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<-----Primer_int2_F----->
Chr12:11328763 ACAGATGTGA GAGGAATTAT CAAGAGGAAA AATACATTTA GTATAATCTC ATTTACATAA AGTTTGAAAA ACATTTTTAA TAATTGTAAT TTATTACATT
Variant NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Chr12:11328663 GGTGATAAAA CTCTACAGTG AAACATGAGT GATCATGATA ACAATTGGAA TAGTCAAGAG GGAGGAAAAAT ATCAACAAGA AGACATATAT TGGGATTATC
Variant NNNNNNNNNN NNNNNNNNNN NNNNNNGAGT GATCATGATA ACAATTGGAA TAGTCAAGAG GGAGGAAAAAT ATCAACAAGA AGACATATAT TGGGATTATC

Chr12:11328563 TGGATGGCTG GCAAATCTTT TTTTCTTACC AATGTGTGGT AACCTCCATG TTAATGTTAT AATTTTCTCT CTTTCTGTTT CTTTGTGCT ATTACTCTCT
Variant TGGATGGCTG GCAAATCTTT TTTTCTTACC AATGTGTGGT AACCTCCATG TTAATGTTAT AATTTTCTCT CTTTCTGTTT CTTTGTGCT ATTACTCTCT

Chr12:11328463 ATATGTATGT TATGCTCCAC AATAAAAAAT GTTTAAAAAG CAGAAACATA AAGTATATTT CTAAGTATAA AATTAGGGTG ATACAGCATA TTCTCATAGA
Variant ATATGTATGT TATGCTCCAC AATAAAAAAT GTTTAAAAAG CAGAAACATA AAGTATATTT CTAAGTATAA AATTAGGGTG ATACAGCATA TTCTCATAGA

Chr12:11328363 TACCATTGTA ATTAGAGTTT TTGCTGAATA AAGGAGAATA GAGCATTATG GTRACTAAGAA ATCCAAATTA AAATTTAAAA CTTTCTTTT TTTATTTTGA
Variant TACCATTGTA ATTAGAGTTT TTGCTGAATA AAGGAGAATA GAGCATTATG GTRACTAAGAA ATCCAAATTA AAATTTAAAA CTTTCTTTT TTTATTTTGA

Chr12:11328263 GACAGAGTCT CACTCTGTTG CCCAGGCTGG AGTGCAGAAG CACAATCTTG GCTCAGTGCA GCCTCCGTCA CCTGGGCTCA AGTGATTCTC CCATCTCAGC
Variant GACAGAGTCT CACTCTGTTG CCCAGGCTGG AGTGCAGAAG CACAATCTTG GCTCAGTGCA GCCTCCGTCA CCTGGGCTCA AGTGATTCTC CCATCTCAGC

Chr12:11328163 CTCCTGAATA TCTAGGACAA CAGGCGTGCA CCACCACGCC CTGCTAATTT TTTCATTTT TTTTNTTAAG AGTCAGGGTT TTGCCATGTT GCCCAGGCTG
Variant CTCCTGAATA TCTAGGACAA CAGGCGTGCA CCACCACGCC CTGCTAATTT TTTCATTTT TTTTNTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

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Figure S1. A schematic representation of the junction sequence of the large-deletion variant. The junction sequence is aligned with the corresponding sequence in CGSC 2.1.3/panTro3. The large deletion resulted in the whole-gene deletions of *cTAS2R43*, *cTAS2R46*, *cTAS2R63P*, and *cTAS2R64*. Vertical bars (|) within the alignment indicate identical nucleotides. Asterisks (*) within the alignment indicate different nucleotides. This variant sequence was isolated from an eastern chimpanzee (subject 156) using intC_F and int31-63_R as PCR and sequence primers with cutoff base calls of *Q20*. The sequence had no variable positions. We performed BLAT search against CGSC 2.1.3/panTro3 using the sequencing results as queries. The BLAT hits showed that the reverse sequence (623 bp) is consistent with positions of 11,256,872 to 11,324,827 on chromosome 12 (chr12) with identity 99.9 % and spanning 67,956 bp with a large deletion from 11,257,350 to 11,324,679 (67,330 bp). The other BLAT hits did not show close alignments (<92 % identity). The sequence around the large deletion contains retrotransposon sequences (*AluJr*, *LIMEg*, and *LIME3B*).

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          <-----AluJr----->
Chr12:11325112 AGAGTTGGAT TCTCACTCTG TTGTCCAGGC TGGAGTTCAG TGGTAGGATC ATGGCTTACT GCAGTCTGGA ACTCCTGGGC TCAAACCATC CTCCCACCTC

          -----AluJr-----
Chr12:11325012 AGCCTTGTGA GTAGCTTCAC TATGCCTGAC TAACTTTTTC ATTCATTGTA GAGGCAGTTT CGCTGTGTTG CACAGGCTGG TCTTGAAGTC CTGGGTGCTC

          -----AluJr----->
          <-----L1MEg----->
Chr12:11324912 CTGCCCCAGC CTTACAAAAT GTTGGGGTTA TGGGTGTGAG CTACCCTGCC TGGCCAATAA AGGGTCTTAT TGAAAATATT AAGTTGAATA TGCAAGAAGG
          Variant NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNGAATA TGCAAGAAGG
          -----L1MEg-----
Chr12:11324812 AATACAAATT AATGAAAGTG GTAAATATGT GCATAATTCT AAATGAATGT TTAGAAAATA ATAATGTCTT GTTGGGGTAA TTATACAATT GATAAGACAT
          Variant AATACAAATT AATGAAAGTG GTAAATATGT GCATAATTCT AAATGAATGT TTAGAA--A ATAATGTCTT GTTGGGGTAA TTATACAATT GATAAGACAT

          -----L1MEg----->
Chr12:11324712 ATGCAAATGG AAAAAAATAG AATGGAGGTA AAGGTGACAG GAGTAAGTTT AGTTAAATA TTTTCTAAAC TTTTCTATGT CTATGAGGAG ATTTTGAACA
          Variant ATGCAAATGG AAAAAAATAG AATGGAGGTA AAG-----<-----Large deletion----->

          <-----L1ME3B----->
Chr12:11324612 ATGATAATAT AATTCTACTC ATAGGTATAT ATGCAAAGGA ATTGTATCAA ATGATATATG AAAGAATGTT CTAGTAGAAT TATTCATAAC TGTTCAAAAA
          Variant -----<-----Large deletion----->

          -----L1ME3B----->
Chr12:11324512 AGAAACTGGC CAAATACATA TTAAGGTGG ATGAATCATT ACAGTAATTC CATGCAATGG AACAATATAG AGAAGTGAAA AAAAATCACA TGTGCTTGCA
          Variant -----<-----Large deletion----->
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Figure S1. Continued.

