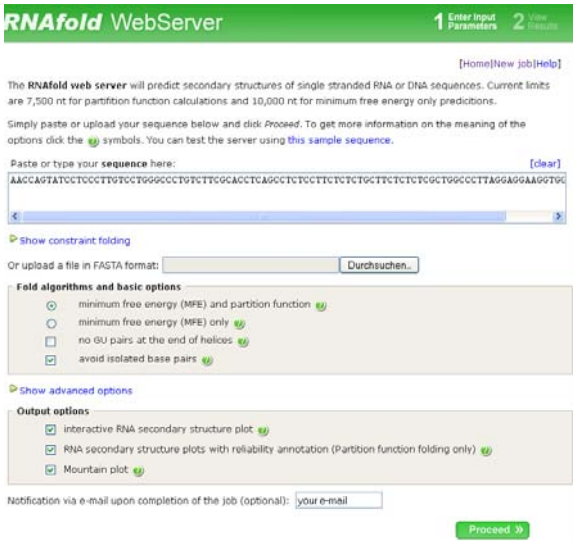
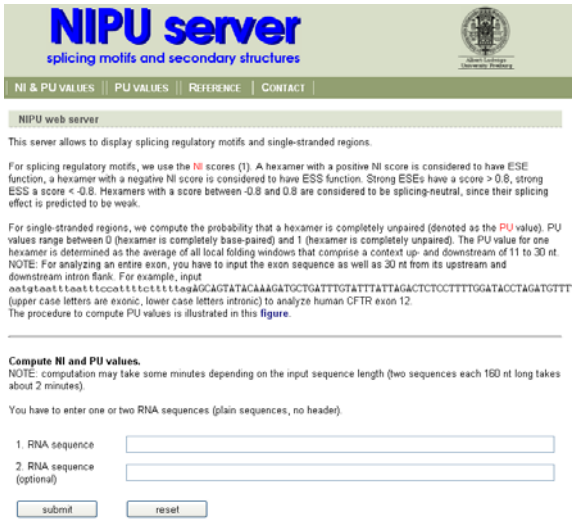
Predicting single-stranded regions



Outcome:
base-pair probability plot

Questions answered:
Which pre-mRNA regions are likely single- or double-stranded.

Predicting if a mutation leads to structural changes



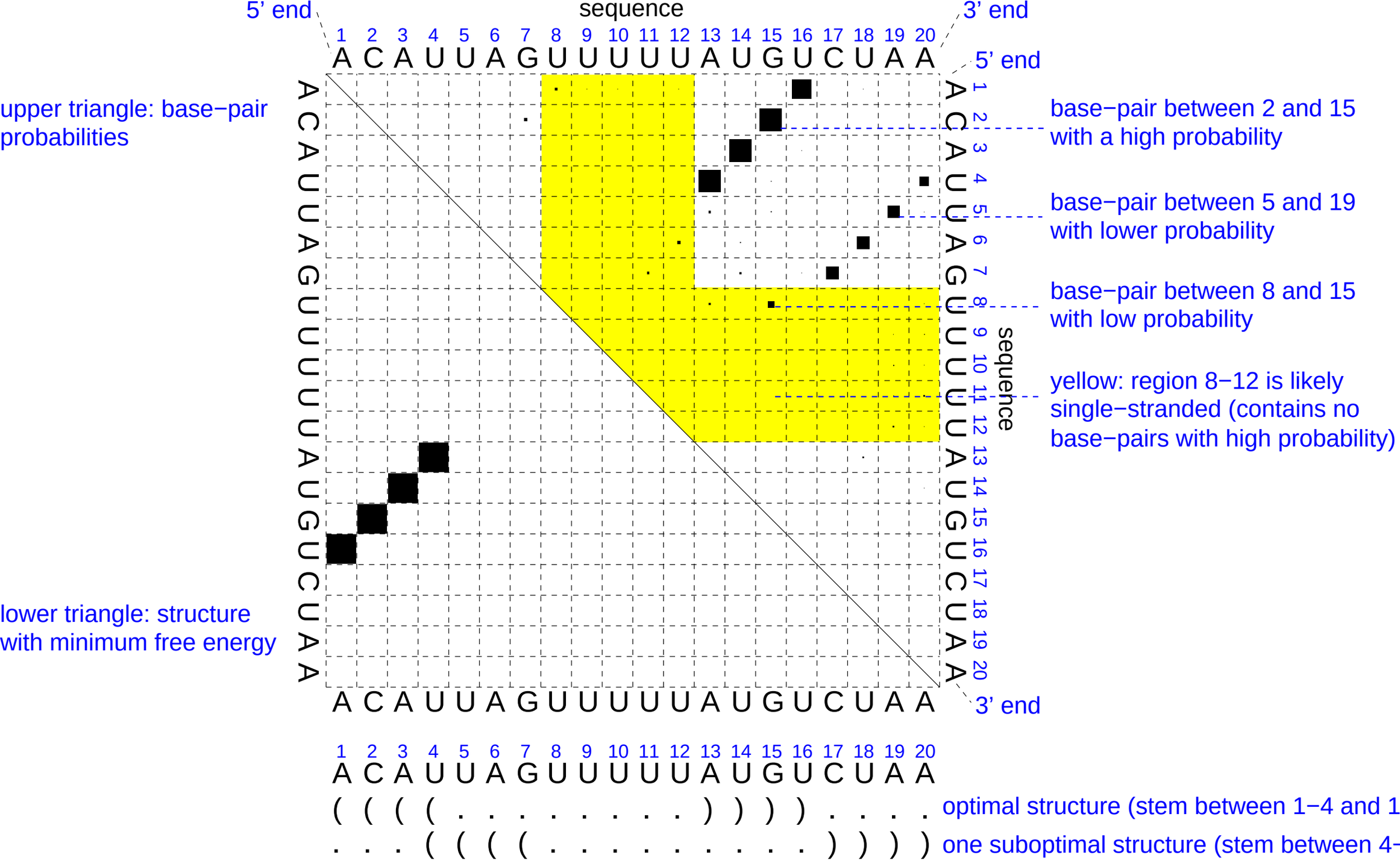
Outcome:
plots showing the single-strandedness of hexamers in the wild-type and mutant sequence

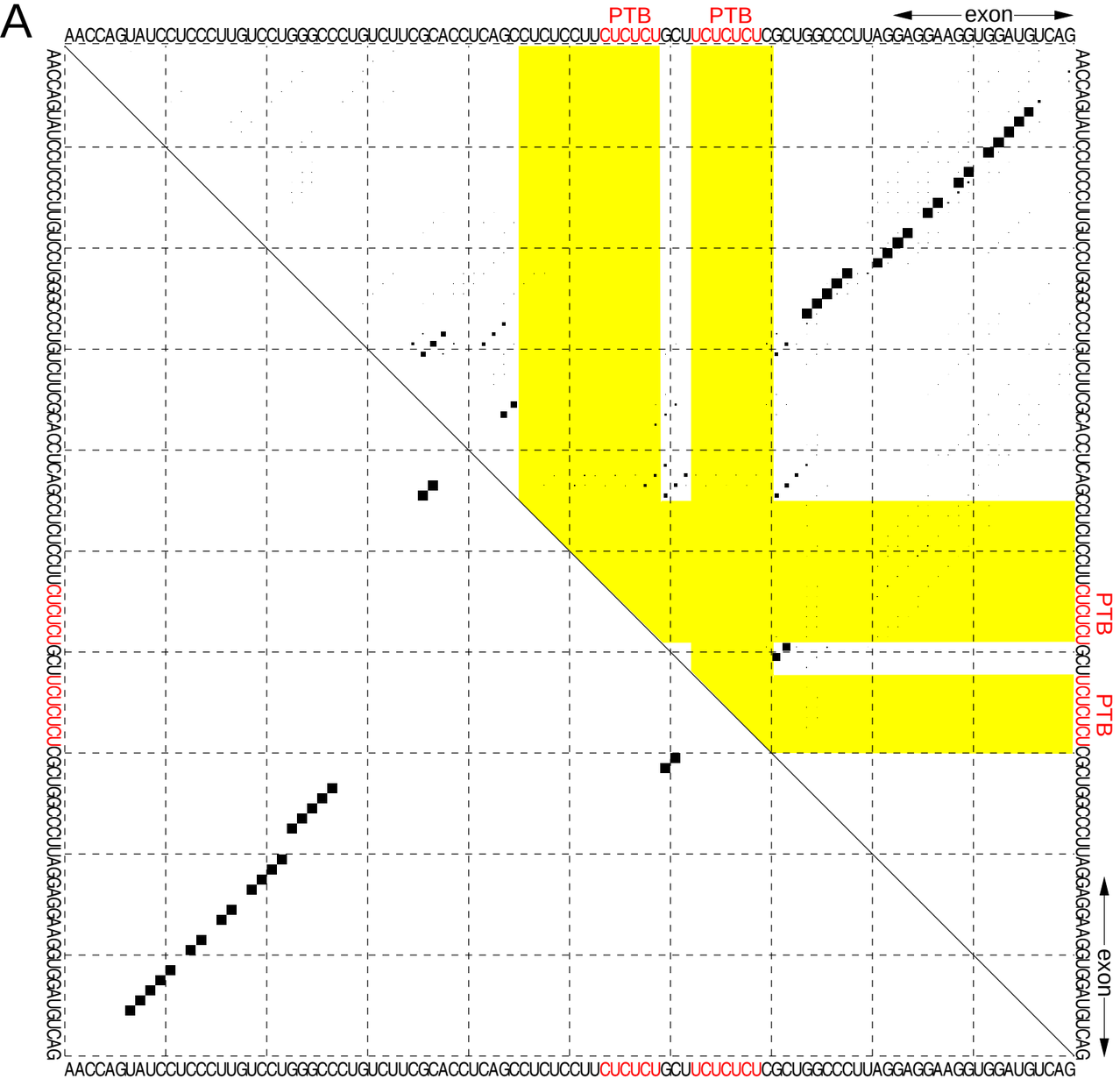
Questions answered:
Which mutations are likely to result in secondary structure changes and which are not.

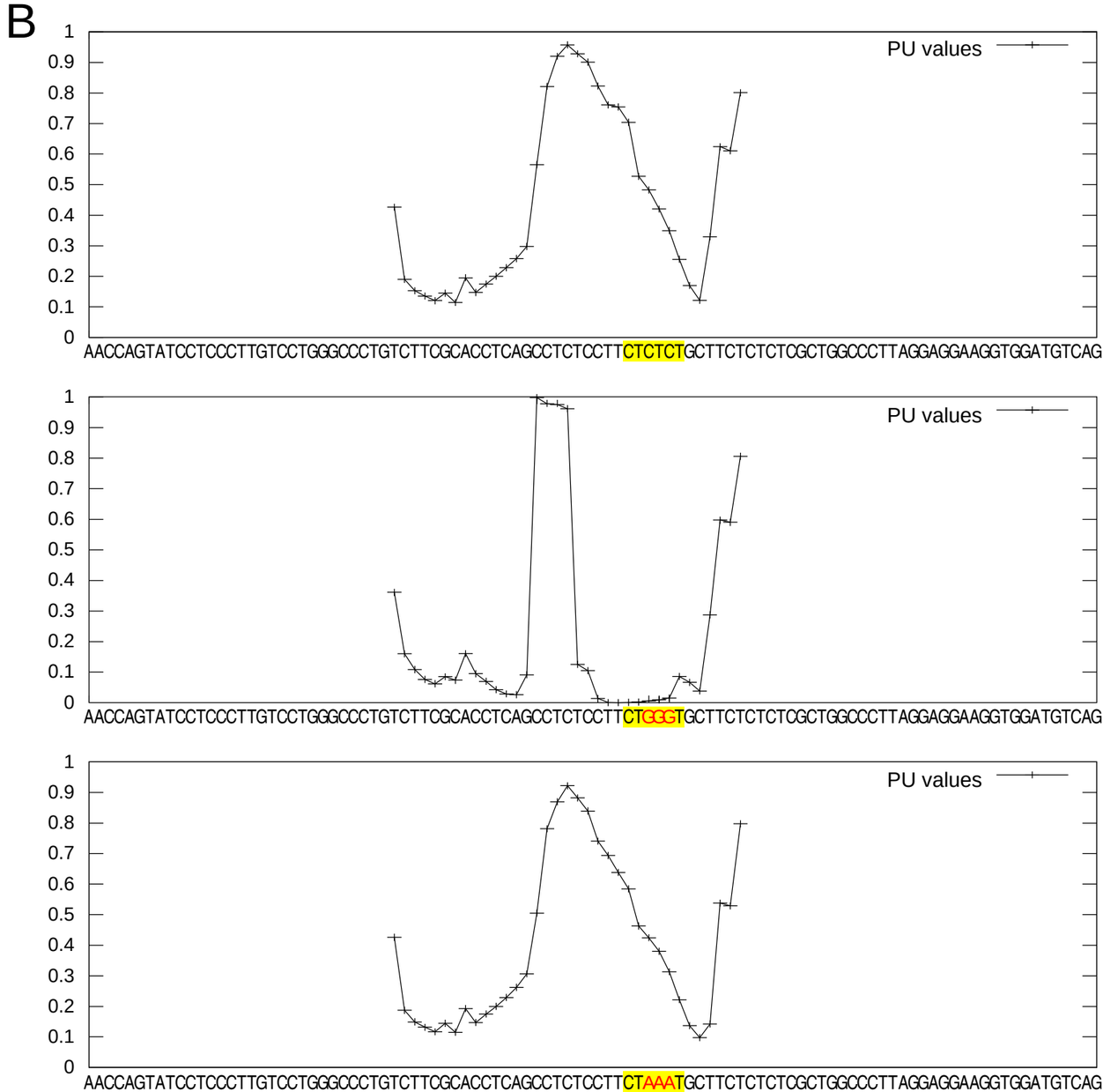
Finding alternative splice events that overlap conserved secondary structures

Outcome:
a list, an annotation track or Genome Browser links of such alternative splice events

Questions answered:
Which alternative splice events might be regulated by conserved secondary structures.


5' end
sequence
3' end
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
A C A U U A G U U U U U A U G U C U A A
5' end
3' end
sequence
upper triangle: base−pair probabilities
lower triangle: structure with minimum free energy
base−pair between 2 and 15 with a high probability
base−pair between 5 and 19 with lower probability
base−pair between 8 and 15 with low probability
yellow: region 8−12 is likely single−stranded (contains no base−pairs with high probability)
((((. . . . .)))) . . . optimal structure (stem between 1−4 and 13−16)
. . . ((((. . . . .)))) one suboptimal structure (stem between 4−7 and 17−20)


A
PTB
PTB
exon
AACCAGUAUCCUCCCUUGUCCUGGGCCCUGUCUUCGCACCUCAGCCUCUCCUUCUCUCUGCUUCUCUCUCGCUGGCCCUUAGGAGGAAGGUGGAUGUCAG
PTB
PTB
exon


B
PU values
AACCAGTATCCTCCCTTGTCCTGGGCCCTGTCTTCGCACCTCAGCCTCTCCTTCTCTCTGCTTCTCTCTCGCTGGCCCTTAGGAGGAAGGTGGATGTCAG
PU values
AACCAGTATCCTCCCTTGTCCTGGGCCCTGTCTTCGCACCTCAGCCTCTCCTTCTGGGTGCTTCTCTCTCGCTGGCCCTTAGGAGGAAGGTGGATGTCAG
PU values
AACCAGTATCCTCCCTTGTCCTGGGCCCTGTCTTCGCACCTCAGCCTCTCCTTCTAAATGCTTCTCTCTCGCTGGCCCTTAGGAGGAAGGTGGATGTCAG