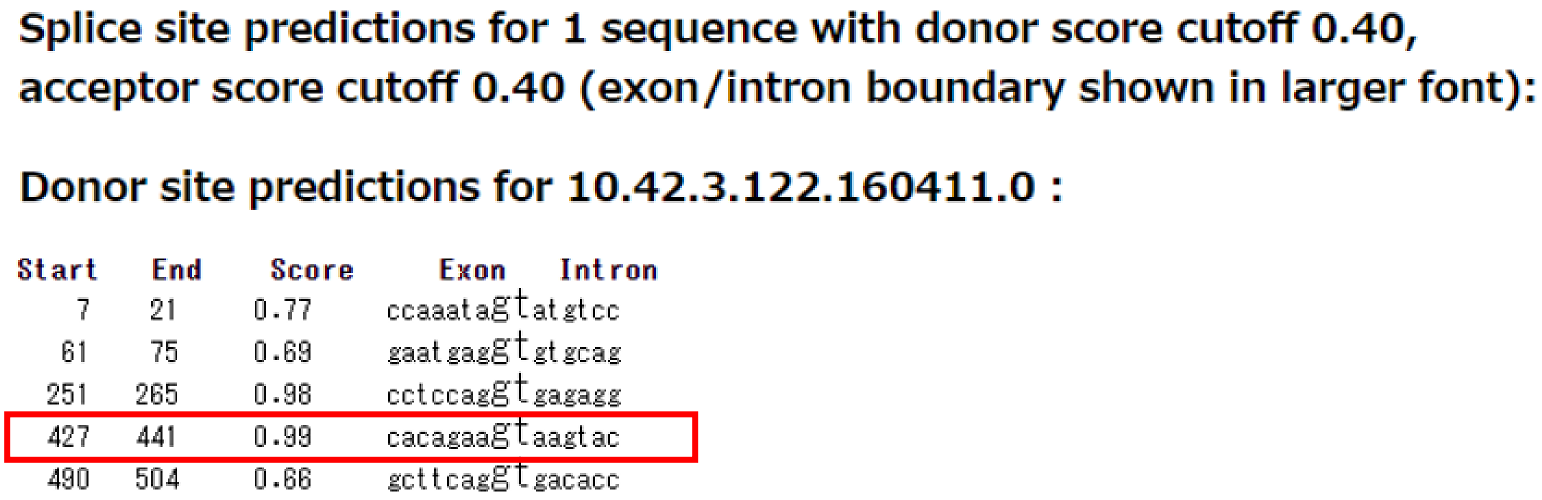
Supplemental Figure S1. In-silico analysis for predicted splice site

http://www.fruitfly.org/seq_tools/splice.html

Wild type

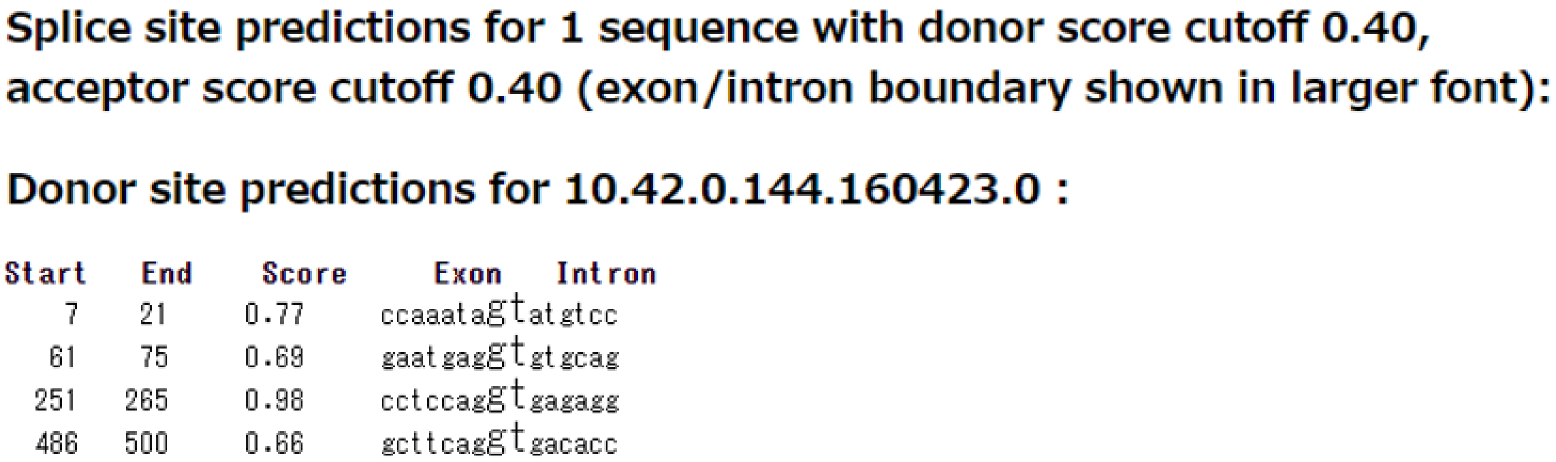


Splice site predictions for 1 sequence with donor score cutoff 0.40, acceptor score cutoff 0.40 (exon/intron boundary shown in larger font):

Donor site predictions for 10.42.3.122.160411.0 :

```
Start    End     Score      Exon    Intron
    7     21     0.77     ccaaatagtatgtcc
   61     75     0.69     gaatgaggtgtgcag
  251    265     0.98     cctccaggtgagagg
  427    441     0.99     cacagaagtaagtac
  490    504     0.66     gcttcaggtgacacc
```

Variant



Splice site predictions for 1 sequence with donor score cutoff 0.40, acceptor score cutoff 0.40 (exon/intron boundary shown in larger font):

Donor site predictions for 10.42.0.144.160423.0 :

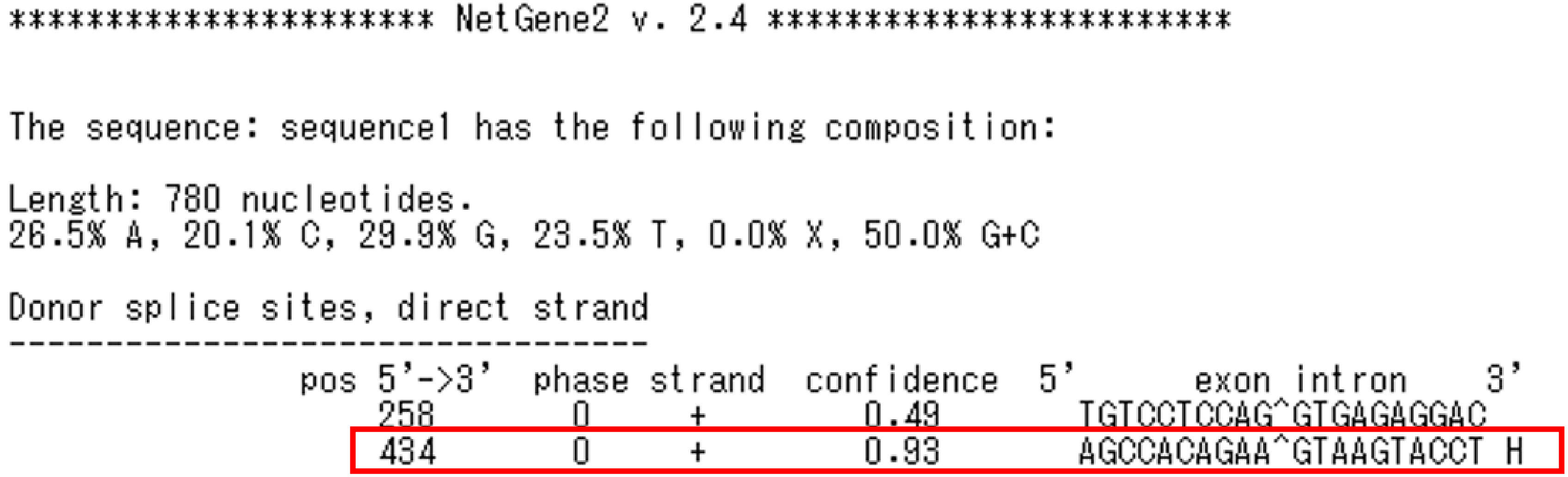
```
Start    End     Score      Exon    Intron
    7     21     0.77     ccaaatagtatgtcc
   61     75     0.69     gaatgaggtgtgcag
  251    265     0.98     cctccaggtgagagg
  486    500     0.66     gcttcaggtgacacc
```

In comparison with the wild type sequence, the normal splicing donor site (red rectangle) is disappeared in the variant sequence.

Supplemental Figure S2. In-silico analysis for predicted splice site

http://www.cbs.dtu.dk/services/NetGene2/

Wild type



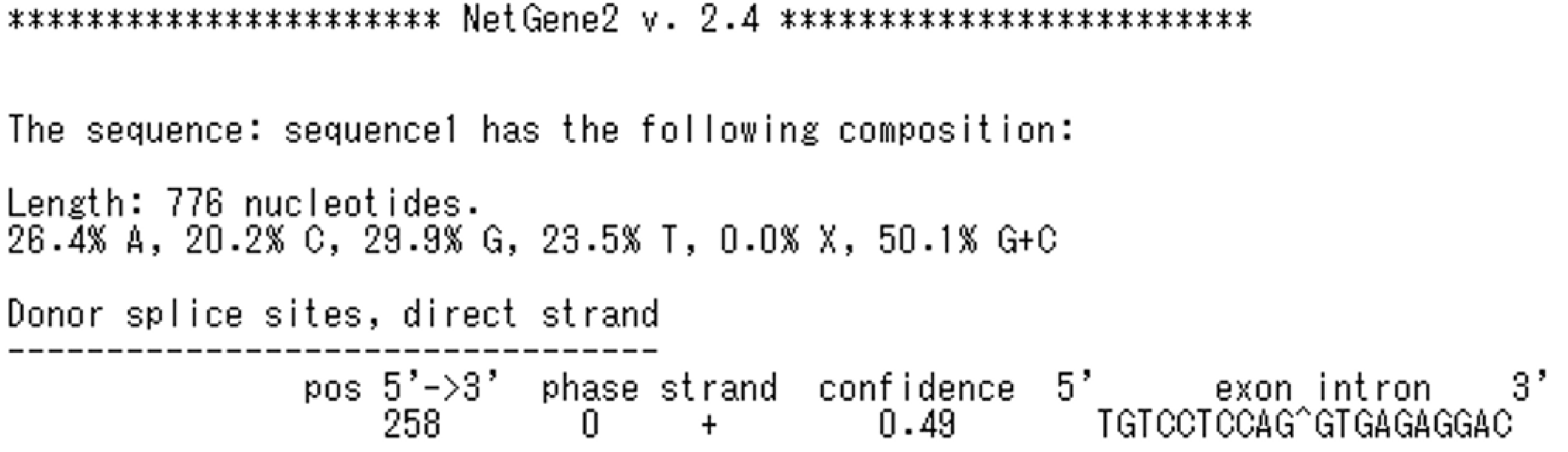
```
********************** NetGene2 v. 2.4 ************************


The sequence: sequence1 has the following composition:

Length: 780 nucleotides.
26.5% A, 20.1% C, 29.9% G, 23.5% T, 0.0% X, 50.0% G+C

Donor splice sites, direct strand
---------------------------------
               pos 5'->3'  phase strand  confidence  5'      exon intron    3'
                   258        0     +          0.49     TGTCCTCCAG^GTGAGAGGAC
                   434        0     +          0.93     AGCCACAGAA^GTAAGTACCT H
```

Variant



```
********************** NetGene2 v. 2.4 ************************


The sequence: sequence1 has the following composition:

Length: 776 nucleotides.
26.4% A, 20.2% C, 29.9% G, 23.5% T, 0.0% X, 50.1% G+C

Donor splice sites, direct strand
---------------------------------
               pos 5'->3'  phase strand  confidence  5'      exon intron    3'
                   258        0     +          0.49     TGTCCTCCAG^GTGAGAGGAC
```

In comparison with the wild type sequence, the normal splicing donor site (red rectangle) is disappeared in the variant sequence.