

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:52:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081776.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_SRR3081776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:52:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,168,977
Mapped reads	1,957,911 / 90.27%
Unmapped reads	211,066 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,128 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	73,159 / 3.37%
Duplication rate	2.89%
Clipped reads	845,810 / 39%

2.2. ACGT Content

Number/percentage of A's	36,134,075 / 27.57%
Number/percentage of C's	24,719,652 / 18.86%
Number/percentage of T's	40,871,275 / 31.18%
Number/percentage of G's	29,347,547 / 22.39%
Number/percentage of N's	1,513 / 0%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.3509
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2.4. Mapping Quality

Mean Mapping Quality	45.38
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2.5. Mismatches and indels

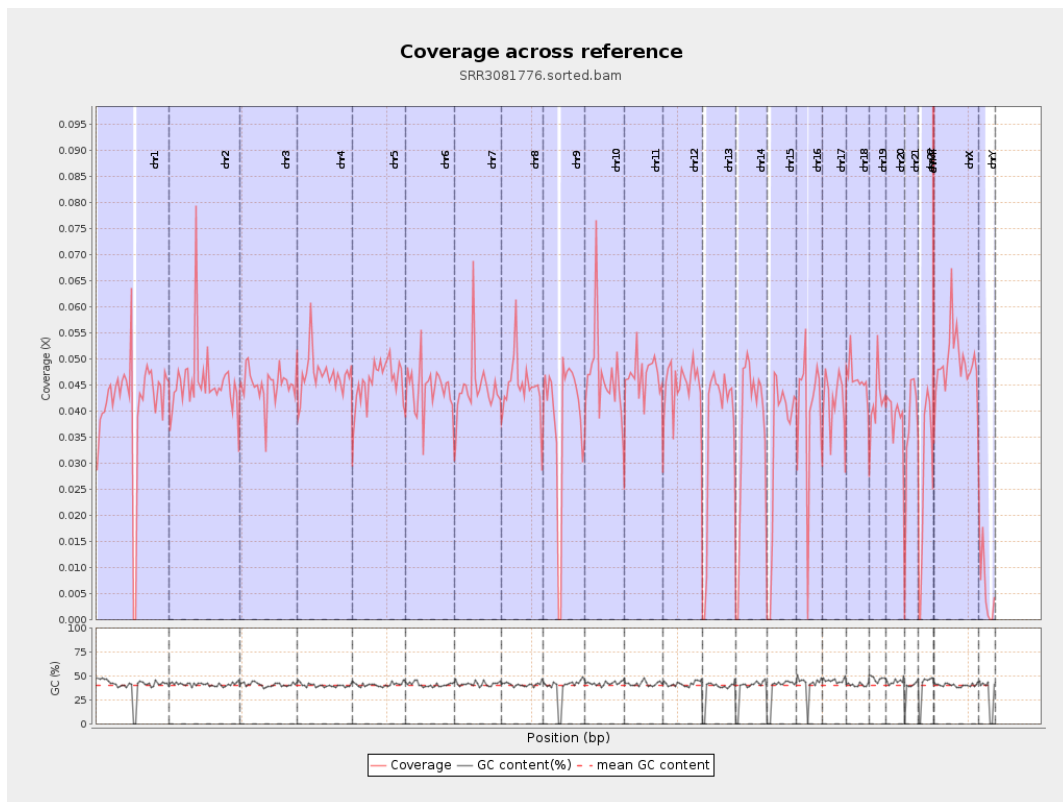
General error rate	0.79%
Mismatches	1,021,391
Insertions	9,655
Mapped reads with at least one insertion	0.49%
Deletions	26,624
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.39%

2.6. Chromosome stats

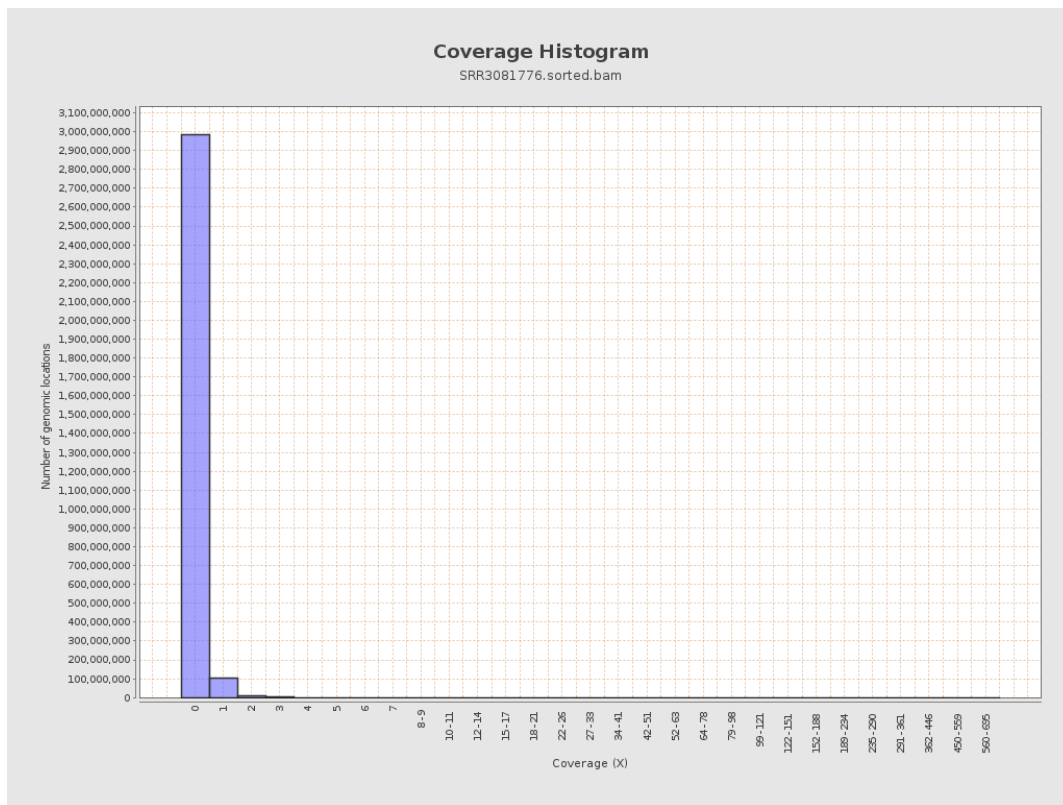
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10273062	0.0412	0.5513
chr2	243199373	11036847	0.0454	0.4266
chr3	198022430	8903124	0.045	0.2382
chr4	191154276	8969251	0.0469	0.2599
chr5	180915260	8282306	0.0458	0.2384
chr6	171115067	7531371	0.044	0.2699
chr7	159138663	7104389	0.0446	0.4552

chr8	146364022	6534475	0.0446	0.4957
chr9	141213431	5466911	0.0387	0.3328
chr10	135534747	6324845	0.0467	0.3904
chr11	135006516	6275575	0.0465	0.3087
chr12	133851895	6032896	0.0451	0.2388
chr13	115169878	4184507	0.0363	0.2119
chr14	107349540	3994699	0.0372	0.2315
chr15	102531392	3499517	0.0341	0.2106
chr16	90354753	3638320	0.0403	0.2561
chr17	81195210	3369031	0.0415	0.2432
chr18	78077248	3611552	0.0463	0.6093
chr19	59128983	2488652	0.0421	0.4578
chr20	63025520	2462359	0.0391	0.2303
chr21	48129895	1746891	0.0363	0.2313
chr22	51304566	1401379	0.0273	0.1837
chrMT	16571	5285	0.3189	0.6483
chrX	155270560	7638743	0.0492	0.2778
chrY	59373566	344989	0.0058	0.1379

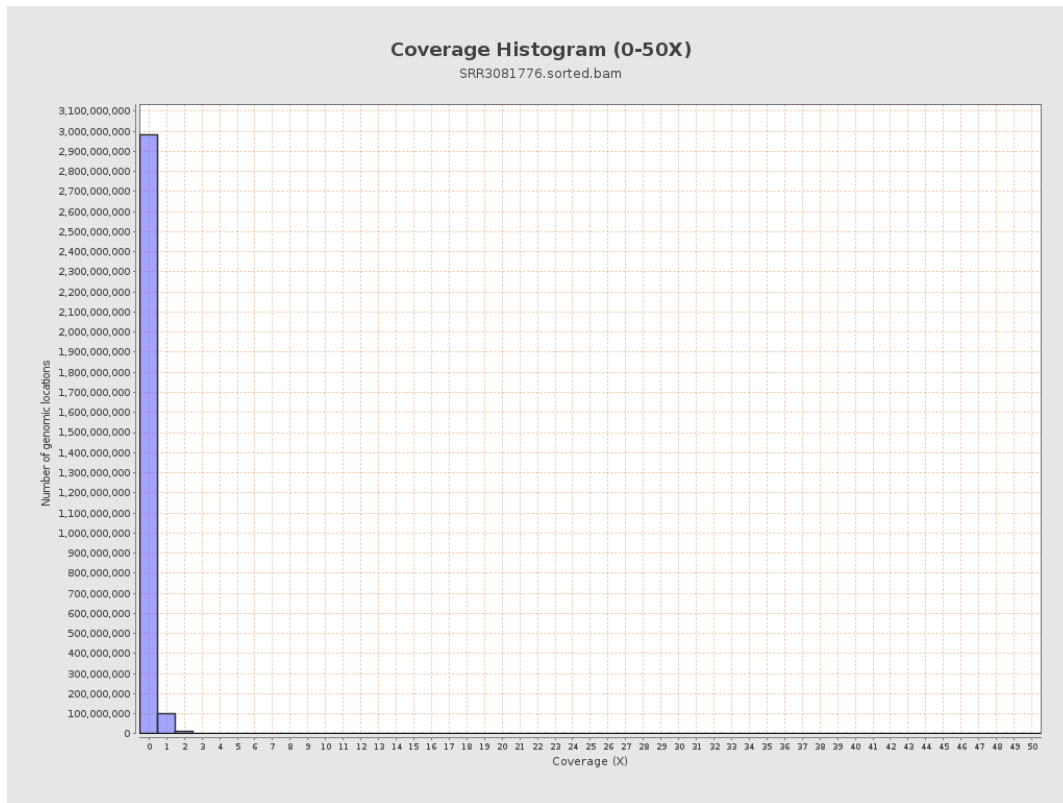
3. Results : Coverage across reference



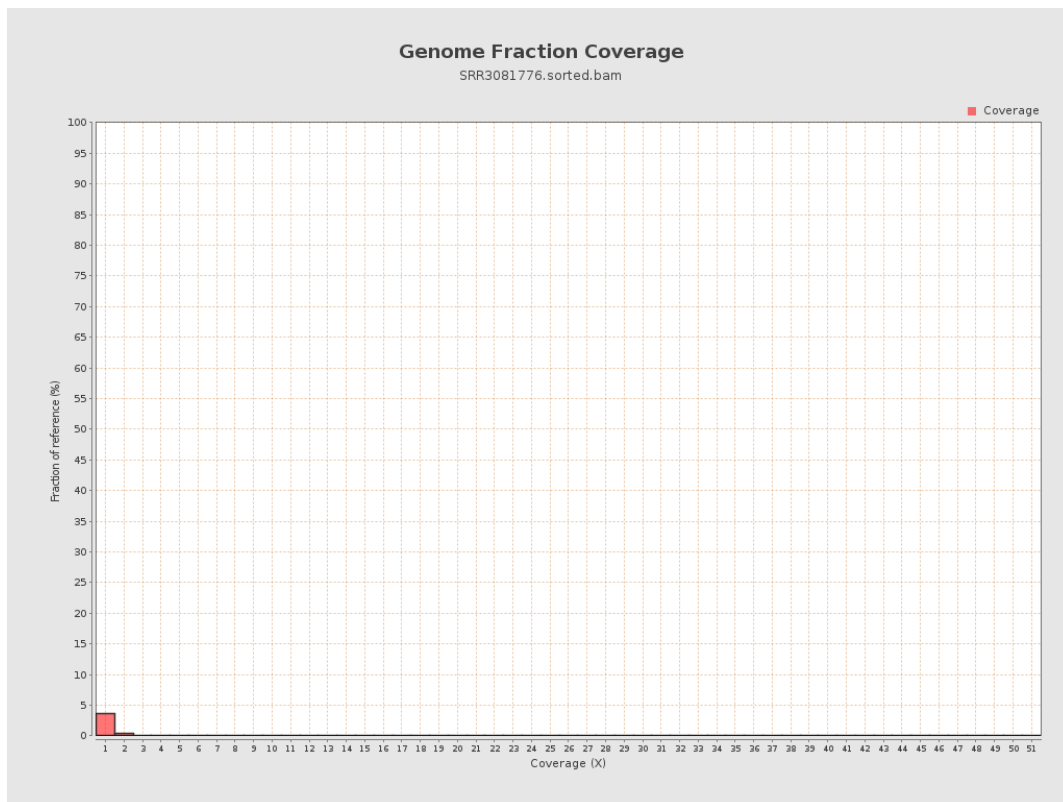
4. Results : Coverage Histogram



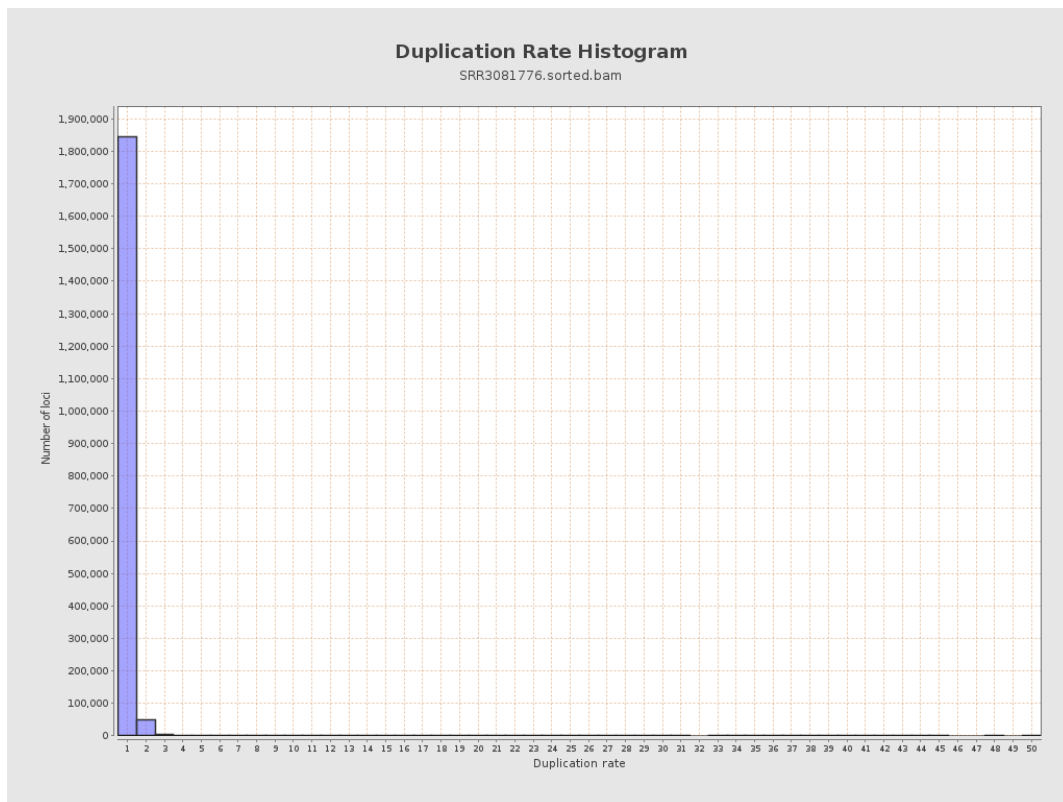
5. Results : Coverage Histogram (0-50X)



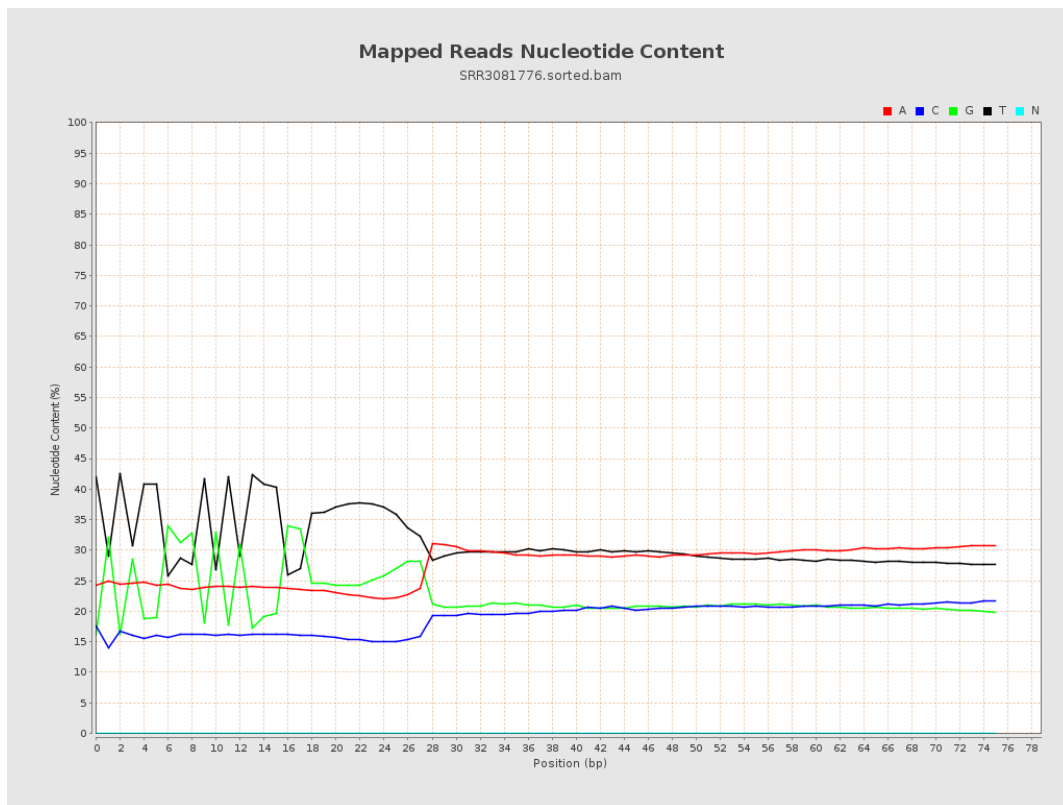
6. Results : Genome Fraction Coverage



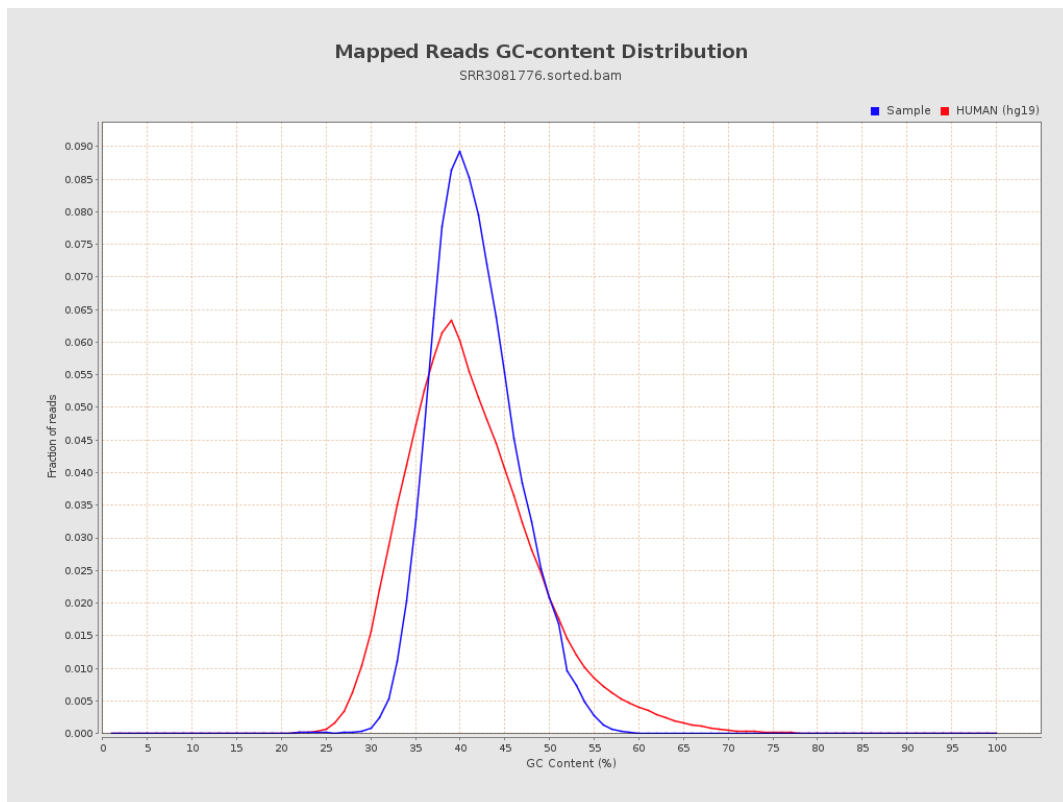
7. Results : Duplication Rate Histogram



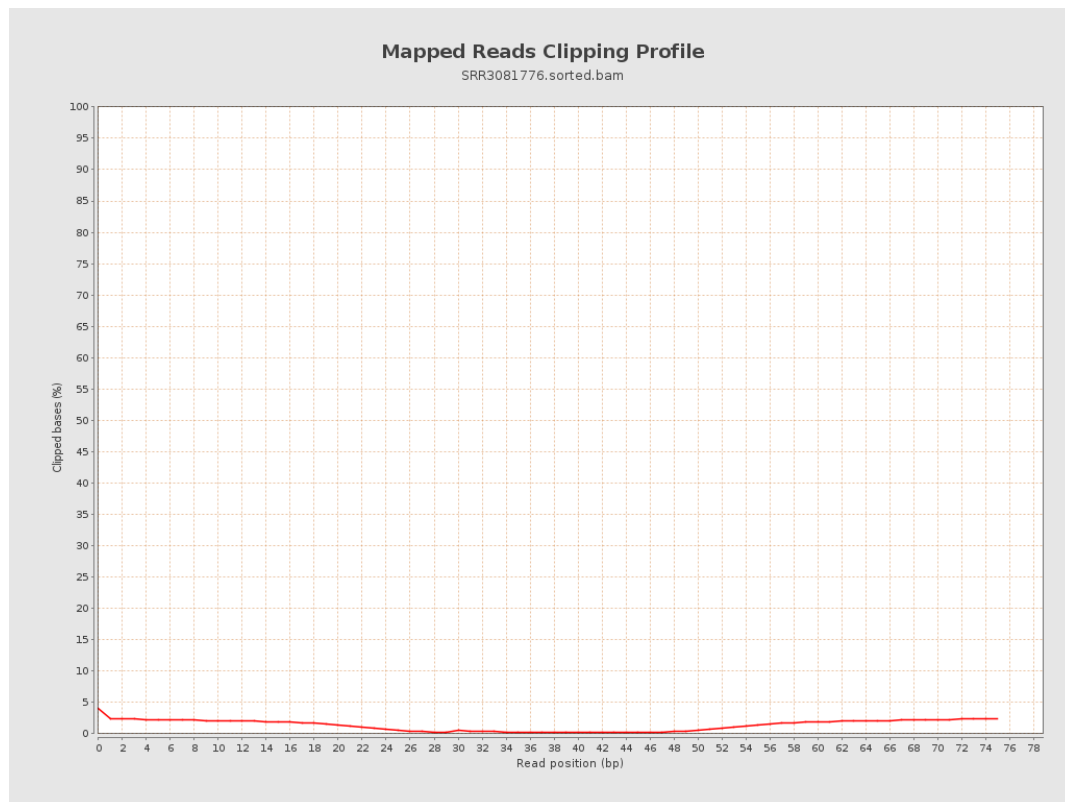
8. Results : Mapped Reads Nucleotide Content



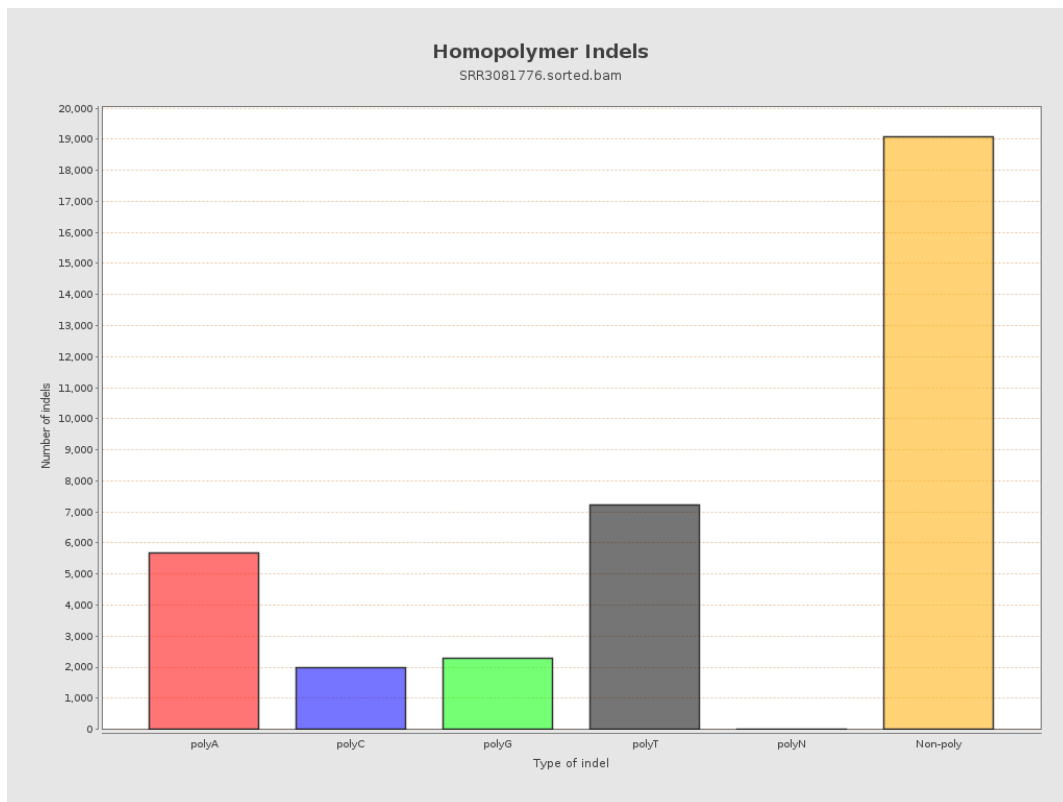
9. Results : Mapped Reads GC-content Distribution



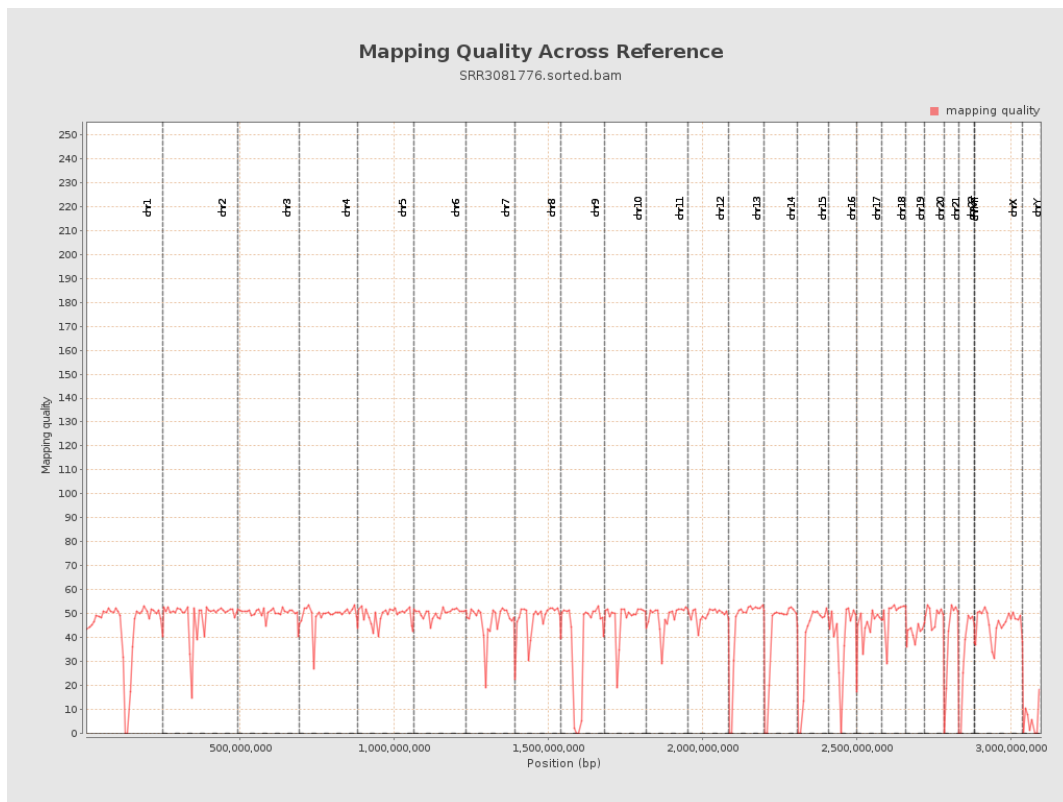
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

