

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/858
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/858 .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/awdata/P26207/P26207_248/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_248_S329_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_248/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_248_S329_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,066,811
Mapped reads	62,586,422 / 91.95%
Unmapped reads	5,480,389 / 8.05%
Mapped paired reads	62,586,422 / 91.95%
Mapped reads, first in pair	31,360,713 / 46.07%
Mapped reads, second in pair	31,225,709 / 45.88%
Mapped reads, both in pair	60,871,359 / 89.43%
Mapped reads, singletons	1,715,063 / 2.52%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	9,439,041 / 13.87%
Clipped reads	14,506,778 / 21.31%

2.2. ACGT Content

Number/percentage of A's	2,663,843,003 / 30.95%
Number/percentage of C's	1,638,940,456 / 19.04%
Number/percentage of T's	2,666,273,545 / 30.97%
Number/percentage of G's	1,639,196,361 / 19.04%
Number/percentage of N's	32,658 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	27.6924
Standard Deviation	238.4267

2.4. Mapping Quality

Mean Mapping Quality	44.64
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2.5. Insert size

Mean	247,919.43
Standard Deviation	2,401,052.2
P25/Median/P75	323 / 426 / 554

2.6. Mismatches and indels

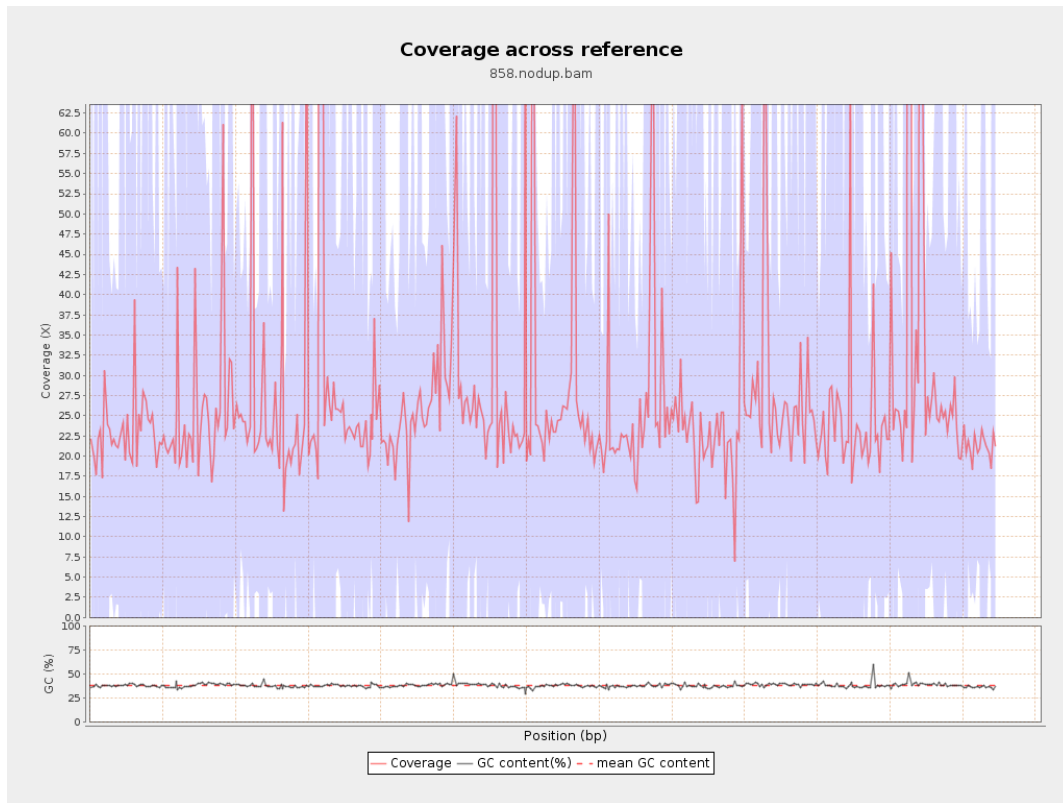
General error rate	2.25%
Mismatches	176,917,958
Insertions	5,949,247
Mapped reads with at least one insertion	8.49%
Deletions	5,774,096
Mapped reads with at least one deletion	8.21%
Homopolymer indels	57.57%

2.7. Chromosome stats

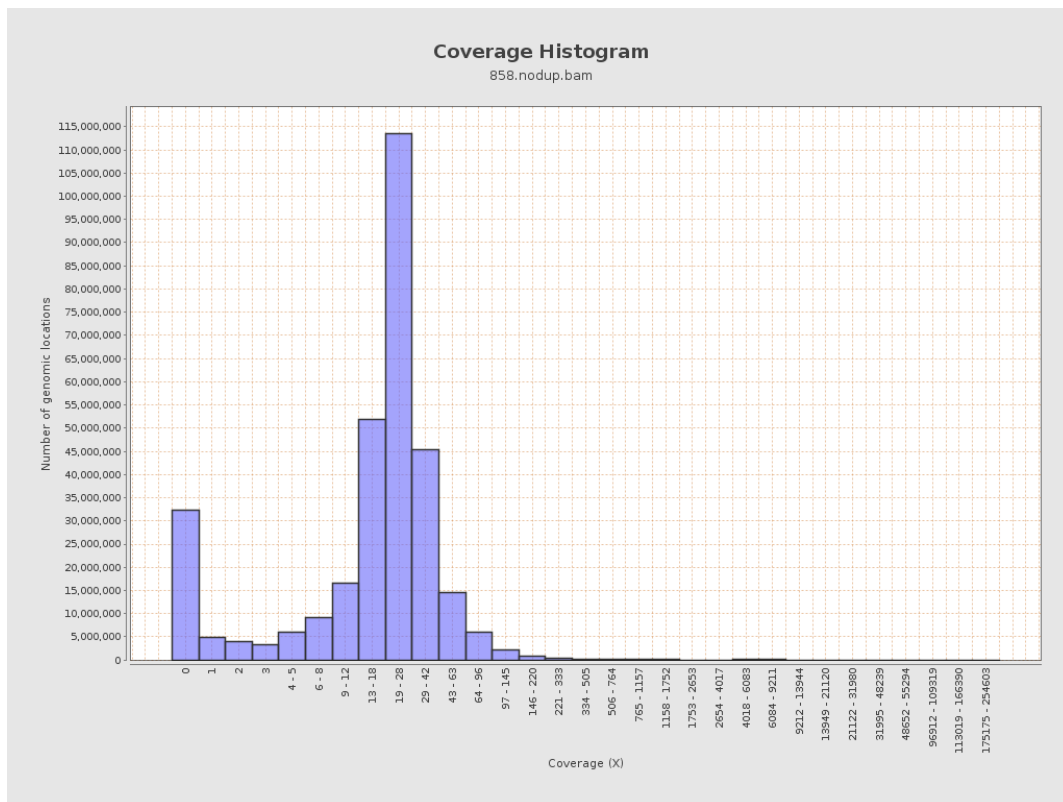
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	674820116	22.7026	85.7379

LT669789.1	36598175	987736164	26.9887	232.3301
LT669790.1	30422129	974201172	32.0228	310.7006
LT669791.1	52758100	1457818517	27.6321	243.6314
LT669792.1	28376109	784054386	27.6308	234.5367
LT669793.1	33388210	849046914	25.4295	162.7427
LT669794.1	50579949	1325237220	26.2008	178.2659
LT669795.1	49795044	1577200277	31.6738	329.2715

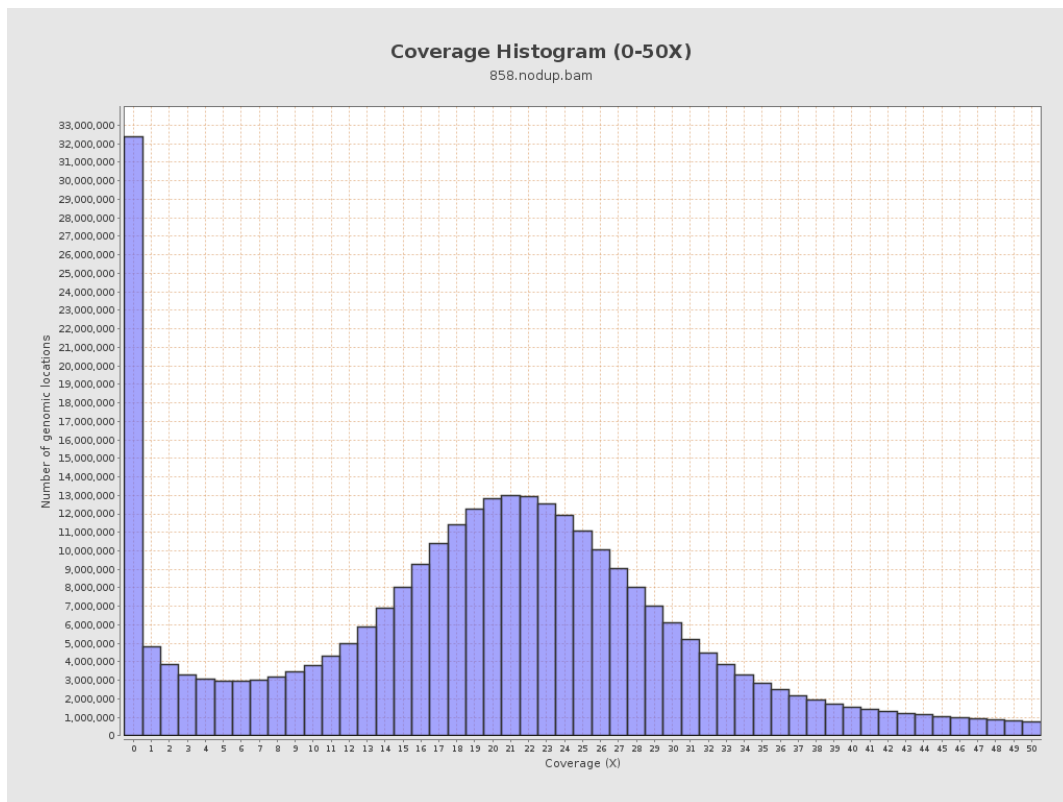
3. Results : Coverage across reference



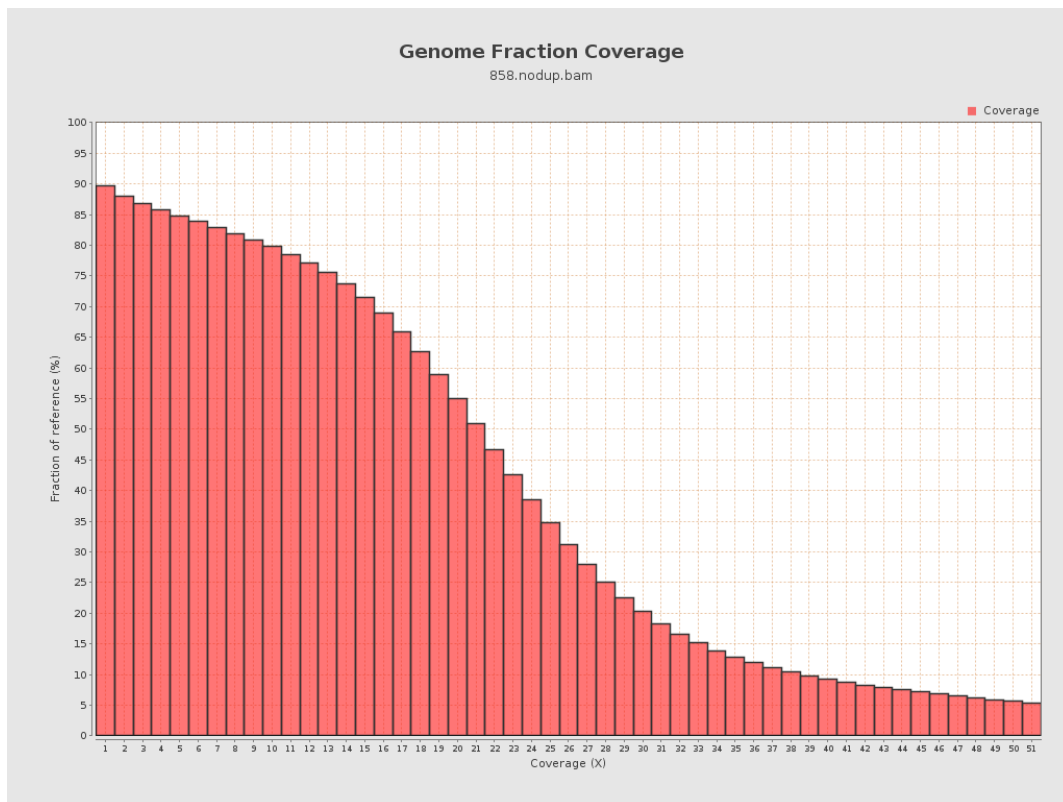
4. Results : Coverage Histogram



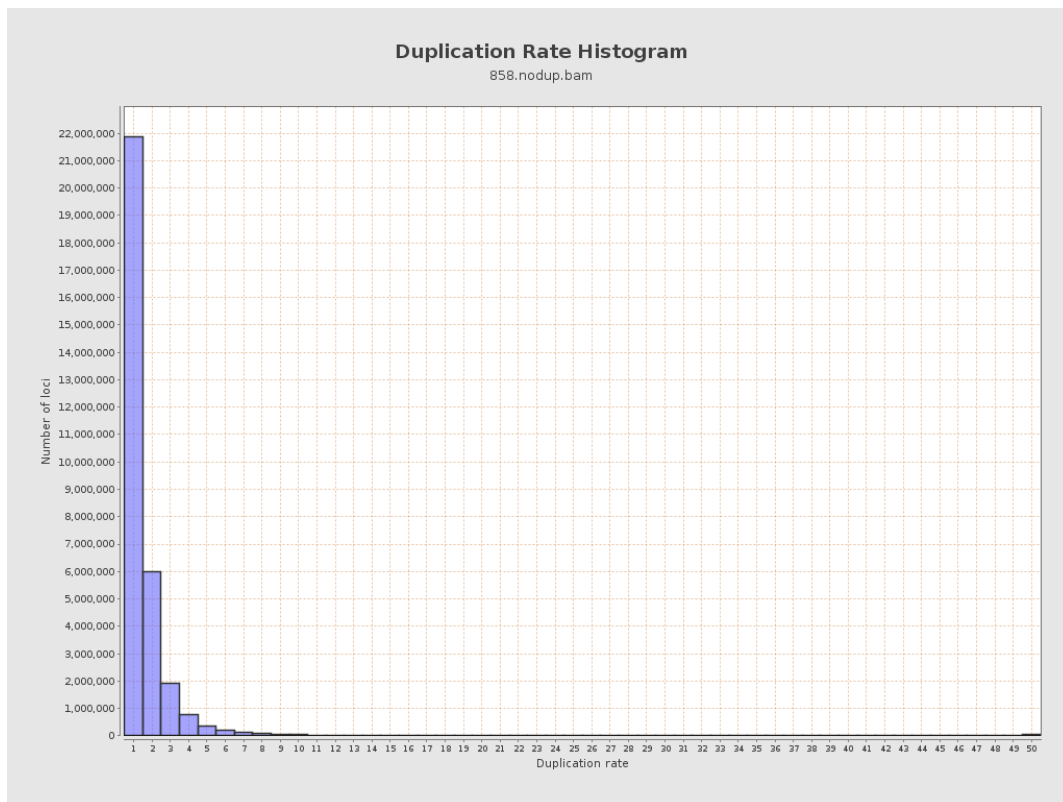
5. Results : Coverage Histogram (0-50X)



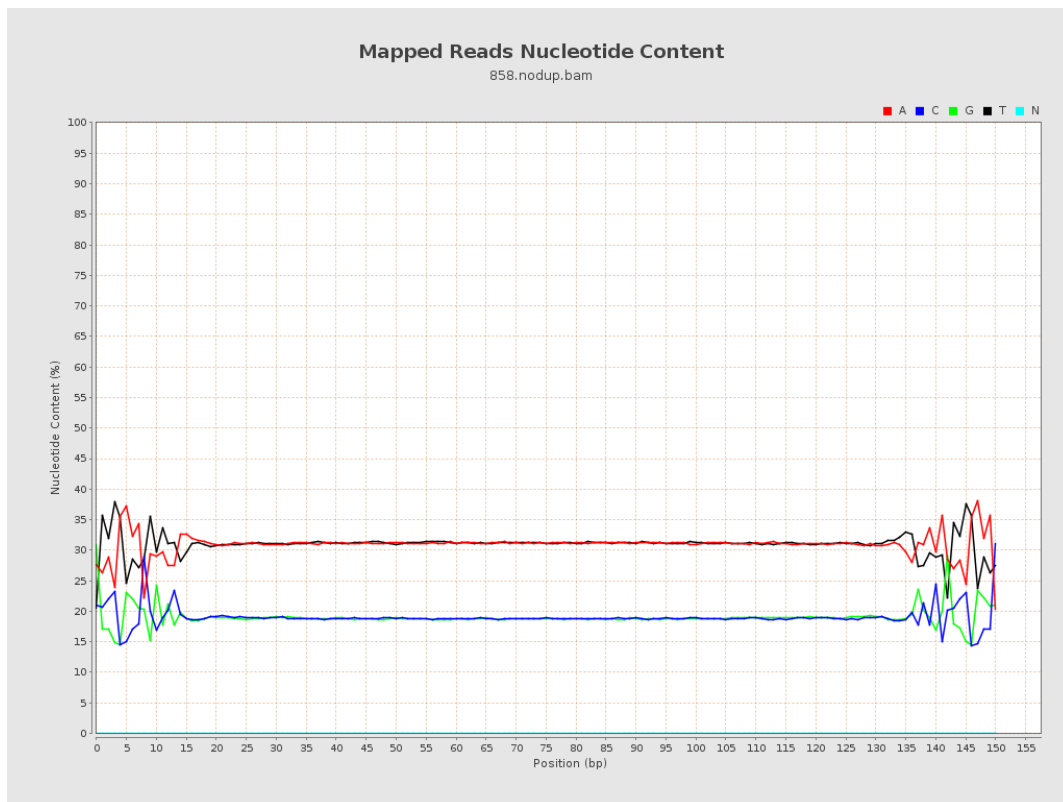
6. Results : Genome Fraction Coverage



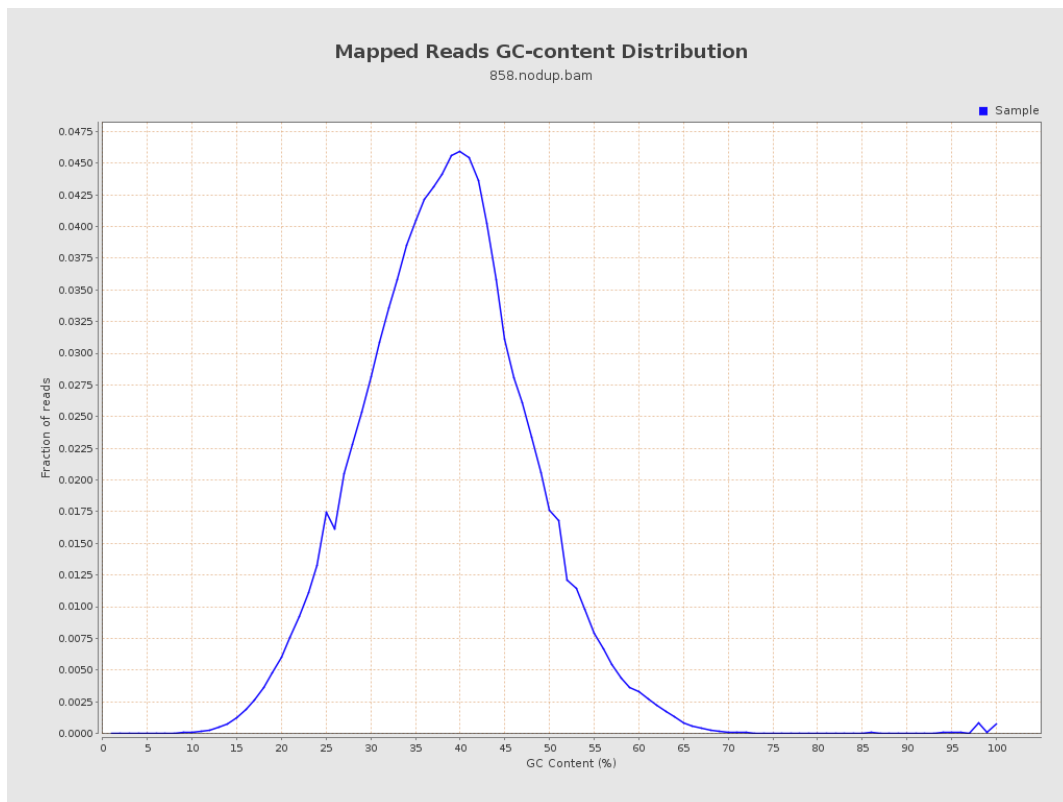
7. Results : Duplication Rate Histogram



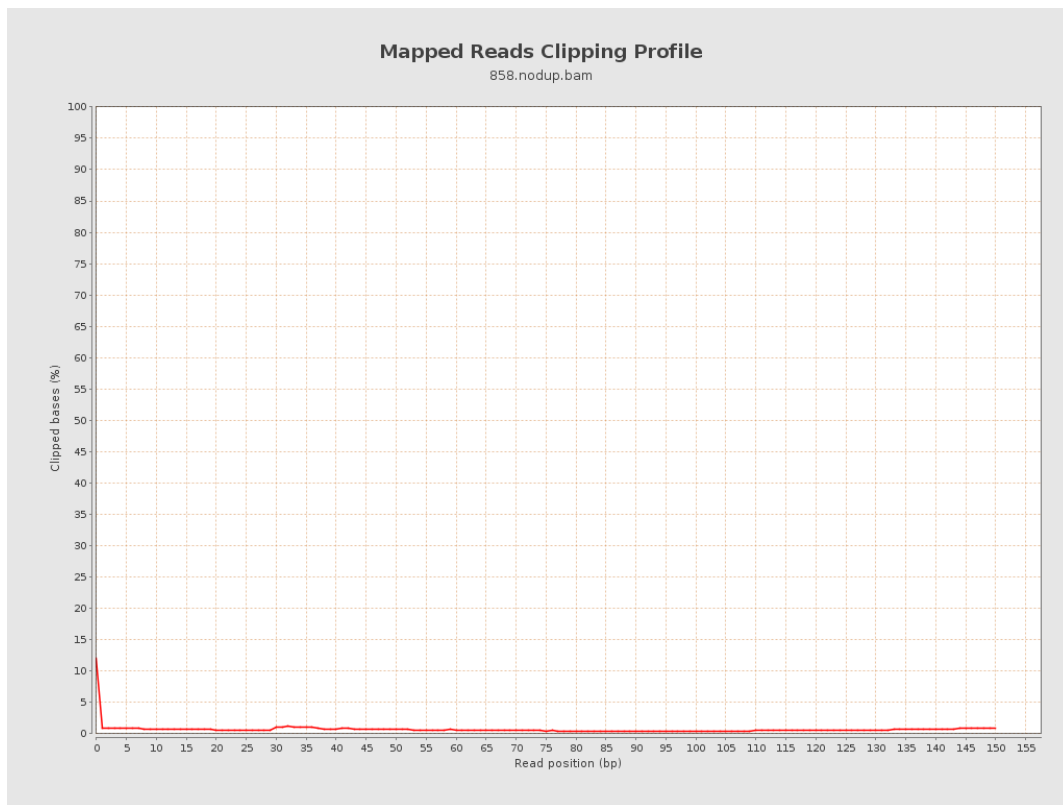
8. Results : Mapped Reads Nucleotide Content



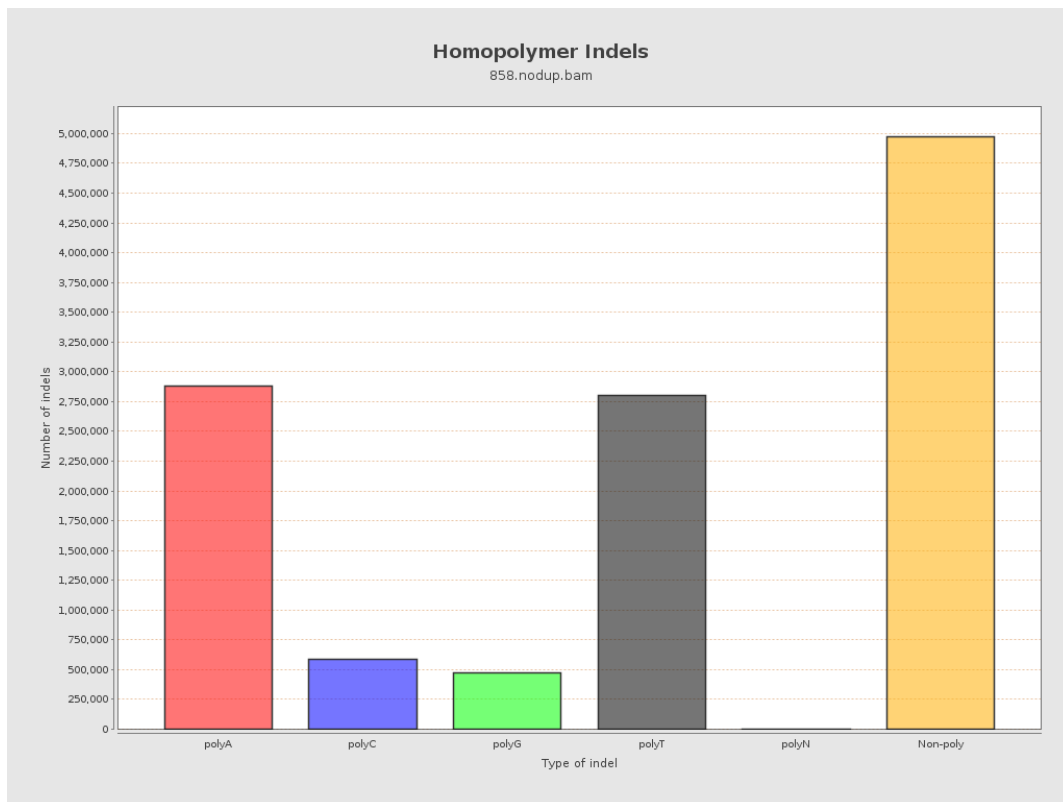
9. Results : Mapped Reads GC-content Distribution



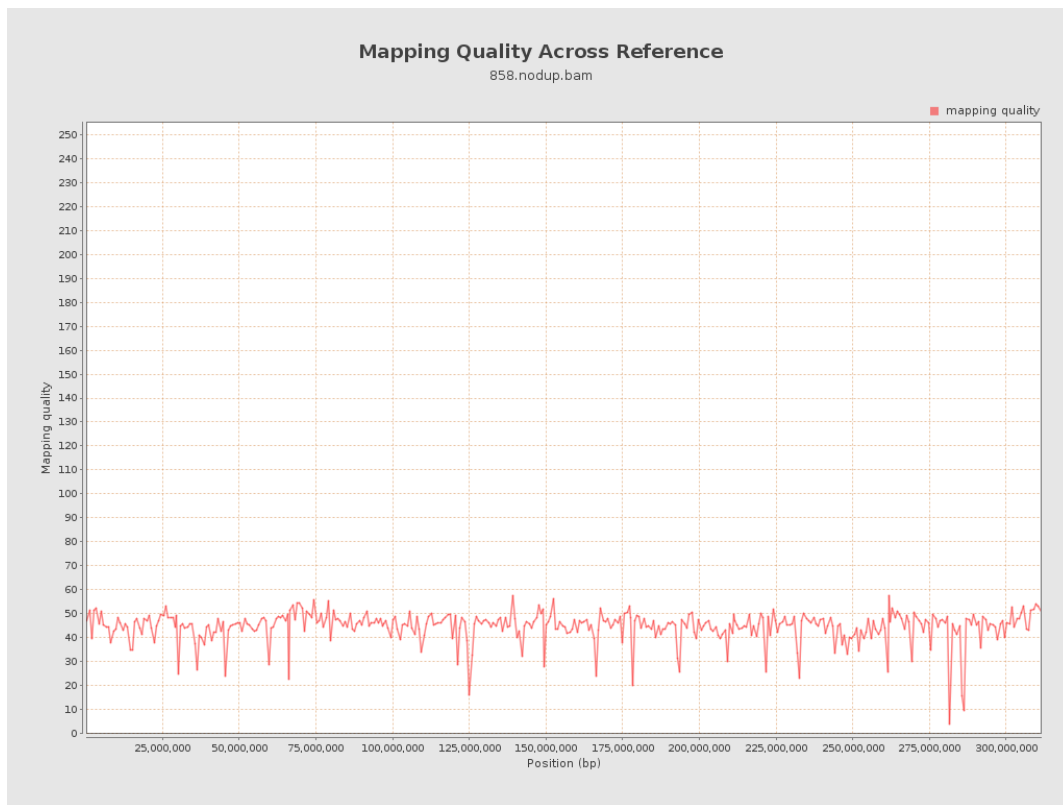
10. Results : Mapped Reads Clipping Profile



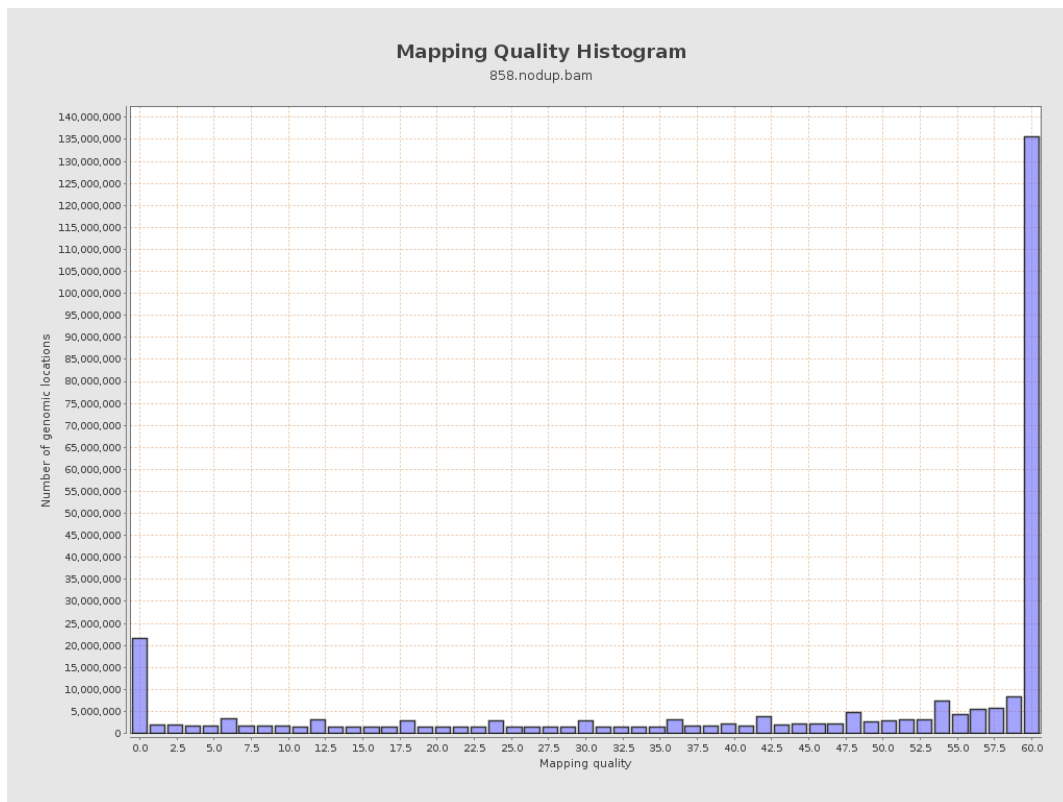
11. Results : Homopolymer Indels



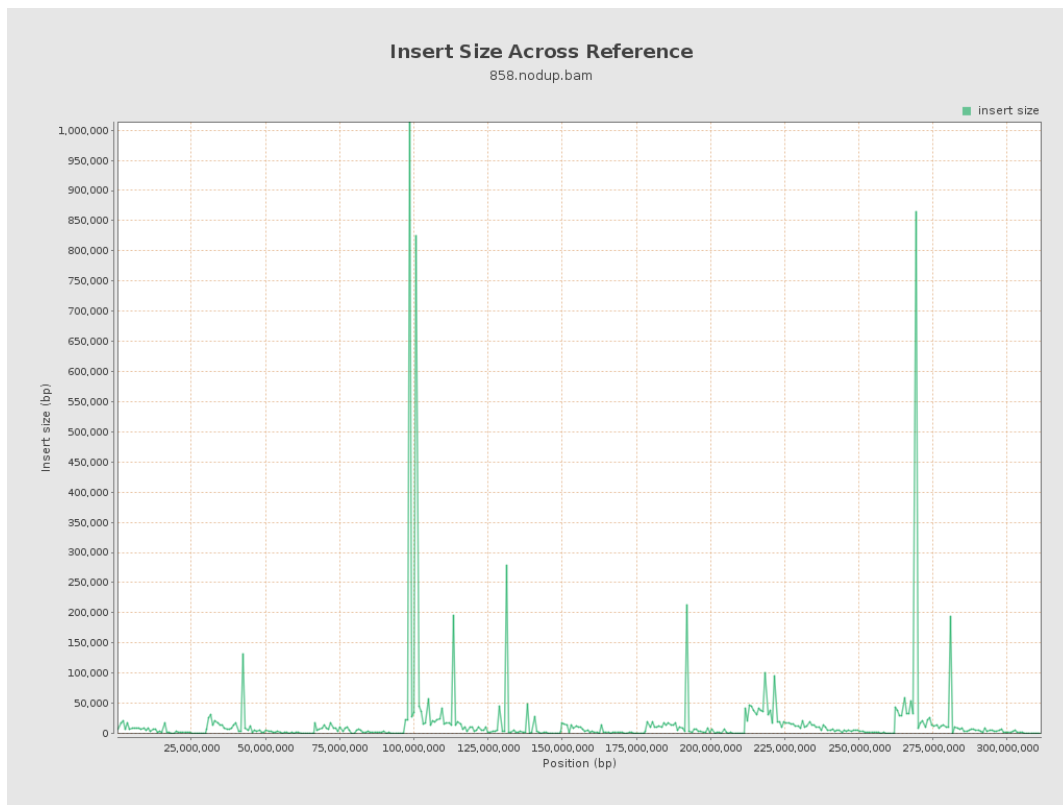
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

