Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/426.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/426.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_229/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_229_S310_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_229/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_229_S310_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,618,769
Mapped reads	62,634,897 / 91.28%
Unmapped reads	5,983,872 / 8.72%
Mapped paired reads	62,634,897 / 91.28%
Mapped reads, first in pair	31,436,882 / 45.81%
Mapped reads, second in pair	31,198,015 / 45.47%
Mapped reads, both in pair	60,830,035 / 88.65%
Mapped reads, singletons	1,804,862 / 2.63%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	10,255,693 / 14.95%
Clipped reads	15,635,091 / 22.79%

2.2. ACGT Content

Number/percentage of A's	2,634,492,728 / 30.82%
Number/percentage of C's	1,638,139,958 / 19.16%
Number/percentage of T's	2,635,943,296 / 30.83%
Number/percentage of G's	1,640,654,627 / 19.19%
Number/percentage of N's	31,927 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	27.503
Standard Deviation	262.8556

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Insert size

Mean	240,331.54
Standard Deviation	2,348,948.24
P25/Median/P75	299 / 397 / 520

2.6. Mismatches and indels

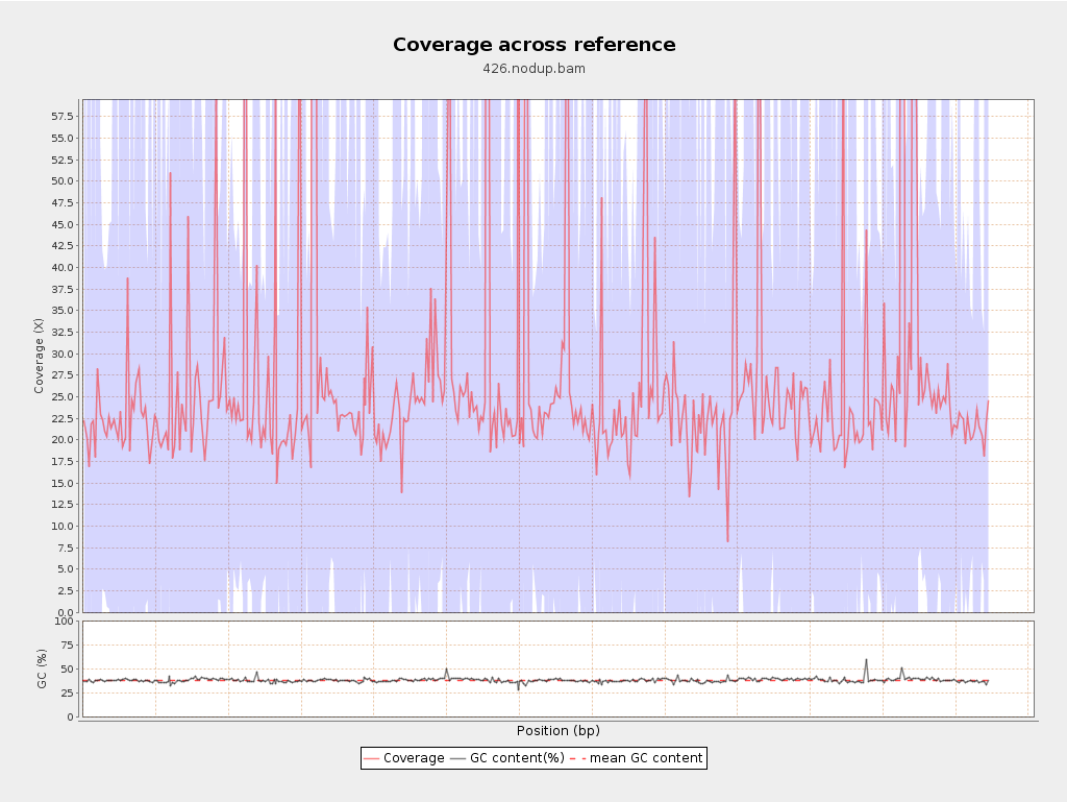
General error rate	2.42%
Mismatches	189,904,313
Insertions	6,060,512
Mapped reads with at least one insertion	8.65%
Deletions	5,861,948
Mapped reads with at least one deletion	8.32%
Homopolymer indels	56.77%

2.7. Chromosome stats

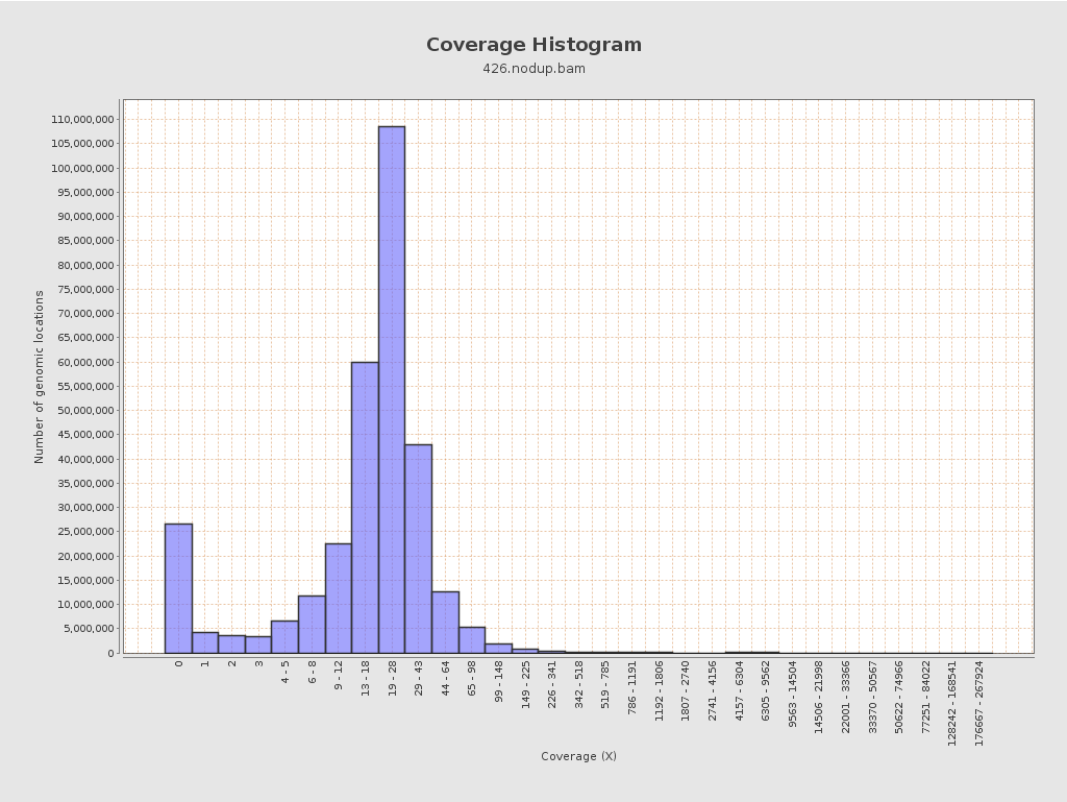
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	657454710	22.1184	89.6365

LT669789.1	36598175	1003212548	27.4115	262.2385
LT669790.1	30422129	989476004	32.5249	334.5307
LT669791.1	52758100	1426952689	27.0471	259.6403
LT669792.1	28376109	786390978	27.7131	262.6812
LT669793.1	33388210	833721729	24.9705	216.6264
LT669794.1	50579949	1289665934	25.4976	202.6776
LT669795.1	49795044	1584203620	31.8145	353.1445

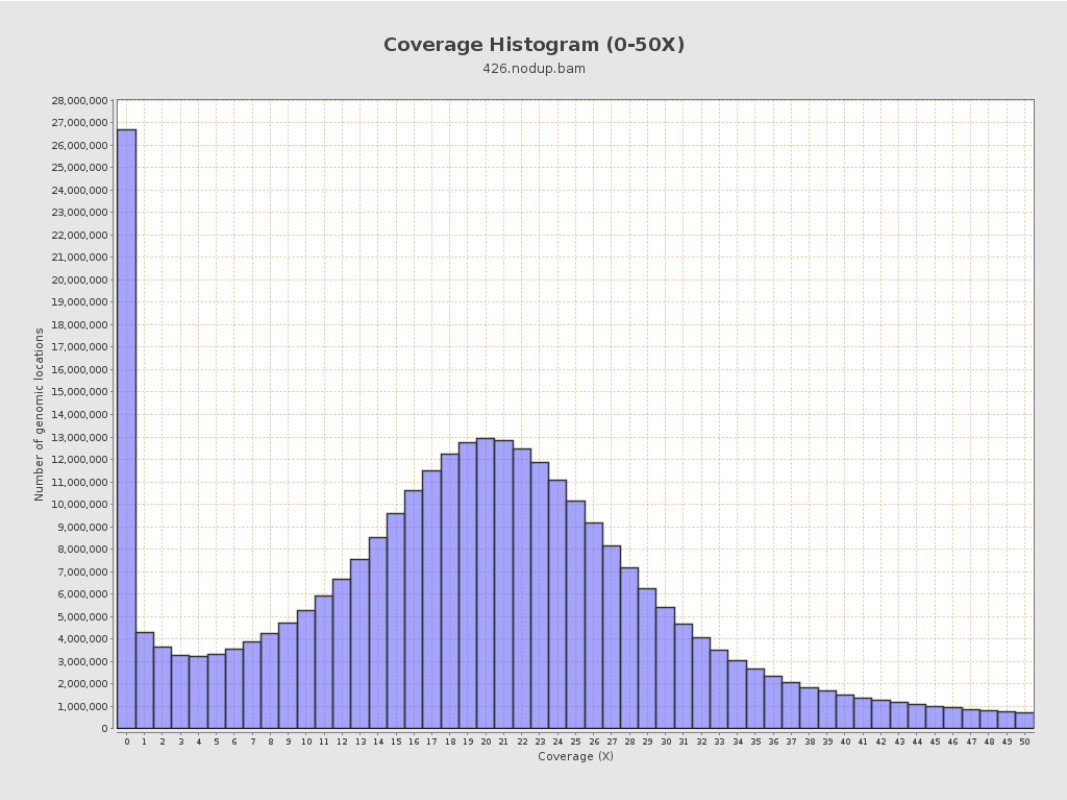
3. Results : Coverage across reference



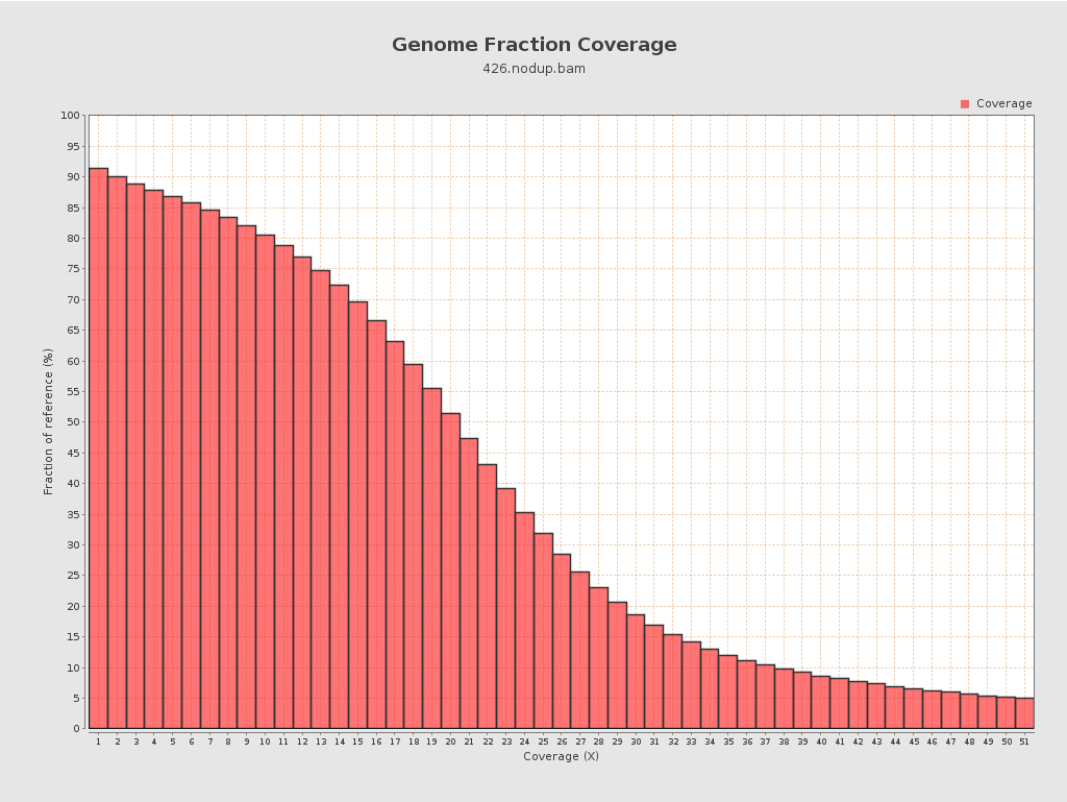
4. Results : Coverage Histogram



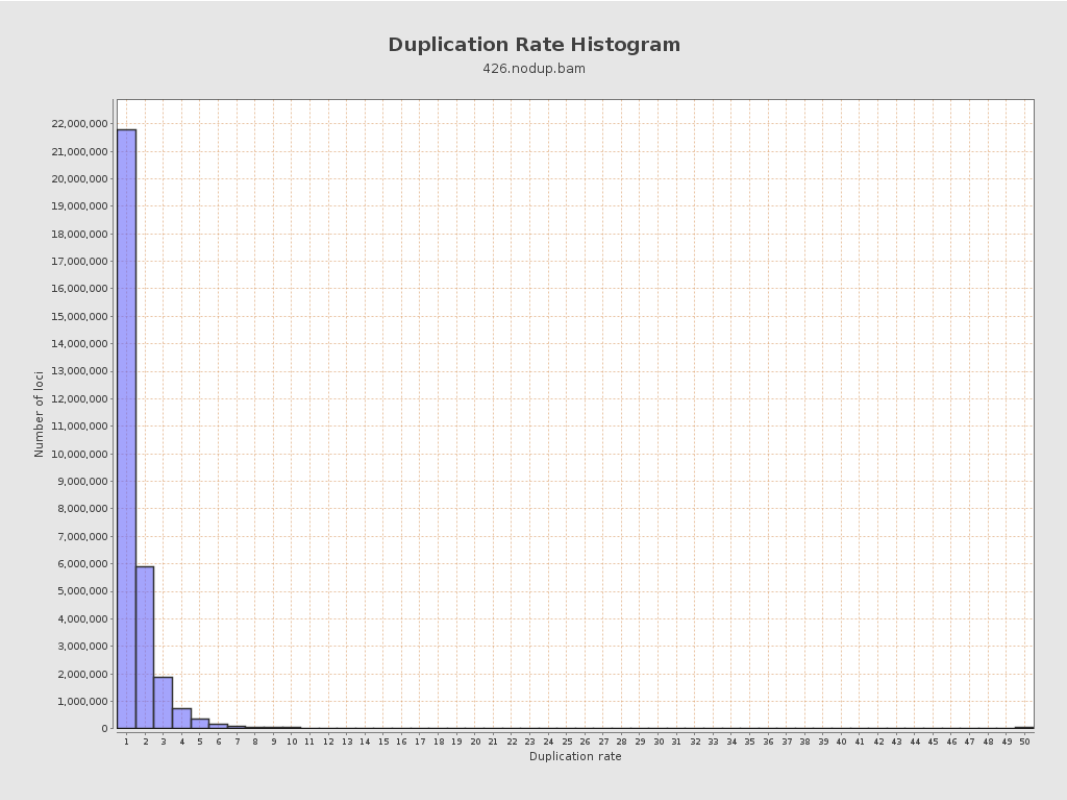
5. Results : Coverage Histogram (0-50X)



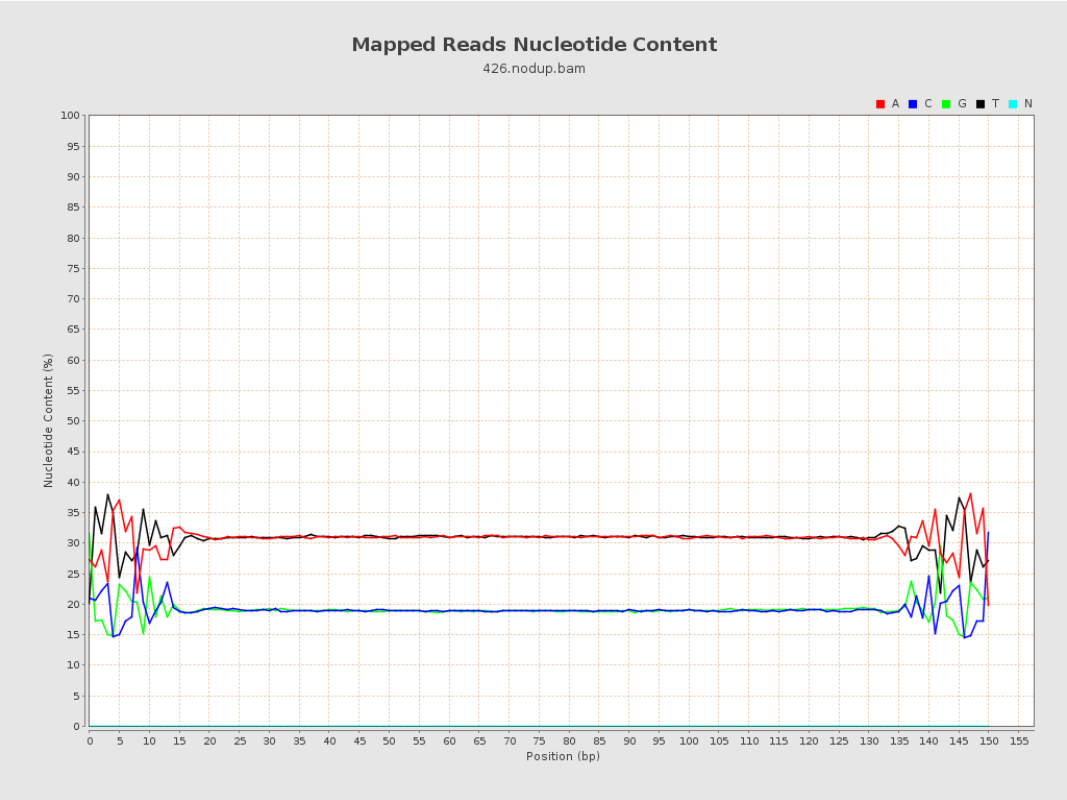
6. Results : Genome Fraction Coverage



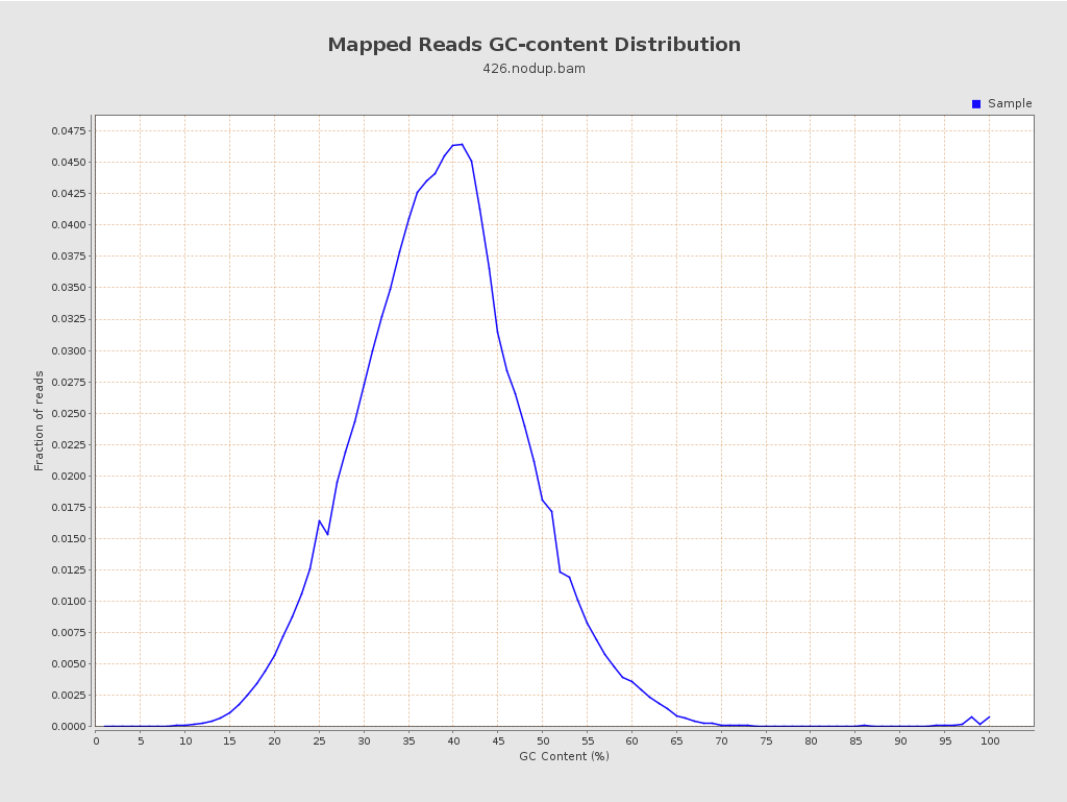
7. Results : Duplication Rate Histogram



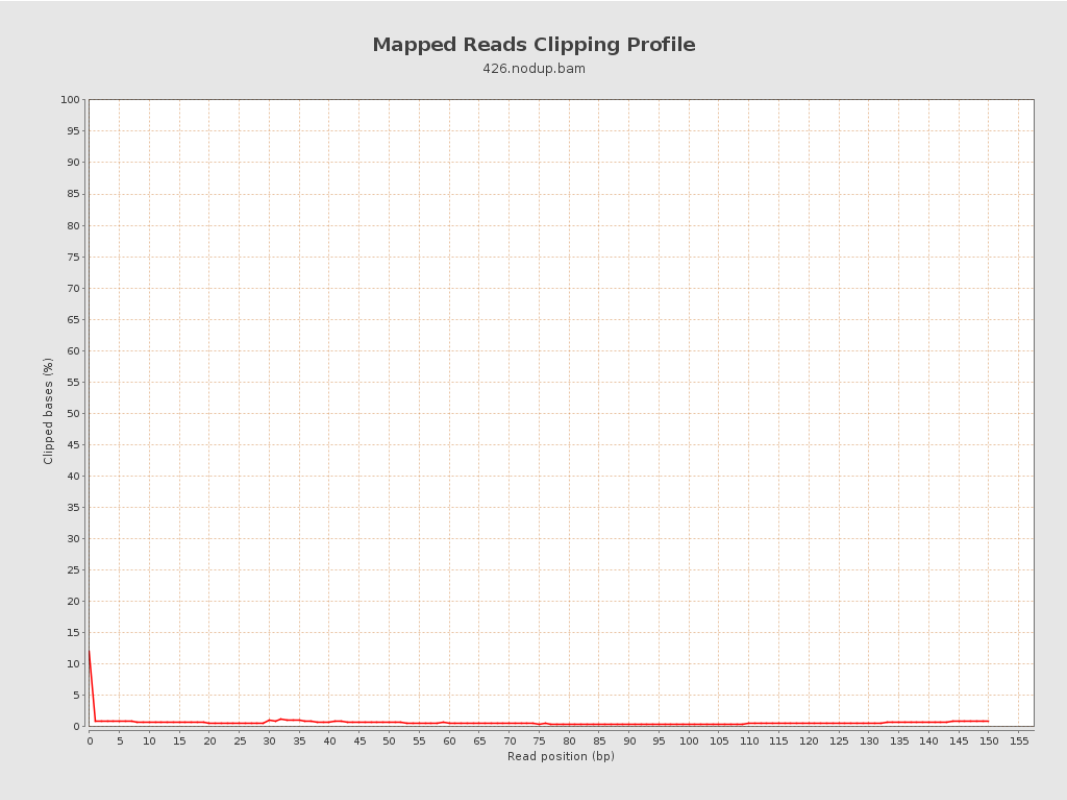
8. Results : Mapped Reads Nucleotide Content



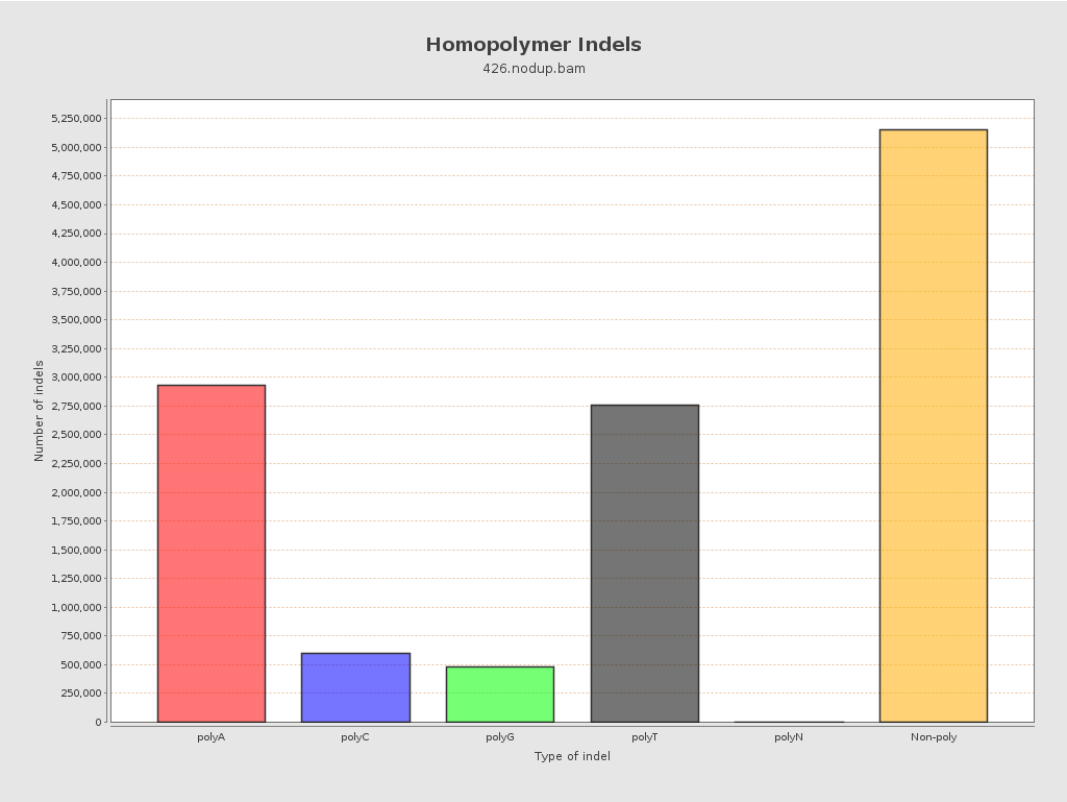
9. Results : Mapped Reads GC-content Distribution



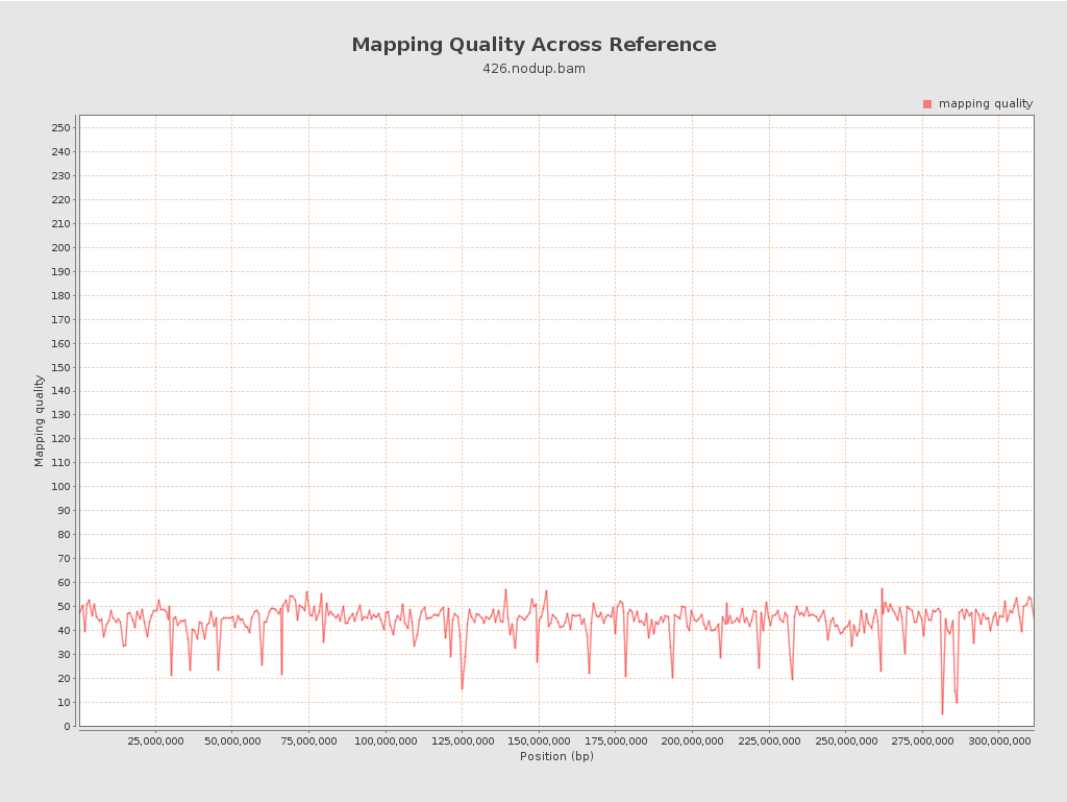
10. Results : Mapped Reads Clipping Profile



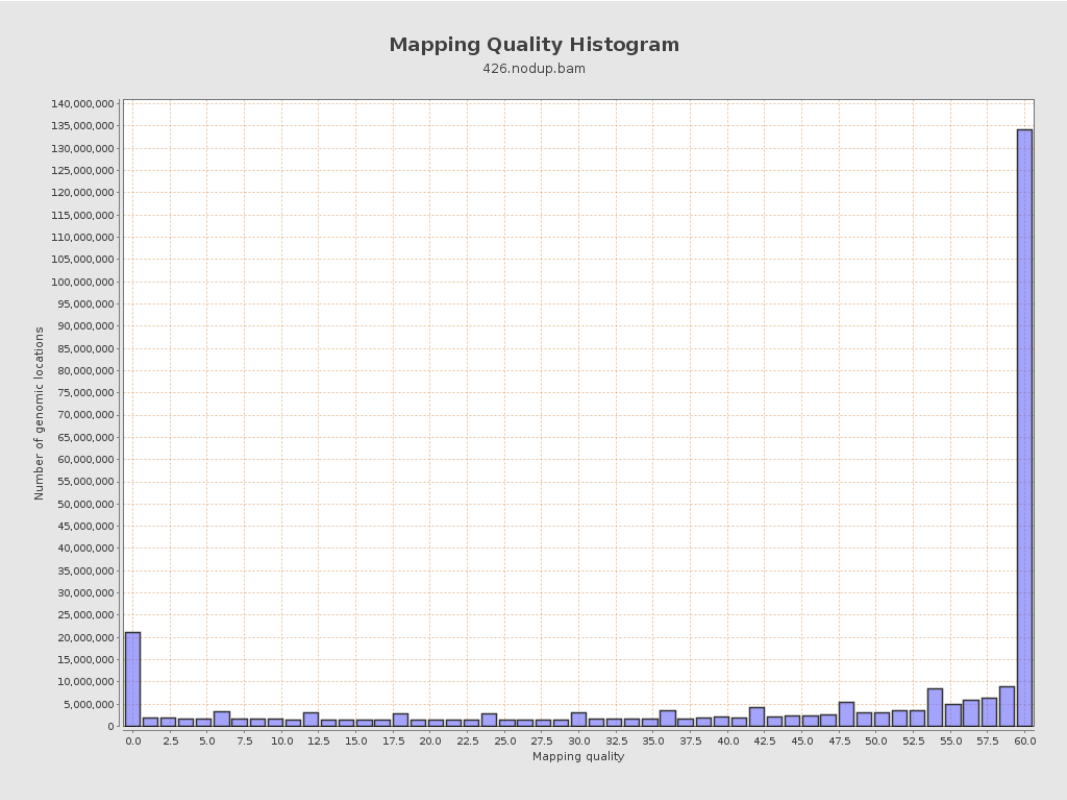
11. Results : Homopolymer Indels



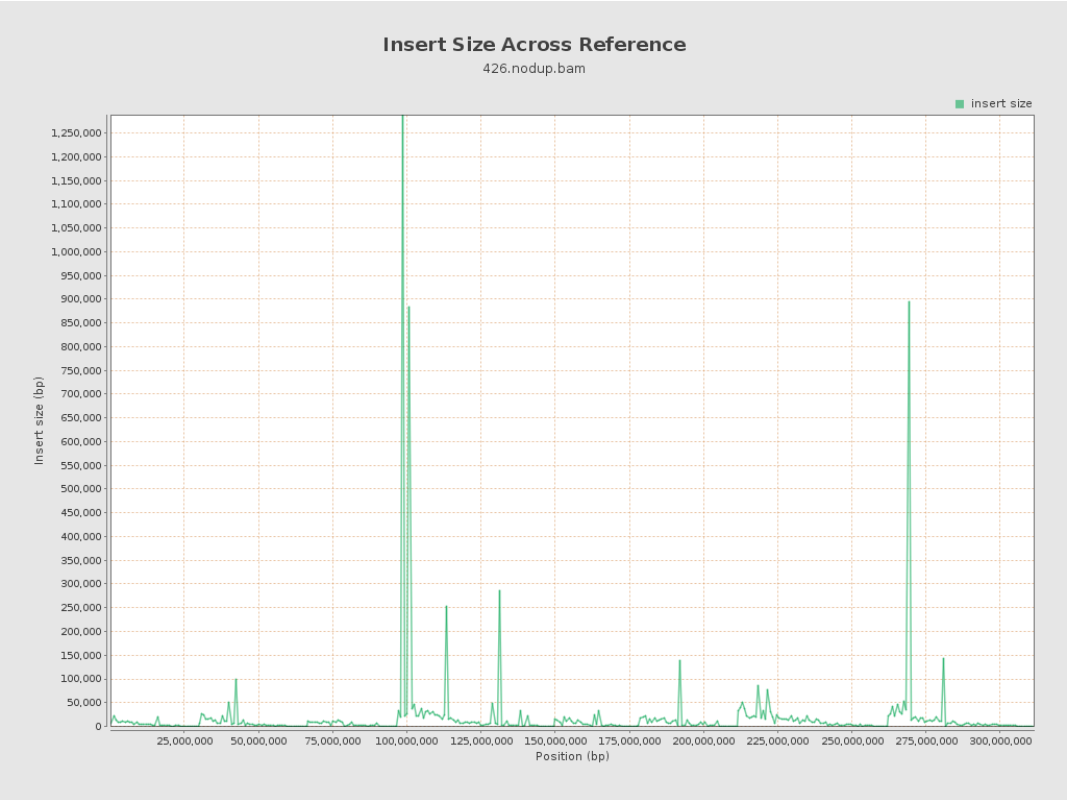
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram