

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:02:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/437
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/437.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_177/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_177_S267_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_177/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_177_S267_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:02:03 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,586,027
Mapped reads	56,372,879 / 93.05%
Unmapped reads	4,213,148 / 6.95%
Mapped paired reads	56,372,879 / 93.05%
Mapped reads, first in pair	28,193,370 / 46.53%
Mapped reads, second in pair	28,179,509 / 46.51%
Mapped reads, both in pair	55,021,605 / 90.82%
Mapped reads, singletons	1,351,274 / 2.23%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	9,133,659 / 15.08%
Clipped reads	12,696,023 / 20.96%

2.2. ACGT Content

Number/percentage of A's	2,406,827,322 / 30.85%
Number/percentage of C's	1,494,163,590 / 19.15%
Number/percentage of T's	2,409,823,068 / 30.89%
Number/percentage of G's	1,491,690,875 / 19.12%
Number/percentage of N's	31,612 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	25.1015
Standard Deviation	206.7827

2.4. Mapping Quality

Mean Mapping Quality	44.36
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2.5. Insert size

Mean	241,552.35
Standard Deviation	2,355,643.84
P25/Median/P75	332 / 435 / 573

2.6. Mismatches and indels

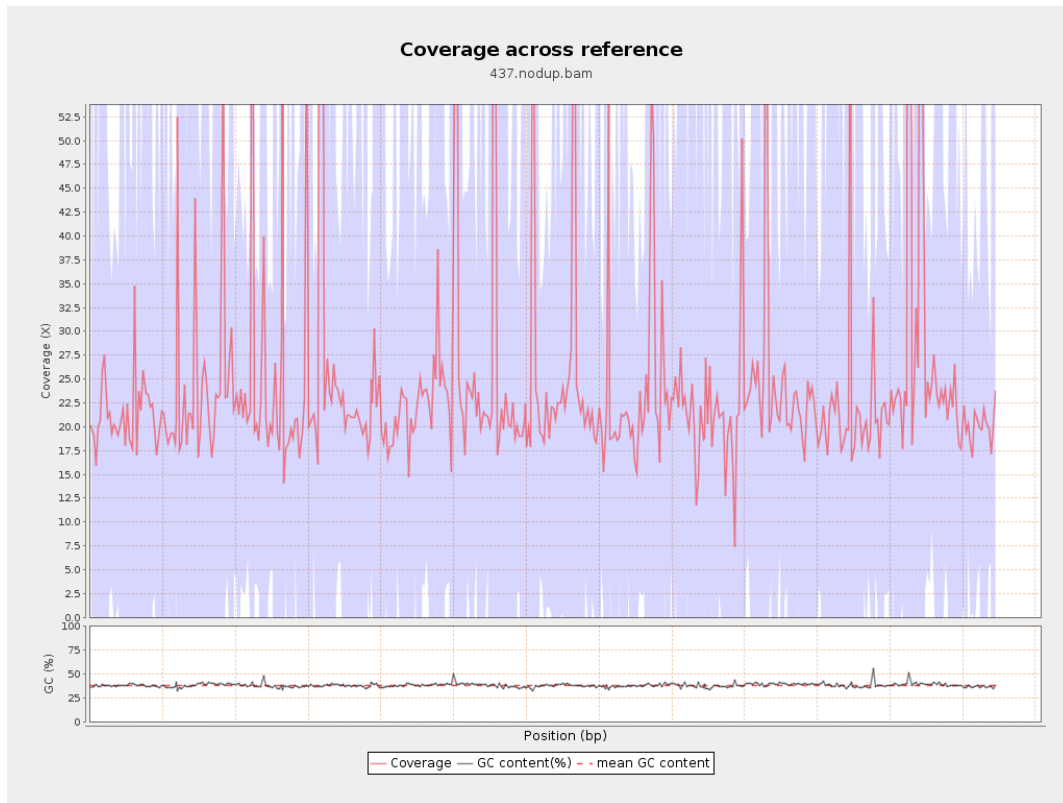
General error rate	2.34%
Mismatches	167,670,025
Insertions	5,400,986
Mapped reads with at least one insertion	8.59%
Deletions	5,368,131
Mapped reads with at least one deletion	8.44%
Homopolymer indels	56.4%

2.7. Chromosome stats

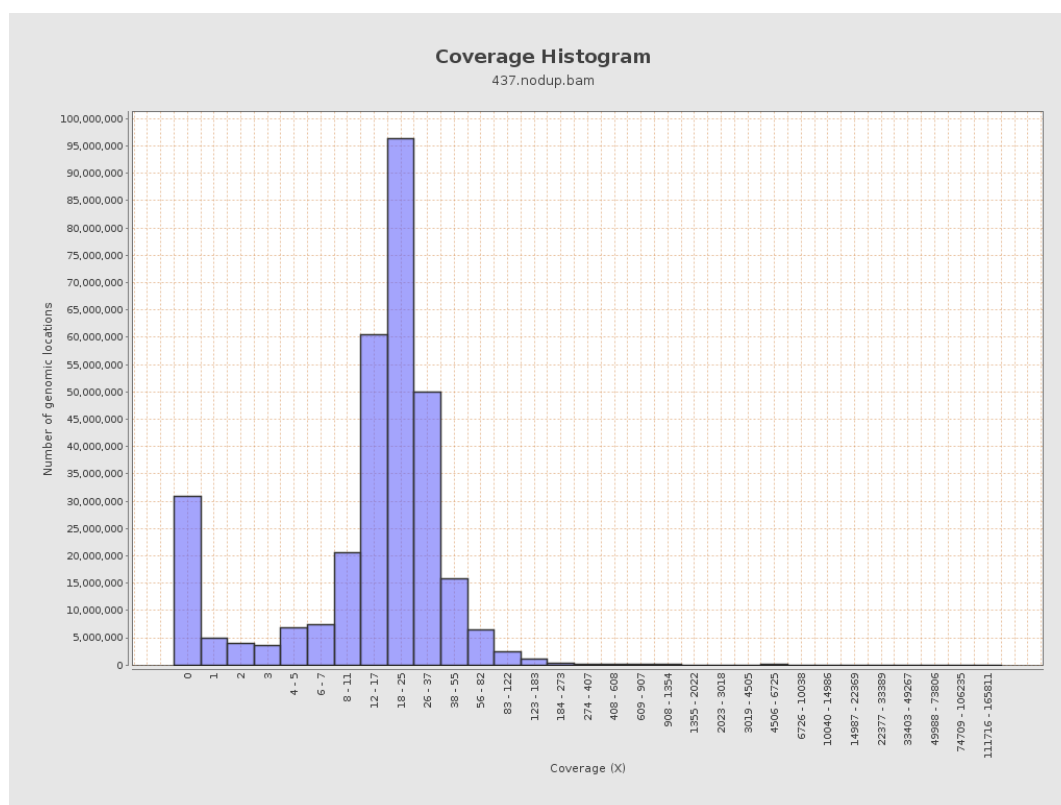
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	624313748	21.0034	81.6234

LT669789.1	36598175	940491281	25.6978	236.364
LT669790.1	30422129	862251026	28.3429	242.7273
LT669791.1	52758100	1290869427	24.4677	213.7169
LT669792.1	28376109	704648030	24.8324	206.0968
LT669793.1	33388210	768151563	23.0067	110.8802
LT669794.1	50579949	1197799118	23.6813	196.0356
LT669795.1	49795044	1434148174	28.801	258.1879

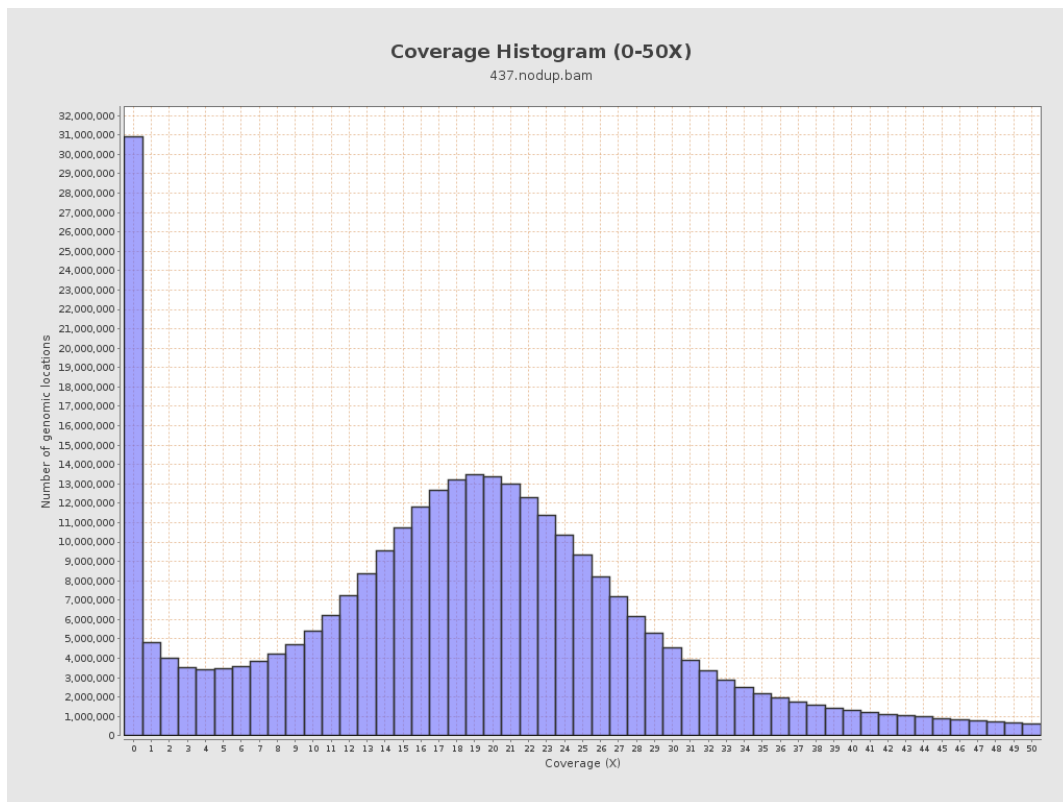
3. Results : Coverage across reference



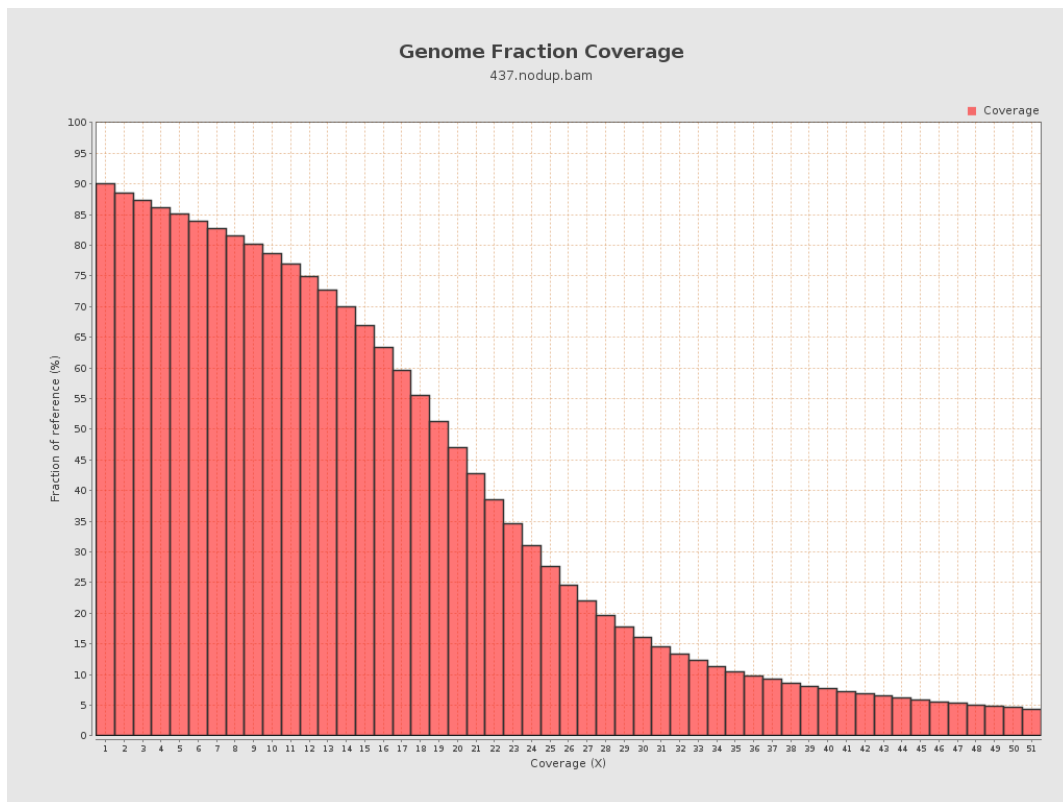
4. Results : Coverage Histogram



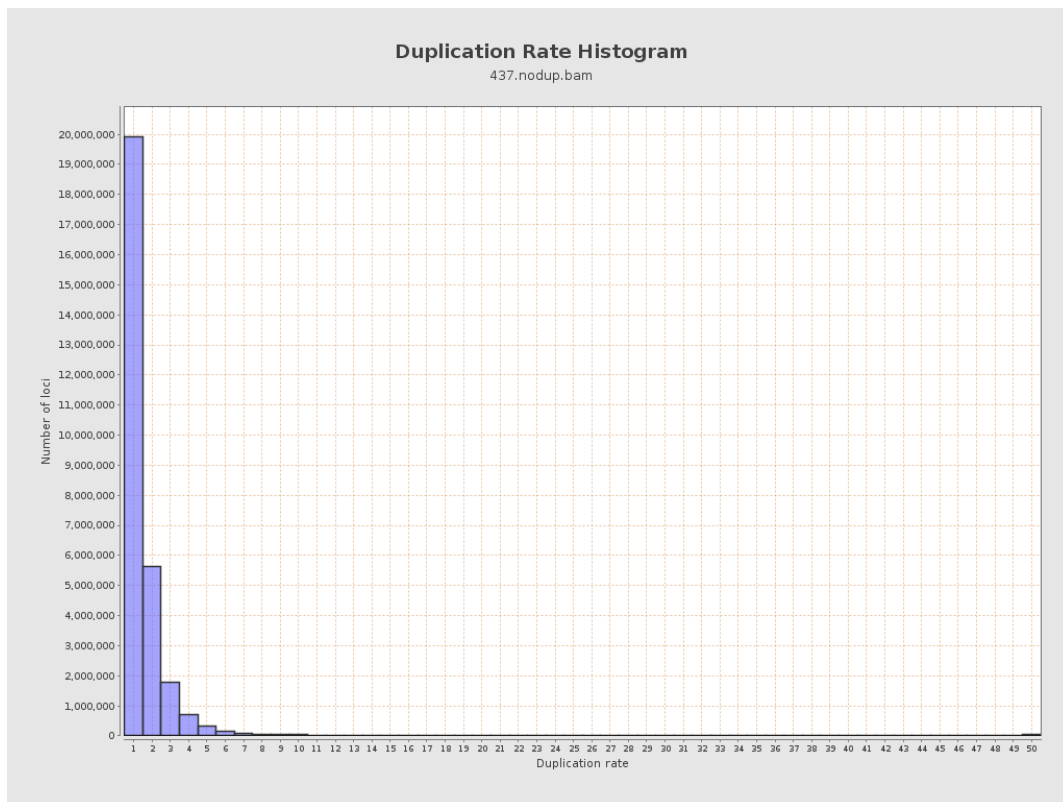
5. Results : Coverage Histogram (0-50X)



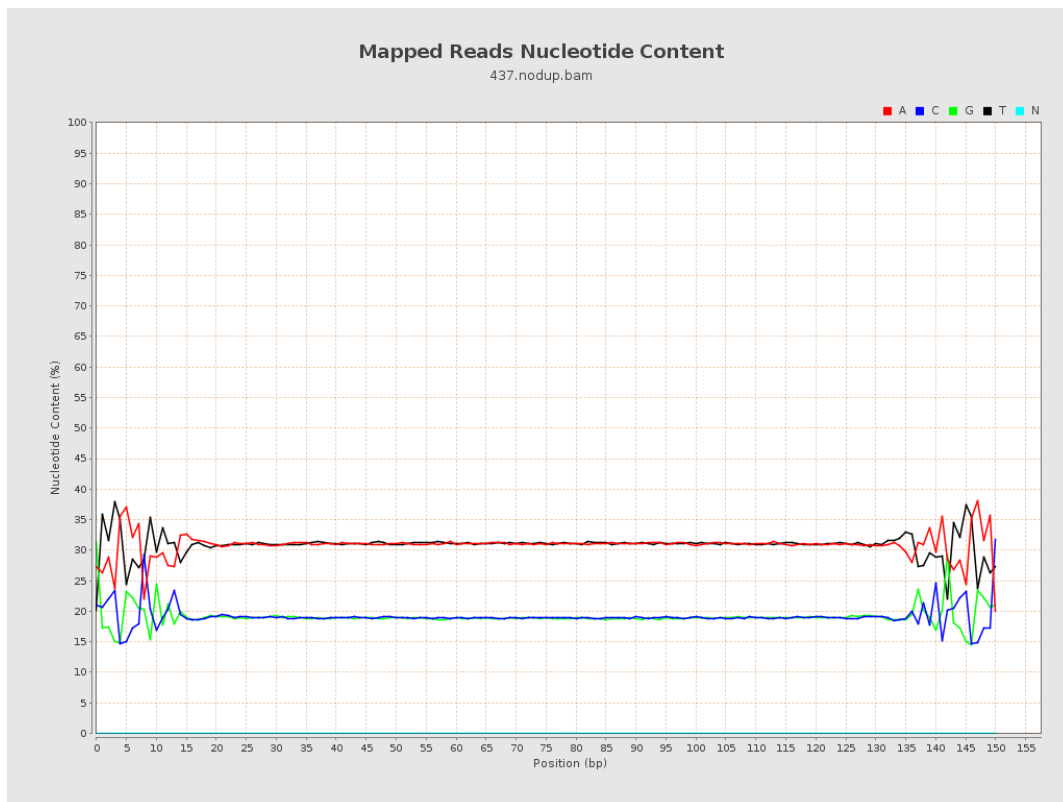
6. Results : Genome Fraction Coverage



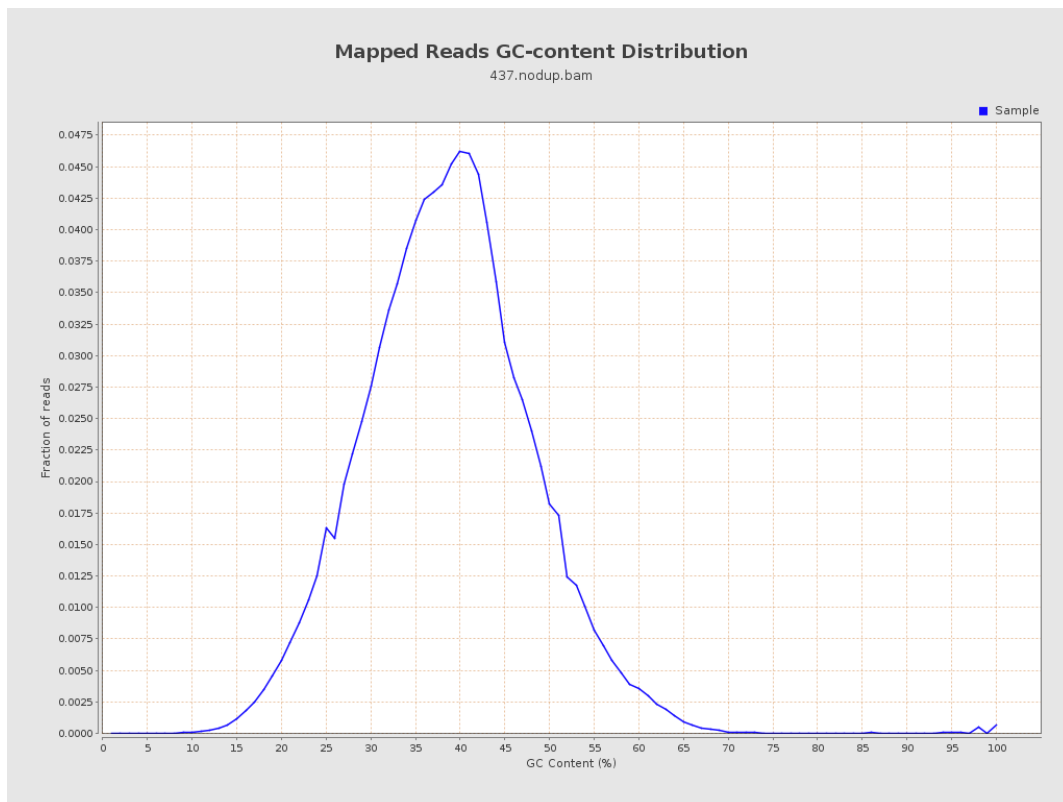
7. Results : Duplication Rate Histogram



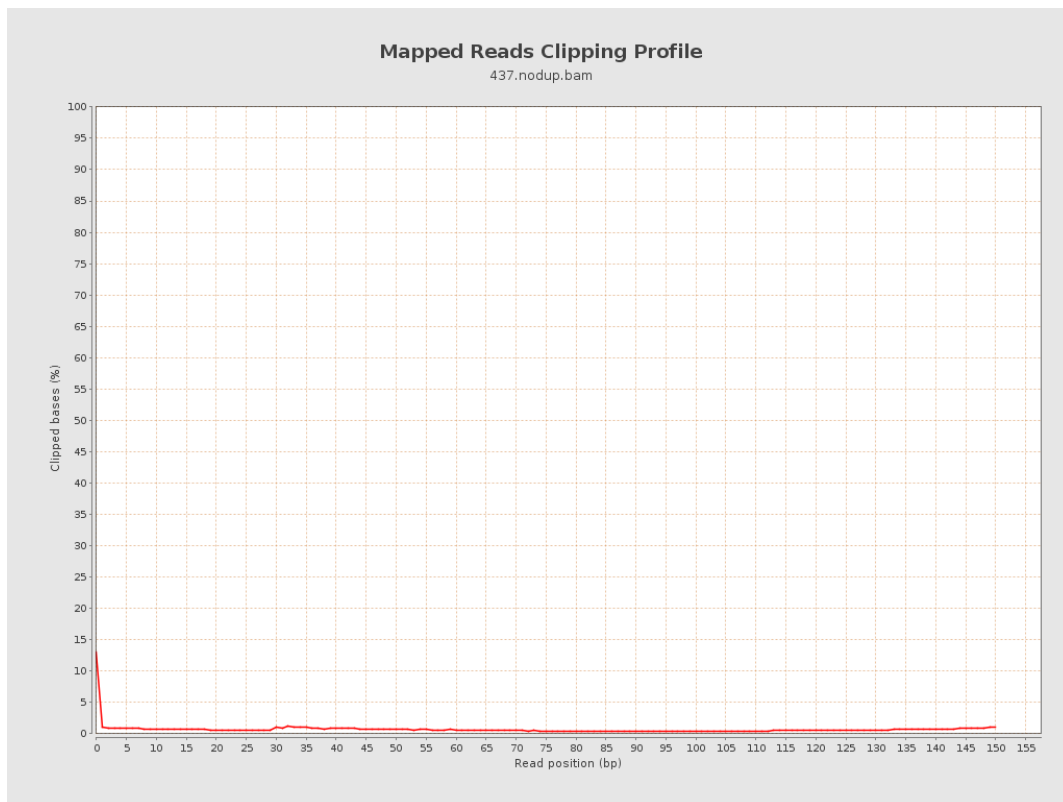
8. Results : Mapped Reads Nucleotide Content



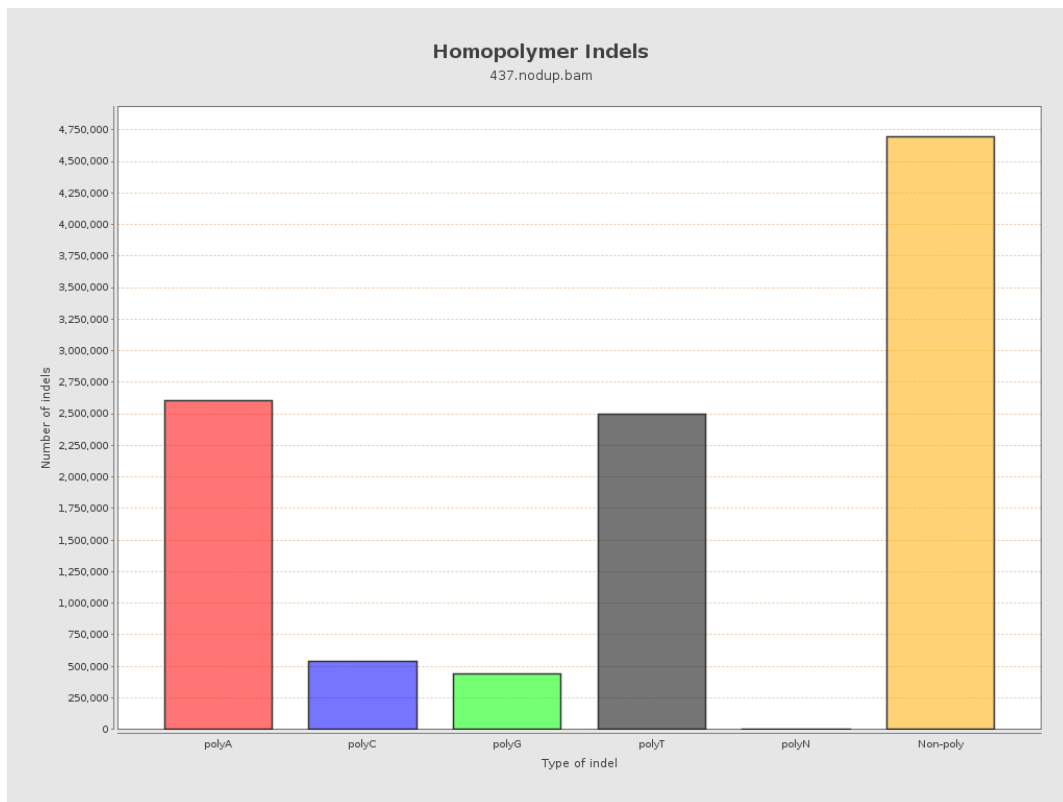
9. Results : Mapped Reads GC-content Distribution



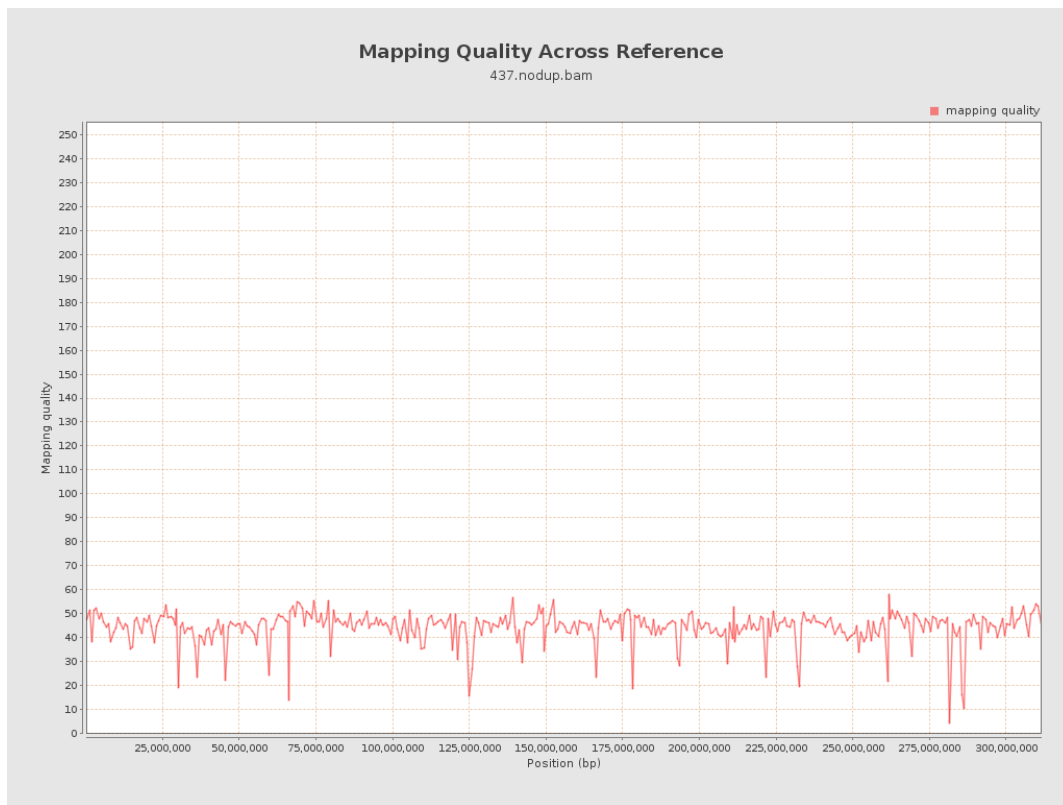
10. Results : Mapped Reads Clipping Profile



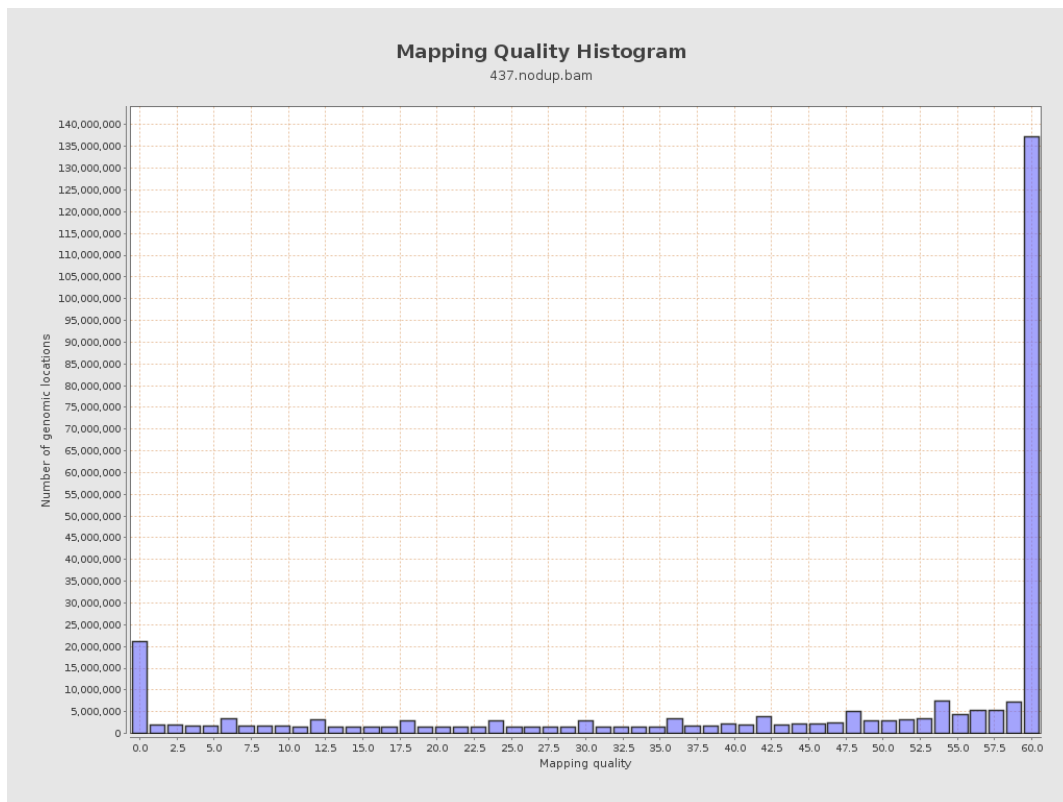
11. Results : Homopolymer Indels



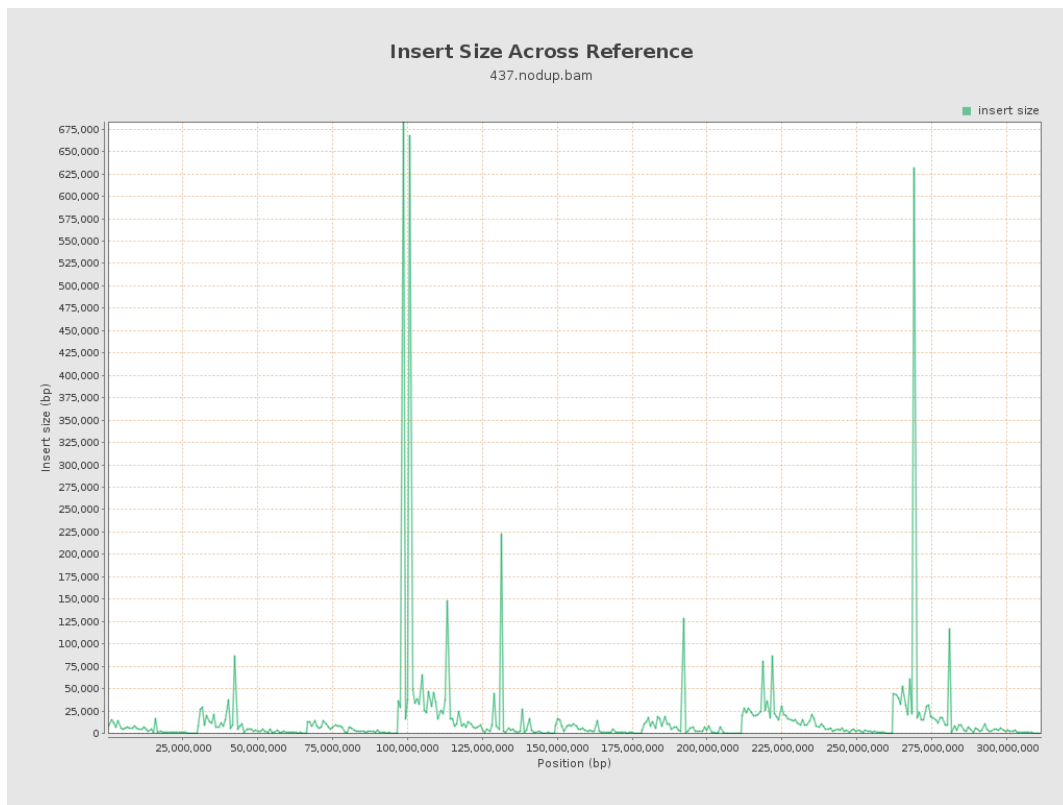
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

