

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2024/03/10 14:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /workdir/FW001Median/FW001Median.dups_rem.bam
-c -nw 400 -hm 3 -sd
```

1.2. Alignment

Command line:	bwa mem -t 16 -a -M -R @RG\tID:pichia\tSM:FW001Median\t PL:ILLUMINA /workdir/new_reference/CBS7435_Sc haffer_plasmids.fasta /workdir/trimmed/FW001Median_1_tri mmed.fastq /workdir/trimmed/FW001Median_2_tri mmed.fastq
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 10 14:35:31 MSK 2024
Size of a homopolymer:	3
Skip duplicate alignments:	yes (only flagged)
Number of windows:	400
BAM file:	/workdir/FW001Median/FW001Media n.dups_rem.bam

2. Summary

2.1. Globals

Reference size	9,447,793
Number of reads	21,497,431
Mapped reads	21,472,968 / 99.89%
Unmapped reads	24,463 / 0.11%
Mapped paired reads	21,472,968 / 99.89%
Mapped reads, first in pair	10,745,414 / 49.98%
Mapped reads, second in pair	10,727,554 / 49.9%
Mapped reads, both in pair	21,446,800 / 99.76%
Mapped reads, singletons	26,168 / 0.12%
Read min/max/mean length	0 / 151 / 147.89
Duplicated reads (flagged)	3,399,018 / 15.81%
Clipped reads	164,848 / 0.77%
Duplicated reads skipped:	3,399,018 / 15.81%

2.2. ACGT Content

Number/percentage of A's	827,528,725 / 30.94%
Number/percentage of C's	509,295,283 / 19.04%
Number/percentage of T's	813,893,674 / 30.43%
Number/percentage of G's	523,682,512 / 19.58%
Number/percentage of N's	53,303 / 0%
GC Percentage	38.62%

2.3. Coverage

Mean	283.087
Standard Deviation	628.4238

2.4. Mapping Quality

Mean Mapping Quality	58.76
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2.5. Insert size

Mean	1,755.99
Standard Deviation	45,151.3
P25/Median/P75	519 / 608 / 710

2.6. Mismatches and indels

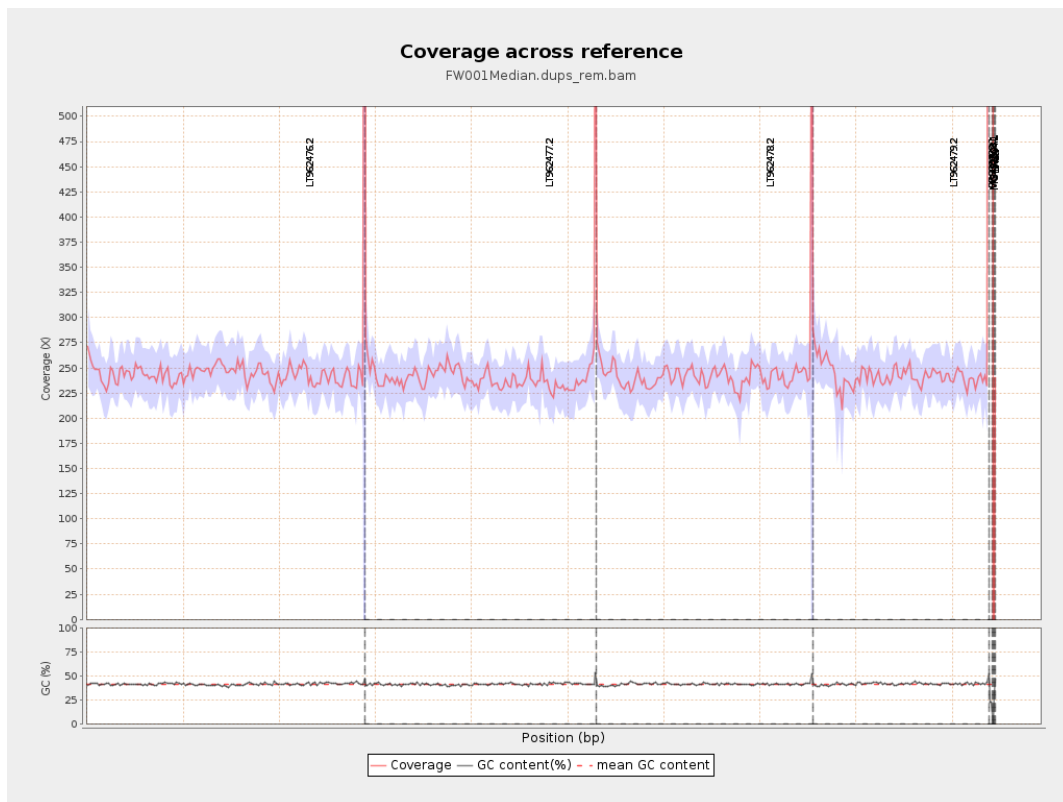
General error rate	0.29%
Mismatches	7,601,730
Insertions	74,860
Mapped reads with at least one insertion	0.31%
Deletions	25,824
Mapped reads with at least one deletion	0.1%
Homopolymer indels	65.08%

2.7. Chromosome stats

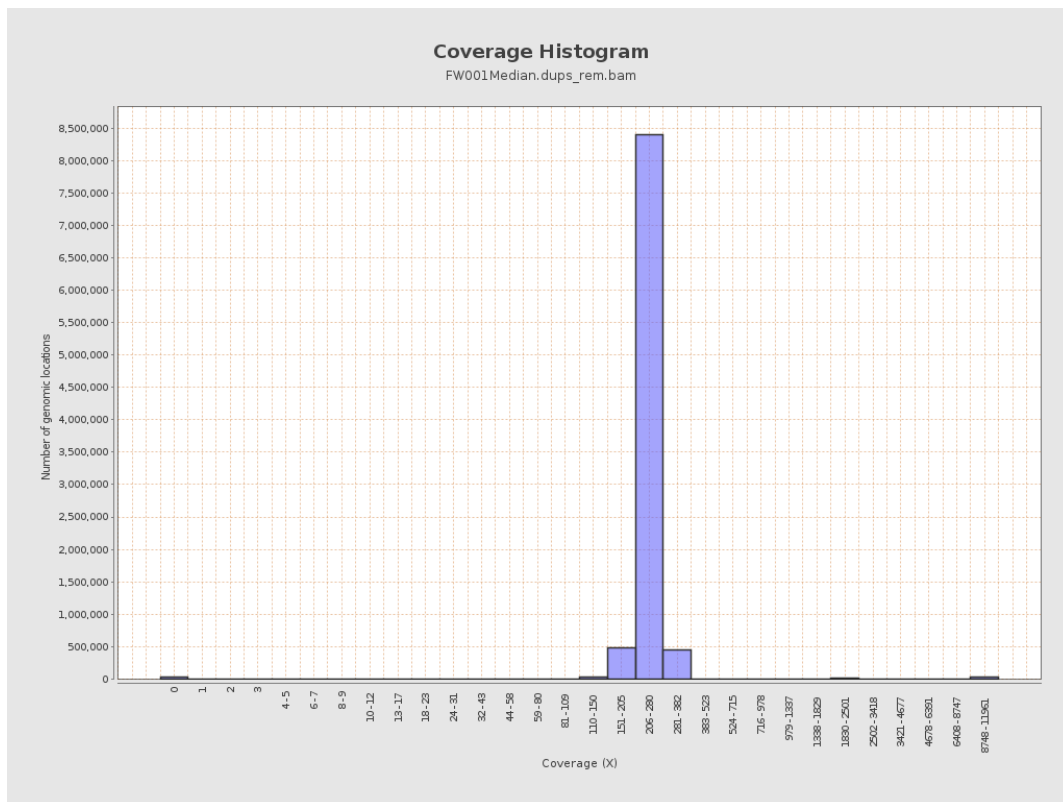
Name	Length	Mapped bases	Mean coverage	Standard deviation

LT962476.2	2895357	720531364	248.8575	146.7532
LT962477.2	2396459	575297505	240.0615	26.6968
LT962478.2	2263464	556576362	245.8958	99.8206
LT962479.2	1827946	452192496	247.3774	105.7108
FR839632.1	35683	368424008	10,324.9169	552.5339
MG491503.1	13092	0	0	0
MG491504.1	9448	151	0.016	0.1254
Linear	6344	1525323	240.4355	32.7903

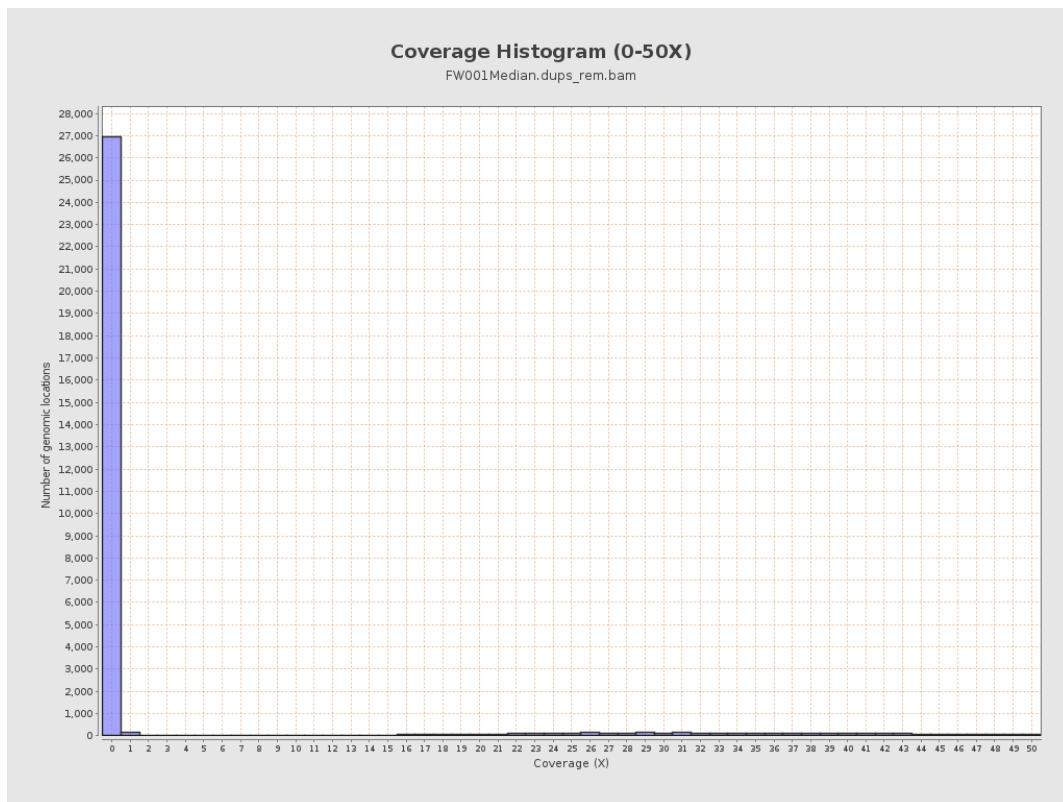
3. Results : Coverage across reference



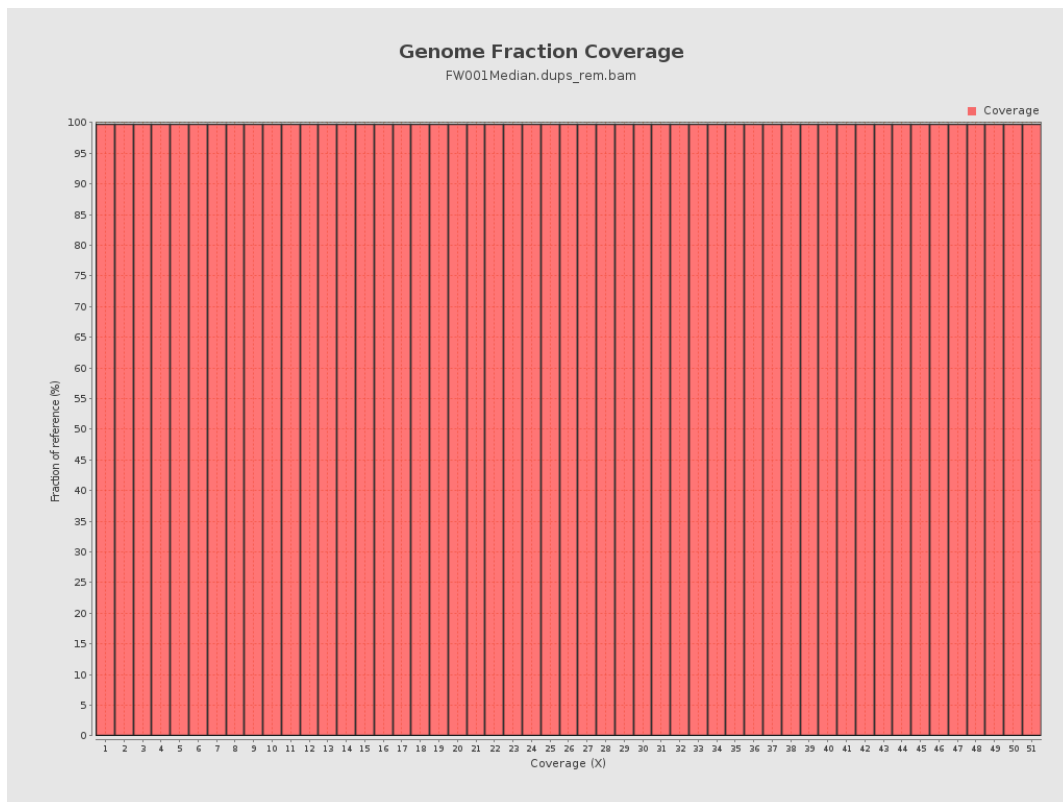
4. Results : Coverage Histogram



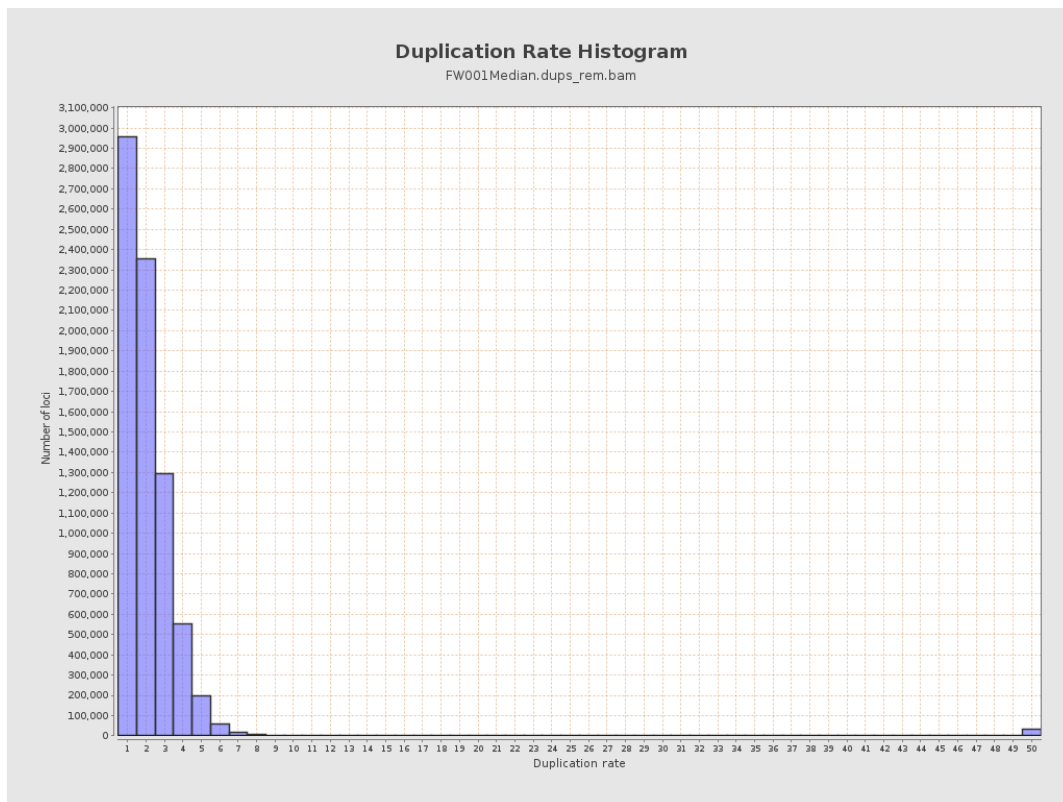
5. Results : Coverage Histogram (0-50X)



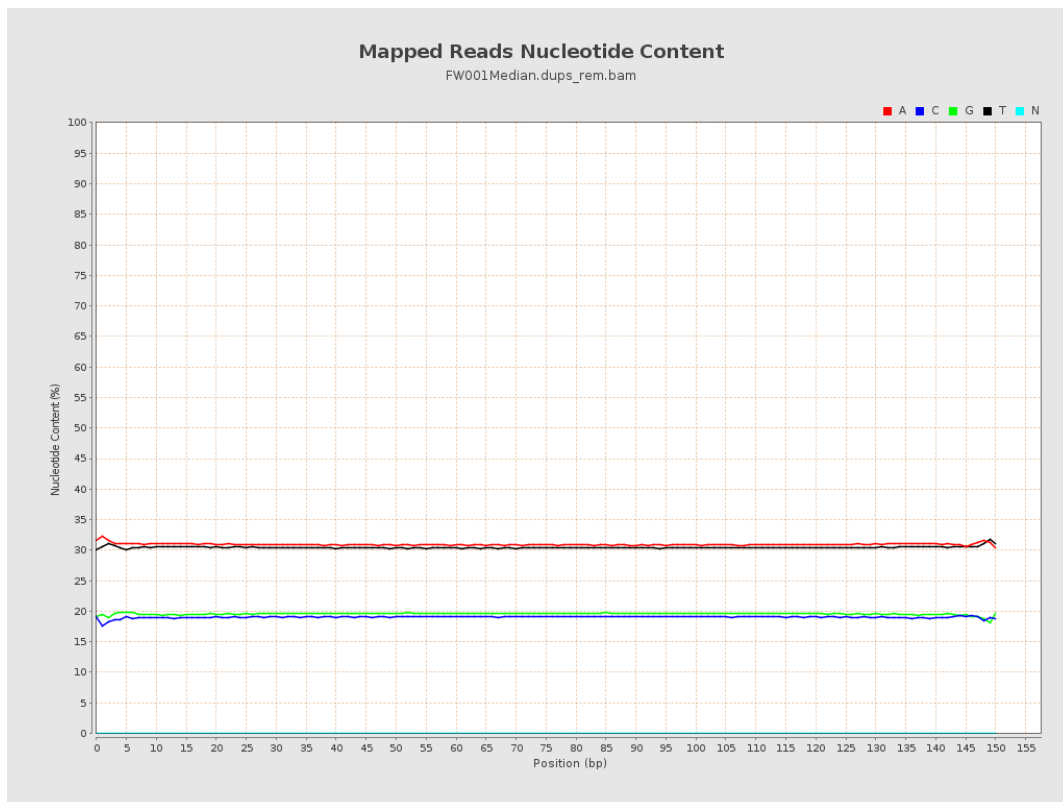
6. Results : Genome Fraction Coverage



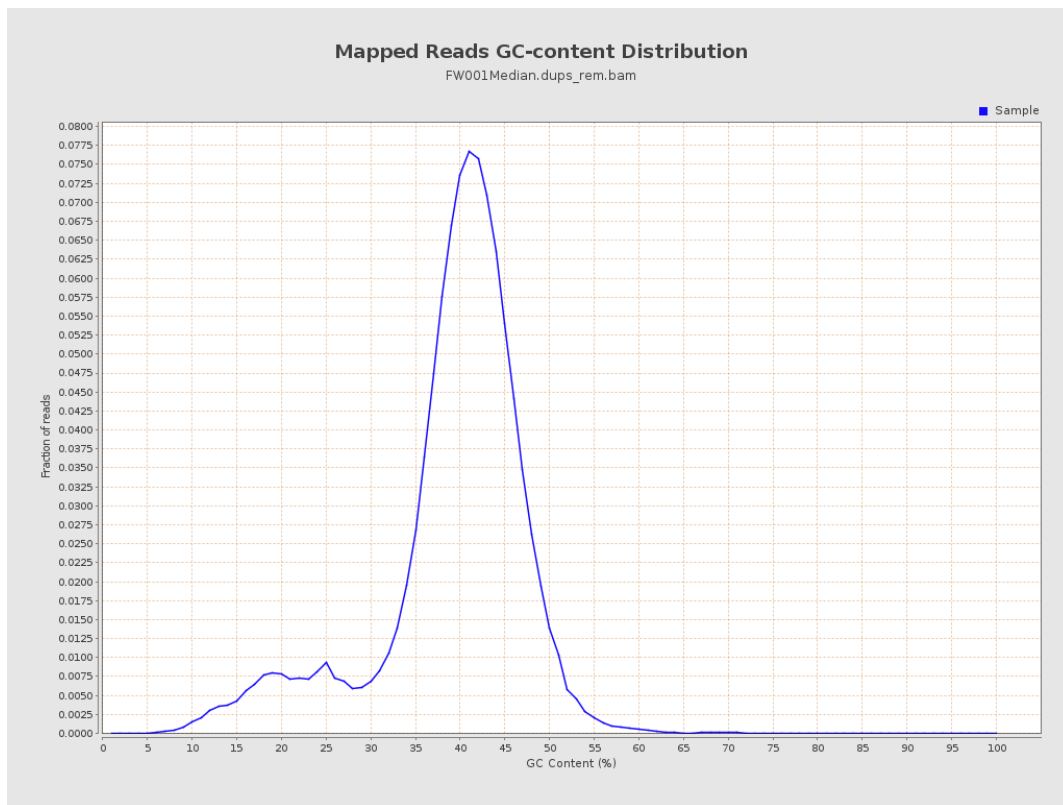
7. Results : Duplication Rate Histogram



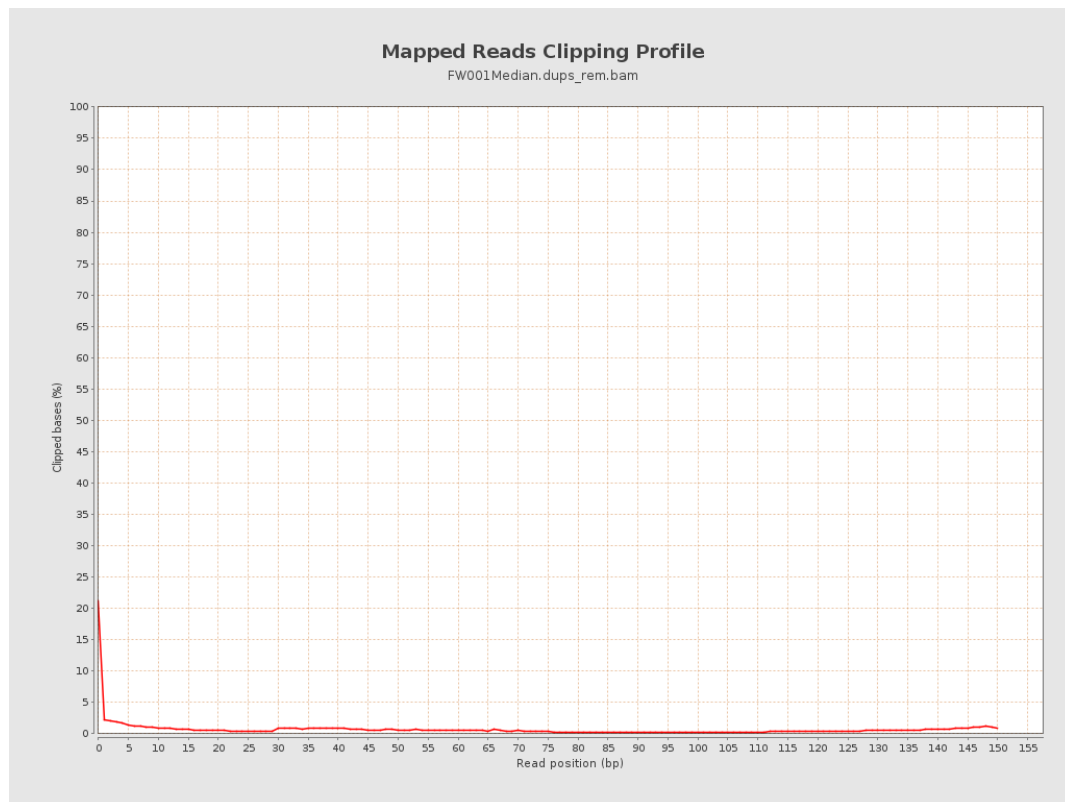
8. Results : Mapped Reads Nucleotide Content



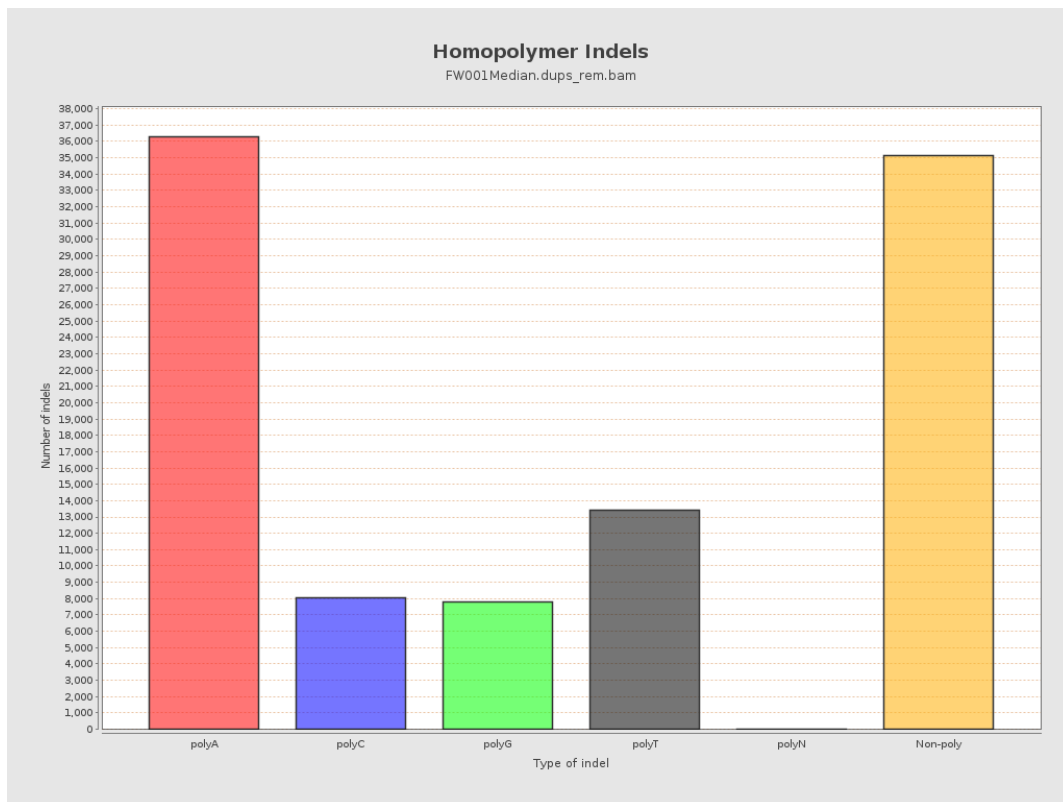
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



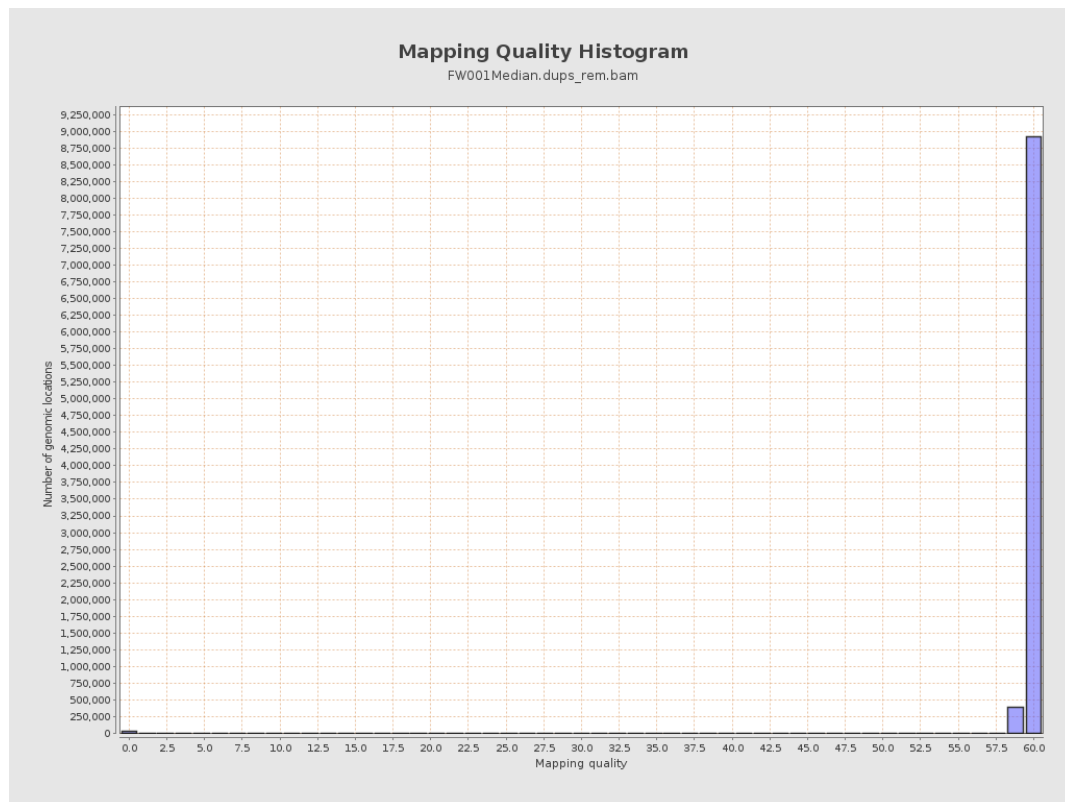
11. Results : Homopolymer Indels



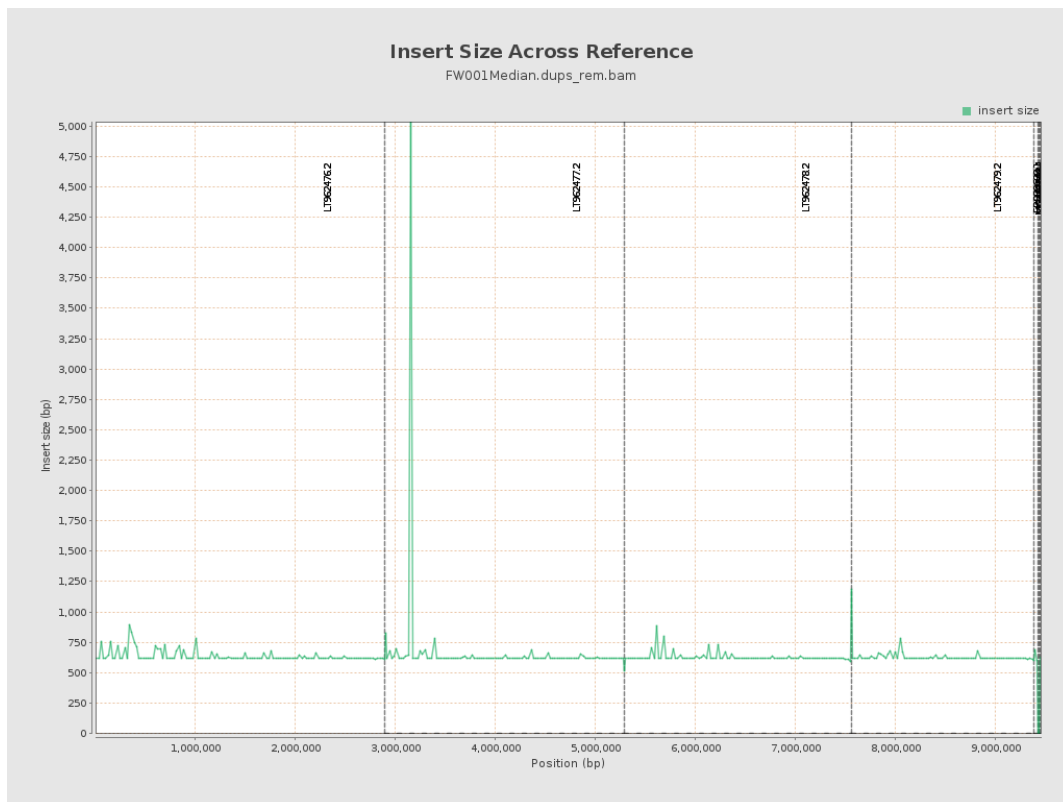
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

