May 2018 Notes from BDGP on clone FI01410 – designed to replace RE19818:

The RE19818 clone indeed has a deletion at position 499 (missing an A) (position 502 of the annotated transcript (FBtr0273263)).  What I should have said is: FI01410 adds that missing A, which extends the reading frame upstream of the annotated start codon, which is found at position 502 of the annotated transcript.  However, the annotated protein is still the uses the start codon at position 502.  I'm guessing the Flybase annotation is based on the Kozak sequence.

FlyBase lists the RE clone as being 3115bp while the FI clone as 3116bp, which is consistent with how we generated the FI clone.

Here is a link to the RE19818 sequence:   
<https://sina.lbl.gov/cgi-bin/labtrack/community_query/cloneReport.pl?_submitted=1&search=&dgrc=&clone_id=RE19818&_submit=Enter>

and to the Genbank record:  
<http://www.ncbi.nlm.nih.gov/sites/entrez?term=BT021303&cmd=Search&db=nucest&QueryKey=1>

Likewise, for FI01410:  
<https://sina.lbl.gov/cgi-bin/labtrack/community_query/cloneReport.pl?_submitted=1&search=&dgrc=&clone_id=FI01410&_submit=Enter>

and the Genbank record:  
<http://www.ncbi.nlm.nih.gov/sites/entrez?term=BT044557.1&cmd=Search&db=nucest&QueryKey=1>

I'm also attaching the Flybase transcript record.  And a file name "sims", which contains the alignments of both the RE and FI clones to the Flybase annotated transcript (as separate alignments, not multi-).

-Ken