Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/665.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/665.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_221/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_221_S302_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_221/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_221_S302_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:26 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	56,502,179
Mapped reads	52,089,431 / 92.19%
Unmapped reads	4,412,748 / 7.81%
Mapped paired reads	52,089,431 / 92.19%
Mapped reads, first in pair	26,121,172 / 46.23%
Mapped reads, second in pair	25,968,259 / 45.96%
Mapped reads, both in pair	50,611,626 / 89.57%
Mapped reads, singletons	1,477,805 / 2.62%
Read min/max/mean length	30 / 151 / 147.95
Duplicated reads (flagged)	8,171,539 / 14.46%
Clipped reads	13,039,717 / 23.08%

2.2. ACGT Content

Number/percentage of A's	2,190,179,002 / 30.84%
Number/percentage of C's	1,357,843,886 / 19.12%
Number/percentage of T's	2,193,306,904 / 30.89%
Number/percentage of G's	1,359,976,375 / 19.15%
Number/percentage of N's	26,976 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	22.8439
Standard Deviation	226.3709

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Insert size

Mean	250,434.23
Standard Deviation	2,399,151.37
P25/Median/P75	319 / 429 / 562

2.6. Mismatches and indels

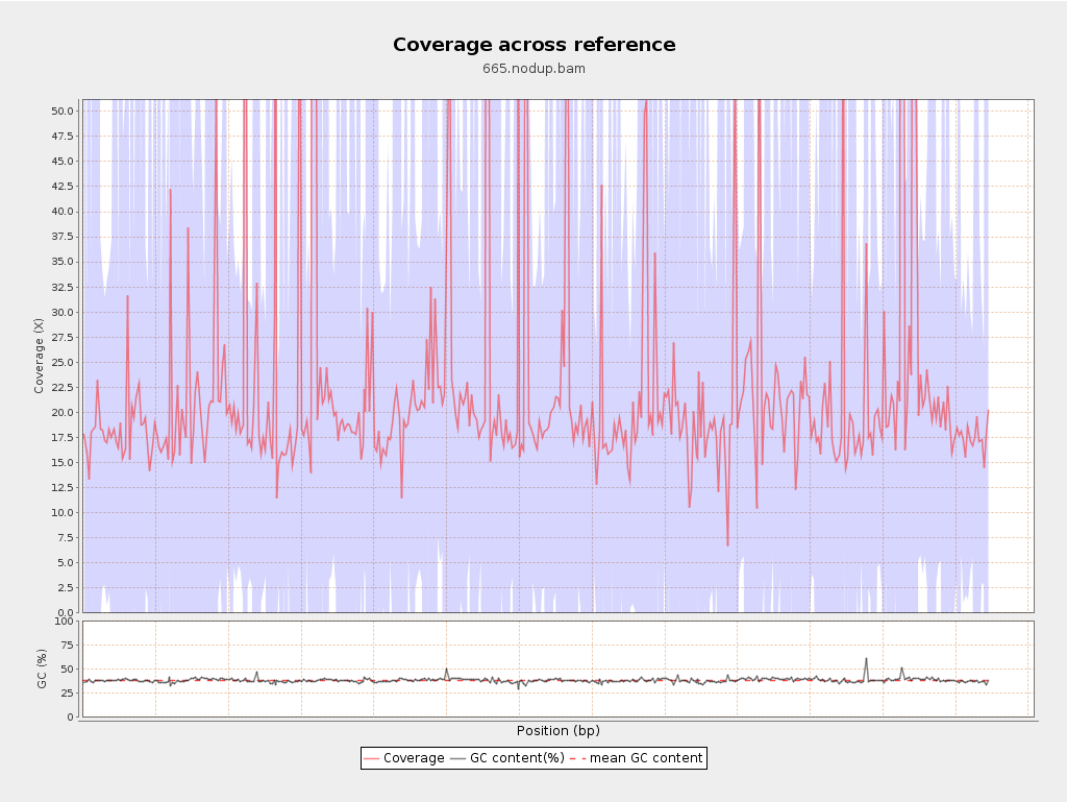
General error rate	2.36%
Mismatches	153,213,293
Insertions	5,105,459
Mapped reads with at least one insertion	8.76%
Deletions	4,805,282
Mapped reads with at least one deletion	8.2%
Homopolymer indels	56.76%

2.7. Chromosome stats

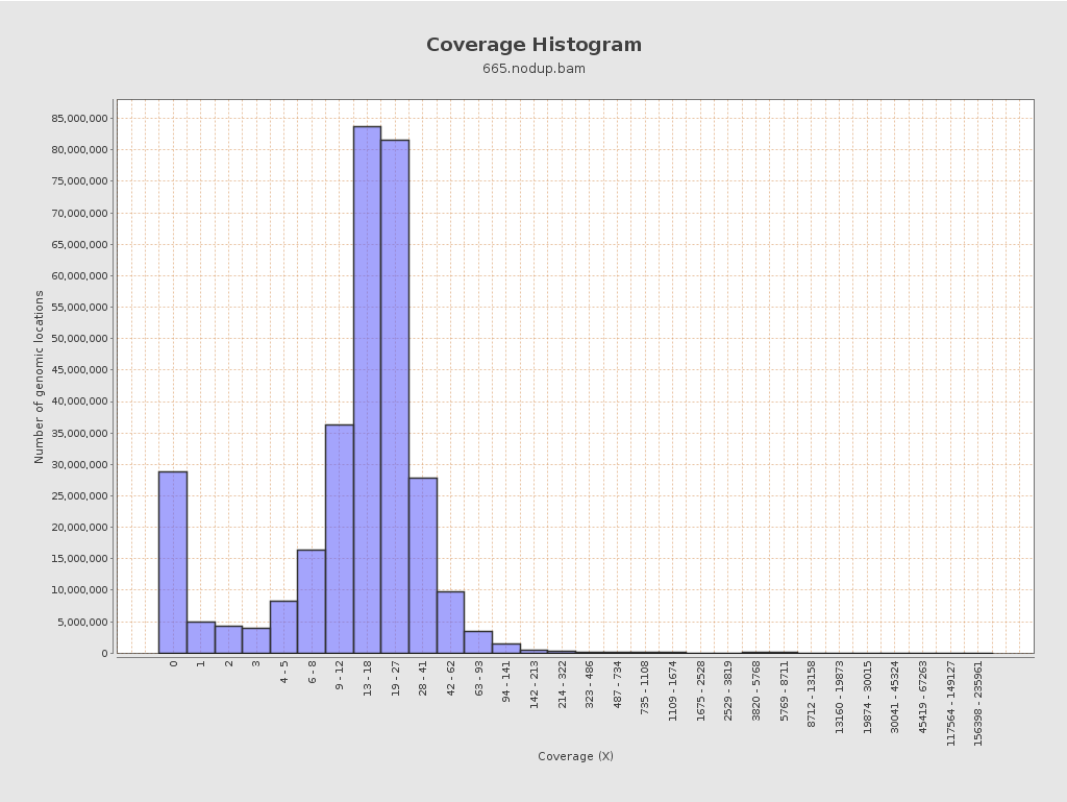
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	538123099	18.1038	80.5816

LT669789.1	36598175	843471139	23.0468	228.2118
LT669790.1	30422129	830358873	27.2946	295.3851
LT669791.1	52758100	1199006824	22.7265	230.6369
LT669792.1	28376109	649011022	22.8717	245.9459
LT669793.1	33388210	686521829	20.5618	144.1281
LT669794.1	50579949	1074558645	21.2448	170.0927
LT669795.1	49795044	1298069762	26.0683	301.7638

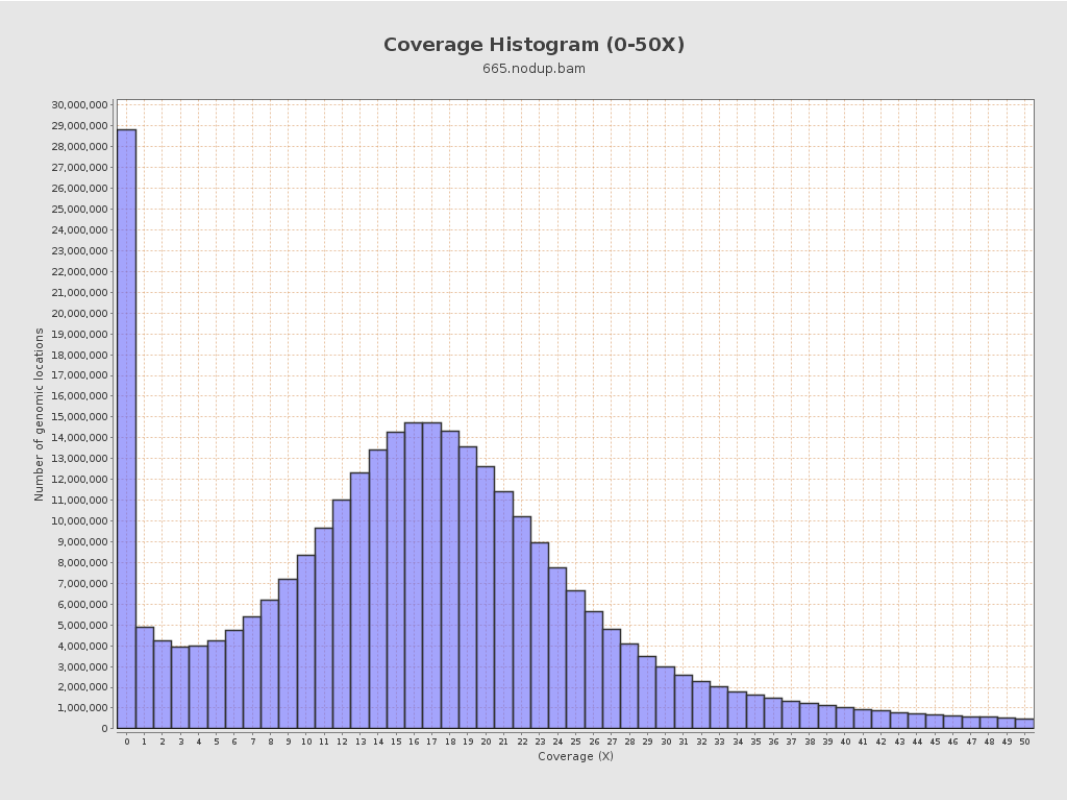
3. Results : Coverage across reference



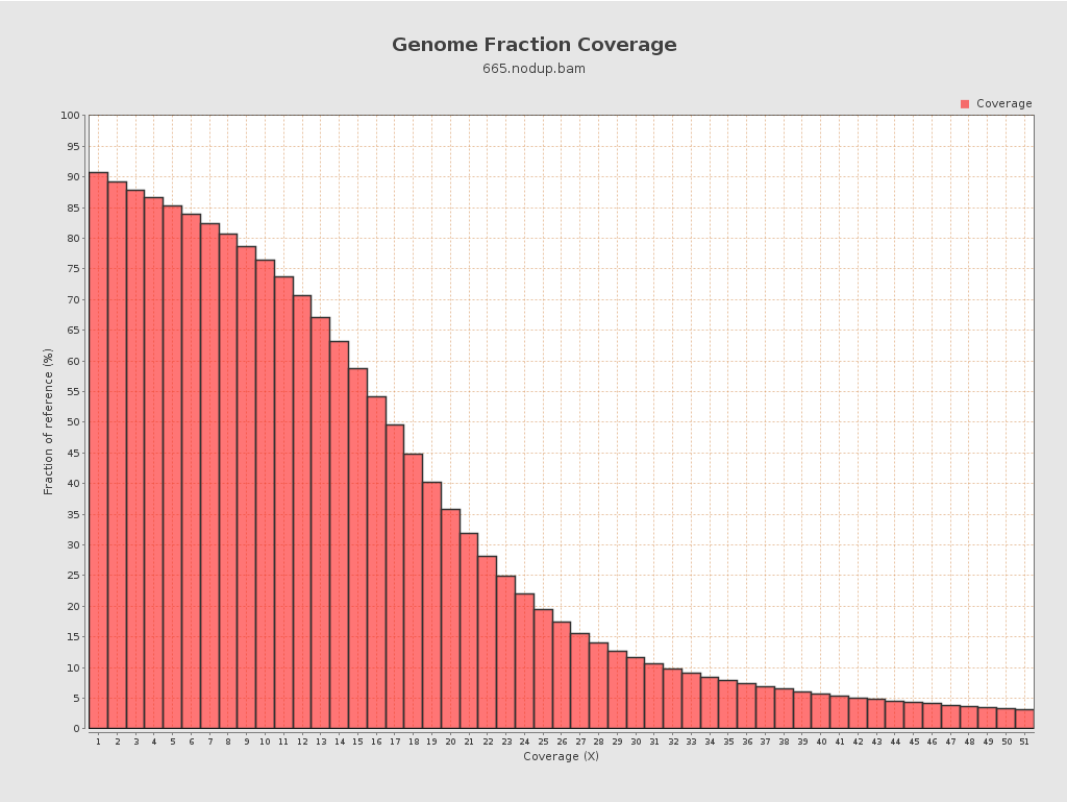
4. Results : Coverage Histogram



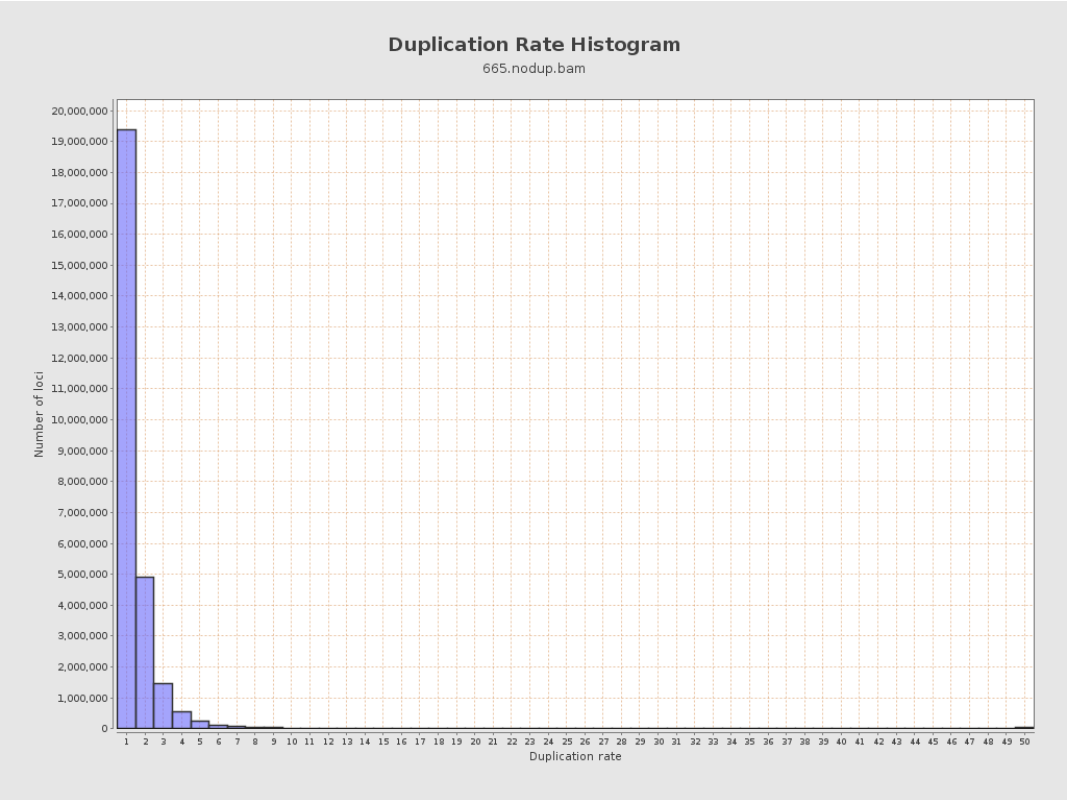
5. Results : Coverage Histogram (0-50X)



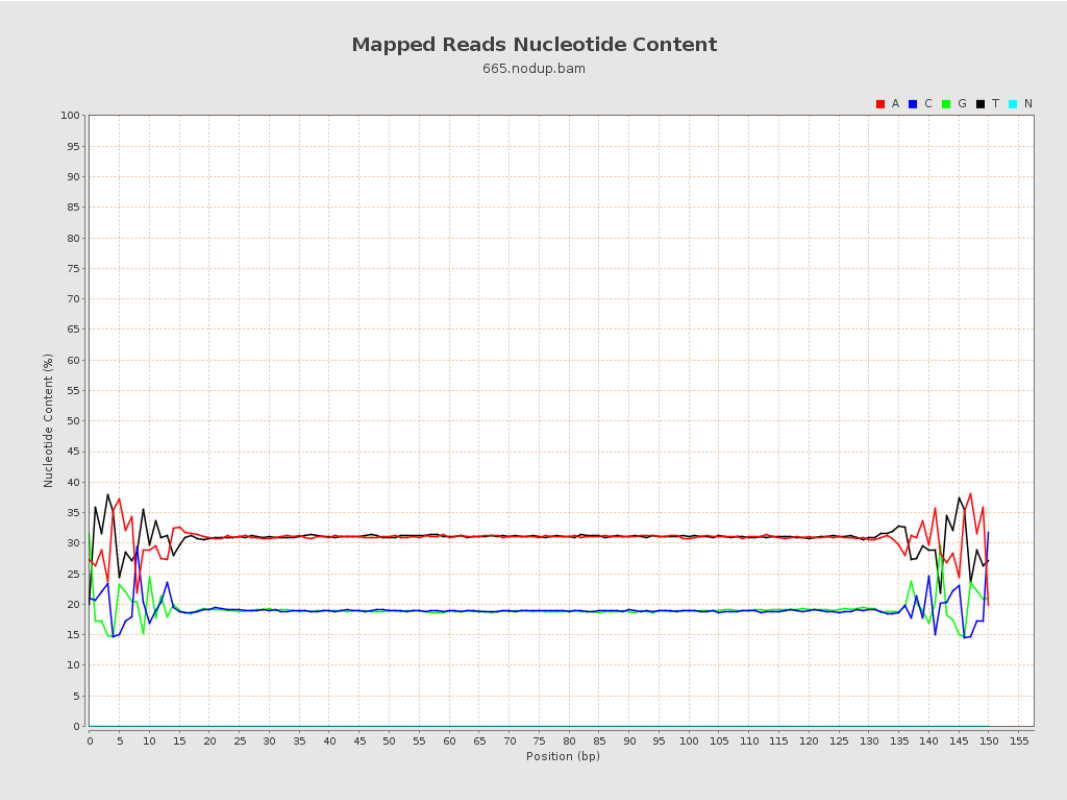
6. Results : Genome Fraction Coverage



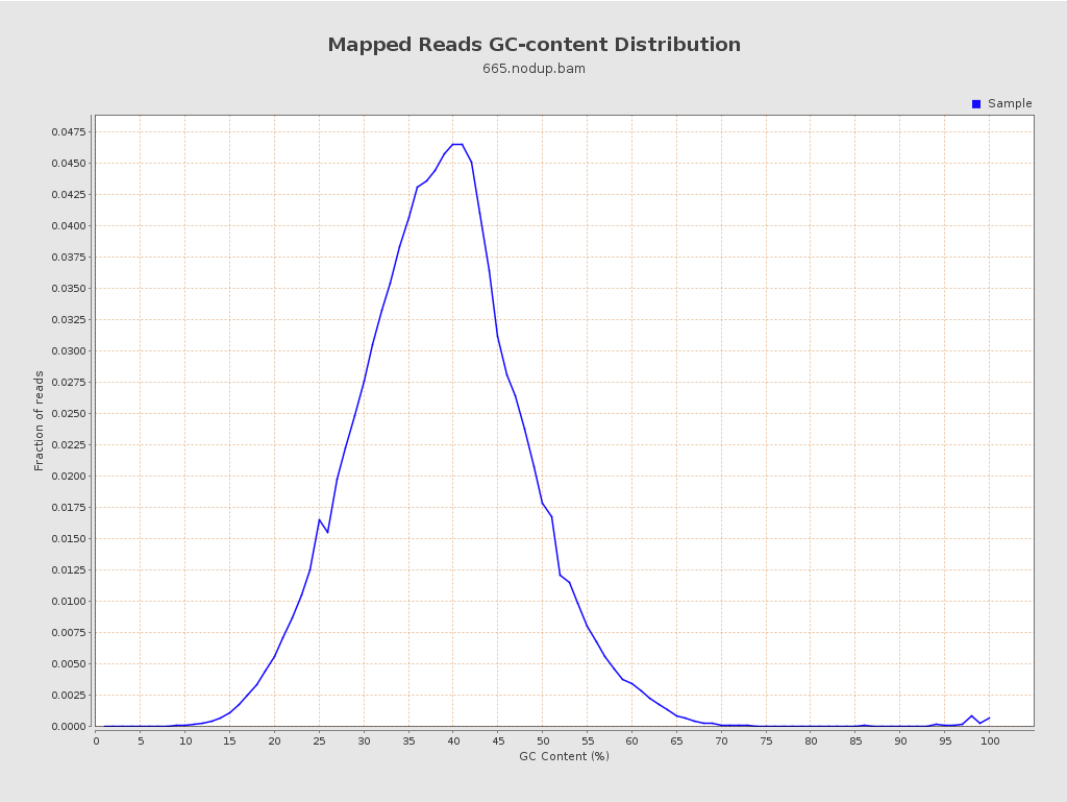
7. Results : Duplication Rate Histogram



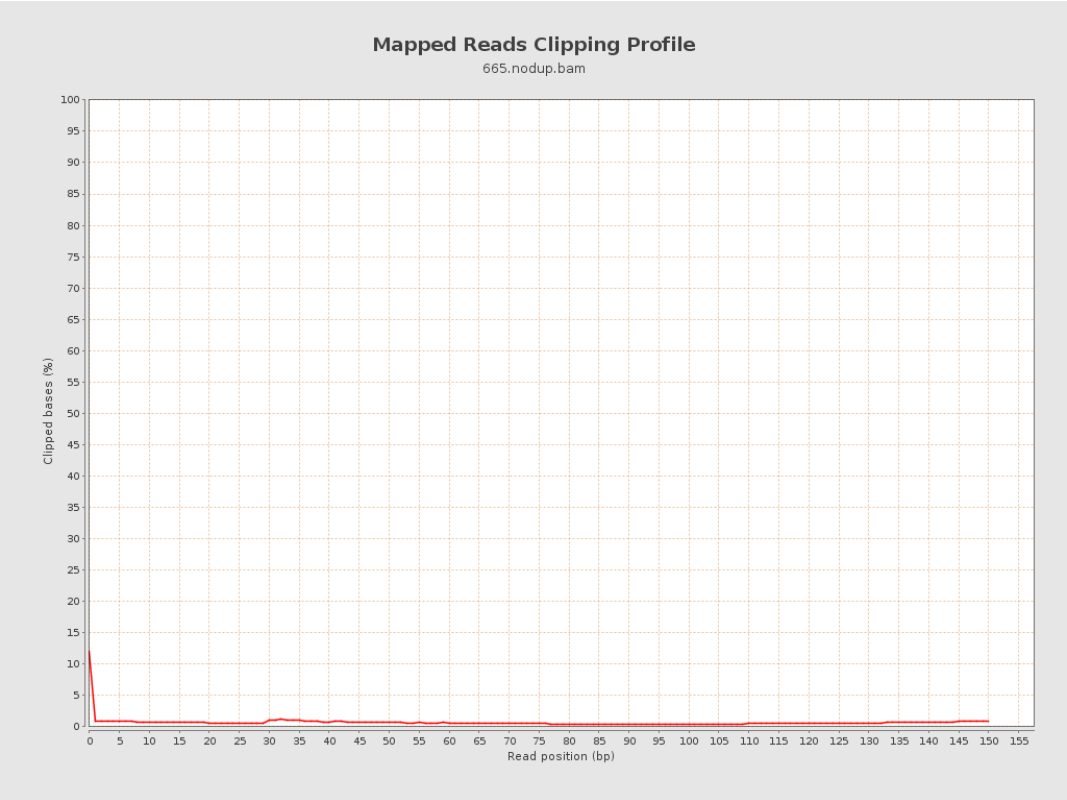
8. Results : Mapped Reads Nucleotide Content



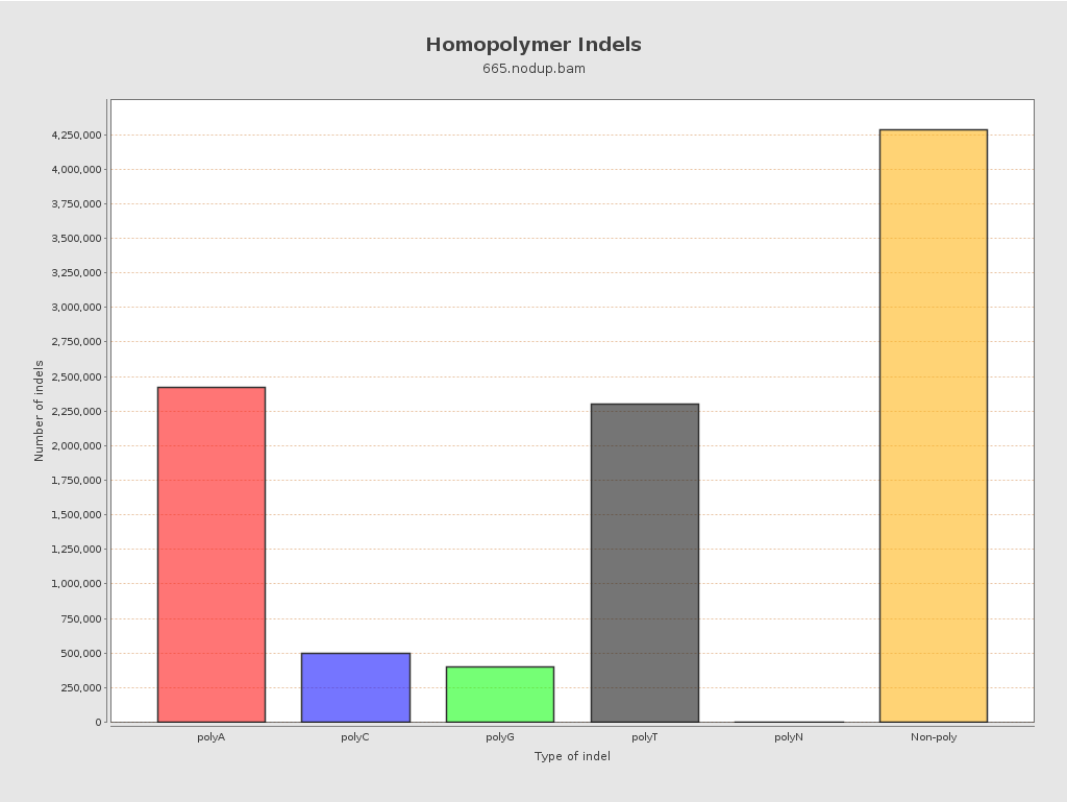
9. Results : Mapped Reads GC-content Distribution



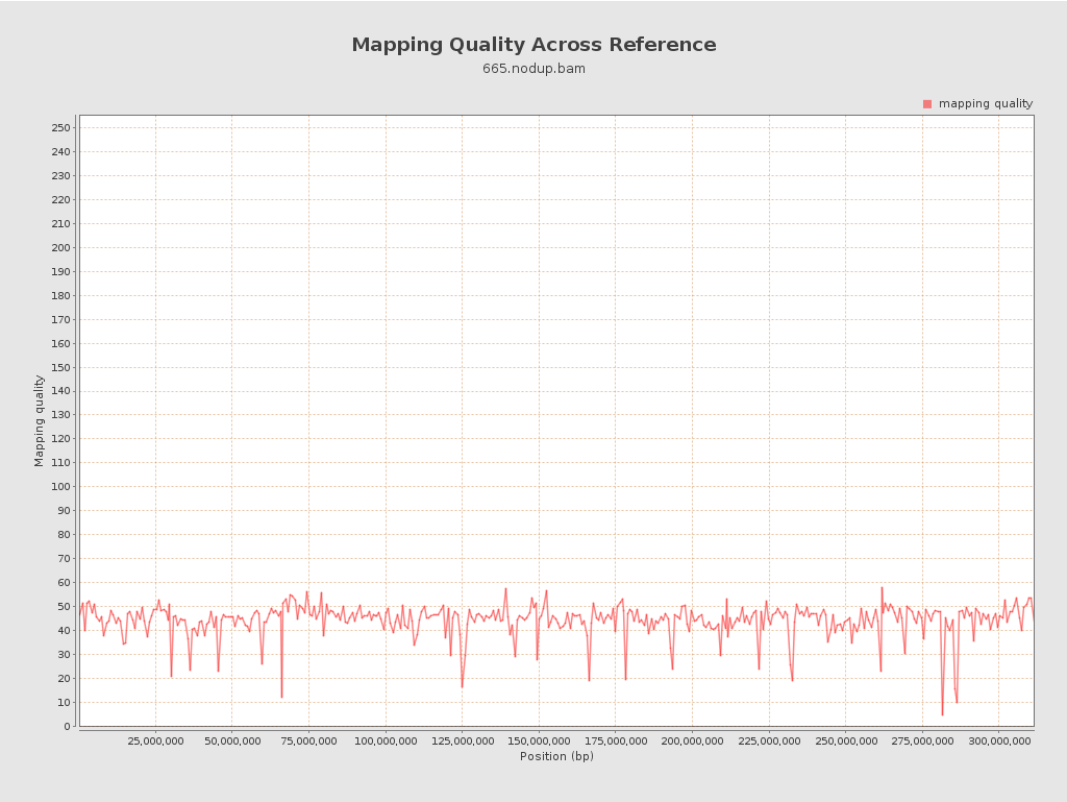
10. Results : Mapped Reads Clipping Profile



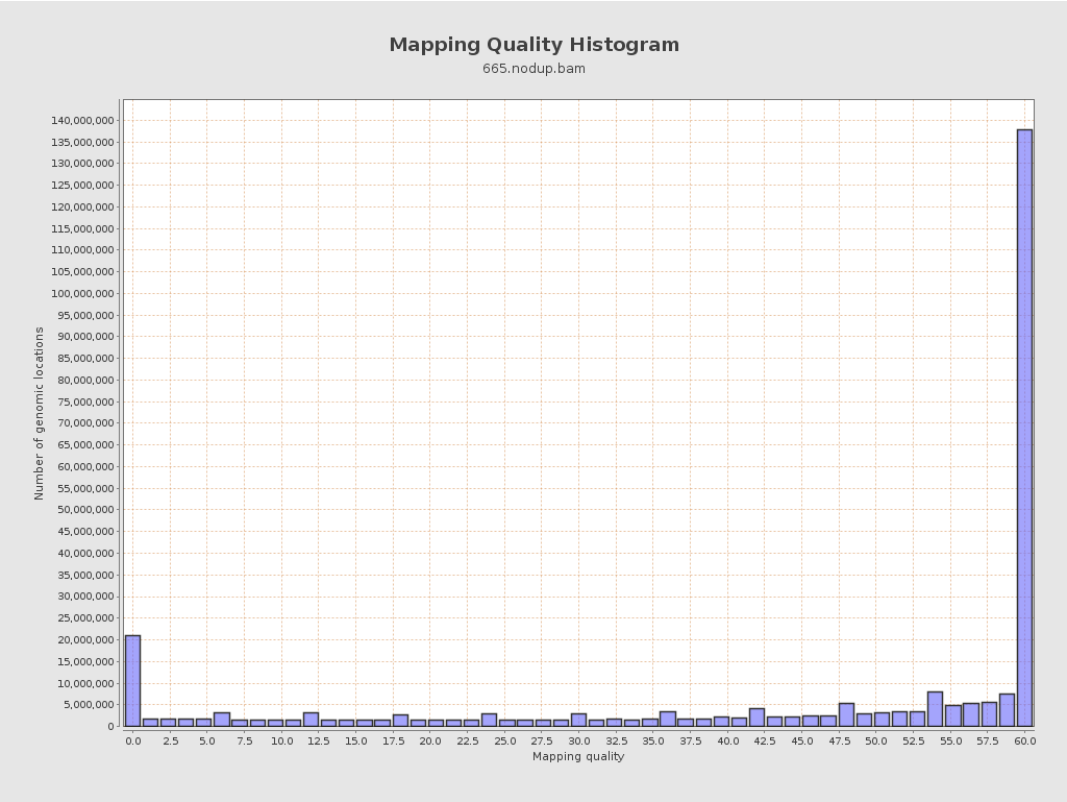
11. Results : Homopolymer Indels



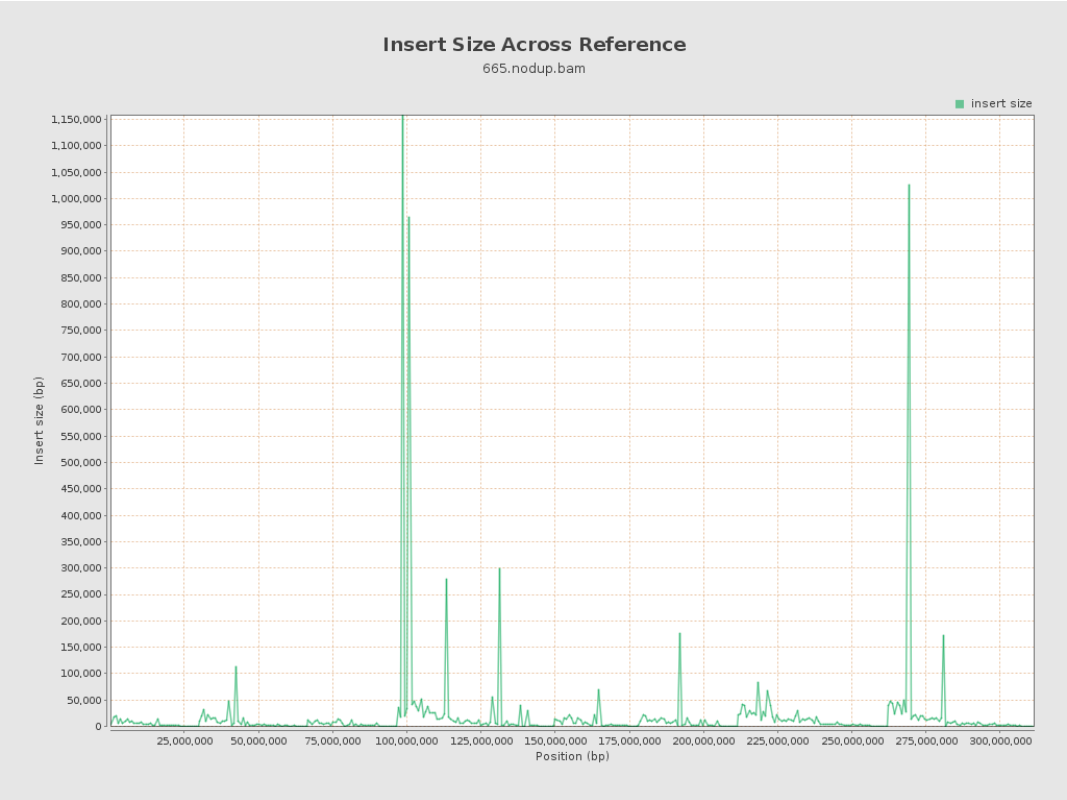
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram