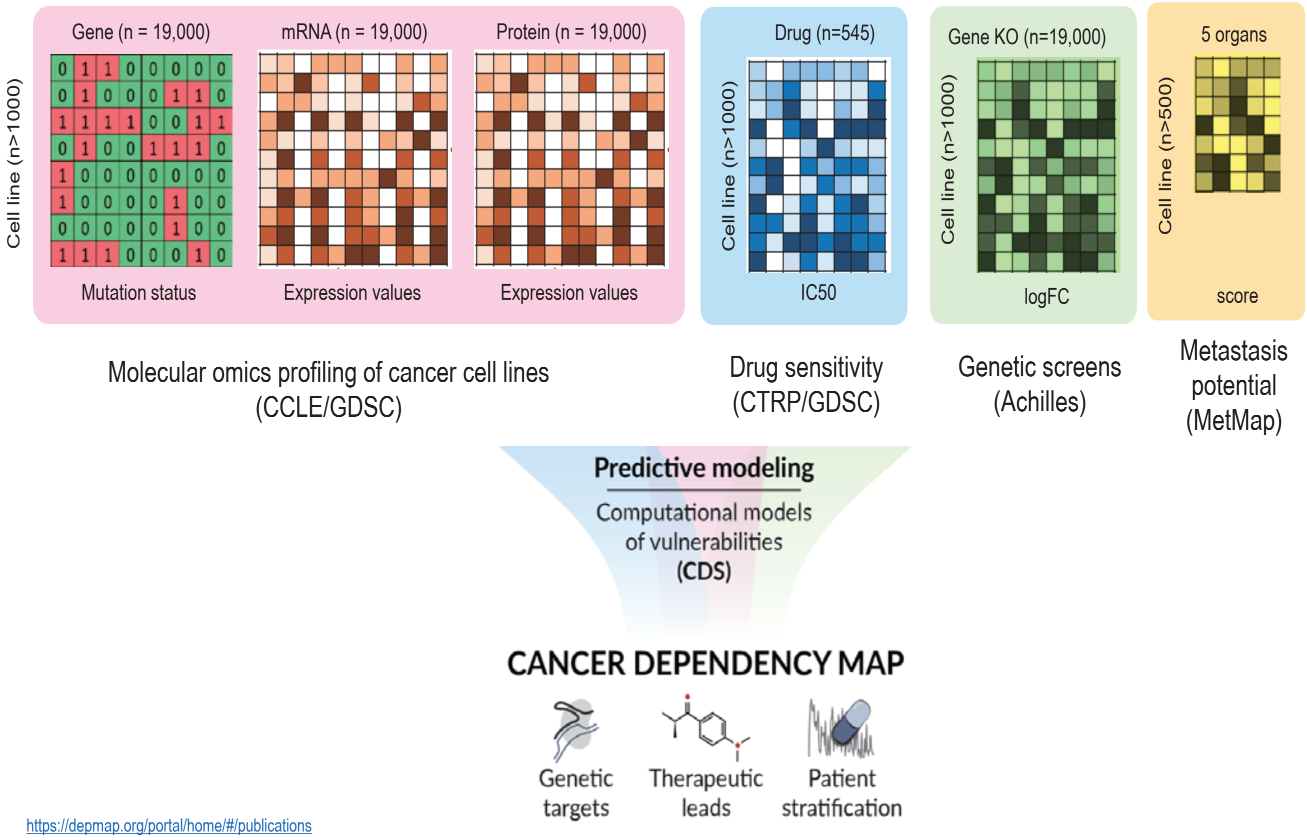
DepMap 리소스



https://depmap.org/portal/home/#/publications

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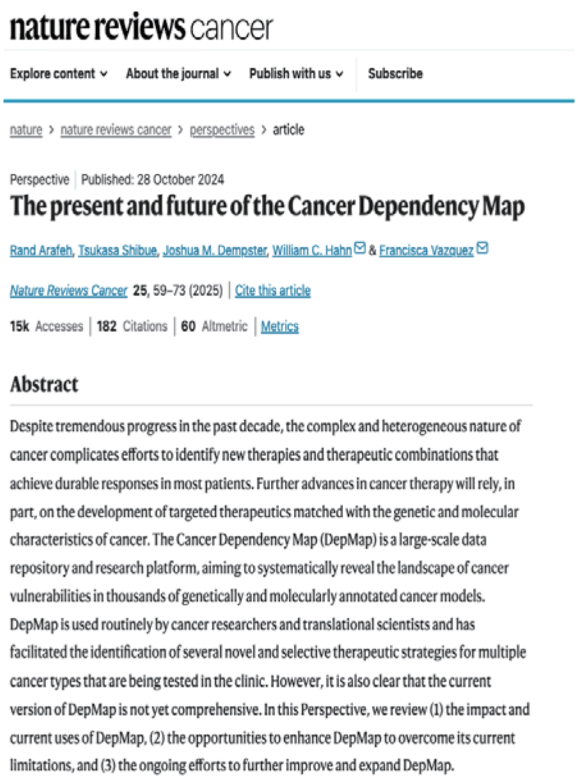
DepMap 데이터 활용 사례 분류



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Perspective | Published: 28 October 2024

The present and future of the Cancer Dependency Map

Rand Arafeh, Tsukasa Shibue, Joshua M. Dempster, William C. Hahn & Francisca Vazquez

Nature Reviews Cancer 25, 59–73 (2025) | Cite this article

15k Accesses | 182 Citations | 60 Altmetric | Metrics

Abstract

Despite tremendous progress in the past decade, the complex and heterogeneous nature of cancer complicates efforts to identify new therapies and therapeutic combinations that achieve durable responses in most patients. Further advances in cancer therapy will rely, in part, on the development of targeted therapeutics matched with the genetic and molecular characteristics of cancer. The Cancer Dependency Map (DepMap) is a large-scale data repository and research platform, aiming to systematically reveal the landscape of cancer vulnerabilities in thousands of genetically and molecularly annotated cancer models. DepMap is used routinely by cancer researchers and translational scientists and has facilitated the identification of several novel and selective therapeutic strategies for multiple cancer types that are being tested in the clinic. However, it is also clear that the current version of DepMap is not yet comprehensive. In this Perspective, we review (1) the impact and current uses of DepMap, (2) the opportunities to enhance DepMap to overcome its current limitations, and (3) the ongoing efforts to further improve and expand DepMap.

1. Drug sensitivity & biomarker discovery
2. Drug's mechanisms of action
3. Gene-gene interactions
4. Synthetic-lethal dependencies
5. Computational tool development

Arafeh R et al. Nat Rev Cancer. 2025 doi: 10.1038/s41568-024-00763-x

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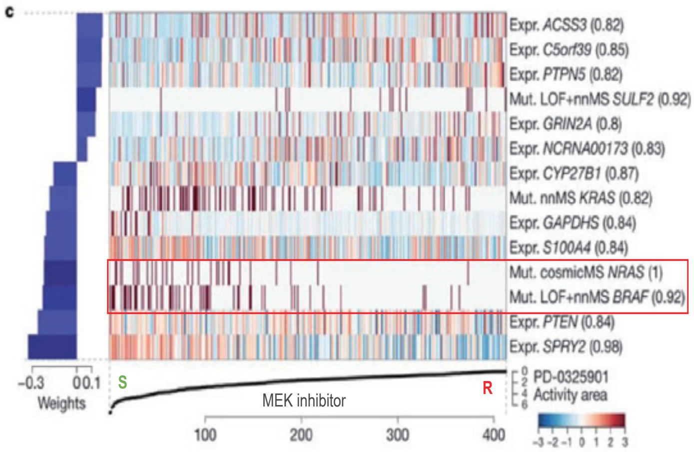
Drug sensitivity & biomarkers – CCLE & GDSC

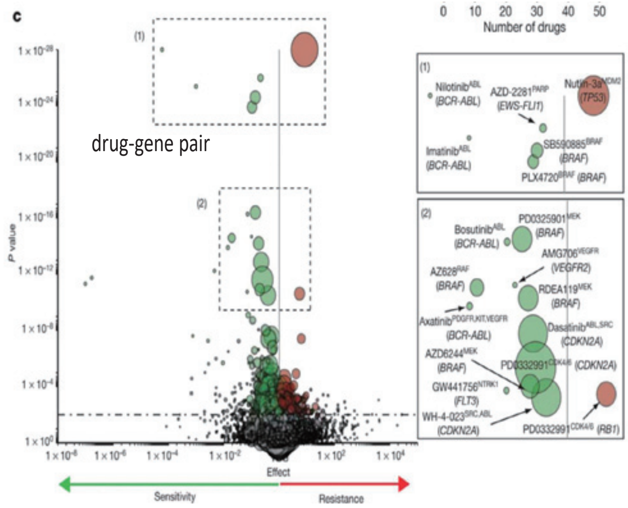
CCLE Cancer Cell Line Encyclopedia

GDSC² Genomics of Drug Sensitivity in Cancer

Pharmacological profiles for **24 anticancer drugs** across 479 cell lines

Pharmacological profiles for **130 anticancer drugs** across 507 cell lines





Elastic Net regression analysis
"Activating mutations in *BRAF* and *NRAS* were among the top four predictors of sensitivity in models generated for the MEK inhibitor PD-0325901."
MEK inhibitors target MAPK pathway, downstream of RAF

Multivariate ANOVA
BCR-ABL rearrangement : ABL inhibitors
BRAF mutations: MEK1/MEK2 inhibitors
TP53 mutations: MEM2 inhibitor

Barretina J, et al., Nature. 2012

Garnett MJ et al., Nature. 2012

Drug's mechanisms of action (MOA)

News & Views

molecular systems biology

The Cancer Dependency Map enables drug mechanism-of-action investigation

Francisca Vazquez* & Jesse S Boehm**

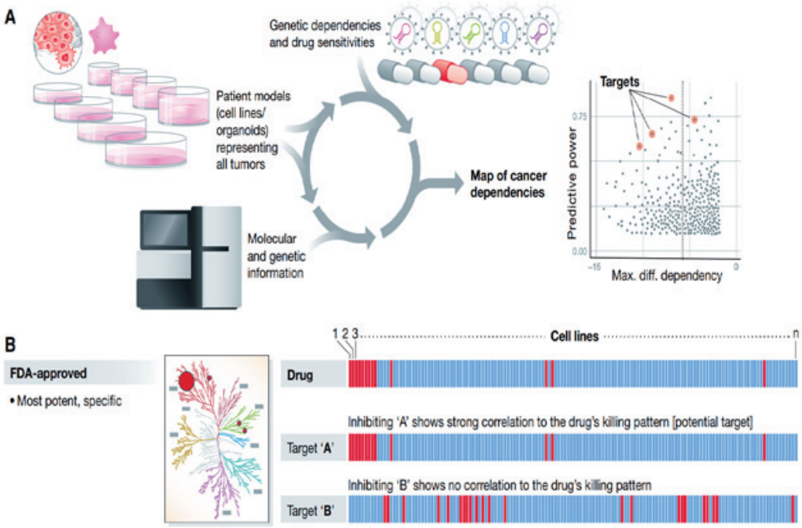
How do small molecules exert their effects in mammalian cells? This seemingly simple question continues to represent one of the fundamental challenges of modern translational science and as such has long been the subject of intense scientific scrutiny. In their recent study, Garnett and colleagues (Gonçalves *et al*, 2020) demonstrate proof-of-concept for a new way to attack this problem systematically for Oncology drugs, by identifying correlated CRISPR- and drug-killing profiles in the Cancer Dependency Map dataset.

Mol Syst Biol. (2020) 16: e9757
See also: **E Gonçalves et al** (2020)

In the case of cancer, several promising new genomic frontiers are now emerging that are beginning to accelerate progress in MoA. First, the use of genetic RNAi or CRISPR modifier screens to identify rescue or sensitization to anti-cancer drug killing has been a powerful approach (Jost & Weissman, 2018; Colic *et al*, 2019). Second, the use of gene expression and/or high content imaging as a surrogate measurement has enabled the assessment of "connectivity" in signature space (e.g., between a known perturbation and that of a small molecule) (Subramanian *et al*, 2017). Despite these advances, such approaches are typically limited to specific cancer contexts.

cancer drugs with largely known that the correlation in viability bet of ~17,000 genetic knockouts an 397 established drugs across 484 di lines should rediscover the Mo examples of success have been re broad-scale study of this new us Cancer Dependency Map data become possible recently.

Through an extensive series of s linear regression analyses, they de the merits of this approach. They fi 26% of cases, the killing pattern of is directly phenocopied by the CRIS pattern of the known drug targ investigate the 264 cases in which t



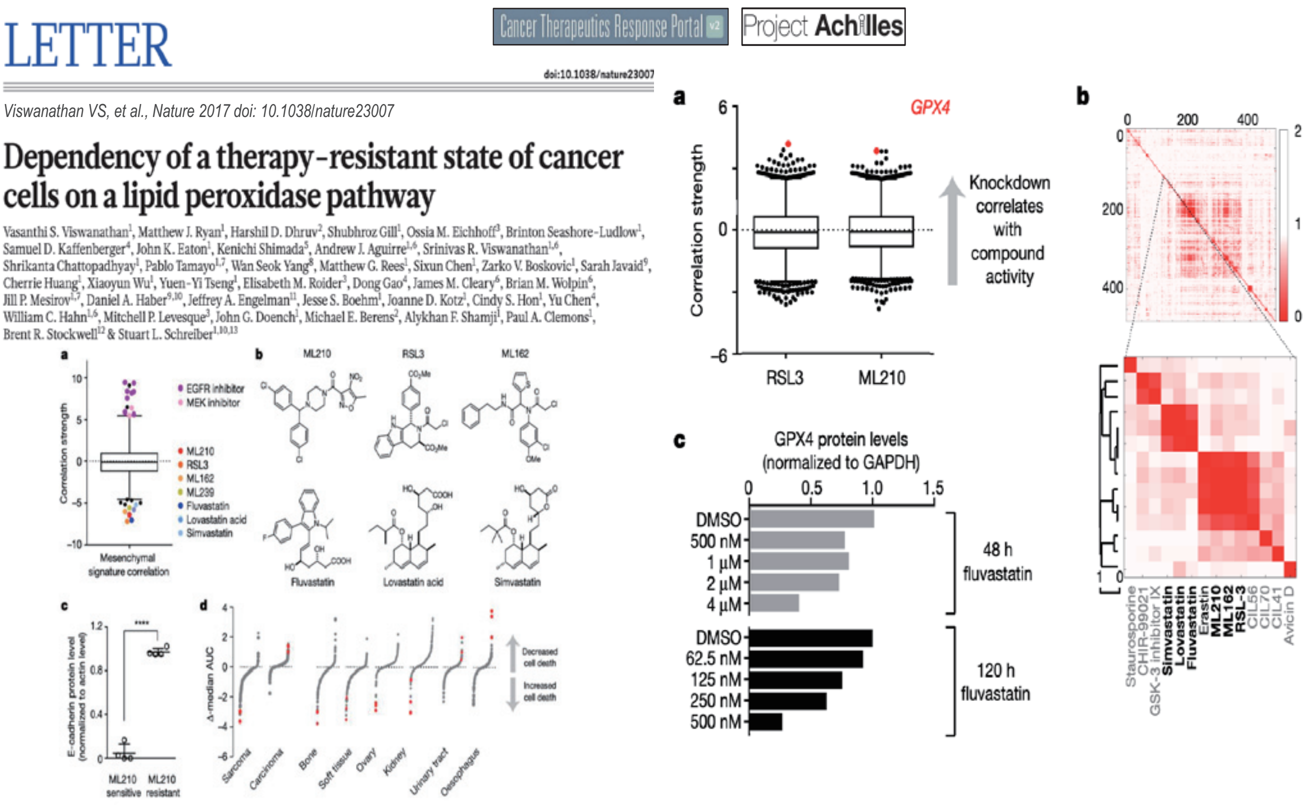
Project Achilles

Cancer Therapeutics Response Portal v2

Correlations of **genetic dependencies** and **drug sensitivities** across cell lines can inform small molecule target(s) identification and mechanism-of-action. Red bars: cell killing; blue bars: no cell killing.

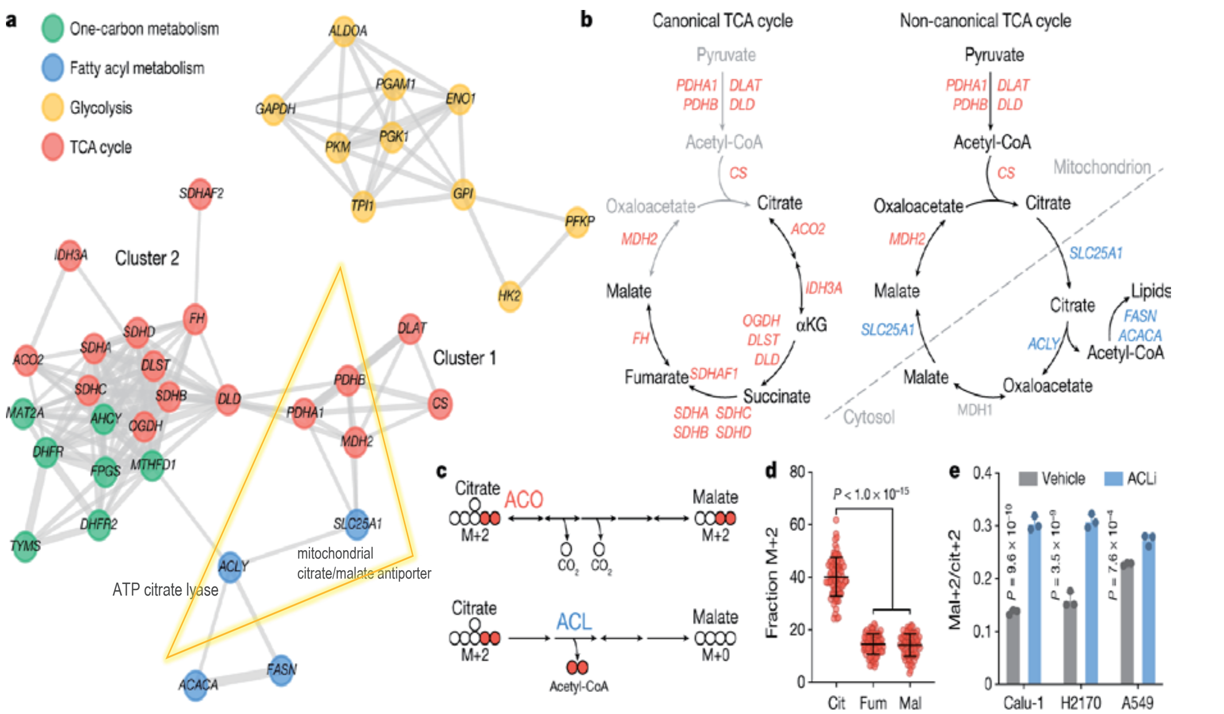
Vazquez F, et al., Mol Syst Biol. 2020

Drug sensitivity & MOA



A search for compounds against **cancer cell lines with mesenchymal gene expression signatures** has identified a handful of compounds that selectively kill these cells (ML210, RSL3, and ML162).
The mechanisms of action of these compounds converged on lipid peroxide reduction by **glutathione peroxidase 4 (GPX4)**, a process known to be critical to the regulation of ferroptosis.

Gene-gene interactions



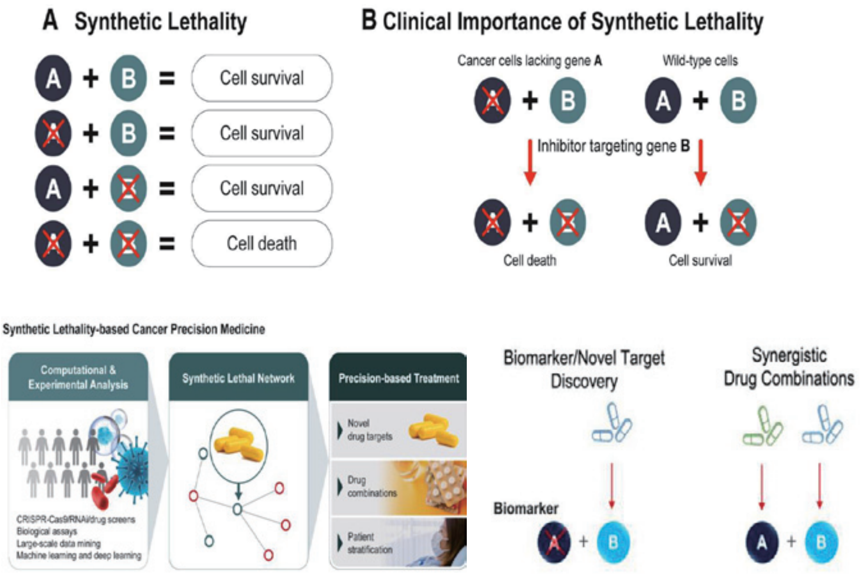
Networks representing gene essentiality score correlations between genes from the indicated pathways
→ Subsequent experimental analyses uncovered an alternative pathway of acetyl-CoA oxidation in the TCA cycle that involves the processing of citrate to malate in the cytosol.

Arnold PK, et al., Nature. 2022

Synthetic-lethal dependencies

CCLE Cancer Cell Line Encyclopedia

Project Achilles



Schäffer AA, et al., Med. 2024

Table 1 | Therapeutic targets identified by the Cancer Dependency Map

Target	Strategy for dependency discovery	Compound	Trial stage	ClinicalTrials.gov ID	Ref.
PRMT5	shRNA screening in *CDKN2A*-deficient cancer cells with collateral deletion of *MTAP*	GSK3326595	II	NCT04676516	60
		AZD3470	I/II	NCT06130553	61
		AZD3470	I/II	NCT06137144	62
		MRTX1719	I/II	NCT05245500	63
		SCR-6920	I	NCT05528055	64
		PF-06939999	I	NCT03854227	65
		TNG462	I/II	NCT05732831	66
		TNG908	I/II	NCT05275478	67
		PRT543	I	NCT03886831	68
		PRT811	I	NCT04089449	69
		JNJ-64619178	I	NCT03573310	70
		AMG 193	I/II	NCT05094336	71
		AMG 193	I/II	NCT05975073	72
		AMG 193	I	NCT06333951	73
MAT2A	shRNA screening in *CDKN2A*-deficient cancer cells with collateral deletion of *MTAP*	S095035	I	NCT06188702	74
		IDE397	I	NCT04794699	75
		ISM3412	I	NCT06414460	76
WRN	CRISPR and RNAi screening in cancer cells with MSI	RO7589831	I	NCT06004245	77
		HRO761	I	NCT05838768	78
PKMYT1	CRISPR screening in cancer cells with *CCNE1* amplification	RP-6306	I	NCT05147350	79
		RP-6306	I	NCT05147272	80
		RP-6306	I	NCT06107868	81
		RP-6306	I	NCT04855656	82
SMARCA2	shRNA screening in *SMARCA4*-mutant cancer cells	PRT3789	I	NCT05639751	83
		FHD-286	I	NCT04891757	84

Arafeh R et al. Nat Rev Cancer. 2025

Computational algorithm development

SCIENCE ADVANCES | RESEARCH ARTICLE

CANCER

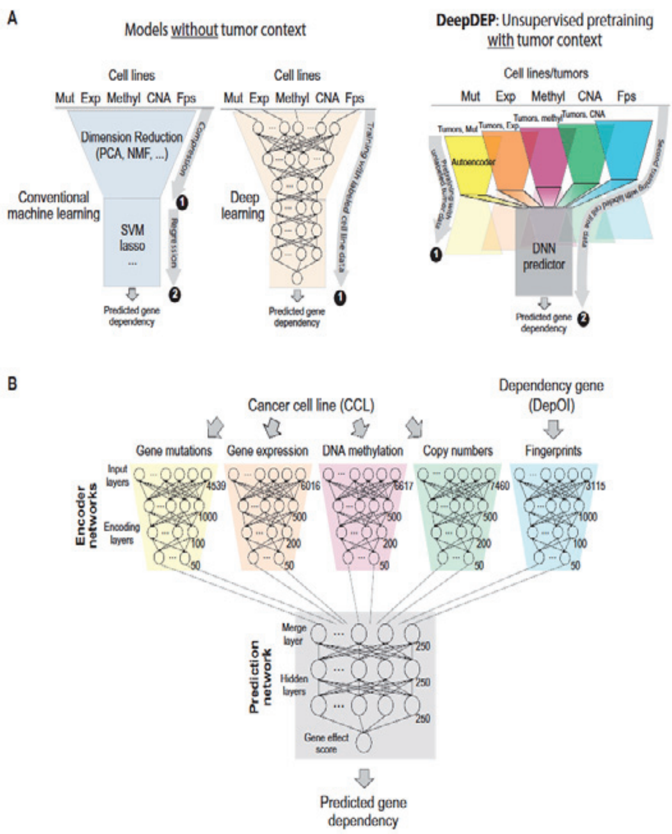
Predicting and characterizing a cancer dependency map of tumors with deep learning

Yu-Chiao Chiu[1], Siyuan Zheng[1,2], Li-Ju Wang[1], Brian S. Iskra[1], Manjeet K. Rao[1,3], Peter J. Houghton[1,4], Yufei Huang[5,6]*, Yidong Chen[1,2]*

Genome-wide loss-of-function screens have revealed genes essential for cancer cell proliferation, called cancer dependencies. It remains challenging to link cancer dependencies to the molecular compositions of cancer cells or to unscreened cell lines and further to tumors. Here, we present DeepDEP, a deep learning model that predicts cancer dependencies using integrative genomic profiles. It uses a unique unsupervised pretraining that captures unlabeled tumor genomic representations to improve the learning of cancer dependencies. We demonstrated DeepDEP's improvement over conventional machine learning methods and validated the performance with three independent datasets. By systematic model interpretations, we extended the current dependency maps with functional characterizations of dependencies and a proof-of-concept in silico assay of synthetic essentiality. We applied DeepDEP to pan-cancer tumor genomics and built the first pan-cancer synthetic dependency map of 8000 tumors with clinical relevance. In summary, DeepDEP is a novel tool for investigating cancer dependency with rapidly growing genomic resources.

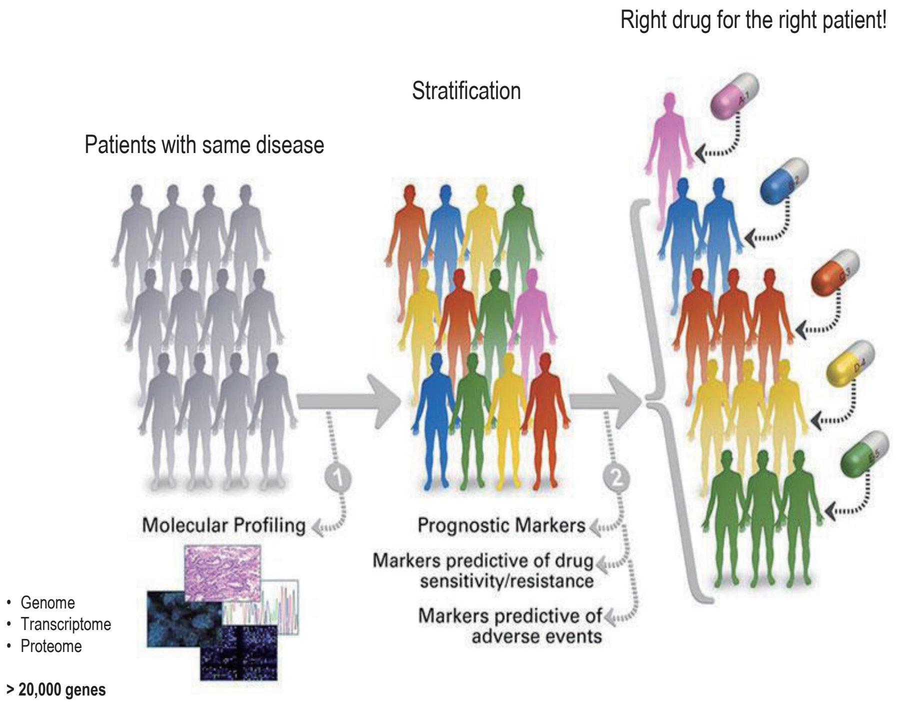
CCLE Cancer Cell Line Encyclopedia

Project Achilles



Yu-Chiao Chiu et al., Sci. Adv. 2021. DOI:10.1126/sciadv.abh1275

DepMap informs pharmacogenomics



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Pharmacogenomics

21 languages

Article Talk

From Wikipedia, the free encyclopedia

WIKIPEDIA
The Free Encyclopedia

For the journal, see Pharmacogenomics (journal).

This article **may be too technical for most readers to understand.** Please help improve it to make it understandable to non-experts, without removing the technical details. *(May 2024)* *(Learn how and when to remove this message)*

Pharmacogenomics, often abbreviated "**PGx**", is the study of the role of the genome in drug response. Its name (*pharmaco-* + *genomics*) reflects its combining of pharmacology and genomics. Pharmacogenomics analyzes how the genetic makeup of a patient affects their response to drugs.[1] It deals with the influence of acquired and inherited genetic variation on drug response, by correlating DNA mutations (including point mutations, copy number variations, and structural variations) with pharmacokinetic (drug absorption, distribution, metabolism, and elimination), pharmacodynamic (effects mediated through a drug's biological targets), and immunogenic endpoints.[2][3][4]

Pharmacogenomics aims to develop rational means to optimize drug therapy, with regard to the patients' genotype, to achieve maximum efficiency with minimal adverse effects.[5] It is hoped that by using pharmacogenomics, pharmaceutical drug treatments can deviate from what is dubbed as the "one-dose-fits-all" approach. Pharmacogenomics also attempts to eliminate trial-and-error in prescribing, allowing physicians to take into consideration their patient's genes, the functionality of these genes, and how this may affect the effectiveness of the patient's current or future treatments (and where applicable, provide an explanation for the failure of past treatments).[6][7] Such approaches promise the advent of precision medicine and even personalized medicine, in which drugs and drug combinations are optimized for narrow subsets of patients or even for each individual's unique genetic makeup.[8][9]

Part of a series on
Genetics

Key components [show]
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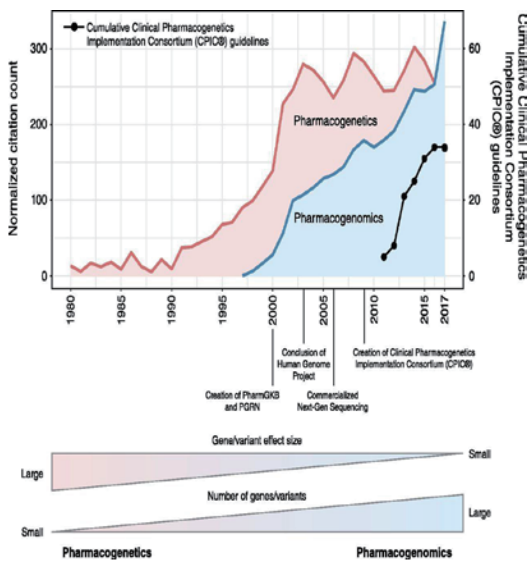
Personalized medicine [show]
Category
V • T • E

Pharmacogenetics vs. pharmacogenomics [edit]

The term *pharmacogenomics* is often used interchangeably with *pharmacogenetics*. Although both terms relate to drug response based on genetic influences, there are differences between the two. **Pharmacogenetics** is limited to monogenic phenotypes (i.e., single gene-drug interactions). **Pharmacogenomics** refers to polygenic drug response phenotypes and encompasses transcriptomics, proteomics, and metabolomics.



Solomon M. et al., CJASN May 2018

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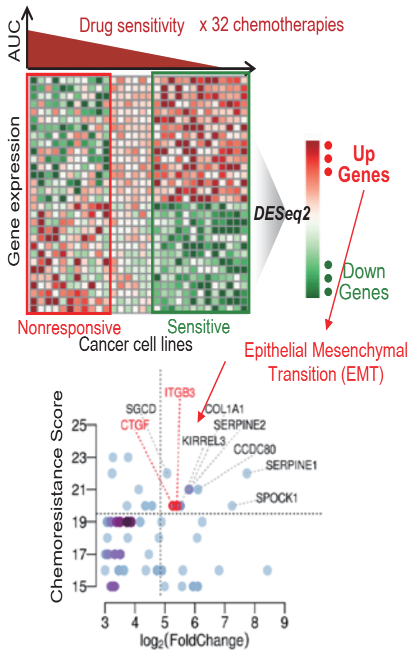
Pharmacogenomic studies using DepMap data

Approach 1

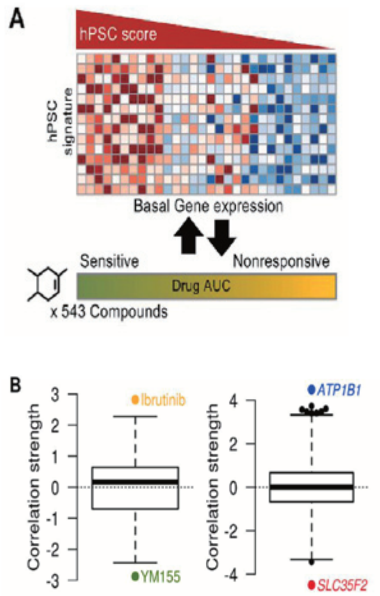
Therapeutic targets for treating chemoresistance



Hong SK et al., Molecular Cancer 2018

Approach 2

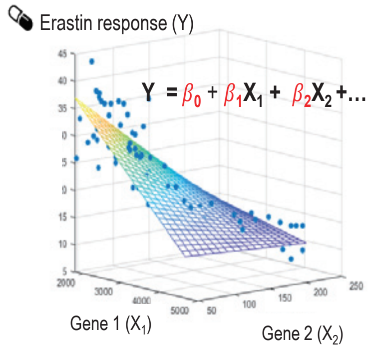
Compounds targeting undifferentiated hPSC



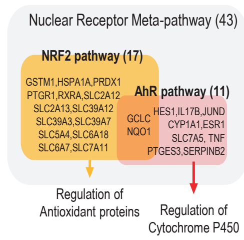
Kim KT et al., Biomaterials 2020

Approach 3

Biomarkers of erastin sensitivity



ElasticNet regression → NRF2 + AhR downstream genes



Kwon OS et al., Redox Biology 2020

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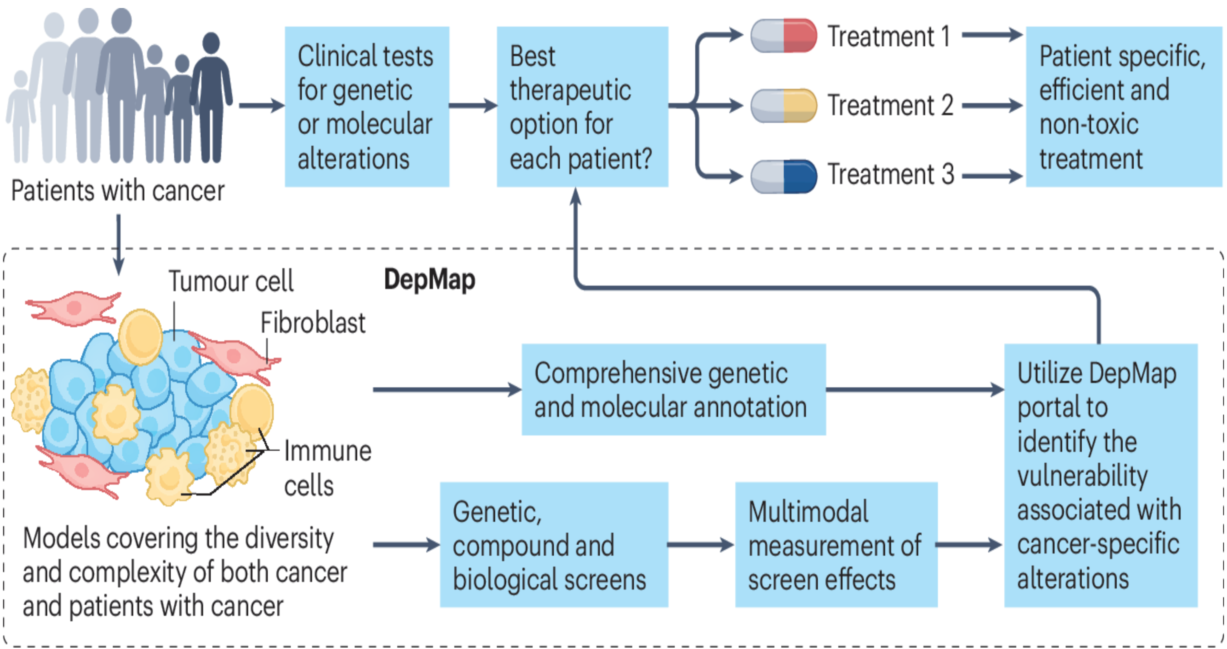
Summary

DepMap aims to identify unique and specific cancer dependencies to facilitate personalized treatments.



Arafeh R et al. Nat Rev Cancer. 2025 doi: 10.1038/s41568-024-00763-x

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Summary

DepMap은 통합 플랫폼이자 표준 인프라

통합 플랫폼	핵심 데이터베이스	활용 범위
멀티오믹스 + 기능유전체 + 약물반응	CCLE · GDSC · CTRP · PRISM Achilles · MetMap	타겟/바이오마커 발굴 약물 MOA, gene-gene interactions Synthetic lethality

DepMap informs pharmacogenomics !

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