Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1180
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1180 .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_443/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_443_S418_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_443/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_443_S418_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	62,237,036
Mapped reads	57,259,150 / 92%
Unmapped reads	4,977,886 / 8%
Mapped paired reads	57,259,150 / 92%
Mapped reads, first in pair	28,681,508 / 46.08%
Mapped reads, second in pair	28,577,642 / 45.92%
Mapped reads, both in pair	55,567,383 / 89.28%
Mapped reads, singletons	1,691,767 / 2.72%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	9,929,778 / 15.95%
Clipped reads	13,366,090 / 21.48%

2.2. ACGT Content

Number/percentage of A's	2,424,656,431 / 30.82%
Number/percentage of C's	1,509,024,260 / 19.18%
Number/percentage of T's	2,430,486,278 / 30.89%
Number/percentage of G's	1,503,877,730 / 19.11%
Number/percentage of N's	26,915 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	25.3109
Standard Deviation	241.1213

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Insert size

Mean	262,942.67
Standard Deviation	2,470,562.47
P25/Median/P75	346 / 455 / 595

2.6. Mismatches and indels

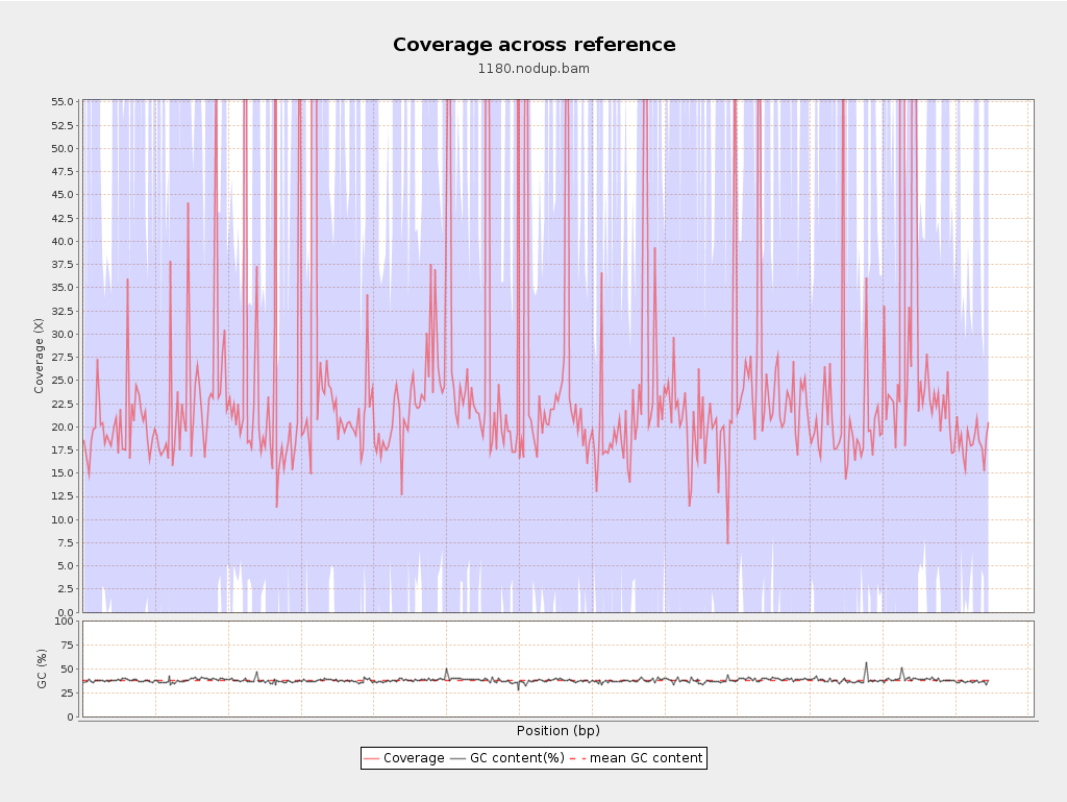
General error rate	2.32%
Mismatches	166,663,195
Insertions	5,616,029
Mapped reads with at least one insertion	8.75%
Deletions	5,343,645
Mapped reads with at least one deletion	8.28%
Homopolymer indels	57.11%

2.7. Chromosome stats

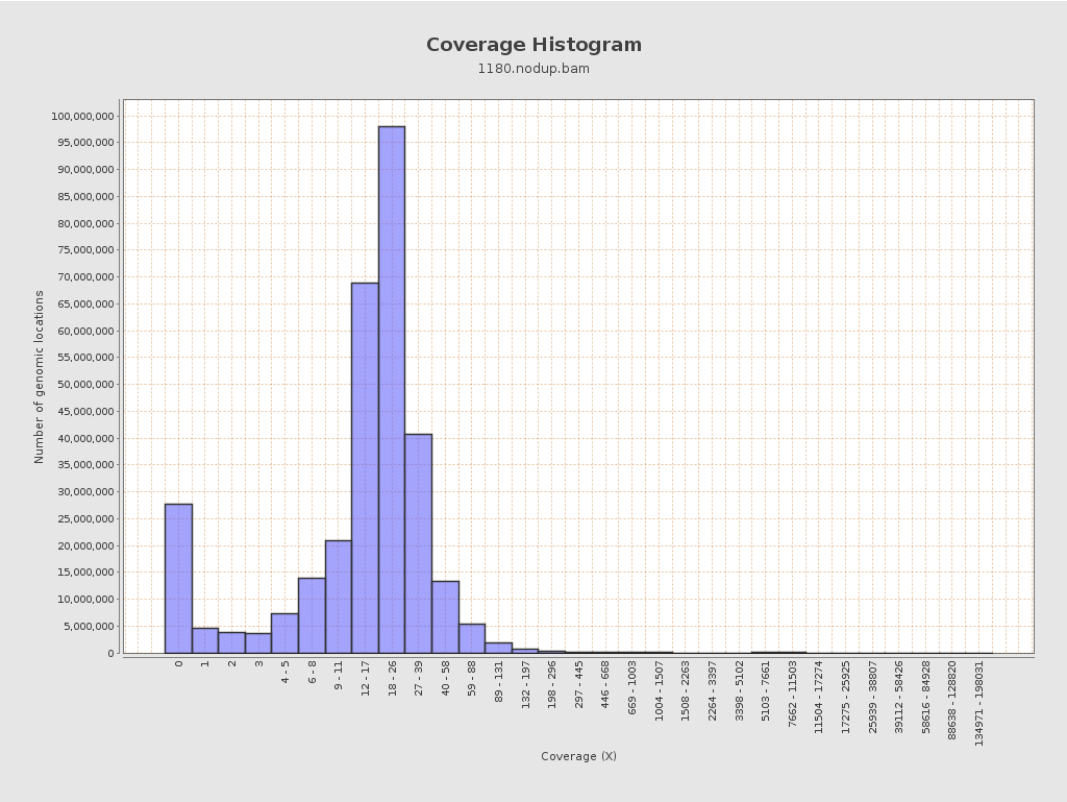
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	588061654	19.7838	90.9622

LT669789.1	36598175	931326214	25.4473	257.1057
LT669790.1	30422129	912912495	30.0082	327.3474
LT669791.1	52758100	1329549481	25.2009	251.9484
LT669792.1	28376109	708409707	24.965	240.9426
LT669793.1	33388210	764009073	22.8826	157.5858
LT669794.1	50579949	1202138921	23.7671	194.5609
LT669795.1	49795044	1451542049	29.1503	298.9708

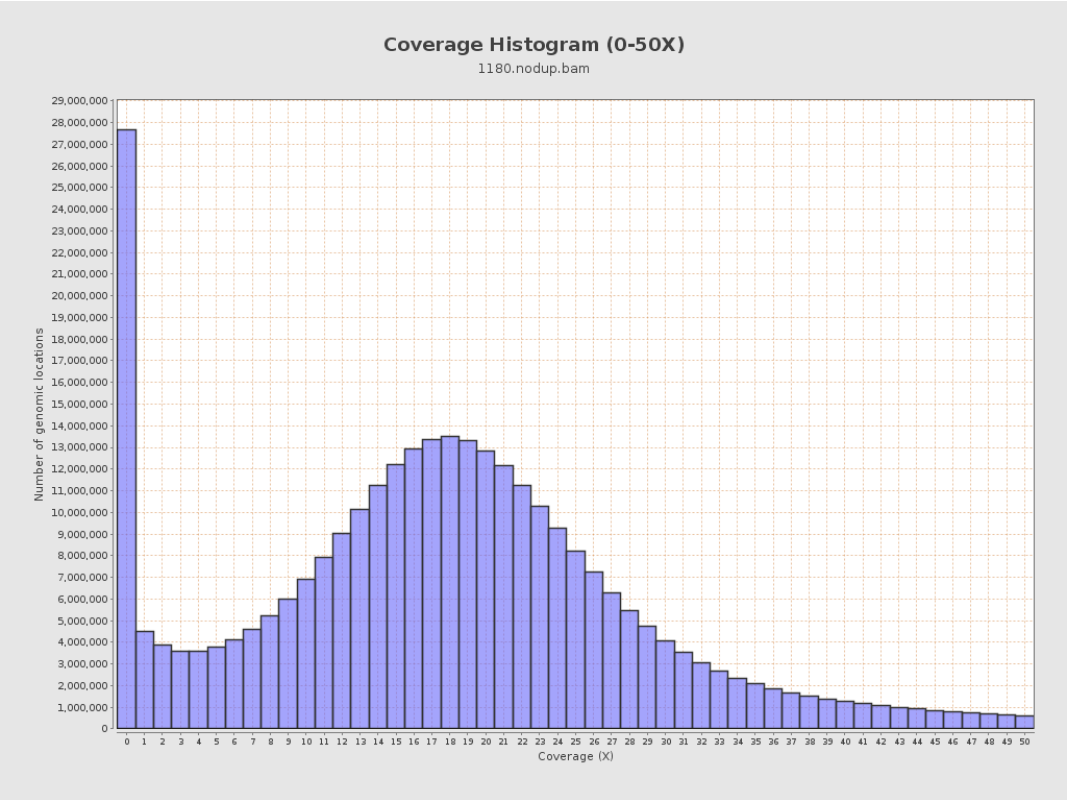
3. Results : Coverage across reference



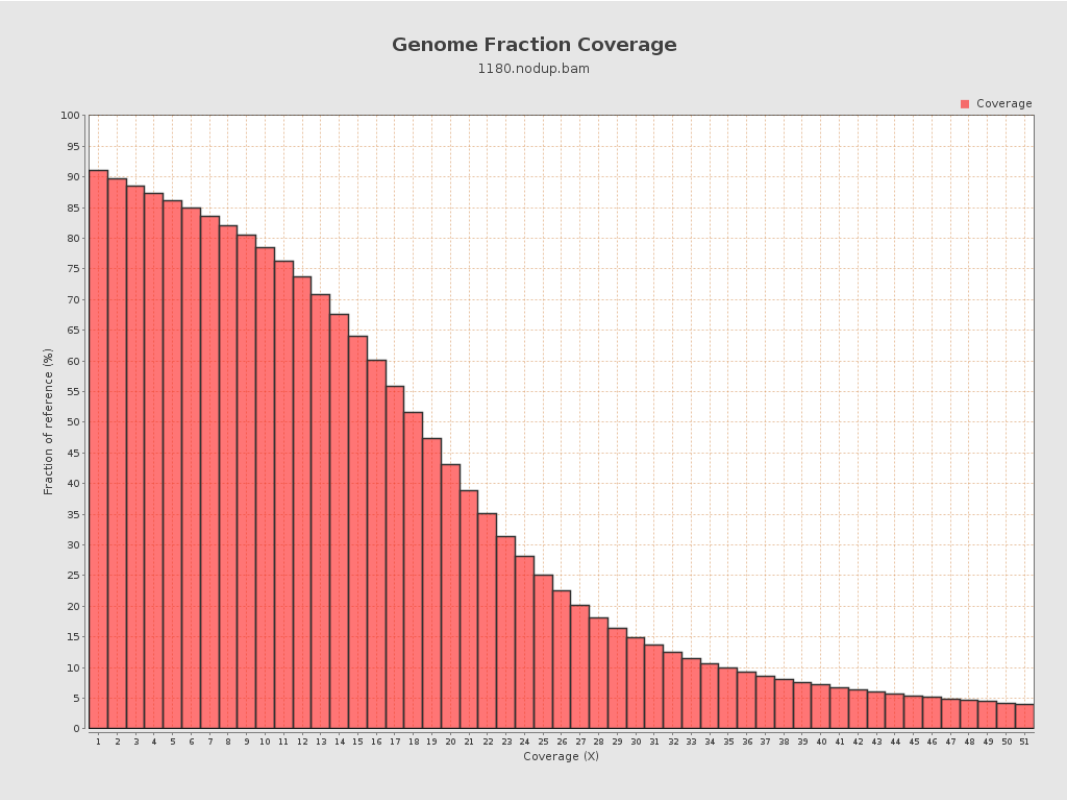
4. Results : Coverage Histogram



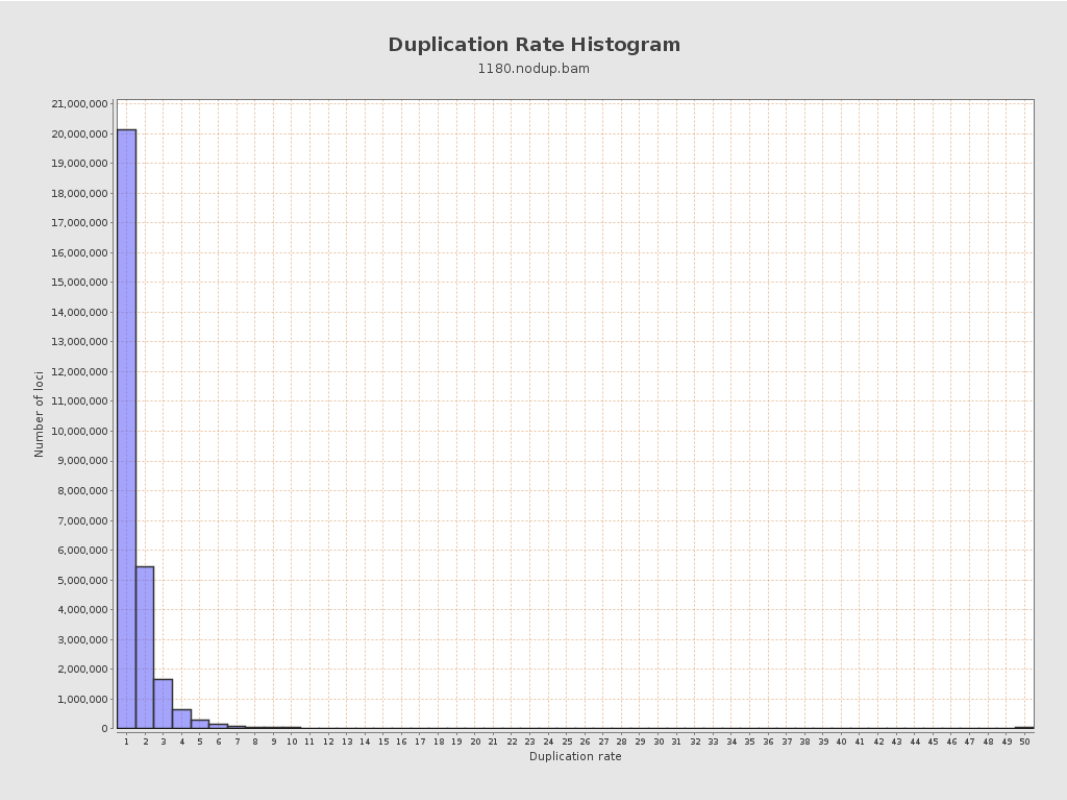
5. Results : Coverage Histogram (0-50X)



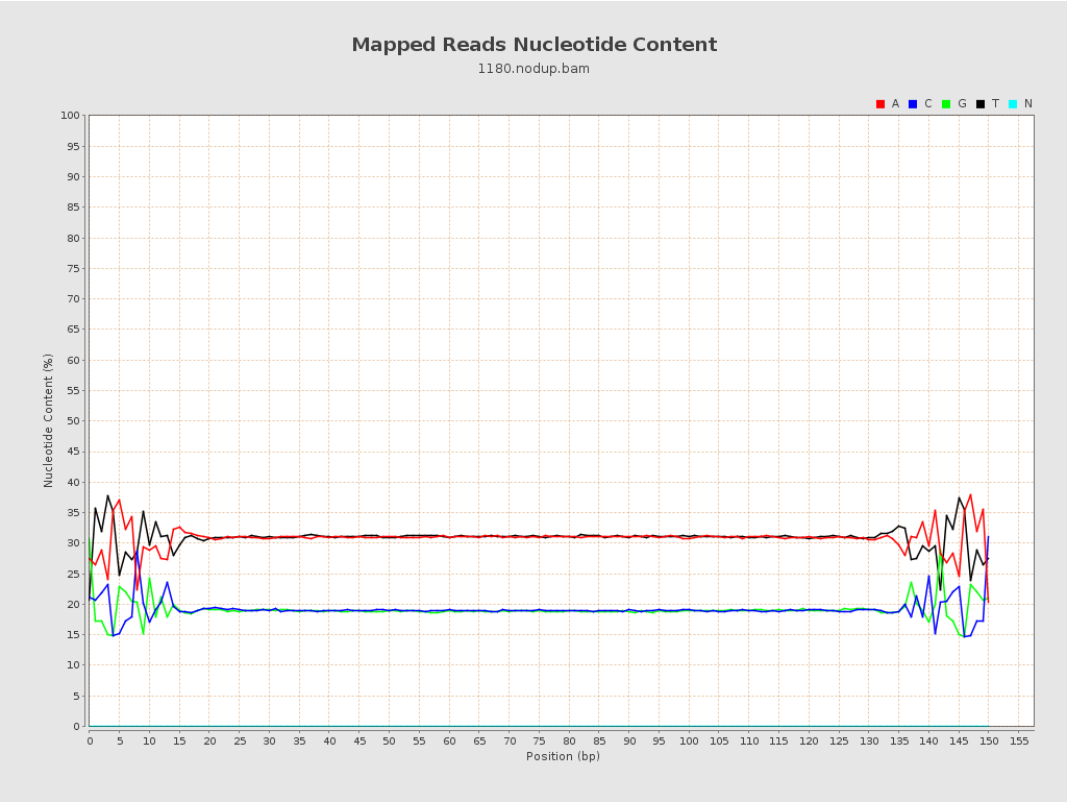
6. Results : Genome Fraction Coverage



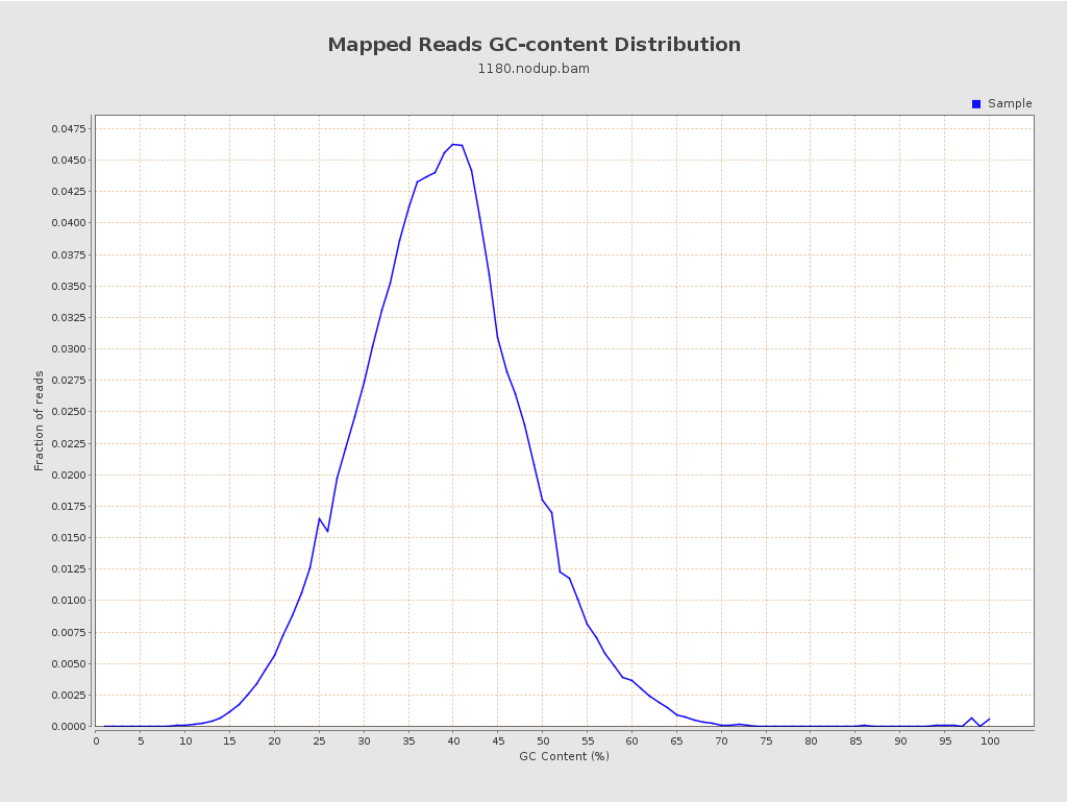
7. Results : Duplication Rate Histogram



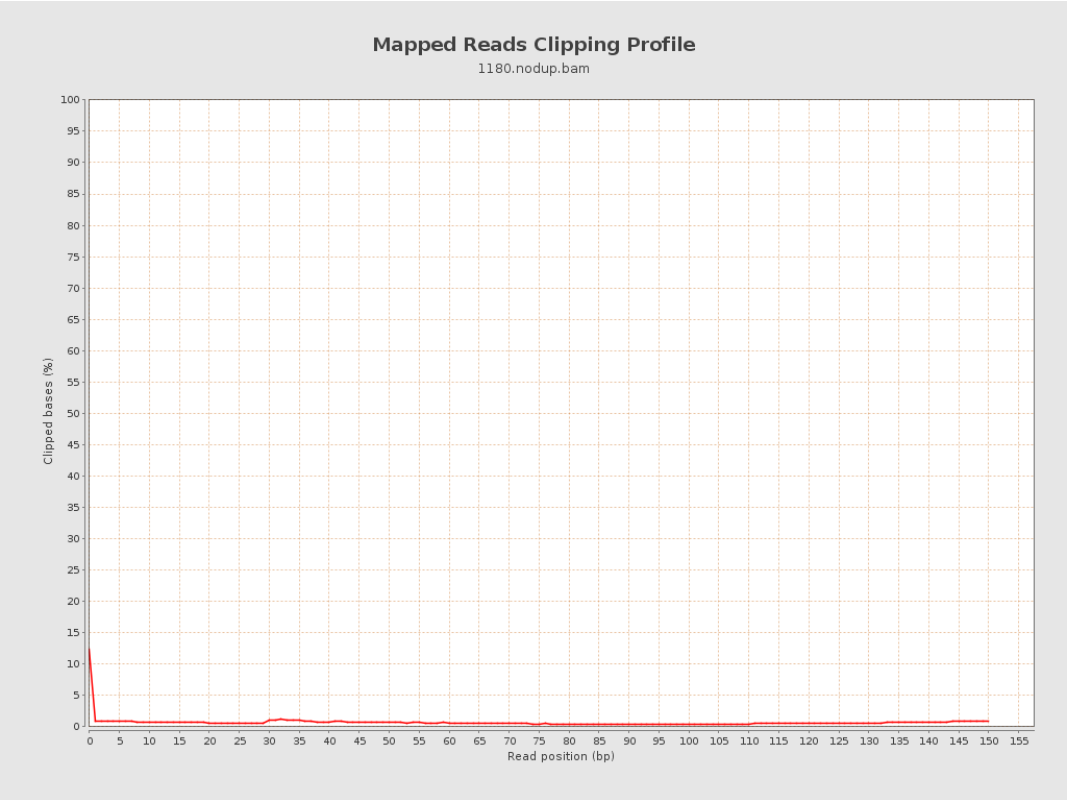
8. Results : Mapped Reads Nucleotide Content



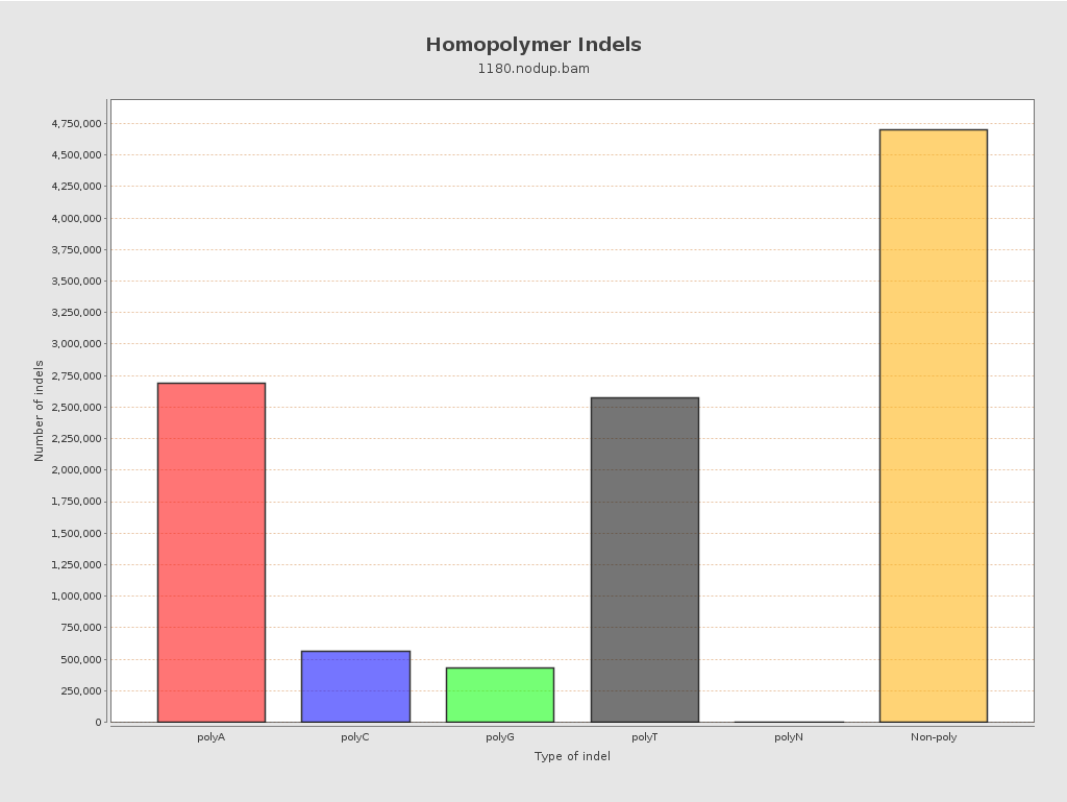
9. Results : Mapped Reads GC-content Distribution



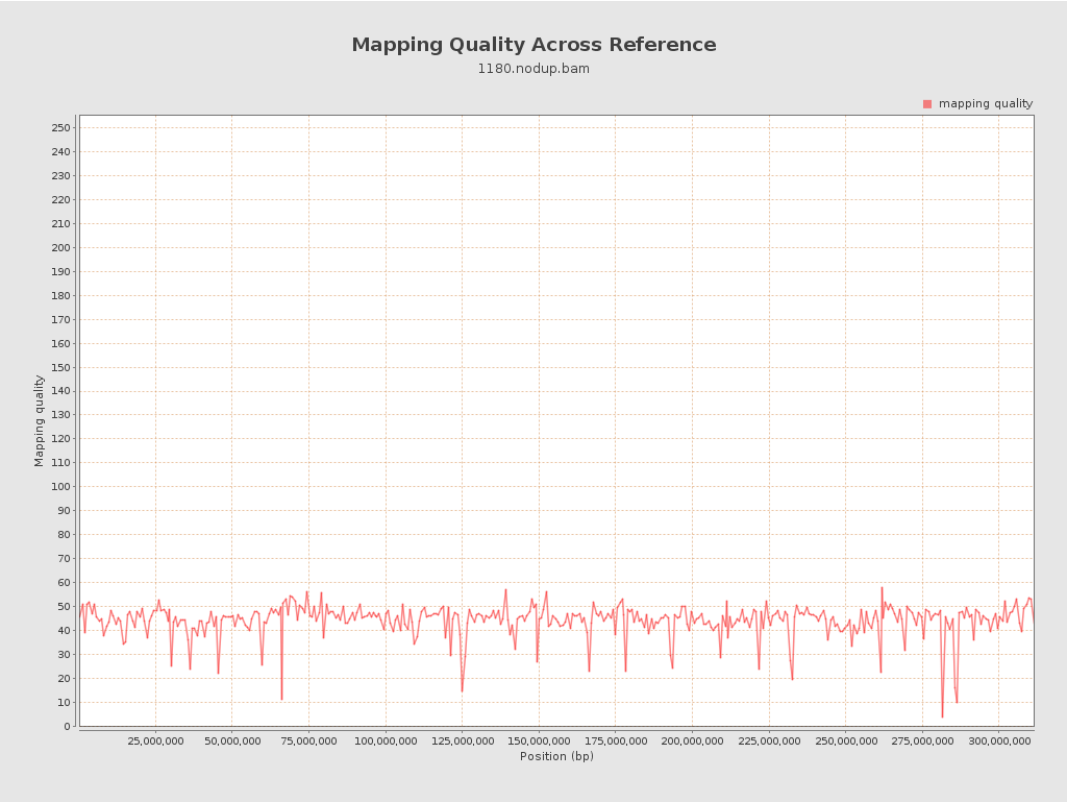
10. Results : Mapped Reads Clipping Profile



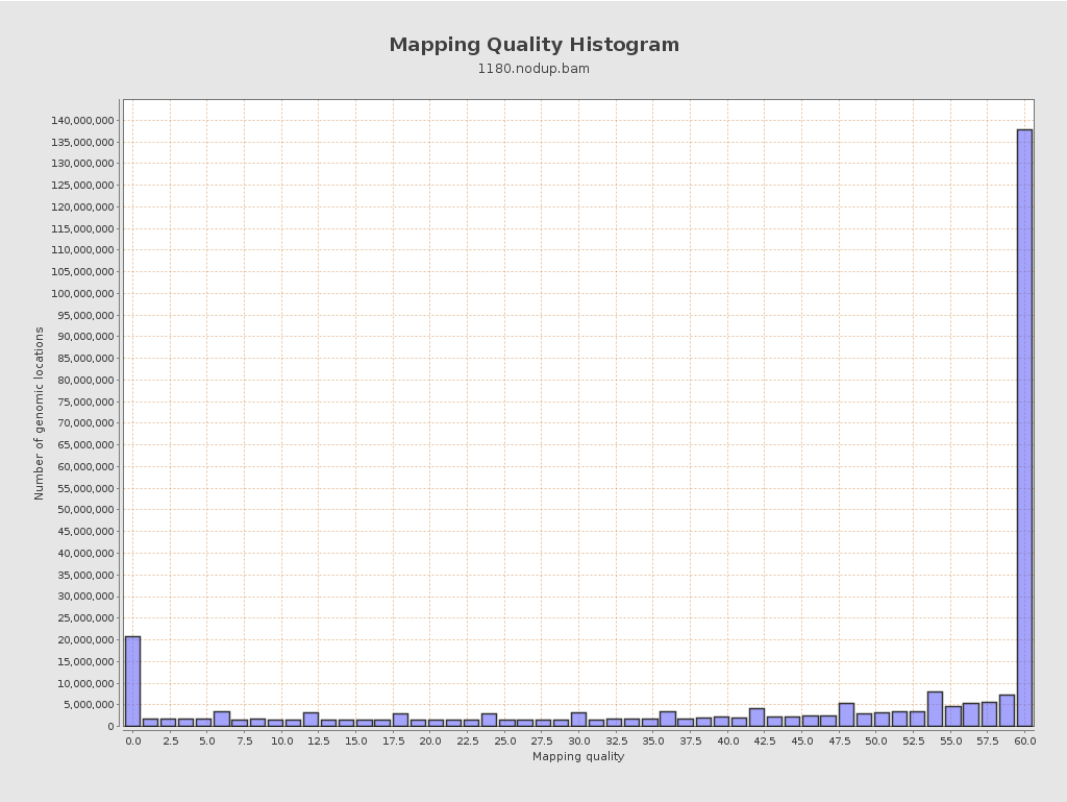
11. Results : Homopolymer Indels



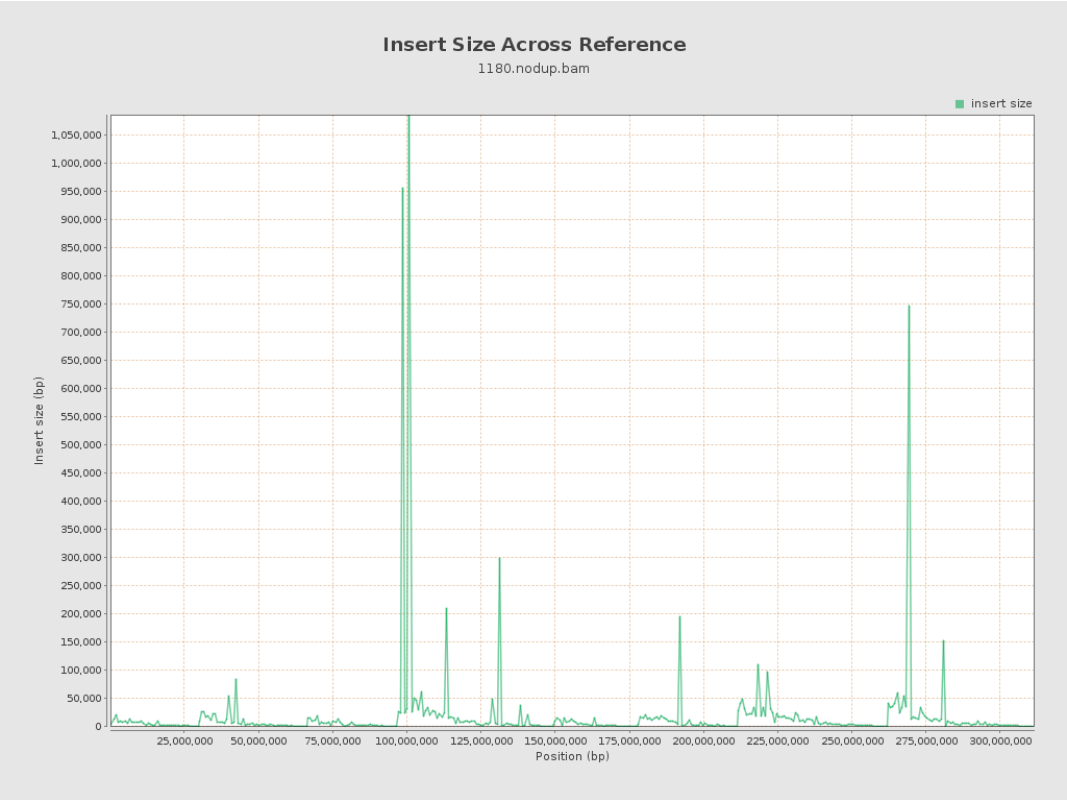
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram