Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/510.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/510.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_454/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_454_S429_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_454/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_454_S429_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,666,214
Mapped reads	72,940,696 / 91.56%
Unmapped reads	6,725,518 / 8.44%
Mapped paired reads	72,940,696 / 91.56%
Mapped reads, first in pair	36,496,433 / 45.81%
Mapped reads, second in pair	36,444,263 / 45.75%
Mapped reads, both in pair	70,757,131 / 88.82%
Mapped reads, singletons	2,183,565 / 2.74%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	13,006,211 / 16.33%
Clipped reads	16,716,461 / 20.98%

2.2. ACGT Content

Number/percentage of A's	3,112,986,343 / 30.95%
Number/percentage of C's	1,916,375,530 / 19.05%
Number/percentage of T's	3,119,346,903 / 31.01%
Number/percentage of G's	1,910,138,529 / 18.99%
Number/percentage of N's	32,842 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	32.3595
Standard Deviation	293.892

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Insert size

Mean	251,609.77
Standard Deviation	2,416,129.32
P25/Median/P75	344 / 451 / 593

2.6. Mismatches and indels

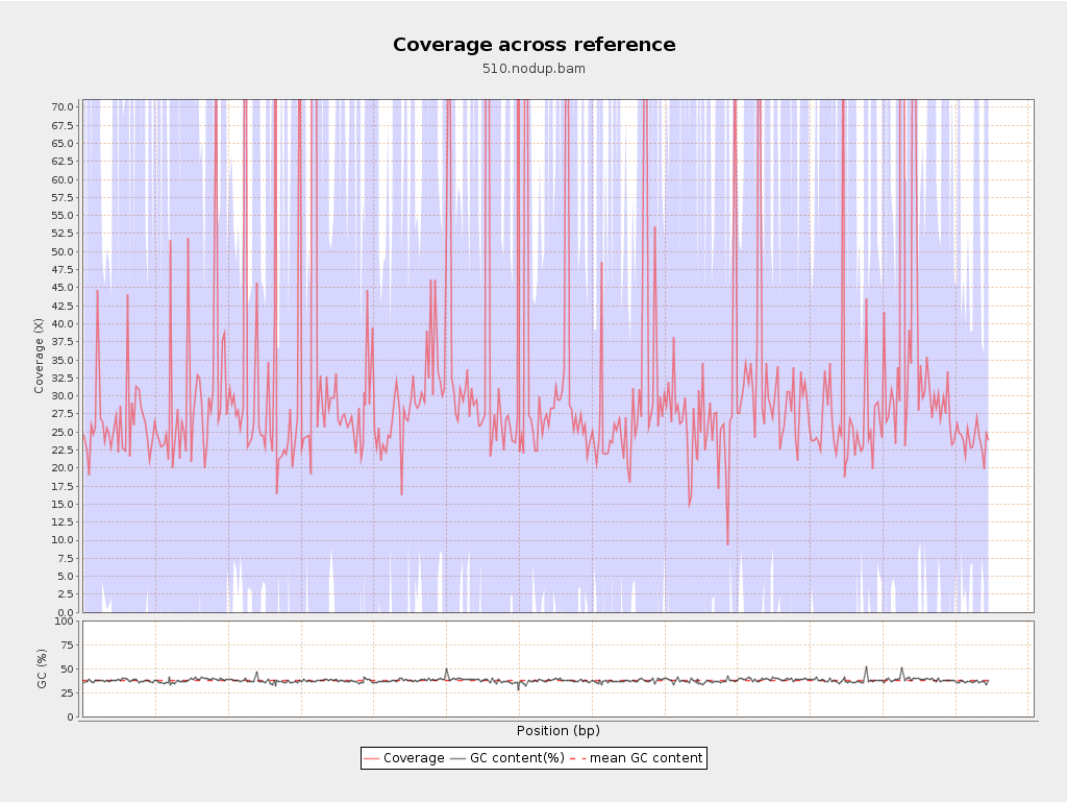
General error rate	2.38%
Mismatches	219,680,371
Insertions	7,208,372
Mapped reads with at least one insertion	8.82%
Deletions	6,924,189
Mapped reads with at least one deletion	8.42%
Homopolymer indels	57.14%

2.7. Chromosome stats

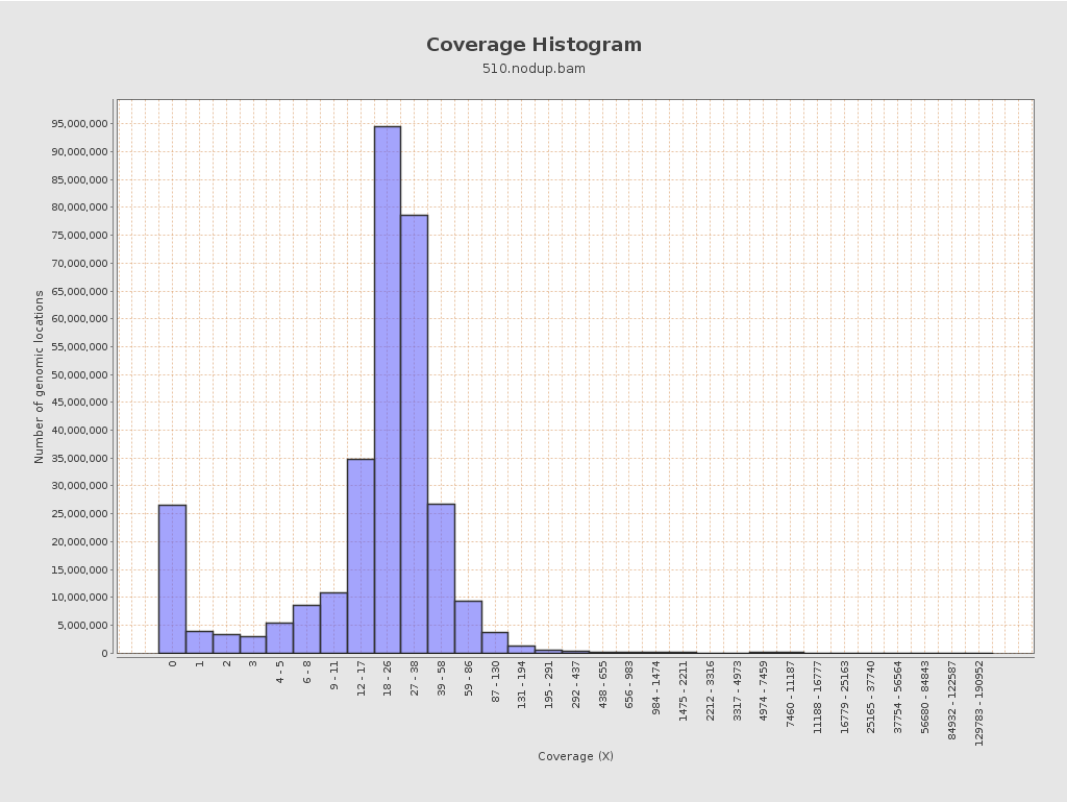
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	771606515	25.9587	110.1627

LT669789.1	36598175	1181813652	32.2916	313.578
LT669790.1	30422129	1157974719	38.0636	408.617
LT669791.1	52758100	1704745259	32.3125	301.9339
LT669792.1	28376109	927966337	32.7024	332.1648
LT669793.1	33388210	977179528	29.2672	197.9208
LT669794.1	50579949	1544367899	30.5332	247.7724
LT669795.1	49795044	1818934435	36.5284	332.9852

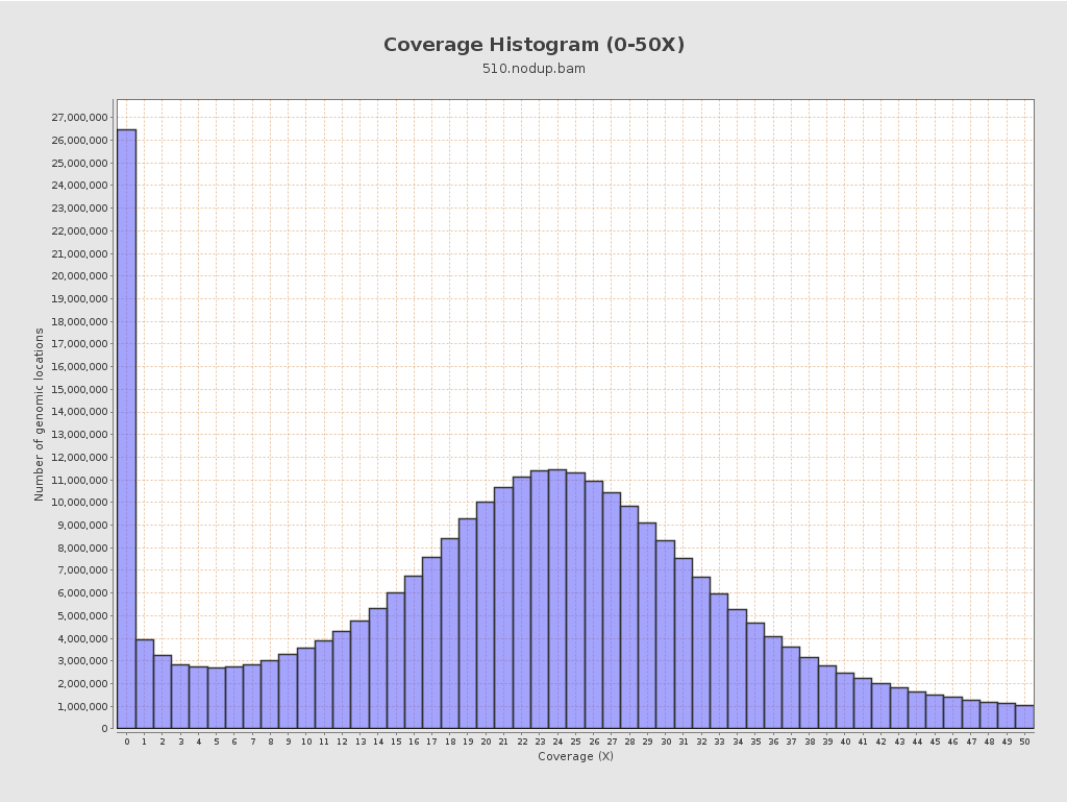
3. Results : Coverage across reference



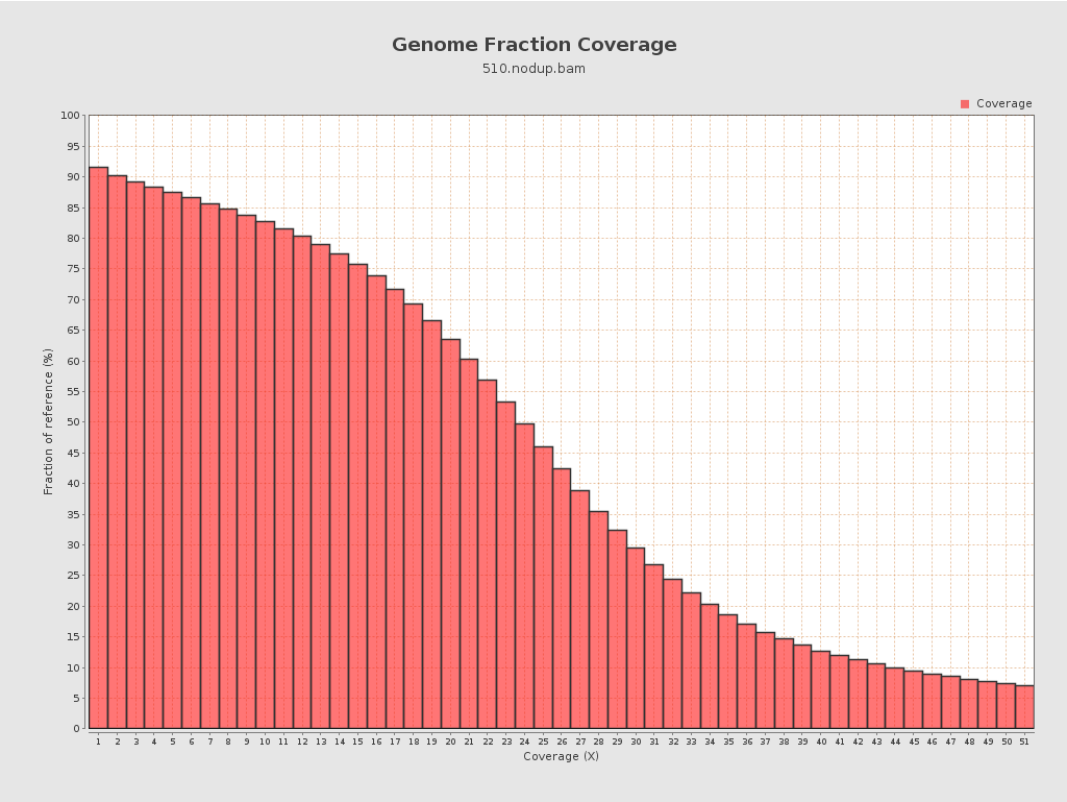
4. Results : Coverage Histogram



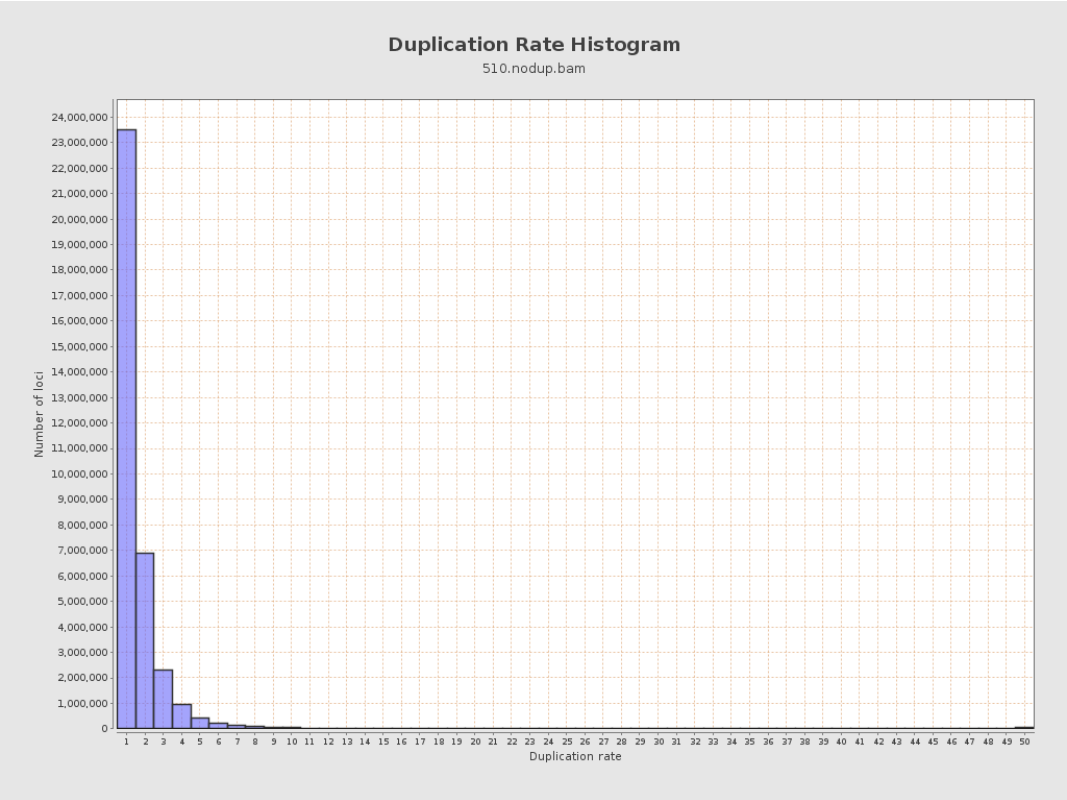
5. Results : Coverage Histogram (0-50X)



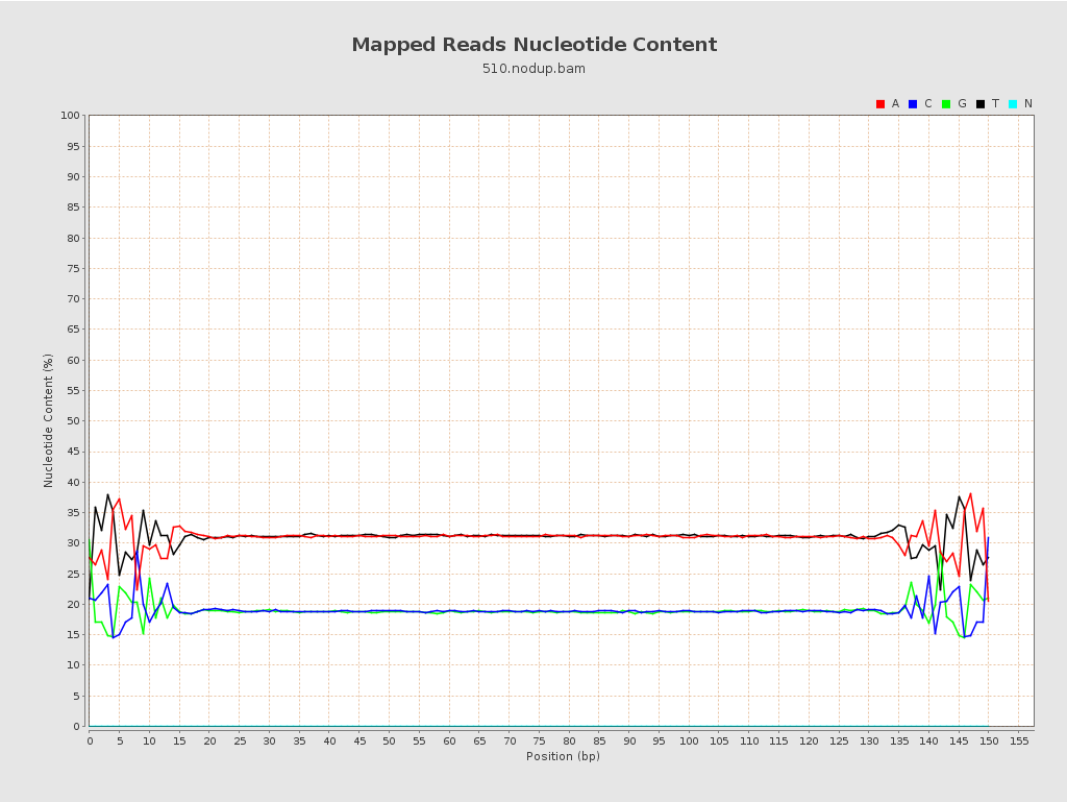
6. Results : Genome Fraction Coverage



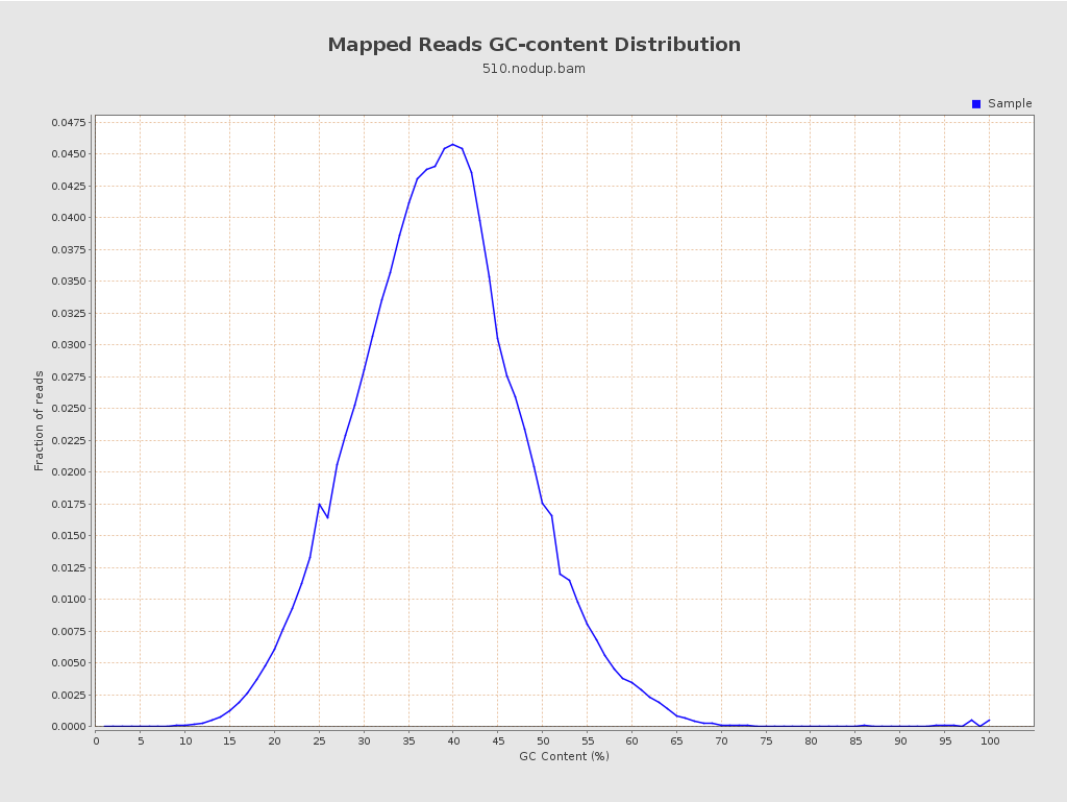
7. Results : Duplication Rate Histogram



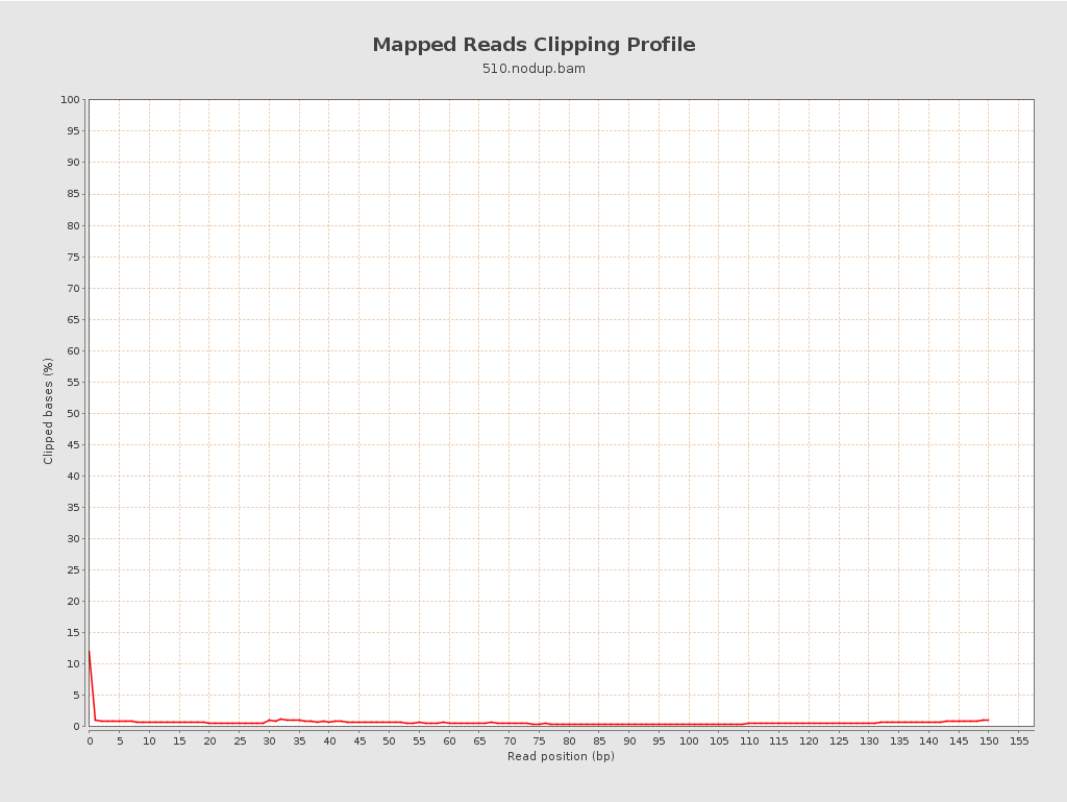
8. Results : Mapped Reads Nucleotide Content



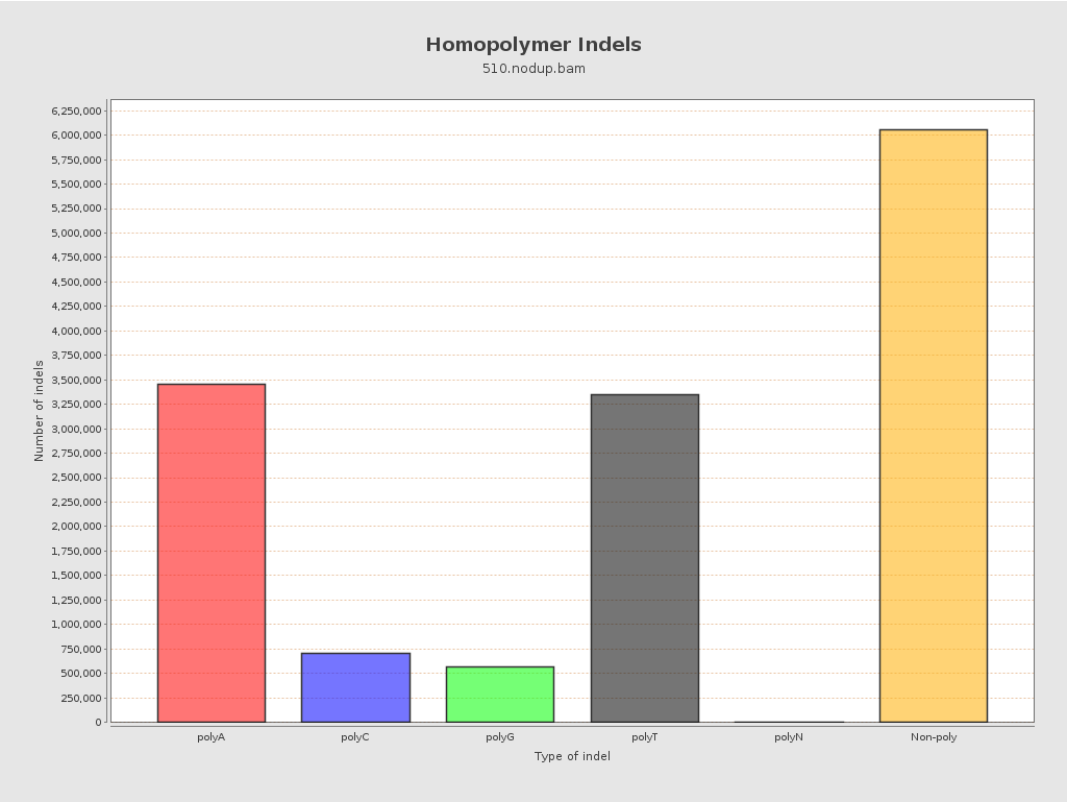
9. Results : Mapped Reads GC-content Distribution



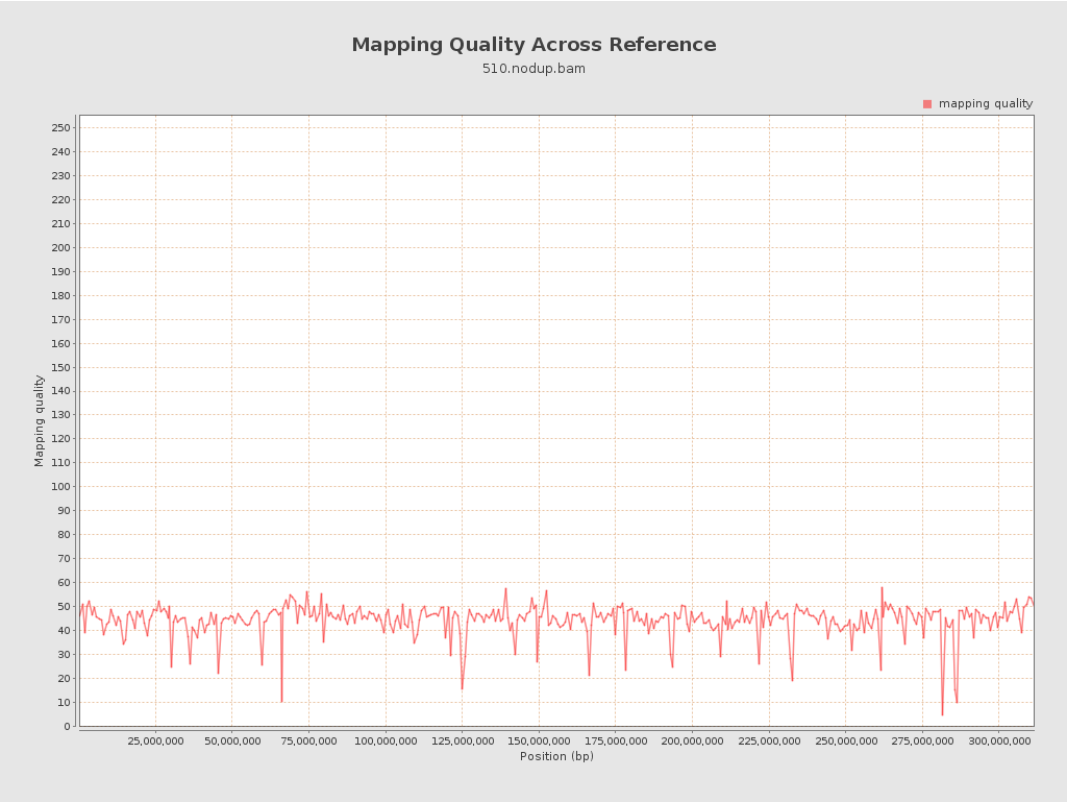
10. Results : Mapped Reads Clipping Profile



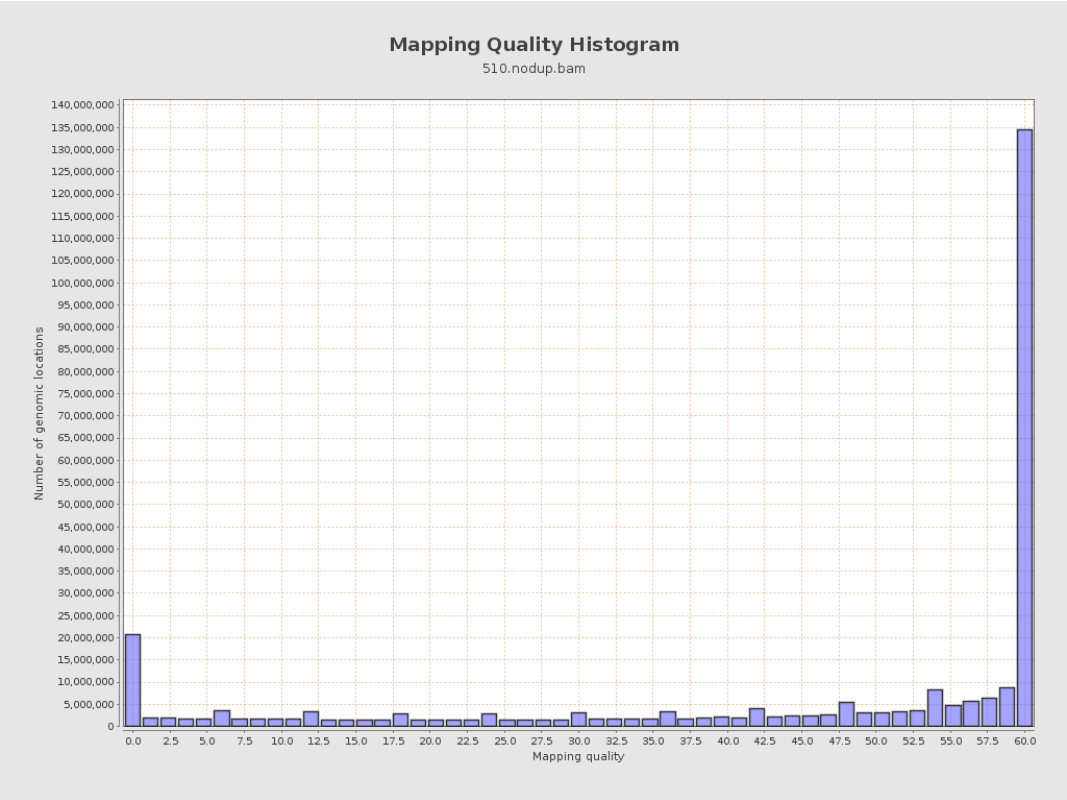
11. Results : Homopolymer Indels



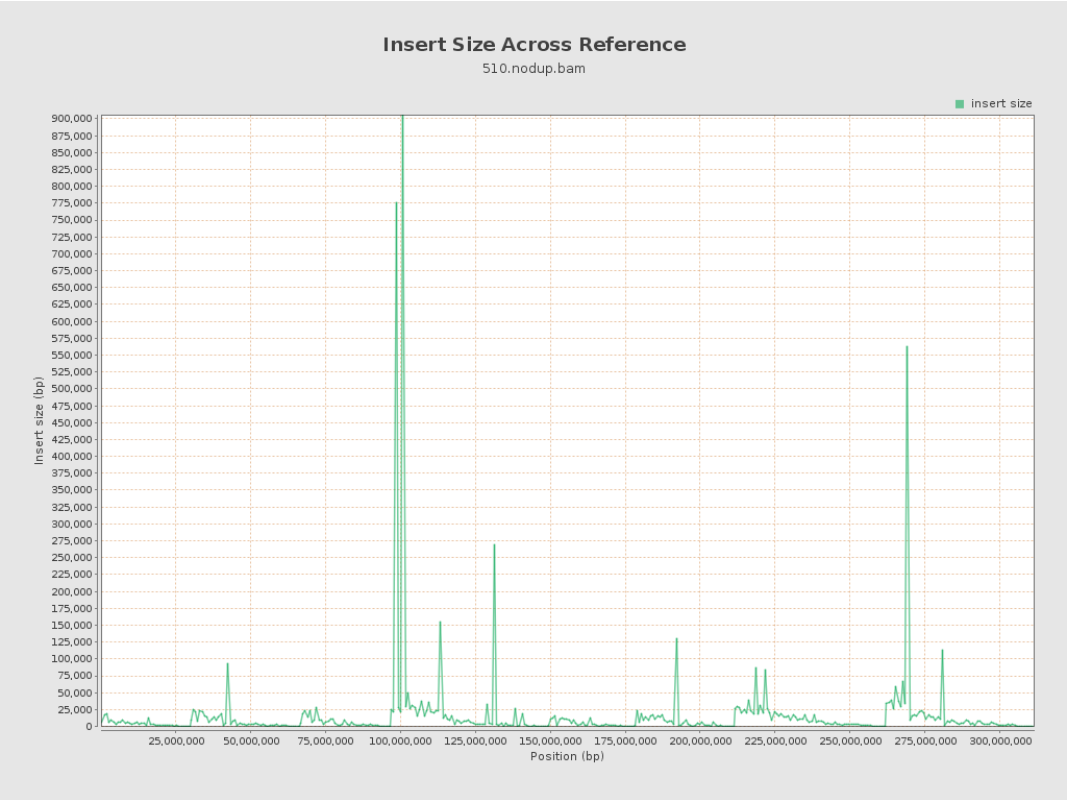
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram