# Rational cell culture optimization enhances experimental reproducibility in cancer cells

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Abstract
Optimization of experimental conditions is critical in ensuring robust experimental
reproducibility. Through detailed metabolomic analysis we found that cell culture conditions
significantly impacted on glutaminase (GLS1) sensitivity resulting in variable sensitivity and
irreproducibility in data.
Baseline metabolite profiling highlighted that untreated cells underwent significant changes
in metabolic status. Both the extracellular levels of glutamine and lactate and the intracellular
levels of multiple metabolites changed drastically during the assay. We show that these
changes compromise the robustness of the assay and make it difficult to reproduce.
We then devised 'metabolically rationalized standard' assay conditions, in which
glutaminase-1 inhibition reduced glutamine metabolism differently in both cell lines assayed,
and decreased the proliferation of one of them. The adoption of optimized conditions such
as the ones described here should lead to an improvement in reproducibility and help
eliminate false negatives as well as false positives in these assays.
Keywords: Cell culture, metabolomics, cancer cell lines, non-small cell lung cancer, drug discovery.

#### 36 1 Introduction

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Reproducibility has increasingly become a topic of concern in biomedical research<sup>1,2</sup>. 38 Scientists acknowledge that they fail to reproduce even their own experiments, let alone 39 those of their colleagues around the globe<sup>3</sup>. When testing a potential anticancer drug, a 40 novel and potent allosteric inhibitor specific for the glutaminase-1 enzyme (EC 3.5.1.2), we 41 42 initially experienced a similar irreproducibility. Our focus on metabolomics led us to 43 experiments that then produced an explanation for the lack of reproducibility, and employed a more comprehensive assay development approach which we believe can be of benefit for 44 45 the scientific community.

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47 One of the initial steps in the development of therapeutic agents for cancer involves testing these agents *in vitro* using human cancer cell lines as experimental models<sup>4,5</sup>. Using primary 48 cell lines in culture, the effects of compounds or perturbations on cell proliferation, DNA 49 50 replication or cell death is generally investigated over a period of time. These types of read-51 out are highly dependent on cell physiology and as such these assays need to fulfill a number of conflicting conditions. On the one hand, cells need to be kept in culture long 52 53 enough to attain a steady state and for the effects of treatments to be observed. On the 54 other hand, they should not be kept there too long because of the gradual accumulation of waste products that can be inhibitory or toxic to cells, such as lactate and ammonia<sup>6</sup>. The 55 56 concentration of nutrients will fall over time, pH will change, and as cells grow and divide, 57 space may become limiting. As cell density increases, effects of paracrine signaling become 58 more pronounced and as cells reach confluence, contact inhibition may suppress proliferation. Although cancer cells are able to proliferate for some time after reaching 59 60 confluence by then accumulating on top of one another, this crowding still limits individual 61 cells' access to nutrients and growth factors<sup>7</sup>, eventually resulting in cell cycle arrest and apoptosis, but long before then, in shifts in cell metabolism. Cell viability assays are affected 62 63 by the metabolic state of the cells and therefore any shift in metabolic states during the 64 assay, and particularly different shifts between sensitive and resistant cell lines, would confound the outcome of such assays. 65

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Recently, Haibe-Kains *et al.* highlighted multiple inconsistencies between two large-scale
pharmacogenomic studies, the Cancer Genome Project (CGP<sup>8</sup>) and the Cancer Cell Line
Encyclopedia (CCLE<sup>9</sup>), *viz.* the sensitivity profiles of common cell lines and drugs<sup>10</sup>. It has
been suggested that differences in the cell culture conditions were amongst the reasons for

these discrepancies<sup>11</sup> and that consistency should be achievable with appropriate laboratory 71 and analysis protocols<sup>12</sup>. For example, for each cell line the CGP study determined the 72 73 seeding density that ensured that each was still in the growth phase at the end of the assay (~70% confluence), whilst the seeding density was not reported for the CCLE study<sup>8</sup>. In 74 75 addition, for adherent cells, the test compound was added 'around 12-24 hours' after 76 seeding cells and studied over a further 72-84 hours in the CCLE study, whereas in the 77 CGP study this was added 1 day after seeding and assayed 72 hours after treatment. This 78 lack of standardized and well-described culture conditions is common to most literature in 79 this field (see refs. <sup>13-19</sup> for examples). Living cells are complex; they adjust to altering 80 environments, by quick metabolic or somewhat slower gene-expression regulation and this 81 may readily change the extent to which any target limits cell physiology and survival. This 82 can make results of drug targeting studies irreproducible unless the relevant environmental 83 conditions are well controlled at the appropriate time scale. Both academia and the 84 pharmaceutical industry recognize the necessity of much more thorough standardization to improve reproducibility <sup>20</sup>. 85

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87 The metabolic performance of the cell lines during drug targeting assays is not assessed 88 routinely, or at least not reported. Metabolic changes could have strong implications for 89 therapeutic targets in, or affected by, intermediary metabolism. Metabolic enzymes involved 90 in cellular proliferation and growth have been identified as altered in cancers, either through 91 the expression of cancer-specific isoforms, through mutations, or through altered expression levels<sup>21</sup>. And it is precisely these targets that are witnessing revived interest of late<sup>22,23</sup>: these 92 altered metabolic pathways are now being targeted directly, used to enhance the efficacy of 93 94 existing therapeutic agents or to overcome resistance to current treatment strategies for cancer. In addition, anti-cancer drugs that do not target metabolism itself are often assayed 95 96 in survival based assays. If metabolism is so involved in cell survival, its variability and 97 during survival based assays could therefore be a prime cause of irreproducibility of the 98 outcome of the many experimental assays. We thus investigated whether variability in 99 cellular metabolic status is linked with different phenotypic responses.

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Here we show how culture conditions widely used to investigate the effects of an inhibitor of the glutaminase-1 enzyme on cell proliferation and metabolism, result in drastic and rapid changes in the metabolic state of the cells, compromising the robustness and reproducibility of the results. We then present the pipeline we engage in such cases in order to identify

these changes and to optimize culture conditions accordingly. The reward is a robust studyof the effects of a potentially important anti-proliferative agent.

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### 109 2 Results

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To investigate the effect of an inhibitor (GLS1i) of the glutaminase-1 enzyme (GLS1, 111 112 EC 3.5.1.2), on cell metabolism and proliferation, we started by employing culture conditions 113 that are widely used in the scientific literature for proliferation assays and should enable the application of metabolomics<sup>13-19</sup>. We seeded cells at a density of  $8 \times 10^5$  cells/well in 1 mL of 114 115 culture media 24 hours prior to commencing the experiment at a time point denoted as time 116 0 by adding 1.0  $\mu$ M of a GLS1 inhibitor (see Materials and Methods section 1.2). The effect 117 of this inhibitor on cell survival was determined 48-hours later. We used two cell lines, A549 118 and H358, that are dependent on glutamine for proliferation<sup>24</sup>, but differ in sensitivity to a novel and potent inhibitor of GLS1 activity developed jointly by AstraZeneca and Cancer 119 120 Research Technology: proliferation of A549 cells is inhibited by this 'GLS1i', whereas 121 proliferation of H358 cells is insensitive to GLS1 inhibition (Figure S1).

# 122 **2.1** The problem: the inhibitor does not seem to work

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We had expected that treatment with a GLS1 inhibitor would lead to a reduced consumption 124 125 of glutamine, a reduced production of glutamate, an increased intracellular concentration of 126 glutamine, a reduced intracellular concentration of glutamate and reduced intracellular 127 concentrations of all TCA cycle intermediates, particularly in the GLS1i sensitive A549 cell 128 lines. The initially observed effects of GLS1i treatment were very different to what we expected (Table 1): GLS1i treatment did not affect cell numbers in either cell line when 129 130 compared to control treatment (Figure S2a). Equally unexpectedly, the amount of glutamine 131 consumed was reduced to a much greater extent in the resistant cell line than in the 132 sensitive cell line (Figure 1a). Intracellular glutamine concentrations were raised in treated 133 conditions in both cell lines (Figure 1b), particularly in the resistant H358 cell lines compared 134 to controls, in agreement with our expectations. However, intracellular glutamate concentrations were reduced in the GLS1i resistant H358 cell lines only (Figure 1c). The 135 136 abundance of TCA cycle intermediates, such as alpha-ketoglutarate ( $\alpha$ -KG), citrate and 137 fumarate, was unaffected by treatment of A549 cells with GLS1i. Only a-KG was reduced in 138 H358 cells (Figure S3).

A first clue on what could be responsible for the lack of effect of the metabolic inhibitor on the cell proliferation and the paradoxical effects on metabolism, was the extracellular concentration of glutamine at the end of this assay: this was very close to undetectable levels, suggesting that during the assay cells had been subject to a concentration of glutamine varying between 2mM and 0 mM. In the absence of glutamine, an inhibitor of glutaminase should perhaps not be expected to have any effect; either directly or due to metabolic rewiring.

## 147 **2.2** Explanation: The cellular environment is uncontrolled

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To understand why GLS1i treatment in the above assay failed to show any significant effects on proliferation or metabolism by A549 and H358 cells we examined the changes in cell numbers and intracellular and extracellular metabolites with enhanced time resolution (Figure 2 and Figure S4).

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154 Our results suggest that, throughout the course of the assay, the cells' environment in 155 control conditions was changing in ways that would be expected to interfere with the cells' internal state<sup>25</sup>. Firstly, the concentration of lactate in spent media 1 hour into the assay was 156 already above 10 mM in both cell lines (Figure 2a). H358 cells had already secreted nearly 157 158 20 mM of lactate by this point, suggesting that most of the glucose available in culture media 159 had already been consumed. In H358 cells this increase in lactate continued over the time 160 points sampled, but in A549 cells the concentration of lactate reached its maximum level of 161 around 14 mM 6 hours post dosing. Secondly, the concentration of glutamine in spent media 162 was already reduced by  $\geq$  70% 1 hour into the assay in both cell lines and undetectable by 163 24 hours and 48 hours post dose in A549 cells and H358 cells, respectively (Figure 2b).

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165 The fluctuating environment that the cells were exposed to in this assay likely contributed to 166 the changes in the specific growth rate of these cells: a small increase in cell numbers was observed over the first 24 hours post dosing (Figure 2c) but was much slower than the 167 expected growth kinetics of these two cell lines<sup>26</sup>. Moreover, between 24 and 48 hours post 168 169 dosing, the number of cells in control conditions seemingly *decreased*. This could be due to the depletion of glutamine, glucose or other essential substrates not measured, to the 170 171 increases in the concentration of lactate, to the resulting decrease in pH, or to contact 172 inhibition of the cells. Deprivation of nutrients and growth factors has been shown to lead to 173 cell cycle arrest and subsequently cell death in NSCLC cell lines indicating that this is a 174 possible explanation for the changes seen in cell numbers in this type of assay<sup>27-29</sup>. The drastic reductions in glutamine could influence normal cell metabolism and physiology, as a 175 176 result of forcing cells to switch to alternative fuel sources and to deal with the problem of ammonium toxicity<sup>6</sup>. Indeed, the intracellular concentration of glutamine fell drastically 177 178 throughout the assay, as did the abundance of other metabolites, albeit to a smaller extent 179 (Figure S4). The high concentration of secreted lactate in spent media is likely to be accompanied by drastic acidification of culture media and cellular damage<sup>30,31</sup>; the culture 180 181 media had a buffering capacity of around 20 mM/pH unit, whilst some 20 mM of lactic acid 182 may have been produced, a large proportion of which was likely derived from glucose.

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184 Our results suggest that these commonly used assay conditions are unsuitable for185 comparing inhibitors of molecular targets with each other.

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# 187 2.3 Assay optimization: Reducing the seeding density and increasing culture 188 volume stabilizes cellular state

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Increasing the volume of culture media alone from 1 to 3 mL was not sufficient to avoid 191 192 these problems of variations in metabolic state (Figure S5): Whilst this reduced the 193 magnitude of changes in the extracellular concentrations of glucose and glutamine, these 194 key nutrients were still close to depletion 72 hours after seeding. pH changes remained 195 within acceptable ranges in A549 cells, but not in H358 cells where pH changed by > 1 pH 196 unit. A slight improvement in the proliferation of these two cell lines was observed but this 197 was still much slower than expected. Confluence was reached early into the assay (24-36 hours after seeding) when the cell lines were seeded at a density of  $8 \times 10^5$  cells/well 198 199 (Figure 3, upper purple line). This, together with the drastic reductions in nutrient 200 concentrations through the assay, may account for the reduced rate of proliferation observed in our previous assays as a result of the induction of cell cycle arrest and apoptosis<sup>7,27-29,32</sup>. 201

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Indeed, we observed steadier metabolic conditions and cell proliferation when the initial seeding density of cells was reduced *and* the volume of culture media increased from 1 to 3 mL (Figure 3 and Figure S5). The period of time during which cells were able to grow exponentially was also increased (Figure 3). Ensuring that confluence remained below ~ 80 % throughout the assay window (24–72 hours post seeding), or that this level of confluence was reached as late as possible in the assay, required a significant reduction in the initial

seeding density of cells, and this was cell-line specific. The time required to recover from reseeding also differed between cell lines and was affected by the initial seeding density. This initial lag phase was very short in duration for A549 cells (< 6 hours) compared to the approximately 24 hours required by H358 cells (Figure 3), which extended beyond 24 hours when H358 cells were seeded at  $2 \times 10^5$  cells/well. These differences in growth kinetics could well compromise inhibitor assays.

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216 Lowering the initial seeding density of cells also reduced the magnitude of changes in the 217 concentrations of key nutrients such as glucose and glutamine (Figure S5b and c), and in pH 218 (Figure S5a) throughout the assay window (24-72 hours post seeding). In the case of the 219 H358 cell line, using these conditions, assays beyond 48 hours after seeding may not be 220 suitable since these cells displayed a high rate of glucose consumption (Figure S5b) and the 221 corresponding lactate secretion would lead to significant reductions in pH (Figure S5a). When H358 cells were seeded at 3 x 10<sup>5</sup> cells/well, the concentration of glucose reached 222 limiting levels (~2 mM) 72 hours after seeding, which would constitute 48 hours post dosing 223 224 in an assay where treatment was applied 24 hours after seeding (Figure S5b).

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We conclude that, in order to ensure that (1) cells are in exponential growth from 24 hours after seeding, (2) confluence is reached as late as possible, and (3) changes in glucose, glutamine and pH are kept to a minimum, the volume of culture media should be increased up to 3 mL and seeding density reduced according to individual cell line growth kinetics. In our case, seeding A549 cells at a density of  $2 \times 10^5$  cells/well or less, and H358 cells at around  $3 \times 10^5$  cells/well in 3 mL of culture media, fulfills these criteria.

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# 233 2.4 Optimized in vitro culture conditions enable successful hypothesis validation 234 and discovery

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236 To validate the expected improvement in assay performance we then seeded A549 and H358 cells at a density of  $1.5 \times 10^5$  and  $3 \times 10^5$  cells/well respectively in 3 mL of media in a 237 6 well plate format. Cells were growing exponentially at rates comparable to those reported 238 239 in the literature<sup>26</sup> (Figure S6) throughout the assay in control conditions. From plates prepared in parallel, the levels of various metabolites in cell and spent media extracts as well 240 241 as cell numbers were measured for 24 hours after treatment with 1 µM of the GLS1 inhibitor. 242 In agreement with our expectations (Table 1), treatment with the GLS1 inhibitor over 24 243 hours led to a reduction in cell numbers of around 20% in A549 cells but not in H358 cell 244 lines (Figure 4a). Throughout the assay, the changes in the cells' environment were now 245 minimal in both cell lines regardless of treatment conditions (Figure 4b-f): the concentrations 246 of glucose and glutamine were reduced by less than 50% over the assay and the lactate secreted caused a pH drop < 1 unit under these improved assay conditions. The amount of 247 248 glutamine consumed appeared reduced in both cell lines by treatment with the GLS1 249 inhibitor although these changes were small and only statistically significant in A549 cells: 250 the achieved stability of culture conditions had the consequence that differences in cellular 251 metabolism were no longer strongly reflected in the changes of the exometabolome, such 252 that assay conditions were now under control and steady.

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254 We therefore assessed intracellular metabolism to investigate whether, under the optimized 255 conditions, the predicted effects of GLS1i on intracellular metabolites were observed that 256 had not been observed under the previous unstable conditions (Table 1). Our results confirm 257 that the glutaminase inhibitor engaged with the intended target: large reductions (p < 0.01) in 258 glutamate were observed in both cell lines (Figure 5a). Only minor increases in the 259 concentration of glutamine were seen, probably as a result of rapid equilibration with the 260 external medium via the glutamine transporter (Figure 5b). The intracellular abundance of 261 TCA cycle intermediates was also affected by GLS1i treatment in both cell lines (Figure 5c-262 e).

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Our results confirm that the optimized culture conditions devised here provide a robust and stable environment in which to reproducibly assay the effects of a GLS1 inhibitor on cell metabolism and proliferation.

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#### 268 3 Discussion

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270 The assay with which we started this study failed to demonstrate any consistent effects of 271 glutaminase inhibition on either glutamine metabolism or proliferation in these two cancer 272 cell lines: addition of the inhibitor to cells (A549) known to be sensitive to the inhibitor, had 273 no apparent effect on their proliferation (Figure S2a). Conversely, the glutamine metabolism 274 by cells (H358) that are *in*sensitive to the same inhibitor was reduced to a much greater 275 extent than that by sensitive (A549) cells (Figure 1). We then demonstrated that these 276 inconsistencies were artifacts, for one, because most glutamine had been depleted in the 277 pre-incubation period (Figure 1b and 2b) leaving too little glutamine for effects of the inhibitor 278 to become statistically noteworthy.

With our improved assay conditions we were able to show that the glutaminase inhibitor (GLS1i) does have an effect on glutamine metabolism of both cell lines, but that only the proliferation of the A549 cells is reduced (Figure 4). GLS1 inhibition was also apparent from the changes in levels of intracellular metabolites in both cell lines, but with distinct differences between sensitive (A549) and resistant (H358) cell lines (Figure 5).

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286 Our findings highlight the importance of *in vitro* assay optimization for the assessment of the 287 potential of metabolic, and probably also other, inhibitors as anti-cancer drugs that impact on 288 cellular metabolism. Variability in the metabolic state during the assay may well create false 289 positives and false negatives because intermediary and energy metabolism is full of 290 pleiotropic implications. Importantly perhaps, the implications of our findings are unlikely to 291 be limited to studies of metabolic inhibitors. Other inhibitors, such as those of cell signaling 292 or transcription require even longer cell incubations, and may therefore be compromised 293 even more by changes in the levels of metabolites such as ATP, NADH, acetyl-CoA and 294 glutamate that cross-talk widely. Even though metabolism may not be the drug target in 295 these cases, its perturbation due to inappropriate culture conditions, might produce a false 296 response. And since the drug may well affect metabolism indirectly, the impact of metabolic 297 status could be overlooked in both control and treated conditions.

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299 Perhaps even more so than this, our results should warn against the straightforward 300 implementation of historically-fixed sets of conditions for drug assays in cell lines. Living 301 cells are complex enough to engage in all sorts of metabolic changes, these changes may well differ between individual cell lines, and the metabolome is sensitive to such changes 302 well before the metabolic fluxes produced by the cells are<sup>33</sup>. We therefore advocate that 303 304 reports on drug assays are accompanied by a thorough description of the experimental 305 procedure used as well as by a metabolic characterization of the cells during the assay, 306 such as in the workflow we demonstrated here. After all, such characterization has become 307 possible over recent years.

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Indeed, reports in the literature regarding the characteristics of cell lines under basal and perturbed conditions may have overlooked changes in the metabolic environment of cells or high cell density. Such aspects are typically not reported or measured and may contribute to the irreproducibility of the results when repeating the assay in a different laboratory. Such irreproducibility is fueling the reproducibility debate<sup>1,2</sup>.

315 Not only do our results highlight the need for reporting experimental 'details' concerning 316 culture conditions, they also show a way towards rationalizing and standardizing these. 317 Required details would include, but not be limited to, information on the source of cell lines 318 and passage number (or at least whether all cells used were below a certain passage 319 number), number of cells per well at the time of seeding and throughout the assay, 320 density/confluence throughout the assay, volume of culture media used, details of cell 321 culture flasks used, length of assay (from time of seeding), choice of cell culture medium 322 (including concentrations of all components) and sera (concentration used and source), and 323 how concentrations of key nutrients (e.g. glucose and glutamine) and pH change throughout 324 the assay. This would complement existing efforts for standardization across biomedical research<sup>34-36</sup> and improve reproducibility, transparency and evaluation of the experimental 325 data, points that are of critical concern<sup>37</sup>. 326

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328 A number of reporting guidelines for the results of biological assays have been in existence 329 for some time, e.g. the Minimum Information About a Microarray Experiment (MIAME) 330 standard. MIAME is now a reporting requirement for a number of funding agencies and journals<sup>38</sup>. Similarly, there are now minimum reporting standards in use for metabolomics <sup>35</sup>, 331 proteomics<sup>36</sup> and systems biology models<sup>39</sup>. Since 2008, the Minimum Information for 332 333 Biological and Biomedical Investigations (MIBBI) project has acted as a repository for the 334 many minimum reporting guidelines that have since been created; there are now over 40 for 335 the biological and biomedical sciences (https://biosharing.org/standards/, accessed 04 July 336 2016).

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The assay developed and discussed here, as well as the contention that it should be accompanied by metabolic analyses of the assay cell lines, should contribute to improved assay reproducibility in cell biology and drug discovery.

# 342 Figures and Tables

Table 1: Predicted versus observed effects of treatment with the GLS1i inhibitor using the prevalent culture conditions compared with the optimized culture conditions devised in this study.

Predicted effect of	GLS1i treatment	Prevalent culture conditions	Optimized culture conditions
in sensitive A549	cells		
Cell numbers $\downarrow$		×	<ul> <li>✓</li> </ul>
Glutamine consump	Glutamine consumption $\downarrow$		<ul> <li>✓</li> </ul>
Glutamate productio	Glutamate production $\downarrow$		<ul> <li>✓</li> </ul>
Glutamine (intracellu	Glutamine (intracellular) $\uparrow$		<ul> <li>✓</li> </ul>
Glutamate (intracellu			<ul> <li>✓</li> </ul>
TCA cycle	α-KG↓	×	×
intermediates	Citrate ↓	×	<ul> <li>✓</li> </ul>
(intracellular):	Fumarate $\downarrow$	×	<ul> <li>✓</li> </ul>
in resistant H358	Bcells		
Cell numbers uncha	Cell numbers unchanged		<ul> <li>✓</li> </ul>
Glutamine consump	tion $\downarrow$	~	~
Glutamate productio	n↓	×	~
Glutamine (intracellular) $\uparrow$ Glutamate (intracellular) $\downarrow$		<ul> <li></li> </ul>	~
		~	<ul> <li>✓</li> </ul>
TCA cycle	α-KG↓	<ul> <li>✓</li> </ul>	<ul> <li>✓</li> </ul>
intermediates	Citrate ↓	×	×
(intracellular)	Fumarate $\downarrow$	×	~

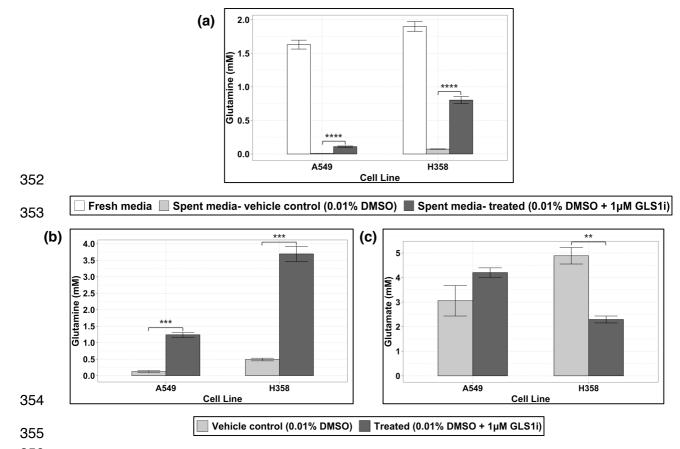
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- 346 significantly as predicted at p < 0.05
- 347 **X** : not significantly as predicted, i.e. p > 0.05.

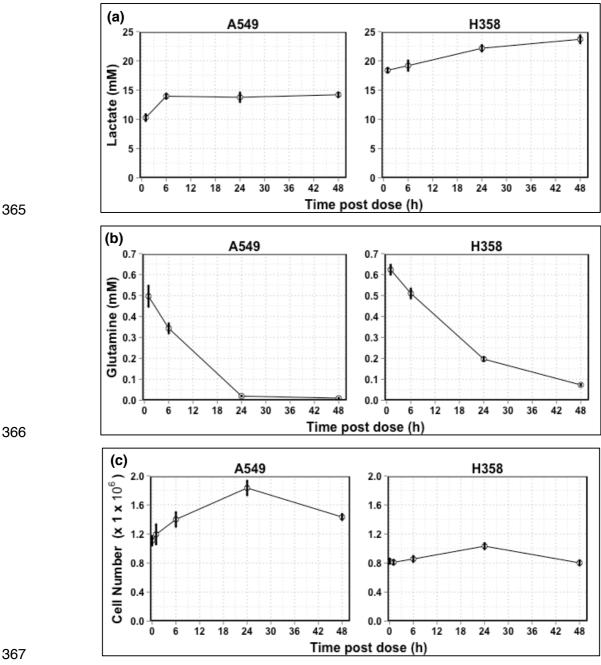
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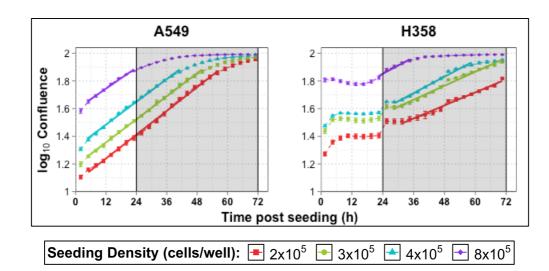


356 Figure 1: Glutamine and glutamate concentrations 48 hours after treatment with 0.01% DMSO ± 1 µM 357 GLS1i using a prevalent assay method. A549 and H358 are known as sensitive and resistant cell lines, 358 respectively, vis-à-vis glutaminase 1 inhibitors. Concentrations of (a) extracellular glutamine (b) intracellular 359 glutamine and (c) intracellular glutamate measured by LC-UV after 24 h of treatment with 0.010 % DMSO ± 1.0 360 µM (final concentrations) GLS1i. For this single experiment, measurements were performed in triplicate for control and treated conditions. Cells had been seeded at a density of 8x10<sup>5</sup> cells/well in 1 ml of culture media 24 361 362 h prior to commencing the experiment. Shown are the mean ± SEM for the 3 technical replicates per cell line 363 and treatment condition. Unadjusted p-values of the differences between control and treated samples obtained 364 using a two-tailed Student's t-test are denoted with asterisks: \*\*:  $p \le 0.01$ ; \*\*\*:  $p \le 0.001$ ; \*\*\*\*:  $p \le 0.0001$ .





369 Figure 2: Changes with time after seeding of the state of a cell culture in a traditional assay in vehicle 370 control (0.01% DMSO) and treatment conditions. (a) Lactate (measured by LC-MS) and (b) glutamine 371 (measured by LC-UV) in spent medium. (c) Number of live cells per well as measured using the Trypan blue 372 exclusion technique using a Countess automated cell counter (Thermo Scientific, Loughborough, UK). Zero time 373 corresponds to 24 hours after seeding of cells into a medium containing 10 mM of glucose, 2 mM of glutamine, in 374 addition to dialyzed fetal calf serum, vitamins and both essential and non-essential amino acids at concentrations 375 well below 1mM except for arginine (0.95 mM) and glutamine (2 mM), as shown in Table M1 in Materials and 376 Methods. The cell lines were: A549 (left) and H358 (right). For this single experiment, measurements were 377 performed in triplicate. Shown are the mean ± SEM for the 3 technical replicates per cell line in control 378 conditions.



#### 380

381 Figure 3: Confluence of A549 and H358 cells over 72 hours after seeding at different initial densities

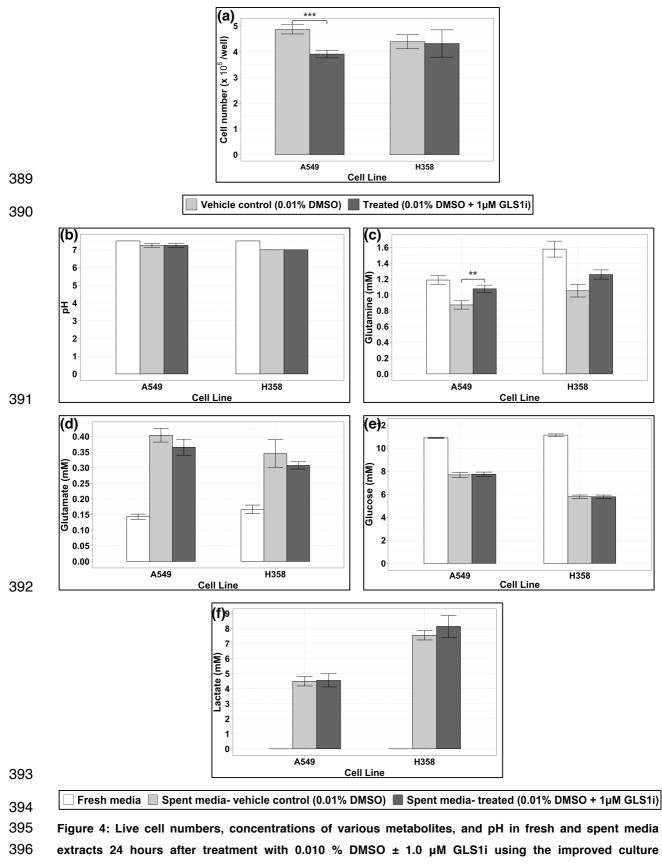
382 when the volume of culture media was increased to 3 mL. Shown are the changes in  $\log_{10}$  confluence over 383 time measured by live content cell imaging Incucyte HD system (Essen Bioscience) when A549 and H358 cells 384 were seeded at a density of  $8 \times 10^5$ ,  $4 \times 10^5$ ,  $3 \times 10^5$  and  $2 \times 10^5$  cells/well. For this single experiment,

measurements were performed in triplicate for control and treated conditions. Shown are the mean ± SEM for the

386 3 technical replicates per cell line and treatment condition. Shaded area denotes the assay window in a prevalent

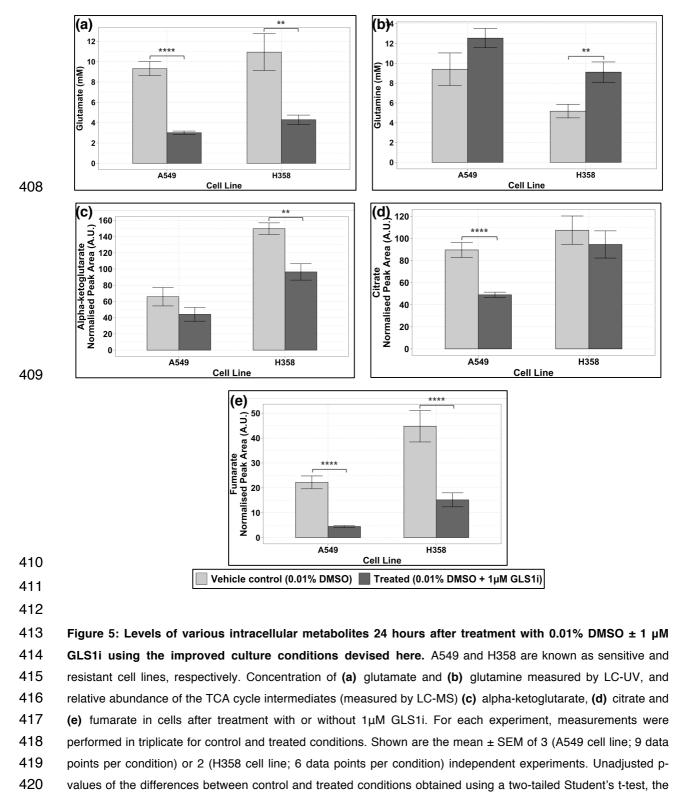
387 assay where samples would be taken over 48 hours from the time of dosing (24 hours after seeding). Solid lines

 $\label{eq:states} 388 \qquad \text{are a fitted linear model for the exponential growth phase of cells.}$ 



conditions devised here. (a) Live cell numbers as measured by automated microscopy following Hoechst
 staining and fixation (See Materials and Methods 1.6). (b) pH of fresh and spent media samples measured using
 MColorpHast indicator strips. Concentration of (c) glutamine, (d) glutamate, (e) glucose and (f) lactate in fresh

400 and spent media samples after treatment with or without 1.0 µM GLS1i measured by LC-UV (glutamine and 401 glutamate), Accu-Chek Aviva Blood Glucose Meter System (glucose) and LC-MS (lactate). For each experiment, 402 measurements were performed in triplicate for control and treated conditions. Shown are the mean ± SEM of 3 403 (A549 cell line; 9 data points per condition) or 2 (H358 cell line; 6 data points per condition) independent 404 experiments. Note that glutamine concentrations in fresh media used for A549 and H358 cells fell by an average 405 of ~27 % and ~5 % respectively over the duration of the assay. Unadjusted p-values of the differences between 406 control and treated conditions obtained using a two-tailed Student's t-test are denoted with asterisks: \*\*:  $p \le 0.01$ ; 407 \*\*\*: p ≤ 0.001.



421 results of which are denoted with asterisks: \*\*:  $p \le 0.01$ ; \*\*\*:  $p \le 0.001$ ; \*\*\*\*:  $p \le 0.001$ .

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430

## 431 5 Author Contributions

432 MWM and HVW established the aim and strategy of the study and 433 designed the experiments, which MWM performed. FO, RB, and CB provided advice and 434 expertise on the design of the experiments, data acquisition and analysis. SEC, BP and SP 435 (see acknowledgements) proposed the experimental system of glutaminase inhibition in 436 human non-small cell lung cancer cell lines. MWM, HVW and FO wrote the paper with 437 advice and guidance provided by RB and CB.

438

# 439 6 Competing financial interests

440 The authors declare that they have no competing financial interests.

#### 442 7 References

443		
444	1.	Prinz, F., Schlange, T. & Asadullah, K. Believe it or not: how much can we rely on published data on potential drug
445		targets? Nature Reviews Drug Discovery 10, 712–712 (2011).
446	2.	Errington, T. M. <i>et al.</i> An open investigation of the reproducibility of cancer biology research. <i>eLife Sciences</i> <b>3</b> , e04333
447		(2014).
448	3.	Baker, M. 1,500 scientists lift the lid on reproducibility. Nature 533, 452-454 (2016).
449	4.	Shoemaker, R. H. The NCI60 human tumour cell line anticancer drug screen. Nat Rev Cancer 6, 813-823 (2006).
450	5.	León, Z., García-Cañaveras, J. C., Donato, M. T. & Lahoz, A. Mammalian cell metabolomics: Experimental design and
451		sample preparation. ELECTROPHORESIS 34, 2762–2775 (2013).
452	6.	Schneider, M. The importance of ammonia in mammalian cell culture. Journal of Biotechnology 46, 161–185 (1996).
453	7.	Freshney, R. I. in Culture of Cells for Tissue Engineering 1–22 (John Wiley & Sons, Inc., 2006).
454		doi:10.1002/0471741817.ch1
455	8.	Garnett, M. J. et al. Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature 483, 570-
456		575 (2012).
457	9.	Barretina, J. et al. The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity.
458		Nature <b>483</b> , 603–307 (2012).
459	10.	Haibe-Kains, B. <i>et al.</i> Inconsistency in large pharmacogenomic studies. <i>Nature</i> <b>504</b> , 389–393 (2013).
460	11.	Hatzis, C. <i>et al.</i> Enhancing reproducibility in cancer drug screening: how do we move forward? <i>Cancer Research</i> <b>74</b> ,
461 462	10	4016–4023 (2014).
463	12. 13.	Haverty, P. M. <i>et al.</i> Reproducible pharmacogenomic profiling of cancer cell line panels. <i>Nature</i> <b>533</b> , 333–337 (2016).
464	13.	Wise, D. R. <i>et al.</i> Myc regulates a transcriptional program that stimulates mitochondrial glutaminolysis and leads to glutamine addiction. <i>Proceedings of the National Academy of Sciences</i> <b>105</b> , 18782–18787 (2008).
465	14.	Yuneva, M., Zamboni, N., Oefner, P., Sachidanandam, R. & Lazebnik, Y. Deficiency in glutamine but not glucose
466		induces MYC-dependent apoptosis in human cells. <i>The Journal of Cell Biology</i> <b>178</b> , 93–105 (2007).
467	15.	Le, A. et al. Glucose-Independent Glutamine Metabolism via TCA Cycling for Proliferation and Survival in B Cells. Cell
468		Metab. 15, 110–121 (2012).
469	16.	Mullen, A. R. et al. Reductive carboxylation supports growth in tumour cells with defective mitochondria. Nature 481,
470		385–388 (2011).
471	17.	Metallo, C. M. et al. Reductive glutamine metabolism by IDH1 mediates lipogenesis under hypoxia. Nature 481, 380-
472		384 (2011).
473	18.	DeBerardinis, R. J. et al. Beyond aerobic glycolysis: Transformed cells can engage in glutamine metabolism that
474		exceeds the requirement for protein and nucleotide synthesis. Proceedings of the National Academy of Sciences 104,
475		19345–19350 (2007).
476	19.	Hassanein, M. et al. SLC1A5 Mediates Glutamine Transport Required for Lung Cancer Cell Growth and Survival.
477		<i>Clinical Cancer Research</i> <b>19,</b> 560–570 (2013).
478	20.	Cook, D. et al. Lessons learned from the fate of AstraZeneca's drug pipeline: a five-dimensional framework. Nature
479		<i>Reviews Drug Discovery</i> <b>13</b> , 419–431 (2014).
480	21.	Schulze, A. & Harris, A. L. How cancer metabolism is tuned for proliferation and vulnerable to disruption. <i>Nat Rev</i>
481 482	00	Cancer <b>491</b> , 364–373 (2012).
483	22.	Zhao, Y., Butler, E. B. & Tan, M. Targeting cellular metabolism to improve cancer therapeutics. <i>Cell Death Dis</i> <b>4</b> , e532 (2012)
483 484	23.	(2013). Vander Heiden, M. G. Targeting cancer metabolism: a therapeutic window opens. Nature Reviews Drug Discovery <b>10</b> ,
485	20.	671–684 (2011).
486	24.	van den Heuvel, A. P. J., Jing, J., Wooster, R. F. & Bachman, K. E. Analysis of glutamine dependency in non-small
487	-	cell lung cancer. <i>Cancer Biology &amp; Therapy</i> <b>13</b> , 1185–1194 (2012).
488	25.	Birsoy, K. <i>et al.</i> Metabolic determinants of cancer cell sensitivity to glucose limitation and biguanides. <i>Nature</i> <b>508</b> ,
489		108–112 (2014).

490	26.	Prower M. Corney, D. N. Cie, H. K. Cozder, A. E. & Minne, J. D. Crewth of Call Lines and Clinical Specimene of
491	20.	Brower, M., Carney, D. N., Oie, H. K., Gazdar, A. F. & Minna, J. D. Growth of Cell Lines and Clinical Specimens of
	07	Human Non-Small Cell Lung Cancer in a Serum-free Defined Medium. <i>Cancer Research</i> <b>46</b> , 798–806 (1986).
492	27.	Tinnemans, M. M. et al. S-phase arrest of nutrient deprived lung cancer cells. Cytometry <b>19</b> , 326–333 (1995).
493	28.	Ishii, T. et al. Nutritional deficiency affects cell cycle status and viability in A549 cells: role of p27Kip1. Cancer Lett.
494		<b>213</b> , 99–109 (2004).
495	29.	Qie, S. et al. Glutamine depletion and glucose depletion trigger growth inhibition via distinctive gene expression
496		reprogramming. Cell Cycle 11, 3679–3690 (2014).
497	30.	Huang, W. et al. A proposed role for glutamine in cancer cell growth through acid resistance. Cell Research 23, 724-
498		727 (2013).
499	31.	LaMonte, G. et al. Acidosis induces reprogramming of cellular metabolism to mitigate oxidative stress. Cancer Metab
500		<b>1</b> , 23 (2013).
501	32.	Zinninger, G. F. & Little, J. B. Proliferation kinetics of density-inhibited cultures of human cells, a complex invitro cell
502		system. Cancer Research 33, 2343–2348 (1973).
503	33.	Raamsdonk, L. M. et al. A functional genomics strategy that uses metabolome data to reveal the phenotype of silent
504		mutations. Nat Biotechnol 19, 45–50 (2001).
505	34.	Brazma, A. et al. Minimum information about a microarray experiment (MIAME)- toward standards for microarray data.
506		Nat. Genet. 29, 365–371 (2001).
507	35.	Fiehn, O. et al. The metabolomics standards initiative (MSI). Metabolomics 3, 175–178 (2007).
508	36.	Taylor, C. F. et al. The minimum information about a proteomics experiment (MIAPE). Nat Biotechnol 25, 887-893
509		(2007).
510	37.	The Academy of Medical Sciences. Reproducibility and reliability of biomedical research: improving research practice.
511		http://www.acmedsci.ac.uk/viewFile/56314e40aac61.pdf
512	38.	Taylor, C. F. et al. Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the
513		MIBBI project. Nat Biotechnol <b>26,</b> 889–896 (2008).
514	39.	Le Novère, N. et al. Minimum information requested in the annotation of biochemical models (MIRIAM). Nat Biotechnol
515		<b>23,</b> 1509–1515 (2005).
0.0		20, 1010 (2000).