

1 JUB

Adapter or scaffold protein which participates in the assembly of numerous protein complexes and is involved in several cellular processes such as cell fate determination, cytoskeletal organization, repression of gene transcription, mitosis, cell-cell adhesion, cell differentiation, proliferation and migration. Contributes to the linking and/or strengthening of epithelia cell-cell junctions in part by linking adhesive receptors to the actin cytoskeleton. May be involved in signal transduction from cell adhesion sites to the nucleus. Plays an important role in regulation of the kinase activity of AURKA for mitotic commitment. Also a component of the IL-1 signaling pathway modulating IL-1-induced NFKB1 activation by influencing the assembly and activity of the PRKCZ-SQSTM1-TRAF6 multiprotein signaling complex. Functions as an HDAC-dependent corepressor for a subset of GFI1 target genes. Acts as a transcriptional corepressor for SNAI1 and SNAI2/SLUG-dependent repression of E-cadherin transcription. Acts as a hypoxic regulator by bridging an association between the prolyl hydroxylases and VHL enabling efficient degradation of HIF1A. Positively regulates microRNA (miRNA)-mediated gene silencing. Negatively regulates the Hippo signaling pathway and antagonizes phosphorylation of YAP1.

This gene seems to be downregulated within the wildtype, whereas for the Ebola infected cells for the 23h probe an upregulation was observed. In contrast, the Marburg infected cells after 23h show downregulation. Interestingly, upstream transcripts in all probes were observed.

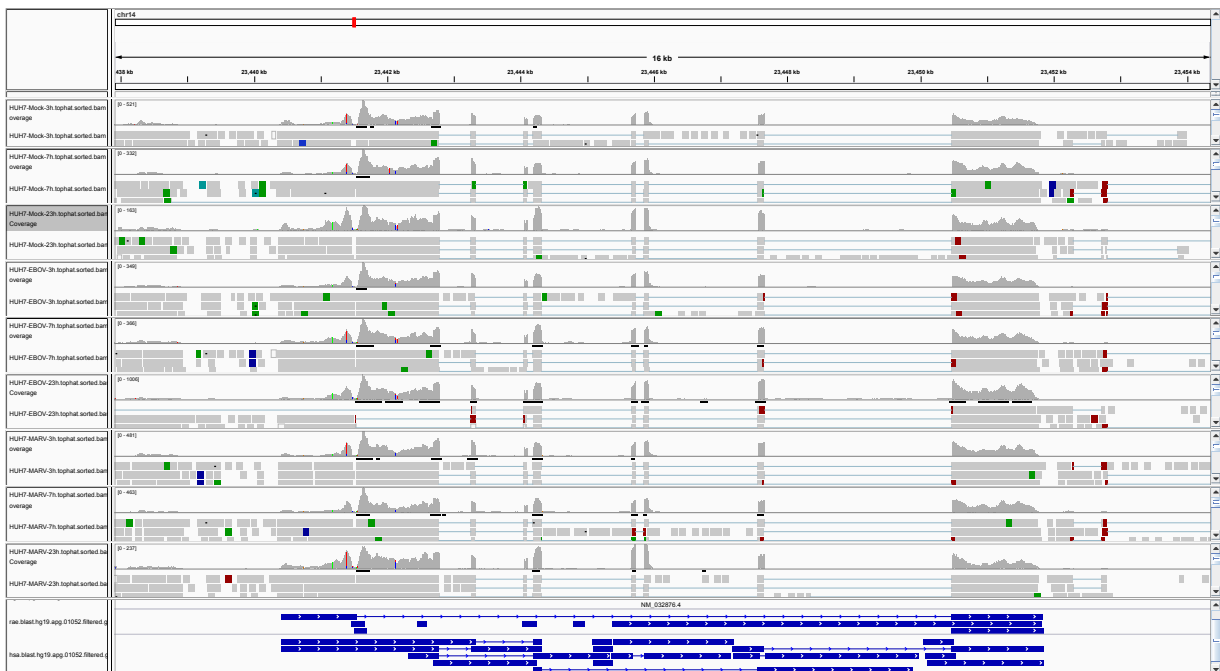


Figure 1: IGV Genome Browser screenshot of gene JUB.

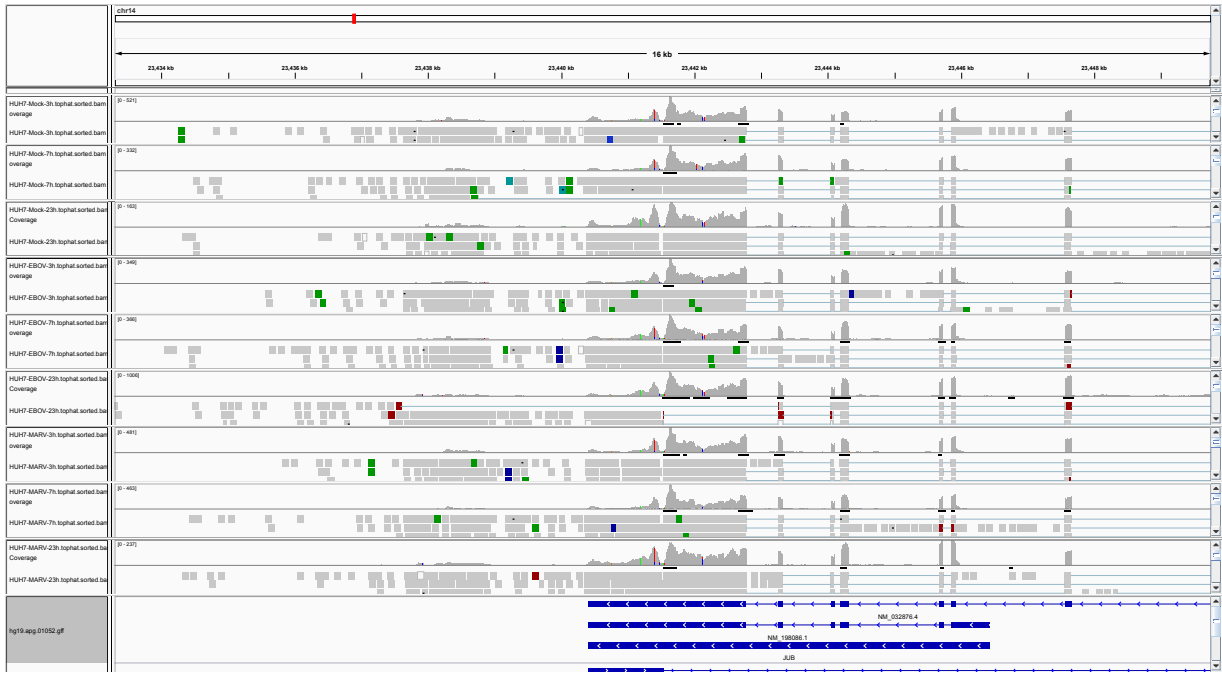


Figure 2: IGV Genome Browser screenshot of upstream region of gene JUB.

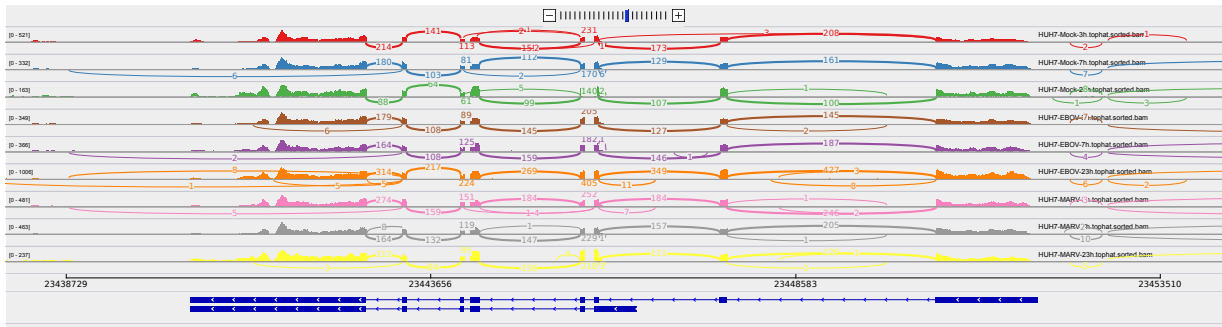


Figure 3: Sashimi plot of gene JUB.

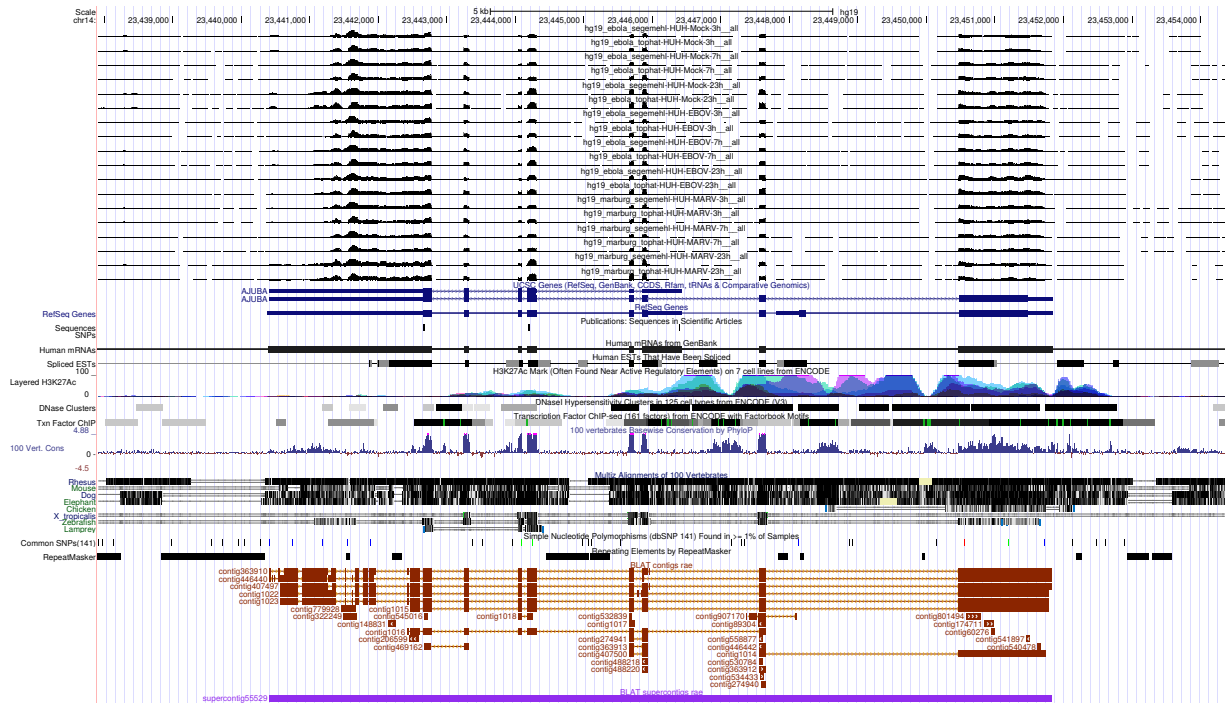


Figure 4: UCSC Genome Browser screenshot of gene *JUB*.