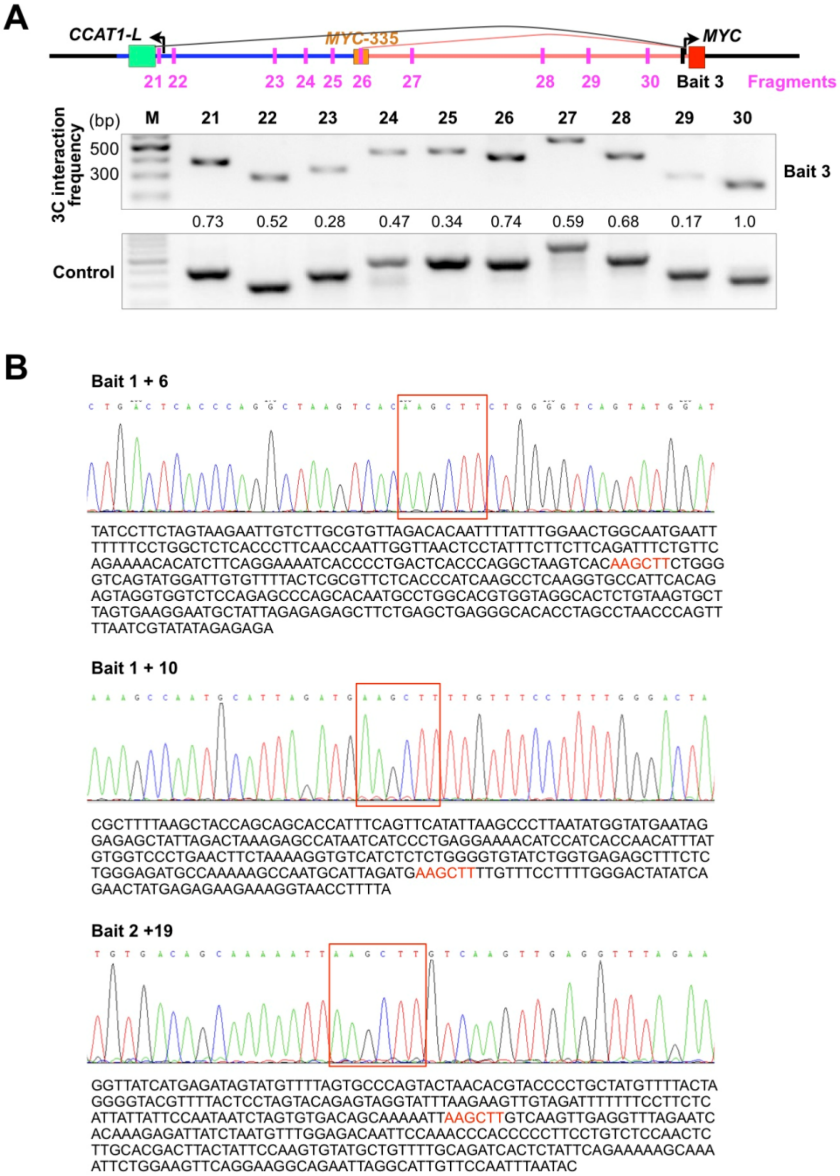

Bait 1 + 6

TATCCTTCTAGTAAGAATTGTCTTGCGTGTTAGACACAATTTTATTTGGAACTGGCAATGAATT
TTTTTCCTGGCTCTCACCCTTCAACCAATTGGTTAACTCCTATTTCTTCTTCAGATTTCTGTTC
AGAAAACACATCTTCAGGAAAATCACCCCTGACTCACCCAGGCTAAGTCACAAGCTTCTGGG
GTCAGTATGGATTGTGTTTTACTCGCGTTCTCACCCATCAAGCCTCAAGGTGCCATTCACAG
AGTAGGTGGTCTCCAGAGCCCAGCACAATGCCTGGCACGTGGTAGGCACTCTGTAAGTGCT
TAGTGAAGGAATGCTATTAGAGAGAGCTTCTGAGCTGAGGGCACACCTAGCCTAACCCAGTT
TTAATCGTATATAGAGAGA

Bait 1 + 10

CGCTTTTAAGCTACCAGCAGCACCATTTCAGTTCATATTAAGCCCTTAATATGGTATGAATAG
GAGAGCTATTAGACTAAAGAGCCATAATCATCCCTGAGGAAAACATCCATCACCAACATTTAT
GTGGTCCCTGAACTTCTAAAAGGTGTCATCTCTCTGGGGTGTATCTGGTGAGAGCTTTCTC
TGGGAGATGCCAAAAAGCCAATGCATTAGATGAAGCTTTTGTTTCCTTTTGGGACTATATCA
GAACTATGAGAGAAGAAAGGTAACCTTTTA

Bait 2 +19

GGTTATCATGAGATAGTATGTTTTAGTGCCCAGTACTAACACGTACCCCTGCTATGTTTTACTA
GGGGTACGTTTTACTCCTAGTACAGAGTAGGTATTTAAGAAGTTGTAGATTTTTTTCCTTCTC
ATTATTATTCCAATAATCTAGTGTGACAGCAAAAATTAAGCTTGTCAAGTTGAGGTTTAGAATC
ACAAAGAGATTATCTAATGTTTGGAGACAATTCCAAACCCACCCCCTTCCTGTCTCCAACTC
TTGCACGACTTACTATTCCAAGTGTATGCTGTTTTGCAGATCACTCTATTCAGAAAAAGCAAA
ATTCTGGAAGTTCAGGAAGGCAGAATTAGGCATTGTTCCAATTTAATAC

Supplementary information, Figure S5 Characterization of the long-range chromatin interaction between the *MYC* promoter and its upstream regulatory elements (related to Figures 4 and 5). (A) Multiple chromatin loops in the upstream region of *MYC* in HT29 cells. Physical map of the region spanning a 550 kb distance with *CCAT1* (*MYC*-515) at one end and *MYC* at the other, interrogated by 3C. Top, the position of the constant fragment containing *MYC* promoter is marked by a black bar (bait 3); positions of Hind III restriction target fragments are marked by pink bars. Bottom, 3C interaction frequencies of the constant fragment with each other fragment. The results revealed that the increased interaction between *MYC*-335 and the *MYC* promoter and between *MYC*-335 and *MYC*-515. The relative abundance of each 3C PCR product was determined using ImageJ, normalized by each corresponding input signal and the bait PCR product (set as 1.0), and labeled underneath.(B) Examples of Sanger sequencing of the 3C PCR products from the examined long-range chromatin interaction regions. Hind III restriction sites are marked with red rectangle lines, nucleotides in the upstream of the Hind III restriction site are from one chromatin region (for example, *MYC*-335, bait1) and nucleotides in the downstream of the Hind III restriction site are from another chromatin region in distance (for example, the *MYC* promoter, #6). The majority of the 3C products were verified in this way to make sure the accuracy of the PCR products.