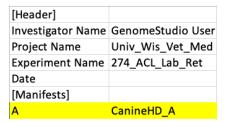
Instructions to Load Raw Intensity Data (*.idat) Files into GenomeStudio

- **Step1.** Download the comma-delimited text (Lab_Ret_ACL_GenomeStudio_Sample_Sheet.csv) Sample Sheet from Dryad
- **Step2.** Download all raw intensity data (*.idat) files from Dryad into one folder (Data Repository)
- **Step3.** Download the Manifest File for the CanineHD BeadChip desired CanFam annotation from Illumina's website into one folder (Manifest Repository)

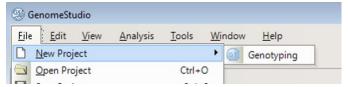
 https://support.illumina.com/downloads/caninehd_product_files.html

CanineHD_A.bpm was used for this analysis

If you are using a different CanineHD BeadChip Manifest File. The header of the Sample Sheet needs to be changed in the two sections highlighted below.



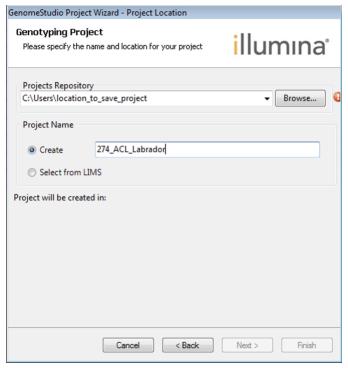
- **Step4.** Download GenomeStudio Software from Illumina's website https://support.illumina.com/array/array_software/genomestudio/downloads.html
- **Step5.** Start GenomeStudio and go to File -> New Project -> Genotyping



This will launch the GenomeStudio Project Wizard



Step6. Choose a project name and the location (Project Repository) you want the project saved



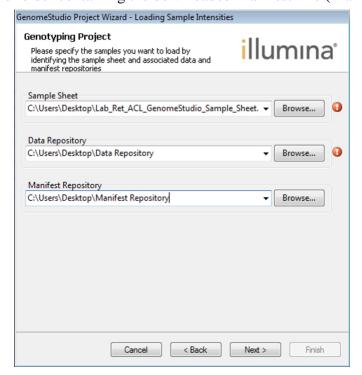
Click Next to advance



Choose the option "Use sample sheet to load sample intensities" Click Next to advance

Step7. Browse to specify the location of the downloaded (.csv) Sample Sheet (from Step1), the location of the folder containing all of the downloaded raw intensity data (*.idat) files (Data Repository from Step2), and the location of the folder containing the downloaded Manifest File (Manifest Repository from

Step3)



Click Next to advance

Step8. Click Finish



Step9. Follow Illumina's provided instructions for creation of a Custom Cluster File https://www.illumina.com/content/dam/illumina-marketing/documents/products/technotes/custom-cluster-file-cnv-tech-note-770-2017-017.pdf