**Code for obtaining genes counts and obtained statistics**

================================================================================================

htseq-count -i gene\_name -m union -s no 3\_S246\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 8017381

\_\_ambiguous 1894979

\_\_too\_low\_aQual 1836940

\_\_not\_aligned 2661793

\_\_alignment\_not\_unique 30791905

htseq-count -i gene\_name -m union -s no 4\_S247\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 8650707

\_\_ambiguous 1910786

\_\_too\_low\_aQual 1864054

\_\_not\_aligned 2758202

\_\_alignment\_not\_unique 22915669

htseq-count -i gene\_name -m union -s no 5\_S248\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 10645995

\_\_ambiguous 1833506

\_\_too\_low\_aQual 1940857

\_\_not\_aligned 2903423

\_\_alignment\_not\_unique 30076802

htseq-count -i gene\_name -m union -s no 6\_S249\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 7824162

\_\_ambiguous 1859356

\_\_too\_low\_aQual 1644652

\_\_not\_aligned 1860310

\_\_alignment\_not\_unique 23816094

htseq-count -i gene\_name -m union -s no 10\_S250\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 5901553

\_\_ambiguous 1545346

\_\_too\_low\_aQual 2099779

\_\_not\_aligned 1432766

\_\_alignment\_not\_unique 13815975

htseq-count -i gene\_name -m union -s no 11\_S251\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 4443268

\_\_ambiguous 1636577

\_\_too\_low\_aQual 1552418

\_\_not\_aligned 1587881

\_\_alignment\_not\_unique 15577872

htseq-count -i gene\_name -m union -s no 13\_S252\_L004.sam hg38\_ucsc.annotated.gtf > PatCouTxt

\_\_no\_feature 5914111

\_\_ambiguous 783529

\_\_too\_low\_aQual 792339

\_\_not\_aligned 984482

\_\_alignment\_not\_unique 8953275