

Technology R&D



CRISPR KO, a, i pooled screens



CRISPR KO arrayed screen



siRNA, miRNA arrayed screens



Compound screening



Nucleofection



High Content Imaging



Live imaging



3D characterisation and screening



Metabolism



High throughput, single cell proteomics

Welcome to VCFG PR...



PRIME - Project Management Portal

VCFG News

Aug2022

Customised image analysis



High throughput screening coupled with Imaging transcriptomics in 2D and 3D models

Prof Kaylene J. Simpson

Peter MacCallum Cancer Centre

Sir Peter MacCallum Department of Oncology, and

Department of Biochemistry and Pharmacology, University of Melbourne

Australia



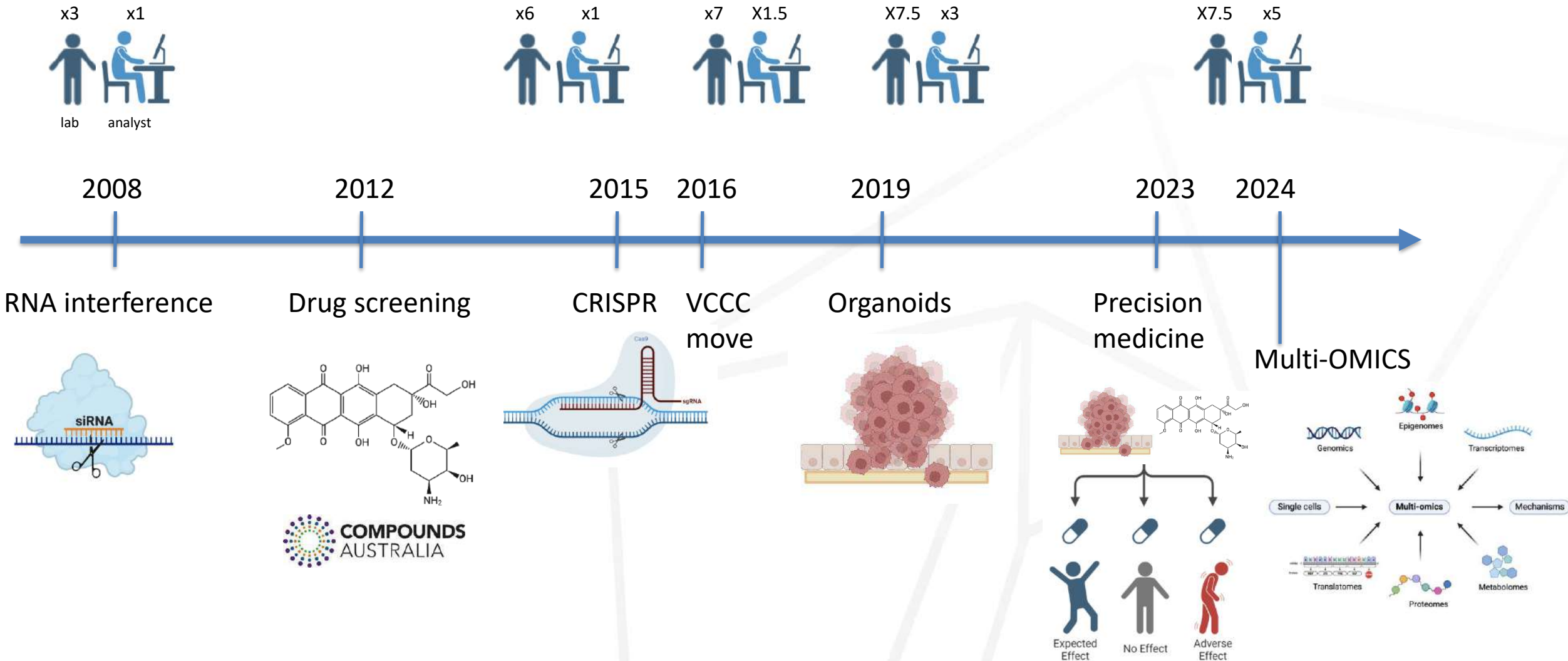
@VCFGconnect

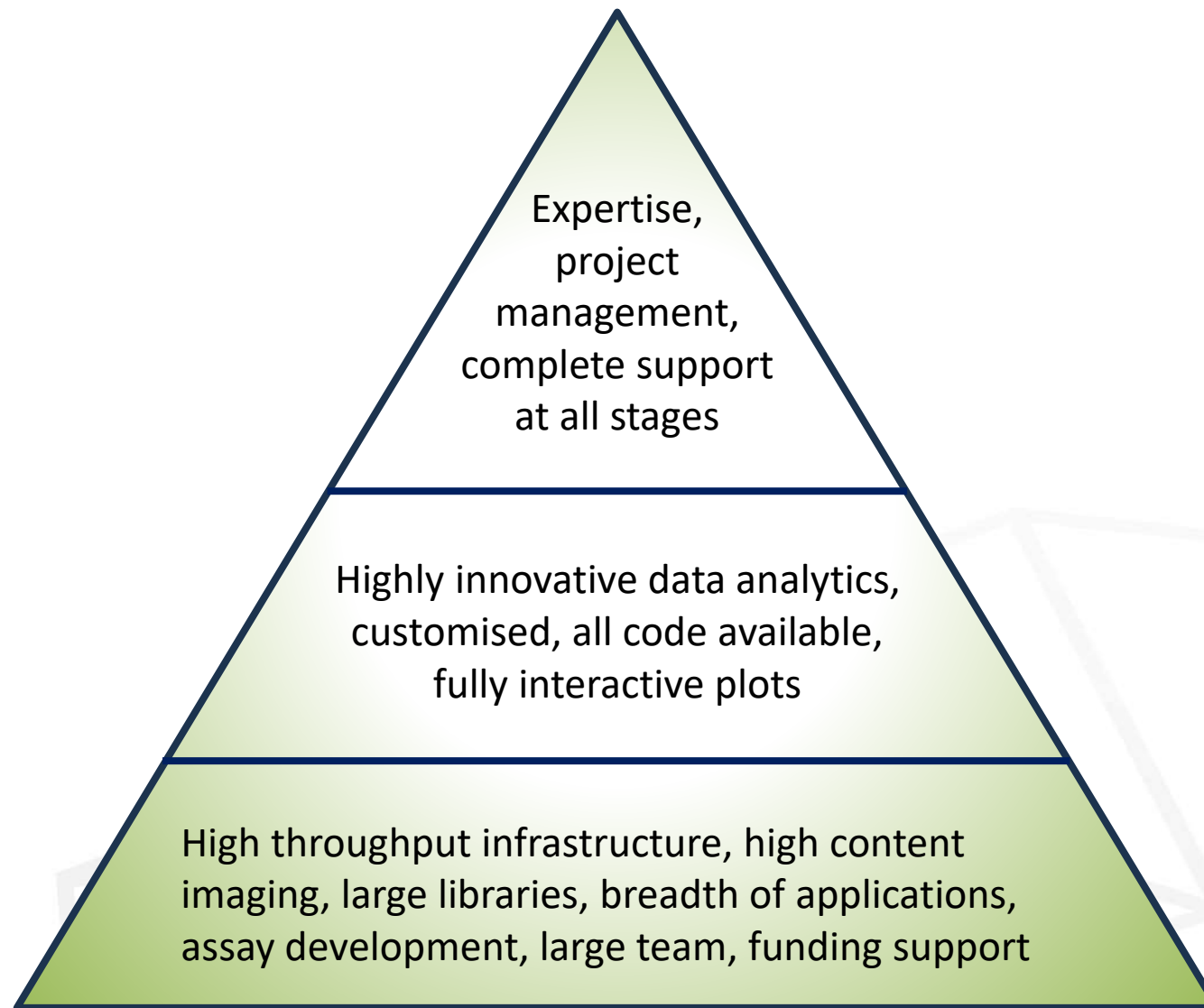


Peter Mac
Peter MacCallum Cancer Centre
Victoria Australia

A core facility needs to evolve, adapt, develop new tools, know what's coming

Data analysis and project management is critical





innovation | discovery | impact

Enabling discovery and driving translational medicine with high throughput technologies

Start with a discussion

- ✓Generate a screen plan
- ✓Define a grant aim
- ✓NCRIS voucher award



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Select your model

- ✓2D suspension
- ✓2D adherent
- ✓3D spheroids/ organoids
- ✓Complex co-culture

Select your perturbation

- ✓Compound library
- ✓BYO compounds
- ✓RNAi, CRISPR

Define your readout

- ✓Plate reader
- ✓Imaging
- ✓Flow cytometry
- ✓Sequencing (CRISPR)

Screening at any
scale with the



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Introduction to the lab

- ✓Lab induction
- ✓Instrument training
- ✓Protocol development

Optimisation, Assay dev

- ✓Dose-curves
- ✓Cell density
- ✓Live/fixed endpoint
- ✓Reporter assays

Run your screen

- ✓Weeks to months
- ✓Researcher-driven or Fee-for-Service
- ✓Concurrent Quality Control (QC) analyses

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Screening at any
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Hit selection

- ✓Decisions to make
- ✓Plan secondary screen

Data analytics

- ✓Basic options
- ✓Advanced options
- ✓Customisation
- ✓Machine learning

Screen QC output

- ✓Controls (pos/neg)
- ✓Z-prime factor
- ✓Variability (%CV)

Start with a discussion

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Detailed target follow up

- ✓Lots of discussion
- ✓Your lab
- ✓Back in VCFG
- ✓Precinct partners

Integrate OMICS

- ✓Metabolomics (MA)
- ✓Transcriptomics (MGC)
- ✓Proteomics (MGC/MSPF)

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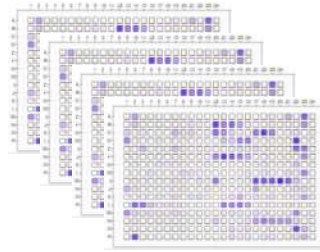
Screen QC output

- ✓Controls (pos/neg)
- ✓Z-prime factor
- ✓Variability (%CV)

Discovery - high throughput screening concept

- Unbiased interrogation
- Best model to replicate your biology
- Thousands of genes (CRISPR, RNAi)
- Thousands of compounds
- Iterative data analysis to generate 'hit' lists

Primary screen

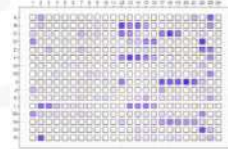


~thousands

*High throughput assay
Adherent or suspension
Multiple lines*



Secondary screen

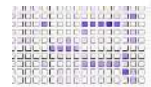


~hundreds

*Validation of primary screen
More difficult, expensive
Multiplex readouts
Lower throughput*



Tertiary screen



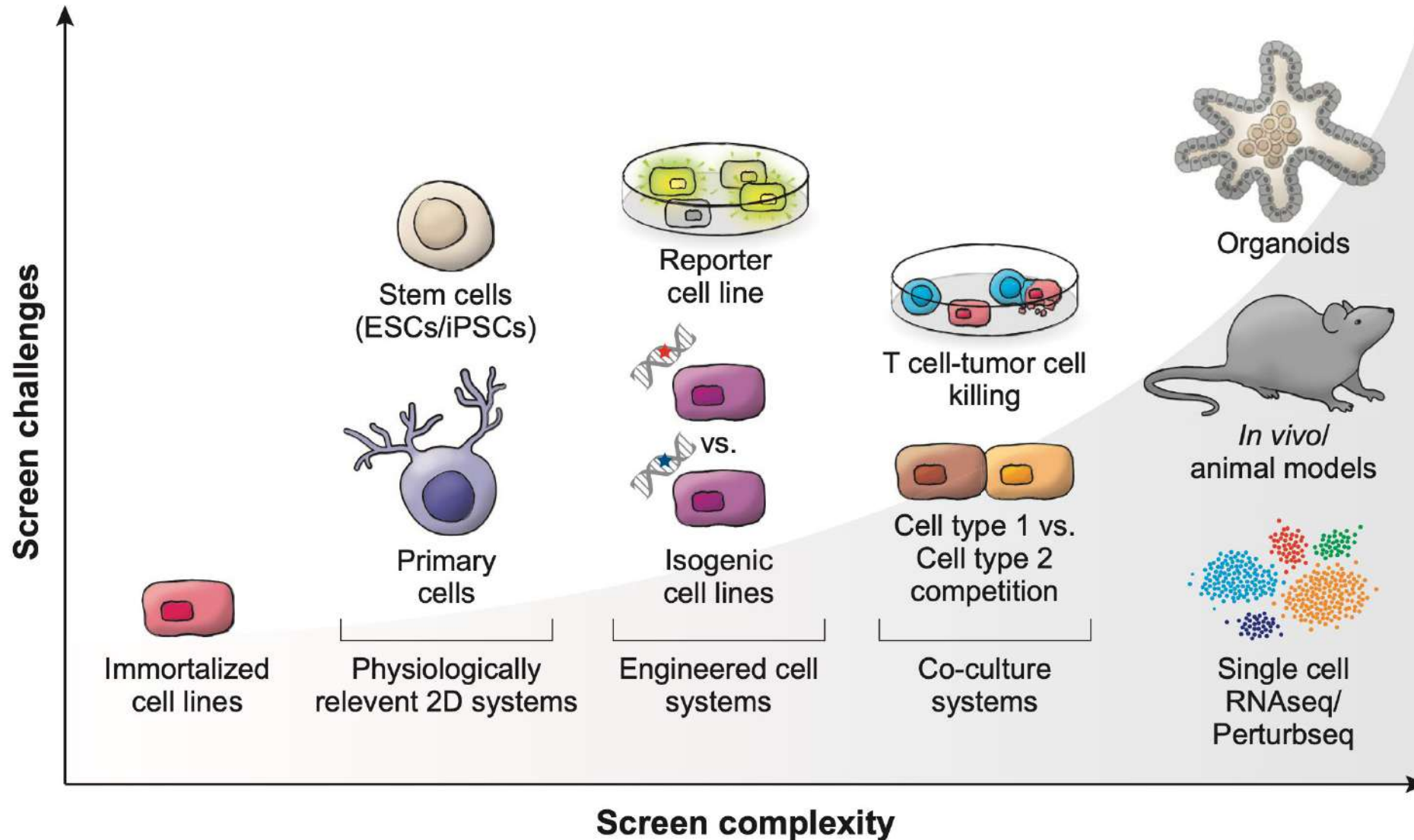
~100

*High confidence
Multiple lines
Orthogonal assays*

~10



Orders of complexity with experimental approaches



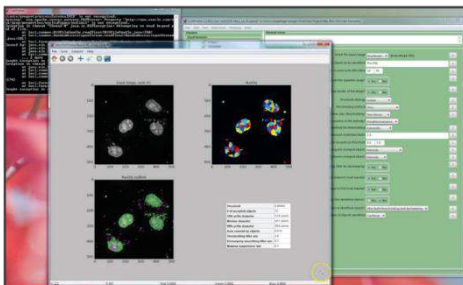
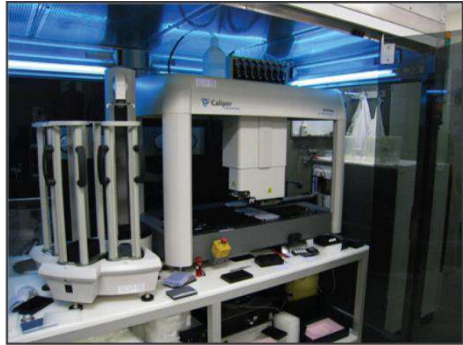
Key infrastructure

- Personal liquid handling workstation – cell dispense, media change, fix/stain
 - BioTek 406 x3, BioTek MFX
- Big robotics – large capacity, flexible movement options with precision small volumes
 - Sciclone, Janus G3
- Plate reader – basic and advanced functionality, kinetic, automated
 - Cytation 3, Cytation 5, Cytation C10
- Microscope – live, widefield, confocal, magnification, speed, throughput, automated
 - CellInsight PRO x 3; Cytation 5 and C10; Incucyte x 2
- Automated plate sealer
 - Plate loc
- Drug dispenser (BYO compounds and controls)
 - Tecan D300e
- Liconics incubator
- Access to Flow through Research Flow Core

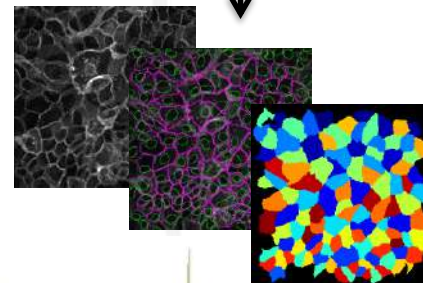
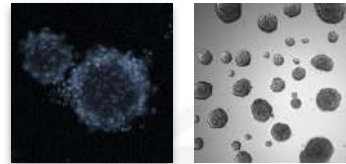
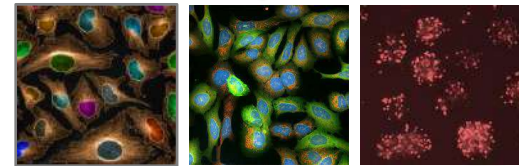
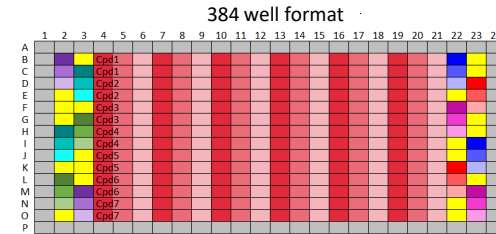
VCFG model ‘researcher driven – staff assisted’



Arrayed screening workflow



3-7 days



Library delivery

Compounds (Compounds Australia)
CRISPR and RNAi whole human genome libraries

Data acquisition

Biological relevance - 2D adherent, suspension, 3D matrices

Image, plate reader, flow cytometry

CellInsight PRO's
Cytation 5 & C10
Novocyte

Data analysis

Fundamental QC
Basic to advanced options
Machine learning innovation
Fully customised



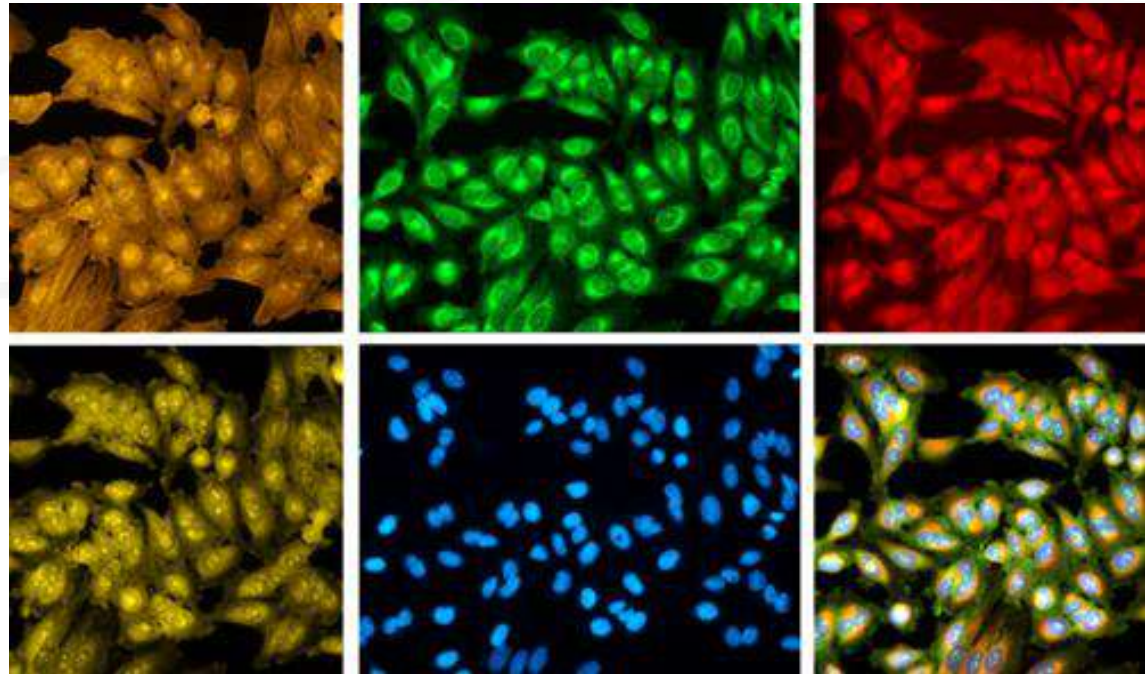
Cell painting to quantify cell biology

Cell Painting is a high-content, multiplexed image-based assay used for cytological profiling.

Up to six fluorescent dyes are used to label different components of the cell including the nucleus, endoplasmic reticulum, mitochondria, cytoskeleton, Golgi apparatus, and RNA.

Imaging and analysis extracts thousands of features to profile cells and elucidate behaviour.

Reference compounds/controls required



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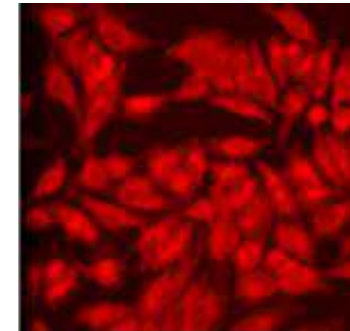
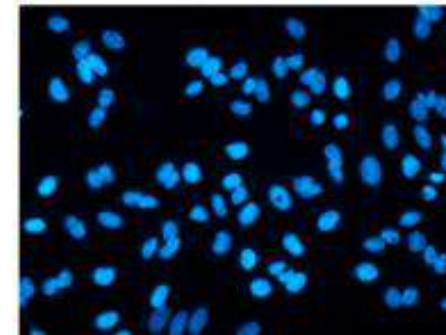
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Depending on scale – cell painting may be a secondary screen

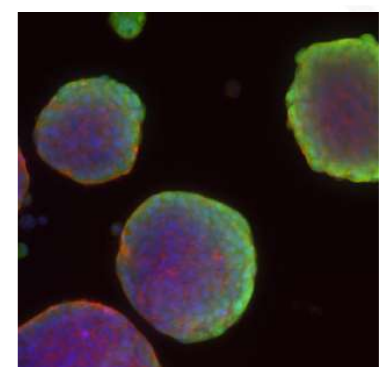
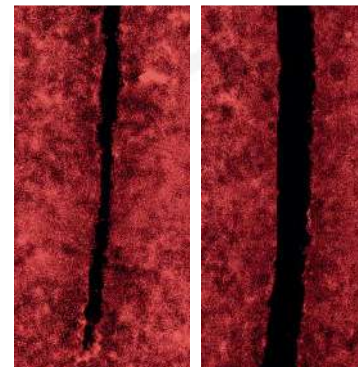
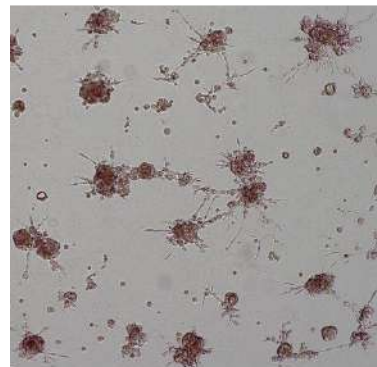
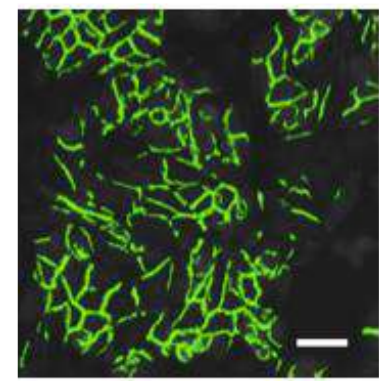
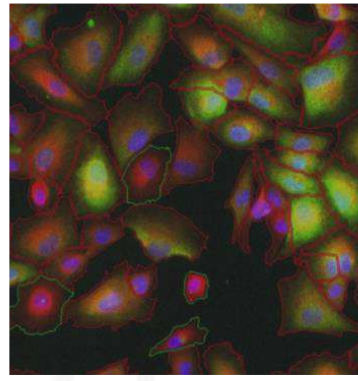
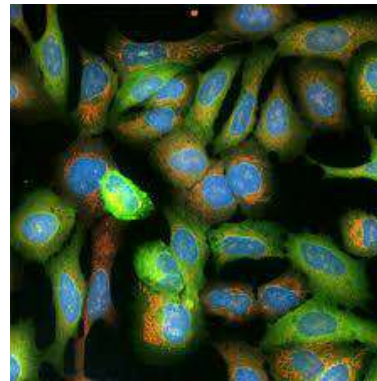
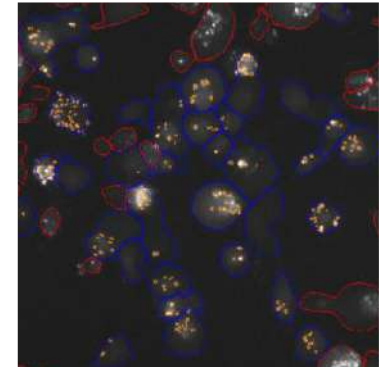
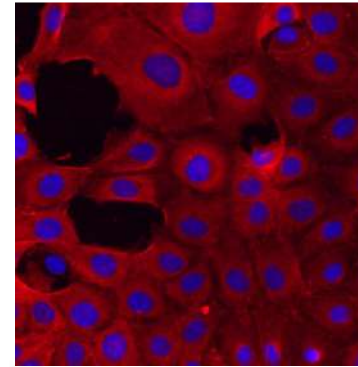
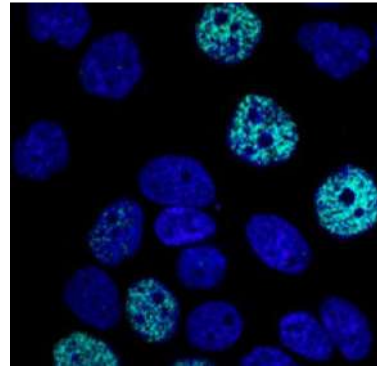
Still powerful to do less and include biological targets of interest



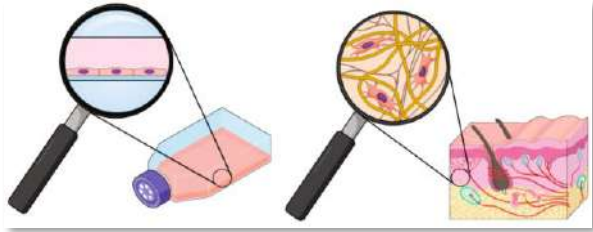
Target X

HCS screens – great diversity possible

drug resistance/sensitivity
cell death
cell size (senescence)
cell cycle
cell morphology
cell motility and metastases
host-pathogen interactions
3D morphogenesis
complex co-cultures
multi-parametric readouts
complex single cell phenotyping
protein modification
protein location
reporter assays, transcriptional activation
internalization/secretion



Working in a more translatable model system

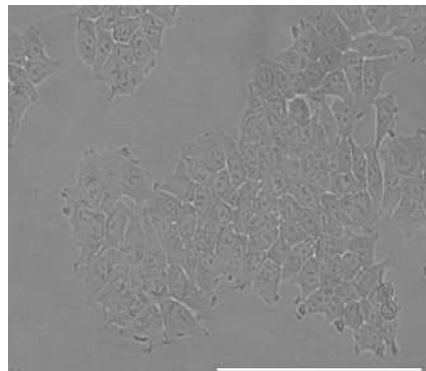


2D cells grown on flat plastic – not very physiological

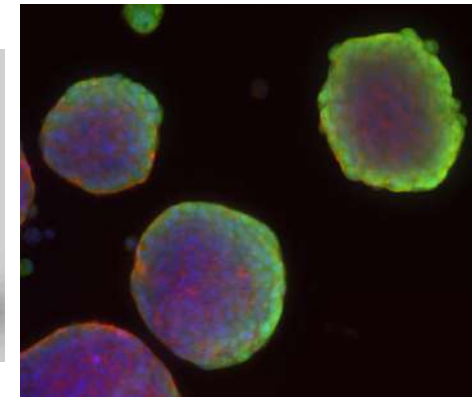
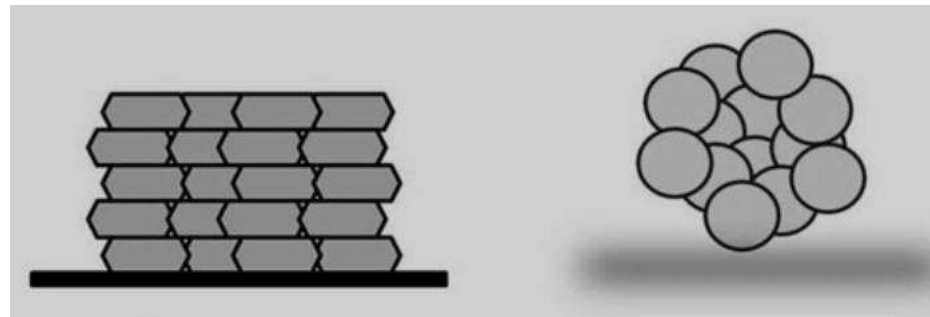
- drug discovery in 2D can fail at clinical trials

3D cells cultured in a matrix full of growth factors and supporting scaffolds

- more closely replicates the microenvironment in the body
- allows cell growth in all planes
- allows us to co-culture different cell types that more closely model a disease
- ideal setting for cells derived directly from a patient
- or cells cultured from a patient in a mouse

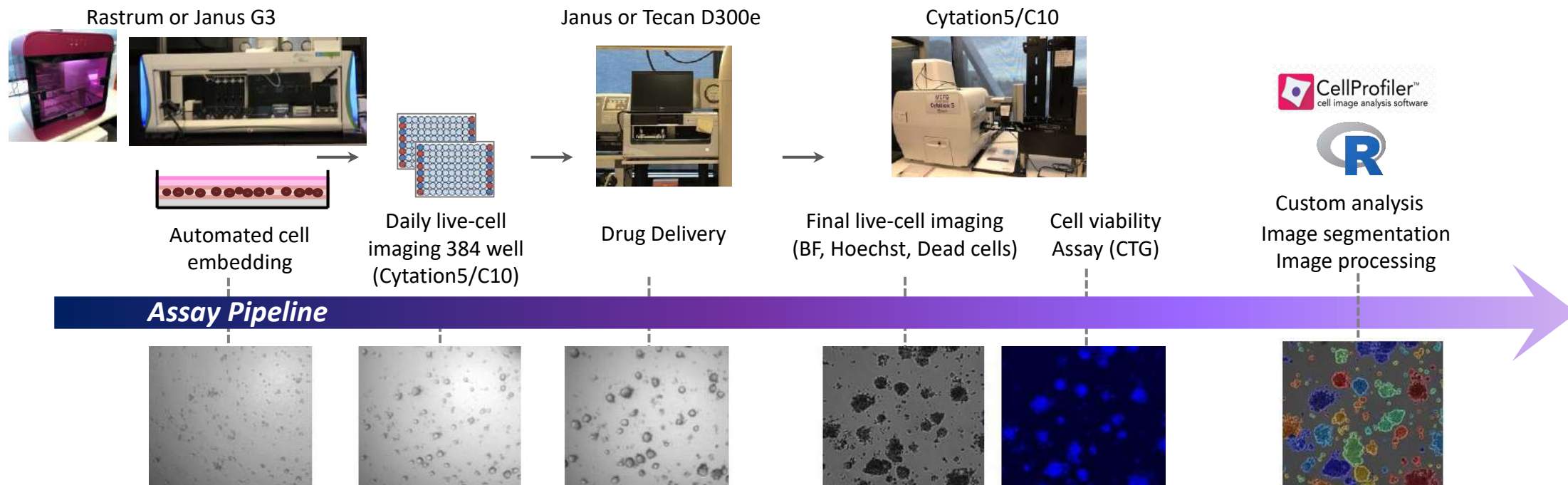


MCF7 cells grown in 2D



MCF7 cells grown in 3D

Automated 3D pipeline



Automated 3D pipeline

- Growth kinetics
- Drug screens
- Immune cell killing/ infiltration
- Single organoid population data
- Phenotypic clustering

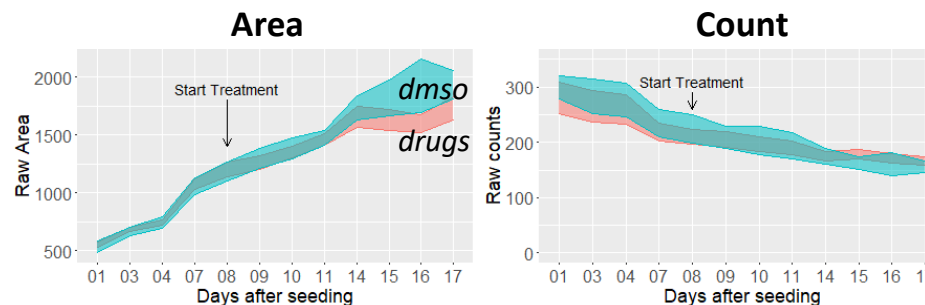
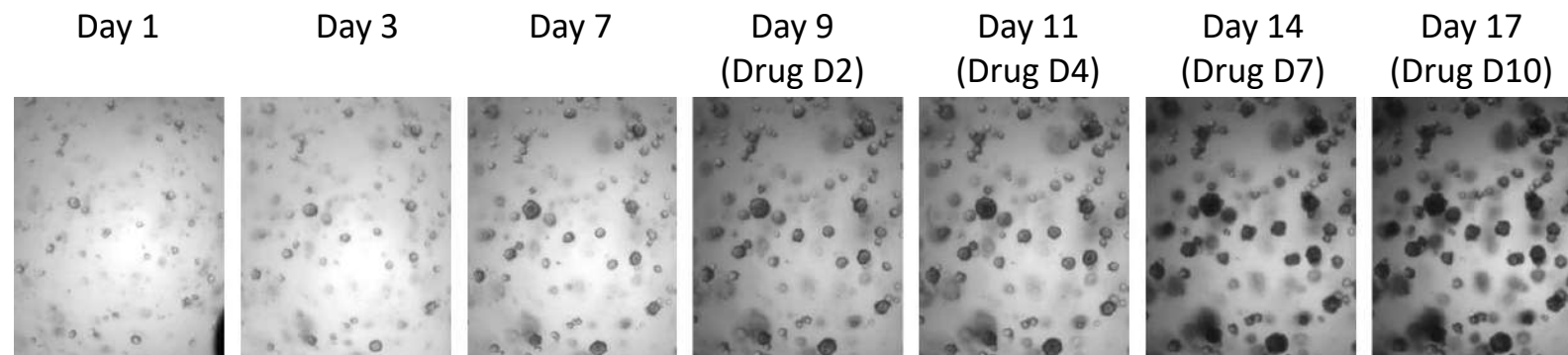
Basic characterisation

- organoid area
- organoid number

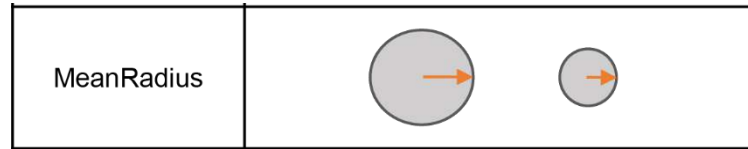
Prostate PDX – growth and death time course

PDX/PDO/cell lines

- Pancreatic
- Colorectal
- Prostate
- Ovarian
- Oesophageal
- Genito-urinary
- Cancer unknown primary
- + Cell lines (breast, prostate)



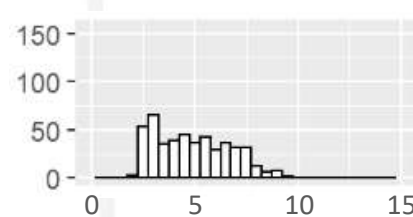
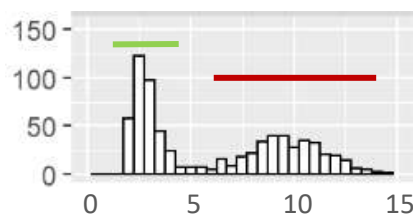
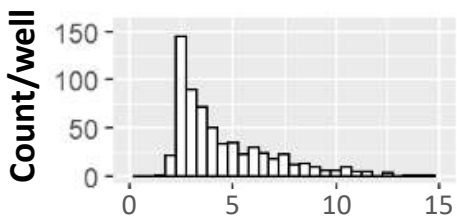
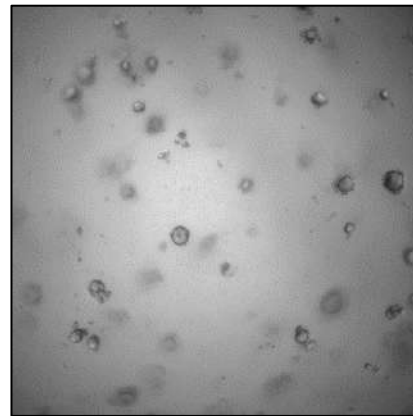
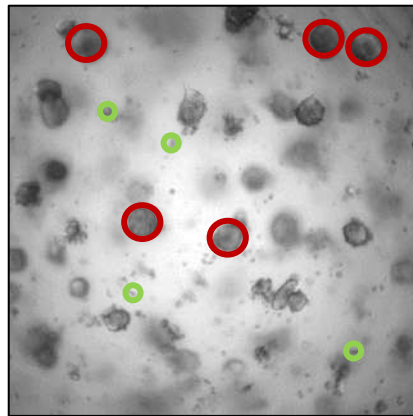
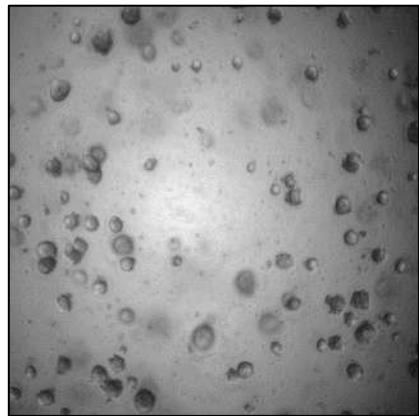
Quantify structure dynamics, organoid size in a whole population



Prostate PDX 1

Prostate PDX 2

Prostate PDX 3



Cancer of Unknown Primary

Day 5 (drug Day 0)

Day 10 (drug Day 5)

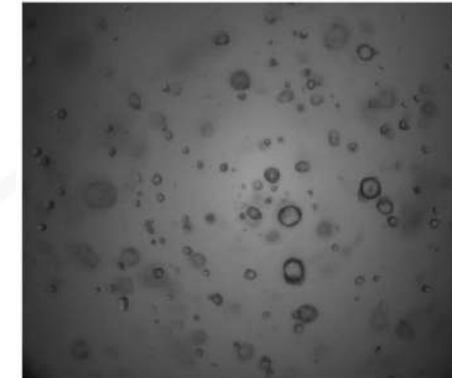


Plate2 Growth-D05_Drug-D00

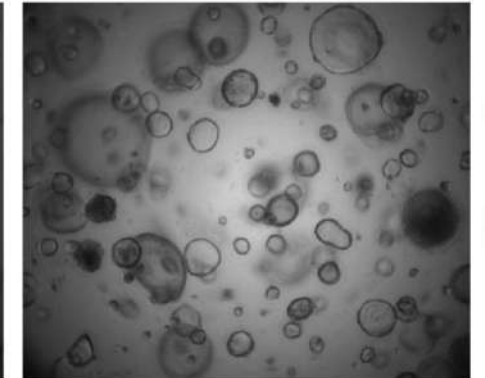


Plate2 Growth-D10_Drug-D05

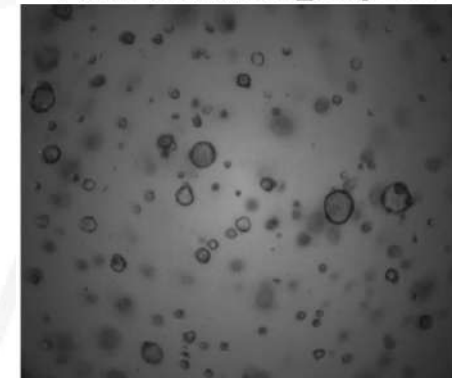


Plate1 Growth-D05_Drug-D00

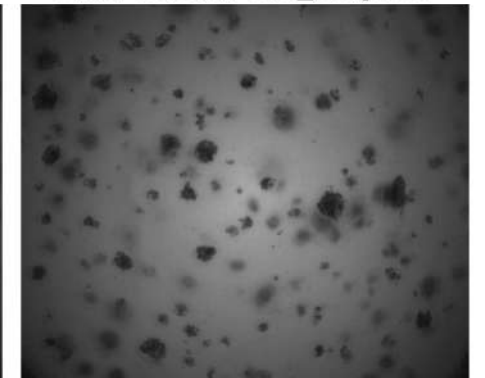


Plate1 Growth-D10_Drug-D05



Fixing and staining in Matrigel in situ - a grand challenge

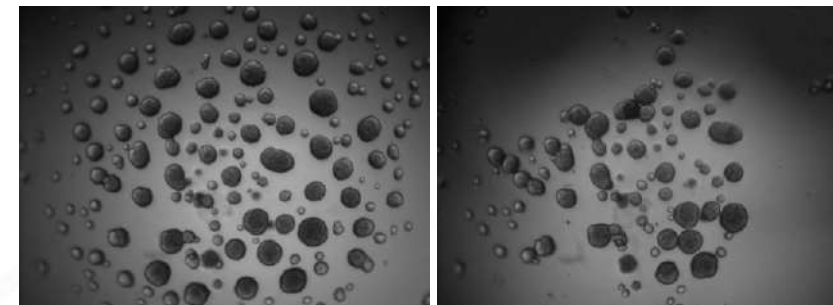
Problem 1 - fixing

- PFA depolymerises Matrigel
- Fixing changes structural integrity (shrink, swell)
- Shift in position means no relational imaging quantitation
- Total structure loss/disintegration

Solution:

Tried numerous agents, settled on 0.3% glutaraldehyde, 10 mins, RT

MCF7 2% embedding



unfixed

fixed

Fixing and staining in Matrigel in situ - a grand challenge

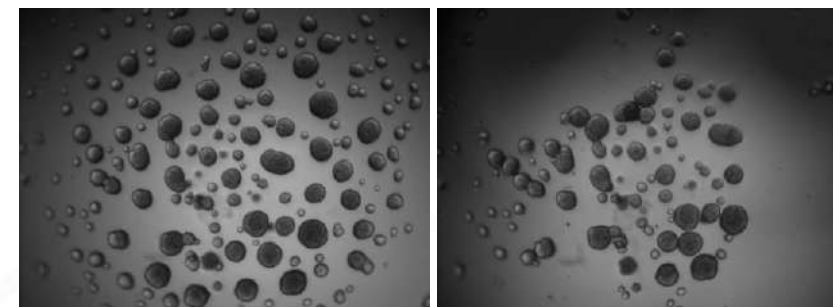
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fixed

Problem 2- background

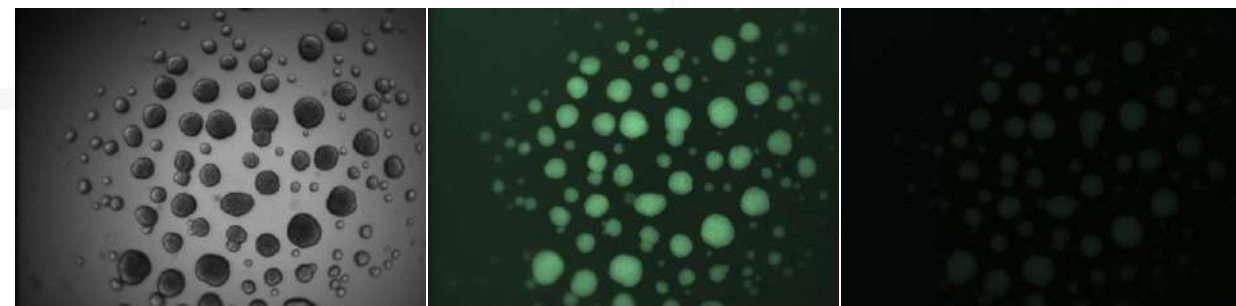
Fixing in matrigel leaves high autofluorescence

Solution:

Quenching – identify agent: Sodium Borohydride

- creates hydrogen gas
- modify concentration
- length of incubation
- temperature of incubation

Time post fixation – must be less than 1 week



fixed

not quenched

quenched

High multiplex parameter staining – discriminates drug response

MCF7 cells – culture endpoint
20X magnification
Single structure, single cell

Suite of markers available

PI (dead)

Image IT Dead

Phalloidin (actin)

Ki67 – (proliferation)

Caspase 3/7

Concanavalin A (membrane)

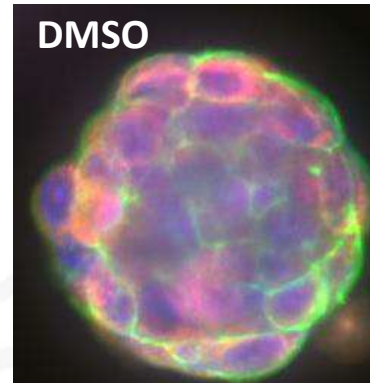
SYTO14 – (nucleic acid stain)

WGA – (membrane, Golgi)

Histone H3 – (chromatin)

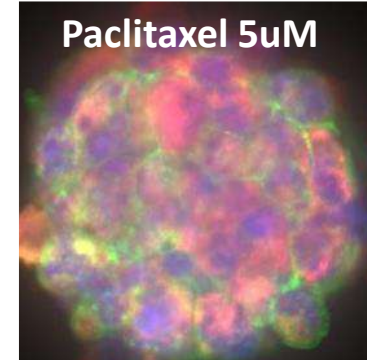
Mitotracker (mitochondria)

Cell painting

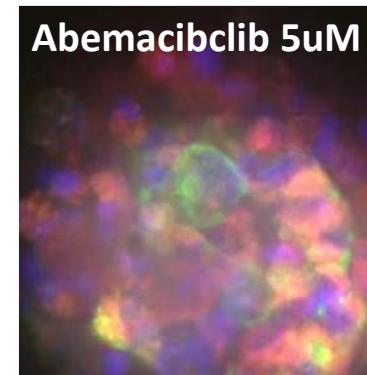


DMSO

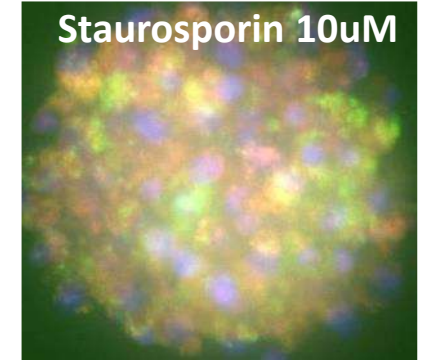
DAPI (Nuclei)
Phalloidin (Actin)
pH3 (mitosis)
Mitochondria



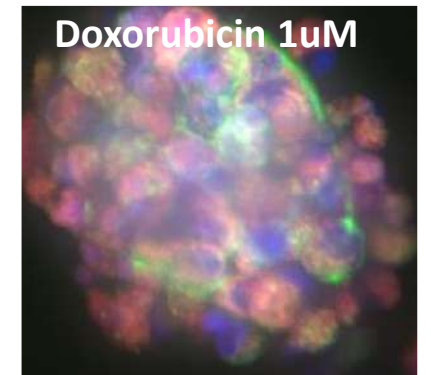
Paclitaxel 5uM



Abemaciclib 5uM



Staurosporin 10uM



Doxorubicin 1uM

Data analytics – Cellular phenotyping and hit identification

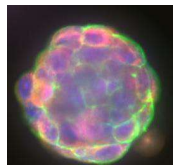
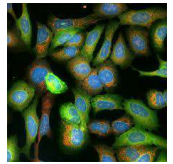
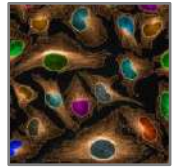
Images

Viability/toxicity/cell cycle

Cell features

Clustering Phenotypic signatures

Biological information



Cell Painting

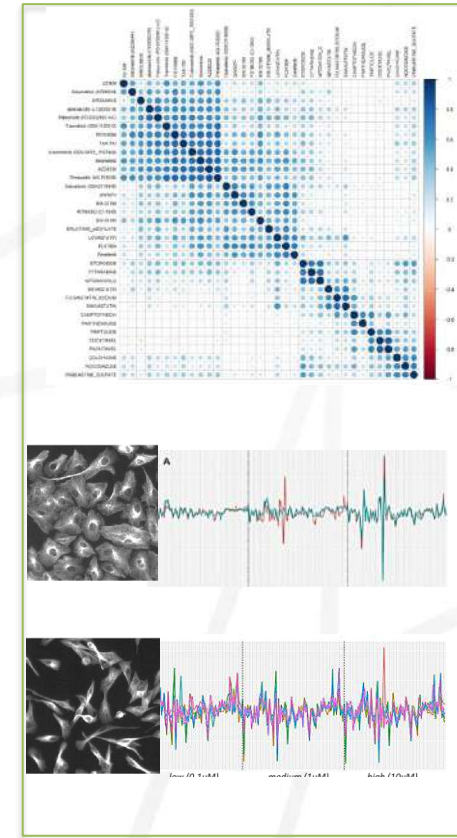
2D

- Intensity
- Area/Shape
- Texture
- Neighbors

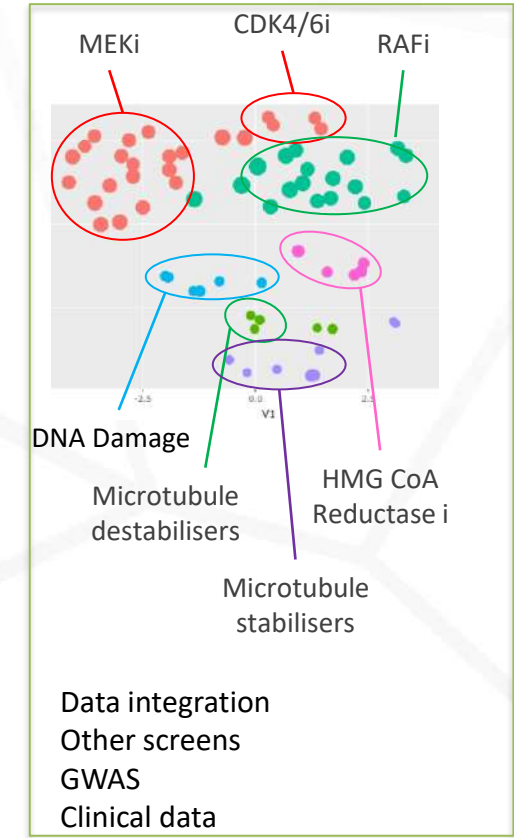
Extraction of cell features (~1,000 per image)

3D

Imaging feature	Schematic representation
Area	
MeanRadius	
Eccentricity	
FormFactor	
MeanIntensity	
Texture	



Feature reduction



Data integration
Other screens
GWAS
Clinical data

Data integration

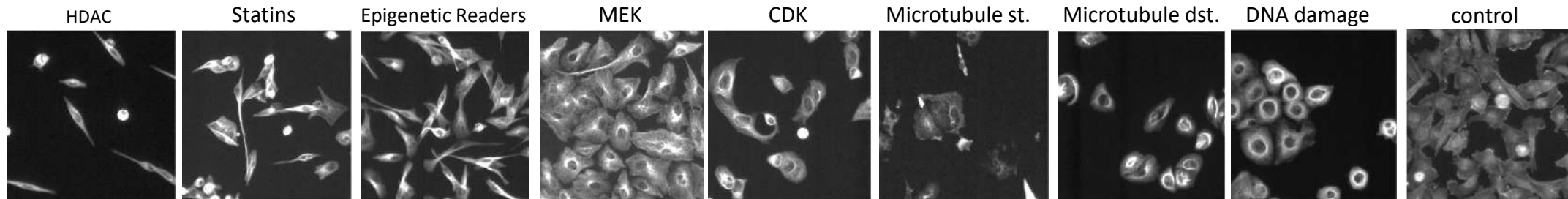
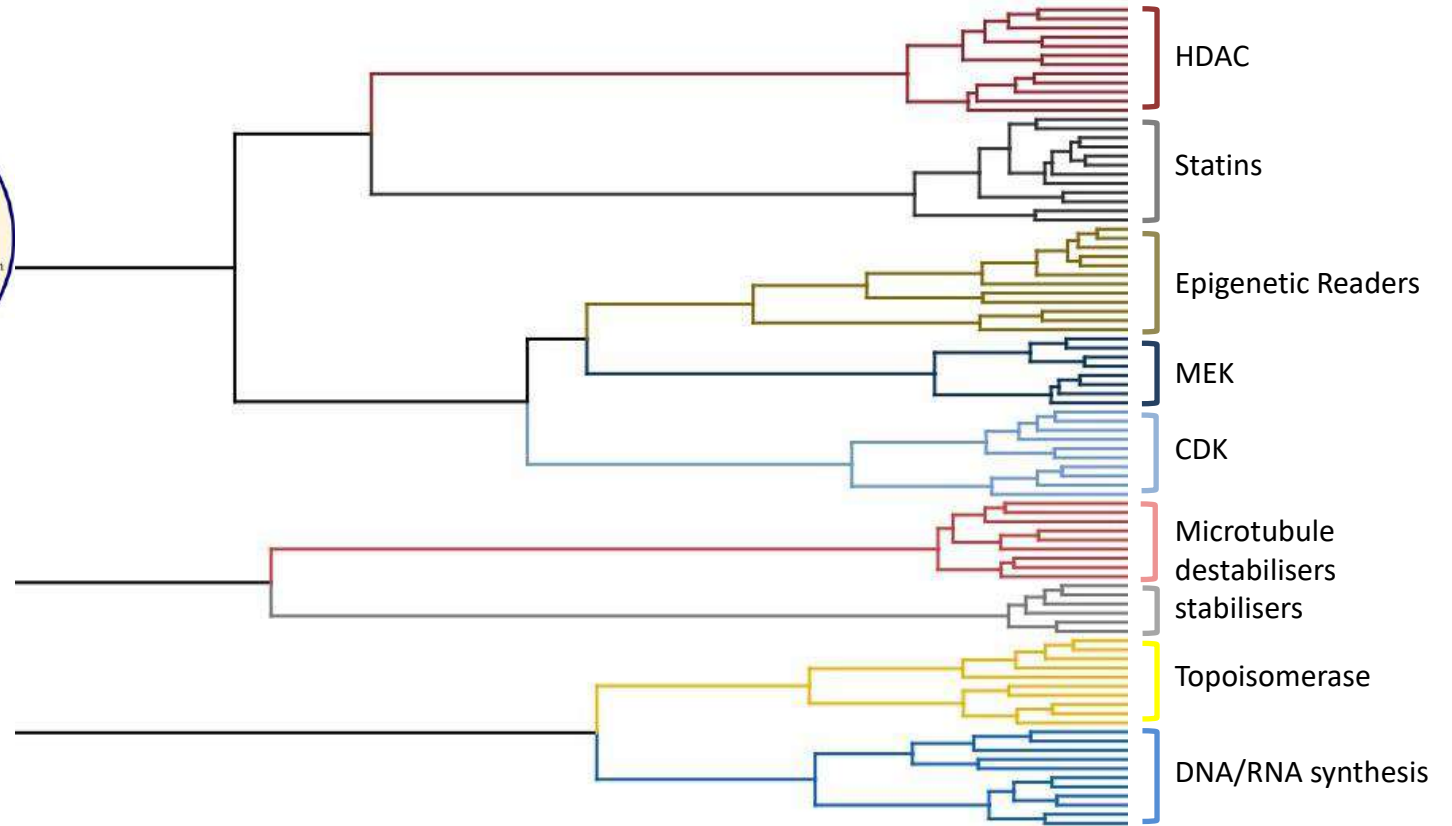
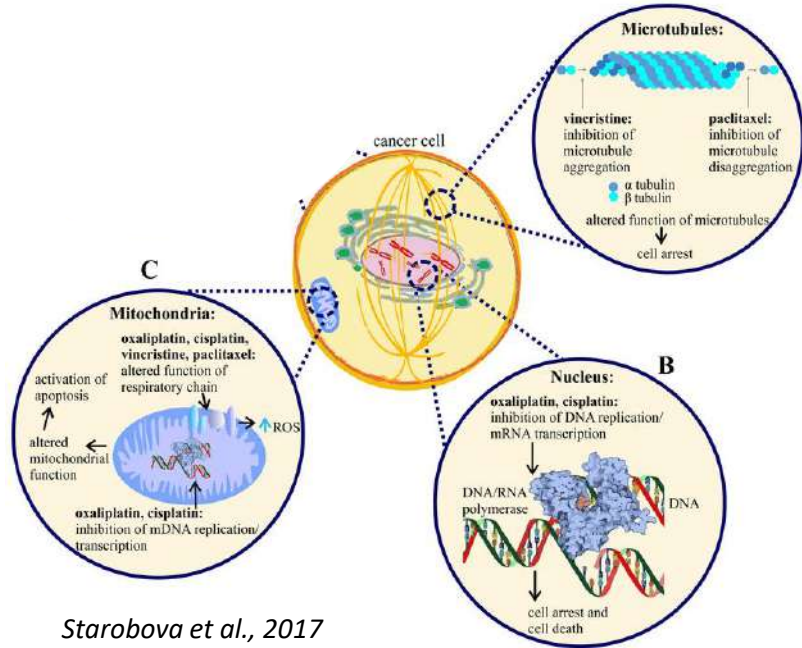


Phenotypic clustering

Mechanism of action cancer reference compound library:

69 compounds – multiple doses

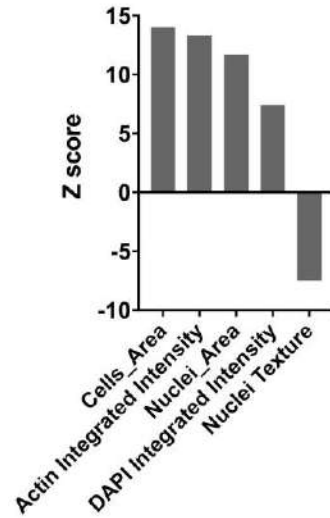
DNA damage, cytoskeleton, epigenetic changes, .A



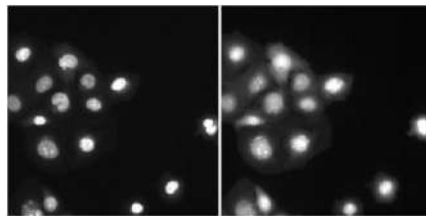
MDA-MB-231

Top features identifying each cluster – towards mechanism of action

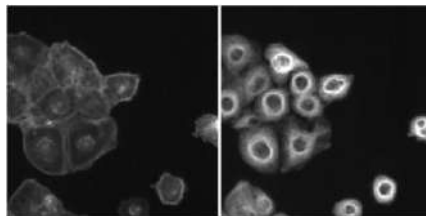
DNA Damage inducers



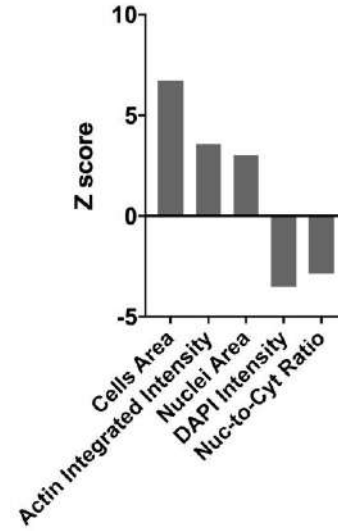
DAPI CellMask



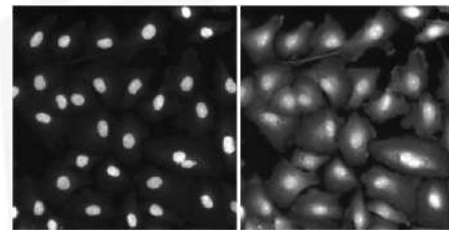
Actin Tubulin



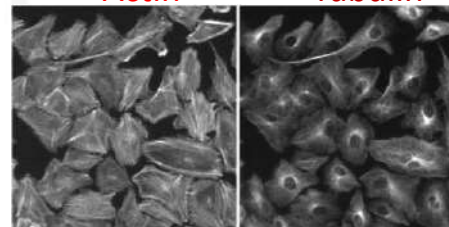
MEK inhibitors



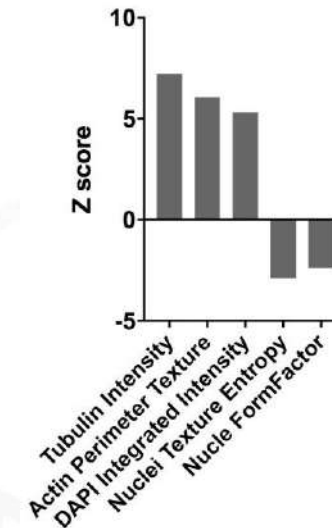
DAPI CellMask



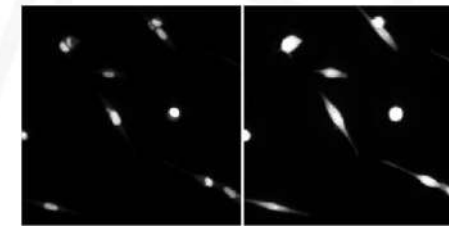
Actin Tubulin



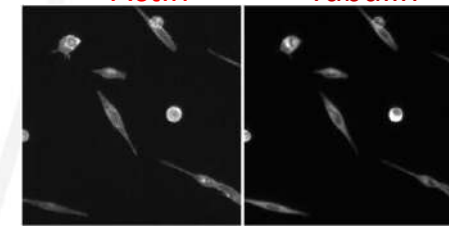
HDAC inhibitors



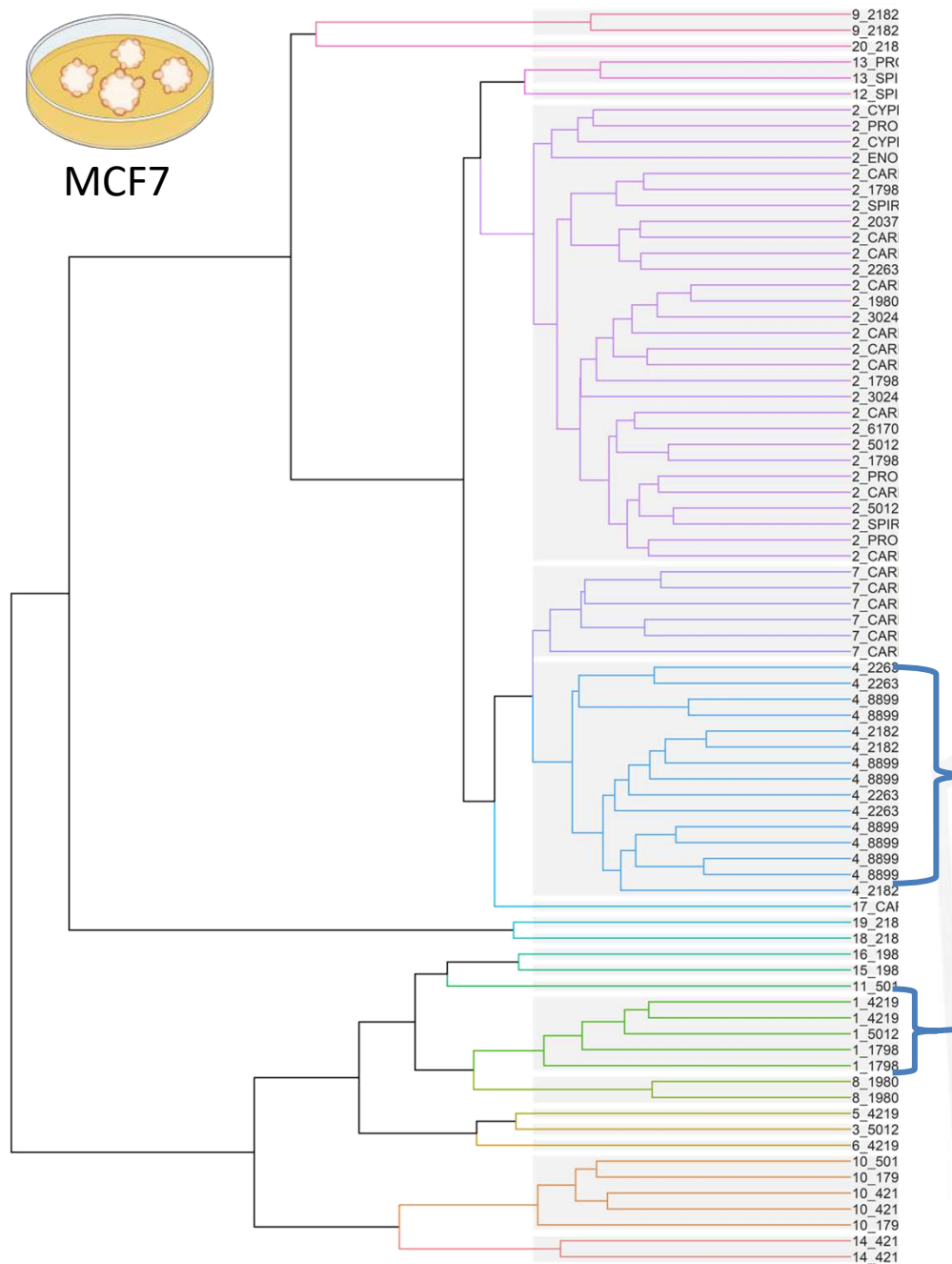
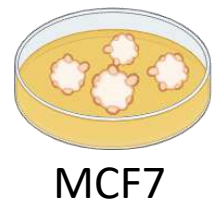
DAPI CellMask



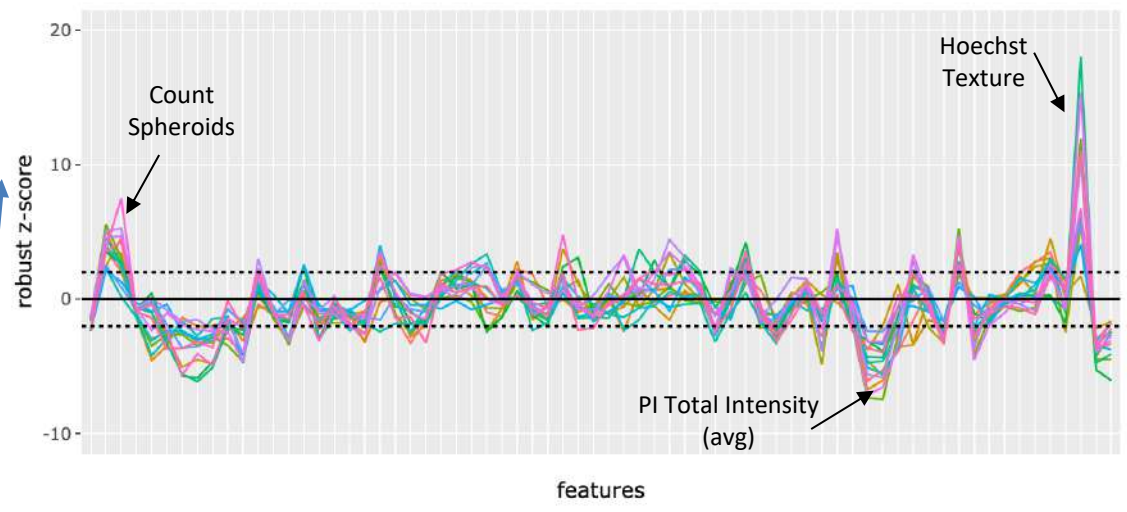
Actin Tubulin



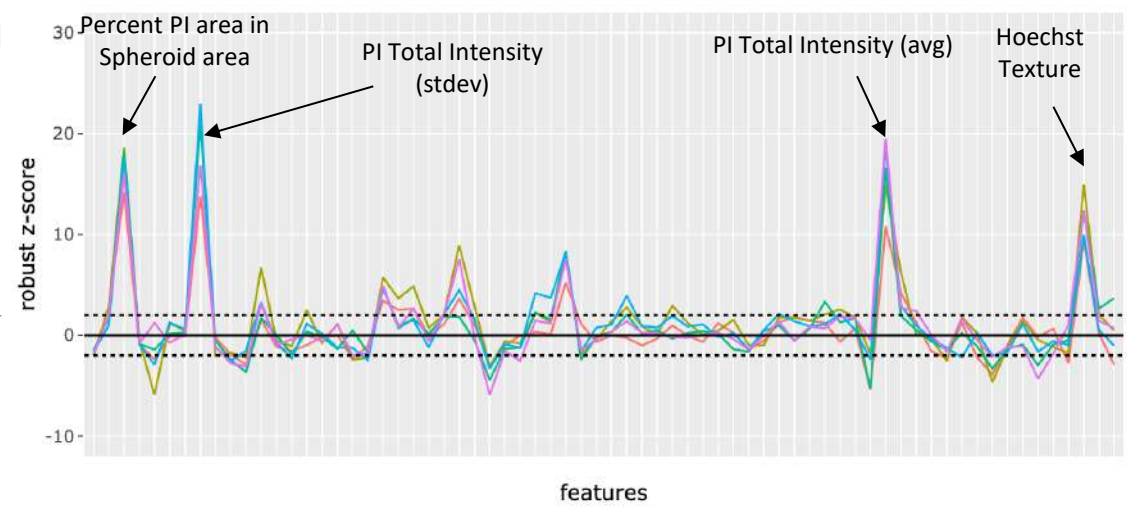
3D compound screen - clusters similar phenotypes



Compound Signatures: Cluster 4

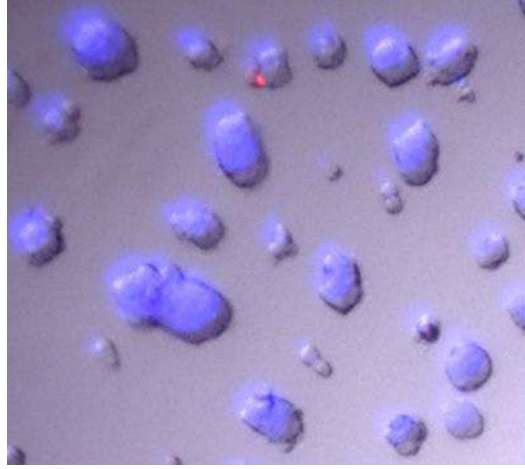


Compound Signatures: Cluster 1

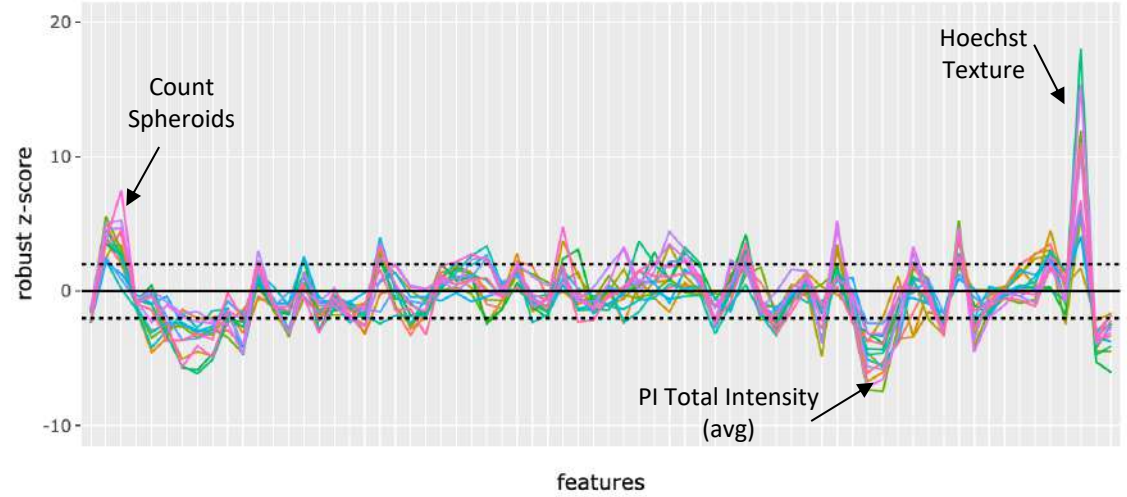


3D compound screen - clusters similar phenotypes

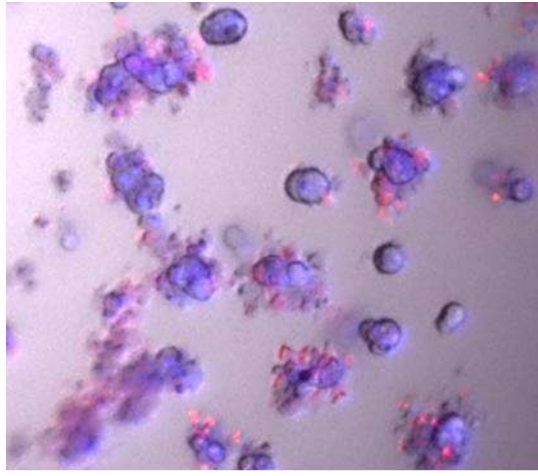
Compound X1 (C4)



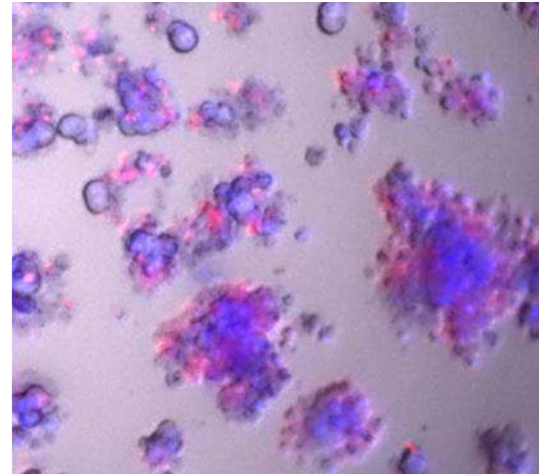
Compound Signatures: Cluster 4



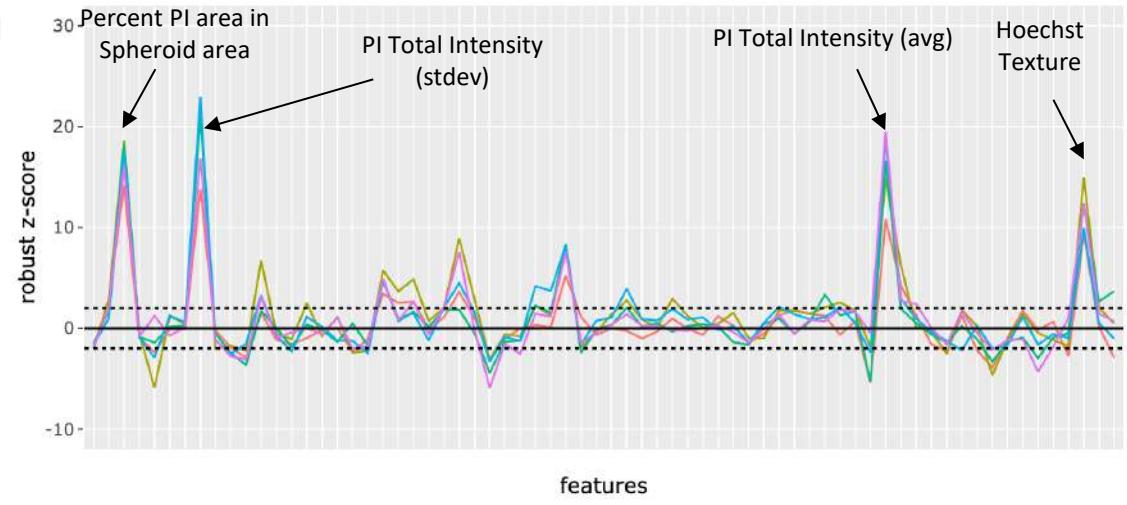
Compound X2 (C1)



Compound X3 (C1)



Compound Signatures: Cluster 1

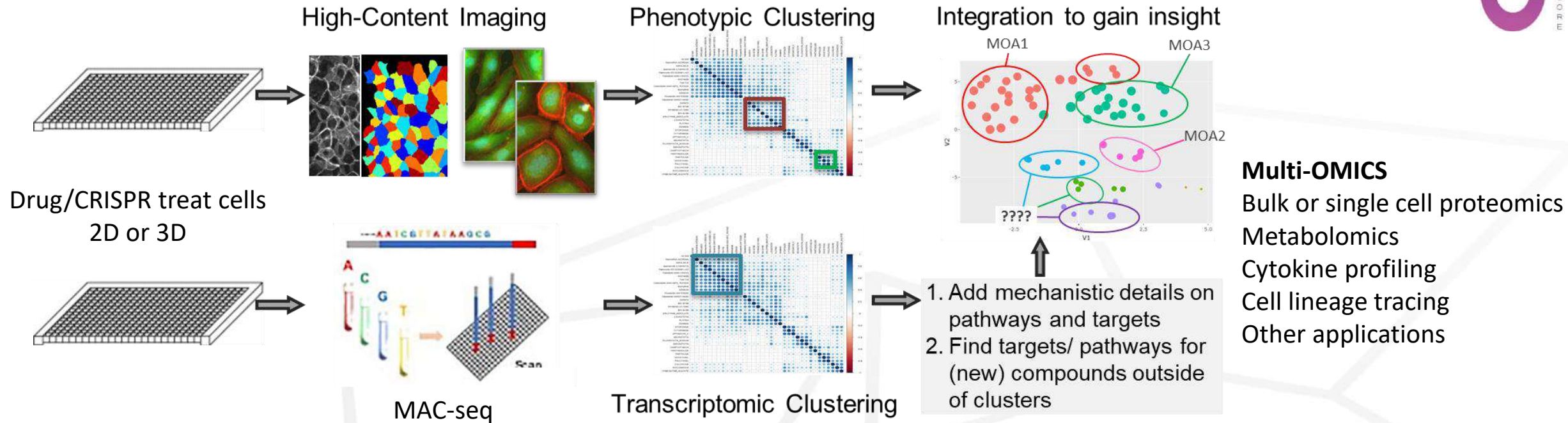


High-throughput transcriptomics (MAC-seq – multiplexed analysis of cells)

384 well format

In situ RNA extraction with barcoded wells

Bulk RNA seq



Screen vignettes

- 1 Drug screen for low grade ovarian carcinoma using high content imaging
 - Dr Kathleen Pishas, Dr Dane Cheasley
- 2 Drug screen for immunomodulatory targets using flow cytometry
 - Emily Derrick, A/Prof Paul Beavis, Eva Orlowski-Oliver
- 3 Organoids in personalised medicine – colorectal patients
 - Dr Anshini Jain, Prof Rob Ramsay, A/Prof Alexander Heriot, A/Prof Nick Clemons
- 4 Immune cell 3D complex co-culture screening – profiling CAR-T cells
 - Dr Milton Mui, A/Prof Nick Clemons

We are sharing unpublished work

“Enabling discovery and driving translational medicine with high throughput technologies”



1- High-throughput strategies to discover synergistic drug combinations for low-grade serous ovarian carcinomas.

Scaled discovery

Single agent screening

6760 compounds

- FDA library
- Kinase inhibitors
- Epigenetics

Focus set of targets

Combinatorial screening

2D and 3D

Hit ID
79 targets

Synergy with
Standard of care

MAC-seq

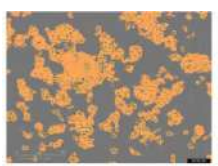
Cell lines

12 LGSOC
1 normal line



Characterisation

Cell banking; DNA pellets, IHC
Growth kinetics
Pilot screen



Day 1: Plate cells

Day 2: Add compounds

Day 5: Fix/Stain Cells

Day 5+: Image Cells

Analyse Data

Hit Selection

Screening

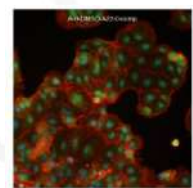
72 hours treatment
0.1; 1; 10uM

Staining

DAPI nuclei
Cell mask – membrane
Phalloidin – actin cytoskeleton

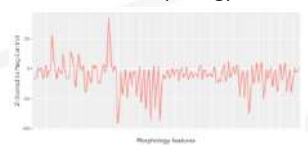
Imaging

10x and 20X

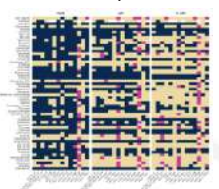


Custom analysis pipelines

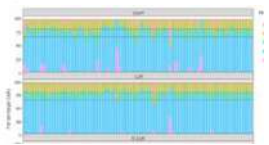
Cell Morphology



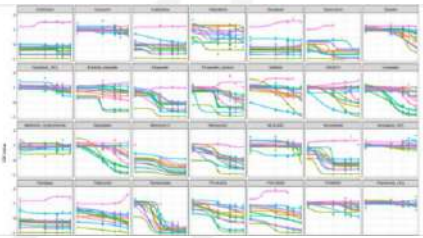
Viability



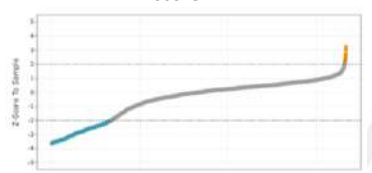
Cell Cycle



Dose response curves

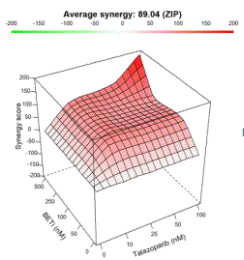


Z-score

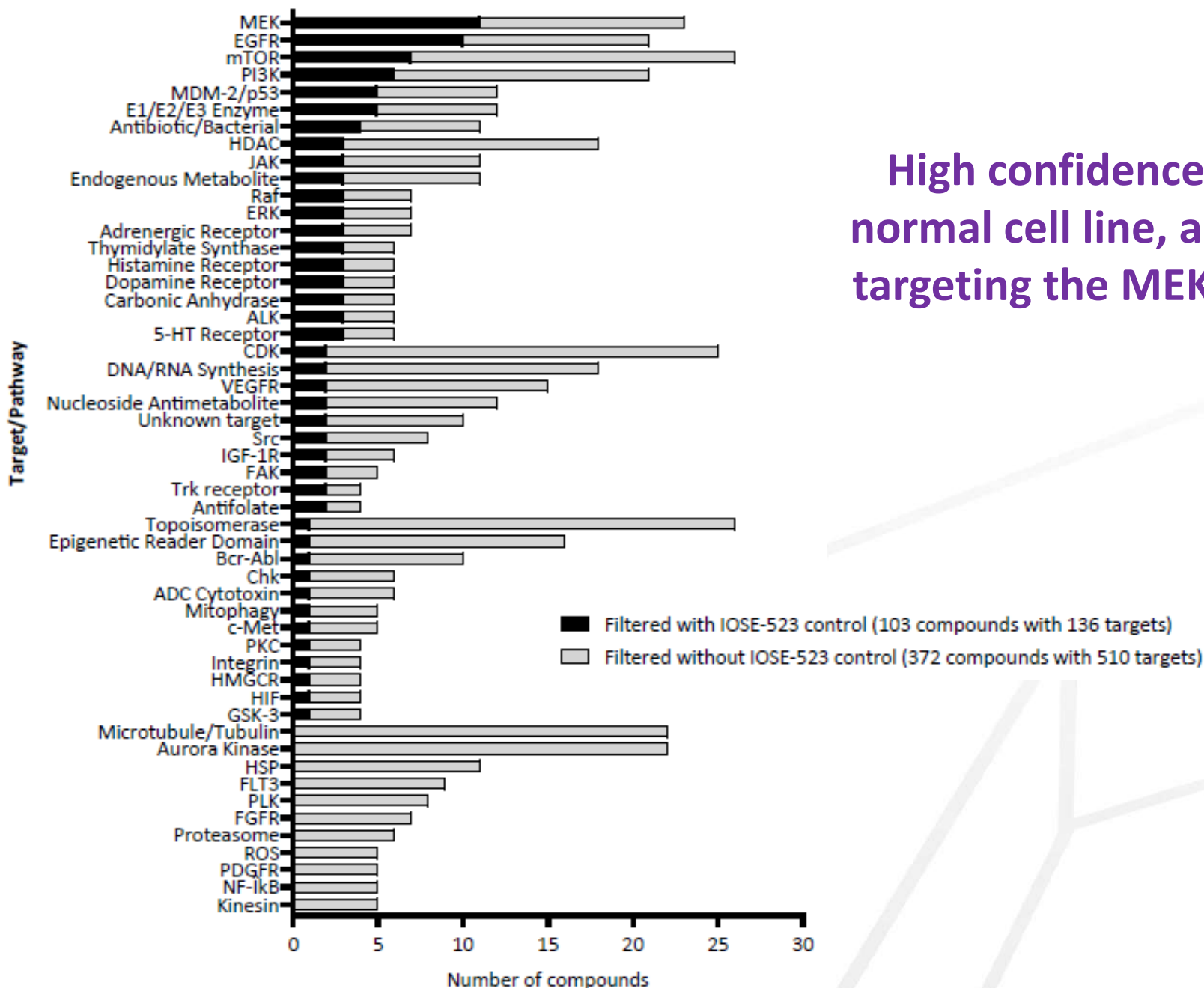


Data integration

Molecular data
Clinical data



High confidence hits with no effect in the normal cell line, are enriched for compounds targeting the MEK, EGFR and mTOR pathway

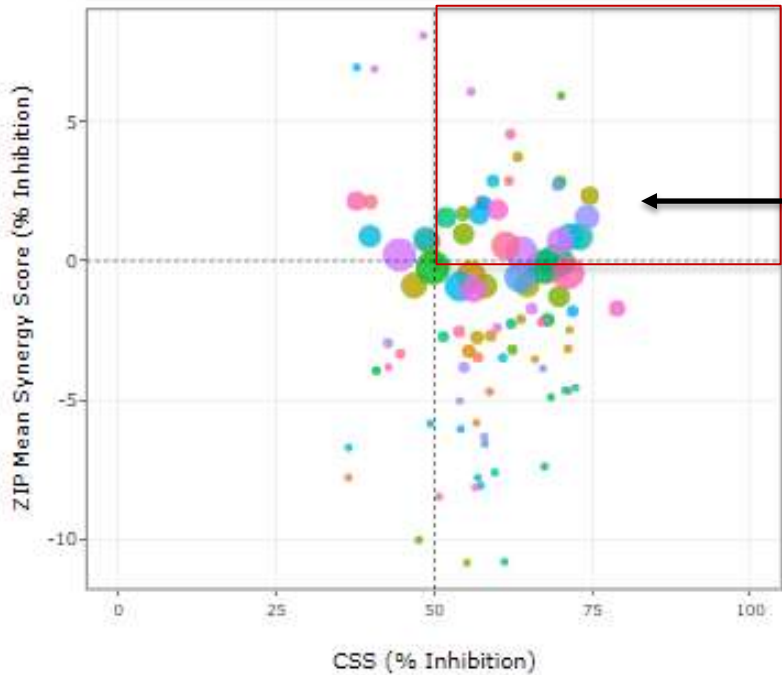


EGFR and MEK inhibitors synergise

Pair-wise synergy interaction study

- 6x6 dose grid
- 6 anchors (standard of care + experimental) in combo with 79 hits
- screening 4 cell lines

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A																								
B																								
C																								
D																								
E																								
F																								
G																								
H																								
I																								
J																								
K																								
L																								
M																								
N																								
O																								
P																								

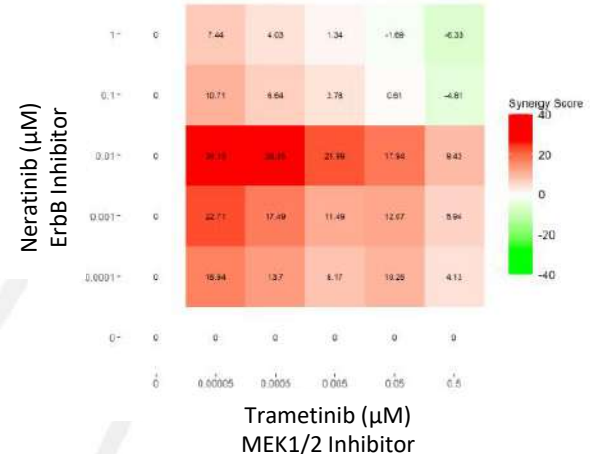


Pelitinib
(EGFR small molecule)
synergistic hits

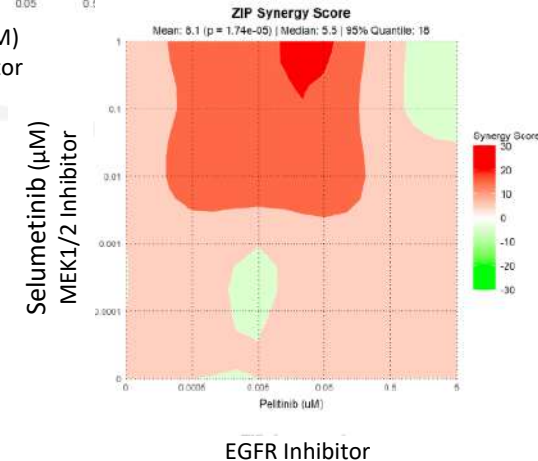
ZIP Synergy Score
Mean: 11.49 (p = 3.06e-08) | Median: 10.3 | 95% Quantile: 24.15



ZIP Synergy Score
Mean: 10.26 (p = 2.57e-05) | Median: 9.43 | 95% Quantile: 27.22



Trametinib (µM)
MEK1/2 Inhibitor

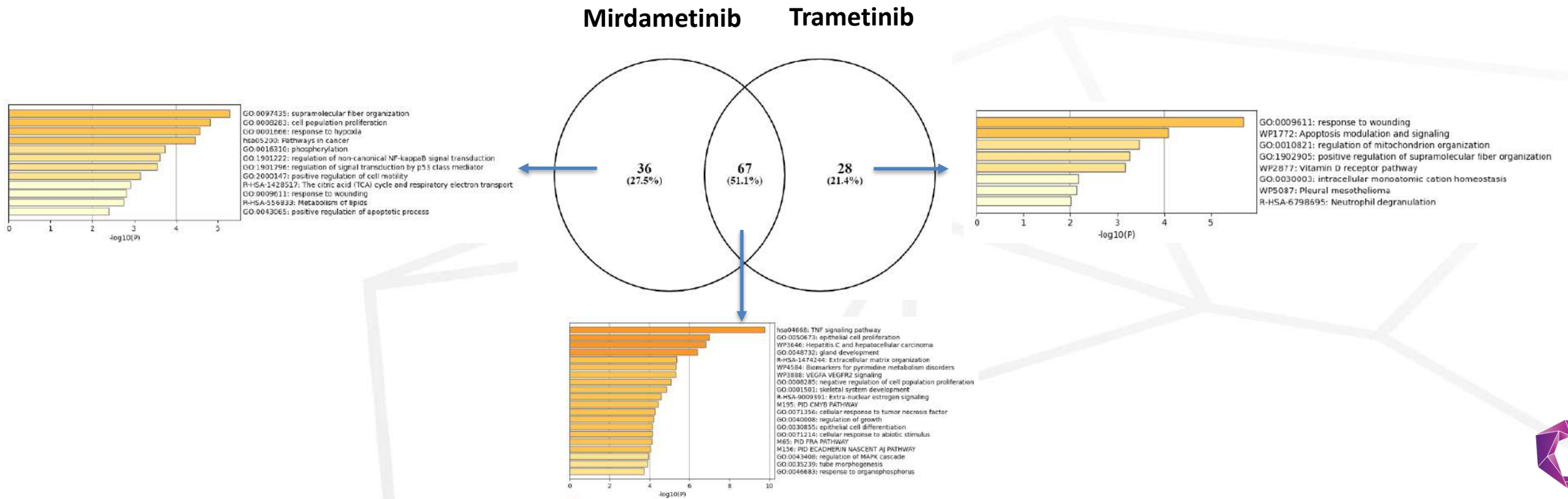


Pelitinib (µM)
EGFR Inhibitor

MAC-seq reveals transcriptional programs driving drug sensitivity

Comparing transcriptional profiles driving drug sensitivity between a series of i) EGFR and ii) MEK inhibitors

VOA-4698 cells, 1 μ M, 24hrs



Dr Kathleen Pishas – record holder! Largest screen in VCFG

13 cell lines screened with >3500 compounds
685 x 384 well plates = 263040 wells of data

~2.5 hours imaging per plate
1712.5 hours = 72 days!
Feb 2021 start and still going

PMC codes

Pilot

PMC37
PMC78
PMC83
PMC88
PMC95
PMC96

Primary

PMC101 PMC122
PMC102 PMC137
PMC103 PMC146
PMC104 PMC147
PMC107 PMC150
PMC108 PMC152
PMC109 PMC155
PMC110 PMC156
PMC113 PMC184
PMC114 PMC185
PMC117
PMC118

Validation/3D/MAC-seq

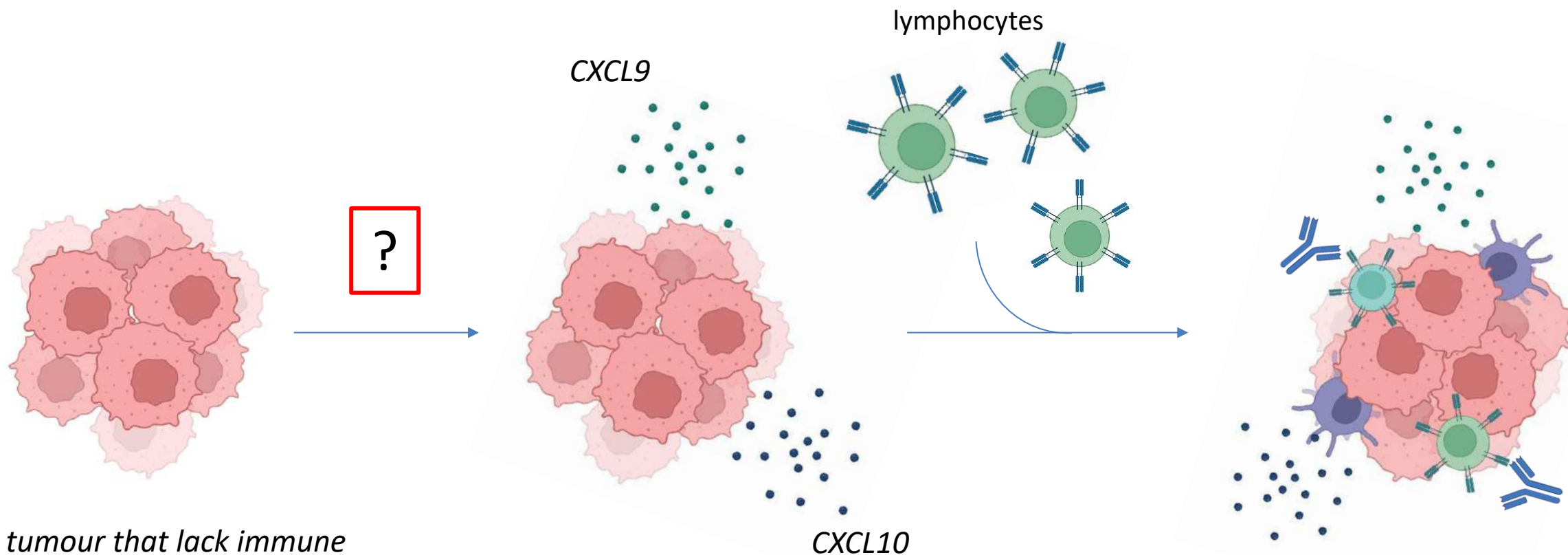
PMC220
PMS28
PMS29
PM3D94
PMC3D104
PM3D110
PM3D113
PM3D130



2- T cell infiltration model – mouse macrophage

CXCL9 and CXCL10 are chemokines induced by IFN γ

Play a role to induce chemotaxis, promote differentiation and multiplication of leukocytes, and cause tissue extravasation.



Cold tumour that lack immune cell infiltrate are CXCL9_{low}

Not responsive to Immune Checkpoint Blockade (ICB)

Hot tumour are CXCL9_{high}

Responsive to ICB

What agents can drive tumours make more CXCL9/10?

Identify novel immunomodulatory drugs to enhance CXCL9/10 expression

Day 1 AM

Plate cells
@ 10K/well
BioTek 406

Day 1 Midday

Add compound library
(20480 compounds)
Janus G3

Day 1 PM

Add IFN γ (0.625ng/mL,
prepared at 10X)
BioTek 406

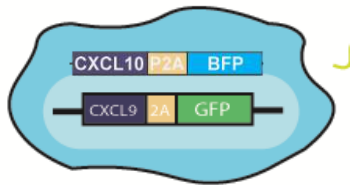
Day 2 AM

Lift cells,
fix with 2% PFA
BioTek 406

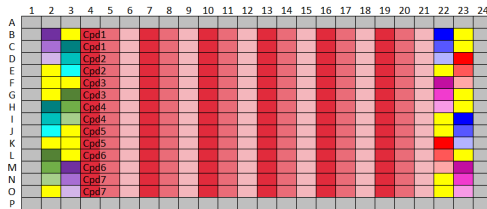
Day 3++

Flow cytometry

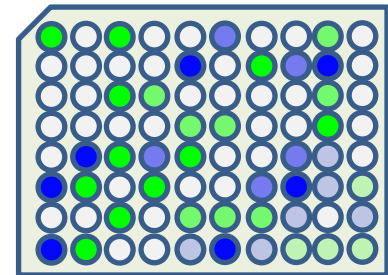
Read MFI of
GFP and BFP
3 systems



CXCL9-P2A-GFP
CXCL10-T2A-BFP



72 x 384 well plates
Single dose compound 10uM

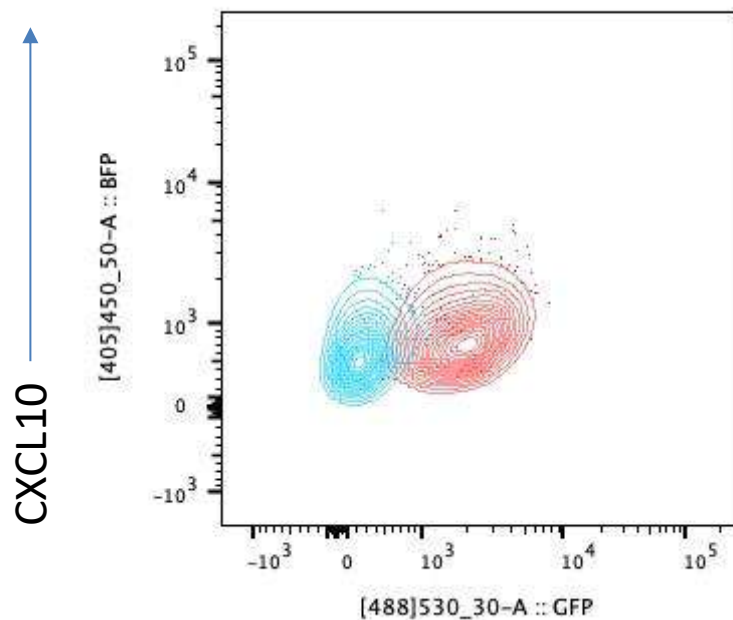


High viability
Exclude toxic targets

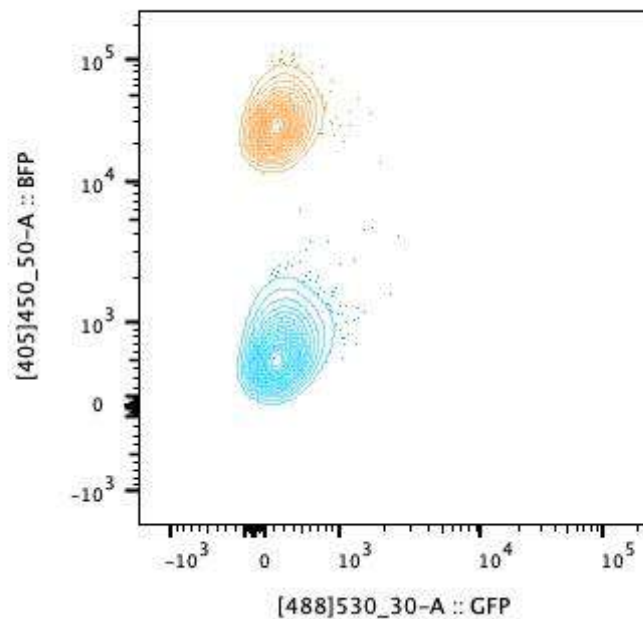
Example compounds

Blue = IFN γ -stimulated DMSO control.

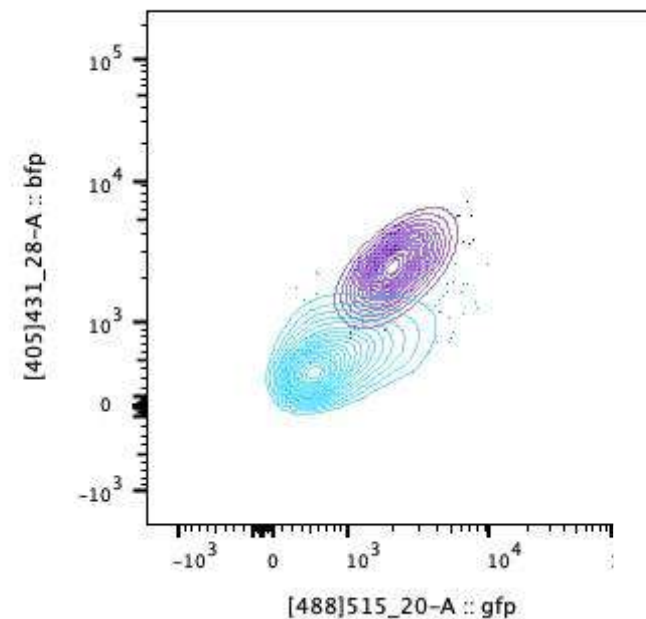
Modifies CXCL9 expression



Modifies CXCL10 expression



Modifies CXCL9&10 expression



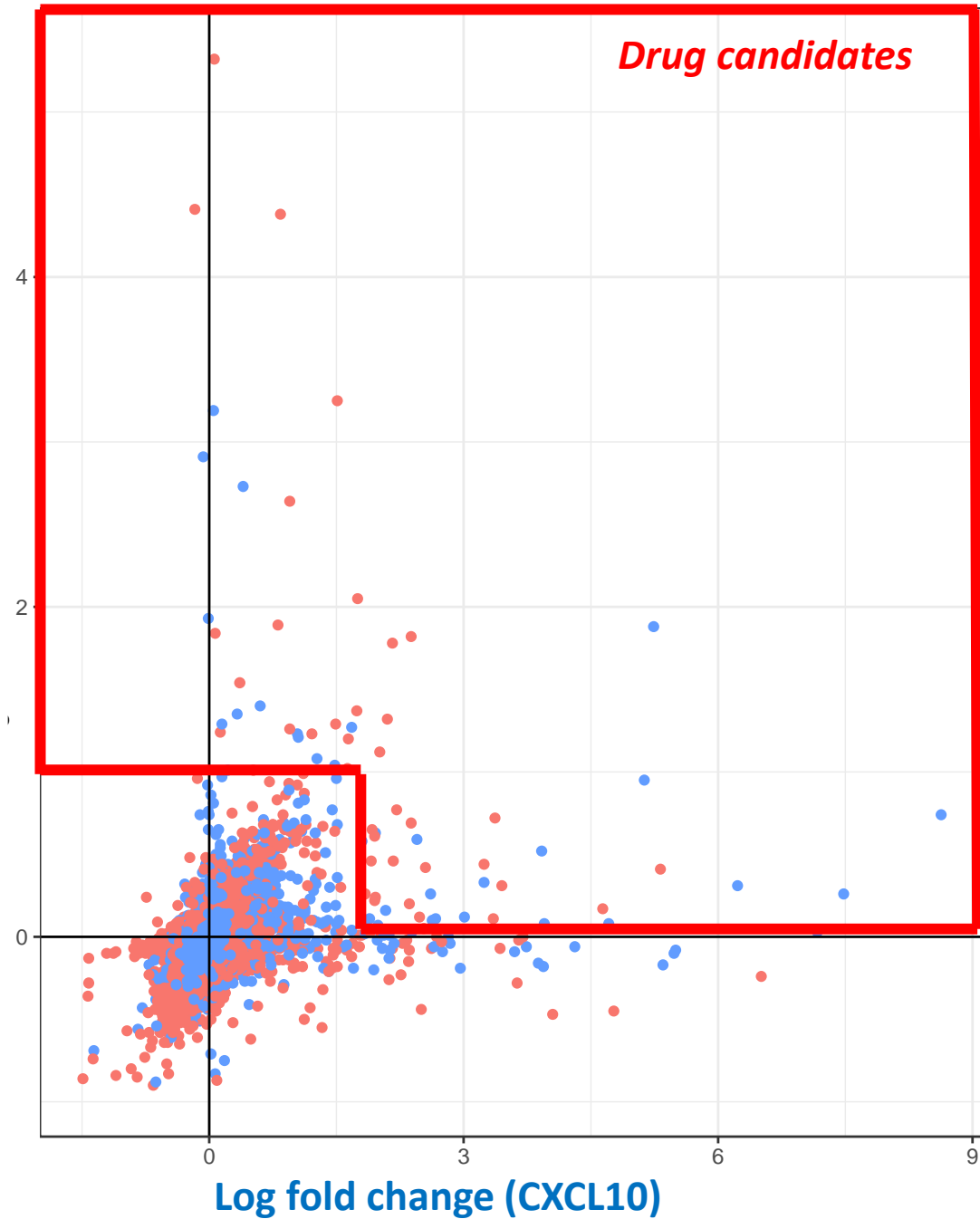
CXCL9

Primary screen outcomes

20480 compounds screened

- CXCL10 log fold change > 1.85
 - CXCL9 log fold change > 0.7
 - Counts > 100 (toxicity)
- Short listed 138 compounds

Log fold change (CXCL9)



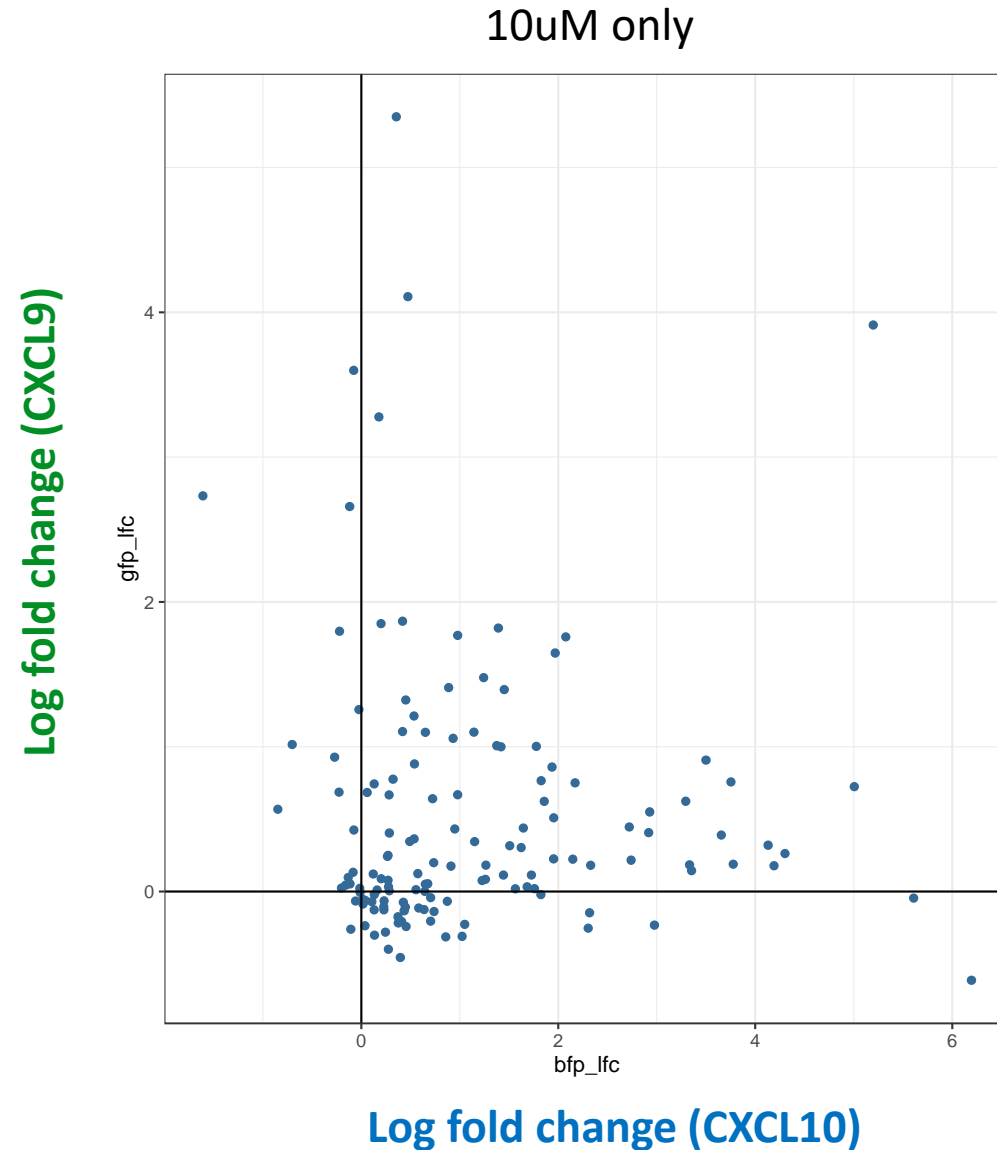
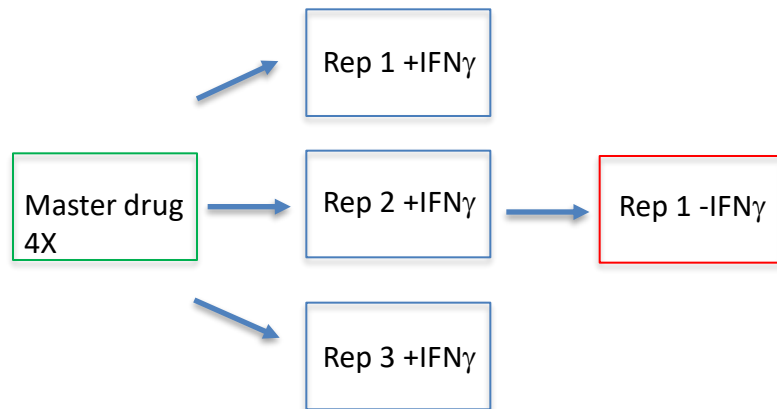
Instrument

- A3
- Fortessa
- LSR

Drug candidates – validation screen

Secondary screen containing 138 compounds

4-point dose curve (10, 3, 1, 0.1 uM, ± IFN γ) in triplicate



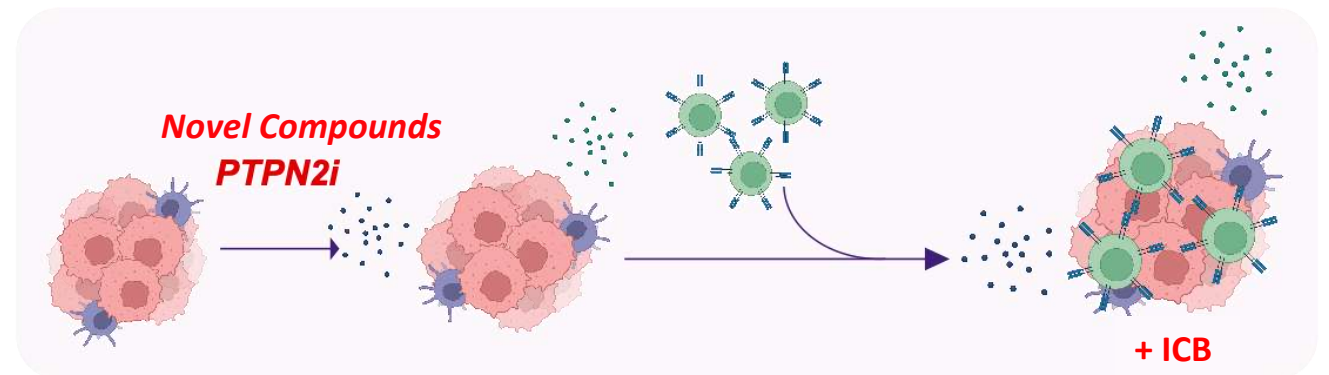
80/138 Drugs validated

High confidence targets for detailed mechanistic study – clinical relevance

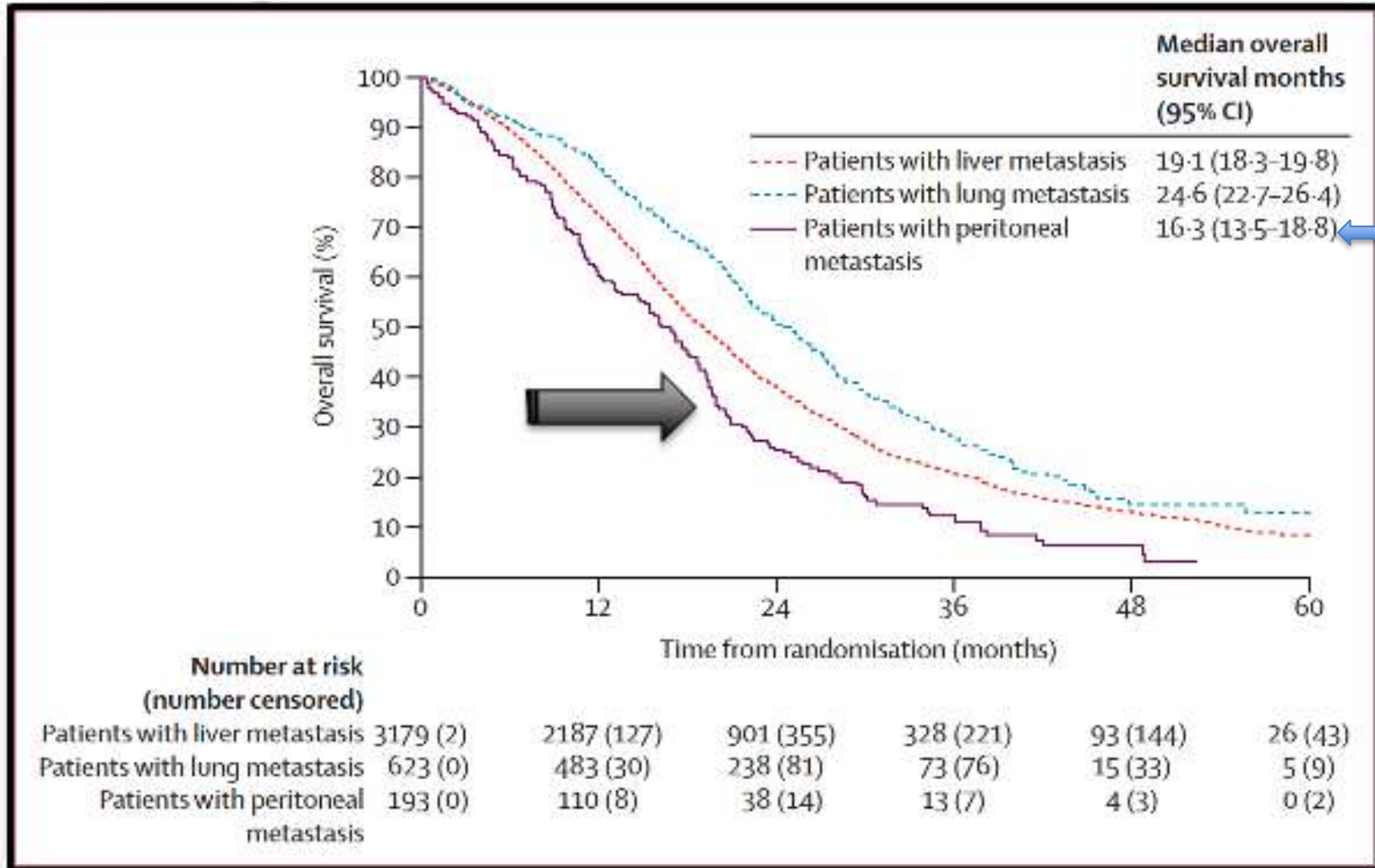
- Selecting best 15-20 drugs:
 - ~5 CXCL9 only
 - ~5 CXCL10 only
 - ~5 modulate CXCL9 & CXCL10
 - Some drugs modulating CXCL9/10 expression **without** IFN γ
- Validate in human primary macrophages.
 - Chemokine production
 - RNAseq for mechanistic insight

Novel compounds improve CXCL9/10 expression in tumors, and subsequently make them more responsive to ICB.

These may be more specific in modulating chemokine production than PTPN2 inhibitors (less adverse reactions).



3- Personalised approach to Colorectal Peritoneal Metastases (CRPM)



Worse prognosis compared to nonperitoneal metastases (liver, lung)

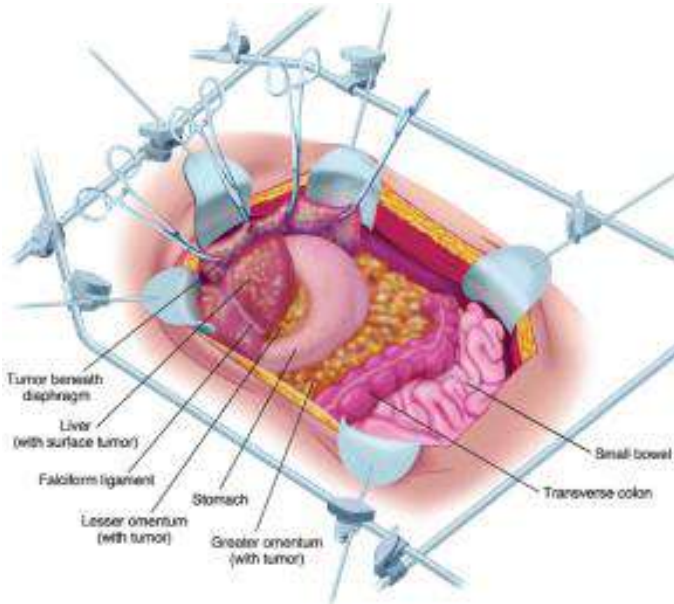
Supportive care → 3-5 months

Systemic Chemotherapy → 16 months

- Limitations**
- Tumour biology
 - Poor drug penetration
 - Drug Resistance

Treatment options for Colorectal Peritoneal Metastases

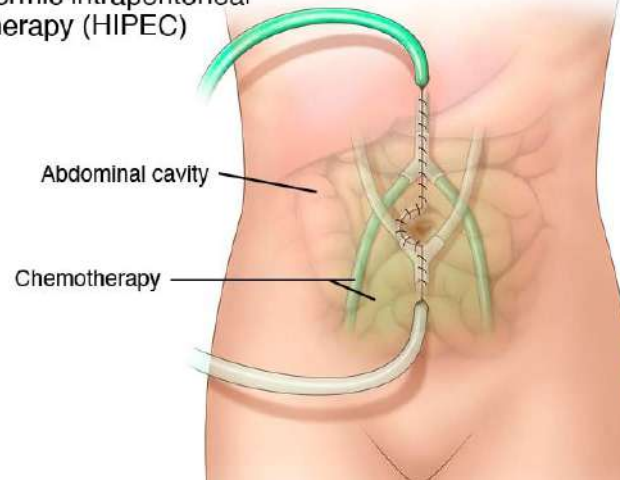
Cytoreductive Surgery (CRS)



Sugarbaker PH. 2016 Jul;48:42-9.

Heated Intraperitoneal Chemotherapy (HIPEC)

Hyperthermic intraperitoneal
chemotherapy (HIPEC)



© Mayo Clinic

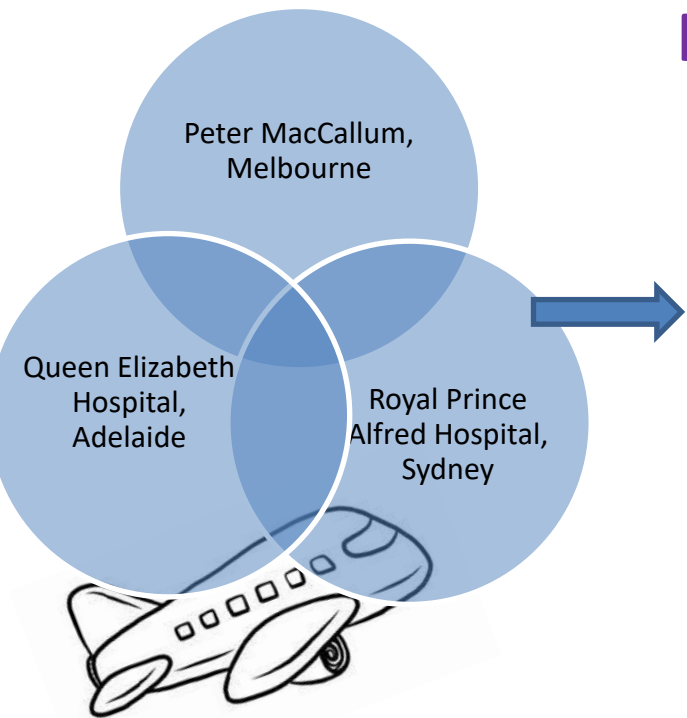
Well selected patients with good
cytoreductive surgery

→ can improve outcomes

But does HIPEC provide oncological
benefit in addition to the surgery?



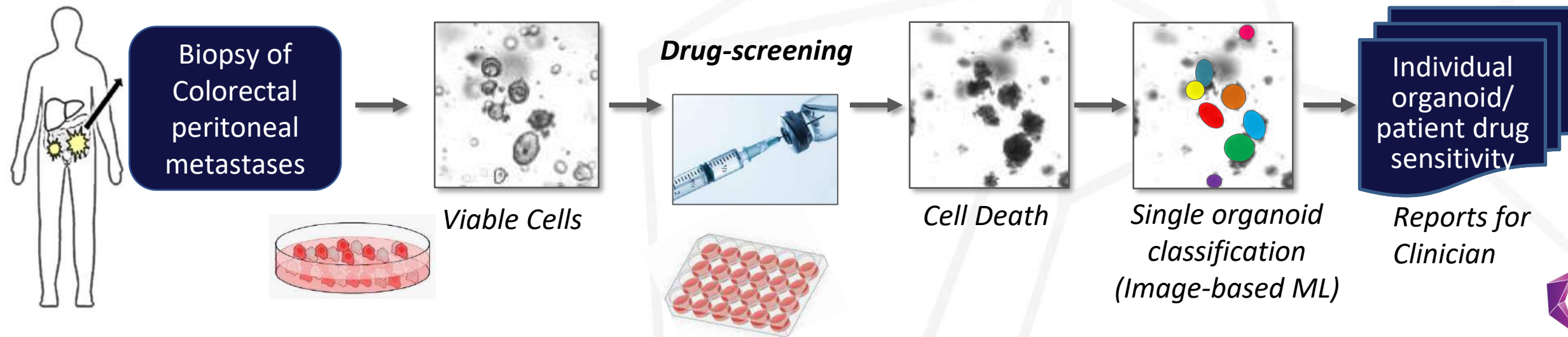
Feasibility study design



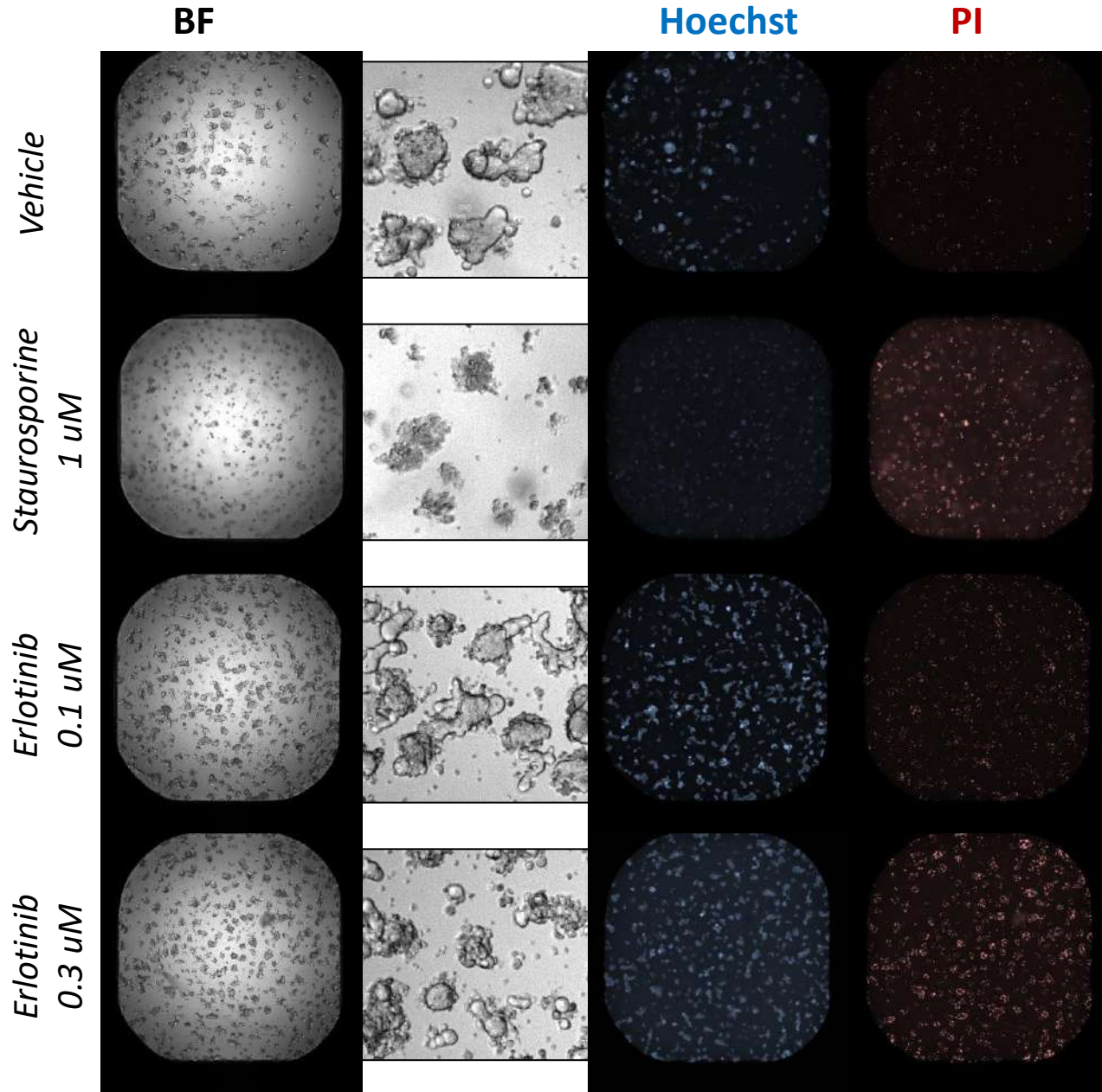
Biopsied, transported and organoids cultured and drug screened at PMCC

Image analysis and generation of Reports

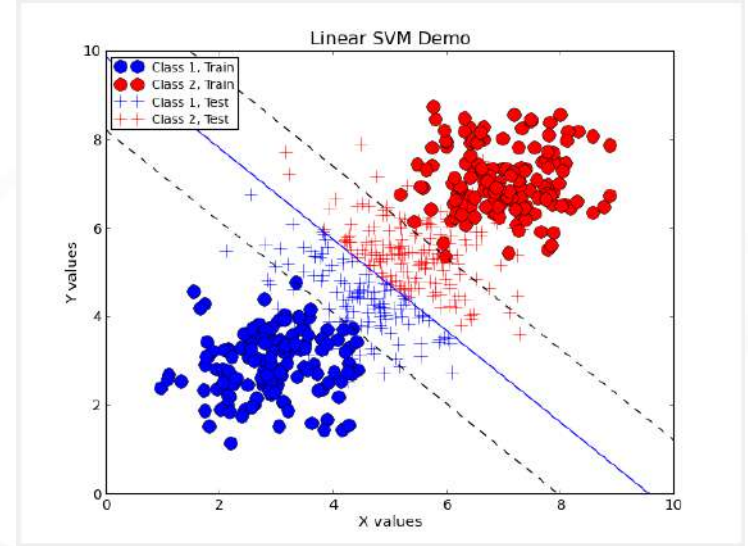
Determine feasibility of inter-site transfer and success rate of organoid culture and drug screening within **4 weeks**



Support Vector Machine learning based on imaging data



Build SVM algorithm for every patient



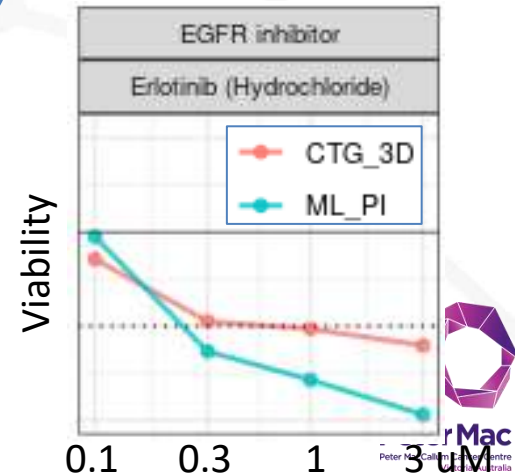
100% alive

100% dead

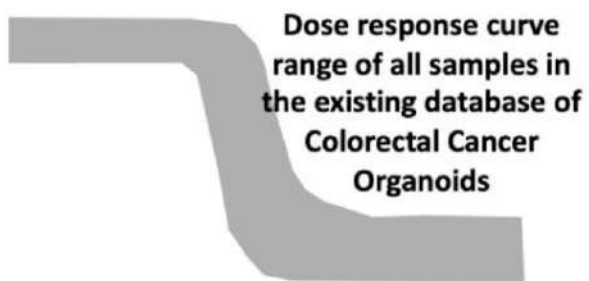
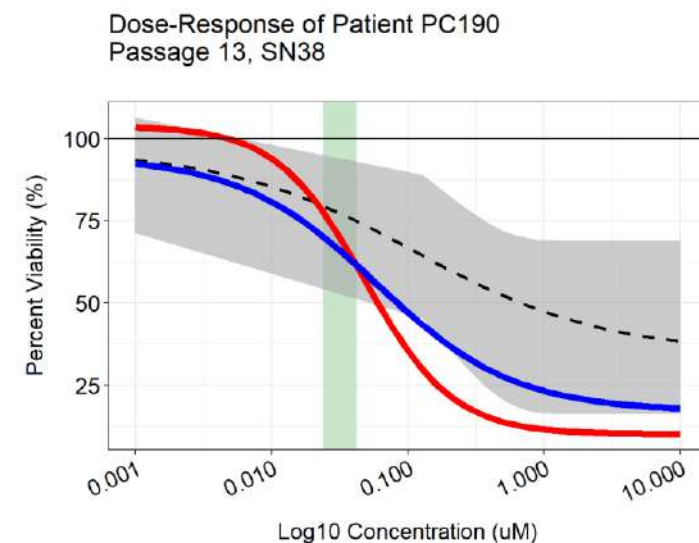
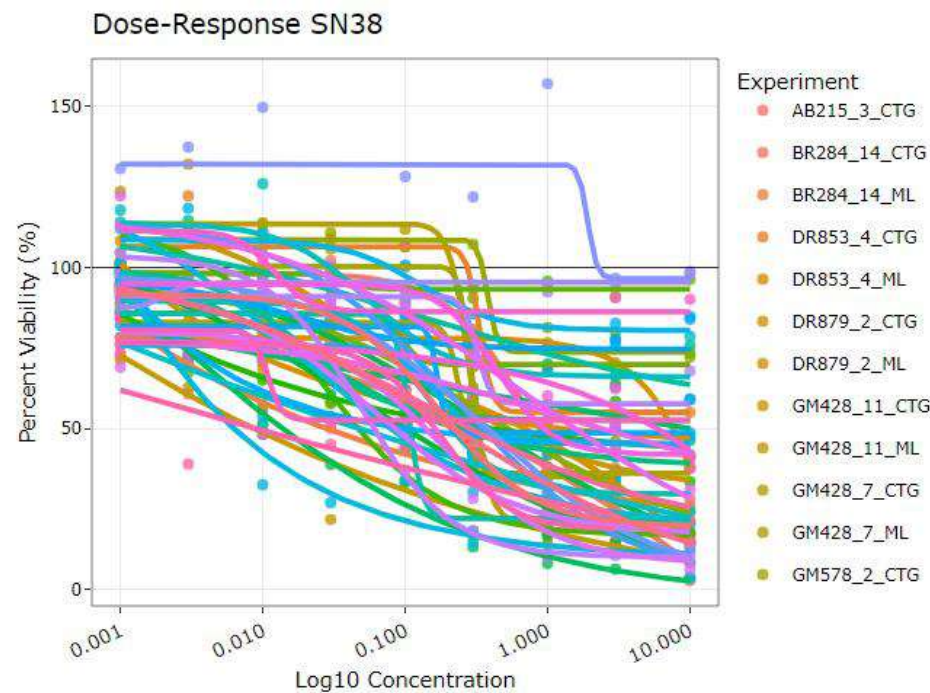
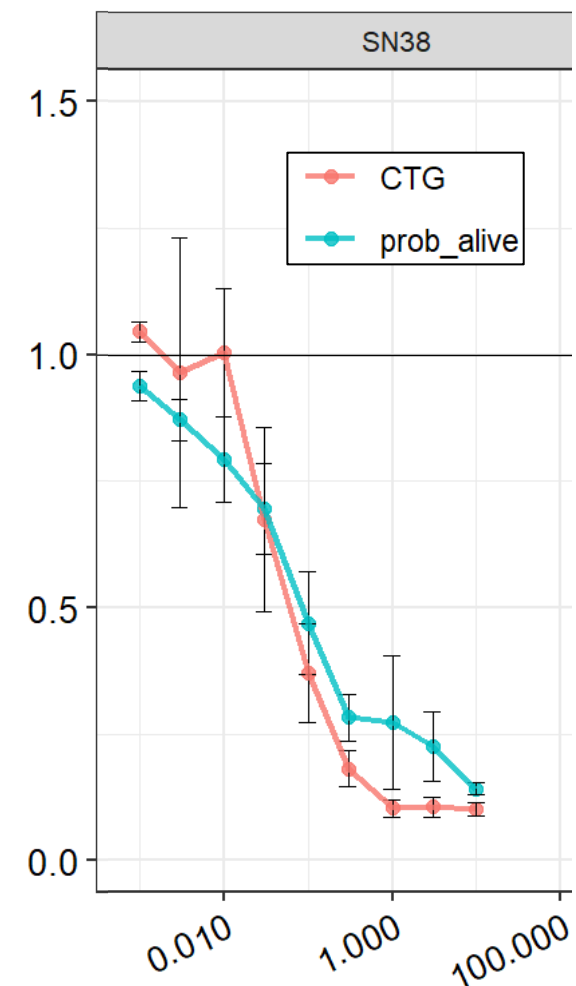
?

Predict unknown conditions

?



How do we benchmark a patient's response?

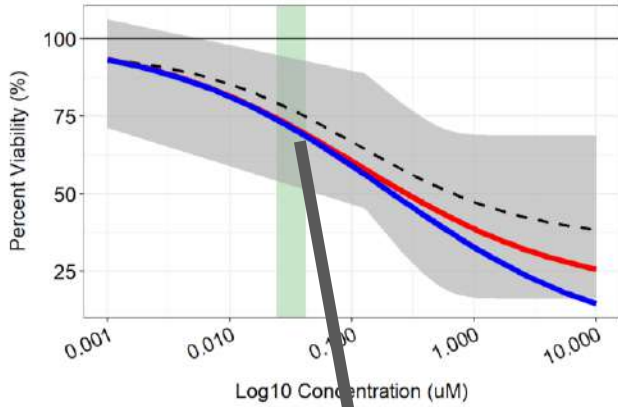


Clinically relevant
concentration ranges
determined in the clinical
cohort

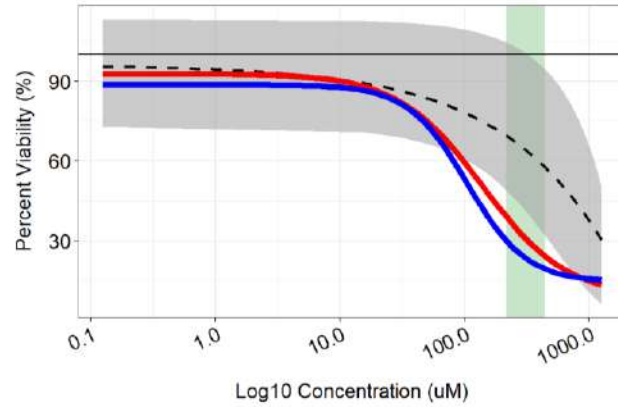
--- Colorectal Cancer Cohort's Mean Dose-response curve

How do we benchmark a patient's response?

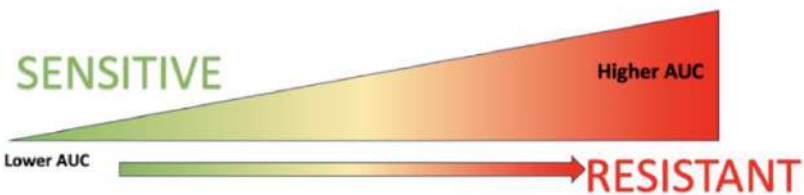
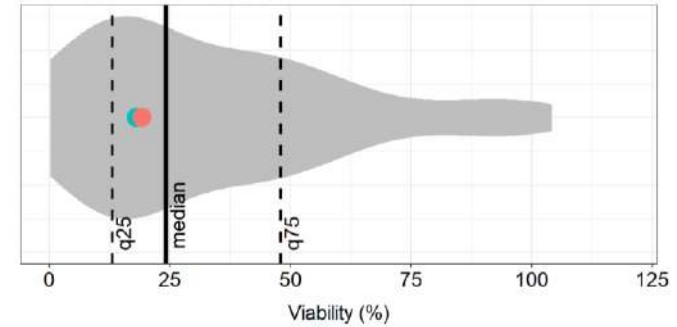
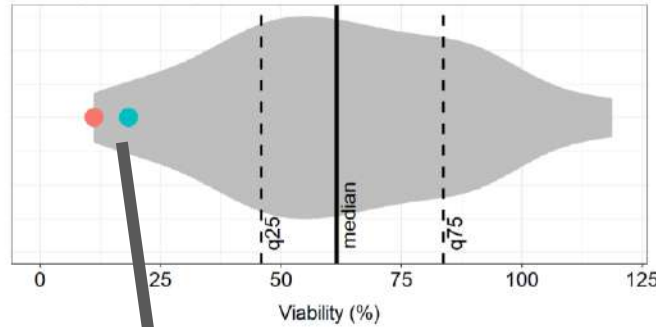
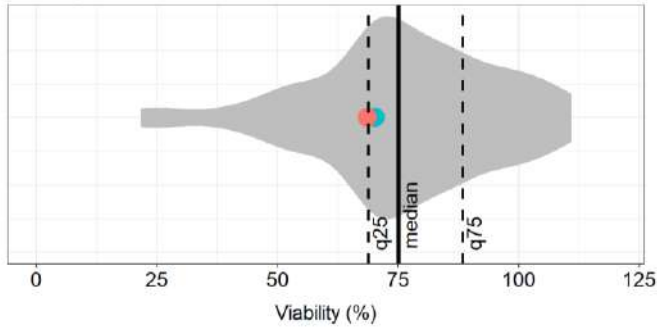
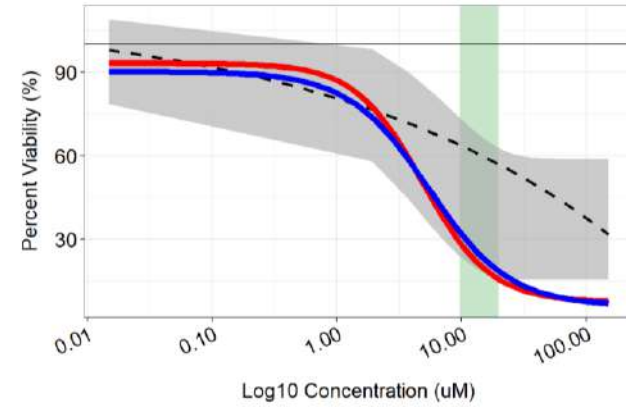
Irinotecan (SN38)



Oxaliplatin



Mitomycin C



More sensitive to Oxaliplatin than 98% of patients in our database

Awaiting clinical response data now



4- Modelling immunotherapy in organoids

Immunotherapy efficacy *in vitro* have been assessed using cell lines with engineered reporters such as Luciferase in **2D**, or luminescent based whole well assay.

There is a lack of translational tool and a read out that encompasses the cellular heterogeneity to apply to primary cells.

Most endpoint assays don't capture kinetic information of cell therapy, a late stage end point will likely include non-specific cytokine killing.



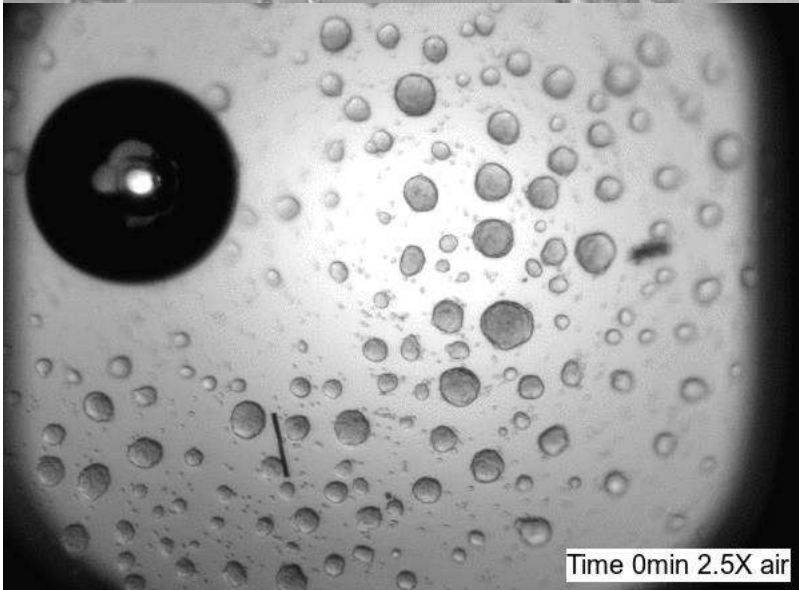
Complex co-culture immuno-oncology

MCF7 spheroids with activated NK92 cells - two different effector:target ratios

Cytation 5



300 cells per well

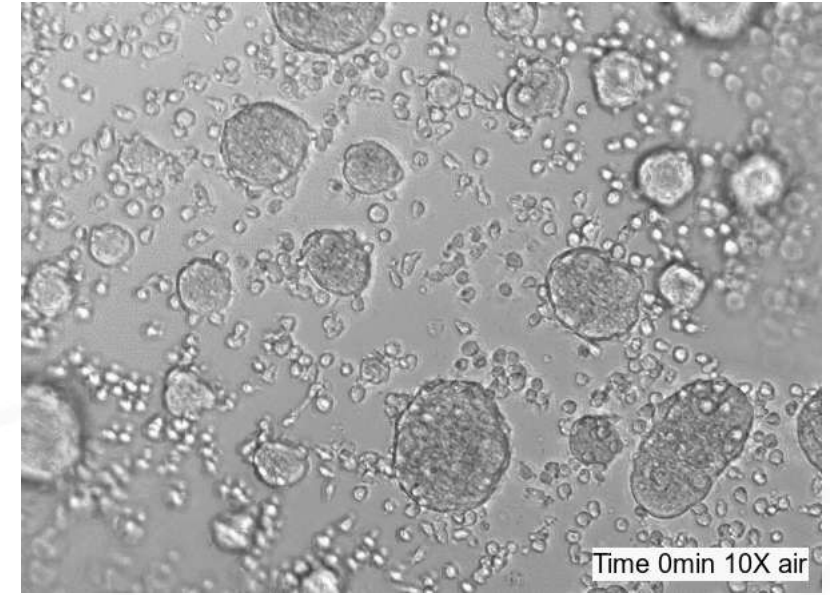


Day 4 MCF7 cells

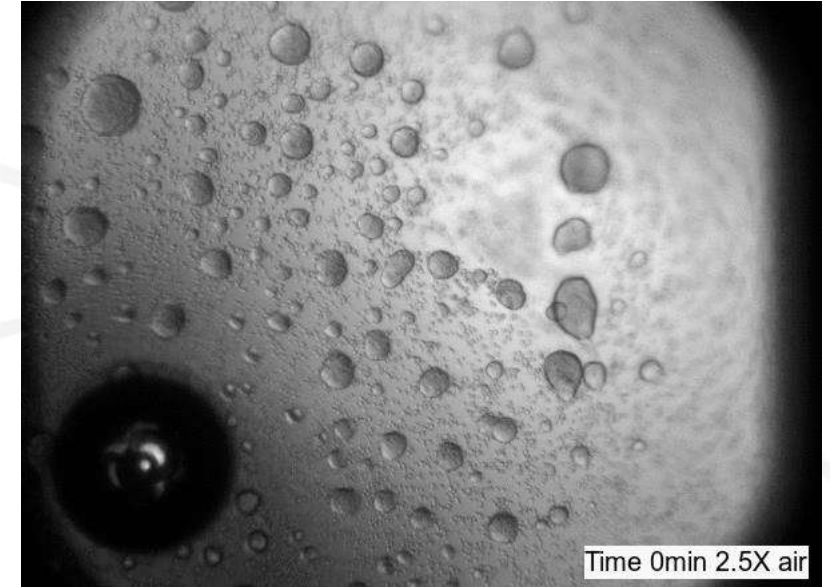
30 minute intervals for 30 hours

10x

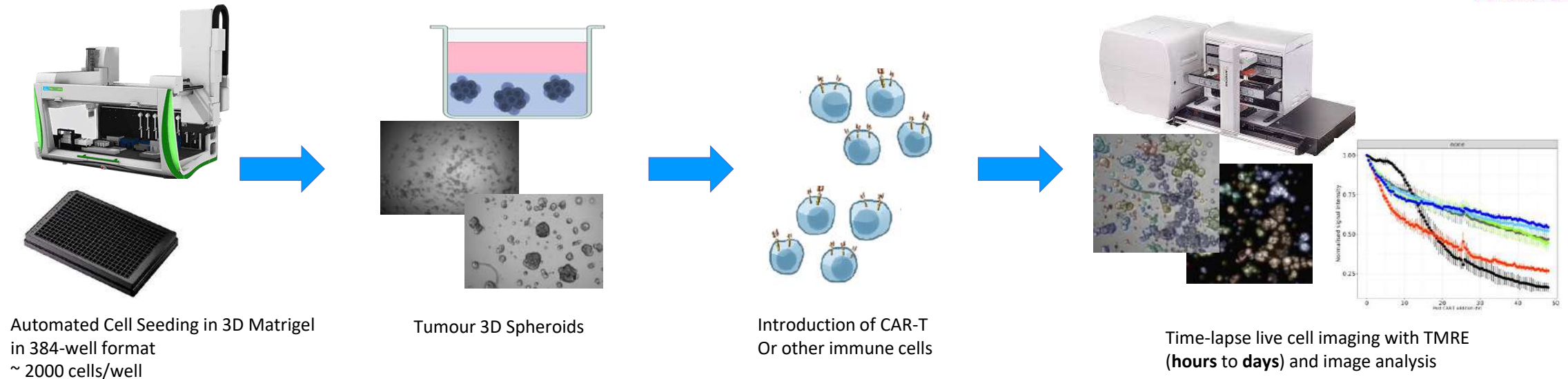
2000 cells per well



2.5x



High-throughput 3D Immune Co-culture Screening Platform



Key points

- Minimal cell material requirement
- High-throughput with real kinetic resolution
- Tumour heterogeneity in 3D
- Scalable and expandable platform for multi-omics assay

Live-image tracking over time ✓

Endpoint parallel readout such as CellTiter-Glo ✓

Flow ✓

MAC-seq (deconvolution of tumor and CAR-T transcriptome) ✓

A bottom-up approach to reconstruct miniaturised models for “micro-environment” for *in vitro* high-throughput screening

CAR-T induced cell death of colorectal spheroids

Using different ratios of CAR-T cells

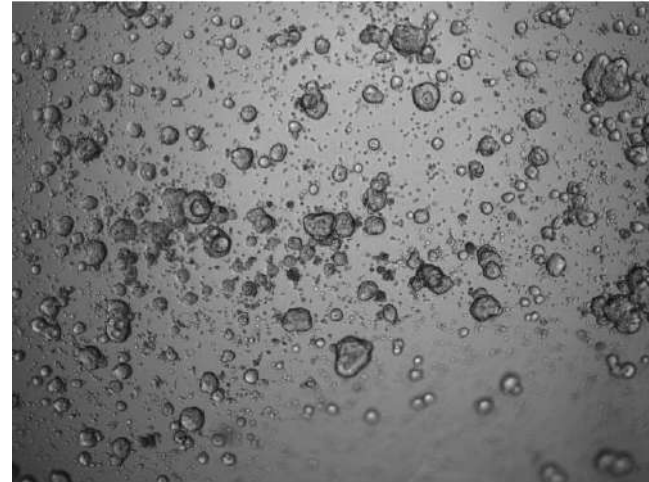
Loss of TMRE is “dose” dependent.

We can measure each individual spheroid in the well for a whole well population heterogeneity readout

Lews-Y CAR-T 1:1 CRC

Patient JF016

Lews-Y CAR-T 5: 1 CRC

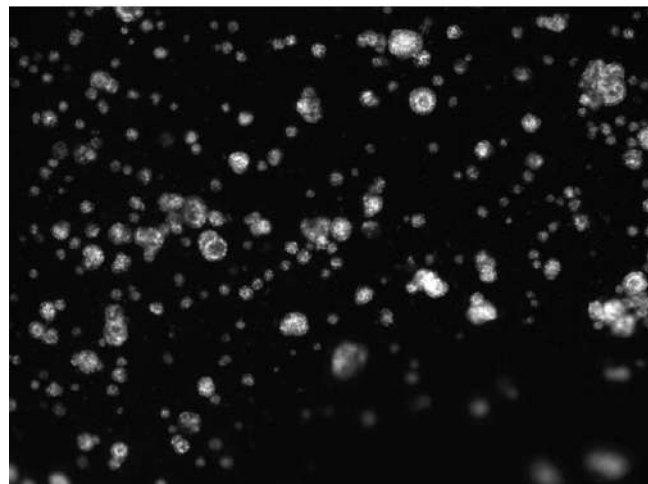


4X_JF016_CAR-T_20000_cells_none_0hr

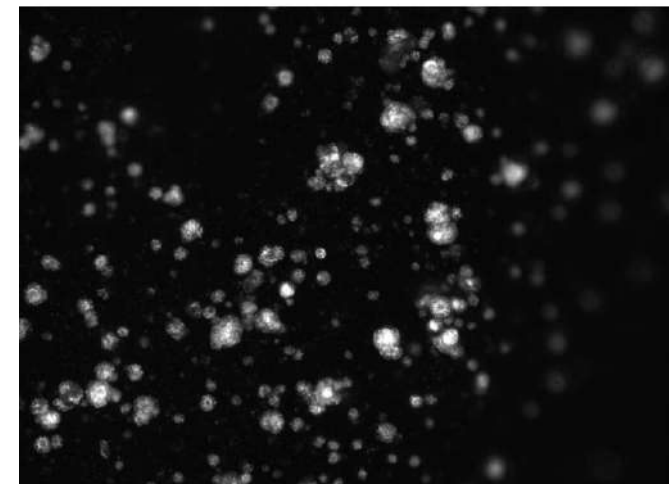


4X_JF016_CAR-T_100000_cells_none_0hr

Bright Field



4X_JF016_CAR-T_20000_cells_none_0hr

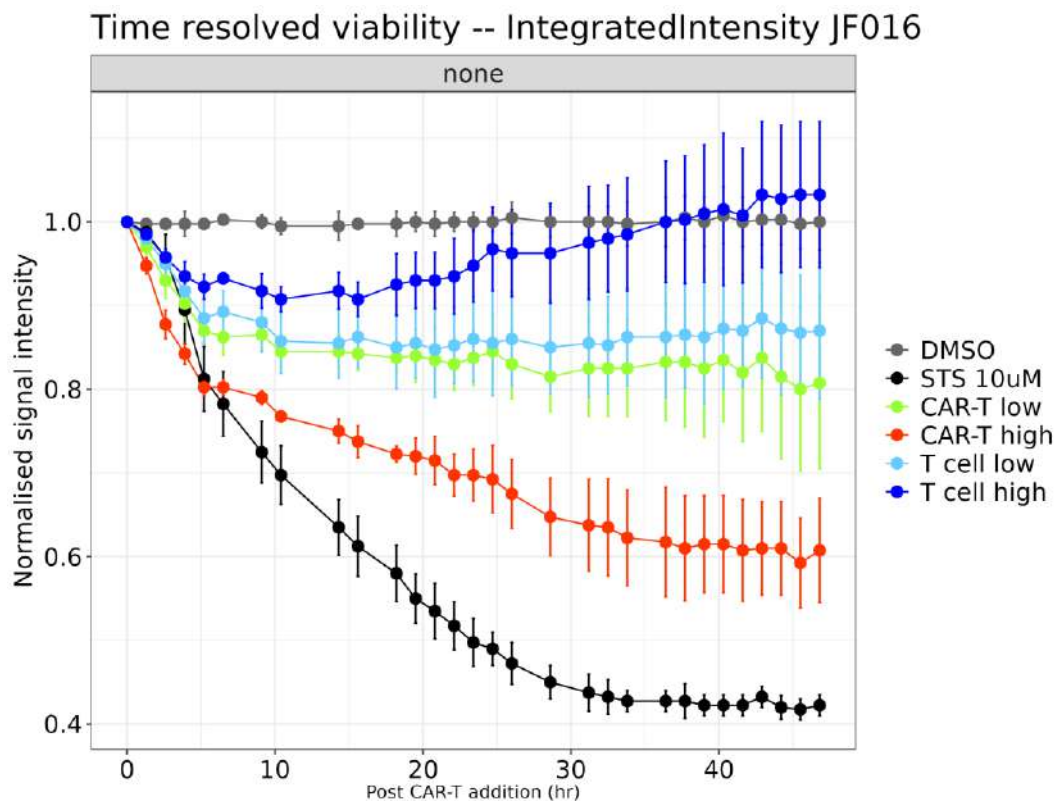


4X_JF016_CAR-T_100000_cells_none_0hr

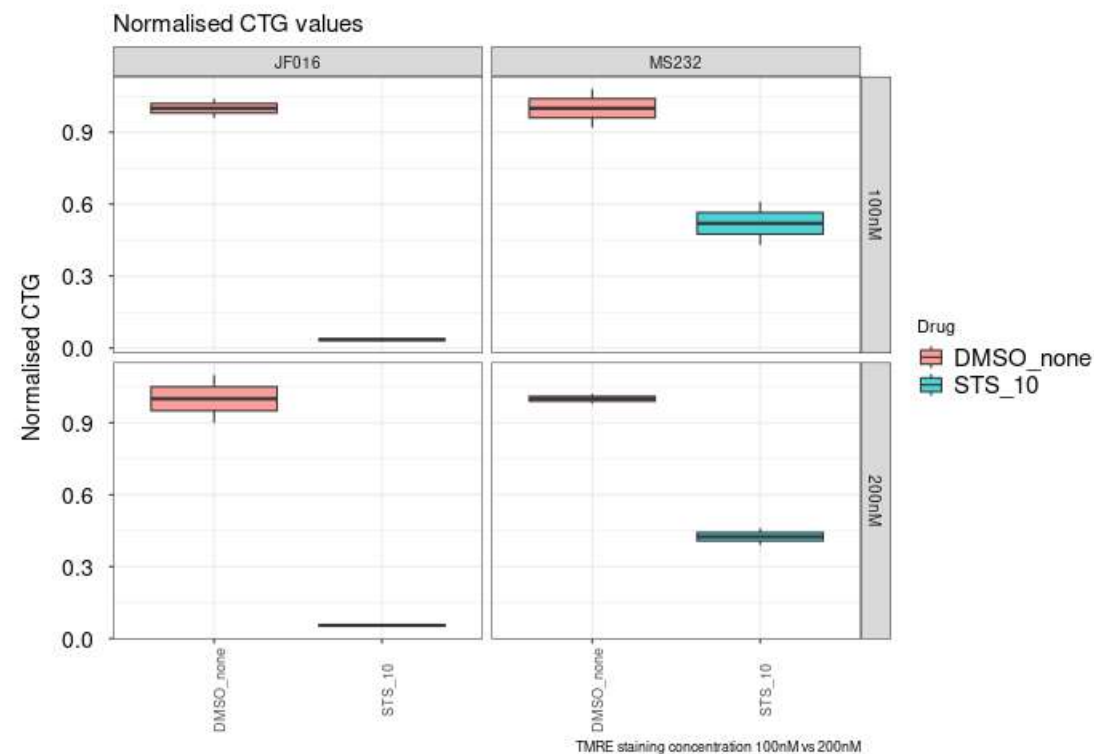
TMRE



Using TMRE to quantify spheroids over time with Cell titre glo endpoint viability



Different ratios of CAR-T and untransduced T cells
Staurosporine 10uM killing agent



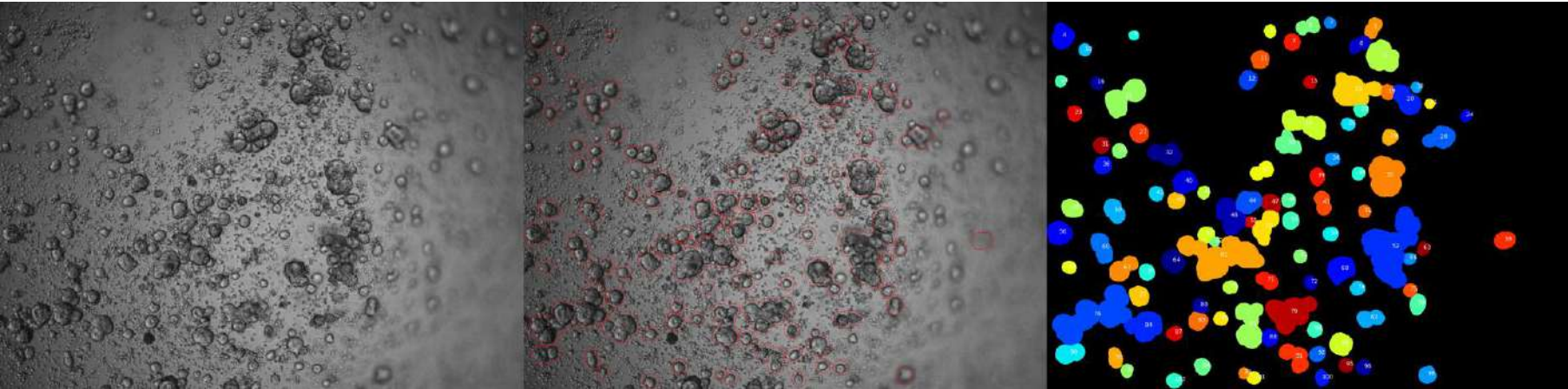
Single spheroid level image analysis and object tracking

Bright Field

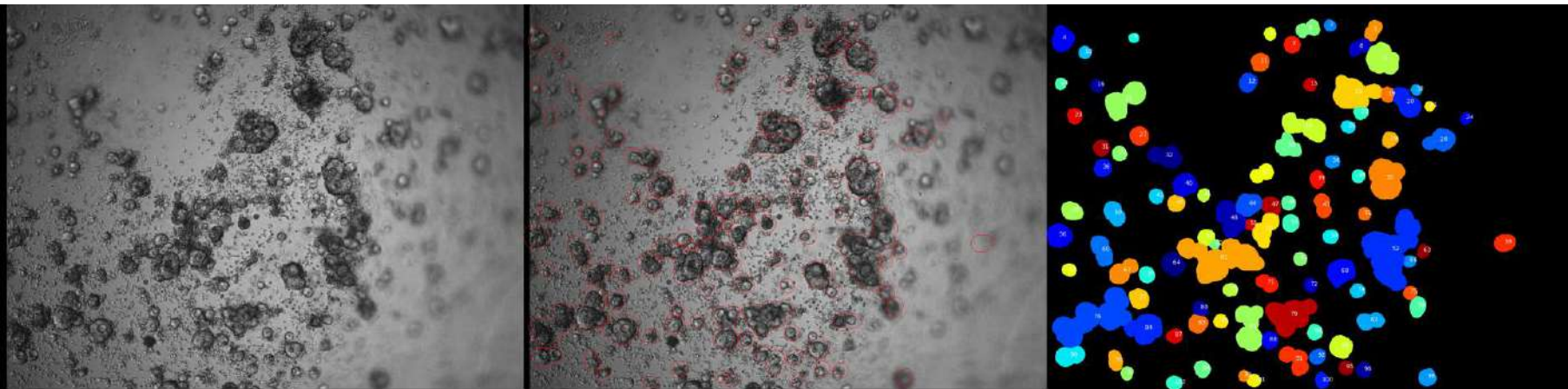
Object detection

Object Tracking

Time 0

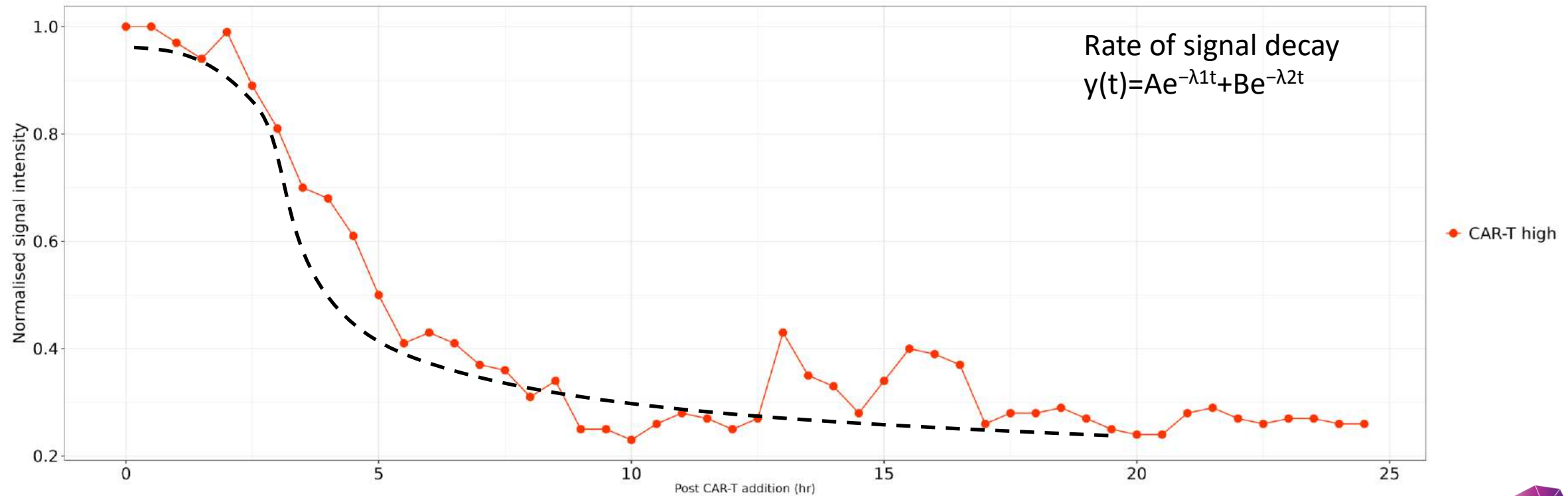


Time 6hr



Single spheroid level image analysis and object tracking

TMRE signal change for a given single spheroid over time
Summarise heterogeneity into a single number

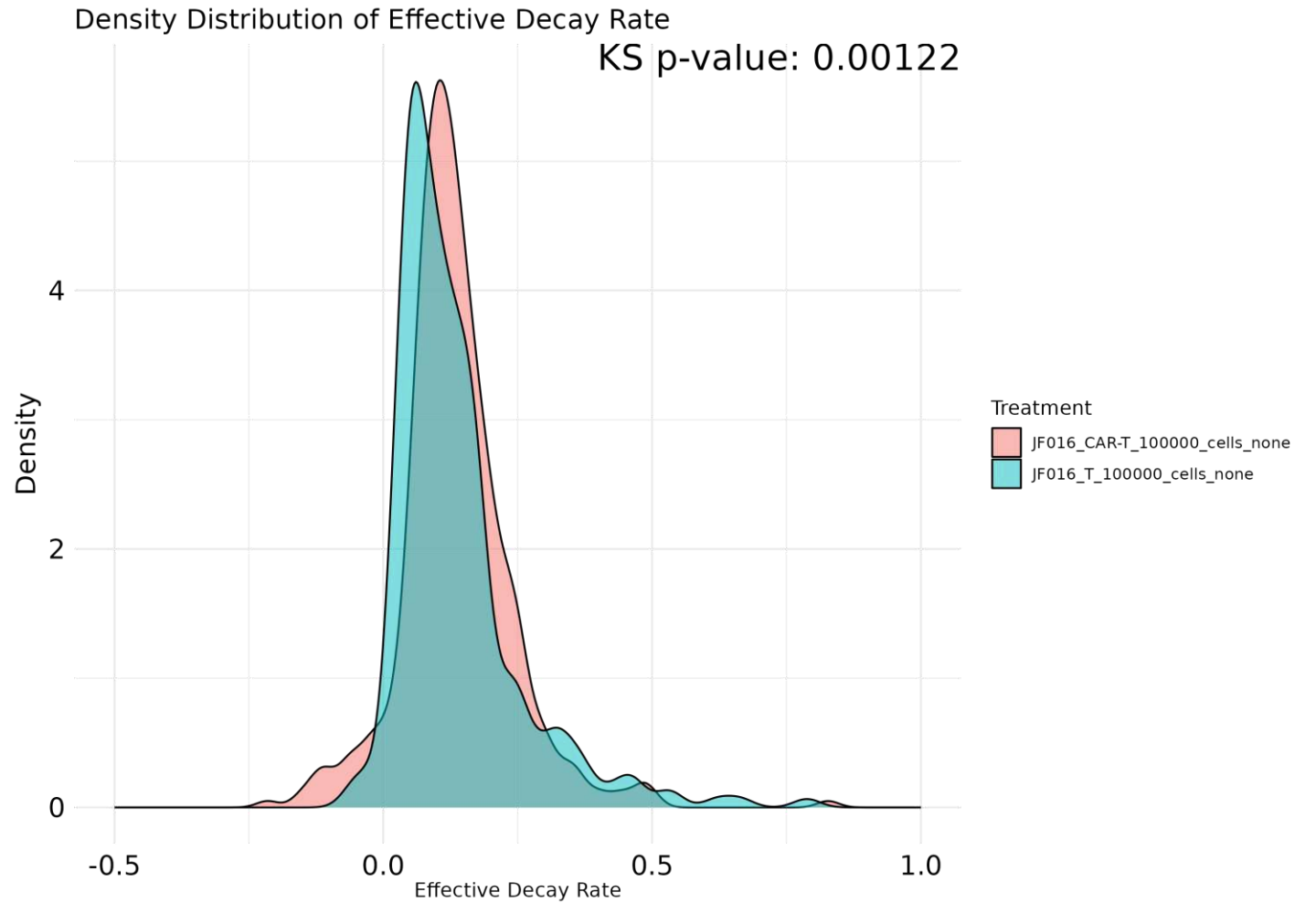


Comparison between 2 samples aggregating single spheroids

plot out the decay rate for every structure per treatment.

compare the 2 distributions using a Kolmogorov-Smirnov test.

CAR-T high dose **significantly** faster death.

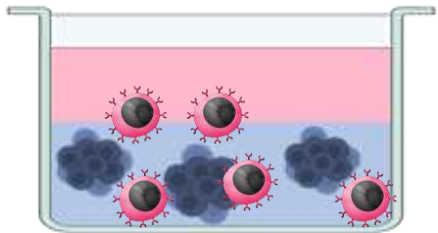


Can we use MAC-seq to quantify signaling differences in presence of CAR-T cells?

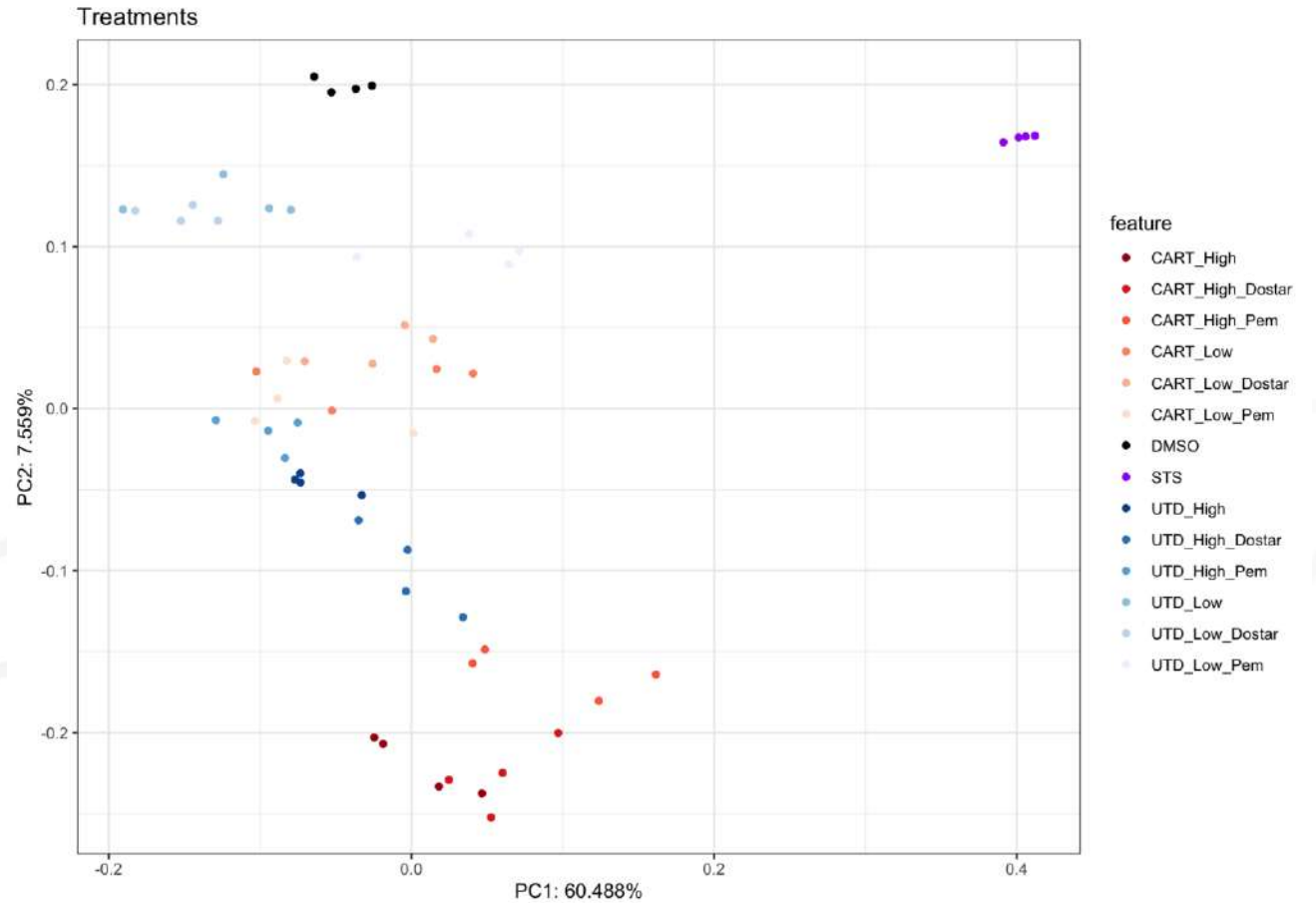
Using JF016 samples 24hr timepoint



CRC alone

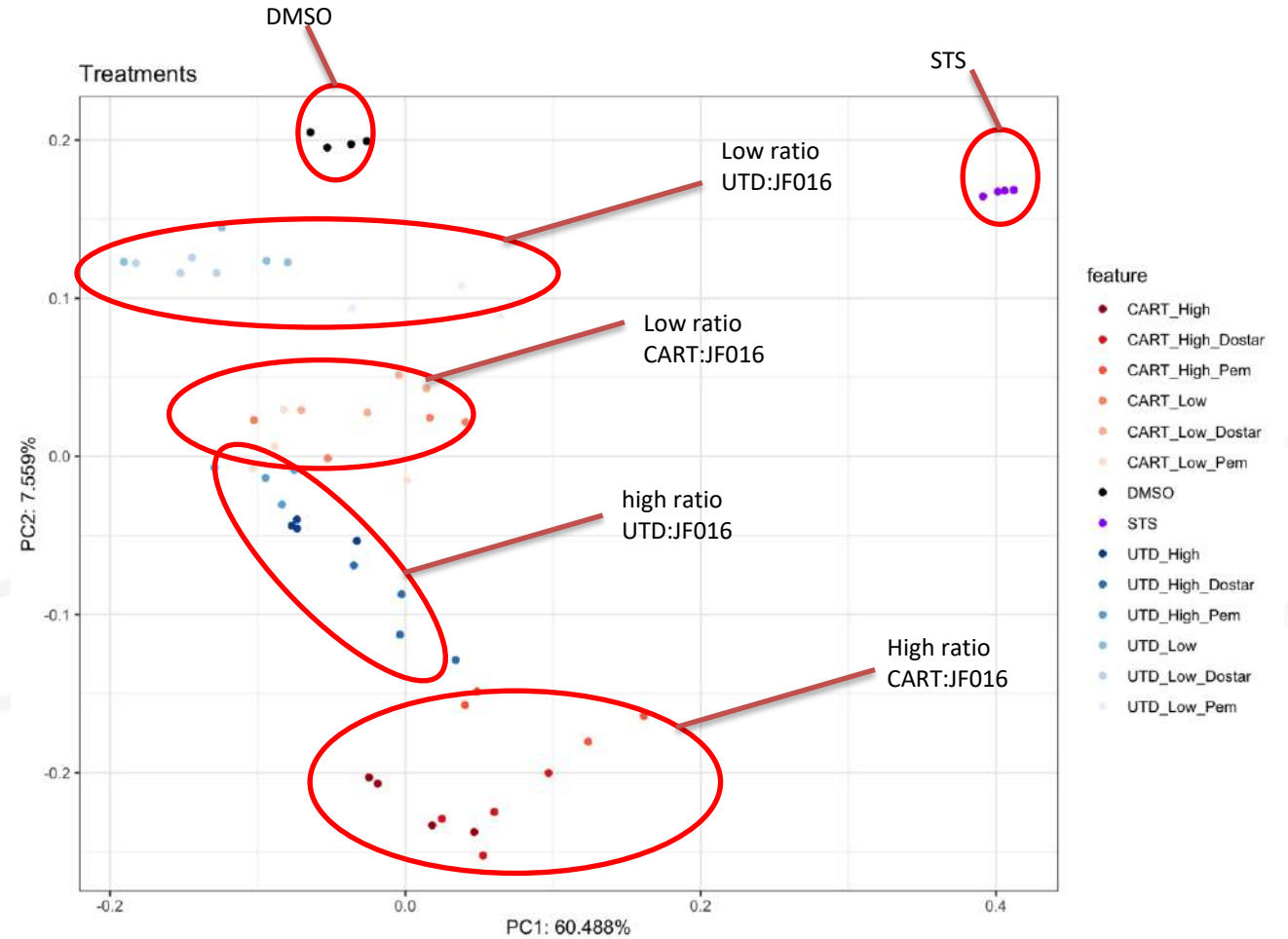


CRC with
- CAR-T
- Untransduced T cells



We can discriminate the RNA profiles of each treatment condition

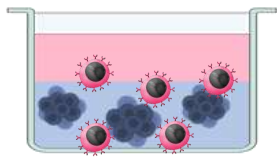
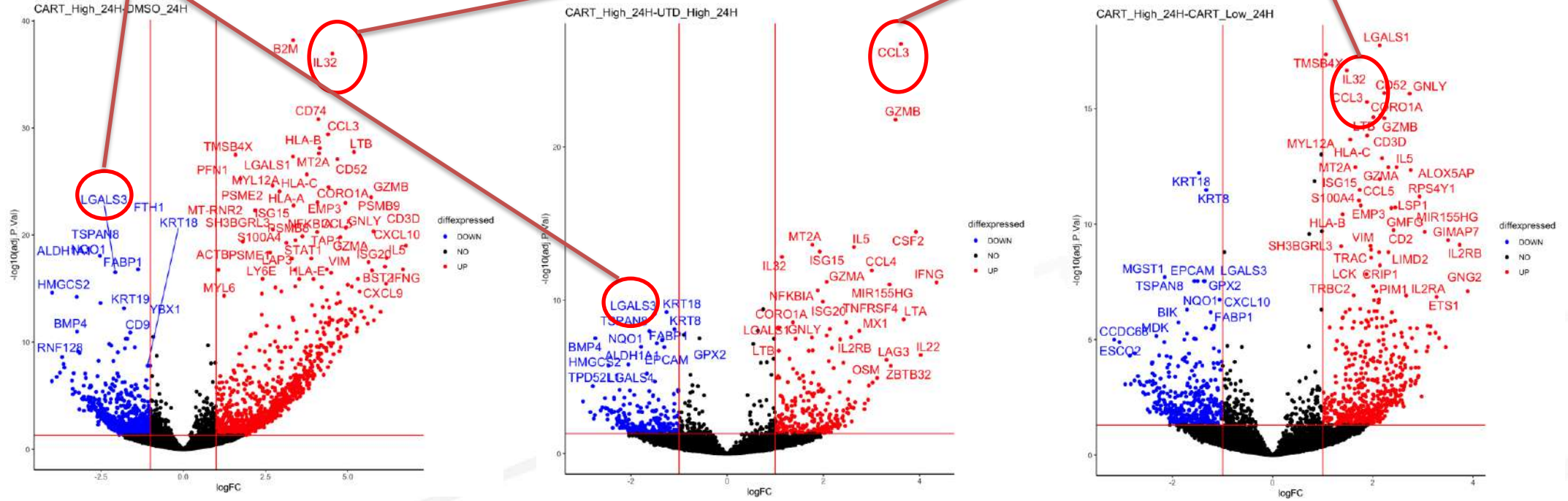
Each dot is the transcriptome of that treatment well.



Differential expression of co-culture conditions

Required for efficient T cell killing

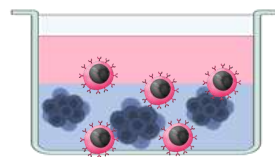
Galectin-3 promotes secretion of proteases that decrease epithelium integrity in human colon cancer cells



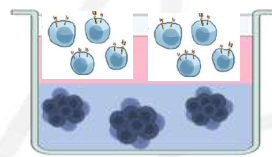
CAR-T



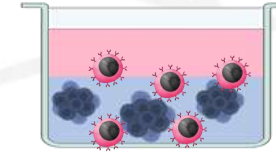
CRC alone



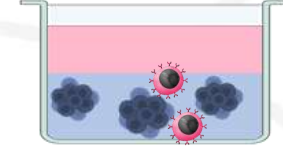
CAR-T



Untransduced T cells



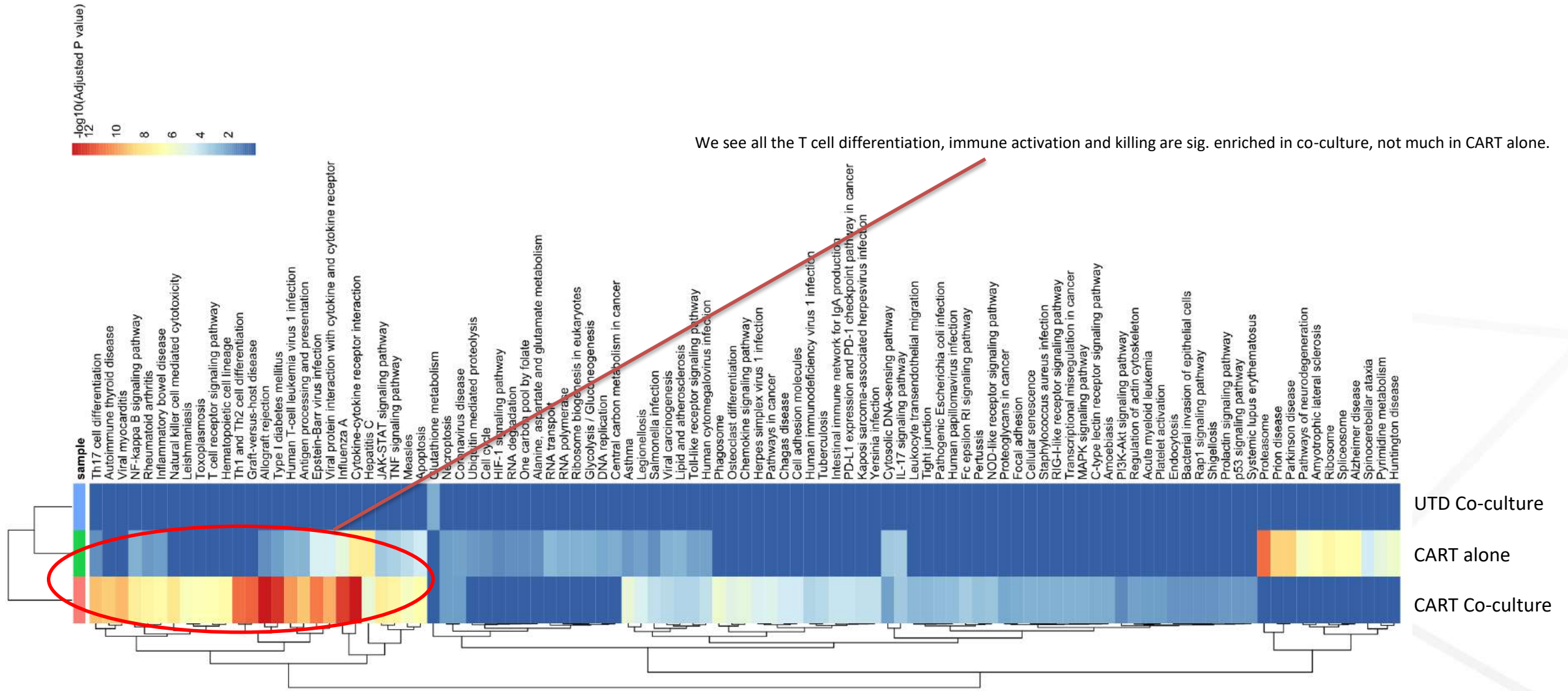
CAR-T high



CAR-T low



Co-culture identifies different expression signature



Multi-OMICS up next..

Currently working on more immunology focussed assays, drugs and CRISPR

Develop the high throughput flow applications (Novocyte with Hudson plate crane), particularly liquid handling multiplexed staining

Developing assays with Metabolomics Australia (Bio21) to quantify metabolite signalling

Working with Mass Spectrometry and Proteomics (Bio21) to miniaturise

Data integration pipelines



VCFG team – an innovative and collaborative partnership



- Prof Kaylene Simpson – Head, project management, grant support, strategy
- Dr Susanne Ramm – 2IC, R&D lead, compound screening, imaging and analysis
- Dr Mark Li – 3D screen support, fee for service and analysis, tech development
- Karla Cowley – 2D data analyst, high content microscopy, IT/server liaison
- Dr AnnRann Wong – Data analysis, screen support, fee for service projects
- Xin Liu – MAC-seq, RNA-seq, spatial transcriptomics, joint with VCFG, MGC and Bioinformatics
- Hasan Quraishi – Integrating MAC-seq with high content screening, Masters of Data Analytics (Monash)
- Jennii Luu – Lab manager, automation specialist, screening method development
- Robert Vary – Equipment training, screen support, fee for service, CRISPR
- Dr Ada Koo – Assay development, high throughput metabolomics (Bio21), iLAB management
- Kavya Pamulapati – Equipment training, maintenance, screen support
- Dr Twishi Gulati – PA National service Coordinator (NCRIS), CRISPR, business development
- Louise Scerri - administration



Organoid Nexus 2024: High Throughput Innovation Meeting

When: November 7, 2024

Time: 8:45am arrival for 9am start, concludes at 5:15pm

Where: Bio21 Institute, 30 Flemington Rd, Parkville VIC

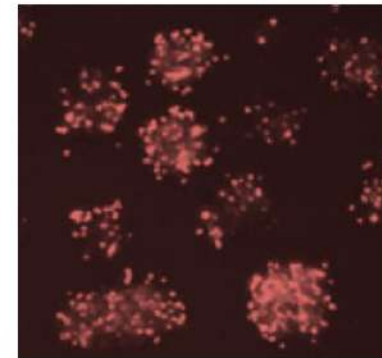
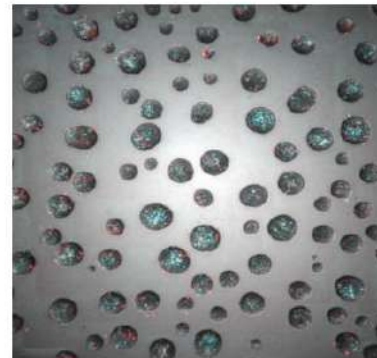
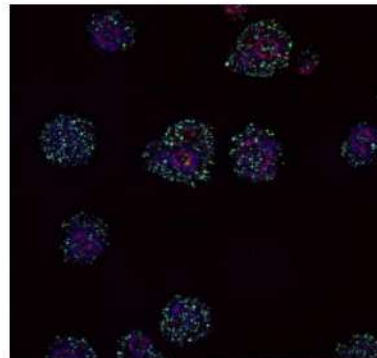
Attendance: In-person only

Cost: \$27.50 per person (incl. GST)

Presentation EoI deadline: October 16, 2024

Registration deadline: October 30, 2024

Interstate travel awards available



Functional High Throughput Technologies
AUSTRALIA