Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/662.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/662.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_257/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_257_S338_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_257/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_257_S338_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:09 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,839,694
Mapped reads	67,293,667 / 93.67%
Unmapped reads	4,546,027 / 6.33%
Mapped paired reads	67,293,667 / 93.67%
Mapped reads, first in pair	33,746,105 / 46.97%
Mapped reads, second in pair	33,547,562 / 46.7%
Mapped reads, both in pair	65,752,355 / 91.53%
Mapped reads, singletons	1,541,312 / 2.15%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	10,282,636 / 14.31%
Clipped reads	15,635,081 / 21.76%

2.2. ACGT Content

Number/percentage of A's	2,872,742,421 / 30.9%
Number/percentage of C's	1,777,879,002 / 19.12%
Number/percentage of T's	2,874,518,092 / 30.92%
Number/percentage of G's	1,771,656,474 / 19.06%
Number/percentage of N's	34,974 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	29.9092
Standard Deviation	259.665

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Insert size

Mean	232,439.63
Standard Deviation	2,286,239.22
P25/Median/P75	316 / 414 / 538

2.6. Mismatches and indels

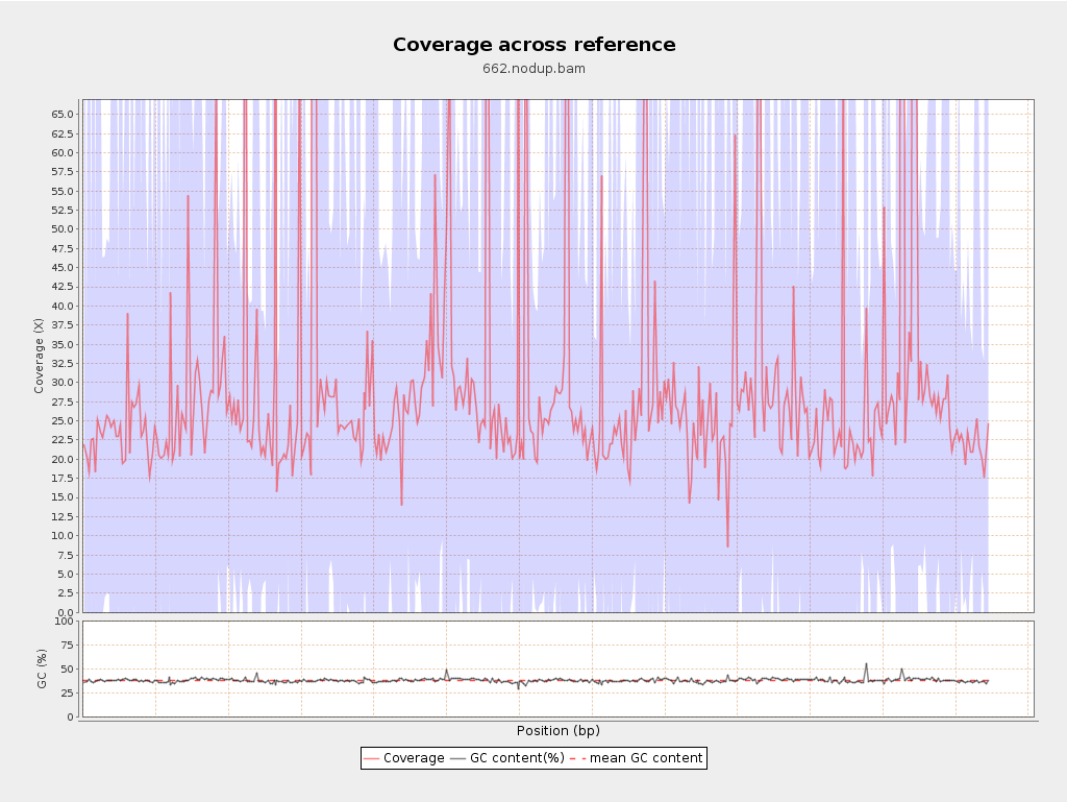
General error rate	2.39%
Mismatches	204,535,935
Insertions	6,404,754
Mapped reads with at least one insertion	8.53%
Deletions	6,444,265
Mapped reads with at least one deletion	8.5%
Homopolymer indels	56.91%

2.7. Chromosome stats

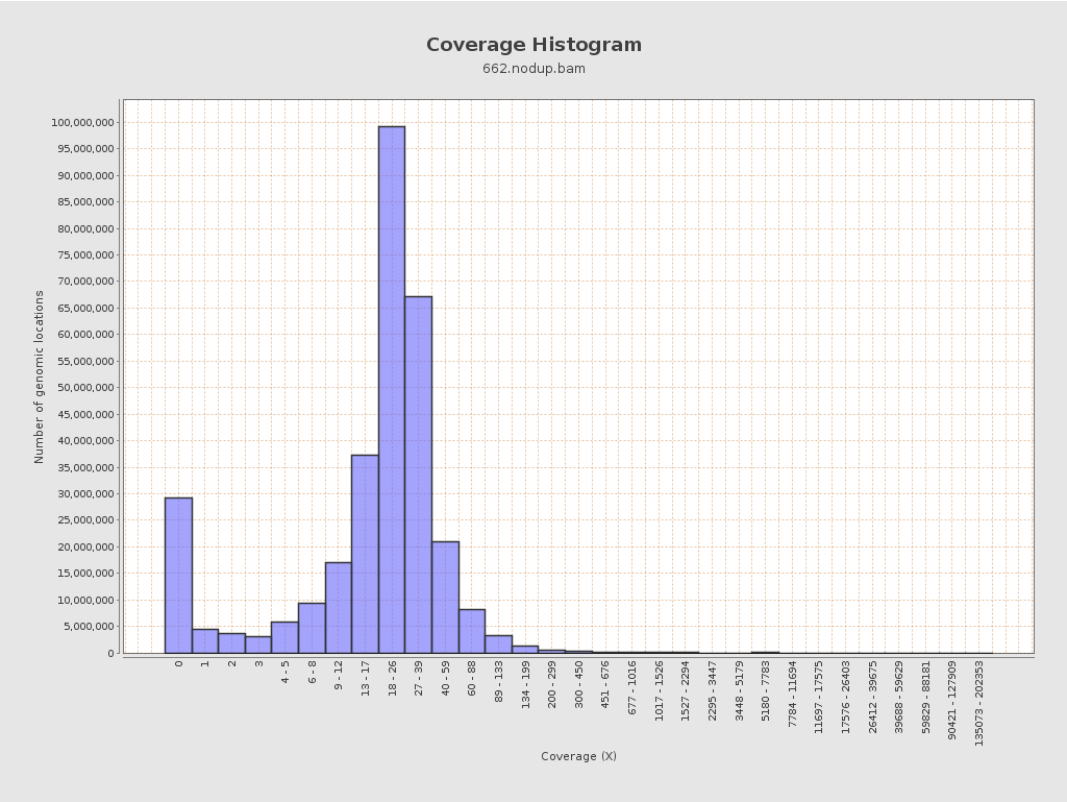
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	690958745	23.2456	75.2151

LT669789.1	36598175	1101214598	30.0893	251.8278
LT669790.1	30422129	993500113	32.6572	283.9679
LT669791.1	52758100	1577136490	29.8937	226.6058
LT669792.1	28376109	832544567	29.3396	292.5748
LT669793.1	33388210	925501738	27.7194	177.7627
LT669794.1	50579949	1445090512	28.5704	208.2012
LT669795.1	49795044	1755029155	35.2451	392.7631

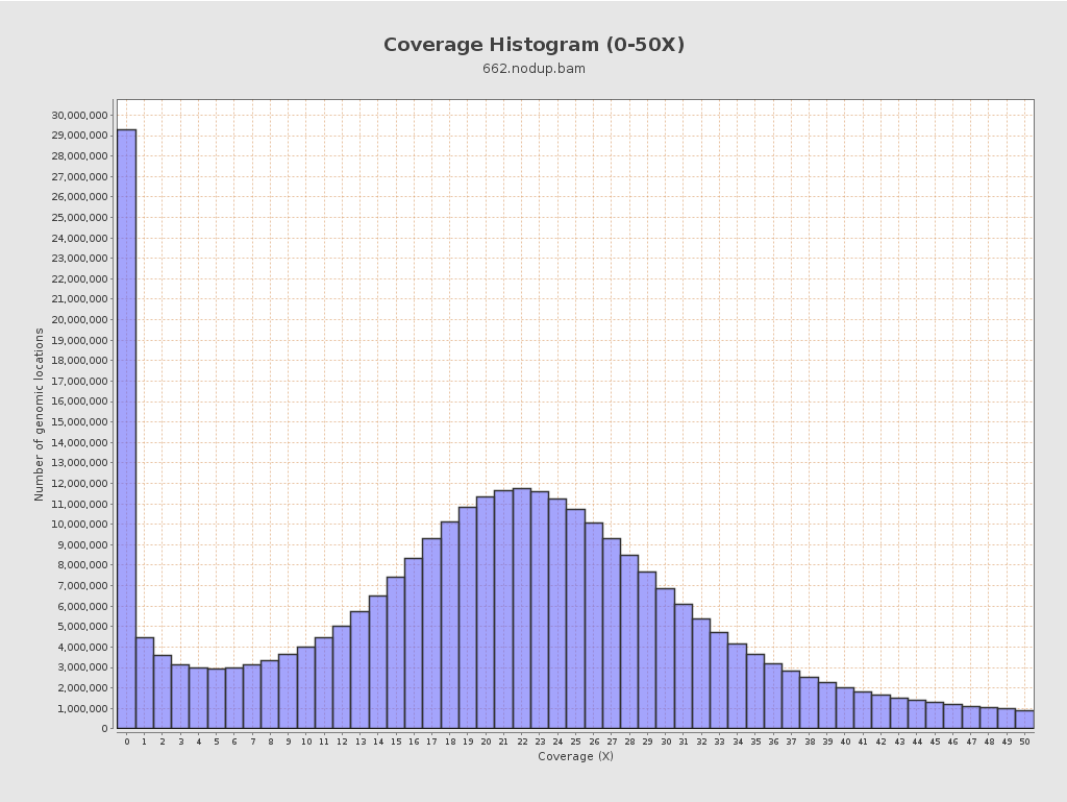
3. Results : Coverage across reference



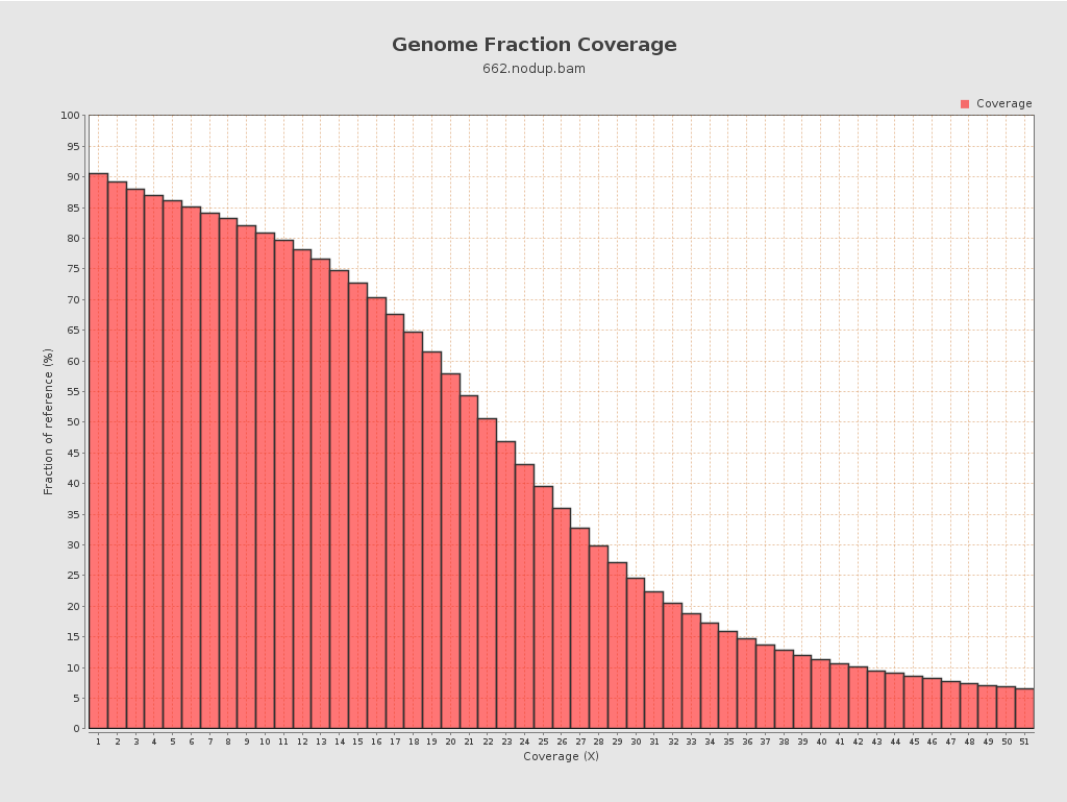
4. Results : Coverage Histogram



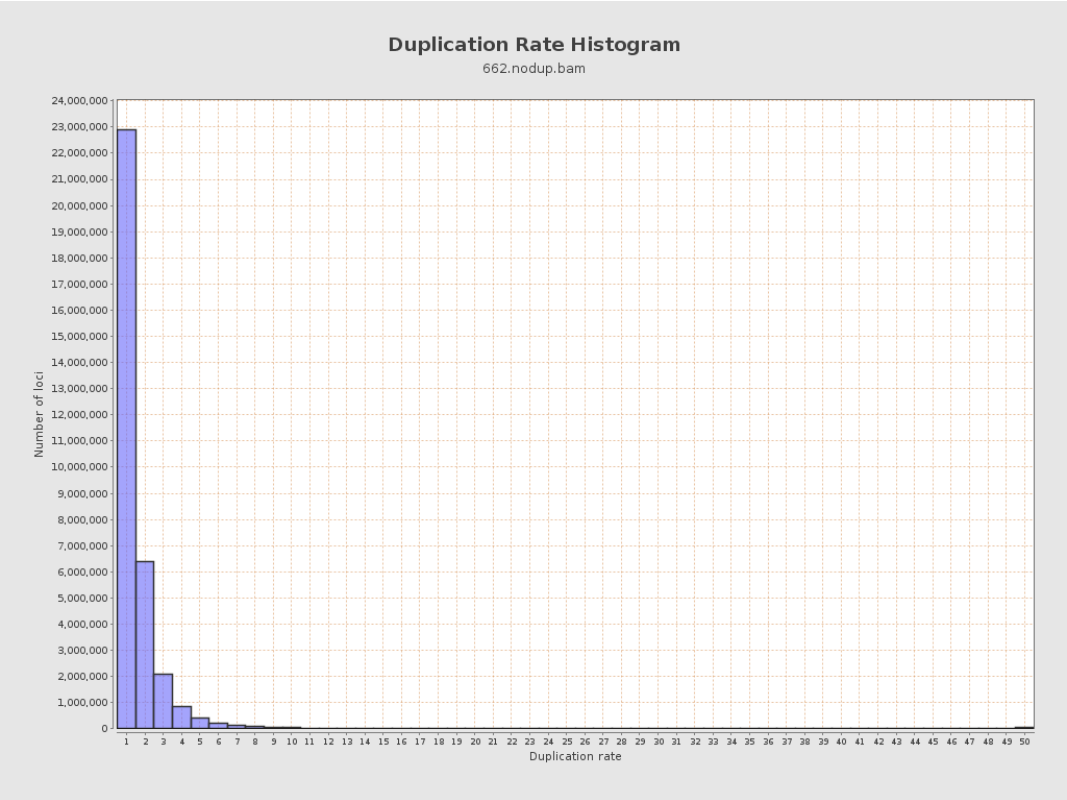
5. Results : Coverage Histogram (0-50X)



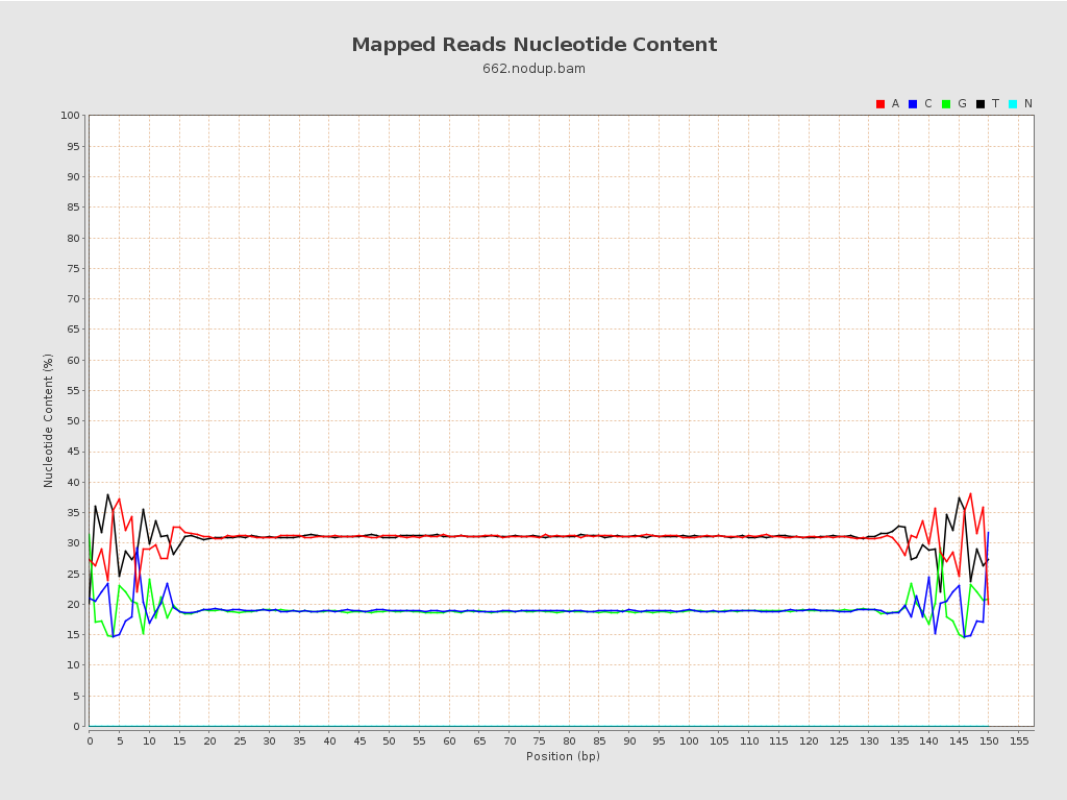
6. Results : Genome Fraction Coverage



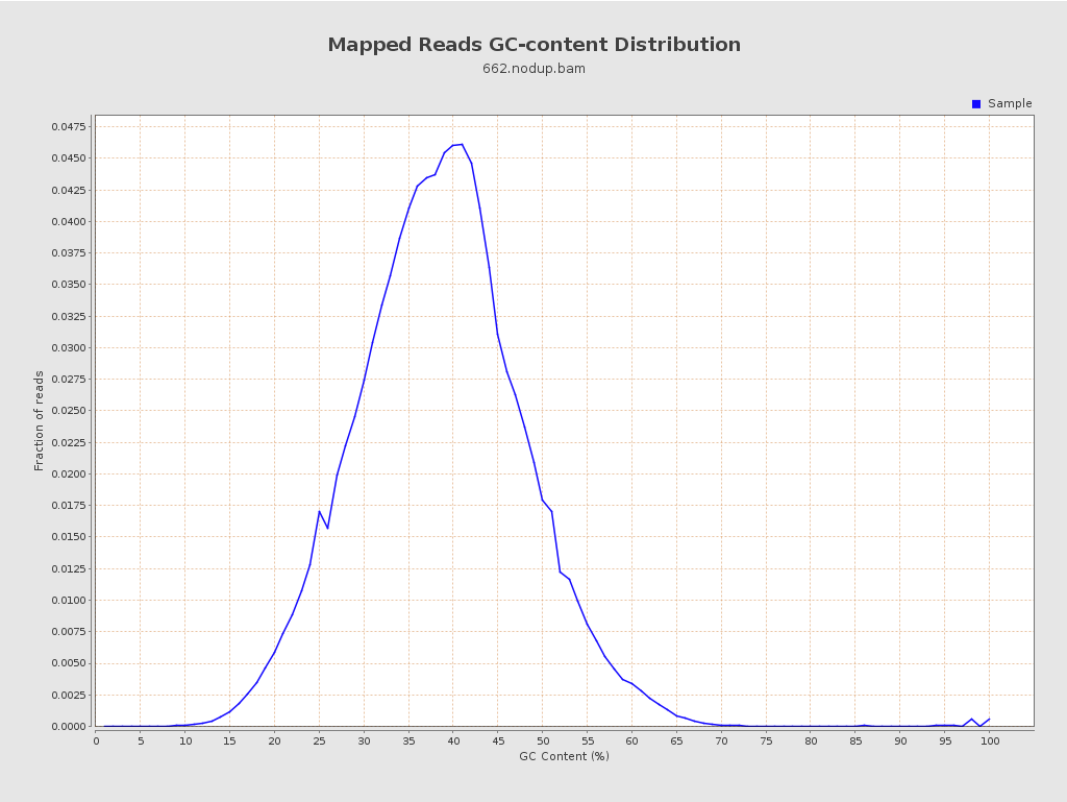
7. Results : Duplication Rate Histogram



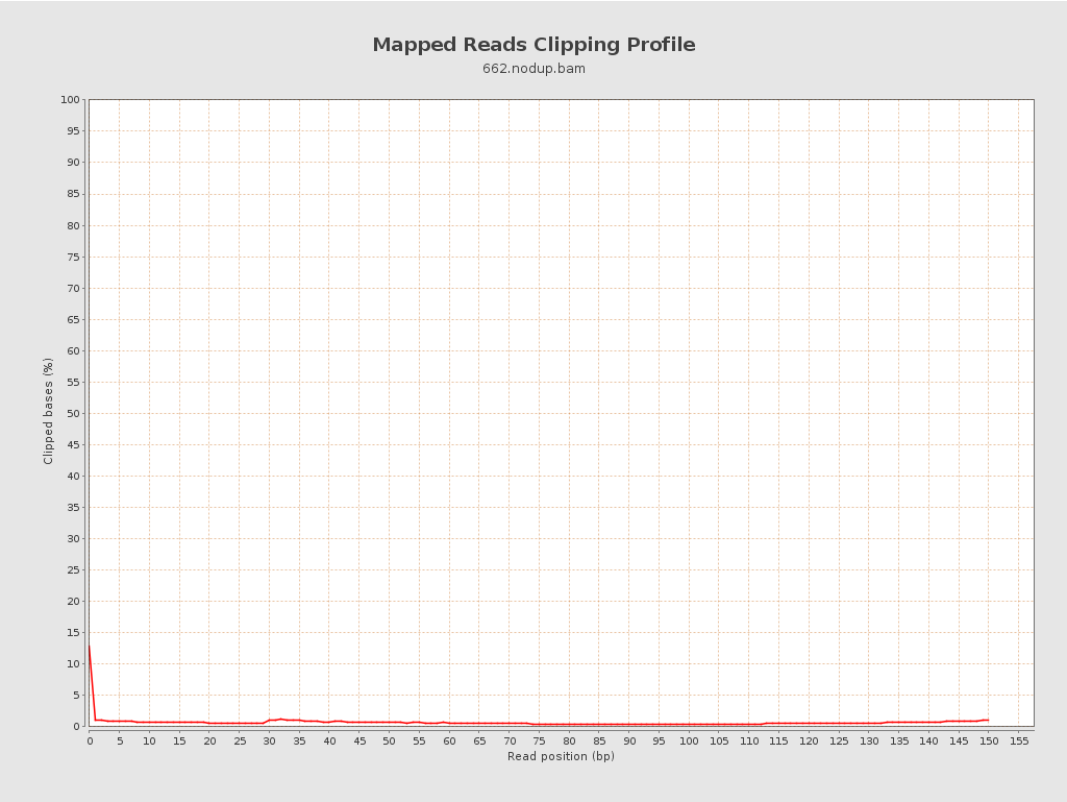
8. Results : Mapped Reads Nucleotide Content



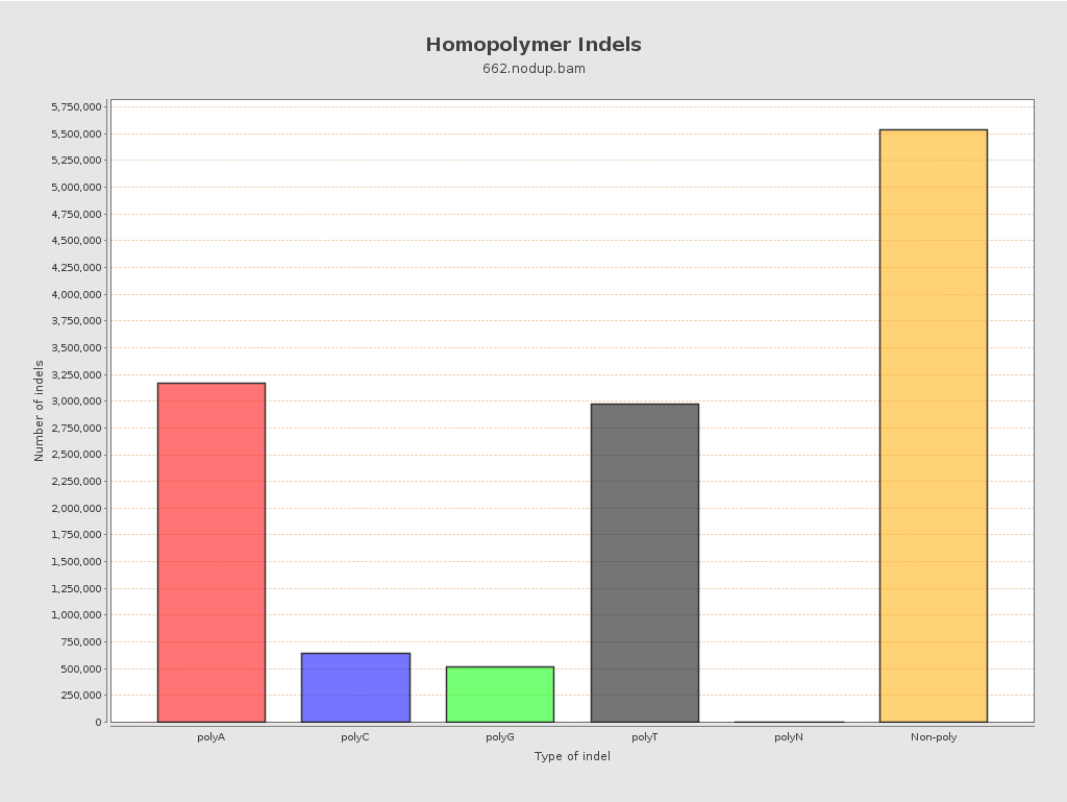
9. Results : Mapped Reads GC-content Distribution



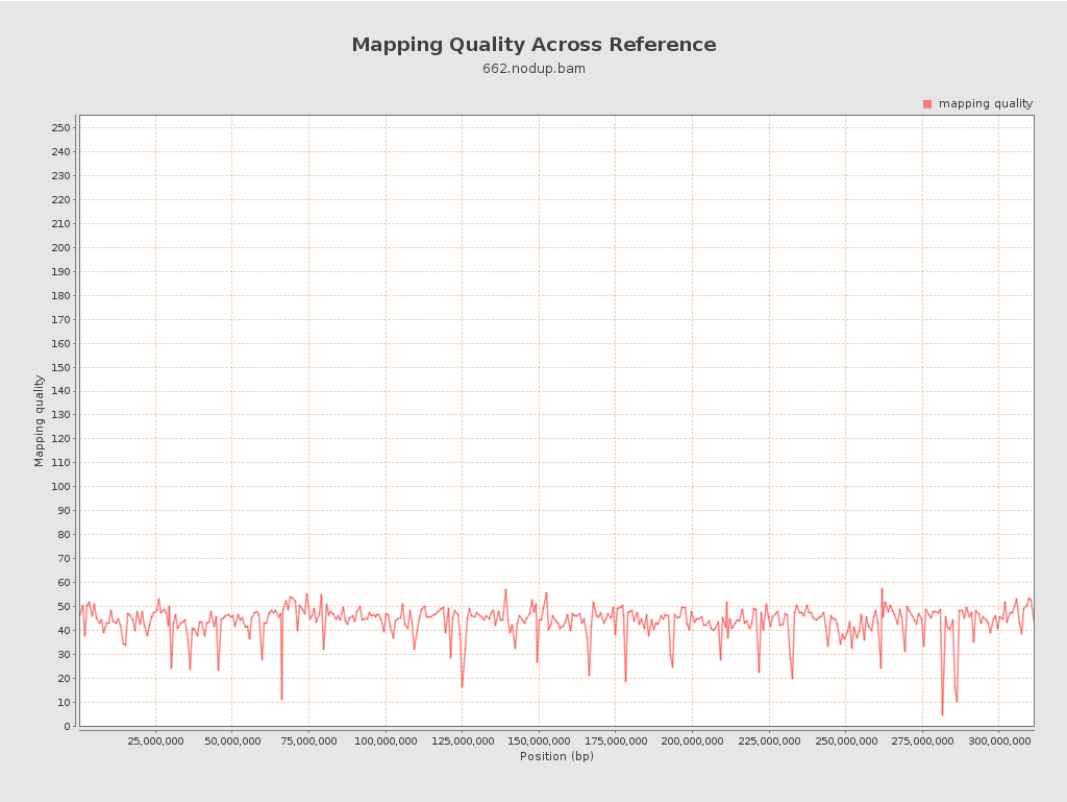
10. Results : Mapped Reads Clipping Profile



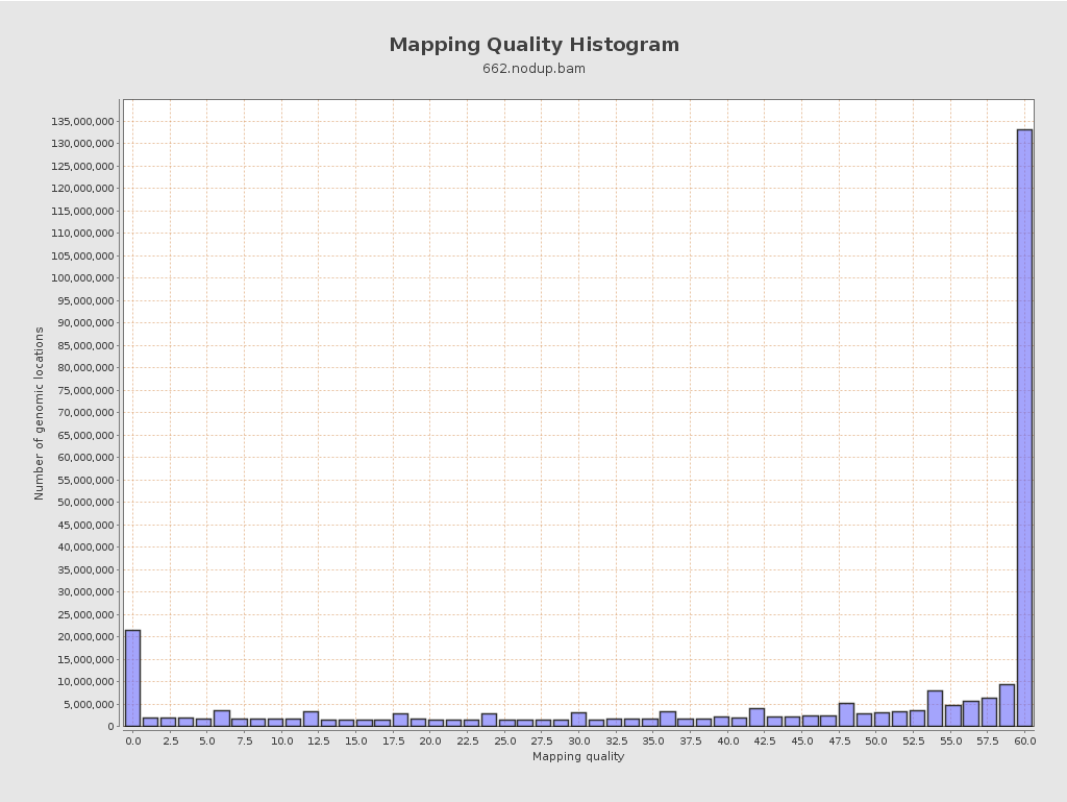
11. Results : Homopolymer Indels



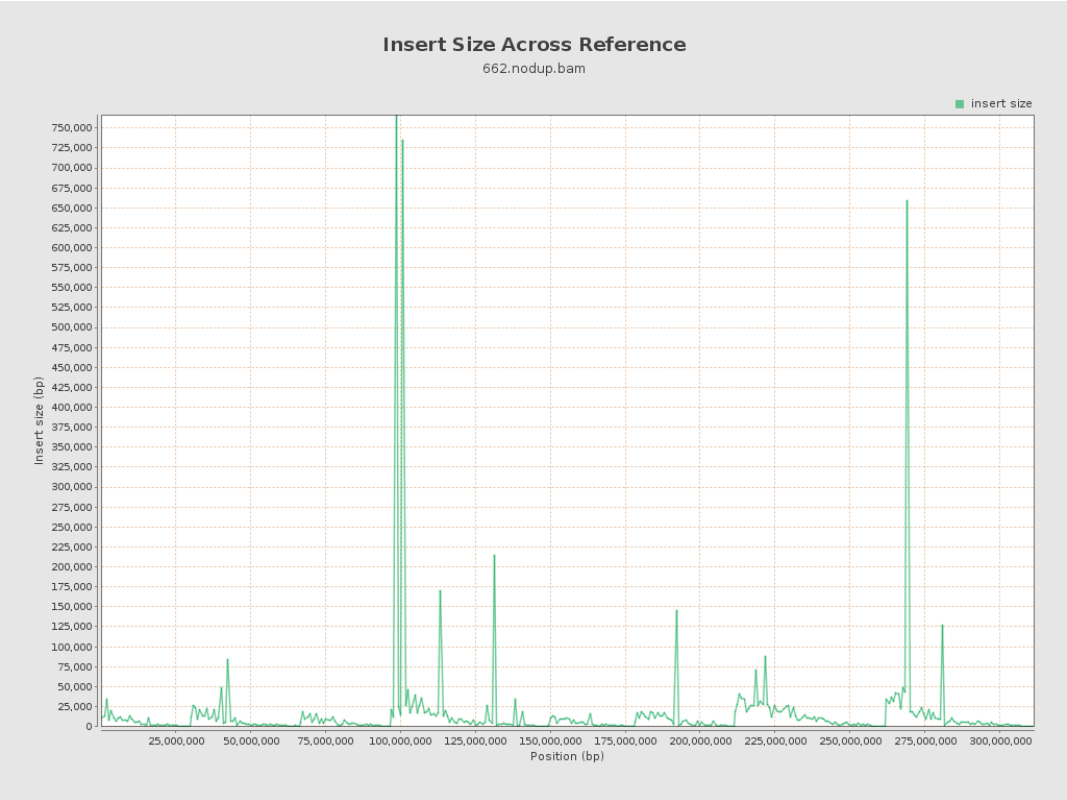
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram