Intra-epithelial non-canonical Activin A signalling safeguards prostate progenitor quiescence

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Abstract

The healthy prostate is a relatively quiescent tissue. Yet, prostate epithelium overgrowth is a common condition during ageing, associated with urinary dysfunction and tumorigenesis. For over thirty years, TGF-β ligands have been known to induce cytostasis in a large variety of epithelia, but the intracellular pathway mediating this signal in the prostate, as well as its relevance for quiescence, have remained elusive.

Here, using mouse prostate organoids to model epithelial progenitors, we found that intra-epithelial non-canonical Activin A signalling inhibited cell proliferation in a Smad-independent manner. Mechanistically, Activin A triggered Tak1 and p38 MAPK activity, leading to p16 and p21 nuclear import. Spontaneous evasion from this quiescent state occurred upon prolonged culture, due to reduced Activin A secretion, a condition associated with DNA replication stress and aneuploidy. Organoids capable to escape quiescence *in vitro* were also able to implant with increased frequency into immunocompetent mice.

Our study demonstrates that non-canonical Activin A signalling safeguards epithelial quiescence in the healthy prostate, with potential implications for the understanding of cancer initiation, and the development of therapies targeting quiescent tumour progenitors.

Introduction

The healthy prostate is a relatively quiescent tissue during adulthood[1,2]. In contrast, the overgrowth of the prostatic epithelium is one of the most common conditions experienced by ageing men, being linked with urinary dysfunction and tumorigenesis[3]. The molecular mechanisms causing exit from quiescence are poorly understood. Chronic inflammation – potentially induced by infection (*e.g.,* prostatitis)[4–6], chemical damage (*e.g.,* urine reflux)[7], physical trauma (e.*g.,* corpora amylacea)[8], dietary carcinogens[9], obesity[10], hormonal imbalance (*e.g.*, low systemic androgen levels)[11,12], and ageing[13] – has been implicated in DNA damage, oxidative stress, and atrophy, leading to a proliferative response[14,15]. Considering the high frequency of these events, it would be logical to hypothesize specialized mechanisms to safeguard epithelial quiescence, but they have been rarely investigated.

It has long been known that Transforming Growth Factor β (TGF-β) signalling inhibits the proliferation of a large variety of epithelial cell types[16,17], including those of the prostate[18]. SMAD factors are the canonical intracellular mediators of this signalling, but additional non-canonical pathways can also be triggered by TGF-β receptors[19,20]. In gastrointestinal (GI) carcinomas (*e.g.*, pancreas, colon), the canonical pathway is frequently mutated[21,22]. However, outside of the GI tract, TGF-β/SMAD components are rarely inactivated in tumours, leaving unexplained the nature of the intracellular signalling responsible for the cytostatic effect of TGF-β[23,24].

Enhanced Tgf-β signalling has been linked with the presence of quiescent epithelial progenitors in the proximal/periurethral region of the mouse prostate[25,26]. Recent single-cell studies have confirmed the enrichment of a variety of epithelial progenitors – basal, luminal proximal (LumP), and periurethral (PrU) cells – in this anatomical district, though also present at low frequency in the distal compartment[27–32]. Such cells are known to be particularly quiescent during homeostasis[33,34], but also to exhibit extensive regenerative potential in *ex-vivo* assays[31,35].

Thus, the TGF-β induced cytostatic response in epithelial progenitors may be relevant for the control of quiescence, but the complexity of this pathway, the lack of interpretable genetic alterations in patients, and the heterogeneous cellular composition of the prostate, have so far hampered mechanistic investigations. Here, we reasoned that prostate organoid models[36,37] – in combination with orthotopic transplantation approaches – may provide a biologically relevant, and experimentally amenable, system for addressing this question.

87 ## Results

88 **Mouse prostate organoid cultures enable the continuous expansion of epithelial progenitors in**
89 **a near-physiological manner.**

90 Initially, we set out to assess whether mouse prostate organoids are a representative and
91 informative model for the study of the prostate epithelium, in light of recent discoveries on prostate
92 cellular heterogeneity and dynamics[27,28,30–32,34,38]. Considering our interest in signalling, we focused
93 on a culture method in defined media conditions. This protocol relies on a mix of growth factors and
94 inhibitors, including Egf, Noggin, R-spondin 1, the Tgf-β receptors inhibitor A83-01, and
95 dihydrotestosterone (ENRAD)[36]. We generated a biobank of mouse prostate organoids, starting from
96 bulk populations of cells from distinct prostate lobes and mouse strains (Fig. 1a, Supplementary Fig
97 S1). In line with previous studies[36,37], we found that, upon tissue dissociation, only a small fraction
98 of cells (approx. 1%) was capable to generate organoids in culture, and that organoid-forming
99 efficiency increased over passages, suggesting enrichment for epithelial progenitors (Fig. 1b). To gain
100 greater insights, we longitudinally tracked organoid formation – from single cells to fully formed
101 organoids – and we observed a progressive expansion of cells expressing the progenitor epithelial
102 surface antigen Sca-1 (encoded by *Ly6a*) (Fig. 1c)[31,35]. Thereafter, the level of Sca-1 appeared to be
103 stable over a long culture period (*e.g.*, 10 weeks). To extend our observations, we performed
104 transcriptomic analyses on three organoid lines derived from distinct mouse prostate lobes (Fig. 1d,e).
105 Consistently with enrichment for epithelial progenitors, organoids expressed high levels of genes
106 specific for the proximal and periurethral compartments (*e.g.*, *Psca*, *Tacstd2*, and *Ly6d*), as well as
107 basal (*e.g.*, *Krt5*, *Krt14, Trp63*) and luminal marker genes (*e.g., Krt8*, *Ar, Foxa1*). In contrast, distal
108 luminal markers were barely detectable (*e.g., Nkx3.1*, *Pbsn*, *Sbp*). Histological (H&E) and
109 immunofluorescent (IF) analyses confirmed that prostate organoids, for the most part, are made up
110 of a bilayer of cuboidal cells, displaying progenitor marker proteins (*e.g.*, Krt7, Ppp1r1b), and
111 resembling the cyto-architecture of the periurethral/proximal compartment (Fig. 1f-h). As expected
112 for periurethral/proximal cells – which are known to be castration resistant – mouse prostate
113 organoids were reversibly dependent on androgen for lumen formation, but not for their survival
114 (Supplementary Fig. S2).

115 The epithelium of the prostate is characterized by a slow cellular turnover. In contrast, prostate
116 organoids appeared to proliferate indefinitely – while retaining low levels of genomic instability
117 (Supplementary Fig. S3) – raising the question of how culture conditions enable persistent cycling in
118 a near-physiological manner. Either an excess of stimulatory cues in culture, or a lack of inhibitory

119 ones – or both – may explain the shift from homeostatic quiescence *in vivo* to unrestrained mitotic
120 activity *in vitro*. Using a 'n -1 approach' for assessing the requirement for growth factors and
121 inhibitors in culture (Supplementary Fig. S4a), we found that prostate organoids are strictly dependent
122 on Egf, with sub-nanogram concentration levels being sufficient for cell cycle progression
123 (Supplementary Fig. S4b,c). Still – based on ligand/receptor expression patterns – Egf signalling
124 alone is unlikely to explain the excess of proliferation in culture. Indeed, *Egf* is highly transcribed by
125 distal luminal cells in the adult prostate[28], and progenitor cells express the Egf receptor *in vivo* –
126 independently of their proximal or distal location – at levels comparable to those observed *in vitro*
127 (Supplementary Fig. S4d). Therefore, we focused on the requirement for the Tgf-β receptor inhibitor
128 A83-01 for the continuous expansion of mouse prostate organoid cultures.

129 **Intra-epithelial non-canonical Activin A signalling is a key mediator of the Tgf-β induced**
130 **cytostatic response in mouse prostate organoids.**

131 Upon A83-01 withdrawal, organoids displayed a marked reduction in EdU incorporation
132 within 24 hours, demonstrating a cytostatic response in this model (Fig. 2a, Supplementary Fig. S5a).
133 A83-01 is a potent inhibitor of three type-I Tgf-β family receptors, and two of them - Acvr1b and
134 Tgfbr1 (also known as Alk4 and Alk5) – were found to be expressed in prostate organoids
135 (Supplementary Fig. S5b). Paracrine and autocrine ligand-receptor interactions have been
136 demonstrated to negatively regulate epithelial proliferation[16,39] leading us to investigate the release
137 of Tgf-β ligands in organoid cultures. We employed a click-chemistry approach to enrich for secreted
138 proteins released in the culture medium, followed by mass-spectrometry analysis[40]. Over multiple
139 experiments, we consistently recovered Activin A peptides (encoded by the *Inhba* gene) in the
140 organoid supernatant, and only in one instance, a Tgfb1 peptide (Fig. 2b). We were also able to
141 immunolocalize Acvr1b in organoid cells, and in progenitor cells *in vivo* (Fig. 2c), with an expression
142 pattern similar to Egfr (Supplementary Fig. S4d). Replacement of A83-01 with Follistatin - a well-
143 known Activin A inhibitor[41] – was sufficient to sustain proliferation, revealing a prominent role for
144 the latter in inducing a cytostatic response (Fig. 2d). To gain greater insights on the downstream
145 pathway, we boosted Tgf-β receptor activity by combining A83-01 withdrawal with the
146 supplementation of distinct ligands. Activin A was found to enhance the non-canonical arm of Tgf-β
147 signalling – mediated by the Tgf−β activated kinase, Tak1 (encoded by the *Map3k7* gene), and the
148 downstream p38 MAPKs – as well as the accumulation of the cell cycle inhibitor p21 (Fig. 2e). In
149 contrast, Tgfb1 increased the activity of the canonical Tgf-β pathway – via Smad2/3 phosphorylation,
150 but with little, if any, alteration of p21 levels. This dichotomy prompted us to functionally test the

151 role of the canonical, and non-canonical pathway, respectively. Disruption of the canonical pathway,
152 via shRNA-mediated silencing of Smad4, did not alter the cytostatic response upon A83-01
153 withdrawal (Supplementary Fig. S6). In contrast, the inhibition of either Tak1 or the structurally
154 related p38α and p38β MAPKs – using a variety of inhibitors (Fig. 2f,g; Supplementary Fig. S7a,b)
155 – was sufficient to ensure organoid expansion in the absence of Tgf-β receptor blockade.

156 TGF-β receptors, and cytokine-stimulated receptors (*e.g.*, IL-1, TNF, type-I interferons), are
157 known to converge on TAK1-p38 MAPK signalling to activate a variety of downstream factors
158 controlling immune- and stress-related responses, including well-characterized transcriptional
159 programmes[42–45]. By combining bulk-RNA sequencing and biochemical approaches, we confirmed
160 that in the absence of Tgf-β receptors inhibition, Tak1-p38α/β signalling resulted in phosphorylation
161 and nuclear shuttling of immune-related transcription factors (*e.g.*, Stat1/2, NF-kB), which led to the
162 transcription of immune related gene sets (*e.g.,* induced by TNF or type-I interferons)[46], as well as to
163 the phosphorylation of the stress-related kinase Mapkapk2 (Fig. 2h,i; Supplementary Fig. S7c-f).
164 Importantly, Tak1-p38 MAPK activity was associated with the nuclear accumulation of the key cell
165 cycle inhibitors p21 and p16 (Fig. 2h).

166 Collectively, our data demonstrated that intra-epithelial non-canonical Activin A signalling
167 induce a cytostatic response in mouse prostate organoids.

168 **Evasion from the Tgf–β induced cytostatic response via downregulation of intra-epithelial**
169 **Activin A signalling.**

170 We reasoned that our biobank may offer the opportunity to discover mechanisms of evasion
171 from the Tgf–β induced cytostatic response, mediated by intra-epithelial Activin A signalling, in an
172 unbiased manner. Therefore, we attempted to culture multiple prostate organoid lines in the absence
173 of A83-01, waiting for the potential emergence of clones capable to thrive in these conditions. Out of
174 nine prostate organoid lines (from three distinct mice), six were irreversibly lost within few weeks.
175 Still, three lines survived for an extended period, with two of them eventually adapting to the absence
176 of A83-01 and recovering the ability to be passaged at clonal density (Fig. 3a,b; Supplementary Fig.
177 S8). We performed bulk-RNA sequencing on the C57#1 DLP organoid line in the presence of A83-
178 01, one day after inhibitor withdrawal, and upon adaptation; additionally, we sequenced the C57#3
179 DLP organoid line in control conditions and following adaptation (Fig. 3c). We focused on
180 transcriptional alterations shared by both lines displaying adaptation to A83-01 withdrawal. First, we
181 noticed that gene signatures associated with ATR signalling were strongly upregulated upon

182 adaptation (Fig. 3d), indicating potential DNA replication stress in S-phase, a finding consistent with
183 phosphorylation of the cell cycle Checkpoint kinase 1 (Chek1) (Fig. 3e). Of note, in the adapted
184 C57#1 DLP line we detected widespread genomic instability and telomere doublets, a hallmark of
185 DNA replication stress, while retaining an intact Trp53 pathway (Fig. 3f-h; Supplementary Fig. S9).
186 Second, in both adapted organoid lines, we observed the downregulation of immune-related
187 transcriptional programmes (*e.g.*, type-I interferon stimulated genes), suggesting an impairment of
188 non-canonical Activin A signalling (Supplementary Fig. S10). Consistently, we found that adapted
189 organoid lines significantly reduced Activin A secretion in culture (Fig. 3i), and that exogenous
190 Activin A (but not Tgfb1) was sufficient to restore the cytostatic response (Fig. 3j,k; Supplementary
191 Fig. S11).

192 Thus, mouse prostate organoids are capable to dampen the Tgf-β induced cytostatic response
193 by downregulation of intra-epithelial Activin A signalling.

194 **Mouse prostate organoids with reduced intra-epithelial Activin A signalling display enhanced**
195 **engraftment upon syngeneic transplantation.**

196 We wondered whether a reduced intra-epithelial Activin A signalling may release the
197 progenitor proliferative potential in response to basal growth stimuli, within the relative quiescent
198 microenvironment of the adult prostate epithelium. To test this hypothesis, we orthotopically
199 transplanted dissociated mouse prostate organoid cells into immunocompetent syngeneic mice (Fig.
200 4a). Donor cells were injected into the extensive branchial structures of the distal anterior prostate, to
201 avoid damage to the delicate proximal ducts, and maximize the probability of retention. Implantation
202 of donor cells into an immunocompetent host tissue characterized by a slow turnover can be
203 considered challenging. Still, we found that, in comparison to control organoid cells, organoid cells
204 adapted to grow without A83-01 implanted with high frequency (Fig. 4b), and gave rise to dysplastic
205 foci, characterized by elevated mitotic index, cuboidal histology and nuclear atypia (Fig. 4c,d).

206 We conclude that intra-epithelial non-canonical Activin A signalling safeguards quiescence
207 in prostate progenitors.

208 Discussion

209 Signalling pathways ensure coordination of tissue development, homeostasis, regeneration,
210 and their disruption can lead to disease. The molecular bases of specific signals are difficult to
211 investigate, due to the challenges of disentangling cellular cross talks *in vivo*, and of establishing
212 representative models *in vitro*. More recently, organoid models in defined media conditions have

213 opened new opportunities for the study of epithelia[47]. Benchmarking of these models with their
214 corresponding *in vivo* counterpart is paramount for the correct experimental interpretations[48]. Here,
215 we demonstrated that mouse prostate organoid cultures enable the continuous expansion of epithelial
216 progenitors *in vitro*, including basal, LumP and PrU cells. Such cell types are predominantly found
217 near the urethra *in vivo*, but also in the distal prostate compartment at low frequency. Our work
218 revealed that progenitor proliferation is dynamically regulated by the antagonistic equilibrium
219 between Egf and non-canonical Activin A signalling, respectively – with at least partial reduction of
220 the latter required for cell cycle progression. The rationale perturbation of additional biochemical
221 signals, and mechanical cues, may enhance progenitor differentiation towards distal luminal cells in
222 culture.

223 It has long been known that the broad family of TGF-β signals induces a cytostatic response
224 in a large variety of epithelial cells, but the specific pathway acting in the prostate has remained
225 poorly understood. Earlier studies pointed to the importance of the Tgf-β family ligand Activin[49,50].
226 At the mechanistic level, DePinho and colleagues initially focused on the role of Smad4 as a
227 proliferative barrier in a *Pten*-loss driven mouse model of prostate cancer[51]. Follow-up studies from
228 the same group and others, carried out in humans and mice, have led to a more complex view[52,53],
229 with the involvement of both canonical and non-canonical pathways.

230 We propose a prominent role for non-canonical Activin A signalling in safeguarding
231 quiescence in prostate epithelial progenitors (Fig. 4e). Our model may be relevant beyond tissue
232 homeostasis and the response to inflammation. Genes encoding for core components of the non-
233 canonical Activin A signalling pathway (*e.g.*, *ACVR2A, MAP3K7*) are frequently lost in prostate
234 cancer, based on large cohorts of patients in the U.S.A.[54] and in China[55]. Moreover, *MAP3K7* loss
235 has been linked to genomic instability in human prostate cancer cell lines[56] and found to promote an
236 aggressive transcriptional programme in prostate tumours, based on a recent systematic pan-cancer
237 analysis[57]. In contrast, genetic alterations rarely affect TGFB1 receptors (*e.g.*, *TGFBR2*) or SMAD
238 factors (*e.g., SMAD4*), and enhanced canonical TGF-β signalling has been reported upon metastatic
239 relapse in a small group of advanced prostate cancer patients[58]. We speculate that loss of the non-
240 canonical TGF-β arm could impair the cytostatic response, while sparing the well-known
241 transforming potential of the TGF-β canonical pathway.

242 Tak1/p38-MAPK signalling stimulated two main sets of effector proteins in prostate
243 progenitors. On the one hand, we observed the nuclear translocation of key negative cell cycle
244 regulators (*e.g.*, p16 and p21). On the other hand, using biochemical and transcriptional analyses, we
245 demonstrated the activation of a broad transcriptional response, reminiscent of those induced by

246 inflammatory cytokines and pathogens. These findings are in line with recent observations on the
247 immune function of structural cells[59] and suggest a cross talk between the epithelial and immune
248 compartments, beyond the well-known mechanisms of anti-microbial defence. Prostate progenitors
249 – and, perhaps, other types of epithelia cells – may have the ability to signal changes in their
250 proliferative status and, immune cells may have the capability to adjust their function in response.

251 To test the relevance of intra-epithelial non-canonical Activin A signalling for the
252 enforcement of quiescence in prostate progenitors, we performed experiments *in vitro* and *in vivo*.
253 Our long-term organoid cultures – in the absence of Tgf-β receptor blockade – revealed that cells
254 capable to re-enter cell cycle had downregulated Activin A secretion. Moreover, those cells were also
255 capable to implant and proliferate at increased frequency *in vivo*. While stromal sources of Tgf-β
256 ligands have been previously described in the prostate[25,26], our study is the first to demonstrate a key
257 role for intra-epithelial signalling.

258 Notably, dysregulation of non-canonical Activin A signalling was associated to DNA
259 replication stress and genomic instability, a finding that may be relevant for tumour initiation. Indeed,
260 distal LumP cells have been shown to serve as cell-of-origin for prostate cancer[30]. In this regard, our
261 orthotopic transplantation approach may be particularly relevant for investigating the tumorigenic
262 potential of distal progenitor cells.

263 Finally, P38 MAPK inhibitors are currently being tested in phase 1/2 clinical trials[60].
264 Quiescent tumour progenitors – induced by the broad family of TGF-β signals - are emerging as key
265 mediators of chemotherapy resistance in solid malignancy[61]. In advanced prostate cancers with a
266 genetically intact Activin A non-canonical pathway, P38 MAPK inhibitors may force tumours
267 progenitors out of quiescence, improving the efficacy of standard chemotherapy regimens[62]. While
268 the complexity and pleiotropy of TGF-β signalling has historically complicated drug development[63],
269 the elucidation of cell- and context-specific pathways may lead to novel therapeutic opportunities.

270 Methods

271 **Mice.**

272 Animal experiments were performed according to the European Communities Council Directive
273 (2010/63/EU) and approved by the Italian Ministry of Health and the University of Trento Animal
274 Welfare Committee (642/2017-PR). Wild-type C57BL/6J (JAX # 000664) mice were purchased from
275 the Jackson Laboratory. Wild-type BALB/c (CRL # 028) and CD-1 (CRL # 022) mouse strains were
276 obtained from the Charles River Laboratories.

277 **Isolation of mouse prostate tissue.**

278 The anterior (AP), dorso-lateral (DLP) and ventral prostate (VP) lobes were dissected individually,
279 using a transverse cut at the intersection of each lobe with the urethra. Paired lobes were collected for
280 organoid cultures, histology and immunostaining studies.

281 **Dissociation of mouse prostate tissue to single cells**.

282 Prostate tissue was minced into small pieces, washed, resuspended into a digestion buffer -including
283 Collagenase II (1 mg/mL; Life Tech, 17101015) and Dispase II (10 mg/mL; Life Tech 17105041),
284 and transferred into a gentleMACS C tube (Miltenyi Biotec). Tissue fragments were processed by
285 alternating mechanical disruption - using the gentleMACS Dissociator (A.01 -C tube programme) –
286 and enzymatic digestion -incubating the solution at 37 °C on a tube rotator for 15 minutes. After three
287 cycles, the cell suspension was pelleted, resuspended in TrypLE (Life Tech, 12605010), and
288 incubated for 5 minutes at 37 °C. After two washes, the cell suspension was filtered through a 70 µm
289 strainer and counted.

290 **3D prostate organoid cultures.**

291 Dissociated prostate cells were resuspended in 80% growth factor-reduced basement matrix (either
292 Matrigel®,Corning, 356231; or BME-2®,AMSBIO, 3533) and seeded at the concentration of
293 approximately 50,000 cells/mL, by depositing at least six 40 µL drops at the bottom of a non-tissue
294 culture treated plate. Basement matrix domes were left to solidify for 15 minutes and covered with
295 ENRAD medium – including Egf (50 ng/mL; PeproTech, 315-09), Noggin (100 ng/mL; PeproTech,
296 120-10C), R-Spondin1 (10% conditioned medium), A83-01 (200 nM; Tocris, 2393) and
297 dihydrotestosterone (10 nM; Merck, 10300) – supplemented with Y-27632 (10 µM; Calbiochem,
298 146986-50-7), as previously described[64]. Organoids were cultured in a standard tissue culture
299 incubator, with medium replacement every 2-3 days. After 6 days from the initial seeding, organoids
300 were imaged with a Leica MZ16F stereomicroscope and organoid forming efficiency was calculated.
301 For subsequent passages, the basement membrane was dissolved using a recovery solution –
302 including Dispase II (1 mg/mL) – and organoids were dissociated to small clumps/single cells as
303 described above, using TrypLE. Following the first passage, organoids were seeded at the
304 concentration of approximately 25,000 cells/mL.

305 **Lentiviral transduction of organoids.**

306 Organoids were dissociated to single cells, and approximately 50,000 cells were transduced for each
307 condition. Spinoculation was performed in a low-adhesion 96 well-plate using 0.6 RTU of lentiviral
308 solution, supplemented with polybrene (4 µg/mL; Sigma Aldrich, H9268) and complete medium
309 (ENRAD) to reach a final reaction volume of 300 µL. The plate was sealed with parafilm and
310 centrifuged for 1 hour at 600 g. Afterwards, the cells were resuspended in 200 µL of complete medium

311 (ENRAD), supplemented with Y-27632 (10 μM), and incubated in suspension at 37 °C for 4-6 hour.
312 After centrifugation, the cell pellet was resuspended in 80% basement matrix and seeded as described
313 above. Antibiotic selection was initiated two days post-transduction. The following plasmids were
314 used: pLenti-AIB-EGFP (kindly donated by Massimo Pizzato), pSUPER-retro-puro-Smad4
315 (Addgene #89829) and pSUPER-retro-puro-GFP shRNA (Addgene #30519).

316 **Treatments with growth factors and small molecule inhibitors.**

317 Growth factors and small molecules used in this study are described in Supplementary Table 1.

318 **Flow cytometry.**

319 Organoids were dissociated to single cells as described above. For cell surface antigen expression
320 analysis, cells were incubated with anti-Cd24a-APC and Sca-1-PE-Cy7 antibodies (1:800 dilution) at
321 4°C for 20-30 minutes, followed by one wash with FACS buffer (1% FBS, 1mM EDTA). Cells were
322 resuspended in FACS buffer, supplemented with 1 μM propidium iodide (Life Tech, P3566) for dead
323 cell exclusion, before proceeding to the analysis. For DNA content analysis, cells were resuspended
324 in 100 μl ice-cold PBS and transferred to a 15 ml tube. About 900 μl of ice-cold EtOH 70% were
325 added dropwise while agitating the cell suspension on a vortex. Cells were then fixed for at least 2
326 hours at -20°C before proceeding with 3 washing steps in PBS, alternated by centrifugation (700 g, 5
327 min) with no brake. Afterwards, cell pellet was resuspended in 100 μL of DNAse-free RNAseA (0.5
328 μg/mL; Life Tech, 12091021) and incubated for 10 min at 37 °C. Cells were incubated with 100 μL
329 of propidium iodide (50 μg/mL) for 30 minutes, at room temperature, before proceeding to the
330 analysis. For cell cycle analysis, organoids were treated with 10 μM EdU for 3 hours. Afterwards,
331 organoids were harvested, dissociated into single cells, and filtered through a 30 μm strainer. Cells
332 were pelleted and stained with the Click-iT™ Plus EdU Alexa Fluor™ 488 Flow Cytometry Assay
333 Kit (Thermo Fisher Scientific, C10632), according to the manufacturer protocol. After the
334 incorporation of the fluorescent probe, cells were incubated with TO-PRO™-3 Iodide (Life Tech,
335 T3695) to stain for DNA content, before proceeding to the analysis. Flow cytometry was performed
336 with a FACS Canto (BD) analyser, and data analysed with Flow Jo v.10.

337 **Histology, immunostaining, and live imaging.**

338 Organoids were cultured for 5-7 days, released from the basement membrane as described above,
339 seeded in a neutralized collagen type-I solution (Corning, 354249), and cultured for additional 24
340 hours, before proceeding to fixation in 4% paraformaldehyde (Sigma Aldrich, P6148) for 5 hours, at
341 room temperature. Prostate tissue was harvested and immediately fixed using the same conditions.
342 Paraffin embedding and 5 μm sectioning were carried out according to standard procedures. For
343 immunofluorescence studies, antigen retrieval was performed using a citrate-based buffer (pH 6.0)

344 (Vector Lab, H3300). Slides were incubated in blocking solution (5% FBS + 0.1% Triton-X in PBS),
345 before proceeding to staining with primary antibodies, at 4°C, overnight. After three washes,
346 spectrally distinct fluorochrome-conjugated antibodies were incubated for 2 hours at room
347 temperature. After three additional washes, samples were counterstained with Hoechst 33342
348 (Abcam, ab145597), and the coverslip was applied, using FluorSave mounting medium (Merck,
349 345789). For immunohistochemistry studies, a similar protocol was followed, but using biotin-
350 conjugated secondary antibodies. The detection was performed using the Vectastain® Elite ABC
351 Peroxidase kit (Vector Labs, PK-6100) according to the manufacturer instructions. The final reaction
352 was blocked by washing slides with water, and coverslips were applied using the DPX mounting
353 medium (Sigma, 06522). For haematoxylin and eosin (H&E) staining, deparaffinised sections were
354 incubated with Gill haematoxylin (Merck, GH5232) for 2 minutes and washed with water. Samples
355 were washed with ethanol, incubated with eosin Y (Merck, HT110132) for 3 minutes, washed again
356 twice with ethanol, and treated with xylene, before mounting the coverslips in phenol based mounting
357 medium. For immunostaining with anti-Egfr and anti-Acvr1b antibodies, the urogenital apparatus
358 was isolated, snap-frozen in 2-methyl-buthanol cooled in liquid nitrogen, and cryo-sectioned at 20
359 µm. Tissue slides were fixed in 4% paraformaldehyde for 20 minutes at room temperature, before
360 proceeding as described above. For live imaging, organoids were stably transduced with pLenti-AIB-
361 EGFP. Images were acquired using either a Zeiss Axio Imager M2, or a Zeiss Axio Observer Z1
362 Apotome, or a Leica TCS SP8 Confocal. Image analysis was performed with the Zeiss ZEN software
363 or ImageJ (v.2.0.0-rc-69/1.52i)[65]. Primary antibodies are listed in Supplementary Table 2.

364 **RNA extraction.**

365 Total RNA was extracted using the RNeasy Plus Micro kit (Qiagen, 74034) according to the
366 manufacturer instructions, and analysed with an Agilent BioAnalyzer 2100 to confirm integrity (RIN
367 > 8), before proceeding with downstream applications.

368 **End-point semi-quantitative and quantitative real-time PCR.**

369 RNA was retrotranscribed into cDNA using the iScript™ cDNA synthesis kit (BioRad, 1708891).
370 End-point PCR was performed using Phusion Universal qPCR Kit (Life Tech, F566L), with PCR
371 products visualized by standard gel electrophoresis. For quantitative real-time gene expression
372 analysis, the qPCRBIO SyGreen Mix (PCRBiosystems, PB20.14-05) was used according to the
373 manufacturer instructions. At least three independent biological replicates were run for each sample,
374 using the CFX96 Real Time PCR thermocycler (Bio-Rad). The data were processed using Bio-Rad
375 CFX Manager software (v.3.1), while gene expression quantification and statistical analyses were

376 performed with GraphPad PRISM (v.6.01). Primer sequences are included in Supplementary Table
377 3.

378 **RNA sequencing and data analysis.**

379 cDNA libraries were prepared with TruSeq stranded mRNA library prep Kit (Illumina, RS-122-2101)
380 using 1 µg of total RNA. RNA sequencing was performed on an Illumina HiSeq 2500 Sequencer
381 using standard Rapid Run conditions at the Next-Generation Sequence Facility of University of
382 Trento. The obtained reads were 100 bp long, single ends, and 25 million on average for each sample.
383 FASTQ file from Illumina HiSeq2500 sequencing machine underwent adapter removal and quality-
384 base trimming using Trimmomatic-v0.35. Genomic alignments were performed onto the Mouse
385 genome (mm10 assembly version) using STAR-v2.6.0 aligner with a maximum mismatch of two and
386 default settings for all other parameters. Then, uniquely mapped reads were selected and processed
387 with HTSeq-count v0.5.4 tool to obtain gene-level raw counts based on GRCm38.92 Ensembl
388 (www.ensembl.org) annotation. Genes with CPM (Counts Per Million) < 1 in all replicates were
389 considered unexpressed and hence removed from the analysis. TMM (Trimmed Mean of M values)
390 normalization and CPM conversion were next performed to obtain gene expression levels for
391 downstream analyses. For each comparison, differential expression testing was performed using the
392 edgeR-3.20.9 statistical package. According to the edgeR workflow, both common (all genes in all
393 samples) and separate (gene-wise) dispersions were estimated and integrated into a Negative
394 Binomial generalized linear model to moderate gene variability across samples. For each comparison,
395 genes having a log Fold-change outside the range of +/-1.5 and a FDR q-value equal or smaller than
396 0.01 were considered as differentially expressed between the two groups.

397 **Gene Set Enrichment Analysis (GSEA).**

398 For the gene set enrichment analysis, the GSEA software (v4.0.3) was run in the 'pre-ranked' mode
399 using the Fold-change as a ranking metric and an FDR enrichment threshold of 0.25. Gene sets were
400 directly obtained from the Molecular Signature (MSig) database (http://
401 software.broadinstitute.org/gsea/msigdb) focusing on all available sets reported in the following
402 MSigDB collections: C2 (curated gene sets): Biocarta, Kegg, Reactome; C5 (Gene ontology):
403 Biological Processes, Cellular Component, Molecular Function; C6 (oncogenic signatures) and C7
404 (immunologic signatures).

405 **Principal Component Analysis (PCA).**

406 PCA was performed using the DESeq2 R-package[66] as follows: normalized counts (CPM) were firstly
407 converted into a DESeqDataset object through a DESeqDatasetFromMatrix function with default
408 parameters and transformed through the variantStabilizingTransformation function to stabilize

409 variance-mean relation across samples. Then, transformed data was analyzed by PCA (plotPCA
410 function) generating a two-dimensional space where the two first components are represented.

411 **Subcellular Fractionation and Western blotting.**

412 Cell pellets from organoid cultures were obtained as previously described and lysed in fresh RIPA
413 buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1% Triton X-100, 1% sodium deoxycholate, 1%
414 NP-40) supplemented with protease (Halt™ protease inhibitor cocktail, Life Tech, 87786) and
415 phosphatase inhibitors (Phosphatase-Inhibitor Mix II solution, Serva, 3905501). Nuclear/cytoplasmic
416 fractionation was performed using NE-PER Nuclear and Cytoplasmic Extraction Kit (Life Tech,
417 78833) according to the manufacturer instructions. Protein concentrations were measured using the
418 BCA Protein Assay Kit (Pierce™ BCA Protein Assay kit, Thermo Fisher Scientific, 23225) and a
419 Tecan Infinite M200 Plate Reader.

420 Protein extracts were resolved via SDS-PAGE, transferred to polyvinylidene difluoride (PVDF)
421 membrane (Merck, GE10600023) using a wet electroblotting system (Bio-Rad). The membranes
422 were blocked with 5% non-fat dry milk or 5% BSA in TBS-T (50 mM Tris-HCl, pH 7.5, 150 mM
423 NaCl, 0.1% Tween20) for 1 hour, at room temperature, and then incubated with gentle shaking with
424 designated primary antibodies overnight, at 4°C. Membranes were incubated with HRP-conjugated
425 secondary antibody in blocking buffer for 1 hour at room temperature. Immunoreactive bands were
426 detected using ECL LiteAblot plus kit A+B (Euroclone, GEHRPN2235) with an Alliance LD2 device
427 and software (UVITEC). Primary antibodies are provided in Supplementary Table 4.

428 **Click-it chemistry-based mass spectrometry analysis.**

429 Organoids were seeded at the approximate concentration of 50,000 cells/ml, depositing seven 40 ul
430 domes *per* individual well of a 6-well non-tissue culture plate. Three wells were used for each
431 condition. Following methionine depletion (2 hours), organoids were grown overnight at 37 °C with
432 L-azidohomoalanine (AHA) medium. Conditioned supernatants were collected, supplemented with
433 protease inhibitors, and stored at -80 °C until further processing. CLICK-IT enrichment of AHA-
434 labelled secreted proteins was performed with the Click-iT™ protein enrichment kit (Thermo Fisher
435 Scientific, C10416) as previously described[67,68]. Following trypsin digestion, peptides were purified
436 by reversed-phase (C18) stage-tip purification[69]. LC-MS/MS analysis was performed by an EASY-
437 LC 1000 coupled to a Q-Exactive mass spectrometer (Thermo Fisher Scientific). LC-MS/MS data
438 analysis was conducted using the MaxQuant/Perseus software suite.

439 **Enzyme-linked immunosorbent assay (ELISA).**

440 Activin A quantification was performed using the corresponding Quantikine ELISA Kit (R&D
441 Systems, DAC00B) according to the manufacturer instructions.
442 **Karyotype analysis.**
443 Organoid cultures were treated with nocodazole (15 μM; Sigma, SML1665) for 5 hours. Organoids
444 were recovered from basement membrane, and 900 μL/sample of 50 mM KCl were added to the cell
445 pellet dropwise, followed by 10 minutes of incubation at 37 °C. After centrifugation (200 g, 5
446 minutes) 900 μL/sample of Carnoy's fixative (methanol/acetic acid 3:1) was added dropwise.
447 Samples were resuspended and incubated for 10 minutes at 37 °C, followed by three washes with
448 methanol/acetic acid 2:1. Approximately 25,000 cells/samples were resuspended in 50 μL and
449 dropped from at least 1 meter of height, directly on a glass slide. After air-drying, the glass slide was
450 incubated with Hoechst 33342, at room temperature, for 10 minutes, and then washed with
451 methanol/acetic acid 2:1 for 5 minutes. After air-drying, coverslips were mounted with ProLong Gold
452 Antifade (Invitrogen, P36934). Images were acquired at the Zeiss Observer Z1 microscope and
453 analysed with ImageJ (v2.0.0-rc-69/1.52i)[65].
454 **Multicolor FISH (M-FISH), Chromosome painting and Telomeric FISH**
455 For M-FISH, fixed cells were dropped onto glass slides and hybridized with the 21XMouse
456 Multicolor FISH Probe Kit (MetaSystems, D-0425-060-DI), as previously described[70]. Briefly, the
457 slides were denatured in 0.07 N NaOH and then rinsed in a graded ethanol series. The probe mix was
458 denatured using a MJ mini personal thermal cycler (Bio-Rad) with the following program: 5 minutes
459 at 75 °C, 30 seconds at 10 °C, and 30 minutes at 37 °C. The probe was added to the slides and the
460 coverslip was sealed using rubber cement. The samples were then hybridized in a humidified chamber
461 at 37 °C for 48 h, washed in saline-sodium citrate (SSC) buffer for 5 min at 75 °C, and finally
462 counterstained with DAPI (Abcam, 6843.2), in Vectashield mounting medium. Metaphases were
463 visualized and captured using a Zeiss Axio-Imager M1 microscope. The karyotyping and cytogenetic
464 analysis of each single chromosome was performed using the M-FISH module of the ISIS software
465 (MetaSystems). A total of 25 metaphases for each sample spreads were analysed in two independent
466 experiments.
467 For chromosome painting, fixed cells were dropped onto glass slides and hybridized with
468 enumeration XMP painting probes specific for chromosomes X (red label) and chromosome Y (green
469 label) (MetaSystems, D-1420-050-OR, D-1421-050-FI) following the manufacturer instructions.
470 Briefly, probes were applied to the slides, denatured at 75 °C for 2 minutes, and then incubated at 37
471 °C overnight. The slides were washed in SSC and counterstained with DAPI in antifade reagent
472 (MetaSystems, D-0902-500-DA). Metaphases were visualized and captured using a Zeiss Axio-

473 Imager M1 microscope. A total of 100 metaphases were analysed for each sample in two independent
474 experiments.
475 For telomeric FISH, staining was performed as previously described[71]. Briefly, slides and the Cy3
476 linked telomeric (TTAGGG)3 PNA probe, (DAKO Cytomatation, K5326) were co-denatured at 80
477 °C for 3 minutes, and hybridized for 2 hours at room temperature, in a humidified chamber. After
478 hybridization, slides were washed and then dehydrated with an ethanol series and air dried. Finally,
479 slides were counterstained with DAPI and Vectashield. Images were captured at 63× magnification
480 using a Zeiss Axio-Imager M1 microscope, and the telomere signals were analysed using the ISIS
481 software (MetaSystems). Telomere doublets frequency was calculated as the ratio between the
482 number of doublets signals and the total number of chromosomes in each metaphase analysed[72]. At
483 least 20 metaphases in two independent experiments were analysed.

484 **Orthotopic organoid transplantation**

485 Orthotopic transplantation of organoids into the prostate of syngeneic immune-competent C57BL/6J
486 mice was performed adapting a previously published method[73]. Organoids were dissociated as
487 described above, with 50,000 cells *per* injection resuspended in 10 μL of 50% basement matrix,
488 supplemented with methylene blue (as tracer). Upon abdominal incision of the host, the left anterior
489 prostate lobe was exposed, and injected into the distal part. The contralateral lobe was injected with
490 saline as negative control. Mice were regularly monitored and sacrificed after 6 months for tissue
491 collection and histopathological analysis.

492 **Statistical analysis and reproducibility**

493 No statistical methods were used to predetermine sample size. The *in vitro* experiments were not
494 randomized, and the investigators were not blinded to allocation during experiments and outcome
495 assessment. The *in vivo* transplantation experiments were randomized, and the investigators were
496 blinded to allocation during experiments and outcome assessment. The *in vitro* experiments were
497 carried out on organoid lines derived from at least two distinct animals and repeated at least three
498 independent times. The *in vivo* transplantation experiments were based on two distinct organoid lines
499 and were repeated at least two independent times. Data collection was performed using Microsoft
500 Office Excel 2016–2018 and statistical analysis was performed using GraphPad Prism 6 software.
501 The number of replicates, the format of the data, and the statistical tests are indicated in figure legends.
502 p-values < 0.05 were considered significant.

503 **Data availability**

RNA sequencing datasets have been deposited on BioProject with the dataset identifier PRJNA659468. All other data supporting the findings of this study are available from the corresponding authors upon reasonable request.

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694 Author contributions

695 F.C. made initial observations. F.C. and A.L. designed the project. F.C., V.F. and A.L. planned the
696 experiments. F.C. and V.F. carried out and analysed the majority of the wet-lab based experiments.
697 A.Ala. executed subcellular fractionation and western blot experiments, D.D.F. performed the
698 experiments on Egf signalling, M.D.P., M.Z., M.C., and E.B., contributed to the generation of
699 organoid lines and to the *in vitro* experiments. M.L. and M.G. executed Click-it mass spectrometry
700 experiments and analysed the data. A. Be. contributed to flow cytometry. S.G. executed the
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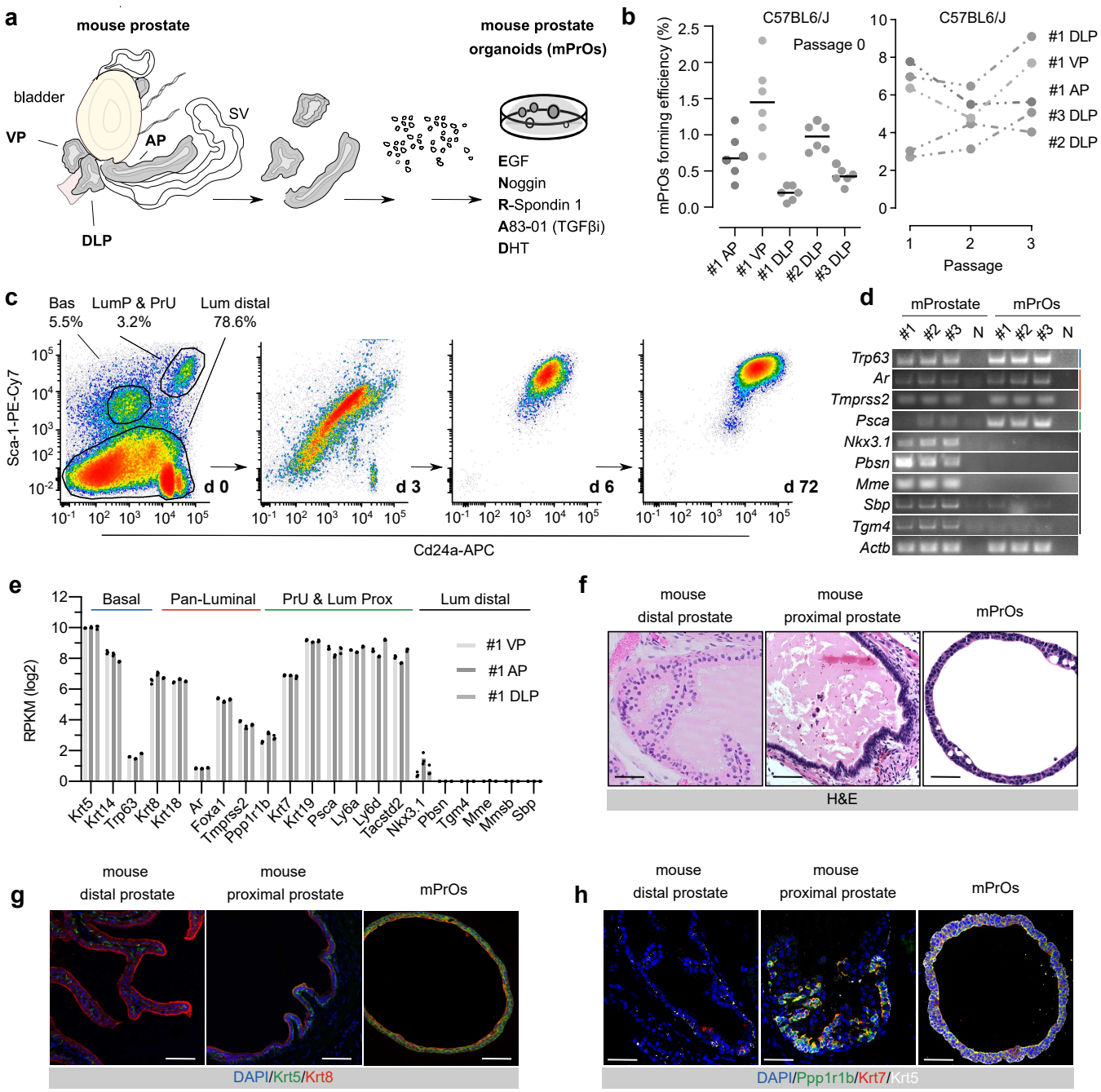
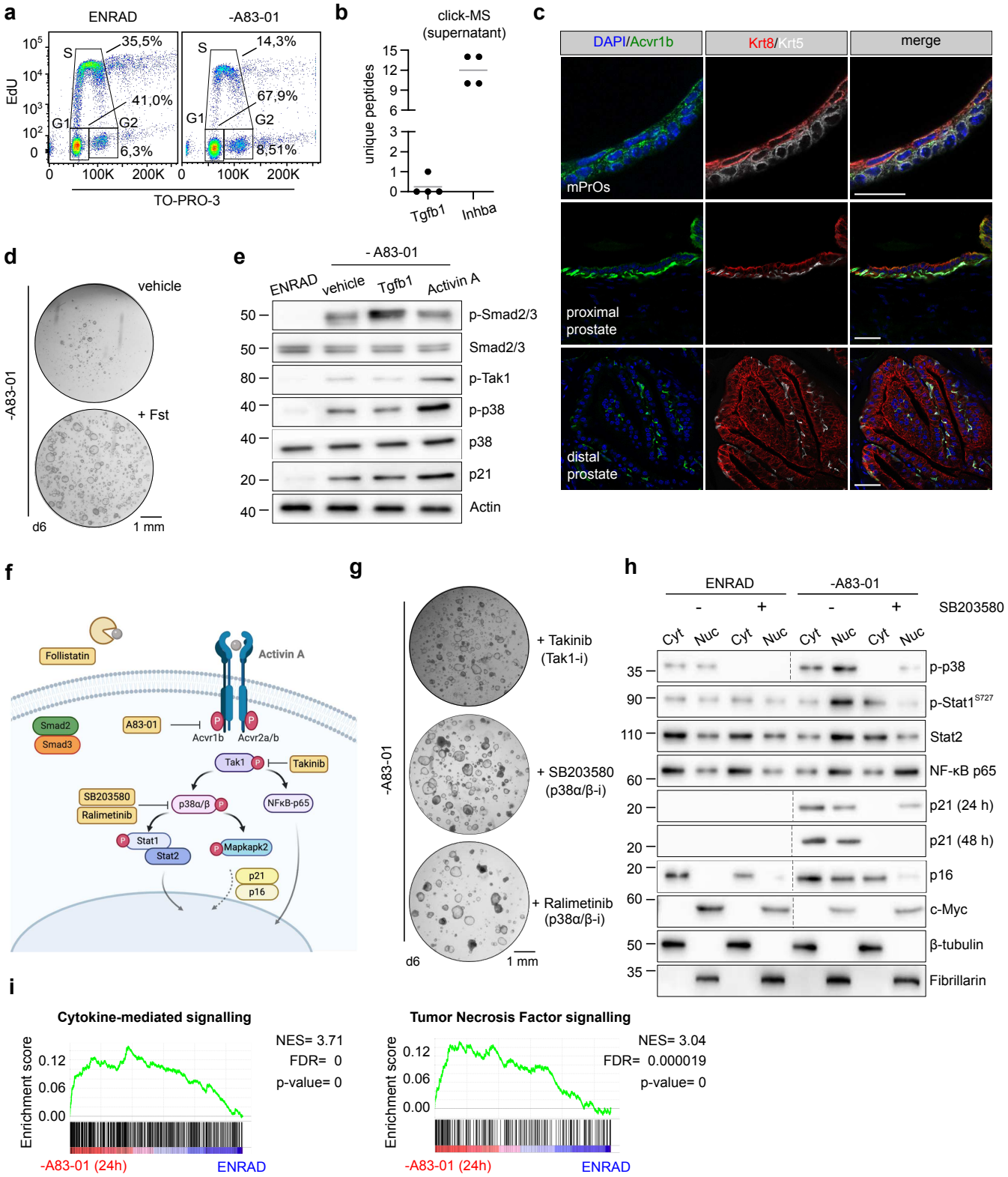
708 **Competing interests**

709 Authors declare no competing interests.



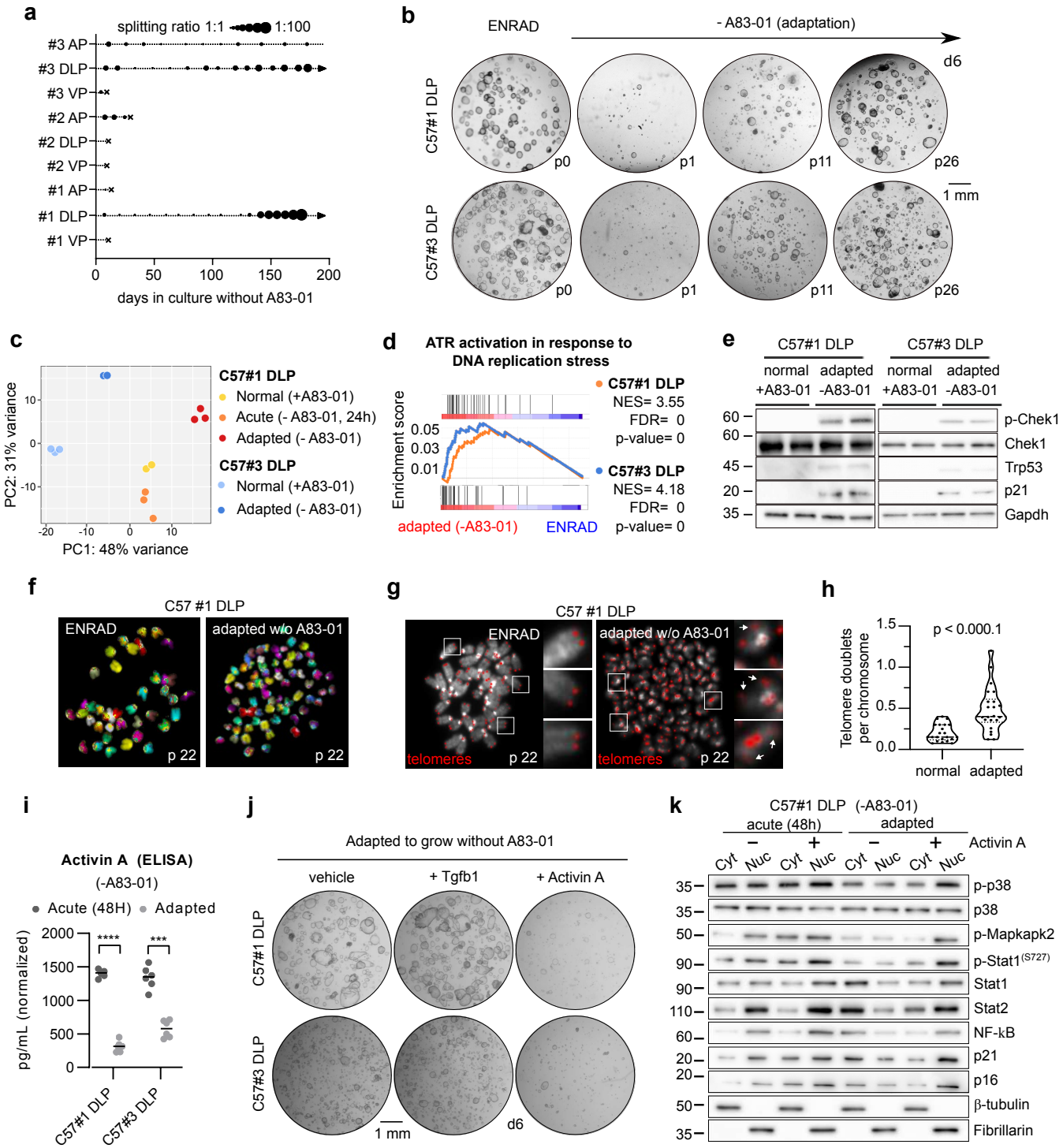
Mouse prostate organoids are highly enriched in epithelial progenitor cells

a. Schematic diagram describing organoid culture derivation (AP, Anterior Prostate; DLP, Dorso-Lateral Prostate; VP, Ventral Prostate; SV, Seminal Vesicle; DHT, dihydrotestosterone).
b. Mouse prostate organoid forming efficiency. Efficiency at derivation (left; data points are shown with crossing line representing mean value). Efficiency at passage 1-3 (right; n≥ 3 per organoid line/passage; data are presented as mean).
c. Representative longitudinal flow-cytometry analysis of dissociated organoid cells (Bas, Basal; LumP, Luminal Proximal; PrU, Periurethral; Lum Distal, Luminal Distal).
d. End-point RT-PCR analysis for selected marker genes.
e. Bulk-RNAseq analysis (n=3; individual data points are shown with bar graphs representing mean value).
f. Representative Haematoxylin-Eosin (H&E) staining of mouse prostate tissue and organoid sections (scale bars = 50 μm).
g. Representative Immunofluorescence (IF) analysis for selected markers in mouse prostate tissue and organoid sections (scale bars = 50 μm).
h. IF staining for selected markers in mouse prostate tissue and organoid sections (scale bars = 50 μm).



Intra-epithelial non-canonical Activin A signalling mediates the Tgf-β induced cytostatic response in mouse prostate organoids

a. Cell cycle analysis by flow cytometry (EdU *vs.* TO-PRO-3) in complete medium (ENRAD) or in the absence of A83-01 (24 hours).
b. Detection of proteins secreted by mouse prostate organoids in culture based on click-chemistry enrichment and mass spectrometry analysis (n=4; data points are shown with crossing line representing mean value).
c. IF analysis for selected markers in mouse prostate tissue and organoid sections (scale bar = 50 μm).
d. Representative stereoscopic images of mouse prostate organoids cultured in the absence of A83-01, with or without Follistatin (Fst, 500 ng/mL, 6 days).
e. Western blot (WB) analysis in mouse prostate organoids for selected canonical and non-canonical Tgf-β signalling mediators, and the cell cycle inhibitor p21 (Activin A, 50 ng/mL; Tgfb1, 500 ng/mL; 24 hours).
f. Schematic view of the non-canonical Activin A pathway, including inhibitors used for the experiments described in this figure.
g. Representative stereoscopic images of mouse prostate organoids following treatment with Takinib (Tak1 inhibitor; 5 μM, 6 days), SB203580 (p38α/β inhibitor; 10 μM, 6 days) or the structurally unrelated Ralimetinib (p38α/β inhibitor; 1 μM, 7 days).
h. Nuclear fractionation and WB analysis in mouse prostate organoids for selected signalling mediators and cell cycle regulators, in the presence or absence of SB203580 (p38α/β inhibitor; 10 μM, 24 hours).
i. Gene set enrichment analysis (GSEA) plots displaying significant enrichment for cytokine-mediated and Tumour Necrosis Factor (TNF) signalling in mouse prostate organoids cultured without A83-01 (24 hours) versus complete medium (ENRAD).



Evasion from the Tgf-β induced cytostatic response occurs via downregulation of intra-epithelial Activin A signalling and leads to DNA replication stress and genomic instability.

a. Diagram depicting the expansion of mouse prostate organoid cultures in the absence of the Tgf-β ligand inhibitor A83-01 (arrow = continuous expansion; dot = passage; cross = culture loss).

b. Representative stereoscopic images of C57BL/6J DLP #1 and # 3 mouse prostate organoid lines during adaptation in the absence of A83-01.

c. Principal Component Analysis (PCA) based on bulk RNA-sequencing of C57#1 DLP and C57#3 DLP mouse prostate organoids grown in normal conditions (ENRAD), upon acute A83-01 depletion (-A83-01, 24 hours) (C57#1 DLP only) or following adaptation (-A83-01, long-term).

d. Gene set enrichment analysis (GSEA) plot displaying significant enrichment for activation of ATR signalling in mouse prostate organoid lines (C57#1 DLP, top; C57#3 DLP, bottom) adapted to grow in the absence of A83-01 *vs.* normal control organoids cultured in complete medium (ENRAD).

e. WB analysis in C57#1 and C57# 3 DLP mouse prostate organoid lines adapted to grow in the absence of A83-01 *vs.* normal control organoids cultured in complete medium (ENRAD). Immunoblots are displayed for Chek1 (ATR signalling mediator), Trp53 and p21.

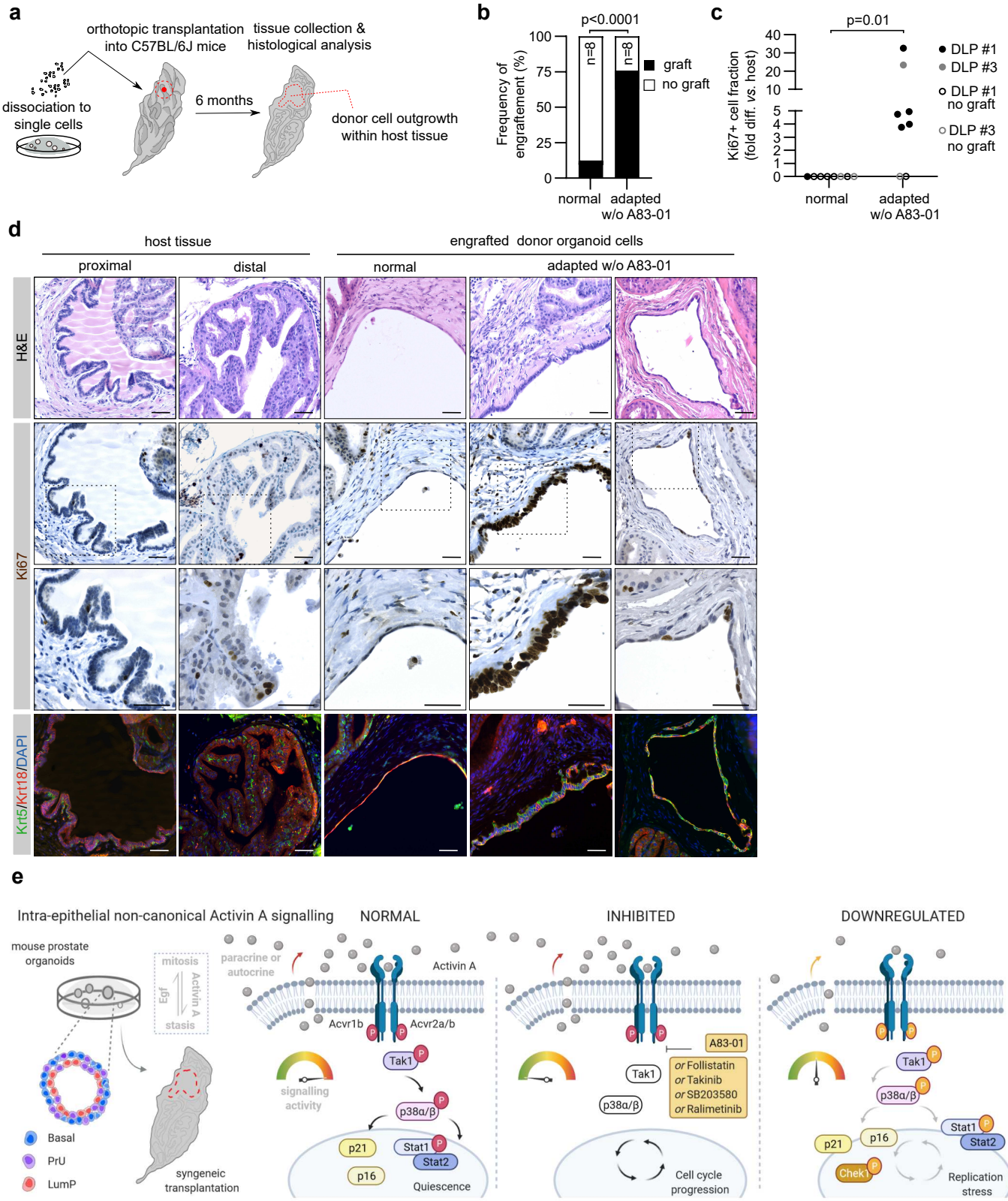
f. Representative spectral karyotype (SKY) images of metaphase spreads obtained from C57#1 DLP mouse prostate organoids cultured in normal conditions (ENRAD) or upon adaptation without A83-01. Widespread genomic instability is observed following adaptation.

g-h. Representative telomere FISH images - and quantification - in C57#1 DLP mouse prostate organoids cultured in normal conditions (ENRAD) or upon adaptation without A83-01. Widespread telomeric instability is observed following adaptation.

i. Enzyme-linked immunosorbent assay (ELISA) for Activin A expression in the supernatant of C57#1 and C57# 3 DLP mouse prostate organoid lines, upon acute A83-01 removal (48 hours) or long-term adaptation. Two-way ANOVA, Sidak's test, p-value *** (<0.001), **** (<0.0001).

j. Representative stereoscopic images of C57#1 and C57# 3 DLP mouse prostate organoid lines adapted to the absence of A83-01 and subsequently treated with either Tgfb1 (500 ng/mL, 6 days) or Activin A (50 ng/mL, 6 days).

k. WB analysis in the C57#1 DLP mouse prostate organoid line upon acute removal (24 hours) or long-term adaptation to A83-01 removal, in the presence or absence of Activin A (50 ng/mL, 24 hours).



Enhanced engraftment of mouse prostate organoids with reduced Activin A signalling into immunocompetent hosts.

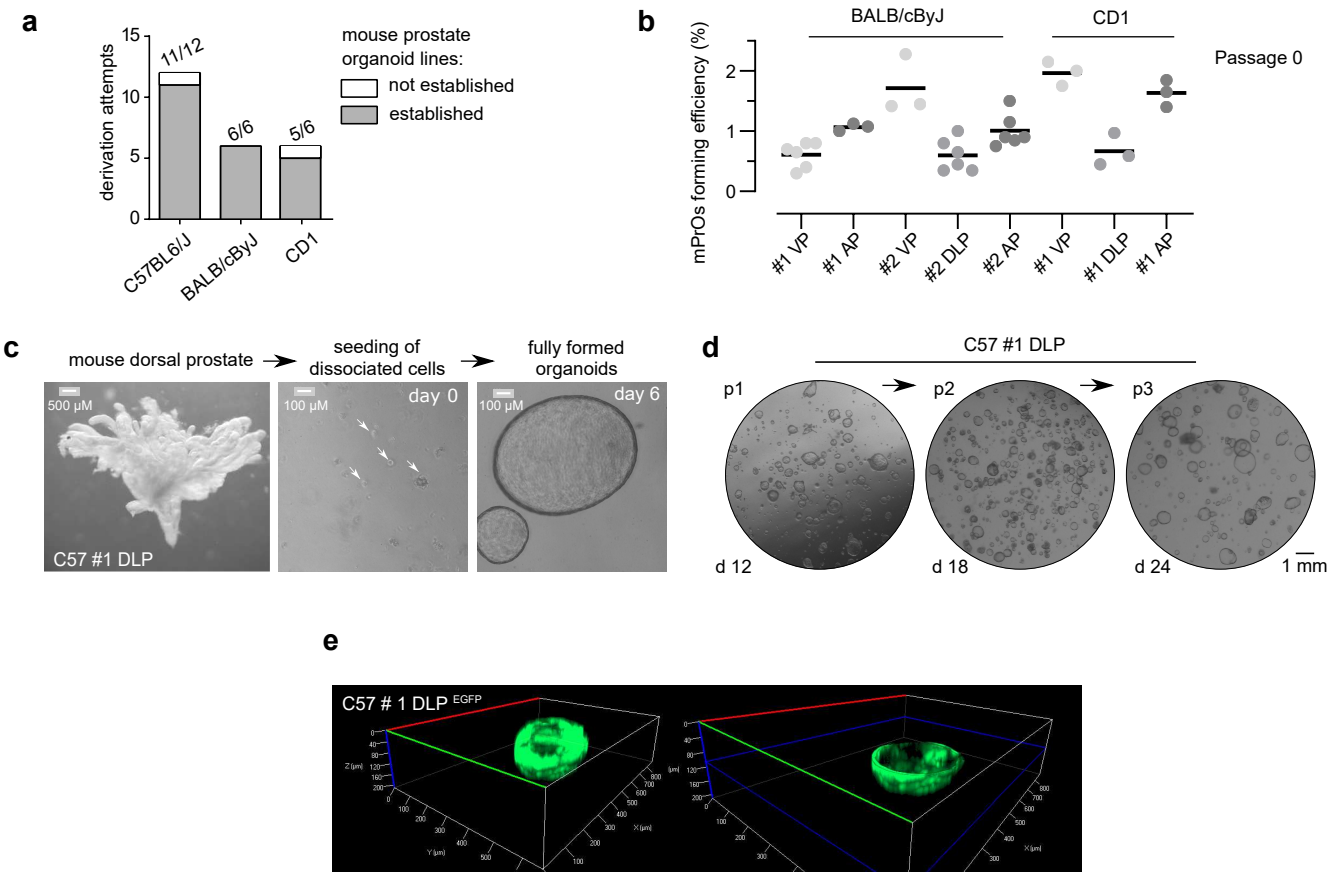
a. Schematic view of the orthotopic transplantation strategy into the anterior prostate lobe of immunocompetent syngeneic C57BL/6J mice.

b. Frequency of engraftment (%) of mouse prostate organoid lines (C57#1 DLP and C57#3 DLP) expanded in complete medium (normal) or adapted to the absence of A83-01 (binomial test (two-tailed)).

c. Normalized mitotic (Ki67+) cell index in grafts of mouse prostate organoid lines (C57#1 DLP and C57# 3 DLP) expanded in complete medium conditions (normal) or adapted to the absence of A83-01 (non-parametric Mann-Whitney test).

d. Representative H&E, IF, and immunohistochemistry (IHC) analyses of host prostate tissue and engrafted donor organoid cells (scale bar = 50 μm).

e. Intra-epithelial non-canonical Activin A signalling safeguards prostate progenitor quiescence. In normal circumstances, autocrine or paracrine Activin A triggers Tak1/p38 Mapk non-canonical signalling - antagonizing the pro-proliferative Egf pathway and enforcing cellular quiescence. Mechanistically, Tak1/p38 Mapk activity leads to p16 and p21 nuclear translocation - as well as to Stat1/2-dependent transcription of type-I interferon genes. Prostate organoid cultures require the suppression of this non-canonical signalling for continuous expansion, which can be achieved at different levels of the signalling cascade, using multiple inhibitors. Organoids with reduced levels on intra-epithelial Activin A signalling can be selected *in vitro*, and display enhanced engraftment efficiency *in vivo*, upon orthotopic transplantation into syngeneic hosts. Notably, the partial down-regulation of this pathway is associated with DNA replication stress and genomic instability.



Establishment of a mouse prostate organoid biobank

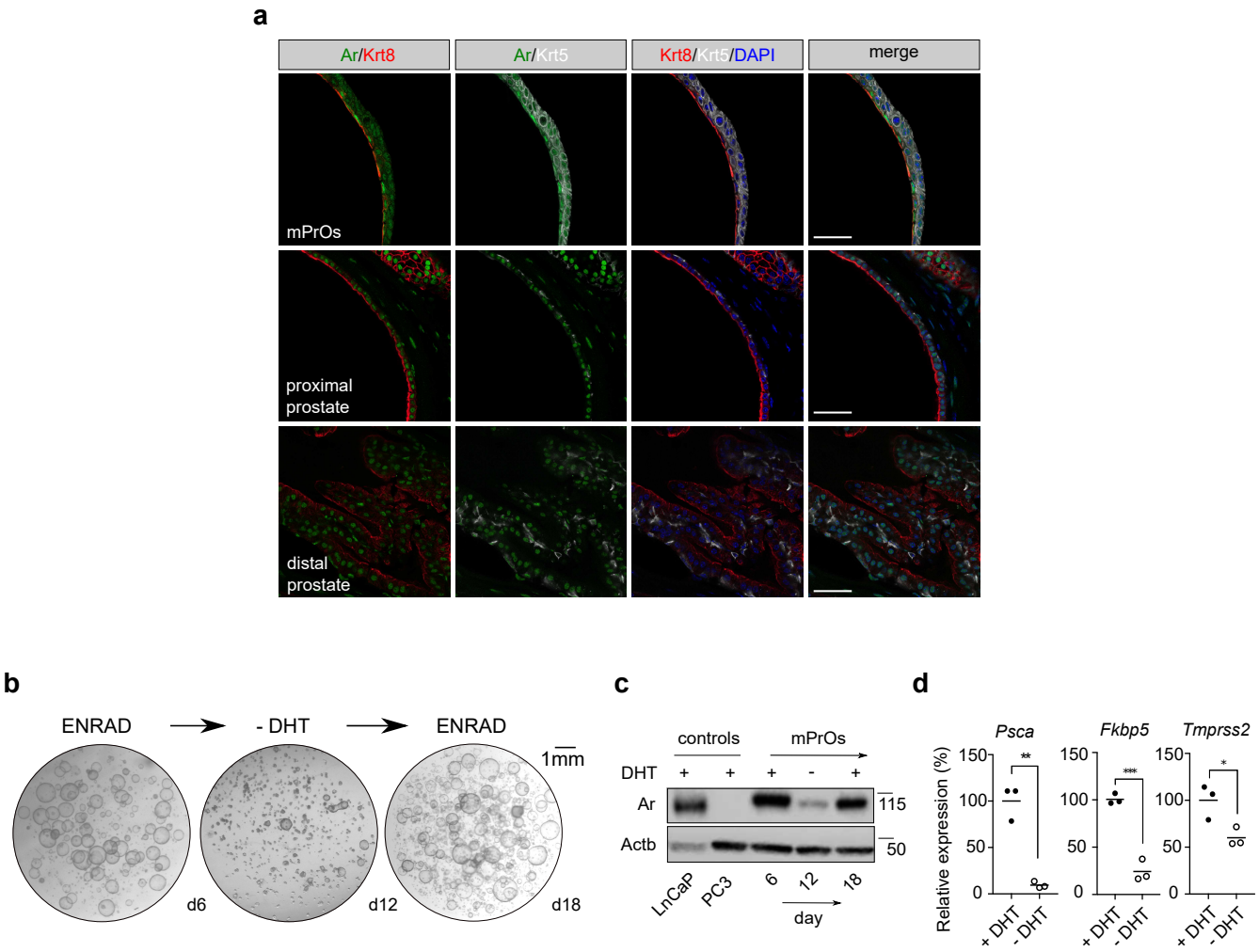
a. Prostate organoid derivation rate from distinct mouse strains.

b. Mouse prostate organoid forming efficiency at derivation. Data points are shown with crossing line representing mean value.

c. Representative stereoscopic images at different stages of mouse prostate organoid derivation.

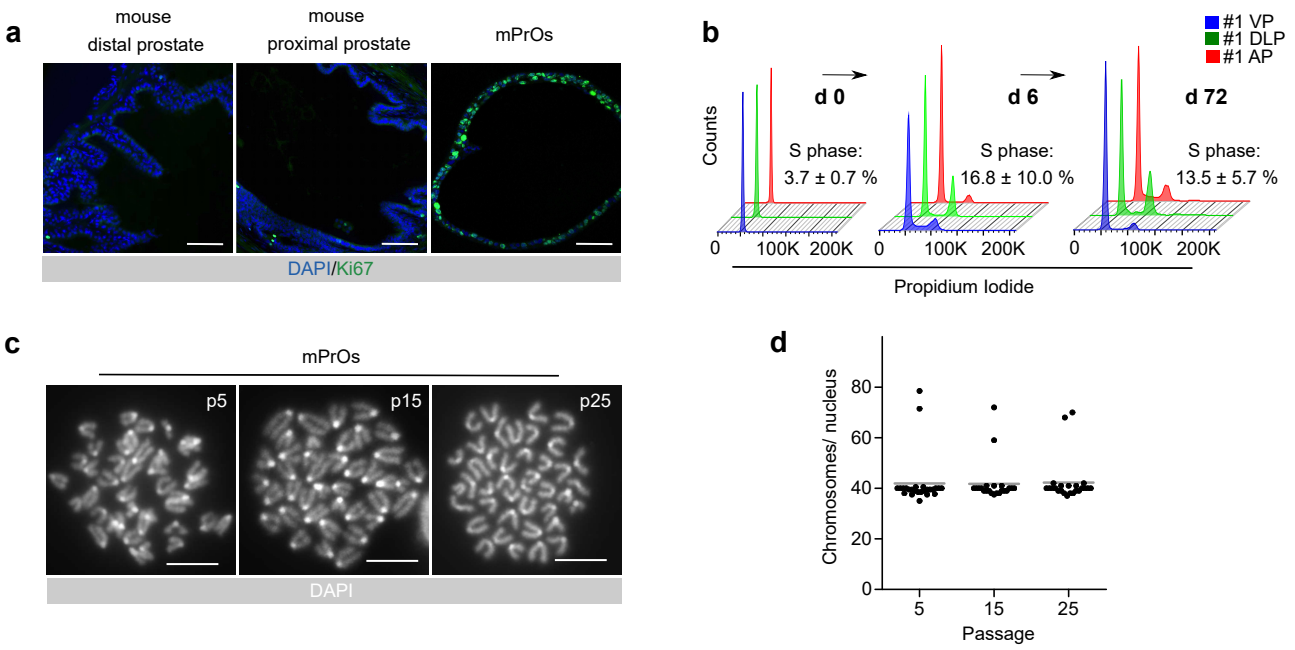
d. Representative stereoscopic images of mouse prostate organoid cultures during subsequent passages.

e. Representative 3D reconstruction of a fully formed mouse prostate organoid based on live epifluorescent microscopic analysis (1 µm section x 300 planes). On the right side, only the bottom half of the organoid is displayed.



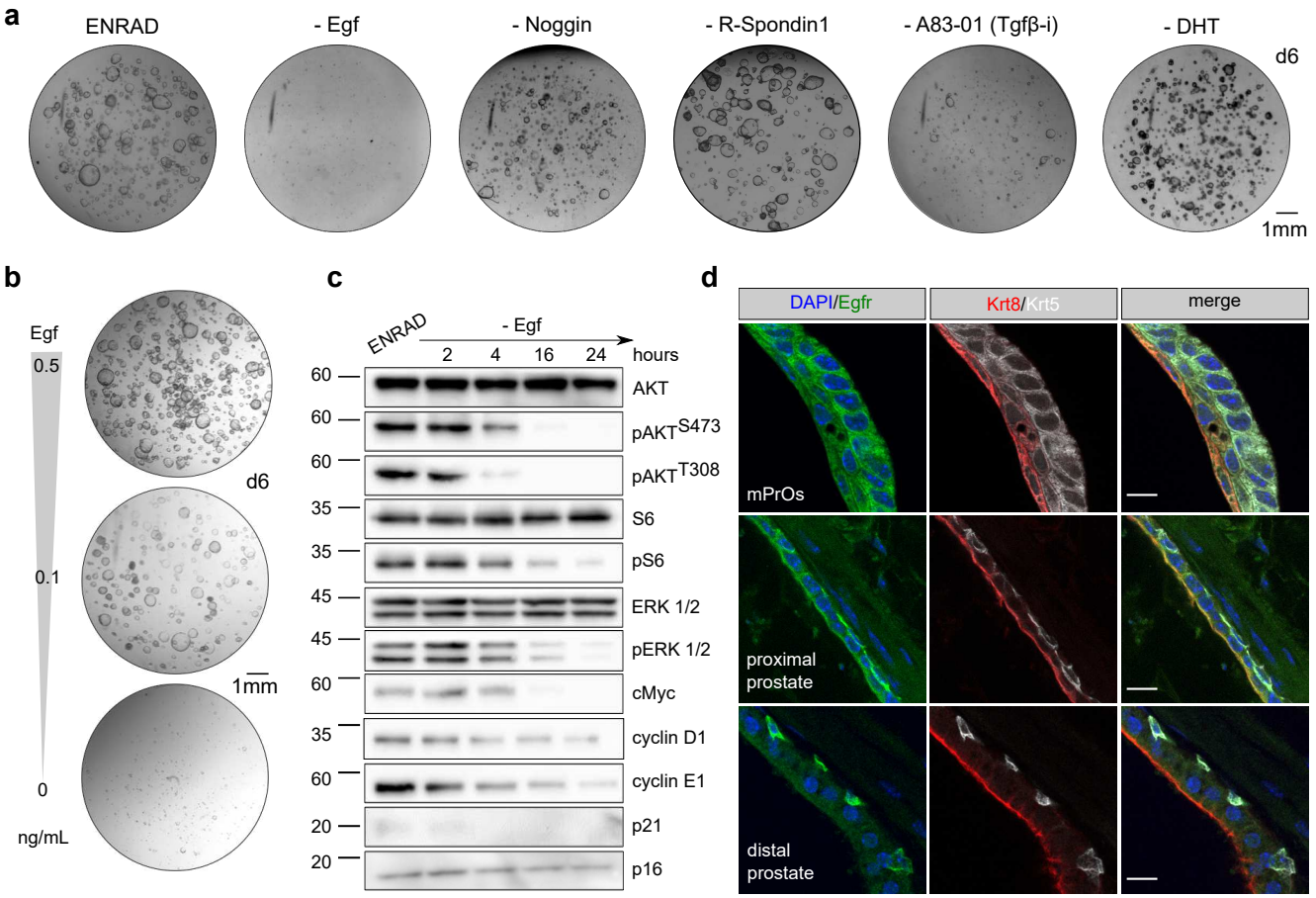
Mouse prostate organoids are dependent on androgen signalling for lumen formation - but not for survival

a. Immunofluorescence analysis for selected markers in mouse prostate tissue and organoid sections (scale bars = 50 µm).
b. Stereoscopic images of mouse prostate organoids experiencing transient dihydrotestosterone (DHT) removal (androgen cycling). Lumen formation necessitates androgen signaling.
c. Western blot analysis for Androgen receptor (Ar) expression in mouse prostate organoids experiencing androgen cycling, and control cell lines expressing (LnCaP) or not expressing (PC3) the receptor.
d. qRT-PCR mRNA expression analysis for selected androgen-responsive genes in the presence or absence of DHT. Data points are shown with crossing line representing mean value. Student's t-test, two-tailed, p-value * (<0.05), ** (<0.01), *** (<0.001).



Low levels of genomic instability in fast cycling mouse prostate organoids

a. Immunofluorescence staining for Ki67 in mouse prostate tissue and organoid sections (scale bars = 50 µm)
b. Flow cytometry analysis for DNA content
c. Representative karyotypes (scale bars = 10 µm)
d. Quantification of karyotype analysis. Data points are shown with crossing line representing mean value.



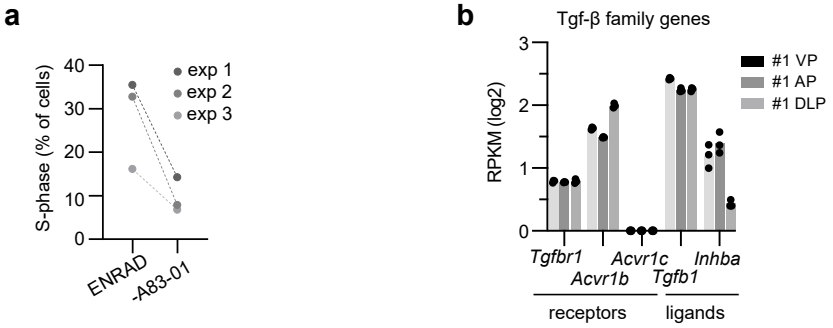
Mouse prostate organoids rely on Egf signalling for continuous proliferation

a. Representative stereoscopic images of mouse prostate organoid grown in complete medium (ENRAD) vs. medium depleted of individual growth factors/inhibitors. Mouse prostate organoids necessitate of both Egf and the Tgf-β inhibiitor A83-01 for continuous expansion. Within the period of observation, removal of Noggin or R-Spondin 1 has no clear consequence in culture. Please note that organoids failed to form a lumen in the absence of dihydrotestosterone (DHT).

b. Stereoscopic images of mouse prostate organoids cultured in the presence of reduced levels (0.5, 0.1 ng/mL) or in the absence of Egf.

c. Western blot analysis in mouse prostate organoids for selected signalling mediator and cell cycle regulator proteins.

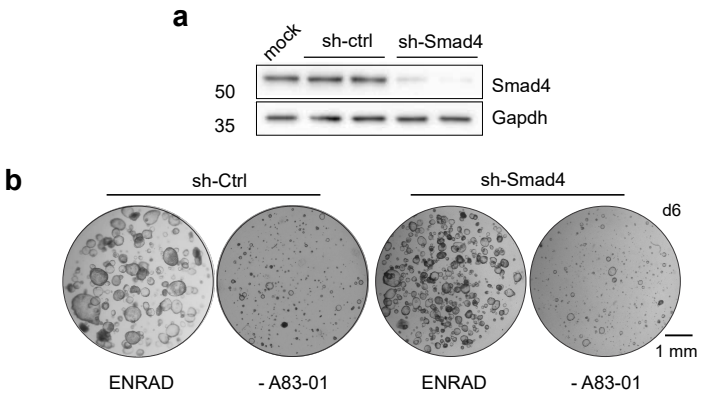
d. Immunofluorescence analysis for selected markers in mouse prostate tissue and organoid sections (scale bars = 10 µm).



Inhibition of Tgf-β receptors is required for cell cycle progression in mouse prostate organoids

a. Quantification of cells undergoing S-phase based on flow cytometry (EdU *vs*. TO-PRO-3) in complete medium (ENRAD) or in the absence of A83-01 (24 hours). (Related to Fig 2a; n=3, individual data points are shown.)

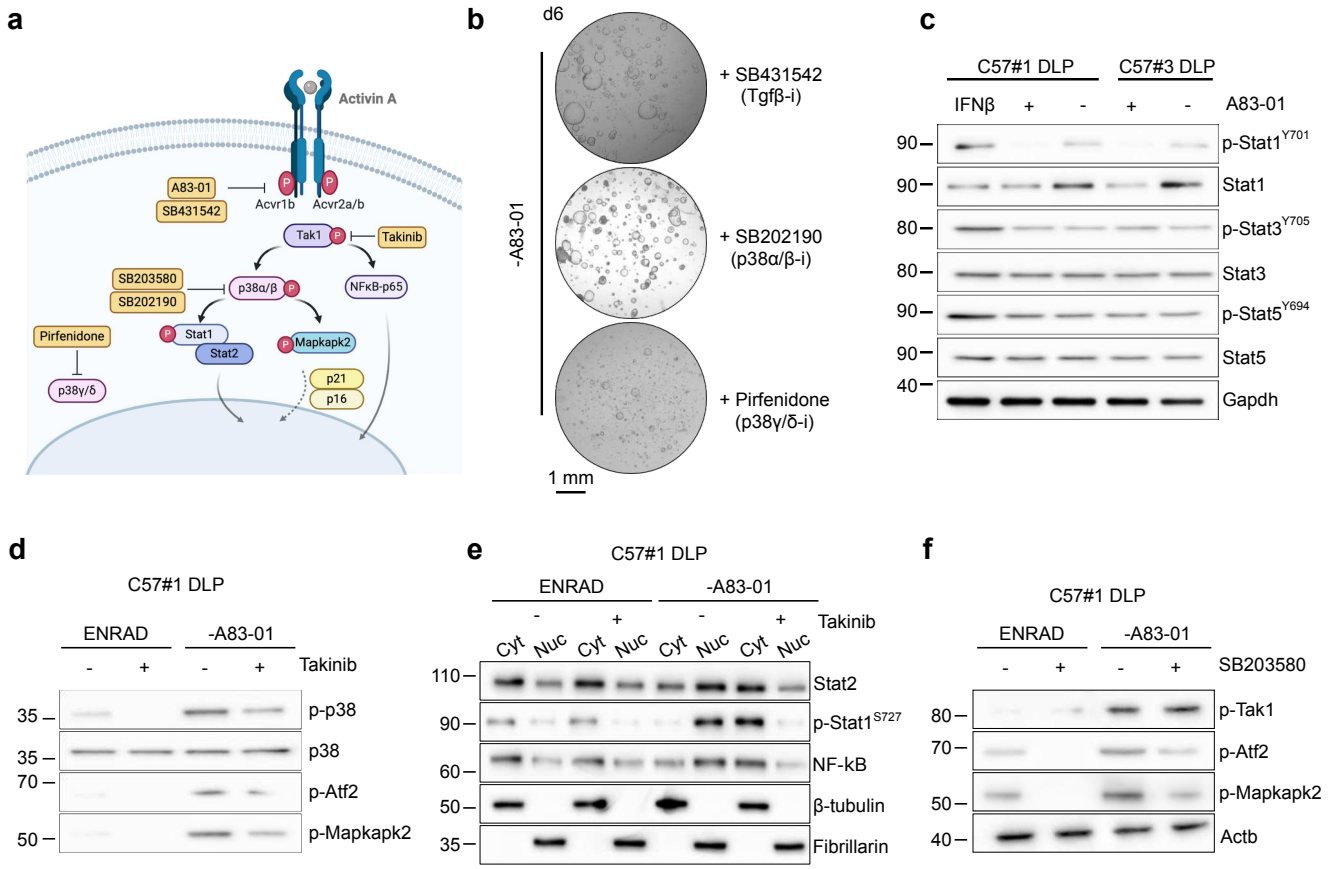
b. mRNA expression levels for selected Tgf-β family receptors and ligands. Bulk-RNAseq analysis (n=3; individual data points are shown with bar graphs representing mean value).



Canonical Smad signalling is dispensable for Tgf-β induced quiescience in prostate organoids

a. Western blot analysis for Smad4 in mouse prostate organoids upon short-hairpin RNA mediated knockdown (sh-Smad4) and in control conditions (sh-Ctrl).

b. Representative stereoscopic images of control (sh-Ctrl) and Smad4 knocked down (sh-Smad4) mouse prostate organoids in normal growth condition (ENRAD) and following A83-01 withdrawal (-A83-01).



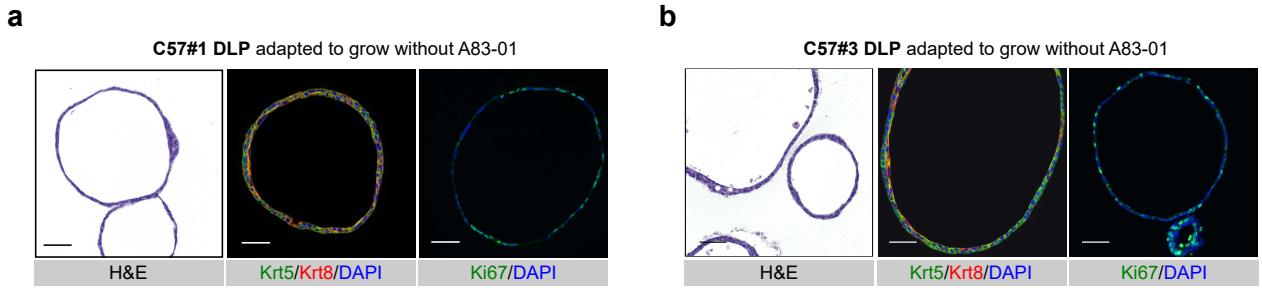
Tak1/p38 MAPK signalling activates immune- and stress-related pathways in prostate organoids

a. Schematic view of the non-canonical Activin A signalling pathwaty, including inhibitors used for the experiments described in this figure.

b. Representative stereoscopic images of mouse prostate organoids grown in the absence of A83-01 and in the presence of either SB431542 (Tgfβ-receptor inhibitor; 10 μM, 6 days), or SB202190 (p38α/β inhibitor; 10 μM, 6 days), or Pirfenidone (p38γ/δ inhibitor; 10 μM, 6 days).

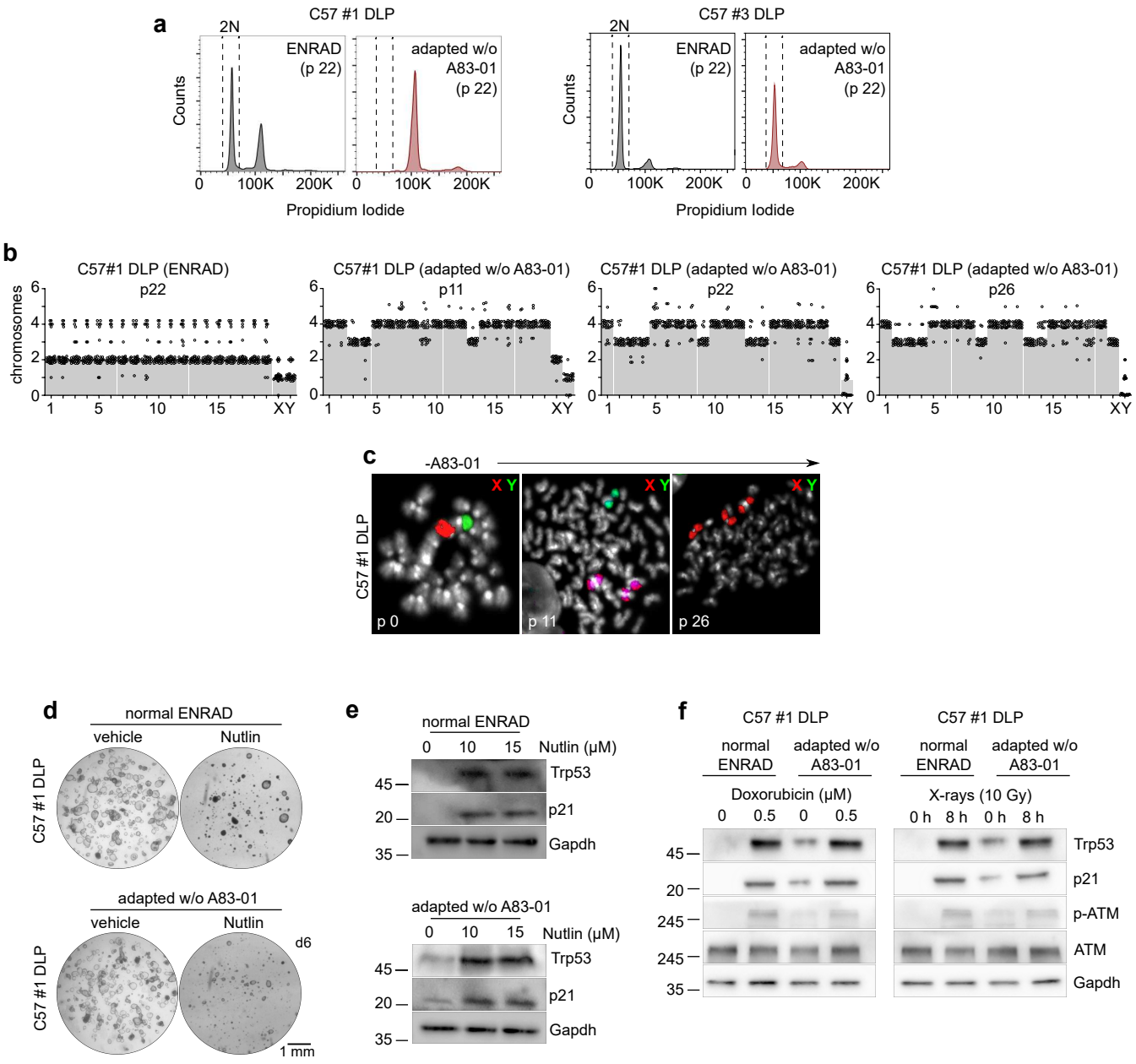
c. Western blot analysis in mouse prostate organoids for canonical IFN signalling mediators upon acute A83-01 withdrawal (IFNβ; 50 ng/mL, 6 days).

d-f. Western blot analysis in mouse prostate organoids for key components of the non-canonical Tgf-β pathway and IFN signalling upon acute A83-01 withdrawal and concomitant inhibition of either Tak1 (Takinib; 5 μM, 24 hours) (**d**, **e**) or p38α/β (SB203580; 10 μM, 24 hours) (**f**).



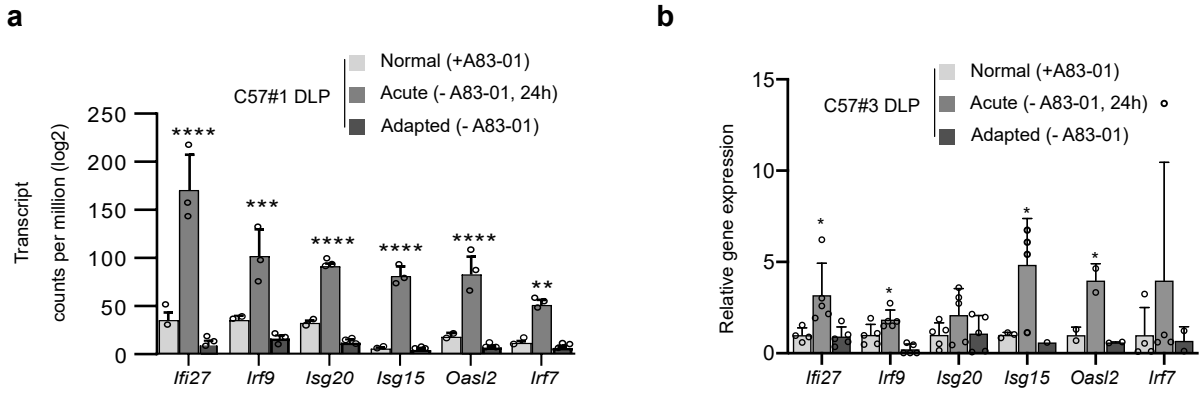
Mouse prostate organoids adapted to the absence of the Tgf-b receptor inhibitor A83-01 retain quasi-normal cellular identities and cytoarchitecture

a-b. Representative H&E and immunofluorescence analyses of C57#1 and C57#3 DLP mouse prostate organoids upon adaptation to A83-01 withdrawal (scale bar = 50 µm). Please note the adapted organoids retain a pattern of cytokeratins expression consistent with normal cellular identities, including basal, luminal P (lumP) and peri-uretheral (PrU)



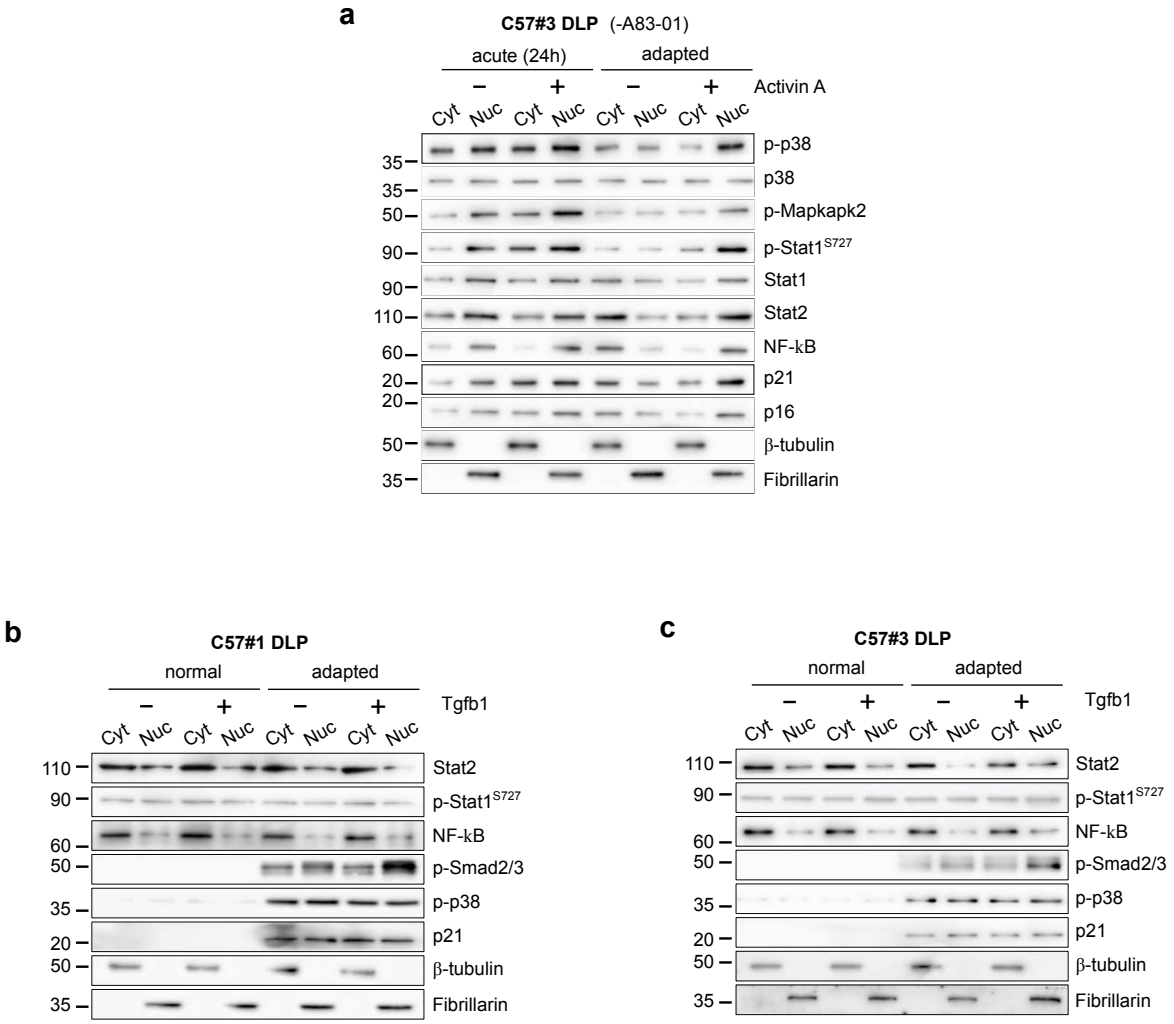
C57#1 DLP mouse prostate organoids adapted to the absence of A83-01 in culture display widespread genomic instability while retaining an intact p53 pathway

a. DNA content analysis in C57#1 DLP and C57#3 DLP mouse prostate organoid lines.
b. Quantification of spectral karyotype (SKY) longitudinal analysis in C57#1 DLP mouse prostate organoids undergoing adaptation to the absence of A83-01 in culture (related to Fig 3f). During adaptation, an early genome duplication event is observed followed by selective chromosome loss and gains, and leading to subtetraploidy.
c. Representative dual-colour FISH images for X and Y chromosomes in C57#1 DLP mouse prostate organoids during adaptation to the absence of A83-01 in culture. This analysis confirmed a progressive sex chromosome imbalance during adaptation.
d. Representative stereoscopic images of C57 #1 DLP mouse prostate organoids treated with Nutlin, or vehicle as control.
e. Western blot analysis of C57 #1 DLP mouse prostate organoids described in **d**.
f. Western blot analysis in C57 #1 DLP mouse prostate organoids treated with doxorubicin or X-rays. C57#1 DLP mouse prostate organoids retain a functional p53 pathway.



Non- canonical Activin A signalling regulates type-I interferon genes in mouse prostate organoids

a-b. mRNA expression levels for selected type-I IFN response genes in C57#1 and C57#3 DLP mouse prostate organoids cultured in complete medium (normal), upon acute A83-01 withdrawal (acute), and adapted to grow without A83-01 (adapted). Transcription of type-I interferon genes is enhanced upon A83-01 withdrawal and reduced upon adaptation (n=3, bulk-RNAseq analysis (a) or qPCR (b); individual data points are shown with bar graphs representing mean value and standard deviation; two-way ANOVA, Tukey's test, p-value * (<0.05), ** (<0.01), *** (<0.001), **** (<0.0001).



Restoration of Activin A signalling – not Tgb1 – leads to cytostasis in organoid lines (C57 #1 and #3) adapted to grow in the absence of A83-01.

a. Western blot analysis of C57#3 DLP mouse prostate organoid line upon acute removal (24 hours) or adapted to grow without A83-01, in the presence or absence of Activin A (50 ng/mL, 24 hours).
b. Western blot analysis of C57#1 DLP normal or adapted to grow without A83-01 mouse prostate organoid lines, in the presence or absence of Tgfb1 (500 ng/mL, 24 hours).
c. Western blot analysis of C57#3 DLP normal or adapted to grow without A83-01 mouse prostate organoid lines, in the presence or absence of Tgfb1 (500 ng/mL, 24 hours).

Supplementary Table 1: Growth factors and small molecules

Treatment	Catalogue #	Concentration
Activin A	R&D, 338-AC	50 ng/mL
Tgfb1	SinoBiol, 50698-M08H	500 ng/mL
Follistatin	PeproTech, 120-13	500 ng/mL
SB203580	Tocris, 1202	10 μM
SB202190	PeproTech, 1523072	10 μM
SB431542	Sigma Aldrich, S4317	10 μM
Ralimetinib*	Selleckchem, S1494	1 μM
Pirfenidone	Cayman, 13986	10 μM
Takinib	Sigma-Aldrich, SML2216	5 μM
IFNβ	SinoBiol, 50708-MCCH5	50 ng/mL

*Organoids were pre-treated with Ralimetinib (1 μM) for 24 hours before being seeded for the experiments.

Supplementary Table 2: Primary antibodies used for IF, IHC and flow cytometry

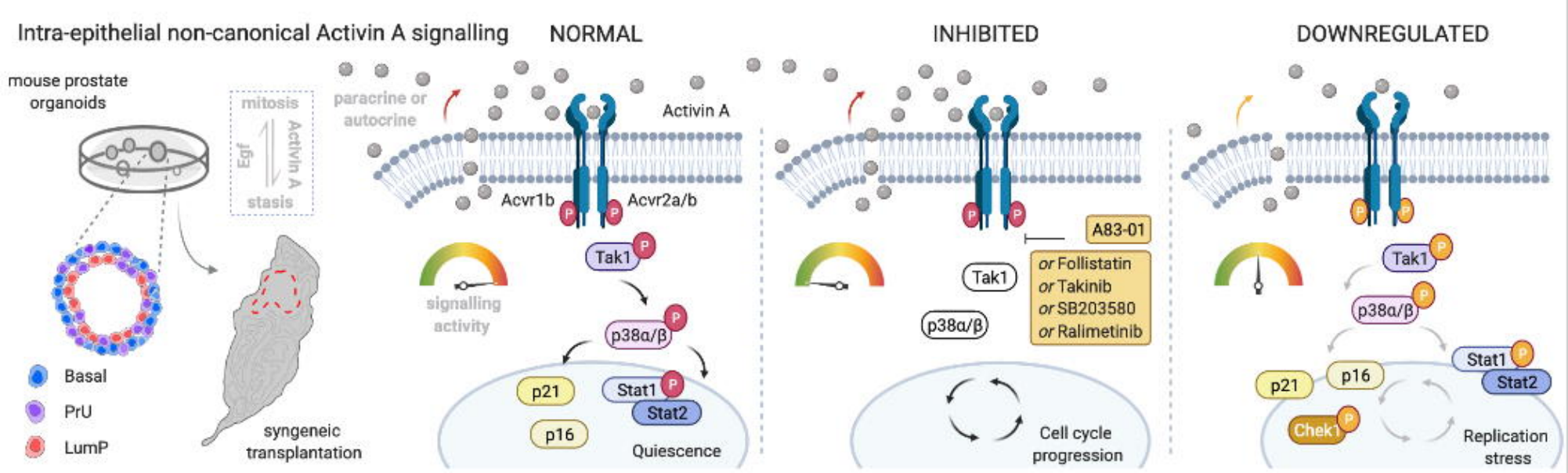
Antigen	Catalogue #	Dilution
Krt5	BioLegend, 905901	1:500
Krt8	Merk, MAB329	1:200
Krt7	Abcam, ab68459	1:250
Krt8/18	Abcam, ab53280	1:1000
Ki67	eBioscience, 14-5698-82	1:200
Egfr	Abcam, ab52894	1:200
Acvr1b	R&D Systems, AF1477	1:500
Ppp1r1b	Invitrogen, MA5-14968	1:400
Ar	Santa Cruz Biotech, SC-816	1:500
Cd24a	eBioscience, BMS17-0242-82	1:800
Sca-1	BioLegend, 122514	1:800

Supplementary Table 3: Primers used for end-point and quantitative PCR

Gene	Primers Sequence
Ifi27	*fw:* 5'-ggcttccattgtctccaaga-3'
	rv: 5'-accttcagtgctccaagtgc-3'
Isg20	*fw:* 5'-cttctgaaaggcaagctggt-3'
	*rv:*5'-tcttgtgtagcaggcgctta-3'
Irf9	*fw:* 5'-ctctttgttcagcgcctttg-3'
	rv-5'-tcccagaaatgtagggttgc-3'
Isg15	*fw:* 5'-gagctagagcctgcagcaat-3'
	rv: 5'-taagaccgtcctggagcact-3'
Oasl2	*fw:* 5'-ctccggttggtgaagttctg-3'
	rv: 5'-gtcgcggtagtttacgagga-3'
Irf7	*fw: 5'*-gaagaccaacttccgctgtg-3'
	rv: 5'-agcattgctgaggctcactt-3'
Trp63	*fw:* 5'-agaacggcgatggtacgaag-3'
	rv: 5'-tctcacgacctctcactggt-3'
Ar	*fw:* 5'-gccaggagtggtgtgtgccg-3'
	rv: 5'-aagttgcggaagccaggcaagg-3'
Tmprss2	*fw:* 5'-gccgcctccggagatttaag-3'
	rv: 5'-aggtgaccctgagttcaatgc-3'
Psca	*fw:* 5'-gctcactgcaaccatgaaga-3'
	rv: 5'-gctaagtaggtggccagcag-3'
Nkx3.1	*fw:* 5'-cggaccctaggagggactc-3'
	rv: 5'-cacctgagtgtgagagaaggc-3'
Mme	*fw:* 5'-ctccaacttctccccaatccc-3'
	rv: 5'-tcgagcagctgattttatgcagt-3'
Pbsn	*fw:* 5'-tgcacagtatgaagggagcat-3'
	rv: 5'-tccgtgtccatgatacgctg-3'
Fkbp5	*fw:* 5'-agccgggaagcctaagtttg-3'
	rv-5'-acttgcctcccttgaagtaca-3'
Tgm4	*fw:* 5'-ctagagtcttgacagggctgc-3'
	rv-5'-tggtactcggatgtgtggtg-3'
Sbp	*fw:* 5'-ccagattgtaccacaaaccctc-3'
	rv-5'-ccgtcctccagaaggaagtc-3'
Sdha	*fw:* 5'-tggtgagaacaagaaggcatca-3'
	rv: 5'-cgcctacaaccacagcatca-3'
Tbp	*fw:* 5'-cggtcgcgtcattttctccgc-3'
	rv: 5'-gtggggaggccaagccctga-3'
Actb	*fw:* 5'-atccagctcctagcacgcacg-3'
	rv: 5'-gtccccgctttgcgcaggtg-3'
Gapdh	*fw:* 5'-gagagtgtttcctcgtcccg-3'
	rv: 5'-actgtgccgttgaatttgcc-3'

Supplementary Table 4: Primary antibodies used for western blot

Antigen	Catalogue #	Dilution
β-Actin	Merk, A2228	1:2000
β-Tubulin	Santa Cruz Biotech, sc-5274	1:4000
Akt	CST, 9272	1:2000
Akt phosphoSer473	CST, 4060	1:1000
Akt phosphoThr308	CST, 9275	1:1000
Ar	Santa Cruz Biotech, sc-816	1:500
Atf2 anti-phosphoThr71	CST, 9221	1:1000
Atm	CST, 2873	1:1000
Atm phosphoSer1981	CST, 5883	1:1000
c-Myc	Abcam, ab32072	1:1000
Chk1	CST, 2360	1:1000
Chk1 phosphoSer35	CST, 2348	1:1000
Cyclin D1	Abcam, ab134175	1:1000
Cyclin E1	CST, 20808	1:1000
Erk	CST, 9102	1:1000
Erk phosphoThr202/Tyr204	CST, 4370	1:1000
Fibrillarin	Abcam, ab4566	1:500
Gapdh	Thermo Fisher, MA515738	1:4000
Krt5	BioLegend, 905901	1:500
Krt8/18	Abcam, ab53280	1:1000
Mapkapk2 phosphoThr334	CST, 3041	1:1000
p16	Abcam, ab211542	1:500
p21	Abcam, ab109520	1:500
p38	CST, 9212	1:1000
p38 phosphoThr180/Tyr182	CST, 9215	1:500
Smad2 phosphoSer465/467	CST, 8828	1:1000
Smad2/3	CST, 8685	1:1000
Smad4	Santa Cruz Biotech, sc-7966	1:1000
Stat1	BD Biosciences, 610186	1:1000
Stat1 phosphoSer727	CST, 9177	1:1000
Stat1 phosphoTyr701	CST, 9171	1:1000
Stat2	CST, 4597	1:1000
Stat3	CST, 9132	1:1000
Stat3 phosphoTyr705	CST, 9131	1:1000
Stat5	CST, 9358	1:1000
Stat5 phosphoTyr694	CST, 9359	1:1000
Tak1	CST, 5206	1:1000
Trp53	Abcam, ab26	1:500


Intra-epithelial non-canonical Activin A signalling
NORMAL
INHIBITED
DOWNREGULATED
mouse prostate organoids
mitosis
Activin A
Egf
stasis
Basal
PrU
LumP
syngeneic transplantation
paracrine or autocrine
Activin A
Acvr1b
Acvr2a/b
P
signalling activity
Tak1
p38α/β
p21
p16
Stat1
Stat2
Quiescence
A83-01
or Follistatin
or Takinib
or SB203580
or Ralimetinib
Cell cycle progression
Chek1
Replication stress