Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:12:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524623.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_SRR10524623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524623.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:12:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,105,460
Mapped reads	1,962,314 / 93.2%
Unmapped reads	143,146 / 6.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,287 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	102,875 / 4.89%
Duplication rate	4.06%
Clipped reads	1,964,460 / 93.3%

2.2. ACGT Content

Number/percentage of A's	29,458,519 / 25.72%
Number/percentage of C's	21,184,384 / 18.49%
Number/percentage of T's	34,911,195 / 30.48%
Number/percentage of G's	28,999,792 / 25.32%
Number/percentage of N's	788 / 0%
GC Percentage	43.81%

2.3. Coverage

Mean	0.037

Standard Deviation	0.3138

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

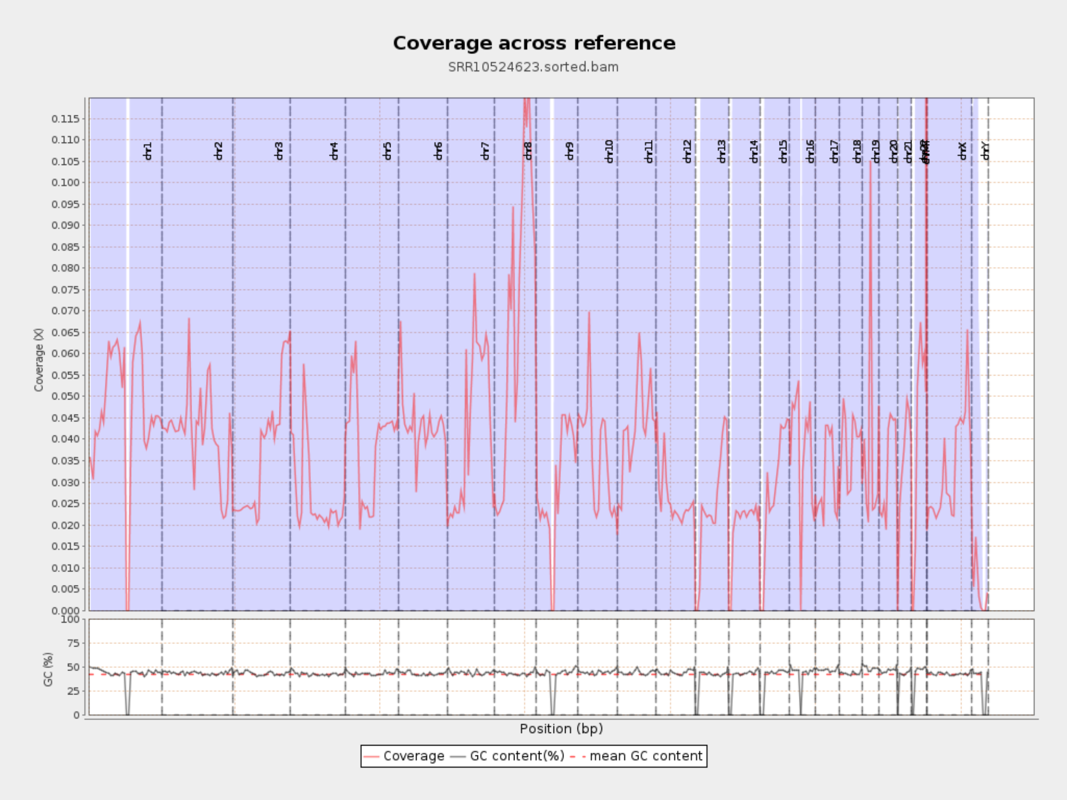
General error rate	0.48%
Mismatches	534,435
Insertions	6,651
Mapped reads with at least one insertion	0.34%
Deletions	21,707
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.53%

