Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/642.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/642.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_427/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_427_S402_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_427/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_427_S402_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:36 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,716,615
Mapped reads	62,791,389 / 94.12%
Unmapped reads	3,925,226 / 5.88%
Mapped paired reads	62,791,389 / 94.12%
Mapped reads, first in pair	31,464,617 / 47.16%
Mapped reads, second in pair	31,326,772 / 46.95%
Mapped reads, both in pair	61,419,750 / 92.06%
Mapped reads, singletons	1,371,639 / 2.06%
Read min/max/mean length	30 / 151 / 147.88
Duplicated reads (flagged)	9,713,632 / 14.56%
Clipped reads	14,469,426 / 21.69%

2.2. ACGT Content

Number/percentage of A's	2,671,231,776 / 30.79%
Number/percentage of C's	1,667,400,492 / 19.22%
Number/percentage of T's	2,674,650,179 / 30.83%
Number/percentage of G's	1,663,498,622 / 19.17%
Number/percentage of N's	29,950 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	27.9175
Standard Deviation	235.5554

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Insert size

Mean	255,185.5
Standard Deviation	2,397,793.57
P25/Median/P75	347 / 455 / 595

2.6. Mismatches and indels

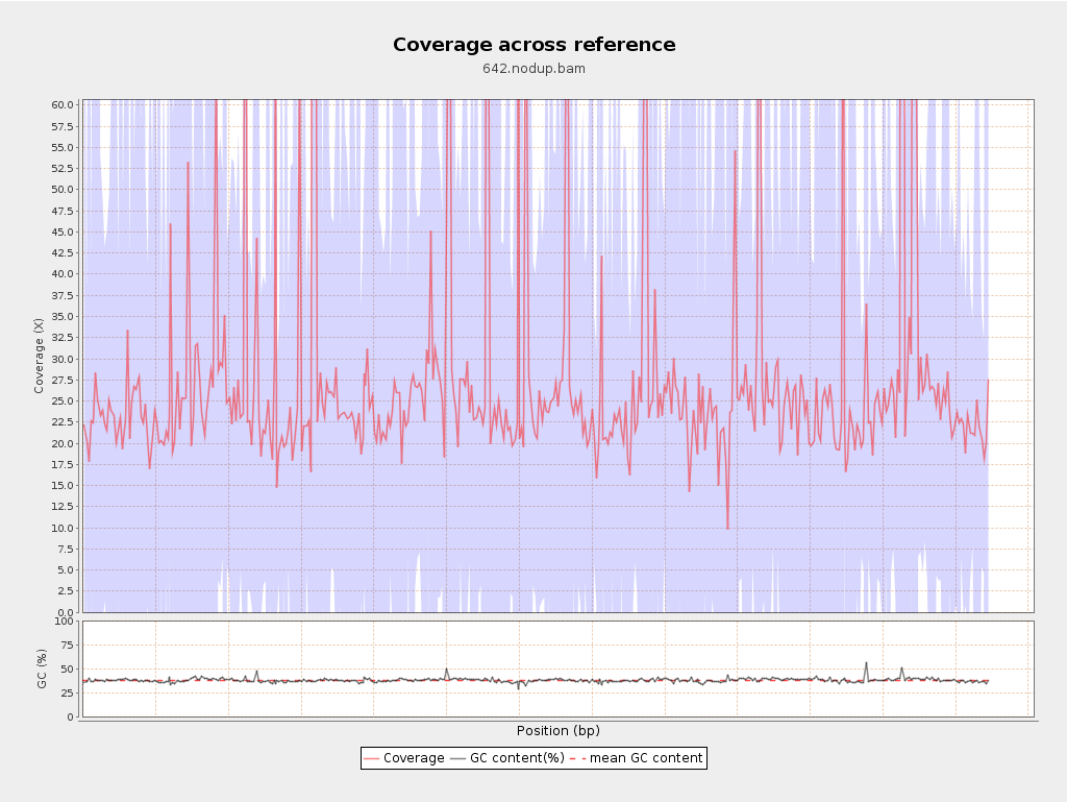
General error rate	2.37%
Mismatches	188,857,137
Insertions	6,052,783
Mapped reads with at least one insertion	8.65%
Deletions	6,201,201
Mapped reads with at least one deletion	8.73%
Homopolymer indels	56.22%

2.7. Chromosome stats

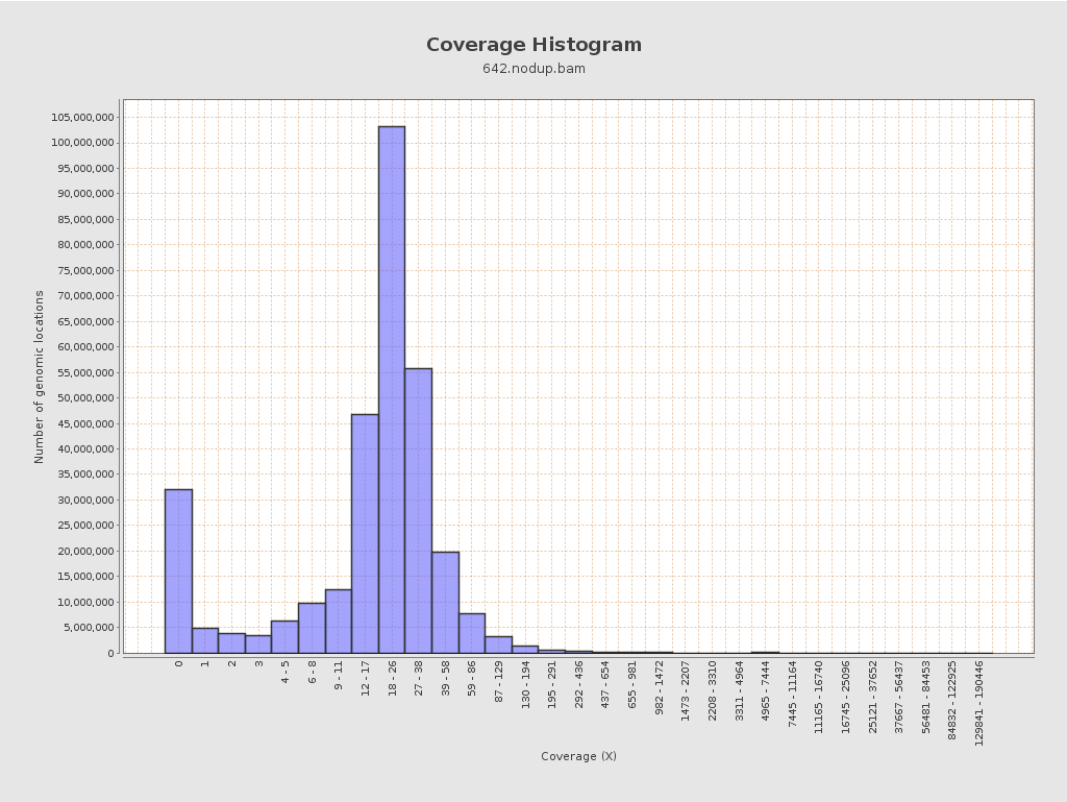
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	677980738	22.8089	86.9619

LT669789.1	36598175	1059280178	28.9435	262.8103
LT669790.1	30422129	911101906	29.9487	236.7678
LT669791.1	52758100	1448107404	27.4481	225.9744
LT669792.1	28376109	780639904	27.5105	226.4961
LT669793.1	33388210	871599886	26.105	154.5837
LT669794.1	50579949	1342478902	26.5417	214.9265
LT669795.1	49795044	1609066093	32.3138	333.781

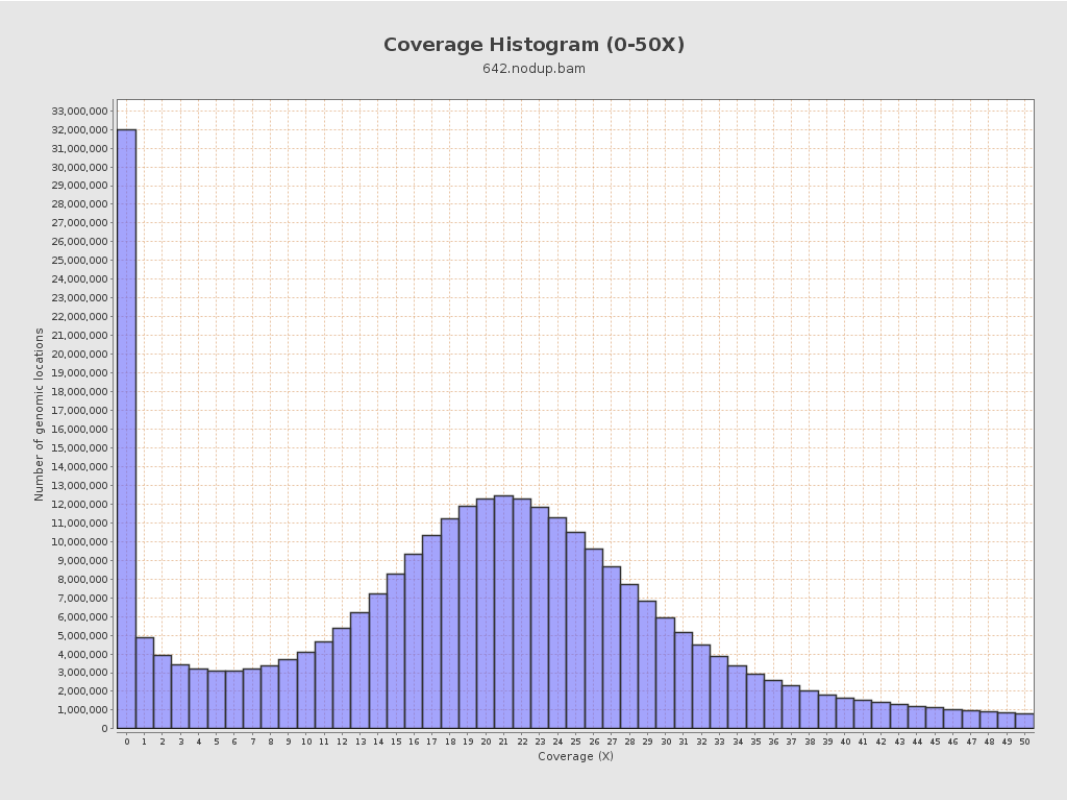
3. Results : Coverage across reference



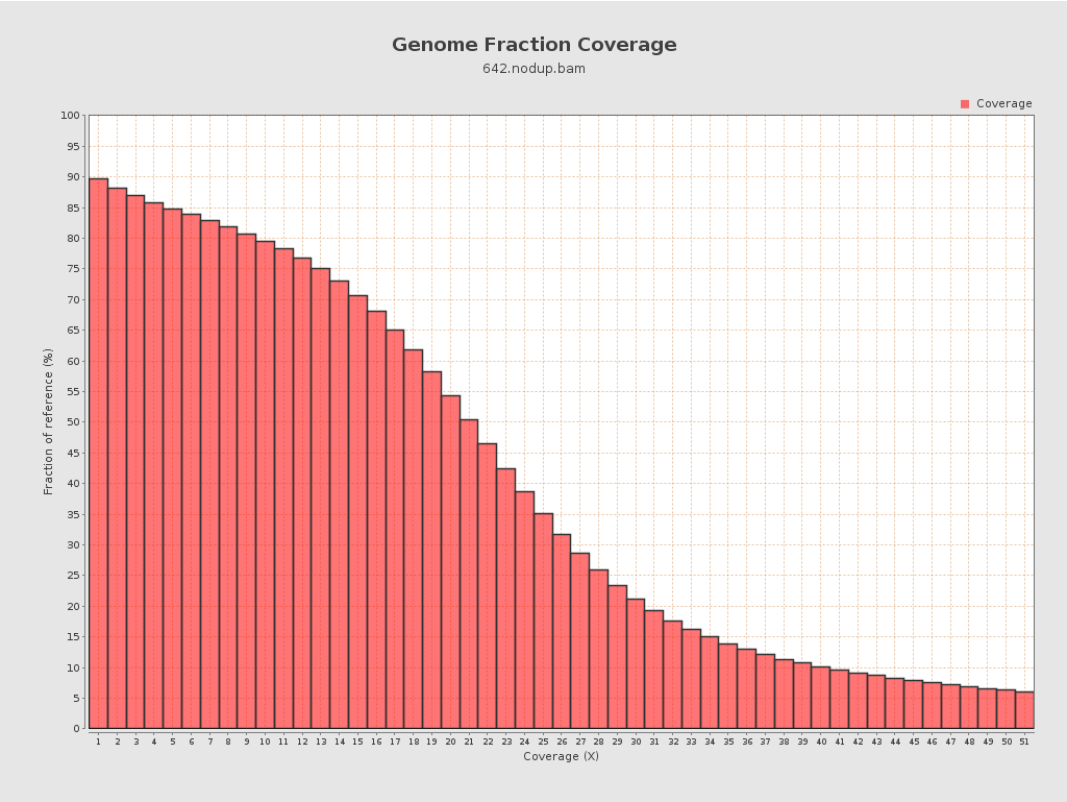
4. Results : Coverage Histogram



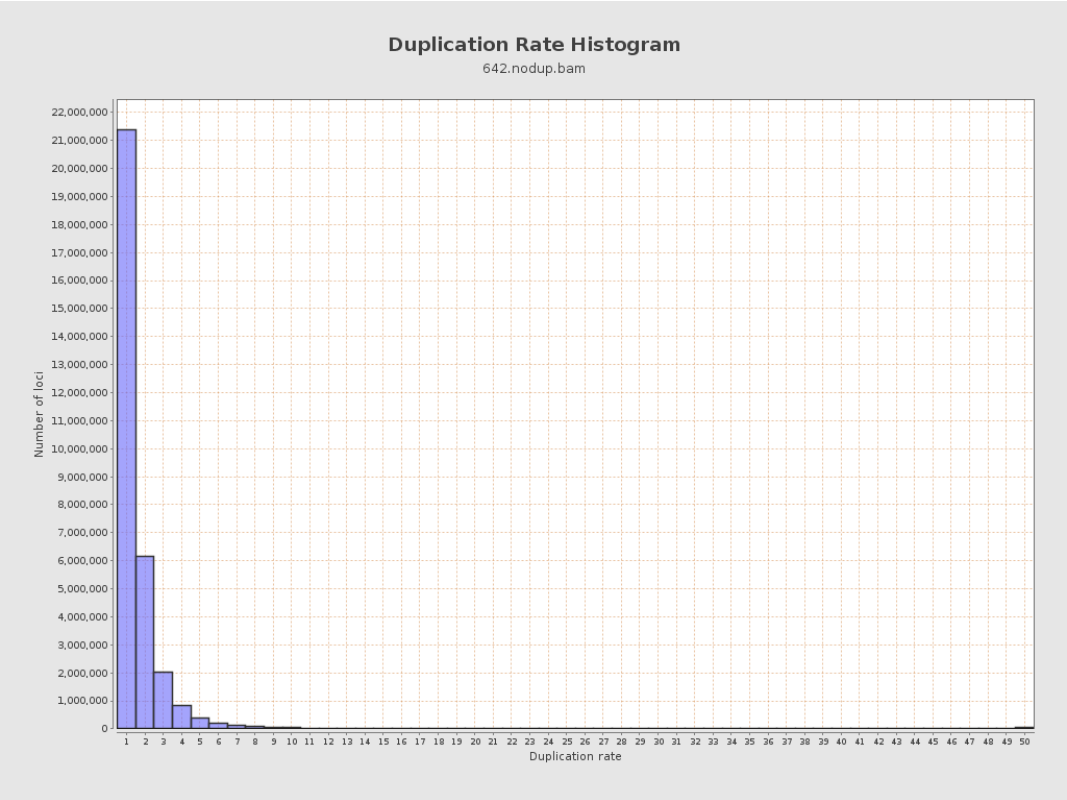
5. Results : Coverage Histogram (0-50X)



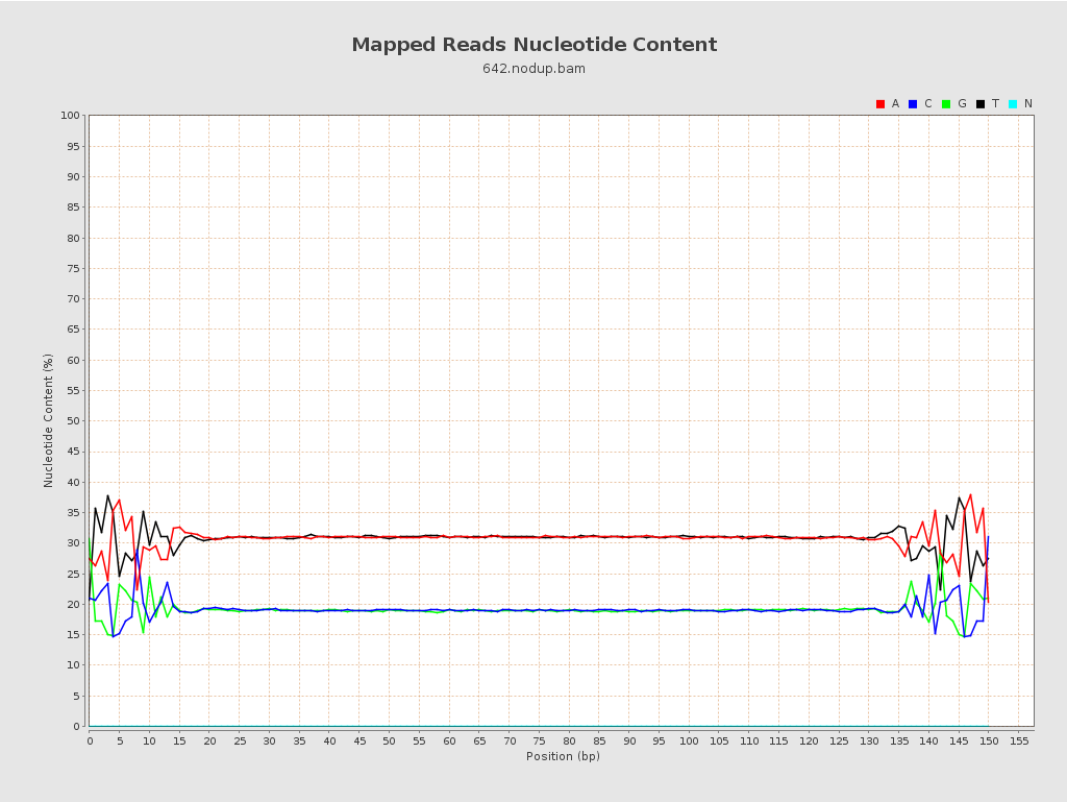
6. Results : Genome Fraction Coverage



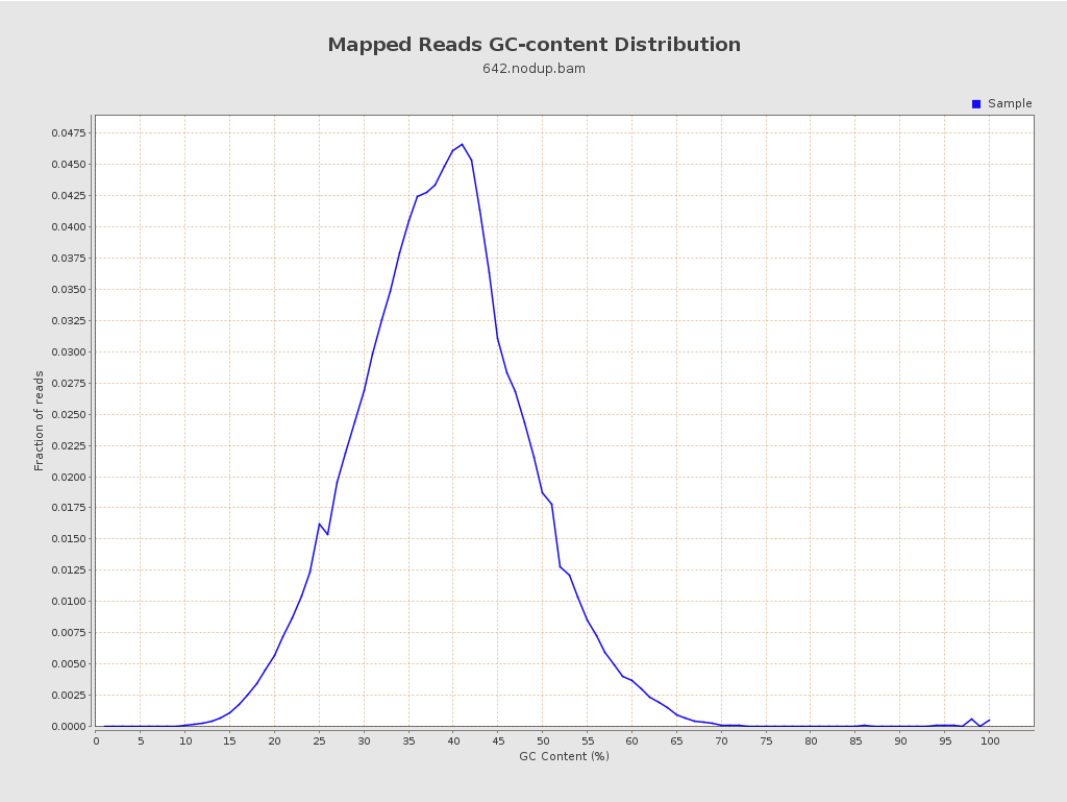
7. Results : Duplication Rate Histogram



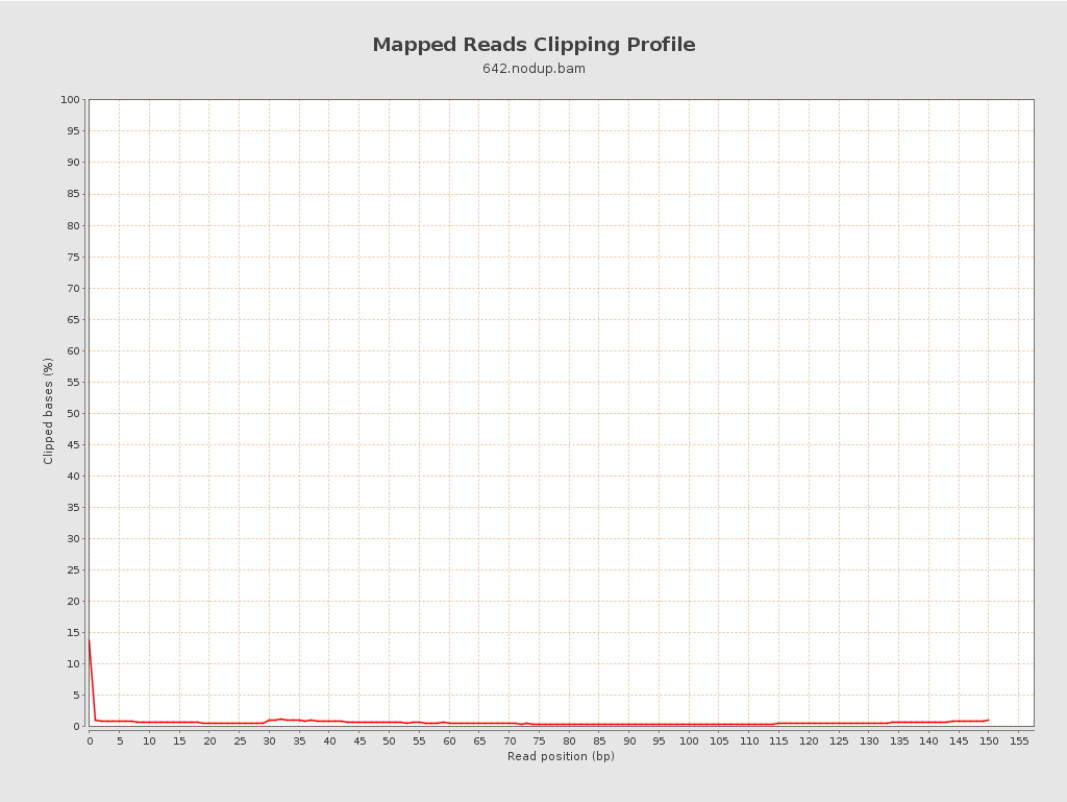
8. Results : Mapped Reads Nucleotide Content



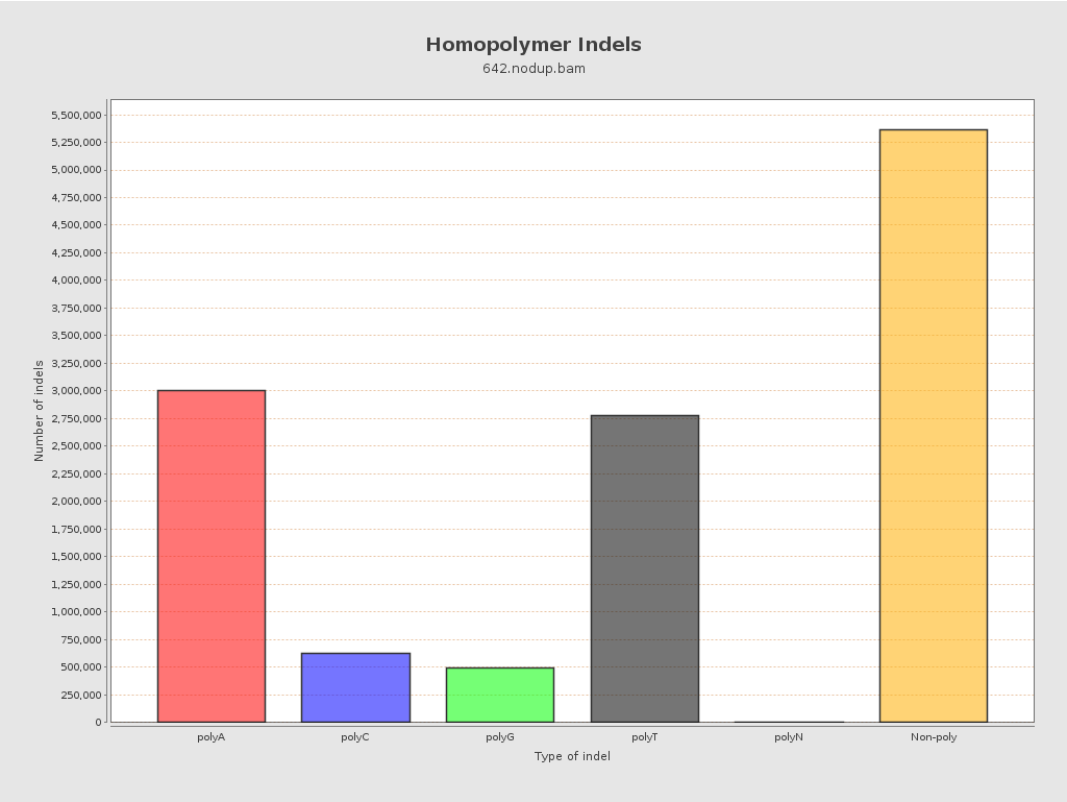
9. Results : Mapped Reads GC-content Distribution



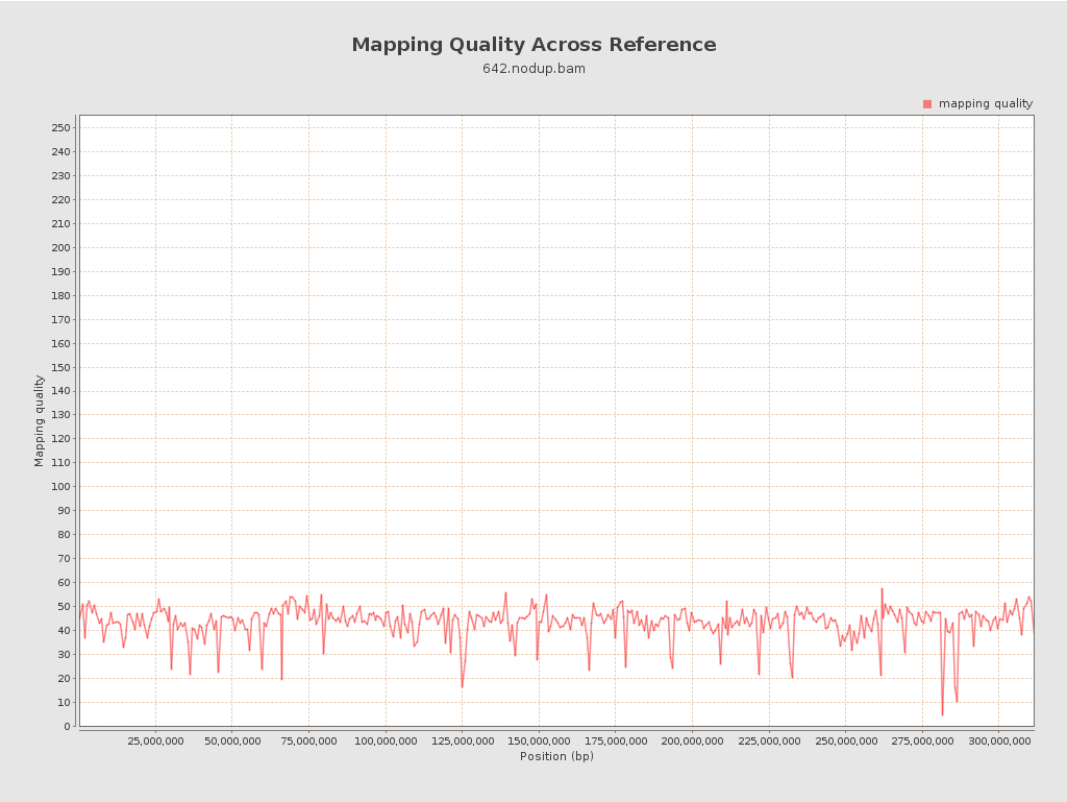
10. Results : Mapped Reads Clipping Profile



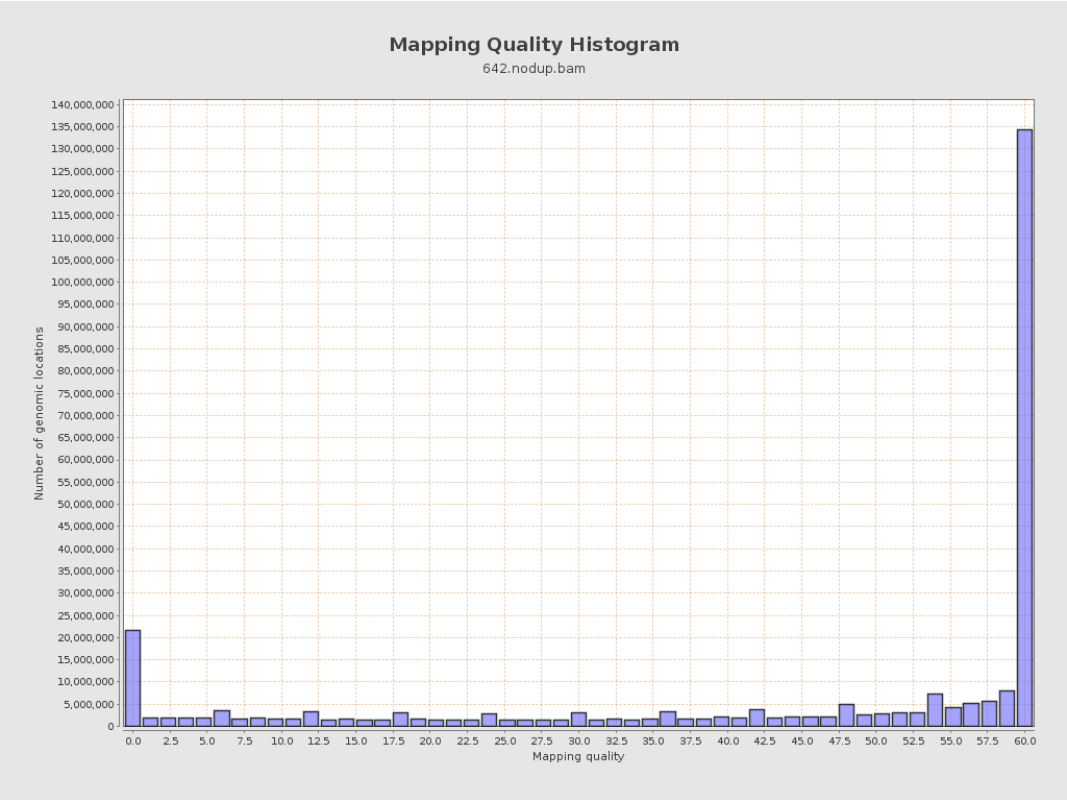
11. Results : Homopolymer Indels



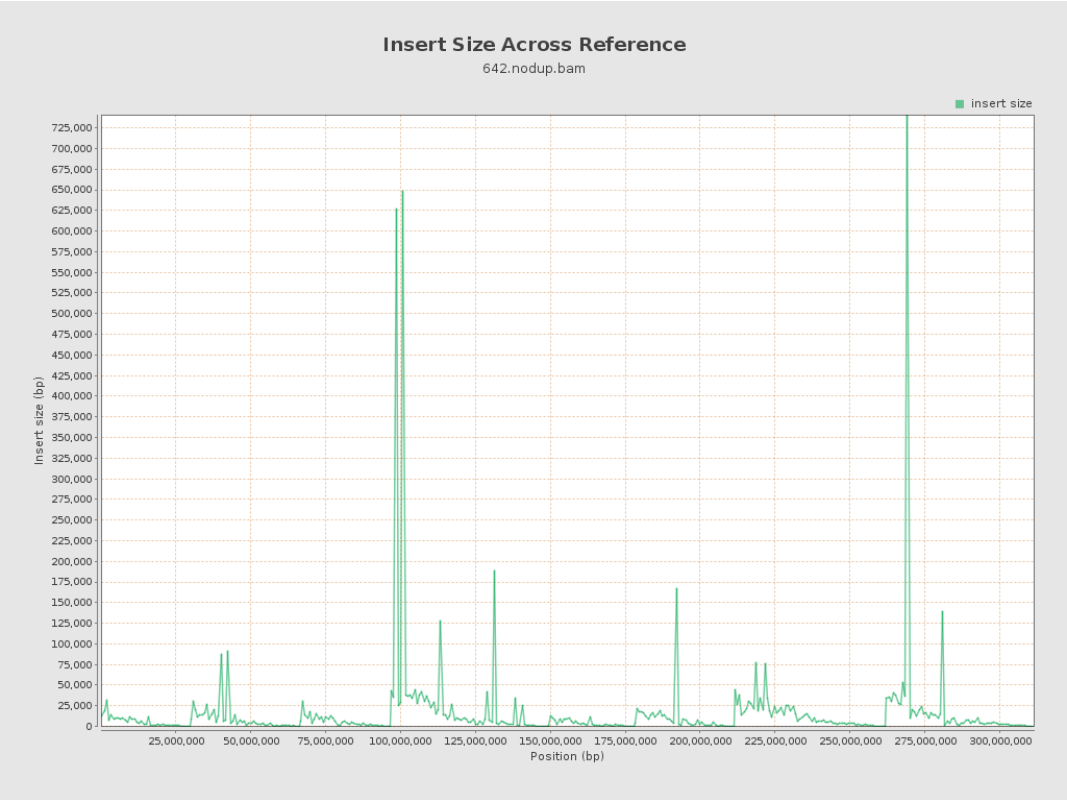
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram