

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:11:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008778.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_SRR6008778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:11:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,093,255
Mapped reads	957,588 / 87.59%
Unmapped reads	135,667 / 12.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,394 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	44,297 / 4.05%
Duplication rate	3.86%
Clipped reads	455,735 / 41.69%

2.2. ACGT Content

Number/percentage of A's	17,164,083 / 27.16%
Number/percentage of C's	12,169,865 / 19.26%
Number/percentage of T's	19,489,645 / 30.84%
Number/percentage of G's	14,282,046 / 22.6%
Number/percentage of N's	93,219 / 0.15%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.2141
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2.4. Mapping Quality

Mean Mapping Quality	44.51
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2.5. Mismatches and indels

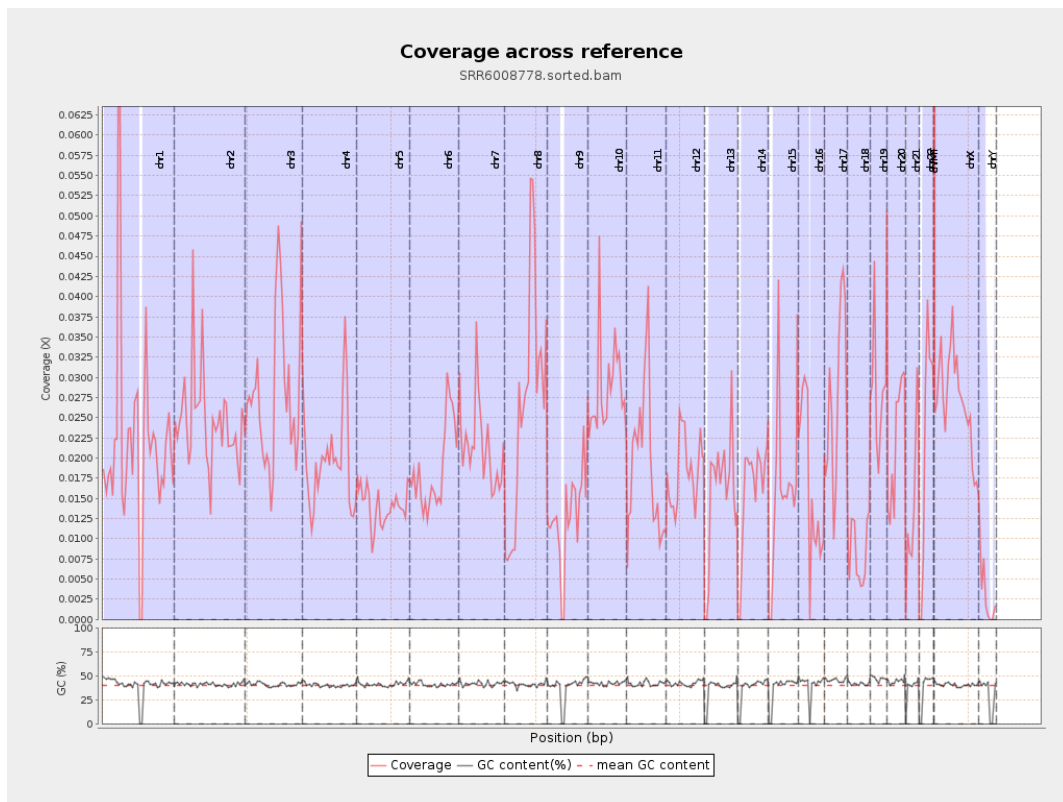
General error rate	0.87%
Mismatches	540,608
Insertions	4,485
Mapped reads with at least one insertion	0.46%
Deletions	18,007
Mapped reads with at least one deletion	1.86%
Homopolymer indels	44.86%

2.6. Chromosome stats

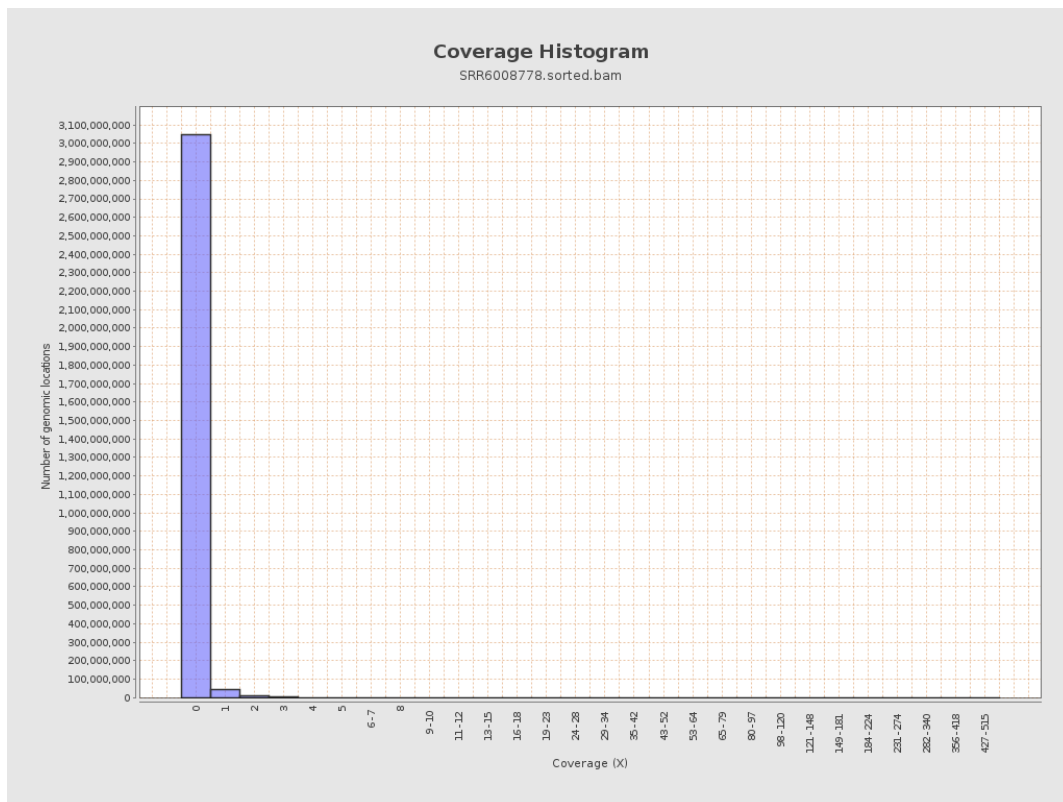
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5384819	0.0216	0.2609
chr2	243199373	5950545	0.0245	0.2924
chr3	198022430	5486378	0.0277	0.2047
chr4	191154276	3795174	0.0199	0.1716
chr5	180915260	2536812	0.014	0.1424
chr6	171115067	3196194	0.0187	0.1737
chr7	159138663	3422230	0.0215	0.2595

chr8	146364022	3898215	0.0266	0.3161
chr9	141213431	1765003	0.0125	0.1526
chr10	135534747	3877791	0.0286	0.2772
chr11	135006516	2639868	0.0196	0.1979
chr12	133851895	2455349	0.0183	0.1632
chr13	115169878	1788225	0.0155	0.1508
chr14	107349540	1701380	0.0158	0.1538
chr15	102531392	1627528	0.0159	0.1524
chr16	90354753	1479386	0.0164	0.1709
chr17	81195210	2227488	0.0274	0.2182
chr18	78077248	609614	0.0078	0.2078
chr19	59128983	1695597	0.0287	0.2379
chr20	63025520	1388028	0.022	0.181
chr21	48129895	696389	0.0145	0.1491
chr22	51304566	1146799	0.0224	0.1812
chrMT	16571	71375	4.3072	3.4057
chrX	155270560	4211779	0.0271	0.21
chrY	59373566	178606	0.003	0.0815

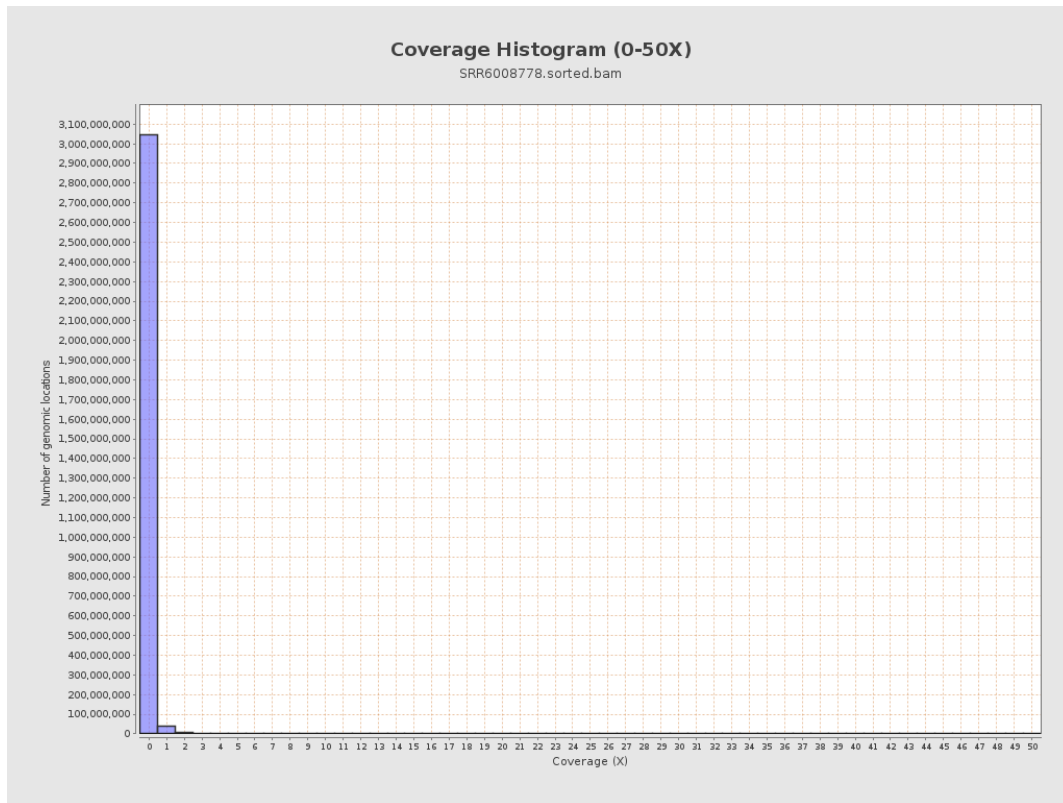
3. Results : Coverage across reference



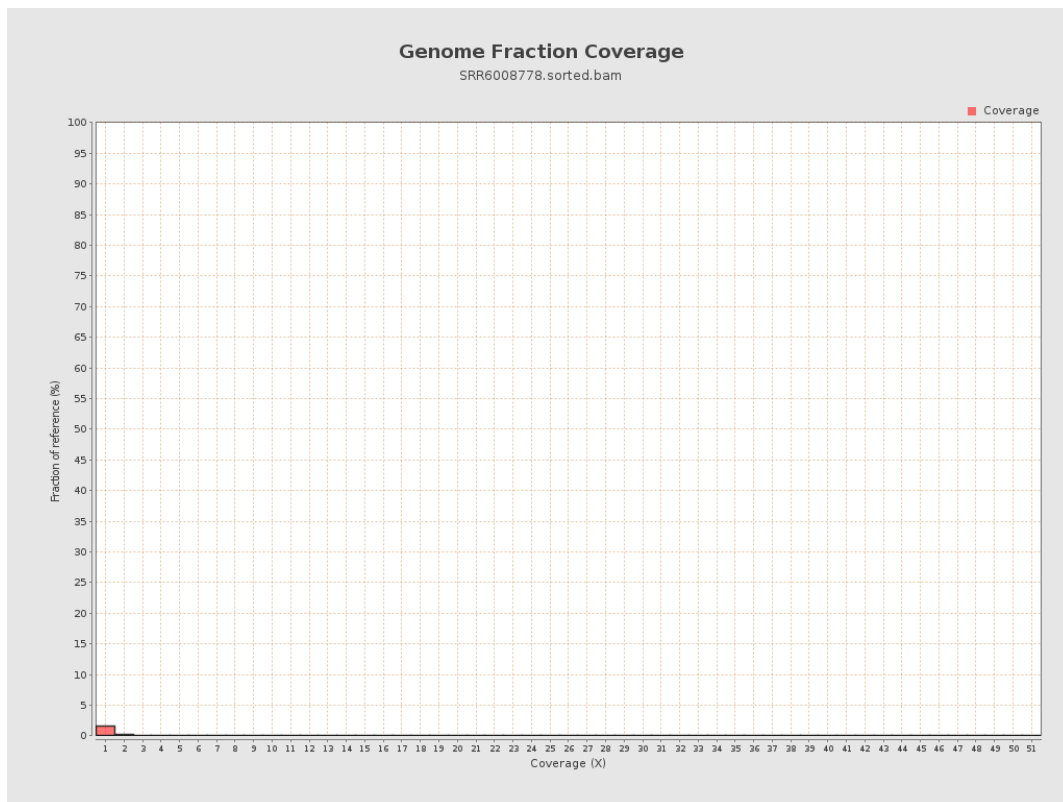
4. Results : Coverage Histogram



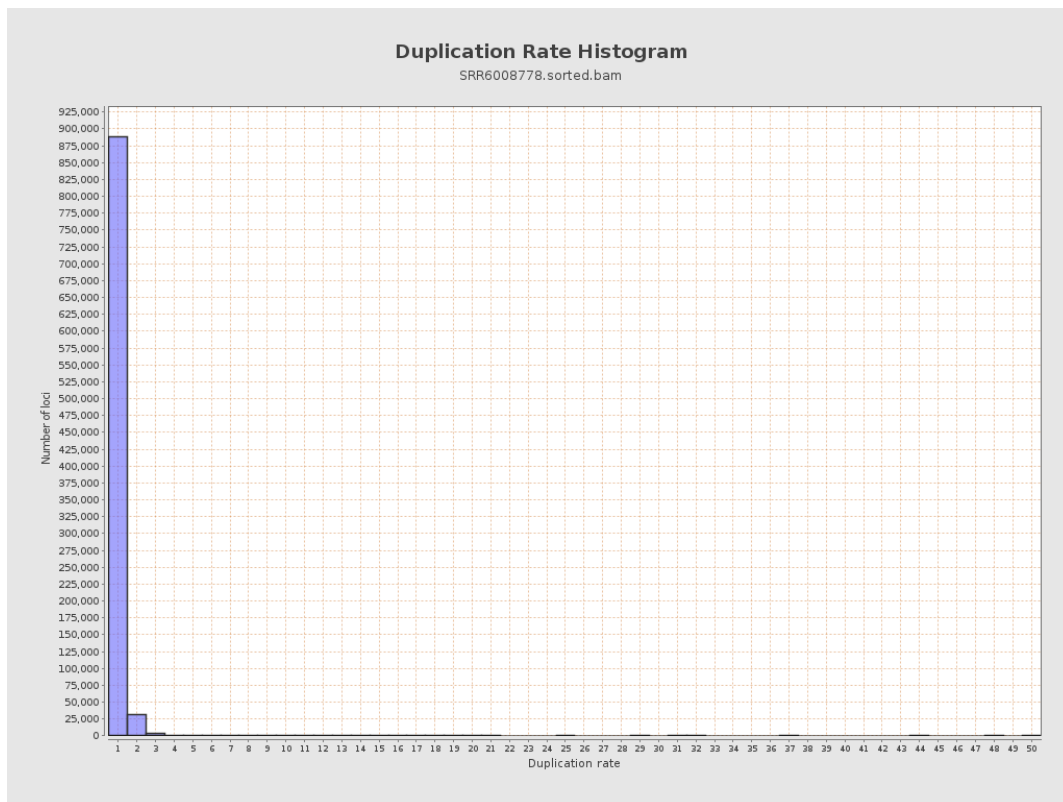
5. Results : Coverage Histogram (0-50X)



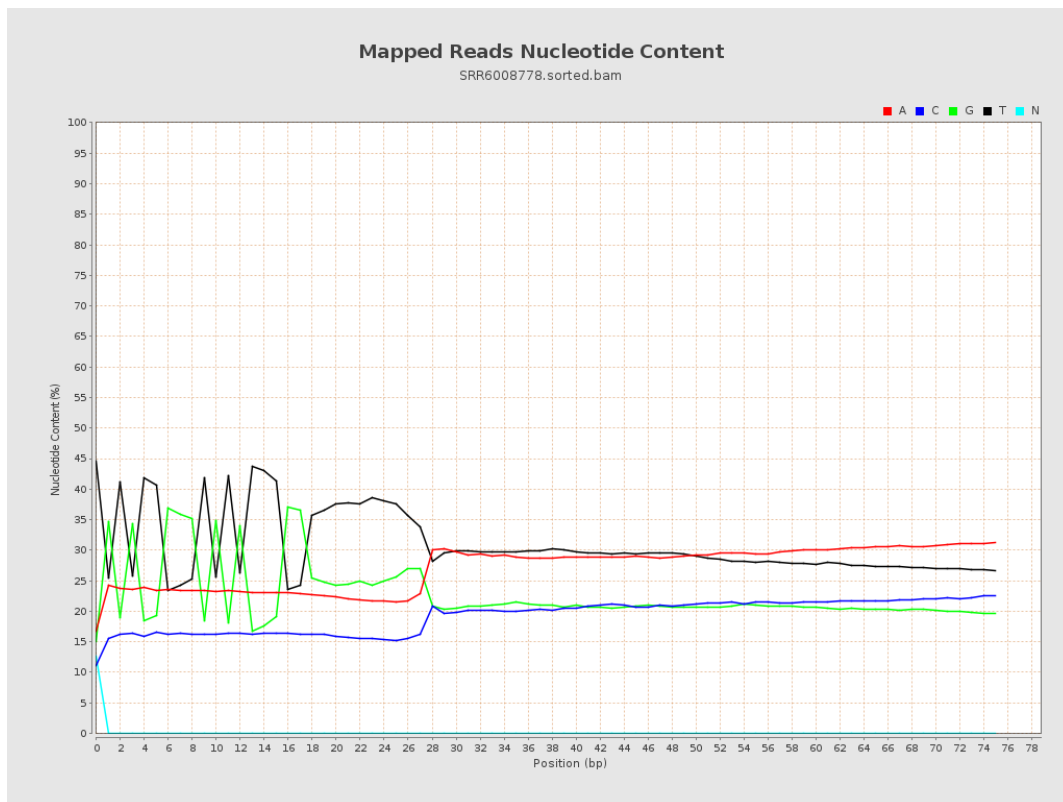
6. Results : Genome Fraction Coverage



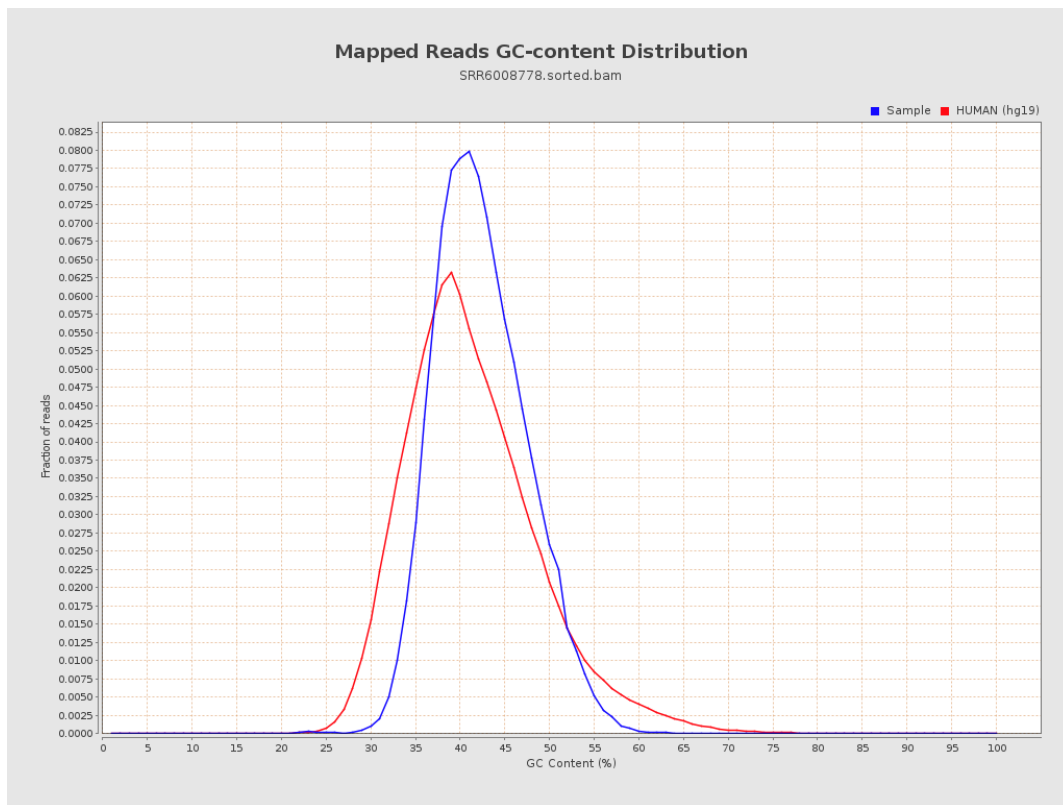
7. Results : Duplication Rate Histogram



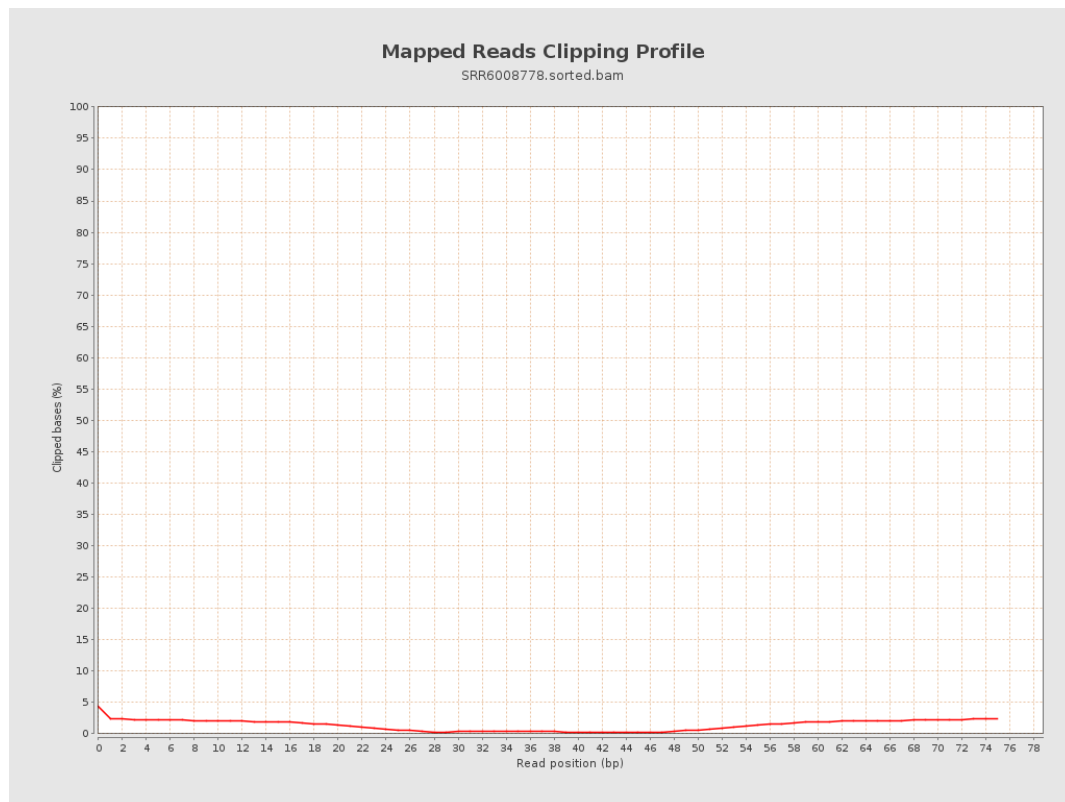
8. Results : Mapped Reads Nucleotide Content



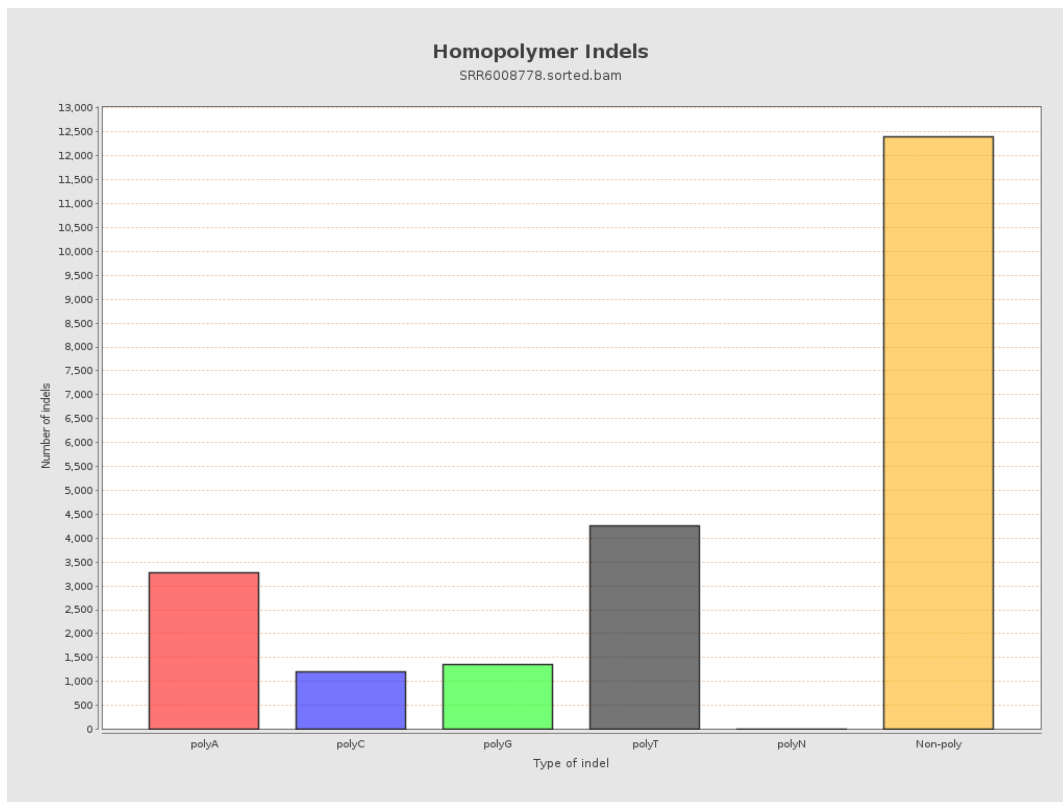
9. Results : Mapped Reads GC-content Distribution



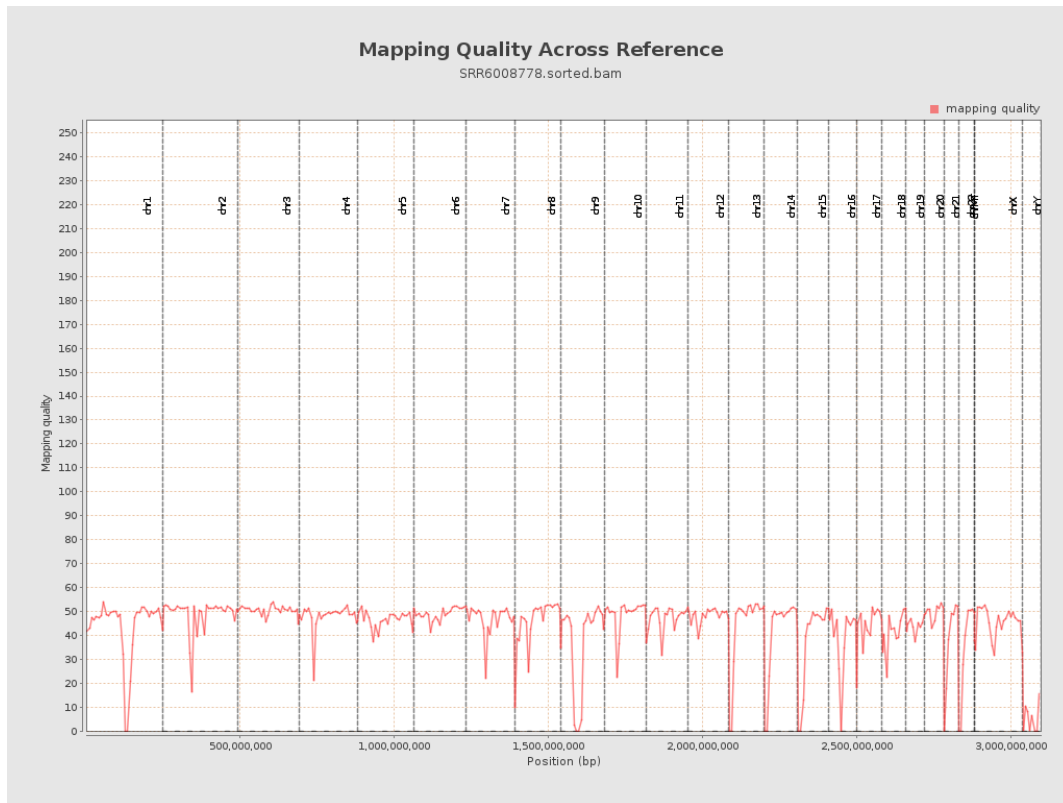
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

