Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:47:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/466.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/466.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_250/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_250_S331_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_250/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_250_S331_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:47:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	113,825,176
Mapped reads	106,925,924 / 93.94%
Unmapped reads	6,899,252 / 6.06%
Mapped paired reads	106,925,924 / 93.94%
Mapped reads, first in pair	53,545,633 / 47.04%
Mapped reads, second in pair	53,380,291 / 46.9%
Mapped reads, both in pair	104,969,955 / 92.22%
Mapped reads, singletons	1,955,969 / 1.72%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	17,101,263 / 15.02%
Clipped reads	24,376,512 / 21.42%

2.2. ACGT Content

Number/percentage of A's	4,575,309,447 / 30.94%
Number/percentage of C's	2,820,019,630 / 19.07%
Number/percentage of T's	4,576,074,657 / 30.94%
Number/percentage of G's	2,817,585,058 / 19.05%
Number/percentage of N's	55,013 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	47.5766
Standard Deviation	384.3801

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Insert size

Mean	214,030.45
Standard Deviation	2,189,981.12
P25/Median/P75	304 / 404 / 530

2.6. Mismatches and indels

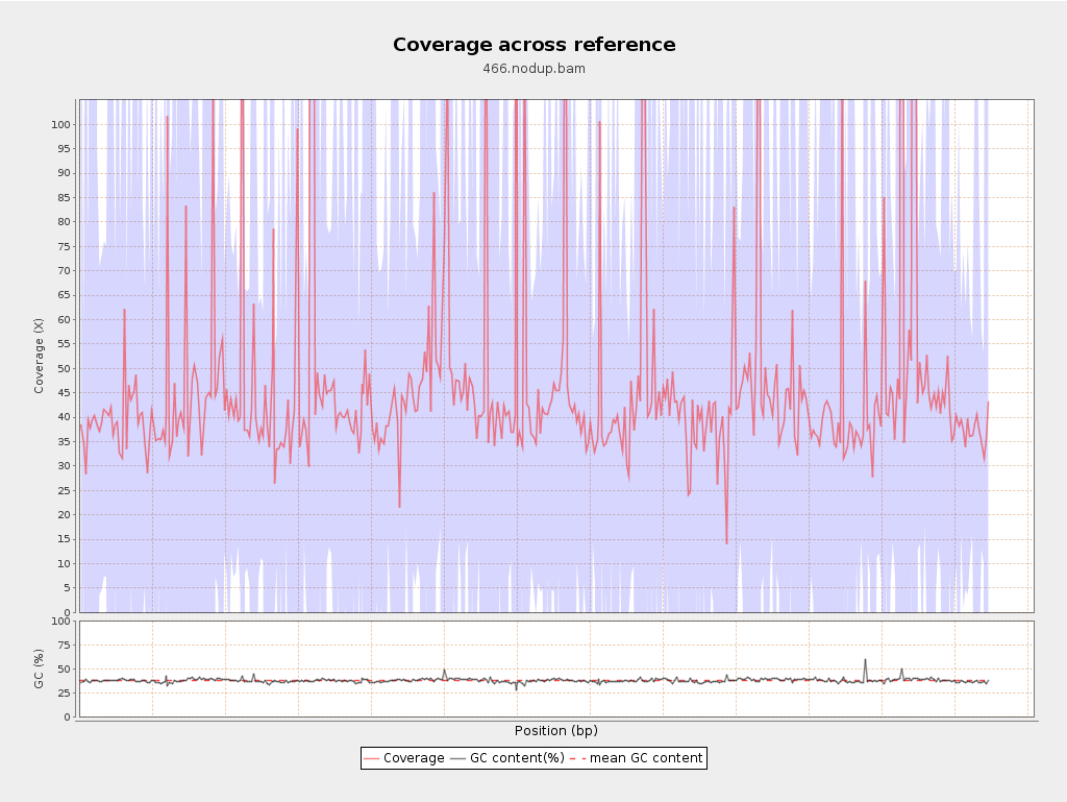
General error rate	2.25%
Mismatches	306,305,166
Insertions	9,736,958
Mapped reads with at least one insertion	8.19%
Deletions	10,002,664
Mapped reads with at least one deletion	8.32%
Homopolymer indels	56.86%

2.7. Chromosome stats

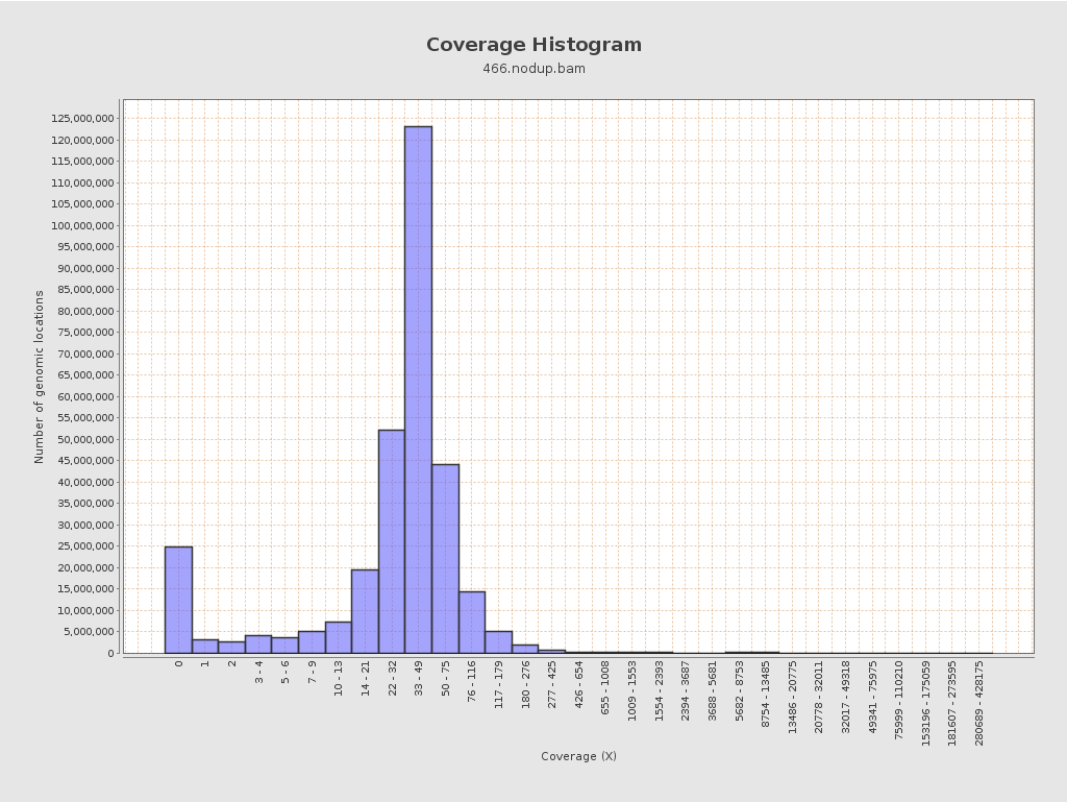
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1153374626	38.8024	108.4492

LT669789.1	36598175	1746543895	47.7222	353.9339
LT669790.1	30422129	1539522653	50.6054	365.4173
LT669791.1	52758100	2477938061	46.9679	286.2121
LT669792.1	28376109	1338906467	47.1843	400.4085
LT669793.1	33388210	1492260409	44.6942	277.223
LT669794.1	50579949	2264735607	44.7754	305.7266
LT669795.1	49795044	2813587854	56.5034	647.4852

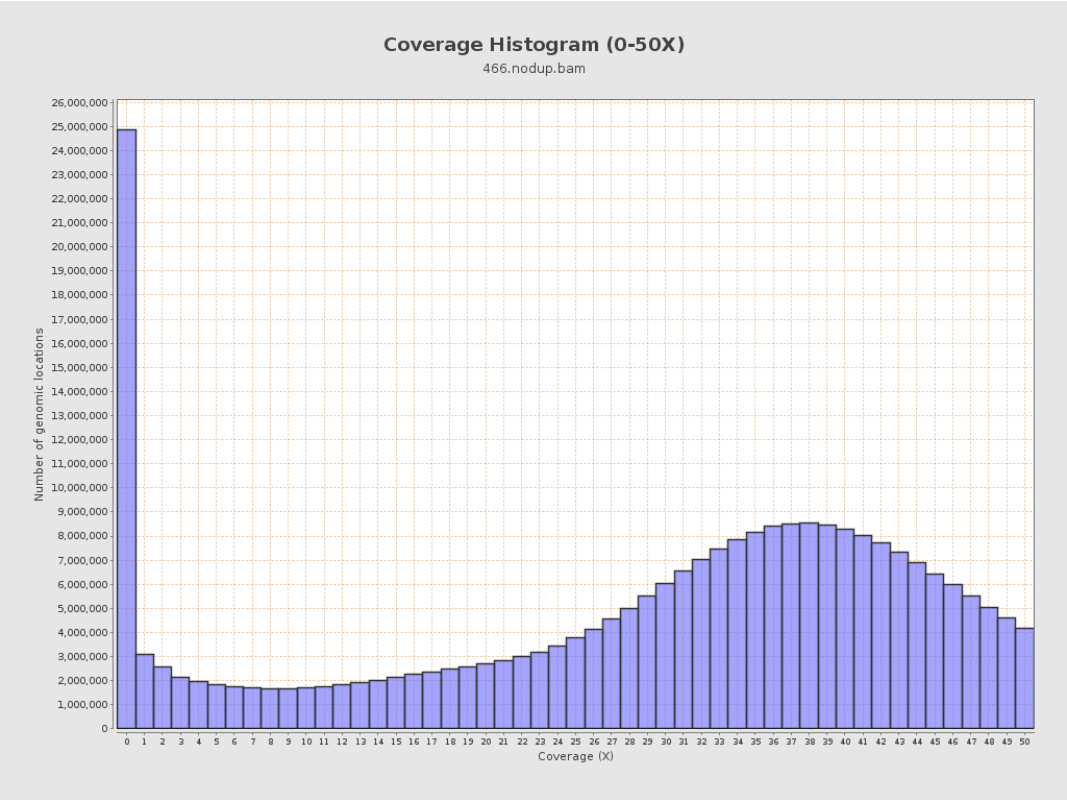
3. Results : Coverage across reference



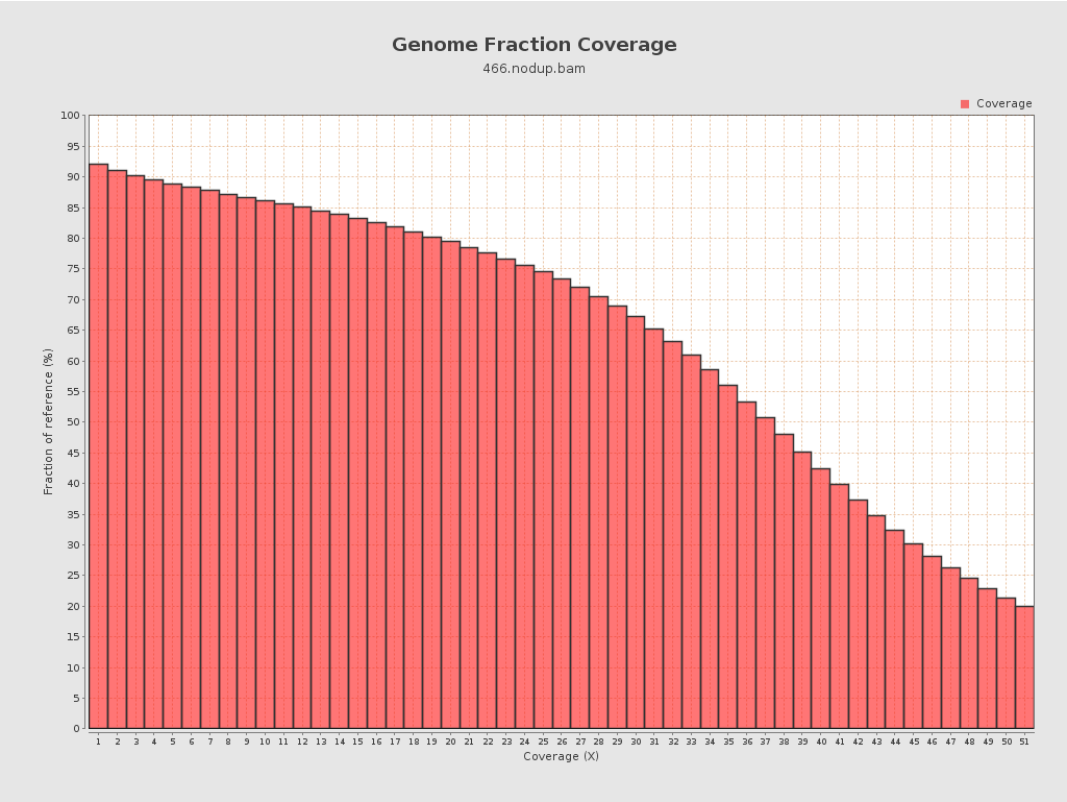
4. Results : Coverage Histogram



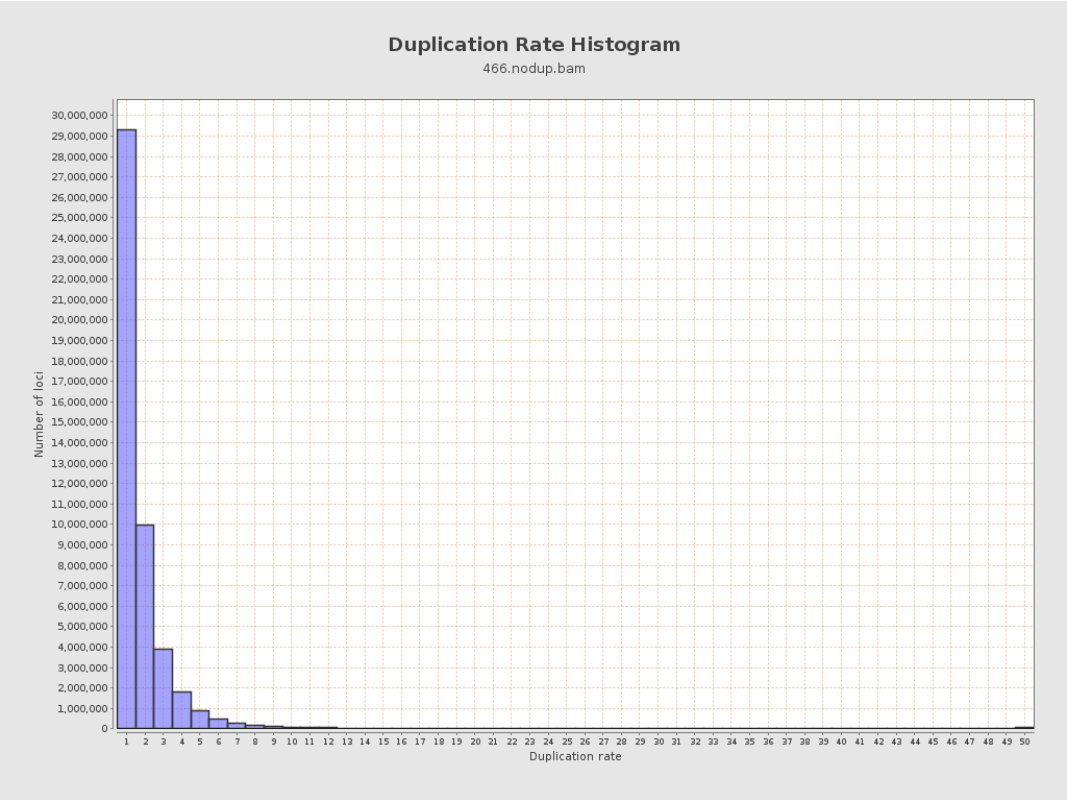
5. Results : Coverage Histogram (0-50X)



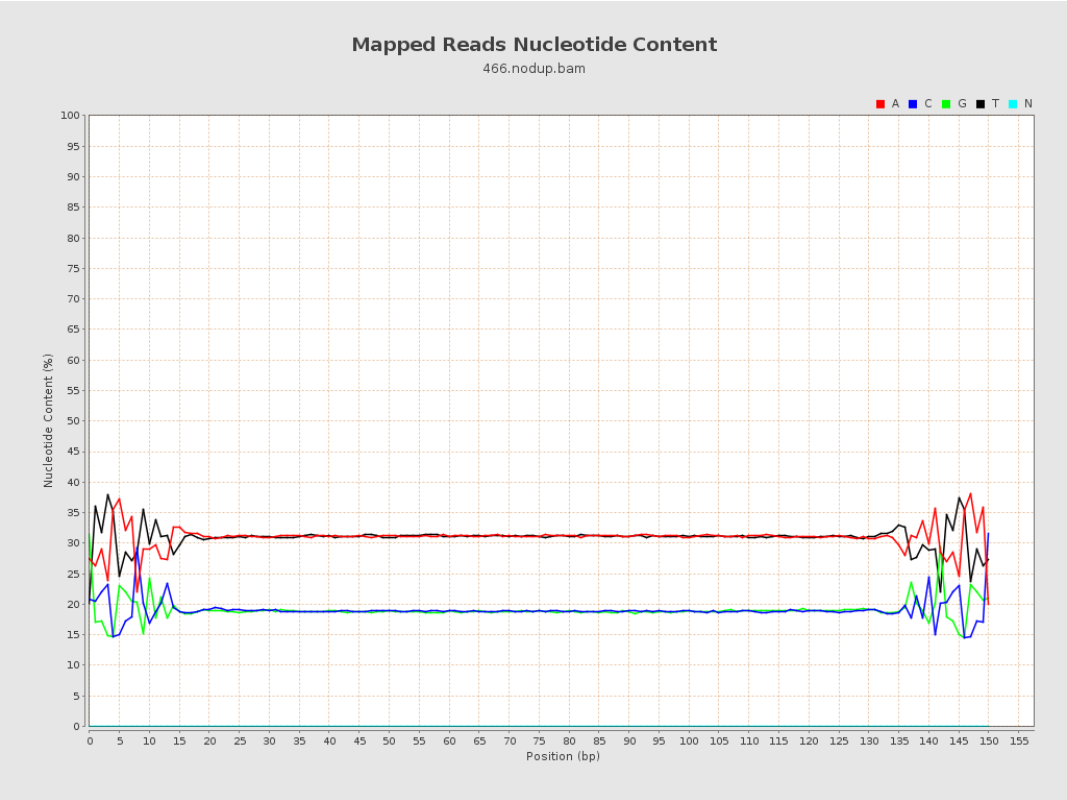
6. Results : Genome Fraction Coverage



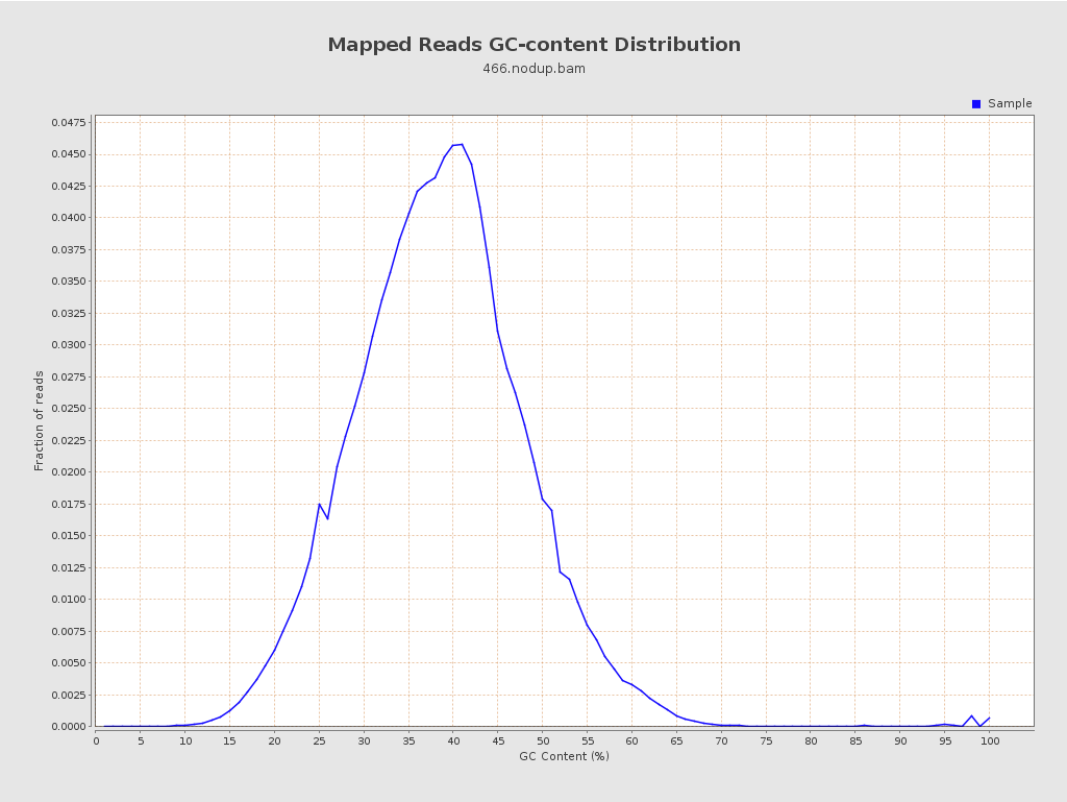
7. Results : Duplication Rate Histogram



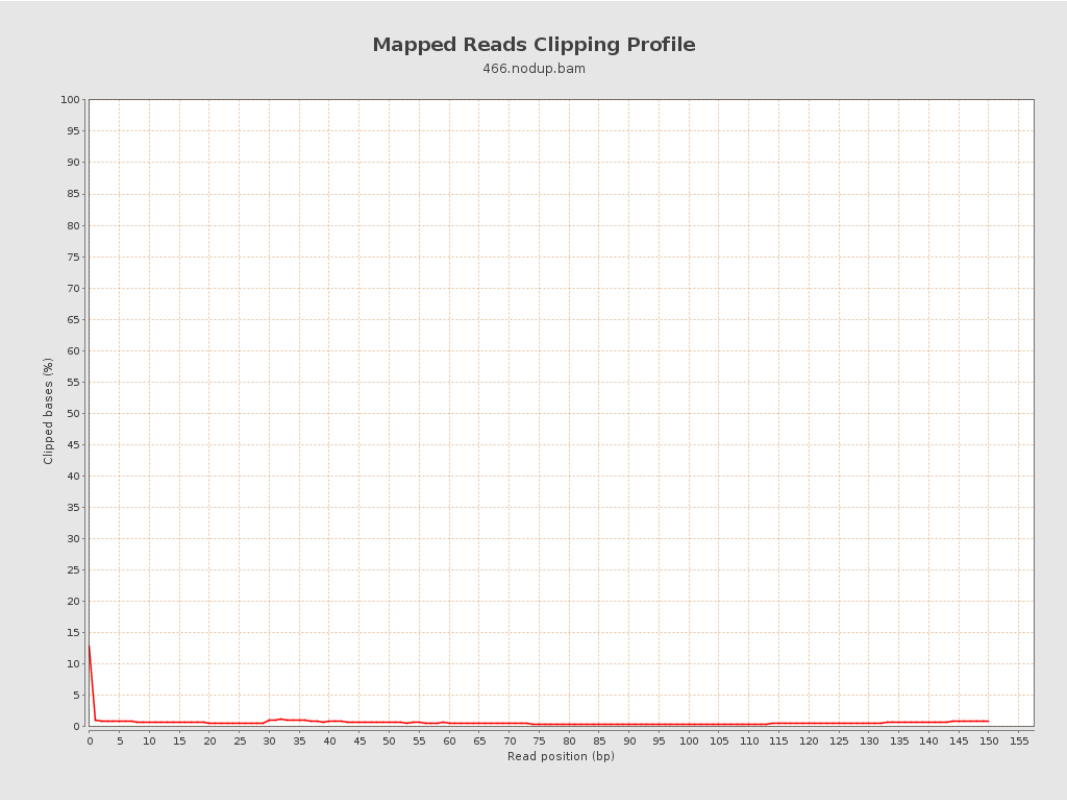
8. Results : Mapped Reads Nucleotide Content



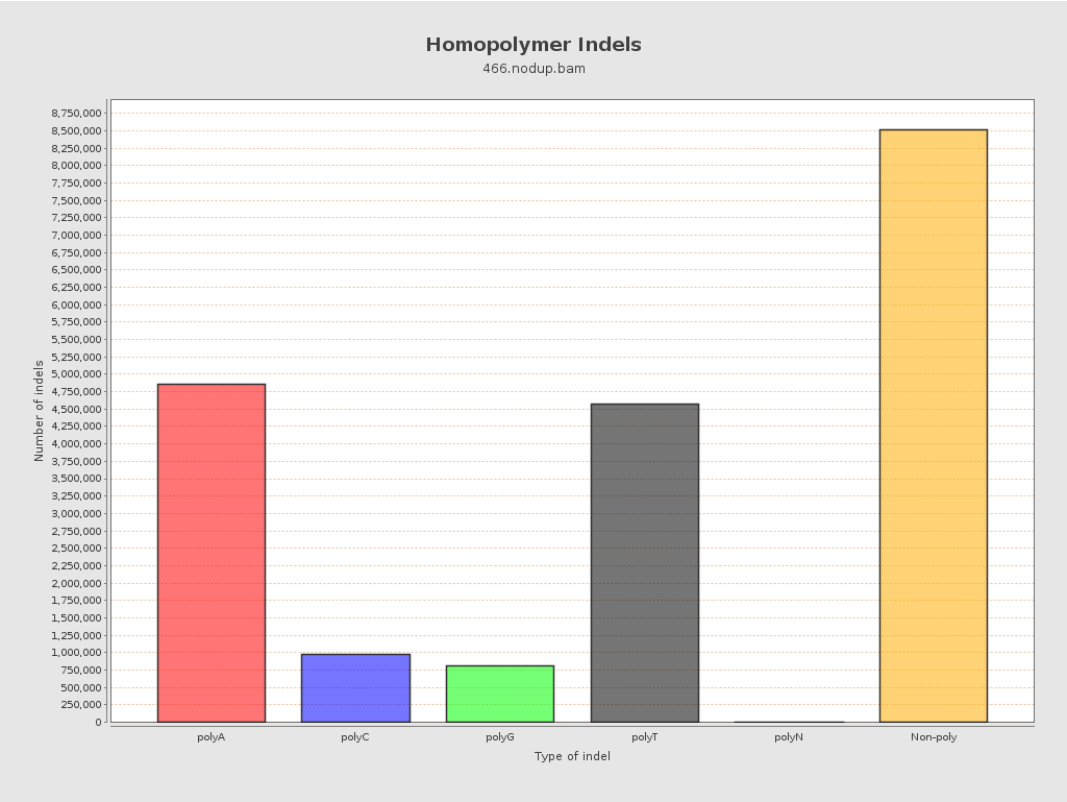
9. Results : Mapped Reads GC-content Distribution



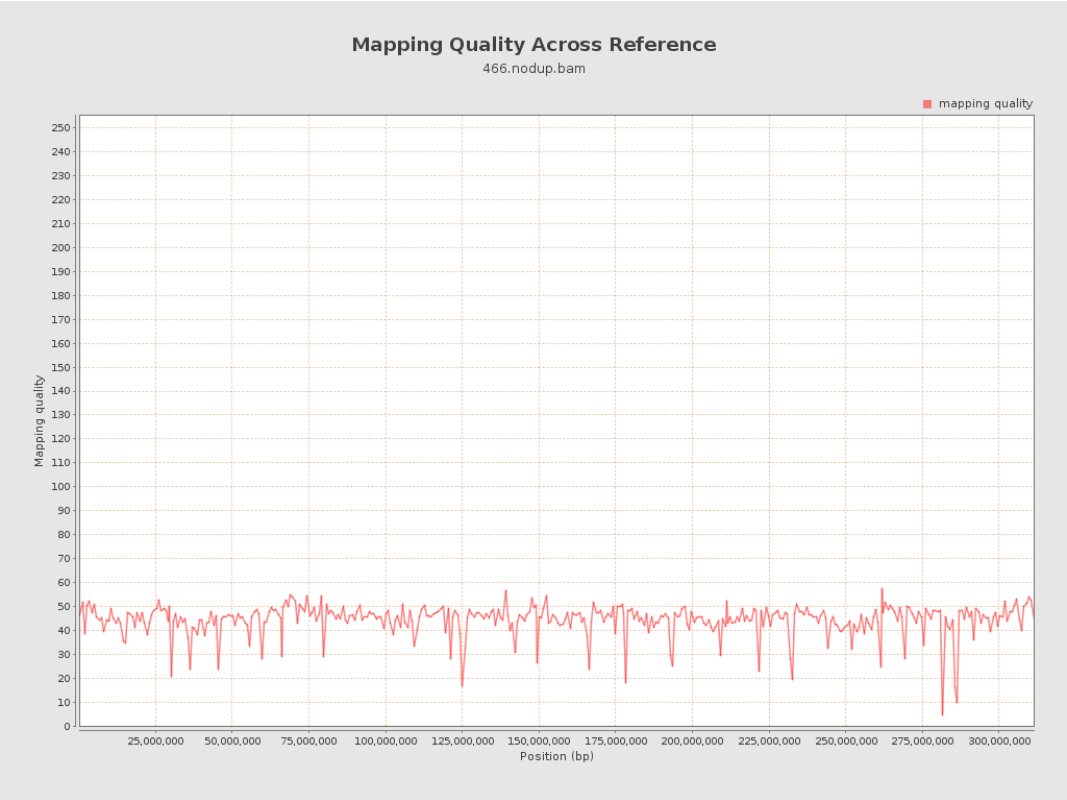
10. Results : Mapped Reads Clipping Profile



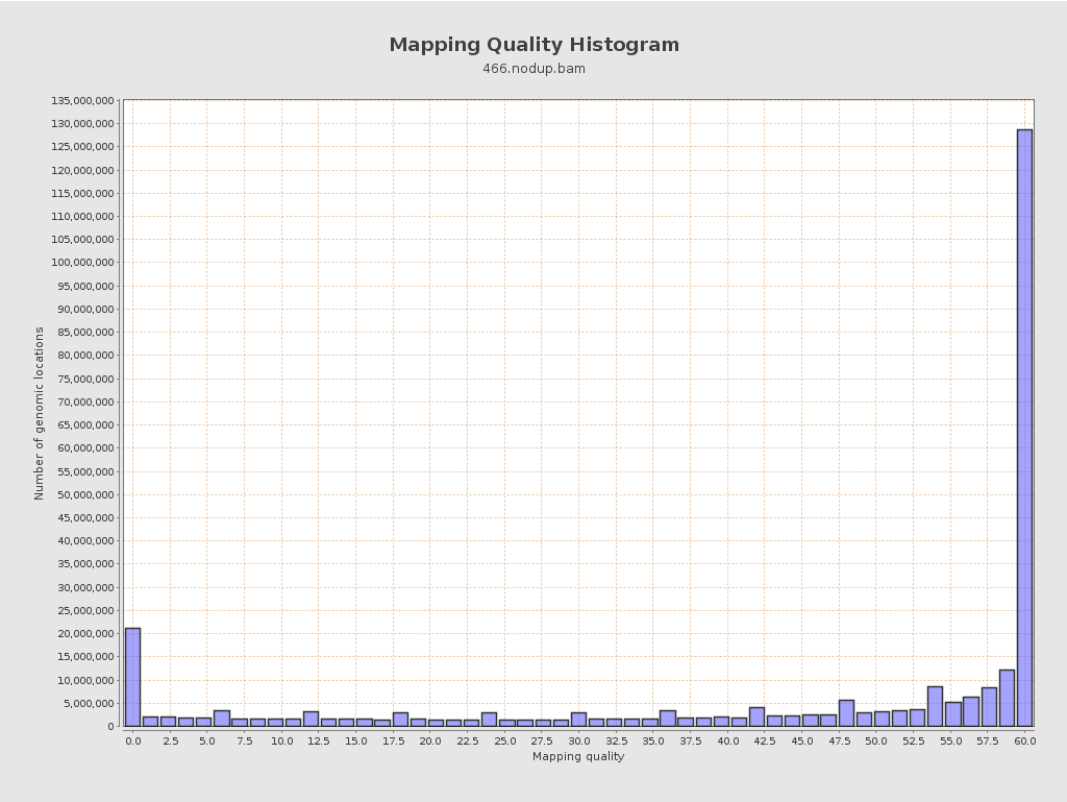
11. Results : Homopolymer Indels



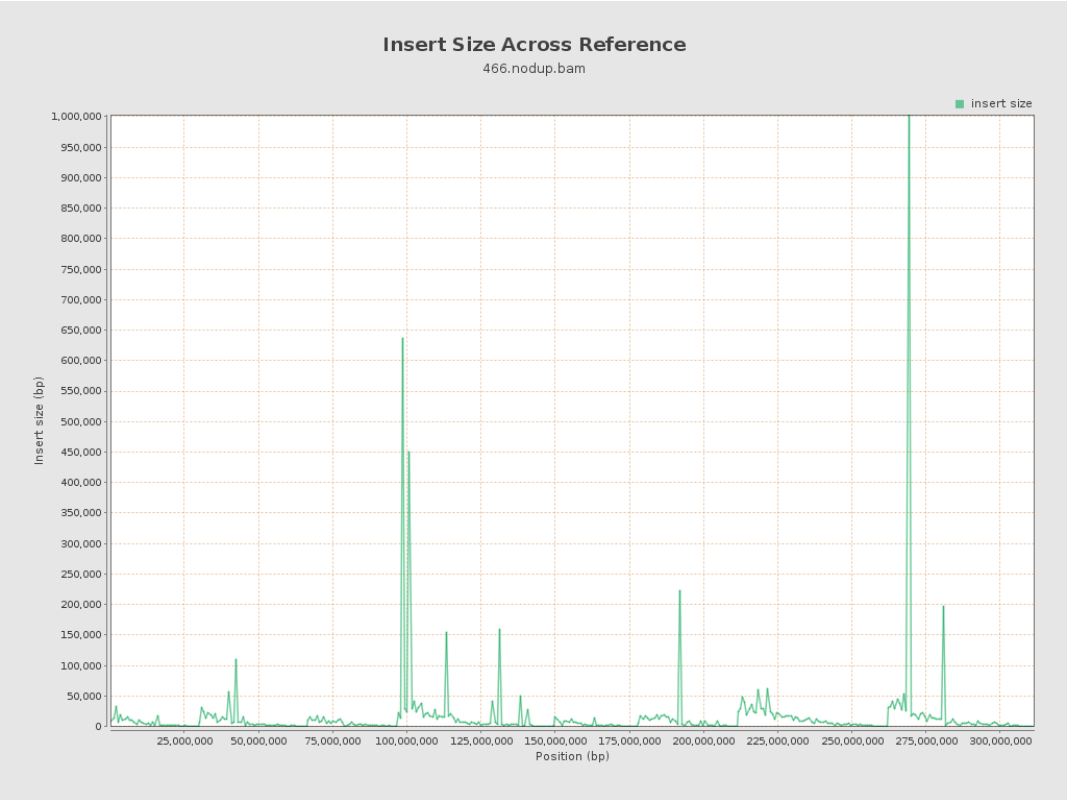
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram