

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:44:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/503
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/503 .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_461/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_461_S436_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_461/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_461_S436_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:44:32 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	100,137,067
Mapped reads	94,875,086 / 94.75%
Unmapped reads	5,261,981 / 5.25%
Mapped paired reads	94,875,086 / 94.75%
Mapped reads, first in pair	47,515,089 / 47.45%
Mapped reads, second in pair	47,359,997 / 47.3%
Mapped reads, both in pair	93,157,295 / 93.03%
Mapped reads, singletons	1,717,791 / 1.72%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	14,889,969 / 14.87%
Clipped reads	20,537,047 / 20.51%

2.2. ACGT Content

Number/percentage of A's	4,078,424,956 / 30.87%
Number/percentage of C's	2,525,627,497 / 19.12%
Number/percentage of T's	4,083,221,857 / 30.91%
Number/percentage of G's	2,523,325,586 / 19.1%
Number/percentage of N's	45,455 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	42.5022
Standard Deviation	304.3512

2.4. Mapping Quality

Mean Mapping Quality	43.59
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2.5. Insert size

Mean	239,211.48
Standard Deviation	2,311,272.97
P25/Median/P75	335 / 442 / 586

2.6. Mismatches and indels

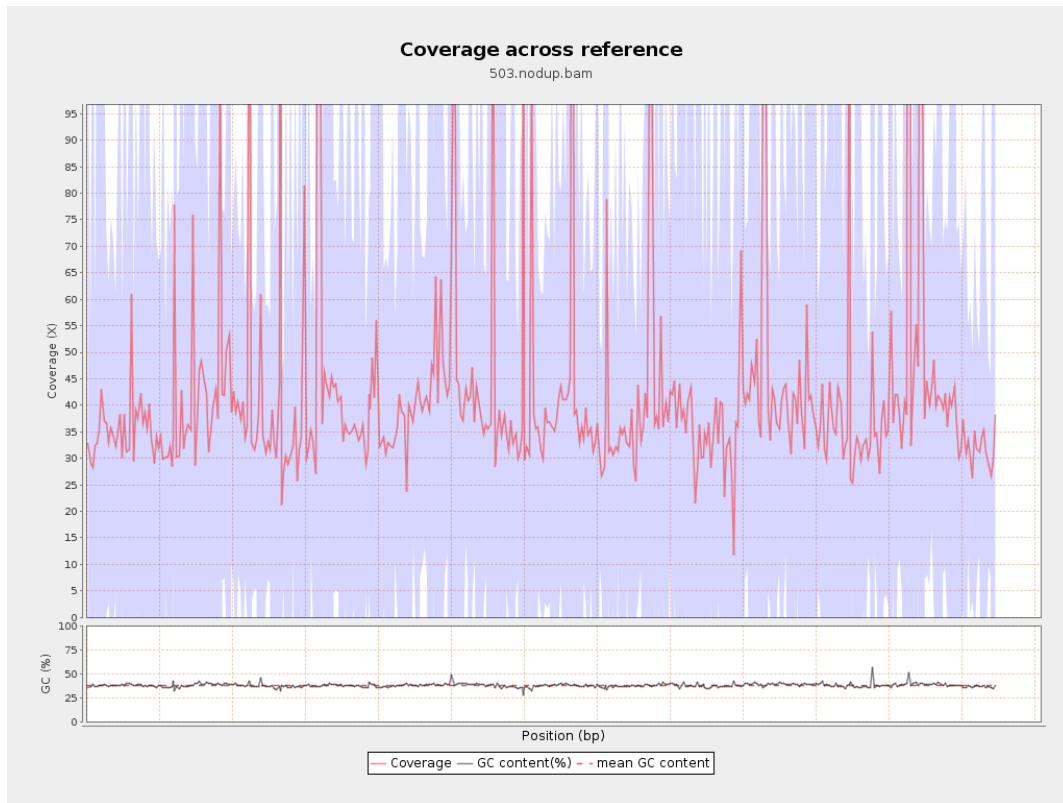
General error rate	2.28%
Mismatches	277,195,680
Insertions	8,856,327
Mapped reads with at least one insertion	8.39%
Deletions	9,142,027
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.3%

2.7. Chromosome stats

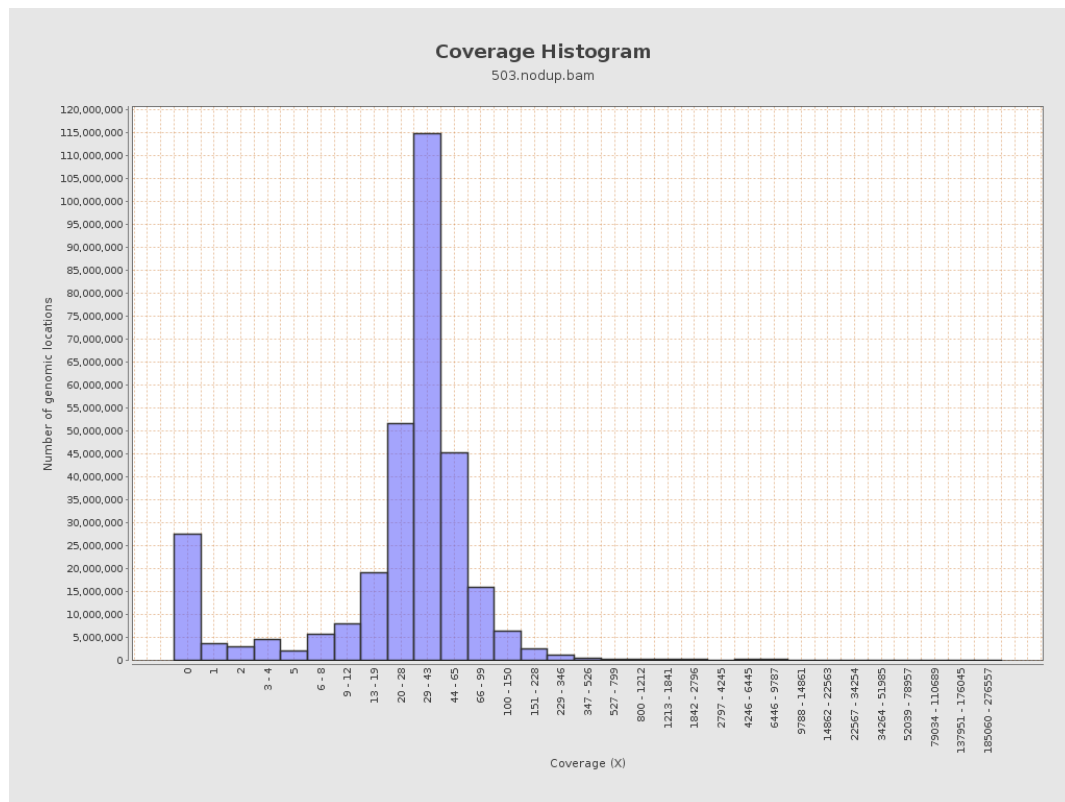
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1034052216	34.7881	90.0704

LT669789.1	36598175	1612904003	44.0706	335.4247
LT669790.1	30422129	1315627804	43.2458	259.171
LT669791.1	52758100	2235721496	42.3768	270.0729
LT669792.1	28376109	1194401170	42.0918	408.9151
LT669793.1	33388210	1345454404	40.2973	236.1566
LT669794.1	50579949	2103387439	41.5854	263.0942
LT669795.1	49795044	2403918814	48.2763	413.2855

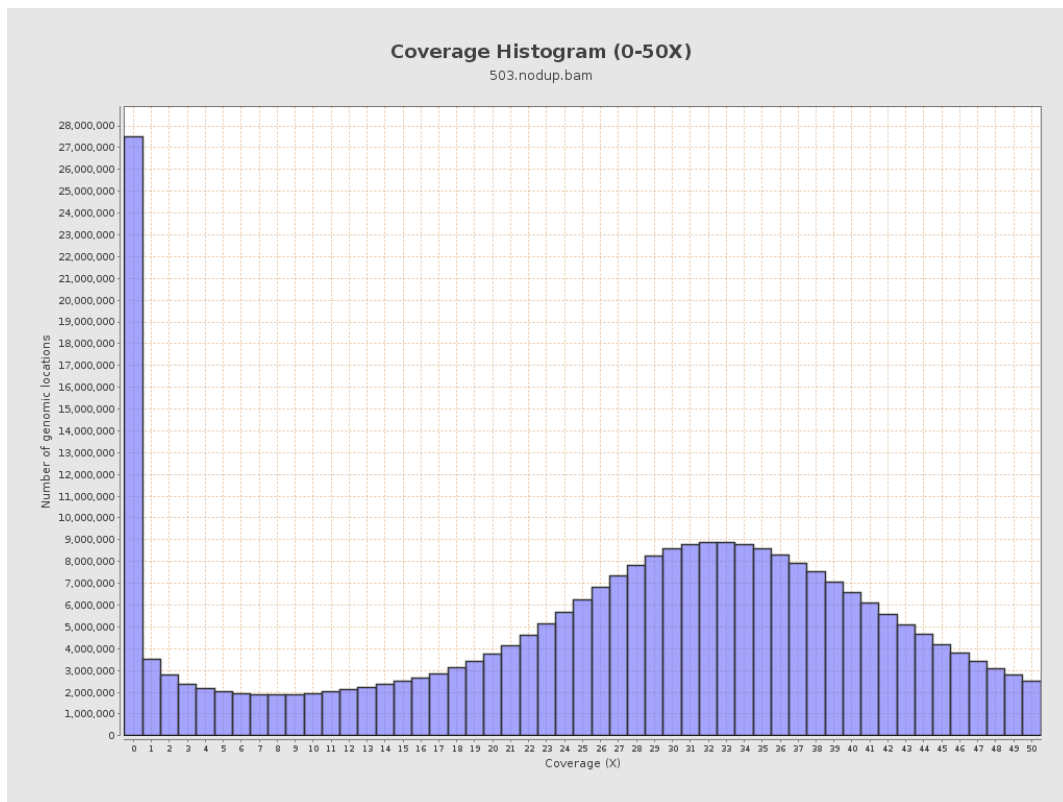
3. Results : Coverage across reference



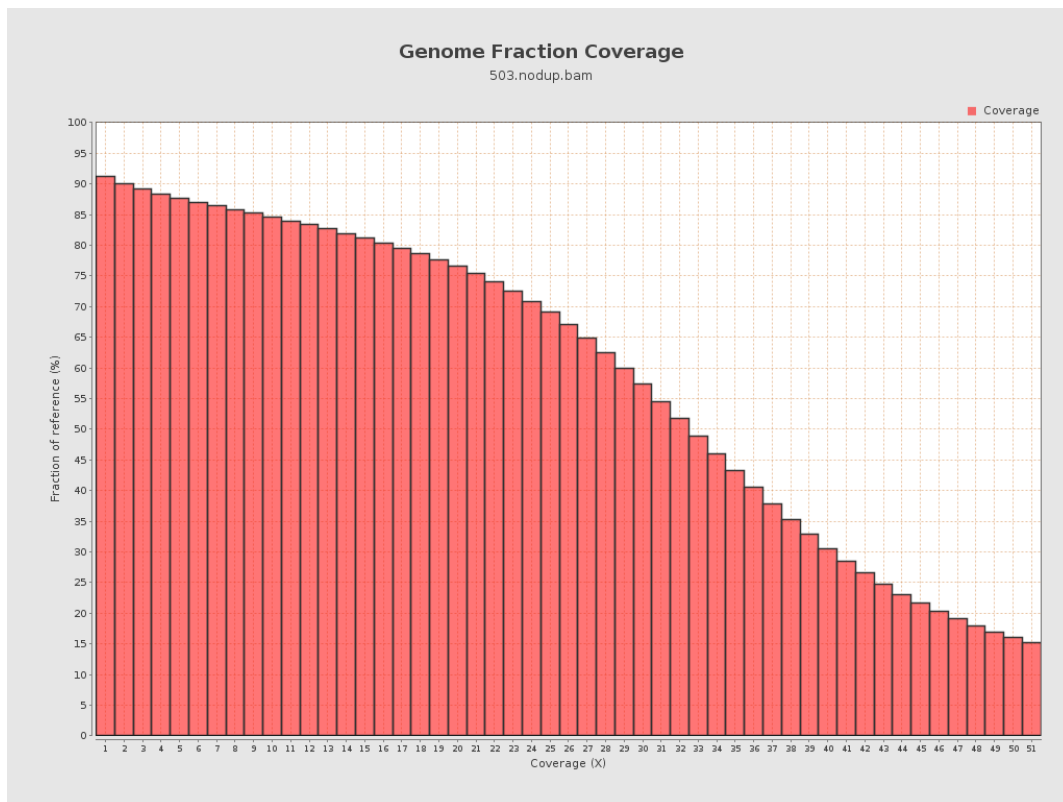
