Sequence alignment figure.

Block 1:
```
logo         TGCTTA..TC CGGCTACGGAGGACTCCTTGCTGTGTAGGCCTGTGTTCATTCTAGGGGTCAGTTGTCTGGCAGATGGGCTTAGAGTTGGAGTACCTCATCTTATTCCCTGCCTGAATCTG
Proband pri  TGCTTAGTCTCGGCTACGGAGGACTCCTTGCTGTGTAGGCCTGTGTTCATTCTAGGGGTCAGTTGTCTGGCAGATGGGCTTAGAGTTGGAGTACCTCATCTTATTCCCTGCCTGAATCTG  120
Proband sec  TGATTAMTCGCGGCTACGGAGGACTCCTTGCTGTGTAGGCCTGTGTTCATTCTAGGGGTCAGTTGTCTGGCAGATGGGCTTAGAGTTGGAGTACCTCATCTTATTCCCTGCCTGAATCTG  120
RefSeq       ...............                                                                                                            0
```

Block 2:
```
Proband pri  CTGTTTTCTTCTGCAGCCCGGGGACGTCTGGACCTTGCCAGACCAGTGCCACACCGTGACTTGCCAGCCAGATGGCCAGACCTTGCTGAAGAGTCATCGGGTCAACTGTGACCGGGGGCT  240
Proband sec  CTGTTTTCTTCTGCAGCCCAGGGACGTCTGGACCTTGCCAGACCAGTGCCACACCGTGACTTGCCAGCCAGATGGCCAGACCTTGCTGAAGAGTCATCGGGTCAACTGTGACCGGGGGCC  240
RefSeq       ...............CCCGGGGACGTCTGGACCTTGCCAGACCAGTGCCACACCGTGACTTGCCAGCCAGATGGCCAGACCTTGCTGAAGAGTCATCGGGTCAACTGTGACCGGGGGCT  104
```

Block 3:
```
Proband pri  GAGGCCTTCGTGCCCTAACAGCCAGTCCCCTGTTAAAGTGGAAGAGACCTGTGGCTGCCGCTGGACCTGCCCCTGTGAGTCCTTTGCTTCTCCAGCCAGGGCAGCGTCAAAGGGGCAGTG  360
Proband sec  GAGGCCTTCATGCCCTAACAGCCAGTCCCCTGTTAAAGTGGAAGACACCTGTGGCTGCCGCTGGACCTGCCCCTGTGAGTCCTTTGCTTCTCCAGCCAGGGCAGCGTCAAAGGGGCAGTG  360
RefSeq       GAGGCCTTCGTGCCCTAACAGCCAGTCCCCTGTTAAAGTGGAAGAGACCTGTGGCTGCCGCTGGACCTGCCCCT...............                                  178
```

Block 4:
```
Proband pri  TTTTAGCTTGGAGATCTTCCGNCCTTGTGACTGTGGCTGTACCACNACCTCCTGCCTTCACGACGNGGTAAGGACAGCTTGGCTATNAGCTATCAGTTAATAGTTTACTC.ATTTATTTA  479
Proband sec  CTTTAGCTTGGAGATCTSGKGNCWCRATGACAGTGGKGGGTTTAKNSCTATCTGGKTTGCCGCGGNAGTATTGKATGGTCGCCSATNAMTTSTC.KYTRSTAACMTGGKTTGSGTACTAA  479
RefSeq       ...............                                                                                                          178
```

Block 5:
```
Proband pri  TTGCTGTCAGTTTATCCTTCTATCCACCCATCCATTCATCCATCCACCTNCNCNTTCCTAACGAANCGAGCG.  551
Proband sec  ATGGTGTGAGTTTATCCATGTATCCARC.AKTCKSARTGGRRAGGAGKGANKNANRCCRGGARMAKNRASCRY  551
RefSeq       ...............                                                          178
```

X non conserved
X ≥50% conserved