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).
Figure S1. Continued.
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