4. Results : Coverage Histogram



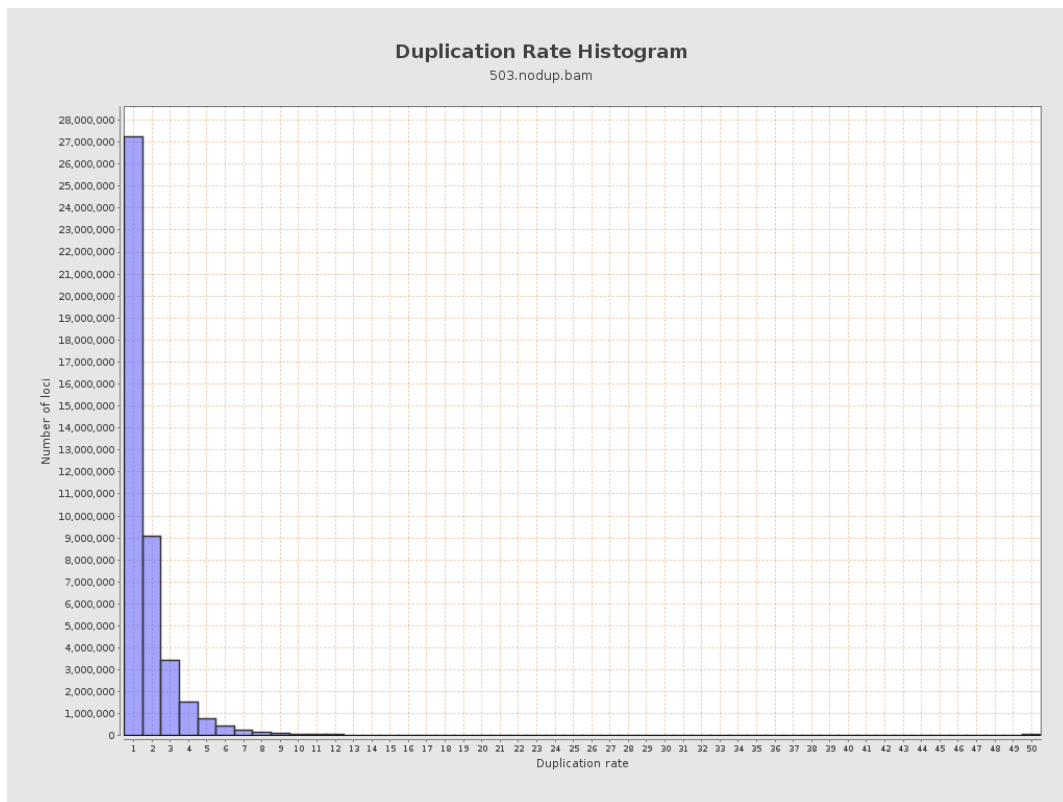
5. Results : Coverage Histogram (0-50X)



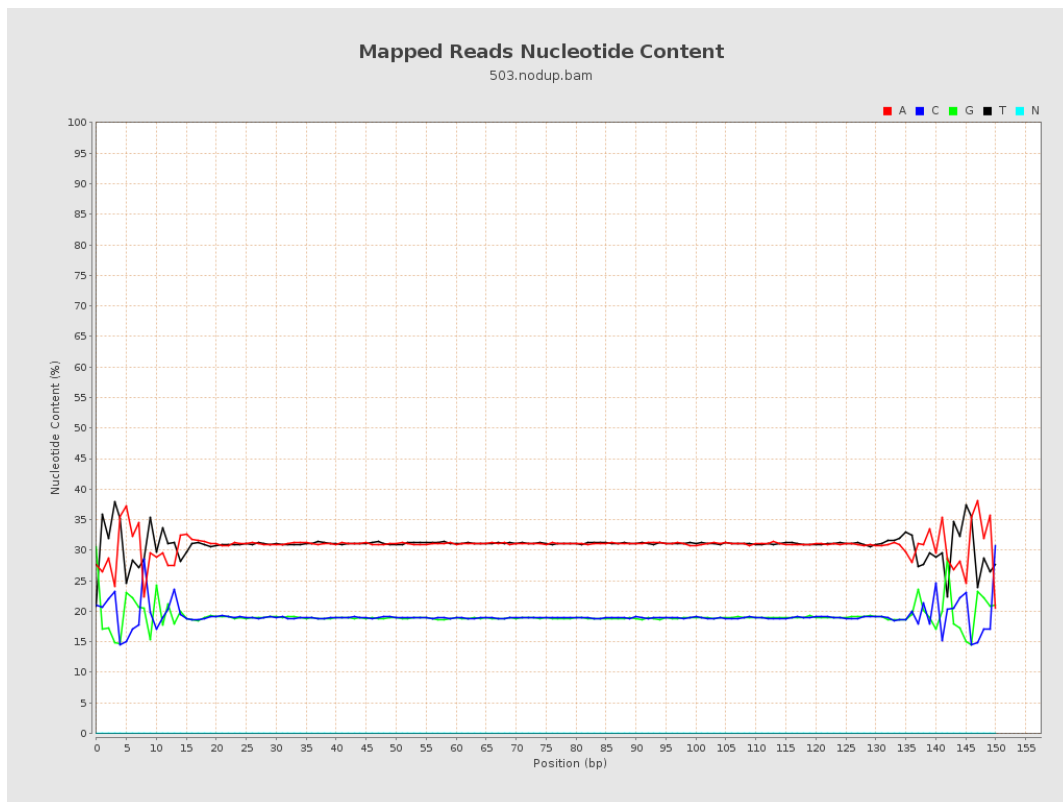
6. Results : Genome Fraction Coverage



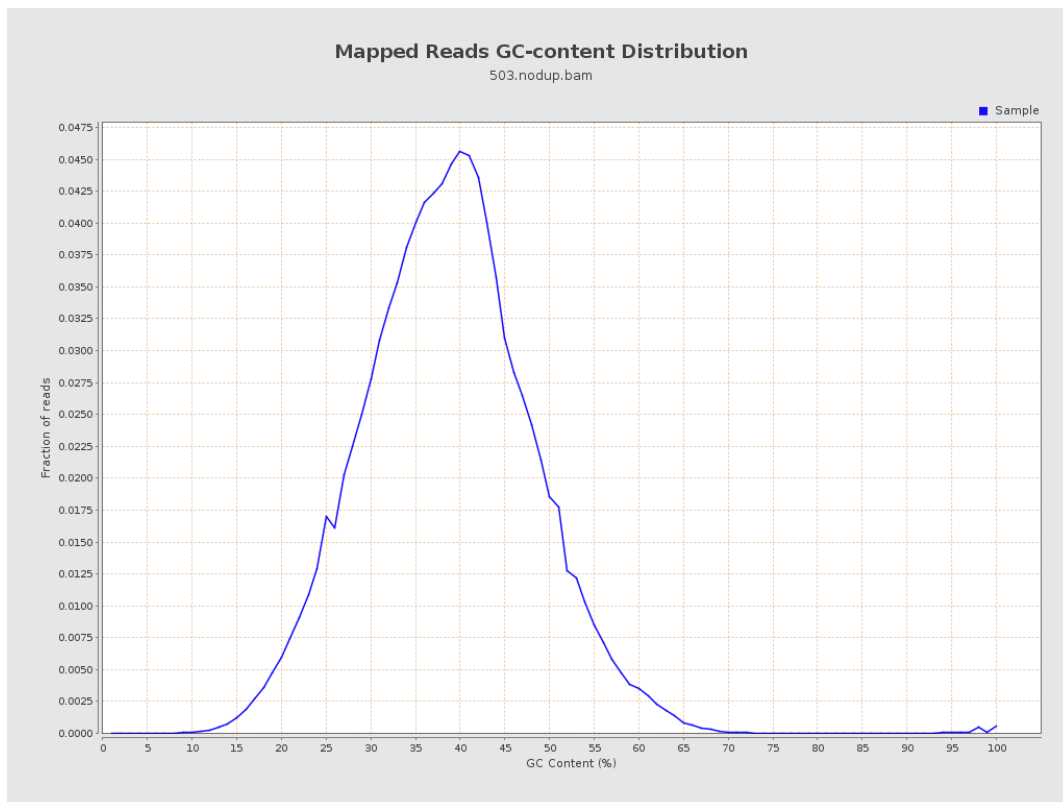
7. Results : Duplication Rate Histogram



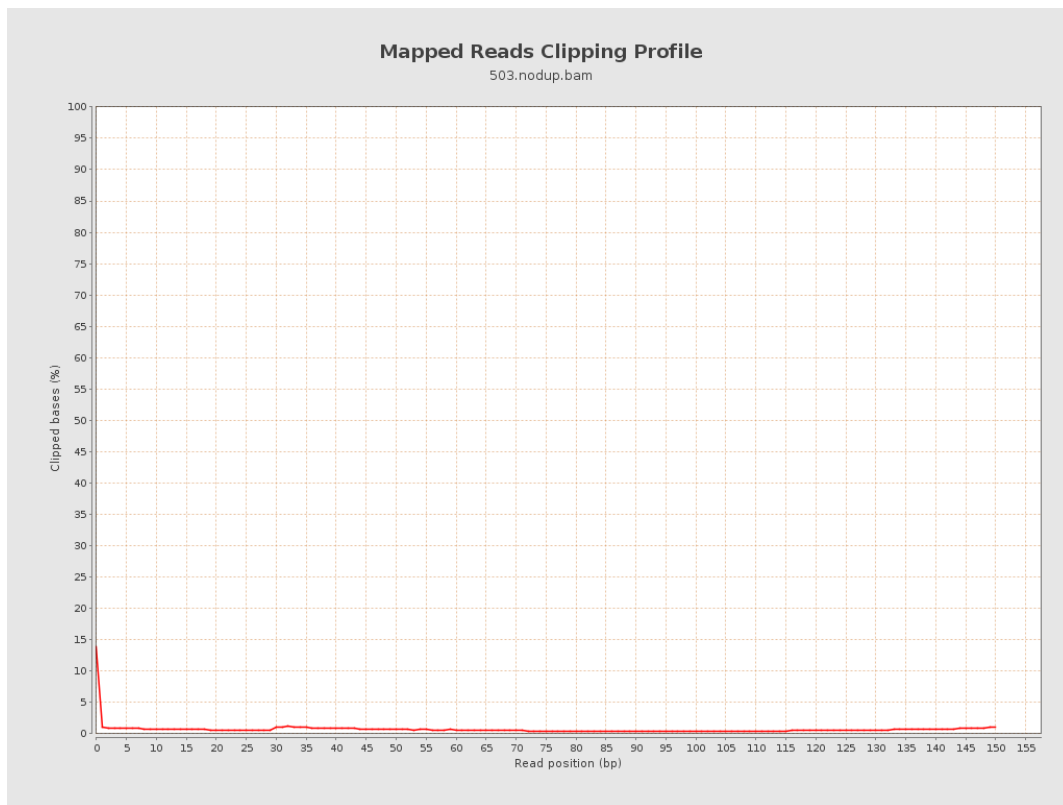
8. Results : Mapped Reads Nucleotide Content



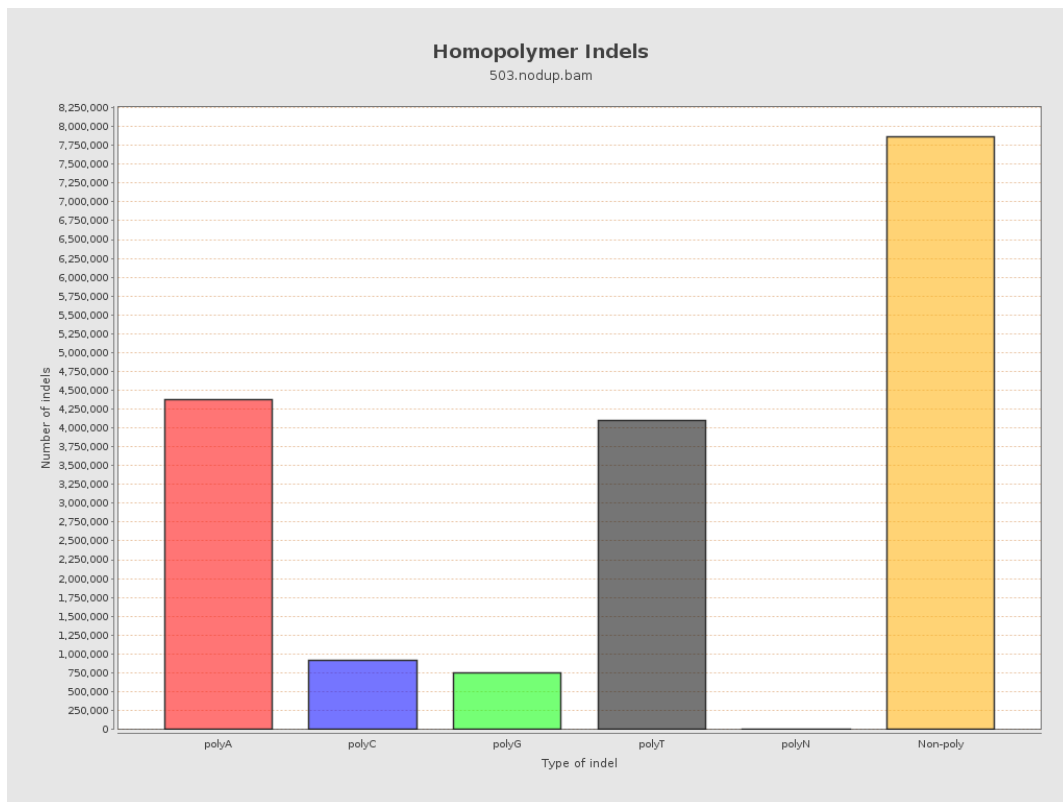
9. Results : Mapped Reads GC-content Distribution



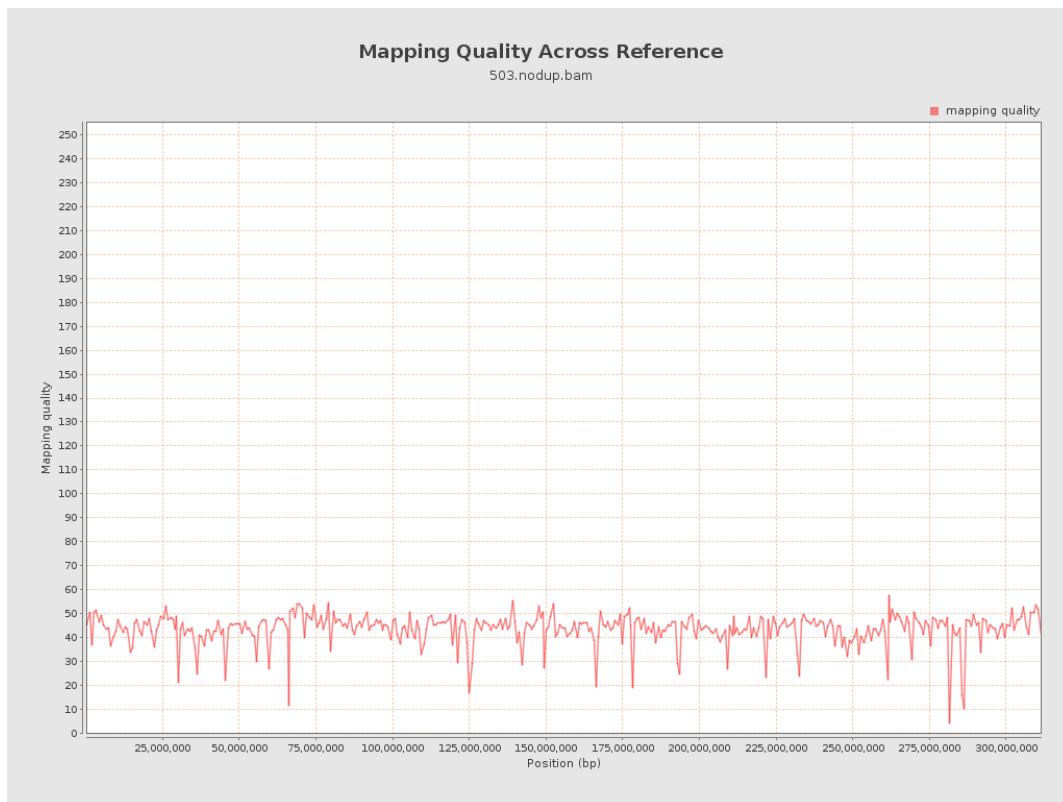
10. Results : Mapped Reads Clipping Profile



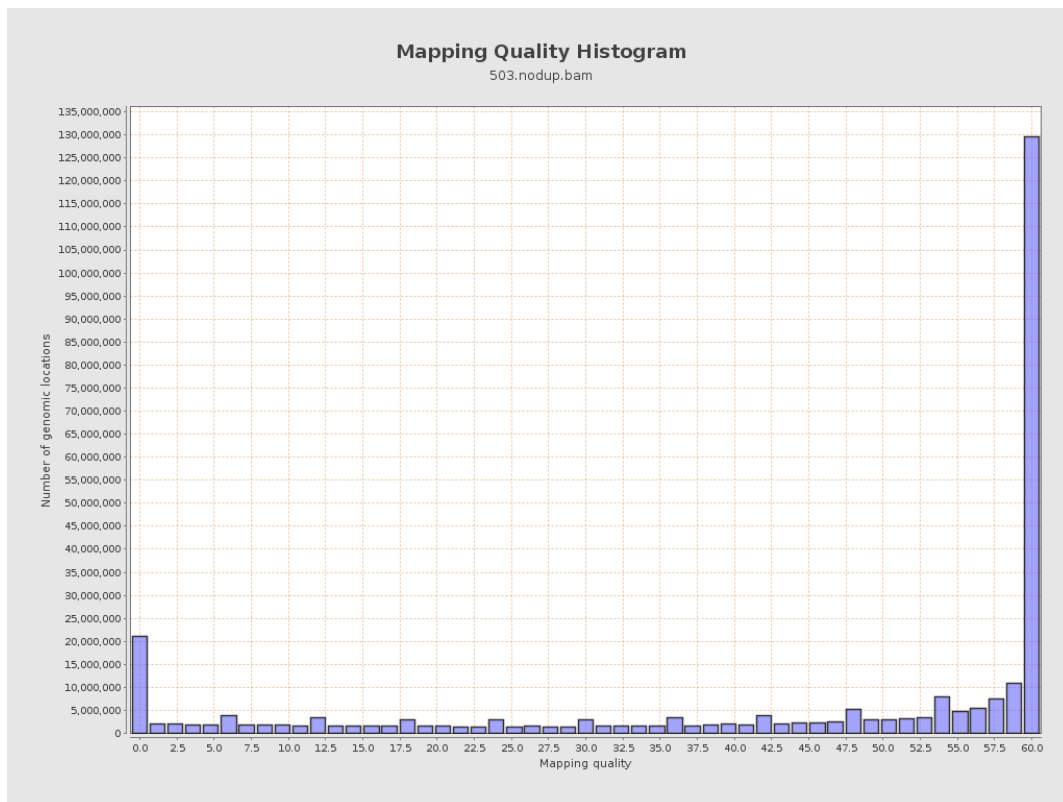
11. Results : Homopolymer Indels



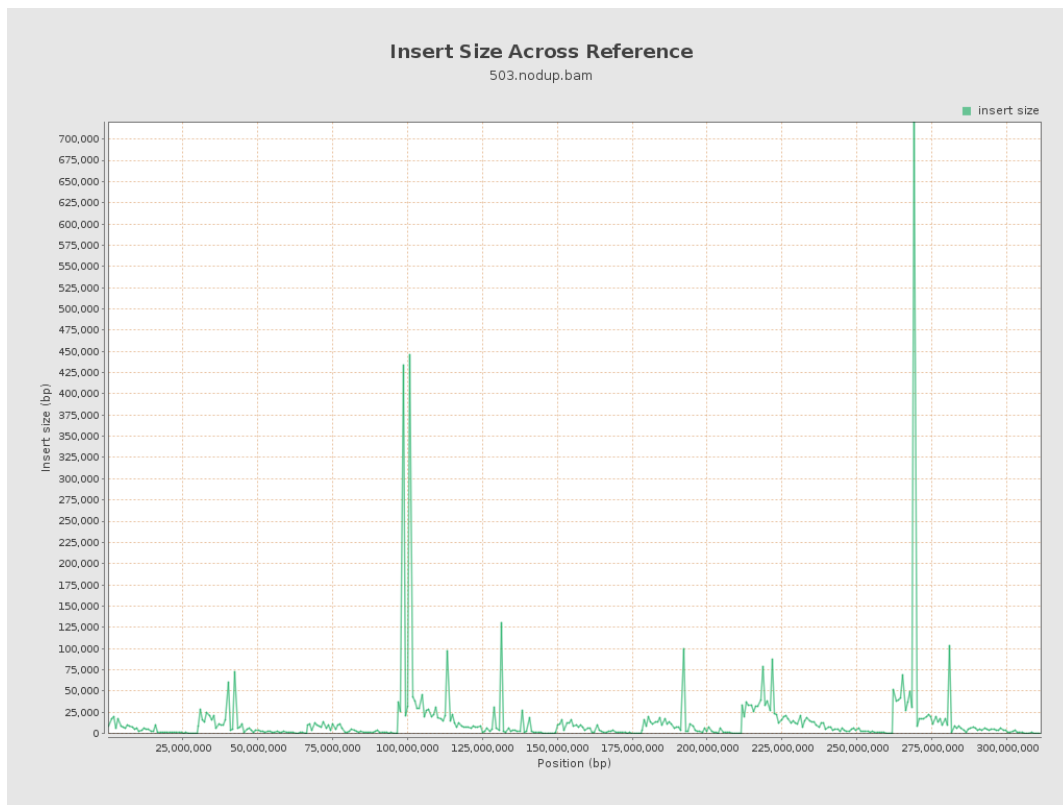
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

