



# MERCURIUS™

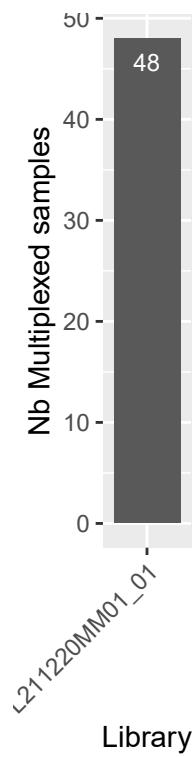
Library preparation and sequencing  
data analysis report 2022-01-24

**Project name (ID): AMP0035**

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## Library preparation summary

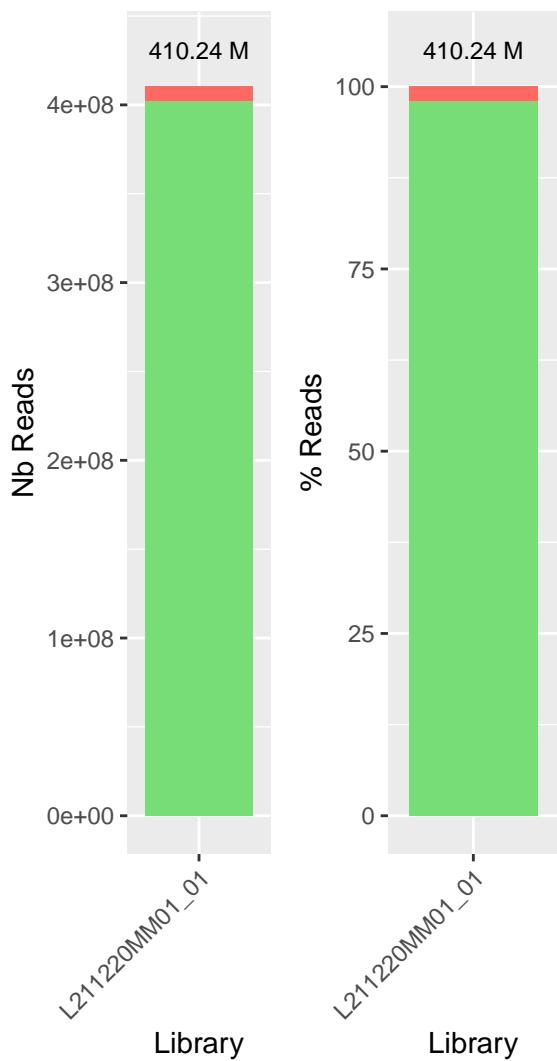
| Library        | Nb of samples | Avg RNA/sample, ng |
|----------------|---------------|--------------------|
| L211220MM01_01 | 48            | 1247.39            |



## Library sequencing summary

| Library        | PF_reads    | Demultiplexed reads | % Demultiplexed | Avg. demultiplexed reads/sample |
|----------------|-------------|---------------------|-----------------|---------------------------------|
| L211220MM01_01 | 410,238,057 | 401,987,022         | 97.99           | 8,374,730                       |

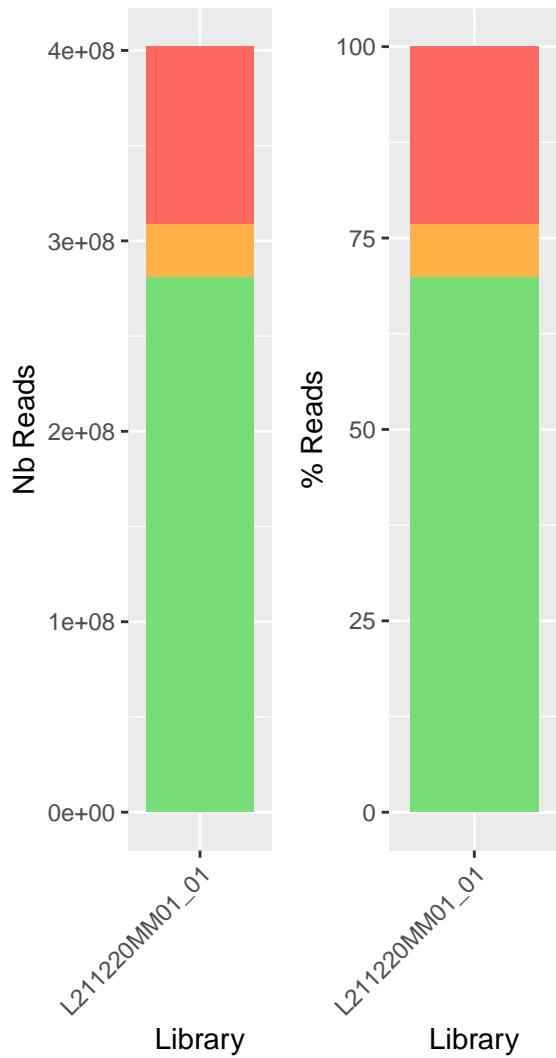
█ Not demultiplexed █ Demultiplexed



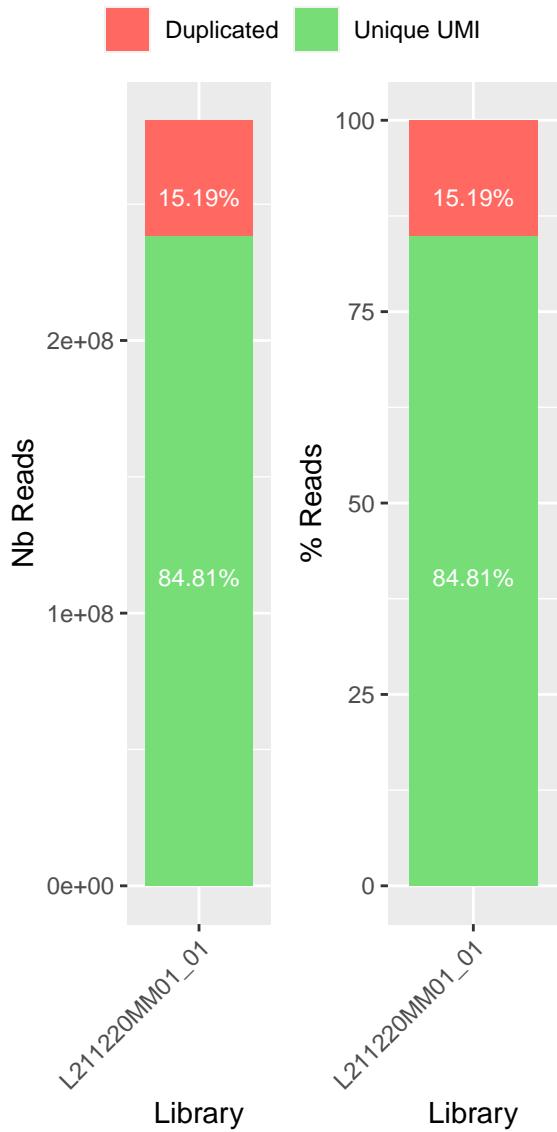
## Library alignment summary

| Library        | Genome assembly  | % Mapped to genome<br>(from demultiplexed) | % Mapped to exons<br>(from demultiplexed) |
|----------------|--|--|---|
| L211220MM01_01 | mus_musculus<br>GRCm38 (mm10)<br>(Ensembl release 102) | 76.79                                      | 69.85                                     |

 Not aligned    No feature    Mapped to exons

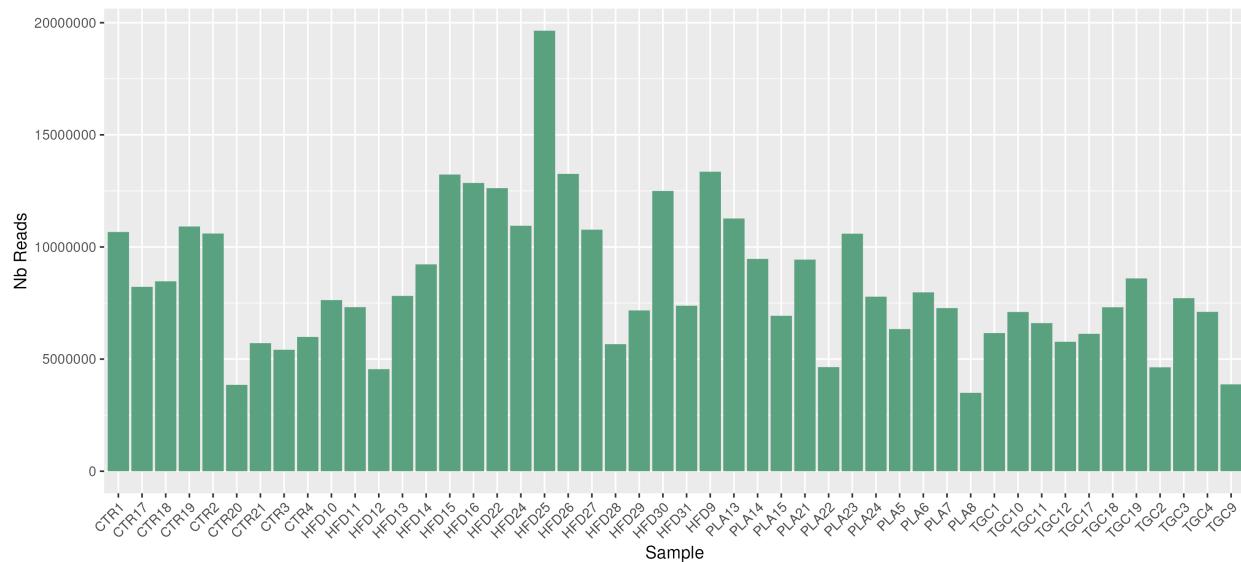


## Library UMI duplication summary

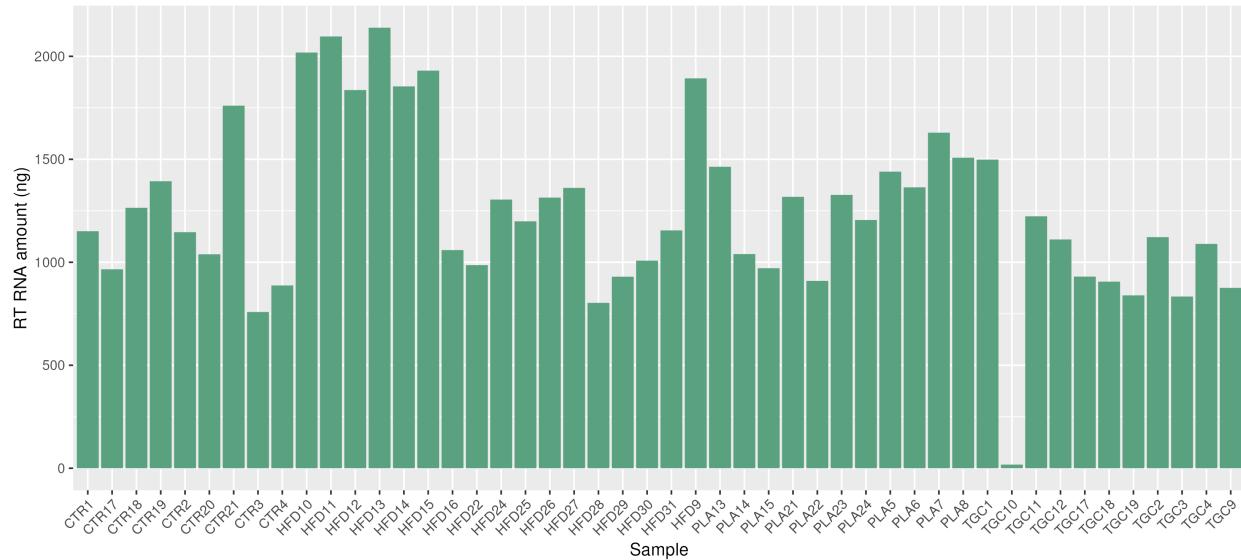


# Library L211220MM01\_01, per sample summary

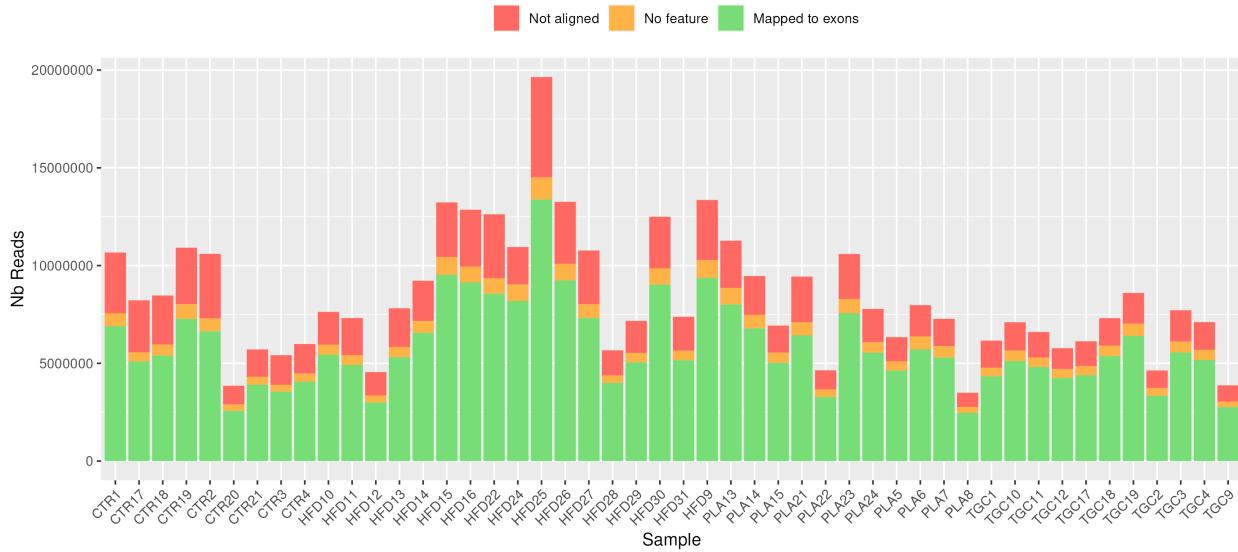
## 1. Number of sequencing reads per sample



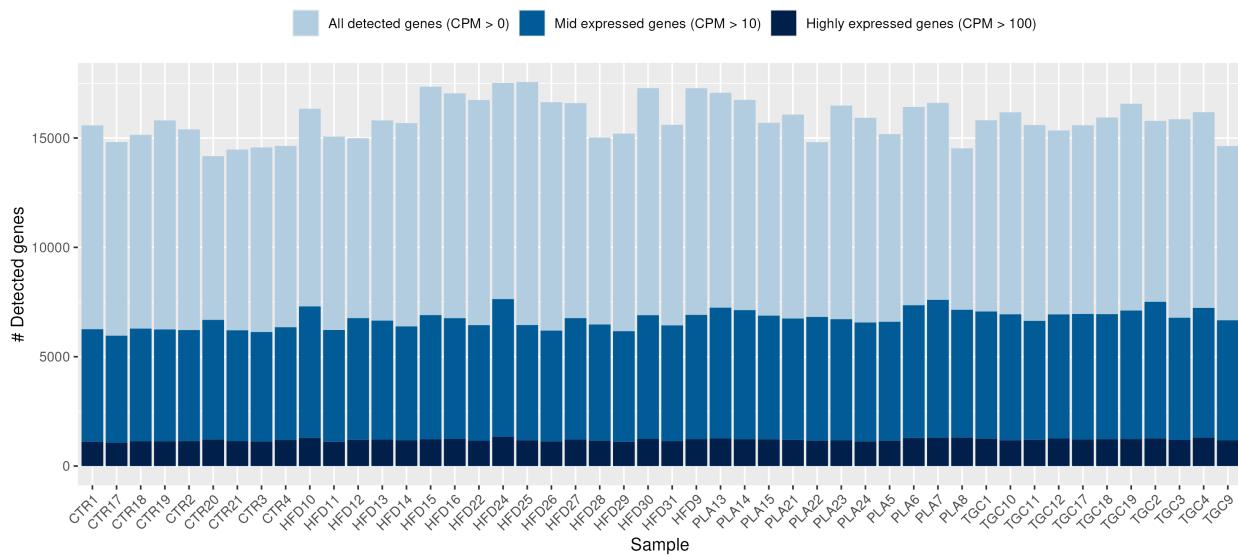
## 2. RT RNA amount (ng), per sample



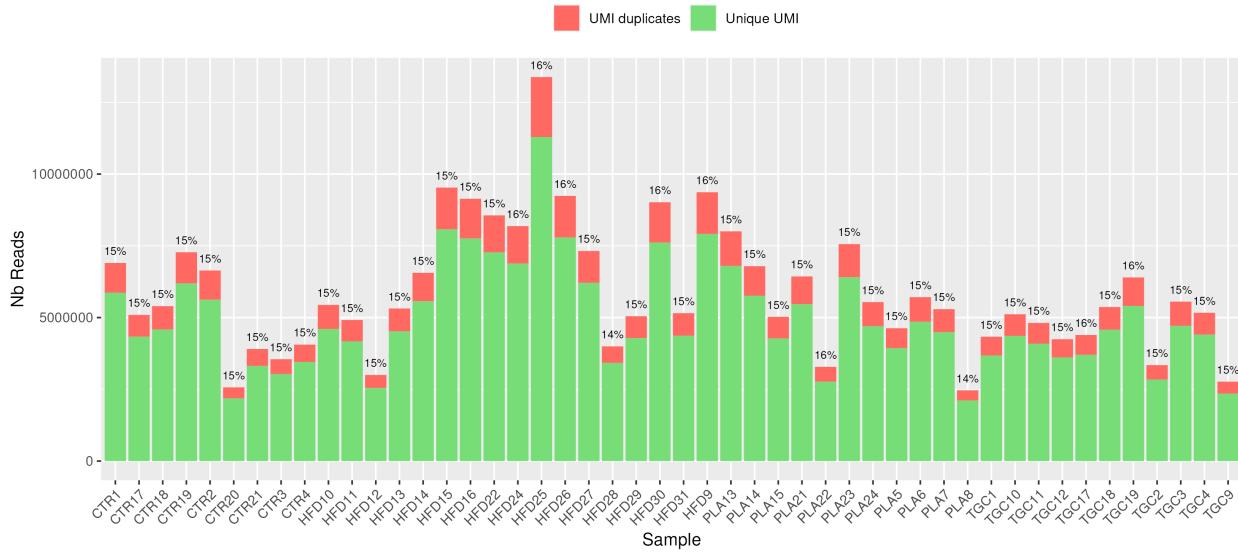
### 3. Alignment stats, per sample



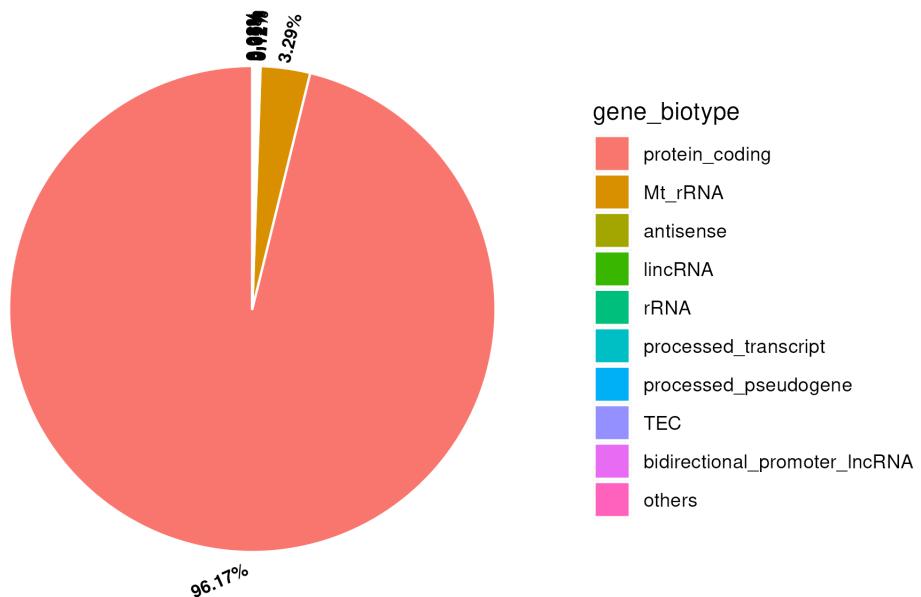
### 4. Detected genes, per sample



## 5. UMI duplicates, per sample



## 6. Biotypes, across samples



## 7. Most expressed genes, across samples

