

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/142
6
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1426 .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_490/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_490_S465_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_490/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_490_S465_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:26:14 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	50,268,081
Mapped reads	47,676,491 / 94.84%
Unmapped reads	2,591,590 / 5.16%
Mapped paired reads	47,676,491 / 94.84%
Mapped reads, first in pair	23,888,937 / 47.52%
Mapped reads, second in pair	23,787,554 / 47.32%
Mapped reads, both in pair	46,752,246 / 93.01%
Mapped reads, singletons	924,245 / 1.84%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	6,677,685 / 13.28%
Clipped reads	10,475,230 / 20.84%

2.2. ACGT Content

Number/percentage of A's	2,036,165,329 / 30.72%
Number/percentage of C's	1,277,481,669 / 19.27%
Number/percentage of T's	2,041,403,748 / 30.8%
Number/percentage of G's	1,273,570,863 / 19.21%
Number/percentage of N's	22,145 / 0%
GC Percentage	38.49%

2.3. Coverage

Mean	21.3253
Standard Deviation	180.7384

2.4. Mapping Quality

Mean Mapping Quality	43.97
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2.5. Insert size

Mean	239,330.7
Standard Deviation	2,311,360.05
P25/Median/P75	365 / 482 / 635

2.6. Mismatches and indels

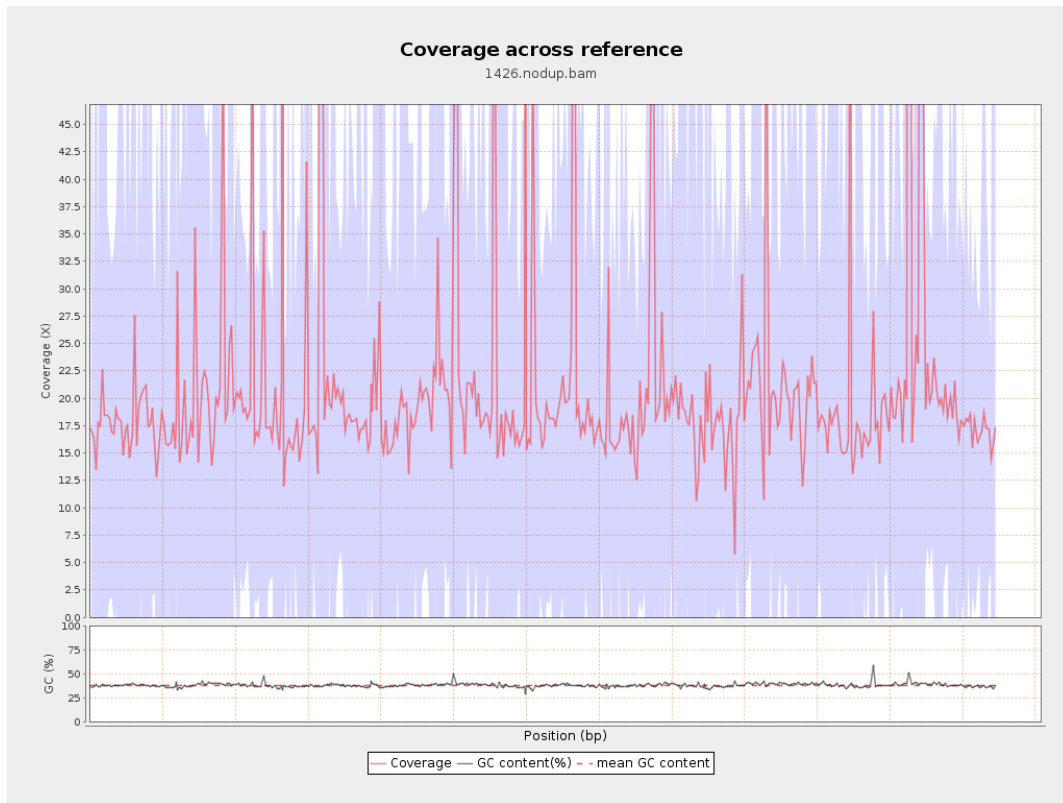
General error rate	2.3%
Mismatches	140,695,315
Insertions	4,374,282
Mapped reads with at least one insertion	8.25%
Deletions	4,512,737
Mapped reads with at least one deletion	8.4%
Homopolymer indels	55.65%

2.7. Chromosome stats

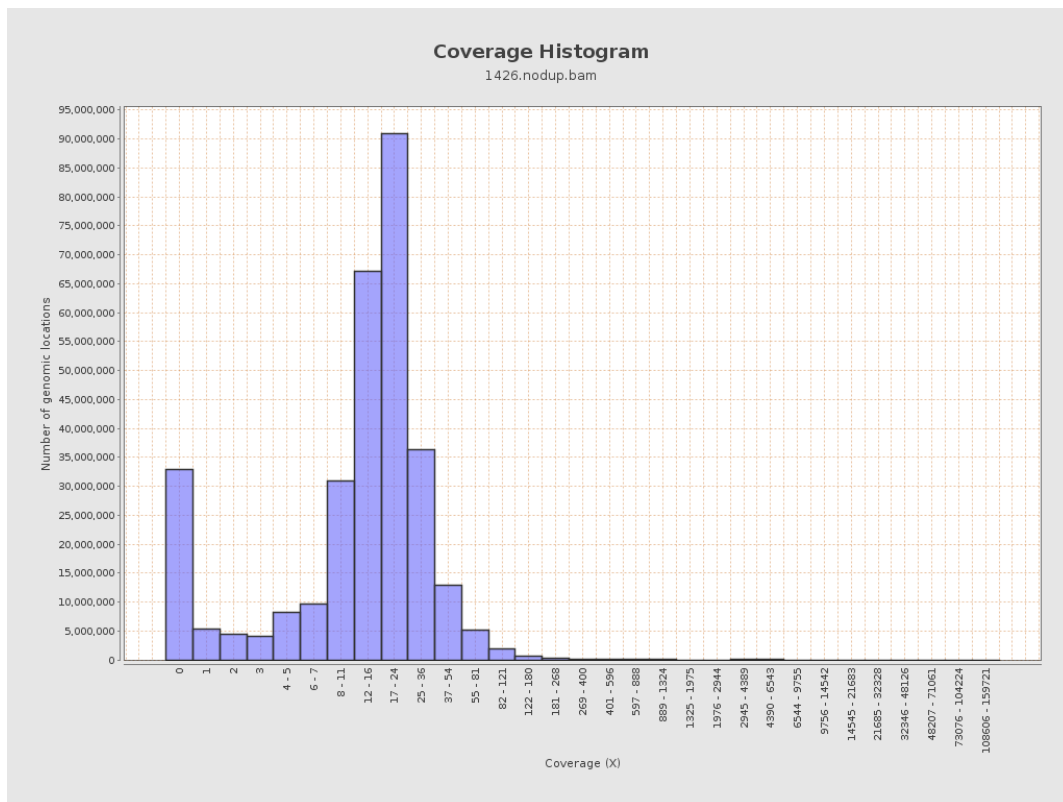
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	525026843	17.6632	62.1969

LT669789.1	36598175	781231111	21.3462	182.4608
LT669790.1	30422129	671669211	22.0783	143.4724
LT669791.1	52758100	1099191432	20.8346	160.905
LT669792.1	28376109	599095472	21.1127	204.1117
LT669793.1	33388210	662814914	19.8518	115.3575
LT669794.1	50579949	1022051403	20.2067	158.3309
LT669795.1	49795044	1284788663	25.8015	281.9544

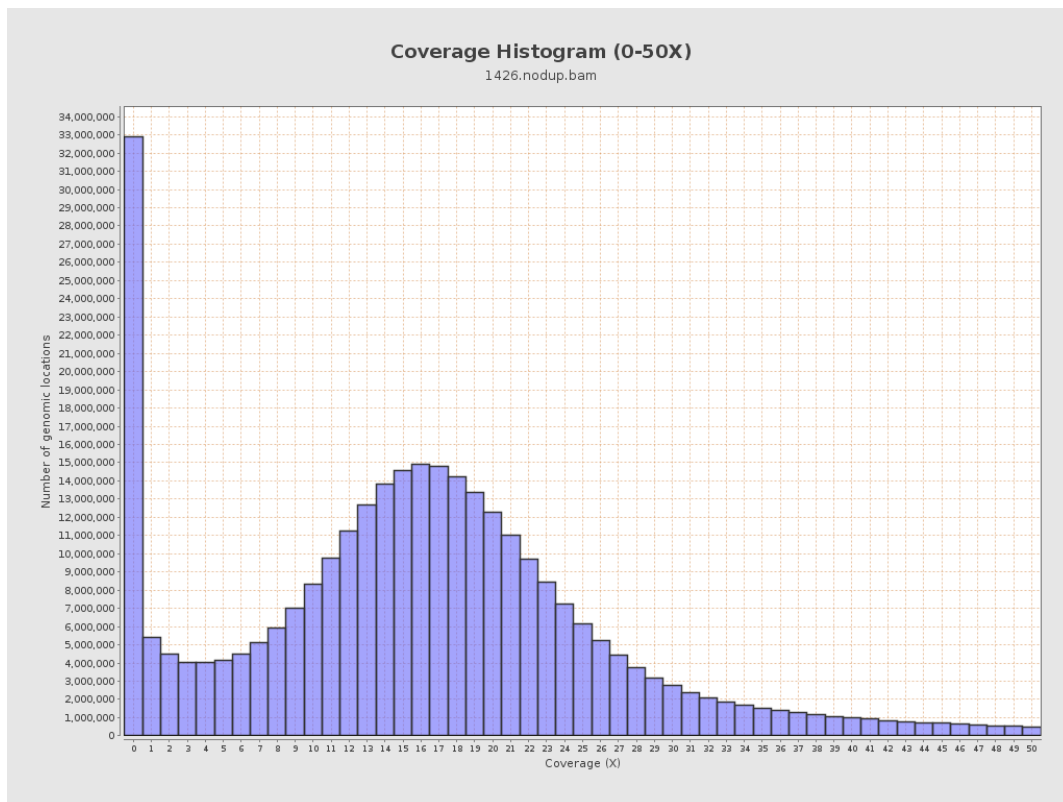
3. Results : Coverage across reference



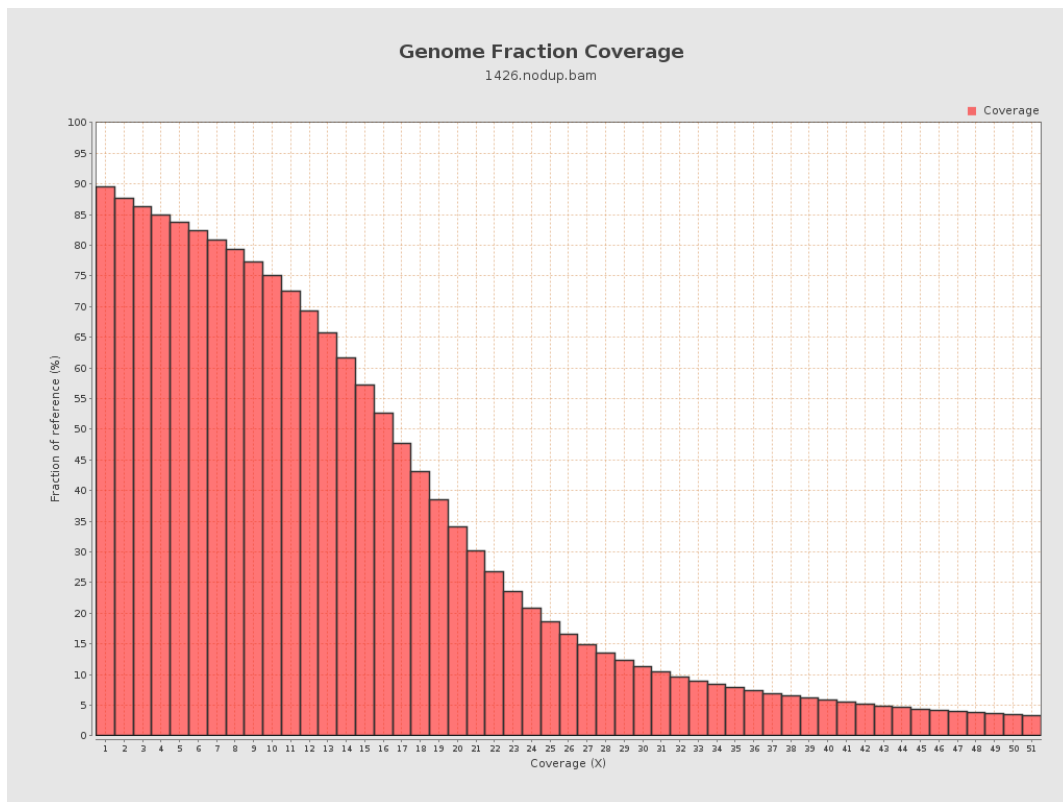
4. Results : Coverage Histogram



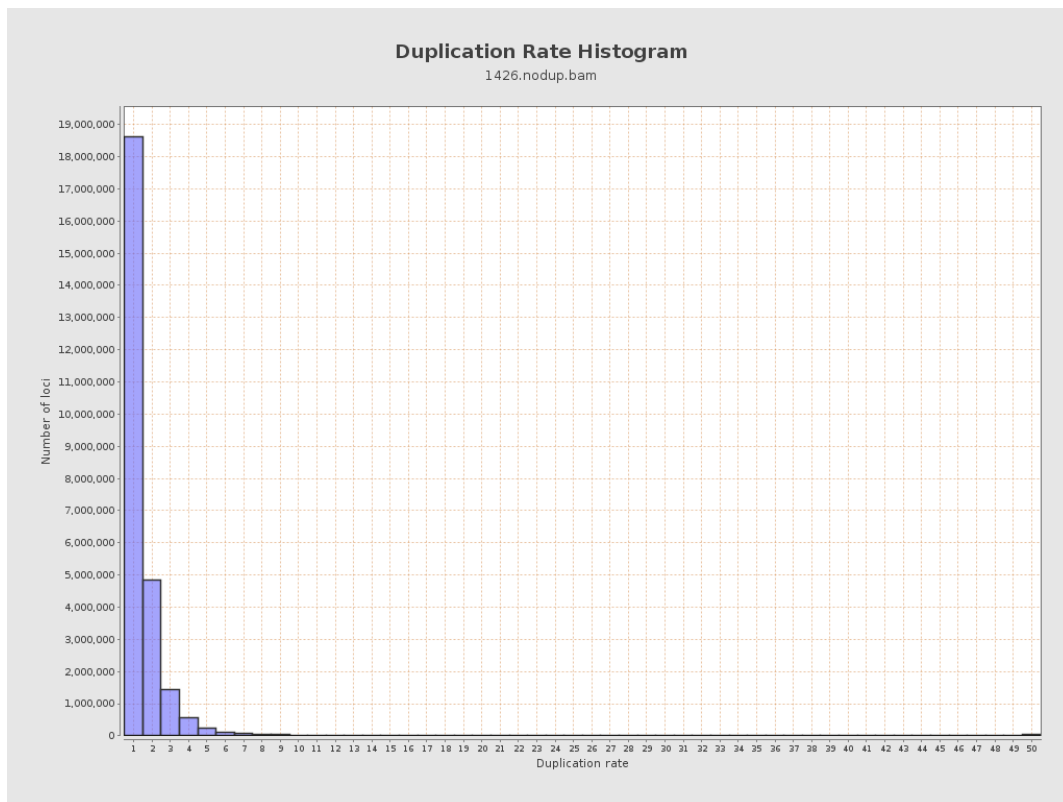
5. Results : Coverage Histogram (0-50X)



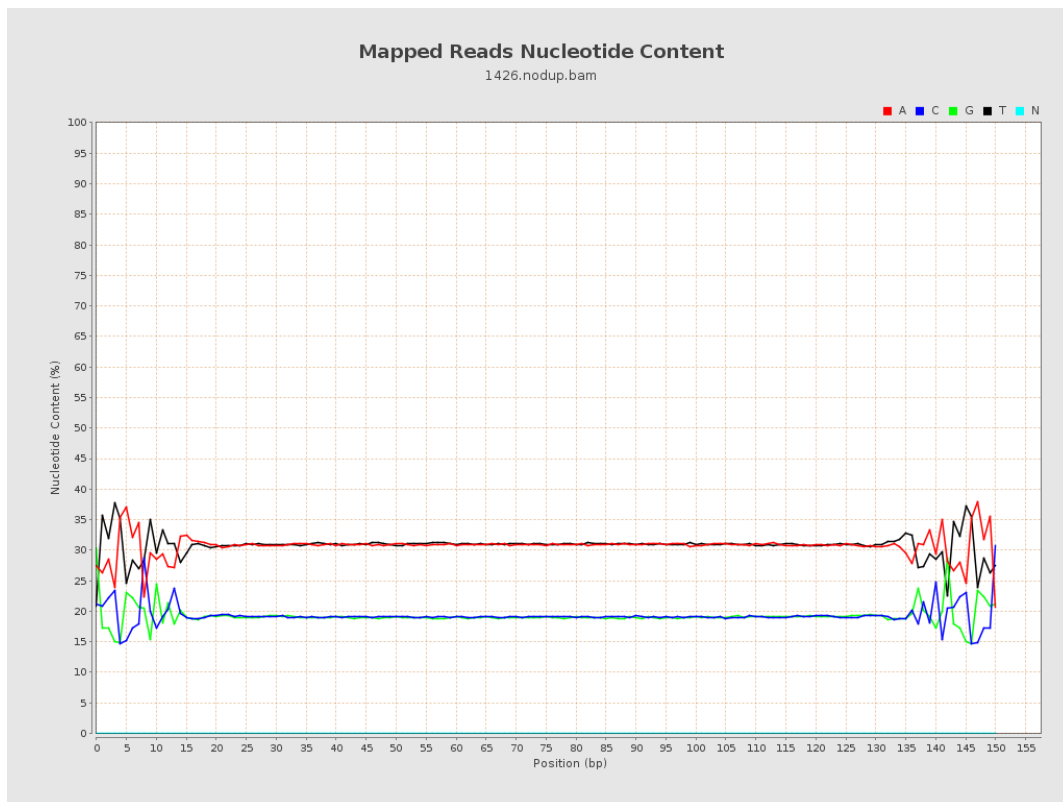
6. Results : Genome Fraction Coverage



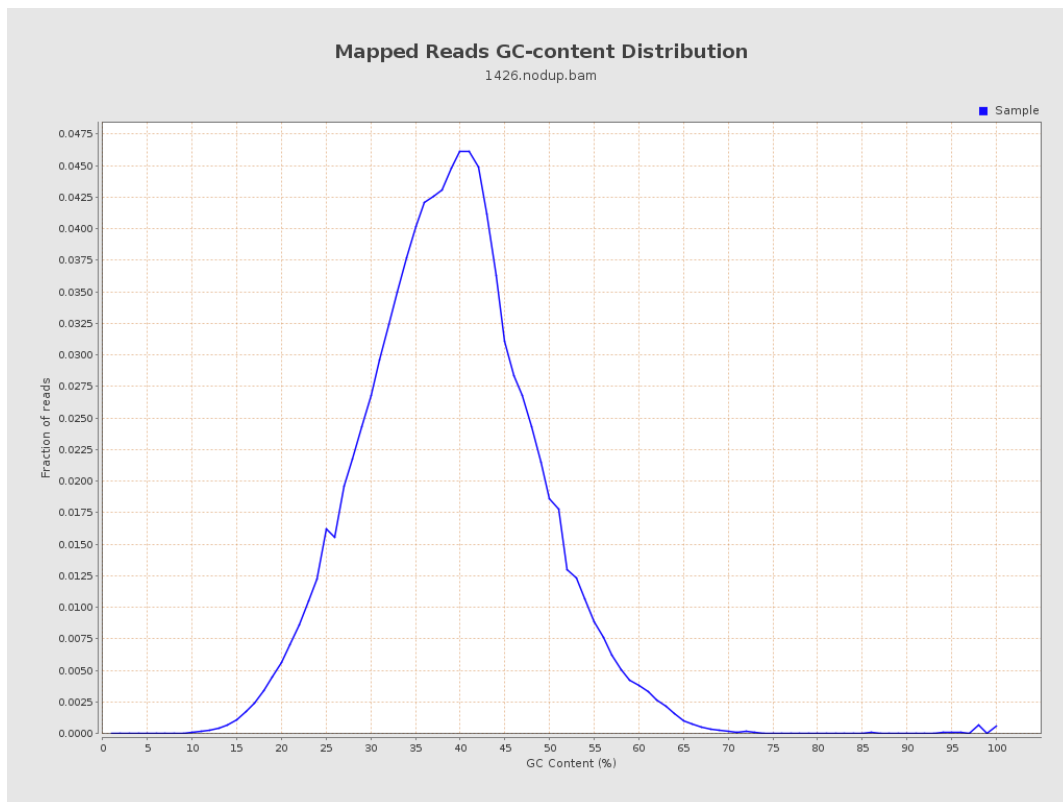
7. Results : Duplication Rate Histogram



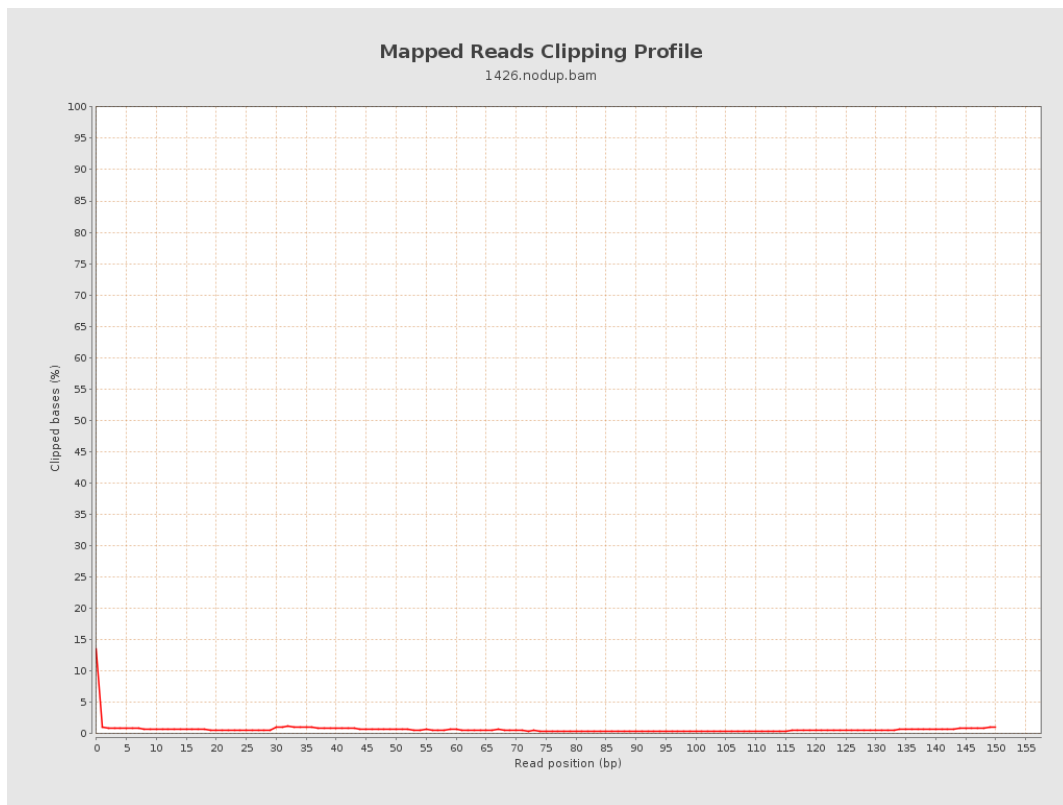
8. Results : Mapped Reads Nucleotide Content



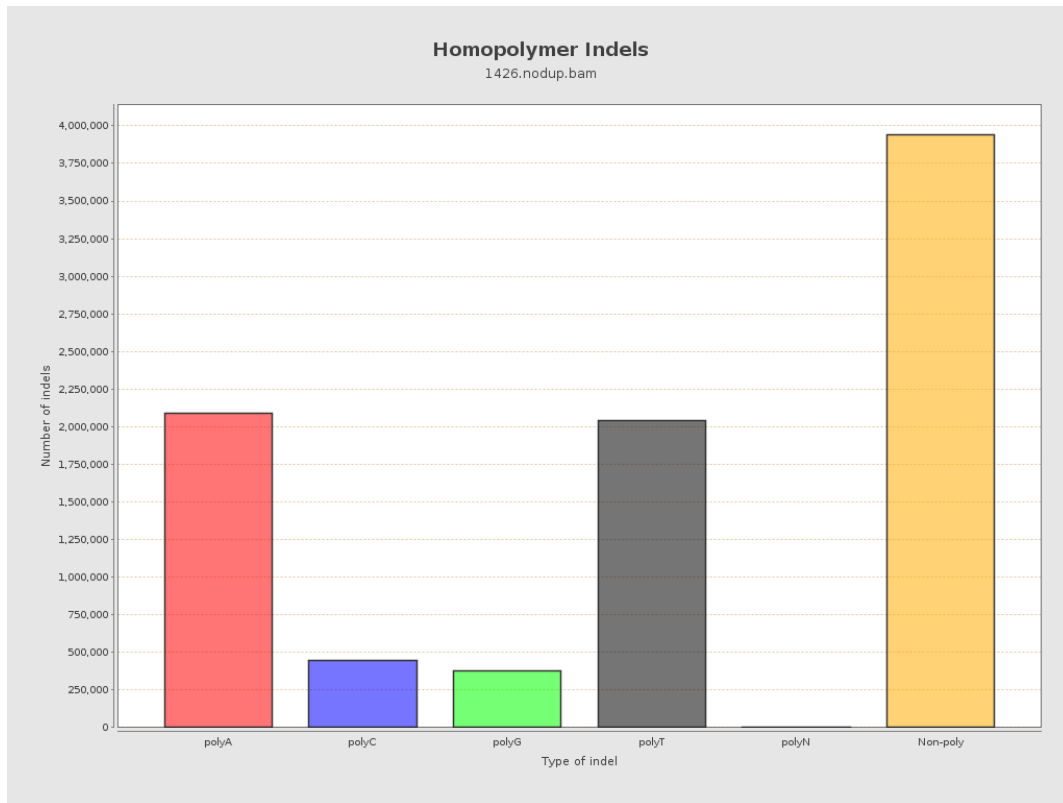
9. Results : Mapped Reads GC-content Distribution



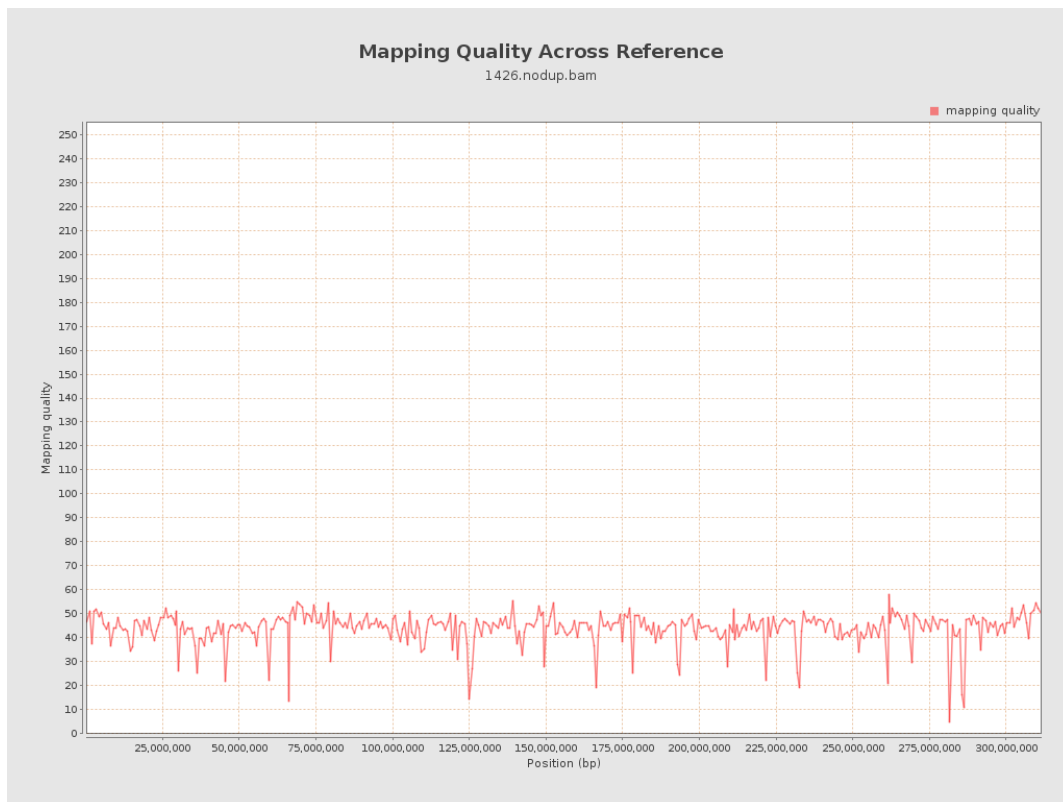
10. Results : Mapped Reads Clipping Profile



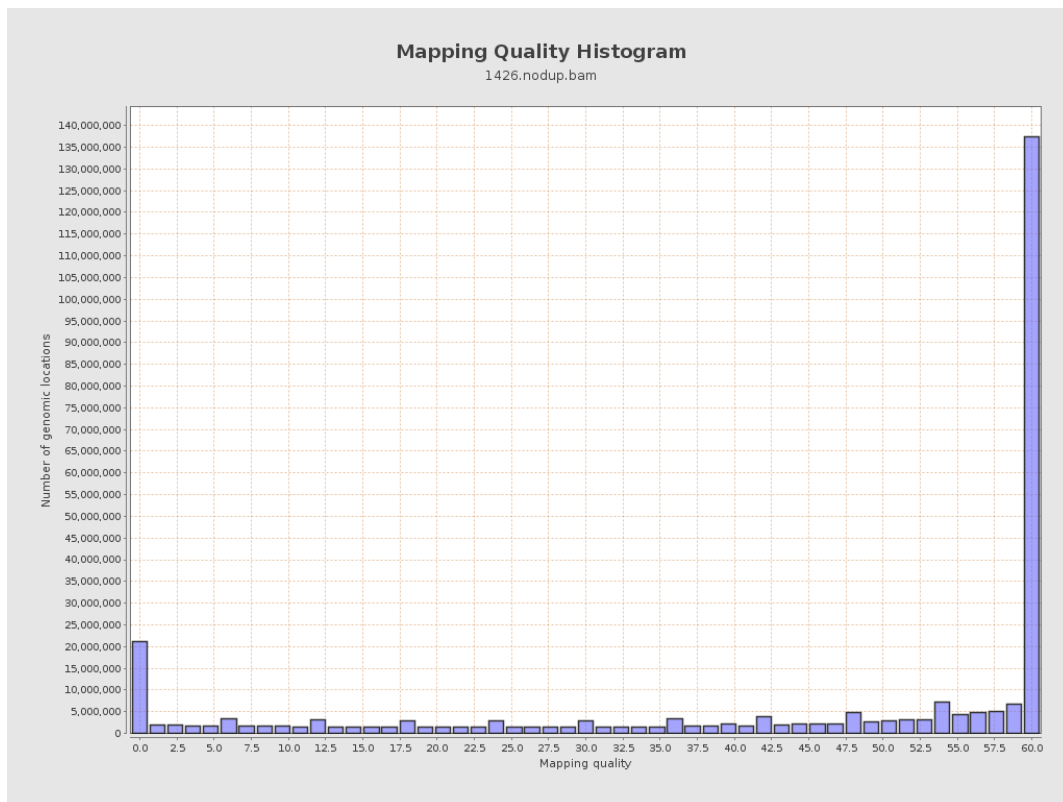
11. Results : Homopolymer Indels



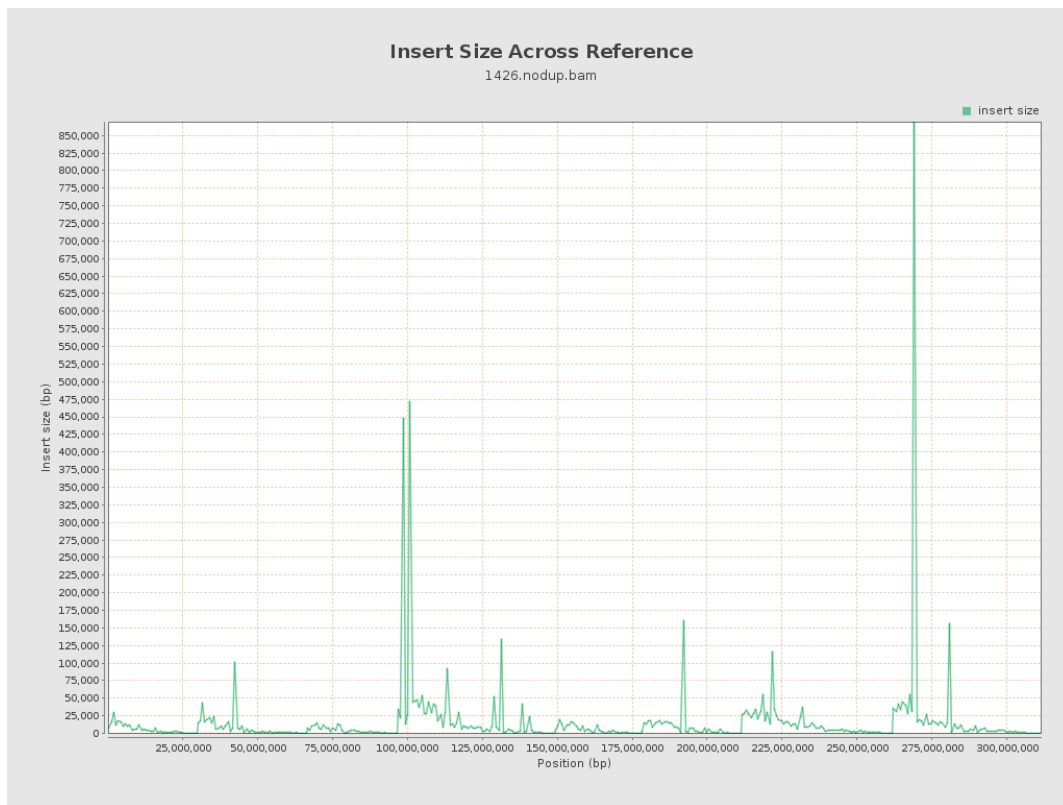
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

