

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:22:25

1. Input data & parameters

1.1. QualiMap command line

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

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1433 .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_469/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_469_S444_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_469/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_469_S444_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:22:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	41,025,937
Mapped reads	38,647,986 / 94.2%
Unmapped reads	2,377,951 / 5.8%
Mapped paired reads	38,647,986 / 94.2%
Mapped reads, first in pair	19,368,762 / 47.21%
Mapped reads, second in pair	19,279,224 / 46.99%
Mapped reads, both in pair	37,787,521 / 92.11%
Mapped reads, singletons	860,465 / 2.1%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	5,451,463 / 13.29%
Clipped reads	8,437,695 / 20.57%

2.2. ACGT Content

Number/percentage of A's	1,658,117,881 / 30.84%
Number/percentage of C's	1,029,170,441 / 19.14%
Number/percentage of T's	1,662,042,011 / 30.92%
Number/percentage of G's	1,026,610,033 / 19.1%
Number/percentage of N's	18,233 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	17.2958
Standard Deviation	137.2985

2.4. Mapping Quality

Mean Mapping Quality	44.01
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2.5. Insert size

Mean	255,805.45
Standard Deviation	2,414,330.37
P25/Median/P75	388 / 503 / 647

2.6. Mismatches and indels

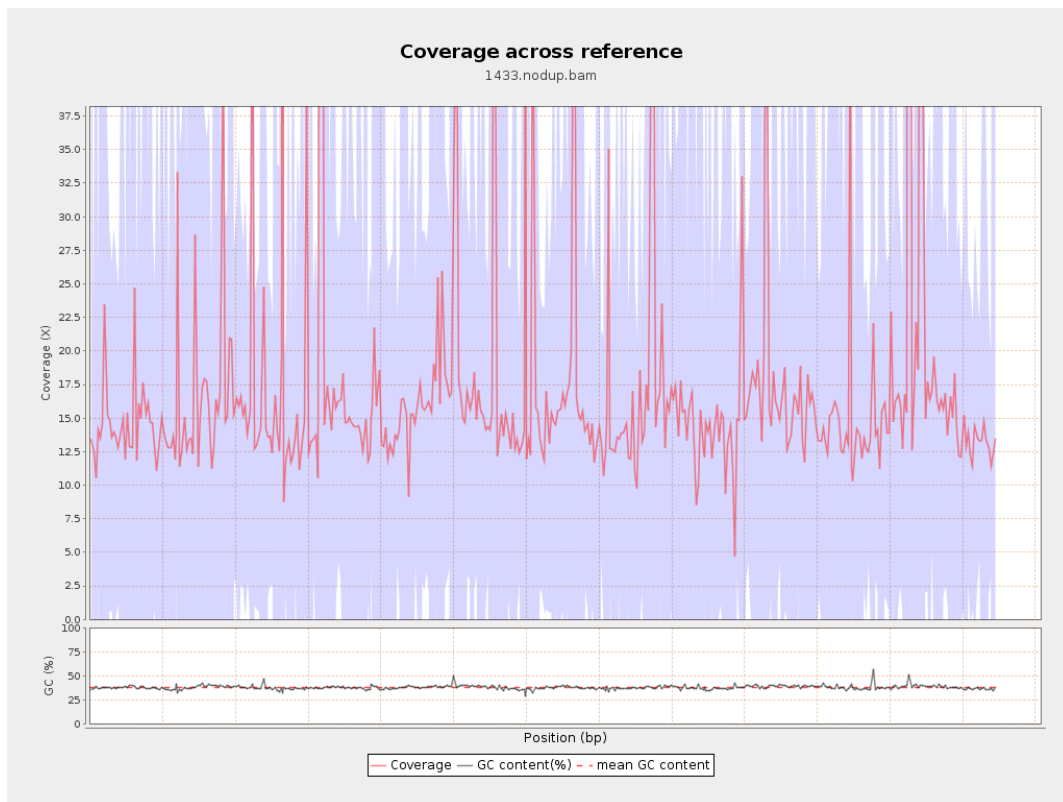
General error rate	2.34%
Mismatches	115,806,950
Insertions	3,617,569
Mapped reads with at least one insertion	8.4%
Deletions	3,703,541
Mapped reads with at least one deletion	8.51%
Homopolymer indels	56.31%

2.7. Chromosome stats

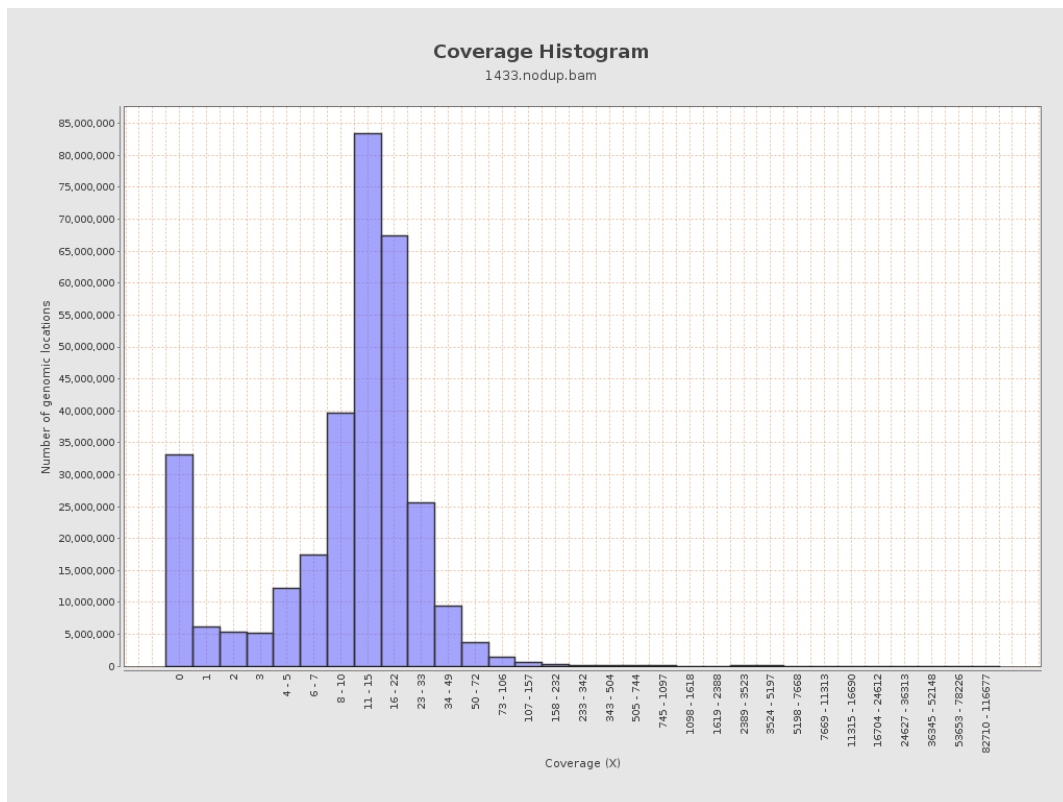
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	426320007	14.3425	42.3097

LT669789.1	36598175	636176264	17.3827	144.7715
LT669790.1	30422129	560913318	18.4377	141.9093
LT669791.1	52758100	898491556	17.0304	118.9546
LT669792.1	28376109	480234569	16.9239	138.318
LT669793.1	33388210	553792398	16.5865	140.1717
LT669794.1	50579949	827949996	16.3691	121.3493
LT669795.1	49795044	1006231689	20.2075	187.5086

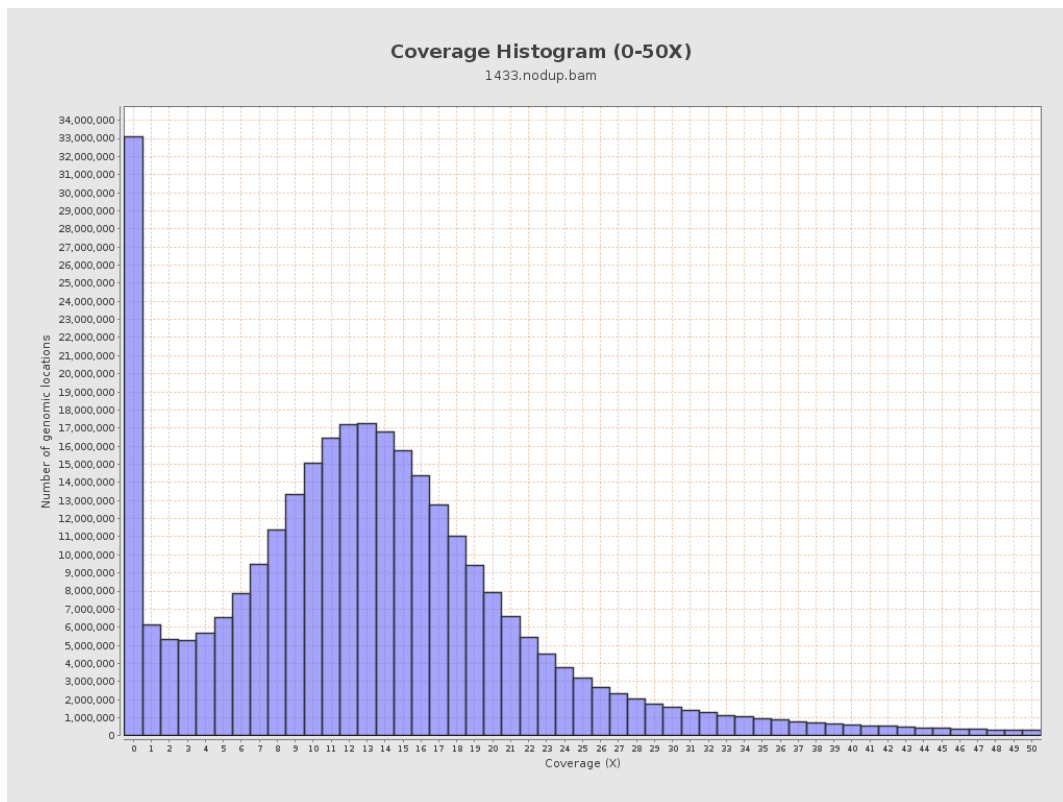
3. Results : Coverage across reference



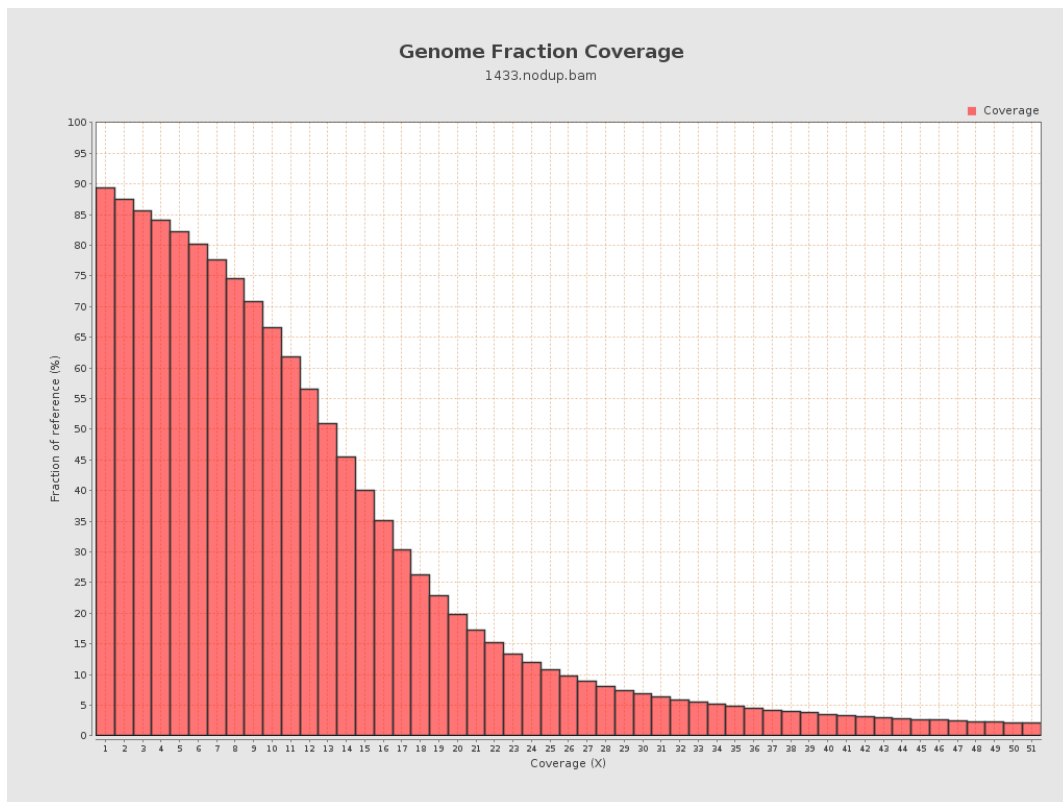
4. Results : Coverage Histogram



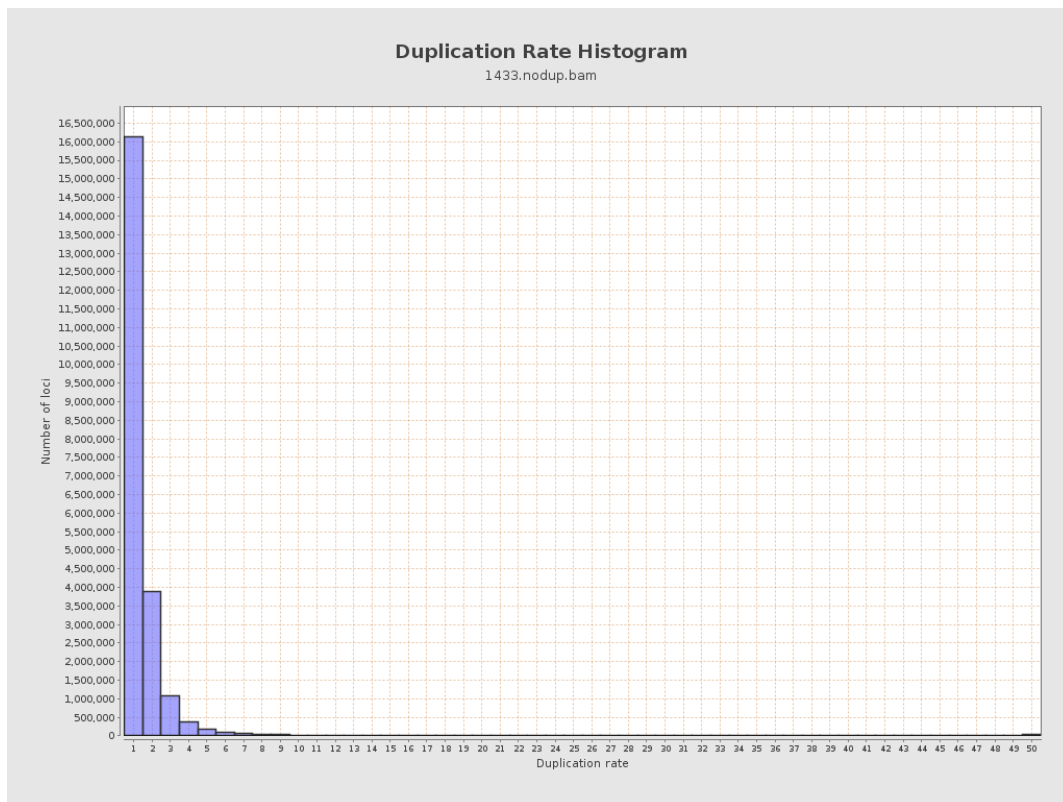
5. Results : Coverage Histogram (0-50X)



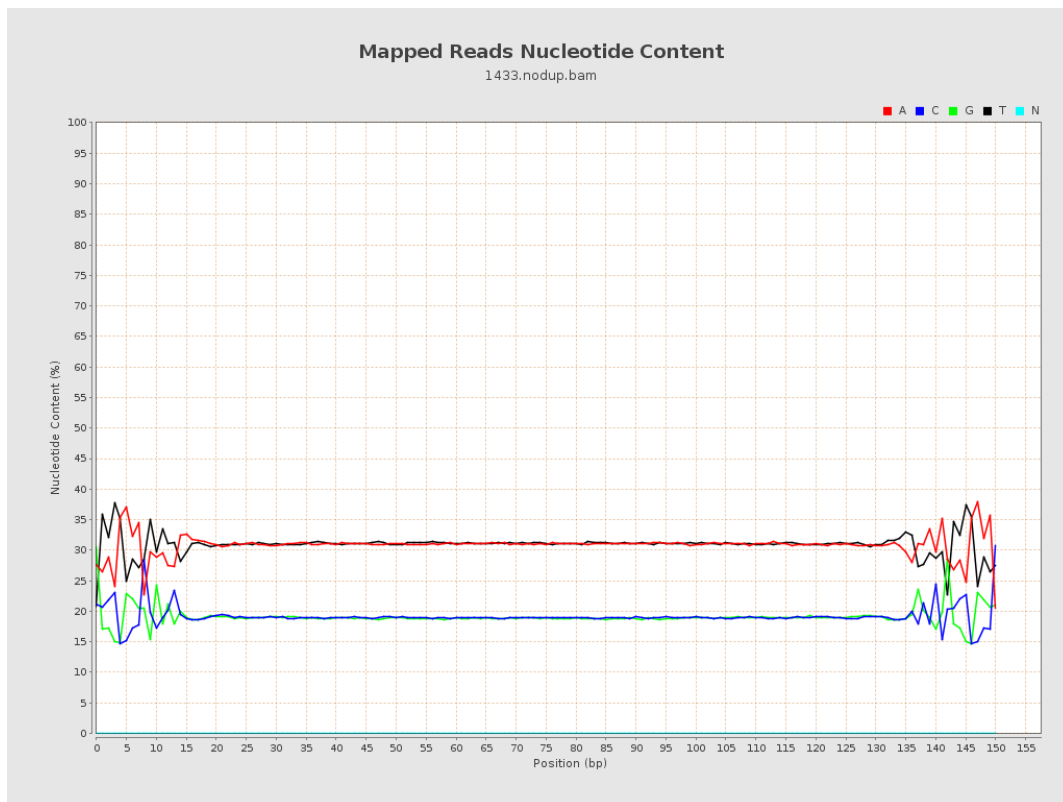
6. Results : Genome Fraction Coverage



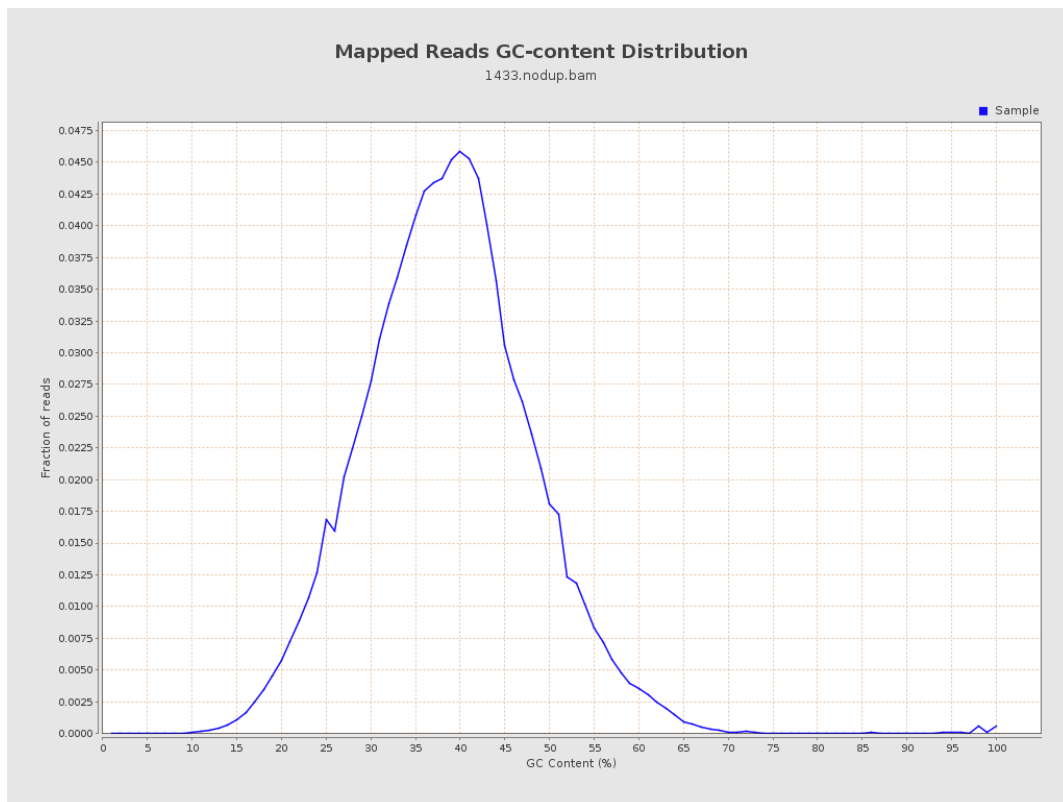
7. Results : Duplication Rate Histogram



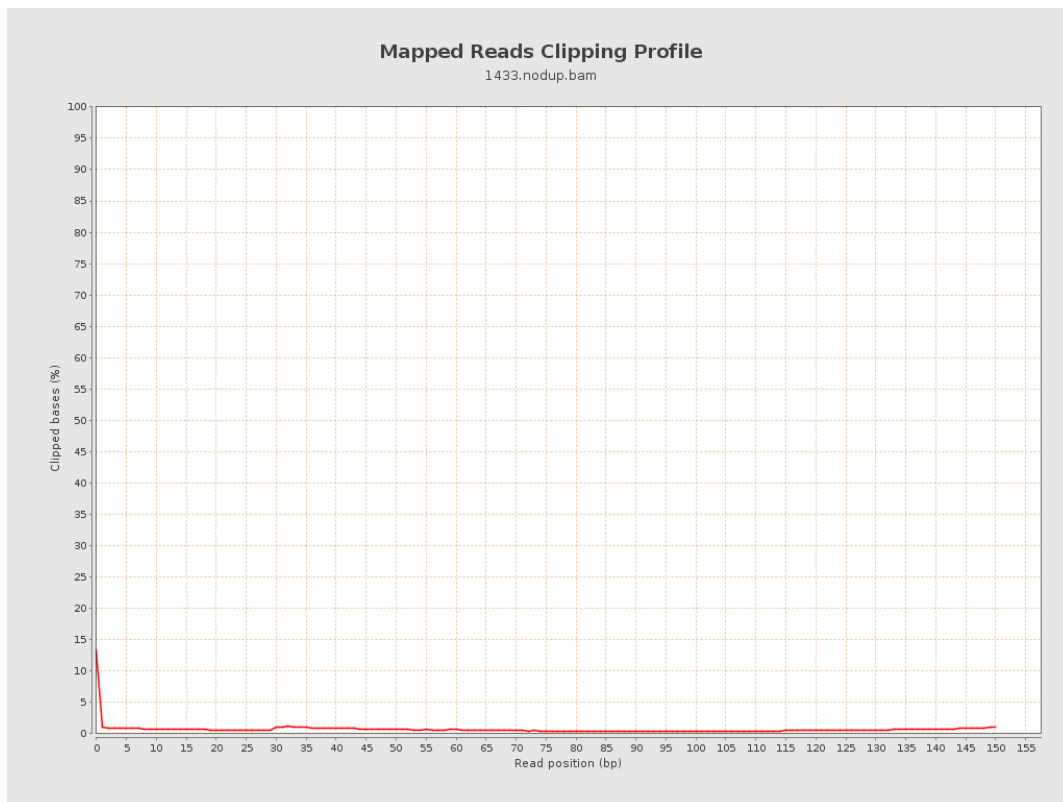
8. Results : Mapped Reads Nucleotide Content



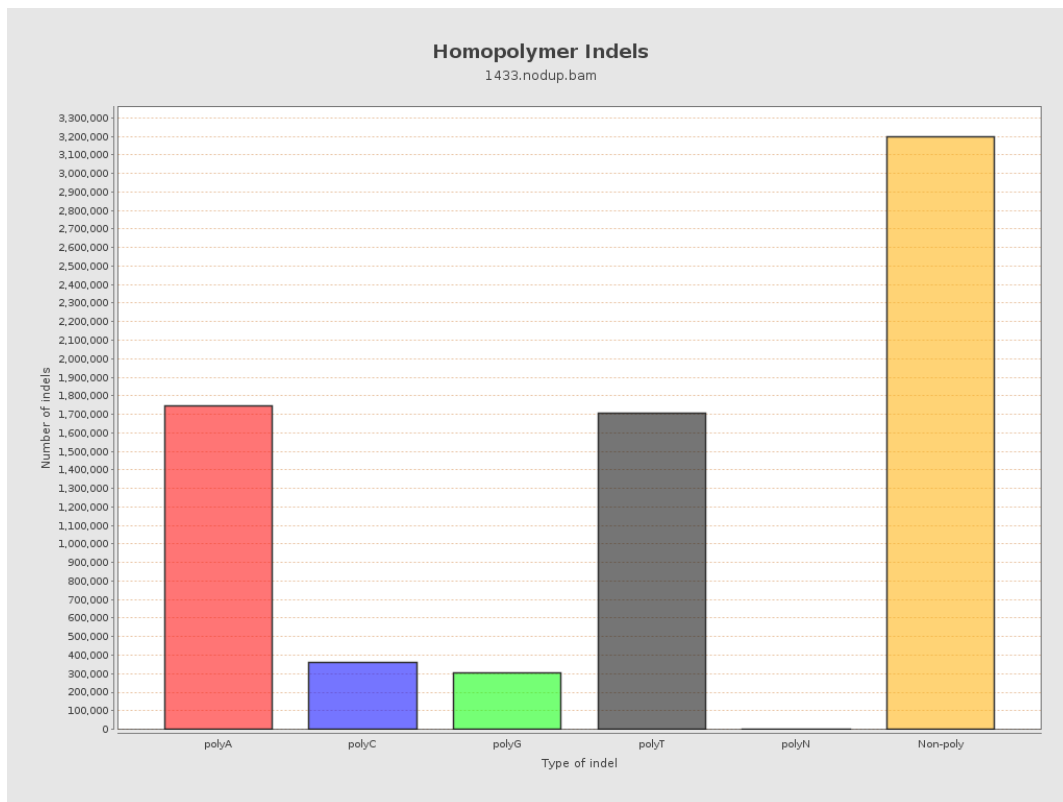
9. Results : Mapped Reads GC-content Distribution



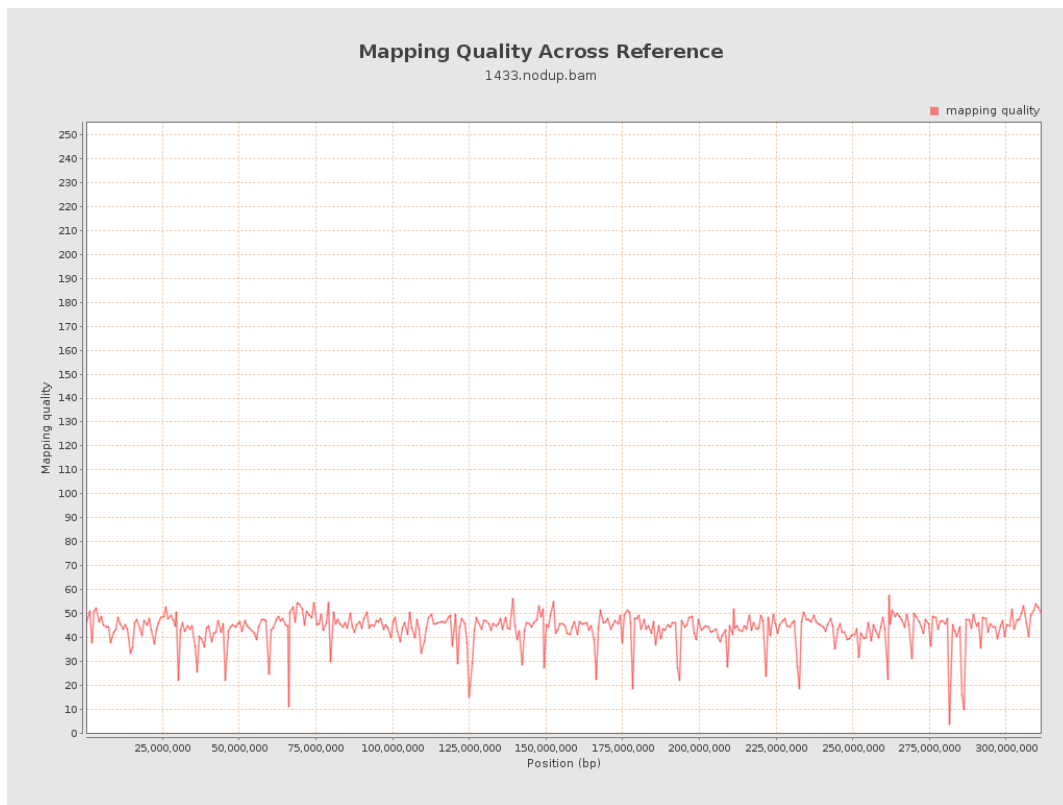
10. Results : Mapped Reads Clipping Profile



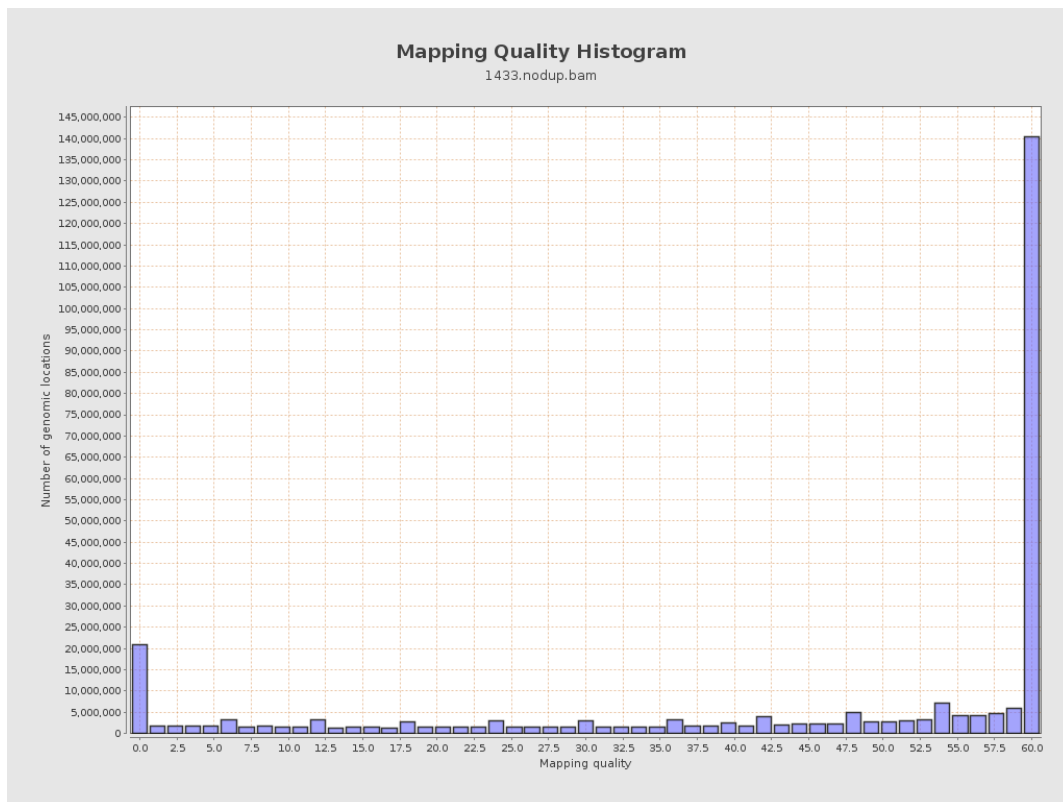
11. Results : Homopolymer Indels



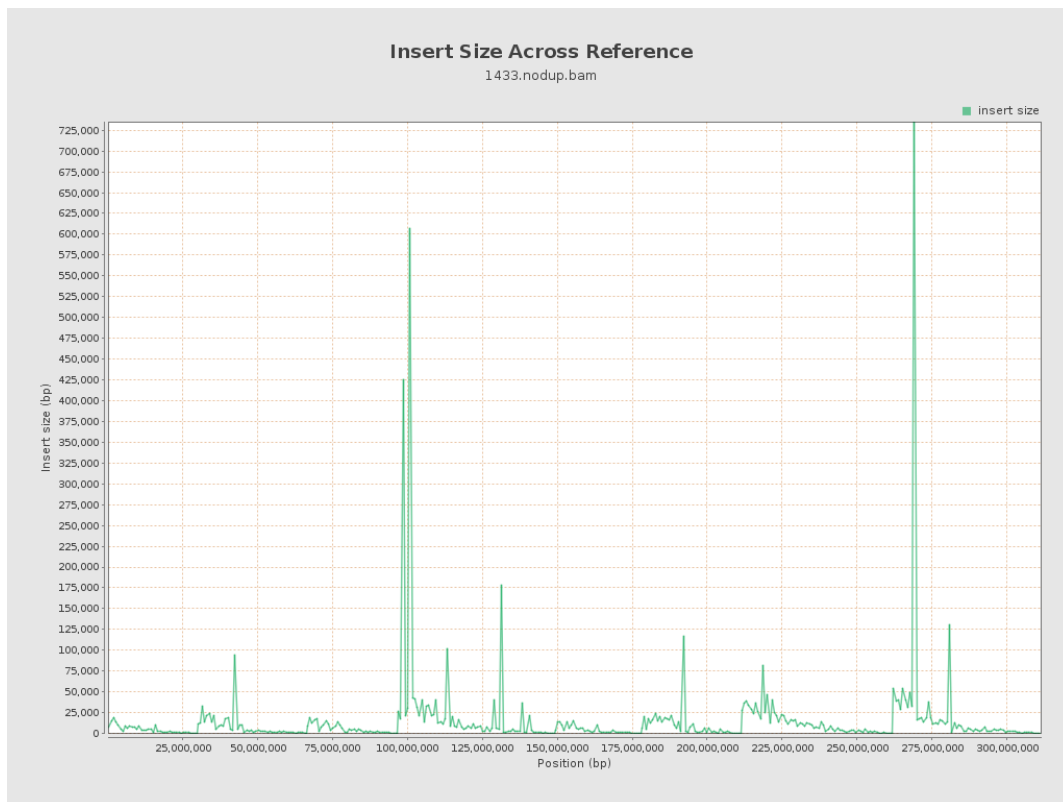
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

