**Week of April 2, 2023**

https://github.com/DesireeWilson/FinalProject

I am working by myself. This week, I performed a summary table using “gtSummary.” Based on the summary table, most of the samples are tumor stages 1 and 2. This is an important find because umor stages 1 and 2 are considered early stage; all the more reason to find biomarkers associated with outcome (remission vs metastasis). Now, this week, I will perform differential gene expression analysis on the following genes in Gleason low (less than 7) vs Gleason high (greater than 7): MYBPC1, SLC7A4, CDC42EP5, BCAS1, PAK1IP1, ANPEP, SLC23A1, HS.270778, GLB1L2, GCNT2, TNFRSF19, CUX2, POTEG, NCAPD3, LOC728606, SLC22A3, C9ORF61, SRD5A2, FLJ31568, SERPINF2, PGM5, LOC645993, ZDHHC8P, CNTNAP2, F12, CXCL14, CTHRC1, ZNF467, CDC20. From here, I will also perform survival analysis as well.

| **Characteristic** | **N = 94***1* |
| --- | --- |
| bcrRelapse |  |
| N | 48 (51%) |
| N/A | 1 (1.1%) |
| Y | 45 (48%) |
| clinicalStage |  |
|  | 1 (1.1%) |
| T1c | 41 (44%) |
| T2a | 34 (36%) |
| T2b | 4 (4.3%) |
| T2c | 1 (1.1%) |
| T3a | 9 (9.6%) |
| Tx | 3 (3.2%) |
| UNKNOWN | 1 (1.1%) |
| tumorGleason |  |
| 10=5+5 | 1 (1.1%) |
| 5=3+2 | 2 (2.1%) |
| 6=2+4 | 1 (1.1%) |
| 6=3+3 | 17 (18%) |
| 7=3+4 | 37 (39%) |
| 7=4+3 | 19 (20%) |
| 8=3+5 | 1 (1.1%) |
| 8=4+4 | 4 (4.3%) |
| 9=4+5 | 8 (8.5%) |
| 9=5+4 | 1 (1.1%) |
| unknown | 3 (3.2%) |
| *1* n (%) | |