

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238243.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:35:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	819,029
Mapped reads	308,754 / 37.7%
Unmapped reads	510,275 / 62.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,833 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	45,287 / 5.53%
Duplication rate	8.43%
Clipped reads	214,360 / 26.17%

2.2. ACGT Content

Number/percentage of A's	5,177,958 / 28.24%
Number/percentage of C's	3,776,994 / 20.6%
Number/percentage of T's	5,367,586 / 29.28%
Number/percentage of G's	4,008,112 / 21.86%
Number/percentage of N's	2,455 / 0.01%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0059

Standard Deviation	0.2644
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2.4. Mapping Quality

Mean Mapping Quality	42.1
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2.5. Mismatches and indels

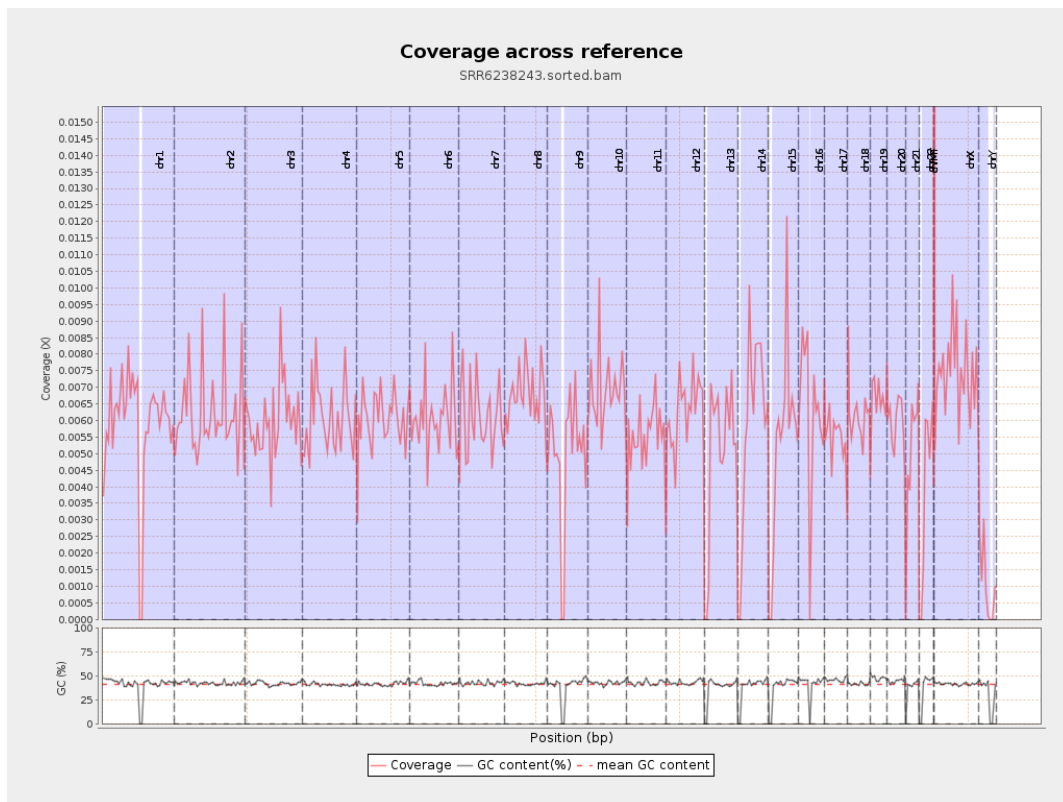
General error rate	1.01%
Mismatches	182,702
Insertions	1,604
Mapped reads with at least one insertion	0.51%
Deletions	4,739
Mapped reads with at least one deletion	1.52%
Homopolymer indels	44.14%

2.6. Chromosome stats

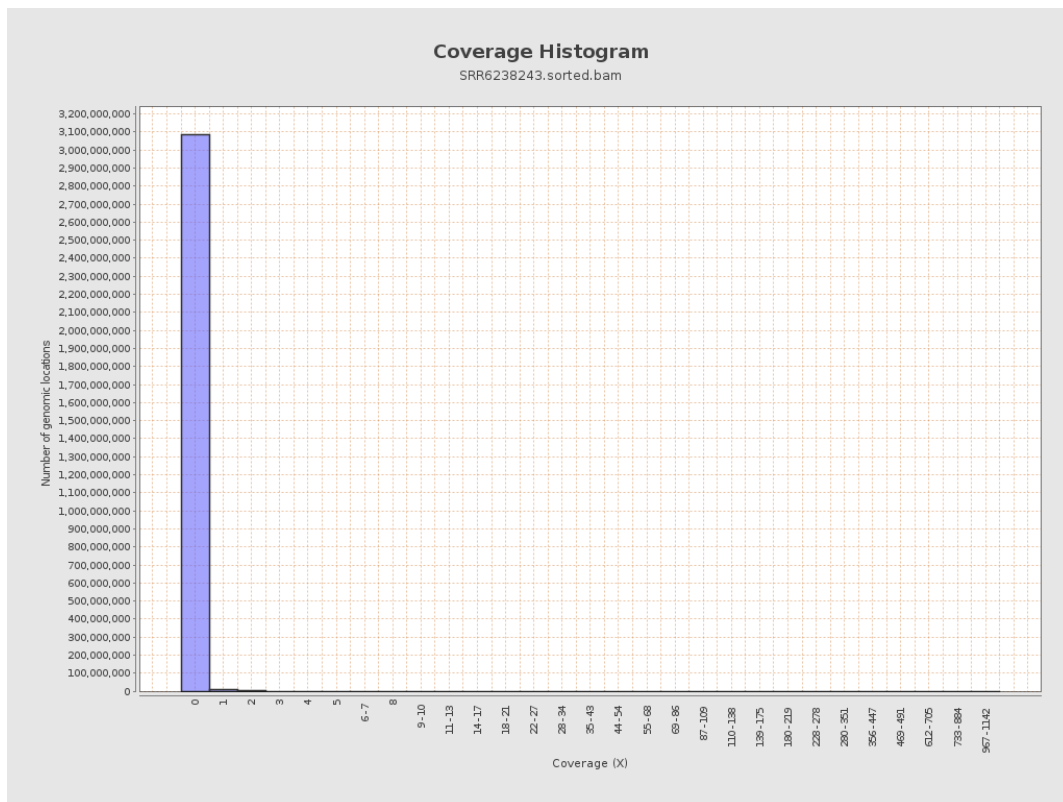
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1464434	0.0059	0.2747
chr2	243199373	1514517	0.0062	0.3764
chr3	198022430	1194336	0.006	0.1638
chr4	191154276	1162232	0.0061	0.2069
chr5	180915260	1113091	0.0062	0.1791
chr6	171115067	1043144	0.0061	0.2582
chr7	159138663	969291	0.0061	0.1771

chr8	146364022	985670	0.0067	0.1892
chr9	141213431	700527	0.005	0.1401
chr10	135534747	932910	0.0069	0.1653
chr11	135006516	758260	0.0056	0.1269
chr12	133851895	842942	0.0063	0.162
chr13	115169878	572170	0.005	0.2293
chr14	107349540	633769	0.0059	0.5885
chr15	102531392	542537	0.0053	0.6673
chr16	90354753	554654	0.0061	0.141
chr17	81195210	440716	0.0054	0.1526
chr18	78077248	478864	0.0061	0.1428
chr19	59128983	394128	0.0067	0.1342
chr20	63025520	372840	0.0059	0.1348
chr21	48129895	243829	0.0051	0.1109
chr22	51304566	202084	0.0039	0.1037
chrMT	16571	9130	0.551	1.2421
chrX	155270560	1153284	0.0074	0.2802
chrY	59373566	61372	0.001	0.0672

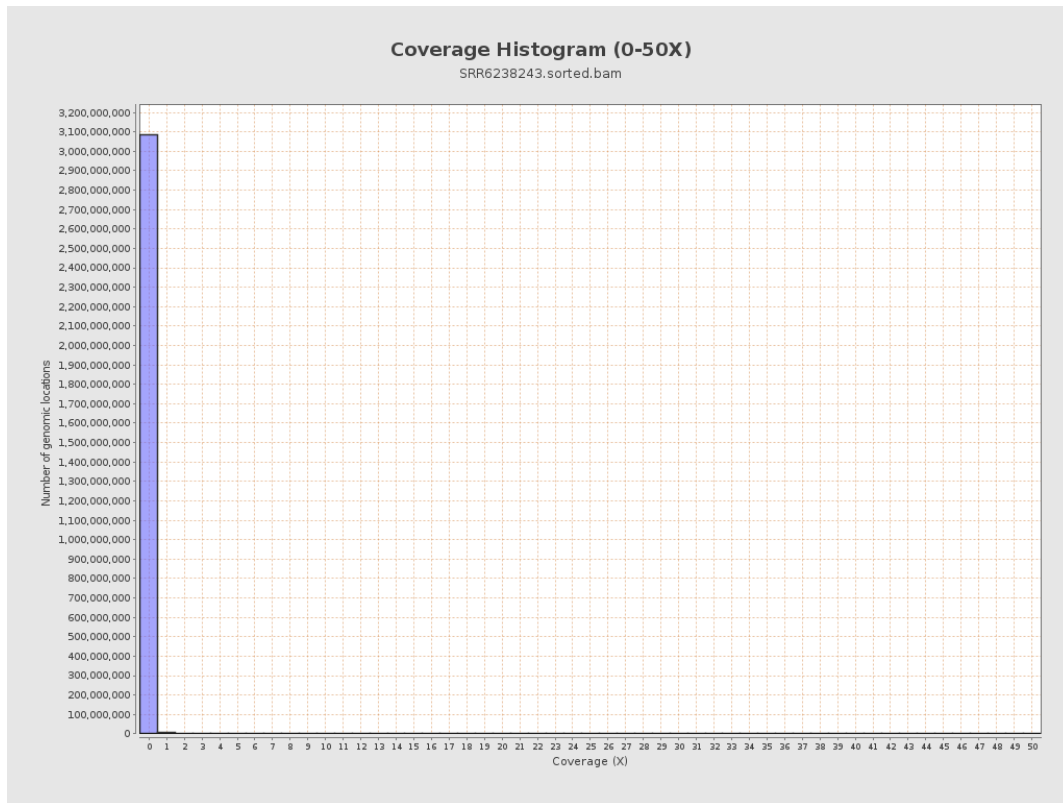
3. Results : Coverage across reference



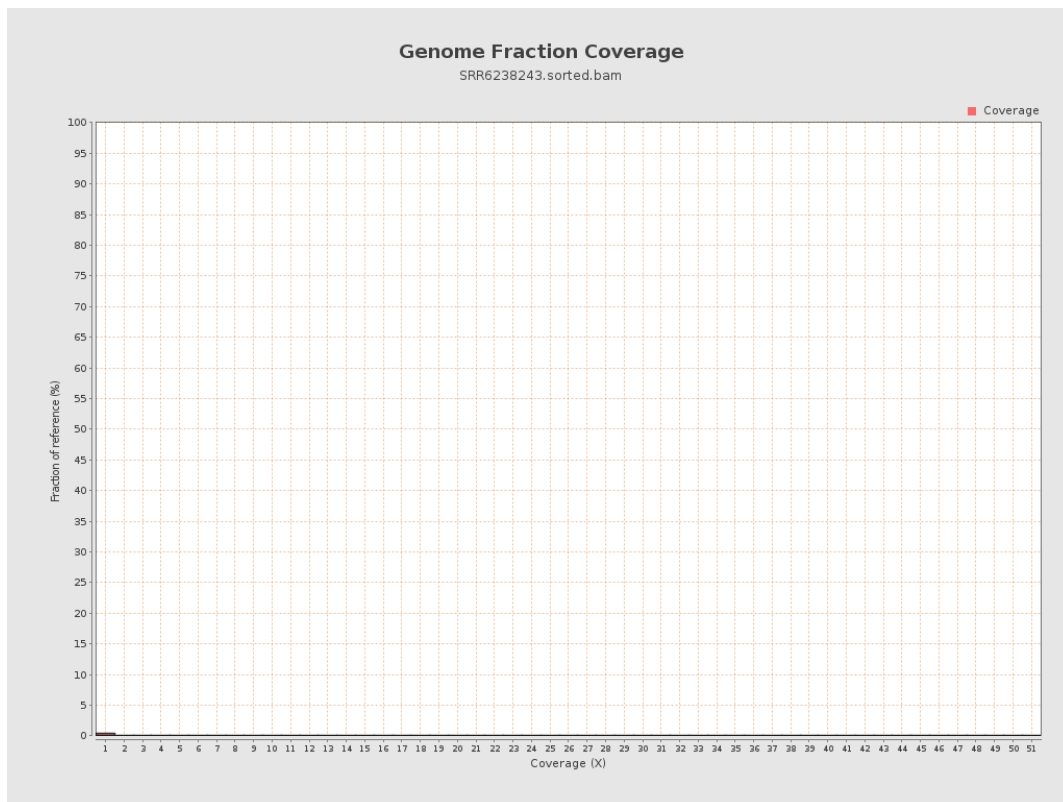
4. Results : Coverage Histogram



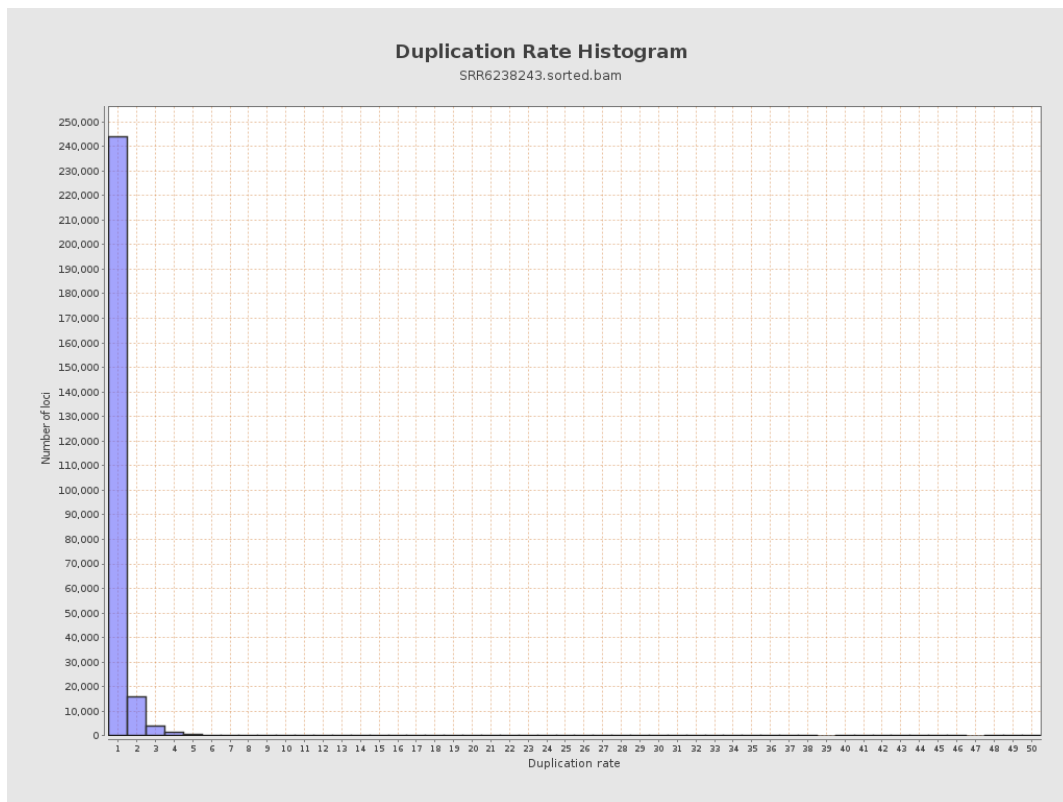
5. Results : Coverage Histogram (0-50X)



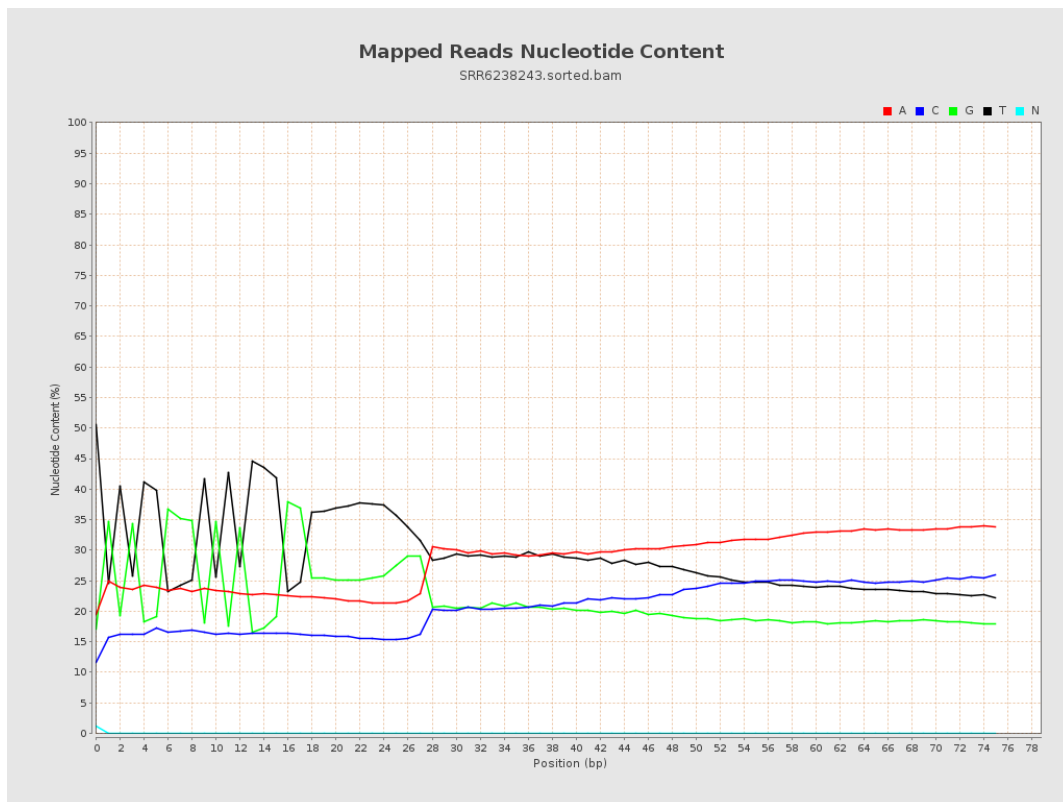
6. Results : Genome Fraction Coverage



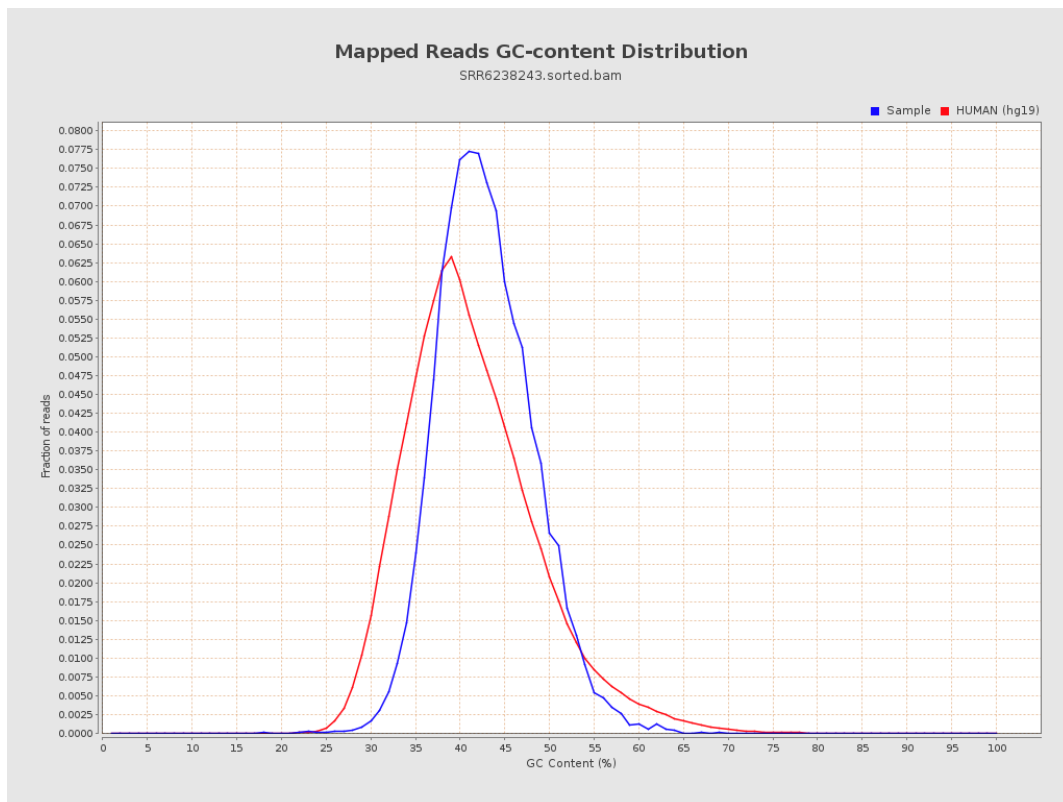
7. Results : Duplication Rate Histogram



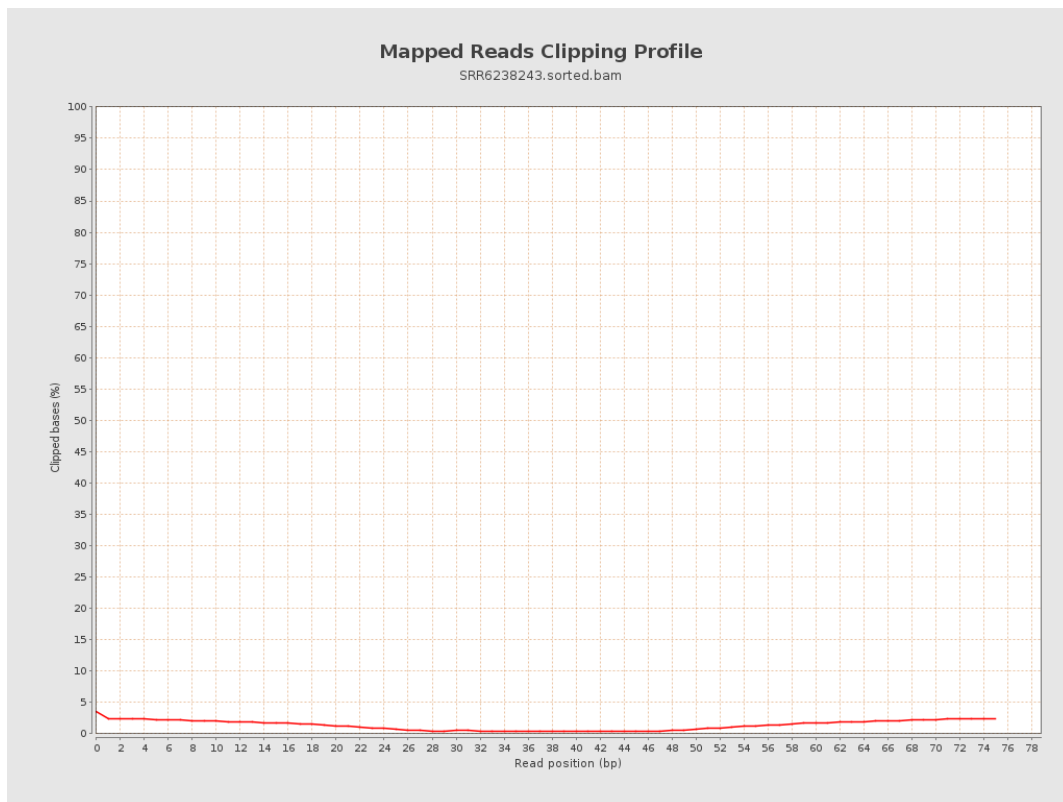
8. Results : Mapped Reads Nucleotide Content



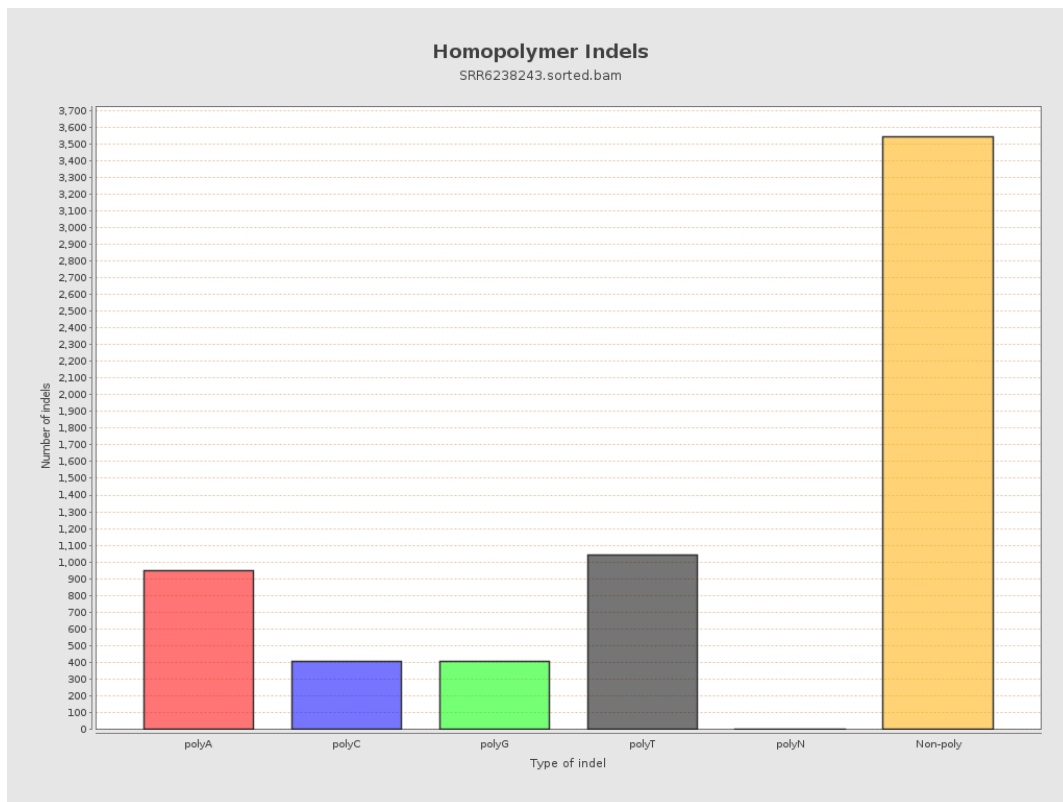
9. Results : Mapped Reads GC-content Distribution



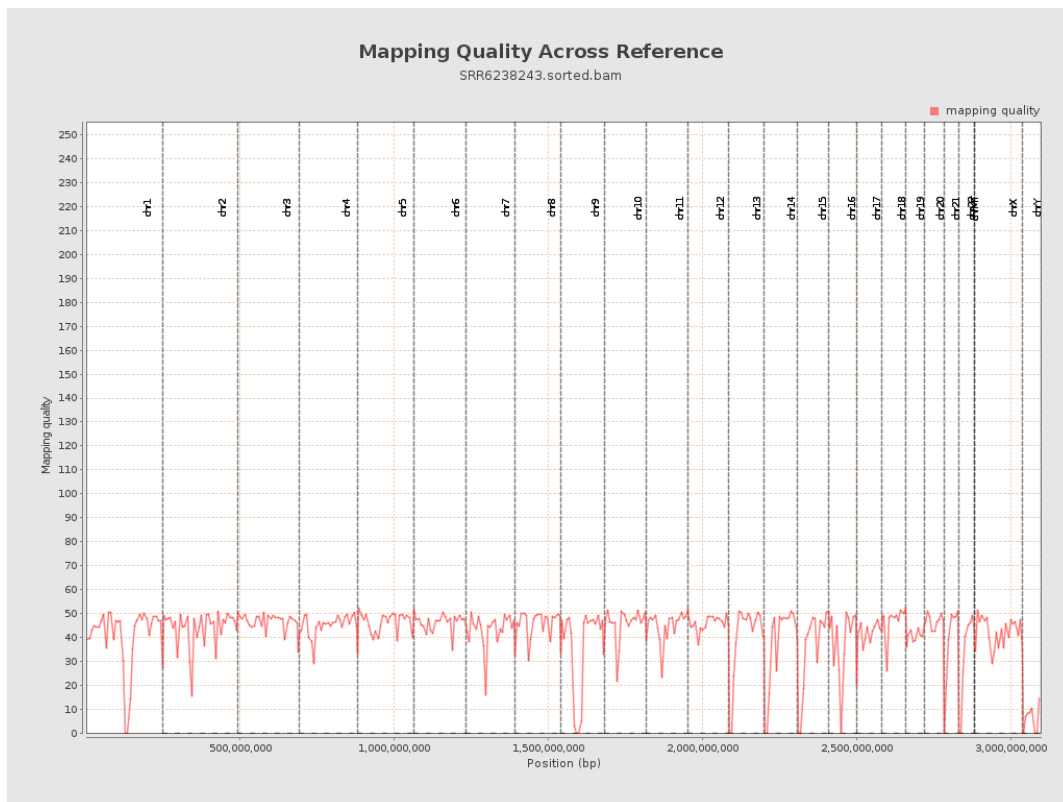
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

