Mapping quality cutoff of 5 input:

```
(base) [crandall@KITT realdata]$ bwa mem reference.fasta JC_1119.R1.fq.gz JC_1119.R2.fq.gz -I 200,40 -t 3 -B 3 -O 5 -L 20,5 2>/dev/null | mawk '!/\t[2-9].[SH].*/' | mawk '!/[2-9].[SH]\t/'| samtools view -@16 -q 5 -SbT reference.fasta - | samtools flagstat - > relaxed.stats
(base) [crandall@KITT realdata]$ bwa mem reference.fasta JC_1119.R1.fq.gz JC_1119.R2.fq.gz -I 200,40 -t 3 -L 20,5 2>/dev/null | mawk '!/\t[2-9].[SH].*/' | mawk '!/[2-9].[SH]\t/'| samtools view -@16 -q 5 -SbT reference.fasta - | samtools flagstat - > normal.stats
(base) [crandall@KITT realdata]$ paste <(cut -f1 -d + relaxed.stats) <(cut -f1 -d + normal.stats) <(cut -f4-10 -d " " relaxed.stats)
```

Mapping quality cutoff of 5 output:

```
2217934 2206471 in total (QC-passed reads + QC-failed reads)
2217934 2206471 primary
0       0       secondary
0       0       supplementary
0       0       duplicates
0       0       primary duplicates
2217934 2206471 mapped (100.00% : N/A)
2217934 2206471 primary mapped (100.00% : N/A)
2217934 2206471 paired in sequencing
1131358 1123539 read1
1086576 1082932 read2
2103108 2092133 properly paired (94.82% : N/A)
2169304 2157042 with itself and mate mapped
48630   49429   singletons (2.19% : N/A)
66004   64712   with mate mapped to a different chr
66004   64712   with mate mapped to a different chr
```

Mapping quality cutoff of 10 input:

```
(base) [crandall@KITT realdata]$ bwa mem reference.fasta JC_1119.R1.fq.gz JC_1119.R2.fq.gz -I 200,40 -t 3 -B 3 -O 5 -L 20,5 2>/dev/null | mawk '!/\t[2-9].[SH].*/' | mawk '!/[2-9].[SH]\t/'| samtools view -@16 -q 10 -SbT reference.fasta - | samtools flagstat - > relaxed.stats
(base) [crandall@KITT realdata]$ bwa mem reference.fasta JC_1119.R1.fq.gz JC_1119.R2.fq.gz -I 200,40 -t 3 -L 20,5 2>/dev/null | mawk '!/\t[2-9].[SH].*/' | mawk '!/[2-9].[SH]\t/'| samtools view -@16 -q 10 -SbT reference.fasta - | samtools flagstat - > normal.stats
(base) [crandall@KITT realdata]$ paste <(cut -f1 -d + relaxed.stats) <(cut -f1 -d + normal.stats) <(cut -f4-10 -d " " relaxed.stats)
```

Mapping quality of 10 output:

```
2201764 2192629 in total (QC-passed reads + QC-failed reads)
2201764 2192629 primary
0       0       secondary
0       0       supplementary
0       0       duplicates
0       0       primary duplicates
2201764 2192629 mapped (100.00% : N/A)
2201764 2192629 primary mapped (100.00% : N/A)
2201764 2192629 paired in sequencing
1119342 1117075 read1
1082422 1075554 read2
2100814 2089604 properly paired (95.42% : N/A)
2157734 2147053 with itself and mate mapped
44030   45576   singletons (2.00% : N/A)
56754   57277   with mate mapped to a different chr
56754   57277   with mate mapped to a different chr
```