2.6. Chromosome stats

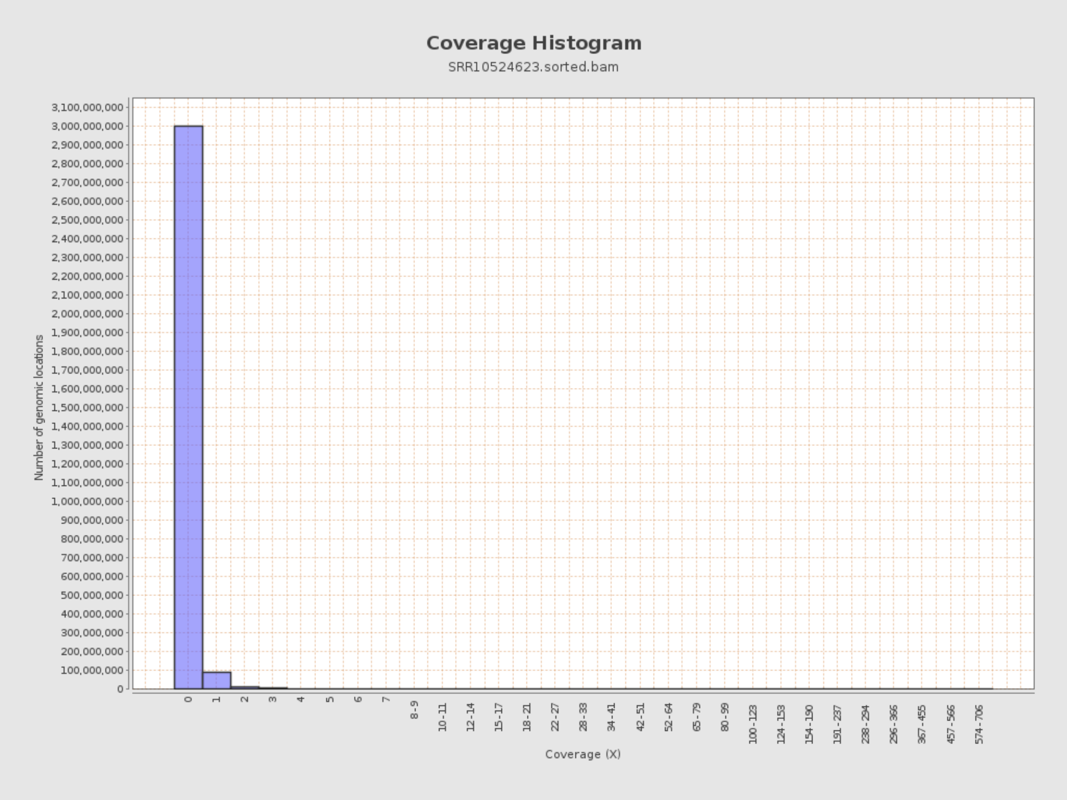
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11747329	0.0471	0.5521
chr2	243199373	10142810	0.0417	0.3655
chr3	198022430	7251384	0.0366	0.2173
chr4	191154276	5109167	0.0267	0.2189
chr5	180915260	7071979	0.0391	0.2243
chr6	171115067	7454526	0.0436	0.2572
chr7	159138663	6915071	0.0435	0.4174

chr8	146364022	10237580	0.0699	0.408
chr9	141213431	4103905	0.0291	0.2758
chr10	135534747	4943388	0.0365	0.3226
chr11	135006516	5795350	0.0429	0.2997
chr12	133851895	3495896	0.0261	0.1907
chr13	115169878	2813459	0.0244	0.1786
chr14	107349540	2104669	0.0196	0.1698
chr15	102531392	2900523	0.0283	0.2022
chr16	90354753	3382626	0.0374	0.2362
chr17	81195210	2520512	0.031	0.2086
chr18	78077248	3059794	0.0392	0.4508
chr19	59128983	2243799	0.0379	0.3989
chr20	63025520	2121425	0.0337	0.2172
chr21	48129895	1660355	0.0345	0.2297
chr22	51304566	2057690	0.0401	0.2281
chrMT	16571	10724	0.6472	0.9377
chrX	155270560	5161769	0.0332	0.2426
chrY	59373566	286518	0.0048	0.1319

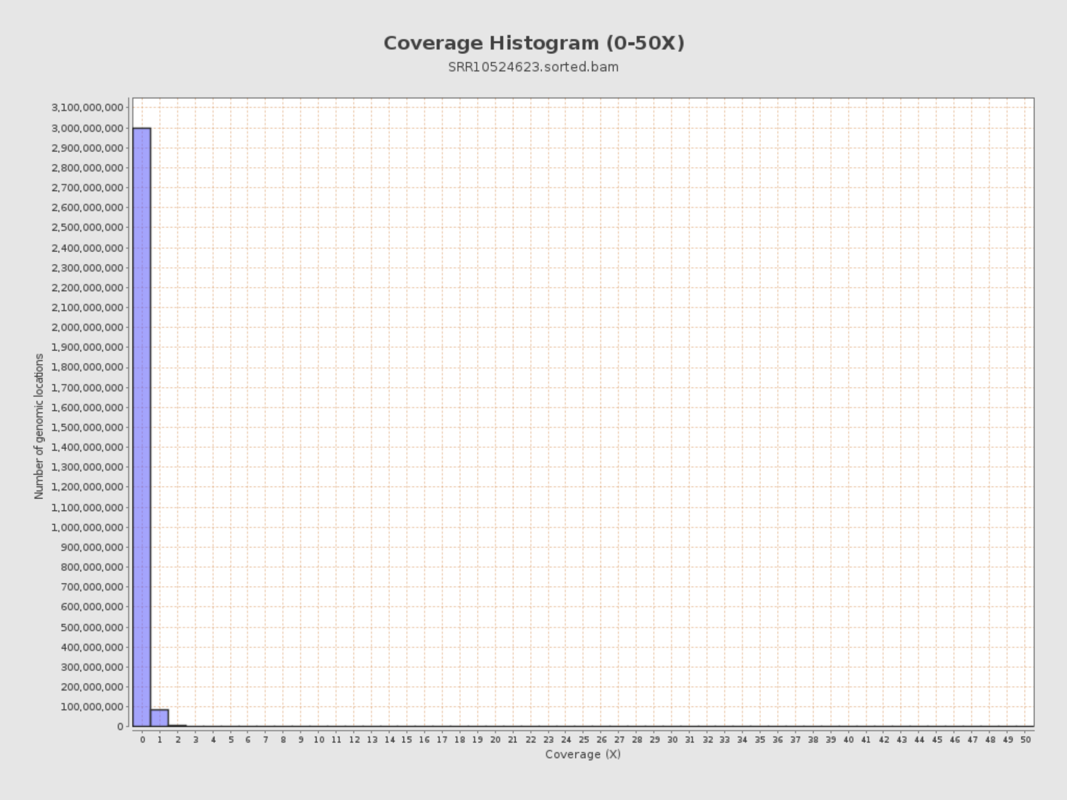
3. Results : Coverage across reference



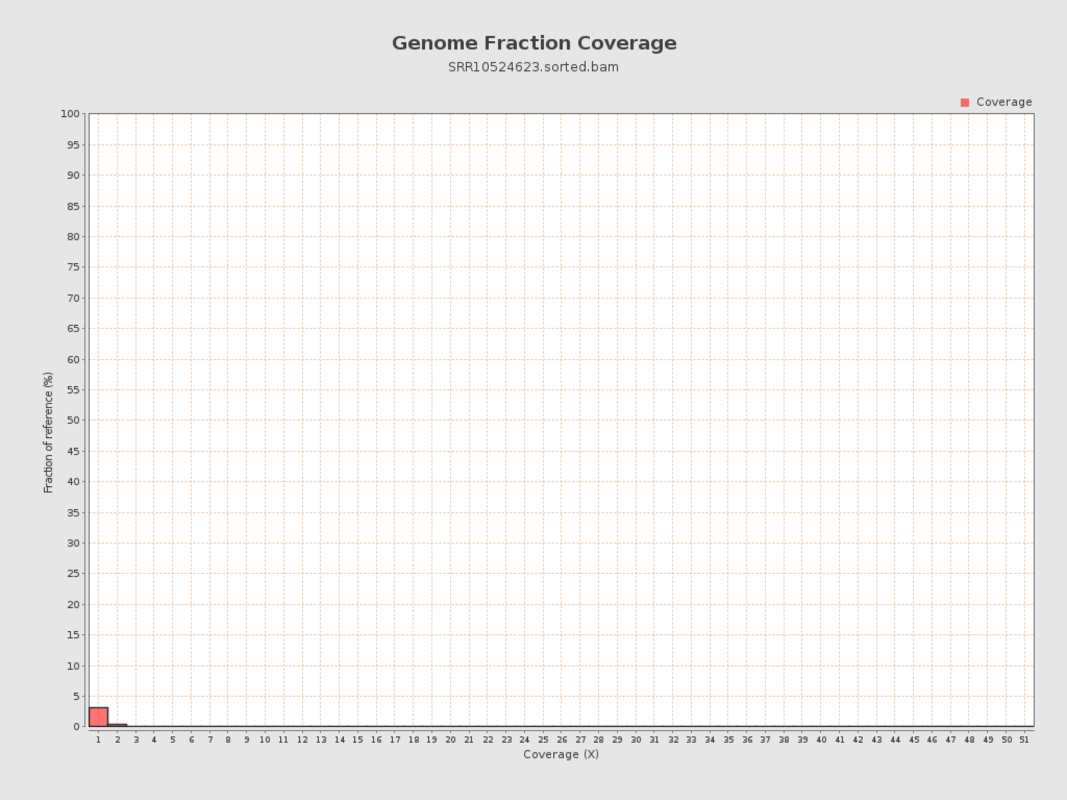
4. Results : Coverage Histogram



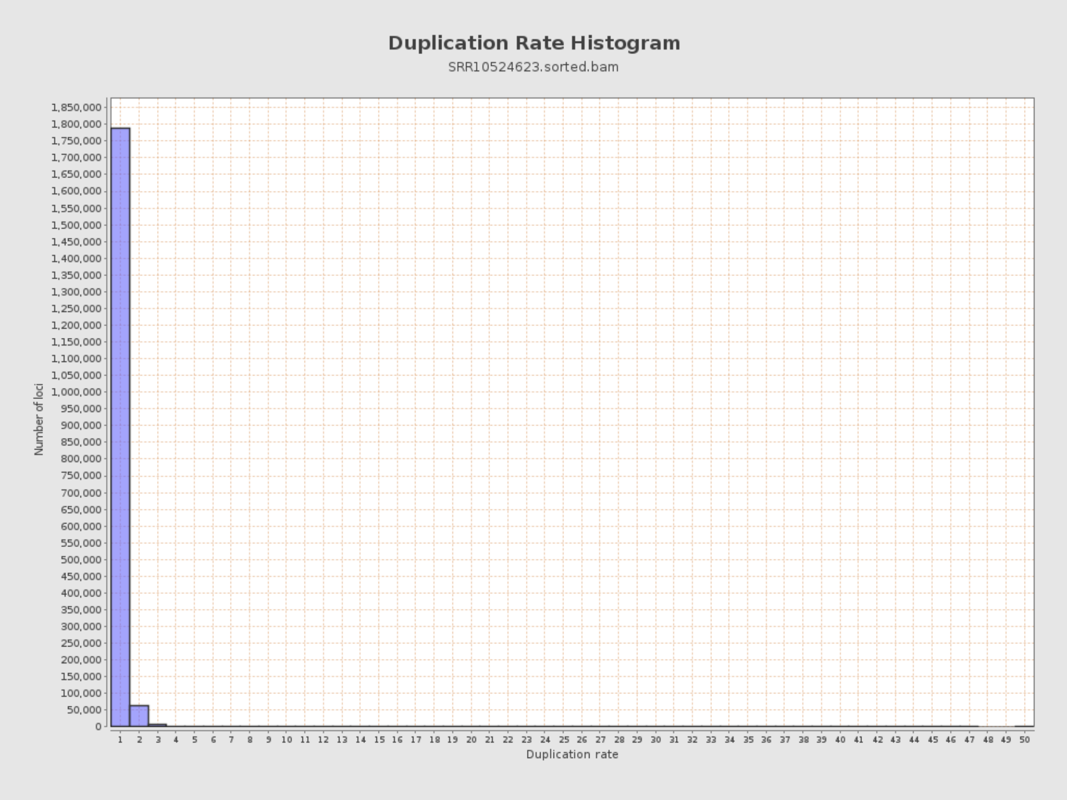
5. Results : Coverage Histogram (0-50X)



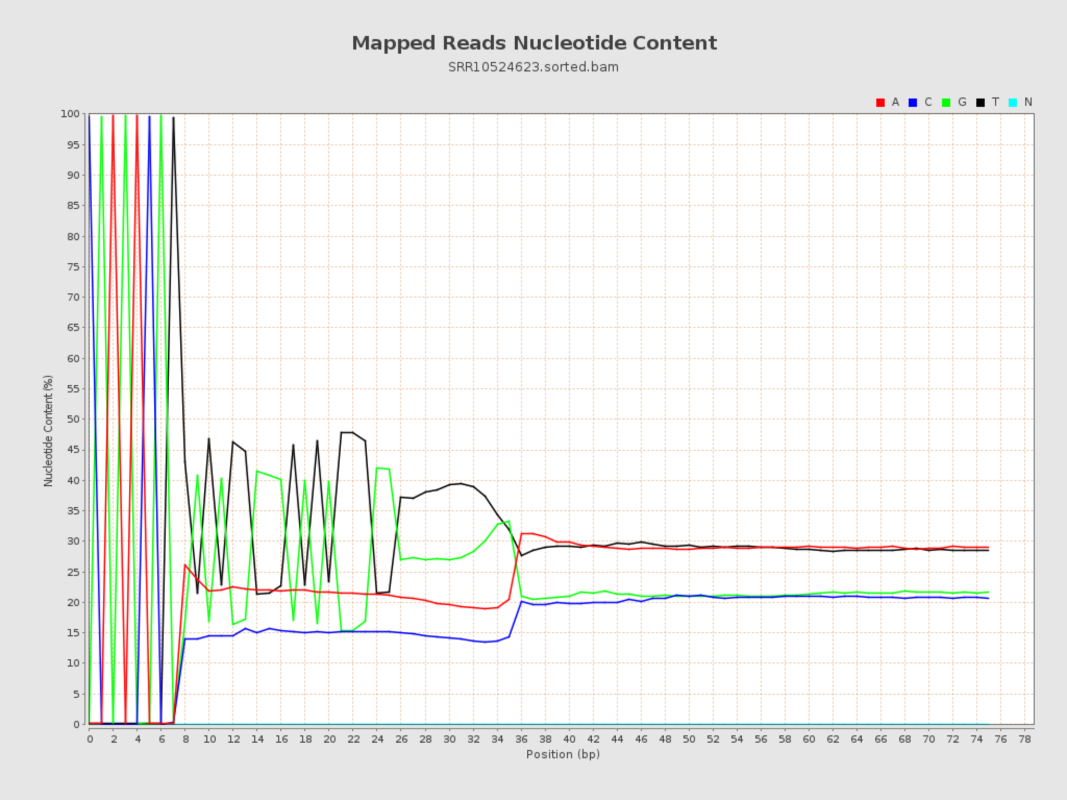
6. Results : Genome Fraction Coverage



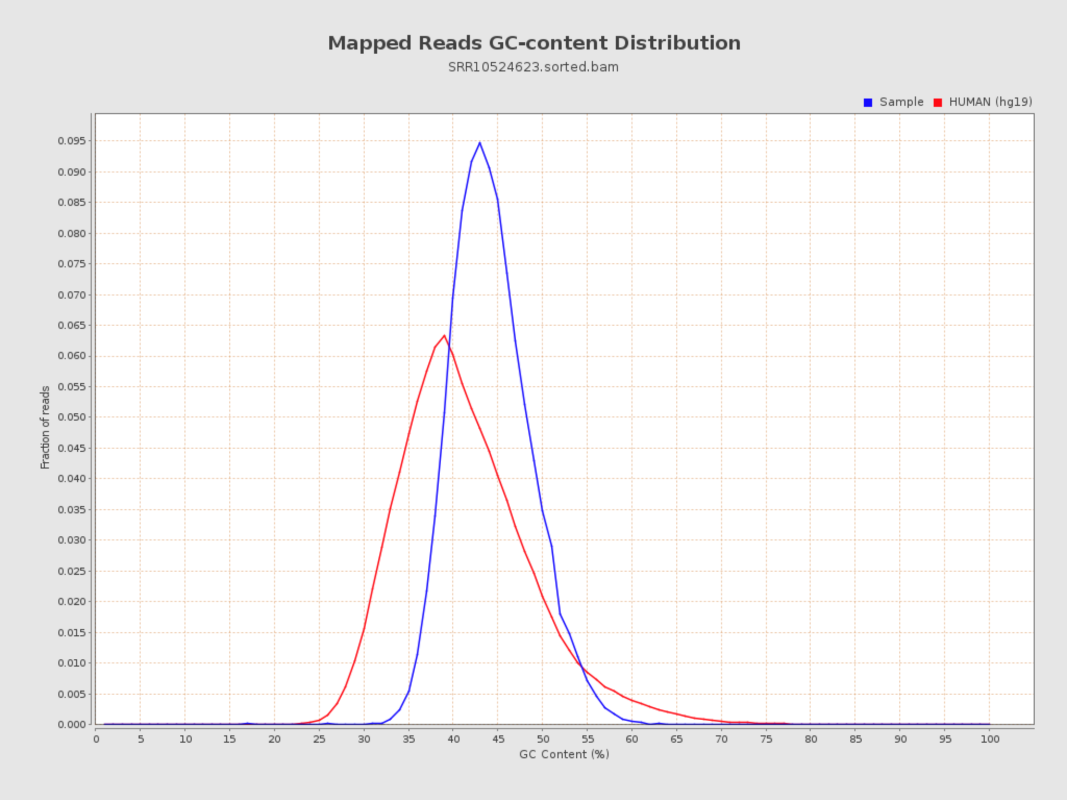
7. Results : Duplication Rate Histogram



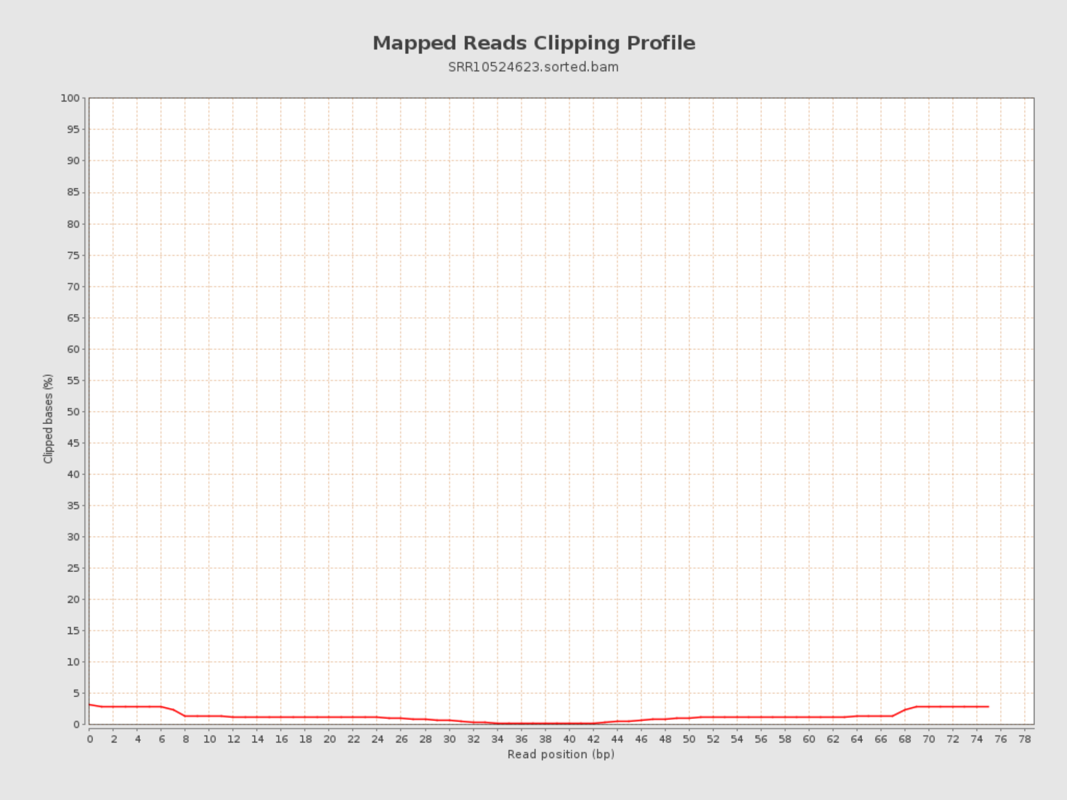
8. Results : Mapped Reads Nucleotide Content



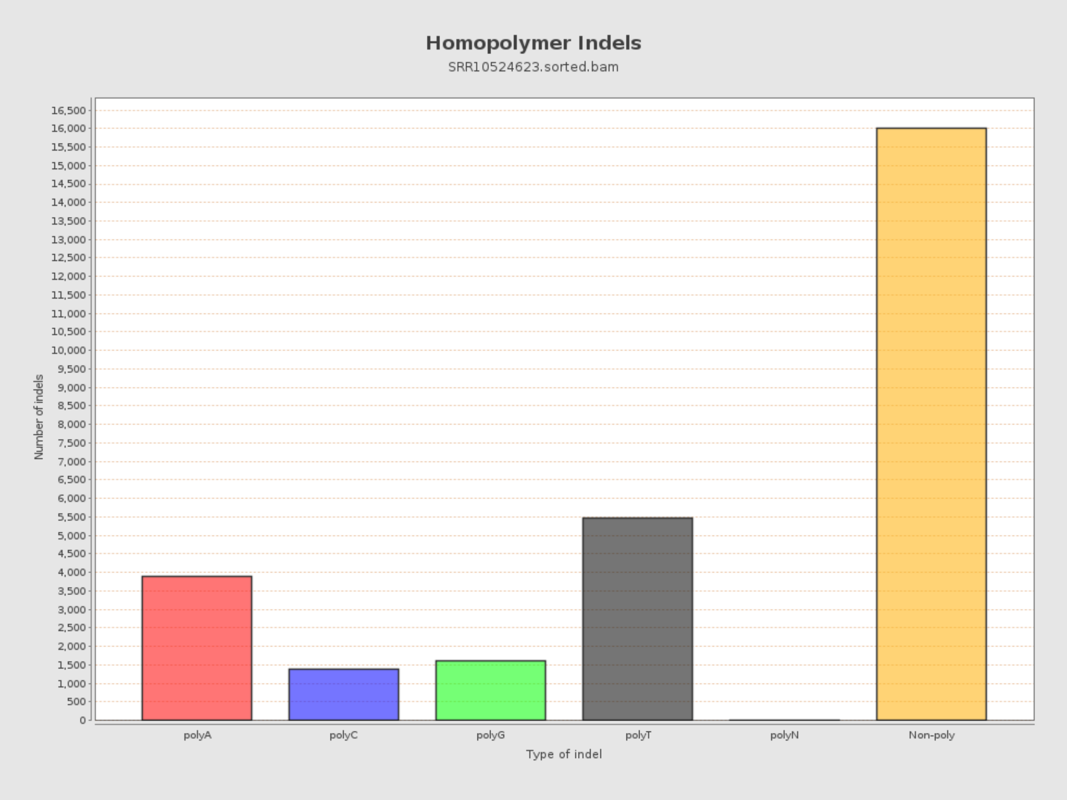
9. Results : Mapped Reads GC-content Distribution



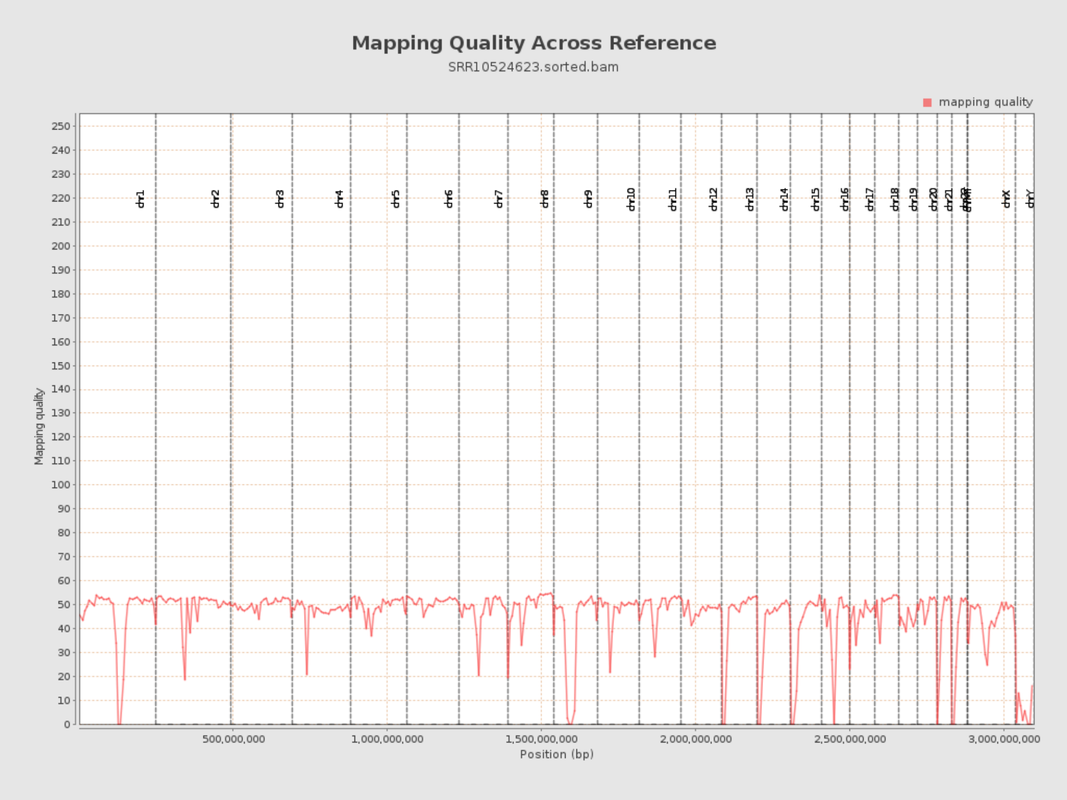
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram