```
Read1                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
Read2                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
Read3                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
Read4                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
Read5                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
Read6                  GGCCACCCCTGTG-CCCCCACAGGGGACTCCGA
ReferenceRepeatingUnit GGCCACCCCTGTGCCCCCCCACAGGGGACTCCGA
                       *************  *******************
```

Figure S10: **Frameshift in *CEL* gene.** Multiple alignment of sequenced reads and reference repeating unit shows a deletion in diabetes patient genome. Due to low PCR amplification in GC rich VNTR region (84.8%), the coverage of VNTR region is 14× and 6 reads support the deletion.