Hsf1 and the molecular chaperone Hsp90 support a "rewiring stress response" leading to an adaptive cell size increase in chronic stress

Short title: Cells adapt to chronic stress with size increase

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Abstract

Cells are exposed to a wide variety of internal and external stresses. Whereas many studies have focused on cellular responses to acute and severe stresses, little is known about how cellular systems adapt to sublethal chronic stresses. Using mammalian cells in culture, we discovered that they adapt to chronic mild stresses, notably proteotoxic stresses such as heat, by increasing their size and translation, thereby scaling the amount of total protein. These adaptations render them more resilient to persistent and subsequent stresses. We demonstrate that Hsf1, well known for its role in acute stress responses, is required for the cell size increase, and that the molecular chaperone Hsp90 is essential for coupling the cell size increase to augmented translation. We term this translational reprogramming the "rewiring stress response", and propose that this protective process of chronic stress adaptation contributes to the increase in size as cells get older, and that its failure promotes aging.

Introduction

Stress has shaped the interactions between organisms and their environment since the origin of the first cell (*Kultz, 2020b*). Throughout their lifetime, cells and organisms are exposed to different kinds of environmental and cell-intrinsic stresses such as heat, genotoxic agents, oxidative agents, alterations of external pH, hypoxia, nutrient deficiency, osmotic changes, protein misfolding and aggregation, and various pathological conditions (*Kristensen et al., 2020*). While intense acute stresses can cause lethal damage, in a physiological environment, cells are mostly exposed to mild and often chronic stresses, so that cells have a chance to adapt (*Bijlsma and Loeschcke, 2005; Kultz, 2020a*). For example, body or tissue temperature increases of only a few degrees constitute a mild heat stress at the cellular level (*Mainster et al., 1970; Evans et al., 2015; van Norren and Vos, 2016; Baker et al., 2020; Rzechorzek et al., 2022*). Similarly, the ecosystem may contain several pollutants that cause a continuous mild oxidative stress (*Taborsky et al., 2021*). Cells and organisms cannot easily escape such stresses and must therefore adapt.

Because cells and organisms need to live with such lifelong stresses, evolution has endowed them with highly conserved stress response pathways (*Liu et al., 1997*). Heat-shock factor 1 (Hsf1), a transcription factor, is the master regulator of cellular stress management (*Li et al., 2017*). Hsf1 governs a protective transcriptional program known as the heat-shock response (HSR), which involves the selective transcription of stress response proteins known as heat-shock proteins (Hsps), most

of which are molecular chaperones (*Lindquist and Craig, 1988; Richter et al., 2010; Vihervaara and Sistonen, 2014*). Molecular chaperones collectively promote the initial folding of newly made proteins, the refolding of unfolded or misfolded proteins, the dissociation of protein aggregates, and the degradation of terminally misfolded or aggregated, and potentially toxic, proteins (*Hartl et al., 2011*). Overall, this process of maintaining protein homeostasis is known as proteostasis. During acute stress of different kinds, apart from the Hsf1-mediated transcriptional response, eukaryotic cells elicit a specific adaptive stress response, known as the integrated stress response (ISR). The ISR reprograms translation to avoid overloading the proteostasis system (*Persson et al., 2020*). In the ISR, global cap-dependent protein translation is reduced, while the translation of some proteins, needed to deal with the challenge, is specifically enhanced.

Hsps are not only required for cells to respond to stress. Even without stress, cells need a basal level of Hsps for folding nascent polypeptide chains, refolding partially denatured or misfolded proteins, or for their degradation (*Balchin et al., 2016*). Hsps are categorized into different families based on their molecular weights. Among those, Hsp90 is essential for the viability and growth of eukaryotic cells and organisms, and it is a major hub of cellular proteostasis through a large number of client proteins (*Taipale et al., 2010; Echeverria et al., 2011; Johnson, 2012; Fierro-Monti et al., 2013; Bhattacharya et al., 2020; Bhattacharya and Picard, 2021*). It is one of the most abundant proteins in cells (*Nollen and Morimoto, 2002; Mollapour et al., 2010; Finka and Goloubinoff, 2013*), and in mammals, a large fraction of it is indeed required during prenatal development, and for tissues and cells (*Bhattacharya et al., 2022*). In mammalian cells, there are two different cytosolic

Hsp90 isoforms, which are encoded by two different genes, Hsp90α (encoded by the gene *HSP90AA1)* and Hsp90β (encoded by *HSP90AB1*) (*Sreedhar et al., 2004*). Hsp90α is the more stress-inducible isoform whereas Hsp90β is more constitutively expressed. There are extensive overlapping functional similarities between the two Hsp90 isoforms, which are 84% identical in humans, but there is also some evidence for isoform-specific functions (*Maiti and Picard, 2022*). However, to what extent mammalian cells require these two isoforms during stress adaptation is not clear.

Cellular stress responses, molecular chaperones, and proteostasis are interconnected with cellular and organismal aging (*Labbadia and Morimoto, 2015; Hipp et al., 2019; Bhattacharya and Picard, 2021*). Although the process of aging is broadly influenced by genetic, epigenetic, and extrinsic factors, it is increasingly apparent that most of these factors ultimately interface with cellular stress response mechanisms (*Kourtis and Tavernarakis, 2011; Vilchez et al., 2014; Lu et al., 2020*). One of the hallmarks of aging is cellular senescence (*Childs et al., 2015; McHugh and Gil, 2018; Calcinotto et al., 2019*), which is characterized by a number of features, including a larger cell size. Earlier studies claimed that, as cells become senescent, they stop dividing. But since cell growth, defined as the addition of cell mass, continues, senescent cells become larger (*Hayflick and Moorhead, 1961; Mitsui and Schneider, 1976; Adolphe et al., 1983; Yang et al., 2011*). That is why cells of older mammalian indiviuals are often two or three times larger than those of younger ones (*Cristofalo and Kritchevsky, 1969; Treton and Courtois, 1981; Demidenko and Blagosklonny, 2008; Mammoto et al., 2019*). Remarkably, recent studies have established that a larger cell size is not a consequence, but rather the cause of senescence. If cells fail to scale the amount of their macromolecules as

they become larger, this causes cytoplasmic dilution and induces senescence (*Neurohr et al., 2019; Lanz et al., 2022*). The question remains why mammalian cells increase their size to the point of becoming senescent. There are a number of indications that some cells increase their size in response to external cues or functional needs (*Dhawan et al., 2007; Boehlke et al., 2010; Hall et al., 2012; Samak et al., 2016*). However, it is poorly understood whether the cell size itself is the target of regulation or a byproduct of some other adaptation (*Ginzberg et al., 2015*).

Here we report that mammalian cells gradually enlarge their size to adapt to chronic mild stress (or "chronic stress" for short). Whereas the cellular response to acute stress has been extensively characterized (*Richter et al., 2010; Somero, 2020*), little is known about how cells adapt to chronic mild stress and to what extent certain Hsps or molecular chaperones are involved. We exposed cells to several chronic stresses to investigate these issues, notably also the role of specific cytosolic Hsp90 isoforms. We discovered that in response to chronic stress cells increase their size in an Hsf1-dependent fashion, and that their adaptation to chronic stress is different from the response to acute stress. Unlike acute stress, which causes a shutdown of global translation to reduce the protein burden, chronic stress induces global translation to increase the amount of total proteins. Hsp90, irrespective of its isoform, supports the increase in translation and, through this adaptation, the cell size increase.

Results

A mammalian cell model to study the effects of chronic mild stress

To study how mammalian cells adapt to chronic stress, we applied several stressors, such as mild heat shock (HS), hypoxia, sodium arsenite, and the protein misfolding agent L-azetidine-2-carboxylic acid (AZC), to several cell lines (Figure 1A - figure supplement 1A). To gage the level of chronic stress, which we would consider mild for a given stressor, we decided that it would be the duration or the intensity, where cell death is ≤10%. To determine the chronic mild HS conditions, we kept all cell lines at different temperatures for seven days. We found the threshold for chronic HS to be 39 °C for HEK293T (HEK) and HCT116 cancer cells, and 40 °C for A549 cancer cells and the normal epithelial cell line RPE1. For hypoxia, we determined that 4 days of hypoxia (1% oxygen) are the appropriate threshold for chronic hypoxic stress. For both sodium arsenite and AZC, 5 μM for 5 days is an appropriate threshold for oxidative and proteotoxic stresses, respectively.

Chronic mild stress causes an increase in cell size

While we were checking cell death by flow cytometry to optimize the threshold for the different chronic stresses, we noticed that in all types of chronic stresses, cells increased their size over time (Figure 1B - figure supplement 1B), as indicated by the forward scatter (FSC) intensity, which is proportional to the diameter (d) of the cell (*Tzur et al., 2011*). Measuring the cell diameter by microscopy (figure supplement 1C) confirmed the size increase suggested by the FSC values after 7 days of mild HS, verifying that FSC values can be used as a proxy for cell diameter. Assuming cells in suspension are a round ball, note that a 10% increase in cell diameter translates to more than a 30% increase in cell volume since volume = $(4/3) \times \pi \times (d/2)^3$. It is well supported that mammalian cells control their size via modulation of

the cell cycle (*Ginzberg et al., 2015; Miettinen et al., 2017; Varsano et al., 2017; Cadart et al., 2018*). Specifically, a lengthening of the G1 phase is responsible for cell size increases. Hence, we determined whether this increase in cell size is caused by a cell cycle arrest. After seven days of chronic HS, we checked the cell cycle profiles of HEK and A549 cells (Figure 1C). Interestingly, the two cell lines showed different cell cycle patterns in chronic HS. While A549 cells have a slightly increased G1 population, HEK cells maintain a similar cell cycle profile. We repeated the analyses at different time points of chronic HS and found that at the initiation of chronic stress, there is a substantial number of cells in the G1 population for both cell lines (Figure 1D). Over time, the cell cycle stabilizes in a cell line-specific fashion, suggesting that cells are able to adapt to chronic HS. Importantly, despite the stabilization of the cell cycle during continued chronic stress, cells maintain an enlarged cell size (Figure 1E) with an almost equal proliferation rate (Figure 1F-G - figure supplement 1D) in the beginning of the stress or after 7 days of stress adaptation. To check if this cell size enlargement is reversible, we put the cells back at 37°C after 7 days of chronic HS. During this recovery period at 37°C, both HEK and A549 cells returned to their usual size (Figure 1H), and A549 cells also reverted back to a normal cell cycle profile (Figure 1I - figure supplement 1E).

A minimal level of Hsp90 is required for chronic stress adaptation

A key question is how cells cope with and adapt to these chronic stresses. A complex network of molecular chaperones and their respective co-chaperones acts as a buffer to the myriad of changes during stress (*Bijlsma and Loeschcke, 2005; Richter et al., 2010; Horwich, 2014; Labbadia and Morimoto, 2015*). The cytosolic

Hsp90 isoforms are the most abundant molecular chaperones (*Jakob and Buchner, 1994; Mayer and Bukau, 1999; Young et al., 2001; Picard, 2002*). Since Hsp90 had been found to support the size increase of cardiomyocytes following myocardial infarction (*Tamura et al., 2019*), we wondered whether it plays any role in the stress-induced cell size increase, and if so, which one of the two cytosolic Hsp90 isoforms, that is Hsp90α or Hsp90β (*Maiti and Picard, 2022*). To address this, we used our human Hsp90α knockout (KO) and Hsp90β KO HEK and A549 cells (Figure 2A) (*Bhattacharya et al., 2022*). Note that hereafter we will refer to cells lacking one *or* the other isoform as Hsp90α/β KO cells and that their basal cell sizes are essentially indistinguishable from those of their respective wild-type cells. We observed that the loss of either one of the two isoforms makes them vulnerable to different chronic stresses (Figure 2B - figure supplement 2A). However, even in the absence of one Hsp90 isoform, cells enlarged their size during chronic HS, and hypoxic and oxidative stress conditions (Figure 2C-D - figure supplement 2B-C). This suggests that the stress-induced cell size increase is not directly associated with a particular cytosolic Hsp90 isoform.

The canonical Hsf1 activity regulates the cell size increase in response to chronic stress

Hsf1 is an evolutionarily conserved transcription factor that mediates the cytoprotective HSR throughout the eukaryotic kingdom (*Anckar and Sistonen, 2011; Gomez-Pastor et al., 2018*). It is well established that Hsf1 activity increases in response to acute stresses (*Li et al., 2017*). During stress, mammalian Hsf1 monomers in the cytosol are activated to form trimers, which localize to the nucleus,

bind DNA sequences known as heat shock elements (HSE), and trigger the transcription of target genes (*Vihervaara and Sistonen, 2014*). It has been proposed that Hsp90 controls Hsf1 activity by titrating Hsf1 under non-stress conditions (*Zou et al., 1998; Leach et al., 2012; Lee et al., 2013; Hentze et al., 2016; Kijima et al., 2018*). Using an Hsf1 reporter plasmid, we found that Hsp90α/β KO cells, and most prominently Hsp90α KO cells, have a higher basal level of Hsf1 activity (Figure 3A). In Hsp90α/β KO cells, the higher basal Hsf1 activity could be due to a larger number of Hsp90-free Hsf1 molecules. We did observe that there is more Hsf1 in the nucleus of Hsp90α/β KO cells in non-stressed conditions (Figure 3B), and yet Hsf1 becomes even more nuclear in cells of all three genotypes during chronic HS (Figure 3B). This also translates to a higher Hsf1 activity, as we could observe with a Hsf1 reporter assay (Figure 3C). To characterize the proteomic changes associated with Hsp90α/β KO and chronic HS, we performed quantitative label-free proteomic analyses of cells maintained in non-stressed conditions, and after one day and four days of HS. The proteomic data confirmed the increased basal Hsf1 activity that we had seen in Hsp90α/β KO cells with the Hsf1 reporter assay. Many proteins whose expression was known to be regulated by Hsf1 proved to be upregulated in Hsp90α/β KO cells (figure supplement 3A and source data 1). Under chronic HS, cells of all three genotypes were able to increase the expression of several Hsf1 target genes (Figure 3D), reminiscent of what we had seen with the Hsf1 reporter assay. Thus, cells are perfectly capable of mounting a HSR in the absence of either one of the two Hsp90 isoforms, suggesting that their increased vulnerability to stress may be due to something else.

To obtain more direct experimental evidence for a role of Hsf1 in the cell size increase induced by chronic HS, we overexpressed WT Hsf1 and a transcriptionally defective Hsf1 mutant (*Kijima et al., 2018*) in HEK, A549, and RPE1 cells. We observed a strong induction of basal Hsf1 activity in cells overexpressing WT Hsf1 but not the mutant form (figure supplement 3B), correlating with an increase in cell size under normal non-stress conditions (Figure 3E). Taken together, our observations suggest a correlation between the canonical transcriptional Hsf1 activity and cell size. We further strengthened this correlation by determining the effect of inducing Hsf1 activity pharmacologically with capsaicin, which is known to trigger a calcium influx and HSR through the vanilloid receptor TRPV1 (*Hagenacker et al., 2005; Bromberg et al., 2013*). We found that A549 cells of all three genotypes display a capsaicin-induced and dose-dependent transcriptional Hsf1 activity (figure supplement 3C) and cell size increase (figure supplement 3D). Collectively, these results indicate that the transcriptional Hsf1 activity is sufficient to cause a cell size increase. To determine whether Hsf1 is necessary for the cell size increase, we used RNA interference to knock down Hsf1 expression in A549 WT and Hsp90α KO cells (figure supplement 3E). Hsf1 knockdown cells exposed to chronic HS failed to display Hsf1 activity (figure supplement 3F), and could not increase their cell size during adaptation to chronic HS (Figure 3F).

So far, we have only shown results obtained with established human cell lines. We also explored the link between Hsp90 and Hsf1 activity in mouse adult fibroblasts (MAFs) established from mice with only a single allele for cytosolic Hsp90 left. These are both homozygous *hsp90α* KO and heterozygous *hsp90β* KO, and will be referred

to as 90αKO 90βHET (*Bhattacharya et al., 2022*). These MAFs proved to be substantially bigger than WT MAFs (figure supplement 3G), and to display a several-fold higher basal Hsf1 activity (figure supplement 3H). It should be emphasized that these MAFs were obtained from adult mice that had escaped the stringent developmental attrition of embryos with this genotype through translational reprogramming of Hsp90β expression (*Bhattacharya et al., 2022*). This may explain why these mutant MAFs, unlike WT MAFs, could not augment their Hsf1 activity nor increase their size any further in chronic HS (figure supplement 3I-J). At this point, we conclude that the HSR correlates with cell size during chronic stress, and that both outcomes are mediated by Hsf1.

Hsp90α/β KO cells overall maintain their chaperome and proteome complexity during chronic stress

Under normal physiological conditions, cells maintain proteostasis through a complex network of molecular chaperones and co-chaperones, a protein collective referred to as the cellular chaperome (*Joshi et al., 2018; Yan et al., 2020*). Cellular adaptation to stress does not only require increased Hsf1 activity, but it is also modulated by complex functional relationships between Hsf1 and the cellular chaperome (*Li et al., 2017*). Even though the HSR in chronic stress is not impaired by the loss of one of the Hsp90 isoforms, Hsp90α/β KO cells gradually die off during the chronic HS adaptation period (Figure 2B). This raises the question whether the chaperome is compromised in the absence of Hsp90α or β. Using the proteomic data sets mentioned above, we focused on the protein levels of all molecular chaperones and co-chaperones at 37°C and in chronic HS at different time points. This analysis

revealed that Hsp90α/β KO cells could still maintain or increase expression of molecular chaperones and co-chaperones during chronic HS (Figure 4A). Immunoblots confirmed the upregulation of the heat-inducible molecular chaperones Hsp90α (in some instances also Hsp90β), Hsp70, Hsp40, and Hsp27 throughout the chronic stress in cells of all three genotypes (Figure 4B - figure supplement 4A). This suggests that the chaperome of Hsp90α/β KO cells is not compromised by chronic stress. Similarly, at the whole proteome level, standardized to the same amount of protein, and although there are genotype-specific differences, the proteome remained complex during chronic stress indicating that proteostasis was largely intact (figure supplement 4B). Next, we analyzed the Hsp90 interactome. We found that the Hsp90α or Hsp90β KO cells could largely maintain the Hsp90 interactors throughout the chronic stress. These data demonstrate that one Hsp90 isoform is sufficient to support most interactors (Figure 4C - figure supplement 4C-D).

To address the protein folding ability of Hsp90α/β KO cells more directly, we performed an *in vivo* refolding assay with exogenously expressed firefly luciferase subjected to unfolding by a short HS at 43 °C. Surprisingly, we found that Hsp90α/β KO cells do even better than WT cells under basal conditions (37° C) (Figure 4D). The KO cells also showed an increased luciferase refolding ability when they were cultured for 2 days at 39 °C prior to luciferase unfolding (Figure 4E). This higher refolding activity of the Hsp90α/β KO cells at 37° C might be due to some other molecular chaperones being more highly expressed than in WT cells (Figure 4B). Similarly, Hsp90α/β KO cells might do better than WT cells under chronic HS because of their ability to further increase the levels of other molecular chaperones,

such as Hsp27, Hsp40, and Hsp70, during chronic HS. So far, these observations suggest that a reduced level of Hsp90 is at least in part functionally compensated by other molecular chaperones in these assays.

A normal level of Hsp90 is required to maintain the cytoplasmic protein density in chronic stress

If Hsp90α/β KO cells do as well or even better than WT cells for almost all parameters investigated so far, what causes them to be more sensitive to stress (Figure 2B)? It is known that when cells grow larger, it is critical for them to maintain a constant cellular protein concentration (*Kempe et al., 2015; Lin and Amir, 2018; Berenson et al., 2019; Lanz et al., 2022*). To achieve this, cells need to increase the total amount of proteins proportionately to their size increase (*Neurohr et al., 2019*), a process that can be referred to as scaling. Uncoupling of protein synthesis and cellular volume causes a dilution of the cytoplasm, which results in cellular senescence and aging. We tested cytoplasmic density by measuring the mobility of EGFP *in vivo* using fluorescence recovery after photobleaching (FRAP) experiments (figure supplement 5A). We calculated the t-half values and diffusion rates (*Persson et al., 2020*), and found that only WT cells could maintain the same cytoplasmic density under chronic HS as at 37 °C (Figure 5A - figure supplement 5B-D). Hsp90α/β KO cells of both cell lines showed lower t-half values and higher diffusion coefficients in chronic stress indicating that they have a reduced cytoplasmic density (Figure 5A - figure supplement 5B-D). This observation suggests that a full complement of cytosolic Hsp90 is necessary to maintain the cytoplasmic density with the increase of cell size in chronic stress. There is no significant difference between

Hsp90α/β KO cells, which indicates that total Hsp90 levels rather than a specific isoform are critical for maintaining the cytoplasmic density.

If the cytosol is more diluted, this should be reflected in the total amount of proteins. Therefore, we collected the same number of non-stressed and stressed enlarged cells after one day and four days of chronic HS, lysed them in the same amount of lysis buffer, and measured the protein concentrations in the lysates. We found that after four days of chronic stress, the total amount of proteins was higher in WT cells, whereas it decreased in Hsp90α/β KO cells (figure supplement 5E). Quantitation by flow cytometric analysis of total cellular protein stained with an amine-reactive dye revealed qualitatively similar results. The total amount of proteins per cell increased with cell size in WT but not in Hsp90α/β KO cells (Figure 5B - figure supplement 5E). These results demonstrate that cells are unable to maintain the ratio of total protein to cell size in chronic stress when Hsp90 levels are reduced.

Normal levels of Hsp90 are required to scale protein biosynthesis during stress-induced cell size enlargement

One of the key features of the acute stress response of mammalian cells is a global inhibition of translation (*Liu et al., 2013; Shalgi et al., 2013; Advani and Ivanov, 2019; Jobava et al., 2021*). We demonstrated here that WT cells exposed to chronic stress increase the total amount of proteins as they get larger, raising the question of how they do it. Revisiting our proteomic data set, we saw that the levels of ribosomal proteins are least reduced in WT compared to Hsp90α/β KO cells under chronic stress (Figure 5C). A reduction of the core machinery of translation may explain why

Hsp90α/β KO cells have decreased amounts of total proteins compared to WT in chronic stress. However, it does not explain the observation of the increased amount of total proteins in WT cells under chronic stress. To address this issue, we checked global translation by labelling nascent polypeptide chains with a fluorescent version of puromycin, which allows measurements for individual cells by flow cytometry. We saw a strong increase of labelled nascent polypeptides in WT cells both on day 1 (figure supplement 5F) and day 4 (Figure 5D) of adaptation to chronic HS. By comparison, Hsp90α/β KO cells failed to maintain the same rate of protein biosynthesis under chronic HS (Figure 5D - figure supplement 5F). While the stress-adapted bigger cells have a higher level of total translation (Figure 5D), it is known that acute HS causes ribosomal dissociation from mRNA, which results in a translational pause (*Shalgi et al., 2013*). Polysome profiling of WT cells adapted to stress for four days showed that the polysome profiles of cells grown at 37 °C or in chronic HS are largely similar (Figure 5E). Similar peaks of single ribosomal particles (40S and 60S), monosomes (80S), and polysomes (both small and large) suggest that the association of ribosomes and mRNAs in WT cells is not affected during adaptation to chronic stress. This raises the question of whether the ISR is not triggered when the stress is chronic. To address this, we did puromycin labeling at earlier time points of chronic HS. We observed that at the beginning of chronic stress (4 h), reminiscent of the ISR (*Persson et al., 2020*), translation is reduced as seen by flow cytometry (figure supplement 5G) and puromycin labelling of nascent chains detected by immunoblotting (figure supplement 5H). Moreover, cells of all three genotypes displayed an increased inhibitory phosphorylation of the eukaryotic translation initiation factor 2A (eIF2α), a hallmark of the ISR (*Pakos-Zebrucka et al.,*

2016; Wek, 2018), after 4 h of HS (Figure 5F - figure supplement 5I). After having been exposed to chronic HS for one day and more, cells increase total translation, to an even higher level than the basal translation at 37 °C (figure supplement 5G), consistent with the higher translation rate observed by puromycin labeling of nascent chains (Figure 5D - figure supplement 5F). As cells remained in chronic HS, the phosphorylation of eIF2α only dropped in WT but not Hsp90α/β KO cells. These findings indicate that at the very beginning of chronic HS, an ISR is induced with the accompanying inhibitory phosphorylation of eIF2α and global reduction of translation. WT cells but not Hsp90α/β KO cells, once adapted to the stress, recover normal or even increased global translation. Translational recovery of WT cells is also reflected in several other translation markers and regulators. We could see an increase in the phosphorylation of mTOR, 4EBP1, and S6 during adaptation to chronic HS (Figure 5G - figure supplement 5I). Thus, it is primarily this recovery, which constitutes a critical and Hsp90-dependent aspect of stress adaptation.

The mTOR complex 1 (mTORC1) is known to regulate cell size by regulating cellular translation (*Fingar et al., 2002*). Hsf1 in a non-transcriptional mode has been linked to regulating organ and cell size by preserving mTORC1 activity (*Su et al., 2016*). And yet, we saw that Hsp90α/β KO cells increase their size in chronic HS despite failing to augment global translation. We therefore determined cell size and translation at different time points following exposure to chronic HS (Figure 5H). In contrast to WT cells for which cell size and translation appear to be coupled, Hsp90α/β KO cells increase cell size while translation is still reduced. Thus, cell size and translation must be coupled for adaptation to chronic stress. It remains to be

seen how Hsp90α/β KO cells manage to increase their size without a concomitant scaling of translation and to what extent the mTORC1-mediated regulation of translation is involved.

Hsp90α/β KO cells are efficient at maintaining cellular proteostasis under normal unstressed conditions

In experiments presented above, we showed that the loss of one Hsp90 isoform does not impair the protein refolding ability (Figure 4D-E), but reduces translation under chronic stress. Proteolysis is complementary to translation and folding, and crucial to prevent cytotoxicity by eliminating damaged proteins (*Hipp et al., 2019*). Cells promote the degradation of terminally misfolded proteins via the autophagy-lysosomal pathway (ALP) or the ubiquitin-proteasome system (UPS) (*Glickman and Ciechanover, 2002; Klaips et al., 2018*). We performed an *in vivo* activity assay for the UPS, which involved the transient expression and flow cytometric quantitation of a degradation-prone ubiquitin-GFP fusion protein (Ub-R-GFP) and its stable counterpart (Ub-M-GFP) as a control (*Dantuma et al., 2000*). We observed no significant differences in the UPS activity of Hsp90α/β KO cells compared to WT cells at 37 °C (figure supplement 6A). We checked the ALP by measuring the autophagic flux using a mCherry-GFP-LC3 reporter (*Leeman et al., 2018*). Here also, we observed that the autophagic flux remains unchanged in Hsp90α/β KO cells (figure supplement 6B). These results lead us to conclude that one Hsp90 isoform is sufficient to maintain cellular proteostasis under normal, unstressed conditions.

A normal level of Hsp90 is required to maintain cellular proteostasis in chronic stress

We recently reported that Hsp90α/β KO HEK cells accumulate insoluble proteins in long-term mild HS (*Bhattacharya et al., 2022*). We therefore checked the above-mentioned cellular proteostasis axes after four days of adaptation to chronic stress. We found that the absence of either one of the two Hsp90 isoforms causes a deficit in UPS activity *in vivo* (Figure 6A) and autophagic flux (Figure 6B). Hsp90α/β KO cells subjected to chronic HS also had reduced proteasomal activity when measured *in vitro* (Figure 6C). When we expressed the aggregation-prone model protein EGFP-Q74 (*Narain et al., 1999*) in stress-adapted Hsp90α/β KO cells, more and larger aggregates of EGFP-Q74 were readily detectable (Figure 6D - figure supplement 6C). This suggests that Hsp90α/β KO cells cannot efficiently maintain proteostasis in chronic stress. Since Hsp90α KO and Hsp90β KO cells are largely affected the same way, we conclude that there is no isoform specificity for maintaining proteostasis during stress, but that total Hsp90 levels above a certain threshold might be the critical parameter.

Enlarged cells are more resistant to subsequent stress

We hypothesized that the stress-induced cell size enlargement is a protective adaptation. To address this, we induced the enlargement or reduction of cell size with different inhibitors and examined how cell size affects cell survivability (Figure 7A). At first, we enlarged the A549 WT and Hsp90α/β KO cells by treating them with a CDK4/6 inhibitor (Figure 7B), which is known to promote a G1 arrest-associated increase in cell size (*Neurohr et al., 2019*). In contrast to what we had seen with

chronic HS, upon becoming bigger in response to treatment with the CDK4/6 inhibitor, Hsp90α/β KO cells were able to scale the amount of total proteins (figure supplement 7A-B). This demonstrates that scaling total protein is possible even in the absence of one Hsp90 isoform and a reduced amount of total Hsp90 when cells are not in chronic HS. We showed above that Hsp90α/β KO cells were dying in chronic HS, possibly because they could not scale their protein with increasing cell size. We therefore wondered whether Hsp90α/β KO cells, enlarged with prior treatment with the CDK4/6 inhibitor, might be more resistant to chronic HS because they would already have scaled their total protein. After treatment with CDK4/6 inhibitors for three days, we washed off the inhibitors and subjected the cells to chronic HS for three days. We observed that cells that were already enlarged due to the CDK4/6 inhibitor treatment did not get even bigger in chronic HS. As predicted, these pre-enlarged Hsp90α/β KO cells were more resistant and less prone to apoptosis and cell death (Figure 7B). Thus, when given a chance to get bigger with protein scaling, even cells lacking one Hsp90 isoform are more resistant to chronic stress.

We further explored the connection between increase in cell size and scaled protein, and stress resistance with other stresses and cell lines. We treated the cells pre-enlarged with the CDK4/6 inhibitor with an acutely toxic concentration of sodium arsenite for one day. Again, pre-enlarged A549 cells of all three genotypes and the normal RPE1 cells were more resistant to this subsequent stress (figure supplement 7C). We then wondered whether reducing cell size would have the opposite effect. We treated HEK and A549 WT, and Hsp90α/β KO cells with rapamycin to inhibit

mTOR-induced cell growth (*Fingar et al., 2002*) (Figure 7C - figure supplement 7D). Cell size was indeed reduced after three days of rapamycin treatment (Figure 7C - figure supplement 7D). Surprisingly, we found that even in the presence of rapamycin cells enlarged their size under chronic HS, albeit not up to the level of cells without rapamycin pretreatment. More of these comparatively smaller rapamycin-treated WT cells were apoptotic than of the bigger cells not treated with rapamycin (Figure 7C - figure supplement 7D). The increased cell death could also be due to the translational inhibition, in light of the fact that WT cells display increased total translation and mTOR activity to adapt to chronic stress (Figure 5G - figure supplement 5I). In contrast, we observed that comparatively smaller rapamycin-treated Hsp90α/β KO cells were less prone to apoptosis than the non-treated bigger cells. It remains to be seen whether the ratio of total protein to cell size is slightly more favorable in Hsp90α/β KO cells under these conditions. To further support the importance of mTOR, we treated the larger cells adapted to chronic HS with rapamycin. We observed that WT cells became more apoptotic when we added rapamycin after three days of stress adaptation (Figure 7C - figure supplement 7D). As rapamycin pre-treatment failed to restrict the cell size increase caused by chronic stress, we then tried to limit the cell size increase with serum starvation (figure supplement 7E). We observed that even serum-starved cells enlarged their size in additional chronic stress as they did with rapamycin. Here again, the size enlargement was not up to the level of non-starved cells. We observed that the serum-starved smaller WT cells died more under stress than the non-starved bigger cells (figure supplement 7E). As with the rapamycin treatment, in most cases, the serum-starved smaller Hsp90α/β KO cells survived better than the bigger non-

starved cells. In both experiments, we did not succeed in preventing the cell size increase upon exposing cells to chronic HS. As a control experiment, we subjected smaller cells obtained with cycloheximide or rapamycin treatment to an acute stress with arsenite for one day. We found that smaller cells were more sensitive to acute stress irrespective of Hsp90 isoform and levels (figure supplement 7F). The above-mentioned control experiments also argue that stress resistance is not *per se* afforded by increased autophagy, as induced by rapamycin, nor by cellular quiescence as induced, for example, by starvation.

We then wondered what would happen if we limited the cell size increase by limiting the available space (Figure 7D). We used RPE1 cells, as these cells always grow in single layers and do not grow on top of each other once they are entirely confluent. We observed that at 37°C, once they become confluent, they do not stop dividing, but become smaller and smaller (Figure 7E-F). In contrast, in chronic HS, over time, they enlarge their size and keep dividing when seeded at low density. Next, we seeded a comparatively higher number of cells, such that the culture plate would already be confluent from the beginning, and put it in chronic HS. We observed that the cells in the 'already-confluent' plate at 37 °C kept dividing and shrinking, without obvious cell death (Figure 7E-F). However, in chronic HS, the cells in the 'already-confluent' plate, while they were initially able to enlarge their size to some extent, when their size eventually shrank because of the limited space, they started dying off (Figure 7F).

Adaptation to chronic stress requires cytosolic Hsp90 above a threshold level irrespective of Hsp90 isoform

So far, our experiments did not reveal any obvious functional differences between the two cytosolic Hsp90 isoforms. This supports the conclusion that the observed phenotypes in chronic stress, rather than being linked to a specific isoform, are due to below threshold levels of total Hsp90. To address this more directly, we exogenously overexpressed Hsp90α or Hsp90β as mCherry or EGFP fusion proteins, respectively, in Hsp90α/β KO cells. This caused an overall increase in total Hsp90 levels (Figure 7G). The transfected cells were subjected to chronic HS. After four days, we checked the scaling of total protein by loading an equal volume of cell lysate on a protein gel (see Materials and Methods for details). We found that when the total levels of Hsp90 are elevated by either one of the two isoforms, Hsp90α/β KO cells are able to scale total protein under chronic HS (Figure 7G). This result complements our previous findings that Hsp90α/β KO cells become more resistant to chronic HS upon increasing total Hsp90 levels, irrespective of Hsp90 isoform (*Bhattacharya et al., 2022*).

Discussion

It is now increasingly recognized that exposure to mild environmental stressors is not necessarily detrimental to the organism. Instead, such experiences may foster a resistant or adapted phenotype through hormesis (*Agathokleous and Calabrese, 2022*). Hormesis is a core mechanism of developmental plasticity by which an

organism's response to a stressor varies with exposure (*Schirrmacher, 2021*). In contrast, hormetic priming is confined to specific temporal windows and can be considered a preparation to cope with stress. The biological process of aging is claimed to be associated with hormesis (*Gems and Partridge, 2008*). Therefore, physiological cellular responses to mild rather than severe stresses may be more important to address in order to comprehend the biology of aging.

Cell size enlargement is a prerequisite for chronic stress adaptation

We report that cells adapt to chronic stress by gradually enlarging their size, through a process coupled with increased translation. Stress-induced cell size enlargement is a step towards stress adaptation as part of an intrinsic stress response. Even when we used inhibitors known for restricting the cell size, chronic stress still induced a cell size increase (Figure 7 - figure supplement 7). This suggests that cell size enlargement is a necessity for cells to adapt to prolonged stress. Cell size enlargement has also been linked to cellular senescence, which is a state of long-term cell cycle arrest (*Childs et al., 2015; McHugh and Gil, 2018; Calcinotto et al., 2019*). In contrast, stress-adapted bigger cells continue to proliferate. It has been reported that bigger cells, when they cannot scale their cellular macromolecules, suffer from cytoplasmic dilution and become senescent (*Neurohr et al., 2019*). The adaptive cell size enlargement in response to chronic stress is coupled with increased translation, which enables cells to maintain their cytoplasmic density and macromolecular crowding. Maintaining macromolecular crowding is necessary to control the kinetics of cellular reactions and to avoid an aging-related deterioration of cellular biochemical processes (*Mourao et al., 2014*). Hence, the adaptive cell size

increase in response to chronic stress is different from that associated with cellular senescence. Our observations demonstrate that the coupling of cell size enlargement and translation is essential for cells to adapt to chronic stress. Failure to do so causes their elimination during stress exposure, as we observed with Hsp90-deficient cells.

Hsp90 enables the rewiring of the stress response

Hsp90-deficient cells subjected to chronic stress suffer from cytoplasmic dilution. For long-term survival under intrinsic or environmentally imposed chronic stress, cells must maintain an equilibrium of protein synthesis, maintenance, and degradation (*Labbadia and Morimoto, 2015; Hipp et al., 2019*). Our results indicate that Hsp90 is a key molecule for sustaining translation under these conditions. Unlike during the ISR, in which global cap-dependent protein translation is specifically reduced by the hyperphosphorylation of eIF2α (*Costa-Mattioli and Walter, 2020; Persson et al., 2020*), during adaptation to chronic stress, we observed a different phenomenon, which we term "rewiring stress response" (RSR). During RSR, cells initially reduce global translation as happens during an ISR. Then, they turn global translation back on, even when they continue to be exposed to the same stress. This leg of the response requires a threshold level of Hsp90. A hallmark of these transitions is the phosphorylation status of eIF2α and its accompanying impact on global translation. At the beginning of a chronic stress, eIF2α is hyperphosphorylated and global translation is inhibited, whereas prolonged exposure to chronic stress results in the reduction of eIF2α phosphorylation and resumption of translation (Figure 5D-F - figure supplement 5F-I). Thus, the dephosphorylation of eIF2α is central to this

phase of the RSR, as it is to terminating the ISR (*Pakos-Zebrucka et al., 2016*). While WT cells switch translation back on, the status of eIF2α phosphorylation and puromycin labeling show that Hsp90α/β KO cells are unable to support this transition, even though they continue to express stress-inducible chaperones and co-chaperones at high levels (Figure 4). It appears that Hsp90-deficient cells are stuck at the ISR stage of the RSR. While the ISR is a powerful survival strategy in acute stress, it fails to support the survival of Hsp90-deficient cells during chronic stress adaptation. The ability to mount a RSR is pivotal for the adaptation of cells to chronic stress. The translational recovery and the expression of some of the stress-inducible genes in response to acute stress of the endoplasmic reticulum and oxidative stress depend on protein phosphatase 1 (PP1) and its regulator GADD34 (*Novoa et al., 2003; Carrara et al., 2017; Krzyzosiak et al., 2018*). However, our proteomic data indicated that there are no significant changes of PP1 or GADD34 protein levels when one compares cells of different genotypes and stress conditions. Hence, what factors and mechanisms allow cells to transition to RSR remains to be discovered. We report here that a threshold level of total Hsp90 is important to turn on the RSR, not the presence of a particular Hsp90 isoform. If one experimentally elevates the levels of either one of the isoforms, cells can activate the RSR (Figure 7G).

Larger cells may be more stress-resistant because of above-threshold levels of macromolecules

When acute stress triggers the ISR, cells only translate selected proteins. With persistent intense stress, the ISR cannot support proteostasis and shifts cells toward apoptosis (*Tian et al., 2021*). When stress is chronic, cells need more than this

limited set of proteins. This is where the RSR comes in, allowing cells to get bigger, and to accumulate more protein molecules, and potentially other macromolecules, per cell. It is conceivable that there is an evolutionarily optimized range or a minimal threshold level for all macromolecules, and that this depends on the specific biological needs of a given cell type subjected to a particular type of stress (Figure 7H). If the absolute numbers per cell of certain molecules are more important than concentration to adapt and to survive under chronic stress, then bigger cells, which have larger stocks of those molecules, may be better at coping with limited damage than smaller cells. This may even apply to proteins involved in translation, including ribosomal proteins, which did not fully scale even in WT cells. As long as individual cells are above the threshold levels for all relevant macromolecules, they can adapt. Hence, growing bigger is an adaptive response that confers higher stress resistance.

This notion is also supported by our recent findings with mouse KOs (*Bhattacharya et al., 2022*). When we reduced the number of alleles for the cytosolic Hsp90 isoforms from four to one, only embryos that could reestablish the threshold levels of Hsp90 protein by translational reprogramming survived and displayed no apparent phenotype, despite the fact that Hsp90 levels were still lower than those of WT littermates (*Bhattacharya et al., 2022*). There is also evidence that cells can maintain favorable macromolecular crowding by reducing the concentration of highly abundant proteins. The mTORC1 pathway modulates the effective diffusion coefficient within the cytoplasm by reducing the number of ribosomes (*Delarue et al., 2018*). This can avoid increasing molecular crowding, which has been shown to hinder the kinetics of biochemical reactions (*Trappe et al., 2001; Zhou et al., 2008; Miermont et al., 2013;*

Mourao et al., 2014). Increased macromolecular crowding might affect protein folding, final shape, conformational stability, binding of small molecules, enzymatic activity, protein-protein interactions, protein-nucleic acid interactions, and pathological aggregation (*Kuznetsova et al., 2014*). Hence, cells that are exposed to prolonged proteotoxic stress might try to maintain a threshold of all the required proteins instead of scaling all proteins at a particular concentration, while tuning molecular crowding to maintain optimal cytoplasmic diffusion coefficients.

Hsf1-dependent cell size enlargement drives the activation of translation in chronic stress

We found that cell size enlargement during chronic stress depends on Hsf1 activity. This is reminiscent of prior evidence that demonstrated that Hsf1 is linked to the regulation of cell size in different tissues in mammals (*Sakamoto et al., 2006; Koya et al., 2013; Su et al., 2016; Obi et al., 2019*). Hsf1 had been reported to maintain cell growth in a noncanonical way by preserving mTORC1 activity and translation by binding and inactivating the kinase JNK, a known inhibitor of mTORC1 activity (*Su et al., 2016*). In contrast, the cell size increase in response to chronic stress appears to be a canonical Hsf1-mediated HSR phenomenon, which is upstream and independent of the scaling of cellular translation. This is supported by several experiments. Hsp90α/β KO cells subjected to chronic stress could increase their size despite reduced translation. Chronic stress still induced an increase of cell size upon inhibition of translation with rapamycin or cycloheximide, or by serum starvation (Figure 7 - figure supplement 7). We conclude from all of these observations that increased translation is not necessary for cells to increase their size under chronic

stress. WT cells start enlarging their size as a response to chronic stress and then translation follows to scale total protein levels. Hsp90α/β KO cells also increase their size in response to stress but fail to couple that to translation, which causes cytoplasmic dilution.

Aging as a failure to adapt to chronic stress

Overall, our findings are relevant to understanding aging. It is well established that mammalian cells get bigger as they grow older (*Cristofalo and Kritchevsky, 1969; Treton and Courtois, 1981; Demidenko and Blagosklonny, 2008; Mammoto et al., 2019*). We speculate that cells enlarge their size with aging as a protective adaptation to accumulating intra- and extracellular stressors. As long as cells manage to scale the biosynthesis of macromolecules such as proteins, their increasing size mitigates the impact of aging. Eventually, the accumulation of stressors cannot completely prevent the development of features of aging.

Our findings may have implications for rejuvenation therapies aimed at delaying or even reverting cellular aging (*Blagosklonny, 2019*). Treatment with the mTORC1 inhibitor rapamycin has been reported to improve the function of aged cells and to lengthen the life span of laboratory animals (*Hansen et al., 2007; Selman et al., 2009; Bjedov et al., 2010*). Despite the low doses that are experimentally used to prevent an age-related decline, there are several adverse side effects. Our data indicate that treatment with mTORC1 inhibitors should be personalized based on the cellular stress level. For healthy cells, where translation plays a vital role in chronic stress adaptation, long-term treatment with rapamycin might affect cellular

homeostasis and precipitate aging, or even induce apoptosis. For aged cells with a weakening proteostatic system, rapamycin may rejuvenate cells by reducing translation and inducing autophagy. This is supported by our observation that Hsp90α/β KO cells, where proteostasis is compromised, rapamycin treatment helped the cells to survive better under chronic stress (see also ref.*Bhattacharya et al., 2022*). We conclude that rather than running the risk of inducing premature aging with prolonged rapamycin treatment from a relatively early age, efforts should focus on developing compounds that induce Hsp90 expression and/or activity, which one could expect to delay aging.

Physiological changes of cell size

Our observations demonstrate that changes of cell size do not have to be the result of physical constraints, but can be a regulated adaptation. There is evidence for changes in cell size that are induced by physiological conditions (*Ginzberg et al., 2015*), and, of course, aging would be one of them. For example, for rat pancreatic β-cells, insulin secretion, metabolic activity, and global protein production rates are positively correlated with cell size (*Bernal-Mizrachi et al., 2001*). In the kidney, epithelial cells modulate their size in response to fluid flow rates (*Boehlke et al., 2010*). Muscle fibers increase their size in an Hsf1-mediated response to heat generated by exercise (*Obi et al., 2019*). Hsf1 null mice cannot increase the size of their skeletal muscle cells (*Koya et al., 2013*). Furthermore, Hsf1 plays a critical role in the adaptive increase of the size of cardiac cells (*Sakamoto et al., 2006*). In many organs, when cell numbers decrease due to aging, this is compensated by an increase in cell size to maintain the overall functional capacity (*Ginzberg et al.,*

2015). Pancreatic β cells increase their size by over 25% during pregnancy in response to increased insulin demand (*Dhawan et al., 2007*). Similarly, the size of the liver increases during pregnancy through hepatocyte hypertrophy (*Milona et al., 2010*), and liver organ and cell size undergo circadian oscillations (*Sinturel et al., 2017*). Hepatocyte size was also found to increase in organisms continuously exposed to toxic environments (*Hall et al., 2012*). These examples support the idea that it is advantageous for a specific cell type to adopt a specific size under particular physiological conditions. Based on our findings with chronic stress, it would be worth investigating whether Hsp90 more generally supports translational scaling in the context of these physiological changes in cell size.

Limitations of this study

Hsf1 mediates the cell size increase stimulated by chronic stress, but how chronic stress is sensed and relayed to Hsf1 remains to be established. The underlying mechanism may not be exactly the same as the one involved in mediating acute stress, which itself remains poorly understood. Furthermore, how Hsf1 induces the cell size increase is unknown, and the role of Hsp90 in stimulating translation needs to be dissected in more detail, which undoubtedly would be very challenging considering that many of the factors involved in translation are likely to be Hsp90 clients.

Materials and Methods

Cell lines and cell culture

Human embryonic kidney HEK293T cells (ATCC, CRL-3216), A549 human lung epithelial carcinoma cells (ATCC, CCL-185) (as well as the corresponding Hsp90α/β KO cell lines), and RPE1 human retinal epithelial cells (ATCC, CRL-4000), HCT116 human colon carcinoma cells (ATCC, CCL-247) were maintained in Dulbecco's Modified Eagle Media (DMEM) supplemented with GlutaMAX (Thermo Fisher Scientific #31966047), 10% fetal bovine serum (FBS) (PAN-Biotech #P40-37500), and penicillin/streptomycin (100 u/ml) (Thermo Fisher Scientific #15070063) with 5% CO_2 in a 37 °C humidified incubator. We have previously established and characterized MAFs (*Bhattacharya et al., 2022*). Experiments related to MAFs were performed with the cells at 12–24 passages. Human Hsp90α (*HSP90AA1*) and Hsp90β (*HSP90AB1*) KO HEK and A549 cells were generated by the CRISPR/Cas9 gene-editing technology, as reported earlier (*Bhattacharya et al., 2020; Bhattacharya et al., 2022*). For transient transfections, cells were initially seeded at 2×10^5 per 2 ml in 6-well plates and transfected using PEI MAX 40K (Polysciences Inc. # 24765-100) (1:3 DNA to PEI ratio), except for A549 and its corresponding Hsp90α/β KO cell lines. For transient transfection of A549 cells, Lipofectamine LTX (Invitrogen #15338030) was used as directed in the manufacturer's protocol. Cell culture media were changed after 6-8h of transfection. Additional chronic stress or treatments were applied 24 h after transfection.

Plasmids

For the transient overexpression of WT and mutant Hsf1, plasmids pcDNA-Flag HSF1 wt and pcDNA-Flag HSF1 C205, respectively, were used (a gift from Len Neckers (*Kijima et al., 2018*)). The plasmid pcDNA-Flag HSF1 C205 allows

expression of the Hsf1 mutant comprising only the N-terminal 205 amino acids. pcDNA3.1(+) (Thermo Fisher Sci. # V79020) was used as the empty vector control. For transient overexpression of Hsp90α and Hsp90β, plasmids pCherry.90α, and pEGFP.90β were used (*Picard et al., 2006*). pmCherry-C1(*Picard et al., 2006*) and pEGFP-C1 (Clontech #6084-1) were used as respective vector control. The autophagy reporter plasmid FUW mCherry-GFP-LC3 was a gift from Anne Brunet (Addgene #110060) (*Leeman et al., 2018*). Plasmids Ub-M-GFP and Ub-R-GFP were a gift from Nico Dantuma (Addgene #11939) (*Dantuma et al., 2000*). The Hsf1 reporter plasmid HSE (WT)-Luc was a gift from Ueli Schibler (*Reinke et al., 2008*). Plasmid pEGFP-Q74 was a gift from David Rubinsztein (Addgene # 40261) (*Narain et al., 1999*). Plasmid pRL-CMV was from Promega (#E2261), and pSpCas9(BB)-2A-Puro (PX459) a gift from Feng Zhang (Addgene # 48139) (*Kirschke et al., 2014*). Plasmid pGL3-CMV.Luc was a gift from Laurent Guillemot (University of Geneva). For knocking down Hsf1, oligonucleotides (see Table 1 of *Supplementary file 1*) were purchased from Microsynth, annealed, and cloned into pLKO.1 (Addgene #10878). The VSV-G envelope expressing plasmid pMD2.G, and the lentiviral packaging plasmid psPAX2 were gifts from Didier Trono.

Lentiviral particle generation and gene knockdown

5×10^6 HEK cells in a 10 cm plate were co-transfected with plasmids pLKO.1shHSF1-1 or pLKO.1shHSF1-2 (5 µg), pMD2.G (1.25 µg), and psPAX.2 (3.75 µg) with PEI MAX 40K (Polysciences Inc., # 24765-100) (1:3 DNA to PEI ratio). Suspensions of lentiviral particles were collected and added to the medium of WT and Hsp90α/β KO A549 cells to knock down the expression of Hsf1. Lentiviral

control particles were similarly generated and used to express a non-targeting shRNA (not known to target any human mRNA) from plasmid pLKO.1. Transduced cells were selected with 4 µg/ml puromycin (Cayman Chemical # 13884) and used as a pool for further experiments. Knockdowns were validated by immunoblot analyses.

Chronic mild stress models

Heat shock: To induce chronic HS, HEK and its respective Hsp90α/β KO cells, and HCT116 cells were cultured at 39 °C; A549 and its respective Hsp90α/β KO cells, RPE1 cells, and MAFs were cultured at 40 °C. The seeding density was 0.5 - 2× 10^6 cells per 15 cm dish depending on the cell line. Depending on the aim of the experiment, cells were cultured in HS for different time spans as mentioned in the respective figure legends.

Hypoxia: Cells were cultured with 1% O_2 and 5% CO_2 in a 37 °C humidified incubator for a maximum of 4 days. The seeding density was 0.5 - 2× 10^6 cells per 10 cm dish, depending on the cell line. For HEK and its respective Hsp90α/β KO cells, 5 ml fresh medium was added every day to counter the acidification of the culture medium.

Oxidative stress: To generate chronic mild oxidative stress, 5-10 µM sodium arsenite (Ars) was added to the cell culture medium for 4 days.

Proteotoxic stress: For chronic mild proteotoxic stress, 5 µM L-azetidine-2-carboxylic acid (AZC) (Sigma #P8783) was added to the culture medium for 4 days.

Acute oxidative stress model

To generate acute oxidative stress, 2-5 × 10^5 cells were cultured with 25-40 μM sodium arsenite for 1 day.

Measurement of cell size

Cells were detached with trypsin/EDTA (PAN-Biotech #P10-024100), collected in complete medium, and thoroughly washed in Tris-buffered saline (TBS). Single-cell suspensions were resuspended in 100–200 μl (PBS) containing 2.5 µg/ml propidium iodide (PI) (Cayman Chemical #14289-10), for 10 min at room temperature (RT). Cells were analyzed with FACS Gallios flow cytometer (Beckman Coulter), and data were analyzed with the FlowJo software package. Cell populations were gated for size measurements based on the value of the forward scatter (FSC) (figure supplement 8A). We made the assumption that trypsinized cells are round in shape, and therefore, that the respective FSC values are proportional to the diameter of the cells. The PI-positive population was excluded from the size measurement analysis. The respective FSC value was converted to a % value. Control experiments showed that initially preparing the cell suspension in medium containing 5% FCS rather than PBS had no impact on the measured values. However, cell size can be changed if cells are in apoptosis. For the experiments where apoptosis could be observed, cells were stained with PI and annexin V (Biolegend #640906) as described below. Cells positive for PI and annexin V were excluded from the size measurement analysis. Again, controls showed that the annexin V buffer had no impact. For all flow cytometric analyses mentioned here or below, a minimum of 10,000 cells were analyzed for each sample. Additionally, cell diameter was also determined by image analysis using an Innovatis Cedex XS cell counter (Roche) set to auto-calculation.

Cell death assays

PI staining: Cells were stained with PI as mentioned above and then analyzed by flow cytometry.

Annexin V-FITC staining: Following a specific treatment, cells were harvested by trypsinization, washed in phosphate-buffered saline (PBS), and resuspended in 100 μl annexin V-binding buffer (10 mM HEPES pH 7.4, 150 mM NaCl, 2.5 mM $CaCl_2$). 5 μl annexin V-FITC and PI to 2.5 µg /ml were added to the cells and incubated for 15 min at 4 °C.

Cell cycle analyses

Cells were harvested as detailed above. Next, cells were fixed with 70% ice-cold ethanol, washed in PBS, and treated with 100 µg/ml RNase A at RT for 5 min, then incubated with PI to 50 µg/ml for 15–20 min at RT before flow cytometric analysis. Apoptotic cells were identified by the quantitation of the SubG0 (<2n DNA) cell population (figure supplement 8B).

Cell proliferation assays

Crystal violet staining: To determine the rate of cell proliferation under chronic HS, 5 × 10^5 cells/well were seeded into 6-well plates and cultured in chronic HS condition as mentioned earlier or at 37 °C. For the heat-adapted cells, they were cultured under chronic HS for 1 week before this assay. One plate was harvested as a control before chronic HS treatment (Day 1). Plates were harvested after 2, 3, and 4 days

from seeding. The proliferation of cells was quantitated by crystal violet staining. Briefly, cells were washed with PBS, incubated with 4% formaldehyde in PBS for 20 min, washed again with PBS, then incubated with 0.1% crystal violet solution in distilled water for 30 min. The wells were washed thoroughly with distilled water and air-dried overnight. Crystals were dissolved in glacial acetic acid, and the absorbance was measured at 595 nm with a Cytation 3 Image Reader (Agilent).

Cell counting: To determine the impact of chronic HS on cell proliferation, HEK and A549 cells were seeded at a density of 3–5 × 10^6 cells per 20 ml in a 15 cm plate and subjected to mild HS at 39 °C and 40 °C for HEK and A549 cells, respectively. A parallel set was maintained at 37 °C as control. Every 7 days, cells were harvested by trypsinization and counted using a hemocytometer under the light microscope with the trypan blue exclusion assay.

Phase contrast and fluorescence microscopy

Cellular morphology and cell culture density were analyzed using an inverted light microscope (Olympus CK2), and phase contrast images were captured with a Dino-lite camera using the software DinoXcope. To visualize the impact of chronic HS on the actin network, cells were grown under chronic HS conditions on a poly-L-lysine-coated coverslip for 4 days, before being washed with PBS and fixed with 3% glyoxal solution (*Richter et al., 2018*). Actin was stained with Phalloidin-Alexa488 (Thermo Fisher Scientific #A12379), and the nucleus was stained with diamidino-2-phenylindole dye (DAPI) (1:30,000 in PBS, from 1 mg/ml stock solution (Thermo Fisher Scientific #62248)). Coverslips were mounted on glass slides using Mowiol.

Cells were visualized, and images were captured with a fluorescence microscope (Zeiss, Germany).

Hsf1 activity assay

To check the Hsf1 activity at 37 °C, under chronic HS, and upon capsaicin treatment, at first, 4×10^4 cells per 400 μl were seeded in 24-well plates. Cells were co-transfected with the Hsf1 luciferase reporter plasmid HSE (WT)-Luc and the Renilla luciferase internal transfection control (plasmid pRL-CMV). 24h after transfection, cells were cultured under chronic HS conditions for 2 days or in capsaicin (10-250 µM) for 4 days. Then, cells were lysed, and firefly and Renilla luciferase activities were measured using the Dual-Luciferase detection kit (Promega #E1910) with a bioluminescence plate reader (Citation, BioTek). Firefly luciferase activities were normalized to those of Renilla luciferase. The corresponding fold change of Hsf1 activity under chronic HS was normalized to their respective Hsf1 activity at 37 °C. In experiments where Hsf1 activity was measured after overexpressing WT or mutant Hsf1, HSE (WT)-Luc and pRL-CMV were co-transfected with the respective expression plasmids.

FRAP experiments

FRAP experiments were carried out on a Leica SP8 confocal microscope using a 63x oil immersion objective. For *in vivo* measurements of cytoplasmic density, cells were transiently transfected with EGFP expression plasmid pEGFP-C1. Fluorescence was bleached within a circular area of 10 µm^2 with homogeneous fluorescence within the cytoplasm and a background zone outside the cell. After

bleaching, images were taken every 1.29 seconds for HEK and its corresponding Hsp90α/β KO cells and 0.22 seconds for A549 and its corresponding Hsp90α/β KO cells for a total of 30 images. The data were used for the calculation of t-half and diffusion coefficients by a one-phase exponential association function, and recovery curves were built using GraphPad Prism 8 (GraphPad Software, Inc., La Jolla, CA).

Protein extraction and analysis

Quantification of cellular protein: To quantify the amount of total soluble protein per cell, 5 x 10^6 cells per experimental condition were harvested, pellets were washed at least twice with PBS, and then lysed in ice-cold lysis buffer (20 mM Tris-HCl pH 7.4, 2 mM EDTA, 150 mM NaCl, 1.2% sodium deoxycholate, 1.2% Triton X-100, protease inhibitor cocktail (Thermo Fisher Scientific #78429), and phosphatase inhibitor cocktail (Thermo Fisher Scientific #78420)). Cell lysates were sonicated for 15 min at high power with the Bioruptor sonicator (Diagenode). Protein quantification was performed using the Bradford reagent (Biorad #5000001), measuring absorbance at 595 nm. To visualize the amount of total protein in each experimental condition, the same volume of cell lysates was mixed with SDS sample buffer and run on 10% SDS-PAGE, and proteins were stained with Coomassie blue for 1 h and de-stained overnight in water.

Analysis of cell size to total protein ratio: Cells from different experimental conditions were fixed for 10 min in 4% formaldehyde, washed with PBS, and permeabilized in 100% methanol for 10 min at -20 °C. Methanol was removed, and cells were washed once with 0.2 M sodium bicarbonate, followed by staining in 0.5 ml 0.2 M sodium

bicarbonate containing 50 mg/ml Alexa Fluor 488 NHS Ester (succinimidyl ester) (Thermo Fisher Scientific #A20100) for 30 min at RT. Cells were then analyzed using flow cytometry. The amount of protein per cell was quantitated as log of the mean fluorescent intensity (MFI) values (detected in the FL1 channel, i.e. MFI-FL1). Relative cell size was deduced from the FSC values (see above).

Assay of protein translation: To measure *de novo* protein translation, cells were seeded at a density of 1.2–1.5 × 10^6 per 10 ml in a 10 cm plate. Cells were then treated with 1 µM puromycin for 0–2.5 h, while being cultured at 37 °C or 39 °C. Cells were harvested and lysed in lysis buffer (20 mM Tris-HCl pH 7.4, 2 mM EDTA, 150 mM NaCl, 1.2% sodium deoxycholate, 1.2% Triton-X100, 200 mM iodoacetamide, protease inhibitor cocktail). 75 µg of clarified cell lysates were separated by 10% SDS-PAGE and immunoblotted for newly synthesized proteins or polypeptides with anti-puromycin antibodies. The intensities of the corresponding lanes reflect the total amount of global protein translation for that time point. To determine *de novo* protein translation at the single cell level in relation to cell size, cells were maintained at 39 °C for 4 h, 1 day, and 4 days. Nascent polypeptides were labelled using Click-iT Plus OPP Alexa Fluor 594 (Thermo Fisher Scientific #C10457) as described in the manufacturer's protocol. Briefly, O-propargyl-puromycin (OPP) (2 µM) was added to cultured cells up to 4 h after the above-mentioned incubation at 39 °C. In parallel, a control set was done at 37 °C. Cells were then washed with PBS, fixed in 3.7% formaldehyde in PBS, permeabilized in 0.5% Triton X-100 in PBS, and incubated at RT for 15 min. The permeabilization buffer was washed off with PBS. Click-iT Plus OPP reaction cocktail was added and incubated for 30 min at RT,

protected from light. The reaction cocktail was removed and washed once with 1 ml of Click-iT Reaction Rinse Buffer, further washed with PBS, and kept in PBS until newly synthesized proteins were quantitated using flow cytometry (figure supplement 9) and expressed as log MFI values, and relative to cell size.

Immunoblot analyses: Lysates of cells (20–100 µg) were subjected to SDS-PAGE and transferred onto a nitrocellulose membrane (GVS Life Science) with a wet blot transfer system (VWR #BTV100). Membranes were blocked with 2–5% non-fat dry milk or bovine serum albumin in TBS with 0.2% Tween 20 (TBST) and incubated with primary antibodies overnight at 4°C. Then they were washed with TBST, incubated with the corresponding secondary antibodies for 1 h at RT, and developed using the WesternBright chemiluminescent substrate (Advansta #K-12045-D50). Images were captured using a LI-COR Odyssey or Amersham ImageQuant 800 image recorder. The EZ-Run Prestained Protein Ladder (Thermo Fisher Scientific) or the AcuteBand Prestained Protein ladder (Lubioscience) were used as protein molecular weight markers. Details of primary and secondary antibodies are given in Table 2 of *Supplementary file 1*.

Autophagic flux measurement

Cells seeded in 6-well plate at a density of 4×10^5 per 2 ml were transfected with the autophagy reporter plasmid FUW mCherry-GFP-LC3 as described above. 24 h after transfection, cells were subjected to chronic HS for 2 days. Cells were harvested by trypsinization, and GFP- and mCherry-positive cells were measured by flow cytometry (figure supplement 10A). The autophagic flux was measured by

calculating the ratio of the MFI of mCherry and GFP-positive cells. A higher relative ratio of mCherry/GFP is indicative of a higher autophagic flux.

In vivo UPS activity assay

Cells seeded at a density of 5×10^5 per 2 ml in 6-well plates were transfected with plasmids Ub-M-GFP and Ub-R-GFP for expression of stable and degradation-prone GFP, respectively (*Dantuma et al., 2000*). The next day, the medium was changed, and cells were cultured at 37 °C or 39 °C for 2 days. Cells were then harvested by trypsinization and GFP-positive cells were quantitated by flow cytometry. The *in vivo* UPS activity was expressed as the MFI of Ub-M-GFP-positive cells minus the MFI of Ub-R-GFP-positive cells (figure supplement 10B). Fold change of UPS activity in HS was normalized to the corresponding activity at 37 °C. Fold change of UPS activity of Hsp90α/β KO cells was also normalized to the fold change relative to WT cells.

In vivo luciferase refolding assay

Cells cultured at 37 °C or cells adapted at 39 °C for 2 days were transfected with the luciferase expression vector pGL3-CMV.Luc. Cells were subjected to an acute HS at 43 °C for 15 min to denature luciferase, followed by incubation at 37 °C for the control cells or at 39 °C for the heat-adapted cell for 1–3 h to allow refolding of luciferase. Cells were harvested by centrifugation and lysed with the Passive Lysis Buffer of the Dual-Luciferase detection kit (Promega). 10 μl cell extract was mixed with an equal volume of firefly luciferase assay substrate from the kit, and the luciferase luminescence signals were measured with a bioluminescence plate reader (Citation, BioTek).

In vitro proteasomal activity assay

Cells cultured at 37 °C or at 39 °C were harvested and washed. Cell pellets were resuspended in lysis buffer (25 mM Tris-HCl pH 7.4, 250 mM sucrose, 5 mM $MgCl_2$, 1% IGEPAL, 1 mM DTT, 1 mM ATP) and incubated for 10–15 min on ice. Samples were centrifuged at 16,100 × g for 20 min, and supernatants were collected for the proteasomal activity assay. Equal amounts of protein (50 μg) for each sample were diluted in proteasomal reaction buffer (50 mM Tris-HCl pH 7.4, 5 mM $MgCl_2$, 1 mM DTT, 1 mM ATP) in a 96-well opaque bottom white plate and 50 μM N-succinyl-Leu-Leu-Val-Tyr-7-amino-4-methyl-coumarin (suc-LLVY-AMC) (Enzo Life Sciences, #BML-P802-0005) was added to each well. AMC fluorescence was measured at 460 nm for 5–60 min, with an excitation at 380 nm. All fluorescence measurements were recorded using a plate reader (Cytation 3, BioTek).

Protein aggregation

To analyze polyglutamine (polyQ) protein aggregation within cells, cells were seeded on glass coverslips and transfected with the plasmid pEGFP-Q74 and 24 h after transfection, cells were placed at 39 °C and the respective controls at 37 °C. 42 h after transfection, cells were fixed with 4% paraformaldehyde and mounted on glass slides using Mowiol. EGFP-positive cells were visualized, and images were captured with a fluorescence microscope (Zeiss, Germany).

Increase and reduction of cell size with various inhibitors

To increase the cell size, 2×10^5 cells in 3 ml were seeded in 6-well plates and treated with the Cdk4/6 inhibitor abemaciclib (MedChemExpress, #HY-16297A-5MG) at 50-100 nM for 2-3 days. At this point, one experimental set was harvested. To reduce the cell size, 2×10^5 cells in 3 ml were seeded in 6-well plates, and treated with 5-10 nM rapamycin (Sigma-Aldrich, #553210), or 100 ng/ml cycloheximide (CHX) for 2-3 days. Alternatively, cell size was reduced by replacing the standard growth medium 24 h after seeding with medium containing only 1% FBS. Parallel sets that were not harvested were washed with fresh medium and subjected to other stress treatments. Cell size and cell death were determined by flow cytometry as described above.

Proteomic analyses

Protein digestion: HEK WT and their respective Hsp90α/β KO cells were cultured at 37 °C, and at 39 °C for 1 day and 4 days. Cells were harvested and snap-frozen. Replicate samples were digested according to a modified version of the iST method (named miST method) (*Kulak et al., 2014*). Briefly, frozen cell pellets were resuspended in 3 ml miST lysis buffer (1% sodium deoxycholate, 100 mM Tris pH 8.6, 10 mM DTT). Resuspended samples were sonicated and heated at 95 °C for 5 min. After quantification with tryptophan fluorescence, 100 µg of samples in 50 µl buffer were diluted 1:1 (v:v) with water. Reduced disulfides were alkylated by adding ¼ volume of 160 mM chloroacetamide (final 32 mM) and incubating at 25 °C for 45 min in the dark. Samples were adjusted to 3 mM EDTA and digested with 1.0 µg Trypsin/LysC mix (Promega #V5073) for 1 h at 37 °C, followed by a second 1-h digestion with a second aliquot of 0.5 µg trypsin. To remove sodium deoxycholate, two sample volumes of isopropanol containing 1% trifluoroacetic acid (TFA) were

added to the digests, and the samples were desalted on a strong cation exchange (SCX) plate (Oasis MCX; Waters Corp., Milford, MA) by centrifugation. After washing with isopropanol/1% TFA, peptides were eluted in 200 μl of 80% acetonitrile, 19% water, 1% (v/v) NH_3.

Peptide fractionation for library construction: After redissolution of samples in 1.0 ml of loading buffer (2% acetonitrile with 0.05% TFA), aliquots (10 µl) of samples were pooled and separated into 6 fractions by off-line basic reversed-phase (bRP) using the Pierce High pH Reversed-Phase Peptide Fractionation Kit (Thermo Fisher Scientific). The fractions were collected in 7.5, 10, 12.5, 15, 17.5, and 50% acetonitrile in 0.1% triethylamine (~pH 10). Dried bRP fractions were redissolved in 40 µl loading buffer, and 4 µl were injected for LC-MS/MS analyses.

LC-MS/MS: LC-MS/MS analyses were carried out on a TIMS-TOF Pro (Bruker, Bremen, Germany) mass spectrometer interfaced through a nanospray ion source ("captive spray") to an Ultimate 3000 RSLCnano HPLC system (Dionex). Peptides were separated on a reversed-phase custom-packed 40 cm C18 column (75 µm ID, 100 Å, Reprosil Pur 1.9 μm particles, Dr. Maisch, Germany) at a flow rate of 0.250 µl /min with a 2-27% acetonitrile gradient in 93 min followed by a ramp to 45% in 15 min and to 90% in 5 min (all solvents contained 0.1% formic acid). Identical LC gradients were used for DDA and DIA measurements.

Library creation: Raw Bruker MS data were processed directly with Spectronaut 15.4 (Biognosys, Schlieren, Switzerland). A library was constructed from the DDA bRP

fraction data by searching the reference human proteome (www.uniprot.org; accessed on September 3rd, 2020, containing 75,796 sequences). For identification, peptides of 7-52 AA length were considered, cleaved with trypsin/P specificity, and a maximum of 2 missed cleavages. Carbamidomethylation of cysteine (fixed), methionine oxidation and N-terminal protein acetylation (variable) were the modifications applied. Mass calibration was dynamic and based on a first database search. The Pulsar engine was used for peptide identification. Protein inference was performed with the IDPicker algorithm. Spectra, peptide and protein identifications were all filtered at 1% FDR against a decoy database. Specific filtering for library construction removed fragments corresponding to less than 3 AA and fragments outside the 300-1800 m/z range. Also, only fragments with a minimum base peak intensity of 5% were kept. Precursors with less than 3 fragments were also eliminated, and only the best 6 fragments were kept per precursor. No filtering was done on the basis of charge state, and a maximum of 2 missed cleavages was allowed. Shared (non-proteotypic) peptides were kept. The library created contained 119,573 precursors mapping to 91,154 stripped sequences, of which 35,119 were proteotypic. These corresponded to 8,632 protein groups (12,252 proteins). Of these, 959 were single hits (one peptide precursor). In total 701,091 fragments were used for quantitation.

DIA quantitation: Peptide-centric analysis of DIA data was done with Spectronaut 15.4 using the library described above. Single hits proteins (defined as matched by one stripped sequence only) were kept in the Spectronaut analysis. Peptide quantitation was based on XIC area, for which a minimum of 1 and a maximum of 3

(the 3 best) precursors were considered for each peptide, from which the median value was selected. Quantities for protein groups were derived from inter-run peptide ratios based on MaxLFQ algorithm (Cox et al 2014). Global normalization of runs/samples was done based on the median of peptides.

Data processing and statistical tests: All subsequent analyses were done with the Perseus software package (version 1.6.15.0). Intensity values were log2-transformed, and after assignment to groups, t-tests were carried out with permutation-based FDR correction for multiple testing (Q-value threshold <0.01). The difference of means obtained from the tests was used for 1D enrichment analysis on associated GO/KEGG annotations as described (Cox and Mann, 2012). The enrichment analysis was also FDR-filtered (Benjamini-Hochberg, Q-val<0.02). The data of the proteomic analysis are supplied as source data 1.

Ribosome and polysome fractionation

Polysome fractionation was performed at the “BioCode: RNA to Proteins” core facility of the Faculty of Medicine of the University of Geneva. Cells were cultured at 37 °C or 39 °C for 4 days. Before harvesting the cells, 100 μg/ml CHX was added to the medium, and cells were maintained in the respective incubator for 15-20 min. Cells were then harvested and washed in ice-cold PBS containing 100 μg/ml CHX, snap-frozen and proceeded to the next steps. Cells were weighed, and resuspended in lysis buffer (50 mM Tris-HCl pH 7.4, 100 mM KCl, 1.5 mM $MgCl_2$, 1.5% Triton X-100, 1 mM DTT, 100 μg/ml CHX, 1 mg/ml heparin, 25 u/ml Turbo DNase I (Roche, #04716728001), 25 u/μl SUPERaseIn RNase inhibitor (Invitrogen, #AM2694),

protease inhibitors (Roche, #04693132001)) at 200 μl lysis buffer per 100 μg pellet. Cell suspensions were passed through a 25G needle 10-12 times. Cell debris were pelleted at 20,000 g at 4 °C for 20 min. The total RNA concentration of the supernatant was determined. Cell lysates containing 350 μg of total RNA were loaded onto linear 20-60% sucrose gradients prepared with the gradient buffer (50 mM Tris-HCl pH 7.4, 100 mM KCl, 1.5 mM $MgCl_2$, 1 mM DTT, 100 μg/ml CHX). Ribosomes/polysomes were centrifuged at 247,600 g (38,000 rpm) in a SW41 Ti rotor (Beckman Coulter, #331362) for 3 h 30 min at 4 °C. Fractionated ribosomes/polysomes were measured and collected using a density gradient fractionation system (ISCO).

General data analyses

Data processing and analyses were performed using GraphPad Prism (version 8).

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Author contributions: S.M. and D.P. conceived the study; S.M. designed and performed most of the experiments, analyzed most of the data, prepared the figures and wrote the drafts; K.B. contributed in designing some experiments, performed proteasome activity assays, and prepared figures; D.W. performed some Western blots; D.H. contributed in FRAP measurements and analysis; O.P performed the polysome profiling; L.B. did the cloning of shRNA constructs and their initial validation; N.H. contributed to the proteomic data analyses; D.P. supervised the work, contributed to the design of the experiments, wrote, and critically edited the manuscript. All authors have read and agreed to the published version of the manuscript.

Competing interests: Authors declare that they have no competing interests.

Data and materials availability: The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD039672, and for a subset they are available in source data 1. All other data needed to evaluate the conclusions in the paper are presented in the paper, and/or the Supplementary Materials.

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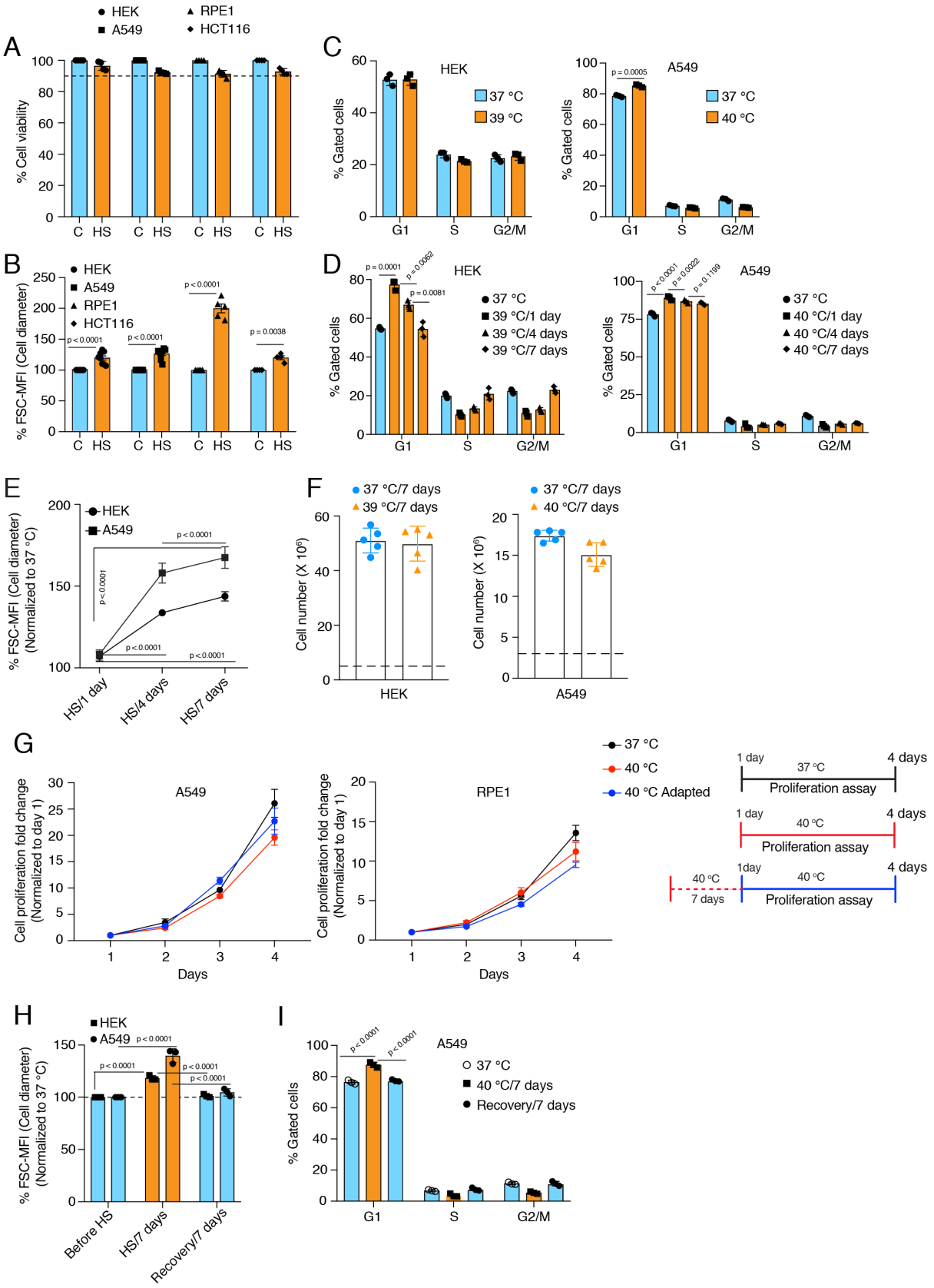
A
HEK
A549
RPE1
HCT116
% Cell viability
C HS C HS C HS C HS
B
% FSC-MFI (Cell diameter)
p < 0.0001
p = 0.0038
C
HEK
37 °C
39 °C
A549
40 °C
% Gated cells
G1 S G2/M
p = 0.0005
D
p = 0.0001
p = 0.0062
p = 0.0081
39 °C/1 day
39 °C/4 days
39 °C/7 days
40 °C/1 day
40 °C/4 days
40 °C/7 days
p = 0.0022
p = 0.1199
E
% FSC-MFI (Cell diameter) (Normalized to 37 °C)
HS/1 day
HS/4 days
HS/7 days
F
37 °C/7 days
39 °C/7 days
40 °C/7 days
Cell number (X 10^6)
G
Cell proliferation fold change (Normalized to day 1)
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1 day
4 days
Proliferation assay
7 days
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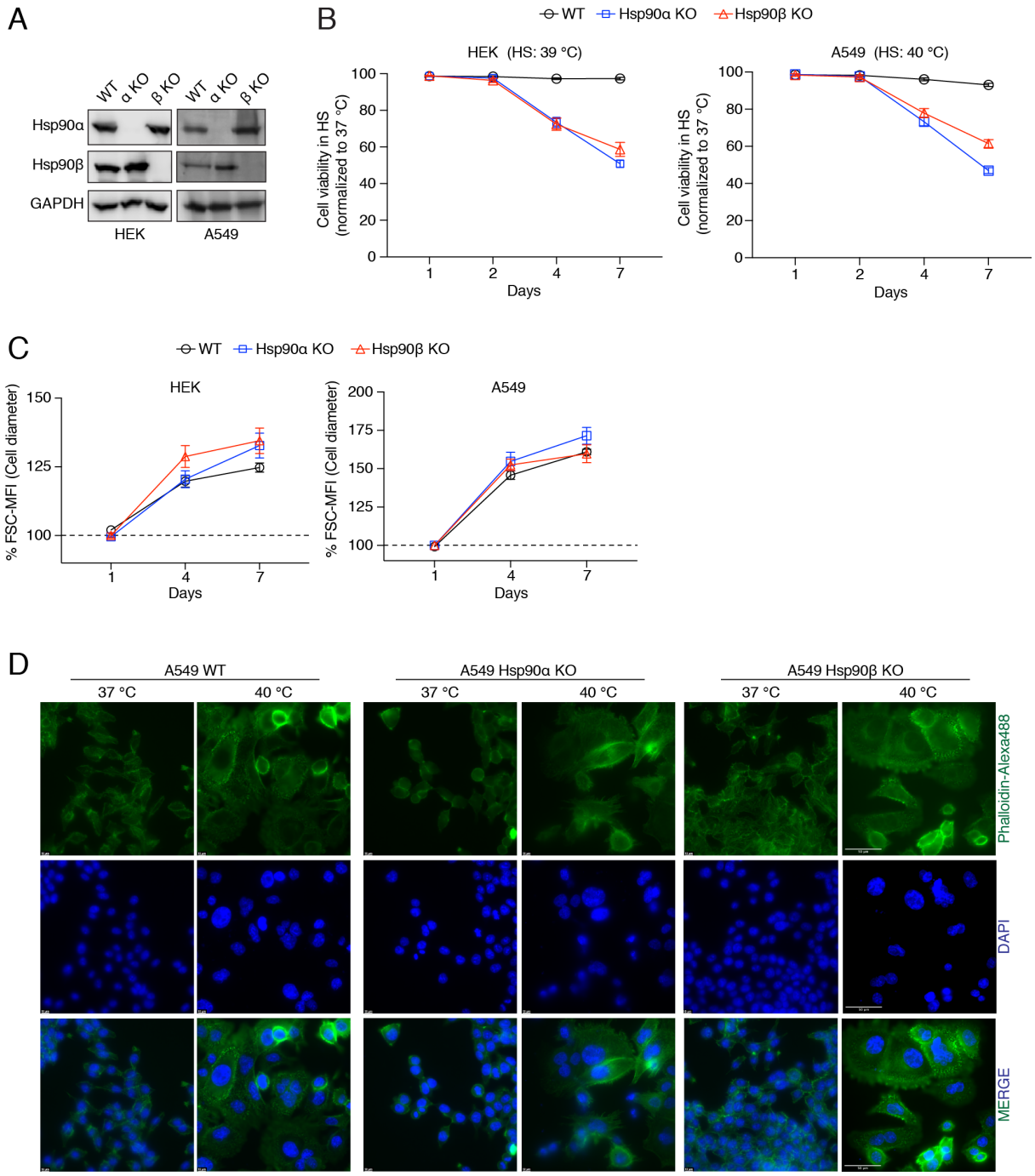
Before HS
HS/7 days
Recovery/7 days
I
Recovery/7 days

Figure 1. Cells increase their size in response to chronic stress. (A) Flow cytometric quantification of cell viability under chronic HS for 7 days (HS = 39°C for HEK and HCT116 cells; HS = 40 °C for A549 and RPE1 cells) (n = 4 biologically independent samples). **(B)** Flow cytometric quantification of cell size after 7 days of chronic HS (biologically independent samples: n = 6 for HEK and A549; n = 5 for RPE1; n = 4 for HCT116). **(C** and **D)** Flow cytometric analysis of cell cycle (n = 3 biologically independent samples). **(E)** Flow cytometric quantification of cell size during different time intervals of chronic HS (n = 4 biologically independent samples). **(F)** Proliferation of HEK and A549 cells at the indicated temperature for the indicated period presented as cell numbers. Cells were seeded at a density of 5 x 10^6 and 3 x 10^6 per 15 cm plate for HEK and A549 cells, respectively. The numbers of live cells counted after 7 days are plotted (n = 5 biologically independent experiments). **(G)** Proliferation of A549 and RPE1 cells measured with a crystal violet assay (n = 3 biologically independent experiments). The adapted cells were maintained at 40 °C for one week before this experimental start point and continued at 40 °C during the experiment. See scheme of the experiment on the right. **(H)** Flow cytometric quantification of cell size in chronic HS and recovery (n = 3 biologically independent samples). (**I)** Flow cytometric analysis of cell cycle in chronic HS and post HS recovery (n = 3 biologically independent samples). The data are represented as mean values ± SEM for all bar and line graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.


A
WT
α KO
β KO
WT
α KO
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Hsp90α
Hsp90β
GAPDH
HEK
A549
B
WT
Hsp90α KO
Hsp90β KO
HEK (HS: 39 °C)
A549 (HS: 40 °C)
Cell viability in HS (normalized to 37 °C)
Days
C
HEK
A549
% FSC-MFI (Cell diameter)
Days
D
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
37 °C
40 °C
Phalloidin-Alexa488
DAPI
MERGE

Figure 2. **Cells are unable to adapt to chronic stress in the absence of one of the cytosolic Hsp90 isoforms. (A)** Immunoblots of Hsp90α and Hsp90β in WT HEK and A549 cells, and their respective Hsp90α/β KO cells. GAPDH serves as the loading control (α KO; Hsp90α KO and β KO; Hsp90β KO) (representative images of n = 4 biologically independent experiments). **(B)** Flow cytometric quantification of cell viability of HEK, A549, and their respective Hsp90α/β KO cells in chronic HS at different time points during a period of 7 days (n = 5 biologically independent samples). Note that the X axis does not have a linear scale and that lines connecting the data points are drawn as a visual aid. **(C)** Flow cytometric quantification of cell size in chronic HS at different time points during a period of 7 days (HS = 39 °C for HEK and 40 °C for A549) (n = 4 biologically independent samples) The data are represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests. **(D)** Fluorescence microscopy images of A549 WT and Hsp90α/β KO cells after 4 days of chronic HS. The cytoskeleton is stained with phalloidin-Alexa488 (green), and the nucleus is stained with DAPI (blue). Images were captured with a fluorescence microscope (Zeiss, Germany). The scale bars on the images on the far right are 50 μM (images are representative of n = 2 biologically independent experiments).

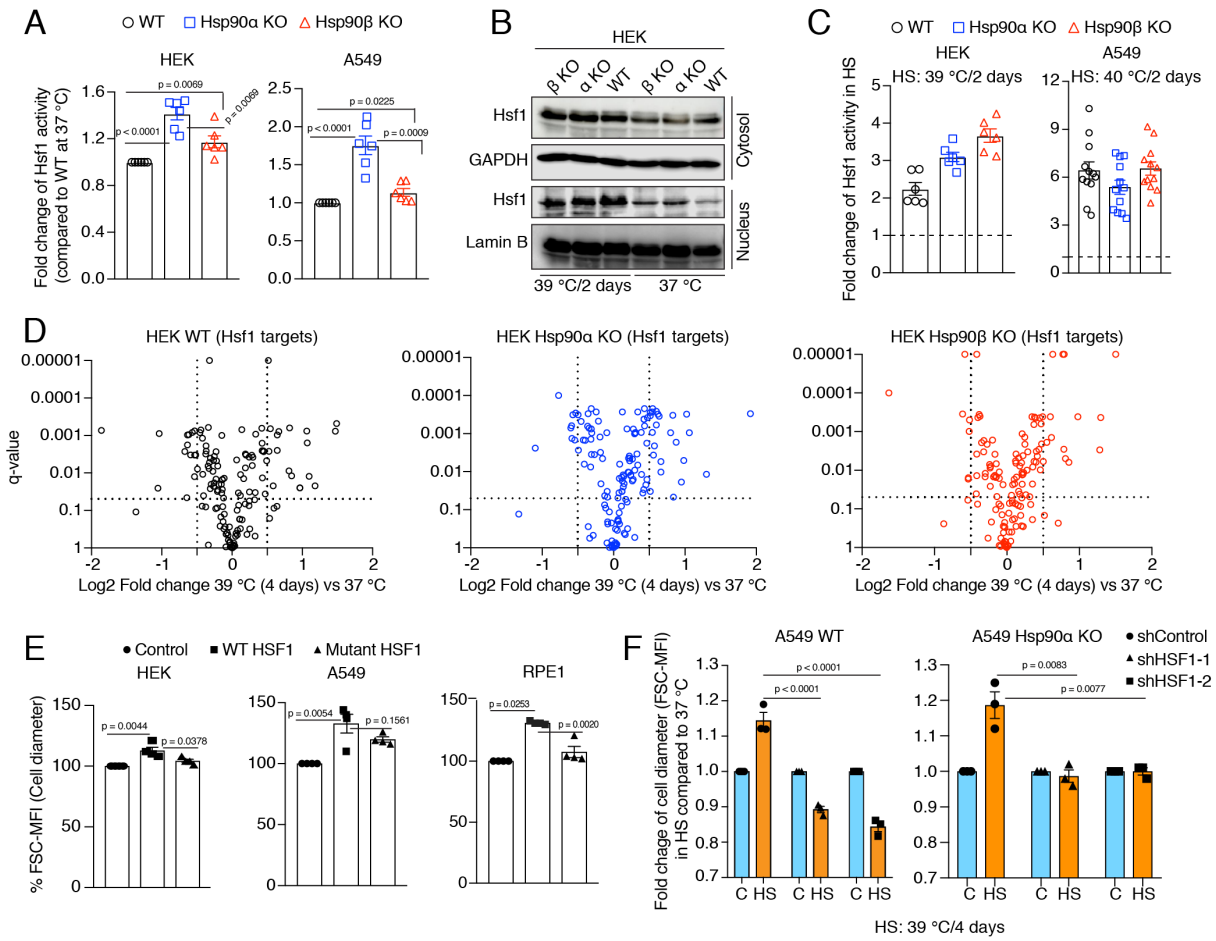


Figure 3. Hsf1 regulates cell size in response to stress. (A) Fold change of Hsf1 activity of HEK WT, A549 WT, and their respective Hsp90α/β KO cells at 37 °C as measured by luciferase reporter assay (n = 3 biologically independent samples and 2 experimental replicates each time). (**B**) Immunoblots of Hsf1 in the cytosolic and nuclear fractions of HEK WT and Hsp90α/β KO cells (α KO, Hsp90αKO; β KO, Hsp90βKO). GAPDH and lamin B1 serve as loading controls (representative blots of n = 2 biologically independent experiments). (**C**) Fold change of Hsf1 activity of HEK WT, A549 WT, and their respective Hsp90α/β KO cells in chronic HS as measured by luciferase reporter assay (n = 3 biologically independent samples, and 2 experimental replicates each time for HEK; n = 3 biologically independent samples, and 4 experimental replicates each time for A549). **(D)** Volcano plots of the

normalized fold changes in protein levels of some core Hsf1 target genes (list obtained from https://hsf1base.org/) in chronic HS, determined by quantitative label-free proteomic analysis of Hsp90α/β KO and WT HEK cells. Molecular chaperones, whose expression is regulated by Hsf1, are excluded from this dataset. Each genotype was compared with its respective 37 °C control (n = 3 biologically independent samples). Log2 fold changes of > 0.5 or < -0.5 with a p-value of < 0.05 were considered significant differences for a particular protein. **(E)** Flow cytometric quantification of cell size of HEK, A549, and RPE1 cells upon overexpression of WT Hsf1 (with plasmid pcDNA-Flag HSF1 wt) or mutant Hsf1 (pcDNA-Flag HSF1 C205 (*Kijima et al., 2018*), retaining only the first 205 amino acids), and with plasmid pcDNA3.1(+) as empty vector control. Transfected cells to be measured were identified on the basis of their coexpression of EGFP (n = 4 biologically independent experiments). **(F)** Flow cytometric quantification of cell size in chronic HS after knockdown of Hsf1 in A549 WT and Hsp90αKO cells. Here the chronic HS for A549 cells is at 39 °C instead of 40 °C to reduce HS-induced damage in Hsf1 knockdown conditions (n = 3 biologically independent samples). **(G)** Flow cytometric quantification of cell cycle in HS after knockdown of Hsf1 in A549 WT and Hsp90αKO cells. The data are represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

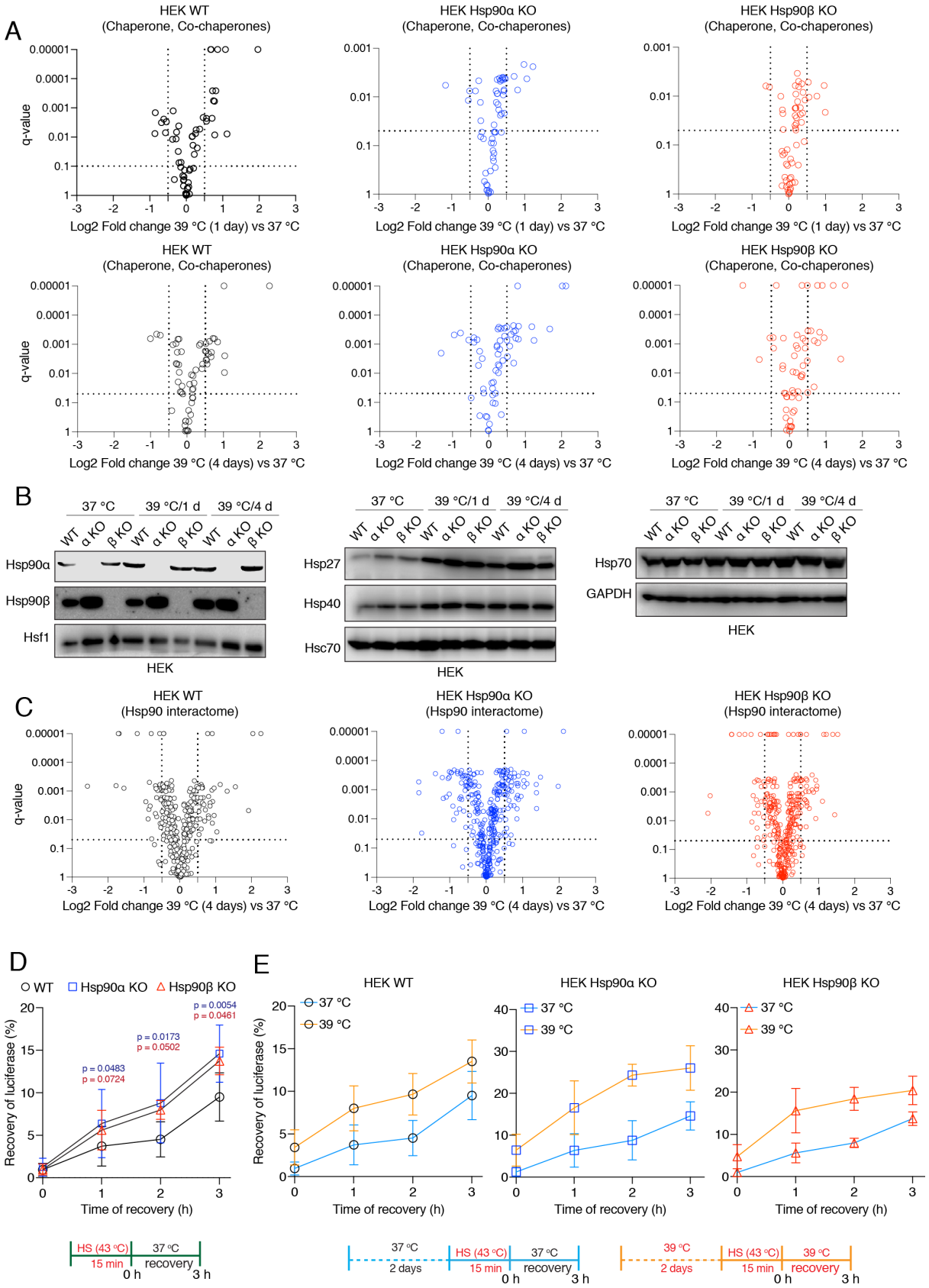

A
HEK WT
(Chaperone, Co-chaperones)
HEK Hsp90α KO
(Chaperone, Co-chaperones)
HEK Hsp90β KO
(Chaperone, Co-chaperones)
q-value
Log2 Fold change 39 °C (1 day) vs 37 °C
Log2 Fold change 39 °C (4 days) vs 37 °C
B
37 °C
39 °C/1 d
39 °C/4 d
WT
α KO
β KO
Hsp90α
Hsp90β
Hsf1
Hsp27
Hsp40
Hsc70
Hsp70
GAPDH
HEK
C
HEK WT
(Hsp90 interactome)
HEK Hsp90α KO
(Hsp90 interactome)
HEK Hsp90β KO
(Hsp90 interactome)
D
WT
Hsp90α KO
Hsp90β KO
Recovery of luciferase (%)
Time of recovery (h)
p = 0.0483
p = 0.0724
p = 0.0173
p = 0.0502
p = 0.0054
p = 0.0461
HS (43 °C)
15 min
37 °C
recovery
0 h
3 h
E
HEK WT
HEK Hsp90α KO
HEK Hsp90β KO
37 °C
39 °C
2 days
39 °C

Figure 4. Hsp90α/β KO cells maintain chaperones, co-chaperones, and Hsp90 interactors during chronic stress adaptation. (A) Volcano plots of the normalized fold changes of molecular chaperones and co-chaperones of cells subjected to 1 and 4 days of chronic HS determined by quantitative label-free proteomic analysis of Hsp90α/β KO and WT HEK cells. Each genotype was compared with its respective 37 °C control (*n* = 3 biologically independent samples)**. (B)** Immunoblots of different molecular chaperones in HEK WT and Hsp90α/β KO cells (α KO, Hsp90αKO; β KO, Hsp90βKO). GAPDH serves as the loading control for all three panels (representative of n = 2 independent experiments). **(C)** Volcano plots of the normalized fold changes of Hsp90 interactors (list obtained from https://www.picard.ch/Hsp90Int) in 4 days of chronic HS determined by quantitative label-free proteomic analysis of Hsp90α/β KO and WT HEK cells. Each genotype was compared with its respective 37 °C control (n = 3 biologically independent samples). For all volcano plots, Log2 fold changes of > 0.5 or < -0.5 with a p-value of < 0.05 were considered significant differences for a particular protein. **(D** and **E)** *In vivo* refolding of heat-denatured luciferase of control cells (blue line) and cells heat-adapted to 39 °C (orange line). Luciferase activity before the acute HS (at 43 °C) is set to 100% (n = 3 biologically independent samples). See scheme of the experiment below. Note the different scales of the Y axes of the bar graphs in panel E. The data are represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests. The p-values for Hsp90α and Hsp90β KO cells are in blue and red, respectively. All the p-values are for comparisons to the respective WT.

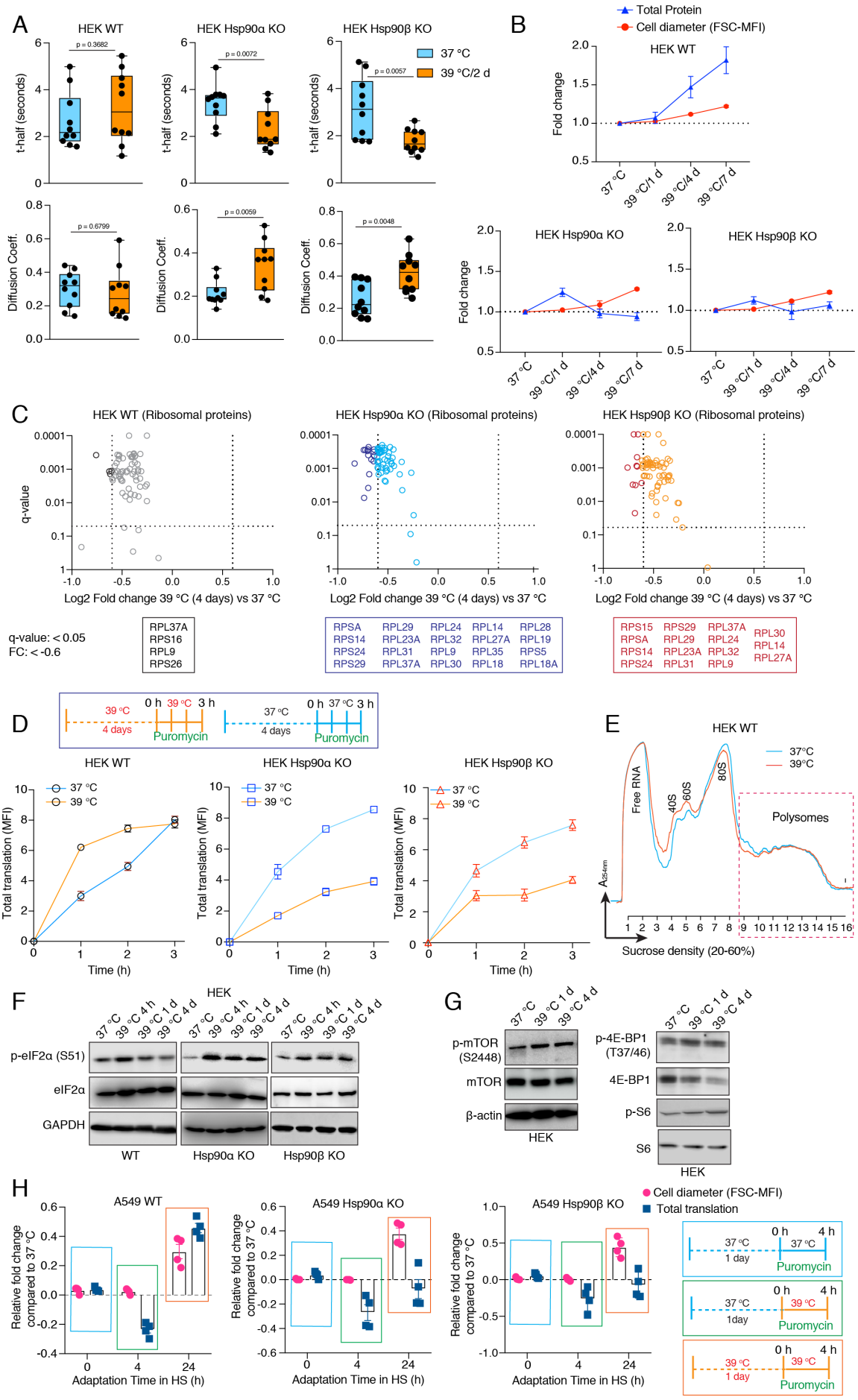

A
HEK WT
HEK Hsp90α KO
HEK Hsp90β KO
37 °C
39 °C/2 d
t-half (seconds)
Diffusion Coeff.
p = 0.3682
p = 0.0072
p = 0.0057
p = 0.6799
p = 0.0059
p = 0.0048
B
Total Protein
Cell diameter (FSC-MFI)
Fold change
37 °C
39 °C/1 d
39 °C/4 d
39 °C/7 d
C
HEK WT (Ribosomal proteins)
HEK Hsp90α KO (Ribosomal proteins)
HEK Hsp90β KO (Ribosomal proteins)
q-value
Log2 Fold change 39 °C (4 days) vs 37 °C
q-value: < 0.05
FC: < -0.6
RPL37A RPS16 RPL9 RPS26
RPSA RPL29 RPL24 RPL14 RPL28 RPS14 RPL23A RPL32 RPL27A RPL19 RPS24 RPL31 RPL9 RPL35 RPS5 RPS29 RPL37A RPL30 RPL18 RPL18A
RPS15 RPS29 RPL37A RPSA RPL29 RPL24 RPS14 RPL23A RPL32 RPS24 RPL31 RPL9 RPL30 RPL14 RPL27A
D
39 °C
4 days
0 h 39 °C 3 h
Puromycin
37 °C
0 h 37 °C 3 h
HEK WT
HEK Hsp90α KO
HEK Hsp90β KO
37 °C
39 °C
Total translation (MFI)
Time (h)
E
HEK WT
37°C
39°C
Free RNA
40S
60S
80S
Polysomes
Sucrose density (20-60%)
F
HEK
37 °C
39 °C 4 h
39 °C 1 d
39 °C 4 d
p-eIF2α (S51)
eIF2α
GAPDH
WT
Hsp90α KO
Hsp90β KO
G
p-mTOR (S2448)
mTOR
β-actin
HEK
p-4E-BP1 (T37/46)
4E-BP1
p-S6
S6
H
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
Cell diameter (FSC-MFI)
Total translation
Relative fold change compared to 37 °C
Adaptation Time in HS (h)
0 h 4 h
37 °C
1 day
Puromycin
1day
39 °C

Figure 5. Hsp90α/β KO cells suffer from cytoplasmic protein dilution during adaptation to chronic stress. (A) FRAP experiments with control and heat-adapted live cells expressing EGFP. The respective box plots show the t-half values of recovery of EGFP fluorescence and the apparent EGFP diffusion coefficients (n= 10 cells from 2 biologically independent experiments). **(B)** Fold change of cell size (represented by the FSC-MFI values) and total proteins (determined as MFI-FL1 values) in chronic HS as analyzed by flow cytometry. Cells were fixed, and total proteins were stained using Alexa Fluor 488 NHS ester (n = 3 biologically independent experiments). Lines connecting the data points are drawn as a visual aid. **(C)** Volcano plots of the normalized fold changes of the ribosomal proteins (list obtained from http://ribosome.med.miyazaki-u.ac.jp/) after 4 days of chronic HS determined by quantitative label-free proteomic analysis in Hsp90α/β KO and WT HEK cells. Each genotype was compared with its respective 37 °C control (n= 3 biologically independent samples). Log2 fold changes of > 0.6 or < -0.6 with a p-value of < 0.05 were considered significant differences for a particular protein. The box below the volcano plot shows the corresponding names of the proteins that were significantly downregulated. **(D)** Flow cytometric analysis of total translation of HEK WT and Hsp90α/β KO cells at 37 °C and after 4 days of chronic HS (see scheme of the experiment on the top). Nascent polypeptide chains were labeled with OP-puromycin during cell culture, and the incorporation of puromycin at different time points was analyzed (n = 4 experimental samples). **(E)** Representative polysome profiles of HEK WT cells at 37 °C and after 4 days of chronic HS (representative of n = 2 biologically independent experiments). **(F** and **G)** Immunoblots of some of the translation-related proteins. GAPDH and β-actin serve as loading controls (images

are representative of n = 2 independent biological samples). **(H)** Relative fold changes of total translation and cell size in the early phase of adaptation to chronic HS (see schemes of experiments on the right) for A549 WT and Hsp90α/β KO cells**.** The data are represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

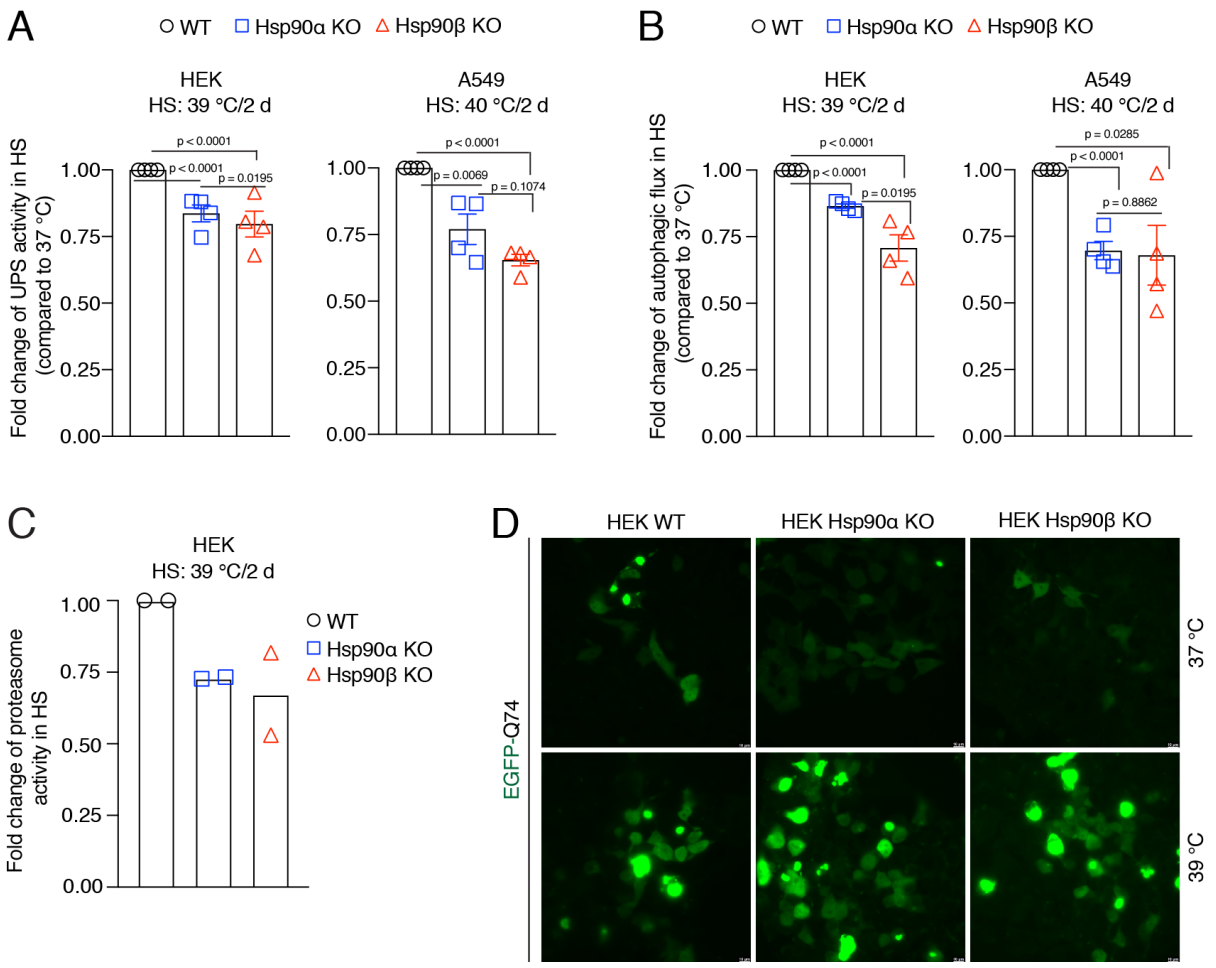


Figure 6. Hsp90 is crucial for cellular proteostasis during adaptation to chronic stress. (A) Flow cytometric determination of the *in vivo* UPS activity in chronic HS compared to 37 °C, using the Ub-M-GFP and Ub-R-GFP reporter proteins (n = 4 biologically independent samples). **(B)** Flow cytometric measurement of autophagic flux in chronic HS compared to 37 °C, using a mCherry-GFP-LC3 reporter. Flux is calculated as the ratio of the mean fluorescence intensities of mCherry and GFP-positive cells (n = 4 biologically independent samples). **(C)** *In vitro* steady-state proteasomal activity with lysates of HEK WT, and Hsp90α and Hsp90β KO cells determined by measuring fluorescence of the cleaved substrate suc-LLVY-AMC (n = 2 biologically independent samples). **(D)** Fluorescence micrographs of cells

expressing the fusion protein EGFP-Q74 visible as aggregates with green fluorescence. The scale bar in micrographs indicates 10 µm (images are representative of n = 2 independent biological samples). The data are represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

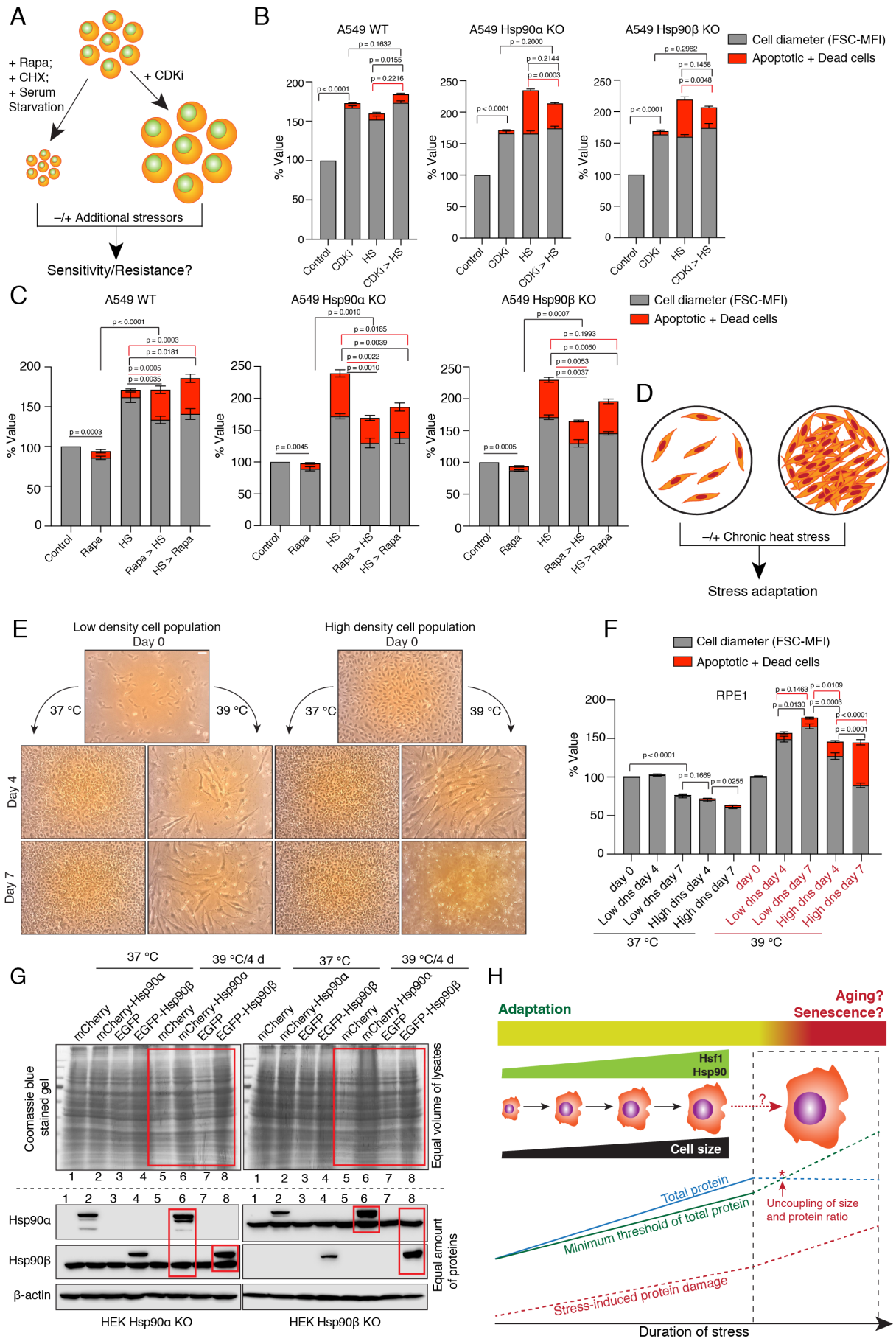

A
+ Rapa;
+ CHX;
+ Serum
Starvation
+ CDKi
–/+ Additional stressors
Sensitivity/Resistance?
B
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
Cell diameter (FSC-MFI)
Apoptotic + Dead cells
% Value
Control
CDKi
HS
CDKi > HS
C
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
Cell diameter (FSC-MFI)
Apoptotic + Dead cells
% Value
Control
Rapa
HS
Rapa > HS
HS > Rapa
D
–/+ Chronic heat stress
Stress adaptation
E
Low density cell population
Day 0
High density cell population
Day 0
37 °C
39 °C
Day 4
Day 7
F
Cell diameter (FSC-MFI)
Apoptotic + Dead cells
RPE1
% Value
day 0
Low dns day 4
Low dns day 7
High dns day 4
High dns day 7
37 °C
39 °C
G
37 °C
39 °C/4 d
mCherry
mCherry-Hsp90α
EGFP
EGFP-Hsp90β
Coomassie blue stained gel
Equal volume of lysates
Hsp90α
Hsp90β
β-actin
Equal amount of proteins
HEK Hsp90α KO
HEK Hsp90β KO
H
Adaptation
Aging?
Senescence?
Hsf1
Hsp90
Cell size
Total protein
Minimum threshold of total protein
Uncoupling of size and protein ratio
Stress-induced protein damage
Duration of stress

Figure 7. Enlarged cells are more resistant to additional stress. (A) Scheme of cell size enlargement or reduction experiments. CHX, cycloheximide; CDKi, CDK4/6 inhibitor. **(B)** Cell size was first enlarged by treating cells with 100 nM CDKi for 3 days; then, cells were washed and subjected to chronic HS at 40 °C for 3 more days (CDKi > HS). Cell size (% FSC-MFI; grey part of the bars) and cell death (% annexin V and PI-positive; red part of the bars) were measured by flow cytometry. The values for cell size and death in the different experimental conditions are normalized to the respective 37 °C controls (n = 3 biologically independent experiments). **(C)** Cells were first pretreated with 7.5 nM rapamycin (Rapa) for 3 days to reduce the cell size. After that, the cells were subjected to chronic HS at 40 °C for 3 days (Rapa > HS). HS > Rapa, the two treatments were done the other way around. The cell size (% FSC-MFI) and relative cell death (% annexin V and PI-positive) were quantified by flow cytometry. The values for cell size and death in different experimental conditions are normalized to the respective 37 °C control (n = 3 biologically independent experiments). **(D)** Scheme of experiments aimed at determining impact of limiting physical space on cell size increase. **(E** and **F)** Phase-contrast micrographs of RPE1 cells seeded in different numbers to restrict the space for cell size increase during adaptation to chronic HS (representative images of n = 4 biologically independent experiments). The cell size (% FSC-MFI) and relative cell death (% annexin V-PI positive) are quantified by flow cytometry. For the bar graphs, the values for cell size and death in different conditions are normalized to the low density (dns) cell population at 37 °C day 0 (n = 4 biologically independent experiments). The data are represented as mean values ± SEM for all bar graphs. **(G)** Immunoblots in the lower panels show the endogenous Hsp90α and Hsp90β, and the exogenously

overexpressed larger fusion proteins of Hsp90α (as mCherry-Hsp90α) and Hsp90β (as EGFP-Hsp90β), with red boxes highlighting samples with exogenous Hsp90. Images of the Coomassie-stained gels in the upper panels show the corresponding levels of total proteins with red boxes indicating lanes for samples from cells subjected to chronic HS (representative images of n = 2 biologically independent experiments). **(H)** Schematic representation of impact of chronic mild stress on cells. Wild-type cells initially adapt by enlarging their size and increasing total protein to maintain a minimum threshold level of functional proteins. The right part of the scheme (surrounded by a stippled box), shows what may happen if stress persists for much longer: cell size enlargement and translation are uncoupled, and because of protein damage, which continues to accumulate, cells become senescent and/or die.

Figure supplements with legends

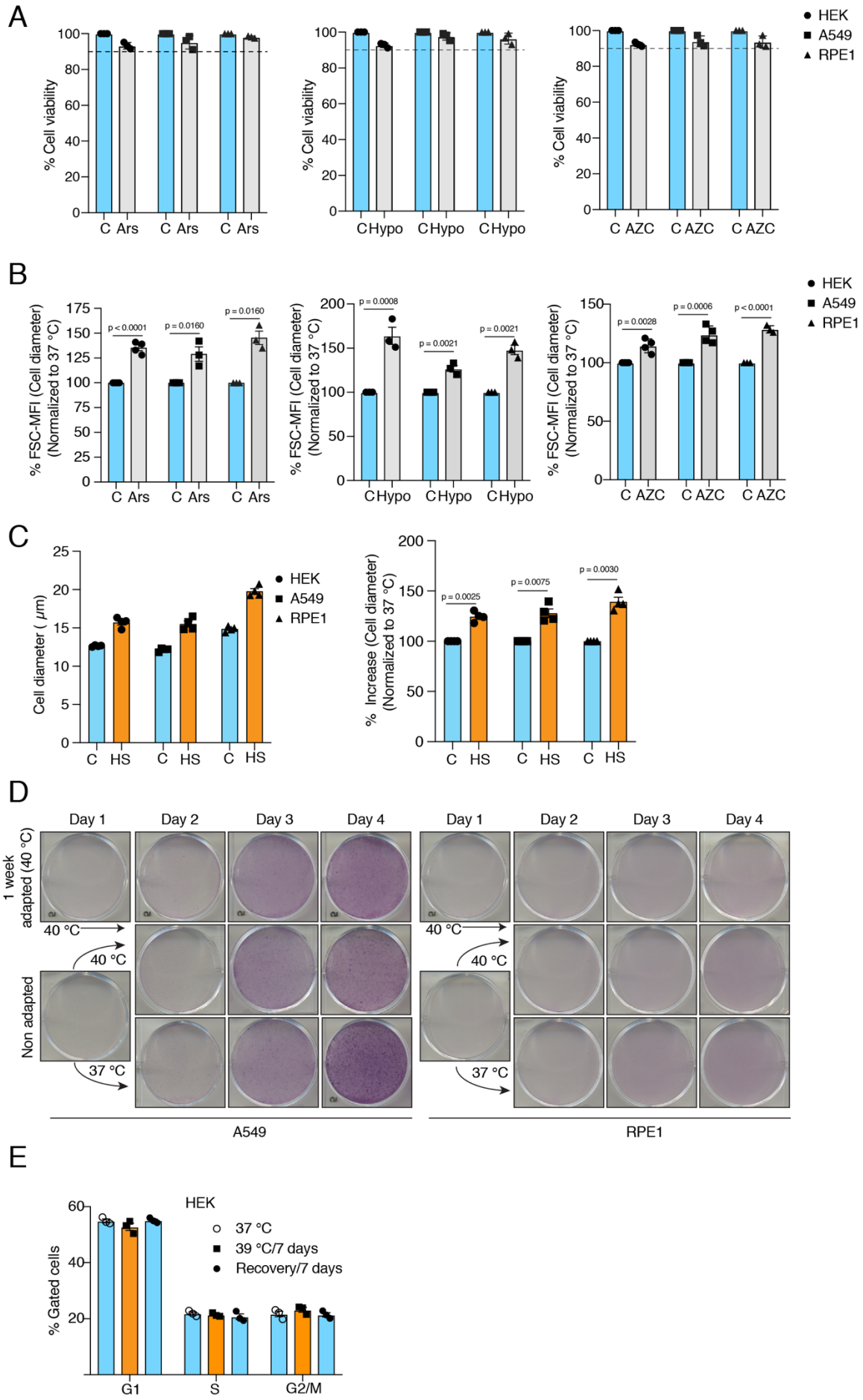

A
% Cell viability
C Ars
C Hypo
C AZC
HEK
A549
RPE1
B
% FSC-MFI (Cell diameter) (Normalized to 37 °C)
p < 0.0001
p = 0.0160
p = 0.0008
p = 0.0021
p = 0.0028
p = 0.0006
p < 0.0001
C
Cell diameter (μm)
% Increase (Cell diameter) (Normalized to 37 °C)
p = 0.0025
p = 0.0075
p = 0.0030
C HS
D
Day 1
Day 2
Day 3
Day 4
1 week adapted (40 °C)
Non adapted
40 °C
37 °C
A549
RPE1
E
% Gated cells
37 °C
39 °C/7 days
Recovery/7 days
G1
S
G2/M

Figure supplement 1. Cells increase their size in response to different types of chronic stress. (A) Flow cytometric quantification of cell viability after 4 days of 10 μM sodium arsenite (Ars), 1% hypoxia (Hypo), or L-azetidine-2-carboxylic acid (AZC) treatment (5 μM) (n = 3 biologically independent samples for Ars, Hypo, and AZC, respectively, for all cell lines). **(B)** Flow cytometric quantification of cell size after 4 days of treatment with 10 μM sodium arsenite (Ars), 1% hypoxia (Hypo), or 5 μM L-azetidine-2-carboxylic acid (AZC) (n = 4, 3, and 4 for Ars, Hypo, and AZC, respectively for HEK; for A549, n = 3, 3, and 4 for Ars, Hypo, and AZC, respectively; for RPE1, n = 3, 3, and 3 biologically independent samples for Ars, Hypo, and AZC, respectively). **(C)** Cell diameters of cells subjected to 7 days of mild HS, measured with an automated cell counter; the bar graph on the left shows absolute values whereas the one on the right shows the same data as % changes relative to cells left at control conditions (samples C); n = 4 samples. **(D)** Scanned images of plates with crystal violet-stained cells (representative images of n = 3 independent experiments). **(E)** Flow cytometric analysis of cell cycle after 1 week in chronic HS and post HS recovery (n = 3 biologically independent samples). The data are represented as mean values ± SEM for all bar and line graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

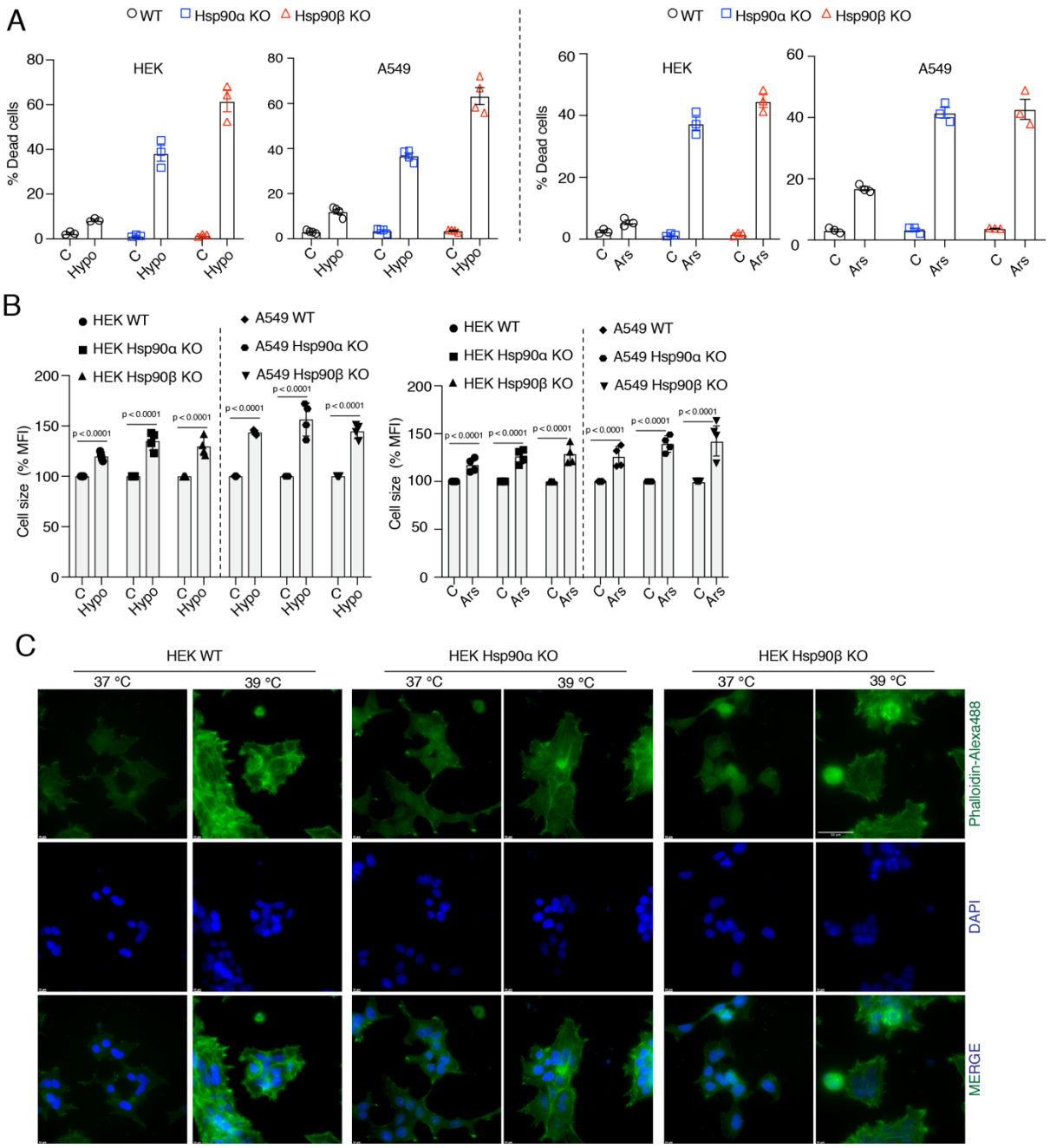


Figure supplement 2. Cells are unable to adapt to chronic stress in the absence of one of the Hsp90 isoforms. (A) Flow cytometric quantification of cell death of A549 WT and Hsp90α/β KO cells after 4 days in 1% hypoxia (Hypo) and 10 μM sodium arsenite (Ars) treatment (n = 3 biologically independent samples). **(B)** Flow cytometric quantification of cell size after 4 days in 1% hypoxia (Hypo) and 10 μM sodium arsenite (Ars) treatment (n = 4 biologically independent samples). **(C)** Fluorescence microscopy images of HEK WT and Hsp90α/β KO cells after 4 days of chronic HS. The cytoskeleton is stained with Phalloidin-Alexa488 (green), and the nucleus is stained with DAPI (blue). The scale bar in the top right micrograph is 50 μM (images are representative of n = 2 biologically independent experiments). The data are

represented as mean values ± SEM for all bar graphs. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

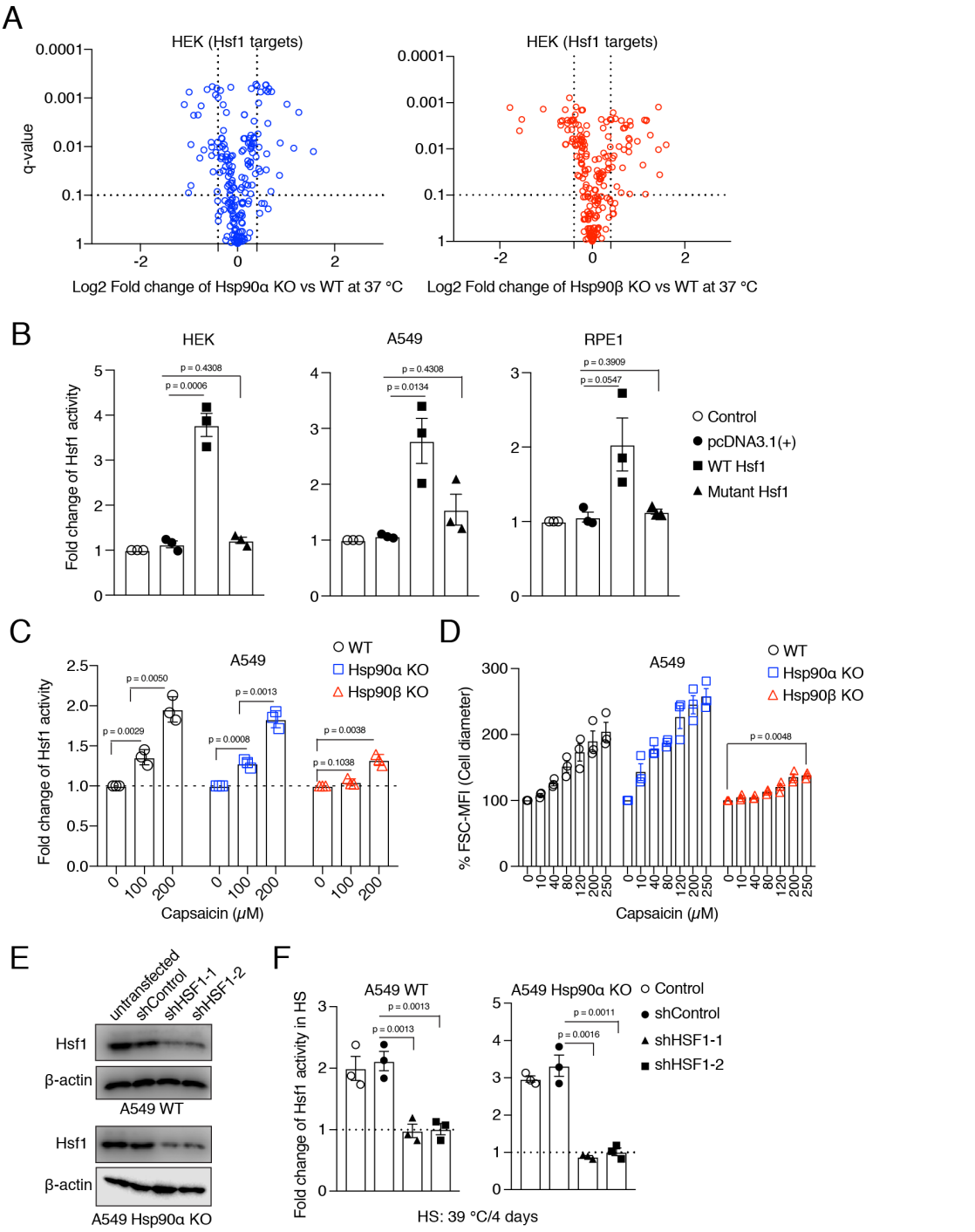

A
HEK (Hsf1 targets)
q-value
Log2 Fold change of Hsp90α KO vs WT at 37 °C
Log2 Fold change of Hsp90β KO vs WT at 37 °C
B
HEK
A549
RPE1
Fold change of Hsf1 activity
Control
pcDNA3.1(+)
WT Hsf1
Mutant Hsf1
C
A549
WT
Hsp90α KO
Hsp90β KO
Capsaicin (μM)
D
% FSC-MFI (Cell diameter)
E
untransfected
shControl
shHSF1-1
shHSF1-2
Hsf1
β-actin
A549 WT
A549 Hsp90α KO
F
A549 WT
A549 Hsp90α KO
Fold change of Hsf1 activity in HS
HS: 39 °C/4 days
shHSF1-1
shHSF1-2
G
MAFs (WT)
MAFs (90αKO 90βHET)
H
I
HS: 40 °C/2 days
C
HS
J

Figure supplement 3. Hsf1 induces cell size in response to stress. (A) Volcano plots of the normalized fold changes in protein levels of some of the core Hsf1 target genes (list obtained from https://hsf1base.org/) in Hsp90α/β KO cells compared to WT HEK as determined by quantitative label-free proteomic analysis. Molecular chaperones, whose expression is regulated by Hsf1, are excluded from this dataset (n = 3 biologically independent samples). Log2 fold changes of > 0.5 or < -0.5 with a p-value of < 0.05 were considered significant differences for a particular protein. **(B)** Fold change of Hsf1 activity of HEK, A549, and RPE1 cells upon overexpressing WT and mutant Hsf1 in combination with EGFP, as measured with the Hsf1 luciferase reporter. Control is transfected with only Hsf1 reporter plasmid and pEGFP-C1, those are common to all the experimental conditions; (n = 3 biologically independent samples). **(C)** Fold change of Hsf1 activity in A549 WT, Hsp90α KO, and Hsp90β KO cells after 4 days of capsaicin treatment as measured by luciferase reporter assay (n = 3 biologically independent samples). **(D)** Flow cytometric quantification of cell size after 4 days of capsaicin treatment of Hsp90α/β KO and WT A549 cells (n = 3 biologically independent samples). **(E)** Immunoblots of Hsf1 after Hsf1 knockdown in A549 WT and Hsp90α KO cells. β-actin serves as the loading control (representative of n = 2 independent experiments). **(F)** Fold change of Hsf1 activity in A549 WT and Hsp90α KO cells in chronic HS after Hsf1 knockdown as measured by luciferase reporter assays. Here the chronic HS for A549 cells is 39 °C to instead of 40 °C to reduce HS-induced damage in Hsf1 knockdown conditions (n = 3 biologically independent samples). **(G)** Flow cytometric quantification of cell size of mouse fibroblast. (90αKO, 90β HET), homozygous *hsp90α* KO, heterozygous *hsp90β* KO cells (n = 6 biologically independent samples). **(H)** Fold change of Hsf1 activity in (90αKO, 90β HET) MAFs compared to WT at 37 °C, as measured by luciferase reporter assays (n = 3 biologically independent samples). **(I)** Fold change of Hsf1 activity in MAFs subjected to chronic HS (orange bars) compared to 37 °C (blue bars), as measured by luciferase reporter assay (n = 3 biologically independent samples). **(J)** Flow cytometric quantification of cell size of MAFs subjected to chronic HS (orange bars) by comparison to 37 °C (blue bars) (n = 4 biologically independent samples). The data are represented as mean values ± SEM for all bar graphs. Where indicated, the statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

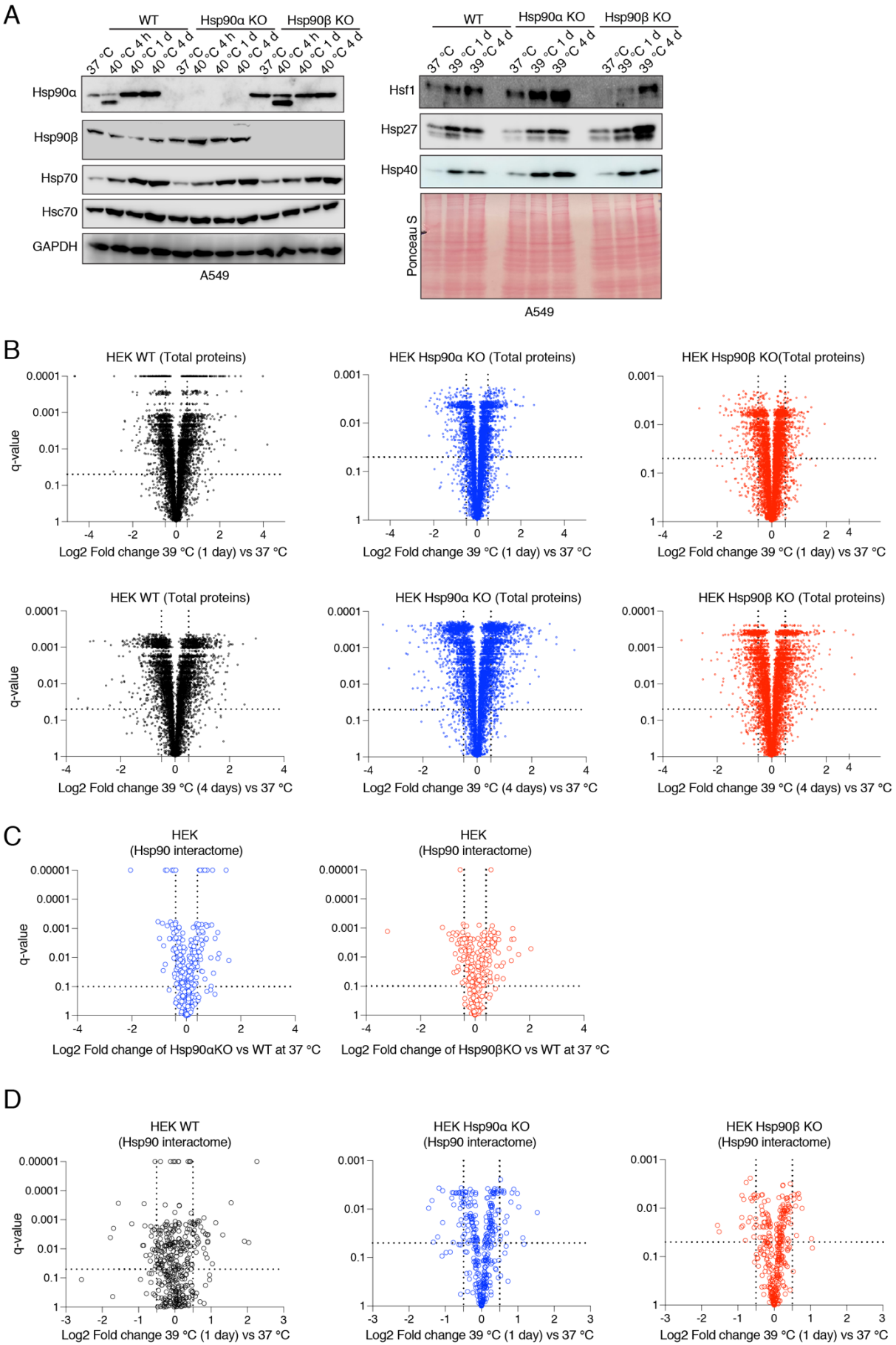

A
WT
Hsp90α KO
Hsp90β KO
37 °C
40 °C 4 h
40 °C 1 d
40 °C 4 d
Hsp90α
Hsp90β
Hsp70
Hsc70
GAPDH
A549
39 °C 1 d
39 °C 4 d
Hsf1
Hsp27
Hsp40
Ponceau S
B
HEK WT (Total proteins)
HEK Hsp90α KO (Total proteins)
HEK Hsp90β KO(Total proteins)
HEK Hsp90β KO (Total proteins)
q-value
Log2 Fold change 39 °C (1 day) vs 37 °C
Log2 Fold change 39 °C (4 days) vs 37 °C
C
HEK
(Hsp90 interactome)
Log2 Fold change of Hsp90αKO vs WT at 37 °C
Log2 Fold change of Hsp90βKO vs WT at 37 °C
D
HEK WT
(Hsp90 interactome)
HEK Hsp90α KO
(Hsp90 interactome)
HEK Hsp90β KO
(Hsp90 interactome)

Figure supplement 4. Hsp90α/β KO cells maintain total proteins and Hsp90 interactors in chronic stress. (A) Immunoblots of some molecular chaperones of A549 WT and Hsp90α/β KO cells (α KO, Hsp90αKO; β KO, Hsp90βKO). GAPDH and the Ponceau S-stained nitrocellulose filter serve as loading controls. **(B)** Volcano plots of the normalized fold changes of total proteins of cells subjected to chronic HS for 1 and 4 days determined by quantitative label-free proteomic analysis of Hsp90α/β KO and WT HEK cells. Each genotype was compared with its respective 37 °C control (n = 3 biologically independent samples) **(C)** Volcano plots of the normalized fold changes of Hsp90 interactors (list obtained from https://www.picard.ch/Hsp90Int) in Hsp90α/β KO HEK cells compared to WT as determined by quantitative label-free proteomic analysis (n = 3 biologically independent samples). **(D)** Volcano plots of the normalized fold changes of Hsp90 interactors in cells subjected to 1 day of chronic HS determined by quantitative label-free proteomic analysis. Each genotype was compared with its respective 37 °C control (n = 3 biologically independent samples)**.** For all volcano plots Log2 fold changes of > 0.5 or < -0.5 with a p-value of < 0.05 were considered significant differences for a particular protein.

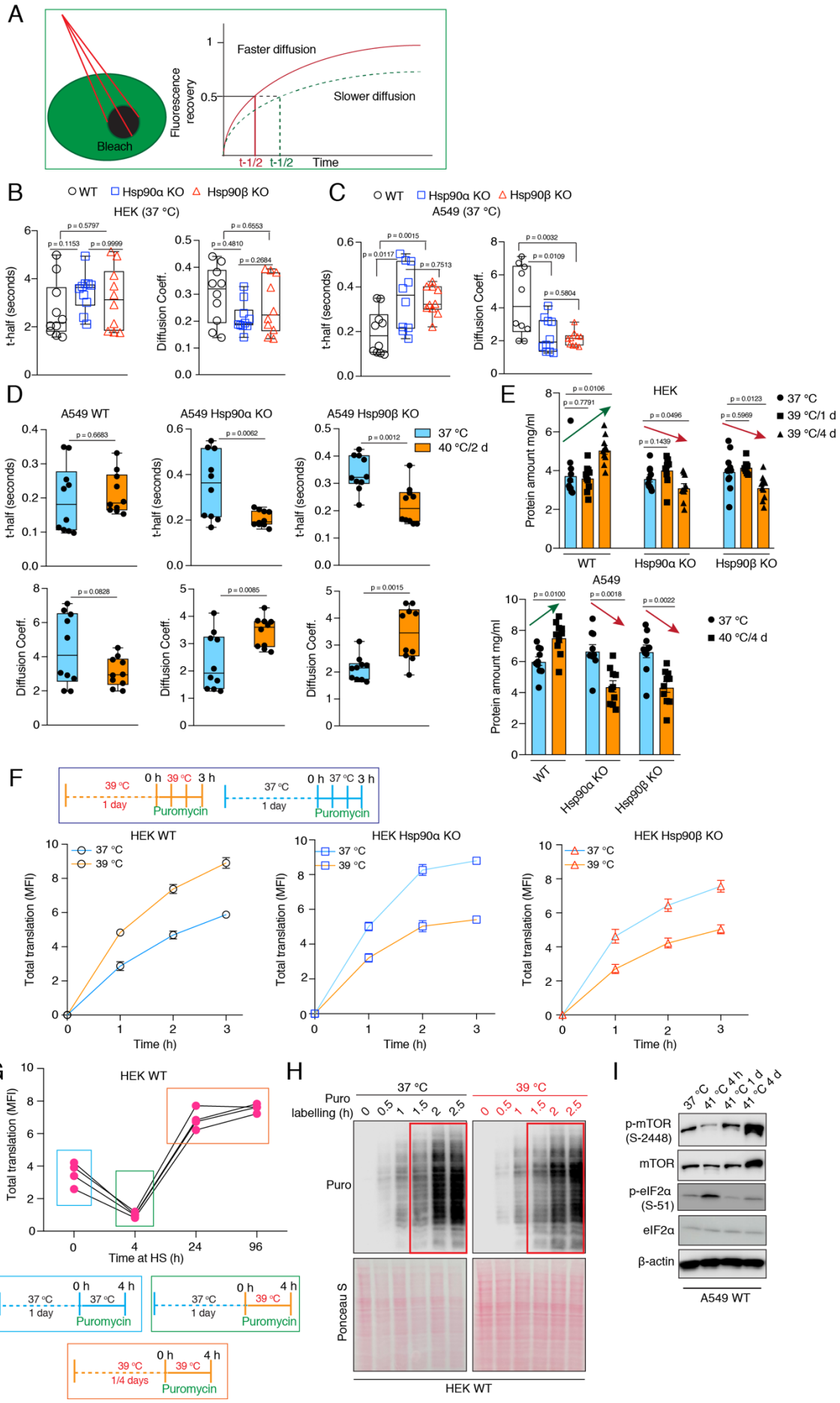

A
Bleach
Fluorescence recovery
Faster diffusion
Slower diffusion
t-1/2 t-1/2 Time
B
WT Hsp90α KO Hsp90β KO
HEK (37 °C)
t-half (seconds)
Diffusion Coeff.
C
A549 (37 °C)
D
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
37 °C
40 °C/2 d
E
HEK
37 °C
39 °C/1 d
39 °C/4 d
Protein amount mg/ml
A549
40 °C/4 d
F
39 °C 1 day Puromycin
37 °C 1 day Puromycin
HEK WT
HEK Hsp90α KO
HEK Hsp90β KO
Total translation (MFI)
Time (h)
G
HEK WT
Time at HS (h)
37 °C 1 day Puromycin
39 °C 1 day Puromycin
39 °C 1/4 days Puromycin
H
Puro labelling (h)
Puro
Ponceau S
HEK WT
I
p-mTOR (S-2448)
mTOR
p-eIF2α (S-51)
eIF2α
β-actin
A549 WT

Figure supplement 5. Cells maintain cytoplasmic density and total protein ratio during stress-induced cell size increase. (A) Scheme of the FRAP experiments. **(B** to **D)** FRAP experiments with live cells expressing EGFP. The respective box plots represent the t-half values of recovery of EGFP fluorescence and the apparent EGFP diffusion coefficients (n= 10 cells from 2 biologically independent experiments). **(E)** Protein amount in cell lysates (5,000 cells lysed in 200 μl lysis buffer) of control cells and cells adapted to chronic HS as measured by Bradford assay. **(F)** Flow cytometric analysis of global translation of HEK WT and Hsp90α/β KO cells at 37 °C and after 1 day under chronic HS. See scheme of the experiment on the top. Nascent polypeptide chains were labeled with OP-puromycin during cell culture, and the incorporation of puromycin at different time points was analyzed (n = 4 experimental samples). **(G)** Total translation of HEK WT cells during a 4 h time span during different phases of chronic HS**. (H)** Immunoblot analysis of global translation as indicated by incorporation of puromycin into nascent polypeptides during the first 4 h of shifting cells to chronic HS conditions, compared to cells remaining at 37 °C. The 0 h time point of puromycin labelling serves as a negative control, and the Ponceau S-stained nitrocellulose filter as loading control (representative images from n = 2 biologically independent experiments) **(I)** Immunoblots of some of the translation-related proteins in A549 cells. β-actin serves as the loading control.

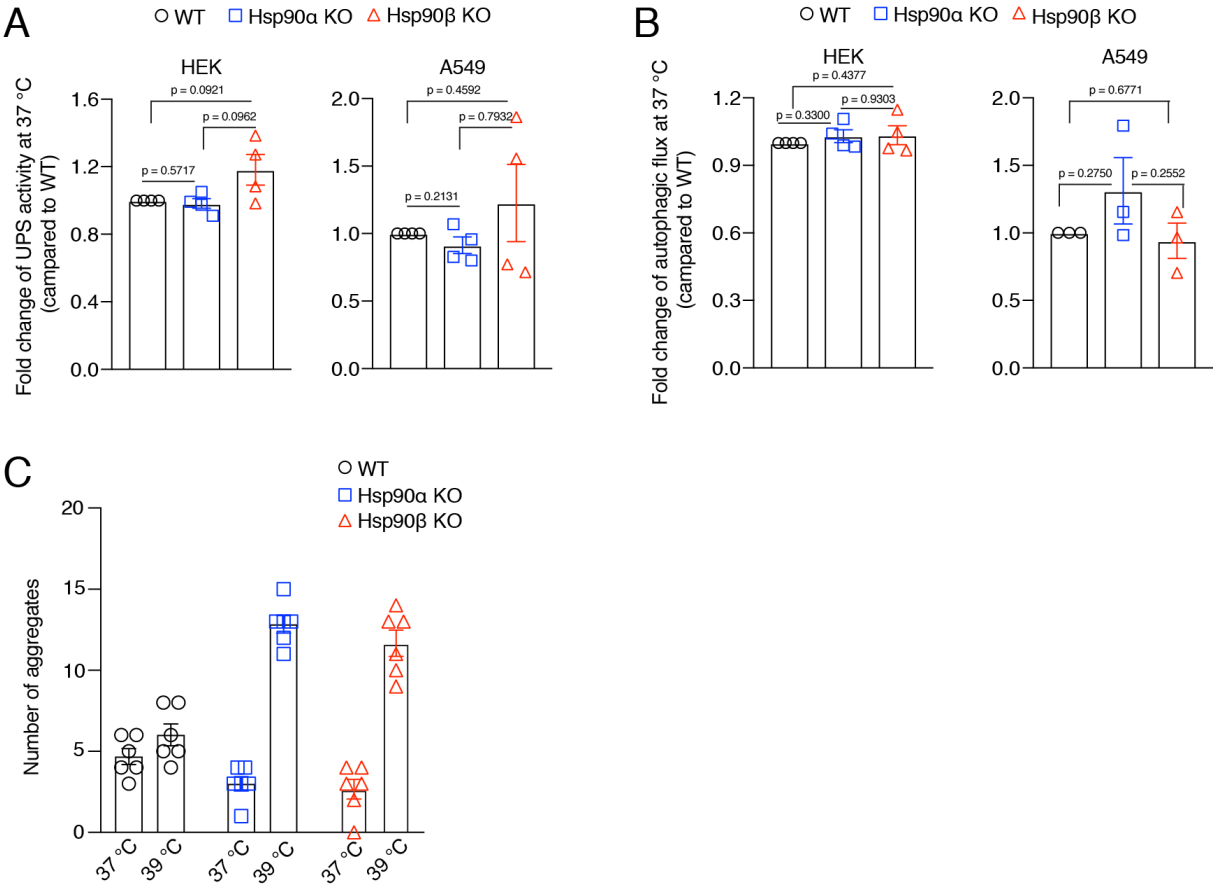


Figure supplement 6. Hsp90α/β KO cells maintain WT levels of protein degradation activities in unstressed conditions. (A) Flow cytometric determination of the *in vivo* UPS activity using the Ub-M-GFP and Ub-R-GFP reporter plasmids (n = 4 biologically independent samples). (**B**) Flow cytometric measurement of autophagic flux using a mCherry-GFP-LC3 reporter. Flux is calculated as the ratio of the mean fluorescence intensities of mCherry and GFP-positive cells (n = 4 biologically independent samples). (**C**) Quantification of the number of EGFP-Q74 aggregates from 6 representative micrographs such as the ones of Fig. 6D. For each bar data obtained from six representative macrographs. The data are represented as mean values ± SEM for all bar graphs, standardized to the respective WT values set to 1. The statistical significance between the groups was analyzed by two-tailed unpaired Student's t-tests.

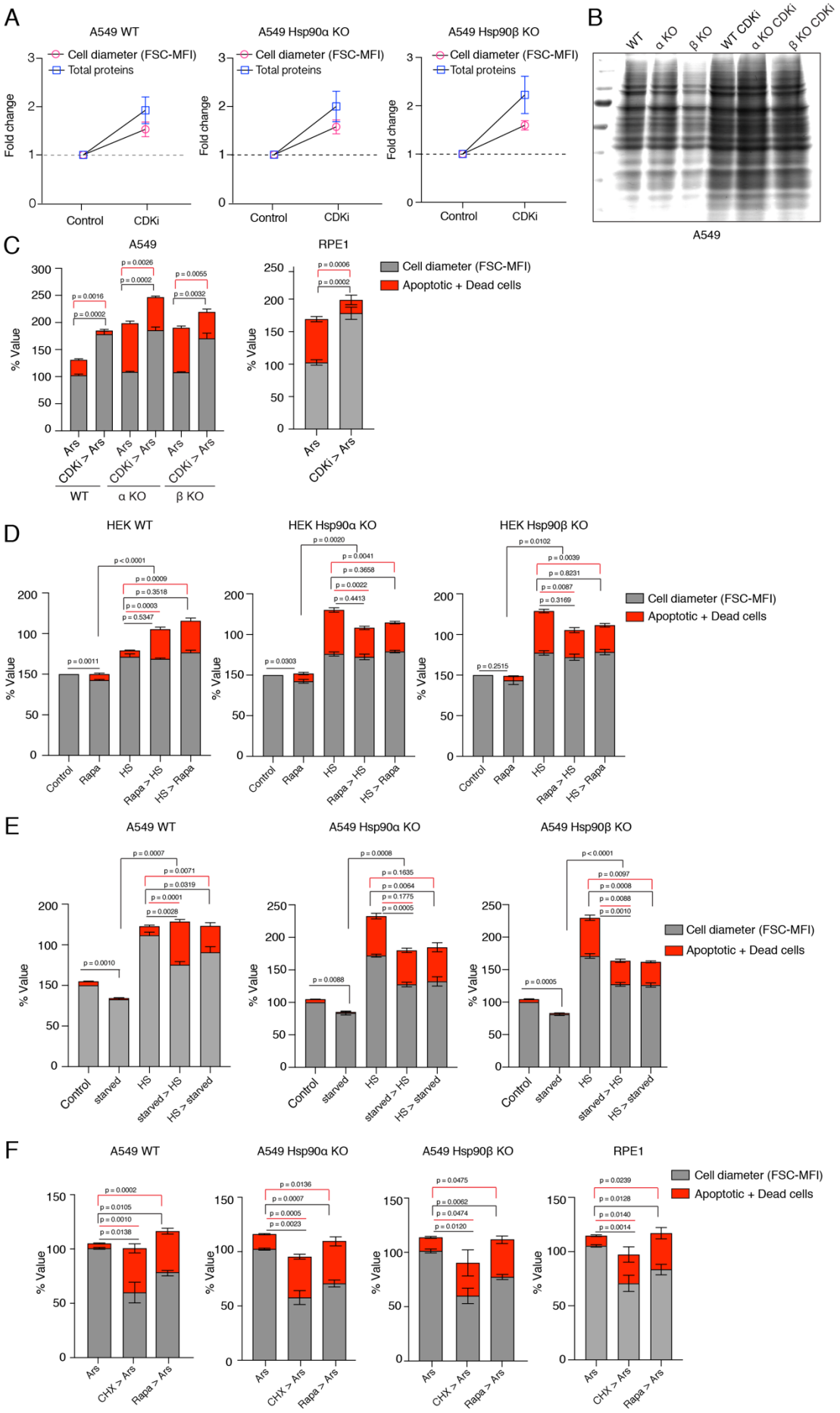
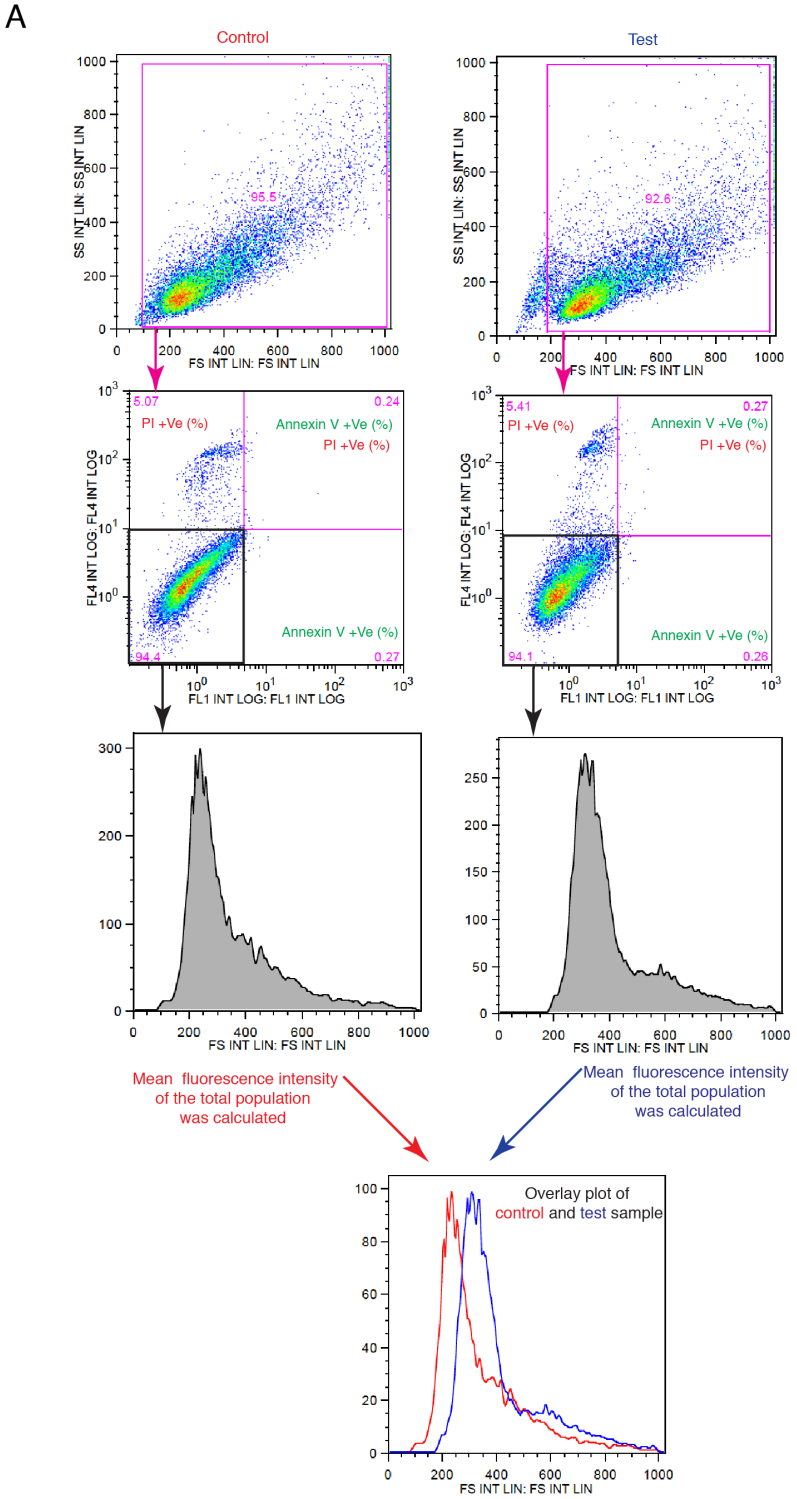

A
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
Cell diameter (FSC-MFI)
Total proteins
Fold change
Control
CDKi
B
WT
α KO
β KO
WT CDKi
α KO CDKi
β KO CDKi
A549
C
A549
RPE1
% Value
Ars
CDKi > Ars
WT
α KO
β KO
Cell diameter (FSC-MFI)
Apoptotic + Dead cells
D
HEK WT
HEK Hsp90α KO
HEK Hsp90β KO
Control
Rapa
HS
Rapa > HS
HS > Rapa
E
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
starved
starved > HS
HS > starved
F
A549 WT
A549 Hsp90α KO
A549 Hsp90β KO
RPE1
CHX > Ars
Rapa > Ars

Figure supplement 7. Smaller cells are more susceptible to additional stress. (A) Cell size was enlarged by treating cells with 100 nM CDKi for 3 days. Fold change of cell size (represented by the FSC-MFI values) and total proteins (determined as MFI-FL1 values) were analyzed by flow cytometry. Cells were fixed, and total proteins were stained using Alexa Fluor 488 NHS ester (n = 3 biologically independent experiments). **(B)** Coomassie-stained protein gel showing protein samples from equal numbers of cells treated or not with CDKi (representative images of n = 2 biologically independent experiments). **(C)** Cell size was enlarged by treating cells with CDKi for 3 days, before cells were treated with sodium arsenite (40 μM) for 3 days. Cell size (% MFI) and cell death (% annexin V and PI-positive) are measured by flow cytometry. α KO, Hsp90α KO; β KO, Hsp90β KO cells. **(D)** Order of treatment experiment as in Fig. 7C, but with HEK cells. Cell size (% MFI) and relative cell death (% annexin V and PI-positive) are quantified by flow cytometry. The values for cell size and death in the different experimental conditions are normalized to the respective 37 °C controls (n = 3 biologically independent experiments). **(E)** Cell size was reduced by serum starvation (starved) for 3 days before subjecting cells to chronic HS for 3 additional days (starved > HS). HS > starved, the two treatments were done the other way around (HS > starved). Cell size (% MFI) and relative cell death (% annexin V-PI positive) were quantified by flow cytometry and normalized to the respective 37 °C controls (n = 3 experimental samples). **(F)** Order of treatment experiment with CHX and rapamycin to reduce cell size first for 3 days and then subjecting cells to oxidative stress with 10 μM sodium arsenite (Ars) for 1 day. Cell size (% MFI) and relative cell death (% annexin V and PI-positive) were quantified by flow cytometry and normalized to the Ars single treatment controls (n = 3 experimental samples).

A


Control
Test
SS INT LIN: SS INT LIN
FS INT LIN: FS INT LIN
95.5
92.6
FL4 INT LOG: FL4 INT LOG
FL1 INT LOG: FL1 INT LOG
PI +Ve (%)
Annexin V +Ve (%)
5.07
0.24
94.4
0.27
5.41
0.27
94.1
0.26
Mean fluorescence intensity of the total population was calculated
Mean fluorescence intensity of the total population was calculated
Overlay plot of control and test sample

B

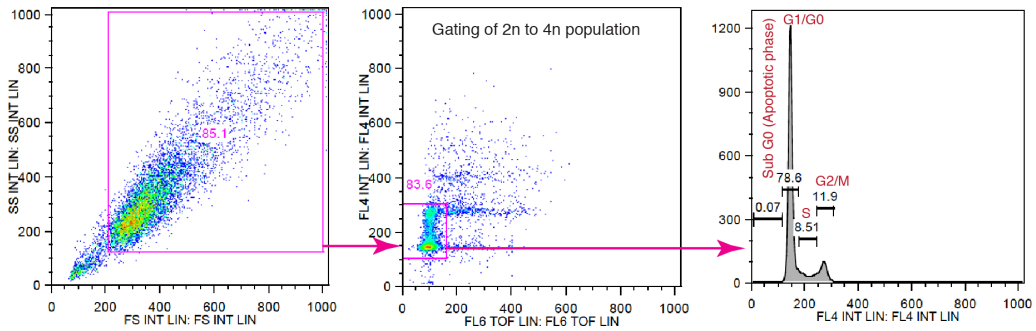

SS INT LIN: SS INT LIN
FS INT LIN: FS INT LIN
85.1
Gating of 2n to 4n population
FL4 INT LIN: FL4 INT LIN
FL6 TOF LIN: FL6 TOF LIN
83.6
Sub G0 (Apoptotic phase)
G1/G0
G2/M
S
0.07
78.6
11.9
8.51

Figure supplement 8. Schematic representation of the flow cytometric strategies for cell size and cell cycle analyses. (**A**) Gating and analysis strategy for cell size; relevant to Fig. 1B, E and H, Fig. 2C, Fig. 5B and H, Fig. 7B-C and F, figure supplements 1B, 2B, 3D, G and J, and 7A and C-F. For size measurements, cell populations were gated based on the values of the forward scatter (FSC). (**B**) Gating and analysis strategy for cell cycle; relevant to Fig. 1C-D and I, and figure supplement 1D.

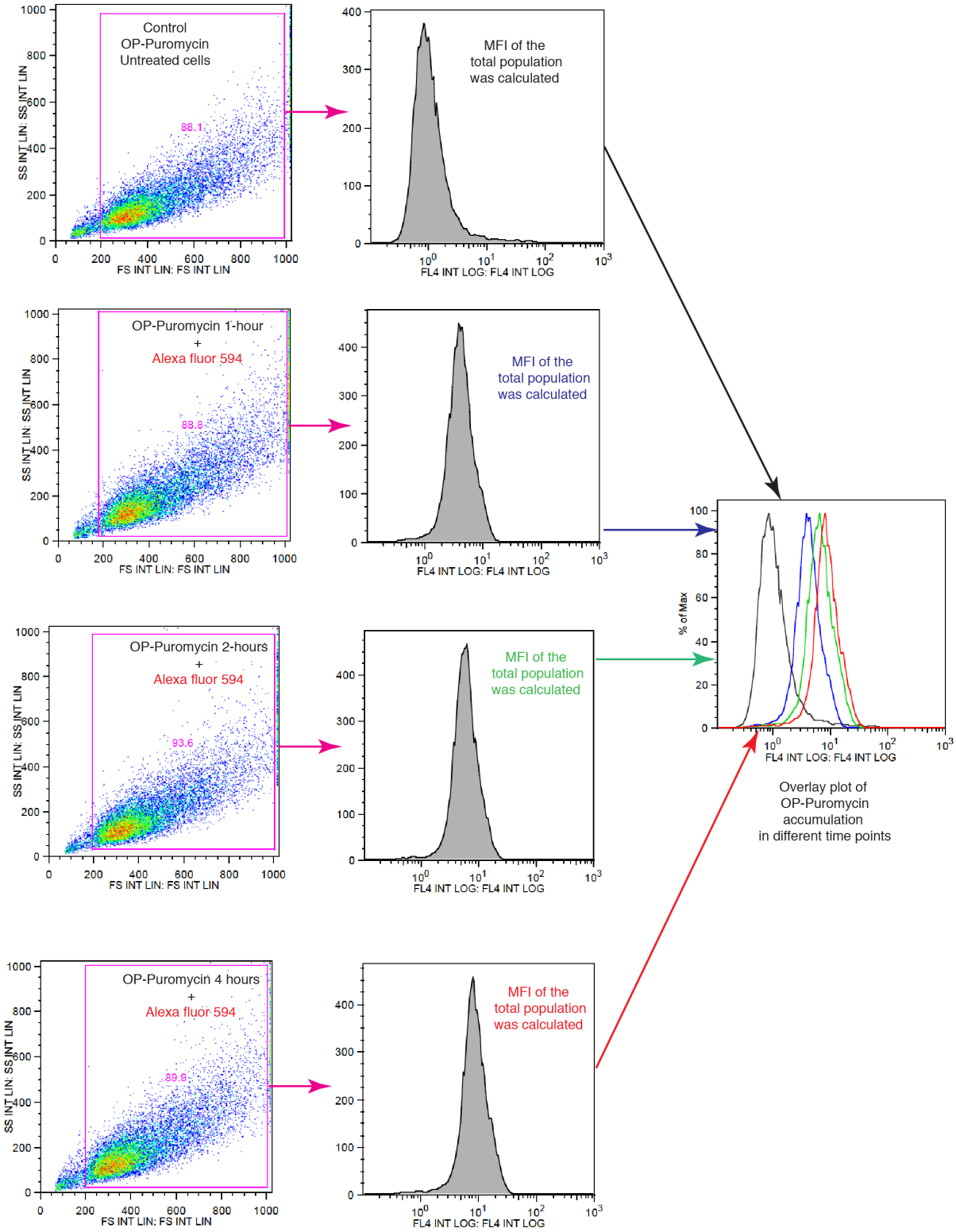


Figure supplement 9. Schematic representation of the flow cytometric strategies to measure translation. Relevant to Fig. 5D and H, and figure supplement 5F-G.

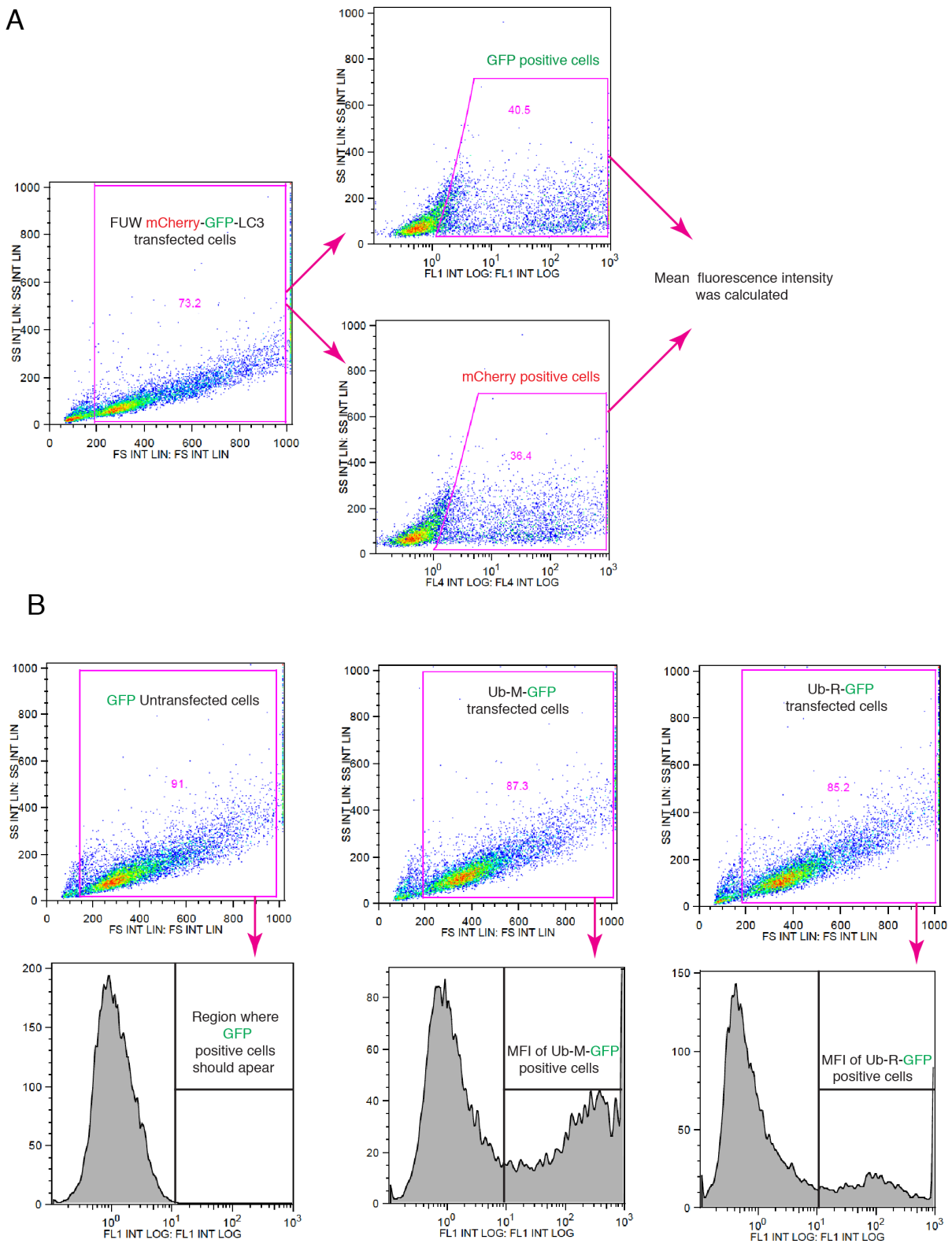


Figure supplement 10. Schematic representation of the flow cytometric strategies for measuring autophagic flux and *in vivo* UPS activities. (**A**) Gating strategy for autophagic flux measurements, relevant to Fig. 6B and figure supplement 6B. (**B**) Gating strategy for measuring UPS activity; related to Fig. 6A and figure supplement 6A.

Supplementary file 1

Table 1. List of oligonucleotides used to generate the expression vectors for the shRNAs shHSF1-1 and shHSF1-2.

shRNA	Oligo name	Sequence 5’ to 3’
shHSF1-1	HSF1 shRNA 3UTR forward	5'-CCG GGC AGG TTG TTC ATA GTC AGA ACT CGA GTT CTG ACT ATG AAC AAC CTG CTT TTT G-3'
	HSF1 shRNA 3UTR reverse	5'-AAT TCA AAA AGC AGG TTG TTC ATA GTC AGA ACT CGA GTT CTG ACT ATG AAC AAC CTG C-3'
shHSF1-2	HSF1 shRNA CDS forward	5'-CCG GCC AGC AAC AGA AAG TCG TCA ACT CGA GTT GAC GAC TTT CTG TTG CTG GTT TTT G-3'
	HSF1 shRNA CDS reverse	5'-AAT TCA AAA ACC AGC AAC AGA AAG TCG TCA ACT CGA GTT GAC GAC TTT CTG TTG CTG G-3'

Table 2. List of antibodies used in this study.

Antigen/Antibody	Supplier	Catalog #	Host	Clonality	Dilution
anti-GAPDH	HyTest Ltd.	5G4	Mouse	monoclonal	1:1000
anti-Hsp25/27	StressMarq	SMC-114	Mouse	monoclonal	1:1000
anti-Puromycin	Sigma-Aldrich	MABE343	Mouse	monoclonal	1:22000
anti-Lamin B1	Cell Signaling Technology	12586	Rabbit	monoclonal	1:1000
anti-Hsp40/Hdj1	Enzo Lifesciences	ADI-SPA-400	Rabbit	polyclonal	1:1000
anti-Hsf1	Enzo Lifesciences	ADI-SPA-901	Rabbit	polyclonal	1:1000
anti-Hsp70	StressMarq	SMC-100	Mouse	monoclonal	1:1000
anti-Phospho-eIF2α (Ser51)	Cell Signaling Technology	3597	Rabbit	monoclonal	1:1000
anti-eIF2α	Cell Signaling Technology	9722	Rabbit	polyclonal	1:1000
anti-Hsp90α (9D2)	Enzo Lifesciences	ADI-SPA-840	Rat	monoclonal	1:1000
anti-Hsp90β (scFv H90-10)	Geneva Antibody Facility	ABCD_A0870	Mouse	monoclonal	1:2000
anti-mTOR	Cell Signaling Technology	2983	Rabbit	monoclonal	1:2000
anti-Phospho-mTOR (Ser2448)	Cell Signaling Technology	2971	Rabbit	polyclonal	1:1000
anti-Phospho-S6 Ribosomal Protein (Ser235/236)	Cell Signaling Technology	4858	Rabbit	monoclonal	1:1000
anti-S6 Ribosomal Protein	GeneTex	GTX130450	Rabbit	polyclonal	1:1000
anti-Hsc70	StressMarq	SMC-151	Mouse	monoclonal	1:2000
anti-beta-Actin	Cell Signaling Technology	3700	Mouse	monoclonal	1:2000
anti-4E-BP1(N1C3)	GeneTex	GTX109162	Rabbit	polyclonal	1:1000
anti-phospho-4E-BP1(Thr37/46)	GeneTex	GTX133182	Rabbit	polyclonal	1:1000

Source data files

Available as separate files:

- **Source data 1**: Excel file with a subset of the proteomic data of WT and Hsp90α/β KO HEK293T cells. In the supplied Excel file, the following abbreviations (column headers) are used: 37C-WT, WT cells cultured at 37 °C; 39C-1d-WT, WT cells cultured at 39 °C for 1 day; 39C-4d-WT, WT cells cultured at 39 °C for 4 days; 37C-a-KO, Hsp90α KO cells cultured at 37 °C, 39C-1d-a-KO, Hsp90α KO cells cultured at 39 °C for 1 day; 39C-4d-a-KO, Hsp90α KO cells cultured at 39 °C for 4 days; 37C-b-KO, Hsp90β KO cells cultured at 37 °C; 39C-1d-b-KO, Hsp90β KO cells cultured at 39 °C for 1 day; 39C-4d-b-KO, Hsp90β KO cells cultured at 39 °C for 4 days.
- **Source data 2**: Excel file with all primary data for graphs.
- **Source data 3**: Pdf file with original immunoblots (with indications of molecular weights) for the main figures.
- **Source data 4**: Pdf file with original immunoblots (with indications of molecular weights) for the figure supplements.