Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1155
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1155 .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_139/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_139_S229_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_139/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_139_S229_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,467,941
Mapped reads	57,308,652 / 93.23%
Unmapped reads	4,159,289 / 6.77%
Mapped paired reads	57,308,652 / 93.23%
Mapped reads, first in pair	28,701,394 / 46.69%
Mapped reads, second in pair	28,607,258 / 46.54%
Mapped reads, both in pair	55,970,207 / 91.06%
Mapped reads, singletons	1,338,445 / 2.18%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	9,341,557 / 15.2%
Clipped reads	12,984,184 / 21.12%

2.2. ACGT Content

Number/percentage of A's	2,446,324,099 / 30.86%
Number/percentage of C's	1,517,629,848 / 19.15%
Number/percentage of T's	2,448,293,109 / 30.89%
Number/percentage of G's	1,514,050,356 / 19.1%
Number/percentage of N's	33,112 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	25.4993
Standard Deviation	215.6135

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Insert size

Mean	235,056.78
Standard Deviation	2,301,574.64
P25/Median/P75	318 / 419 / 553

2.6. Mismatches and indels

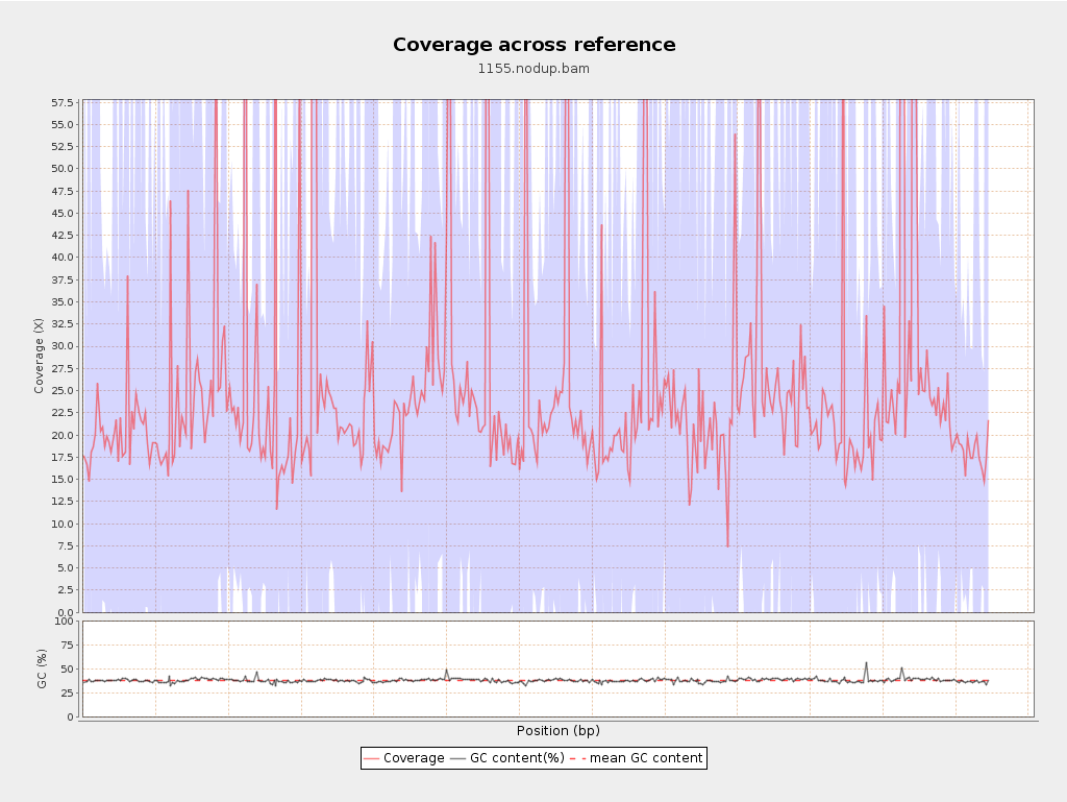
General error rate	2.33%
Mismatches	170,133,162
Insertions	5,444,822
Mapped reads with at least one insertion	8.52%
Deletions	5,474,453
Mapped reads with at least one deletion	8.49%
Homopolymer indels	56.84%

2.7. Chromosome stats

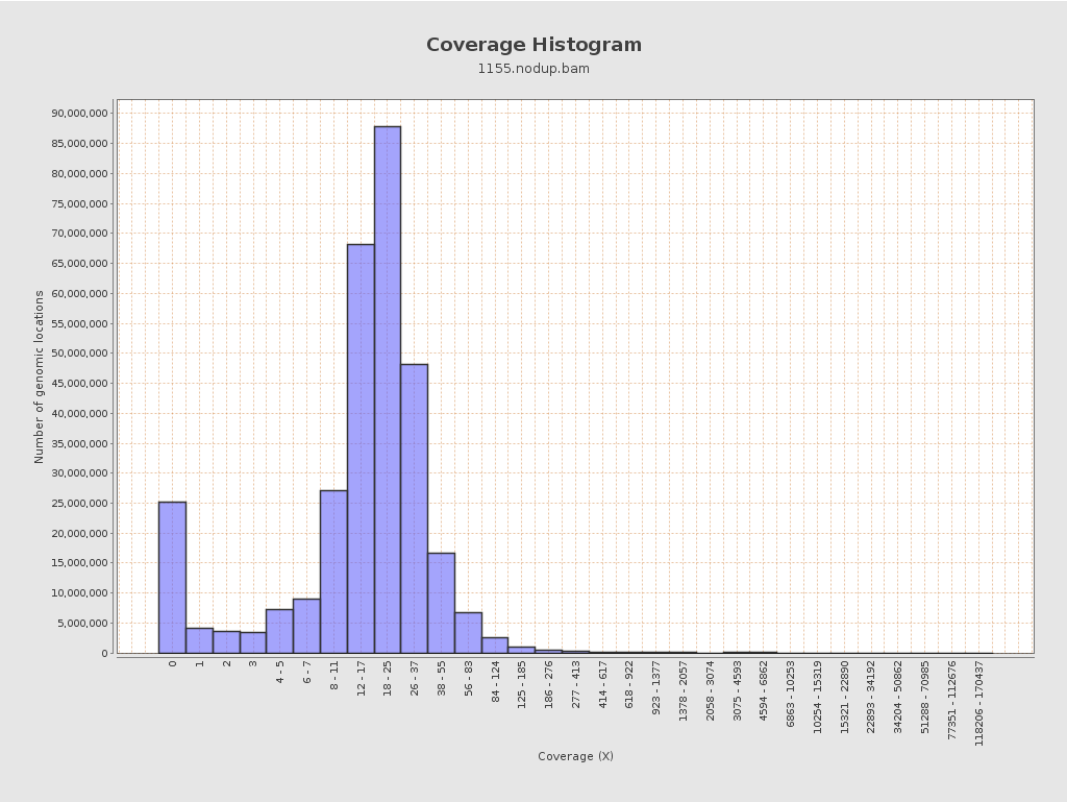
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	589392718	19.8286	68.8602

LT669789.1	36598175	976453121	26.6804	238.016
LT669790.1	30422129	837557332	27.5312	247.1606
LT669791.1	52758100	1352335001	25.6327	207.4329
LT669792.1	28376109	701065798	24.7062	255.4496
LT669793.1	33388210	791379681	23.7024	155.1479
LT669794.1	50579949	1265321013	25.0163	196.3183
LT669795.1	49795044	1433143191	28.7808	266.5775

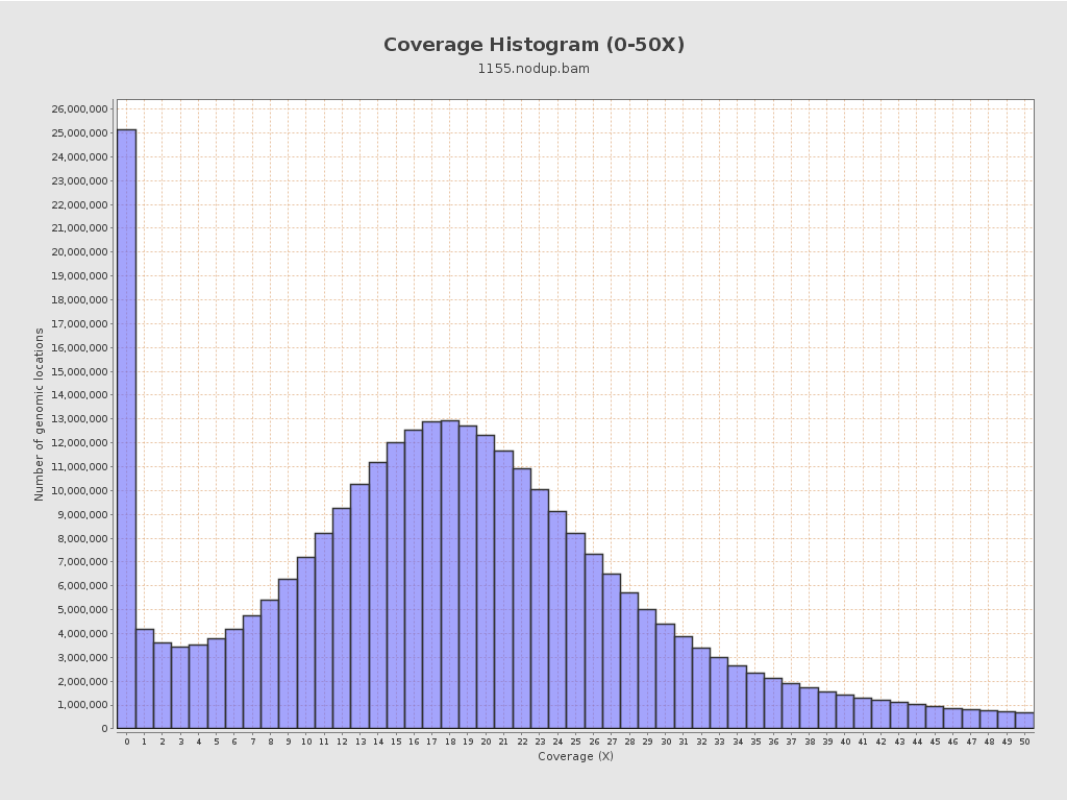
3. Results : Coverage across reference



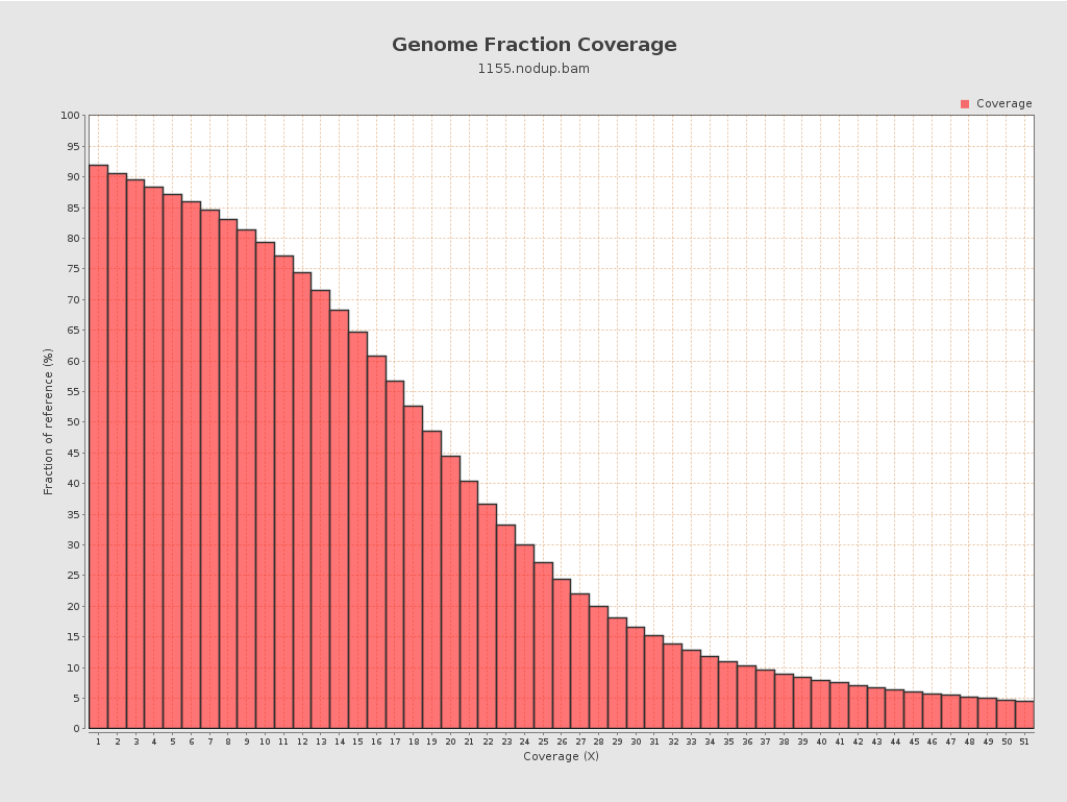
4. Results : Coverage Histogram



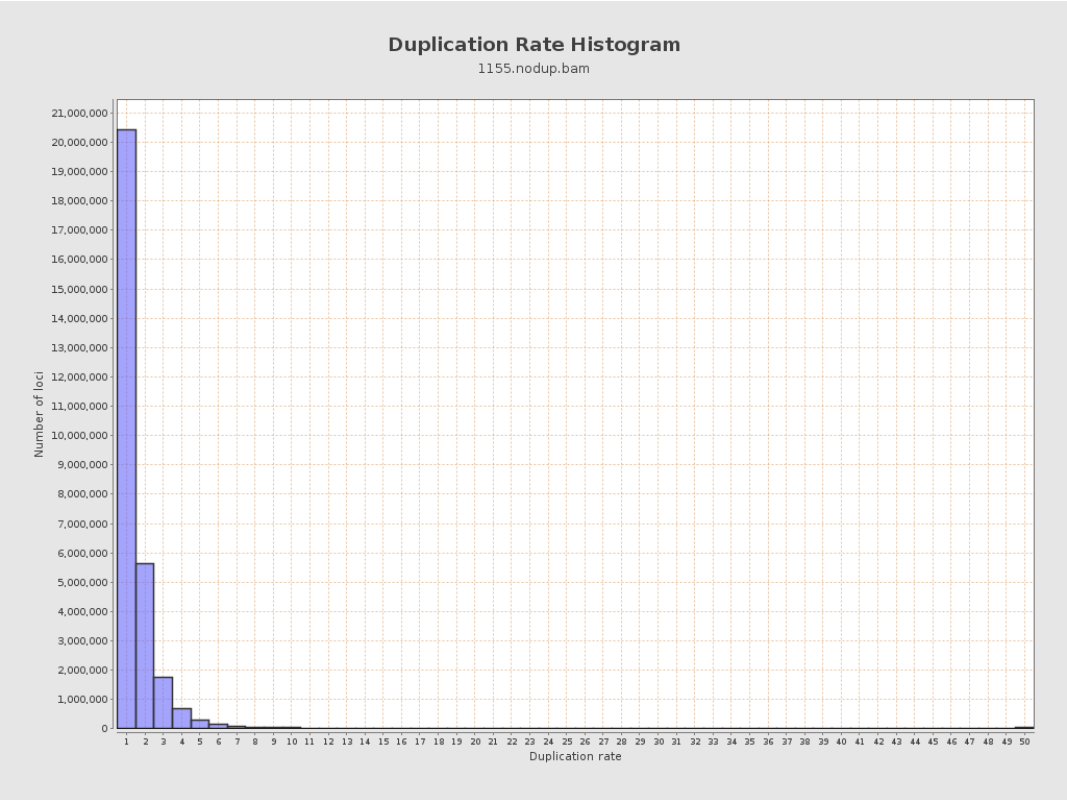
5. Results : Coverage Histogram (0-50X)



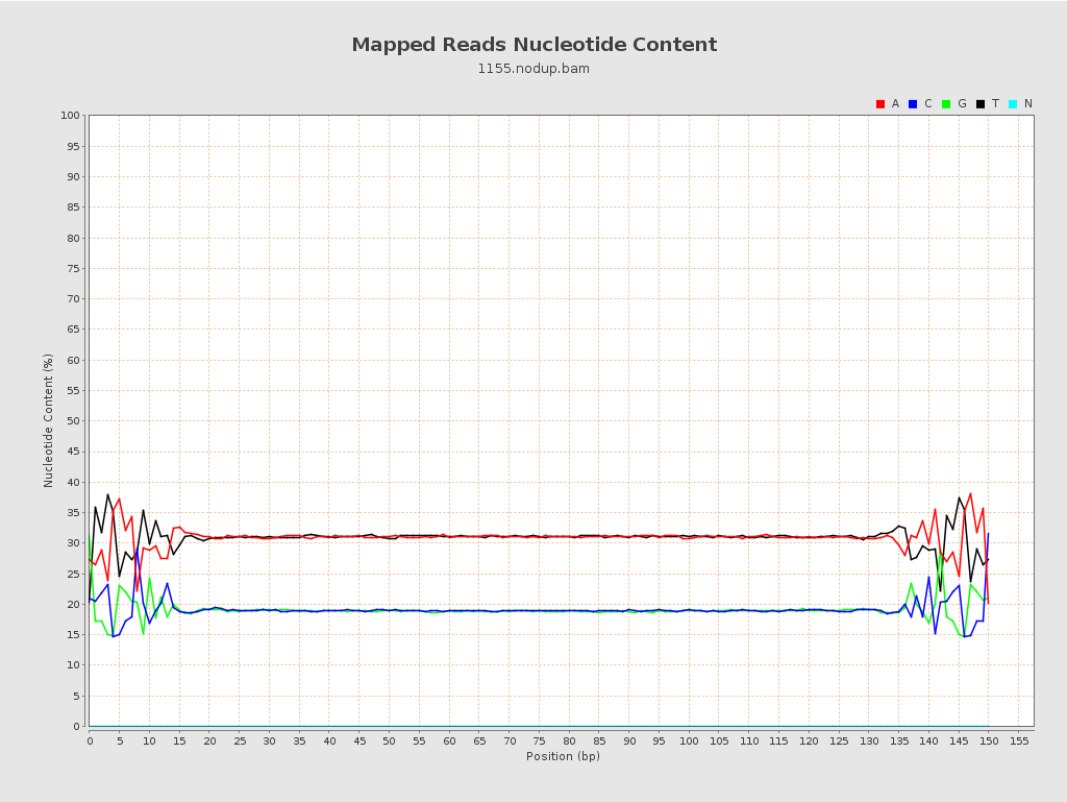
6. Results : Genome Fraction Coverage



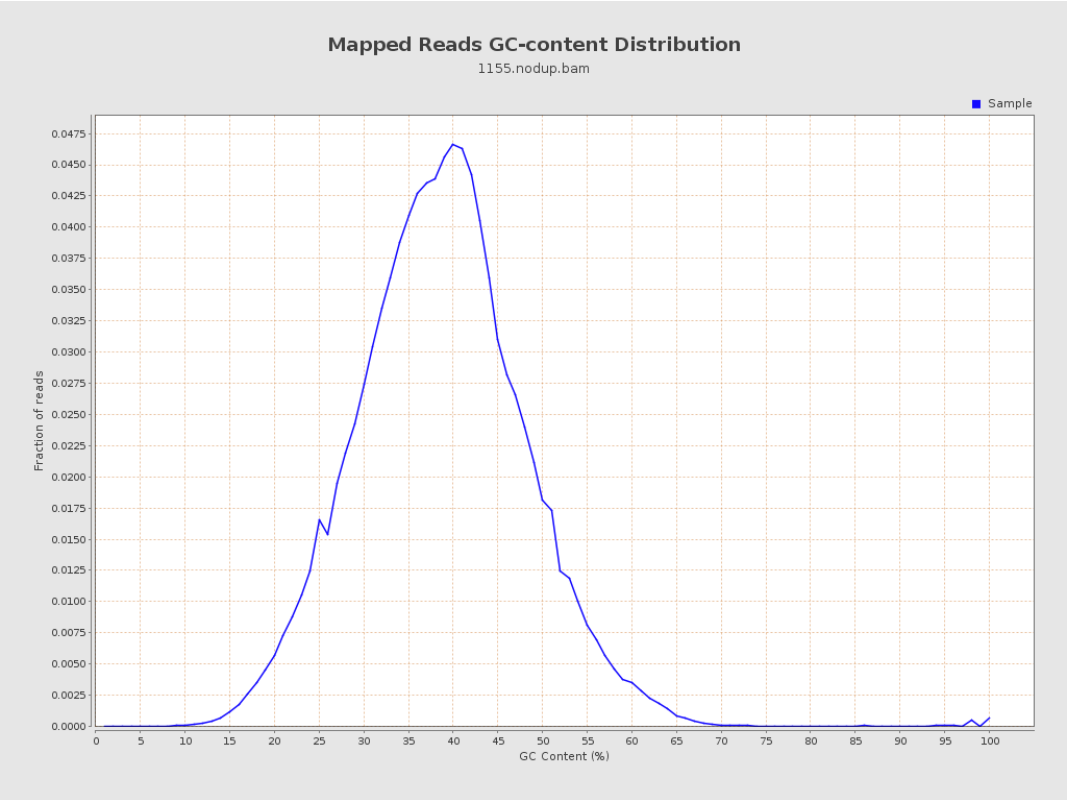
7. Results : Duplication Rate Histogram



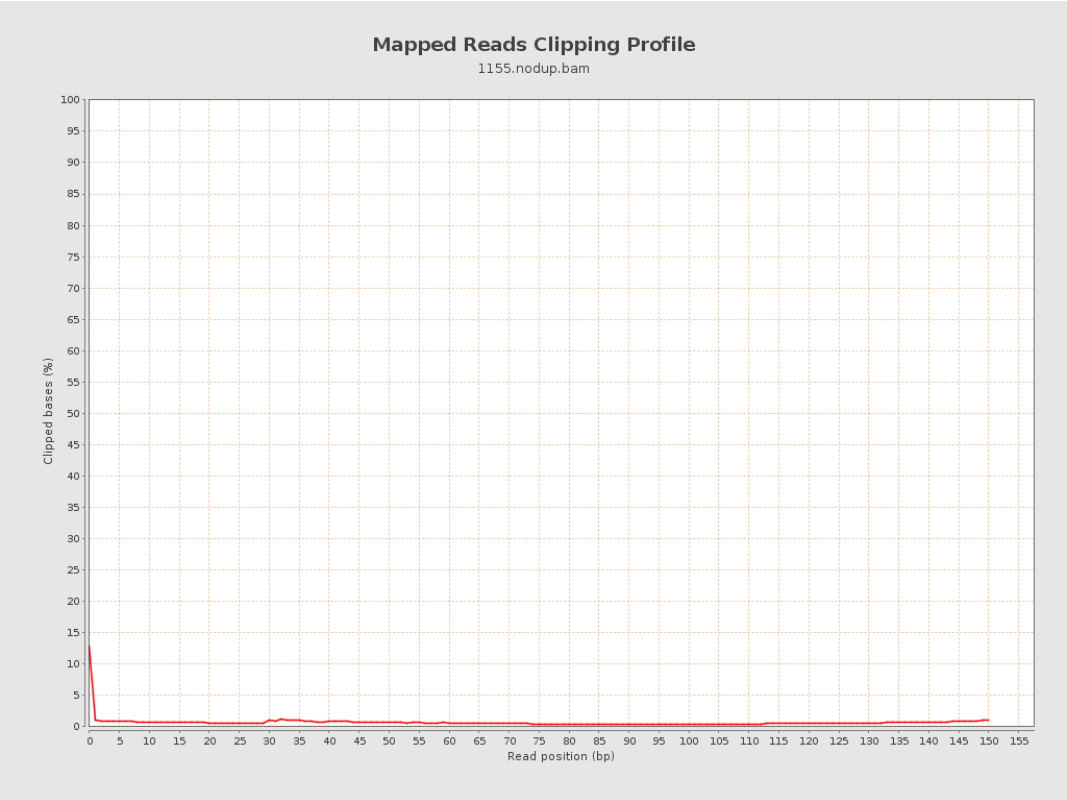
8. Results : Mapped Reads Nucleotide Content



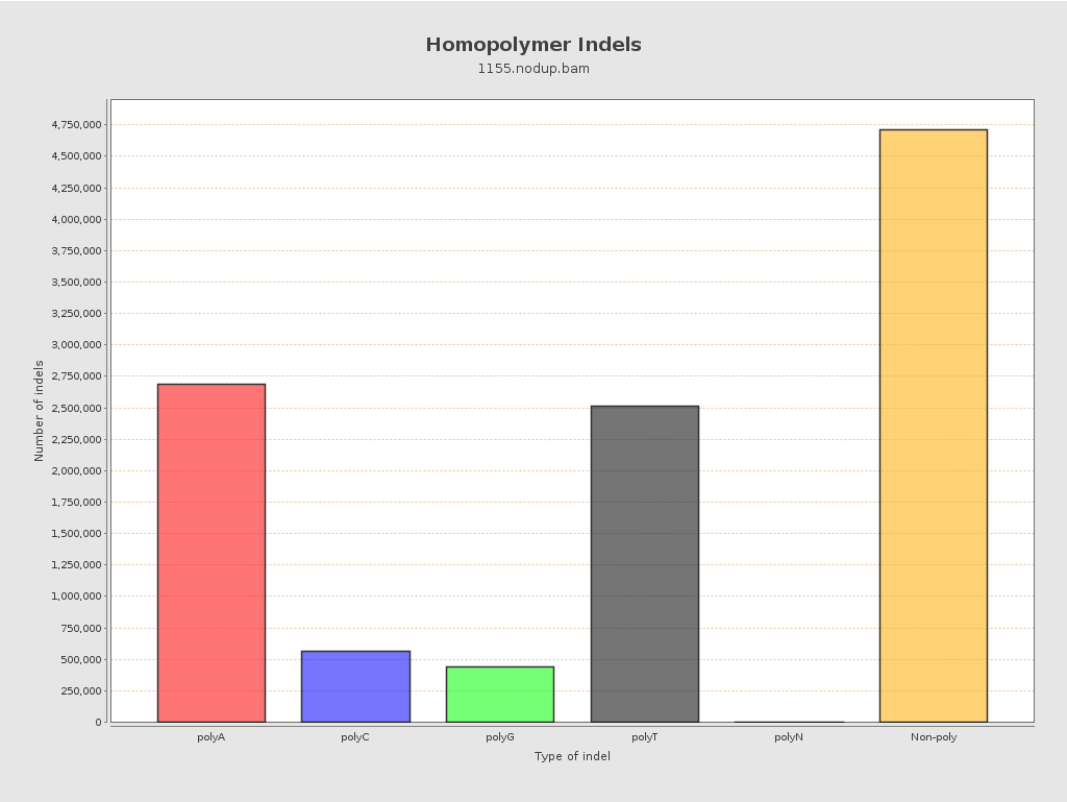
9. Results : Mapped Reads GC-content Distribution



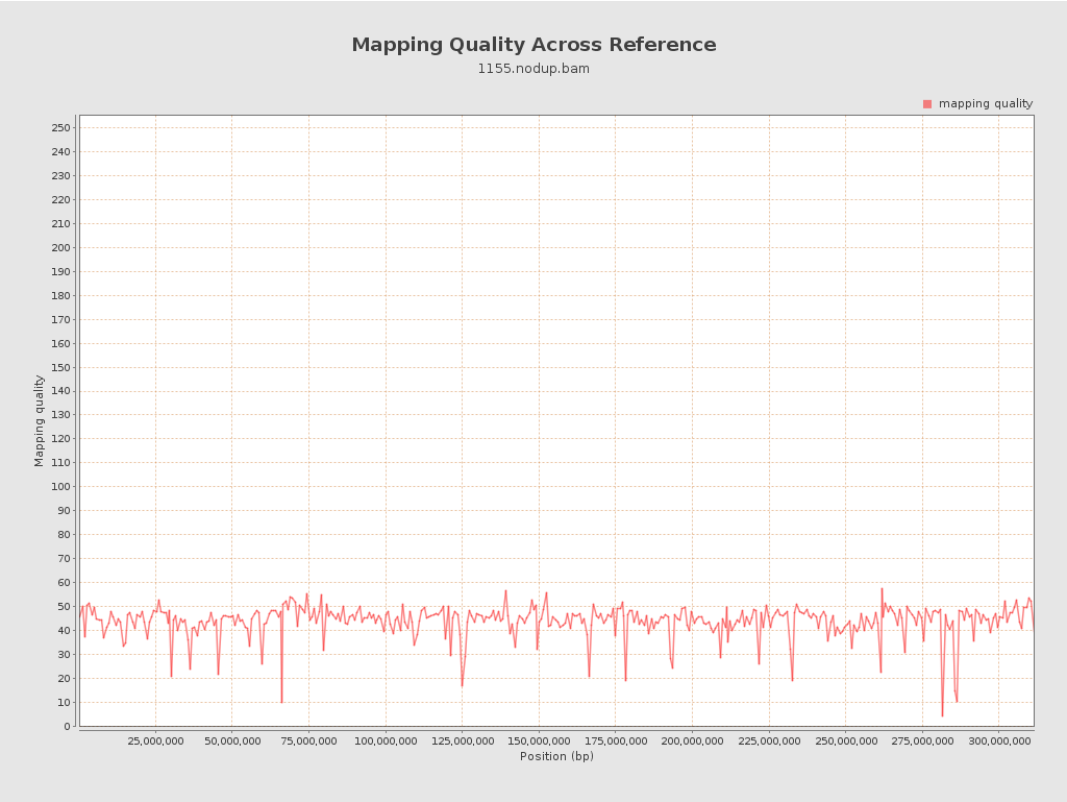
10. Results : Mapped Reads Clipping Profile



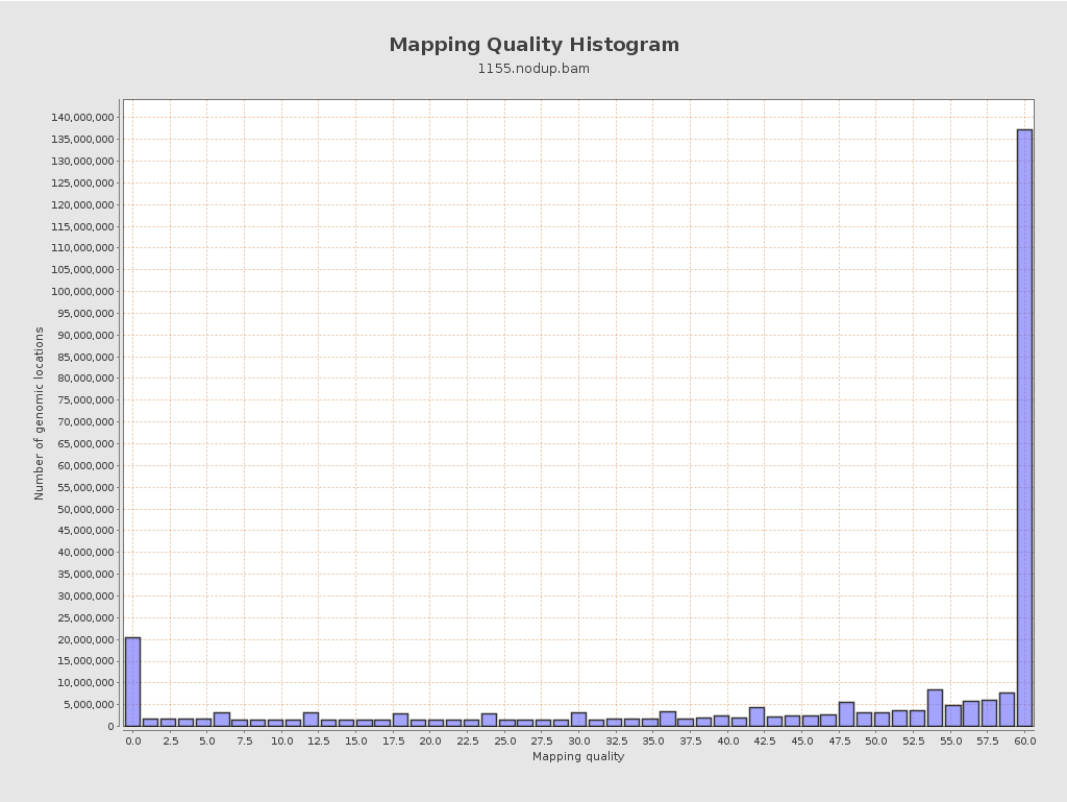
11. Results : Homopolymer Indels



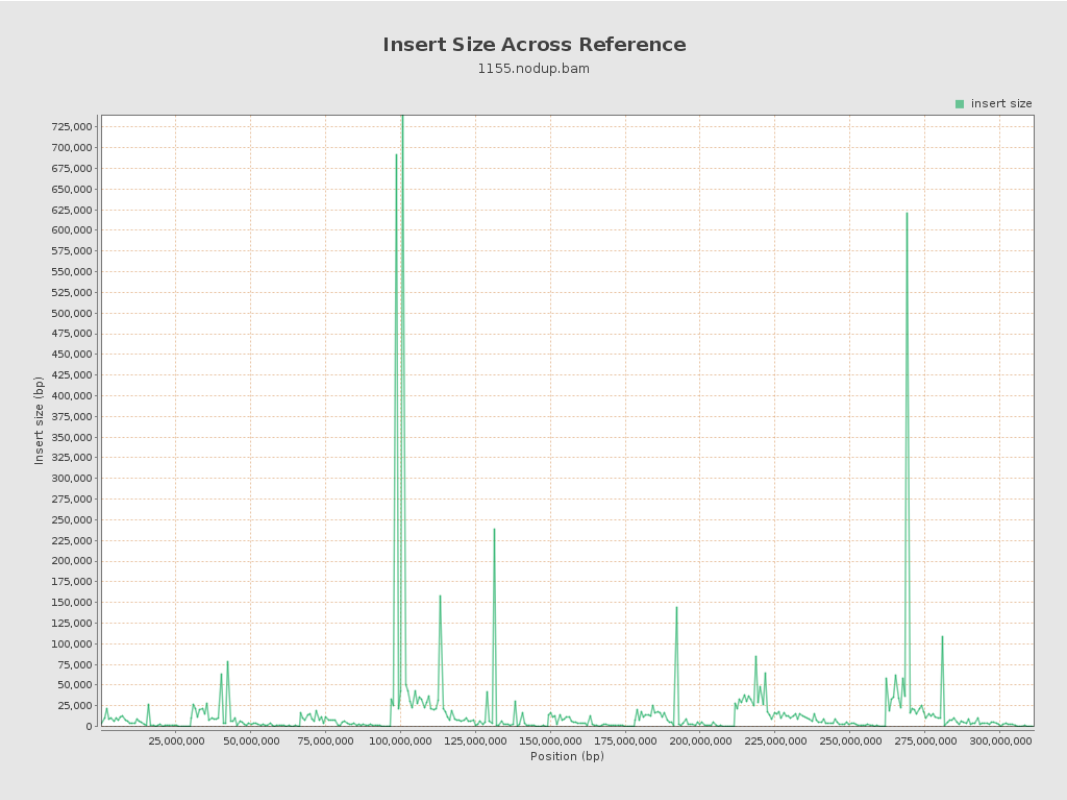
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram