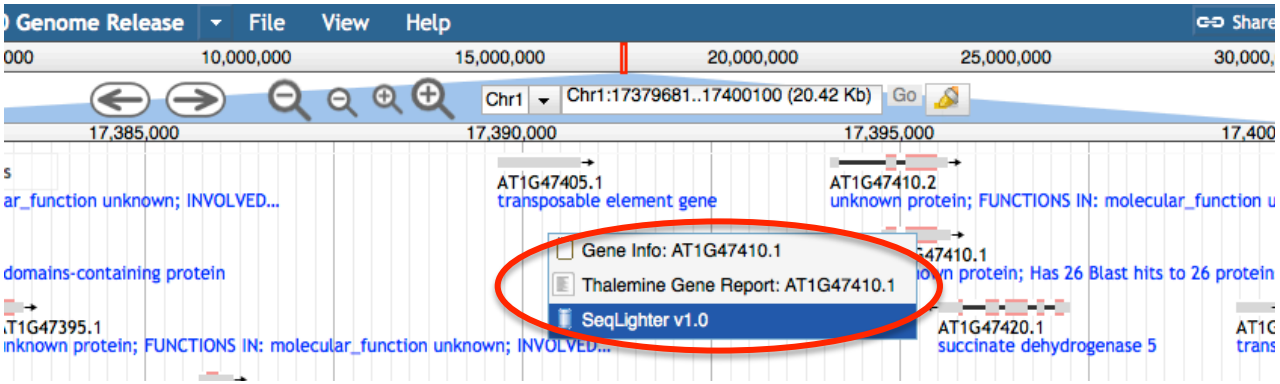
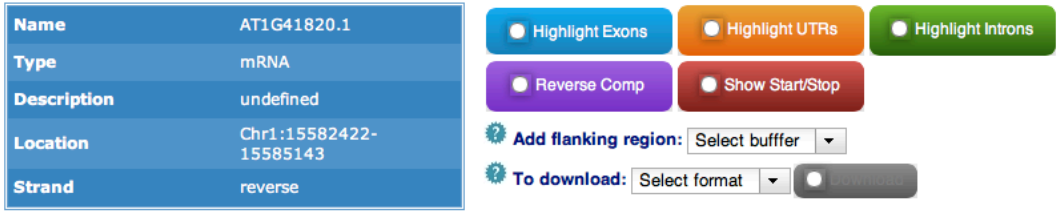
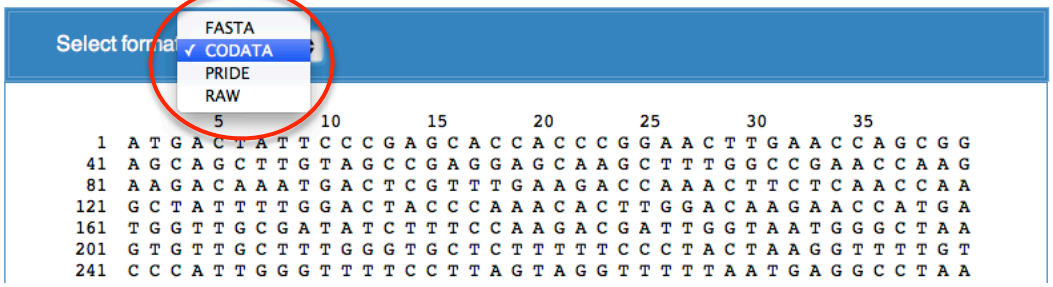
Welcome to SeqLighter v1.0!

[1] To launch the sequence viewer, right click a gene model on the 'Protein Coding Gene Models' track. Select SeqLighter v1.0 on the dropdown menu.

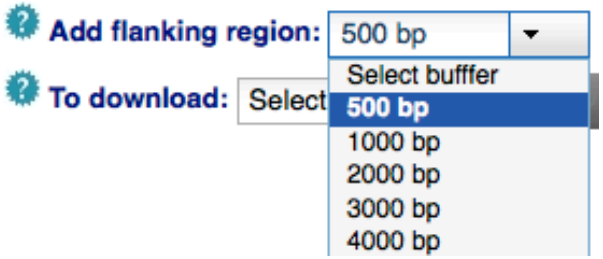


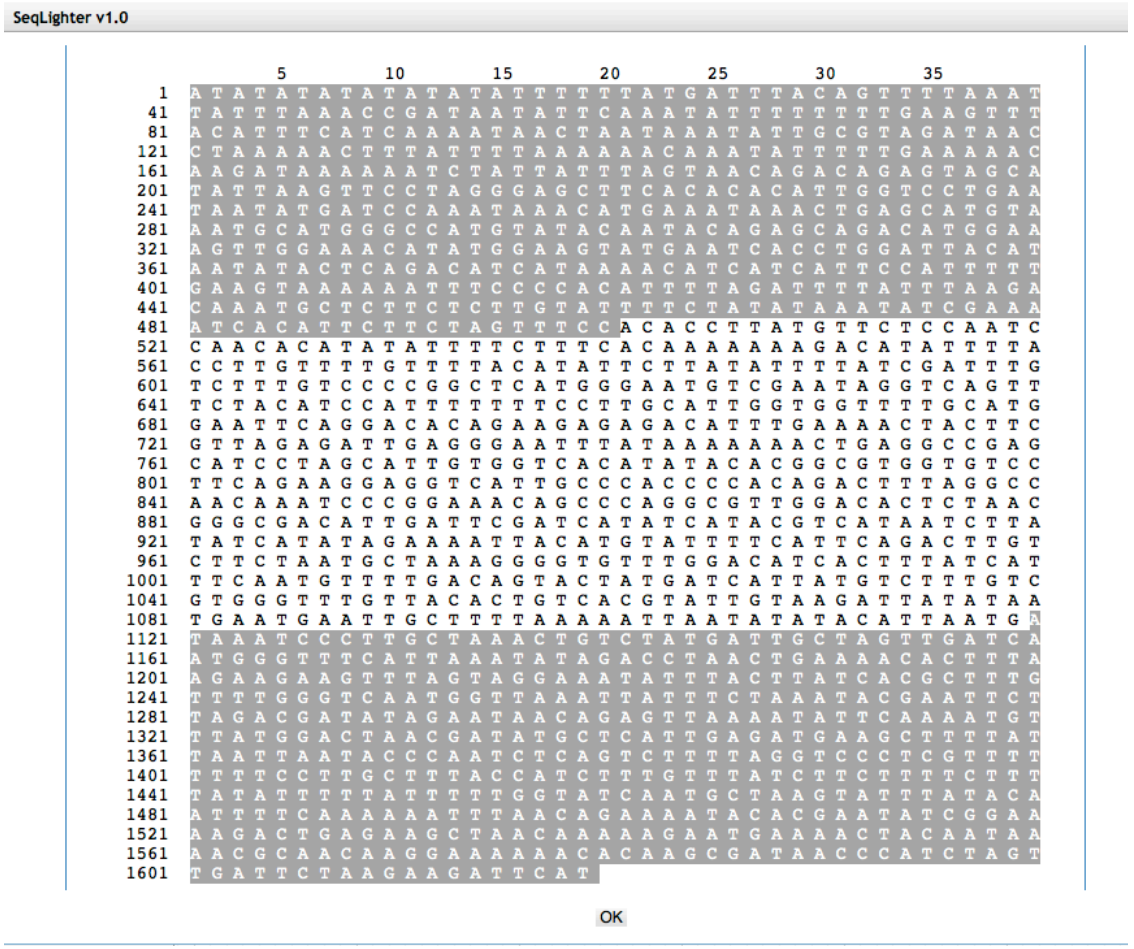
[2] This will launch a popup screen displaying the nucleotide sequence of the selected gene model. The default format is in CODATA and there are other sequence formats such as FASTA, PRIDE, and RAW to choose from.



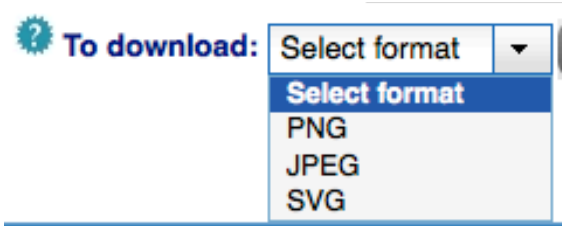


[3] Flanking Sequence: An option to add upstream and downstream sequences of the gene model is available in 500bp, 1K, 2K, 3K and 4K. When one of these are selected, the additional sequence is highlighted in grey. Note: The flanking sequences will not available in the downloaded image.

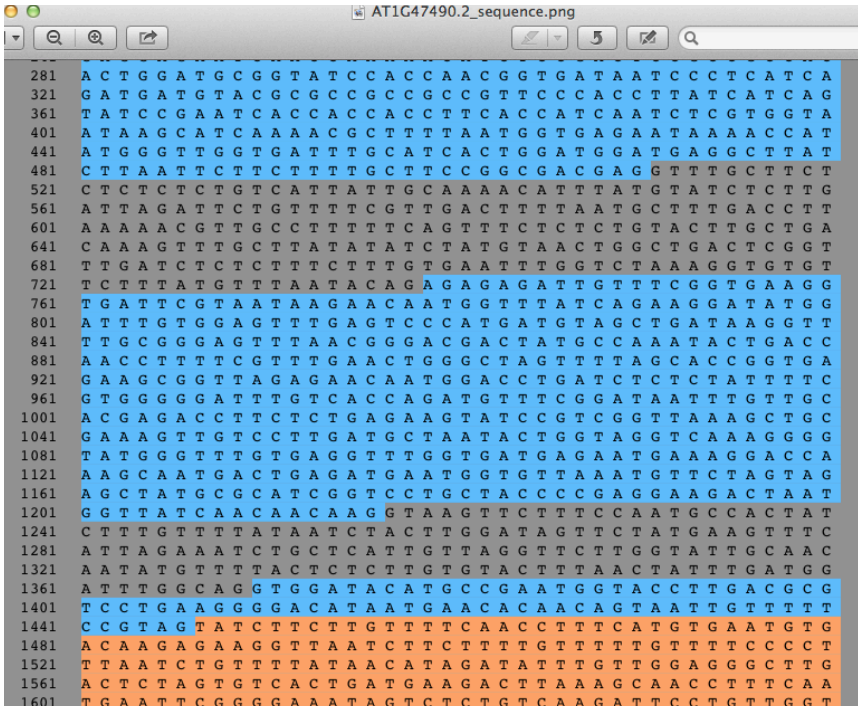




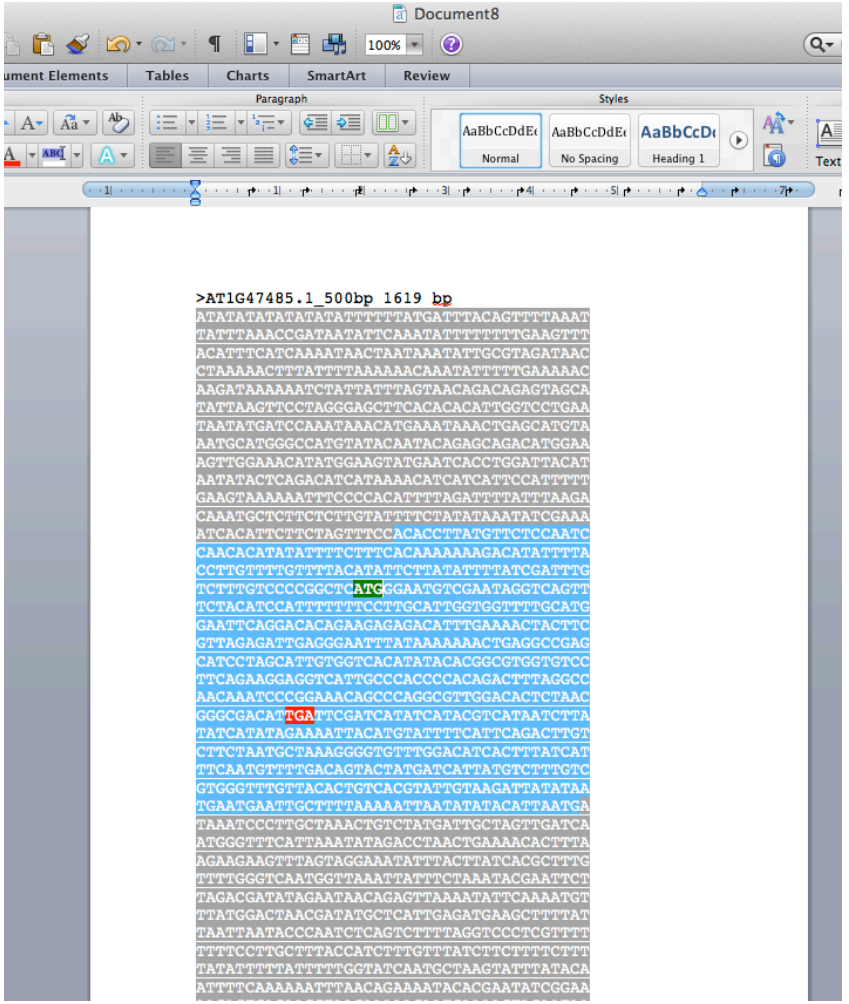
[4] The downloadable formats include PNG, JPEG and SVG. In addition, copying and pasting of the elements in the sequence box will retain any selected highlights. Note: The downloaded images will only be in CODATA format.



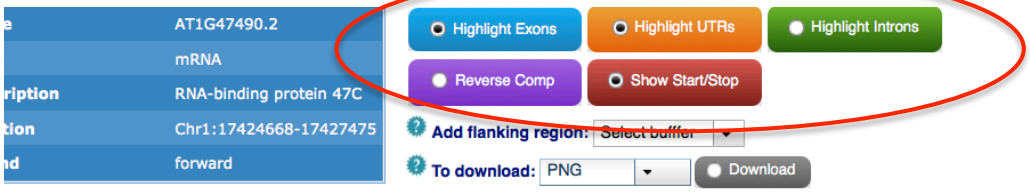
PNG format

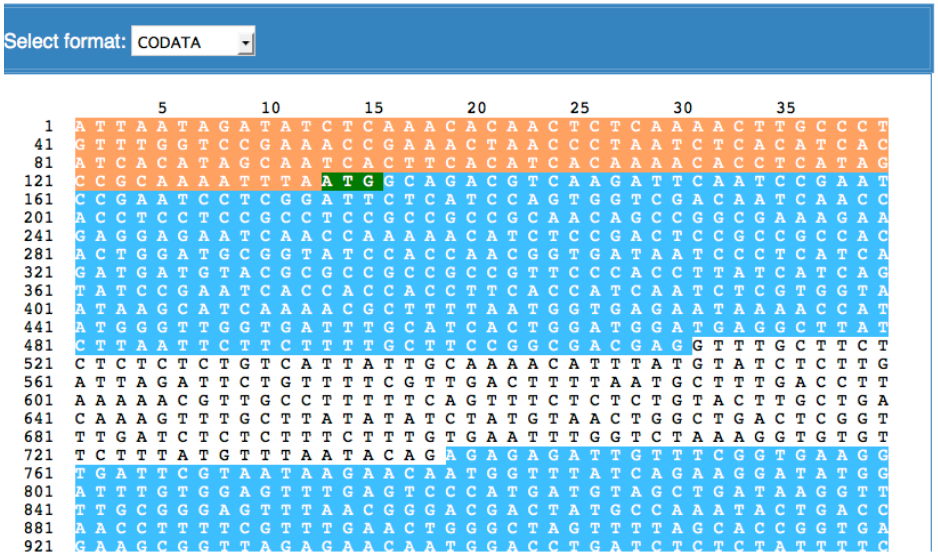


Copy and paste will retain the highlighted regions.



[5] Highlighting options for exons, introns, utrs and start/stop codon is available. In addition, reverse complement of the selected sequence [including flanking regions] is available. When reverse complement is enabled, other highlighting options will not be available. The highlighting is available for all of the sequence formats such as FASTA, PRIDE, CODATA and RAW.





This sequence widget was built using the BioJs sequence viewer component.
http://biojs.net/jenkins/target/registry/Biojs.Sequence.html