

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/413
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/413.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/awdata/P26207/P26207_171/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_171_S261_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_171/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_171_S261_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:13 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,818,645
Mapped reads	70,727,476 / 93.29%
Unmapped reads	5,091,169 / 6.71%
Mapped paired reads	70,727,476 / 93.29%
Mapped reads, first in pair	35,420,227 / 46.72%
Mapped reads, second in pair	35,307,249 / 46.57%
Mapped reads, both in pair	69,055,850 / 91.08%
Mapped reads, singletons	1,671,626 / 2.2%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	12,556,084 / 16.56%
Clipped reads	15,873,126 / 20.94%

2.2. ACGT Content

Number/percentage of A's	3,017,960,673 / 30.81%
Number/percentage of C's	1,880,240,809 / 19.19%
Number/percentage of T's	3,022,542,342 / 30.85%
Number/percentage of G's	1,875,836,427 / 19.15%
Number/percentage of N's	41,251 / 0%
GC Percentage	38.34%

2.3. Coverage

Mean	31.5196
Standard Deviation	269.4051

2.4. Mapping Quality

Mean Mapping Quality	43.86
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2.5. Insert size

Mean	245,177.42
Standard Deviation	2,360,264.42
P25/Median/P75	329 / 429 / 563

2.6. Mismatches and indels

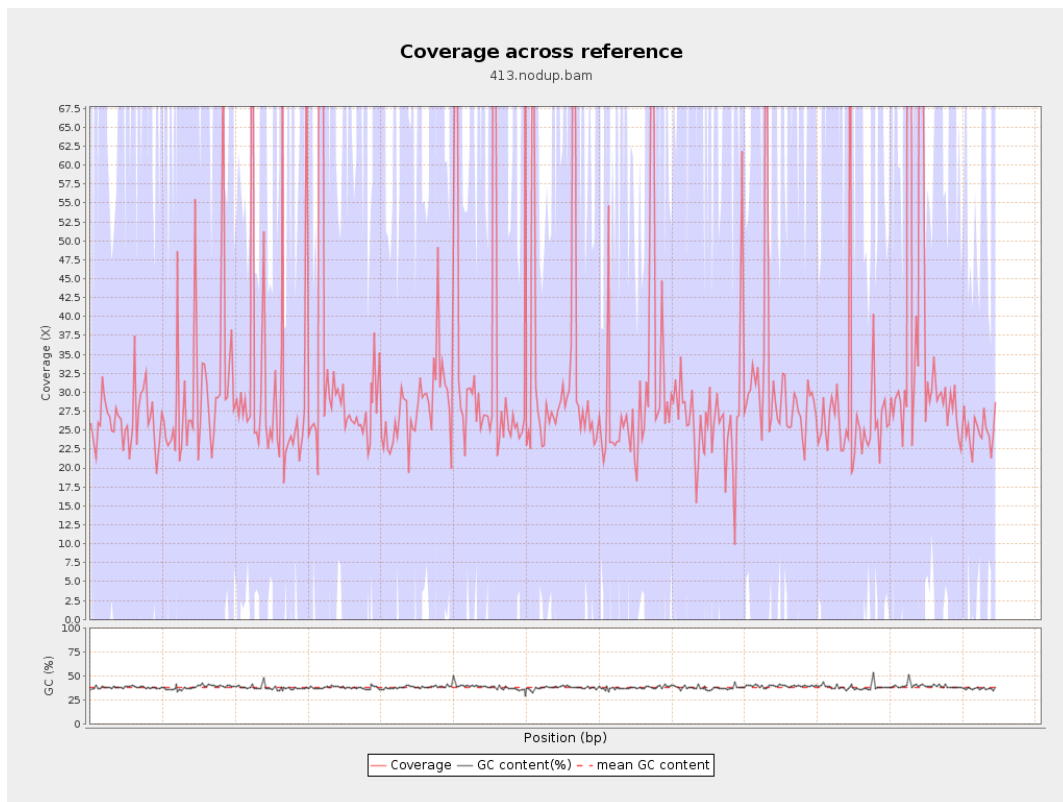
General error rate	2.34%
Mismatches	210,821,534
Insertions	6,857,898
Mapped reads with at least one insertion	8.69%
Deletions	6,896,267
Mapped reads with at least one deletion	8.63%
Homopolymer indels	56.19%

2.7. Chromosome stats

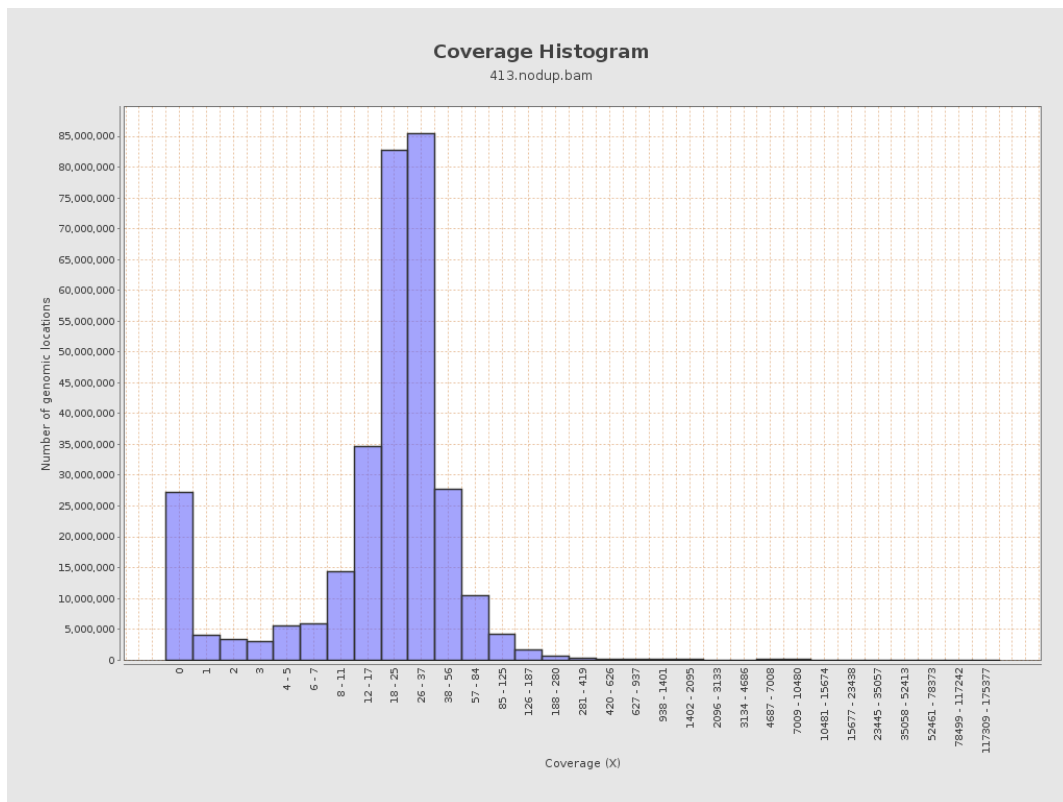
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	773325225	26.0166	100.2899

LT669789.1	36598175	1165624684	31.8493	289.4581
LT669790.1	30422129	1065851061	35.0354	291.0475
LT669791.1	52758100	1630465136	30.9045	268.317
LT669792.1	28376109	892165443	31.4407	286.5748
LT669793.1	33388210	979015368	29.3222	175.1236
LT669794.1	50579949	1501781264	29.6912	240.1367
LT669795.1	49795044	1814609035	36.4416	364.179

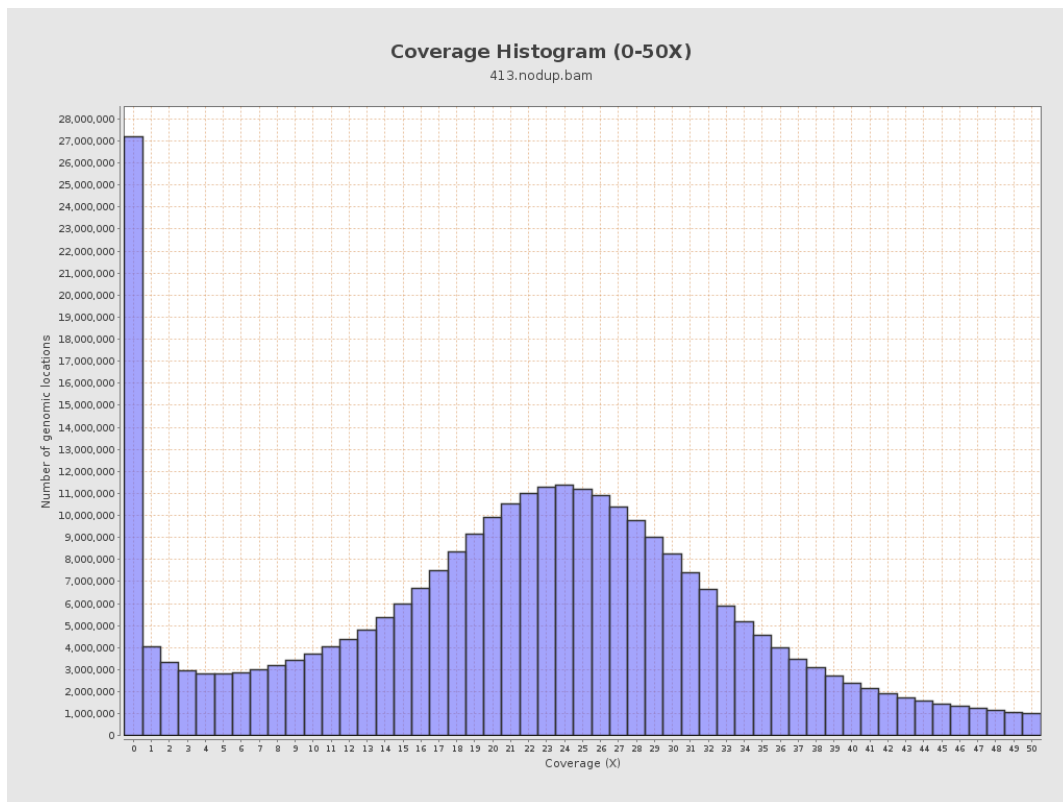
3. Results : Coverage across reference



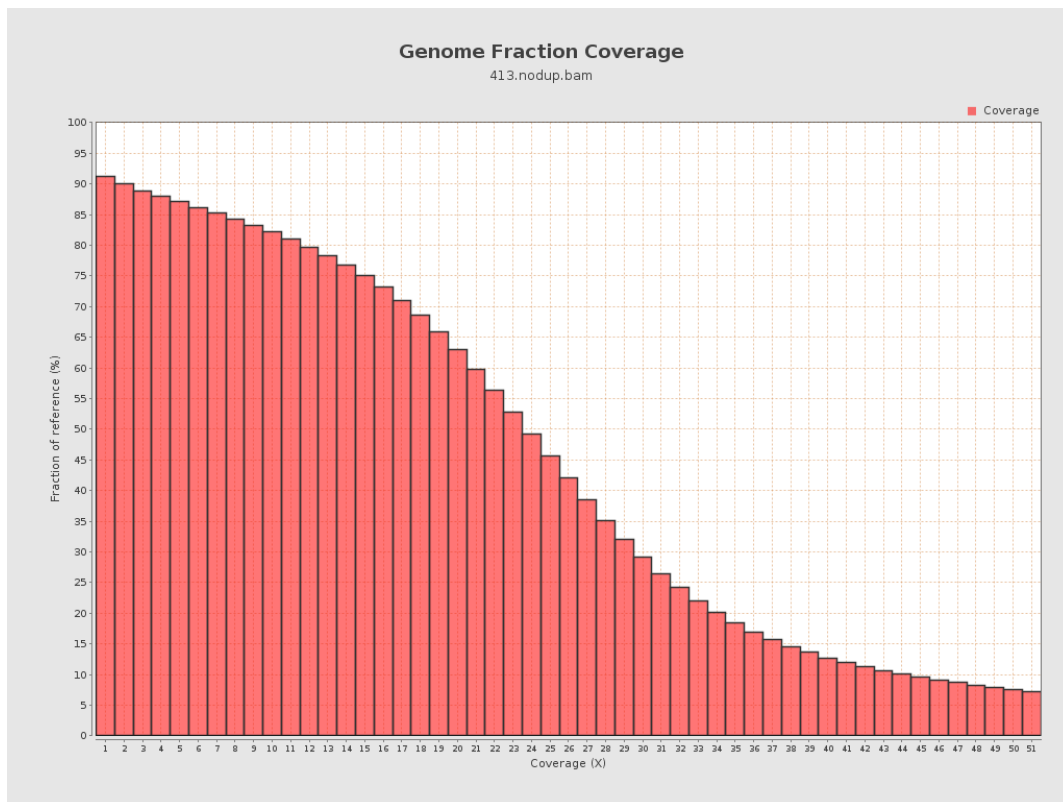
4. Results : Coverage Histogram



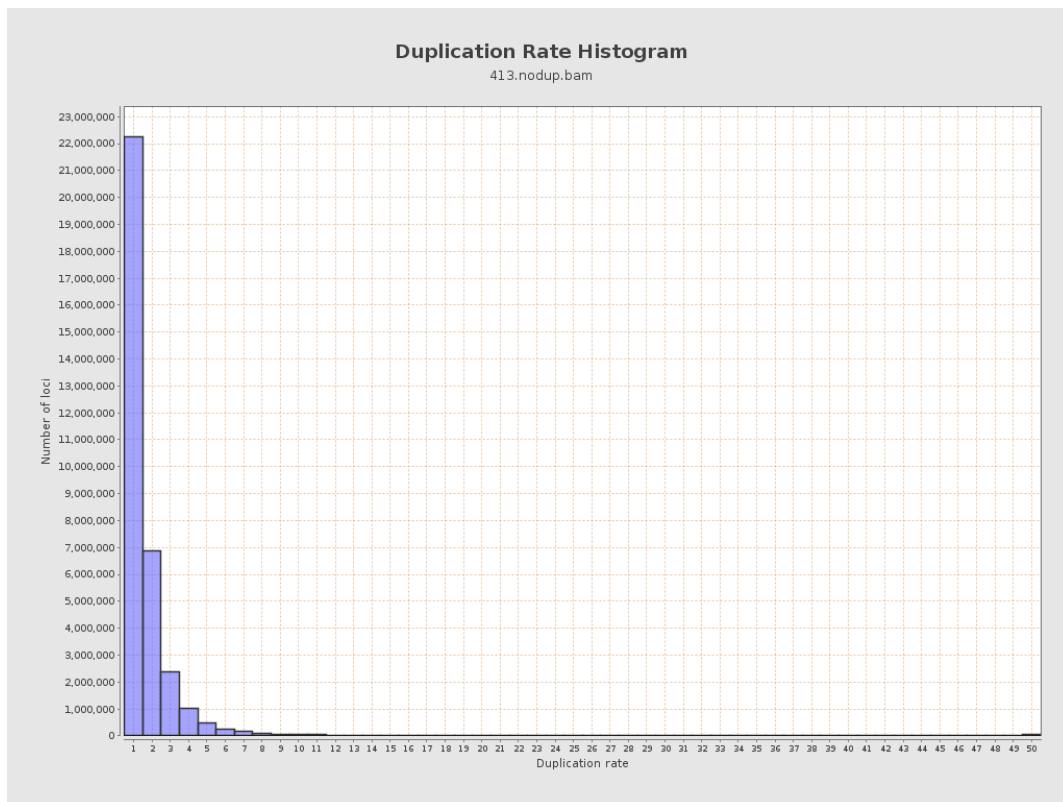
5. Results : Coverage Histogram (0-50X)



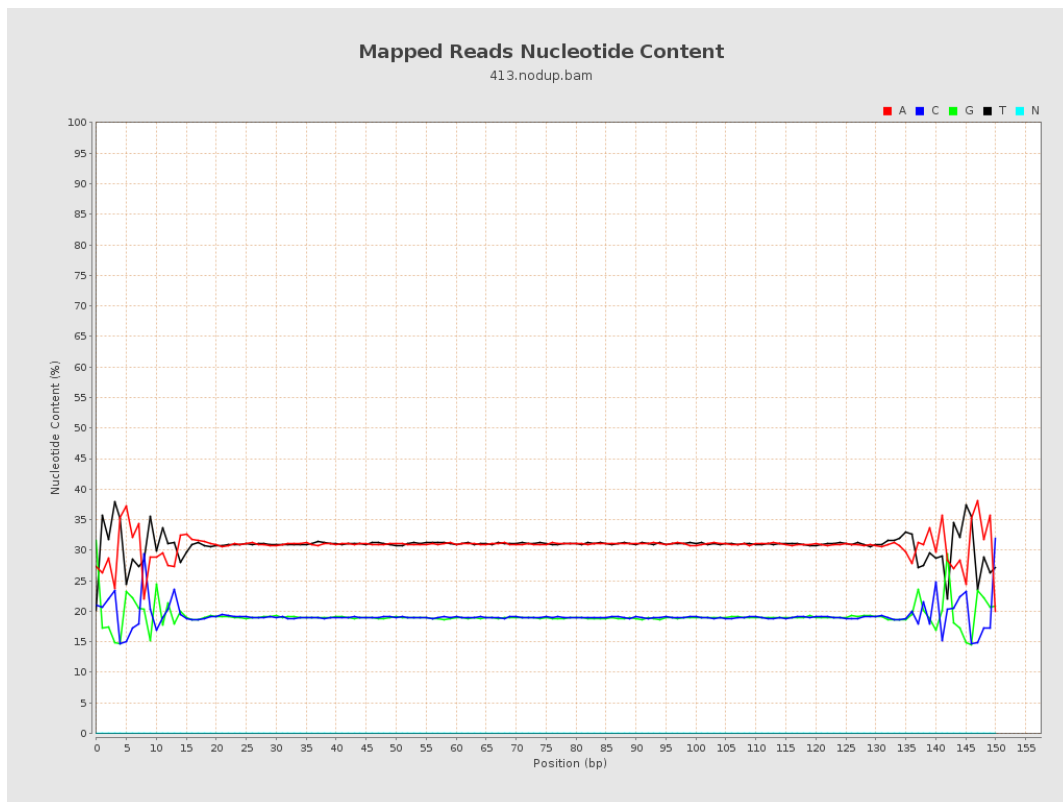
6. Results : Genome Fraction Coverage



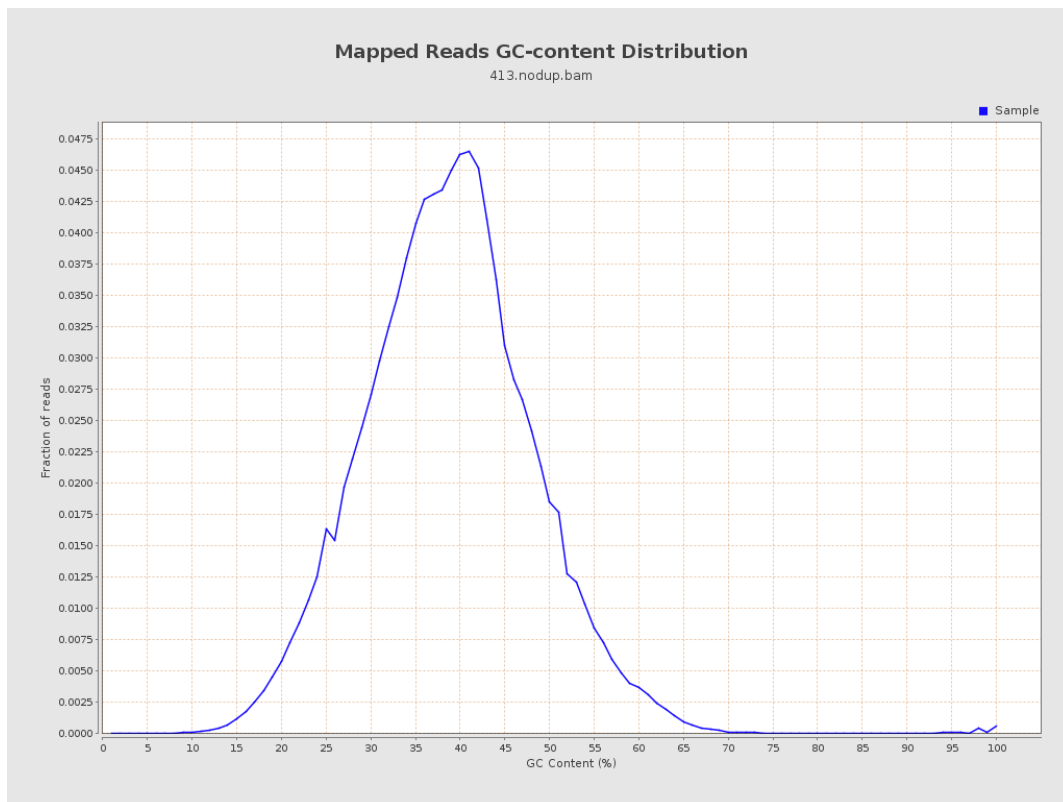
7. Results : Duplication Rate Histogram



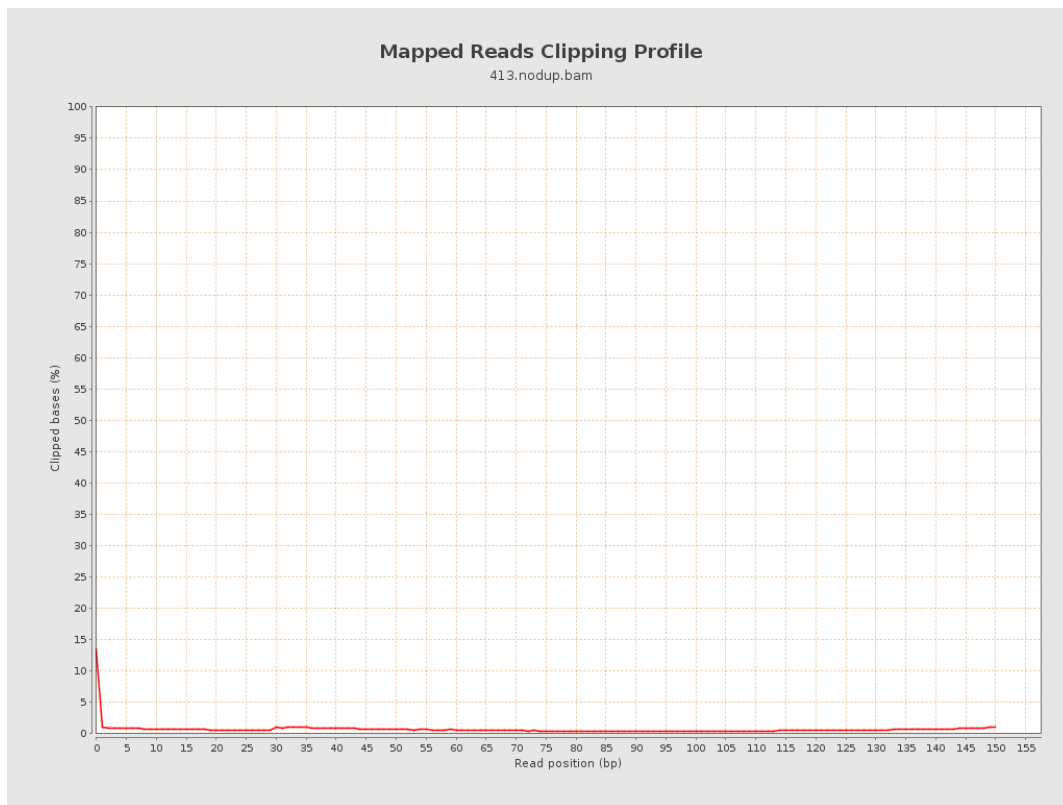
8. Results : Mapped Reads Nucleotide Content



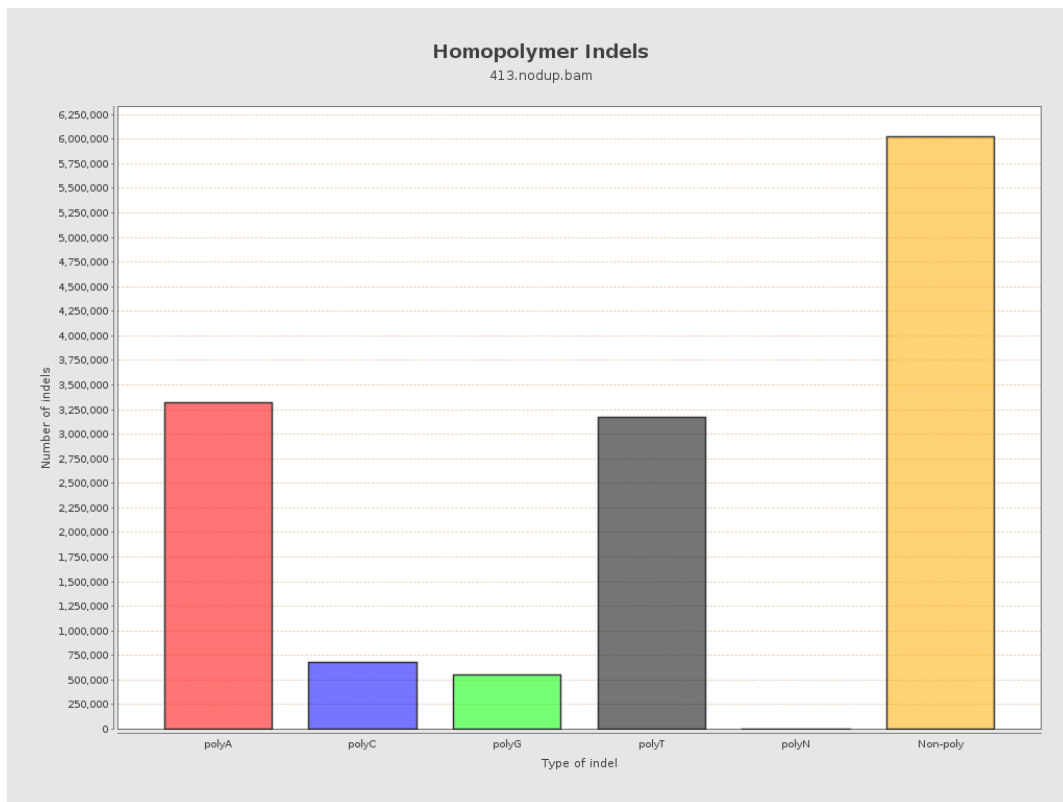
9. Results : Mapped Reads GC-content Distribution



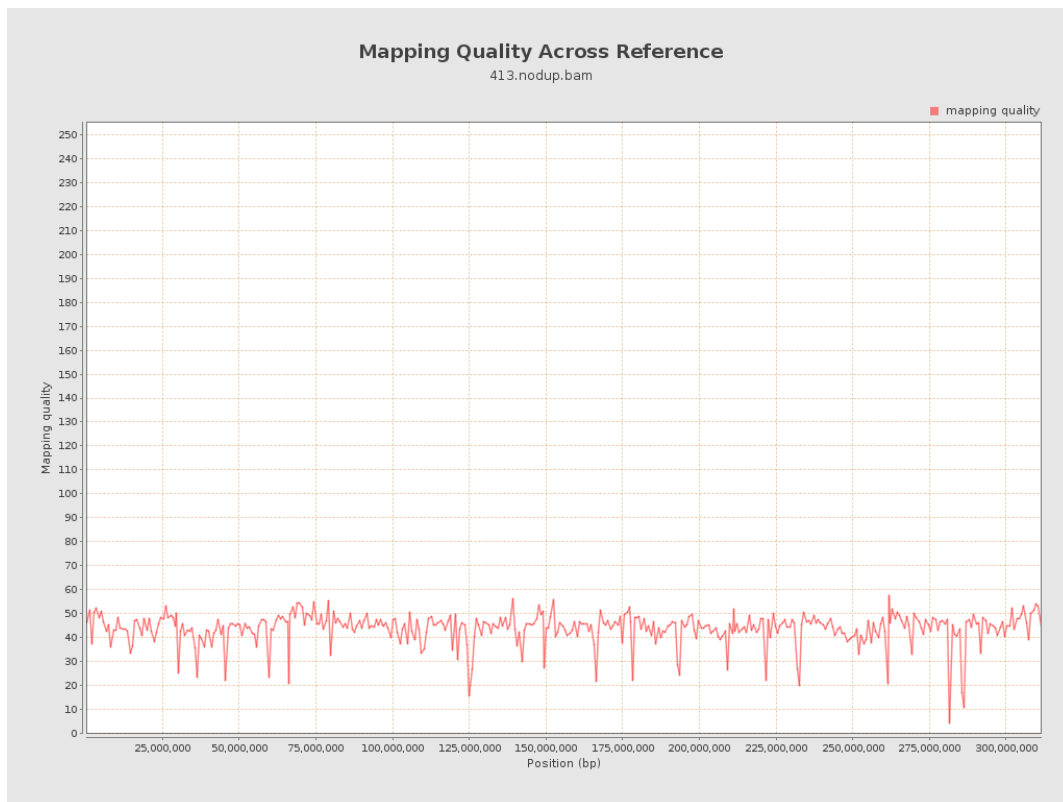
10. Results : Mapped Reads Clipping Profile



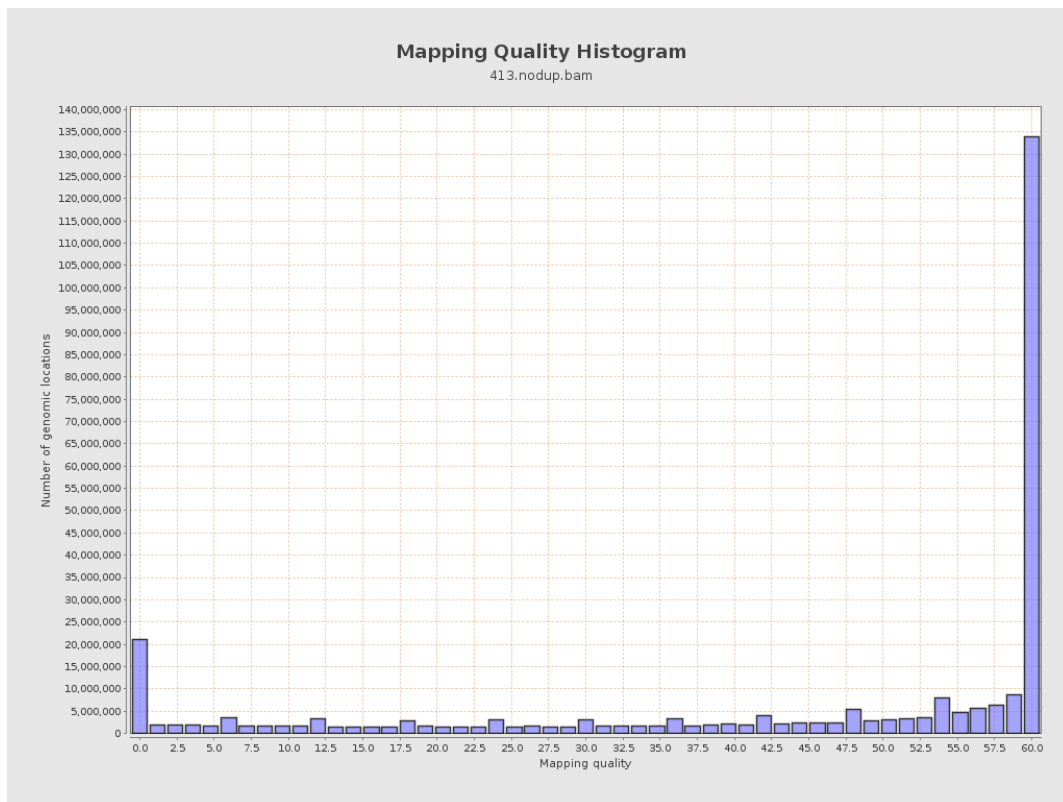
11. Results : Homopolymer Indels



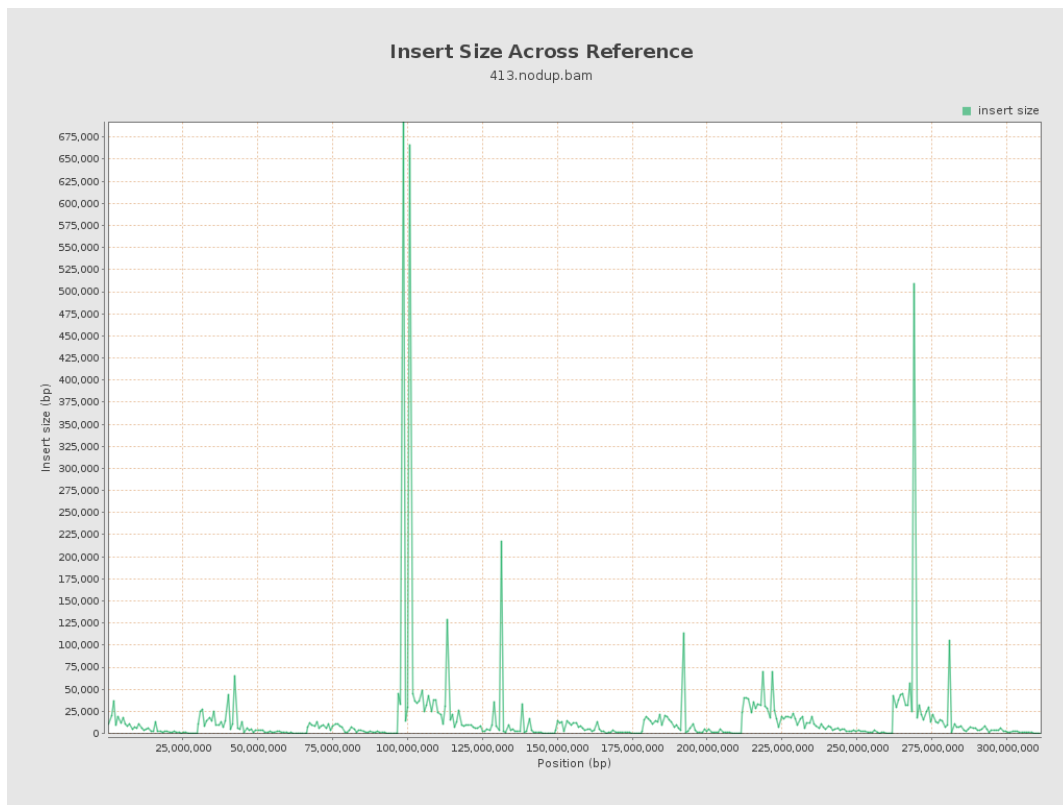
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

