

Heat Shock Factor 1 forms condensates and restructures the yeast genome before activating target genes

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Linda S Rubio, Suman Mohajan, David S Gross 

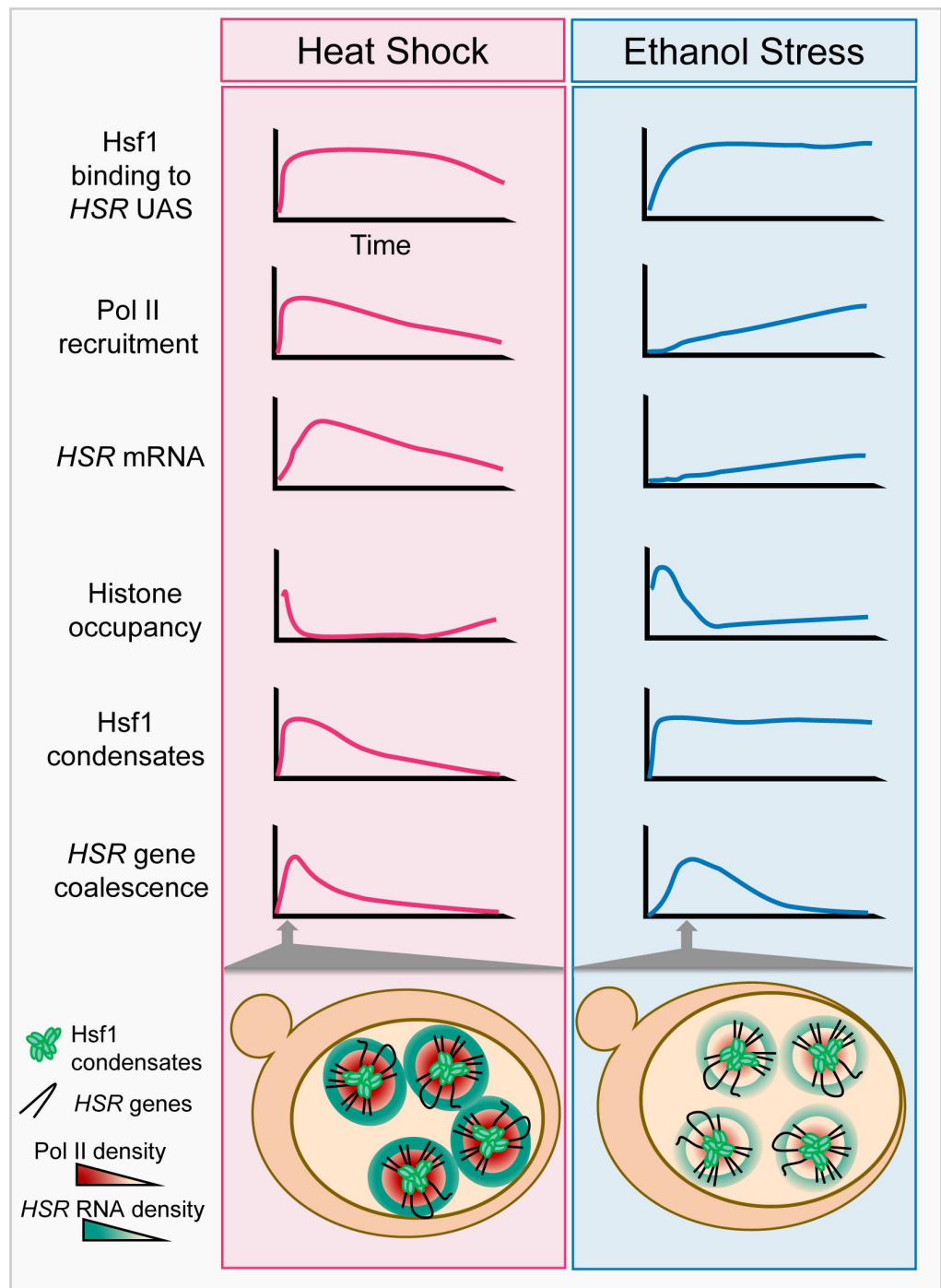
Department of Biochemistry and Molecular Biology, Louisiana State University Health Sciences Center, Shreveport, LA 71130

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Abstract

In insects and mammals, 3D genome topology has been linked to transcriptional states yet whether this link holds for other eukaryotes is unclear. Using both ligation proximity and fluorescence microscopy assays, we show that in *Saccharomyces cerevisiae*, *Heat Shock Response (HSR)* genes dispersed across multiple chromosomes and under the control of Heat Shock Factor (Hsf1) rapidly reposition in cells exposed to acute ethanol stress and engage in concerted, Hsf1-dependent intergenic interactions. Accompanying 3D genome reconfiguration is equally rapid formation of Hsf1-containing condensates. However, in contrast to the transience of Hsf1-driven intergenic interactions that peak within 10-20 min and dissipate within 1 h in the presence of 8.5% (v/v) ethanol, transcriptional condensates are stably maintained for hours. Moreover, under the same conditions, Pol II occupancy of *HSR* genes and RNA expression are detectable only later in the response and peak much later (>1 h). This contrasts with the coordinate response of *HSR* genes to thermal stress (39°C) where Pol II occupancy, transcription, intergenic interactions, and formation of Hsf1 condensates are all rapid yet transient (peak within 2.5-10 min and dissipate within 1 h). Therefore, Hsf1 forms condensates, restructures the genome and transcriptionally activates *HSR* genes in response to both forms of proteotoxic stress but does so with strikingly different kinetics. In cells subjected to ethanol stress, Hsf1 forms condensates and repositions target genes before transcriptionally activating them.

Graphical Abstract



eLife assessment

This is a **valuable** contribution to our understanding of how different cell stressors (ethanol or heat-shock) elicit unique responses at the genomic and topographical level under the regulation of yeast transcription factor Hsf1, providing **solid** evidence documenting the temporal coupling (or lack thereof) between Hsf1 aggregation and long-range communication among co-regulated heat-shock loci versus chromatin remodeling and transcriptional activation. A particular strength is the combination of genomic and imaging-based experimental approaches applied to genetically engineered in vivo systems.

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Introduction

Genomes of higher eukaryotes are organized into multiple hierarchical levels. Chromosomes are segregated within individual territories, and within chromosomal territories active and inactive regions are separated into topologically associated domains (TADs) (Wendt & Grosfeld, 2014 [DOI](#)). Within TADs, DNA loops are formed to permit the interaction between enhancers or silencers and the promoters of their target loci. Although this hierarchy suggests a static view of the genome, recent studies have suggested that the genome is quite dynamic, as multiple points of interaction form in response to developmental cues and other stimuli. This dynamic restructuring ranges from the interactions between co-regulated genes (Fanucchi et al., 2013 [DOI](#); Papantonis et al., 2012 [DOI](#); Park et al., 2014 [DOI](#); Schoenfelder et al., 2010 [DOI](#)), to the convergence of enhancers dispersed across multiple chromosomes into a hub that regulates a single gene (Monahan & Lomvardas, 2015 [DOI](#)), to the reorganization of the genome that occurs in the zygote (Schulz & Harrison, 2019 [DOI](#)).

Despite its evolutionary distance, the yeast *Saccharomyces cerevisiae* also possesses an organized genome. Centromeres are located in a cluster at the spindle pole body, while chromosomal arms are extended with telomeres and the nucleolus located at the opposite side of the nucleus (Duan et al., 2010 [DOI](#)), resulting in a Rabl-like configuration (Taddei & Gasser, 2012 [DOI](#)). And as in higher eukaryotes, the budding yeast genome is organized into TAD-like structures (Eser et al., 2017 [DOI](#)) subdivided into smaller loop domains (Hsieh et al., 2015 [DOI](#)). Also as is the case in mammalian cells, the yeast genome is not static. Genes, including *INO1*, *GAL1* and *GAL10*, have been observed to reposition from the nuclear interior to the nuclear periphery upon their activation (Brickner et al., 2019 [DOI](#); Brickner & Walter, 2004 [DOI](#); Cabal et al., 2006 [DOI](#); Casolari et al., 2004 [DOI](#); Dieppois et al., 2006 [DOI](#); Green et al., 2012 [DOI](#)). In response to methionine starvation, several Met4-regulated genes have been observed to cluster (Du et al., 2017 [DOI](#); Lee et al., 2024 [DOI](#)).

More dramatic still are *Heat Shock Response* (*HSR*) genes under the regulation of Heat Shock Factor 1 (Hsf1). Upon exposure to acute thermal stress (heat shock [HS]), *HSR* genes dispersed across multiple chromosomes transcriptionally activate and engage in novel *cis*- and *trans*-intergenic interactions between one another – principally although not exclusively involving coding regions – that culminate in their coalescence into intranuclear foci (Chowdhary et al., 2017 [DOI](#), 2019 [DOI](#)). These stress-induced foci, comprised of Hsf1 and components of the transcriptional machinery, form quickly, rearrange rapidly and dissolve suddenly (Chowdhary et al., 2022 [DOI](#)). As such, Hsf1 clusters exhibit properties of biomolecular condensates, defined as self-organized membrane-free compartments enriched in specific macromolecules that may or may

not be phase-separated (Banani et al., 2017). Hsf1 condensate formation elicited by heat shock, like that of *HSR* gene interactions, parallels the kinetics of induction and attenuation of Hsf1-dependent genes (Chowdhary et al., 2017, 2022).

The Hsf1-driven heat shock response is a fundamental, evolutionarily conserved transcriptional program characterized by the gene-specific transcription factor (TF) Hsf1, its DNA recognition element (heat shock element (HSE)) and a core set of target genes encoding molecular chaperones and co-chaperones (reviewed in (Verghese et al., 2012)). In absence of proteotoxic stress, yeast Hsf1 is bound by Hsp70 and its co-chaperone Sis1 in the nucleoplasm (Feder et al., 2021; Krakowiak et al., 2018; Pepper et al., 2019; Zheng et al., 2016). Upon encountering stress, Hsp70 is titrated by unfolded proteins, particularly orphan ribosomal proteins located in the nucleolus and nascent polypeptides in the cytosol (Albert et al., 2019; Ali et al., 2023; Tye et al., 2019; Tye & Churchman, 2021). This results in the release of Hsf1 which then trimerizes and binds to HSEs located upstream of ~50 genes whose transactivation is dependent on this factor (Pincus et al., 2018). Once proteostasis is reestablished, excess Hsp70 binds Hsf1, inactivating it, thereby closing the negative feedback loop that regulates Hsf1 transcriptional activity (Krakowiak et al., 2018; Zheng et al., 2016). Note that in yeast, a fraction of Hsf1 is constitutively trimeric and it is this species that binds high-affinity HSEs even under non-stressful conditions (Giardina & Lis, 1995; Pincus et al., 2018).

In addition to thermal stress, Hsf1 can be activated by chemical stressors such as ethanol. Ethanol is a metabolite of glucose breakdown that budding yeast cells secrete into their surroundings. Ethanol production helps yeast outcompete other microbes in the environment (Liti, 2015; Piškur et al., 2006; Rozpedowska et al., 2011). Furthermore, once glucose is depleted, ethanol serves as an alternative carbon source (Piškur et al., 2006). Given this strategic use of ethanol, it is of fundamental importance for yeast to have a mechanism in place to respond to the stress that ethanol elicits. Similar to thermal stress, exposure to ethanol causes a large number of cellular perturbations including disruption of the plasma membrane (Piper et al., 1994); disruption of the H^+ ATPase and intracellular acidification (Rosa & Sá-Correia, 1991, 1996; Triandafillou et al., 2020); production of reactive oxygen species (Bandas & Zakharov, 1980; Davidson et al., 1996); depolymerization of the actin cytoskeleton (Homoto & Izawa, 2018; Tan et al., 2017); cell cycle arrest (Johnston & Singer, 1980; Kubota et al., 2004); disruption of mRNP transport to the daughter cell and formation of stress granules (Grouši et al., 2009; Kato et al., 2011); global inhibition of transcription and translation (Bresson et al., 2020; Gasch et al., 2000); and formation of protein aggregates (Piper, 1995; Plesset et al., 1982; Stanley et al., 2010). The cell counteracts many of these perturbations through the enhanced production of molecular chaperones (Altamirano et al., 2024; Verghese et al., 2012).

Here, we investigate activation of the HSR in yeast exposed to 8.5% ethanol (ethanol stress (ES)) and compare it to the response induced by exposure to 39°C (HS). We find that like HS, exposure to ES induces transcription of Hsf1-regulated *HSR* genes and induces concerted intergenic interactions between them. In contrast to HS, however, Hsf1 condensate formation and *HSR* intergenic interactions cells peak well before transcription. The delay in transcriptional induction may be linked to a widespread increase in nucleosome occupancy that occurs upon exposure of cells to ethanol. At longer times of ethanol exposure, *HSR* gene transcript accumulation continues to increase while *HSR* gene coalescence has already dissipated. Likewise, ES-induced Hsf1 condensates are present for a prolonged period, in contrast to HS-induced condensates that begin to dissipate shortly after they appear. Collectively, our data indicate that different stimuli drive distinct transcription, chromatin, topologic and condensation phenomena, yet all are dependent on Hsf1.

Results

Thermal stress and ethanol stress elicit distinct proteotoxic responses in yeast

Saccharomyces cerevisiae in the wild metabolizes glucose and other sugars into ethanol, which the yeast secretes into the environment to suppress microbial competition. Therefore, it is likely that yeast has evolved mechanisms to contend with ethanol toxicity. Indeed, a common laboratory strain (W303) retains viability when cultivated in the presence of 8.5% ethanol, although its ability to proliferate is diminished (**Figure 1A, B**). As assessed by the presence of Hsp104-containing foci (a measure of protein aggregation (Liu et al., 2010)), the rate of cytosolic protein aggregation is similar in cells exposed to either 8.5% ethanol or 39°C thermal stress (**Figures 1D and 1E**; see **Figure 1C** for experimental design). However, it is notable that the number and volume of Hsp104 foci, and by extension protein aggregation, is substantially higher in cells subjected to ethanol stress.

We next investigated the subcellular localization of the Hsp70 co-chaperone, Sis1, in cells exposed to ethanol versus thermal stress. Previous work has shown that Sis1 is diffusely localized within the nucleus under control conditions where it promotes binding of Hsp70 to Hsf1, thereby repressing the HSR (Feder et al., 2021). In response to acute HS, Sis1 relocates to nucleolus where it forms a perinucleolar ring, and to the cytoplasm where it forms cytosolic clusters that colocalize with Hsp104 and spatially associate with the endoplasmic reticulum (Feder et al., 2021). Consistent with these previous observations, we observed rapid relocation of Sis1 in response to a 39°C HS. It formed a ring-like structure within 2.5 min consistent with a perinuclear location. Such relocation lasted at least 60 min and spatially separated Sis1 from Hsf1 (**Figures 2A and 2B**). A similar result was obtained when cells were exposed to 42°C. In response to ES, Sis1 remained largely co-localized with Hsf1 within the nucleoplasm although some enrichment at the nuclear periphery was evident. This was the case whether cells were exposed to 5% or 8.5% ethanol (**Figures 2A and 2B**). In addition, a 60 min exposure to 8.5% ethanol resulted in the formation of prominent cytosolic Sis1 puncta that were less evident in the HS sample (**Figure 2A**). These observations suggest that these two stressful treatments elicit a qualitatively distinct response. Experiments described below provide further support for this possibility.

Ethanol stress induces transcriptional activation of Hsf1-dependent genes but with delayed kinetics and reduced expression compared to thermal stress

To gain further insight into the mechanism by which *S. cerevisiae* contends with ethanol-induced proteotoxicity, we assessed the kinetics of transcriptional activation of *HSR* genes in cells exposed to ethanol stress. Cells were cultivated to early log phase in rich YPD medium, then ethanol was added to a final concentration of 8.5% and cell aliquots were removed at 0-, 10-, 20- and 60-min. Transcription was terminated through addition of sodium azide (see Materials and Methods). A parallel culture was exposed to an instantaneous 30° to 39°C heat shock and cells were removed at the corresponding time points. Transcription was terminated as above.

While cells exposed to heat shock displayed a rapid and substantial increase in *HSR* mRNA levels (typically >10-fold increase within 10 min of thermal upshift), those exposed to ethanol stress only weakly induced the same cohort of genes (**Figure 3A**). However, while HS induced a transient increase in RNA expression, ES induced a sustained increase that was evident at all Hsf1-dependent genes tested (**Figure 3– figure supplements 1 and 2**). A corresponding immunoblot analysis of two Hsf1 targets, Hsp104 and Btn2, strengthens the notion that HS induces

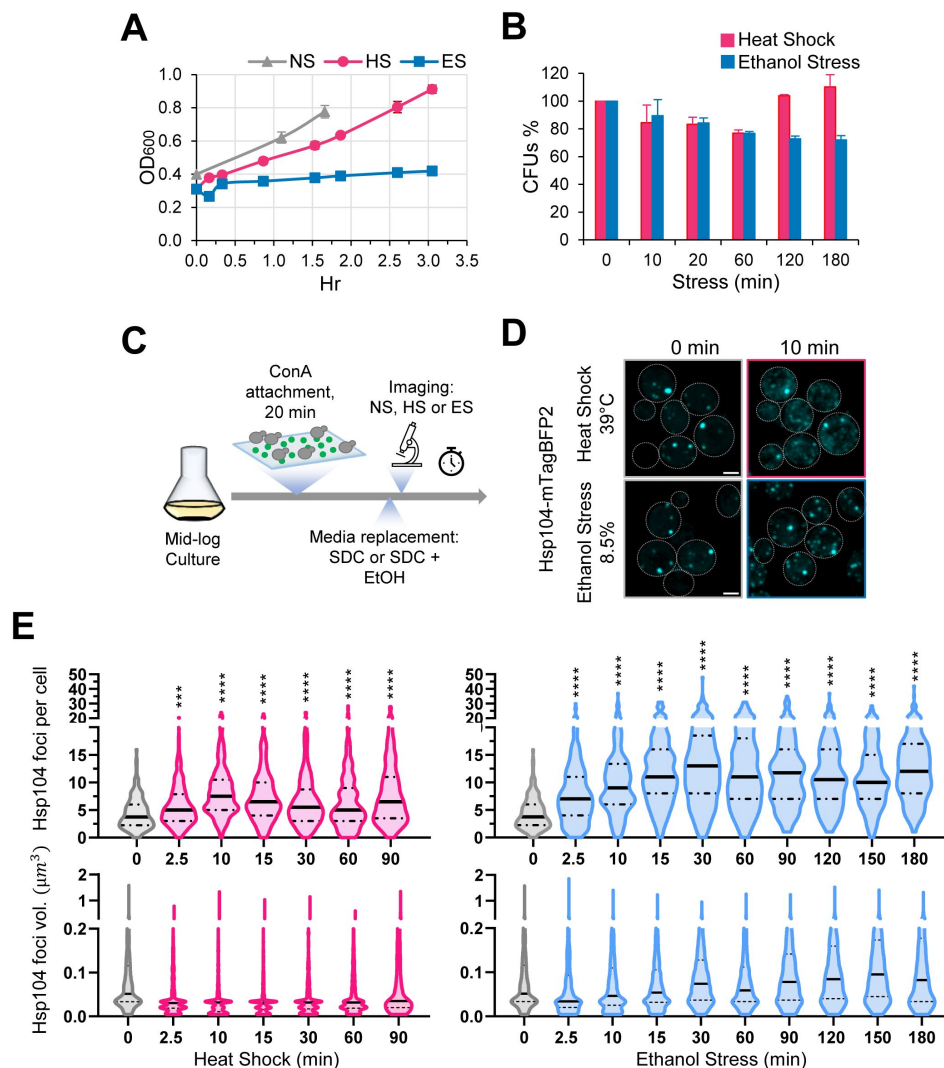


Figure 1.

Thermal and chemical stresses used in this study elicit distinct proteotoxic responses.

(A) Growth curve of strain W303-1B grown in liquid culture (YPDA). Mid-log phase cultures were diluted to OD₆₀₀=0.4 and shifted to different conditions: no stress (NS, 25°C), heat shock (HS, 39°C), or ethanol stress (ES, 8.5% v/v, 25°C). OD₆₀₀ was monitored over time. Means and SD are shown. N=2.

(B) Viability assay of W303-1B cells following exposure to heat shock (25° to 39°C upshift for the indicated time) or ethanol stress (8.5% v/v ethanol for the indicated time at 25°C). An aliquot was taken from each condition at the listed stress timepoints and diluted in rich media. Cells were spread on YPDA plates and grown at 30°C for 3 days. Colony forming units (CFUs) were determined using ImageJ/FIJI. Plotted are percentages of CFUs of stressed cells normalized to those of the 0 min control. Graphs depict means + SD. N=2.

(C) Experimental strategy for imaging Hsp104 foci. Cells were attached to a concanavalin A (ConA)-coated surface, followed by heat shock or ethanol stress treatment (see Materials and Methods). Synthetic complete media (SDC) was supplemented with ethanol to a final concentration of 8.5% for ES samples. Scale bar: 2 μm.

(D) Both heat shock and ethanol stress induce formation of Hsp104 foci. DPY1561 cells were attached to a VAHEAT substrate using Concanavalin A and subjected to an instantaneous heat shock (25° to 39°C) or to ethanol stress (25°C, 8.5% v/v). 0 min control was kept at 25°C without stress. Hsp104-mTagBFP2 foci were visualized by confocal microscopy. Shown are maximal projections of 11 z-planes, taken with an interplanar distance of 0.5 μm. Scale bar: 2 μm.

(E) Cells subjected to the above treatments were assayed for Hsp104 puncta number and volume. An average of 200 cells per timepoint, per condition, was quantified using Imaris image analysis software (v.10.0.1). For this analysis, we made the assumption that the diffuse Hsp104 clusters seen in HS cells are comparable to the compact Hsp104 foci in ES cells. N=2. Significance was determined by Mann Whitney test, stress (T≥2.5 min) vs. no stress. ***, *p*<0.001; ****, *p*<0.0001.

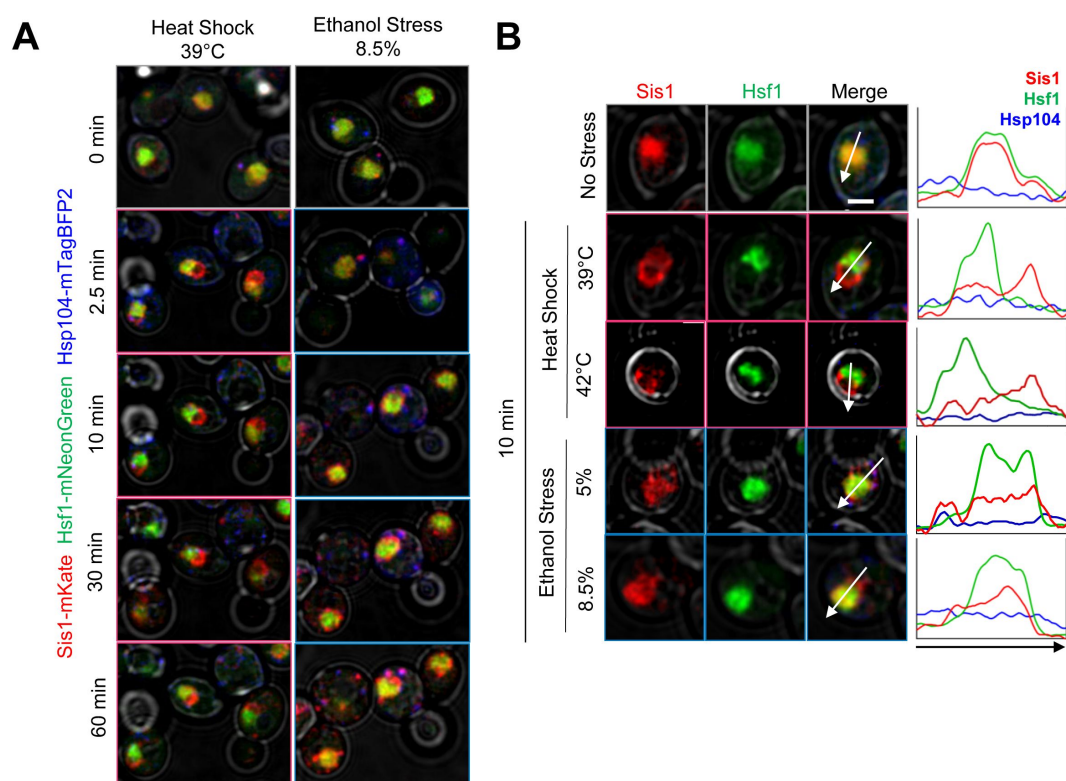


Figure 2.

Heat shock and ethanol stress elicit distinct patterns of Sis1 subcellular relocalization.

(A) Live cell confocal microscopy of the diploid strain LRY033 expressing Sis1-mKate, Hsf1-mNeonGreen, and Hsp104-mTagBFP2. Cells were treated as in [Figure 1D](#). 11 z-planes were captured with an interplanar distance of 0.5 μm . Shown is a representative plane for each timepoint.

(B) Subcellular localization analysis of Sis1, Hsf1 and Hsp104 in cells subjected to no stress (25°C), heat shock (at 39°C or 42°C) or ethanol stress (at 5% or 8.5% v/v (25°C)) for 10 min. Cells from strain LRY033 were treated as described in [Figure 1D](#). A representative plane is shown for each condition. Line profiles are plotted for each channel on the right. Arrows were drawn to bisect the nucleus. Scale bar: 2 μm .

a rapid yet transient response whereas ES induces a delayed, yet far more sustained increase in gene expression (**Figure 3–figure supplement 3** [↗](#)). In the case of *HSP12* and *HSP26*, whose transcription is under the dual regulation of Msn2 and Hsf1, exposure to heat shock resulted in a high level of induction as previously observed ([Chowdhary et al., 2019](#) [↗](#)) yet exposure to 8.5% ethanol failed to cause detectable activation during the first 20 min (**Figure 3B** [↗](#); **Figure 3–figure supplement 1** [↗](#)). Nonetheless, as described below, both *HSP12* and *HSP26* respond to acute ethanol stress but do so through their inducible and dramatic 3D genomic repositioning.

Pol II recruitment and histone eviction are delayed in ethanol-stressed cells and this correlates with a transient, widespread increase in nucleosome density

The delayed transcriptional response of *HSR* genes in ES-versus HS-treated cells prompted us to investigate occupancy of Hsf1, RNA Pol II and histones at these genes over a time course. A possible explanation for the delay in activation in cells exposed to ethanol stress is less rapid (or reduced) Hsf1 binding to the genes' upstream regulatory regions. To explore this possibility, we exposed cells to either thermal or chemical stress and processed them for chromatin immunoprecipitation (ChIP) analysis. As previously observed ([Kim & Gross, 2013](#) [↗](#); [Pincus et al., 2018](#) [↗](#); [Sekinger & Gross, 2001](#) [↗](#)), occupancy of Hsf1 at its target loci increases many-fold following a brief heat shock (**Figure 4B** [↗](#), left, dark red; see **Figure 4A** [↗](#) for location of primers). Hsf1 occupancy typically declines after 60 min of continuous thermal stress and in the case of *TMA10*, dissociation begins much sooner. In response to ethanol stress, Hsf1 occupancy steadily increased, in most cases reaching maximal levels by 20 min and plateauing thereafter (**Figure 4B** [↗](#), left, black). These results suggest that ethanol stress induces binding of Hsf1 to its cognate HSEs to a degree similar to heat shock, yet such binding is more gradual. Moreover, given the above, Hsf1's binding to these sites fails to elicit a corresponding transcriptional response.

In light of this disconnect between Hsf1 binding and *HSR* mRNA production, we evaluated abundance of the large subunit of Pol II at representative genes over the same time course. In response to heat shock, Rpb1 is rapidly recruited to the promoters and coding regions of each *HSR* gene, peaking within 2.5 min and then gradually declining over the next ~60 min (**Figure 4B** [↗](#), middle, red and pink traces). By contrast, its occupancy is noticeably delayed in cells exposed to ethanol stress (blue traces), consistent with reduced transcript levels (**Figure 4–figure supplement 1B** [↗](#)). The increase in *HSR* mRNA in heat-shocked cells parallels, yet consistently lags, the abundance of Pol II within *HSR* gene coding regions (**Figure 4–figure supplement 1A** [↗](#)). This delay in reaching peak accumulation may reflect contributions beyond RNA synthesis, such as transient enhanced stability of *HSR* transcripts during the acute phase of heat shock.

To obtain further insight into the chromatin landscape present during the two stresses, we assayed histone H3 abundance as a measure of nucleosome density. In response to heat shock, nucleosomes are rapidly displaced over the promoter and coding regions of strongly expressed *HSR* genes (*HSP82*, *HSP104* and *SSA4*); a similar, albeit less robust, response is observed for *TMA10* and *HSP12*. Following this initial phase (~20 min), nucleosomes reassemble over these genes and in certain cases return to their original density by 60 min (**Figure 4B** [↗](#), right, red and pink traces). This dramatic and dynamic remodeling has been previously observed ([Kremer & Gross, 2009](#) [↗](#); [Zhang et al., 2014](#) [↗](#); [Zhao et al., 2005](#) [↗](#)). In contrast, ethanol stress elicits a transient increase in H3 abundance over all five genes (**Figure 4B** [↗](#), right, blue traces). This apparent increase in chromatin compaction is not restricted to *HSR* genes; a variety of unrelated loci, including a stress-responsive, Msn2-regulated gene (*PGM2*), two constitutively expressed genes (*TUB1*, *ACT1*), two genes assembled into SIR-dependent heterochromatin (*HMLa1*, *YFR057w*) and a non-transcribed region (*ARS504*) also exhibit a transient increase in nucleosome density in ethanol-exposed cells (**Figure 4–figure supplement 2A** [↗](#)).

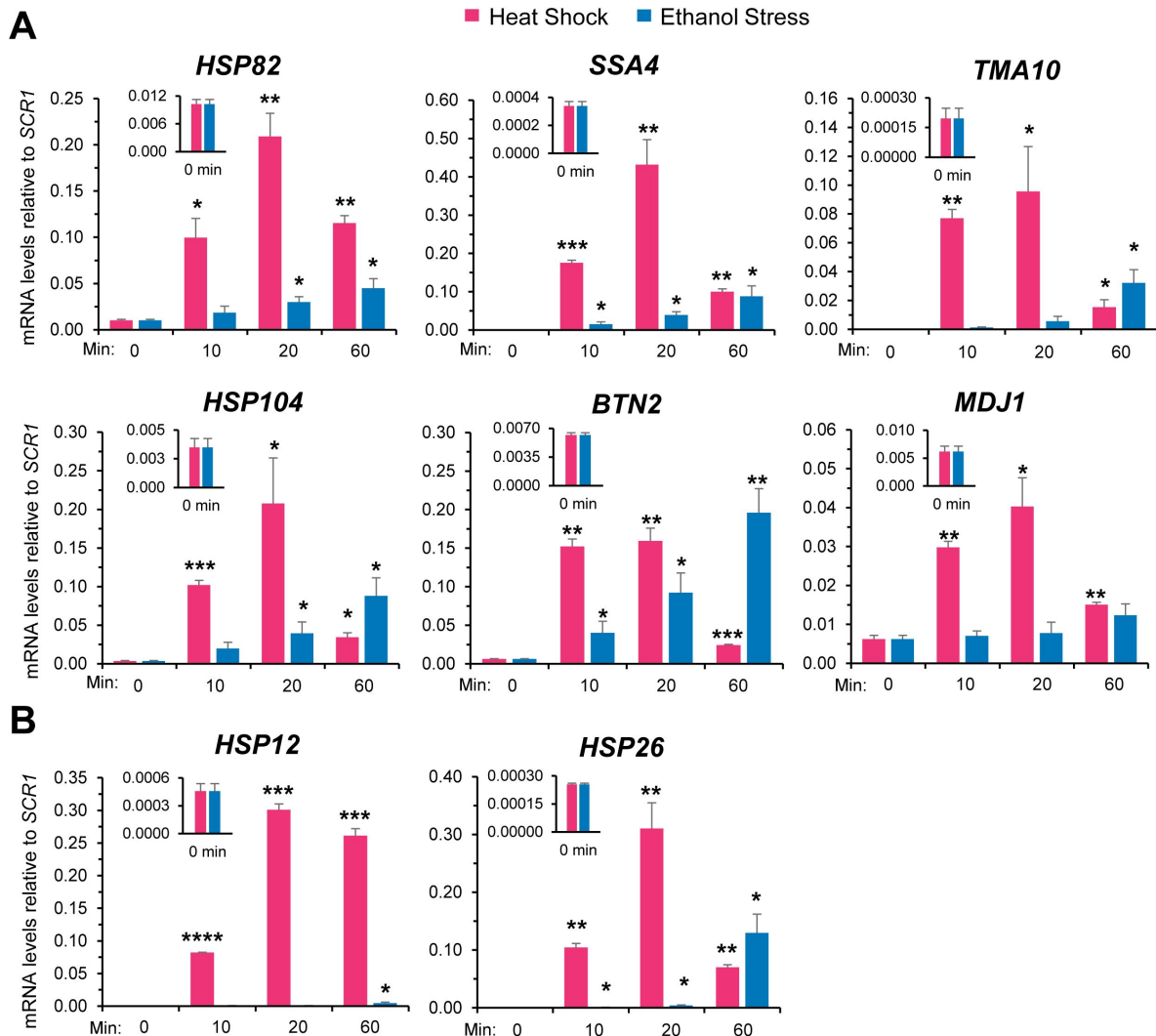


Figure 3.

Ethanol stress transcriptionally induces Heat Shock Response (HSR) genes but with markedly slower kinetics than thermal stress.

(A) RNA abundance of Hsf1-dependent HSR genes was determined by Reverse Transcription-qPCR in strain W303-1B. Heat shock was performed at 39°C; ethanol stress was done using 8.5% (v/v) ethanol at 25°C. Insets display transcript abundance using a zoomed-in scale. Depicted are means + SD. N=2, qPCR=4. Statistical analysis: T-test, one-tailed, no stress vs. stress conditions. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$.

(B) As in (A), but the Hsf1-, Msn2-dual regulated genes HSP12 and HSP26 were evaluated. *, $p < 0.05$; ***, $p < 0.001$; ****, $p < 0.0001$.

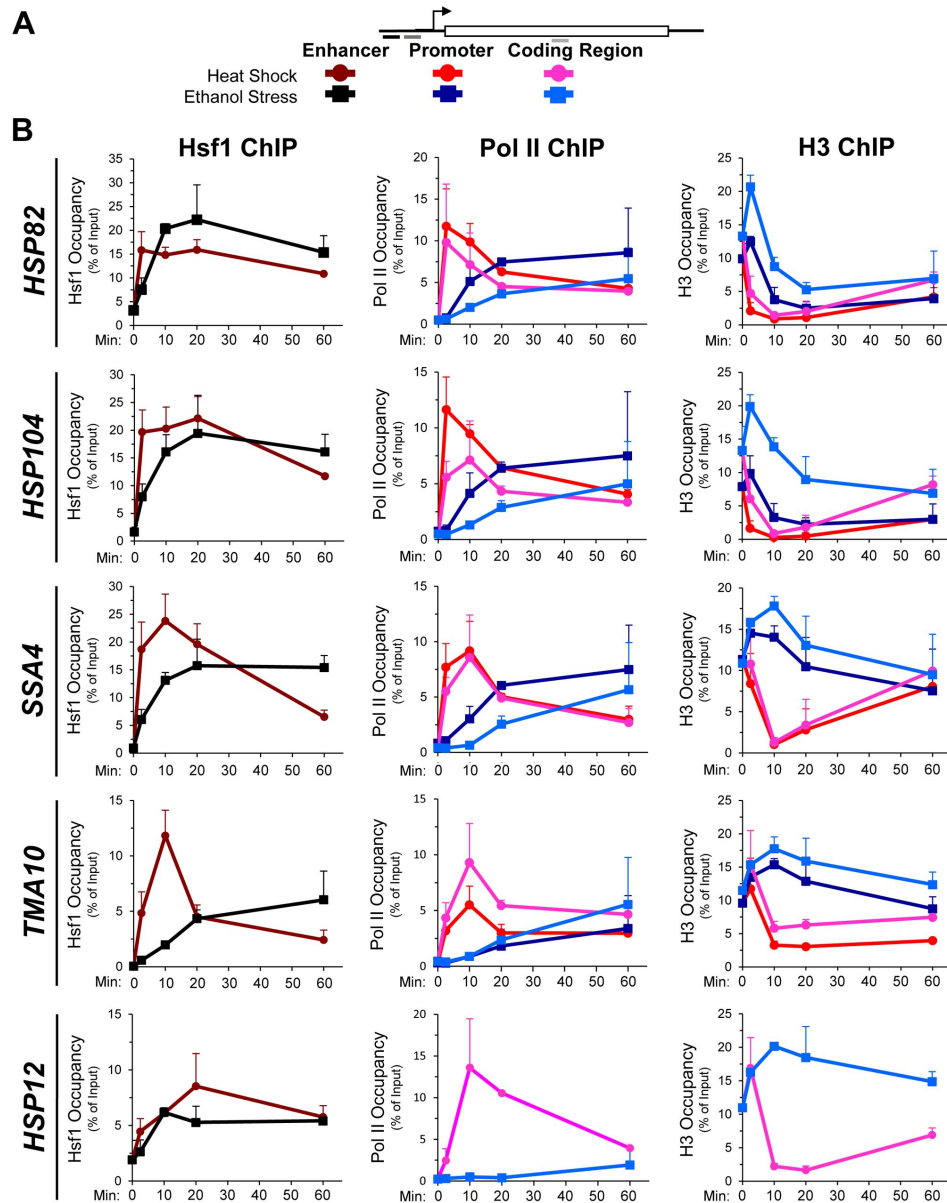


Figure 4.

Hsf1 and Pol II recruitment to *HSR* genes is delayed in ethanol stressed cells, while histone occupancy transiently increases.

(A) Map of a representative *HSR* gene depicting locations of primers used for chromatin immunoprecipitation (ChIP) analysis. Heat shock: shades of red and pink. Ethanol stress: shades of blue.

(B) ChIP analysis of Hsf1, Pol II (Rbp1) and histone H3 occupancy to the enhancer (UAS), promoter and coding regions of the indicated genes. Mid-log cultures of strain BY4741 were subjected to the indicated times of heat shock (39°C) or ethanol stress (8.5% v/v, 25°C). Time points evaluated for all three factors: 0, 2.5, 10, 20 and 60 min. Antibodies raised against full-length Hsf1, CTD of Rbp1 or the globular domain of Histone H3 were used (see **Materials and Methods**). ChIP signals were normalized to input. Shown are means + SD. N=2, qPCR=4.

In agreement with this idea, chromatin volume (as assessed by the signal arising from an H2A-mCherry protein fusion) decreases upon exposure of cells to ethanol stress (and much more transiently to heat stress; **Figure 4-figure supplement 2[B, C]**). These data suggest that the increase in nucleosome density antagonizes Pol II recruitment and its subsequent release into the coding regions of *HSR* genes in ES cells. Once Pol II has been stably recruited, elongation and concomitant histone eviction ensues (**Figure 4B**). Altogether, our ChIP data indicate that Hsf1 binds to its target enhancers less readily in ethanol-stressed than in thermally stressed cells. This impediment to Hsf1 occupancy is magnified by a corresponding, and more severe, hindrance to Pol II recruitment resulting in a pronounced delay in *HSR* gene transcription.

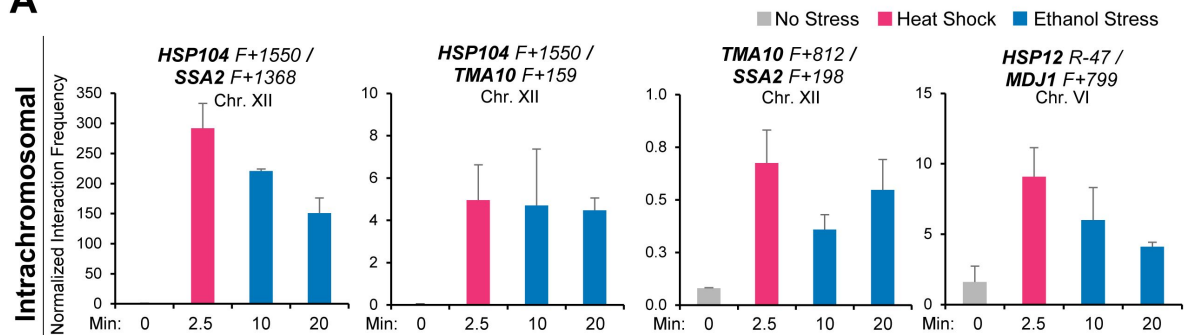
Acute ethanol stress induces rapid and profound 3D genomic repositioning of *HSR* loci

An intriguing feature of *HSR* genes is the fact that they coalesce into discrete intranuclear foci in response to heat shock. Such interactions have been documented using both molecular (chromosome conformation capture (3C)) and imaging (fluorescence microscopy) approaches (Chowdhary et al., 2017, 2019, 2022; Rubio & Gross, 2023). Intriguingly, physical interactions specifically involve Hsf1 targets irrespective of their location in the genome. Other loci, including adjacent, transcriptionally active genes, show little or no tendency to interact with Hsf1-dependent genes. Such *cis*- and *trans*-interactions principally involve gene coding regions and are highly dynamic, typically peaking at 2.5 min and dissipating by 30- to 60-min. The kinetics of HS-induced coalescence often, although not always, correlate with kinetics of transcriptional induction; they also parallel the formation of Hsf1 condensates (Chowdhary et al., 2017, 2019, 2022) as discussed further below.

Given these previous observations, we wished to know if ethanol stress induced similar 3D genome restructuring. It seemed unlikely that such topological changes would occur during the initial phase of ES since only weak Pol II occupancy and low *HSR* transcript levels are observed (**Figures 3, 4**). However, as shown in **Figure 5**, exposure to 8.5% ethanol triggered frequent intergenic interactions between Hsf1 targets during the first 10 min as revealed by Taq I-3C, a highly sensitive, quantitative version of 3C (Chowdhary et al., 2020) (see **Figure 5 - figure supplement 1** for location of 3C primers). Both intra- and interchromosomal interactions can be detected. Moreover, the interaction frequencies following this exposure in most cases equaled, and in some instances exceeded, those detected in cells heat-shocked for 2.5 min (**Figures 5A, 5B**), when peak 3C interactions occur in thermally stressed cells (Chowdhary et al., 2017). A detailed kinetic analysis revealed that intergenic interactions elicited by ethanol stress, similar to those induced by thermal stress, are highly dynamic: detectable within 2.5 min, peak shortly thereafter (within 10-20 min) and largely attenuate by 60 min (**Figures 5** and **6A**).

It has been previously suggested that a functional link exists between gene looping and transcriptional activation (Ansari & Hampsey, 2005; O'Sullivan et al., 2004). Indeed, gene loops and other intragenic interactions (Chowdhary et al., 2017) are readily detected within *HSR* genes in cells exposed to ethanol. However, as is the case with intergenic interactions, these topological changes are kinetically uncoupled from both transcription and Pol II occupancy. They are detected quite early (within 2.5 min), peak soon thereafter (at 10 min) and attenuate by 60 min (**Figure 6B** and **Figure 5 - figure supplement 2**). Taken together, our 3C and expression analyses indicate that 3D genomic repositioning and intragenic looping of *HSR* genes precedes the maxima of transcript levels and Pol II occupancy. Moreover, for certain loci (e.g., *HSP12* and *HSP26*), they argue that neither transcription nor Pol II recruitment is required to drive 3D topological changes in these genes. Further evidence in support of this is provided below.

A



B

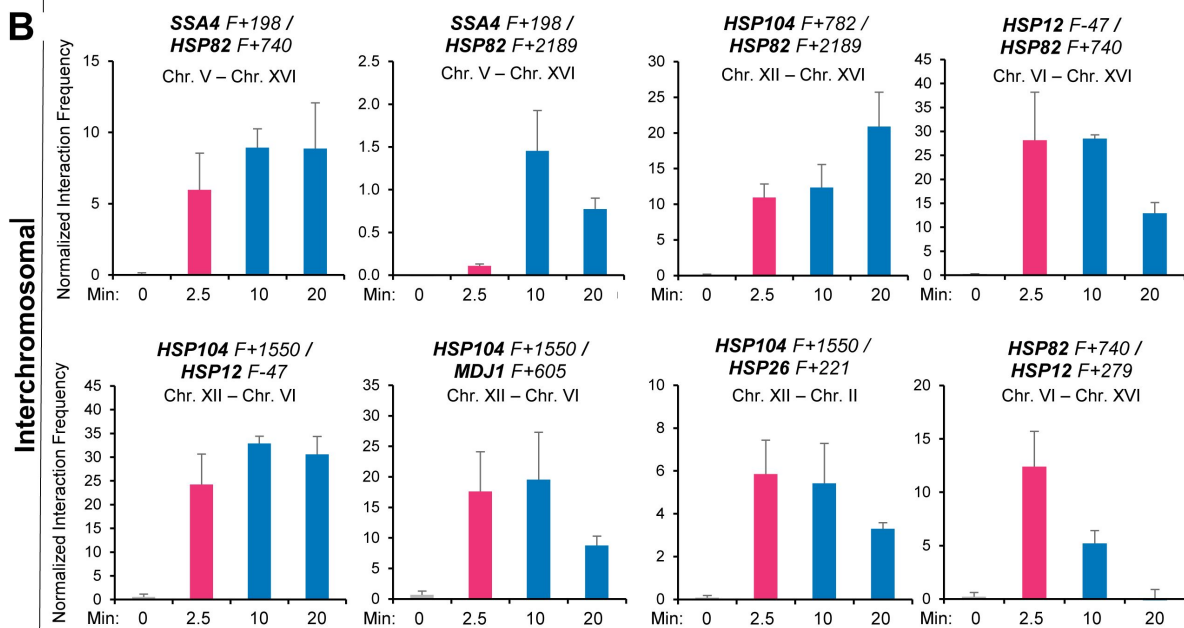


Figure 5.

Ethanol stress induces intergenic interactions between *HSR* genes that are comparable to those induced by acute thermal stress.

(A) Intrachromosomal (*cis*) interactions between *HSR* genes were analyzed by Taq I-3C. W303-1B cells were instantaneously shifted from 30° to 39°C for 2.5 min (HS) or exposed to 8.5% v/v ethanol at 30°C for 10 or 20 min (ES). No stress samples were kept at 30°C. Location of Taq I coordinates are provided in [Figure 5-figure supplement 1](#). F (forward) primers are positioned near the indicated Taq I restriction site. 3C signals were normalized to the 3C signal derived from using a naked genomic DNA template. Graphs depict means + SD; N=2; qPCR=4.

(B) Interchromosomal (*trans*) interactions between *HSR* genes were performed as in (A).

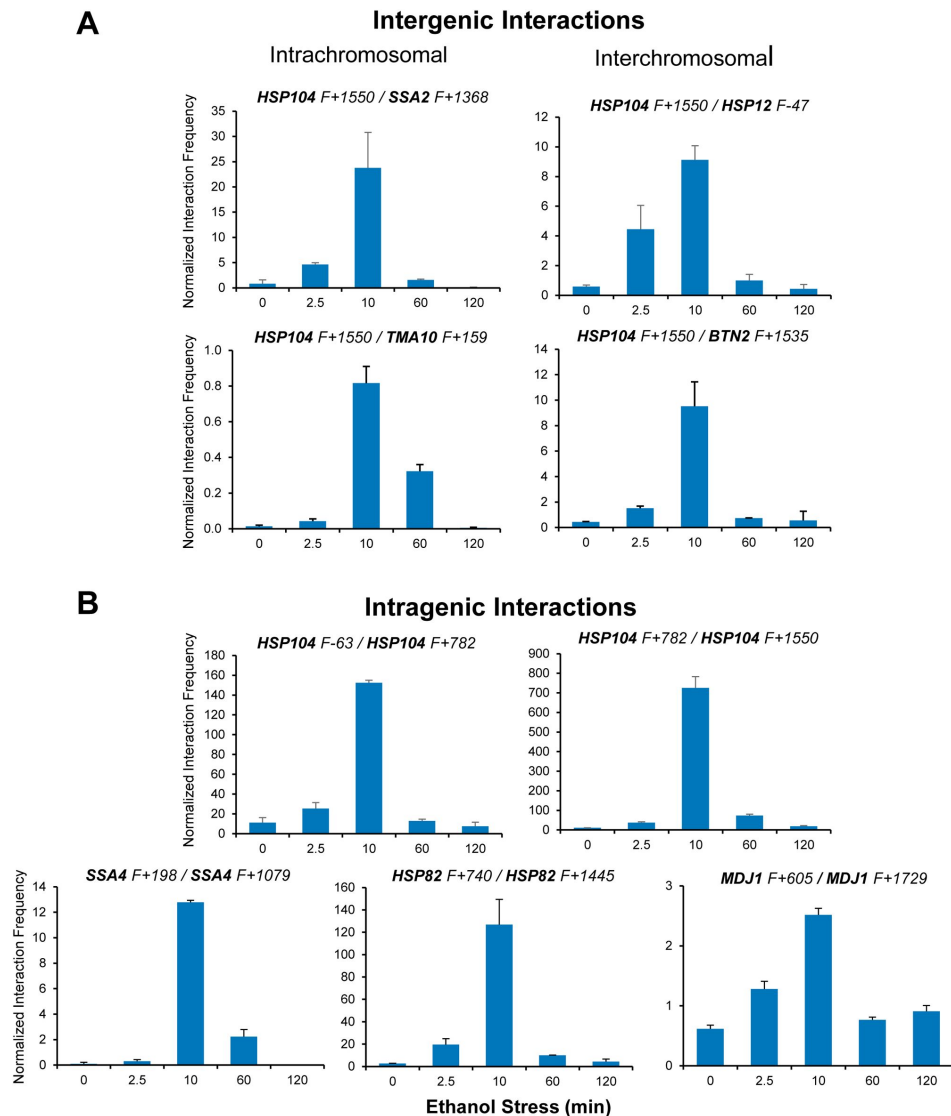


Figure 6.

Ethanol-induced *HSR* gene interactions are detectable by 2.5 min but typically dissipate within 60 min

(A) Taq I-3C analysis of intergenic interactions occurring during ethanol stress was conducted as described in [Figure 5](#). All samples were kept at 25°C. Plotted are means + SD. N=2, qPCR=4.
(B) As in (A), but for intragenic interactions.

Live cell imaging reveals that *HSR* genes coalesce to a similar degree under ethanol stress and heat stress conditions

To provide an orthogonal line of evidence for *HSR* gene interaction, we employed fluorescence microscopy to image live cells bearing *LacO*-tagged *HSP104* and *TetO*-tagged *TMA10* loci in cells expressing GFP-LacI and TetR-mCherry fusion proteins. Both genes are located on Chromosome XII, on opposite arms, and are physically separated by the nucleolus (100-200 rDNA repeats) that lies between them (Duan et al., 2010) (schematically depicted in **Figure 7-figure supplement 1A**). In the absence of stress, fluorescence signals representing these two genes are typically well-separated (**Figure 7-figure supplement 1B**, 0 min). Upon heat shock, they rapidly converge, usually within 2.5 min. Upon exposure to ethanol, gene convergence is also observed, albeit less rapidly (**Figure 7-figure supplement 1B**; see also below). Despite the slight delay, these results demonstrate that *HSP104* and *TMA10* coalesce in ethanol stressed cells and do so with similar frequency as in thermally stressed cells (**Figure 7-figure supplement 1C**), consistent with the 3C analysis described above.

Having confirmed the physical interaction of Hsf1-dependent genes under ethanol stress, we assessed the transcriptional status of coalesced genes. Our RT-qPCR analysis indicated that the increase in *HSR* mRNA levels in ES-induced cells is delayed compared to those in HS-induced cells (**Figure 3C**). To obtain insight into *HSR* gene transcription kinetics in single cells, we integrated a stem loop array (24xMS2) upstream of *HSP104*, allowing production of a chimeric transcript visualized upon binding of the MCP-mCherry fusion protein (Haim et al., 2007). This strain also harbored *LacO*-tagged *HSP104* and *HSP12* genes and expressed GFP-LacI (schematically illustrated in **Figure 7A**). We were unable to detect an MCP-mCherry focus adjacent to *HSP104* under no stress conditions (**Figure 7B**; 0 min), consistent with very low *HSP104* basal transcript levels (**Figure 3A**). Heat shock induced rapid coalescence between *HSP104* and *HSP12*, as well as transcription from *HSP104*. These phenomena were detectable by 2.5 min as a merged signal of the chimeric transcript and the two GFP-labeled genes (**Figure 7B**). This visualization method allowed us to quantify the percentage of the population that is actively engaged in transcription, revealing that during heat shock, transcription and coalescence are positively correlated (**Figure 7[C, F]**). Consistent with this, after *HSP104* transcription declined (10 min HS), so did *HSP104*-*HSP12* coalescence (**Figure 7 – figure supplement 1D**).

A detailed single cell analysis supports the strong spatiotemporal correlation between *HSR* gene coalescence and transcription in heat-shocked cells (**Figure 7D**). In contrast, under ethanol stress, *HSP104* RNA was not detected until 5-10 min (and in most cases not until 10 min) even though *HSP12* and *HSP104* coalesced as early as 2.5 min (**Figure 7E**; **Figure 7 – figure supplement 1D**). Indeed, such an analysis suggests temporal uncoupling between *HSR* gene coalescence and *HSR* gene transcription in ethanol stressed cells (**Figure 7F**). Underscoring the disconnect between 3D genome repositioning and transcription is the fact that in ethanol stressed cells, enhanced *HSP12* RNA levels were undetectable until 60 min (**Figure 3B** and **Figure 3 – figure supplement 1**). Collectively, our RT-qPCR, 3C and imaging data argue that ethanol stress induces striking topological changes in *HSR* genes within the first 10-20 min and that these are accompanied by a minimal increase in transcript levels. This provides a sharp contrast to heat-shocked cells where there exists a strong temporal correlation between *HSR* gene transcription and *HSR* gene repositioning (**Figure 7F**).

Ethanol stress induces rapid formation of long-lived Hsf1 condensates

Recently, TF condensates have been proposed as a mechanism for transcriptional regulation (Bojja et al., 2018; Cho et al., 2018; Hnisz et al., 2017; Nair et al., 2019; Sabari et al., 2018). Heat shock-activated Hsf1 forms small nuclear condensates (diameter of ≤ 300 nm) that localize at

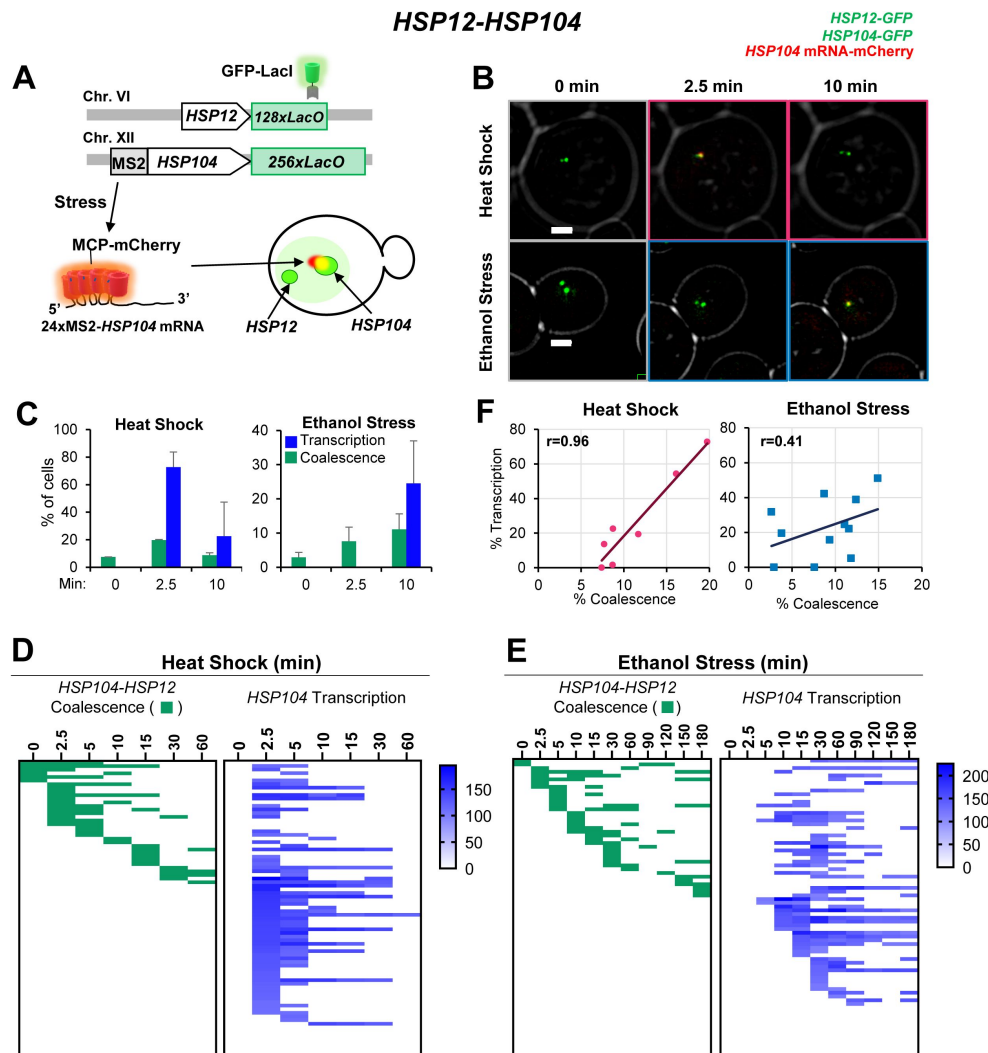


Figure 7.

***HSR* gene transcription and coalescence are strongly correlated in heat-shocked but not ethanol-stressed cells.**

(A) *HSP12* and *HSP104* are flanked by *LacO* arrays in the heterozygous diploid strain VPY705. In addition, *HSP104* has a 24xMS2 loop array integrated within its 5'-UTR. MCP-mCherry binds to the nascent chimeric *HSP104* transcript and is visualized as a red dot adjacent to the gene which appears as a green dot.

(B) Live cell confocal fluorescence microscopy of strain VPY705 heat-shocked at 39°C using a VAHEAT device or exposed to 8.5% ethanol at 25°C for the indicated times. An Olympus spinning disk confocal microscope system was used for imaging. Scale bar: 2 μ m.

(C) Quantification of VPY705 cells treated as above and scored for the coalescence of *HSP104*-*HSP12* and the presence of chimeric MS2 $\times$ 24-*HSP104* mRNA. Cells were scored positive for coalescence only when a single green dot could be visualized in the nucleus across the 11 z-planes. Transcription was scored as positive only when a red dot above background could be seen near the large green dot (*HSP104*). Approximately 40 cells were scored per timepoint, per condition. Graphs represent means $\pm$ SD. N=2.

(D) Single cell analysis of *HSP12*-*HSP104* coalescence (green) and *HSP104* transcription (blue) at discrete timepoints over a heat shock time course. Each row in the transcription analysis corresponds to the same cell in the coalescence analysis. Blue gradient represents the intensity of mCherry signal in each cell.

(E) As in (D) but for ethanol stress.

(F) Scatter plot showing the correlation (r) between percent transcription and percent coalescence in HS and ES cells (derived from D and E). Each plotted value corresponds to a different stress timepoint (see also **Figure 7 - figure supplement 1D**).

HSR gene loci in both human (Zhang et al., 2022) and budding yeast cells (Chowdhary et al., 2022), and their presence positively correlates with *HSR* gene transcriptional activity. The tendency of Hsf1 to form condensates may be linked to its extensive intrinsically disordered structure (Figure 8A), a feature proposed to be critical for the biomolecular condensation of proteins (reviewed in (Alberti et al., 2019; Banani et al., 2017)). Additionally, nuclear stress bodies comprised of HSF1 bound to satellite III DNA repeats in human cells have been described (Jolly et al., 1997, 2002), although formation of these large foci (diameter of several μm) is independent of the sites of active *Heat Shock Protein* genes and their presence may repress *HSR* gene activation (Gaglia et al., 2020).

Given the temporal link between Hsf1 condensation and transcription established in heat-shocked yeast cells, we anticipated that the appearance of Hsf1 condensates in ethanol-stressed cells would be delayed relative to what is seen in heat-shocked cells. However, we found that ethanol stress induced formation of Hsf1-GFP condensates as rapidly as did heat shock. These were visible in virtually all ES cells as early as 2.5 min, paralleling their rapid appearance in HS cells (Figure 8B–D). However, in contrast to the rapid dissolution of condensates in HS cells, those formed in cells exposed to 8.5% ethanol showed no evidence of dissipating even after 60 min of continuous exposure (Figure 8B, D). An independent analysis of Hsf1 tagged with a monomeric GFP, mNeonGreen, gave virtually identical results: >90% of cells exhibited Hsf1 puncta as early as 2.5 min and such puncta were stably maintained for 150 min (Figure 8 – figure supplement 1). Moreover, in a further analysis they were still visible at 5.5 h (data not shown). Therefore, in 8.5% ethanol-stressed cells, formation of Hsf1 condensates is uncoupled from *HSR* gene transcription and their maintenance is uncoupled from *HSR* gene repositioning. An important implication is that although condensates may initiate or promote *HSR* gene repositioning, they cannot maintain the 3D restructured state of the genome.

Does the enhanced stability of ES-induced puncta arise from the nature of the stress or its intensity? To test this, we examined the behavior of yeast cells exposed to a lower concentration of ethanol. As shown in Figure 8 – figure supplement 1, Hsf1 puncta formed in >95% of 5% ethanol-treated cells within 2.5 min, resembling what was seen in cells exposed to either 8.5% ethanol or 39°C HS. Yet such puncta dissipated in a majority of 5% ES cells within 30 min, resembling the case with HS but strongly contrasting to what was seen with 8.5% ethanol. Therefore, although 5% and 8.5% ES elicit a similar pattern of Sis1 subcellular relocalization, one that is distinct from that caused by either a 39° or 42°C HS (Figure 2), it is the greater intensity of 8.5% ethanol stress, not its intrinsic nature, that most closely correlates with the stability of Hsf1 condensates.

Hsf1 and Pol II are required for *HSR* gene interactions in response to both heat shock and ethanol stress

The above analyses reveal several unexpected differences in the way yeast responds to ethanol stress versus heat stress. Given these differences, we asked whether either Hsf1 or RNA Pol II are required for the repositioning of *HSR* genes in response to ethanol stress; both have been shown to be necessary for 3D genome restructuring in response to heat shock (Chowdhary et al., 2019, 2022). To do so, we used the auxin-induced degradation system to conditionally degrade Hsf1 and the Rpb1 subunit of RNA Pol II in appropriately engineered strains. As schematically summarized in Figure 9A, cells expressing degron-tagged Hsf1 or Rpb1 were pre-treated with 1 mM indoleacetic acid (IAA) for 30–40 min, at which time each protein was >90% degraded (Figure 9 – figure supplement 1A). Although minimal short-term growth defects were detectable, loss of Rpb1 and Hsf1 resulted in loss of cell viability at all temperatures (Figure 9 – figure supplement 1 [B, C]).

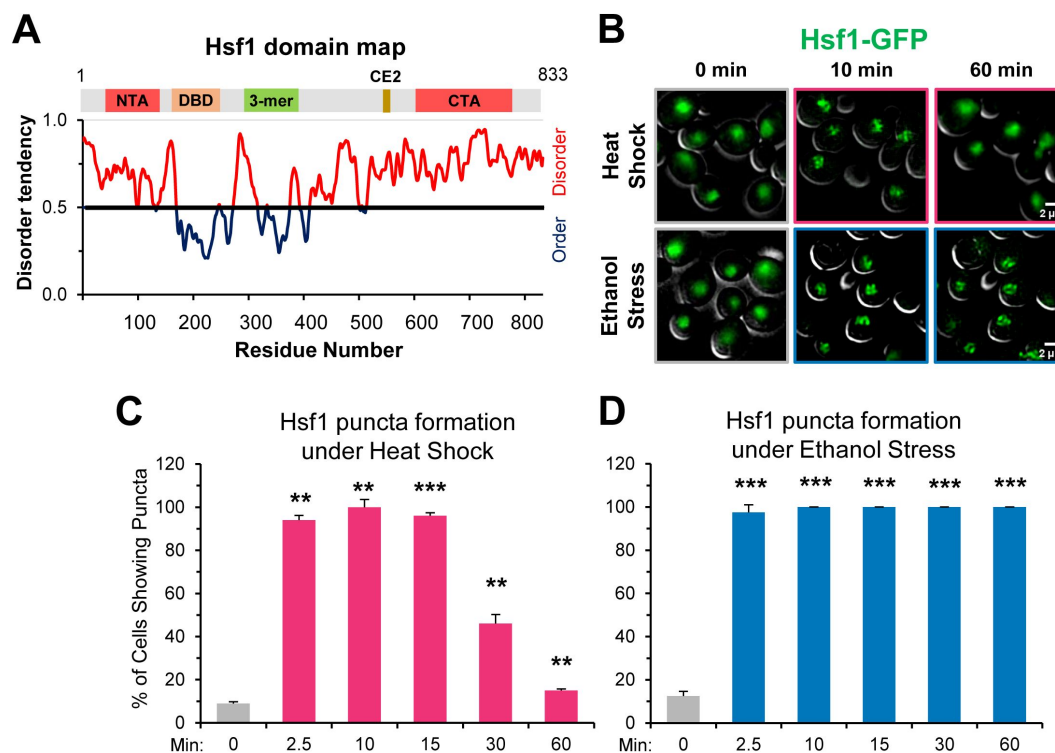


Figure 8.

Ethanol stress induces rapid formation of long-lasting Hsf1 condensates

(A) Hsf1 is a transcription factor bearing N- and C-terminal domains with high disorder tendency (determined by IUPRED2). NTA, N-terminal activator; DBD, DNA binding domain; 3-mer, trimerization domain; CE2, conserved element 2 (Hsp70 binding site); CTA, C-terminal activator.

(B) Hsf1-GFP condensates form in response to ethanol stress. Diploid cells expressing Hsf1-GFP (ASK741) were grown in synthetic complete medium supplemented with adenine (SDC + Ade) and mounted onto ConA-coated coverslips. Live cell widefield microscopy was performed on cells exposed to either heat shock (38°C) or ethanol stress (8.5% v/v) or left untreated (25°C). A representative plane is shown for each condition out of 11 z-planes imaged (interplanar distance of 0.5 μ m). Scale bar: 2 μ m.

(C) ASK741 cells were subjected to a 38°C heat shock for the indicated times and scored for the presence of Hsf1 condensates. A cell was scored as positive if it contained at least one clearly defined puncta. Approximately 200 cells were evaluated per timepoint. A one-tailed t-test was used to assess significance (stress versus no stress condition). N=2. **, $p < 0.01$; ***, $p < 0.001$.

(D) ASK741 cells were exposed to 8.5% v/v ethanol for the indicated times and the presence of Hsf1 condensates were scored from a total of 200 cells per timepoint. Significance was determined as in (C).

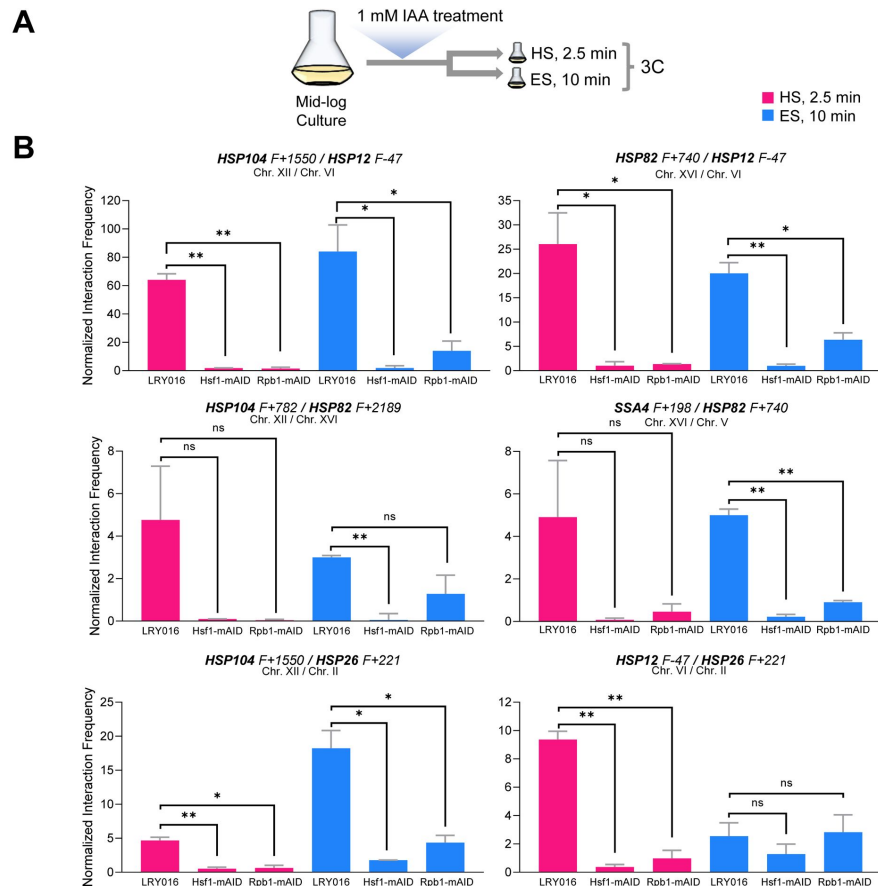


Figure 9.

Hsf1 and Pol II are critically required for *HSR* gene interactions in response to either heat shock or ethanol stress

(A) Experimental strategy. Degron-tagged cells were treated with 1 mM IAA at 25°C for 30-40 min prior to exposure to either heat shock (HS, 39°C for 2.5 min) or ethanol stress (ES, 8.5% v/v ethanol for 10 min) followed by HCHO crosslinking and 3C analysis.

(B) Strains LRY016 (W303-1B; OsTIR1), LRY100 (LRY016; Hsf1-mAID) and LRY102 (LRY016; Rpb1-mAID) were subjected to the above protocol and physical interactions between the indicated chromosomal loci were detected by Taq I-3C as in [Figure 5](#). Representative interchromosomal interactions are shown. Graphs represent means + SD. Statistical significance between the indicated interaction frequencies was determined using a one-tailed t-test. *, $p < 0.05$; **, $p < 0.01$; ns, not significant. A no stress sample, maintained at 30°C for 10 min following IAA treatment and then crosslinked, was handled in parallel. No signal above background was detected for any pairwise test.

Consistent with previous observations (Chowdhary et al., 2019 [↗](#)), intergenic interactions between *HSR* genes, located on the same or different chromosomes, were nearly obviated in cells conditionally depleted of either Hsf1 or Rpb1 and then heat shocked (**Figure 9B** [↗](#) and data not shown). While a similar strong dependence on Hsf1 is observed in 8.5% ethanol-treated cells, close inspection of the data suggests that residual *HSR*-*HSR* gene interactions are retained in Rpb1-depleted cells for certain loci. Particularly noteworthy is the inducible interaction between *HSP12* and *HSP26*, genes co-regulated by Msn2 and Hsf1. Neither is detectably activated following a 10-min exposure to ethanol (**Figure 3B** [↗](#)), yet the genes engage in an intergenic interaction that is unaffected by prior degradation of Rpb1 (**Figure 9B** [↗](#)). Together with the kinetic uncoupling of *HSR* gene repositioning with Pol II recruitment/transcription and the relative permanence of Hsf1 condensates described above, these observations raise the possibility that 8.5% (v/v) ethanol-induced Hsf1 condensates are compositionally different from those formed in response to heat shock and drive *HSR* gene repositioning and transcription in a mechanistically distinct way (see **Figure 10** [↗](#) for model).

Discussion

Ethanol stress induces *HSR* gene transcription, *HSR* gene coalescence and formation of Hsf1 condensates

Here we have shown that exposure of budding yeast to a high, but sub-lethal, concentration of ethanol strongly stimulates the binding of Hsf1 to the upstream regulatory regions of *HSR* genes. Unexpectedly, such binding – which is evident as early as 2.5 min – does not lead to concurrent recruitment of Pol II and transcription of *HSR* genes. Instead, Pol II recruitment and transcription are delayed, typically for 10 min or longer. As exposure to 8.5% ethanol causes a global yet transient increase in H3 occupancy – which we interpret as an increase in the compaction of chromatin (see below) – the increase in nucleosome density may present a barrier to both Pol II recruitment and elongation. In addition, another feature of heat shocked-induced Hsf1 activation, repositioning of *HSR* genes within the 3D genome, is observed in cells exposed to ethanol. However, unlike transcription, this phenomenon occurs rapidly and is transient, resembling what is observed in heat shocked cells. The lack of temporal linkage between *HSR* gene transcription and *HSR* intergenic interactions is consistent with the idea that *HSR* gene coalescence and transcription are distinct phenomena and that Hsf1 can instigate long-range changes in 3D genome structure independently of inducing transcription. Thus, Hsf1 represents an example of a gene-specific TF that has functions independent of regulating transcription (discussed further below).

It has recently been demonstrated that in response to heat shock, inducible transcriptional condensates drive 3D genome reorganization in budding yeast. This conclusion arose from several features, including the tight temporal linkage between Hsf1 condensation and *HSR* intergenic interactions and the similar sensitivity of these two phenomena to the aliphatic alcohol, 1,6-hexanediol (Chowdhary et al., 2022 [↗](#)). Similar to previous observations of heat-shocked cells (and confirmed here), we have found that in cells exposed to 8.5% ethanol, Hsf1 forms discrete puncta within 2.5 min. However, Hsf1-containing condensates formed in response to 8.5% ES are stable – persisting for hours – while such assemblies dissipate within 30 min in cells exposed to HS. In addition, while Hsf1 condensates formed as rapidly in cells exposed to 5% versus 8.5% ethanol, those formed in the presence of 5% ethanol proved to be transient, resembling their counterparts in HS cells. Relevant to this observation is the finding that Hsf1 activation in yeast exposed to 5% ethanol is dependent on the misfolding of nascent proteins, while in cells exposed to 8% ethanol, Hsf1 activation is dependent on the misfolding of both nascent and mature proteins (Tye & Churchman, 2021 [↗](#)). Therefore, the persistence of Hsf1 condensates in 8.5% ethanol may derive from widespread unfolded mature proteins that are more difficult to refold than short nascent polypeptides attached to ribosomes.

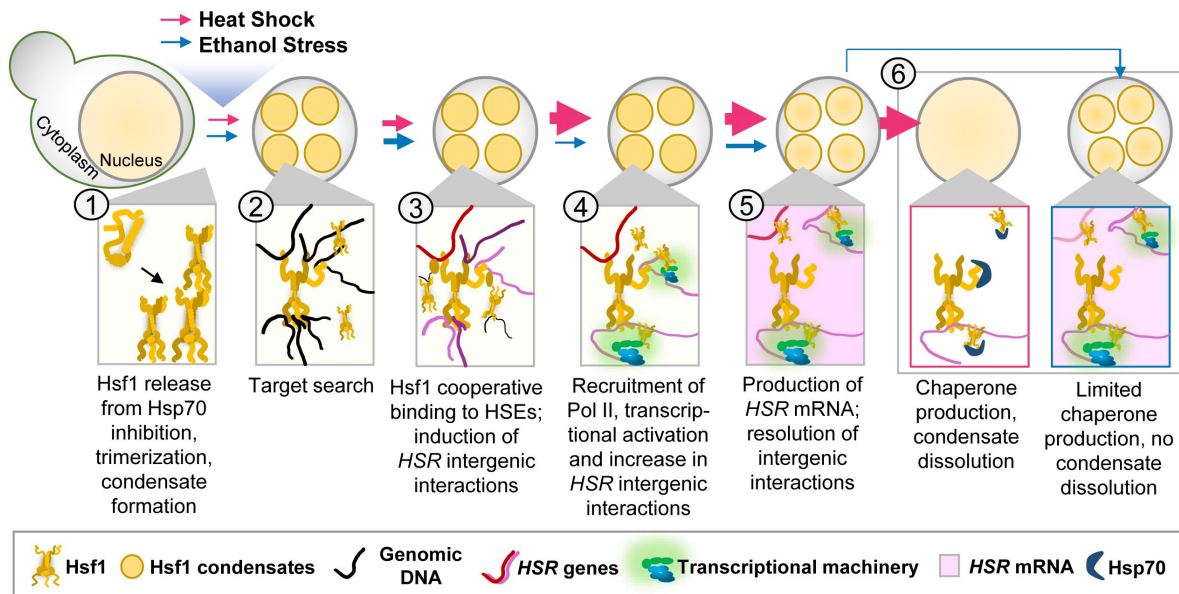


Figure 10.

Hsf1 forms condensates, restructures the genome and transcriptionally activates *HSR* genes in response to both thermal and chemical stresses but does so with strikingly different kinetics.

Heat Shock (pink arrows): *S. cerevisiae* cells exposed to heat shock (30° to 39°C upshift) undergo protein misfolding (proteotoxicity), leading to chaperone titration and activation of Hsf1 accompanied by formation of Hsf1 condensates (1). Rapid target search is hypothesized to occur via multivalent interactions between Hsf1's activation domains and chromatin-bound proteins (Brodsky et al., 2020) (2). Subsequently, Hsf1 cooperatively binds HSEs and induces the 3D reorganization of *Heat Shock Responsive (HSR)* genes (3). Simultaneously, RNA Pol II is recruited to *HSR* genes and transcription is induced (4). Productive transcription (pink shading) ensues, followed by dissolution of *HSR* gene interactions (5). Rapid export of *HSR* mRNAs (Zander et al, 2016) facilitates production of chaperone and cytoprotective proteins, which aid in restoration of proteostasis and disassembly of Hsf1 condensates (Chowdhary et al, 2022) (6). Thickness of arrows (for both HS and ES) symbolizes rapidity and/or magnitude of the subsequent step.

Ethanol Stress (blue arrows): Exposure to 8.5% (v/v) ethanol induces proteotoxicity, titration of chaperones, and subsequent activation of Hsf1, triggering formation of condensates (1, 2). Condensates may aid Hsf1 target search by facilitating the multivalent interactions described above (2). Hsf1 then binds HSEs, inducing *HSR* gene repositioning (3). Subsequently, Pol II is recruited and transcriptionally activated (3). Ethanol stress-induced interactions dissipate well before maximal *HSR* gene transcriptional induction is achieved (5). The weak transcriptional *HSR* gene output, coupled with suppressed *HSR* mRNA export under ES (Izawa et al, 2008), results in a low level of chaperone synthesis (6) that fails to resolve proteotoxicity. This likely contributes to the persistence of Hsf1 condensates.

Additional features might account for the way in which these two proteotoxic stresses elicit the HSR in budding yeast. For example, while ethanol denatures proteins similar to thermal stress (Furutani & Izawa, 2022 [↗](#); Kato et al., 2011 [↗](#)), it impacts the cell at other levels. Actively growing yeast preferentially consume sugars and even in the presence of oxygen can produce ethanol (Dashko et al., 2014 [↗](#)). This change in carbon source, termed the diauxic shift, is marked by a reduction in growth rate due to the less efficient generation of energy as well as accumulation of waste products and depletion of nutrients (Herman, 2002 [↗](#)). Consistent with activation of the HSR, this physiological adjustment is accompanied by increased chaperone synthesis (Piper, 1995 [↗](#); Piper et al., 1994 [↗](#)) as well as an increase in the activity of alcohol metabolism-related enzymes. Such an adaptation likely takes time. In contrast to the gradual increase in ethanol that occurs under natural conditions, here we have imposed an instantaneous ethanol shock. The addition of ethanol elicits a heat shock transcriptional response and synthesis of chaperones. The cell growth arrest seen here (**Figure 1A** [↗](#)) may arise as part of the adaptive program deployed upon encountering ethanol stress, such as a transition into quiescence. However, we fail to see activation of Msn2 targets, a signature of quiescence (Breedon & Tsukiyama, 2022 [↗](#)), early in the exposure to ES at a time when Hsf1 itself is activated (**Figure 3B** [↗](#)). While other possibilities exist, our results suggest that the activation of programs involved in proteome protection are likely the first line of defense against sudden ethanol stress. Salient differences by which yeast cells respond to heat versus ethanol stress are summarized in **Table 1** [↗](#); a model summarizing the Hsf1 response under both HS and ES conditions is provided in **Figure 10** [↗](#).

Exposure to ethanol transiently induces the global compaction of chromatin

An important observation is that exposure of cells to 8.5% ethanol leads to a widespread increase in H3 ChIP signal that we interpret as increased compaction of chromatin. Although this effect is temporary, both euchromatic and heterochromatic regions are impacted, and this is consistent with measurements of total chromatin volume that reveal a decrease lasting nearly 60 min. A similar outcome was recently reported for both yeast and mammalian cells exposed to aliphatic di-alcohols (Itoh et al., 2021 [↗](#); Meduri et al., 2022 [↗](#)). It is probable that the effect of ethanol exposure is nearly instantaneous since, as discussed above, ethanol is known to denature proteins (Kato et al., 2019 [↗](#)), likely by dehydration (disruption of biomolecules' hydration shell). While such denaturation may contribute to chromatin compaction, the effect is reversible, possibly due to refolding / renaturation mediated by Hsp70 and other molecular chaperones whose intracellular concentration increases during ethanol exposure. As mentioned above, this temporary increased density of chromatin could suppress Pol II recruitment and subsequent elongation. Also not ruled out is a direct effect of 8.5% ethanol on one or more components of the Pol II machinery. Possible advantages of chromatin compaction could be to downregulate global transcription, as well as to limit chromatin damage by reactive oxygen species or other potentially damaging molecules present in the cell during ethanol stress (Bradley et al., 2021 [↗](#); Costa et al., 1997 [↗](#); Davidson et al., 1996 [↗](#); Davidson & Schiestl, 2001 [↗](#); Shen et al., 2020 [↗](#); Voordeckers et al., 2020 [↗](#)).

A novel function for a TF that is uncoupled from regulating the transcription of its target gene

A key finding is that in response to ethanol stress, *HSR* genes reposition and Hsf1 condensates form well before transcription of Hsf1-dependent genes peaks, and in certain cases, is even detected. This suggests that Hsf1 has a function distinct from transactivating its target genes: it drives *HSR* gene repositioning that culminates in their physical coalescence. Likewise, deletion of the N-terminal IDR (NTA, amino acids 1-140; see **Figure 8A** [↗](#)) was observed to have little effect on *HSR* gene transcription during an acute heat shock yet formation of Hsf1 condensates and intergenic 3C interactions were suppressed (Chowdhary et al., 2022 [↗](#)). Furthermore, as discussed

Parameter	Heat Shock (39°C)	Ethanol Stress (8.5% v/v)
Hsf1 binding to HSEs	Rapid, peak at 2.5 min	Slight delay, peak at 10 min
Pol II recruitment to <i>HSRs</i>	Rapid, peak at 2.5 min	Severely delayed, detection starts at 10 min
Histone H3 occupancy at <i>HSRs</i>	Rapid depletion	Transient increase, followed by gradual depletion
Genome compaction ¹	Transient	Sustained
<i>HSR</i> gene transcription	Rapid	Delayed
<i>HSR</i> gene coalescence	Rapid, transient	Slightly delayed, transient
Hsf1 condensates	Rapidly induced, transient, well defined	Rapidly induced, stable, poorly defined

¹ As inferred from enhanced H3 ChIP signal at non-Hsf1 regulated loci.

Table 1.

Kinetics of select nuclear phenomena in response to heat shock and ethanol stress

above, recruitment of Hsf1 to its target HSEs is delayed in response to ES versus HS. Nevertheless, formation of Hsf1 condensates occurs with similar kinetics under both conditions, well prior to the peak of Hsf1 DNA binding in ES cells. This suggests the possibility that two types of Hsf1 clusters exist: one that is DNA-bound and the other that hovers over the *HSR* genes. It is possible that this cloud-forming Hsf1 cluster aids in target searching, by analogy with Gal4 that can also form clusters without binding DNA (Meeussen et al., 2023 [↗](#)).

Conclusion

While Hsf1 is known to induce interactions between transcriptionally active *HSR* genes in response to heat shock, here we have demonstrated a similar role for this transcription factor in response to ethanol stress. Despite minimal *HSR* gene transcription during the initial 10 min exposure to ethanol, *HSR* genes engage in robust physical interactions, rivaling those seen for 2.5 min HS. This interaction correlates with an increase in definition of Hsf1 condensates yet is not accompanied by concurrent recruitment of Pol II to promoters, perhaps due to the compaction of chromatin in ethanol-stressed cells. Hsf1 therefore forms condensates and drives 3D repositioning of its target genes without appreciably activating these genes. Furthermore, Hsf1 does this through formation of condensates that may be materially different than those that form in response to HS. Our results also argue that formation of TF clusters, while sufficient for TF DNA binding and 3D genome restructuring, are not sufficient to drive transcription. Additional factors and/or activities – such as the opening of chromatin – are necessary. Further research into the biophysical properties, molecular regulation, and functional consequences of HSF1 condensates will deepen our understanding of how cells respond to both thermal and chemical stress and maintain cellular homeostasis.

Materials and Methods

Yeast Strain Construction

The *HSF1-mNeonGreen* (*HSF1-mNG*) diploid strain LRY033 expressing a yeast-optimized version of mNeonGreen, derived from *Branchiostoma lanceolatum* (Shaner et al., 2013 [↗](#)), and co-expressing Sis1-mKate and Hsp104-BFP (Blue Fluorescent Protein; mTagBFP2) was created as follows. First, DPY1561 (Feder et al., 2021 [↗](#)) was crossed to W303-1B to create strain LRY031. This diploid was sporulated and a strain homozygous for *HSF1* and retention of one allele each of *SIS-mKate* and *HSP104-mTagBFP2* was obtained after back crossing. The resultant diploid was named LRY032. LRY032 was transformed with a PCR amplicon containing 50 bp of homology sequences flanking the stop codon, targeting the mNG tag to *HSF1* at its C-terminus flanked by the *HIS3* selectable marker. The plasmid template for this amplification was pFA6a-link-ymNeonGreen-SpHis5 (Botman et al., 2019 [↗](#)). LRY033 is heterozygous for *HSF1-mNG*, *SIS1-mKate* and *HSP104-mTagBFP2*.

Other strains were created as follows. LRY037 was constructed using the *HSF1*-targeted *mNeonGreen* amplicon to transform strain W303-1B. LRY040 was constructed by transforming LRY037 with an amplicon containing *RPB3-mCherry::hphMX6*, obtained using genomic DNA from strain SCY004 (Chowdhary et al., 2022 [↗](#)) as template. LRY100 and LRY102 were constructed using LRY016 (Rubio & Gross, 2023 [↗](#)) as recipient of the mini-degron tag amplified from pHyg-AID*-9myc (Morawska & Ulrich, 2013 [↗](#)), targeted to the C-terminus of *HSF1* and *RPB1*, respectively.

A complete list of strains as well as plasmids and primers used in strain construction are listed in **Supplemental File 1 – Tables 1, 2 [↗](#), 3.**

Yeast Culture and Treatment Conditions

Cells were grown at 30°C in YPDA (1% w/v yeast extract, 2% w/v peptone, 2% w/v dextrose and 20 mg/L adenine) to mid-log density ($OD_{600} = 0.6 - 0.8$). For ethanol stress, the cell culture was mixed with an equal volume of YPDA containing 17% v/v ethanol (yielding a final concentration of 8.5%) and incubated at 25°C for different lengths of time as indicated in the figures. For heat shock, the mid-log culture was mixed with an equal volume of 55°C YPDA medium to achieve an instantaneous temperature upshift to 39°C, and the culture was maintained at 39°C for the indicated times. The no stress samples were diluted with an equivalent volume of YPDA and maintained at 25°C. Samples were kept at their respective temperatures using a water bath with constant shaking.

Cell Viability and Growth Assays

Cell Viability Assay

Cells were grown at 30°C in YPDA to $OD_{600}=0.6$ and then diluted to $OD_{600}=0.4$ using an equivalent volume of medium as described above for ethanol stress, heat shock or the no stress control (YPDA at 25°C). Cells were kept under these conditions for 3 h; during this time aliquots were taken at different timepoints and diluted 1:26,000 for plating onto YPDA. Plates were incubated at 30°C for 3 days then scanned. Colonies were quantified using ImageJ/Fiji (v. 1.53t) (Schindelin et al., 2012 [↗](#)) - “Analyze Particles” option. The number of colony-forming units (CFUs) obtained in stress samples were normalized to the no stress samples and expressed as a percentage of the number of CFUs obtained in the no stress sample.

Growth Assay

Cells were grown in liquid culture and subjected to the same treatments as described above. OD_{600} readings of each sample were taken at intervals over 3 h (see **Figure 1** [↗](#)). The average OD_{600} from two samples was plotted versus time.

Spot Dilution

Spot dilution was conducted as described previously (Rubio & Gross, 2023 [↗](#)).

Auxin Induced Degradation

Cells expressing the F-box protein oTIR1 in combination with a degron-tagged protein were grown in YPDA medium to mid-log phase and indole-3-acetic acid (IAA) was then added to a final concentration of 1 mM IAA stocks [10 mg/mL (57 mM)] were prepared fresh in 95% ethanol and filter-sterilized before use. For immunoblot analysis, cells were treated for varying times up to 1 h prior to metabolic arrest using 20 mM sodium azide, followed by cell harvesting. 0 min control samples were treated with vehicle alone (1.7% v/v ethanol). For growth curve analysis, samples were kept at 30°C with constant shaking and aliquots were removed at various timepoints to monitor OD_{600} . For 3C analysis, cells were similarly grown in YPDA to $OD_{600}=0.6$, then treated with 1 mM IAA for either 30 min (LRY016 and LRY100) or 40 min (LRY102) prior to cell cross-linking and subsequent cell harvesting.

Reverse Transcription-qPCR (RT-qPCR)

RT-qPCR was conducted as previously described using 25 mL cell culture aliquots (Rubio & Gross, 2023 [↗](#)). Transcription was terminated via addition of sodium azide to a final concentration of 20 mM (Lee & Garrard, 1991 [↗](#)). PCR primers used are listed in **Supplemental File 1 – Table 4**.

Immunoblot Analysis

Immunoblotting was performed as previously reported using 20 mL cell culture aliquots (Rubio & Gross, 2023 [↗](#)).

Chromatin Immunoprecipitation

Chromatin immunoprecipitation was performed as previously described (Chowdhary et al., 2019 [↗](#)) with modifications. Briefly, cells from a 50 mL mid-log culture were exposed to 8.5% v/v ethanol and fixed using 3.01% formaldehyde (HCHO), resulting in a net concentration of 1%. Glycine was then added to 0.363 M glycine to quench excess formaldehyde. We note that HCHO is consumed in a reaction with ethanol. Since 8.5% ethanol equals 1.46 M, acetal formation at 1:2 stoichiometry consumes 0.730 M (2.01%) of HCHO, leaving an effective concentration of 0.363 M (1%). The reaction resulting in formation of an acetal is illustrated in **Figure 11** [↗](#).

For heat shock, cells from a 50 mL mid-log culture were fixed with 1% (0.363 M) formaldehyde following 39°C upshift for the times indicated (**Figure 4** [↗](#); **Figure 4 – figure supplements 1** [↗](#) and **2** [↗](#)). Glycine was then added at a final concentration of 0.363 M to quench unreacted formaldehyde. Chromatin lysates, prepared as previously described (Chowdhary et al., 2019 [↗](#)), were incubated using 20% of the lysate with one of the following antibodies: 1.5 µL of anti-Hsf1 (Erkine et al., 1996 [↗](#)), 1.5 µL anti-Rpb1 antiserum (Zhao et al., 2005 [↗](#)), or 1 µL of H3 antibody (Abcam, ab1791). Incubation of lysate with antibody was done for 16 h at 4°C. Chromatin fragments bound to antibody were captured on Protein A-Sepharose beads (GE Healthcare) for 16 h at 4°C. Wash, elution, and DNA purification were conducted as described (Chowdhary et al., 2019 [↗](#)).

The ChIP DNA template was quantified by qPCR (7900HT Fast Real Time PCR System, Applied Biosystems). A standard curve was generated using genomic DNA and ChIP DNA quantities were deduced by interpolation. The qPCR signal for each primer combination was normalized relative to the corresponding signal arising from the input DNA. Primers used in ChIP analysis are listed in **Supplemental File 1 – Table 5**.

Taq I chromosome conformation capture (Taq I-3C)

TaqI-3C was performed as previously described (Rubio & Gross, 2023 [↗](#)). A master cell culture was grown at 30°C in YPDA from OD₆₀₀=0.15 to a final OD₆₀₀=0.8. Aliquots of 50 mL were used for each condition. Heat shock and ethanol stress were conducted as described above. Primers for analysis of 3C templates are listed in **Supplemental File 1 – Table 6**.

Fluorescence Microscopy

Widefield Fluorescence Microscopy

For **Figure 7 – figure supplement 1 [B, C]** [↗](#) and **Figure 8** [↗](#), cells were grown at 30°C in Synthetic Complete Dextrose (SDC) medium supplemented with 0.1 mg/mL adenine to early log phase. From this culture, 90 µL were removed and cells were immobilized onto a concanavalin A (ConA, Sigma Aldrich, 100 µg/mL in ddH₂O)-coated coverslip for 20 min. The medium was then removed and replaced by either SDC or SDC + 8.5% v/v ethanol. The coverslip was mounted onto a concave microscope slide to reduce media evaporation (2-Well Concavity Slide, Electron Microscopy Sciences). Images were acquired using an AX70 Olympus epifluorescence microscope across 11 z-planes with 0.5 µm of interplanar distance. Filter set 89021 (Chroma Technology) and a Photometrics Prime 95B camera were used to image GFP and mCherry. SlideBook Software version 6.0.15 (Intelligent Imaging Innovations) was used for image capturing and z-axis stepping motor operation (Ludl Electronic products).

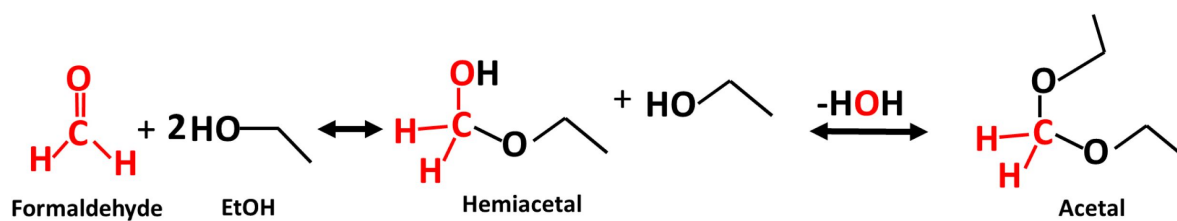


Figure 11.

Acetal formation reaction (McMurry, 2012 [🔗](#))

For heat shock, No Stress (NS) control images were taken using an Olympus Ach 100/1.25-NA objective coupled to a heating device (Biopetechs objective heater system). Heat-shocked sample imaging was done by rotating the objective away from the coverslip, switching the heating system on, and allowing it to reach 38°C before returning the objective to the coverslip for an instantaneous heat shock. The same field of view on the coverslip was imaged for both NS and HS timepoints. For ethanol stress, an Olympus UPlanFl 100/1.4-NA objective was used for image acquisition. Analysis of the images after acquisition was done using ImageJ (v. 1.52).

In the *HSP104-TMA10* coalescence analysis, cells in which the fluorophore-tagged genes had undergone replication (two green or two red fluorescent spots, indicative of late S/G2 phase) were excluded from the analysis. The locations of the two tagged loci were analyzed over 11 different z-planes, encompassing the whole nucleus. Cells were deemed coalescence positive if they displayed colocalized, non-resolvable fluorophore signals with a distance of <0.4 μm between centroids.

Spinning Disk Confocal Microscopy

For all other imaging, cells were grown as described above and image acquisition was done using an UPlan Apo 100x/1.50 NA objective in an Olympus Yokogawa CSU W1 Spinning Disk Confocal System coupled to sCMOS cameras (Hamamatsu Fusion) controlled by cellSens Dimension software. A 50 μm pinhole disk was used for imaging in combination with 10% of laser power employed for excitation using 405 nm, 488 nm, and 561 nm lasers. Z-stacks were captured as for widefield fluorescence. For heat shock, cells were attached to a VAHEAT substrate (Interference GmbH, Germany) (Icha et al., 2022 [DOI](#)) using ConA as above. The substrate was mounted onto the VAHEAT holder and control images were captured before heat was applied. Samples were instantaneously heated to 39° or 42°C. The substrate reservoir was covered with a coverslip to prevent media evaporation. Imaging was done over multiple timepoints as indicated in the figures. For ethanol stress, cells were mounted onto a coverslip as above, petroleum jelly was used to hold the coverslip against the concave slide and to reduce media evaporation. The slide was inverted and placed on the stage for visualization at room temperature.

Image reconstruction and analysis was done using FIJI/ImageJ (v. 1.53t) (Schindelin et al., 2012 [DOI](#)). Hsp104-BFP (LRY033) and Hsf1-mNeonGreen (LRY040) foci count and volume were performed using the “Cells” feature in Imaris v.10.0.0. The background fluorescence was used to delimit the region of interest (ROI). This ROI was then used to quantify the number of foci per cell. For Hsp104, the ROI (whole cell) was delimited to volumes between 20 and 140 μm^3 (Uchida et al., 2011 [DOI](#)). Foci size was measured to an average of 0.4 μm in diameter, which was used to train Imaris to recognize foci of distinct sizes [“Different Spot Sizes (Region Growing)” option]. A similar approach was taken to identify the nucleus (as the cell) and the Hsf1 foci (as nucleus) using the “Cells” feature in Imaris. Nuclei with volume of 10 $\mu\text{m}^3 \pm 3.7 \mu\text{m}^3$ were used for the analysis (Larson et al., 2011 [DOI](#)). Data obtained from these analyses were plotted using GraphPad Prism 8. Plot profile for signal arising from Hsf1-mNeonGreen, Sis1-mKate, and Hsp104-BFP was done using ImageJ/FIJI.

For analysis of transcription in VPY705, *24xMS2-HSP104* mRNA was visualized using the signal arising from MCP-mCherry binding to the chimeric transcript. Cells were interrogated for transcription by assaying the presence of an mCherry focus adjacent to *HSP104-LacO₂₅₆* bound by LacI-GFP. The high background signal from MCP-mCherry made it difficult to assess the localization of transcripts once they dissociated from the *HSP104*-tagged gene.

Statistical Tests

The statistical significance of the differences in mean values for a variety of assays was determined as specified in the figure legends using GraphPad Prism 8.

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Author Contributions

Linda S. Rubio, Conceptualization, Investigation, Visualization, Methodology, Formal Analysis, Writing – original draft, Writing – review and editing; Suman Mohajan, Investigation, Visualization, Methodology, Formal Analysis; David S. Gross, Conceptualization, Resources, Visualization, Validation, Supervision, Funding Acquisition, Writing – original draft, Writing – review and editing.

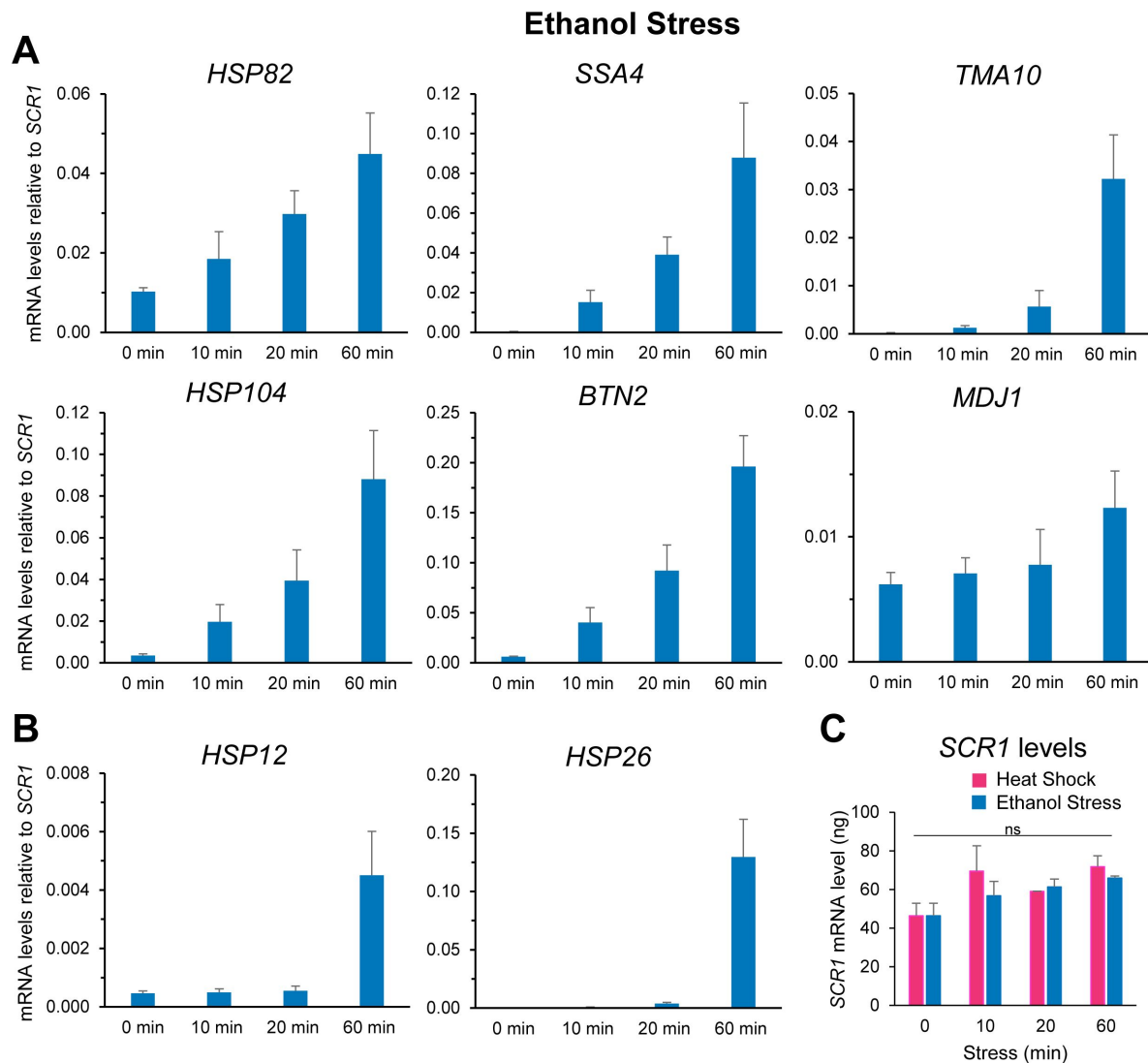


Figure 3 – figure supplement 1.

Ethanol stress transcriptionally induces *HSR* genes.

(A) RNA abundance of Hsf1-dependent genes was determined as in [Figure 3](#). Cells were exposed to 8.5% (v/v) ethanol at 25°C for the indicated times. Depicted are means + SD. N=2, qPCR=4.

(B) As in (A), but the Hsf1-, Msn2-dual regulated genes *HSP12* and *HSP26* were evaluated.

(C) Quantification of *SCR1* mRNA levels used for normalization of transcripts, analyzed by RT-qPCR. N=2, qPCR=4. A one-way ANOVA test (GraphPad Prism 8.0) was performed. ns (not significant), P>0.05.

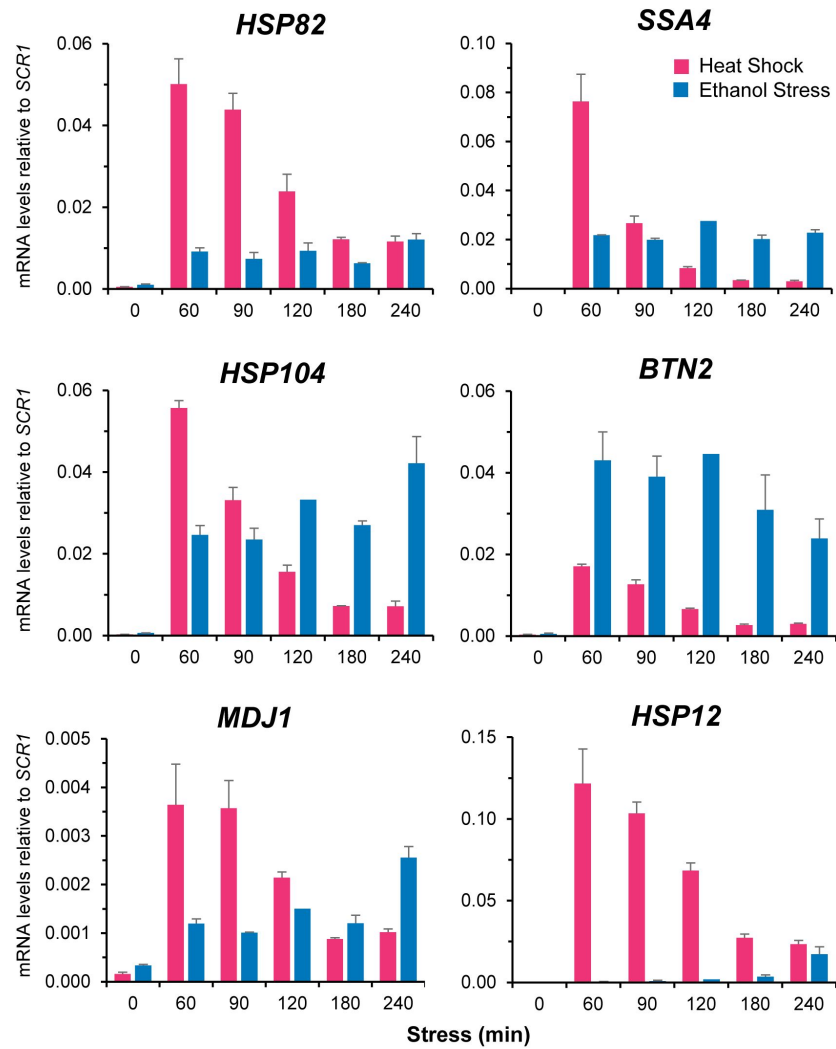


Figure 3 – figure supplement 2.

In response to chronic heat stress *HSR* mRNA levels gradually attenuate, whereas in response to chronic ethanol stress they remain constant.

Abundance of *HSR* mRNAs was determined by RT-qPCR. Experiment was conducted as described in [Figure 3](#) except longer time points were evaluated. Depicted are means + SD. N=2, qPCR=4.

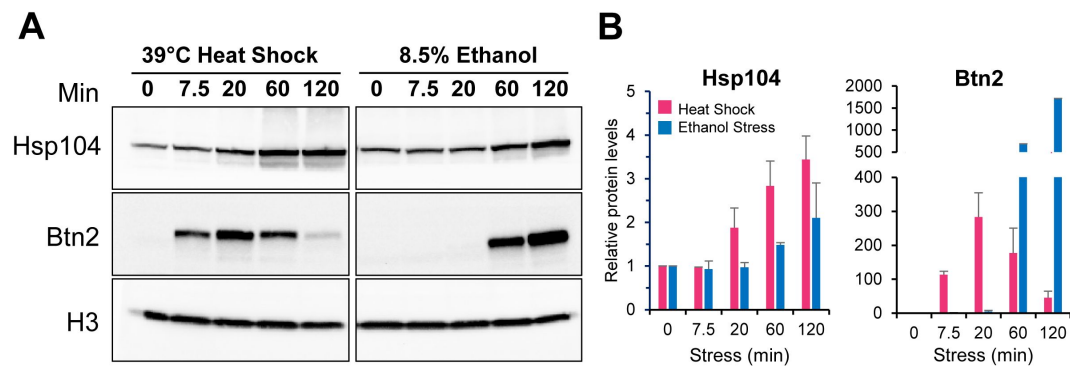


Figure 3 – figure supplement 3.

Induced HSR protein production is evident early during heat shock while it is delayed during ethanol stress.

(A) Analysis of chaperone levels by Immunoblot. Strain W303-1B was exposed to constant heat shock or ethanol stress conditions for different timepoints. Levels of Histone H3, Hsp104, and Btn2 were monitored using antibodies against endogenous proteins. Histone H3 serves as the loading control.

(B) Quantification of Hsp104 and Btn2 protein levels, samples were treated as described in (A). Protein levels were normalized to histone H3 and 0 min timepoints. Shown are means + SD. N=2.

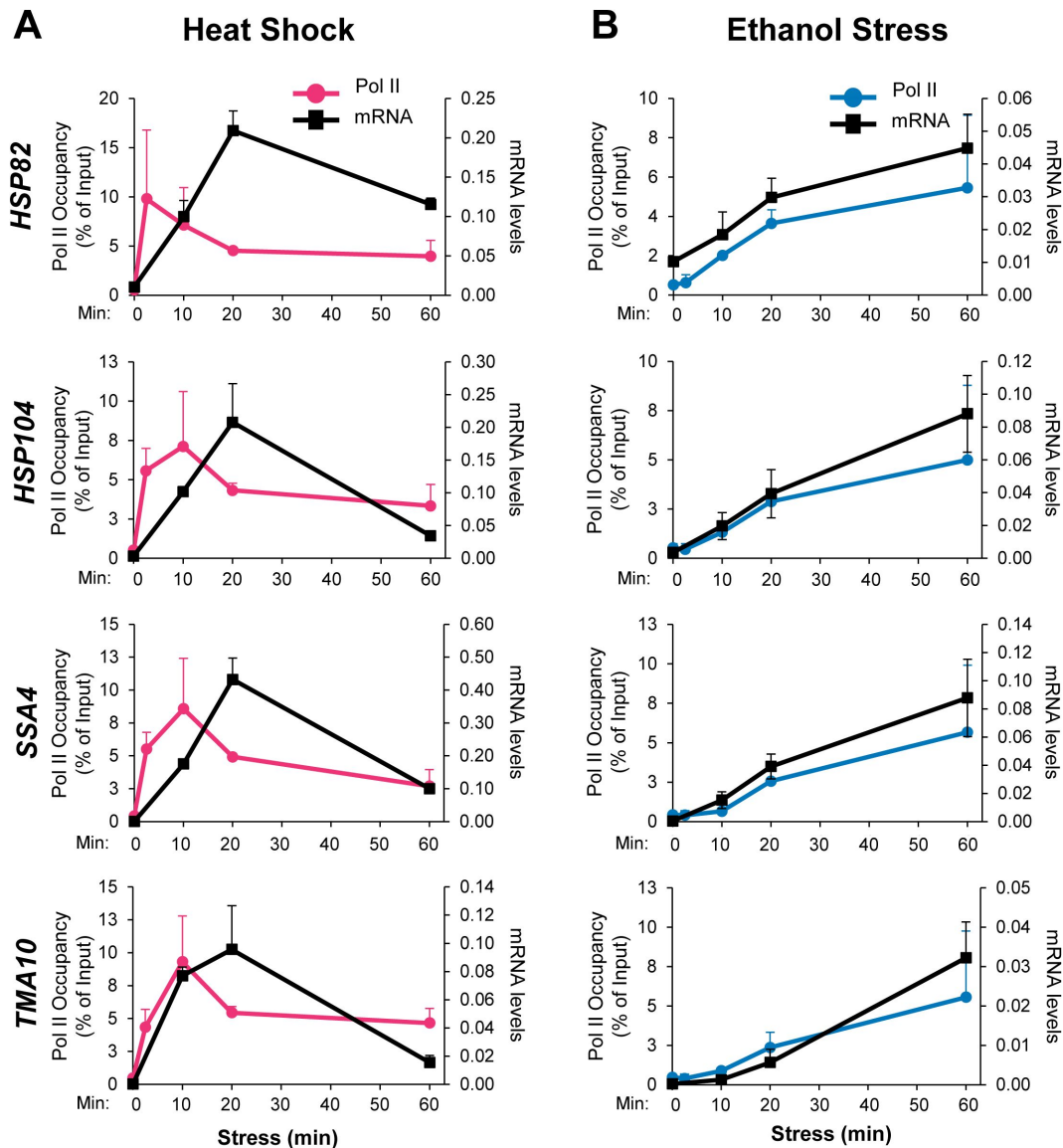


Figure 4 – figure supplement 1.

Pol II occupancy of the indicated *HSR* genes vs. their mRNA levels in cells subjected to either heat shock or ethanol stress. (A) Pol II ChIP and RT-qPCR data of the indicated *HSR* genes in cells exposed to HS are co-plotted to allow comparison of the occupancy of Pol II (over ORF) versus the corresponding transcript levels. Data derived from **Figures 2A** and **3**. (B) As above, except for ethanol stress.

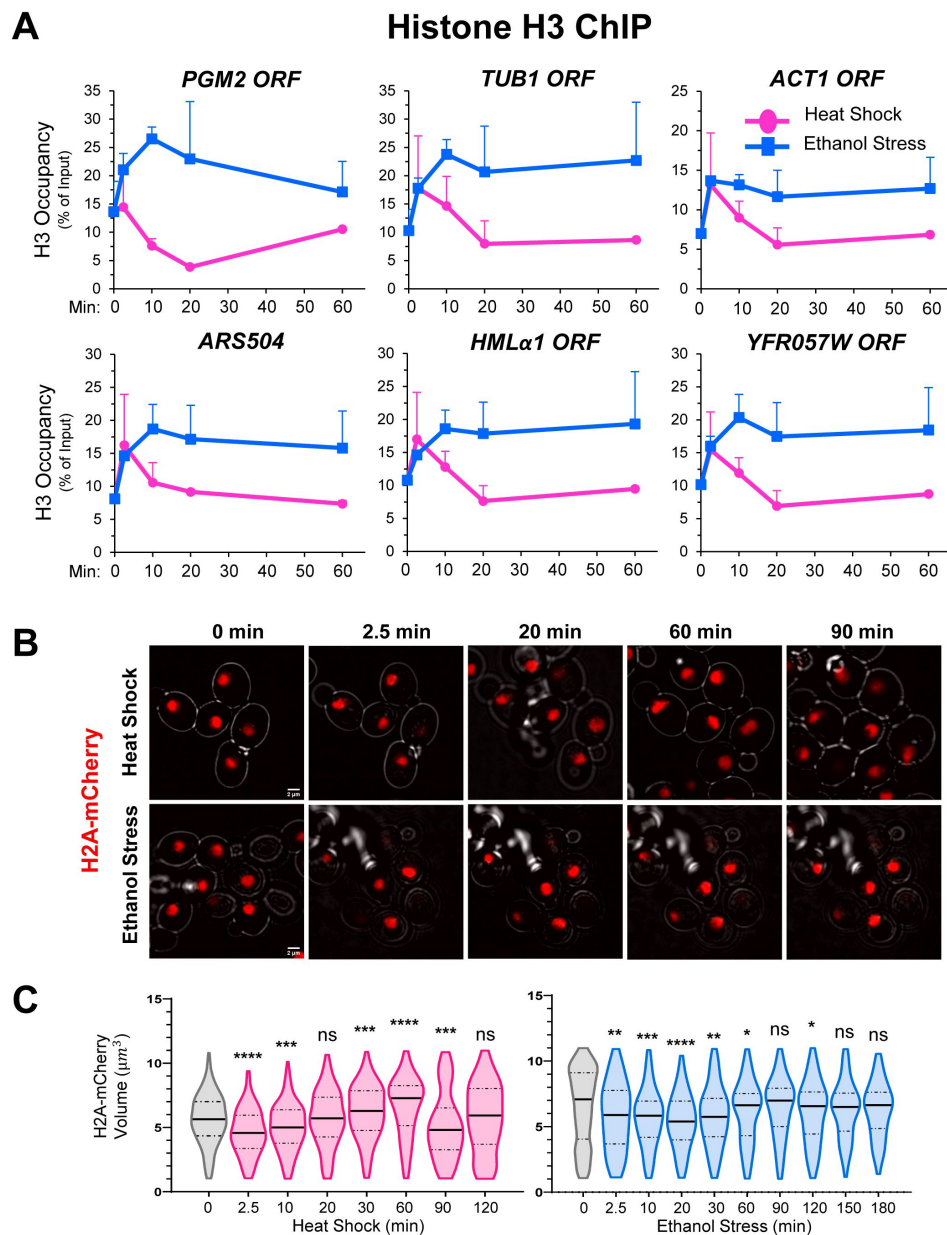


Figure 4 – figure supplement 2.

Ethanol and thermal stresses induce chromatin compaction.

(A) ChIP analysis of histone H3 occupancy at inducible (*PGM2*), constitutive (*ACT1*, *TUB1*), and inactive/silenced loci (*ARS504*, *HMLα1*, *YFR057W*). Experiment was carried out and data quantified as in [Figure 3B](#). Shown are means + SD. N=2, qPCR=4.

(B) Live cell confocal fluorescence microscopy of the diploid strain DBY1447. Histone H2A-mCherry was used to measure chromatin volume in cells cultivated in SDC medium at 25°C and then subjected to thermal (39°C) or ethanol stress (8.5% v/v) for the times indicated. VAHEAT device was used for heat shock (see Materials & Methods). Imaging was done across 11 z-planes with 0.5 μm of interplanar distance. Representative single plane images are shown. Scale bar: 2 μm.

(C) Violin plots depicting H2A-mCherry volume measurements of DBY1447 cells treated as in (B). An average of 100 cells per timepoint, per condition, were evaluated. H2A-mCherry volume was determined using 3D Objects Counter in ImageJ/Fiji (v. 1.54f). Statistical significance between no stress (0 min) and stress (2.5 – 180 min) samples was determined using Mann Whitney U Test. N=2. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; ****, $p < 0.0001$; ns, not significant.

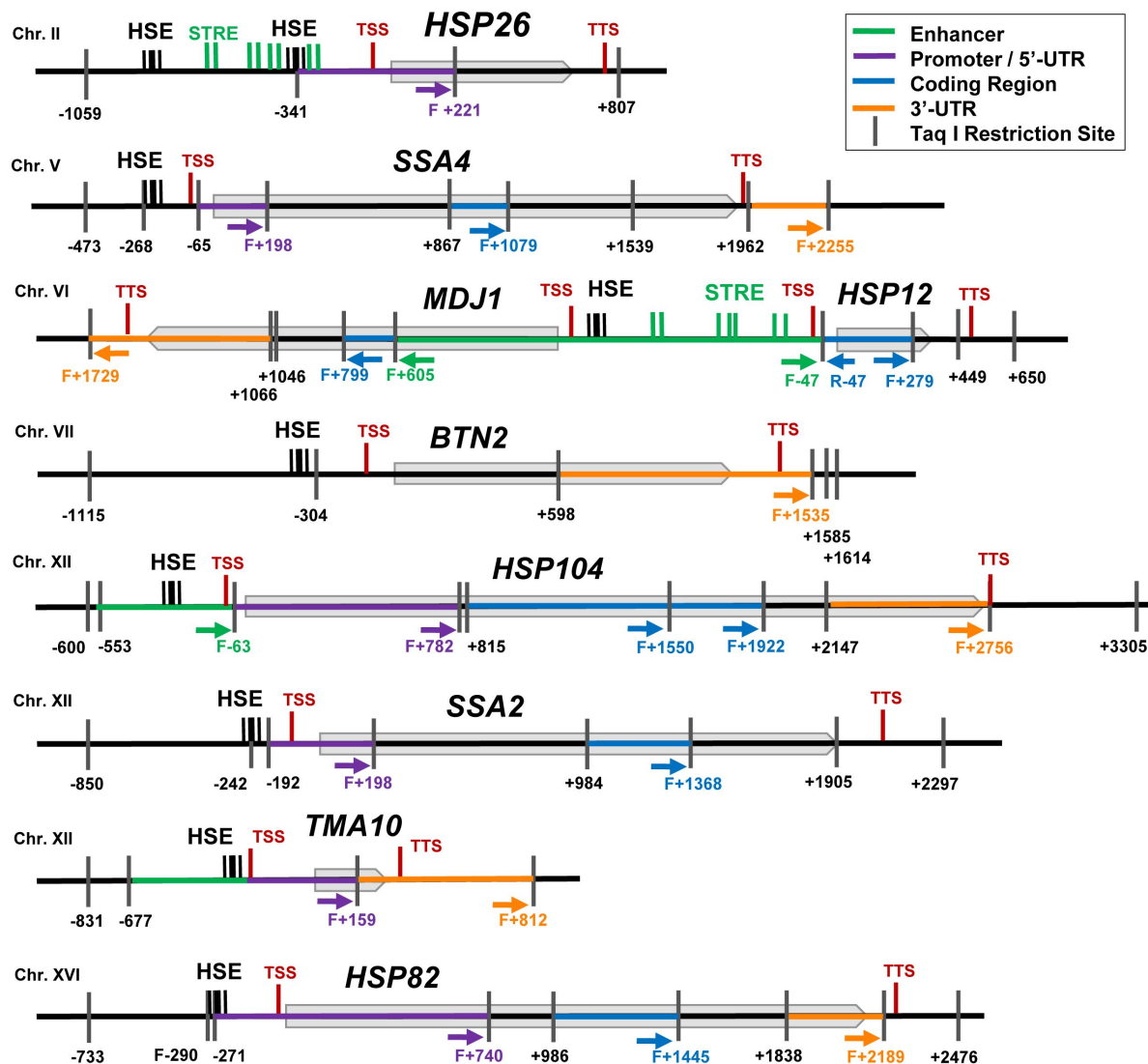


Figure 5-figure supplement 1.

Physical maps of genes used in this study.

Taq I restriction sites are numbered relative to the ATG (+1) codon. Coding regions are represented by grey boxes. Locations of Hsf1 binding sites (Heat Shock Elements (HSEs)) are shown as triple black vertical lines. Stress Responsive Elements (STREs) (Msn2 binding sites) are shown as green vertical lines (shown only for select genes). The primers used to analyze 3C interactions are represented as arrows. TSS, Transcription Start Site. TTS, Transcription Termination Site.

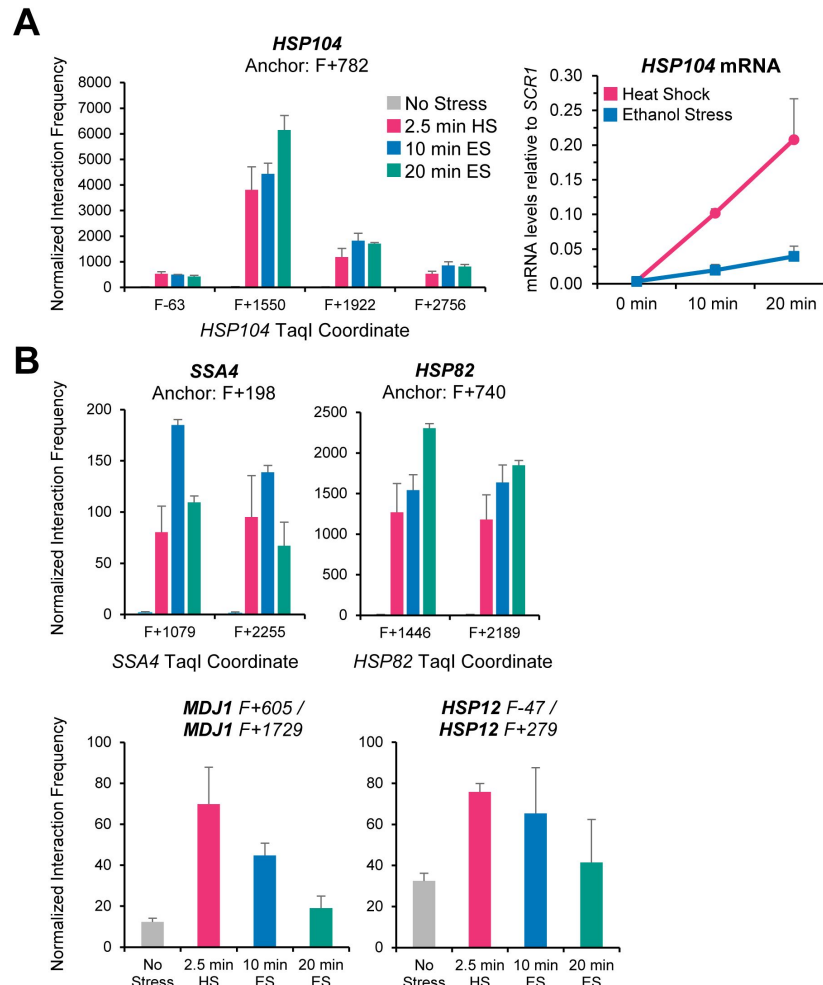


Figure 5-figure supplement 2.

Intragenic interaction frequency induced by ethanol stress is comparable to those induced by thermal stress, despite modest transcriptional output.

(A) Comparison of *HSP104* intragenic interactions (left) with *HSP104* mRNA levels (right). Samples from strain W303-1B were exposed to thermal (HS, 39°C) or ethanol stress (ES, 8.5%) for the indicated times. Intragenic interactions were analyzed by Taq I-3C; mRNA data are from [Figure 3A](#). Locations of Taq I restriction sites are in [Figure 5-figure supplement 1](#). Depicted are means + SD. N=2, qPCR=4.

(B) Taq I-3C analysis of intragenic interactions of the indicated Hsf1 target genes. Analysis and symbols as in (A).

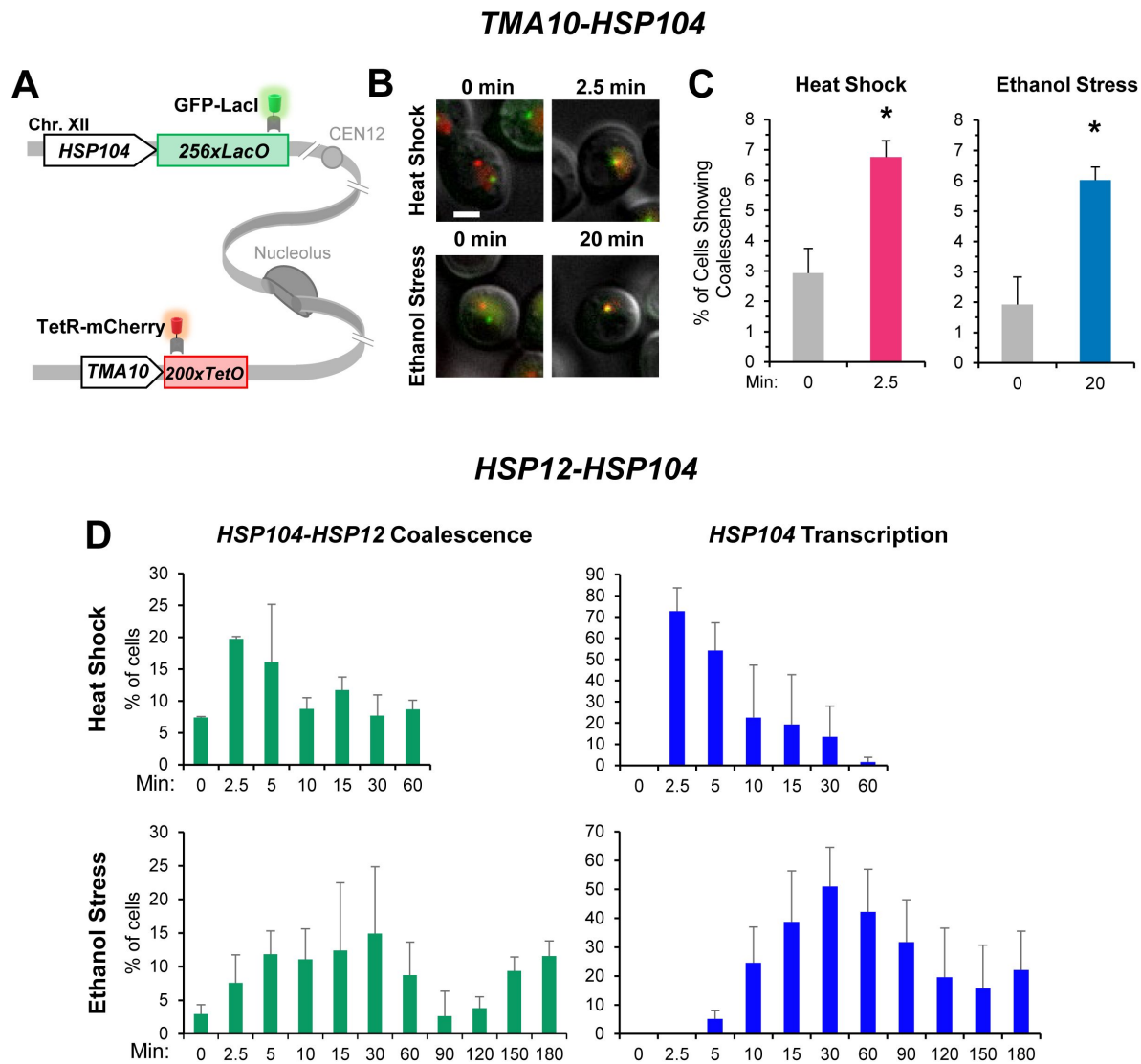


Figure 7-figure supplement 1.

HSR gene coalescence and transcription are temporally uncoupled in ethanol stressed cells.

(A) Relative location of *HSP104* and *TMA10* on Chr. XII in the diploid strain ASK727. One allele of *HSP104* is flanked by an integrated *LacO*₂₅₆ array and one allele of *TMA10* is flanked by a *TetO*₂₀₀ array. ASK727 also expresses GFP-LacI and TetR-mCherry (N- and C-terminal fusion, respectively) to allow visualization of the two genes as a green and red dot, respectively. (B) Live cell widefield fluorescence microscopy of ASK727. Cells were immobilized onto ConA-coated coverslips and exposed to either heat shock (25°C to 38°C upshift) or ethanol stress (8.5% v/v; 25°C) for the indicated times (see Materials & Methods). 11 z-planes with 0.5 µm interplanar distance were captured for each condition. A representative z-plane is shown per condition. Scale bar: 2 µm.

(C) ASK727 cells, treated as in B, were scored for colocalization of *HSP104* and *TMA10* upon exposure to either heat shock or ethanol stress. A cell was scored as positive when the highest intensity signal from both genes overlapped in the same z-plane. An average of 70 cells were evaluated per condition, per timepoint. Displayed are means + SD. N=2. A one-tailed t-test was performed to assess significance. *, $p < 0.01$. Note: we interpret *HSP104*-*TMA10* coalescence observed at T=0 min to principally reflect coincidental overlap given absence of 3C signal under the no stress condition. A similar consideration applies to the *HSP104*-*HSP12* gene pair analyzed below.

(D) VPY705 cells were subjected to heat shock (39°C; VAHEAT device) or ethanol stress (8.5%) for the indicated times and imaged using an Olympus Spinning Disk Microscope System. Imaging was acquired over 11 z-planes, with 0.5 µm of distance between planes. Left: Percentage of cells showing coalescence between GFP-labeled alleles of *HSP104* and *HSP12*. Right: Percentage of cells in the population displaying an mCherry dot (MCP-mCherry bound *HSP104* transcripts) colocalizing with the GFP-labeled *HSP104* gene. An average of 40 cells per timepoint per condition were scored. Graphs depict means + SD. N=2.

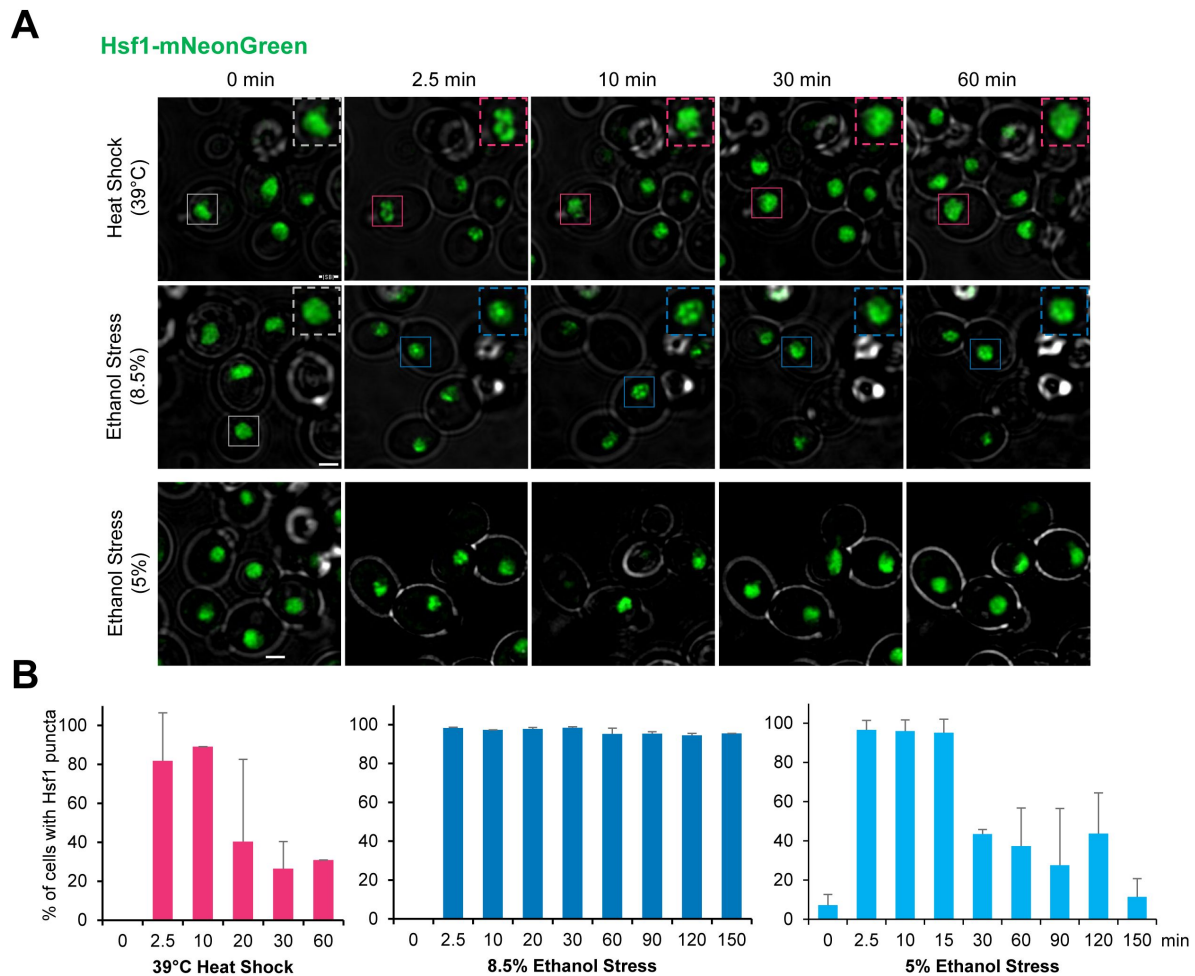


Figure 8-figure supplement 1.

Hsf1-mNeonGreen rapidly forms condensates in response to both thermal and ethanol stress.

(A) Visualization of Hsf1-mNeonGreen (LRY040 haploid strain) exposed to heat shock (39°C) or ethanol stress (8.5% or 5% v/v, 25°C). Control (0 min) was kept at 25°C. Single plane is shown, from an 11 z-planes stack taken with 0.5 μ m of interplanar distance. Dashed box represents zoom-in of a representative cell for that time point (continuous box). Scale bar: 2 μ m (B) Cells treated as in (A) were scored for the presence of Hsf1-mNeonGreen foci using Imaris software (v.10.0.0. See Materials and Methods). Depicted is the percentage of cells in the population displaying Hsf1 foci. Average cells scored per condition, per timepoint: 150. N=2. Shown are means + SD.

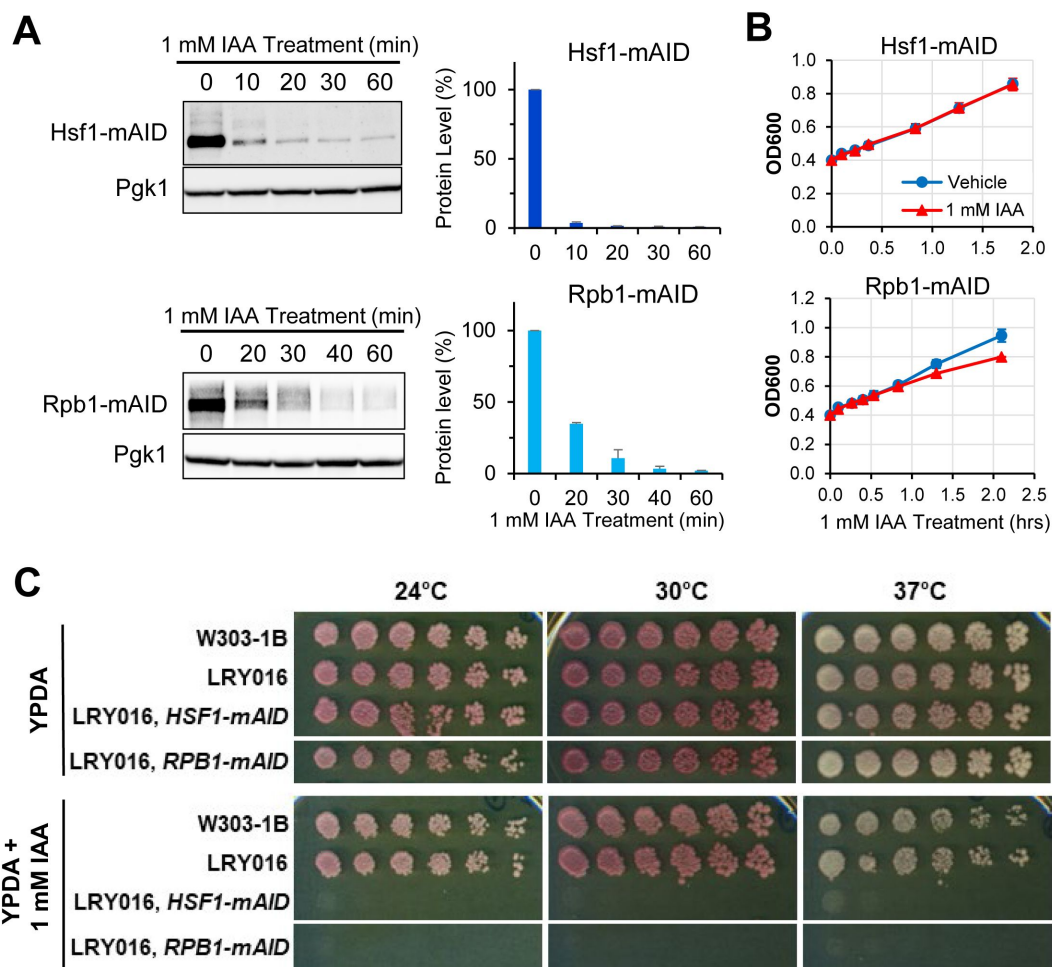


Figure 9-figure supplement 1.

Hsf1 and Rpb1 are efficiently degraded in degron-tagged strains following addition of auxin.

(A) Analysis of protein degradation by Immunoblot. Strains LRY100 and LRY102 (Hsf1-mAID and Rpb1-mAID, respectively) were grown in YPDA to mid-log phase and subjected to 1 mM IAA treatment for different lengths of time. Cells were harvested and processed by Western blot. cMyc antibody was used to visualize mAID tagged proteins, endogenous Pgk1 serves as the loading control. Quantification of mAID tagged protein levels is shown on the right. Normalization was done to Pgk1 and 0 min samples. Shown are means + SD. N=2.

(B) Growth curve assay of LRY100 and LRY102 cells exposed to 1 mM IAA. Cells were pre-grown in YPDA to mid-log phase, then diluted with equivalent volume of YPDA + IAA in ethanol (vehicle) for a final concentration of 1 mM IAA and 1.7% ethanol or just 1.7% ethanol (vehicle-treated control). Samples were incubated with shaking at 25°C, aliquots were removed to monitor OD₆₀₀ at the indicated times. Plots depict means + SD. N=2.

(C) Spot dilution analysis of cells from the indicated strains. Cells were pre-grown to early log phase, diluted to OD₆₀₀=0.5 in autoclaved distilled water, then serially diluted 1:3. A 6×8 applicator was used to spot cells on YPDA or YPDA + 1 mM IAA plates. Incubation was done at the indicated temperatures for 3 days.

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Editors

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Sofia Araújo

University of Barcelona, Barcelona, Spain

Reviewer #2 (Public Review):

Significance:

Rubio *et al.* study the behavior of the transcription factor Hsf1 under ethanol stress, examining its distribution within the nucleus and the coalescence of heat shock response genes in budding yeast. In comparison to the heat shock response, the response to ethanol stress shows similar gene coalescence and Hsf1 binding. However, there is a notable delay in the transcriptional response to ethanol, and a disconnect between it and the appearance of

irreversible Hsf1 condensates/puncta, highlighting important differences in how Hsf1 responds to these two related but distinct environmental stresses.

Overview and general concerns (from the original review):

The authors studied how yeast responds to ethanol stress (8.5%) and compared it to the heat shock response (from 25°C to 39°C). They observed a more gradual increase in the expression of heat shock response (HSR) genes during ethanol stress compared to heat shock. Additionally, the recruitment of Hsf1 and Pol II to HSR genes, and the inter- and intrachromosomal interactions among these genes, showed slower kinetics under ethanol stress. They attribute the delay in transcriptional response to chromatin compaction induced by ethanol. Despite this delay, these interactions persisted longer. Hsf1 clusters, previously documented during the heat shock response, were also observed during ethanol stress and persisted for an extended period. The conditional degradation of Hsf1 and Rpb1 eliminated most inter- and intrachromosomal interactions for heat shock responsive genes in both ethanol stress and heat shock conditions, indicating the importance of these factors for long distance interactions between HSR genes. Overall, this manuscript provides novel insights into the differential behavior of HSR genes under different stress conditions. This contributes to the broader understanding of how different stressors might elicit unique responses at the genomic and topographical level under the regulation of transcription factor Hsf1.

The central finding of the study highlights the different dynamics of Hsf1, Pol II, and gene organization in response to heat shock versus ethanol stress. However, one important limitation to consider is that the two chosen conditions may not be directly comparable. For a balanced assessment, the authors should ideally expose yeast to various ethanol concentrations and different heat shock temperatures, ensuring the observed differences stem from the nature of the stressor rather than suboptimal stress intensity. At the very least, an additional single ethanol concentration point on each side of 8.5% should be investigated to ensure that 8.5% is near the optimum. In fact, comparing the number of Hsp104 foci in the two conditions in Fig. 1E and F suggests that the yeast is likely experiencing different intensities of stress for the chosen heat shock condition and ethanol concentration used in this study.

A second significant concern is the use of the term "Hsf1 condensate". Chowdhary et al.'s 2022 Molecular Cell study highlighted an inhomogeneous distribution and rapid dynamics of Hsf1 clustering upon heat shock, with sensitivity to 1,6-hexandiol, which is interpreted as evidence for condensation by LLPS. But this interpretation has been criticized severely by McSwiggen et al. Genes Dev 2019 and Mussacchio EMBO J 2022. It is important to mention that 1,6-hexandiol is known to affect chromatin organization (Itoh et al. Life Science Alliance 2021). Describing such clusters as 'condensates' without further experimental evidence is premature. I encourage authors to settle on their neutral term 'puncta' which they use interchangeably with 'condensate' so as not to confuse the reader. The dynamic binding and unbinding of the low-abundance Hsf1 at coalescent chromatin target sites might explain the liquid-like properties of these clusters without the need for invoking the phase-separation hypothesis. While Hsf1 clusters exhibit features consistent with phase-separated condensates, other equally plausible alternative mechanisms, such as dynamic site-specific interactions (Mussacchio, EMBO J, 2022), should also be considered. This is best left for the discussion where the underlying mechanism for puncta formation can be addressed.

Comments on revised version:

The authors have addressed the majority of my comments effectively. The new Sis1 experiment provides a clear illustration of a distinctive response to ethanol and heat. This work offers a comprehensive perspective on Hsf1 in stress response from multiple angles. I have two additional comments to improve the paper without re-review:

(Original point #3) Could the authors clarify the differences between DPY1561 and the original strain used? There appears to be missing statistical analysis for Figure 1E at the bottom.

(Original point #4) In the new Figure 7F, '% transcription' and '% coalescence' are presented. My understanding is that Figures 7D and 7E aim to demonstrate the correlation between HSP104 transcription (a continuous variable) and HSP104-HSP12 coalescence (a binary variable) at the single-cell level. However, averaging the data across cells masks individual variations and potential anti-correlations. The authors could explore statistical methods that handle correlations between a continuous variable and a binary variable. Alternatively, consider converting 'HSP104 transcription' to a binary variable and then performing a chi-square test to assess the association.

<https://doi.org/10.7554/eLife.92464.2.sa2>

Reviewer #3 (Public Review):

This is an interesting manuscript that builds off of this group's previous work focused on the interface between Hsf1, heat shock protein (HSP) mRNA production, and 3D genome topology. Here the group subjects the yeast *Saccharomyces cerevisiae* to either heat stress (HS) or ethanol stress (ES) and examines Hsf1 and Pol II chromatin binding, Histone occupancy, Hsf1 condensates, HSP gene coalescence (by 3C and live cell imaging), and HSP mRNA expression (by RT-qPCR and live cell imaging). The manuscript is well written, and the experiments seem well done, and generally rigorous, with orthogonal approaches performed to support conclusions. The main findings are that both HS and ES result in Hsf1/Pol II-dependent intergenic interactions, along with formation of Hsf1 condensates. Yet, while HS results in rapid and strong induction of HSP gene expression and Hsf1 condensate resolution, ES result in slow and weak induction of HSP gene expression without Hsf1 condensate resolution. Thus, the conclusion is somewhat phenomenological - that the same transcription factor can drive distinct transcription, topologic, and phase-separation behavior in response to different types of stress. While identifying a mechanistic basis for these results would be a tough task perhaps beyond the scope of this study, it would nevertheless be helpful to place these results in context with a series of other studies demonstrating across various organisms showing Hsf1 driving distinct activities dependent on the context of activation. Perhaps even more importantly, this work left out PMID: 32015439 which is particularly relevant considering that it shows that it is human HSF1 condensate resolution rather than simple condensate formation that is associated with HSF1 transcriptional activity - which are similar to the findings here with this particular dose of HS resulting in resolution and high transcriptional activity versus ES resulting in resolution failure and lower activity. It is also worth noting that the stresses themselves are quite different - ethanol can be used as a carbon source and so beyond inducing proteotoxic stress, the yeast are presumably adapting to this distinct metabolic state. Basically, it is not clear whether these differences are due to the dose of stress, versus we are looking at an early timepoint as ES initiates a genome-wide chromatin restructuring and gene expression reprogramming that goes beyond a response to proteotoxic stress. This reviewer is not suggesting a barrage of new experiments, but perhaps discussion points to contextualize results.

Comments on latest version:

The authors have addressed my concerns.

<https://doi.org/10.7554/eLife.92464.2.sa1>

Author response:

The following is the authors' response to the original reviews.

Public Reviews:

Reviewer #1:

Overall, the conclusions appear appropriately supported by the data, and the data appear of high quality.

Strengths:

The particular strengths of the paper include an impressive combination of genomic and imaging-based approaches and insightful genetically engineered cell systems. The manuscript reports interesting and potentially important findings. The text is generally very well written, the ideas are clearly explained, and the reasoning is easy to follow.

Weaknesses:

The main weakness seems to be that the heat and ethanol shock approaches likely elicit pleiotropic effects, and therefore it is a challenge to test the causal relationship between various observations. Nevertheless, even as indirect effects might contribute to some of the authors' observations, the results are definitively worth reporting.

We agree that these two proteotoxic stresses can impact cell physiology in multiple ways and discuss this on lines 132-143 and 500-519. Moreover, in this revision we have more rigorously quantified the extent of proteotoxic stress elicited by the 39°C heat shock and 8.5% ethanol stress (Figure 1E; see response 1 to Reviewer 2). We have additionally added new Figure 2 that reveals an important difference in the way Hsf1 and its negative regulator, the Hsp70 co-chaperone Sis1, respond to HS and ES. This difference is evident at two different intensities for each stress as described in more detail below (see response 1 to Reviewer 2).

Presentation of some of the data could be improved.

We agree and have made improvements/data additions to multiple figures: Figure 1E; Figures 3A, B; Figures 4A, B; Figure 7 (data drawn from original Fig. 6 and Fig. 6 – fig. suppl. 1 and reorganized); Fig. 8B; Figure 9; Figure 10. Corresponding enhancements to the supplemental figures have been made as well.

Reviewer #2:

(1) The central finding of the study highlights the different dynamics of Hsf1, Pol II, and gene organization in response to heat shock versus ethanol stress. However, one important limitation to consider is that the two chosen conditions may not be directly comparable. For a balanced assessment, the authors should ideally expose yeast to various ethanol concentrations and different heat shock temperatures, ensuring the observed differences stem from the nature of the stressor rather than suboptimal stress intensity. At the very least, an additional single ethanol concentration point on each side of 8.5% should be investigated to ensure that 8.5% is near the optimum. In fact, comparing the number of Hsp104 foci in the two conditions in Fig. 1E and F suggests that the yeast is likely experiencing different intensities of stress for the chosen heat shock condition and ethanol concentration used in this study.

We thank the reviewer for this important suggestion. In this revision, we have included an enhanced analysis of the yeast cellular response to each of these stresses. As illustrated in

revised Figure 1, the two stresses used throughout this study – 39°C heat shock and 8.5% ethanol stress – both elicit a proteotoxic response, as assayed by the de novo formation of Hsp104 clusters. While 10 min exposure to 8.5% ethanol results in the formation of multiple discrete (spherical) foci, a 10 min exposure to the elevated temperature leads the appearance of multiple, largely diffuse Hsp104 clusters, some of which are spherical (new Fig. 1D). The difference in morphology notwithstanding, we have attempted to quantify these clusters using Imaris v. 10.0.1 image analysis software; the results are depicted in Fig. 1E. Such quantification suggests that 8.5% ethanol elicits a more intense stress than exposure to 39°C. A caveat is that it is unclear whether diffuse Hsp104 clusters are comparable to compact Hsp104 foci (see response 3 below).

Beyond the apparent difference in intensity, a new analysis presented in new Figure 2 reveals that heat shock, elicited by temperature upshift to either 39°C or 42°C, induces relocalization of the J-protein Sis1 – a key negative regulator of Hsf1 – from the nucleoplasm to the nucleolar periphery. Sis1’s perinucleolar ring localization agrees with previous findings of 39°C heat-shocked cells (Feder et al., 2021). Ethanol stress, whether 5% or 8.5%, initially causes Sis1 to relocalize diffusely throughout the nucleus and cytosol. At 10 min, Sis1 localizes to the periphery of the nucleus, thereby providing a marked contrast to what is observed in response to heat shock. These new results are described on lines 174-191.

Taking these two observations together, we asked whether a less severe ethanol stress (5%) would induce Hsf1 puncta. It does, and as rapidly as 8.5% ethanol (data are presented in revised Figure 8-figure supplement 1). Interestingly, in the presence of 5% ethanol, Hsf1 puncta begin to dissolve at 30 min. This strongly contrasts with the case when cells are exposed to 8.5% ethanol (Figure 8; Figure 8-figure supplement 1). As we state in this revision (lines 414-424), the sustained presence of condensates that we originally observed is likely the consequence of the intensity of the proteotoxic stress elicited by exposure to 8.5% ethanol; analogous responses to these two stress conditions have been observed before (lines 495-501).

(2) A second significant concern is the use of the term "Hsf1 condensate". Chowdhary et al.'s 2022 Molecular Cell study highlighted an inhomogeneous distribution and rapid dynamics of Hsf1 clustering upon heat shock, with sensitivity to 1,6-hexandiol, which is interpreted as evidence for condensation by LLPS. However this interpretation has been criticized severely by McSwiggen et al. Genes Dev 2019 and Mussacchio EMBO J 2022. It is important to mention that 1,6-hexandiol is known to affect chromatin organization (Itoh et al. Life Science Alliance 2021). Describing such clusters as 'condensates' without further experimental evidence is premature.

While we appreciate and largely agree with the point made by this reviewer, we prefer to maintain the term “condensate”. Banani et al (2017) originally defined “biomolecular condensate” to mean selforganized membrane-free compartments that concentrate specific biomolecules. It was never meant to imply LLPS although its widespread use in the literature has led to that implication. We clarify our use of this term on lines 99-104.

(3) Figure 1: Why does ethanol stress at 0 min display a larger number of Hsp104 foci per cell than heat shock at the same time? How are foci defined by the authors? In Fig. 1D, there are many smaller puncta. A comparative assessment of the number and size of foci for heat shock and ethanol stress would be beneficial.

We thank the reviewer for raising this point and have addressed it as follows. First, we repeated the assay with a different strain (DPY1561) and increased the number of cells assayed from 40 to 200. This larger sample size created the same T=0 baseline for both stresses (Figure 1E). Second, we define Hsp104 foci as diffraction-limited structures with a diameter of ~0.4 µm (lines 747-749). Third, employing Imaris v. 10.0.1, we quantified foci size (= volume) and a summary graph has been added to Figure 1E that also displays the number

of foci per cell. In the legend to this figure, we point out that to conduct this analysis we assumed that the diffuse Hsp104 clusters seen in HS cells are comparable to the compact Hsp104 foci in ES cells (lines 1169-1171).

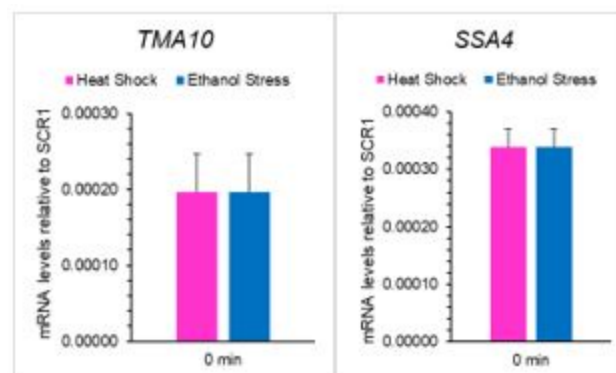
(4) Figure 2: Selecting a housekeeping gene with consistent expression levels is crucial for meaningful qPCR analysis. Do *SCR1* mRNA levels fluctuate during heat shock or ethanol stress?

We thank the reviewer for this question. In revised Figure 3 – figure supplement 1C we provide a new graph (reproduced here) revealing that the levels of *SCR1* do not significantly change under either heat shock or ethanol stress relative to the non-stressed control (0 min). One-way ANOVA analysis was performed for both HS and ES and *p* values were 0.094 and 0.083, respectively (calculated using GraphPad Prism 8).

(5) Additionally, certain genes, such as *TMA10* and *SSA4*, lack visible bars at time 0. Are these levels undetectable? The varying y-axis scales are confusing; presenting data as relative fold changes could offer a clearer perspective.

Transcript levels for all genes evaluated here are detectable, even in the basal unstressed state. They are not visible on the histogram for certain genes at T= 0 due to the prodigious fold-increase in RNA elicited by heat shock. However, to address this concern, we have added a bar graph inset displaying basal transcript levels for each gene in revised Figure 3. We reproduce data for *SSA4* and *TMA10* in the graphs below. In addition, we present transcript levels in new Figure 3 - figure supplement 1 for cells subjected to ethanol stress to allow a better appreciation of their increase over time.

Author response image 1.



(6) Line 239: The evidence for chromatin compaction is unconvincing. An increase in H3 occupancy by ChIP might indicate a reduction in histone exchange dynamics but may not relate to overall chromatin compaction. The authors use H2A-mCherry to suggest a decrease in chromatin volume, but this data is not persuasive. Did the authors observe any changes in nuclear size? Perhaps quantifying chromatin compaction more directly, using signal intensity per volume, would be informative.

To address this concern, we attempted to quantify integrated density for H2A-mCherry using Image J software. While the volume decreased for both stresses, the integrated density only increased for ethanol stress. We speculate that this may be due to photobleaching which has been reported for heat shock. The combination of heat and acidic pH contribute to loss of fluorescence signal (Alkaabi et al., 2005). While the integrated density supports the idea of

global chromatin compaction in the ethanol stress condition, given the above concerns with the HS sample we elected to not present these data.

(7) Line 340: The claim of a "strong spatiotemporal correlation" isn't evident from the data. Could correlation coefficients be provided? There is potential anti-correlation in Fig. 6 - Figure Supplement 1C.

We thank the reviewer for this excellent suggestion. We now present an analysis of the correlation between HSP104 – HSP12 coalescence and HSP104 transcription for both HS and ES time courses, using single cell data of Figures 7D, 7E and Figure 7- suppl. 1D. This analysis is presented in new Figure 7F.

(8) Figure 8: The WT data in Fig 8 seem inconsistent with Fig. 4 (e.g. the interaction frequency for HSP104 and SSA2). Are these fluctuations between experiments, or are they side effects of IAA treatment? The use of ethanol as an IAA solvent vehicle raises concerns. It would be beneficial if the authors could demonstrate that 1.7% ethanol in the control does not induce ethanol stress.

We acknowledge that there existed an inconsistency in the magnitude of intergenic interaction frequencies reported in the two experiments for HSP104 and SSA2. Some of this might be attributed to the fact that different strains were used, W303-1B in Figure 4 and LRY016 (W303-1B; *LEU2::pGPD1osTIR1*) in Figure 8. Nonetheless, in each experiment there was a prodigious fold-increase in interaction frequency over the no stress (T= 0 min) control for both HS and ES conditions and moreover, in each experiment the magnitude of this interaction was greater for the 2.5 min HS sample vs. the 10 min ES sample. However, to obviate this concern, we have removed the HSP104-SSA2 analysis from Figure 9 (corresponds to original Fig. 8).

Regarding the second point, we cannot entirely rule out the concern that the 1.7% ethanol vehicle might impact 3C interaction frequencies. It is unlikely to be significant, however, given that most other pairwise tests evaluated in the two experiments (Figs. 5 and 9) resulted in similar 3C values. In particular, there was no consistent trend towards higher (or lower) interaction frequencies in the IAA experiment of Fig. 9.

Reviewer #3:

*This is an interesting manuscript that builds off of this group's previous work focused on the interface between Hsf1, heat shock protein (HSP) mRNA production, and 3D genome topology. Here the group subjects the yeast *Saccharomyces cerevisiae* to either heat stress (HS) or ethanol stress (ES) and examines Hsf1 and Pol II chromatin binding, Histone occupancy, Hsf1 condensates, HSP gene coalescence (by 3C and live cell imaging), and HSP mRNA expression (by RT-qPCR and live cell imaging). The manuscript is well written, and the experiments seem well done, and generally rigorous, with orthogonal approaches performed to support conclusions...While identifying a mechanistic basis for the results [presented here] would be a tough task perhaps beyond the scope of this study, it would nevertheless be helpful to place these results in context with a series of other studies...importantly, this work left out PMID: 32015439 (HSF1 phase transition mediates stress adaptation and cell fate decisions) which is particularly relevant considering that it shows that it is human HSF1 condensate resolution rather than simple condensate formation that is associated with HSF1 transcriptional activity - which is similar to the findings here with this particular dose of HS resulting in resolution and high transcriptional activity versus ES resulting in resolution failure and lower activity.*

We thank the Reviewer for pointing out this oversight. In this revision, we cite Gaglia et al., 2020 and several others reporting HSF1 foci formation in human cells exposed to heat shock. The single cell analysis of Gaglia et al argued that dissolution of large HSF1 foci (aka “nuclear stress bodies”), typically several μm in diameter and localized over satellite III DNA repeats (Jolly et al., 1997, 2002), correlates with HSP gene activation. Importantly, these condensates are postulated to act as reservoirs of HSF1, sequestered away from HSP genes (Gaglia et al., 2020). In contrast, Zhang et al., 2022 has shown that human HSF1 inducibly forms small condensates ($\sim 300\text{ nm}$) that localize over HSP genes and whose formation directly correlates with HSP gene activation (we discuss the Jolly, Gaglia and Zhang findings on lines 382-394). Likewise, our work shows that in yeast, Hsf1 inducibly forms small, dynamic clusters that colocalize with *HSR* genes within 2.5 min of exposure to elevated temperature; these dissolve $\sim 20\text{-}60$ min later (Figure 8 and Figure 8-supp. 1). In concert with Hsf1 condensate formation, *HSR* gene repositioning and transcription/ Pol II recruitment are likewise evident within 2.5 min. Therefore, in HS cells there exists coordinate induction of condensate formation, Pol II recruitment, transcription and intergenic interactions (for a detailed kinetic analysis of *HSR* gene interactions, see Figures 5 and 6 of Chowdhary et al, 2017). This tight temporal relationship is absent in ethanol stressed cells (Figures 3, 4, 5, 6, 7, 8; summarized in Figure 10 and Table 1).

It is also worth noting that the stresses themselves are quite different - ethanol can be used as a carbon source and so beyond inducing proteotoxic stress, the yeast are presumably adapting to this distinct metabolic state. Basically, it is not clear whether these differences are due to the dose of stress, versus we are looking at an early timepoint as ES initiates a genome-wide chromatin restructuring and gene expression reprogramming that goes beyond a response to proteotoxic stress. This reviewer is not suggesting a barrage of new experiments, but perhaps discussion points to contextualize results.

We thank the reviewer for this suggestion and in our revised manuscript discuss these issues (lines 414-424 and 486-498 [5% vs. 8.5% ethanol]; lines 500-519 [ethanol as a metabolite]).

Recommendations for the authors:

Reviewer #1:

(1) In Figure 1E, the number of foci in control (0 min) cells is very different for the two conditions. Could the authors clarify/check this? Based on the mean numbers at time point 0, the control cells for the ethanol treatment already contain about 10-20 Hsp104 foci, compared to around 5 foci per cell in the control for heat shock.

We thank the reviewer for raising this point and have repeated the assay with a different strain (DPY1561). And as shown in Figure 1E, have confirmed that the control samples have similar number of foci.

(2) In the same Figure 1E, is the P-value relative to the control or the same time point in the other treatment? A comparison across treatments would be necessary to support the claim in lines 168-171 of the text.

The statistical analysis (Mann Whitney test) was performed by comparing each stress timepoint to the no stress control. We clarify this in the figure legend.

(3) In Figure 1D, the heat-shock condition shows the same cells that are used in the control, but the cells in the ethanol-shock condition are different. This is a bit visually

misleading compared to the experimental setup shown in panel 1C. The authors could show the control cells for the ethanol condition as well.

We thank the reviewer for this excellent suggestion and have added the 0 min image for the ethanol stress conditions.

(4) In Figure 7B adding images at 60min would help underscore the point that the condensates are stable in ethanol shocked cells.

We appreciate this suggestion as well and have included a 60 min timepoint for both stresses (Figure 8B).

Reviewer #2:

(1) Line 113: Has it not been established that yeast Hsf1 is constitutively trimeric?

In yeast, only a fraction of Hsf1 is thought to be constitutively trimeric and it is this species that binds high-affinity HSEs even under non-stressful conditions (Giardina & Lis, 1995; Pincus et al., 2018). We have added this clarification to the text (lines 121-123).

(2) Ethanol can precipitate proteins, especially in rich media like YPD. Did the authors notice any protein precipitation? If yes, how do they account for effects due to nutrient loss by precipitation?

This is an interesting point, but we did not notice any precipitates in either rich or synthetic liquid media containing 8.5% (v/v) ethanol for any of the time points used in the experiments.

(3) Figure 3: The figure appears incomplete. Can enhancer, promoter, coding region, and 3'UTR be shown consistently for all genes examined?

In response to this point, we have simplified this figure (new Fig. 4) by uniform presentation of factor occupancy at enhancer, promoter, and coding region loci for all but one of the genes evaluated. For *HSP12* (330 bp), we were unable to distinguish promoter from coding region since the average sonicated chromatin fragment obtained using a Bioruptor is ~300 bp. Therefore, we evaluated only the *HSP12* coding region for Pol II and histone H3 occupancy.

(4) Figure 4: The comparison between heat shock at 2.5 min and ethanol stress at later points is puzzling. Why not use consistent time points as in Fig. 3?

Time points for the two stresses examined in this figure (new Fig. 5) were selected to represent times of peak intergenic interaction between *HSR* genes. These times were derived from our earlier analysis of 3C interactions during a heat shock time course (Figs. 5, 6 of Chowdhary et al., 2017) and ES data presented in this study, including Fig. 4 (Pol II ChIP time course) and Fig. 6 (3C time course). Data presented in Figs. 5 and 6 are consistent with the notion that intergenic interactions in cells subjected to ethanol stress are delayed relative to those observed in heat shocked cells, peaking in most cases at ~10 min (vs. ~2.5 min for heat stress (Chowdhary et al., 2017)).

(5) Figure 5: Fig. 5B top panel seems to show color inconsistencies for bars at 0 and 120 min. Also, the xaxis on the top left panel seems to have a typo; should it read "10," not "0?"

We thank the reviewer for the observation. We changed the graphs in new Figure 6 to display the same color for all time points. We also fixed the typo.

(6) Line 302: The evidence presented supports maximal mRNA levels, but the claim of "maximal transcription" requires support from nascent RNA analysis.

We agree that RT-qPCR measures mRNA abundance, not nascent transcription. We have changed the text to refer to "transcript levels" where pertinent (lines 301-302; 1331-1332).

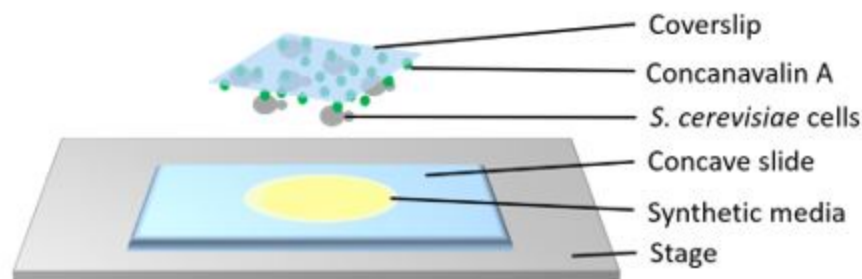
(7) How long do loci remain coalescent during heat shock versus ethanol stress? Both 3C and imaging analyses do not differentiate between frequency and duration, which seems essential for understanding interaction dynamics.

We thank the reviewer for this excellent question. In new Fig. 7D,E (data drawn from Fig. 6 – fig. suppl. 1), HSR gene coalescence detected in single cells over a HS or ES time course is charted. Interpretable data exist for a small number of cells. Moreover, for both HS and ES states, in certain cells coalescence between the representative Hsf1 target genes *HSP104* and *HSP12* dissolves and then reappears. With this caveat in mind, the data suggest that *HSP104*-*HSP12* coalescence can last at least 15 min in HS cells and up to 30 min in ES cells. We have not emphasized this point in the manuscript since a far more comprehensive analysis – beyond the scope of this study – is required.

(8) For longer analyses, how do the authors accommodate potential ethanol concentration changes due to evaporation?

For liquid cultures, we relied on maintaining minimal changes in the vapor pressure within the experimental vessel; to facilitate that, flasks were tightly covered to minimize evaporation and temperature was kept at 25°C. For most molecular analyses (RT-qPCR, ChIP, 3C), we confined our analysis to the first 60 min. For microscopy, the samples were encased within a concave slide, covered by a coverslip, as illustrated below. In addition, to tightly seal the coverslip on the slide we used petrolatum. This arrangement minimized evaporation.

Author response image 2.



(9) Figure 9: This legend seems to have an incomplete sentence: "(represented using ...)."

We have substituted an entirely new model in this revised manuscript (new Figure 10) that omits the use of an ellipsis. (We had used it to symbolize a delay in the appearance of HSR gene transcription in ES cells.)

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