Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:48

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/IT6
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/IT6 .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_485/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_485_S460_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_485/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_485_S460_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	54,326,372
Mapped reads	50,833,230 / 93.57%
Unmapped reads	3,493,142 / 6.43%
Mapped paired reads	50,833,230 / 93.57%
Mapped reads, first in pair	25,479,417 / 46.9%
Mapped reads, second in pair	25,353,813 / 46.67%
Mapped reads, both in pair	49,869,753 / 91.8%
Mapped reads, singletons	963,477 / 1.77%
Read min/max/mean length	30 / 151 / 147.87
Duplicated reads (flagged)	7,014,885 / 12.91%
Clipped reads	11,698,284 / 21.53%

2.2. ACGT Content

Number/percentage of A's	2,166,388,448 / 30.73%
Number/percentage of C's	1,357,631,540 / 19.26%
Number/percentage of T's	2,167,670,393 / 30.75%
Number/percentage of G's	1,357,002,057 / 19.25%
Number/percentage of N's	24,130 / 0%
GC Percentage	38.51%

2.3. Coverage

Mean	22.6834
Standard Deviation	183.3693

2.4. Mapping Quality

Mean Mapping Quality	42.58

2.5. Insert size

Mean	269,967.12
Standard Deviation	2,437,785.91
P25/Median/P75	366 / 478 / 626

2.6. Mismatches and indels

General error rate	2.48%
Mismatches	161,005,825
Insertions	4,965,520
Mapped reads with at least one insertion	8.77%
Deletions	5,281,121
Mapped reads with at least one deletion	9.19%
Homopolymer indels	55.52%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	552422502	18.5849	61.7097

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LT669789.1	36598175	871016095	23.7994	191.82
LT669790.1	30422129	696567896	22.8968	145.1311
LT669791.1	52758100	1188960330	22.5361	169.703
LT669792.1	28376109	629106888	22.1703	206.377
LT669793.1	33388210	735258619	22.0215	179.4863
LT669794.1	50579949	1131263478	22.3658	174.5454
LT669795.1	49795044	1264519261	25.3945	246.7847

3. Results : Coverage across reference
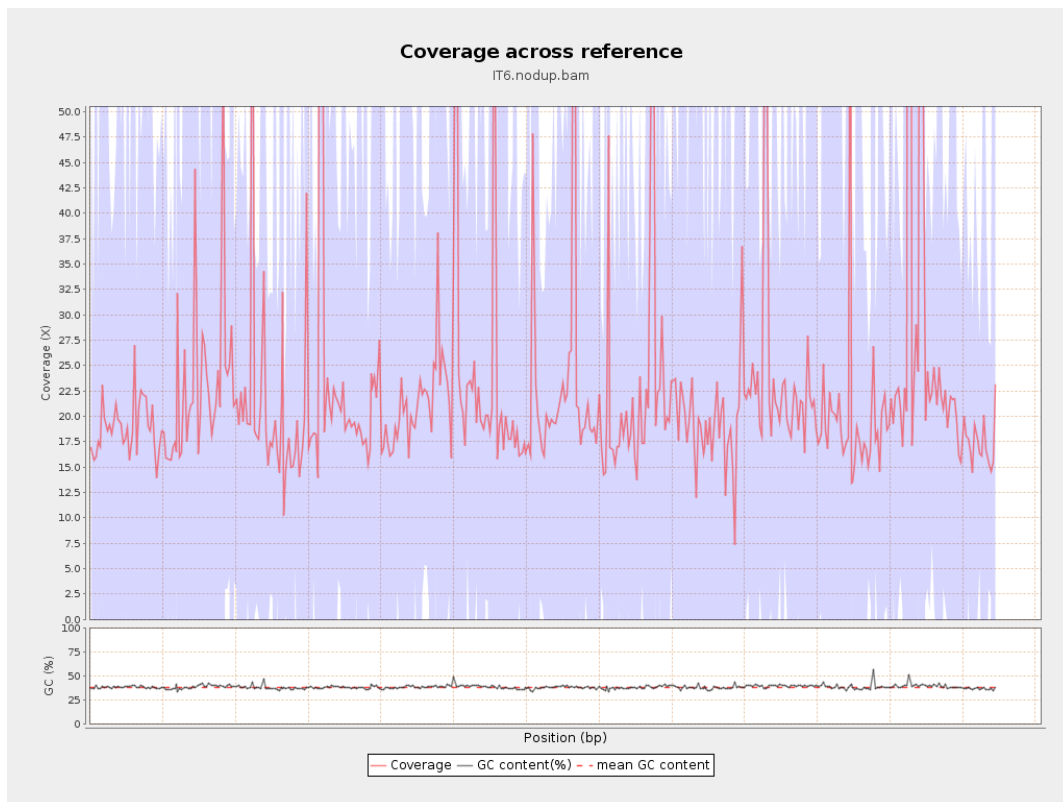
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
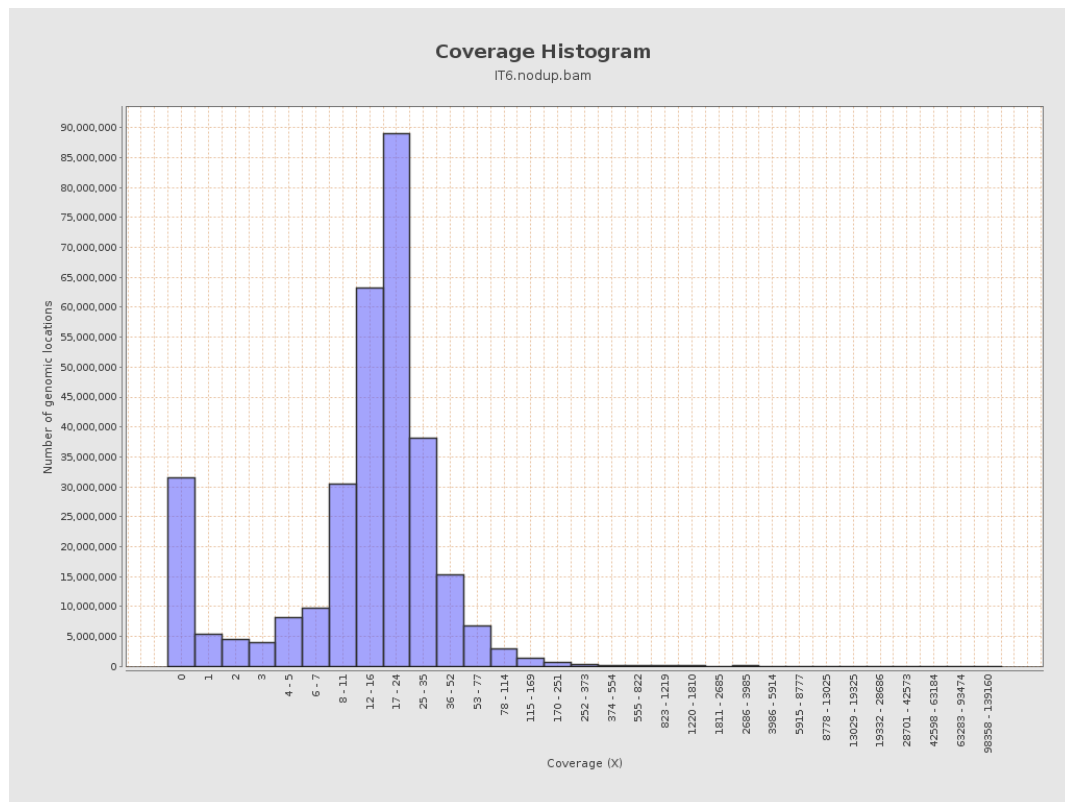
Coverage Histogram (0-50X)
IT6.nodup.bam
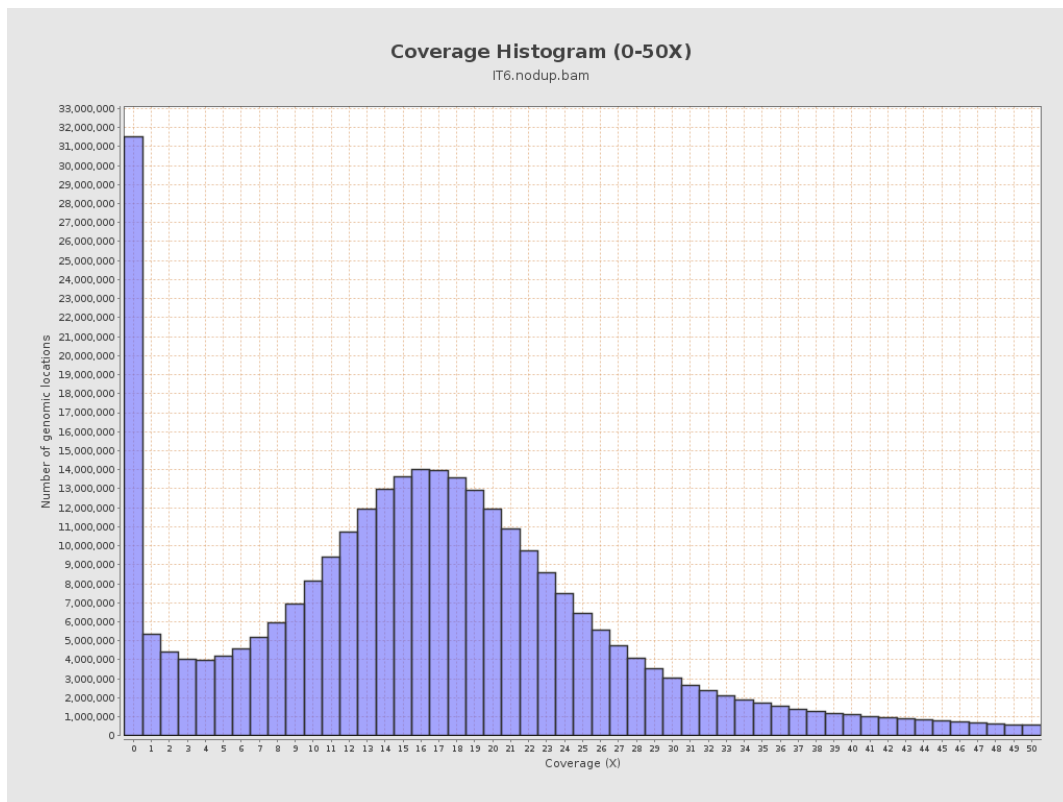
6. Results : Genome Fraction Coverage
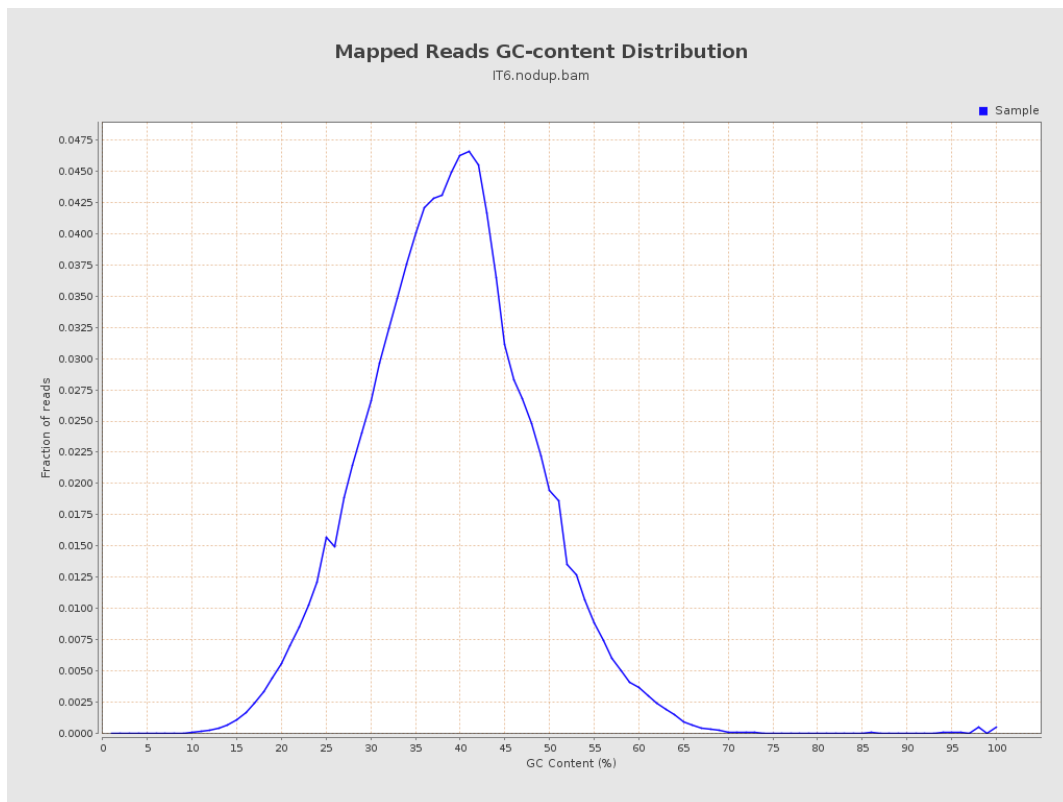

Genome Fraction Coverage
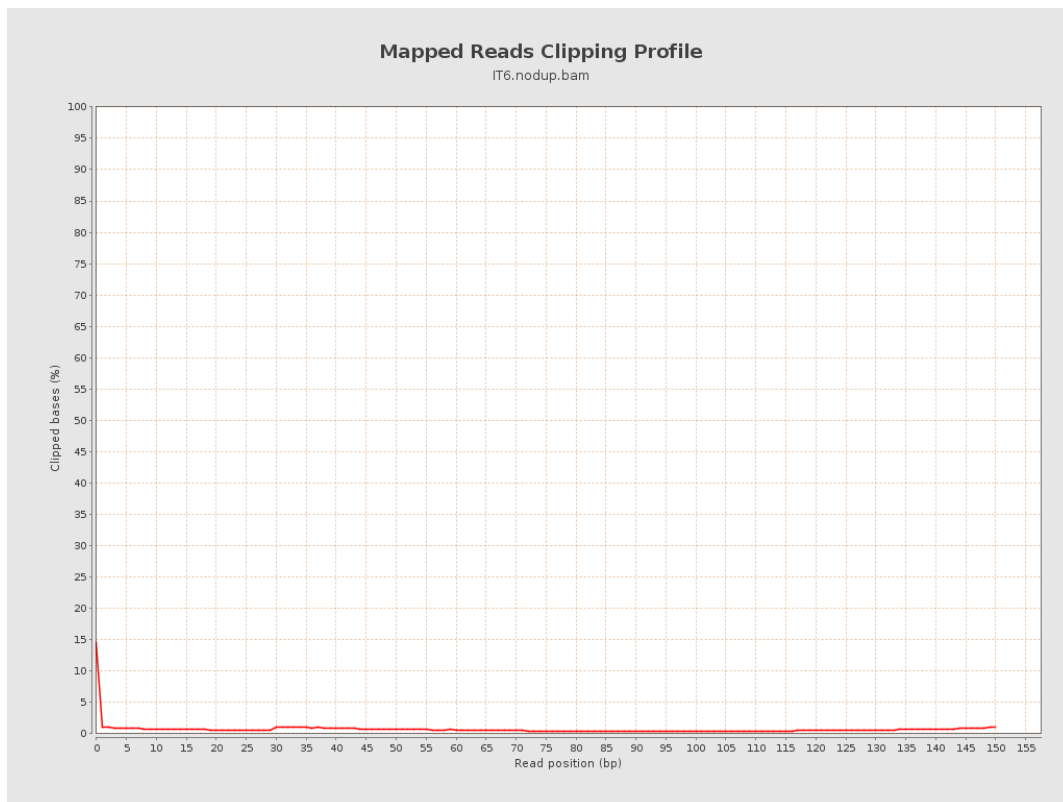IT6.nodup.bam
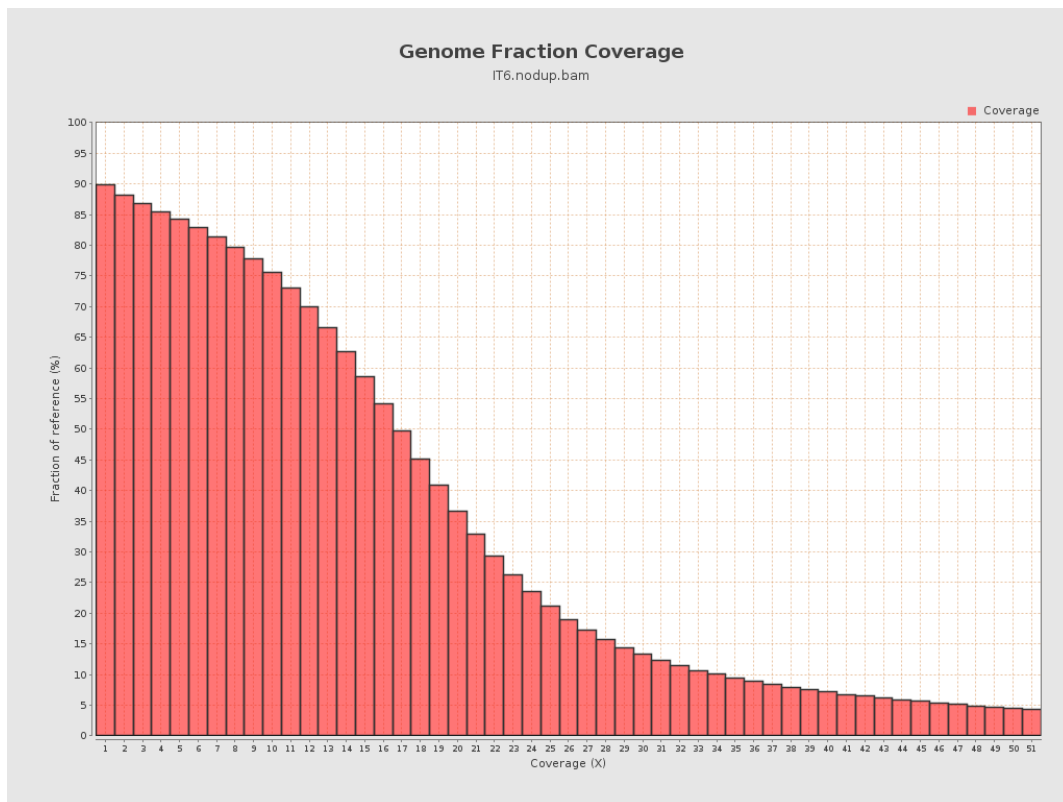
7. Results : Duplication Rate Histogram
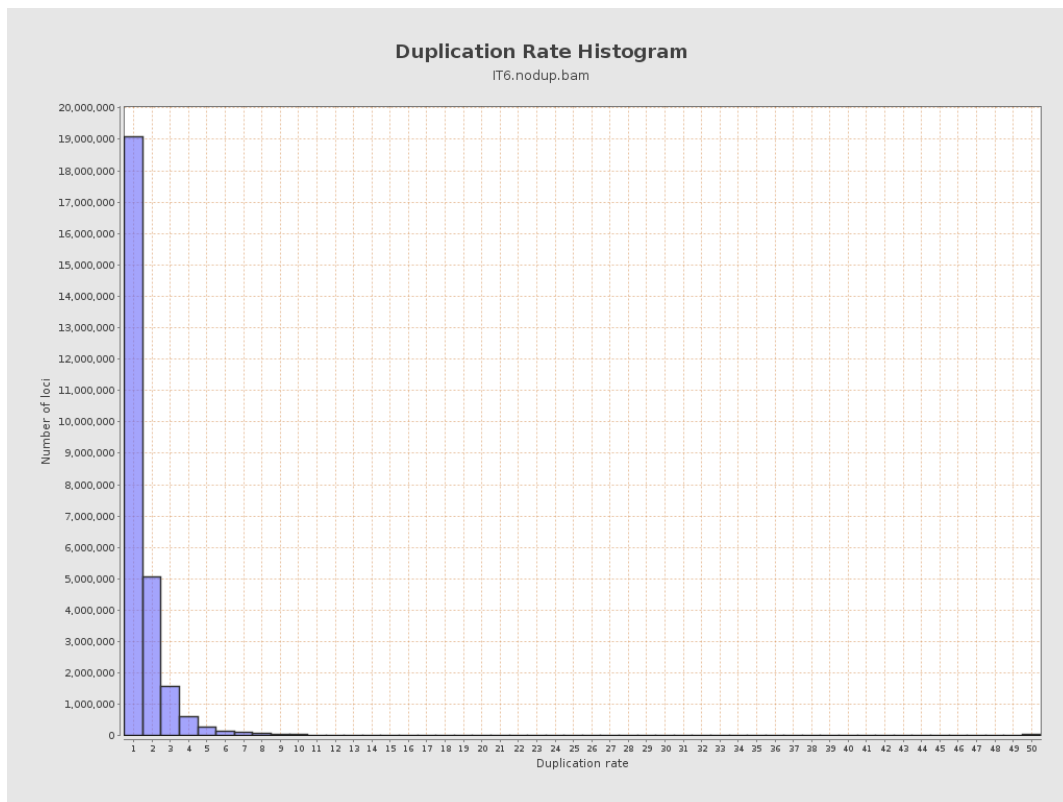
8. Results : Mapped Reads Nucleotide Content
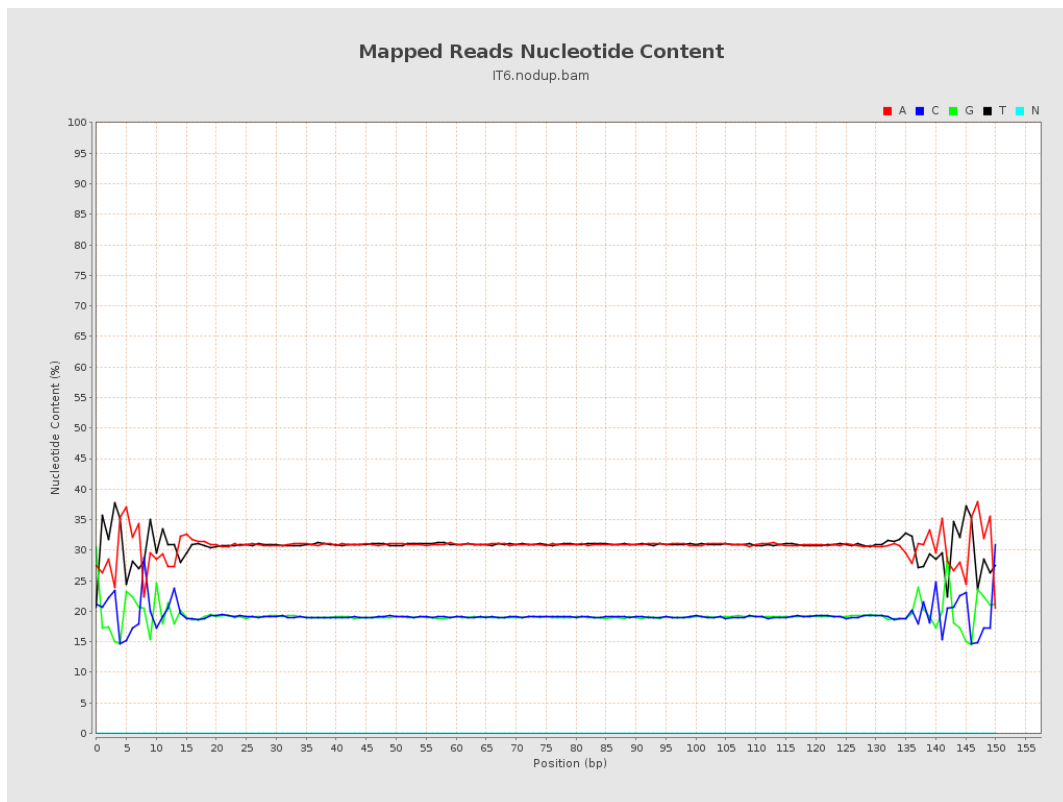
9. Results : Mapped Reads GC-content Distribution

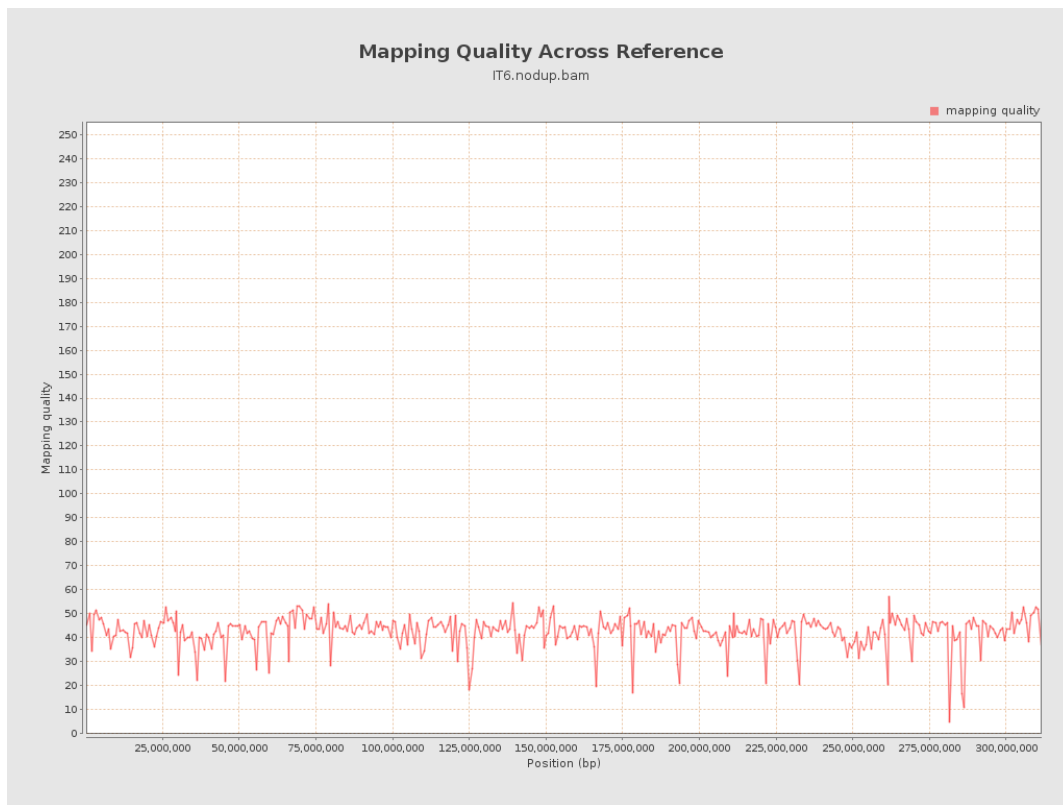# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
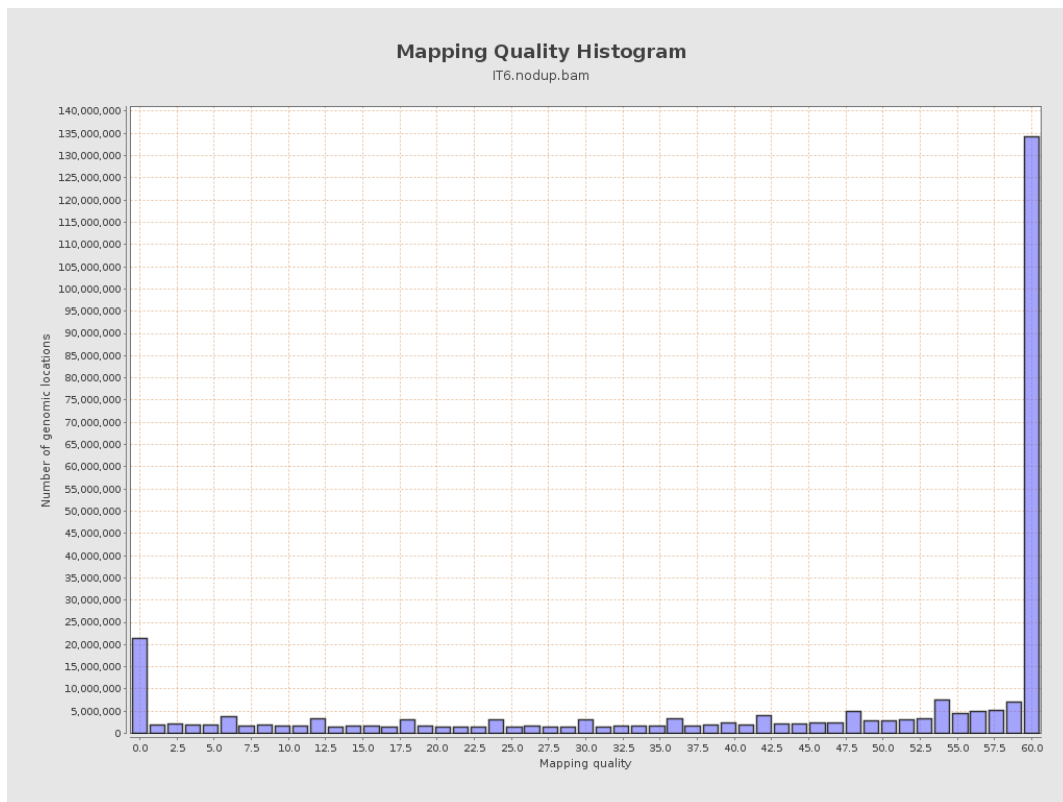IT6.nodup.bam

11. Results : Homopolymer Indels
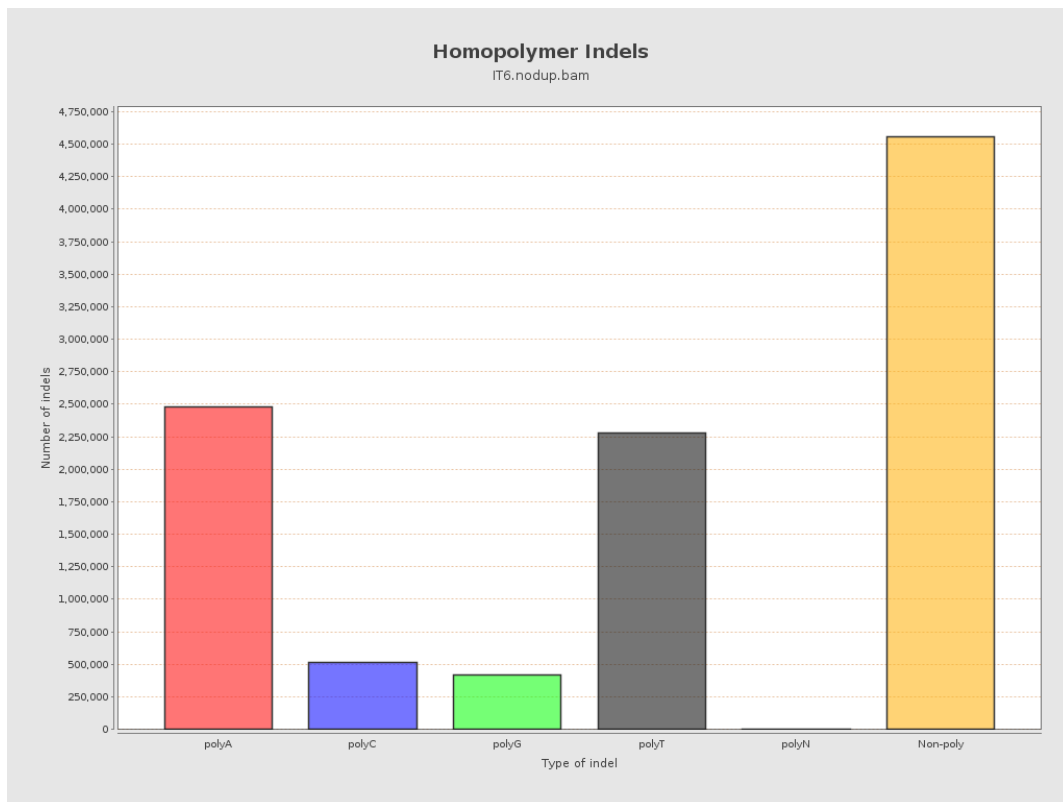
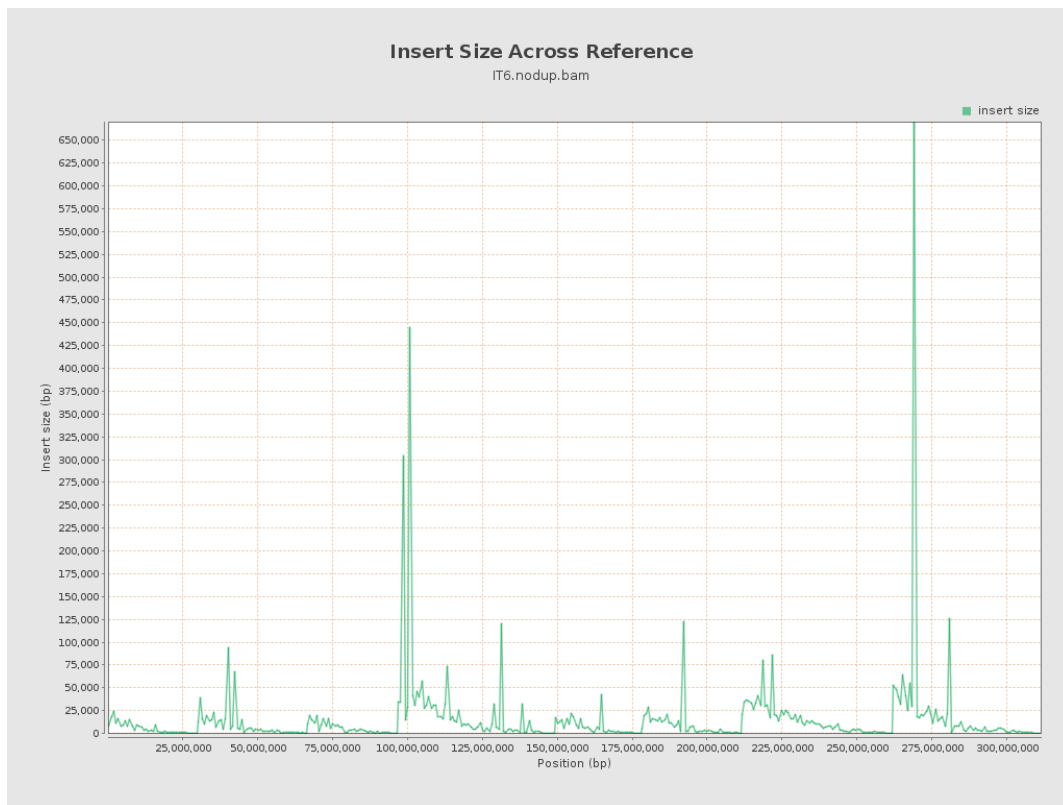# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram