

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/123
0
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1230 .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_130/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_130_S220_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_130/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_130_S220_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:25 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,796,945
Mapped reads	67,336,425 / 92.5%
Unmapped reads	5,460,520 / 7.5%
Mapped paired reads	67,336,425 / 92.5%
Mapped reads, first in pair	33,729,985 / 46.33%
Mapped reads, second in pair	33,606,440 / 46.16%
Mapped reads, both in pair	65,531,850 / 90.02%
Mapped reads, singletons	1,804,575 / 2.48%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	11,760,175 / 16.15%
Clipped reads	15,541,187 / 21.35%

2.2. ACGT Content

Number/percentage of A's	2,871,886,831 / 30.91%
Number/percentage of C's	1,773,816,521 / 19.09%
Number/percentage of T's	2,874,943,983 / 30.94%
Number/percentage of G's	1,771,744,238 / 19.07%
Number/percentage of N's	38,461 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	29.8978
Standard Deviation	245.7698

2.4. Mapping Quality

Mean Mapping Quality	43.67
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2.5. Insert size

Mean	259,948.82
Standard Deviation	2,436,480.03
P25/Median/P75	334 / 435 / 568

2.6. Mismatches and indels

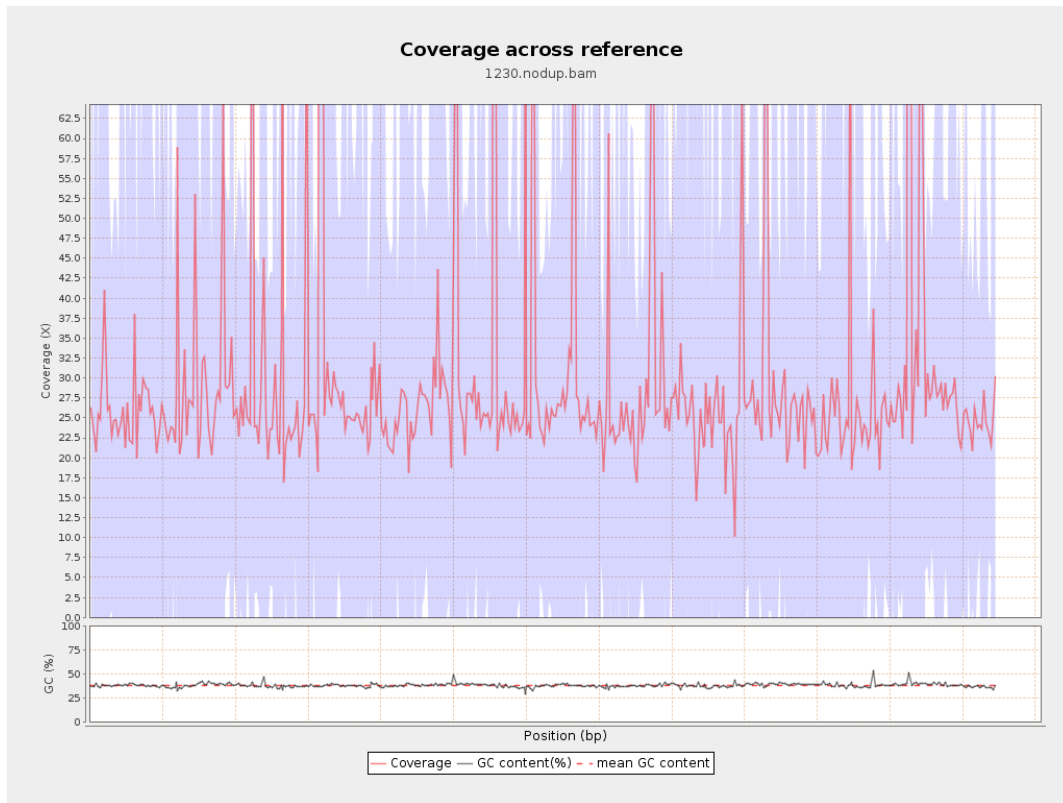
General error rate	2.4%
Mismatches	204,069,982
Insertions	6,738,414
Mapped reads with at least one insertion	8.95%
Deletions	6,650,133
Mapped reads with at least one deletion	8.72%
Homopolymer indels	56.47%

2.7. Chromosome stats

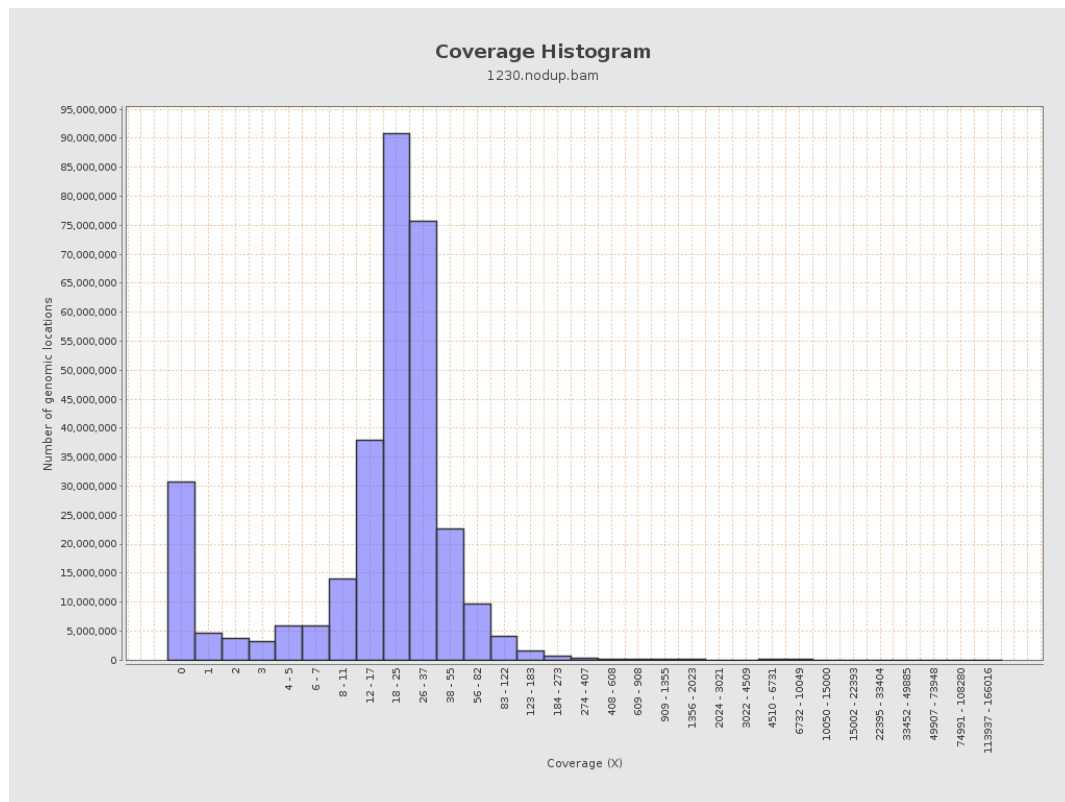
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	759378763	25.5474	102.5094

LT669789.1	36598175	1121932114	30.6554	280.8521
LT669790.1	30422129	1057505313	34.7611	317.5678
LT669791.1	52758100	1535660652	29.1076	264.2777
LT669792.1	28376109	851319068	30.0013	255.0508
LT669793.1	33388210	931941247	27.9123	165.2175
LT669794.1	50579949	1418940491	28.0534	226.971
LT669795.1	49795044	1640746216	32.95	265.3858

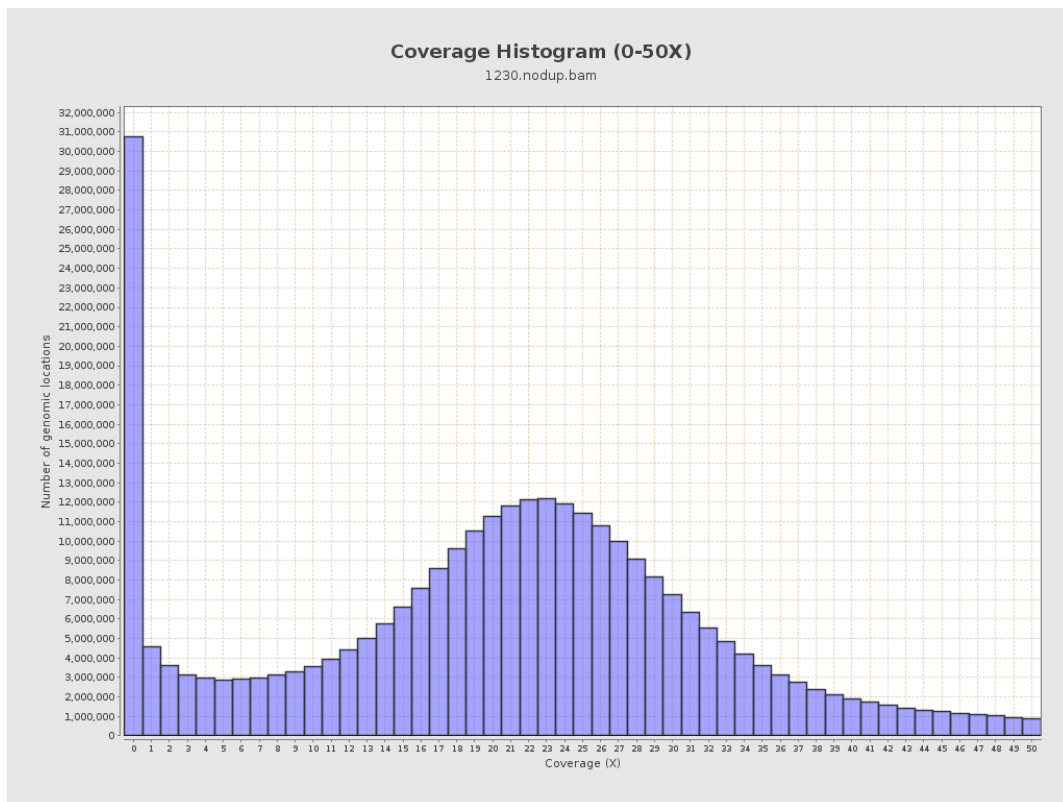
3. Results : Coverage across reference



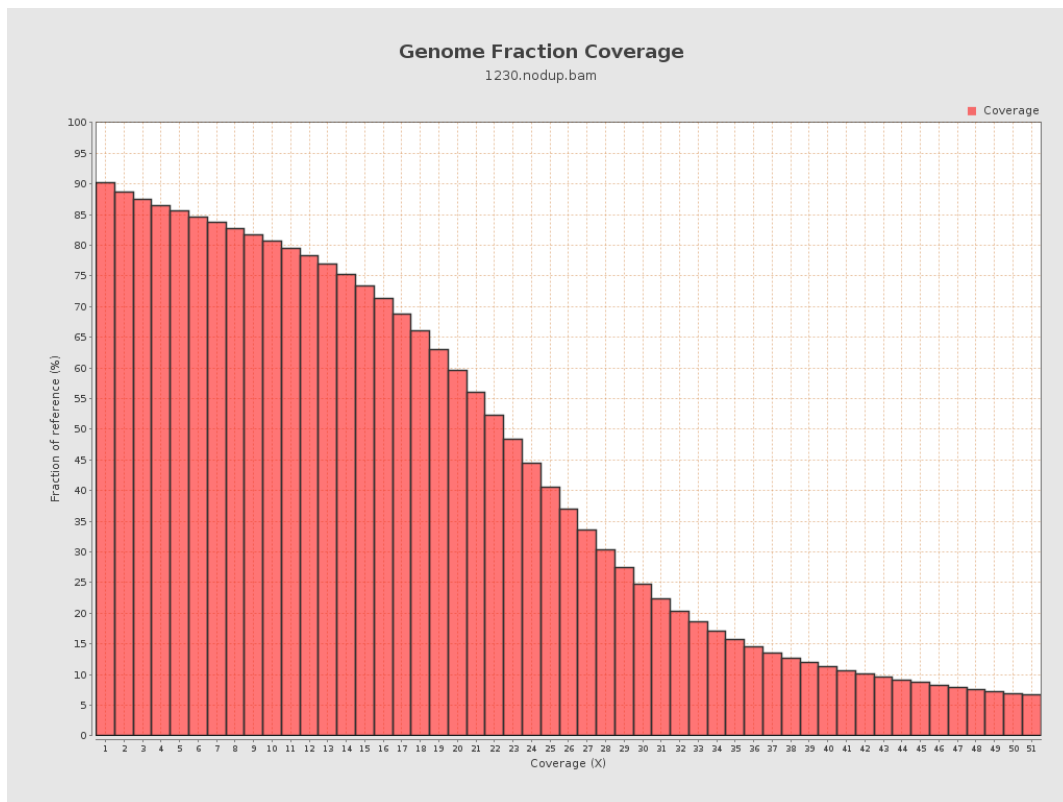
4. Results : Coverage Histogram



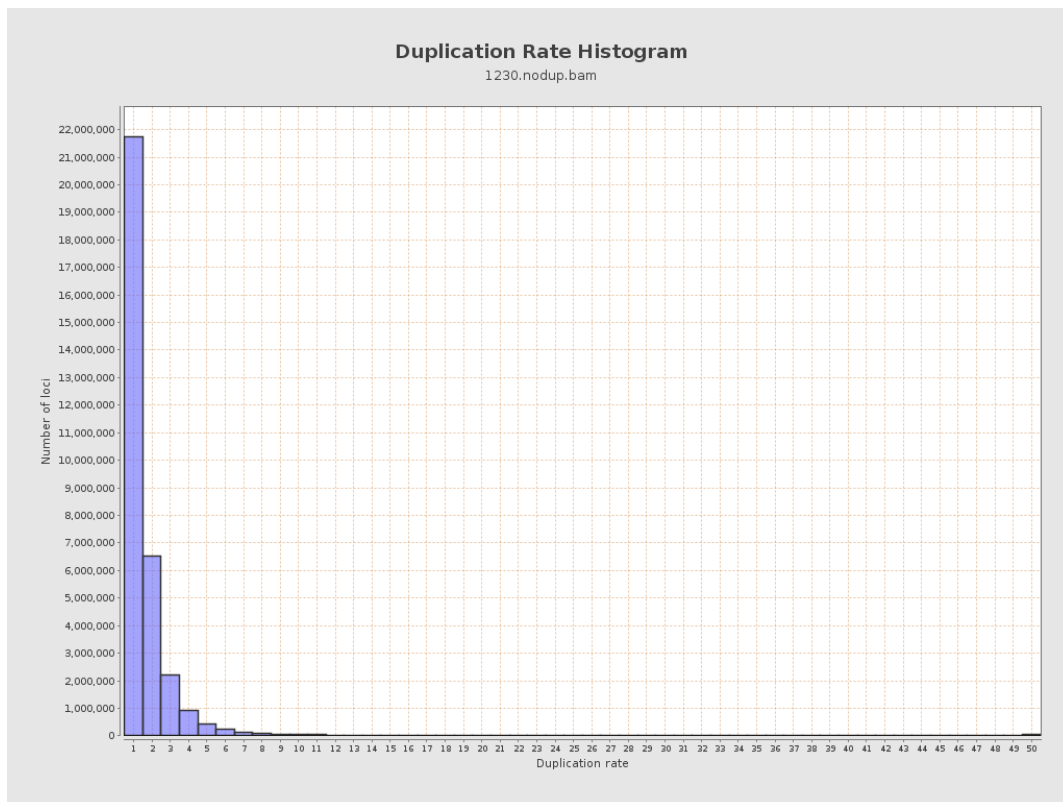
5. Results : Coverage Histogram (0-50X)



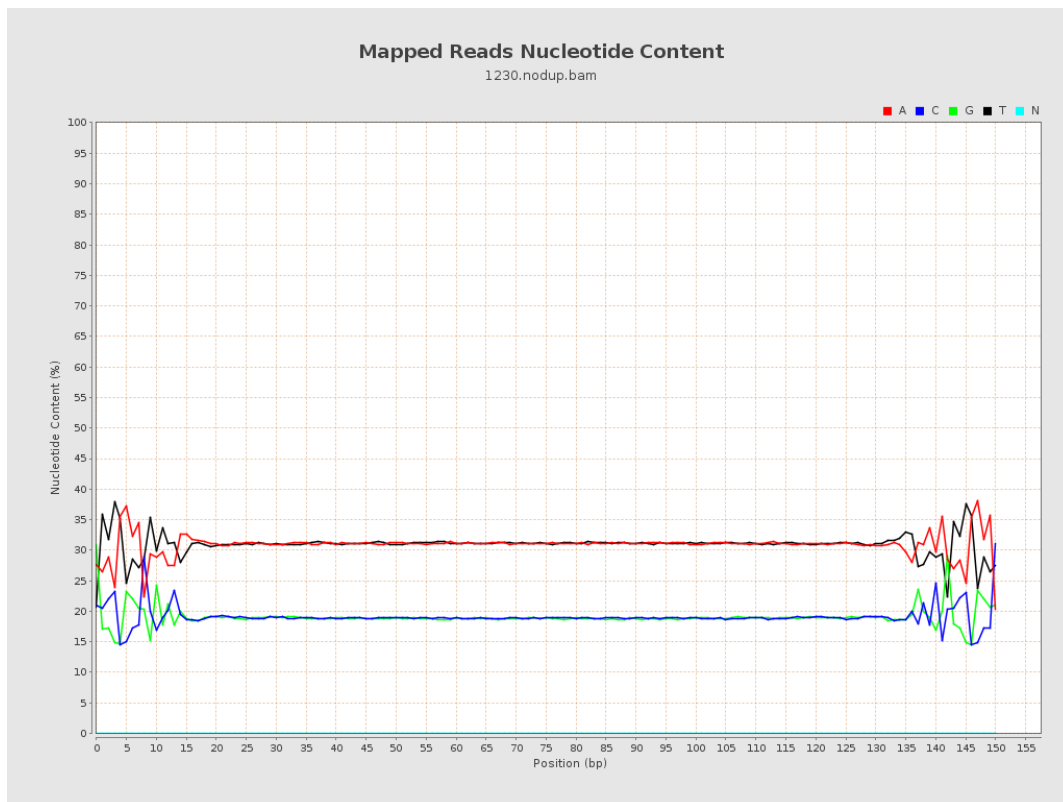
6. Results : Genome Fraction Coverage



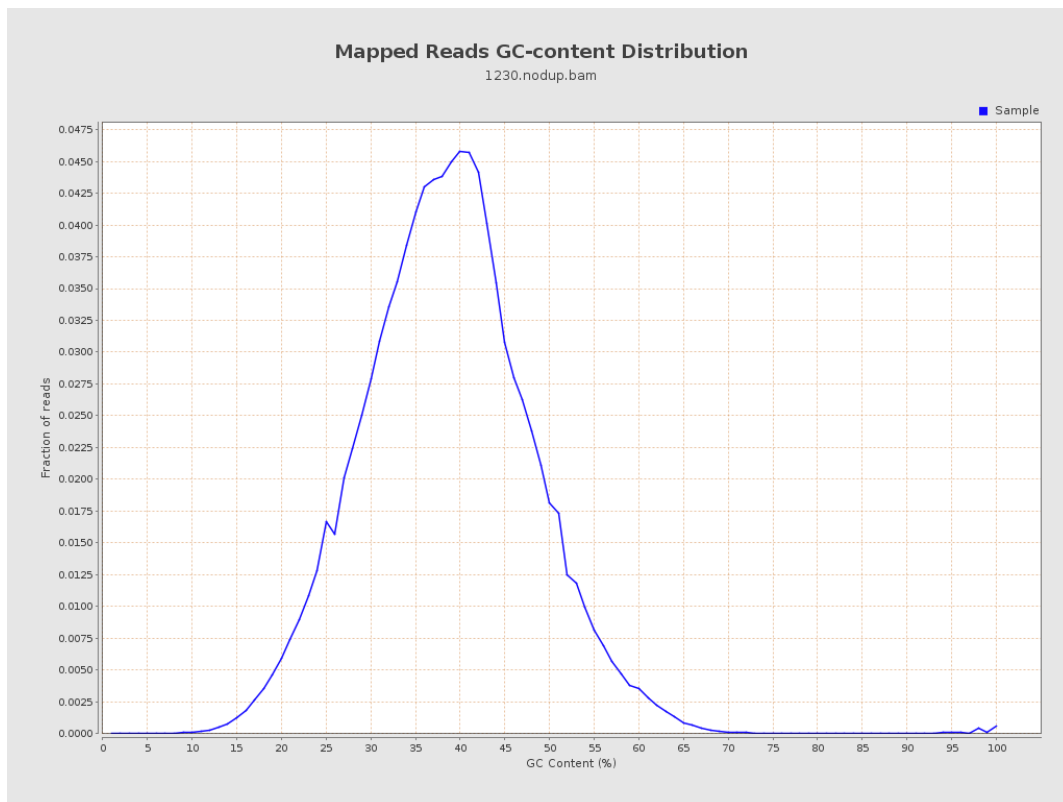
7. Results : Duplication Rate Histogram



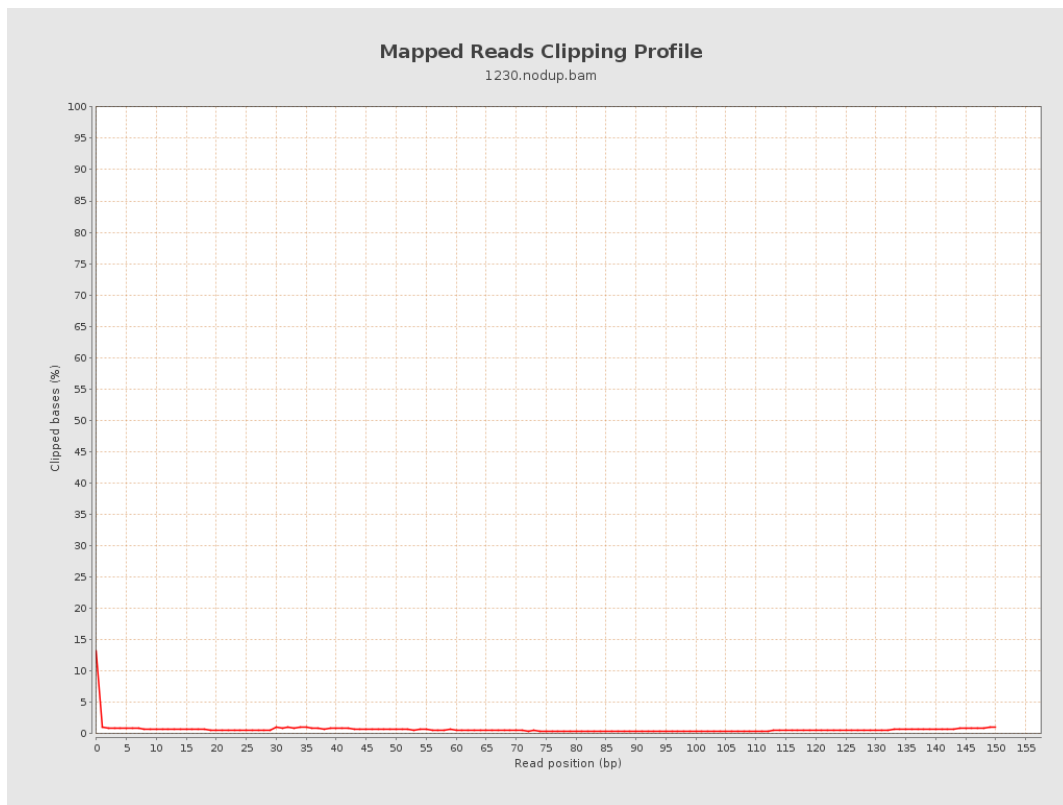
8. Results : Mapped Reads Nucleotide Content



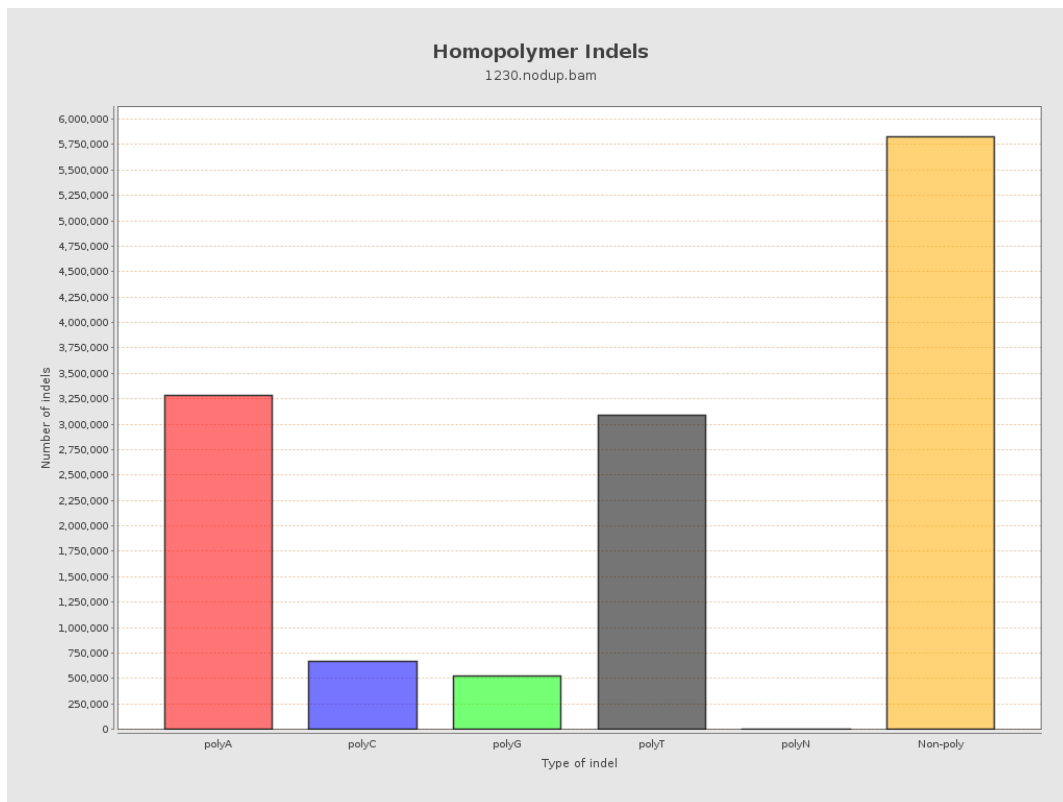
9. Results : Mapped Reads GC-content Distribution



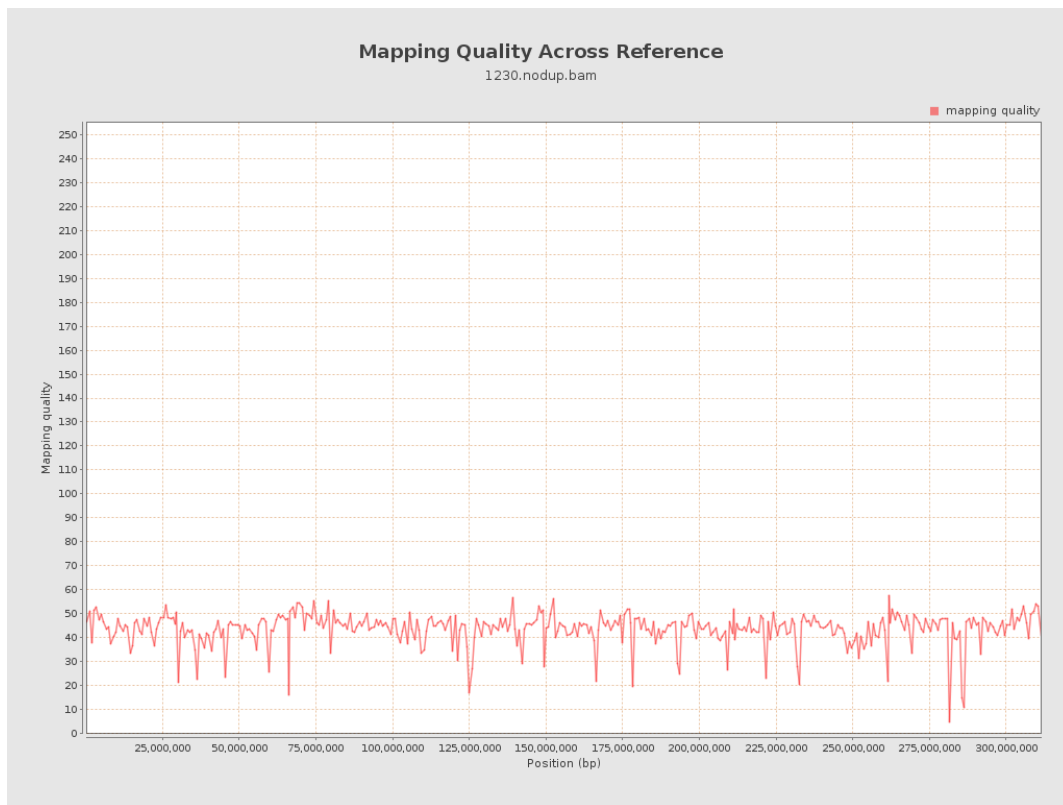
10. Results : Mapped Reads Clipping Profile



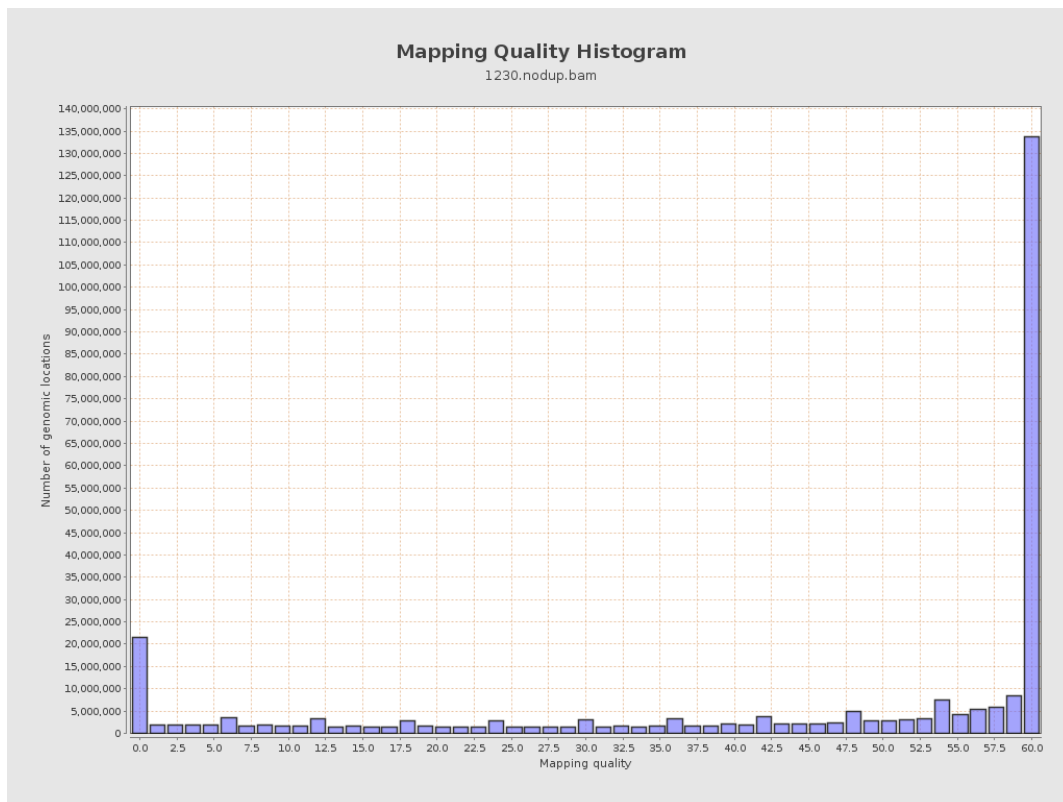
11. Results : Homopolymer Indels



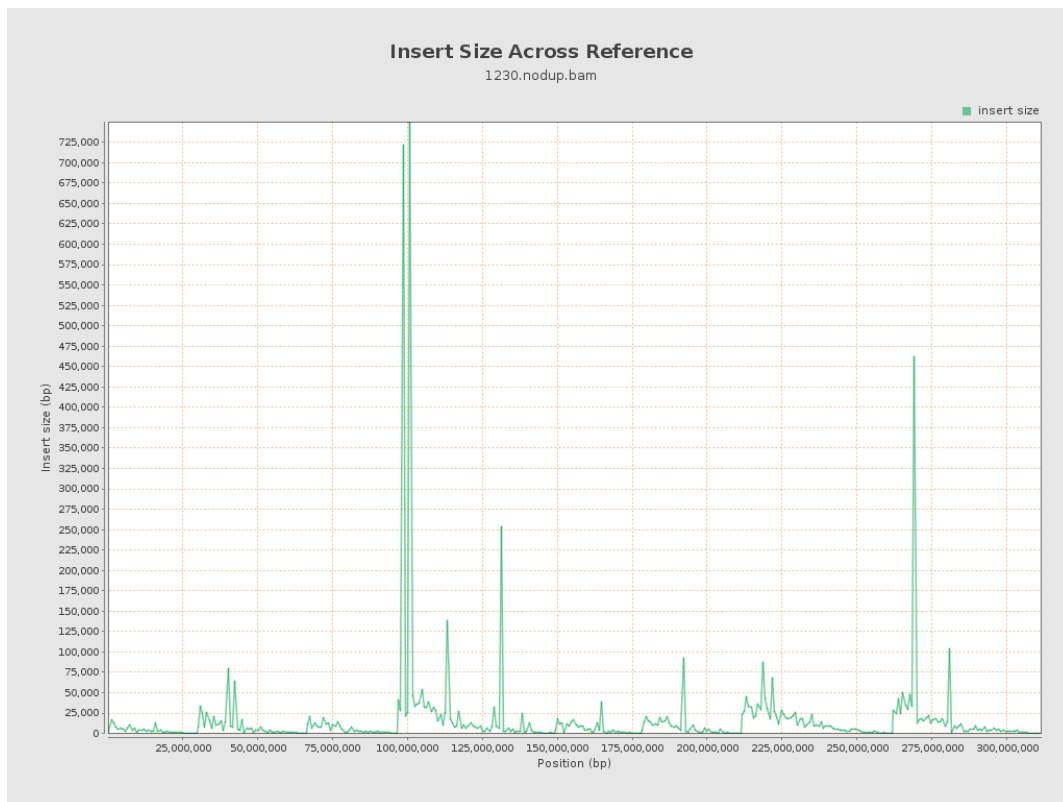
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

