

1 **Midkine noncanonically suppresses AMPK activation through**
2 **disrupting the LKB1-STRAD-Mo25 complex**

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18

19 **ABSTRACT**

20

21 Midkine (MDK), an extracellular growth factor, regulates signal transduction and
22 cancer progression by interacting with receptors, and it can be internalized into the
23 cytoplasm by endocytosis. However, its intracellular function and signaling regulation
24 remain unclear. Here, we show that intracellular MDK interacts with LKB1 and
25 STRAD to disrupt the LKB1-STRAD-Mo25 complex. Consequently, MDK decreases
26 the activity of LKB1 to dampen both the basal and stress-induced activation of AMPK
27 by glucose starvation or treatment of 2-DG. We also found that MDK accelerates
28 cancer cell proliferation by inhibiting the activation of the LKB1-AMPK axis. In
29 human cancers, compared to other well-known growth factors, MDK expression is
30 most significantly upregulated in cancers, especially in liver, kidney and breast
31 cancers, correlating with clinical outcomes and inversely correlating with *PRKAA1*
32 (encoding AMPK α 1) expression and phosphorylated AMPK levels. Our study
33 elucidates an inhibitory mechanism for AMPK activation, which is mediated by the
34 intracellular MDK through disrupting the LKB1-STRAD-Mo25 complex.

35

36 INTRODUCTION

37 AMP-activated protein kinase (AMPK), consisting of catalytic subunit α and
38 regulatory subunit β and γ (Lin & Hardie, 2018), is the core cellular energy sensor and
39 regulator (Garcia & Shaw, 2017). Under energy stress conditions, an elevated cellular
40 AMP/ATP ratio induces conformational changes in the AMPK heterotrimer and
41 induces the exposure of the AMPK α Thr172 site (Hardie, 2018, Oakhill, Steel et al.,
42 2011), which can be phosphorylated by upstream kinases (Carling, 2017).
43 Phosphorylation at Thr172 leads to the activation of AMPK (Hawley, Davison et al.,
44 1996, Suter, Riek et al., 2006), which directly phosphorylates a series of substrates to
45 postpone energy-consuming processes, such as cell proliferation and fatty acid
46 synthesis, and to promote energy-producing procedures, including catabolism and
47 autophagy (Goodman, Liu et al., 2014, Mihaylova & Shaw, 2011). AMPK is closely
48 related to diverse diseases (Rider, 2016), including dual and controversial roles in
49 cancer (Faubert, Vincent et al., 2015, Jeon & Hay, 2015, Russell & Hardie, 2020).
50 Although defined as a tumor suppressor by many studies (Faubert, Boily et al., 2013,
51 Houde, Donzelli et al., 2017, Huang, Wullschleger et al., 2008, Vara-Ciruelos,
52 Dandapani et al., 2019), AMPK promotes cancer progression under certain conditions
53 by rescuing cancer cells from nutrient deficiency (Eichner, Brun et al., 2019,
54 Laderoute, Calaoagan et al., 2014, Saito, Chapple et al., 2015, Shaw, 2015).

55 LKB1, CAMKK β and TAK1 are upstream kinases of AMPK that all
56 phosphorylate AMPK α at the Thr172 site (Goodman et al., 2014). Among these
57 proteins, the serine/threonine kinase LKB1 mediates the best-characterized classical

58 AMPK activation route(Woods, Johnstone et al., 2003), especially in cancer cells. In
59 contrast to most kinases, which are usually phosphorylated and activated by upstream
60 kinases, LKB1 forms a heterotrimer with pseudokinase STRAD and scaffolding
61 protein Mo25 and then undergoes self-phosphorylation at multiple amino acids to
62 self-induce its kinase activity (Hawley, Boudeau et al., 2003, Zeqiraj, Filippi et al.,
63 2009a, Zeqiraj, Filippi et al., 2009b). Some studies have demonstrated that disruption
64 of the LKB1-STRAD-Mo25 complex decreases AMPK α Thr172 phosphorylation
65 levels and attenuates AMPK activity (Lin, Elf et al., 2015).

66 Midkine (MDK, encoded by the *MDK* gene) is a pleiotrophin family growth
67 factor that plays vital roles in different physiological processes, such as embryo and
68 nerve development, blood pressure control, inflammation and immune response
69 (Kadomatsu, Bencsik et al., 2014, Muramatsu, 2010, Sorrelle, Dominguez et al., 2017,
70 Yoshida, Sakakima et al., 2014). MDK is highly expressed in different types of cancer
71 (Kato, Shinozawa et al., 2000, Meng, Tan et al., 2015, Shaheen, Abdel-Mageed et al.,
72 2015) and promotes tumor progression by positively regulating cell proliferation,
73 invasion and migration (Rawnaq, Dietrich et al., 2014, Sun, Hu et al., 2017, Xu, Qu et
74 al., 2009, Yao, Li et al., 2014). The molecular weight of mature MDK is 13 kD after
75 the cleavage of the signal peptide (Muramatsu, 2014). As a secreted protein, MDK
76 binds transmembrane receptors (Kadomatsu, Kishida et al., 2013), including PTP ξ ,
77 ALK, Notch2 and LRP1, and thus activates intracellular signaling (Herradon,
78 Ramos-Alvarez et al., 2019, Kadomatsu et al., 2013, Kishida, Mu et al., 2013, Lorente,
79 Torres et al., 2011, Muramatsu, Zou et al., 2000). It has also been reported that

80 extracellular MDK can be transported into the cytosol by endocytosis and then enter
81 the nuclei where it undergoes proteasomal degradation, but the intracellular functions
82 of MDK are still unclear (Dai, Shao et al., 2008, Shibata, Muramatsu et al., 2002,
83 Suzuki, Shibata et al., 2004).

84 Here, we report that MDK suppresses AMPK activation in the cytoplasm instead
85 of acting as an extracellular ligand. In the cytosol, MDK interacts with LKB1 and
86 STRAD to depolymerize the LKB1-STRAD-Mo25 complex and reduce LKB1
87 activity, consequently reducing the phosphorylation of AMPK α . Decreasing the
88 cellular MDK expression level or maintaining the extracellular localization of MDK
89 elevates AMPK α phosphorylation in cells. In cancer cells, MDK promotes cell
90 proliferation by suppressing the LKB1-AMPK axis, and MDK expression correlates
91 with clinical outcomes and inversely correlates with LKB1/AMPK signaling pathway
92 activation. Therefore, our study reveals a previously undescribed molecular function
93 and mechanism of MDK, which may facilitate further clinical application of MDK in
94 targeted cancer therapy.

95 **RESULTS**

96 **Midkine suppresses AMPK activation in an intracellular localization-dependent**
97 **manner**

98 Most previous MDK studies focused on identifying the transmembrane receptors of
99 MDK to connect the secreted MDK with intracellular signaling. Very few studies
100 have reported that extracellular MDK can be internalized into cells by endocytosis
101 and localize near the nucleus to regulate rRNA synthesis (Dai, 2009, Dai et al., 2008).
102 To confirm this localization, we examined the transport and relocalization of MDK.
103 Consistent with previous studies, MDK was secreted into the cell medium of HepG2
104 and HCCLM3 cells expressing high levels of MDK (Fig 1A), and this secreted MDK
105 was internalized into Bel-7402, SMMC-7721 and MHCC97H cells not expressing
106 MDK (Figs 1B and EV1A and B). This internalized intracellular MDK was found 15
107 minutes after MDK-overexpressing cell culture medium (or conditioned medium, CM)
108 treatment (Figs EV1A and B), suggesting that the intracellular relocalization of MDK
109 was efficient in MDK non-expressed cells. However, intracellular MDK was mostly
110 localized in the cytoplasm, not in the nucleus (Figs 1C and EV1C and D). This
111 phenomenon indicated that MDK may possess an unexplored function in the
112 cytoplasm.

113 To identify the MDK-regulated cell signaling pathways, we first performed a
114 pathway enrichment analysis. Interestingly, we found that the AMPK signaling
115 pathway was the most highly correlated with MDK among the pathways (Fig 1D). To

116 further examine the relationship between MDK and the AMPK pathway, we tested the
117 level of phosphorylated AMPK α at Thr172 in MDK-knockdown and
118 MDK-overexpressing cells. In both Bel-7402 and MHCC97H cells, the
119 overexpression of MDK inhibited the level of phosphorylated AMPK α during glucose
120 starvation, 2-DG stimulation or FBS deprivation (Figs 1E, F and G, and EV1E). In
121 contrast, knocking down MDK expression by shRNA led to elevated levels of
122 AMPK α phosphorylation (Figs 1H and EV1F and G), and restoring MDK expression
123 decreased AMPK α phosphorylation (Fig EV1F and G). Taken together, these results
124 suggest that MDK suppresses AMPK activation in human cancer cells.

125 MDK is well known to be secreted after posttranslational modification. Although
126 a number of studies have reported that extracellular MDK can be transported into
127 cells, the function of intracellular MDK remains unclear. Therefore, to understand
128 whether internalized cellular MDK is critical for AMPK repression, we investigated
129 the effect of extracellular MDK on AMPK activation. We collected CM containing
130 secreted MDK from MDK-overexpressing MHCC97H cells and then used it to
131 culture MDK-deficient MHCC97H parental cells. Upon the application of CM from
132 MDK-overexpressing cells, the intracellular MDK level increased in a time-dependent
133 manner, and this treatment, which triggered AKT phosphorylation as previously
134 reported (Sandra, Harada et al., 2004), decreased LKB1 and AMPK α phosphorylation
135 (Fig 1I). In addition, Bel-7402 cells cultured with control CM exhibited increased
136 AMPK activation after 2-DG treatment, however, the cells cultured with CM from
137 MDK-overexpressing showed decreased AMPK activation, even after 2-DG treatment

138 (Fig EV1H).

139 Next, to further clarify whether the intracellular relocalization of MDK is
140 indispensable for AMPK suppression, we induced the transportation of MDK into the
141 cytoplasm. MDK is a heparin-binding protein(Iwasaki, Nagata et al., 1997,
142 Kadomatsu et al., 2013). Heparin is a sulfated glycosaminoglycan polymer that can
143 bind MDK and restrict its movement to the inside of cells (Kishida & Kadomatsu,
144 2014, Muramatsu, Yokoi et al., 2011). By adding heparin to the medium of the
145 HCCLM3 cells, the intracellular MDK level decreased dramatically, and MDK
146 significantly accumulated in the cell culture medium (Fig 1J). Heparin reduced
147 intracellular MDK and obviously elevated AMPK α phosphorylation in the HCCLM3
148 cells (Fig 1J). In contrast, knocking down MDK did not alter AMPK α
149 phosphorylation levels in cells during heparin application (Fig 1J), excluding the
150 possibility that AMPK is activated by heparin. Similarly, heparin decreased the
151 intracellular MDK level in the MDK-overexpressing cells and promoted AMPK α
152 phosphorylation but did not alter the AMPK activity in the Bel-7402 control cells (Fig
153 EV1I). Additionally, heparin caused decreased intracellular MDK levels and elevated
154 AMPK α phosphorylation in MDK-CM-treated Bel-7402 and MHCC97H cells (Fig
155 1K and L). In summary, these results indicate that intracellular MDK suppresses
156 AMPK phosphorylation in a cytosol-dependent manner and corroborates findings
157 indicating an intracellular function for MDK.

158 **Midkine associates with AMPK subunits and its upstream regulating factors**

159 Since MDK regulates the phosphorylation of LKB1 and AMPK, we tried to reveal the

160 underlying mechanisms by which MDK functions. First, we isolated MDK-associated
161 protein complexes in HEK293T cells through tandem affinity purification followed by
162 mass spectrometry (MS) analysis. According to their biological functions, the
163 MDK-associated proteins were classified into different groups (Fig EV2A). We found
164 that some MDK-associated proteins belonged to LKB1 substrates, AMPK regulators
165 or metabolic regulation factors (Figs 2A and EV2A). Interestingly, MDK associated
166 with the LKB1 substrates MARK and SIK3 of AMPK family proteins, and the
167 well-studied AMPK ubiquitination regulators USP10 and UBE2O were also added to
168 the prey list (Fig 2A).

169 The specific interaction between MDK and the AMPK α subunit, as well as the
170 well-studied AMPK upstream kinases LKB1 and CAMKK β , was confirmed by
171 pull-down assays (Figs 2B and EV2B and C). Additionally, MDK form complex with
172 endogenous AMPK signaling components such as LKB1, STRAD α/β , AMPK $\alpha 1/2$,
173 AMPK γ and CAMKK β in MDK-transduced HEK293T cells (Fig 2C). Furthermore,
174 coimmunoprecipitation (co-IP) assays showed that LKB1 can be detected in
175 endogenous MDK immunoprecipitates from HCCLM3 cells (Fig 2D) and that
176 endogenous MDK is pulled down with endogenous LKB1 immunoprecipitates from
177 HCCLM3 and HepG2 cells (Fig 2E and F). Interestingly, we noticed that STRAD α
178 and Mo25a, which bind LKB1 and facilitate LKB1 activation, showed different
179 interaction ability with MDK (Figs 2D-H and EV2B and C). STRAD α was associated
180 with both endogenous and exogenous MDK; however, Mo25a was not detected in the
181 either the endogenous co-IP or exogenous pull-down assays (Figs 2C, D, G and H,

182 and EV2B and D). These results suggested that MDK may inhibit the protein
183 machinery of LKB1-Mo25-STRAD.

184 Considering that LKB1 phosphorylates AMPK α at Thr172, we wondered
185 whether MDK interacts with LKB1 and AMPK α directly or indirectly via the
186 kinase-substrate reaction. To test this hypothesis, we stably expressed MDK in
187 LKB1-deficient A549 cells and found that AMPK α was detected only in the MDK
188 coprecipitates from LKB1-reconstituted A549 cells (Fig EV2D). This result indicated
189 that the interaction between MDK and AMPK may be dependent on LKB1. LKB1
190 contains a kinase domain in the middle of its amino acid sequence (Fig EV2E).
191 Although AMPK α was associated with different forms of LKB1 (the full length
192 protein, the N-terminus with the kinase domain only and the C-terminus only), MDK
193 interacted only with the NK domain (amino acids 1-309), which was similar to
194 STRAD and Mo25 (Fig EV2E and F). In summary, we discovered that both MDK and
195 AMPK α are physically associated with LKB1 through its N-terminal kinase domains
196 in cells.

197 **Midkine suppresses AMPK α activation through interacting with LKB1**

198 LKB1 and calcium/calmodulin-dependent protein kinase kinase β (CAMKK β) are
199 well-known AMPK upstream kinases, and both kinases can phosphorylate the AMPK
200 α subunit at the Thr172 site (Fogarty, Ross et al., 2016, Woods et al., 2003). Although
201 MDK associates with LKB1 and CAMKK β (Fig 2B and C), whether MDK regulates
202 AMPK α activities through LKB1 or CAMKK β remains unclear. Interestingly, the
203 activity of LKB1 and AMPK α was increased in MDK-knockdown Hep3B and

204 HCCLM3 cells (Fig 3A and B). In contrast, restoring MDK expression in these
205 knockdown cells recovered LKB1 activity and AMPK α phosphorylation (Fig 3A and
206 B), suggesting that MDK contributed to the LKB1-modulated AMPK α suppression.
207 Furthermore, in LKB1-deficient A549 cells, MDK overexpression did not alter
208 AMPK α phosphorylation levels until LKB1 expression was restored (Fig 3C and D),
209 indicating that MDK suppressed AMPK α activation through LKB1. In HCCLM3 cells,
210 AMPK α phosphorylation was elevated when the intracellular MDK levels were
211 decreased by heparin treatment, but the effect of heparin was attenuated in
212 LKB1-knockdown cells (Fig 3E). These results indicated that LKB1 is involved in the
213 MDK-induced regulation of AMPK activity.

214 To understand whether MDK mediates AMPK signaling through CAMKK β , we
215 used CAMKK β activator A23187 to treat MDK-restoring MHCC97H cells. The
216 overexpression of MDK suppressed AMPK activation upon DMSO treatment;
217 however, AMPK α phosphorylation was elevated regardless of the MDK expression
218 after CAMKK β activator A23187 treatment (Fig 3F). In agreement with this, A23187
219 stimulated AMPK α activation regardless of the level of MDK or LKB1 expression,
220 while MDK suppressed AMPK α phosphorylation in the presence of LKB1 during
221 glucose starvation (Fig 3C and D). Considering these results, we speculated that MDK
222 mediates AMPK activity through LKB1.

223 **Midkine disrupts LKB1-STRAD-Mo25 complex**

224 LKB1, a serine/threonine kinase, forms a heterotrimeric complex with pseudokinase
225 STRAD and scaffolding-like adaptor Mo25a and undergoes conformational change

226 and self-phosphorylation to achieve full activation (Zeqiraj et al., 2009a). Our results
227 demonstrated that MDK-mediated repression of AMPK activation relied on LKB1
228 (Fig 3C-E), and the level of MDK expression was correlated with LKB1
229 phosphorylation (Fig 3A and B). In addition, we found that MDK physically interacts
230 with LKB1 and STRAD (Fig 1B-H). Considering that the formation of the
231 LKB1-STRAD-Mo25a complex necessary for LKB1 activity, we surmised that MDK
232 affects the stability of the LKB1-STRAD-Mo25 heterotrimer.

233 To investigate this hypothesis, we performed coimmunoprecipitation assays with
234 LKB1 from MDK-transduced cells. The overexpression of MDK significantly
235 inhibited the formation of the LKB1-STRAD-Mo25a complex in endogenous LKB1
236 immunoprecipitates from HEK293T cells (Fig 4A). In contrast, knocking down MDK
237 increased the level of STRAD and Mo25 in the endogenous LKB1-containing
238 immunoprecipitates from HCCLM3 cells (Fig 4B). Furthermore, to prevent the
239 phosphorylation of LKB1 from affecting this interaction, we expressed FLAG-tagged
240 wild-type (WT) and kinase dead (KD, K78L) LKB1 in HEK293T cells. As previously
241 reported, both the WT and KD LKB1 bound strongly to STRAD and Mo25a (Fig
242 EV3A). Next, we simultaneously expressed FLAG-tagged LKB1-KD and SFB-tagged
243 AMPK α 1 in HEK293T cells. The coimmunoprecipitation assays showed that MDK
244 overexpression decreased the binding of STRAD and Mo25a to LKB1; however, it
245 did not affect the LKB1-AMPK interaction (Figs 4C and EV3B). Moreover, gradually
246 increasing MDK in the HEK293T cells was accompanied by gradually decreased
247 LKB1-STRAD-Mo25a association, although the LKB1-AMPK α interaction was not

248 affected (Fig 4D). In contrast, gradually increasing MDK expression affected neither
249 the association of AMPK α with the regulatory β and γ subunits nor the
250 LKB1-AMPK α interaction (Figs 4E and EV3C). To further evaluate the impact of
251 secretion on MDK function, we deleted the three amino acids from 20 to 22 in MDK
252 signal peptide, and named MDK-Del. MDK-Del showed a strong defect in the
253 cleavage of signal peptide and could not be detected in the medium (Fig EV3D). Similar
254 to the wild type MDK, MDK-Del interact with LKB1 in cells and attenuated the
255 interaction of LKB1 to STRAD and Mo25 (Fig EV3E and F). Taken together with the
256 association of MDK with LKB1 and STRAD, these results suggest a mechanism by
257 which MDK binds to LKB1 and STRAD and inhibits the formation of the
258 LKB1-STRAD-Mo25a complex, leading to a decrease in LKB1 activity and AMPK α
259 phosphorylation.

260 **Midkine expression is upregulated in cancers**

261 To explore the expression of growth factors in different cancers, we analyzed the
262 expression levels of well-studied growth factors in The Cancer Genome Atlas (TCGA)
263 database. Among these proteins, MDK showed the highest upregulated expression in
264 different types of cancers, even higher than that of established growth factors such as
265 VGF, EGF and TGFB1 (Figs 5A and B, and EV4A), indicating important roles for
266 MDK in cancer. Indeed, cancer was the disease most frequently related to MDK in the
267 disease enrichment analysis (Fig EV4B).

268 To further examine the expression of MDK in practical samples, we collected 36
269 pairs of liver cancer tissues and adjacent noncancer tissues. MDK expression was

270 significantly upregulated in the cancer tissues compared to its expression in the
271 adjacent normal tissues (Figs 5C and D, and EV4C). In addition, we also examined
272 MDK expression through tissue microarray assay (TMA), which contained 75 pairs of
273 liver cancer and adjacent normal tissue samples, by immunohistochemistry (IHC).
274 Similarly, MDK was highly expressed in the cancer tissues compared to its expression
275 in the adjacent normal tissues (Figs 5E and F, and EV4D). Notably, higher MDK
276 expression correlated with poor prognosis in both the TCGA liver hepatocellular
277 carcinoma (LIHC) and kidney renal clear cell carcinoma (KIRC) cohorts (Fig 5G and
278 H). Taken together, MDK is highly expressed in most cancers, which suggests that
279 MDK plays important functions in cancer progression.

280 **Midkine promotes cancer cell proliferation, invasion and tumorigenesis**

281 To clarify the function of MDK in tumorigenesis, we performed both loss-of-function
282 and gain-of-function analyses of MDK in different cancer cell lines. First, we
283 determined the expression level of MDK in a panel of human cancer cell lines. MDK
284 was highly expressed in most cancer cell lines compared to its expression in
285 immortalized normal human liver cells and mammary epithelial cells; however, in
286 some cancer cell lines, MDK expression was almost negligible (Fig EV5A and B).
287 This negative expression of MDK may be due to gene methylation in the *MDK*
288 genomic region or transcriptional regulation in particular cancer cells instead of
289 genome deletion (Fig EV5C).

290 Considering these expression assessment results, we generated MDK-transduced
291 and short hairpin RNA (shRNA) knockdown cell lines (Figs 6A, E and G and

292 EV5D). Two independent MDK shRNAs both decreased the proliferation of
293 HCCLM3 and HepG2 cells (Figs 6B and F, and EV5 E). In contrast, transducing
294 MDK expression vector in MHCC97H and Bel-7402 cells increased their
295 proliferation (Figs 6C and D, and EV5F). In addition, restoring MDK expression in
296 MDK-knockdown HCCLM3 and HepG2 cells recovered their proliferation ability
297 (Figs 6E and E, and EV5D and E). We also examined the effect of MDK on cell
298 motility and anchorage-independent growth. Knocking down MDK expression
299 significantly decreased the invasion ability of BT549 cells (Fig 6G), and the
300 overexpression of MDK increased the colony-forming ability of Bel-7402 cells in soft
301 agar (Fig 6H). However, MDK-overexpressing cells did not affect wound healing
302 migratory ability (Fig EV5G). To explore the function of MDK in tumor growth *in*
303 *vivo*, we subcutaneously injected MDK-knockdown or reconstituted HCCLM3 cells
304 and control cells into nude mice. Mice with MDK shRNA-expressing cancer cells
305 produced smaller tumor, measured by volume, and lighter tumor, measured by weight,
306 throughout the experiment than mice transplanted with the control shRNA-infected
307 cells or MDK-reconstituted HCCLM3 cells (Fig 6I-K). In contrast,
308 MDK-overexpressing MHCC97H cells accelerated tumor growth and tumor weight *in*
309 *vivo* (Fig EV5H and I). Furthermore, the tumors formed by MHCC97H cells
310 overexpressing MDK exhibited downregulated AMPK α phosphorylation compared
311 with the tumors formed by control MHCC97H cells (Fig EV5J). Taken together, these
312 results indicate that MDK promotes the proliferation and tumorigenicity of human
313 cancer cells; however, the mechanism by which intracellular MDK derives

314 tumorigenesis remains unclear.

315 **Midkine promotes cancer progression by negatively regulating AMPK signaling**

316 MDK has been reported to promote tumor progression in a diverse manner, but the
317 definitive mechanism remains unclear. Our results showed that MDK accelerated
318 tumor cell proliferation, invasion and *in vivo* tumorigenesis (Fig 6). AMPK is mainly
319 activated under energy stress conditions and suppresses cell division to reduce energy
320 consumption(Gonzalez, Hall et al., 2020). To investigate the role of AMPK in
321 MDK-modulated cell proliferation, we performed a colony forming assay under
322 normal and low-glucose conditions. As expected, MDK-overexpressing cells showed
323 an accelerated proliferation rate under both conditions, and we also observed that,
324 compared to the effects under normal conditions, the overexpression of MDK
325 significantly promoted cell proliferation under low-glucose conditions (Fig EV6A
326 and B). However, knocking down MDK did not alter the mitochondrial oxygen
327 consumption rate (OCR) or extracellular acidification rates (ECARs) (Fig EV6C and
328 D), thus indicating that MDK did not affect glycolysis or mitochondrial oxidative
329 phosphorylation.

330 Furthermore, to determine whether MDK decreases LKB1 activity to suppress
331 AMPK activation and thus contributes to cell proliferation, we expressed LKB1
332 shRNA and CAMKK β shRNA in MDK-depleted HCCLM3 cells. Knocking down
333 LKB1, but not CAMKK β , reversed the inhibitory effects of MDK shRNA on cell
334 proliferation and colony formation (Figs 7A and B, and EV6E-H). In addition,
335 reconstitution of LKB1 in its deficient Hela cells, significantly inhibited the cell

336 proliferation caused by MDK overexpression (Fig EV6I-K).

337 To understand whether MDK affects AMPK-related signaling pathways in
338 different cancers, we performed a gene expression correlation-based gene set
339 enrichment analysis (GSEA). The results showed that MDK expression is negatively
340 correlated with the AMPK signaling pathway in several different cancers, such as
341 liver cancer, kidney cancer and breast cancer (Figs 7C and EV7A and B). The IHC
342 analysis of the HCC tissues revealed that MDK protein expression is negatively
343 correlated with p-AMPK α expression (Fig 7D), and high MDK expression correlates
344 with poor prognosis for HCC patients (Fig 7E and Supplementary Table 1).

345 Next, to investigate the relevance of our findings to human cancer, we analyzed
346 gene expression data from TCGA and Gene Expression Omnibus (GEO) datasets. We
347 found a significant negative correlation between *MDK* and the *PRKAA1* or *STK11*
348 (encoding LKB1) transcript levels in the GSE76427 dataset (Fig 7F). On the other hand,
349 MDK showed strong negative correlations with the expression of *PRKAA1* and the
350 activity of AMPK in the TCGA database (Figs 7G and H, and EV7C and D; see the
351 Methods section for the estimation of AMPK activity). Next, we examined the
352 prognostic value of *MDK* with *PRKAA1* or AMPK using the TCGA dataset of KIRC
353 tumors from 531 patients. The patients with simultaneous high expression levels of
354 *MDK* and low expression levels of *PRKAA1* or low AMPK activity had shorter
355 overall survival in the KIRC cohort (Fig 7I and J). In summary, targeting the high
356 expression of MDK may provide therapeutic benefits in human cancers.

357 **DISCUSSION**

358 MDK is a growth factor belonging to the pleiotrophin family. This definition, in
359 association with its secretory nature, inspired receptor identification research seeking
360 to elucidate the working mechanism of MDK. Several receptors that bind MDK have
361 been identified: ALK, LRP1, Notch2 and PTP ξ (Chen, Bu et al., 2007, Gungor,
362 Zander et al., 2011, Huang, Hoque et al., 2008, Lorente et al., 2011, Muramatsu et al.,
363 2000, Sakaguchi, Muramatsu et al., 2003); however, none of these receptors have high
364 affinity for MDK. MDK was also found to be internalized by cells after secretion, but
365 this point has been largely ignored in previous MDK functional studies. In the present
366 study, we not only confirmed the intracellular transport of MDK (Fig 1B and I-L) but
367 also show the high efficiency of this translocation (Fig EV1A and B). In addition,
368 heparin treatment caused a large decrease in intracellular MDK (Fig 1J-L), indicating
369 that most intracellular MDK was the result of extracellular transport. These results
370 suggested that MDK has highly efficient transportability, which enables it to play
371 important roles in the cytoplasm. However, the detailed internalization mechanism of
372 MDK warrants future investigation.

373 Indeed, here, we reveal previously undescribed functions of intracellular MDK to
374 modulate LKB1 activity by disrupting the formation of the LKB1-STRAD-Mo25
375 complex by directly associating with LKB1 and STRAD (Figs 2B-H and 4A-E and
376 EV3A, B , E and F). The LKB1-STRAD-Mo25 complex is the major upstream
377 activator of the energy-sensing AMPK (Hawley et al., 2003). However, LKB1
378 exhibits weak catalytic activity in cells, and its activation is predominantly stimulated
379 by STRAD and MO25 (Boudeau, Baas et al., 2003, Boudeau, Scott et al., 2004,

380 Hawley et al., 2003, Zeqiraj et al., 2009a). MDK inhibits LKB1 activity by
381 depolymerizing the LKB1-STRAD-Mo25 complex (Fig 2 and Fig 4), and its
382 inhibition directly suppressed AMPK activation in cells (Fig 2). Thus, we elucidated a
383 new intracellular function and molecular mechanism of MDK (Fig 7), which will
384 inform us as we further investigate whether this mechanism commonly mediates the
385 activity of other proteins.

386 The expression of MDK has been reported to be upregulated in diverse types of
387 cancer (Filippou, Karagiannis et al., 2020), which was confirmed in our study (Figs
388 5A-F and EV4). The elevated expression of MDK was accompanied by decreased
389 patient survivals (Figs 5G and H, and 7I and J), suggesting that MDK serves as a
390 prognostic marker. It has been reported that MDK promotes cancer progression by
391 regulating diverse processes, including cell proliferation, invasion, migration and
392 apoptosis (Dai, Wang et al., 2019, Jono & Ando, 2010, Olmeda, Cerezo-Wallis et al.,
393 2017, Takei, Kadomatsu et al., 2001, Yin, Luo et al., 2002). Consistent with these
394 multiple functions, MDK participates in diverse cellular signaling pathways
395 (Kadomatsu et al., 2013), such as the AKT, ERK and Notch2/JAK pathways(Kishida
396 et al., 2013, Lopez-Valero, Davila et al., 2020, Sandra et al., 2004, Stoica, Kuo et al.,
397 2002). In this study, we found that MDK suppresses the activation of AMPK (Figs
398 1D-I and 3A-F), which is usually regarded as a tumor suppressor. It will be interesting
399 to know whether MDK contributes to cancer progression through AMPK signaling or
400 other pathways, such as by activating AKT, which we discovered (Figs 1I and J, and
401 EV1E). MDK increases cell proliferation and colony formation under normal and

402 low-glucose culture conditions (Figs 6A-F and H and EV5D-F, EV6A and B), even
403 though MDK did not affect glycolysis or mitochondrial oxidative phosphorylation
404 (Fig EV 6C and D). Therefore, our study proved that the inhibition of AMPK activity
405 by MDK may occur only through LKB1 activity in cancer cells.

406 AMPK, as a master energy sensor, is activated under energy stress conditions to
407 modulate a series of cell behaviors for maintaining survival, including the repression
408 of cell proliferation. Although AMPK is usually considered to be a tumor suppressor,
409 several studies have also reported that AMPK promotes tumor progression by
410 protecting tumor cells under energy stress conditions (Shaw, 2015). These findings
411 indicate that some individual cases may manifest specific regulatory mechanisms.
412 Here, we also found that the expression of MDK was upregulated overall, but some
413 individuals showed the opposite expression trend (Figs 5B-F, and EV4C and D). It
414 will be interesting to determine the AMPK phosphorylation level and tumor
415 development stage in low-MDK tumors. MDK has been widely presumed to be a
416 diagnostic marker of several different cancers, but the ambiguous regulatory
417 molecular mechanism has postponed its utilization. Here, we elucidate the molecular
418 mechanism by which MDK modulates tumor progression, including the suppression
419 of AMPK signaling, to provide more clues to advance the clinical application of MDK
420 in cancer diagnosis and prognosis.

421

422 **ACKNOWLEDGMENTS**

423 We thank members of the Dr. Piao laboratory for helpful discussion. This study is
424 supported by National Natural Science Foundation of China grants (No.81972625, No.

425 81672440, No.81602155, No.21907093), Dalian Science and Technology Innovation
426 Funding (2019J12SN52), Innovation program of science and research from the DICP,
427 CAS (DICP ZZBS201803).

428 **AUTHOR CONTRIBUTIONS**

429 H-l.P. and T.X. conceived the project, H-l.P. supervised the project. T.X. and H-l.P. the
430 designed project and T.X performed most of experiments, D.C. performed
431 computational data analysis, T.X., D.C. and H-l.P. analyzed data. X.L, N.Z., W.W.,
432 H.C., T.L., R.Y., W.O., H.Q., J.K., C.Z., and S.L. provided significant intellectual
433 input. T.X. and H-l.P. wrote the manuscript with input from all other authors.

434 **DECLARATION OF INTERESTS**

435 All authors declare no competing interest.

436

437 **FIGURE LEGENDS**

438 **Figure 1 | Midkine suppresses AMPK activation in an intracellular**
439 **localization-dependent manner**

440 **A.** Western blotting of MDK and β -actin in the HepG2, HCCLM3, Bel-7402 and
441 SMMC-7721 cell lysate and conditioned medium (CM).

442 **B.** Western blotting of MDK and β -actin in the Bel-7402 and SMMC-7721 cells with
443 or without CM from MDK-overexpressing MHCC97H cells.

444 **C.** Western blotting of MDK, β -tubulin and Lamin B1 in the cytoplasmic and nuclear
445 fractions of the MHCC97H cells transduced with MDK and the control cells.

446 **D.** Signaling pathway enrichment assay with MDK-correlated genes based on the
447 TCGA database.

448 **E.** Western blotting of the Bel-7402 cells transduced with MDK and the control cells
449 treated with different concentrations of glucose (25 mM and 1 mM) for 2 hours.

450 **F.** Western blotting of the Bel-7402 cells transduced with MDK and the control cells
451 with or without 10 mM 2DG treatment for 4 hours.

452 **G.** Western blotting of the MHCC97 cells transduced with MDK and the control cells
453 at different times during glucose starvation.

454 **H.** Western blotting of the HCCLM3 cells transduced with two independent MDK
455 shRNAs with or without 10 mM 2DG treatment for 4 hours.

456 **I.** Western blotting of the MHCC97H cells at different time points of CM treatment.
457 CM is from MDK-overexpressing MHCC97H cells.

458 **J.** Western blotting of the HCCLM3 cells transduced with MDK shRNA1 and the

459 control cells with or without heparin treatment (30 $\mu\text{g/ml}$) for 4 hours under 10 mM
460 2DG culture conditions.

461 **K and L.** Western blotting of the Bel-7402 (K) and MHCC97H (L) cells with or
462 without combined treatment with MDK-overexpression CM and heparin (30 $\mu\text{g/ml}$).

463 **Figure 2 | Midkine associates with AMPK subunits and its upstream regulating**
464 **factors**

465 **A.** AMPK kinase subunit and LKB1 substrates were identified as MDK-associated
466 proteins in HEK293A cells by tandem affinity purification–mass spectrometry. Bait
467 MDK protein is marked in red. AMPK α is marked in blue. The right column of
468 numbers represents unique peptide number/total peptide number.

469 **B and C.** MDK associates with LKB1, CAMKK β and AMPK subunits. The indicated
470 constructs were expressed in the HEK293T cells for 24 hours, and cell lysates were
471 subjected to pull-down assays with S protein beads.

472 **D.** MDK was immunoprecipitated from HCCLM3 cells and subjected to Western blot
473 analysis with antibodies against LKB1, Mo25a, STRAD α and MDK.

474 **E and F.** LKB1 was immunoprecipitated from HCCLM3 (E) and HepG2 (F) cells and
475 subjected to Western blot analysis with antibodies against MDK, Mo25a, STRAD α
476 and LKB1.

477 **G and H.** HEK293T cells were cotransfected with MDK-HA and Flag-tagged LKB1
478 (G) or Myc-tagged Mo25a (H) and coimmunoprecipitated with HA primary antibody
479 and subjected to Western blot analysis with antibodies against LKB1, HA, Mo25a and
480 MDK.

481 **Figure 3 | Midkine suppresses AMPK α activation through LKB1**

482 **A and B.** Western blot analysis of the Hep3B cells transduced with MDK shRNA1
483 and restored MDK in the MDK-knockdown cells (A) and the HCCLM3 cells
484 transduced with two independent MDK shRNAs and restored MDK in the
485 MDK-knockdown cells after 4 hours of 10 mM 2-DG treatment (B). Western blot
486 analysis was performed with antibodies against p-LKB1, LKB1, p-AMPK α , AMPK α ,
487 MDK and β -actin.

488 **C and D.** Western blot analysis of the A549 cells transduced with LKB1 alone or in
489 combination with MDK and the control cells with glucose starvation for 2 hours (C)
490 and the A549 cells transduced with LKB1 alone or in combination with MDK and the
491 control cells with DMSO or A23187 (10 μ g/ml) treatment or glucose starvation for 2
492 hours (D). Western blot analysis was performed with antibodies against p-AMPK α ,
493 AMPK α , LKB1, MDK and β -actin.

494 **E.** Western blot analysis of p-AMPK α , AMPK α , LKB1, MDK and β -actin in the
495 HCCLM3 cells transduced with LKB1 shRNA and the control cells with or without
496 heparin (30 μ g/ml) treatment and 10 mM 2-DG treatment for 4 hours.

497 **F.** Western blot analysis of p-AMPK α , AMPK α , MDK and β -actin from the
498 MHCC97H cells transduced with MDK-Myc and the control cells treated with DMSO
499 or A23187 (10 μ g/ml).

500 **Figure 4 | Midkine depolymerized LKB1-STRAD-Mo25 complex**

501 **A and B.** LKB1 was immunoprecipitated from the HEK293T cells transduced with
502 MDK-HA (A) and the HCCLM3 cells transduced with MDK shRNA1 (B), and then,

503 Western blot analysis was performed with antibodies against STRAD α , Mo25a, MDK
504 and LKB1.

505 **C.** LKB1 was immunoprecipitated from the HEK293T cells transduced with
506 MDK-HA and the control cells followed by Western blotting with antibodies against
507 AMPK α , STRAD α , Mo25a, HA and FLAG. The indicated constructs were expressed
508 in the HEK293T cells for 48 hours, and the cell lysates were subjected to
509 coimmunoprecipitation with primary LKB1 and IgG antibodies.

510 **D and E.** HEK293T cells were cotransfected with different doses of MDK-HA and
511 SFB-tagged LKB1 (D) or SFB-tagged AMPK α 1 (E), pulled down with S protein
512 beads and subjected to Western blot analysis with antibodies against STRAD α ,
513 Mo25a, LKB1, MDK and AMPK subunits.

514 **Figure 5 | Midkine expression is upregulated in cancer**

515 **A.** Pan-cancer evaluation of the expression and prognostic impact of growth factors.
516 The color of each rectangle represents the log₂ transformed fold change (Log₂FC) of
517 the mRNA expression for the corresponding growth factor between tumor and normal
518 tissues, and the white rectangles indicate either a Log₂FC value equal 0 or differences
519 between tumor and normal tissues that are not significant (linear model approach of
520 limma, $P > 0.01$). The purple and green circles represent high gene expression
521 correlated with good and poor prognosis, respectively (log rank test, $P < 0.01$). The left
522 bars represent the numbers of cancer types in which a growth factor is upregulated in
523 the tumor tissues compared with the normal tissues ($P < 0.01$, log₂FC > 1). The
524 growth factors are ranked by the numbers, and only the top 25 factors are shown.

525 **B.** Boxplots of the differences in MDK expression in paired normal and tumor tissues
526 of eight types of cancers. The centers of the boxes represent the median values. The
527 bottom and top boundaries of the boxes represent the 25th and 75th percentiles,
528 respectively. The whiskers indicate 1.5-fold of the interquartile range. The dots
529 represent points falling outside this range. The paired P-values were calculated based
530 on Wilcox tests.

531 **C and D.** The expression of MDK in 36 pairs of matched adjacent nontumor (NT)
532 and cancer (Ca) tissues as detected by Western blotting (C), and the distribution of
533 MDK expression in both the NT and Ca samples as represented by boxplots with the
534 expression value normalized by ImageJ software (D).

535 **E and F.** Immunohistochemical staining of MDK in representative adjacent nontumor
536 and HCC specimens (E) and boxplots of the distributions of MDK expression status
537 in 75 paired paraffin-embedded tissues (F). Scale bar, 200 μm .

538 **G and H.** Kaplan-Meier survival curves of LIHC (G) and KIRC (H) patients with
539 data stratified by the expression levels obtained from the TCGA database.

540 **Figure 6 | Midkine promotes cancer cell proliferation, invasion and**
541 **tumorigenesis**

542 **A and B.** Western blotting of MDK and β -actin in HCCLM3 cells transduced with
543 two independent MDK shRNAs (A) and representative images and growth curves of
544 the HCCLM3 cells with MDK knocked down (B).

545 **C and D.** Western blot analysis of MDK, Myc, HA and β -actin in the
546 MDK-transduced MHCC97H cells (C) and representative images and cell growth

547 curves of MHCC97H cells overexpressing MDK (D).

548 **E and F.** Western blot analysis of MDK and β -actin in the HCCLM3 cells transduced
549 with MDK shRNA1 and restored MDK in the MDK-knockdown cells (E) and
550 representative images and cell growth curves of the HCCLM3 cells transduced with
551 MDK shRNA1 and restored MDK in the MDK-knockdown cells (F).

552 **G.** Western blotting of MDK and HSP90 in the BT549 cells transduced with two
553 independent MDK shRNAs and representative images and invaded cell numbers of
554 BT549 cells with MDK knocked down. $n=3$ wells per group. Scale bar, 200 μm .

555 **H.** Western blotting of MDK and β -actin in the MDK-overexpressing Bel-7402 cells
556 and representative images and clone numbers of the Bel-7402 cells with restored
557 MDK expression. $n=3$ wells per group, Bar=200 μm .

558 **I-K.** Tumor images (I), growth curve (J) and weight (K) after subcutaneously
559 injecting mice with HCCLM3 cells transduced with MDK shRNA or reconstituted
560 MDK in MDK-knockdown cells.

561

562 **Figure 7 | Midkine promotes cancer progression by negatively regulating AMPK**
563 **signaling**

564 **A and B.** Colony forming assay of the HCCLM3 cells transduced with LKB1 shRNA
565 or in combination with MDK shRNA. Images (A) and quantification (B) of colony
566 formation. $n=3$ wells per group. Scale bar, 200 μm .

567 **C.** GSEA results showing the negative correlations between MDK and the AMPK
568 signaling pathway based on the TCGA LIHC and KIRC cohorts. Genes in the

569 RNA-seq data were ranked by the Pearson coefficients of the correlations between the
570 genes and *MDK*, and the ranked gene list was utilized as the input for the GSEA
571 software program.

572 **D and E.** Scatter plots showing the inverse correlation of MDK with p-AMPK α
573 expression and MDK expression in human hepatocellular carcinoma tumors (D),
574 Kaplan-Meier survival curves of HCC patients with data stratified by MDK
575 expression levels (E) ($n=74$).

576 **F.** Scatter plots showing the inverse correlation of *MDK* with *PRKAA1* (encoding
577 AMPK α 1) and *STK11* (encoding LKB1) expression and MDK expression in the
578 GSE76427 data set ($n=115$).

579 **G and H.** Scatter plots showing the inverse correlation of MDK with *PRKAA1* and
580 AMPK in the TCGA LIHC and KIRC cohorts (LIHC $n=371$, KIRC $n=531$). Gene
581 expression was obtained from RNA-seq data from the TCGA. AMPK activity was
582 estimated by the expression of their downstream target genes. Statistical significance
583 in (d-h) was determined by Pearson correlation test. R: Pearson correlation coefficient.
584 R, Spearman rank correlation coefficient.

585 **I and J.** Kaplan-Meier survival curves of the TCGA KIRC patients with data
586 stratified by the expression levels of both *MDK* and *PRKAA1* (I) or the expression of
587 *MDK* and the activity of AMPK (J). HL: MDK is high, *PRKAA1* or AMPK is low;
588 LH: MDK is low, *PRKAA1* or AMPK is high. Median expression/activity levels were
589 utilized as the thresholds for high and low separation.

590 **K.** Schematic cartoon of the MDK mechanisms of action: high MDK expression

591 depolymerizes the LKB1-STRAD-Mo25 complex and subsequently suppresses the

592 activity of AMPK signaling in human cancers.

593

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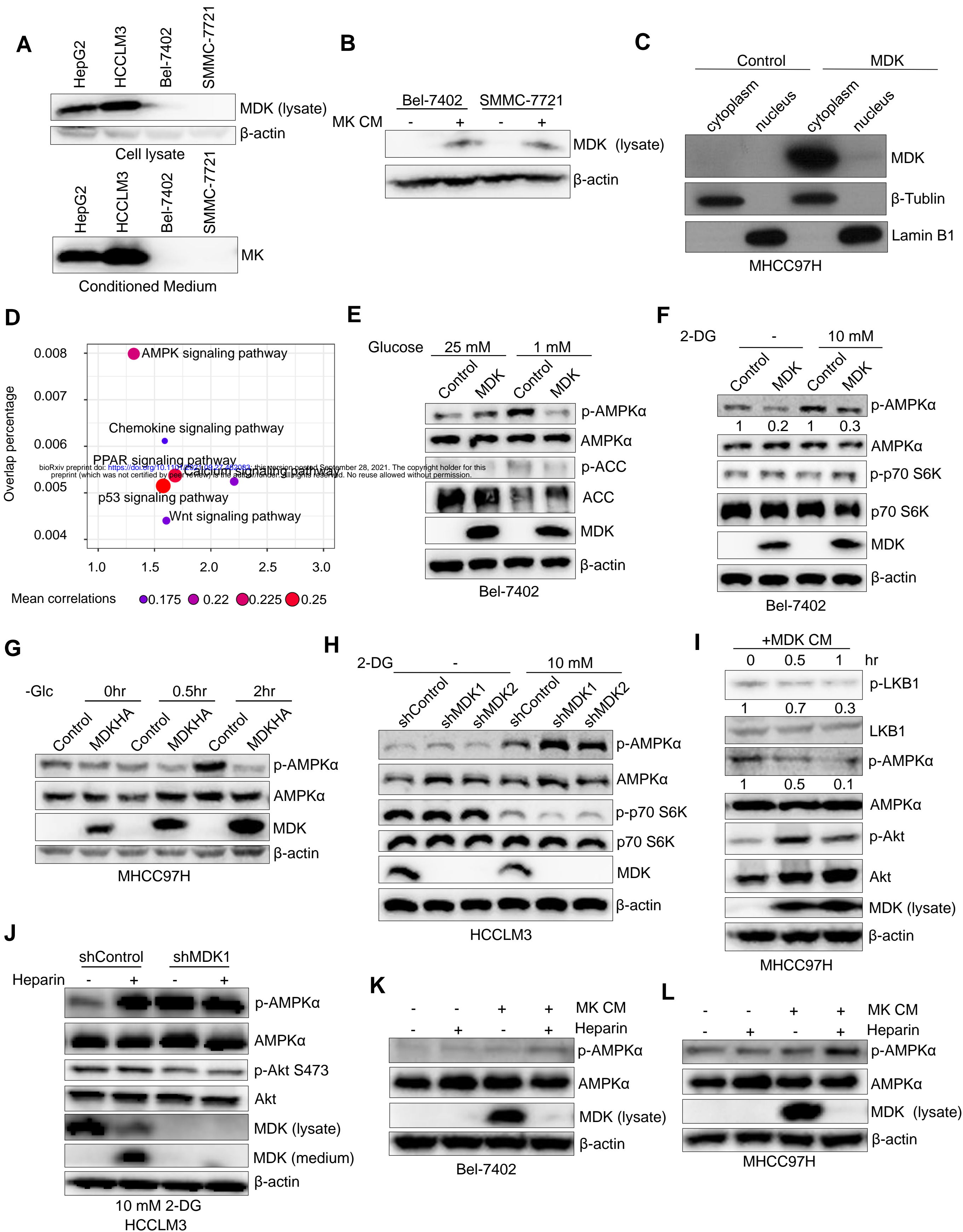
Fig 1

Fig 2

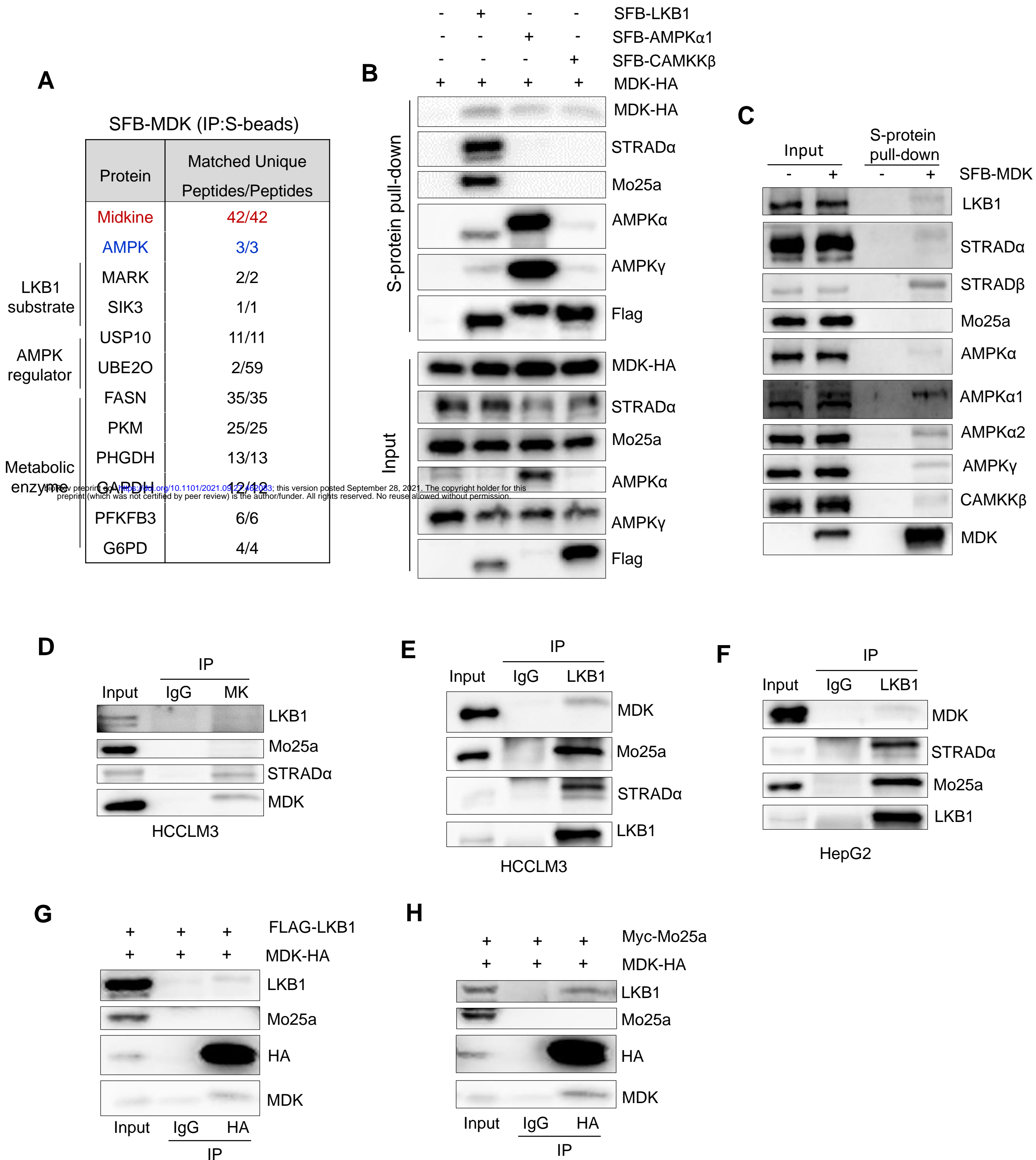


Fig 3

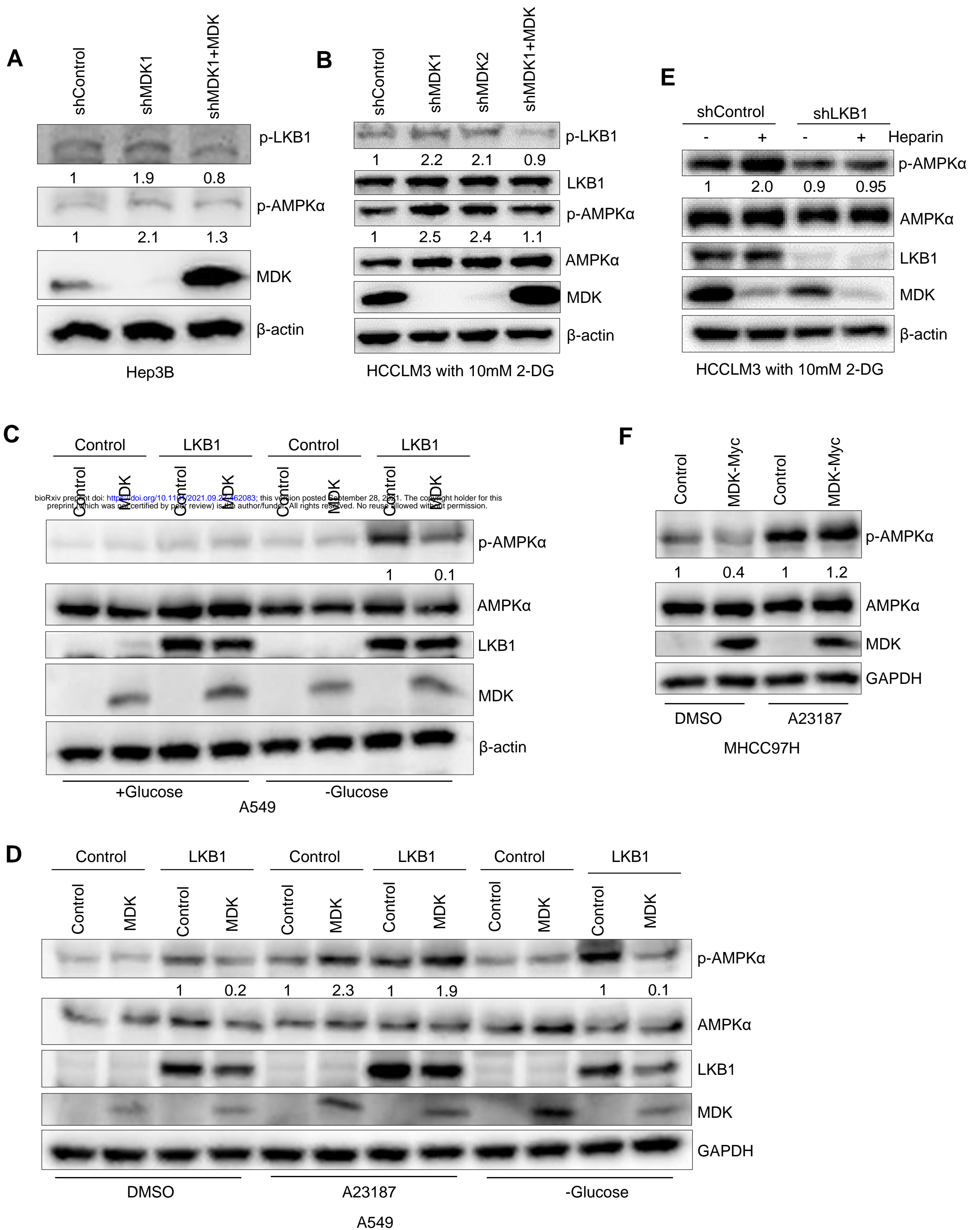


Fig 4

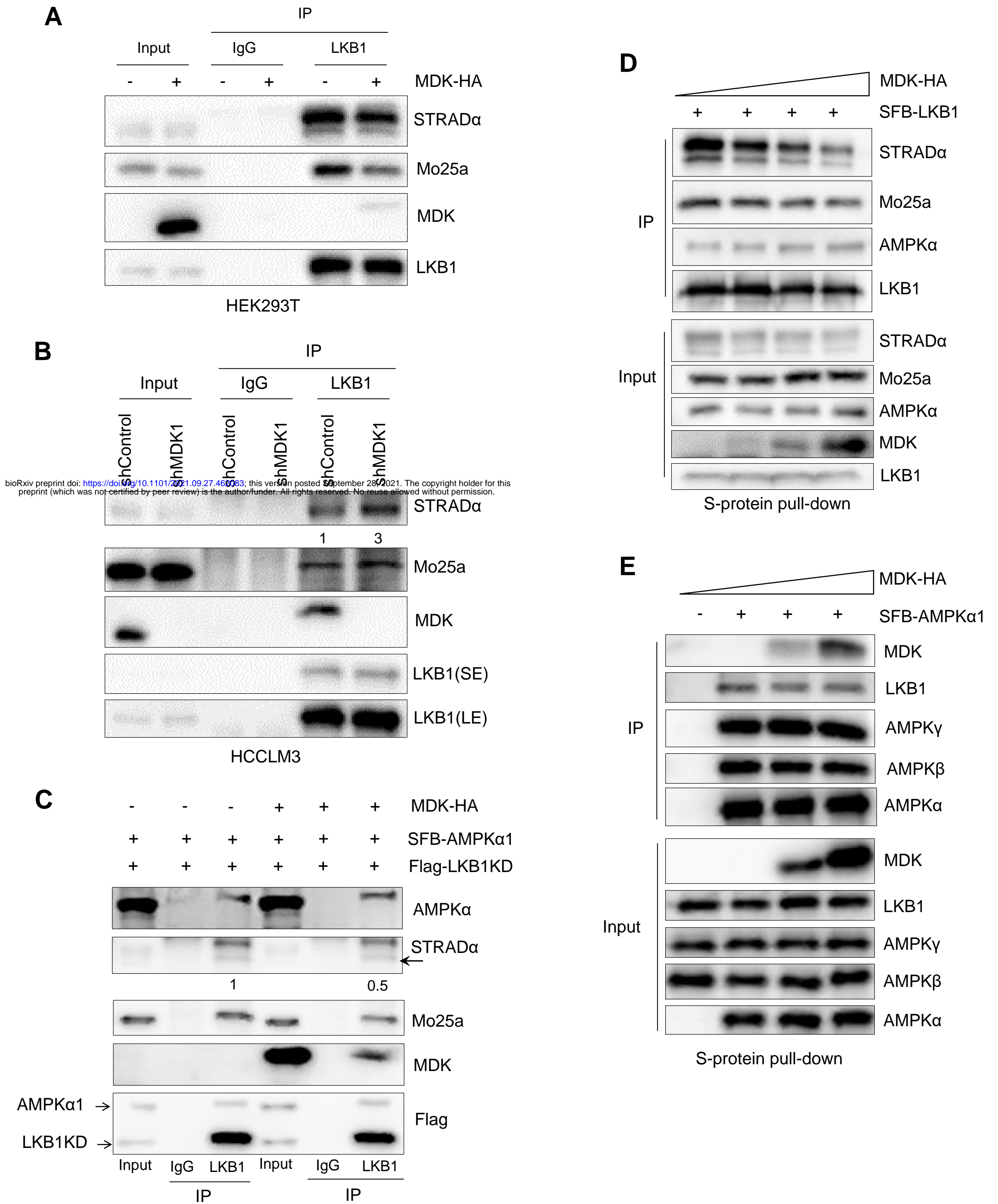


Fig 5

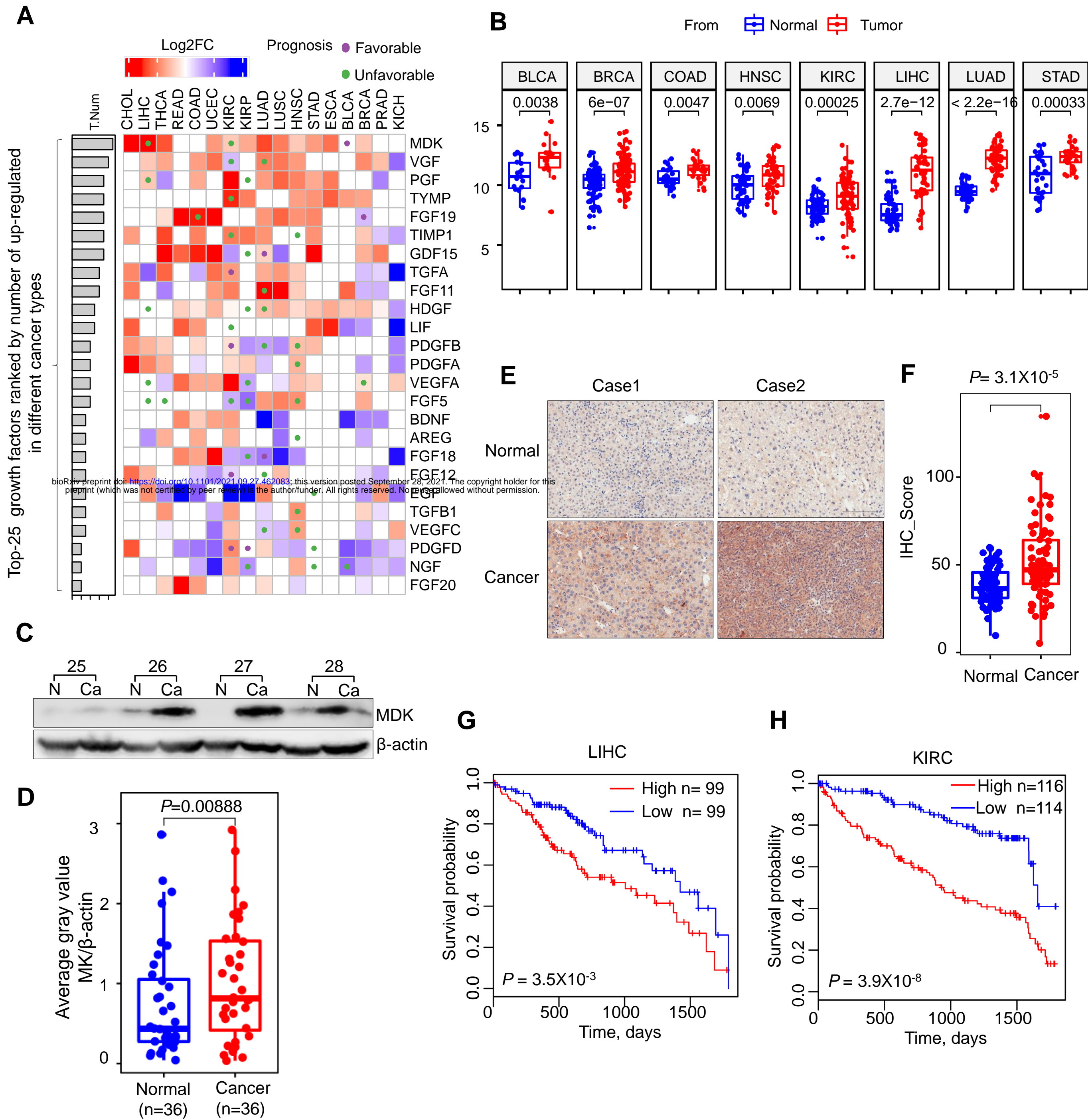


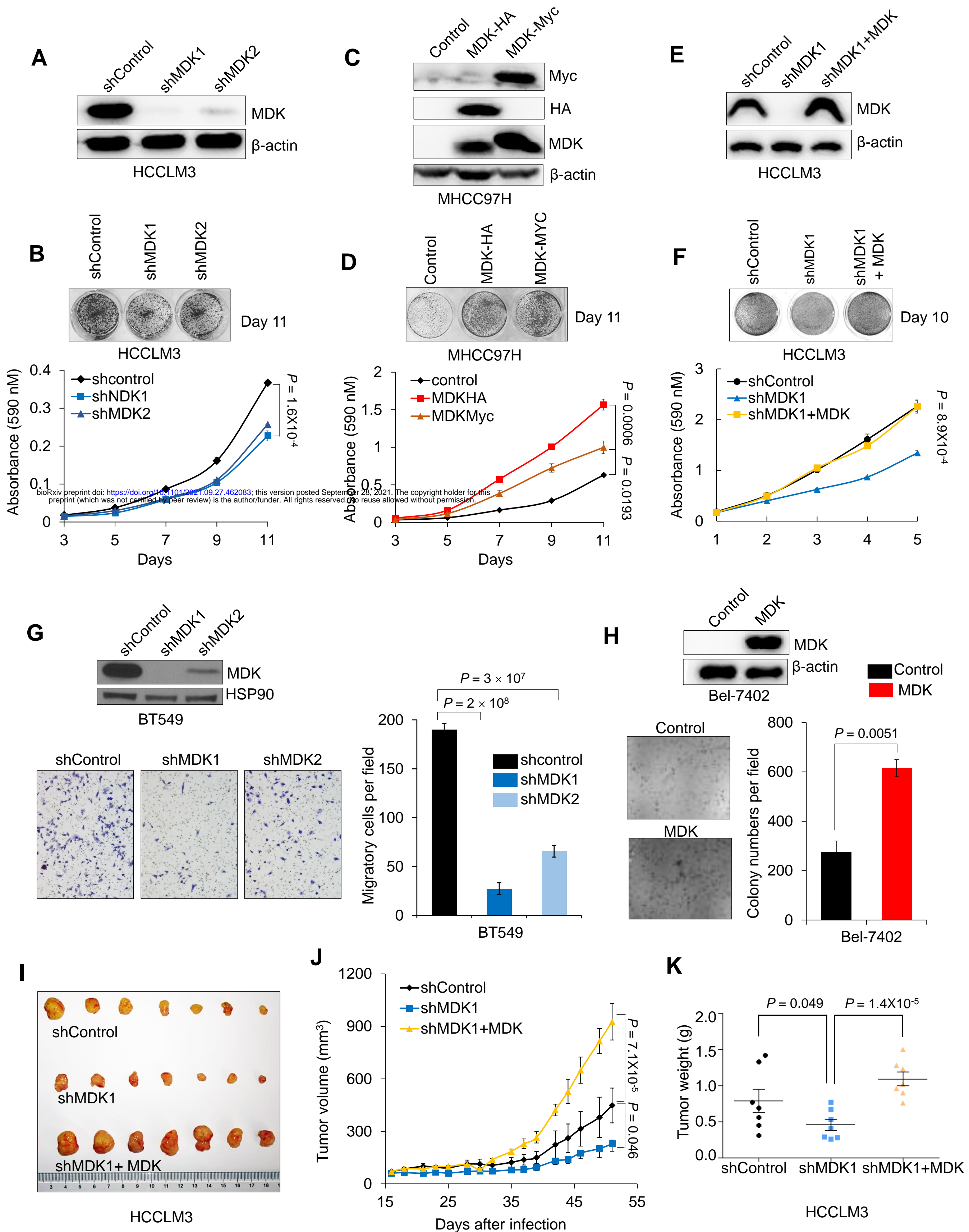
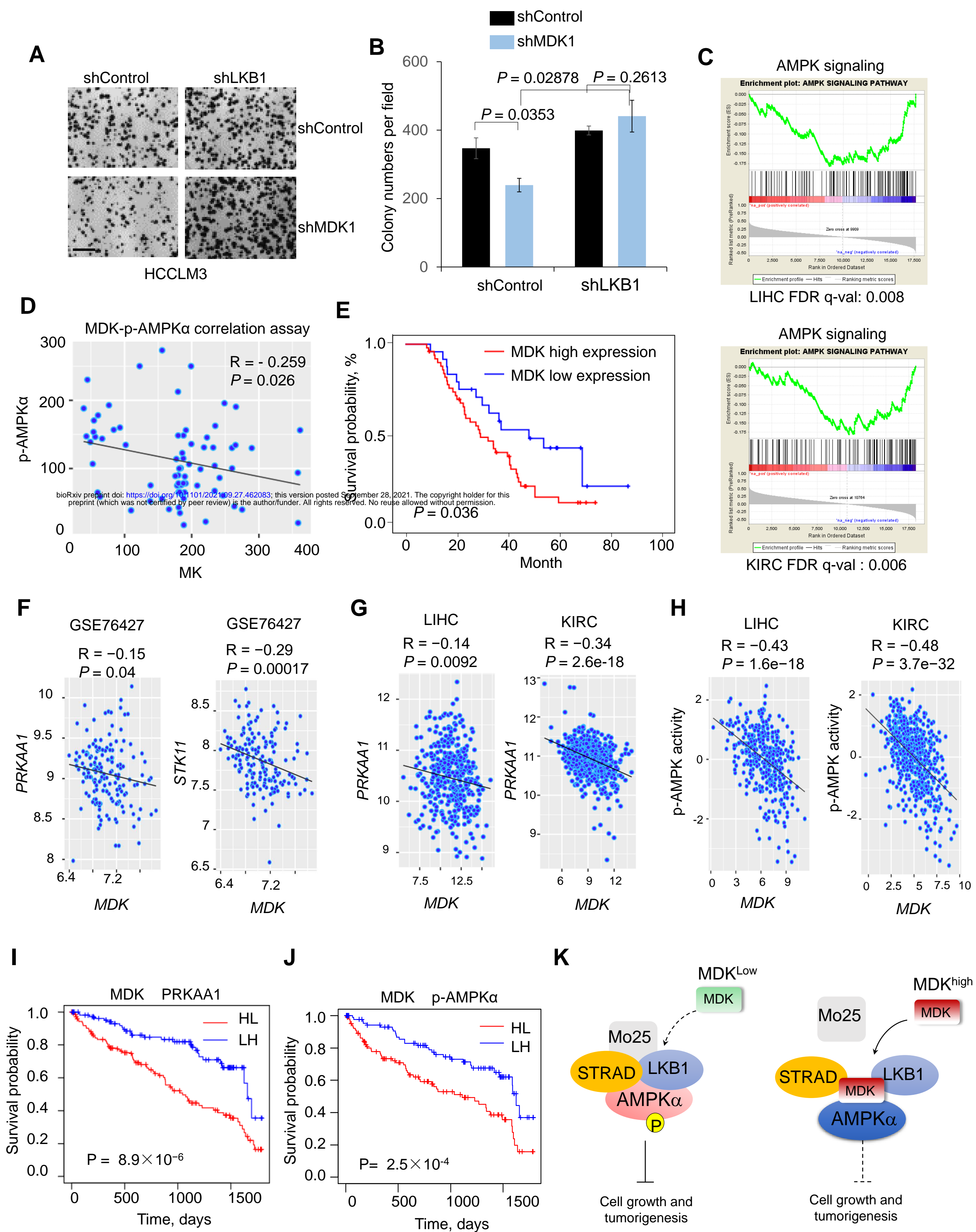
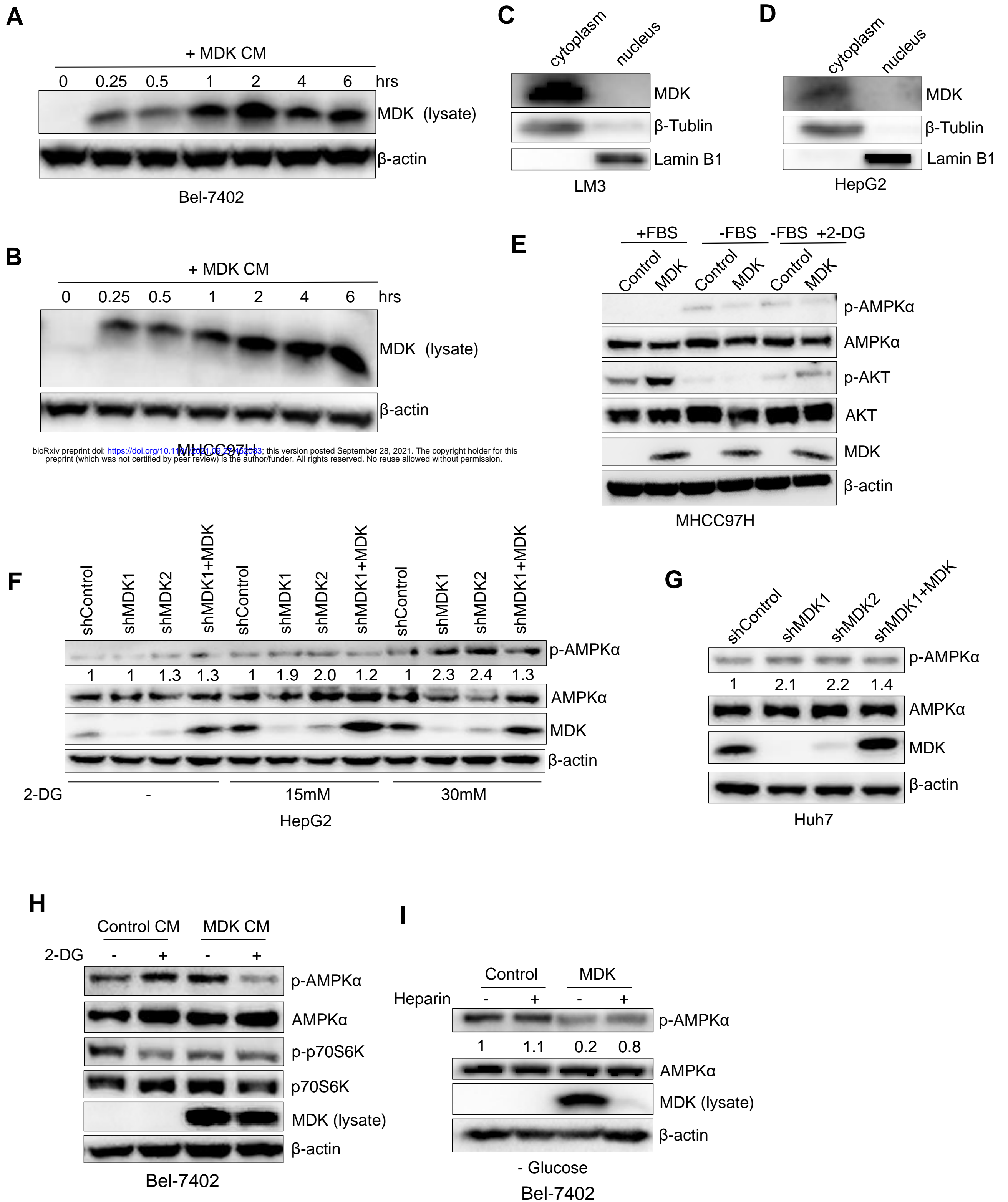
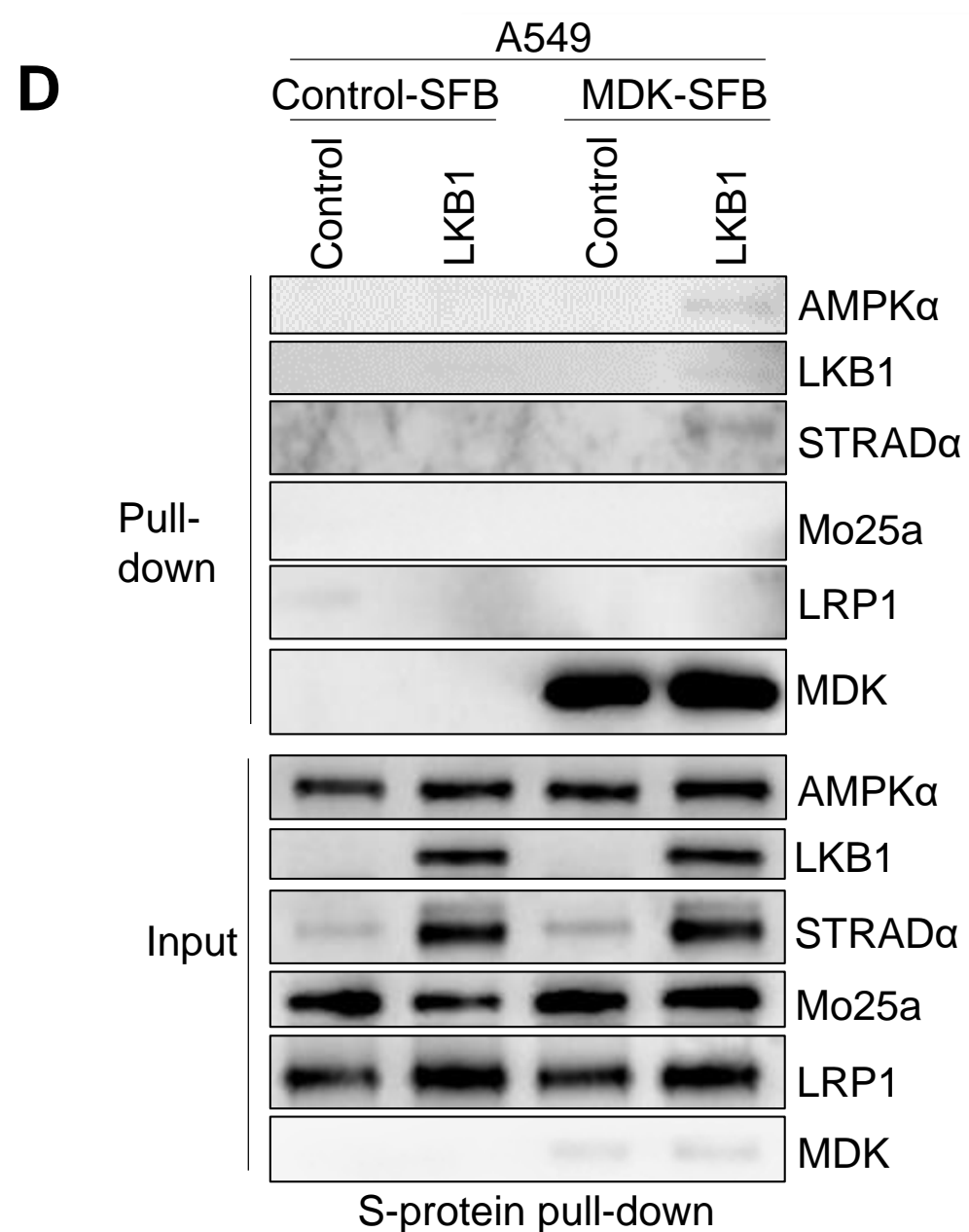
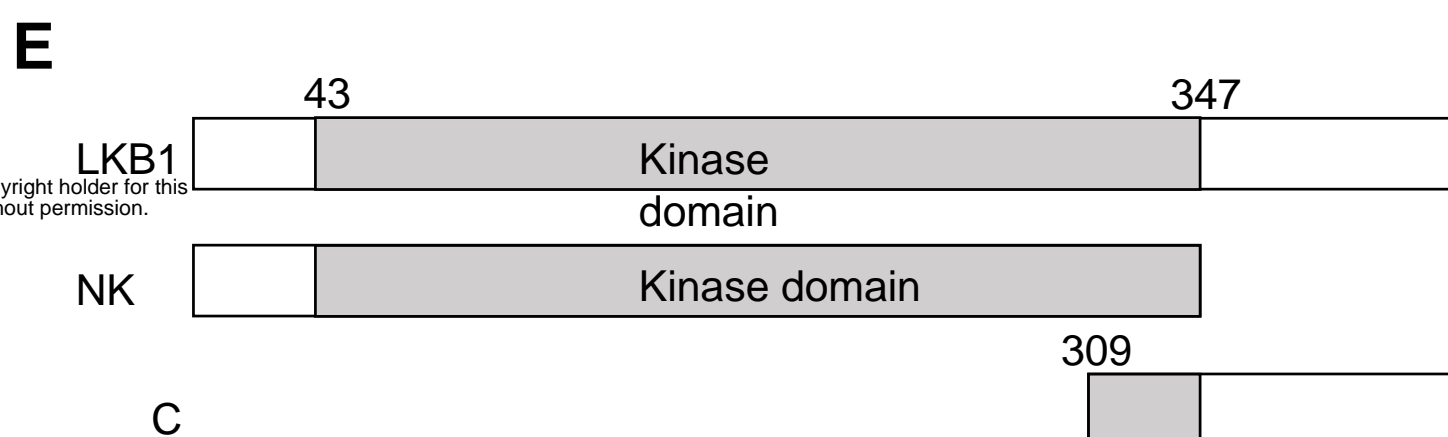
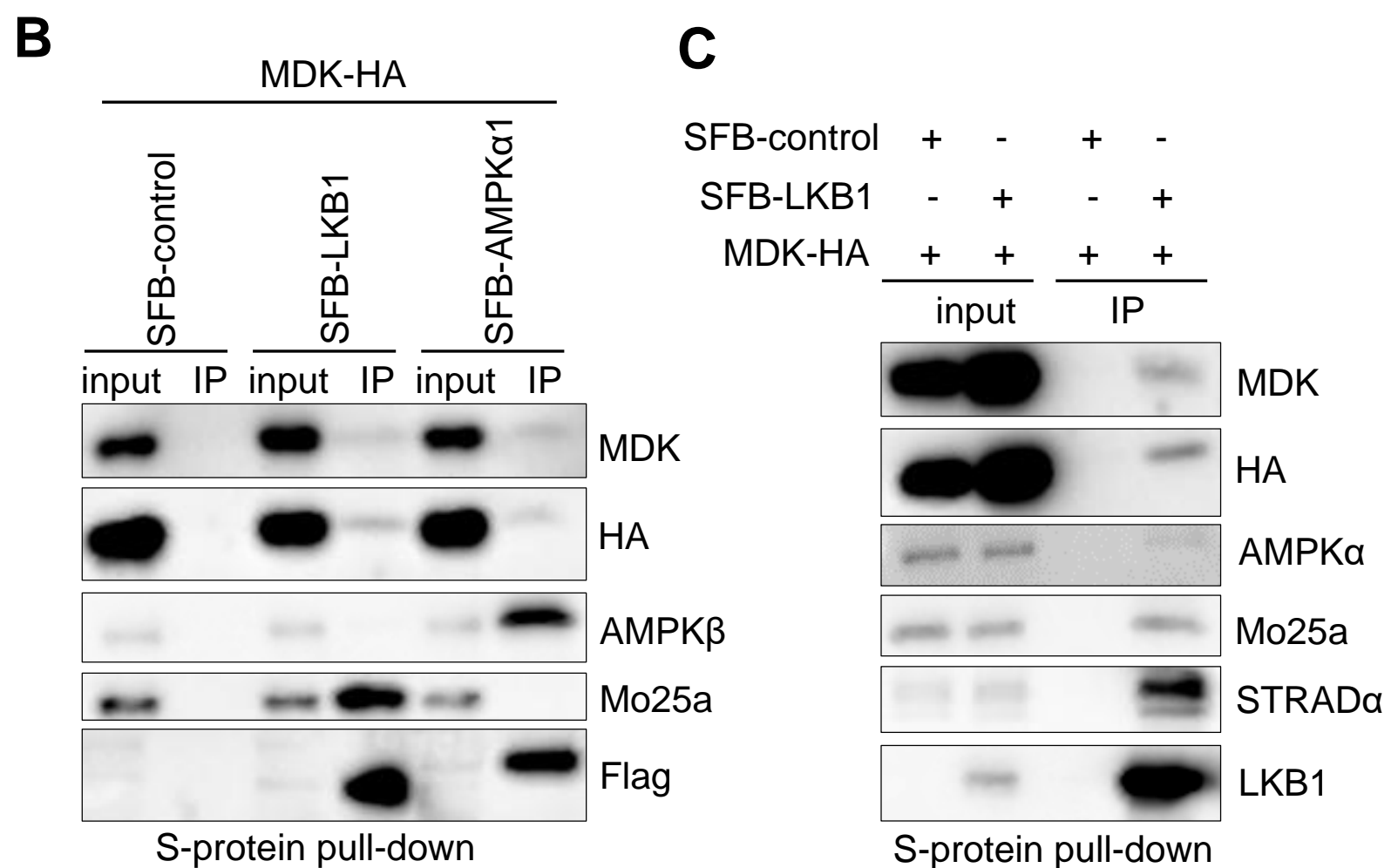
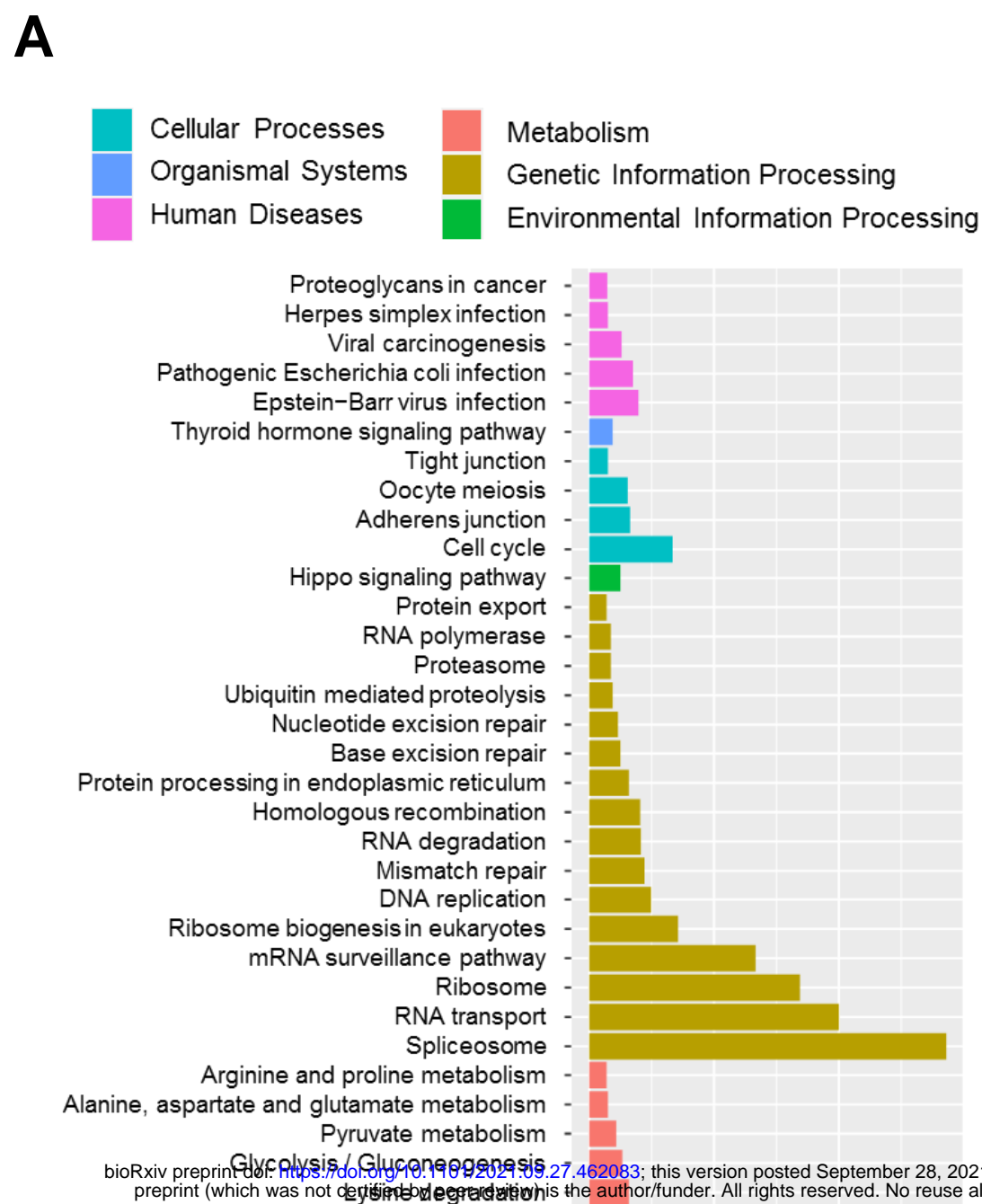
Fig 6

Fig 7

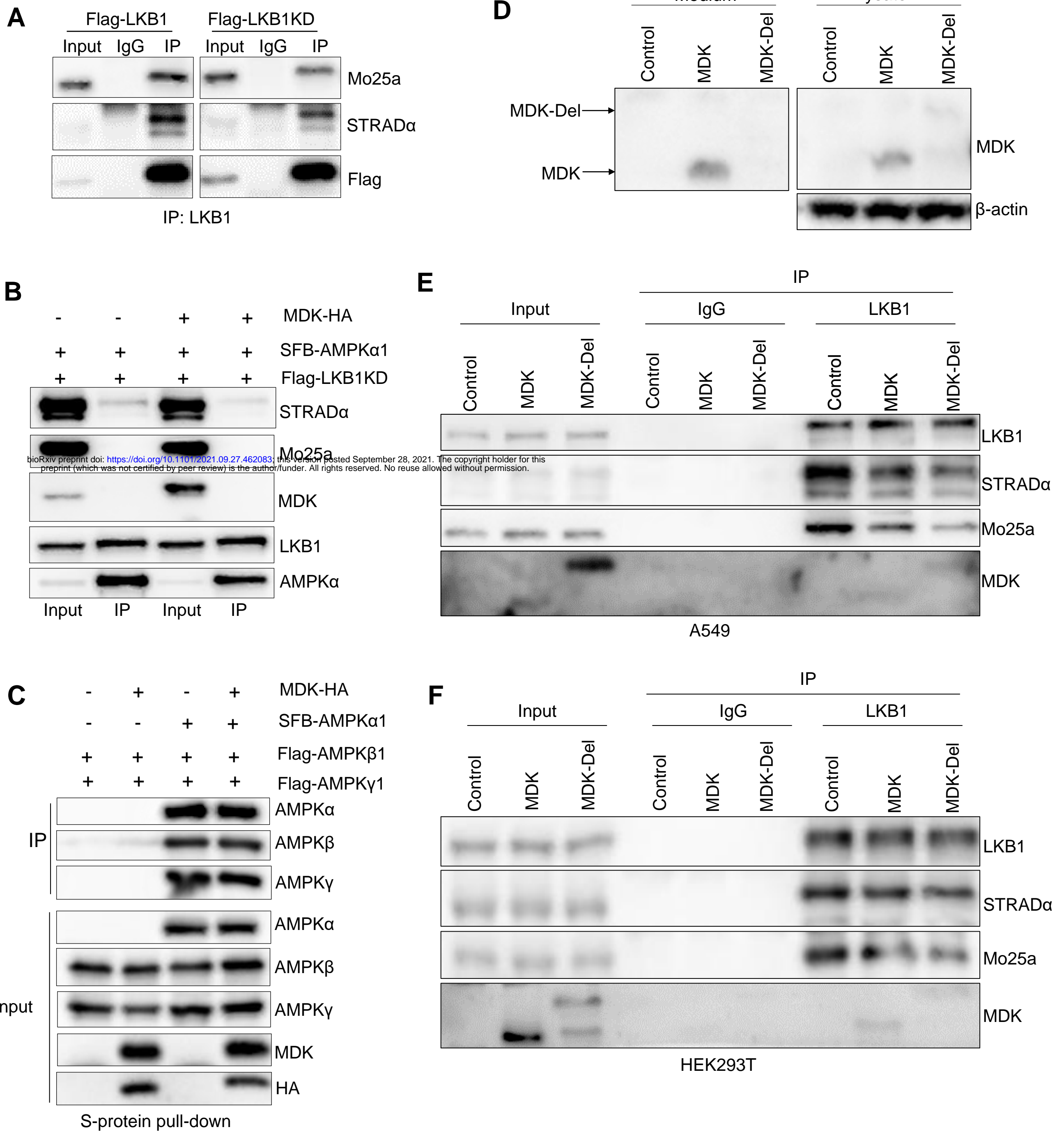
Expanded View Fig 1



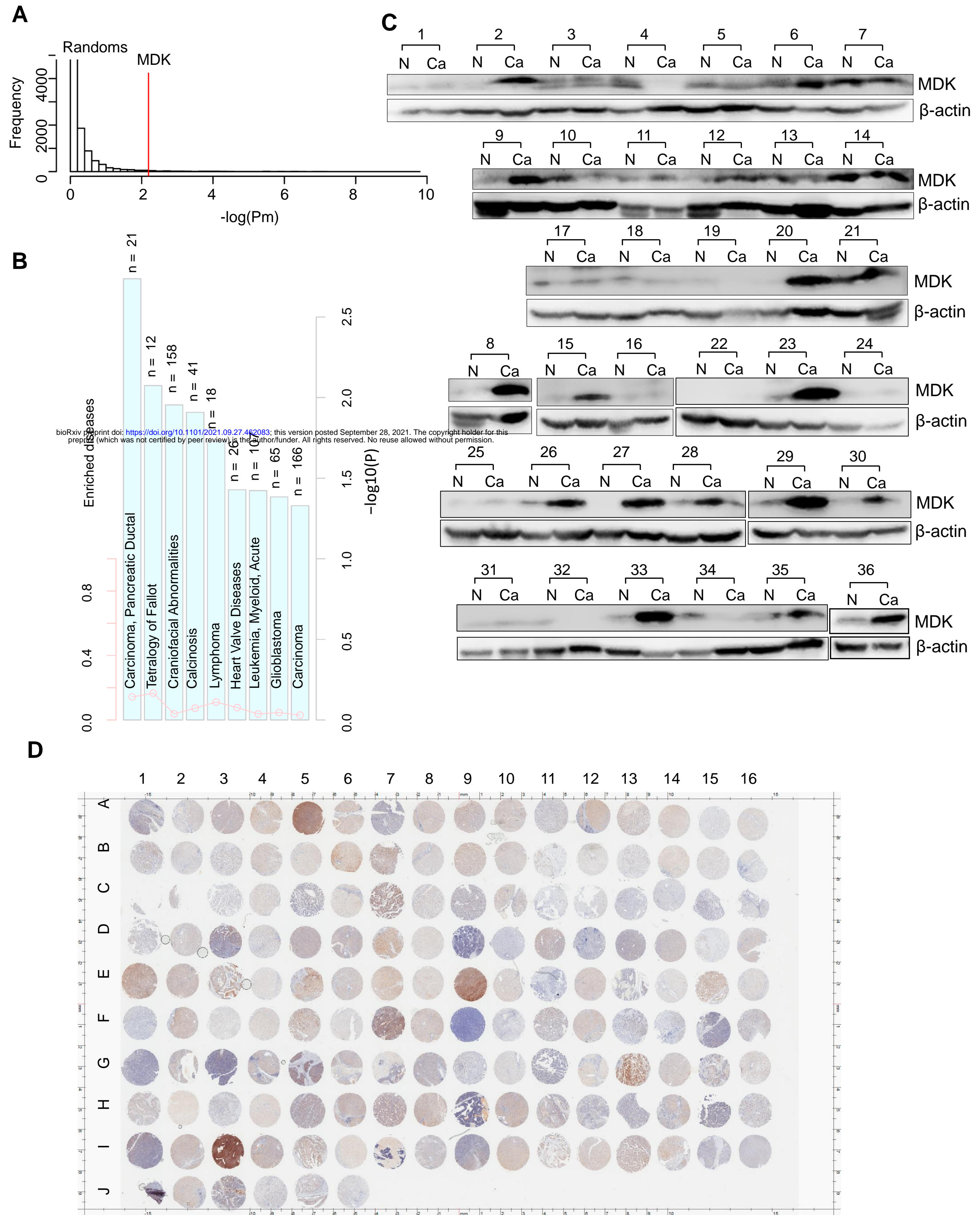
Expanded View Fig 2



Expanded View Fig 3

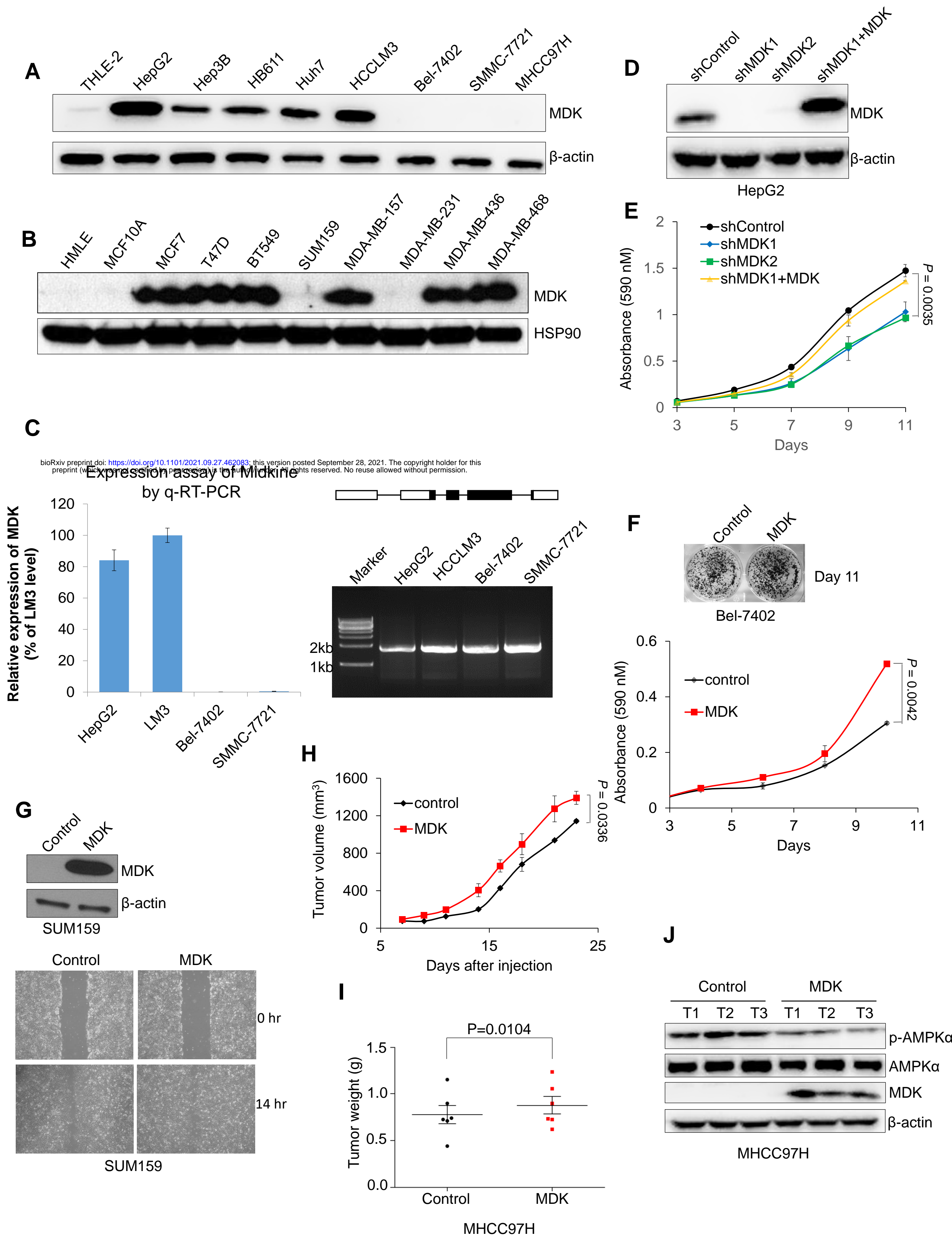


Expanded View Fig 4



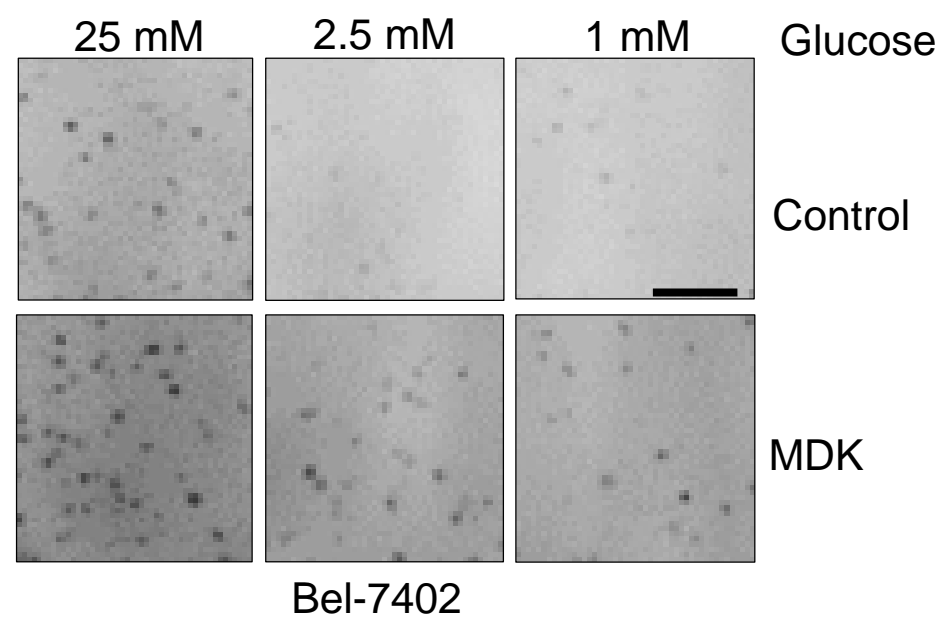
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Expanded View Fig 5

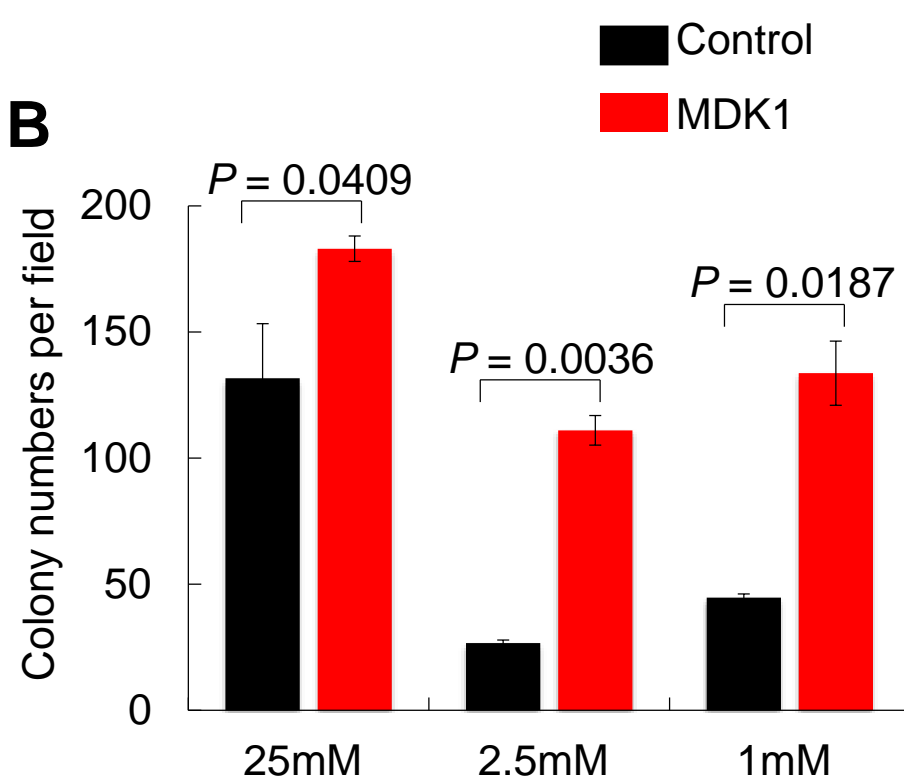


Supplementary Fig 6

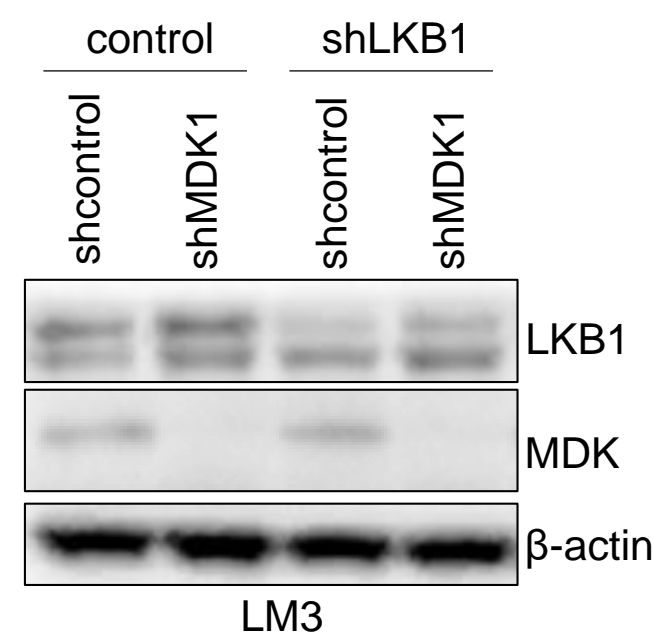
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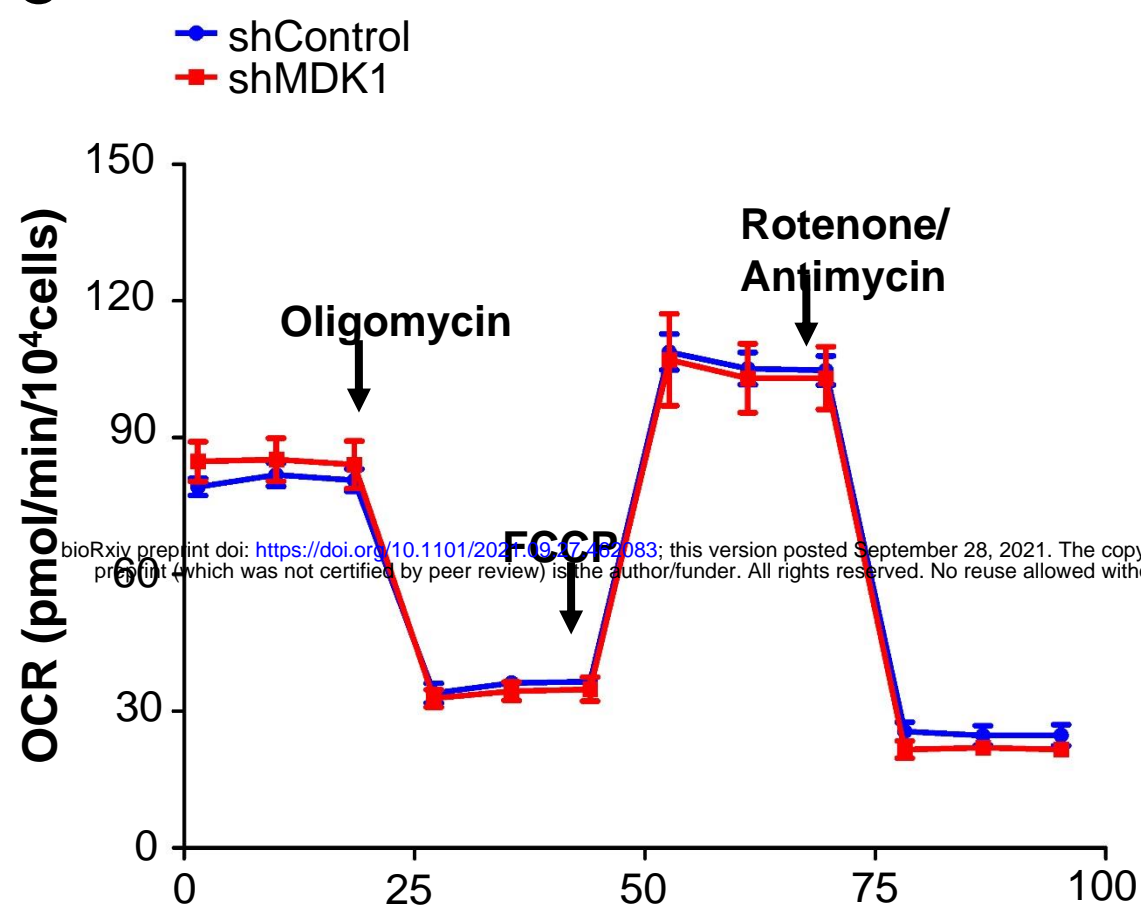
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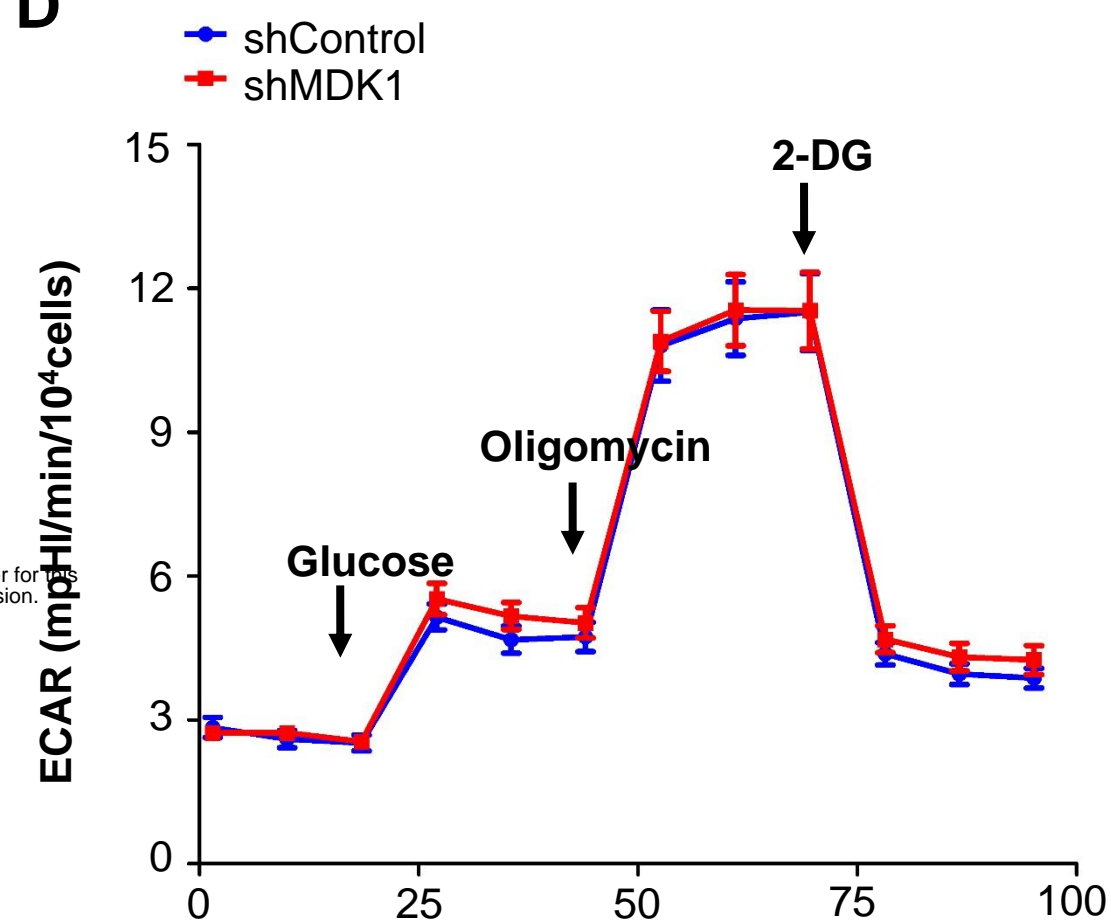
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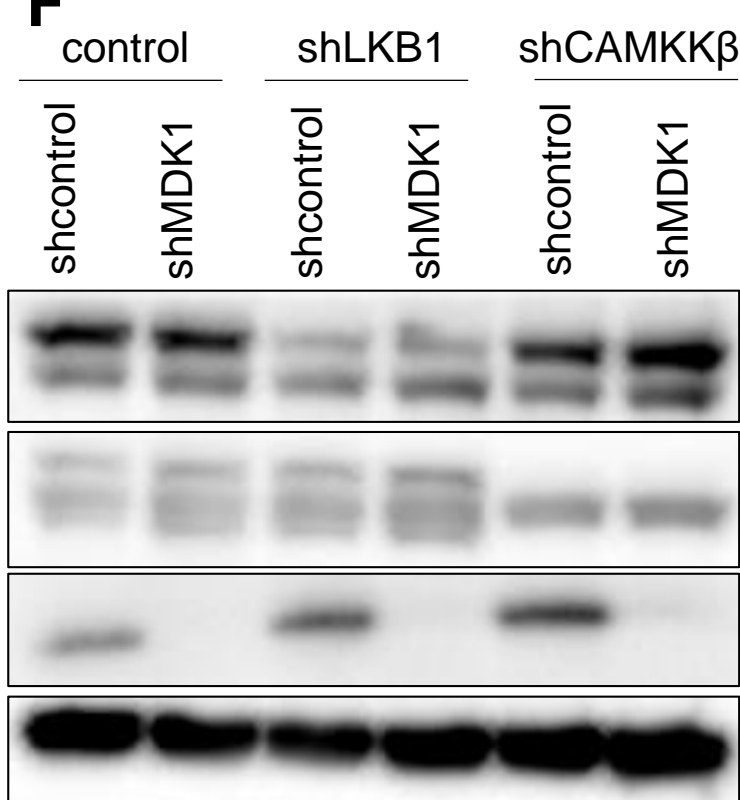
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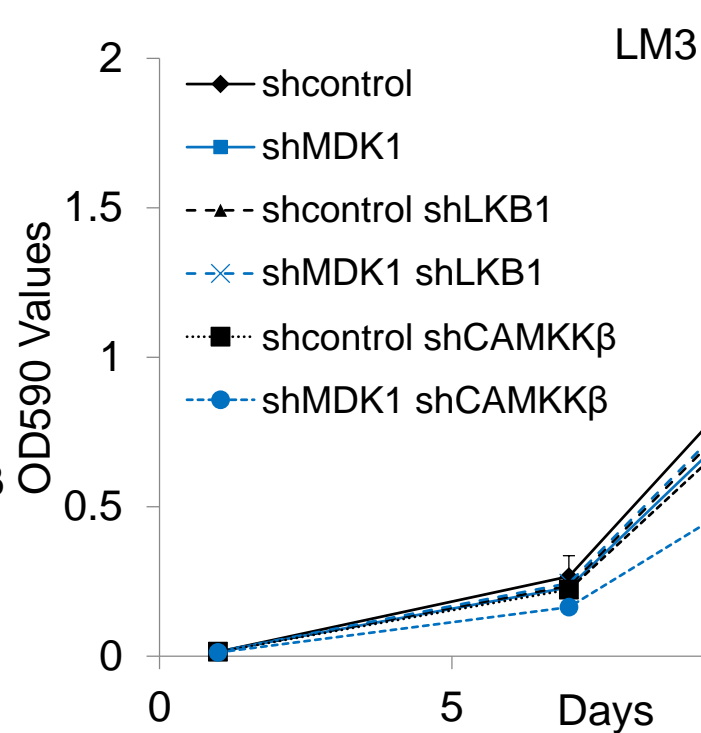
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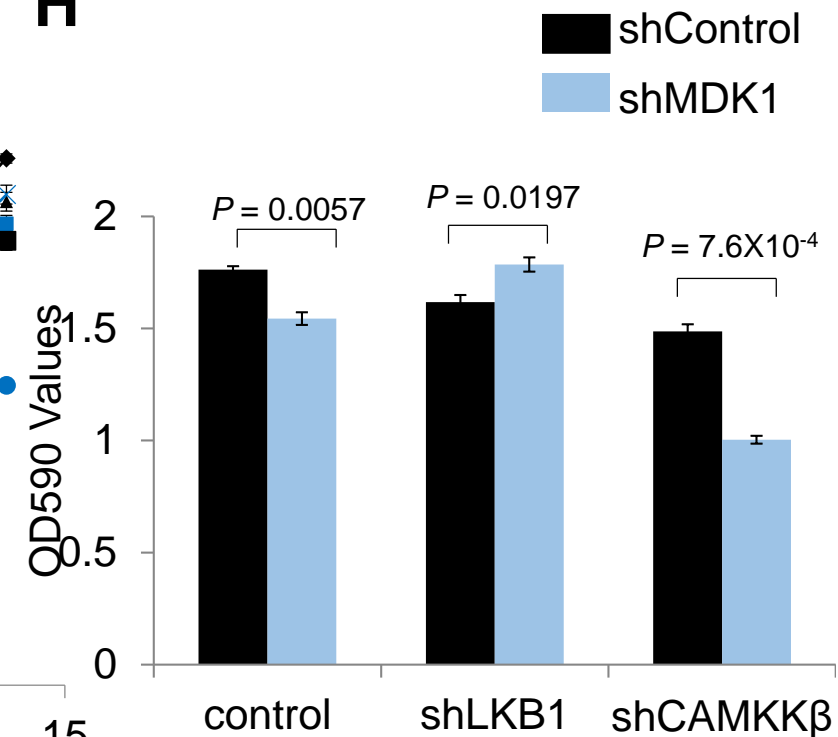
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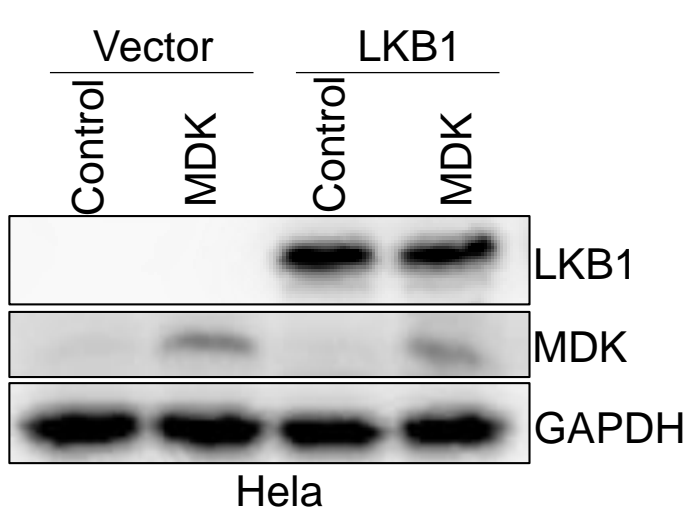
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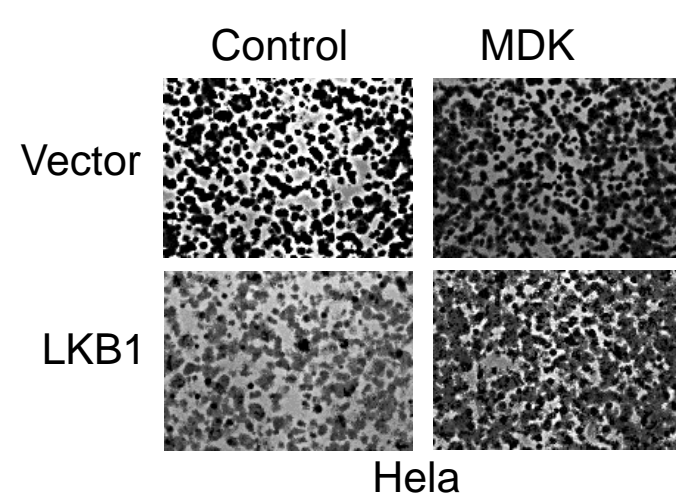
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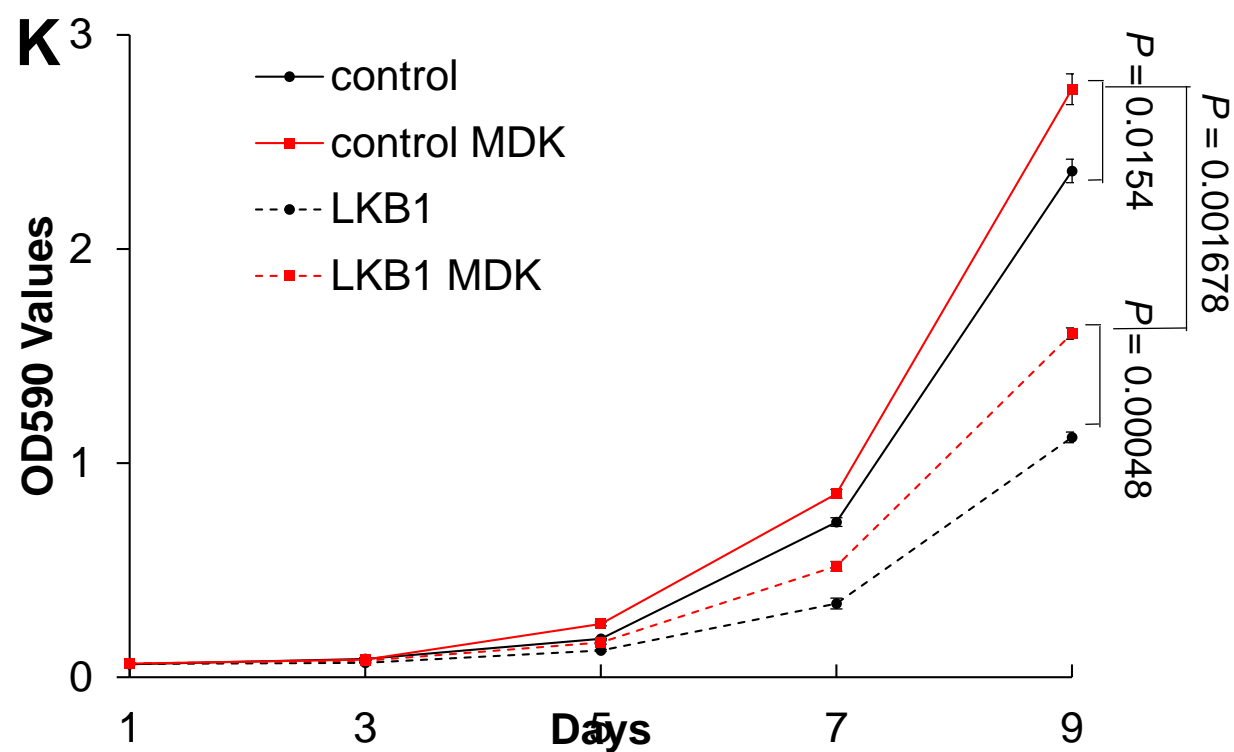
I



J



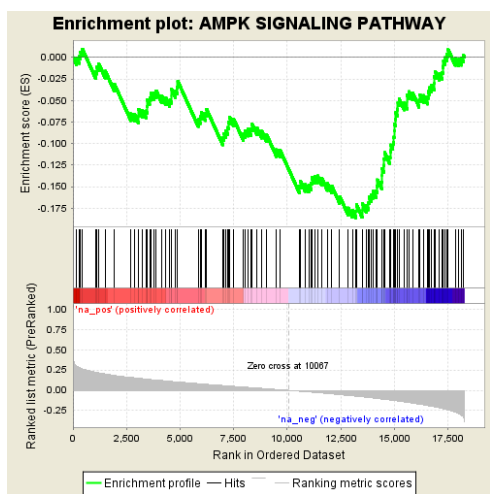
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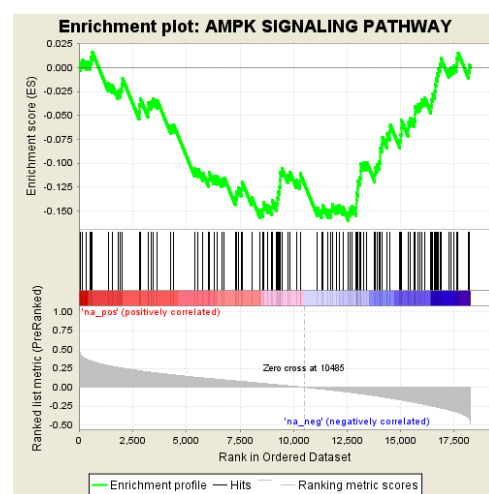
Supplementary Fig 7

A

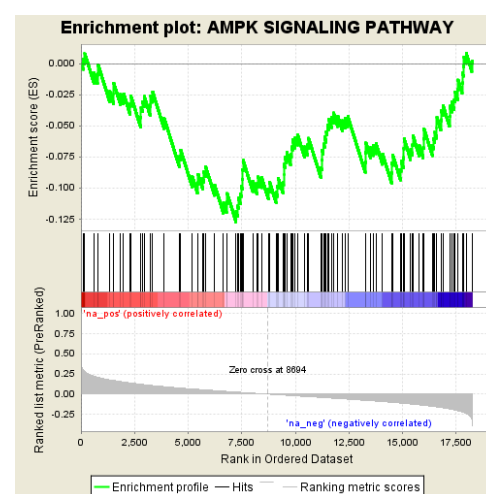
BRCA FDR q-val: 0.005



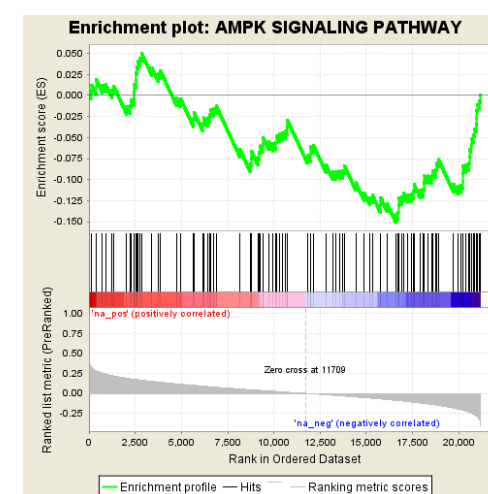
PRAD FDR q-val: 0.02



LUAD FDR q-val: 0.062

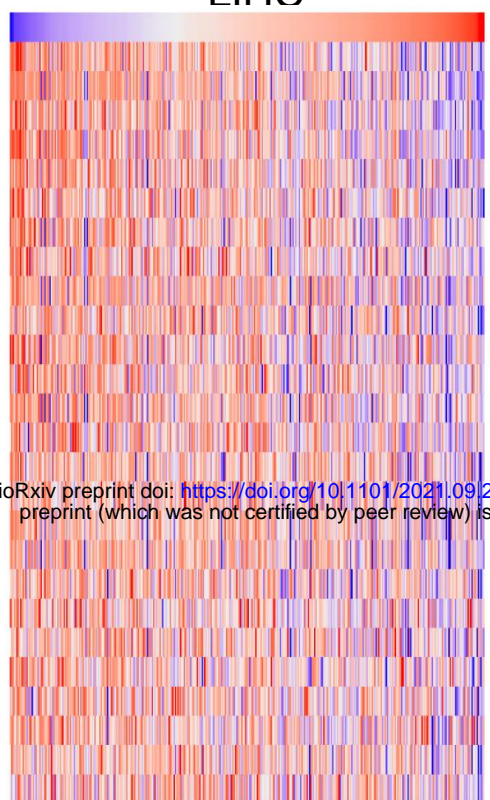


GSE76327 FDR q-val: 0.05



B

LIHC



KIRC

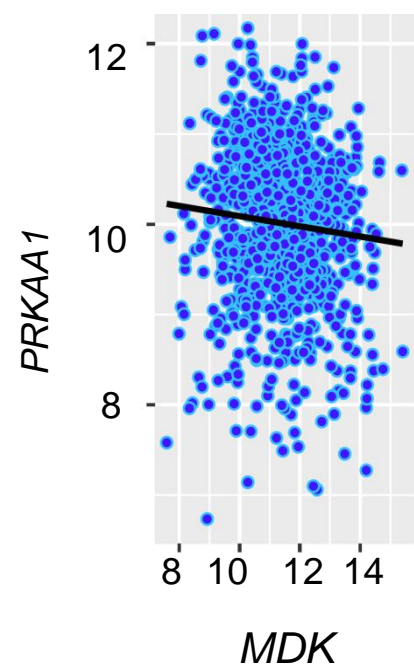


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C

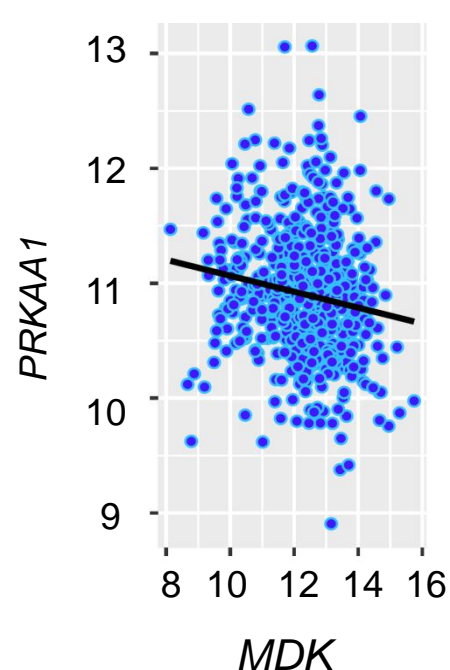
BRCA

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 $P = 0.0043$



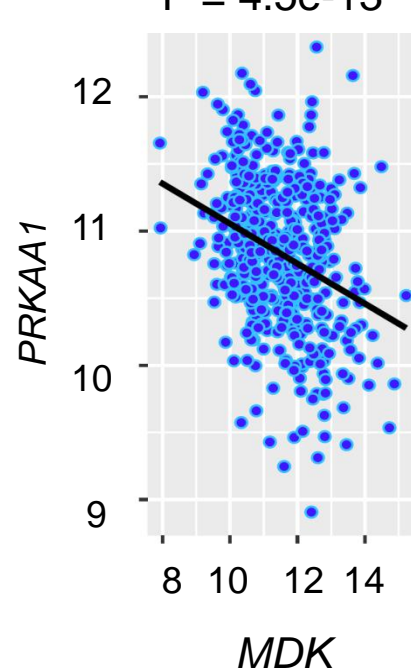
LUAD

$R = -0.15$
 $P = 0.00042$



PRAD

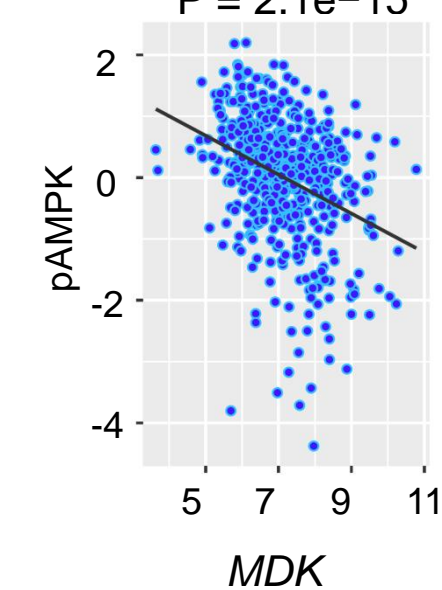
$R = -0.32$
 $P = 4.5e-13$



D

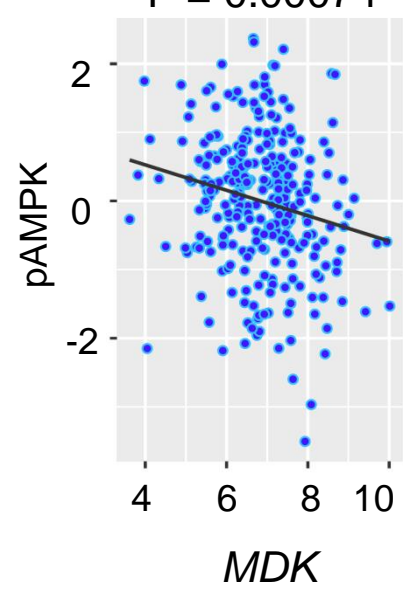
PRAD

$R = -0.35$
 $P = 2.1e-15$



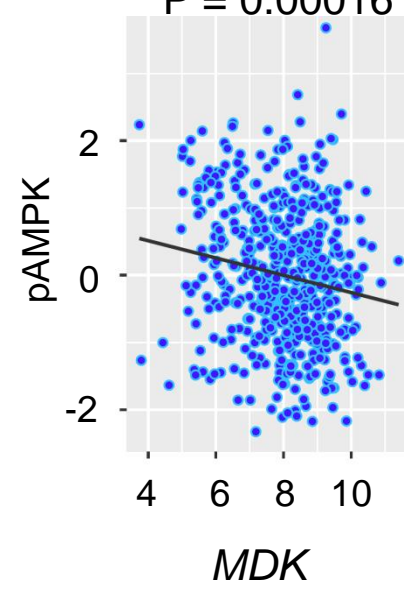
COAD

$R = -0.2$
 $P = 0.00074$



LUAD

$R = -0.17$
 $P = 0.00016$



KIRP

$R = -0.29$
 $P = 4.9e-7$

