

1 PEG10

This is a paternally expressed imprinted gene that encodes transcripts containing two overlapping open reading frames (ORFs), RF1 and RF1/RF2, as well as retroviral-like slippage and pseudoknot elements, which can induce a -1 nucleotide frame-shift. ORF1 encodes a shorter isoform with a CCHC-type zinc finger motif containing a sequence characteristic of gag proteins of most retroviruses and some retrotransposons. The longer isoform is the result of -1 translational frame-shifting leading to translation of a gag/pol-like protein combining RF1 and RF2. It contains the active-site consensus sequence of the protease domain of pol proteins. Additional isoforms resulting from alternatively spliced transcript variants, as well as from use of upstream non-AUG (CUG) start codon, have been reported for this gene. Increased expression of this gene is associated with hepatocellular carcinomas.

PEG10 is very highly expressed in human cells. In Ebola- and Marburg-infected cells, it is significantly down-regulated after 23h of infection. In addition, there seems to be a processed site at the 5' end of the gene, which also shows a lower expression in Ebola- and Marburg infected cells after 23h. Although reads that map to this site have mate pairs very far away. In the bat homolog, we observe an approx. 10-fold lower expression, which is of a more constant nature across the various conditions.

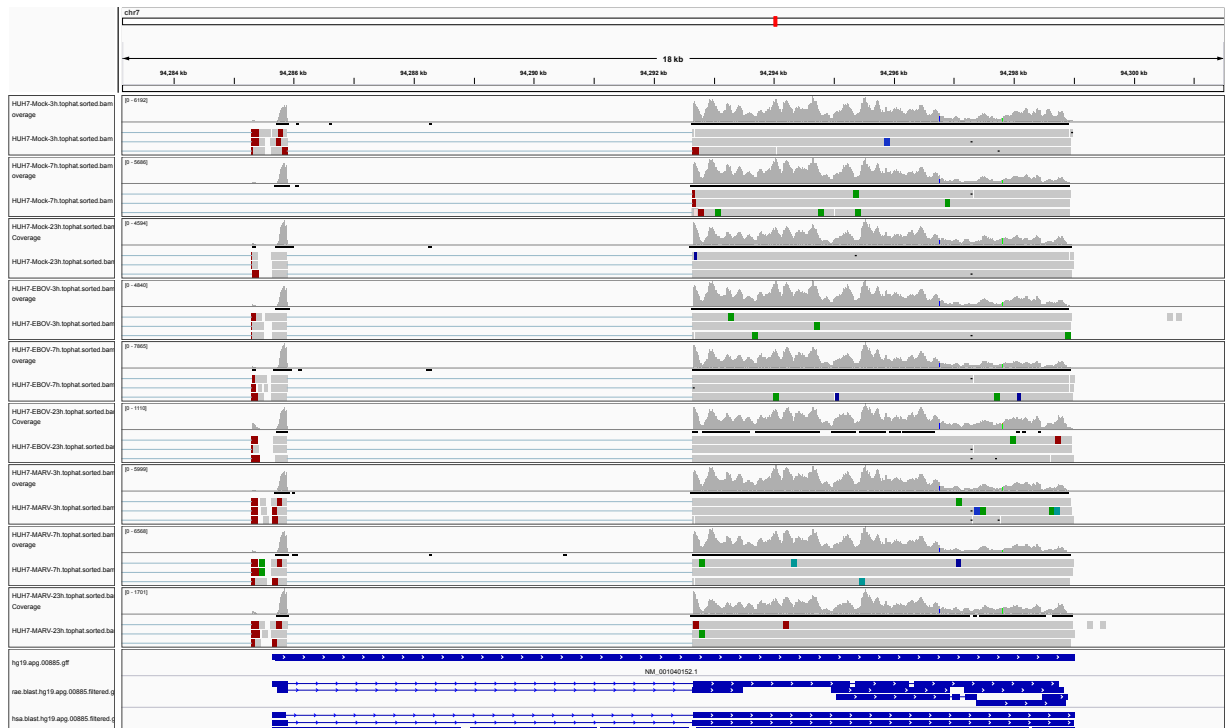


Figure 1: IGV Genome Browser screenshot of gene PEG10.

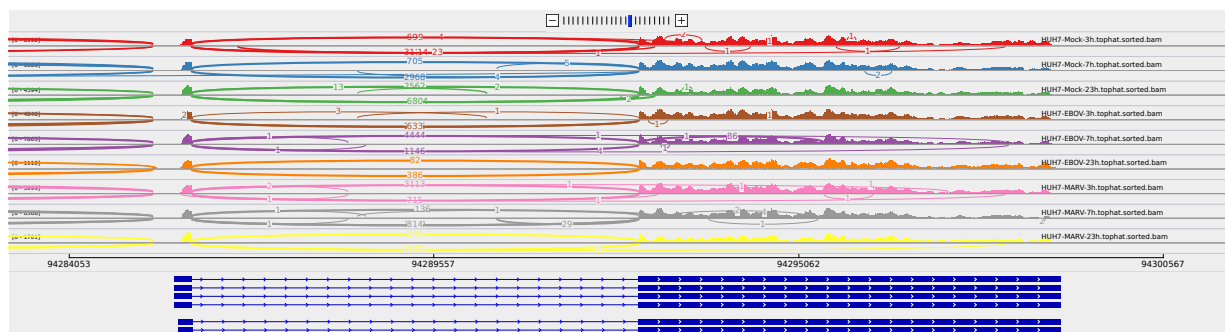


Figure 2: Sashimi plot of gene PEG10.

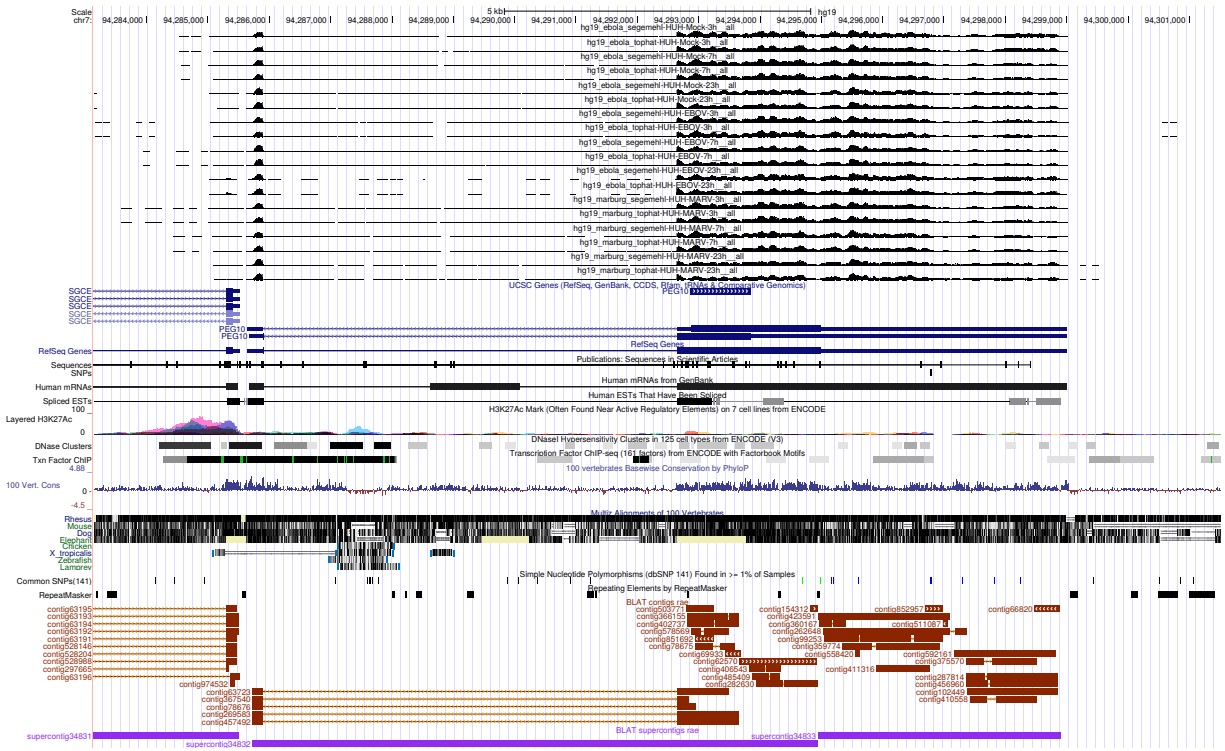


Figure 3: UCSC Genome Browser screenshot of gene PEG10.

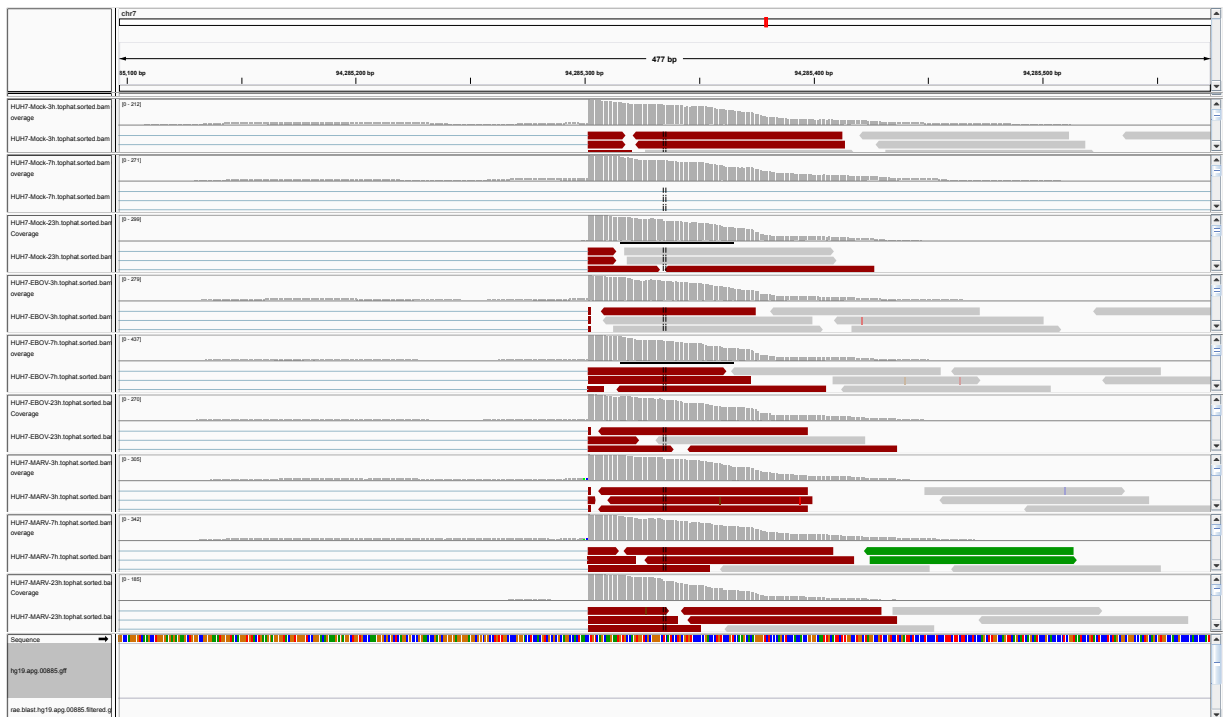


Figure 4: IGV Genome Browser screenshot of potential processing site 5' of gene PEG10.