## **Demultiplexing Overview**

My demultiplexing script took two hours and thirty-seven minutes to run after leaving all the files open. This was a significant reduction from my initial 8 hours when I opened and closed each file every time, I used it. I used a very strict quality score cutoff of 32 which resulted in a large number of reads being placed into the unknown file. This score was chosen as my demultiplexing script takes the average quality score of a line so outliers would not cause an entire sequence line to be discarded. The script does not explicitly test if barcodes contain an N. This is intentional because any barcode containing an N will not be in the list of known barcodes, so that record will be placed in unknown. My script does not check if there are any N I chose to report my percentages as a percentage of the reads that correctly ended up in a barcoded file. The barcode, followed by the count, followed by the percentage is reported below. Also included is a heatmap of all barcode combinations, and a bar graph of all barcode counts, unknown counts and index hopped counts. These are found in the graphs folder.

Barcode	Count	Percent
CTCTGGAT	28273074	11%
TACCGGAT	59803610	22%
AGAGTCCA	9424161	3.5%
GTAGCGTA	6425781	2.4%
ATCATGCG	8385008	3.1%
AACAGCGA	7418886	2.8%
TCGACAAG	3174898	1.2%
TCGAGAGT	9284990	3.5%
CGGTAATC	3730418	1.4%
TAGCCATG	8657718	3.2%
TCTTCGAC	34156815	13%
CTAGCTCA	14820156	5.5%
TATGGCAC	9086426	3.4%
ACGATCAG	6841163	2.5%
GATCTTGC	3054876	1.1%
AGGATAGC	7217701	2.7%
TGTTCCGT	13452889	5.0%
GCTACTCT	5780573	2.1%
CGATCGAT	4834036	1.8%
GTCCTAAG	7309039	2.7%
GATCAAGG	5204218	1.9%
TCGGATTC	3638673	1.4%
CACTTCAC	3369605	1.3%
ATCGTGGT	5606619	2.1%