

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/502
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/502.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_411/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_411_S386_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_411/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_411_S386_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:36 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,134,722
Mapped reads	75,324,367 / 95.18%
Unmapped reads	3,810,355 / 4.82%
Mapped paired reads	75,324,367 / 95.18%
Mapped reads, first in pair	37,755,798 / 47.71%
Mapped reads, second in pair	37,568,569 / 47.47%
Mapped reads, both in pair	73,971,626 / 93.48%
Mapped reads, singletons	1,352,741 / 1.71%
Read min/max/mean length	30 / 151 / 148.12
Duplicated reads (flagged)	12,348,940 / 15.6%
Clipped reads	16,373,033 / 20.69%

2.2. ACGT Content

Number/percentage of A's	3,235,469,748 / 30.82%
Number/percentage of C's	2,015,535,537 / 19.2%
Number/percentage of T's	3,234,564,398 / 30.82%
Number/percentage of G's	2,010,709,247 / 19.16%
Number/percentage of N's	35,827 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	33.7687
Standard Deviation	252.0718

2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Insert size

Mean	232,269.56
Standard Deviation	2,272,136.38
P25/Median/P75	344 / 451 / 593

2.6. Mismatches and indels

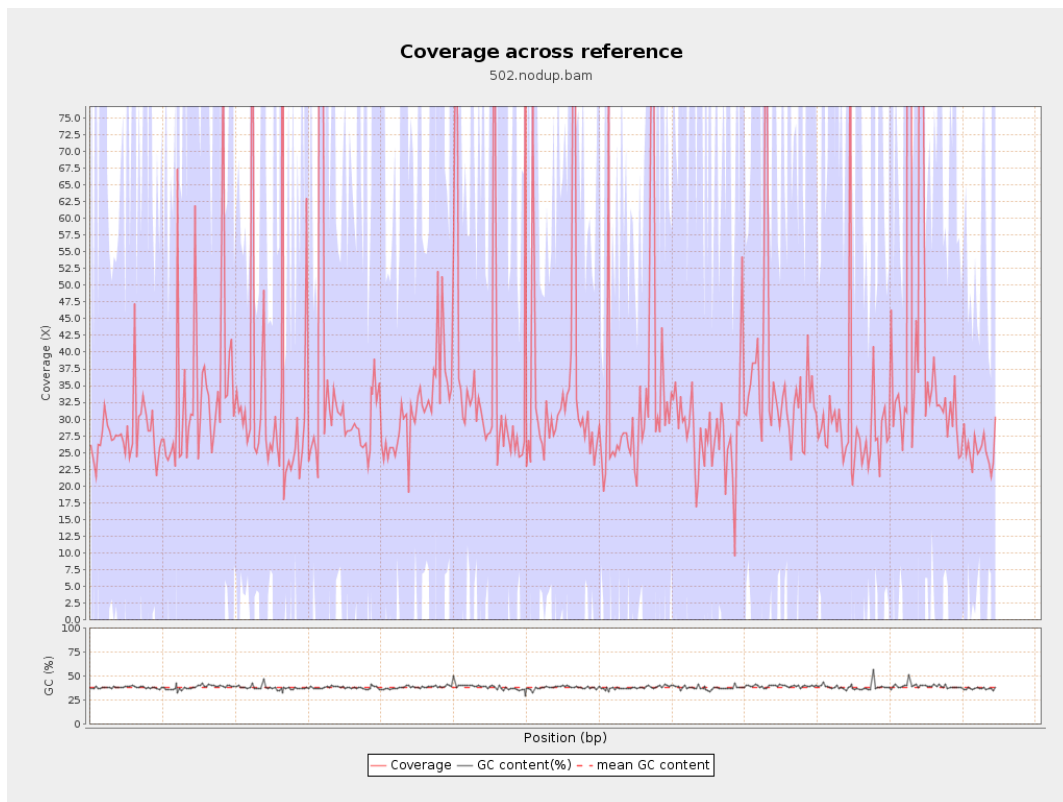
General error rate	2.32%
Mismatches	225,073,449
Insertions	6,891,398
Mapped reads with at least one insertion	8.24%
Deletions	7,254,832
Mapped reads with at least one deletion	8.58%
Homopolymer indels	56.41%

2.7. Chromosome stats

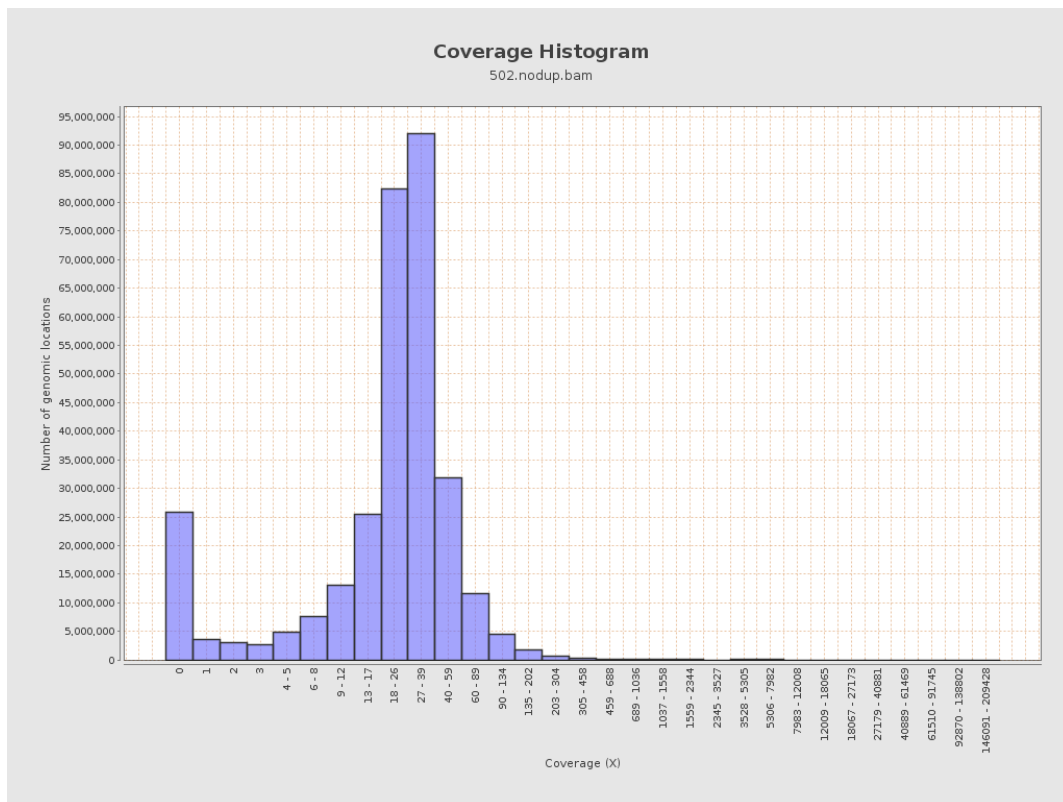
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	814896398	27.4151	69.9755

LT669789.1	36598175	1290163094	35.2521	275.857
LT669790.1	30422129	1047664910	34.4376	240.7115
LT669791.1	52758100	1757880810	33.3196	205.394
LT669792.1	28376109	933296899	32.8902	273.0521
LT669793.1	33388210	1071507492	32.0924	196.3422
LT669794.1	50579949	1662988192	32.8784	245.1671
LT669795.1	49795044	1945347913	39.0671	359.5412

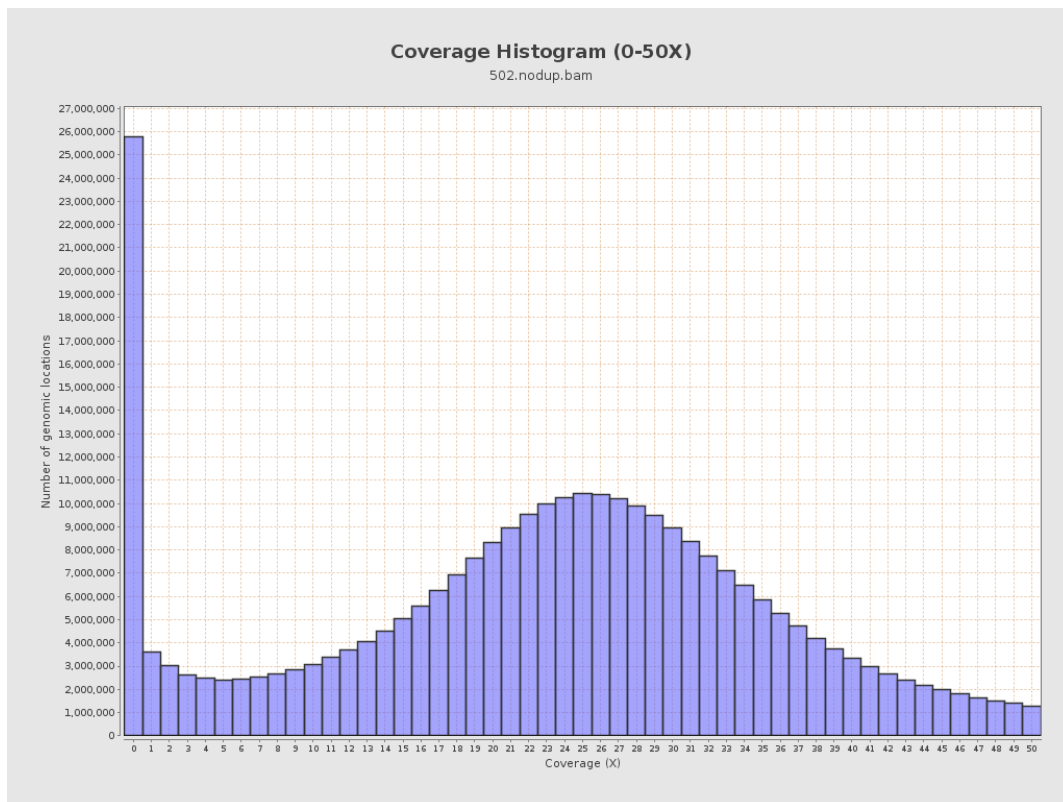
3. Results : Coverage across reference



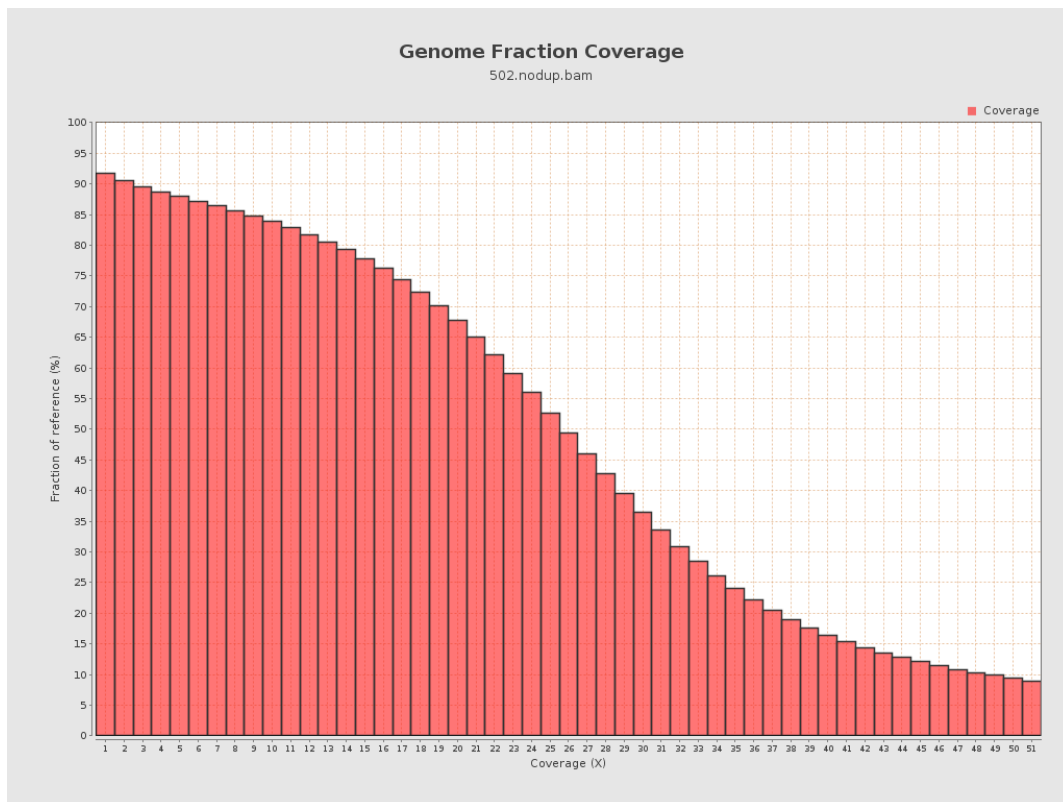
4. Results : Coverage Histogram



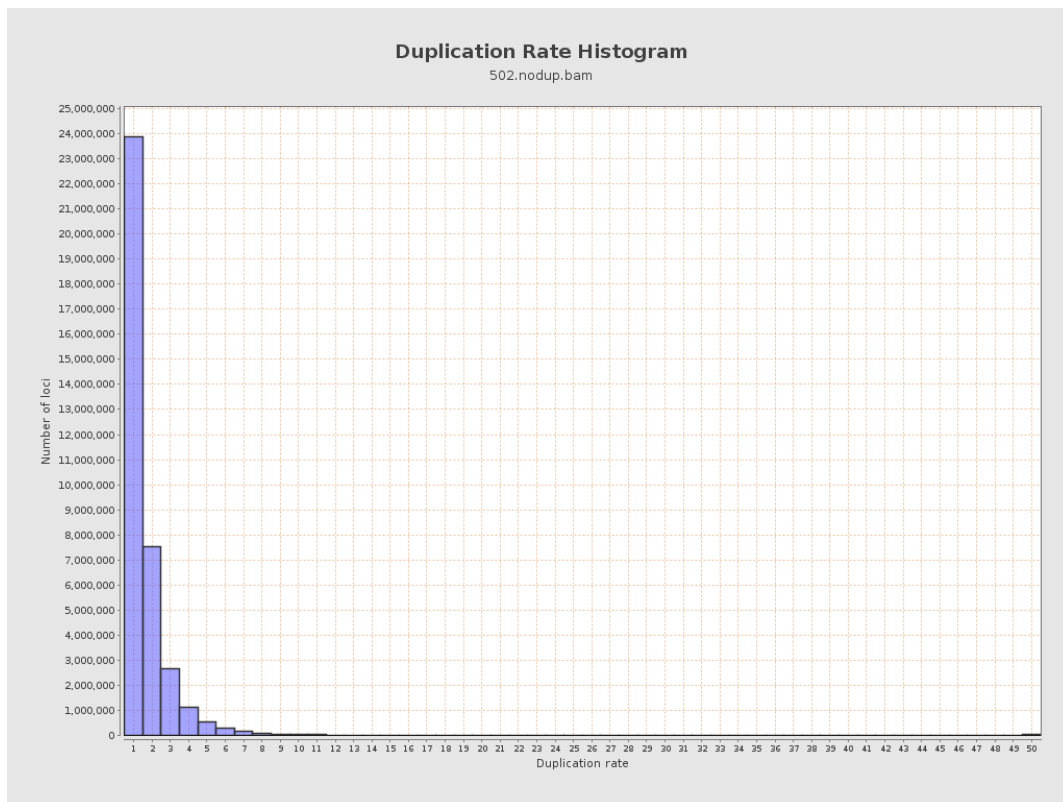
5. Results : Coverage Histogram (0-50X)



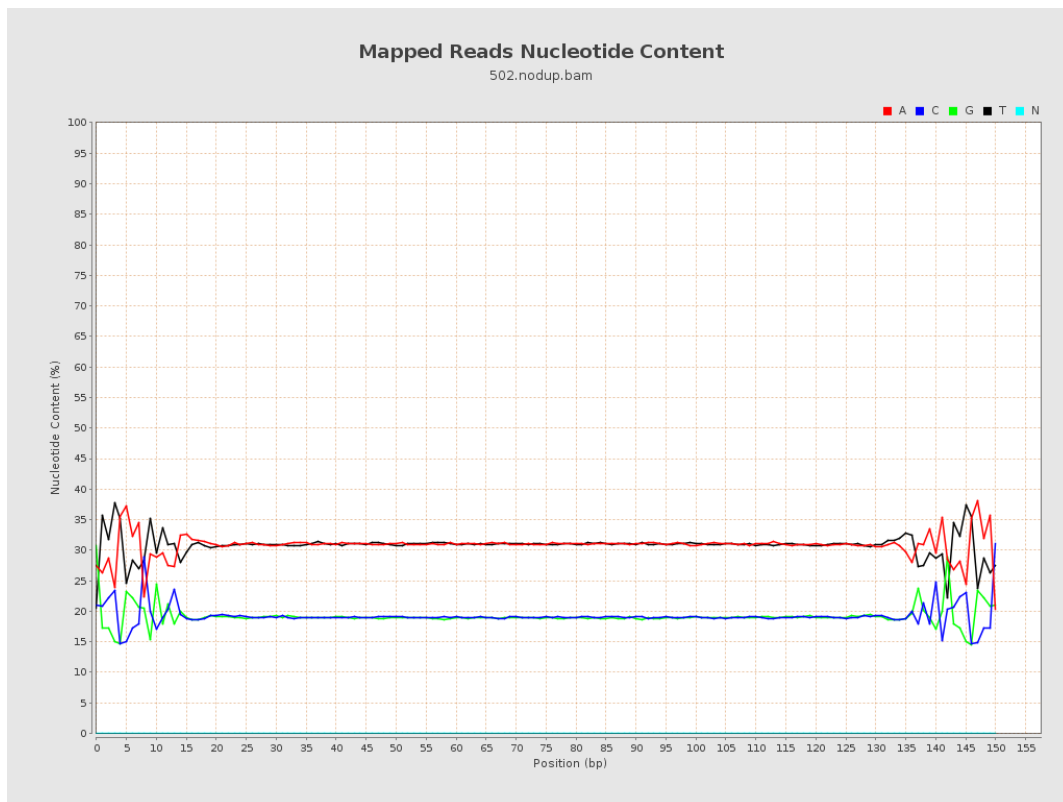
6. Results : Genome Fraction Coverage



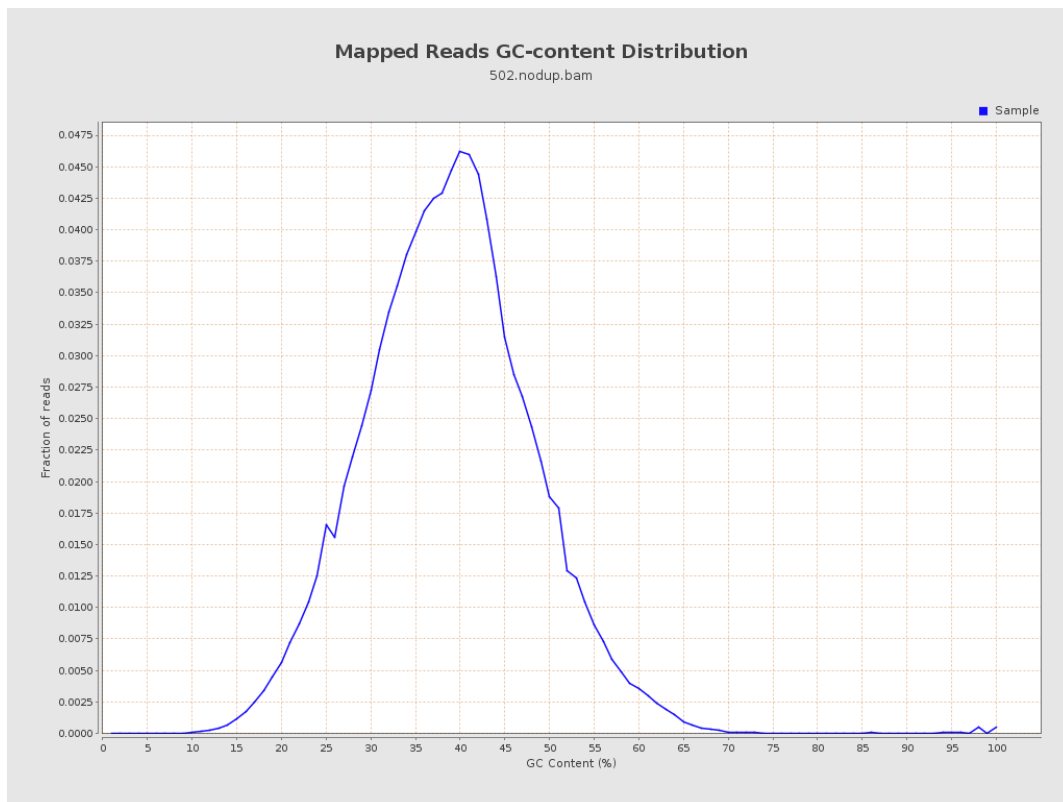
7. Results : Duplication Rate Histogram



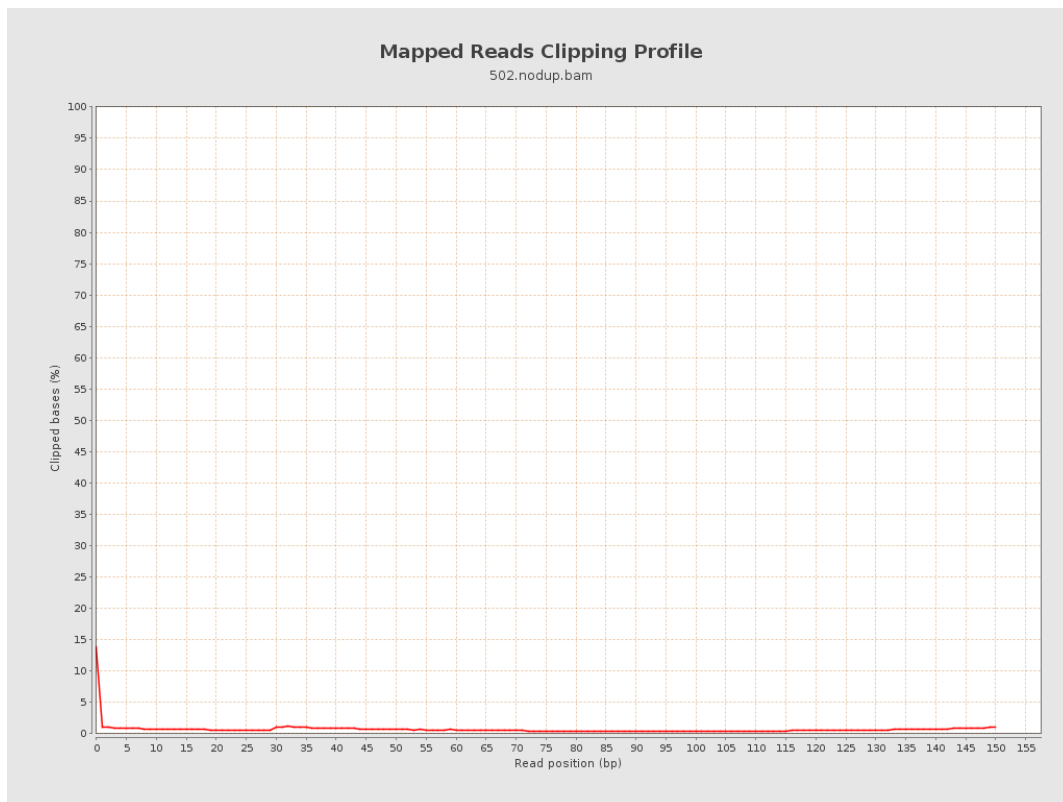
8. Results : Mapped Reads Nucleotide Content



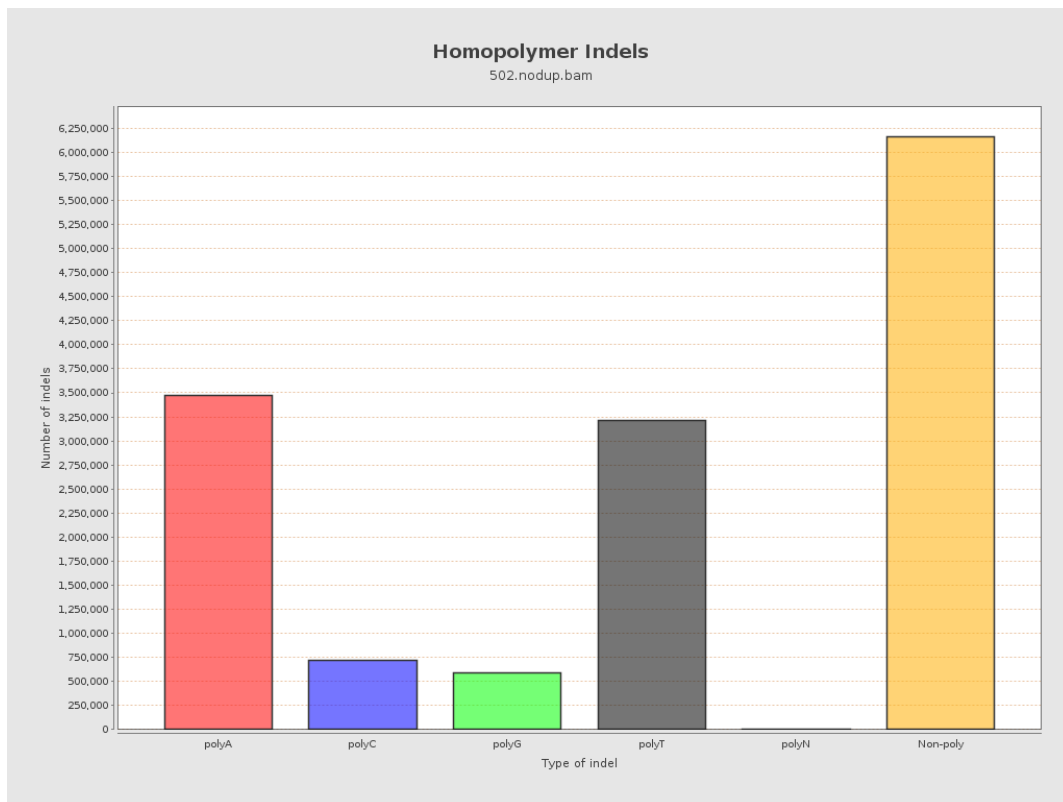
9. Results : Mapped Reads GC-content Distribution



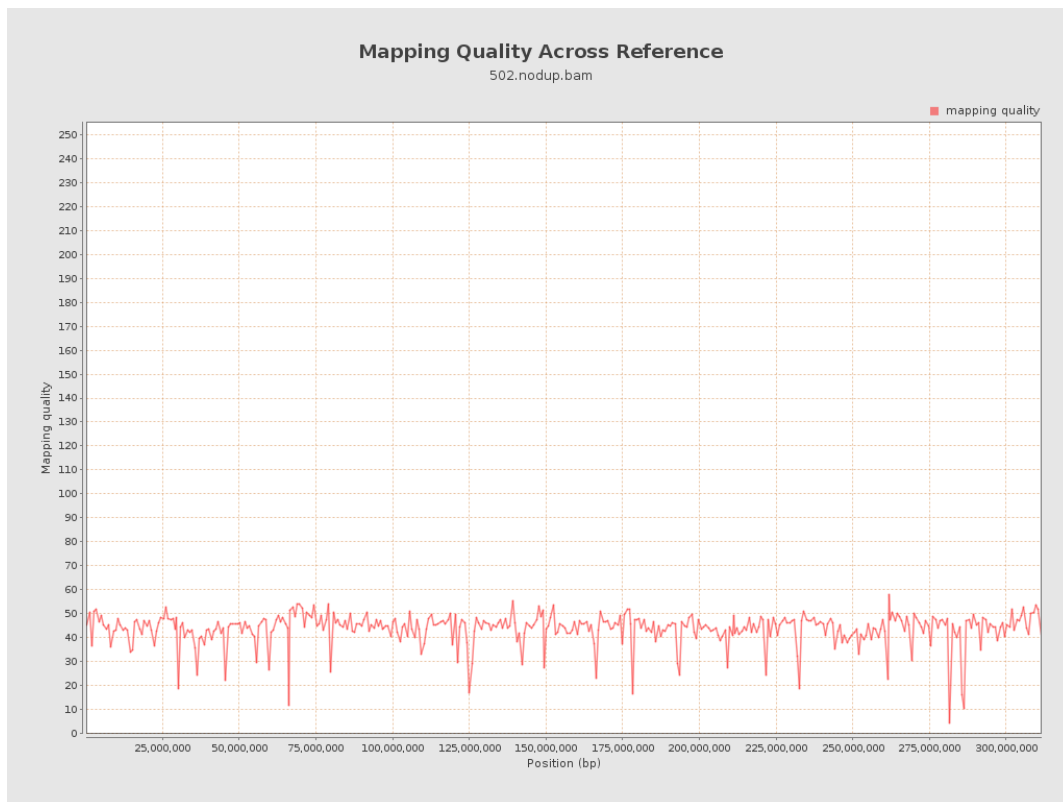
10. Results : Mapped Reads Clipping Profile



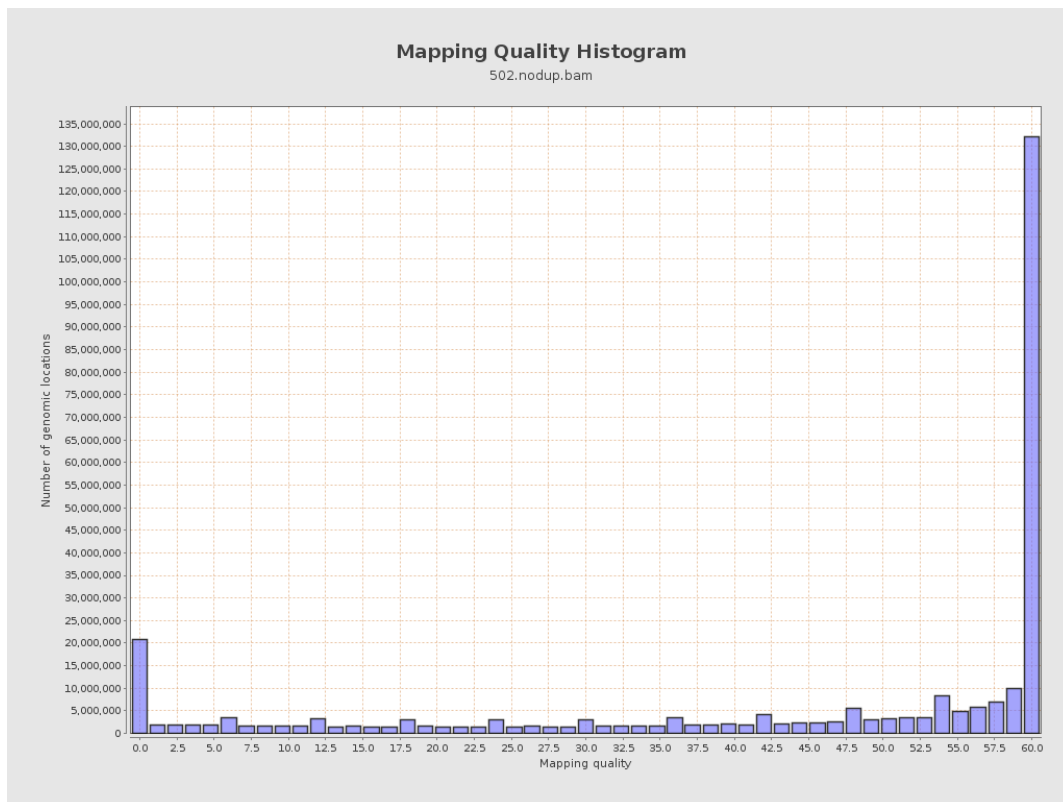
11. Results : Homopolymer Indels



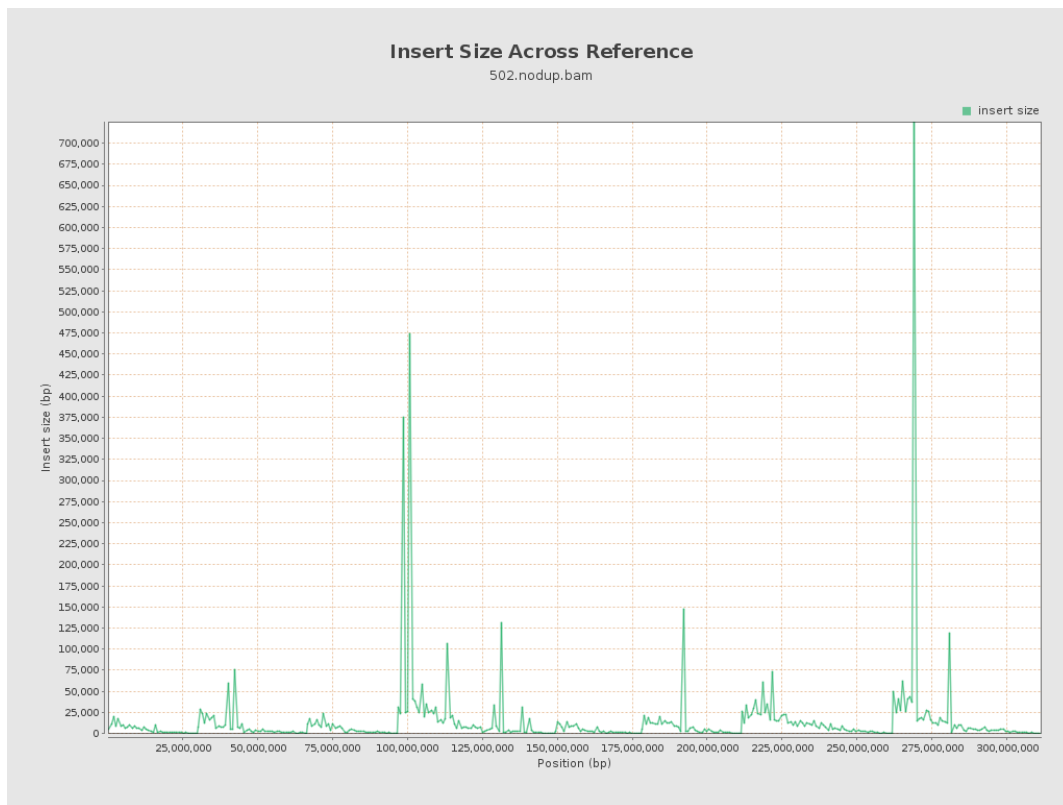
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

