Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1113
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1113 .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_478/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_478_S453_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_478/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_478_S453_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:30:08 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,496,693
Mapped reads	58,186,392 / 94.62%
Unmapped reads	3,310,301 / 5.38%
Mapped paired reads	58,186,392 / 94.62%
Mapped reads, first in pair	29,166,680 / 47.43%
Mapped reads, second in pair	29,019,712 / 47.19%
Mapped reads, both in pair	57,007,319 / 92.7%
Mapped reads, singletons	1,179,073 / 1.92%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	8,947,248 / 14.55%
Clipped reads	12,722,535 / 20.69%

2.2. ACGT Content

Number/percentage of A's	2,495,458,363 / 30.8%
Number/percentage of C's	1,558,757,130 / 19.24%
Number/percentage of T's	2,495,410,103 / 30.8%
Number/percentage of G's	1,552,341,061 / 19.16%
Number/percentage of N's	27,210 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	26.0648
Standard Deviation	217.2298

2.4. Mapping Quality

Mean Mapping Quality	43.56

2.5. Insert size

Mean	250,755.6
Standard Deviation	2,365,343.88
P25/Median/P75	375 / 489 / 641

2.6. Mismatches and indels

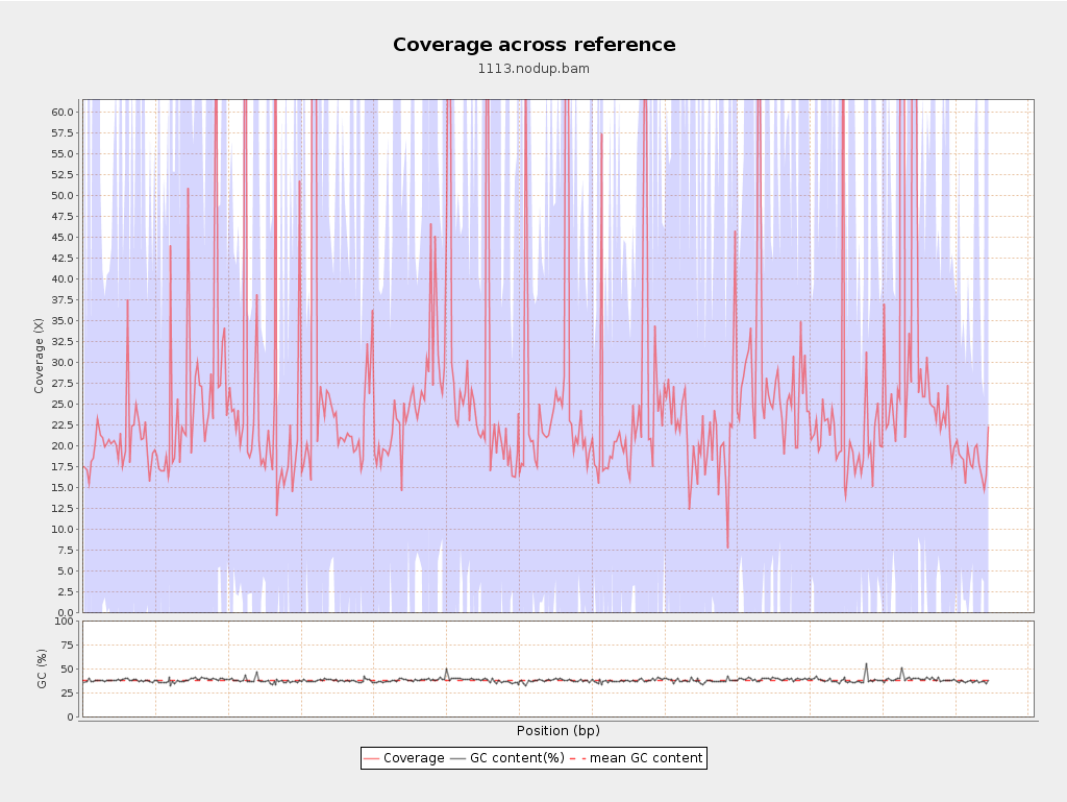
General error rate	2.36%
Mismatches	176,821,761
Insertions	5,464,033
Mapped reads with at least one insertion	8.45%
Deletions	5,619,375
Mapped reads with at least one deletion	8.59%
Homopolymer indels	56.3%

2.7. Chromosome stats

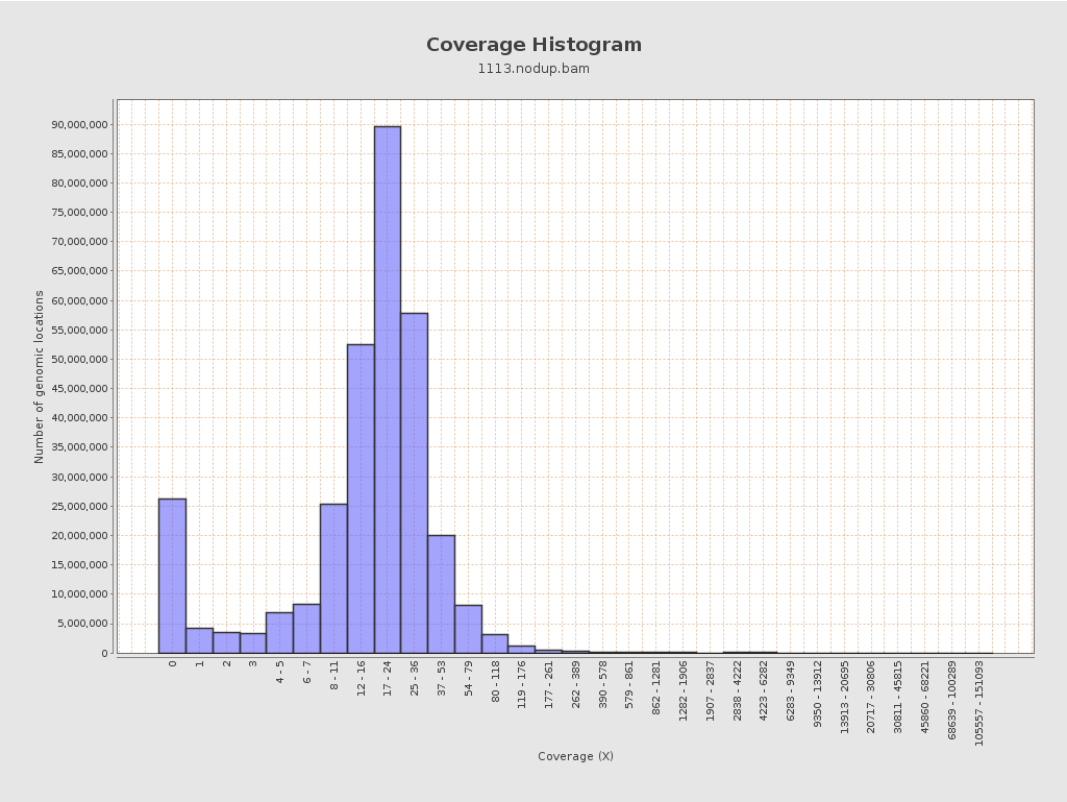
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	595231578	20.0251	58.9273

LT669789.1	36598175	999461912	27.3091	229.9675
LT669790.1	30422129	802957643	26.3939	200.6357
LT669791.1	52758100	1392785232	26.3995	191.6048
LT669792.1	28376109	718727567	25.3286	297.8166
LT669793.1	33388210	798601550	23.9187	117.4837
LT669794.1	50579949	1308412166	25.8682	205.9029
LT669795.1	49795044	1506698543	30.258	296.6343

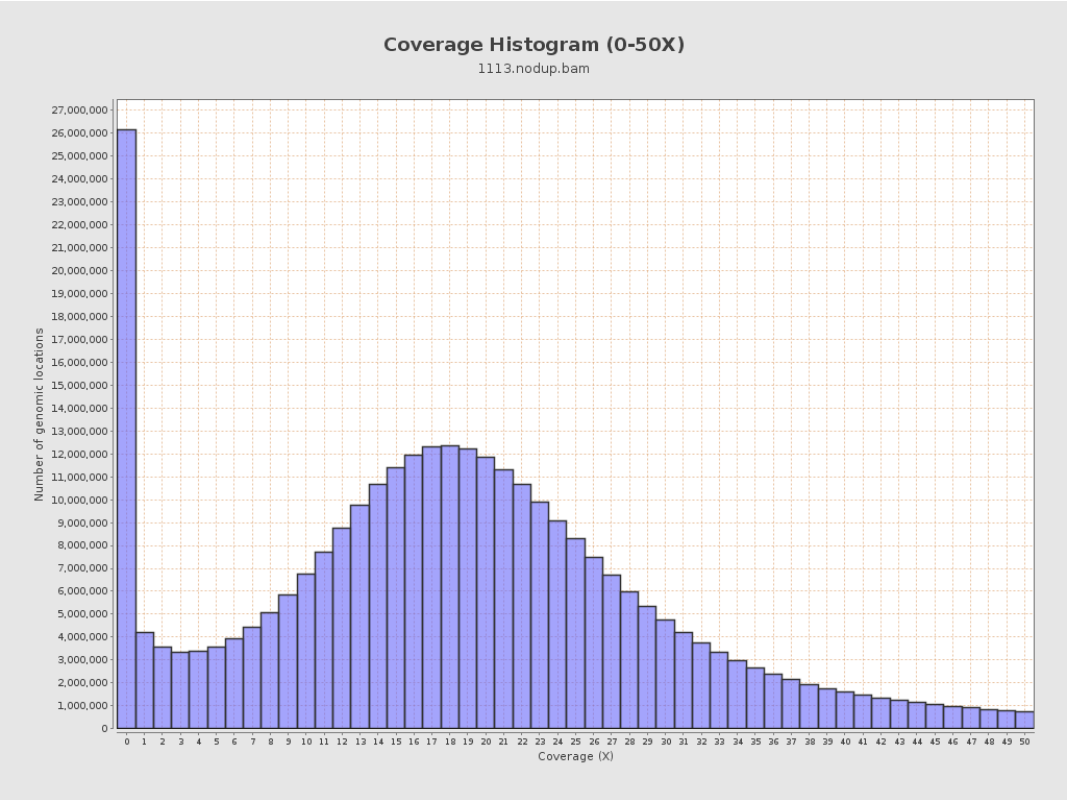
3. Results : Coverage across reference



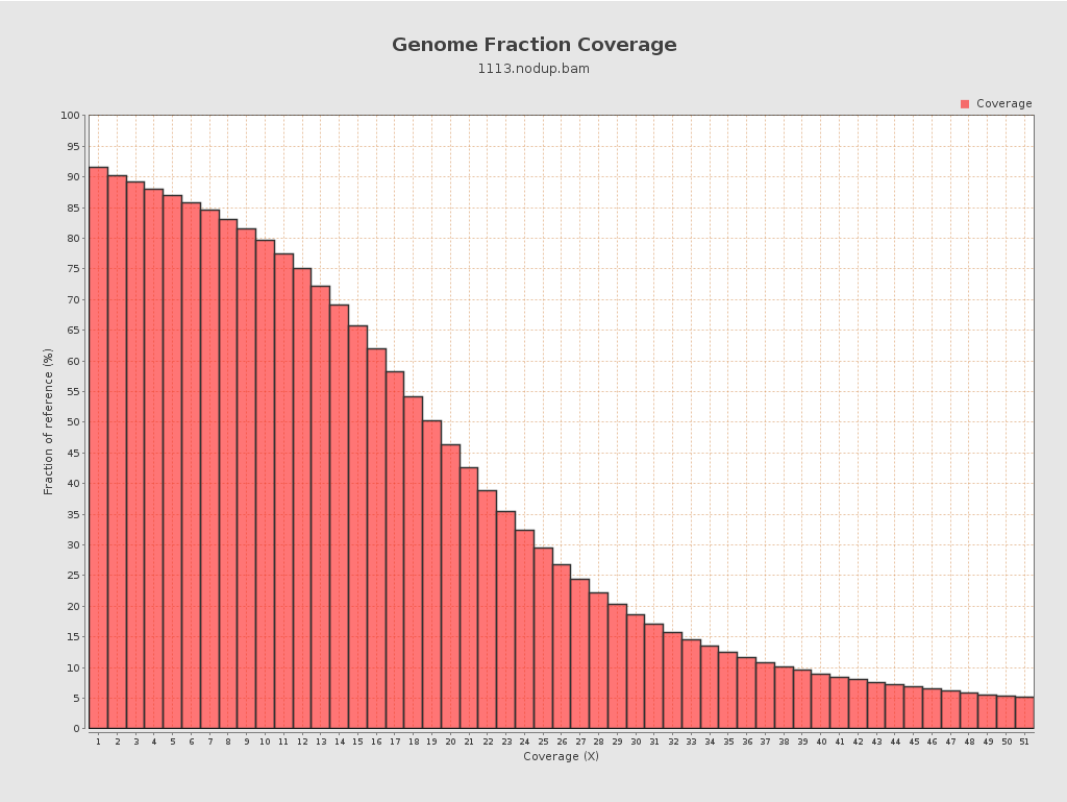
4. Results : Coverage Histogram



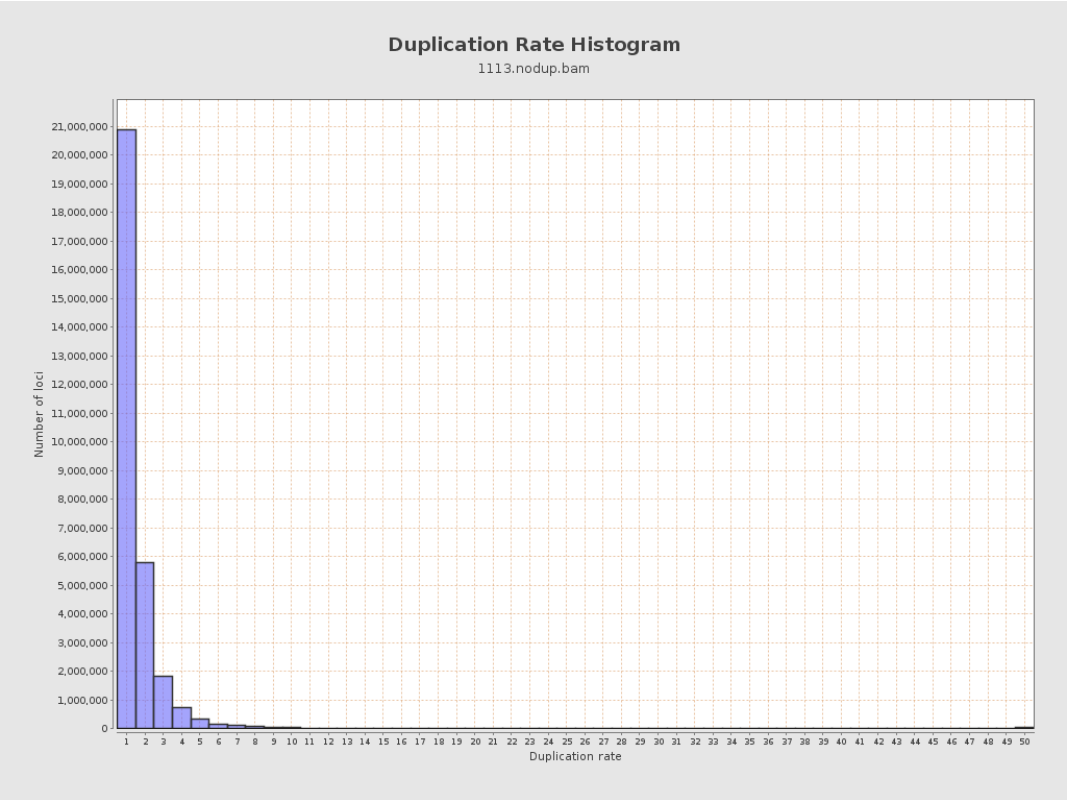
5. Results : Coverage Histogram (0-50X)



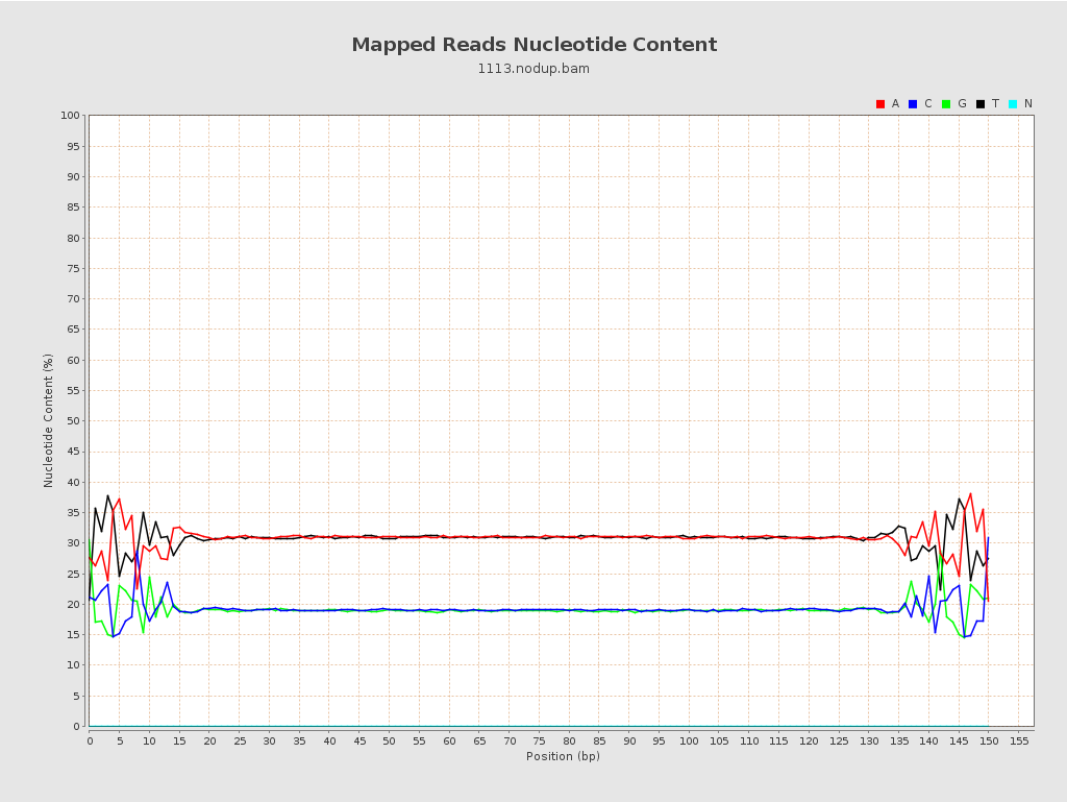
6. Results : Genome Fraction Coverage



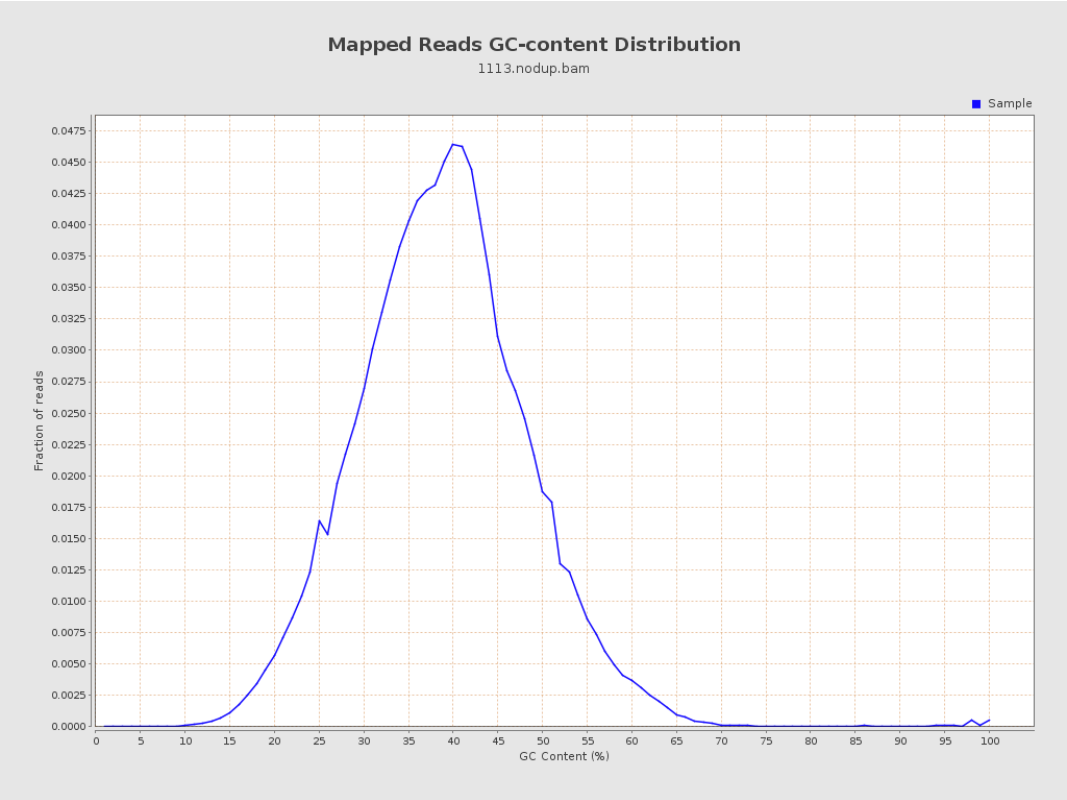
7. Results : Duplication Rate Histogram



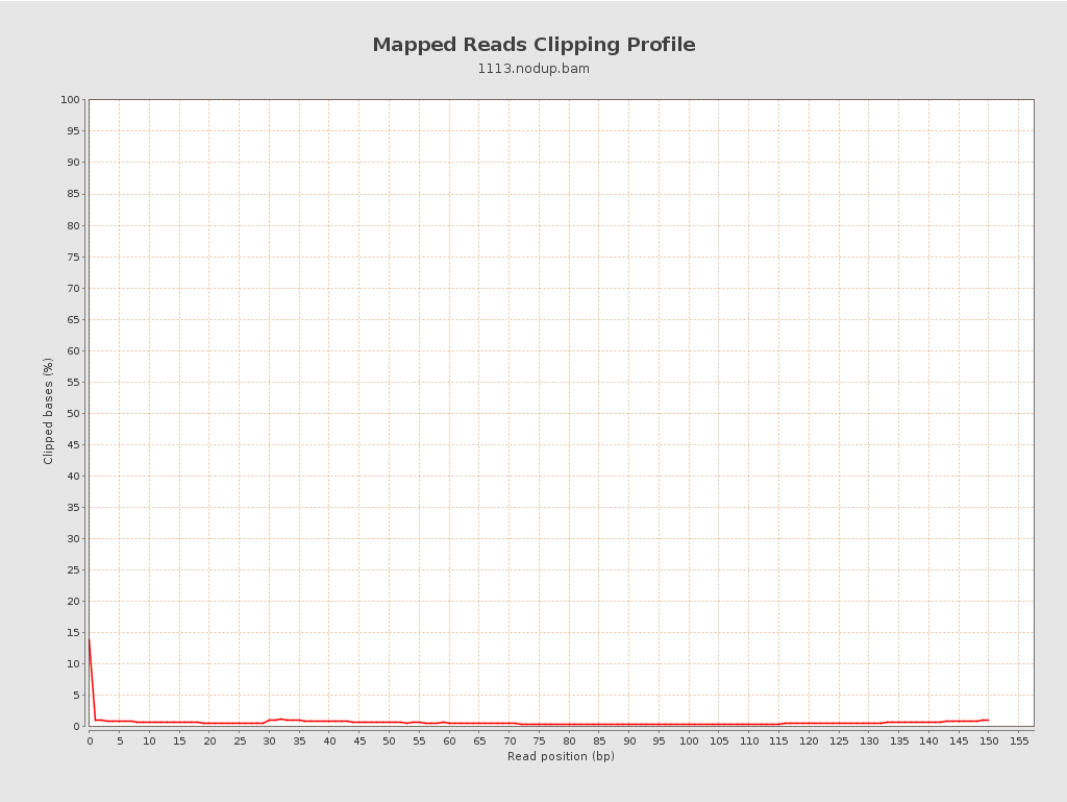
8. Results : Mapped Reads Nucleotide Content



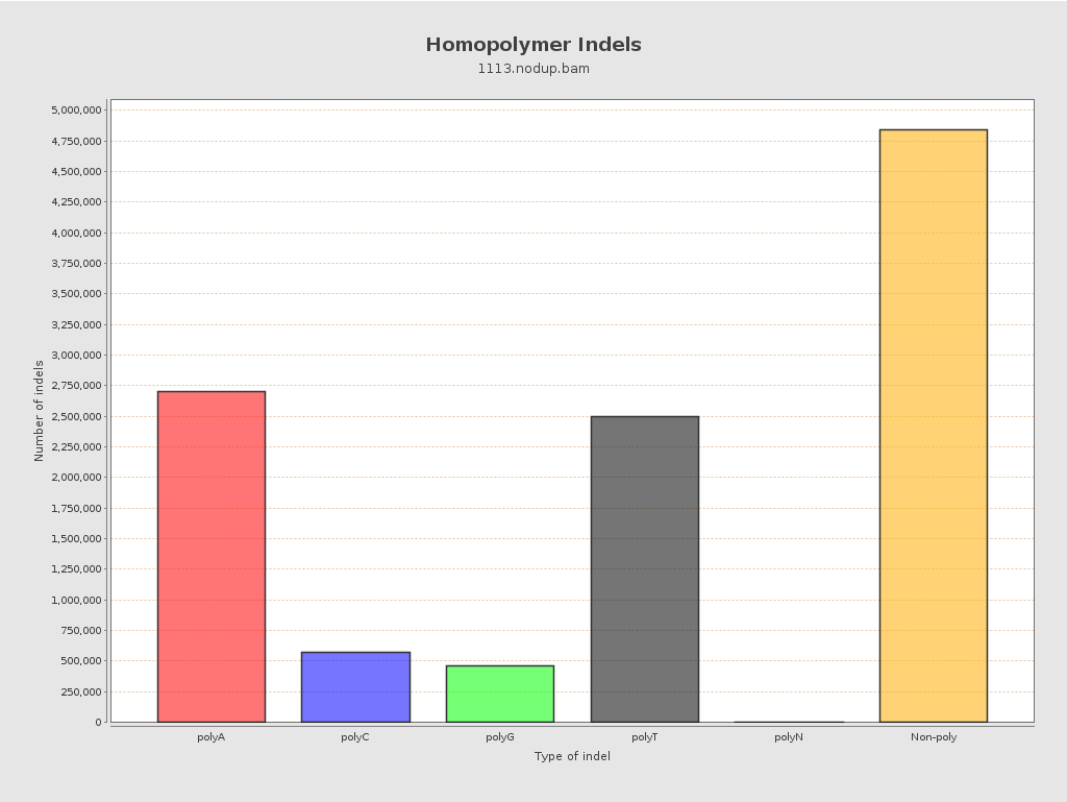
9. Results : Mapped Reads GC-content Distribution



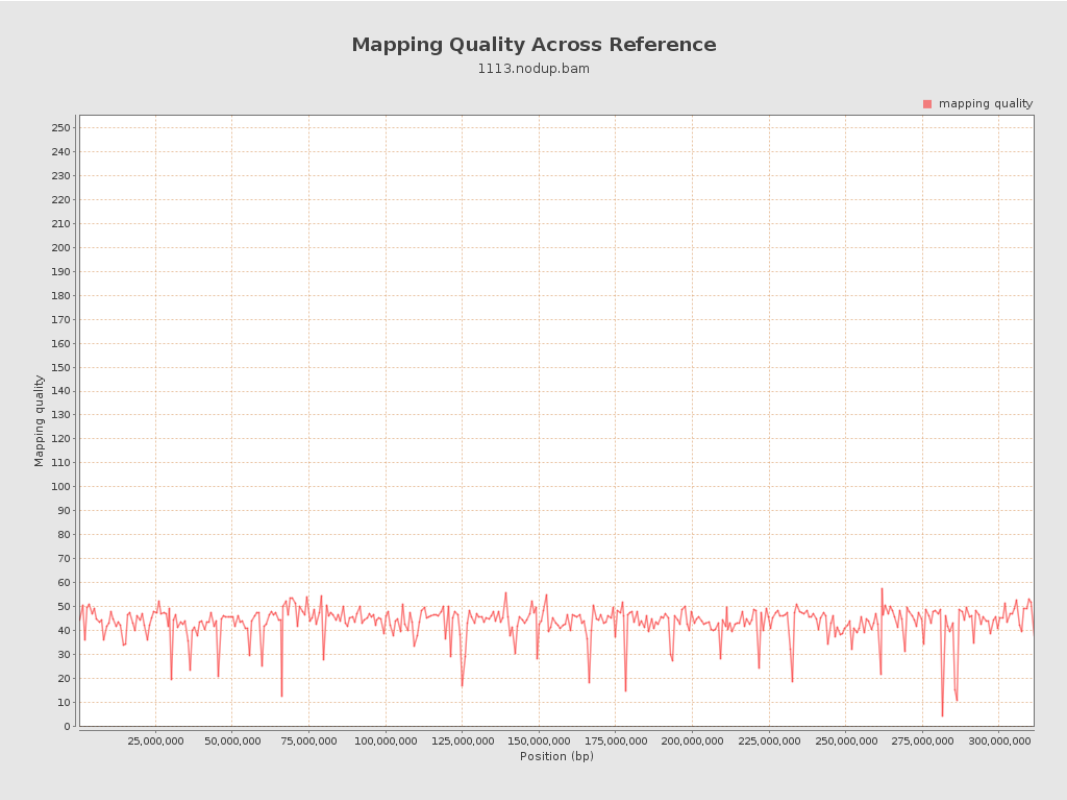
10. Results : Mapped Reads Clipping Profile



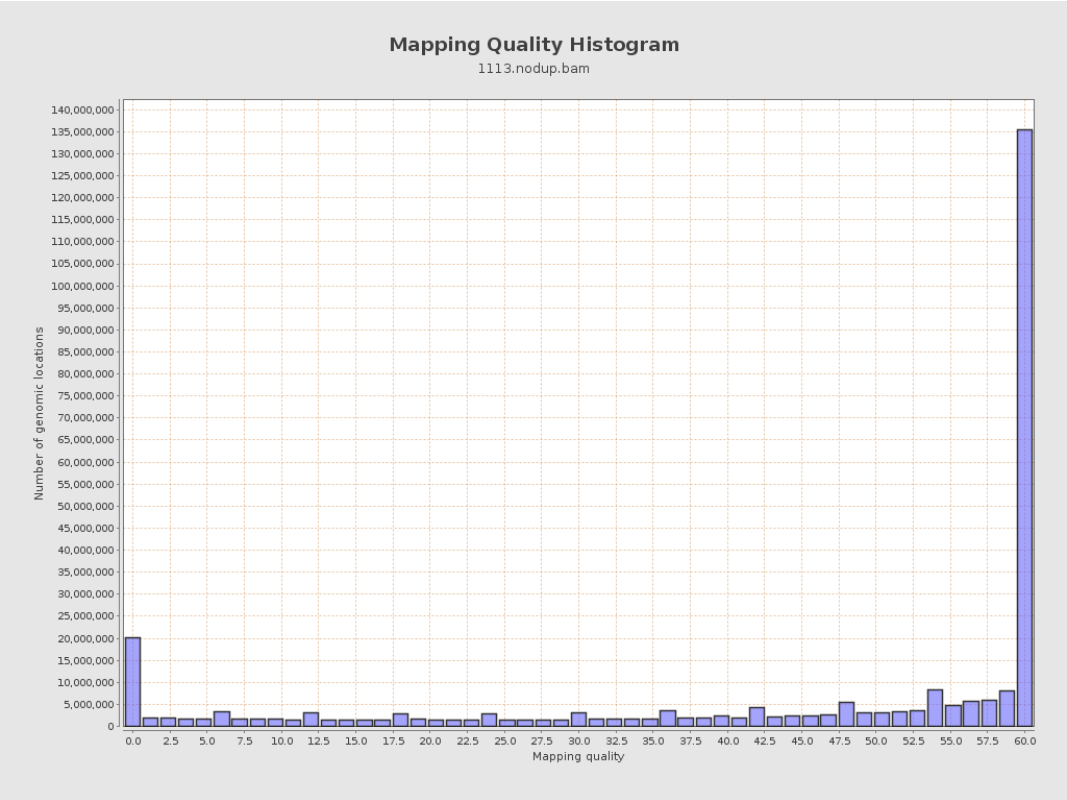
11. Results : Homopolymer Indels



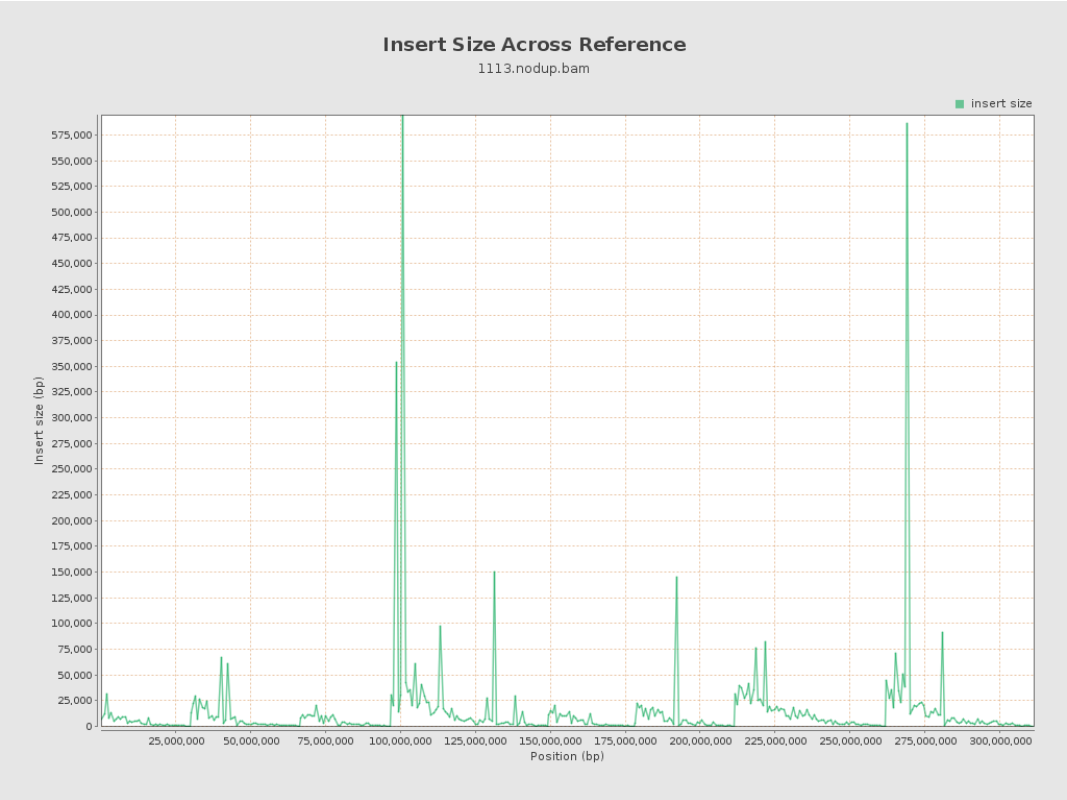
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram