

Supplemental Figures

AT5G15960 (+)

AT5G15960 - stress-responsive protein (KIN - KIN1) x

HELP

iCLIP-seq	RNA-seq	Details	Settings
Symbol KIN1			
Brief Description stress-responsive protein (KIN1) / stress-induced protein (KIN1)			
Computational Description KIN1; BEST Arabidopsis thaliana protein match is: stress-responsive protein (KIN2) / stress-induced protein (KIN2) / cold-responsive protein (COR6.6) / cold-regulated protein (COR6.6) (TAIR:AT5G15970.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLINK).			
Curator Summary cold and ABA inducible protein kin1, possibly functions as an anti-freeze protein. Transcript level of this gene is induced by cold, ABA, dehydration and osmoticum (mannitol). However, protein activity of GUS fused to the promoter of this gene is inhibited by cold treatment, suggesting an inhibition of the protein by increased transcript level.			
Gene Ontology ▶ 8 values			
Plant Ontology ▶ 10 values			
Interactions AT3G21630 AT4G09000 AT5G65430			

Supplemental Figure 1: Screenshot of the SEQing Details tab. This separate tab displays extended information about the selected gene in tabular format and delivers background information directly through SEQing. These data can be loaded into SEQing by specifying a Tab-separated values file using the parameter `-adv_desc`.

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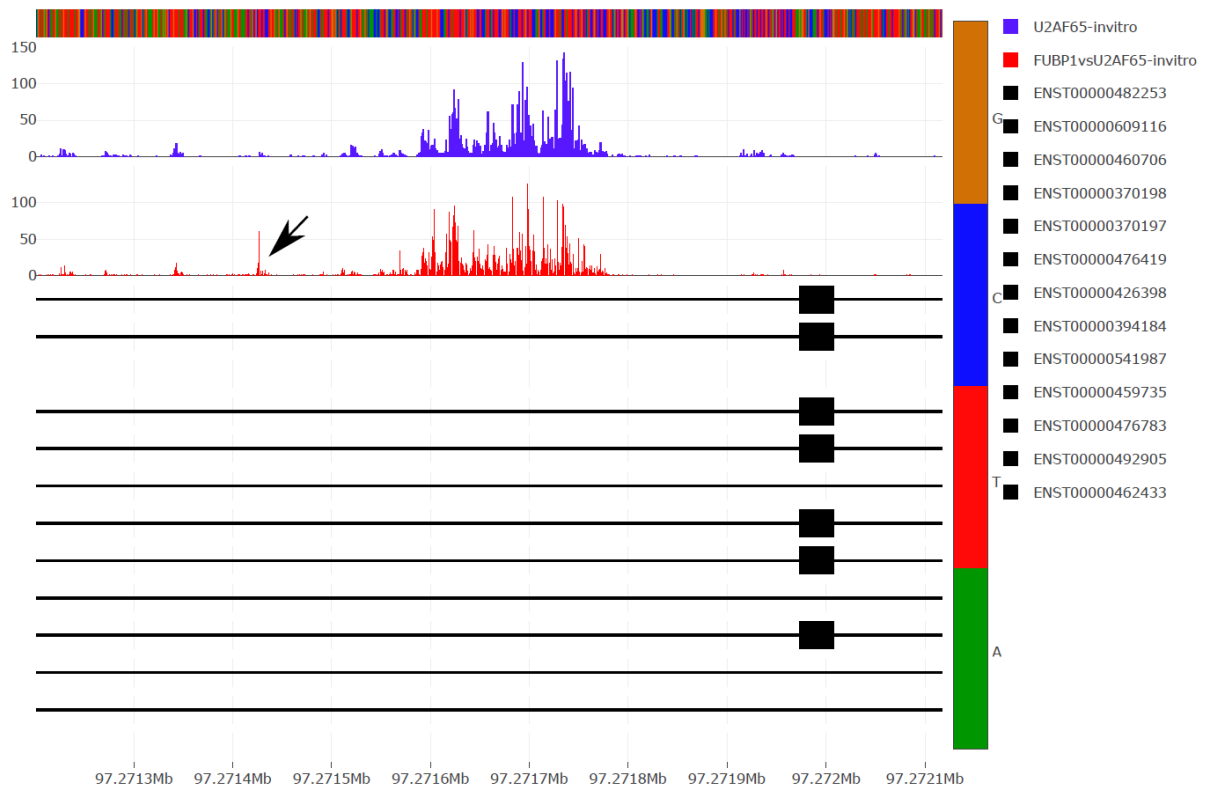
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iCLIP-seq	RNA-seq	Details	Settings
iCLIP Settings AtGRP7-LL24k R: 88 G: 151 B: 255 CONFIRM	Coverage plot settings Col2 R: 255 G: 165 B: 0 CONFIRM	Splice event plot settings A3 R: 0 G: 0 B: 255 CONFIRM	iCLIP-seq plot settings iCLIP plot scale Binding site plot scale RNA-seq plot settings Coverage plot scale Event plot scale Legend Colorbar Margin Image export format: svg

Supplemental Figure 2: Screenshot of the SEQing Settings tab. The display options for each data track can be modified manually in this tab. Track colors can be set individually for each data track, whereas track heights are adjustable globally for the iCLIP and RNA-seq tab. The file format in which the images should be exported is switchable between .png and .svg. The .svg export is the default setting.

PTBP2 (ENSG00000117569)



Supplemental Figure 3: Visualization of U2 Auxiliary Factor 2 (U2AF2) crosslink sites on the Polypyrimidine Tract Binding Protein 2 (PTBP2) gene using SEQing. The exported image, created by SEQing, depicts a genomic window from one of the U2AF2 targets, Polypyrimidine Tract Binding Protein 2 (PTBP2). The data tracks show *in vitro* crosslink sites from U2AF2 alone and from U2AF2 together with the cofactor Far Upstream Element Binding Protein 1 (FUBP1). It is demonstrated that the presence of the FUBP1 protein influences U2AF2 binding. The area marked by the arrow points to a U2AF2 binding site in the presence of FUBP1 protein. Below the data tracks reside known transcript annotations of the PTBP2 gene. A track legend, color coding of the bases and transcript isoform accessions are featured on the right side of the exported image.