

# Editing Annotations

Change Annotation Type

Get Sequence  
Get GFF3  
Zoom to Base Level  
Edit Information (alt-click)

Change annotation type

Delete  
Merge  
Split  
Duplicate  
Make Intron  
Move to Opposite Strand

Set Translation Start  
Set Translation End  
Set Longest ORF  
Set Readthrough Stop Codon

Set as 5' end  
Set as 3' End  
Set both Ends

Set to Downstream Splice Donor  
Set to Upstream Splice  
Set to Downstream  
Set to Upstream Splice

Undo  
Redo  
Show History

gene  
pseudogene  
rRNA  
snRNA  
snoRNA  
tRNA  
ncRNA  
miRNA  
repeat\_region  
transposable\_element

Edit Associations

- PubMed / dbxref
- Metadata
  - key/value
  - status
  - comments

Edit Additional Structural Data (right-click popup)

History of Structural Edits

| History                    |                    |                  |        |
|----------------------------|--------------------|------------------|--------|
| Operation                  | Editor             | Date             | Revert |
| Add transcript             | nathandunn@ibl.gov | 6/14/16 12:53 PM | ↑      |
| Set translation end        | nathandunn@ibl.gov | 6/14/16 12:53 PM | ⏮      |
| Set readthrough stop codon | nathandunn@ibl.gov | 6/14/16 12:53 PM | ↓      |
| Change annotation type     | nathandunn@ibl.gov | 6/14/16 12:53 PM | ⏭      |

# Editing Annotation Panel

The image shows a screenshot of the 'Editing Annotation Panel' interface, which is divided into several sections and tabs. The main section on the left has tabs for 'Details', 'DbXref', 'Comment', and 'Attributes'. The 'Details' tab is active, showing fields for 'Type' (repeat\_region), 'Status' (with a dropdown menu open showing 'No status selected', 'allgood', and 'allbad'), 'Name' (Apple2-00001), 'Synonyms', 'Description' (mRNA with CDSs but no UTRs), 'Location' (13488 - 17000 strand(-)), 'Ref Sequence' (ctgA), 'Owner', 'Created', and 'Updated'. A callout box labeled 'Define and select status' points to the 'Status' dropdown. Below the 'Details' tab, there are tabs for 'Prefix' and 'Accession'. The 'Prefix' tab is active, showing a 'Prefix' field and a 'PMID' field. A callout box labeled 'Add and verify pubmed' points to the 'PMID' field. To the right of the main section, there is a 'Comment' section with a 'Comment' tab and a 'Comment' field. A callout box labeled 'Predefined comments' points to the 'Comment' field. Below the 'Comment' section, there is a 'Tag' field and a 'Value' field. A callout box labeled 'Can select predefined keys / values per organism and type' points to the 'Tag' field. A dropdown menu is open next to the 'Tag' field, showing 'Select canned value' and 'valueall'.

**Define and select status**

**Predefined comments**

**Add and verify pubmed**

**Can select predefined keys / values per organism and type**