

CountTableGenerator

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9/1/2017

```
transcriptome_fasta %>% length()

## [1] 80320
seqs_csv %>% nrow()

## [1] 70178
ma1_num_seq <- mas[[1]] %>% nrow()
for(ma in 2:length(mas)){
  assertthat::assert_that(nrow(mas[[ma]]) == ma1_num_seq)
}
print(ma1_num_seq)

## [1] 67626
seqs_csv$Status %>% table()

## .
##      0      1      2      3
## 10660 38268 16754  4496
seqs_csv$Paralog.. %>% table()

## .
##      0      1      2      3      4      5      6      7      8      9     10     11
## 65682 3231  871  263   72   27   15    6    4    3    2    2
table(seqs_csv$Status, seqs_csv$Paralog..)

##
##           0      1      2      3      4      5      6      7      8      9     10
## 0 10660      0      0      0      0      0      0      0      0      0      0
## 1 38268      0      0      0      0      0      0      0      0      0      0
## 2 16754      0      0      0      0      0      0      0      0      0      0
## 3      0 3231  871  263   72   27   15    6    4    3    2
##
##           11
## 0      0
## 1      0
## 2      0
## 3      2
seqs_csv <- seqs_csv %>%
  dplyr::rowwise() %>%
  dplyr::mutate(SeqType = ifelse(grepl("CONTIG",ID),
                                "CONTIG",
                                ifelse(grepl("F5",ID),
                                        "SINGLETON",
                                        "UNKNOWN")))
```

```
seqs_csv$SeqType %>% table()
```

```
## .  
##   CONTIG SINGLETON  
##   24301      45877
```

```
table(seqs_csv$SeqType, seqs_csv$Status)
```

```
##  
##           0      1      2      3  
##   CONTIG   4601  7209 11116 1375  
##   SINGLETON 6059 31059  5638 3121
```

```
table(seqs_csv$SeqType, seqs_csv$Paralog..)
```

```
##  
##           0      1      2      3      4      5      6      7      8      9  
##   CONTIG   22926 1197   144   27      5      2      0      0      0      0  
##   SINGLETON 42756 2034   727  236     67     25     15      6      4      3  
##  
##           10     11  
##   CONTIG      0      0  
##   SINGLETON    2      2
```