Differential Gene Expression Column Headers:

- gene_id: The unique identifier for the gene (e.g., from Ensembl, depend on reference annotation used).
- **gene_name:** The actual gene name (e.g., BRCA1, P53), which is easier to recognize compared to the gene ID.
- **sample 1:** The label for the first sample group.
- **sample_2:** The label for the second sample group.
- **status:** The status of the differential expression test for the gene. Common statuses include:
 - OK:
 - o **NOTEST:** There was an issue performing the test (e.g., insufficient data).
- Average FPKM (The test was successful. Sample 1): The average Fragments Per Kilobase of transcript per Million mapped reads (FPKM) value for all replicates in sample 1.
- Average FPKM (Sample 2): The average FPKM value for all replicates in sample 2.
- **log2_fold_change:** The log2-transformed fold change in expression between sample 1 and sample 2. A positive value means the gene is more highly expressed in sample 2, while a negative value means higher expression in sample 1.
- **test_stat:** The test statistic from the differential expression analysis, used to assess the significance of the difference between the two samples.
- **p_value:** The p-value indicating the significance of the differential expression. A smaller p-value suggests a more statistically significant difference between the two groups.
- q_value: The False Discovery Rate (FDR)-adjusted p-value, which accounts for multiple testing to minimize false positives.
- **significant**: Indicates whether the gene is significantly differentially expressed based on the q-value. Typically, this will be either "yes" or "no."
- sample_1_0 FPKM, sample_1_1 FPKM, sample_1_2 FPKM: The FPKM values for each biological replicate of sample 1. The numbers (_0, _1, _2) represent individual replicates within this group.
- sample_2_0 FPKM, sample_2_1 FPKM, sample_2_2 FPKM: The FPKM values for each biological replicate of sample 2. Again, the numbers represent the individual replicates.