Naming convention for RNA files:

**For raw data:**

NS.1720.004.NEBNext\_dual\_i7\_185---NEBNext\_dual\_i5\_185.2\_R1.fastq.gz

NS.1720.004.NEBNext\_dual\_i7\_185---NEBNext\_dual\_i5\_185.2\_R2.fastq.gz

This corresponds to **D1FS-1**, as found in laneInfo.xlsx.

Would give file name AS\_D\_L1\_F\_S\_S1\_L004\_R1.fastq.gz

**Where:**

AS = Artificial Selection

D = Down, or selected for lower sociability

L1 = Lineage (Ranges from L1 – L4)

F = Female, Sex

S = Sociability Arena, (Experiment matched)

S1 = Biological Sample (Ranges from S1 – S3)

L004 = Flowcell Lane