

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:47:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238070.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_SRR6238070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:47:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,250,958
Mapped reads	643,257 / 51.42%
Unmapped reads	607,701 / 48.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,471 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	39,318 / 3.14%
Duplication rate	5.34%
Clipped reads	496,023 / 39.65%

2.2. ACGT Content

Number/percentage of A's	10,530,639 / 28.39%
Number/percentage of C's	6,895,474 / 18.59%
Number/percentage of T's	11,332,535 / 30.55%
Number/percentage of G's	8,336,015 / 22.47%
Number/percentage of N's	1,946 / 0.01%
GC Percentage	41.06%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1464
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.21
----------------------	-------

2.5. Mismatches and indels

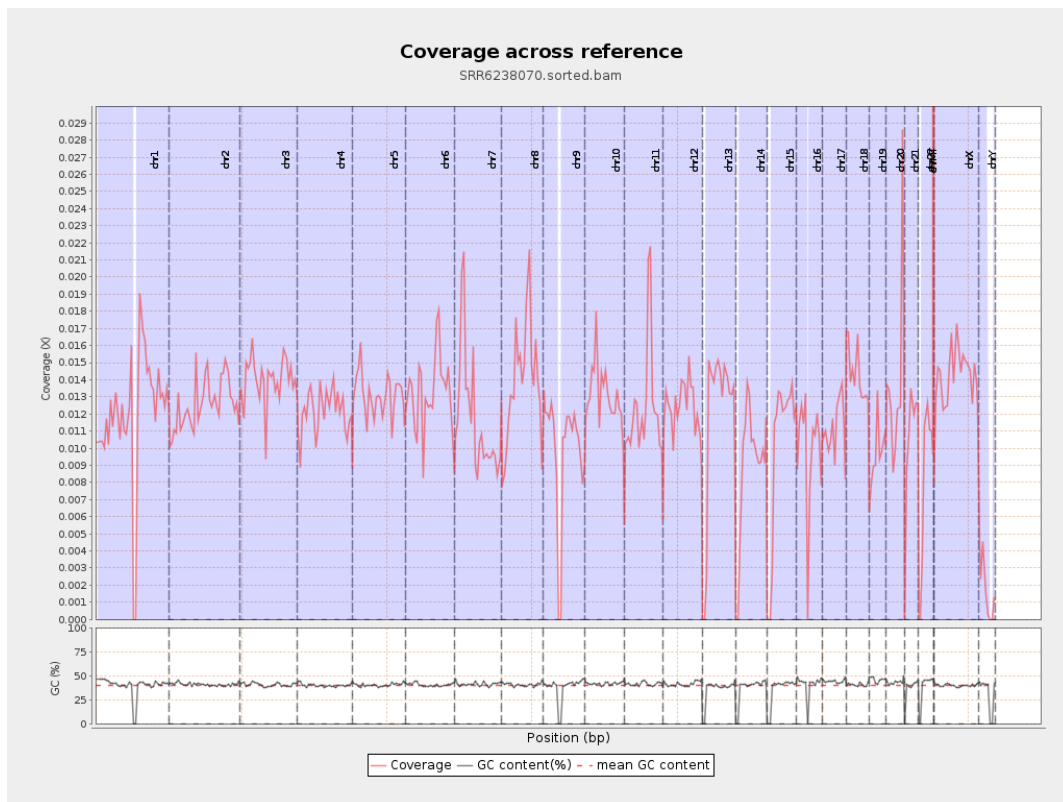
General error rate	0.79%
Mismatches	289,560
Insertions	2,797
Mapped reads with at least one insertion	0.43%
Deletions	10,897
Mapped reads with at least one deletion	1.68%
Homopolymer indels	45.57%

2.6. Chromosome stats

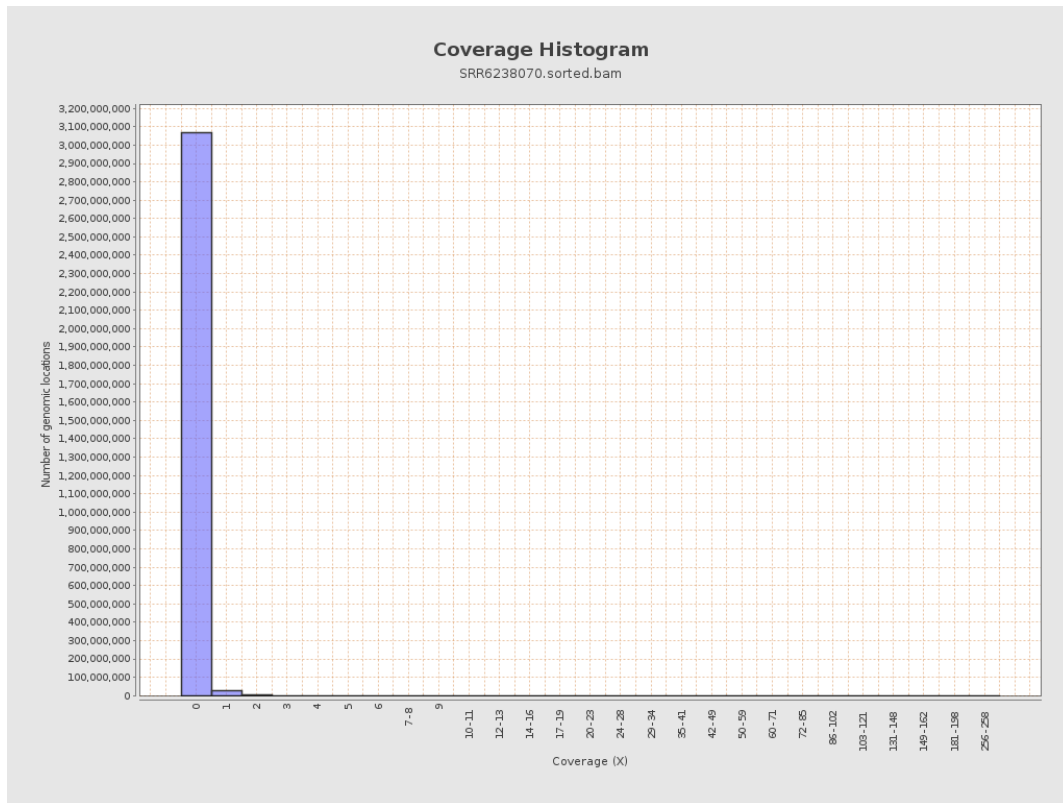
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2995833	0.012	0.1737
chr2	243199373	3060661	0.0126	0.1823
chr3	198022430	2771690	0.014	0.1426
chr4	191154276	2323103	0.0122	0.1339
chr5	180915260	2365093	0.0131	0.1381
chr6	171115067	2263417	0.0132	0.149
chr7	159138663	1869450	0.0117	0.1549

chr8	146364022	2016717	0.0138	0.1717
chr9	141213431	1382200	0.0098	0.1277
chr10	135534747	1786785	0.0132	0.1518
chr11	135006516	1666775	0.0123	0.1414
chr12	133851895	1662538	0.0124	0.1356
chr13	115169878	1353710	0.0118	0.1308
chr14	107349540	949103	0.0088	0.1175
chr15	102531392	1033273	0.0101	0.1215
chr16	90354753	888068	0.0098	0.1194
chr17	81195210	903920	0.0111	0.1272
chr18	78077248	1114715	0.0143	0.174
chr19	59128983	575880	0.0097	0.1424
chr20	63025520	889502	0.0141	0.1428
chr21	48129895	507598	0.0105	0.1244
chr22	51304566	404651	0.0079	0.1043
chrMT	16571	31076	1.8753	1.9016
chrX	155270560	2196910	0.0141	0.1463
chrY	59373566	100678	0.0017	0.049

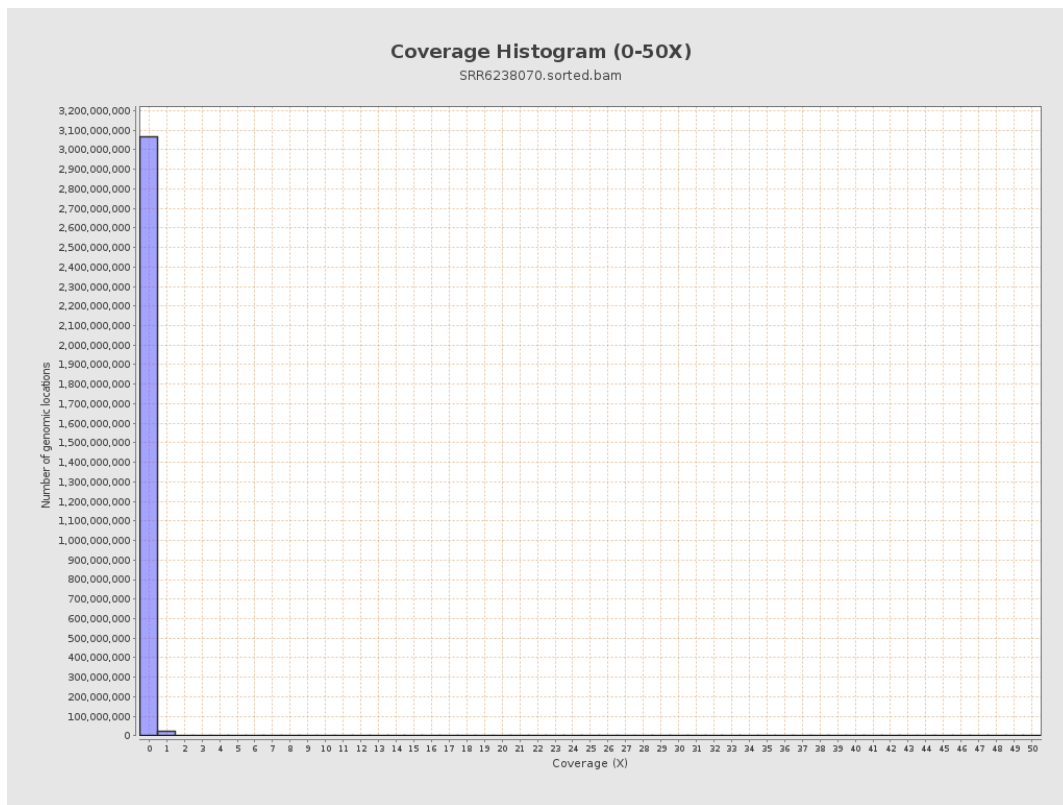
3. Results : Coverage across reference



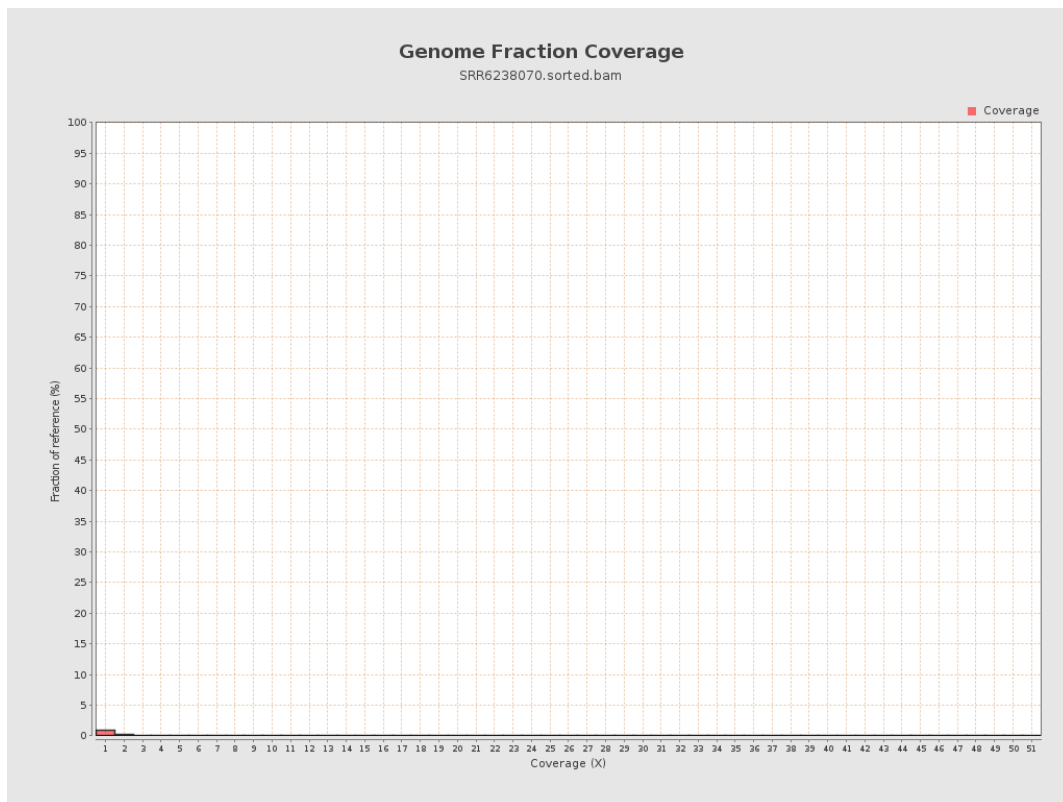
4. Results : Coverage Histogram



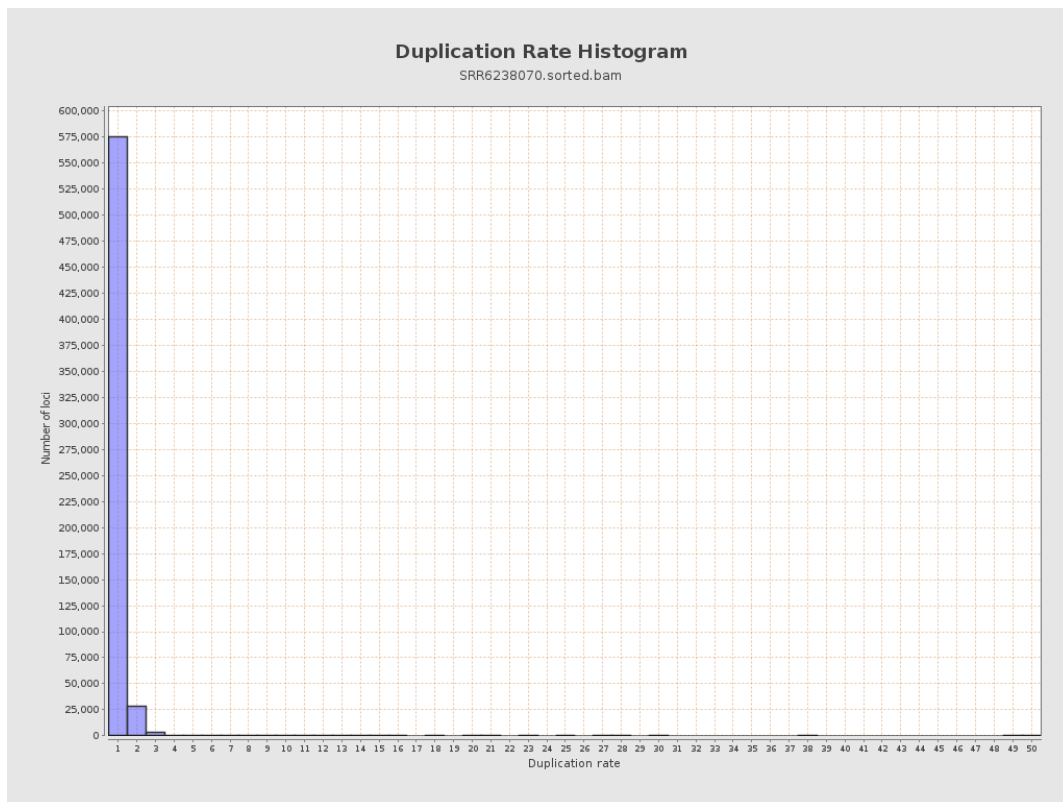
5. Results : Coverage Histogram (0-50X)



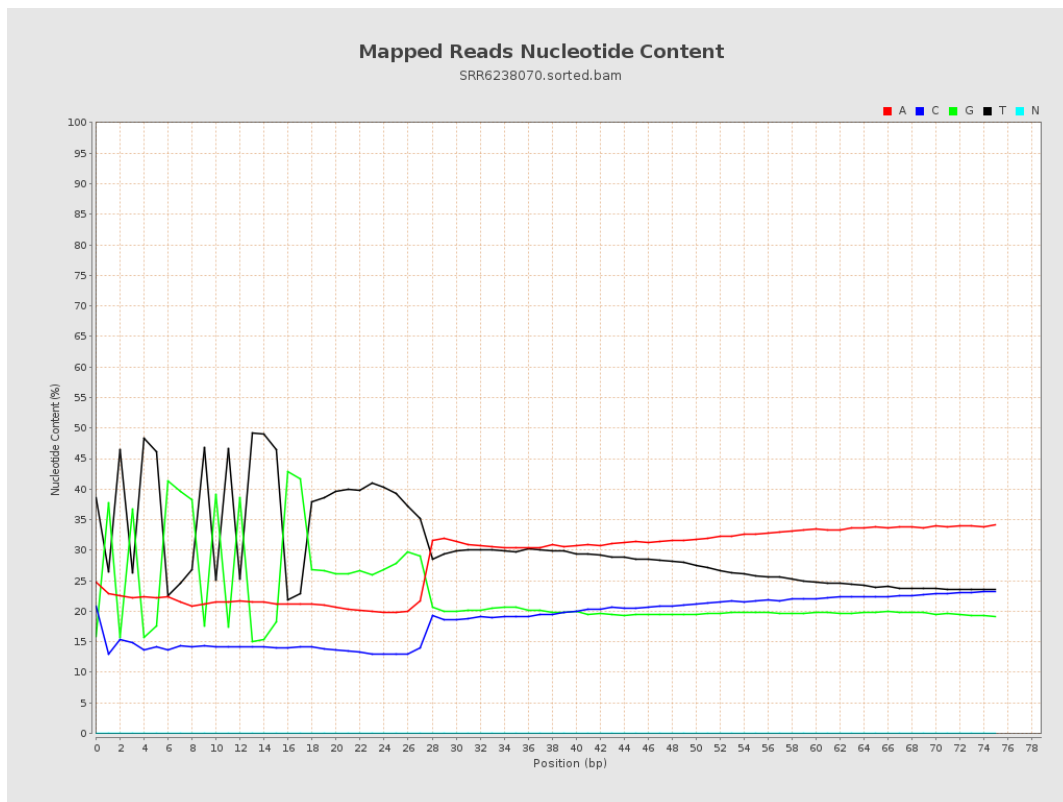
6. Results : Genome Fraction Coverage



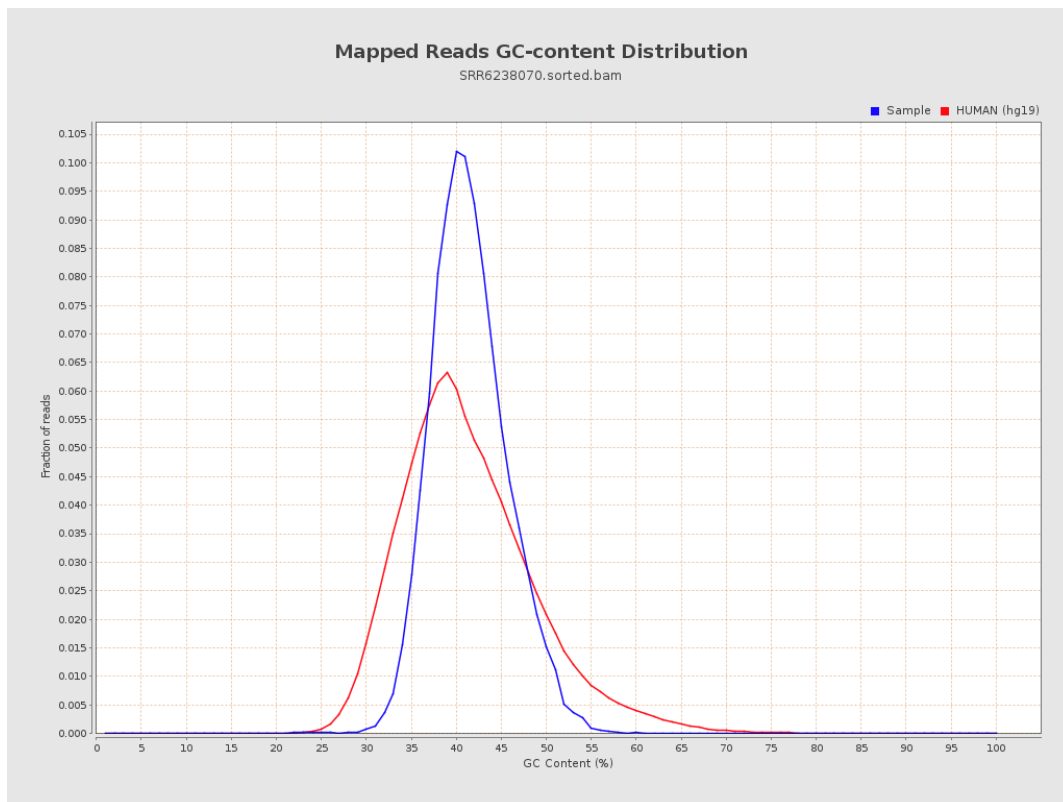
7. Results : Duplication Rate Histogram



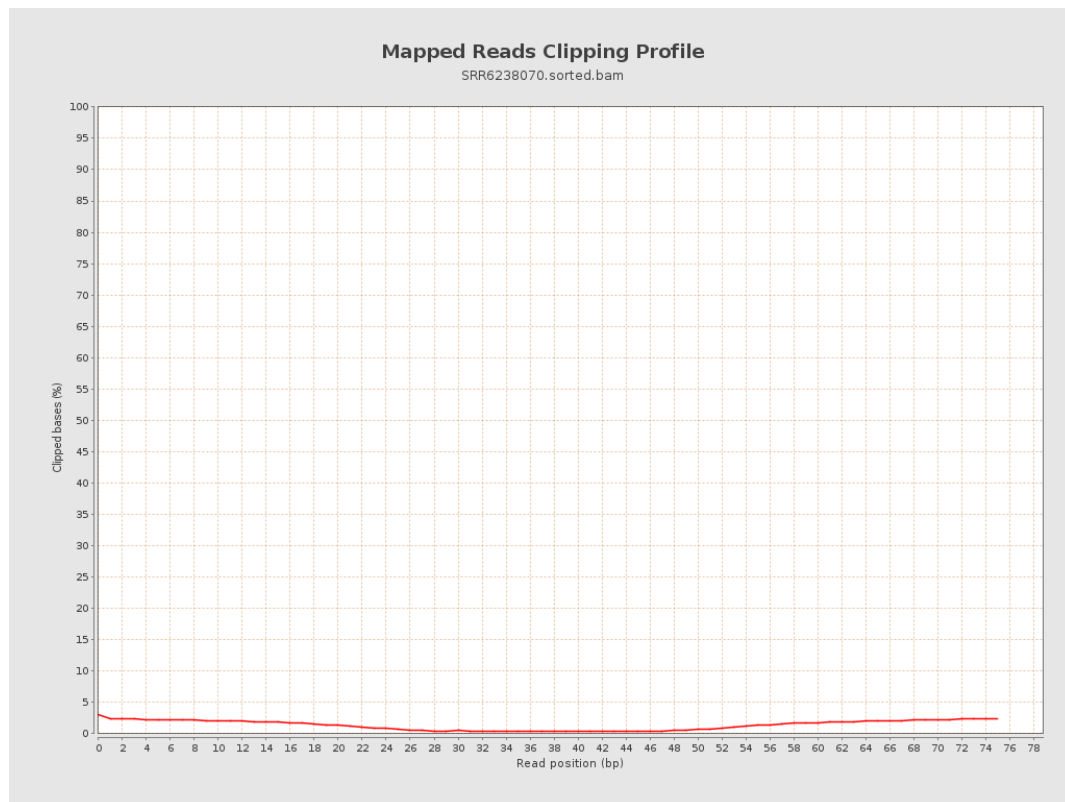
8. Results : Mapped Reads Nucleotide Content



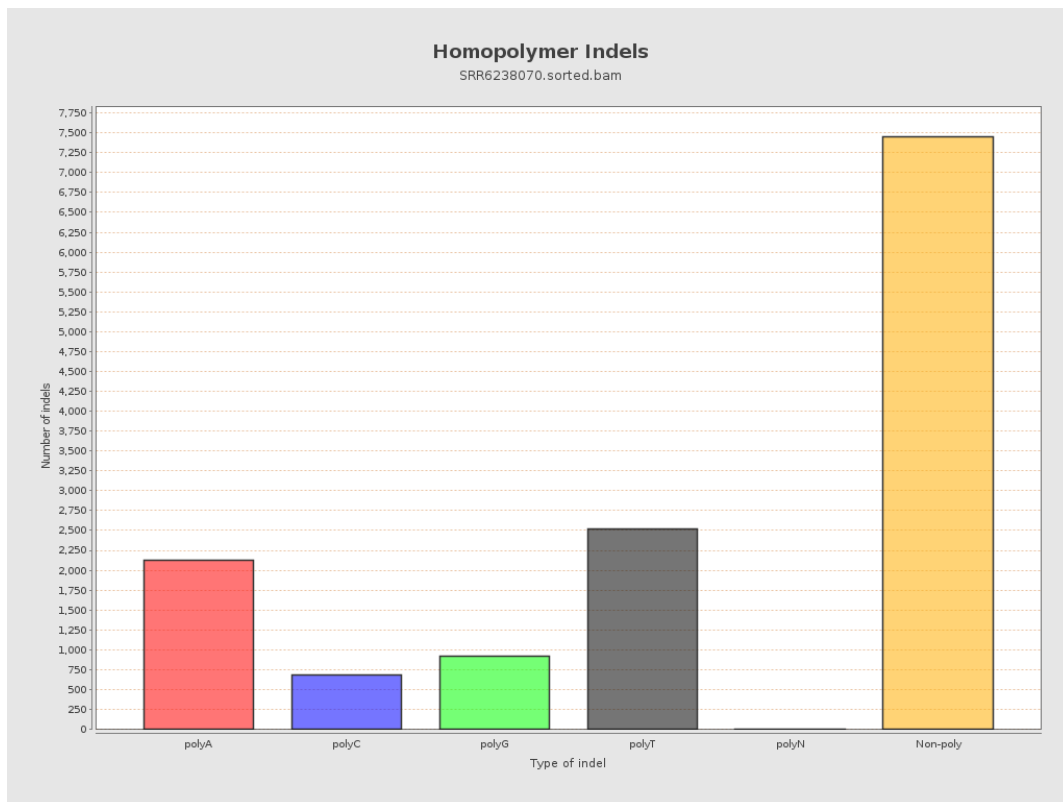
9. Results : Mapped Reads GC-content Distribution



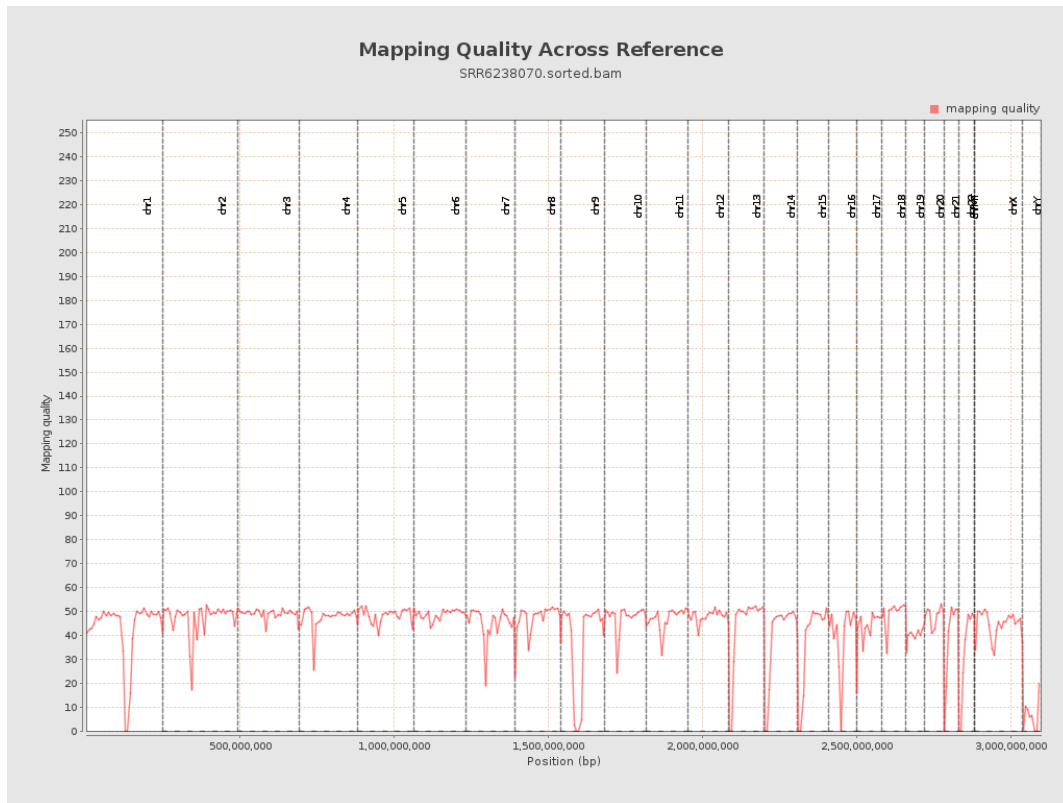
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

