Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/465.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/465.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_237/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_237_S318_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_237/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_237_S318_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:42 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,773,044
Mapped reads	73,379,063 / 93.15%
Unmapped reads	5,393,981 / 6.85%
Mapped paired reads	73,379,063 / 93.15%
Mapped reads, first in pair	36,755,332 / 46.66%
Mapped reads, second in pair	36,623,731 / 46.49%
Mapped reads, both in pair	71,670,504 / 90.98%
Mapped reads, singletons	1,708,559 / 2.17%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	11,207,843 / 14.23%
Clipped reads	17,234,087 / 21.88%

2.2. ACGT Content

Number/percentage of A's	3,124,478,086 / 30.95%
Number/percentage of C's	1,924,703,872 / 19.06%
Number/percentage of T's	3,126,688,936 / 30.97%
Number/percentage of G's	1,919,844,714 / 19.02%
Number/percentage of N's	38,382 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	32.479
Standard Deviation	268.2981

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Insert size

Mean	229,857.19
Standard Deviation	2,287,947.2
P25/Median/P75	304 / 400 / 517

2.6. Mismatches and indels

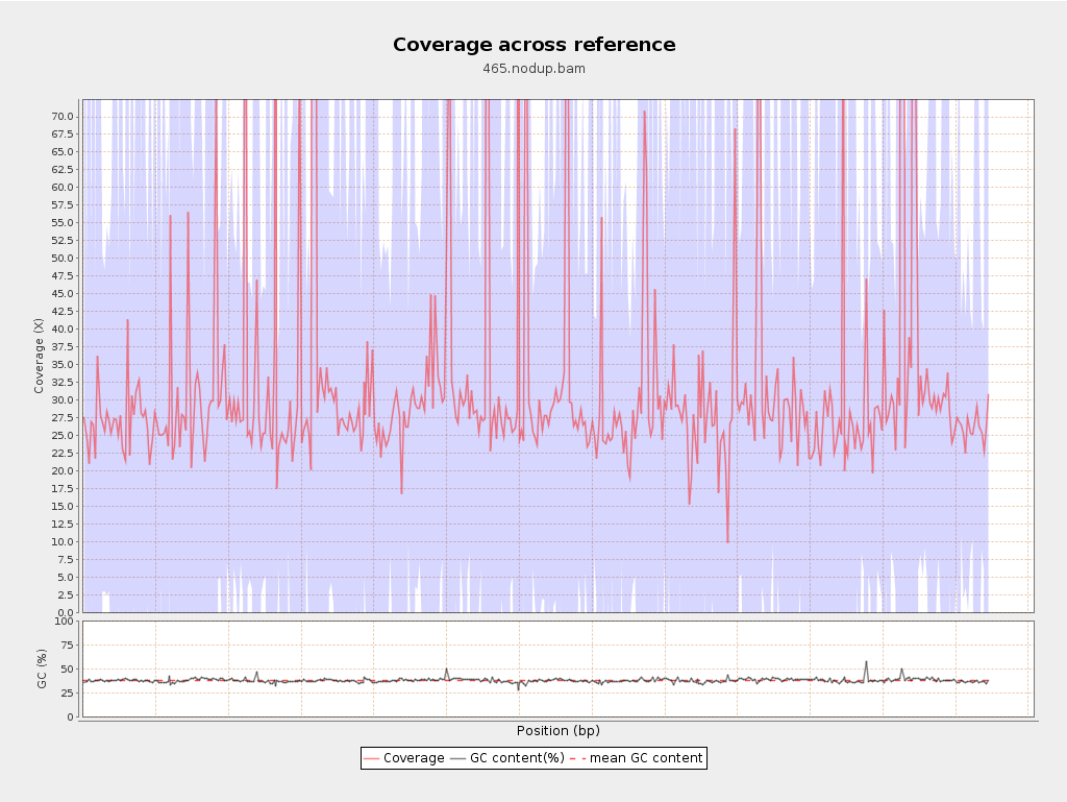
General error rate	2.29%
Mismatches	211,686,375
Insertions	7,056,225
Mapped reads with at least one insertion	8.61%
Deletions	6,971,969
Mapped reads with at least one deletion	8.41%
Homopolymer indels	56.89%

2.7. Chromosome stats

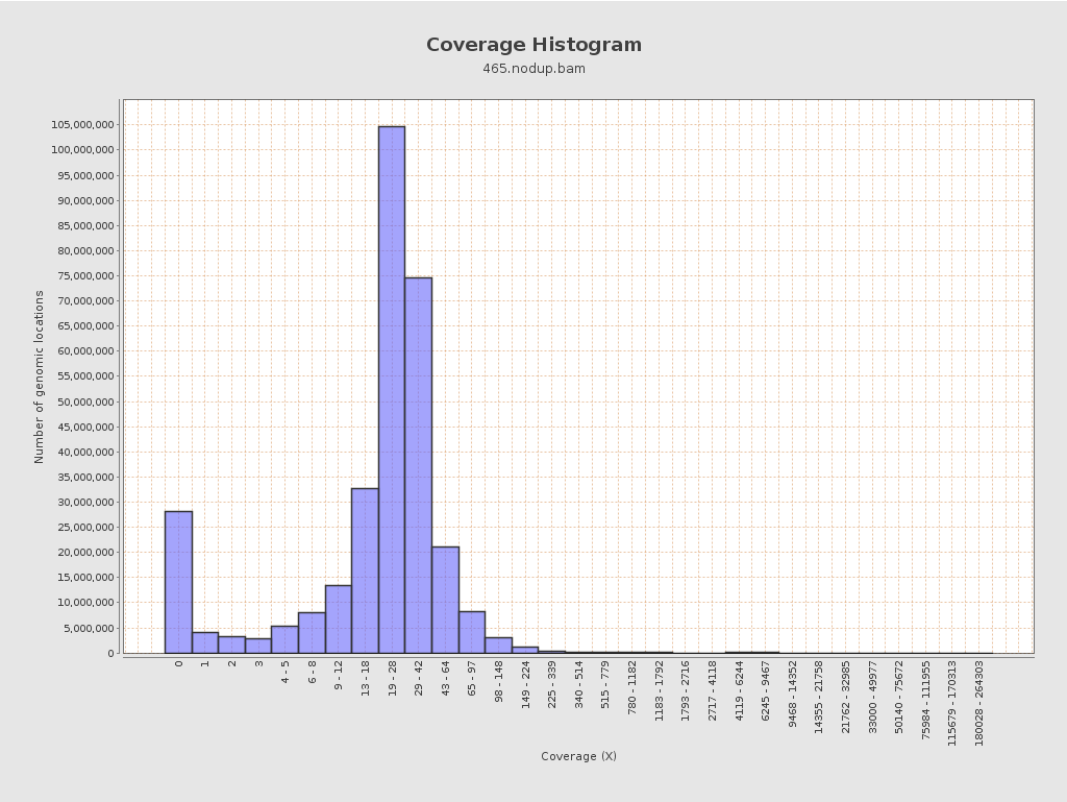
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	798156393	26.8519	84.8417

LT669789.1	36598175	1200287415	32.7964	287.4662
LT669790.1	30422129	1124310648	36.957	317.2043
LT669791.1	52758100	1680380481	31.8507	252.2422
LT669792.1	28376109	930781181	32.8016	300.1258
LT669793.1	33388210	977648197	29.2812	142.8723
LT669794.1	50579949	1548072775	30.6065	224.3253
LT669795.1	49795044	1862183607	37.397	374.6929

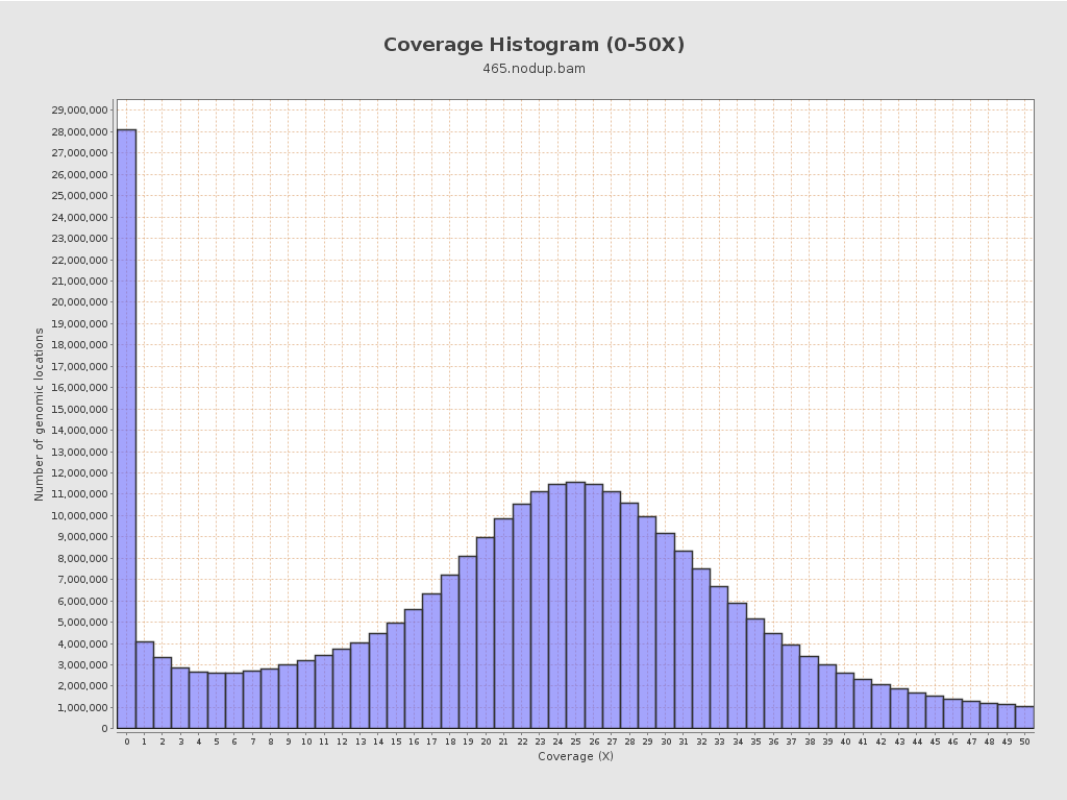
3. Results : Coverage across reference



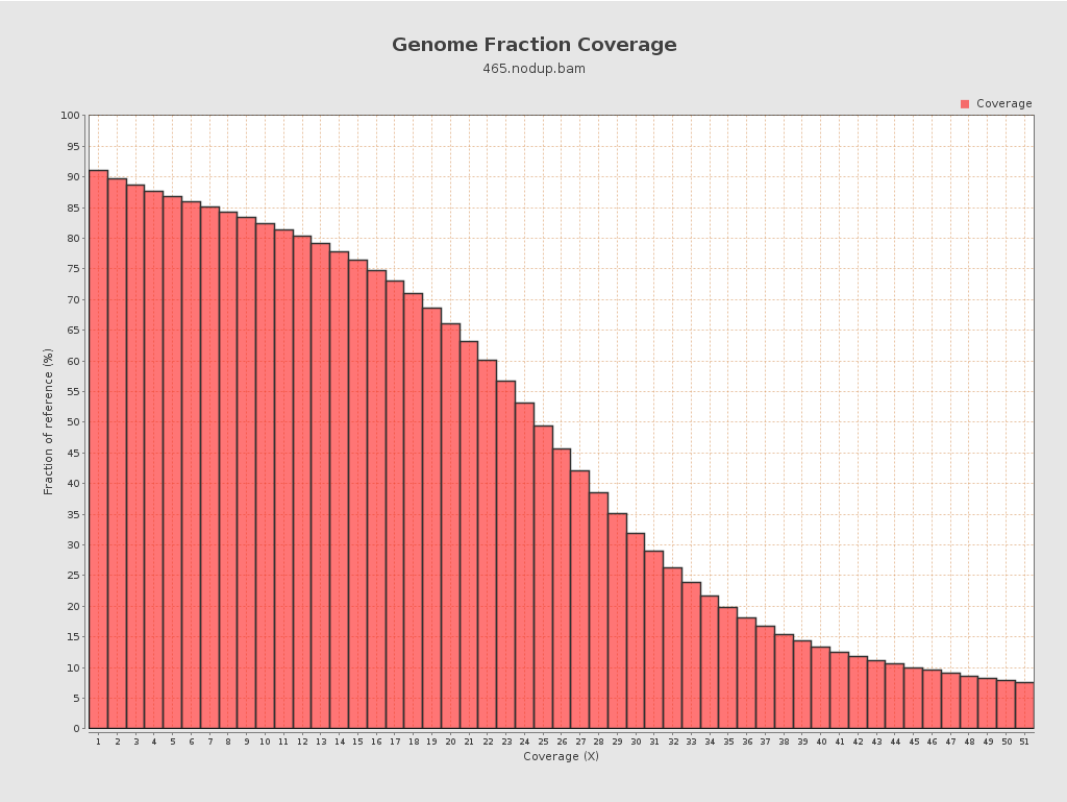
4. Results : Coverage Histogram



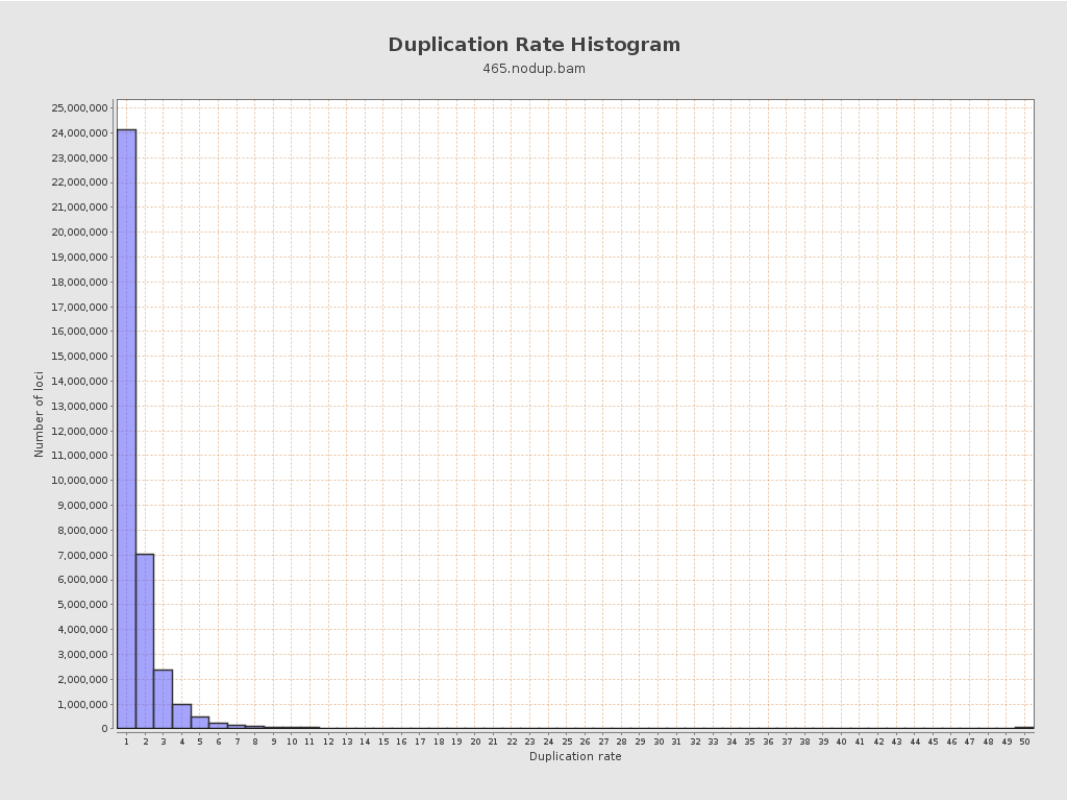
5. Results : Coverage Histogram (0-50X)



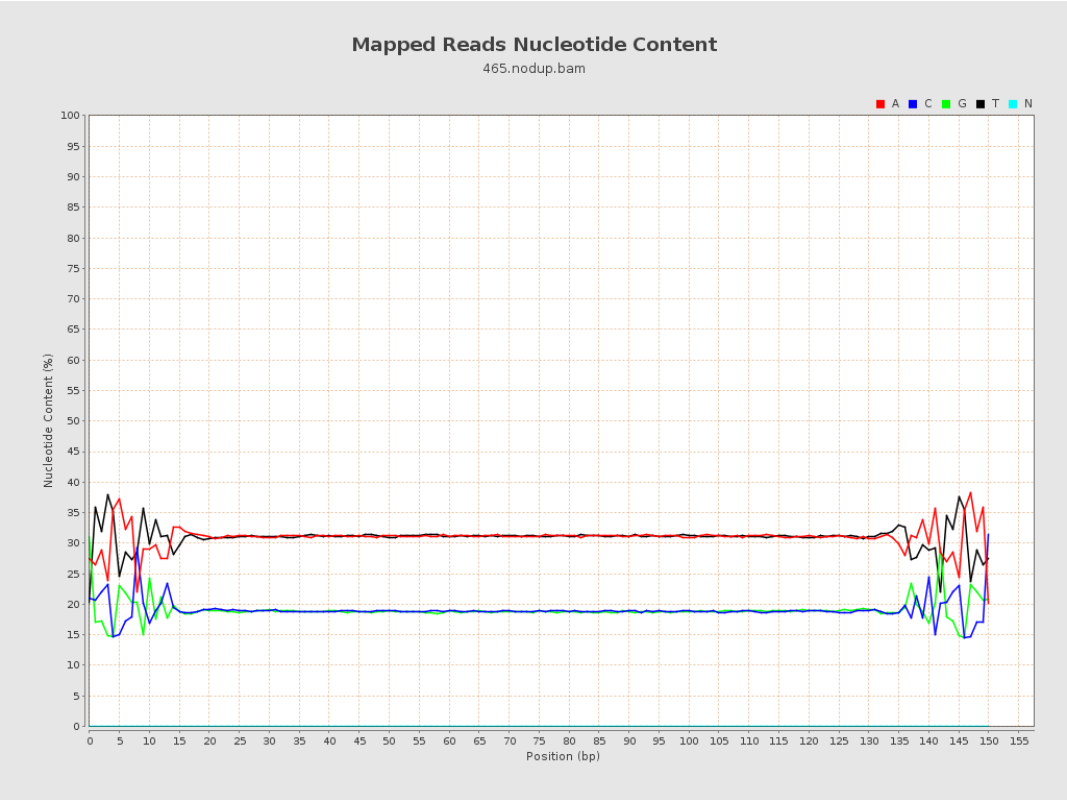
6. Results : Genome Fraction Coverage



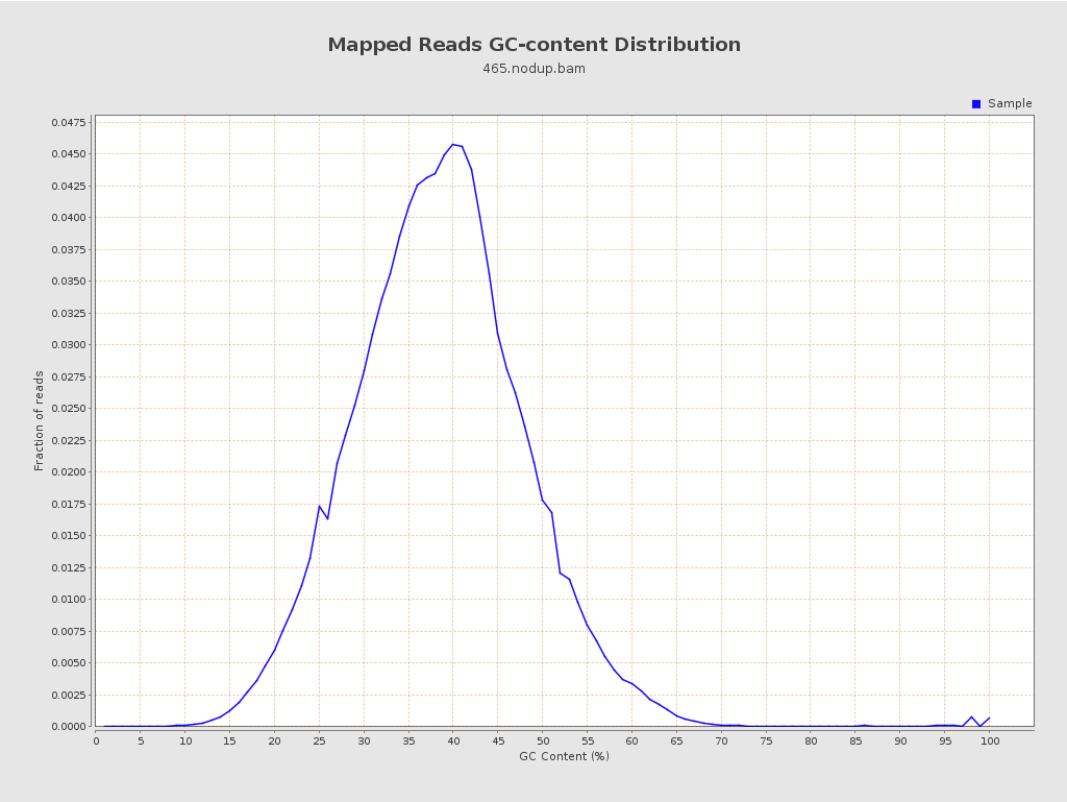
7. Results : Duplication Rate Histogram



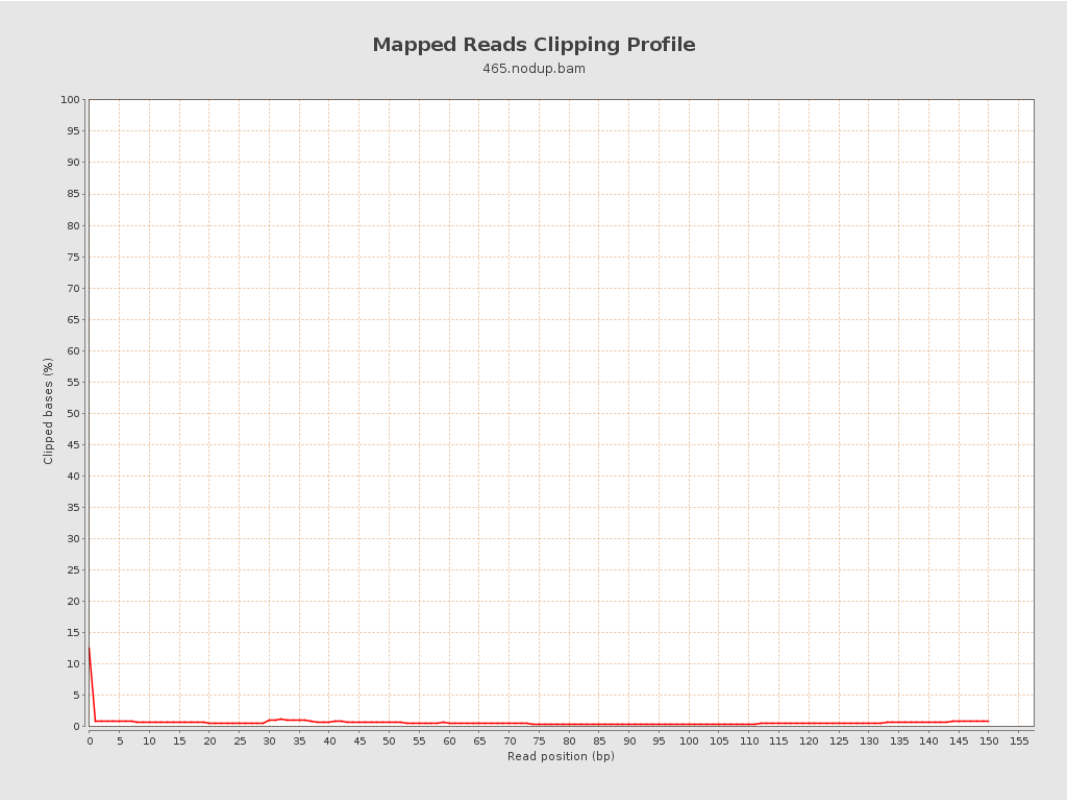
8. Results : Mapped Reads Nucleotide Content



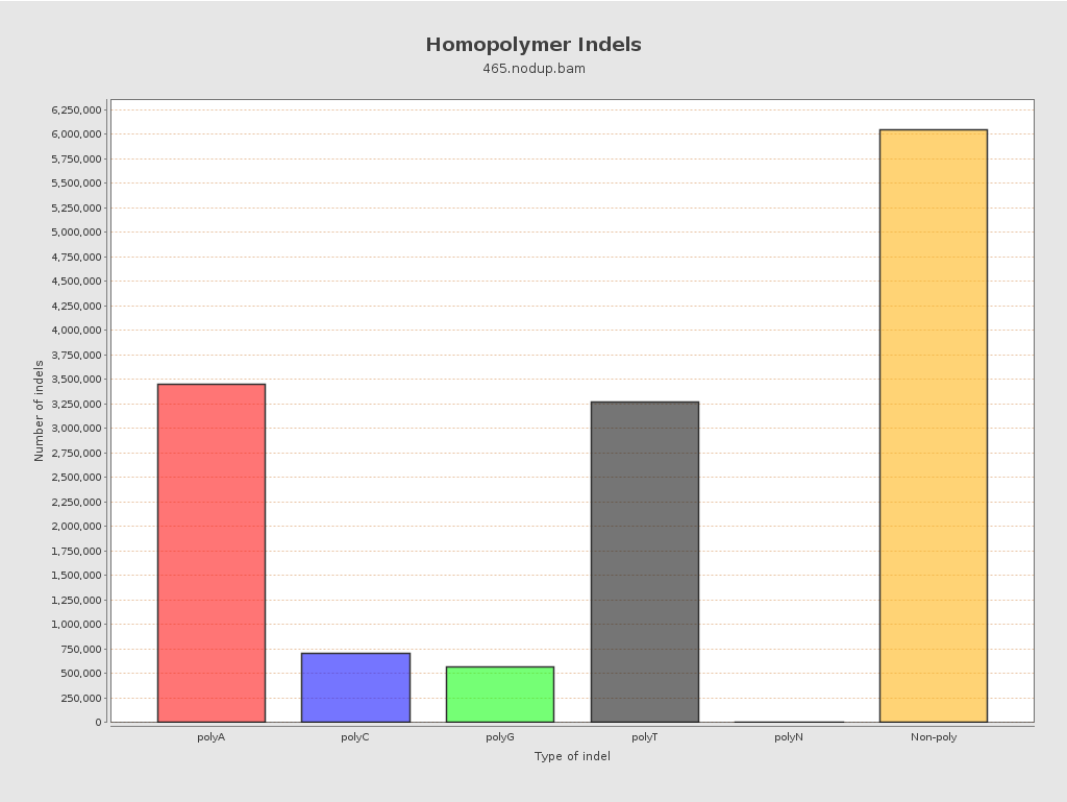
9. Results : Mapped Reads GC-content Distribution



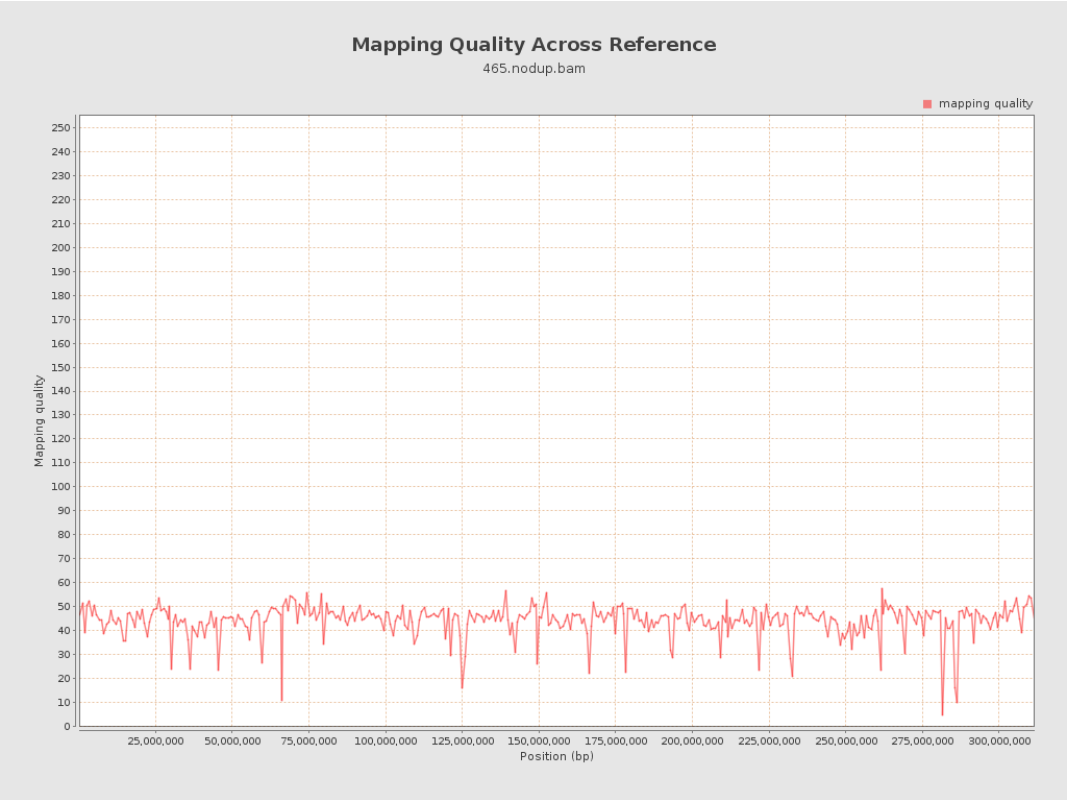
10. Results : Mapped Reads Clipping Profile



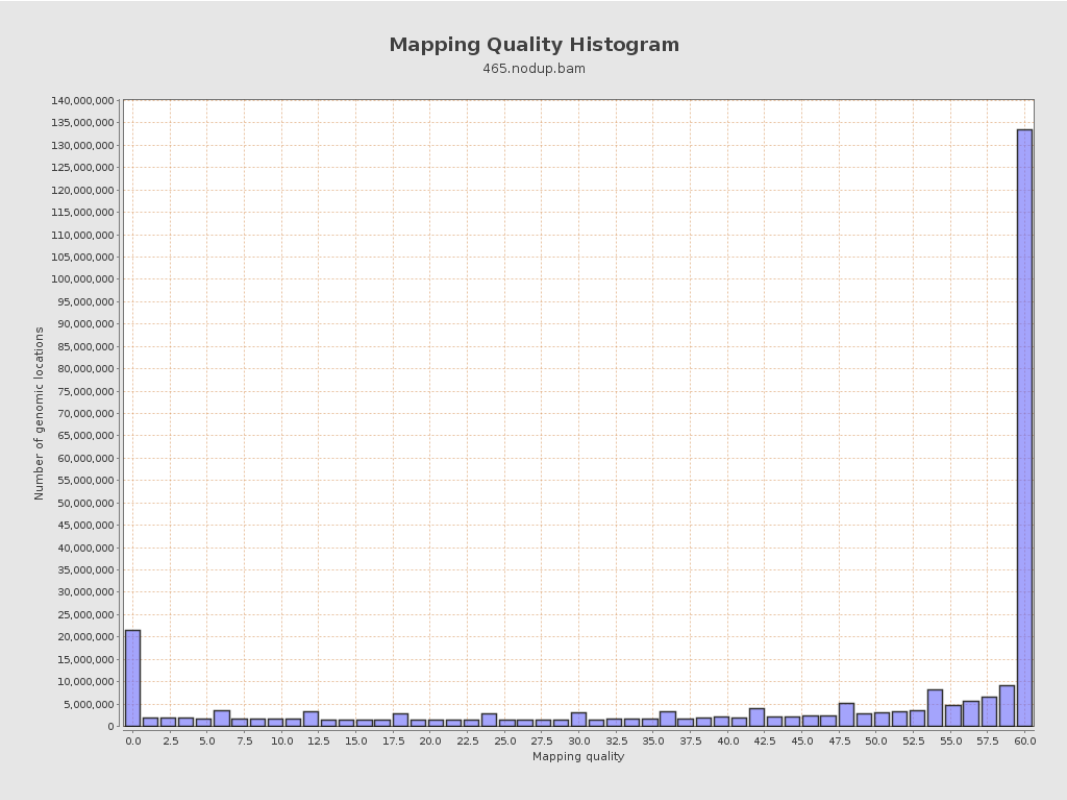
11. Results : Homopolymer Indels



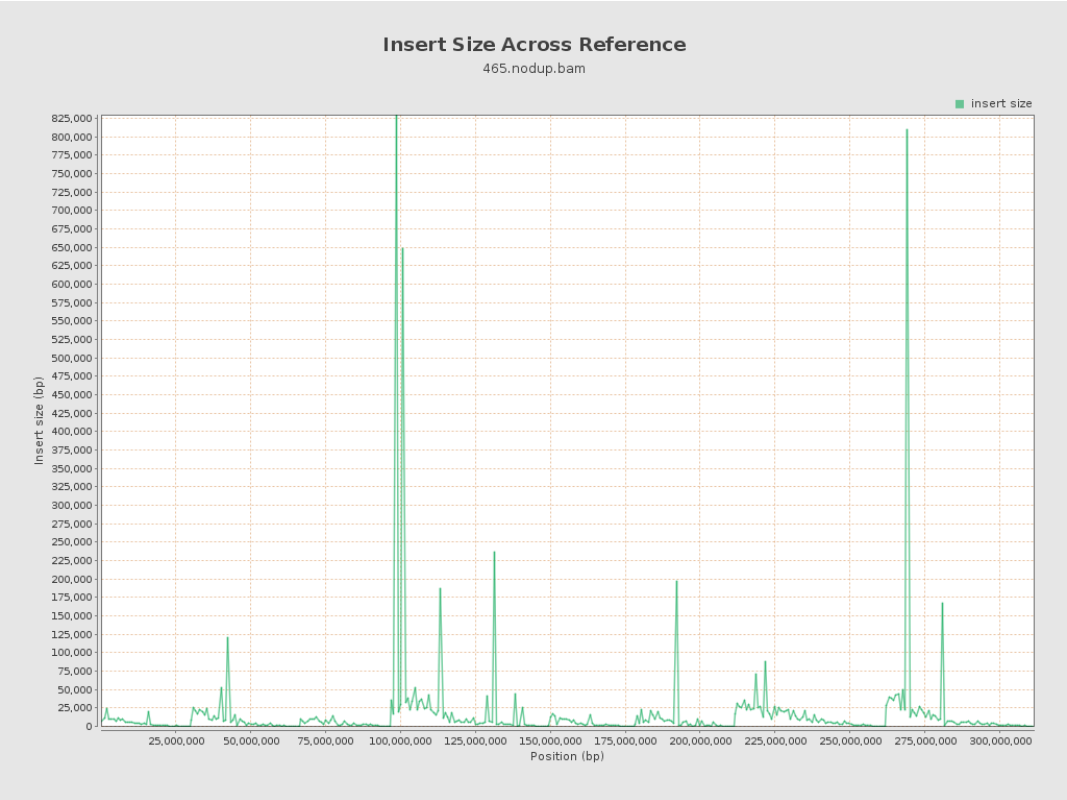
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram