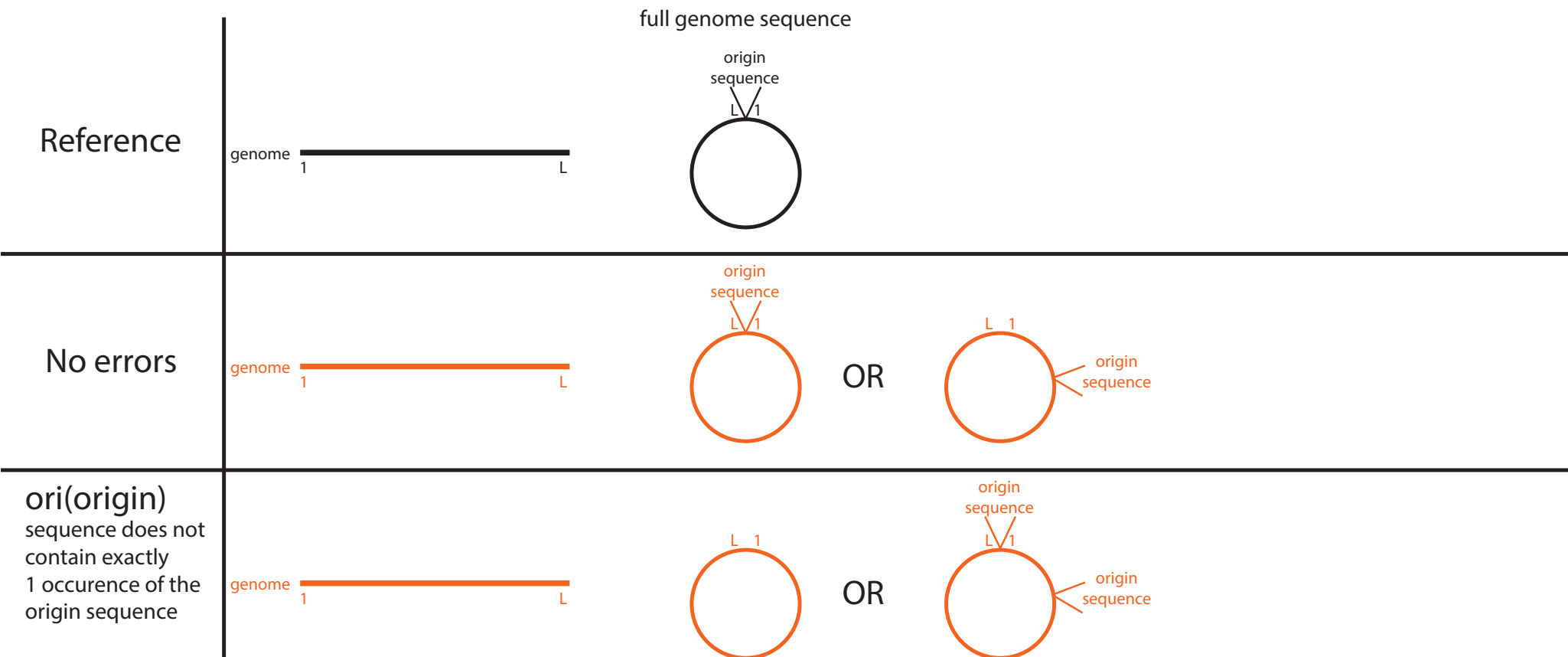



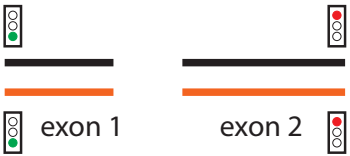
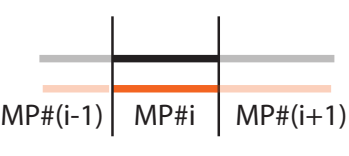


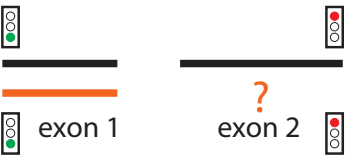
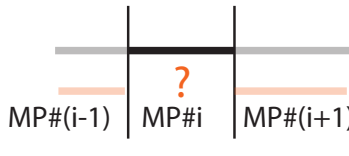
ori: there is not exactly 1 occurrence of the origin sequence



Example output from annotation script:

HQ693428	N/A	N/A	ori	there is not exactly 1 occurrence of origin sequence [0 occurrences]
----------	-----	-----	-----	--

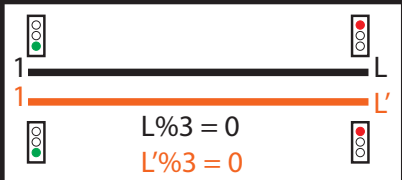
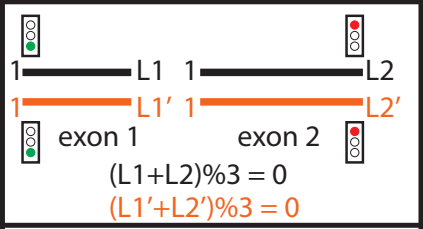
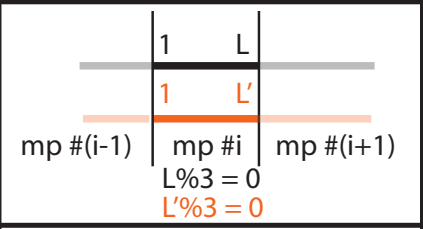
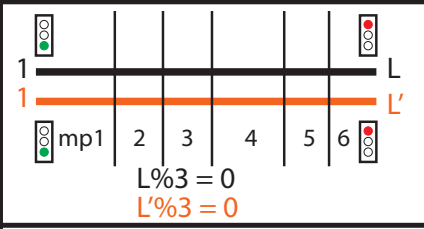
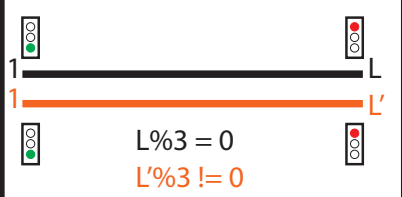
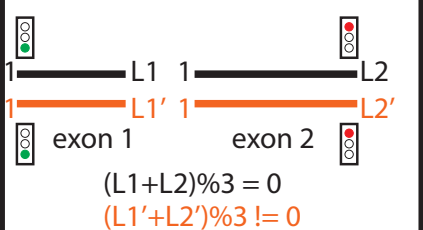
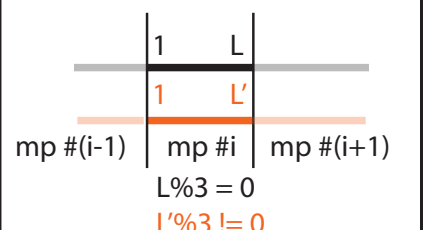
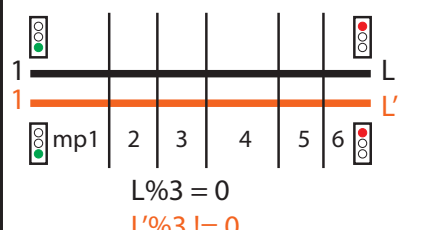
nop: unable to identify homologous feature

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
nop (no prediction) homology search yielded no prediction				N/A

Example output from annotation script:

AM421536      1   CDS#1   nop   unable to identify homologous feature


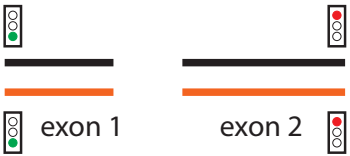
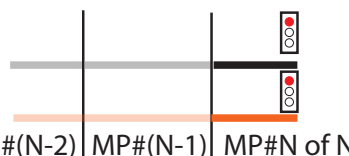
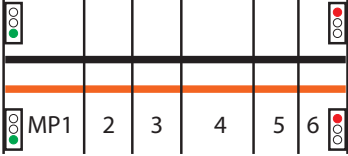
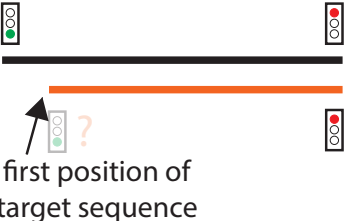
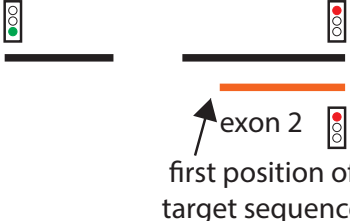
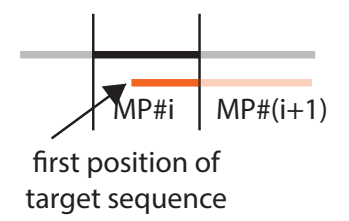
nm3: length of nucleotide feature is not a multiple of 3

