

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/464
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/464.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_249/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_249_S330_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_249/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_249_S330_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:29:56 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	62,282,389
Mapped reads	58,516,829 / 93.95%
Unmapped reads	3,765,560 / 6.05%
Mapped paired reads	58,516,829 / 93.95%
Mapped reads, first in pair	29,317,218 / 47.07%
Mapped reads, second in pair	29,199,611 / 46.88%
Mapped reads, both in pair	57,310,435 / 92.02%
Mapped reads, singletons	1,206,394 / 1.94%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	7,734,093 / 12.42%
Clipped reads	13,165,260 / 21.14%

2.2. ACGT Content

Number/percentage of A's	2,508,240,217 / 30.97%
Number/percentage of C's	1,542,029,068 / 19.04%
Number/percentage of T's	2,508,935,166 / 30.98%
Number/percentage of G's	1,538,622,779 / 19%
Number/percentage of N's	30,004 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	26.0515
Standard Deviation	198.1068

2.4. Mapping Quality

Mean Mapping Quality	44.62
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2.5. Insert size

Mean	220,855.38
Standard Deviation	2,236,050.02
P25/Median/P75	309 / 405 / 526

2.6. Mismatches and indels

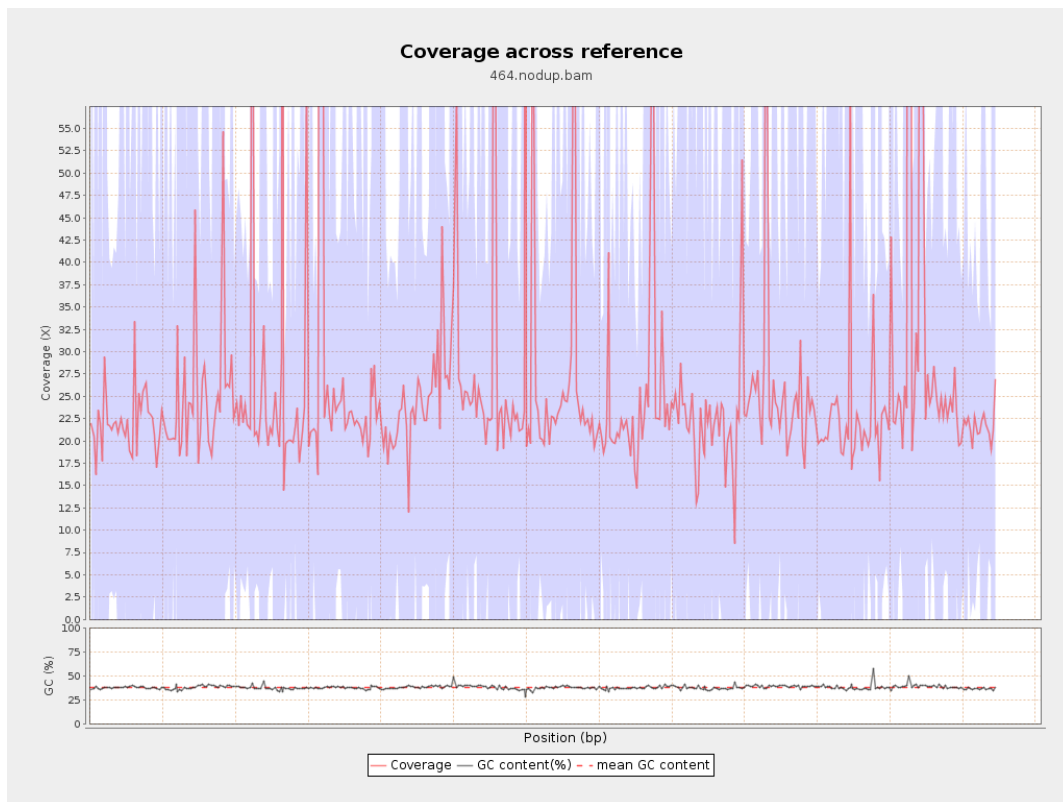
General error rate	2.25%
Mismatches	166,708,737
Insertions	5,464,927
Mapped reads with at least one insertion	8.38%
Deletions	5,518,798
Mapped reads with at least one deletion	8.38%
Homopolymer indels	57.3%

2.7. Chromosome stats

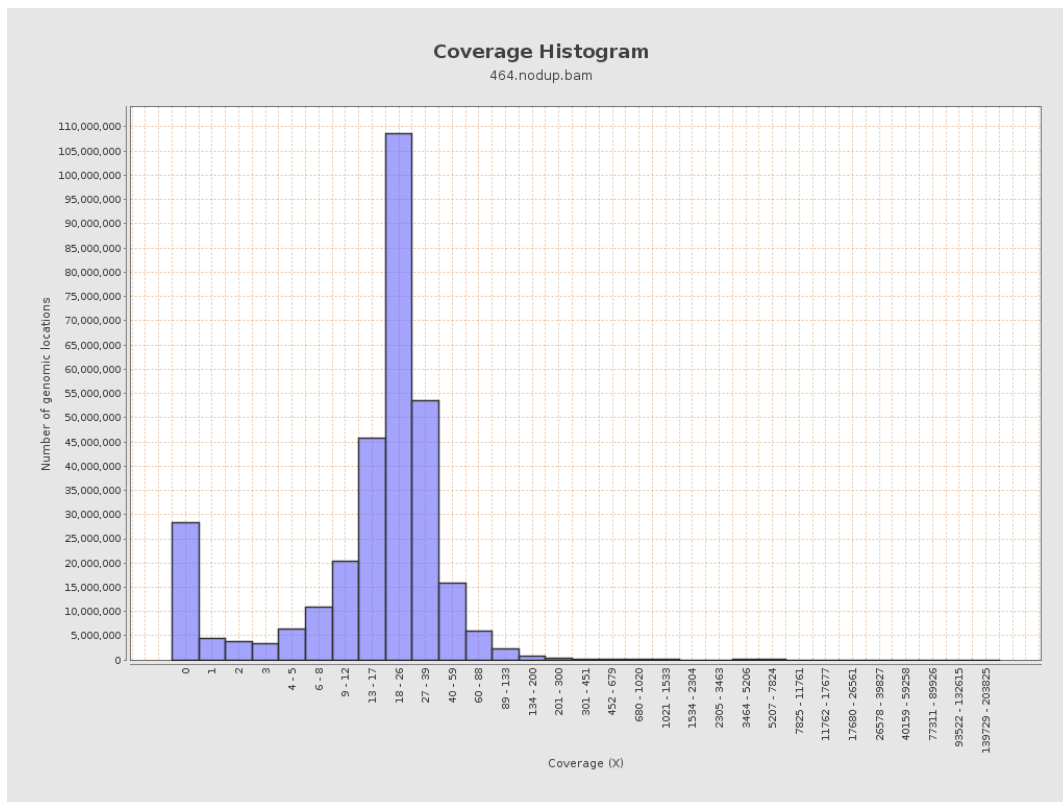
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	650819894	21.8952	60.8607

LT669789.1	36598175	966813756	26.417	203.7756
LT669790.1	30422129	879530662	28.9109	232.1867
LT669791.1	52758100	1355432863	25.6915	174.1918
LT669792.1	28376109	742445546	26.1645	206.7819
LT669793.1	33388210	805062614	24.1122	138.6754
LT669794.1	50579949	1234536520	24.4076	162.2428
LT669795.1	49795044	1484115270	29.8045	289.4373

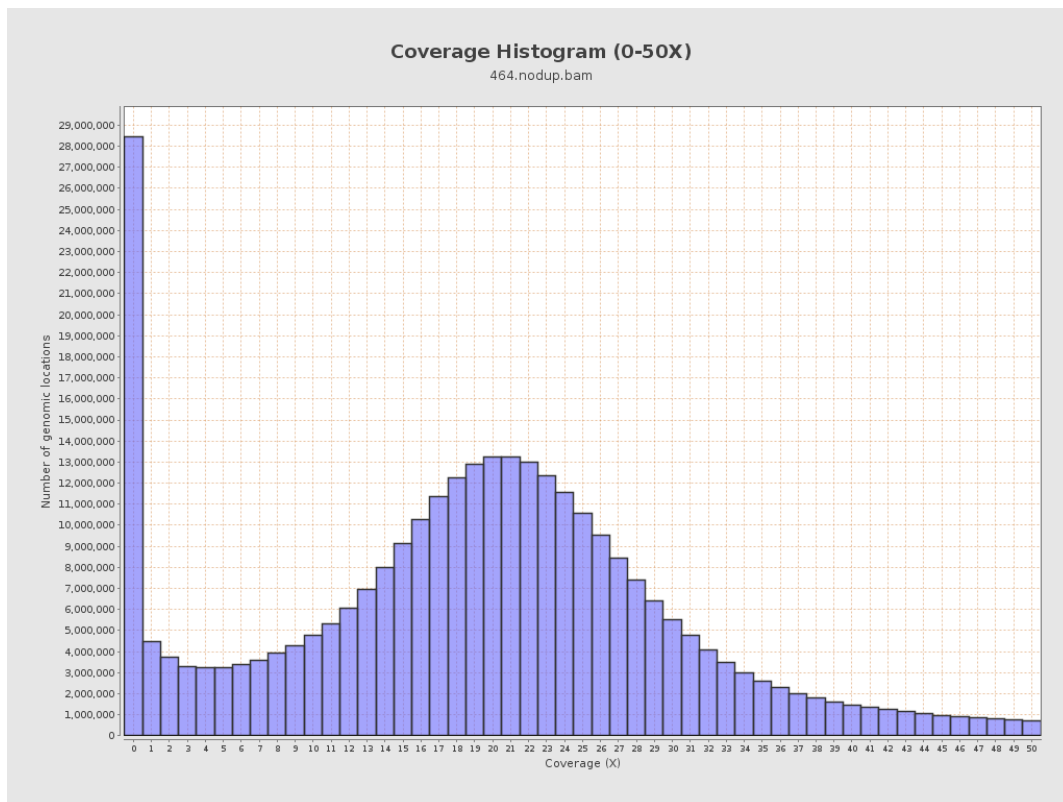
3. Results : Coverage across reference



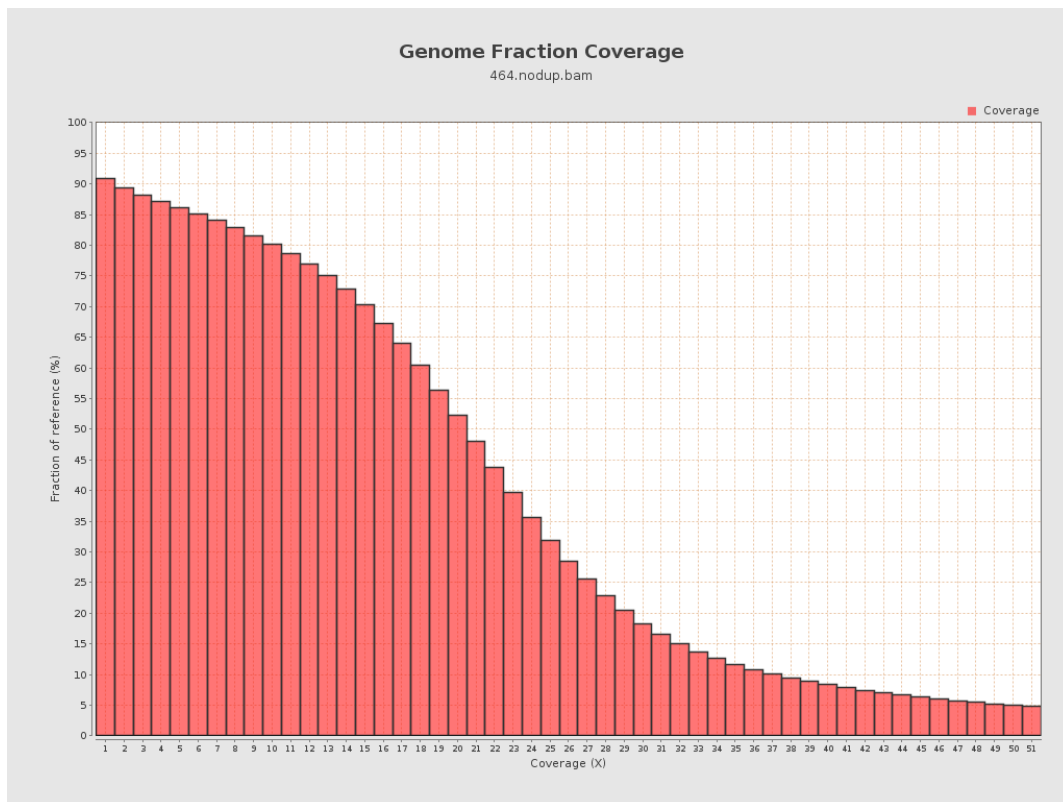
4. Results : Coverage Histogram



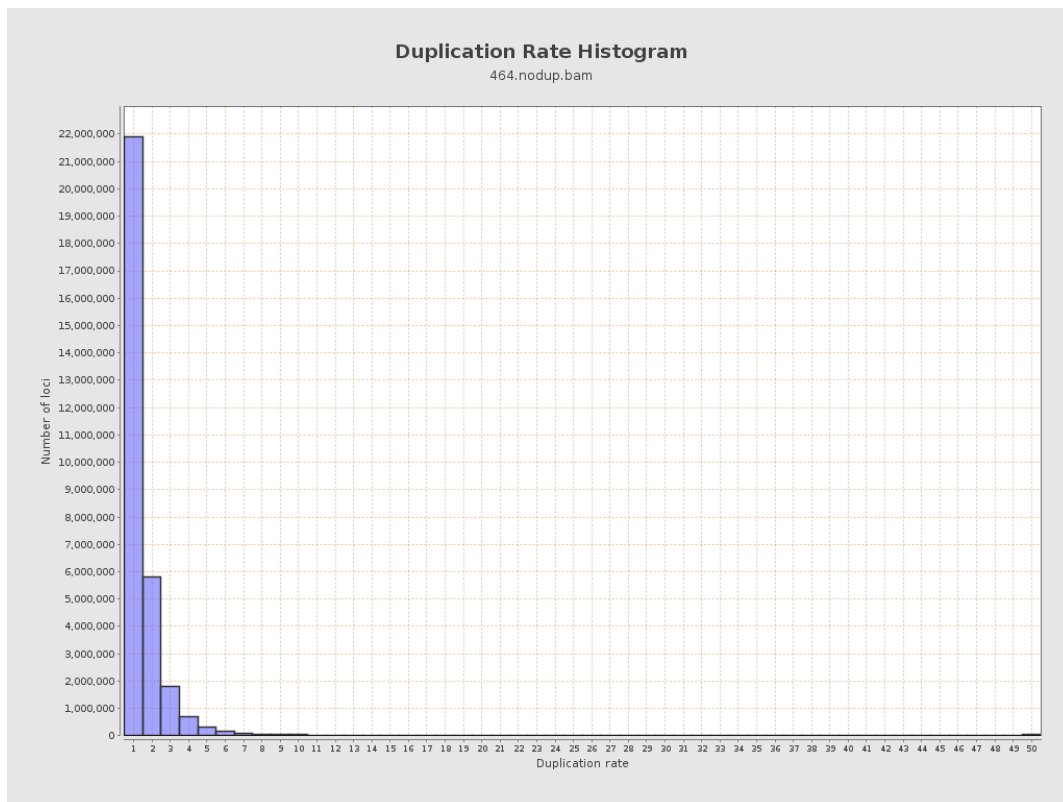
5. Results : Coverage Histogram (0-50X)



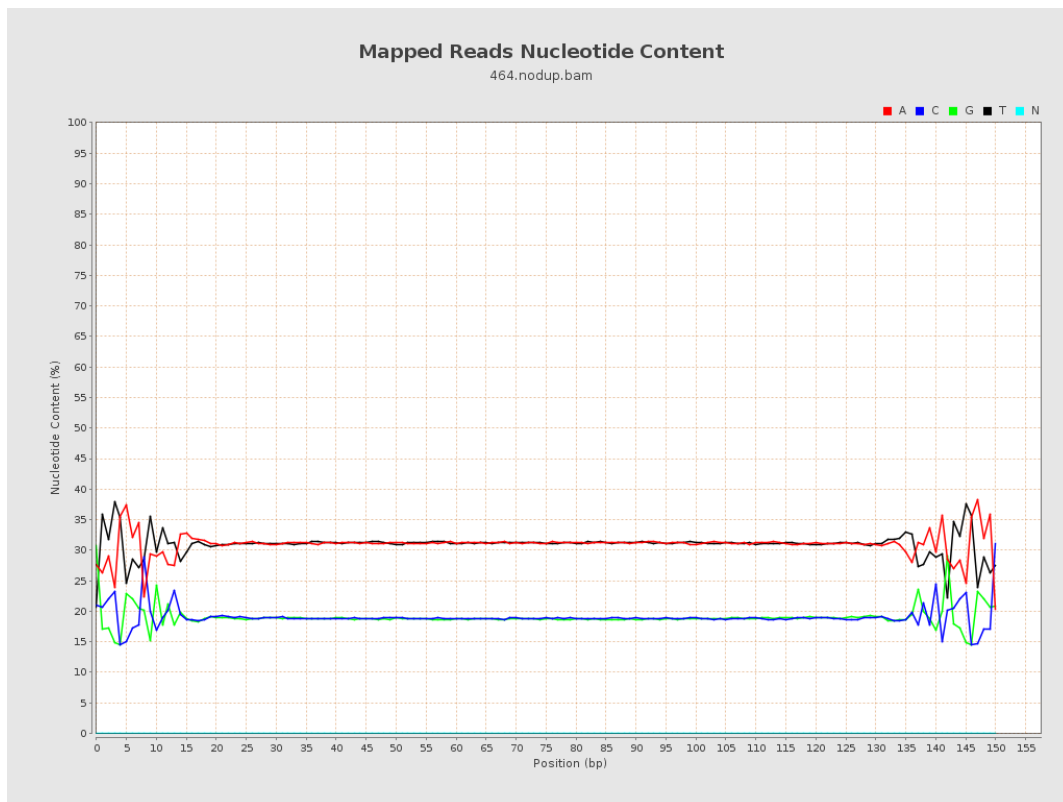
6. Results : Genome Fraction Coverage



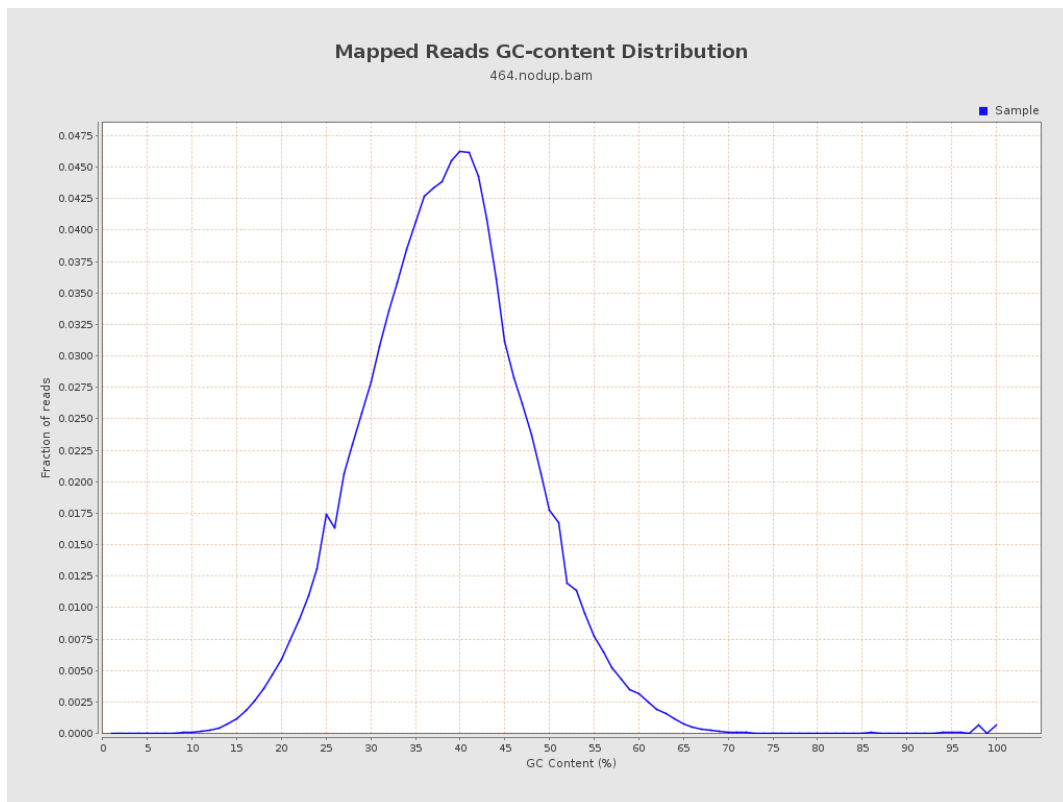
7. Results : Duplication Rate Histogram



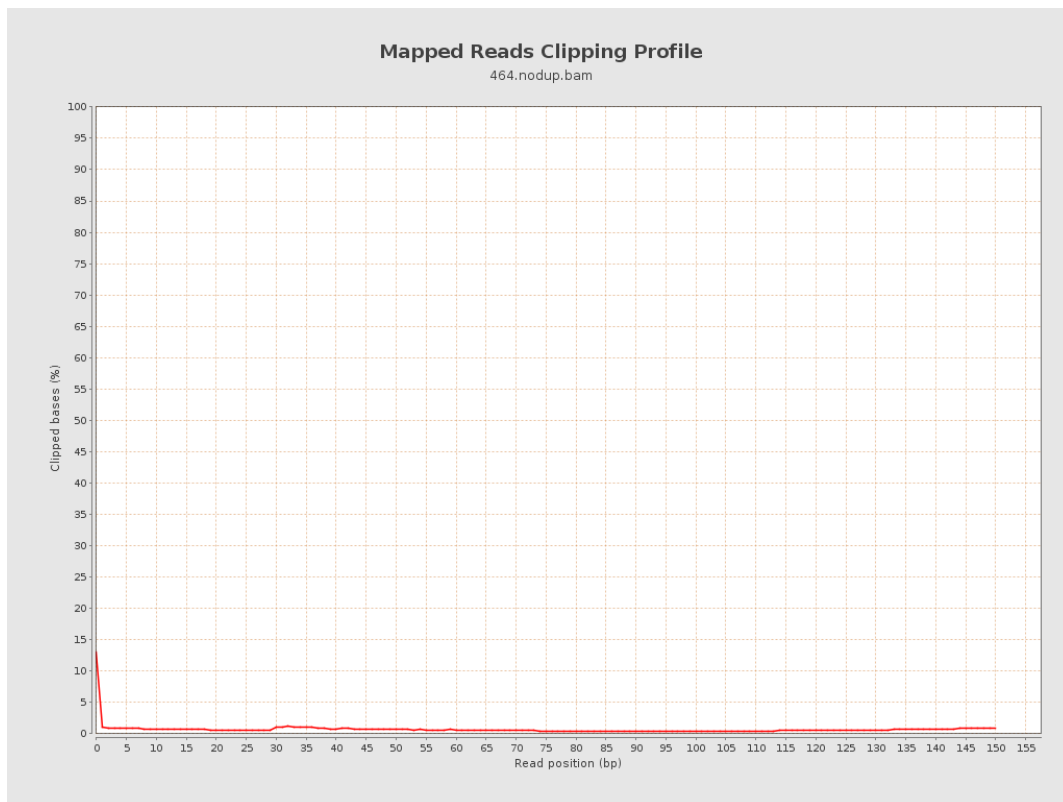
8. Results : Mapped Reads Nucleotide Content



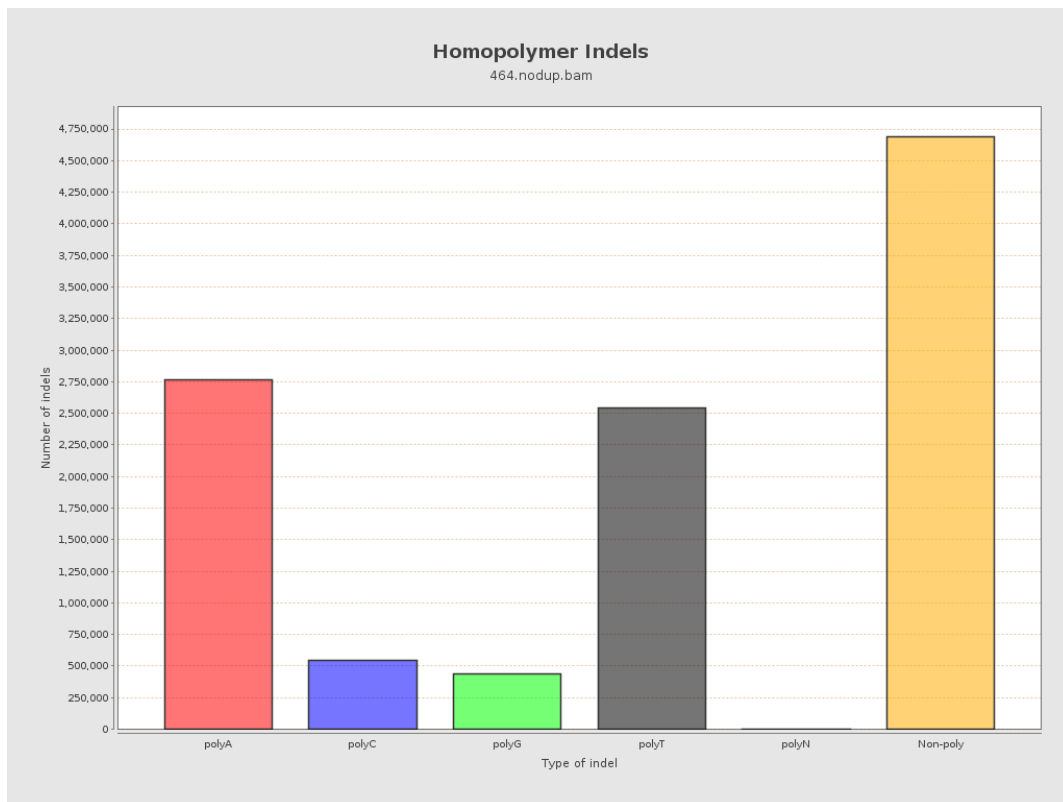
9. Results : Mapped Reads GC-content Distribution



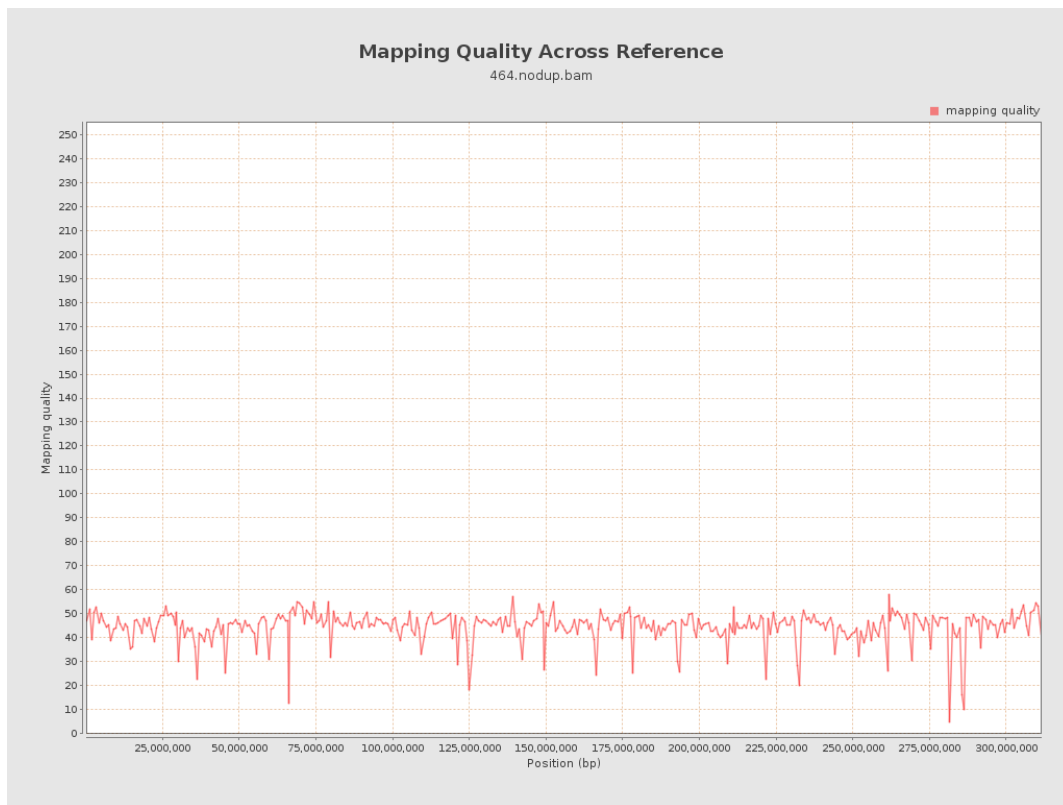
10. Results : Mapped Reads Clipping Profile



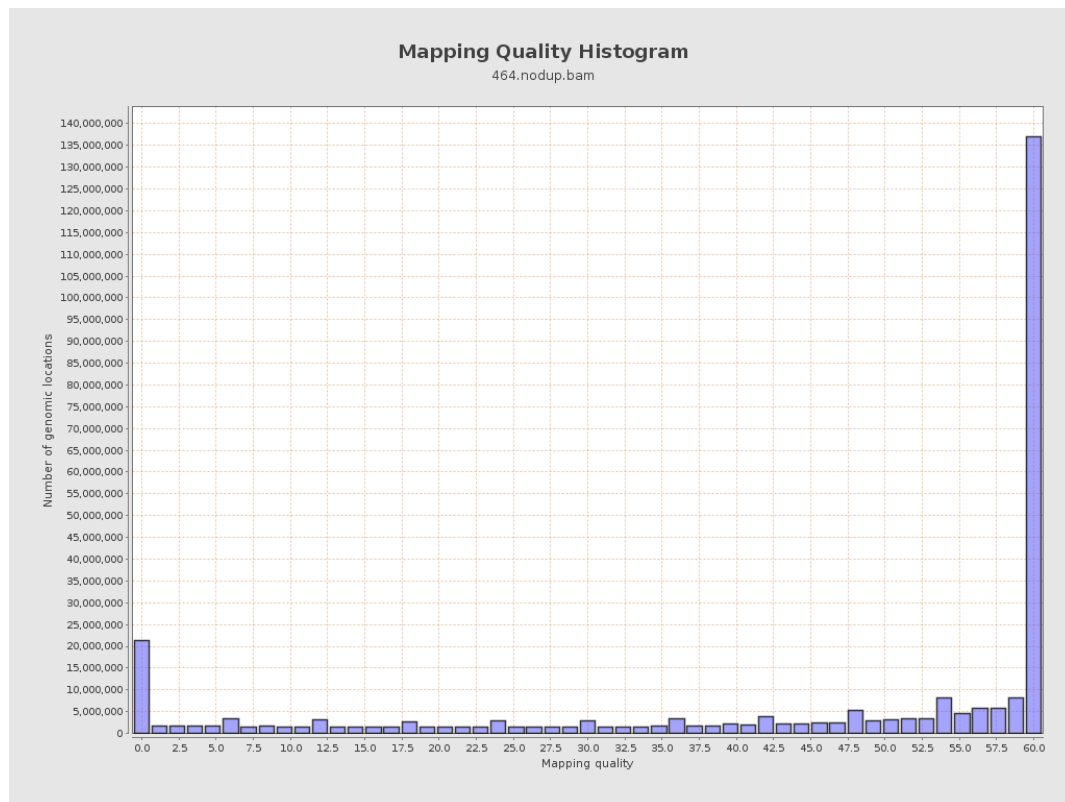
11. Results : Homopolymer Indels



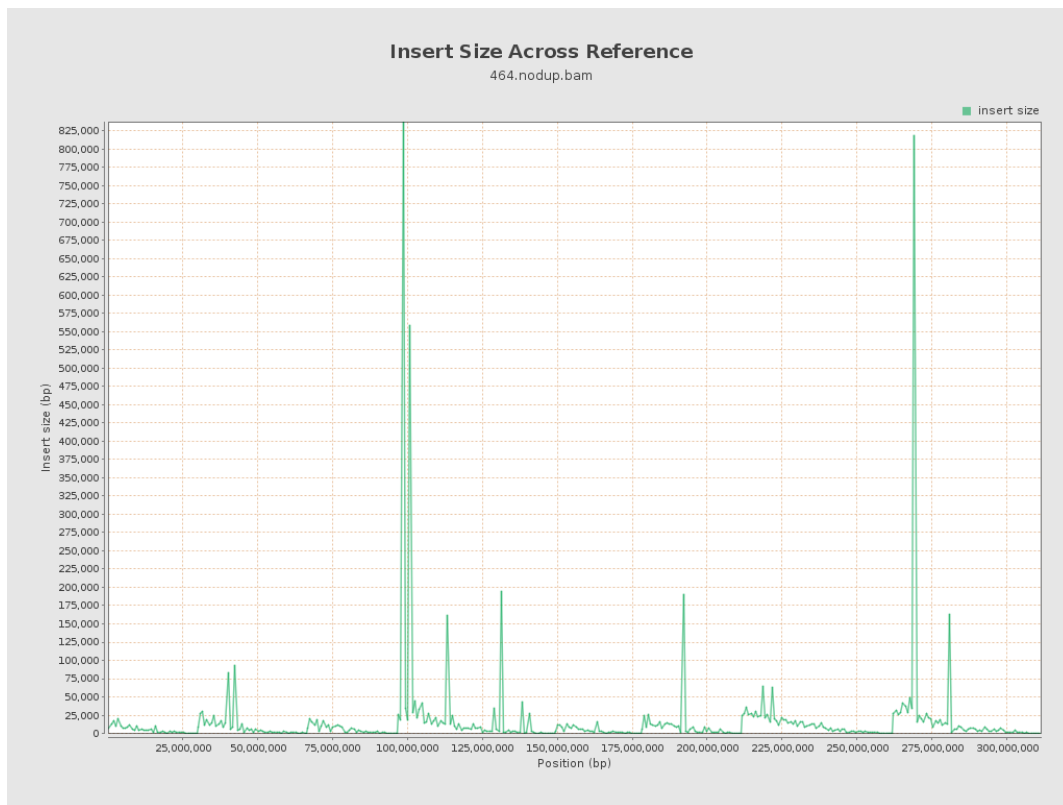
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

