The mechanical regulation of RNA binding protein hnRNPC in the failing heart

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ABSTRACT

Cardiac pathologies are characterized by intense remodeling of the extracellular matrix (ECM) that eventually leads to heart failure. Cardiomyocytes respond to the ensuing biomechanical stress by re-expressing fetal contractile proteins via transcriptional and post-transcriptional processes, like alternative splicing (AS). Here, we demonstrate that the heterogeneous nuclear ribonucleoprotein C (hnRNPC) is upregulated and relocates to the sarcomeric Z-disk upon ECM pathological remodeling. We show that this is an active site of localized translation, where the ribonucleoprotein associates to the translation machinery. Alterations in hnRNPC expression and localization can be mechanically determined and affect the AS of numerous mRNAs involved in mechanotransduction and cardiovascular diseases, like Hippo pathway effector YAP1. We propose that cardiac ECM remodeling serves as a switch in RNA metabolism by impacting an associated regulatory protein of the spliceosome apparatus. These findings offer new insights on the mechanism of mRNAs homeostasis mechanoregulation in pathological conditions.

KEYWORDS

Heart failure; alternative splicing; mechanotransduction; RNA-binding proteins; hnRNPC.

48 **INTRODUCTION**

49 The onset and progression of aging-associated pathologies is paralleled by continuous local
50 extracellular matrix (ECM) remodeling. This remodeling serves as a compensatory strategy for
51 tissues to cope with altered conditions [1]. ECM remodeling is perceived and transmitted within a
52 cell through the modulation of cytoskeleton-propagated intracellular tension [2] that eventually
53 affects tissue-specific cell responses and function [3,4]. Cardiac pathologies are a prime example of
54 how ECM remodeling can impact on cell functionality, here affecting muscle contractility and
55 organ pumping [5]. Independently of the etiology, cardiac remodeling confers a major shift in
56 cardiomyocyte contractile function by inducing changes in signaling axes [6], metabolic pathways [7],
57 and the overall epigenetic landscape [8]. Such changes eventually trigger modifications in the
58 cardiomyocyte genetic program to increase cell contractility and favor cell survival [9]. Reactivation
59 of the fetal cardiac genetic program is a hallmark of the pathological heart, as observed in
60 pressure overload-induced hypertrophy [10].

61 Besides transforming the transcriptional landscape, post-transcriptional events, such as alternative
62 splicing (AS), RNA editing and transport, translation and degradation are also affected in cardiac
63 disease [11]. In particular, changes in AS in the pathological heart lead to alterations in the
64 expression level of numerous sarcomeric and ion channel genes associated with cardiac
65 pathologies, being determinants of cardiomyopathies and, eventually, of heart failure (HF) [12]. The
66 mechanisms presiding over RNA homeostasis permit prompt cellular adaptation to changes in the
67 external environment. This process is mainly controlled via RNA binding proteins (RBPs) that
68 physically associate with and guide RNAs through all steps of post-transcriptional control. Given
69 the importance of RBPs in RNA metabolism, their expression must be tightly controlled.

70 Among the RBPs, heterogeneous nuclear ribonucleoproteins (hnRNPs) represent a large family of
71 proteins that comprise nuclear ribonucleoprotein complexes consisting of RNA and proteins, and
72 help control mRNA dynamics [13]. Under stress conditions, hnRNPs may relocalize to a different
73 cellular compartment, undergo post-transcriptional modification, and/or exhibit altered protein
74 expression; all of these events can affect the metabolism of essential transcripts needed for cell
75 adaptation [14,15]. Indeed, the mislocalization and deregulation of hnRNPs has been associated with
76 the onset of several pathologies, including cancer, Alzheimer's disease and fronto-temporal lobe
77 dementia [16].

78 Emerging data suggest that RNA homeostasis can be controlled by mechanical cues [17–19], but the
79 molecular basis of such processes is largely unknown. One hypothesis is that mechanical stress
80 arising from the surrounding environment could affect RNA dynamics by either altering RBP
81 function or localization [20,21]. However, this process requires that components of the RNA
82 processing apparatus respond to mechanical cues generated during ECM remodeling.
83 In this study, we show ischemic and chronic cardiac pathologies are accompanied by the altered
84 expression of the RBP heterogeneous nuclear ribonucleoprotein C (hnRNPC). The protein adopts a
85 peculiar sarcomeric distribution and associates to the translation machinery upon pathological
86 ECM remodeling. Moreover, we provide evidence that hnRNPC intracellular localization can be
87 controlled by the increased biomechanical stress generated by cardiac ECM remodeling and show
88 the relocation of a fraction of the protein from the nucleus is sufficient to affect the AS of
89 transcripts coding for components of the mechanosensitive Hippo pathway. This pathway is
90 known to be heavily involved in the progression of cardiac diseases [22,23].
91 Therefore, we propose hnRNPC acts as a mechanosensitive switch affecting RNA metabolism in
92 the pathological heart.
93

RESULTS

The RNA-binding protein hnRNPC is upregulated in the diseased heart

The intense ECM remodeling occurring in cardiac pathologies can alter tissue integrity and impair organ function [5], but the underlying molecular mechanisms are unclear. We first asked whether this phenomenon was associated with a common genetic signature in both ischemic and non-ischemic heart diseases. To do so, we analyzed four published expression profiling array datasets obtained from ischemic (mouse myocardial infarction, MI) [24] and non-ischemic (mouse and human HF) [25–27] cardiac diseases and looked for common molecular function terms among the upregulated genes in the pathological heart (**Supplementary Data 1).**

We found that 11-17% of the significantly upregulated genes in MI and HF hearts (FC>1.5) shared the RNA binding (GO:0003723) annotation (**Fig. 1a; Supplementary Data 1**). When browsing the genes encoding RBPs, we found 82 RBPs that were upregulated in both mouse datasets and four that were upregulated in both human heart failure (HF) datasets. We identified hnRNPC as the only common upregulated gene among all four datasets (**Fig. 1b**). hnRNPC is a core ribonucleoprotein that is ubiquitously distributed and best known for its role as a splicing regulator [28–30]. Increased levels of this RBP have been associated with several pathological conditions [31–33]. Its upregulation in diseased cardiomyocytes has been recently confirmed by single cell RNA-sequencing in a model of ischemia-reperfusion [34].

Consistently, our *in silico* expression array analyses showed that hnRNPC was upregulated 1.52 fold 48 h after MI and 1.77 fold in HF in mice, and from 1.68 to 4.2 fold in HF patients (**Supplementary Fig. 1a**; **Supplementary Data 1**).

Given the consistent alteration in the expression level of hnRNPC in both ischemic and non-ischemic cardiac pathologies, we further analyzed its expression in heart tissue specimens obtained from a cohort of 17 patients diagnosed with end-stage HF and undergoing cardiac transplantation. As a healthy control, we used non-transplantable hearts from deceased (healthy) donors (**Supplementary Fig. 1b, c; Supplementary Table 1**). Both RT-qPCR and western blot analyses confirmed that hnRNPC gene (**Fig. 1c**) and protein (**Fig. 1d**) expression were reproducibly upregulated in failing human hearts. These results support that hnRNPC expression is upregulated in HF. This phenomenon seems to happen independently of the etiology of the disease, since no

significant difference is found in ischemic vs non-ischemic heart diseases (Supplementary Fig. 1d, e).

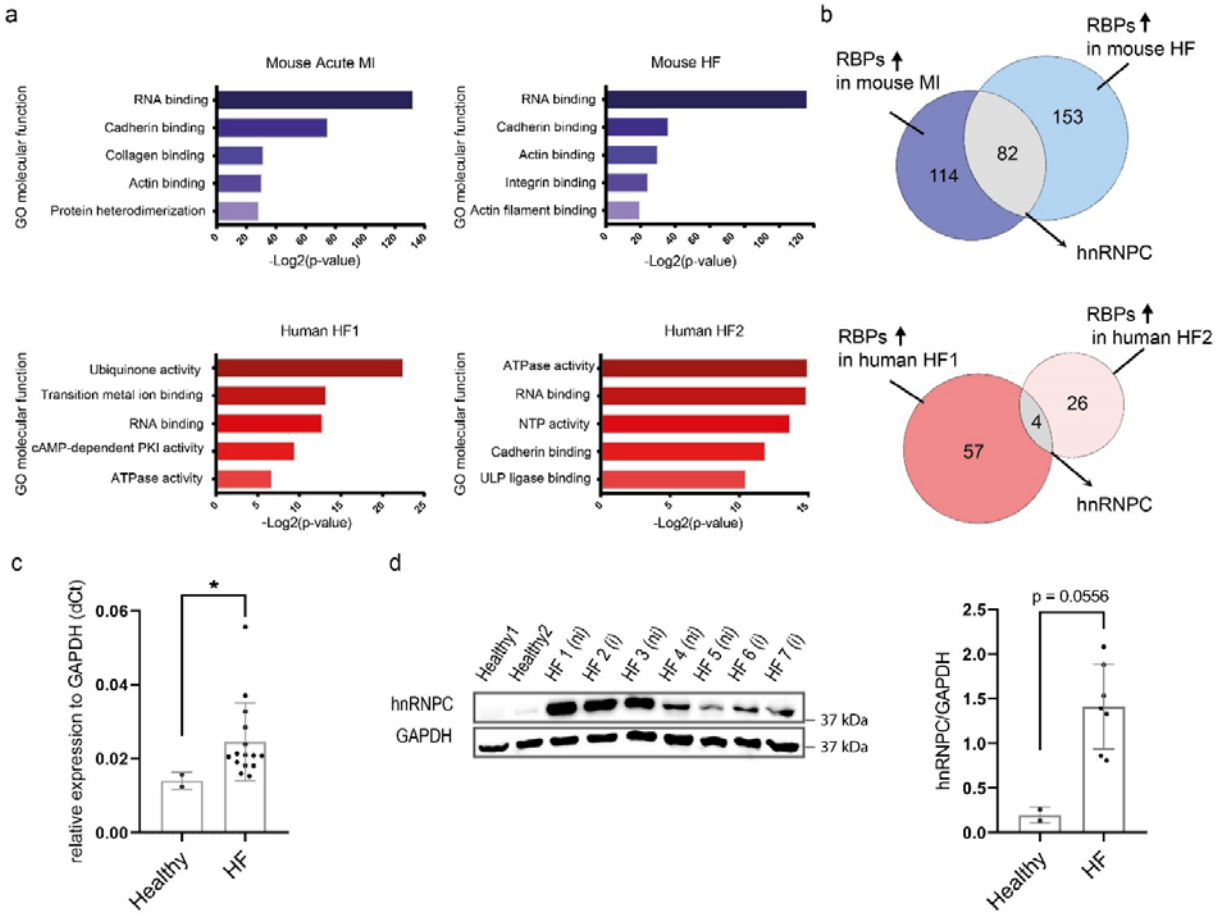


Figure 1: **The RNA-binding protein hnRNPC is upregulated in the diseased heart. a)** Top: Gene ontology (GO) annotation of the significantly upregulated genes (FDR < 0.1; FC > 1.5) identified by expression profiling array of murine hearts (left ventricle) exposed to myocardial infarction (48 h post-MI) as compared to sham operated (left) and of MerCreMer (MCM) murine hearts with peak dysfunction (day 10 post-tamoxifen treatment) as compared to control (right). Bottom: Gene ontology (GO) annotation of the genes found significantly upregulated by expression profiling array analysis of failing (HF) human heart as compared to healthy human heart in two datasets: HF1 (left) (FDR < 0.05; FC > 1.8) and HF2 (FDR < 0.1; FC > 1.5) (right). **b)** Top: Genes found upregulated by *in silico* analysis of profiling array data 48 h post-MI and in HF mouse heart tissues that encode for proteins involved in RNA binding (GO: 0003723). Bottom: Genes found upregulated by *in silico* analysis of profiling array data of HF1 and HF2 encoding for proteins involved in RNA binding (GO: 0003723). **c)** RT-qPCR analysis of hnRNPC RNA expression in HF (N = 15; n = 2) compared to healthy human hearts (N = 2; n = 2). **d)** Western blot analysis (left) and relative quantification (right) of hnRNPC protein expression in samples of HF (1-7) (N = 7; n = 3) and healthy (1-2) (N = 2; n = 3) heart tissues. HF (i) and HF (ni) indicate ischemic and non-ischemic samples, respectively. GAPDH was used for total protein loading normalization. Data are presented as mean ± S.D.; *p < 0.05; p-values were determined by Mann-Whitney test. See also **Supplementary Fig. 1** and **Supplementary Data 1**.

hnRNPC interacts with components of the myofibril in pathological heart

144 The participation of hnRNPs to pre-mRNA processing and mRNA dynamics is defined by their
145 cellular localization and by their interaction with specific interactors. To investigate hnRNPC
146 binding partners and how these might change upon HF, we pulled down the endogenous protein
147 in human end-stage failing and healthy heart samples and quantitatively analyzed the
148 immunoprecipitated complexes by tandem mass tag spectrometry (TMT-MS, **Fig. 2a**). We
149 identified 194 unique proteins interacting with hnRNPC in failing hearts, and 127 in healthy
150 samples: only 55 interactors were common to both conditions (**Fig. 2b; Supplementary Data 2;**
151 **Supplementary Methods**).
152
153 We weighted the specific HF and healthy interactor proteins for their abundances in the hnRNPC-
154 IP complexes and used the resulting data to build proteomaps based on the KEGG database [35]. This
155 approach allowed us to visualize how the hnRNPC interactome composition changes in the
156 pathology with a focus on the function of its binding partners (**Fig. 2c** and **Supplementary Data 2**).
157 We found that hnRNPC mainly interacted with components of the spliceosome complex in both
158 healthy and diseased hearts, consistent with its acknowledged function in RNA splicing [29,30]. More
159 interestingly, HF-specific interactors returned a common annotation for cardiac muscle
160 contraction and cytoskeletal proteins (**Fig. 2c**), suggesting that hnRNPC might display a distinct
161 localization in the pathological heart (**Supplementary Fig. 2a**).
162
163 We next performed gene ontology analysis of hnRNPC interactors in healthy and diseased heart to
164 identify which cellular component they belonged to. This analysis revealed that HF-specific
165 hnRNPC interactors included proteins belonging to the myofibril. For example, components of the
166 myofilament, sarcomere and the cardiac troponin complex were found bound to the RBP, almost
167 exclusively in HF (**Fig. 2d; Supplementary Fig. 2b**). Together with the annotation for cytosolic and
168 polysomal ribosome, which was significant for hnRNPC interactors in HF samples, these data
169 support a differential localization of the protein in the pathological heart.
170

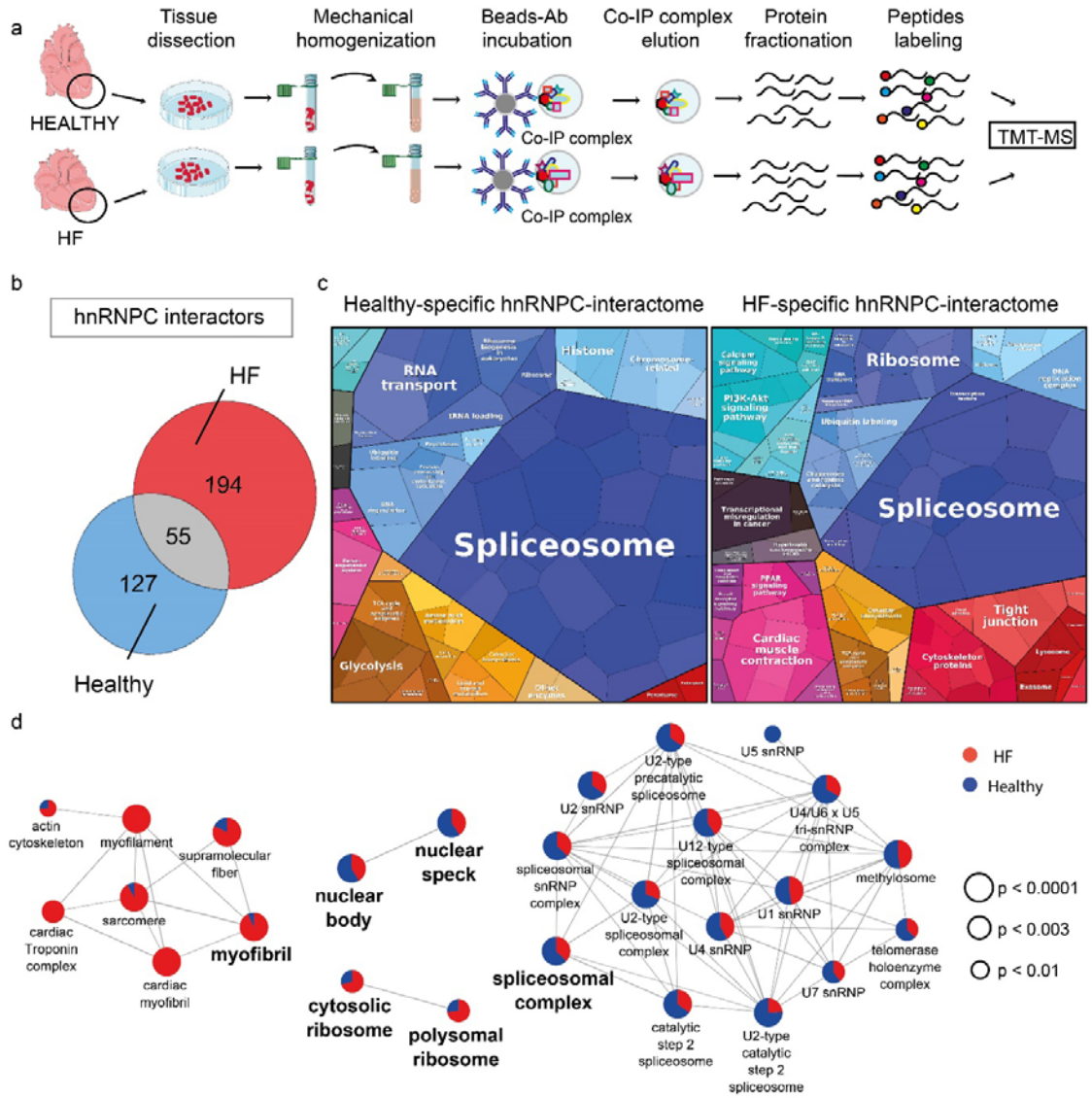


Figure 2: hnRNPC interacts with components of the myofibril in pathological heart. a) Graphical representation of the strategy adopted to identify hnRNPC interactors in the healthy human and failing heart (HF) *in vivo* by endogenous protein immunoprecipitation followed by tandem mass tag spectrometry (TMT-MS). **b)** The number of unique and shared proteins found in the hnRNPC interactome in human healthy (N=2) and HF (N=2) heart tissue by TMT-MS. **c)** Proteomaps (based on the KEGG database) representing the quantitative composition of the hnRNPC interactome in healthy and HF human hearts with a focus on protein function. Proteins are weighted for their abundance in the immunoprecipitated samples. **d)** Network representation of the cellular components Gene Ontology (GO) categories enriched in the hnRNPC interactome in healthy (red) and HF (blue) heart tissue. The size of the node indicates the Bonferroni adjusted Term p-values. See also **Supplementary Fig. 2** and **Supplementary Data 2**.

hnRNPC localizes to the Z-disk of the sarcomeric apparatus in the pathological heart

hnRNPC is predominantly localized in the nucleus. Given its interaction with components of the contractile apparatus and ribosomal proteins in the failing heart, we hypothesized hnRNPC could have a different localization under this condition. To confirm our hypothesis, we used confocal

186 microscopy to investigate hnRNPC intracellular localization in the human myocardium. Besides
187 being localized in the nucleus of cardiomyocytes, we also detected hnRNPC in the cytoplasm of the
188 contractile cells in the failing heart, with a characteristic striated pattern closely following the
189 distribution of cardiac troponin T (**Fig. 3a**). Using structured-illumination microscopy (SIM) to
190 resolve the subcellular distribution of the protein in the human pathological heart, we observed
191 that hnRNPC was localized at the Z-disc of the sarcomeres in HF (**Fig. 3b; Supplementary Fig. 3a**)
192 with a lateral resolution of ~125 nm. The shuttling of a fraction of the protein in the diseased heart
193 was confirmed by western blot analysis. This experiment also indicated a significant reduction in
194 hnRNPC nuclear expression in the pathological heart (Supplementary Fig. 3b).
195
196 To understand whether hnRNPC sarcomeric distribution can be considered a common feature of
197 cardiac pathologies, we analyzed its localization in a mouse model of MI generated by left anterior
198 descending (LAD) coronary artery ligation in C57BL/6 mice [36] (**Supplementary Fig 3c, d)**. We
199 stained the infarction border and the distal zone of the infarcted myocardium with an antibody
200 directed against hnRNPC at day 4 post-MI, when the tissue is stormed by intense inflammatory
201 response and at day 21 post-MI, when the acute phase is resolved and the scar is stabilized [5]. As
202 expected, hnRNPC showed a characteristic nuclear localization in both the healthy and ischemic
203 heart. When co-stained with troponin T2 (TNNT2), hnRNPC displayed a clear sarcomeric pattern in
204 cardiomyocytes located at the infarct border zone 21 days post-MI. A similar pattern could be
205 detected at the earlier time-point (day 4 post-MI). Image analysis clarified the co-localization
206 between hnRNPC and TNNT2 was only significant at day 21 post-MI as compared to sham-
207 operated, day 4 post-MI. No such phenomenon was found far from the infarct, at the distal zone
208 (**Fig. 3c**). These results suggest that hnRNPC translocates to the sarcomeres in cardiomyocytes at
209 the border zone of the infarction where it interacts with components of the sarcomere. This
210 process seems to start right after the ischemic insult and consolidates during the chronic MI stage.
211 To further confirm hnRNPC sarcomeric localization in failing hearts, we performed a proximity
212 ligation assay (PLA) with TNNT2 (**Fig. 3d**; **Supplementary Data 2; Supplementary Methods**). We
213 found that hnRNPC and TNNT2 are located within 40 nm of each other in HF and that the number
214 of interactions, as indicated by PLA dots, was significantly lower in healthy hearts (**Fig. 3d**). We
215 also confirmed the physical interaction between hnRNPC and other sarcomeric proteins (FHL2,

216 PDLIM5, MYH7) identified by TMT-MS in HF but not in the healthy heart by co-
217 immunoprecipitation analysis (**Fig. 3e**).
218 In order to further corroborate hnRNPC interaction with FHL2 and PDLIM5, we pulled the two
219 endogenous proteins down in 2 HF samples and resolved the interacting proteins (**Supplementary**
220 **Data 3**). hnRNPC presence was confirmed in both IP preparations by MS analysis and by western
221 blot (**Supplementary Fig. 3e; Supplementary Data 3**). Interestingly, FHL2, PDLIM5 and hnRNPC
222 interactomes returned 143 common binding partners in the failing heart (**Supplementary Fig. 3f**)
223 with a common annotation for actin cytoskeleton and myofibril component (**Supplementary Fig.**
224 **3g**; **Supplementary Data 3**).
225 Altogether, these results indicate that hnRNPC localizes to the contractile apparatus in both
226 ischemic and non-ischemic diseased hearts. The sarcomeric distribution of hnRNPC in HF suggests
227 this protein might have distinct functions in physiological and pathological conditions.

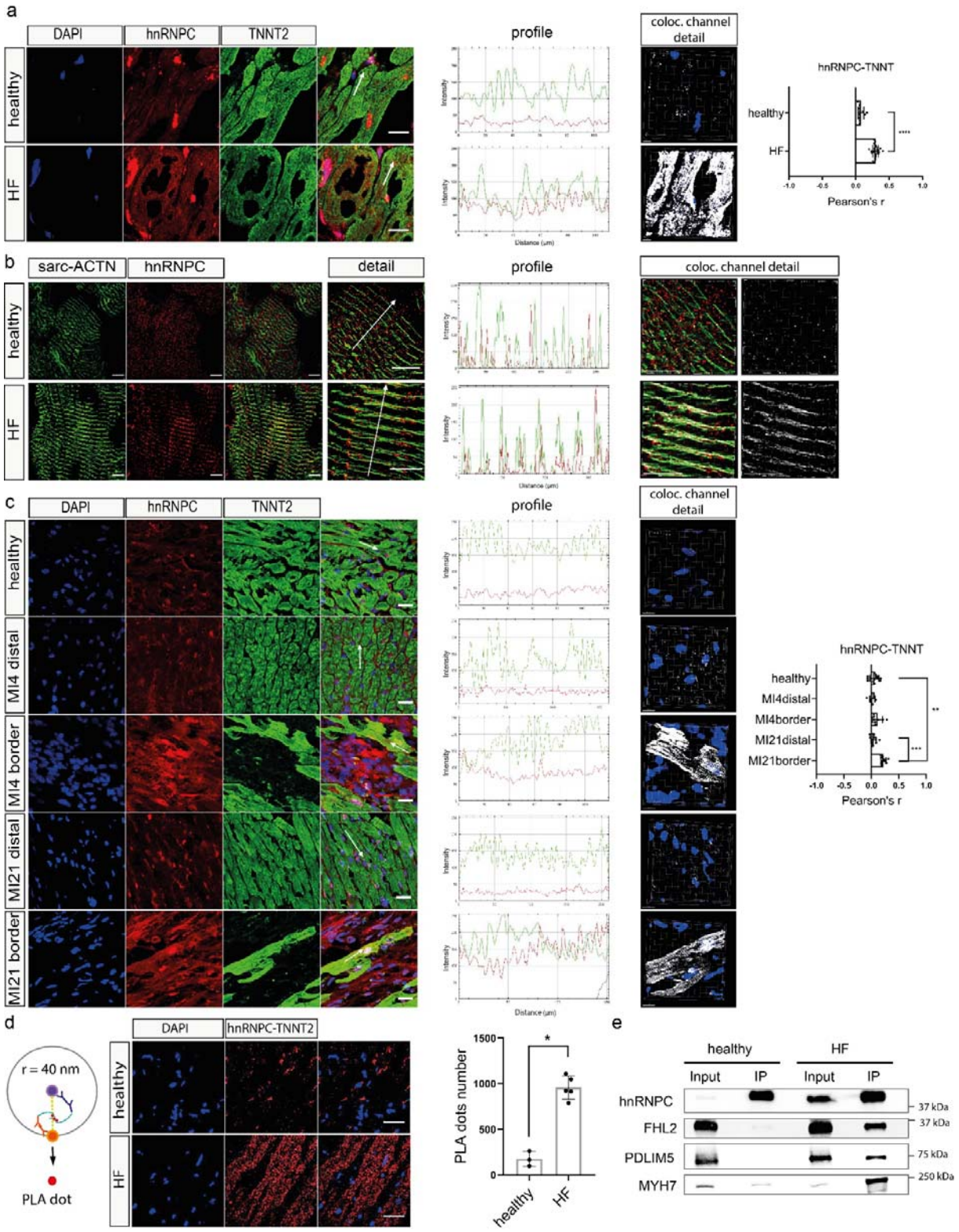


Figure 3: hnRNPC is localized at the Z-disk of the sarcomeric apparatus in the pathological heart. a) Representative confocal microscopy images depicting hnRNPC (red) localization in healthy (N=2) or failing (HF) (N=3) human heart tissue. Cardiomyocytes are stained with cardiac troponin T2 antibody (TNNT2, green) and the nuclei are

counterstained with DAPI (blue). The image analysis shows hnRNPC (red) distribution across the sarcomere, as identified by TNNT2 staining. The area analyzed is indicated by the white arrow in the microscopic image. The detail shows the colocalization (white) of red and green channels. Pearson's coefficient was calculated by Imaris ($n \geq 11$). Data are presented as mean ± S.D.; ****$p < 0.0001$; Mann-Whitney test. Scale bar = 20 µm; Scale bar of detail = 5 µm. **b)** Representative super-resolution image and image analysis of hnRNPC (red) sarcomeric distribution in failing HF. The sarcomere is counterstained by sarcomeric alpha actinin (sarc-ACTN, green). The area analyzed is indicated by the white arrow in the microscopic image. The detail shows the colocalization (white) of red and green channels. Scale bar = 5 µm. **c)** Representative confocal images showing the localization and relative profile of hnRNPC (red) in healthy and at the infarction proximity (border zone), or distal areas of infarcted mouse heart 4- and 21-days post-MI. Cardiomyocytes are stained with cardiac troponin T (TNNT2, green) and the nuclei are counterstained with DAPI (blue). The area analyzed is indicated by the white arrow in the microscopic image. The detail shows the colocalization (white) of red and green channels. Pearson's coefficient was calculated by Imaris ($n \geq 8$). Data are presented as mean ± S.D.; ***$p < 0.001$; **$p < 0.01$; Mann-Whitney test. Scale bar = 10 µm. **d)** Representative confocal images and relative quantification of the results obtained from Proximity Ligation Assay (PLA) by using antibodies against hnRNPC and TNNT2 in healthy ($N = 3$; $n \geq 12$) and HF ($N = 5$; $n \geq 13$) human heart tissue. Red dots identify areas where the proteins are found to be within 40 nm of each other. The nuclei are counterstained with DAPI (blue). Data are presented as mean ± S.D.; *$p < 0.05$; Mann-Whitney test. Scale bar = 50 µm. **e)** Western blot analysis of three sarcomeric proteins (FHL2, PDLIM5 and MYH7) in hnRNPC immunoprecipitated samples (IP) or total lysate (input) in healthy and failing human heart (HF). See also **Supplementary Fig. 3** and **Supplementary Data 3**.

hnRNPC binds transcripts encoding components of cardiomyocytes contractile apparatus in HF

To understand the role of hnRNPC at the sarcomere in HF, we next determined which transcripts it physically binds. To do so, we carried out RNA-binding protein-immunoprecipitation (RIP) followed by high-throughput sequencing (RIP-seq) in three human HF samples (**Fig. 4a; Supplementary Methods**). We first confirmed the specificity of the antibody in control RIP experiments in which a mouse IgG antibody showed no hnRNPC immunoprecipitation (**Supplementary Fig. 4a**). Next, we found that the distribution of reads on genomic regions (intron/exon, 5'UTR, 3'UTR, CDS) in the hnRNPC-IP library mostly mapped to intronic regions (63%), followed by coding DNA sequences (CDS, 22%), 3' (13%) and 5' (2%) untranslated regions (UTRs) (**Fig. 4b**). After browsing the POSTAR2 database, we confirmed that 2,487 out of 2,629 RNA targets found in our RIP-seq experiment harbored at least one binding site for hnRNPC [37] (**Supplementary Fig. 4b**).

Next, we calculated the number of reads mapping to a specific region (intron/exon, 5'UTR, 3'UTR, CDS) for each gene. By this approach, we could define two groups of targets: the transcripts enriched in intronic and those enriched in exonic reads (exon, CDS, 5' and 3' UTRs) (**Supplementary Fig. 4c; Supplementary Data 4; Supplementary Methods**). The large proportion of intronic hits is consistent with the documented role of hnRNPC in pre-mRNA splicing [28]. Although RBPs are known to exert their control on pre-mRNA splicing also by binding to exonic splicing enhancers or silencers [38]), we hypothesized that the exon-enriched targets found in the

271 pathological heart could represent mature RNAs that might be informative as to hnRNPC activity
272 at the sarcomere.
273 We then performed gene ontology analysis of hnRNPC-targets to understand to which cellular
274 component they belonged to. Here, we identified that the intron-enriched targets (1,681) mostly
275 belonged to nucleus, cytoskeleton and adhesion categories, while 18.8% of all annotated I-band
276 components were hnRNPC targets (**Fig. 4c, Fig. 4d**). Among the intron-enriched targets belonging
277 to the I-band category, we found transcripts such as LDB3, CACNA1C, DMD, PDLIM5, for which an
278 alteration in AS has been previously assigned to the occurrence of cardiac pathologies [12,39].
279 Moreover, we found splicing regulators among the hnRNPC targets (including RBM20, MBNL2,
280 CELF1-2, RBFOX1-2) that are involved in heart development and disease [40,41]. These findings
281 indicate that hnRNPC could exert both a direct and indirect role in splicing control of sarcomeric
282 transcripts affecting the post-transcriptional regulation of other RBPs. Selected hnRNPC intron-
283 enriched targets, showing high read coverage on intronic regions, as obtained by Integrative
284 Genomics Viewer (IGV), are shown in **Fig. 4e** and in **Supplementary Fig. 4d.**
285
286 We performed a similar cellular component enrichment analysis of the hnRNPC exon-enriched
287 targets and identified a significant enrichment for the myofibril, troponin complex, A and I bands
288 of the sarcomeres (**Fig. 4f**). Titin (*TTN*), cardiac muscle alpha actin (*ACTC1*) and troponin I (*TNNI3*)
289 contractile apparatus transcripts were found among hnRNPC targets (**Fig. 4g; Supplementary Fig.
290 4e**). When we analyzed the enriched biological processes by these exon-enriched hnRNPC targets,
291 we found that these targets were mainly involved in muscle structure development (22), filament
292 sliding (9), contraction (14) and myofibril assembly (9) (**Supplementary Fig. 4f**). By comparison, the
293 intron-enriched targets were principally associated with the regulation of signal transduction
294 (472), cell communication (513), cytoskeletal organization (209) and heart development (113)
295 (**Supplementary Fig. 4g**).
296
297 These data demonstrate that hnRNPC interacts with intron-enriched transcripts, confirming its
298 well-known function as a splicing regulator. On the other hand, hnRNPC also binds exon-enriched
299 transcripts that are enriched in RNAs encoding myofibril components.

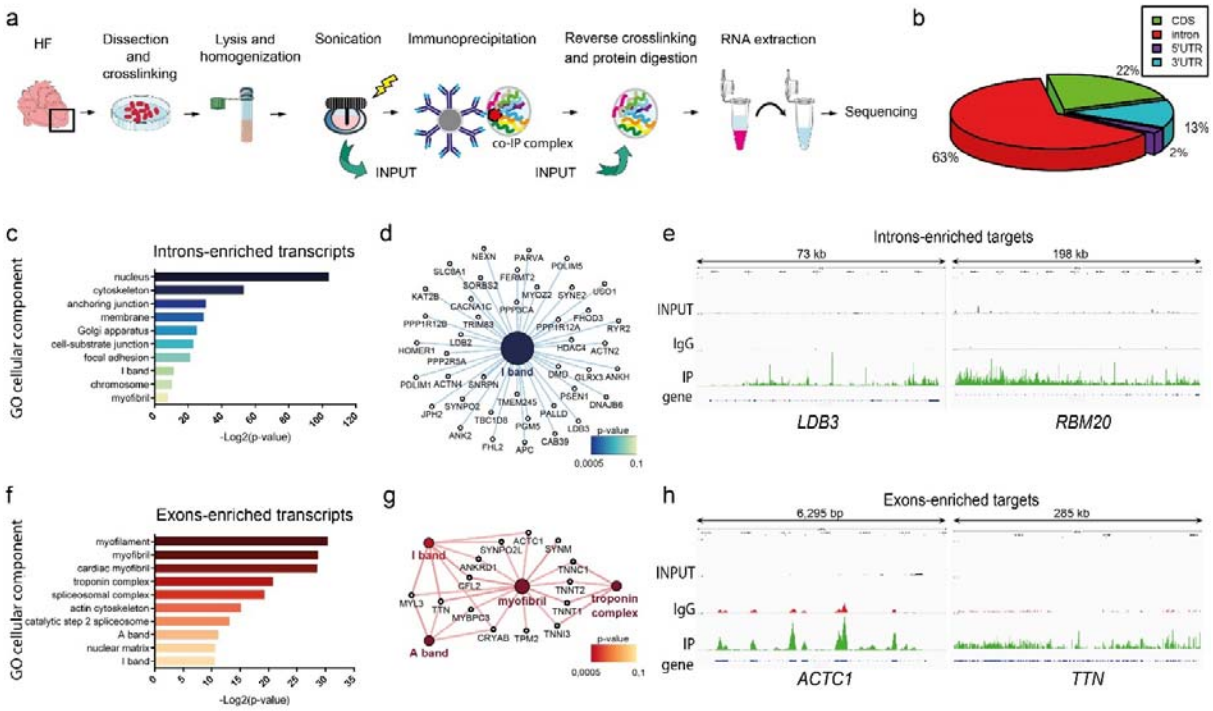


Figure 4: hnRNPC binds transcripts encoding components of cardiomyocytes contractile apparatus in HF. **a)** Graphical representation of the strategy adopted to identify hnRNPC RNA targets in human heart failure (N = 3) (HF) *in vivo* by endogenous RNA immunoprecipitation followed by sequencing. **b)** Genomic distribution of the read counts showing the percentage of reads mapping on specific genomic regions (intron/exon, 5'UTR, 3'UTR, CDS) in immunoprecipitated samples (N = 3). **c)** Cellular components Gene Ontology (GO) categories significantly enriched in intron-enriched transcripts (log2 intron/exon ratio > 1) bound to hnRNPC in HF. **d)** GO network of I band cellular components and the intron-enriched transcripts within this network that bind hnRNPC (p-value corrected with Bonferroni = 0.00037). The size of the node is proportional to the number of hnRNPC targets belonging to the ontology. **e)** Individual gene representation of intron-enriched hnRNPC targets: read coverage is displayed in INPUT (black), IgG (red) and IP (green) samples. **f)** Cellular components GO categories significantly (p-value < 0,05) enriched in exon-enriched transcripts (log2 intron/exon ratio < -1) bound to hnRNPC in HF. **g)** GO network of cellular components of interest enriched (Group p-value corrected with Bonferroni = 9.43E-07) in exon-enriched RNAs that bind hnRNPC in HF. The size of the node is proportional to the number of hnRNPC targets belonging to the ontology. **h)** Individual gene representation of exon-enriched hnRNPC targets: read coverage is displayed in INPUT (black), IgG (red) and IP (green) samples. See also **Supplementary Fig. 4** and **Supplementary Data 4**.

ECM pathological remodeling induces hnRNPC association to the translation machinery at the sarcomere

Because hnRNPC exon-enriched targets comprised mainly mRNAs encoding sarcomeric proteins and we found hnRNPC localized at the sarcomere in HF, we queried the role of hnRNPC at this site. *TTN*, *ACTC1* and *TNNI3* transcripts, found among hnRNPC exon-enriched targets, are translated at the sarcomeres in the rat heart, in a process dubbed as 'localized translation' [42,43]. Localized translation allows for the spatio-temporal control of contractile protein synthesis at the

324 sarcomeric site [43,44]. Previous reports have shown ribosomes are present at the sarcomeres in the
325 rat heart, where localized translation ensures that contractile proteins are readily replaced during
326 sarcomere remodeling [43,45]. Consistently, our TMT-MS analysis identified nine ribosomal proteins
327 in the hnRNPC interactome in the failing heart (**Supplementary Fig. 5a**) which accounted for the
328 ribosome annotation found in GO cellular component analysis (**Fig. 2d**). To confirm the presence
329 of the ribosomes at the sarcomeric structure, we labeled the evolutionarily conserved RPS6
330 ribosomal protein (which was a potential hnRNPC interactor in our TMT-MS analysis) in healthy
331 and HF cardiac tissue sections. We found a typical sarcomeric cross-striated pattern, as confirmed
332 by TNNT2 decoration, in both groups (**Supplementary Fig. 5b**). We observed a similar pattern in
333 the sarcomeres of cardiomyocytes residing both at the distal and at border zones of myocardial
334 infarction, as well as in healthy cardiomyocytes in the murine heart (**Supplementary Fig. 5c**).
335
336 As we found that hnRNPC relocated to the sarcomeres in HF and confirmed the presence of the
337 ribosomes at this site in the human heart, we asked whether sarcomeres could be a site of
338 localized translation in human cardiomyocytes. Therefore, we derived contractile cardiomyocytes
339 from human induced pluripotent stem cells (iPSC-CMs) through an established protocol [46]. In
340 differentiated cells, we first confirmed RPS6 presence at the sarcomeres by co-localization analysis
341 of the protein with cardiac TNNT2 (**Fig. 5a**). Next, we performed a ribopuromycylation assay that
342 exploits puromycin mimicry of aminoacylated tRNA to visualize the active sites of translation
343 (**Supplementary Fig. 5d**). Here, puromycin (PMY) could be incorporated in the contractile
344 apparatus of human iPSC-CMs, thus demonstrating human cardiomyocyte sarcomeres are active
345 sites of protein translation (**Fig. 5b**).
346
347 Next, we queried whether hnRNPC associates to the translation machinery when localized at the
348 sarcomeres in the pathological heart. To do this, we adopted an original reductionist approach
349 that proved effective at reproducing some key mechanical features of pathological cardiac ECM
350 remodeling by decellularizing healthy and diseased human heart tissue (dECMs) [23,47]. We used the
351 homogenized dECMs to coat the surface of cell culture plates. Next, we seeded contractile iPSC-
352 CMs on healthy and pathological dECMs and combined ribopuromycilation with PLA assay to
353 investigate whether hnRNPC localized close to the active translation sites, as indicated by PMY
354 staining (**Fig. 5c**). The analysis showed the presence of PLA dots, corresponding to hnRNPC–PMY

proximity, in TNNT2-positive cells cultured on pathological dECMs but not in iPSC-CMs grown on healthy dECMs (**Fig. 5d**). These data confirm that sarcomeres are active sites of RNA translation and that hnRNPC localizes to those sites as a result of cardiac ECM pathological remodeling.

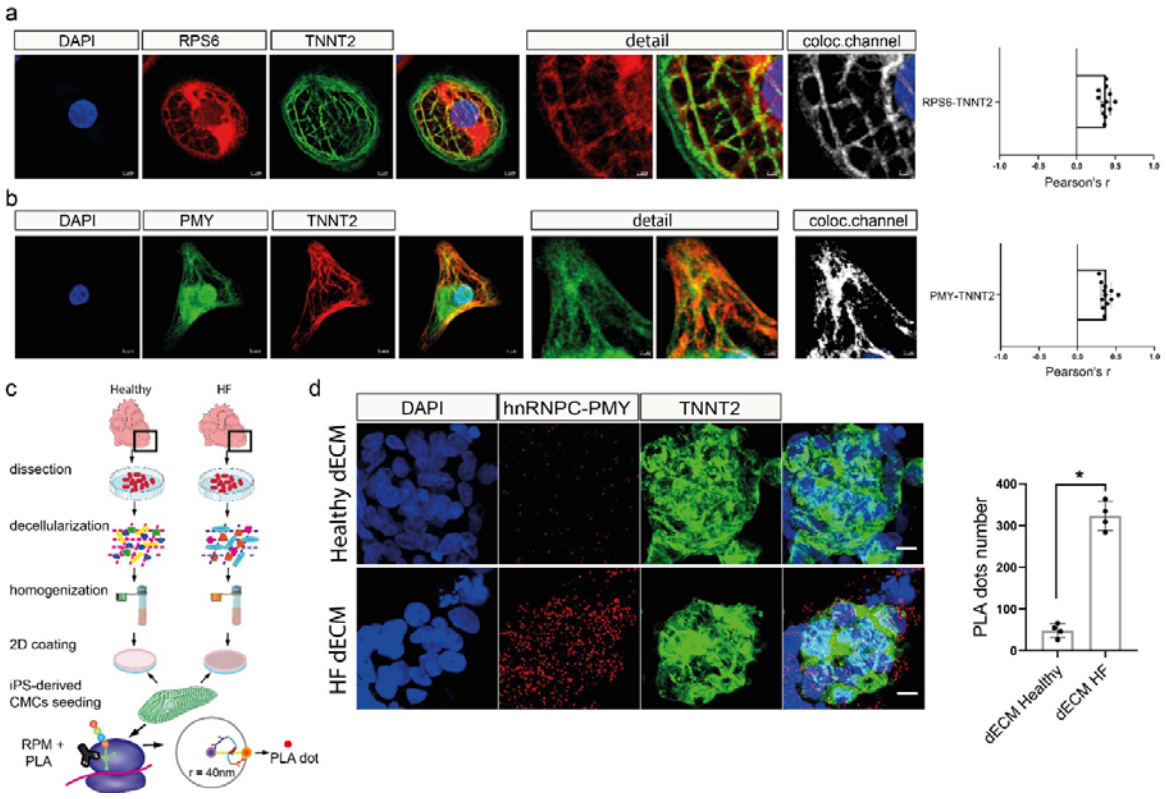


Figure 5: hnRNPC associates to the translation machinery at the sarcomere following ECM pathological remodeling. a) Representative confocal image of ribosomal protein S6 (RPS6, red) localization in iPSC-derived contractile cardiomyocytes (N = 3). Sarcomeric units are identified by cardiac troponin T (TNNT2, green) staining and nuclei are counterstained with DAPI (blue). The detail shows a magnified area of a single cardiomyocyte in which the colocalization of red and green channels has been quantified using Imaris software (n = 12). Data are presented as mean ± S.D. Scale bar = 5 µm; Scale bar of detail = 2 µm. **b)** Representative confocal microscopy images of single iPSC-derived cardiomyocytes labeled with anti-puromycin antibody (PMY, green) after puromycin incorporation (N = 3). Sarcomeric units are identified by cardiac troponin T (TNNT2, red) staining and the nuclei are counterstained with DAPI (blue). Colocalization analysis of the green and red channels was quantified by Imaris software (n = 12). Data are presented as mean ± S.D. The detail shows a magnified area of a single cardiomyocyte. Scale bar = 5 µm; Scale bar of detail: 2 µm. **c)** Description of the ribopuromycilation and Proximity Ligation Assay (PLA) used to investigate the occurrence of localized translation at the sarcomeres in iPSC-derived cardiomyocytes grown onto decellularized matrices obtained from either healthy or failing human hearts. **d)** Representative confocal microscopy images of PLA using antibodies against PMY and hnRNPC in iPSC-derived beating cardiomyocytes grown onto HF or healthy decellularized heart matrices. The cardiomyocytes were labeled with cardiac troponin T (TNNT2, green). Red dots indicate that the proteins are within 40 nm of each other. The nuclei are counterstained with DAPI (blue). Data are presented as mean ± S.D. (N = 4; n = 6). *p < 0.05; Mann-Whitney test. Scale bar = 10 µm. See also **Supplementary Fig.5**.

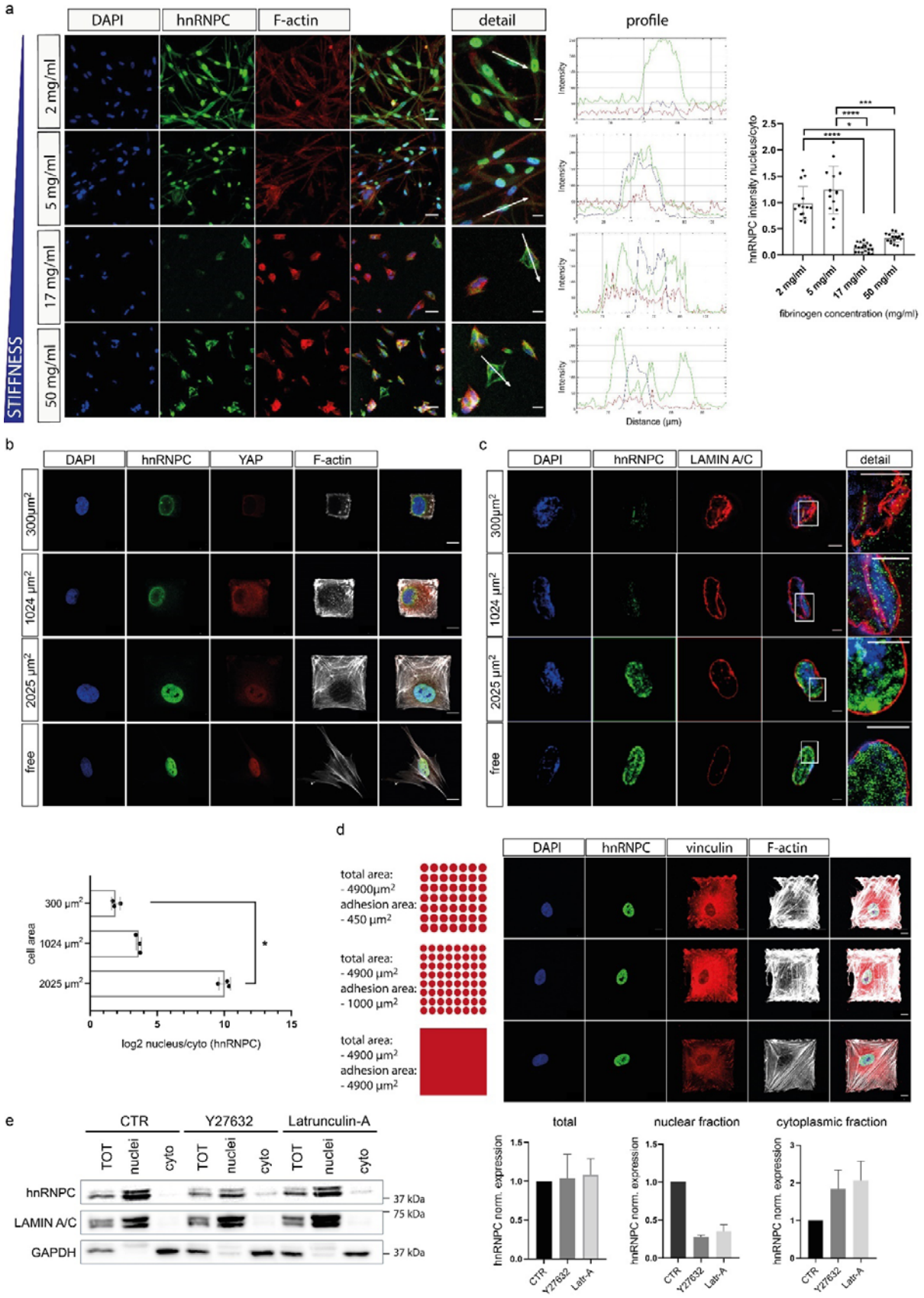
hnRNPC intracellular localization is controlled by cell spreading and cytoskeletal tension

380 Thus far we have shown that cardiac ECM pathological remodeling induces hnRNPC shuttling to
381 the active sites of translation at the sarcomere. Pathological remodeling is a complex
382 phenomenon modifying the chemical composition and the mechanical properties of cardiac ECM
383 [5,23]. We tried to disentangle the role of mechanical cues in hnRNPC localization. We hence adopted
384 surfaces with the same chemical composition and controlled rigidities (1.5 vs 28 kPa) and repeated
385 the ribopuromycilation assay followed by PLA on iPSC-CMs. The elasticity values chosen do not
386 exactly match those found in the living heart, but are in the same kPa range. More importantly,
387 these values have been shown to induce mechanosensor activation in other cell systems [48–50].
388 Here we found hnRNPC localization to the sites of active translation, as detected by PMY
389 interaction, was sensitive to the stiffness of the substrate, since PLA signal was significantly
390 different on substrates with different elasticities. This result suggests that substrate stiffness *per*
391 *se* can induce hnRNPC shuttling (**Supplementary Fig. 6a**).

392 In order to corroborate this result, we challenged normal human dermal fibroblasts (NHDFs), a
393 model of highly mechano-responsive cells, with different mechanical stimuli and analyzed hnRNPC
394 distribution. Here, we used a fibrin-based 3D culture system, whose mechanical properties can be
395 tuned in a physiological range by modulating the fibrinogen concentration in the presence of
396 constant levels of thrombin [51] (**Supplementary Fig. 6b**). We embedded NHDFs into the hydrogels
397 and analyzed hnRNPC localization after 48 hours. We additionally stained F-actin and cell nuclei to
398 monitor cell ability to spread within the hydrogels, indicative of the degree of cytoskeletal tension.
399 We observed that NHDFs spread well in soft (2 mg/ml and 5 mg/ml fibrinogen) hydrogels, but
400 failed to elongate as the stiffness of the fibrin gel increased (17 mg/ml fibrinogen). At the highest
401 fibrinogen concentration (50 mg/ml), the cells were unable to acquire an elongated morphology
402 (**Supplementary Fig. 6c**). Image analysis demonstrated that hnRNPC nuclear localization correlated
403 with the NHDF volume and with the cellular ability to spread within soft hydrogels, with hnRNPC
404 translocation to the cytoplasm characteristic of cells confined into stiff fibrin gels (**Fig. 6a;**
405 **Supplementary Fig. 6c**). These data suggest that hnRNPC nuclear localization might be controlled
406 by the ability of cells to develop intracellular tension and spread within the surrounding milieu.

407 To corroborate our hypothesis, we used fibronectin-coated micro-patterned surfaces to precisely
408 control single cell area [49,50,52]. We stained NHDFs with a specific antibody against hnRNPC and
409 used YAP as an example of a mechanosensitive protein whose localization depends on intracellular

410 tension and cell spreading [49,50]. Confocal analysis showed that hnRNPC localized at the nucleus in
411 cells that were confined to bigger areas (2,025 μm^2) or free to spread. By contrast, the protein
412 shuttled to the perinuclear region of cells constrained on smaller surfaces (1,024 and 300 μm^2)
413 (**Fig. 6b; Supplementary Fig. 6d**). To resolve the intracellular distribution of the protein, we
414 counterstained the nuclear structure with Lamin A/C and visualized the cells by structured
415 illumination microscopy (SIM). Here we found that hnRNPC egressed the nucleus and acquired a
416 perinuclear localization in constrained cells, with a peculiar distribution close to Lamin A/C nuclear
417 invaginations (**Fig. 6c**). We repeated the same experiment using iPSC-CMs and again observed that
418 hnRNPC nuclear localization was also sensitive to cell spreading in contractile cells
419 (**Supplementary Fig. 6e**).
420 Having shown that hnRNPC nuclear localization required the cell to spread in 2D and 3D, we next
421 performed in depth experiments to clarify whether the shuttling of the protein was driven by the
422 availability of adhesion sites within the local ECM or by the transmission of intracellular tension.
423 We first designed single cell fibronectin-coated micropatterned arrays that keep the cell area
424 constant (4,900 μm^2), while reducing the number of fibronectin adhesion spots [49]. When we
425 decreased the adhesion area (1,000 and 450 μm^2), we saw no significant effect on hnRNPC
426 nuclear localization (**Fig. 6d**).
427
428 We concluded that adhesion did not affect hnRNPC localization, and decided to inhibit the
429 transmission of intracellular tension by treating NHDFs with pharmacological inhibitors of either
430 the RhoA/ROCK pathway (Y27632) or F-actin polymerization (Latrunculin A) [2,53]. We analyzed
431 hnRNPC localization in the nucleus and cytoplasm by cell fractionation followed by western
432 blotting, and detected a significant decrease in nuclear hnRNPC and the concomitant increase in
433 its cytoplasmic expression in cells treated with the pharmacological inhibitors (**Fig. 6e**). These data
434 are consistent with the hypothesis that the inhibition of intracellular tension determines a
435 reduction in hnRNPC nuclear expression and the shuttling of a fraction of the protein to the
436 cytoplasm.


a
DAPI
hnRNPC
F-actin
detail
profile
STIFFNESS
2 mg/ml
5 mg/ml
17 mg/ml
50 mg/ml
Intensity
Distance (µm)
hnRNPC intensity nucleus/cyto
fibrinogen concentration (mg/ml)
b
DAPI
hnRNPC
YAP
F-actin
300µm²
1024 µm²
2025 µm²
free
c
DAPI
hnRNPC
LAMIN A/C
detail
cell area
log2 nucleus/cyto (hnRNPC)
d
total area:
- 4900µm²
adhesion area:
- 450 µm²
total area:
- 4900 µm²
adhesion area:
- 1000 µm²
total area:
- 4900 µm²
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DAPI
hnRNPC
vinculin
F-actin
e
CTR
Y27632
Latrunculin-A
TOT
nuclei
cyto
hnRNPC
LAMIN A/C
GAPDH
37 kDa
75 kDa
37 kDa
total
nuclear fraction
cytoplasmic fraction
hnRNPC norm. expression
CTR
Y27632
Latr-A

437

Figure 6: hnRNPC intracellular localization is mechanically controlled. a) Left: Representative confocal microscopy images showing hnRNPC (green) expression in normal human dermal fibroblasts (NHDFs) embedded for 48 h in fibrin-based hydrogels with an increasing fibrinogen concentration and stiffness. Cellular F-actin was labeled with Phalloidin (red) and the nuclei were counterstained with DAPI (blue). Image analysis shows the quantification of signal distribution in NHDFs embedded for 48 h in fibrin-based hydrogels with controlled stiffness. Right: Quantification of the hnRNPC in the nucleus/cytoplasm distribution in fibrin-gels with increasing fibrinogen concentration and stiffness. For each experimental condition, data are presented as mean ± S.D. from N ≥ 7 independent fields of acquisition; *p < 0.05; ***p < 0.001; ****p < 0.0001, Kruskal-Wallis test followed by Dunn's multiple comparison test. **b)** Top: confocal analysis of individual cells grown onto 300, 1024, 2025 μm^2 micropatterns coated with fibronectin. The cells were labeled with anti-hnRNPC (green), Alexa Fluor 647 Phalloidin, anti-Lamin A/C (red) and the nuclei were counterstained with DAPI (blue). Bottom: Barplot representation of hnRNPC nucleus/cytoplasm distribution in single cells seeded onto 300, 1024, 2025 μm^2 micropatterns (N = 3; n ≥ 8); *p < 0.05; Kruskal-Wallis test followed by Dunn's multiple comparison test. **c)** Representative super-resolution images of individual cells grown onto 300, 1024, 2025 μm^2 micropatterns coated with fibronectin. The cells were labeled with anti-hnRNPC (green) and anti-Lamin A/C (red). Nuclei were counterstained with DAPI. **d)** Left: Annotation of micropattern properties (cell area and adhesion area) and a schematic top view of the fibronectin distribution in the micropatterns. Red color indicates fibronectin-covered area. Right: Confocal images of single NHDFs grown onto the indicated micropatterns and labeled with anti-vinculin (red), anti-hnRNPC (green), Alexa Fluor 546 Phalloidin and DAPI (blue) (N = 3; n = 5). **e)** Western blot analysis (left) and quantification (right) of hnRNPC expression in cellular (TOT), nuclear and cytoplasmic fractions of NHDFs treated or not (CTR) with Latrunculin-A and Y27632 inhibitors. GAPDH was used for loading normalization of the total and cytoplasmic fractions. Lamin A/C was used to normalize protein loading in the nuclear fraction. Band intensities corresponding to hnRNPC in the nuclear and cytoplasmic fractions were quantified using Bio-Rad Image Lab software. Data are presented as mean ± S.D. (N = 3). See also **Supplementary Fig. 6**.

hnRNPC regulates the AS of genes involved in mechanotransduction

We have so far demonstrated that a fraction of hnRNPC is distributed to the sarcomeres in HF, and its expression in the nucleus is reduced (**Supplementary Fig. 3b**). This data suggests a decreased contribution of the ribonucleoprotein to the splicing process (**Fig. 2c)**. Moreover, we found that altered cytoskeletal tension affects hnRNPC subcellular localization. As hnRNPC is associated to the spliceosome and mainly nuclear in physiological conditions, we studied which changes in terms of AS events would cause the reduced contribution of hnRNPC to the splicing process. We therefore knocked down (KD) hnRNPC in NHDFs using two independent siRNAs (**Fig. 7a**) and analyzed the abundance of RNA splicing variants by high throughput genome-wide RNA-seq. We then adopted the multivariate analysis of transcript splicing (MATs) statistical algorithm to quantify the changes in AS driven by hnRNPC downregulation. We identified the differential splicing of 2,032 RNA transcripts (FDR< 0.01 and |ΔPSI| ≥ 0.1) in the KD cells, as compared to the scrambled control transfected cells (**Supplementary Data 5; Supplementary Methods**). Consistent with previous reports [30,54], most of the splicing events affected by hnRNPC KD consisted of skipped

477 exons (SE: 78,95%), followed by mutually exclusive exons (MXE: 14,85%), alternative 3'-5' splice
478 sites (A3SS: 3,76% and A5SS: 2,15%) and intron retention (IR: 0,3%) (**Fig. 7b**). Pathway enrichment
479 analysis of the 2,032 differentially spliced genes in hnRNPC KD cells revealed that the splicing of
480 numerous genes involved in cell mechanotransduction, integrin-mediated cell adhesion and focal
481 adhesion was affected (**Fig. 7c**). In particular, 15 components of the Hippo signaling pathway, a
482 mechanosensitive molecular axis involved in heart development [22] and diseases [52,55], displayed
483 altered AS upon hnRNPC silencing (**Supplementary Data 6**).
484 Among the 15 genes belonging to Hippo pathway which displayed altered splicing upon hnRNPC
485 depletion we found the main effector, Yes Associated Protein 1 (YAP1). *YAP1* gene encodes for
486 multiple protein isoforms (**Fig. 7d**). The distinct co-transcriptional fingerprints of the splicing
487 variants are known to depend upon the presence of one (YAP1-1) or two (YAP1-2) WW domains
488 [56,56]. The exon 4, which encodes for the second WW domain in YAP1-2 isoforms, was found
489 differentially spliced in hnRNPC-depleted cells by RNA-seq. We thus designed primers that
490 recognize 9 isoforms of YAP1 and analyzed the relative abundance of those including or not exon 4
491 in hnRNPC-depleted cells by RT-qPCR. Interestingly, we found that hnRNPC depletion significantly
492 affected the inclusion of exon 4 in YAP1 transcript and the overall balance among YAP1-1 and
493 YAP1-2 splicing variants (**Fig. 7d, e Supplementary Fig. 7a**). These results were confirmed in
494 hnRNPC-depleted iPSC-CMs (**Supplementary Fig. 7b, c**).
495 Additionally, we obtained similar results by treating NHDF with inhibitors of cytoskeletal tension,
496 hence we established that the mechanical displacement of hnRNPC from the nucleus affects the
497 expression of YAP1-1 isoforms (**Fig. 7e**).

498 In order to validate this set of data, we analyzed the expression of CD44 isoforms, whose
499 alternative splicing has been proven mechanosensitive [57]. As expected, here we found CD44
500 isoform abundance was also affected by hnRNPC depletion as well as by the treatment with
501 inhibitors of tension both in NHDFs and iPSC-CMs (**Supplementary Fig. 7d, e**). We also validated
502 the splicing events occurring in MYLK and COL6A3 transcripts in hnRNPC KD cells by RT-qPCR
503 (**Supplementary Fig. 7f, g**).
504 Next, we compared the differentially spliced genes in hnRNPC KD cells to the RNAs known to
505 harbor hnRNPC binding sites (as documented in the POSTAR database). We found as many as
506 1,738 among the 2,032 transcripts had at least one hnRNPC binding site and could, in principle,
507 interact with this RBP (**Supplementary Fig. 7h**). In order to check that those were true hnRNPC

508 targets, we performed individual-nucleotide resolution Cross-Linking and ImmunoPrecipitation
509 (iCLIP). This approach allowed us to map precisely hnRNPC-RNA interactions and relate them to
510 the previously detected hnRNPC-dependent splicing events in NHDF cells (**Supplementary Fig. 8a,**
511 **b; Supplementary Data 7; Supplementary Methods**). A total of 1,470,396 uniquely mapped
512 hnRNPC crosslink events were identified, which cluster into 13,567 binding sites in 5,536
513 transcripts (**Supplementary Data 7**). As a control, we found the majority of hnRNPC crosslink
514 events to be located within introns, with high coverage of Alu elements, in good agreement with
515 previous results obtained in other cell types [28,29] (**Supplementary Fig. 8c, d**). While 58% of the
516 crosslink events mapped to coding sequences, several non-coding hnRNPC targets were also
517 identified, including MALAT-1, a long non coding RNA whose interaction with hnRNPC has already
518 been described [58] (**Supplementary Fig. 8e-g**).
519 Next, we matched the results of AS events in hnRNPC KD cells with those obtained by iCLIP. In
520 particular, we searched for all transcripts directly bound by hnRNPC to determine whether they
521 displayed AS in hnRNPC-depleted cells. We ultimately detected 748 transcripts physically
522 interacting with hnRNPC in NHDFs that were differentially spliced in the absence of the protein
523 (**Fig. 7f; Supplementary Data 7**). Among those, we confirmed the presence of seven components
524 of the Hippo pathway (**Fig. 7g; Supplementary Data 6**), on which hnRNPC binding occurred in
525 intronic regions surrounding exons alternatively spliced in hnRNPC-depleted cells (**Fig. 7h, i;**
526 **Supplementary Fig. 9a, b).** This was the case for YAP1 transcript, for which, the RNA-binding
527 protein iCLIP coverage in the proximity of the hnRNPC-dependent exon 4 could be confirmed (**Fig.**
528 **7h, i**). The data were validated by independent iCLIP-PCR assay for three selected hnRNPC targets:
529 YAP1, CD44 and MYLK (**Supplementary Fig. 10 a, b**).
530 In summary, these results suggest that hnRNPC participates in the regulation of AS of pre-mRNAs
531 encoding genes involved in mechanotransduction.

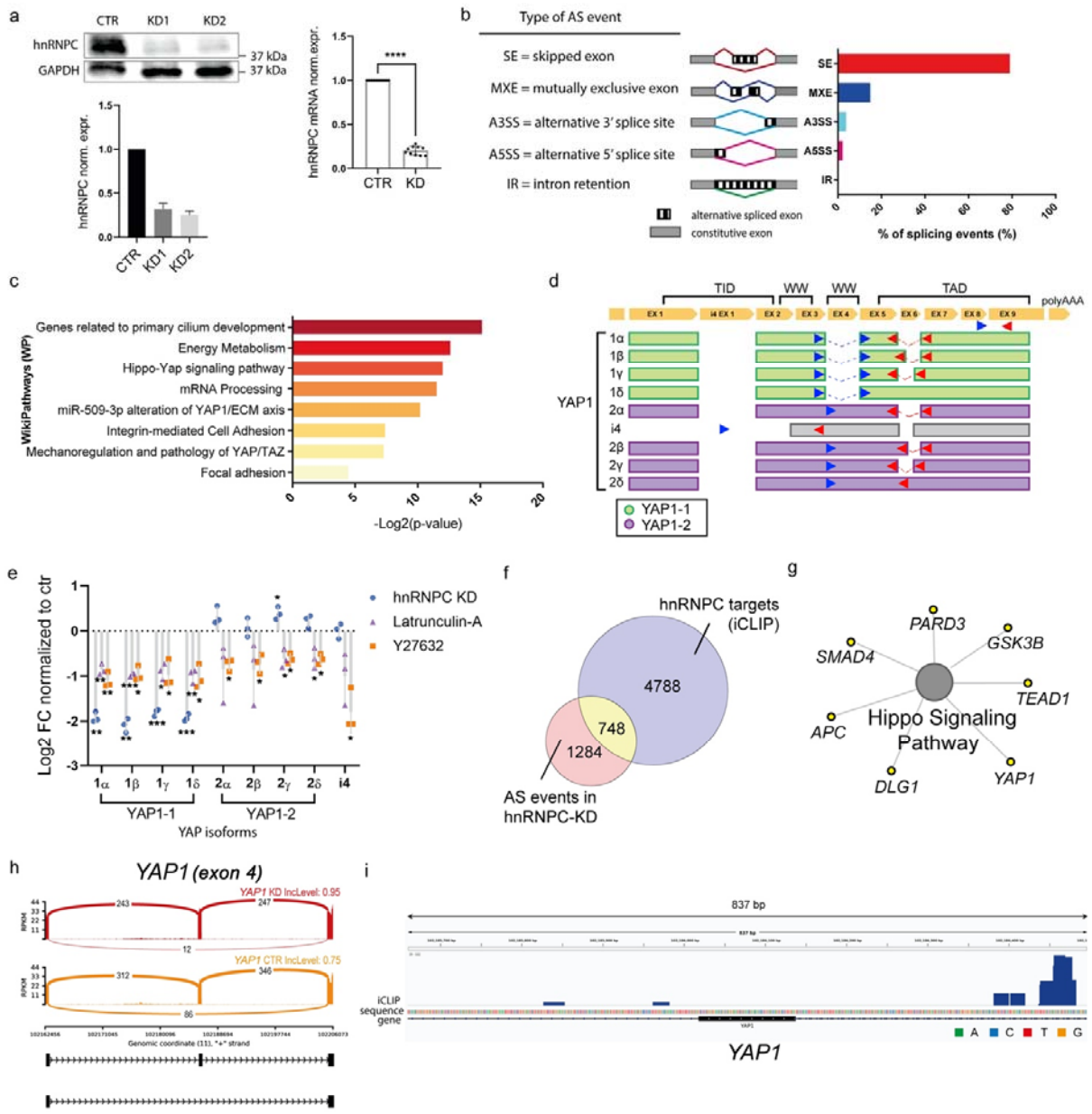


Figure 7: hnRNPC regulates the alternative splicing of genes involved in mechanotransduction. a) Left: Western blot analysis (top) and relative quantification (bottom) of hnRNPC protein expression in normal human dermal fibroblasts (NHDF) transfected with hnRNPC siRNA constructs (KD1 and KD2) or with a control siRNA construct (CTR). Protein expression was assessed 96 h after the transfection. GAPDH was used for total protein loading normalization. Data are presented as mean ± S.D. (N = 3). Right: histogram representation of the results obtained by RT-qPCR analysis of hnRNPC RNA expression in NHDFs 96 h after transfection with hnRNPC (KD) or control siRNAs (CTR). Data are presented as mean ± S.D. (N = 10). ****p < 0.0001, Mann-Whitney test**. b)** The percentage of splicing events occurring in hnRNPC KD cells classified into the five major categories of alternative splicing (AS), as obtained by Multivariate analysis of transcript splicing (MATs). **c)** Gene ontology (GO) analysis showing the main pathways found significantly enriched (p-value < 0.05) in genes displaying altered splicing in hnRNPC KD cells using the WikiPathways database. **d)** Schematic representation of protein-coding YAP1 isoforms. Coding regions (CDS) of four YAP1-1, four YAP1-2, and YAP-i4 isoforms are aligned and corresponding protein domains (TEAD-binding domain (TBD), WW domains, TRANS-activating-domain (TID) with N-terminal coiled-coil domain and N terminal PDZ motif) are shown.

546 Blue and red arrows represent the approximate binding sites of forward and reverse primers, respectively. **e)** Dotplot
547 representation of YAP isoforms mRNA expression (Log2FC) in NHDF upon hnRNPC-depletion (blue) or upon 24h
548 treatment with latrunculin-A (purple) or rock inhibitor (Y27632) (orange). Each result is compared to its relative
549 control. Superimposed bars represent the as mean ± S.D. (N = 3). *p < 0.05; **p < 0.01; ***p < 0.001; One-sample t-
550 test. **f)** Venn diagram representation of the common transcripts identified as hnRNPC targets by hnRNPC iCLIP-seq
551 data that were also found differentially spliced (AS events) in hnRNPC KD in NHDF cells. **g)** GO network representation
552 of the RNA targets of hnRNPC displaying altered splicing upon hnRNPC silencing and belonging to Hippo signaling
553 Pathway (HSA04390). **h)** Sashimi plot depicting YAP1 skipped exon (SE) AS event (exon 4) in hnRNPC KD cells. **i)**
554 Individual gene representation of hnRNPC binding on YAP1 transcript: the iCLIP average (N = 3) is shown in blue.
555
556
557 **hnRNPC regulates the AS of genes involved in cardiovascular diseases**
558 We next used our iCLIP and alternative splicing analyses to validate the RNA-IP results obtained in
559 the diseased human heart **(Fig. 4).** We figured this approach might help us unveil the direct targets
560 of hnRNPC in the pathological heart, where the RBP levels and localization are perturbed **(Fig. 1c,**
561 **d; Fig. 3a, b).** We matched the three datasets to identify 389 common transcripts which are
562 physically bound by hnRNPC in the failing hearts and undergo alternative splicing in its absence
563 (**Fig. 8a; Supplementary Data 8**). Among them, we again confirmed the presence of the
564 components of the Hippo pathway (**Supplementary Data 6**).
565
566 The Comparative Toxicogenomics Database (CTD) annotation of the transcripts targeted for gene–
567 disease associations yielded cardiovascular, cancer and neurological diseases as the main
568 represented categories (**Fig. 8b; Supplementary Data 8**). In particular, 41 hnRNPC direct targets
569 belonging to the cardiovascular disease category displayed AS in hnRNPC KD cells (**Fig. 8c;**
570 **Supplementary Data 8**). We confirmed the importance of hnRNPC depletion in exon inclusion by
571 visualizing the splice junction of selected transcripts belonging to this category and by highlighting
572 hnRNPC binding sites on those transcripts (**Fig. 8d, e**).
573
574 Taken together, these results indicate that mechanical cues induce hnRNPC shuttling to the
575 sarcomeres, where the RBP localizes in close proximity to the translation apparatus. A reduction
576 in hnRNPC nuclear localization and in its contribution to the splicing process affect the AS of
577 mechanosensitive transcripts and RNAs involved in cardiovascular diseases.

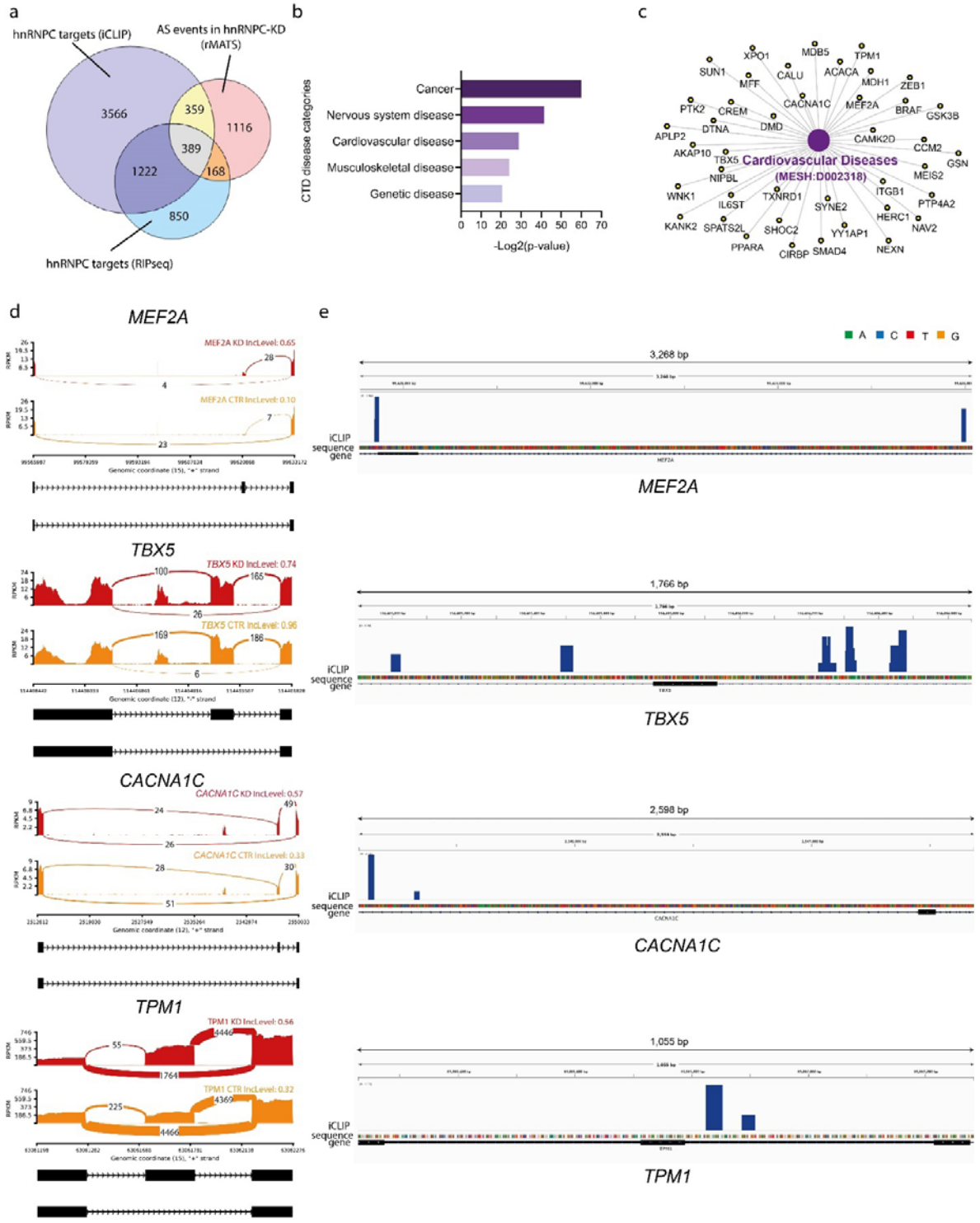


Figure 8. hnRNPC regulates AS of genes involved in cardiovascular diseases. a) Venn diagram representation of the transcripts common to the following datasets: iCLIP-seq in NHDFs, RNAseq AS-analysis in hnRNPC KD NHDF and hnRNPC RNA-IP in failing human hearts. **b)** Gene Ontology (GO) analysis of the 389 transcripts common to the three datasets as obtained by Comparative Toxicogenomics Database (CTD). **c)** GO network representation of the transcripts belonging to Cardiovascular Disease (MESH: D002318) category and common to the three datasets analyzed: iCLIP-

585 seq, AS (rMATS) in *HNRNPC* KD NHDF and hnRNPC RNA-IP in failing human hearts. **d)** Sashimi plots depicting
586 representative skipped exon AS events in *MEF2A*; *TBX5*; *CACNA1C* and *TPM1* belonging to Cardiovascular Disease
587 category of the CTD database. **e)** Individual gene representation of hnRNPC binding: the iCLIP average (N = 3) is shown
588 in blue. See also **Supplementary Data 6-8**.
589

590 **DISCUSSION**

591 Cardiac pathologies are characterized by a profound modification of the composition and
592 mechanics of the local ECM — a phenomenon referred to as ventricular remodeling. This process
593 impairs cardiomyocyte contractility and thus contributes to the progressive deterioration of heart
594 function [5]. The active cardiomyocyte response to ventricular remodeling is considered a
595 compensatory mechanism that aims to minimize the detrimental effects of the increased
596 biomechanical stress on cardiac output, while protecting the integrity and the pumping activity of
597 the organ [59].
598
599 Here we performed an *in silico* analysis of published expression profiling array datasets obtained
600 from ischemic and non-ischemic heart, with the aim of identifying molecular mediators that help
601 ensure cell adaptation to the new demands of the pathological organ by reshaping gene
602 expression. We observed a general upregulation of RBP expression in the pathological heart in
603 humans and in mice, independently of the etiology of the pathology. We identified hnRNPC among
604 the RBPs consistently altered in the diseased heart; the upregulation of this abundant nuclear
605 protein, which has so far mainly been studied for its role as a splicing factor [28–30], has been
606 independently confirmed by single cell RNA sequencing in cardiomyocytes [34]. The expression of
607 hnRNPC gene was found consistently upregulated in pathological heart, where higher
608 concentration of the protein suggest post-transcriptional processes might be at play to increase
609 protein stability.
610
611 We took hnRNPC forward for further analyses – employing quantitative proteomics, super-
612 resolution microscopy and PLA to disclose that hnRNPC shuttles out of the nucleus and localizes to
613 the sarcomeres of cardiomyocytes in the pathological heart. We confirmed this observation by
614 biochemical analyses, and found that the protein settles at the Z-disc, where it physically interacts
615 with components of the contractile apparatus, including Troponin T2, PDLIM5, FHL2 and MYH7.
616
617 hnRNPC upregulation has been associated with different pathologies, including atherosclerosis
618 and pre-atherosclerotic intimal hyperplasia [33], neurodegenerative diseases [31] and some forms of
619 cancer (e.g. gastric cancer) [60]; however, modifications in its localized function have not been
620 described in pathological conditions. Indeed, most hnRNPs shuttle between the nucleus and the

621 cytoplasm; hence their interaction with specific binding partners can be considered as an indicator
622 of their function at specific cell compartments. Interestingly, in chemoresistant gastric cancer,
623 hnRNPC was found upregulated and localized to the cytoplasm and membrane, but its function in
624 these compartments was not questioned [60]. Our mass spectrometry analysis of hnRNPC-
625 interacting proteins in diseased human heart samples confirmed that hnRNPC protein interacts
626 with the spliceosome, as previously demonstrated [61]. However, the presence of spliceosome
627 components was reduced in hnRNPC interactome in failing hearts compared to healthy hearts.
628 Interestingly, the presence of proteins belonging to the cytoskeleton, the sarcomere and the
629 ribosome specifically in the failing heart interactome suggested hnRNPC activity might be modified
630 in pathological conditions.

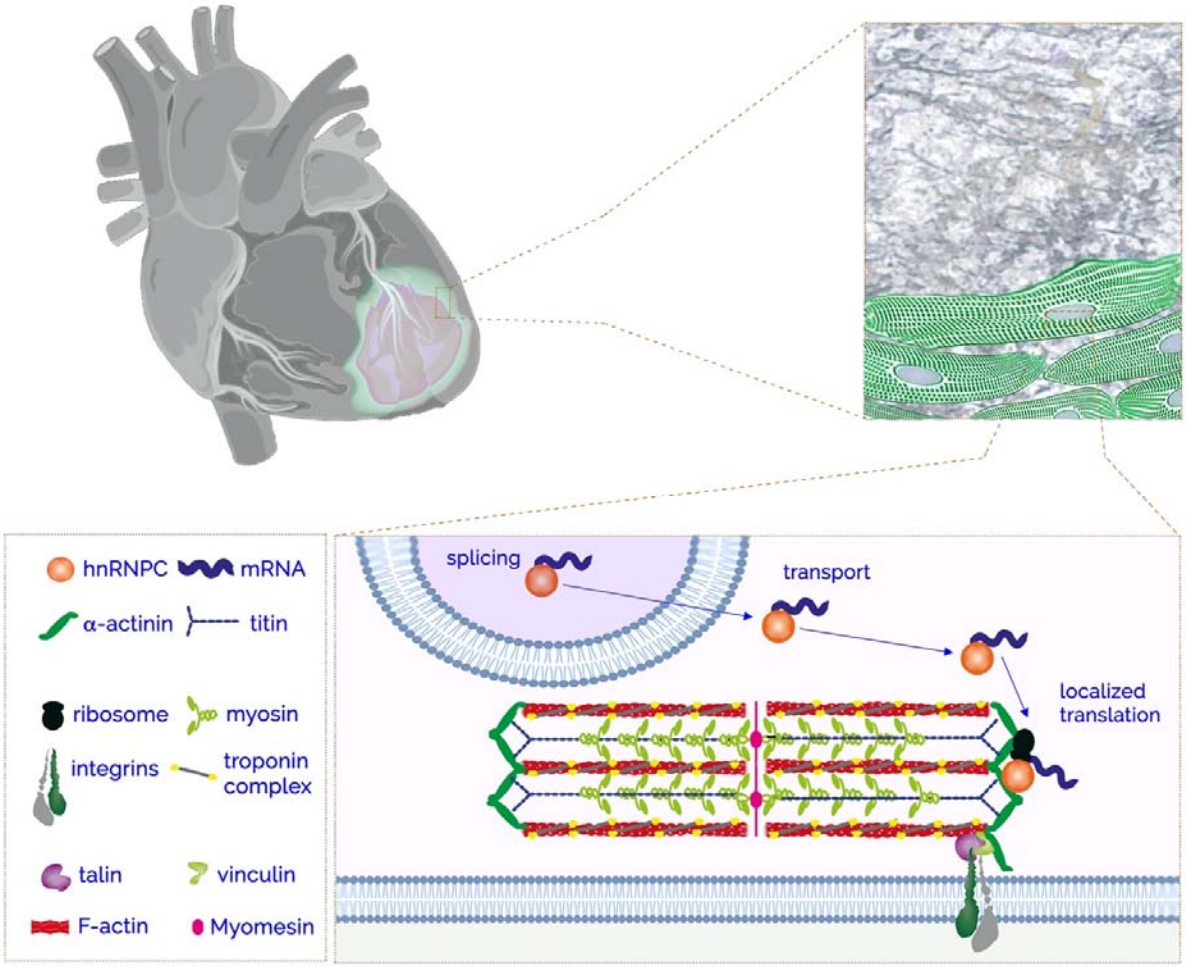
631 To determine how RBP function changes in diseased heart, we performed RIP-seq and identified
632 several specific exon-enriched hnRNPC-bound RNAs in the failing heart, mostly encoding for
633 sarcomeric proteins. Some of these mRNAs, including titin (*TTN*), cardiac muscle alpha actin
634 (*ACTC1*) and cardiac troponin I3 (*TNNI3*) are translated locally at the sarcomeric site [42,43]. Together
635 with the evidence that hnRNPC interacts with ribosomal proteins at the sarcomere, these data led
636 us to hypothesize that hnRNPC shuttling to the contractile apparatus in the failing heart could be
637 associated with the localized translation of transcripts encoding for contractile proteins.

638 Localized translation has been described in different cell types, including neurons [62], fibroblasts [63]
639 and myoblasts [64], as a strategy aimed at maximizing the synthesis of needed proteins directly at
640 the site of exploitation. Indeed, hnRNPC was previously found in RNA granules in neurons together
641 with mRNAs involved in synaptic remodeling, which are transported to the subsynaptic site and
642 translated in response to an input [65]. Sarcomeres serve as sites of active translation in the rat
643 heart, where the translation machinery and mRNAs encoding for sarcomeric proteins are
644 distributed in a cross-striated pattern [43]. We used iPSC-derived cardiomyocytes to visualize the
645 active incorporation of PMY (an indicator of active translation) at the sarcomere, where ribosome
646 components are found. By coupling decellularized extracellular matrices obtained from healthy
647 and diseased human hearts with ribopuromycilation and PLA, we found that the pathological ECM
648 induces hnRNPC recruitment to the sarcomeric active sites of translation.

649 Because cardiac ECM remodeling is associated with mechanical stress, we used 3D hydrogels with
650 controlled stiffness and micropatterned surfaces to demonstrate that a fraction of hnRNPC can

651 shuttle outside of the nucleus when the transmission of intracellular tension is hindered. We
652 confirmed that its shuttling to the cytoplasm is precipitated in constrained cells not able to
653 propagate intracellular tension. It thus seems that the mechanical stress associated with ECM
654 remodeling serves as a switch for hnRNPC redistribution from the nucleus to the sarcomere,
655 presumably to modulate its role in RNA homeostasis. Given hnRNPC shuttling out of the nucleus
656 and its reduced interaction with spliceosomal components, we investigated the effect of hnRNPC
657 depletion on pre-mRNAs AS. To mimic a situation in which hnRNPC function in splicing is reduced,
658 we induced its shuttling from the nucleus by pharmacological inhibitors of tension in NHDFs,
659 which are known to be extremely sensitive to mechanical cues. Together with the results obtained
660 by hnRNPC knock down in the same cell type and iPSC-derived cardiomyocytes, these experiments
661 indicate hnRNPC depletion from the nucleus affects the AS of mechanosensitive transcripts and
662 genes involved in cardiovascular diseases. Next, we used iCLIP-seq to confirm the presence among
663 hnRNPC direct targets of components of the Hippo pathway, a molecular axis involved in
664 organogenesis and whose dysregulation has been associated to numerous pathologies [66],
665 including those affecting the heart [22,52,55,67]. In particular, we found that the mechanically induced
666 hnRNPC displacement from the cell nucleus or its depletion affect the inclusion of YAP1 exon 4.
667 This splicing event is of particular relevance, since the exon encodes for the second WW domain, a
668 domain known to directly control the protein interaction with TEAD transcription factor and thus
669 its DNA binding activity [49]. This switch towards the expression of YAP1 isoforms with two WW
670 domains (YAP1-2) has been recently described by our research group in human pathological hearts
671 [56].
672 Going forward, questions remain as to which upstream factors are involved in hnRNPC regulation
673 in failing hearts and what is the specific role of hnRNPC at the translation sites
674 (repressor/activator).
675 Indeed, although our data suggest an involvement of hnRNPC in localized translation at the
676 sarcomeric site in HF, future work is needed to elucidate whether hnRNPC plays a direct role in
677 this process and its relevance in the establishment and progression of cardiac diseases.
678 The presence of the hnRNPC transcript in our RIP- and iCLIP-seq analyses suggests that hnRNPC
679 could regulate its own RNA post-transcriptionally. RBPs were previously proposed to bind and
680 regulate the fate of their transcripts in an autoregulatory feedback [68]. Further studies are thus

681 needed to elucidate whether hnRNPC adopts this mechanism to regulate its expression and
682 function in cardiac pathologies.
683 In conclusion, our results on the regulation of hnRNPC localization and function unveil a novel
684 mechanism by which RNA homeostasis could undergo mechanical regulation following
685 pathological cardiac ECM remodeling (**Fig. 9**). Future experiments that study the mechanical
686 control of RNA homeostasis and the players involved are now warranted, as the ability of RNA
687 binding proteins (RBPs) to serve as possible mechanosensors could explain how ECM mechanics
688 can directly affect cell differentiation and function by controlling RNA fate in a stage-specific
689 manner.



690

691 **Figure 9: Graphical representation of hnRNPC displacement in the pathological heart.**

692

693 **Methods**

694 **Study approval**

695 This study was performed in accordance with the ethical standards of the Centre of Cardiovascular
696 and Transplantation Surgery and was approved by the Ethics Committee of St. Anne's University
697 Hospital, Brno, Czech Republic. The experiments were done according to the Declaration of
698 Helsinki (2000) of the World Medical Organization. Experiments involving mice were approved by
699 the Instituto de Biologia Molecular e Celular – Instituto de Engenharia Biomédica (IBMC-INEB)
700 Animal Ethics Committee and the National Direção Geral de Veterinária (permit no: 022793), and
701 conformed with Directive 2010/63/EU of the European Parliament.

702

703 **Patient-derived heart samples**

704 Diseased heart tissue samples (N=17) were obtained from left ventricle of patients diagnosed with
705 end-stage heart failure undergoing cardiac transplantation or ventricular assist device
706 implantation. The classification of ischemic (N = 8) and non-ischemic (N = 9) heart failure is defined
707 based on the patient anamnesis, as per the International Statistical Classification of Diseases and
708 Related Health Problems (ICD-10). Healthy hearts (N=3) obtained from deceased organ donors
709 without a history of cardiac disease were used as a control (**Supplementary Table 1)**.

710

711 **Mouse model of myocardial infarction (MI)**

712 MI was experimentally induced by ligating the left anterior descending coronary artery in
713 C57BL/6 adult mice (9-10 weeks), as previously described [36] (**Supplementary Methods**). Mice
714 hearts cohort was composed of 4 days post-MI (acute MI), 21 days post-MI (chronic MI), sham-
715 operated (no ligation of the coronary artery) (**Supplementary Fig. 3b**). All animal experiments
716 were approved by the local Ethics Committees.

717

718 **Proximity Ligation Assay**

719 The proximity ligation assay (PLA) was performed on fixed (4% PFA) heart tissue slices and cells
720 using DuoLink PLA technology probes and reagents (**Supplementary Table 2**) and following the
721 manufacturer's protocol (**Supplementary Methods**).

722

723 **Ribopuromycilation**

724 Ribopuromycilation protocol (RPM) to visualize active sites of translation was performed following
725 the original RPM protocol – Procedure A[66,67] (**Supplementary Methods**; **Supplementary Fig. 5d**).
726 The RPM experiments were performed on beating cardiomyocytes between days 20 and 30 of
727 differentiation.

728

729 **Cell culture, differentiation, transfection, treatment and micropatterning**

730 Culture of the human induced pluripotent stem cell line DF 19-9-7T (iPSC) (WiCell, Madison, WI,
731 USA) and normal human dermal fibroblasts (NHDF, ATCC) as well as cardiac differentiation is
732 detailed in **Supplementary Methods**. Cardiac troponin T (**Supplementary Table 2**) was used as
733 sarcomeric marker of iPSC-derived cardiomyocytes. Treatment of cells with inhibitors of
734 cytoskeletal tension, 3D cultures in fibrin gels and micropatterning are detailed in **Supplementary**
735 **Methods**.
736 *HNRNPC* knockdown was performed as previously described[27]. Detailed procedures for siRNA
737 transfection, qRT-PCR and western blotting are described in **Supplementary Methods**.

738

739 **Protein Immunoprecipitation (IP)**

740 For the IP of hnRNPC-binding proteins, 100 mg of tissue from the human heart apex was used for
741 each IP and control sample (**Fig. 2a**). The sample was washed in ice-cold PBS, dissected and
742 mechanically homogenized in 1ml of Lysis Buffer using 3.0 mm Zirkonia beads and Beadbug
743 homogenizer. Dynabeads Protein G (50 µl/sample) were incubated with 200 µl primary antibody
744 (5 µg/sample) for 45 min at 4 °C. Heart lysates were incubated with antibody conjugated
745 Dynabeads overnight at 4°C. The proteins were then eluted by incubation with 100 µl 8M Urea on
746 a shaker (20 min at RT). The eluates were then processed for mass spectrometry analysis
747 (**Supplementary Methods; Supplementary Table 2)**.

748

749 **Mass spectrometry**

750 After protein immunoprecipitation, the samples were digested with trypsin using the FASP
751 method. The digested peptides were labeled using TMT pro16-plex isobaric mass tagging reagents
752 (Thermo Scientific) and the fractions were analyzed on an Orbitrap Fusion™ Lumos™ Tribrid™
753 mass spectrometer interfaced with an Easy-nLC1200 liquid chromatography system (Thermo
754 Fisher Scientific). The IP/IgG abundances were calculated for each sample. A protein was

755 considered successfully immunoprecipitated when a ratio > 1.5 was detected in both biological
756 replicates. See also **Supplementary Methods** and **Supplementary Table 2**.
757
758 **RNA Immunoprecipitation (RIP)**
759 To immunoprecipitate hnRNPC-binding RNAs, 100 mg tissue from the human heart apex was used
760 for each IP and control sample. In brief, the heart samples were dissected, cross-linked in 1% (v/v)
761 formaldehyde, mechanically dissociated in 1 ml Polysome Lysis Buffer (PLB) using 3.0 mm Zirkonia
762 beads and a Beadbug homogenizer and sonicated. Dynabeads Protein G (100 µl/sample) were
763 incubated with 10 µg of primary antibody (sc-32308, sc-2025) for 1 h at 4 °C. Cross-linked lysate
764 was incubated with antibody-conjugated Dynabeads overnight at 4°C. Reverse cross-linking was
765 performed and the proteins were digested by incubation with Proteinase K (60 µg/sample) for 1.5
766 h at 55 °C on a shaker. RNA extraction was then performed following standard phenol:chloroform
767 phase separation. The protocol is depicted in **Fig. 4a** and detailed in **Supplementary Methods**.
768
769 **RNA sequencing, RIP-seq and alternative splicing (AS) analysis**
770 A sequencing library was prepared using a NEBNext Ultra II Directional Kit (New England Biolabs,
771 MA, USA). For the RIP-sequencing, the immunoprecipitated RNA was used as an input into the
772 total RNA library preparation protocol; control input RNA was first rRNA depleted using QIAseq
773 Fastselect HMR Kit (Qiagen, Germany). For the alternative splicing analysis, 200-300 ng total RNA
774 was used as an input into the polyA enrichment module protocol. Samples were fragmented and
775 transcribed into cDNA. Following universal adapter ligation, the samples were barcoded using dual
776 indexing primers. The RNA resultant from RIP of heart tissue or resultant from NHDF transfection
777 with hnRNPC siRNA and the respective control construct was sequenced on an Illumina Nextseq
778 550 sequencer (Illumina, CA, USA) to 25-35 million single-end 75bp reads and >50 million paired-
779 end 75 bp reads per sample, respectively. Detailed sequencing procedure and analysis are
780 available in the expanded methods section (**Supplementary Methods; Supplementary Table 2**).

781 **Individual-nucleotide resolution UV crosslinking and immunoprecipitation (iCLIP) of**
782 **hnRNPC1/C2**

783 NHDFs were grown to 85-90% confluency and exposed to 150 mJ/cm2 at 254 nm in a Stratalinker
784 2400 on ice. Cell pellets were resuspended in 1ml of ice-cold lysis buffer (**Supplementary**

785 **Methods**). The insoluble fraction was removed by centrifugation at 20.000g for 20 min at 4°C and
786 the supernatant was used for the iCLIP experiment. Dynabeads Protein G (Invitrogen) (100
787 µl/sample) were incubated with 15 µg of anti HNRNPC1/C2 antibody (Santa Cruz) in a total volume
788 of 100 µl of lysis buffer for 1 h at RT. Antibody coupled beads were mixed with 1ml of soluble cell
789 lysate and incubated for 1hour on a rotator at 4°C. Dephosphorylation, radiolabeling (γ-ATP) and
790 3' end adapter ligation was carried out on the protein-RNA complex. The resultant Protein-RNA
791 complex was resolved on a gradient NuPAGE gel and blotted onto nitrocellulose membrane. Post-
792 autoradiography the membrane was cut between 48-100kDa size and Proteinase K treatment was
793 performed to isolate RNA. The cDNA libraries were prepared as previously described [69] with slight
794 modifications. The purified library was analyzed by 75bp single end high-throughput sequencing at
795 Illumina HiSeq2500. Protocol and reagents are detailed in **Supplementary Methods and**
796 **Supplementary Table 2**. A schematic representation of the protocol can be found in
797 **Supplementary Fig. 7f**.
798
799 **Decellularization of human myocardial tissue and preparation of ECM coating**
800 The decellularization protocol was performed as previously described[23,70] **(Supplementary**
801 **Methods)**. The ECM-enriched scaffold was mechanically disrupted and used as 2D coating for cell
802 culture (**Fig. 5c, d**).
803
804 **Microscopy and image analysis**
805 Histology, immunohistochemistry and immunocytochemistry are detailed in **Supplementary**
806 **Methods**. A Zeiss LSM 780 confocal microscope with 40x (1.3 NA) oil-immersion or 20x air (0.8 NA)
807 objective lenses was used for image acquisition. ImageJ and Imaris software were used for image
808 quantification (**Supplementary Methods**). For the Masson's Trichrome analysis, a slide scanner
809 Zeiss Axio Scan Z1 microscope was used to visualize whole tissues using the bright-field mode and
810 a 10x objective. Super-resolution imaging was performed using a 3D-SIM Deltavision OMX with a
811 60x objective (1.42 NA).
812
813 **Statistical Analyses**
814 All data are expressed as the mean ± standard deviation (S.D.) unless otherwise specified. The
815 statistical analyses were performed by using GraphPad Prism v. 6.0 software package. The null

816 hypothesis was rejected when $P < 0.05$. The number of biological (N) and technical (n) replicates
817 and the statistical tests used are indicated in figure legends and in the Source Data file.

818 **Data Availability**

819 All data supporting the findings of this study are available as Supplementary Data. Sequencing
820 data have been deposited to GEO database under the reference series GSE155474 and
821 GSE169068. The Mass Spectrometry proteomics data have been deposited to the
822 ProteomeXchange Consortium via the PRIDE partner repository under the dataset identifier
823 PXD020663.

824

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851

852 **Author contributions**

853 FM: Conceptualization, Experimental Design and Execution; ARP: Experimental Execution; VHE:
854 Bioinformatics analysis; NMV, SV: iCLIP-sequencing; HD: Experimental Execution; VHO: human
855 tissue harvesting and patient anamnesis; FC, FCAR: Superresolution microscopy, manuscript
856 drafting; WSA, APG: RNA-IP protocol setting and data interpretation; MAOC: paper
857 conceptualization and drafting; SP, GF: project supervision, paper conceptualization and drafting.

858

859 **Declaration of interests**

860 The authors declare no competing interests.

861

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