Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1119
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1119 .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_290/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_290_S371_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_290/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_290_S371_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	64,335,706
Mapped reads	59,959,431 / 93.2%
Unmapped reads	4,376,275 / 6.8%
Mapped paired reads	59,959,431 / 93.2%
Mapped reads, first in pair	30,033,862 / 46.68%
Mapped reads, second in pair	29,925,569 / 46.51%
Mapped reads, both in pair	58,773,852 / 91.35%
Mapped reads, singletons	1,185,579 / 1.84%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	8,256,958 / 12.83%
Clipped reads	13,598,581 / 21.14%

2.2. ACGT Content

Number/percentage of A's	2,561,363,432 / 30.85%
Number/percentage of C's	1,590,479,053 / 19.15%
Number/percentage of T's	2,563,054,077 / 30.87%
Number/percentage of G's	1,588,720,704 / 19.13%
Number/percentage of N's	31,895 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	26.7151
Standard Deviation	218.6467

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Insert size

Mean	223,065.22
Standard Deviation	2,226,967.79
P25/Median/P75	302 / 396 / 518

2.6. Mismatches and indels

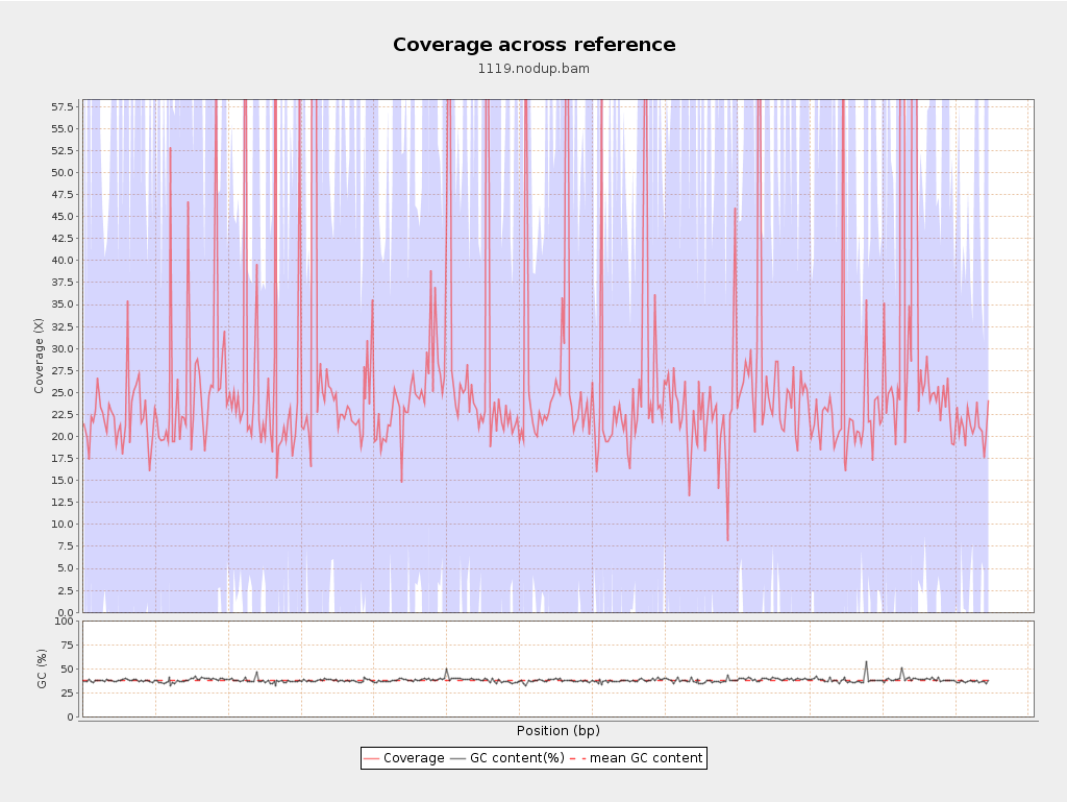
General error rate	2.32%
Mismatches	177,224,929
Insertions	5,636,750
Mapped reads with at least one insertion	8.45%
Deletions	5,771,854
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.19%

2.7. Chromosome stats

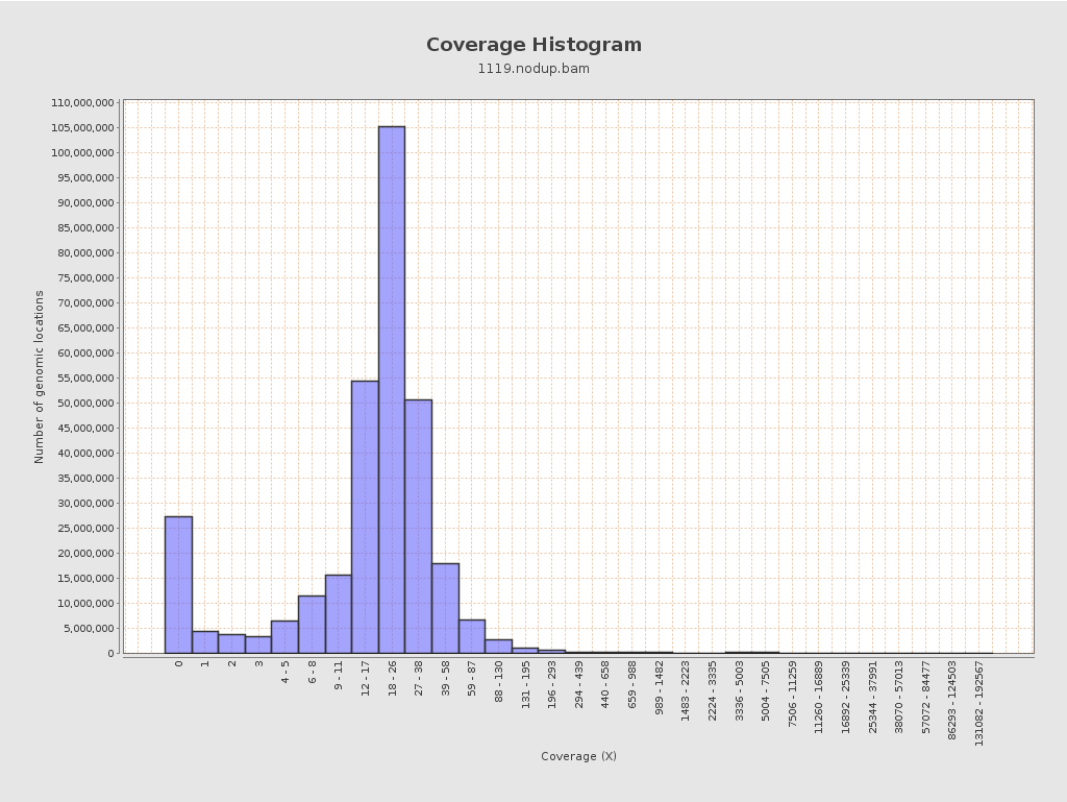
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	652823649	21.9626	63.1982

LT669789.1	36598175	995772894	27.2083	221.6793
LT669790.1	30422129	874677219	28.7513	213.3774
LT669791.1	52758100	1387148546	26.2926	187.4359
LT669792.1	28376109	745173240	26.2606	252.2398
LT669793.1	33388210	827953391	24.7978	149.4957
LT669794.1	50579949	1274354232	25.1949	179.4699
LT669795.1	49795044	1567649821	31.482	334.1423

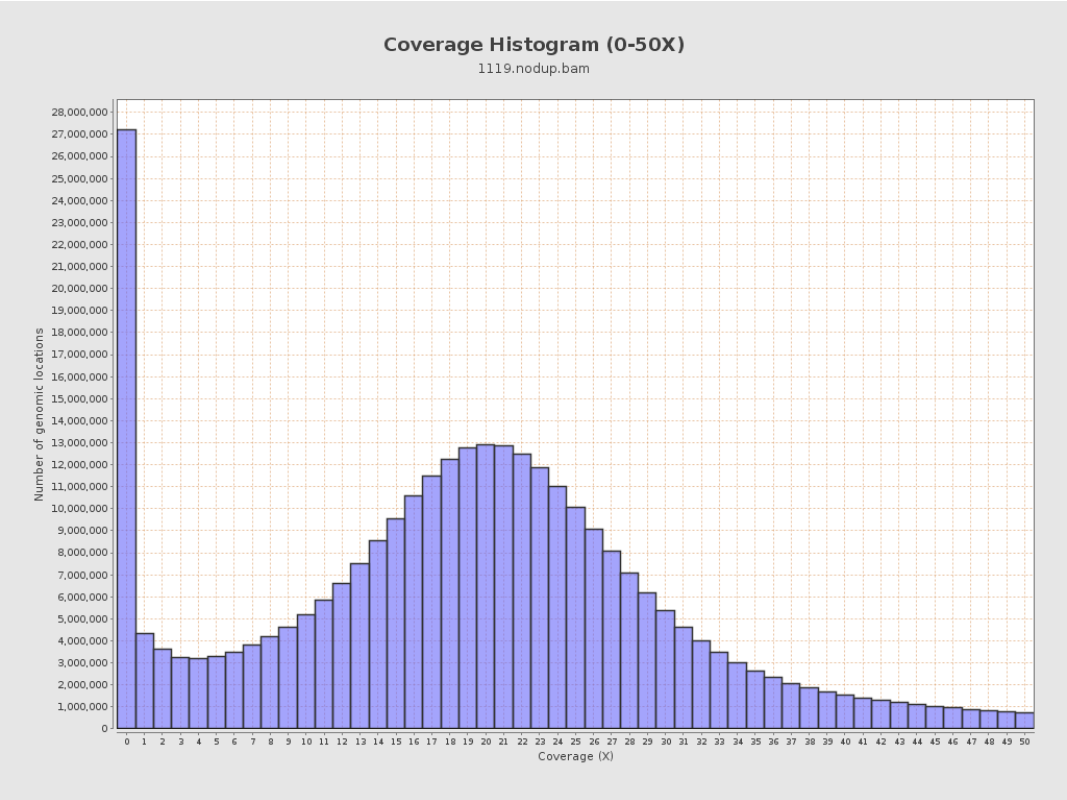
3. Results : Coverage across reference



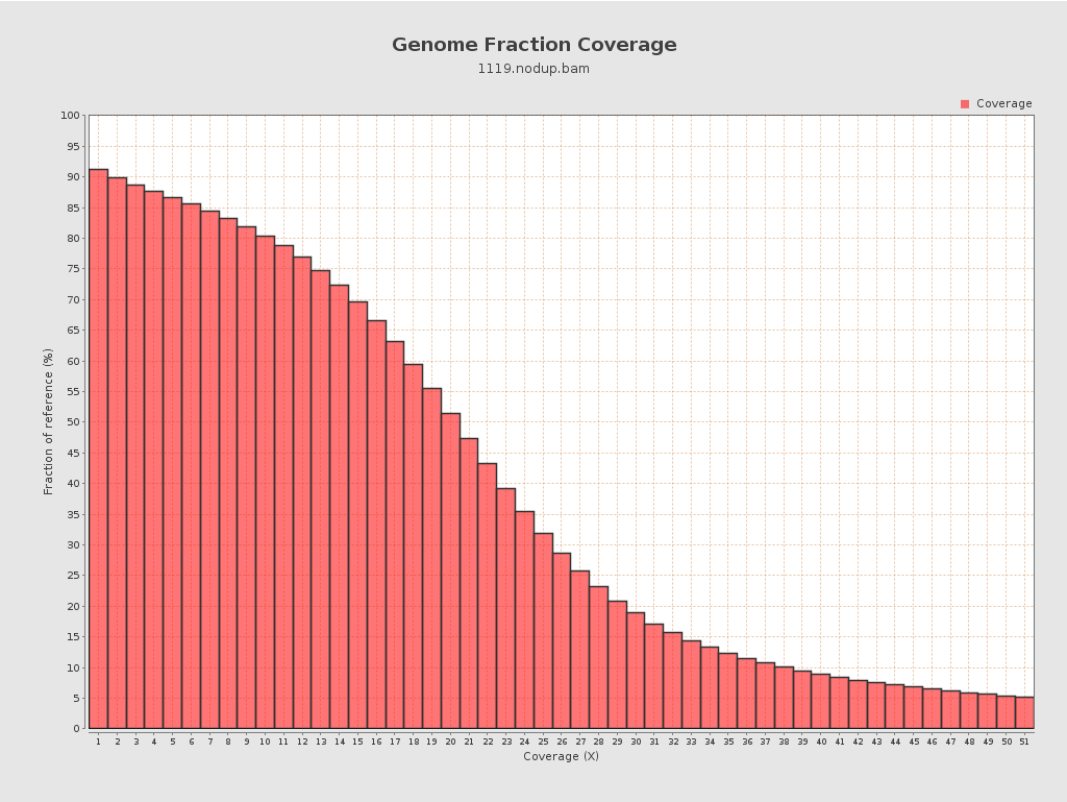
4. Results : Coverage Histogram



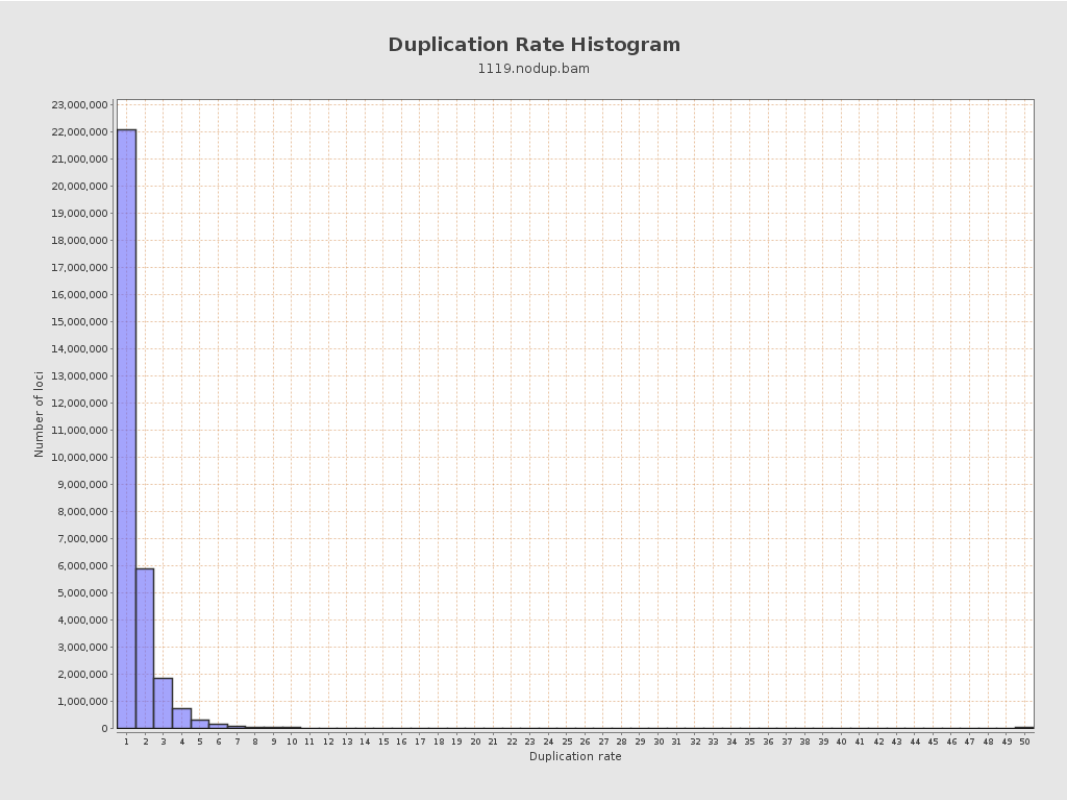
5. Results : Coverage Histogram (0-50X)



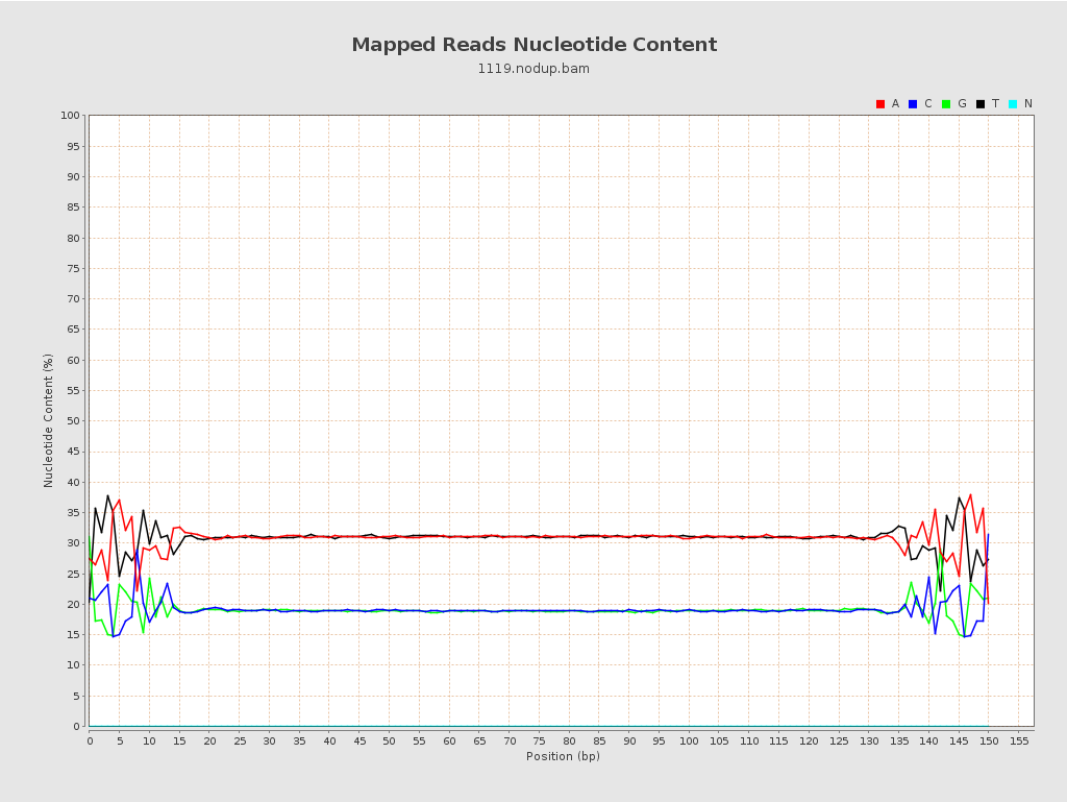
6. Results : Genome Fraction Coverage



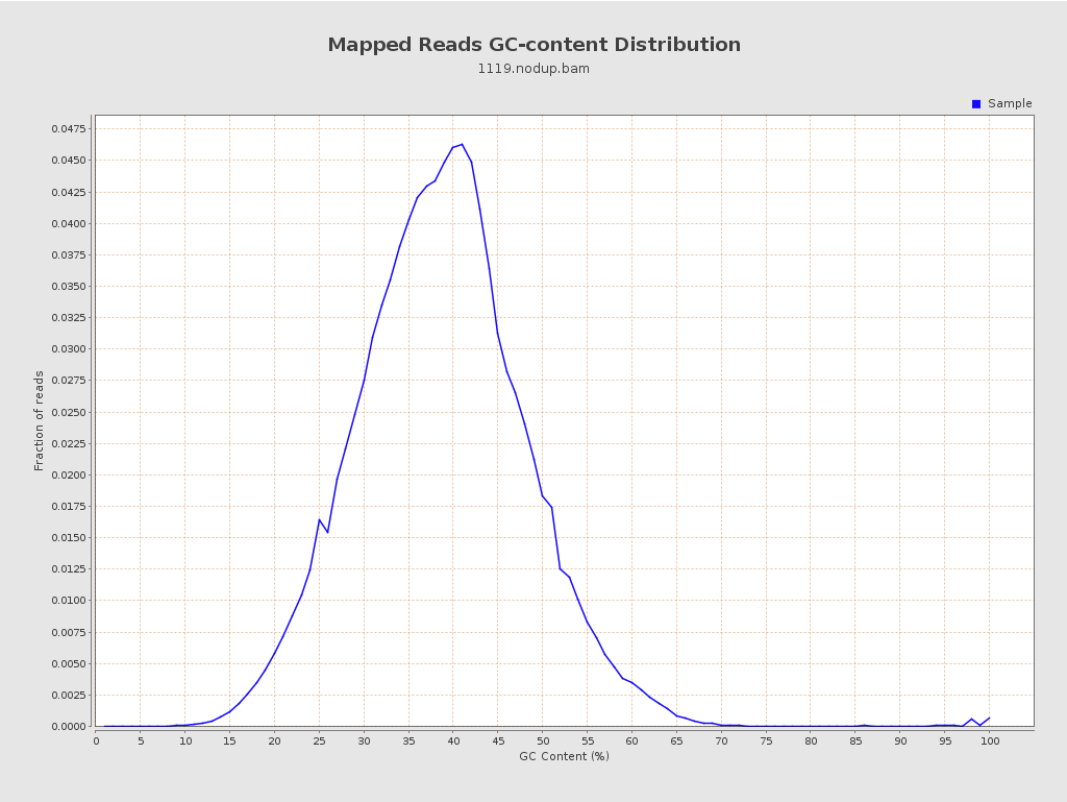
7. Results : Duplication Rate Histogram



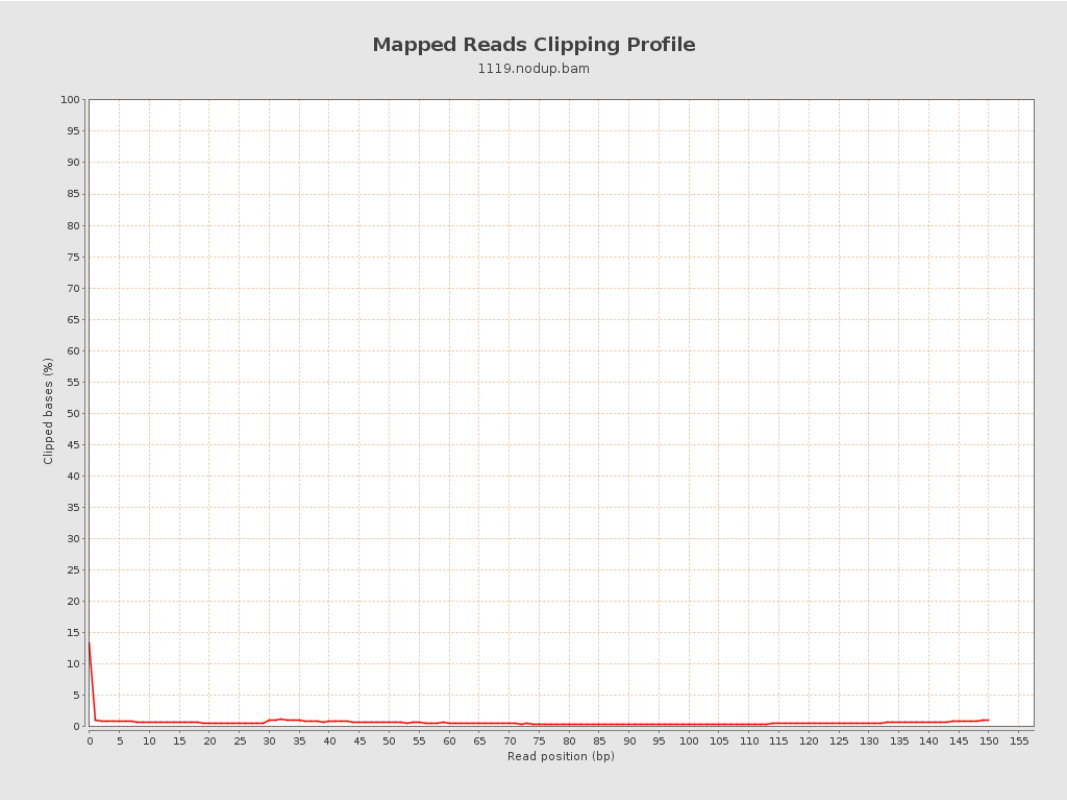
8. Results : Mapped Reads Nucleotide Content



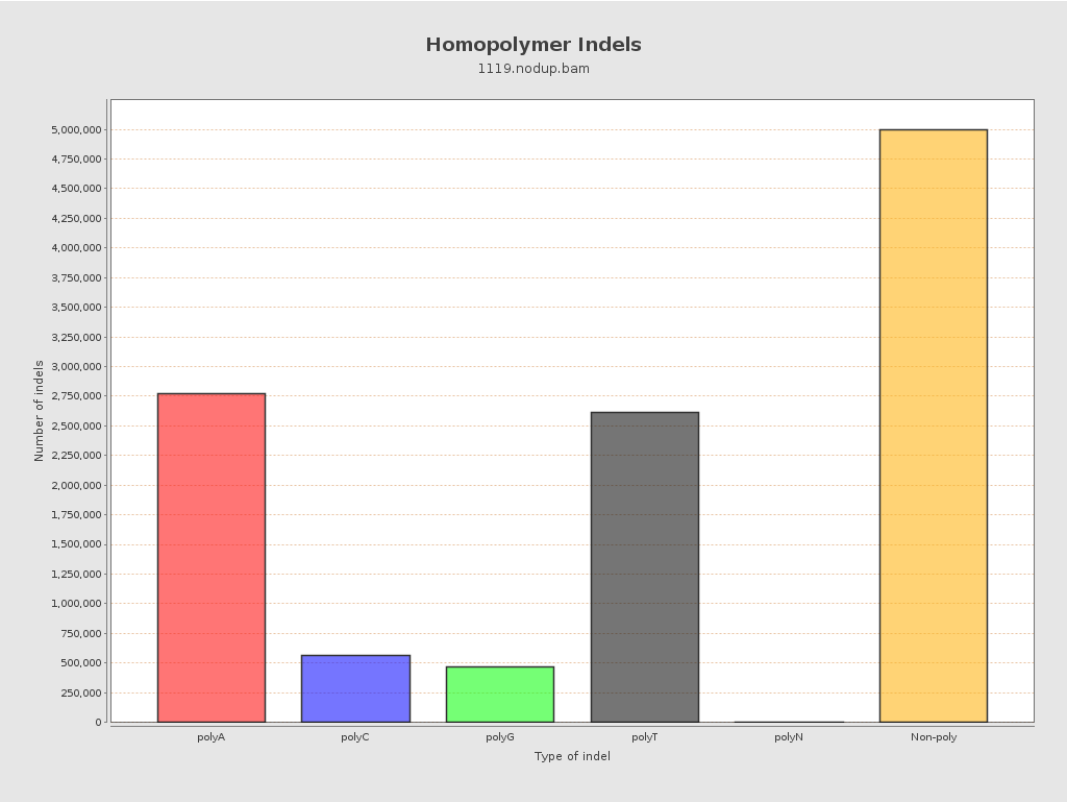
9. Results : Mapped Reads GC-content Distribution



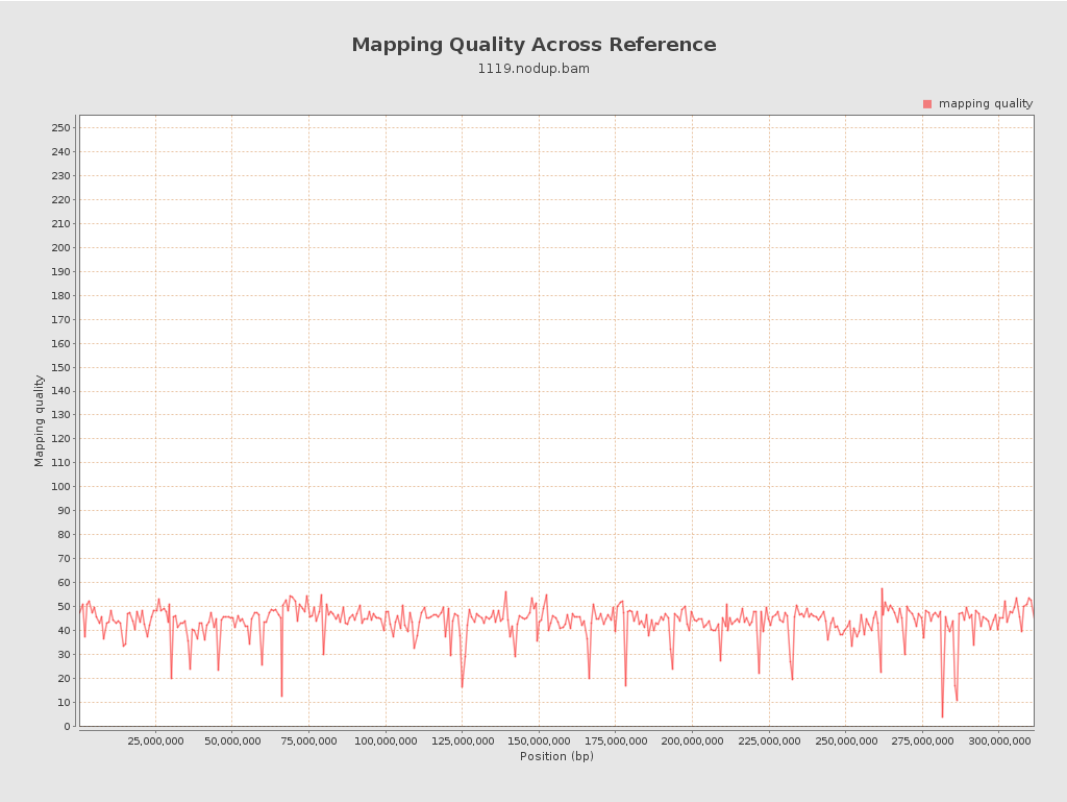
10. Results : Mapped Reads Clipping Profile



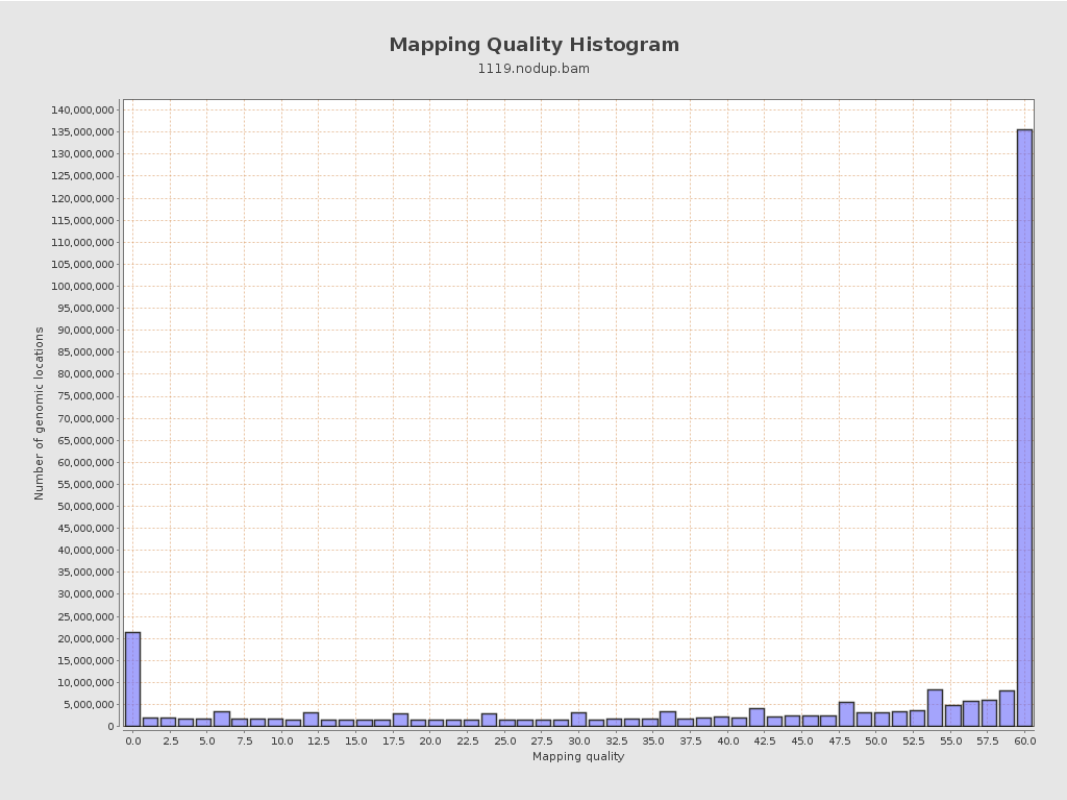
11. Results : Homopolymer Indels



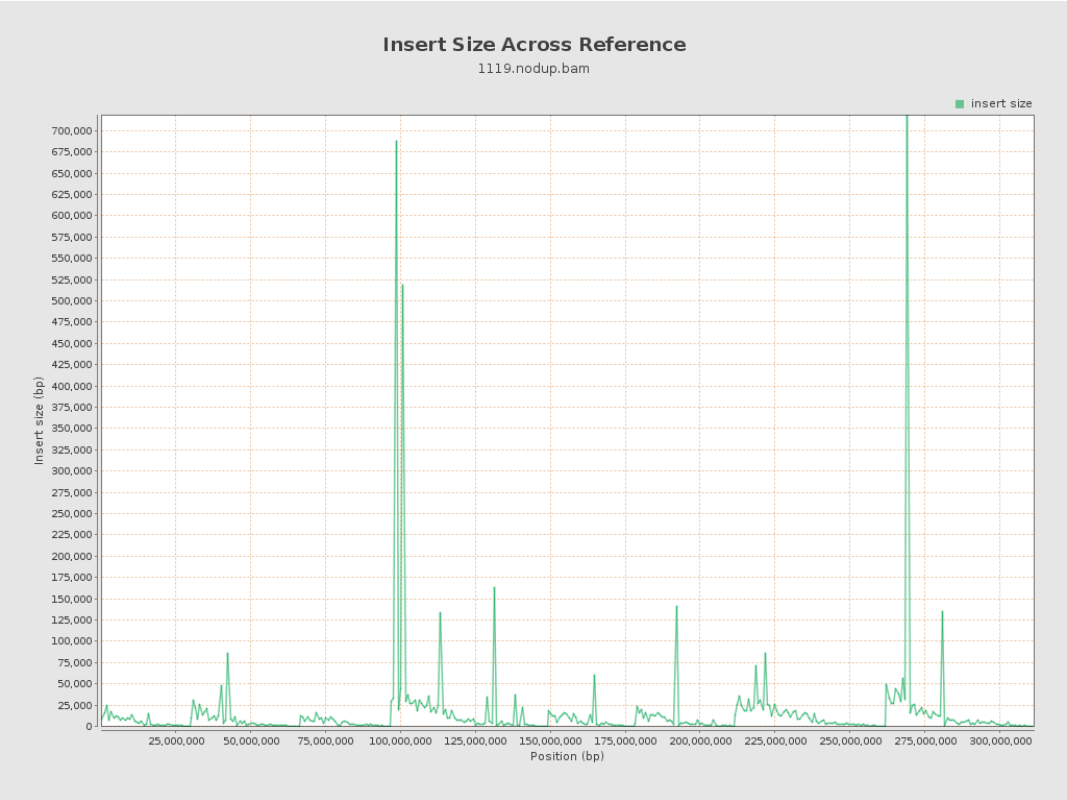
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram