Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:29:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524423.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_SRR10524423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524423.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:29:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,348,254
Mapped reads	2,177,703 / 92.74%
Unmapped reads	170,551 / 7.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,776 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	121,129 / 5.16%
Duplication rate	4.06%
Clipped reads	2,181,098 / 92.88%

2.2. ACGT Content

Number/percentage of A's	32,299,218 / 25.15%
Number/percentage of C's	26,124,039 / 20.34%
Number/percentage of T's	39,274,929 / 30.58%
Number/percentage of G's	30,720,457 / 23.92%
Number/percentage of N's	12,932 / 0.01%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.4019

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

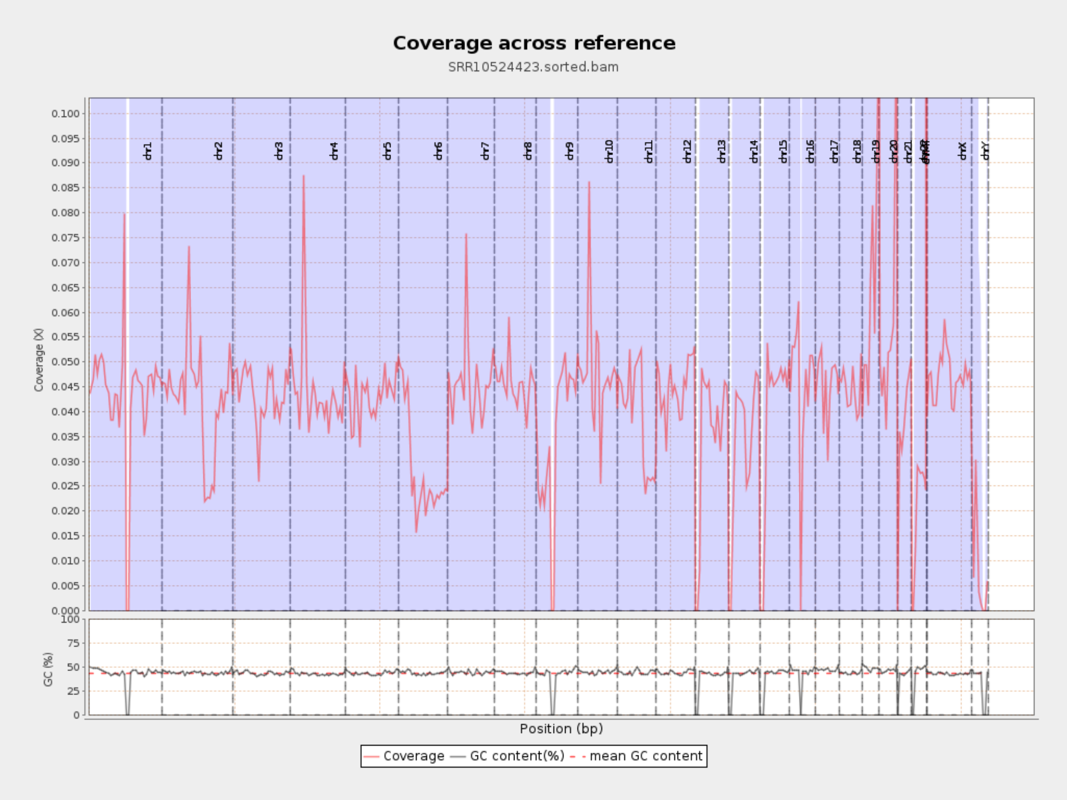
General error rate	0.52%
Mismatches	649,902
Insertions	8,998
Mapped reads with at least one insertion	0.41%
Deletions	23,788
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.87%

2.6. Chromosome stats

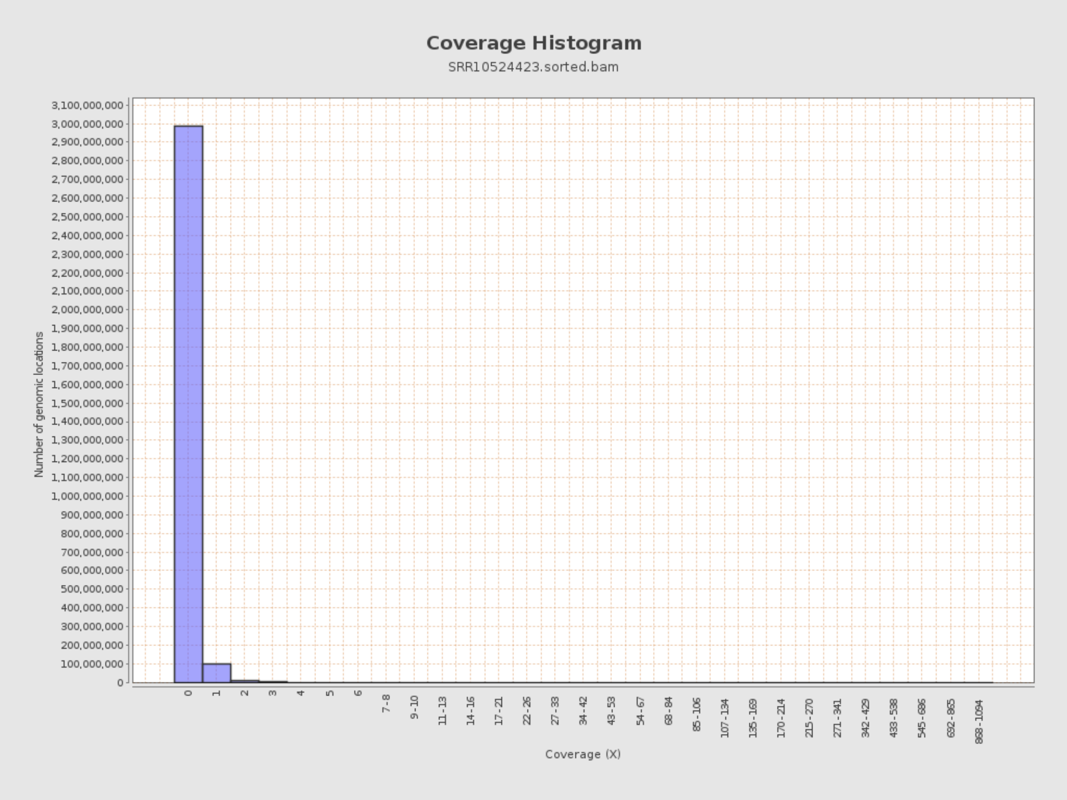
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10821803	0.0434	0.8631
chr2	243199373	10384159	0.0427	0.4888
chr3	198022430	8634343	0.0436	0.2399
chr4	191154276	8426043	0.0441	0.3253
chr5	180915260	7763820	0.0429	0.2354
chr6	171115067	4870305	0.0285	0.2076
chr7	159138663	7269895	0.0457	0.5315

chr8	146364022	6673976	0.0456	0.3109
chr9	141213431	4777970	0.0338	0.2698
chr10	135534747	6479403	0.0478	0.4309
chr11	135006516	5312681	0.0394	0.2998
chr12	133851895	6011920	0.0449	0.2486
chr13	115169878	4000229	0.0347	0.2131
chr14	107349540	3582428	0.0334	0.2176
chr15	102531392	3978683	0.0388	0.2263
chr16	90354753	4097845	0.0454	0.2644
chr17	81195210	3657624	0.045	0.2806
chr18	78077248	3463916	0.0444	0.4826
chr19	59128983	3928589	0.0664	0.5597
chr20	63025520	3748687	0.0595	0.2978
chr21	48129895	1775842	0.0369	0.2877
chr22	51304566	998222	0.0195	0.1618
chrMT	16571	41245	2.489	2.3744
chrX	155270560	7296538	0.047	0.2749
chrY	59373566	473947	0.008	0.2665

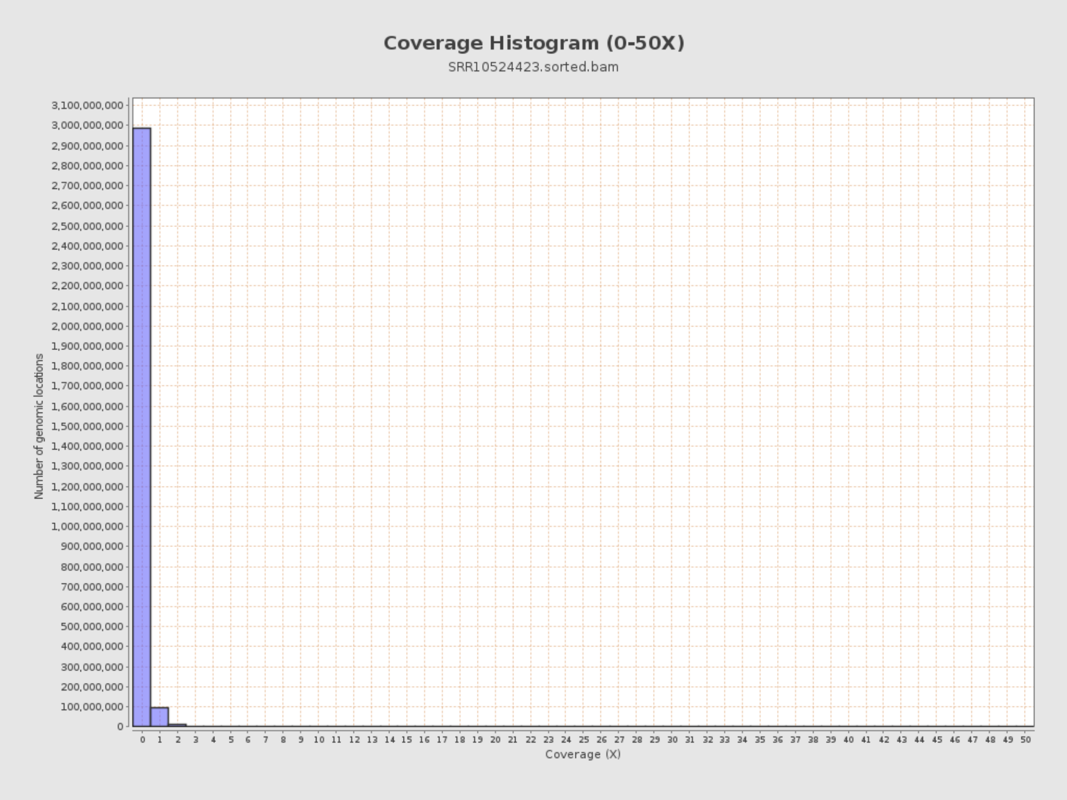
3. Results : Coverage across reference



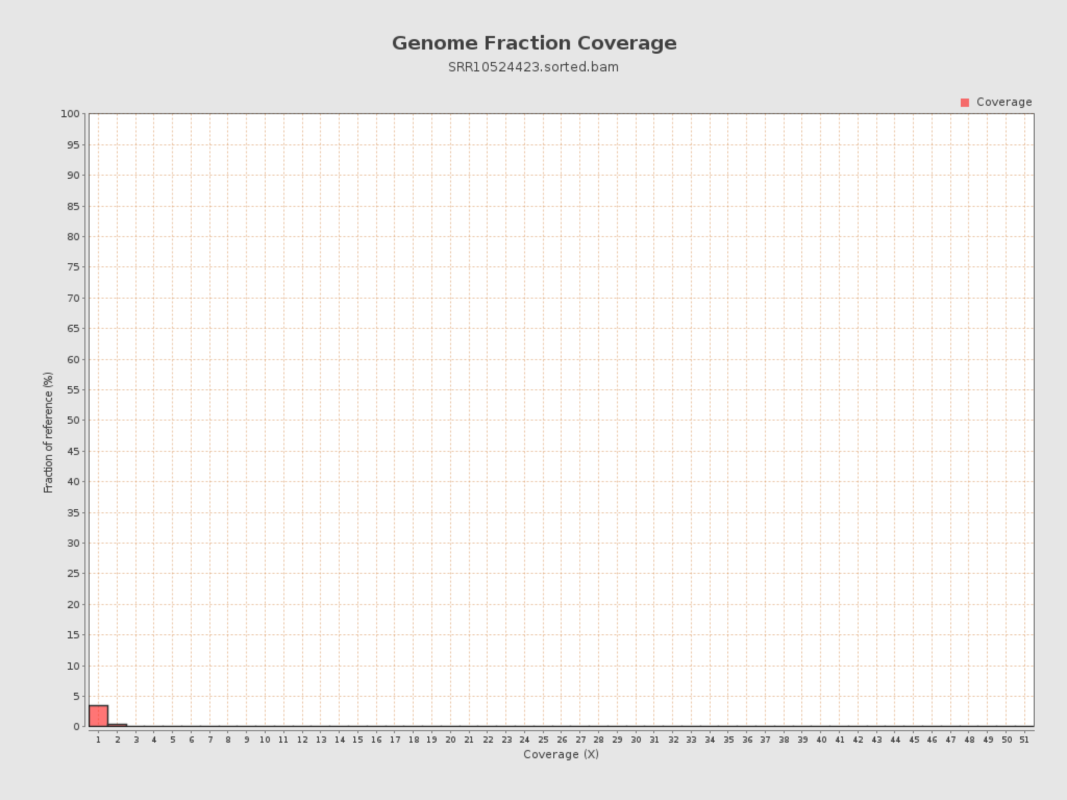
4. Results : Coverage Histogram



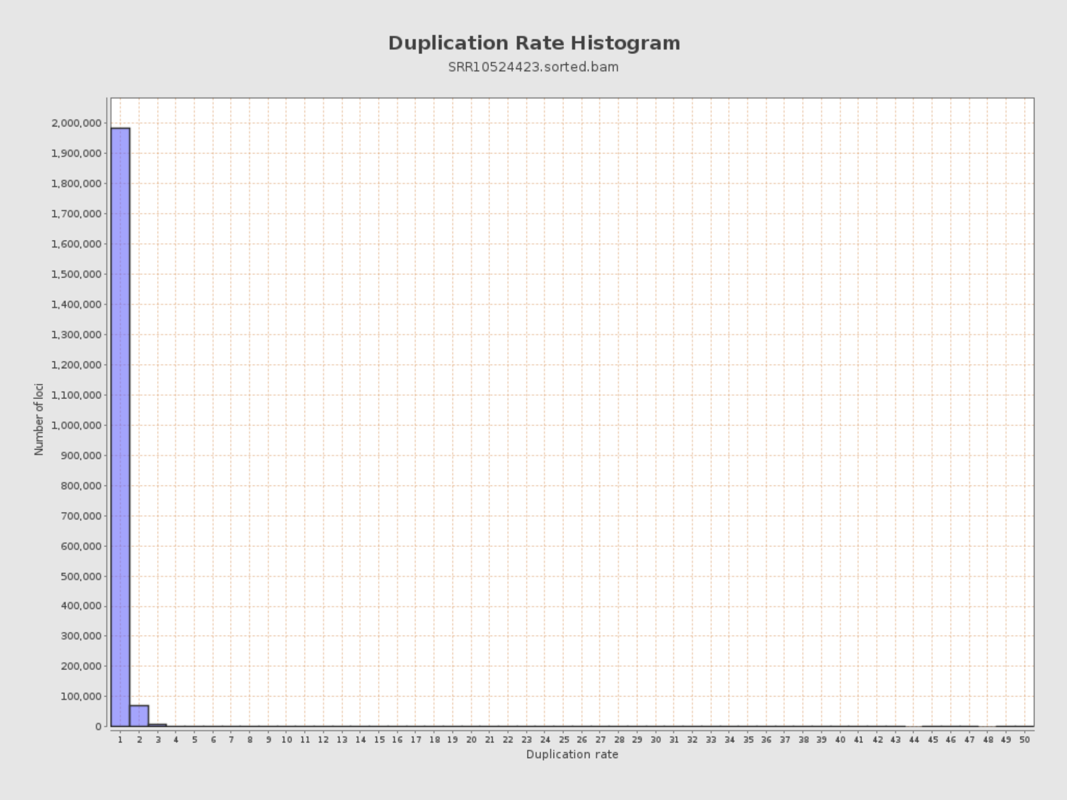
5. Results : Coverage Histogram (0-50X)



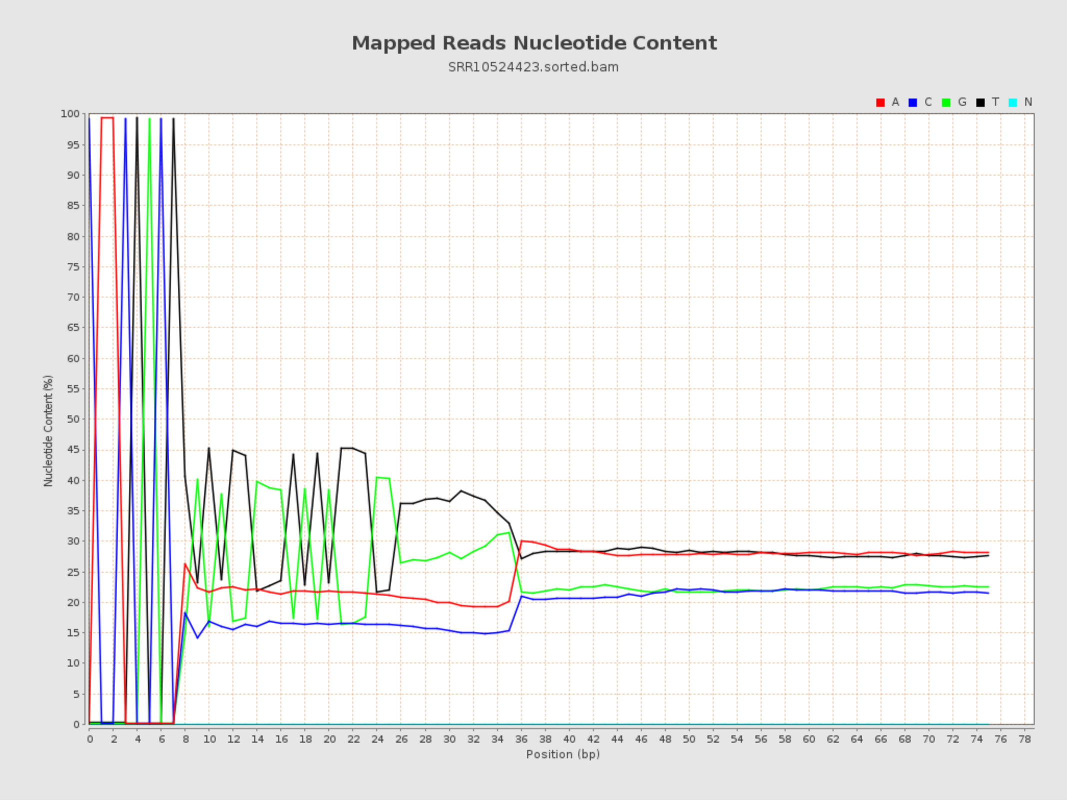
6. Results : Genome Fraction Coverage



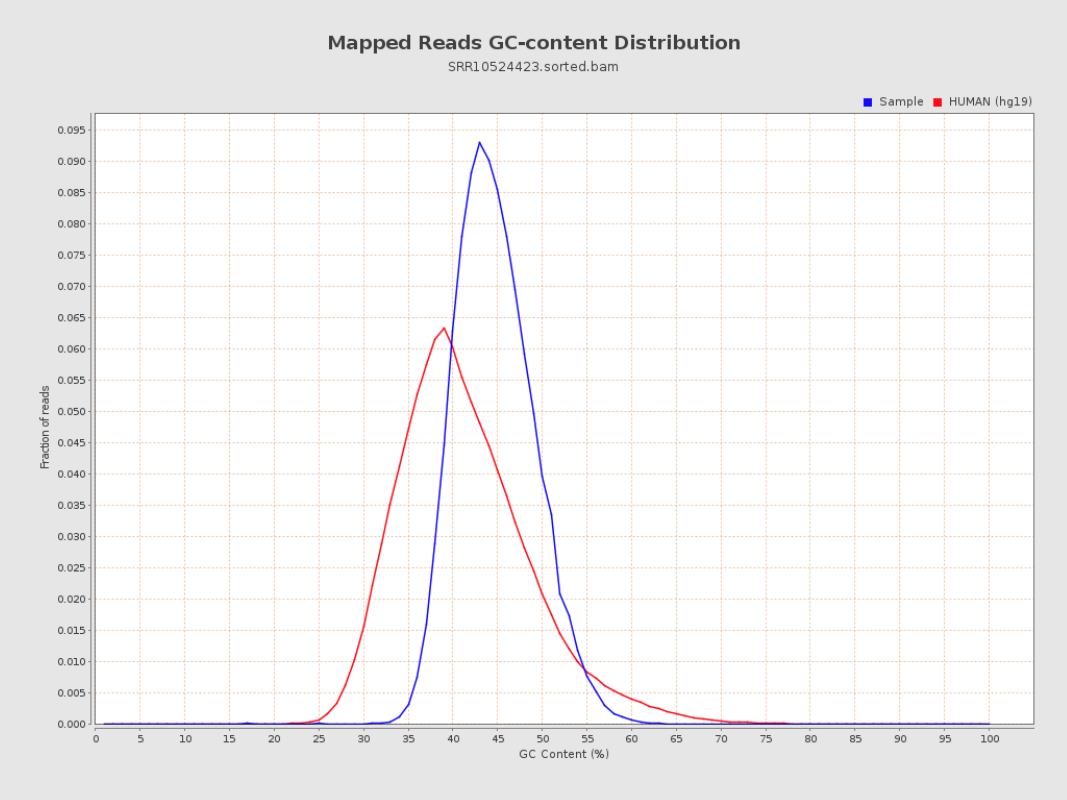
7. Results : Duplication Rate Histogram



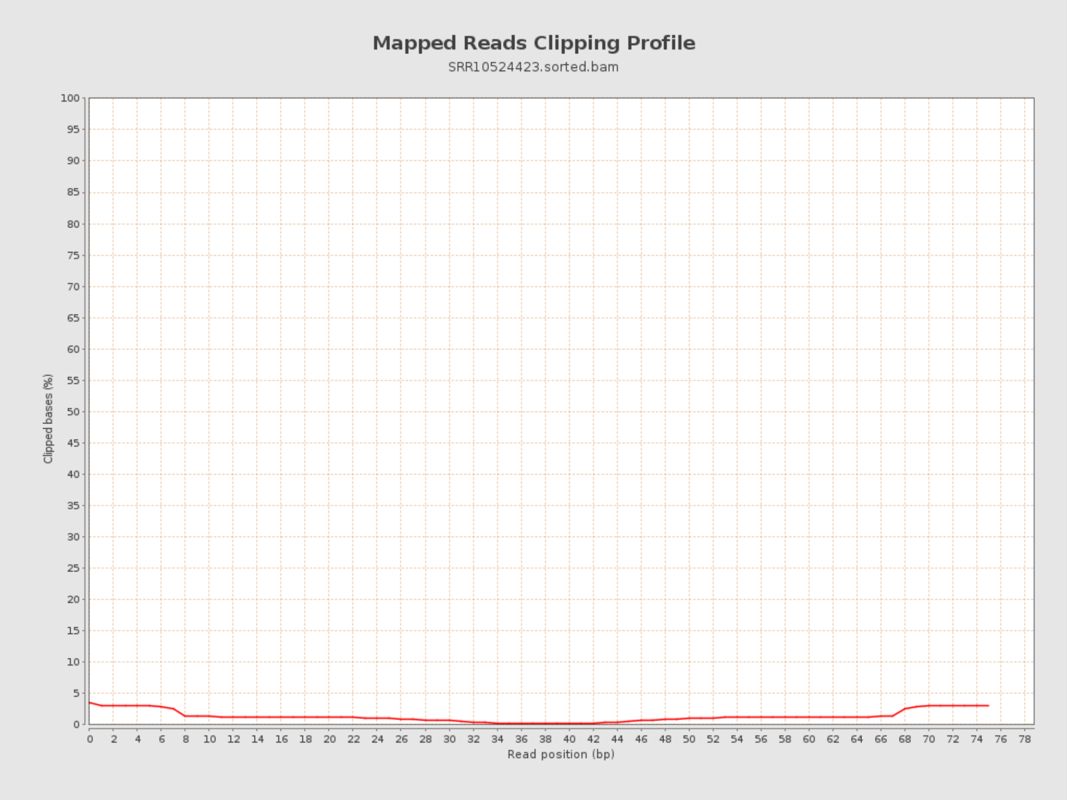
8. Results : Mapped Reads Nucleotide Content



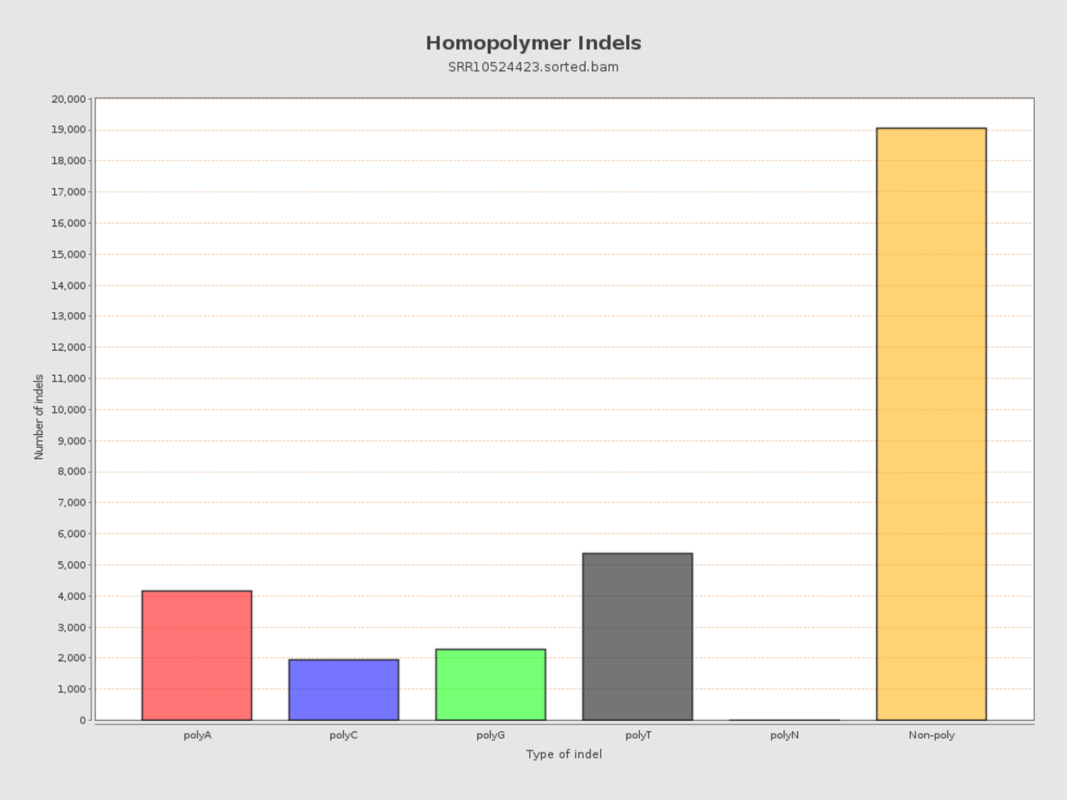
9. Results : Mapped Reads GC-content Distribution



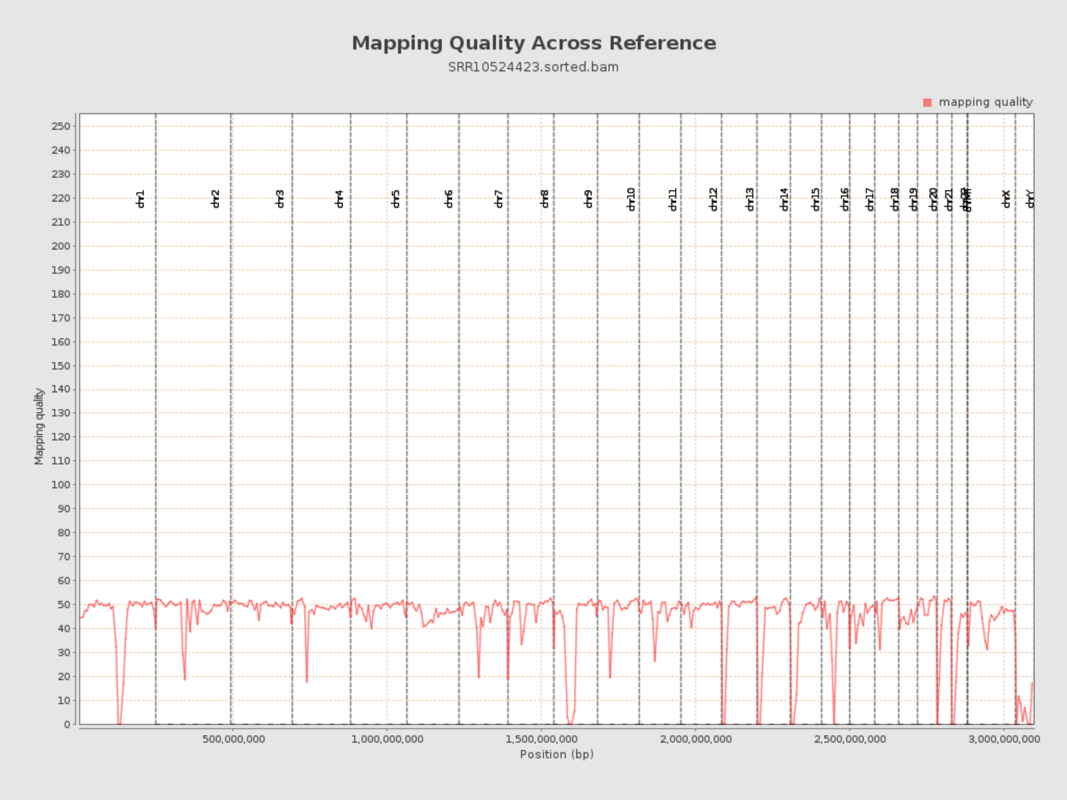
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram