Supplemental Figure 3. Chimpanzee-specific numts aligned with human homologous nuclear site and chimpanzee mtDNA.

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P:1:168        AAAACATACAACACACACACACACACACACACATTGGATGATGCCAATGTTTCAG...CGATGTGCAGGAAGAGGCAGATGCACACATACACATACACATGCACAGCACAAAATTATAACATAACACC
H:1:168        AAAACATACAACACACACACACACACACACA-------------------- ---...-------------------------------------CACACGCACAGCACAAAATTATAACATAACACC
P:M:14438      GCCCATAAAGGCTGTTGCTATGGTTGTGAGCAAGAGGATAATGCCAATGTTTCAG...CGATGTGTAGGAAGAGGCAGATAAAAAATATTGAGGCGCCGTTAGCGTGGAGGTAGCGGATGATCCAACC

P:1:179        CATGGTACTGGTACCAAAACAGAGATATAGACCAATGGAACAGAAGGGGACTGATCTAAAACA...ACCGCGGTAGCTGGCACACAGAGCCCTCAGAAATAATGCCGCATATCTACAACCATCTGAT
H:1:179        CATGGTACTGCTACCAAAACAGAGATATAGACCAATGGAACAGAA-------------------...-------------------CAGAGCCCTCAGAAATAATGCCGCATATCTACAACCATCTGAT
P:M:309        TATCAGCTGGAGTTTTTTACAACTCAGGTGAATTTTAGCTTTATGGGGGGGTGATCTAAAACA...ACCGCGGTGGCTAGCACGAAATTGACCAACCCTGAGGTTAGTATGGCTTAGTTAAACTTTC

P:1:213        AGGATACCTCAAAGTAGGGATCCACAGGCTAAGGGGAGATTAATAGTT...TAATGTTAGCAGTTAGACGGTGGATTTAACTATTTTGTGAATTGCAATTGGTTAAGGAAGA
H:1:213        AGGATACCTCAGAGTAGGGATCCACAGGCTATAGG-------------...--------------------TGGATTTAACTATTTTATGAATTGCAATTGGTTAAGGAAGA
P:M:8419       AGGATTAGAATTGTGAAGATAATGAGTGCATAGGGTAGATTGATAGTT...TAATGTTAGCGGTTAGACGTACGGCTAAGGCTATTGGTTGAATGAGTAGGCTAATAGTTTC

P:1:8.3        GGACCACAGGTGCGCACCACCTGACCCGGGGCTACTGCTCGTAATGCGCC...GAGGATTGAGTAAACTCCTATCTCTATCTATTTAGTAGAGATAGGAGTTTTG
H:1:8.3        GGACCACAGGTGCGCACCACCTGACCCGGCTCATT---------------...---------------------TTTTGCATCTTTAGTAGAGATAGGAGTTTTG
P:M:3061       GCTAGAGTGACTTCGTATGAGATTGTTTGGGCTACTGCTCGTAGTGCACC...GAGGATTGAGTAAACGGCTAGGCTGGAGGTGGCTAGAATAAATAGGAGGCCT

P:1:97         CTTTCACTGTTGTAAAAATTGTCCCTGTCATGAAACCGACCTGGATTACTCCGGTCTGAAC...GTAAACCCTATTGTTGATATGGACTCTGGAATAGTCCTACTTATTTCCTAAGACTTTCCTTG
H:1:97         CTTTCACTGTTGTAAAAATTGTCCCTGTCATGA-----------------------------...--------------------------------CACCTACTTATTTCCTAAGACTTTCCTTG
P:M:2368       CTTTCGTACAGGGAGAAATTTAGAACAGATAGAAACCGACCTGGATTACTCCGGTCTGAAC...GTAAACCCTATTGTTGATATGGACTCTGGAATAGGATTGCGCTGTTATCCCTAGGGTAACTT

P:2a:101       CCACGTGTGCATGACAAGCCCACCCCCAATATCCAGCCTCCTCAGACTCATTGGACCAG...TTGTAATTACTGTGGCCCCTCAGAATCCAAGTTTAGGTCTTTGAATTTCAACTGCTTCTGC
H:2a:101       CCACGTGTGCATGACAAGCCCACCCCCAATATCCA-------------------------...------------------------------AGTTTAGGTCTTTGAATTTCAACTGCTTCTGC
P:M:14582      AAGAATCGTGTAAGGGTAGGGCTGTCTACTGAGTAGCCTCCTCAGACTCACTGGACCAG...TTGTAATTACTGTGGCTCCTCAGAAGGATATTTGGCCTCATGGGAGGACATAGCCCATAAA

P:2a:83        TTGTTTTTGTCAGGTTTGTCAAAGATCAGATGGTTGTAGCGCCTTCCCCAATAAATGATATTATCTC...CCTAATCGCAATAGCATTCCTAATGCTAACCGAAAGATGTGTGGTGTTATTTCTGAGG
H:2a:83        TTGTTCTTGTCAGGTTTGTCAAAGATCAGATGGTTGT-----------------------------...----------------------------------AGATGTGTGGTGTTATTTCTGAGG
P:M:2578       GTACGAAAGGACAAGAGAAATGAGGCCTACTTCACAAAGCGCCTTCCCCAATAAATGATATTATCTC...CCTAATCGCAATAGCATTCCTAATGCTAACCGAACGAAAAATTCTAGGCTACATACAA

P:2b:105       TCTCCCTCTGCCTCTCTCTCATAAGGATATACGCCTAGAAGGAATAATACTATCACTATTC...TACTAGTCTCAATCTCTAACACATACGGCCTAGGTGACTGCATCTAGGGCCCATTCTAATAAGC
H:2b:105       TCTCCCTCTGCCTCTCTCTCATAAGGATATACG-----------------------------...-----------------------------------TGACTGCATCTAGGGCCCATTCTAATAAGC
P:M:9982       ATATCGCTCACACCTAATATCTTCCCTACTATGCCTAGAAGGAATAATACTATCACTGTTC...TACTAGTTTCAATCTCTAACACATATGGCTTAGACTACGTACATAACCTAAACCTACTCCAATG

P:2b:111       GACCTCTCTGAGCTTCAGTTTCCTCATCTGTTGGGTCTCATGAGTTGGAGTGTAGGAGAAA...AGCCGATGAAGAGTTGGAATAGGTTGTTGTTACCTGGGGATAATTCTCAAAAGGCAGGTGGGAA
H:2b:111       GACCTCTCTGAGCTTCAGTTTCCTCATCTGT-----------------------------...------------------------------TACCTGGGGATAATTCTCAAAAGGCAGGTGGGAA
P:M:12157      CTGTATTAGTACTTAGGAGGATTATTTGTTGTGGATCTCATGAGTTGGAGTGTAGGAGAAA...AGCCGATGAAGAGTTGGAATAGGTTGTTAGCGGTGACTAGGATTAGTATAGTAATTAGGAAGAT

P:2b:16        AATTTCTTTTTCAGATTGTTCACTGTTTAGGCGTCCGGGAATTGCGTCTGTTT...GGCTTCAACTGGGAAATGCTATATAGAATTTTTATAGAAATGCTAACAATTTTTATGTTAGTTTTGTATC
H:2b:16        AATTTCTTTTTCAGATTGTTCACTGTTG------------------------...-----------------------------TCATATAGAAATGCTAACAATTTTTATGTTAGTTTTGTATC
P:M:7433       TCGTGTGGCGGTGAAAGTGGTTTGGTTTAGGCGTCCGGGAATTGCGTCTGTTT...GGCTTCAACTGGGAGGACCACTCGGTTATCAACGTCAAGGAGTCGTAGATCACCTGGTTCTAGAAATAAT
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P:2b:18        CACCACTTACTGGCAATGCAAAATTTTTGAGTTGGCTGTTACTACGAGGGCTATGTGG...ACATGAGGAAGGGATAGGTGTCCCTTCCATAAAACAGGAGAGATACTATTTTGGAGAGCTG
H:2b:18        CACCACTTACTGGCAATGCAAAATTTTTGAGTT-------------------------...-------------------GTCCCTTCCATAAAACAGGAGGGATACTATTTTGGAGAGCTG
P:M:10950      GCCGGTGAAGCTTCAGGGGGTTTGGATGAGAATGGCTGTTACTACGAGGGCTATGTGG...ACATGAGGAAGGGATAGGCTATATGTTTTGTTAGGGGGTTGAGGATGAGTGTGAGGCGTAT

P:2b:39        AAGATGGCTACAGAGTGTTGCCTCATCCTTGGGCATGGGGATTTTATTTTGAGCTTGTTGGTTAGGTAATTGAGGTCTAGGGCTGTCAGAAGCCCTTATTGACTTGGGCAACCTAGGCTTCCCAGCTT
H:2b:39        AAGGTGGCTACAGAGTGTTGCCTCATCCTTGGGC-------------------------------------------------------------TATTGACTTGGGCAACCTAGGCTTCCCAGCTT
P:M:13246      AATCCGAGTATATTAGAGAAGTGAAATGTATATAGTGGGGATTTTATTTTGAGCTTGCTGGTTAGGTAATTGAGGTCTAGGGCTGTTAGAAGTCCTAGGGAAGTAACGCCTAGGGCTGTAAGTTTTAA

P:3:147        GGGCTAAGAAGACGTGCTGTTGAATTGGTATACGGCAGTGATATTAATAATTTTCATGGTTTGAGAAGCCTTCGCTTCAAAACGTACTCCCTGTGGAACTGATTGAAAATGGTTTCTTTTTCCTTGAC
H:3:147        GGGCTAAGAAGACGTGCTGTTGAATTGGTATA---------------------------------------------------------CTCCCTGTGGAATTGATTGAAAATGGTTTCTTTTTCCTTGAC
P:M:6710       CCTATCATCCGTAGGCTCATTTATCTCCCTGACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTTGCTTCAAAACGAAAAGTCCTAATAGTAGAAGAGCCCTCCGCAAACCTGGAATGAC

P:3:169        TTGAACTTGTAGTTTGATGTAATAAATAAAGCATCCGTGTTATACTTCACAACAATTCTAATCCTATGGAAATTTATGTTGCCATGTTTAGGGAAGGACTGAATTAATTCTAAGAATAAAG
H:3:169        TTGAACTTGGAGTTTGATGTAATAAATAAA-------------------------------------TGGAAATTTATGTTGCCATGTTTTGGGAAGGACTGAATTAATTCTAAGAATAAAG
P:M:15223      AGCTACCCCTTCATCACCATCGGACAAATAGCATCCGTATTATACTTCACAACAATCCTAATCCTAATACCAATCGCCTCTCTAATCGAAAACAAAATACTTGAATGAACCTGCCCTTGTA

P:3:193        GGACAATTAAAGTAGGACTCCTGACCCTTTGTGAGCTTTCTACCACTCCAGCTTAGC...GCATCACCCCACTGAATCCCCTAGAAGTCCCACCAAAGGTGCTTTGCTTGTGTATACTTTATAT
H:3:193        GGACAATTAAAGTAGGACTCCTGACCCGTCTT-------------------------...-----------------------------CCACCAAAGGTGCTTTGCTTGTGTATACTTTATAT
P:M:8920       CTCAGAAGTTTTTTTCTTTGCAGGATTTTTTGAGCTTTCTACCACTCCAGCCTAGC...GTATTACCCCACTAAATCCCCTAGAAGTCCCACTCCTAAACACATCTGTATTACTCGCATCAGG

P:3:24         GAATAAGTGTCCCAAGTGGAAGATTCCTTGGGAAGGAATCTTCCTAAGGAAGTCGGAGTGGGAGGTGATT...GAAGTGCTGTTAGGGAAAGAACATTTTACTGTTCGTATCTTTAGGTTACACAGC
H:3:24         GAATAAGTGTCCCAAGTGGAAGA-----------------------------------------------...--------------GAAAGAACATTTTACTGTTCGTATCTTTAGGTTACACAGC
P:M:14736      GAATAAGCCAAGGATATCTTTGATTGTGTAGTAGGGGTGGAAGGTAATTTTGTCGGAGTGGGAGGTGATT...GAAGTGTTGTTAGGGCTGTGATGATGAAGGGTAAGATAAAGTGGAAGGTGAAGA

P:3:53         CCTGTCTCTCTCCCTTTAGACTCCTGAGCCACCTCCAGCCTAGCCGTTT...TAGCCCAAAAGTGGGGGATACACCCTGGAGGAGAGATCTGTGAGAATGTGTGAAAAGCTCCCGC
H:3:53         CCTGTCTCTCTCCCTTTAGACTCCTGT----------------------...---------AGTGGGGGATACACCCTGGAGGAGAGATCTGTGAGAATGTGTGAAAAGCTCCTGC
P:M:3042       CTTAACTTAGGCCTCCTATTTATTCTAGCCACCTCCAGCCTAGCCGTTT...TAGCCCAAACAATCTCATACGAAGTCACTCTAGCCATTATCCTACTGTCAACGCTACTAATAAG

P:3:92         TTACTAGATATAAACATATATTGAAAATAATCAGAAGGGTGCGTTCATAATTTGAGTTTGCTAGGCAGAATAGTAATGAGGATGTAAGTCCGTGGGCGATTATGAGAAAGAAACATGACGATGAGGTAG
H:3:92         TTACTAGATATAAACATATATTGAAAATAATTAG--------------------------------------------------------------------------AAACATGACAATGAGGTAG
P:M:11120      TTTGAAGTCCTTGGGAGAGAATTATGATGCGACTGTGGGTGCGTTCATAATTTGAGTTTGCTAGGCAGGATAATAATGAGGATGTAAGTCCGTGGGCGATTATGAGGATAATTGCGCCGGTGAAGCTTC

P:5:60         TTCTTTCACCTTTAACCAAAGAGGGTGGTTTAGATGGTTGGGTTGTGCTCCGAGGTCGCCCCAA...CCATAGGGTCTGGTTTCCAAGATTCTAACCTGACCTCGCATTCTGTCATTCTACC
H:5:60         TTCTTTCACCTTTAACCAAAGAGGGTGGTTTAGATGGTT--------------------------...---------------TCCAAGATTCTAACCCGACCTCGCATTCTGTCATTCTACC
P:M:2142       TTTGACTGGTGAGGTCTTAGCATGTATTGCTCGGAGGTTGGGTTGTGCTCCGAGGTCGCCCCAA...CCATAGGGTCTTCTCGTCTTGTTATGTTATGCCCGCCTCTTCACGGGTAGGTCAA

P:5:87         CCAATCCTCAAATCTCTCCTCTACTTCTCCTTTGATTATGCCTTTTTGGGTTGAGGTGGTAATGGAACTGCAGTGGTTATCTCATTGGTTATCTCATTCAATCAAATGG
H:5:87         CCAATCCTCAAATCTCTCCTCTACTTCTCC-------------------------------------ACTGCAGTGGTTATCTCATTGGTTATCTCATTCAATCAAATGG
P:M:13473      GAGAGGGAAGAAAAAAGAGAGGAAATAAAGTTTGATCATGCCTTTTTGGGTTGAGGTGGTAATGGAAGCGGAGATTTGGTACTGTGAAATTGTTTTAGGTAATAGTTTC
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P:6:10         TTGTGCTCTACTGAGAATGGTACTGCAGCAAGTACCATT...CCGTAAAGGGGTAT..ACCTCCTAGGTGATC...CCTACACAATTCTCCGATCTGATTGACTGAAATGAAAAAATAATAATAATCC
H:6:10         TTGTGCTCTACTGAGAAGGA-----------------------------------..----------------------------------GACTGACTGACTGAAATGAAAAAATAATAATAATCC
P:M:10796      TAGCCACCTAATTTTAAGAGTACTGCAGCAAGTACCATT...CCGTAAAGGGGTAT..TCCTCCTAGGCGATC...CCTACACAATCCTCCGATCCATCCCCAACAAACTAGGAGGCGTCCTCGCCCT

P:6:105        GAAGTCTAGATAATATCCAACCTCATTAAATTTATTTCCCTATATCGCACCTACGTTCAATATTACAGATGAGCATACCGTAATTAAATTTATTCCCTATAGAGATATTCTTCAGATGCTGAAAGAAATGTTT
H:6:105        GAAATCTAGATAATATCCAACCTCGTTAAATTTA-----------------------------------------------------------CTCCCTATAGAGATATTCTTCAGATGCTGAAAGAAATGTTT
P:M:16144      GTCGCAGTATCTGTCTTTGATTCCTGCCCCATTGTATTATTTATCGCACCTACGTTCAATATTACGACCTAGCATACCTACTAAAGTGTGTTGATTAATTAATGCTTGCAGGACATAACAACAGCAGCAAAA

P:6:109        AATCATCATCAAATCATCACCAAAGCAAATCAGCTCAACTAGGCCTTCACC...CATCTGCCTGCGACAAACTCTATAGGGTTTTTGTTGTTGTTGCTGTTGTTGTGTTTTTTTGTTTGTTTTTTGA
H:6:109        AATCATCATCAAATCATCACCAAAG--------------------------...------------------TCTATAGGGTTTTTTTTGTTGTTG-------TTTTTGTTTTTGTTTGTTTTTTGA
P:M:10938      TAGGCTTCCTCCTAGCAGCAGCAGGCAAATCAGCTCAACTAGGCCTTCACC...CATCTGCCTGCGACAAACAGACCTAAAATCGCTCATTGCATACCCTTCAGTCAGCCACATAGCCCTCGTAGTA

P:6:158        CCAGCACTTTGGGAGGCCAAGGGCTGTGAGTTTTAAGTAAAGTGGGATTGTCA...TTGGAGTAGAAACCTGTGAGAAAGGGCATTCAGGTCTGGAGTTCGACACCAGCCTGACTAACATGGAGAAAC
H:6:158        CCAGCACTTTGGGAGGCCAAGGCGGGCG-------------------------...----------------------GATCACCTCAGGTCTGGAGTTCAAGACCAGCCTGACTAACATGGAGAAAC
P:M:12889      TCCTAGGGAAGTAACGCCTAGGGCTGTAAGTTTTAAGTAAAGGGGAATTGTCA...TTGGAGTAGAAACCTGTGAGGAAGGGTATTCCTGCTAATGCTAGGCTCCCAATGGTGAGGGAGGTTGAAGTG

P:6:165        CCTTTGCACAGAGCCTTGCAGTCTGCAGTGGTTAGATTTTTCTATGTAGCTGTTGAGTTGTGGTAGTCACCCCTGATTTTTTTTTTTTTTTTTGGAGACTGAATCTCTCTCTTTTGCCCAGGCTGG
H:6:165        CCTTTGCACAGAGCCTTGCAGTCTGCAGTGATAT--------------------------------TCACCCCTGG-------TTTTTTTTTTTCGAGACTGAATCTCTCTCTTTTGCCCAGGCTGG
P:M:9543       GGATATAGGGTCGAAGCCACATTCGTAAGGGGTAGATTTTTCTATGTAGCTGTTGAGTTGTGGTAGTCAGAATGTGATAATTATCAGTAGTAGGGCTAGAAGGGTATTGGTTATTAAAATTAGGACG

P:6:171        GCCAAGCACAGAGACAGAAAGGATATAATTCCTACGCCTTCTCAGCCGATGAAGAGTTGGAATAGGTTGTTAGCGGTGACTAGGATTAGTAGGTATAGTAGCAGTGCACTTCCCTGTCGCCCTGCTACTC
H:6:171        GCCAAGCACAGAGACA-------------------------------------------------------------------------------------GTGCACTTCCCTGTCGCCCTGCTACTC
P:M:12137      CATCAGCTAATGAGTAGAAAGGATATAATTCCTACGCCTTCTCAGCCGATGAAGAGTTGGAATAGGTTGTTAGCGGTGACTAGGATTAGTATAGTAATTAGGAAGATAAGTAAGTATTTGAAGAATTGGT

P:6:2.1        GGACCACACAAAGTCTTTCATCGGTGATGGTTGATGTGGAGGGTTTTAGGGGTTCTTTAGTGAAGAGTTTTATGGCGTCAGCGAGGACTTCCCCTCCGGATTCCTCCAGACAACCTT
H:6:2.1        GGACCACACAAAGTCTTTCATCA-------------------------------------------------------------GGACTTCCCCTCCGGATTCCTCCAGACAACCTT
P:M:2870       GGGTTGGGGCGGTGATGTAGAGGGTAATGGTTGAAGTGGAGGGTTTTAAGGGTTCTTTAGTGAAGAGTTTTATGGCGTCAGCGAAGGGCTGTAATAGCCCGTAAGGACCTACAATGT

P:6:28         AATTCCAGTTACTTGGGAGGTTGAGGTTCTTAGGTAGCTCATCTGGTTTCGGGGATCTTAGCTTTGGTTCTCTTTGCAAAGTTATTTCTAGTTAATTCATTATGCAATTGCTTGAACCTGGG
H:6:28         AATTCCAGTTACTTGGGAGGCTGAGGCATG-------------------------------------------------------------------------------AGATTGCTTGAACCTGGG
P:M:1268       CATAGACGGGTGTGCTCTTTTAGCTGTTCTTAGGTAGCTCGTCTGGTTTCGGGGGTCTTAGCTTTGGTTCTCTTTGCAAAGTTATTTCTAGTTAATTCATTATGCAAAAGGTACAGGGGTTA

P:6:4.9        AACATTCAAGAAGAGTAATTAGACTTAAGGGACCAGTAAGGGGGGAAATAG...AATAGTGTAAGGAGTATTGGGGCAGTTATAACTGGAAGGTTTTTTTAGTCCATCACTTAAAACACAA
H:6:4.9        AACATTCAAGAAGAGTAATTAGACTTAAT----------------------...------------------------------AACTGGAAGGCTTTTTTAGTCCATCACTTAAAACACAA
P:M:782        TCGGTTGTTGATGAGATGTTTAGAAGTGGGGACCAGTAGAGGGGGGAATAG...AATAGTGTCAGGAGTATGGGGGTAATTATGGTGGGTCATACGGCGGTATTTAGTTGGGGCATTTCAC

P:6:55         GGCCACTTGGAGAAGAGCCCACAGAGACTGAGCCGGCGTCAAAGTATTCAGCTGACTCGCTACACTTCACGGAAGCTTTCAGTCCCCCTTTCCTCCATATTCAAATATCTATCATCC
H:6:55         GGCCACTTGGAGAAGAGCCCACAGAGACTGAG-------------------------------------------CTTTCAGTCCCCCTTTCCTCCATATTCAAATATCTATCATCC
P:M:6267       CACCTCCGCTACCATAATCATTGCTATTCCTACCGGCGTCAAAGTATTCAGCTGACTCGCTACACTTCACGGAAGCAATATGAAATGATCTGCCGCAGTACTCTGAGCCCTAGGGTT
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P:6:67         CACACACACACCACACACACAGAACATACAGTAGATAGCCCCACC...GATCAAACAACCCCCTAGGCATCCCCTACATGCACACACTACATACACATACAATTTTGGTTACTAAGCC
H:6:67         CACACACACCACACACACATT------------------------...-------------------------ACACATGCACACACTACATACACATACAATTTTGGTTACTAAGCC
P:M:14670      CTGGTCCAGTGAGTCTGAGGAGGCTACTCAGTAGACAGCCCTACC...GATCAAATAACCCCCTAGGAATCACCTCCCACTCCGACAAAATTACCTTCCACCCCTACTACACAATCAA

P:7:157        AAGTGTATTATGGTTGGAGGGGCTCAGGGTGTGTGAGAAGGTCTGCGGCTAGGAGTCAGTAAAGCAATTGGCTTAGTGGGCGAAATATTATGCTTTGTTGGTGACAGGAGATGGGAGATCCCGCAA
H:7:157        AAGTGTATTATGGTTGGAGGGGCTCATTGTGTG-------------------------------------------------------------------TGACAGGAGATGGGAGATCTCGCAA
P:M:15098      AGCTTACTGGTTGTCCTCCGATTCAGGTTAGGATGAGGAGGTCTGTGGCTAGGAGTCAGTAAAGCAGTTGGCTTAGTGGGCGAAATATTATGCTTTGTTGTTTGGATGTGTGGAGGACAGGGATTG

P:7:29
       TGATTGTATAGTATTAAGTTTGCCACAATCTTAATTGTGGCAATTAATCTTAATTGTATAGTATTAAGTTTGCATCCCTTCTGGACCCCACGGATGCCCCCCCTCAGATAGGGGTCCCTTAG...TCAAGGTGTAGCCCATG
AGGTGGCAAGATTAATTGTCTTGCCAGGAGAGGAGCATCTATGAATTATTCC
H:7:29  TGATTGTATAGTAGTAAGTTTGCCACAGTCCT-------------------------------------------------------------------------------------------...-----------------
--------------------TACCAGGAGAGGAGCATCTATGAATTATTCC
P:M:15769
       CCAACAGACCTATCTCCCCTTGACAGAACATAGTACATACAACCATACACCGTACATAGCACATTACAGTCAAACCCCTCCTCGCCCCCACGGATGCTCCCCCTCAGATAGGAATCCCTTGG...TCAAGGTGTAGCCTATG
AGGTGGCAAGAAATGGGCTACATTTTCTACCCCAGAAAATTACGATAACCCT

P:7:35         TTCAACTAAATAGAGGACCAGATCAATACTTAACAAACCCACAGGTCCTAAACTATTAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGAGCACAACCTCGGAGCAGTTACCACAAACTGCTCC
H:7:35         TTCAACTAAATAGAGGATCAGAT-----------------------------------------------------------------------------------------GTTACCACAAACTGCTCC
P:M:2175       GAGCTTTAATTCATTAATGCAAACAATACTTAACAAACCTACAGGTCCTAAACTATTAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGAGCACAACCCAACCTCCGAGCAATACATGCTAAGA

P:8:11         GACATATGTGTGTTTGTATGTACATATATTCACGCATGTGTGTGTGTATATATATATACCTCGTGGTA...GATCAAACATCACCCCCCTACTTAATACACATACATATACGTGTCTATATACATACATG
H:8:11         GACATATGTGTGCCTGTGTATGTATGTACATATATACACACACACATATATATATA------------...-------------------------CACACATACATATACGTATCTATATACATACATG
P:M:11062      GCCTGCGACAAACAGACCTAAAATCGCTCATTGCATACCCTTCAGTCAGCCACATAGCCCTCGTAGTA...GATCAAATACCACTCTCCTACTCACAGGATTCAACATACTAATCACAGCCCTGTACTCC

P:8:122        GGCTTGTCTCAAACTCTTGGACTCAAGTGATCCCCCTATGAGCAGGCGCAATAGTCATAG...TTAGCCGTACGTCTAACCGTACGCTAACCATCTACCTCAGCCTCCCAAAGTGCTGGGATTG
H:8:122        GGCTTGTCTCAAACTCTTGGACTCAAGTGATCC-----------------------------...----------------------------ACCTACCTCAGCCTCCCAAAGTGCTGGGATTG
P:M:8260       CCCAACTATCTATAAACCTAGCCATGGCTATCCCCCTATGAGCAGGCGCAGTAGTCATAG...TTAGCCGTACGTCTAACCGCTAACATTACTGCAGGCCACCTACTCATGCACCTAATTGGAA

P:8:134        GGAAGTACTACTACTCATCCTTCAAGGGGGTGAGGATTGTCTTTGGAGTTGTGTTTTATGTTCGATAGTTGAGGGTTGATTACTGTGCATGCTTGTAAGCAATTCAATCCCCACTTCTCTGAAGGGCC
H:8:134        GGAAGTACTACTACTCATCCTTCAAACCT-----------------------------------------------------------------------GCAATTCAATCCCCACTTCTCTGAAGGGCC
P:M:15611      GGGAGATAGGTCTGTTGGTATCGGGGTGGGGGAGGGGTGTCGTTGGAATTGTGTTTTATGTTCGACAGTTGGGAGTTGATTGTTGTGCGTGCTTGTAAGCATGGAGTGAAGGTTTTGATGTGGGAGTG

P:8:0.34       GGGTATATCATGGAAGAAAAACATCTAACCTTCCTCGTCCCCACGGATGCCCCCCGTCAGATAGG...GTATTTTCGTCTGGGGGGTGTGCTTGCTATTGCAGCAGTGTTTACAGTACTGAAAATAA
H:8:0.34       GGGTATATCATGGAAGAAAAACATCTAAGAGA--------------------------------...----------------------------ATAGCAGCAGTGTTTACAGTACTGAAAATAA
P:M:15772      CACCGTACATAGCACATTACAGTCAAACCCCTCCTCGCCCCCACGGATGCTCCCCCTCAGATAGG...GTATTTTCGTCTGGGGGGTGTGCACGCGATAGCATTGCGAAACGCTGGCCCCGGAGCA

P:8:39         GGAGCGCGTCCAGCCGCAGATGCATGGCAATGAATGAAGCGAATAGATTTTC...TTTTATTTTATTTTATTTTATTTTATTTTATCCCAGCTTCCCTAGGATGTGCCCCAATCGGGGAGTAGG
H:8:39         GGAGCGCGTCCAGCCGCAGATGCATTG-------------------------...--------------------------------CCAGCTTCCCTAGGATGTGCCCCAATCGGTGAGTAGG
P:M:7921       CGGCGGGTAAGCCTAGGATTGTGGGGGCAGCGAATGAAGCGAATAGATTTTC...TTTTATGGGTTTTGGTGAGGGGGGTAGATGGTAATTTGAATTTAATATTTTTAGTTGGGTGACGAGAAA
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P:8:48        CTAATTTAAAGTGACACTCACTTTTTGATAACGAACATGTTGGACAGTCTACCCTCCCTTGGCAG...TTCAAATTTCATCTTTTCATTTTGATAAACGAAACAGTGAACACTTGGATTAAGTAGTAATATA
H:8:48        CTAATTTAAAGTGACACTCAC-------------------------------------------...-------------------------------------------TTGGATTAAGTAGTAATATA
P:M:5688      CTTGCATCTGCCATAGTAGAAGCCGGCGCGGGAACAGGTTGAACAGTCTACCCTCCCTTAGCGG...TTCAAATTTCATCTTTAGGCGGTATGCACTTTTAACAGTCACCCCTCAATTAACATGCCCTCCC

P:10:135      GGTGTTTCAAATGAAAAAAACTTGGAATTTGAGGATGAGTGTGAGGCGTATTATGC...CGTAAAGGGGTATTTTTACCATGGTGATAGATGCCATAGAAAATCTATGTAA
H:10:135      GGTGTTTCAAATGAAAAAAACTTGGAATTTCT-----------------------...--------------------CATGGTGATAGATGCCATAGAAAATCTATGTAA
P:M:10786     GGGATAGGCTATATGTTTTGTTAGGGGGTTGAGGATGAGTGTGAGGCGTATTATGC...CGTAAAGGGGTATTTTTACCATGAAAGCCATCGTGTACGCTAGTCATATTAA

P:10:85       TTGCTTTTTAAACACATTTCCTGGTACCTGAGCAGCCACCAATTA...ATCCCAAACATACAACCGAACATACAATGGTATGCAGCCATTGACTTGCAAATGCCTTTTTTTCCATTCC
H:10:85       TTTCTTTTTAAACACATTTCCTGGTACCT----------------...----------------------------GGTATGCAGCCATTGACTTGCAAATGCCTTTTTTTCCATTCC
P:M:1600      AAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA...ATCCCAAACATACAACCGAACTCCTTACACCCAATTGGACCAATCTATTACCCCATAGAAGAACTAATGT

P:11:42       TTCTACATAAAGCATTCTCTATACAGCGAAAATCTATTTGCTTCATTCATTGCCCCCACAATCCTAGGCCTGCCCGCCGCAGTACTGATCATTCTATTCCCCCCTCTATTTGATGGGAAATGTGACC
H:11:42       TTCTACATAAAGTGTTCTCTATACAGCACT--------------------------------------------------------------------------CTCTATTTTATGGGAAATGTGACC
P:M:7950      CAATAAACCCTGAGAACCAAAATGAACGAAAATCTATTCGCTTCATTCGCTGCCCCCACAATCCTAGGCTTACCCGCCGCAGTACTAATCATTCTATTCCCCCCTCTACTGGTCCCCACTTCTAAAC

P:11:90       TTGTGTTTTTTAGCATACTTGAGCTTCTGAATTACCCCCACTGTTAACCCAACACAG...ATCACCTCTAGCATTACCAGTGCTTTTCCCAGAAGGATTGAAGACCAAAGGGATCACC
H:11:90       TTGTGTTTTTTAGCATACTTGAGCTTCTGAAT------------------------...-------------------GTGCTTTTCCCAGAAGGATTGAAGACCAAAGGGATCACC
P:M:1828      CTAATATCTACAATCAACCAACAAGCCATTATTACCCCCGCTGTTAACCCAACACAG...ATCACCTCTAGCATTACCAGTATTAGAGGCACCGCCTGCCCGGTGACATATGTTTAAC

P:12:104      TTTTTTTAGGTTGGGTGAGGGAACTTAGTGGGTTCGATTCTCATAGTCCTAGA...GTCGTAGCGAAATCGGGGATATGCTGTTCGAATTAGTTTAGTGAACAGAAGGAAAGTAATTGAG
H:12:104      TTTTTTTAGGTTGGGTGAGGGAGCTTAGAAAACTCAG----------------...--------------------------GAGGAGCTAGTTTAGTGAACAGAAGGAAAGTAATTGAG
P:M:3540      GGCACGGAGAATTTTGGATTCTCAGGGATGAGTTCGATTCTTATAGTCCTAGA...GTCGTAGCGAAATCGGGGATATGCTGTTCGAATTCATAGGAACAGGGAGGTTAGAAGTAGAGCT

P:12:127      CCATTGGGTCAGGGTTTCTGCACTATAGTCCAAAGAGGAACAGCTCTT...AGAAGAGCTAATGATAGTCCCATCTGGGTTGCCAGAAATATGTTACAGGGAAGG
H:12:127      CCATTGGGTCAGGGTTTCTGCACTATAGTCC--------------------...-----------------CATCTGGGTTGCCAGAAATATGTTACAAGGAAGG
P:M:1515      TAAATCCCCTTGTAAACTTAACTGTTAGTCCAAAGAGGAACAGCTCTT...AGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCC

P:12:33       TTGTCGCCCAGGCTGGAGTGTAGTGGATTTGCGCTGCATGTGCCATTA...TAATATCACTGCTCACTGCGATCTCGGCTCACTGCAACCTCTGCCTGCTGGGTTCAA
H:12:33       TTGTCGCCCAGGCTGGAGTGTAGTGG-----------------------...----------------CGCGATCTCGGCTCACCACAACCTCTGCCTGCTGGGTTCAA
P:M:6709      TAGGGGAAGTAGCATCTTGTAGACCTACTTGCGCTGCATGTGCCATTA...TAATATTACTGCTGTCAGGGAGATAAATGAGCCTACGGATGATAGGACATTTCATGT

P:13:113      AAGAGGTATGGGCTGTTGGGTTTTTCAGCTTAAGGCAAGAAATATTAATTTGCTAAGTTGGTTTTTCACTCAGGTGAAA...GGGTGTGATAGGTGGCAAGGGAAAATGAA
H:13:113      AAGAGGTATGGGCTGTTGGGTTTTTCAGCTTAAGGTAAGAAATATTAATTTGCTAAGTTGGA-----------------...-----------------ATGGAAAATGAA
P:M:3795      TGTGGAGCGGGGGCTTATTTTTTTGGTTAGGATTGGGATAAAAGCTAGTATATTTATTTCTAGGCCTACTCAGGTGAAA...GGGTGTGATAGGTGGCACGGAGAATTTTG

P:13:19       TTTGGGTTTTTTGCTTACAAATACACAAAAACATCAAATTACACAGTCGCATCATAATTCTCTCCCAAGGACTTCAAACTTTACTCCCACTAATAGCCTTTTGATGACTCCGACATATGCAAATTTTT
H:13:19       TTTGGGTTTTTTGCTTACAAATACACAAAAACATCTAA--------------------------------------------------------------------------TGACATATGCAAATTTTT
P:M:111989    ATTATTATCCTGCCTAGCAAACTCAAATTATGAACGCACCCACAGTCGCATCATAATTCTCTCCCAAGGACTTCAAACTCTACTCCCACTAATAGCCTTTTGATGACTCCTGGCAAGCCTCGCTAA
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P:13:61        GATCTTCAGGGTAGGTTGGCAAGCGGTTGGTTCAGGGTATGGGGTTAGCAGCGGTGTATGTGTAGAGACCCAGGAGAGCCAACGAAGTAATTCCAGCCTGGAAAA
H:13:61        GATCTTCAGGGTAGGTTGGCAAGCC--------------------------------------AGAGACCCAGGAGAGCCAATGAAGTAATTCCAGCCTGGAAAA
P:M:16492      TGTGTAGGGGTGTCTTTGGGGTTTGGTTGGTTCAGGGTATGGGGTTAGCAGCGGTATATGTGTTGAGTAGGGTGAGTAGGGGGTTACGTTGCTGGGGCTAGTAGA

P:14:20        GCTGGCCTAACAGGCTGCACACATACAAAGCCTTCATAAATTATTCAACTTCCCACACTATTGAAATTTACCACAACCACCACCCCATCATACTCTTTTACCCATAACACTAATCTCTTCCCTGG
H:14:20        GCTGGCCTAACAGGCTGCAC----ACAAAGCCTATAA-----------------------------------------------------------------AACA-TACTCTCTTCCCTGG
P:M:13706      GGATCCTCCCGAATCAGCCCTGGCCCCTCCCCTTCATAAATTATTCAACTTCCCACGCTATTAAAATTTACCACAACCACCATCCCATCATACCCTTTTACCCATAACACTAATCCTACCTCCAT

P:14:24        AAGAGGTTCTTAAGTGATGAAGGTACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTAGTAAGTTAAGCAGAGTGAGTATC
H:14:24        AAAAGGTTCTTAAGTGATGAAGGTA-------------------------------------------------------------------------AGTTAAGCAGAGTGAATATC
P:M:1328       AGAACCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACC

P:14:43        AACTCTACAAGATTGGCTTTAGTGTCAATCTAGTAAGGGCTTAGCTTAATTAAAGTG...TGAGGTGGAGTAGTGGAGTACACGCACAGCAGCAACTGCCTAGTGATATCTCTATCTT
H:14:43        AACTCTACAAGATTGGCTTTAGTGTCAATGCT--------------------------...---------------ATGCACACGCACAGCAGCAACTGCCTAGTGATATCTCTATCTT
P:M:4778       AAATGTTTGTGGGTTTAAGTCCCATTAATCTAGTAAGGGCTTAGCTTAATTAAAGTG...TGAGGTGGAGTAGATTAGGCGTAGGTAGAAATAGAGGTTAAGGAGAGTGATGATGGCT

P:15:41        CCAGGCTGAAGTGCAGTGGCACGATCTTGTGTAAGGGTAGGGCTGTCTACTGAGTAGCCTCCTCAGCCTTACTGCAACCTCCGCCTCCCAGGTTCAAGTGATTCTCCTGCC
H:15:41        CCAGGCTGAAGTGCAGTGGCACGATCTTGG--------------------------------------CTTACTGCAACCTCCACCTCCCAGGTTCAAGTGATTCTCCTGCC
P:M:14656      GGTAAGATAAAGTGGAAGGTGAAGAATCGTGTAAGGGTAGGGCTGTCTACTGAGTAGCCTCCTCAGACTCACTGGACCAGGTCTGTTCCGATGTATGGGATAGCGGACAGT

P:15:62        GGTATCTAGATCTTGGTTTATCCTTTCTAGTAATTACAAACCTACTGTCCGC...GAGGCTACTCAGTAGACACTAATTTAATCCAATGAAATTAAGCATGGTCAAGTCACCTACTT
H:15:62        GGTATCTAGATCTTGGTTTATCCTTTC----------------------...-------------------CACTAATTTAATCCAGTGAAATTAAGCATGGTCAAGTCACCTACTT
P:M:1459       GAGGCCAAATATCCTTCTGAGGAGCCACAGTAATTACAAACCTACTGTCCGC...GAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTCACCTTCCACTTTATCTTACCC

P:16:15        TTAATGAAGGCTGGGCACACTGGCTCACGAGGACATAGCCCATAAAG...CATCATTAGACATCACGCCTGTAATCCCAGTACTTTACGAGACCAAGGCAGGCAGATCACC
H:16:15        TTAATGAAGGCTGGGCACACTGGCTCAC-------------------...----------------GCCTGTAATCCCAGCACTTTACGAGACCAAGGCAGGCAGATCACC
P:M:6346       CTCCTCAGAAGGATATTTGGCCTCATGGGAGGACATAGCCCATAAAG...CATCATTAGACATCGTGCTACACGACACATACTACGTCGTAGCCCACTTCCACTACGTTCT

P:16:6.1       GGCATTAACCCACAACTTGCATGAGATTTTCATAGCCGAATACATAAACATTATTATAATAAACACCCTCTCTTGGGGACTTTCAAGCTGTGTTGTCTCATTTGG
H:16:6.1       GGCATTAACCCACAACTTTCATGAGATG-------------------------------------------TCTTGGGGACTTTCAAGCTGTGTTGTCTCATTTGG
P:M:3393       TATGCCGCAGGCCCCTTTGCCCTATTTTTCATAGCCGAATACATAAACATTATTATAATAAACACCCTCACTGCTACAATCTTCCTAGGAGCAACATACAATAC

P:16:85        GGACCCATCCATCCTTTACGATTGCCCTCCTATTGCCCTTACCTTGAGCCCTACAAACAGCCAACCTACCACTAATAGTCACATCATCCAAAGGGAAGCCTCAGCAAACTCGGTCAGG
H:16:85        GGACCCATCCATCCTTTACGATGGGGGG-------------------------------------------------------CTGCTACCAAAGGGAAGCCTCCGCAAACTCGGTCAGG
P:M:9681       TCCTATTATTTGACCTAGAAATTGCCCTCCTATTGCCCTTACCTTGAGCCCTACAAACGGCCAACCTACCACTAATAGTCACATCATCCCTCTTATTAATTACTATCCTAGCCCTAAG

P:17:41        CACATGCTACATAGAAAAAAATTTACAGCCACTTCTCCGGGGCCAGCGTTTCGCAATGCTATCGCGTGCACACCCCCCAGACGAAAATACCAAATGCATGGAAGTAATGTCTACGAACTGATGTG
H:17:41        CACATGCTACATAGAAAAAAATTTACAGCCACTT------------------------------------------------------------------AAAGTAATGTCTACGAACTGATGTG
P:M:16025      CAGGAATCAAAGACAGATACTGCGACATAGGGTGCTCCGGGGCCAGCGTTTCGCAATGCTATCGCGTGCACACCCCCCAGACGAAAATACCAAATGCATGGAAGGCTCCCGTGACTGGTTAATAG
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P:18:1.6       TTGTTTCTAAGAGGTCAGATACTTAGCTGTTCTAAGAACAGCTAAAAGAGCACAC...TAGTTCAACTTTAAATTTACCTCCATGTCTTTCCACAGTTGTGACCTTAAAACAC
H:18:1.6       TTGTTTCTAAGAGGTCAGATACT--------------------------------...--------------------TTCTATGTCTTTCCACAGTTGTGACCTTAAAACAC
P:M:1342       AAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACAC...TAGTTCAACTTTAAATTTACCTACAGAACCCTCTAAATCCCCTTGTAAACTTAAC

P:18:69        AATATAACTTCTTATCAGATATGAATAGCTTTGGGTGCTGATGGTGGAGTTAAAGACTTTTTCTCTGATTTGTCCTTGGAAAAAACTTTATTATTTTATTCAGAATGGCATATTTGG
H:18:69        AATATAACTTCTTATCAGATATGAAGTAT-------------------------------------------------------AATTTTATTATTTTATTCAGAATGGCATATTTGG
P:M:15361      CAGAGAATAGTTTAAATTAGAATCTTAGCTTTGGGTGCTGATGGTGAAGTTAATTACTTTTTCTCTGATTTGTCCTTGGAAGAAAGTTTTCGTTTCCGGTTTACAAGACCGGTGTAT

P:19:15        TTCTCTACTGACCCTCCCCAGGGTGGGTCAGTAAATGCTAGTATAATATTTATATAAATAAGAGGCATTTGGTAAATATGATTATCATAATTCAGCCAACCCAGTCATTGCTCAA
H:19:15        TTCTCTACTGACCCTCCCCAGGGTGA----------------------------------------------------------------------CAGCCAACCCAGTCATTGCTCAA
P:M:9864       CGATATACTAGTATTCCTAGAAGTGAGATGGTAAATGCTAGTATAATATTTATATAAATAAGGGGCATTTGGTAAATATGATTATCATAATTTAATGAGTCGAAATCATTCGTTT

P:19:57        GGCTTGGCCAGAGCAGATCTCTGCCAACGTTACTCGGACTACCC...CCTCTTATTAATTAACGTCGGTGGCAGCTGAGCCTGGTGAGGACACTGGGATGCTCTT
H:19:57        GGCTTGGCCAGAGCAGATCTCG----------------------...-------------------GGTGGCAGCTGAGCCTGGTGAGGACACTGGGATGCTCTT
P:M:6634       TTCCTTGGCCTATCTGGGATGCCCCGACGTTACTCGGACTACCC...CCTCTTATTAATTACTATCCTAGCCCTAAGCCTCGCCTACGAATGATTACAAAAAGGG

P:22:33        TTCTACAACTGCTGTACCAGACCAGTAGGTTTGTAATTACTGTGGCCCCTCAGAAG...GATGATTCAGCCATAGTTTACGTCTCGGGTTTGTCACCCATTTAAGGTTCAATGTTCCCTCTGTT
H:22:33        TTCTACAACTGCTGTACCAGACCAGGCCCGATCTCACT------------------...---------------------TATCTAGGTTTGTGACCCATTTAAGGTTCAATGTTCCCTCTGTT
P:M:14372      TTCCGATGTATGGGATAGCGGACAGTAGGTTTGTAATTACTGTGGCTCCTCAGAAG...GATGATCCAACCATAGTTTACGTCTCGGGTGATGTGGGCGATCGACGAGAAGGCGGTTGAGGCGT
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Yellow highlighted nucleotides represent BLAST-defined homology between chimpanzee mtDNA and the chimp numt region. Boxed nucleotides are the actual nucleotides inserted, as inferred from comparison to human sequence, the proxy for the pre-integration target site. Italicized nucleotides indicate insertions in chimp, or deletions in human. Sequences are labeled by species (H=Homo, P=Pan), followed by chromosome number (or “M” for the mitochondrial genome), followed by beginning position rounded to the nearest Mb for nuclear DNA or nearest bp for mitochondrial DNA.