Alignment Stats

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Contents

1 Params

Params 1: -p 1 –very-sensitive –local -5 4 -3 4 -I 50 -X 250
Params 2: -p 1 –very-sensitive –local -5 4 -3 4 -I 50 -X 10000
Params 3: -p 1 –very-sensitive –local -5 12 -3 4 -I 50 -X 10000
Params 4: -p 1 –very-sensitive –local -N 1 -5 12 -3 4 -I 50 -X 10000

2 Tables

2.1 Stats

```
print(params)
```
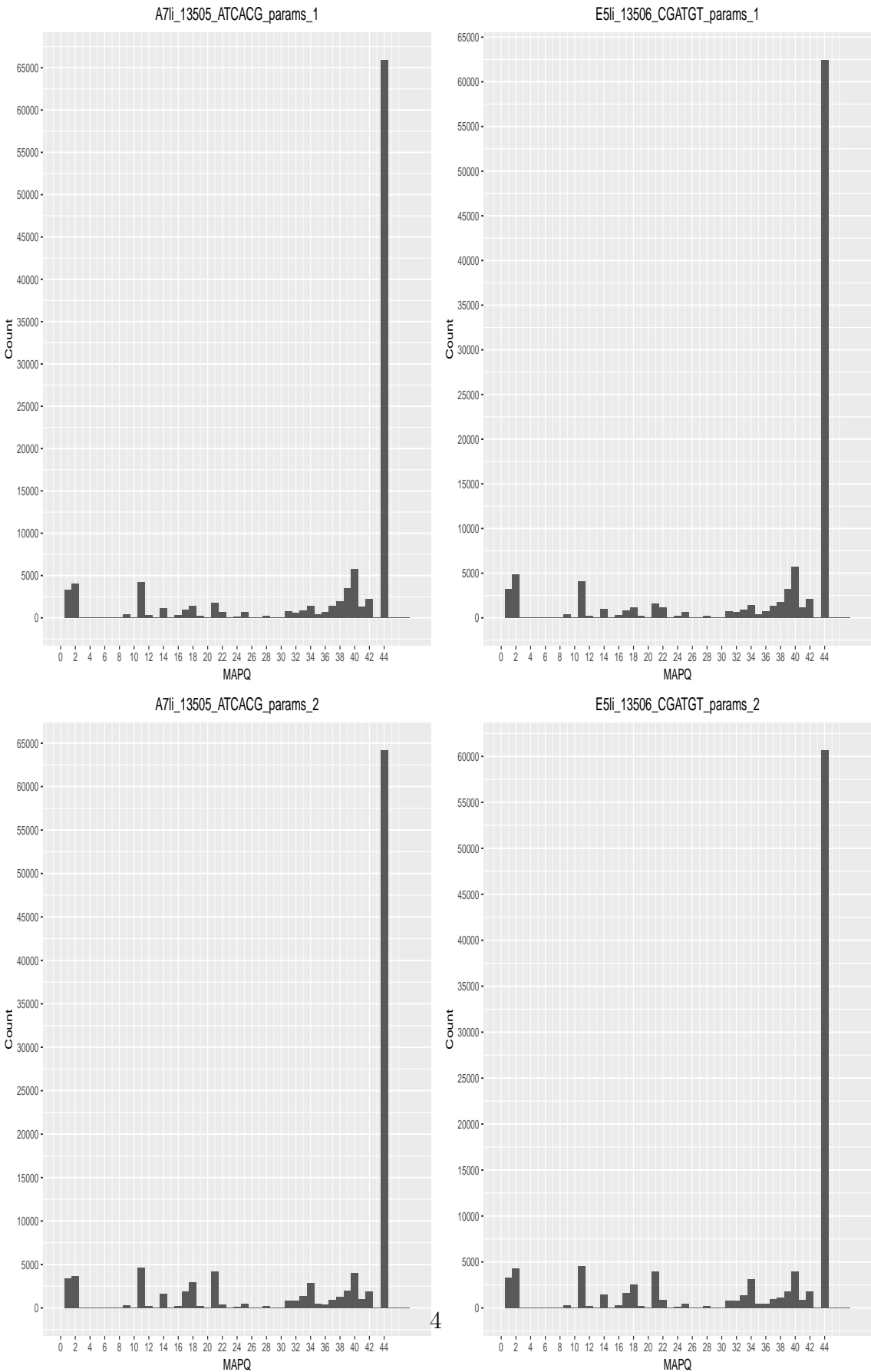
```
##                                Stats A7li__1  E5li__1  A7li__2  E5li__2  A7li__3  E5li__3  A7li__4  E5li__4
## 1           raw total sequences:     110000   110000   110000   110000   110000   110000   110000   110000
## 2             filtered sequences:         0        0        0        0        0        0        0        0
## 3                      sequences:    110000   110000   110000   110000   110000   110000   110000   110000
## 4                      is sorted:         0        0        0        0        0        0        0        0
## 5                  1st fragments:     55000    55000    55000    55000    55000    55000    55000    55000
## 6                 last fragments:     55000    55000    55000    55000    55000    55000    55000    55000
## 7                   reads mapped:    107246   103551   107254   103562   107242   103725   107242   103725
## 8        reads mapped and paired:    106860   102230   106876   102252   106852   102280   106852   102280
## 10                 reads unmapped:      2754     6449     2746     6438     2758     6275     2758     6275
## 11          reads properly paired:     83696    80930    92538    89960    86150    84542    86150    84542
## 13                   reads paired:    110000   110000   110000   110000   110000   110000   110000   110000
## 15               reads duplicated:         0        0        0        0        0        0        0        0
## 17                      reads MQ0:       569      837      551      862      755      983      755      983
## 19                 reads QC failed:         0        0        0        0        0        0        0        0
## 20          non-primary alignments:        0        0        0        0        0        0        0        0
## 21                  total length: 12870000 12870000 12870000 12870000 11990000 11990000 11990000 11990000
## 23                   bases mapped: 12547782 12115467 12548718 12116754 11689378 11306025 11689378 11306025
## 25           bases mapped (cigar): 11949843 11418154 12033129 11499675 11139112 10656163 11139112 10656163
## 27                  bases trimmed:         0        0        0        0        0        0        0        0
## 28               bases duplicated:         0        0        0        0        0        0        0        0
## 29                     mismatches:    146980   142347   142160   136729   124022   121296   124022   121296
## 31                     error rate:         0        0        0        0        0        0        0        0
## 33                 average length:       117      117      117      117      109      109      109      109
## 34                 maximum length:       117      117      117      117      109      109      109      109
## 35                average quality:        35       34       35       34       35       34       35       34
## 36            insert size average:       153      156      185      189      181      186      181      186
## 37 insert size standard deviation:        42       42      121      125      155      162      155      162
## 38           inward oriented pairs:     44729    43407    45504    44180    42242    41497    42242    41497
## 39          outward oriented pairs:      7195     5977     6939     5753    10010     8357    10010     8357
## 40     pairs with other orientation:       64       62       34       32       49       55       49       55
## 41 pairs on different chromosomes:       373      607      134      304      207      377      207      377
```
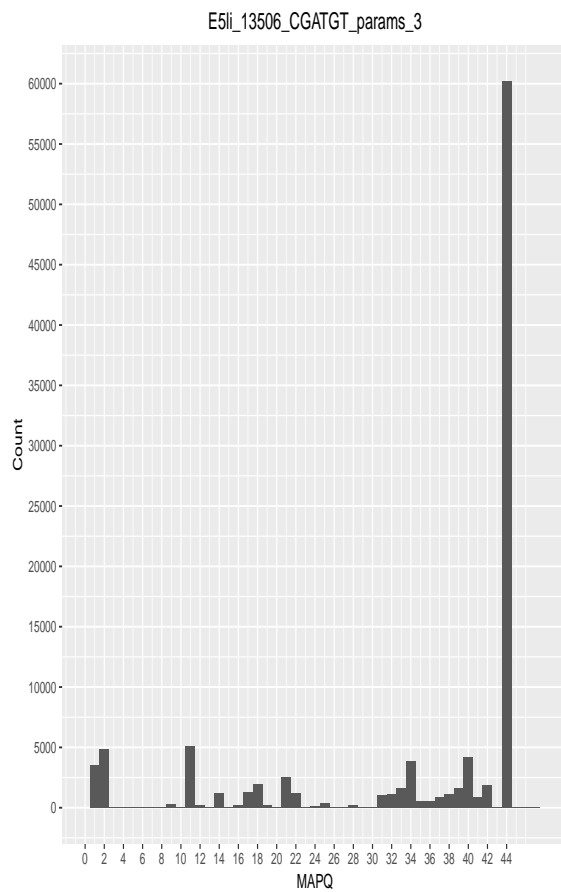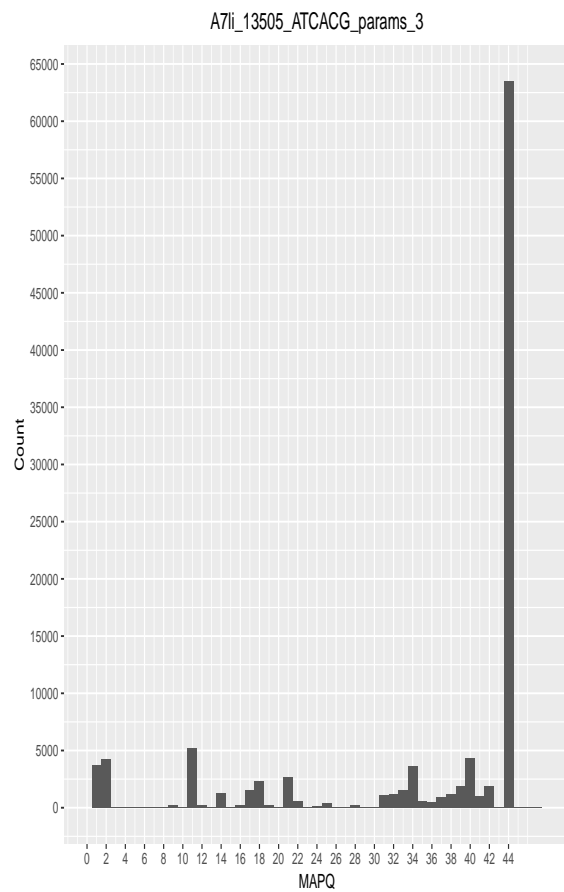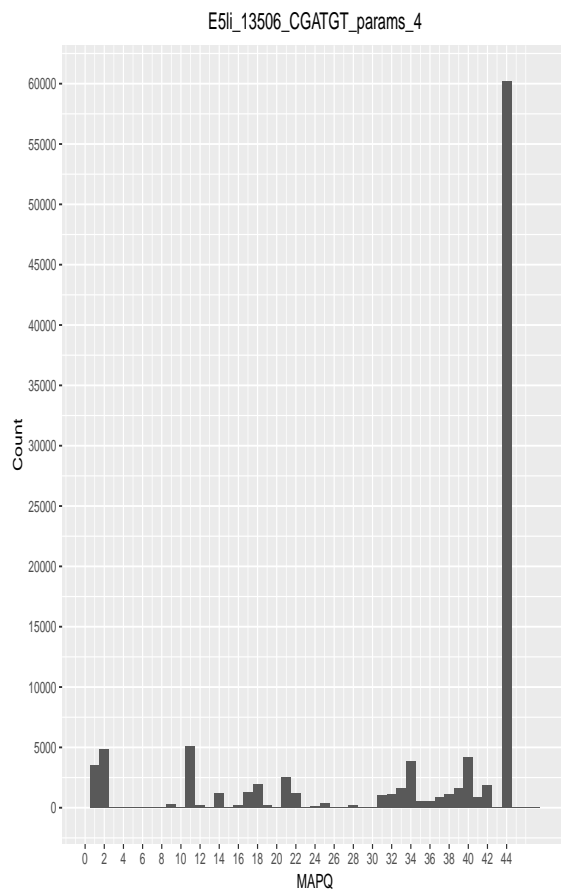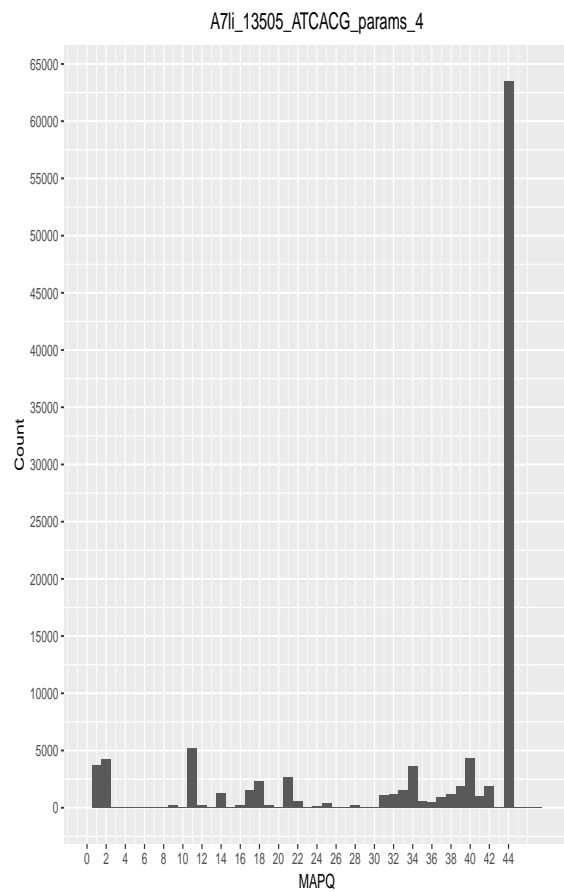
2.2 Average Coverage

	Par 1		Par 2		Par 3		Par 4	
Coding:	0.593	0.549	0.595	0.551	0.550	0.512	0.550	0.512
Non-Coding:	0.398	0.373	0.403	0.378	0.3670	0.347	0.3670	0.347

3 Plots

3.1 MAPQ

A7li_13505_ATCACG_params_3

E5li_13506_CGATGT_params_3

A7li_13505_ATCACG_params_4

E5li_13506_CGATGT_params_4

3.2   Fragment Length

A7li_13505_ATCACG_params_1

E5li_13506_CGATGT_params_1

A7li_13505_ATCACG_params_2

E5li_13506_CGATGT_params_2

A7li_13505_ATCACG_params_3

E5li_13506_CGATGT_params_3

A7li_13505_ATCACG_params_4

E5li_13506_CGATGT_params_4