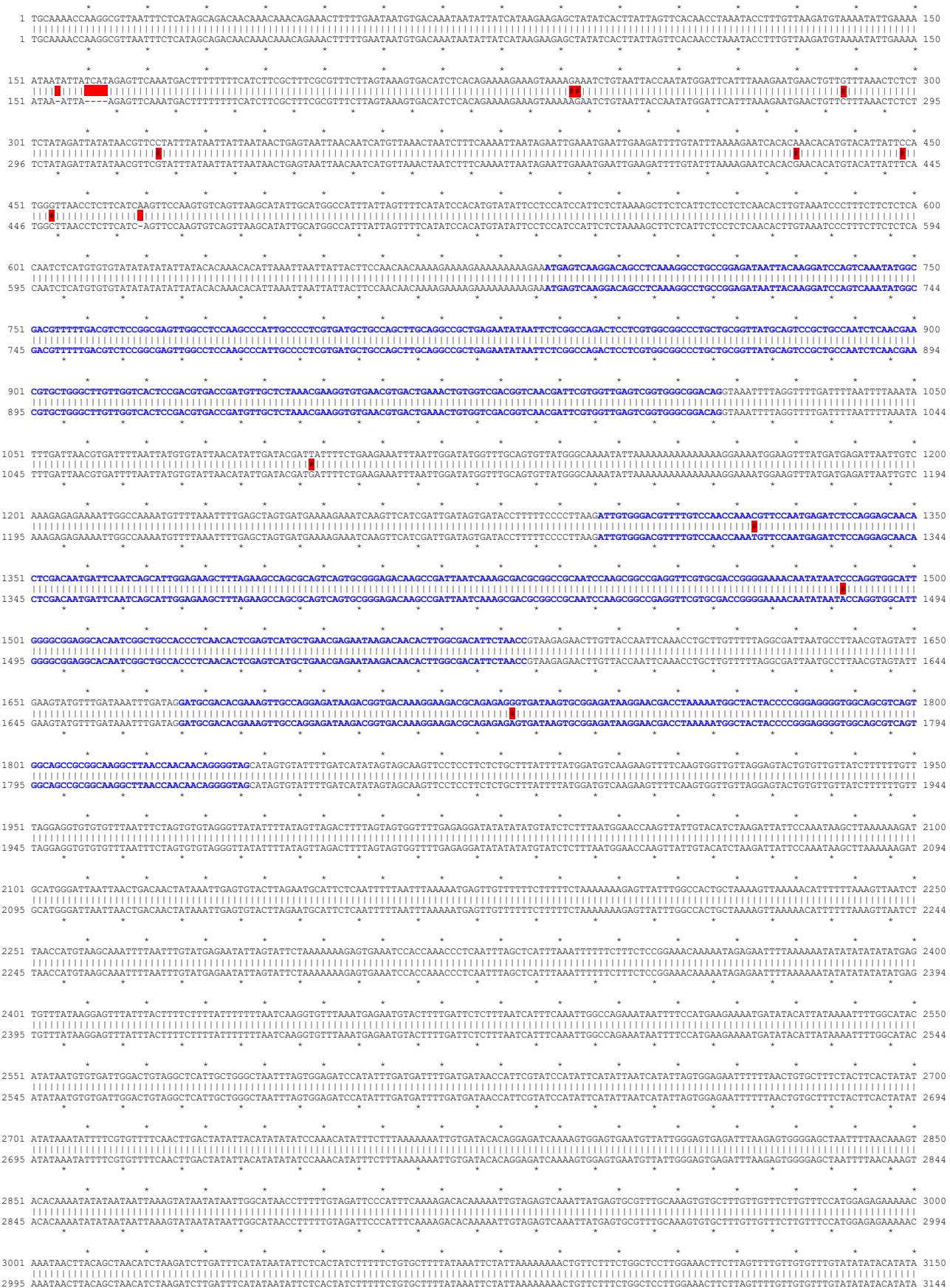


Fig.S1 Alignment of the 14.1-kb genomic DNA sequences from Jin5-508 (upper) and YN (lower). The pair-wise comparison was performed by using the ApE (v2.0.60) software with default parameters. The software is accessible from <http://jorgensen.biology.utah.edu/wayned/ape/>. The variants (SNPs and InDels) were highlighted in red. The blue nucleotide sequences are the three exons of CsGy7G014720 (CsFn17.1) while the orange nucleotide sequences are the the exon of CsGy7G014730.



13351 AGGATTAGTTGGAATAAAAAGAACAAATAAGAACAGAAATACACAATGCCTTGAGAAAGTTATTATTACAGATACTTACATTAACACCTTTTGGTAAGAAGTGCCTGGAGTTGCAGCCACTCCTTTATTTATATATTAACATGAAATGATTA 13500
13345 AGGATTAGTTGGAATAAAAAGAACAAATAAGAACAGAAATACACAATGCCTTGAGAAAGTTATTATTACAGATACTTACATTAACACCTTTTGGTAAGAAGTGCCTGGAGTTGCAGCCACTCCTTTATTTATATATTAACATGAAATGATTA 13494
13501 TGTTTAAACACAGAAAATCATGTTTATAATTTTAAAATAAGCTATTCCAGGGTCACCTTGTAATAATTAACCTGATTCCAAGTCTTATCTGCCACAACAAAACATAAAGATGAATACACAAAAGAAGAAAGGATGTACAAGGCAATAGC 13650
13495 TGTTTAAACACAGAAAATCATGTTTATAATTTTAAAATAAGCTATTCCAGGGTCACCTTGTAATAATTAACCTGATTCCAAGTCTTATCTGCCACAACAAAACATAAAGATGAATACACAAAAGAAGAAAGGATGTACAAGGCAATAGC 13644
13651 ATTCCATAATAGAGCAATTAACCTTTTAAATTTACAGTAAACAGGAGGTTTCAAATGAACAGCCCTTTTGGCAATTTTGTAACTAAGAGAAACTTACAGCGCTCTCCAGAAGTGTGCCAGAAACAAAACCGGGATGTACAA 13800
13645 ATTCCATAATAGAGCAATTAACCTTTTAAATTTACAGTAAACAGGAGGTTTCAAATGAACAGCCCTTTTGGCAATTTTGTAACTAAGAGAAACTTACAGCGCTCTCCAGAAGTGTGCCAGAAACAAAACCGGGATGTACAA 13794
13801 ACCGTTTACCCCCAAGGTTAAATGACATGAACATAAAGTCAACCTGTCCCTAAACACTTACTCAAATGCACCATAAAGAAATCTAGAAAATATTTCTTTGGGGGAATCAGCGCGCGTGGATATCATCATCCCAAAAATGGC 13950
13795 ACCGTTTACCCCCAAGGTTAAATGACATGAACATAAAGTCAACCTGTCCCTAAACACTTACTCAAATGCACCATAAAGAAATCTAGAAAATATTTCTTTGGGGGAATCAGCGCGCGTGGATATCATCATCCCAAAAATGGC 13944
13951 ACTGGTTAGTAAGGCCAGCAAAAAGAGTTCTGCAACACGCATTCTCTGTAGTGGTAGCCAATGAAGATGCAAAAGGTCGAGACAAAAGGATATTAGTAGCTTGGTTTGACAGAATCATACCTGAAGGTTACCGCAACAAAACACTACATTCA 14100
13945 ACTGGTTAGTAAGGCCAGCAAAAAGAGTTCTGCAACACGCATTCTCTGTAGTGGTAGCCAATGAAGATGCAAAAGGTCGAGACAAAAGGATATTAGTAGCTTGGTTTGACAGAATCATACCTGAAGGTTACCGCAACAAAACACTACATTCA 14094
14101 GTTGTGCAATGGCGCAAAAAGAAAACCAAGCAGAAGCTAAGTTTTAGTAGAAGAGTGATCTATTATACAGTGTGGCATGTGTTAATCTGTGAAGCAGACTCCTGTTGATTTGGTAAACAGTTCATCTCAATTCCTCTGCTTCAGAGGTGA 14250
14095 GTTGTGCAATGGCGCAAAAAGAAAACCAAGCAGAAGCTAAGTTTTAGTAGAAGAGTGATCTATTATACAGTGTGGCATGTGTTAATCTGTGAAGCAGACTCCTGTTGATTTGGTAAACAGTTCATCTCAATTCCTCTGCTTCAGAGGTGA 14244
14251 AGATTTGATGATGCTCCAATCATCTTATCATCTCCAGGT 14295
14245 AGATTTGATGATGCTCCAATCATCTTATCATCTCCAGGT 14289