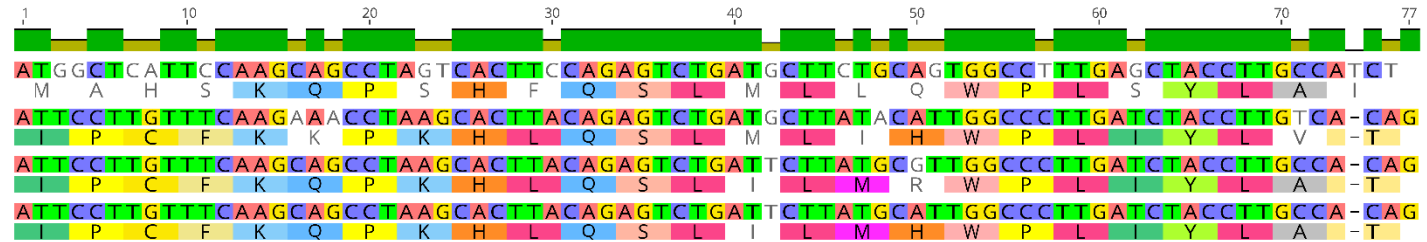


Exon 1

Identity

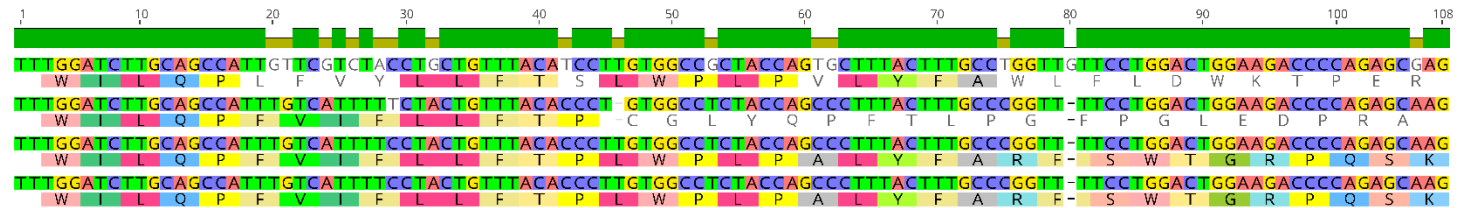
1. *H. sapiens* - Exon1
Frame 1
2. *M. javanica* - NW_023436150.1 - Exon1
Frame 1
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon1
Frame 1
4. *M. pentadactyla* - NW_023454910.1 - Exon1
Frame 1



Exon 2

Identity

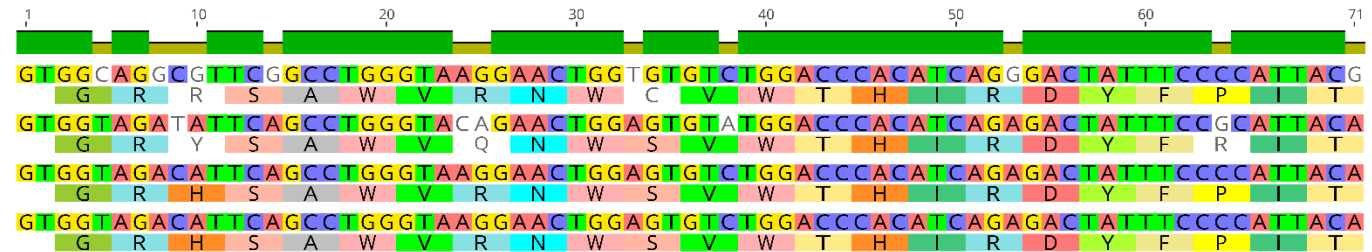
1. *H. sapiens* - Exon2
Frame 3
2. *M. javanica* - NW_023436150.1 - Exon2
Frame 3
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon2
Frame 3
4. *M. pentadactyla* - NW_023454910.1 - Exon2
Frame 3



Exon 3

Identity

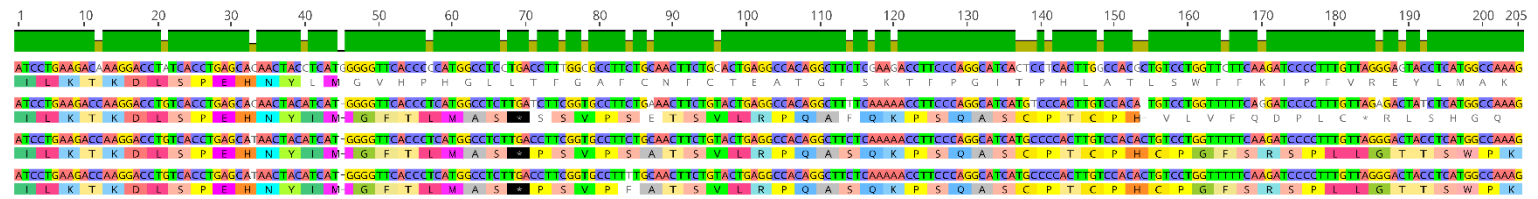
1. *H. sapiens* - Exon3
Frame 3
2. *M. javanica* - NW_023436150.1 - Exon3
Frame 3
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon3
Frame 3
4. *M. pentadactyla* - NW_023454910.1 - Exon3
Frame 3



Exon 4

Identity

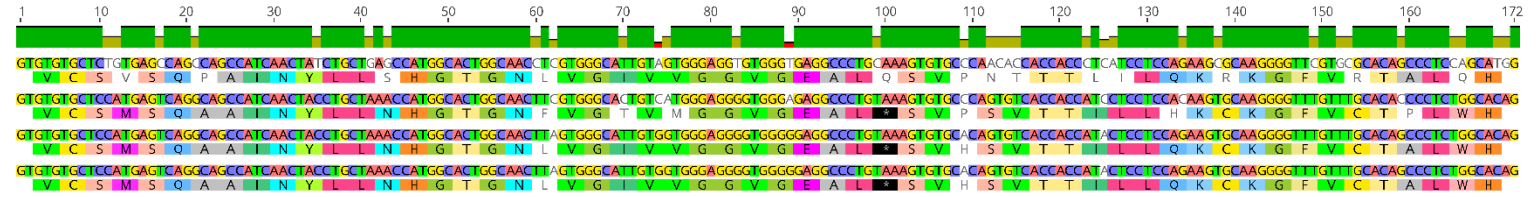
1. *H. sapiens* - Exon4
Frame 1
2. *M. javanica* - NW_023436150.1 - Exon4
Frame 1
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon4
Frame 1
4. *M. pentadactyla* - NW_023454910.1 - Exon4
Frame 1



Exon 5

Identity

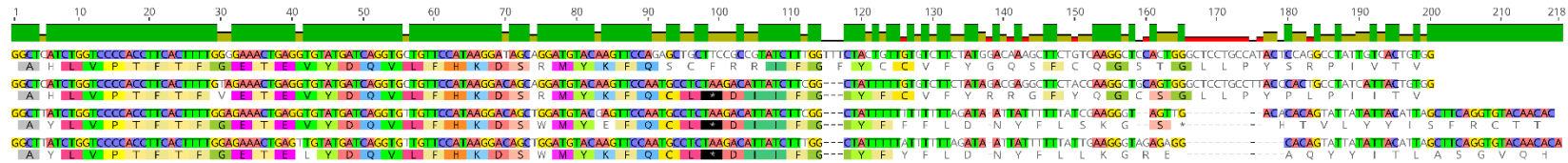
1. *H. sapiens* - Exon5
Frame 3
2. *M. javanica* - NW_023436150.1 - Exon5
Frame 3
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon5
Frame 3
4. *M. pentadactyla* - NW_023454910.1 - Exon5
Frame 3



Exon 6

Identity

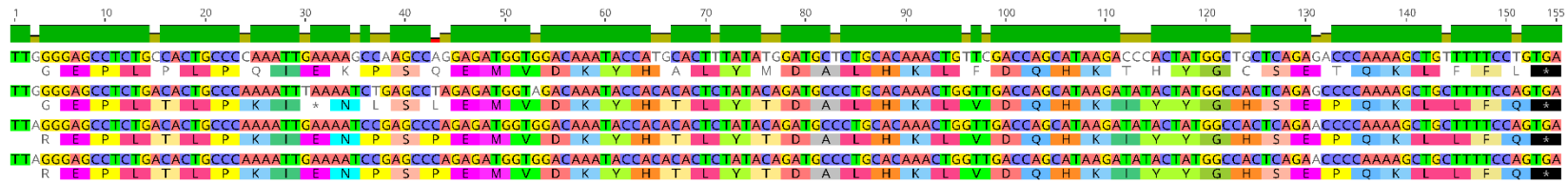
1. *H. sapiens* - Exon6
Frame 2
2. *M. javanica* - NW_023436150.1 - Exon6
Frame 2
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon6
Frame 2
4. *M. pentadactyla* - NW_023454910.1 - Exon6
Frame 2



Exon 7

Identity

1. *H. sapiens* - Exon7
Frame 3
2. *M. javanica* - NW_023436150.1 - Exon7
Frame 3
3. *M. pentadactyla* - JAMXTM010000791.1 - Exon7
Frame 3
4. *M. pentadactyla* - NW_023454910.1 - Exon7
Frame 3



Multiple sequence alignment of each exon from AWAT1 in both *Homo sapiens* (reference), *Manis javanica* (NW_023436150.1) and *Manis pentadactyla* (NW_023454910.1 and JAMXTM010000791.1). Matches in nucleotides and aminoacids are highlighted with a specific color. Gaps (-) present in any of the *Manis* species and not in Human represent deletions, and on the other hand gaps present in Human but not in *Manis* represent insertions. Premature stop codons are represented with (*).

On the top of each exonic analysis there is a graph (denoted in different shades of green) related with the degree of similarity in each nucleotide position in the exon.

