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301 AGGCAGCAGT GGGGAATATT GGACAATGGG CGAAAGCCTG
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421 CCTTGCTGTT TTGACGTTAC CAACAGAATA AGCACCGGCT
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661 GGAAGGAACA CCAGTGGCGA AGGCGACCAC CTGGACTGAT
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721 GCGTGGGGAG CAAACAGGAT TAGATACCCT GGTAGTCCAC
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1321 CGGTGAATAC GTTCCCCGGGC CTTGTACACA CCGCCC