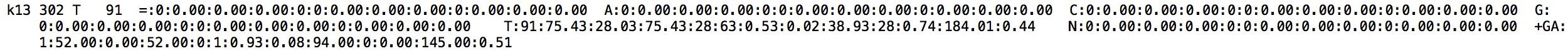
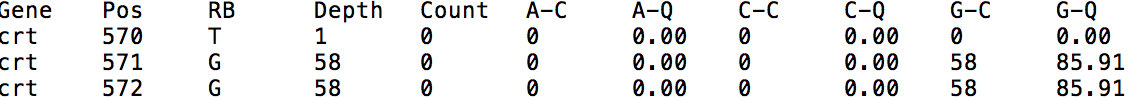
ReadCountMod Description and General Instructions

Description

The readcountMod program is a python script program used to generate readcounts for each base at each position requested. The readcountMod program generates the readcounts using the bam-readcount program which takes in the input of a bam file, fasta file, and a bed file and is able to generate the readcounts for all 4 nucleotide bases and the mapping quality, a feature missing in the .cov excel file found in a Run Folder generated by the IonTorrent PGM. The biggest problem with the bam-readcount program by itself that the readcountMod program addresses is no longer the need to manually input the three file types and the removal of extraneous information provided in the bam-readcount program. The readcountmod program parses through the original readcount file and generates a parsed readcount file which neatly organizes the information and places them in a separate parsed readcount folder.

Original Readcount File: 

Parsed ReadCount File:



In addition to generating the parsed readcount files the program also appends the readcount information to the run excel file found in the run folder. The program correctly appends and aligns the readcount data based on Barcode, Chromosome, and position. The readcountmod program in its totality is able to provide a user friendly and decipherable readcount file, batch processing of bam files to readcount files and in a relatively fast and efficient manner.

Instructions:

What to Input:

The input for the readcountmod program is a folder containing one or more run folder generated by the IonTorrent PGM

Outputs:

1. A folder containing all the bam files found in the run folders
2. A folder containing all the unedited readcounts
3. A folder containing all the parsed readcount files
4. Excel files found in the original run folders with the appended readcount info

What software is needed run readcountmod

1. Python installer
2. Bam-readcount – can be either found on the nyu hpc or can be downloaded locally using homebrew

Reasons why the program might not work

1. Python or bam-readcount not installed
2. Wrong input of runfolder directory --- Remember when inputting the directory

not to use any spaces and that every new directory starts with a ‘/’

Example of proper directory input : /Users/Directory/Directory/Directory/RunFolderName

1. The run folder was modified