Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:35:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524873.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_SRR10524873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524873.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:35:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,796,966
Mapped reads	1,653,054 / 91.99%
Unmapped reads	143,912 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,547 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	50,122 / 2.79%
Duplication rate	2.05%
Clipped reads	1,659,924 / 92.37%

2.2. ACGT Content

Number/percentage of A's	25,419,829 / 26.34%
Number/percentage of C's	17,665,363 / 18.31%
Number/percentage of T's	29,576,609 / 30.65%
Number/percentage of G's	23,818,244 / 24.68%
Number/percentage of N's	12,847 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3029

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

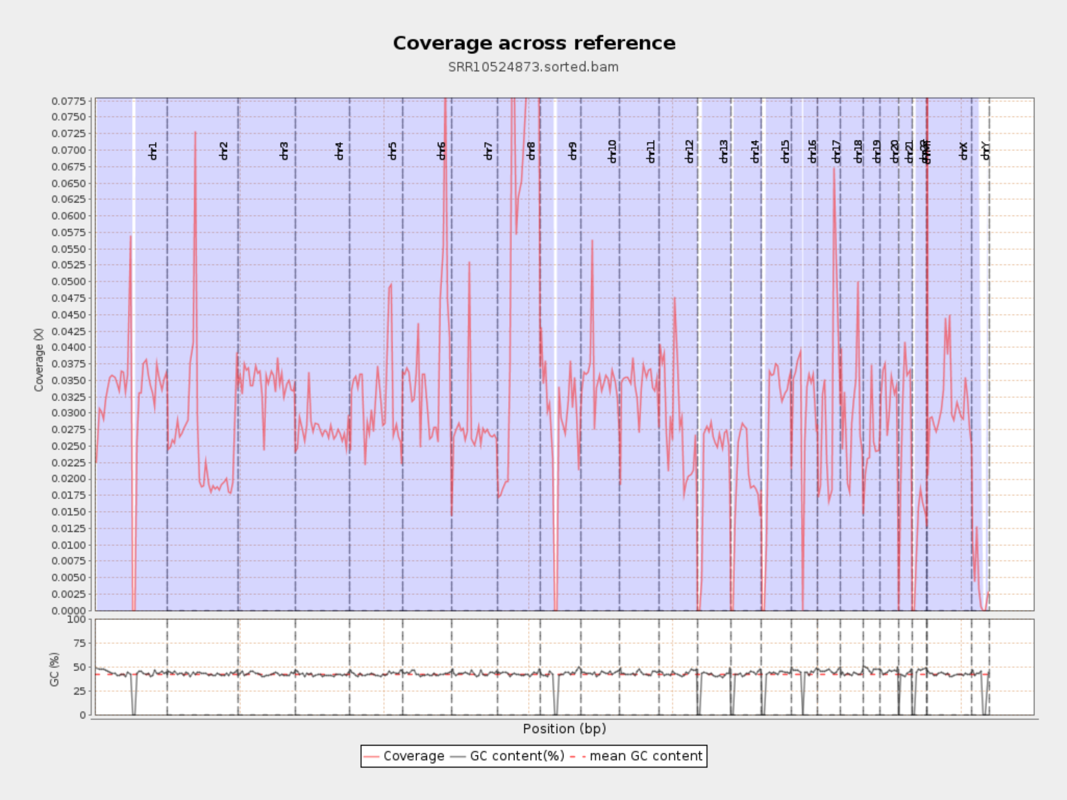
General error rate	0.49%
Mismatches	461,783
Insertions	5,873
Mapped reads with at least one insertion	0.35%
Deletions	17,721
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.06%

2.6. Chromosome stats

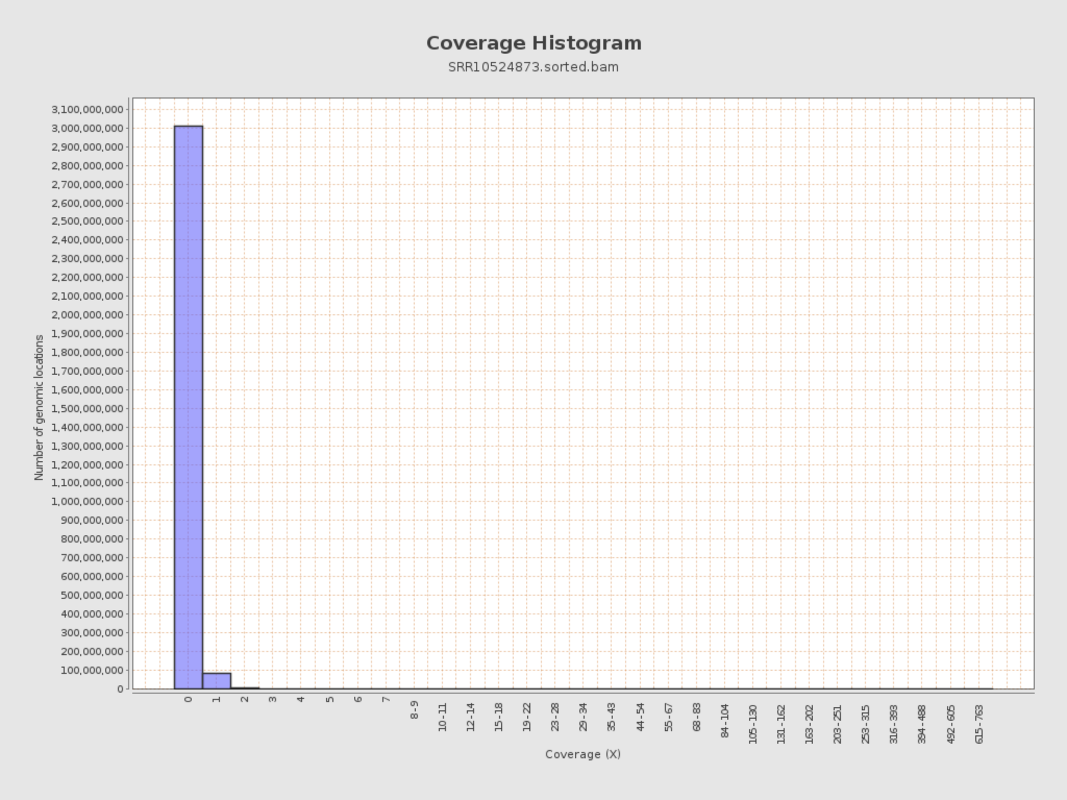
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8034556	0.0322	0.5891
chr2	243199373	6217659	0.0256	0.2996
chr3	198022430	6877563	0.0347	0.2
chr4	191154276	5249234	0.0275	0.1897
chr5	180915260	5856938	0.0324	0.1952
chr6	171115067	6336184	0.037	0.2306
chr7	159138663	4439018	0.0279	0.4177

chr8	146364022	10374935	0.0709	0.4172
chr9	141213431	3986012	0.0282	0.2535
chr10	135534747	4812180	0.0355	0.2804
chr11	135006516	4635837	0.0343	0.2751
chr12	133851895	3821753	0.0286	0.1853
chr13	115169878	2537614	0.022	0.1577
chr14	107349540	2029441	0.0189	0.1654
chr15	102531392	2893720	0.0282	0.1804
chr16	90354753	2764844	0.0306	0.2046
chr17	81195210	2645294	0.0326	0.2209
chr18	78077248	2329543	0.0298	0.4676
chr19	59128983	1480329	0.025	0.4069
chr20	63025520	2054276	0.0326	0.1954
chr21	48129895	1401918	0.0291	0.1939
chr22	51304566	592698	0.0116	0.1144
chrMT	16571	5609	0.3385	0.6258
chrX	155270560	4903622	0.0316	0.2194
chrY	59373566	239741	0.004	0.102

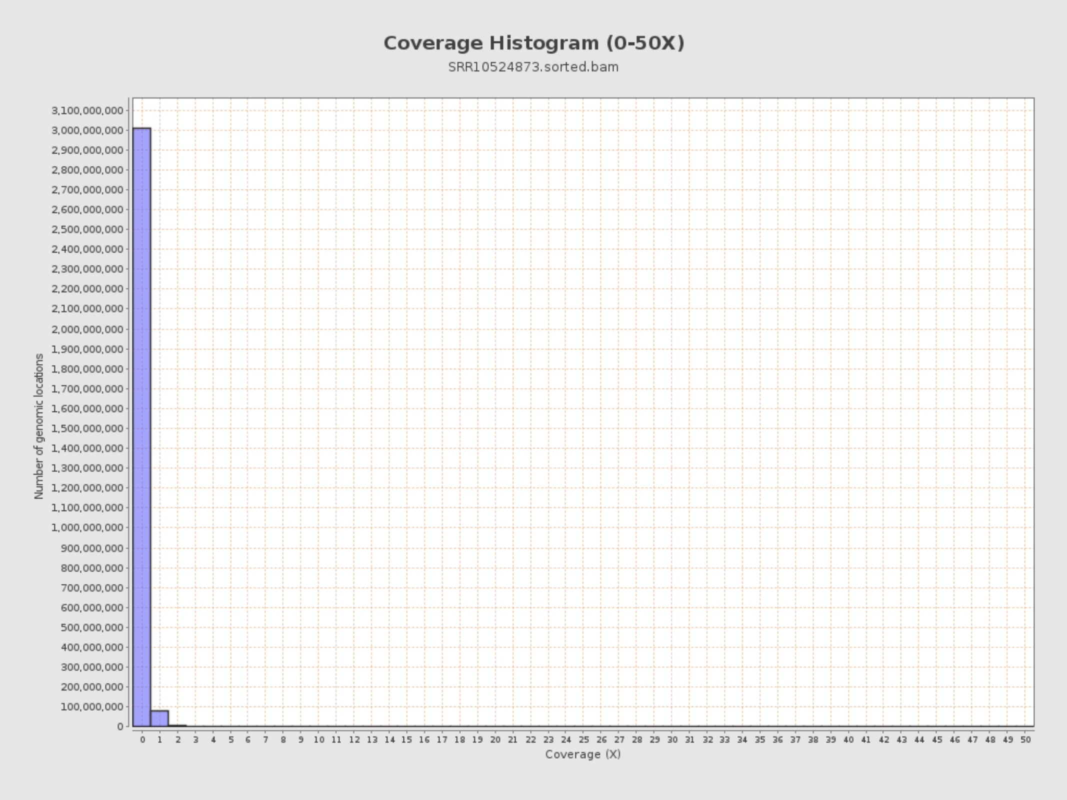
3. Results : Coverage across reference



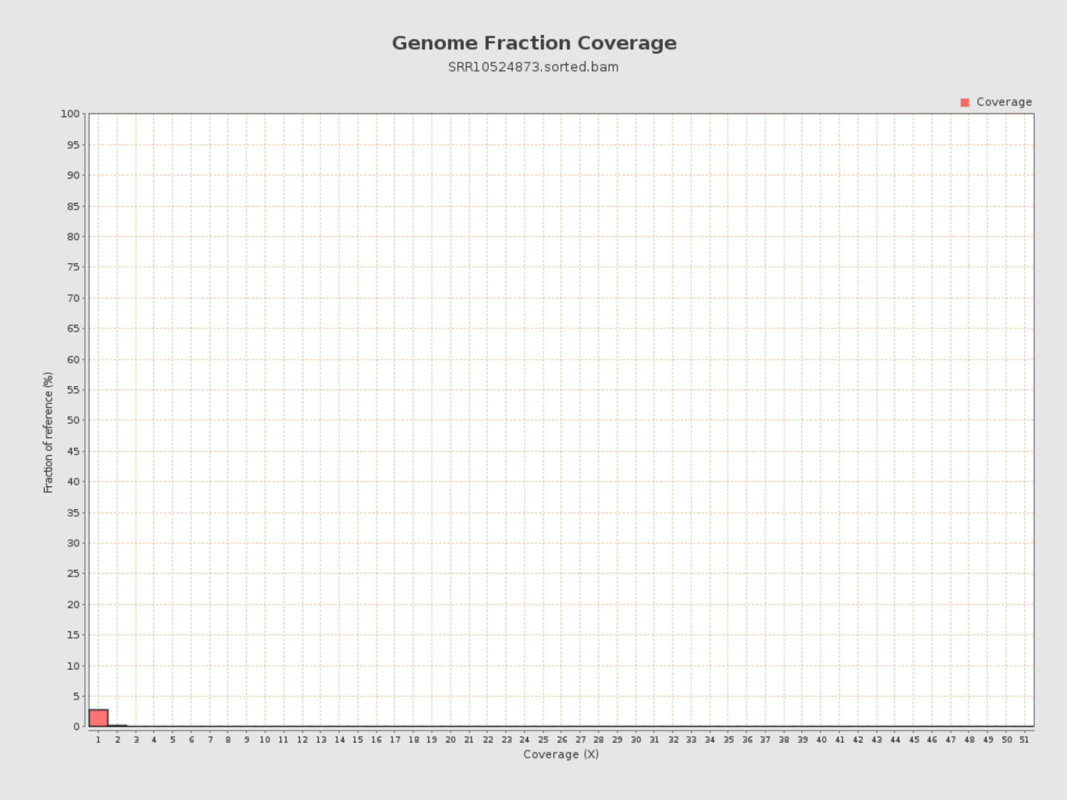
4. Results : Coverage Histogram



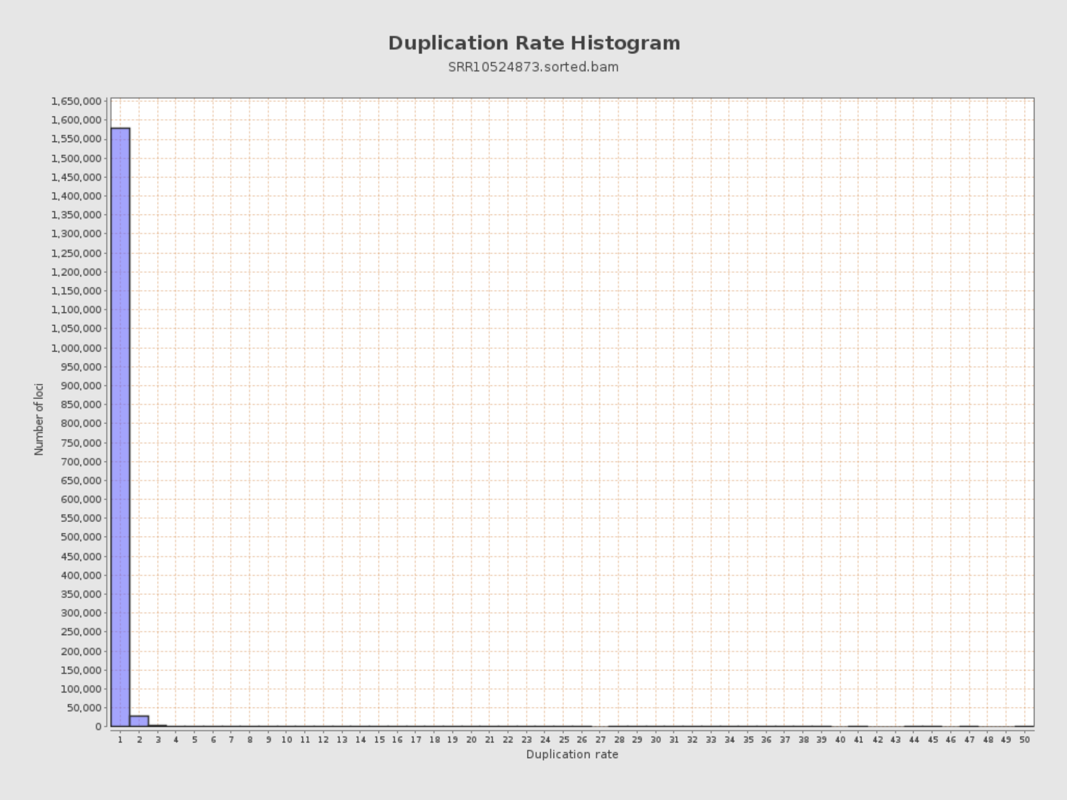
5. Results : Coverage Histogram (0-50X)



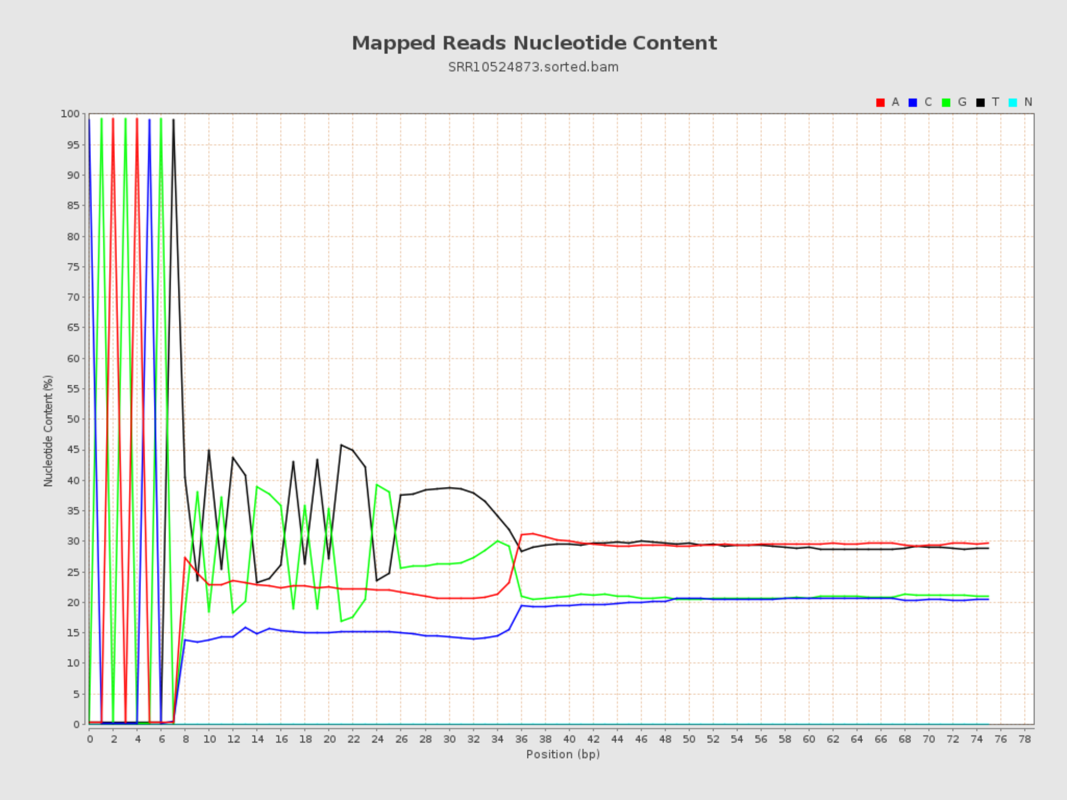
6. Results : Genome Fraction Coverage



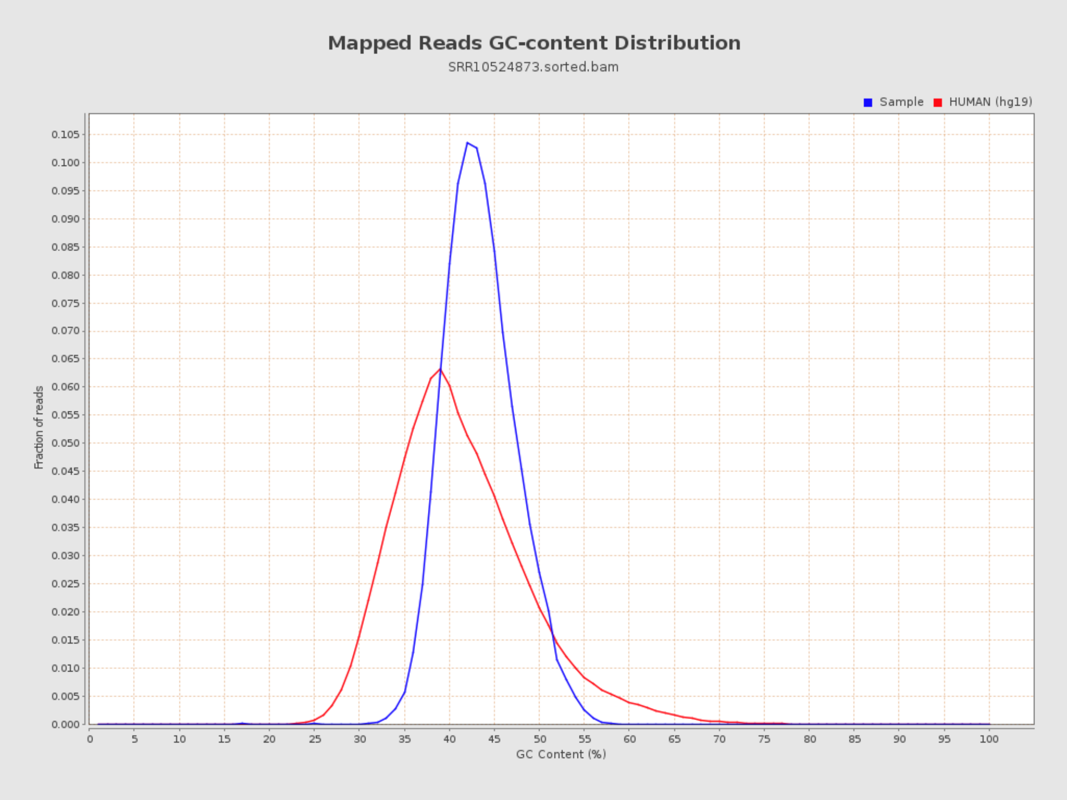
7. Results : Duplication Rate Histogram



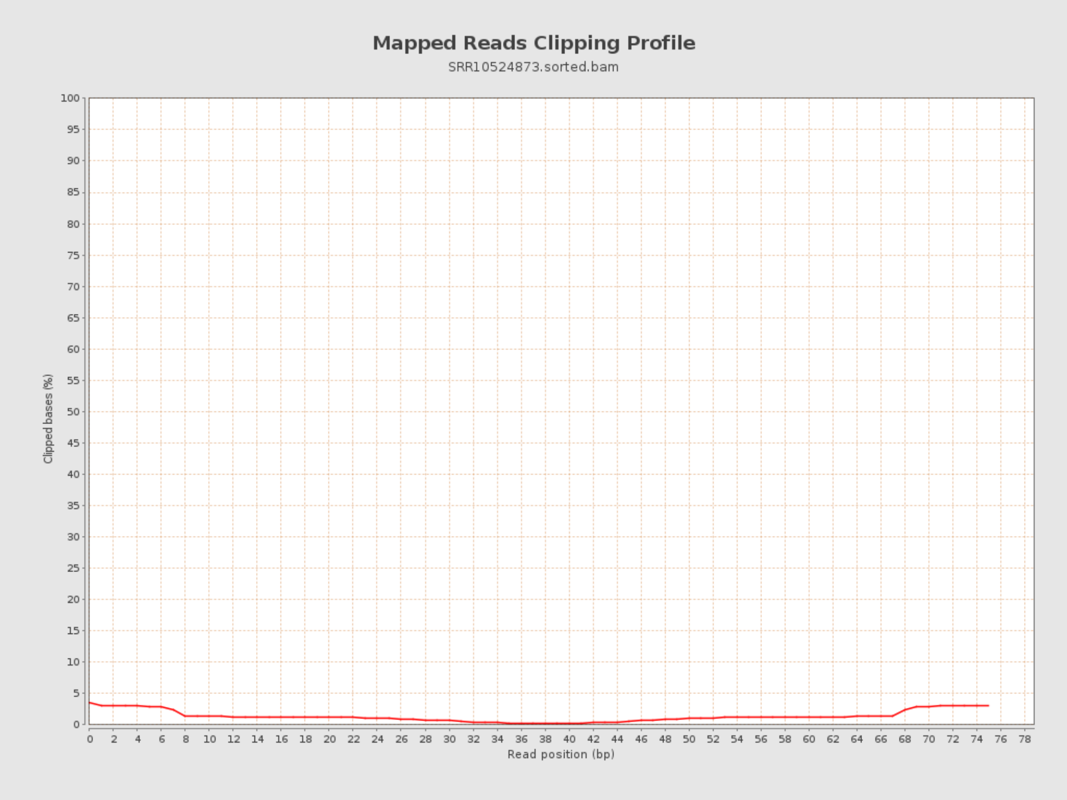
8. Results : Mapped Reads Nucleotide Content



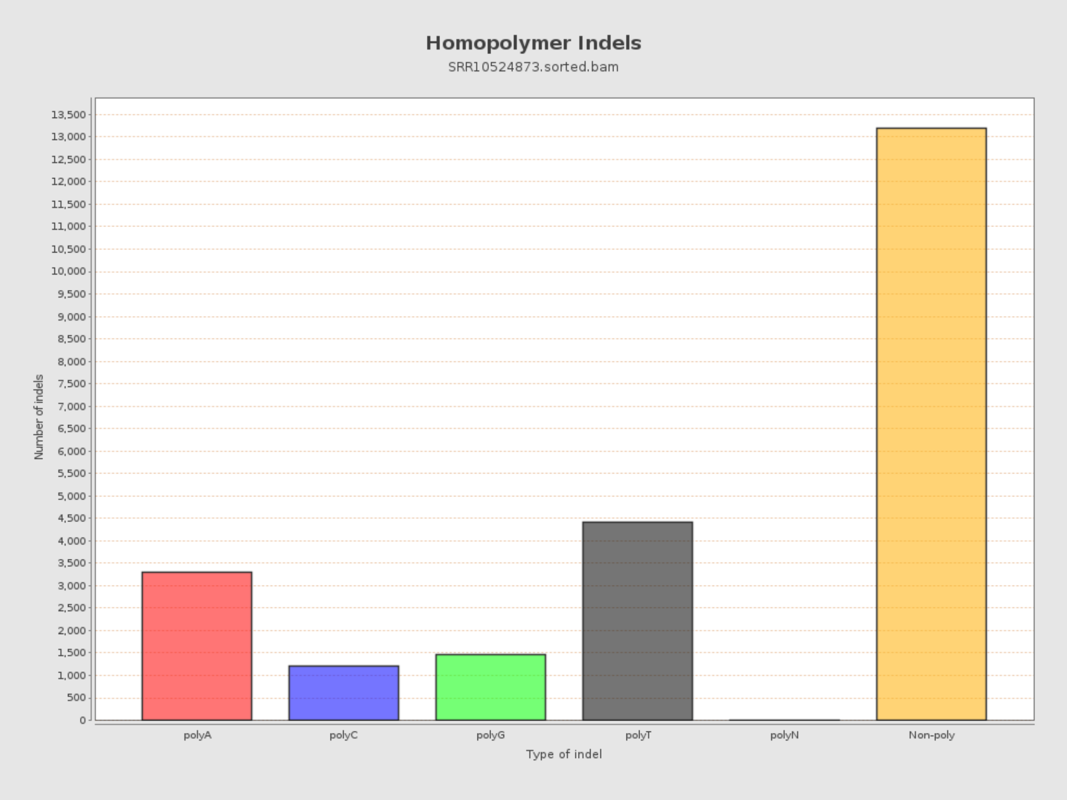
9. Results : Mapped Reads GC-content Distribution



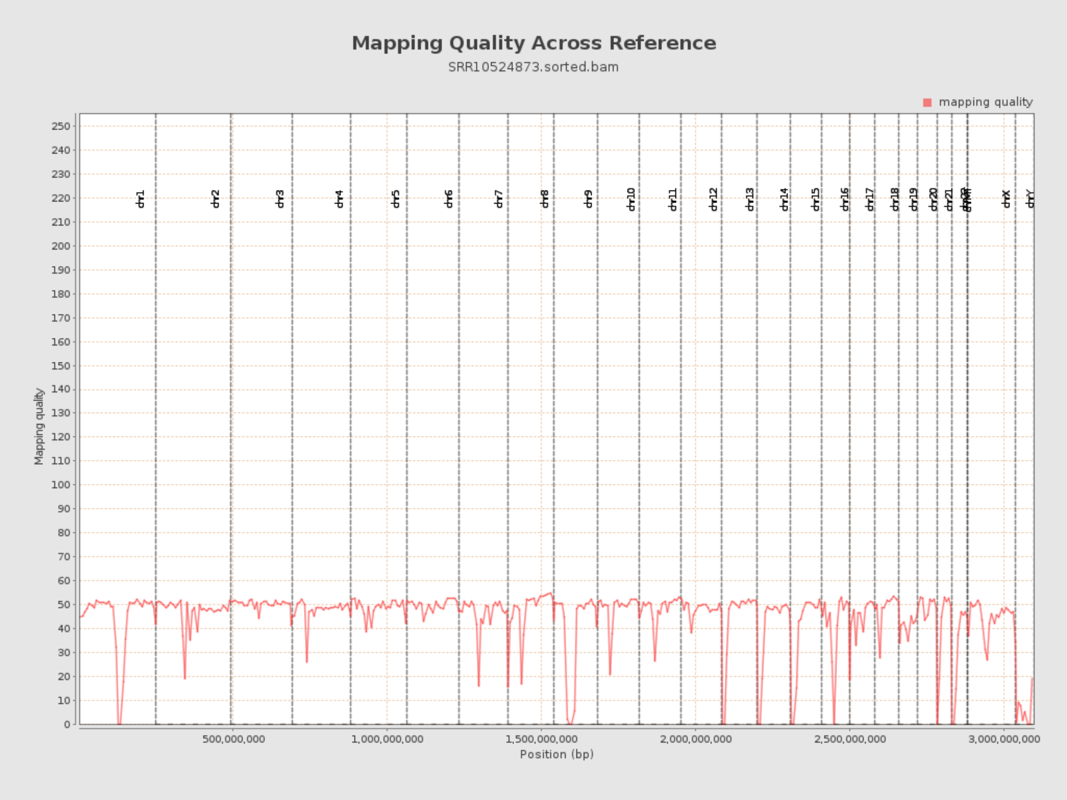
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram