

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:17:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008739.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_SRR6008739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:17:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,019,916
Mapped reads	764,701 / 74.98%
Unmapped reads	255,215 / 25.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,487 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	17,732 / 1.74%
Duplication rate	1.77%
Clipped reads	424,553 / 41.63%

2.2. ACGT Content

Number/percentage of A's	13,420,850 / 27.67%
Number/percentage of C's	8,418,235 / 17.36%
Number/percentage of T's	15,016,625 / 30.96%
Number/percentage of G's	11,645,884 / 24.01%
Number/percentage of N's	2,225 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1627
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.4
----------------------	------

2.5. Mismatches and indels

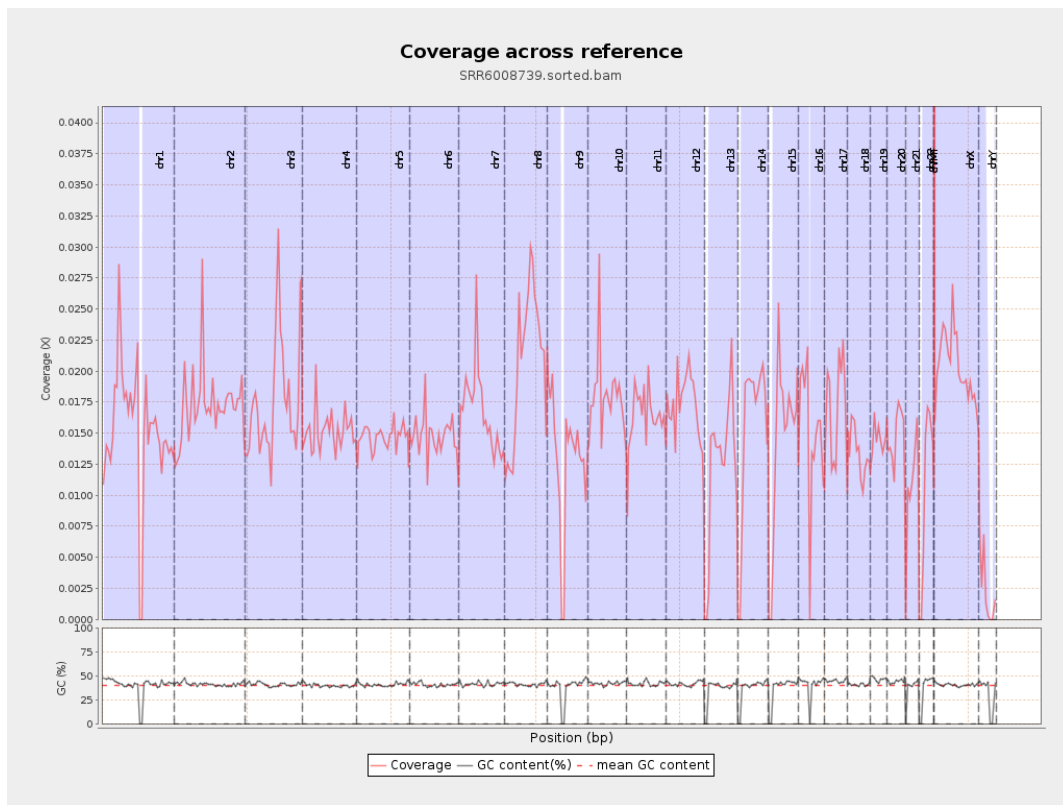
General error rate	0.85%
Mismatches	402,522
Insertions	4,175
Mapped reads with at least one insertion	0.54%
Deletions	15,965
Mapped reads with at least one deletion	2.06%
Homopolymer indels	47.17%

2.6. Chromosome stats

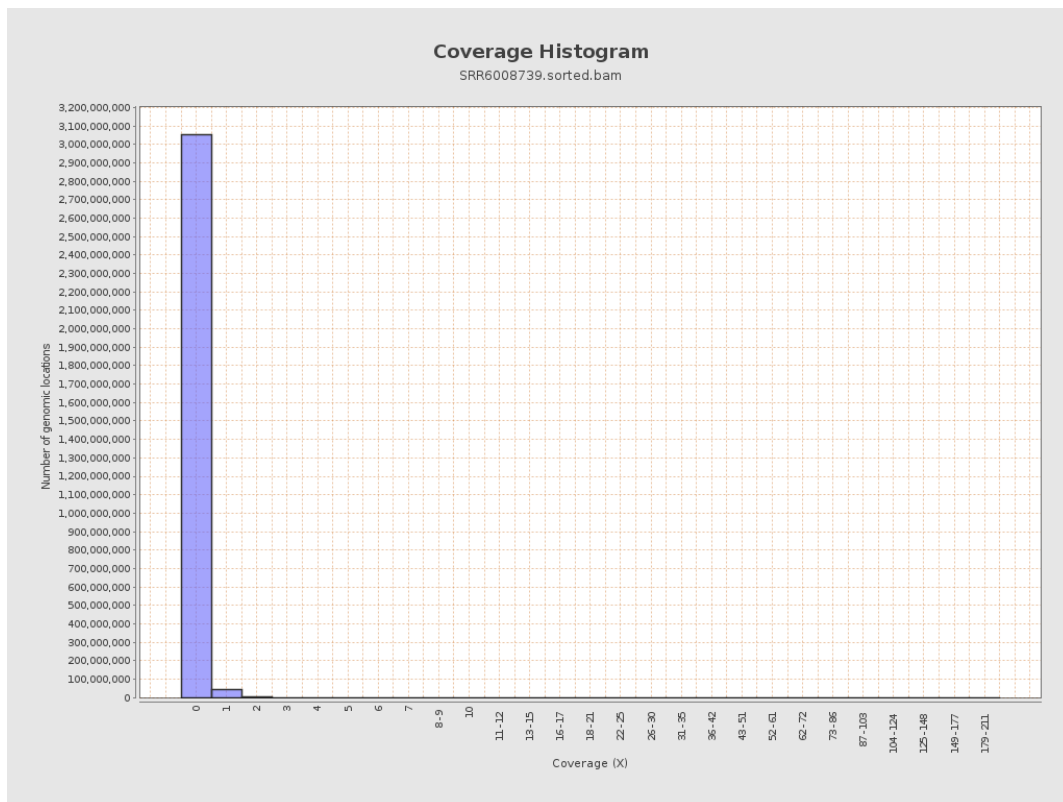
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3783046	0.0152	0.2047
chr2	243199373	4196319	0.0173	0.218
chr3	198022430	3474391	0.0175	0.1383
chr4	191154276	2898469	0.0152	0.1335
chr5	180915260	2668415	0.0147	0.1266
chr6	171115067	2528891	0.0148	0.1478
chr7	159138663	2666533	0.0168	0.2057

chr8	146364022	3036987	0.0207	0.1847
chr9	141213431	1835020	0.013	0.1534
chr10	135534747	2432805	0.0179	0.1763
chr11	135006516	2220320	0.0164	0.1586
chr12	133851895	2316429	0.0173	0.138
chr13	115169878	1418465	0.0123	0.1154
chr14	107349540	1660890	0.0155	0.1344
chr15	102531392	1475910	0.0144	0.1262
chr16	90354753	1336352	0.0148	0.139
chr17	81195210	1370021	0.0169	0.1437
chr18	78077248	1040486	0.0133	0.2322
chr19	59128983	861098	0.0146	0.1743
chr20	63025520	921529	0.0146	0.1295
chr21	48129895	525187	0.0109	0.1131
chr22	51304566	549451	0.0107	0.1074
chrMT	16571	13903	0.839	1.0975
chrX	155270560	3162913	0.0204	0.157
chrY	59373566	136300	0.0023	0.0661

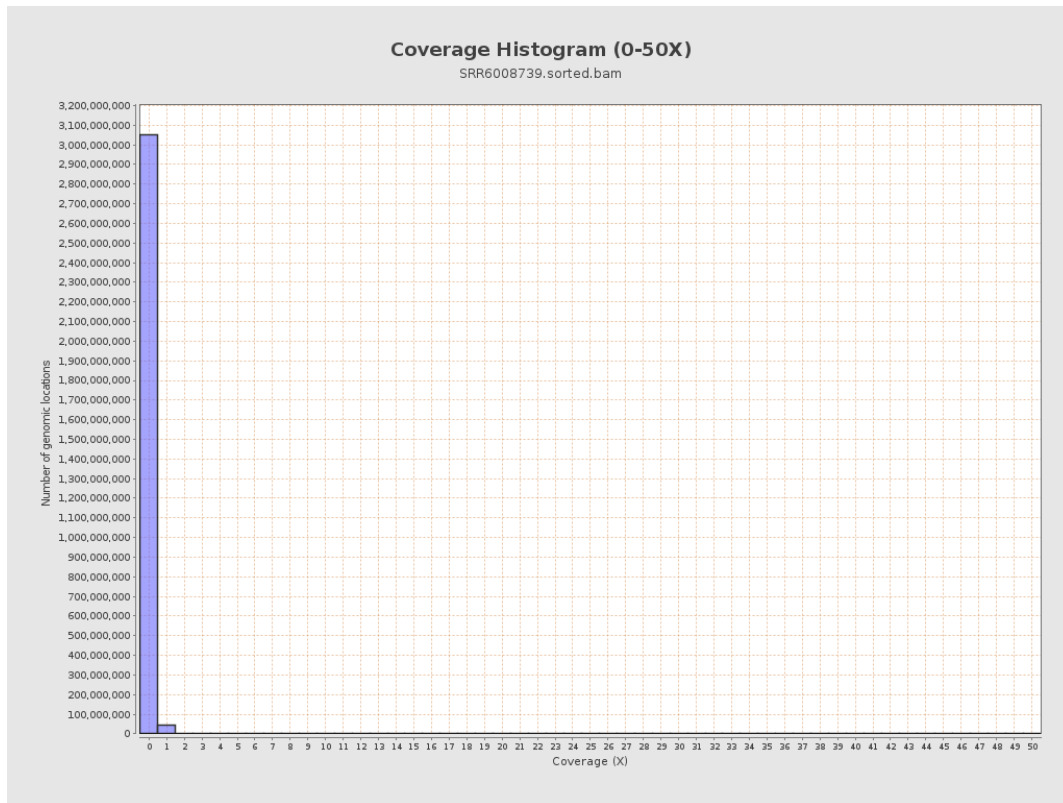
3. Results : Coverage across reference



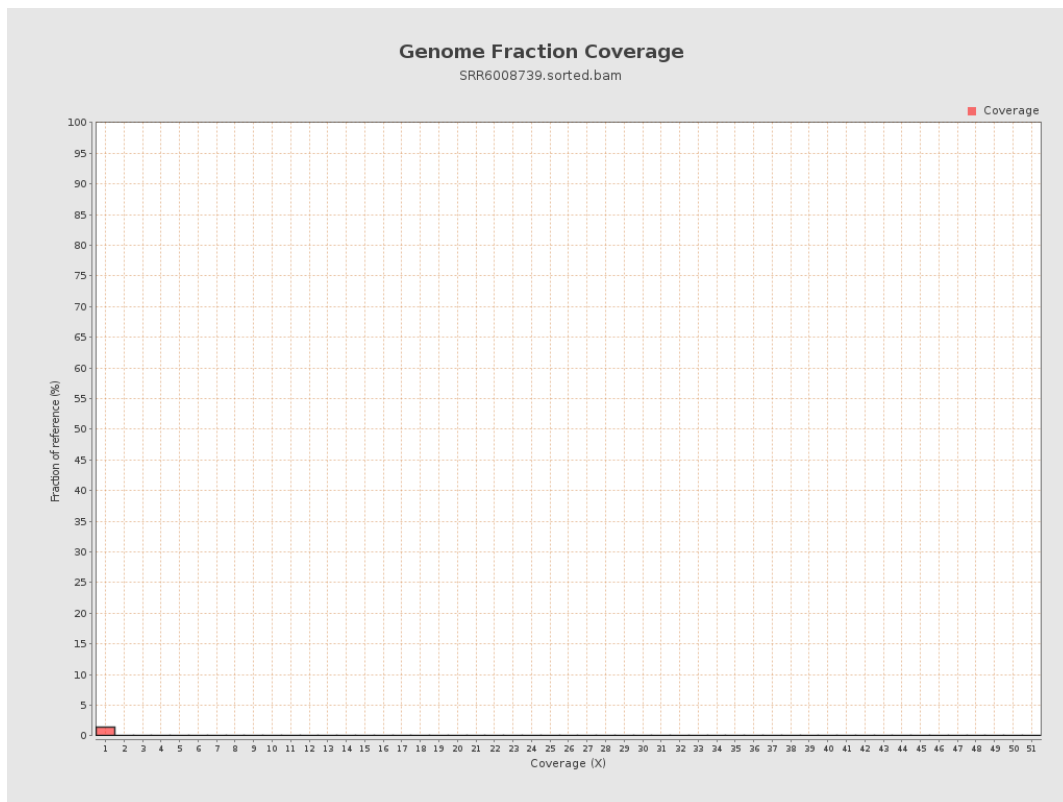
4. Results : Coverage Histogram



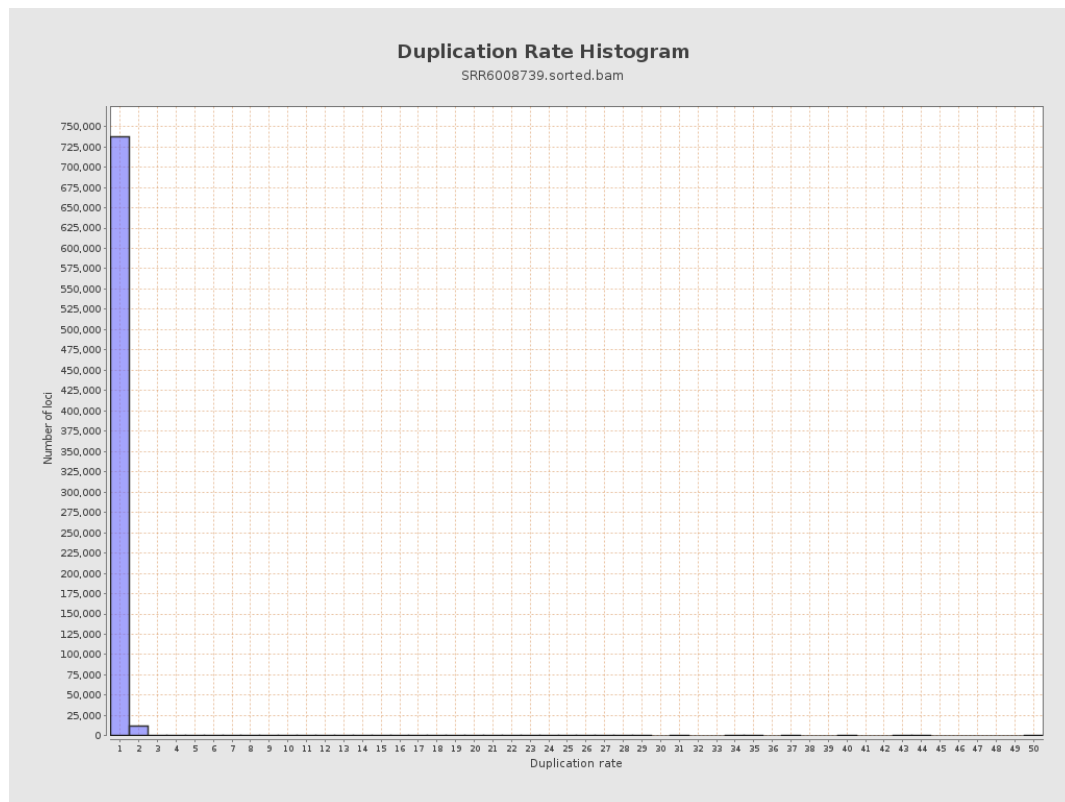
5. Results : Coverage Histogram (0-50X)



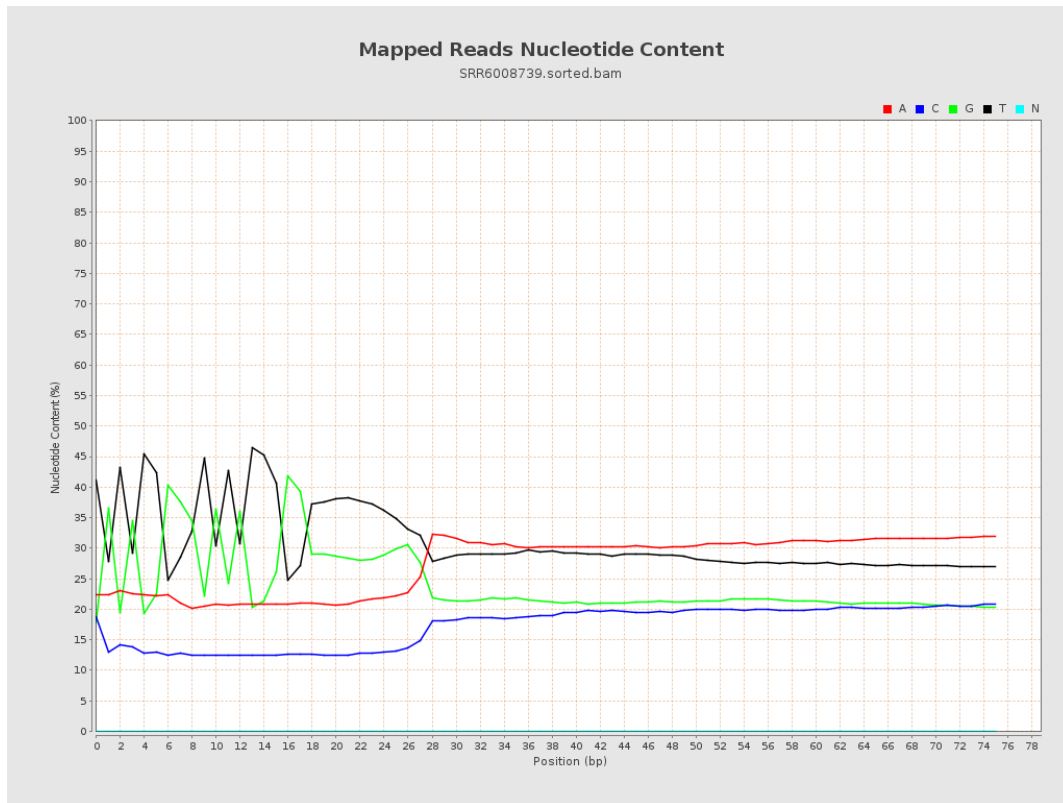
6. Results : Genome Fraction Coverage



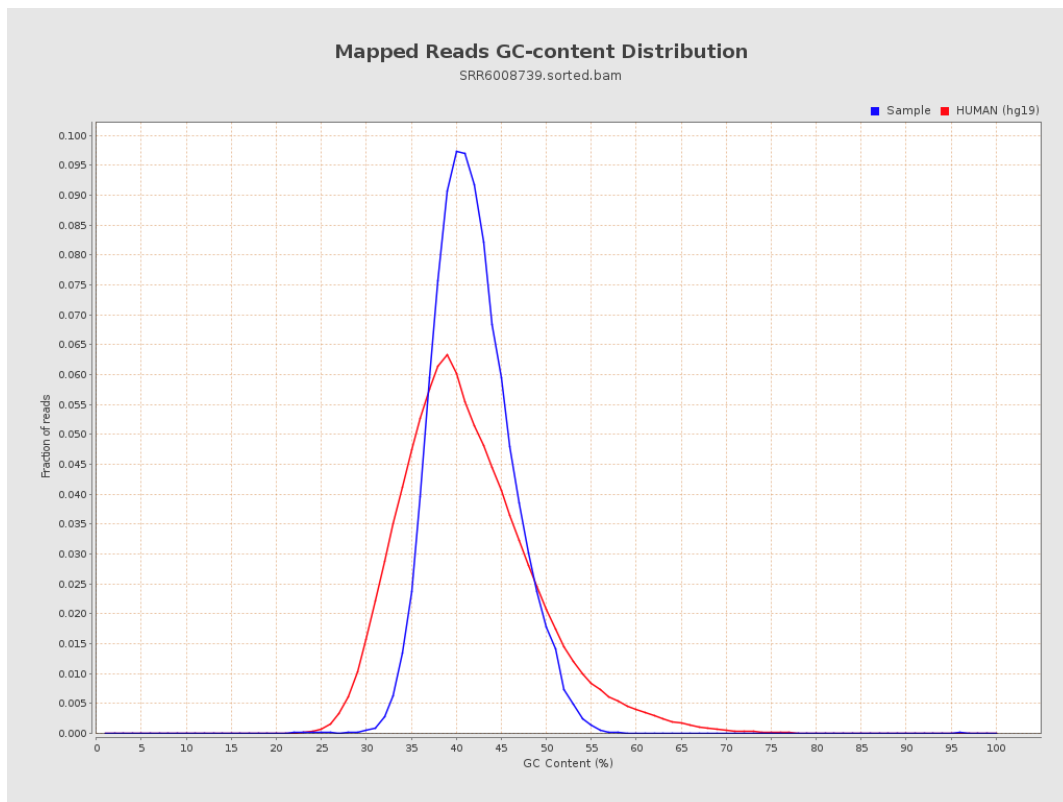
7. Results : Duplication Rate Histogram



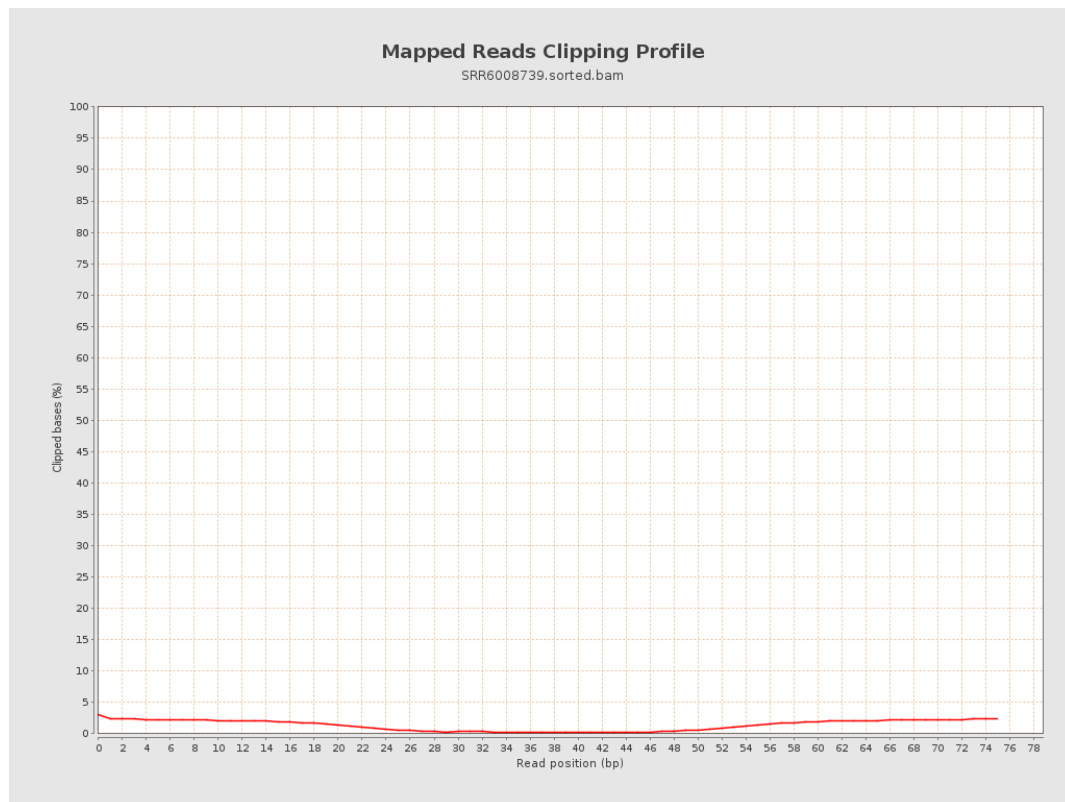
8. Results : Mapped Reads Nucleotide Content



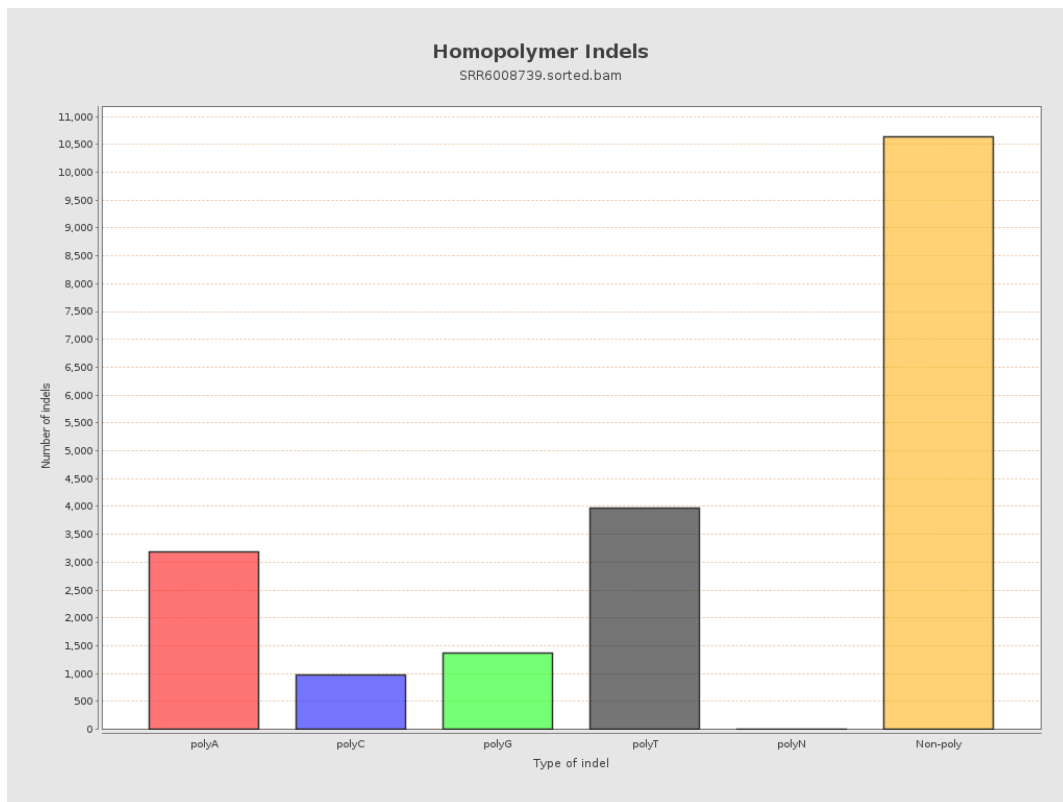
9. Results : Mapped Reads GC-content Distribution



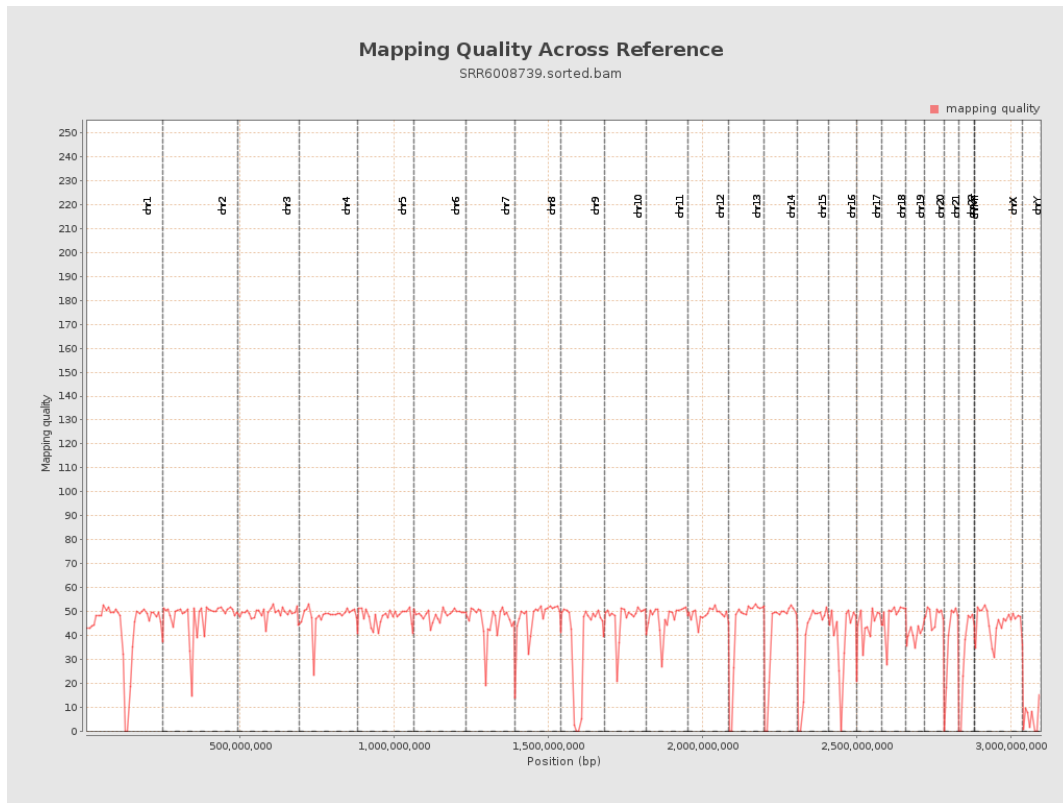
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

