```
                                  10        20        30        40        50
                          ....|....|....|....|....|....|....|....|....|....|
GAPDH NG_007073.2         ACTTGCGCCCCGCTCCCTCTTTCTTTGCAGCAATGCCTCCTGCACCACCA
GAPDH C-1                 CAC.AGTGATT.......................................
GAPDH C-2                 CAC.AGTGATT.......................................
GAPDH C-3                 CAC.AGTGATT.......................................
GAPDH 01.1                -----------.......................----------------
GAPDH 02.1                --------------------------------------------------
GAPDH_Pb1                 ---------------------------------------............

                                  60        70        80        90       100
                          ....|....|....|....|....|....|....|....|....|....|
GAPDH NG_007073.2         ACTGCTTAGCACCCCTGGCCAAGGTCATCCATGACAACTTTGGTATCGTG
GAPDH C-1                 ..................................................
GAPDH C-2                 ..................................................
GAPDH C-3                 ..................................................
GAPDH 01.1                --------------------------------------------------
GAPDH 02.1                ---------------------------------------.......
GAPDH_Pb1                 ............-------------------------------------

                                  110       120       130
                          ....|....|....|....|....|....|
GAPDH NG_007073.2         GAAGGACTCATGGTATGAGAGCTGGGGAAT
GAPDH C-1                 ..............AATCGAA.TCCCGCG
GAPDH C-2                 ..............AATCGAA.TCCCGCG
GAPDH C-3                 ..............AATCGAA.TCCCGCG
GAPDH 01.1                -------------------------------
GAPDH 02.1                ..............---------------
GAPDH_Pb1                 -------------------------------
```