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors	 $L \% 3 = 0$ $L' \% 3 = 0$	 $(L1 + L2) \% 3 = 0$ $(L1' + L2') \% 3 = 0$	 $L \% 3 = 0$ $L' \% 3 = 0$	 $L \% 3 = 0$ $L' \% 3 = 0$
nm3 (not a multiple of 3) length is not a multiple of 3	 $L \% 3 = 0$ $L' \% 3 \neq 0$	 $(L1 + L2) \% 3 = 0$ $(L1' + L2') \% 3 \neq 0$	 $L \% 3 = 0$ $L' \% 3 \neq 0$	 $L \% 3 = 0$ $L' \% 3 \neq 0$

Example output from annotation script:

JF920397      2   MP#2      nm3   length of nucleotide feature is not a multiple of 3 [299]

# b5e: alignment to reference does not extend to 5' end of reference but does extend to 5' boundary of target

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
b5e (5' boundary expected) alignment does not extend to 5' boundary of reference but does extend to 5' boundary of target				N/A

Example output from annotation script:

JN975546

6 MP#6

b5e alignment to reference does not extend to 5' boundary of reference  
 but does extend to 5' boundary of target [1486 nt from 5' end]

b5u: alignment to reference does not extend to 5' end of reference or target

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
b5u (5' boundary unexpected) alignment does not extend to 5' boundary of reference or target				N/A

Example output from annotation script:

KT781411      6   MP#6      b5u   alignment to reference does not extend to 5'  
boundary of reference or target [1494 nt from 5' end]

# b3e: alignment to reference does not extend to 3' end of reference but does extend to 3' boundary of target

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
b3e (3' boundary expected) alignment does not extend to 3' boundary of reference but does extend to 3' boundary of target				N/A

Example output from annotation script:


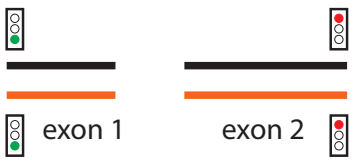
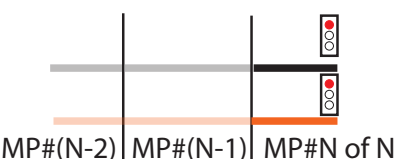
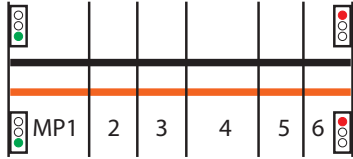

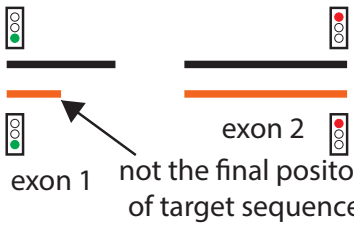

KC597143

8

CDS#2

b3e alignment to reference does not extend to 3' boundary of reference  
 but does extend to 3' boundary of target [394 nt from 3' end]

b3u: alignment to reference does not extend to 3' end of reference or target

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
b3u (3' boundary unexpected) alignment does not extend to 3' boundary of reference or target				N/A

Example output from annotation script:

KC597143

8

CDS#2

b3u alignment to reference does not extend to 3' boundary of reference or target [412nt from 3' end]

olp: lack of an expected overlap with another feature  
or additional unexpected overlap with another feature

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
olp (overlap) feature does not overlap with same set of features as in reference				

Example output from annotation script:

FJ562227      6   CDS#6      olp   feature does not overlap with same set of features as in reference [-(6.1,1.1),-(6.1,7.1)]



str: predicted start of CDS is not valid start codon

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
str (start) predicted CDS start is not a valid start codon			N/A	

Example output from annotation script:

```
KR006962      3  CDS#3      str  predicted CDS start position is not beginning of ATG start codon  
[TNN starting at position 4472 on strand +]
```

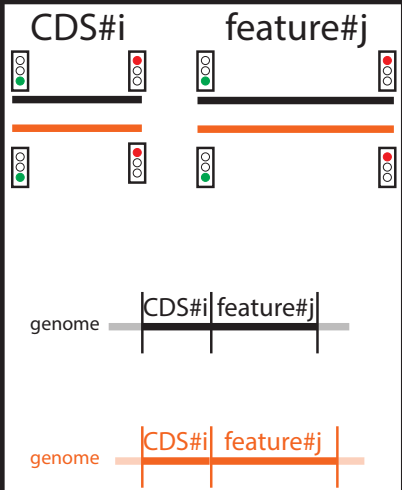
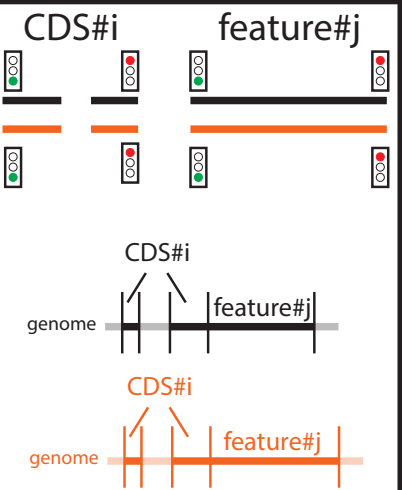
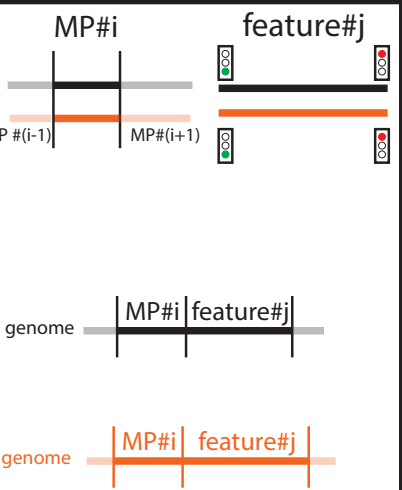
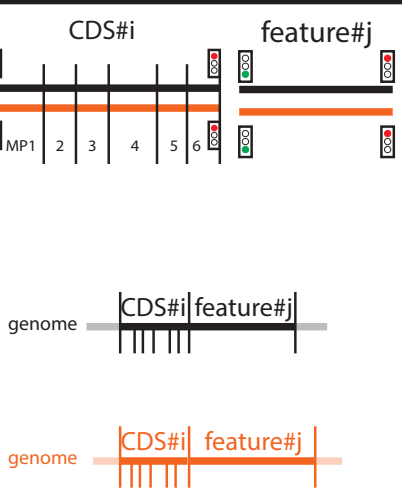
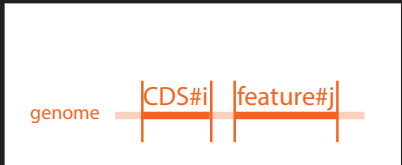



str: predicted start of CDS is not valid start codon

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
str (start) predicted CDS start is not a valid start codon			N/A	

Example output from annotation script:

KR006962	3	CDS#3	str	predicted CDS start position is not beginning of ATG start codon [TNN starting at position 4472 on strand +]
----------	---	-------	-----	---

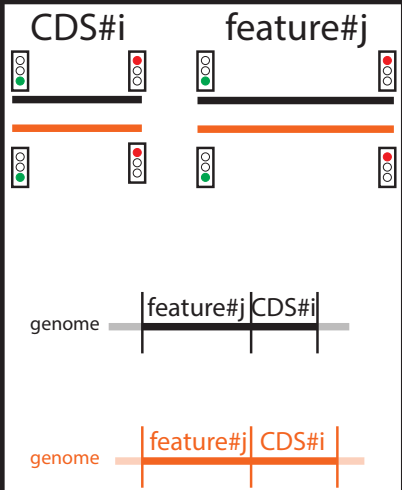
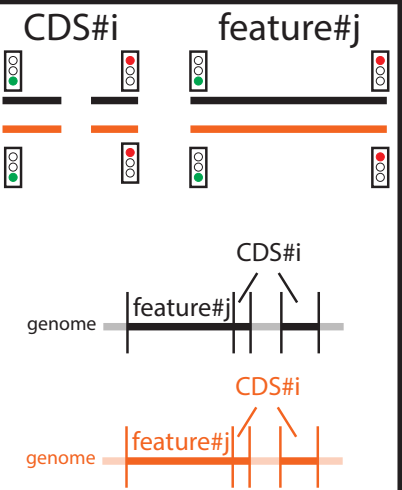
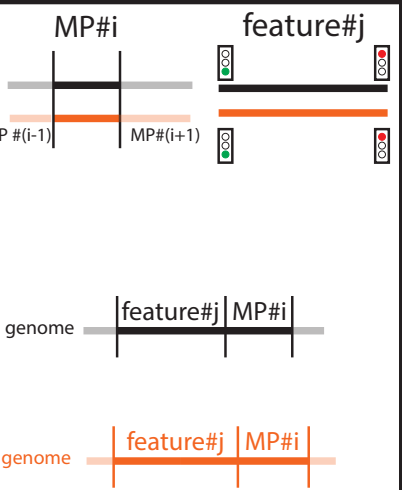
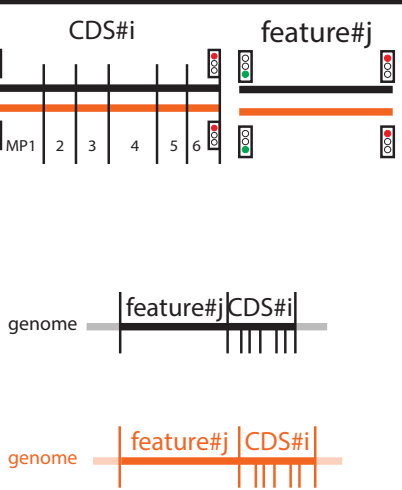




ajb: MP or CDS is not adjacent to same set of features before it as in the reference

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
ajb (adjacent before) mature peptide is not adjacent to expected mature peptide on 5' end				

Example output from annotation script:

KC131141      11   MP#11   ajb   feature (MP or CDS) is not adjacent to same set of  
features before it as in reference [-(11.1,10.1)]

aja: MP or CDS is not adjacent to same set of features after it as in the reference

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP #i)	CDS (made up of mature peptides)
No errors				
aja (adjacent after) mature peptide is not adjacent to expected mature peptide on 3' end				

Example output from annotation script:

CS477302      10   MP#10   aja   feature (MP or CDS) is not adjacent to same set of features after it as in reference [-(10.1,11.1)]

trc: truncation due to an early stop

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
trc (truncation) in-frame stop codon exists 5' of predicted stop				

Example output from annotation script:

```
EU628610      3  CDS#3      trc  in-frame stop codon exists 5' of stop position predicted by homology to reference
                                     [homology search predicted 1796..1356 exon 2 of 2 revised to 1796..1371 (stop shifted 15 nt)]
```


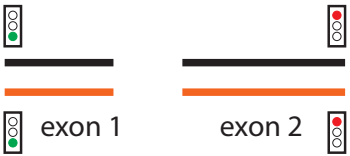
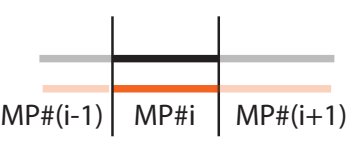
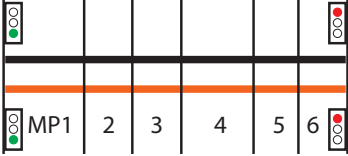
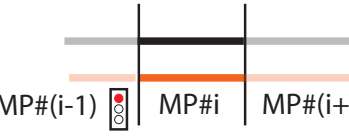
ext: extended feature due to a missing stop codon

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
ext (extension) first in-frame stop codon exists 3' of predicted stop				

Example output from annotation script:

HM631854	14	MP#14	ext	first in-frame stop codon exists 3' of stop position predicted by homology to reference [homology search predicted 7544..10230 revised to 7544..10288 (stop shifted 58 nt)]
HM631854	15	CDS(MP)#1	ext	first in-frame stop codon exists 3' of stop position predicted by homology to reference [homology search predicted 74..10233 revised to 74..10291 (stop shifted 58 nt)]

ntr: mature peptide is not translated because of upstream stop

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
ntr (not translated) mature peptide is not translated due to early stop 5' of predicted start	N/A	N/A		N/A

Example output from annotation script:

```
KC131141      11  MP#11  ntr  mature peptide is not translated because its CDS has an in-frame stop 5' of the mature
                                peptide's predicted start [early stop in mature peptide 10 ending at position 6274]
```

nst: no in-frame stop codon exists 3' of predicted valid start codon

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
nst (no stop) no in-frame stop codon exists 3' of predicted valid start codon				

Example output from annotation script:

HQ234499      15   CDS(MP)#1    nst   no in-frame stop codon exists 3' of predicted valid start codon [inferred stop codon position (3 nt 3' of 10269 on + strand) is off the end of the sequence]




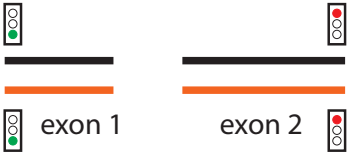
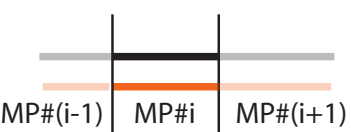
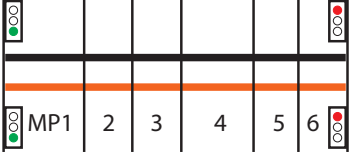
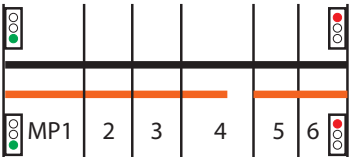
ost: predicted feature is on opposite strand from reference

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
ost (opposite strand) predicted feature is on opposite strand from reference				

Example output from annotation script:

JN644310 15 MP#15 ost predicted feature is on opposite strand from reference


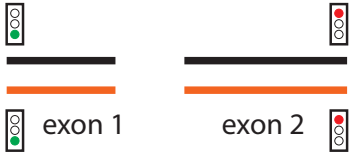
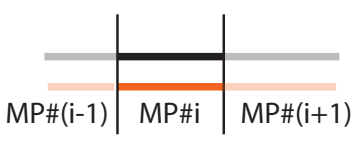
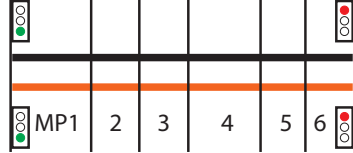
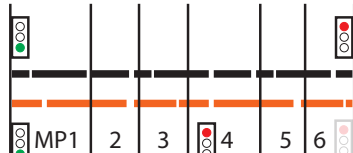
aji: CDS has at least one inconsistent MP adjacency relative to the reference

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
aji (adjacency inconsistency) CDS has at least one inconsistent adjacency relative to reference	N/A	N/A	N/A	

Example output from annotation script:

```
HQ166035      15  CDS#1   aji   CDS comprised of mat_peptides has at least one adjacency inconsistency between
                                2 mat_peptides [MP#9 (4074..4463) not adjacent to MP#10 (4465..4572)]
```


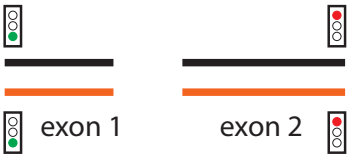
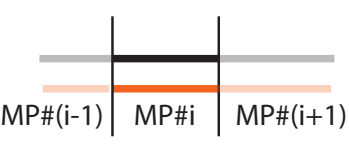
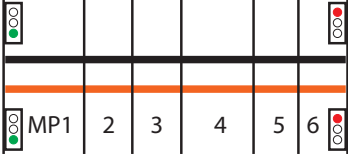
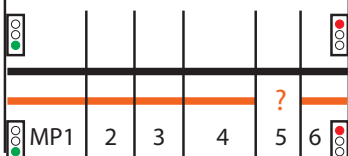
int: CDS has at least one MP that is not translated due to an early stop

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
int (interrupted translation) CDS has at least one mature peptide that is not translated due to early stop	N/A	N/A	N/A	

Example output from annotation script:

```
JN975491      7  CDS(MP)#1   int  CDS comprised of mat_peptides is incomplete: at least one primary mat_peptide
                                is not translated due to early stop (ntr) [MP#2, MP#3, MP#4, MP#5, MP#6]
```

inp: CDS has at least one MP that is not identified

	CDS (single exon)	CDS (multi-exon)	mature peptide (MP#i)	CDS (made up of mature peptides)
No errors				
inp (interrupted prediction) CDS has at least one mature peptide that is not translated due to lack of prediction (nop)	N/A	N/A	N/A	

Example output from annotation script:

```
KC407671      16  CDS(MP)#1   inp  CDS comprised of mat_peptides is incomplete: at least one
                                primary mat_peptide is not identified (nop) [MP#1, MP#3]
```