I wrote a code to score the gap between sequences based on BLOSUM62.matrix.

The gap scores are listed below:

The score of alignment between human sequence and mouse sequence is: 1083.0.

The score of alignment between human sequence and random sequence is: -255.0.

The score of alignment between mouse sequence and random sequence is: -258.0.

In BLOSUM theory, the more acceptable the transmission in nature, the more scores attained.

The score between human and mouse is much higher, and they share similar scores between random sequence, which have confirmed the relation between human and mouse genetically.

The code also counted the Hamming distances between three sequences as follow:

The Hamming distance of alignment between human sequence and mouse sequence is: 23.

The Hamming distance of alignment between human sequence and random sequence is: 210.

The Hamming distance of alignment between mouse sequence and random sequence is: 209.

And these are also the evidence for the conclusion.

If we apply the alignment to sequences with different lengths, the analysis of scoring should depend on the lengths. As the length increases, the same score is expected to indicate less differences.