Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:37:15

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1425
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1425 .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_415/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_415_S390_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_415/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_415_S390_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:37:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,558,407
Mapped reads	76,660,816 / 95.16%
Unmapped reads	3,897,591 / 4.84%
Mapped paired reads	76,660,816 / 95.16%
Mapped reads, first in pair	38,378,614 / 47.64%
Mapped reads, second in pair	38,282,202 / 47.52%
Mapped reads, both in pair	75,367,880 / 93.56%
Mapped reads, singletons	1,292,936 / 1.6%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	11,688,571 / 14.51%
Clipped reads	16,452,784 / 20.42%

2.2. ACGT Content

Number/percentage of A's	3,279,940,592 / 30.7%
Number/percentage of C's	2,062,762,383 / 19.31%
Number/percentage of T's	3,286,786,484 / 30.77%
Number/percentage of G's	2,053,289,389 / 19.22%
Number/percentage of N's	35,315 / 0%
GC Percentage	38.53%

2.3. Coverage

Mean	34.3695
Standard Deviation	261.2207

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Insert size

| Mean	226,818.89
Standard Deviation	2,248,929.51
P25/Median/P75	334 / 437 / 572

2.6. Mismatches and indels

General error rate	2.25%
Mismatches	220,768,745
Insertions	7,030,507
Mapped reads with at least one insertion	8.26%
Deletions	7,345,318
Mapped reads with at least one deletion	8.5%
Homopolymer indels	56.08%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	851852611	28.6584	95.9977

|				
LT669789.1	36598175	1270340368	34.7105	282.3126
LT669790.1	30422129	1063702376	34.9648	222.4096
LT669791.1	52758100	1771143089	33.571	206.8422
LT669792.1	28376109	951345292	33.5263	271.9513
LT669793.1	33388210	1080664314	32.3666	189.778
LT669794.1	50579949	1652514062	32.6713	226.3238
LT669795.1	49795044	2069420911	41.5588	411.126

3. Results : Coverage across reference

Coverage across reference
1425.nodup.bam
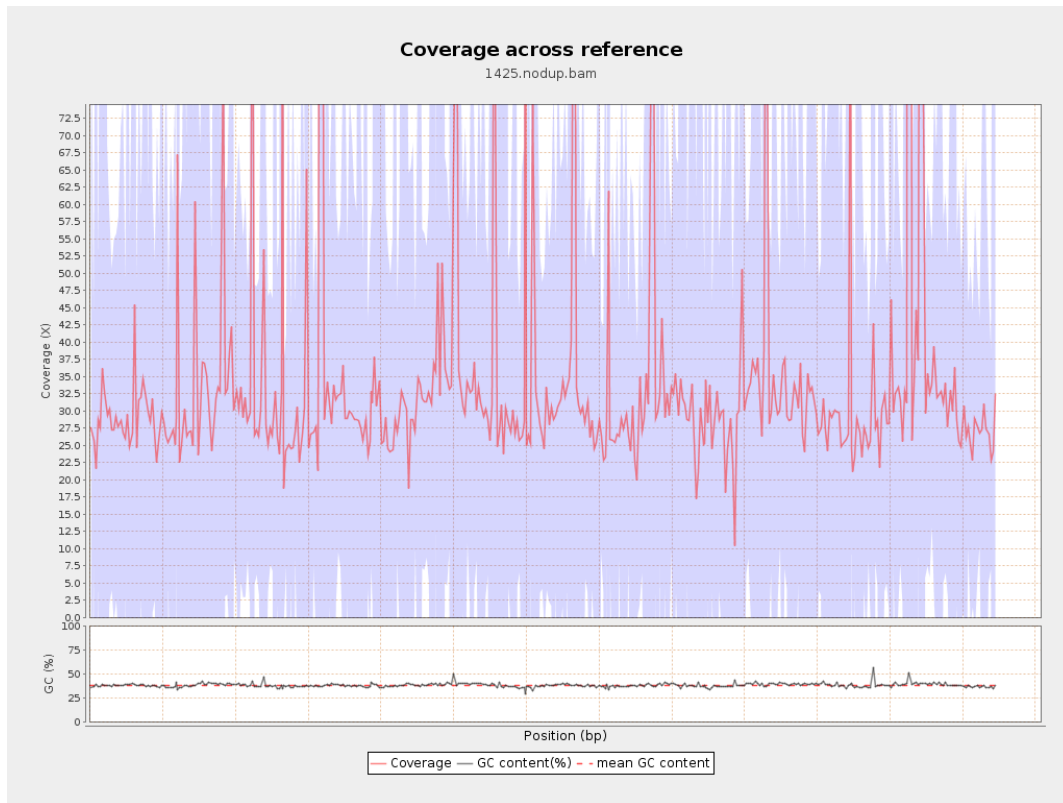
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
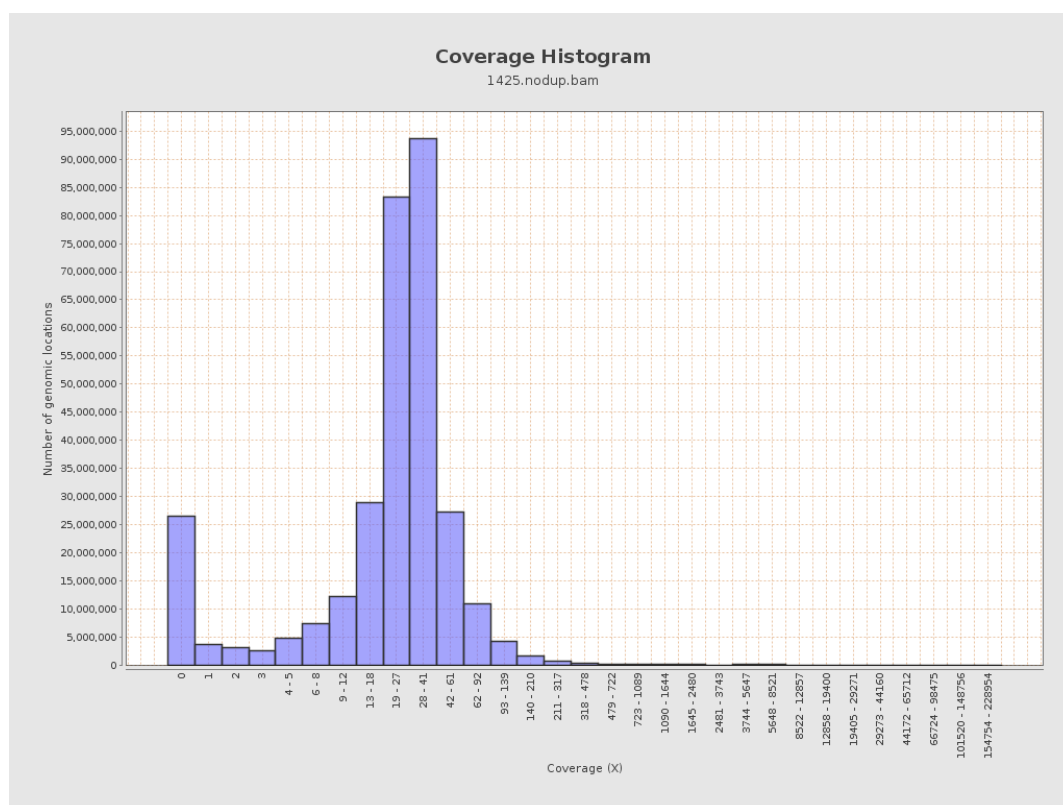
Coverage Histogram (0-50X)
1425.nodup.bam
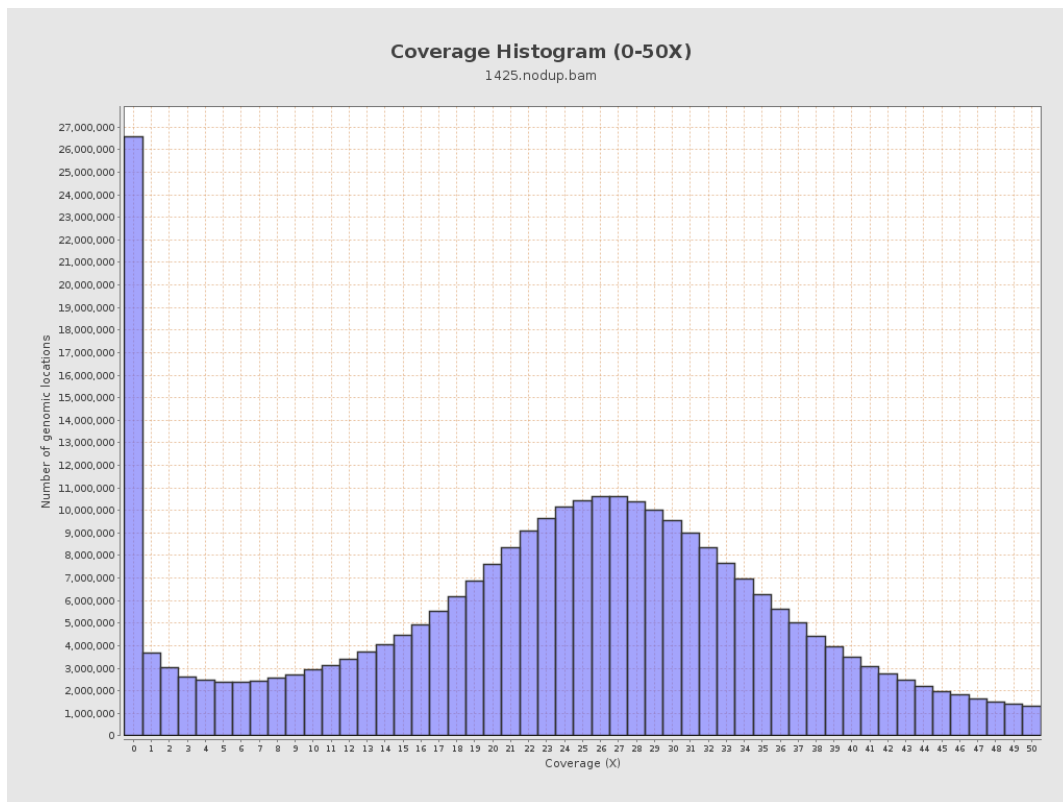
6. Results : Genome Fraction Coverage
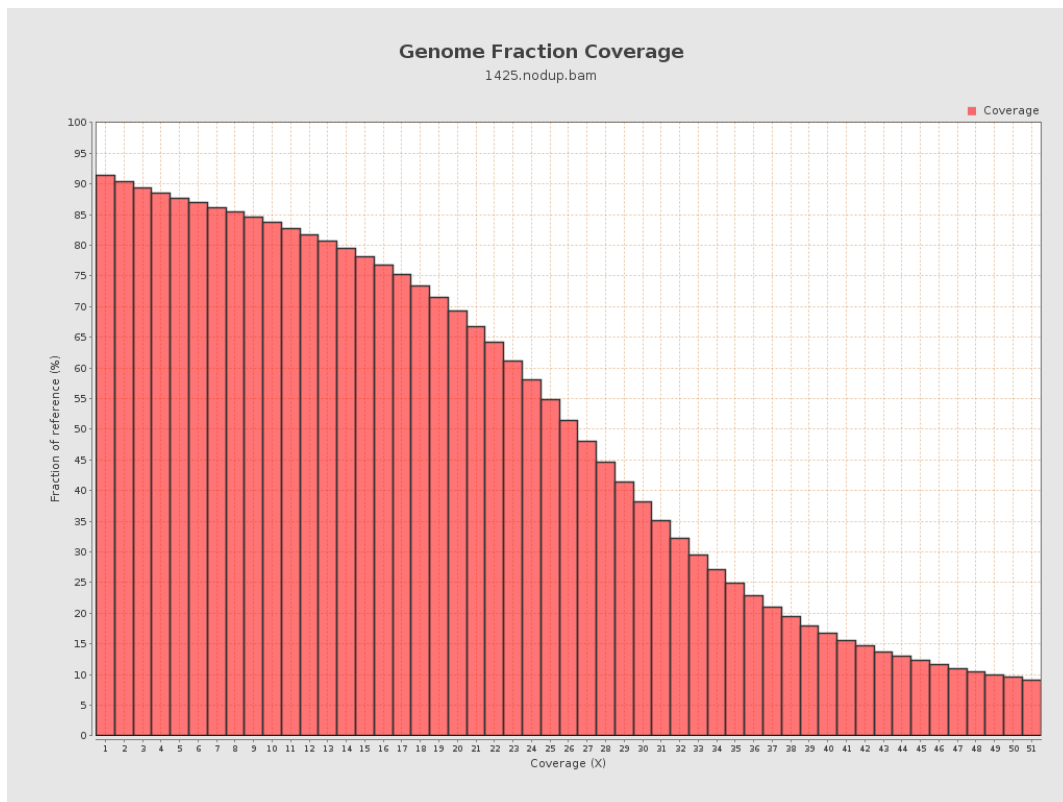
7. Results : Duplication Rate Histogram
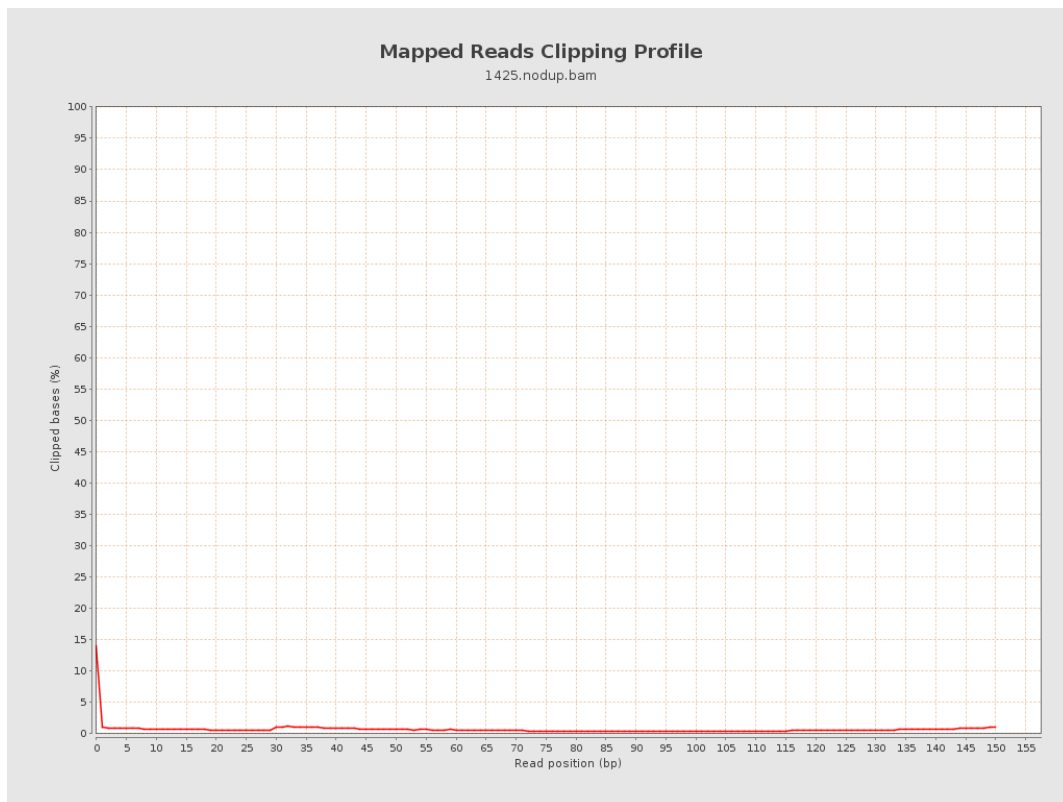

Duplication Rate Histogram
1425.nodup.bam
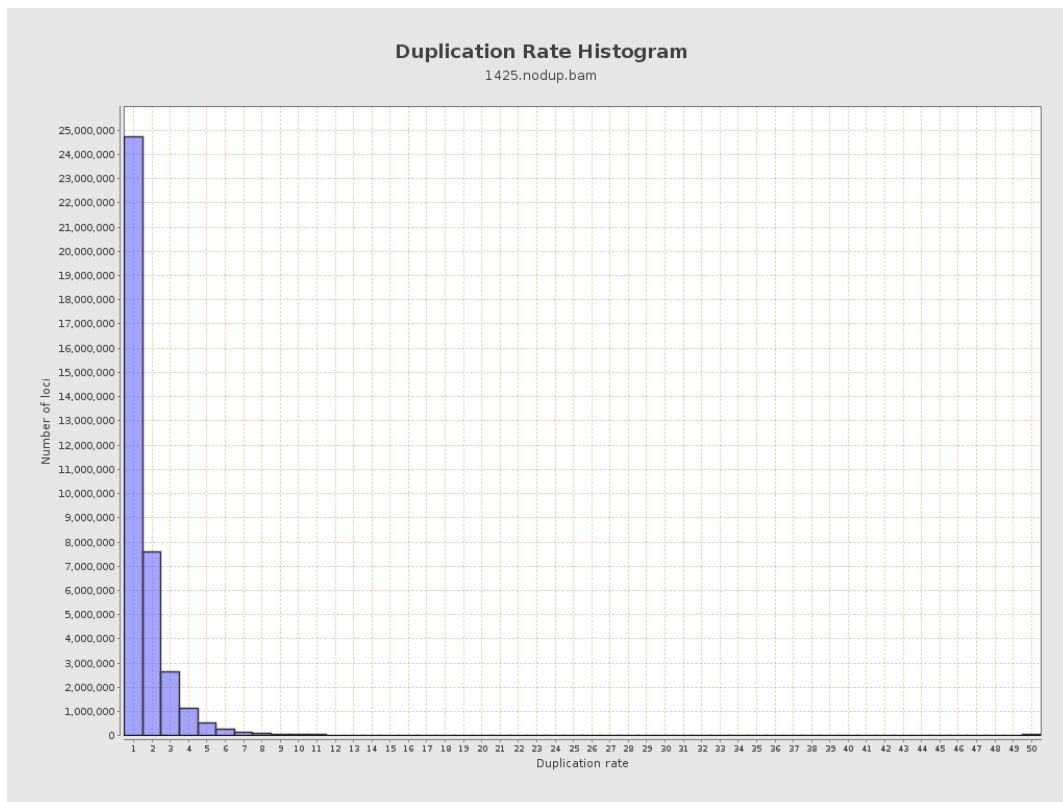
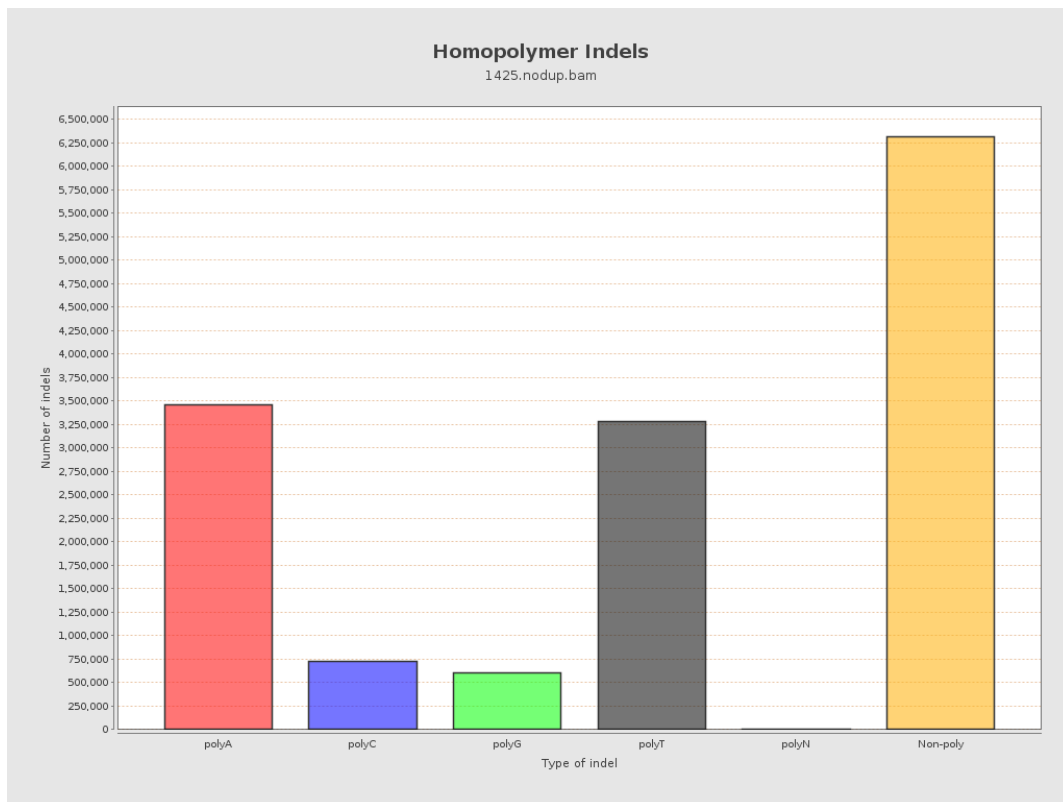# 8. Results : Mapped Reads Nucleotide Content
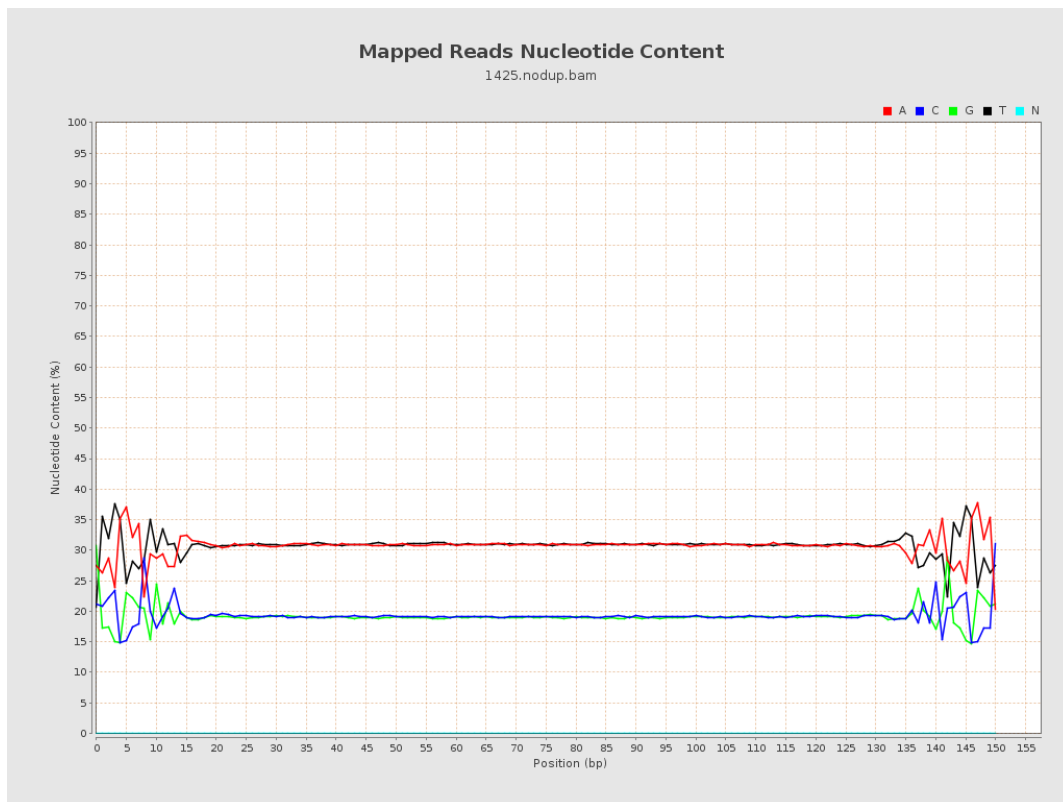
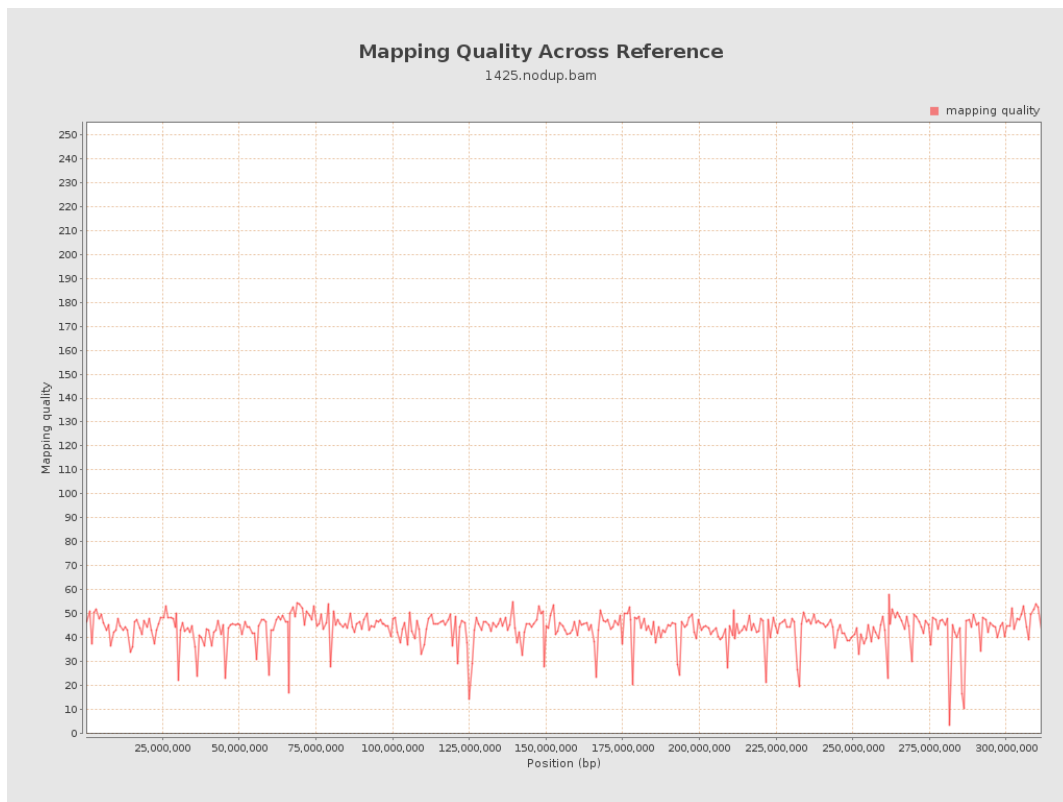# 9. Results : Mapped Reads GC-content Distribution
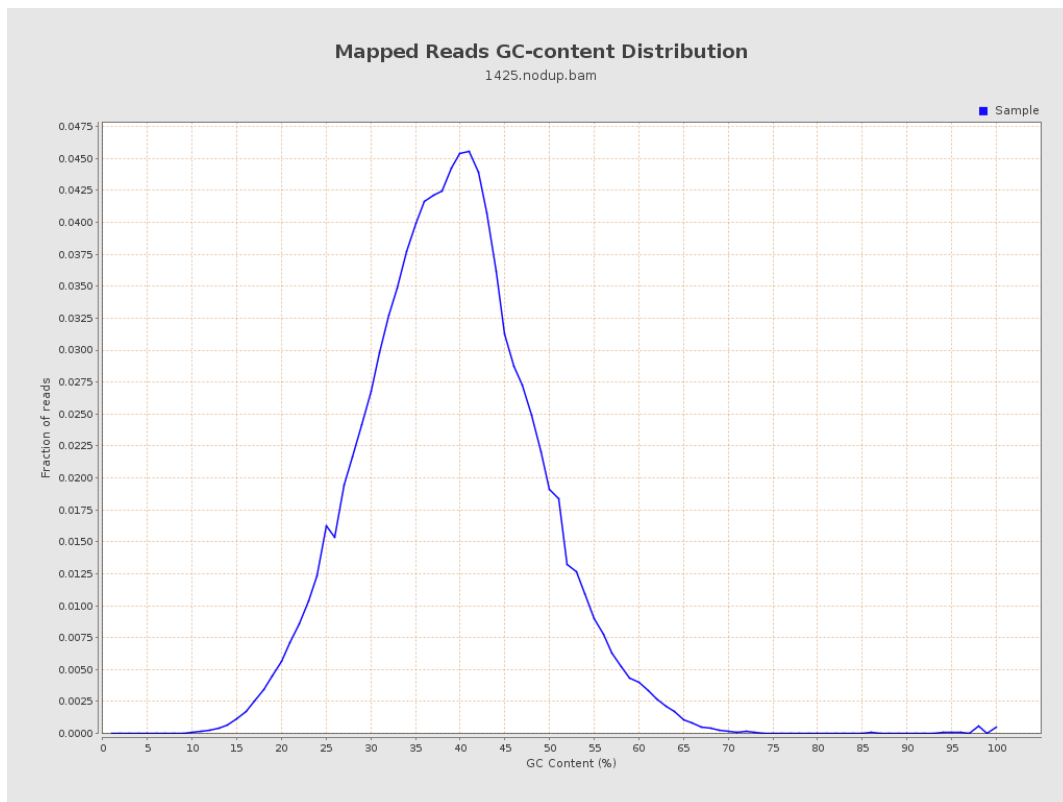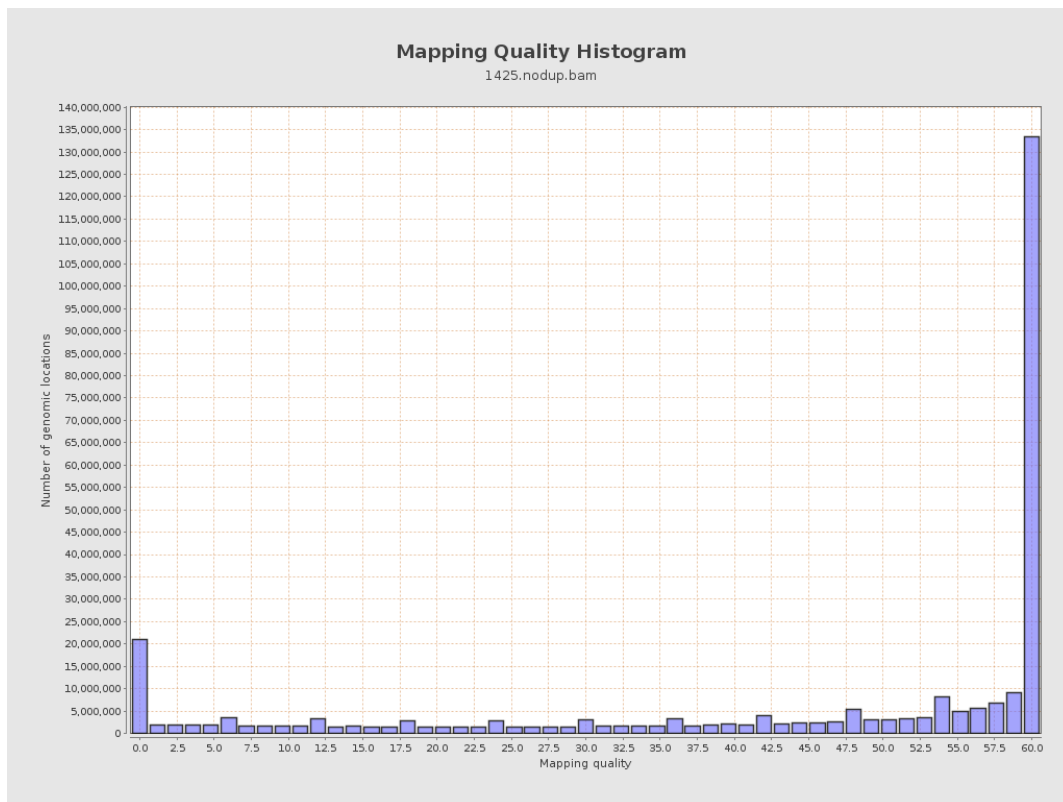
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

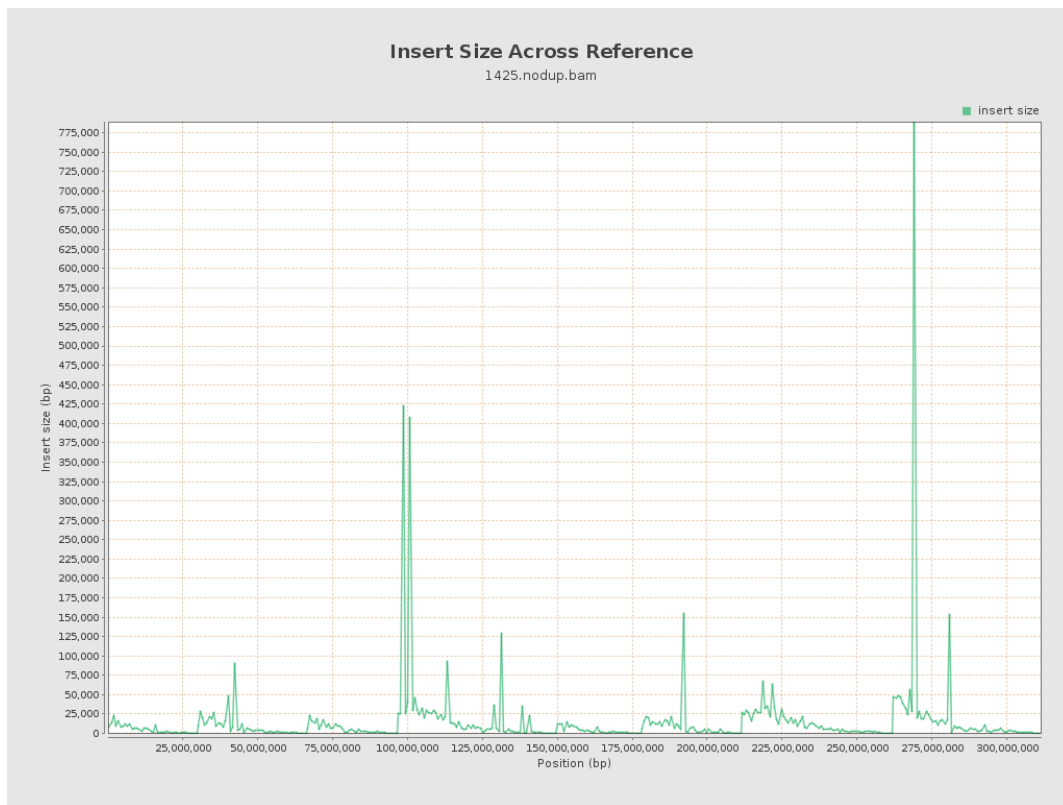# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1425.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
1425.nodup.bam

15. Results : Insert Size Histogram