Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:36:39

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/666
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/666 .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/reference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_417/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_417_S392_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_417/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_417_S392_L004 _R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,262,383
Mapped reads	75,090,769 / 94.74%
Unmapped reads	4,171,614 / 5.26%
Mapped paired reads	75,090,769 / 94.74%
Mapped reads, first in pair	37,630,451 / 47.48%
Mapped reads, second in pair	37,460,318 / 47.26%
Mapped reads, both in pair	73,578,899 / 92.83%
Mapped reads, singletons	1,511,870 / 1.91%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	12,351,806 / 15.58%
Clipped reads	16,149,863 / 20.38%

2.2. ACGT Content

Number/percentage of A's	3,226,590,493 / 30.84%
Number/percentage of C's	2,006,531,862 / 19.18%
Number/percentage of T's	3,230,425,326 / 30.88%
Number/percentage of G's	1,997,473,849 / 19.09%
Number/percentage of N's	37,152 / 0%
GC Percentage	38.28%

2.3. Coverage

Mean	33.6518
Standard Deviation	274.7849

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Insert size

| Mean	235,229.81
Standard Deviation	2,296,677.94
P25/Median/P75	352 / 461 / 608

2.6. Mismatches and indels

General error rate	2.29%
Mismatches	220,660,668
Insertions	6,979,675
Mapped reads with at least one insertion	8.37%
Deletions	7,071,734
Mapped reads with at least one deletion	8.35%
Homopolymer indels	56.39%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	796602281	26.7997	78.5182

|				
LT669789.1	36598175	1272118370	34.7591	302.9184
LT669790.1	30422129	1071793079	35.2307	266.2403
LT669791.1	52758100	1766522191	33.4834	241.7355
LT669792.1	28376109	931370460	32.8223	349.5742
LT669793.1	33388210	1022998042	30.6395	140.5181
LT669794.1	50579949	1640161863	32.4271	243.2134
LT669795.1	49795044	1985742656	39.8783	391.3797

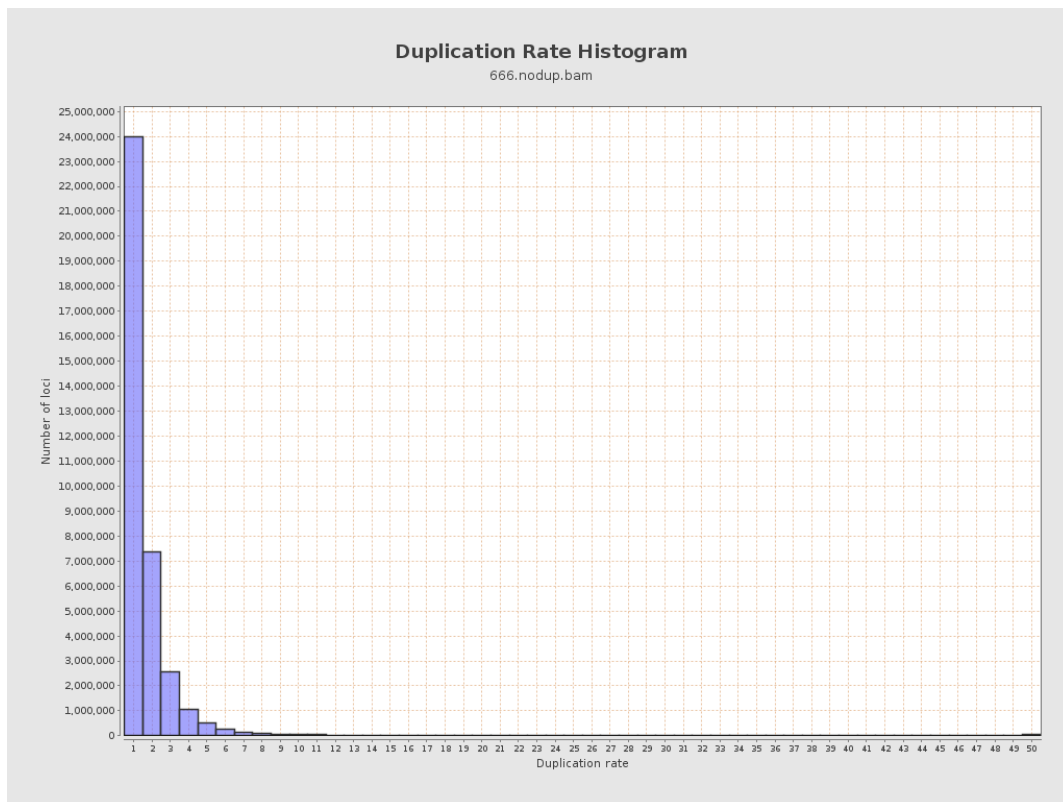# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
666.nodup.bam
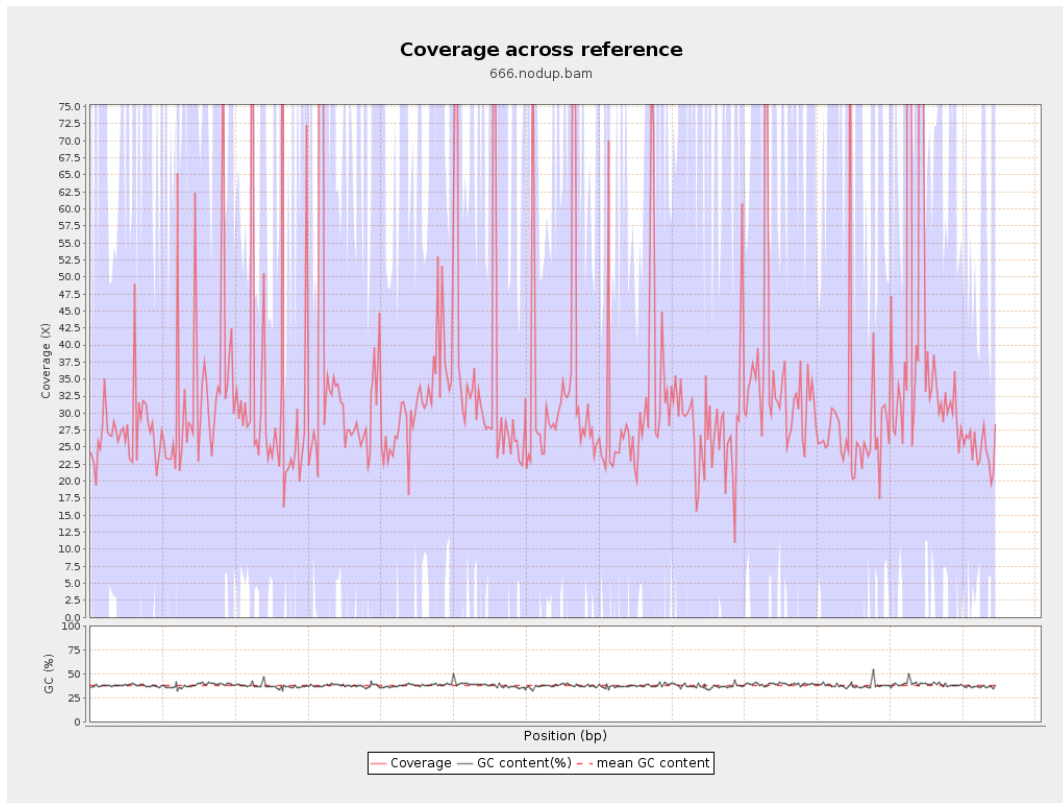
5. Results : Coverage Histogram (0-50X)
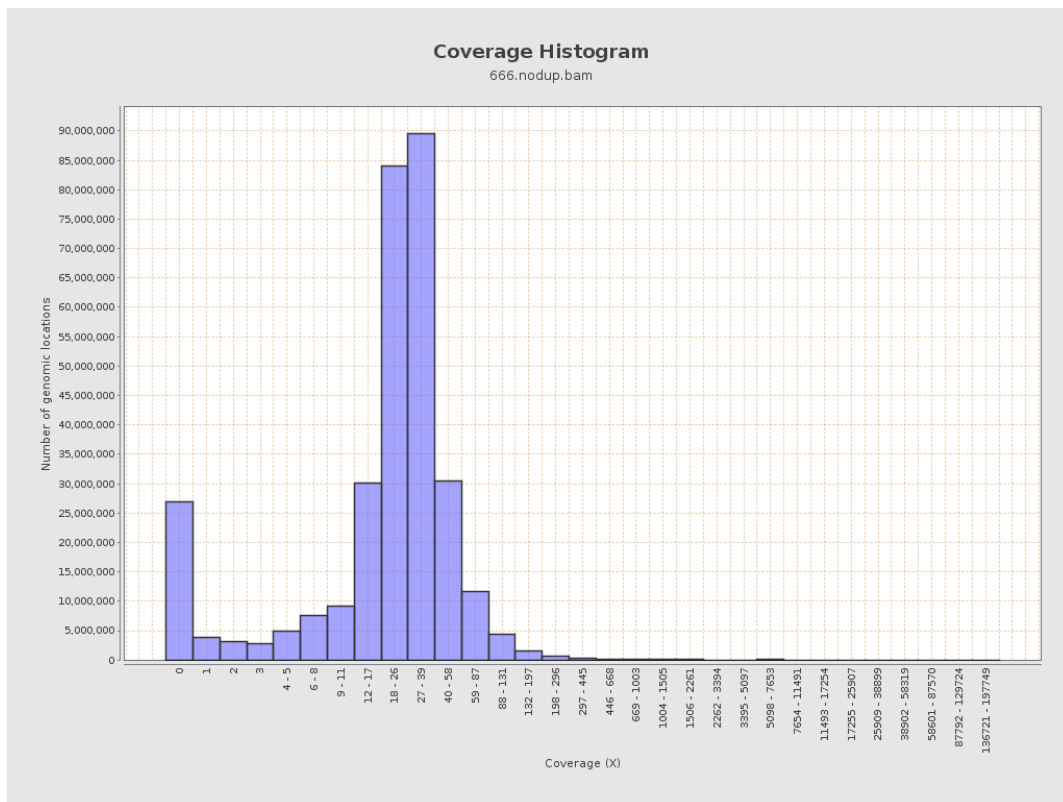
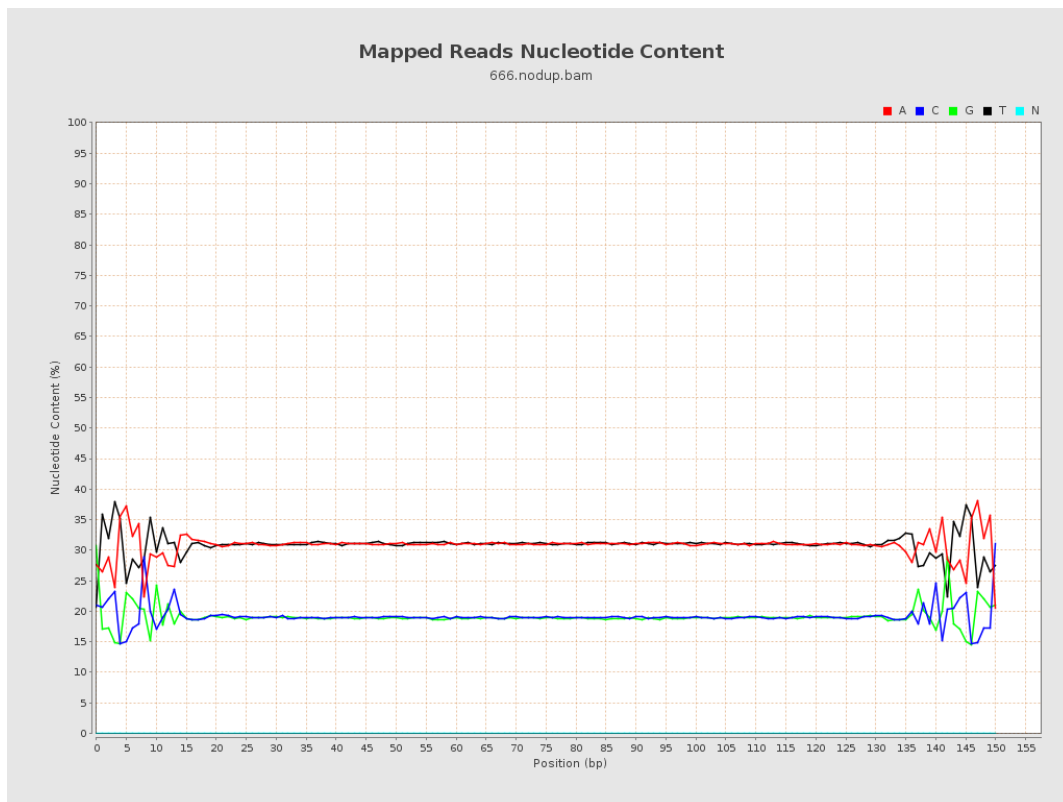Coverage Histogram (0-50X)
666.nodup.bam
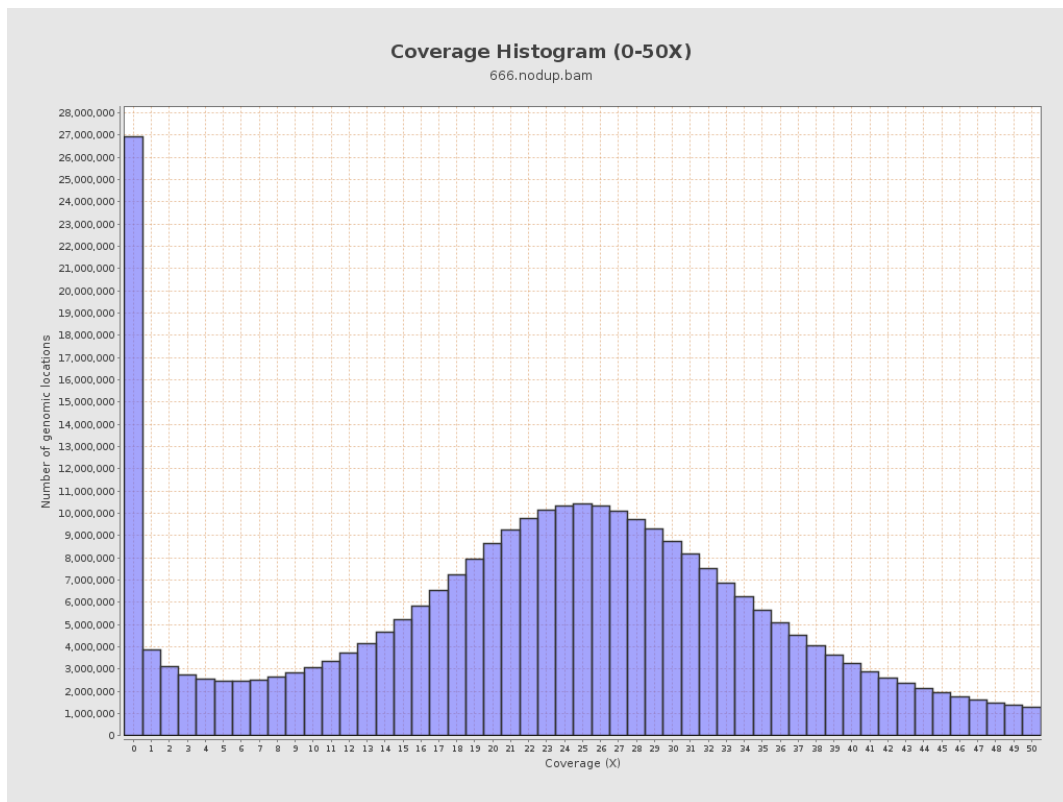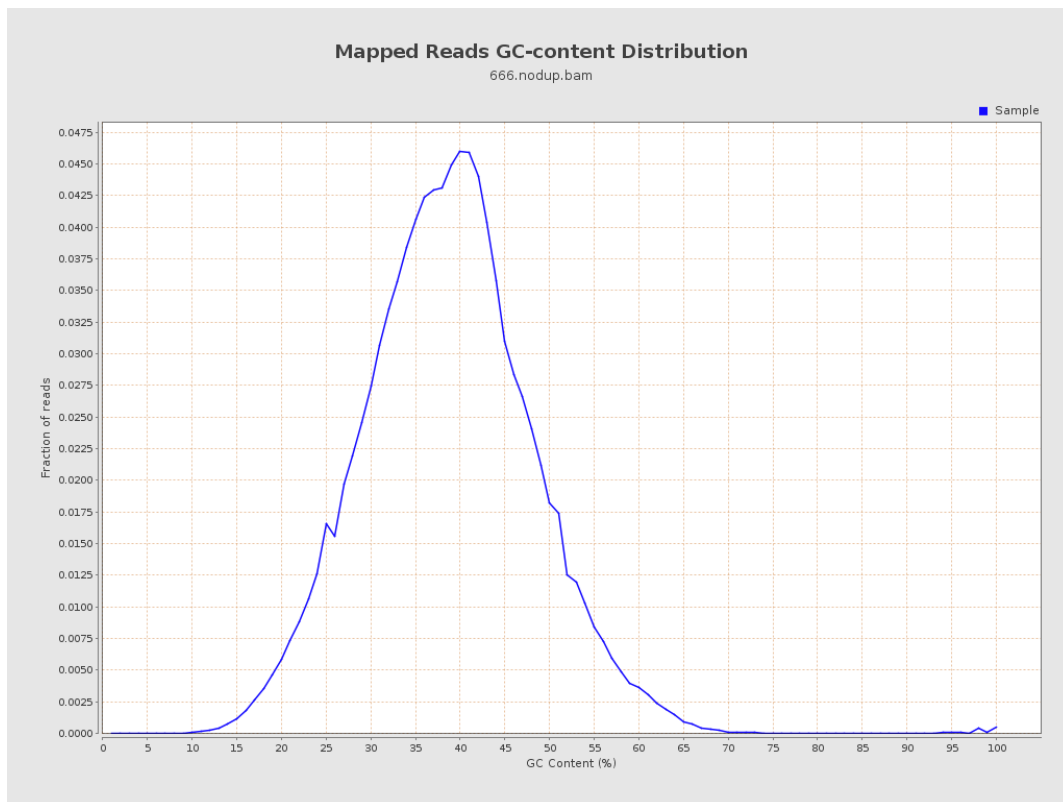
6. Results : Genome Fraction Coverage
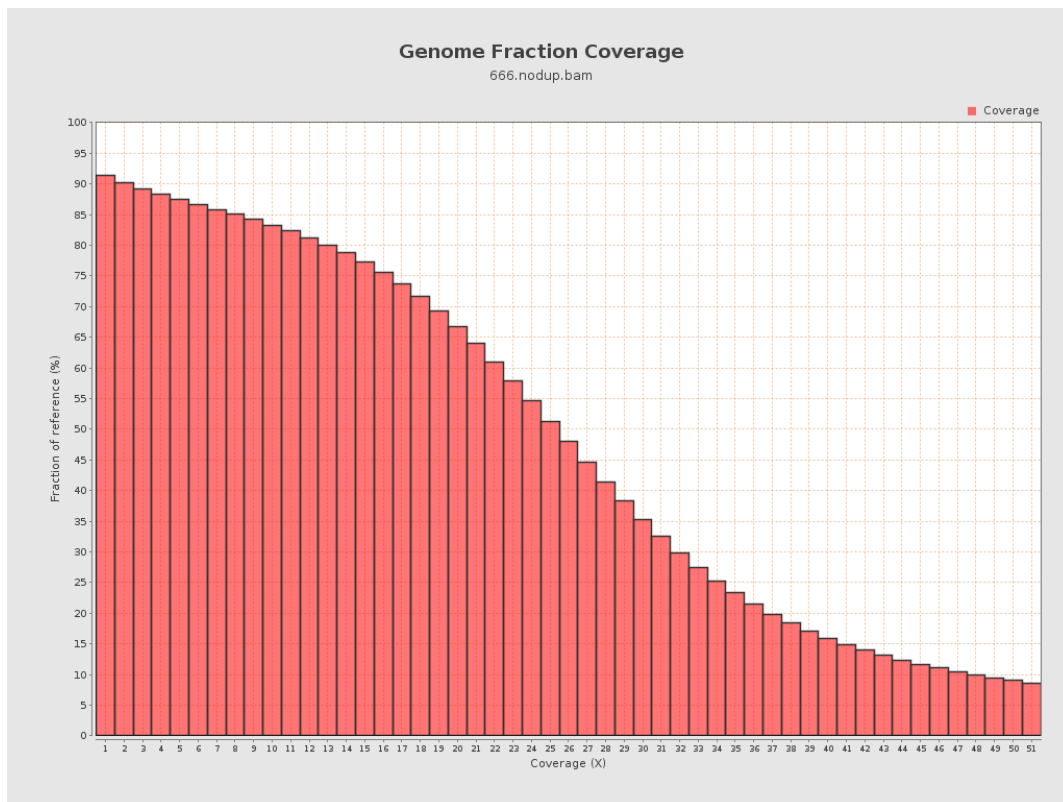
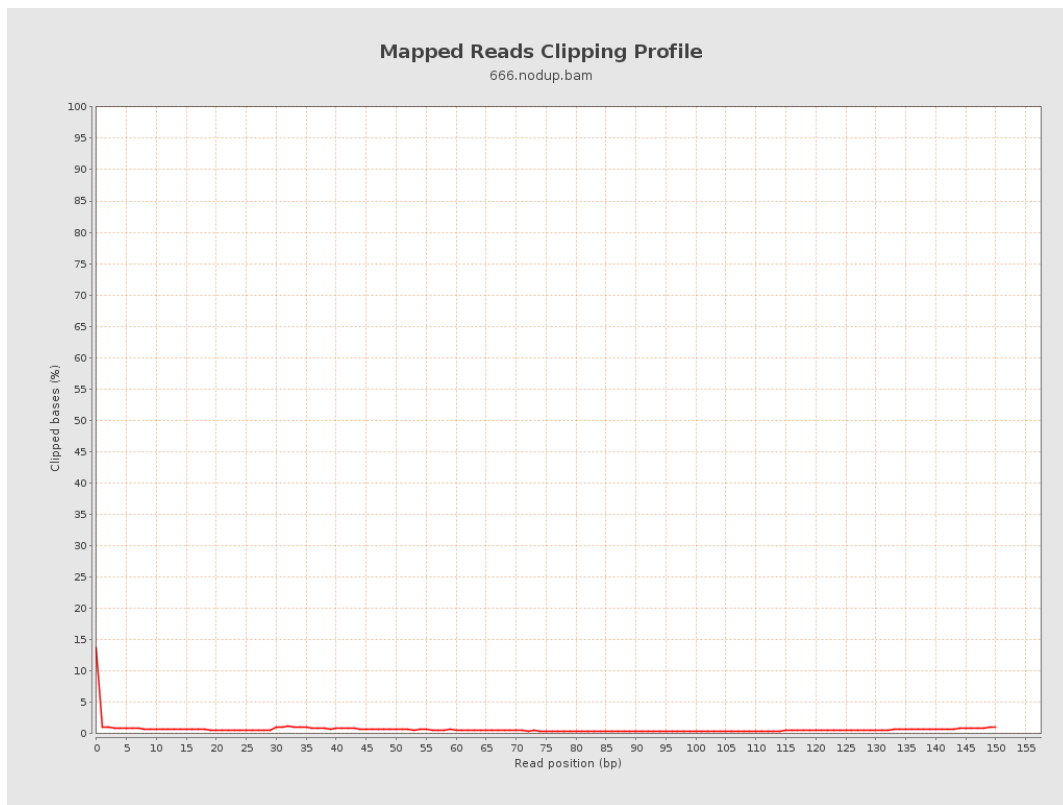# 7. Results : Duplication Rate Histogram
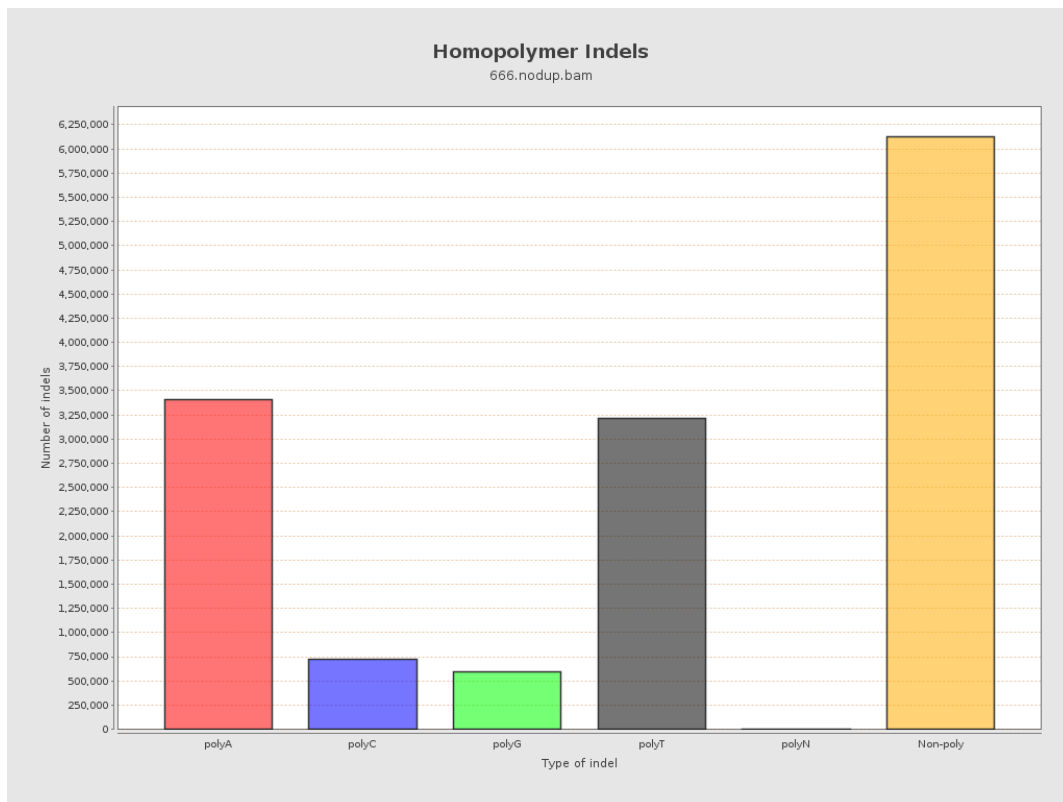
8. Results : Mapped Reads Nucleotide Content
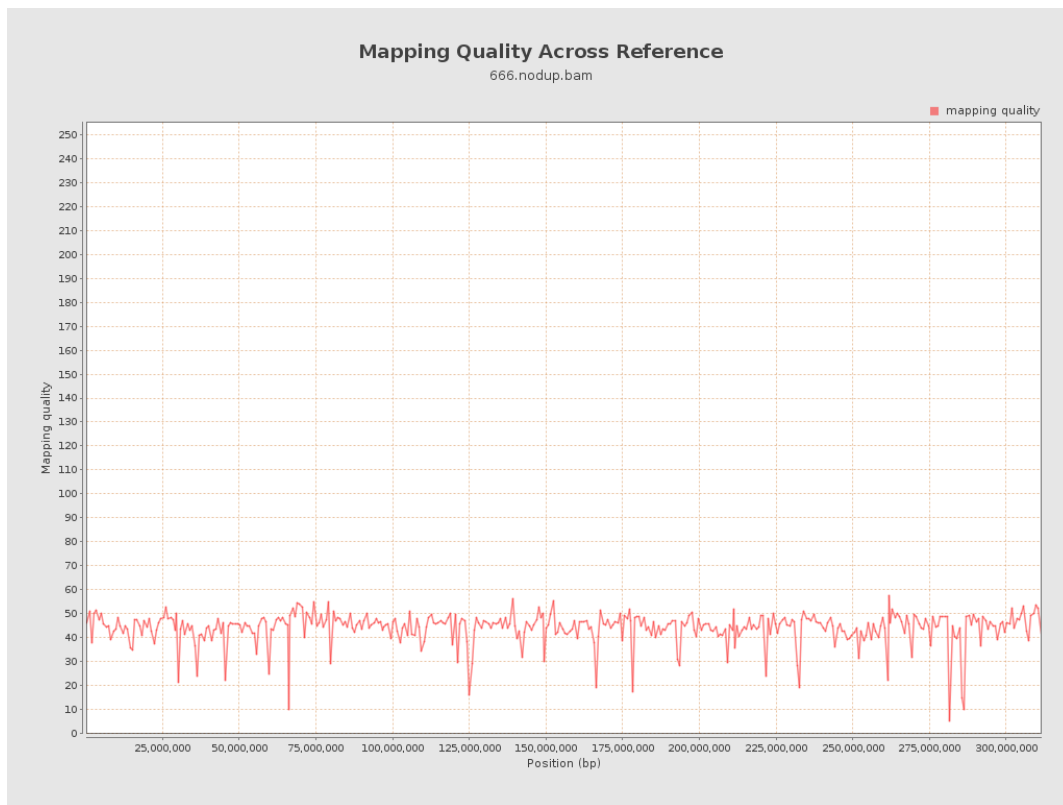
9. Results : Mapped Reads GC-content Distribution
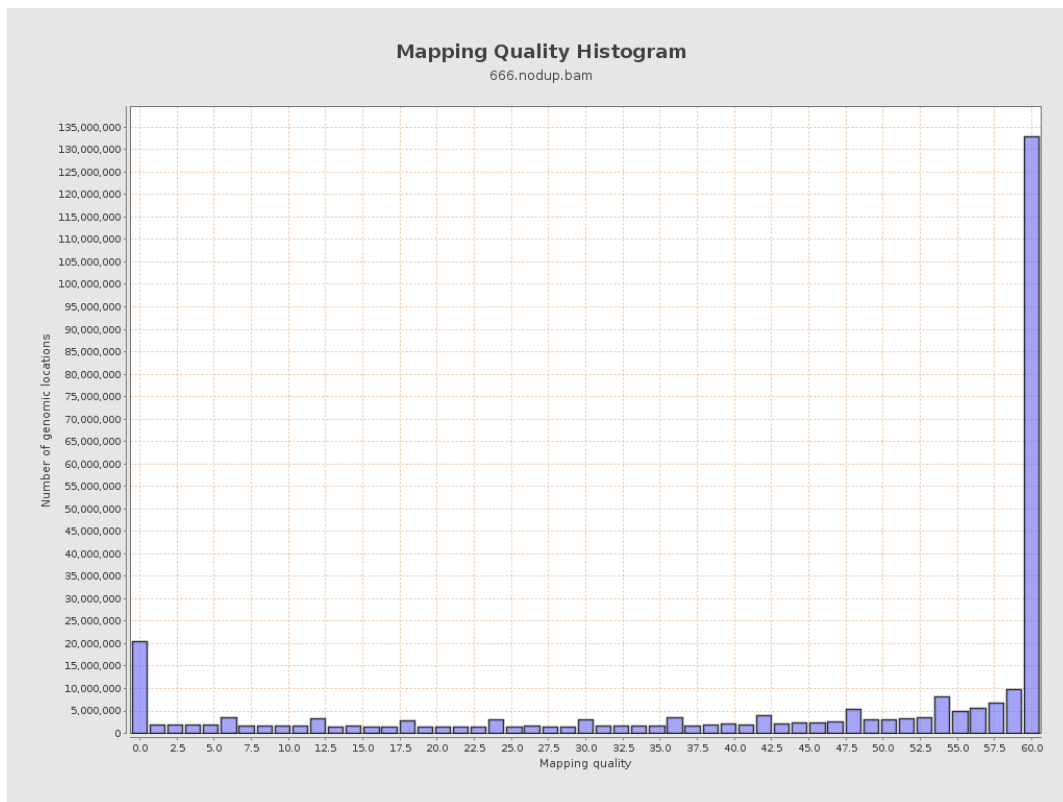
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
666.nodup.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
666.nodup.bam

14. Results : Insert Size Across Reference
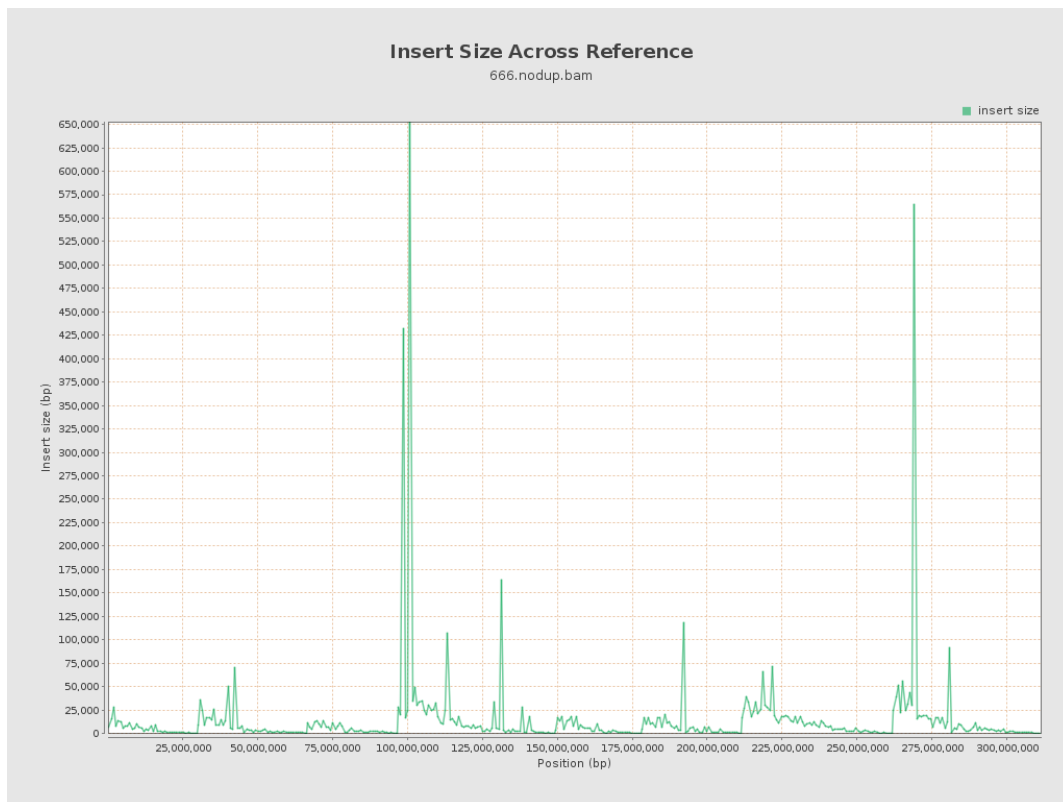
15. Results : Insert Size Histogram