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Genetic Analysis of Homeostasis Iron Regulator (HFE) Gene and Protein in Homo Sapiens and its Future Aspect in Treatment of Classic (Type-I) Hereditary Hemochromatosis

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Abstract:- The HFE gene is present in the genome of various organisms, including Homo sapiens and functions to regulate the amount of iron in the body. With speciation, HFE gene has evolved in the various organisms but organisms having the common ancestry still have the HFE protein structure similar to the ancestral homologues. This has been proved and the applications to this have been extrapolated in this paper. This paper has therefore hypothesized a likely source of the transgenic HFE gene for gene therapy and other therapies that are under development. Besides the hypothesis of transgenic HFE source, the paper also shows the relation of Homo sapiens with its Primate ancestors such as Gorilla gorilla and Pan troglodytes.

The approach to the extrapolation of results was using the Basic Local Alignment Sequence Tool (BLAST) of the Homo sapiens HFE gene (NM_000410.4 Homo sapiens homeostatic iron regulator (HFE), transcript variant 1, mRNA) and then Pairwise alignment of the Closest genes to the Homo sapiens HFE gene. To further strengthen the claim, the Homo sapiens HFE protein was aligned with that of the closest genes that were found using BLAST. The results found that the Pan troglodytes HFE gene was close to 99.35% in identity to the Homo sapiens HFE, whereas Pan troglodytes protein had a 100% match to that of Homo sapiens HFE protein.

Thus the chimpanzee HFE gene can act as a source for the transgenic genes for curing the Classic, Type-I hemochromatosis, wherein the HFE protein synthesized by the body is dysfunctional to regulate the Iron in the body as Iron sensing complex is rendered dysfunctional by the malformed HFE protein which leads to the high amount of iron in the body which causes various problems such as diabetes, liver cirrhosis and etc in the long run.

Keywords:- *Hemochromatosis, HFE Gene, HFE Protein, HFE Trans-Genesis.*

I. INTRODUCTION

Iron is one of the most essential elements in our body. It plays an important role in the production of hemoglobin and facilitation of oxygen transport. Another role of iron is the enhancement of the immune system, by supporting the functions of all cells including those of the immune system. Further, iron content in our body also affects our cognitive function as well as physical features such as hair, skin and nails [1]. Thus, it is crucial for one to properly manage the iron level of one's body.

The HFE gene, or the hemochromatosis gene, is responsible for the production of the Homeostatic Iron Regulator (HFE) protein [2].

- *Features of HFE gene: [ ]*

This gene is placed in the short arm of the 6th chromosome. The cytogenetic location of *HFE* is 6p22.2 (genomic coordinates (GRCh37): (6:26,087,421–26,096,437). The HFE gene contains 7 exons spanning 12 kb. The full-length transcript represents 6 exons[2].

- *The function of HFE protein:*

The HFE protein is located on the surface (cell membrane) of intestinal and liver cells. It interacts with the other protein in surrounding cells and monitors the amount of iron in the body along with the regulation and production of another protein called hepcidin [2].

For monitoring the iron level of a body, the HFE protein utilizes glycoproteins called transferrin (Tf) and transferrin receptor (TfR). The transferrin transports the iron in the bloodstreams to various tissues. The transferrin receptor, which is a membrane-bound protein, which binds the Tf to itself to receive the iron. When the HFE protein is bound to the TfR protein of a cell, the TfR protein cannot bind the Tf protein, which prevents the iron from entering the cells. If the HFE protein is not bound to HFE, then Tf can attach itself to the TfR protein and thus in this way, HFE protein monitors the iron level of a body [2].

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Another function of HFE protein is the regulation of the protein called hepcidin, which is produced in the liver. Hepcidin controls how much iron is absorbed into the body and is released from the body (iron metabolism). Deficiency in hepcidin causes excess iron and overproduction of it leads to decreased iron content. When the HFE protein is attached to the TfR, proteins including hepcidin aren't able to enter the cell, which stops the production of hepcidin. When the HFE isn't bound, the production of hepcidin resumes [2].

➢ *Hereditary Hemochromatosis*

Hereditary Hemochromatosis (HHC) is an autosomal recessive genetic disorder that is caused due to excess accumulation of iron in tissues which leads to organ damage, especially in the liver. It is also referred to as iron overload disorder.

Although HHC is already present at birth, the symptoms of this disease are usually experienced later in life, from around 40 years of age [3].

➢ *Clinical Symptoms and Physical Manifestations in Patients with Hereditary Hemochromatosis[3]:*

>Amenorrhea
>Cardiomyopathies
>Abdominal Pain
>Apathy
>Ascites
>Cirrhosis
>Congestive heart failure
>Diabetes Mellitus
>Hypogonadism
>Hepatocellular Carcinoma
>Loss of Libido
>Weakness
>Weight Loss
>Splenomegaly
>Lethargy
>Impotence
>Osteoporosis
>Testicular atrophy

II. MUTATIONS

➢ *C282Y*

The C282Y mutation is seen in adults with HHC and is the most common mutation. In C282Y mutation the Nucleotide 845 which usually is Guanine is replaced with Adenine which results in the transcribed protein to have Tyrosine instead of Cysteine at Amino acid number 282[4].

➢ *H63D*

The H63D mutation has Guanine in the place of Cytosine a Nucleotide number 184 which in turn causes the transcribed protein to contain Aspartic acid in place of Histidine at Amino acid number 63. In this mutation, an increase in the ferritin concentration and hemoglobin level of a body is observed [4].

III. HFE MECHANISM IN IRON REGULATION

➢ *Role of HFE protein:*

The HFE gene encodes a non-classical MHC (major histocompatibility complex) class I-like protein which can be found on the surfaces of the intestinal cells. By associating with β 2-microglobulin, HFE protein binds with TfR1 (Transferrin Receptor 1) preventing the expression of hepcidin. But, in the case that HFE protein does not bond with TfR1, the receptor gains affinity towards other proteins, primarily, transferrin. This results in hepcidin production, allowing ferrous ions to enter the hepatic cells [5].

However, mutations can occur in HFE genes. C282Y mutation prevents the HFE proteins from reaching the surface of the hepatic cells. This disrupts the disulfide bridges in the extracellular domains of the protein. Such a mutation prevents the linkage of the HFE protein and the TfR1 leading to an iron overload in many of the vital organs, common symptoms of HH type 1 [5].

➢ *Role of Hepcidin:*

Hepcidin synthesized and secreted by hepatocytes in the human liver matures in hepcidin-25 (due to 25-amino acid peptide). It binds with ferroportin (also referred to as IREGI) where they later endocytosis in lysosomes. It is worthy to note that the Hepcidin-25 expression is indirectly correlated with ferroportin. Hence, in situations where there is a temporary lack of iron in the blood, hepcidin protein is suppressed. Soon when the concentrations stabilize, hepcidin is expressed to prevent further iron export into the blood. [6]

In normal conditions, ferritin formed and isolated in hepatocytes can sustain a large number of iron ions with the help of the IRP-IRE regulatory system. In HH, however, the iron overload ferritin begins to denature in lysosomes due to excess iron ions, rather than endocytosis. This results in a redox-active NTBI (non-transferrin bound iron). [6]

This protein releases isolated Fe^{2+} ions which react with hydrogen peroxide. This process is known as hydroxyl radical generation since it produces free radicals of OH. These OH free radicals undergo lipid peroxidation when they bond with lipid peroxides to generate respective radicals. [7]

These toxic lipid radicals disrupt organelle function by weakening the lysosome membrane which further leads to enzyme leakage and eventually cell death. Lysosome fragility can also induce collagen synthesis and in turn fibrosis. Thus it induces tissue damage in the body. [8]

IV. TOOLS

➢ *The tools used for the analysis were:*

➢ *BLAST - Basic Local Alignment Sequence tool [9]:*

BLAST is a bioinformatics tool that is used to find the regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

➢ *Pairwise Sequence Alignment [10]:*

A pairwise sequence alignment (MSA) is a sequence alignment of two biological sequences, generally a protein, DNA, or RNA. In many cases, the input set of query sequences are assumed to have an evolutionary relationship by which they share a linkage and are descended from a common ancestor. From the resulting PSA, sequence homology can be inferred and phylogenetic analysis can be conducted to assess the sequences; shared evolutionary origins.

➢ *EMBOSS [11]:*

Dottup is a commonly used tool for drawing dot plots between two sequences. It looks for places where words of a specified length have an exact match in both sequences and draw a diagonal line over the position of these words. Shorter sequences are more sensitive to shorter regions of similarity but also display random points of similarity and run slower as compared to longer sequences which run faster, display minimum random points of similarity but are less sensitive.

V. ANALYSIS

In the analysis, the BLAST was executed on the Homo sapiens DNA code for HFE gene and based on the results of BLAST, the Pairwise alignment was run on sequences closest to the query entered. The Protein transcribed from the closest DNA sequence found using Pairwise alignment was then analyzed against the Human HFE protein and the results were extrapolated. The sequence of the Homo sapiens HFE gene (NM_000410.4) was acquired from NCBI, alongside sequences of HFE genes from several other species.

➢ *The sample used as a query from Homo sapiens:*

Ascension Number: Homo sapiens HFE gene (NM_000410.4)

Number of Amino Acids in transcribed protein: 348

➢ *Database Used for BLAST:*

nr (All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects)

➢ *BLAST results:*

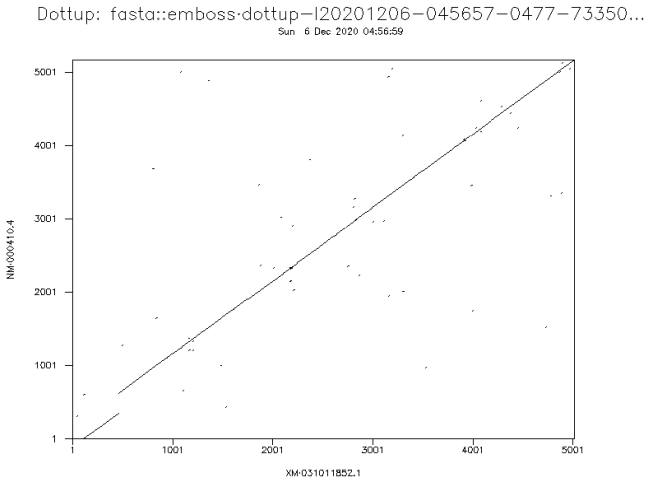
BLAST results showed that the genes ascension number XM_016954624.2 of Gorilla gorilla and XM_031011852.1 of Pan troglodytes were the closest variants to the Homo sapiens HFE gene (NM_000410.4).

➢ *Pairwise alignment of Genes:*

Pairwise alignment of NCBI Reference Sequence: NC_000006.12 and XM_016954624.2:

The results found out that 3189/3211bp of NC_000006.12 and XM_016954624.2 perfectly aligned meaning the alignment was roughly 99.3 percent and Waterman-Eggert score was 9829.

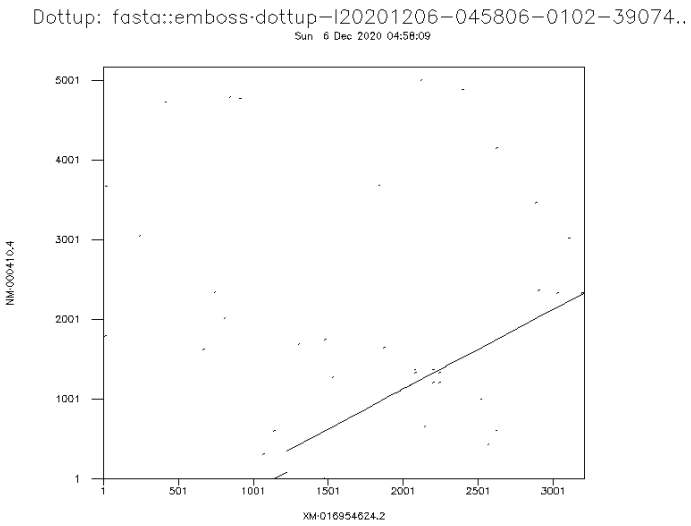
➢ *EMBOSS:*



➢ *Pairwise alignment of NCBI Reference Sequence: NC_000006.12 and XM_031011852.1:*

The results found out that 4664/5015 bp of NC_000006.12 and XM_031011852.1 perfectly aligned, meaning that the alignment was roughly 93.0 percent and Waterman-Eggert score was 23206.

➢ *EMBOSS :*



➢ *Pairwise alignment of proteins:*

Pairwise alignment of Homo sapiens HFE protein vs Gorilla gorilla HFE protein transcribed from XM_031011852.1 gene:

As seen from the result mentioned in (fig.1) all the 345/348 amino acids of Gorilla gorilla HFE protein align with the amino acids of Homo sapiens HFE protein. Therefore there is a 99.1% similarity in the two proteins compared.

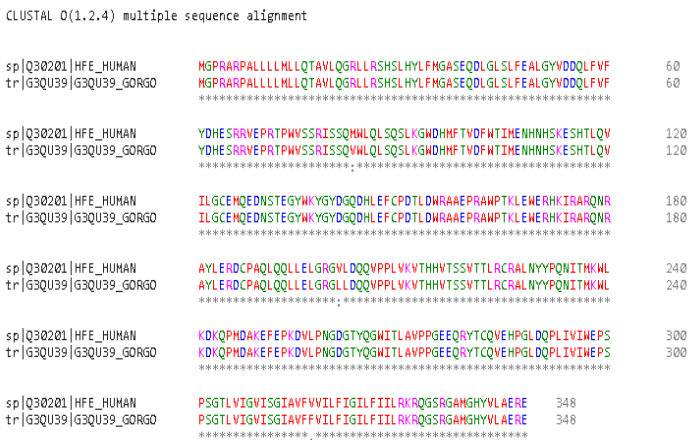


Fig : Pairwise alignment result of Homo sapiens HFE protein V/S Gorilla gorilla HFE protein

Pairwise alignment of Homo sapiens HFE protein vs Pan troglodytes HFE protein transcribed from XM_016954624.2 gene:

As seen from the result mentioned in (fig.1) all the 348/348 amino acids of Pan troglodytes HFE protein align with the amino acids of Homo sapiens HFE protein Therefore there is a 100% similarity in the two proteins compared

Fig : Pairwise alignment result of Homo sapiens HFE protein V/S Pan troglodytes HFE protein

VI. POSSIBLE METHODS OF CORRECTION FOR CLASSIC TYPE-I HHC

The analysis that was run, found out that there is immense scope for interspecies transgenesis of HFE gene to cure the Type-I hemochromatosis. The existing technologies such as embryonic gene therapy, vector-based infusion of the gene and stem cell therapy for it to be expressed in the Human DNA can be possible cures for the treatment of classic type-I HHC in humans. The recent studies pertaining to the use of adenoviruses, Lentivirus and Epstein Barr Virus as vectors for insertion of foreign therapeutic genes have shown great success in the correction of other genetic anomalies such as Hemophilia which can be cured by the expression of correct genetic sequences.

Moreover, the current studies being conducted on the use of adenoviral vector for the correction of Hemophilia[12] gives rise to the fundamental argument of it being used for curing classic type-I Hemochromatosis by insertion of therapeutic sequences of HFE gene as analyzed above in the cells of Homo sapiens, thus reversing the classic type-I hemochromatosis.

Why insertion of HFE gene using Lentiviral and Adenoviral vectors is an impractical approach?

The approach to curing HHC Type-I is impractical with the use of conventional Lentiviral and Adenoviral vectors due to their limitation of the length of DNA they can carry. The adenovirus and Lentivirus vectors are limited to less than 12KB whereas the complete CDS length of the HFE gene in the Homo sapiens is found to be more than 10KB, 12KB[13].

Due to the length of DNA being a constraint we have to use other vectors that are being used for transgenesis of hepatic cells.

➢ *Use of Epstein Barr Virus*

The Epstein Barr Virus holds a large transgenic capacity unlike other virus vectors such as retroviruses and lentiviruses (that are often used as a vector). The EBV virus

can hold up to 120kb as a vector compared to other vectors [14]. This allows EBV to sufficiently accommodate and deliver genomic transgenes for gene therapy.

This can be possible cure for the treatment of classic type-I HHC in humans. The recent studies pertaining to the use of adenoviruses, Lentivirus and Epstein Barr Virus as vectors for insertion of foreign therapeutic genes have shown great success in the correction of other genetic anomalies such as Hemophilia which can be cured by the expression of correct genetic sequences.

Therefore the similar methodologies using the EBV virus as a vector for transgenic HFE gene can be used for the correction of type-I classic HHC in Homo sapiens.

- *Proposal and the case for the use of CRISPR-cas based gene-editing technology and stem cell therapy to reverse C282Y mutation and cure Classic Type-I HHC:*

CRISPR-cas based gene-editing technology has shown immense and tremendous amounts of scope in reversing the single point mutation related genetic diseases such as hemophilia [15].

Therefore based on this model the in vivo experiment for transgenesis of the hepatic cells and the hematopoietic stem cells for reversing the C282Y mutation should be possible by using the CRISPR-cas technology.

VII. CONCLUSION

In our study, we conclude that Homo sapiens variant of the HFE gene, **NM_000410.4 Homo sapiens homeostatic iron regulator (HFE), transcript variant 1, mRNA)** can be substituted with either Gorilla gorilla gene, **XM_031011852.1** or Pan troglodytes gene, **XM_016954624.2.**

The basis of this hypothesis is that the exons of the human gene that was entered as a query against the gene of the Gorilla gorilla and Pan troglodytes had a high degree of similarities as given in the results above. This causes the proteins being transcribed out of the proposed substitute genes to have identical HFE proteins as Homo sapiens (Query protein), 348/348 amino acids similar with Pan troglodytes and 347/348 amino acids similar with Gorilla gorilla.

Thus with the proposed methods of correction combined with the use of transgenic material analyzed using BLAST software we will be able to devise a genetic therapy to cure Classic Type-I HHC.

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APPENDIX:

I. The sequence of Homo sapiens HFE gene (NM_000410.4) :

Homo sapiens homeostatic iron regulator (HFE), transcript variant 1, mRNA

AGAGCTGGGGAAATGGGCCCGCGAGCCAGGCCGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGG
CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGC
TTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTT
TCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACT
TCTGGACTATTATGGAAAATCACAACCACAGCAAGGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAG
AAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGG
ATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAAC
AGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAA
GTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCC
CCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACTAAAGACGTATTGCCC
AATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTG
GAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCA
GTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGAGGA
GCCATGGGGCACTACGTCTTAGCTGAACGTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAG
AGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATTGCCTGAC
GAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCTGCATGCCGGT
GATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCTCC
GTCACCTCAGAGACATACACCTATGTCATTTCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGGGACTTACATG
ATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACATGTATC
TATGCATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTCTCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTT
GGGGATTCTTCCATCTGATTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGT
CCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTTGAAAGG
GGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGA
TGCTACTCTAGTATTCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATG
ATAAGGATGATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTACATGCATTACTGCATGCACTTCTTAC
AATAATTCTATGAGATAGGTACTATTATCCCCATTTCTTTTTTAAATGAAGAAAGTGAAGTAGGCCGGGCACGGTGGCT
CACGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAA
CATGGTGAAACCCCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCAGCTACT
CGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCAGAGCTTGCAGTGAGCCGAGTTTGCGCCACTGCACTC
CAGCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAAATAAAAATAAAAATAAAAAAATGAAAAAAAAAAGAAAGTG
AAGTATAGAGTATCTCATAGTTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCGTTTGATACATCTCA
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CTCTGGAGTCAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGAAG
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ACCAGGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCAAAAGAGTCTTTTTTTTTTTTTTGAGACT

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CTATTGCCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCACTGTAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGT
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CTTTAATAAATGTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTCATCTTGTGTATATACTTAATCGCTT
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GAATTAATCGTGTTTCTTCACTCTAGGGACATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAACCATTCT
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CCTGAACTGGGAACACAACAGAAGGAAAACAAACCACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGAC
TGCTGAGAGGTACAGGCCAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGTCAGTATTTTATAAAACA
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TAACTTCTACACTCTAACATGTAGAATGTTACTACAATATTAAAGTATTTTGTATGACAATTTTATTTGAAAGCCTAGGA
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TAAGGTGTAGAAGAGATAGATATGGTGGATTTGGAGTTGATACTTATATATTTTCTATTTCTTGGATGGATGAATTTGTA
CATTAAAAGTTTTCCATGGCAGAAA

II. Pairwise Alignment result : Homo sapiens v/s Pan troglodytes

>>Pan Troglodytes HFE 3211 bp (3211 nt)
Waterman-Eggert score: 9829; 857.5 bits; E(1) < 0
99.3% identity (99.3% similar) in 1991 nt overlap (351-2341:1221-3211)

```
          360       370       380       390       400       410
Homo  GGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGA
      : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GCAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGA
          1230      1240      1250      1260      1270      1280

          420       430       440       450       460       470
Homo  GGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACT
          1290      1300      1310      1320      1330      1340

          480       490       500       510       520       530
Homo  GGATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GGATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAA
          1350      1360      1370      1380      1390      1400

          540       550       560       570       580       590
Homo  GATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCA
          1410      1420      1430      1440      1450      1460

          600       610       620       630       640       650
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Homo  GTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGAC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGAC
         1470     1480     1490     1500     1510     1520

          660      670      680      690      700      710
Homo  ACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCA
      ::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::
Pan   ACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCCTGAACTACTACCCCCA
         1530     1540     1550     1560     1570     1580

          720      730      740      750      760      770
Homo  GAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACC
         1590     1600     1610     1620     1630     1640

          780      790      800      810      820      830
Homo  TAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::: :
Pan   TAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTATC
         1650     1660     1670     1680     1690     1700

          840      850      860      870      880      890
Homo  CCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   CCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCT
         1710     1720     1730     1740     1750     1760

          900      910      920      930      940      950
Homo  CATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCAGTGGAAT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   CATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCAGTGGAAT
         1770     1780     1790     1800     1810     1820

          960      970      980      990     1000     1010
Homo  TGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   TGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCA
         1830     1840     1850     1860     1870     1880

         1020     1030     1040     1050     1060     1070
Homo  GGGTTCAAGAGGAGCCATGGGGCACTACGTCTTAGCTGAACGTGAGTGACACGCAGCCTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GGGTTCAAGAGGAGCCATGGGGCACTACGTCTTAGCTGAACGTGAGTGACACGCAGCCTG
         1890     1900     1910     1920     1930     1940

         1080     1090     1100     1110     1120     1130
Homo  CAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGC
      :::::::: :::::::::::::::::::::::::::: ::::::::::::::::::
Pan   CAGACTCATTGTGGGAAGGAGACAAAACTAGAGACTCAAAAAGGGAGTGCATTTATGAGC
         1950     1960     1970     1980     1990     2000

         1140     1150     1160     1170     1180     1190
Homo  TCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATTGCCTGACGAACTCCTTGA
      ::::::::::::::: :::::::::::::::::::::::::::: ::::::::::::
Pan   TCTTCATGTTTCAGGACAGAGTTGAACCTAAACATAGAAATTGCCTGAAGAACTCCTTGA
         2010     2020     2030     2040     2050     2060

         1200     1210     1220     1230     1240     1250
Homo  TTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCT
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     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  TTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCT
          2070     2080     2090     2100     2110     2120

          1260     1270     1280     1290     1300     1310
Homo GCATGCCGGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAG
     ::::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  GCATGCCAGTGATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAG
          2130     2140     2150     2160     2170     2180

          1320     1330     1340     1350     1360     1370
Homo CTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAGACATACACCTATGTCATT
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  CTGCATCTAGAGGCTTCCTTCATTTCCTCCGTCACCTCAGAGACATACACCTATGTCATT
          2190     2200     2210     2220     2230     2240

          1380     1390     1400     1410     1420     1430
Homo TCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGGGACTTACATGATTCATTTTA
     :::::::::::::::::::::::::::::::::::::::: ::::::::::::::
Pan  TCATTTCCTATTTTTGGAAGAGGACTCCTTAAATTTGGGGGACTCACATGATTCATTTTA
          2250     2260     2270     2280     2290     2300

          1440     1450     1460     1470     1480     1490
Homo ACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTA
     ::::::::::::::::::::::::::::: ::::::::::::::::::::::::::::
Pan  ACATCTGAGAAAAGCTTTGAACCCTGGGACATGGCTAGTCATAACCTTACCAGATTTTTA
          2310     2320     2330     2340     2350     2360

          1500     1510     1520     1530     1540     1550
Homo CACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTCTCTGTG
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  CACATGTATCTATGCATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTCTCTGTG
          2370     2380     2390     2400     2410     2420

          1560     1570     1580     1590     1600     1610
Homo TTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGA
     :::::::::::::::::::::::::::: ::::::::::::::::::::::::::::
Pan  TTACCCAGTAACTCATCTGTCACCAAGCCCTGGGGATTCTTCCATCTGATTGTGATGTGA
          2430     2440     2450     2460     2470     2480

          1620     1630     1640     1650     1660     1670
Homo GTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAA
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  GTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAA
          2490     2500     2510     2520     2530     2540

          1680     1690     1700     1710     1720     1730
Homo GCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATC
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  GCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATC
          2550     2560     2570     2580     2590     2600

          1740     1750     1760     1770     1780     1790
Homo TTGAAAGGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTG
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan  TTGAAAGGGGTTGTGAAGAGGTGTTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTG
          2610     2620     2630     2640     2650     2660

          1800     1810     1820     1830     1840     1850
Homo CAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCA
     ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
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Pan   CAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCA
          2670     2680     2690     2700     2710     2720

          1860     1870     1880     1890     1900     1910
Homo  CAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATGATAAGGATGATA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   CAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATGATAAGGATGATA
          2730     2740     2750     2760     2770     2780

          1920     1930     1940     1950     1960     1970
Homo  AAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTACATGCATTACTGCATGCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   AAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTACATGCATTACTGCATGCA
          2790     2800     2810     2820     2830     2840

          1980     1990     2000     2010     2020     2030
Homo  CTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCATTTCTTTTTTAAATGAAGA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   ATTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCATTTCTTTTTTAAATGAAGA
          2850     2860     2870     2880     2890     2900

          2040     2050     2060     2070     2080     2090
Homo  AAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   AAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAA
          2910     2920     2930     2940     2950     2960

          2100     2110     2120     2130     2140     2150
Homo  AGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAACCCCA
      :: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   AGTGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAACCCCA
          2970     2980     2990     3000     3010     3020

          2160     2170     2180     2190     2200     2210
Homo  TCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCAGCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   TCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCAGCT
          3030     3040     3050     3060     3070     3080

          2220     2230     2240     2250     2260     2270
Homo  ACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCAGAGCTTGCAGTGAGCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   ACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCAGAGCTTGCAGTGAGCC
          3090     3100     3110     3120     3130     3140

          2280     2290     2300     2310     2320     2330
Homo  GAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAAATA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Pan   GAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAAATA
          3150     3160     3170     3180     3190     3200

          2340
Homo  AAAATAAAAAT
      ::::: :::::
Pan   AAAATTAAAAT
          3210
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III. Pairwise Alignment result 2: Homo sapiens v/s Gorilla gorilla

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>>Gorilla gorilla HFE 5015 bp                    (5015 nt)
 Waterman-Eggert score: 23206;  1309.2 bits; E(1) <  0
93.0% identity (93.0% similar) in 5190 nt overlap (1-5176:111-5015)

          10       20       30       40       50       60
Homo   AGAGCTGGGGAAATGGGCCCGCGAGCCAGGCCGGCGCTTCTCCTCCTGATGCTTTTGCAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill AGAGCTGGGGAAATGGGCCCGCGAGCCAGGCCGGCGCTTCTCCTCCTGATGCTTTTGCAG
          120      130      140      150      160      170

          70       80       90      100      110      120
Homo   ACCGCGGTCCTGCAGGGGCGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ACCGCGGTCCTGCAGGGGCGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGT
          180      190      200      210      220      230

          130      140      150      160      170      180
Homo   GCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAG
          240      250      260      270      280      290

          190      200      210      220      230      240
Homo   CTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCC
       ::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Gorill CTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCTCGAACTCCATGGGTTTCC
          300      310      320      330      340      350

          250      260      270      280      290      300
Homo   AGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCAC
       :::::::::::::::::: ::::::::::::::::::::::::::::::::::::::::::
Gorill AGTAGAATTTCAAGCCAGGTGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCAC
          360      370      380      390      400      410

          310      320      330      340      350      360
Homo   ATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGGAGTCCCAC
       :::::::::::::::::::::::::::::::::::::::: ::::::::::
Gorill ATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAATCACAGCAAGG--------
          420      430      440      450      460

          370      380      390      400      410      420
Homo   ACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGG

Gorill ----------------------------------------------------------


          430      440      450      460      470      480
Homo   AAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGA

Gorill ----------------------------------------------------------


          490      500      510      520      530      540
Homo   GCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCC

Gorill ----------------------------------------------------------


          550      560      570      580      590      600
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Homo   AGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAG

Gorill ------------------------------------------------------------


          610       620       630       640       650       660
Homo   CTGGGGAGAGGTGTTTTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTG
                    ::::::::::::::::::::::::::::::::
Gorill -----------------------------TGCCTCCTTTGGTGAAGGTGACACATCATGTG
                              470       480       490

          670       680       690       700       710       720
Homo   ACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACC
         500       510       520       530       540       550

          730       740       750       760       770       780
Homo   ATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTA
         560       570       580       590       600       610

          790       800       810       820       830       840
Homo   TTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAA
         620       630       640       650       660       670

          850       860       870       880       890       900
Homo   GAGCAGAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GAGCAGAGATATACGTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATC
         680       690       700       710       720       730

          910       920       930       940       950       960
Homo   TGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTT
         740       750       760       770       780       790

          970       980       990      1000      1010      1020
Homo   GTCGTCATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGA
        :::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTCGTAATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGA
         800       810       820       830       840       850

         1030      1040      1050      1060      1070      1080
Homo   GGAGCCATGGGGCACTACGTCTTAGCTGAACGTGAGTGACACGCAGCCTGCAGACTCACT
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::: :
Gorill GGAGCCATGGGGCACTACGTCTTAGCTGAACGTGAGTGACACGCAGCCTGCAGACTCATT
         860       870       880       890       900       910

         1090      1100      1110      1120      1130      1140
Homo   GTGGGAAGGAGACAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTT
       :::::::::::::::::::::::::::::: :::::::::::::::::: ::::::::::
Gorill GTGGGAAGGAGACAAAACTAGAGACTCAAAAAGGGAGTGCATTTATGAGTTCTTCATGTT
         920       930       940       950       960       970

         1150      1160      1170      1180      1190      1200
Homo   TCAGGAGAGAGTTGAACCTAAACATAGAAATTGCCTGACGAACTCCTTGATTTTAGCCTT
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      :::::: :::::::::::::::::::::::::::::: ::::::: ::::::::::::
Gorill TCAGGACAGAGTTGAACCTAAACATAGAAATTGCCTGAAGAACTCCCTGATTTTAGCCTT
        980     990    1000    1010    1020    1030

          1210    1220    1230    1240    1250    1260
Homo  CTCTGTTCATTTCCTCAAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCTGCATGCCGGT
      :::::::::::: :::: :::::::::::::::::::::::::::::::::: ::
Gorill CTCTGTTCATTTTCTCAGAAAGATTTCCCCATTTAGGTTTCTGAGTTCCTGCATGCCAGT
       1040    1050    1060    1070    1080    1090

          1270    1280    1290    1300    1310    1320
Homo  GATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCATCTAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GATCCCTAGCTGTGACCTCTCCCCTGGAACTGTCTCTCATGAACCTCAAGCTGCATCTAG
       1100    1110    1120    1130    1140    1150

          1330    1340    1350    1360    1370    1380
Homo  AGGCTTCCTTCATTTCCTCCGTCACCTCAGAGACATACACCTATGTCATTTCATTTCCTA
      :::::::::::::::::: ::::::::::::::::::::::::::::::::::::
Gorill AGGCTTCCTTCATTTCCTCCATCACCTCAGAGACATACACCTATGTCATTTCATTTCCTA
       1160    1170    1180    1190    1200    1210

          1390    1400    1410    1420    1430    1440
Homo  TTTTTGGAAGAGGACTCCTTAAATTTGGGGGACTTACATGATTCATTTTAACATCTGAGA
      :::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTTTTGTAAGAGGACTCCTTAAATTTGGGGGACTTACATGATTCATTTTAACATCTGAGA
       1220    1230    1240    1250    1260    1270

          1450    1460    1470    1480    1490    1500
Homo  AAAGCTTTGAACCCTGGGACGTGGCTAGTCATAACCTTACCAGATTTTTACACATGTATC
      :::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
Gorill AAAGCTTTGAACCCTGGGACATGGCTAGTCATAACCTTACCAGATTTTTACACATGTATC
       1280    1290    1300    1310    1320    1330

          1510    1520    1530    1540    1550    1560
Homo  TATGCATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTCTCTGTGTTACCCAGTA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TATGCATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTCTCTGTGTTACCCAGTA
       1340    1350    1360    1370    1380    1390

          1570    1580    1590    1600    1610    1620
Homo  ACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGCACAGC
      :::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
Gorill ACTCATCTGTCACCAAGCCCTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGCACAGC
       1400    1410    1420    1430    1440    1450

          1630    1640    1650    1660    1670    1680
Homo  TATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAAGCATCATGGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TATGAAGGCTGTACACTGCACGAATGGAAGAGGCACCTGTCCCAGAAAAAGCATCATGGC
       1460    1470    1480    1490    1500    1510

          1690    1700    1710    1720    1730    1740
Homo  TATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTTGAAAGGGG
      :::::::::::::::::::::::::::::::::::::::::::::::::: ::::::::
Gorill TATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAATATCTGGAAAGGGG
       1520    1530    1540    1550    1560    1570

          1750    1760    1770    1780    1790
Homo  TTGTGAAGAGGTGT-TTTTTCTAATTGGCATGAAGGTGTCATACAGATTTGCAAAGTTTA
      :::::::::::::: :::::::::::::::::: ::::::::::::::::::::::
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Gorill TTGTGAAGAGGTGTCTTTTTCTAATTGGCATGAAGTTGTCATACAGATTTGCAAAGTTTA
      1580     1590     1600     1610     1620     1630

  1800     1810     1820     1830     1840     1850
Homo  ATGGTGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCACAATAATTT
      ::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATGATGCCTTCATTTGGGATGCTACTCTAGTATTCCAGACCTGAAGAATCACAATAATTT
      1640     1650     1660     1670     1680     1690

  1860     1870     1880     1890     1900
Homo  TCTACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATGATAAGGATGAT----------
      ::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TCTACCTGGTCTCTCCTTGTTCTGATAATGAAAATTATGATAAGGATGATGATAATGATG
      1700     1710     1720     1730     1740     1750

    1910     1920     1930     1940     1950     1960
Homo  --AAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTACATGCATTACTGCAT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATAAAAGCACTTACTTCGTGTCCGACTCTTCTGAGCACCTACTTACATGCATTACTGCAT
      1760     1770     1780     1790     1800     1810

    1970     1980     1990     2000     2010     2020
Homo  GCACTTCTTACAATAATTCTATGAGATAGGTACTATTATCCCCATTTCTTTTTTAAATGA
      ::: :::::::::::::::::::::::::::::: ::::::::::::::::::::::
Gorill GCAATTCTTACAATAATTCTATGAGATAGGTACTATCATCCCCATTTCTTTTTTAAATGA
      1820     1830     1840     1850     1860     1870

    2030     2040     2050     2060     2070     2080
Homo  AGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill AGAAAGTGAAGTAGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC
      1880     1890     1900     1910     1920     1930

    2090     2100     2110     2120     2130     2140
Homo  CAAAGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAACC
      :::::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CAAAGCGAGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAACC
      1940     1950     1960     1970     1980     1990

    2150     2160     2170     2180     2190     2200
Homo  CCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CCATCTCTAATAAAAATACAAAAAATTAGCTGGGCGTGGTGGCAGACGCCTGTAGTCCCA
      2000     2010     2020     2030     2040     2050

    2210     2220     2230     2240     2250     2260
Homo  GCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCAGAGCTTGCAGTGA
      :::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::
Gorill GCTACTCGGAAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCAGAACTTGCAGTGA
      2060     2070     2080     2090     2100     2110

    2270     2280     2290     2300     2310     2320
Homo  GCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GCCGAGTTTGCGCCACTGCACTCCAGCCTAGGTGACAGAGTGAGACTCCATCTCAAAAAA
      2120     2130     2140     2150     2160     2170

    2330     2340     2350     2360     2370     2380
Homo  ATAAAAATAAAAATAAAAAAATGAAAAAAAAAAGAAAGTGAAGTATAGAGTATCTCATAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATAAAAATAAAAATAAAAAAATGAAAAAAAAAAGAAAGTGAAGTATAGAGTATCTCATAG
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      2180     2190     2200     2210     2220     2230

    2390     2400     2410     2420     2430     2440
Homo  TTTGTCAGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCGTTTGATACATCTCAG
      ::::::::::::::   ::::::::::::::::::::::::::::::::::::::::::::
Gorill CTTGTCAGTGATAG----AGGTTTCAAACTCAGTCAATCTGACCGTTTGATACATCTCAG
      2240       2250     2260     2270     2280     2290

    2450     2460     2470     2480     2490     2500
Homo  ACACCACTACATTCAGTAGTTTAGATGCCTAGAATAAATAGAGAAGGAAGGAGATGGCTC
      :::::::::::::::::::::::::::::::: ::::::::::::::: :::::::::
Gorill ACACCACTACATTCAGTAGTTTAGATGCCTAGAGTAAATAGAGAAGGAAGTAGATGGCTC
          2300     2310     2320     2330     2340     2350

    2510     2520     2530     2540     2550     2560
Homo  TTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAGCTTGAATCACATGAAGGGGAACAGCAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTCTCTTGTCTCATTGTGTTTCTTCTGAGTGAGCTTGAATCACATGAAGGGGAACAGCAG
          2360     2370     2380     2390     2400     2410

    2570     2580     2590     2600     2610     2620
Homo  AAAACAACCAACTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTCCCTGAAGGAAGGTCC
      :::::::::: ::::::::::::::::::::::::::::::::::::::::::::::::
Gorill AAAACAACCAGCTGATCCTCAGCTGTCATGTTTCCTTTAAAAGTCCCTGAAGGAAGGTCC
          2420     2430     2440     2450     2460     2470

    2630     2640     2650     2660     2670     2680
Homo  TGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTCTTTGGCATTCATTTCTTTGGACCCTA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TGGAATGTGACTCCCTTGCTCCTCTGTTGCTCTCTTTGGCATTCATTTCTTTGGACCCTA
          2480     2490     2500     2510     2520     2530

    2690     2700     2710     2720     2730     2740
Homo  CGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGCTTCACACACGGTGTC
      :::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Gorill CGCAAGGACTGTAATTGGTGGGGACAGCTAGTGGCCCTGCTGGGCTTCACACACAGTGTC
          2540     2550     2560     2570     2580     2590

    2750     2760     2770     2780     2790     2800
Homo  CTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGA
      :::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::
Gorill CTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTCCCTCGATGAAGTGGA
          2600     2610     2620     2630     2640     2650

    2810     2820     2830     2840     2850     2860
Homo  GTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTGGCTTAGAGGATGCCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GTAAGCTCTCTCATTTTGAGATGGTATAATGGAAGCCACCAAGTGGCTTAGAGGATGCCC
          2660     2670     2680     2690     2700     2710

    2870     2880     2890     2900     2910     2920
Homo  AGGTCCTTCCATGGAGCCACTGGGGTTCCGGTGCACATTAAAAAAAAAATCTAACCAGGA
      :::::::::::::: ::::::::: ::::::::::::::::::::::::::::::::::
Gorill AGGTCCTTCCATGGGGCCACTGGGATTCCGGTGCACATTAAAAAAAAAATCTAACCAGGA
          2720     2730     2740     2750     2760     2770

    2930     2940     2950     2960     2970     2980
Homo  CATTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCAAAAGAGTCTTTTTTT
      :: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CACTCAGGAATTGCTAGATTCTGGGAAATCAGTTCACCATGTTCAAAAGAGTCTTTTTTT
          2780     2790     2800     2810     2820     2830
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    2990     3000     3010     3020     3030     3040
Homo  TTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCACTGTAA
      :   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill T----TTGAGACTCTATTGCCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCACTGTAA
           2840     2850     2860     2870     2880

    3050     3060     3070     3080     3090     3100
Homo  CCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCAAGTAGCTGGGATTAC
      :::::::::::::::::::::::::::::::::: :::::::::: ::::::::::::::::
Gorill CCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTAC
      2890     2900     2910     2920     2930     2940

    3110     3120     3130     3140     3150     3160
Homo  AGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCA
      ::::::::::::::::::::::::::::::::::::::::::: :: ::::::::::
Gorill AGGCGTGCACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGATACGGGGTTTCACCA
      2950     2960     2970     2980     2990     3000

    3170     3180     3190     3200     3210     3220
Homo  TGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCCA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TGTTGGCCAGGCTGGTCTCGAACTCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCCA
      3010     3020     3030     3040     3050     3060

    3230     3240     3250     3260     3270     3280
Homo  AAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAAAGAGTCTTAATATAT
      :::::::::::::::::::::::::::::: :: ::::::::::::::::::::::::::
Gorill AAGTGCTGAGATTACAGGTGTGAGCCACCCAGCTCAGCCGTCAAAAGAGTCTTAATATAT
      3070     3080     3090     3100     3110     3120

    3290     3300     3310     3320     3330     3340
Homo  ATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTGGCTGCATAAATGTGG
      ::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Gorill ATATCCAGATGGCATGTGTTTACTTTATGTTACTACATGCATTTGGCTGCATAAATGTGG
      3130     3140     3150     3160     3170     3180

    3350     3360     3370     3380     3390     3400
Homo  TACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATATACAGCTCAGAAGTTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TACAAGCATTCTGTCTTGAAGGGCAGGTGCTTCAGGATACCATATACAGCTCAGAAGTTT
      3190     3200     3210     3220     3230     3240

    3410     3420     3430     3440     3450     3460
Homo  CTTCTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTCTTCTTTTAAACCATTTTCTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CTTCTTTAGGCATTAAATTTTAGCAAAGATATCTCATCTCTTCTTTTAAACCATTTTCTT
      3250     3260     3270     3280     3290     3300

    3470     3480     3490     3500     3510     3520
Homo  TTTTTGTGGTTAGAAAAGTTATGTAGAAAAAAGTAAATGTGATTTACGCTCATTGTAGAA
      ::::: ::::::::::::::::::::::::::::::::::::::::::: :::::::::
Gorill TTTTTCTGGTTAGAAAAGTTATGTAGAAAAAAGTAAATGTGATTTACGCTTATTGTAGAA
      3310     3320     3330     3340     3350     3360

    3530     3540     3550     3560     3570     3580
Homo  AAGCTATAAAATGAATACAATTAAAGCTGTTATTTAATTAGCCAGTGAAAAACTATTAAC
      :::::::::::::::::::::::::::: :::::::::::: ::::::::::::::::
Gorill AAGCTATAAAATGAATACAATTAAAGCTGCTATTTAATTAGCCGGTGAAAAACTATTAAC
      3370     3380     3390     3400     3410     3420
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    3590     3600     3610     3620     3630     3640
Homo  AACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCATATACTTTAATAAAT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill AACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCATATACTTTAATAAAT
    3430     3440     3450     3460     3470     3480

    3650     3660     3670     3680     3690     3700
Homo  GTATATTGTATTGTATACTGCATGATTTTATTGAAGTTCTTGTTCATCTTGTGTATATAC
      ::: :::::::::::::::: :::::::::::: :::::::::::::::::::::::::
Gorill GTACATTGTATTGTATACTGCGTGATTTTATTGATGTTCTTGTTCATCTTGTGTATATAC
    3490     3500     3510     3520     3530     3540

    3710     3720     3730     3740     3750     3760
Homo  TTAATCGCTTTGTCATTTTGGAGACATTTATTTTGCTTCTAATTTCTTTACATTTTGTCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTAATCGCTTTGTCATTTTGGAGACATTTATTTTGCTTCTAATTTCTTTACATTTTGTCT
    3550     3560     3570     3580     3590     3600

    3770     3780     3790     3800     3810     3820
Homo  TACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCGTGTTTCTTCACTCTAGGGA
      ::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Gorill TACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCATGTTTCTTCACTCTAGGGA
    3610     3620     3630     3640     3650     3660

    3830     3840     3850     3860     3870     3880
Homo  CATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAGCAAACCATTCTGAAAGCATA
      ::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Gorill CATTGTCGTCTAAGTTGTAAGACATTGGTTATTTTACCAACAAACCATTCTGAAAGCATA
    3670     3680     3690     3700     3710     3720

    3890     3900     3910     3920     3930     3940
Homo  TGACAAATTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGACTGCTATAAGGCTTC
      ::::::::: ::::::::::::::: ::::::::::::::::::::::::::::::::
Gorill TGACAAATTCTTTCTCTCTTAATATCGTACTATACTGAAAGCAGACTGCTATAAGGCTTC
    3730     3740     3750     3760     3770     3780

    3950     3960     3970     3980     3990     4000
Homo  ACTTACTCTTCTACCTCATAAGGAATATGTTACAATTAATTTATTAGGTAAGCATTTGTT
      : ::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Gorill ATTTACTCTTCTACCTCATAAGGAATATGTTACAATTAATTCATTAGGTAAGCATTTGTT
    3790     3800     3810     3820     3830     3840

    4010     4020     4030     4040     4050     4060
Homo  TTATATTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACCCCAGTCTTCACAGTA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTATATTGGTTTTATTTCACCTGGGCTGAGATTTCAAGAAACACCCCAGTCTTCACAGTA
    3850     3860     3870     3880     3890     3900

    4070     4080     4090     4100     4110     4120
Homo  ACACATTTCACTAACACATTTACTAAACATCAGCAACTGTGGCCTGTTAATTTTTTT-AA
      ::::::::: :::::::::::::::::::::::::::::::::::::::::::::: ::
Gorill ACACATTTCGCTAACACATTTACTAAACATCAGCAACTGTGGCCTGTTAATTTTTTTTAA
    3910     3920     3930     3940     3950     3960

    4130     4140     4150     4160     4170     4180
Homo  TAGAAATTTTAAGTCCTCATTTTCTTTCGGTGTTTTTTAAGCTTAATTTTTCTGGCTTTA
      ::::::: ::::::::: ::::::::::::::::::::::::::::::::::::::::::
Gorill TAGAAATCTTAAGTCCCCATTTTCTTTCGGTGTTTTTTAAGCTTAATTTTTCTGGCTTTA
    3970     3980     3990     4000     4010     4020

    4190     4200     4210     4220     4230     4240
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Homo   TTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTGCATTTTAAATTCTT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TTCATAAATTCTTAAGGTCAACTACATTTGAAAAATCAAAGACCTGCATTTTAAATTCTT
       4030      4040      4050      4060      4070      4080

       4250      4260      4270      4280      4290      4300
Homo   ATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAAGGGTGACACCTGGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATTCACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAAGGGTGACACCTGGT
       4090      4100      4110      4120      4130      4140

       4310      4320      4330      4340      4350      4360
Homo   GGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGATGCAGCGCTGAGGGTTTTC
       :::::::::::::: :::::::::::::: :::: :::::: ::::::::::::::::::::
Gorill GGCCATAGGTAAACGTACCACGGTGGTGCGGTCACCAGACATGCAGCGCTGAGGGTTTTC
       4150      4160      4170      4180      4190      4200

       4370      4380      4390      4400      4410      4420
Homo   CTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAAATCACTTGTAGAGA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAAATCACTTGTAGAGA
       4210      4220      4230      4240      4250      4260

       4430      4440      4450      4460      4470      4480
Homo   AAAGCCCCTGAAAATTTGAGAAAACAAACAAGAAACTACTTACCAGCTATTTGAATTGCT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill AAAGCCCCTGAAAATTTGAGAAAACAAACAAGAAACTACTTACCAGCTATTTGAATTGCT
       4270      4280      4290      4300      4310      4320

       4490      4500      4510      4520      4530      4540
Homo   GGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAACAGAAGGAAAACAAACC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GGAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACACAACAGAAGGAAAACAAACC
       4330      4340      4350      4360      4370      4380

       4550      4560      4570      4580      4590      4600
Homo   ACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGCTGAGAGGTACAGGC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ACTCTGATAATCATTGAGTCAAGTACAGCAGGTGATTGAGGACTGCTGAGAGGTACAGGC
       4390      4400      4410      4420      4430      4440

       4610      4620      4630      4640      4650      4660
Homo   CAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGTCAGTATTTTATAAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CAAAATTCTTATGTTGTATTATAATAATGTCATCTTATAATACTGTCAGTATTTTATAAA
       4450      4460      4470      4480      4490      4500

       4670      4680      4690      4700      4710      4720
Homo   ACATTCTTCACAAACTCACACACATTTAAAAACAAAACACTGTCTCTAAAATCCCCAAAT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ACATTCTTCACAAACTCACACACATTTAAAAACAAAACACTGTCTCTAAAATCCCCAAAT
       4510      4520      4530      4540      4550      4560

       4730      4740      4750      4760      4770      4780
Homo   TTTTCATAAACTCAGTTTTAAACTAACTTTTTTTCAAACCACAATCTGATTTAACAATGA
       :::::::::::::::::::::::::::::::: :::::::::::::::::::::::::
Gorill TTTTCATAAACTCAGTTTTAAACTAACTTTTTT-CAAACCACAATCTGATTTAACAATGA
       4570      4580      4590      4600      4610      4620

       4790      4800      4810      4820      4830      4840
Homo   CTATCATTTAAATATTTCTGACTTTCAAATTAAAGATTTTCACATGCAGGCTGATATTTG
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          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CTATCATTTAAATATTTCTGACTTTCAAATTAAAGATTTTCACATGCAGGCTGATATTTG
          4630      4640      4650      4660      4670      4680

          4850      4860      4870      4880      4890      4900
Homo   TAATTGTGATTCTCTCTGTAGGCTTTGGGTATAATGTGTTCTTTTCCTTTTTTGCATCAG
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill TAATTGTGATTCTCTCTGTAGGCTTTGGGTATAATGTGTTCTTTTCCTTTTTTGCATCAG
          4690      4700      4710      4720      4730      4740

          4910      4920      4930      4940      4950      4960
Homo   CGATTAACTTCTACACTCTAACATGTAGAATGTTACTACAATATTAAAGTATTTTGTATG
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill CGATTAACTTCTACACTCTAACATGTAGAATGTTACTACAATATTAAAGTATTTTGTATG
          4750      4760      4770      4780      4790      4800

          4970      4980      4990      5000      5010      5020
Homo   ACAATTTTATTTGAAAGCCTAGGATGCGTTGACATCCTGCATGCATTTATTACTTGATAT
          :::::::::::::::::::::::::: :::::::::::::: ::::::::::::::::
Gorill ACAATTTTATTTGAAAGCCTAGGATGCCTTGACATCCTGCATACATTTATTACTTGATAT
          4810      4820      4830      4840      4850      4860

          5030      5040      5050      5060      5070      5080
Homo   GCATGCATTCTGGTATCTCAAGCATTCTATTTCTGAGTAATTGTTTAAGGTGTAGAAGAG
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill GCATGCATTCTGGTATCTCAAGCATTCTATTTCTGAGTAATTGTTTAAGGTGTAGAAGAG
          4870      4880      4890      4900      4910      4920

          5090      5100      5110      5120      5130      5140
Homo   ATAGATATGGTGGATTTGGAGTTGATACTTATATATTTTCTATTTCTTGGATGGATGAAT
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Gorill ATAGATATGGTGGATTTGGAGTTGATACTTATATATTTTCTATTTCTTGGATGGATGAAT
          4930      4940      4950      4960      4970      4980

          5150      5160      5170
Homo   TTGTACATTAAAAGTTTTCCATGGCAGAAA
          ::::::::::::::::::::::::::::
Gorill TTGTACATTAAAAGTTTTCCATGGCAGAAA
          4990      5000      5010
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