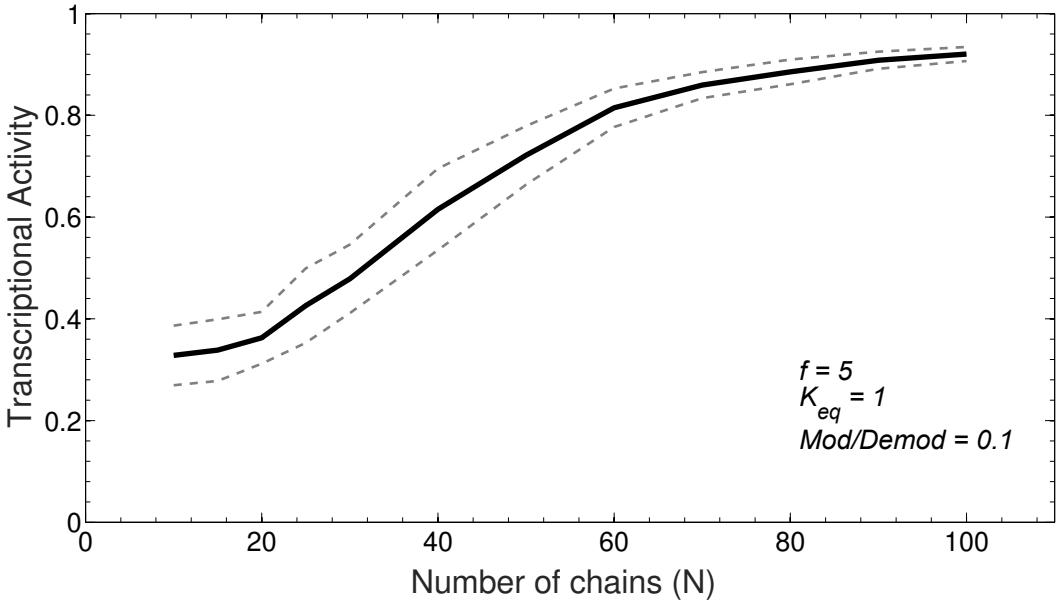
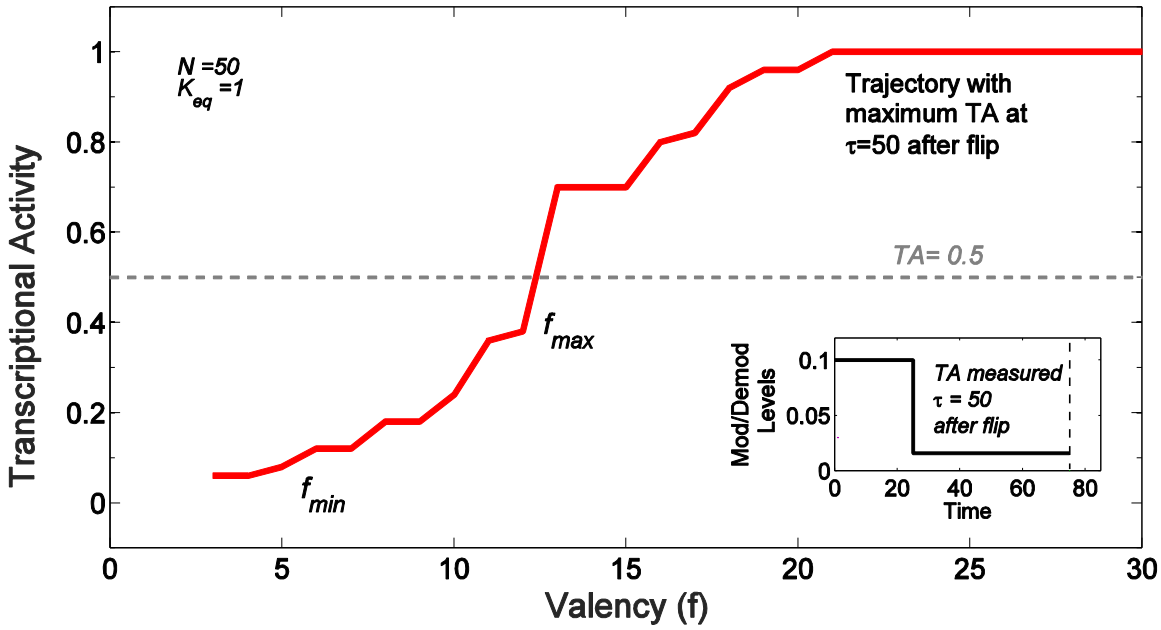
Supplemental Figures

Supplemental Figure 1



Supplemental Figure 1. Dependence of transcriptional activity (TA) on number of chains (N) is depicted above. The proxy for transcriptional activity (TA) is defined as the size of the largest cluster of cross-linked chains, scaled by the total number of chains. The solid lines indicate the mean and the dashed lines indicate twice the standard deviation in 50 simulations. All simulations are done at Modifier/Demodifier=0.1, K_{eq}=1 and *f*=5. TA levels are very different as long as the values of N (or concentration of components) for a SE and a typical enhancer are sufficiently different.

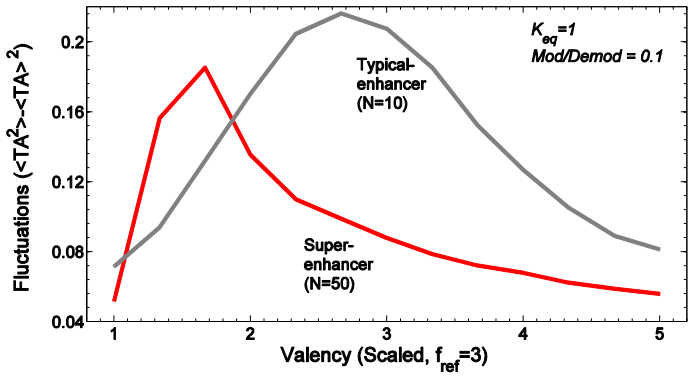
Supplemental Figure 2



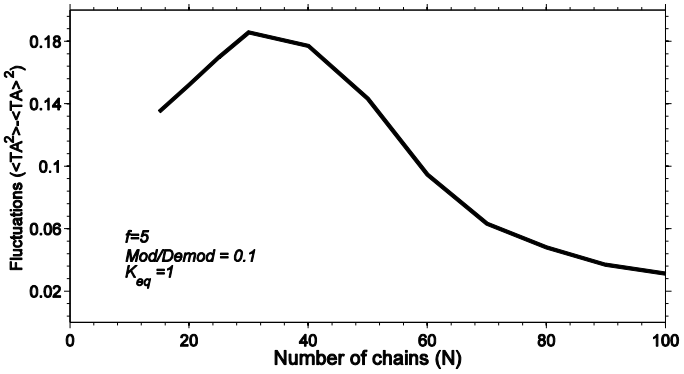
Supplemental Figure 2. Simulations carried out to study disassembly of the gel after a sharp change in the Modifier/Demodifier balance (mimics change in signals). The proxy for transcriptional activity (TA) is defined as the size of the largest cluster of cross-linked chains, scaled by the total number of chains. As depicted in the inset, the ratio of Modifier/Demodifier levels are flipped (at τ=25) from 0.1 to 0.016 and TA is calculated τ=50 time units *post change* in the Modifier/Demodifier balance. All simulations are done for N=50 (model for SE) and K_{eq}=1.The solid line represents the variation in the maximum value of the calculated TA in 250 replicate simulations as valency (f) is changed. Threshold valencies f_{min}, for ensuring cluster formation (see Figure 2C), and f_{max}, to ensure robust disassembly (defined as TA<0.5, dotted line) within τ=50 time units post change in Modifier/Demodifier levels are identified. The specific value of τ=50 time units post change in Modifier/Demodifier values is chosen for illustrative purposes, and determines the value of f_{max}. The qualitative result that there exists a maximal valency above which the gel does not disassemble in a realistic time scale is robust to changes in the chosen value of this time scale.

Supplemental Figure 3

A



B



Supplemental Figure 3. Noise characteristics of super-enhancers and typical enhancers

A. Dependence of fluctuations (or transcriptional noise), measured as variance in Transcriptional activity (TA), on valency are shown for SEs (N=50) and typical enhancers (N=10). The proxy for transcriptional activity (TA) is defined as the size of the largest cluster of cross-linked chains, scaled by the total number of chains. The angular brackets in the definition of the ordinate represent averages over 50 replicate simulations. All simulations are done at Modifier/Demodifier=0.1, K_{eq}=1. The normalized magnitude of the noise, and importantly the range of valencies over which the noise is manifested, are smaller for SEs compared to a typical enhancer. Note, however, that the absolute magnitude of the noise in the vicinity of the phase separation point is larger for bigger values of N.

B. Dependence of fluctuations (or transcriptional noise), measured as variance in Transcriptional activity (TA), on N is shown for f = 5 (the minimal valency required for cluster formation for N=50. All simulations are done at Modifier/Demodifier=0.1 and K_{eq}=1. The proxy for transcriptional activity (TA) is defined as the size of the largest cluster of cross-linked chains, scaled by the total number of chains. The angular brackets in the definition of the ordinate represent averages over 50 replicate simulations.