QC table checklist

1. Check schema
   1. Are all the fields labeled?
   2. Is there a table description?
   3. Do the field labels make sense for all fields?
   4. Are the labels correct?
2. Look at table row number and size
   1. Do these metrics make sense?
3. Scroll through table manually
   1. See if anything stands out - empty columns, etc.
   2. The BigQuery table search user interface is useful for this test run. The test tier points to the isb-etl-open.
      1. [BigQuery table search test tier](https://isb-cgc-test.appspot.com/bq_meta_search/)
      2. [isb-project\_zero](https://console.cloud.google.com/bigquery?authuser=1&folder=&organizationId=&project=isb-project-zero&p=isb-project-zero&d=RNAseq_Gene_Expression&page=table)
   3. Run a manual check in the console with the steps mentioned in step 1
      1. Are all the fields labeled?
      2. Is there a table description?
      3. Do the field labels make sense for all fields?
      4. Are the labels correct?
4. Number of cases on GDC portal versus table?
5. Number of cases / aliquots versus BigQuery metadata table
6. Number of entries per gene - should equal aliquot count
7. Check for any duplicate rows present in the table