A

```
1 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
2 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
3 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
4 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
5 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
6 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
7 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
8 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
9 : GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
10: GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
11: GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
12: GTCCGGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAAATAAAATAAAATAAAAGTAACTACACAGACCACTAGAGTTCTCATAGTAACATGAATGCCATCTG
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B

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1 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
2 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA--------TAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
3 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA----TAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
4 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA----TAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
5 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
6 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
7 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
8 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA--------TAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
9 : GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
10: GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
11: GTCCGACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA----TAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
12: GTCCAACCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAA----TAAATAAATAAATAAATAAATAAATAAATAAATAAAGTAGTGCCCCAAACTCACCCTGGACTCATTACCCTAGCAATCG
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C

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1 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAATAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
2 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
3 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
4 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
5 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
6 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTC-AAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
7 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
8 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
9 : CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTC-AAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
10: CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
11: CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAATAAATAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
12: CTCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAATAAATAAATAAAATAAAAGGTGAGTAATCTTGAATTACATACTCTAGTAATATTTATTTAATTTACTCAGAA
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D

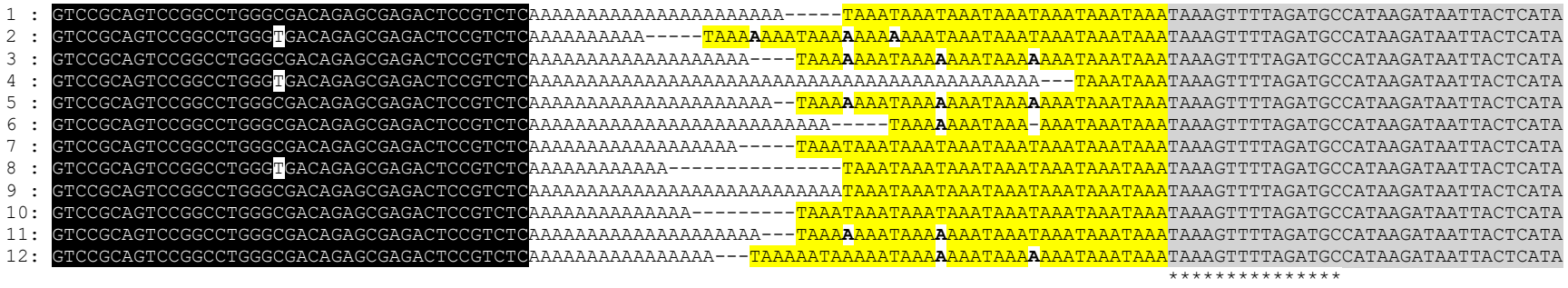

Figure S10. Examples of Alu copies with A-tails containing TA_{3-5} repeats from orthologous loci of different human genomes. The 3'-terminal Alu sequences (highlighted in black) are given together with A-rich tails and flanking sequences (highlighted gray). TA_{3-5} repeats are marked yellow. Asterisks indicate TSDs. **A** exemplifies conserved TA_3 repeats. **B** exemplifies A-tails polymorphic by both the length and number of TA_3 repeats (apparently, resulted from the canonical template slippage in DNA replication). **C** exemplifies A-tails of the same length but with a different number of repeat units. **D** exemplifies a combination of the above **B** and **C** A-tails. The A nucleotides at positions were T could be expected are boldfaced (these can result from errors in the canonical template slippage mechanism). Alu coordinates in the reference genome (GRCh38): **A**, chr21:33819681-33820031; **B**, chr12:113777516-113777146; **C**, chr13:107062743-107062353; and **D**, chr15:85399195-8539958. Other human genomes: 1, HG01243 Puerto Rican; 2, NA24385 Ashkenazim (Caucasian); 3, HG00514 Han Chinese Southern; 4, NA19240 Yoruban (African); 5, HG00733 Puerto Rican; 6, SAMD00243993 Japanese; 7, KOREF_S1 Korean; 8, NA12878 Utah Mormon (Caucasian); 9, AK1 Korean; 10, KOREF Korean; 11, hg38; 12, 2T2.