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pt  AAGTCAGGTCCTCTCGAGATCCTAAGTCCTGCAATACC GCGTATTGCATGATCTA ACCCTGGGTACATTACAAAGTGAAGTC
hs  AAGTCAGGTCCTCTCGAGATCCTAAGTCCTG-AATACC GCGTATTGCATGATCTA GCCCTGGGTACATTACAAAGTCAAGTC

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Supplementary Figure S 5: A section of aligned sequence (which we made up for illustrative purposes). We have already taken human upstream sequence and calculated MTT conservation scores for every 16 bp window. We now take all windows with a particular score and find them in the alignment. Imagine for example that the three windows we have highlighted in blue represent all the windows with a 13 score. We examine the positions adjacent to these, here highlighted in red, and count the number of nucleotides which are the same or different. For our windows with a 13 score, four are the same and two are different. We repeat this for the other possible window scores, creating a table such as supplementary table 1.