Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/955.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/955.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_486/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_486_S461_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_486/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_486_S461_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	76,670,429
Mapped reads	73,591,263 / 95.98%
Unmapped reads	3,079,166 / 4.02%
Mapped paired reads	73,591,263 / 95.98%
Mapped reads, first in pair	36,844,655 / 48.06%
Mapped reads, second in pair	36,746,608 / 47.93%
Mapped reads, both in pair	72,458,629 / 94.51%
Mapped reads, singletons	1,132,634 / 1.48%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	10,982,174 / 14.32%
Clipped reads	15,160,029 / 19.77%

2.2. ACGT Content

Number/percentage of A's	3,178,453,815 / 30.82%
Number/percentage of C's	1,980,987,679 / 19.21%
Number/percentage of T's	3,182,768,329 / 30.86%
Number/percentage of G's	1,971,978,845 / 19.12%
Number/percentage of N's	35,736 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	33.1796
Standard Deviation	240.9999

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	229,319.39
Standard Deviation	2,249,601.83
P25/Median/P75	368 / 481 / 632

2.6. Mismatches and indels

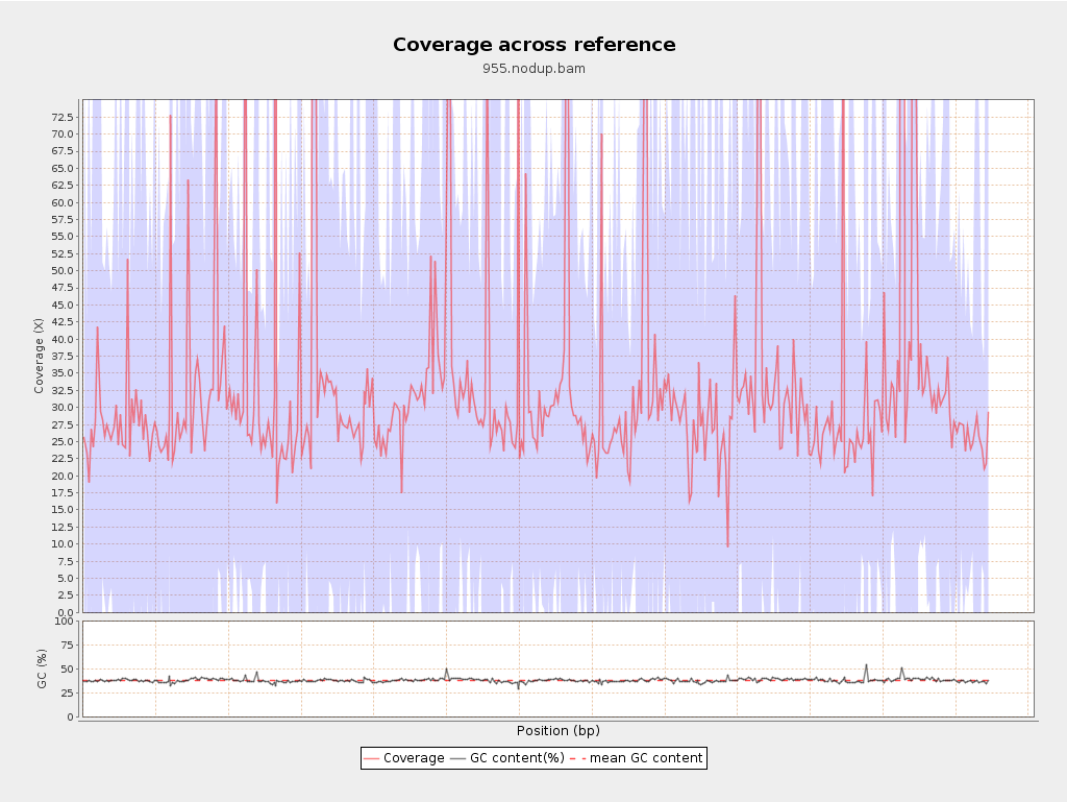
General error rate	2.26%
Mismatches	214,870,694
Insertions	6,566,449
Mapped reads with at least one insertion	8.07%
Deletions	6,888,190
Mapped reads with at least one deletion	8.3%
Homopolymer indels	55.87%

2.7. Chromosome stats

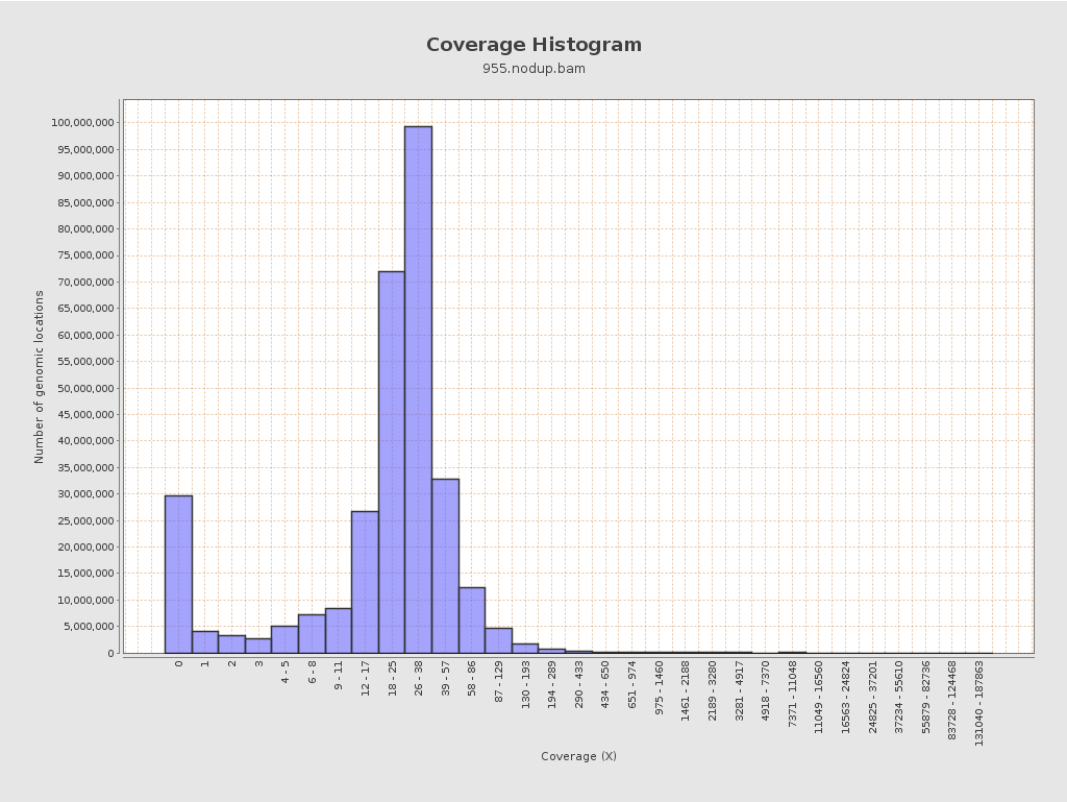
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	812824342	27.3454	64.2634

LT669789.1	36598175	1256381942	34.3291	289.1461
LT669790.1	30422129	999100910	32.8413	182.4949
LT669791.1	52758100	1722473725	32.6485	184.9564
LT669792.1	28376109	905772512	31.9203	266.1769
LT669793.1	33388210	1046314850	31.3379	190.1401
LT669794.1	50579949	1615185952	31.9333	230.3494
LT669795.1	49795044	1982100405	39.8052	352.7199

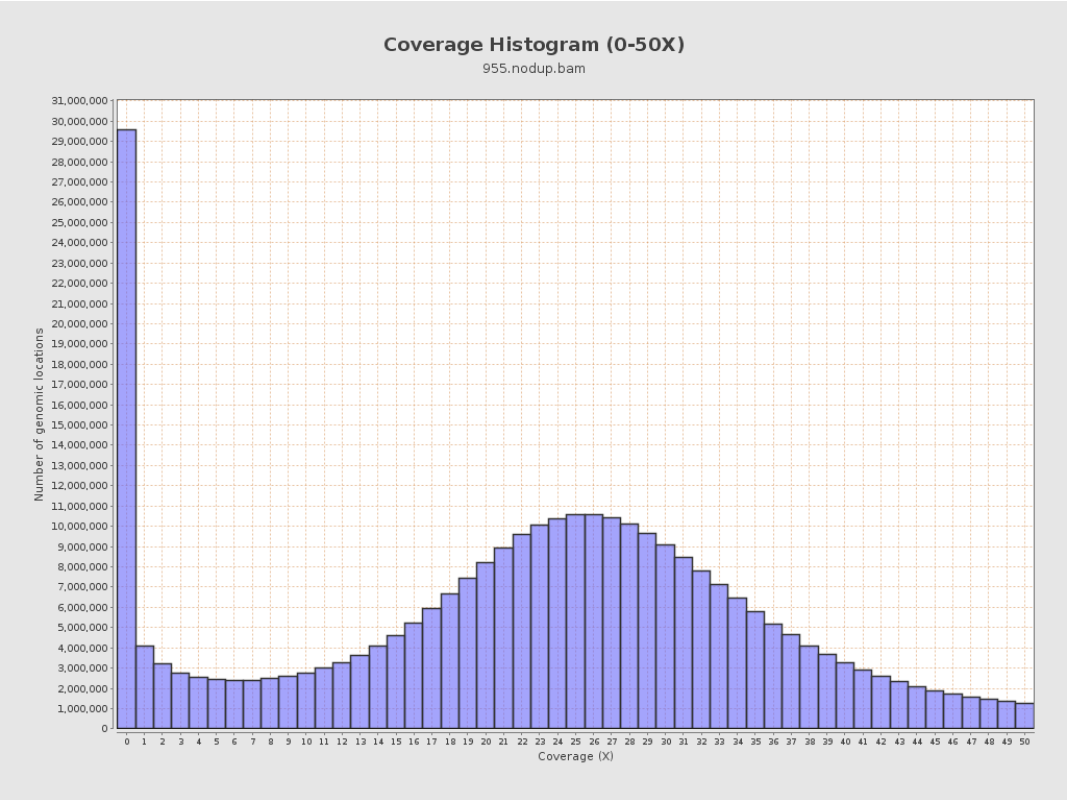
3. Results : Coverage across reference



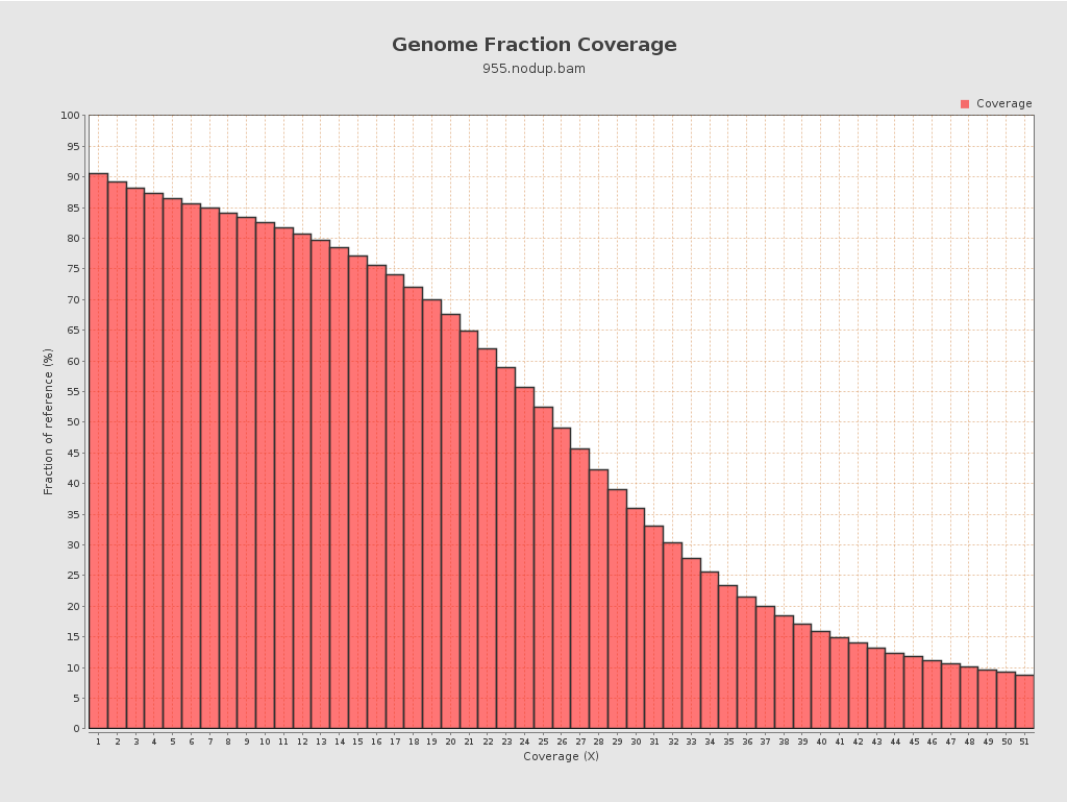
4. Results : Coverage Histogram



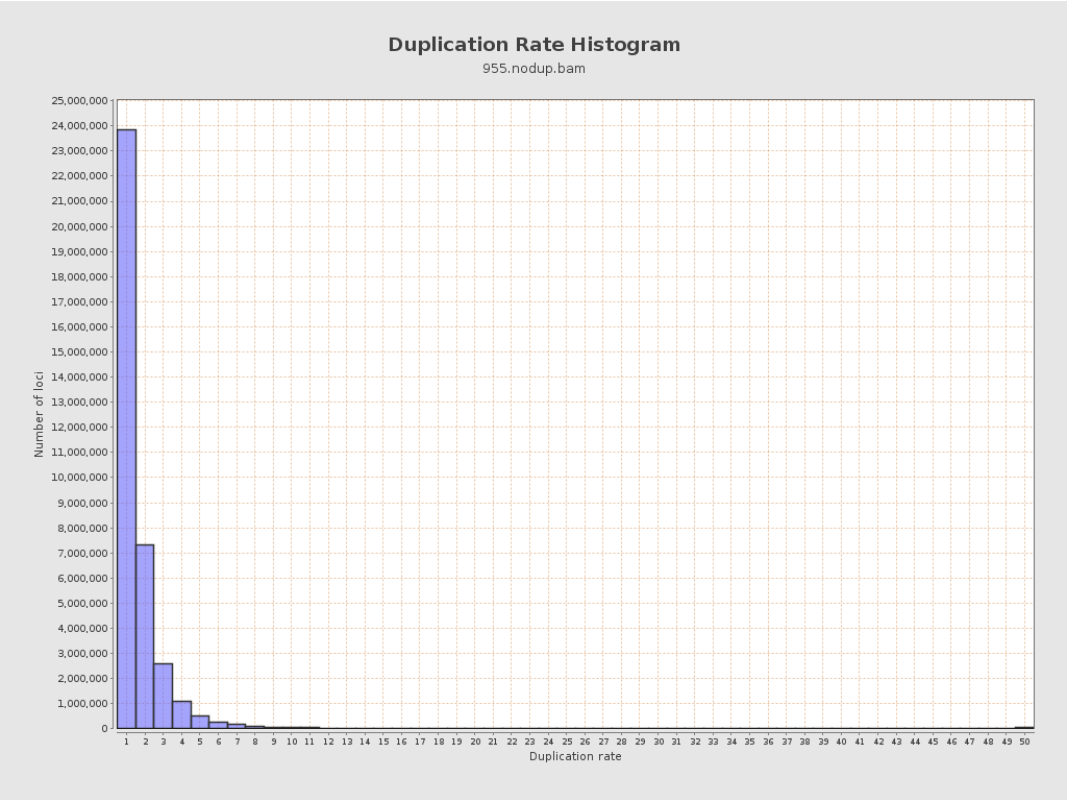
5. Results : Coverage Histogram (0-50X)



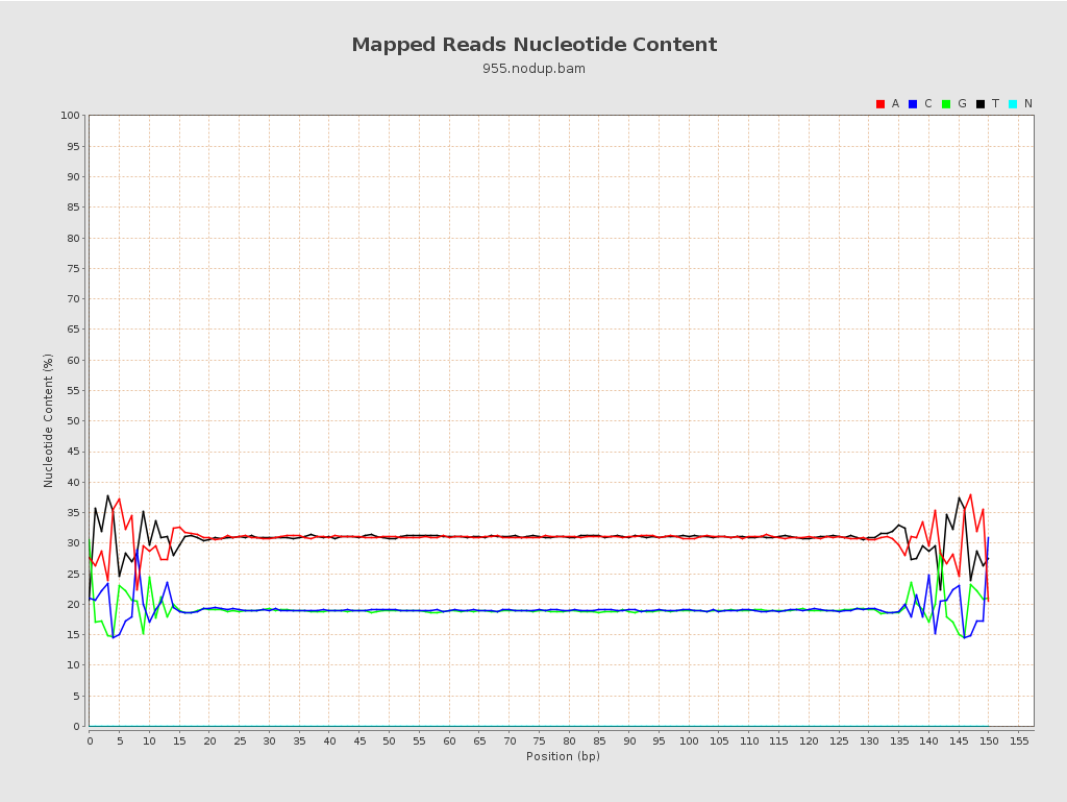
6. Results : Genome Fraction Coverage



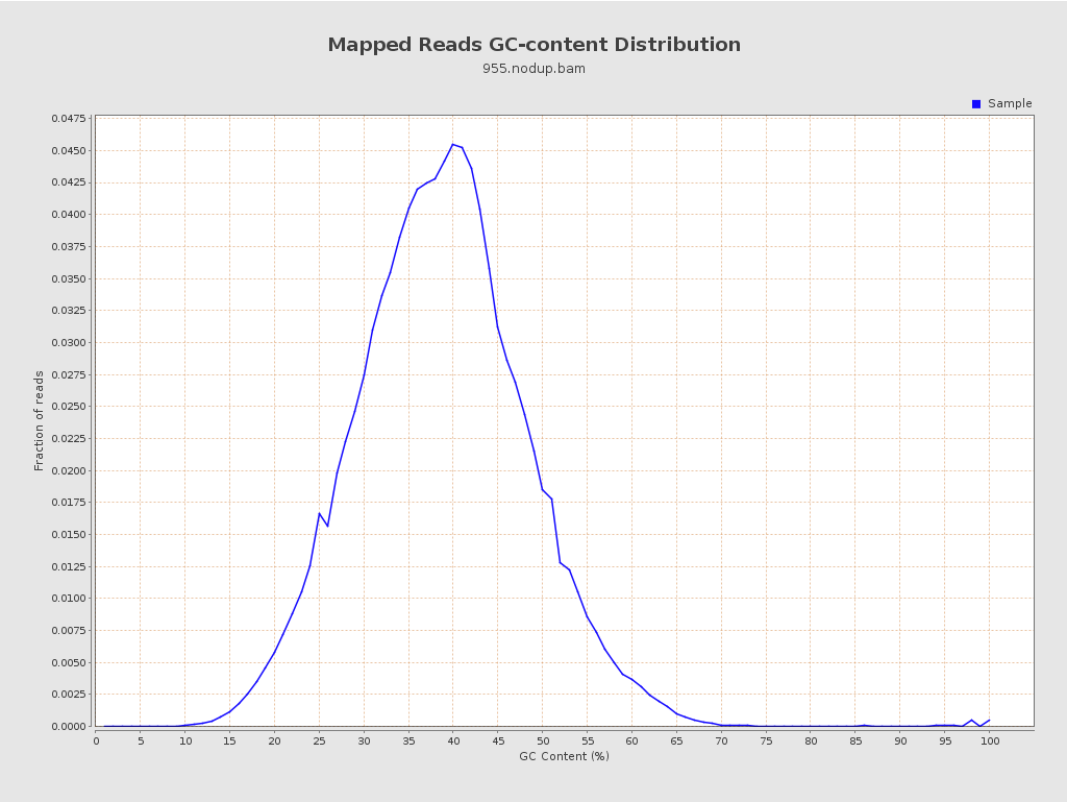
7. Results : Duplication Rate Histogram



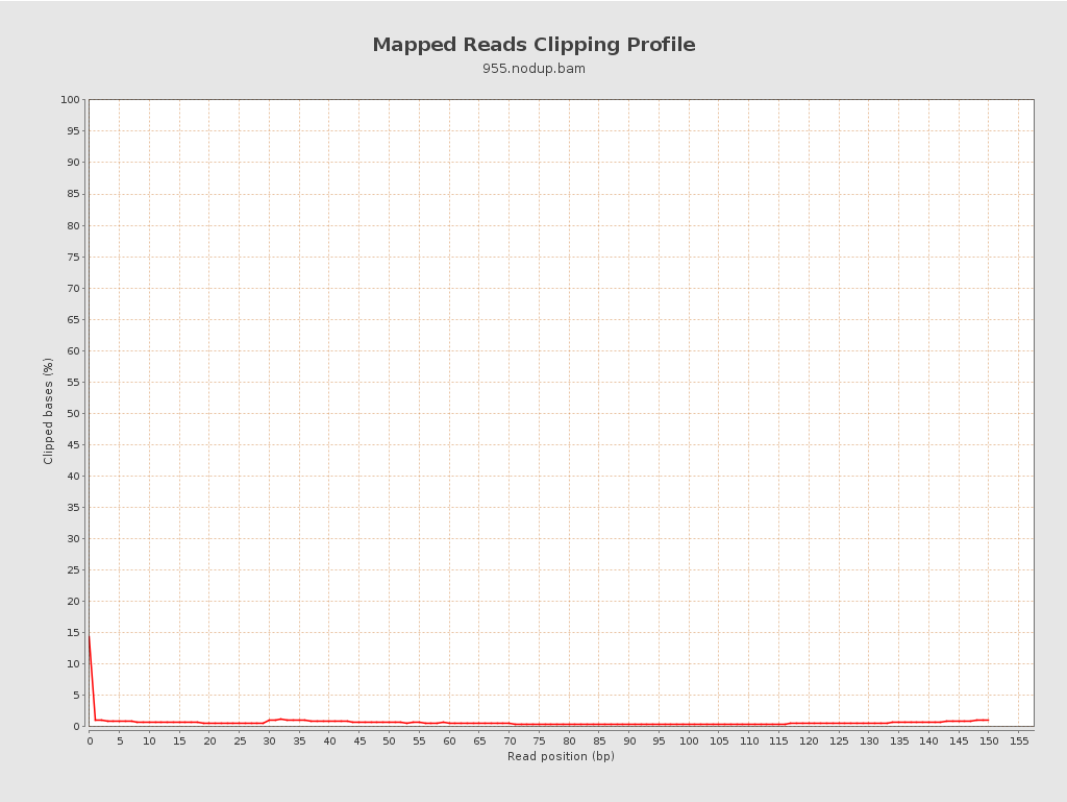
8. Results : Mapped Reads Nucleotide Content



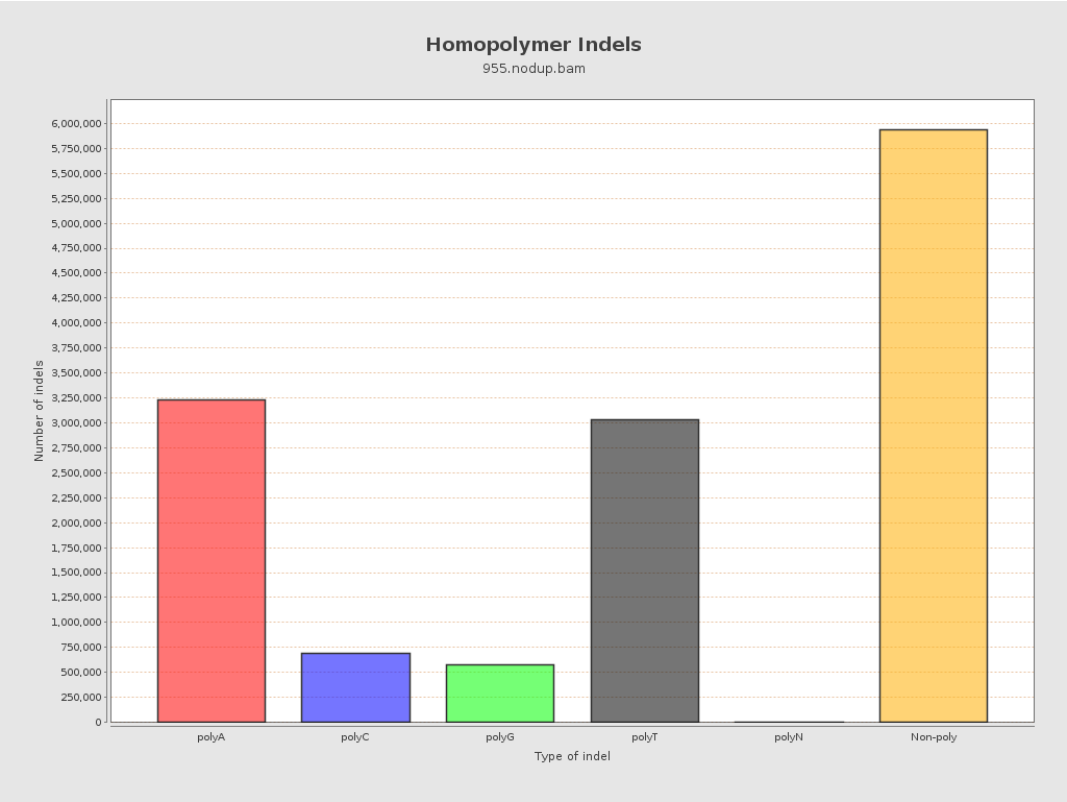
9. Results : Mapped Reads GC-content Distribution



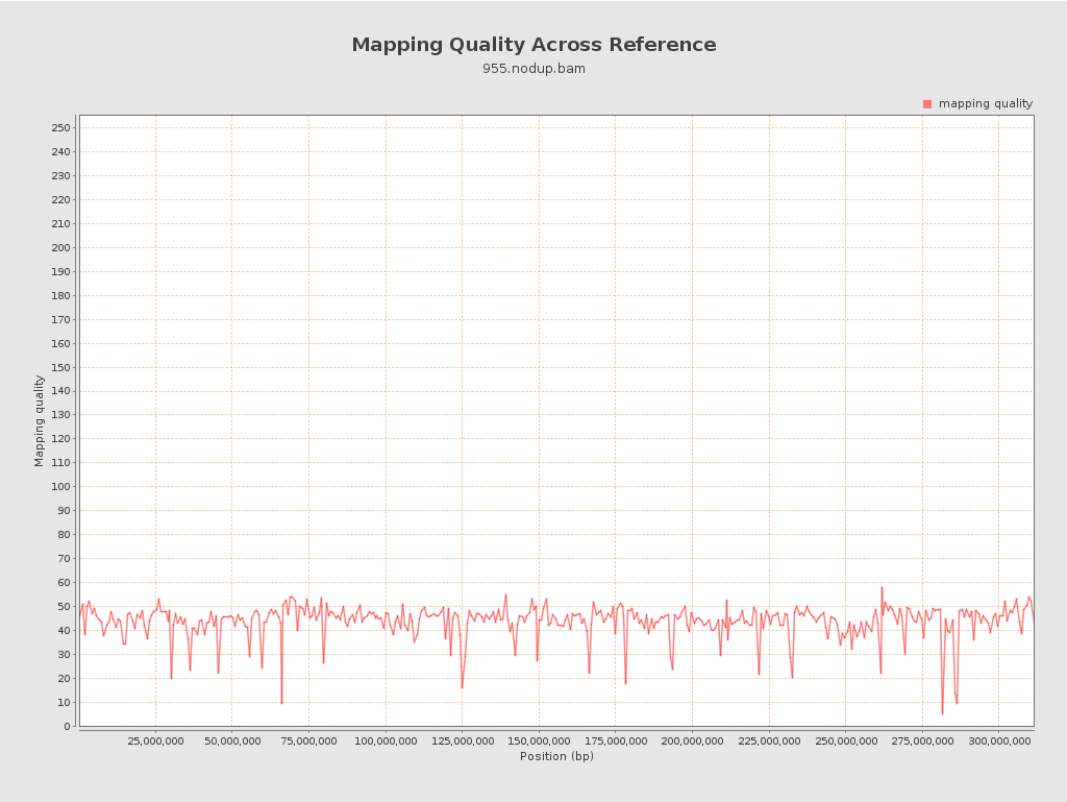
10. Results : Mapped Reads Clipping Profile



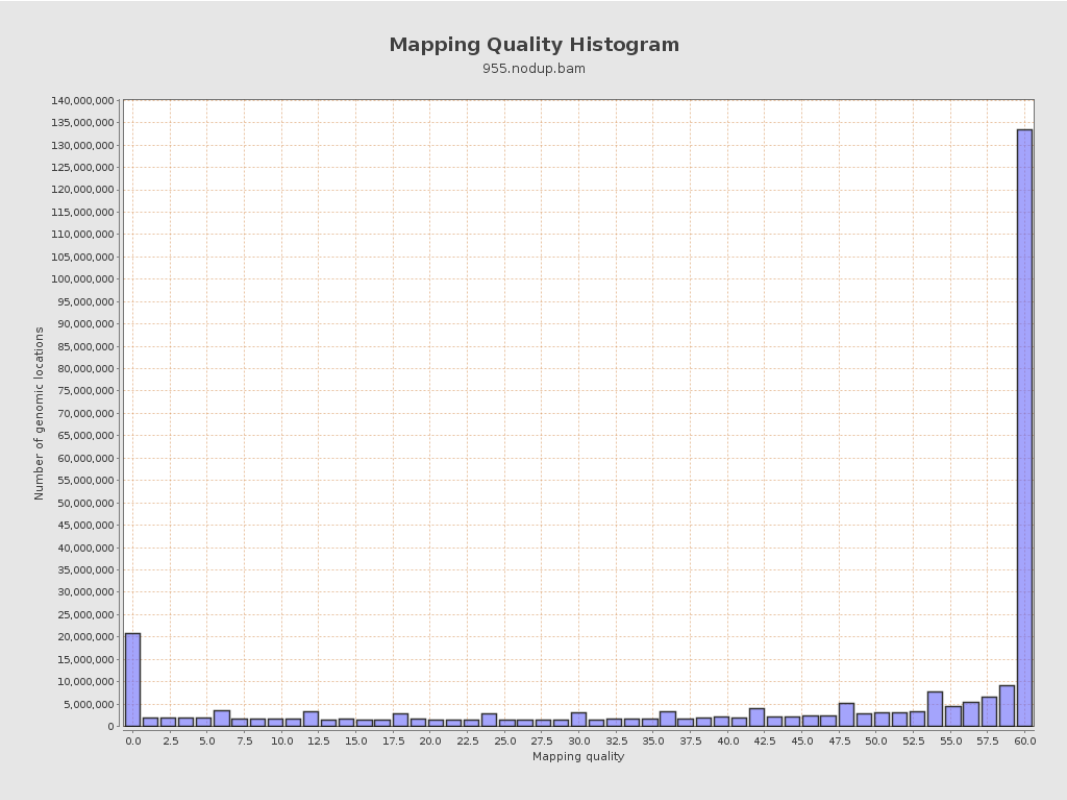
11. Results : Homopolymer Indels



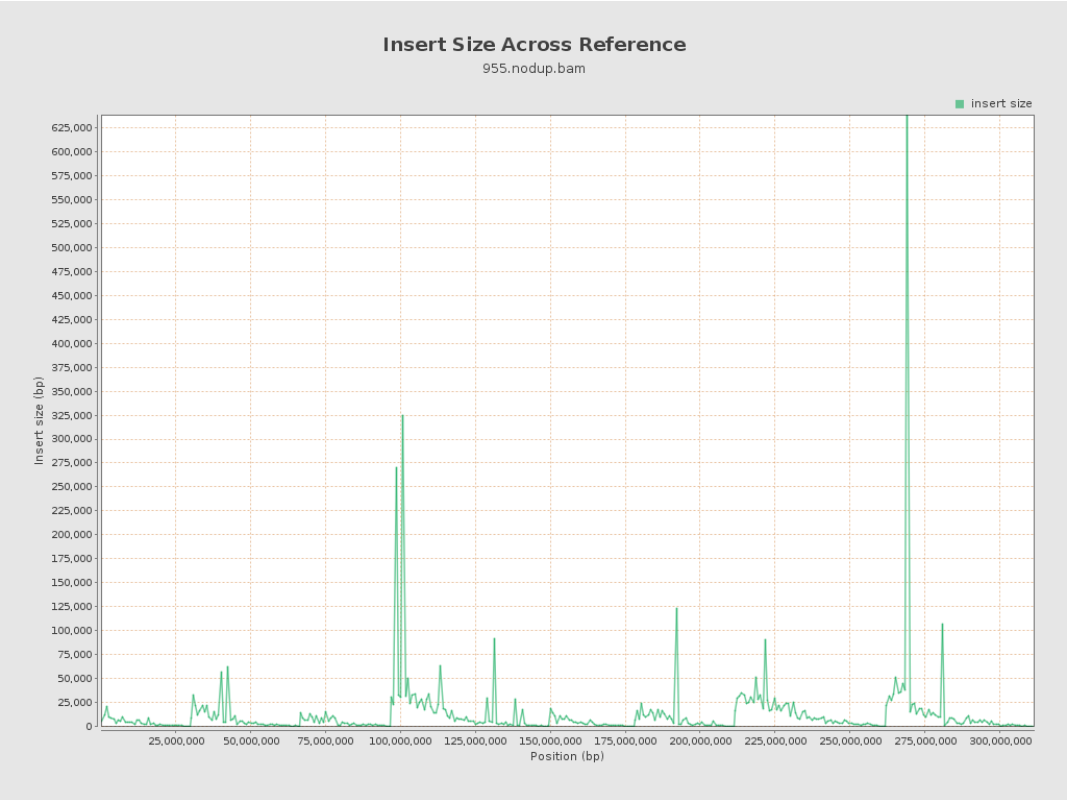
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram