Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:56:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524894.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_SRR10524894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524894.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:56:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,427,178
Mapped reads	2,242,707 / 92.4%
Unmapped reads	184,471 / 7.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,096 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	114,192 / 4.7%
Duplication rate	3.76%
Clipped reads	2,243,421 / 92.43%

2.2. ACGT Content

Number/percentage of A's	31,556,584 / 24.12%
Number/percentage of C's	26,287,304 / 20.09%
Number/percentage of T's	42,251,125 / 32.3%
Number/percentage of G's	30,707,062 / 23.47%
Number/percentage of N's	17,275 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.404

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

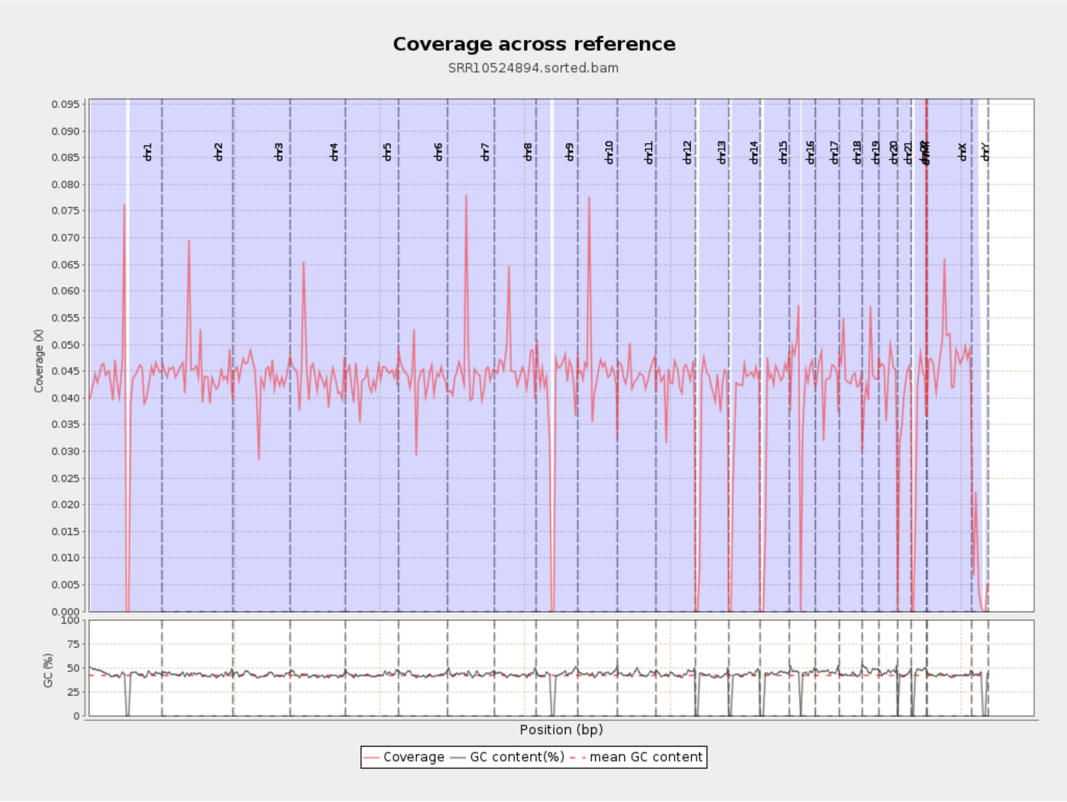
General error rate	0.5%
Mismatches	644,119
Insertions	9,303
Mapped reads with at least one insertion	0.41%
Deletions	24,868
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.65%

2.6. Chromosome stats

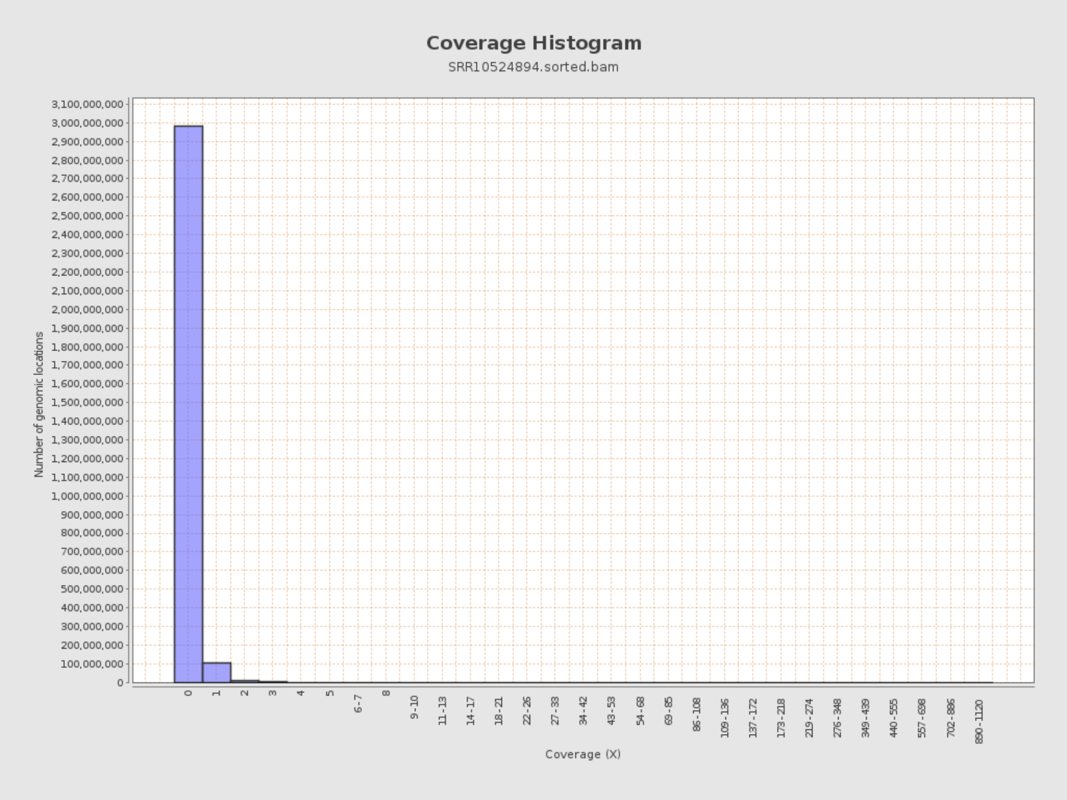
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10472676	0.042	0.8371
chr2	243199373	11037442	0.0454	0.4253
chr3	198022430	8716226	0.044	0.2339
chr4	191154276	8458008	0.0442	0.2639
chr5	180915260	7880822	0.0436	0.2361
chr6	171115067	7508956	0.0439	0.2628
chr7	159138663	7196987	0.0452	0.5535

chr8	146364022	6780815	0.0463	0.385
chr9	141213431	5525744	0.0391	0.3519
chr10	135534747	6250798	0.0461	0.3697
chr11	135006516	6006684	0.0445	0.3659
chr12	133851895	5833200	0.0436	0.2431
chr13	115169878	4145702	0.036	0.2125
chr14	107349540	3972311	0.037	0.2319
chr15	102531392	3708518	0.0362	0.2125
chr16	90354753	3793636	0.042	0.2549
chr17	81195210	3518249	0.0433	0.2604
chr18	78077248	3515174	0.045	0.7144
chr19	59128983	2585161	0.0437	0.5503
chr20	63025520	2794067	0.0443	0.242
chr21	48129895	1735204	0.0361	0.2416
chr22	51304566	1584754	0.0309	0.1961
chrMT	16571	33849	2.0427	1.786
chrX	155270560	7417116	0.0478	0.2916
chrY	59373566	386430	0.0065	0.1615

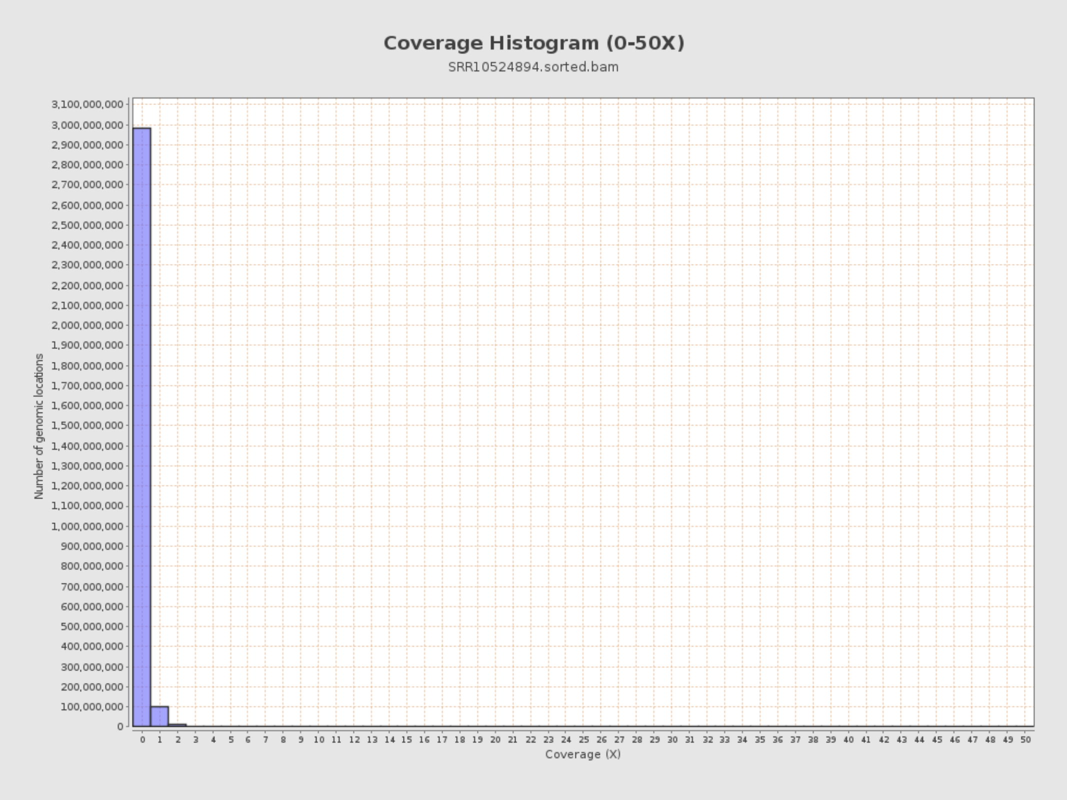
3. Results : Coverage across reference



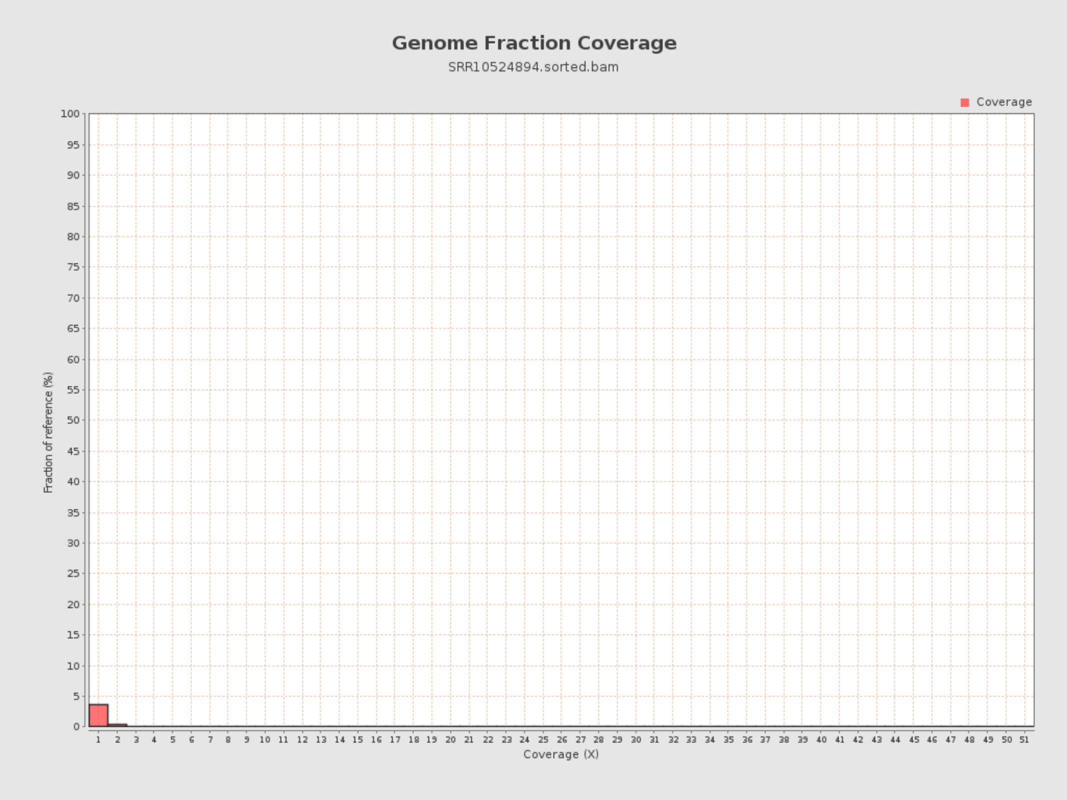
4. Results : Coverage Histogram



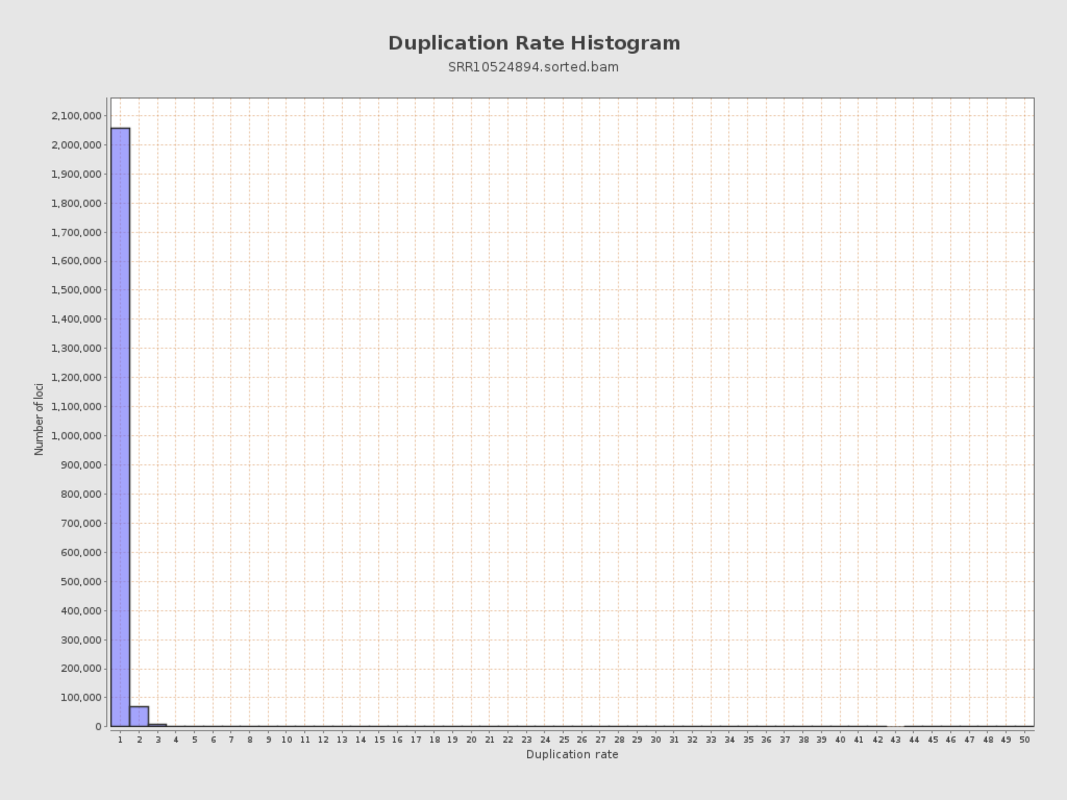
5. Results : Coverage Histogram (0-50X)



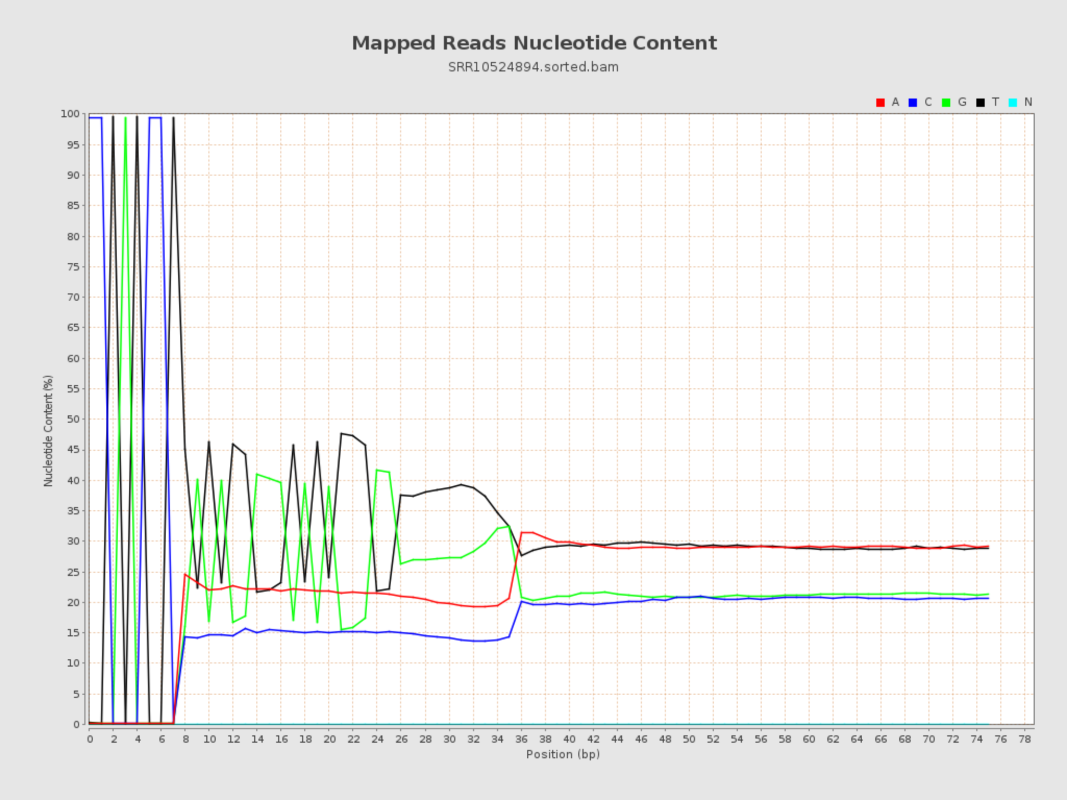
6. Results : Genome Fraction Coverage



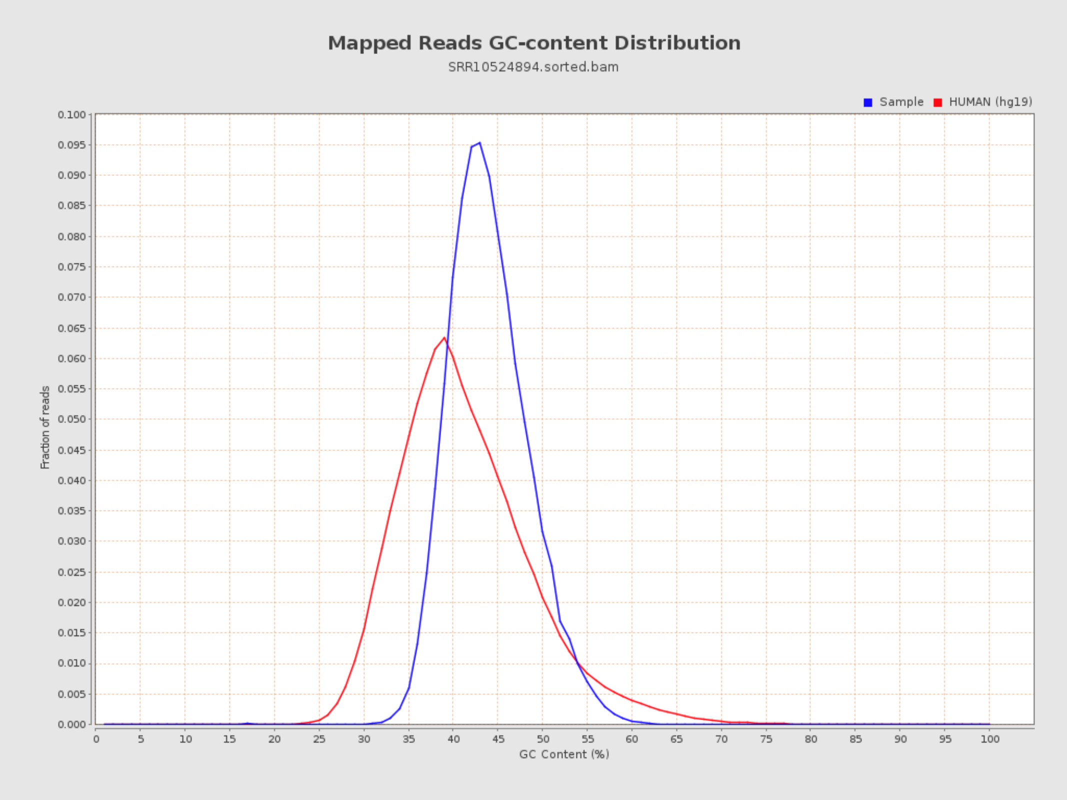
7. Results : Duplication Rate Histogram



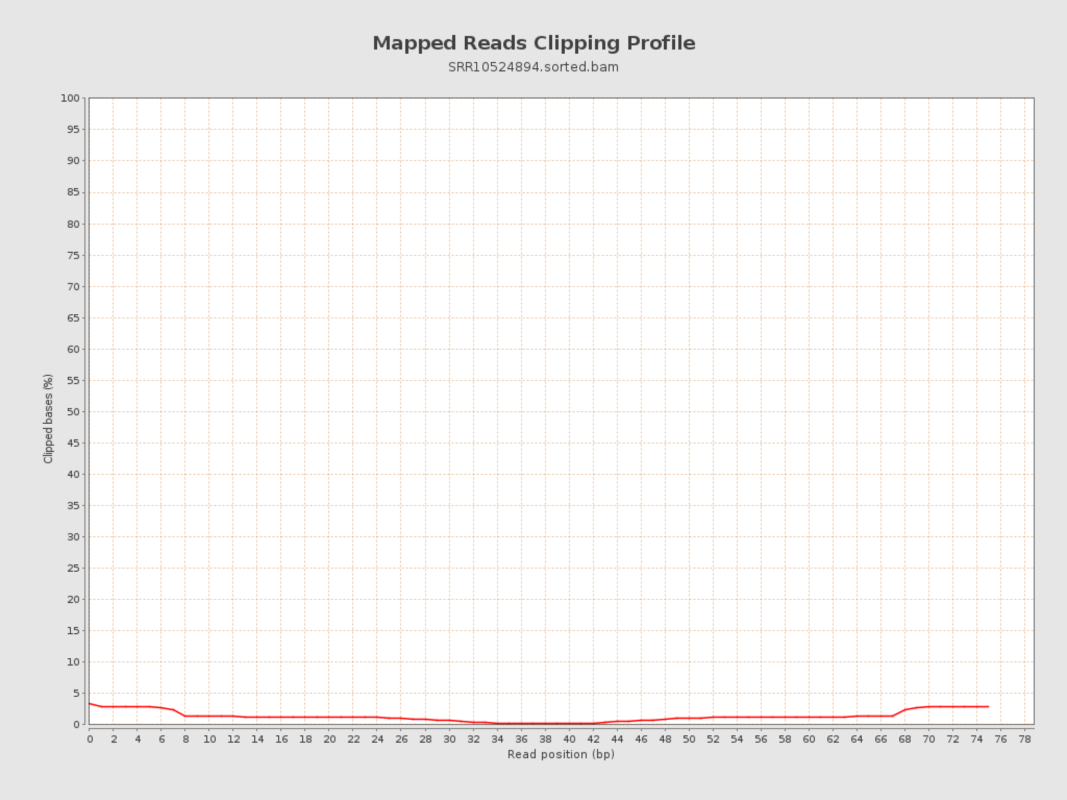
8. Results : Mapped Reads Nucleotide Content



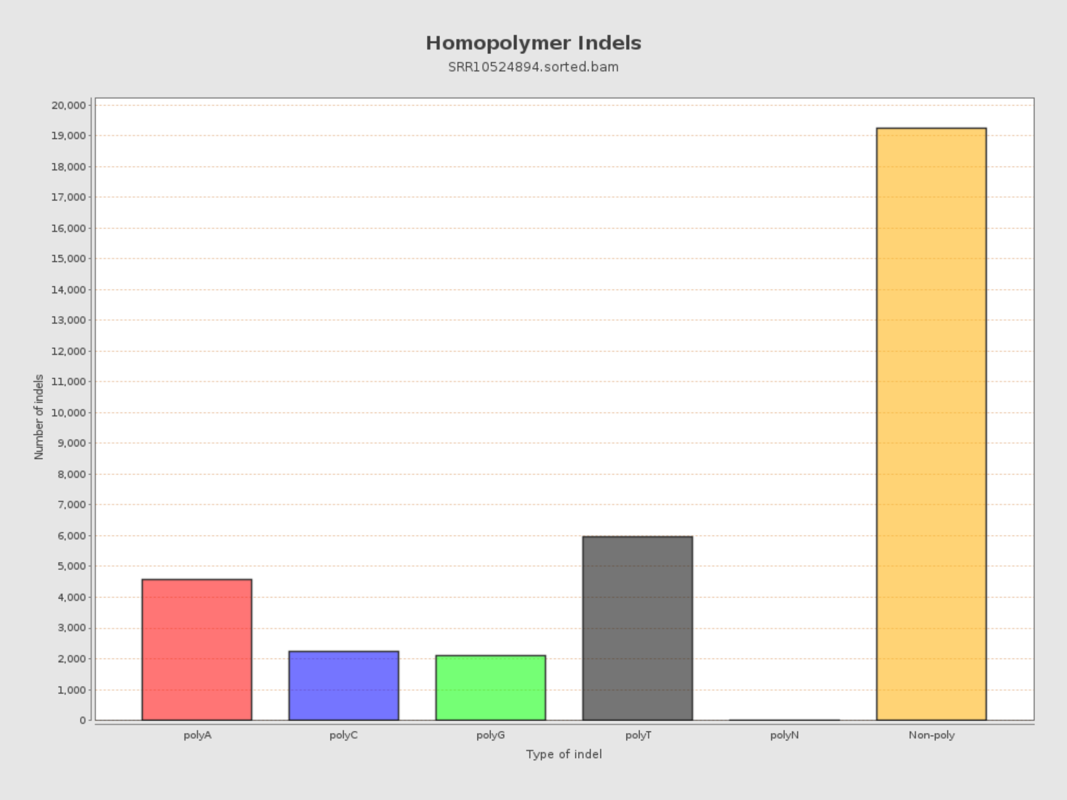
9. Results : Mapped Reads GC-content Distribution



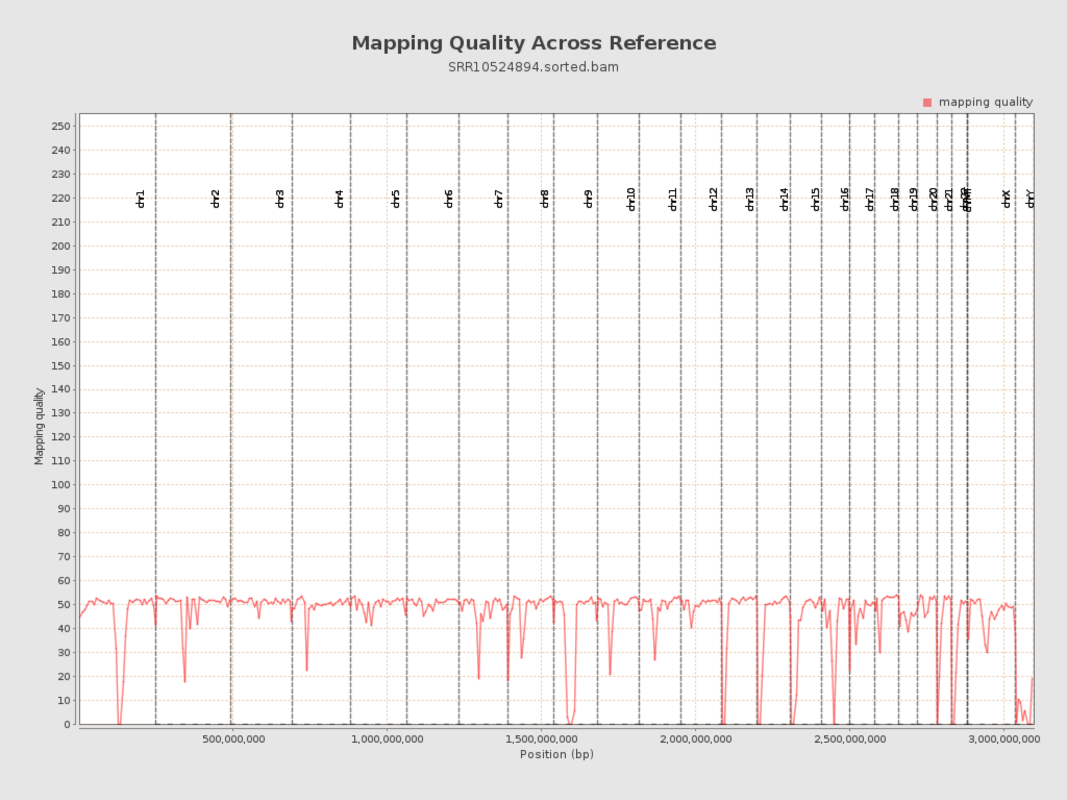
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram