

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:45:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548976.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_SRR1548976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:45:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,826,199
Mapped reads	2,955,479 / 43.3%
Unmapped reads	3,870,720 / 56.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	85,636 / 1.25%
Duplication rate	2.16%
Clipped reads	368,147 / 5.39%

2.2. ACGT Content

Number/percentage of A's	35,612,859 / 30.62%
Number/percentage of C's	22,481,740 / 19.33%
Number/percentage of T's	35,725,242 / 30.71%
Number/percentage of G's	22,492,538 / 19.34%
Number/percentage of N's	6,033 / 0.01%
GC Percentage	38.66%

2.3. Coverage

Mean	0.0376
Standard Deviation	0.3207

2.4. Mapping Quality

Mean Mapping Quality	42.86
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2.5. Mismatches and indels

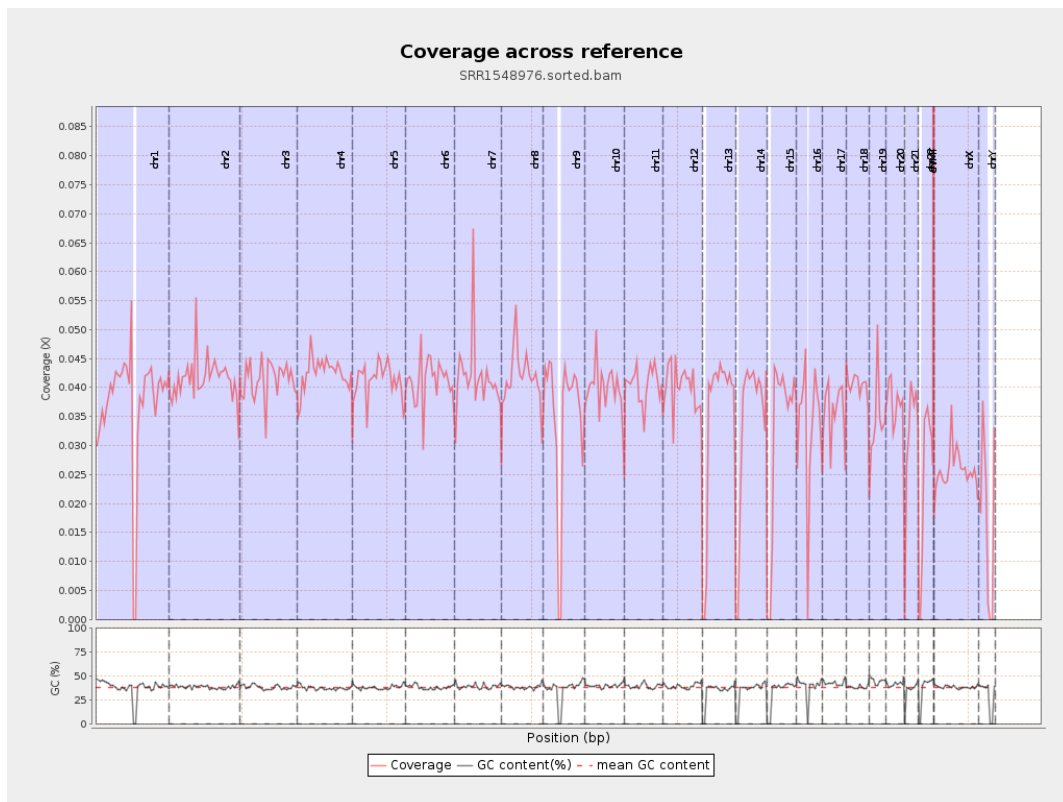
General error rate	0.35%
Mismatches	396,005
Insertions	6,388
Mapped reads with at least one insertion	0.22%
Deletions	13,137
Mapped reads with at least one deletion	0.44%
Homopolymer indels	43.74%

2.6. Chromosome stats

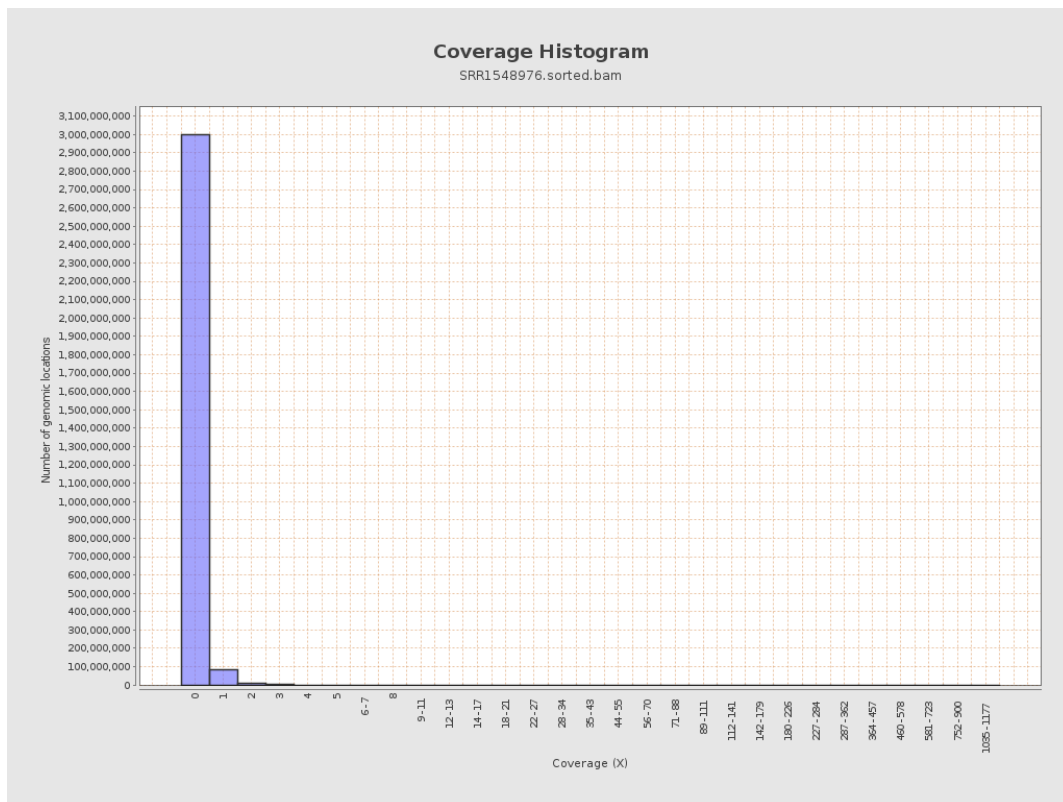
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9327388	0.0374	0.4897
chr2	243199373	10122518	0.0416	0.2987
chr3	198022430	8206588	0.0414	0.2396
chr4	191154276	8122848	0.0425	0.2499
chr5	180915260	7469360	0.0413	0.241
chr6	171115067	7040117	0.0411	0.2643
chr7	159138663	6693928	0.0421	0.4296
chr8	146364022	6125002	0.0418	0.6252

chr9	141213431	4930465	0.0349	0.2643
chr10	135534747	5424657	0.04	0.2698
chr11	135006516	5438660	0.0403	0.2794
chr12	133851895	5353514	0.04	0.2425
chr13	115169878	3979401	0.0346	0.219
chr14	107349540	3594656	0.0335	0.2452
chr15	102531392	3324371	0.0324	0.21
chr16	90354753	3019148	0.0334	0.2187
chr17	81195210	2883608	0.0355	0.2291
chr18	78077248	3166559	0.0406	0.409
chr19	59128983	2046558	0.0346	0.4227
chr20	63025520	2331318	0.037	0.2308
chr21	48129895	1527200	0.0317	0.2259
chr22	51304566	1201839	0.0234	0.2078
chrMT	16571	5806	0.3504	0.6691
chrX	155270560	3989358	0.0257	0.2108
chrY	59373566	1009886	0.017	0.2129

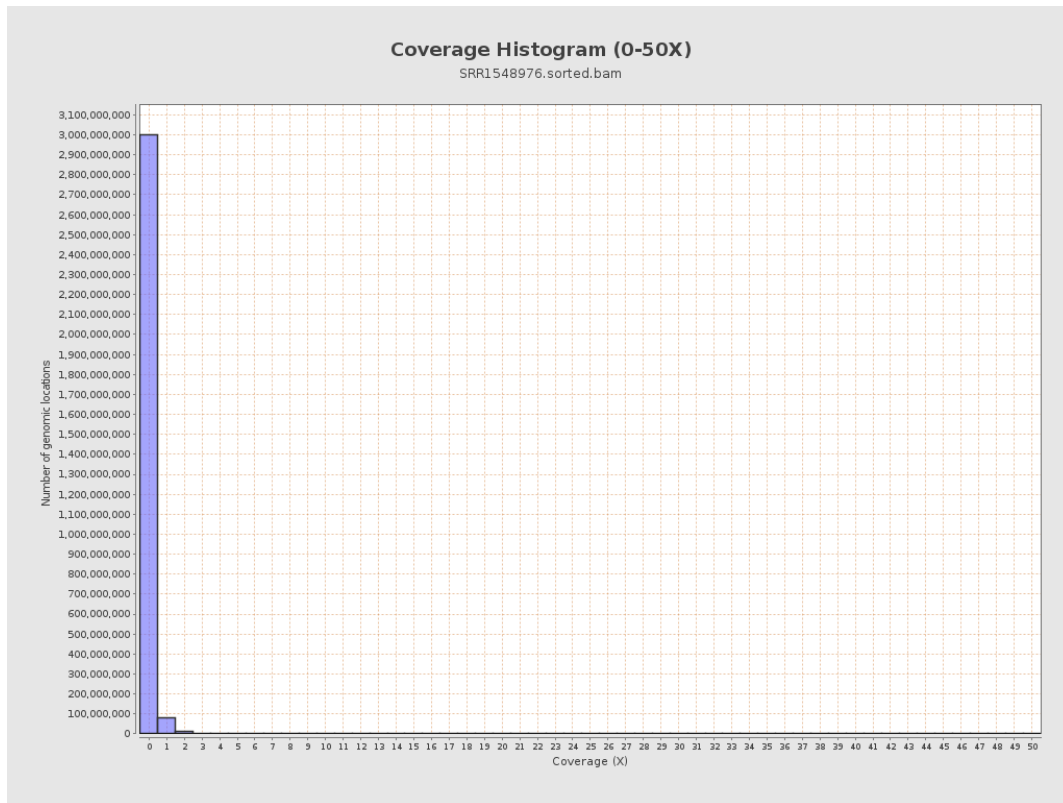
3. Results : Coverage across reference



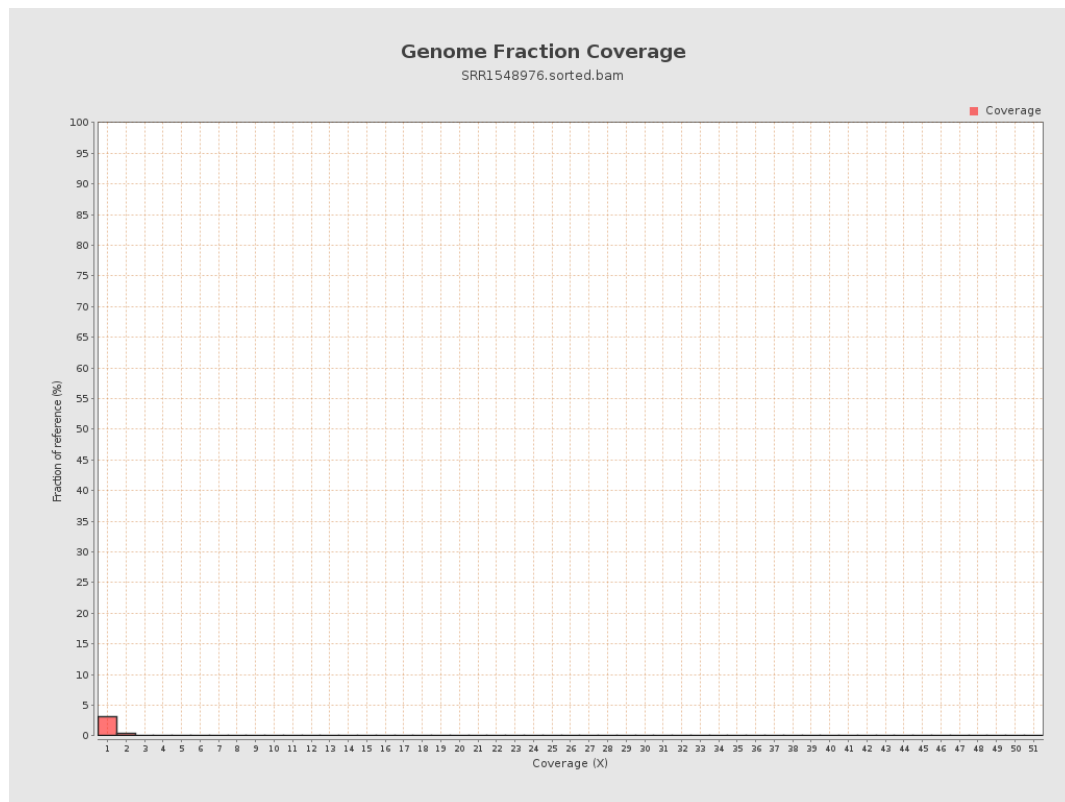
4. Results : Coverage Histogram



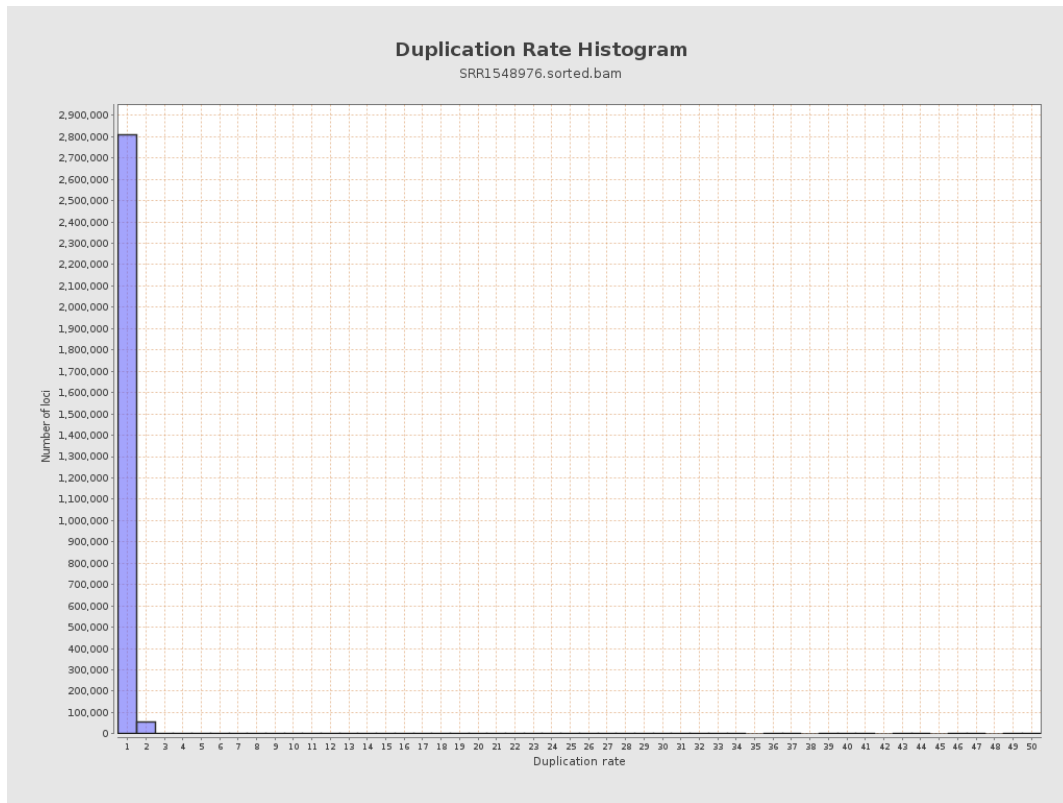
5. Results : Coverage Histogram (0-50X)



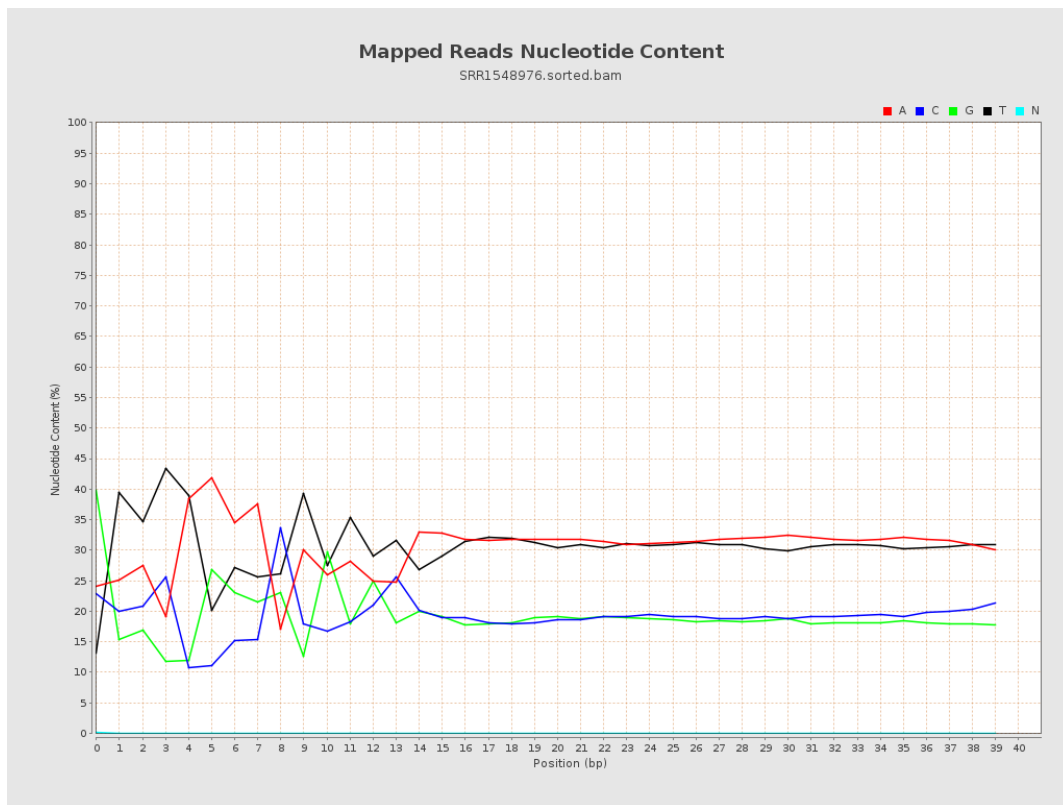
6. Results : Genome Fraction Coverage



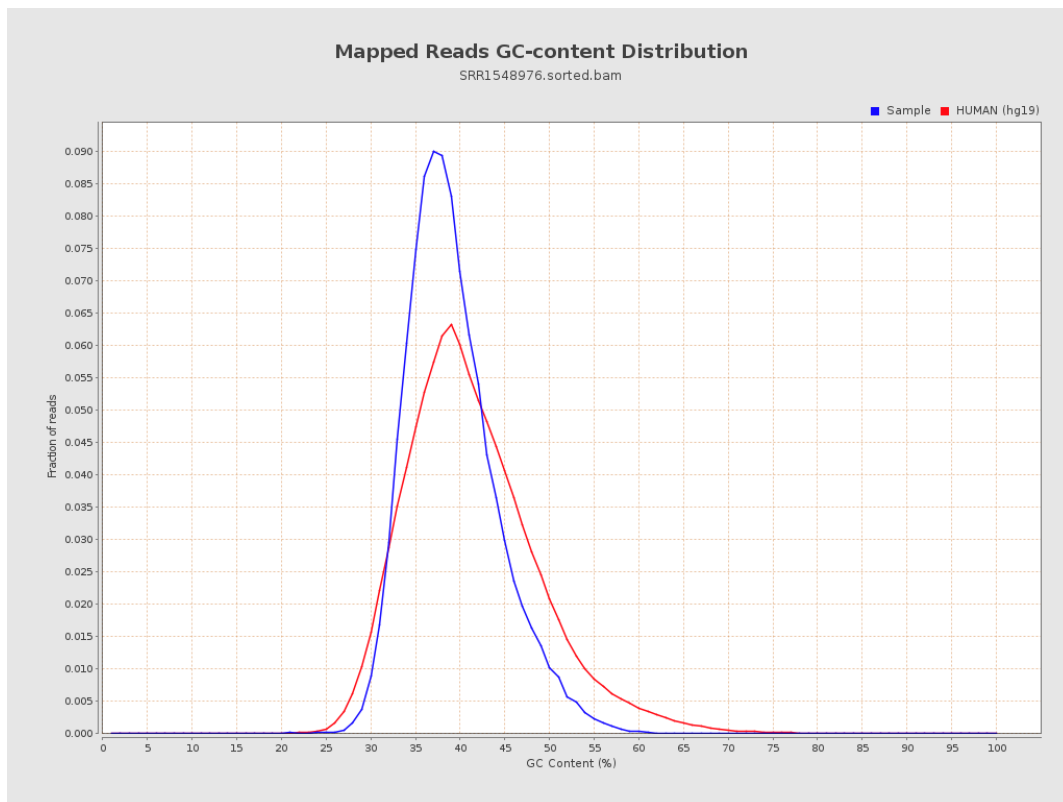
7. Results : Duplication Rate Histogram



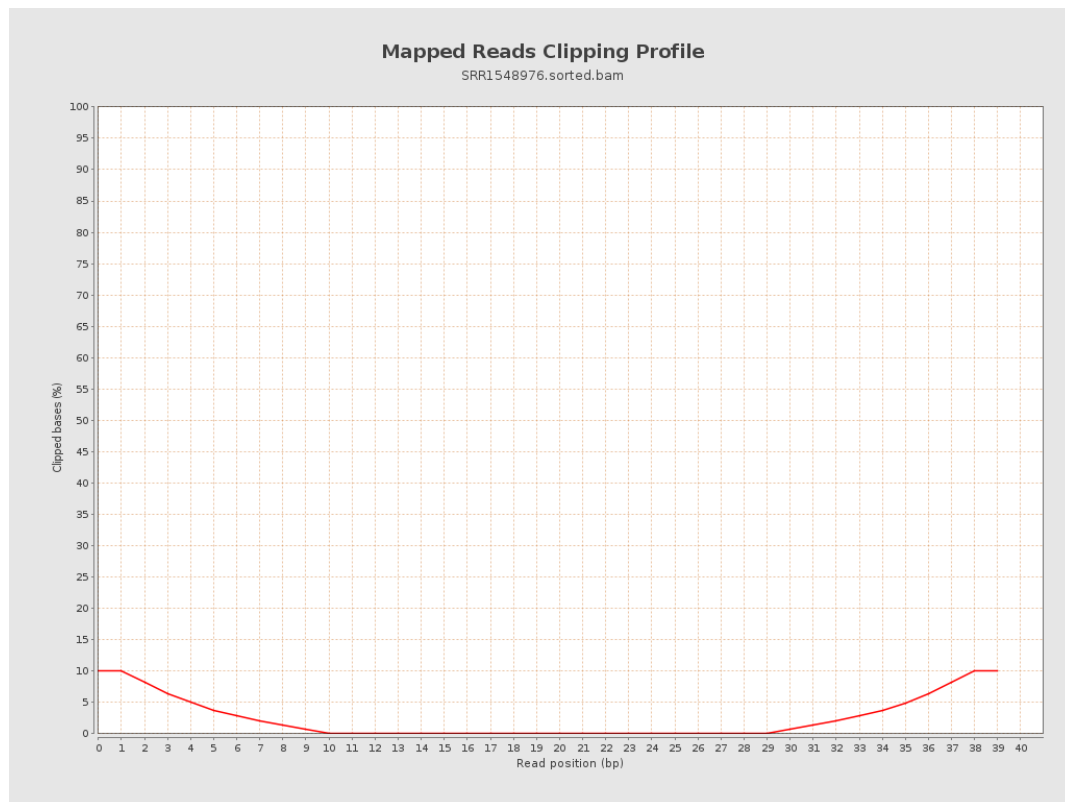
8. Results : Mapped Reads Nucleotide Content



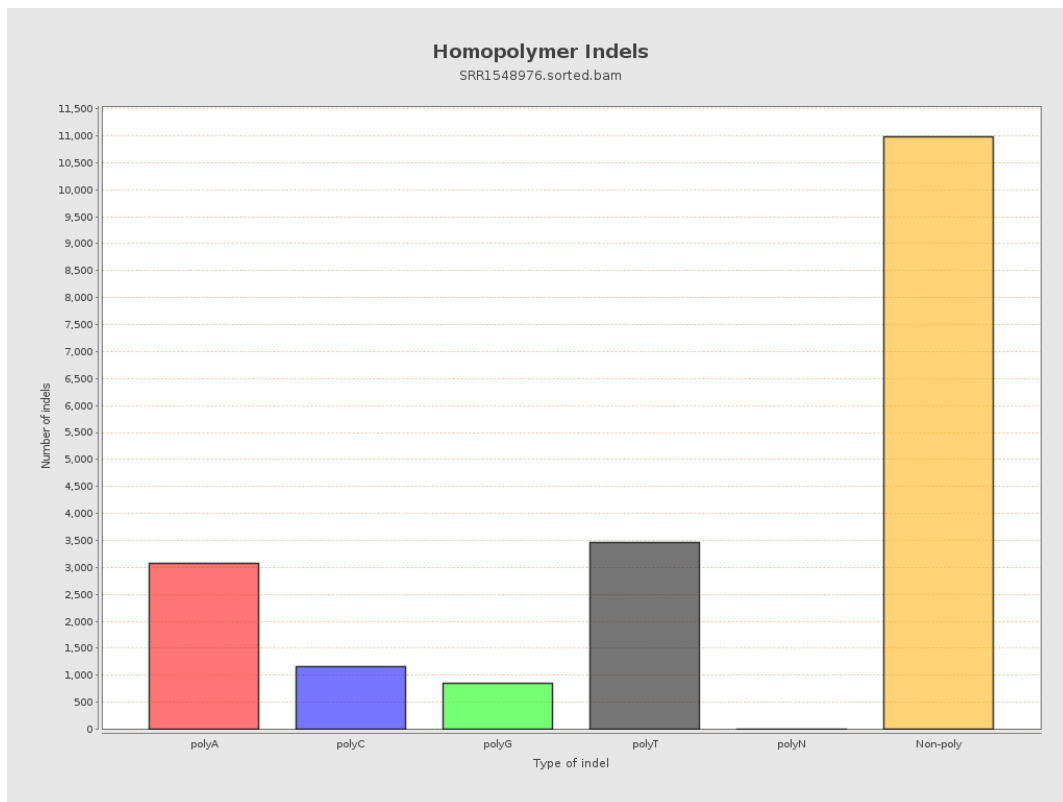
9. Results : Mapped Reads GC-content Distribution



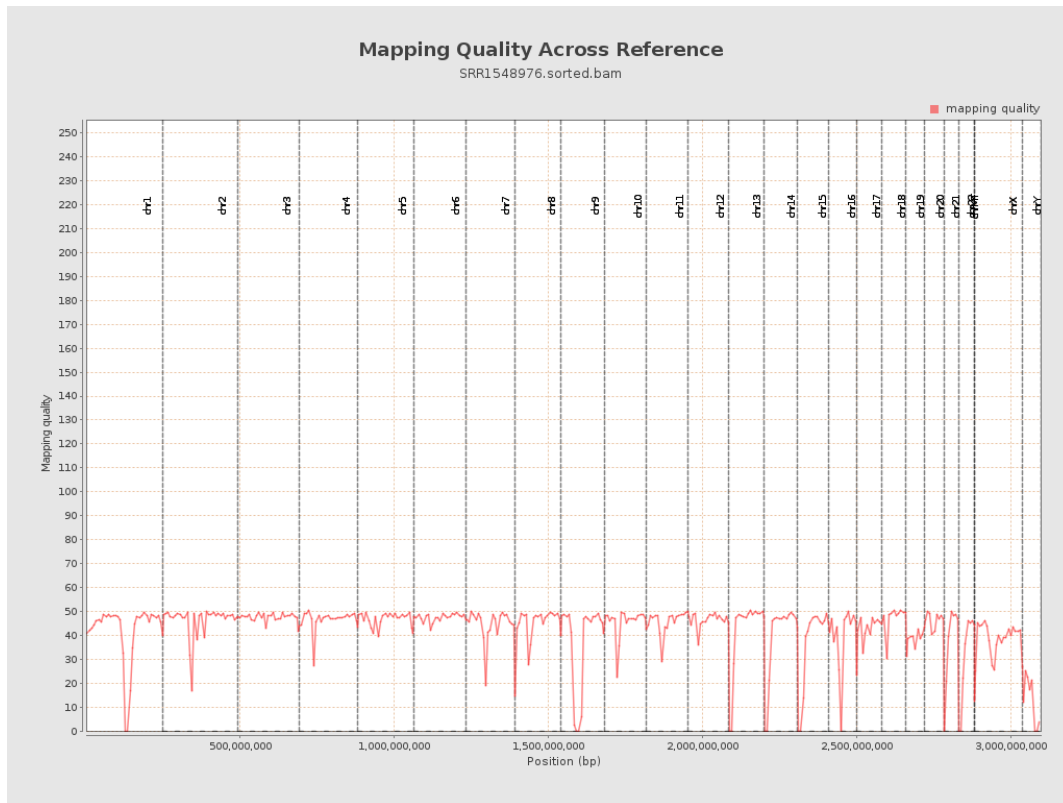
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

