

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/143
6
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1436 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_584/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_584_S151_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_584/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_584_S151_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	43,409,209
Mapped reads	40,454,853 / 93.19%
Unmapped reads	2,954,356 / 6.81%
Mapped paired reads	40,454,853 / 93.19%
Mapped reads, first in pair	20,303,780 / 46.77%
Mapped reads, second in pair	20,151,073 / 46.42%
Mapped reads, both in pair	39,493,183 / 90.98%
Mapped reads, singletons	961,670 / 2.22%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	5,665,607 / 13.05%
Clipped reads	9,760,145 / 22.48%

2.2. ACGT Content

Number/percentage of A's	1,723,642,631 / 30.96%
Number/percentage of C's	1,059,783,276 / 19.04%
Number/percentage of T's	1,725,160,249 / 30.99%
Number/percentage of G's	1,058,086,083 / 19.01%
Number/percentage of N's	38,697 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	17.9071
Standard Deviation	139.2143

2.4. Mapping Quality

Mean Mapping Quality	44.34
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2.5. Insert size

Mean	219,799.59
Standard Deviation	2,233,199.75
P25/Median/P75	311 / 409 / 526

2.6. Mismatches and indels

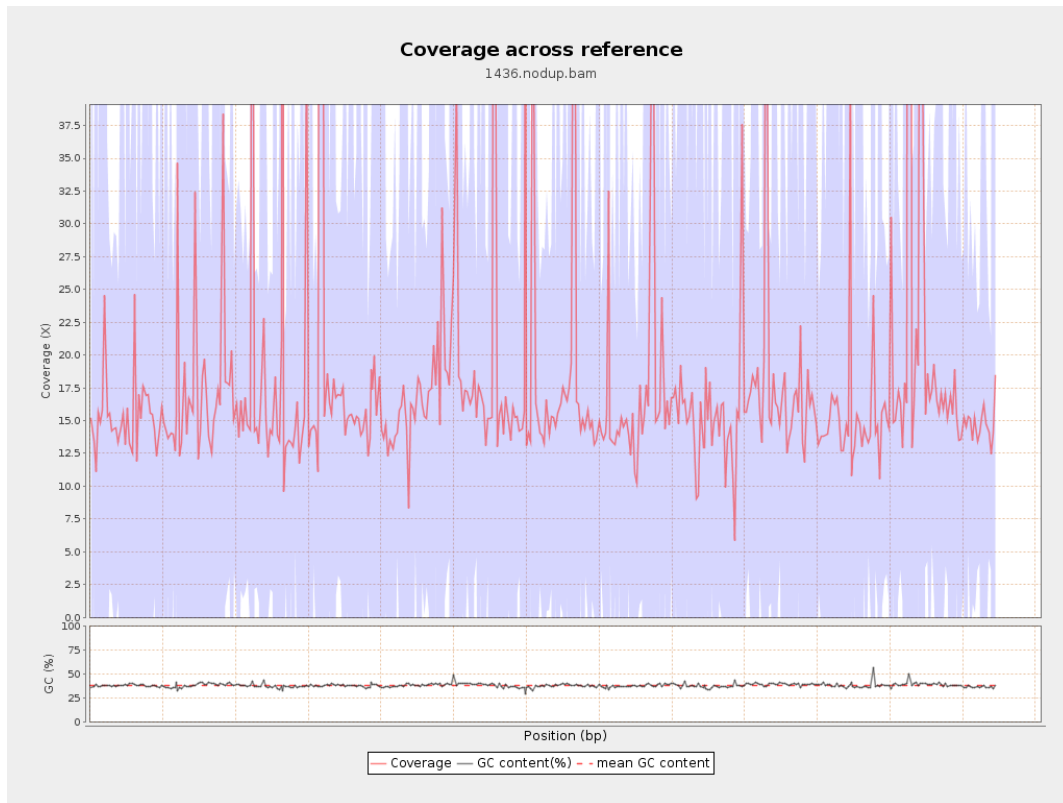
General error rate	2.51%
Mismatches	129,161,906
Insertions	3,749,924
Mapped reads with at least one insertion	8.33%
Deletions	3,724,255
Mapped reads with at least one deletion	8.19%
Homopolymer indels	56.82%

2.7. Chromosome stats

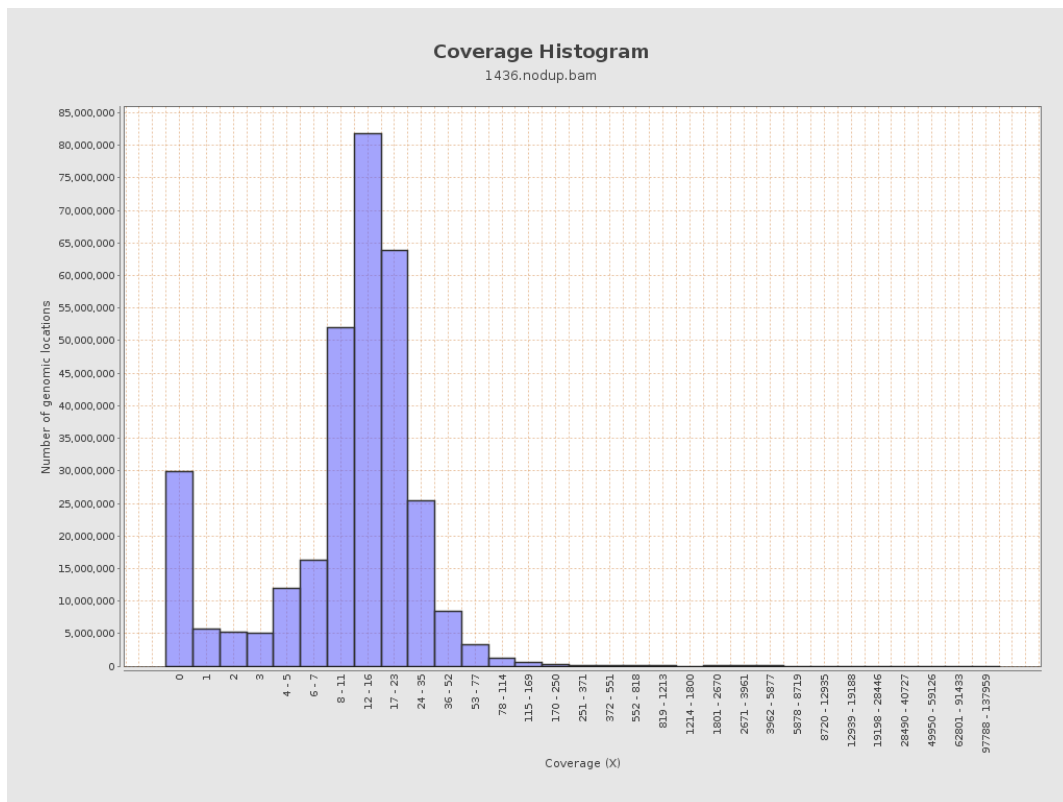
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	449631397	15.1267	46.8885

LT669789.1	36598175	674416832	18.4276	151.2785
LT669790.1	30422129	606548755	19.9377	166.6652
LT669791.1	52758100	933273087	17.6897	128.2166
LT669792.1	28376109	506245334	17.8405	157.3694
LT669793.1	33388210	554699117	16.6136	101.4512
LT669794.1	50579949	849141751	16.7881	115.295
LT669795.1	49795044	1006634536	20.2156	185.0447

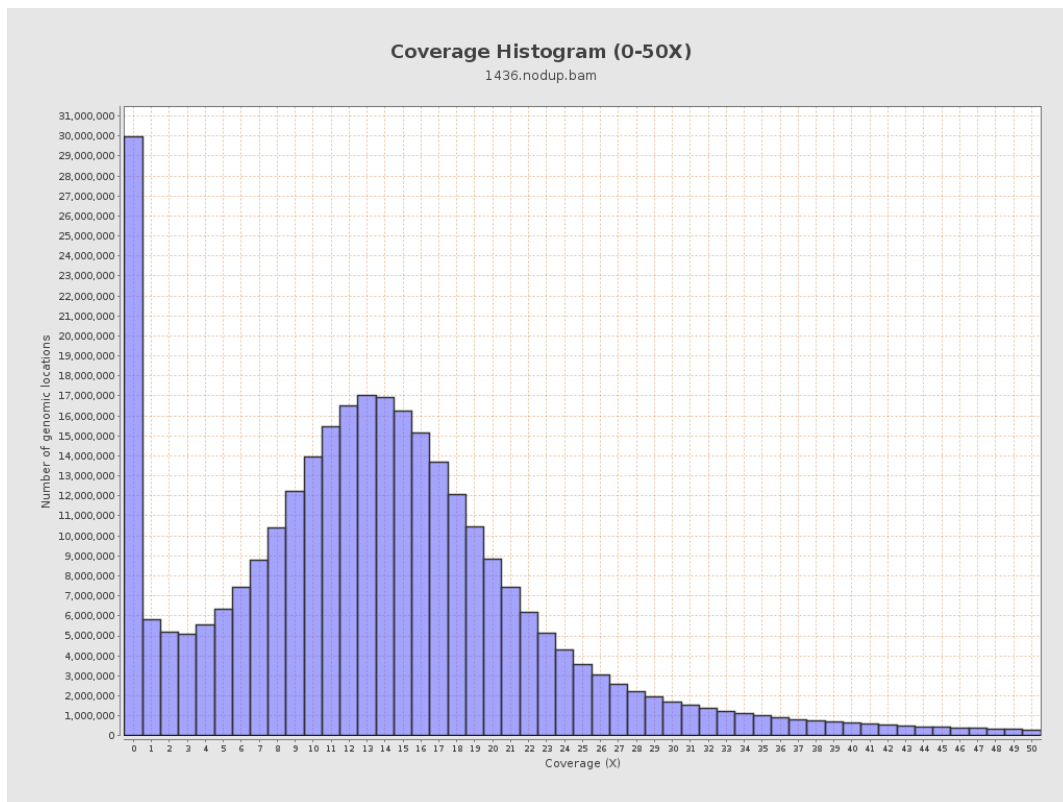
3. Results : Coverage across reference



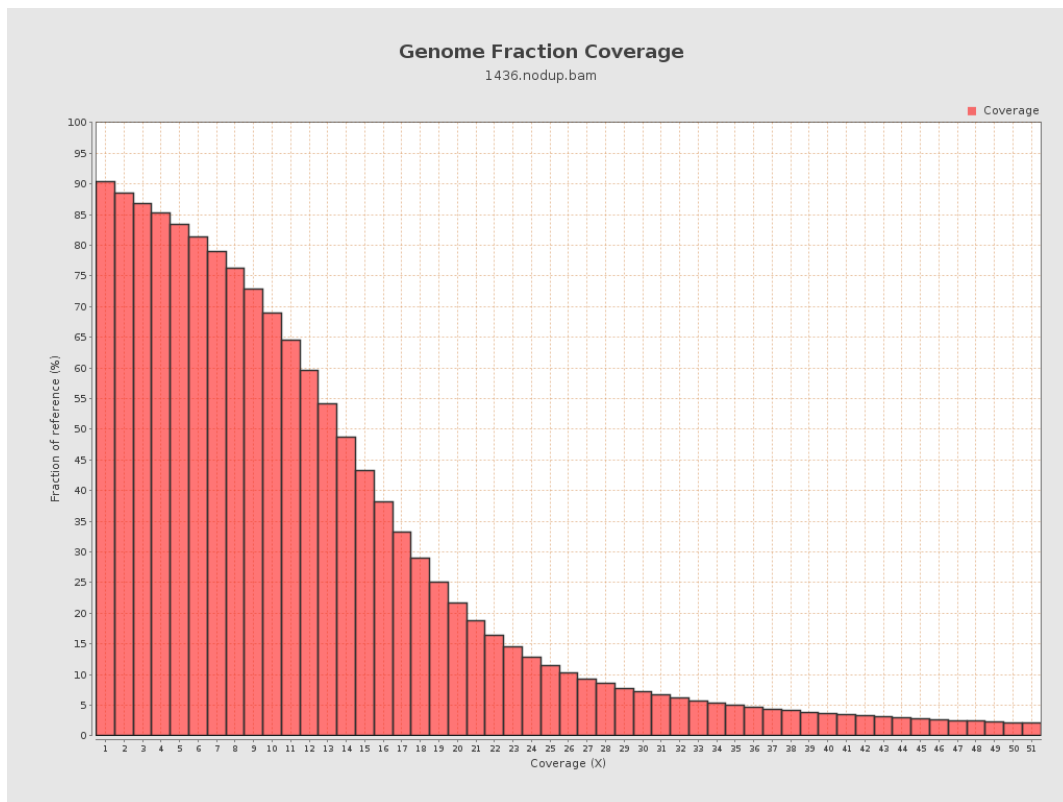
4. Results : Coverage Histogram



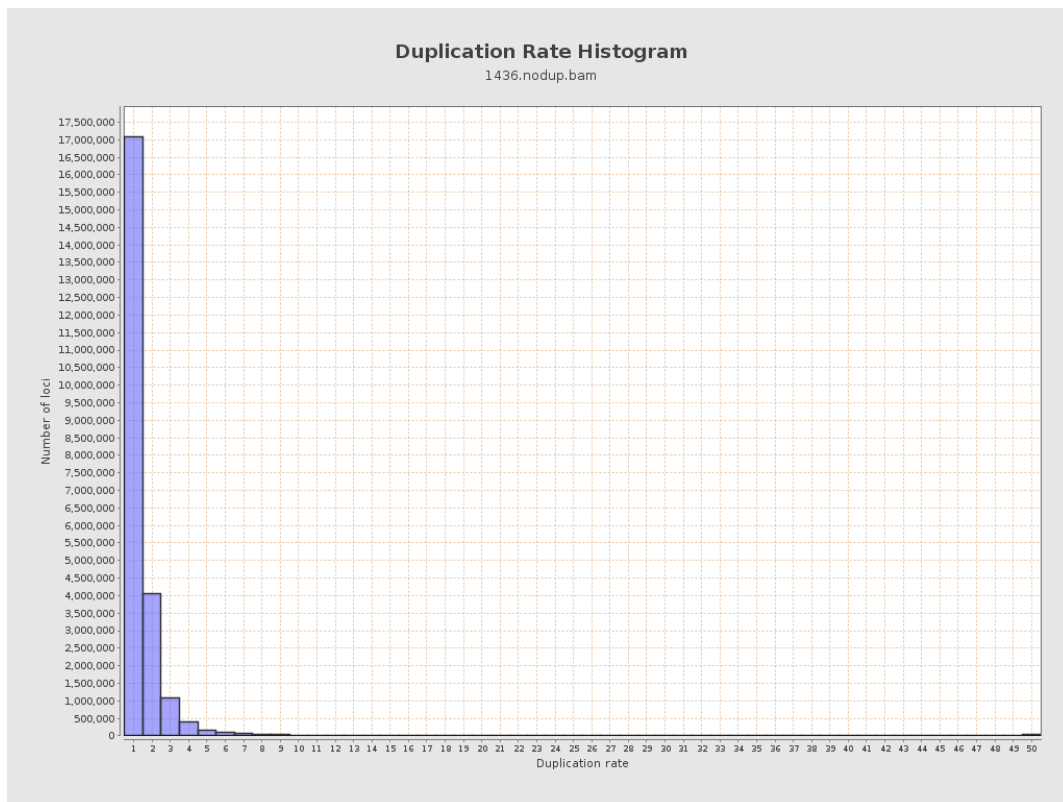
5. Results : Coverage Histogram (0-50X)



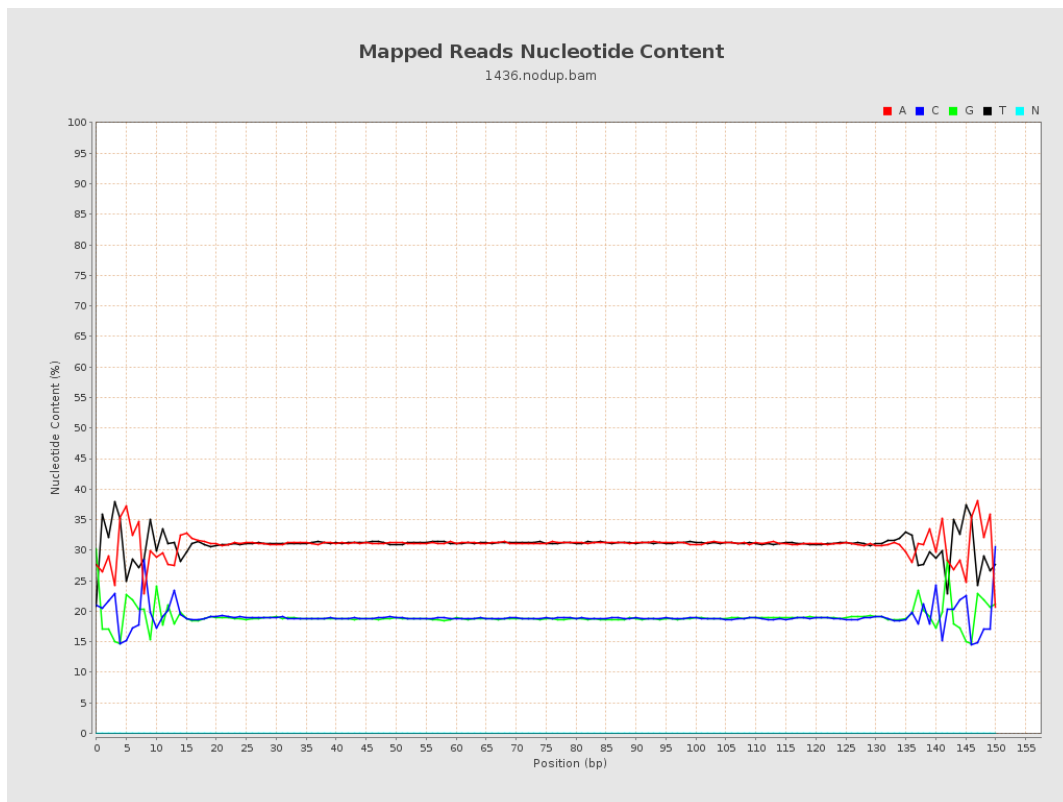
6. Results : Genome Fraction Coverage



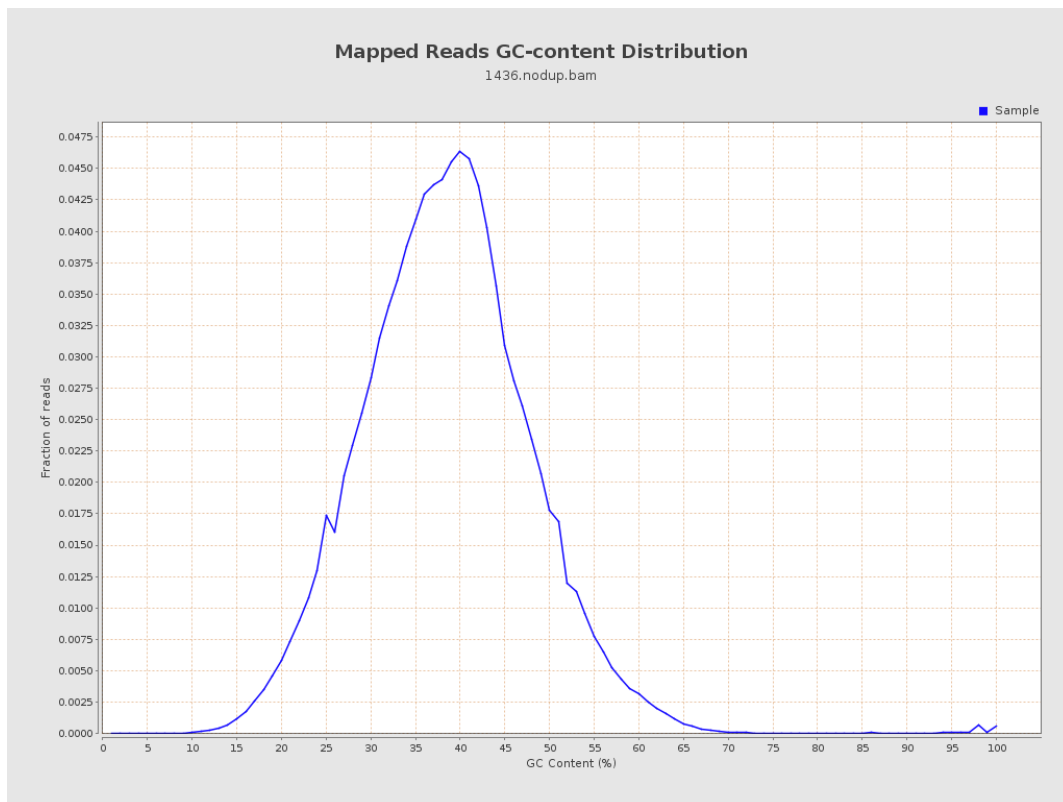
7. Results : Duplication Rate Histogram



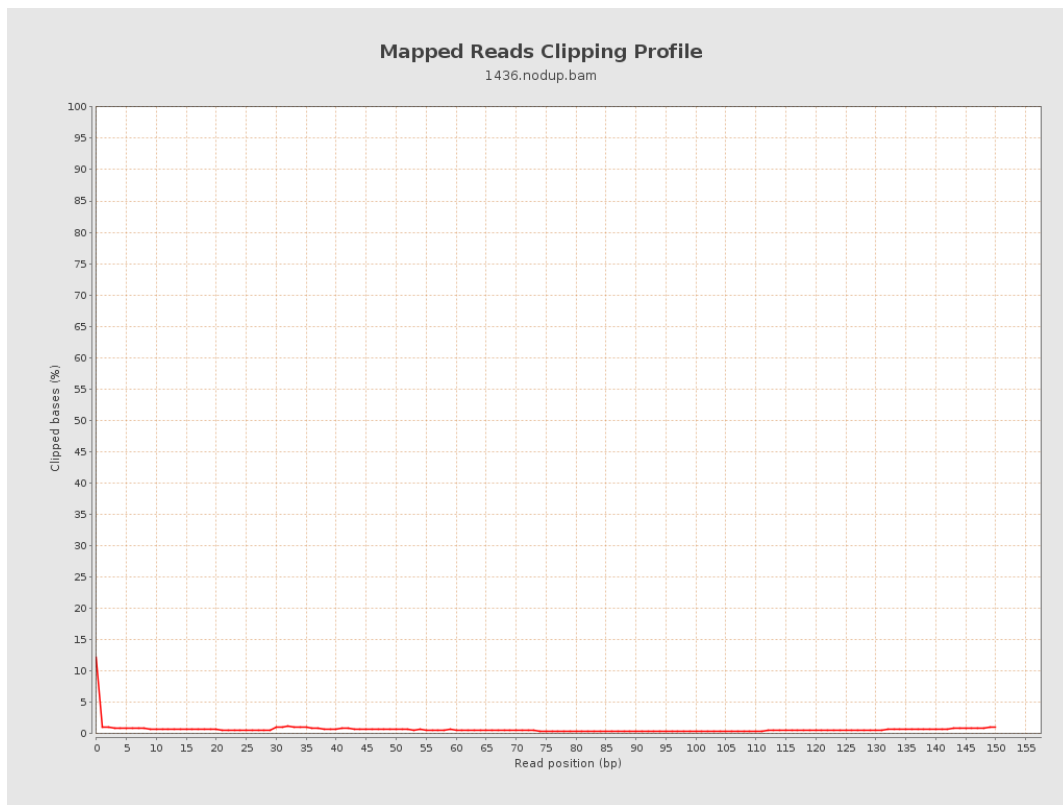
8. Results : Mapped Reads Nucleotide Content



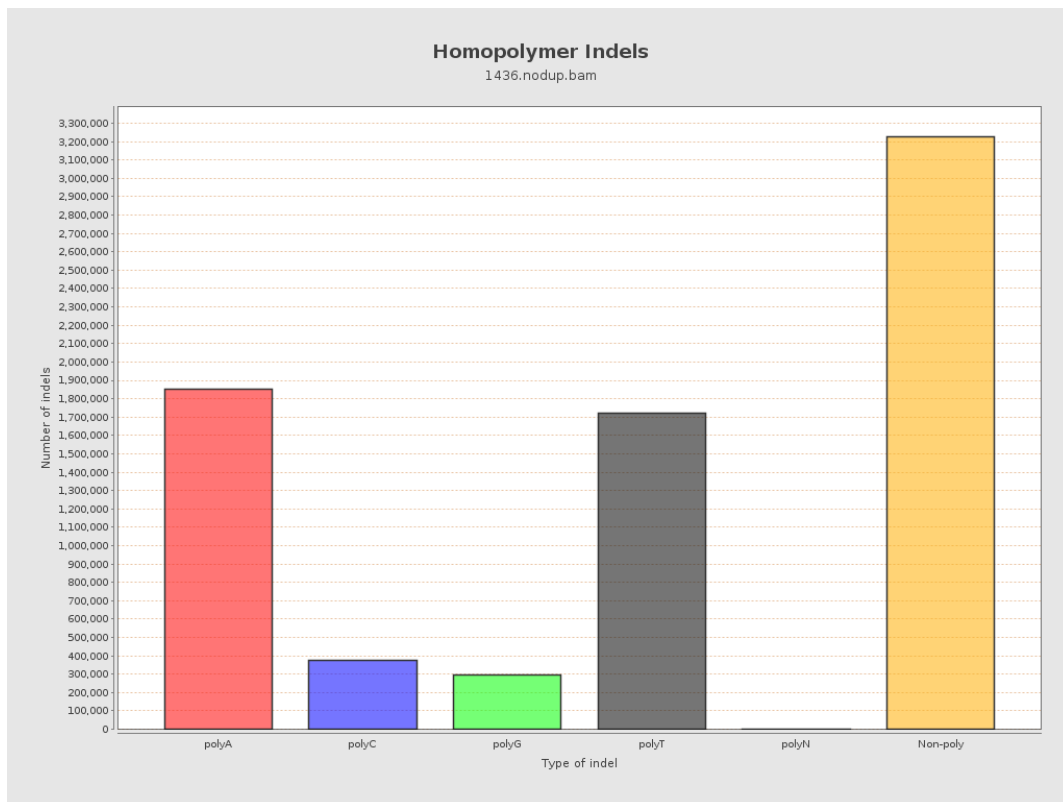
9. Results : Mapped Reads GC-content Distribution



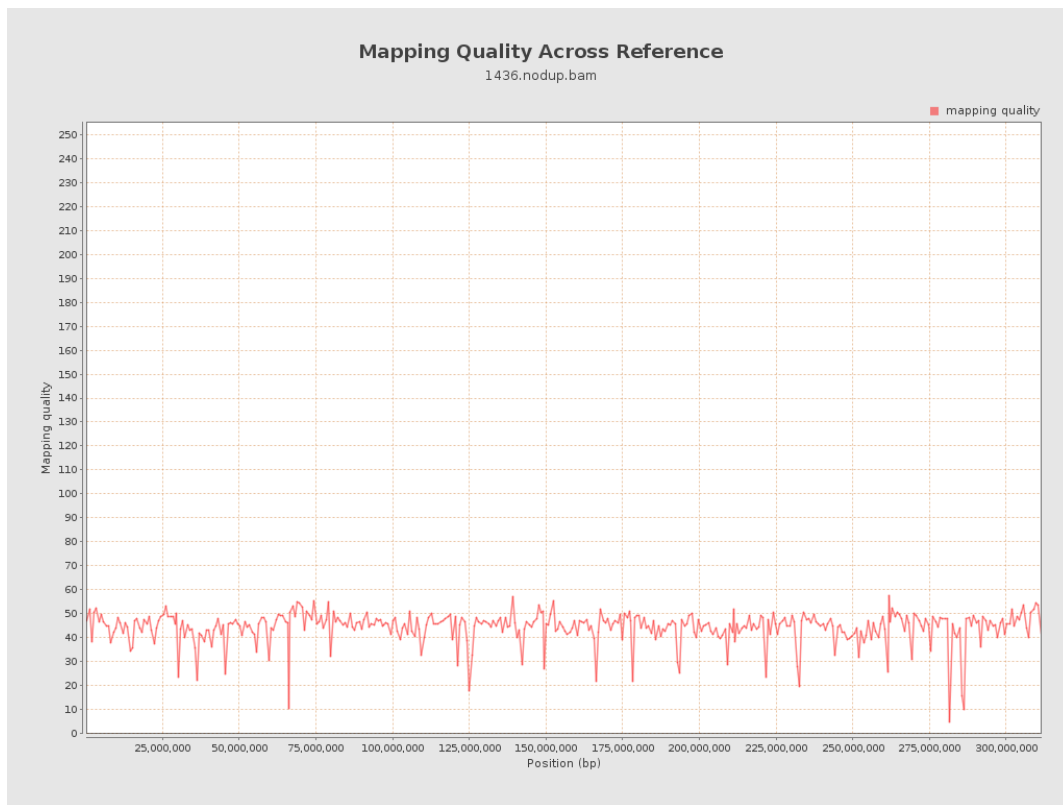
10. Results : Mapped Reads Clipping Profile



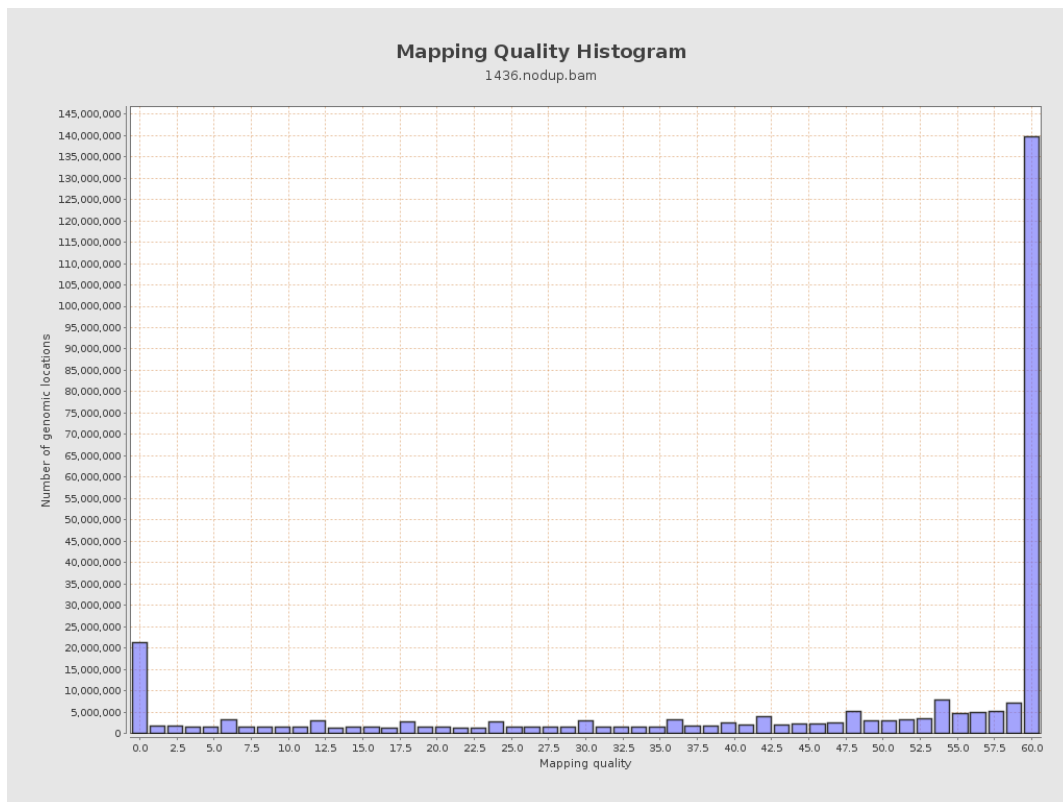
11. Results : Homopolymer Indels



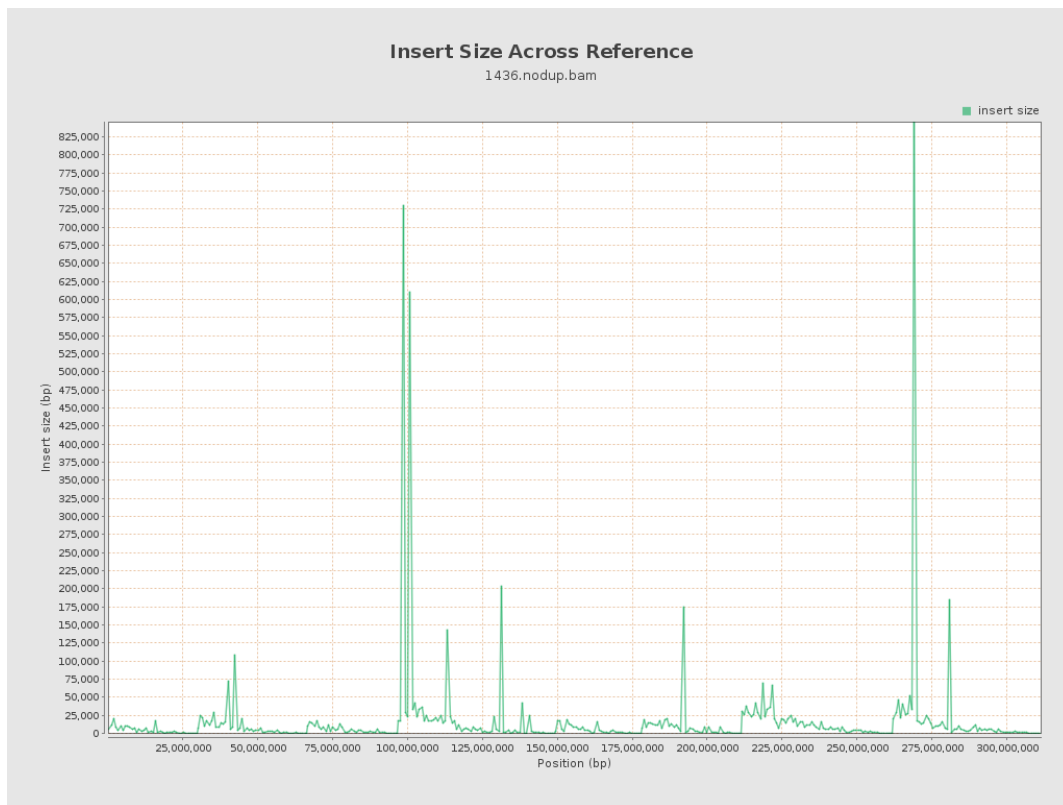
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

