

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/116
6
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1166 .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_451/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_451_S426_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_451/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_451_S426_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:40:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	93,835,346
Mapped reads	89,124,233 / 94.98%
Unmapped reads	4,711,113 / 5.02%
Mapped paired reads	89,124,233 / 94.98%
Mapped reads, first in pair	44,644,973 / 47.58%
Mapped reads, second in pair	44,479,260 / 47.4%
Mapped reads, both in pair	87,489,658 / 93.24%
Mapped reads, singletons	1,634,575 / 1.74%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	13,808,439 / 14.72%
Clipped reads	18,820,720 / 20.06%

2.2. ACGT Content

Number/percentage of A's	3,849,256,035 / 30.94%
Number/percentage of C's	2,371,952,642 / 19.06%
Number/percentage of T's	3,854,584,903 / 30.98%
Number/percentage of G's	2,365,654,070 / 19.01%
Number/percentage of N's	42,441 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	40.0267
Standard Deviation	292.6676

2.4. Mapping Quality

Mean Mapping Quality	44.31
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2.5. Insert size

Mean	232,709.39
Standard Deviation	2,283,758.9
P25/Median/P75	353 / 462 / 608

2.6. Mismatches and indels

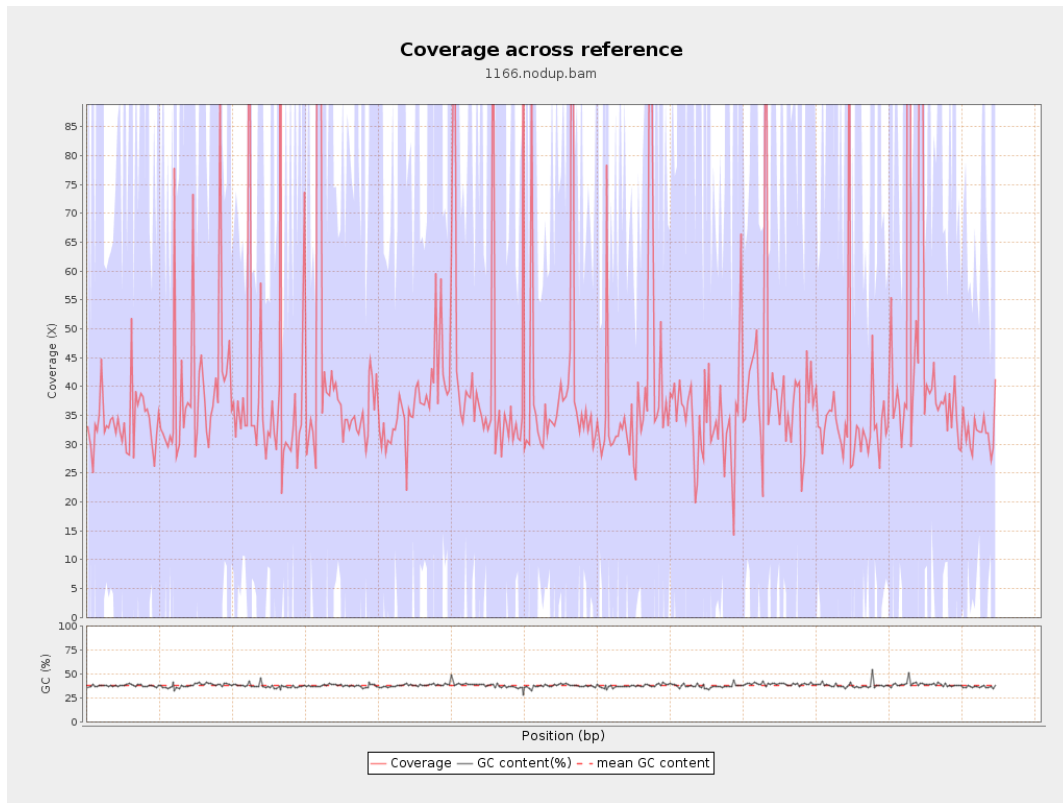
General error rate	2.26%
Mismatches	258,651,391
Insertions	8,319,522
Mapped reads with at least one insertion	8.4%
Deletions	8,558,564
Mapped reads with at least one deletion	8.53%
Homopolymer indels	56.3%

2.7. Chromosome stats

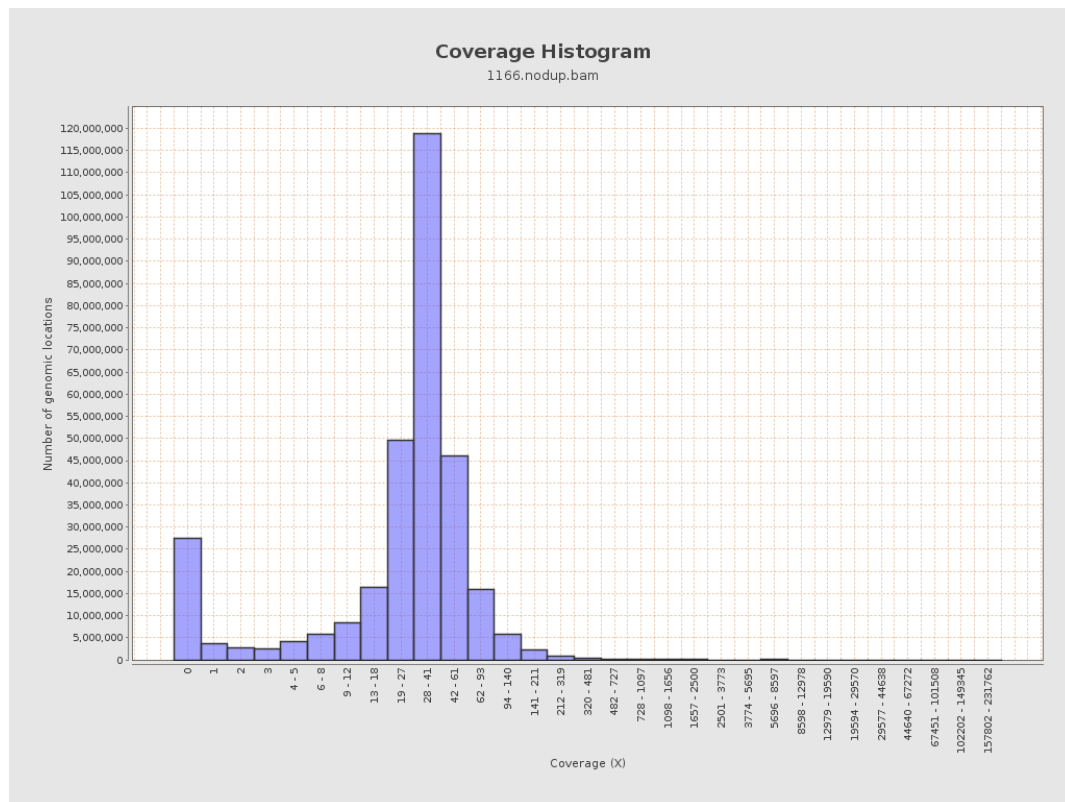
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	992895676	33.4035	83.8049

LT669789.1	36598175	1513427580	41.3525	324.0436
LT669790.1	30422129	1283637091	42.1942	277.2185
LT669791.1	52758100	2065844557	39.1569	240.0054
LT669792.1	28376109	1121865234	39.5356	345.8732
LT669793.1	33388210	1266233027	37.9246	219.6311
LT669794.1	50579949	1937895543	38.3135	273.0217
LT669795.1	49795044	2292204230	46.0328	412.8119

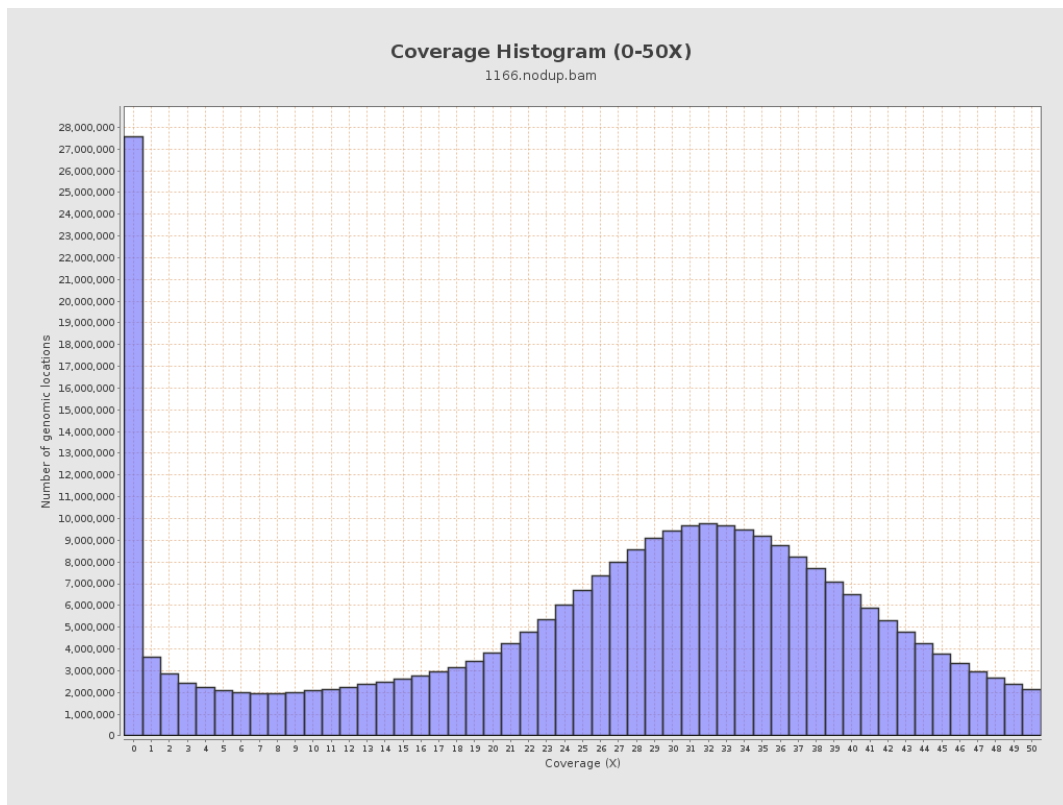
3. Results : Coverage across reference



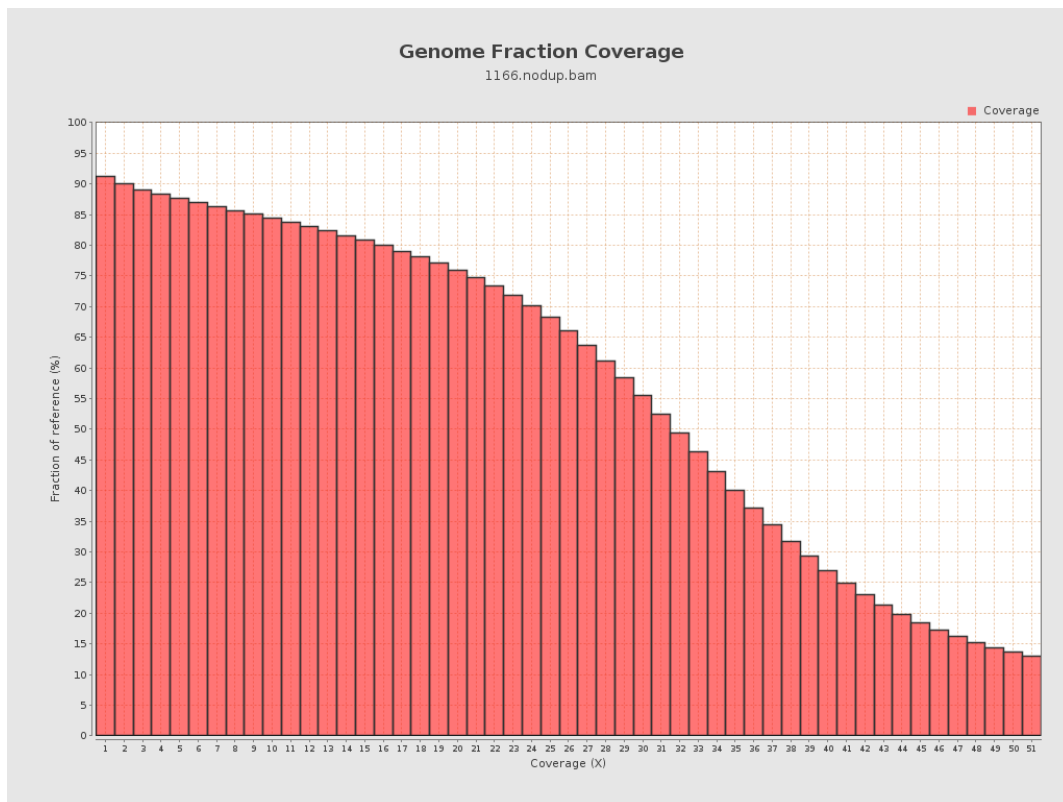
4. Results : Coverage Histogram



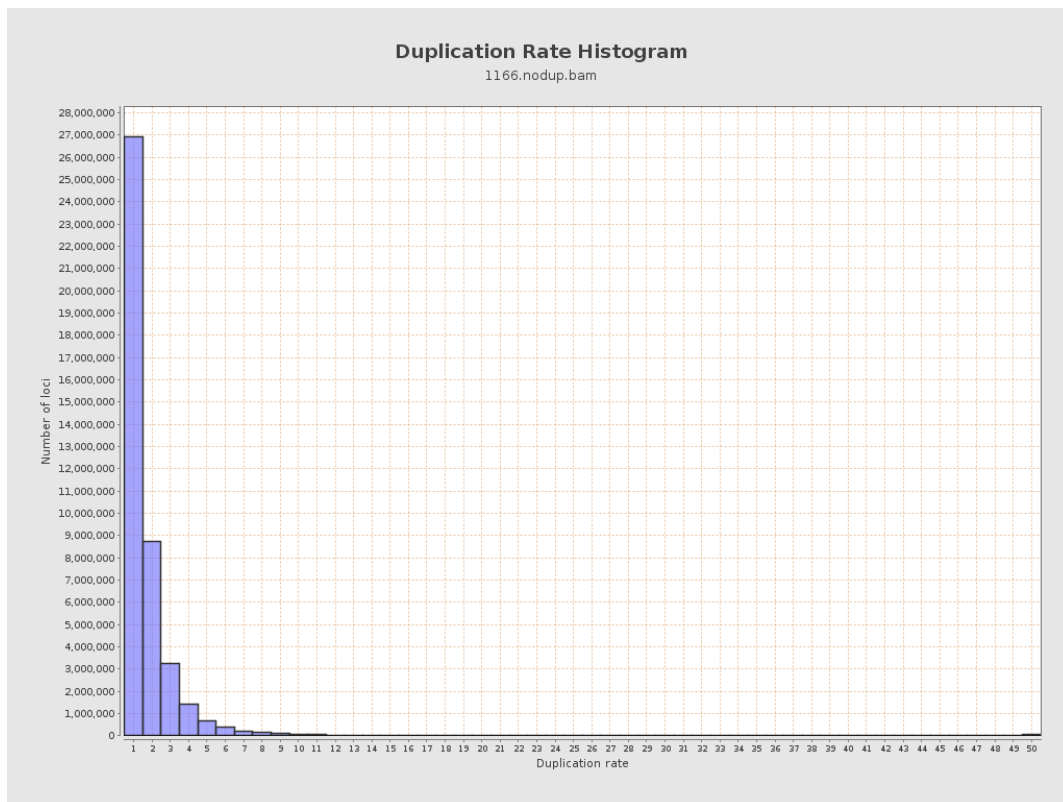
5. Results : Coverage Histogram (0-50X)



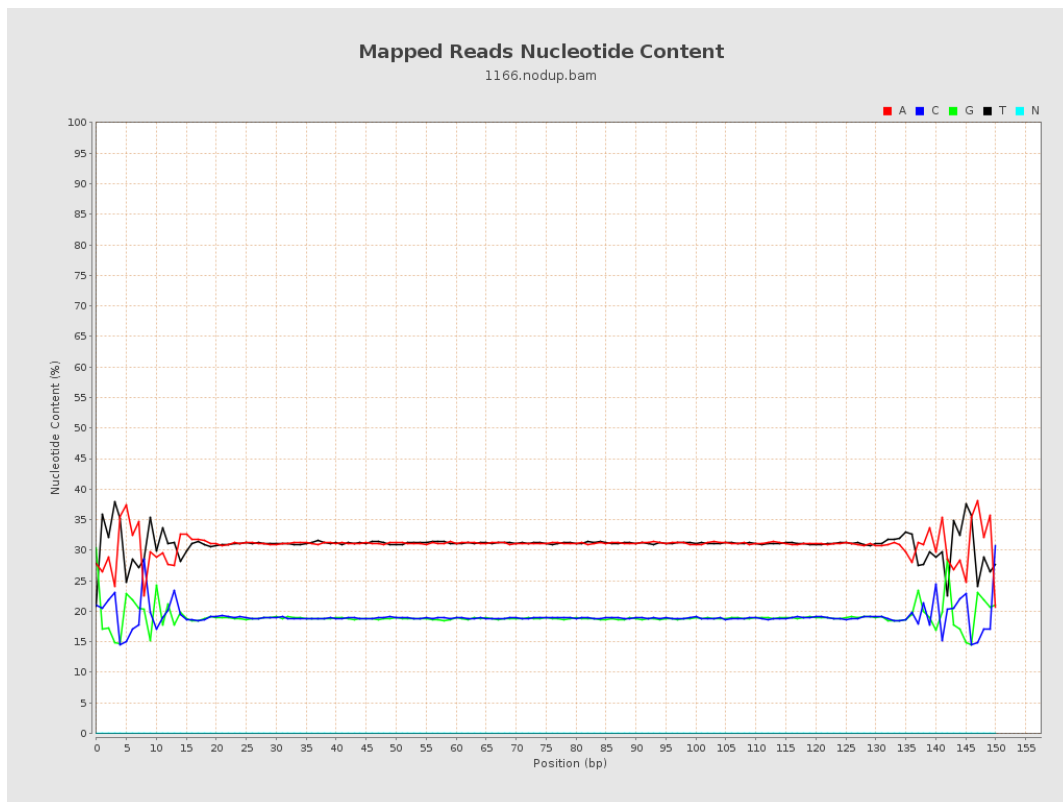
6. Results : Genome Fraction Coverage



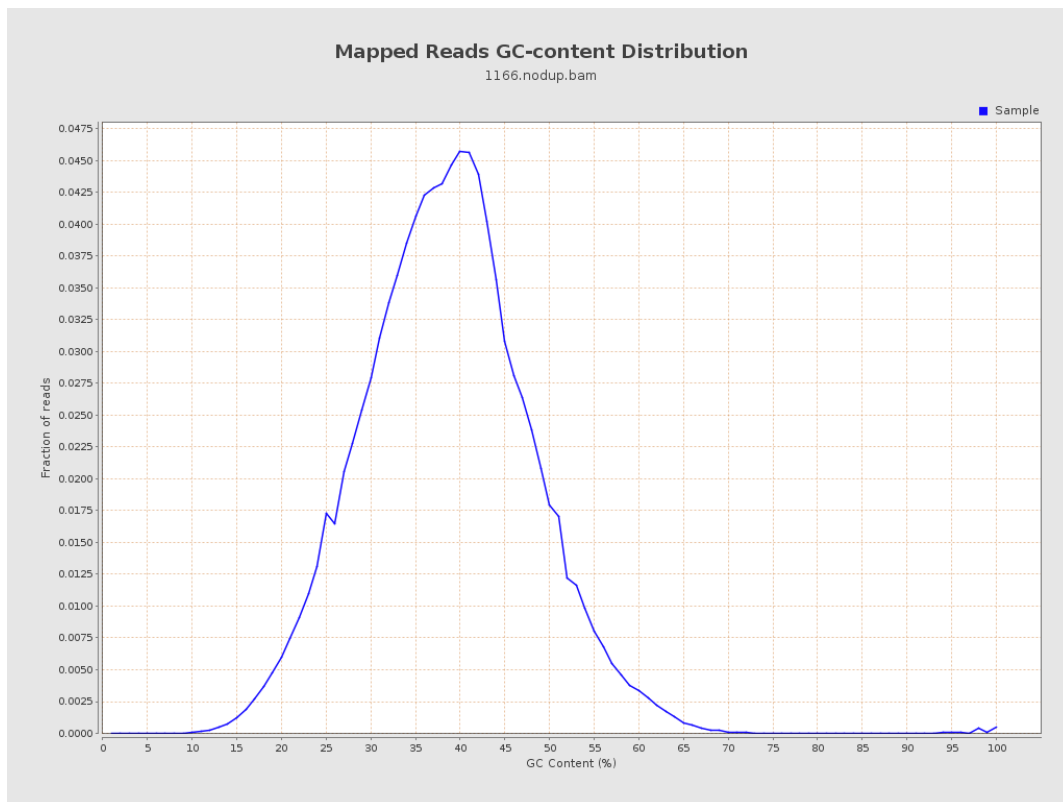
7. Results : Duplication Rate Histogram



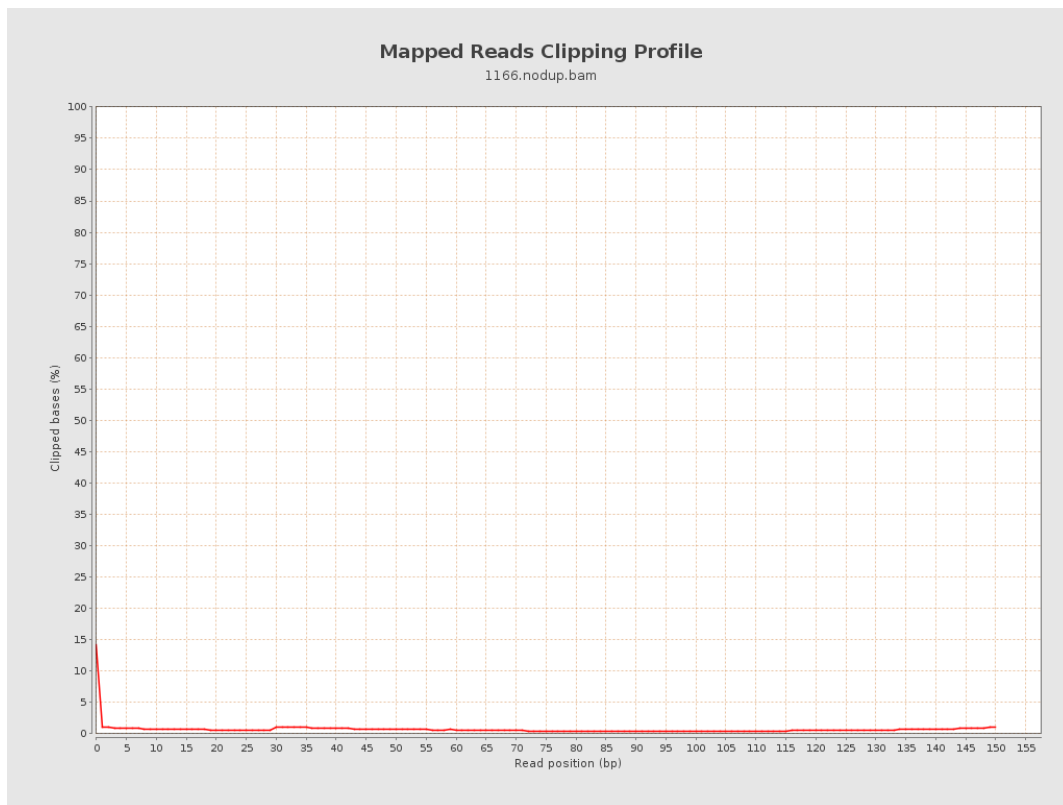
8. Results : Mapped Reads Nucleotide Content



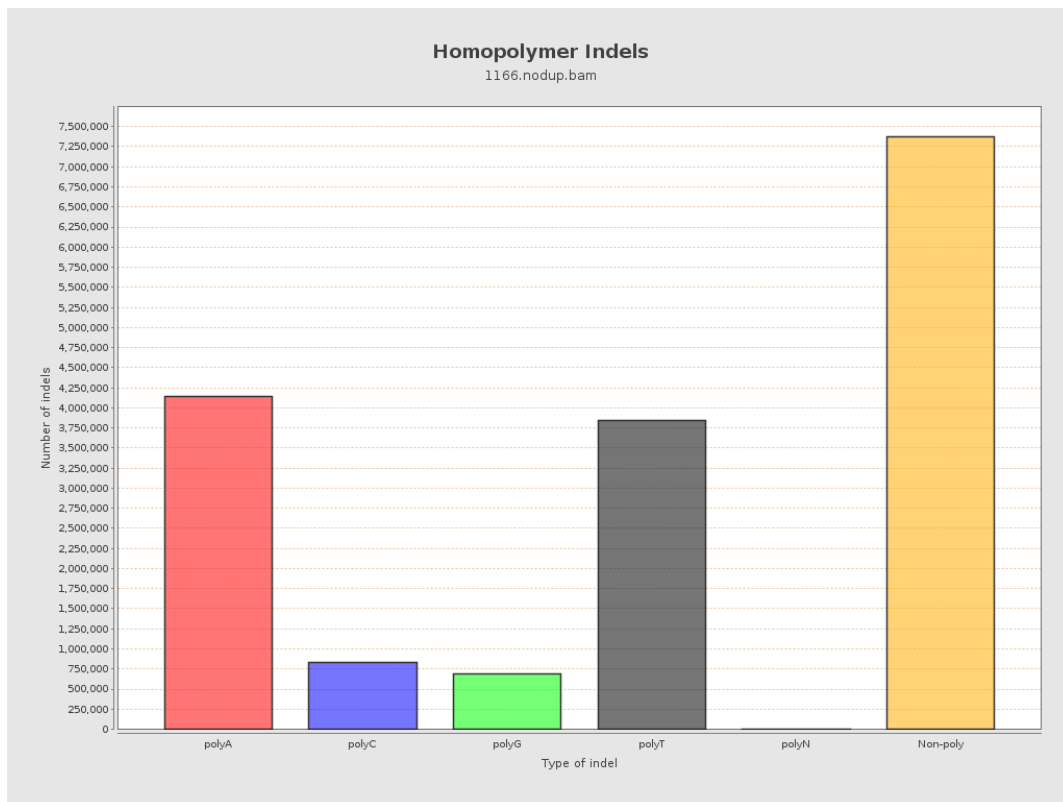
9. Results : Mapped Reads GC-content Distribution



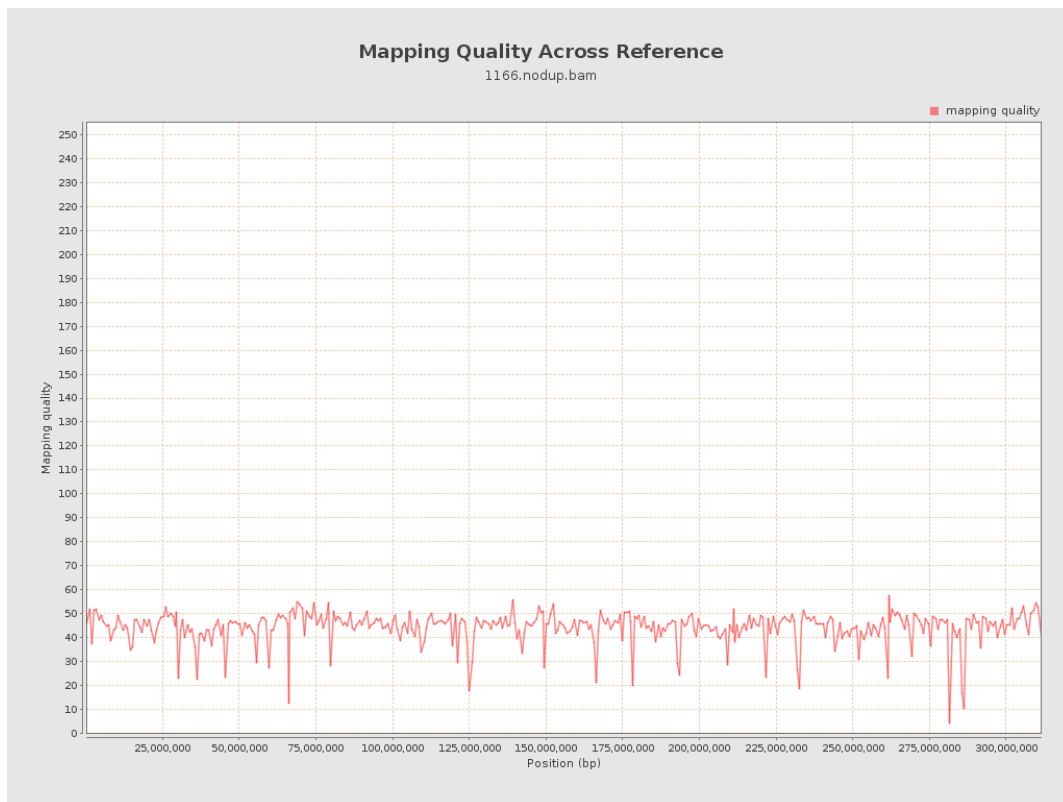
10. Results : Mapped Reads Clipping Profile



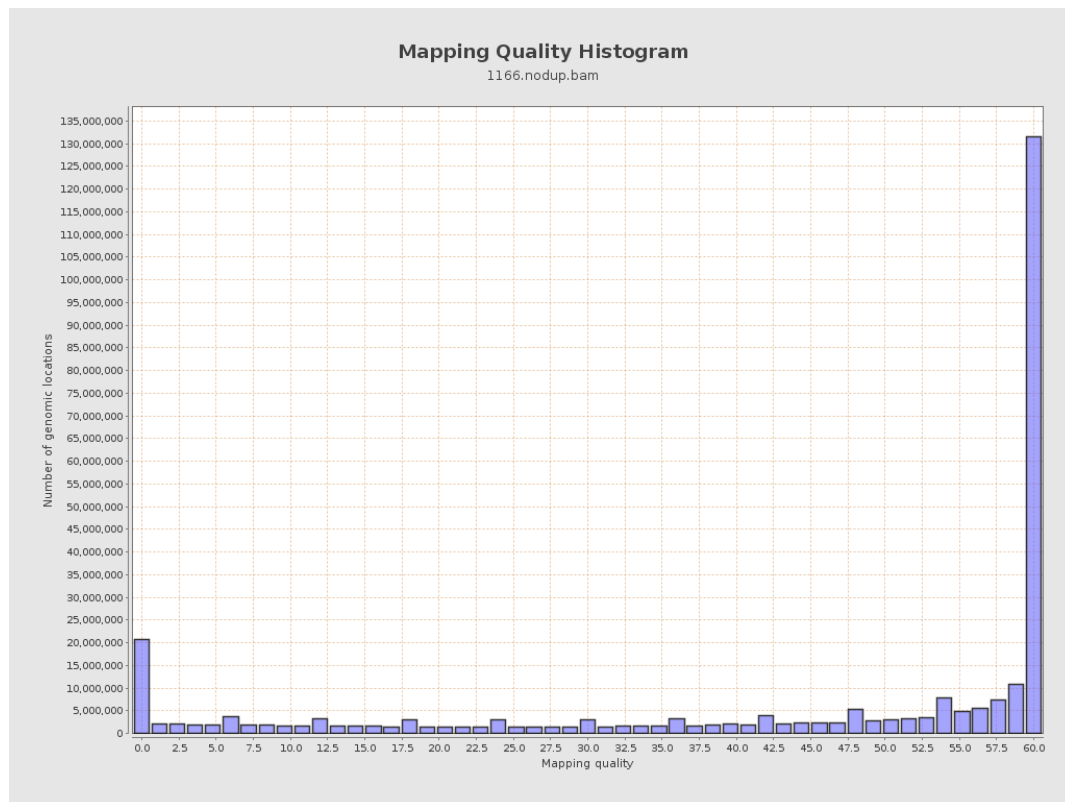
11. Results : Homopolymer Indels



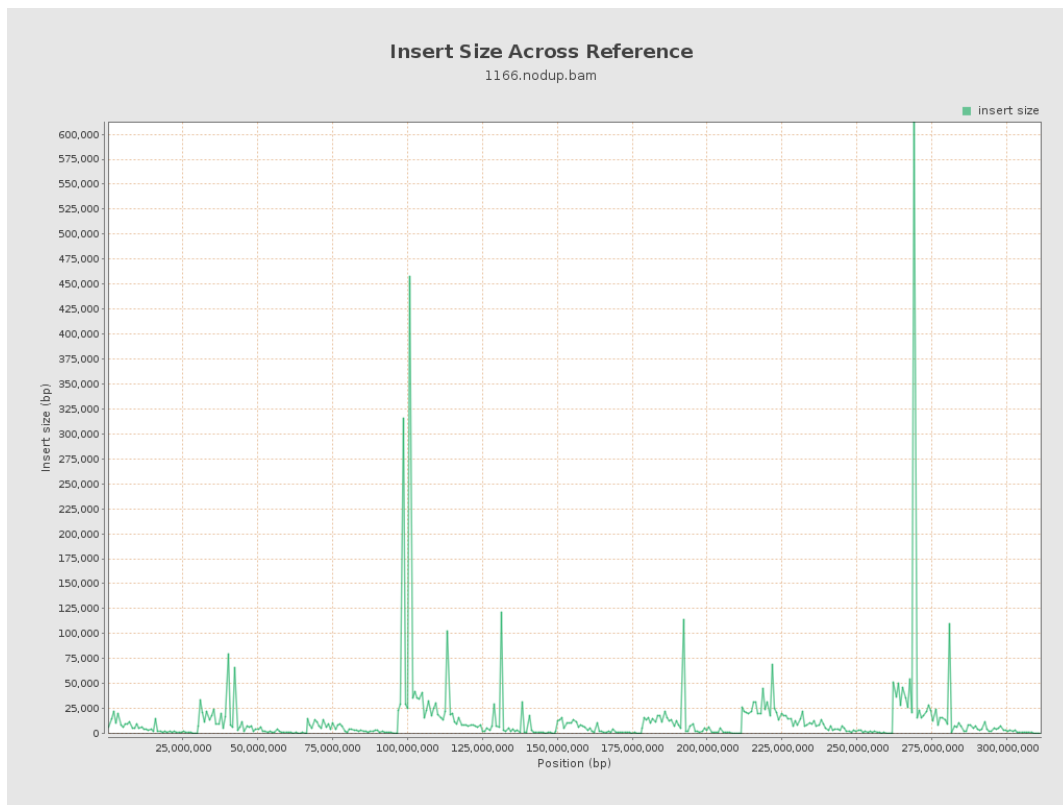
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

