Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/790.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/790.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_266/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_266_S347_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_266/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_266_S347_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,825,204
Mapped reads	60,206,113 / 94.33%
Unmapped reads	3,619,091 / 5.67%
Mapped paired reads	60,206,113 / 94.33%
Mapped reads, first in pair	30,142,793 / 47.23%
Mapped reads, second in pair	30,063,320 / 47.1%
Mapped reads, both in pair	59,005,211 / 92.45%
Mapped reads, singletons	1,200,902 / 1.88%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	9,056,971 / 14.19%
Clipped reads	13,921,766 / 21.81%

2.2. ACGT Content

Number/percentage of A's	2,562,992,122 / 30.76%
Number/percentage of C's	1,603,782,992 / 19.25%
Number/percentage of T's	2,566,166,560 / 30.79%
Number/percentage of G's	1,600,353,407 / 19.2%
Number/percentage of N's	30,608 / 0%
GC Percentage	38.45%

2.3. Coverage

Mean	26.8119
Standard Deviation	232.5495

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Insert size

Mean	233,856.83
Standard Deviation	2,269,598.07
P25/Median/P75	317 / 417 / 547

2.6. Mismatches and indels

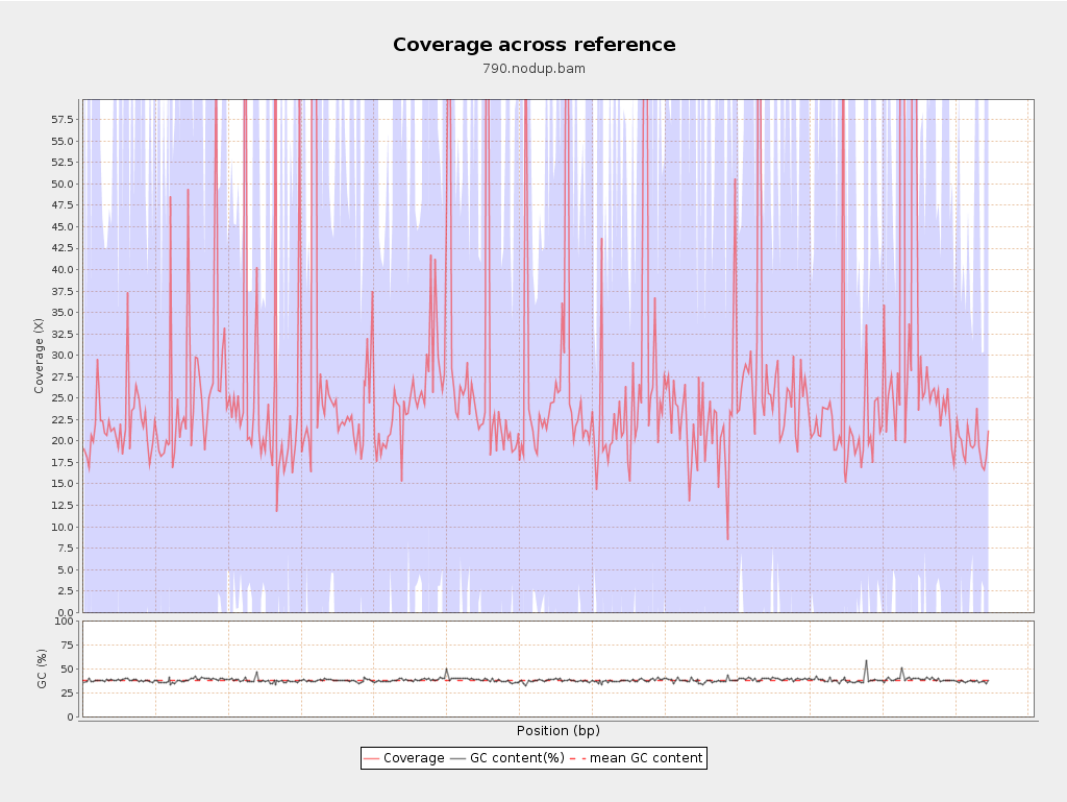
General error rate	2.41%
Mismatches	185,115,905
Insertions	5,739,855
Mapped reads with at least one insertion	8.57%
Deletions	5,893,020
Mapped reads with at least one deletion	8.7%
Homopolymer indels	55.85%

2.7. Chromosome stats

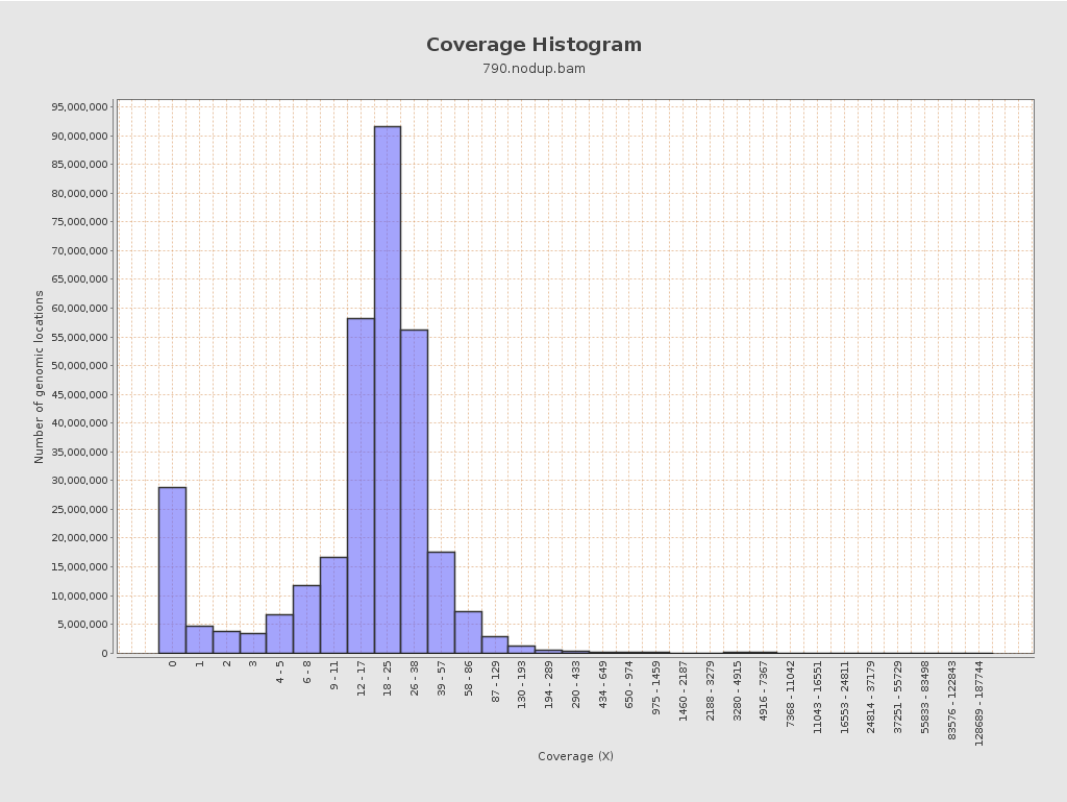
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	639138578	21.5022	65.3447

LT669789.1	36598175	1000569879	27.3393	230.42
LT669790.1	30422129	869087139	28.5676	242.3333
LT669791.1	52758100	1406094276	26.6517	201.8167
LT669792.1	28376109	738072496	26.0103	273.467
LT669793.1	33388210	858108118	25.7009	224.1059
LT669794.1	50579949	1309192617	25.8836	211.0984
LT669795.1	49795044	1535465406	30.8357	310.2546

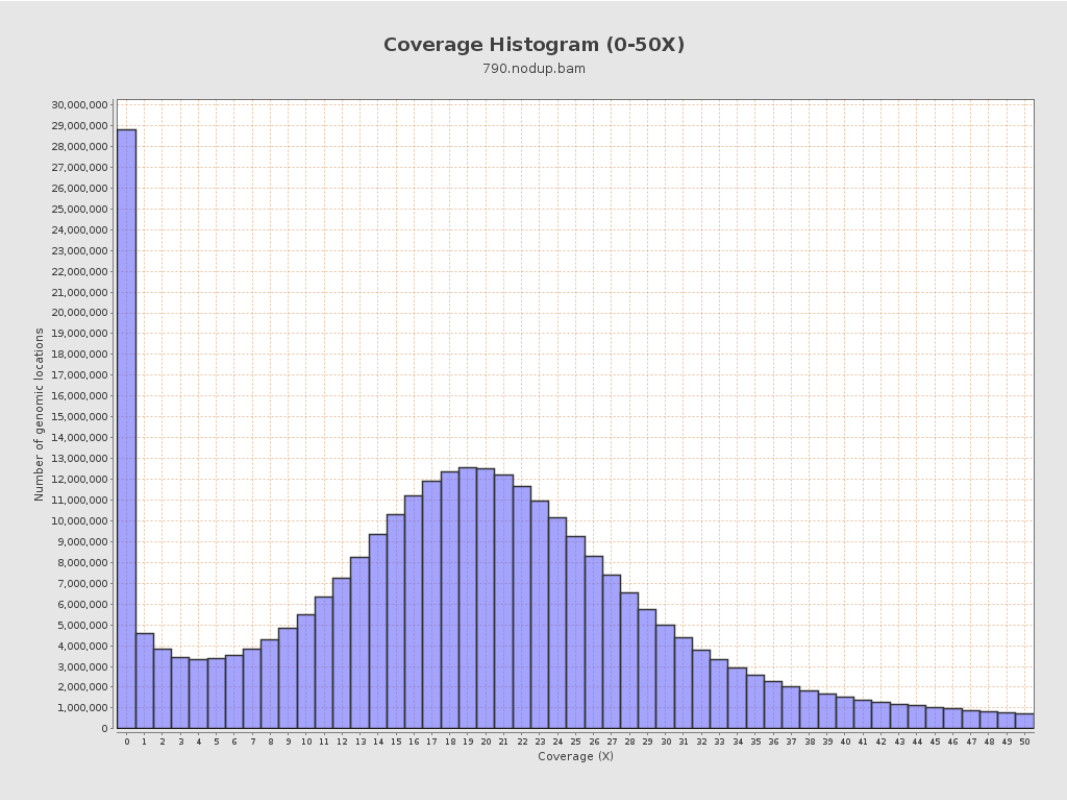
3. Results : Coverage across reference



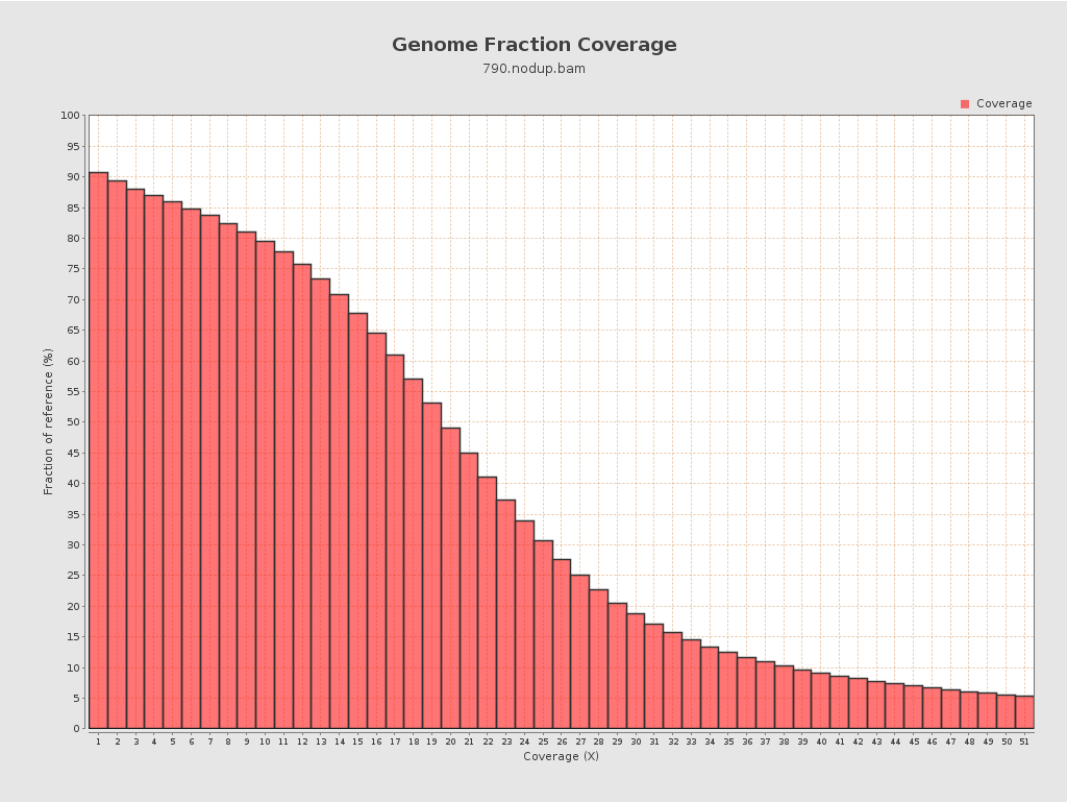
4. Results : Coverage Histogram



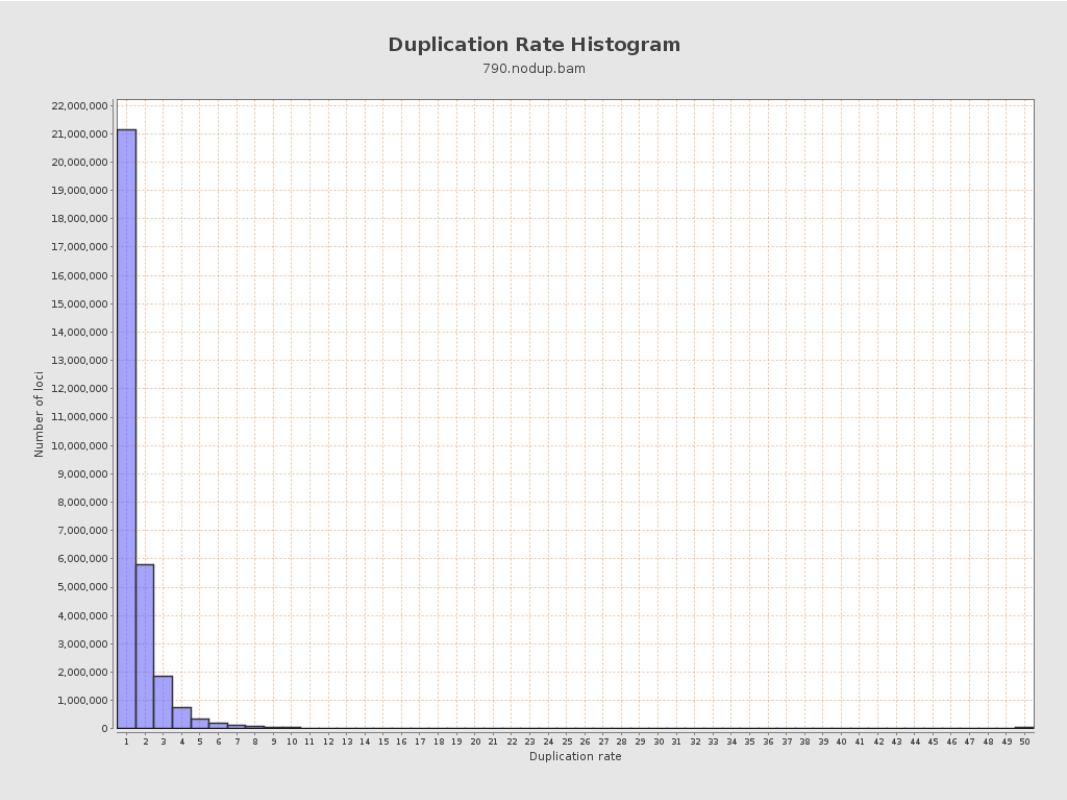
5. Results : Coverage Histogram (0-50X)



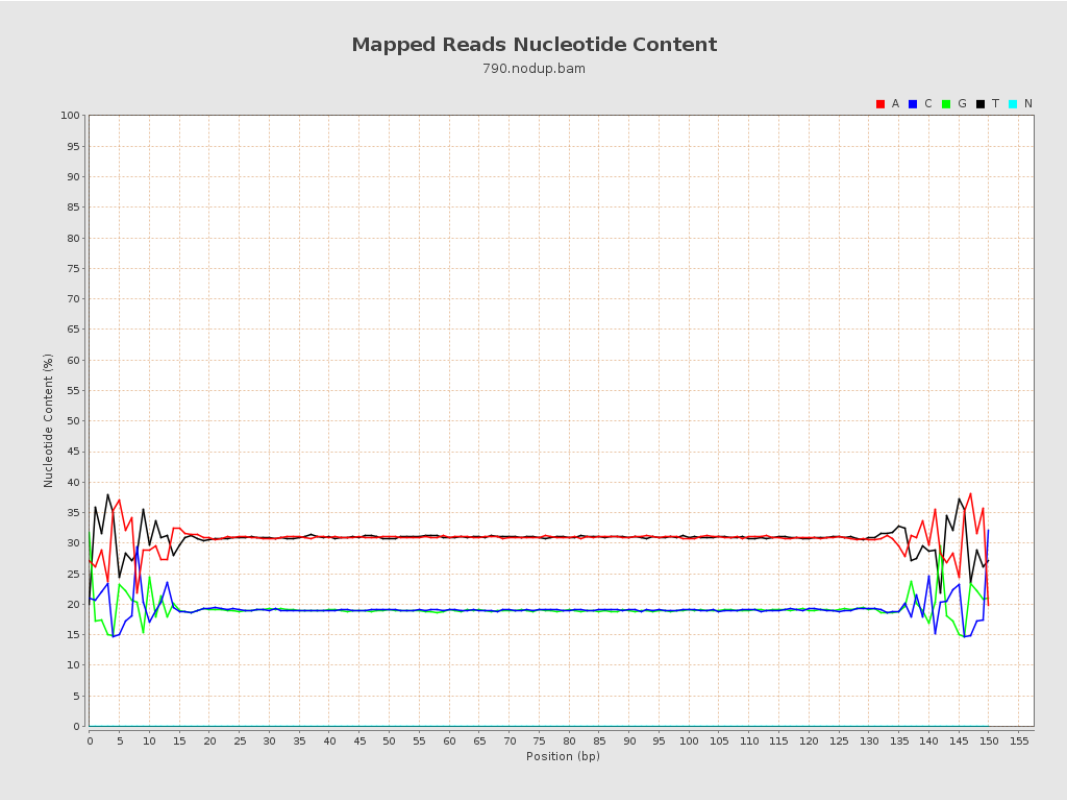
6. Results : Genome Fraction Coverage



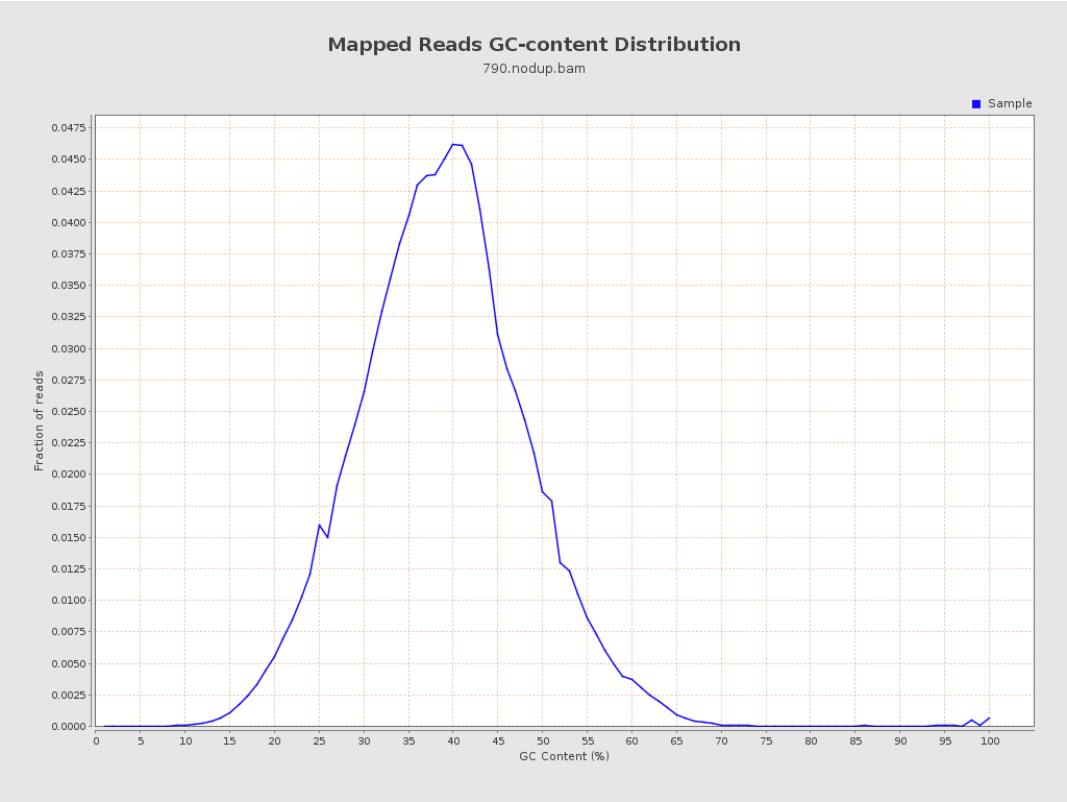
7. Results : Duplication Rate Histogram



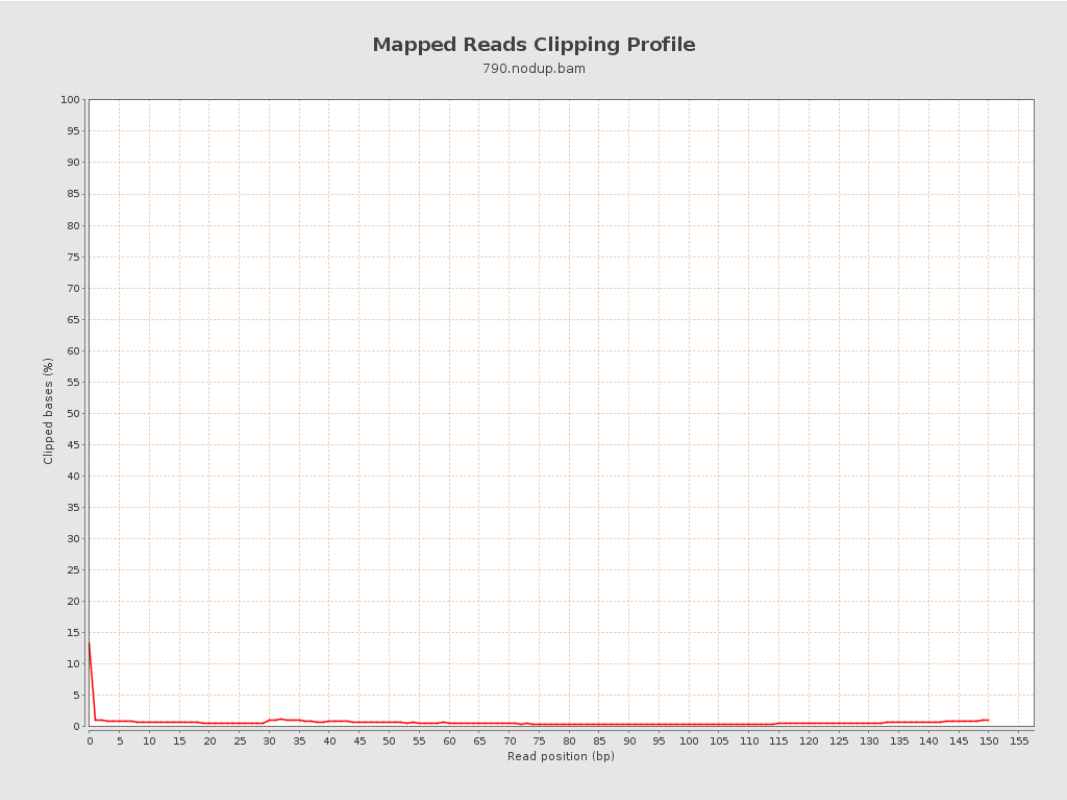
8. Results : Mapped Reads Nucleotide Content



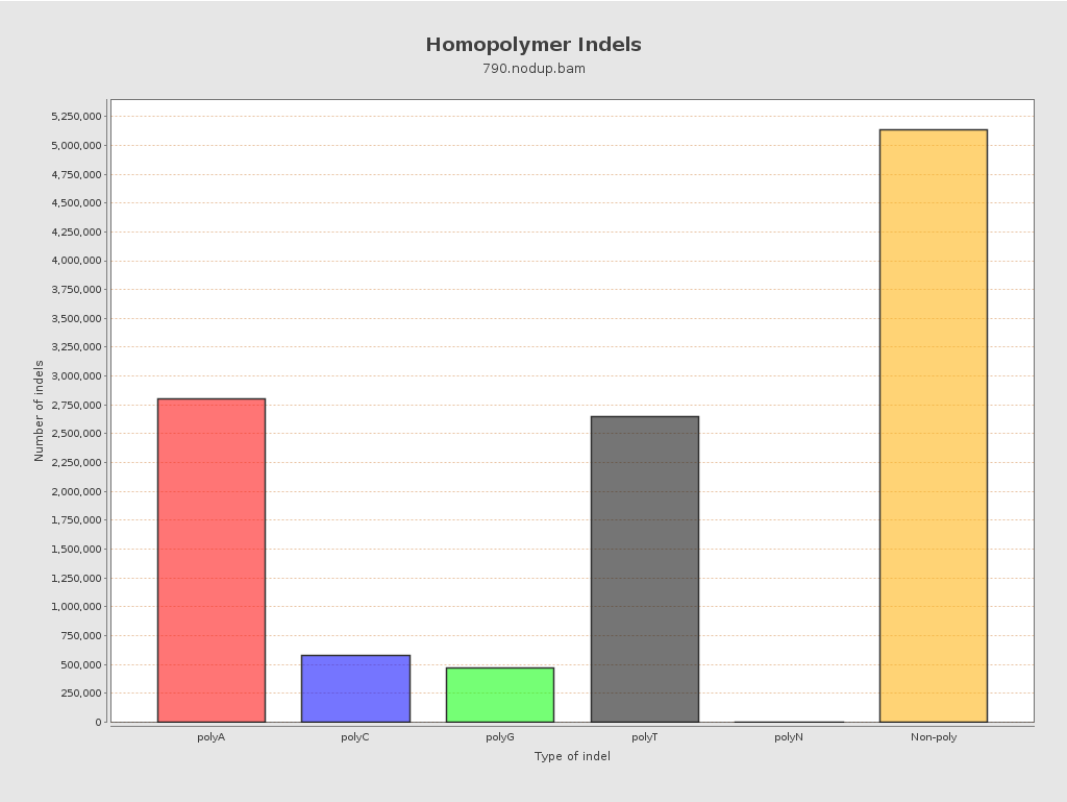
9. Results : Mapped Reads GC-content Distribution



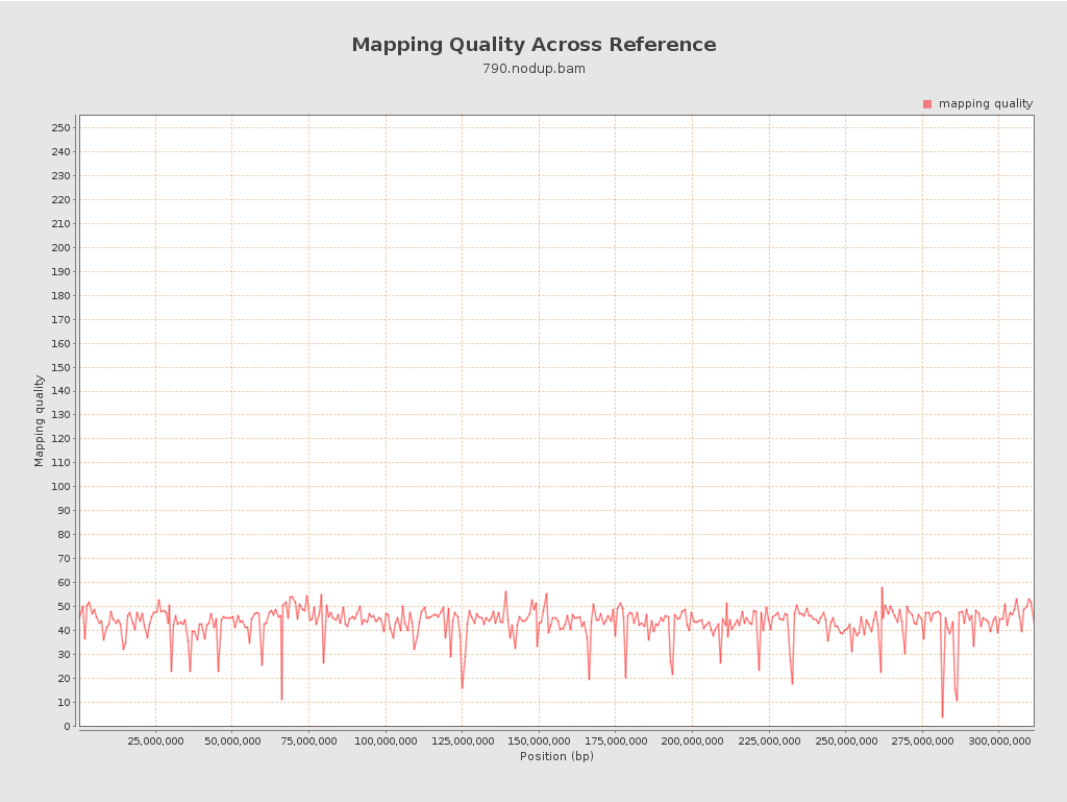
10. Results : Mapped Reads Clipping Profile



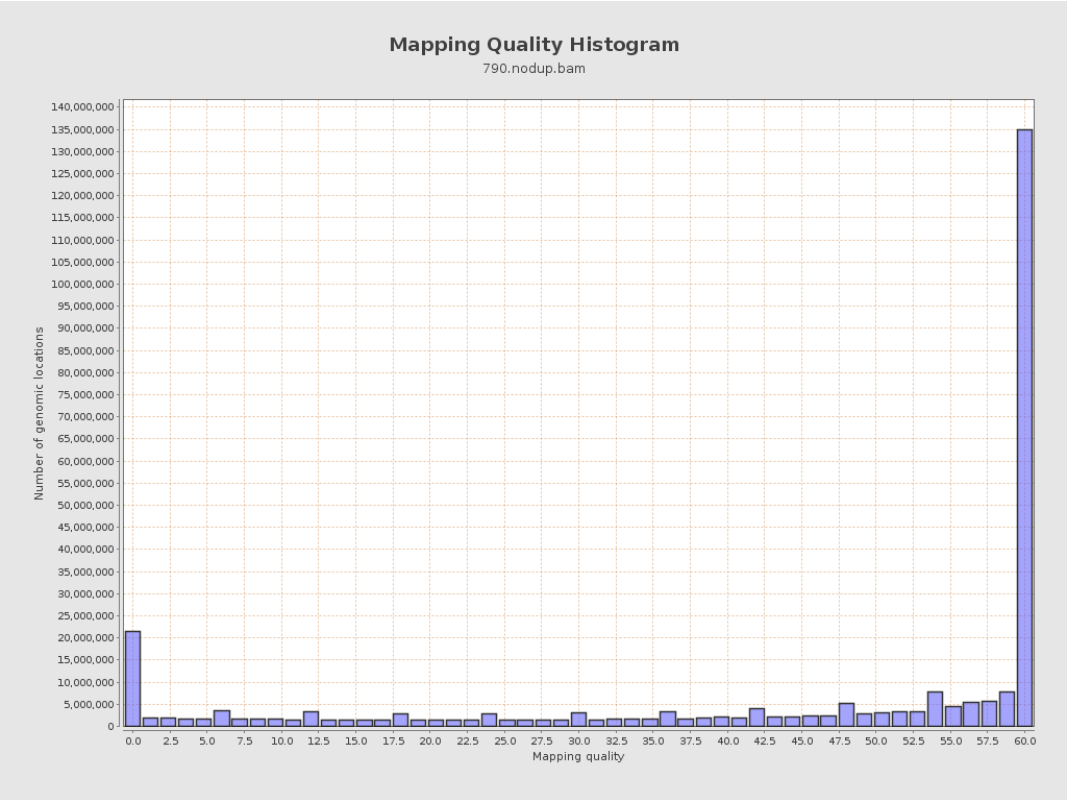
11. Results : Homopolymer Indels



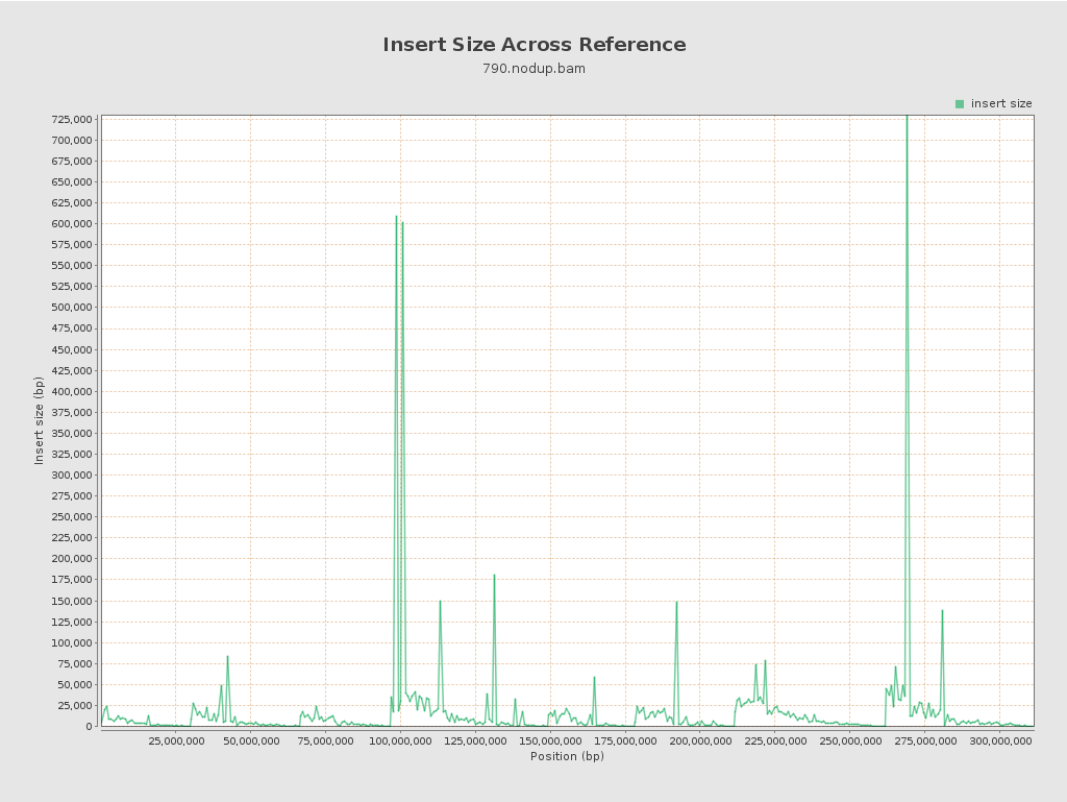
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram