Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:15:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524498.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_SRR10524498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524498.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:15:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,750,866
Mapped reads	2,539,383 / 92.31%
Unmapped reads	211,483 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,629 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	157,178 / 5.71%
Duplication rate	4.69%
Clipped reads	2,539,790 / 92.33%

2.2. ACGT Content

Number/percentage of A's	36,464,078 / 24.7%
Number/percentage of C's	26,242,336 / 17.78%
Number/percentage of T's	46,052,581 / 31.2%
Number/percentage of G's	38,860,171 / 26.32%
Number/percentage of N's	2,963 / 0%
GC Percentage	44.1%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.4033

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

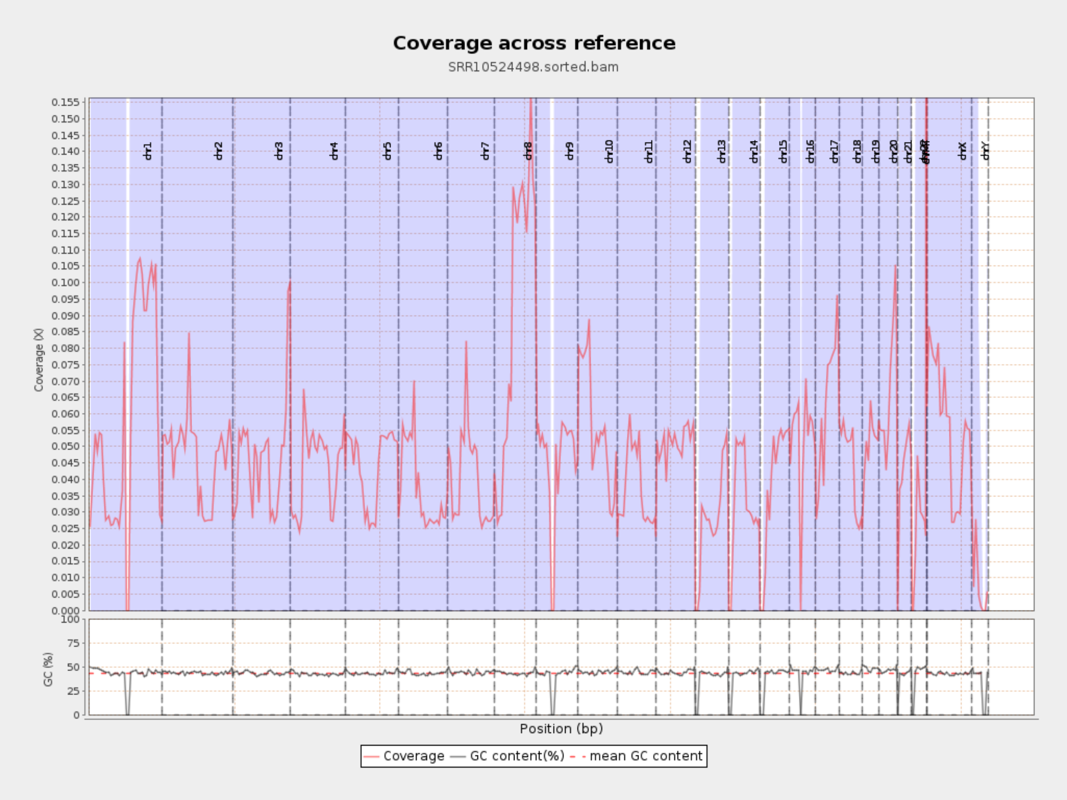
General error rate	0.48%
Mismatches	697,045
Insertions	9,133
Mapped reads with at least one insertion	0.36%
Deletions	27,849
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.66%

2.6. Chromosome stats

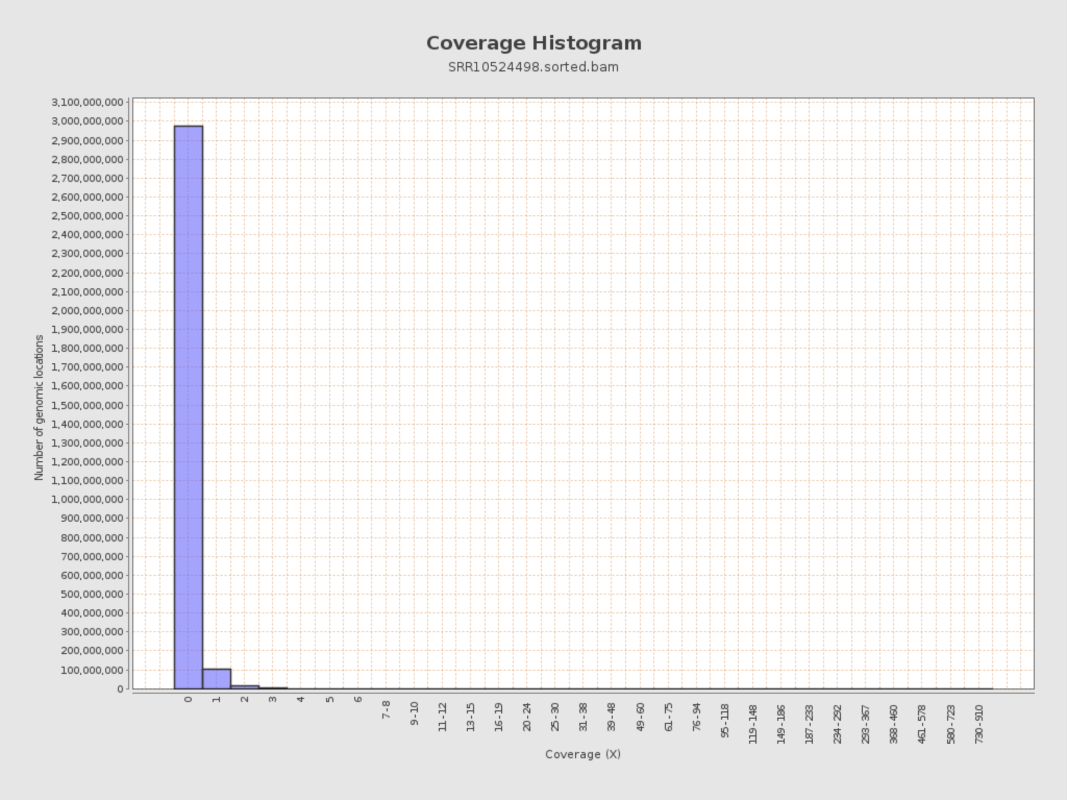
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14501442	0.0582	0.7232
chr2	243199373	11520308	0.0474	0.4749
chr3	198022430	9083827	0.0459	0.2505
chr4	191154276	8336431	0.0436	0.2869
chr5	180915260	8038861	0.0444	0.2473
chr6	171115067	6352716	0.0371	0.3233
chr7	159138663	6379607	0.0401	0.5583

chr8	146364022	13595794	0.0929	0.4316
chr9	141213431	6319716	0.0448	0.3529
chr10	135534747	7728227	0.057	0.4121
chr11	135006516	5051016	0.0374	0.3859
chr12	133851895	6889374	0.0515	0.2681
chr13	115169878	3242017	0.0281	0.1985
chr14	107349540	3503883	0.0326	0.2188
chr15	102531392	3921232	0.0382	0.2414
chr16	90354753	4697767	0.052	0.2958
chr17	81195210	5194169	0.064	0.3191
chr18	78077248	3483954	0.0446	0.6405
chr19	59128983	3014687	0.051	0.5643
chr20	63025520	4259693	0.0676	0.3128
chr21	48129895	2030828	0.0422	0.2697
chr22	51304566	1202943	0.0234	0.1786
chrMT	16571	16918	1.0209	1.3149
chrX	155270560	8826872	0.0568	0.3274
chrY	59373566	477462	0.008	0.2132

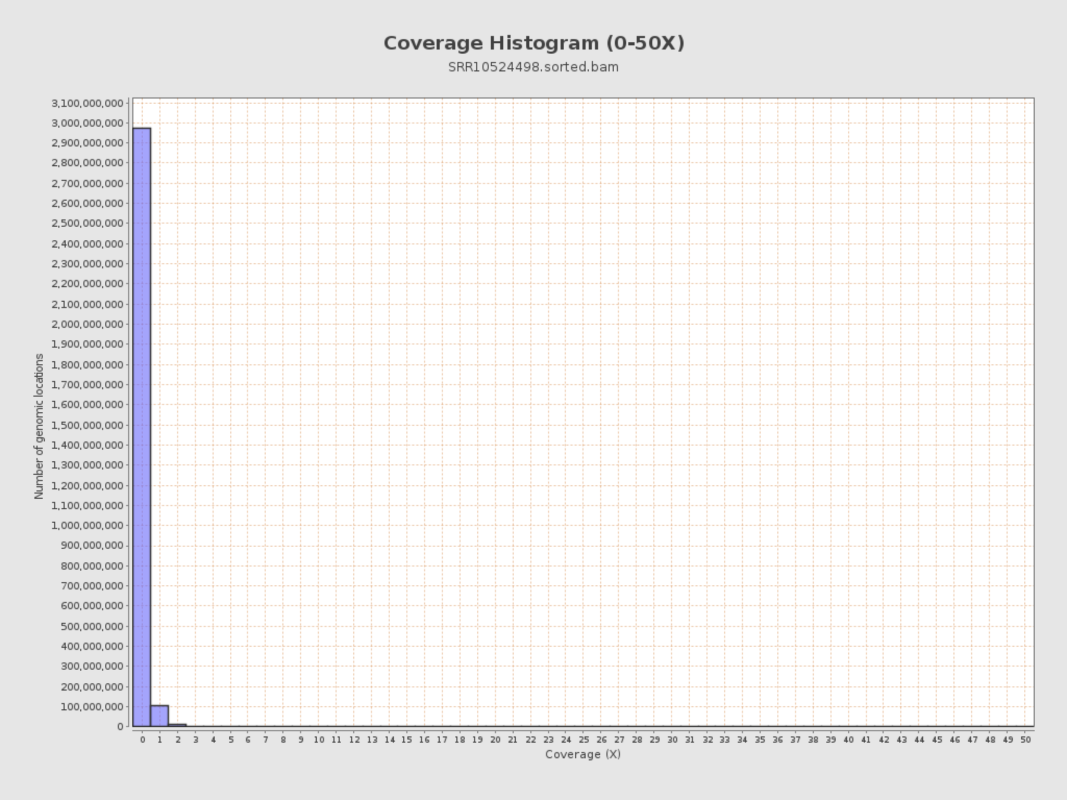
3. Results : Coverage across reference



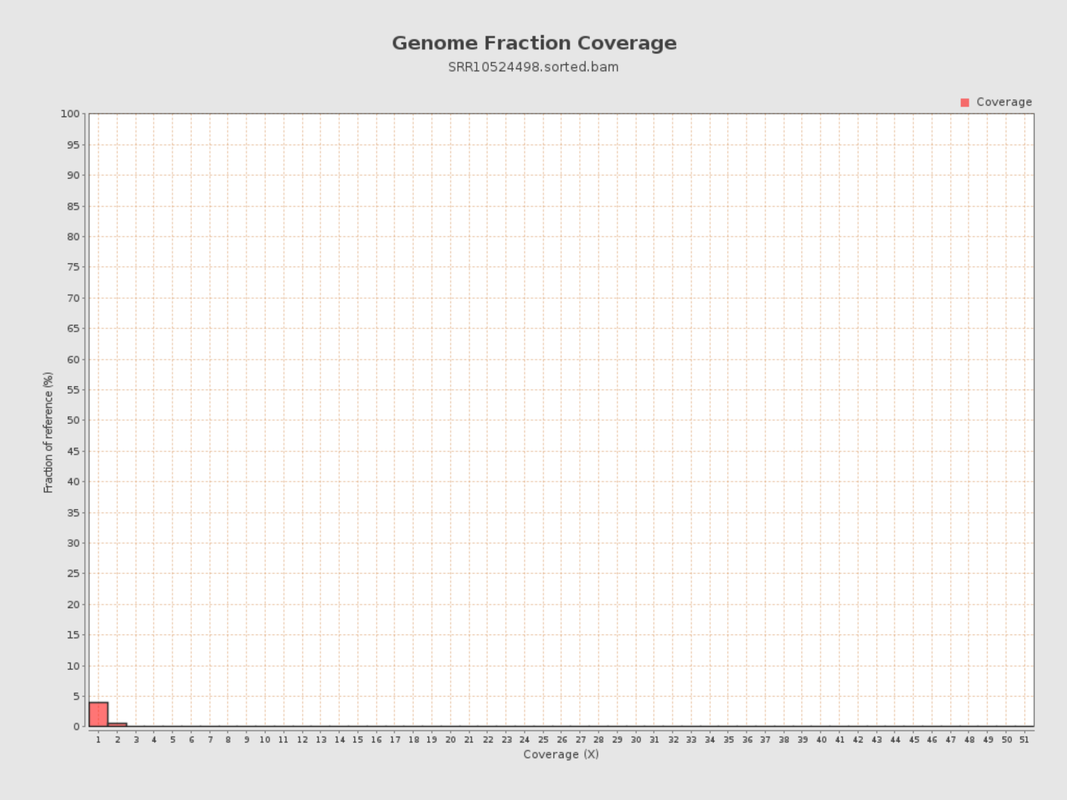
4. Results : Coverage Histogram



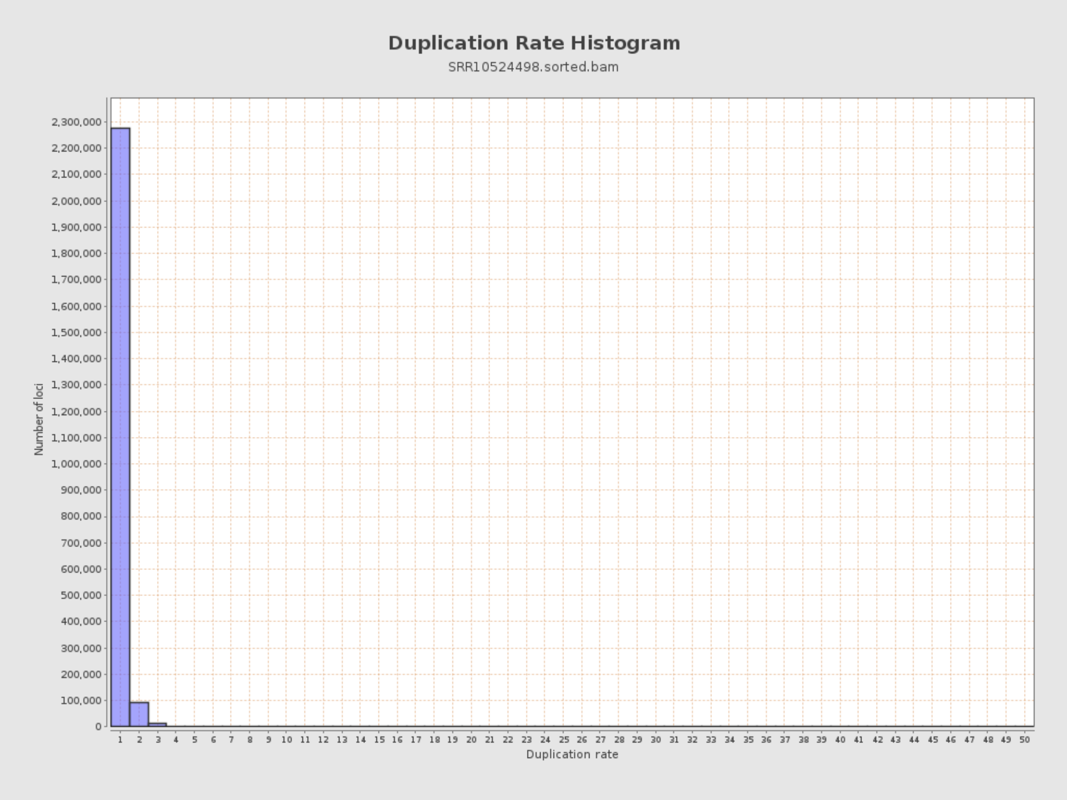
5. Results : Coverage Histogram (0-50X)



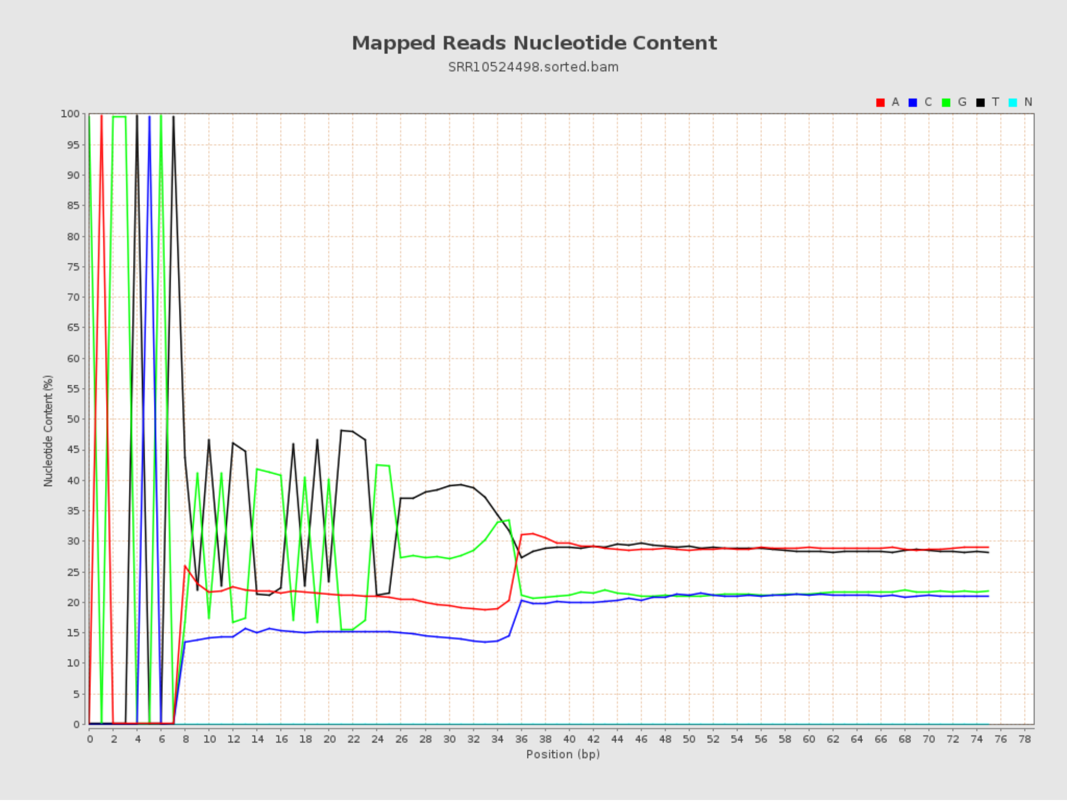
6. Results : Genome Fraction Coverage



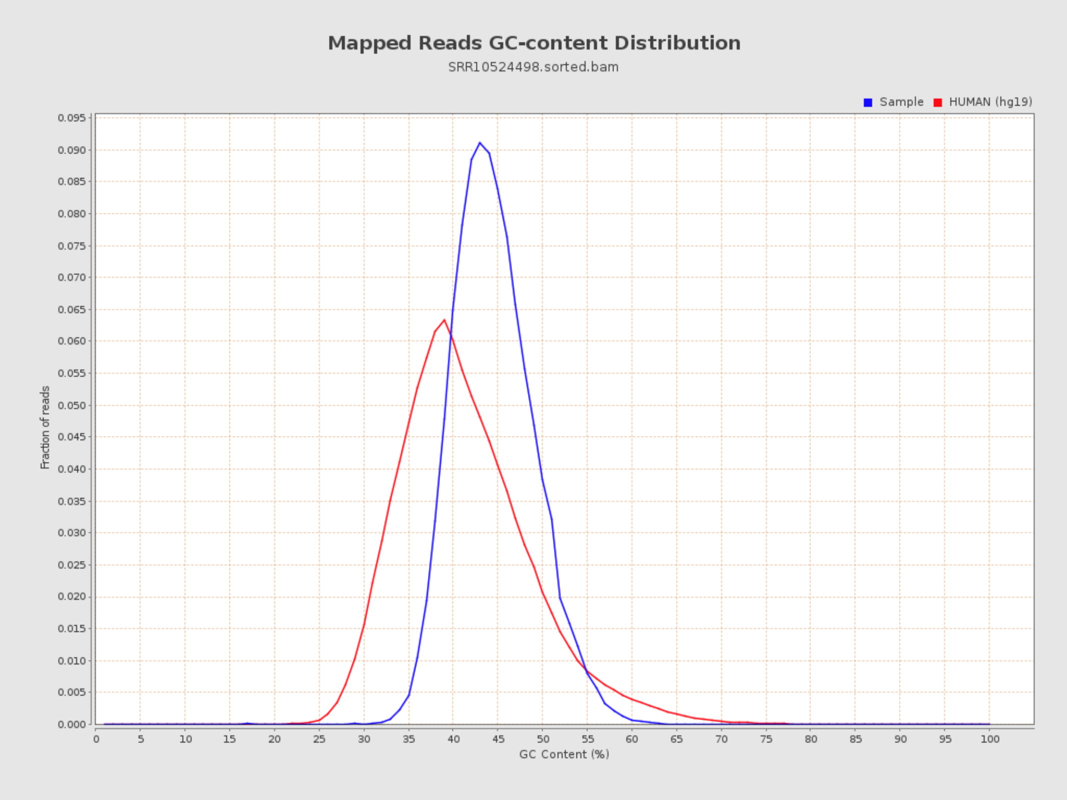
7. Results : Duplication Rate Histogram



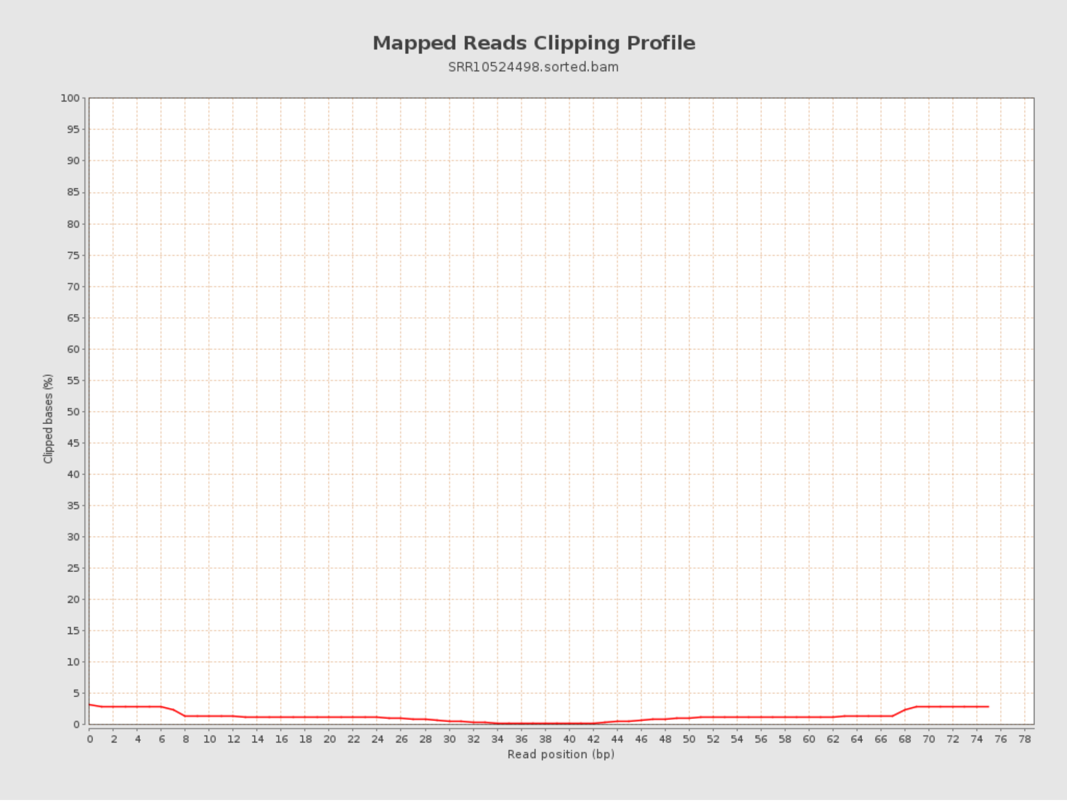
8. Results : Mapped Reads Nucleotide Content



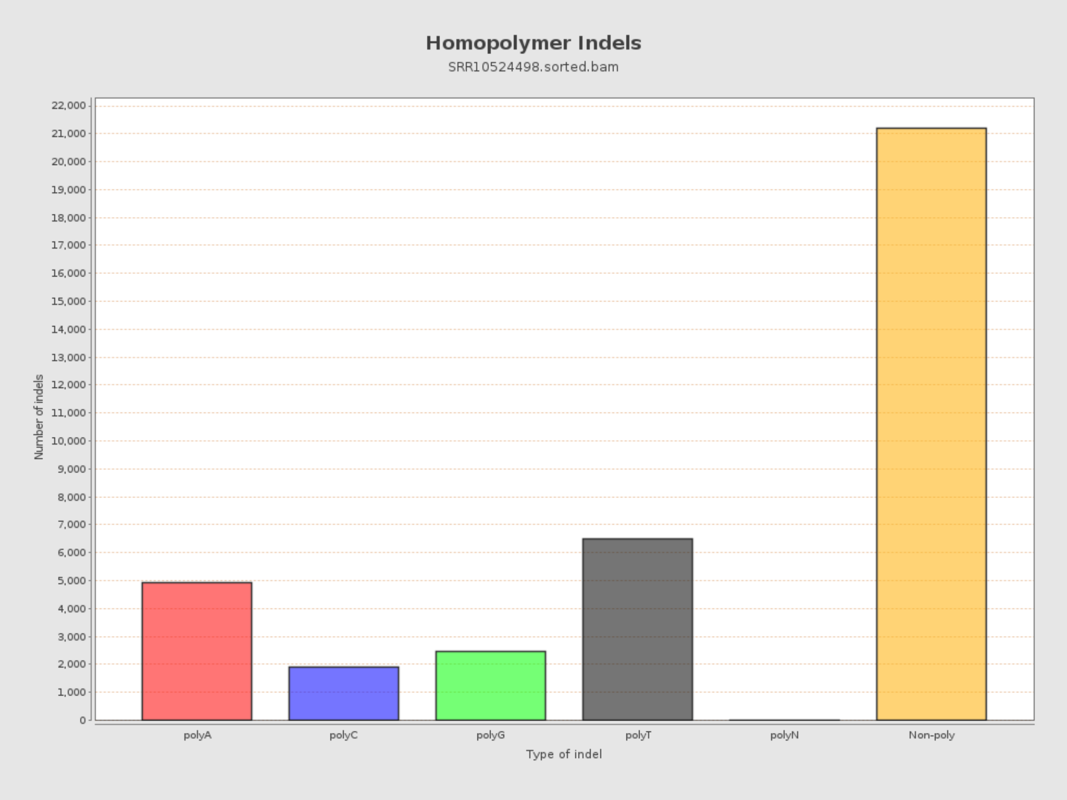
9. Results : Mapped Reads GC-content Distribution



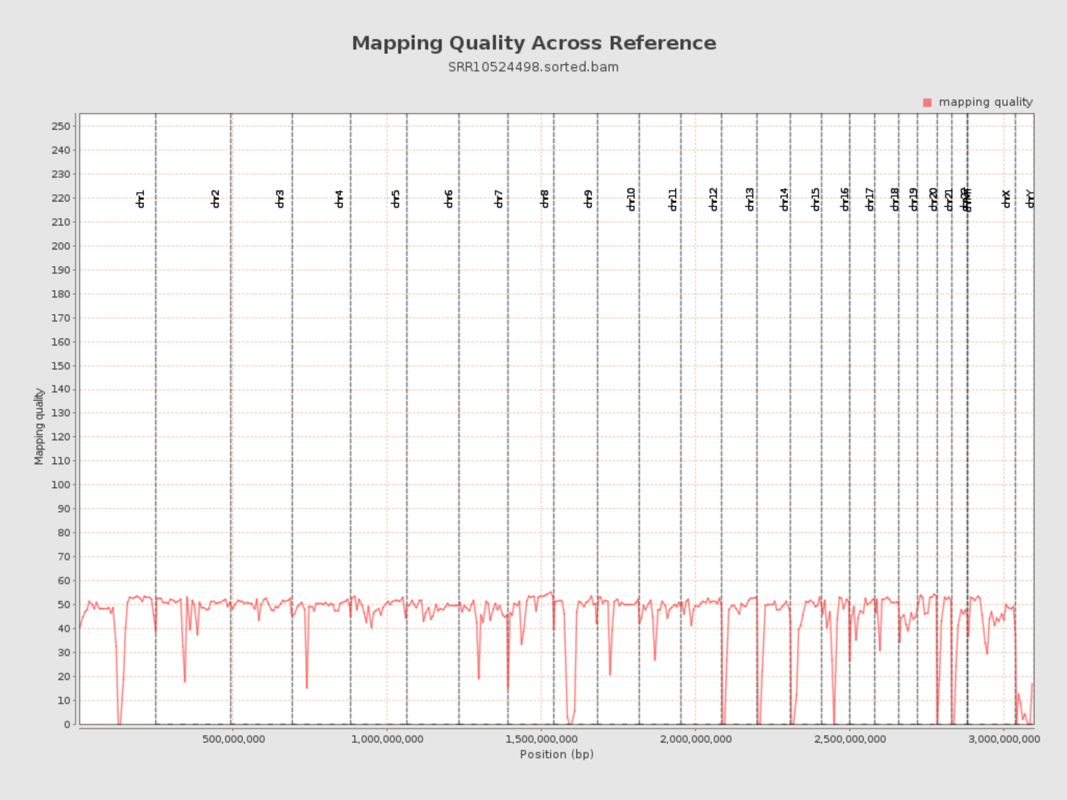
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram