Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1442
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1442 .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_145/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_145_S235_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_145/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_145_S235_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:19 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,278,311
Mapped reads	74,098,287 / 92.3%
Unmapped reads	6,180,024 / 7.7%
Mapped paired reads	74,098,287 / 92.3%
Mapped reads, first in pair	37,126,356 / 46.25%
Mapped reads, second in pair	36,971,931 / 46.05%
Mapped reads, both in pair	72,238,554 / 89.99%
Mapped reads, singletons	1,859,733 / 2.32%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	13,152,385 / 16.38%
Clipped reads	16,847,483 / 20.99%

2.2. ACGT Content

Number/percentage of A's	3,164,676,111 / 30.91%
Number/percentage of C's	1,954,300,722 / 19.09%
Number/percentage of T's	3,170,279,455 / 30.96%
Number/percentage of G's	1,949,608,487 / 19.04%
Number/percentage of N's	42,095 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	32.94
Standard Deviation	274.5124

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Insert size

Mean	235,967.31
Standard Deviation	2,324,706.17
P25/Median/P75	314 / 412 / 542

2.6. Mismatches and indels

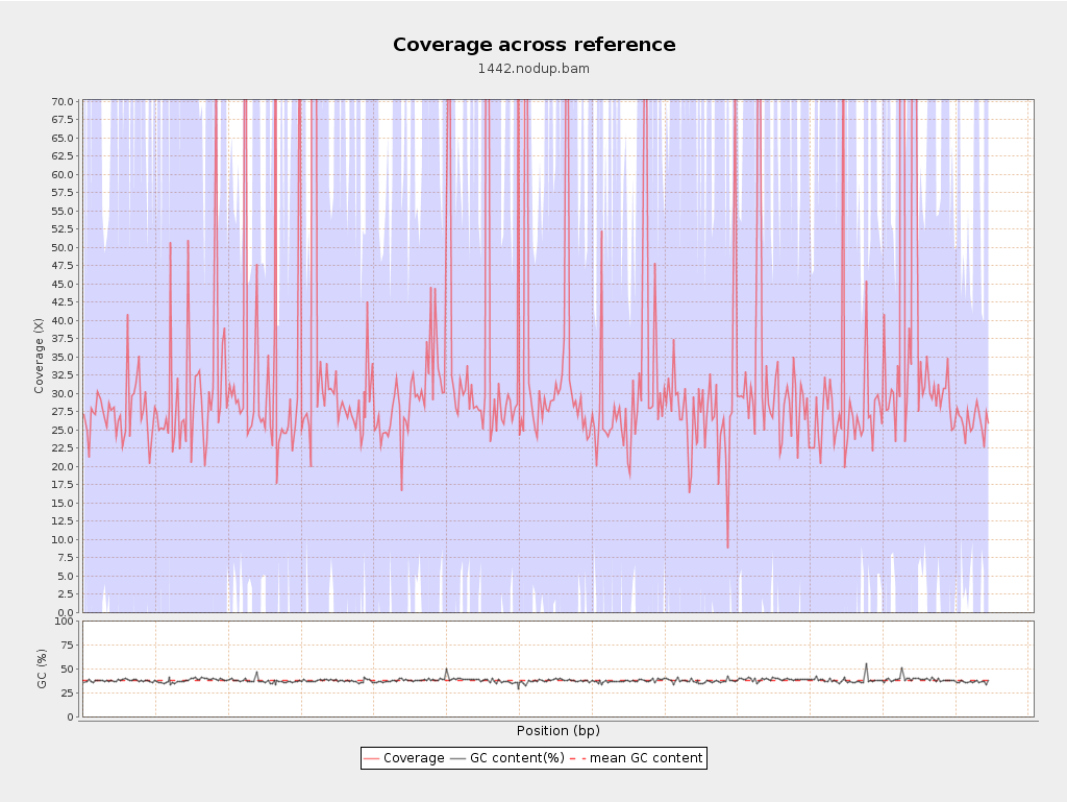
General error rate	2.35%
Mismatches	221,018,793
Insertions	7,068,283
Mapped reads with at least one insertion	8.53%
Deletions	7,043,212
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.97%

2.7. Chromosome stats

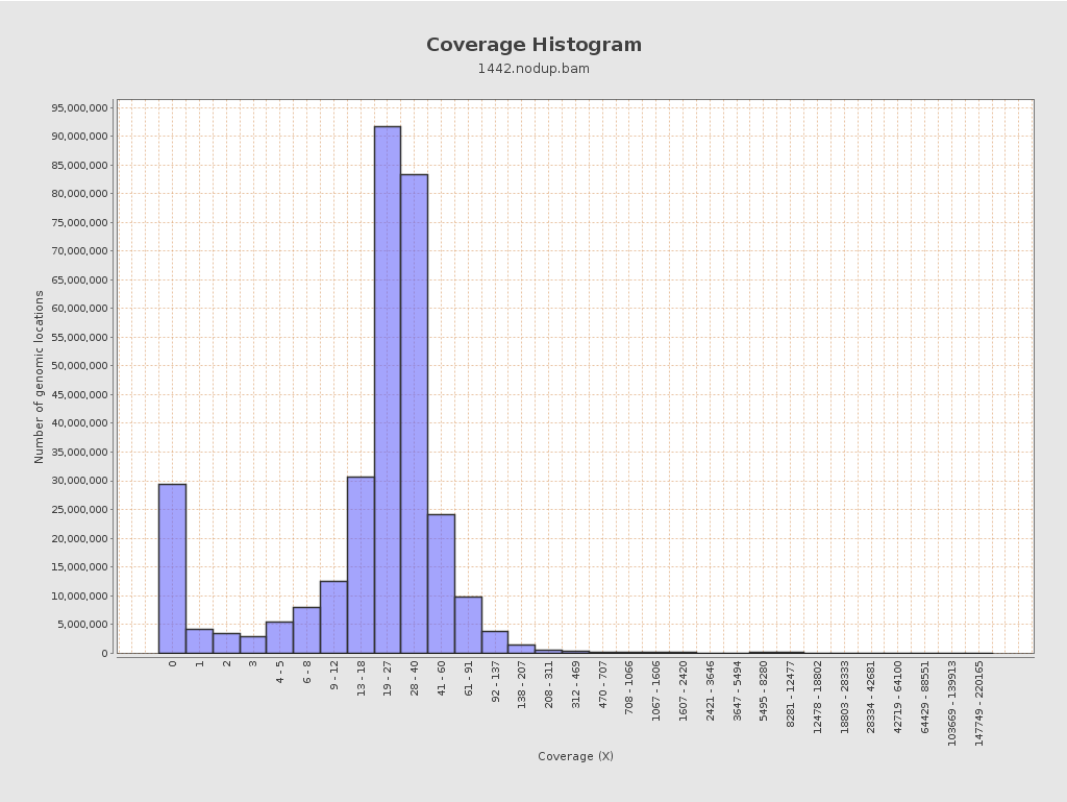
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	807691084	27.1727	94.4331

LT669789.1	36598175	1184122745	32.3547	274.3867
LT669790.1	30422129	1139484499	37.4558	333.4456
LT669791.1	52758100	1709849300	32.4092	261.5903
LT669792.1	28376109	934610807	32.9365	273.0922
LT669793.1	33388210	1004736707	30.0926	176.2684
LT669794.1	50579949	1546855023	30.5824	220.8814
LT669795.1	49795044	1938140576	38.9224	396.9428

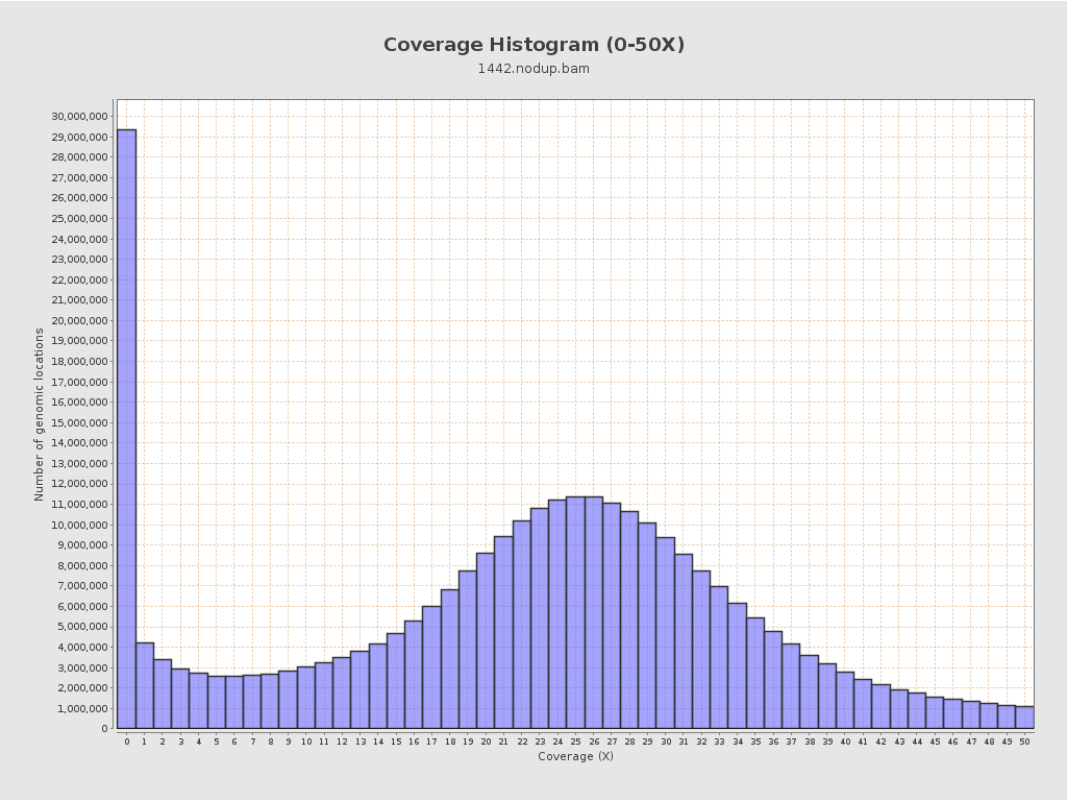
3. Results : Coverage across reference



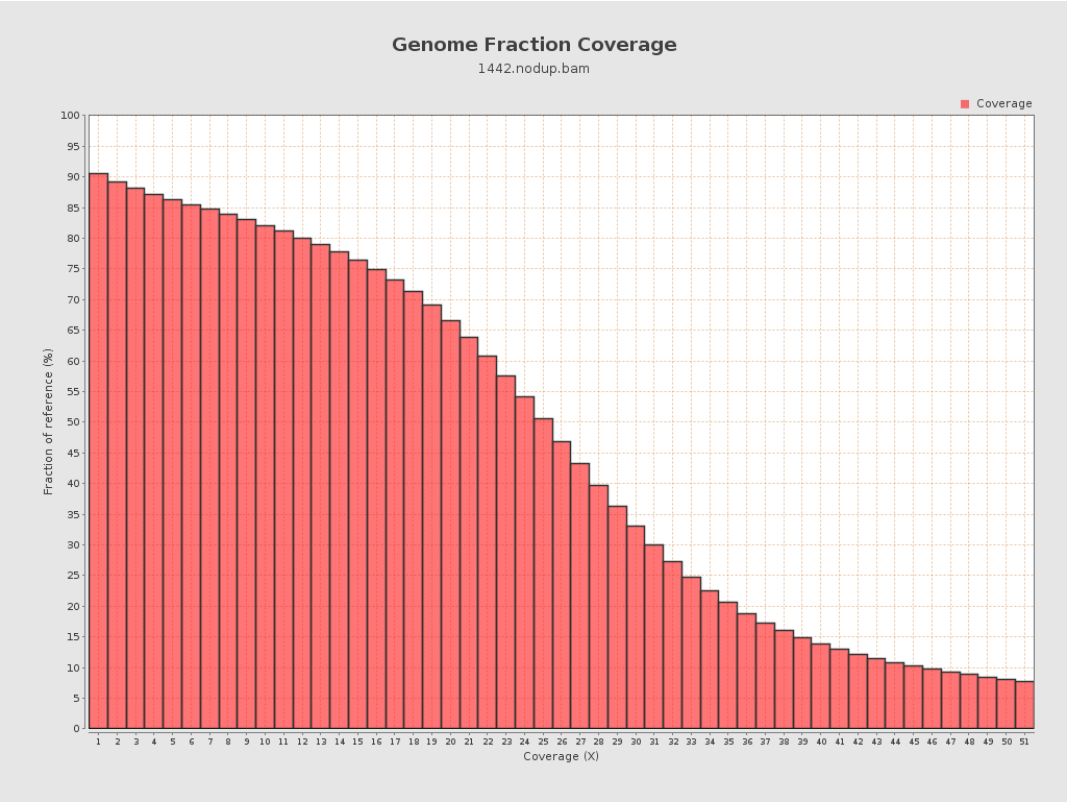
4. Results : Coverage Histogram



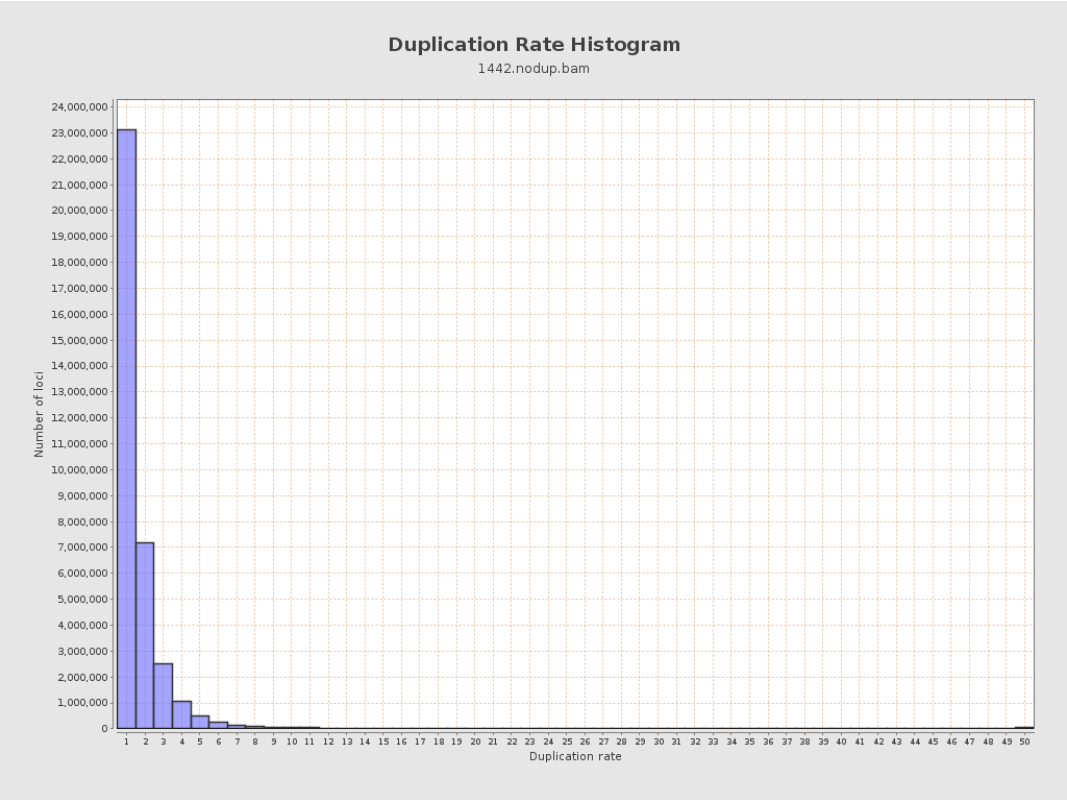
5. Results : Coverage Histogram (0-50X)



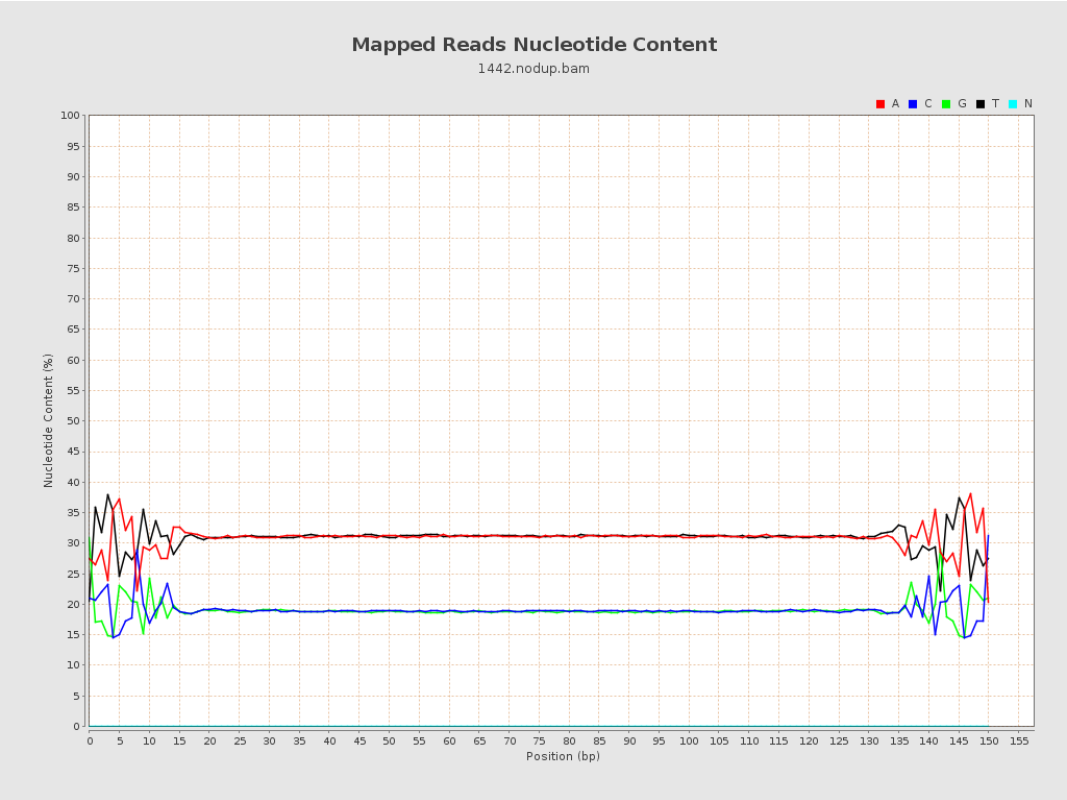
6. Results : Genome Fraction Coverage



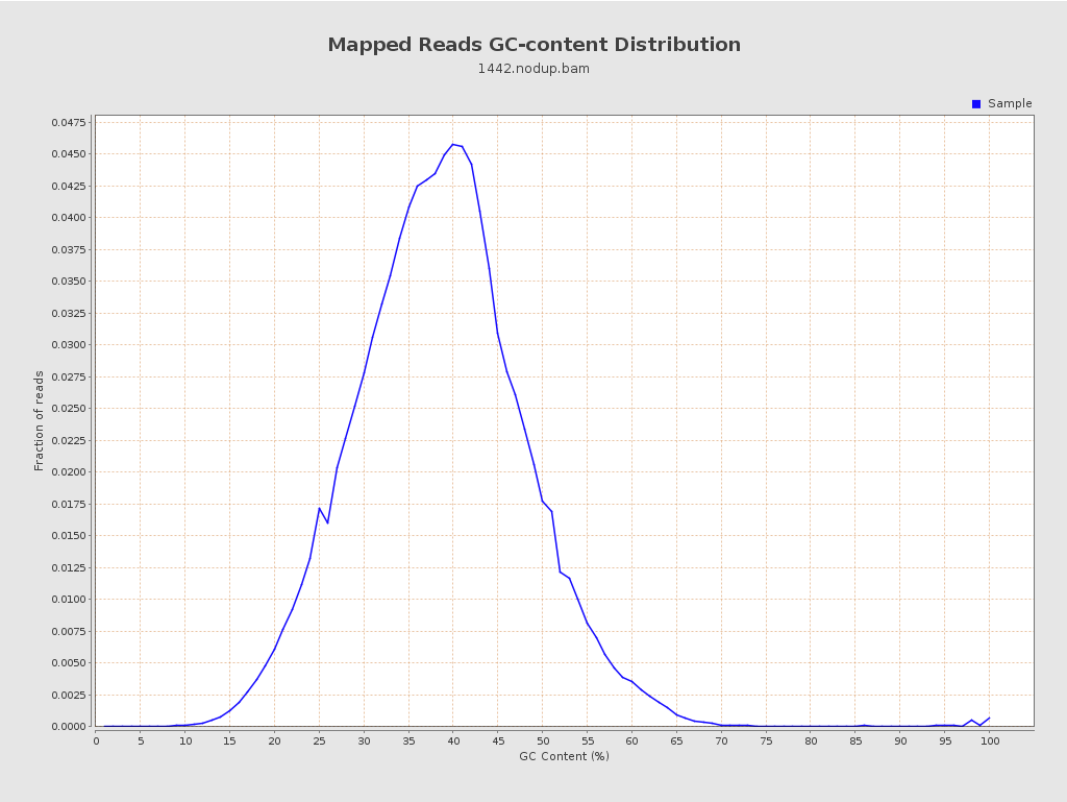
7. Results : Duplication Rate Histogram



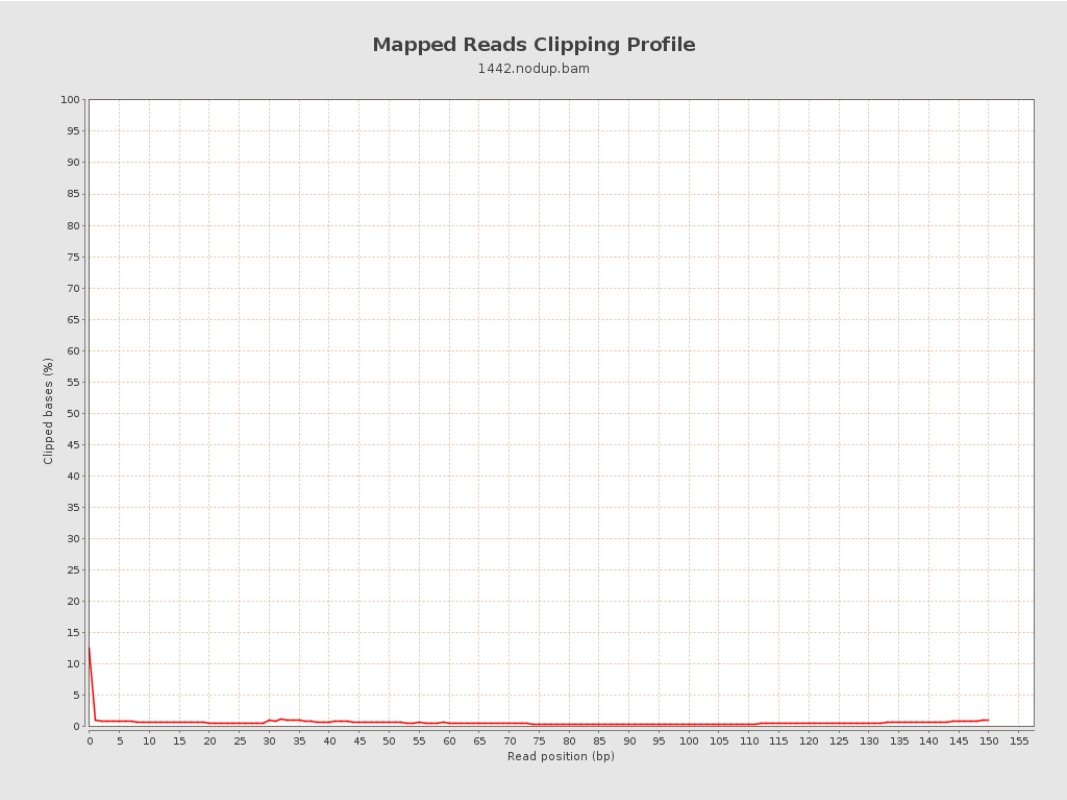
8. Results : Mapped Reads Nucleotide Content



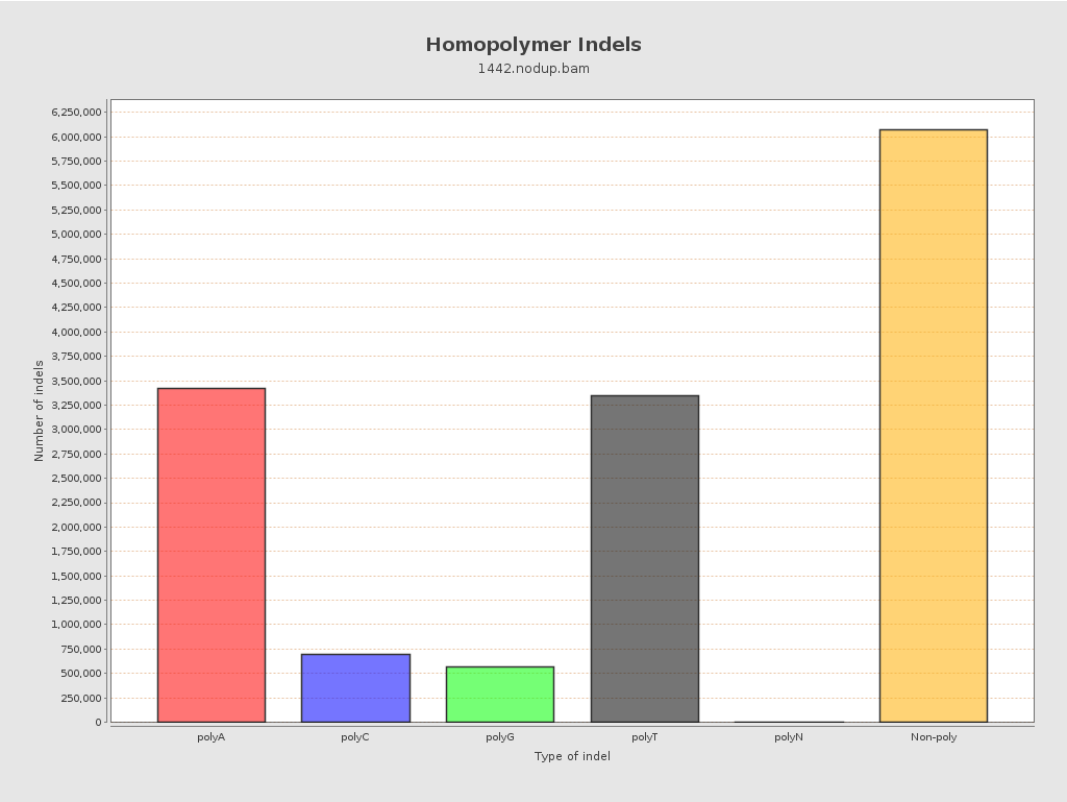
9. Results : Mapped Reads GC-content Distribution



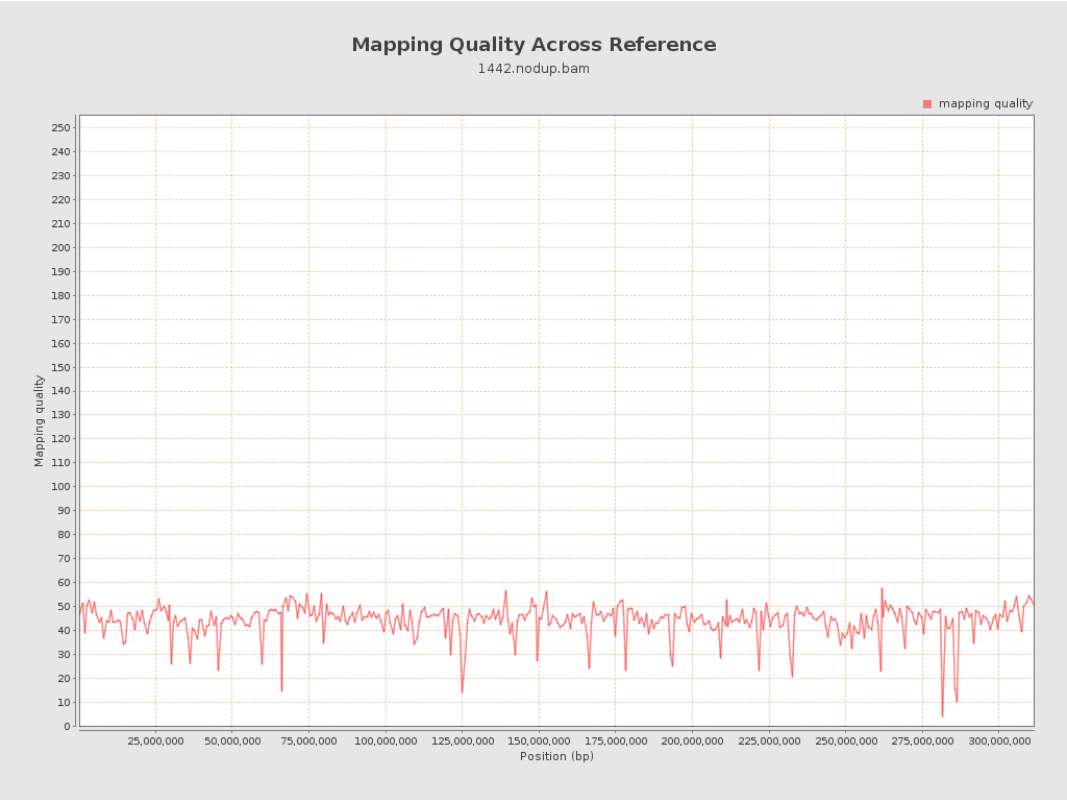
10. Results : Mapped Reads Clipping Profile



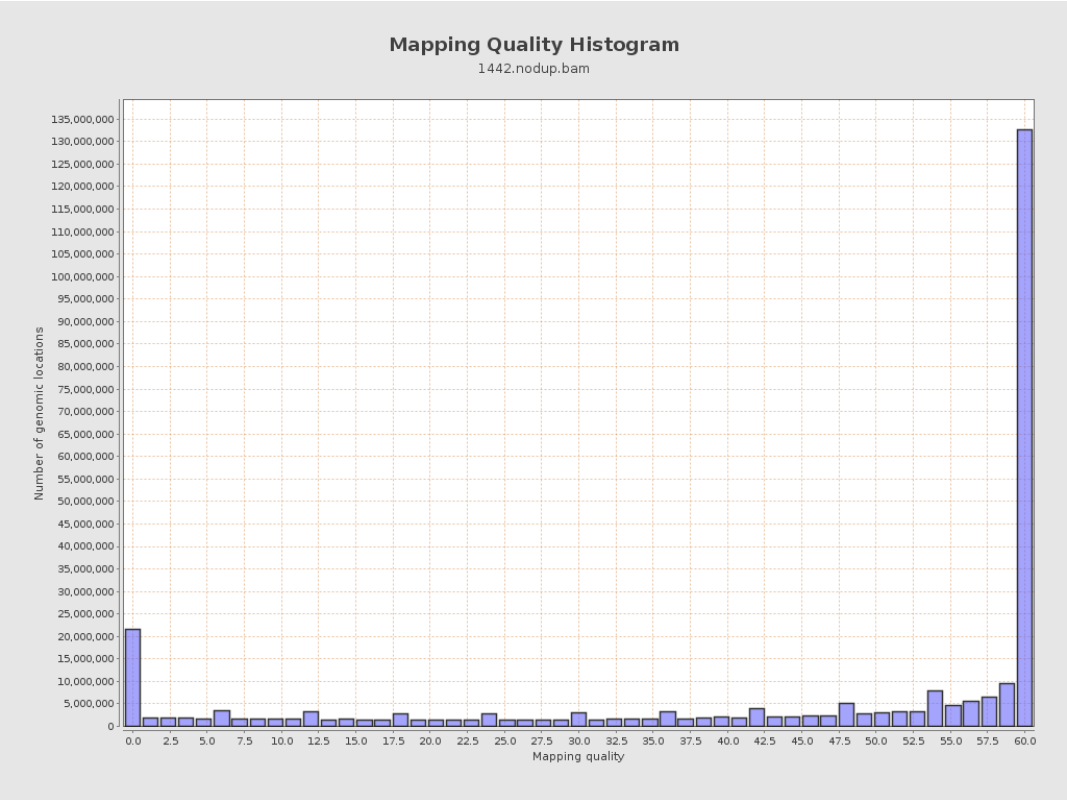
11. Results : Homopolymer Indels



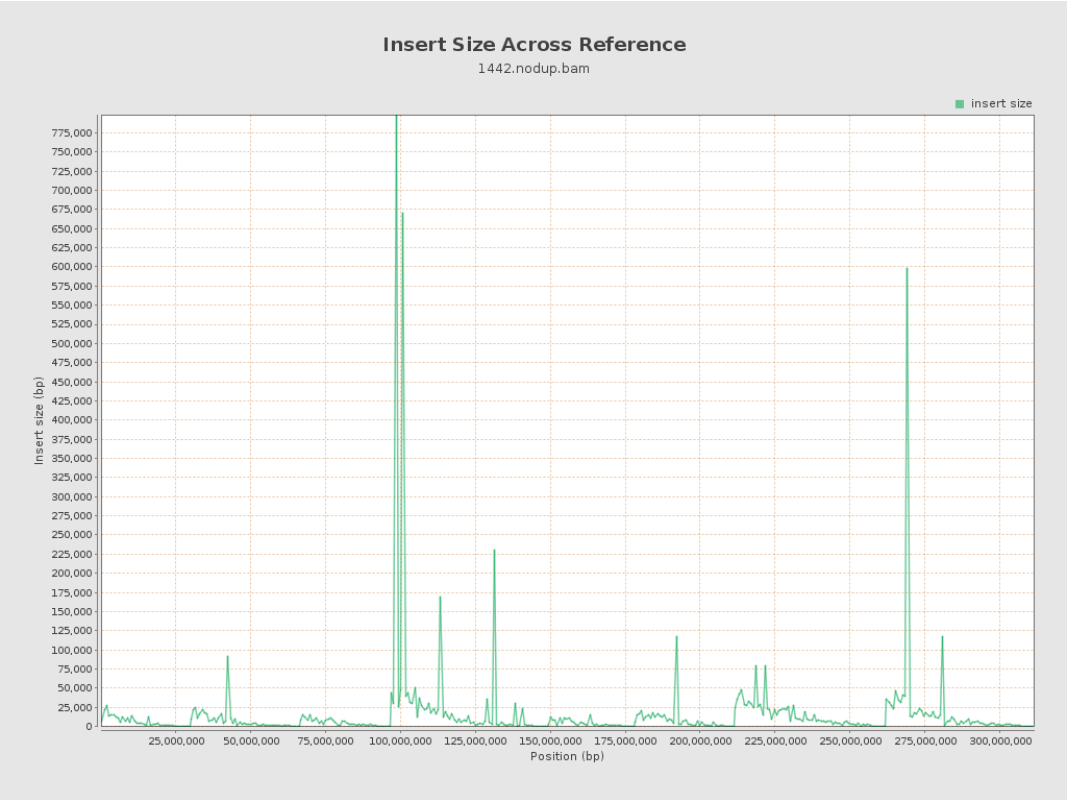
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram