

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548978.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_SRR1548978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:07:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,698,079
Mapped reads	2,913,887 / 43.5%
Unmapped reads	3,784,192 / 56.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	75,708 / 1.13%
Duplication rate	1.91%
Clipped reads	391,368 / 5.84%

2.2. ACGT Content

Number/percentage of A's	35,252,699 / 30.77%
Number/percentage of C's	21,972,959 / 19.18%
Number/percentage of T's	35,298,347 / 30.81%
Number/percentage of G's	22,025,683 / 19.23%
Number/percentage of N's	5,533 / 0%
GC Percentage	38.41%

2.3. Coverage

Mean	0.037
Standard Deviation	0.2999

2.4. Mapping Quality

Mean Mapping Quality	42.6
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2.5. Mismatches and indels

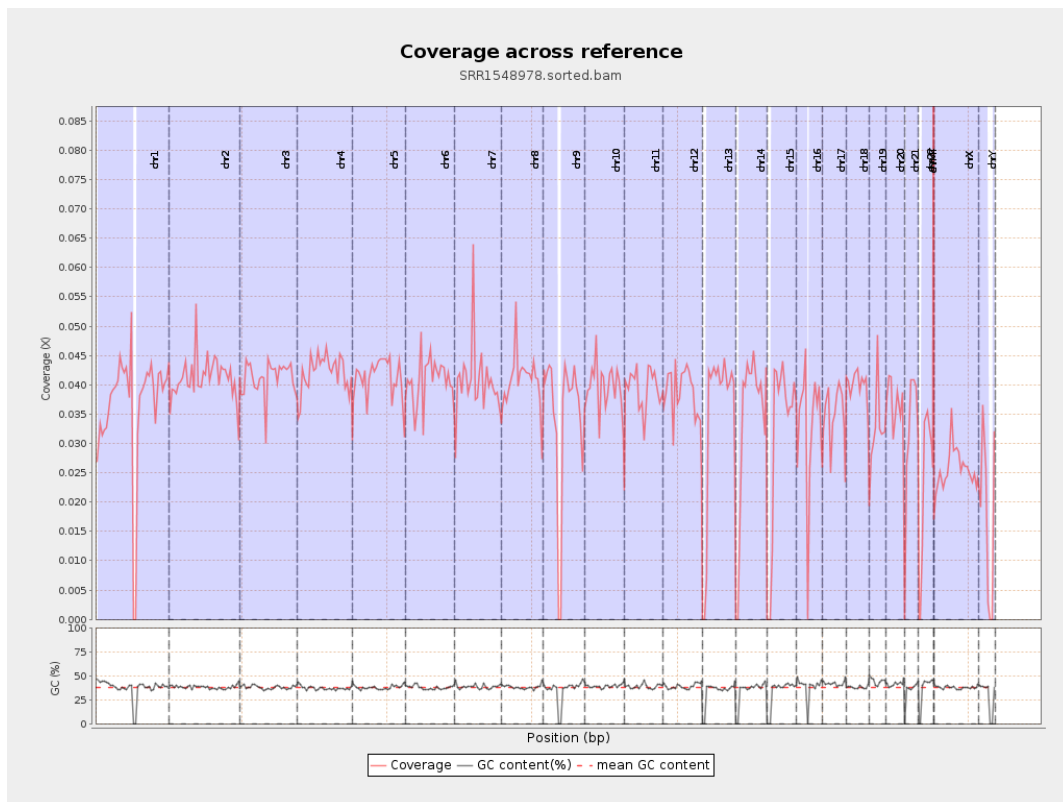
General error rate	0.36%
Mismatches	404,828
Insertions	6,475
Mapped reads with at least one insertion	0.22%
Deletions	13,616
Mapped reads with at least one deletion	0.47%
Homopolymer indels	41.65%

2.6. Chromosome stats

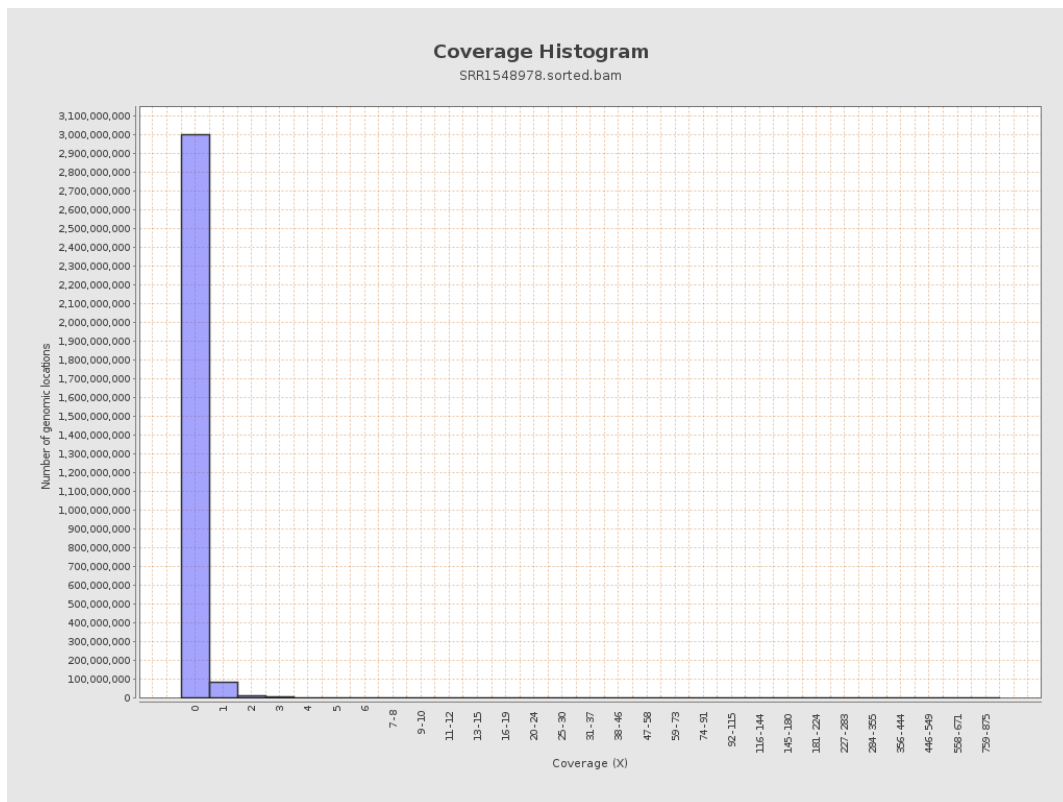
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9115730	0.0366	0.4736
chr2	243199373	10019113	0.0412	0.283
chr3	198022430	8176105	0.0413	0.2344
chr4	191154276	8041892	0.0421	0.2414
chr5	180915260	7456429	0.0412	0.2355
chr6	171115067	6970395	0.0407	0.2509
chr7	159138663	6505955	0.0409	0.4064
chr8	146364022	5962101	0.0407	0.4878

chr9	141213431	4850761	0.0344	0.2511
chr10	135534747	5382533	0.0397	0.2641
chr11	135006516	5284512	0.0391	0.2752
chr12	133851895	5160633	0.0386	0.231
chr13	115169878	3972247	0.0345	0.2133
chr14	107349540	3580282	0.0334	0.2357
chr15	102531392	3251428	0.0317	0.2037
chr16	90354753	2979288	0.033	0.2139
chr17	81195210	2809636	0.0346	0.22
chr18	78077248	3131420	0.0401	0.3998
chr19	59128983	1950110	0.033	0.4247
chr20	63025520	2302210	0.0365	0.2242
chr21	48129895	1534058	0.0319	0.2199
chr22	51304566	1166611	0.0227	0.204
chrMT	16571	2675	0.1614	0.4075
chrX	155270560	3955013	0.0255	0.2053
chrY	59373566	1011015	0.017	0.2035

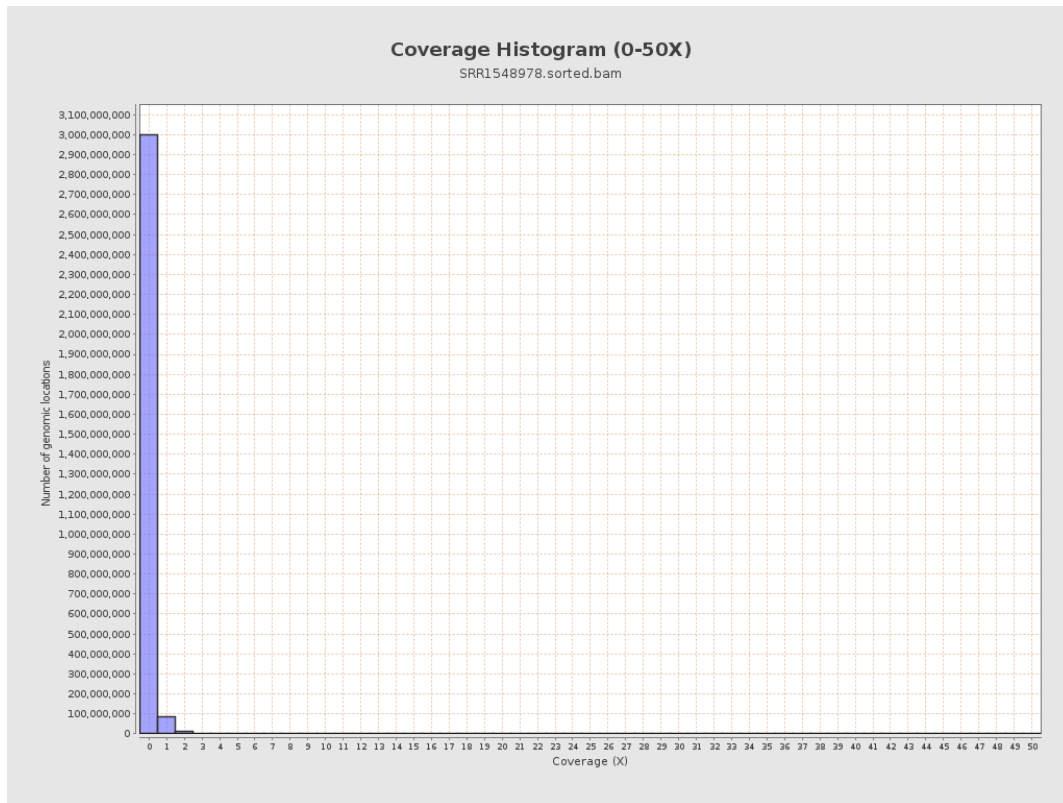
3. Results : Coverage across reference



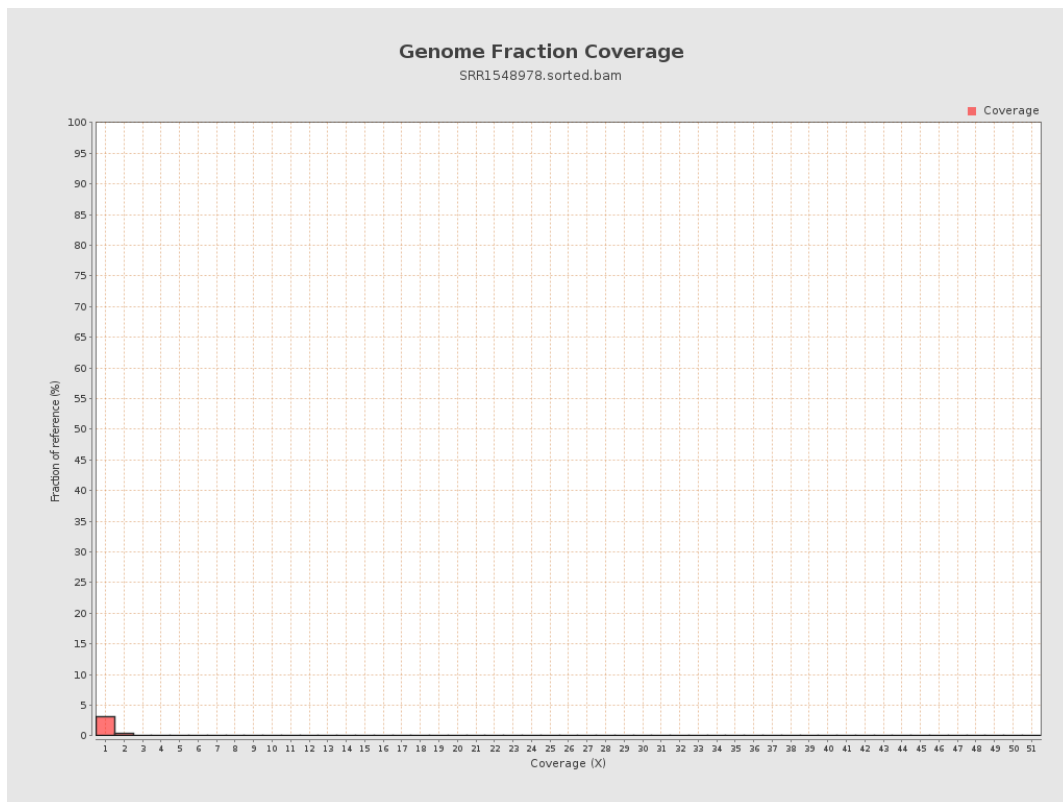
4. Results : Coverage Histogram



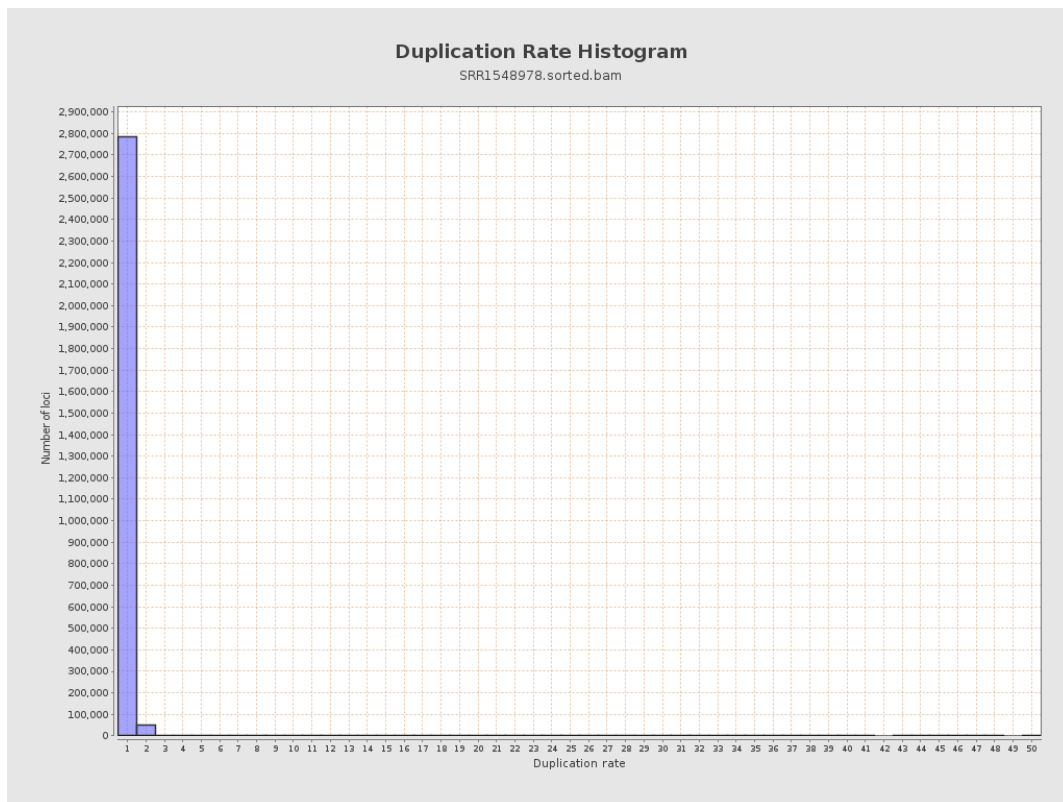
5. Results : Coverage Histogram (0-50X)



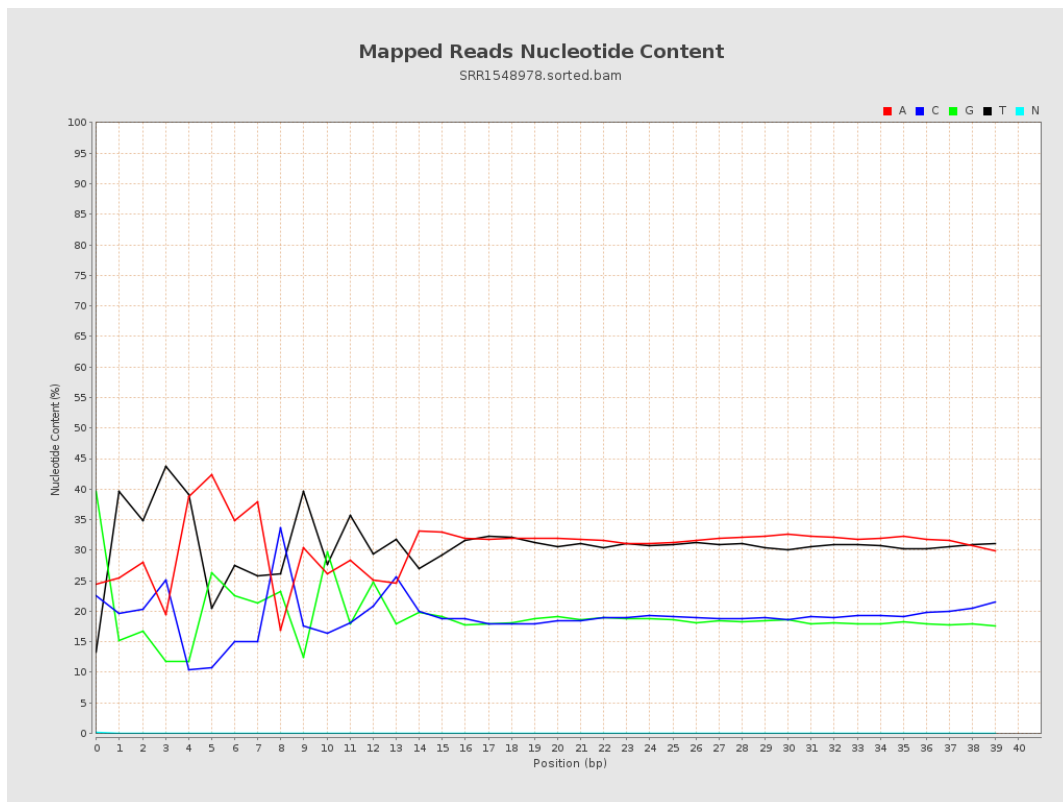
6. Results : Genome Fraction Coverage



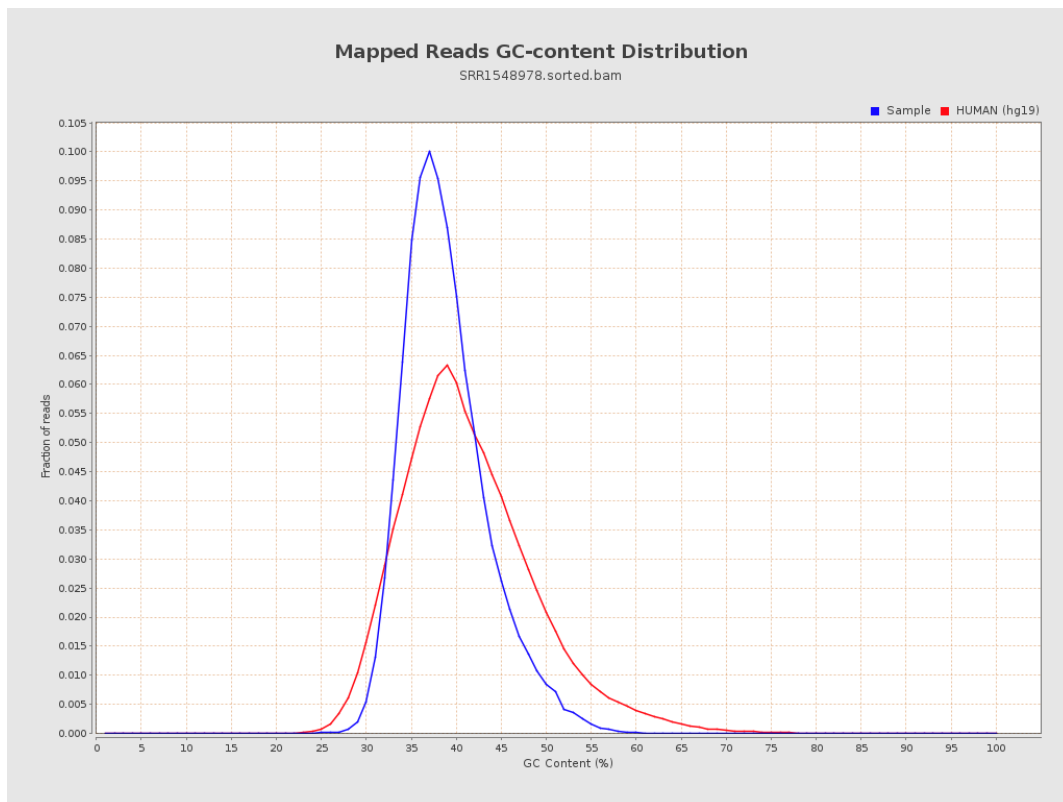
7. Results : Duplication Rate Histogram



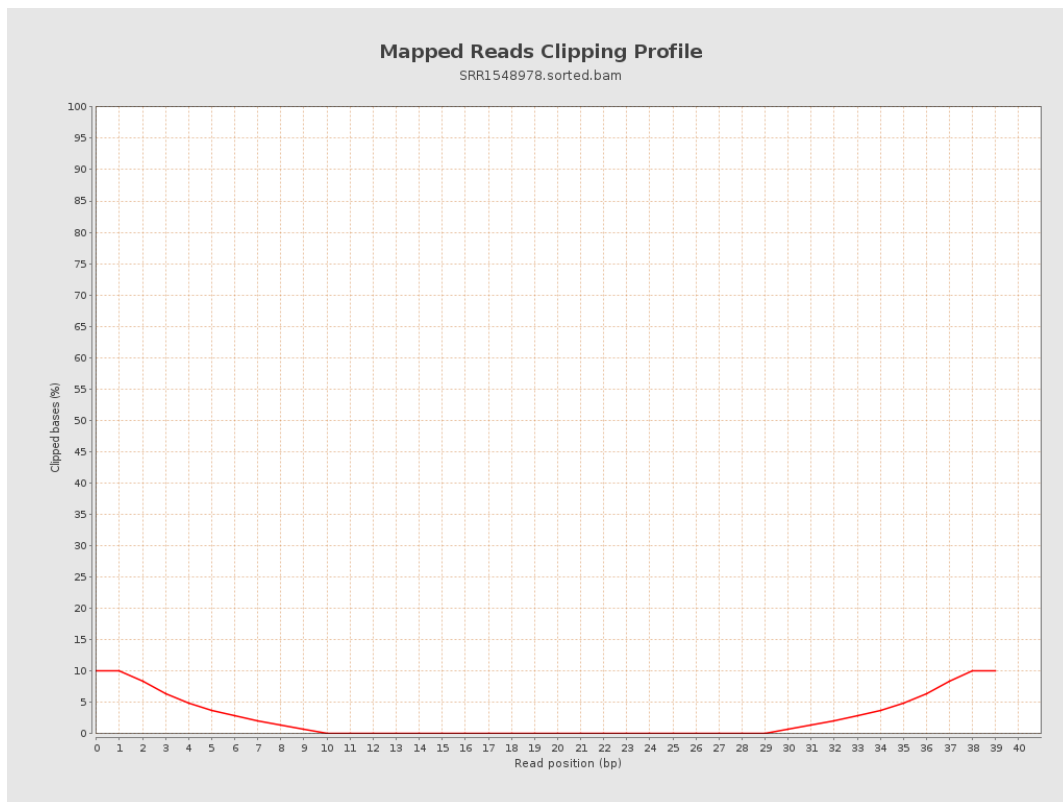
8. Results : Mapped Reads Nucleotide Content



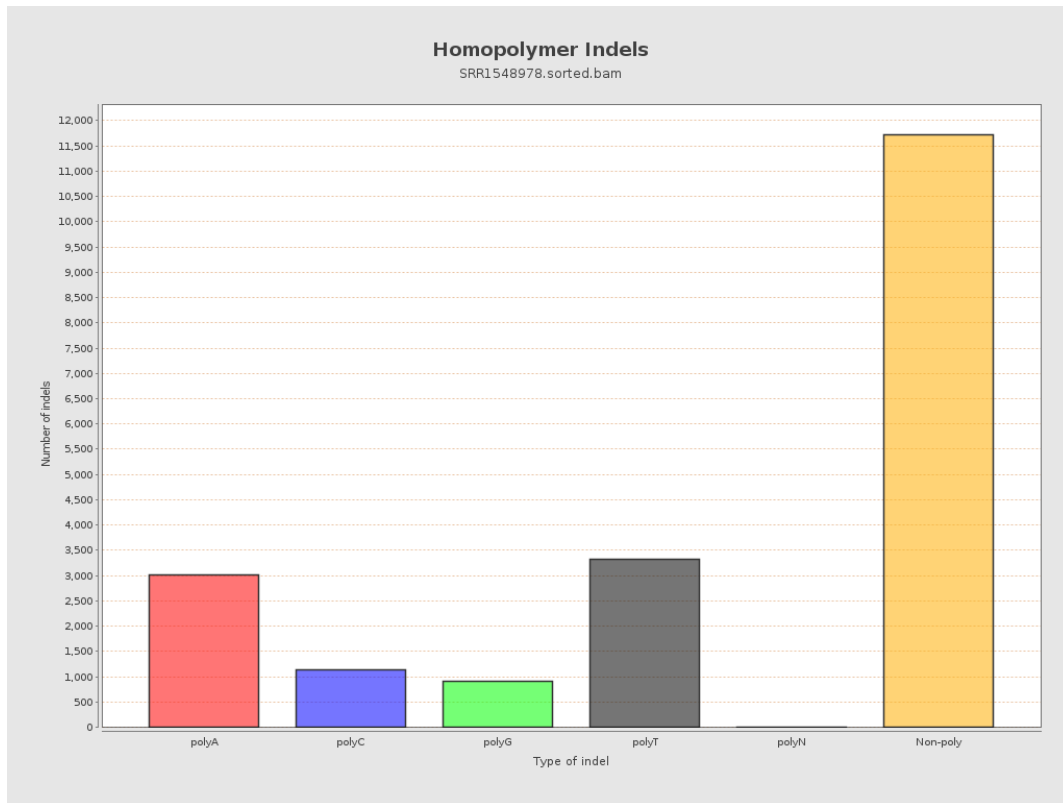
9. Results : Mapped Reads GC-content Distribution



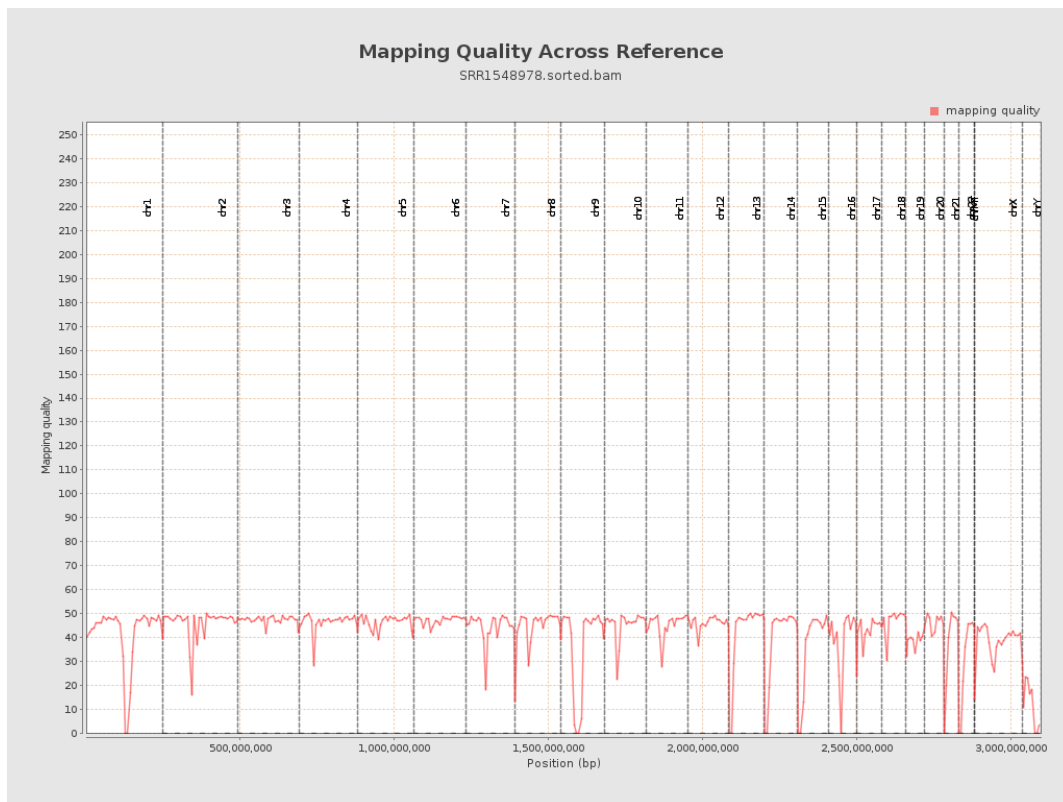
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

