Genomic hallmarks of cellular dormancy in cancer and therapeutic implications

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ABSTRACT

Therapy resistance in cancer is often driven by a subpopulation of cells that are temporarily arrested in a non-proliferative, quiescent or ‘dormant’ state, which is difficult to capture and whose mutational drivers remain largely unknown. We developed methodology to uniquely identify this state from transcriptomic signals and characterised its prevalence and genomic constraints in solid primary tumours. We show dormancy preferentially emerges in the context of more stable, less mutated genomes which maintain *TP53* integrity and lack the hallmarks of DNA damage repair deficiency, while presenting increased APOBEC mutagenesis. We uncover novel genomic dependencies of this process, including the amplification of the centrosomal gene *CEP89* as a driver of dormancy impairment. Lastly, we demonstrate that dormancy underlies unfavourable responses to various therapies exploiting cell cycle, kinase signalling and epigenetic mechanisms in single cell data, and propose a signature of dormancy-linked therapeutic resistance to further study and clinically track this state.

1 INTRODUCTION

2 Quiescence is a widely conserved state of reversible proliferative arrest, essential for the normal
3 development and homeostasis of eukaryotic organisms^{1,2}. During quiescence, cells are halted in the
4 G0 phase of the cell cycle, where they maintain minimal basal activity². In cancer, this temporary
5 cell cycle arrest, also termed cellular dormancy, has been proposed as one of the contributing
6 factors of resistance to treatments that target actively dividing cells, such as chemotherapy³⁻⁵.
7 Moreover, a variety of other pre-existing or acquired resistance scenarios have been explained by a
8 drug-tolerant ‘persister’ cell state represented by slow cycling or entirely quiescent cells^{6,7}. Their
9 presence is associated with minimal residual disease, a major cause of relapse in the clinic⁸. As the
10 neoplastic cells evolve, dormancy can also be employed as a mechanism to facilitate immune
11 evasion^{9,10} or adaptation to new environmental niches during metastatic seeding^{11,12}.

12 Despite increasing evidence for the importance of dormancy in cancer progression, it remains a
13 poorly defined biological programme. Hampering our understanding is the fact that quiescence
14 represents a number of heterogeneous states¹. Canonically, cells can be forced into quiescence
15 through serum starvation, mitogen withdrawal or contact inhibition¹. Cells can also enter dormancy
16 spontaneously in response to cell-intrinsic factors like replication stress¹³⁻¹⁵. This process is
17 controlled by p53¹⁶, which triggers the inhibition of cyclin-CDK complexes by activating p21¹⁴.
18 This in turn allows the assembly of the DREAM complex - a key effector responsible for
19 repression of cell-cycle dependent gene expression¹⁷. Min and Spencer¹⁸ recently demonstrated a
20 much broader systemic coordination of 198 genes underlying distinct types of quiescence by
21 profiling the transcriptomes of cells that entered this state either spontaneously or upon different
22 stimuli. Additionally, proliferation-quiescence decisions can be impacted by oncogenic changes
23 such as *MYC* amplification¹⁹ or altered p38/ERK signalling²⁰.

24 Despite these advances, the identification of dormant cells within tumours presents an ongoing
25 challenge due to their scarcity and lack of universal, easily measurable markers for the activation

and maintenance of this state. As they are often defined by a lack of proliferative markers^{21,22}, quiescent cells can be mistaken for other therapy resistant cell types such as senescent or cancer stem cells^{6,23}. Unlike quiescent cells, which can readily resume their proliferative state, senescent cells are irreversibly arrested¹⁸ while cancer stem cells have a high capacity for self-renewal and sit at the top of the differentiation hierarchy²⁴. Biomarkers of quiescence that are sufficiently specific and robust to be clinically useful are clearly needed.

Furthermore, the extent to which dormancy is enacted through transcriptional or genetic control is unknown^{5,25}, as the mutational processes and genomic changes driving quiescence have not been systematically profiled across cancer tissues. Understanding the evolutionary triggers and molecular mechanisms that enable cancer cells to enter and maintain dormancy would enable us to develop pharmacological strategies to selectively eradicate quiescent cancer cells or prevent them from re-entering proliferative cycles.

To address these challenges, we have developed a new method to uniquely and reliably quantify tumour dormancy using transcriptomic data, and employed it to characterise this phenomenon in bulk and single cell datasets from a variety of solid tumours. We identify and validate mutational constraints for dormancy emergence, hinting at potential new therapeutic targets that could exploit this mechanism. We also demonstrate the relevance of dormancy to responses to a range of compounds targeting cell cycle, kinase signalling and epigenetic mechanisms in single cell datasets, and propose an expression signature that could be employed to detect tumour dormancy-induced treatment resistance.

RESULTS

Evaluating tumour dormancy from transcriptomic data

We hypothesised that primary tumours contain varying numbers of quiescent cells, and this in turn may determine their ability to overcome therapies targeting cycling cells. To capture this elusive

phenotype, we developed a computational framework that would allow us to quantify dormancy signals in bulk and single cell sequenced cancer samples (Figure 1a). We employed 139 differentially expressed genes across five distinct forms of quiescence resulting from serum starvation, contact inhibition, MEK inhibition, CDK4/6 inhibition and spontaneous quiescence, as described by Min and Spencer¹⁸, as markers of a generic quiescence state. The expression levels of these markers were used to derive a score reflecting the relative level of dormancy within individual tumours (see Methods).

We validated multiple scoring methodologies²⁶⁻²⁹ using seven single-cell and bulk datasets³⁰⁻³⁶ where actively proliferating and quiescent cells had been independently profiled (Extended Data Figure 1a, Supplementary Table 1, Methods). A combined Z-score approach had the highest accuracy in detecting signals of dormancy, with a 91% mean performance in classifying cells as quiescent or cycling (Figure 1b, Extended Data Figure 1b). It also outperformed classical cell cycle and dormancy markers, such as the expression of targets of the DREAM complex, CDK2, Ki67 and of mini-chromosome replication maintenance (MCM) protein complex genes - which are involved in the initiation of eukaryotic genome replication (Figure 1c). Importantly, our approach provided a good separation between quiescent and proliferating samples across a variety of cancer types and models including cancer cell lines, 3D organoid cultures, circulating tumour cells and patient-derived xenografts (Supplementary Table 1), thereby demonstrating its broad applicability. Furthermore, the strength of the score appeared to reflect the quiescence depth, i.e. the time the cells stay in quiescence³⁷ (Figure 1d).

We experimentally validated our methodology in nine lung adenocarcinoma cell lines. There was a remarkably good correlation between our predicted quiescence levels and the fraction of quiescent cells, estimated using quantitative, single-cell imaging of phospho-Ser807/811-Rb (PRb, which labels proliferative cells³⁸) and 24 hour EdU proliferation assays (Figure 1e-h). Cells that were negative for either PRb or EdU were defined as quiescent (see Methods, Figure 1e-f). Importantly,

a G1 signature (Methods) was not associated with these experimental measurements, proving our method indeed captures quiescence rather than a prolonged G1 state (Figure 1g-h). The quiescence correlations appeared robust to random removal of individual genes from the signature, with no single gene having an inordinate impact on the score (Extended Data Figure 1c-e). This provided further reassurance that our Z-score based methodology is successful in capturing dormancy signals from bulk tumour data.

Having established a robust framework for quantifying tumour dormancy, we next profiled 8,005 primary tumour samples across 31 solid cancer tissues from The Cancer Genome Atlas (TCGA). After accounting for potential confounding signals from the microenvironment by correcting for tumour purity (see Methods, Extended Data Figure 1f-g), we observed an entire spectrum of dormancy across tumours that ranged from highly dormant to highly proliferative (Figure 2a). Cancers well known to be frequently dormant, such as glioblastoma^{3,30}, were amongst the highest ranked in terms of quiescence, along with kidney and adrenocortical carcinomas (Figure 2b).

As expected, tissues with lower stem cell division rates presented a greater propensity for quiescence (Figure 2c)³⁹. Importantly, we confirmed that our quiescence scores capture a cellular state that is distinct from that of cancer stem cells, marked by signatures associated with high telomerase activity and an undifferentiated state^{40,41}, and that of senescent cells, marked by the Senescence-Associated Secretory Phenotype (SASP) and β -galactosidase activity⁴²⁻⁴⁴ (Figure 2d, Extended Data Figures 2a-d). Our scores also showed strong negative correlations with the expression of proliferation markers (Figure 2d).

Lastly, we confirmed dependencies on the p53/p21/DREAM activation axis: tumours that were proficient in *TP53* or the components of the DREAM complex, as well as those with higher p21 expression, had elevated dormancy levels across numerous tissues (Figure 2e, Extended Data Figures 2e-f), although only 8 out of 139 dormancy genes are directly transcriptionally regulated by p53⁴⁵. Nevertheless, p53 proficiency appears to be a non-obligatory dependency of dormancy,

which is also observed to arise in p53 mutant scenarios in 21% of cases. p53 has also been shown to play a role in preventing the occurrence of larger structural events and polyploidy⁴⁶⁻⁴⁸, potentially explaining the lower dormancy levels we observed in tumours that had undergone whole genome duplication (Figure 2f).

The genomic background of cancer dormancy

After obtaining dormancy estimates for primary tumour samples, we set out to identify potential genomic triggers which might create a favourable background for tumour dormancy. We identified 285 cancer driver genes that were preferentially altered (via mutations or copy number alterations) either in dormant or fast proliferating tumours (Figure 3a). Reassuringly, this list included genes previously implicated in driving cellular quiescence-proliferation decisions such as *TP53* and *MYC*^{16,19}. An additional 10 cancer genes showed signals of positive selection in the context of high dormancy/proliferation (Supplementary Table 2). We also investigated associations with mutagenic footprints of carcinogens (termed “mutational signatures”), which can be identified as trinucleotide substitution patterns in the genome^{49,50}. 15 mutational signatures were linked with dormancy either within individual cancer studies or pan-cancer (Extended Data Figure 2g).

Following the initial prioritisation of putative genomic constraints of dormancy, we sought to identify those events that could best distinguish dormant from fast proliferating tumours, while accounting for tissue effects. An ensemble elastic net selection approach similar to the one described by Pich et al⁵¹ was applied for this purpose (Figure 3b, Methods). Our pan-cancer model identified tissue type to be a major determinant of quiescence levels (Extended Data Figure 3a). It also uncovered a reduced set of 60 genomic events linked with tumour dormancy levels, including SNVs and copy number losses in 17 cancer genes, as well as amplifications of 13 cancer genes (Figure 3c). These events could then be successfully employed to predict quiescence in a separate test dataset, thus internally validating our model (Extended Data Figure 3b).

Reassuringly, a functional *TP53*, lack of *MYC* amplification and lower mutation rates (Figure 3c) were amongst the top ranked characteristics of dormant tumours, which also displayed less aneuploidy. Additionally, we uncovered novel dependencies, such as *CEP89* and *LMNA* amplifications observed in fast cycling tumours, or *ZMYM2* deletions prevalent in dormant samples. p16 (*CDKN2A*) deletions, one of the frequent early events during cancer evolution^{52,53}, were enriched in dormant tumours. *RB1* deletions and amplifications were both associated with a reduction in tumour dormancy, which might reflect the dual role of RB1 in regulating proliferation and apoptosis⁵⁴. Overall, the genomic dependencies of dormancy mainly comprised genes involved in cell cycle pathways, p53 regulation and ubiquitination (most likely of cell cycle targets), TGF- β signalling mediators and RUNX2/3 regulation which have previously been shown to play a role in controlling proliferation and cell cycle entry⁵⁵ (Extended Data Figure 3c).

Our model also calls attention to the broader mutational processes associated with this cellular state. Such processes showed fairly weak and heterogeneous correlations with dormancy within individual cancer tissues (Extended Data Figure 2g), but their contribution becomes substantially clearer pan-cancer once other genomic sources are accounted for. In particular, we identified an association between dormancy and mutagenesis induced by the AID/APOBEC family of cytosine deaminases as denoted by signature SBS2⁴⁹ (Figure 3c). As highlighted by Mas-Ponte and Supek⁵⁶, APOBEC/AID driven mutations tend to be directed towards early-replicating, gene-rich regions of the genome, inducing deleterious events on several genes including *ZMYM2*, which our pan-cancer model has linked with higher dormancy.

In turn, defective DNA mismatch repair, as evidenced by signatures SBS44, SBS20, SBS15, SBS14 and SBS6⁴⁹, was prevalent in fast cycling tumours (Figure 3c). Mismatch repair deficiencies lead to hypermutation in a phenomenon termed “microsatellite instability” (MSI), which has been linked with increased immune evasion⁵⁷. Cancers particularly prone to MSI include colon, stomach and endometrial carcinomas⁵⁸, where this state was indeed linked with lower

quiescence (Figure 3d). Furthermore, dormant tumours were depleted of alterations across all DNA damage repair pathways (Figure 3e).

Our measurements of dormancy also reflected expected cycling patterns across 27 MCF7 strains⁵⁹: cell lines with longer doubling times exhibited higher quiescence (Figure 3f). This coincided with a depletion of *PTEN* mutations, a dependency highlighted by the pan-cancer model.

When checking for dependencies in individual cancer tissues, 27 out of the 28 genes identified by the model were significantly associated with dormancy in at least one tissue, most prominently in breast, lung and liver cancers which also represent the largest studies within TCGA (Figure 3g, top panel). Most of these genomic insults were linked with a decrease in dormancy. In external validation datasets these associations, including deletions in *PTEN* and *LRP1B* or amplifications of *MYC*, *CEP89* or *STAG1*, featured most prominently in the largest cohort of breast cancer samples (Figure 3g, bottom panel).

CEP89 amplification contributes to high tumour proliferation rates

To gain more insight into the underlying biology of cellular dormancy, we sought to experimentally validate associations highlighted by the pan-cancer model. We focused on the impact of *CEP89* activity on quiescence-proliferation decisions due to the high ranking of this putative oncogene in the model, the relatively unexplored links between *CEP89* and cell cycle control, as well as its association with quiescence across a variety of cancer cell lines (Extended Data Figure 4a-c). The function of *CEP89* is not well characterised, however, the encoded protein has been proposed to function as a centrosomal-associated protein^{60,61}. Centrosomes function as major microtubule-organising centres in cells, playing a key role in mitotic spindle assembly⁶² and the mitotic entry checkpoint⁶³. Moreover, centrosomes act as sites of ubiquitin-mediated proteolysis of cell cycle targets⁶⁴, and members of several growth signalling pathways, such as Wnt

and NF- κ B, localise at these structures^{65,66}. Several genetic interactions have also been reported between CEP89 and key cell cycle proteins, including cyclin D2⁶⁷ (Figure 4a).

Our model linked *CEP89* amplification with fast cycling tumours (Figure 3c). Centrosome amplification is a common feature of tumours with high proliferation rates and high genomic instability⁶⁸, and overexpression of centrosomal proteins can alter centriole structure^{69,70}. Indeed, *CEP89* amplified tumours presented elevated expression of a previously reported centrosome amplification signature (CA20)⁶⁸ (Figure 4b), which was strongly anticorrelated with quiescence levels (Figure 4c). Furthermore, *CEP89* expression was prognostic across multiple cancer tissues (Figure 4d) and linked with toxicity of several cancer compounds in cell line models (Extended Data Figure 4d).

We validated this target in the lung adenocarcinoma cell line NCI-H1299 showing high levels of *CEP89* amplification. Cep89 depletion via siRNA knockdown caused a consistent increase in the fraction of quiescent cells as measured by PRb and EdU assays (Figure 4e-f). Thus, we propose *CEP89* as a novel cell proliferation regulator that may be exploited in certain scenarios to control tumour growth.

Dormancy in breast cancer

Due to the variation of dormancy levels across tissues and to increase power, we have taken a pan-cancer approach to capture genomic features that are universally associated with dormancy. However, we acknowledge that the extremely diverse genomic background for cancer development in different tissues might mean that certain genetic alterations may lead to higher or lower propensity of dormancy in a single tissue only. To investigate this further we focused on breast cancer, the largest cancer dataset available from TCGA, where we still have adequate power and balance of dormant/cycling phenotypes to uncover tissue-specific genomic markers of dormancy. A combined ANOVA and random forest classification approach identified 30 genomic events that

could distinguish dormant from fast cycling tumours with a mean accuracy of 74% (Figure 5a). This model recovered the associations with the APOBEC mutational signature SBS2, *TP53* mutation as well as *MYC*, *KLF6*, *LMNA*, *ETV6* and *RAD21* amplification already seen in the pan-cancer model (Figure 5b). All additional associations validated in the METABRIC cohort and were also seen in several other cancers, particularly bladder, lung and lower grade glioma (Figure 5c). Since APOBEC/AID activity has been linked with dormancy in both the pan-cancer and the tissue-specific models, we further investigated its role in breast cancer, where the associated mutation signature SBS2 is relatively prevalent. Indeed, breast cancer samples enriched in APOBEC-associated mutations, defined as mutations attributed to SBS2 and SBS13, presented significantly higher quiescence levels (Figure 5d). Across breast cancer subtypes, the Luminal A subtype showed the highest levels of dormancy, however, Her2+ tumours had the highest incidence of APOBEC associated mutational events, suggesting this subtype may be the most susceptible to APOBEC-linked quiescence (Figure 5e-f).

Characterisation of individual quiescence programmes

While we had previously examined a generic dormancy programme, cancer cells can enter quiescence due to different stimuli¹ and this may inform its aetiology and manifestation. To explore this, we re-scored tumours based on gene expression programmes specific to serum starvation, contact inhibition, MEK inhibition, CDK4/6 inhibition or spontaneously occurring quiescence as defined by Min and Spencer¹⁸ (see Methods). We observed a good correlation between the dormancy estimates representing individual quiescence programmes and the expression of genes associated with the corresponding form of quiescence in the literature (Figure 6a-e, Extended Data Figure 5). CDK4/6 inhibition-induced quiescence levels were further validated using external RNA-seq datasets from cancer cell lines and xenograft mice sequenced before and after treatment with the CDK4/6 inhibitor Palbociclib^{71,72} (Figure 6f, Supplementary

Table 4). Interestingly, we also observed significant differences in spontaneous quiescence scores before and after treatment. Indeed, p21 activity has been linked with the Palbociclib mechanism of action^{73,74}, and this analysis suggests potential similarities between CDK4/6 inhibition and p21-dependent quiescence phenotypes.

Having validated our framework for quantifying stimulus-specific quiescence programmes, we proceeded to estimate the dominant form of quiescence in different cancer types (Figure 6g). We found a range of quiescence aetiologies across most tissues, while a minority of cancers were dominated by a single form of quiescence, e.g. serum starvation in all dormant pheochromocytomas and paragangliomas, contact inhibition in 88% of head and neck carcinomas and CDK4/6 inhibition in 80% of dormant adrenocortical carcinomas. While we do not wish to claim that the dormancy state will have necessarily been induced by the actual predicted stimulus (impossible in the case of CDK4/6 or MEK inhibition, as the analysed samples are all treatment-naïve), we suggest that the downstream signalling cascade may resemble that triggered by such stimuli, e.g. via CDK4/6 or MEK loss of function mutations. Amongst these states, spontaneous quiescence appeared most strongly dependent on p53 functionality (Supplementary Table 3). This points to common transcriptional features of drug-tolerant dormant cells in different cancer settings that could be employed in designing ways to eradicate these cells in the future.

Clinical relevance of tumour dormancy

Overall, dormancy appears to be beneficial for the long-term outcome of cancer patients (Figure 7a, Extended Data Figure 6a). As expected, quiescence levels were increased in stage 1 tumours, although later stages also exhibited occasional elevated dormancy (Extended Data Figure 6b). Indeed, such dormant, indolent tumours could have higher chances of being eradicated earlier in the disease, which is consistent with reported worse prognosis of patients with higher tumour cell proliferation rates and less stable, more mutated genomes⁷⁵. However, outcomes do vary depending

on the quiescence subtype, with worse survival observed upon contact inhibition (Figure 7b). The outcomes also vary by tissue, with lung, colon or esophageal carcinoma patients displaying significantly worse prognosis in the context of dormancy (Figure 7c).

While dormancy may confer an overall survival advantage in most cancers, it can also provide a pool of cells that are capable of developing resistance to therapy^{34,76}. Using our methodology, we indeed observed an increase in quiescence levels in cell lines following treatment with EGFR, BRAF and CDK4/6 inhibitors, as well as conventionally used chemotherapies such as 5-Fluorouracil (5-FU) in multiple bulk RNA-seq datasets (Figure 7d). Furthermore, the recent widespread availability of single-cell transcriptomics offers the opportunity to investigate the impact of quiescence on such therapies with much greater granularity than is allowed by bulk data. Using our quiescence signature and single-cell data from RKO and SW480 colon cancer cell lines treated with 5-FU⁷⁷, we could observe quiescence-proliferation decisions following conventional chemotherapy treatment. Within the p53 proficient cell line RKO, the fraction of quiescent cells increased from 41% to 93% after treatment with a low dose (10 μ M) of 5-FU and persisted at higher doses (Figure 7e-f). In contrast, a comparable increase was not observed in *TP53* mutant SW480 cells, further emphasizing the key role of p53 as a regulator of quiescence (Figure 7g-h). SW480 cells showed higher apoptotic activity following treatment compared to RKO cells, particularly within actively cycling cells, further corroborating that cells capable of entering quiescence may be less vulnerable to this therapy (Extended Data Figure 6c-d).

Similarly, using single cell data from an *EGFR* mutant Non-Small Cell Lung Cancer (NSCLC) cell line treated with the EGFR inhibitor Erlotinib⁷⁸, we predicted that 40% of cells were likely to exist in a dormant state prior to treatment. EGFR inhibition led to a massive decrease in cell numbers immediately after treatment, mostly due to proliferating cells dying off (Extended Data Figures 6e-f), while the proportion of quiescent cells increased to 96% at day 1, indicating an immediate selective advantage for such cells (Figure 7i-j). Interestingly, these cells appear to gradually start

proliferating again in the following days during continuous treatment, with the percentage of proliferating cells approaching pre-treatment levels by day 11 (Figure 7j). The same trend captured by our signature could be observed upon KRAS and BRAF inhibition in different cell line models (Extended Data Figure 6g-j, Supplementary Table 4)^{34,78}. Furthermore, during the first days of treatment the NSCLC cells that survived EGFR inhibition appeared to reside in a state most resembling that induced by serum starvation (Figures 7k-l). Both EGFR kinase inhibitors and serum starvation have been shown to trigger autophagy⁷⁹, which may explain the convergence between this inhibitory trigger and the type of quiescence response. At day 11 most of the remaining dormant cells appeared in a state similar to that preceding the treatment (Figure 7l).

Thus, quiescence appears to explain resistance to broad acting chemotherapy agents as well as targeted molecular inhibitors of the Ras/MAPK signalling pathway, being either selected for, or induced immediately upon treatment, and gradually waning over time as cells start re-entering the cell cycle. Using massively multiplexed chemical transcriptomic data, we also analysed responses to 188 small molecule inhibitors in cell lines at single-cell resolution⁸⁰ (Extended Data Figure 7). We observed a large increase in quiescence following treatment with compounds targeting cell cycle regulation and tyrosine kinase signalling, consistent with our previous results, but also for compounds modulating epigenetic regulation, e.g. histone deacetylase inhibitors - thus highlighting the broad relevance of quiescence.

These analyses showcase our ability to probe the nature of quiescent phenotypes using a defined dormancy signature, which could aid the development of methods to selectively target quiescent drug-resistant persister cells. However, a major challenge of scRNA-seq data analysis is the high percentage of gene dropout, which could impact our ability to evaluate dormancy using the full 139 gene signature. The scRNA-seq datasets we analysed exhibited an average drop-out of 8.5 genes out of the full gene signature. While our scoring method remains robust to such levels of dropout (Extended Data Figure 1c-e), we also employed machine learning to reduce our initial list of 139

markers of dormancy to a robust 35-gene signature, comprised mainly of RNA metabolism and splicing-regulating factors, but also of genes involved in cell cycle progression, ageing and senescence, which could be applied to sparser datasets with larger levels of gene dropout (Methods, Figure 8a-b). The optimised signature of dormancy performed similarly to the initial broadly defined programme in distinguishing highly dormant and fast cycling tumours (Figure 8c), showed an average dropout of only 0.5 genes across the scRNA-seq datasets used in this study (Figure 8d), was similarly prognostic ($p=0.004$) and showed comparable profiles of resistance to treatment (Figure 8e, Extended Data Figure 8). This minimal expression signature could be employed to track and further study emerging quiescence-induced resistance in a variety of therapeutic scenarios.

DISCUSSION

Despite its crucial role in cancer progression and resistance to therapies, dormancy has remained poorly characterised due to the scarcity of suitable models and biomarkers for large-scale tracking in the tissue or blood. Lack of proliferative markers such as Ki67 or CDK2^{21,81} does not uniquely distinguish quiescence from other cell cycle phases, e.g. G1 or S. This study overcame this limitation by employing genes active in different forms of quiescence whose patterns of expression are distinct from markers of a longer G1 phase, senescence or stemness. We demonstrate a robust method for profiling this signature to identify dormancy in bulk and single cell RNA-seq data, its versatility evidenced by high classification accuracies across a variety of solid cancer datasets. More variable performance was observed when applied to hematopoietic stem cells as it was not designed to capture signals in this context (Extended Data Figure 1b).

We show that dormancy is pervasive across different solid cancers and generally associated with more stable, less mutated genomes with intact DNA damage repair pathways. We also find a link between APOBEC mutagenesis and higher levels of dormancy. We identify mutational events

affecting a variety of genes such as *PTEN*, *CEP89*, *CYLD*, *LMNA* that appear unfavourable to dormancy development, thus potentially implicating them in influencing quiescence-proliferation decisions. Among these, we propose *CEP89* amplification as novel biomarker of non-small cell lung primary tumours with low quiescence capacity. Genomic alterations enriched in dormant tumours, such as p16 or *ZMYM2* deletions, were more rare and predominantly captured pan-cancer. Such targets should be further validated and could be exploited to either counteract dormancy or induce it.

Our finding that primary tumour dormancy confers a favourable prognosis could raise a potential limitation of our approach in distinguishing between slow-dividing and drug-tolerant persister cell phenotypes⁶ in bulk transcriptome data. Nevertheless, our methodology is directly extendable to single cell data, where we demonstrate a clear association between existent/emerging quiescence and resistance to multiple cell cycle, kinase signalling and epigenetic targeting regimens in a variety of cancers. Quiescent cells utilise several mechanisms to achieve drug resistance, including upregulation of stress-induced pathways such as anti-apoptotic BCL-2 signalling⁸², anti-ROS programmes¹⁸ or immune evasion¹⁰. Further studies are needed to elucidate if these mechanisms are specific to individual cancer tissues or individual quiescence types.

Overall, our study provides for the first time a pan-cancer view of dormancy and its evolutionary constraints, underlying novel mutational dependencies which could be exploited in the clinic. We propose a tumour dormancy signature which can be measured in bulk tissue or single cells, and could inform therapeutic strategies or risk of relapse. This signature could be assessed in the clinic to track rapidly emerging resistance, e.g. through liquid biopsies or targeted gene panels. We hope these insights can be used as building blocks for future studies into the different regulators of dormancy, including epigenetics and microenvironmental interactions, as well as the mechanisms by which it enables therapeutic resistance both in solid and haematological malignancies.

346 **ONLINE METHODS**

347 **Selection of quiescence marker genes**

348 *Generic quiescence markers:*

349 Differential expression analysis results comparing cycling immortalised, non-transformed human
 350 epithelial cells and cells in five different forms of quiescence (spontaneous quiescence, contact
 351 inhibition, serum starvation, CDK4/6 inhibition and MEK inhibition) were obtained from Min and
 352 Spencer¹⁸. A total of 195 genes were differentially expressed in all five forms of quiescence under
 353 an adjusted p-value cut-off of 0.05. This gene list, reflective of a generic quiescence phenotype,
 354 was subjected to the following refinement and filtering steps: (1) selection of genes with a
 355 unidirectional change of expression across all five forms of quiescence; (2) removal of genes
 356 involved in other cell cycle stages included in the “KEGG_CELL_CYCLE” gene list deposited at
 357 MSigDB; (3) removal of genes showing low standard deviation and low levels of expression within
 358 the TCGA dataset, or which showed low correlation with the pan-cancer expression of the
 359 transcriptional targets of the DREAM complex, the main effector of quiescence, in TCGA.

360 *Quiescence subtype-specific markers:*

361 Gene lists representing spontaneous quiescence, contact inhibition, serum starvation, CDK4/6
 362 inhibition and MEK inhibition programmes were obtained using genes differentially expressed in
 363 each individual quiescence form using an adjusted p-value cutoff of 0.05. The gene lists were
 364 subjected to filtering steps 2 and 3 described above. Following the refinement steps, 10 upregulated
 365 and 10 downregulated genes with highest log2 fold changes were selected for each quiescence
 366 type.

367

368 Dormancy quantification

369 The *GSVA* R package was used to implement the combined z-score²⁶, ssGSEA²⁷ and GSVA²⁸ gene
 370 set enrichment methods. For the above three methods a separate score was obtained for genes
 371 upregulated in quiescence and genes downregulated in quiescence, following which a final
 372 quiescence score was obtained by subtracting the two scores. The singscore single-sample gene
 373 signature scoring method²⁹ was implemented using the *singscore* R package. In addition to these,
 374 we also calculated a mean scaled quiescence score based on the refined list of genes upregulated
 375 and downregulated in quiescence, as well as a curated housekeeping genes from the
 376 “HSIAO_HOUSEKEEPING_GENES” list deposited at MSigDB, as follows:

$$377 \quad QS = \frac{\frac{1}{n} \sum G_U - \frac{1}{n} \sum G_D}{\frac{1}{n} \sum G_H}$$

378 QS = mean scale quiescence score

379 G_U = expression of genes upregulated in quiescence

380 G_D = expression of genes downregulated in quiescence

381 G_H = expression of housekeeping genes

382 n = number of genes in each gene set

383 Quiescence scores for the TCGA cohort were derived from expression data scaled by tumour purity
 384 estimates. The pan-cancer TCGA samples were also classified into “high” or “low” quiescence
 385 groups based on k-means clustering (k=2) on the expression data of 139 quiescence biomarker
 386 genes, following the removal of tissue-specific expression differences using the *ComBat* function
 387 from the *sva* R package⁸³.

388 **Measuring the depth of quiescence**

389 We employed the GSE124109 dataset from Fujimaki et al³⁷ where rat embryonic fibroblasts were
390 transcriptomically profiled as they moved from shallow to deep quiescence over time in the
391 absence of growth signals. The derived quiescence scores using our combined z-score
392 methodology increased from shallow to deep quiescence.

393 **Validation of quiescence scoring methodologies**

394 *Single-cell RNA-sequencing validation datasets:*

395 Datasets were obtained from the ArrayExpress and Gene Expression Omnibus (GEO) databases
396 though the following GEO Series accession numbers: GSE83142, GSE75367, GSE137912,
397 GSE139013, GSE90742 and E-MTAB-4547. Quality control analysis was standardised using the
398 *SingleCellExperiment*⁸⁴ and *scater*⁸⁵ R packages. Normalisation was performed using the *scraper*⁸⁶ R
399 package.

400 *Bulk RNA-sequencing validation datasets:*

401 Datasets were obtained from the GEO database through the following GEO Series accession
402 numbers: GSE93391, GSE114012, GSE131594, GSE152699, GSE124854, GSE135215,
403 GSE99116 and GSE124109. GSE114012 count data were normalised to TPM values using the
404 *GeoTcgaData* R package. All normalised datasets were log-transformed before further analysis.

405 The accuracy with which the quiescence scoring methods could separate proliferating and
406 quiescent samples within the validation datasets was determined by calculating the area under the
407 curve of the receiver operating characteristic (ROC) curves, using the *plotROC* R package.

408

409 **Experimental validation in lung adenocarcinoma cell lines**

410 The average fraction of cancer cells spontaneously entering quiescence was estimated for nine lung
 411 adenocarcinoma cell lines (NCIH460, A549, NCIH1666, NCIH1944, NCIH1563, NCIH1299,
 412 NCIH1650, H358, L23) using EdU and phospho-Rb staining proliferation assays.

413 Cell lines were obtained from ATCC or Sigma and regularly checked for mycoplasma. A549 and
 414 NCIH460 were cultured in DMEM (Gibco). NCIH358, NCIH1299 and NCIH1563 were
 415 maintained in RPMI-1640 (Gibco) supplemented with 5mM sodium pyruvate and 0.5% glucose.
 416 NCIH1944, NCIH1666, NCIH1650 and L23 were grown in RPMI-1640 ATCC formulation
 417 (Gibco). A427 were cultured in EMEM (ATCC). A549, NCIH460, H358, NCIH1299, NCIH1563,
 418 A427 were supplemented with 10% heat inactivated FBS. NCIH1666 with 5% heat-inactivated
 419 FBS and all other cell lines with 10% non-heat inactivated FBS. All cell lines had penicillin-
 420 streptomycin (Gibco) added to 1%. Cells were maintained at 37°C and 5% CO₂. To calculate the
 421 quiescent fraction, A549 and NCIH460 cells were plated at a density of 500 cells/well, and all
 422 other cell lines at a density of 1000/well, in 384well CellCarrier Ultra plates (PerkinElmer) in the
 423 relevant media. 24h later, 5 µM EdU was added and cells were incubated for a further 24h before
 424 fixing in a final concentration of 4% formaldehyde (15 min, RT), permeabilization with PBS/0.5%
 425 Triton X-100 (15 min, RT) and blocking with 2% BSA in PBS (60 min, RT). The EdU signal was
 426 detected using Click-iT chemistry, according to the manufacturer's protocol (ThermoFisher). Cells
 427 were also labelled for phospho-Ser807/811 Rb (PRb) using Rabbit mAb 8516 (CST) at 1:2000 in
 428 blocking solution, overnight at 4°C. Unbound primary antibody was washed three times in PBS
 429 and secondary Alexa-conjugated antibodies were used to detect the signal (ThermoFisher, 1:1000,
 430 1h at RT). Finally nuclei were labelled with Hoechst 33258 (1 µg/ml, 15 min RT) before imaging
 431 on a high-content widefield Operetta microscope, 20x N.A. 0.8. Automated image analysis
 432 (Harmony, PerkinElmer) was used to segment and quantify nuclear signals in imaged cells.

433 Quiescent cells were defined by the absence of EdU or PRb staining, determined by quantification
434 of their nuclear expression (Figure 1e-f).

435 The quiescence scores for cancer cell lines were calculated using corresponding log-transformed
436 RPKM normalised bulk RNA-seq data from the Cancer Cell Line Encyclopedia (CCLE)
437 database⁸⁷.

438 CEP89 was depleted by ON-Target siRNA Pool from Horizon. NCI-H1299 cells were reverse
439 transfected in 384 well plates with 20nM of Non-targeting control (NTC) or CEP89-targeting
440 siRNA using Lipofectamine RNAiMax (ThermoFisher), according to the manufacturer's
441 instructions. Cells were left for 24h, before 5 μ M EdU was added for the final 24h and then cells
442 were processed as above to determine the quiescent fraction. To determine the level of Cep89
443 depletion by western blot, cells were reverse transfected with siRNA in 24 well plates. 48h after
444 transfection, cells were lysed directly in 1x SDS sample buffer with 1mM DTT (ThermoFisher).
445 Samples were separated on pre-cast 4-20% Tris-Glycine gels, transferred to PVDF using the iBlot2
446 system and membranes blocked in blocking buffer (5% milk in TBS) for 1h at RT. The membrane
447 was then cut and the upper half was incubated in 1:1000 Cep89 antibody (Sigma, HPA040056), the
448 bottom half in B-actin antibody 1:2000 (CST; 3700S) diluted in blocking buffer overnight at 4°C.
449 Membranes were washed three times in TBS-0.05% TritonX-100 before being incubated in
450 secondary anti-rabbit (Cep89) or anti-mouse (B-actin) HRP conjugated antibodies (CST 7074P2
451 and CST 7076P2, respectively) diluted 1:2000 in blocking buffer for 1h at RT. Membranes were
452 washed three times again and signal detected using Clarity ECL solution (BioRad) and scanned on
453 an Amersham ImageQuant 800 analyser.

454 **Multi-omics discovery cohort**

455 FPKM normalised RNA-sequencing expression data, copy number variation gene-level data, as
456 well as mutation annotation files aligned against the GRCh38 human reference genome from the

457 Mutect2 pipeline were downloaded using the *TCGABiolinks* R package⁸⁸ for 9,712 TCGA primary
 458 tumour samples across 31 solid cancer types. Haematological malignancies were excluded as the
 459 quiescence markers were derived in epithelial cells and might not be equally suited to capture this
 460 phenotype in blood. For patients with multiple samples available, one RNA-seq barcode entry was
 461 selected for each individual patient resulting in 9,631 total entries. All expression data were log-
 462 transformed for downstream analysis. During quiescence score calculation, expression data for the
 463 primary tumour samples was scaled according to tumour purity estimates reported by Hoadley et
 464 al⁸⁹ to account for potential confounding quiescence signals coming from non-tumour cells in the
 465 microenvironment. Samples with purity estimates lower than 30% were removed, leaving 8,005
 466 samples for downstream analysis.

467 The mutation rates of all TCGA primary tumour samples were determined by log-transforming the
 468 total number of mutations in each sample divided by the length of the exome capture (38Mb).

469 *TP53* functional status was assessed based on somatic mutation and copy number alterations as
 470 described in Zhang et al⁹⁰. *TP53* mutation and copy number for the TCGA tumours were
 471 downloaded from cBioPortal (<http://www.cbioportal.org>). Tumours with *TP53* oncogenic
 472 mutations (annotated by OncoKB) and copy-number alterations (GISTIC score ≤ -1) were assigned
 473 as *TP53* mutant and CNV loss. Tumours without these *TP53* alterations were assigned as *TP53*
 474 wild type. The effects of the *TP53* mutation status on quiescence score were then determined with
 475 a linear model approach with the quiescence score as a dependent variable and mutational status as
 476 an independent variable. The *P* values were FDR-adjusted.

477 APOBEC mutagenesis enriched samples were determined through pan-cancer clustering of
 478 mutational signature contributions as described in Wiecek et al⁹¹. The APOBEC mutagenesis
 479 cluster was defined as the cluster with highest mean SBS2 and SBS13 contribution. This was
 480 repeated 100 times and only samples which appeared in the APOBEC cluster at least 50 times were
 481 counted as being APOBEC enriched.

Aneuploidy scores and whole genome duplication events across TCGA samples were obtained from Taylor et al⁹². Microsatellite instability status for uterine corpus endometrial carcinoma, as well as stomach and colon adenocarcinoma samples were obtained from Cortes-Ciriano et al⁵⁸. Telomerase enzymatic activity “EXTEND” scores were obtained from Noureen et al⁴⁰. Expression-based cancer cell stemness indices were obtained from Malta et al⁴¹. Centrosome amplification transcriptomic signature (CA20) scores were obtained from Almeida et al⁶⁸.

PHATE dimensionality reduction

The *phateR* R package⁹³ was used to perform the dimensionality reduction with a constant seed for reproducibility. The *ComBat* function from the *sva* R package⁹⁴ was used to remove tissue-specific expression patterns from the TCGA RNA-seq data.

Cancer stem cell division estimates

The mean stem cell division estimates for different cancer types used in this study were obtained from Tomasetti and Vogelstein³⁹.

Positive selection analysis

Genes positively selected specifically in samples clustered into low or high dormancy groups were identified based on dN/dS analysis using the *dNdScv* R package⁹⁵, run with default parameters. Genes showing signals of positive selection in either the high dormancy or low dormancy samples which encoded olfactory receptors were discarded from downstream analysis.

Mutational signature estimation

Mutational signature contributions were inferred as described in Wiecek et al⁹¹.

503 Ensemble elastic net regression model

504 The COSMIC database was used to source a list of 723 known drivers of tumorigenesis (Tiers
505 1+2). 285 oncogenes and tumour suppressors from a curated list showed a significant enrichment
506 or depletion of mutations or copy number variants in dormant samples either pan-cancer or within
507 individual TCGA studies.

508 To classify dormant from fast proliferating tumours, the 286 genes were used as input features for
509 an ensemble elastic net regression model along the tumour mutational rate, whole-genome
510 doubling estimates, ploidy, aneuploidy scores, 10 positively selected genes and 15 mutational
511 signatures, which showed a significant correlation with quiescence scores either pan-cancer or
512 within individual TCGA studies. The *caret* R package was used to build an elastic net regression
513 model 1000 times on the training dataset of 3,753 TCGA primary tumour samples (80% of the total
514 dataset). Only samples with at least 50 mutations were used in the model, for which mutational
515 signatures could be reliably estimated. For each of the 1000 iterations, we randomly selected 90%
516 of the samples from the training dataset to build the model. Only features which were included in
517 all 1000 model iterations were selected for further analysis. To test the performance of our
518 approach, a linear regression model was built using the reduced list of genomic features and their
519 corresponding coefficients averaged across the 1000 elastic net regression model iterations. When
520 applying the resulting linear regression model on the internal validation dataset of 936 samples, we
521 found a strong correlation between the observed and predicted quiescence scores ($R = 0.73$, $p <$
522 $2.2e-16$).

523 SHAP values for the linear regression model used to predict quiescence scores were obtained using
524 the *fastshap* R package.

525

526 **Gene enrichment and network analysis**

527 Gene set enrichment analysis was carried out using the *ReactomePA* R package, as well as
528 GeneMania⁹⁶ and ConsensusPathDB⁹⁷. Interactions between CEP89 and other cell cycle
529 components were inferred using the list of cell cycle genes provided by cBioPortal and GeneMania
530 to reconstruct the expanded network with direct interactors (*STAG1*, *CCND2*, *STAT3*). Networks
531 were visualised using Cytoscape⁹⁸.

532 **Gene lists**

533 Genes associated with the G1 phase of the cell cycle were obtained from the curated
534 “REACTOME_G1_PHASE” list deposited at MSigDB.

535 Genes associated with apoptosis were obtained from the curated “HALLMARK_APOPTOSIS” list
536 deposited at MSigDB.

537 Genes associated with the senescence-associated secretory phenotype were obtained from Basisty
538 et al⁴⁴. Lists of genes making up the various DNA damage repair pathways were derived from
539 Pearl et al⁹⁹.

540 Genes associated with contact inhibition were obtained from the curated “contact inhibition” gene
541 ontology term. Genes associated with serum starvation were obtained from the curated
542 “REACTOME_CELLULAR_RESPONSE_TO_STARVATION” list deposited at MSigDB. MEK
543 inhibition was assessed based on the activity of the MAPK pathway as determined using an
544 expression signature (MPAS) consisting of 10 downstream MAPK transcripts¹⁰⁰.

545 **Validation of genomic features of dormancy**

546 For elastic net model feature validation, RNA-seq data was downloaded for six cancer studies from
547 cBioPortal¹⁰¹, along with patient-matched whole-genome, whole-exome and targeted sequencing

data. The 6 datasets used comprise breast cancer (SMC¹⁰² and METABRIC¹⁰³), paediatric Wilms' tumor (TARGET¹⁰⁴), bladder cancer, prostate adenocarcinoma and sarcoma (MSKCC¹⁰⁵⁻¹⁰⁷) studies. The data were processed and analysed in the same manner as the TCGA data. RNA-seq data for 27 MCF7 cell line strains, alongside cell line growth rates and targeted mutational sequencing data were obtained from Ben-David et al⁵⁹.

Genomic dependency modelling in breast cancer

An ANOVA-based feature importance classification was used and identified 30 genomic features most discriminative of samples with lower and higher than average quiescence scores. A random forest model was then built using the identified features and correctly classified samples according to their quiescence state with a mean accuracy of 74% across five randomly sampled test datasets from the cohort.

Survival analysis

Multivariate Cox Proportional Hazards analysis was carried out using the *coxph* function from the *survival* R package. The optimal quiescence score cut-off value of 2.95 was determined using the *surv_cutpoint* function.

Treatment response scRNA-seq and bulk RNA-seq data

Datasets have been obtained from the GEO database through the following GEO Series accession numbers: GSE134836, GSE134838, GSE134839, GSE137912, GSE149224, GSE124854, GSE135215, GSE99116, GSE152699, GSE178839 and GSE139944. The *umap* R package was used for dimensionality reduction with constant seed for reproducibility.

569 Quiescence subtype determination

570 *TCGA cohort studies:*

571 Samples with evidence of dormancy characterised by a generic quiescence score > 0 were further
 572 subclassified based on the most likely form of quiescence exhibited, among CDK4/6 inhibition,
 573 contact inhibition, MEK inhibition, spontaneous quiescence or serum starvation, using subtype-
 574 specific expression signatures. We opted for a conservative approach and classed each dormant
 575 sample into a specific quiescence subtype if the quiescence score for the corresponding programme
 576 was higher than one standard deviation of the distribution across the TCGA cohort, and if the score
 577 was significantly higher than for the remaining programmes when assessed using a Student's t test.
 578 Samples which could not be classified into any of the five quiescence states characterised in this
 579 study were classified as “uncertain”.

580 *Single-cell RNA seq treatment response datasets:*

581 The quiescence subtype of individual single cells was inferred by mapping such individual cells
 582 onto the reference dataset of MCF10A cells reflecting different forms of quiescence obtained from
 583 Min and Spencer¹⁸. The *ComBat* R package was used to remove the study batch effect between the
 584 expression data to be classified and the reference bulk RNA-seq data. PCA dimensionality
 585 reduction analysis was then used on the combined datasets using the *prcomp* R function. For each
 586 patient sample or single-cell expression data entry, a k-nearest neighbour algorithm classification
 587 was performed using the *knn* function from the *class* R package. During the classification the three
 588 nearest reference bulk RNA-seq data points were considered, with two nearest neighbours with
 589 identical class needed for classification.

590

591

592 Optimisation of dormancy signature

593 We investigated if a subset of the 139 quiescence-related genes could act as a more reliable marker
594 of dormancy that would bypass dropout issues in single cell data. This was performed in three
595 steps:

596 *(1) Assessment of individual importance as quiescence marker for a given gene*

597 We collected three high confidence single cell expression datasets separating quiescent from
598 dormant cells. A random forest model was trained on each dataset separately to predict the
599 quiescence state of a given cell based on the expression levels of the 139 genes. The Gini
600 indices corresponding to each gene in the model were normalised to a range of values between
601 0 and 1, which would reflect how important an individual gene was for determining quiescence
602 state relative to the other 138 genes. The procedure was repeated 1000 times for each of the
603 three datasets, and the average Gini coefficients across iterations were stored.

604 *(2) Prioritisation of gene subsets based on cumulative importance in the model*

605 Genes were placed in the candidate subset if their importance metric was above a given
606 threshold in at least one of the datasets. By gradually increasing the threshold from 0 to 1,
607 different gene combinations were produced.

608 *(3) External validation of candidate subsets*

609 The gene combinations in (2) were tested for their ability to predict quiescence. For this, a
610 separate validation dataset was utilized, which contained gene expression levels for the 139
611 genes in the 10 lung cancer cell lines previously employed for experimental validation, along
612 with the quiescence state of the lines as inferred by PRb and EdU staining. For each gene
613 subset, a combined z-score of quiescence was calculated from the expression levels as
614 described previously. The correlations between this z-score and the two experimental
615 measurements of quiescence were used to establish the ability of a gene combination to predict

quiescence. Among the top performing subsets, a 35 gene signature with a mean correlation of 78% between predicted and measured quiescence levels in the test data ($p=0.016$) showed the highest correlation with PRb measurements capturing short-lived quiescence, the more common state observed in single cell treatment datasets. Therefore, this signature was deemed to achieve the best trade-off between gene numbers and signal capture.

The optimised gene signature is available at <https://github.com/secrierlab/CancerDormancy>

Data visualization and basic statistics

Graphs were generated using the ggplot2 and ggpubr R packages. Groups were compared using a two-sided Student's t test, Wilcoxon rank-sum test or ANOVA, as appropriate. P-values were adjusted for multiple testing where appropriate using the Benjamini-Hochberg method.

Data availability

The results published here are in part based upon data generated by the TCGA Research Network: <https://www.cancer.gov/tcga>, METABRIC (<https://ega-archive.org/studies/EGAS00000000083>), MSK-IMPACT (<https://www.mskcc.org/msk-impact>), or deposited at cBioPortal (<https://www.cbioportal.org/>) and GEO (<https://www.ncbi.nlm.nih.gov/geo/>). All data comply with ethical regulations, with approval and informed consent for collection and sharing already obtained by the relevant consortia.

Code availability

All code developed for the purpose of this study can be found at the following repository: <https://github.com/secrierlab/CancerDormancy>

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648 **AUTHOR CONTRIBUTIONS**

649 MS designed the study and supervised the computational analyses. ARB designed and supervised
650 the experimental validation in cell lines. GB supervised the analysis of p53 functional association.
651 AJW developed the dormancy scoring methodology and performed all computational analyses to
652 validate and apply it in bulk and single cell datasets, as well as link it to genomic features. SC
653 performed the experimental validation of quiescence prevalence and CEP89 association with
654 quiescence in cell lines. DK performed the inference of the minimal signature of dormancy
655 applicable in single cell data. MPC performed the random forest modelling and feature selection in
656 breast cancer. LG performed the positive selection analysis. GMT wrote the code for batch effect
657 correction and for PCA mapping of single cell data on a reference dataset. DHJ performed the
658 APOBEC enrichment classification. PZ and LX performed the quiescence comparison of p53 wild
659 type and mutated cancers. MS, AJW, ARB and SC wrote the manuscript, with contributions from
660 all other authors. All authors read and approved the manuscript.

661   **COMPETING INTEREST STATEMENT**

662   None declared.

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884 **FIGURES**

885

886 **Figure 1: Methodology for quantifying cancer dormancy. (a) Workflow for evaluating**

887 dormancy from RNA-seq data. 139 genes differentially expressed in multiple forms of quiescence

888 were employed to score dormancy across cancer tissues. **(b)** Receiver operating characteristic
889 (ROC) curves illustrating the performance of the z-score methodology on separating actively
890 proliferating and quiescent cells in seven single-cell (continuous curves) and bulk RNA-seq (dotted
891 curves) datasets. AUC = area under the curve. **(c)** Compared classification accuracies of the z-score
892 approach and classic cell proliferation markers across the seven single-cell/bulk RNA-seq
893 validation datasets. **(d)** Quiescence levels of embryonic fibroblast cells under serum starvation for
894 various amounts of time. Replicates are depicted in the same colour. **(e)** Representative images of
895 lung cancer cell lines immunostained and analysed to detect the quiescent fraction. Hoechst (labels
896 all nuclei) is in blue, PRb in green and EdU in red in merged image. White dashed circles highlight
897 quiescent cells that are negative for both PRb and EdU signals. Scale bar: 100 μ m. **(f)** Graphs show
898 single cell quantification of PRb and EdU intensities taken from images and used to define the cut-
899 off to calculate the quiescent fraction (QF; green boxes). Images in **(e)** and graphs in **(f)** are taken
900 from the A549 cell line. **(g-h)** Correlation between theoretical estimates of a quiescence or G1 state
901 and the fraction of cells entering quiescence in nine lung adenocarcinoma cell lines, as assessed
902 through **(g)** phospho-Rb assays and **(h)** EdU assays. Mean of n=3 is shown for the average
903 percentage of quiescent cells.

904

Figure 2: Pan-cancer evaluation of dormancy. (a) PHATE plot illustrating the wide spectrum of dormancy-proliferation states across 8,005 primary tumour samples from TCGA. Each sample is coloured according to the relative dormancy level. (b) Variation in tumour dormancy levels across different cancer tissues. (c) Correlation between mean quiescence scores and stem cell division estimates for various tissue types. (d) Correlating tumour dormancy scores with cancer cell stemness (Stemness Index), telomerase activity (EXTEND score) and the expression of several commonly used proliferation markers. The Pearson correlation coefficient is displayed. RC – replication complex. (e) Consistently higher levels of dormancy are detected in samples with functional p53. (f) Lower quiescence scores are observed in tumours with one or two whole genome duplication events. Wilcoxon rank-sum test p-values are displayed in boxplots, * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

Figure 3: Pan-cancer genomic landscape of dormancy. (a) Cancer drivers with mutations or copy number alterations depleted pan-cancer in a dormancy context. Features further selected by

920 the pan-cancer model are highlighted. **(b)** Schematic of the ensemble elastic net modelling
 921 employed to prioritise genomic changes associated with tumour dormancy. **(c)** Genomic events
 922 significantly associated with dormancy, ranked according to their importance in the model (highest
 923 to lowest). Each point depicts an individual tumour sample, coloured by the value of the respective
 924 feature. For discrete variables purple indicates the presence of the feature and green its absence.
 925 The Shapley values indicate the impact of individual feature values on the quiescence score
 926 prediction. **(d)** Dormancy levels are significantly reduced in microsatellite unstable (MSI) samples
 927 in stomach adenocarcinoma (STAD) and uterine corpus endometrial carcinoma (UCEC), with the
 928 same trend (albeit not significant) shown in colon adenocarcinoma (COAD). Wilcoxon rank-sum
 929 test $*p<0.05$; $**p<0.01$. **(e)** Genomic alterations are depleted across DNA repair pathways during
 930 dormancy. Odds ratios of mutational load on pathway in dormancy are depicted, along with
 931 confidence intervals. CS=chromosome segregation; p53=p53 pathway; UR=ubiquitylation
 932 response; CPF=checkpoint factors; TM=telomere maintenance; CR=chromatin remodelling;
 933 TLS=translesion synthesis; NHEJ=non-homologous end joining; NER=nucleotide excision repair;
 934 MMR=mismatch repair; FA=Fanconi Anaemia; BER=base excision repair. **(f)** Dormancy is
 935 increased in cell lines with slow doubling time across MCF7 strains, which also show lower
 936 prevalence of PTEN mutations. **(g)** Tissue-specific changes in quiescence between samples
 937 with/without dormancy-associated deletions (blue), amplifications (red) and SNVs (brown) within
 938 the TCGA cohort (top) and external validation datasets (bottom).

Figure 4: CEP89 amplification is associated with lower tumour dormancy. (a) Network illustrating CEP89 interactions with cell cycle genes (from GeneMania). The edge colour indicates the interaction type, with green representing genetic interactions, orange representing predicted interactions and purple indicating pathway interactions. The edge width illustrates the interaction weight. (b) CA20 scores are significantly increased in TCGA primary tumours containing a CEP89 amplification. (c) Pan-cancer relationship between CA20 scores and tumour quiescence across the TCGA cohort. (d) Cox proportional hazards analysis estimates of the log hazards ratio for the impact of CEP89 expression on patient prognosis within individual cancer studies, after adjusting for tumour stage. Patients with high expression of CEP89 show significantly worse prognosis within ACC, LUSC, LIHC, KIRC and STAD, but significantly better prognosis within HNSC,

950 PAAD and KIRP studies. **(e)** Western blot showing depletion of Cep89 protein 48h after siRNA
 951 transfection of NCI-H1299 cells. Mock is lipofectamine only, NTC is Non-targeting control
 952 siRNA. B-actin is used as a loading control. **(f)** Graphs show that Cep89 depletion in NCI-H1299
 953 cells leads to a reduction in nuclear number and an increase in the fraction of quiescent cells,
 954 measured by an increase in the percentage of EdU negative (24h EdU pulse) and Phospho-Ser
 955 807/811 Rb negative cells. One-Way ANOVA, * $p < 0.05$, ** $p < 0.01$. Mean of $n=3$.

Figure 5: Genomic landscape of breast cancer dormancy. (a) ROC curve illustrating the mean performance of the random forest model for dormancy prediction in breast cancer based on 9

randomisations. **(b)** Impurity criterion information gain for the top ranked genomic events predictive of dormancy in the TCGA BRCA cohort, modelled using random forests. Features also appearing in the pan-cancer model are highlighted in dark purple. WGD = whole-genome doubling. **(c)** Tissue-specific changes in dormancy estimates between samples with and without dormancy-associated amplifications (red) and SNVs (purple), identified by the breast cancer specific random forest model, within the TCGA cohort (top panel) and external validation datasets (bottom panel). **(d)** Dormancy scores are significantly higher in APOBEC mutation-enriched breast cancer samples. **(e)** APOBEC-linked SBS2 mutational burden compared between breast cancer subtypes. **(f)** Association between dormancy scores, APOBEC enrichment and breast cancer subtypes in TCGA.

Figure 7: Impact of cellular dormancy on patient prognosis and treatment response. (a)

Disease-specific survival based on tumour dormancy for patients from TCGA within 15 years of

990 follow up. Patients with high primary tumour dormancy showed significantly better prognosis than
 991 patients with low dormancy. **(b-c)** Hazard ratio ranges illustrating the impact of different forms of
 992 quiescence **(b)** and different tissues **(c)** on patient prognosis, after taking into account potential
 993 confounding factors. Values above 0 indicate significantly better prognosis in the context of high
 994 tumour dormancy. **(d)** Change in quiescence scores inferred from bulk RNA-seq across breast,
 995 pancreatic, colorectal and skin cancer cells in response to treatment with the CDK4/6 inhibitor
 996 Palbociclib, 5-FU or the BRAF inhibitor Vemurafenib. **(e-f)** UMAP plot illustrating the response of
 997 the TP53-proficient RKO colorectal cancer cell line to various 5-FU doses and the corresponding
 998 proportions of cells predicted to be quiescent/proliferating. Each dot is an individual cell, coloured
 999 according to its dormancy level. **(g-h)** The same as previous, but for the TP53-deficient SW480
 1000 cell line. **(i-j)** UMAP plot illustrating the response of individual PC9 NSCLC cells to the EGFR
 1001 inhibitor Erlotinib across several time points and the corresponding proportion of cells predicted to
 1002 be quiescent/proliferating. **(k)** Principal component analysis illustrating the superimposition of
 1003 scRNA-seq profiles (circles) of quiescent NSCLC cells before/after EGFR inhibition onto the bulk
 1004 RNA-seq reference data (triangles) for MCF10A cells occupying various quiescence states. **(l)** The
 1005 proportion of NSCLC cells in **(k)** predicted to occupy different quiescence states across several
 1006 time points.

Figure 8: Optimisation of dormancy signature for use in scRNA-seq data. (a) Methodology for refining the gene signature of dormancy: random forest classifiers are trained to distinguish dormant from cycling tumours on three high confidence datasets; Gini index thresholding is optimised to prioritise a final list of 35 genes. **(b)** Gini index variation, correlation with experimentally measured quiescence via EdU and PRb staining assays, and corresponding p-values are plotted as the number of genes considered in the model is increased. The red dotted line

1014 indicates the threshold chosen for the final solution of 35 genes. The black dotted line indicates the
 1015 threshold for p-value significance. **(c)** Additional external validation of the 35 gene signature acting
 1016 as a classifier of quiescent and proliferation cells in single cell and bulk datasets. **(d)** Dropout in
 1017 single cell data by gene signature. The percentage of genes out of the 35 (red) and 139 (grey) gene
 1018 lists with reported expression across the single-cell RNA-seq datasets analysed in this study. **(e)**
 1019 Proportion of cycling and quiescent cells estimated in single cell datasets of p53 wild type and
 1020 mutant lines treated with 5FU, as well as cells treated with EGFR inhibitors. Data as in Figure 7.

1021

1022 EXTENDED DATA

1023
1024 **Extended Data Figure 1: Quiescence evaluation and validation.** (a) Classification accuracies
1025 measured using the Matthews correlation coefficient (MCC) comparing the combined z-score
1026 quiescence scoring method to other scoring methodologies across the seven single-cell and bulk
1027 RNA sequencing validation datasets. (b) Receiver operating characteristic (ROC) curves

1028 illustrating the accuracy of the combined z-score methodology when separating dormant and
 1029 proliferating hematopoietic stem cells from three publicly available single-cell RNA-seq datasets.
 1030 Datasets used are denoted by their corresponding GEO series accession number and the area under
 1031 the curve (AUC) for each dataset is specified. **(c)** Mean correlation between computationally
 1032 inferred dormancy scores after randomly removing variable number of genes from the dormancy
 1033 signature and the fraction of cells entering quiescence in nine lung adenocarcinoma cell lines, as
 1034 assessed through an EdU staining assay. **(d)** Same as **(c)** but with experimental levels of quiescence
 1035 measured using a phospho-Rb staining assay. **(e)** Mean classification accuracy across 7 bulk and
 1036 single-cell RNA-seq validation datasets after randomly removing variable number of genes from
 1037 the dormancy signature. **(f-g)** PHATE plots displaying the first two principal components obtained
 1038 from dimensionality reduction analysis across 8,005 primary tumour TCGA samples, based on the
 1039 expression of 139 genes differentially expressed across different quiescence programmes before
 1040 (left) and after (right) removal of tissue specific expression patterns. Each primary tumour sample
 1041 is coloured by their corresponding tissue of origin **(f)** or the corresponding quiescence score **(g)**.

1049 samples with low expression (lower quartile of the expression distribution) across TCGA cancer
 1050 types. **(f)** Consistently higher levels of dormancy are detected in samples with a functional
 1051 DREAM complex. TCGA studies where mutations within one of the DREAM components could
 1052 be detected in at least 10 patients are shown. **(g)** Correlation between quiescence levels and
 1053 mutational signature contributions across TCGA cancer types. Only significant correlations are
 1054 displayed (Pearson correlation p-value < 0.05).

1055

1056 **Extended Data Figure 3: Modelling and validating a pan-cancer classifier of dormancy. (a)**

1057 Genomic features and cancer types significantly associated with dormancy, ranked according to

their importance in the pan-cancer linear regression model (from highest to lowest contribution). The genomic features highlighted are identical to Figure 3c, but cancer types are shown here as well. Each point corresponds to one sample and is coloured according to the original value of the respective feature. For discrete variables purple indicates the presence of the feature and green indicates the absence of the feature. For cancer type variables, purple indicates the patient belongs to the specified TCGA cancer type group. The Shapley values indicate whether the quiescence scores predicted by the ensemble elastic net regression model for each patient are increased or decreased depending on the cancer type of each individual as well as specific SNVs, CNV and other genomic features. **(b)** Correlation between the observed quiescence scores within the test dataset (x axis) and scores predicted by the linear regression model using the selected pan-cancer features (y axis). **(c)** Pathways significantly altered in association with tumour dormancy.

Extended Data Figure 4: CEP89 expression is associated with quiescence and has prognostic value. (a-c) CEP89 expression is negatively correlated with quiescence scores in lung **(a)**, pancreas **(b)** and thyroid **(c)** cancer cell lines. The NCI-H1299 cell line where CEP89 activity was tested is highlighted in red. **(d)** Compounds with selective toxicity on cell lines with high CEP89 expression. The volcano plot shows the Pearson correlation coefficients and the corresponding p-values for associations between CEP89 expression and Area Under the dose-response Curve (AUC) for each compound across cell lines from the CCLE.

Extended Data Figure 5: Quiescence subtype validation. Correlation between subtype-specific quiescence estimates and (a) mean expression of CDK4/6, (b) the mean expression of curated

1081 contact inhibition genes, **(c)** MPAS scores, **(d)** mean expression of curated serum starvation genes
 1082 and **(e)** CDKN1A expression, across individual TCGA cancer studies and pan-cancer. The colour
 1083 gradient indicates the strength of the association (positive or negative).

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Extended Data Figure 6: Tumour dormancy relevance to clinical outcome. (a) Multivariate

Cox proportional hazards analysis of the disease specific survival in the TCGA cohort, modelled

1087 on tumour dormancy (binarized by optimised survival cut-off into high, where score > 2.95; and
1088 low, where score <= 2.95) and potential confounding factors. **(b)** Quiescence scores in TCGA
1089 cancers compared across tumour stages. **(c)** The average expression of apoptosis genes compared
1090 between TP53 wild type RKO and TP53 mutant SW480 colorectal cancer cell lines in response to
1091 various 5-FU treatment doses. **(d)** The average expression of apoptosis genes compared between
1092 quiescent and cycling cells within the TP53 WT RKO and TP53 MT SW480 cell lines. **(e)** The
1093 number of NSCLC cells sequenced during the EGFR inhibition treatment time course. **(f)** The
1094 average expression of apoptosis genes compared between quiescent and cycling cells at different
1095 time points during EGFR inhibition treatment. There is a notable increase in apoptotic activity of
1096 cycling cells at day 1. **(g)** Response of melanoma cancer cells to BRAF inhibition treatment across
1097 several time points, illustrated using UMAP plots coloured by quiescence score of individual cells.
1098 **(h)** Response of NSCLC cells to EGFR inhibition via Erlotinib across several time points,
1099 illustrated using UMAP plots coloured by quiescence score of individual cells. **(i)** Response of lung
1100 adenocarcinoma cell lines to KRAS inhibition treatment across several time points, illustrated
1101 using UMAP plots coloured by quiescence score of individual cells. **(j)** Percentage of cells
1102 illustrated in **(g-i)** predicted to be quiescent across the treatment time course.

Extended Data Figure 7: Quiescence dynamics upon various treatment modalities. (a-b)

Percentage of quiescent MCF7 (a) and A549 (b) cells following 24-hour treatment with selected

1106 compounds. Treatments highlighted in blue and red indicate the 30 compounds which showed the
 1107 highest decrease and increase in quiescence levels, respectively, in comparison to the control,
 1108 shown in grey. **(c-d)** The average percentage of quiescent MCF7 **(c)** and A549 **(d)** cells following a
 1109 24-hour treatment with compounds affecting specific pathways. Pathways shown in blue and red
 1110 indicate an average decrease and increase in quiescence respectively in comparison to the control,
 1111 shown in grey.

1112

1113 **Extended Data Figure 8: Application of reduced dormancy signature to scRNA-seq data. (a-**

1114 **c) UMAP plot illustrating the response of (a) the TP53-proficient RKO colorectal cancer cell line**

1115 to various 5-FU doses, **(b)** the TP53-deficient SW480 colorectal cancer cell line to various 5-FU
1116 doses, and **(c)** the P9 NSCLC cell line to the EGFR inhibitor Erlotinib across several timepoints.
1117 Each dot is an individual cell and it is coloured according to its dormancy level, calculated using
1118 the optimised 35 gene signature. **(d)** Principal component analysis illustrating the superimposition
1119 of scRNA-seq profiles (circles) of quiescent NSCLC cells, inferred using the optimised 35 gene
1120 signature, before and after EGFR inhibition onto the bulk RNA-seq reference data (triangles) for
1121 MCF10A cells occupying various quiescence states. The NSCLC cell line quiescence type was
1122 predicted using a k-nearest neighbour algorithm based on the bulk RNA-seq reference.
1123