Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:22:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080777.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_SRR3080777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:22:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,861,337
Mapped reads	2,510,213 / 87.73%
Unmapped reads	351,124 / 12.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,317 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	84,706 / 2.96%
Duplication rate	2.67%
Clipped reads	1,194,708 / 41.75%

2.2. ACGT Content

Number/percentage of A's	47,554,730 / 28.6%
Number/percentage of C's	32,276,845 / 19.41%
Number/percentage of T's	50,530,811 / 30.39%
Number/percentage of G's	35,925,447 / 21.6%
Number/percentage of N's	3,421 / 0%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.3859

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

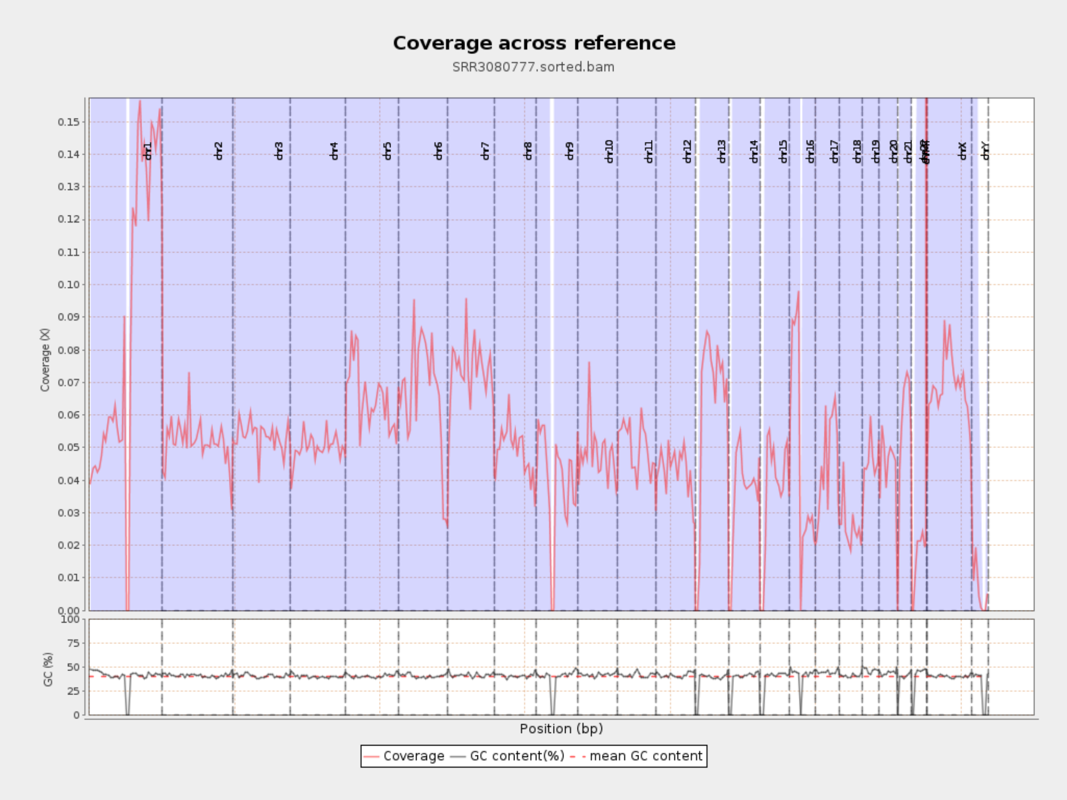
General error rate	0.76%
Mismatches	1,249,338
Insertions	12,509
Mapped reads with at least one insertion	0.49%
Deletions	35,768
Mapped reads with at least one deletion	1.41%
Homopolymer indels	46.75%

2.6. Chromosome stats

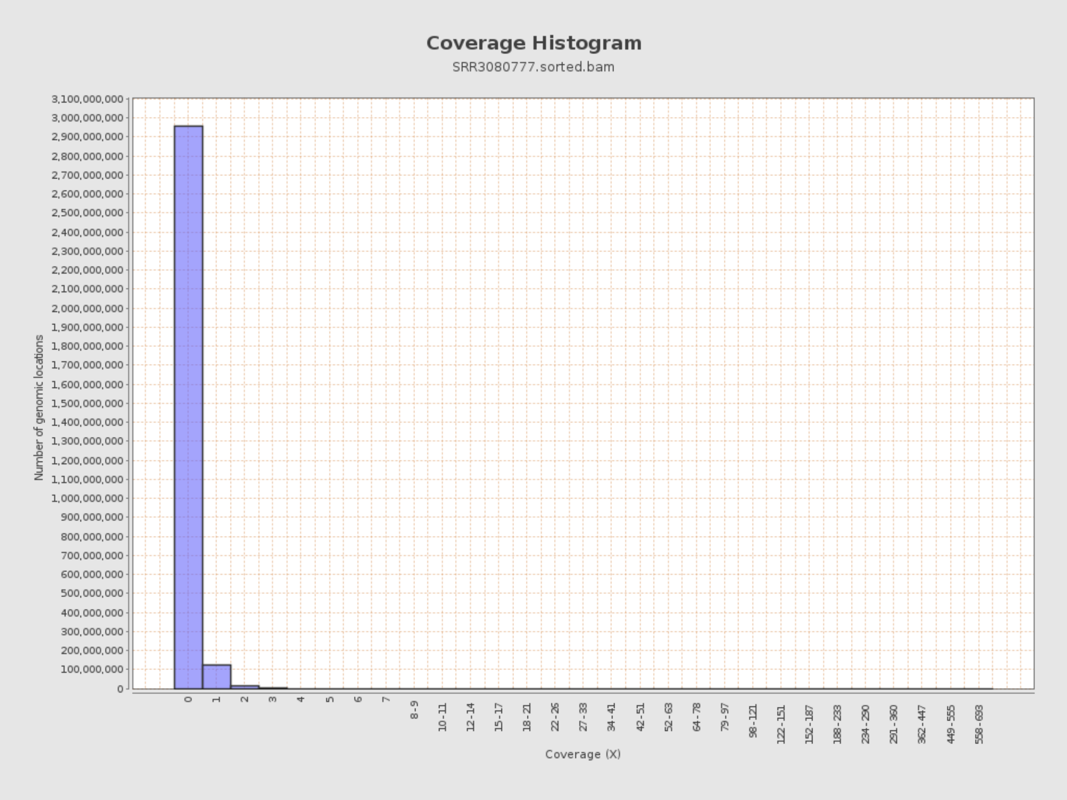
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21600495	0.0867	0.6963
chr2	243199373	12640104	0.052	0.4242
chr3	198022430	10580421	0.0534	0.2632
chr4	191154276	9555827	0.05	0.2632
chr5	180915260	11837635	0.0654	0.2903
chr6	171115067	11504667	0.0672	0.4108
chr7	159138663	11803817	0.0742	0.5208

chr8	146364022	7131083	0.0487	0.4805
chr9	141213431	5563120	0.0394	0.3071
chr10	135534747	6531381	0.0482	0.3708
chr11	135006516	6811414	0.0505	0.2943
chr12	133851895	5799448	0.0433	0.2389
chr13	115169878	7193254	0.0625	0.2852
chr14	107349540	3796941	0.0354	0.2361
chr15	102531392	3786011	0.0369	0.2255
chr16	90354753	4334042	0.048	0.2678
chr17	81195210	3705205	0.0456	0.2502
chr18	78077248	2040578	0.0261	0.5497
chr19	59128983	2707453	0.0458	0.4965
chr20	63025520	2867831	0.0455	0.2531
chr21	48129895	2693632	0.056	0.2799
chr22	51304566	805404	0.0157	0.1388
chrMT	16571	31657	1.9104	1.7515
chrX	155270560	10630642	0.0685	0.3197
chrY	59373566	396580	0.0067	0.1365

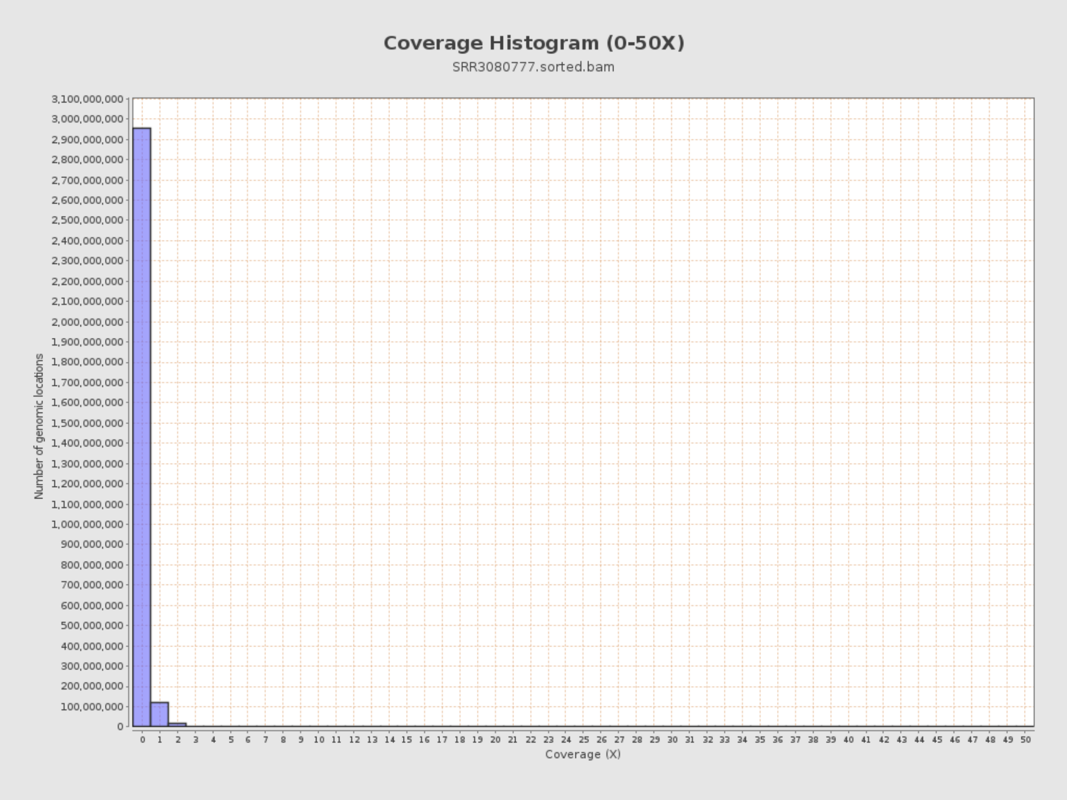
3. Results : Coverage across reference



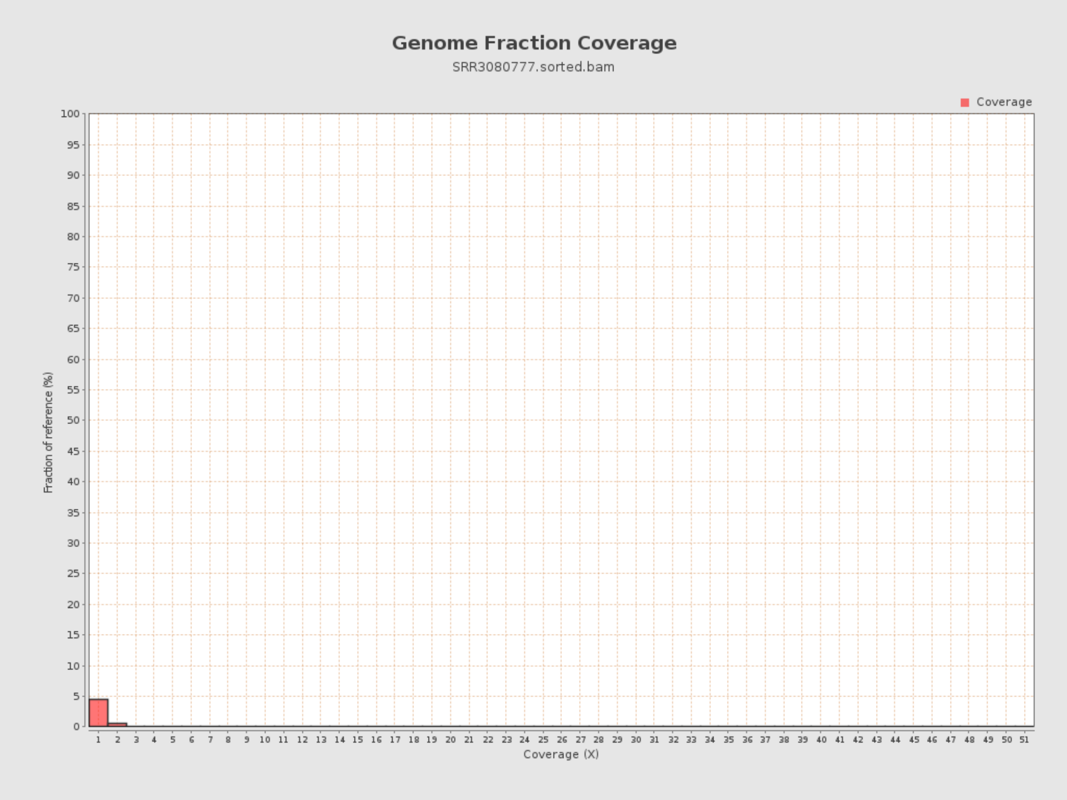
4. Results : Coverage Histogram



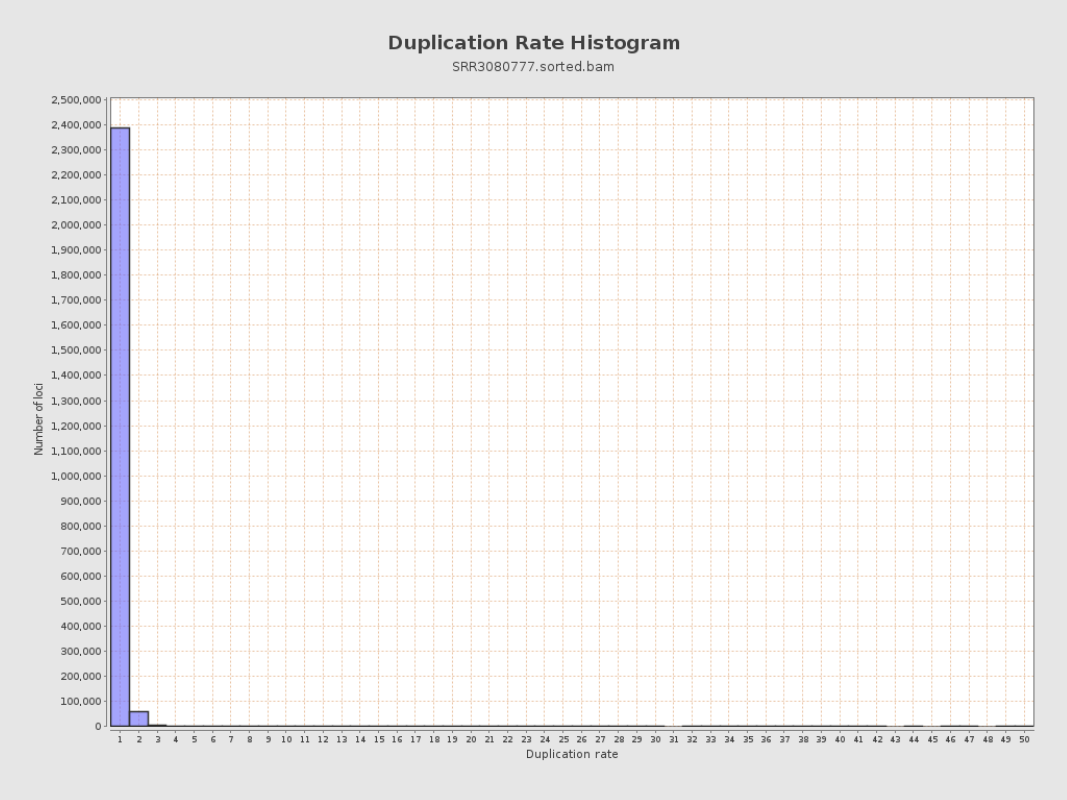
5. Results : Coverage Histogram (0-50X)



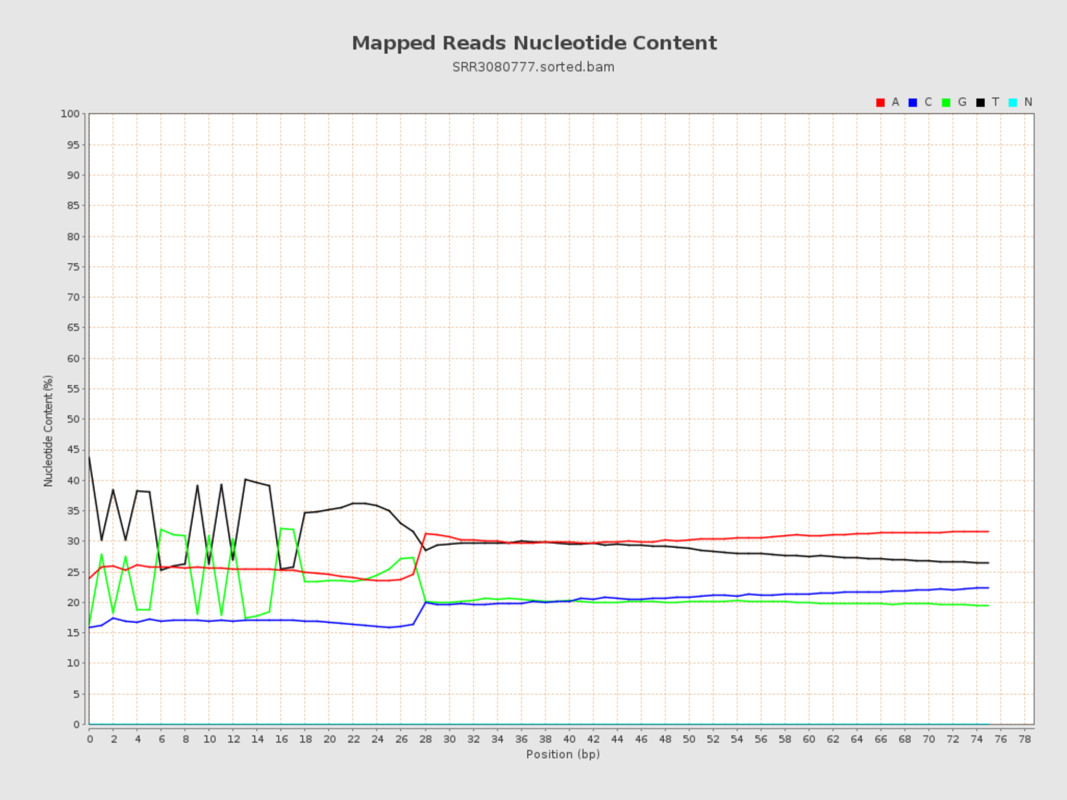
6. Results : Genome Fraction Coverage



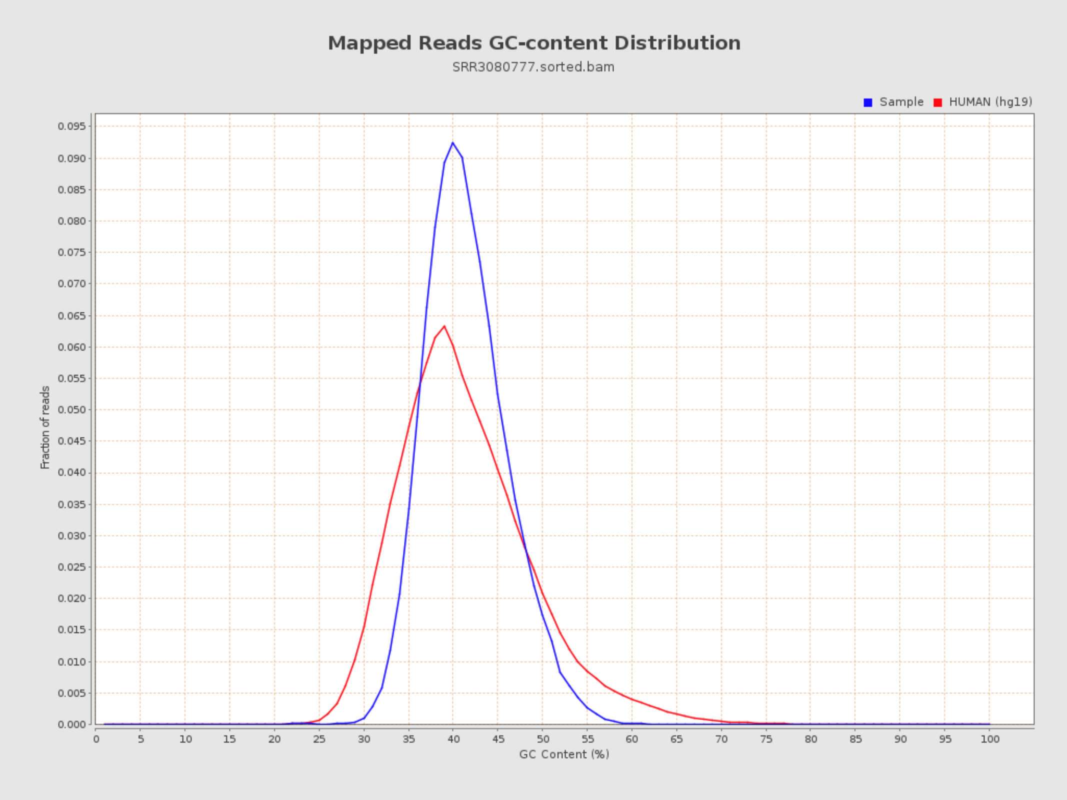
7. Results : Duplication Rate Histogram



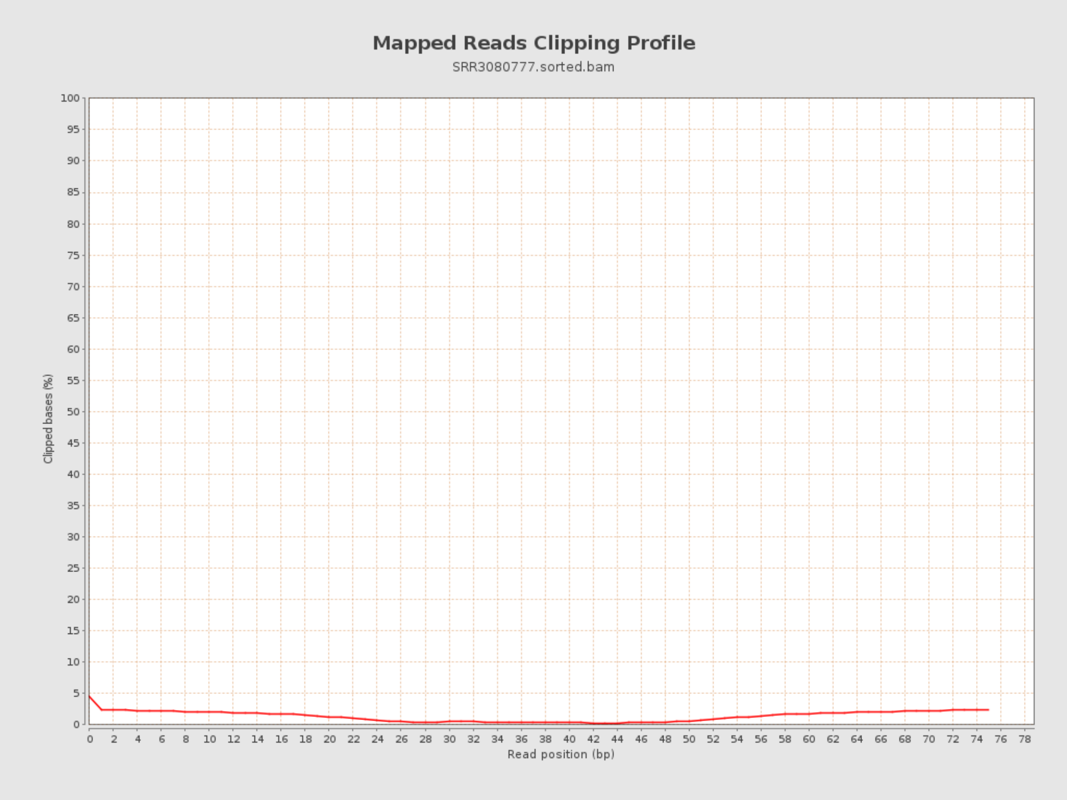
8. Results : Mapped Reads Nucleotide Content



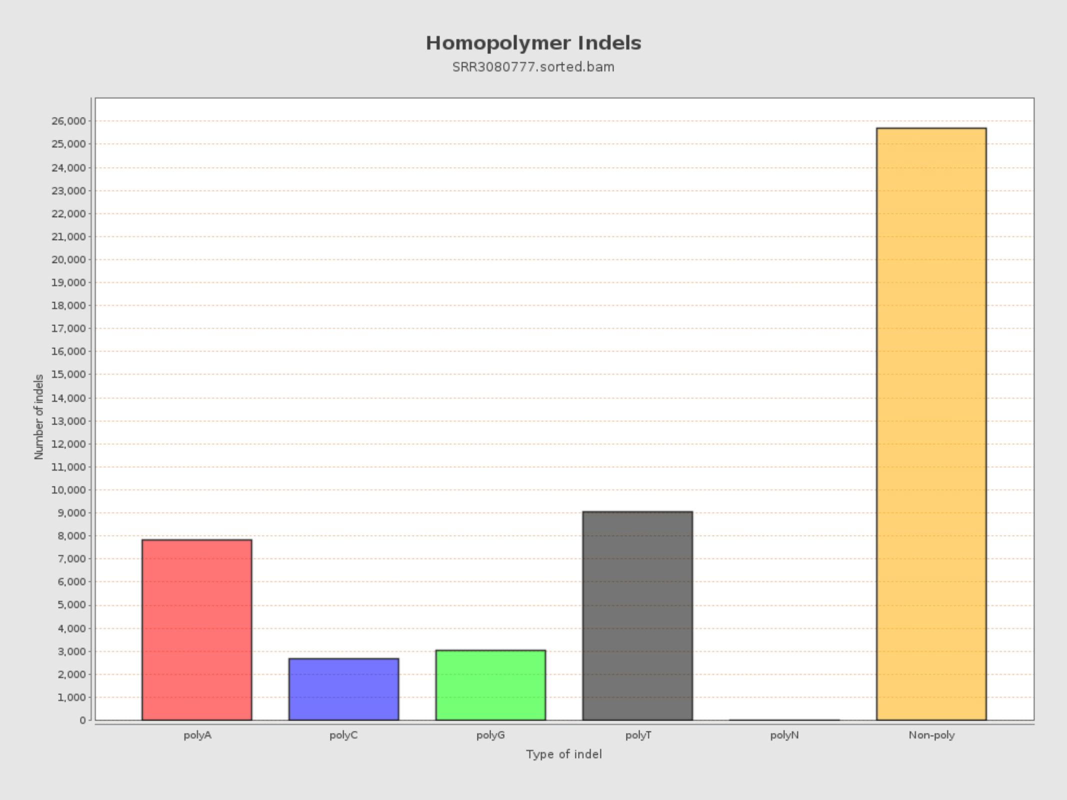
9. Results : Mapped Reads GC-content Distribution



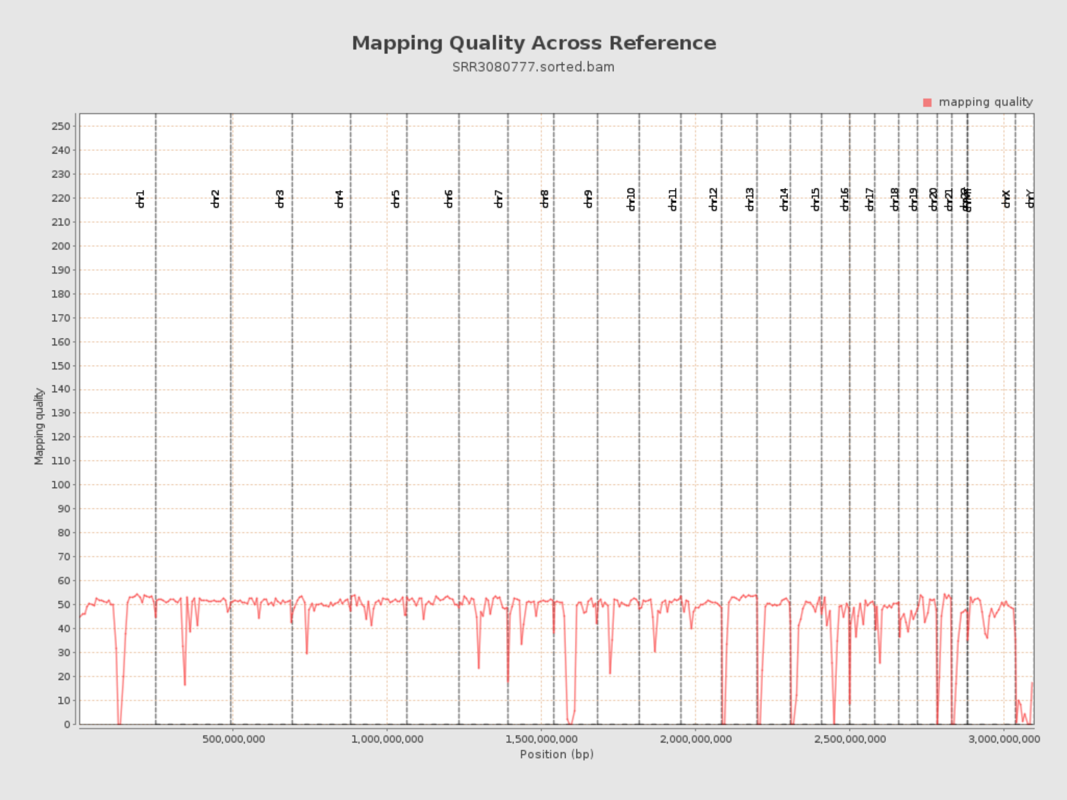
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram