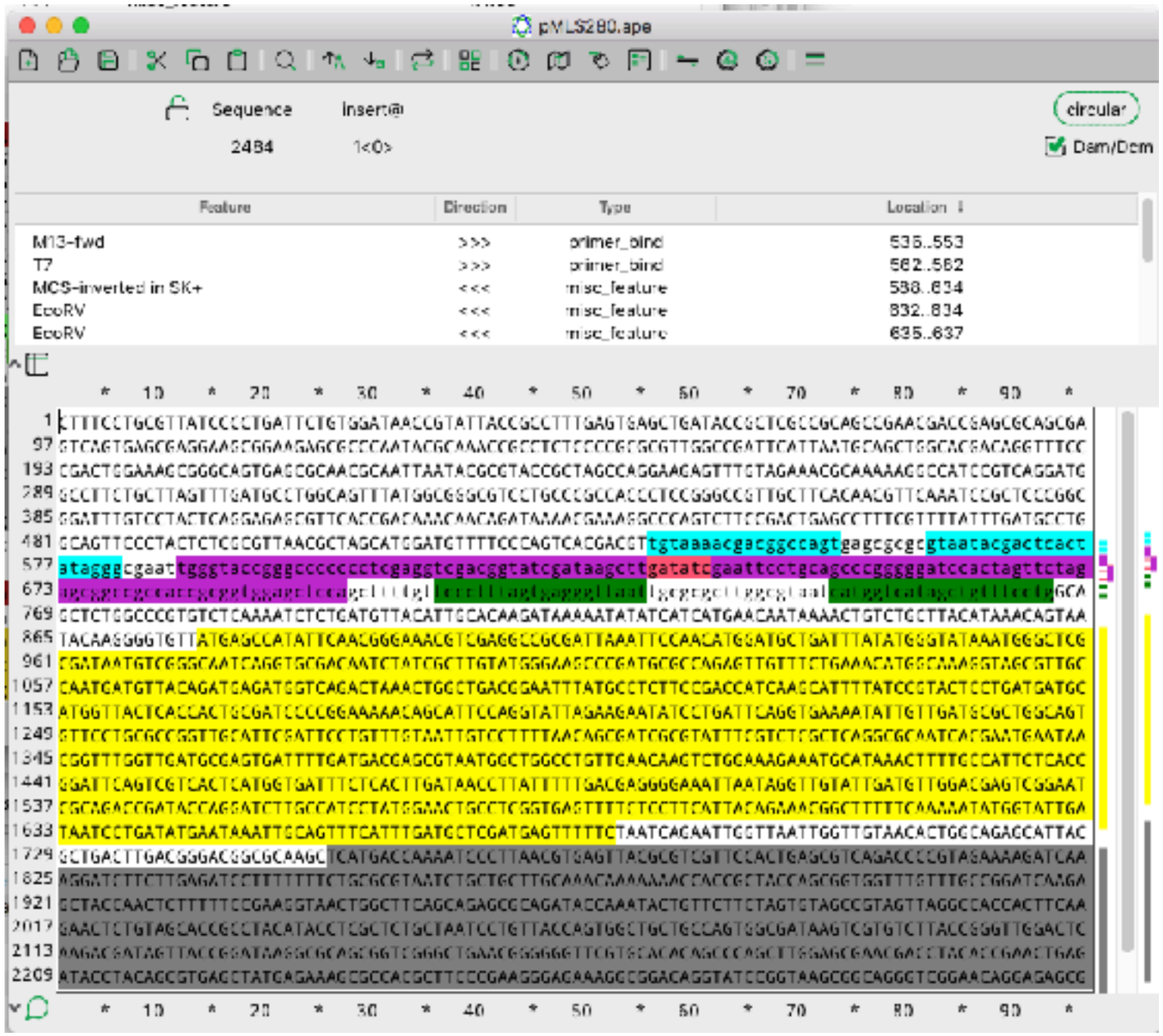
ApE Window

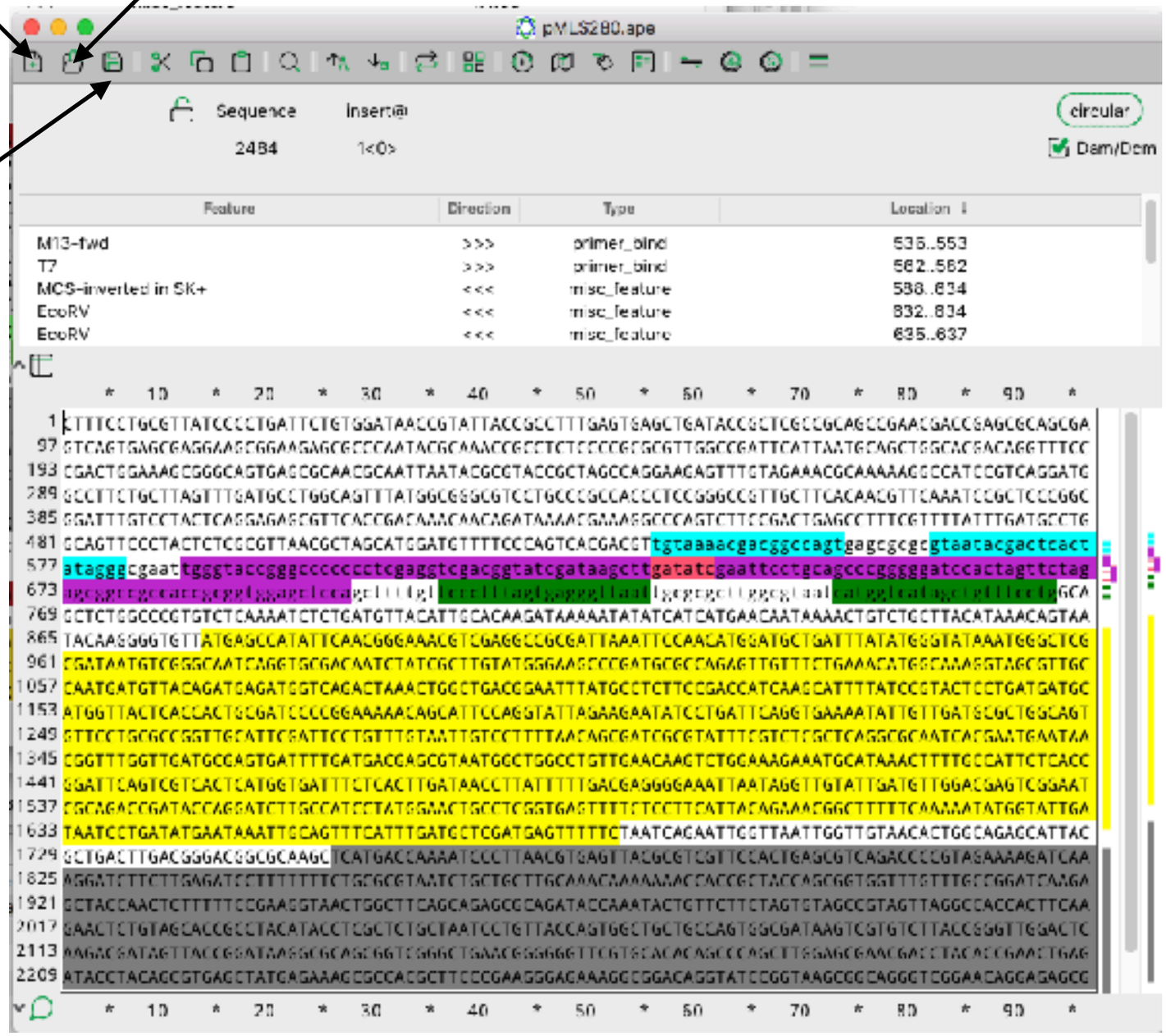

pVLS280.ape
Sequence
2484
Insert@
1<0>
circular
Dam/Dcm
Feature
Direction
Type
Location
M13-fwd >>> primer_bind 535..553
T7 >>> primer_bind 562..562
MCS-inverted in SK+ <<< misc_feature 588..634
EcoRV <<< misc_feature 832..834
EcoRV <<< misc_feature 635..637

ApE Window

New window
Shift: Duplicate selection

Open File

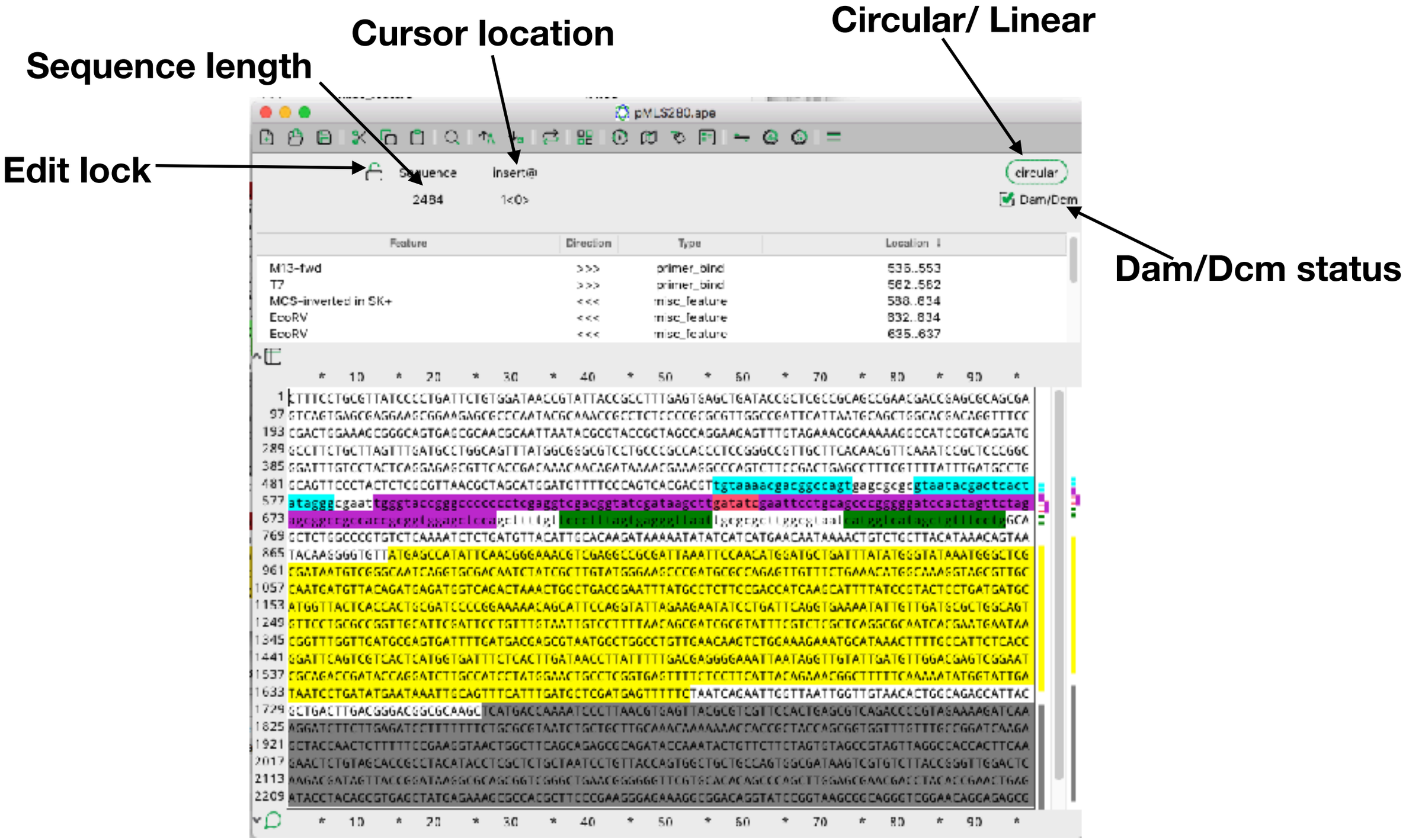
Save window
Shift: Save as



Shortcuts

Command	Function
O	Open
N	New window
D	Duplicate selected region
Shift-D	Duplicate whole sequence
S	Save sequence
Shift-S	Save sequence as…

ApE Window

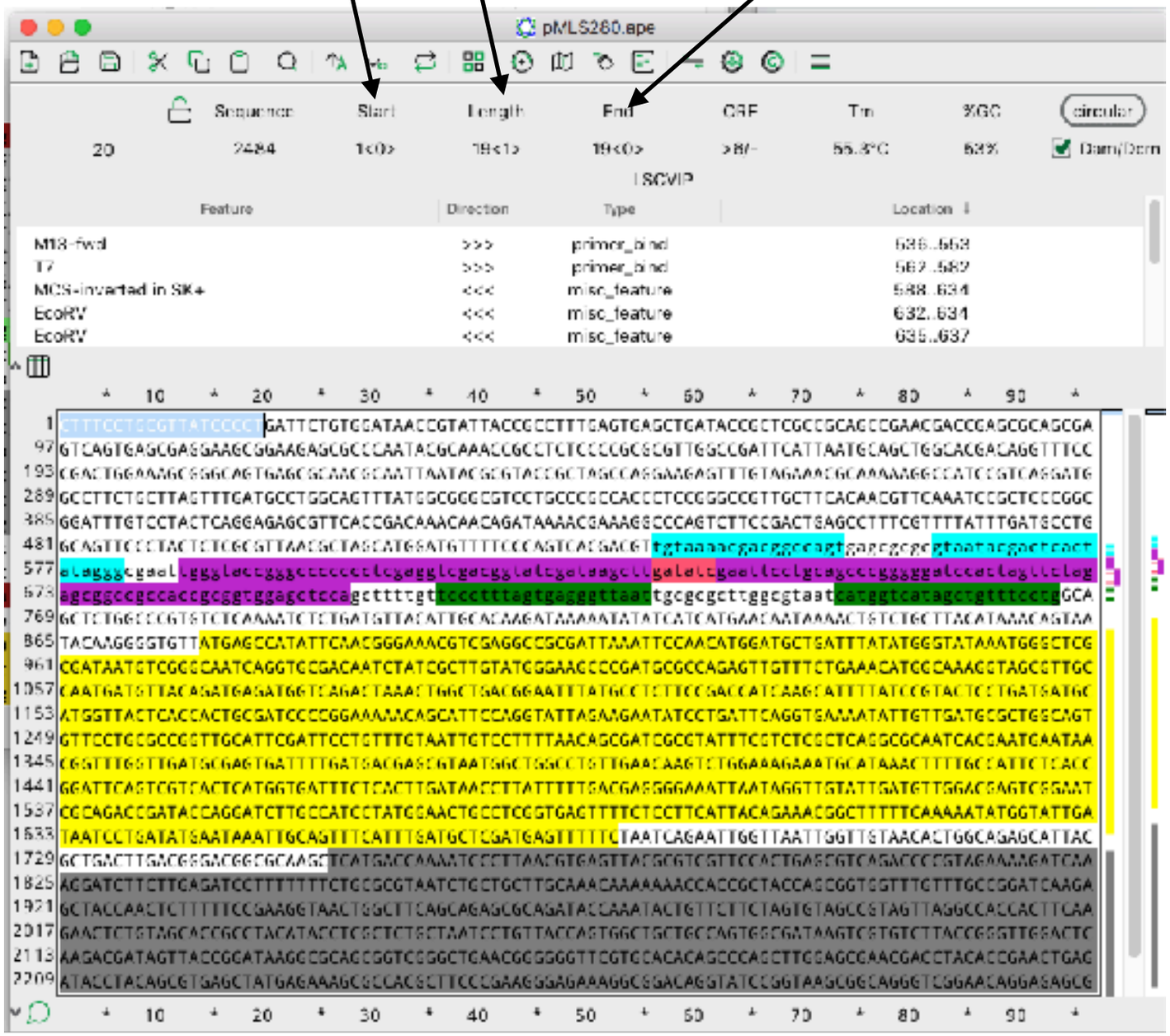

Cursor location
Circular/ Linear
Sequence length
Edit lock
Dam/Dcm status
pVLS280.ape
Sequence
2484
Insert@
1<0>
circular
Dam/Dcm
Feature
Direction
Type
Location
M13-fwd >>> primer_bind 535..553
T7 >>> primer_bind 562..562
MCS-inverted in SK+ <<< misc_feature 588..634
EcoRV <<< misc_feature 632..634
EcoRV <<< misc_feature 635..637

ApE Window

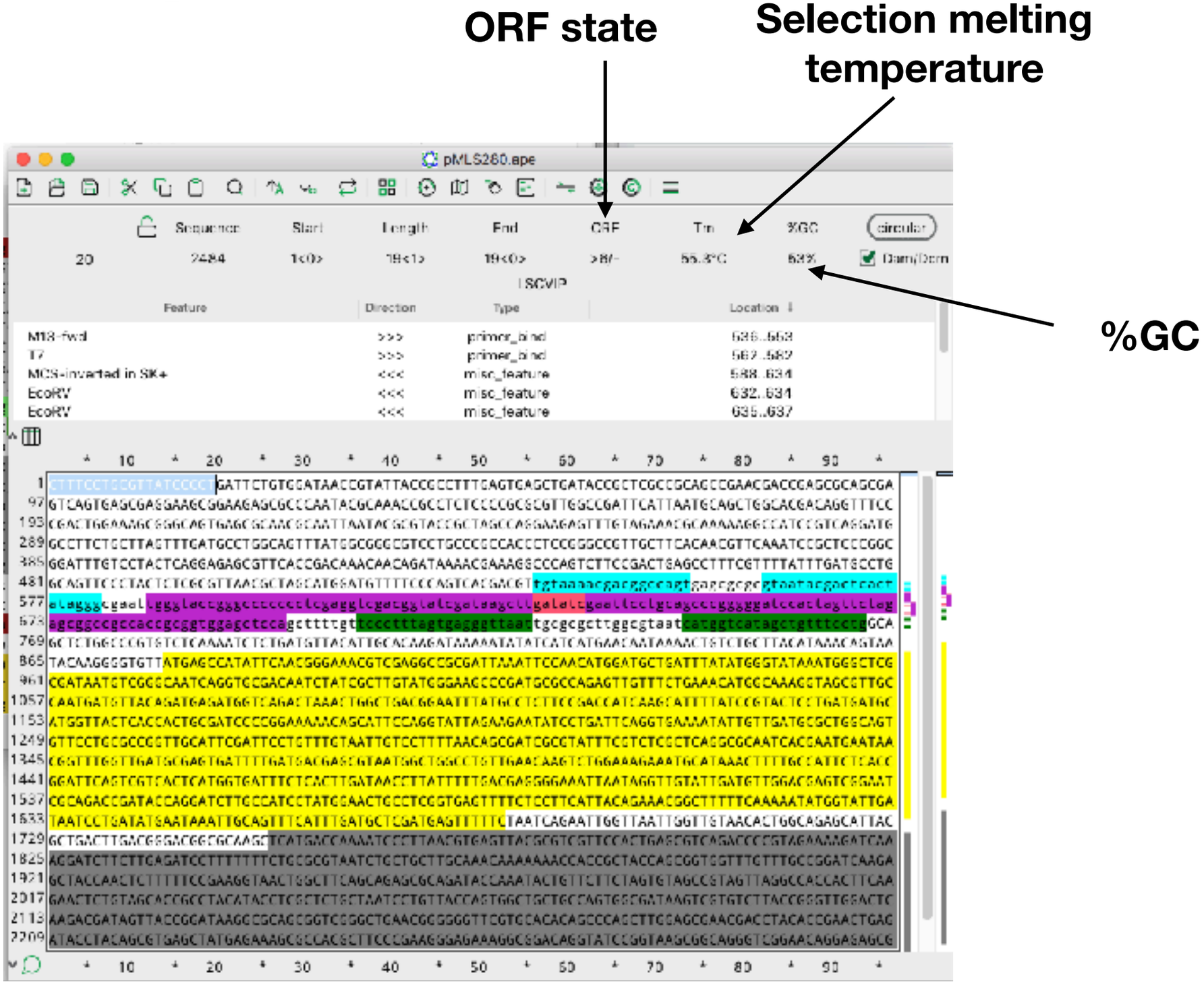
Selection start
double click to set

Selection length

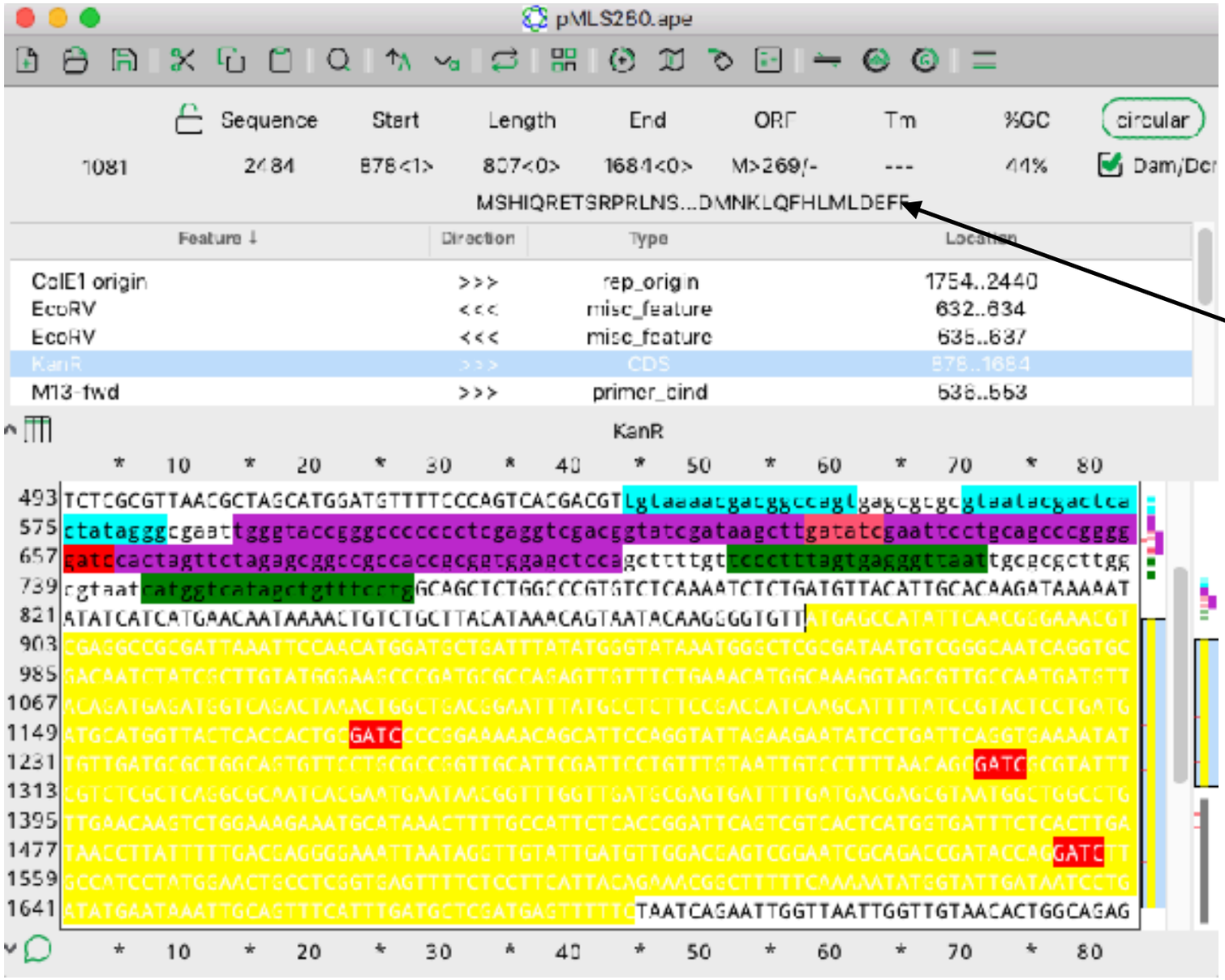
Selection end
double click to set



ApE Window

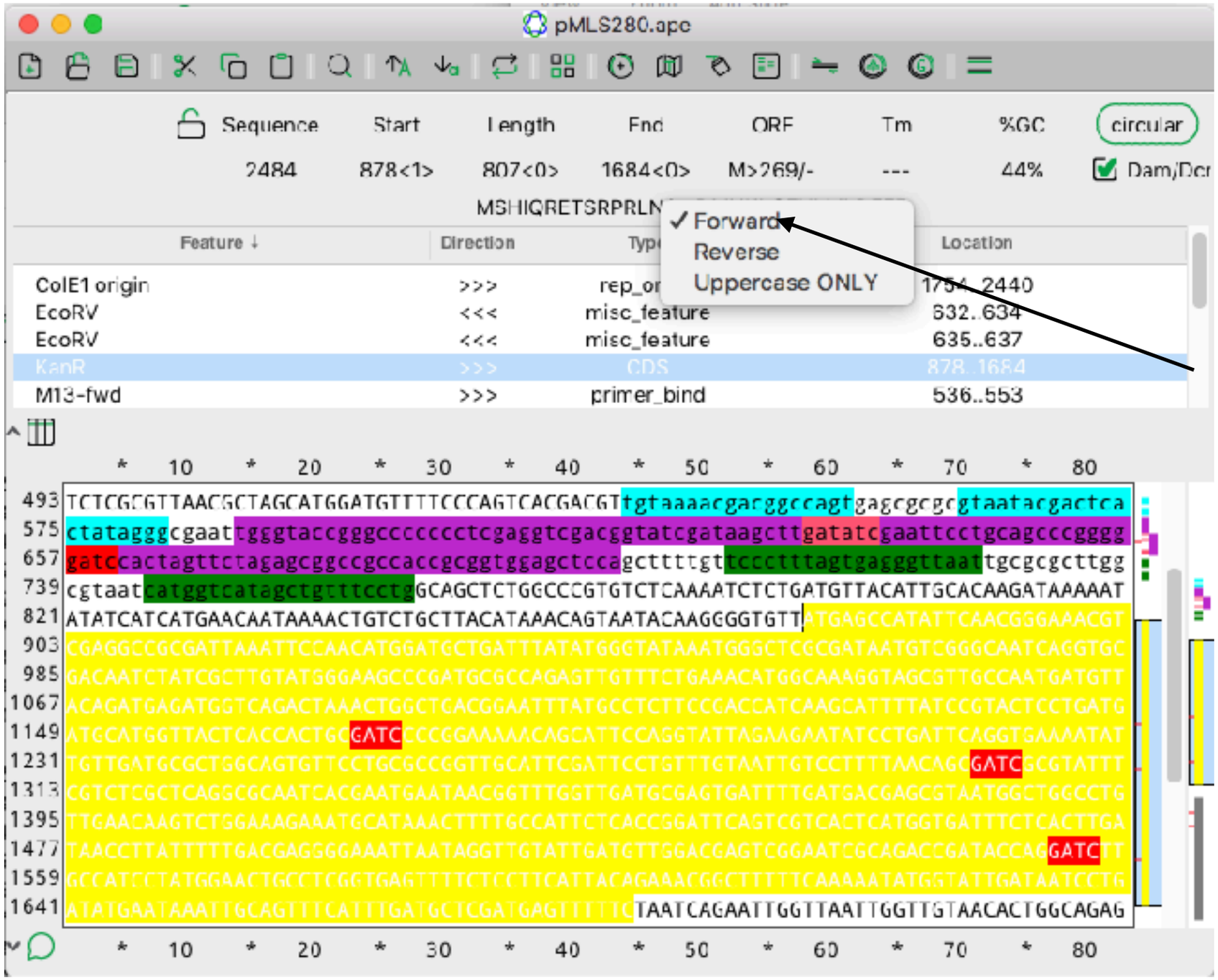

ORF state
Selection melting temperature
%GC
pMLS260.ape
Sequence
Start
Length
End
ORF
Tm
%GC
circular
20
2484
1<0>
19<1>
19<0>
>8/-
55.3°C
63%
Dam/Dcm
SCVIP
Feature
Direction
Type
Location
M13-fwd
>>>
primer_bind
T7
>>>
primer_bind
MCS-inverted in SK+
<<<
misc_feature
EcoRV
<<<
misc_feature
EcoRV
<<<
misc_feature

Selection translation



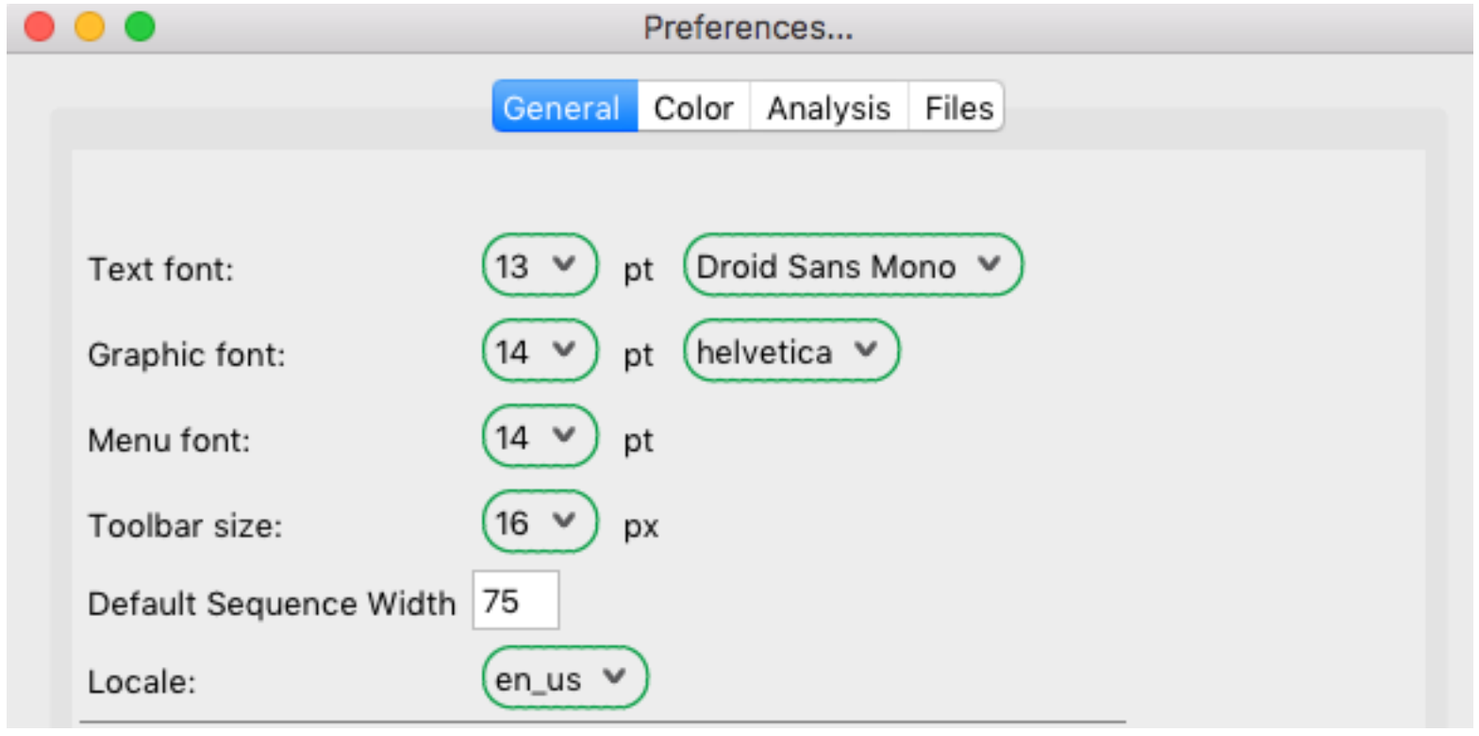
The translation of the selected region is shown here

Selection translation



Right click here to set the translation direction

Preferences

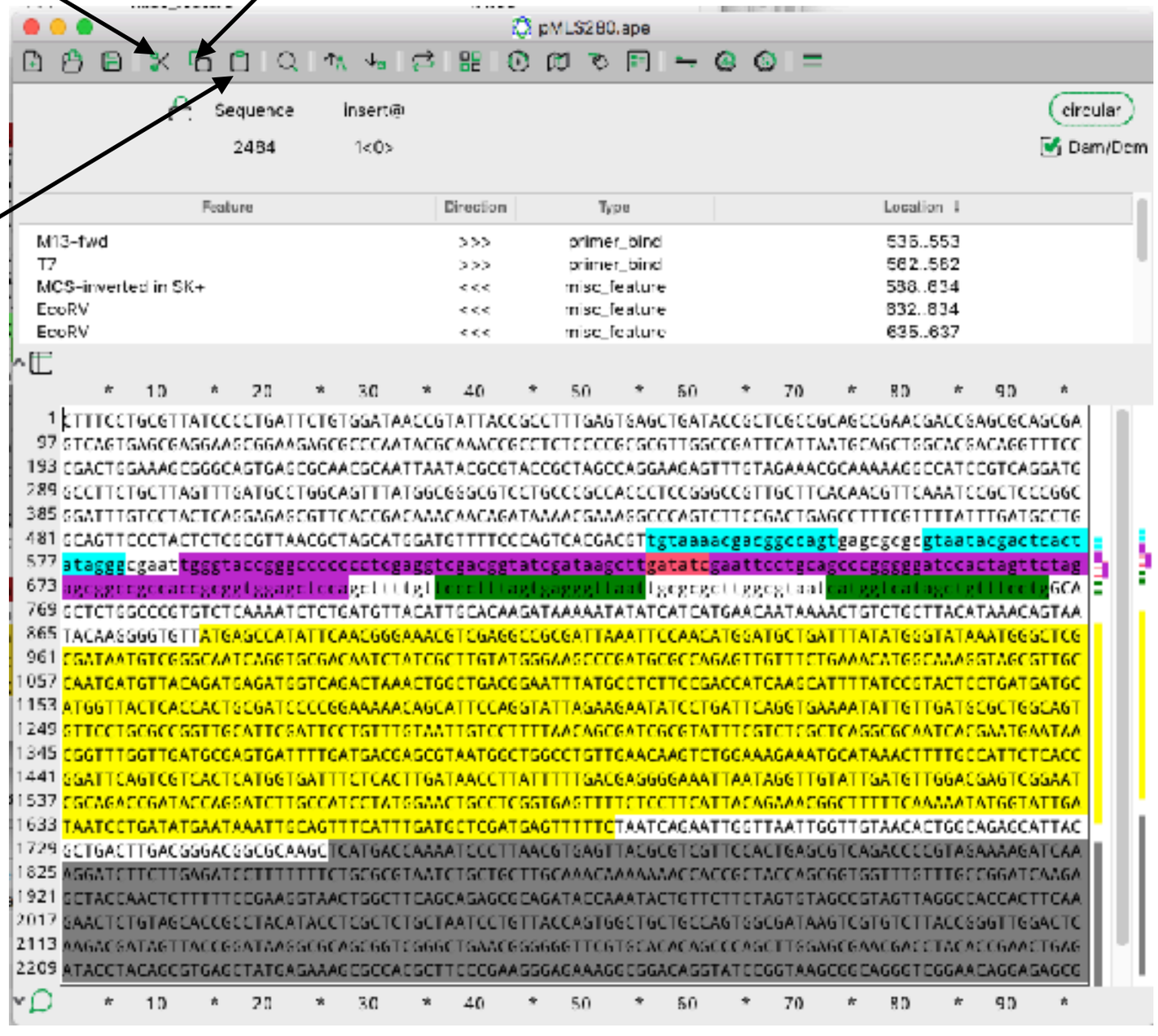


ApE Window

Cut
Shift: Cut rev-com

Copy
Shift: Copy rev-com

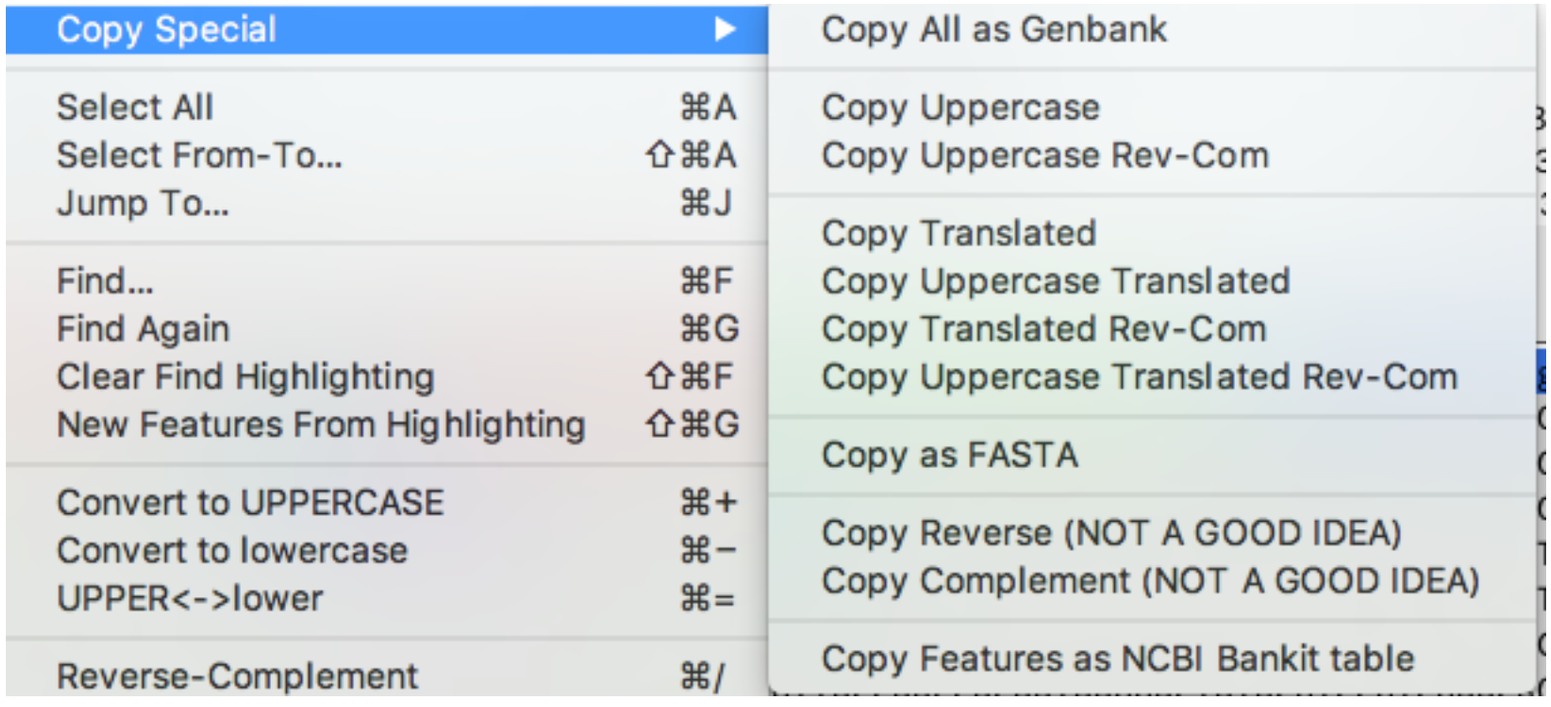
Paste
Shift: Paste rev com



Shortcuts

Command	Function
X	Cut
Shift-X	Cut rev-com
C	Copy
Shift-C	Copy rev-com
V	Paste
Shift-V	Paste rev-com

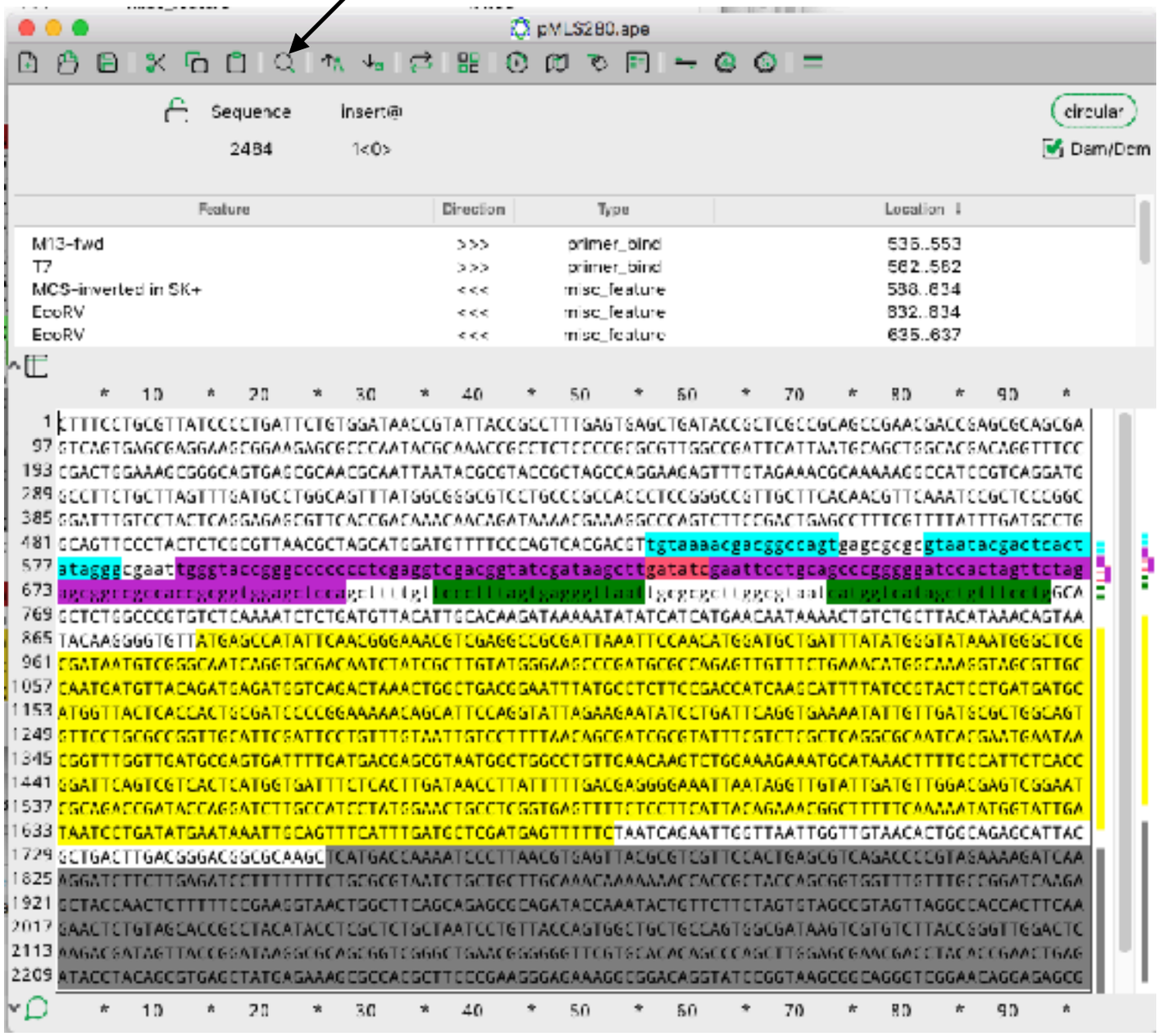
Copy Special



ApE Window

Find

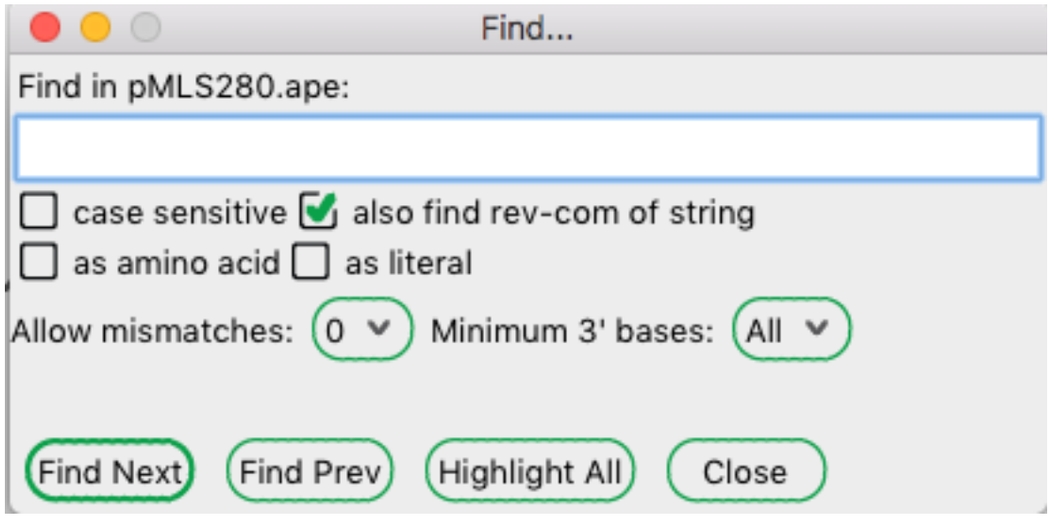
Shift: Clear find highlight



Shortcuts

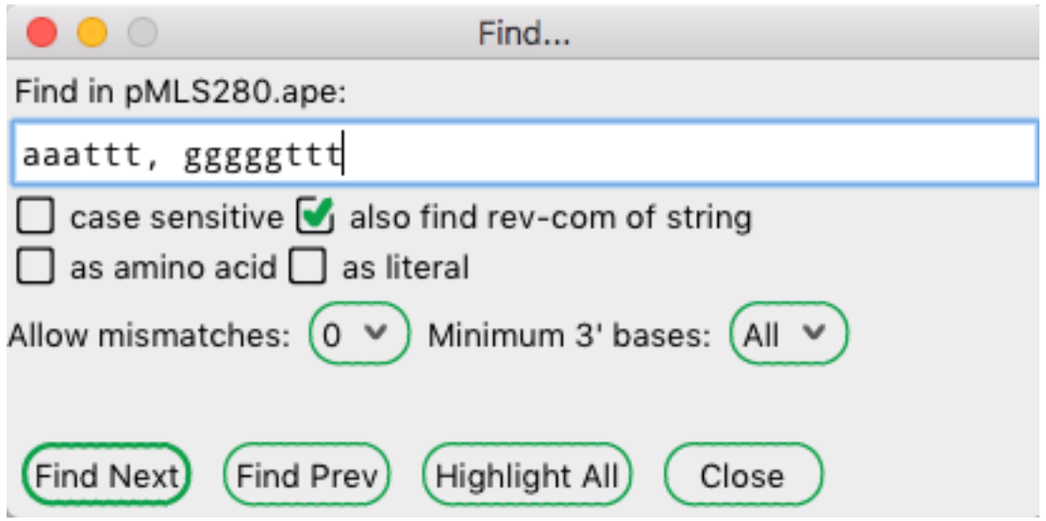
Command	Function
F	Find
Shift-F	Clear find highlight
G	Do find again
Shift-G	New feature from find highlight

Find dialog

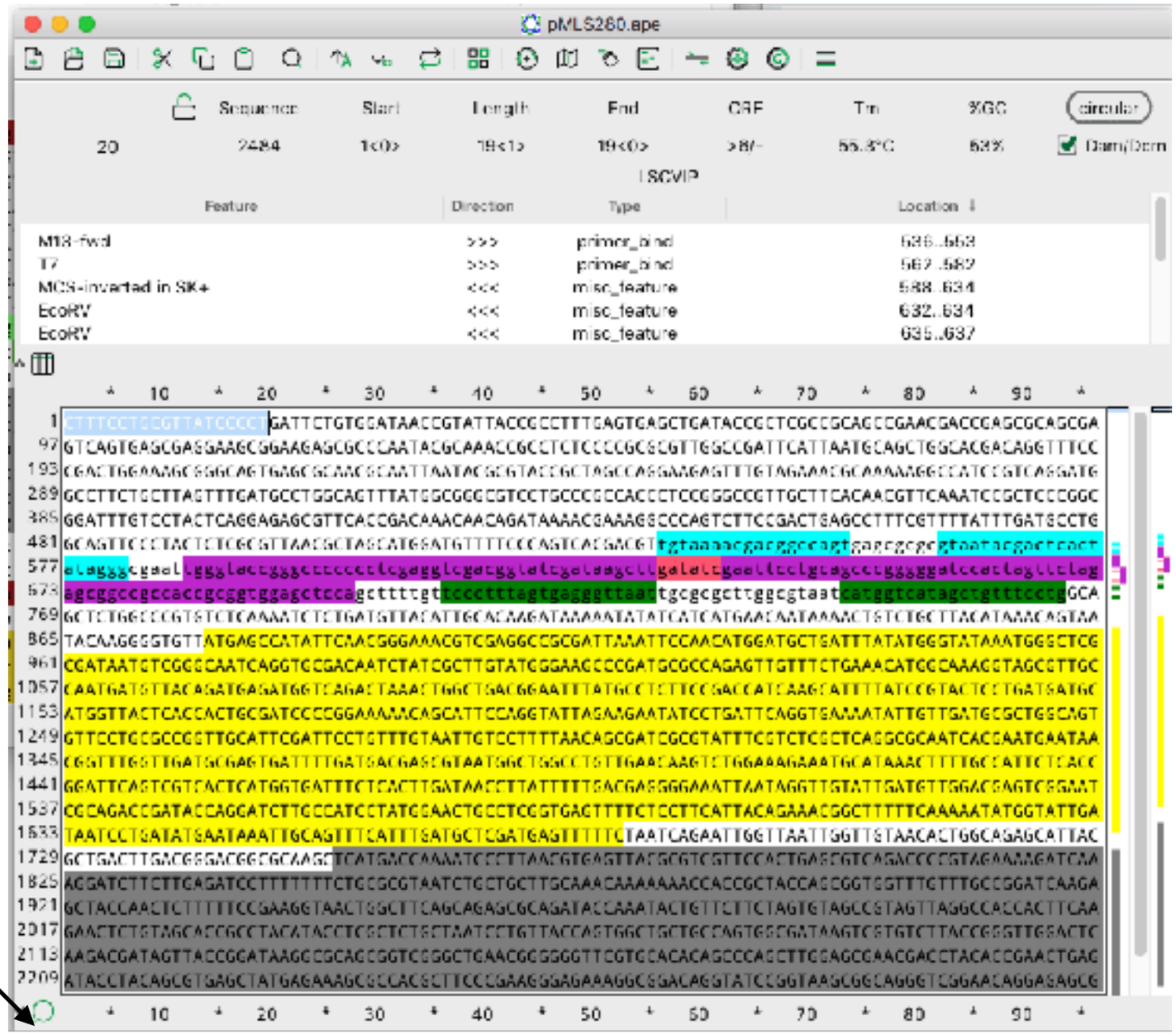

Find...
Find in pMLS280.ape:
case sensitive
also find rev-com of string
as amino acid
as literal
Allow mismatches:
0
Minimum 3' bases:
All
Find Next
Find Prev
Highlight All
Close

Find dialog

You can search for multiple patterns with a comma or bar



ApE Window

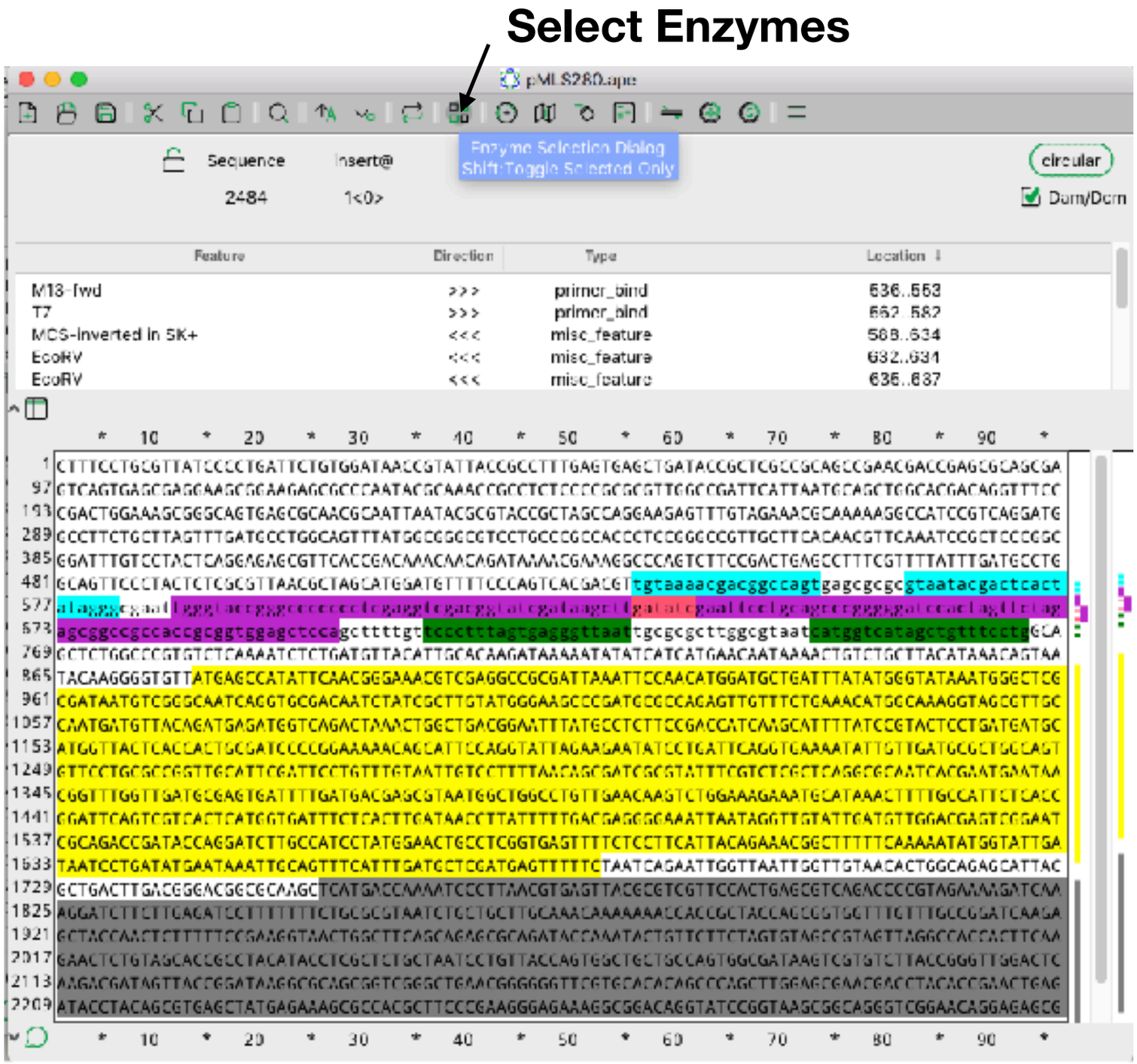


Open this to show the file comment

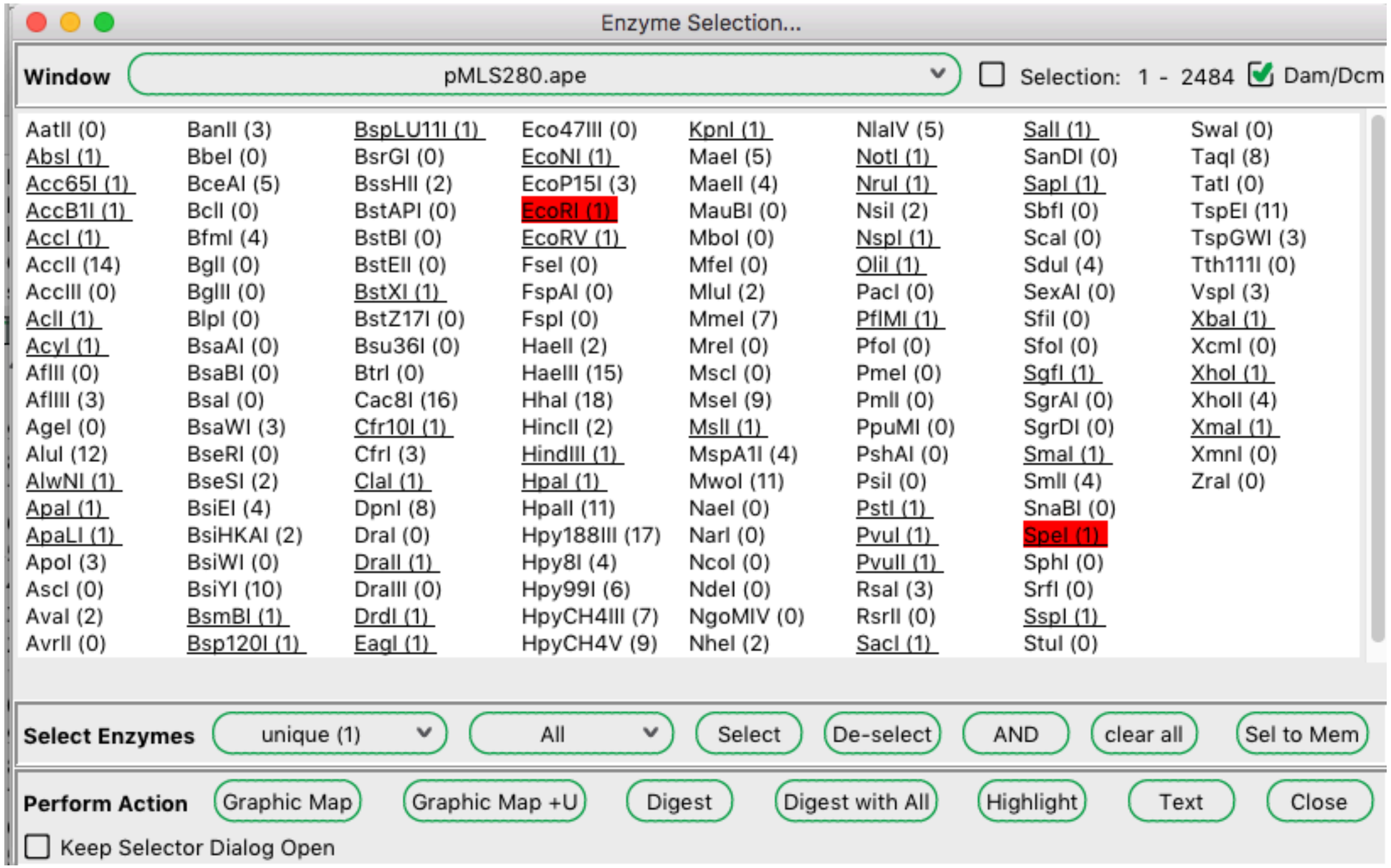
Shortcuts

Command	Function
.	New Feature
K	Add features using feature library
Shift-K	Clear all features

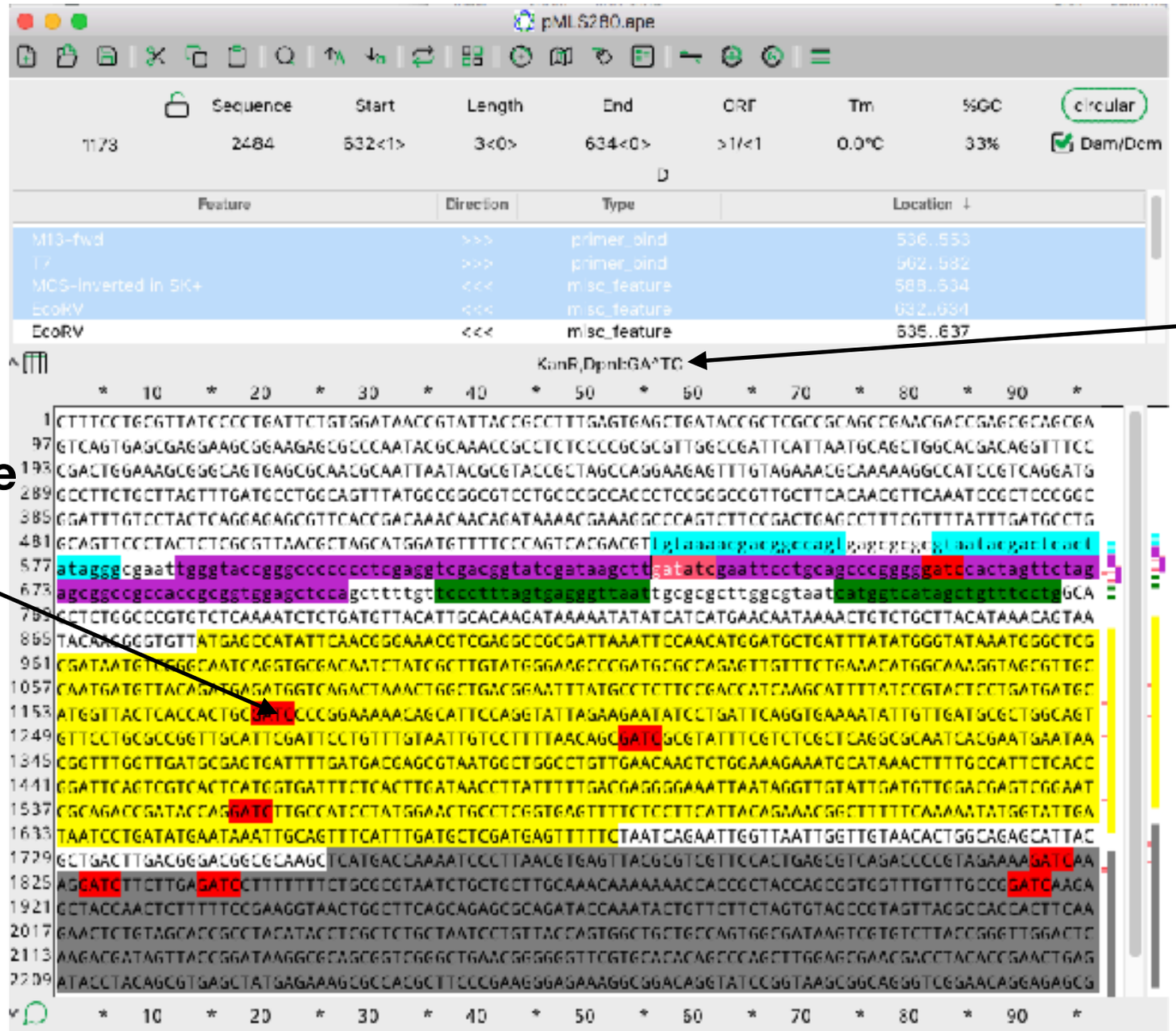
Enzymes


Select Enzymes
pMLS280.ape
Enzyme Selection Dialog
Shift:Toggle Selected Only
Sequence
2484
Insert@
1<0>
circular
Dam/Dcm
Feature
Direction
Type
Location
M13-fwd >>> primer_bind 636..653
T7 >>> primer_bind 662..682
MCS-Inverted in SK+ <<< misc_feature 568..634
EcoRV <<< misc_feature 632..631
EcoRV <<< misc_feature 636..637

Select an enzyme to highlight



Enzyme highlights

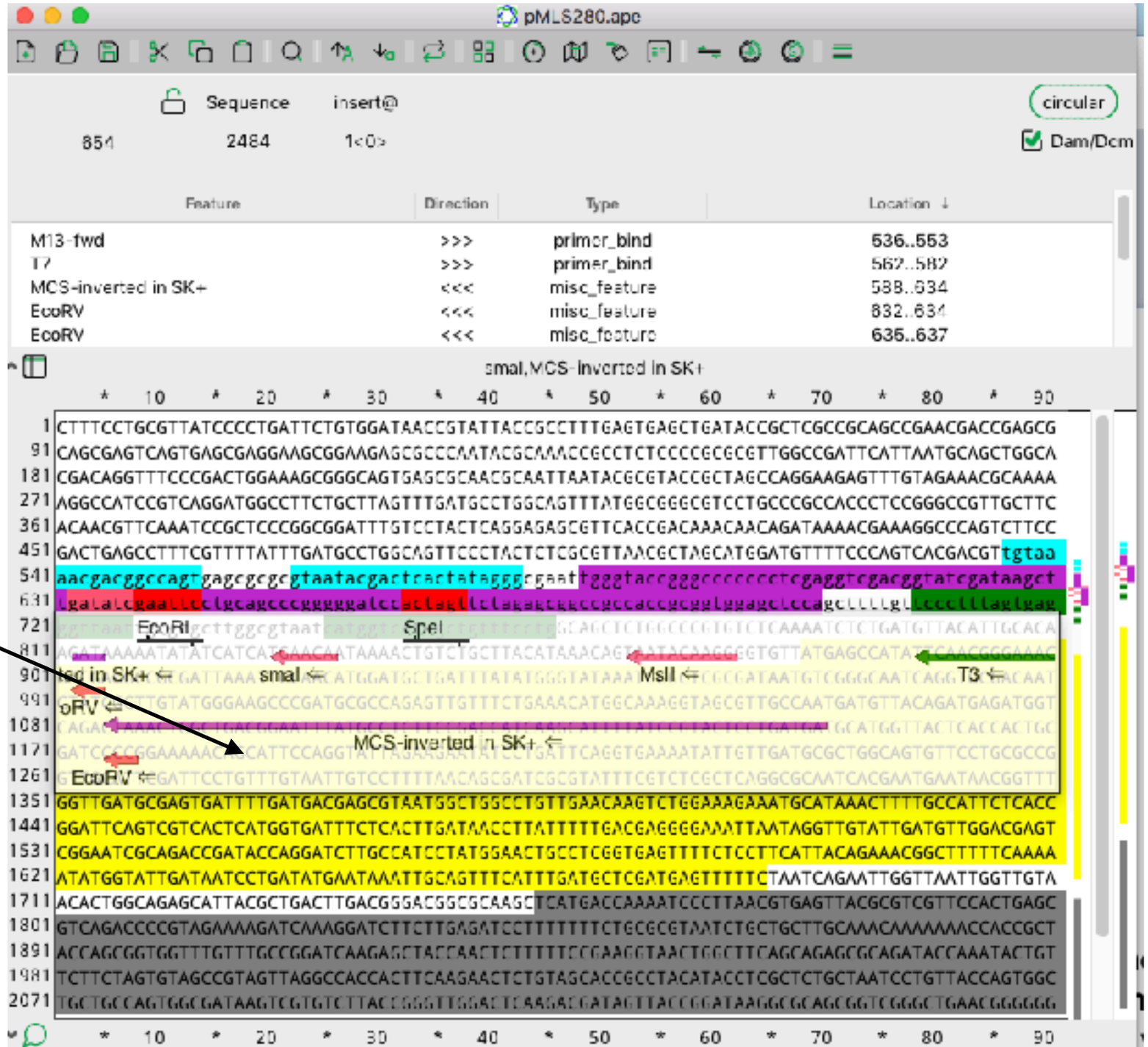


Enzyme name and sequence shows up here when you put the mouse over the sequence

Enzymes can be highlighted

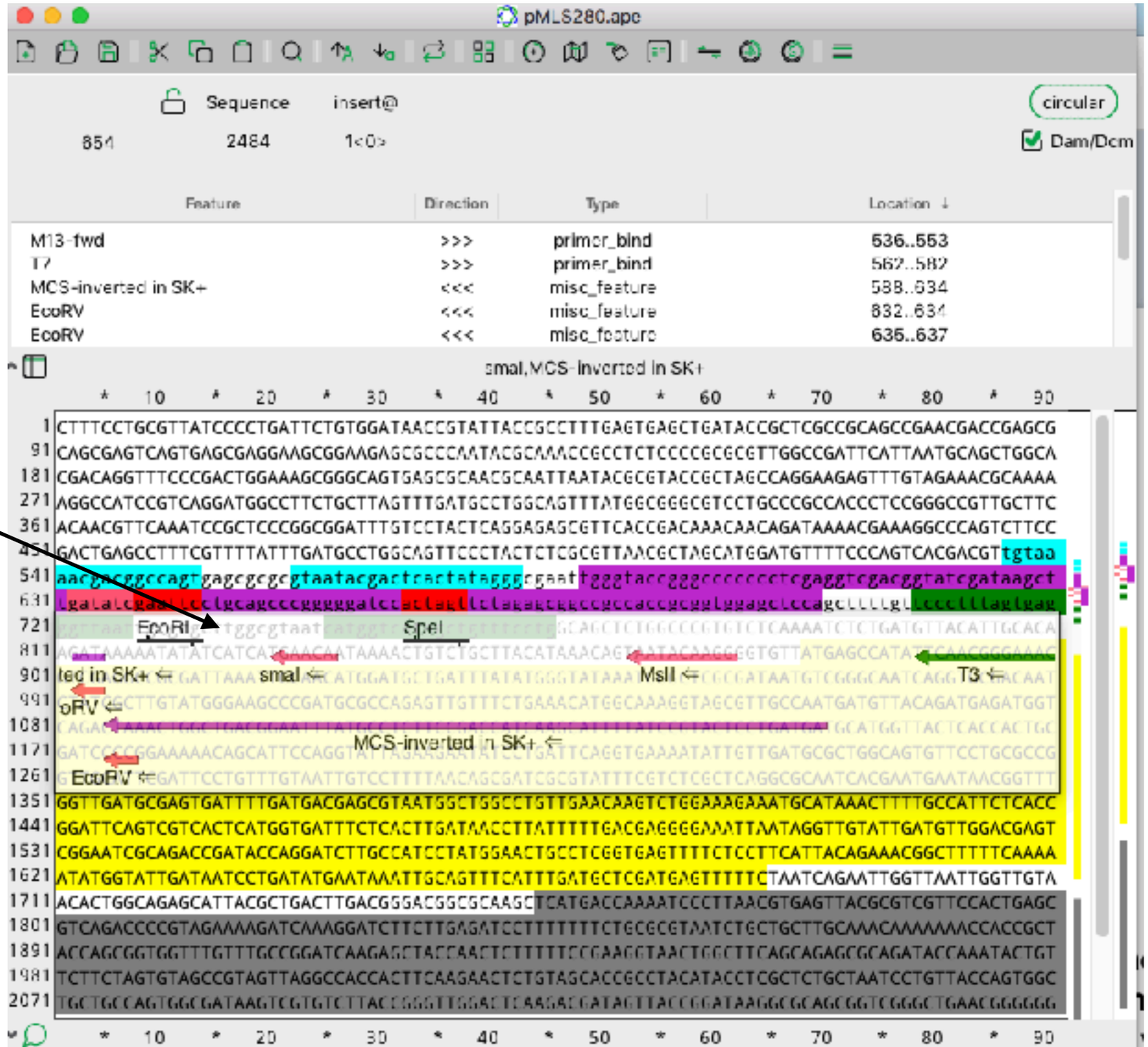
X-ray window

spacebar turns on the X-ray window

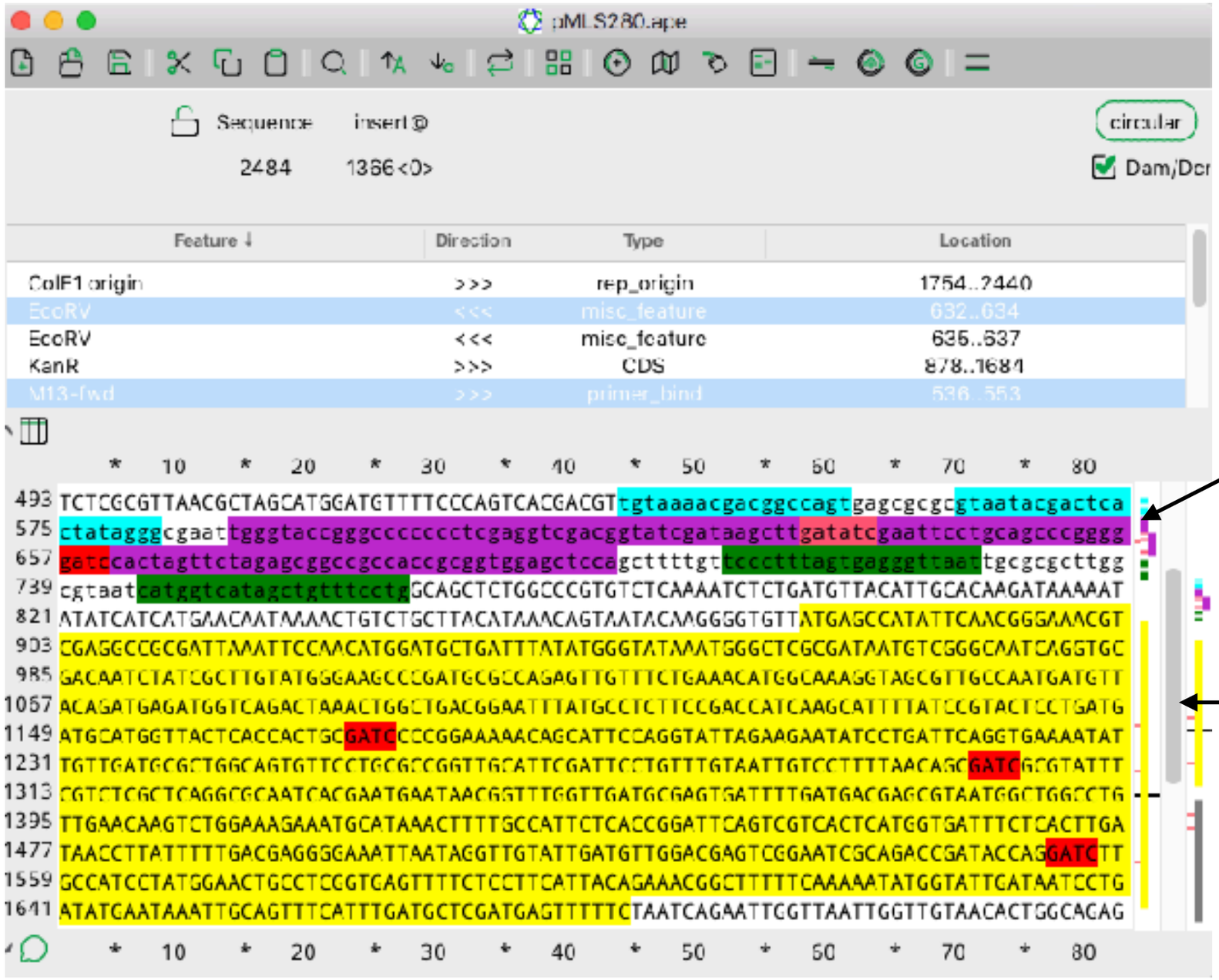


X-ray window

The X-ray window shows all the features and enzyme sites in a row



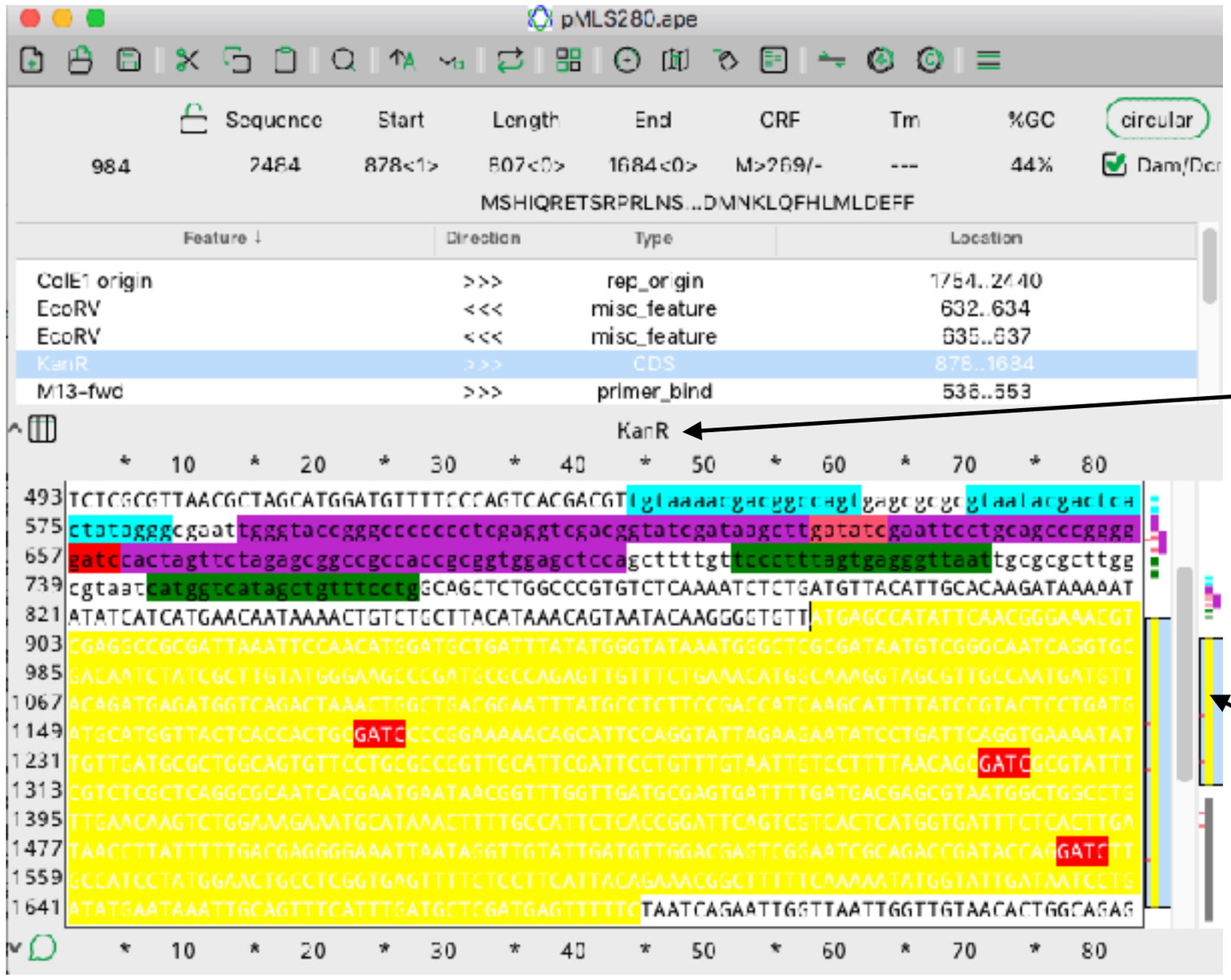
Side maps



First map shows the features in the current lines

Second map shows the features in the whole sequence

Side maps

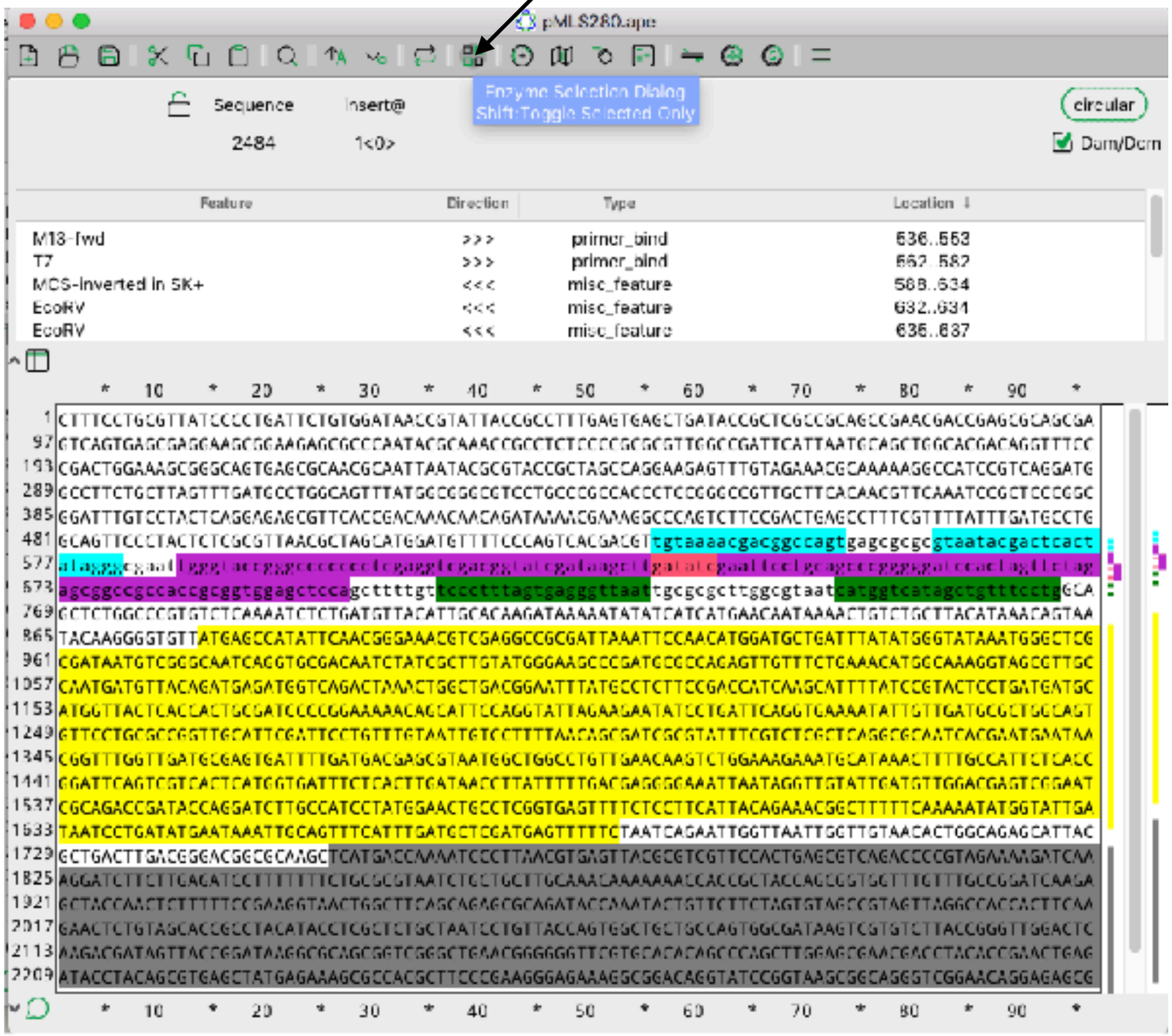


Side map features under the pointer are listed here

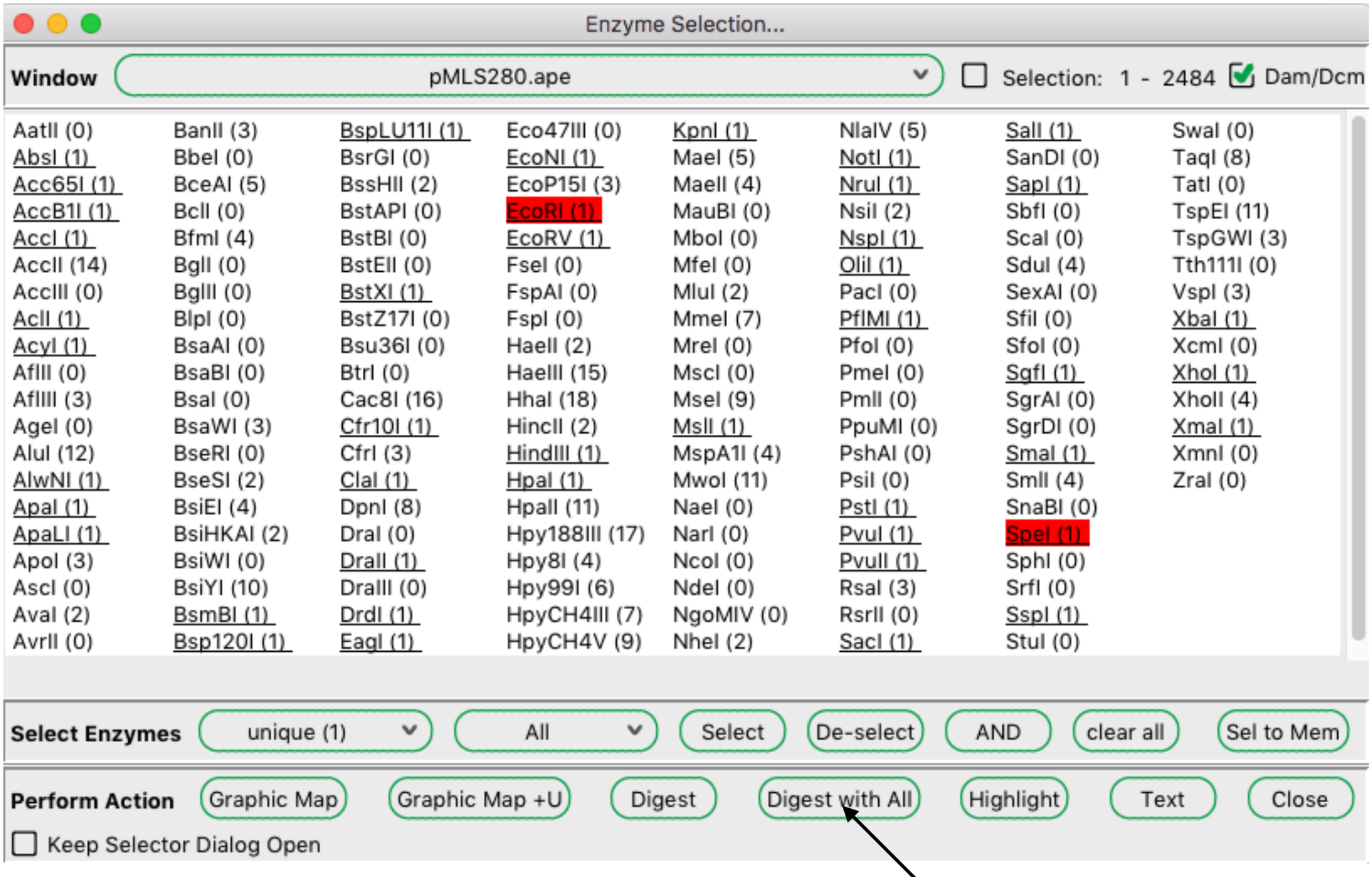
Click on any of these to select a feature in the feature table and set the selection to that feature

Virtual Gel

Select Enzymes

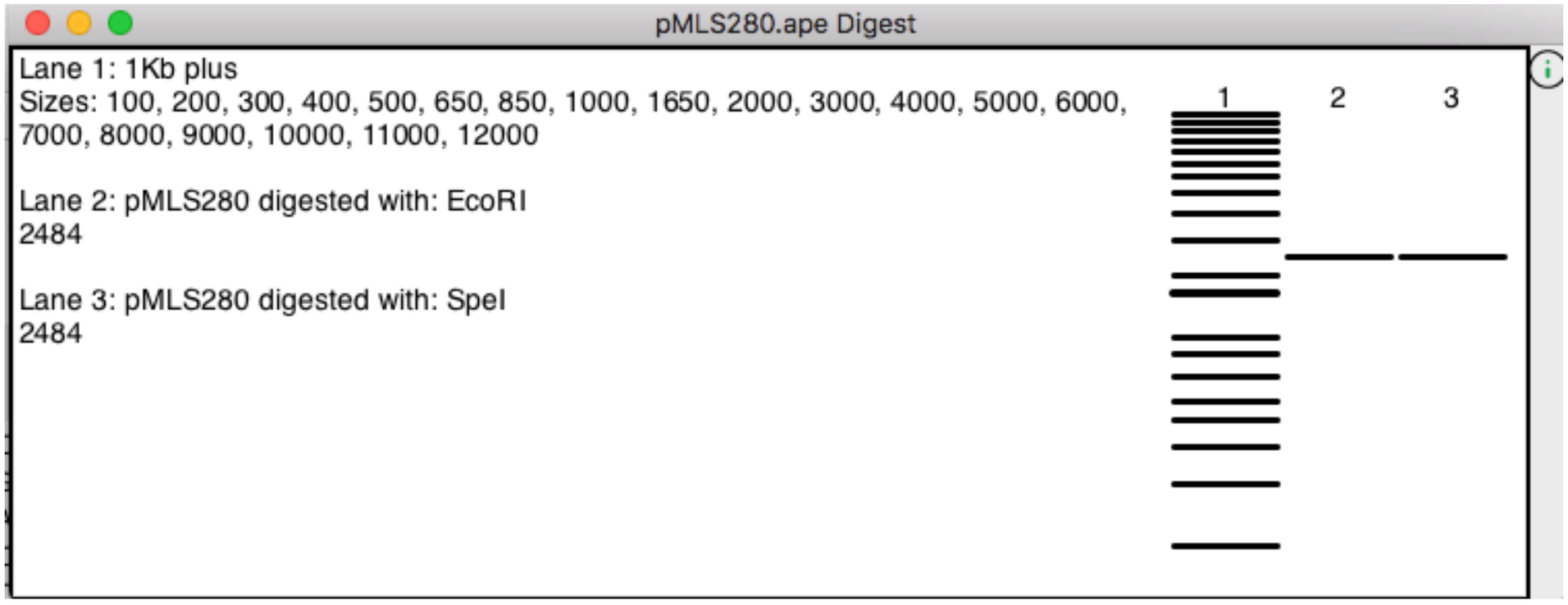


Virtual Gel

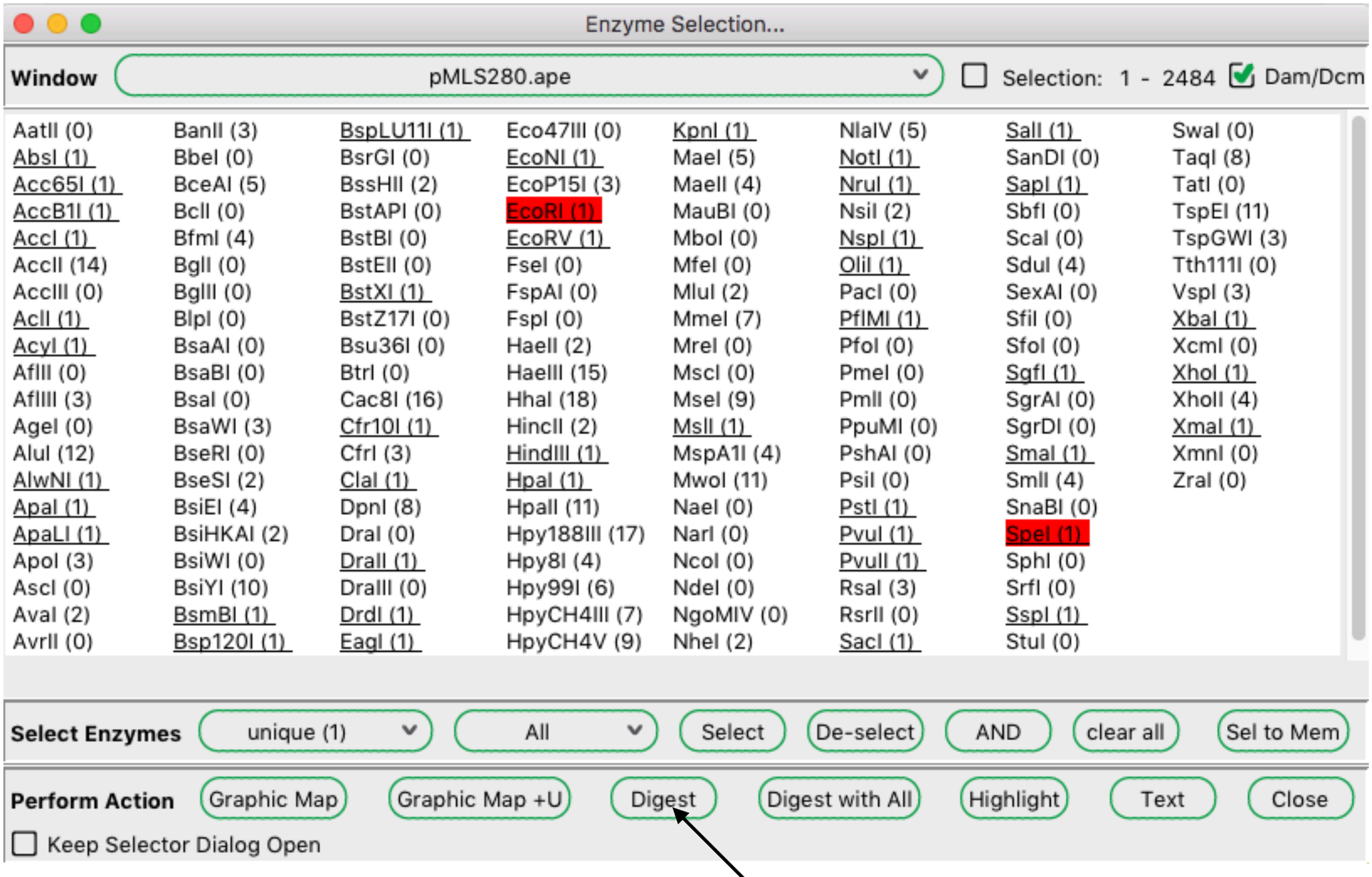


Click here to digest the sequence with each enzyme individually

Virtual Gel

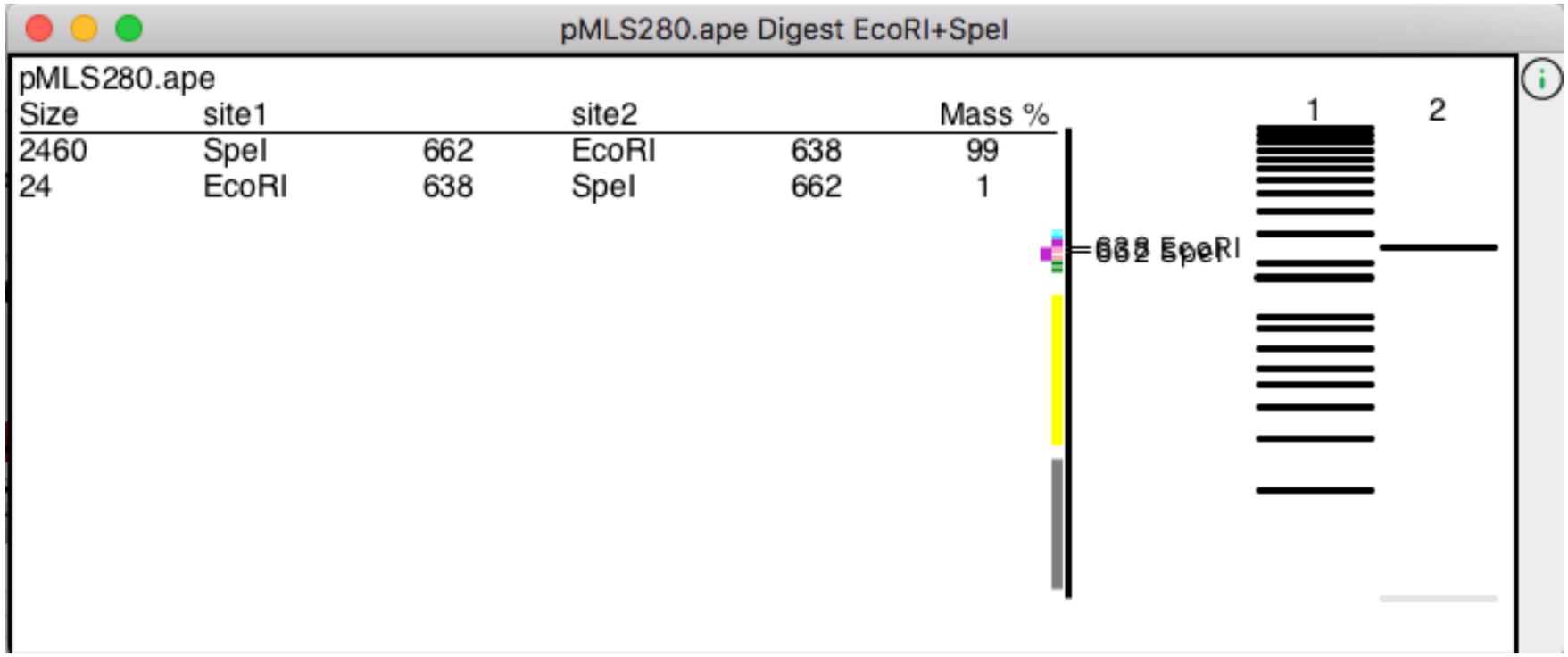

pMLS280.ape Digest
Lane 1: 1Kb plus
Sizes: 100, 200, 300, 400, 500, 650, 850, 1000, 1650, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000
Lane 2: pMLS280 digested with: EcoRI
2484
Lane 3: pMLS280 digested with: SpeI
2484
1
2
3

Virtual Gel

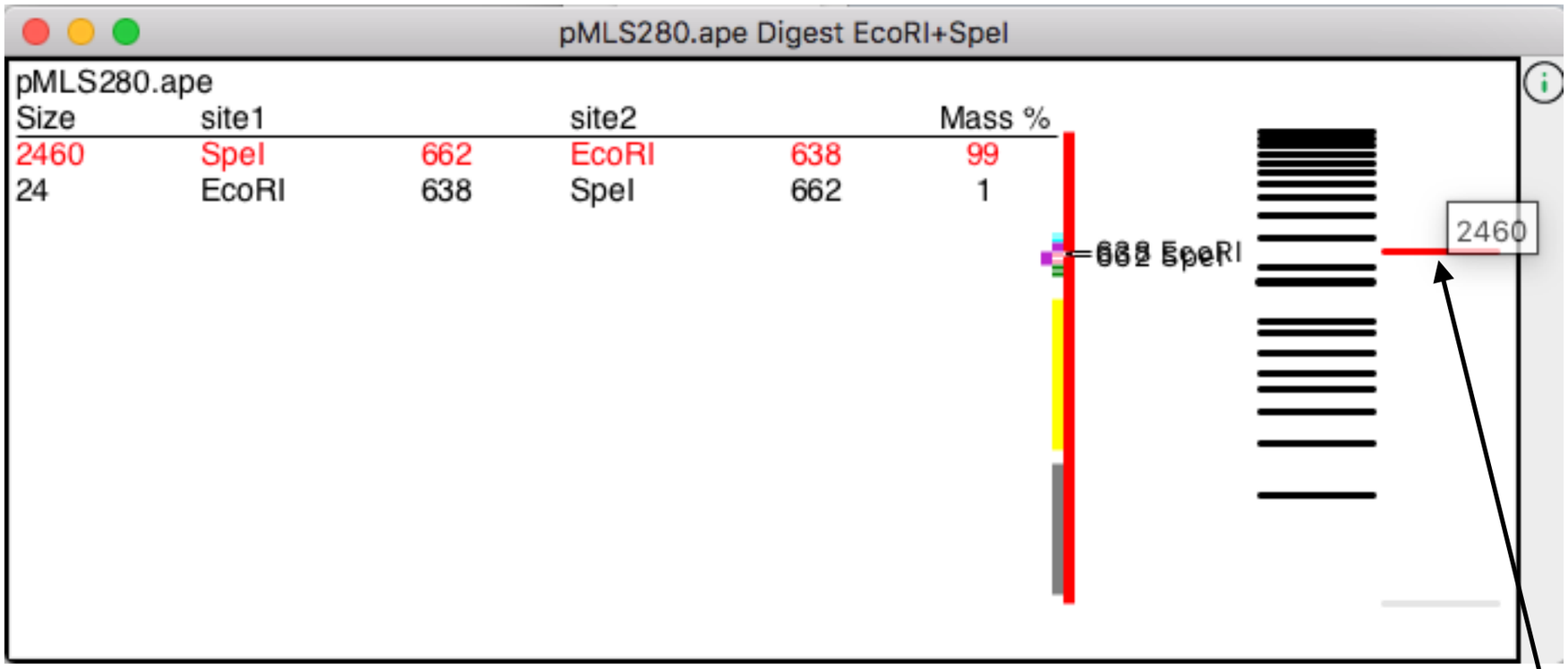


Click here to digest the sequence with each enzyme at one time

Virtual Gel

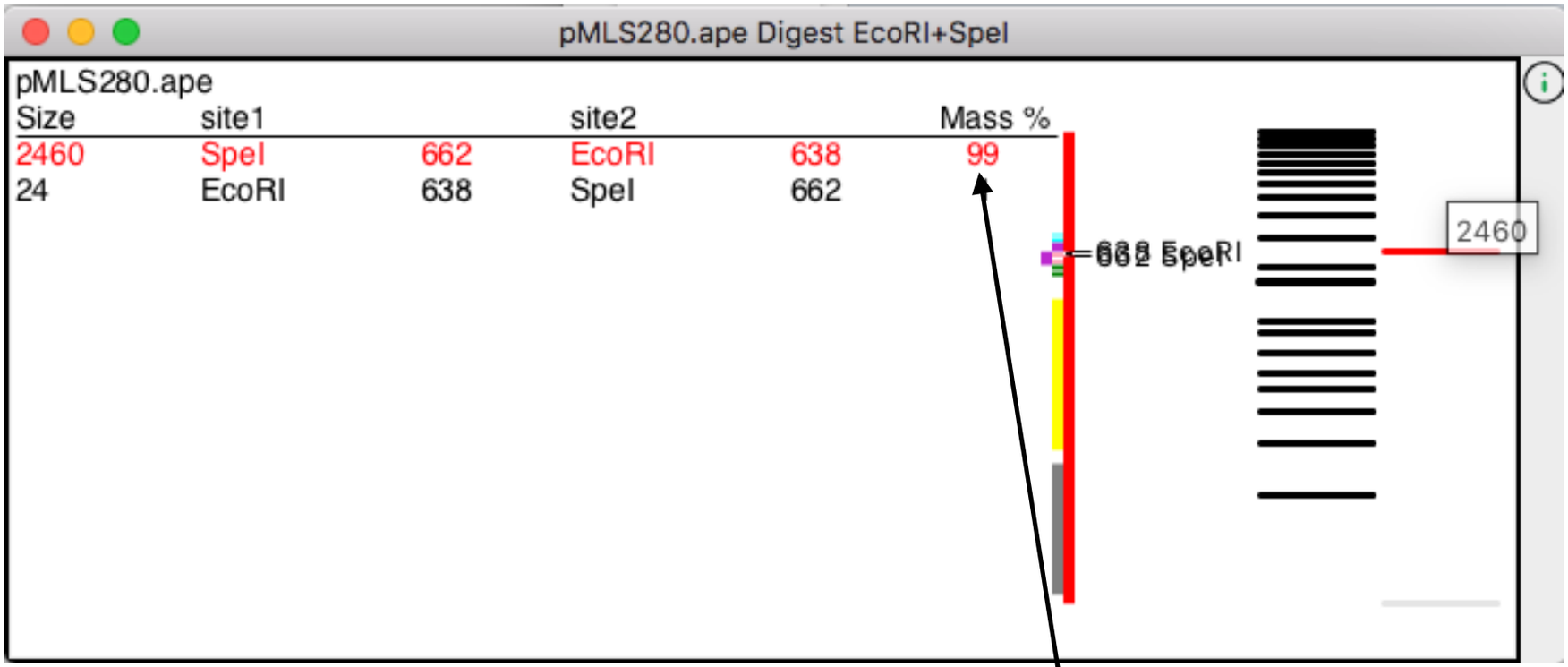

pMLS280.ape Digest EcoRI+SpeI
pMLS280.ape
Size site1 site2 Mass %
2460 SpeI 662 EcoRI 638 99
24 EcoRI 638 SpeI 662 1
1
2
662 SpeI

Virtual Gel



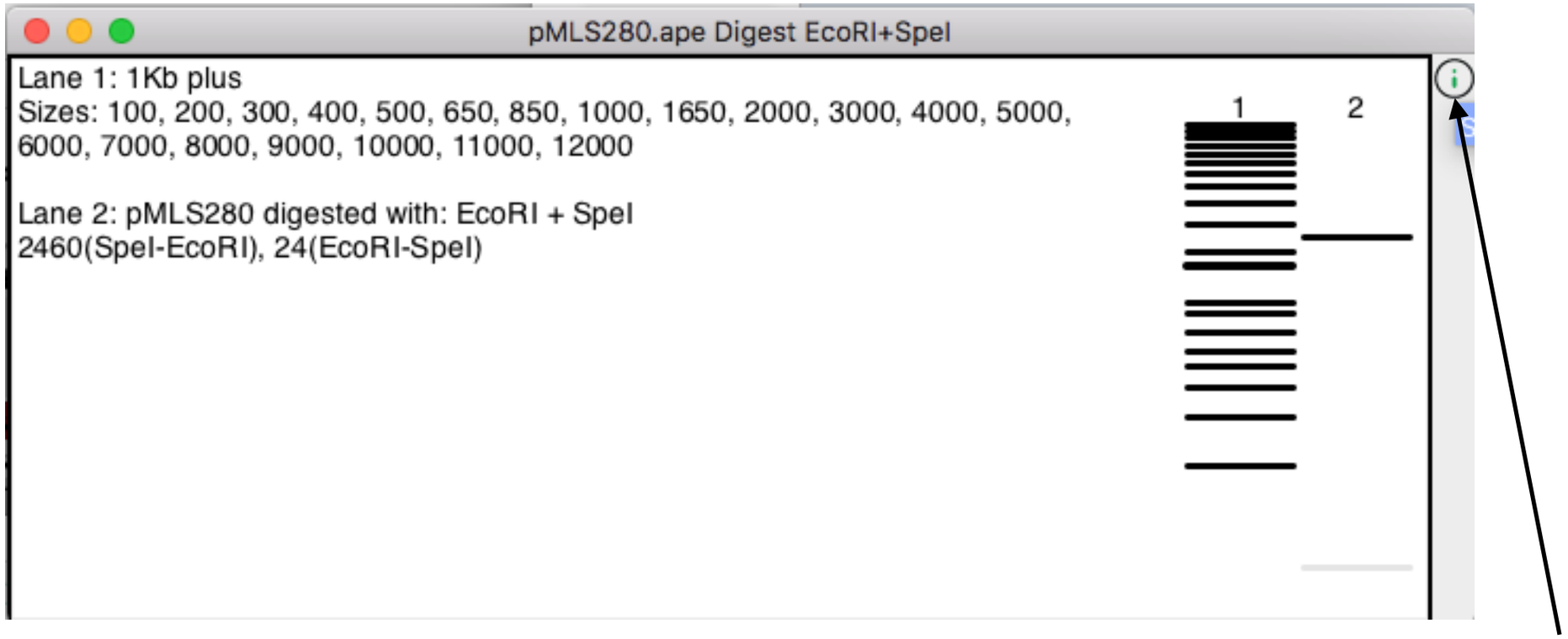
Mouse here to highlight the band
Double-click to select that region in the sequence

Virtual Gel



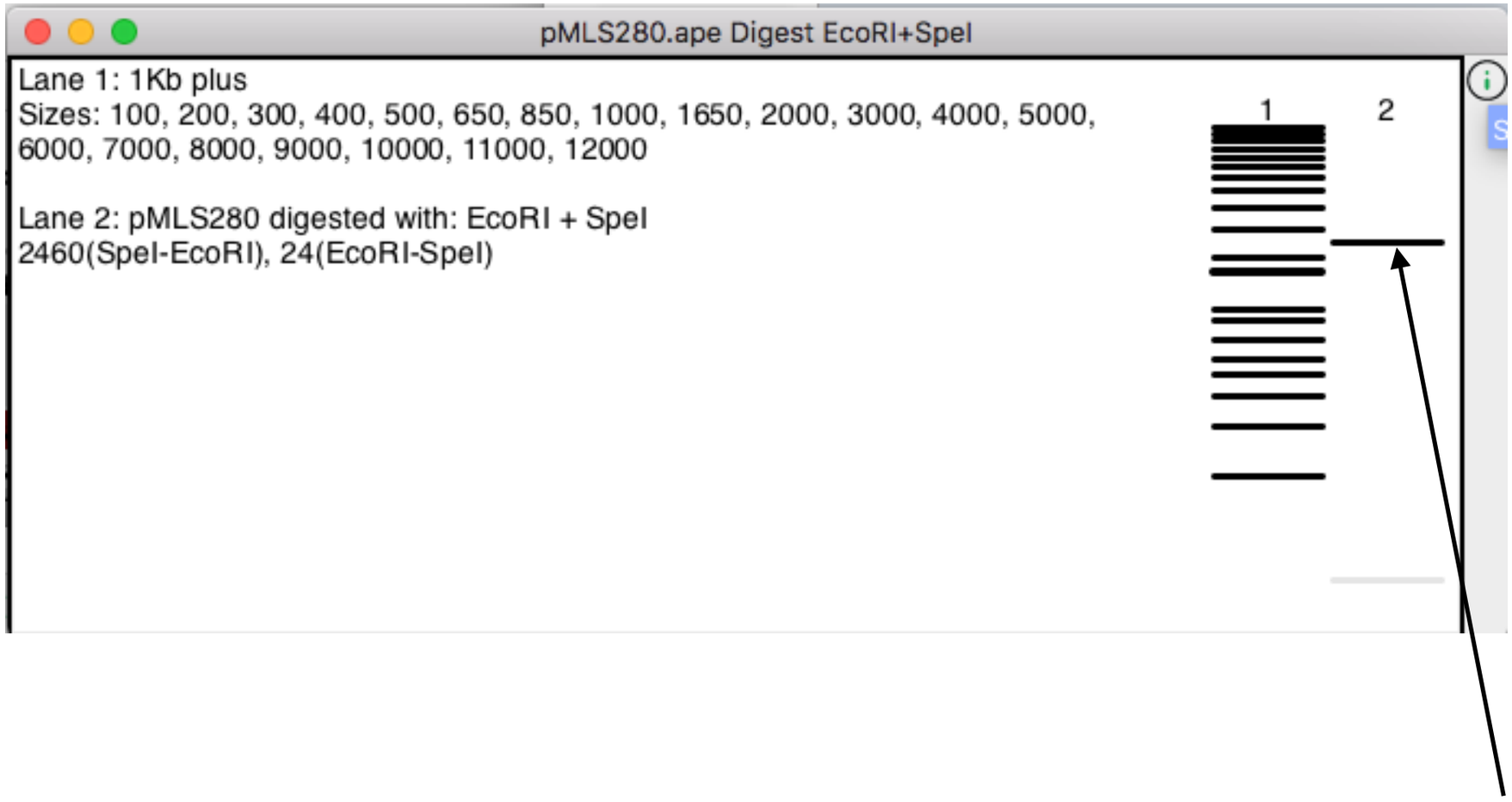
Mass % shows how much of the total DNA each band represents Use this to decide how much DNA to load on a gel. 50 ng is about the least DNA you can see on a gel.

Virtual Gel



Click here to see a list of digest lanes

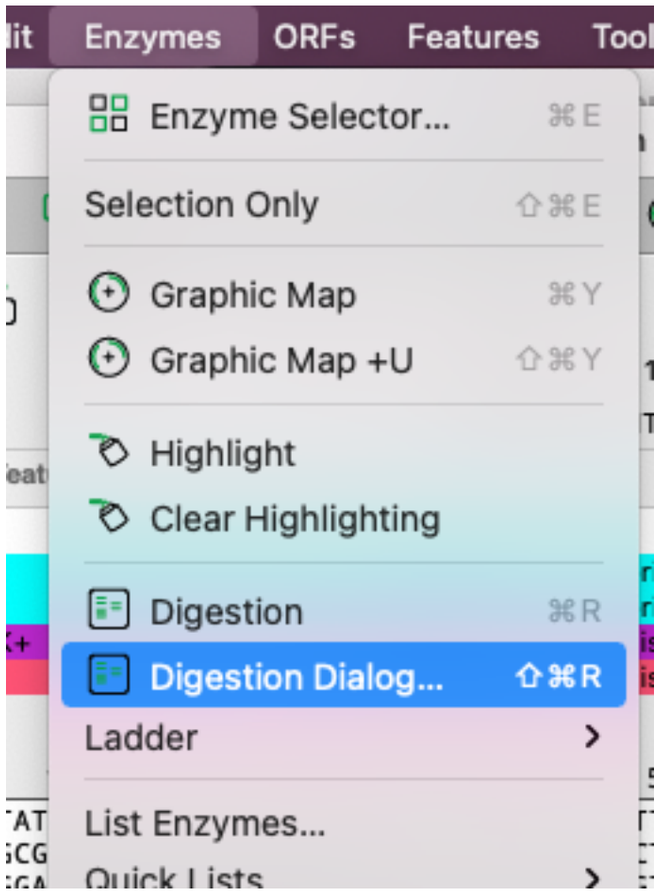
Virtual Gel


pMLS280.ape Digest EcoRI+SpeI
Lane 1: 1Kb plus
Sizes: 100, 200, 300, 400, 500, 650, 850, 1000, 1650, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000
Lane 2: pMLS280 digested with: EcoRI + SpeI
2460(SpeI-EcoRI), 24(EcoRI-SpeI)
1
2
Click and drag lanes to rearrange

Shortcuts

Command	Function
R	Digest with currently selected enzymes
Shift-R	Digest Dialog
E	Enzyme selection dialog
Shift-E	Set all functions to apply to selection

Digestion dialog

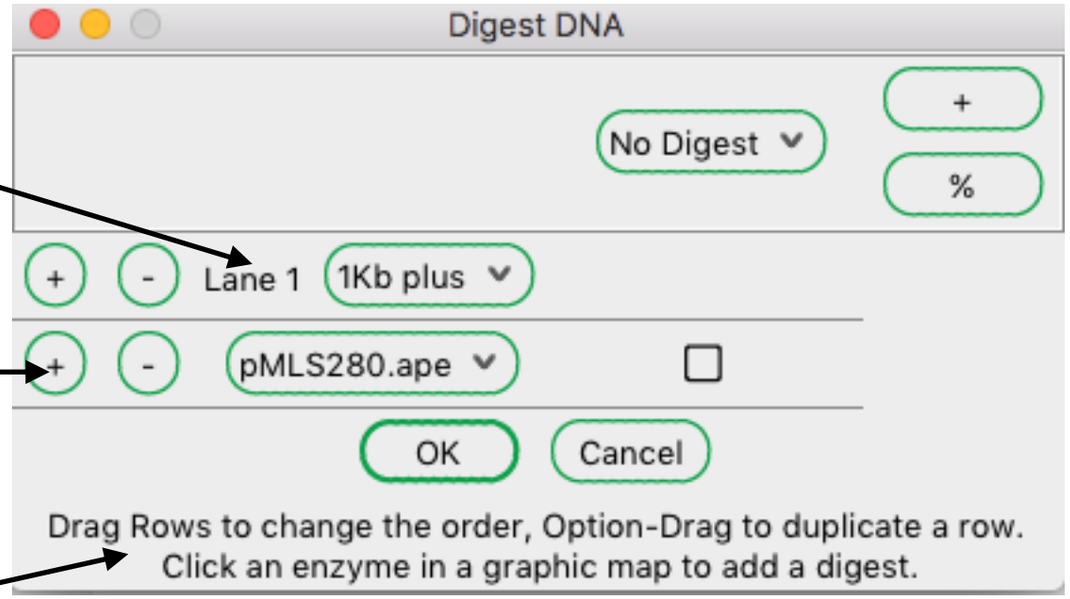


Digestion dialog

Each gel lane is a table row

Add and remove rows with these buttons

Rows can be dragged and duplicated

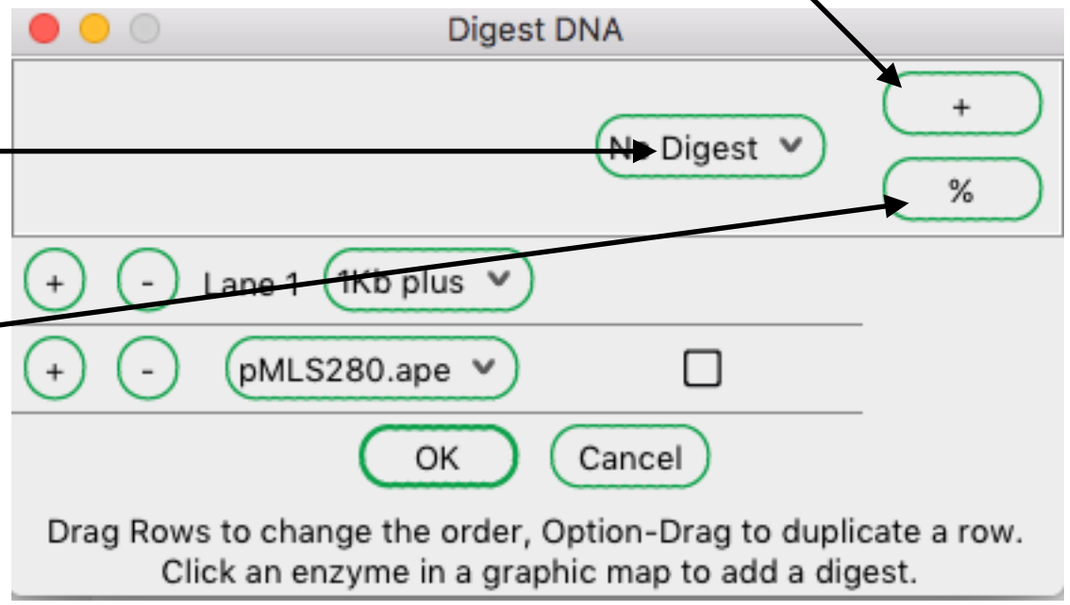


Digestion dialog

Add enzyme columns with this button

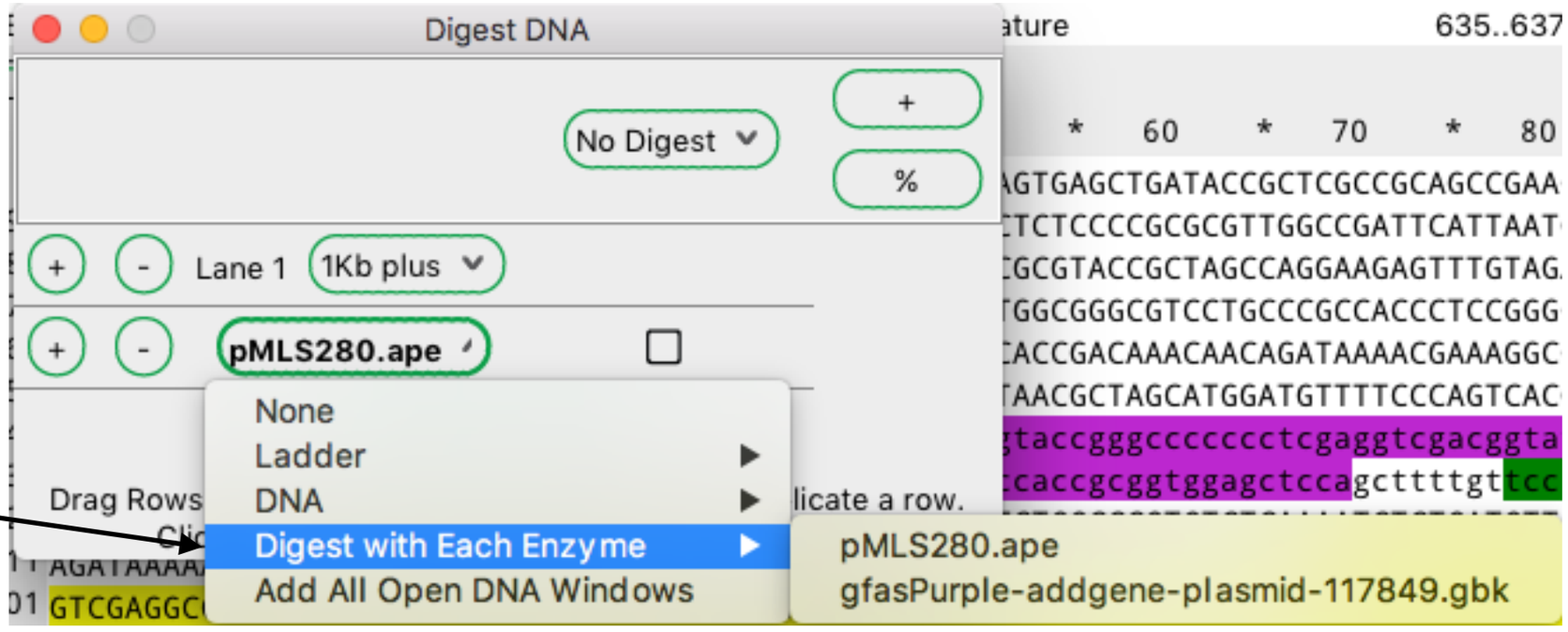
Enzymes for digestions are added here

Show partial digest options with this button



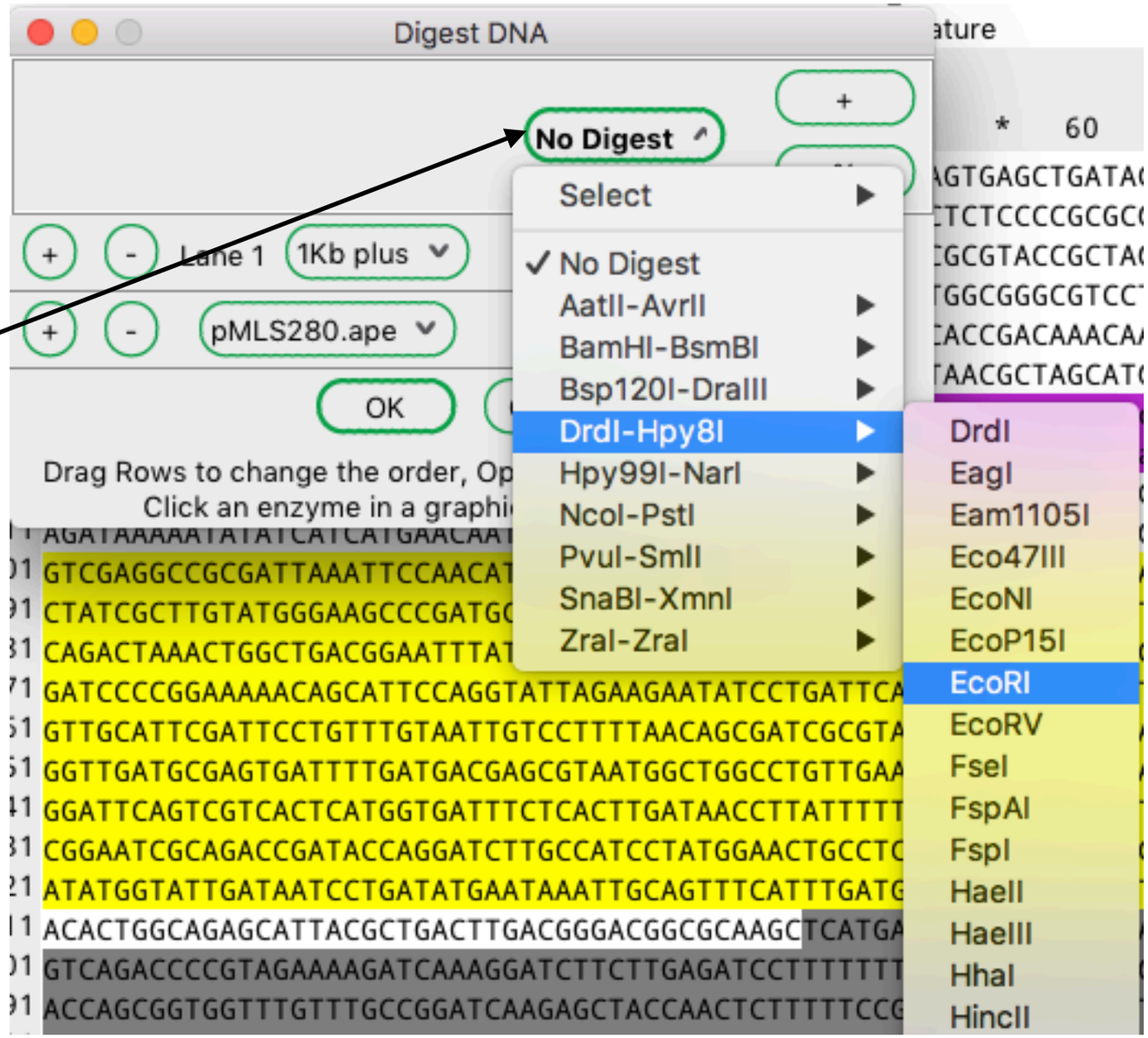
Digestion dialog

Change what is in the lane with this menu

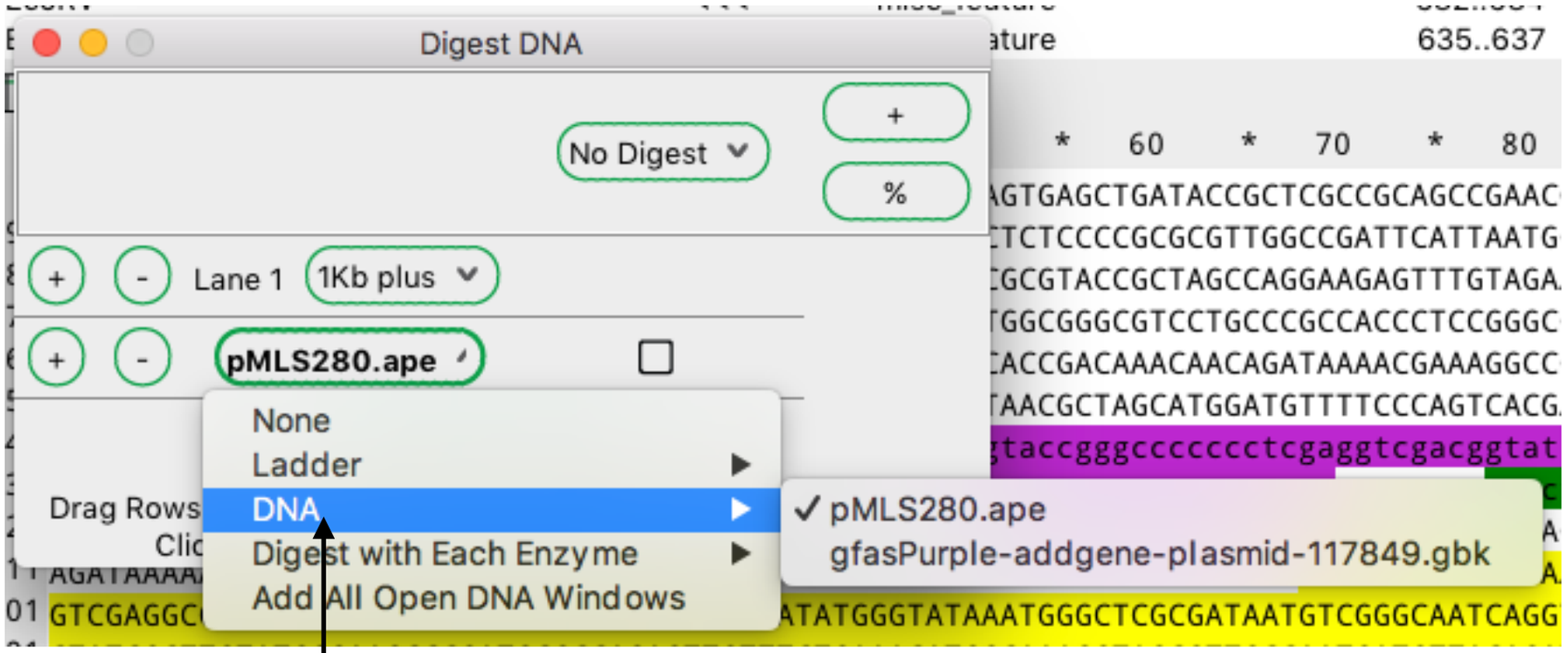


Digestion dialog

Change the enzyme with this menu

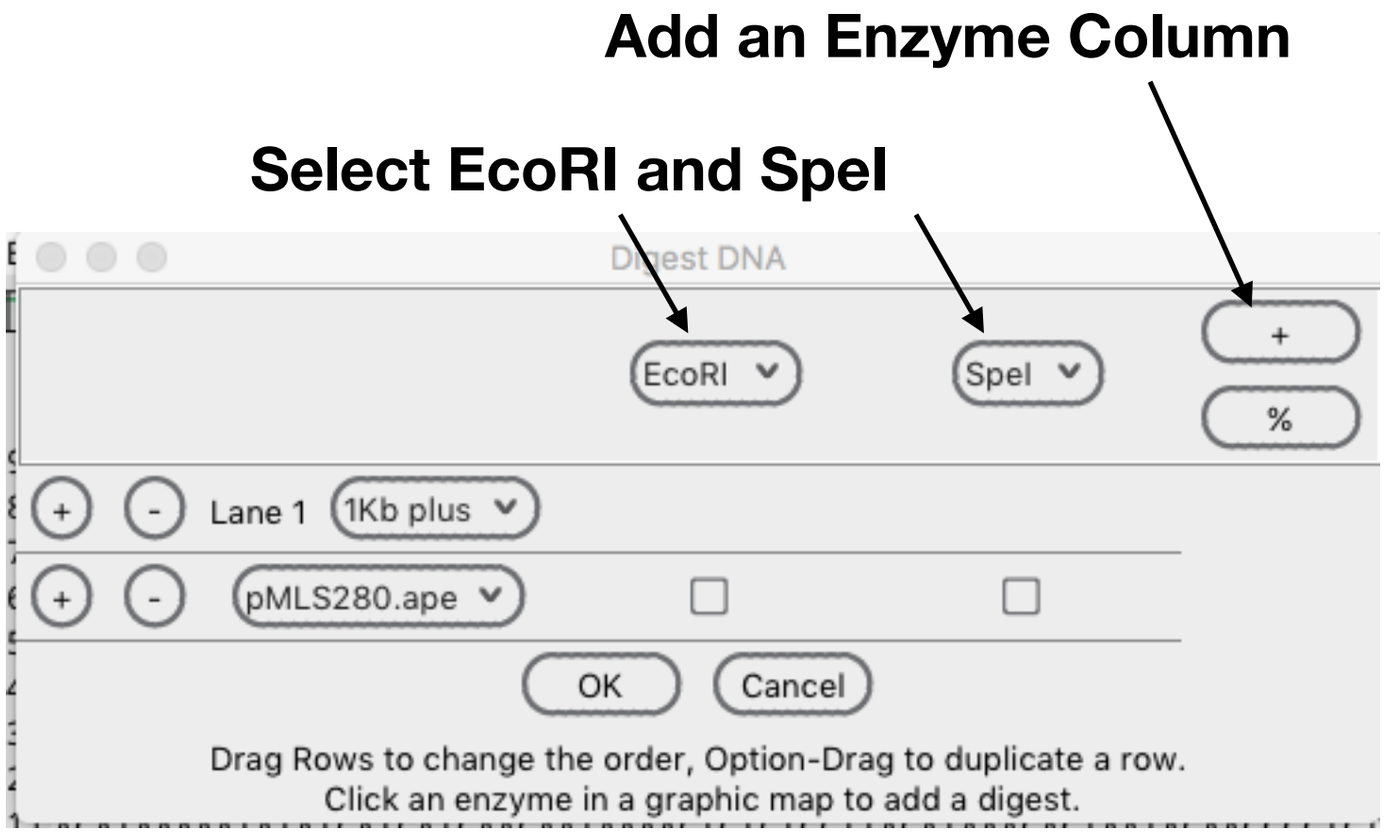


Digestion Dialog

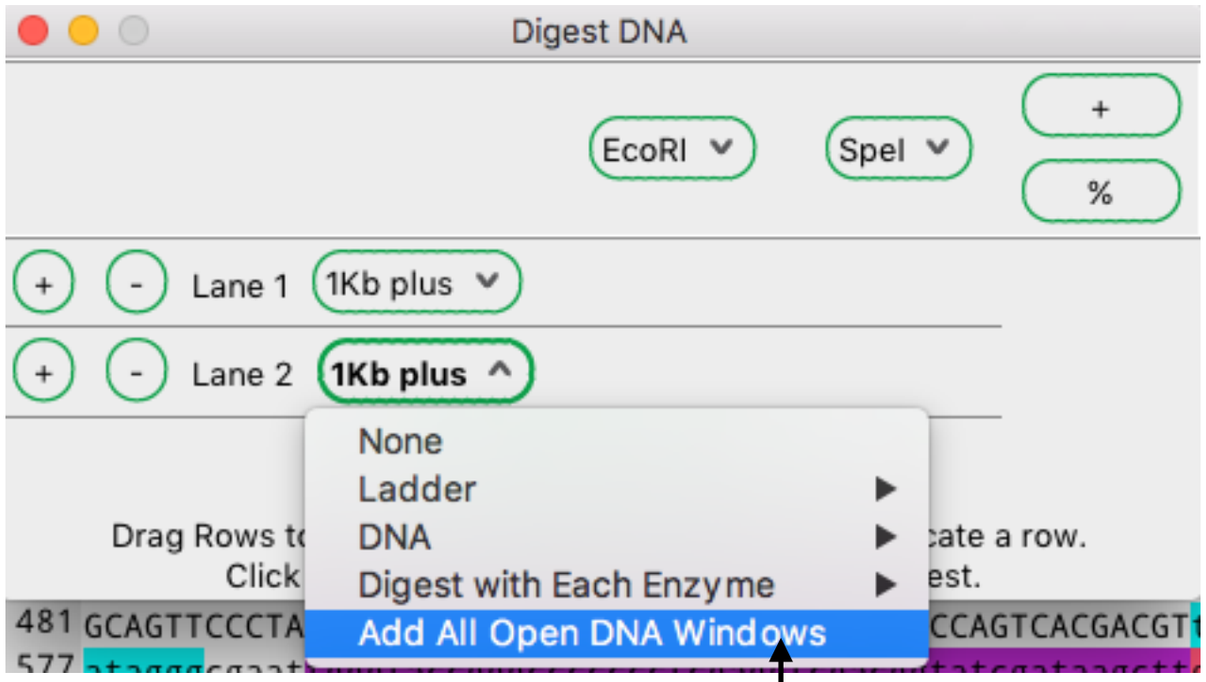


Select the DNA or ladder for each lane

Digestion Dialog

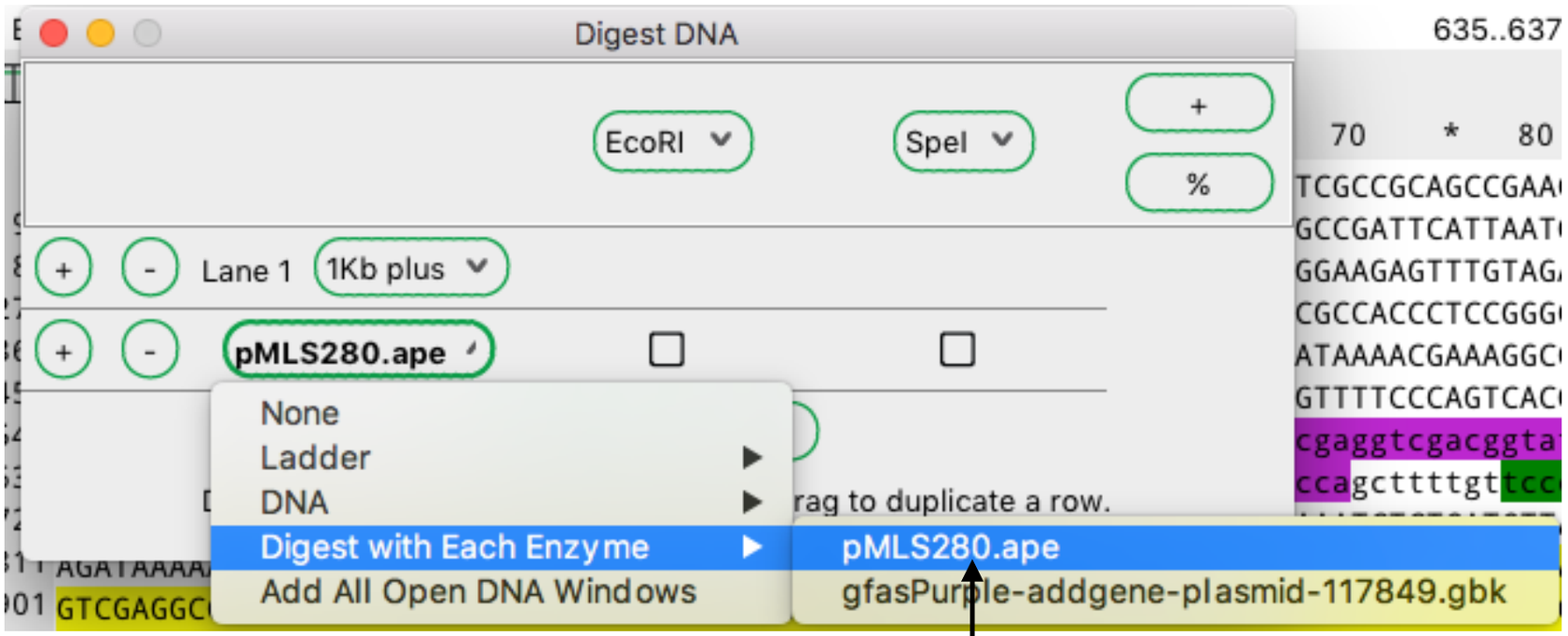


Digestion Dialog



You can also just create a set of new lanes with each open DNA

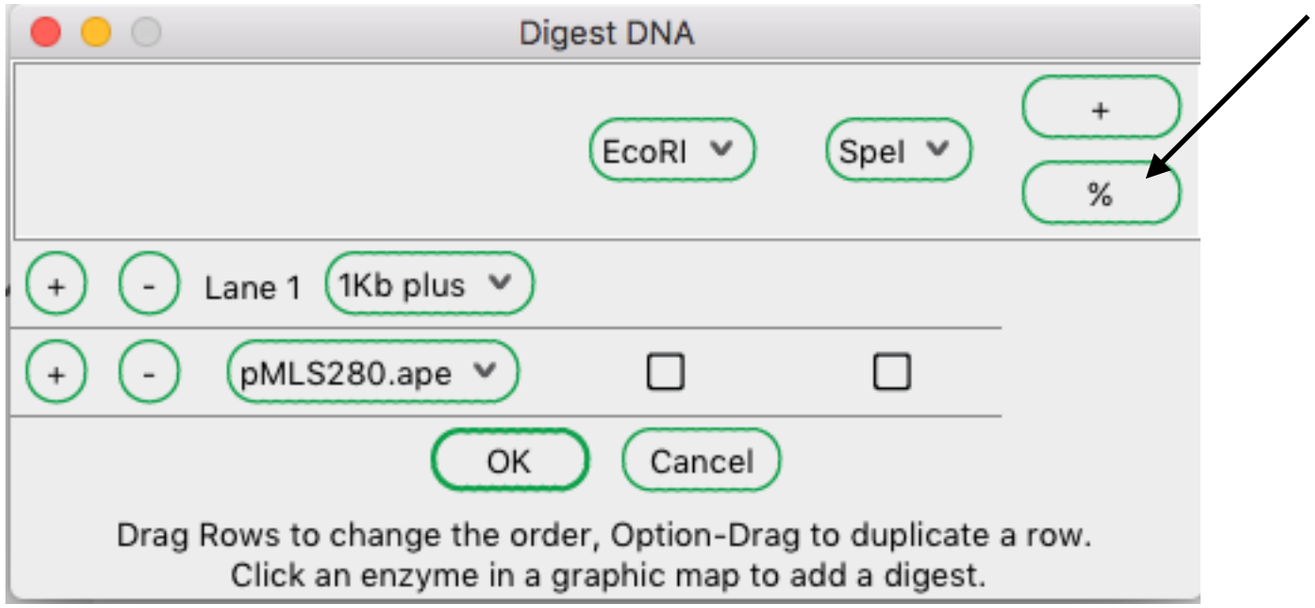
Digestion Dialog



For convenience, you can digest a single DNA with all current enzymes

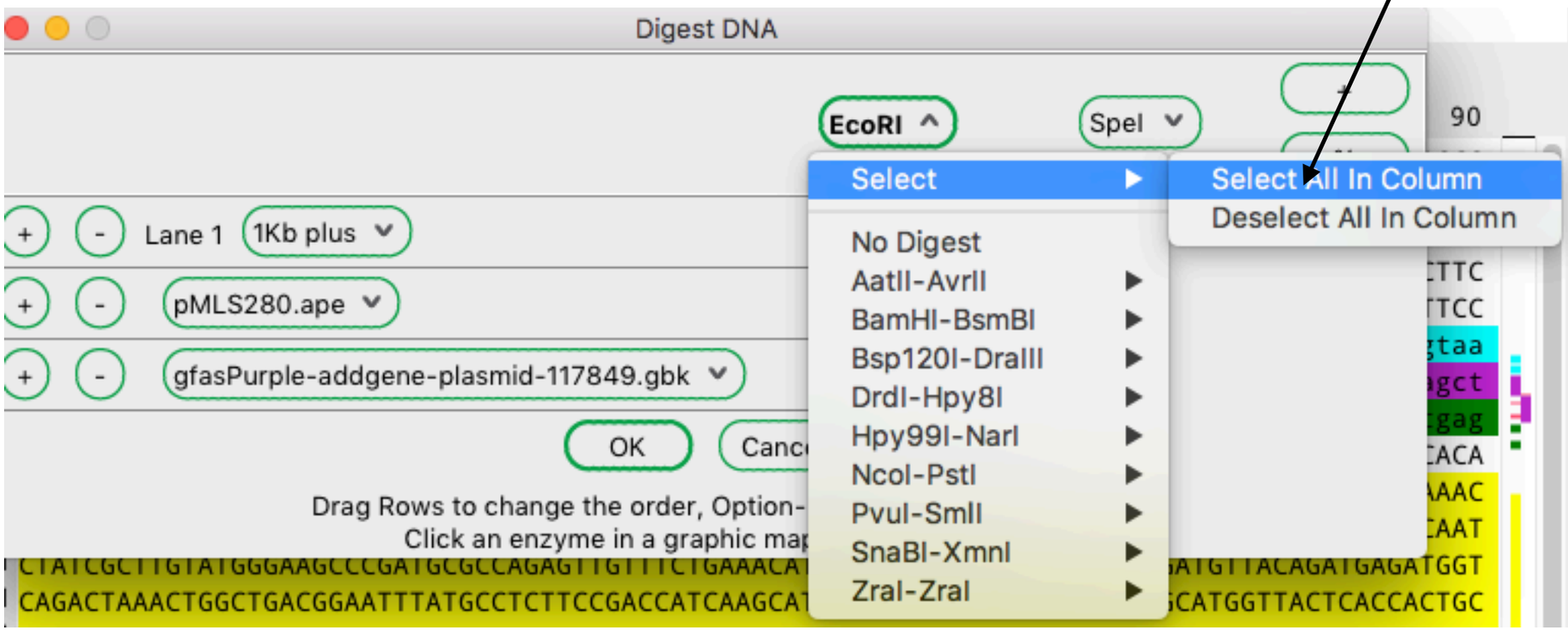
Digestion Dialog

Press this to do partial digests

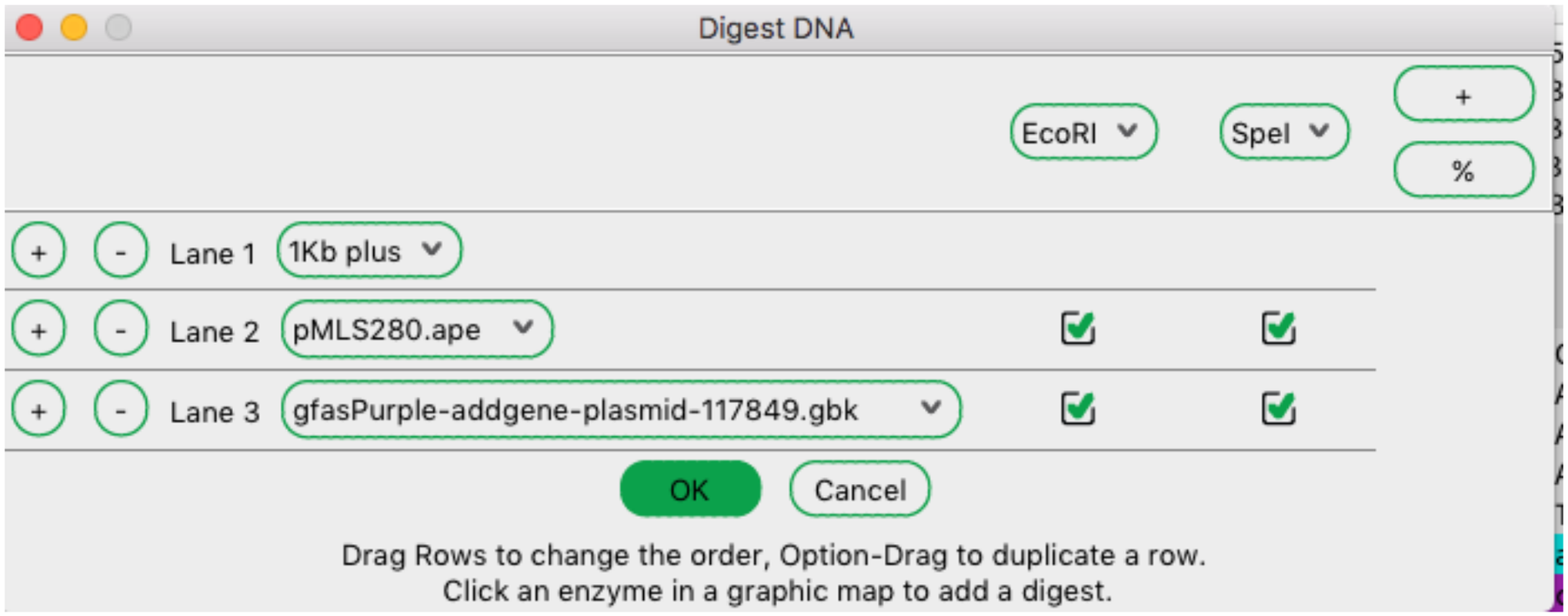


Digestion Dialog

Press this to select EcoRI in all columns

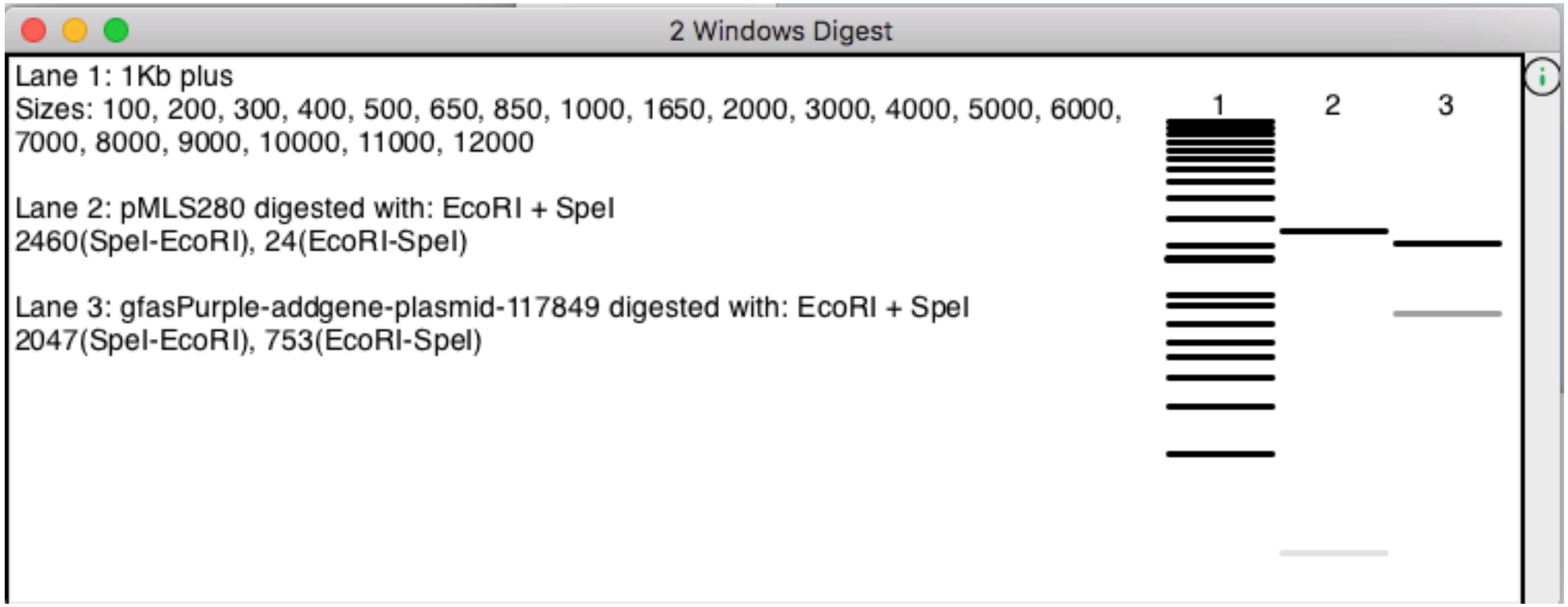


Digestion Dialog



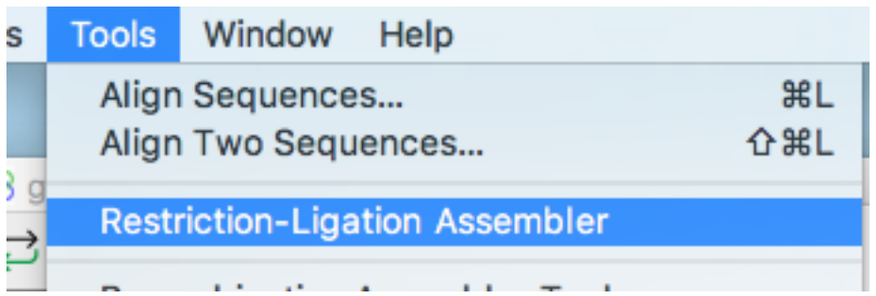
This will digest pMLS280 and gfasPurple with EcoRI and SpeI

Digestion Dialog

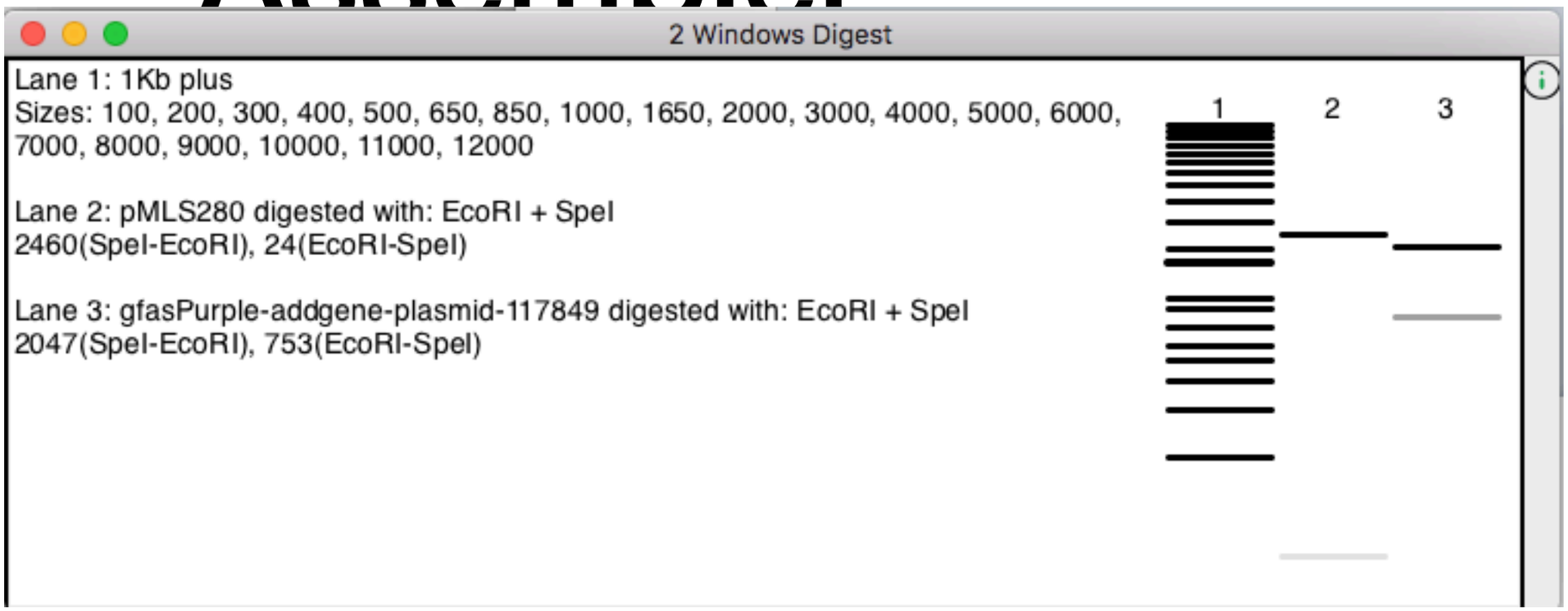


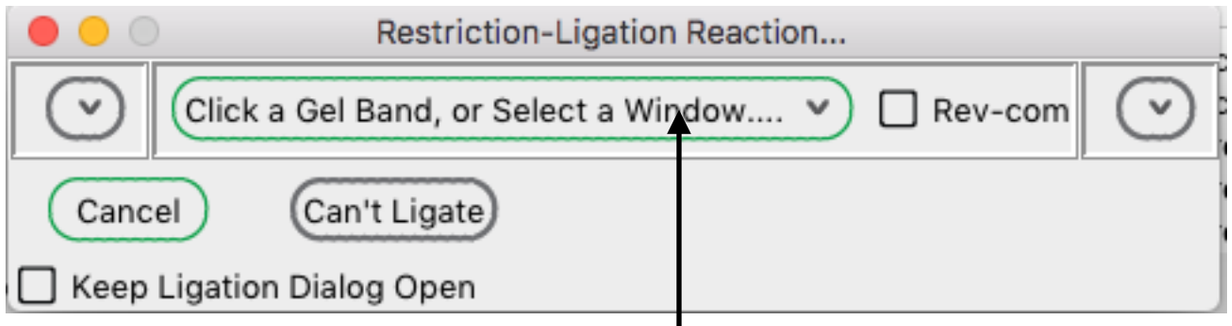
This will digest pMLS280 and gfasPurple with EcoRI and SpeI

Restriction-Ligation Assembler



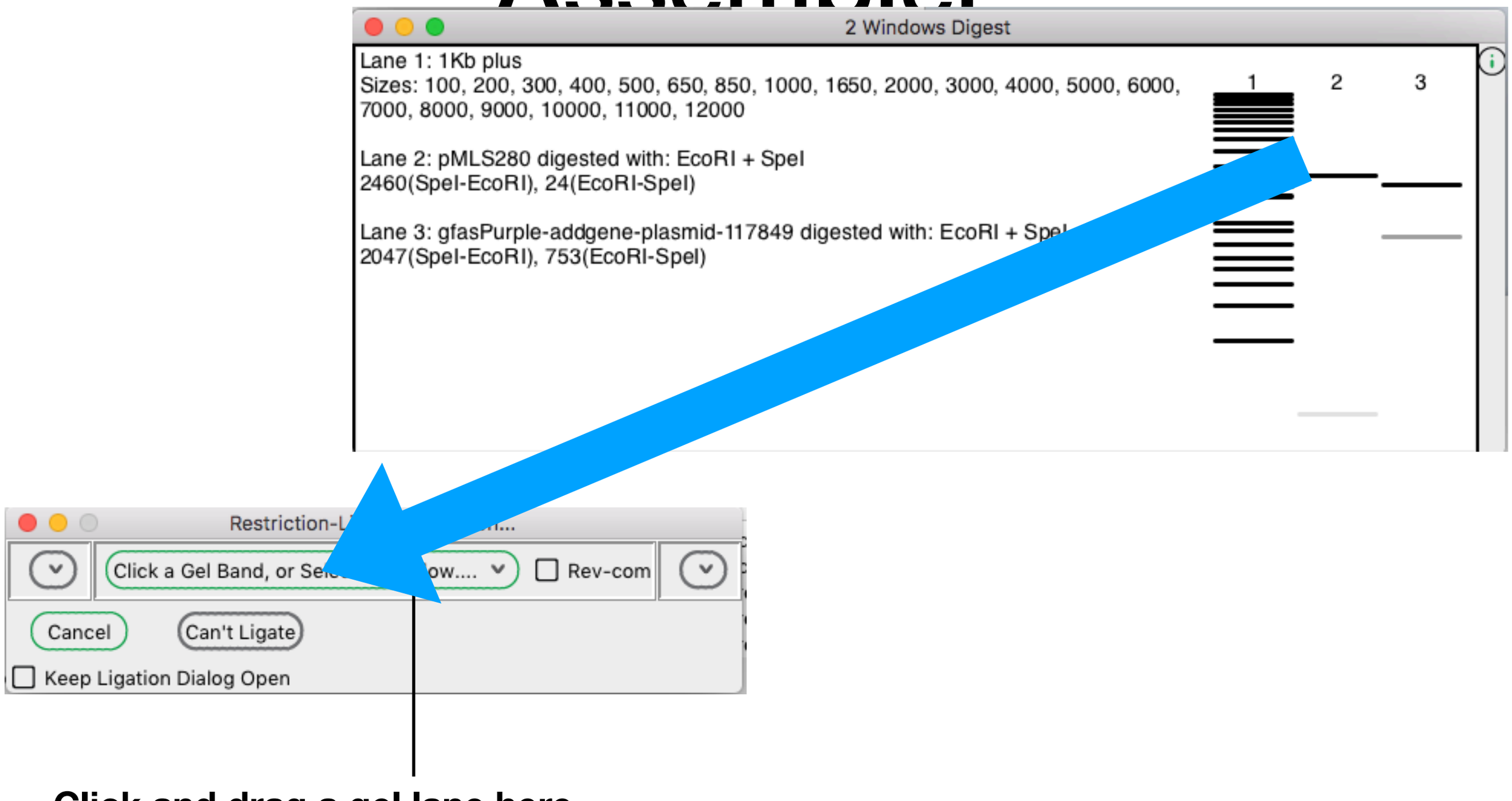
Restriction-Ligation Assembler





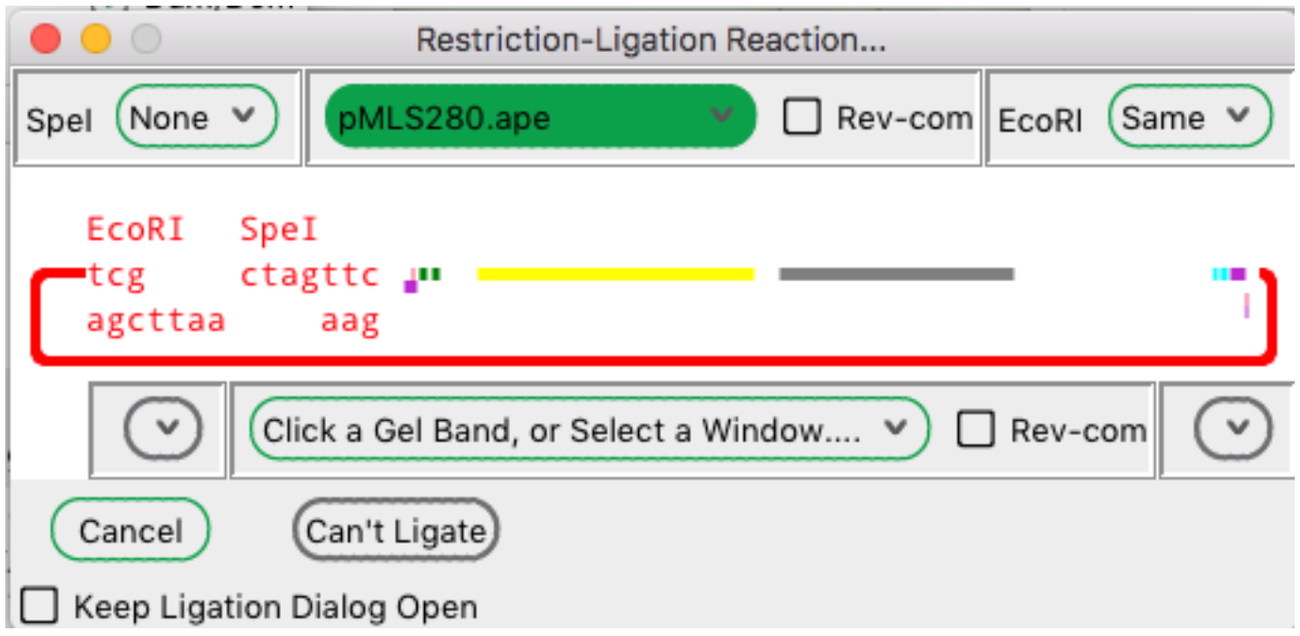
Click and drag a gel lane here

Restriction-Ligation Assembler

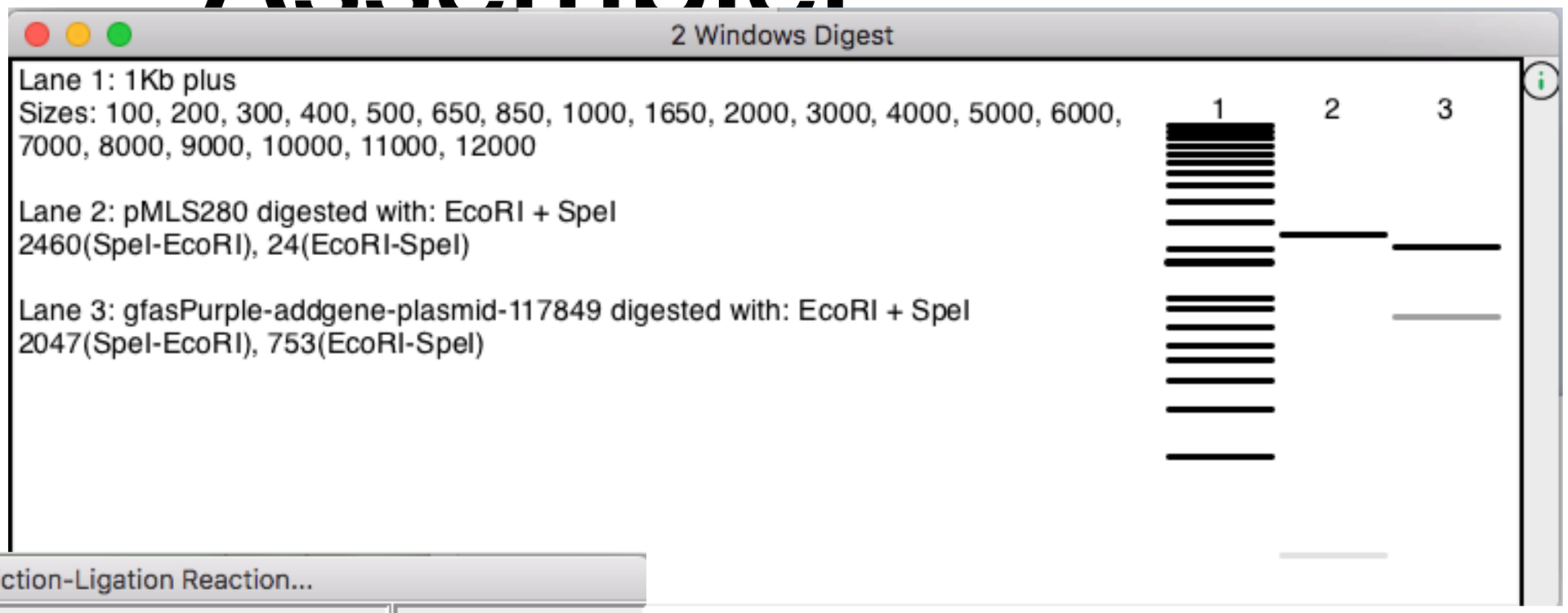


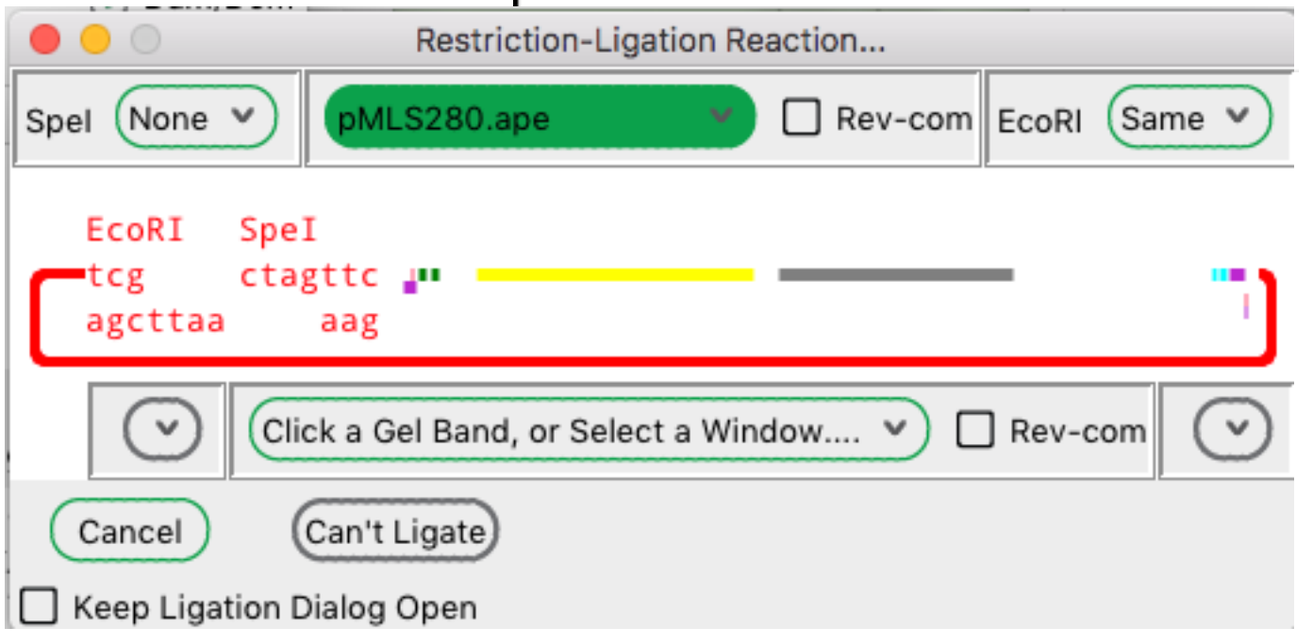
Click and drag a gel lane here

Restriction-Ligation Assembler

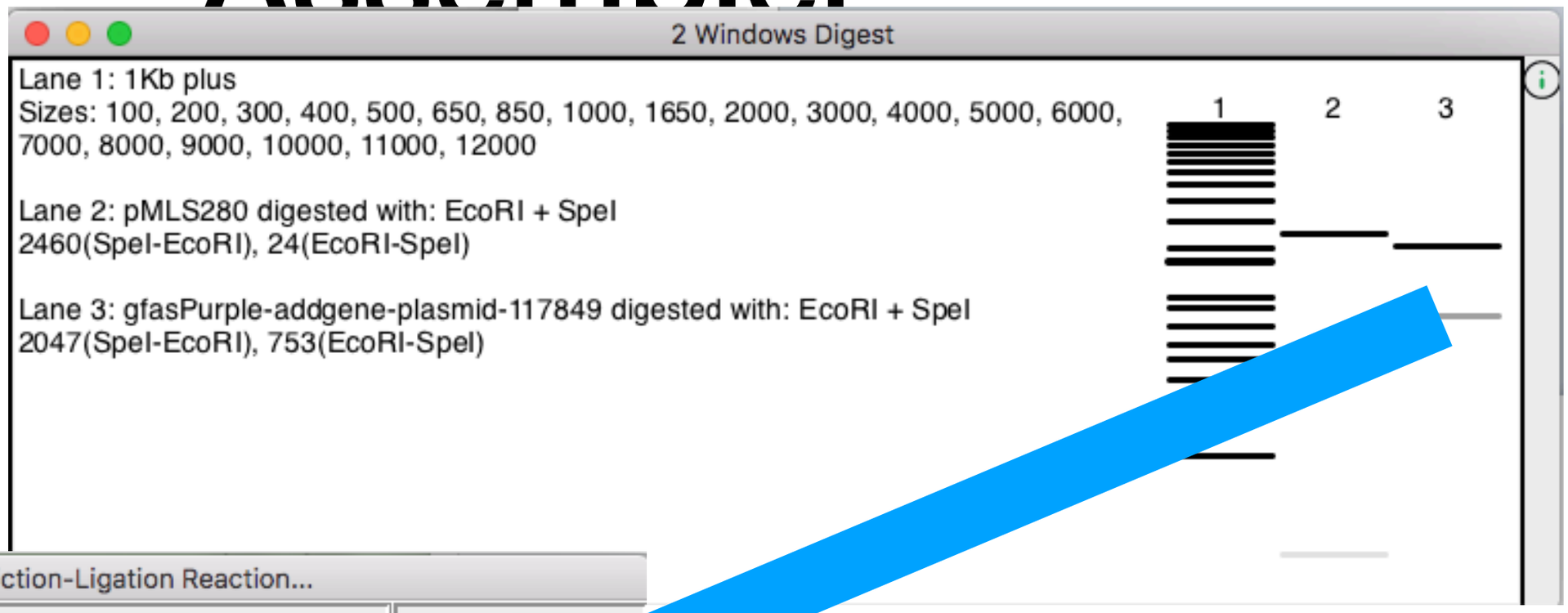


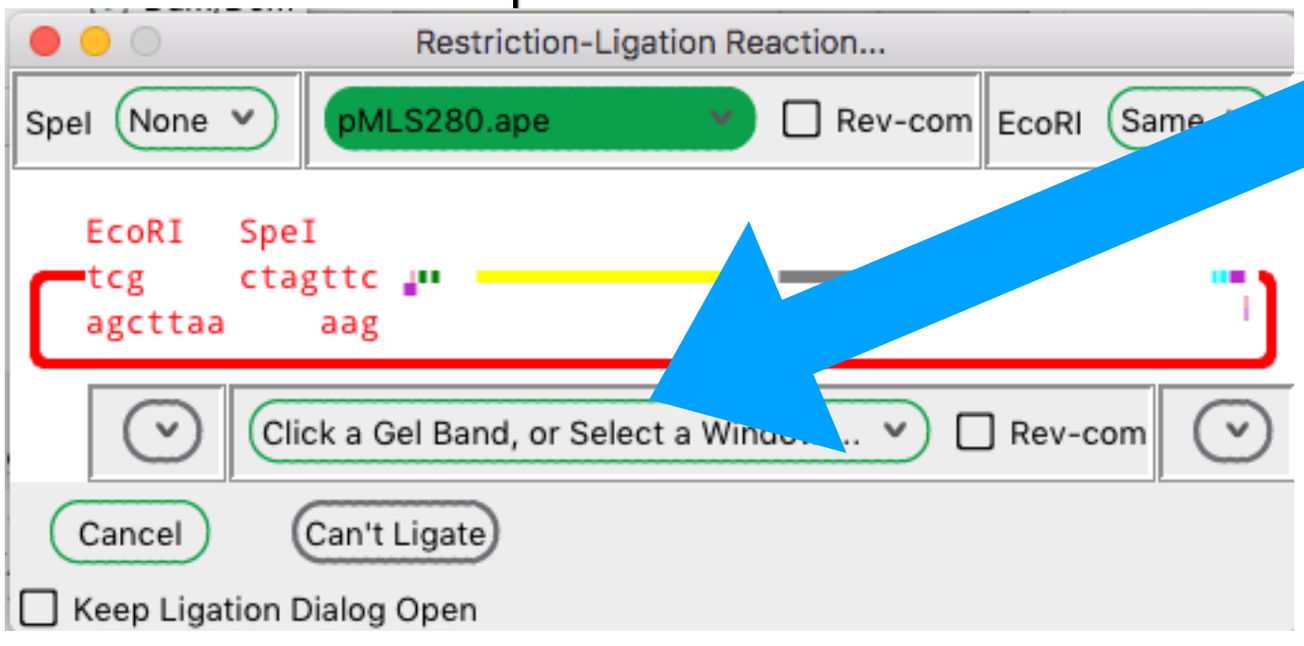
Restriction-Ligation Assembler





Restriction-Ligation Assembler

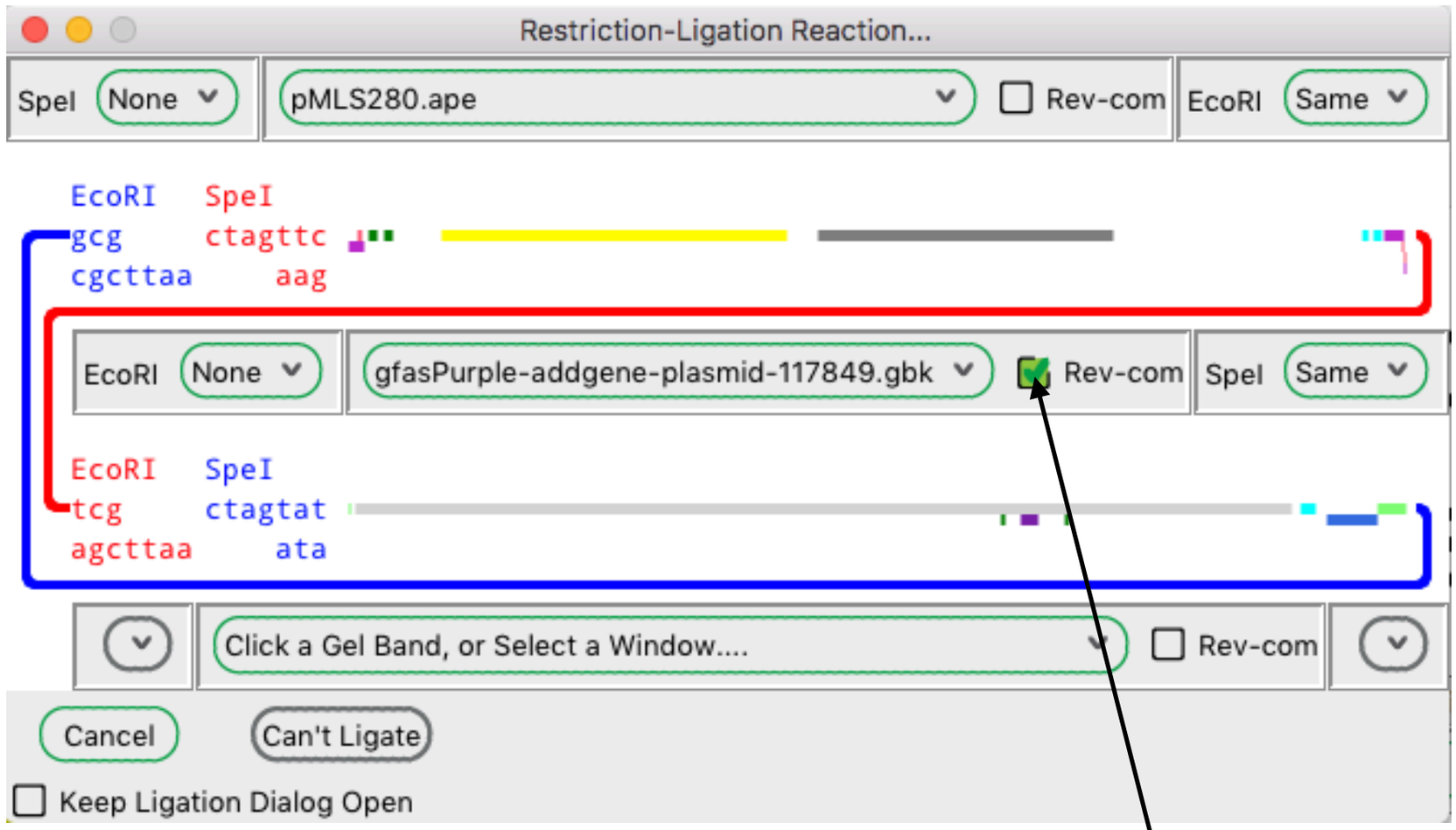




Restriction-Ligation Assembler

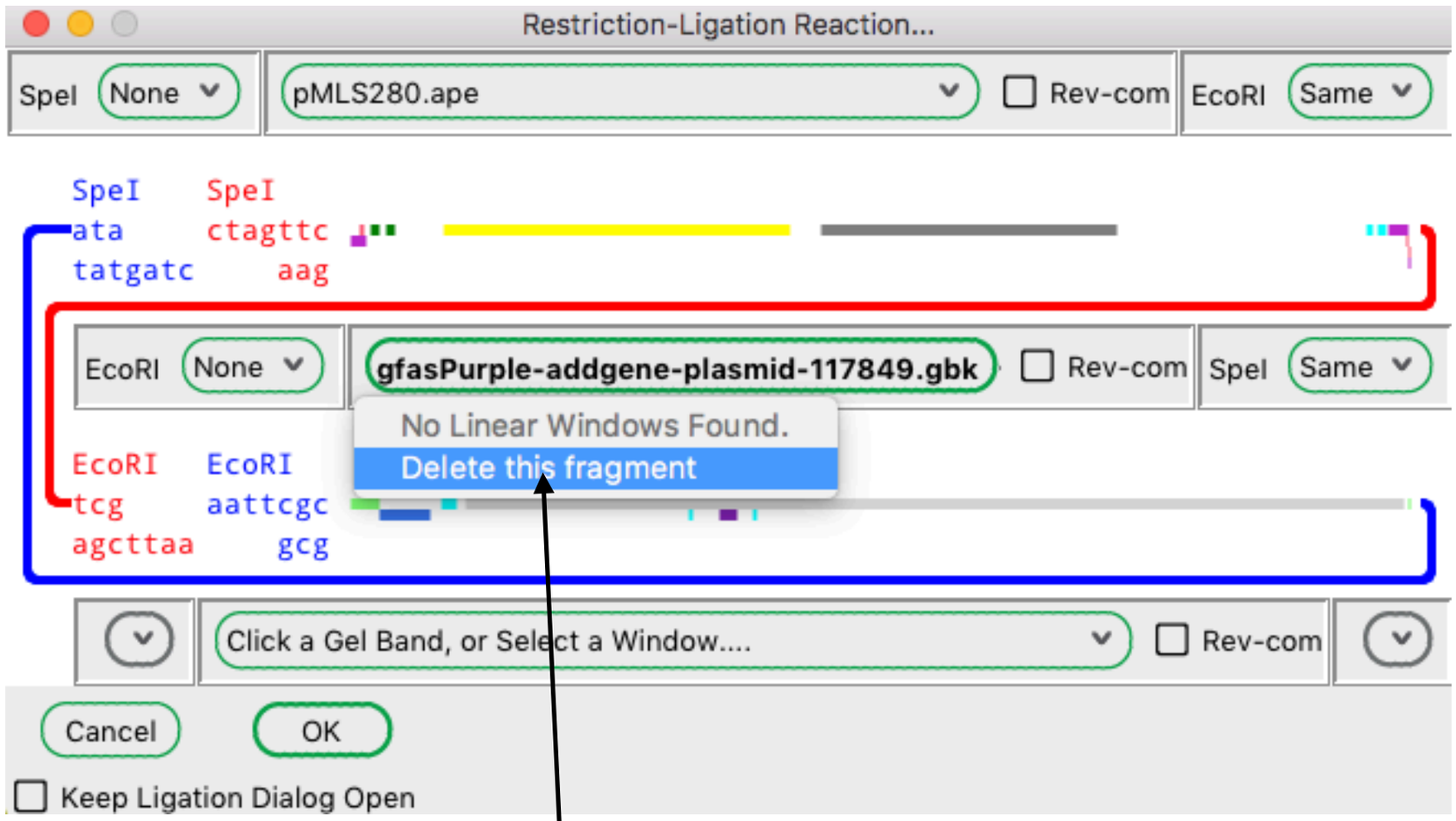
mouse here to see the feature names

Restriction-Ligation Assembler



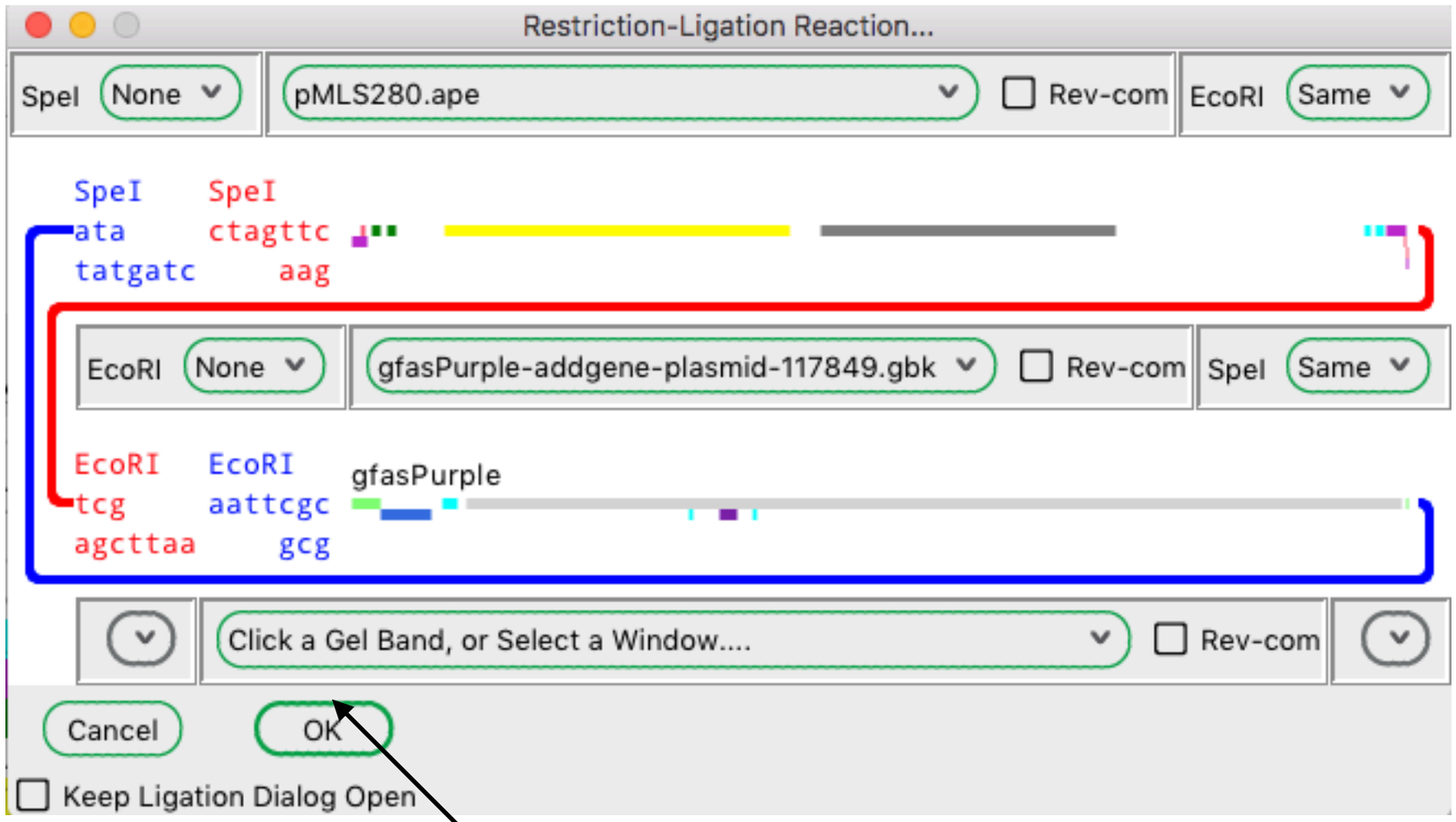
click here to flip a fragment

Restriction-Ligation Assembler



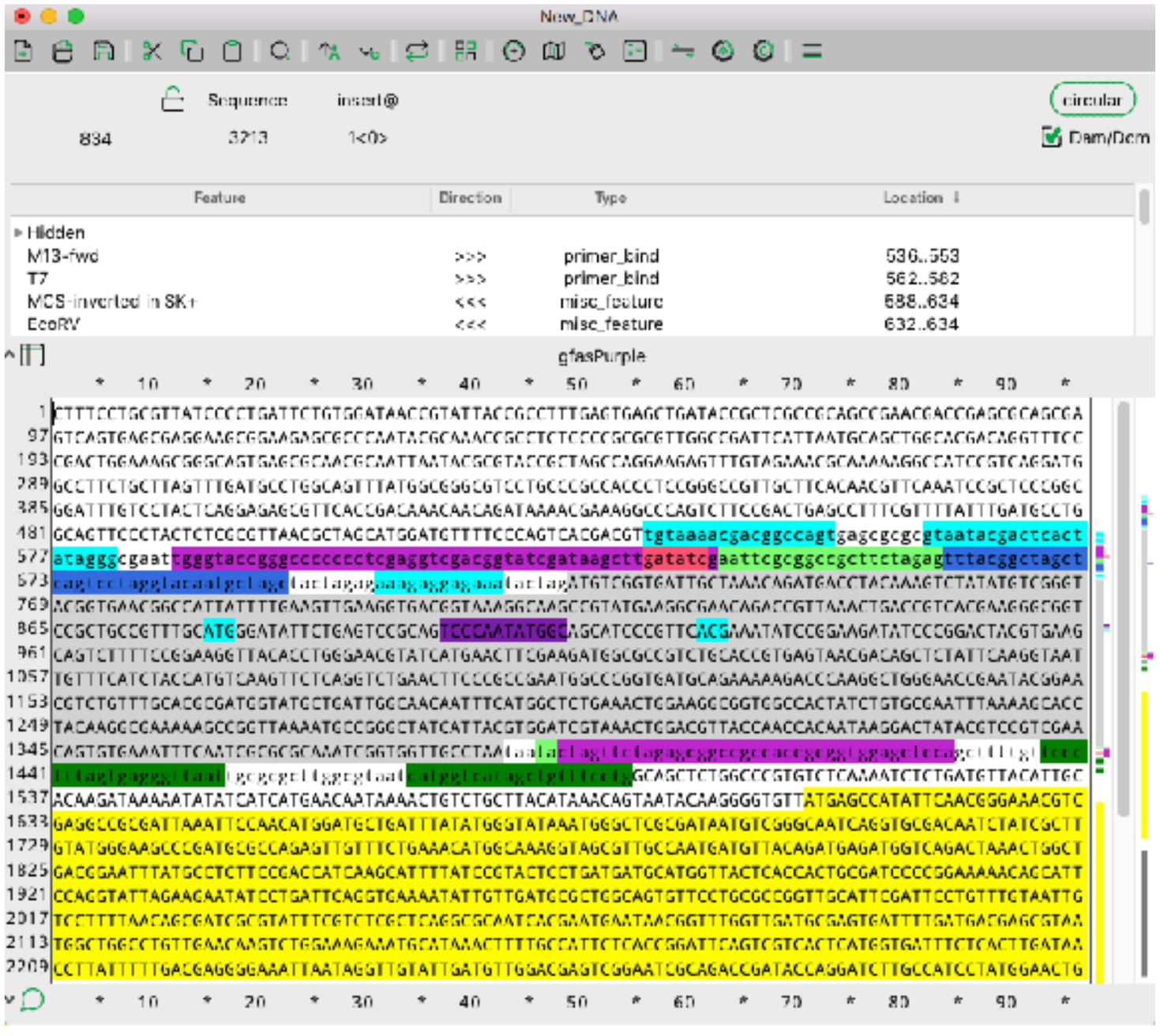
click here to delete a fragment

Restriction-Ligation Assembler

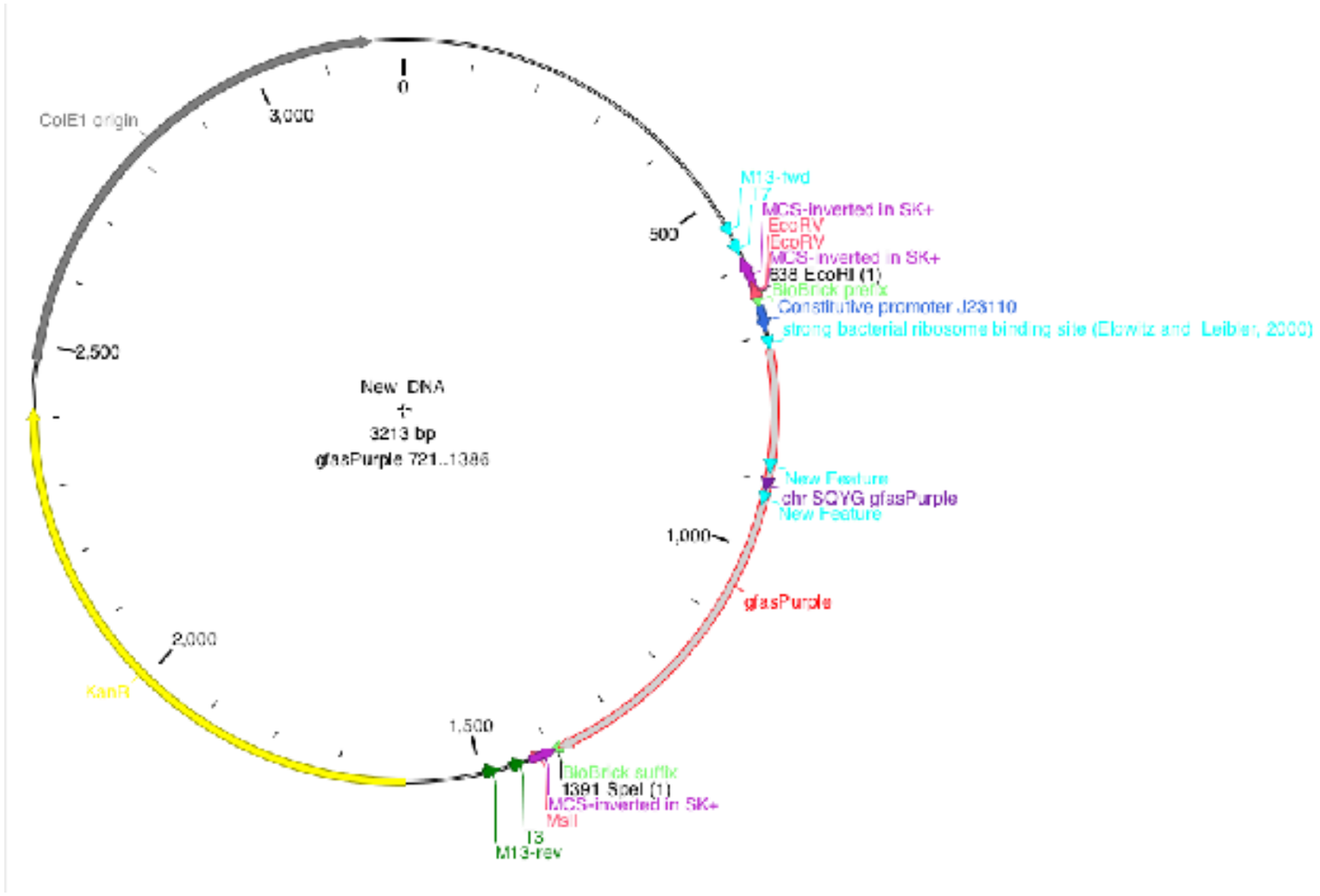


When everything works, you can click OK

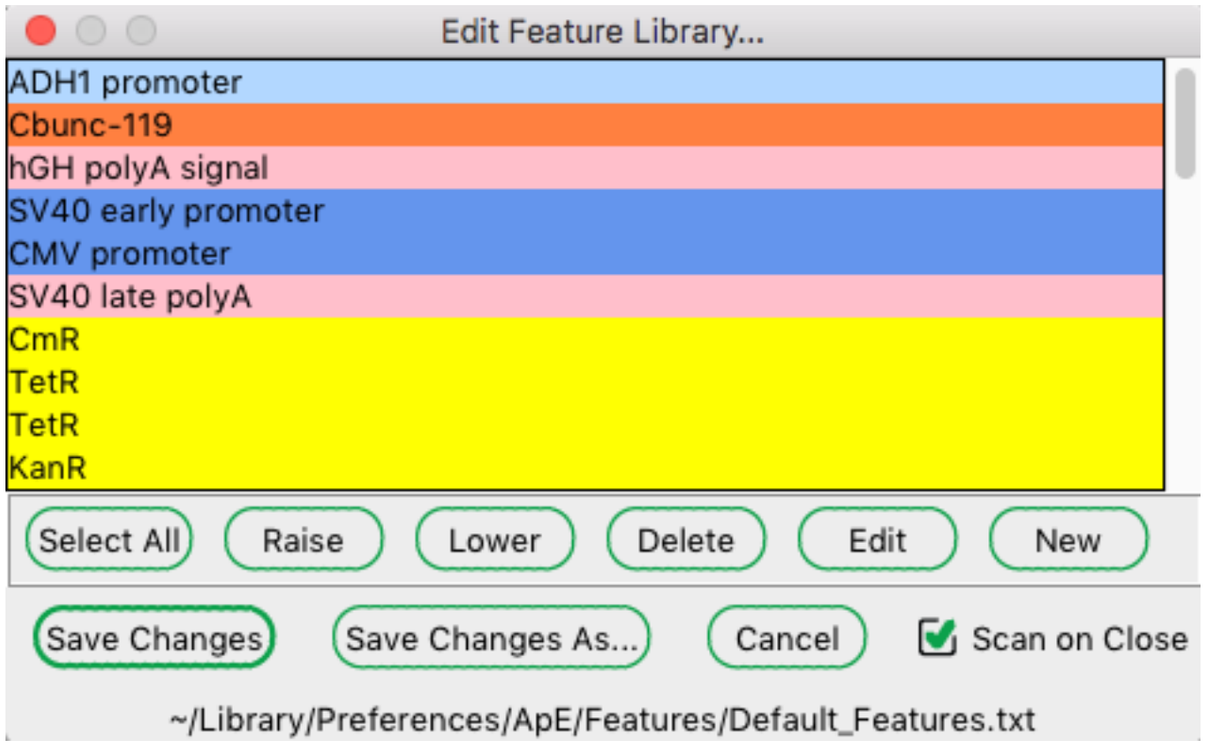
Restriction-Ligation Assembler



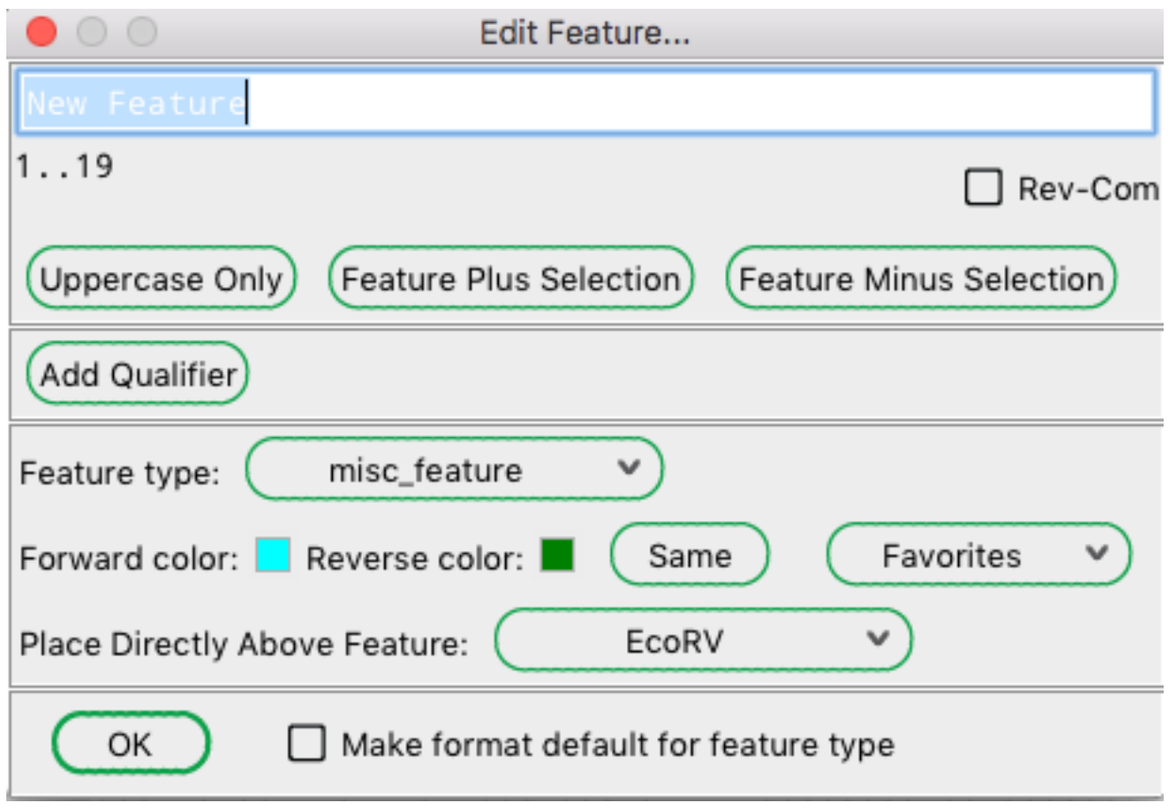
Restriction-Ligation Assembler



Feature library

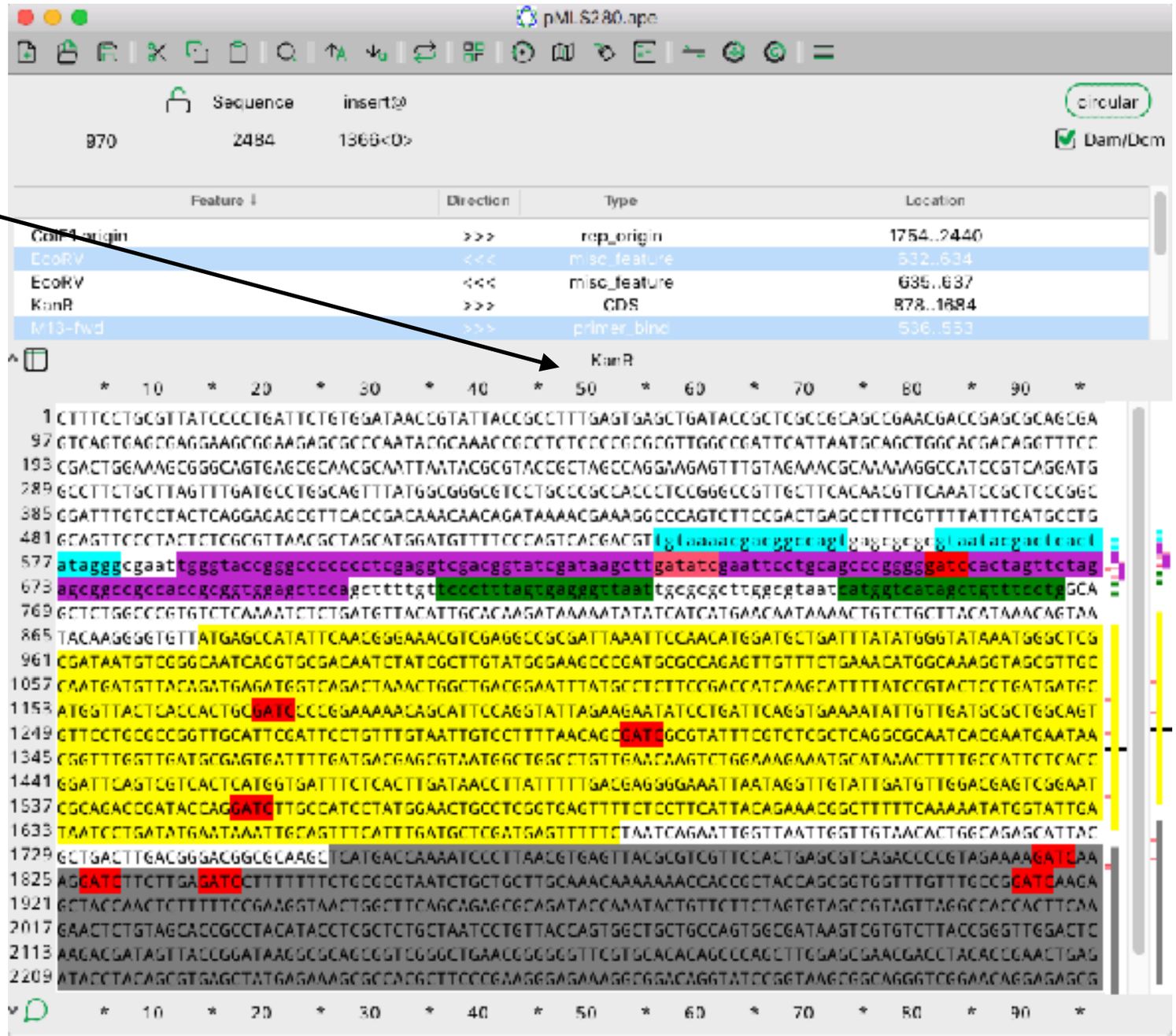


New Feature


Edit Feature...
New Feature
1..19
Rev-Com
Uppercase Only
Feature Plus Selection
Feature Minus Selection
Add Qualifier
Feature type:
misc_feature
Forward color:
Reverse color:
Same
Favorites
Place Directly Above Feature:
EcoRV
OK
Make format default for feature type

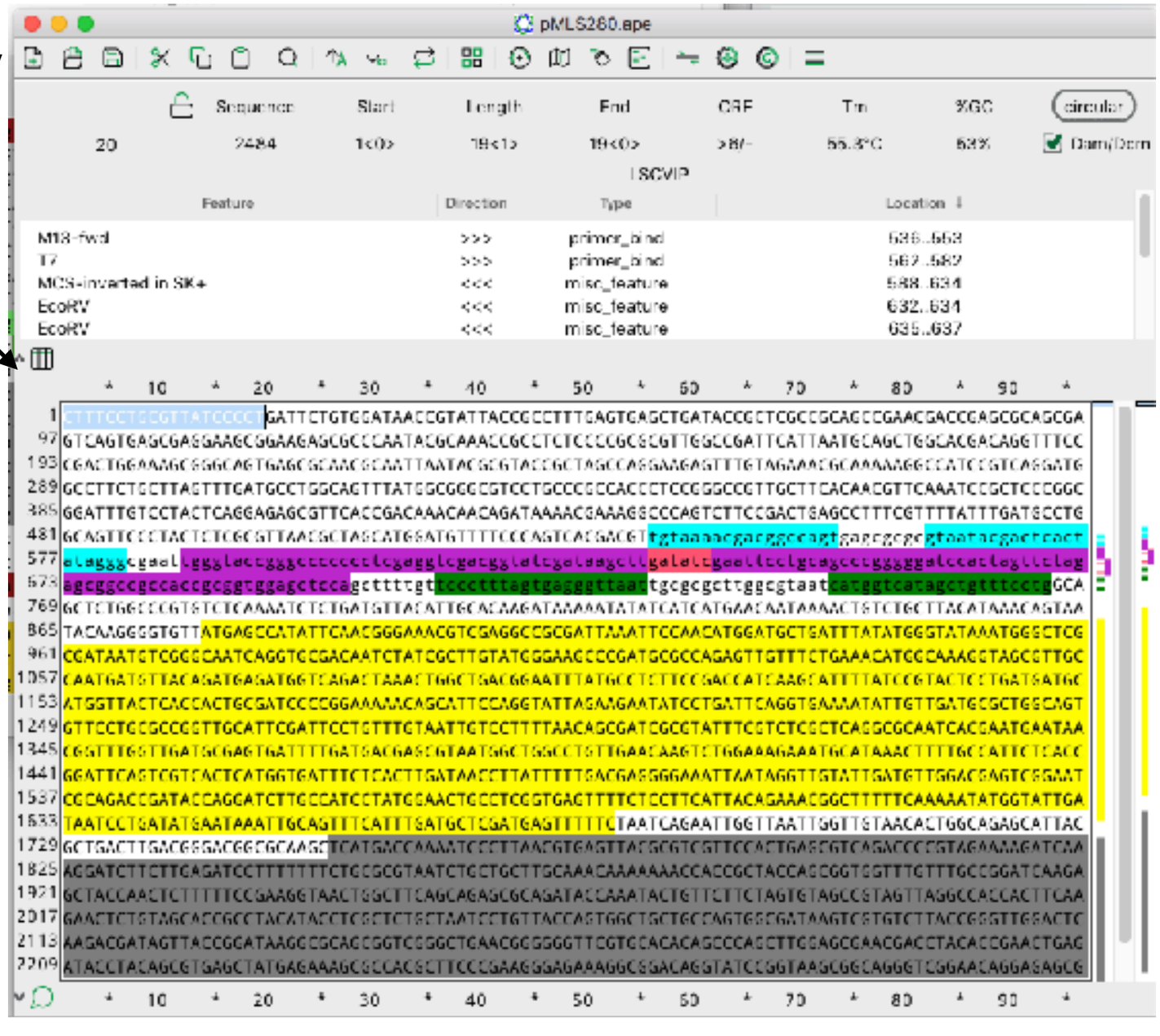
Features

Current features under the mouse pointer are listed here



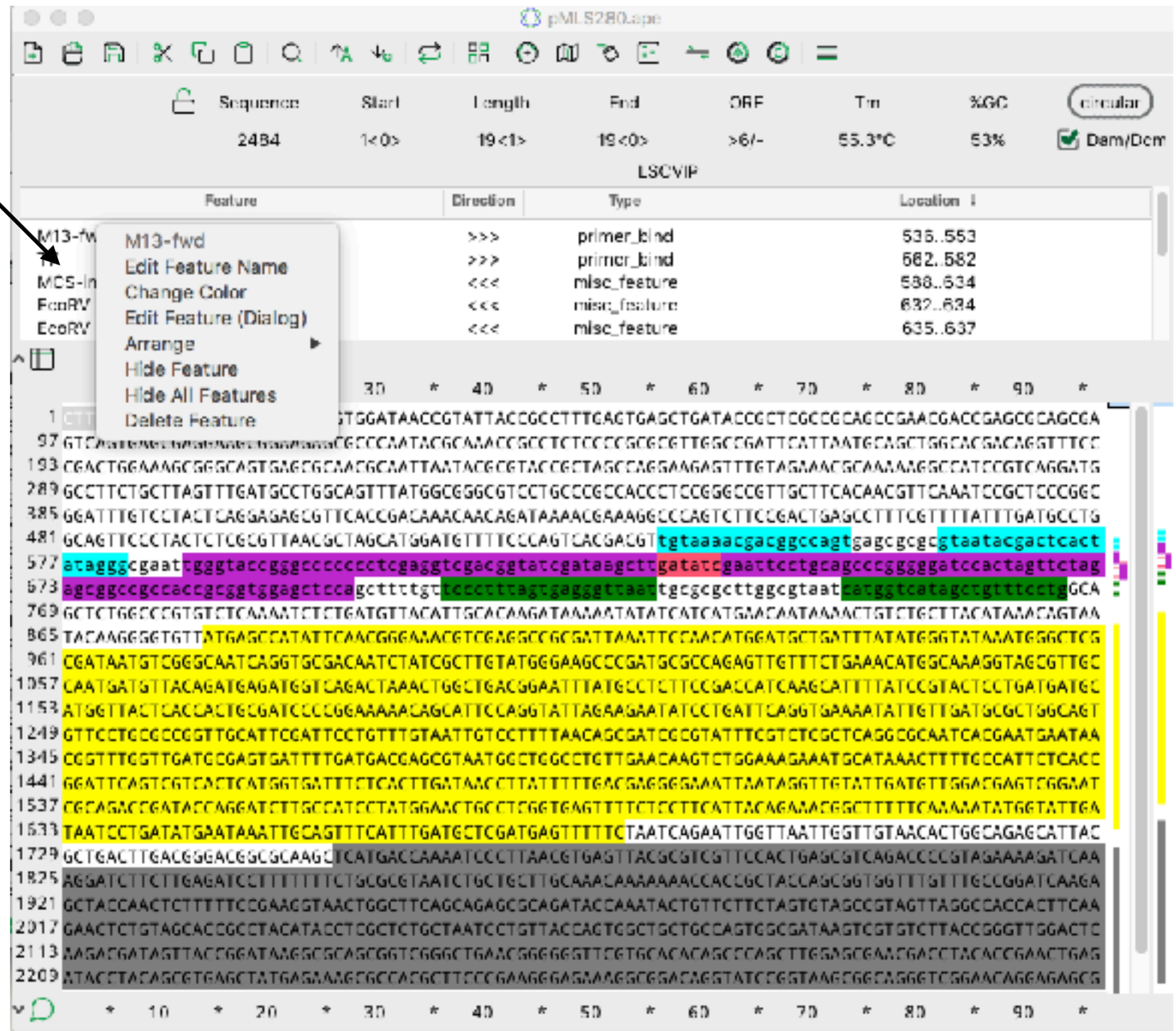
Features

Click this to hide/ show the feature table



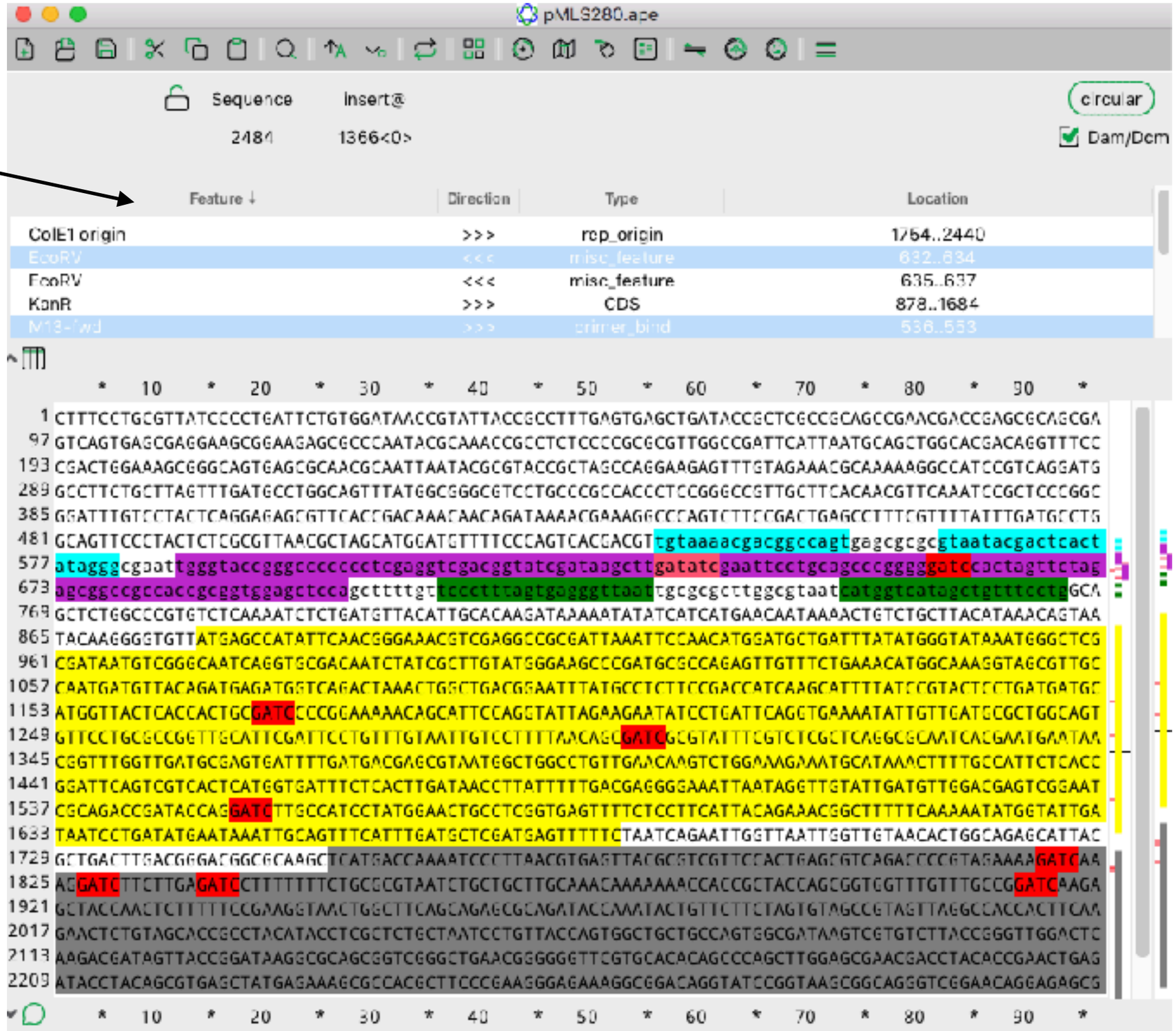
Features

Right-click here to edit a feature



Features

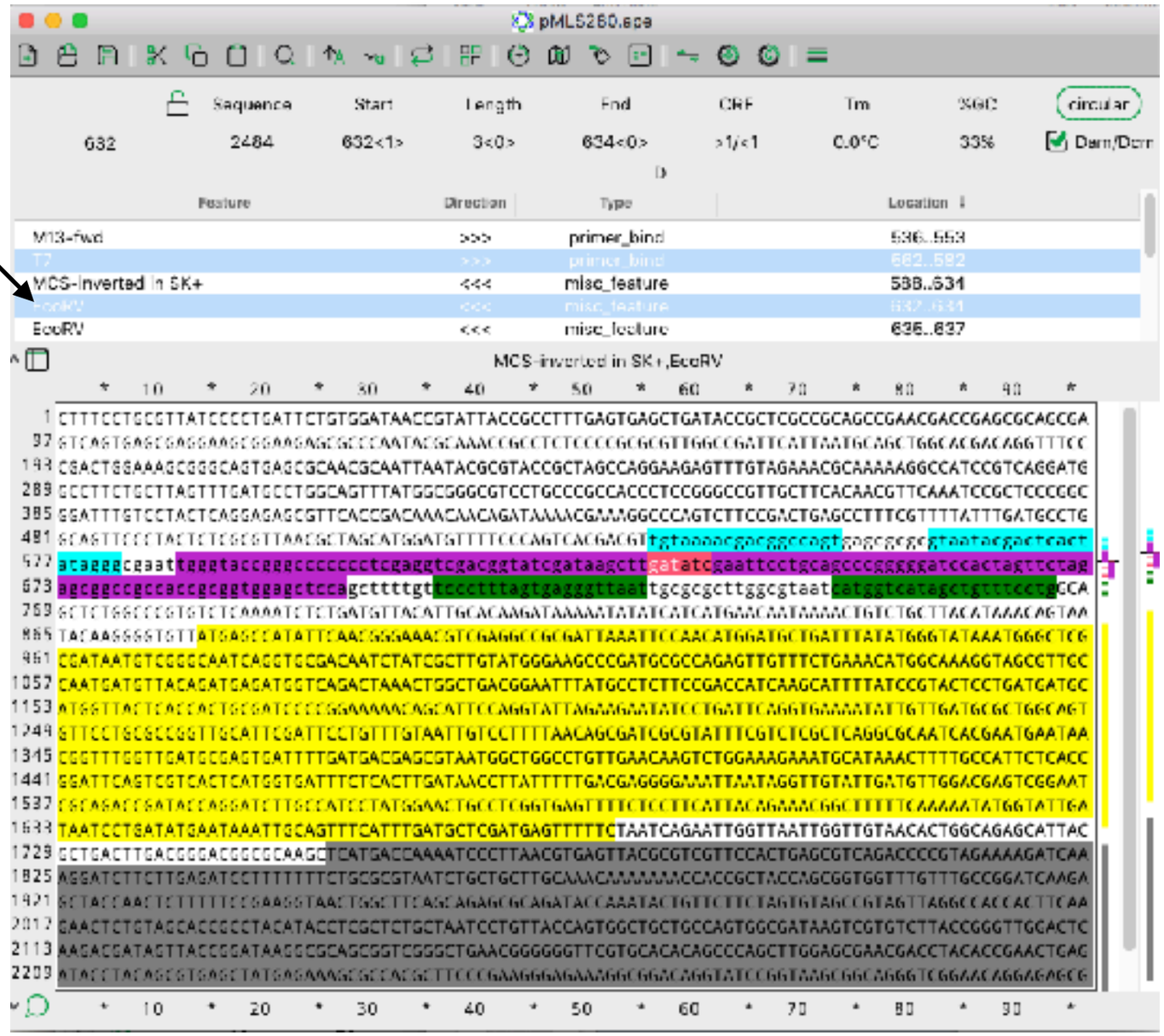
Click this to sort the feature table



Features

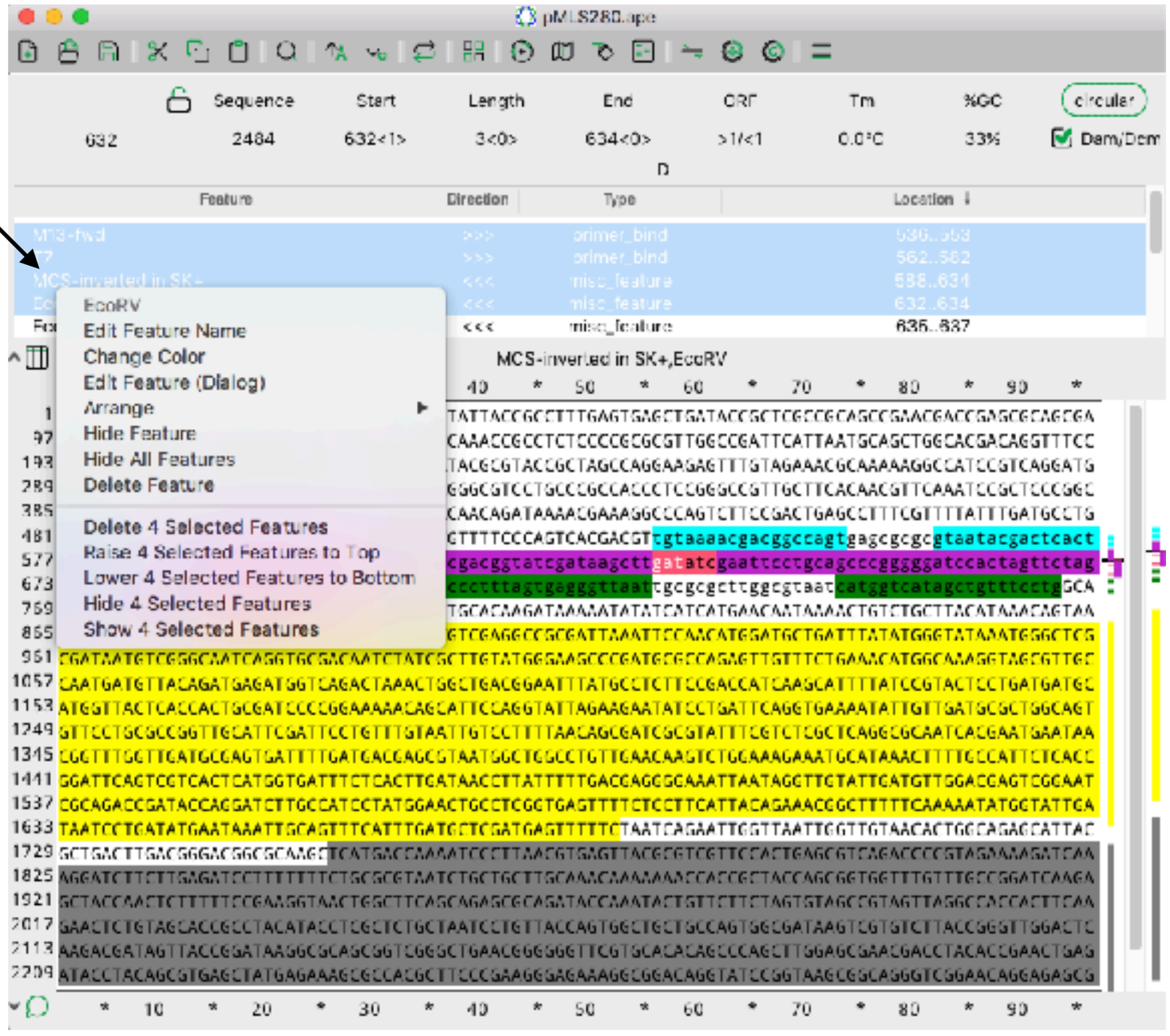
Command-click here to select multiple features

Shift-click here to select a range of features



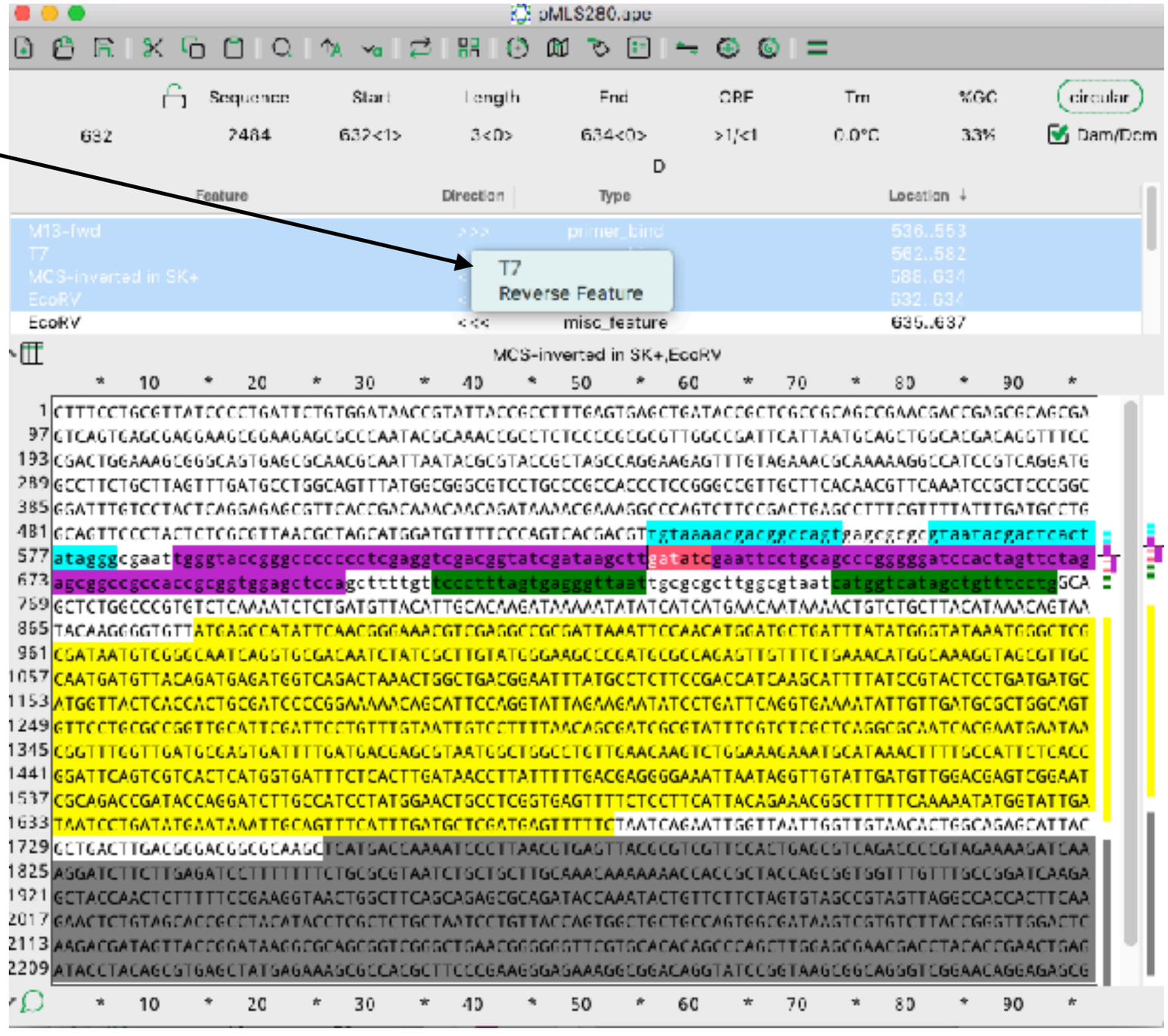
Features

Right-click here to edit a range of features



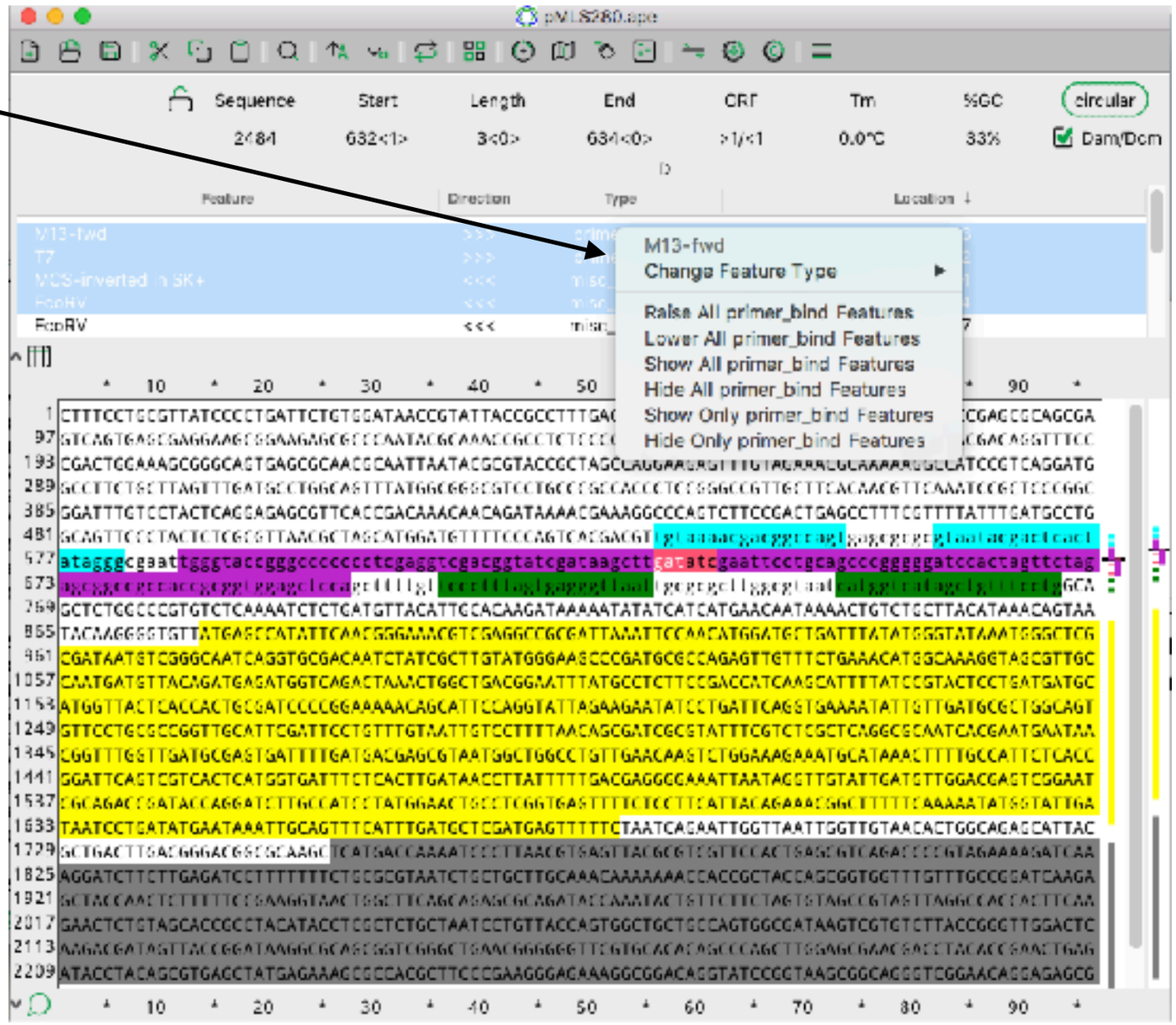
Features

Right-click here to edit a feature's direction

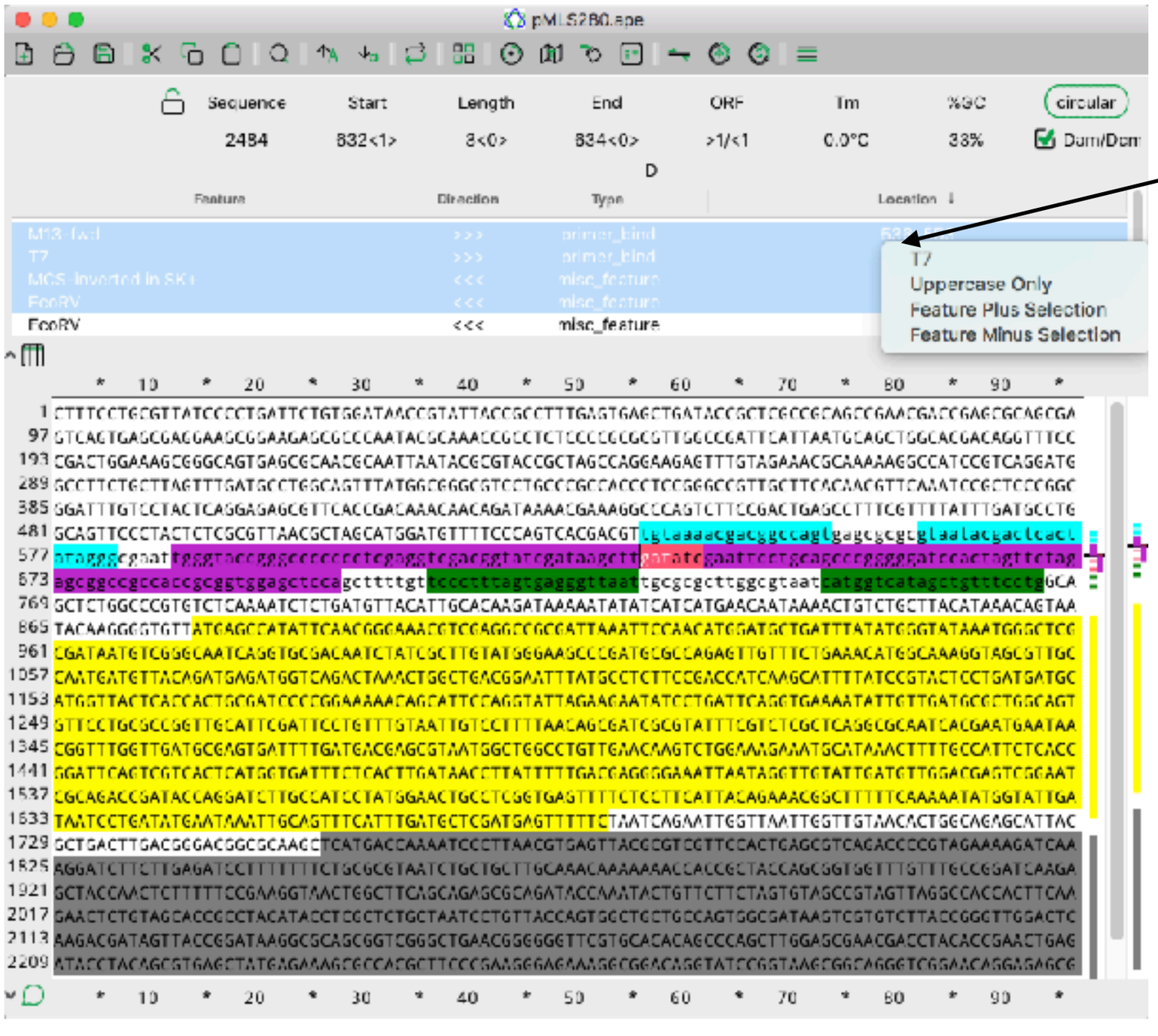


Features

Right-click here to edit a feature's type, or to raise, lower or hide all of a type of feature



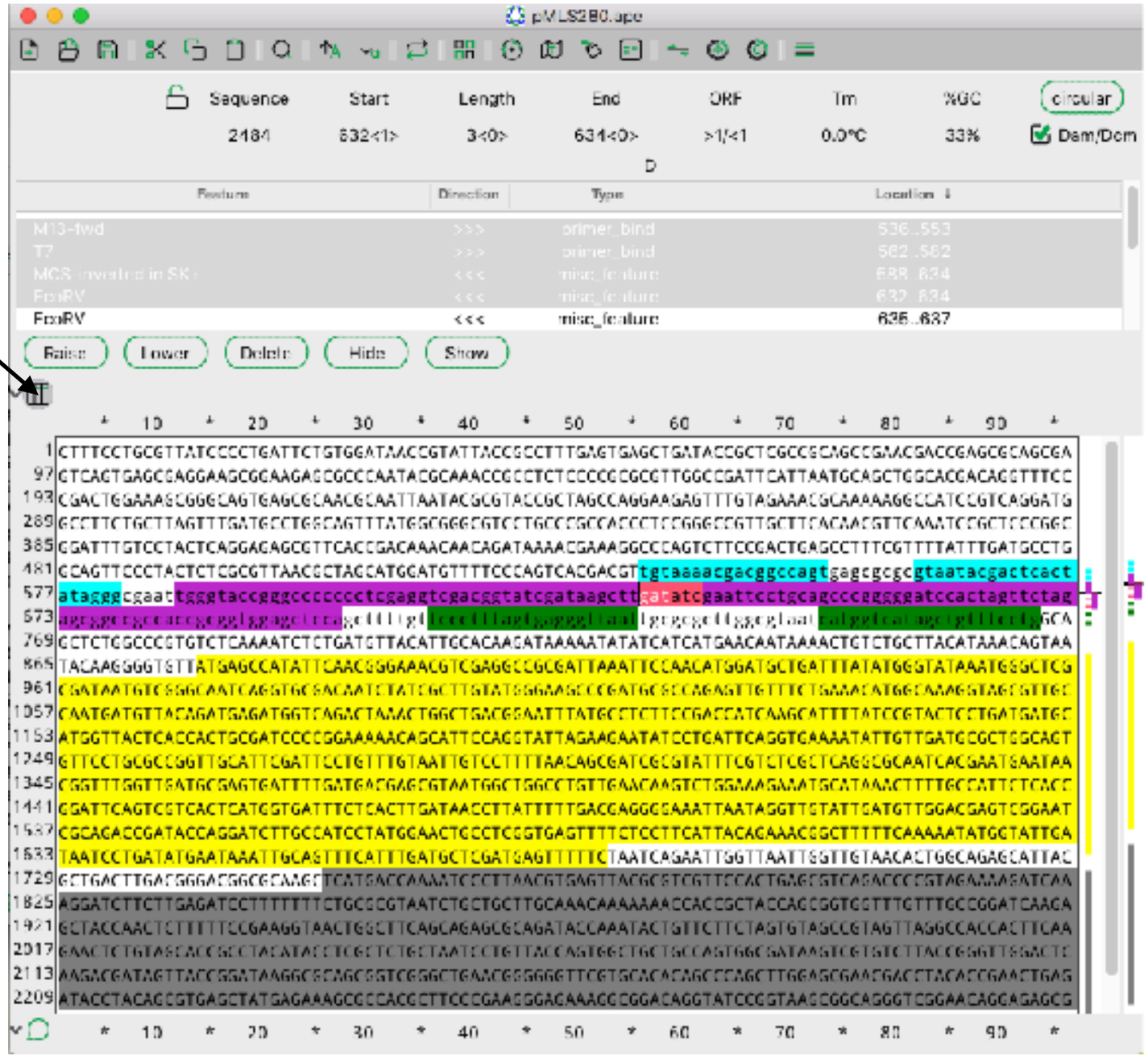
Features



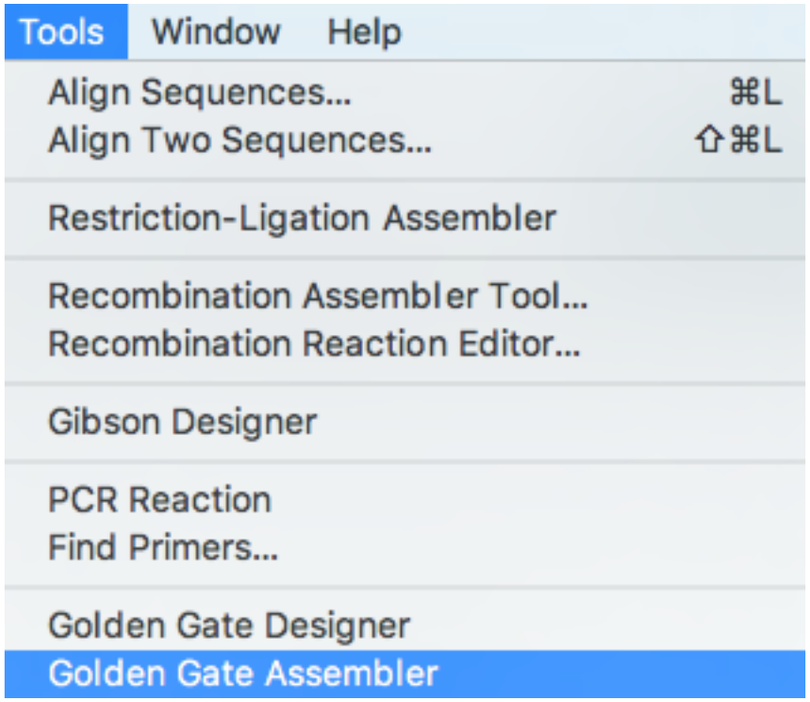
Right-click here to edit a feature's range

Features

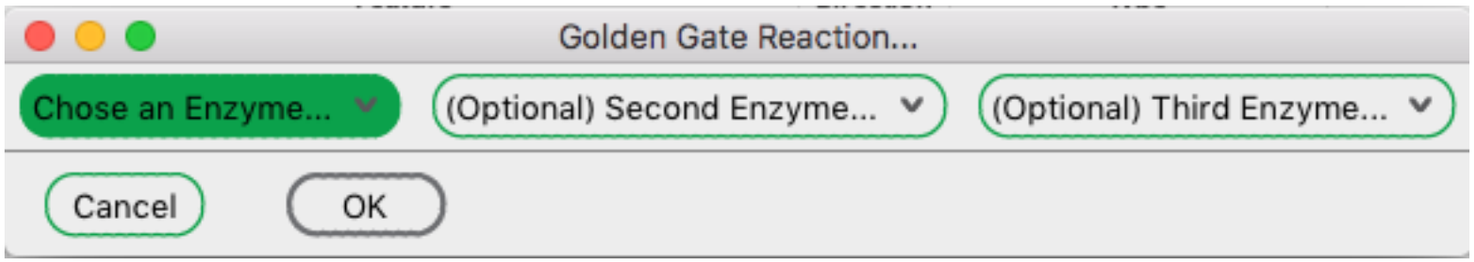
Shift-click this to hide/show the feature table buttons



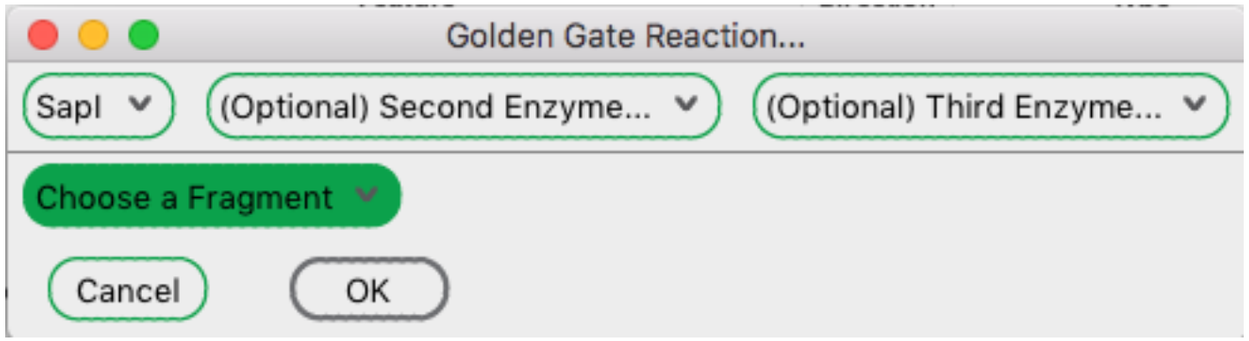
Golden Gate Assembler



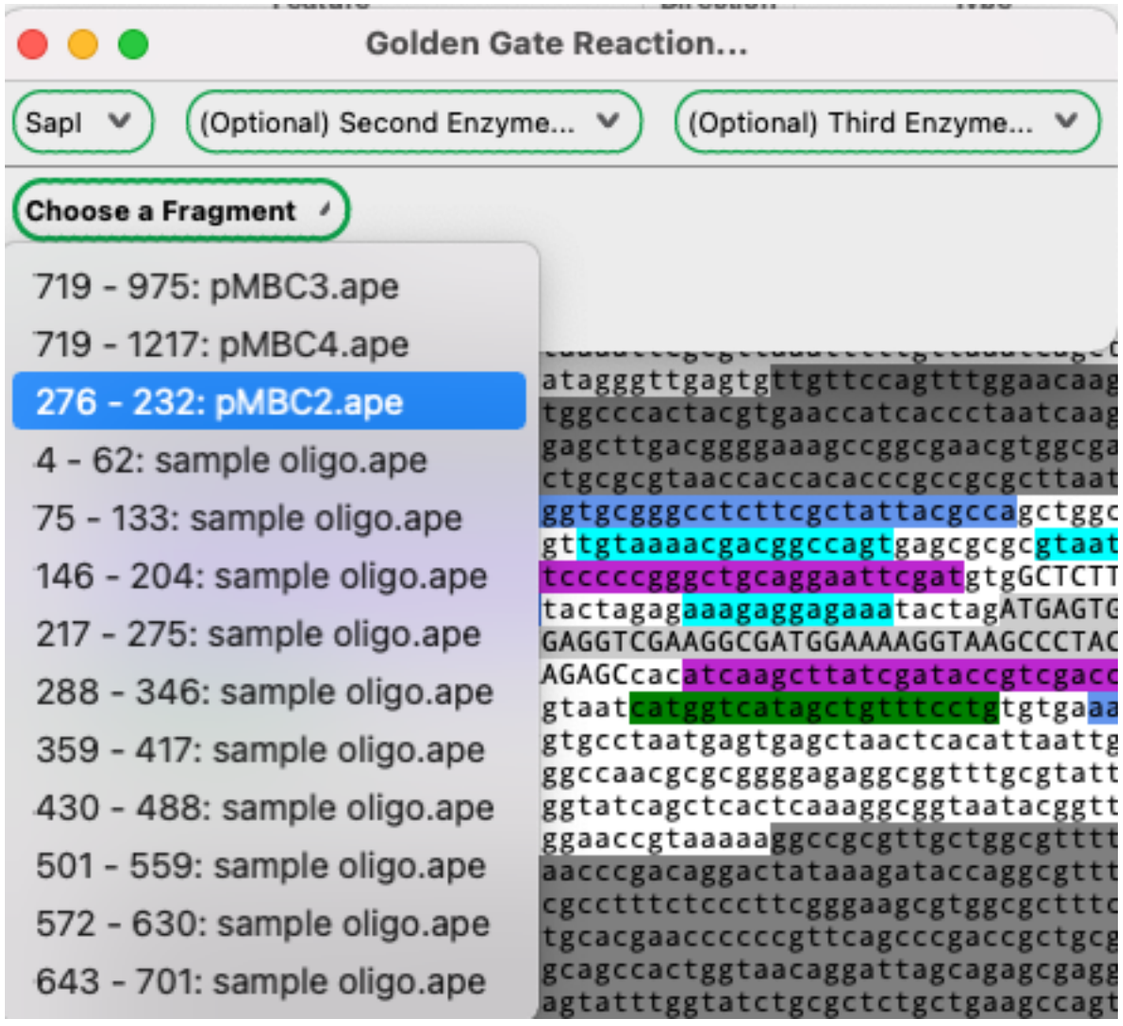
Golden Gate Assembler



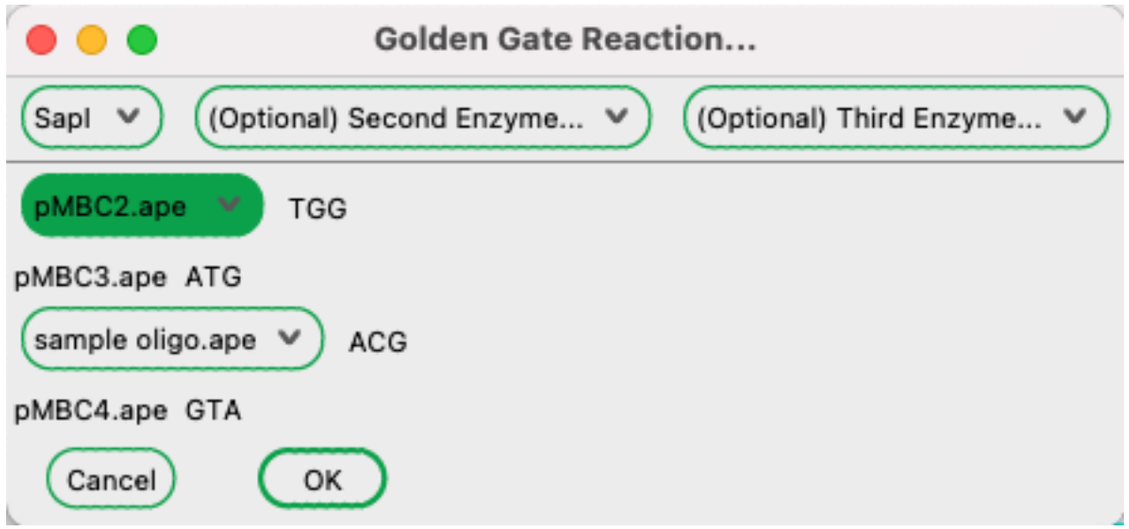
Golden Gate Assembler



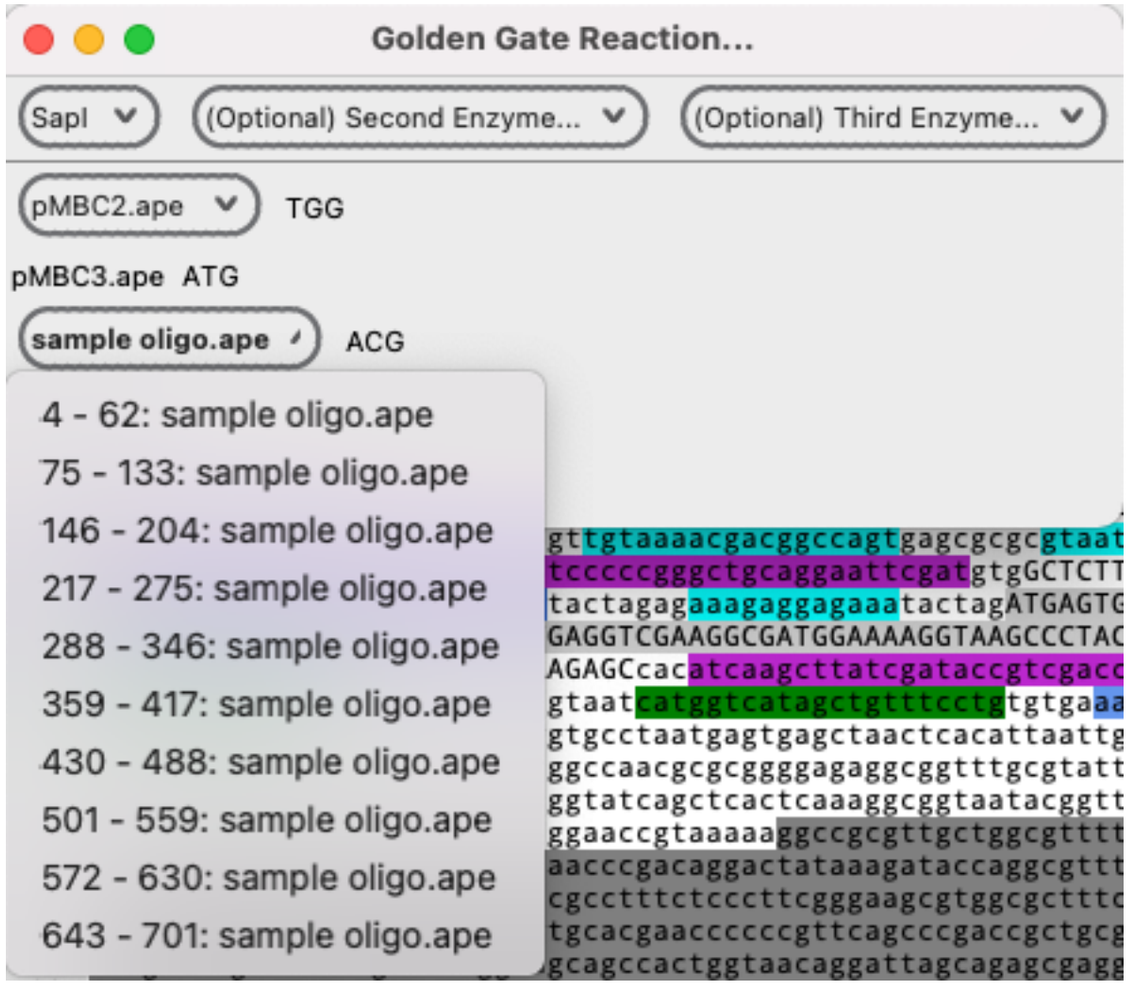
Golden Gate Assembler



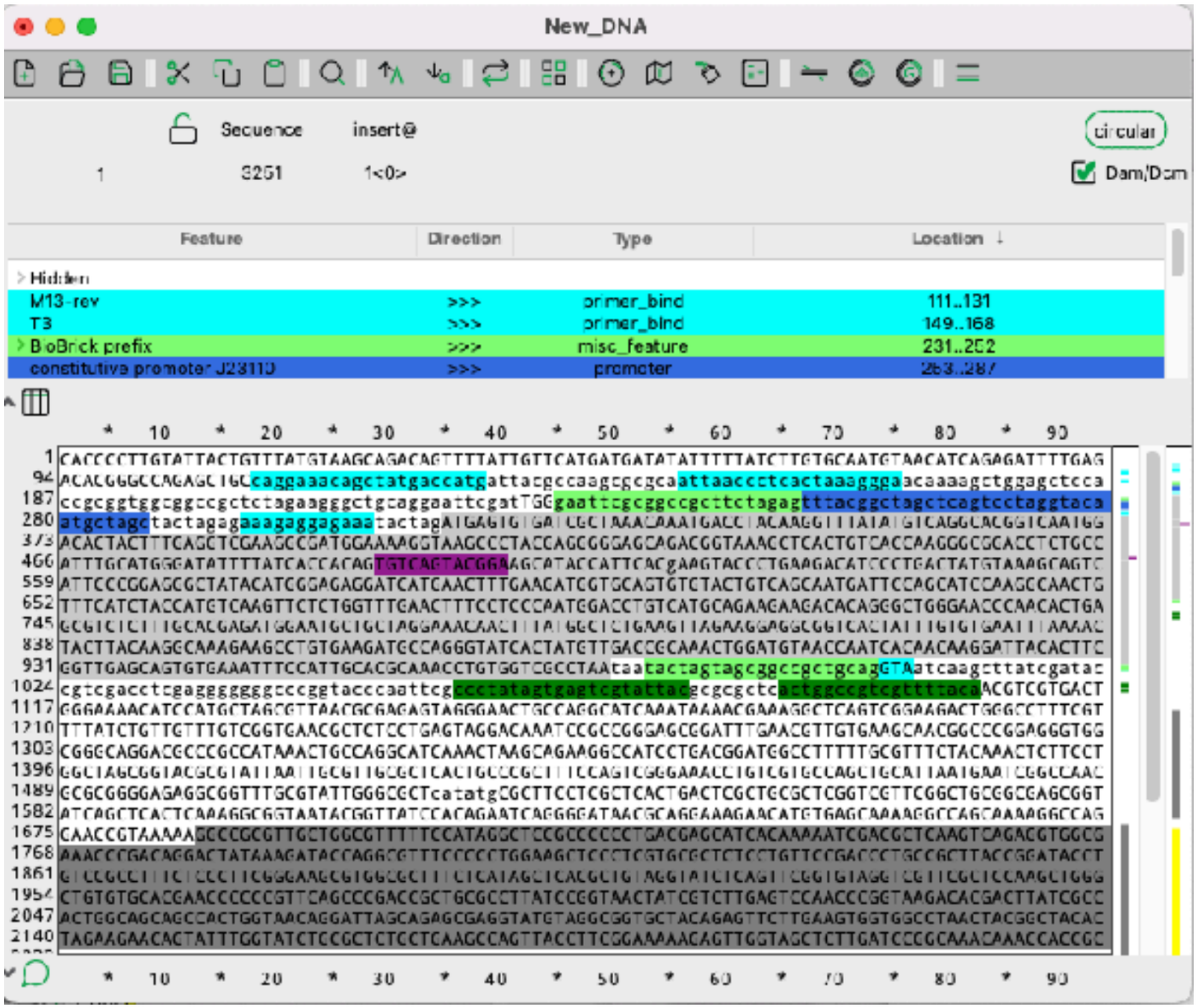
Golden Gate Assembler



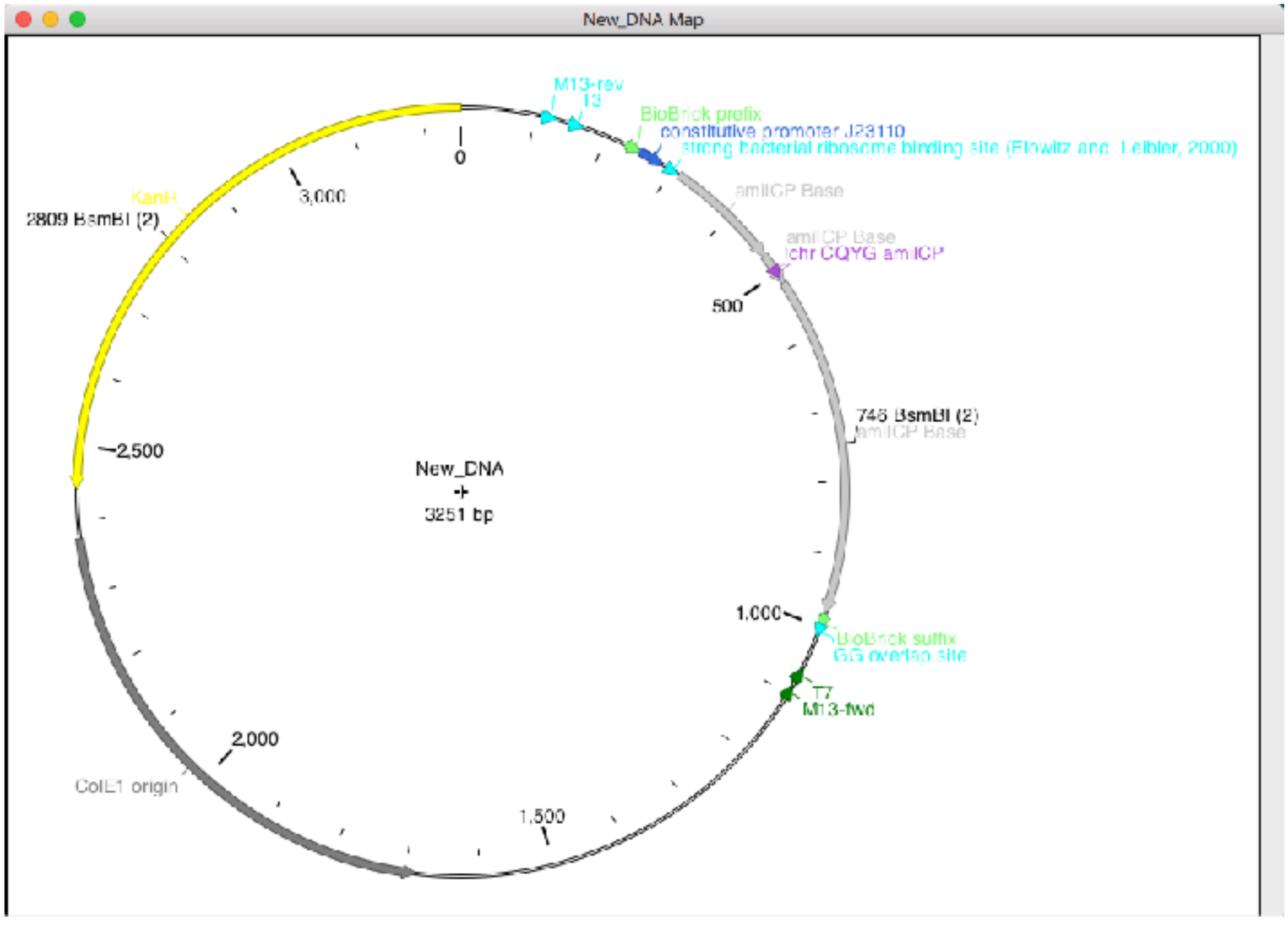
Golden Gate Assembler



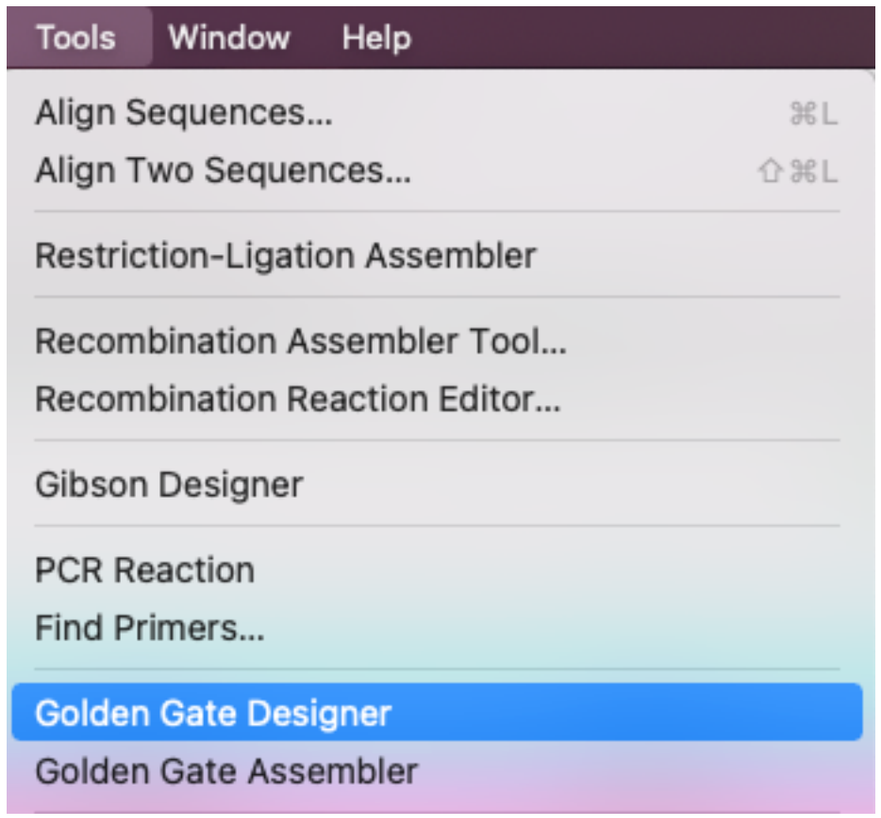
Golden Gate Assembler



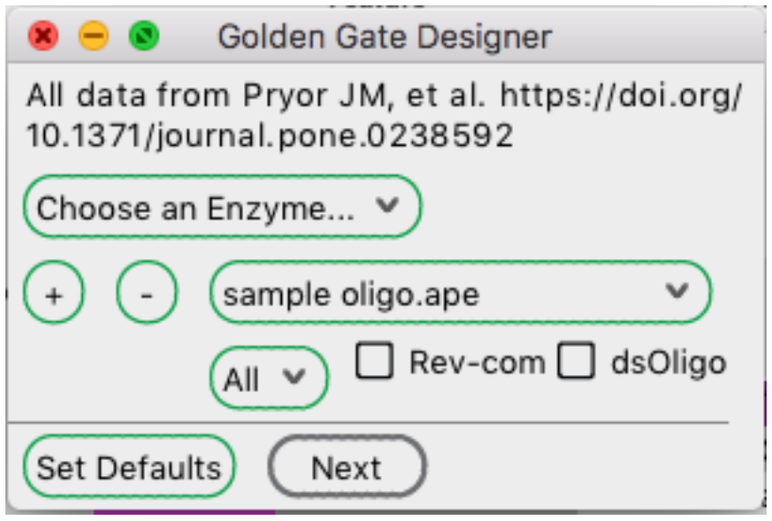
Golden Gate Assembler



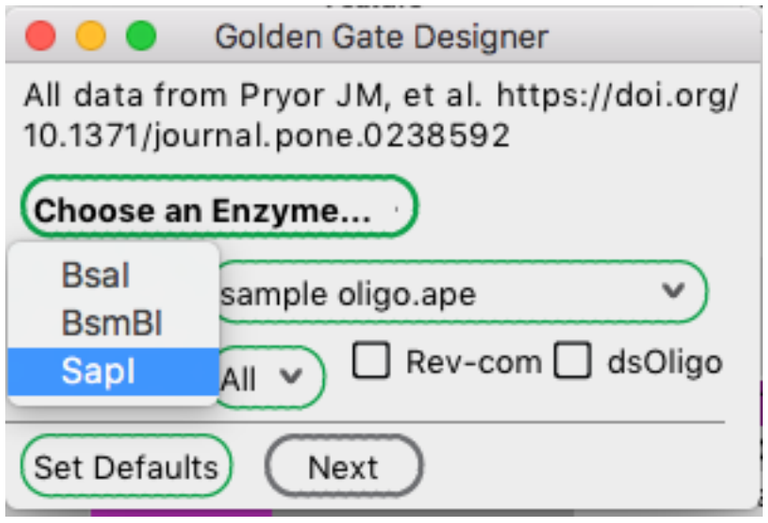
Golden Gate Designer



Golden Gate Designer

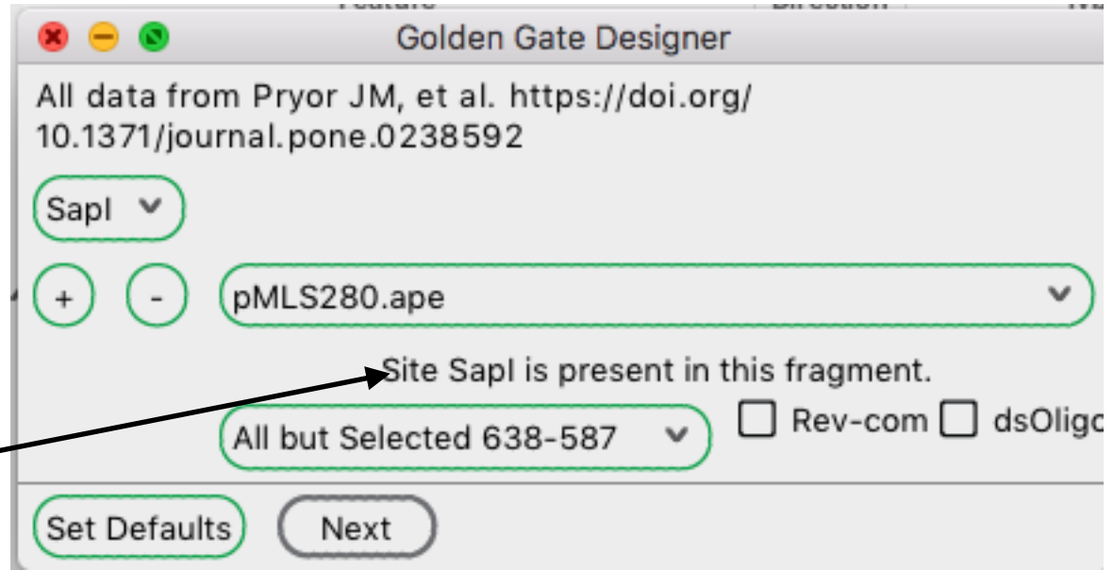


Golden Gate Designer

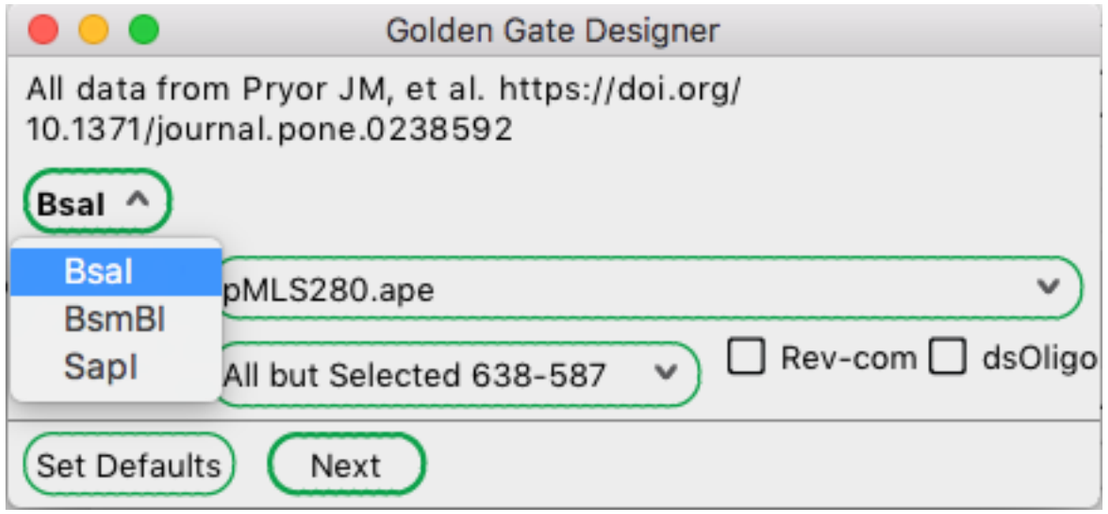


Golden Gate Designer

You can’t use a fragment that has a site already in it

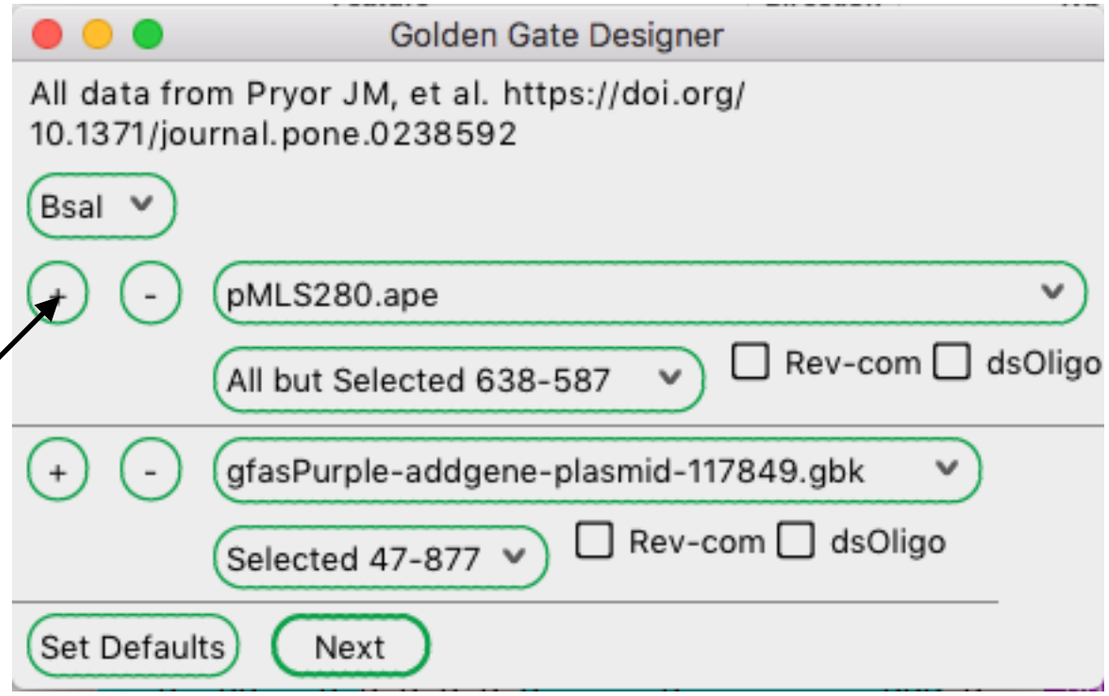


Golden Gate Designer

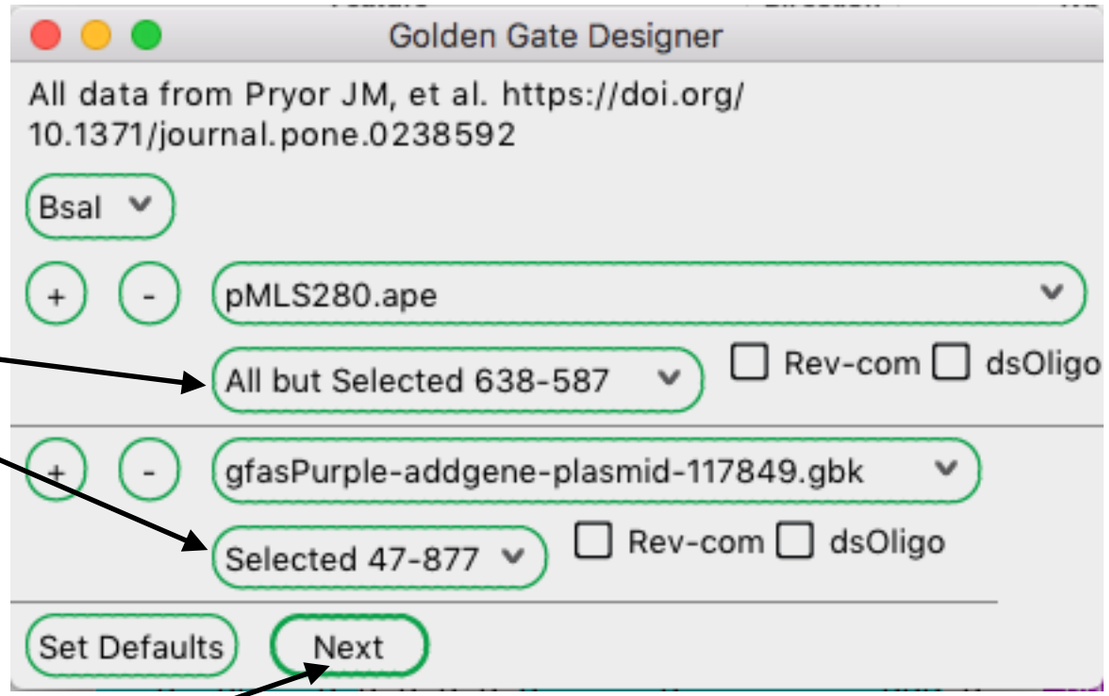


Golden Gate Designer

Add fragments using this button



Golden Gate Designer



Select these ranges

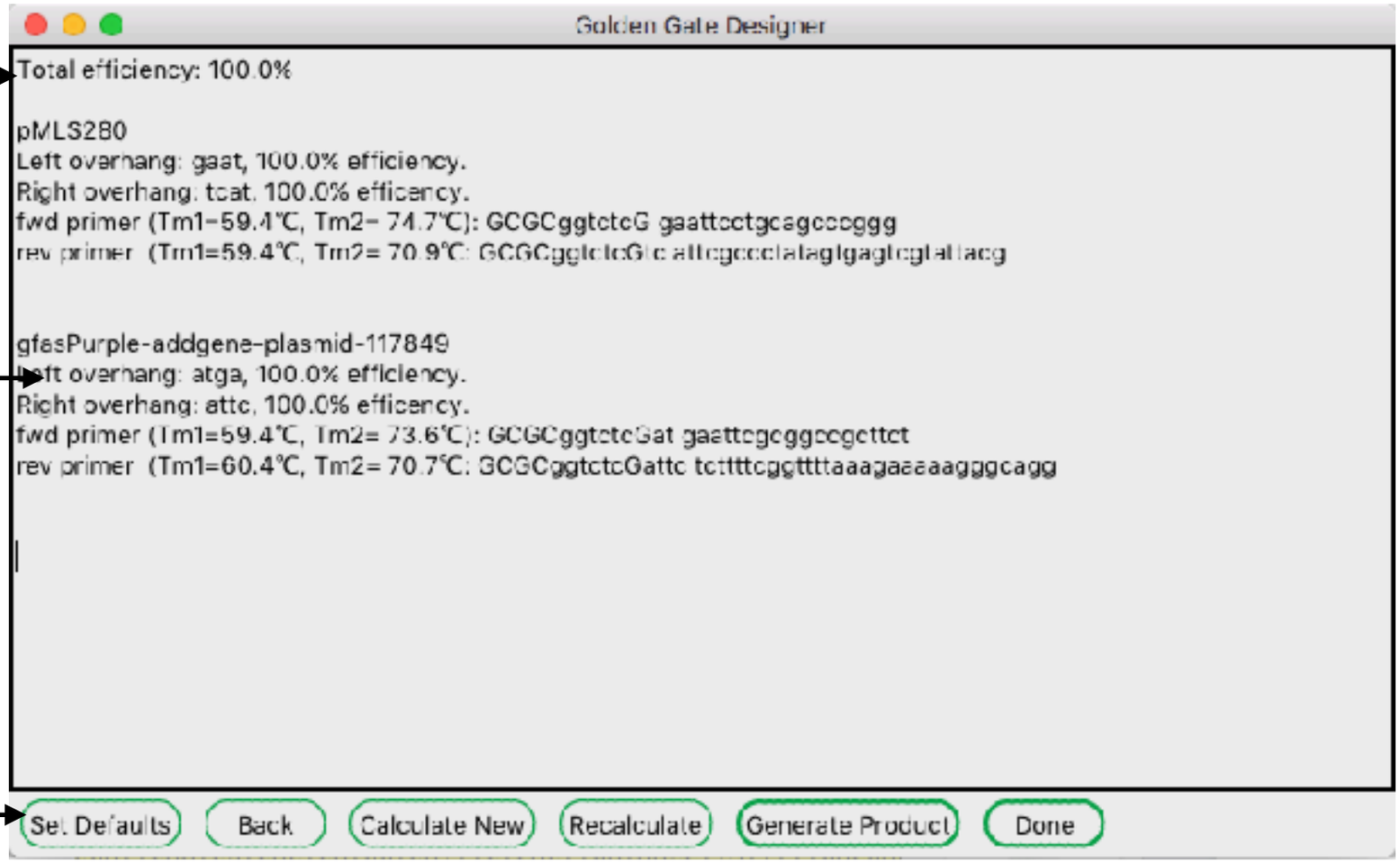
Then click “Next”

Golden Gate Designer

Calculates the total efficiency (on-target to off target)

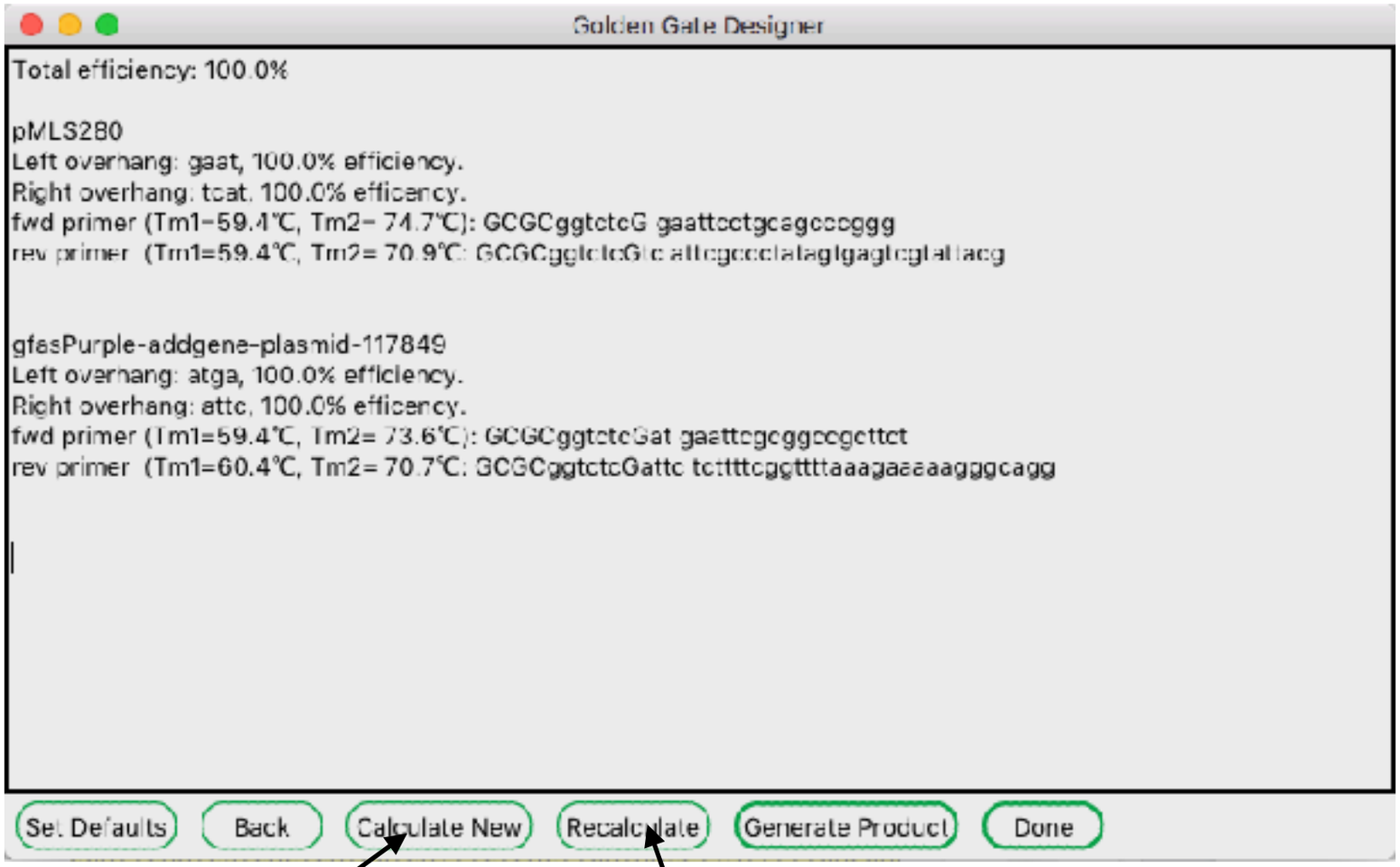
Each fragment and the primers needed

You can set default values here bases



Golden Gate Designer

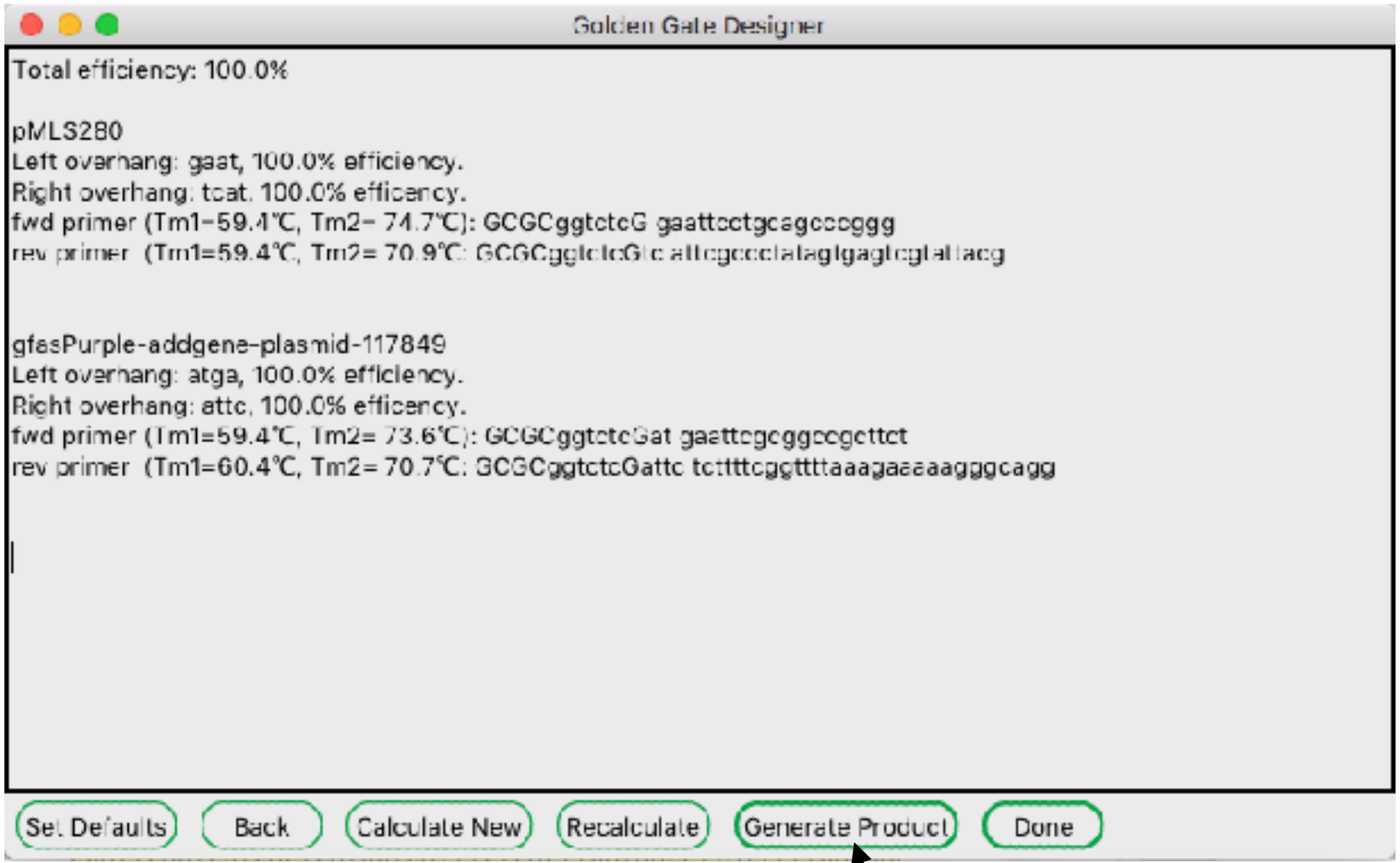
Golden Gate Designer



Re-start the calculation if it's stuck in an unfavorable search

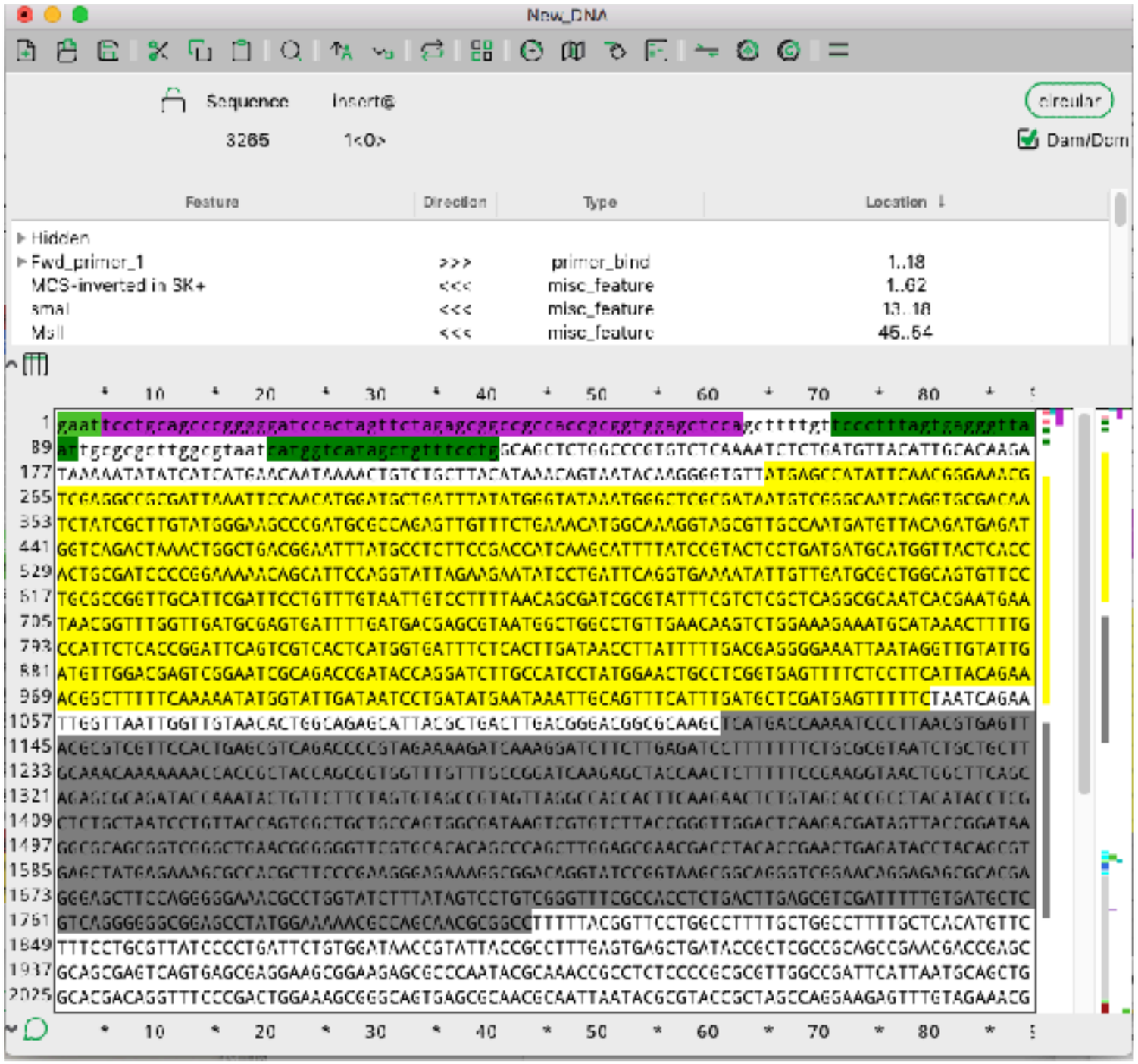
Do a longer calculation from the current search position

Golden Gate Designer

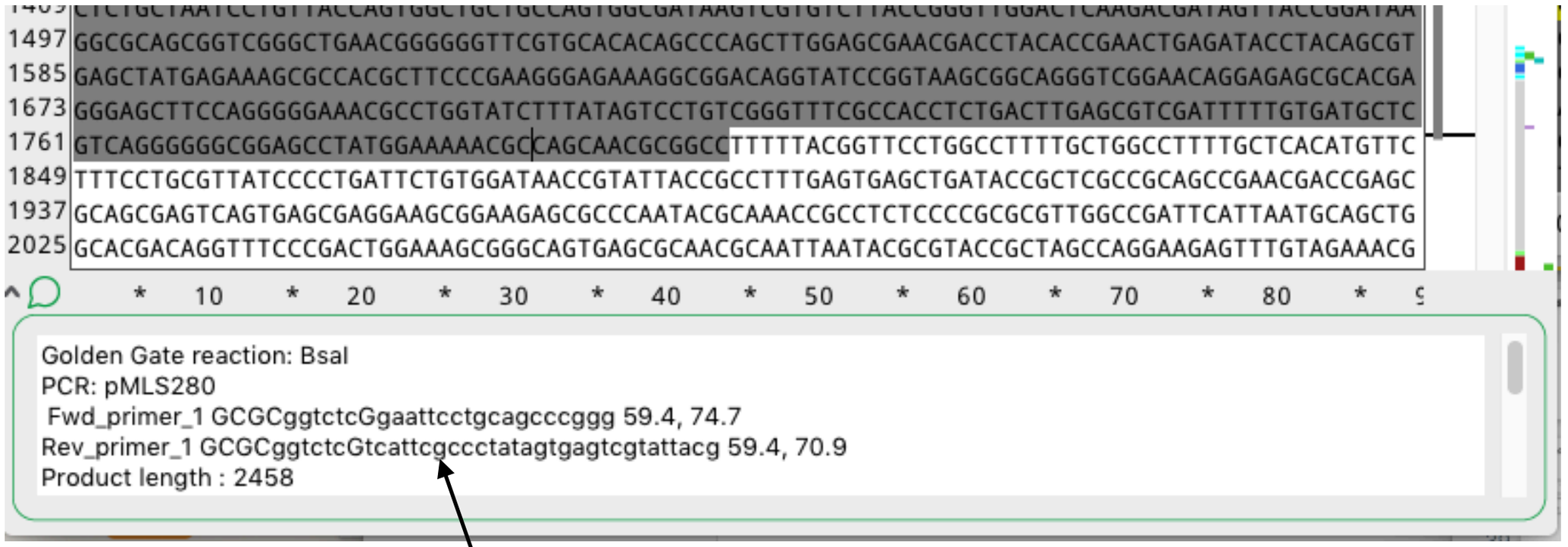


Generate the new product

Golden Gate Designer

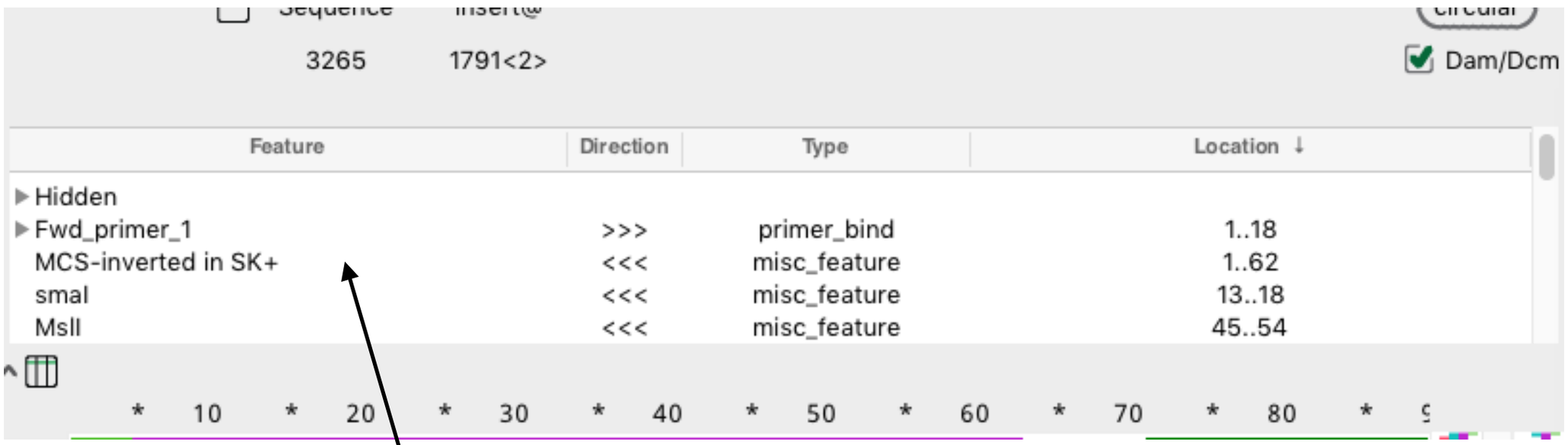


Golden Gate Designer



The primers and PCR conditions are in the comments

Golden Gate Designer

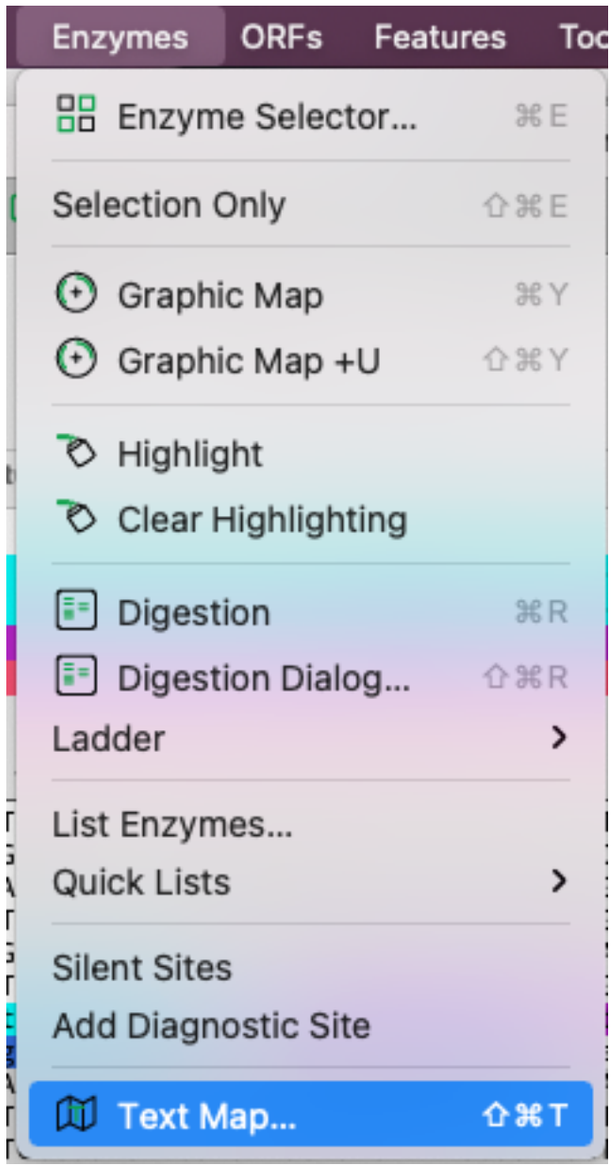


The primers are new features in the feature table

Golden Gate Designer

The primers are new features in the sequence

Text map dialog

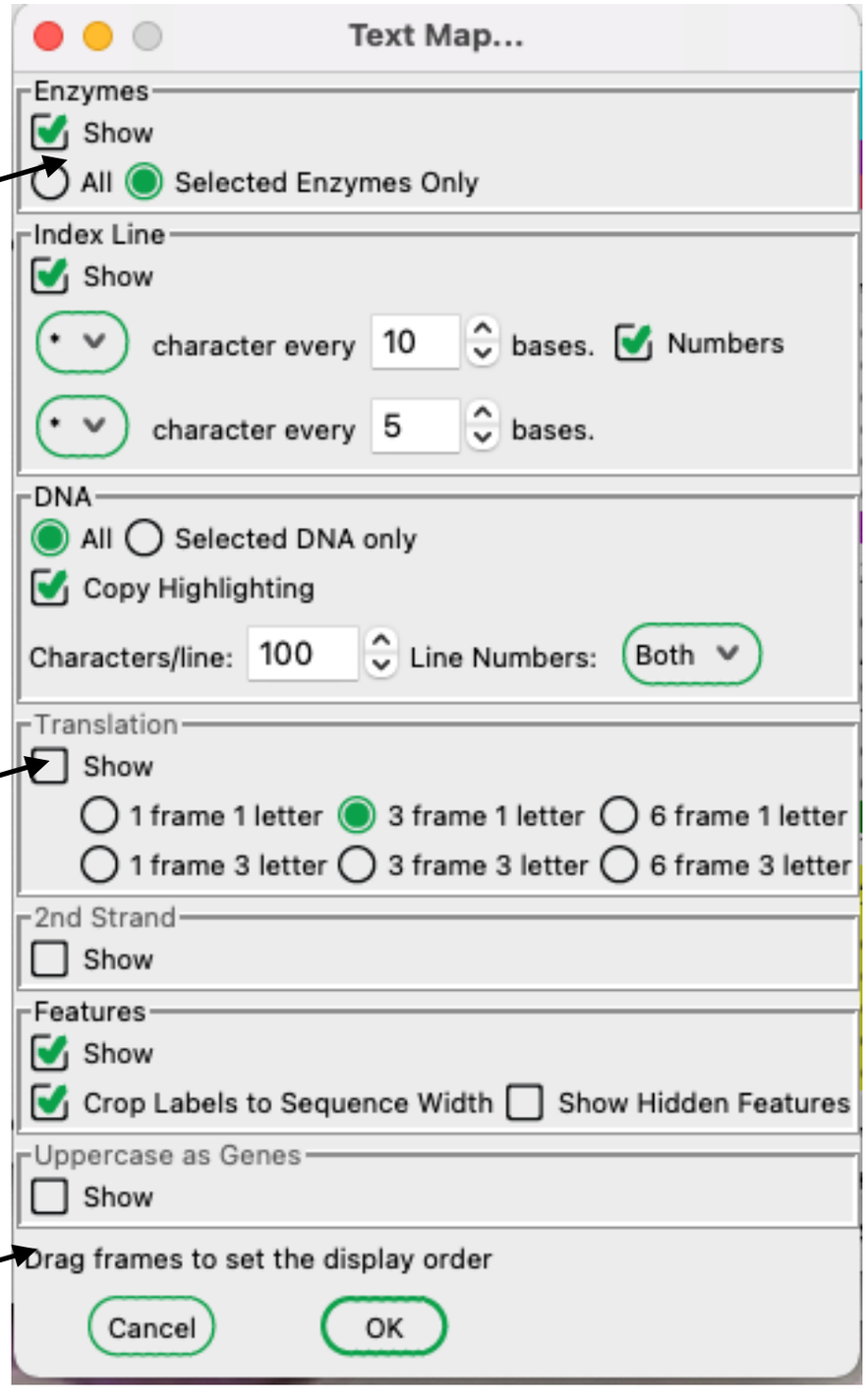


Text map dialog

Each box is an analysis line

Turn off the line by unchecking this box

Drag the frames to change the order



Text map dialog

gfasPurple-addgene-plasmid-117849.gbk Text Map

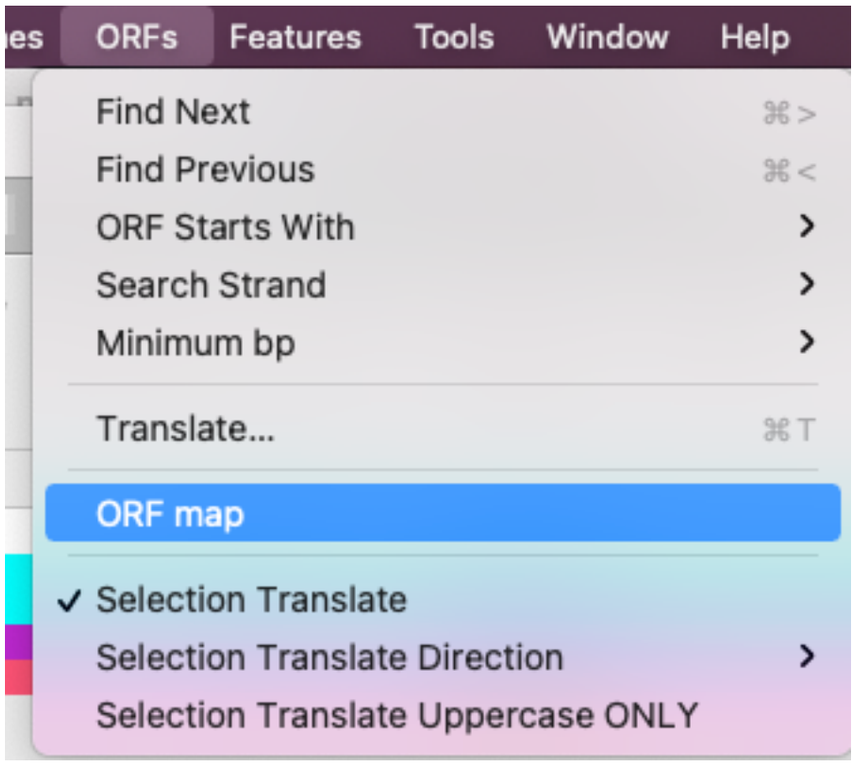
```
Wed Oct 06, 2021 10:18 MDT
gfasPurple-addgene-plasmid-117849.gbk
Text Map
          10        20        30        40        50        60        70        80        90        100
       *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
atttcagataaaaaaaatccttagctttcgctaaggatgatttctggaattcgcggccgcttctagagtttacggctagctcagtcctaggtacaatgct
taaagtctatttttttaggaatcgaaagcgattcctactaaagaccttaagcgccggcgaagatctcaaatgccgatcgagtcaggatccatgttacga
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
bacterial terminator                                  BioBrick prefix       Constitutive promoter J23110

          110       120       130       140       150       160       170       180       190       200
       *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
agctactagagaaagaggagaaatactagATGTCGGTGATTGCTAAACAGATGACCTACAAAGTCTATATGTCGGGTACGGTGAACGGCCATTATTTTGA
tcgatgatctctttctcctctttatgatcTACAGCCACTAACGATTTGTCTACTGGATGTTTCAGATATACAGCCCATGCCACTTGCCGGTAATAAAACT
                            M  S  V  I  A  K  Q  M  T  Y  K  V  Y  M  S  G  T  V  N  G  H  Y  F  E
                            1
>>>                         >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Constitutive promoter J23110 gfasPurple
           >>>>>>>>>>>>
           strong bacterial ribosome binding site (Elowitz and  Leibler, 2000)

         210       220       230       240       250       260       270       280       290       300
      *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
AGTTGAAGGTGACGGTAAAGGCAAGCCGTATGAAGGCGAACAGACCGTTAAACTGACCGTCACGAAGGGCGGTCCGCTGCCGTTTGCATGGGATATTCTG
TCAACTTCCACTGCCATTTCCGTTCGGCATACTTCCGCTTGTCTGGCAATTTGACTGGCAGTGCTTCCCGCCAGGCGACGGCAAACGTACCCTATAAGAC
 V  E  G  D  G  K  G  K  P  Y  E  G  E  Q  T  V  K  L  T  V  T  K  G  G  P  L  P  F  A  W  D  I  L
25
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
gfasPurple
                                                                                  >>>
                                                                                  New Feature

         310       320       330       340       350       360       370       380       390       400
```

ORF map dialog

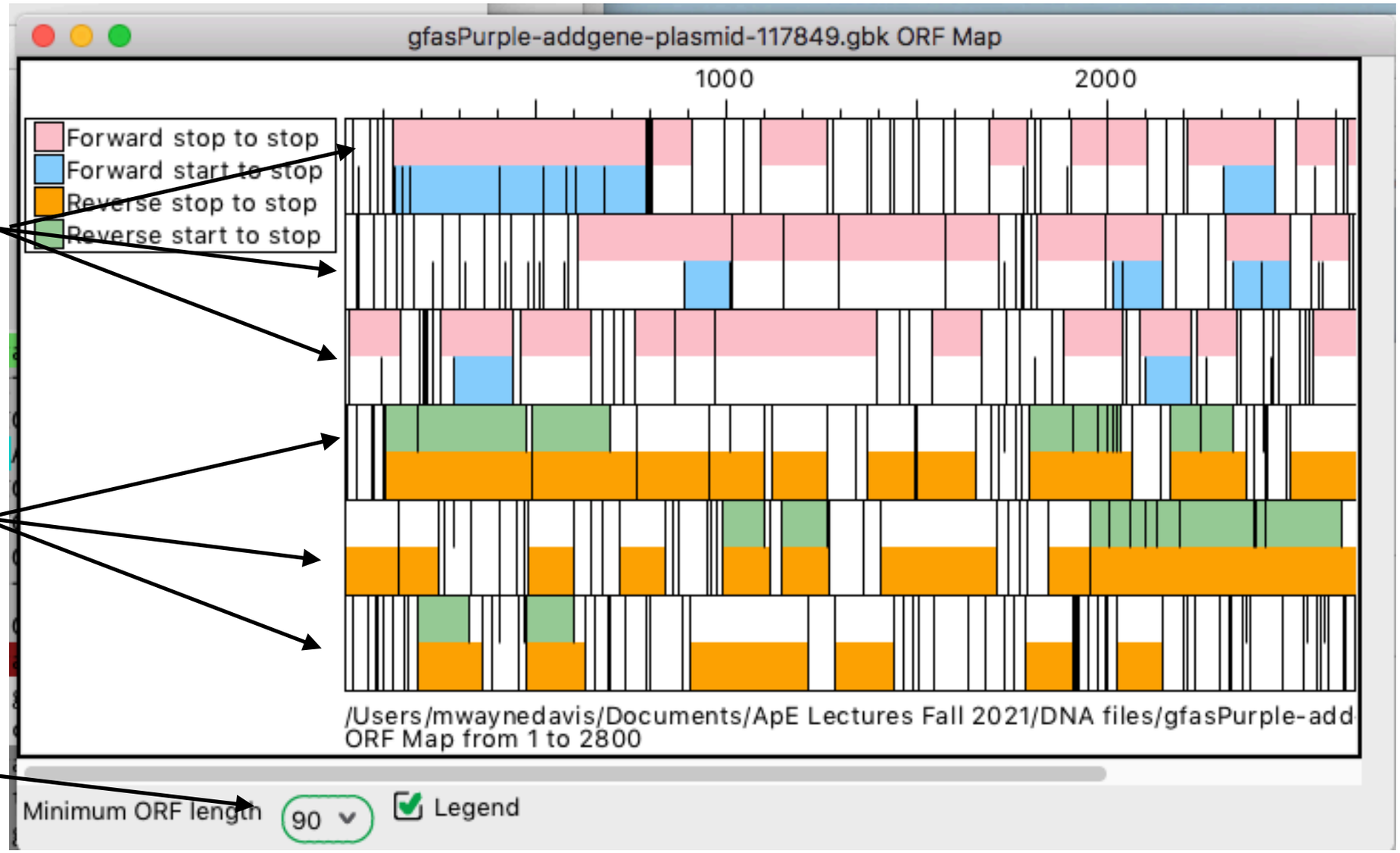


ORF map dialog

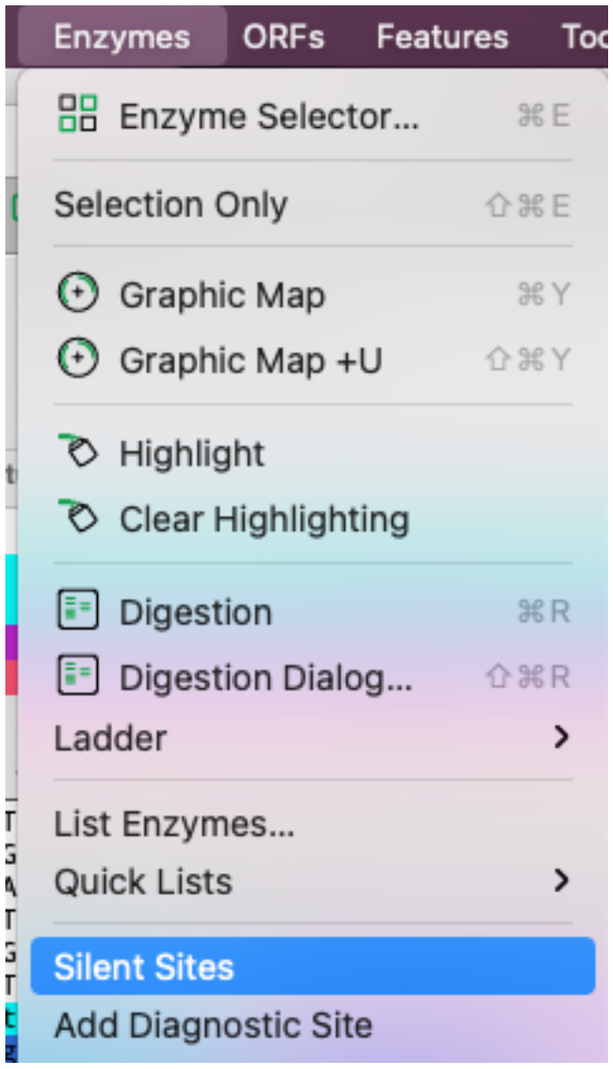
Three forward frames

Three reverse frames

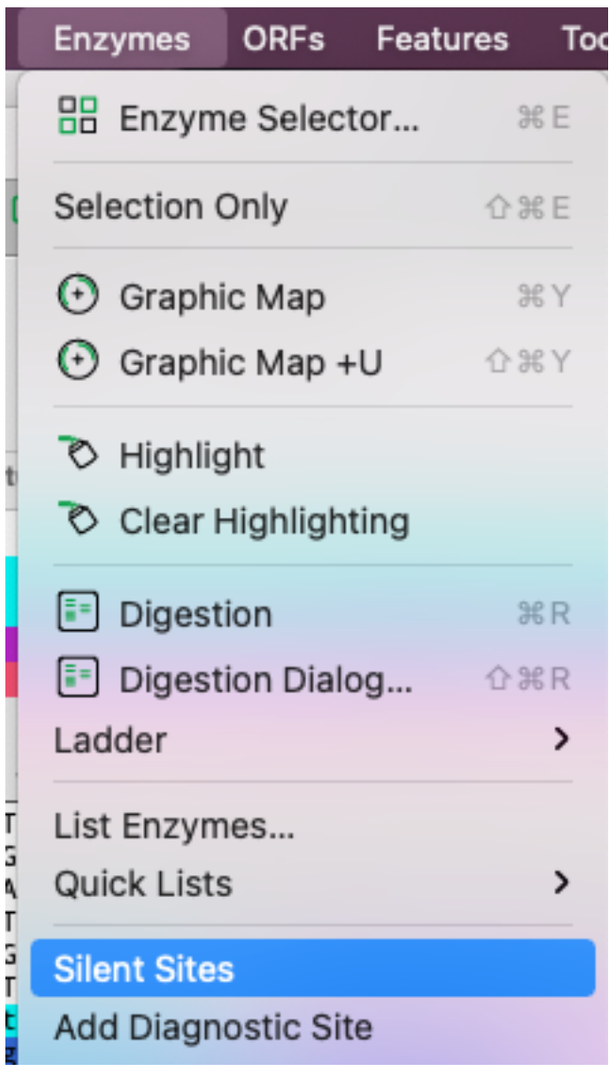
Longer than this are highlighted in color, and can be clicked



Silent/ diagnostic sites dialog

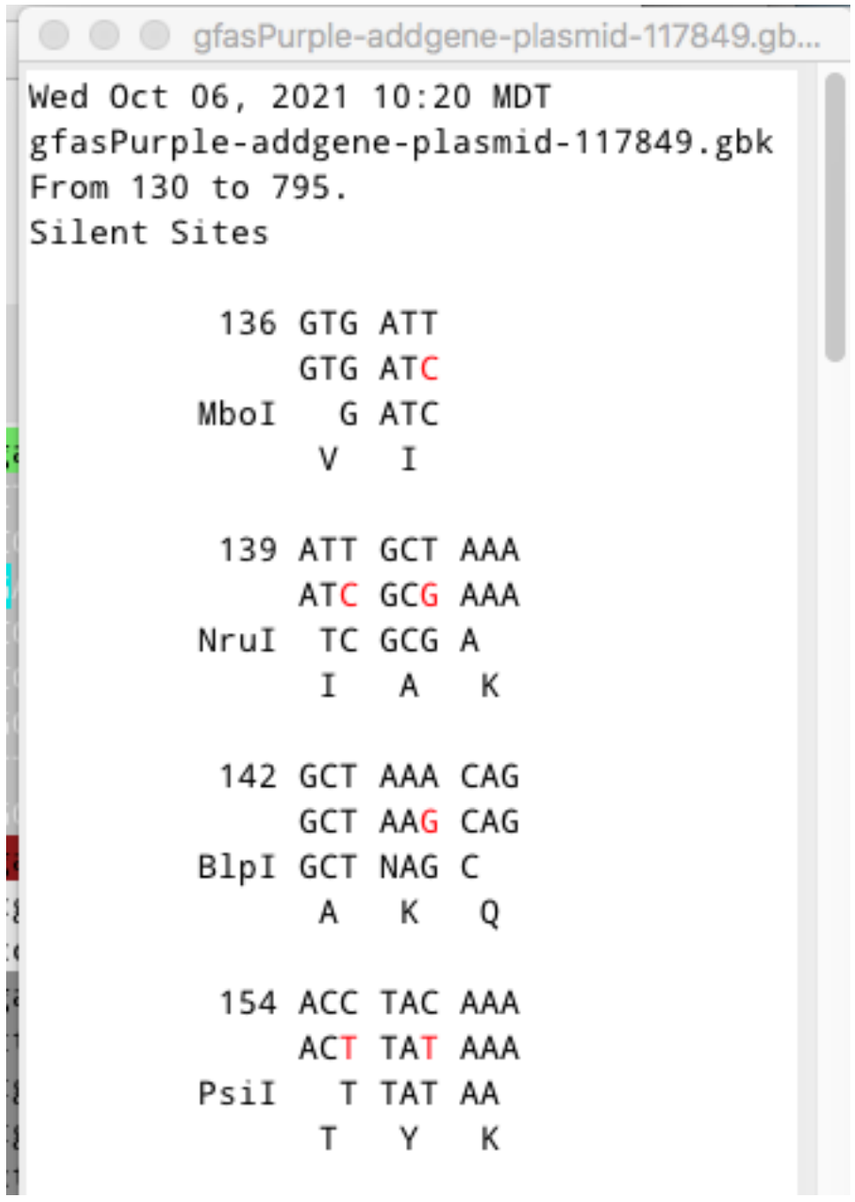


Silent/ diagnostic sites dialog

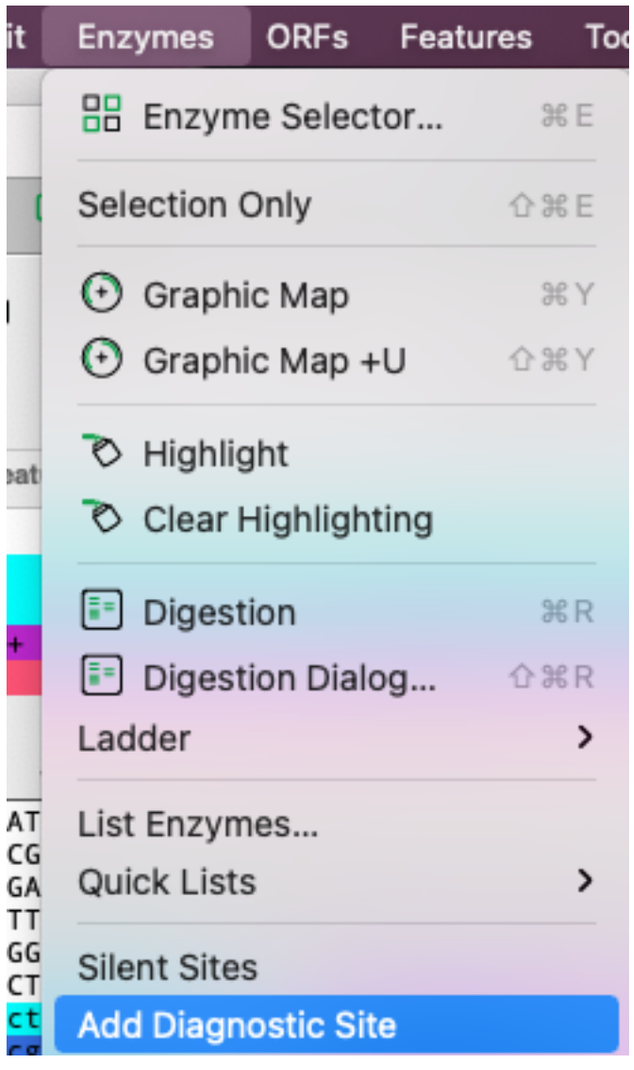


***Select a forward ORF and a set of restriction enzymes before selecting the menu item

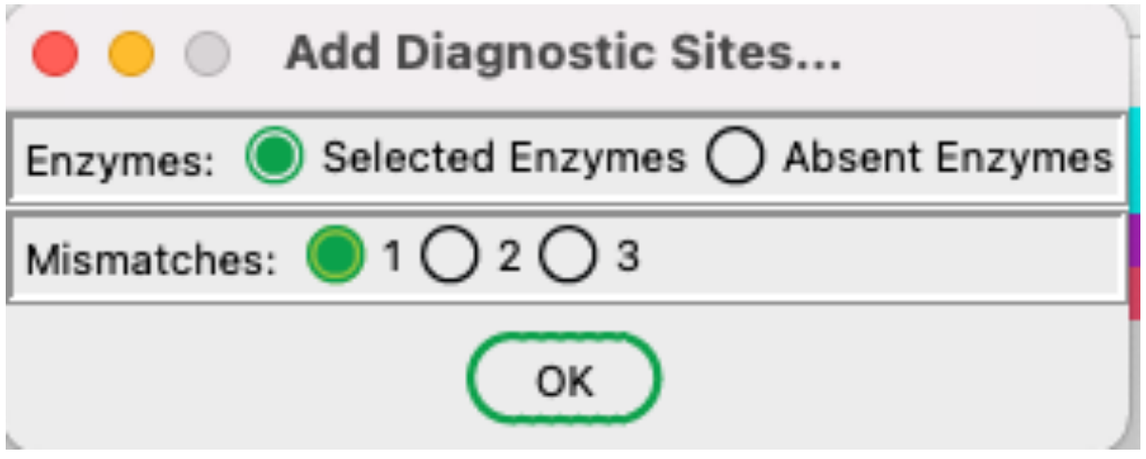
Silent/ diagnostic sites dialog



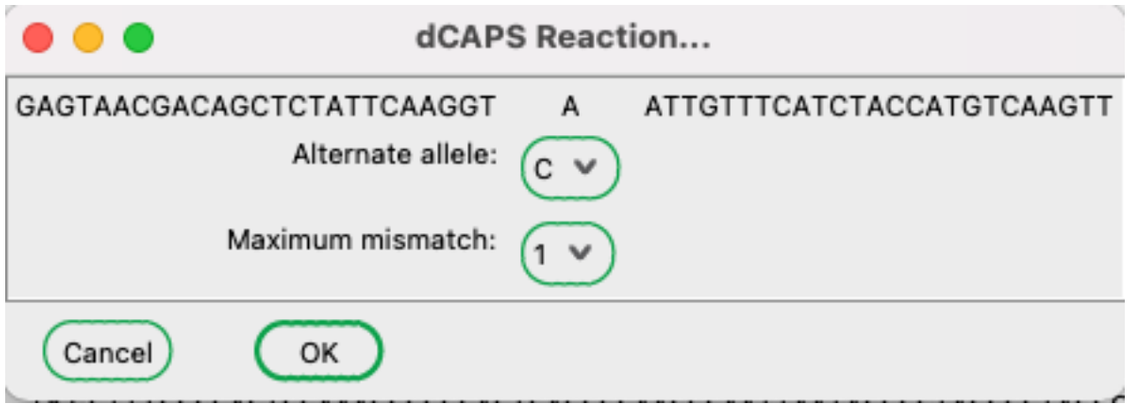
Silent/ diagnostic sites dialog



Select diagnostic site if you are adding a site that is NOT in an ORF



dCAPS dialog



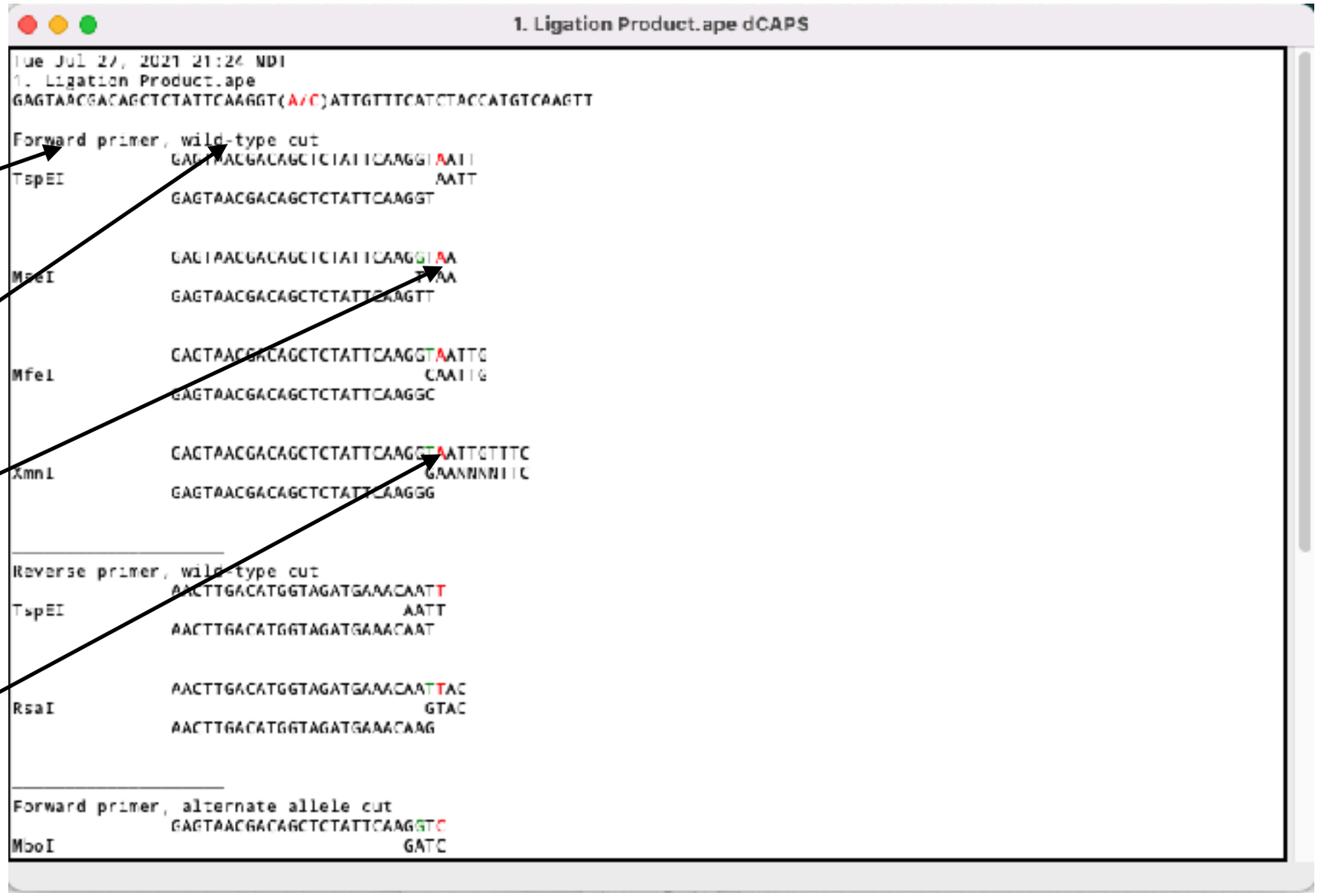
dCAPS dialog

Two orientations

WT or mutant cut

Red is the variant base

Green is a mutant primer base

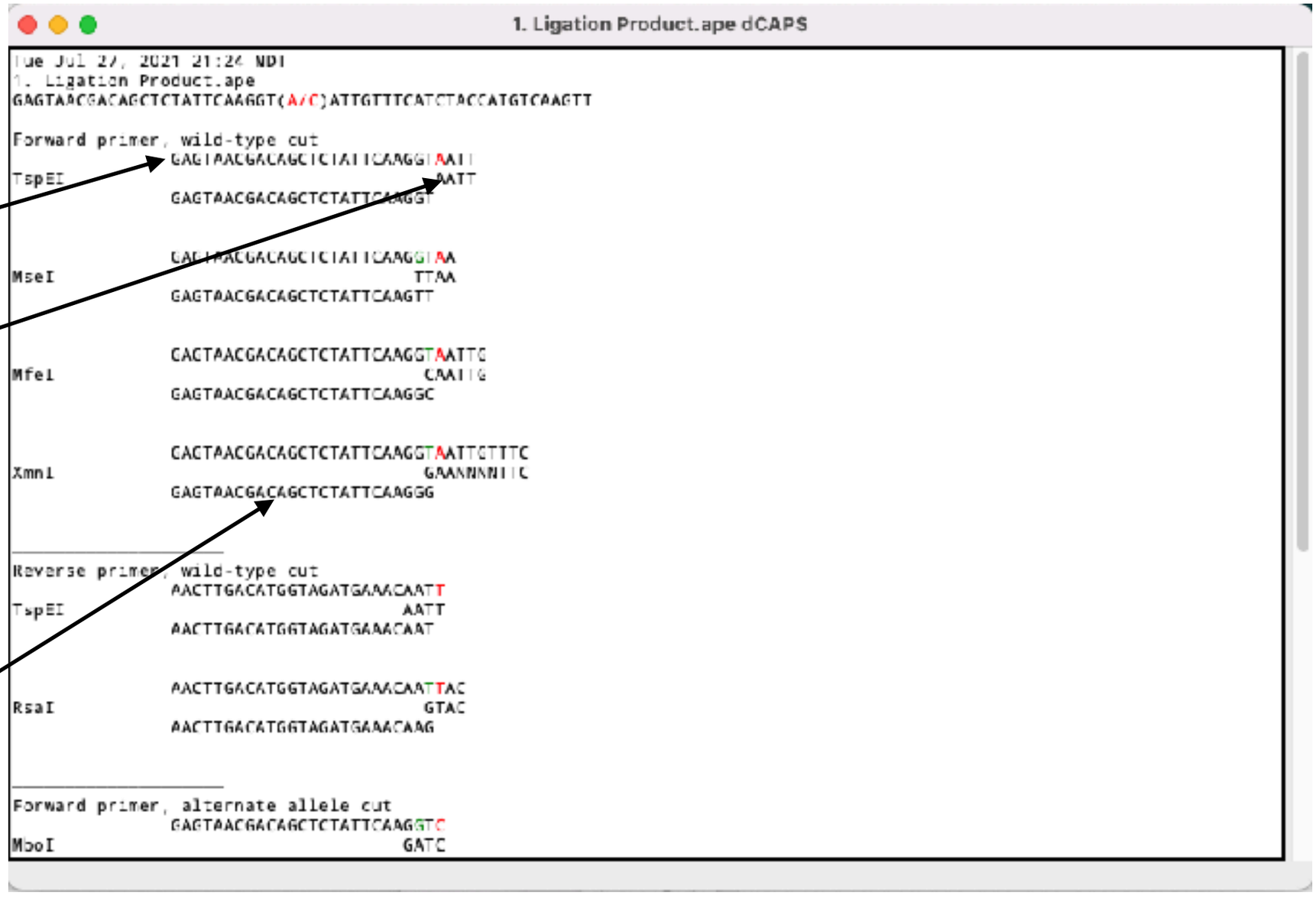


dCAPS dialog

Sequence of the DNA

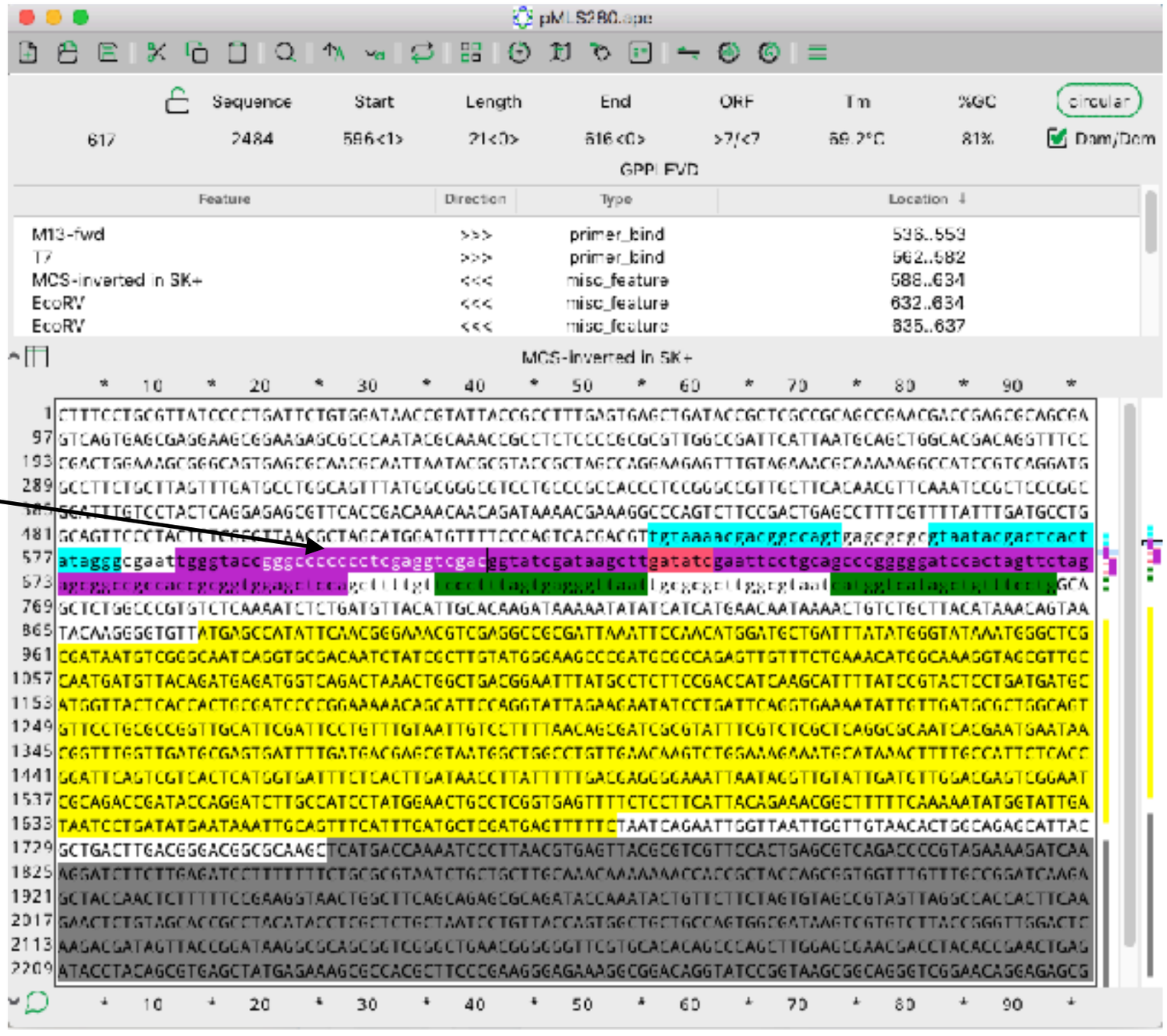
Enzyme recognition sequence

Primer sequence



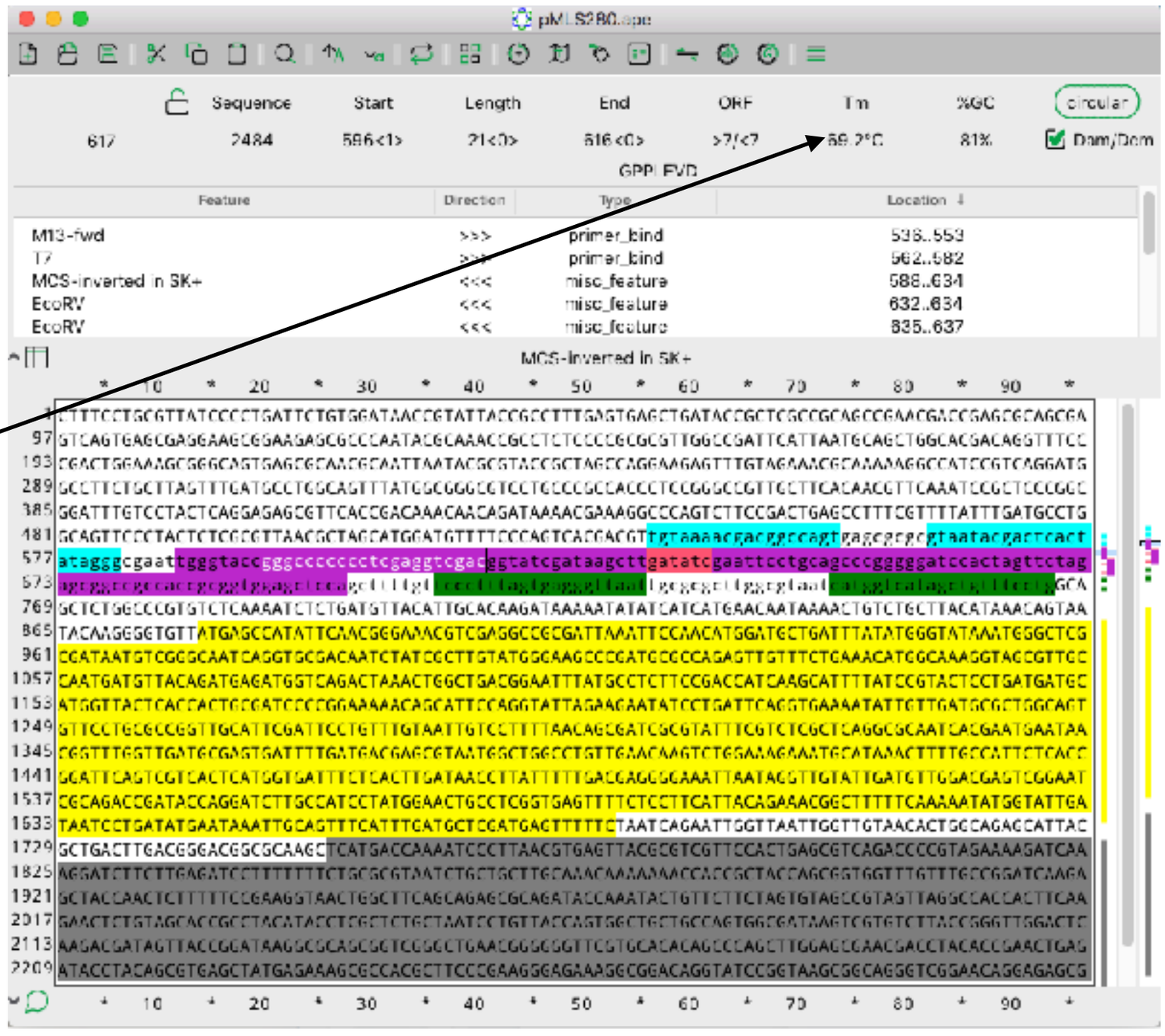
Primers- hand designed

Drag the selection where you want the primer



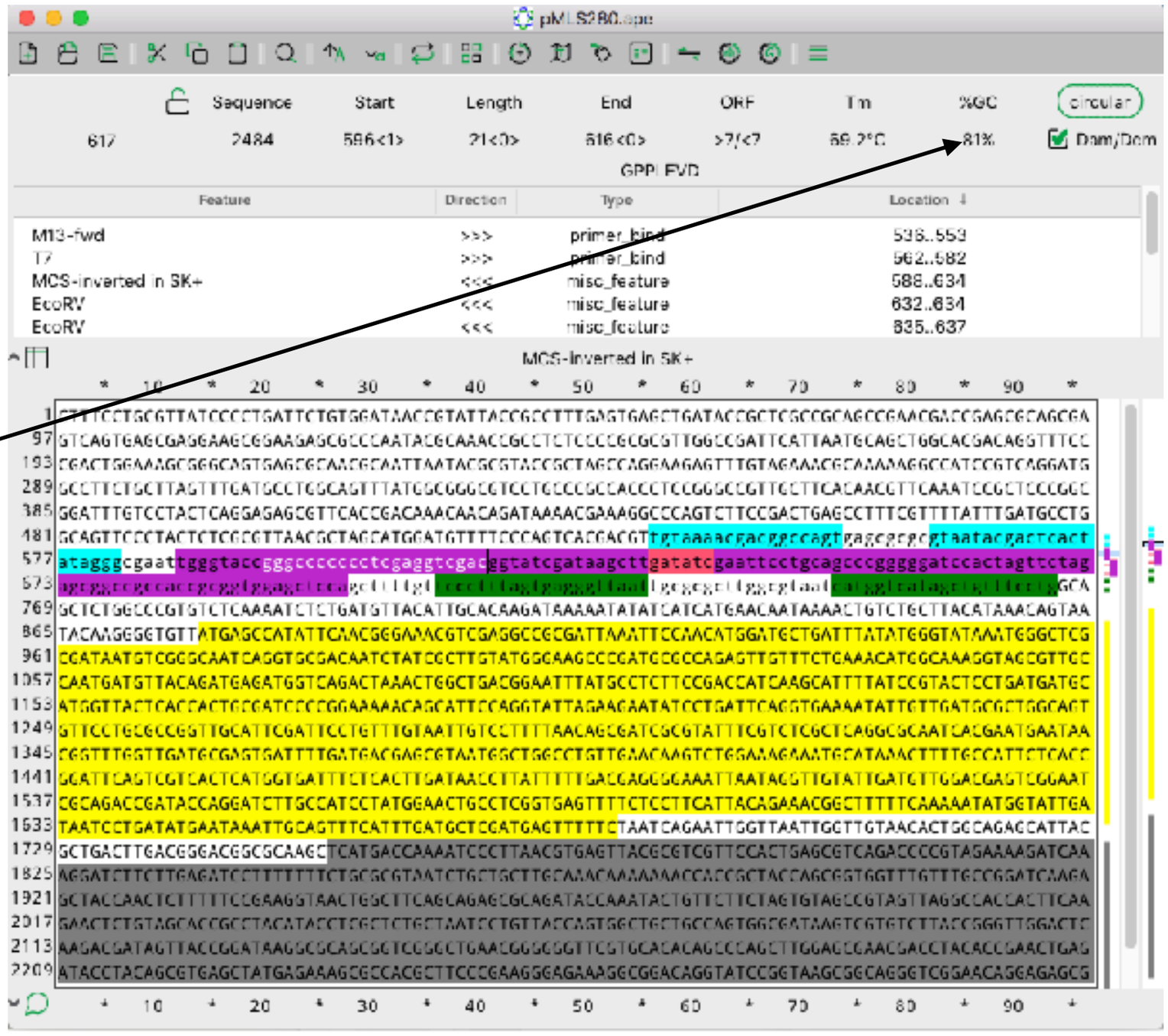
Primers- hand designed

Drag the selection until the Tm is what you want



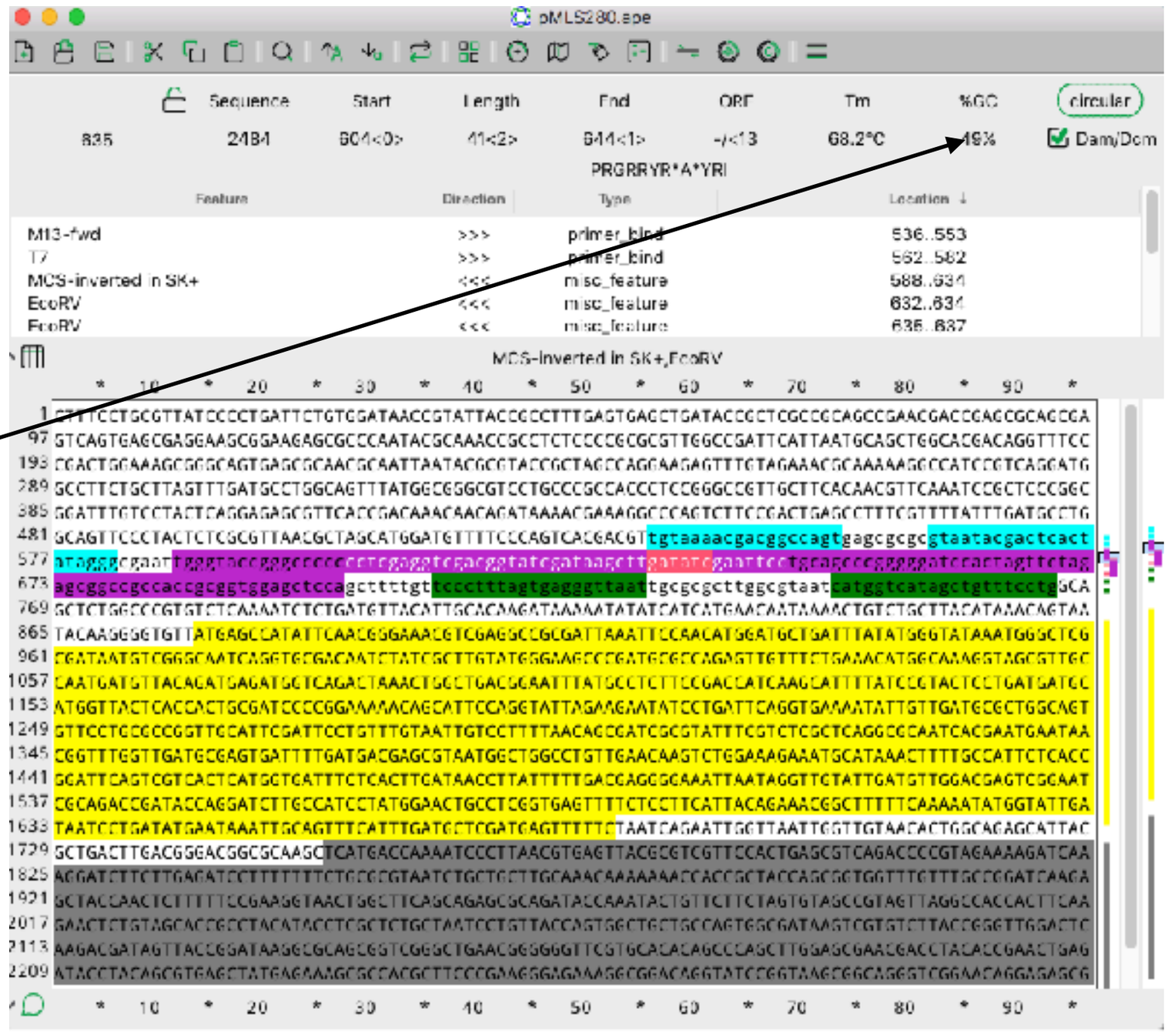
Primers- hand designed

Try to keep the %GC near 50%, if possible

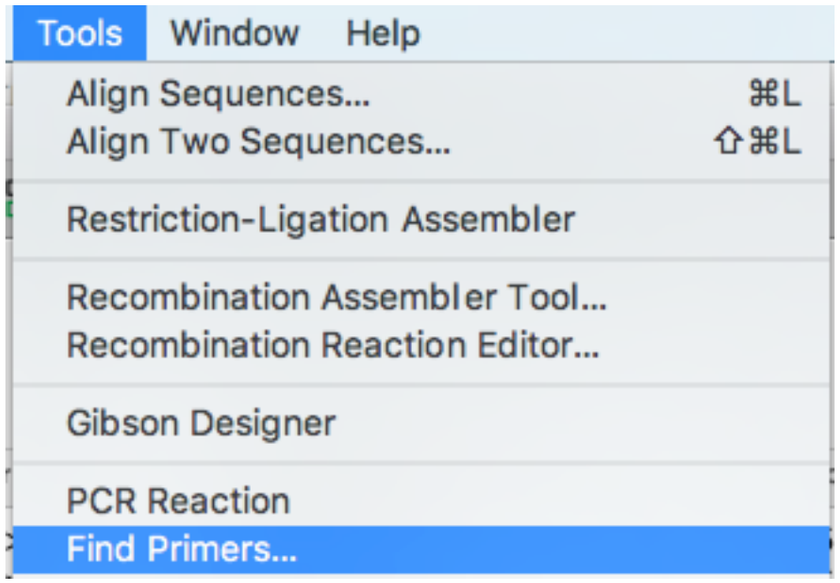


Primers- hand designed

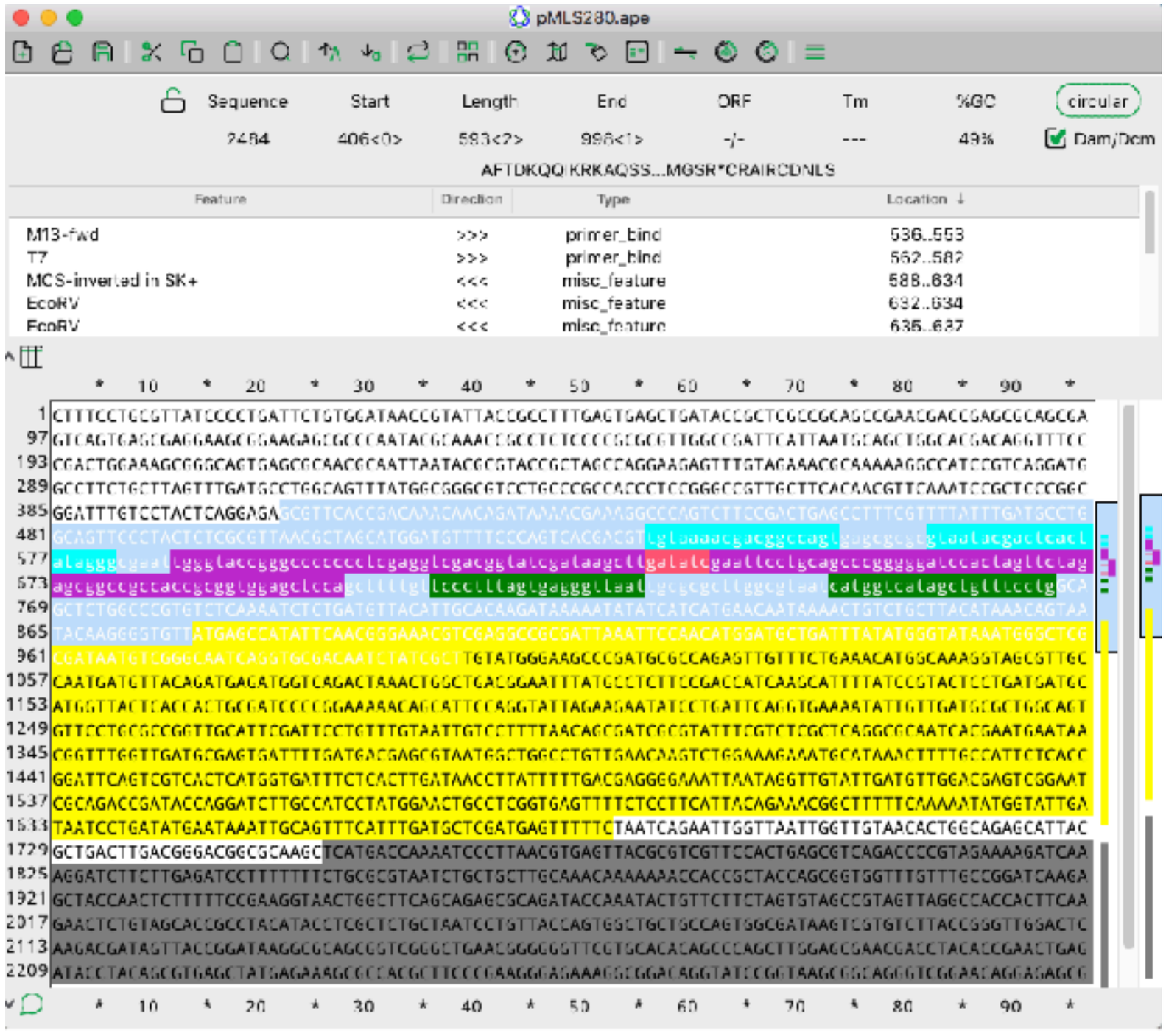
Try to keep the %GC near 50%, if possible



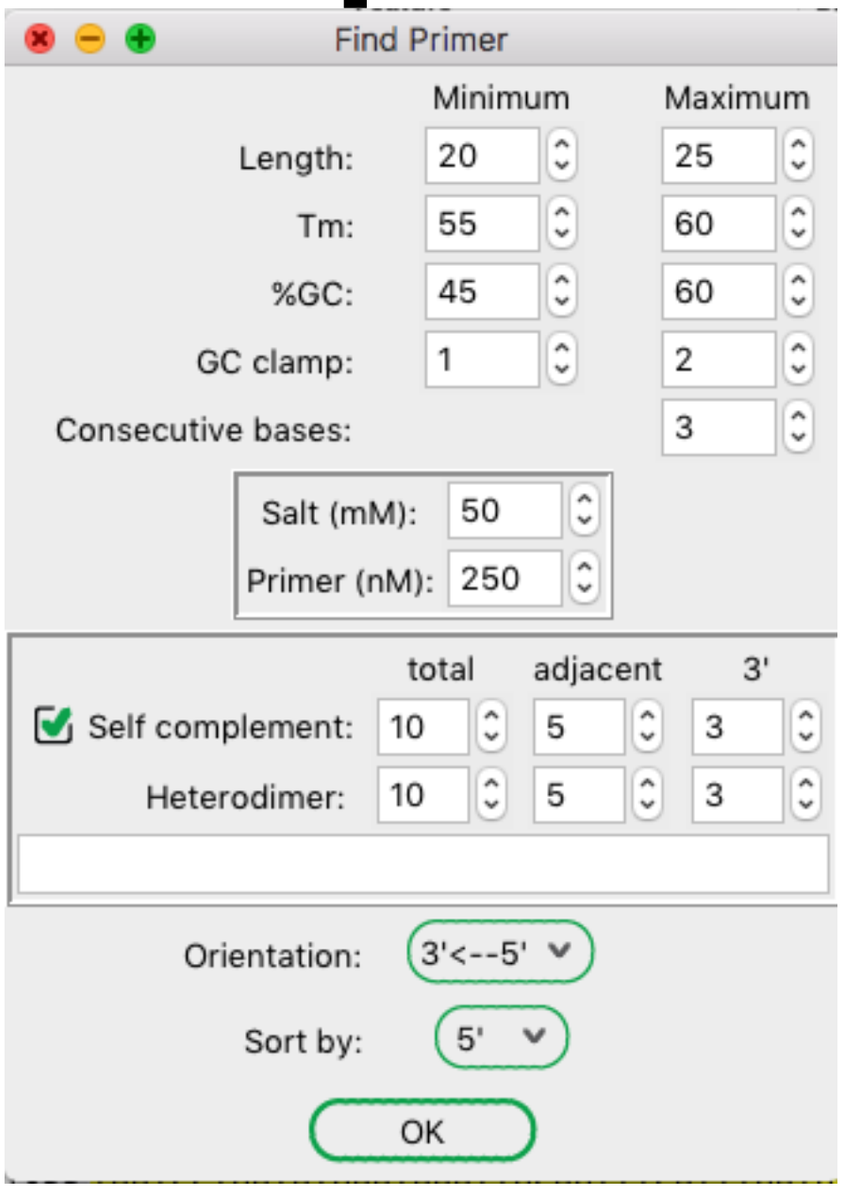
Primers- ApE designed



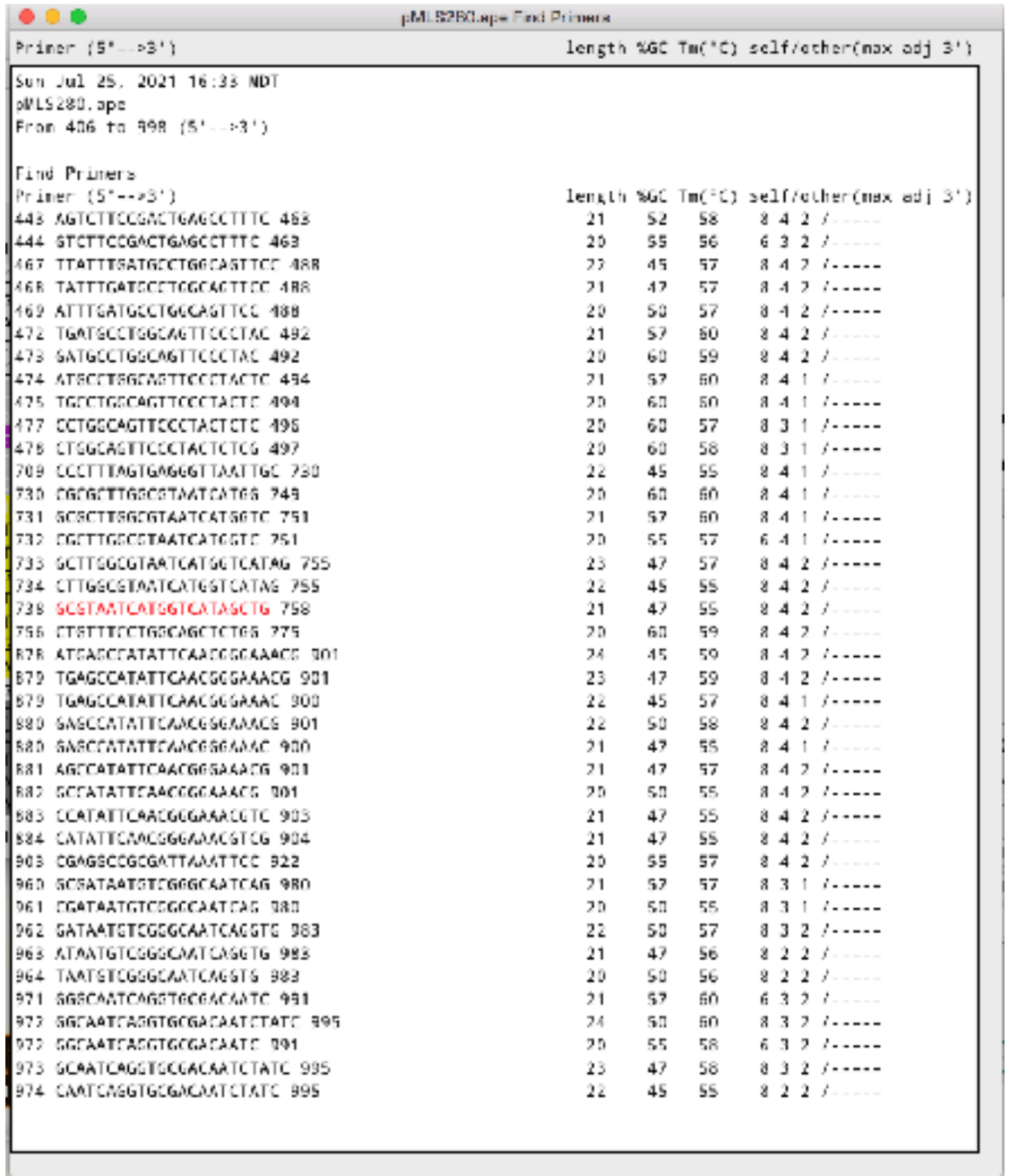
Primers- ApE designed



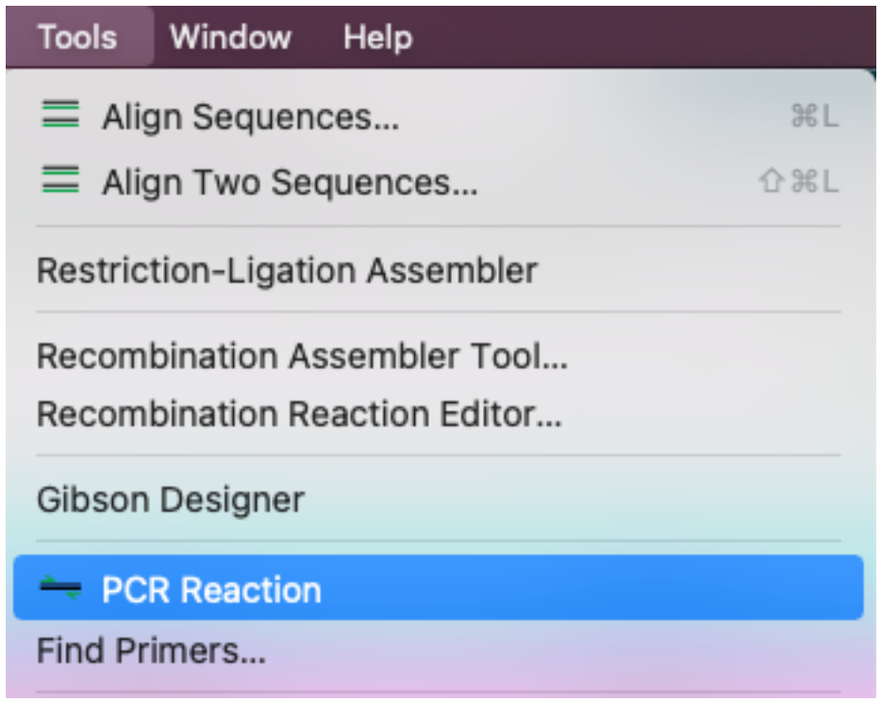
Primers- ApE designed



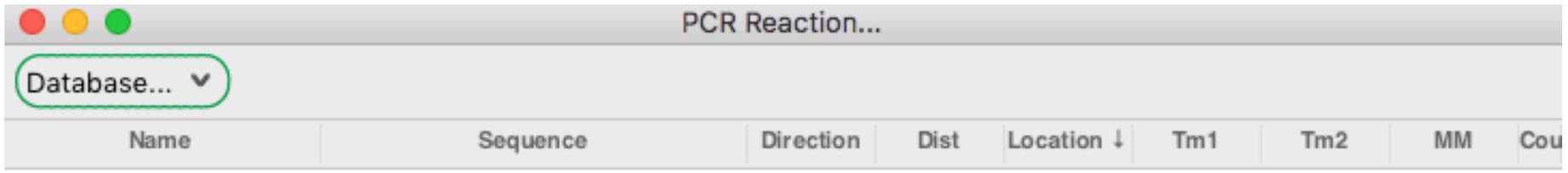
Primers- ApE designed

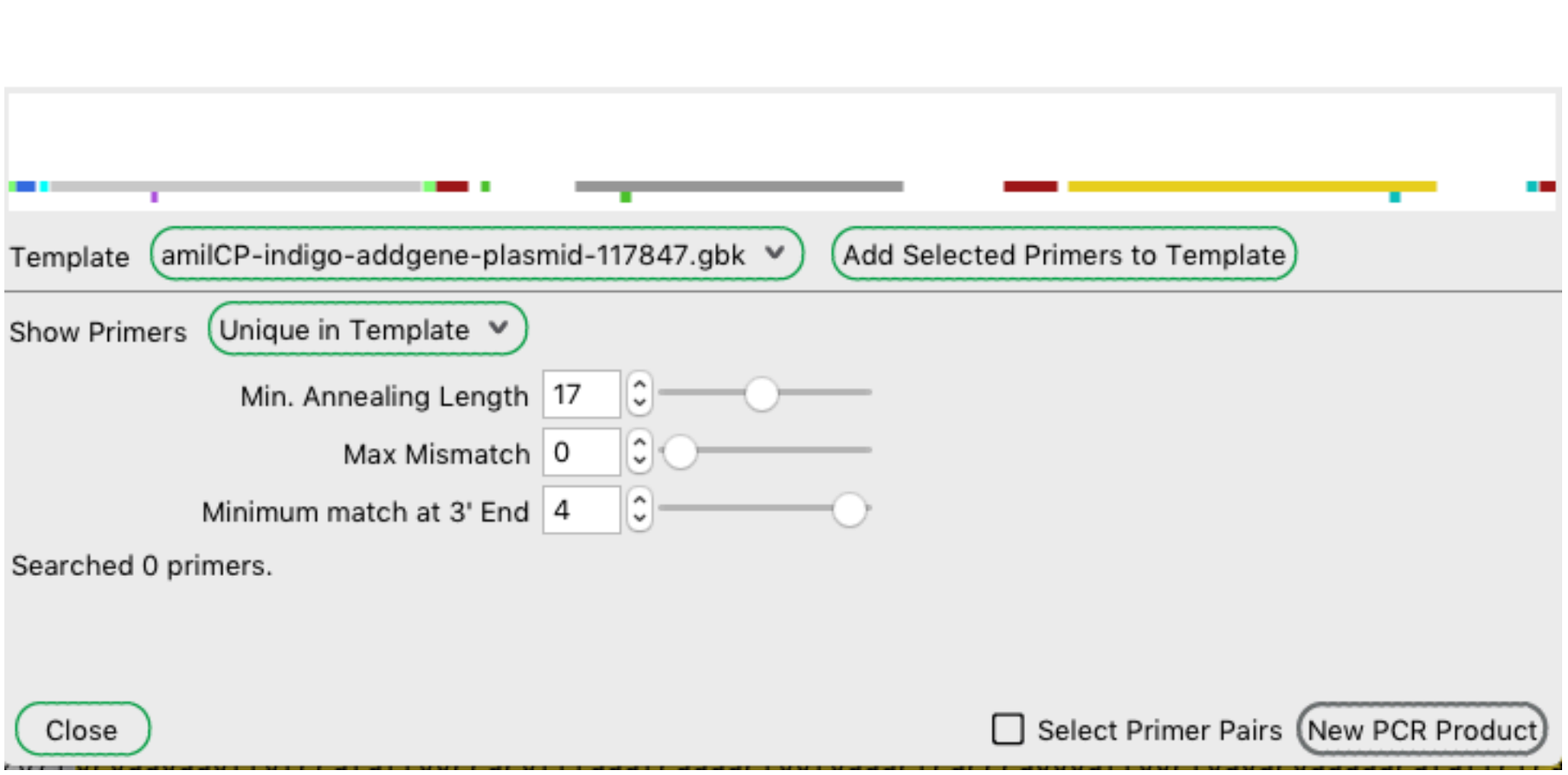


PCR reaction tool

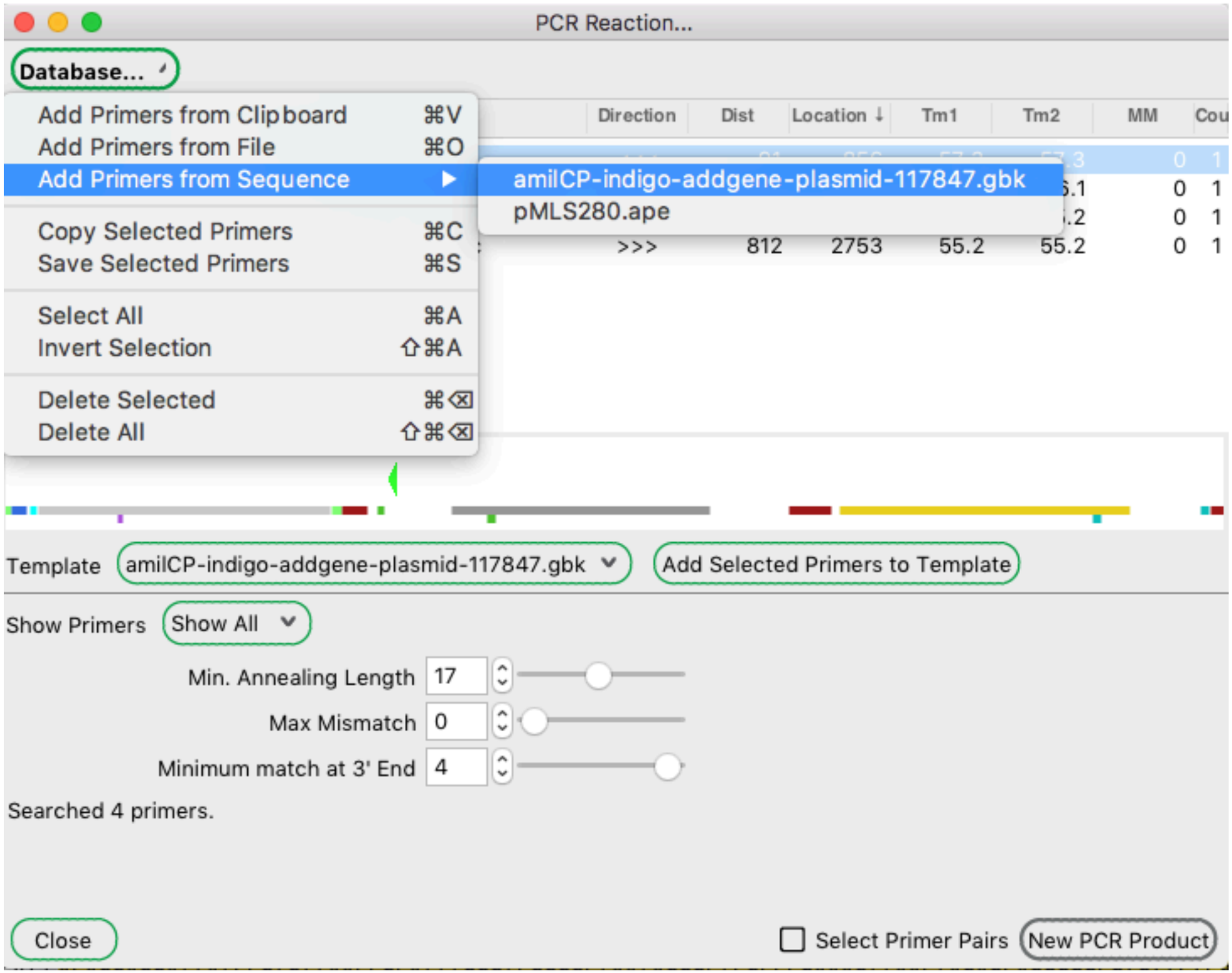


PCR reaction tool





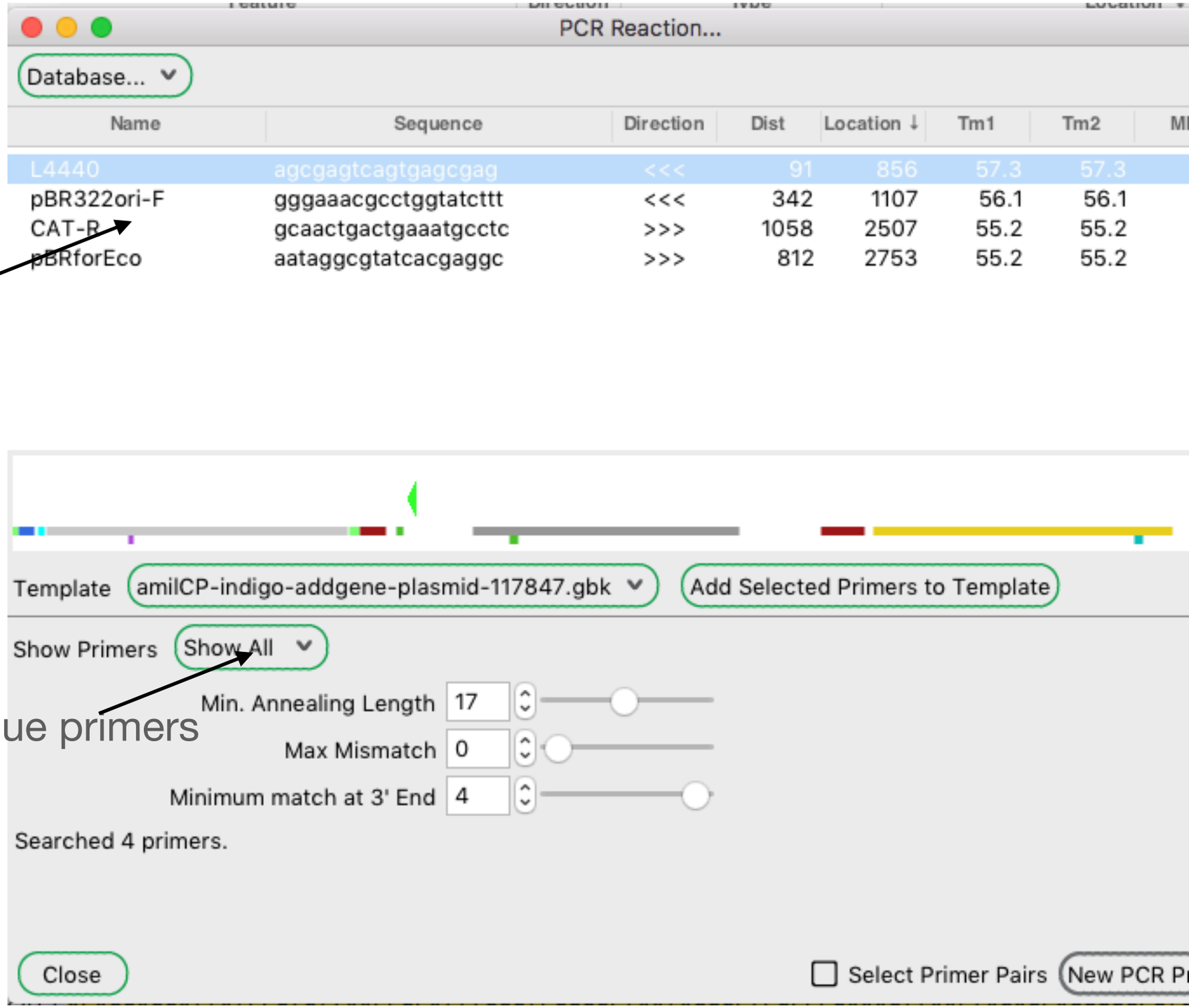
PCR reaction tool



PCR reaction tool

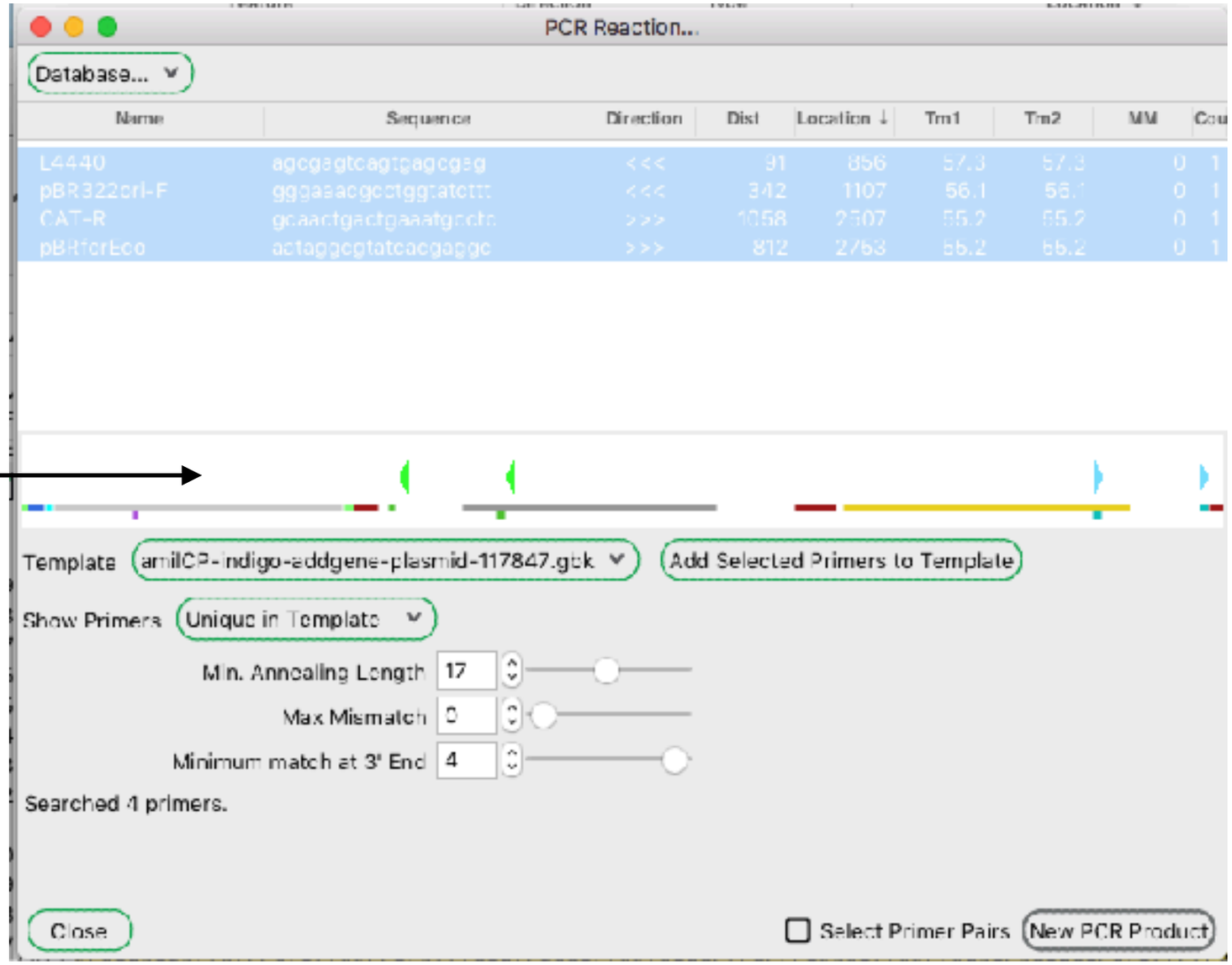
Active primers show up here

Select this to activate just unique primers



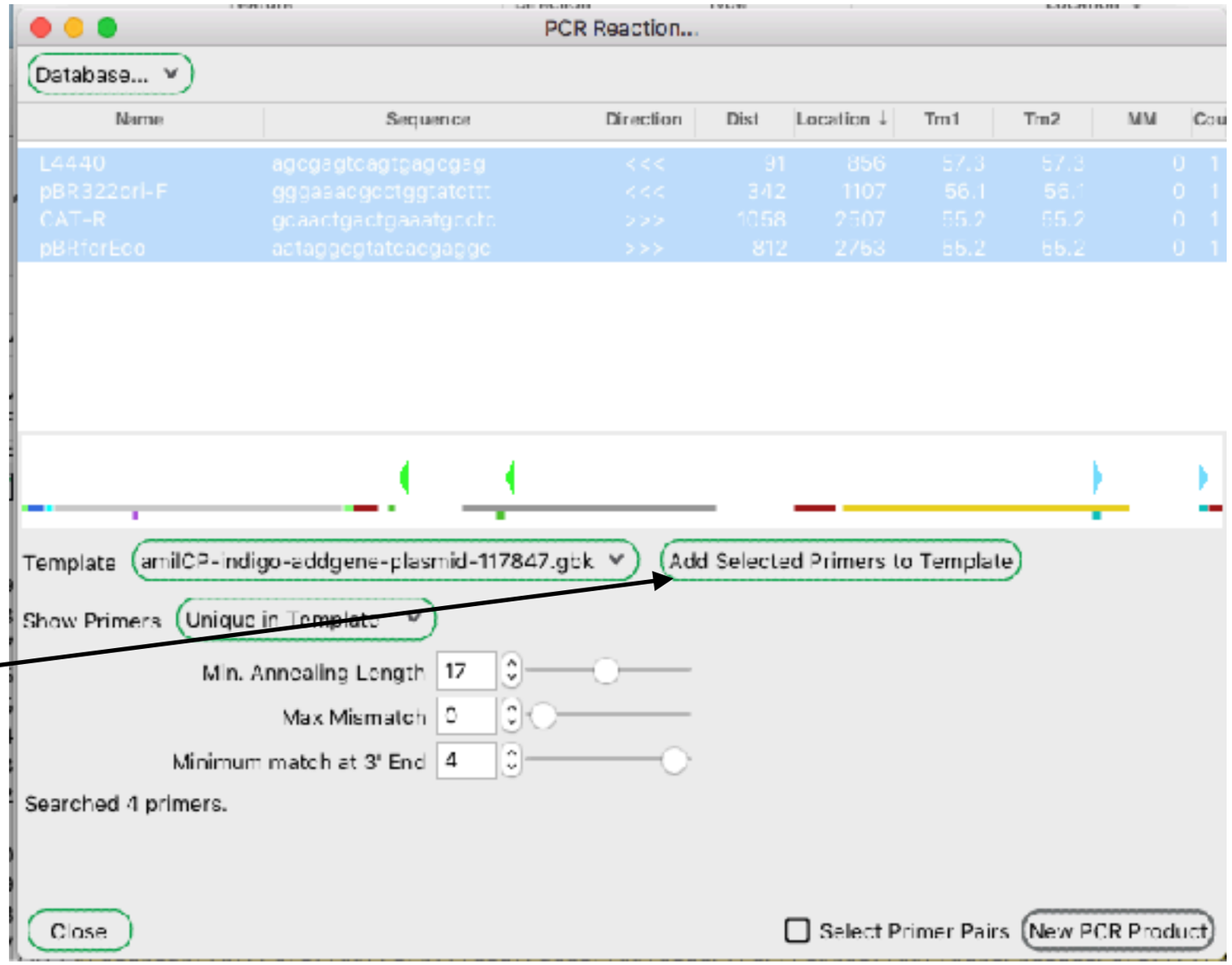
PCR reaction tool

Select primers to show them in the sequence map



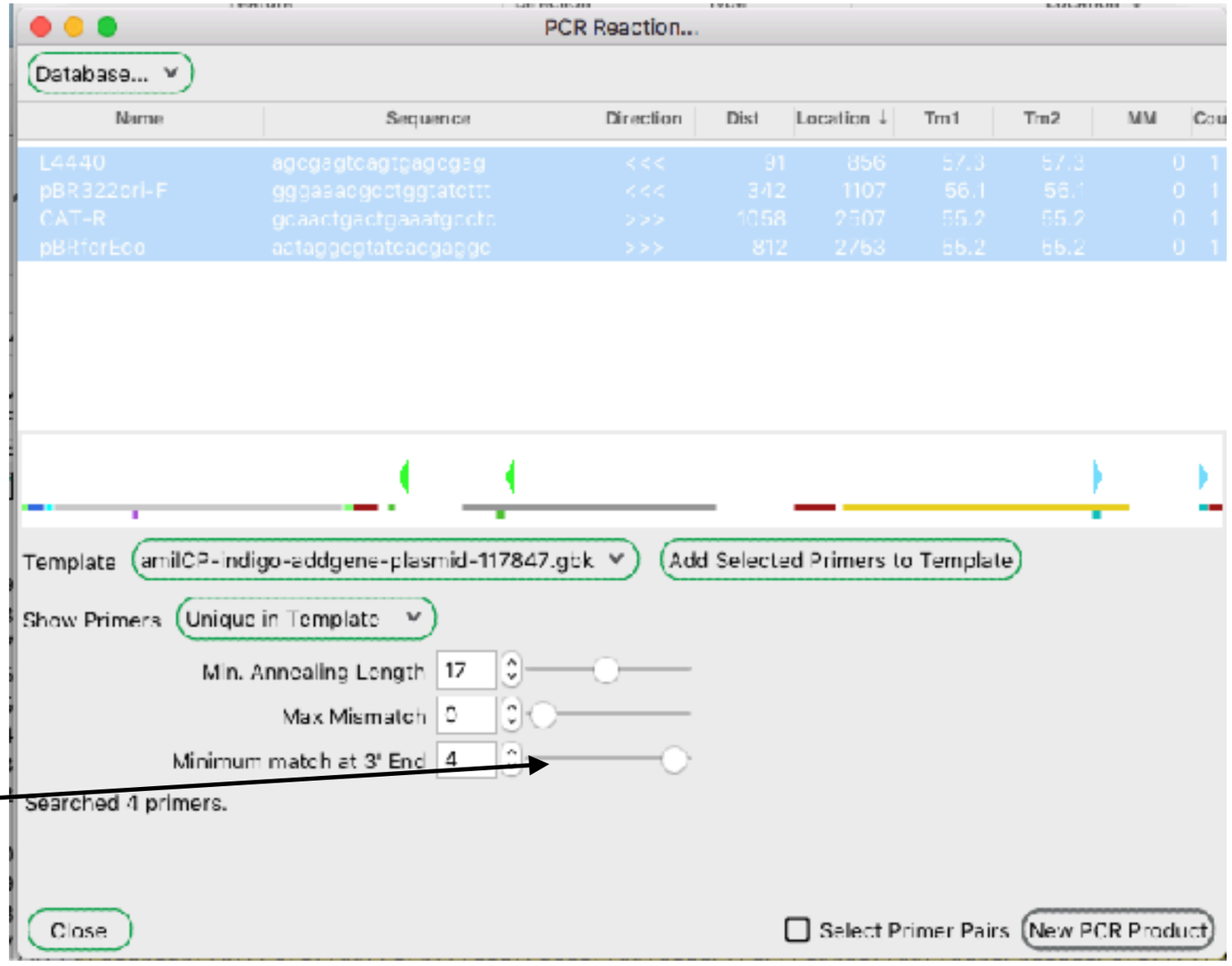
PCR reaction tool

Click here to add selected primers as new primer_bind features



PCR reaction tool

Modify the priming search parameters here



PCR reaction tool

Select all of the class primers and sequences then copy

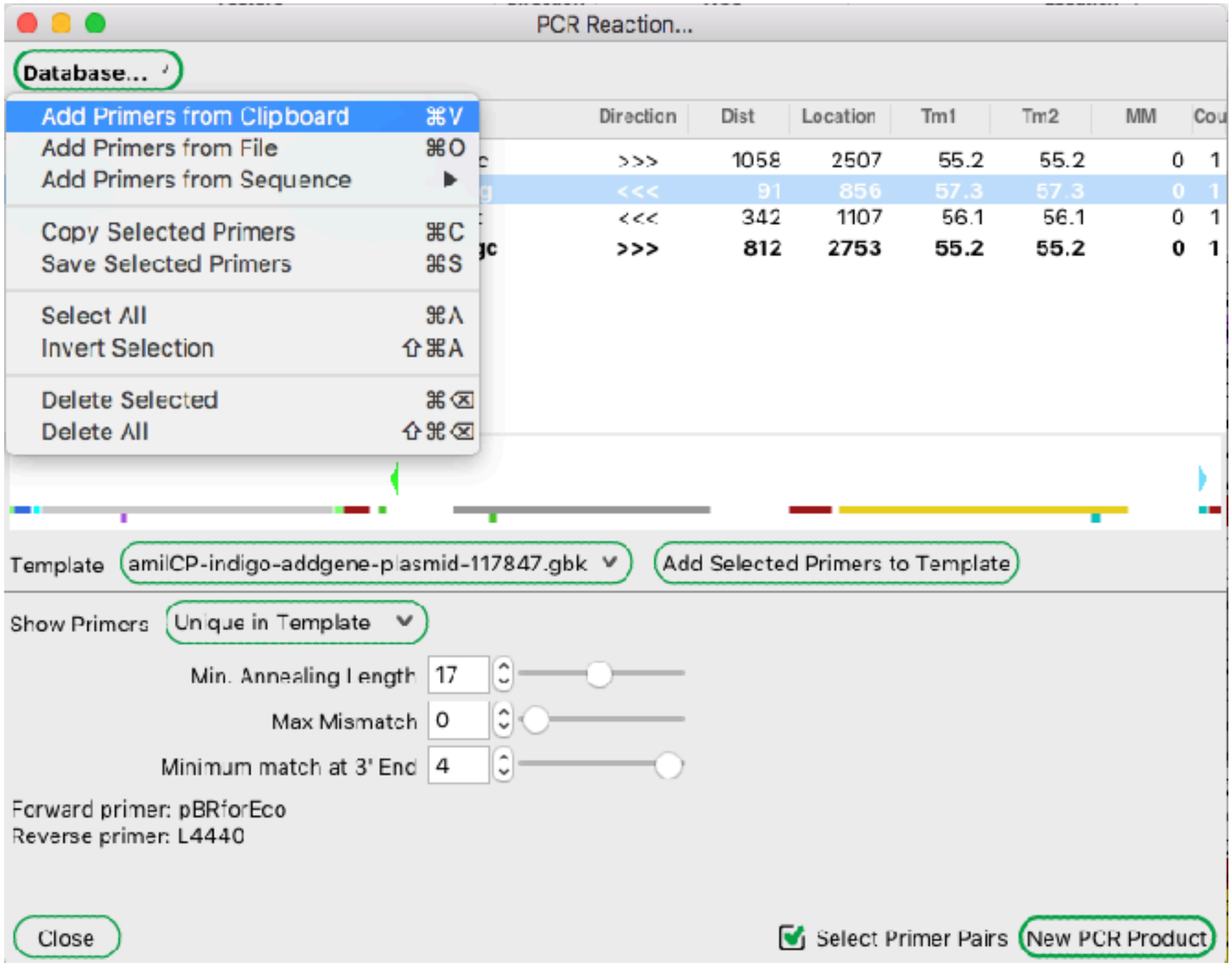
	A	B	C	D
1	oMBC1	gaattcgcggccgcttctagag		
2	oMBC2	agcgagtcagtgagcgaggaagc		
3	oMBC3	gctagccatgtacctaggactgagctag		
4	oMBC4	GCTactagtagcggccgctgcag		
5	oMBC5	tactagagaaagaggagaaatactagAT		
6	oMBC6	ttaTTAGGCGACCACAGGTTTGCG		
7	oMBC7	gtgGCTCTTCgTGGgaattcgcggccgc		
8	oMBC8	gtgGCTCTTCgCA-GCAAATGGCACAGG		
9	oMBC9	gtgGCTCTTCgACgAAGTACCCTGAAGA		
10	oMBC10	gtgGCTCTTCgTACctgcagcggccgct		
11	oMBC11	gtgGCTCTTCgCGTGAATGGTATGCTTC		
12	oMBC12	gtgGCTCTTCgATGGGATATTTTATCAC		
13	oMBC13	gtgGCTCTTCgATGGGATATTTTATCAC		
14	oMBC14	gtgGCTCTTCgATGGGATATTTTATCAC		
15	oMBC15	gtgGCTCTTCgATGGGATATTTTATCAC		
16	oMBC16	gtgGCTCTTCgATGGGATATTTTATCAC		
17	oMBC17	gtgGCTCTTCgATGGGATATTTTATCAC		
18	oMBC18	gtgGCTCTTCgATGGGATATTTTATCAC		
19	oMBC19	gtgGCTCTTCgATGGGATATTTTATCAC		
20	oMBC20	gtgGCTCTTCgATGGGATATTTTATCAC		
21	oMBC21	gtgGCTCTTCgATGGGATATTTTATCAC		
22	oMBC22	/phos/CTGTGGTGATAAAATATCCCAA		
23	oMBC23	/phos/NNKNNKTACGGAAGCATACCATT		
24	oMBC24	ggggacaagtttgtacaaaaaagcaggc		
25	oMBC25	ggggaccactttgtacaagaaagctggg		
26	oMBC26	actggcgtcgttttaca		
27	oMBC27	catggtcatagctgtttcctg		
28	oMBC28	tgtaaaacgacggccagtgaattcgcggccgcttctaga		
29	oMBC29	CAGGGTACTTGGTGAATGGTATGCT		
30	oMBC30	AGCATACCATTCACCAAGTACCCTG		
31	oMBC31	caggaaacagctatgaccatgctgcagcggccgctacta		
32	oMBC32	caggaaacagctatgaccatg		
33	oMBC33	tgtaaaacgacggccagt		
34	oMBC22	CTGTGGTGATAAAATATCCCAAGCAAAT		
35	oMBC23	NNKNNKTACGGAAGCATACCATTCACCA		
36				
37				

PCR reaction tool

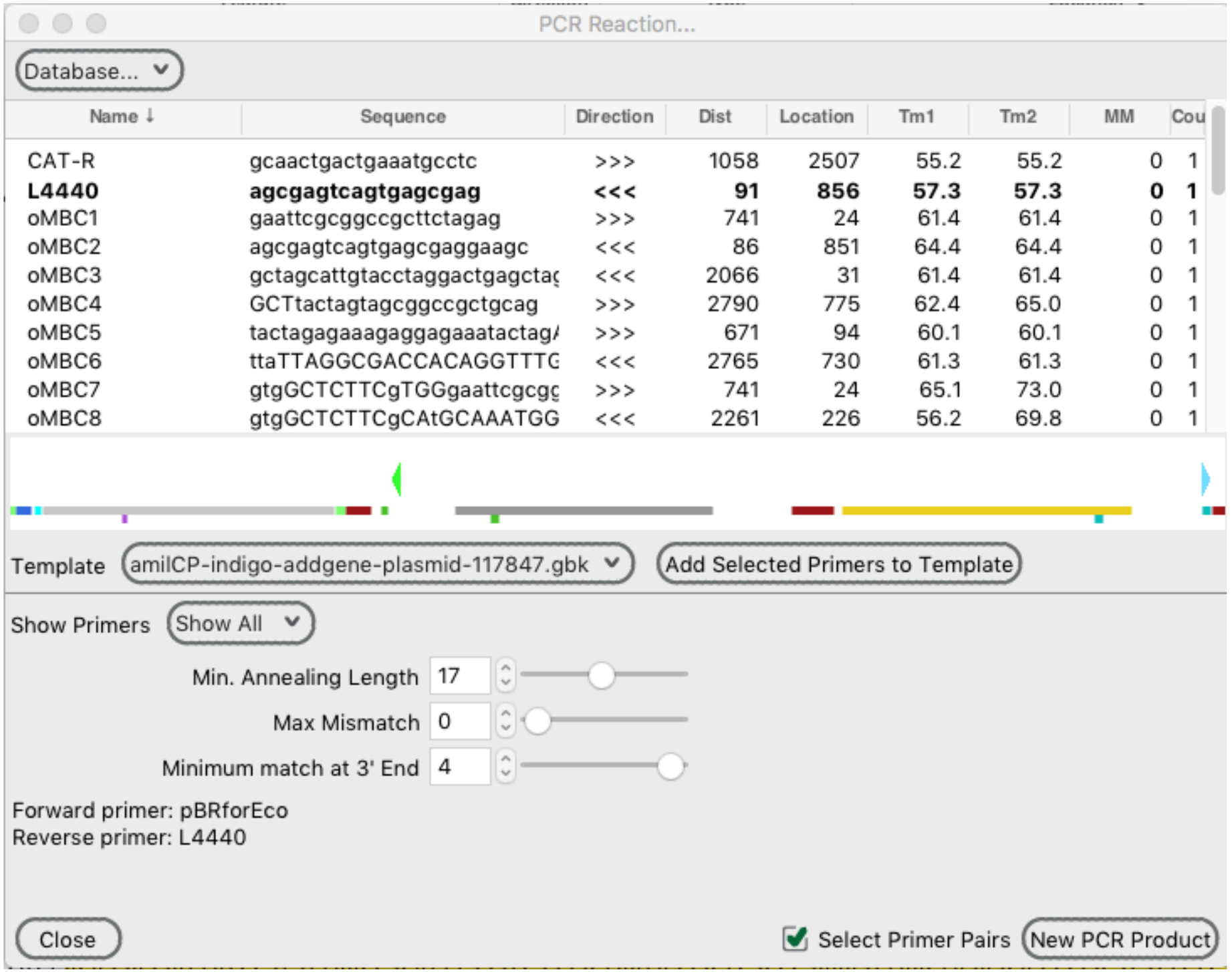
Primers can be:

sequence
name (tab) sequence
name (tab) sequence (tab) note
feature library format

PCR reaction tool

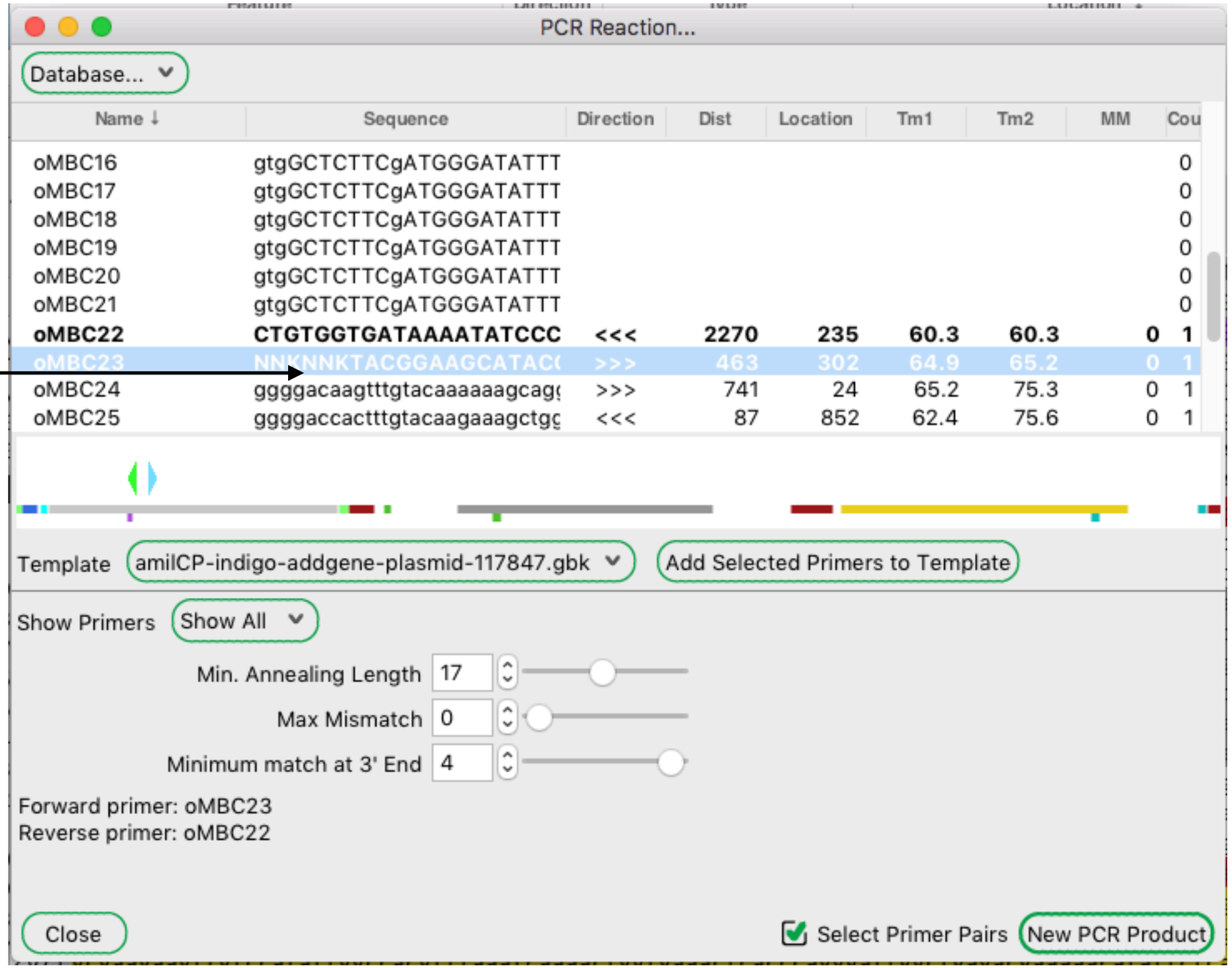


PCR reaction tool

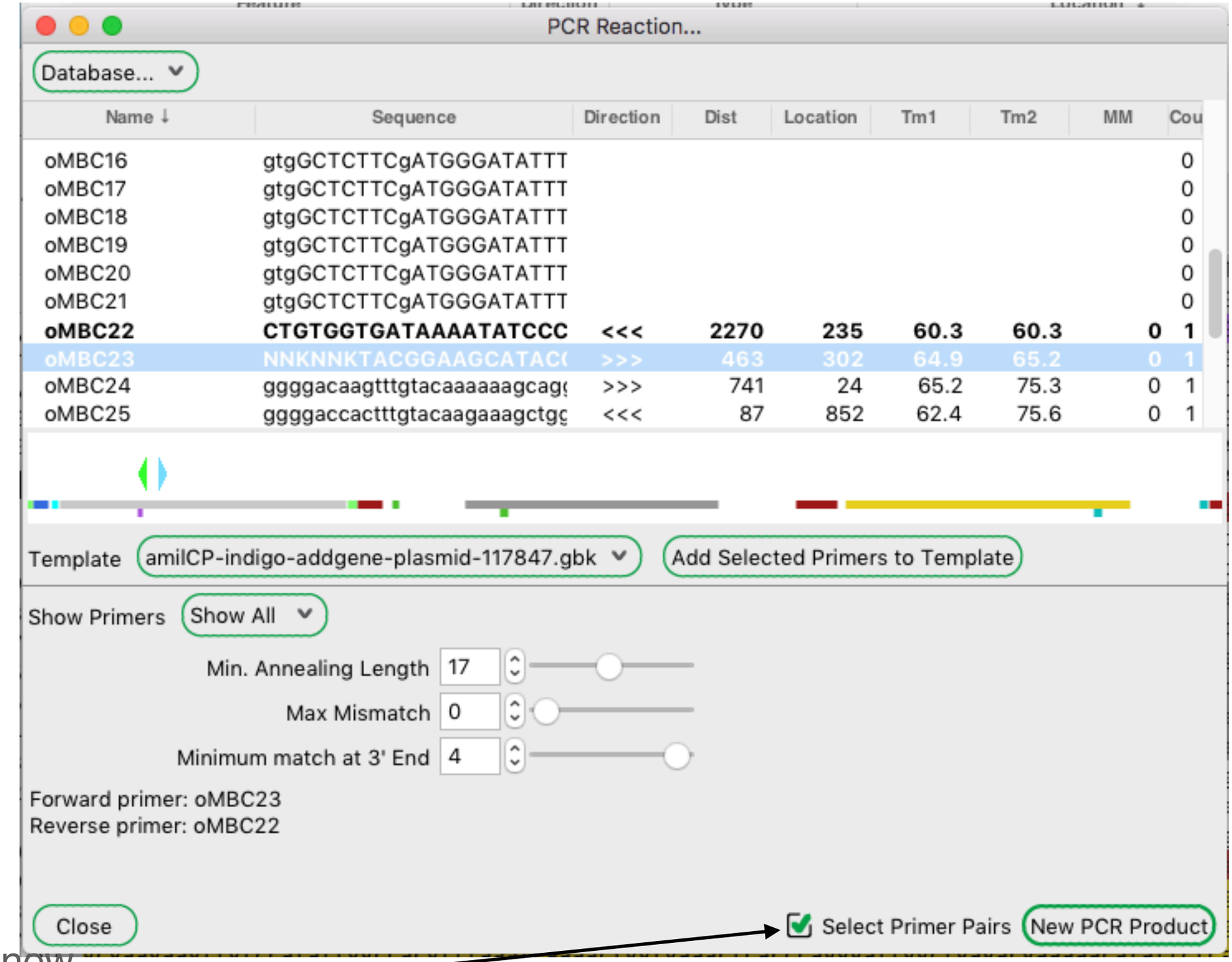


PCR reaction tool

Select oMBC22 and 23 primers.
These are the around the horn mutagenic primers.



PCR reaction tool

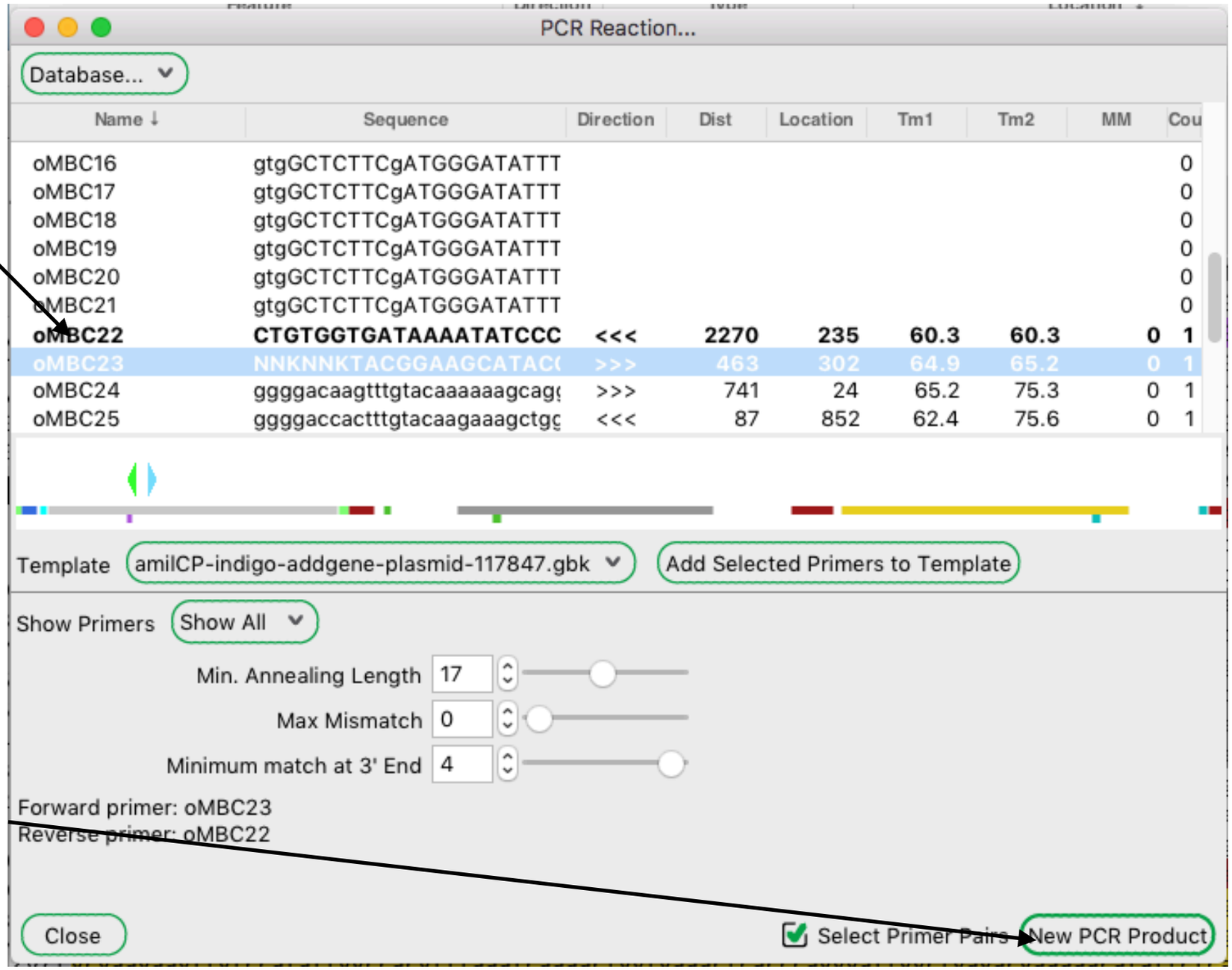


Select this to do a new PCR reaction

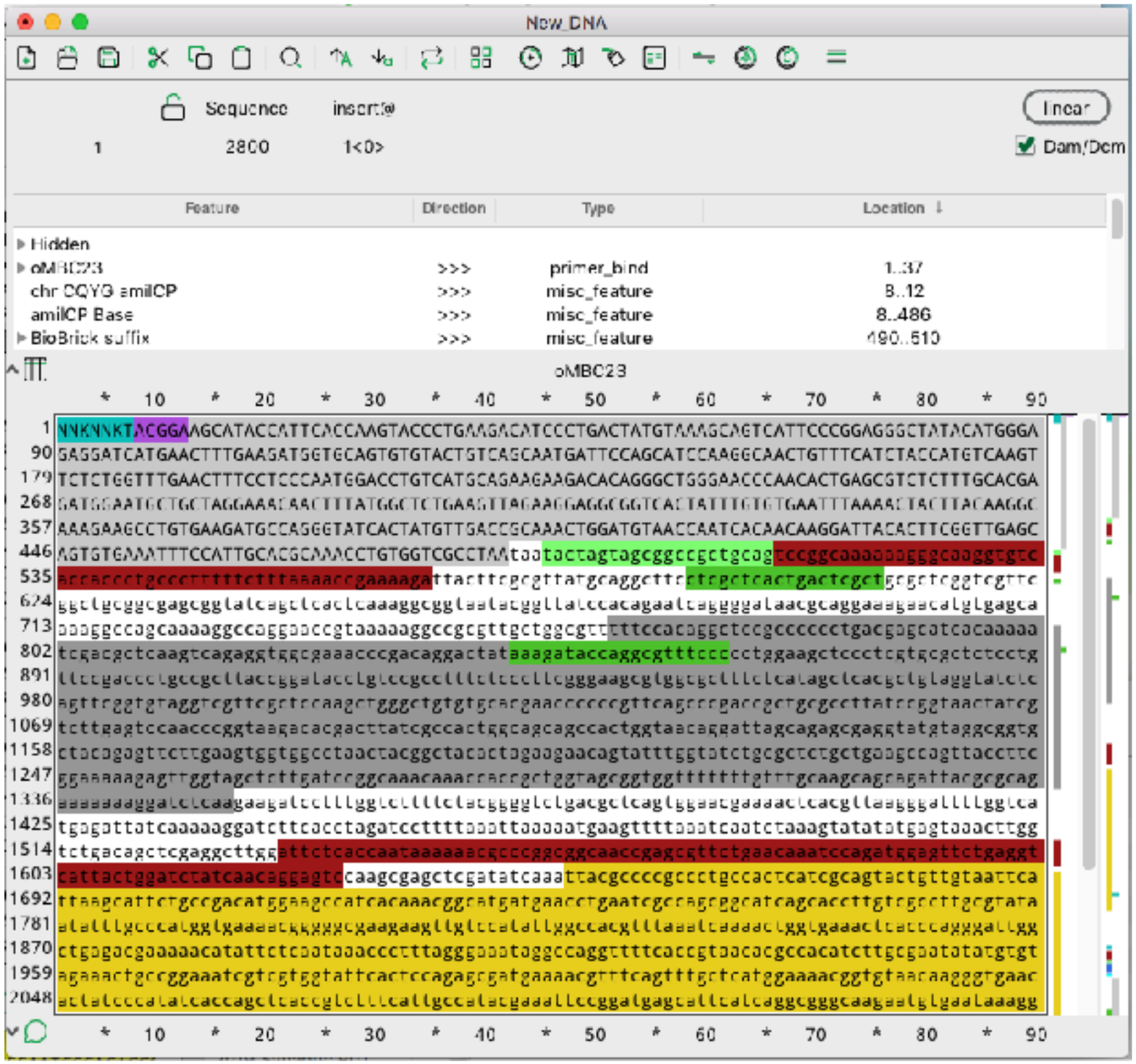
PCR reaction tool

In primer pair mode, only one forward and one reverse primer can be selected. Selected primers are in bold.

New PCR will become active when a pair of primers is selected.



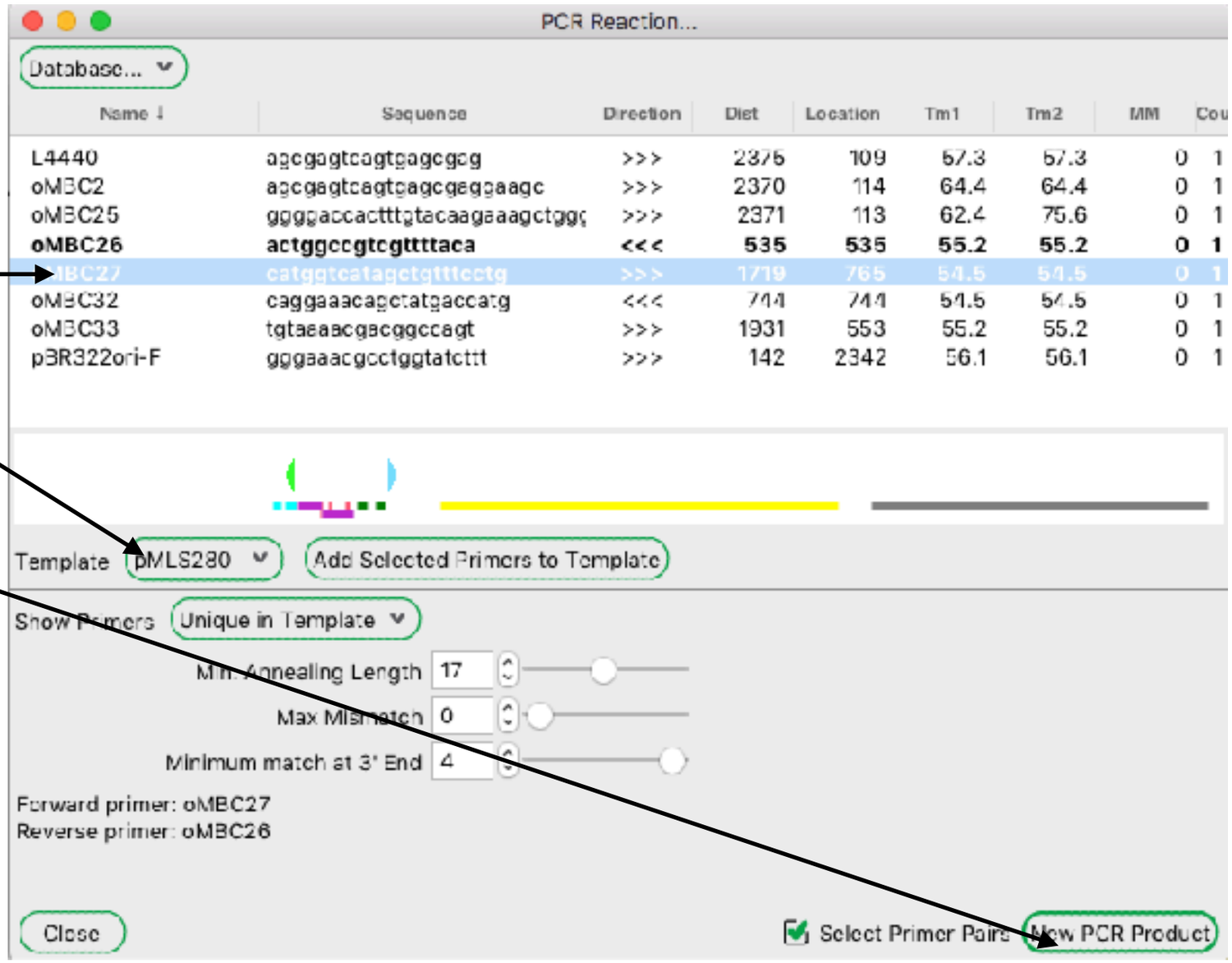
PCR reaction tool



Gibson Designer

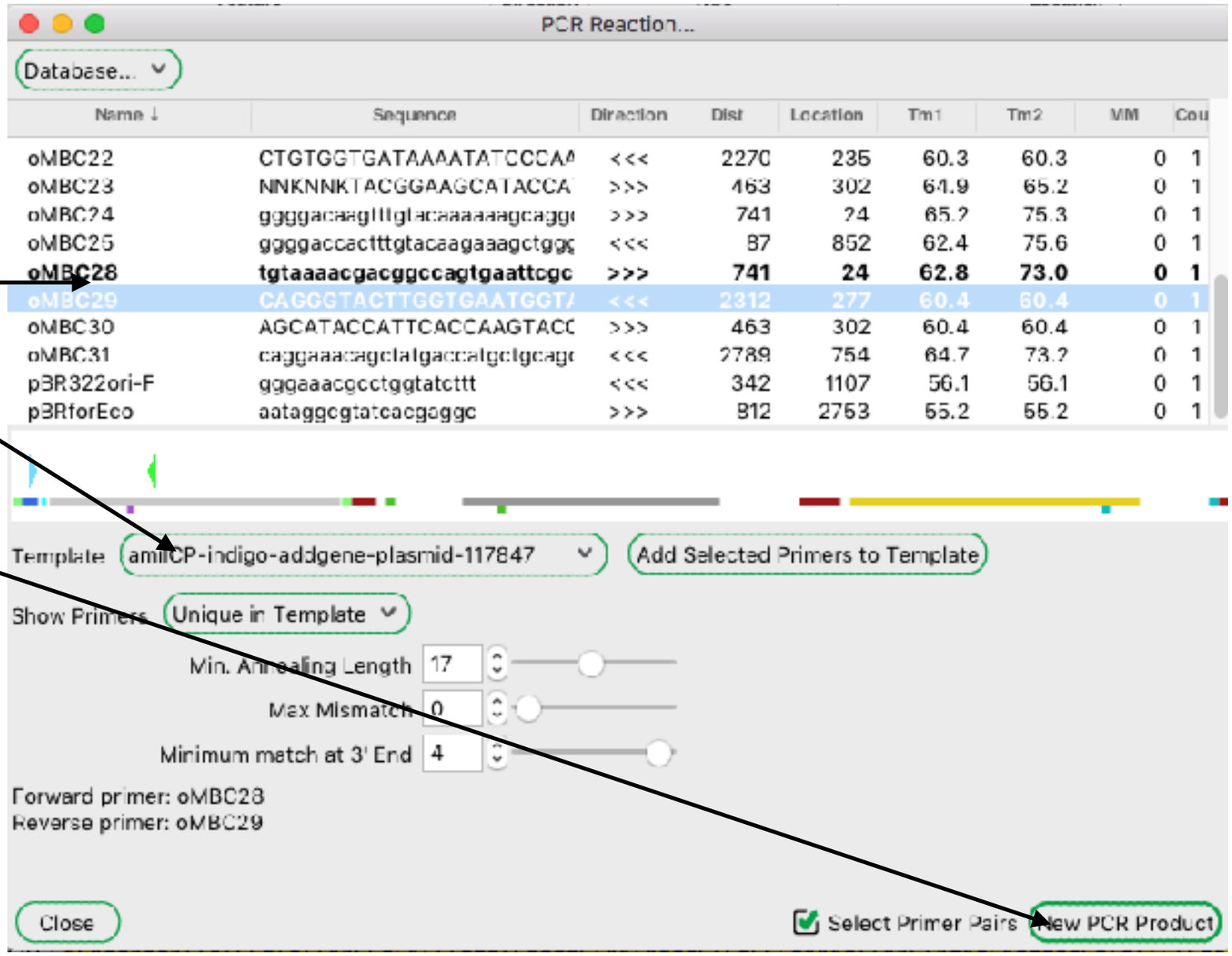
Gibson Designer

Do oMBC26-oMBC27 PCR on pMLS280



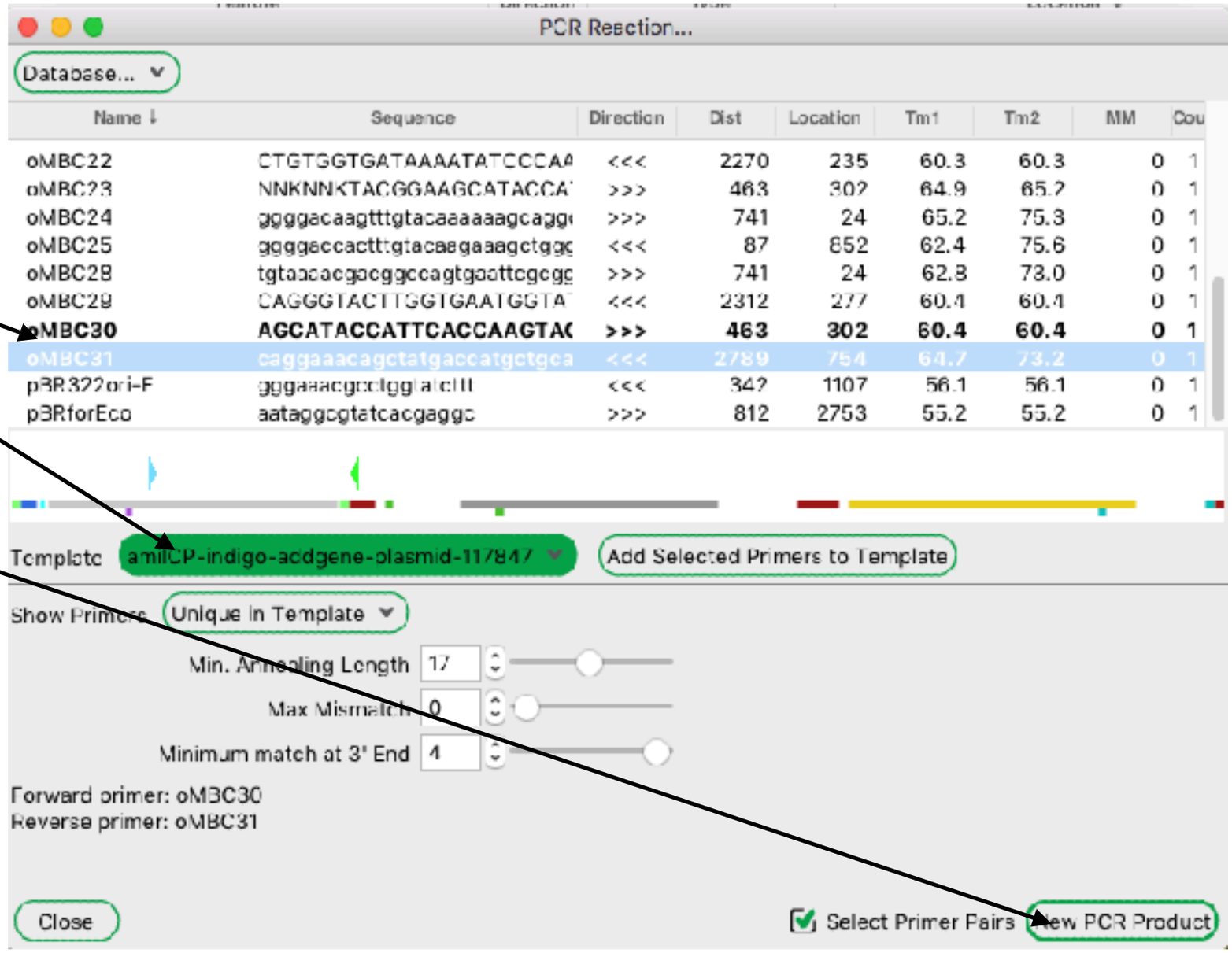
Gibson Designer

Do oMBC28-oMBC29 PCR on amilCP

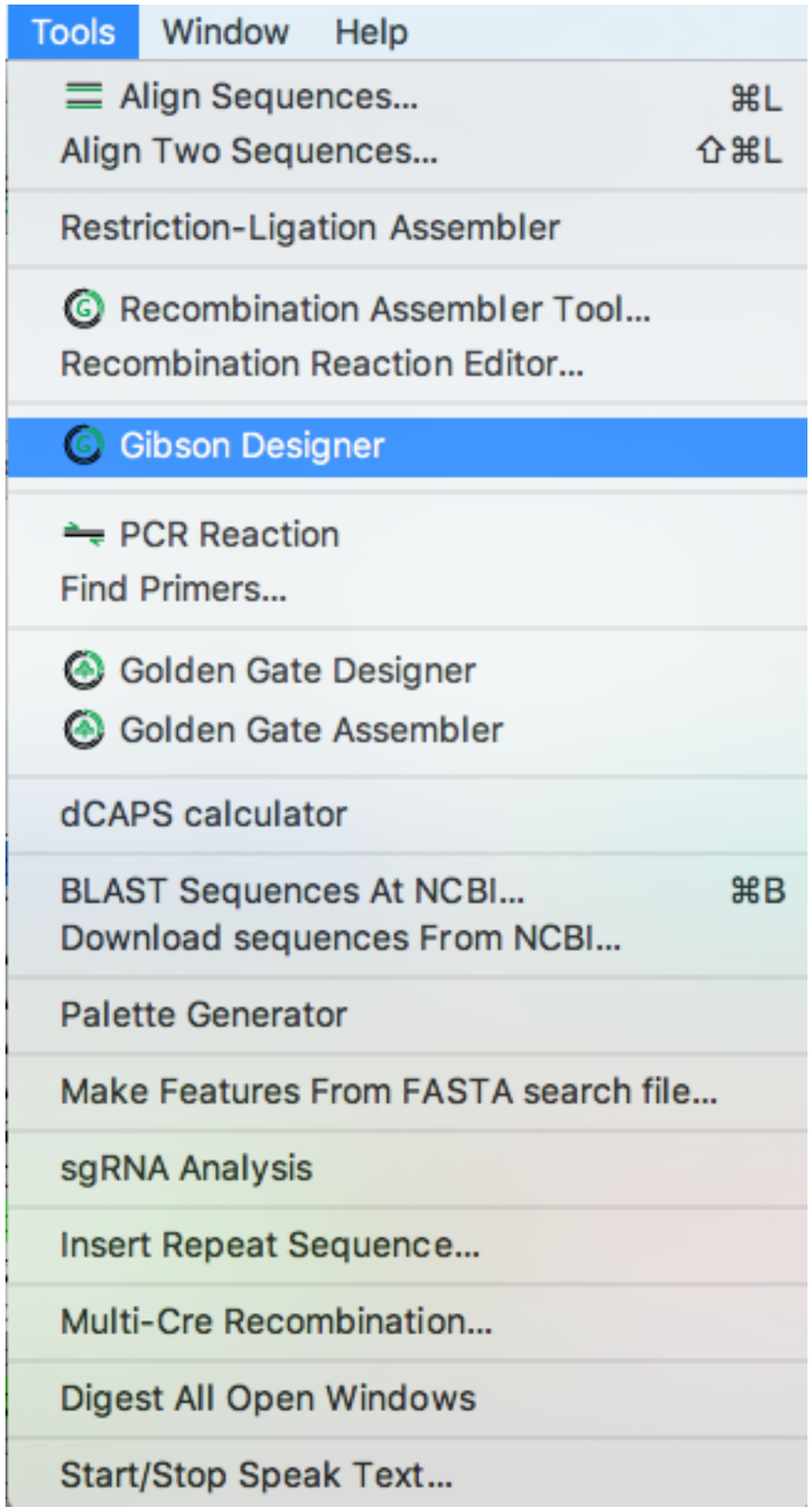


Gibson Designer

Do oMBC30-oMBC31 PCR on amilCP

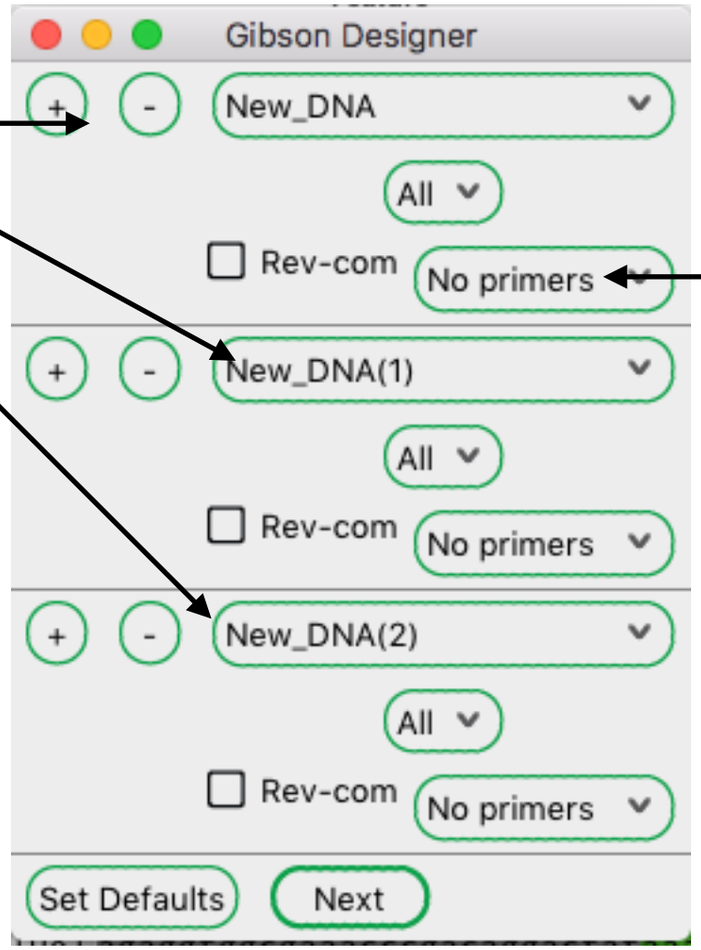


Gibson Designer



Gibson Designer

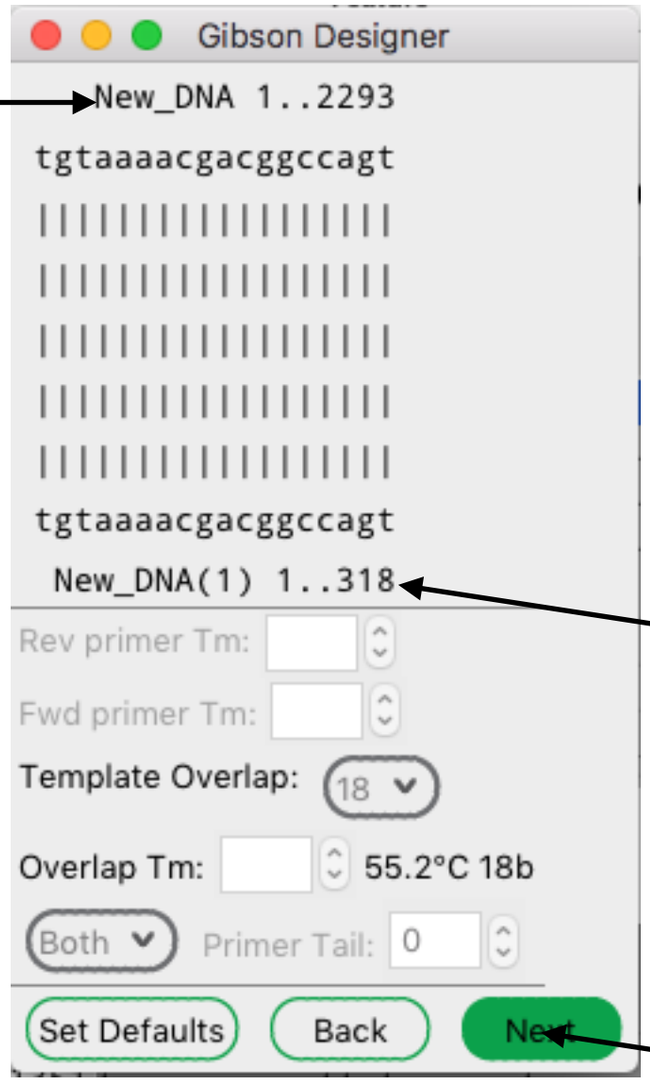
add the three new DNA sequences in order



In this case, we don't need new primers. We are doing a Gibson using someone else's design

Gibson Designer

First fragment

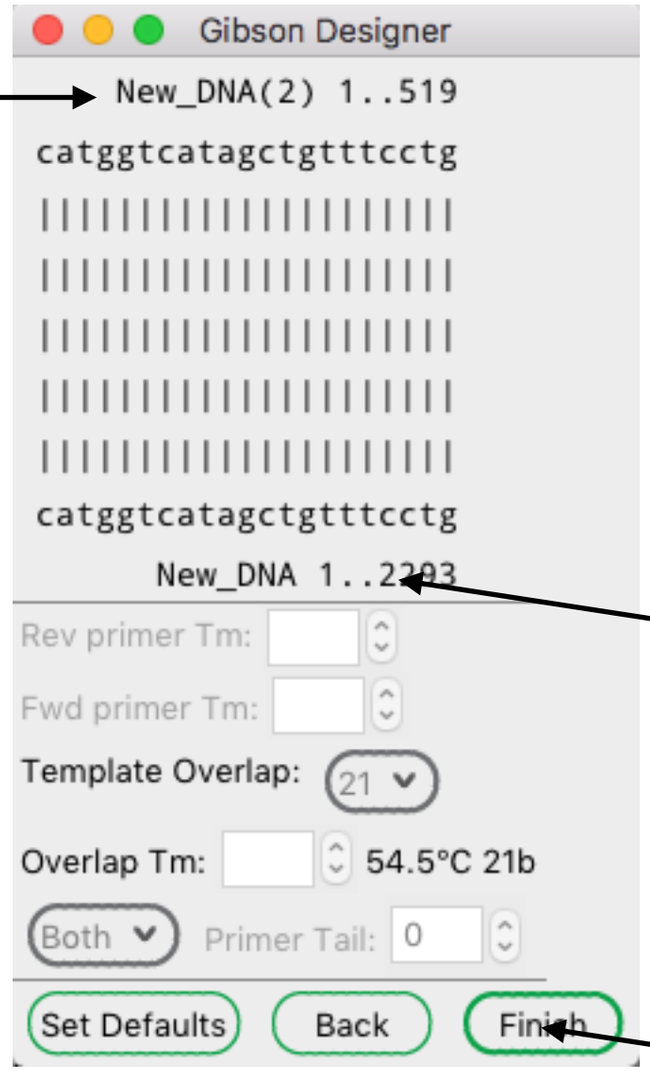


Second fragment

Press next to see each of the three junctions

Gibson Designer

Second fragment



Final fragment

Generate product

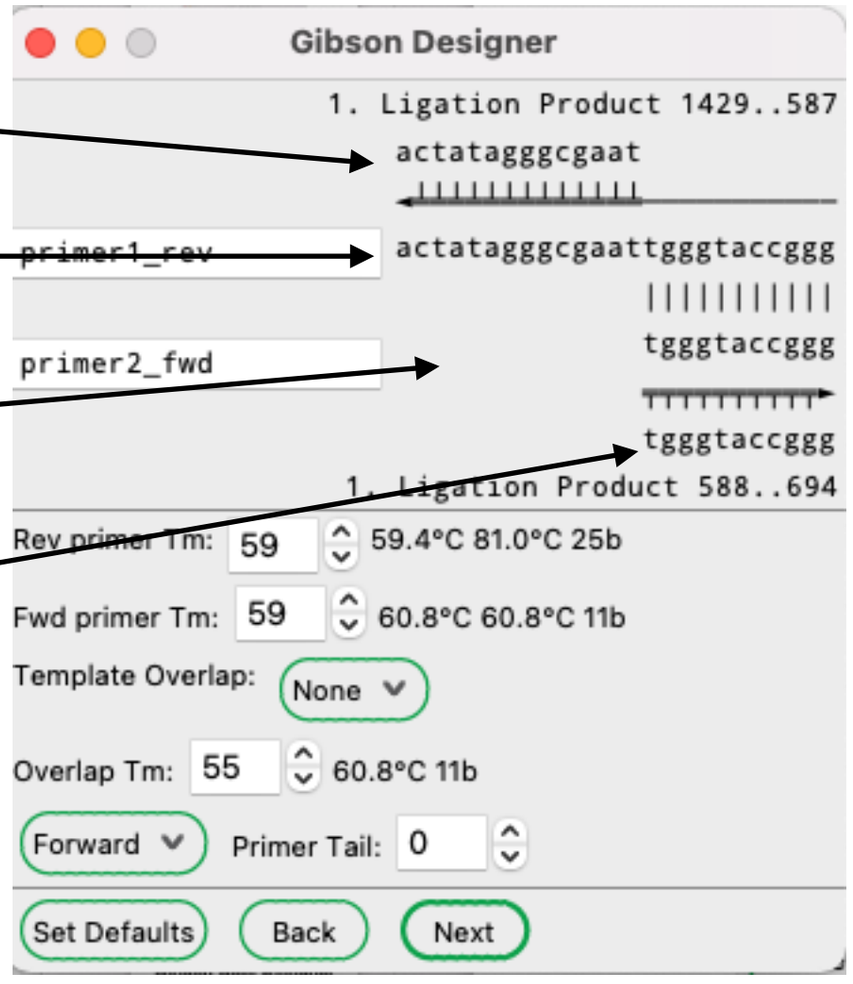
Gibson Designer

The first template sequence

The reverse primer sequence

The forward primer sequence

The second template sequence

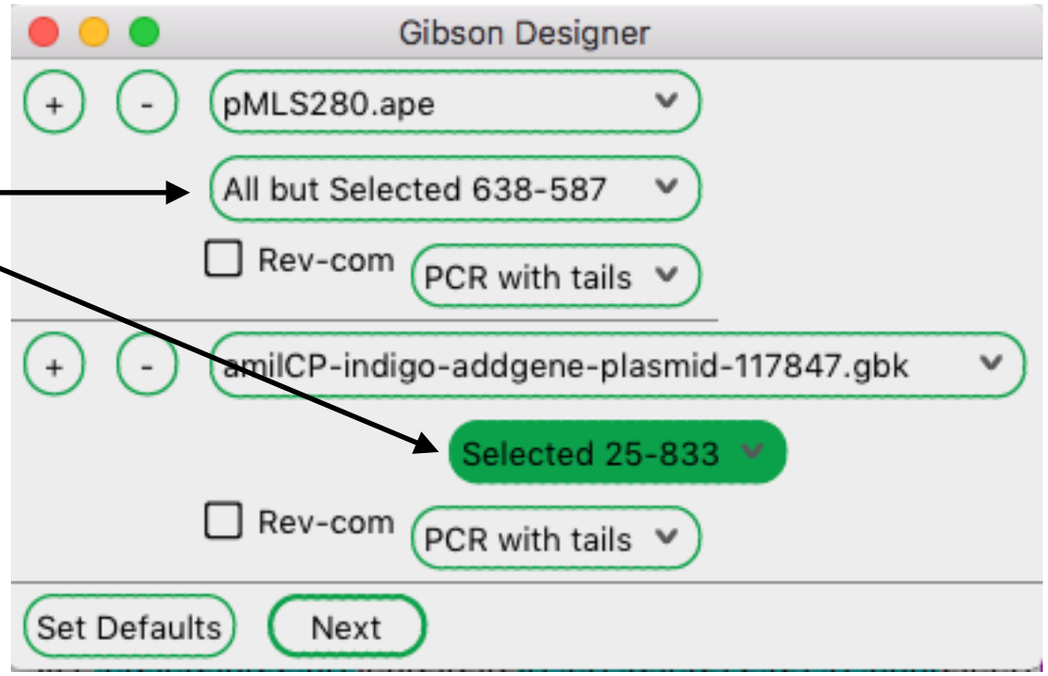


Gibson Designer

Design a new Gibson reaction

Gibson Designer

Use the open plasmids with these selection ranges



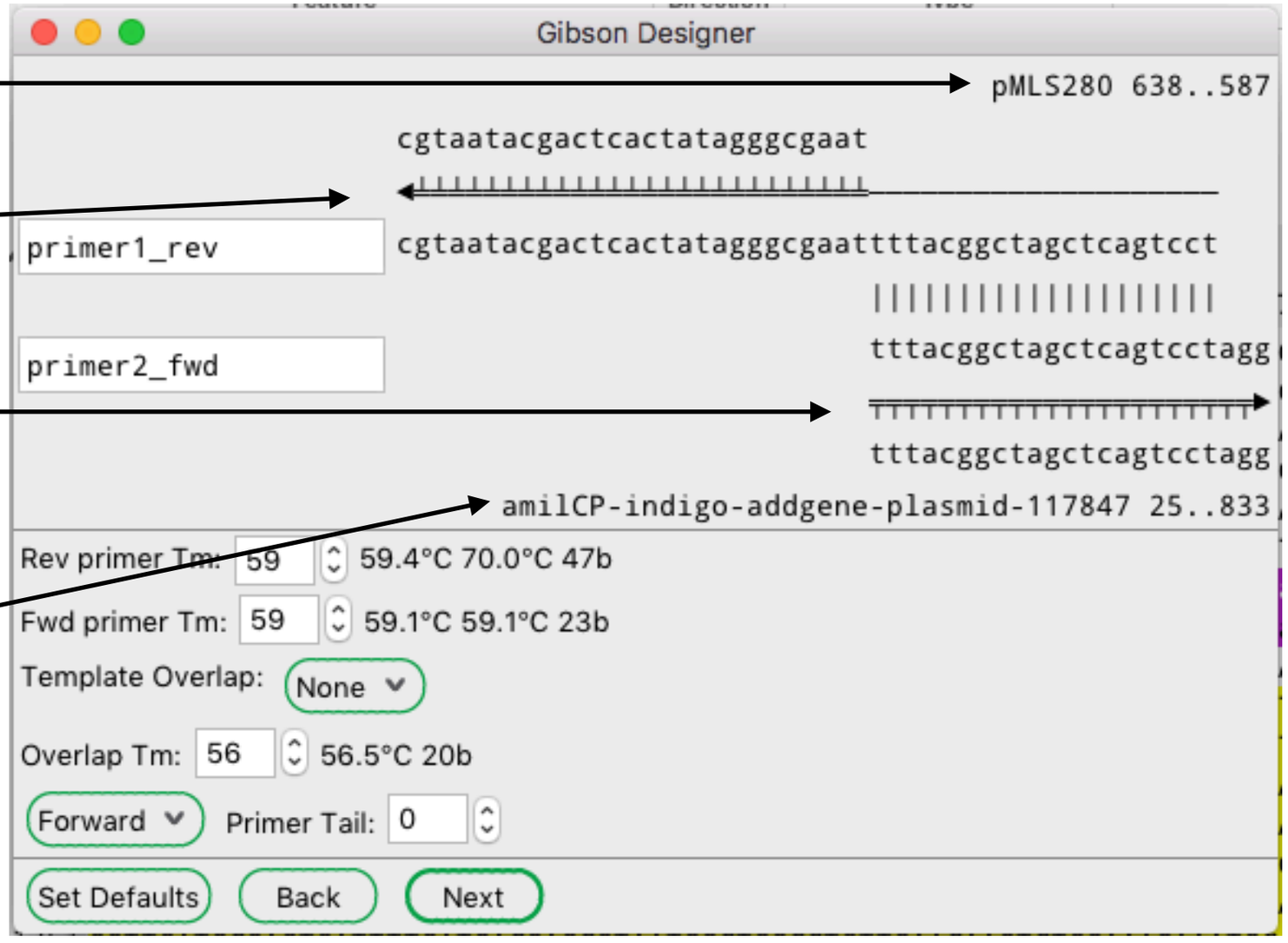
Gibson Designer

First fragment

Reverse primer

Foreward primer

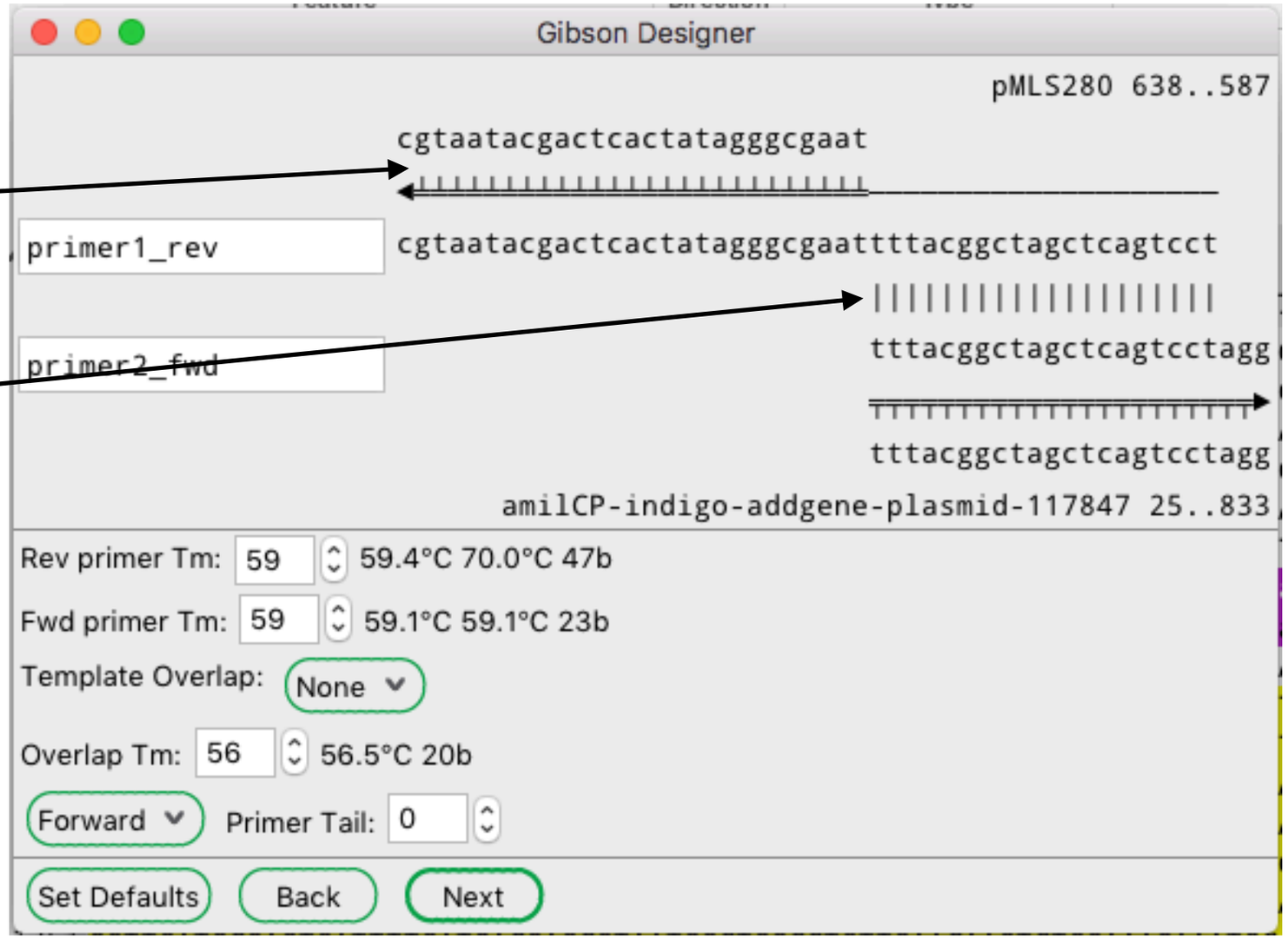
Second fragment



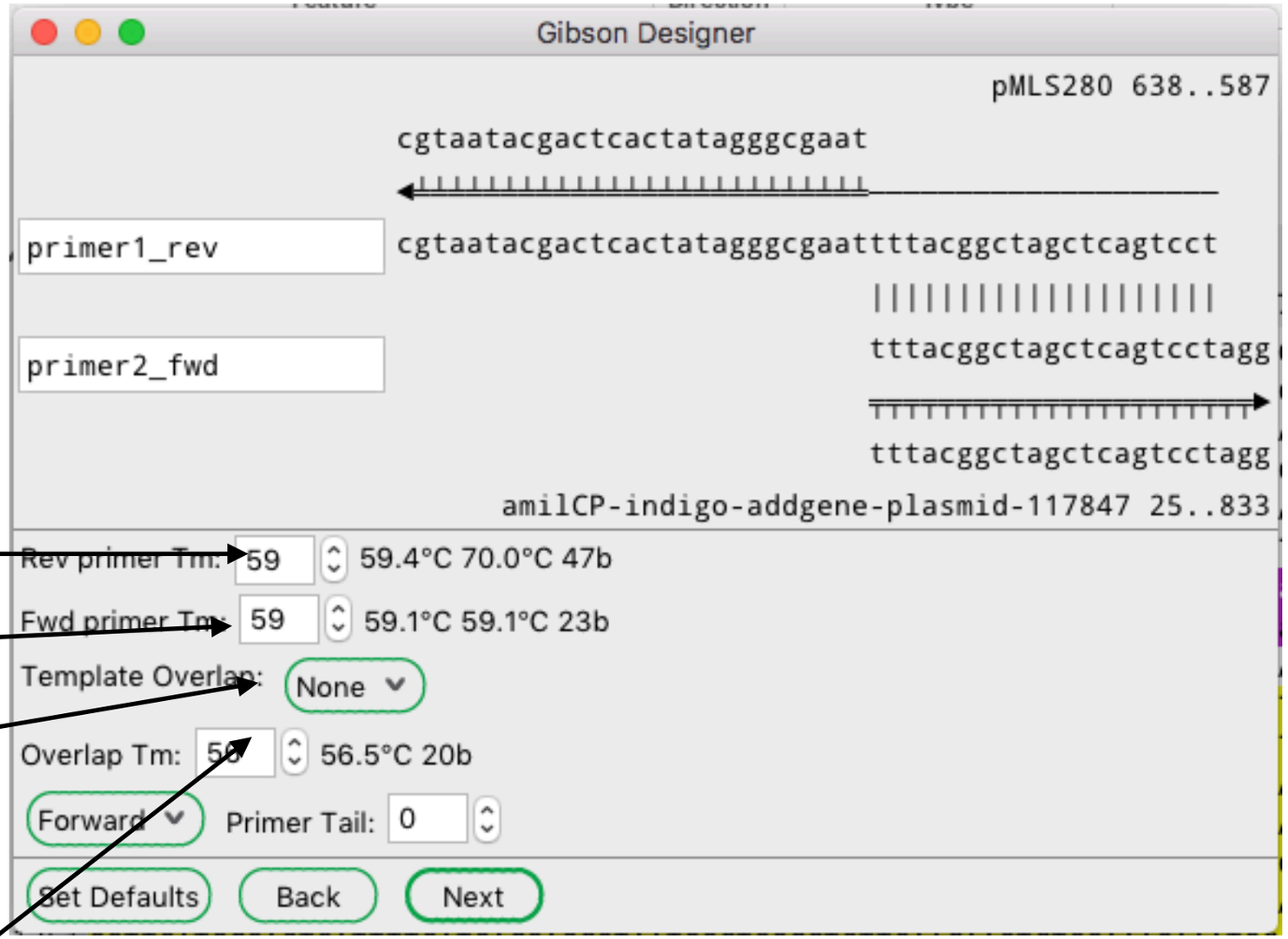
Gibson Designer

priming hybridization

Gibson hybridization



Gibson Designer



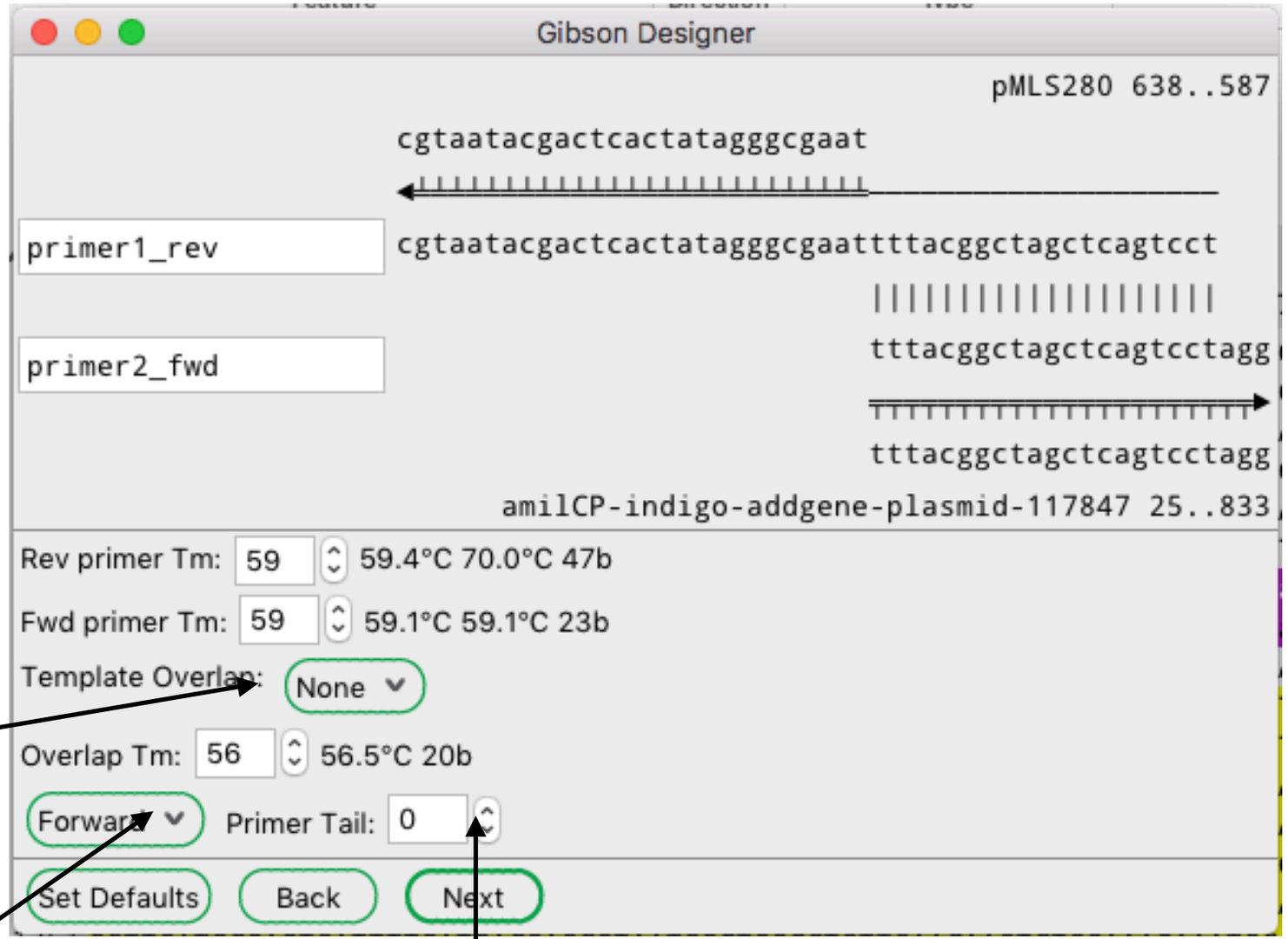
Adjust the Tm

Adjust the Tm

If there is already overlap between the templates, you can use that

Adjust the overlap Tm

Gibson Designer

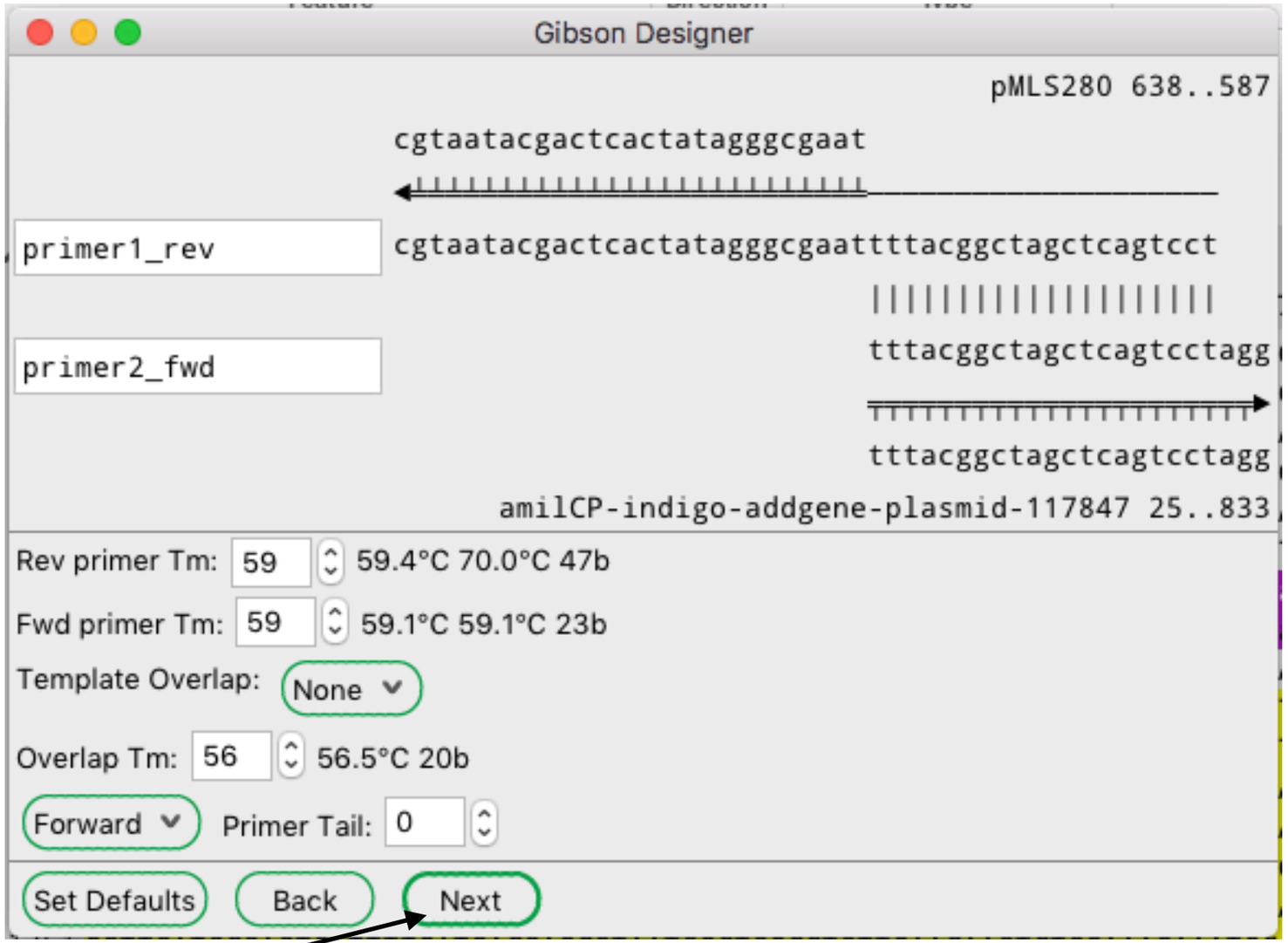


You can also add non-templated sequence here

Set which fragment gets the overlap

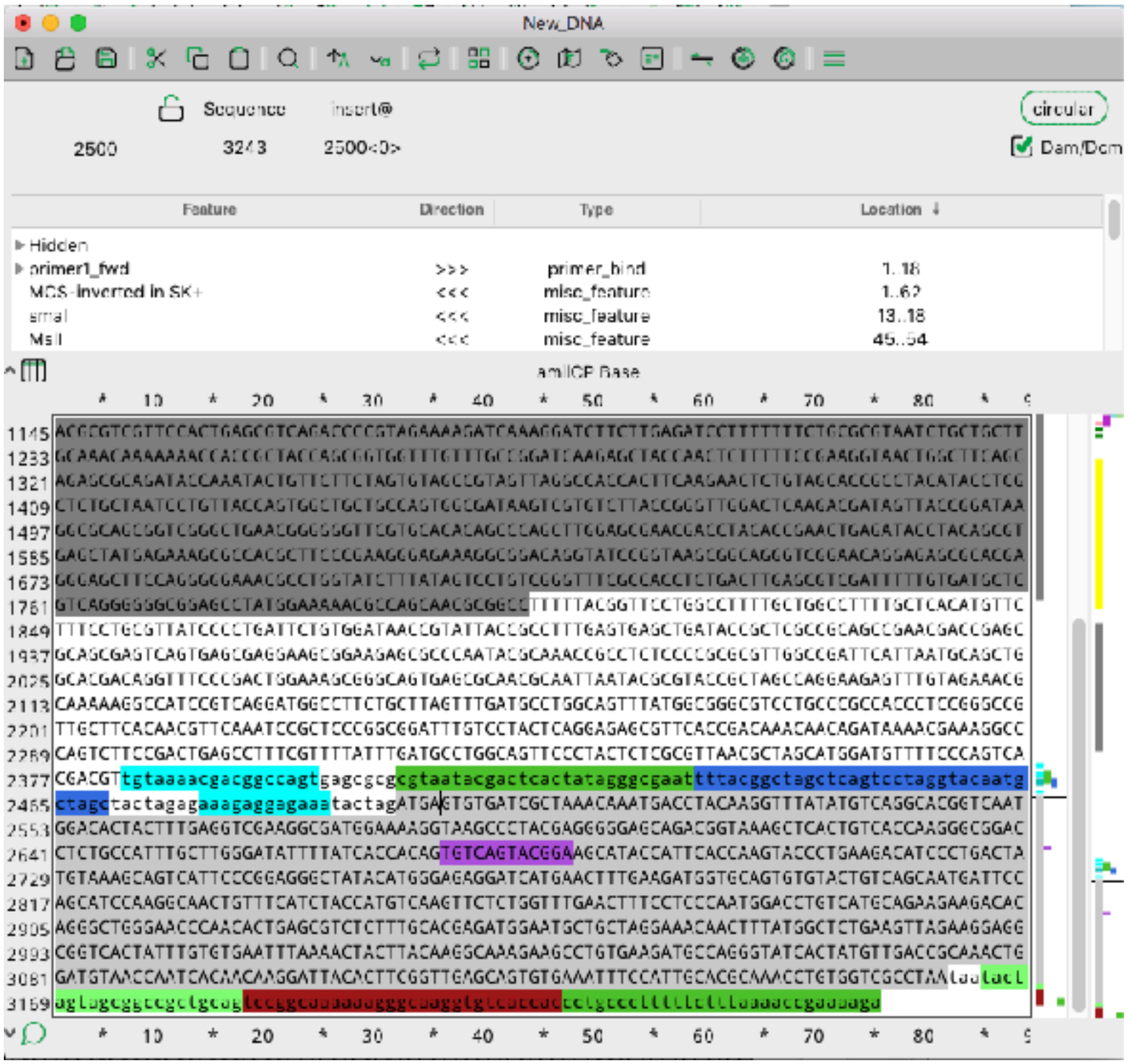
Add overlap to the other side

Gibson Designer



You have to examine each junction

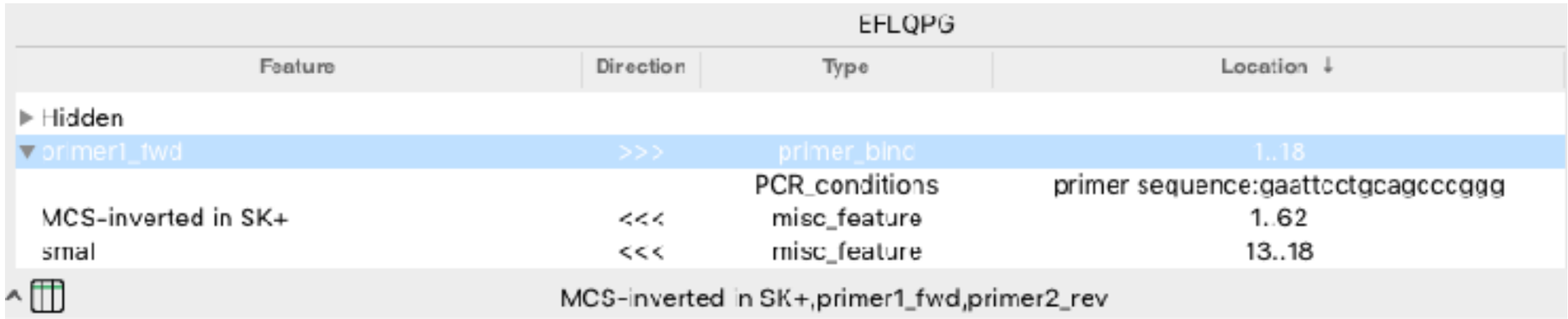
Gibson Designer

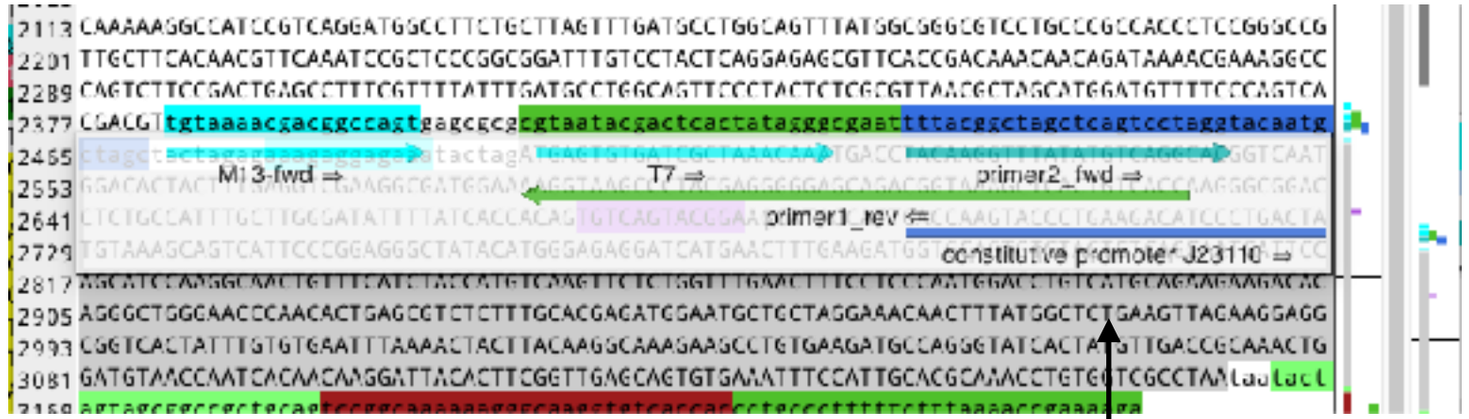


Gibson Designer

Gibson PCR products, primers etc. are in the file comment

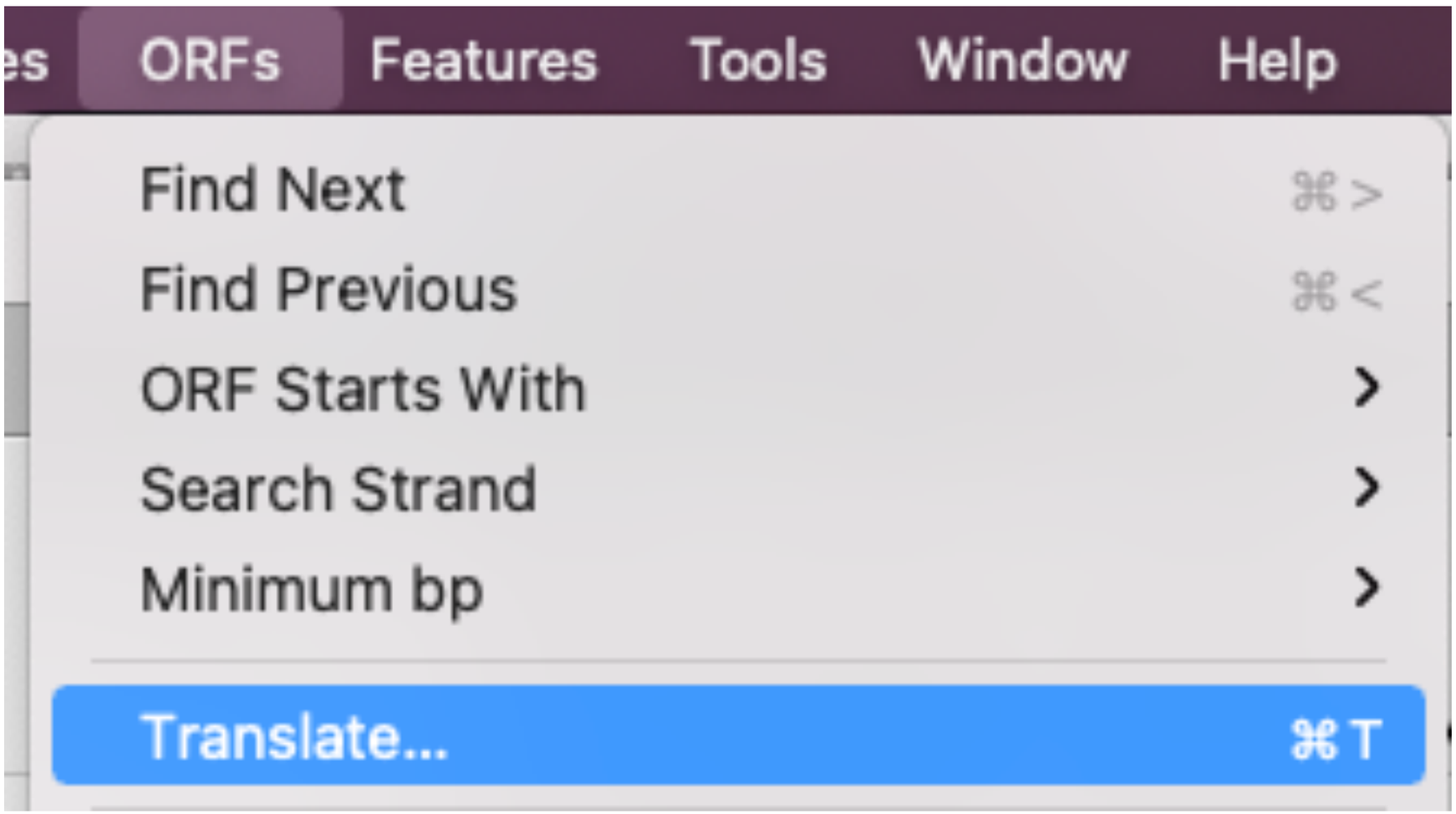
Gibson Designer





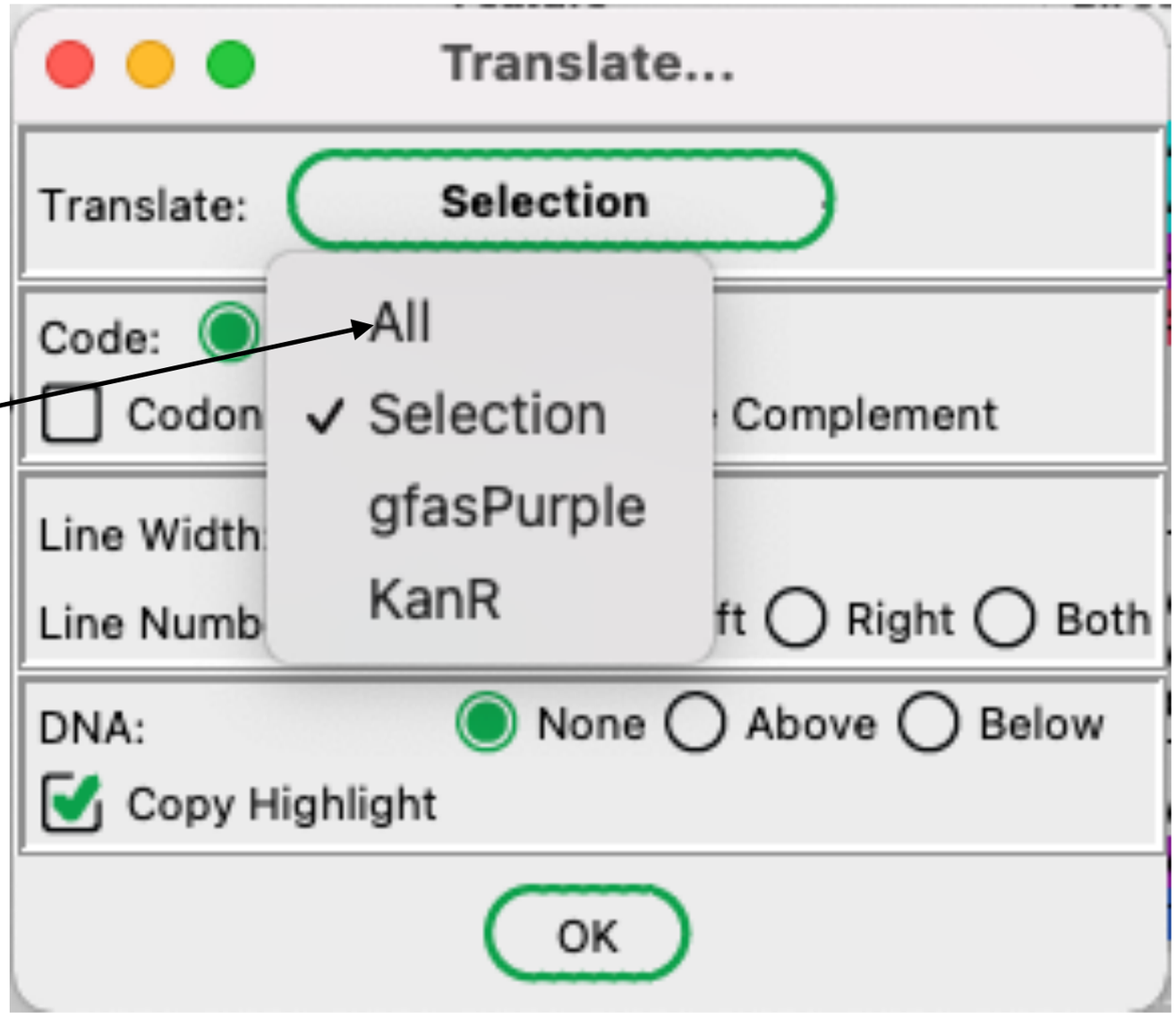
Gibson PCR primers are in the file features

Translation tool



Translation tool

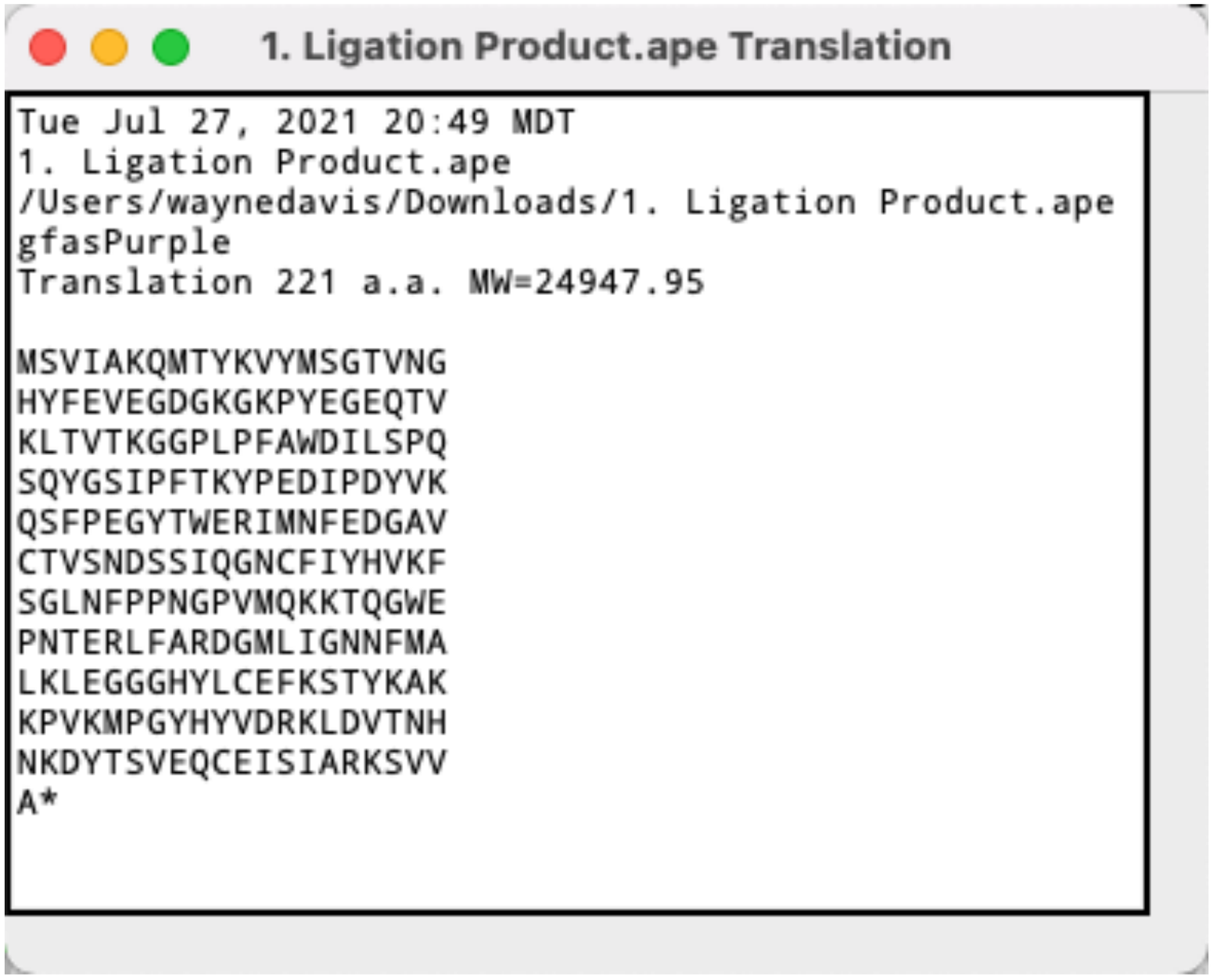
Translate all of a sequence, selected text, or any “CDS” type feature



Translation tool

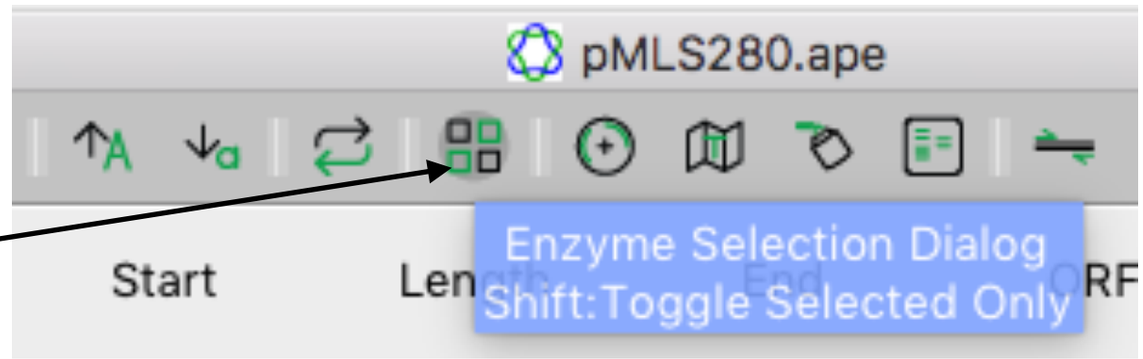
Format the output

Translation tool

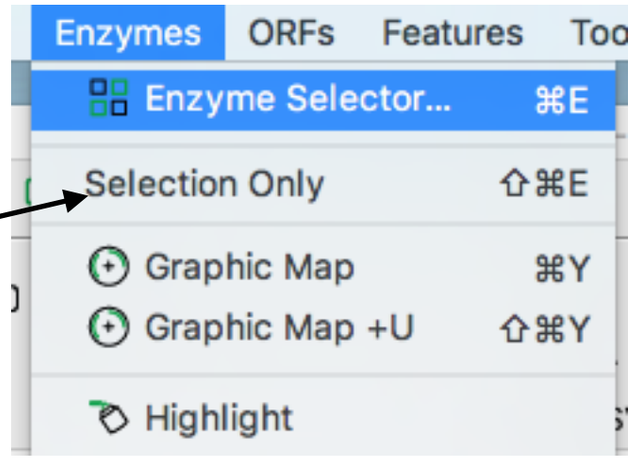


Enzyme Selection

Shift-click to change all tools to apply to selection rather than sequence

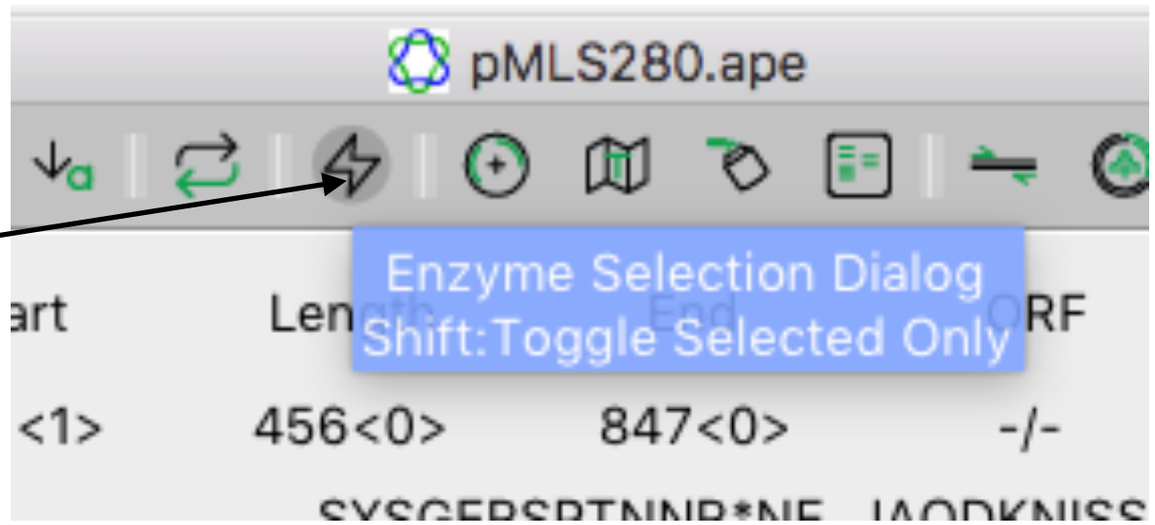


You can select this option to change all tools to apply to selection rather than sequence

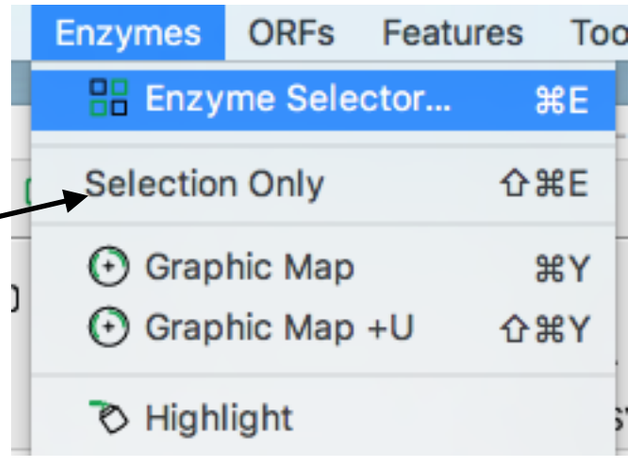


Enzyme Selection

This toolbar icon changes when you have “selection only” applied



You can select this option to change all tools to apply to selection rather than sequence

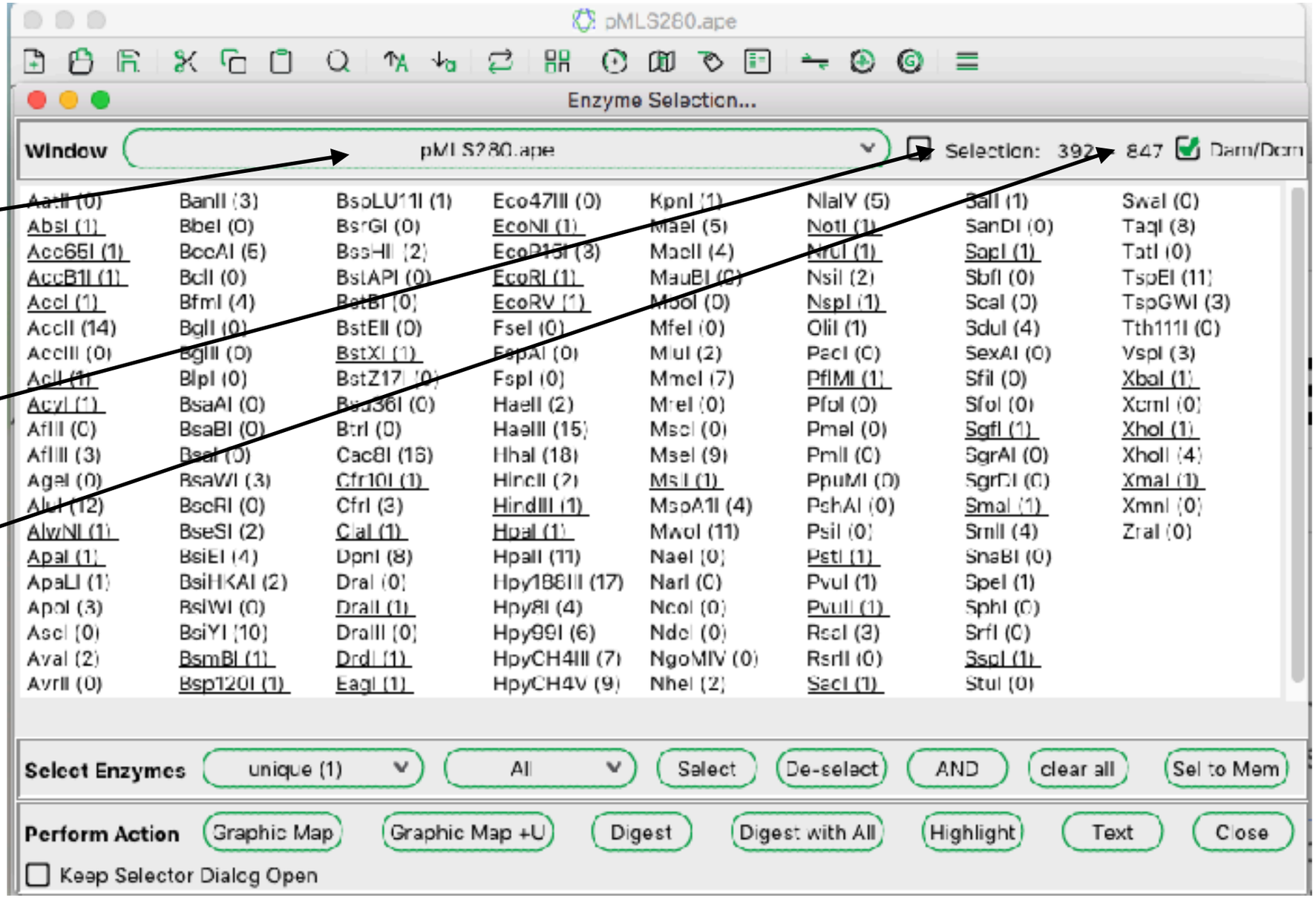


Enzyme Selection

Current window to search

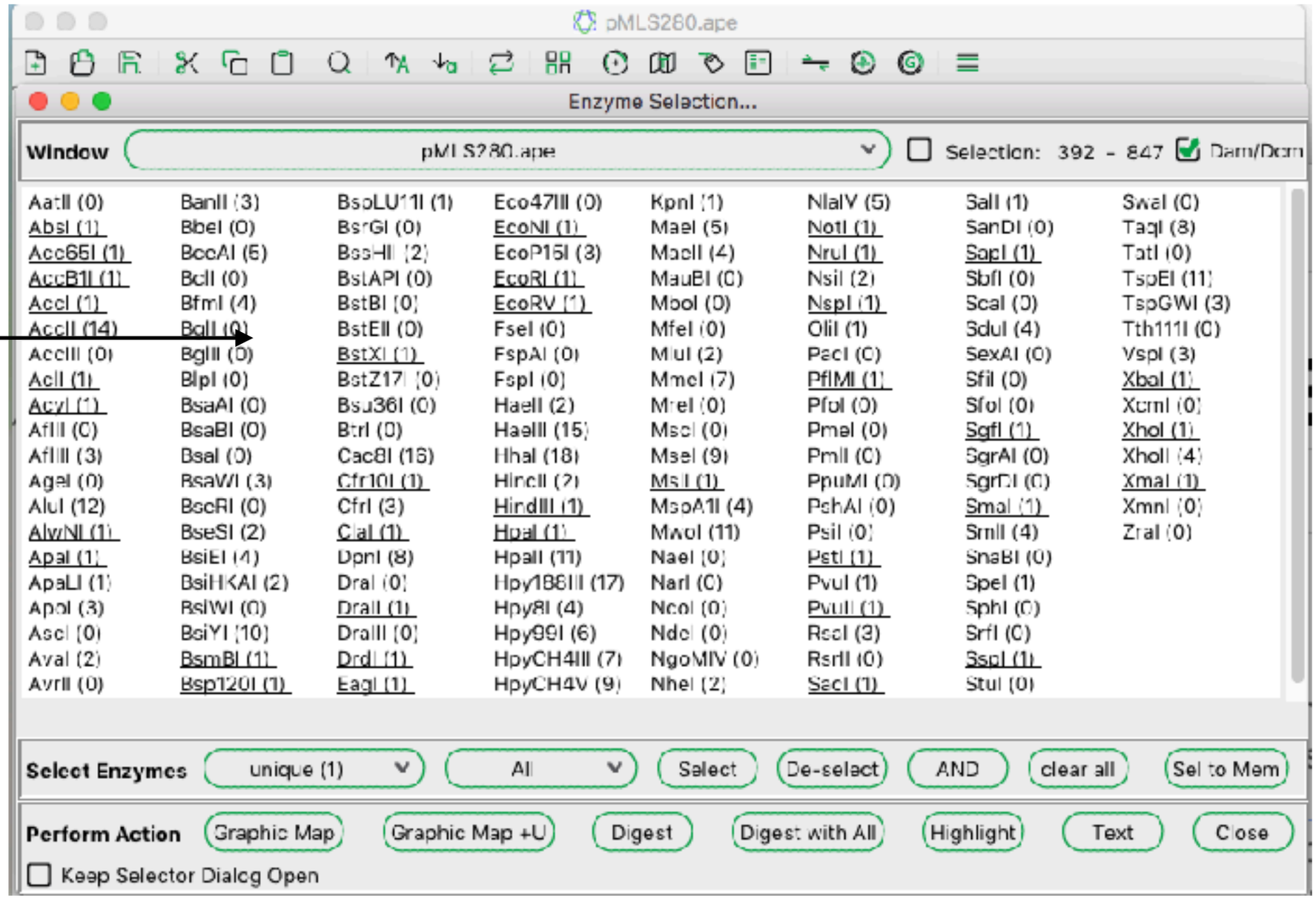
Apply search to selection

Current selection in window (can be changed while the dialog is open)



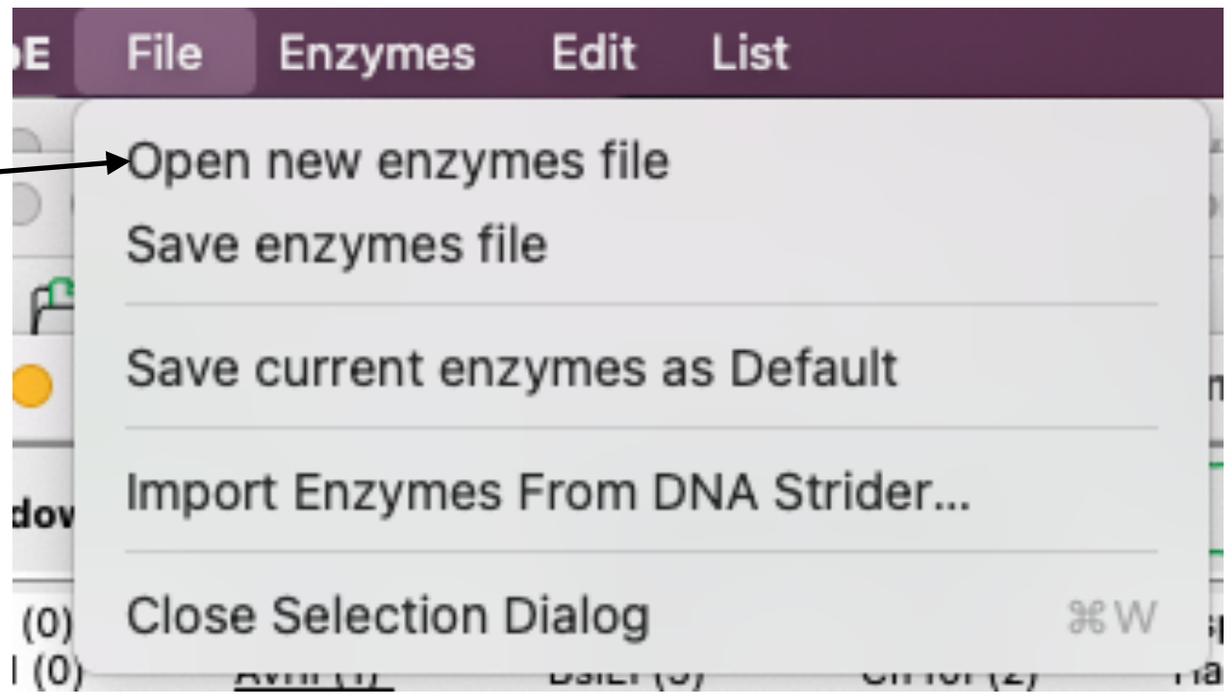
Enzyme Selection

All enzymes are shown here



Enzyme Selection

The current enzymes can be changed by loading new ones using the file menu WHILE THE DIALOG IS OPEN

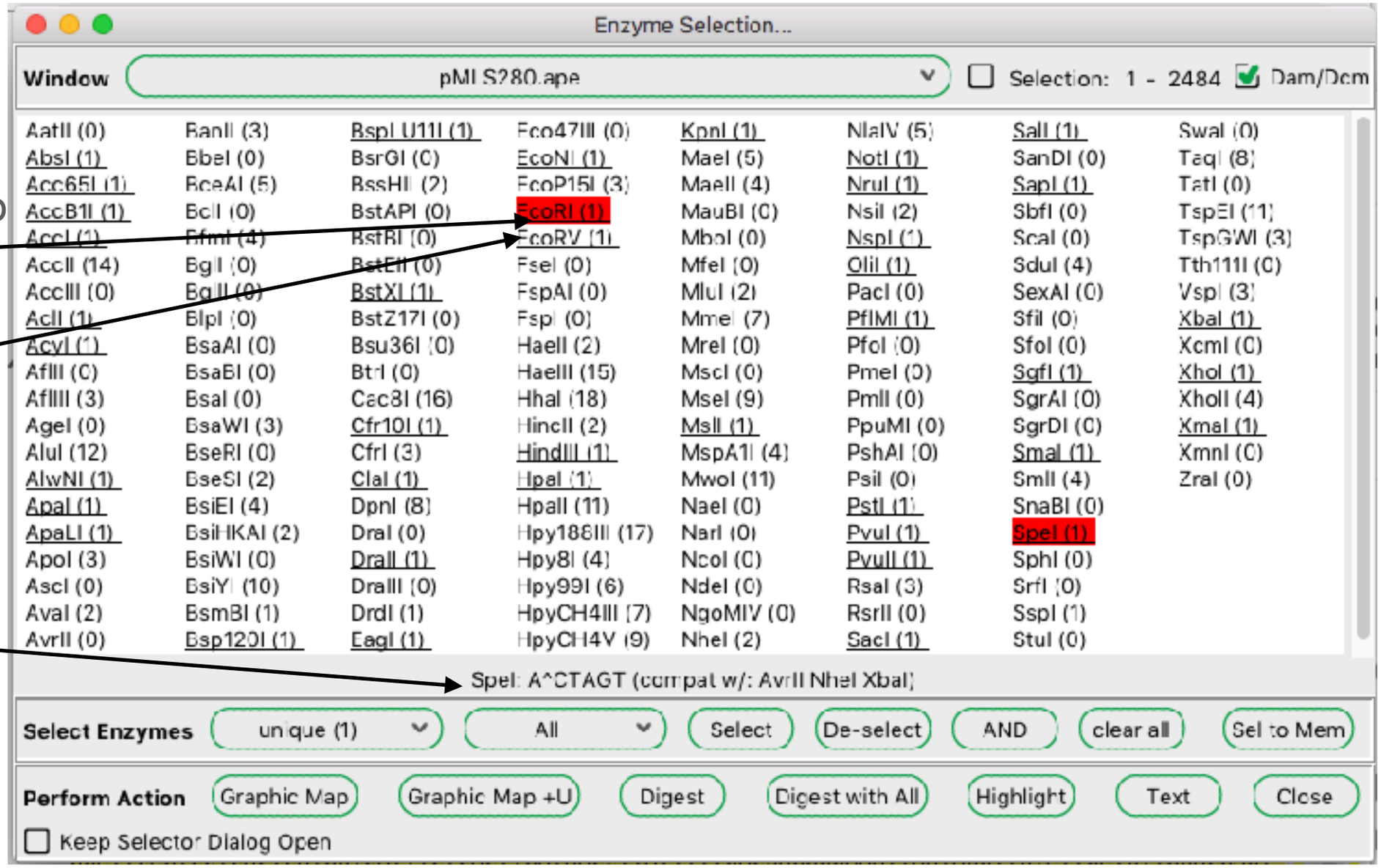


Enzyme Selection

Click on any enzyme to select it

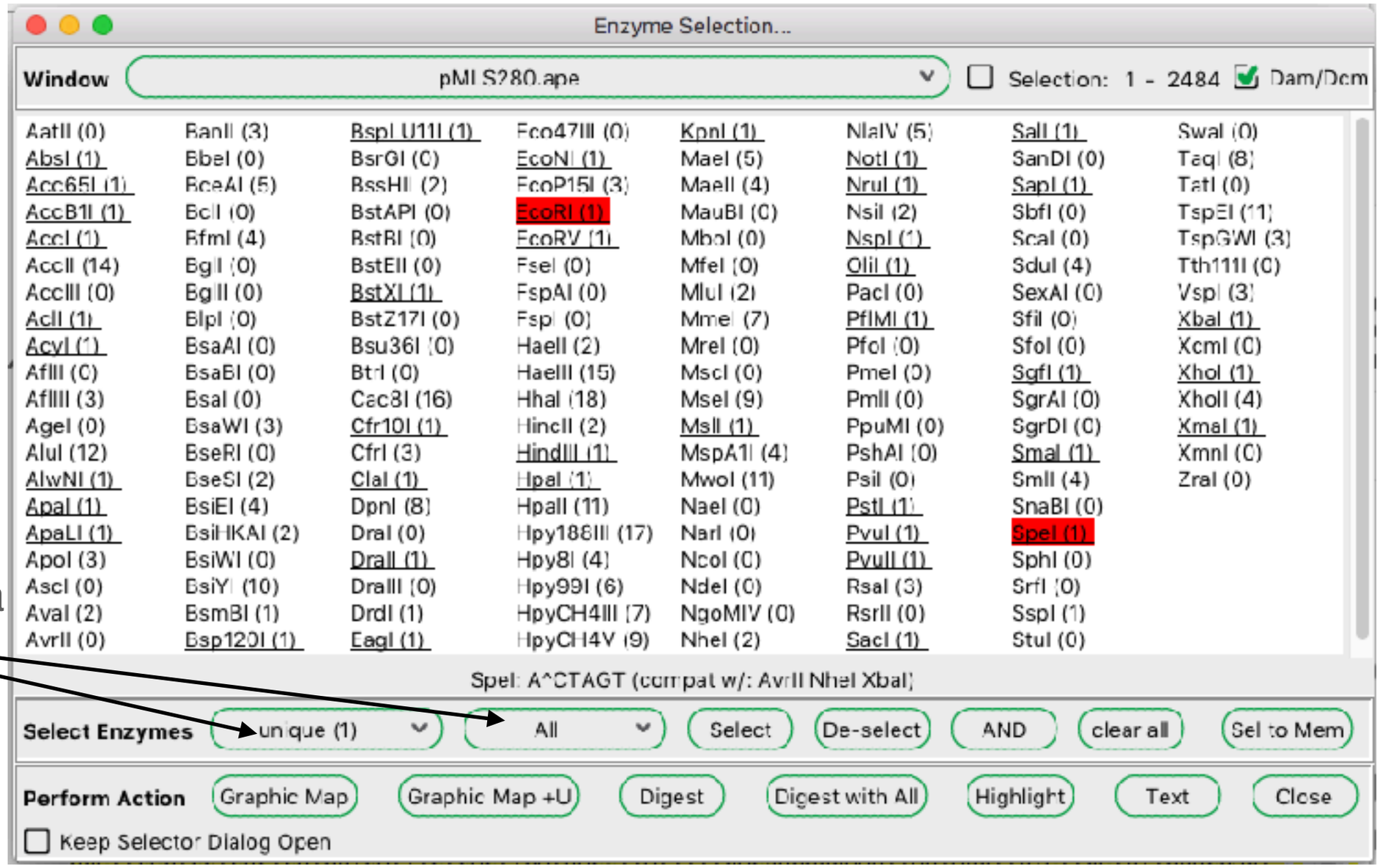
Shift-click on any enzyme to select only that enzyme

The enzyme currently under the mouse is shown here



Enzyme Selection

The selection criteria are shown here

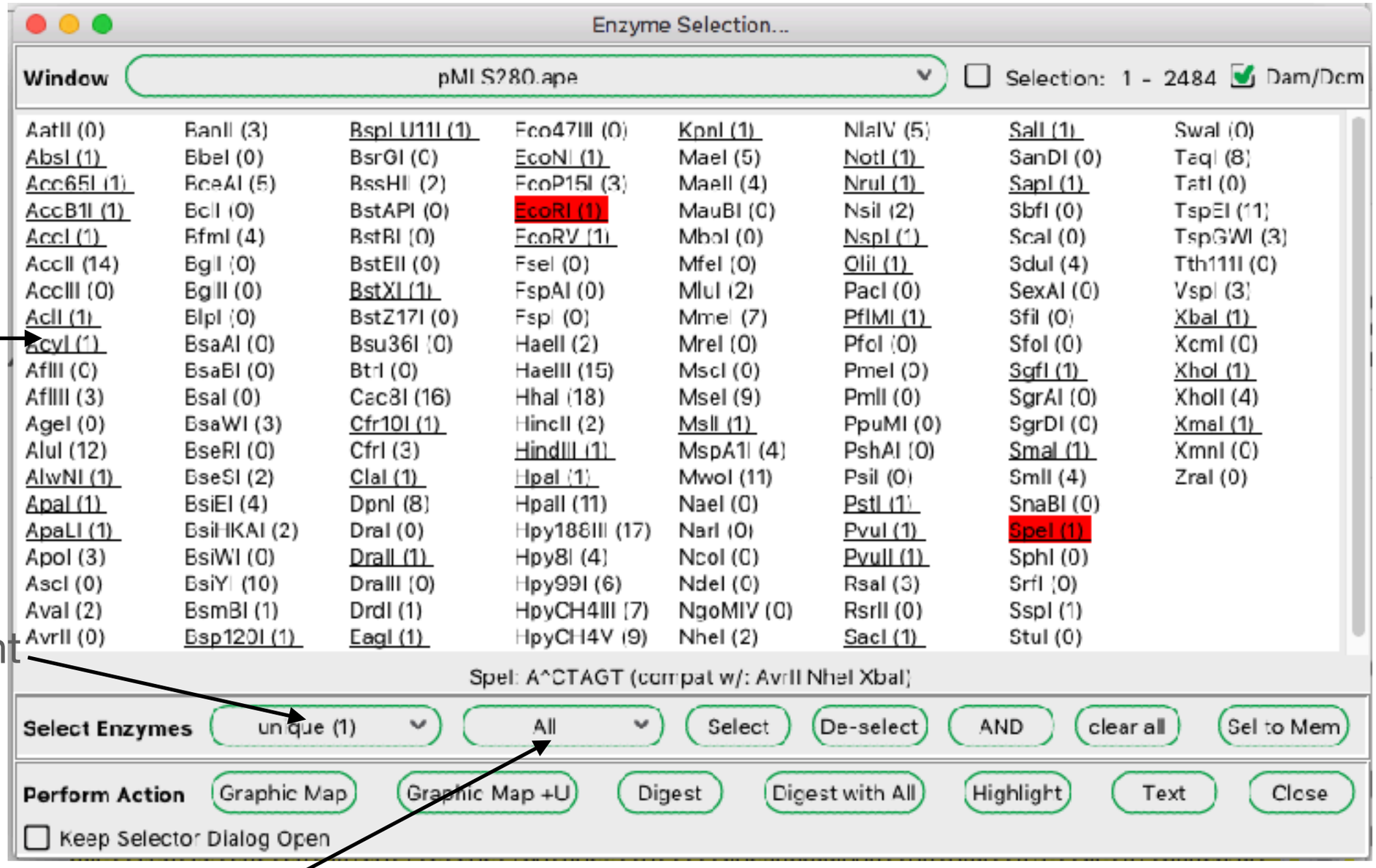


Enzyme Selection

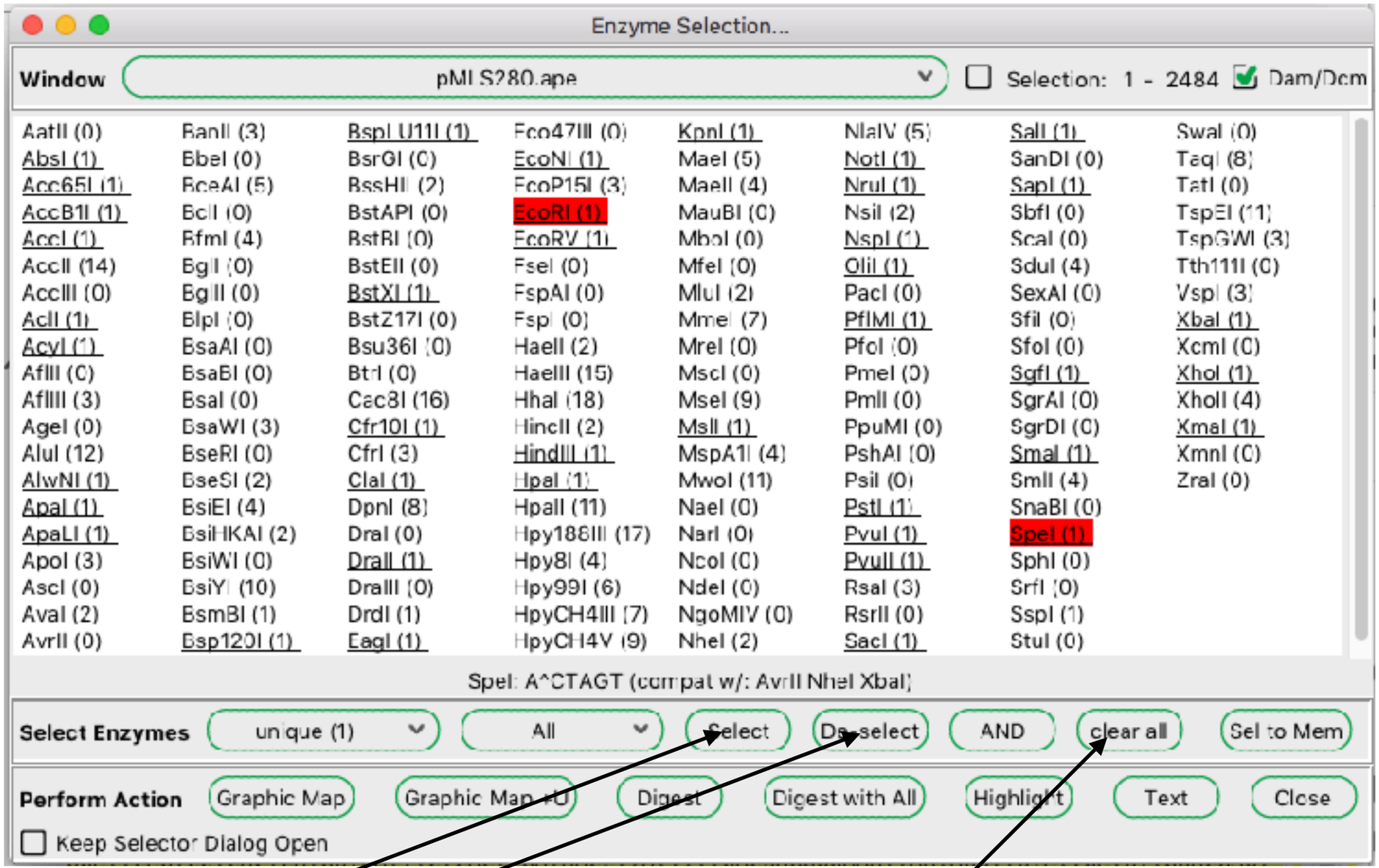
Any enzyme matching both the count AND the group are underlined

This is the count

This is the group



Enzyme Selection

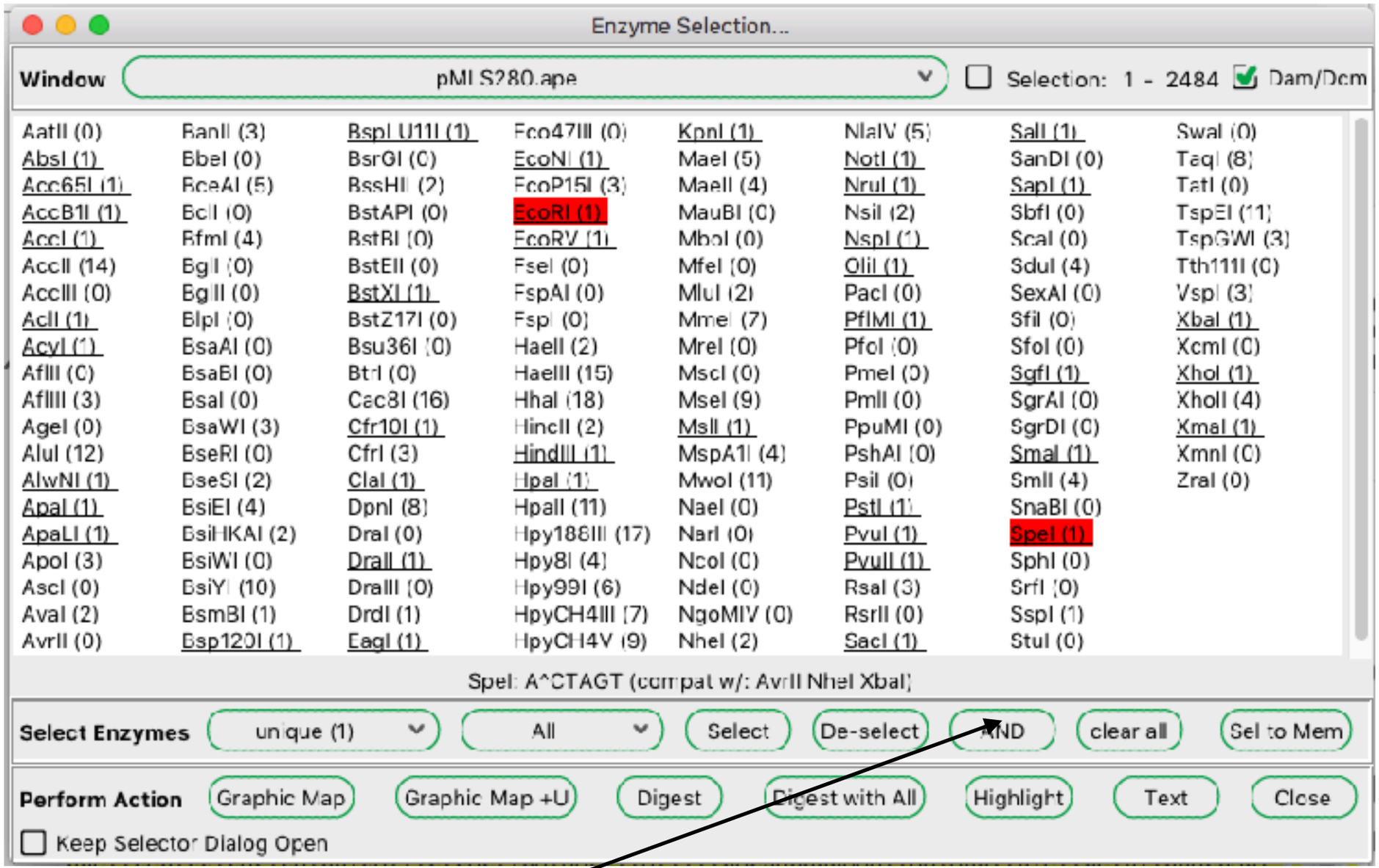


Click here to select all underlined enzymes

Click here to DE-select all underlined enzymes

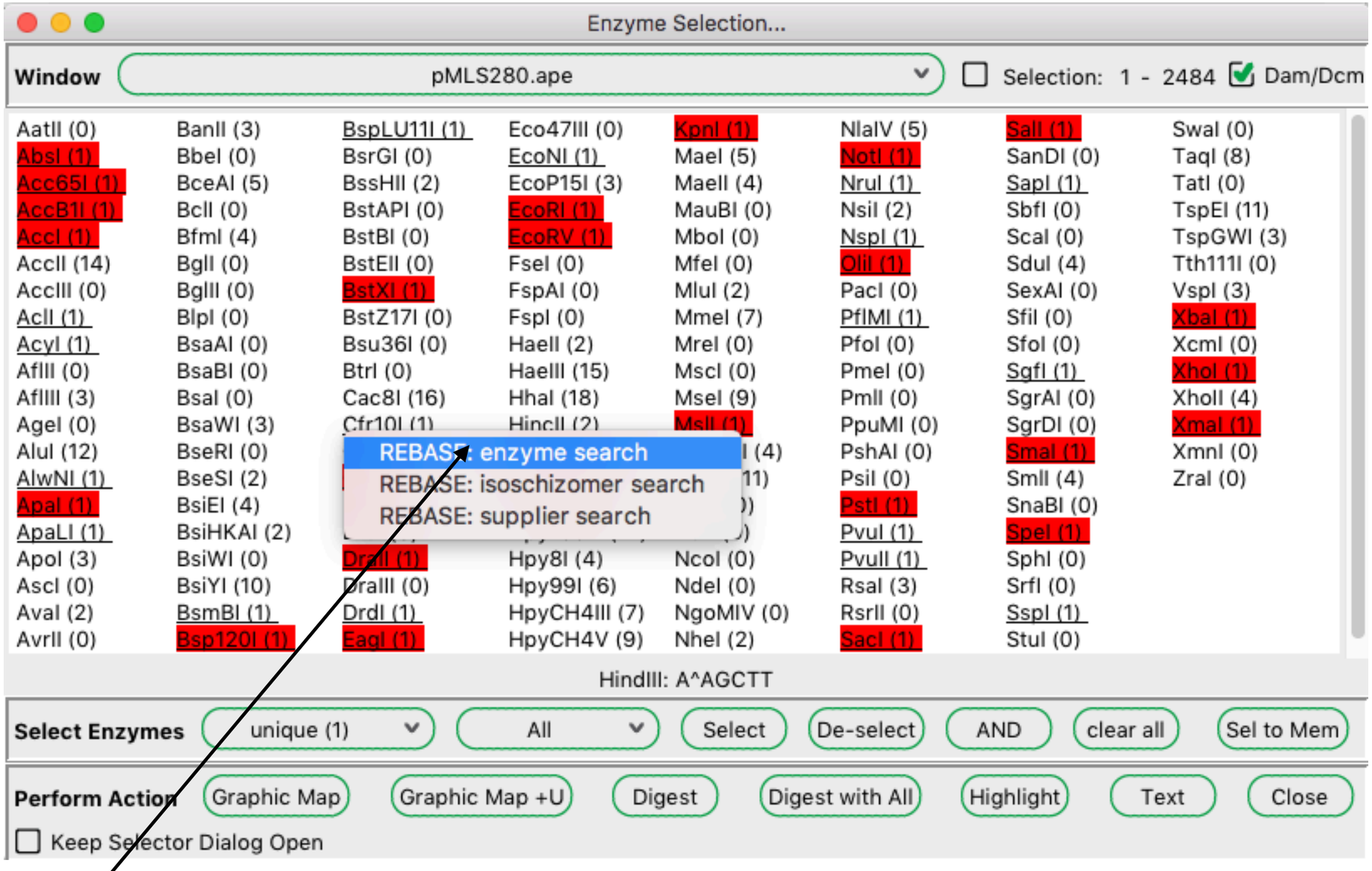
Click here to de-select ALL enzymes

Enzyme Selection



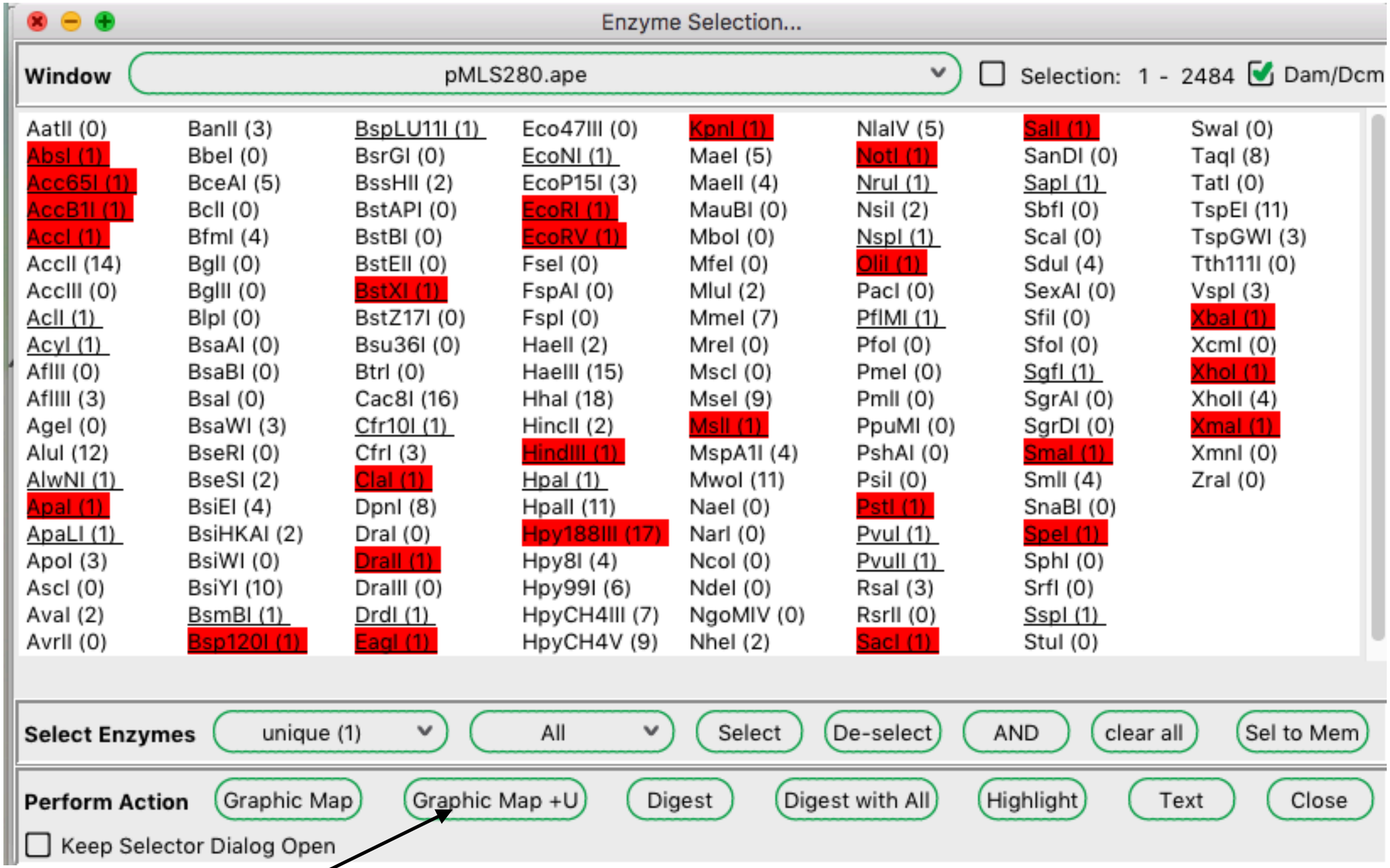
Click here to select only enzymes that are currently selected AND underlined

Enzyme Selection



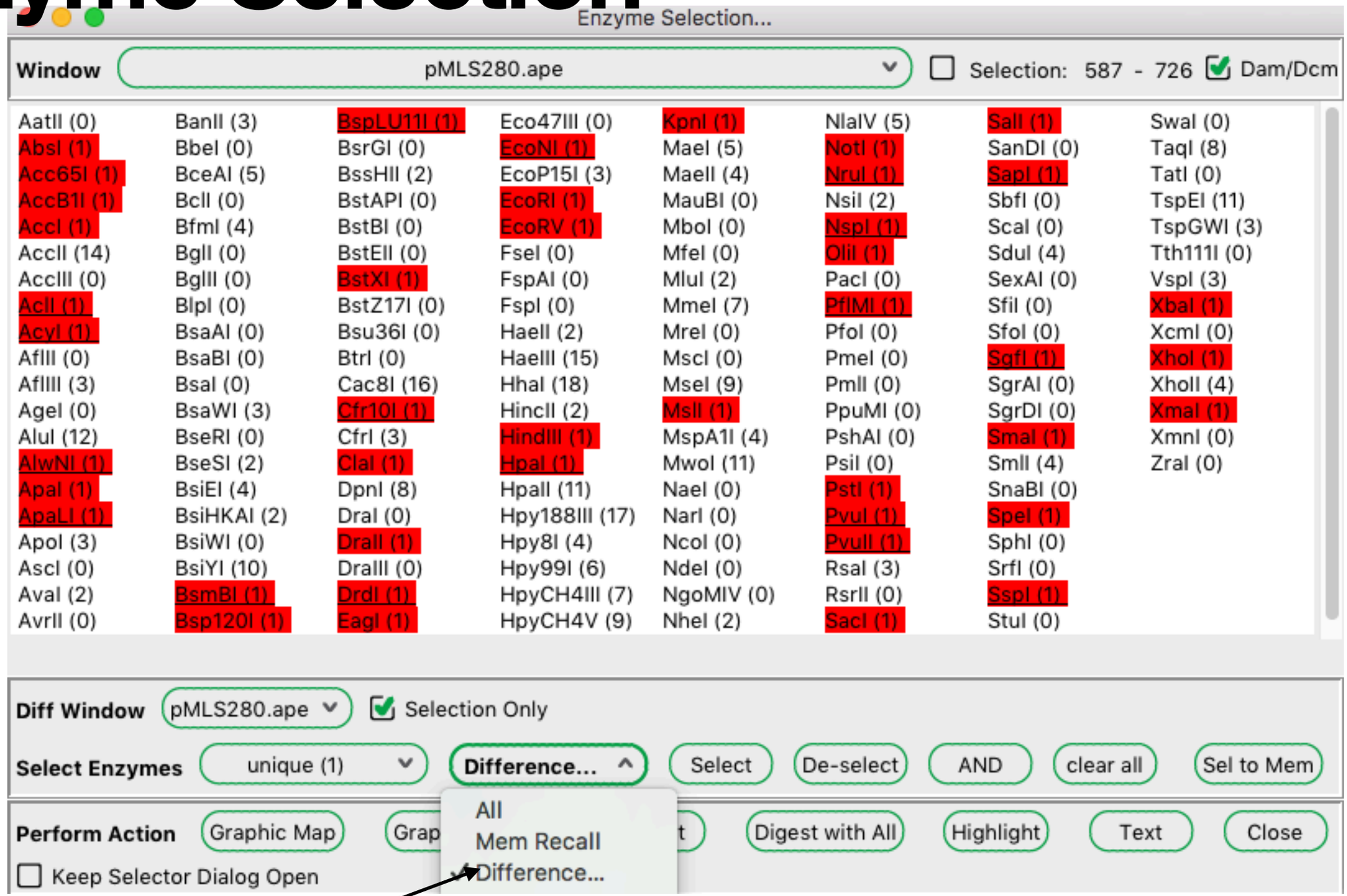
Right-click to search for enzyme info

Enzyme Selection



Click here to do analysis functions

Enzyme Selection

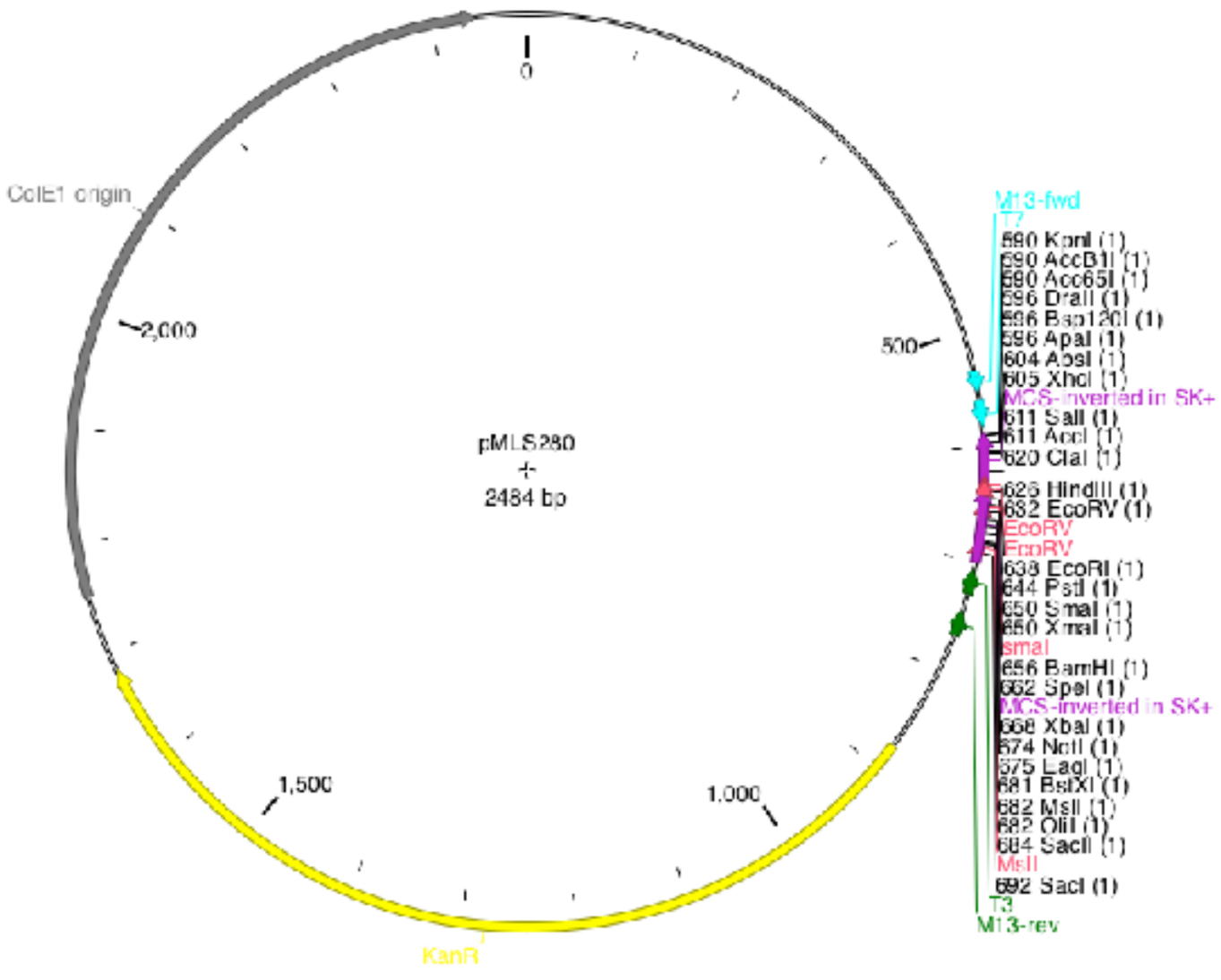


The difference group is special

Enzyme Selection

- Select the MCS in pMLS280
- Open the enzyme selector
- Select all unique enzymes in pMLS280
- Chose the difference group and pMLS280+selection within the difference selector
- Deselect the different enzymes
- Do a graphic map
- What do you see?

Enzyme Selection



Enzyme Selection

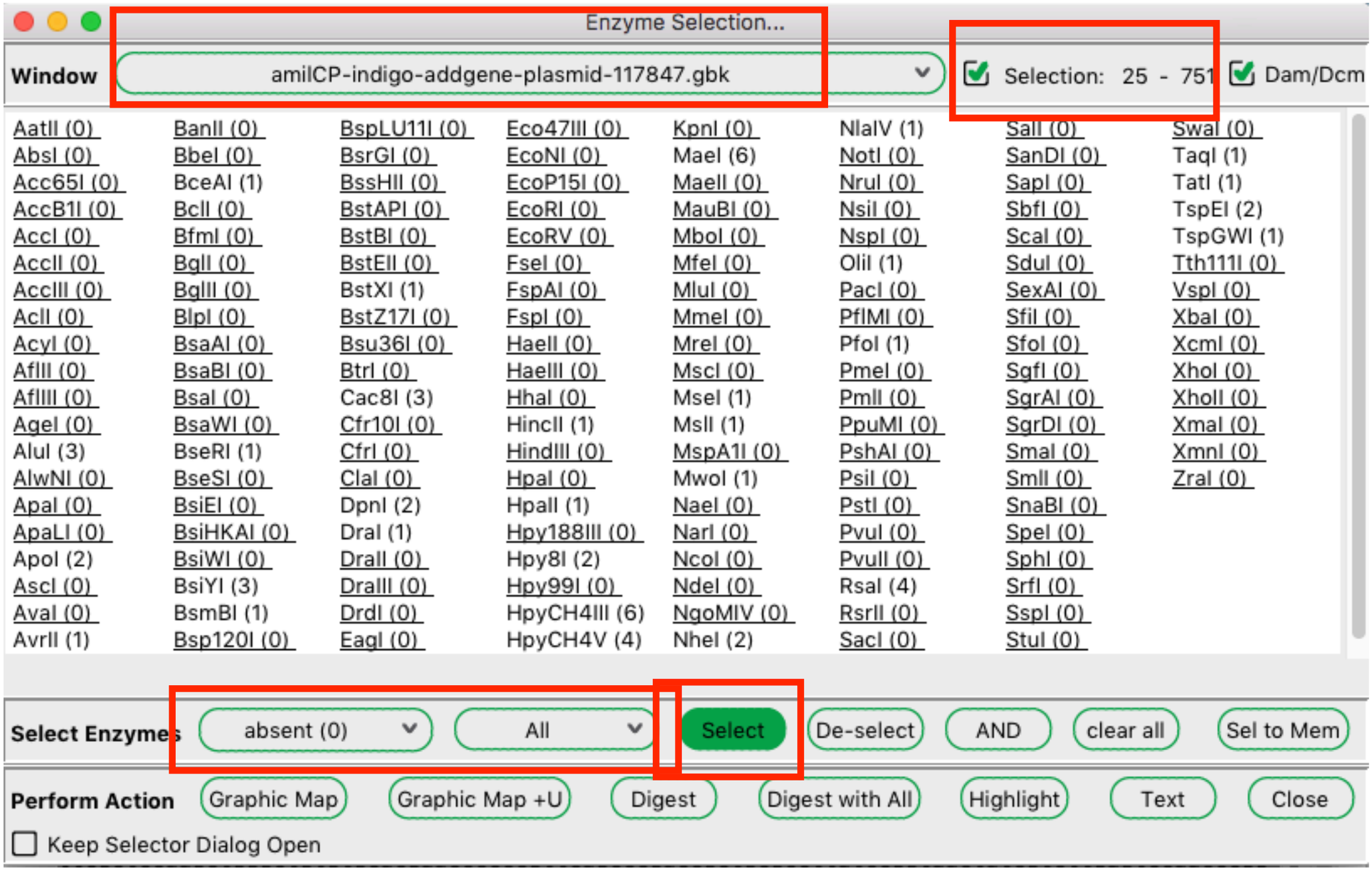
Find enzymes to clone amilCP into pMLS280

Enzyme Selection

- Select from 25 to 751 in amilCP

Enzyme Selection

- select all enzymes that are absent from the selection in amilCP

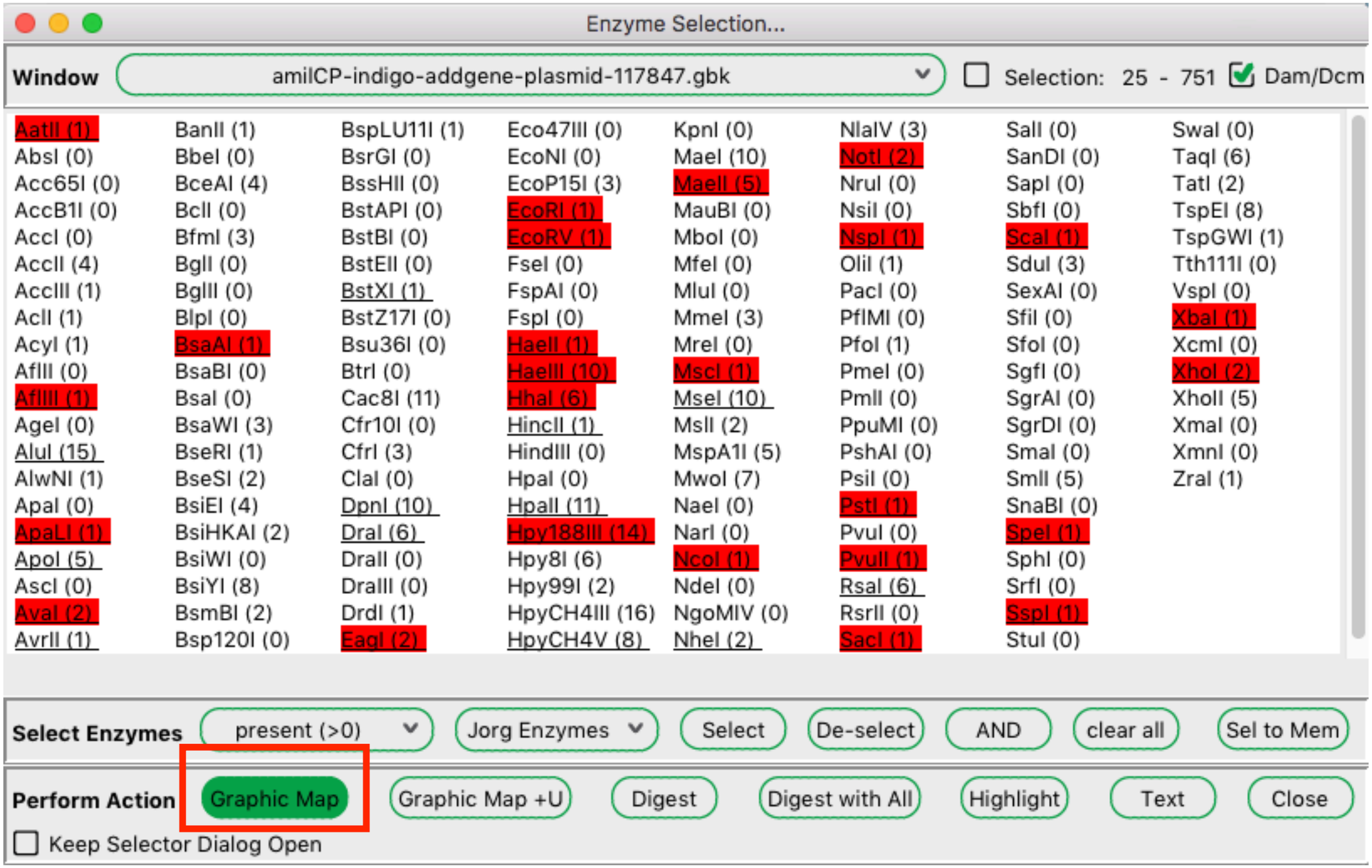


Enzyme Selection

- select all enzymes that are ALSO present somewhere in the plasmid, and in the Jorg collection

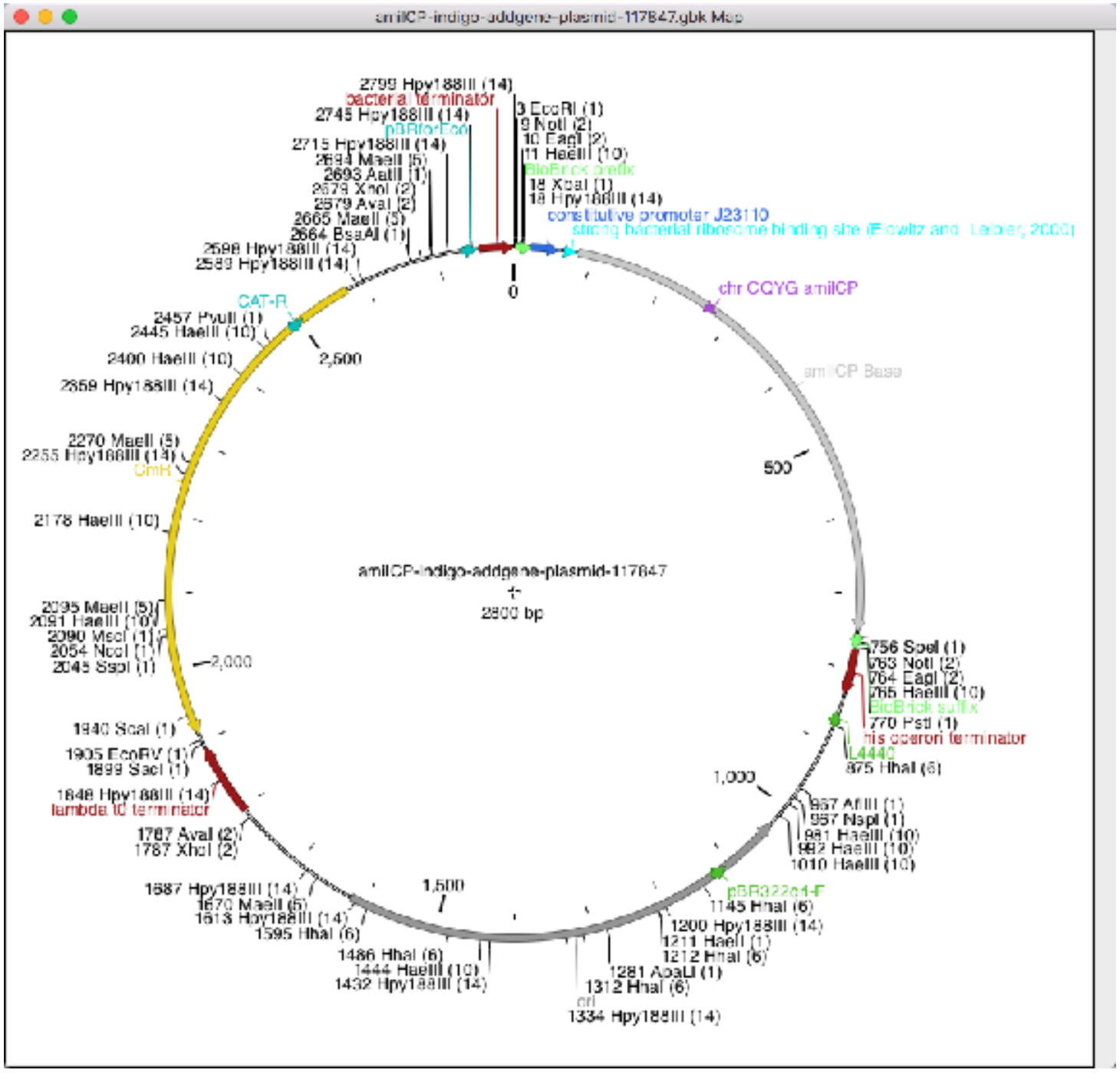
Enzyme Selection

- do a graphic map



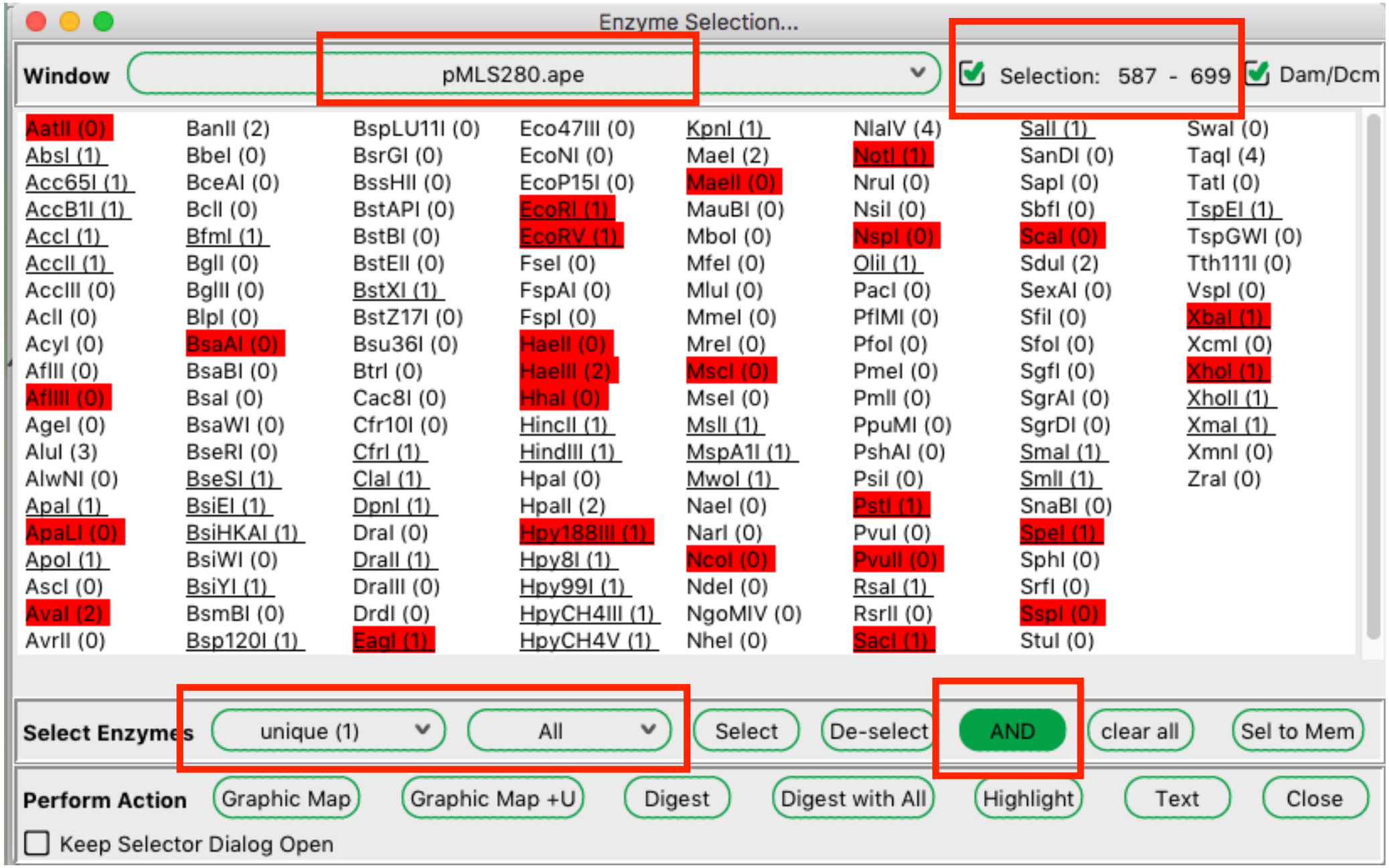
Enzyme Selection

- do a graphic map



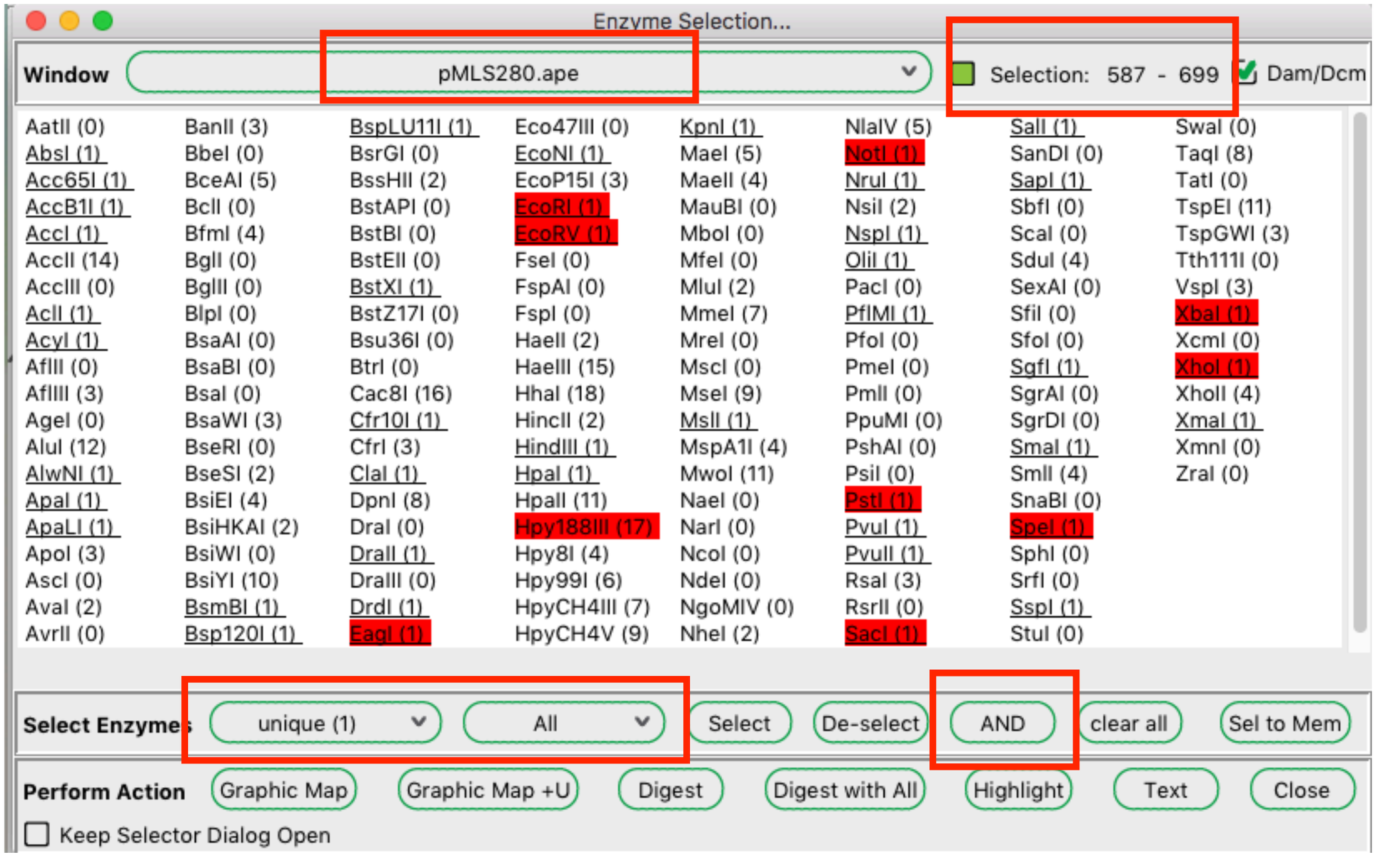
Enzyme Selection

- select all enzymes that are ALSO unique in the pMLS MCS

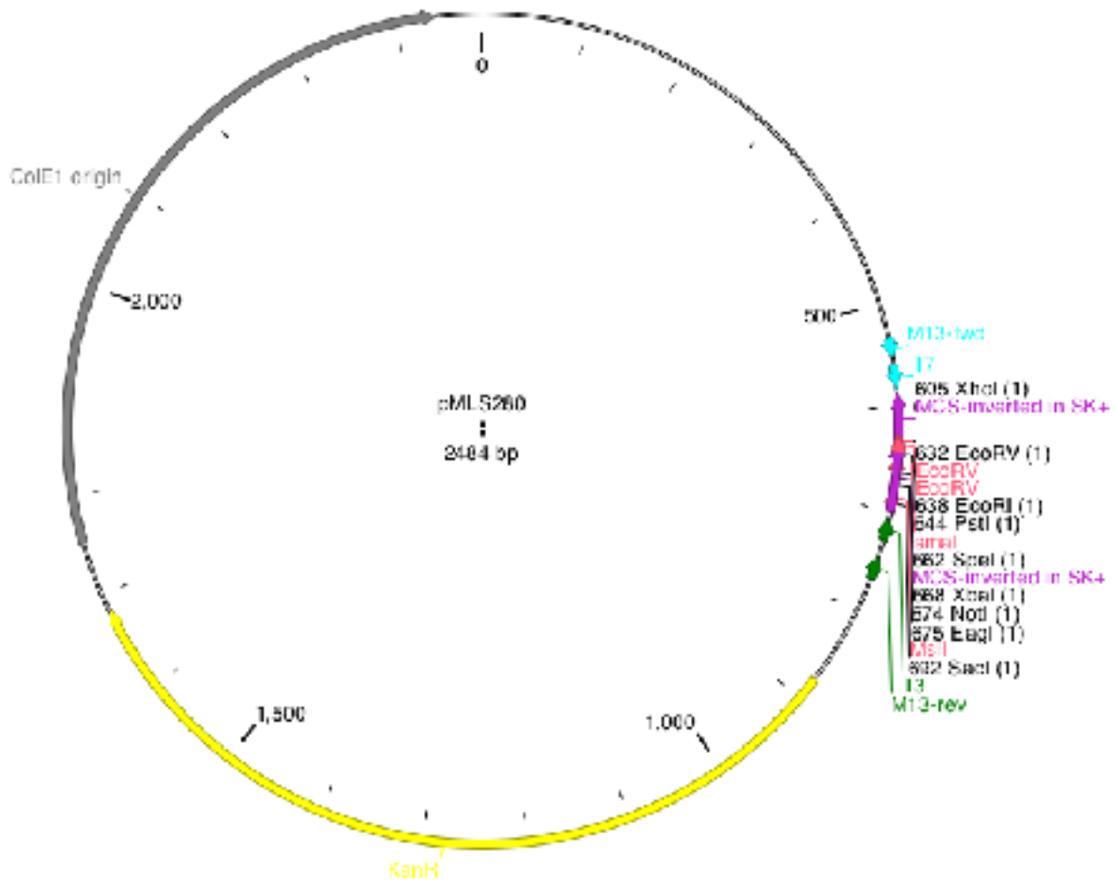


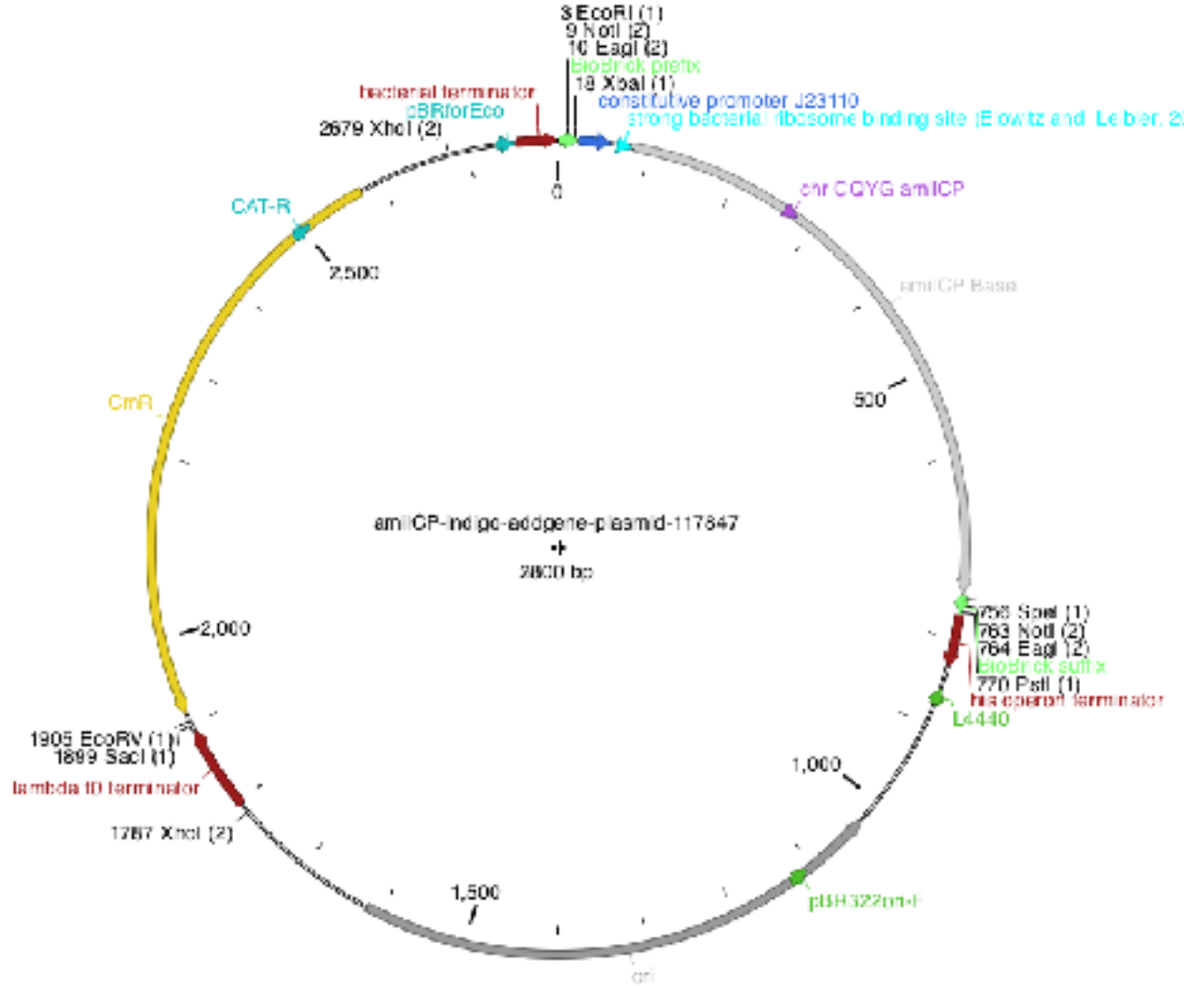
Enzyme Selection

- select all enzymes that are ALSO unique in pMLS

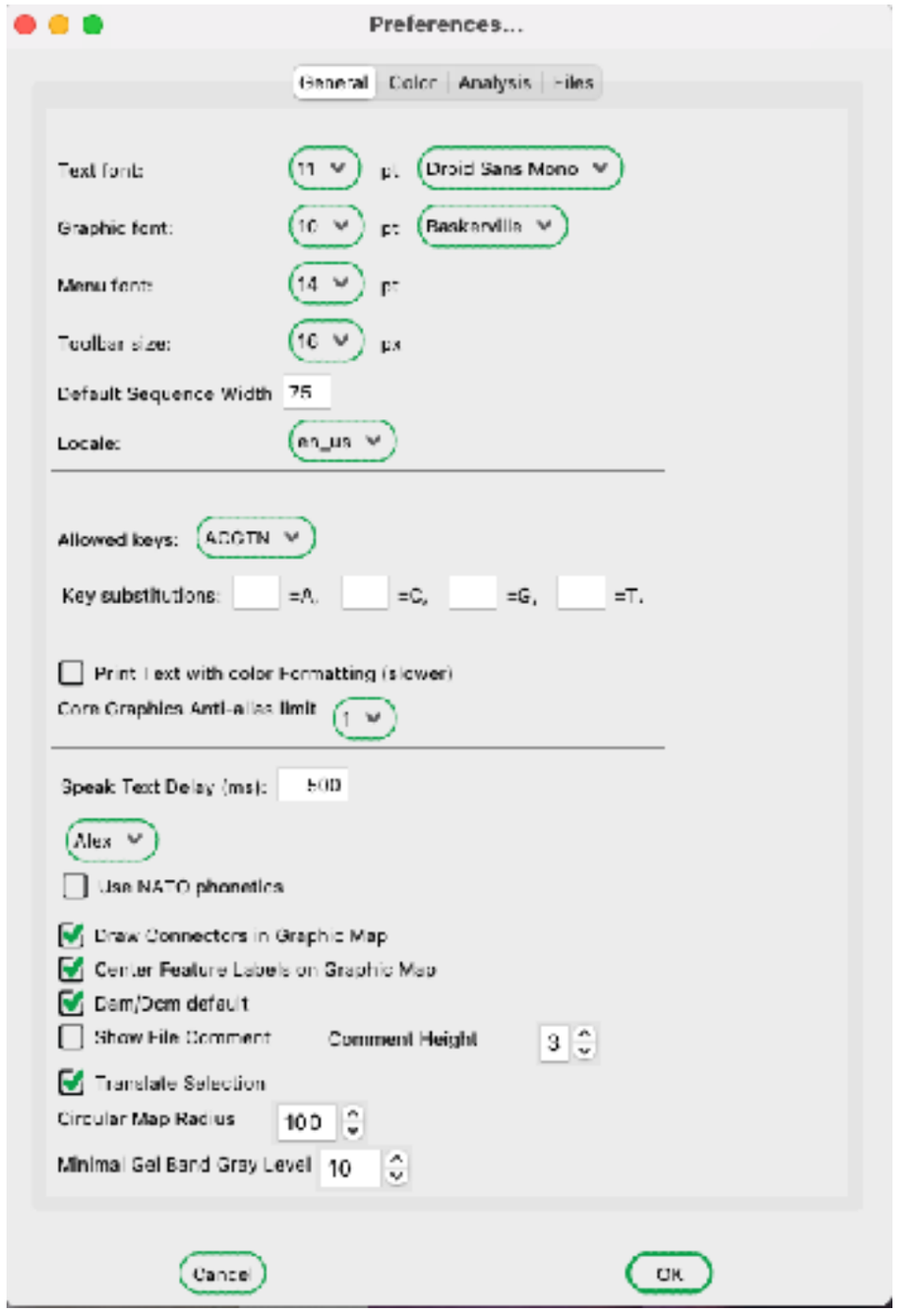


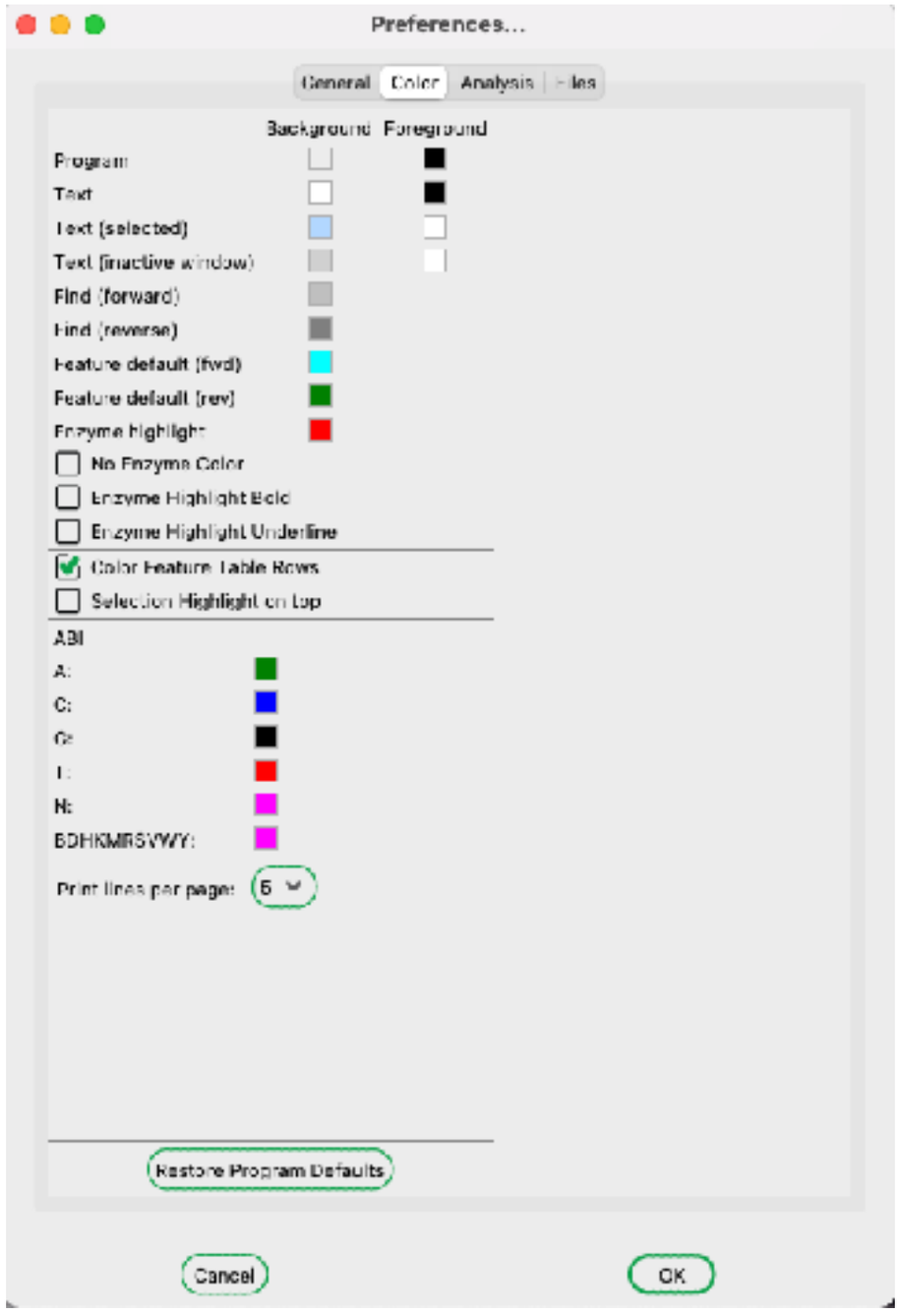
Enzyme Selection



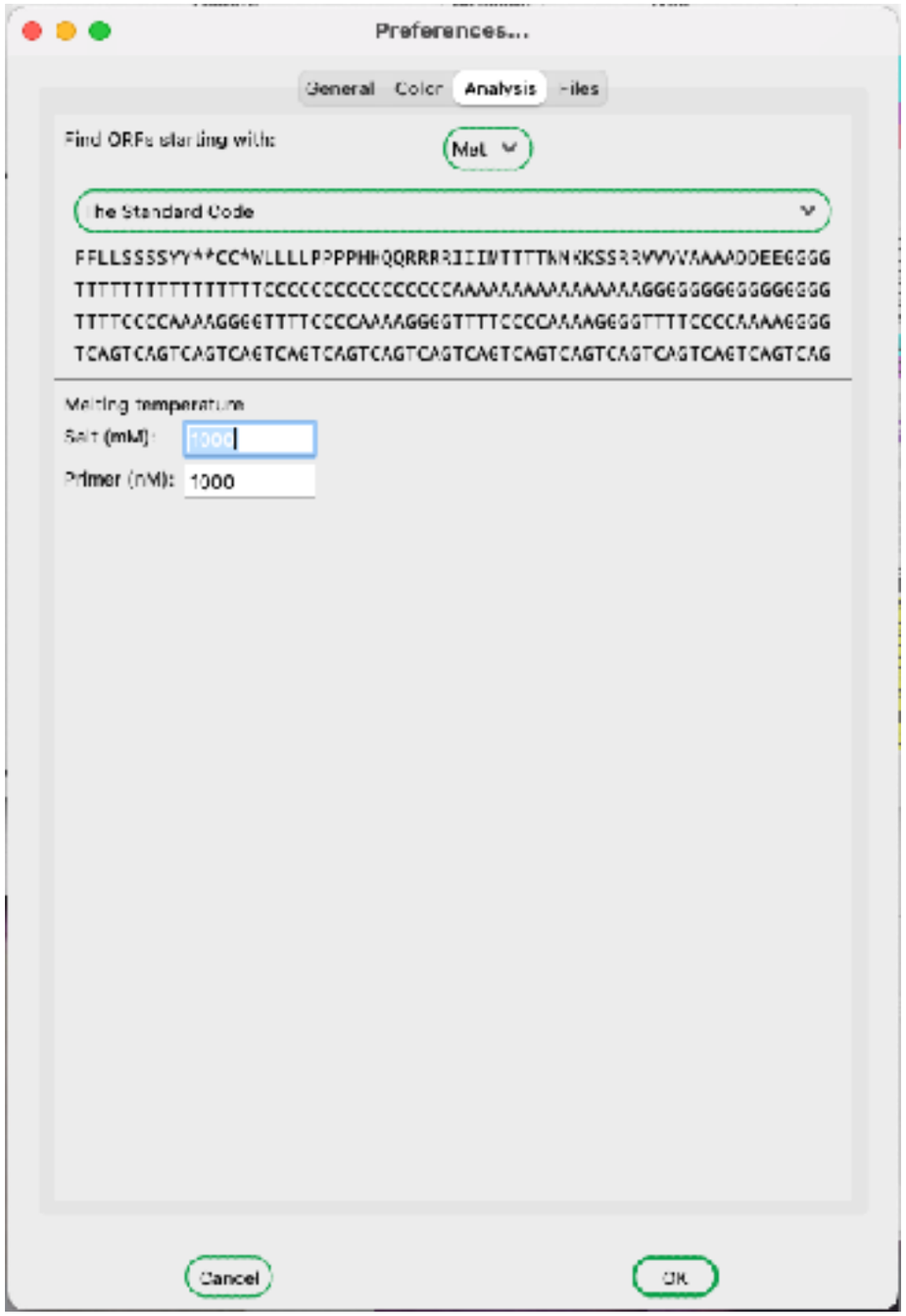


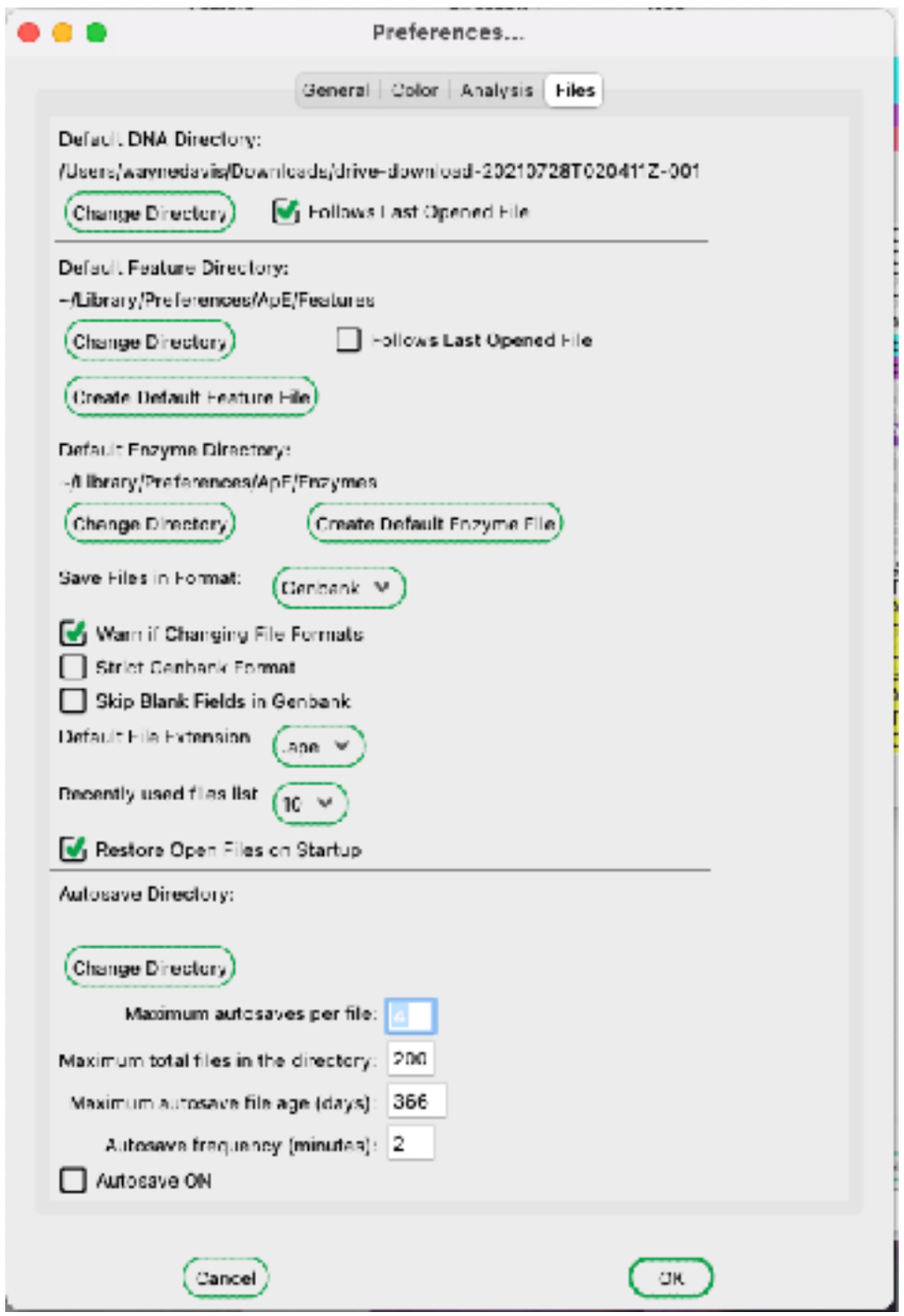
Preferences dialog



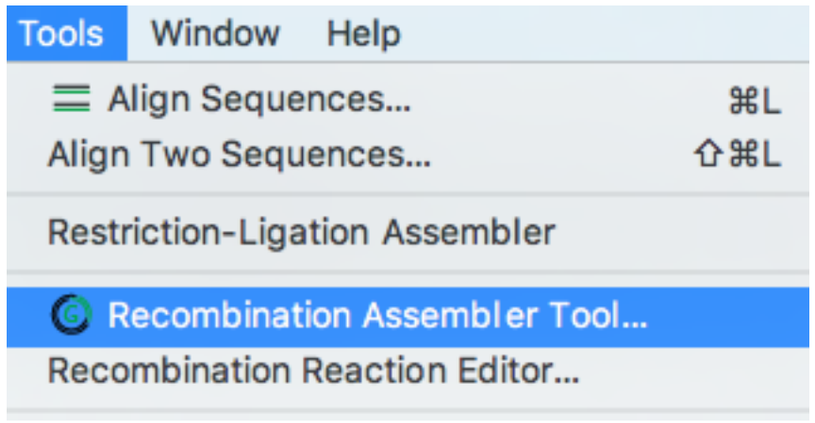


Preferences dialog

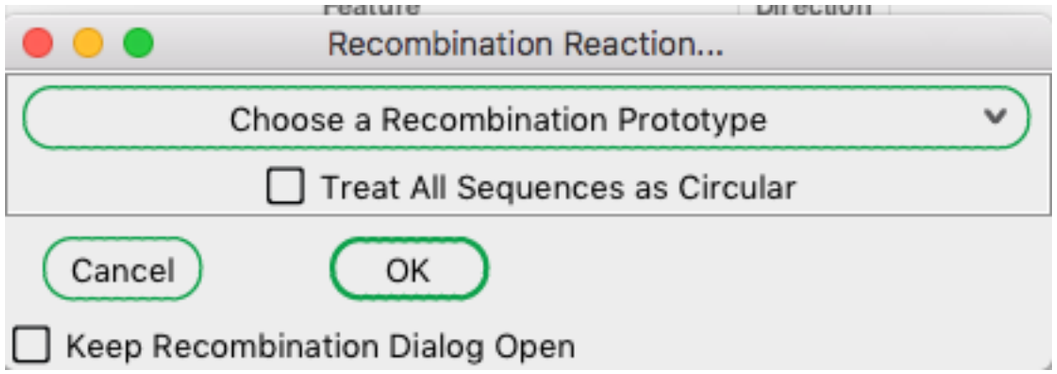


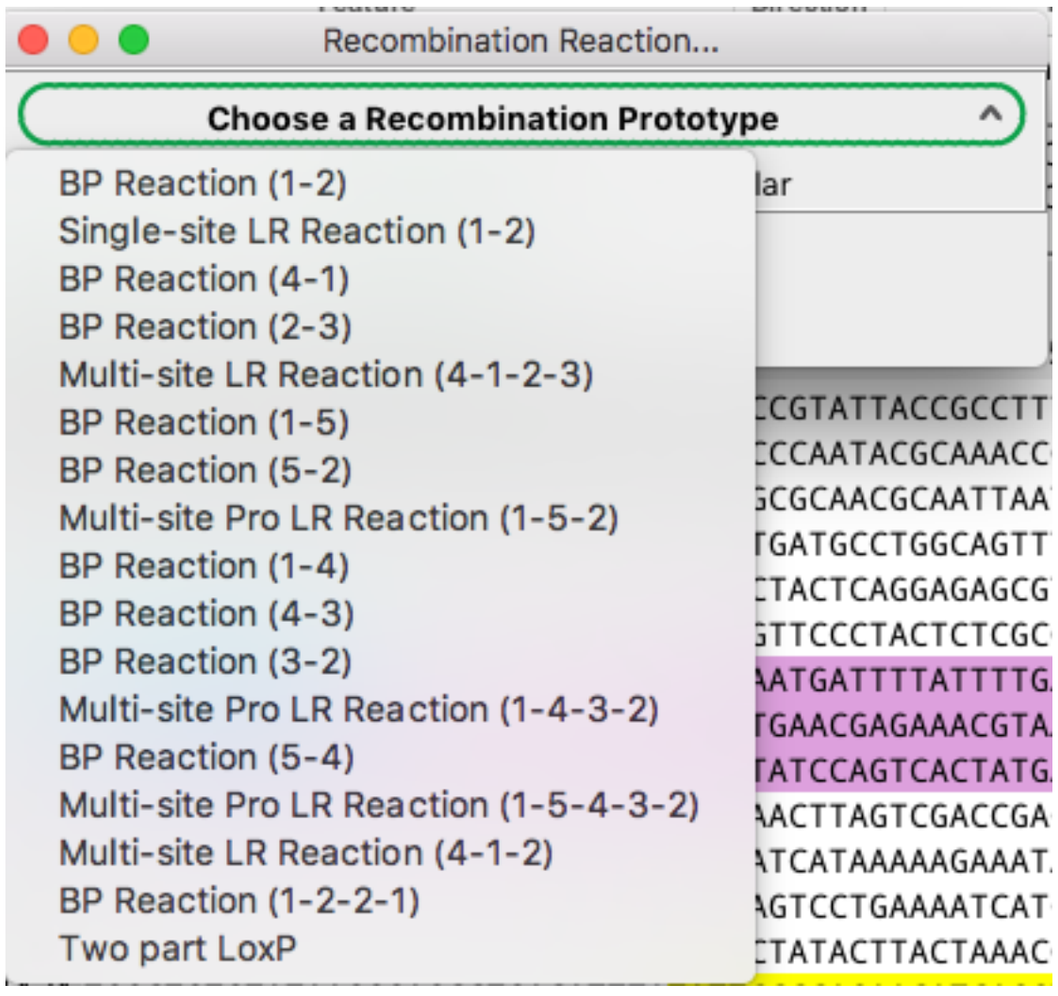


Recombination tool

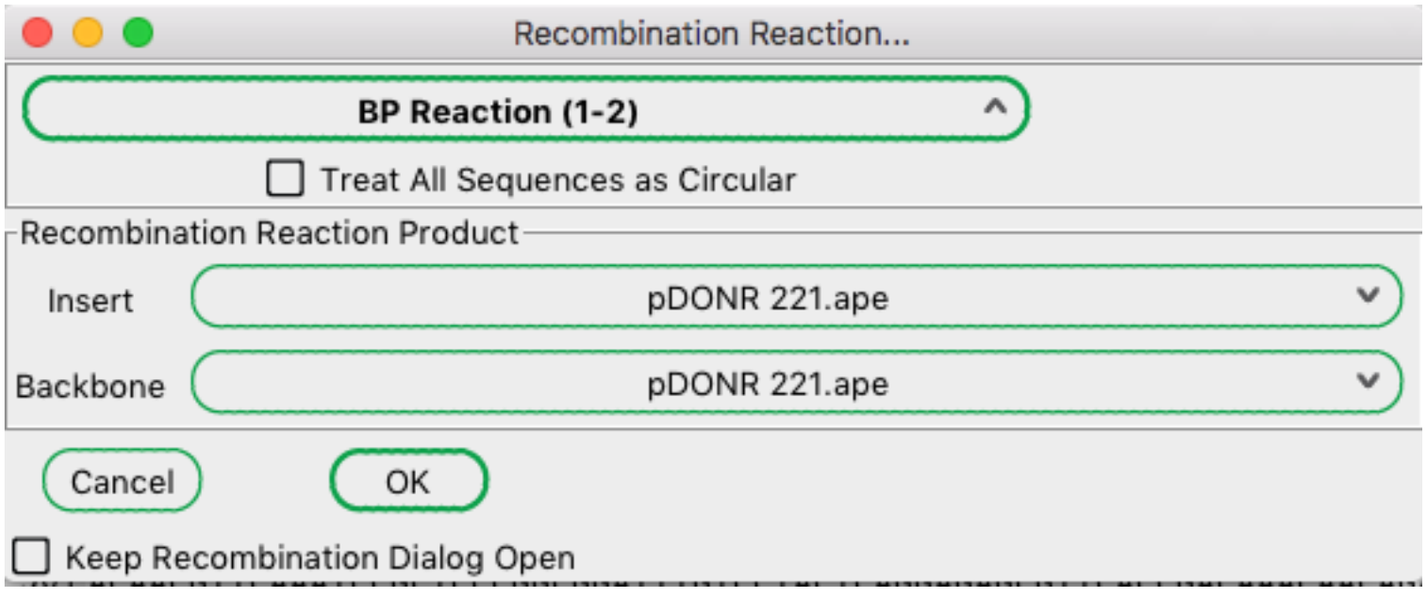


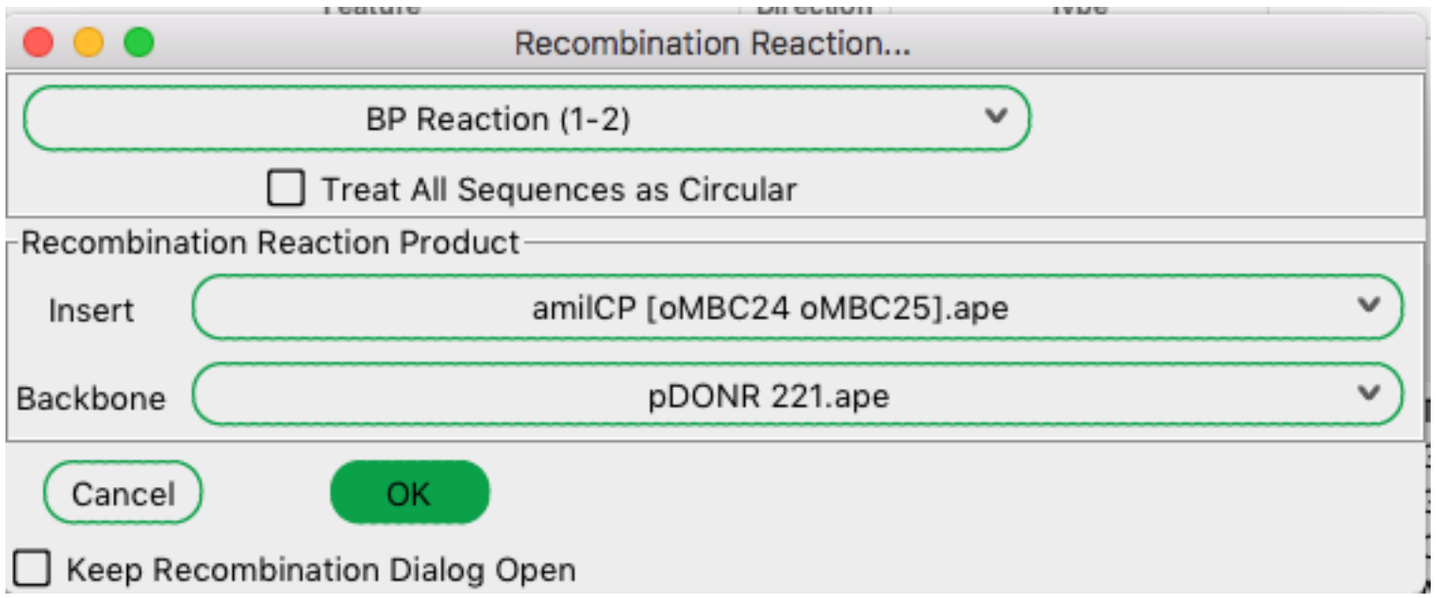
Recombination tool





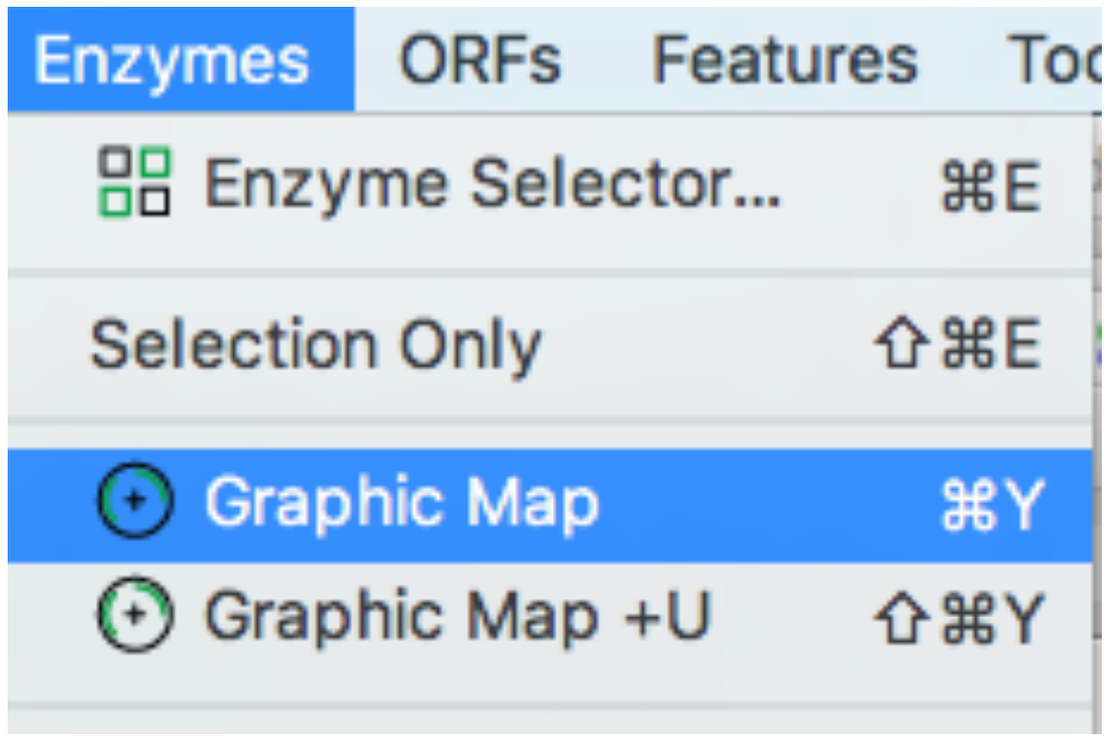
Recombination tool



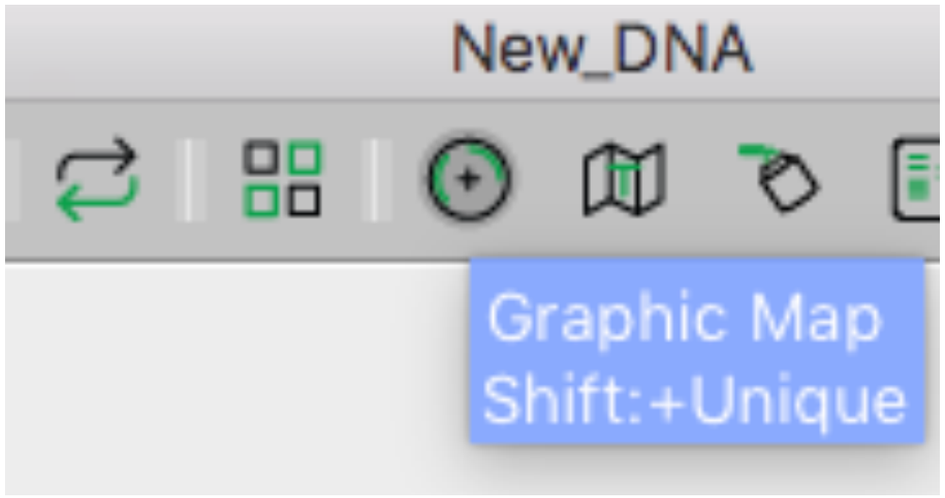


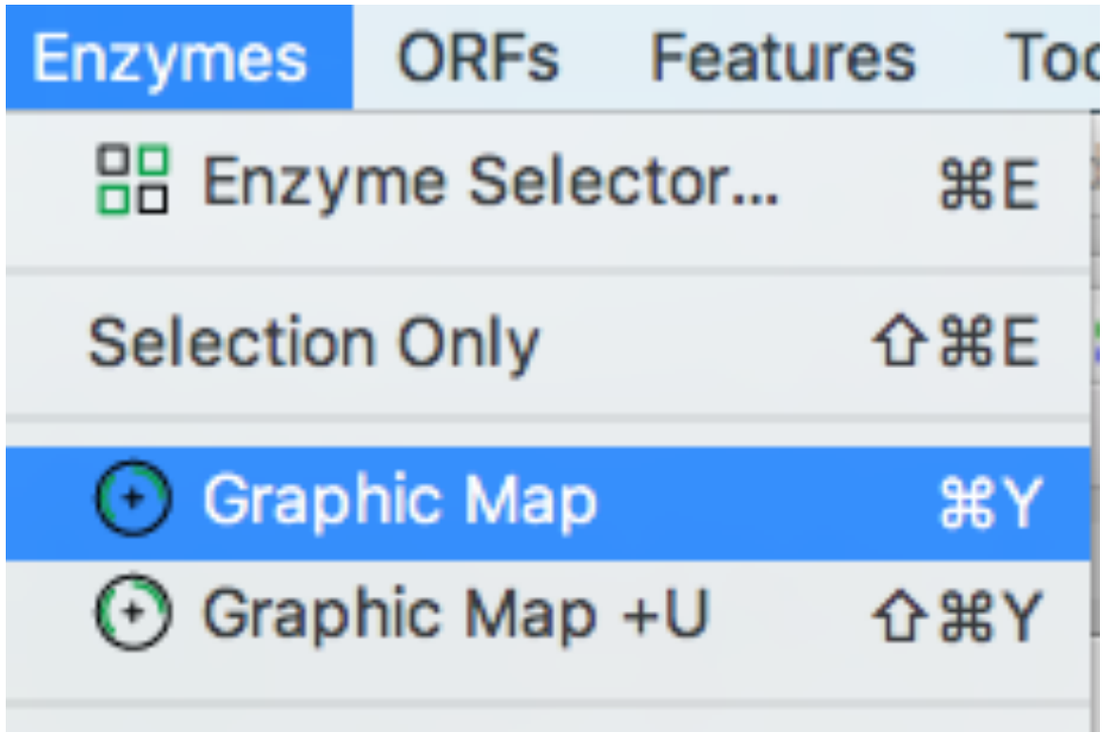
Recombination tool

Graphic Map

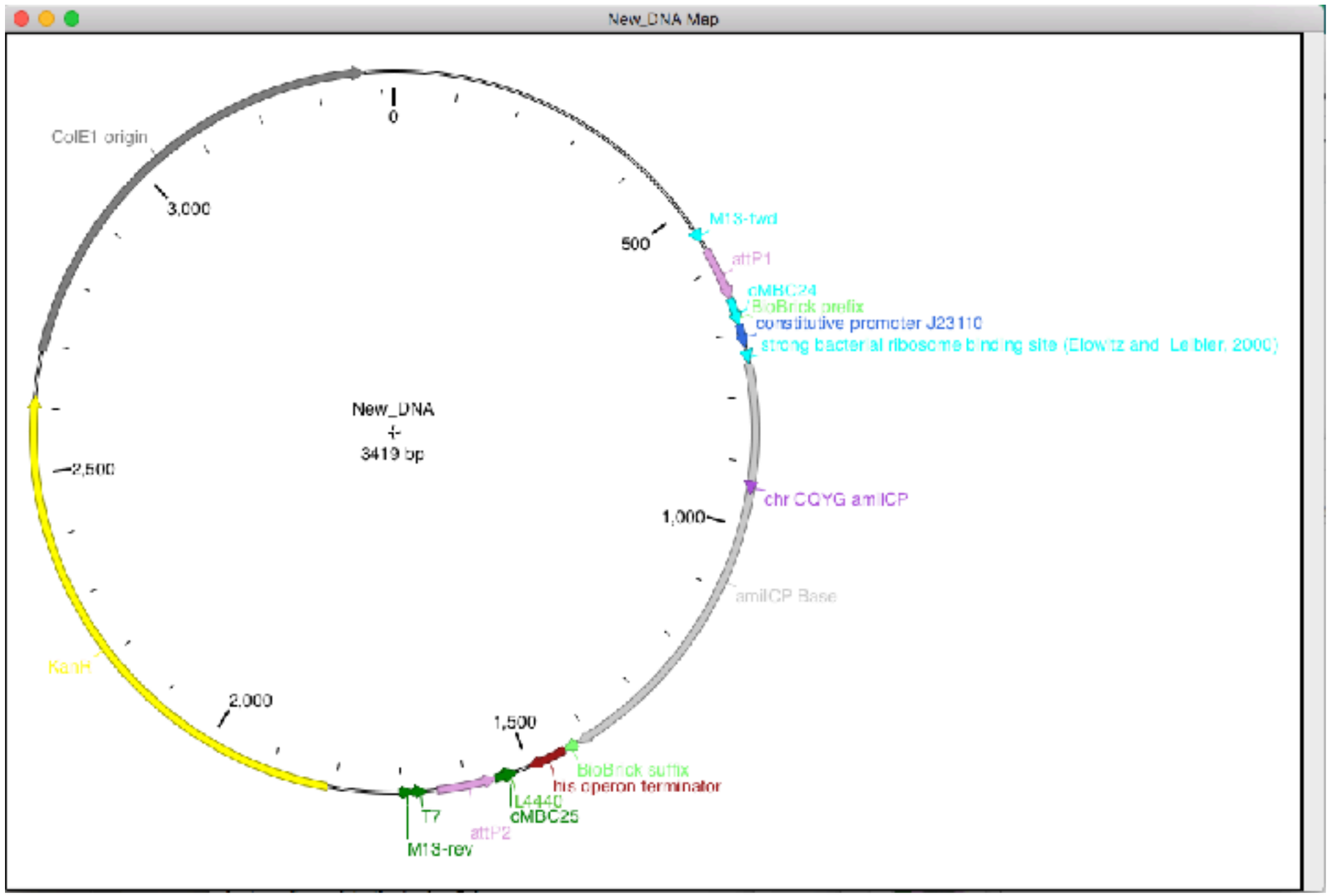

Enzymes
ORFs
Features
Enzyme Selector... ⌘E
Selection Only ⇧⌘E
Graphic Map ⌘Y
Graphic Map +U ⇧⌘Y

Graphic Map


New_DNA
Graphic Map
Shift:+Unique


Enzymes
ORFs
Features
Enzyme Selector... ⌘E
Selection Only ⇧⌘E
Graphic Map ⌘Y
Graphic Map +U ⇧⌘Y

Graphic Map


New_DNA Map
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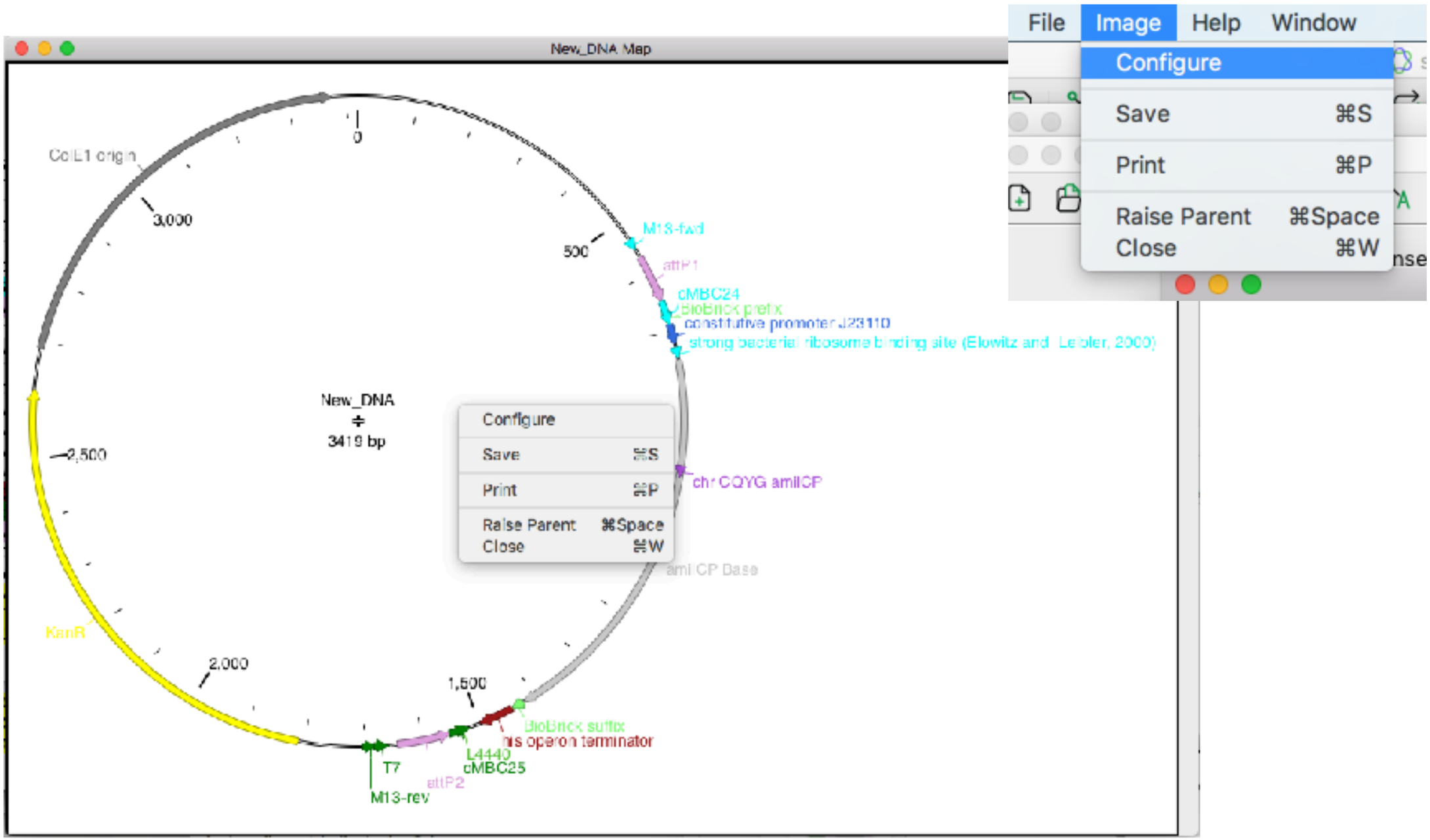
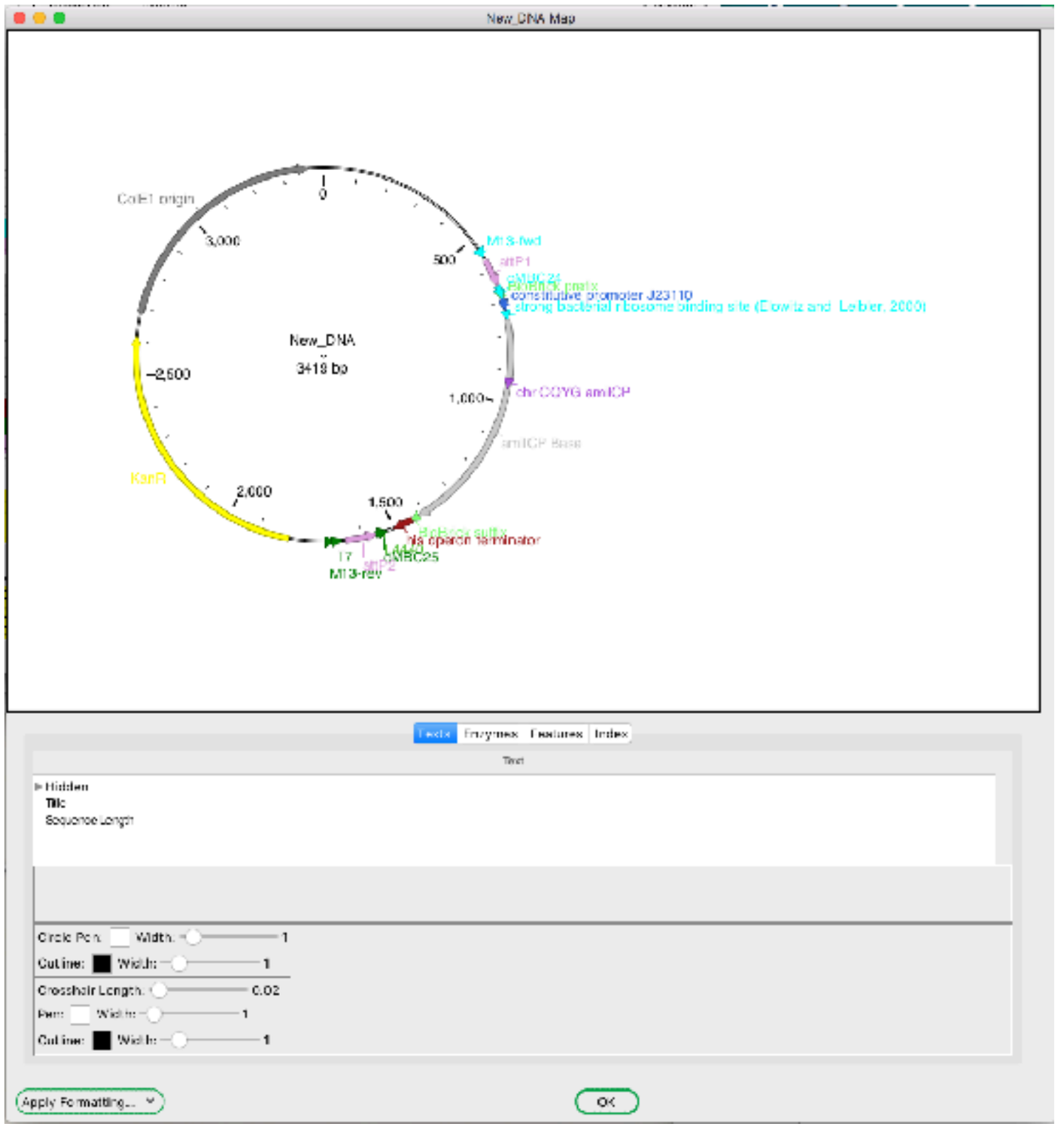
1,500
2,000
2,500
3,000
New_DNA
3419 bp
ColE1 origin
M13-fwd
attP1
cMBC24
BioBrick prefix
constitutive promoter J23110
strong bacterial ribosome binding site (Elowitz and Leibler, 2000)
chr CQYG amilCP
amilCP Base
BioBrick suffix
his operon terminator
L4440
cMDC25
attP2
T7
M13-rev
KanR

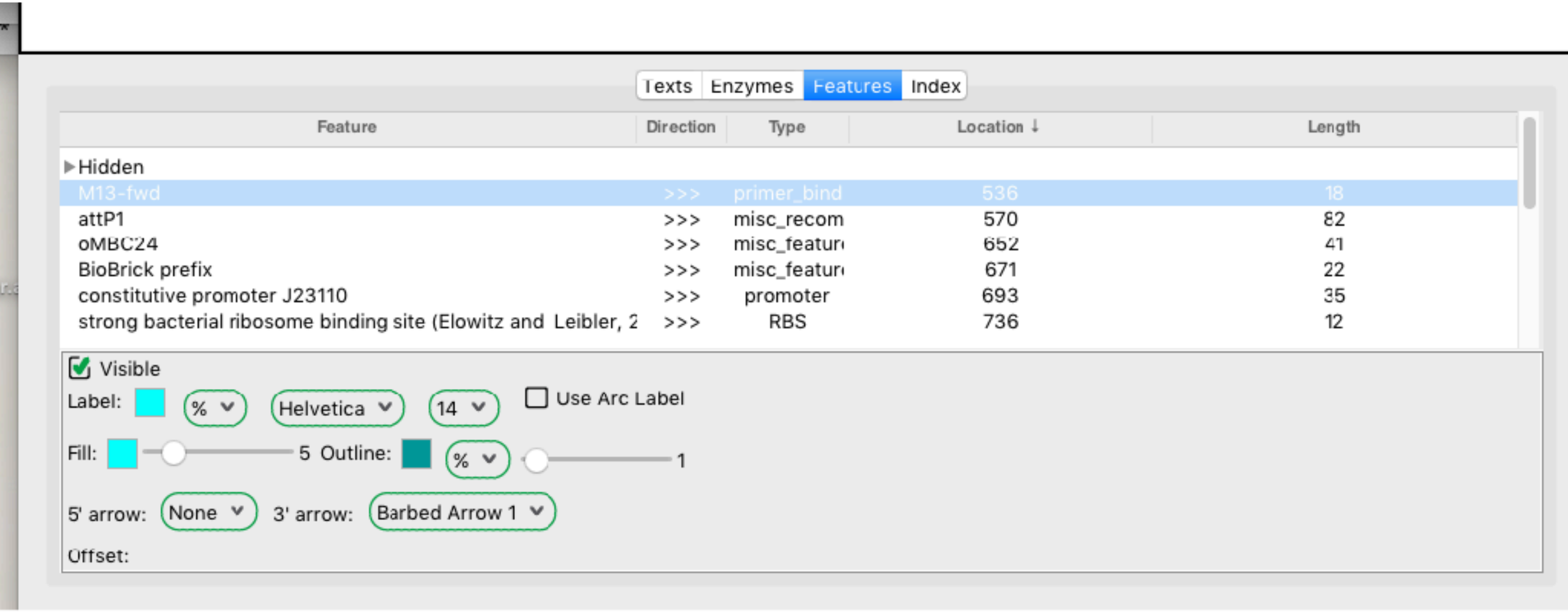
Graphic Map


New_DNA Map
File
Image
Help
Window
Configure
Save ⌘S
Print ⌘P
Raise Parent ⌘Space
Close ⌘W
ColE1 origin
0
500
1,000
1,500
2,000
2,500
3,000
M13-fwd
attP1
cMBC24
BioBrick prefix
constitutive promoter J23110
strong bacterial ribosome binding site (Elowitz and Leibler, 2000)
New_DNA
3419 bp
Configure
Save ⌘S
Print ⌘P
Raise Parent ⌘Space
Close ⌘W
KanR
T7
M13-rev
attP2
L4440
cMBC25
BioBrick suffix
rrnB operon terminator

Graphic Map


New_DNA Map
ColE1 origin
0
3,000
500
M13-fwd
attP1
constitutive promoter J23110
strong bacterial ribosome binding site (Elowitz and Leibler, 2000)
New_DNA
3418 bp
2,500
1,000
chrCO2YG amICP
amICP Base
KanR
2,000
1,500
rrnB operon terminator
M13-rev
Text
Hidden
Title
Sequence Length
Circle Pen: Width: 1
Outline: Width: 1
Crosshair Length: 0.02
Pen: Width: 1
Outline: Width: 1
Apply Formatting...
OK

Graphic Map


Texts
Enzymes
Features
Index
Feature
Direction
Type
Location ↓
Length
▶Hidden
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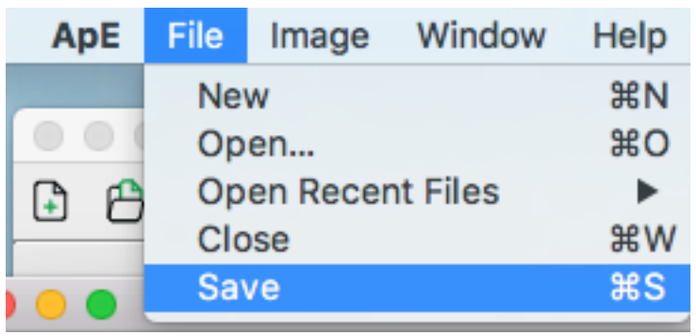
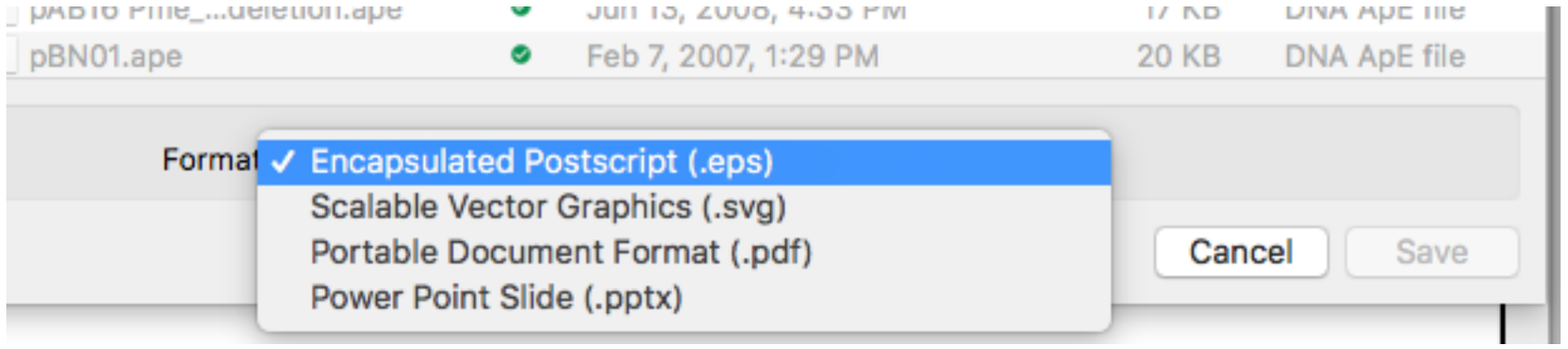
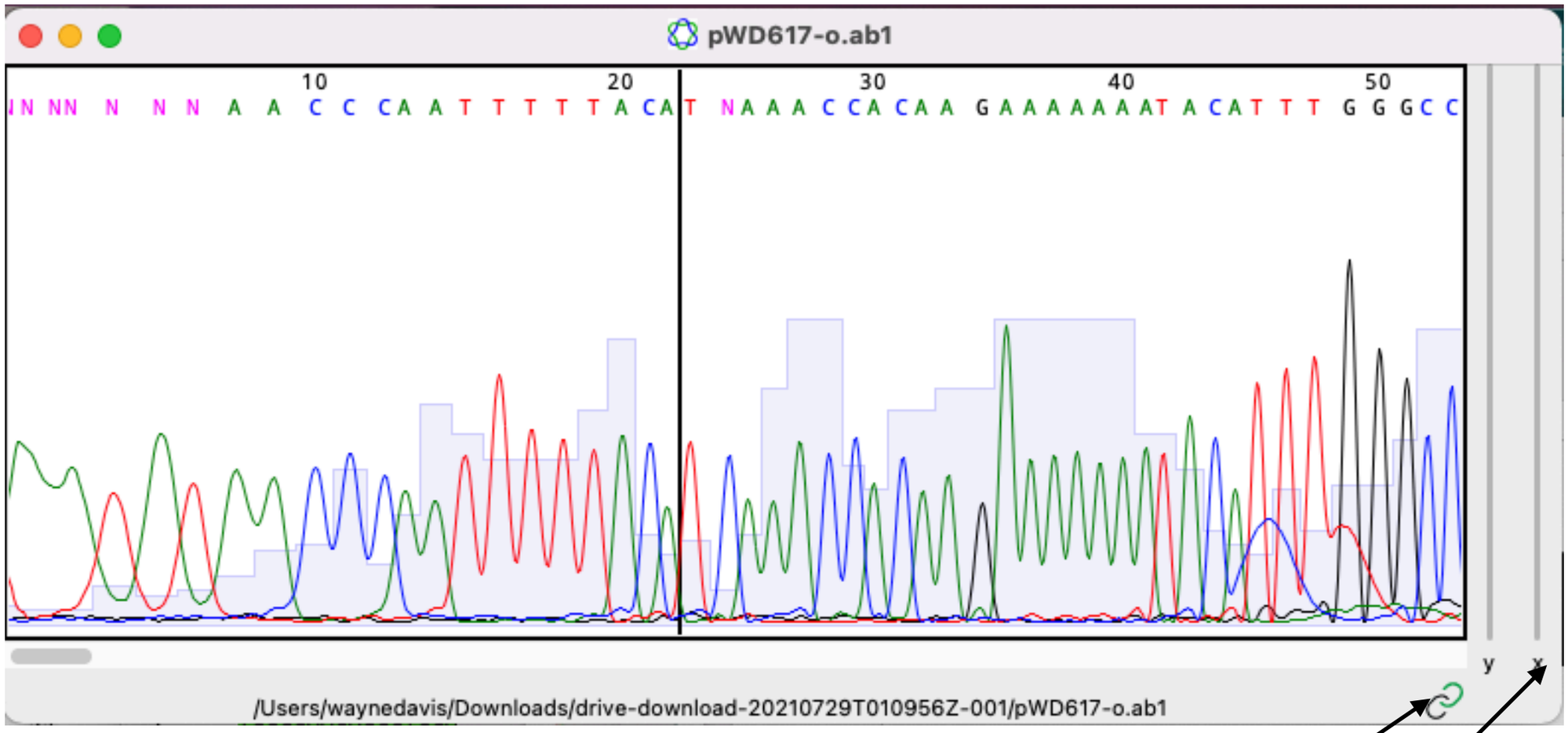
attP1 >>> misc_recom 570 82
oMBC24 >>> misc_featur 652 41
BioBrick prefix >>> misc_featur 671 22
constitutive promoter J23110 >>> promoter 693 35
strong bacterial ribosome binding site (Elowitz and Leibler, 2 >>> RBS 736 12
Visible
Label:
%
Helvetica
14
Use Arc Label
Fill:
5
Outline:
%
1
5' arrow:
None
3' arrow:
Barbed Arrow 1
Offset:

Graphic Map

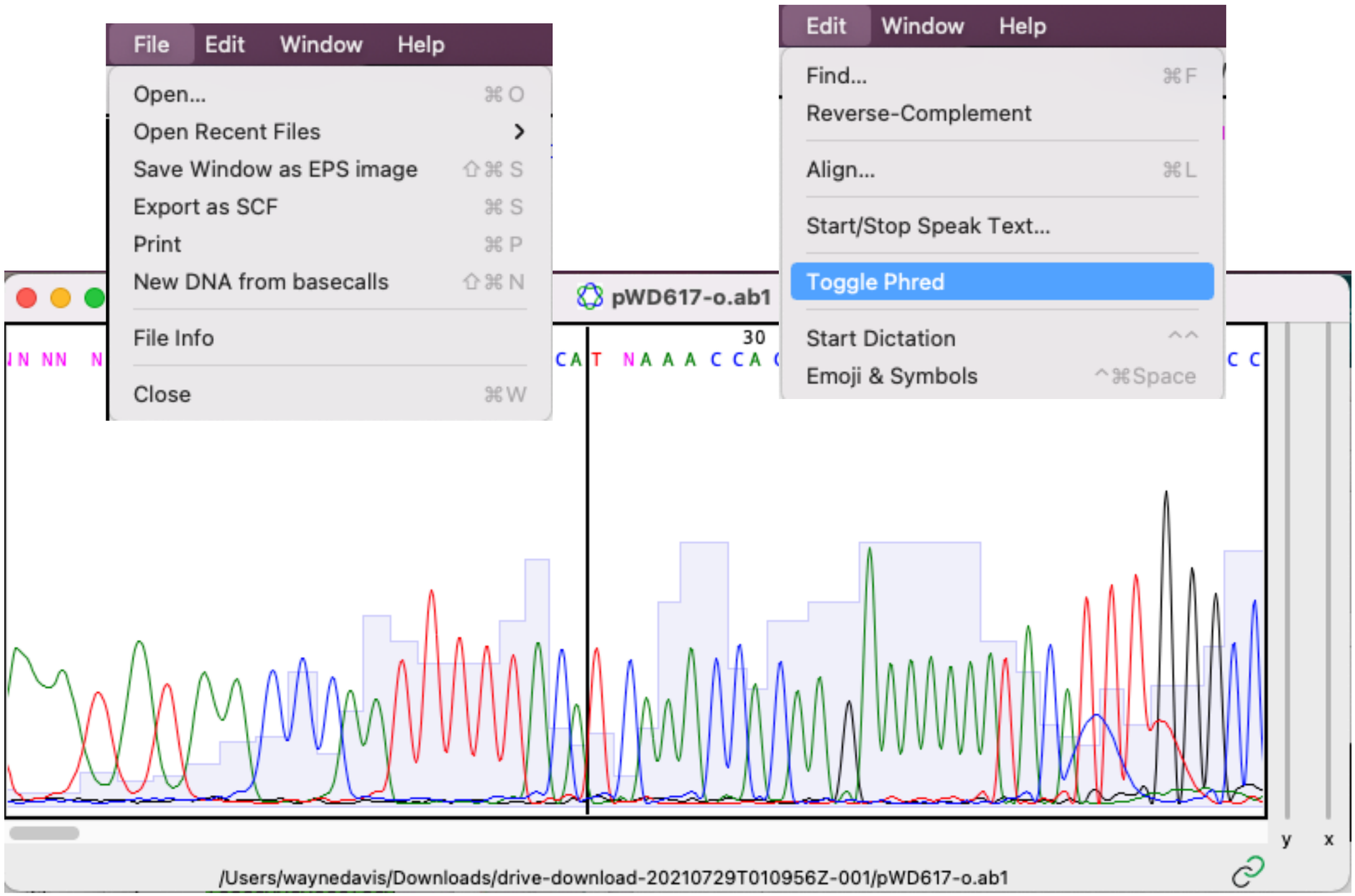

ApE
File
Image
Window
Help
New ⌘N
Open... ⌘O
Open Recent Files ▶
Close ⌘W
Save ⌘S


pBN01.ape
Feb 7, 2007, 1:29 PM
20 KB
DNA ApE file
Format
✓ Encapsulated Postscript (.eps)
Scalable Vector Graphics (.svg)
Portable Document Format (.pdf)
Power Point Slide (.pptx)
Cancel
Save

ABI files


pWD617-o.ab1
10
20
30
40
50
N NN N N N A A C C CA A T T T T T A CA T NA A A C CA CA A G A A A A A A AT A CA T T T G G G C C
y
x
/Users/waynedavis/Downloads/drive-download-20210729T010956Z-001/pWD617-o.ab1
Drag this to a sequence window to add the abi file to a sequence file
Scale

ABI files


File
Edit
Window
Help
Open... ⌘O
Open Recent Files
Save Window as EPS image ⇧⌘S
Export as SCF ⌘S
Print ⌘P
New DNA from basecalls ⇧⌘N
File Info
Close ⌘W
Edit
Window
Help
Find... ⌘F
Reverse-Complement
Align... ⌘L
Start/Stop Speak Text...
Toggle Phred
Start Dictation ^^
Emoji & Symbols ^⌘Space
pWD617-o.ab1
30
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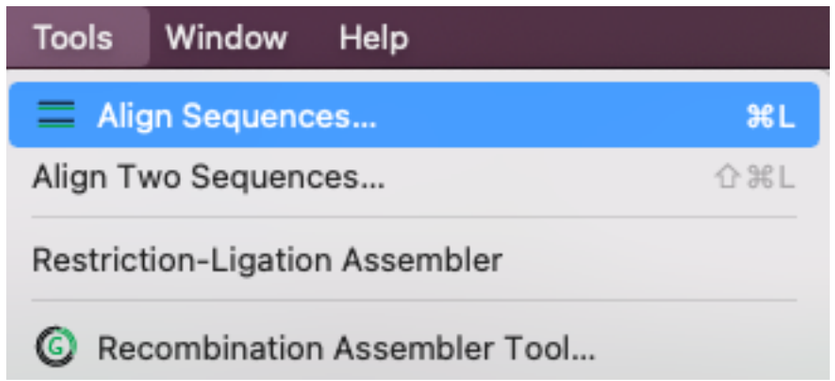
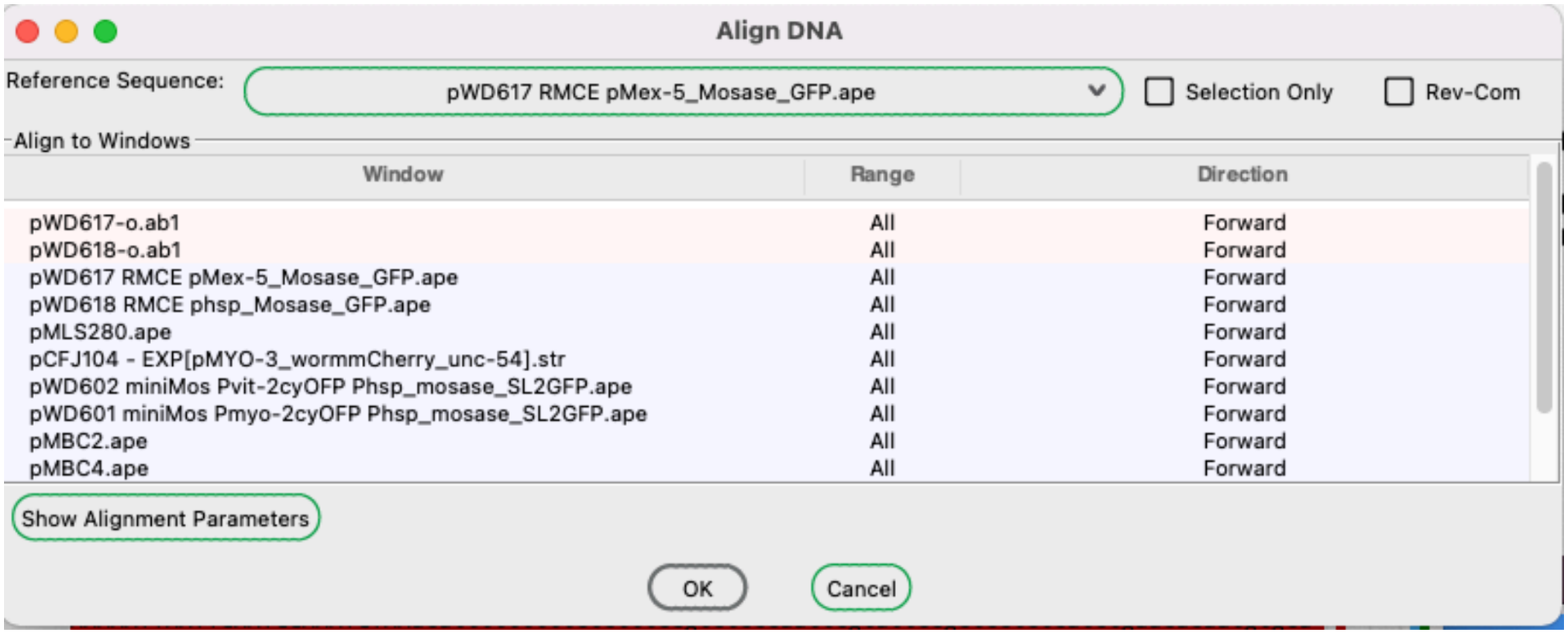
x
/Users/waynedavis/Downloads/drive-download-20210729T010956Z-001/pWD617-o.ab1

Align


Tools
Window
Help
Align Sequences...
⌘L
Align Two Sequences...
⇧⌘L
Restriction-Ligation Assembler
Recombination Assembler Tool...

Align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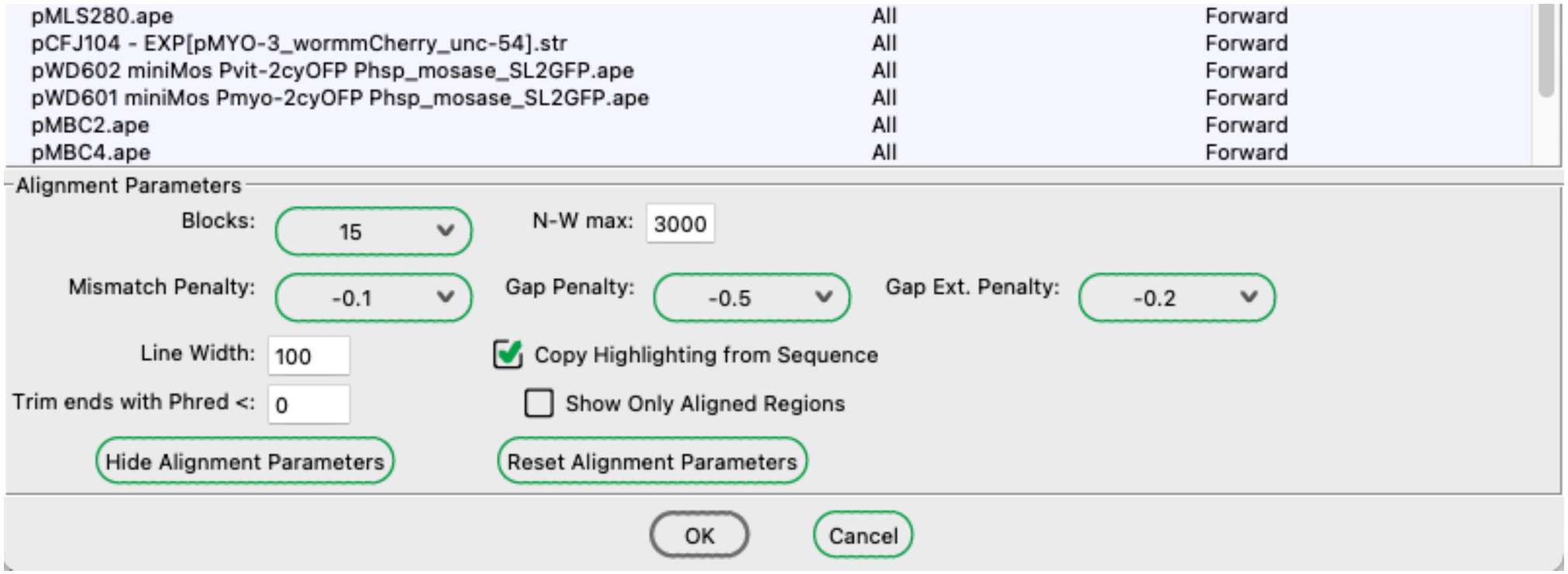
pWD617 RMCE pMex-5_Mosase_GFP.ape
Selection Only
Rev-Com
Align to Windows
Window
Range
Direction
pWD617-o.ab1 All Forward
pWD618-o.ab1 All Forward
pWD617 RMCE pMex-5_Mosase_GFP.ape All Forward
pWD618 RMCE phsp_Mosase_GFP.ape All Forward
pMLS280.ape All Forward
pCFJ104 - EXP[pMYO-3_wormmCherry_unc-54].str All Forward
pWD602 miniMos Pvit-2cyOFP Phsp_mosase_SL2GFP.ape All Forward
pWD601 miniMos Pmyo-2cyOFP Phsp_mosase_SL2GFP.ape All Forward
pMBC2.ape All Forward
pMBC4.ape All Forward
Show Alignment Parameters
OK
Cancel

Align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pWD602 miniMos Pvit-2cyOFP Phsp_mosase_SL2GFP.ape All Forward
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Alignment Parameters
Blocks: 15
N-W max: 3000
Mismatch Penalty: -0.1
Gap Penalty: -0.5
Gap Ext. Penalty: -0.2
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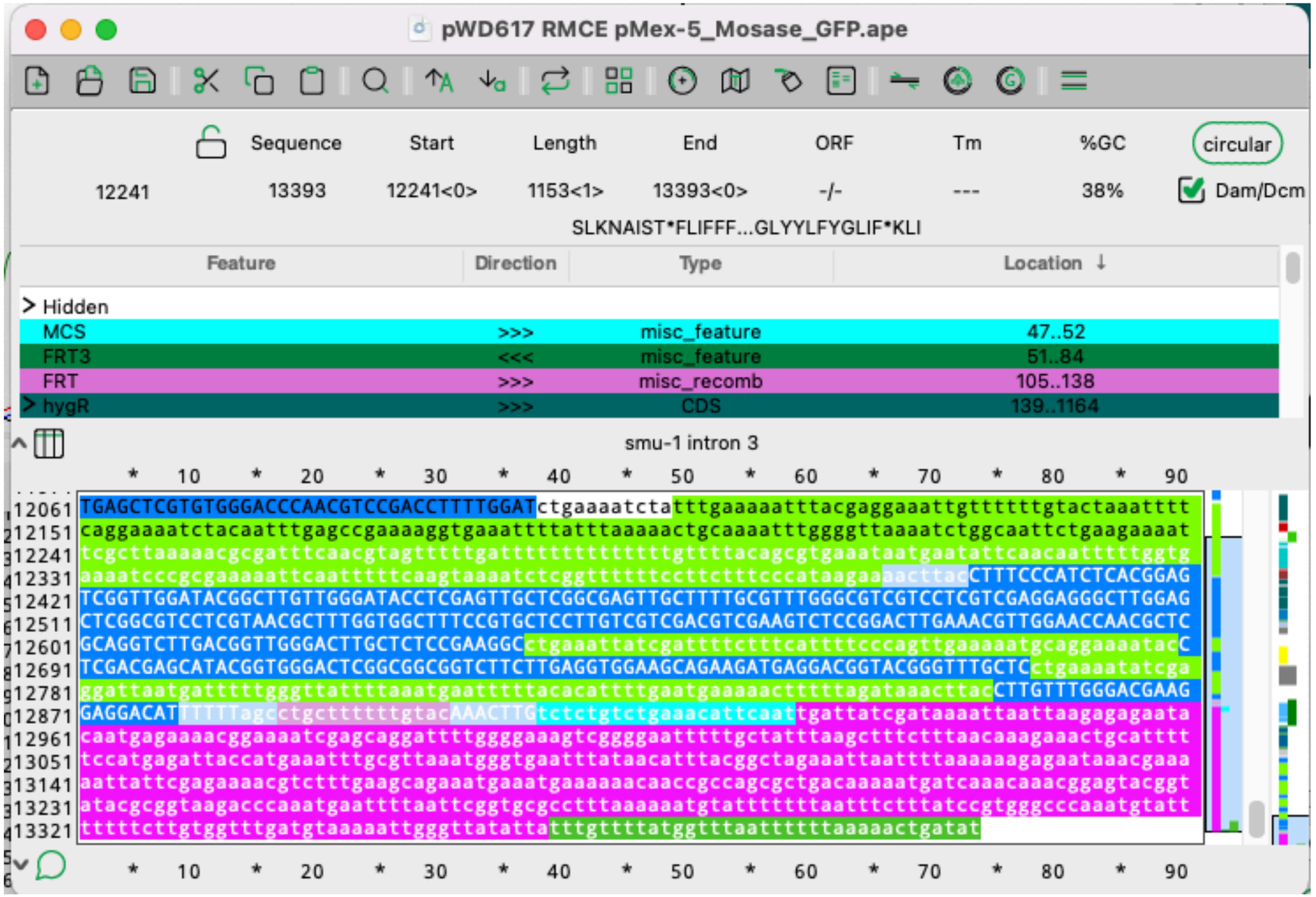
Copy Highlighting from Sequence
Trim ends with Phred <: 0
Show Only Aligned Regions
Hide Alignment Parameters
Reset Alignment Parameters
OK
Cancel

Align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Sequence
Start
Length
End
ORF
Tm
%GC
circular
12241
13393
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1153<1>
13393<0>
-/-

38%
Dam/Dcm
SLKNAIST*FLIFFF...GLYYLFYGLIF*KLI
Feature
Direction
Type
Location
> Hidden
MCS
>>>
misc_feature
47..52
FRT3
<<<
misc_feature
51..84
FRT
>>>
misc_recomb
105..138
> hygR
>>>
CDS
139..1164
smu-1 intron 3
* 10 * 20 * 30 * 40 * 50 * 60 * 70 * 80 * 90
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12511 CTCGGCGTCCTCGTAACGCTTTGGTGGCTTTCCGTGCTCCTTGTCGTCGACGTCGAAGTCTCCGGACTTGAAACGTTGGAACCAACGCTC
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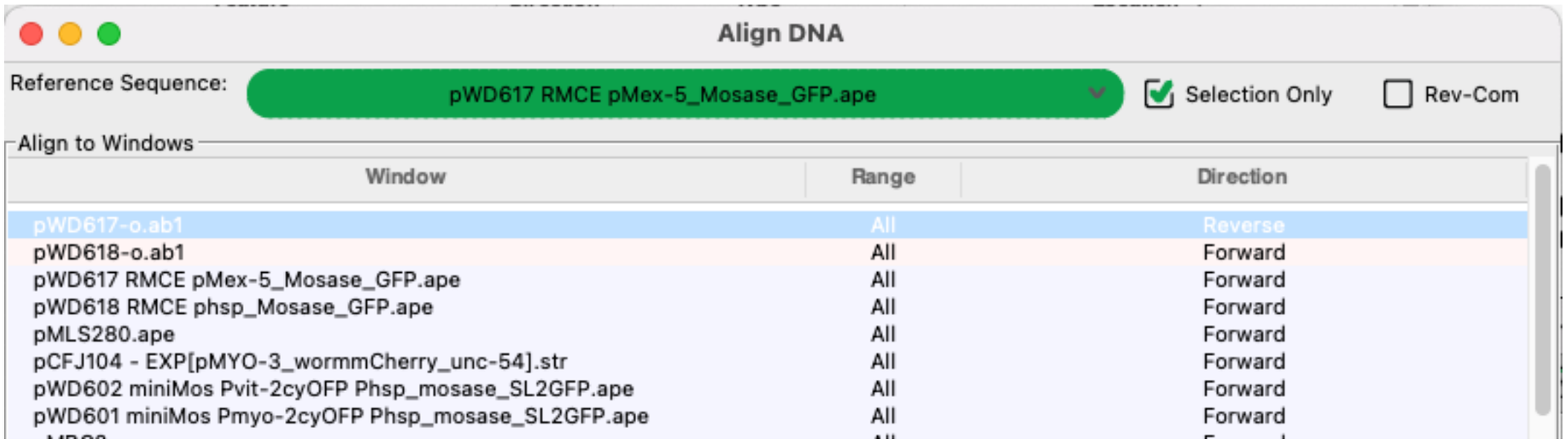
Align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Selection Only
Rev-Com
Align to Windows
Window
Range
Direction
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pWD618-o.ab1 All Forward
pWD617 RMCE pMex-5_Mosase_GFP.ape All Forward
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pMLS280.ape All Forward
pCFJ104 - EXP[pMYO-3_wormmCherry_unc-54].str All Forward
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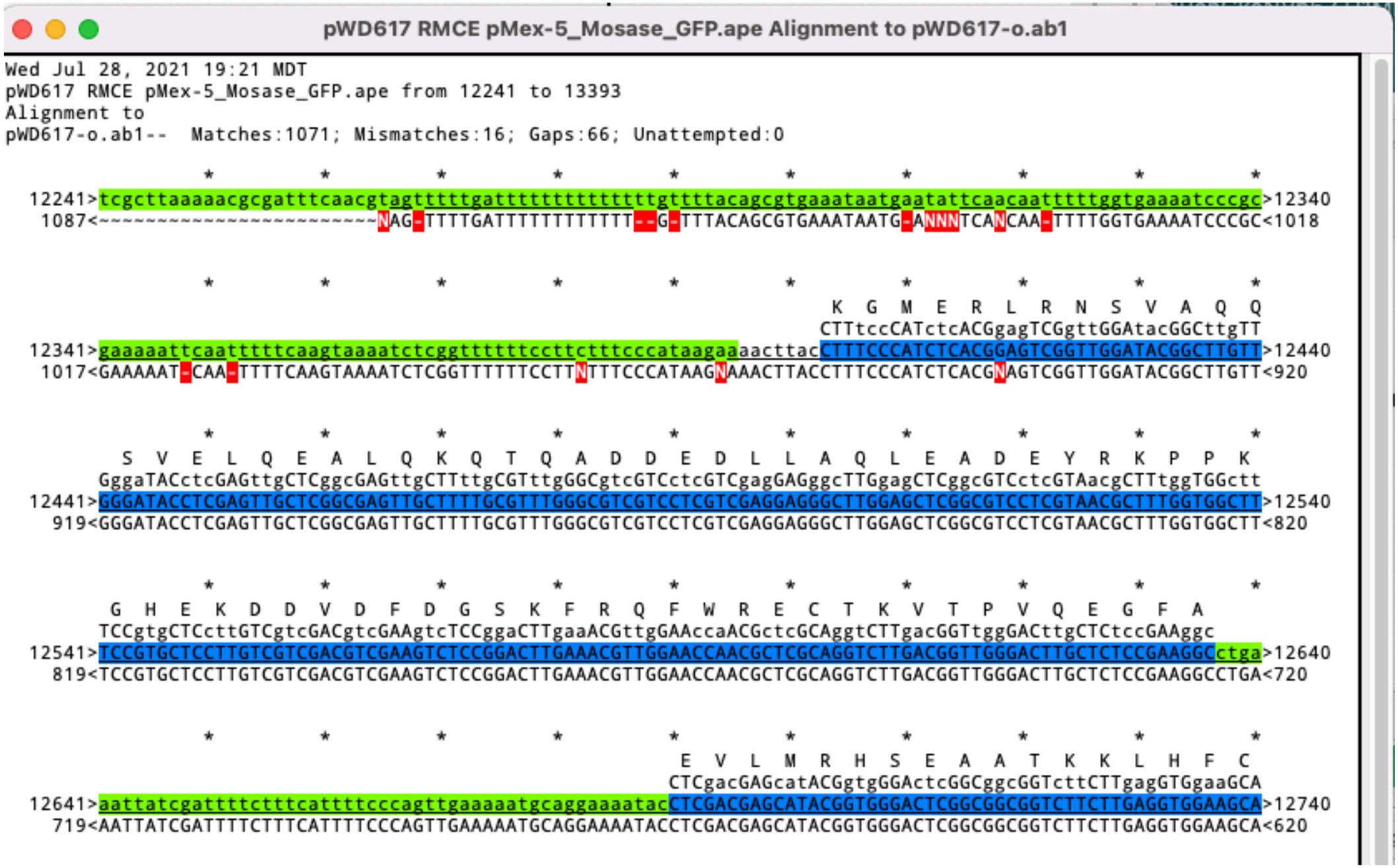
Align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Wed Jul 28, 2021 19:21 MDT
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Alignment to
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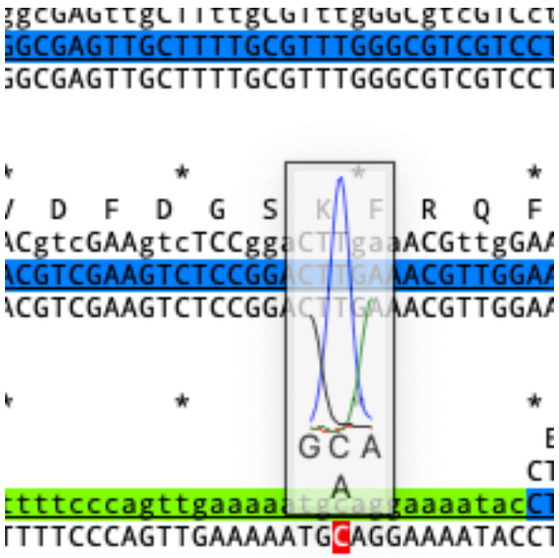
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G C A
A
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