Report: Other HTS Applications

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Nucleosome project

Besides the figures contrasting wildtype and arp8 mutant as well es versus t=0 within each cell type (mutant and wt) for up-regulated (Fig.1) and down-regulated genes (Fig.2), both compared to t=0, we have finally found a good way to give a nice overview over all genes (Fig.3), which also shows the banding pattern of the 1+, 2+, etc. Blue reflects low nucleosome occupancy, while yellow shows high occupancy. The plot ranges from 1000bp upstream to 5kb downstream of the +1 nucleosome. The vertical blue area reflect the nucleosome-free region (NFR) at the transcriptions start-site (TSS) and promotor. The diagonal blue region reflects the NFR a the transcription end-site (TES). The genes are ordered by their length, i.e. the distance from TSS to TES. The values are aligned at the +1 nucleosome.
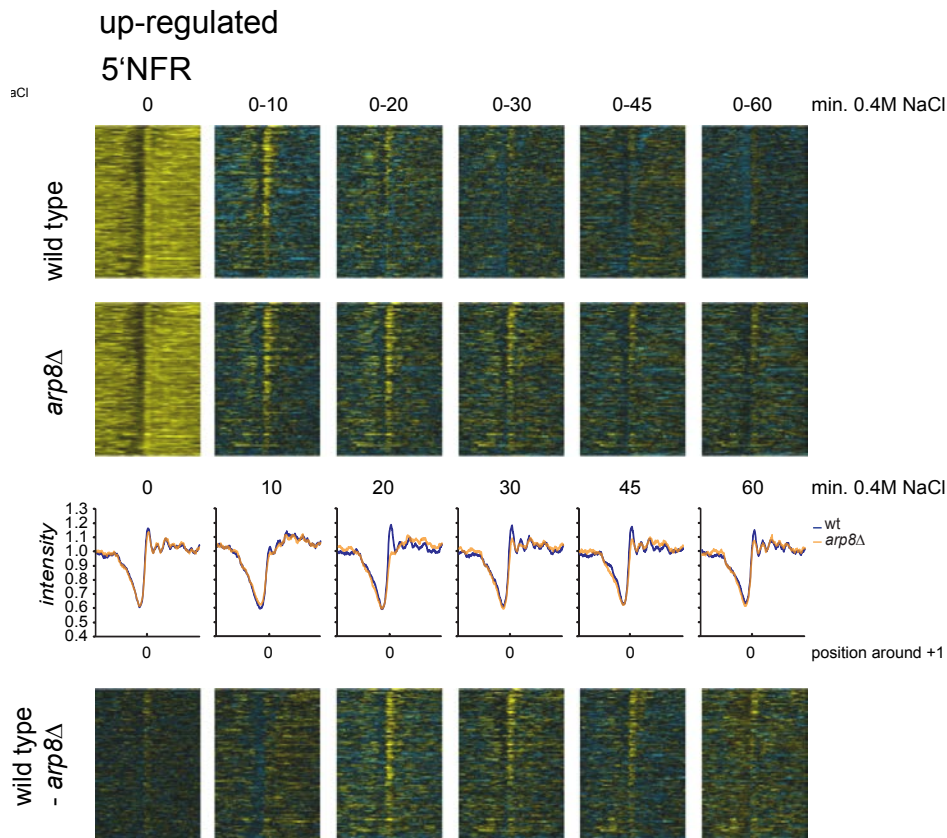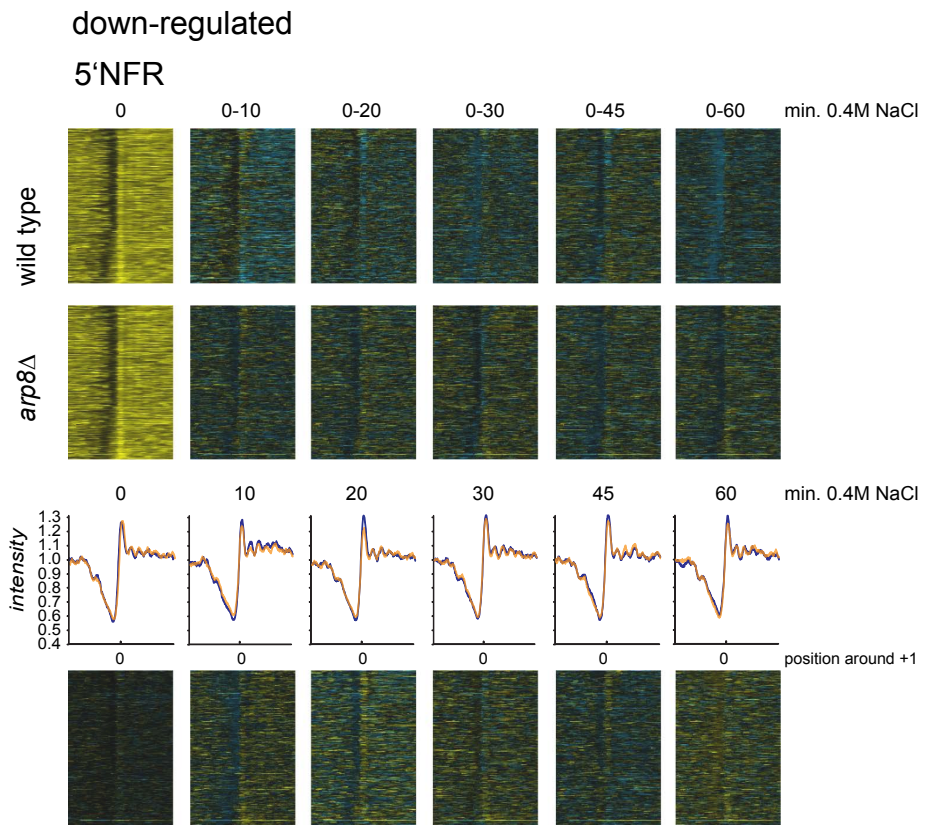

Fig.1

down-regulated

5'NFR

Fig.2

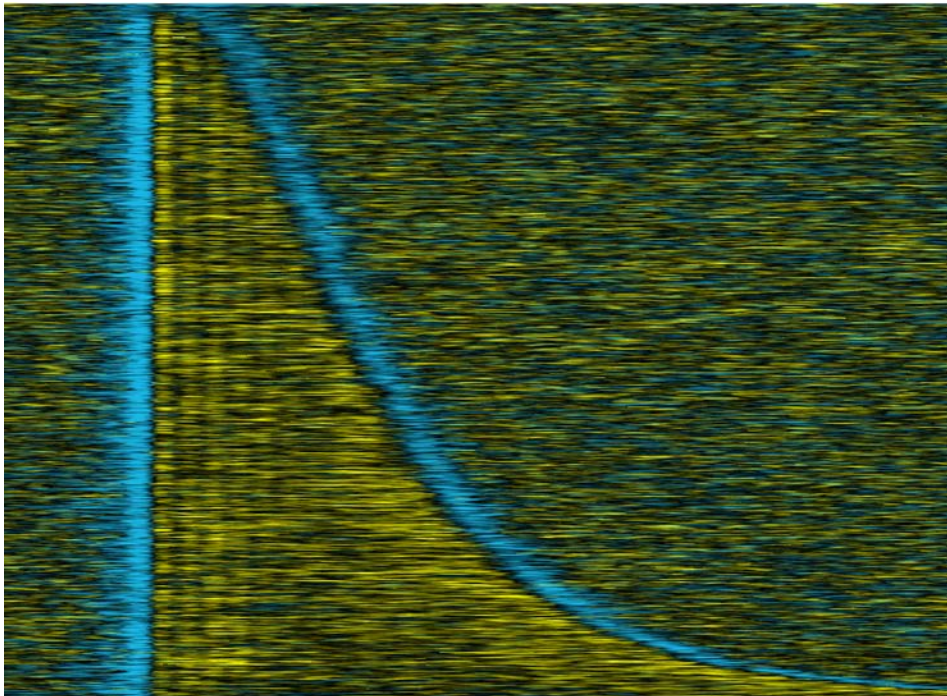

Fig.3

Furthermore, Christoph found out that in all cases of strongly up-regulated genes (compared to t=0), there usually is an (yet unknown) observable transcript in the opposite direction and strand. These are typically the stress-induced transcripts (SITs) reported earlier. It had been suggested by Steinmetz et al. that these may be anti-sense transcripts regulating genes on the opposite strand, i.e. tandem upstream to the strongly up-regulated gene. Currently I am extracting the expression data of all three genes of such cases to be able to measure possible relationships in their expression strength over time after stress-induction.

Christoph, has seen that a strong absolute increase in expression is a much better indicator for a bi-directional transcript, than a strong relative increase (possibly at low levels).

DAGwoman workflow engine

Thomas and I currently writing on a manual for DAGwoman to document all currently supported features. There are currently two requests to use the extended DAGwoman version in an SGE environment.