Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:42:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081730.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_SRR3081730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:42:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,678,115
Mapped reads	2,445,312 / 91.31%
Unmapped reads	232,803 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,860 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	94,271 / 3.52%
Duplication rate	3.18%
Clipped reads	1,029,587 / 38.44%

2.2. ACGT Content

Number/percentage of A's	45,478,483 / 27.64%
Number/percentage of C's	31,632,053 / 19.22%
Number/percentage of T's	50,529,929 / 30.71%
Number/percentage of G's	36,913,968 / 22.43%
Number/percentage of N's	1,785 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0532

Standard Deviation	0.3541

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

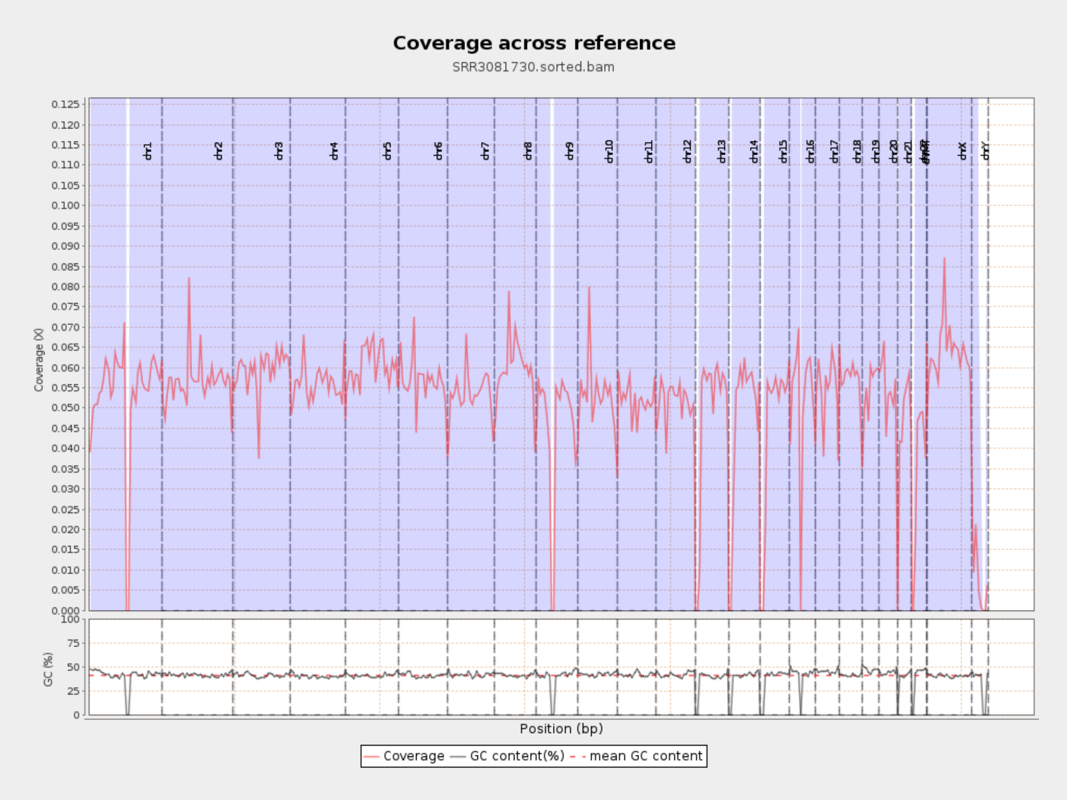
General error rate	0.8%
Mismatches	1,301,144
Insertions	11,201
Mapped reads with at least one insertion	0.45%
Deletions	31,505
Mapped reads with at least one deletion	1.27%
Homopolymer indels	47.08%

2.6. Chromosome stats

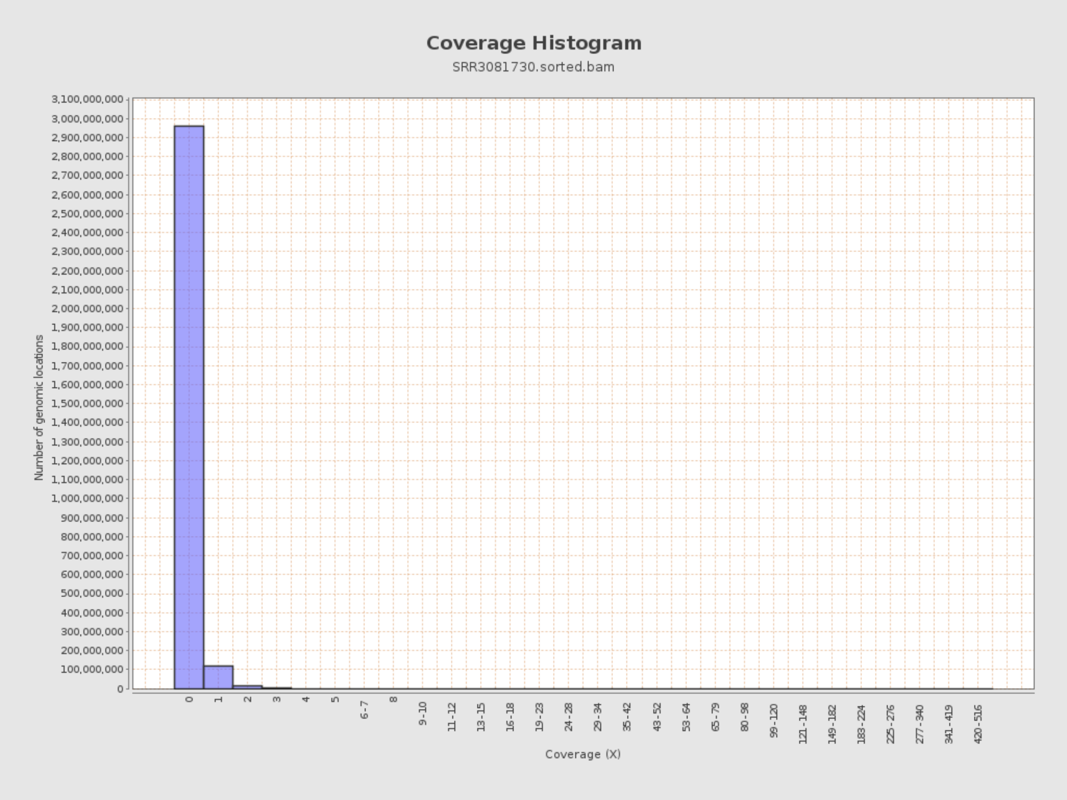
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13254408	0.0532	0.5239
chr2	243199373	13792337	0.0567	0.445
chr3	198022430	11754130	0.0594	0.2824
chr4	191154276	10708113	0.056	0.2893
chr5	180915260	11010365	0.0609	0.2852
chr6	171115067	9724116	0.0568	0.3062
chr7	159138663	8585375	0.0539	0.4066

chr8	146364022	8758593	0.0598	0.4185
chr9	141213431	6419033	0.0455	0.3418
chr10	135534747	7239405	0.0534	0.3902
chr11	135006516	6994775	0.0518	0.315
chr12	133851895	6885944	0.0514	0.2646
chr13	115169878	5447520	0.0473	0.2517
chr14	107349540	4990950	0.0465	0.2623
chr15	102531392	4611852	0.045	0.2487
chr16	90354753	4717268	0.0522	0.2914
chr17	81195210	4409055	0.0543	0.2839
chr18	78077248	4503541	0.0577	0.5448
chr19	59128983	3231377	0.0546	0.4264
chr20	63025520	3421940	0.0543	0.2761
chr21	48129895	2157097	0.0448	0.2617
chr22	51304566	1645489	0.0321	0.2054
chrMT	16571	1100	0.0664	0.2599
chrX	155270560	9915355	0.0639	0.3198
chrY	59373566	433108	0.0073	0.1637

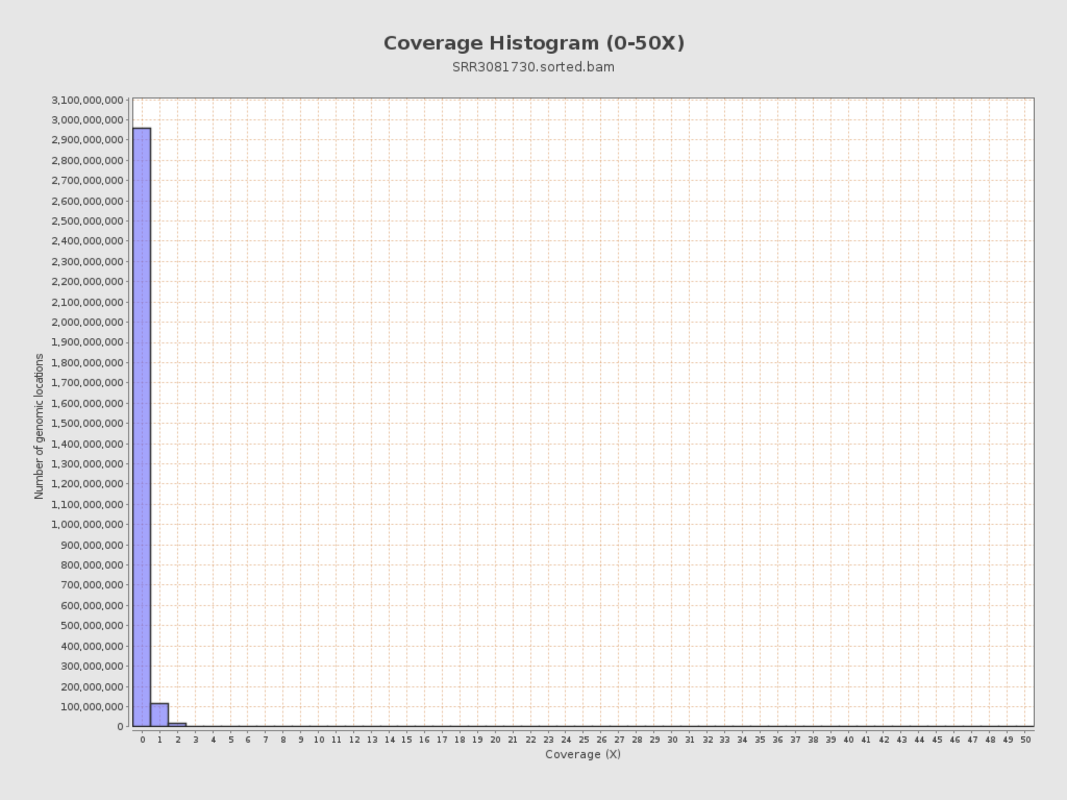
3. Results : Coverage across reference



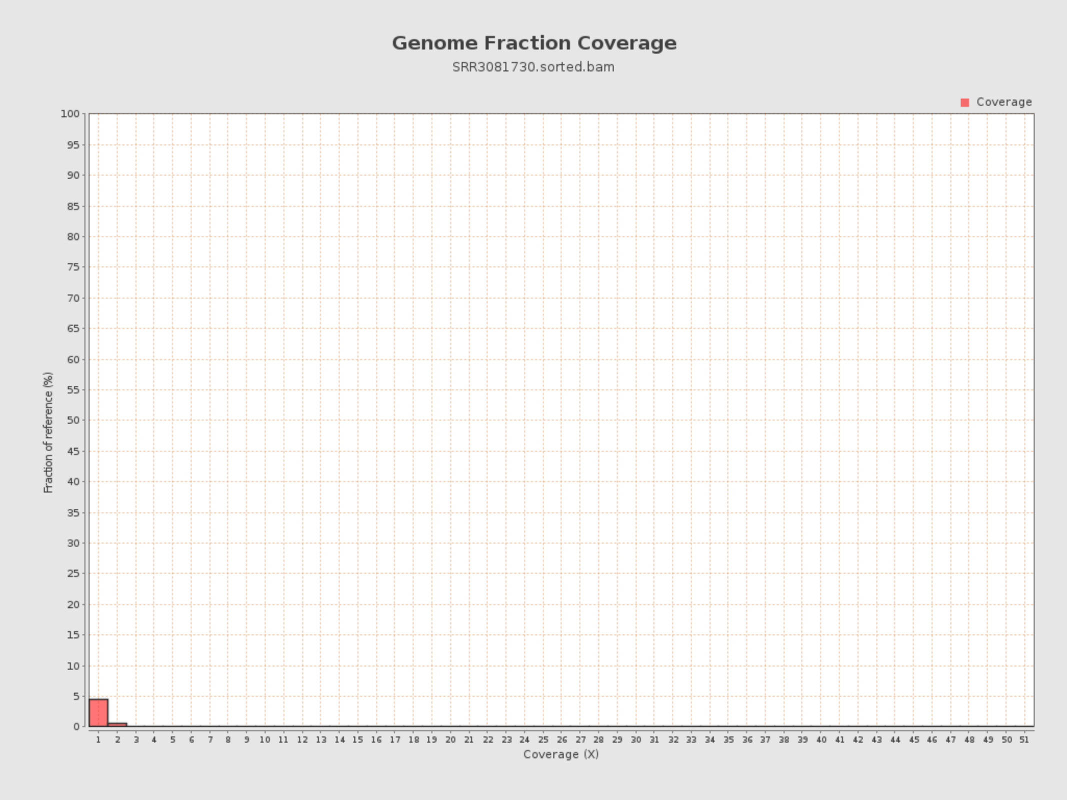
4. Results : Coverage Histogram



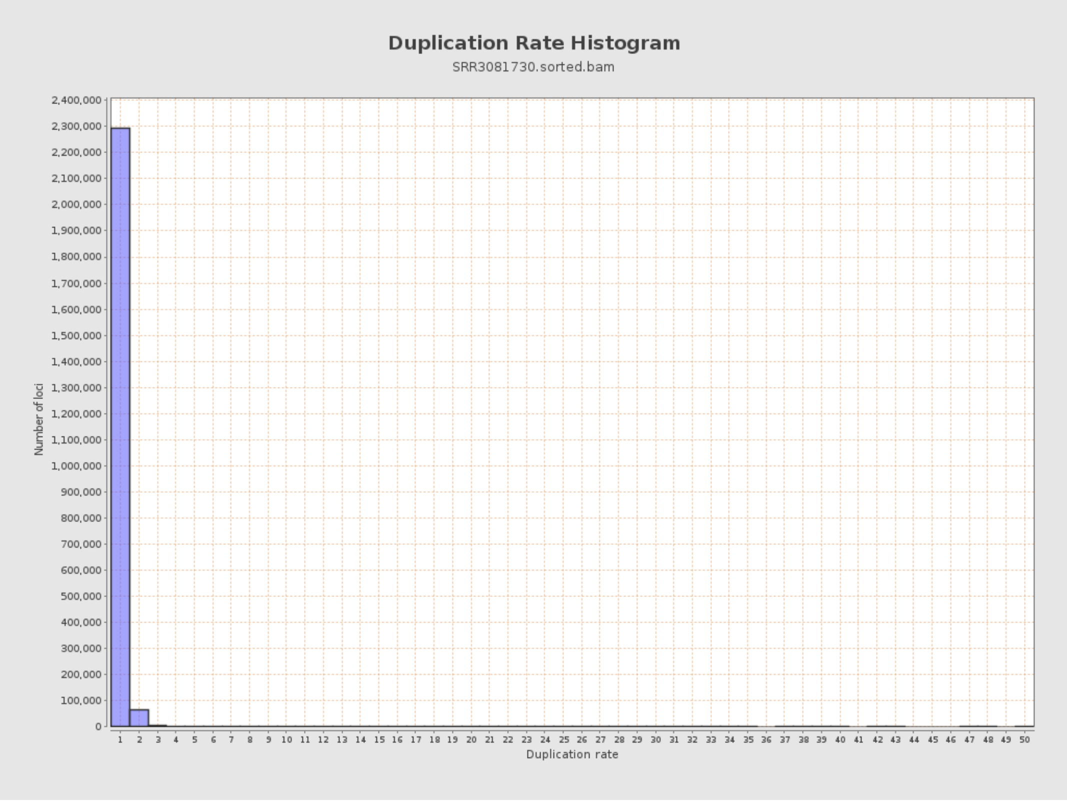
5. Results : Coverage Histogram (0-50X)



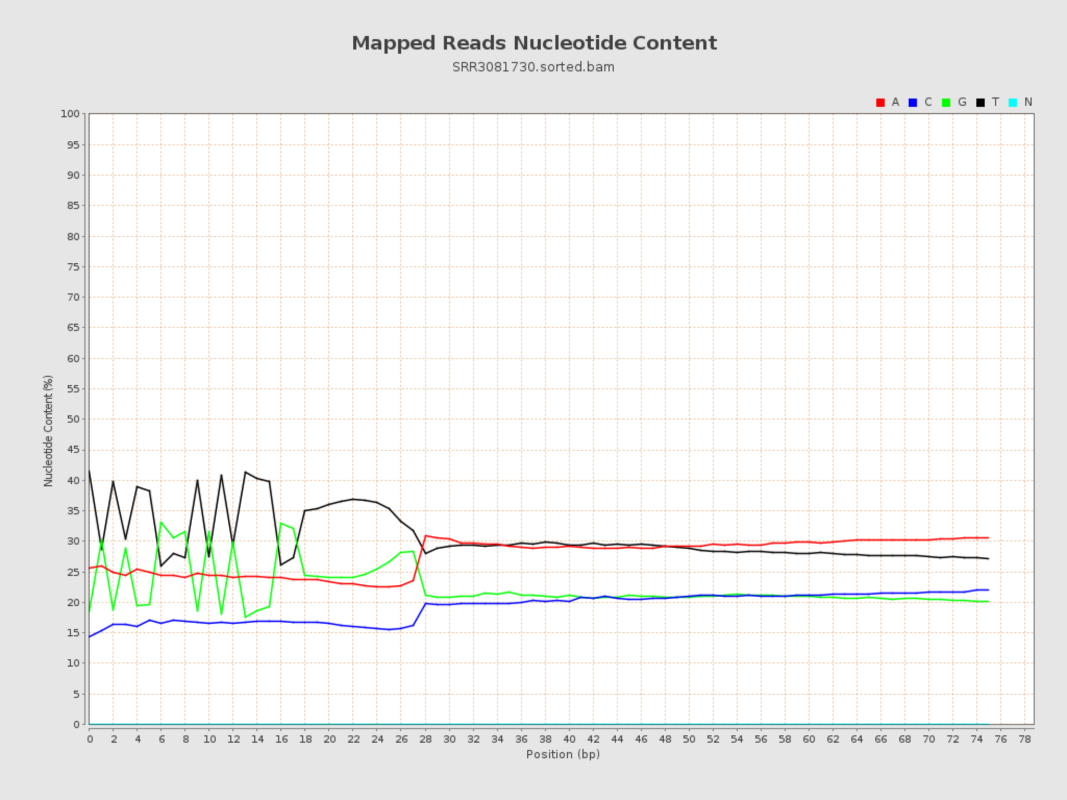
6. Results : Genome Fraction Coverage



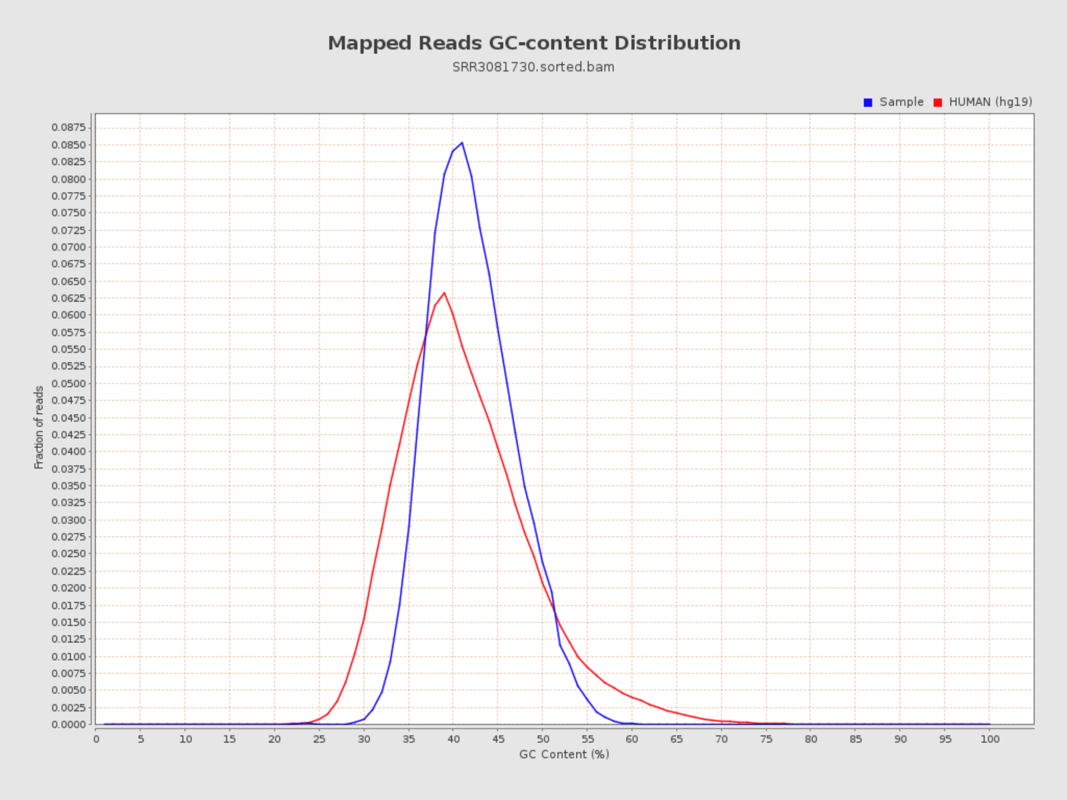
7. Results : Duplication Rate Histogram



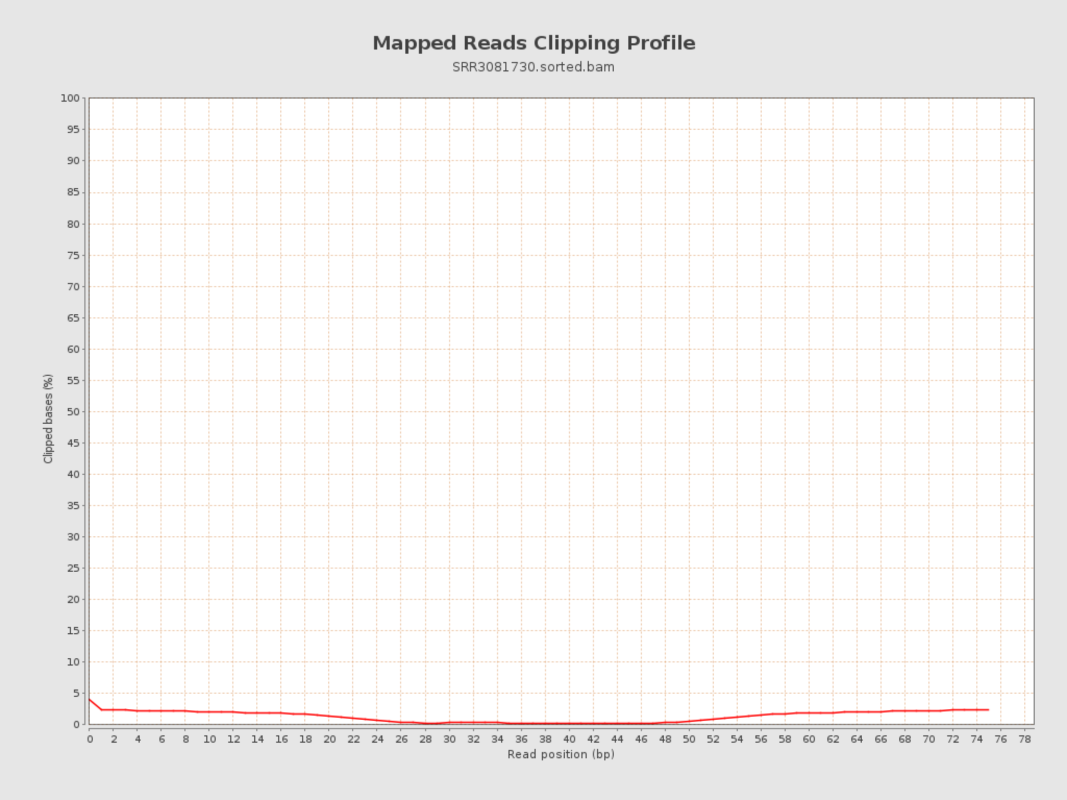
8. Results : Mapped Reads Nucleotide Content



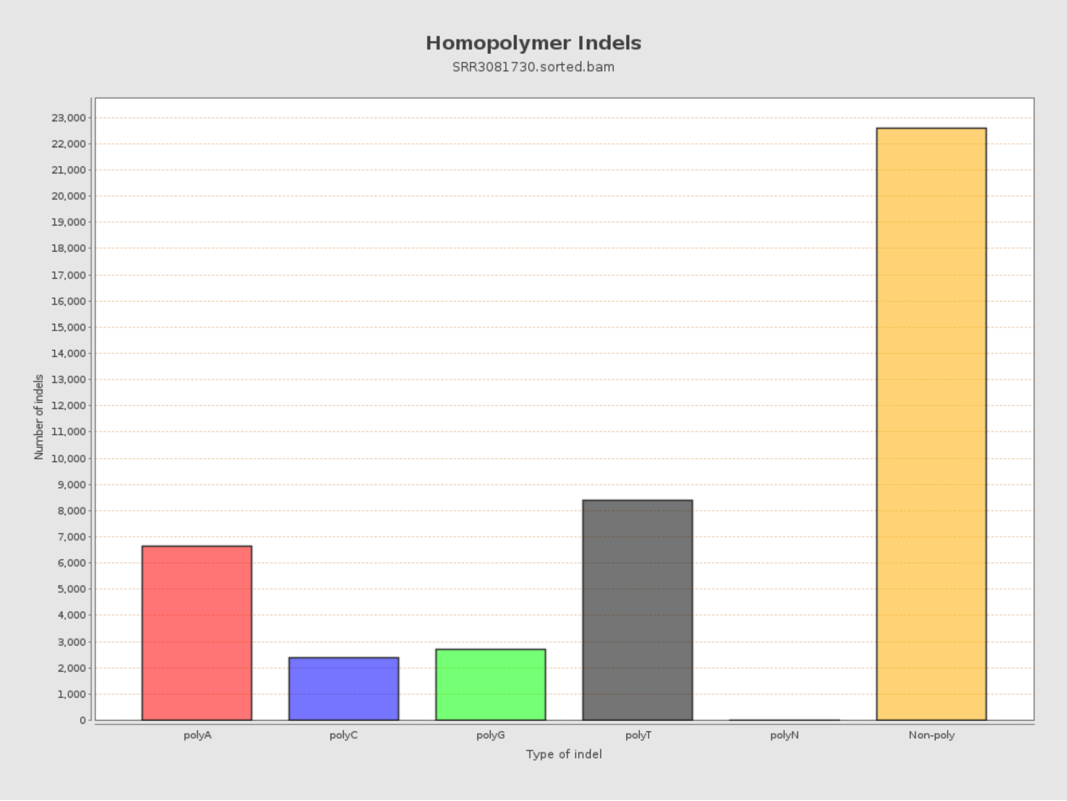
9. Results : Mapped Reads GC-content Distribution



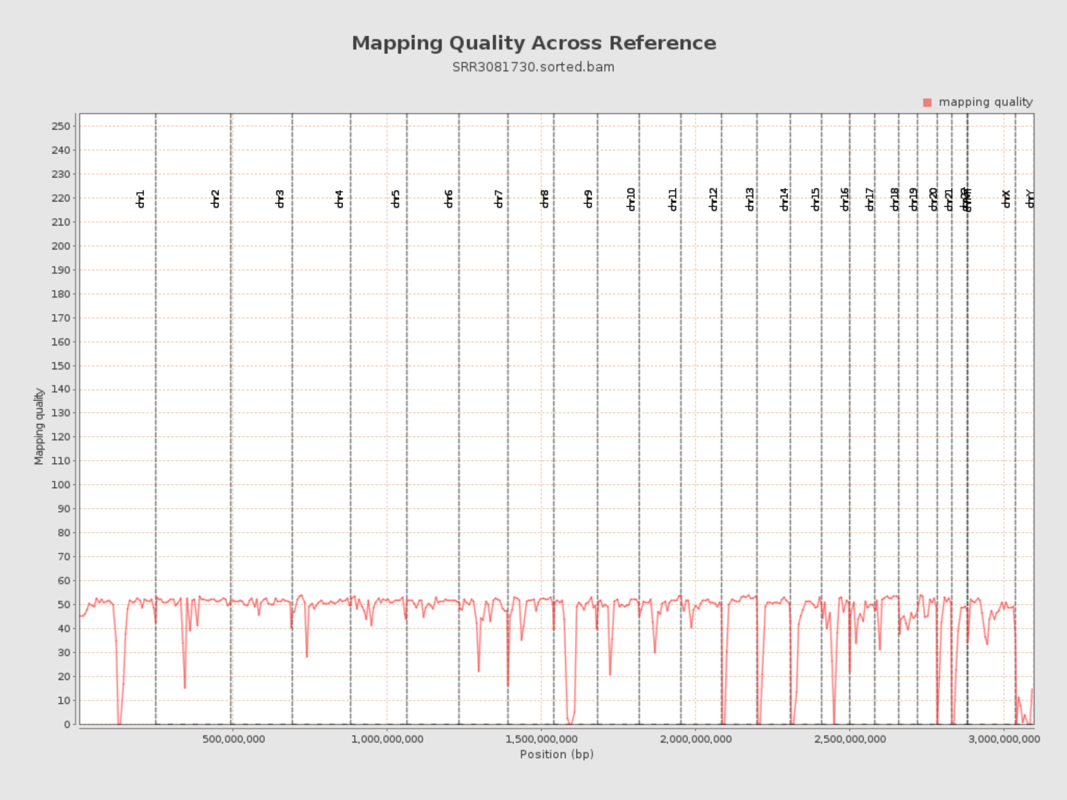
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram