Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081775.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_SRR3081775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,170,735
Mapped reads	1,983,795 / 91.39%
Unmapped reads	186,940 / 8.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,447 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	77,071 / 3.55%
Duplication rate	3.08%
Clipped reads	814,337 / 37.51%

2.2. ACGT Content

Number/percentage of A's	37,048,121 / 27.74%
Number/percentage of C's	25,212,263 / 18.87%
Number/percentage of T's	41,754,013 / 31.26%
Number/percentage of G's	29,562,163 / 22.13%
Number/percentage of N's	1,516 / 0%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.3392

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

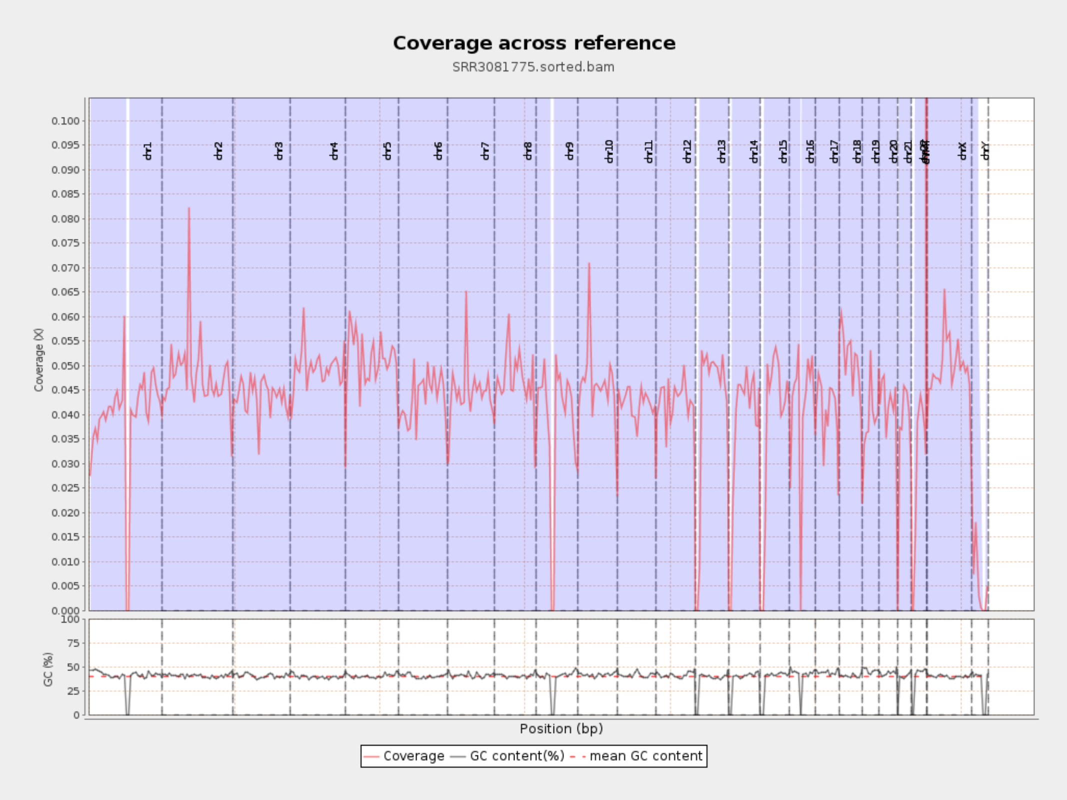
General error rate	0.78%
Mismatches	1,019,473
Insertions	9,445
Mapped reads with at least one insertion	0.47%
Deletions	27,001
Mapped reads with at least one deletion	1.35%
Homopolymer indels	47.17%

2.6. Chromosome stats

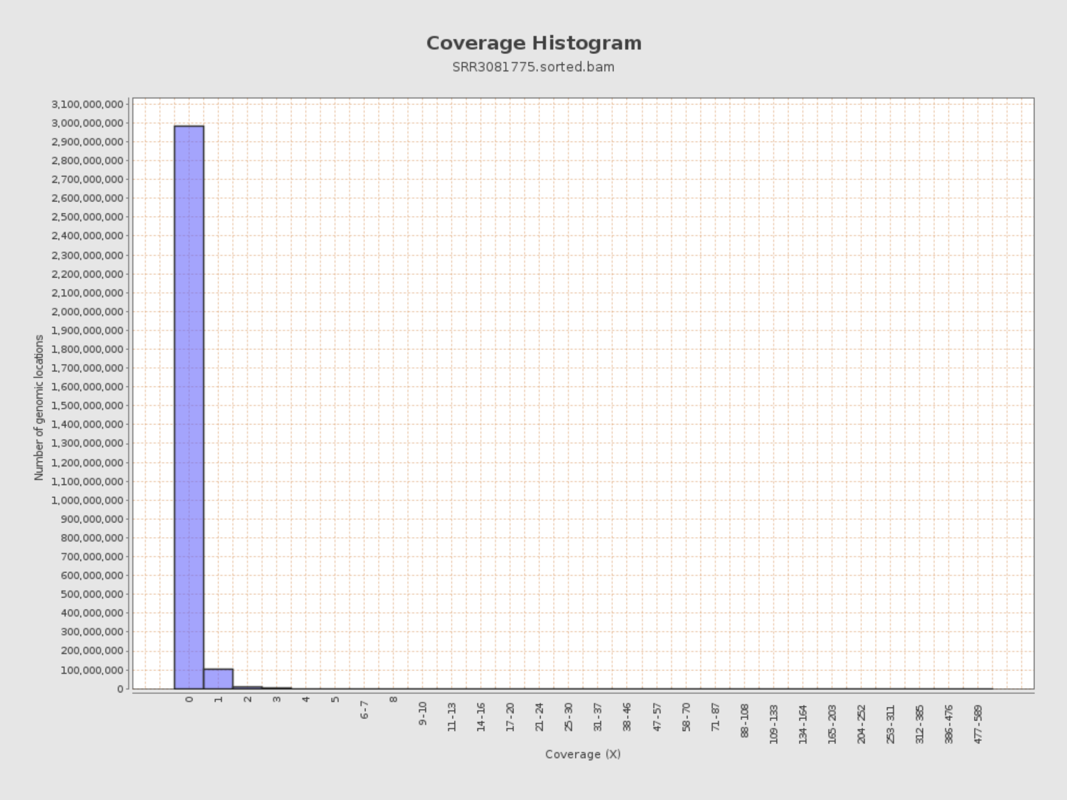
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9845686	0.0395	0.497
chr2	243199373	11767883	0.0484	0.4311
chr3	198022430	8664889	0.0438	0.2362
chr4	191154276	9453040	0.0495	0.268
chr5	180915260	9341339	0.0516	0.2567
chr6	171115067	7433598	0.0434	0.2679
chr7	159138663	7154871	0.045	0.4248

chr8	146364022	6898825	0.0471	0.457
chr9	141213431	5475643	0.0388	0.3475
chr10	135534747	6337465	0.0468	0.3534
chr11	135006516	5658734	0.0419	0.3052
chr12	133851895	5718177	0.0427	0.2347
chr13	115169878	4722736	0.041	0.227
chr14	107349540	3967932	0.037	0.2314
chr15	102531392	3893168	0.038	0.2214
chr16	90354753	3762169	0.0416	0.2609
chr17	81195210	3291407	0.0405	0.241
chr18	78077248	4028738	0.0516	0.5936
chr19	59128983	2328444	0.0394	0.4326
chr20	63025520	2661974	0.0422	0.2399
chr21	48129895	1730799	0.036	0.2336
chr22	51304566	1426757	0.0278	0.1869
chrMT	16571	19901	1.201	1.4583
chrX	155270560	7693484	0.0495	0.2762
chrY	59373566	348628	0.0059	0.1323

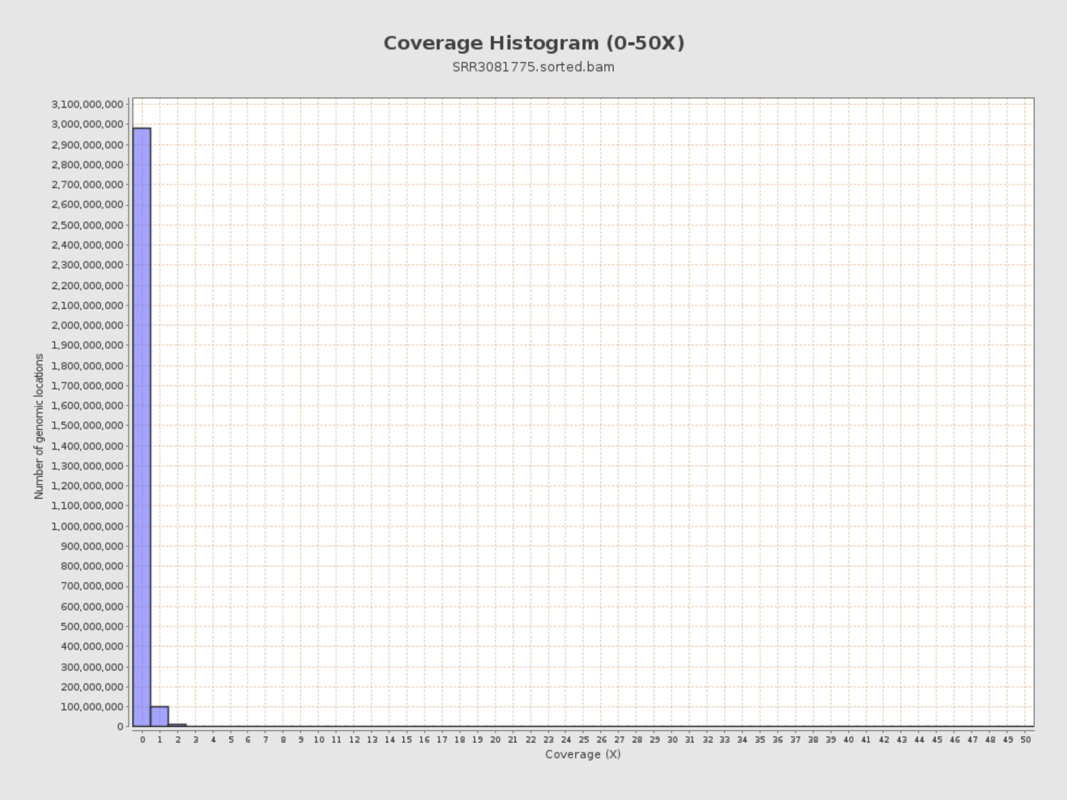
3. Results : Coverage across reference



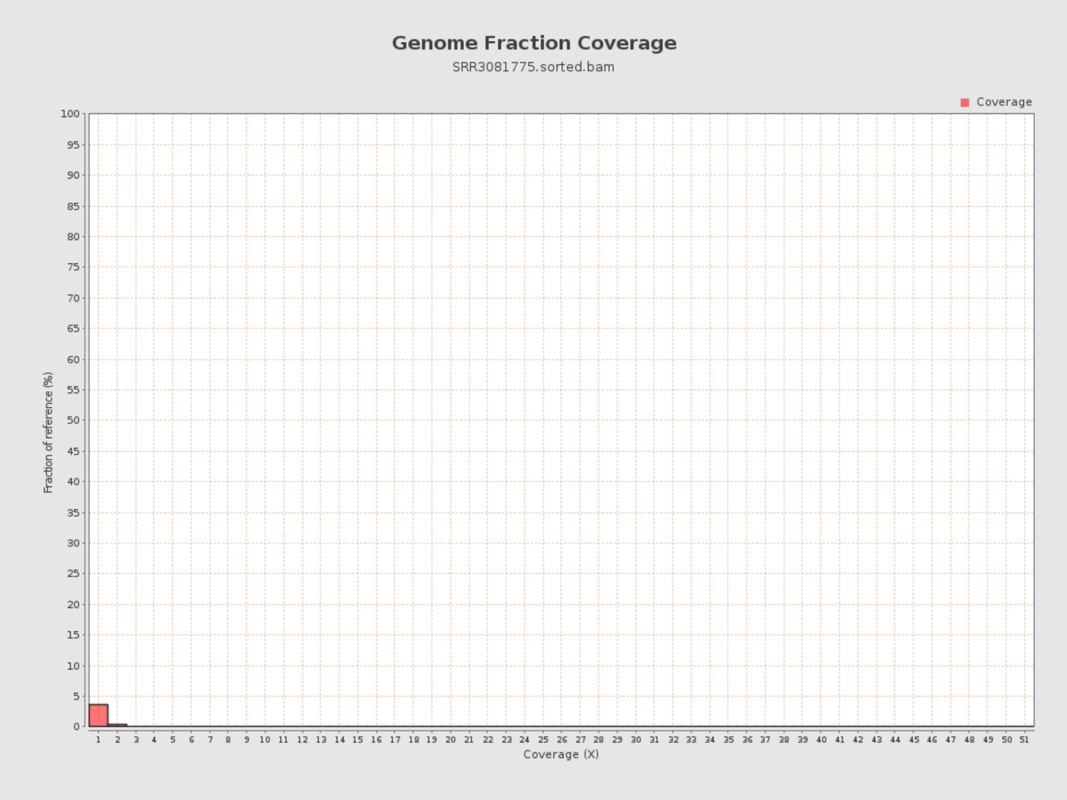
4. Results : Coverage Histogram



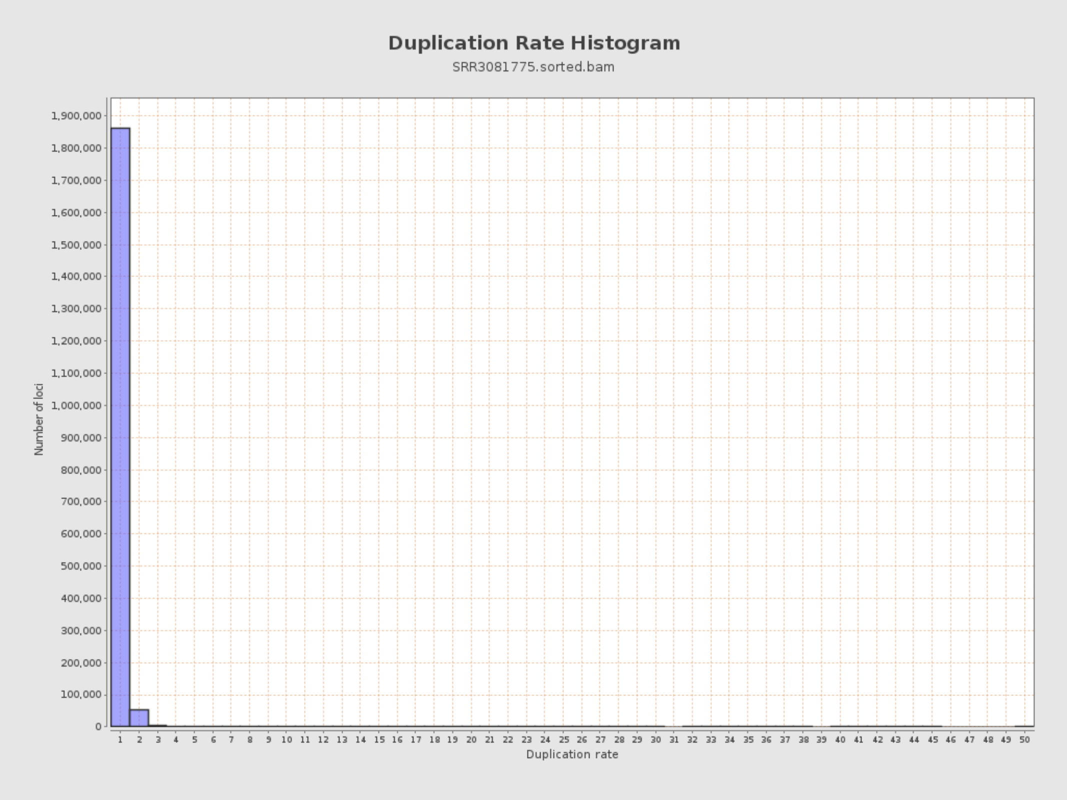
5. Results : Coverage Histogram (0-50X)



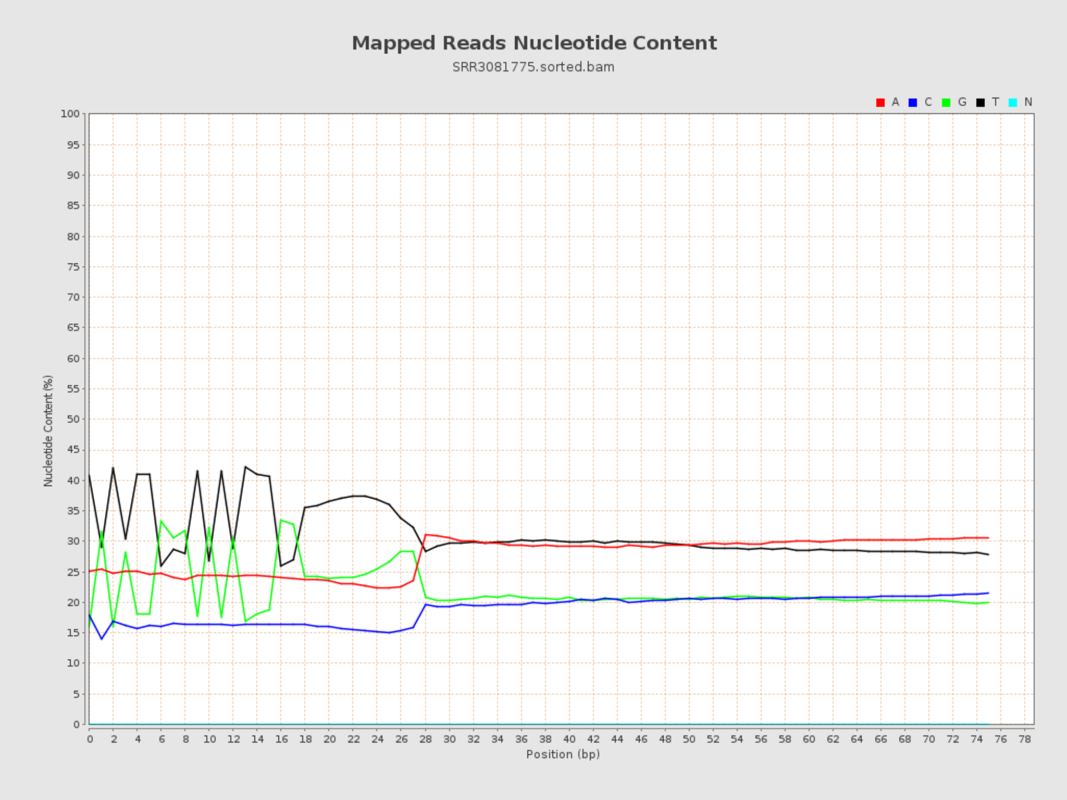
6. Results : Genome Fraction Coverage



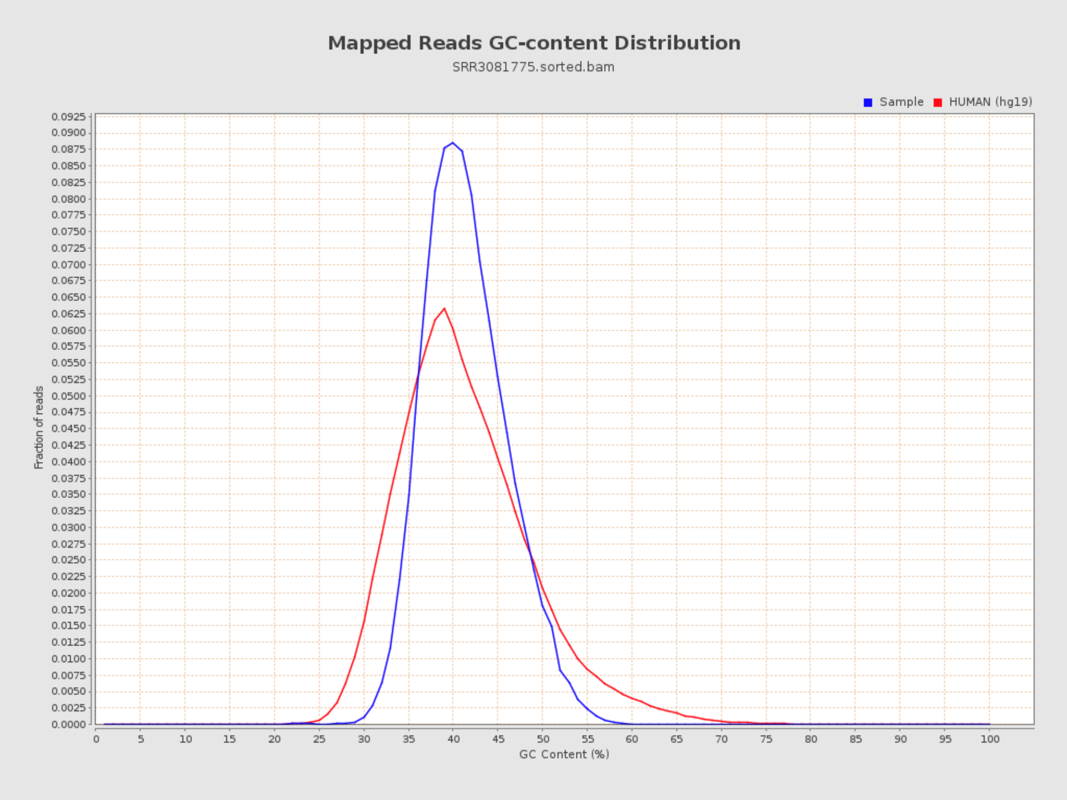
7. Results : Duplication Rate Histogram



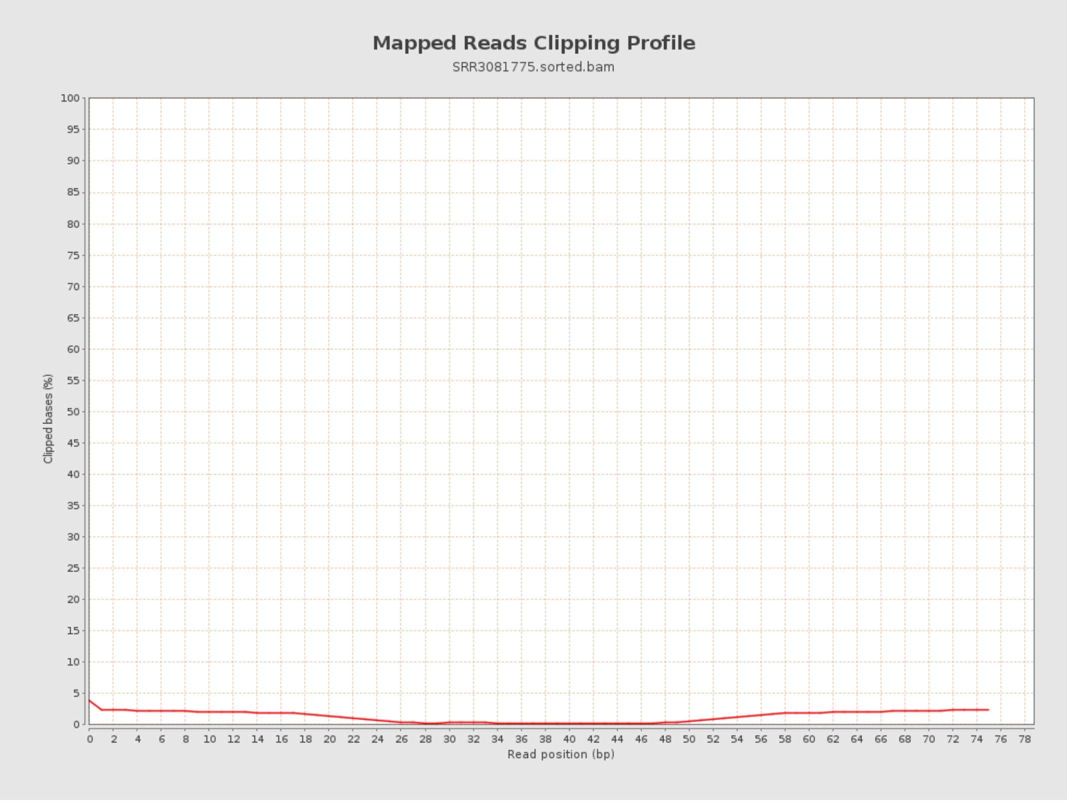
8. Results : Mapped Reads Nucleotide Content



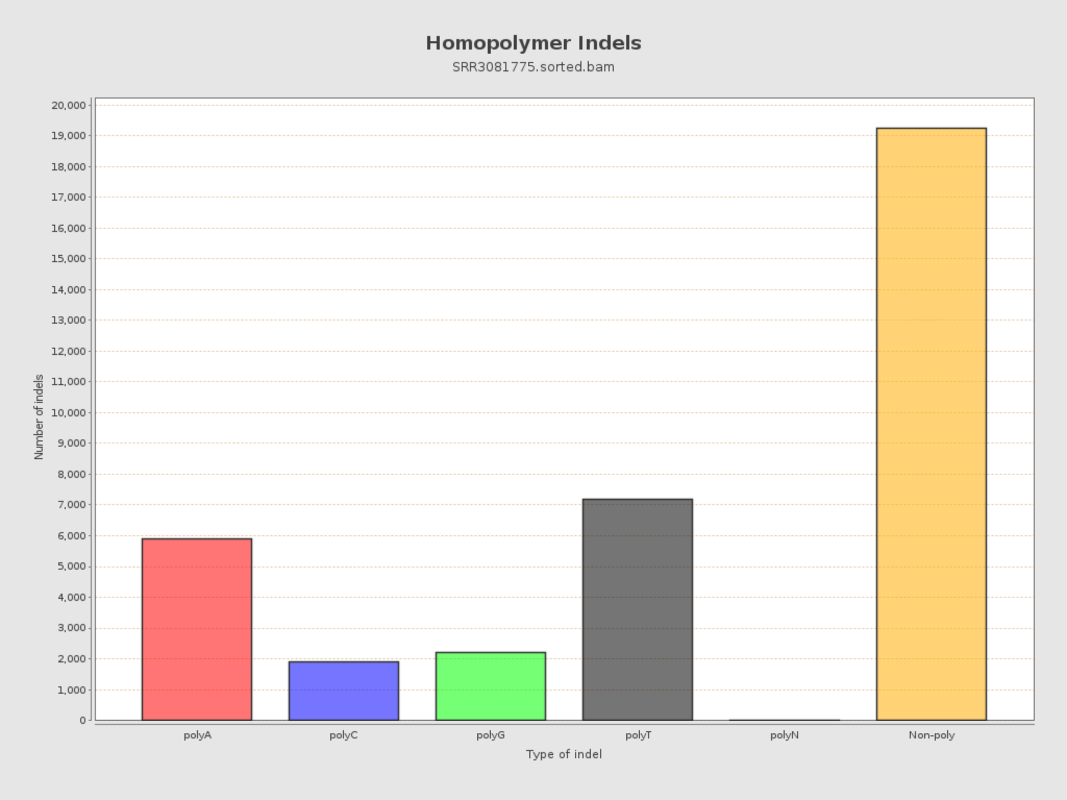
9. Results : Mapped Reads GC-content Distribution



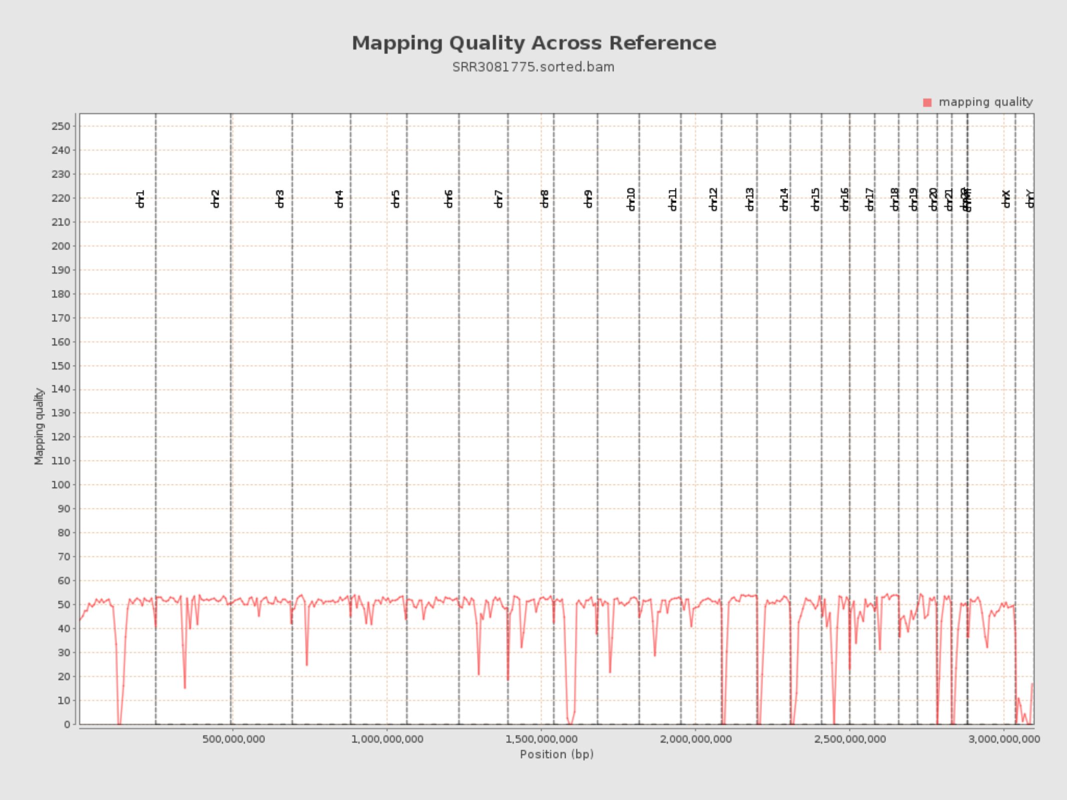
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram