Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/600.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/600.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_283/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_283_S364_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_283/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_283_S364_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:29 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	74,762,294
Mapped reads	68,463,850 / 91.58%
Unmapped reads	6,298,444 / 8.42%
Mapped paired reads	68,463,850 / 91.58%
Mapped reads, first in pair	34,297,755 / 45.88%
Mapped reads, second in pair	34,166,095 / 45.7%
Mapped reads, both in pair	66,413,272 / 88.83%
Mapped reads, singletons	2,050,578 / 2.74%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	11,628,633 / 15.55%
Clipped reads	16,556,708 / 22.15%

2.2. ACGT Content

Number/percentage of A's	2,899,643,642 / 30.89%
Number/percentage of C's	1,791,681,579 / 19.09%
Number/percentage of T's	2,904,814,706 / 30.95%
Number/percentage of G's	1,789,485,662 / 19.07%
Number/percentage of N's	33,721 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	30.1984
Standard Deviation	294.1962

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Insert size

Mean	258,076.41
Standard Deviation	2,433,958.8
P25/Median/P75	320 / 418 / 543

2.6. Mismatches and indels

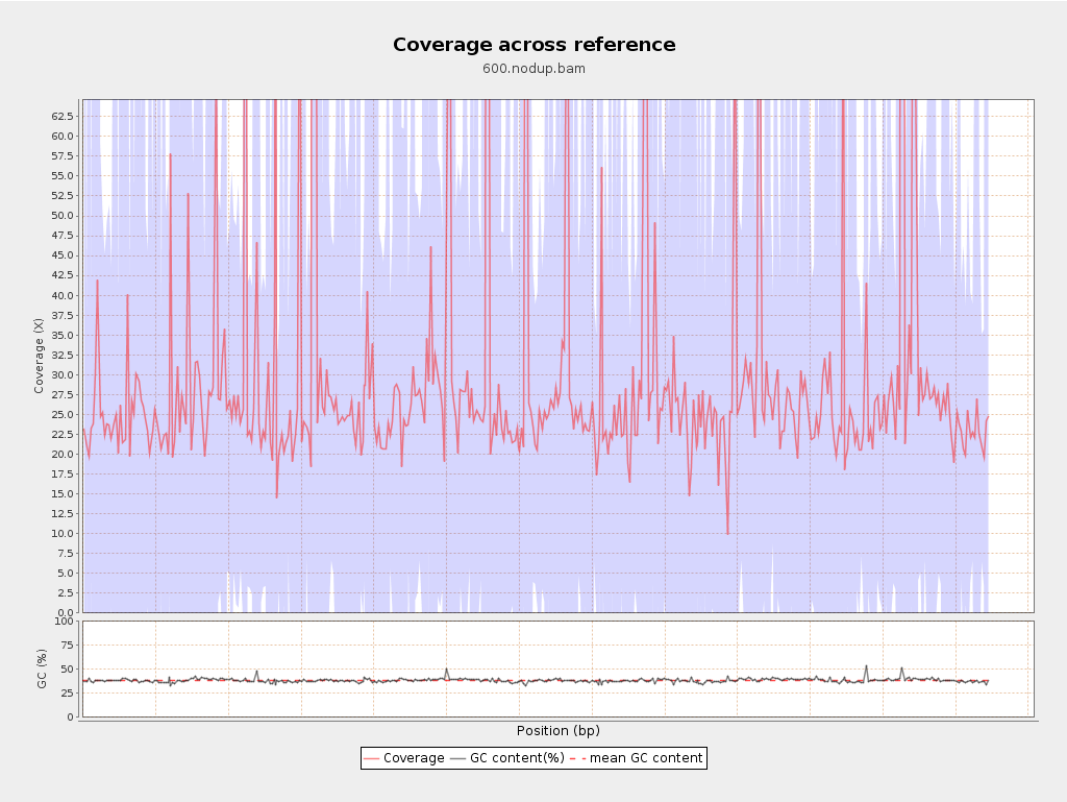
General error rate	2.44%
Mismatches	209,509,841
Insertions	7,008,218
Mapped reads with at least one insertion	9.12%
Deletions	6,799,300
Mapped reads with at least one deletion	8.79%
Homopolymer indels	56.72%

2.7. Chromosome stats

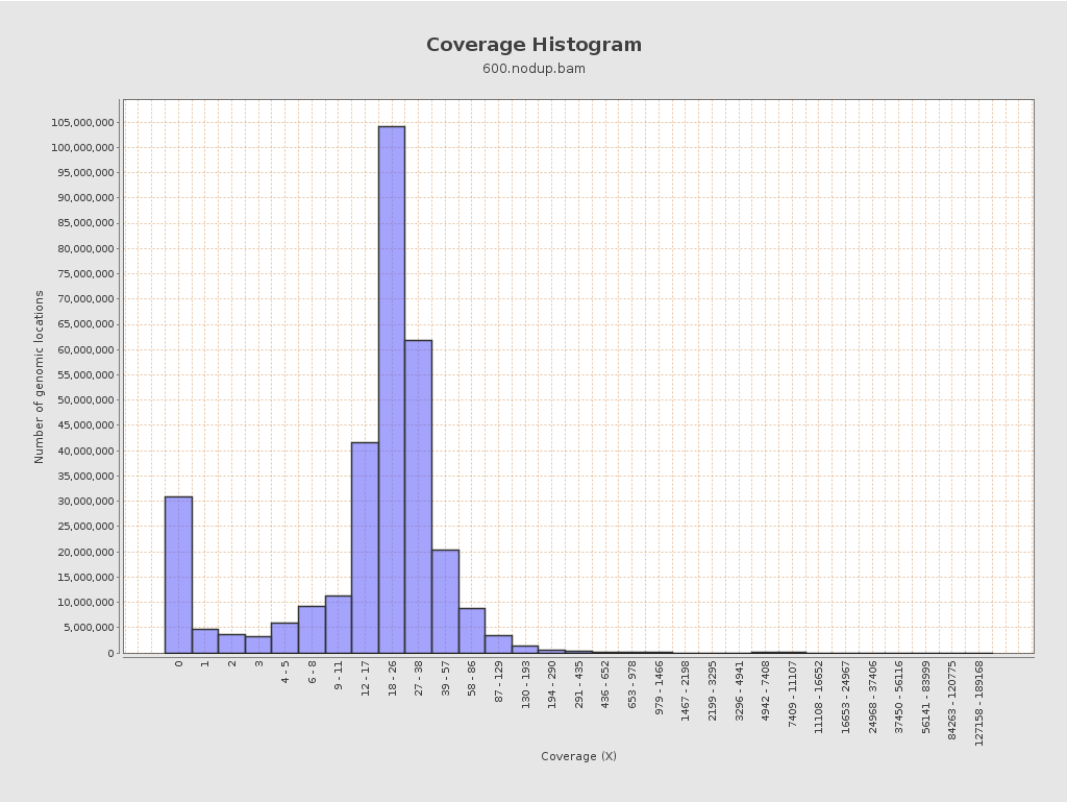
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	730656331	24.5811	119.258

LT669789.1	36598175	1125016221	30.7397	314.7266
LT669790.1	30422129	1099345480	36.1364	401.7386
LT669791.1	52758100	1572765941	29.8109	322.9823
LT669792.1	28376109	847056260	29.851	294.3259
LT669793.1	33388210	949266094	28.4312	244.1034
LT669794.1	50579949	1441187953	28.4933	263.7802
LT669795.1	49795044	1645803988	33.0516	302.0146

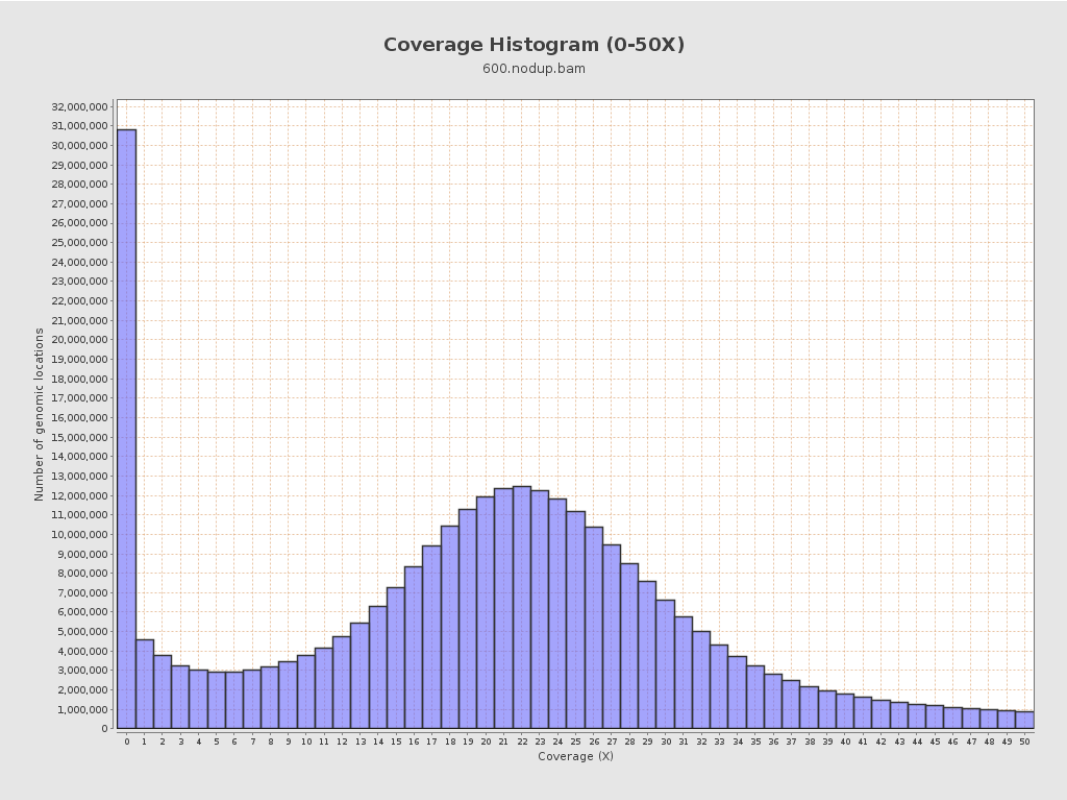
3. Results : Coverage across reference



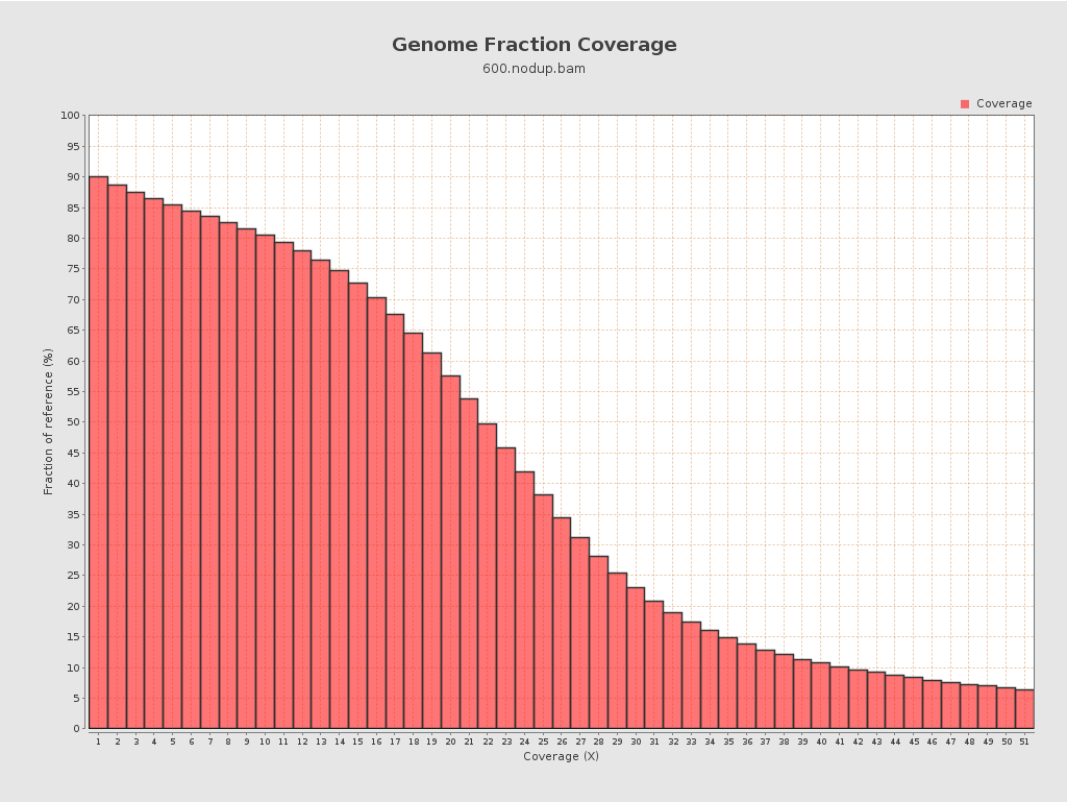
4. Results : Coverage Histogram



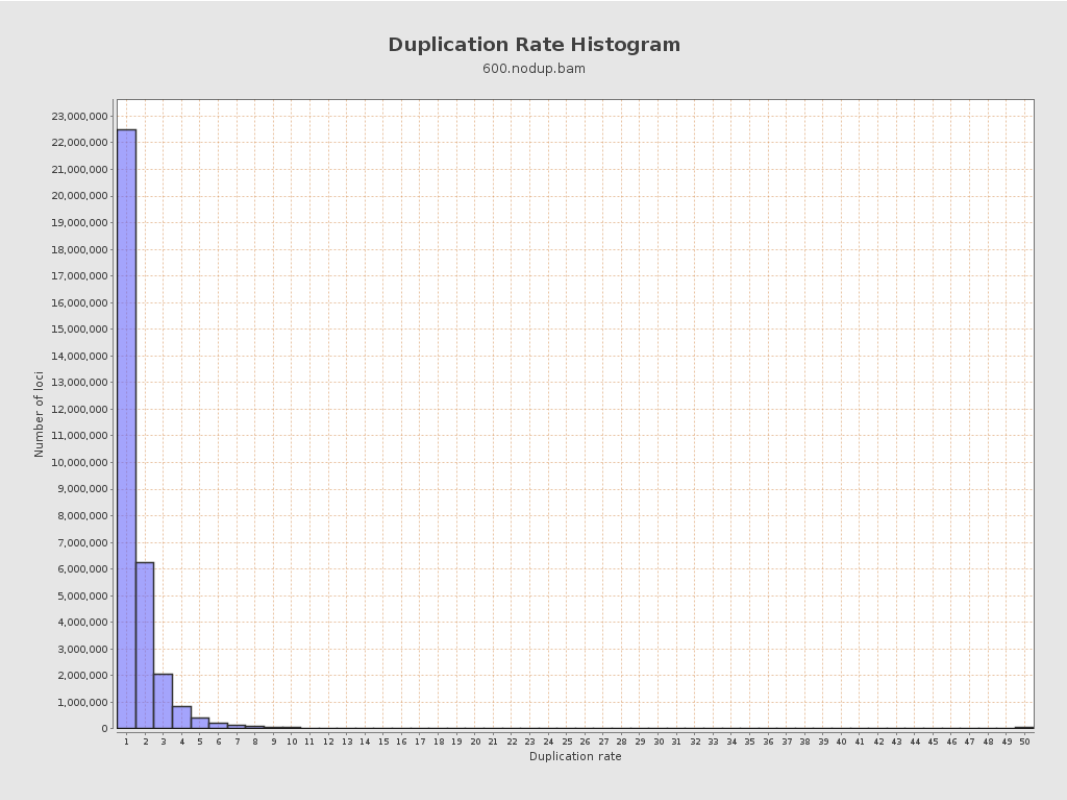
5. Results : Coverage Histogram (0-50X)



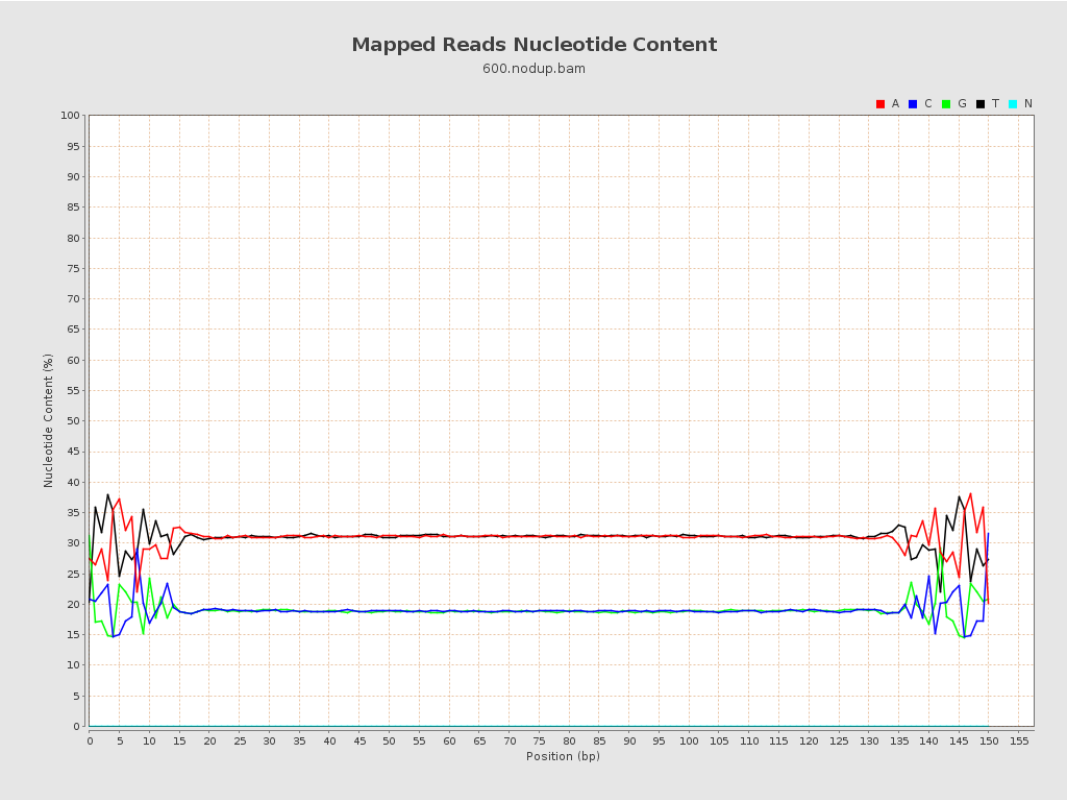
6. Results : Genome Fraction Coverage



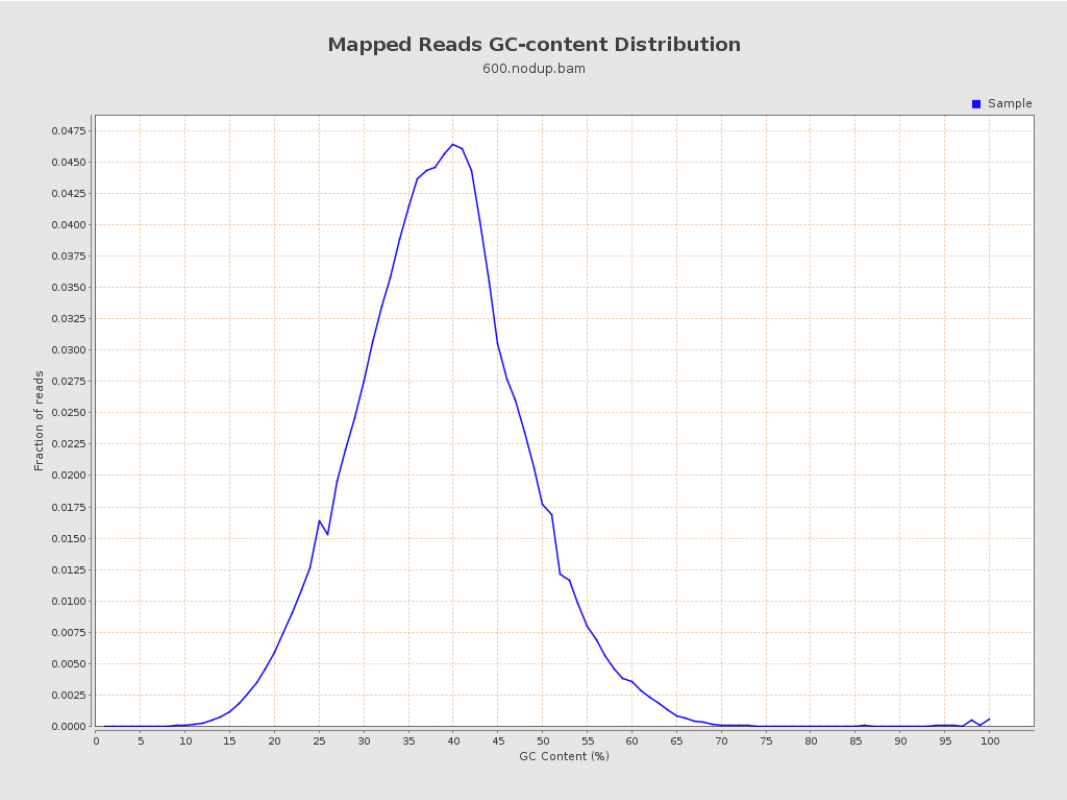
7. Results : Duplication Rate Histogram



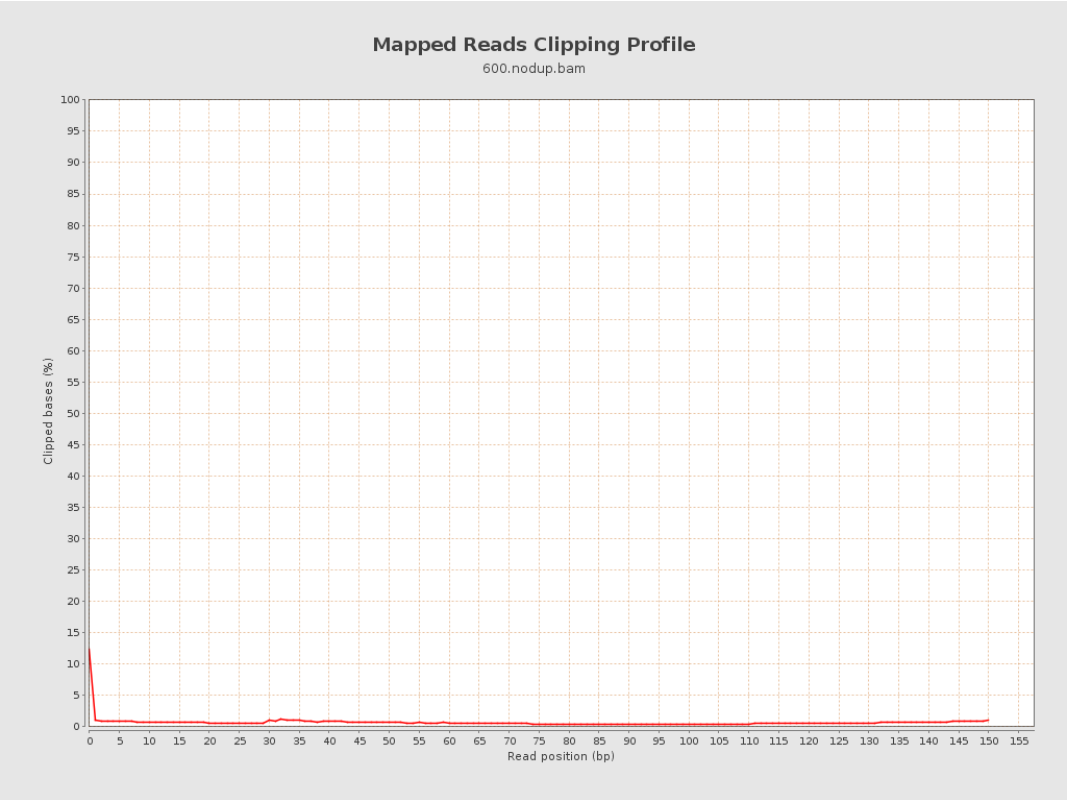
8. Results : Mapped Reads Nucleotide Content



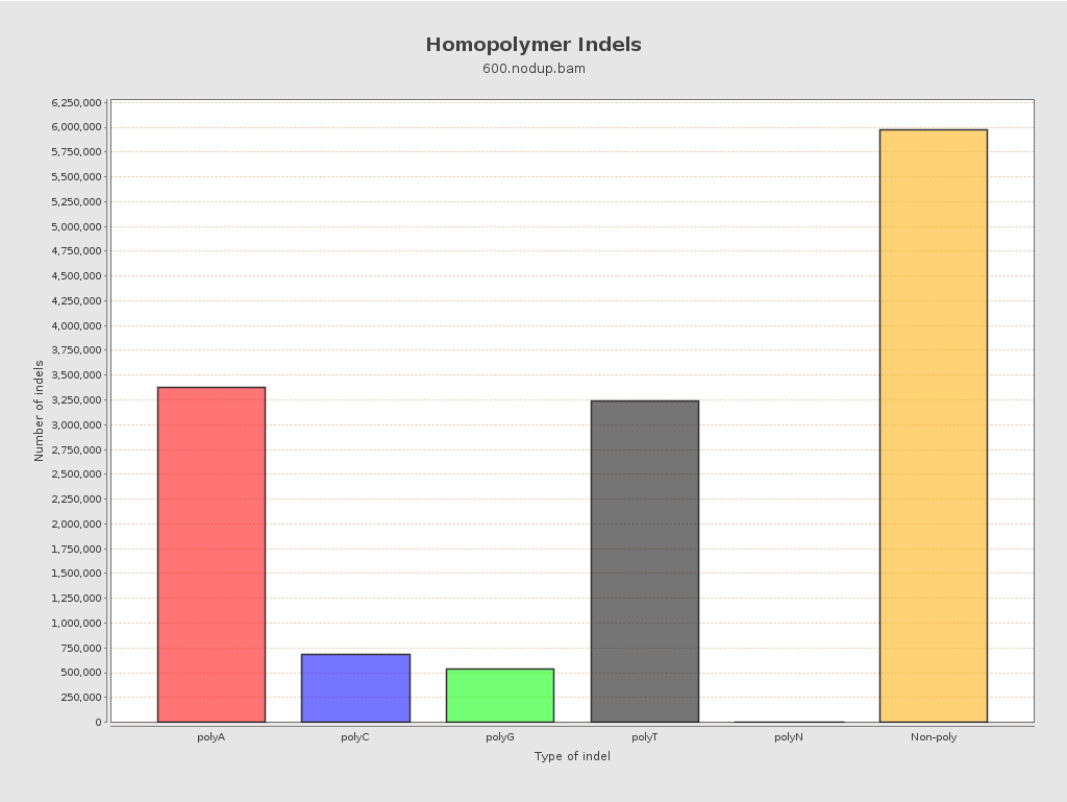
9. Results : Mapped Reads GC-content Distribution



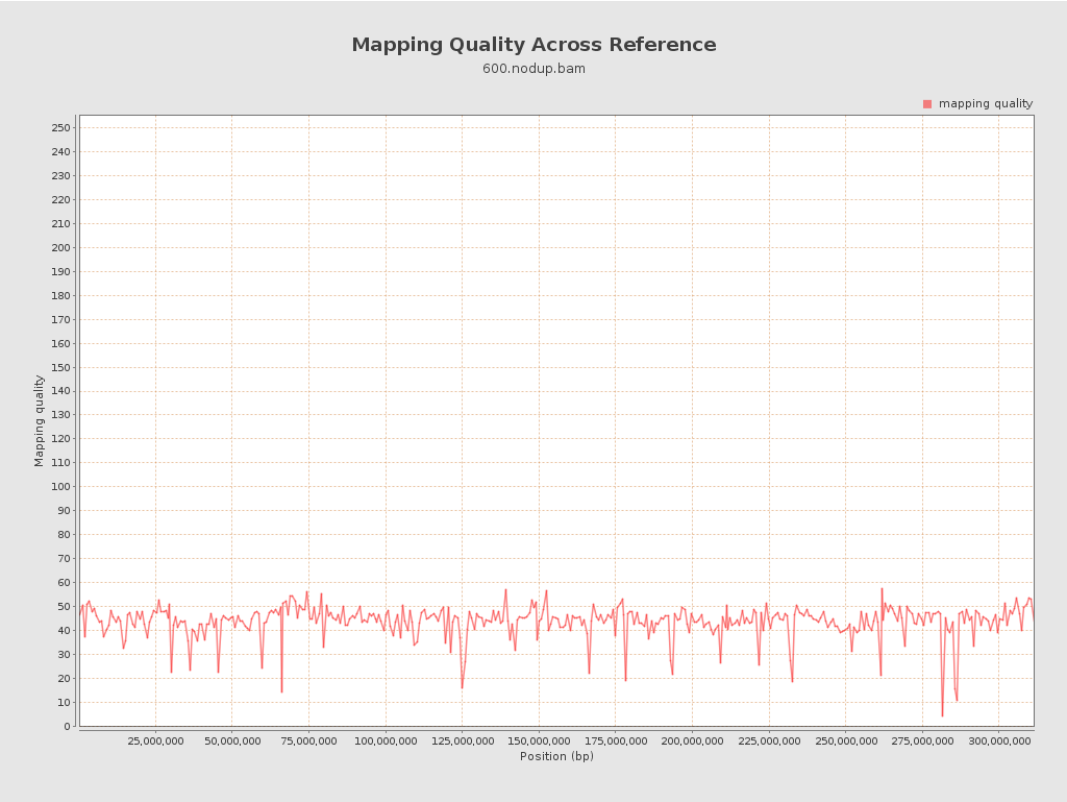
10. Results : Mapped Reads Clipping Profile



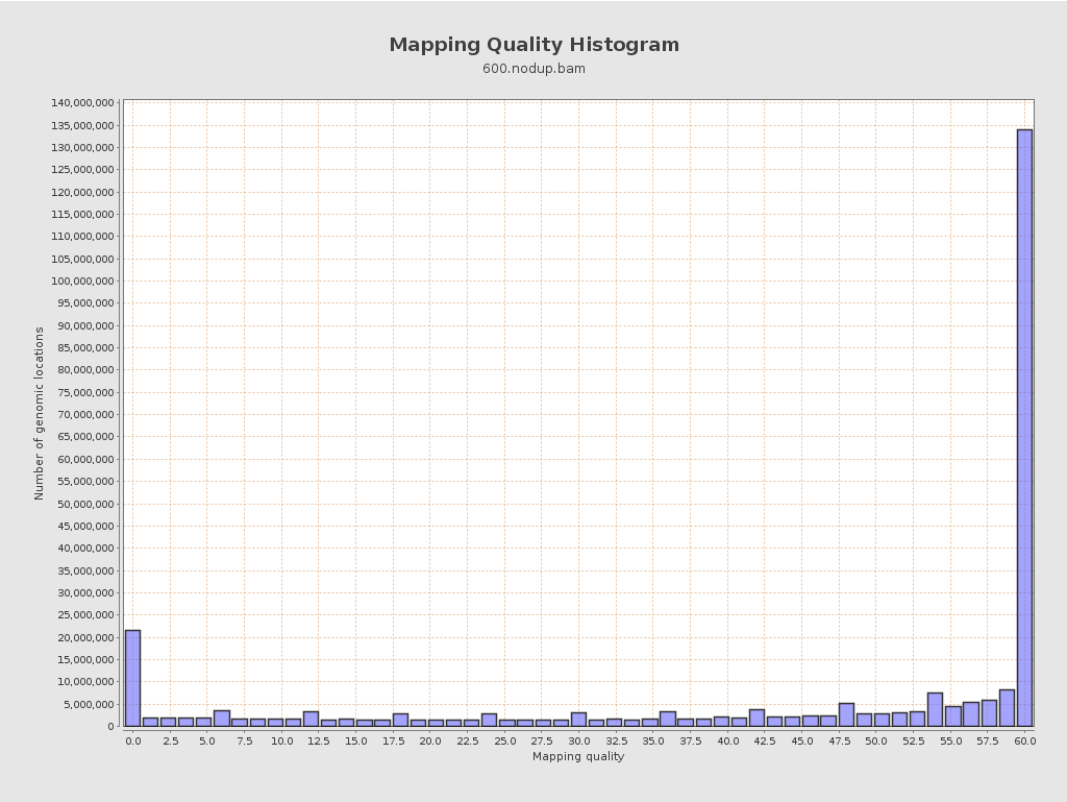
11. Results : Homopolymer Indels



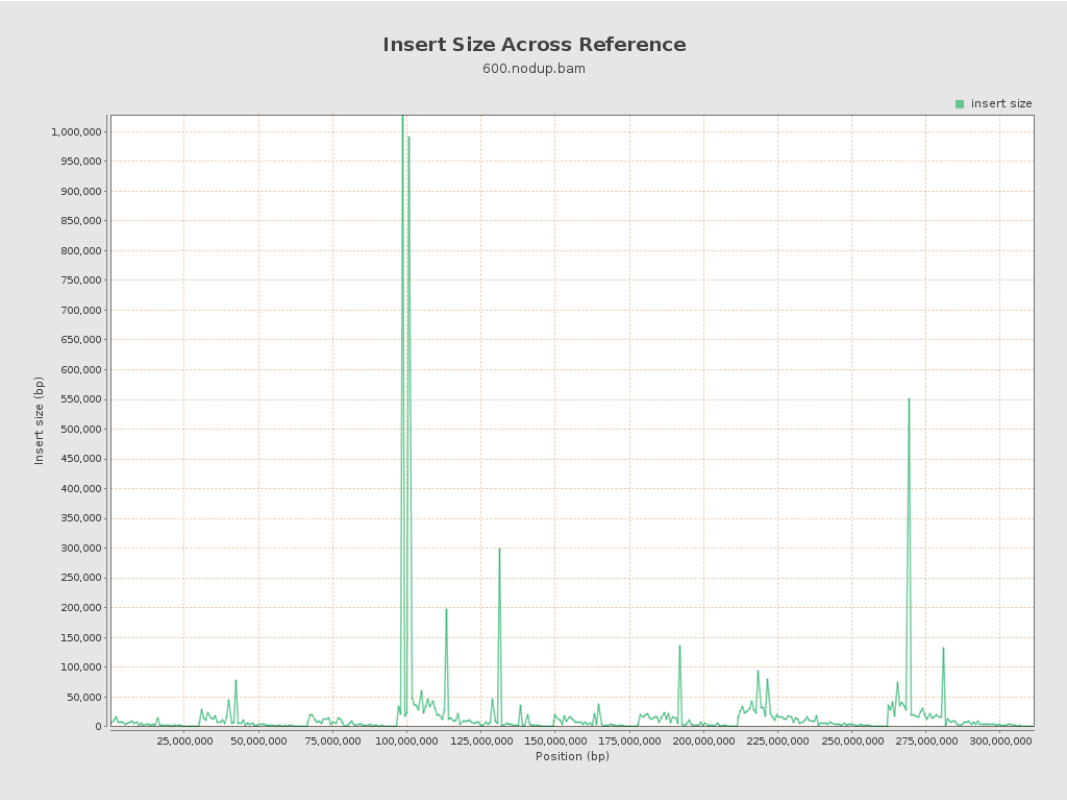
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram