Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/859.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/859.nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_157/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_157_S247_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_157/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_157_S247_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,571,866
Mapped reads	61,047,732 / 93.1%
Unmapped reads	4,524,134 / 6.9%
Mapped paired reads	61,047,732 / 93.1%
Mapped reads, first in pair	30,576,090 / 46.63%
Mapped reads, second in pair	30,471,642 / 46.47%
Mapped reads, both in pair	59,653,916 / 90.97%
Mapped reads, singletons	1,393,816 / 2.13%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	10,181,550 / 15.53%
Clipped reads	13,284,047 / 20.26%

2.2. ACGT Content

Number/percentage of A's	2,618,848,521 / 30.9%
Number/percentage of C's	1,621,204,045 / 19.13%
Number/percentage of T's	2,617,494,265 / 30.88%
Number/percentage of G's	1,618,878,869 / 19.1%
Number/percentage of N's	36,236 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	27.269
Standard Deviation	210.127

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Insert size

Mean	233,740.26
Standard Deviation	2,295,684.13
P25/Median/P75	327 / 427 / 557

2.6. Mismatches and indels

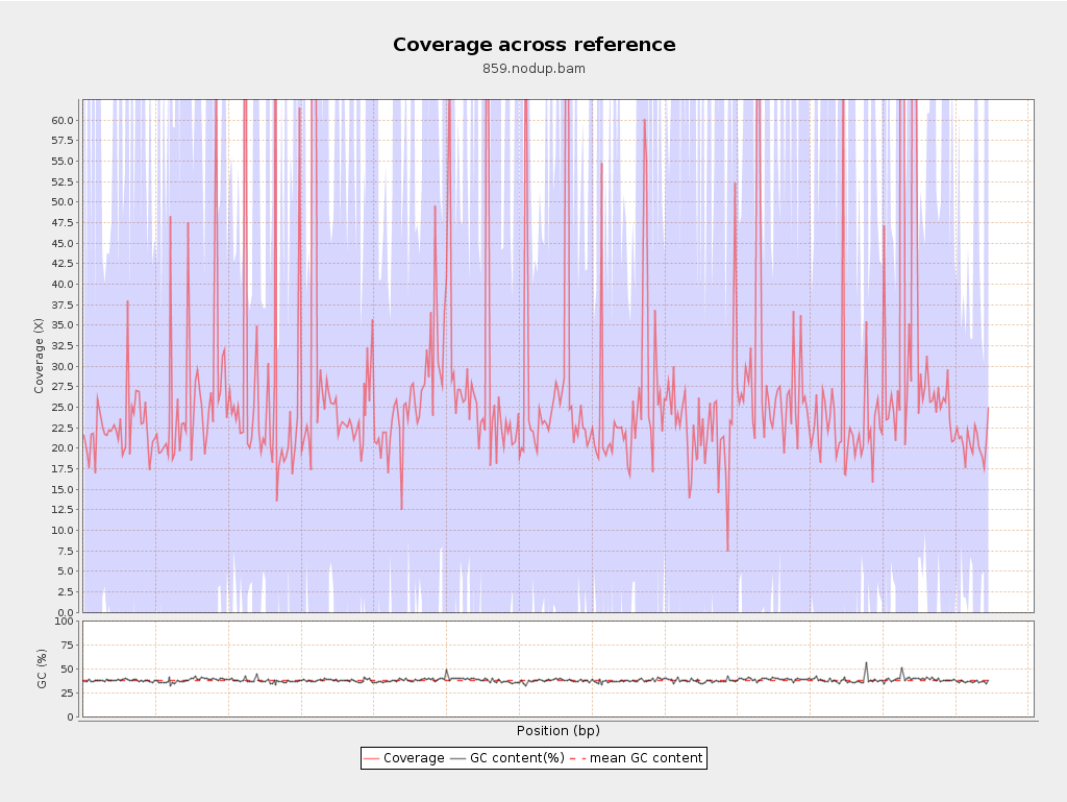
General error rate	2.26%
Mismatches	175,488,794
Insertions	5,686,166
Mapped reads with at least one insertion	8.36%
Deletions	5,743,179
Mapped reads with at least one deletion	8.38%
Homopolymer indels	57.19%

2.7. Chromosome stats

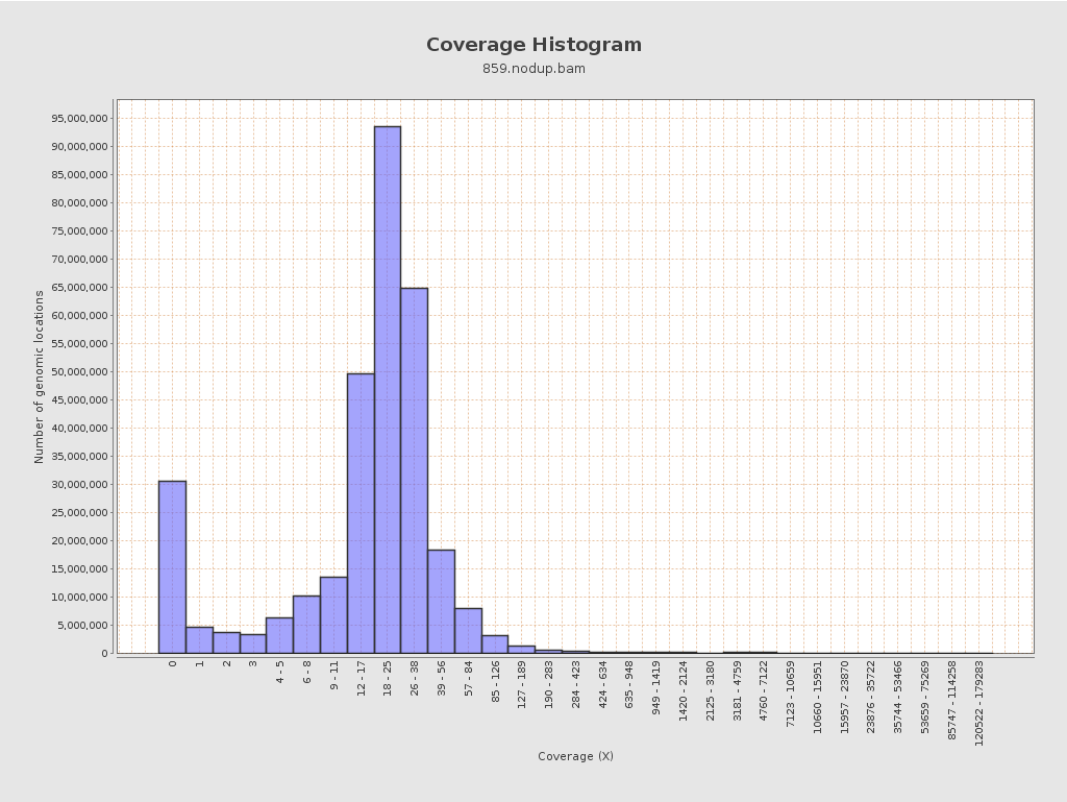
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	659084567	22.1732	61.7977

LT669789.1	36598175	1012299655	27.6598	208.6367
LT669790.1	30422129	893433994	29.3679	227.2428
LT669791.1	52758100	1435739544	27.2136	188.4882
LT669792.1	28376109	769750015	27.1267	281.6876
LT669793.1	33388210	832760319	24.9417	114.9657
LT669794.1	50579949	1337959949	26.4524	172.3484
LT669795.1	49795044	1557148147	31.2711	297.6241

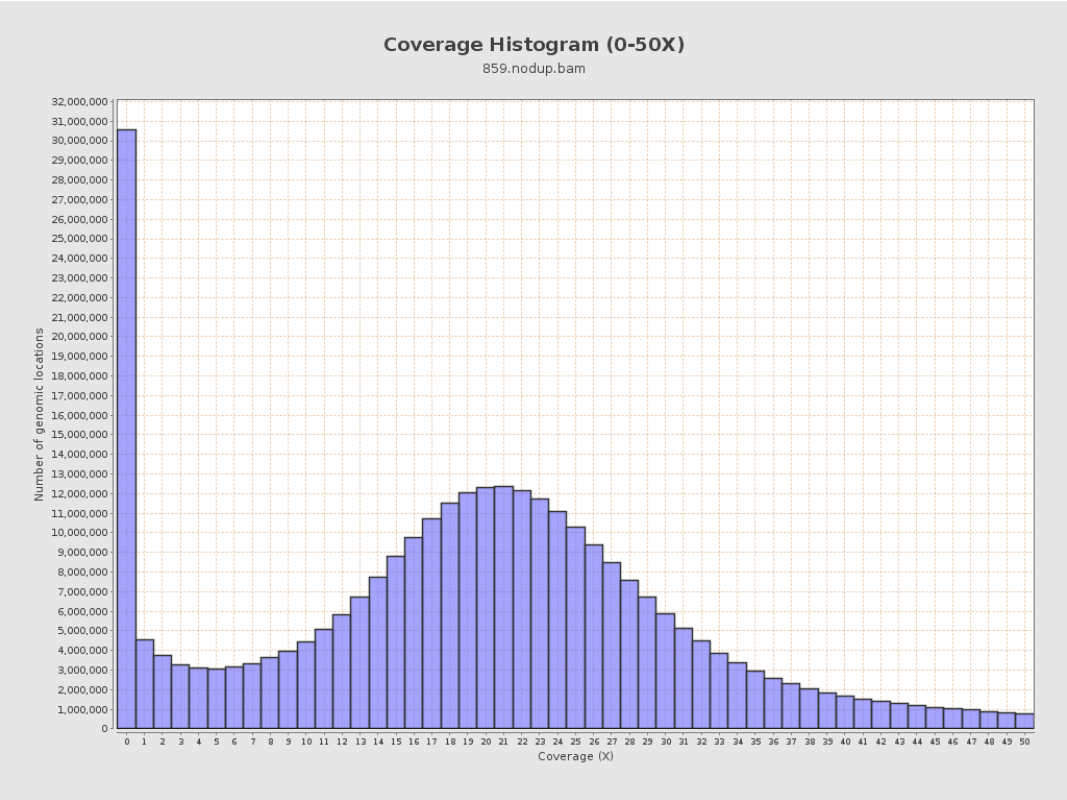
3. Results : Coverage across reference



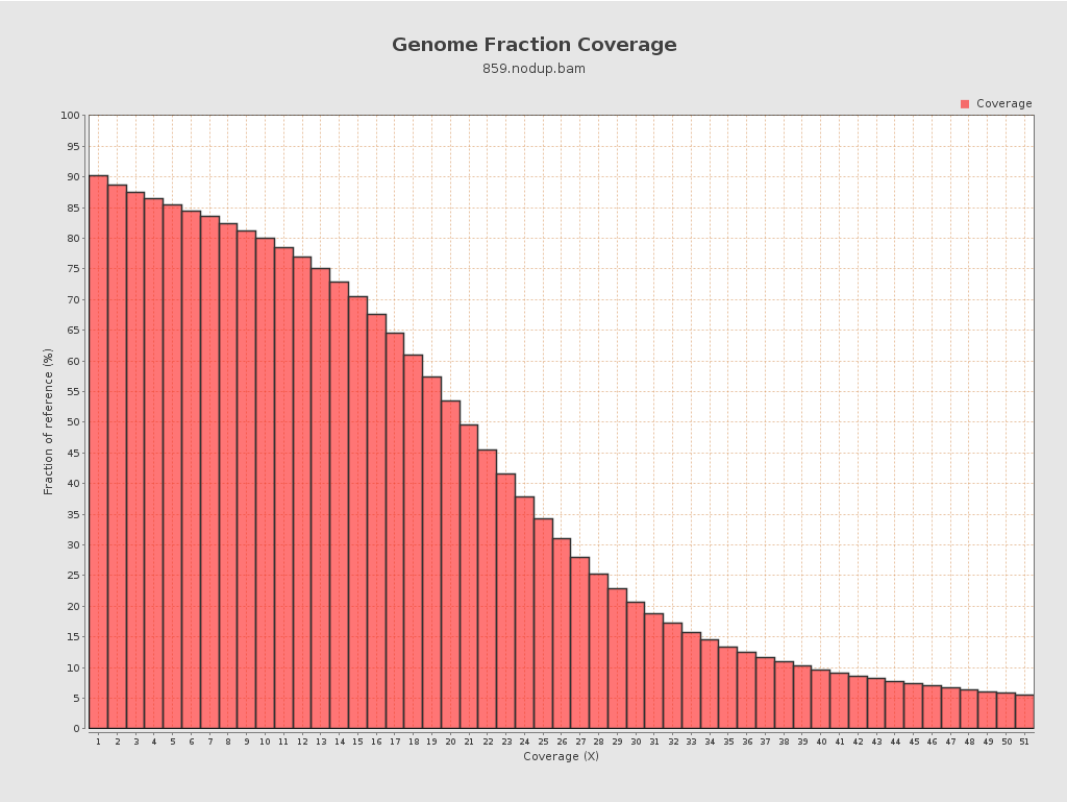
4. Results : Coverage Histogram



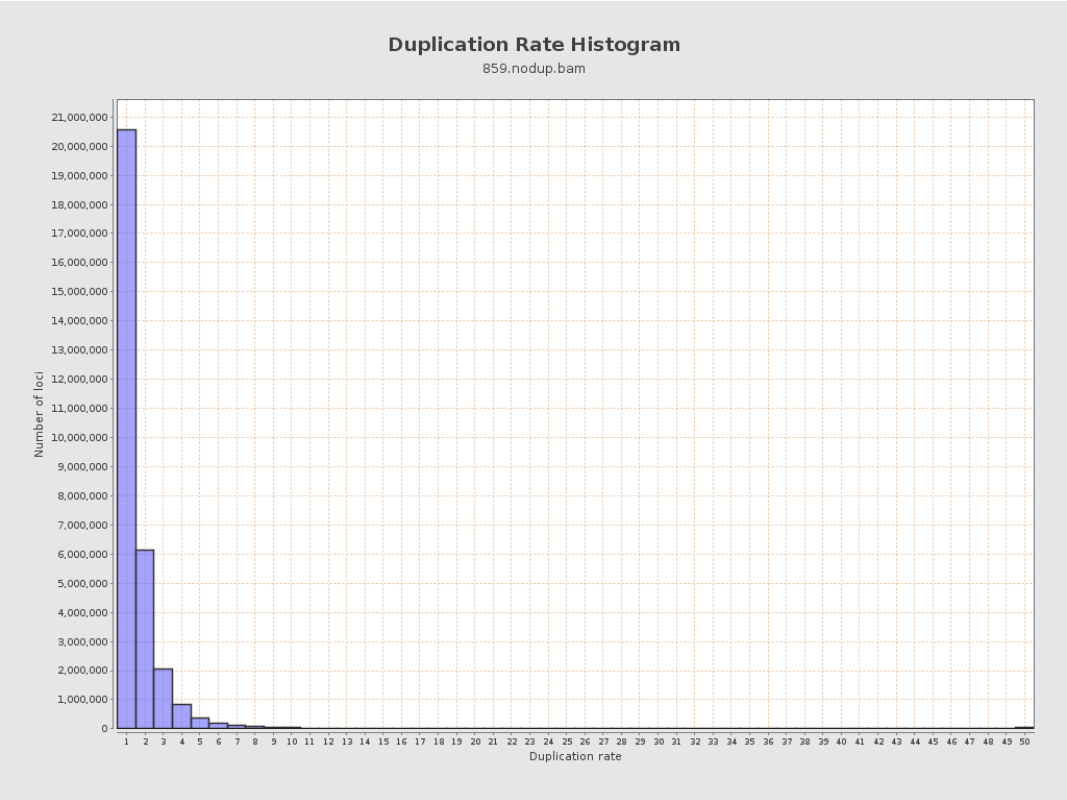
5. Results : Coverage Histogram (0-50X)



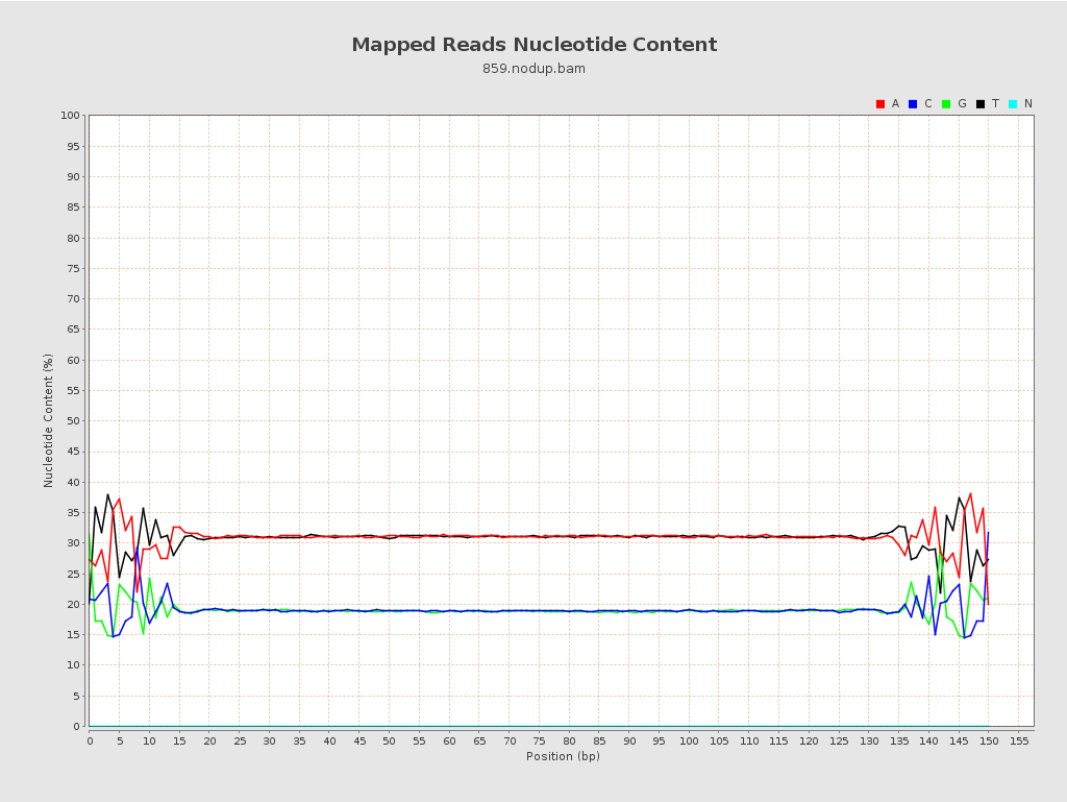
6. Results : Genome Fraction Coverage



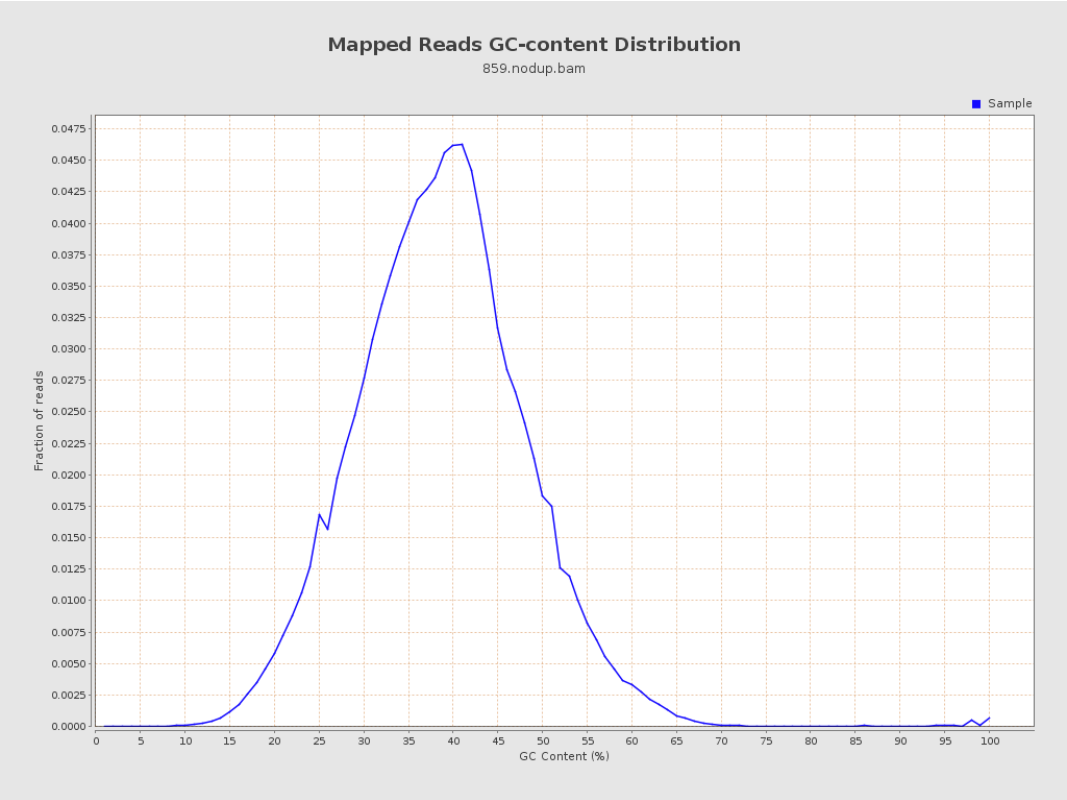
7. Results : Duplication Rate Histogram



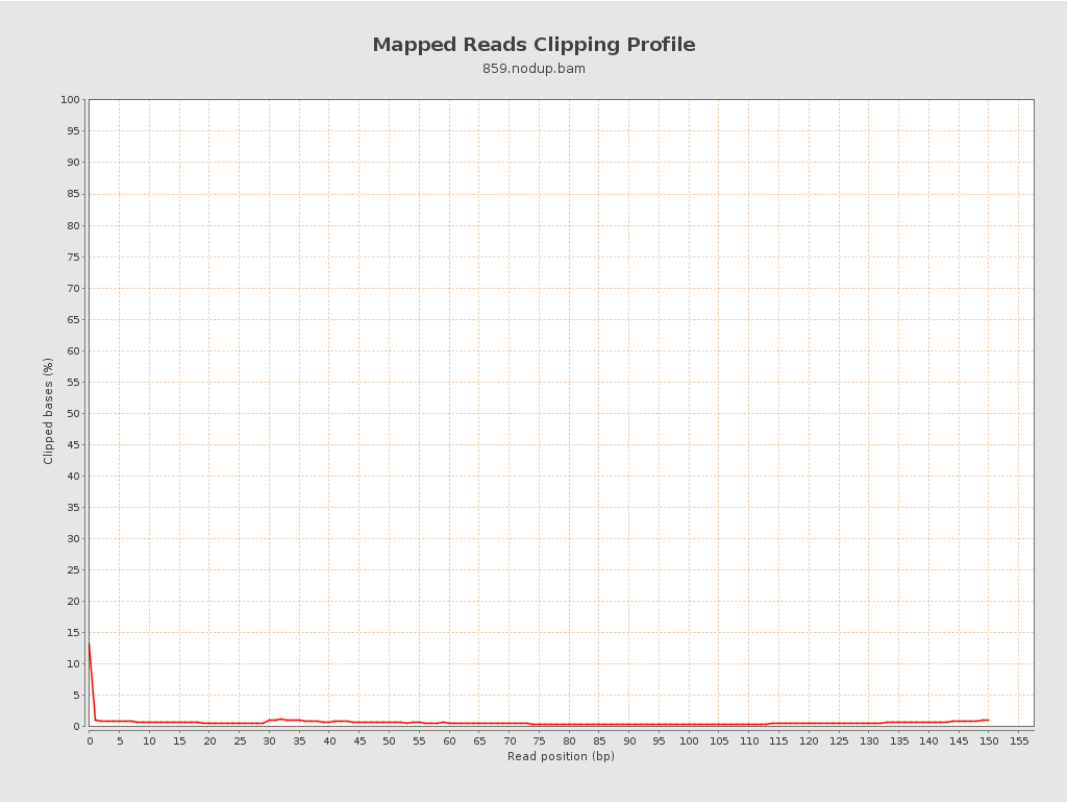
8. Results : Mapped Reads Nucleotide Content



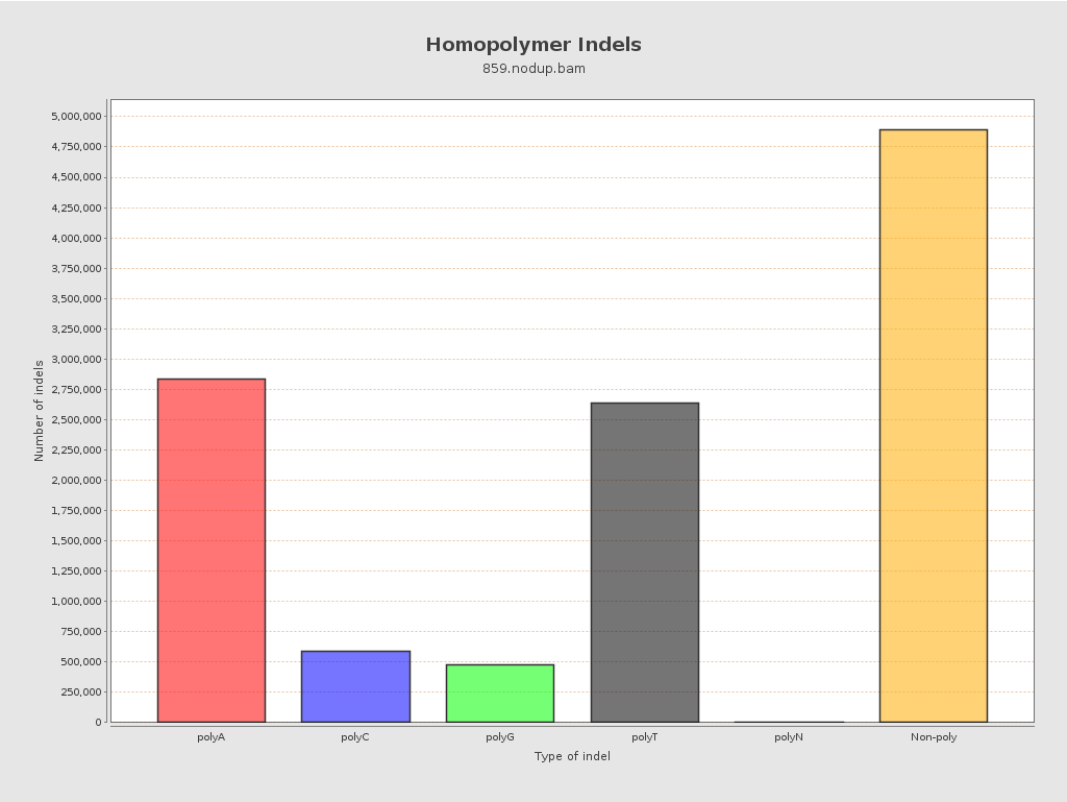
9. Results : Mapped Reads GC-content Distribution



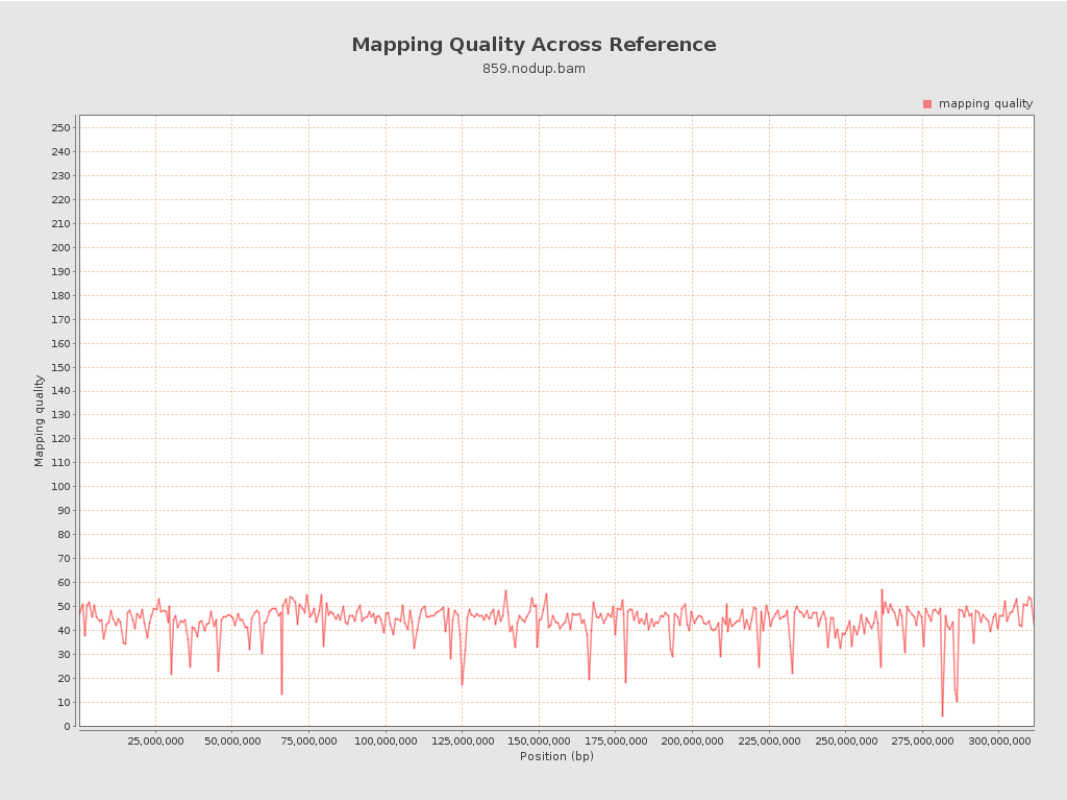
10. Results : Mapped Reads Clipping Profile



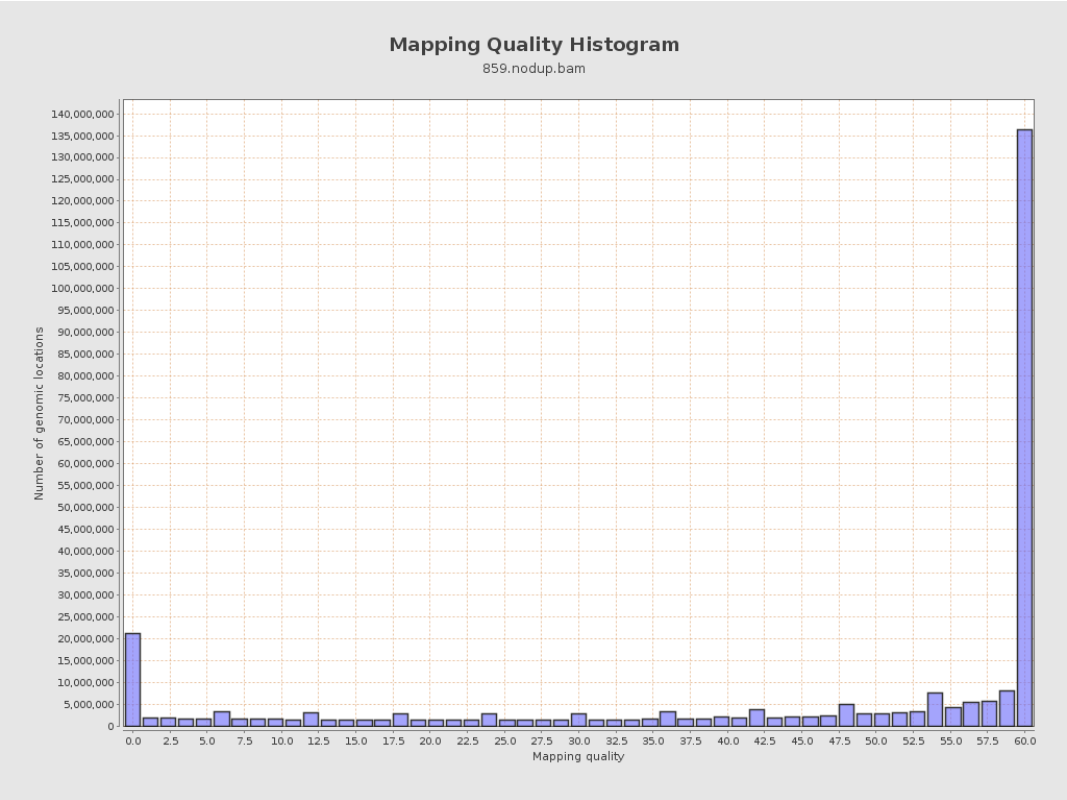
11. Results : Homopolymer Indels



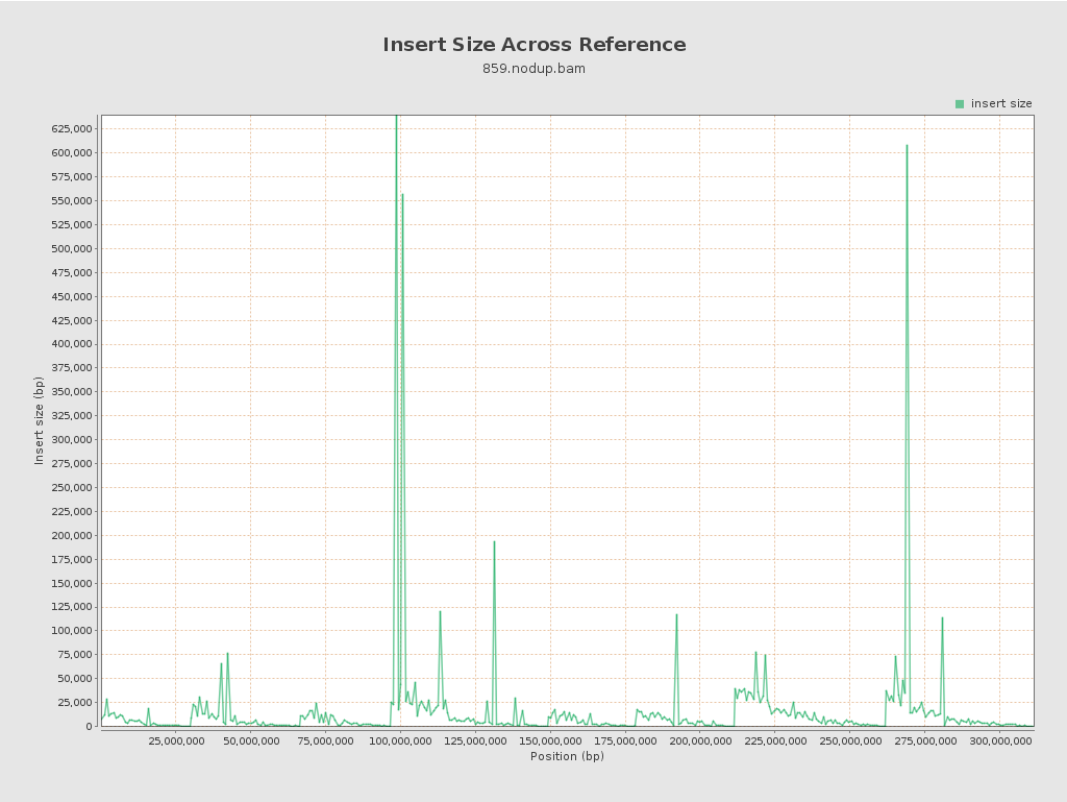
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram