Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:04:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524489.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_SRR10524489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524489.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:04:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524489.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,472
Mapped reads	2,039,234 / 91.55%
Unmapped reads	188,238 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,798 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	77,514 / 3.48%
Duplication rate	2.72%
Clipped reads	2,041,849 / 91.67%

2.2. ACGT Content

Number/percentage of A's	28,105,007 / 24%
Number/percentage of C's	21,748,419 / 18.57%
Number/percentage of T's	37,646,888 / 32.14%
Number/percentage of G's	29,617,166 / 25.29%
Number/percentage of N's	3,462 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3284

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

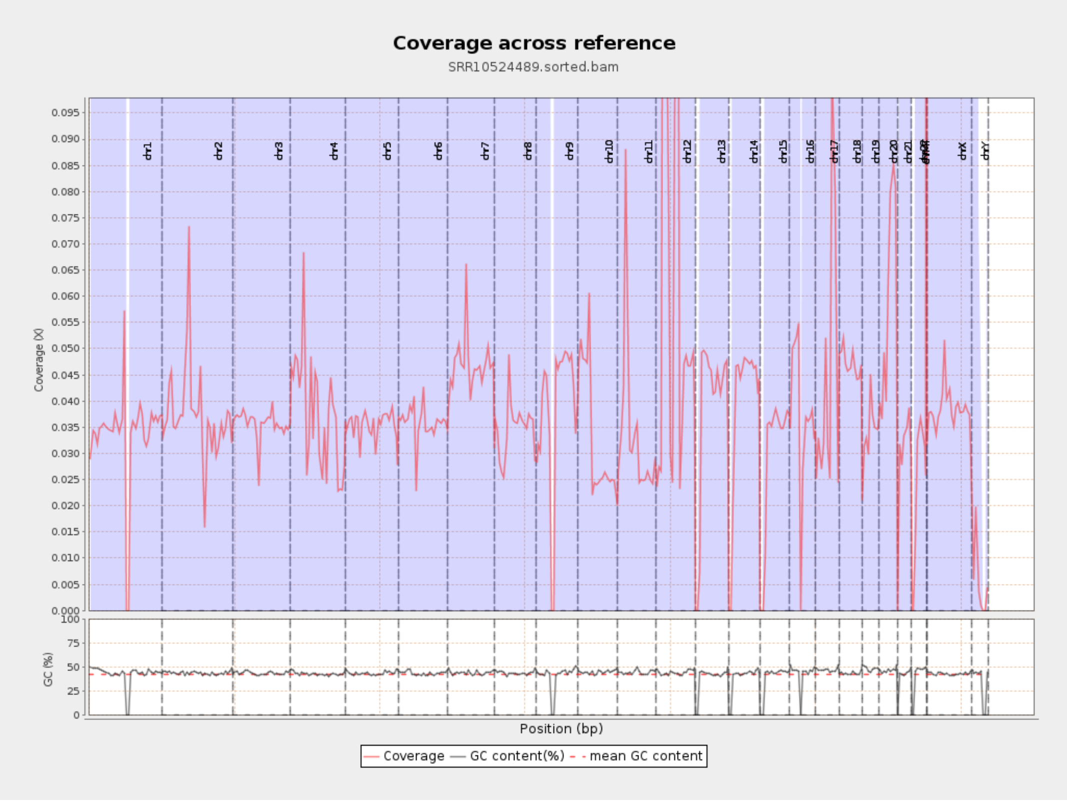
General error rate	0.49%
Mismatches	557,945
Insertions	7,451
Mapped reads with at least one insertion	0.36%
Deletions	19,011
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.22%

2.6. Chromosome stats

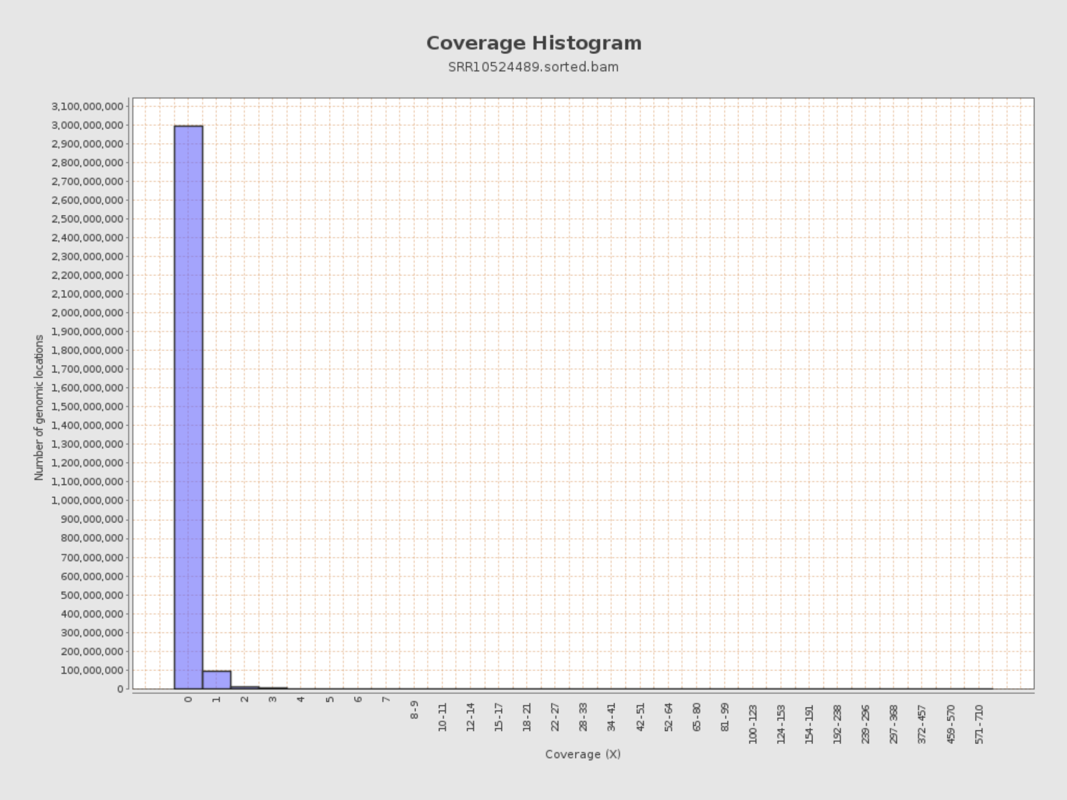
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8374200	0.0336	0.5715
chr2	243199373	9141783	0.0376	0.3559
chr3	198022430	7062000	0.0357	0.2067
chr4	191154276	7205620	0.0377	0.2487
chr5	180915260	6416212	0.0355	0.2107
chr6	171115067	6147650	0.0359	0.233
chr7	159138663	7492191	0.0471	0.4435

chr8	146364022	5117706	0.035	0.3012
chr9	141213431	5400247	0.0382	0.3499
chr10	135534747	4509071	0.0333	0.3202
chr11	135006516	4571862	0.0339	0.2813
chr12	133851895	8743322	0.0653	0.3237
chr13	115169878	4376805	0.038	0.2143
chr14	107349540	4149022	0.0386	0.2324
chr15	102531392	2996834	0.0292	0.1879
chr16	90354753	3404308	0.0377	0.2331
chr17	81195210	3561215	0.0439	0.2407
chr18	78077248	3695054	0.0473	0.5999
chr19	59128983	2042023	0.0345	0.415
chr20	63025520	3771623	0.0598	0.2806
chr21	48129895	1433770	0.0298	0.2259
chr22	51304566	1200031	0.0234	0.1673
chrMT	16571	13427	0.8103	1.0014
chrX	155270560	5979549	0.0385	0.2604
chrY	59373566	347179	0.0058	0.1488

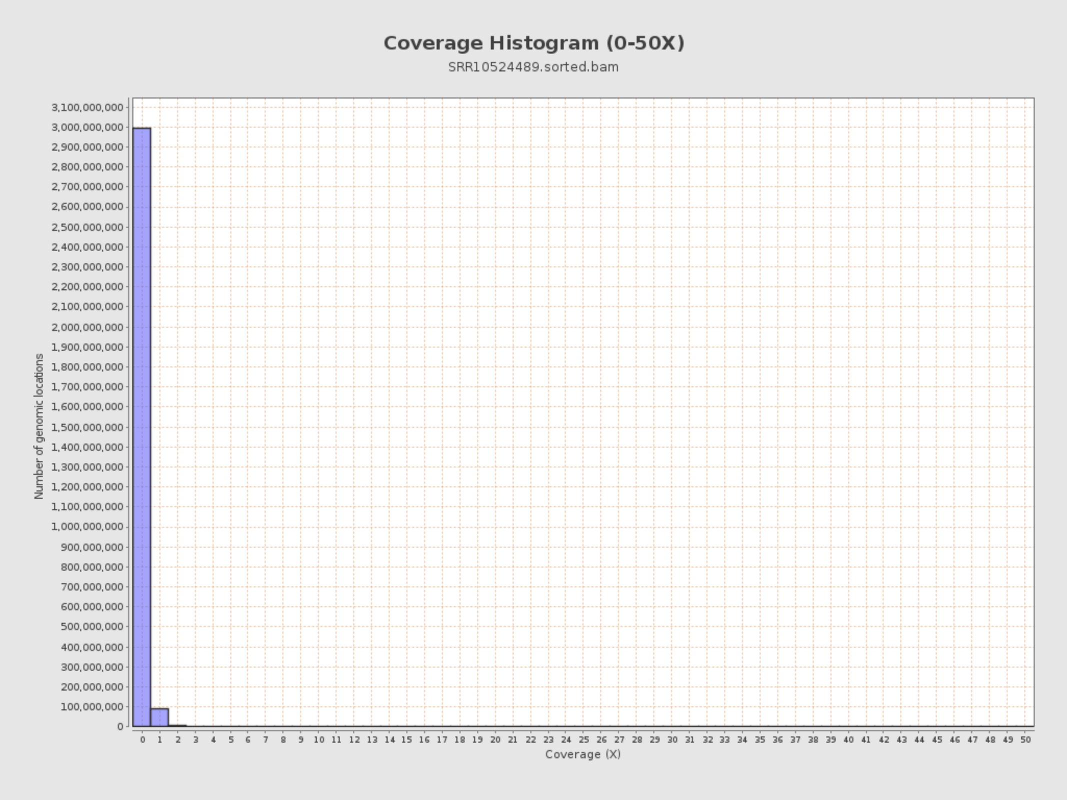
3. Results : Coverage across reference



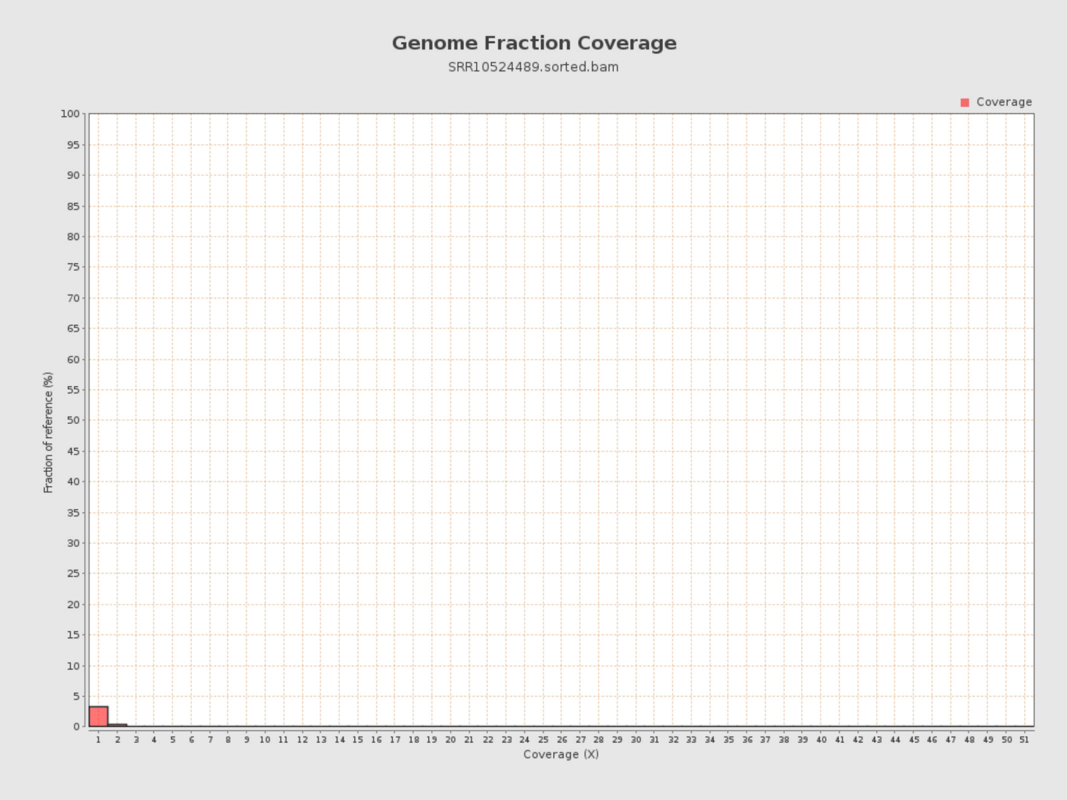
4. Results : Coverage Histogram



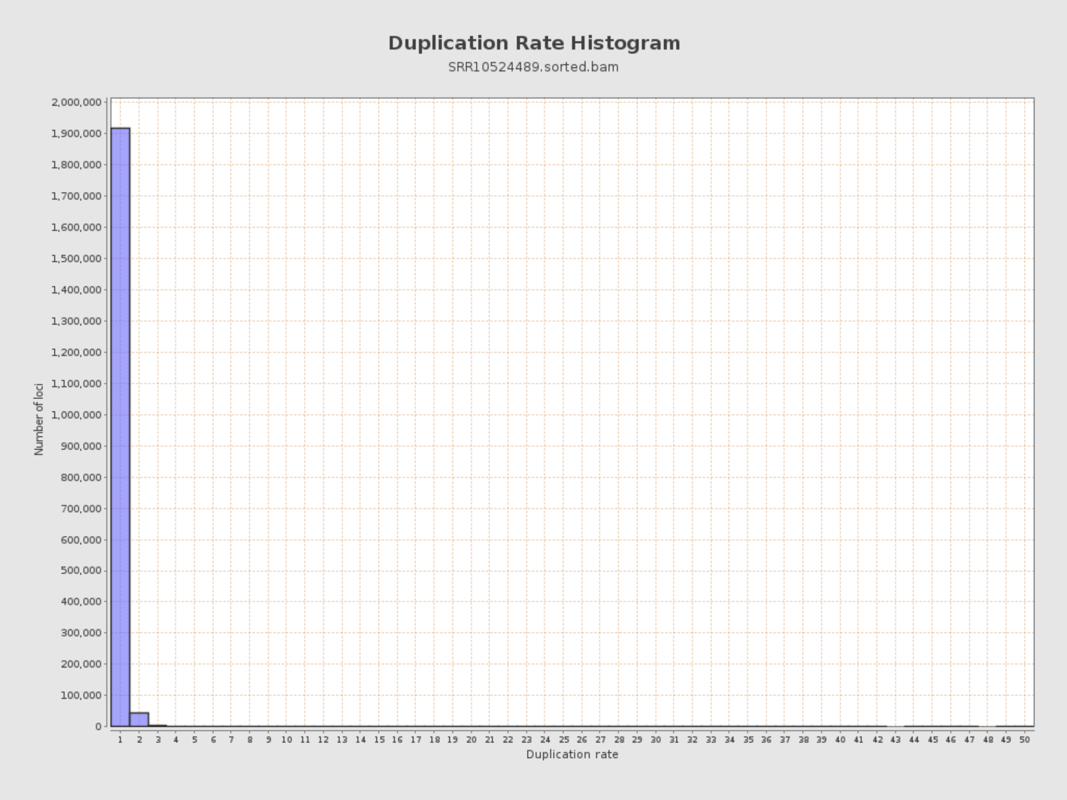
5. Results : Coverage Histogram (0-50X)



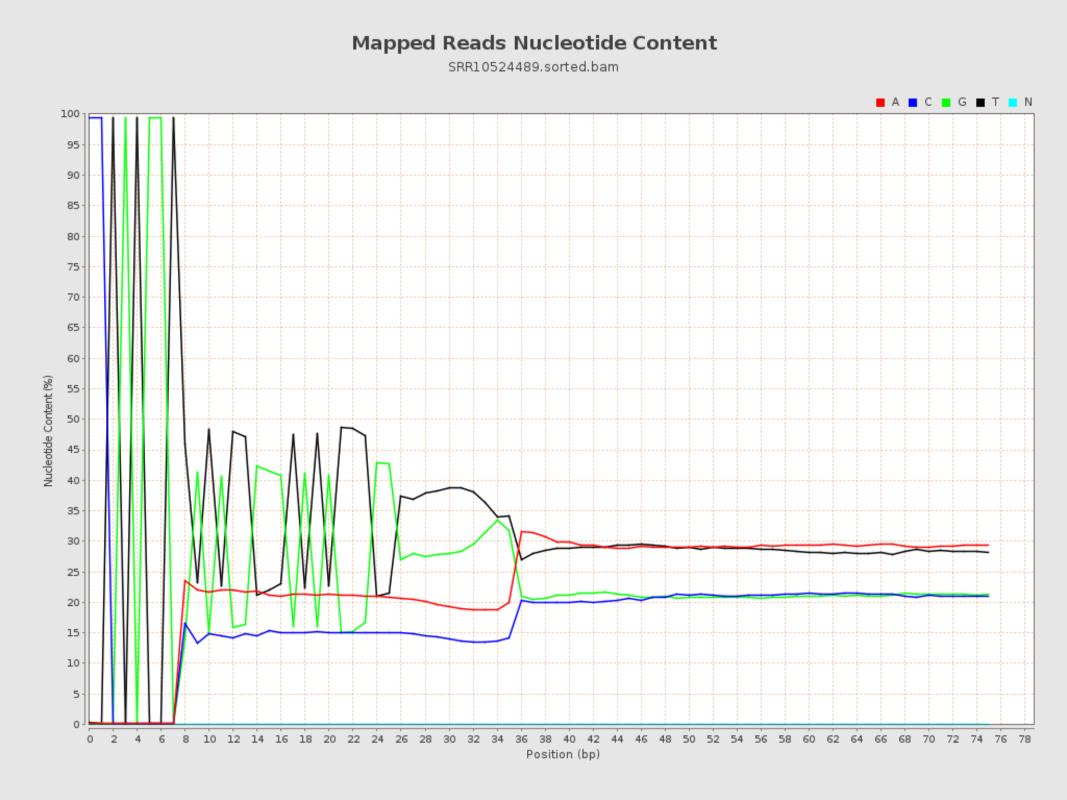
6. Results : Genome Fraction Coverage



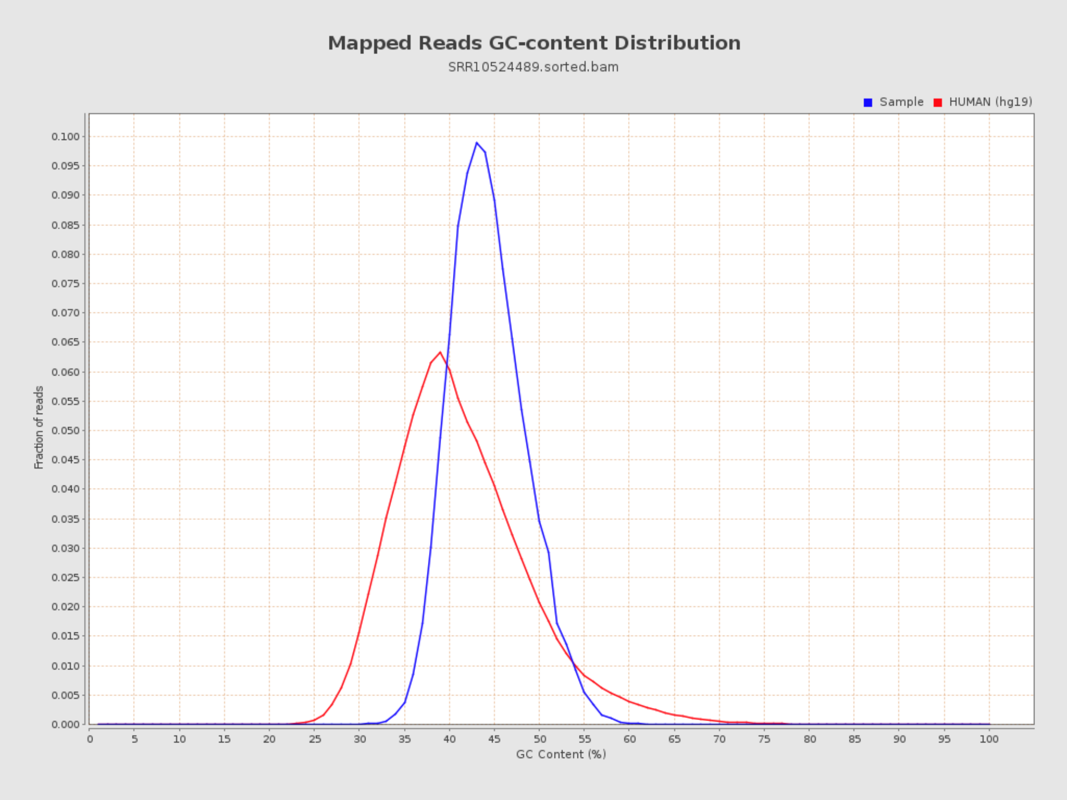
7. Results : Duplication Rate Histogram



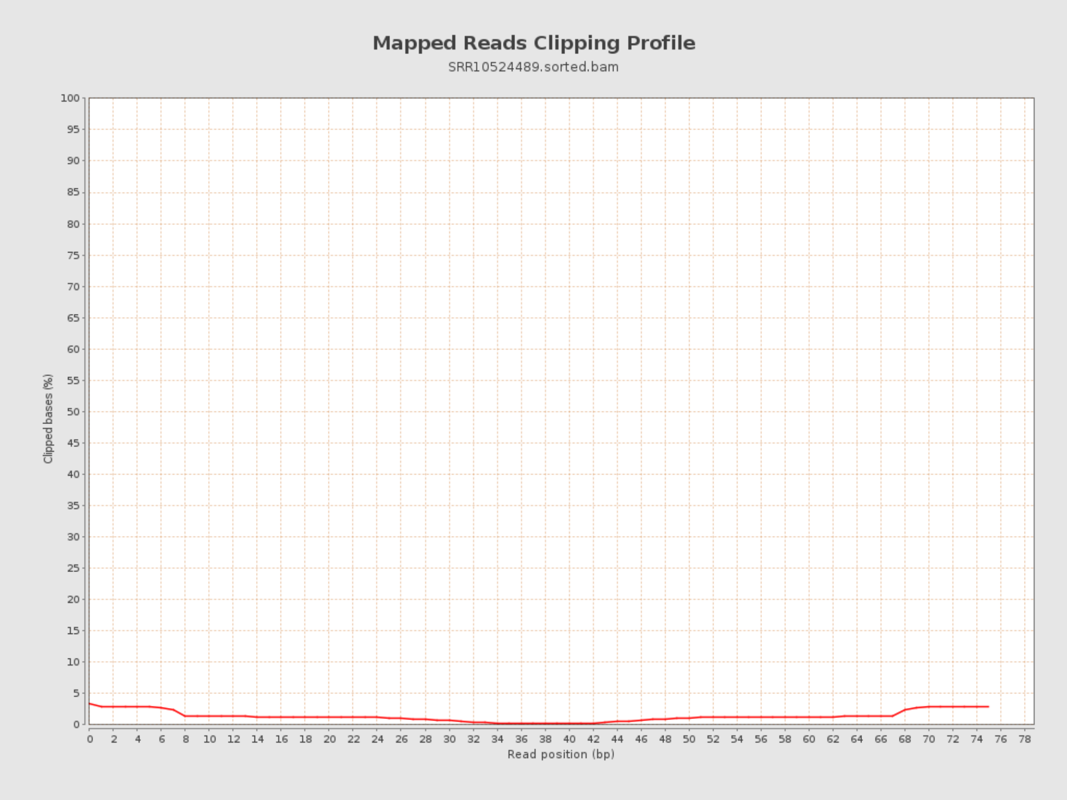
8. Results : Mapped Reads Nucleotide Content



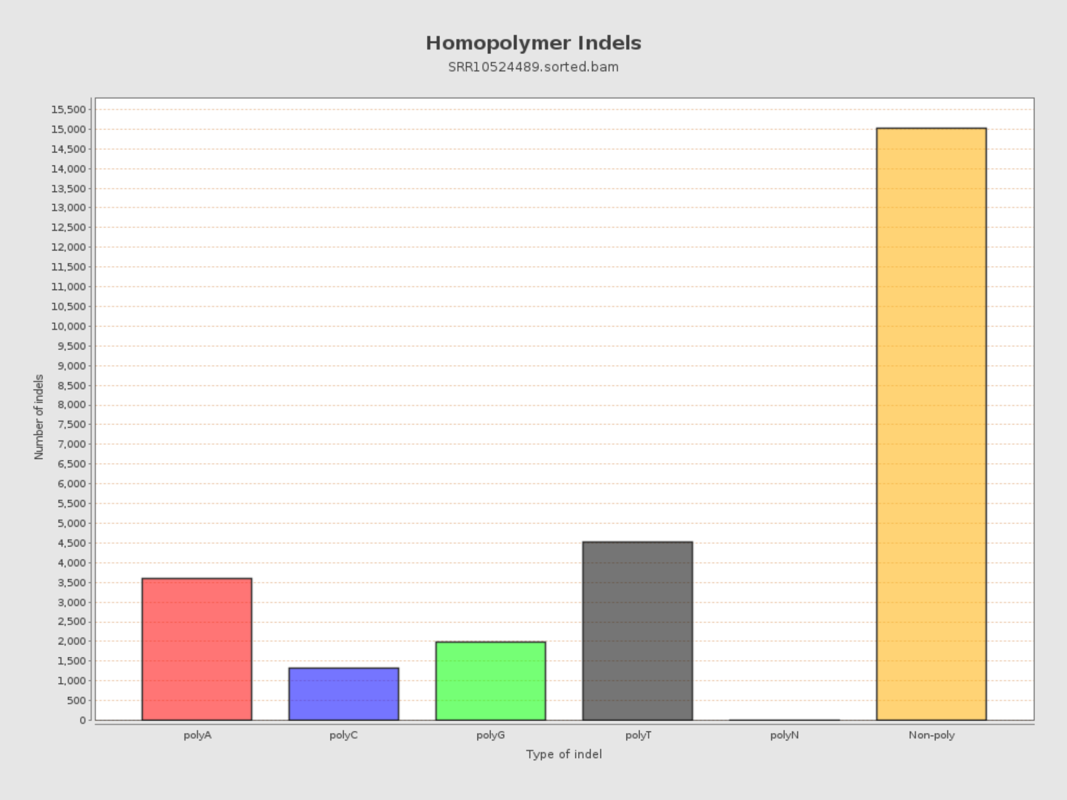
9. Results : Mapped Reads GC-content Distribution



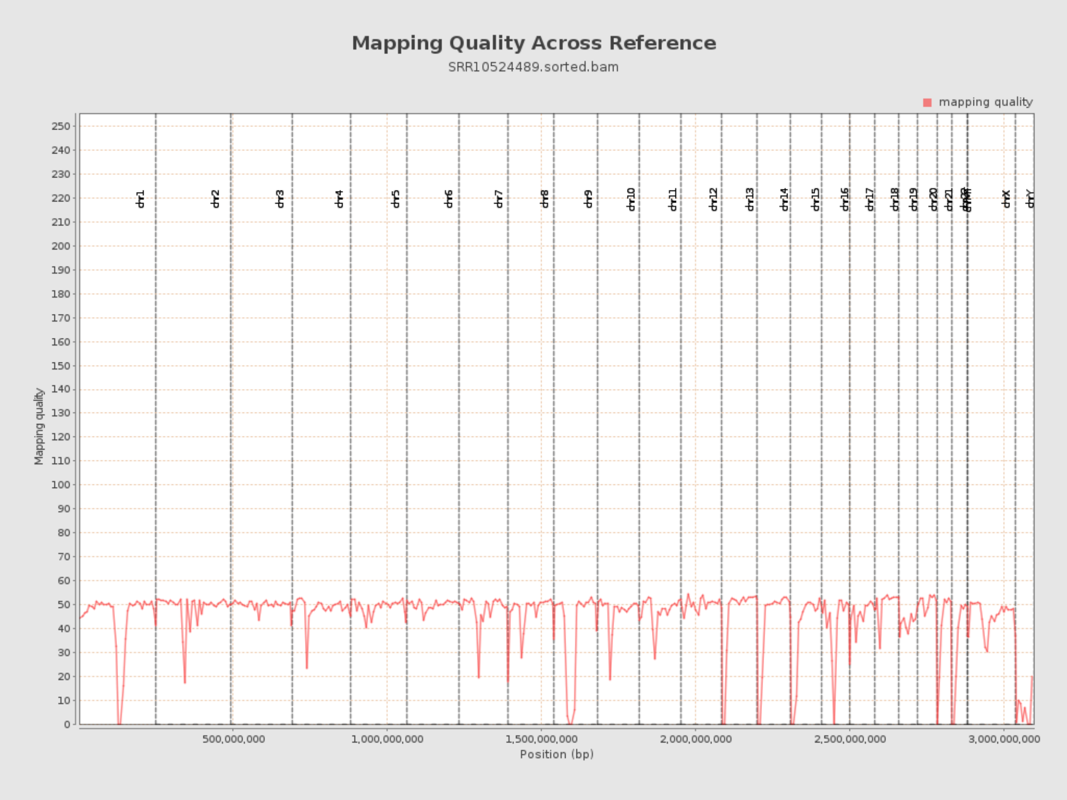
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram