Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:47:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524323.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_SRR10524323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:47:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,136,437
Mapped reads	2,862,743 / 91.27%
Unmapped reads	273,694 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,643 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	132,741 / 4.23%
Duplication rate	3.33%
Clipped reads	2,868,301 / 91.45%

2.2. ACGT Content

Number/percentage of A's	39,866,993 / 24.07%
Number/percentage of C's	31,394,591 / 18.95%
Number/percentage of T's	52,821,506 / 31.89%
Number/percentage of G's	41,532,074 / 25.07%
Number/percentage of N's	23,149 / 0.01%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.4434

2.4. Mapping Quality

Mean Mapping Quality	43.69

2.5. Mismatches and indels

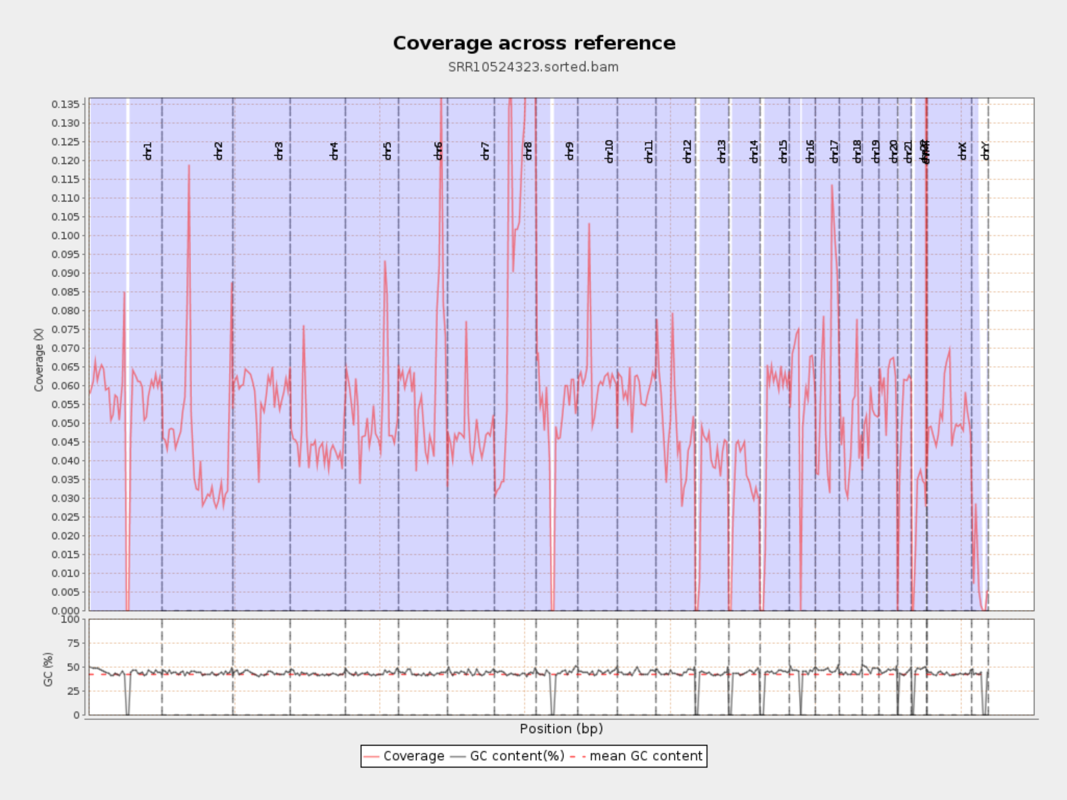
General error rate	0.52%
Mismatches	841,726
Insertions	10,606
Mapped reads with at least one insertion	0.37%
Deletions	26,960
Mapped reads with at least one deletion	0.94%
Homopolymer indels	42.58%

2.6. Chromosome stats

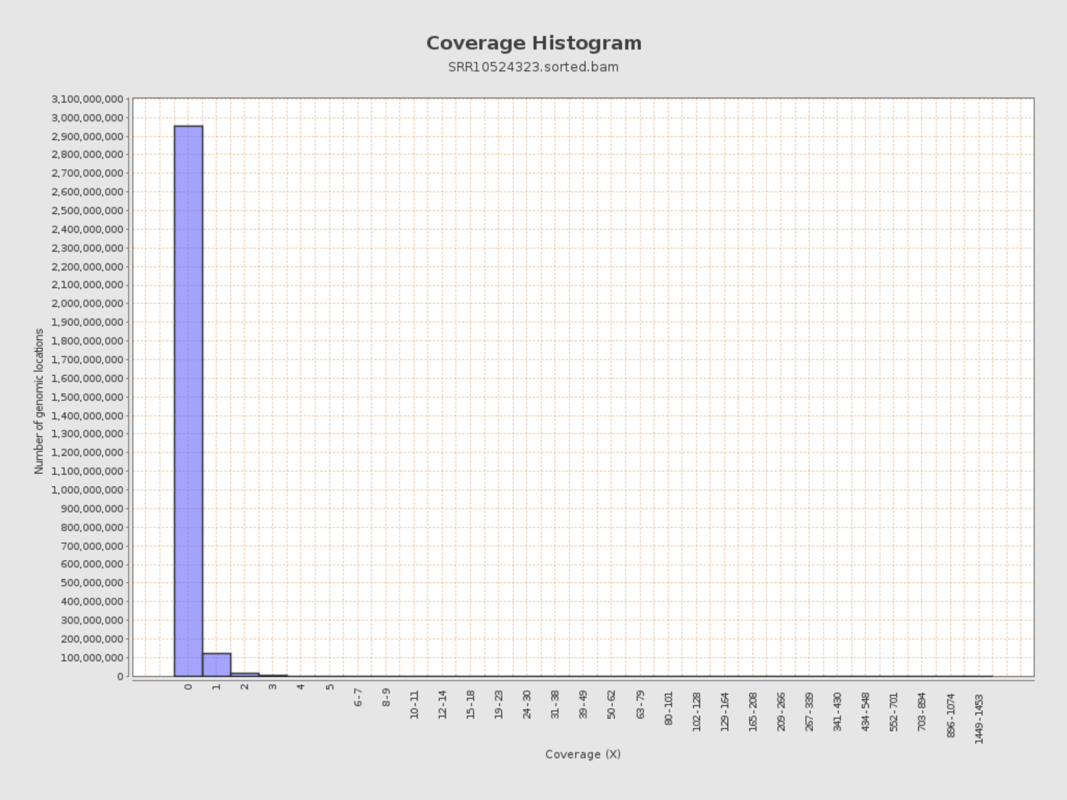
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13967020	0.056	0.8328
chr2	243199373	10719192	0.0441	0.6386
chr3	198022430	11505718	0.0581	0.2771
chr4	191154276	8501695	0.0445	0.2933
chr5	180915260	9652227	0.0534	0.2658
chr6	171115067	10621892	0.0621	0.3182
chr7	159138663	7524406	0.0473	0.5325

chr8	146364022	17089216	0.1168	0.5344
chr9	141213431	6857246	0.0486	0.3335
chr10	135534747	8474800	0.0625	0.4465
chr11	135006516	7940626	0.0588	0.3632
chr12	133851895	6531678	0.0488	0.2592
chr13	115169878	4137129	0.0359	0.2165
chr14	107349540	3424757	0.0319	0.2196
chr15	102531392	5129106	0.05	0.2641
chr16	90354753	5318550	0.0589	0.3024
chr17	81195210	5233170	0.0645	0.3281
chr18	78077248	3796006	0.0486	0.6028
chr19	59128983	2999635	0.0507	0.5646
chr20	63025520	3845431	0.061	0.2973
chr21	48129895	2404341	0.05	0.2932
chr22	51304566	1261425	0.0246	0.18
chrMT	16571	300695	18.1459	10.9725
chrX	155270560	7976347	0.0514	0.3013
chrY	59373566	469701	0.0079	0.2132

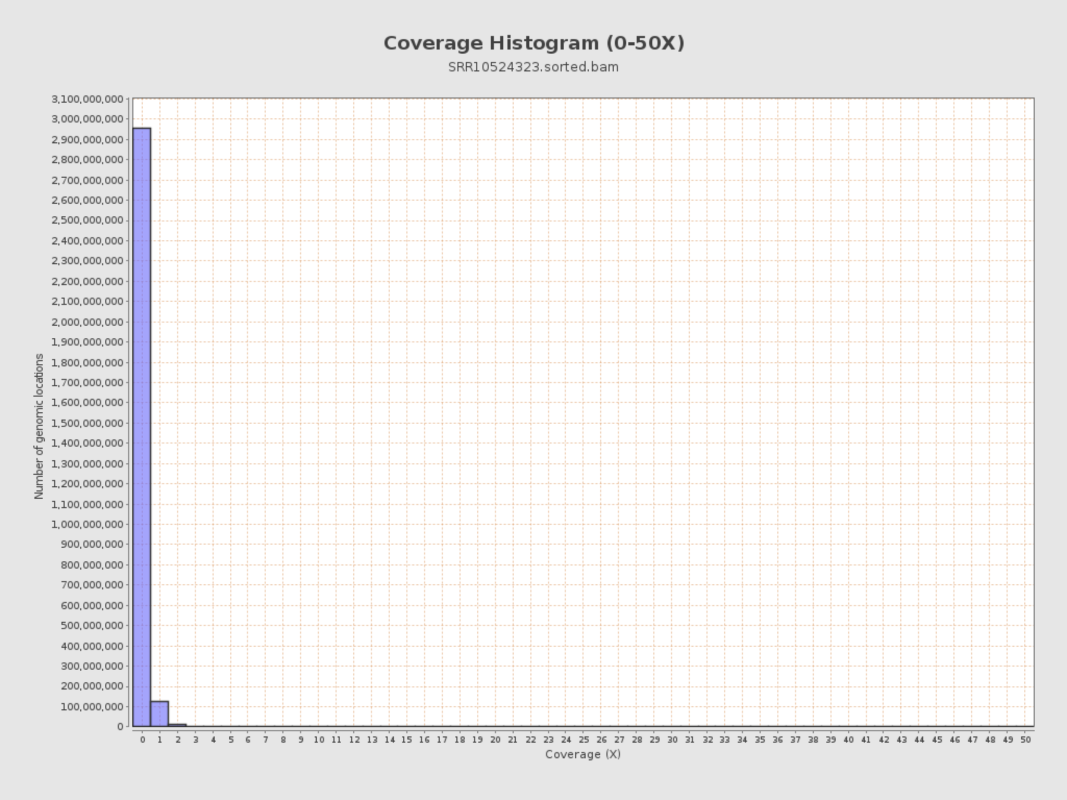
3. Results : Coverage across reference



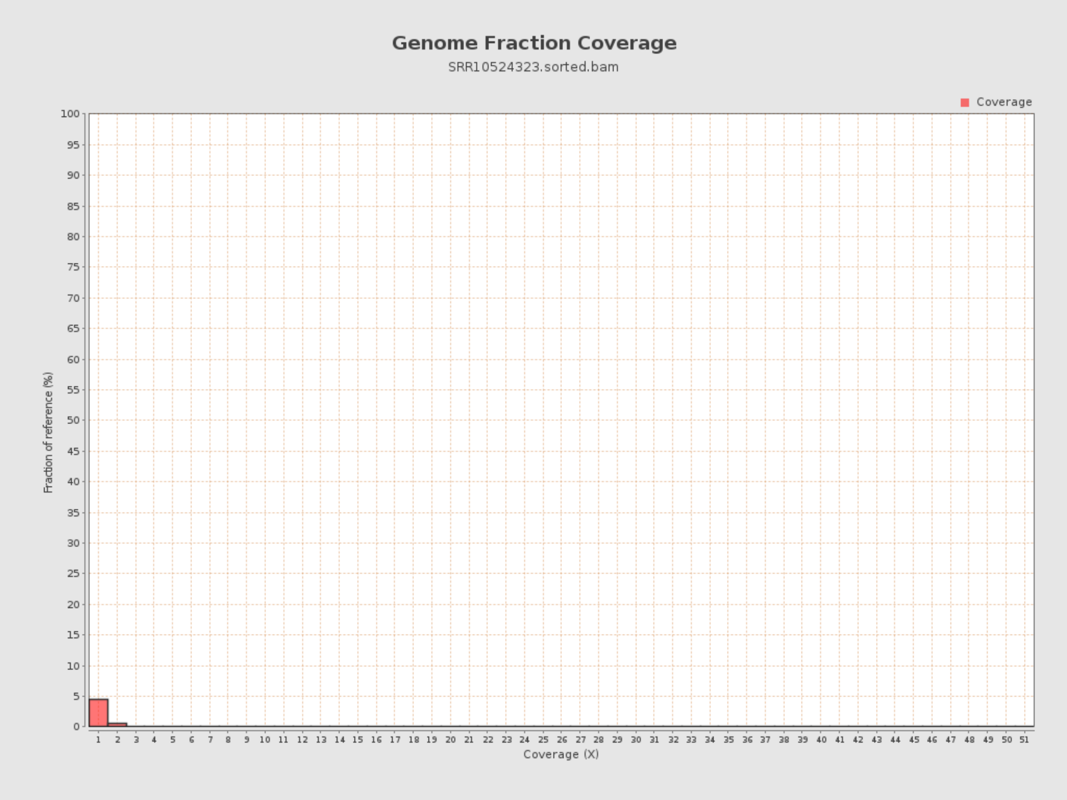
4. Results : Coverage Histogram



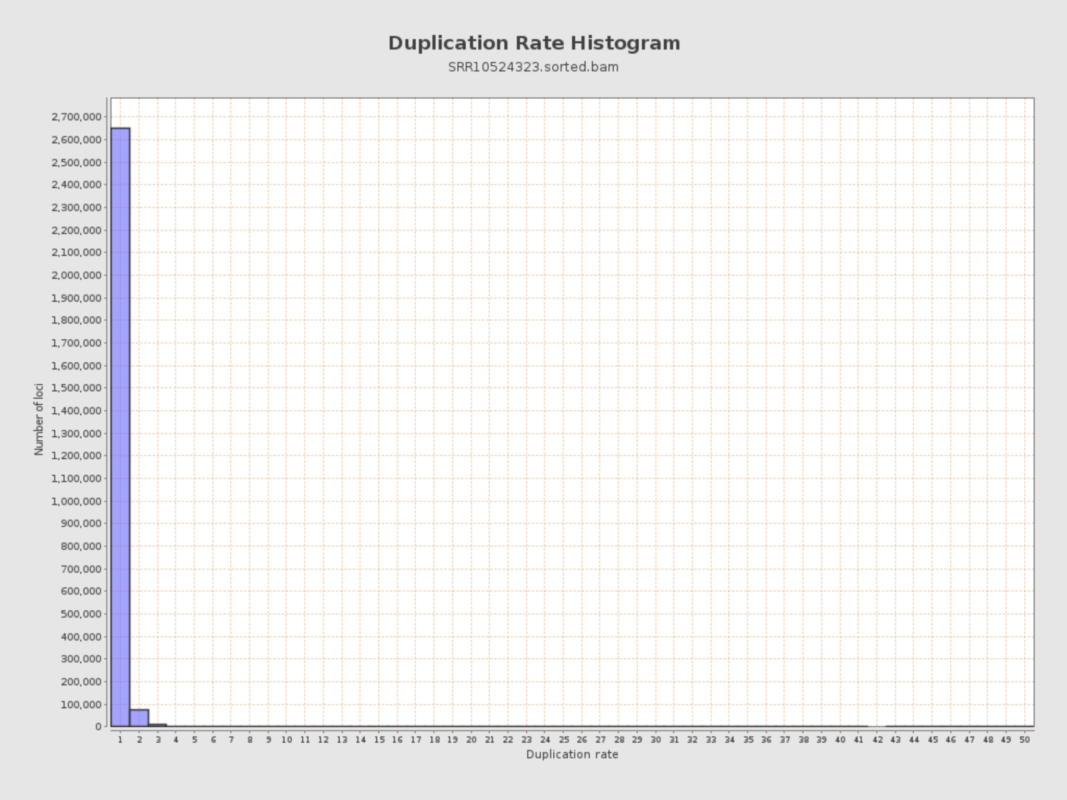
5. Results : Coverage Histogram (0-50X)



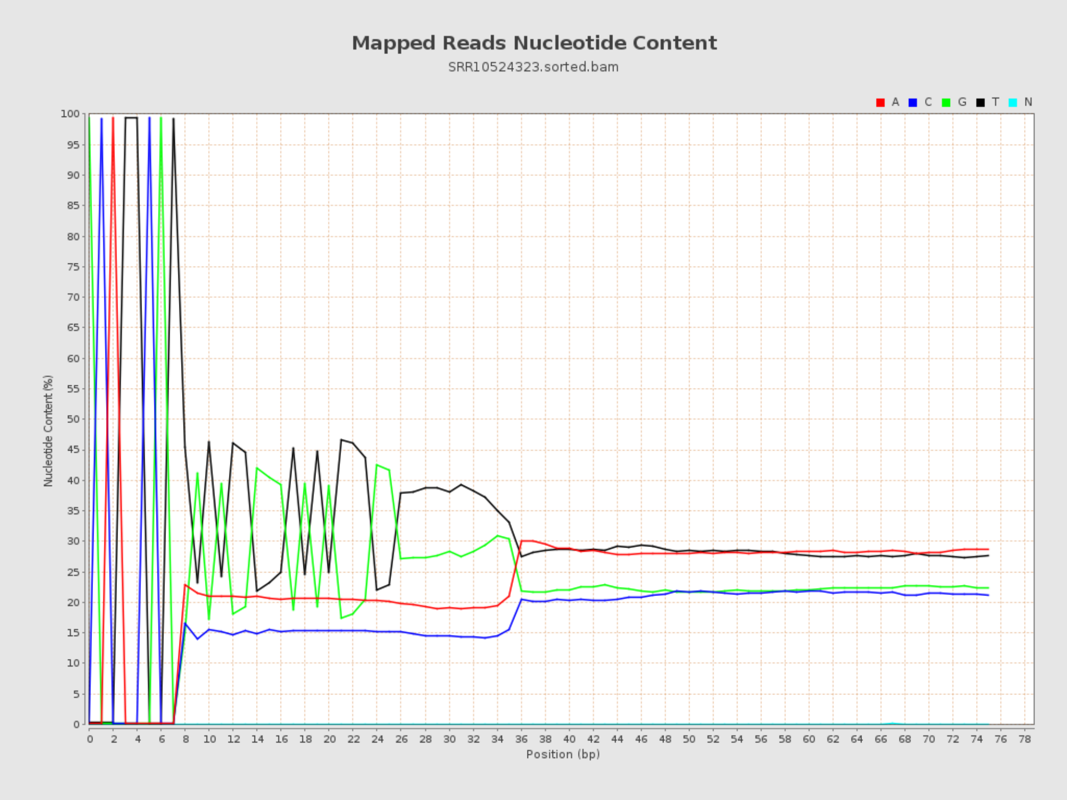
6. Results : Genome Fraction Coverage



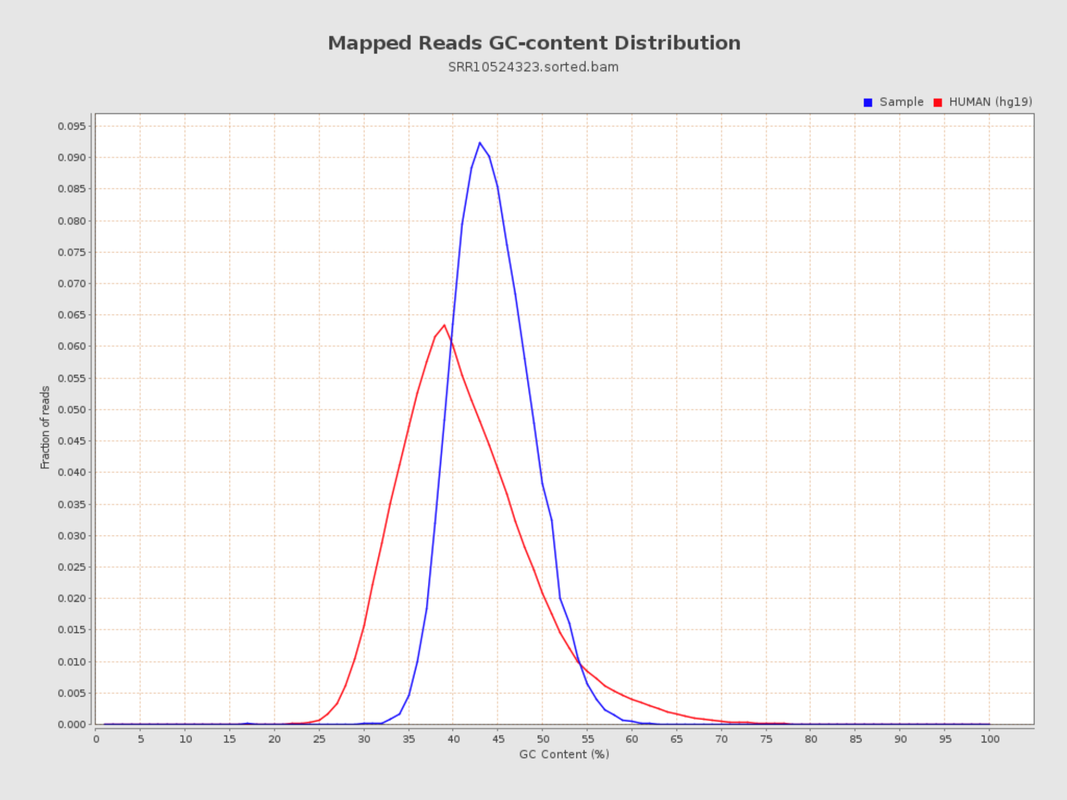
7. Results : Duplication Rate Histogram



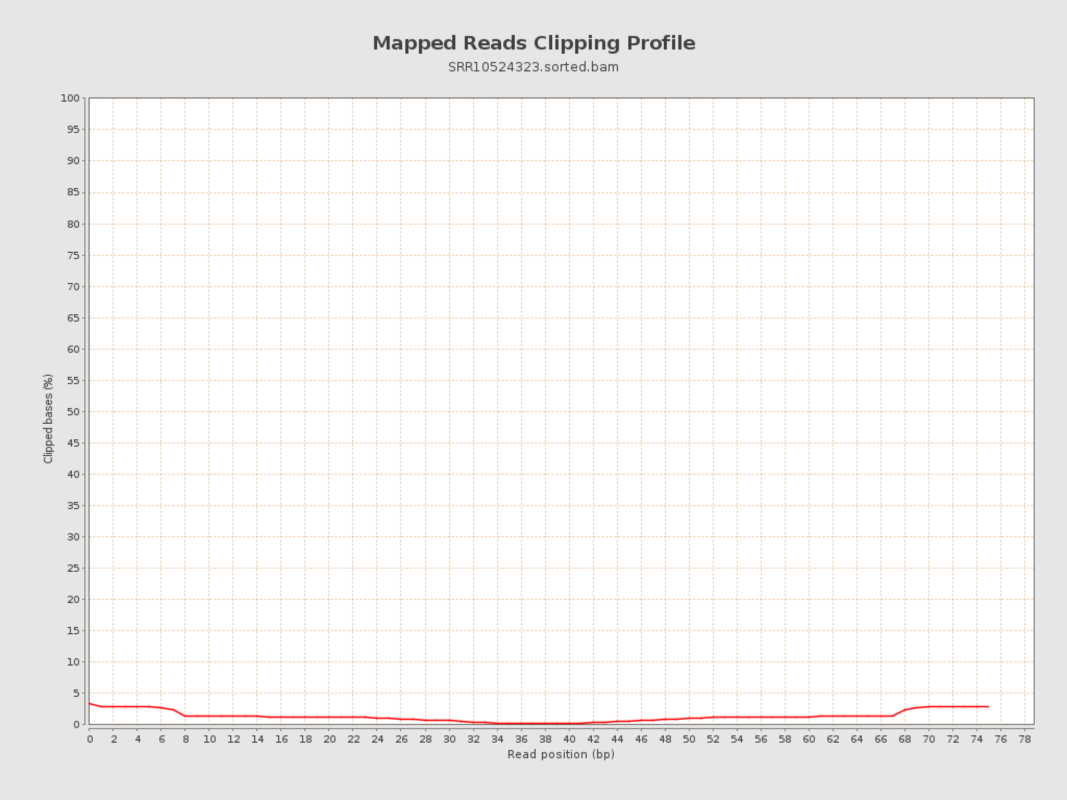
8. Results : Mapped Reads Nucleotide Content



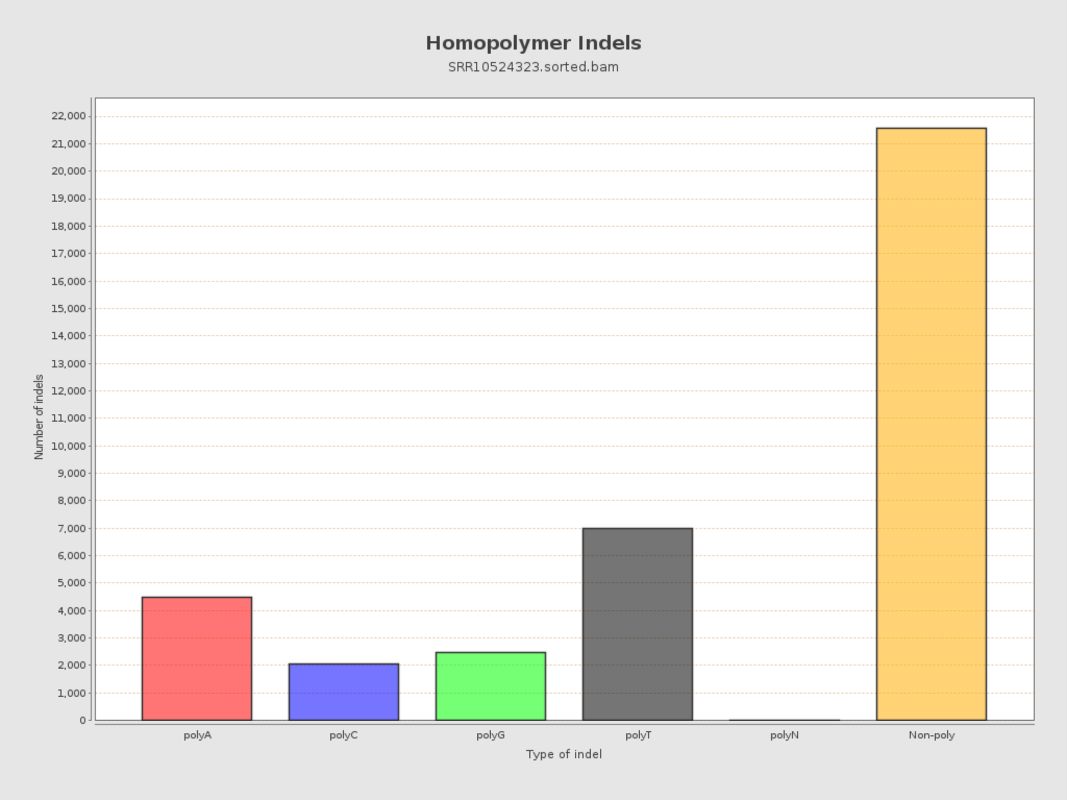
9. Results : Mapped Reads GC-content Distribution



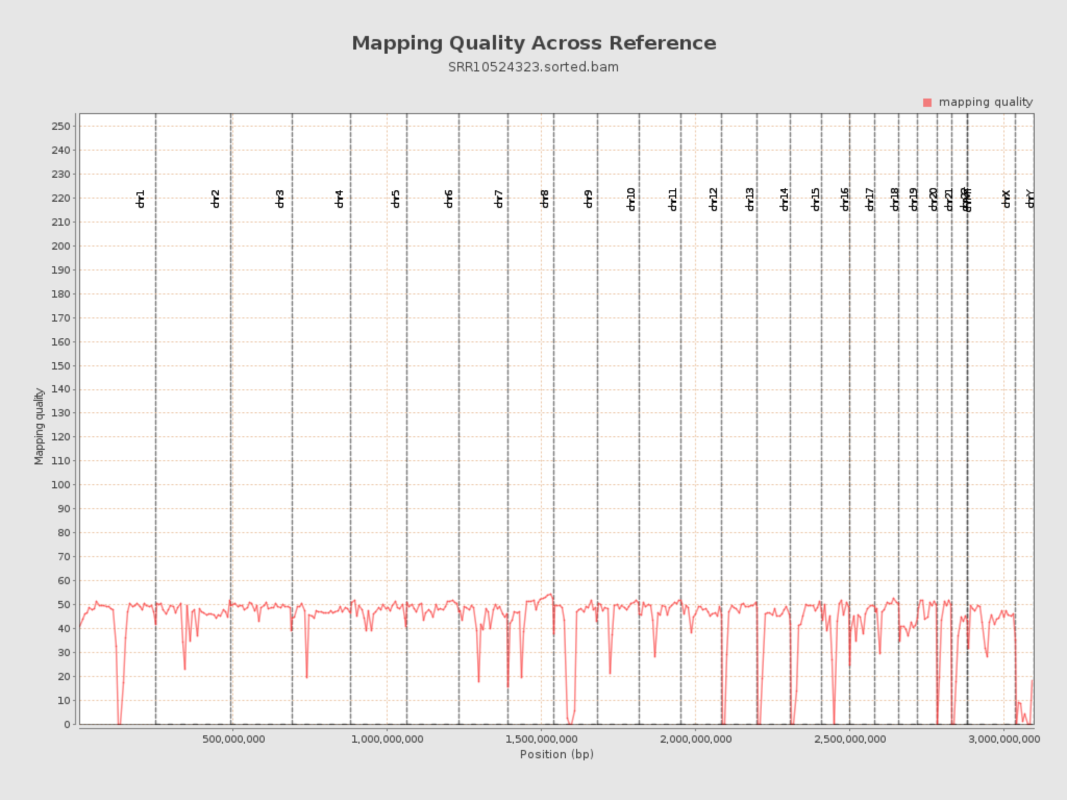
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram