

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/127
3
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1273 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_494/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_494_S469_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_494/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_494_S469_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:34:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	74,699,565
Mapped reads	70,043,797 / 93.77%
Unmapped reads	4,655,768 / 6.23%
Mapped paired reads	70,043,797 / 93.77%
Mapped reads, first in pair	35,095,893 / 46.98%
Mapped reads, second in pair	34,947,904 / 46.78%
Mapped reads, both in pair	68,633,594 / 91.88%
Mapped reads, singletons	1,410,203 / 1.89%
Read min/max/mean length	30 / 151 / 148.37
Duplicated reads (flagged)	10,919,949 / 14.62%
Clipped reads	14,155,958 / 18.95%

2.2. ACGT Content

Number/percentage of A's	3,039,651,139 / 30.97%
Number/percentage of C's	1,870,172,107 / 19.05%
Number/percentage of T's	3,041,251,091 / 30.99%
Number/percentage of G's	1,864,081,593 / 18.99%
Number/percentage of N's	33,559 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	31.5743
Standard Deviation	218.8562

2.4. Mapping Quality

Mean Mapping Quality	44.8
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2.5. Insert size

Mean	228,894
Standard Deviation	2,275,161.65
P25/Median/P75	370 / 478 / 623

2.6. Mismatches and indels

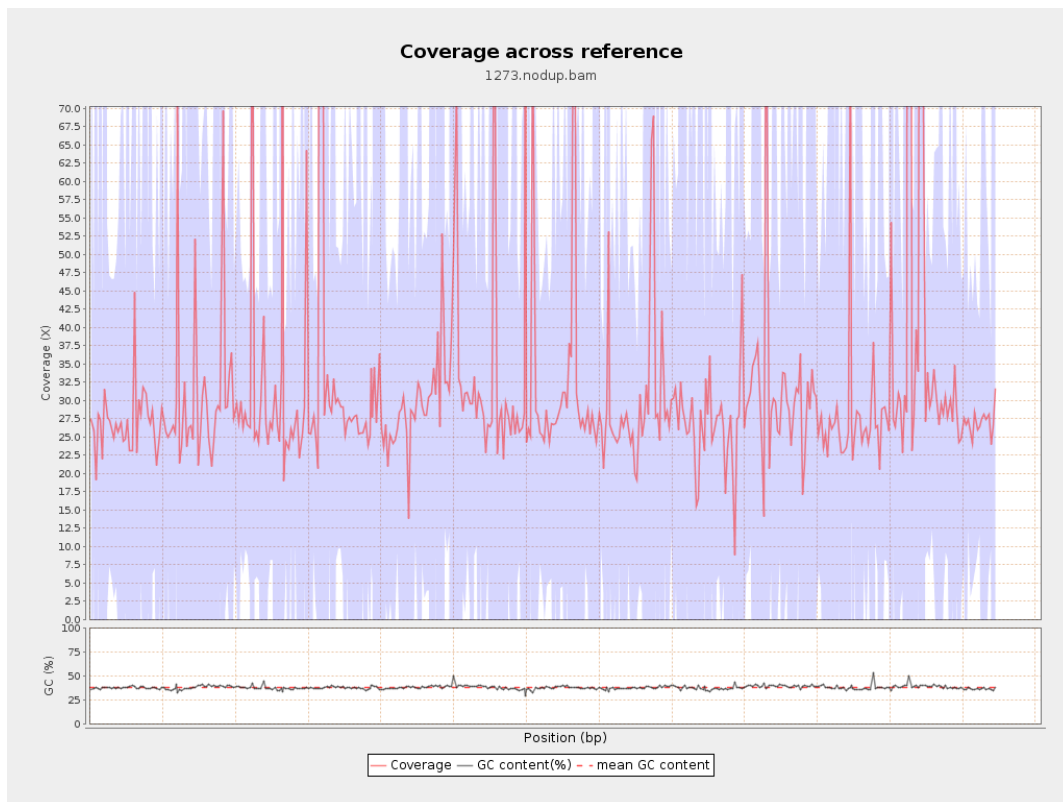
General error rate	2.21%
Mismatches	198,877,702
Insertions	6,354,935
Mapped reads with at least one insertion	8.17%
Deletions	6,488,978
Mapped reads with at least one deletion	8.26%
Homopolymer indels	56.75%

2.7. Chromosome stats

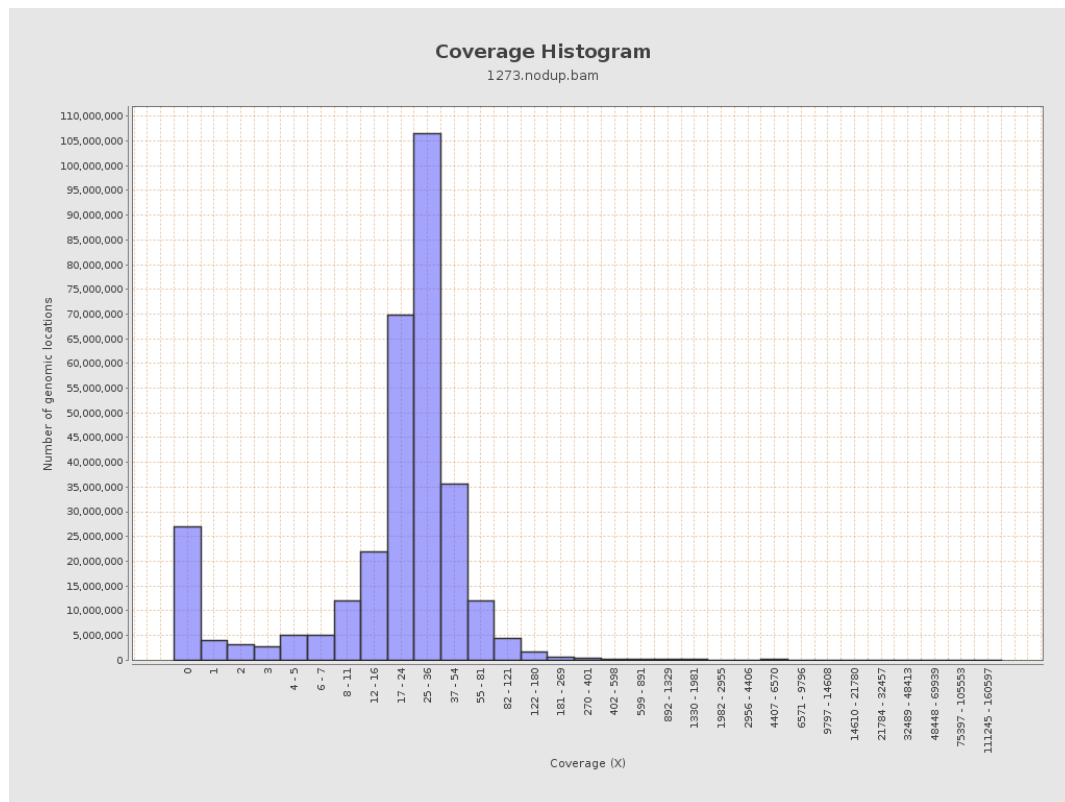
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	796568742	26.7985	59.7525

LT669789.1	36598175	1162527256	31.7646	228.3323
LT669790.1	30422129	1027317828	33.7688	223.0332
LT669791.1	52758100	1628503130	30.8674	180.2049
LT669792.1	28376109	894394891	31.5193	259.1992
LT669793.1	33388210	969983106	29.0517	157.9737
LT669794.1	50579949	1494257246	29.5425	188.0628
LT669795.1	49795044	1866337249	37.4804	321.7437

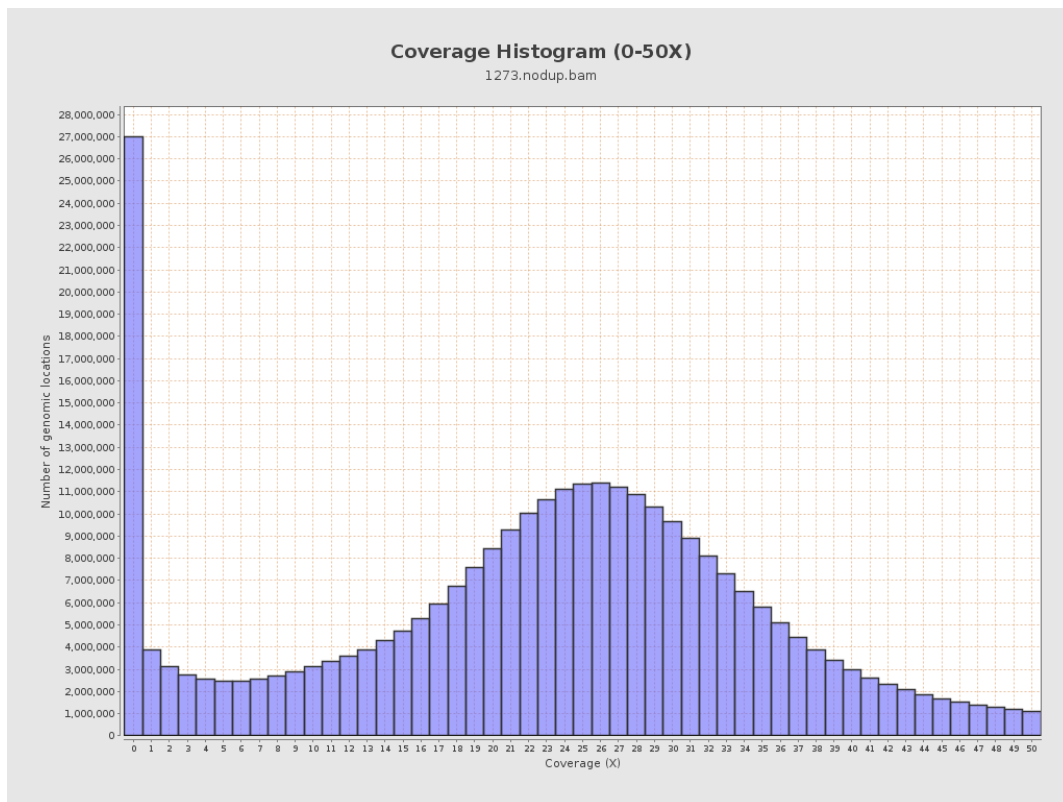
3. Results : Coverage across reference



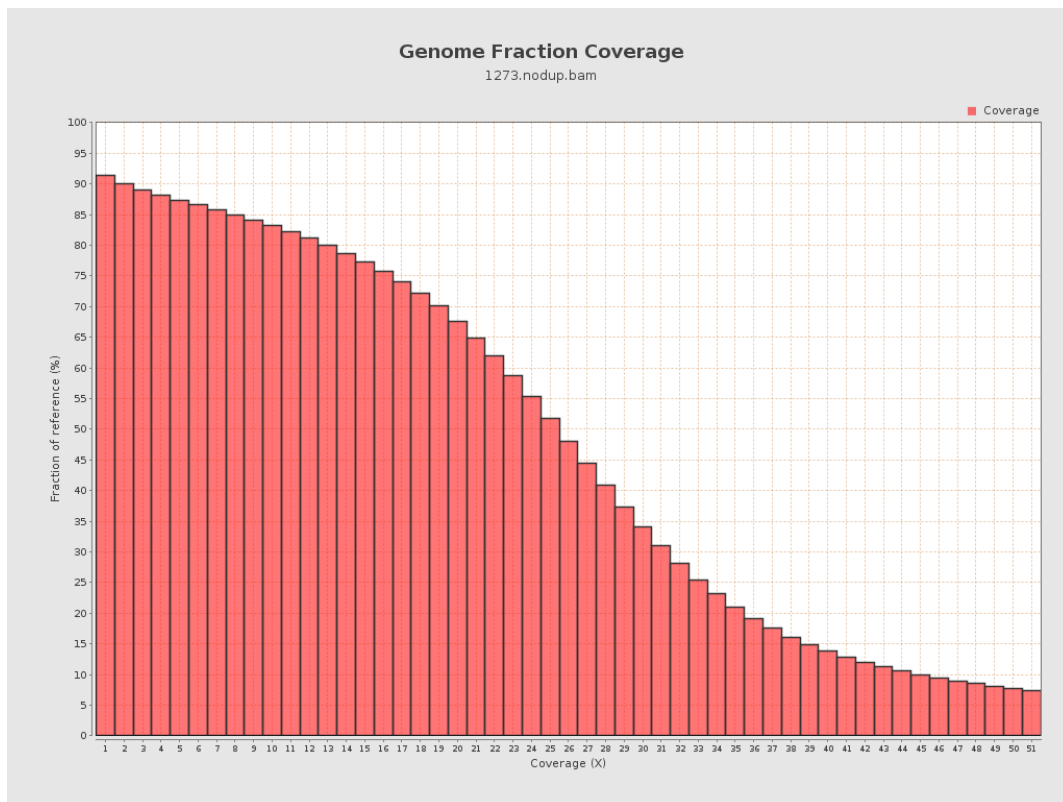
4. Results : Coverage Histogram



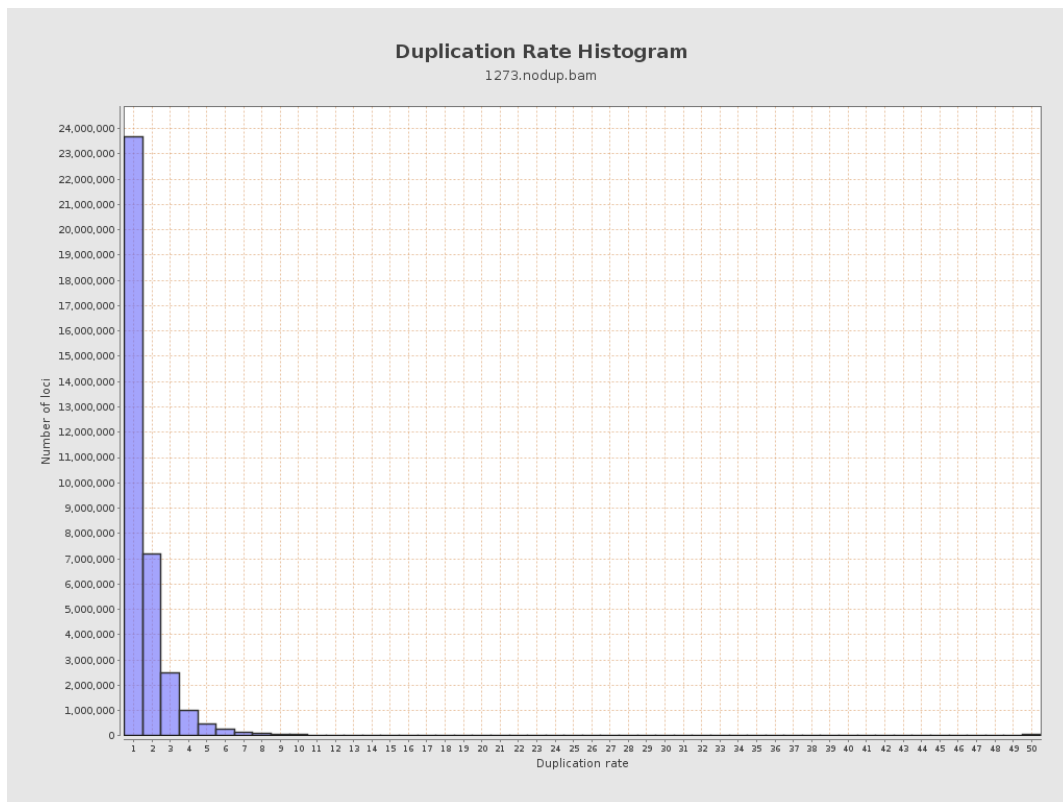
5. Results : Coverage Histogram (0-50X)



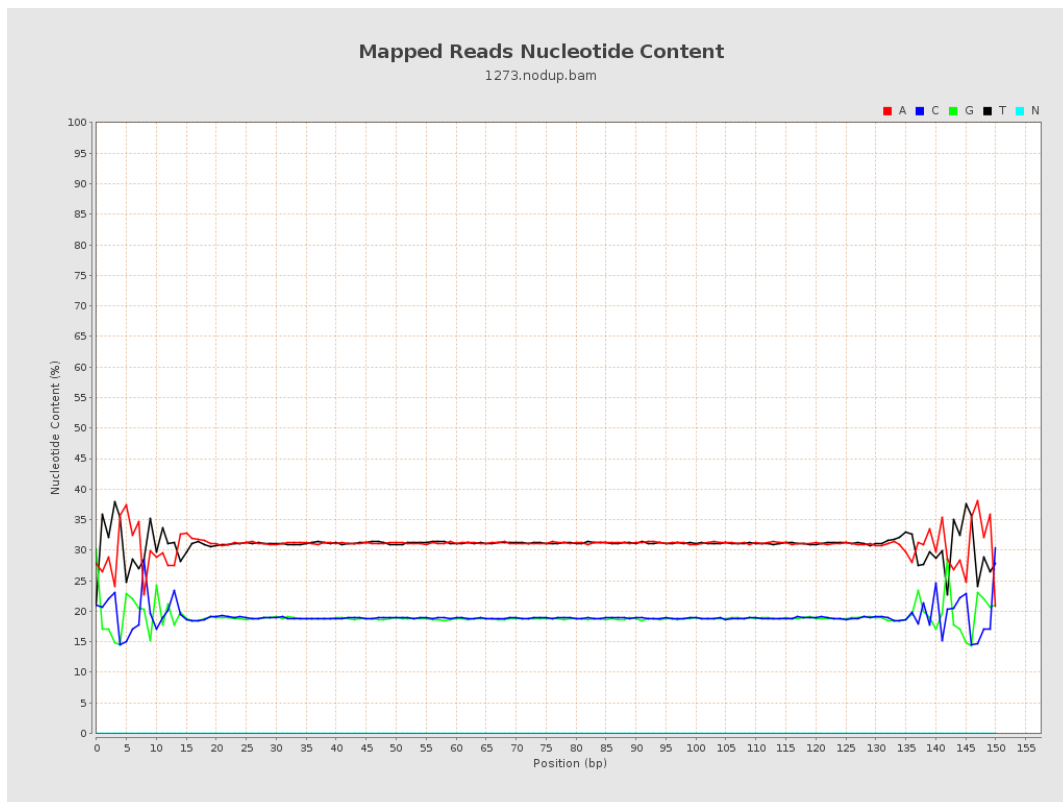
6. Results : Genome Fraction Coverage



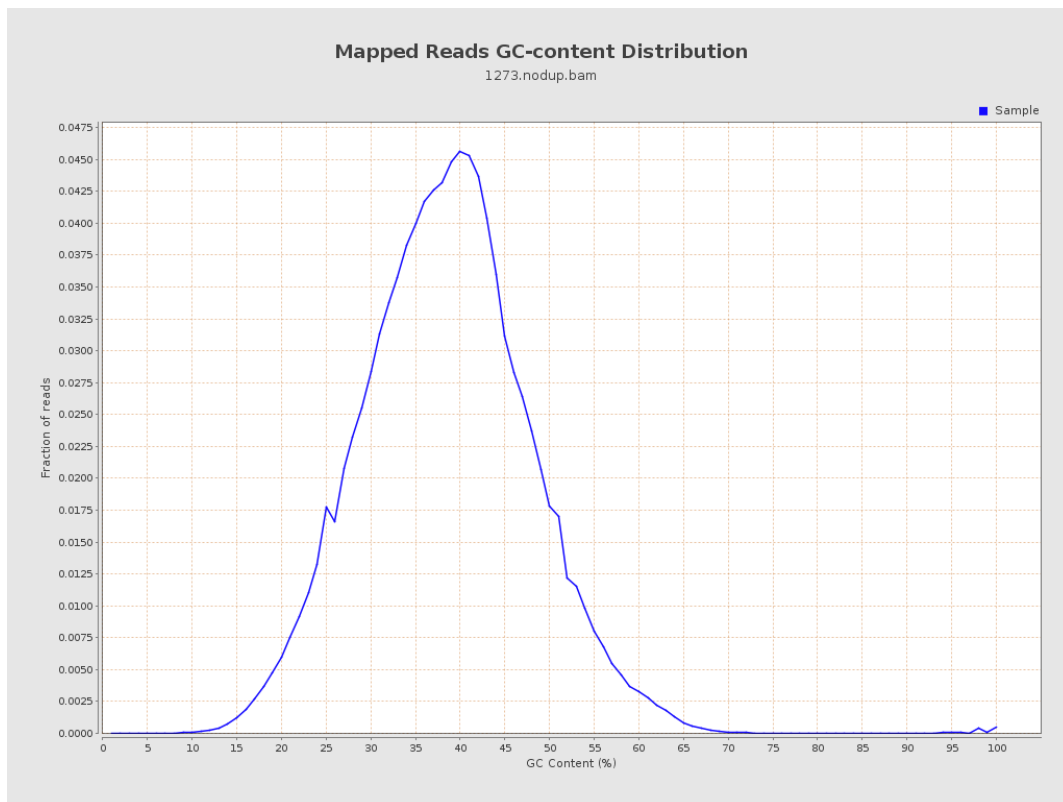
7. Results : Duplication Rate Histogram



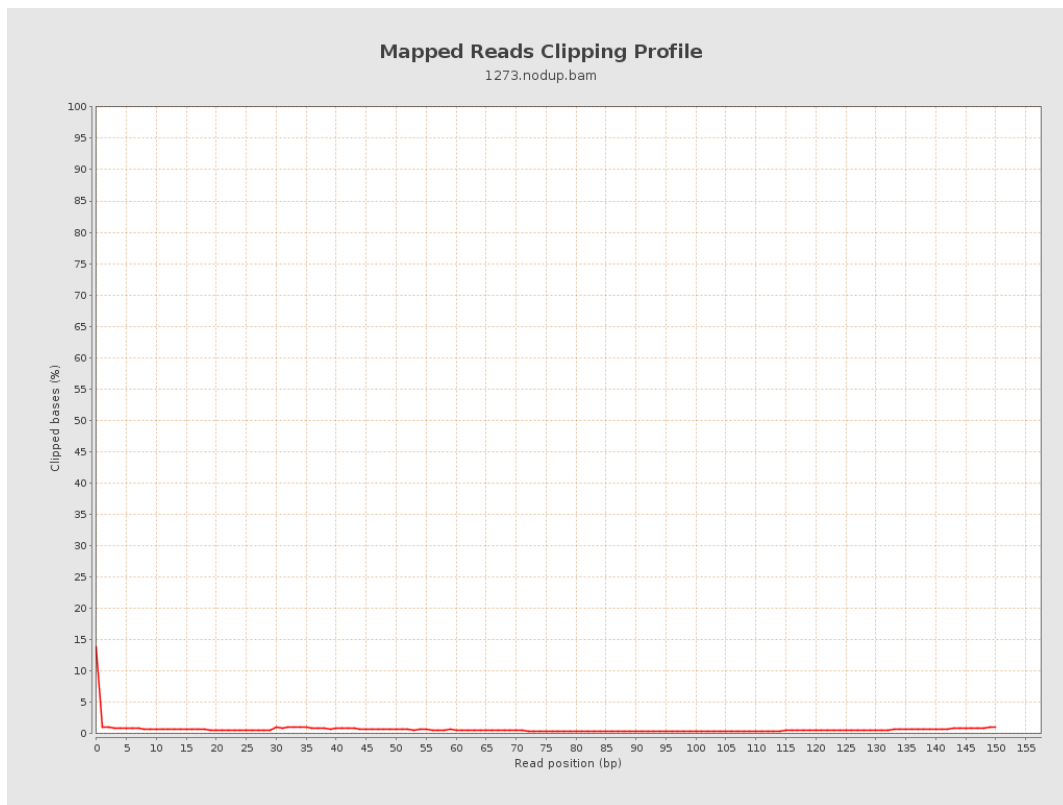
8. Results : Mapped Reads Nucleotide Content



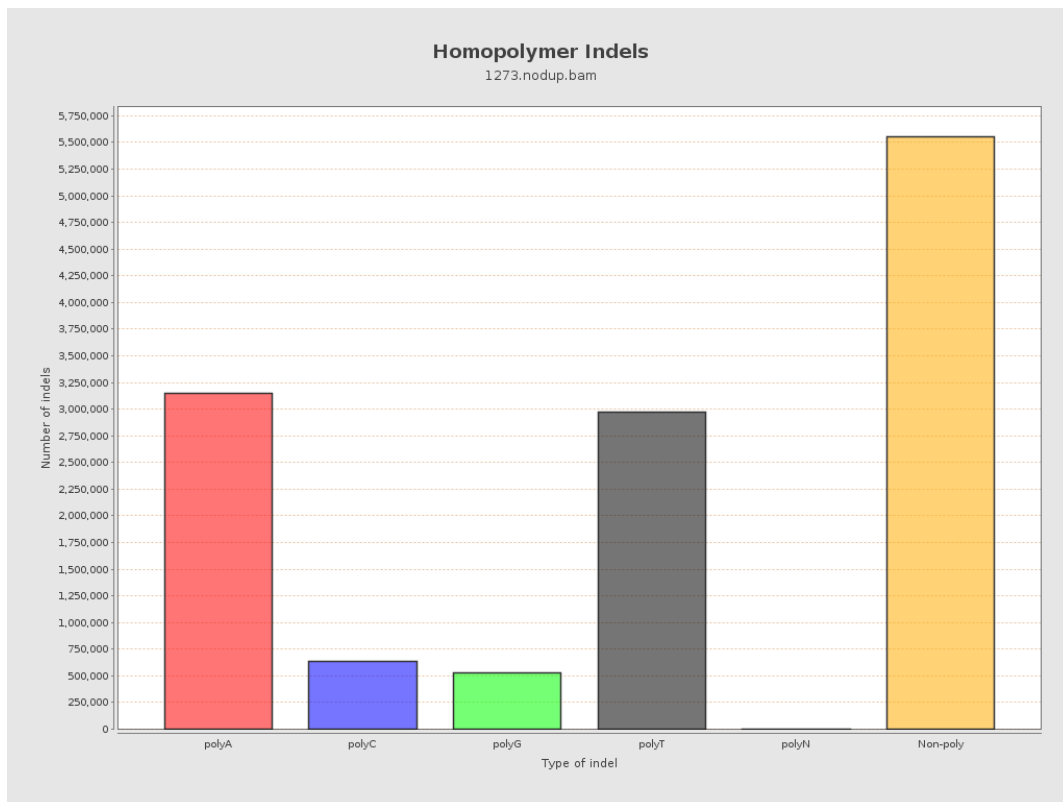
9. Results : Mapped Reads GC-content Distribution



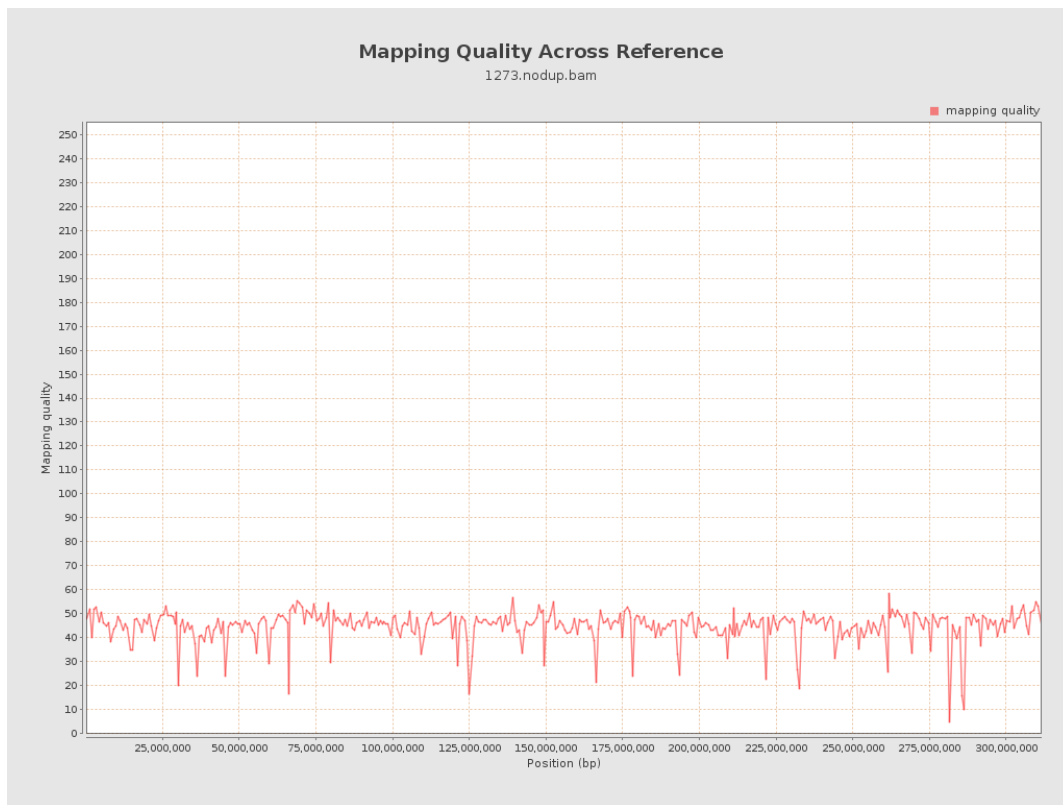
10. Results : Mapped Reads Clipping Profile



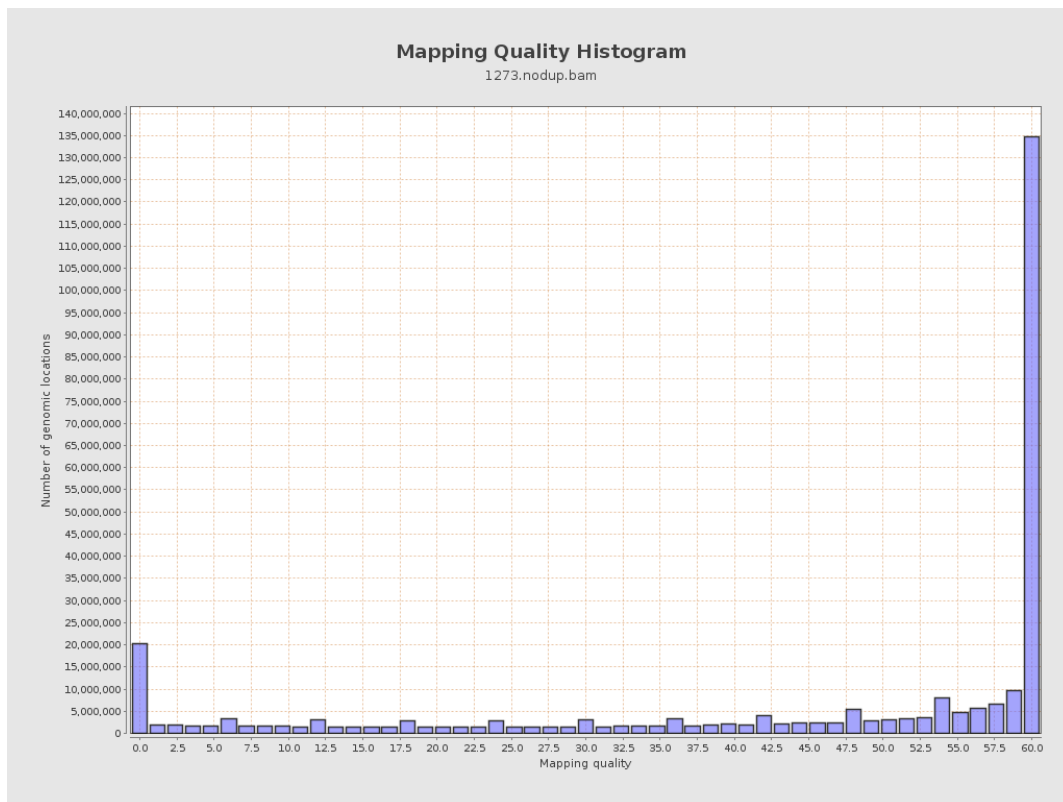
11. Results : Homopolymer Indels



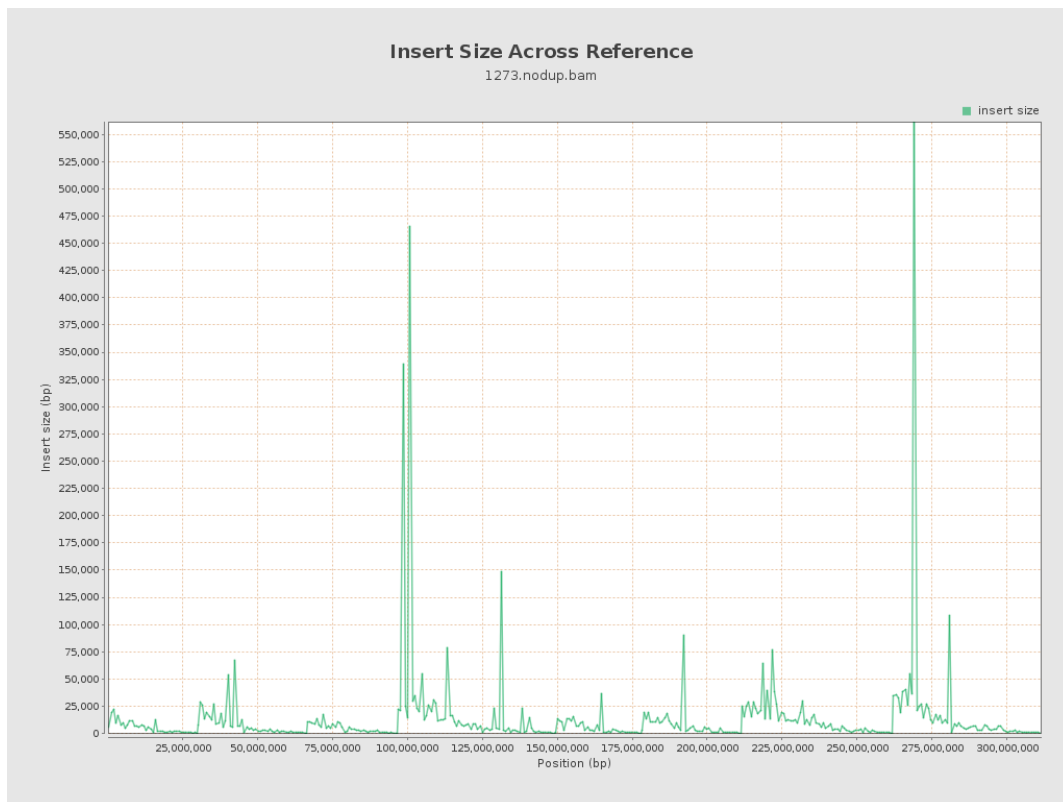
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

