The impact of extracellular matrix on the precision medicine utility of pancreatic cancer patient-derived organoids

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Abstract

The use of patient-derived organoids (PDOs) to characterize therapeutic sensitivity and resistance (pharmacotyping) is a promising precision medicine approach. The potential of this approach to inform clinical decisions is now being tested in several large multi-institutional clinical trials. PDOs are cultivated in extracellular matrix from basement membrane extracts (BMEs) that are most commonly acquired commercially. Each clinical site utilizes distinct BME lots and may be restricted due to the availability of commercial BME sources. However, the impact of different sources and lots of BMEs on organoid drug response is unknown. Here, we tested the impact of BME source and lot on proliferation, chemotherapy and targeted therapy drug response, and gene expression in mouse and human pancreatic ductal adenocarcinoma (PDA) organoids. Both human and mouse organoids displayed increased proliferation in Matrigel (Corning) compared to Cultrex (RnD) and UltiMatrix (RnD). However, we observed no substantial impact on drug response when oragnoids were cultured in Matrigel, Cultrex, or UltiMatrix. We also did not observe major shifts in gene expression across the different BME sources, and PDOs maintained their Classical or Basal-like designation. Overall, we find that BME source (Matrigel, Cultrex, UltiMatrix) does not shift PDO dose-response curves and drug testing results, indicating that PDO pharmacotyping is a robust approach for precision medicine.

Introduction

The 5-year relative survival rate for patients with pancreatic ductal adenocarcinoma (PDA) is 12% (*1*). As the incidence of PDA continues to rise (*2*), strategies to increase survival are imperative. Surgical resection remains the only curative option. However, most patients are ineligible due to the presence of metastasis at the time of diagnosis (*3*). Standard-of-care chemotherapeutic regimens include gemcitabine/nab-paclitaxel and FOLFIRINOX, which demonstrate median survival times of 8.5 and 11.1 months, respectively (*4, 5*). Further, as heterogeneity in tumor biology and treatment response continues to be revealed, personalized medicine approaches are becoming increasingly necessary.

The use of patient-derived organoids (PDOs) has the potential to revolutionize care for patients with PDA (*6*). PDOs are 3D cultures in defined conditions that support propagation of normal, premalignant, and neoplastic cells from primary tissue (*7-11*). Organoid technology has emerged as a promising avenue for precision medicine (*12*). The ability to derive PDA PDOs from surgical resections, rapid autopsies (RAP), and endoscopic ultrasound guided fine needle biopsies allows for a broad sampling of patients with PDA to encompass inter- and intra-patient tumor heterogeneity (*8*). Importantly, PDA PDOs mirror patient tumor genetics, gene expression, and treatment response, situating them as a promising tool for more precision medicine efforts to identify alternative treatment strategies (*8, 13-15*).

As the use of organoids has expanded and become more accessible, variations in culture conditions have been introduced to optimize PDA PDO generation and growth. A number of studies have delineated the impact of the liquid media composition on organoid phenotype, transcriptome, and drug response (*16, 17*). Commercial products to support organoid studies have become more widespread, including a wide variety of basement membrane extracts (BME), which serve as 3D scaffolds. Recent studies have described the use of fully synthetic and defined hydrogels to support organoids of colon, bile duct, and mammary gland origin (*18-21*). However, BMEs derived from Engelbreth-Holm-Swarm (EHS) murine sarcomas, most notably Matrigel

(Corning), but also products such as Cultrex and UltiMatrix (RnD), remain the most widely used

(*19*). EHS-tumor-derived BMEs contain heterogenous mixtures of extracellular matrix proteins,

primarily laminins, collagen IV, entactin, and perlecan, as well as tumor-derived proteins and

growth factors, which contribute to batch-to-batch variability (*18, 19*). Regardless, these BMEs

have historically served as the scaffold for organoid culture. However, the impact of different EHS-

tumor-derived BMEs on organoid growth, chemosensitivity, and global gene expression remains

unclear. Importantly, previous reports have demonstrated the clinical utility and relevance of PDA

PDO pharmacotyping using Matrigel (*8, 13, 15*). These studies and others have prompted the

design of clinical trials based on the use of organoid-guided chemotherapy. However, due to the

CoVID-19 pandemic, severe supply chain issues have limited BME availability. These issues

range from complete inability to secure the same commercial source of BME or dramatic reduction

of available BME within the same lot. The impact of the commercial source and lot of BME on

drug response and prognostic gene expression programs has not been explored, yet is critical for

the deployment of PDO clinical trials.

Here, we report the impact of BME on PDA organoid growth, response to standard-of-care

chemotherapy as well as targeted therapy, and gene expression patterns. While we find that BME

source has a significant and substantial impact on organoid growth, drug response and gene

expression remain consistent across multiple lots and commercial sources. Results from this

study provide insights into selecting BME for organoid culture and for characterizing PDO

sensitivity and resistance to both chemotherapies and targeted therapies, which may assist in

guiding clinical decisions.

Results

BME impacts mouse and human organoid growth

To investigate the influence of BME on organoid growth, human and mouse PDA

organoids (**Supplementary Table 1-2**) were cultivated in Matrigel 04 (lot #1062004) and then

plated in either Matrigel 04, Matrigel 01 (lot #0287001), Cultrex 83 (lot #1564183), Cultrex 87 (lot

#1586187), or UltiMatrix 96 (lot #1637796). Intracellular ATP levels were measured after 4

(mouse) or 6 days of culture (human). Human PDOs and mouse organoids exhibited reduced

growth in Cultrex and UltiMatrix compared to Matrigel (**Figure 1A-B, Supplementary Figure 2**).

Mouse organoid proliferation did not recover even after multiple passages in Cultrex, suggesting

that this growth deficit is not due to a lack of adaptation period (data not shown). In most

experimental replicates across mouse and human organoids, there was no difference in

proliferation between Matrigel lots. In 1 out of 3 experiments, there was a small but significant

decrease (<10%) in growth of hM1F and hF24 in Matrigel 01 compared to Matrigel 04

(**Supplementary Figure 2A-B**). Similarly, 1 out of 2 experiments demonstrated a significant

decrease (24%) in hT1 growth in Matrigel 01 (**Supplementary Figure 2C**). Mouse organoid

mT69B consistently exhibited no significant differences in intracellular ATP levels between

Matrigel lots (n=4/4), while mT69A exhibited 17-23% changes between Matrigel lots (n=2/4)

(**Supplementary Figure 2D-E**). In nearly all hPDO experiments, there was a significant, and

sometimes substantial (e.g., 27% in Cultrex 83 relative to Matrigel 04), reduction in growth when

cultured in either lot of Cultrex or UltiMatrix compared to Matrigel 04 (**Figure 1A, Supplementary**

Figure 2A-B). Mouse organoids exhibited more mixed results across experimental repeats, but

consistently (n=3/4 mT69A, n=4/4 mT69B) exhibited significant, and sometimes substantial (e.g.,

55% decrease in Ultimatrix 96 relative to Matrigel 04), decreased growth in UltiMatrix 96 (**Figure**

1B, Supplementary Figure 2D-E). In the setting of Cultrex, mouse organoid proliferation trended

slower relative to Matrigel. mT69A and B grew significantly slower in Cultrex 83 (A: n=2/4, B: 2/4)

and 87 (A: n=3/4, B: 2/4), while exhibiting no significant difference relative to Matrigel 04 in 25-

50% of the experiments. These data collectively indicate that mouse and human organoids grow

significantly more in Matrigel compared to Cultrex or UltiMatrix. The impact of BME source on

PDO expansion may be potentially problematic for completion of drug testing for patients within

a clinically relevant timeline.

BME has minimal impact on drug response

To investigate the influence of BME on drug response, we measured the dose-response

of both mouse and human organoids to standard-of-care chemotherapies: gemcitabine,

paclitaxel, SN-38 (active metabolite of irinotecan), oxaliplatin, and 5-fluorouracil (5-FU), as well

as the targeted small molecule trametinib (third generation MEKi) (**Supplementary Figure 1**).

Organoids were allowed to reform and then subjected to pharmacotyping. We found that the dose-

response curves for gemcitabine, SN-38, and trametinib across all BMEs were largely overlapping

in both hF24 and hM1F (n=3/3) (**Figure 1C-D**, **Supplementary Figure 3A-B**). The dose response

curves in hT1 were also consistent across BMEs for SN-38 (n=2/2), but exhibited some variability

for gemcitabine (n=1/2) and trametinib (n=1/2) between Matrigel, Cultrex, and Ultimatrix

(Supplementary Figure 3C). Paclitaxel dose-response curves across all BMEs were also largely

overlapping in hM1F (n=3/3) (**Figure 1D**), hT1 (n=2/2) **(Supplementary Figure 3C),** and hF24

(n=2/3) (**Figure 1C, Supplementary Figure 3A).** Oxaliplatin also displayed consistent dose-

response curves regardless of BME hF24 (n=3/3), hM1F (n=2/3), and hT1 (n=2/2) (**Figure 1C-D**,

Supplementary Figure 3A-C). Additionally, 5-FU exhibited overlapping dose-response curves in

hF24 (n=3/3) (**Figure 1C**, **Supplementary Figure 3A**) and hM1F (n=2/3) (**Figure 1D**,

Supplementary Figure 3B). However, we observed more variability in dose-response curves for

5-FU in hT1 as a function of BME in both experimental repeats conducted (**Supplementary**

Figure 3C).

Mouse organoids were less sensitive to all agents tested relative to hPDOs, with

oxaliplatin and 5-FU dose-response curves failing to reach 50% cytotoxicity (**Supplementary**

Figure 3D-E). Gemcitabine and SN-38 mouse organoid dose response curves exhibited no

consistent or substantial shifts when cultured in different BMEs (**Supplementary Figure 3D-E**).

Dose-response curves for trametinib were also largely overlapping regardless of BME for both

mT69A (n=3/4) and mT69B (n=3/4), although both organoid lines were more resistant in 1 out of

4 experimental replicates when cultured in UltiMatrix 96 (**Supplementary Figure 3D-E**). We

observed a similar dose response shift for paclitaxel when mouse organoids were cultured in

Ultimatrix (n=1/4) (**Supplementary Figure 3D-E**). Overall, these data demonstrate that choice of

BME does not induce consistent shifts in dose-response curves for PDOs treated with standard-

of-care chemotherapies or trametinib, suggesting that either Matrigel, Cultrex, or UltiMatrix would

be appropriate for PDO pharmacotyping analyses.

BME does not induce significant alterations in dose-response parameters

We next compared dose-response parameters to gain further insight into subtle changes

in dose response curves both within individual experiments and across all experimental replicates.

Within each individual experimental replicate, we performed statistical analyses to identify

differences in the half maximum inhibitory concentration (IC50s), Hill slope, area under the curve

(AUC), and standard deviation of the residuals (Sy.x) between BME lots and sources (*22*).

We observed a modest number of instances in which IC50s were statistically significant

between BMEs within experimental replicates (**Figure 2A-B, Supplementary Figure 4**).

Significant pairwise comparisons in IC50 were predominantly observed between Matrigel and

Cultrex or between Matrigel and UltiMatrix. Across all organoids, drug treatments, and BME

comparisons, statistical differences between lots of Matrigel (04 vs 01) were observed only once

in a single experimental replicate (Paclitaxel, hF24) (**Supplementary Figure 4A**). Similarly,

statistical differences between lots of Cultrex (83 vs 87) were observed in only two experimental

replicate (SN-38, hM1F; 5-FU, mT69A) (**Supplementary Figure 4B**). These data indicate that lot

within the same BME source has little impact on drug IC50. Differences in IC50s for oxaliplatin

and trametinib were rarely significant, occurring in 1/16 experiments (hT1, Matrigel 04 vs. Cultrex

87) (**Supplementary Figure 4C**) and 2/16 experiments (hM1F, Matrigel 01 vs. UltiMatrix; mT69A,

Matrigel 01 vs. UltiMatrix, Cultrex 87, Cultrex 83 vs. UltiMatrix) (**Supplementary Figure 4B, D**),

respectively. Conversely, we consistently observed statistical differences in gemcitabine IC50

between Matrigel and Cultrex/UltiMatrix in each experimental replicate of hF24 and hM1F (**Figure**

2, **Supplementary Figure 4A-B**), as well as in hT1 (n=1/2), mT69A (n=1/4), and mT69B (n=2/4)

(**Supplementary Figure 4C-E**). Statistical differences in paclitaxel IC50 were observed in hF24

(n=1/3), hM1F (n=1/3), hT1 (n=2/2), and mT69B (n=1/4) (**Supplementary Figure 4A-C, E**).

Lastly, differences in 5-FU IC50 were observed in only one experimental replicate for hF24,

mT69A, and mT69B (**Figure 2A**, **Suppelementary Figure 4D-E**). To further compare differences

in dose-response across experimental repeats, we calculated average IC50 concentrations

(**Figure 2C-D**, **Supplementary Figure 6**). For all hPDOs, we observed no statistically significant

alterations in mean IC50s over experimental repeats calculated for any drug as a function of BME

(**Figure 2C-D**, **Supplementary Figure 6A**). Similarly, mouse organoids exhibited no statistically

significant shifts in drug IC50, regardless of which BME organoids were plated in (**Supplementary**

Figure 6B-C).

Hill slope is another metric of drug potency that has been suggested to offer higher

predictive power than IC50 (*23*). Pairwise comparisons of Hill slope revealed little to no significant

differences among BMEs on a per-drug or per-organoid basis (**Supplementary Figure 5**). The

only instances in which Hill slopes were statistically distinct between BMEs were in mouse

organoids treated with 5-FU, likely due to the resistant nature of these organoids to 5-FU yielding

disparate dose-response curves (**Supplementary Figure 5D-E**).

We also rarely observed changes in average dose-response curve AUCs across BMEs.

Between BME lot, there were not significant AUC differences. AUCs for hF24 treated with

paclitaxel were slightly (1.28- to 1.3-fold) but significantly higher in Cultrex 83 or Cultrex 87

compared to Matrigel 04 (**Figure 2E**). Similarly, calculated AUCs for hM1F treated with

gemcitabine were 1.3-fold higher on average in Cultrex 83 compared to Matrigel 04 (**Figure 2F**).

Lastly, AUCs for mT69A treated with paclitaxel were increased in Ultimatrix 96 compared to

Matrigel 04 (1.28-fold) (**Supplementary Figure 7B**). In all other mouse and human drug-organoid

combinations tested, there were not significant differences in mean AUC across multiple

experiments. These data suggest that while minimal differences in drug response exist, the most

rigorous approach is to complete pharmacotyping analyses using the same commercial BME

source.

We next sought to analyze dose-response curve goodness-of-fit as a parameter of plating

consistency in each BME within and across experimental replicates. We measured Sy.x as an

estimate of goodness-of-fit. In general, higher Sy.x values indicate larger deviations of data points

from the fit regression curve. Sy.x values for Cultrex 83 were relatively consistent across

experimental replicates, with low absolute values (<10%) and low inter-experimental variability

(**Figure 3A-B**). The largest variations in Sy.x across experimental replicates in Cultrex were hF24

treated with SN-38 and 5-FU, and hM1F treated with gemcitabine and oxaliplatin (**Figure 3A-B**).

Sy.x values were larger on average for Cultrex 83 in hM1F treated with oxaliplatin (mean =

20.37%). Cultrex 87 performed consistently as well (ranging from 1.6 – 11.5%), with the most

statistical variance across experiments observed in hF24 treated with gemcitabine (**Figure 3A**).

UltiMatrix 96, relative to the other BMEs, exhibited higher experimental variability in Sy.x values,

with greater variance observed in hF24 treated with gemcitabine (4.1 – 11%) and oxaliplatin (7.6

– 22.3%); and hM1F treated with gemcitabine (4.0 – 15.8%), paclitaxel (4.6 – 14.1%), oxaliplatin

(7.5 – 26%), and trametinib (4.8 – 12.6%) (**Figure 3A-B**). Matrigel 04 yielded consistent and

relatively low Sy.x values (<10%) across all experimental replicates, with the exception of hF24

treated with 5-FU (6.3 – 13.3%) (**Figure 3A**). Similarly, Matrigel 01 demonstrated low and

consistent Sy.x values across treatments, experimental replicates, and hPDOs tested, as

evidenced by low standard deviations and low Sy.x absolute values **(Figure 3A, Supplementary**

Figure 8). Overall, these results indicate better dose-response curve goodness-of-fit from

experiment to experiment when human organoids are cultured in Matrigel.

For mouse organoids, similar trends were observed, albeit with higher absolute Sy.x

values across almost all conditions (range: 4.5 – 40.8%) (**Figure 3C-D**). In general, mouse

organoids are more sensitive to single cell dissociation protocols and have higher growth rates,

both of which contribute to increased variance and necessitate shorter pharmacotyping

experimental time courses (3 days for mouse organoids vs 5 days for hPDOs). Over the course

of 4 experimental replicates, UltiMatrix 96 demonstrated a high degree of statistical variability in

Sy.x values relative to the other BMEs tested, notably for mT69A treated with paclitaxel (9.0 -

24.1%) and oxaliplatin (13.5 - 23.9%), and mT69B treated with gemcitabine (8.81 - 19.8%)

(**Figure 3C-D**). Relative to the other BMEs tested, Cultrex lots also exhibited high levels of

variability in Sy.x. Cultrex 83 exhibited a high degree of variability for mT69A treated with 5-FU

(7.7 - 22.7%) and trametinib (5.9 - 14.7%), and mT69B treated with paclitaxel (6.3 - 17.1%) and

SN-38 (7.3 - 40.8%) (**Figure 3C-D**). Similar variability in Sy.x across experimental replicates was

observed for Cultrex 87 in mT69A treated with oxaliplatin (11.7 - 26.8%) and 5-FU (12.2 - 30.5%),

and mT69B treated with gemcitabine (6.9 - 19.4%), paclitaxel (7.9 - 23.6%), and trametinib (8.2 -

39.9%) (**Figure 3C-D**). Sy.x values were consistent for mT69B treated with paclitaxel when

cultured in Ultimatrix 96 (10.7 - 10.9%) (**Figure 3D**). Both Matrigel 04 and Matrigel 01 showed

relatively consistent Sy.x values in the mouse organoid context but exhibited some biological and

experimental variance. Most notably, mT69A and mT69B are relatively resistant to oxaliplatin and

5-FU and exhibited relatively high Sy.x absolute values (20-30%) in these conditions compared

other drug treatments (**Figure 3C-D**).

Overall, we observed no statistically significant differences in average Sy.x values for both

human and mouse organoids across BMEs and all drugs (**Figure 3, Supplementary Figure 8**).

However, for both human and mouse organoids, both lots of Matrigel exhibited more consistent

Sy.x values across experimental replicates compared to Cultrex or UltiMatrix, as evidenced by

lower variance in Sy.x values across experiments (**Figure 3**). Lot-to-lot variability was more

pronounced for Cultrex compared to Matrigel for both human and mouse organoids. Collectively,

these data indicate that drug dose-response curve fitting is stable across the BMEs tested.

Gene expression and organoid subtype classification are not influenced by BME

Although we did not observe substantial shifts in drug response as a function of BME lot

or source, alterations in intracellular signaling and cell state represented another potential variable

influenced by BME composition. Therefore, we also investigated BME induced changes in gene

expression or PDA subtype classification (*24*). To this end, mouse organoids (mT69A, mT69B,

mT9) and human PDOs (hF24, hM1F, hT1) were each cultured in each BME (Matrigel 04, Matrigel

01, Cultrex 83, Cultrex 87, and Ultimatrix 96) for 3 days and subjected to RNA-seq analyses

(**Supplementary Figure 1**). Multivariate analysis of resultant Z-scores of organoid normalized

counts indicated that both mouse and human samples clustered well based on organoid line

(**Figure 4A**, **Supplementary Figure 9C-D**). However, samples did not cluster significantly based

on BME (**Figure 4A, Supplementary Figure 9C-D, F-G**). Gene expression was largely

unchanged between Matrigel lots in both human and mouse organoids (0-2 differentially

expressed genes, 20 in hM1F) (**Supplementary Figure 9A-B**). Similarly, minimal gene

expression changes were observed in human and mouse organoids between Cultrex lots (0-4

differentially expressed genes) (**Supplementary Figure 9A-B**). Between BME sources, we

observed more changes in gene expression, but these were not consistent between organoid

lines. For example, hT1 (Stage 2B) displayed 522 differentially expressed genes between Matrigel

04 and UltiMatrix, whereas hF24 (Stage 4) and hM1F (Stage 4, lung metastasis) presented 0

(**Supplementary Figure 9A**). Similarly, mT69B (KPC PDA primary tumor) displayed 90

differentially expressed genes between Matrigel 04 and Cultrex 87, whereas mT69A (KPC PDA

metastasis) presented with 13 (**Supplementary Figure 9B**). These results indicate that BME

does not substantially alter PDO gene expression profiles.

Previous work defined molecular subtypes of PDA. Patients with basal-like PDA exhibit

poor prognoses and increased therapeutic resistance compared to the classical subtype (*24*).

Changes to molecular subtype would have major implications on the predictive power of PDOs in

precision medicine approaches. To determine whether BME influenced hPDO subtype

classification, we delineated significant changes to enrichment of basal-like and classical

differentially expressed genes (see **Supplementary File** for gene list). Pairwise comparisons of

subtype gene enrichment indicated no significant difference in basal-like or classical gene

enrichment between Matrigel 04 and Matrigel 01, or between Cultrex 83 and Cultrex 87

(**Supplementary Figure 9E**). Notably, a number of comparisons that were enriched for one

hallmark type were also enriched for the other (**Supplementary Figure 9E**). For instance, hM1F

displayed upregulation of both basal-like as well as classical hallmark genes when cultured in

Cultrex 83, Cultrex 87, or UltiMatrix **(Supplementary Figure 9E)**. Indeed, overall, there was a

greater enrichment for the classical subtype signature, in concordance with previous work

demonstrating that organoid models primarily exhibit RNA states reminiscent of the classical

subtype (*16*). Analysis of individual genes implicated in the etiology of PDA revealed that BME

did not significantly alter hPDO expression levels of *KRAS*, *TP53*, or *CDKN2A.* A slight but

statistically significant increase in *SMAD4* expression was detected in hM1F cultured in Matrigel

01 compared to Matrigel 04 (**Figure 4B**). Similarly, we observed slight yet statistically significant

increases in *ERBB3* in all three hPDOs cultured in Cultrex or UltiMatrix (**Supplementary Figure**

9H). Expression of *EGFR* was increased in hT1 cultured in Cultrex 87 relative to Matrigel 04

(**Supplementary Figure 9H**). However, we did not observe any significant changes in expression

levels of *MYC*, *GATA6*, *MAP2K1*, *MAP2K2*, *SOX9*, *RB1*, *BRCA2*, and *ERBB2*, as well as genes

related to drug resistance such as *HNF1A* and *ABCB1* (**Supplementary Figure 9H**). Overall,

these data indicate that the potential influence of BME on organoid gene expression, cell state,

and subsequent response to targeted therapies, must be carefully considered when developing

protocols for organoid-guided therapy studies.

Discussion

The ability of PDOs to mirror patient genetics, transcriptomics, and drug response in

retrospective studies prompted the onset of several clinical trials to test the benefit of using PDOs

to inform treatment decisions. However, previous studies demonstrated the plasticity of PDOs in

response to varying culture conditions and potential impact on drug response (*16, 17*). With multi-

institutional clinical trials underway, the need to investigate factors that impact the robustness of

PDO genetics, transcriptomics, and drug testing is imperative. Basement membrane extracts are

central to most PDO efforts. Previous studies demonstrated variability in protein composition,

presence of xenogenic bioactive compounds, and scaffold stiffness between batches. Despite

this variability, commercially available BMEs remain critical and prevalent in organoid efforts.

Given the multi-year nature of PDO-related clinical trials, more than one lot of BME will be required

for the duration of these studies. In addition, limitations in availability due to supply chain issues

has necessitated that some efforts switch between alternate commercial sources. However, the

influence of BME source and lot on organoid response to drug treatment was unknown.

To investigate the extent to which BME impacts growth, drug response, and

transcriptomics, we compared various commercially available BMEs on previously established

mouse and human PDA organoids. We consistently observed a decrease in mouse and human

organoid growth when cultured in Cultrex or UltiMatrix compared to Matrigel. While this could

potentially arise from a lack of an adaptation period, multiple passages of mouse organoids in

Cultrex does not rescue their growth rate. Despite this growth deficit, we observed no substantial

shifts in drug response or gene expression as a function of BME source or lot. The generation

efficiency of PDA organoids in Matrigel is 75% (*8*). This study made use of previously established

organoids. Given the impact of BME source on PDO growth, it will be important to delineate the

effect of BME on isolation efficiency in future work. For established organoids, Matrigel, Cultrex,

or UltiMatrix BMEs are all viable options for pharmacotyping experiments. Altogether, this work

demonstrates that precision medicine approaches using organoids are robust, and that ongoing

clinical trials are unlikely to be affected by different lots or commercial sources of BME.

Methods

Organoids and cell culture conditions

Organoids used in this study were generated at Cold Spring Harbor Laboratory (*7, 8, 25*).

Human patient-derived and mouse organoids were cultured as described. In short, mouse

organoid media contained Advanced DMEM/F12, HEPES, Glutamax, Penicillin/Streptomycin,

EGF, FGF-10, Gastrin, A83-01, B27 supplement, *N*-acetylcysteine, nicotinamide, Noggin, and R-

spondin1. For human organoid culture, Wnt3a was also included in the media. Organoid

nomenclature is defined as: hT – human tumor obtained from resection; hF – human fine-needle

biopsy obtained by fine-needle aspiration or core biopsy; hM – human metastasis obtained from

direct resection of metastases following rapid autopsy or VATS resection; mT – murine tumor. All

organoid models were routinely tested for *Mycoplasma* at Salk Institute. Additional hPDO and

mouse organoid characteristics are available in **Table S1** and **Table S2**.

Basement membrane extracts

Both human and mouse organoids were maintained in Corning Matrigel Lot #1062004

during the growth and expansion phase. For pharmacotyping comparisons, organoids were plated

in either Corning Matrigel (Growth Factor Reduced, Phenol Red Free) Lot #1062004 (Matrigel

04), Corning Matrigel (Growth Factor Reduced, Phenol Red Free) Lot #0287001 (Matrigel 01),

RnD Cultrex Reduced Growth Factor BME Lot #1564183 (Cultrex 83), RnD Cultrex Reduced

Growth Factor BME Lot #1586187 (Cultrex 87), or Cultrex UltiMatrix Reduced Growth Factor BME

Lot #1637796 (UltiMatrix 96).

Pharmacotyping of organoids

Organoids were dissociated into single cells using a diluted solution of TrypLE Express

(Thermo Fisher). Equal numbers of single cells (1,500 viable cells per well) were plated in a 20

uL suspension of 10% BME in ultra-low attachment 384 well plates (Corning). Twenty-four hours

after plating, reformation of organoids was visually verified and therapeutic compounds were

applied using a digital dispenser (Tecan). Chemotherapies were tested in triplicate 10-point dose-

response curves. Gemcitabine, paclitaxel, SN-38 (active metabolite of irinotecan), and trametinib

ranged from 0.5nM – 5µM; oxaliplatin and 5-fluorouracil ranged from 50nM – 100µM. Compounds

were dissolved in DMSO, and all treatments were normalized to 0.5% DMSO content. Mouse

organoids underwent treatment for 3 days, while human organoids underwent treatment for 5

days. After treatment, cell viability was assessed using Cell Titer Glo (Promega) per

manufacturer's instructions on a Tecan Spark Cyto plate reader. A four-parameter log-logistic

function with upper limit equal to the mean of the lowest dose values was fit to the data (viability

vs. dose) with Graphpad Prism 9. The half maximal inhibitory concentration (IC50) values, area

under the curve (AUC), and standard deviation of the residuals (Sy.x) for each dose-response

curve were calculated using Graphpad Prism 9. Each pharmacotyping experiment was carried

out at least two times.

RNA isolation

For RNA-seq comparisons, organoids were maintained in Corning Matrigel Lot #1062004

(Matrigel 04) and then plated in either Corning Matrigel (Growth Factor Reduced, Phenol Red

Free) Lot #1062004 (Matrigel 04), Corning Matrigel (Growth Factor Reduced, Phenol Red Free)

Lot #0287001 (Matrigel 01), RnD Cultrex Reduced Growth Factor BME Lot #1564183 (Cultrex

83), RnD Cultrex Reduced Growth Factor BME Lot #1586187 (Cultrex 87), or Cultrex UltiMatrix

Reduced Growth Factor BME Lot #1637796 (Ultimatrix 96). Each BME condition was plated in

triplicate, and organoids were grown for 3 days before harvesting in TRIzol (Life Technologies)

and snap frozen. RNA was isolated using the RNeasy Mini Kit (Qiagen). RNA quality control was

performed for all samples using a Qubit Fluorometer (Life Technologies) and TapeStation (RIN

greater than 8.5) (Agilent) before RNA-seq analyses.

RNA-seq analyses

Library construction was conducted using the Truseq RNA library prep kit (Illumina) with

500ng RNA input. Raw reads were trimmed with Trim Galore v0.4.4_dev

(https://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) and quality-checked with

FastQC v0.11.8 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). Trimmed reads

were then aligned to the hg38 human reference genome with STAR aligner v2.5.3a (*26*), and

converted to gene counts with HOMER's analyzeRepeats.pl script (*27*).

Differential gene expression analysis

Gene counts where normalized and queried for differential expression using DESeq2

v1.30.0 (*28*). For each pairwise comparison, genes with fewer than 10 total raw counts across all

samples were discarded prior to normalization, and genes with an absolute log2foldchange > 1

and an FDR-corrected p-value ≤ 0.05 were pulled as significant.

Statistics

A four-parameter log-logistic function with upper limit equal to the mean of the lowest dose

values was fit to the dose-response data (viability vs. dose) with Graphpad Prism 9. The half

maximal inhibitory concentration (IC50) values, area under the curve (AUC), and standard

deviation of the residuals (Sy.x) for each dose-response curve were calculated using Graphpad

Prism 9. Each pharmacotyping experiment was carried out for n = 2-4 experimental replicates.

Differences among means were analyzed using 1-way ANOVA with Dunnett's multiple

comparisons test. Outliers were determined using Grubbs' test $\alpha = 0.05$.

To compare estimated dose-response curve parameters across different BMEs within an

experimental replicate, t-tests were conducted on the IC50 and Hill slope to test the null

hypothesis of zero difference in the parameters among BMEs using R 4.0.3 and package drc (*22,*

29). The Bonferroni method was used to adjust for multiple comparisons, and a comparison

between a pair of BMEs was considered significant if the *P* value was below 0.05 divided by the

total number of pairwise comparisons. Consequently, pairwise t-tests were considered significant

if $P < 0.00027778$ (hPDO) or $P < 0.00041667$ (mouse organoids).

To assess the model fitting and compare the log-logistic models with other alternatives,

including Weibull models, a sensitivity analysis was conducted. The Akaike Information Criterion

(AIC) was used for the comparison. The four-parameter log-logistic (LL4) model consistently

yielded smaller AIC values, suggesting this model as the most appropriate model-fitting strategy.

Analyses presented from the aforementioned t-tests on IC50 and Hill slope were conducted first

on data fitted with the LL4 model, then on data fitted with Weibull models when appropriate.

Author contributions

JL, SO, and KP maintained organoid cultures, acquired materials, and designed and

conducted the experiments. JL and XL acquired and analyzed the data. KL performed statistical

analysis on RNA-seq data. JZ directed and provided statistical analysis for dose-response curve

comparisons. JL, XL, JZ, and DE wrote the manuscript. DE conceived the project and directed

the experiments.

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Figure legends

Figure 1. Basement membrane extract impacts growth of mouse and human organoids but

does not significantly shift dose-response curves. (**A**) Growth of human patient-derived

organoids hF24 and hM1F cultured in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix

96 for 5 days as determined by levels of intracellular ATP (Cell Titer Glo - CTG). Data represent

mean ± SD. Statistical significance was determined by 1-way ANOVA. ****$P \leq 0.0001$. (**B**) Growth

of mouse organoids mT69A and mT69B cultured in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex

87, or UltiMatrix 96 for 3 days as determined by levels of intracellular ATP (CTG). Data represent

mean ± SD. Statistical significance was determined by 1-way ANOVA. ****$P \leq 0.0001$. (**C**) Dose-

response curves for hF24 treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and

trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data

represent mean ± SD of triplicate values fitted with a four-parameter log-logistic function. (**D**)

Dose-response curves for mT69B treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU,

and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96.

Data represent mean ± SD of triplicate values fitted with a four-parameter log-logistic function.

Figure 2. Basement membrane extracts exert minimal effects on drug IC50 and dose-

response AUC. (**A-B**) P value heatmaps from pairwise comparisons of IC50 between BMEs for

hF24 and hM1F. Each square represents pairwise t-tests. After Bonferroni adjustment, t-tests

were considered significant if $P < 0.00027778$. Statistically significant comparisons are denoted

by an asterisk and orange border. (**C-D**) Gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and

trametinib IC50 values (M) for hF24 and hM1F across different BMEs. Data represent mean ± SD

416 of 3 experimental replicates. (**E-F**) Gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and

417 trametinib AUC values for hF24 and hM1F across the different BMEs. Data represent mean ± SD

418 of 3 experimental replicates. Statistical significance was determined by 1-way ANOVA. $*P \leq 0.05$,

419 $***P \leq 0.001$ vs. Matrigel 04.

421 **Figure 3. Dose-response curve goodness of fit is not significantly altered by basement**

422 **membrane extract.** (**A-B**) Standard deviation of the residuals (Sy.x) for hF24 and hM1F treated

423 with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib across the different BMEs.

424 Data represent mean ± SD of 3 experimental replicates. (**C-D**) Sy.x for mT69A and mT69B treated

425 with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-fluorourical (5-FU), and trametinib across the

426 different BMEs. Data represent mean ± SD of 4 experimental replicates. Outliers were determined

427 using Grubbs' test α = 0.05.

429 **FIgure 4. Human patient-derived organoid gene expression profiles are consistent across**

430 **basement membrane extract types.** (**A**) Expression heatmap of Z-scores of normalized counts

431 of classical or basal-like hallmark genes in hF24, hM1F, and hT1 when cultured in different BMEs.

432 (B) Normalized counts for hallmark PDA genes *KRAS, TP53, SMAD4,* and *CDKN2A*. Data

433 represent mean ± SD of 3 technical replicates. Statistical significance was determined by 1-way

434 ANOVA. $**P \leq 0.01$ vs. Matrigel 04.

436 **Supplementary Figure 1. Experimental outline.** Three biological replicates of human patient-

437 derived organoids and mouse organoids were selected based on primary sample type and

438 disease stage. Each organoid line was expanded to sufficient quantities for experimentation in

439 Matrigel 04. Organoids were then single-cell dissociated and either plated in triplicate in 6-well

440 plates for RNA isolation and subsequent RNA-seq, or plated for pharmacotyping in five 384-well

441 plates in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Organoids were allowed

to recover overnight. Next, organoids were treated with drugs and incubated for 5 days (human

organoids) or 3 days (mouse organoids), followed by Cell Titer Glo to assess organoid viability.

Supplementary Figure 2. Proliferation of human and mouse organoids is not significantly

altered by basement membrane extract. (**A**) Data for n = 3 experimental replicates of hF24

proliferation in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent

mean ± SD. **$P \leq 0.01$, ****$P \leq 0.0001$ vs. Matrigel 04. (**B**) Data for n = 3 experimental replicates

of hM1F proliferation in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data

represent mean ± SD. **$P \leq 0.01$, ****$P \leq 0.0001$ vs. Matrigel 04. (**C**) Data for n = 2 experimental

replicates of hT1 proliferation in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96.

Data represent mean ± SD. ****$P \leq 0.0001$ vs. Matrigel 04. (**D**) Data for n = 4 experimental

replicates of mT69A proliferation in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix

96. Data represent mean ± SD. *$P \leq 0.05$, **$P \leq 0.01$, ****$P \leq 0.0001$ vs. Matrigel 04. (**E**) Data for

n = 4 experimental replicates of mT69B proliferation in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex

87, or UltiMatrix 96. Data represent mean ± SD. **$P \leq 0.01$, ****$P \leq 0.0001$ vs. Matrigel 04.

Supplementary Figure 3. Dose response curves are consistent regardless of basement

membrane extract used. (**A**) Data for n = 3 experimental replicates of hF24 response to

gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib while cultured in Matrigel 04,

Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD. (**B**) Data for n =

3 experimental replicates of hM1F response to gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU,

and trametinib while cultured in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96.

Data represent mean ± SD. (**C**) Data for n = 2 experimental replicates of hT1 response to

gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib while cultured in Matrigel 04,

Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD. (**D**) Data for n =

4 experimental replicates of mT69A response to gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU,

and trametinib while cultured in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96.

Data represent mean ± SD. (**E**) Data for n = 4 experimental replicates of mT69B response to

gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib while cultured in Matrigel 04,

Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD.

Supplementary Figure 4. Statistically significant differences in IC50 within experimental

replicates occur on a per-drug and per-organoid basis. (**A-C**) Heatmaps of *P* values from

pairwise comparisons of IC50 between BMEs for each experimental repeat of hF24 (**A**), hM1F

(**B**), or hT1 (**C**). Each square represents significance of pairwise t-tests. After Bonferroni

adjustment, t-tests were considered significant if *P* < 0.00027778. Statistically significant

comparisons are denoted by an asterisk and orange border. (**D-E**) Heatmaps of *P* values from

pairwise comparisons of IC50 between BMEs for each experimental repeat of mT69A (**D**) or

mT69B (**E**). Each square represents significance of pairwise t-tests. After Bonferroni adjustment,

t-tests were considered significant if *P* < 0.00041667. Statistically significant comparisons are

denoted by an asterisk and orange border.

Supplementary Figure 5. Dose response curve Hill slopes remain consistent across

basement membrane extract culture conditions. (**A-C**) Heatmaps of *P* values from pairwise

comparisons of Hill slope between BMEs for each experimental repeat of hF24 (**A**), hM1F (**B**), or

hT1 (**C**). Each square represents significance of pairwise t-tests. After Bonferroni adjustment, t-

tests were considered significant if *P* < 0.00027778. Statistically significant comparisons are

denoted by an asterisk and orange border. (**D-E**) Heatmaps of *P* values from pairwise

comparisons of Hill slope between BMEs for each experimental repeat of mT69A (**D**) or mT69B

(**E**). Each square represents significance of pairwise t-tests. After Bonferroni adjustment, t-tests

were considered significant if *P* < 0.00041667. Statistically significant comparisons are denoted

by an asterisk and orange border.

Supplementary Figure 6. IC50 values remain consistent across basement membrane extract culture conditions. (**A**) IC50 values (M) for hT1 treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 2 experimental replicates. (**B**) IC50 values (M) for mT69A treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 4 experimental replicates. (**C**) IC50 values (M) for mT69B treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 4 experimental replicates. Outliers were determined using Grubbs' test $\alpha = 0.05$.

Supplementary Figure 7. AUC values are consistent across basement membrane extract culture conditions. (**A**) AUC values for hT1 treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 2 experimental replicates. (**B**) AUC values for mT69A treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 4 experimental replicates. Statistical significance was determined by 1-way ANOVA. *$P \leq 0.05$ vs. Matrigel 04. (**C**) AUC values for mT69B treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-FU, and trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data represent mean ± SD of 4 experimental replicates.

Supplementary Figure 8. Standard deviation of the residuals does not statistically change as a function of basement membrane extract used. Standard deviation of the residuals (Sy.x) for hT1 treated with gemcitabine, paclitaxel, SN-38, oxaliplatin, 5-fluorourical (5-FU), and

trametinib during culture in Matrigel 04, Matrigel 01, Cultrex 83, Cultrex 87, or UltiMatrix 96. Data

represent mean ± SD of 2 experimental replicates. Outliers were determined using Grubbs' test

α = 0.05.

Supplementary Figure 9. Global gene expression profiles are consistent across basement

membrane extract conditions for both mouse and human organoids. (**A**) Differential gene

expression among human patient-derived organoids cultured in Matrigel 04 (MG004), Matrigel 01

(MG001), Cultrex 83 (Cultrex 183), Cultrex 87 (Cultrex 187), or UltiMatrix 96 (Ultimatrix). Numbers

represent total number of genes with an adjusted *P* value of differential expression ≤ 0.05 and an

absolute log2(foldchange) > 1 for all pairwise comparisons of basement membrane extracts within

individual organoid lines and within species. (**B**) Differential gene expression among mouse

organoids cultured in Matrigel 04 (MG004), Matrigel 01 (MG001), Cultrex 83 (Cultrex 183), Cultrex

87 (Cultrex 187), or UltiMatrix 96 (Ultimatrix). Numbers represent total number of genes with an

adjusted *P* value of differential expression ≤ 0.05 and an absolute log2(foldchange) > 1 for all

pairwise comparisons of basement membrane extracts within individual organoid lines and within

species. (**C**) Principal component analysis of human patient-derived organoid gene expression

within species and individual organoid lines. (**D**) Principal component analysis of mouse organoid

gene expression within species and individual organoid lines. (**E**) Heatmaps of basal-like or

classical hallmark gene enrichment between basement membrane extract comparisons for all

human patient-derived organoid lines (top row) and individual lines. Each square represents

significance of enrichment in the differentially expressed genes between two basement

membrane extracts. The differentially expressed genes in the BME listed on the y-axis are queried

for enrichment. Squares are labeled with *P* value. Black squares = ns. (**F**) Expression heatmap

of all genes in human patient-derived organoids cultured in different BMEs. Z-scores of

normalized counts. (**G**) Expression heatmap of all genes in mouse organoids cultured in different

basement membrane extracts. Z-scores of normalized counts. (**H**) Normalized counts for select

genes of interest in hF24, hM1F, and hT1 cultured in different BMEs. Data represent mean ± SD

of 3 technical replicates. *$P \leq 0.05$, **$P \leq 0.01$ vs. Matrigel 04.

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Figure 1

Figure 2A-B

Figure 2C-D

Figure 2E-F

Figure 3A-B

Figure 3C-D

Figure 4

Organoids

Human
hF24 - Stage IV EUS FNA
hM1F - Stage IV lung metastasis
hT1 - Stage IIB resection

Mouse
mT69A - murine metastasis
mT69B - murine primary tumor
mT9 - murine primary tumor

Color key

① Expansion

Matrigel 04

②a Plate for
RNA isolation
RNA-seq/BME

②b Plate for
pharmacotyping/BME

Matrigel 04
Matrigel 01
Cultrex 83
Cultrex 87
UltiMatrix 96

④ Recovery (24h)

10-point dose-response
Tecan d300e
Gemcitabine
Paclitaxel
SN-38
Oxaliplatin
5-FU
Trametinib

⑤ Treatment
Human - 5d
Mouse - 3d

Assay Cell Viability
Cell Titer Glo
Tecan Spark Cyto

*Created with
BioRender.com*

Supplementary Figure 1

Supplementary Table 1

PDO	Origin	Site	Type of sample	Sex	Age	Race	Stage	KRAS (allele frequencies)	TP53 (allele frequencies)	SMAD4 (allele frequencies)	CDKN2A (allele frequencies)
hF24*	H. sapiens	Pancreas	EUS FNA	F	57	Caucasian	4	G12V 82%	F113V (100%)	LOSS (N/A)	DEEP LOSS (N/A)
hM1F*	H. sapiens	Lung	RAP	M	55	Caucasian	4	G12D 73%	R175H (100%)	WT (N/A)	WT (N/A)
hT1*	H. sapiens	Pancreas	Resection	M	65	Caucasian	2B	G12V 39%	R213* (100%)	WT (N/A)	DEEP LOSS (N/A)

*H. Tiriac *et al.*, Organoid Profiling Identifies Common Responders to Chemotherapy in Pancreatic Cancer. *Cancer Discov* **8**, 1112-1129 (2018).

Supplementary Table 2

PDO	Origin	Sex	Site	Type of sample
mT69A	M. musculus	F	Pancreas	KPC B6, PDAC local pancreatic metastasis
mT69B	M. musculus	F	Pancreas	KPC B6, PDAC primary tumor
mT9	M. musculus	F	Pancreas	KPC PDAC primary tumor

Supplementary Figure 2A-C

Supplementary Figure 2D-E

Supplementary Figure 3A

Supplementary Figure 3B

C

Supplementary Figure 3C

Supplementary Figure 3D

Supplementary Figure 3E

Supplementary Figure 4A – IC50

Supplementary Figure 4B – IC50

C

Supplementary Figure 4C – IC50

D

Supplementary Figure 4D – IC50

E

Supplementary Figure 4E – IC50

Supplementary Figure 5A – Hill Slope

Supplementary Figure 5B – Hill Slope

Supplementary Figure 5C – Hill Slope

D

Supplementary Figure 5D – Hill Slope

E

Supplementary Figure 5E – Hill Slope

Supplementary Figure 6A-C

Supplementary Figure 7A-C

Supplementary Figure 8

Cells labeled by number of differentially expressed genes (abs(lfc)>1 and FDR ≤ 0.05)

Cells labeled by number of differentially expressed genes (abs(lfc)>1 and FDR ≤ 0.05)

Supplementary Figure 9A-B

Supplementary Figure 9C-D

Supplementary Figure 9E

F Expression Heatmap of All Genes
Z-Scores of Human Organoid Normalized Counts

G Expression Heatmap of All Genes
Z-Scores of Mouse Organoid Normalized Counts

Supplementary Figure 9F-G

H

Supplementary Figure 9H

Supplementary Figure 9H