Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:07:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524593.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_SRR10524593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524593.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:07:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,285,006
Mapped reads	2,123,321 / 92.92%
Unmapped reads	161,685 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,726 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	125,312 / 5.48%
Duplication rate	4.54%
Clipped reads	2,121,431 / 92.84%

2.2. ACGT Content

Number/percentage of A's	32,738,738 / 26.46%
Number/percentage of C's	22,781,706 / 18.41%
Number/percentage of T's	37,926,411 / 30.65%
Number/percentage of G's	30,273,988 / 24.47%
Number/percentage of N's	904 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.04

Standard Deviation	0.346

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

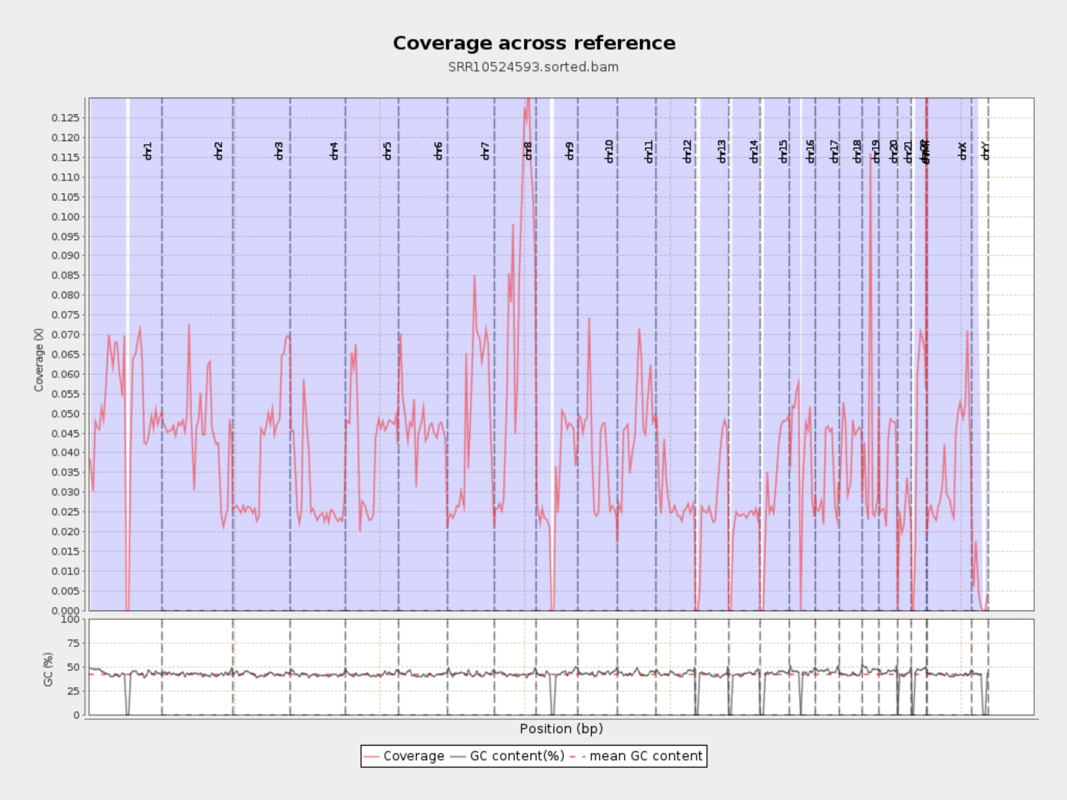
General error rate	0.49%
Mismatches	590,926
Insertions	9,335
Mapped reads with at least one insertion	0.44%
Deletions	23,171
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.95%

2.6. Chromosome stats

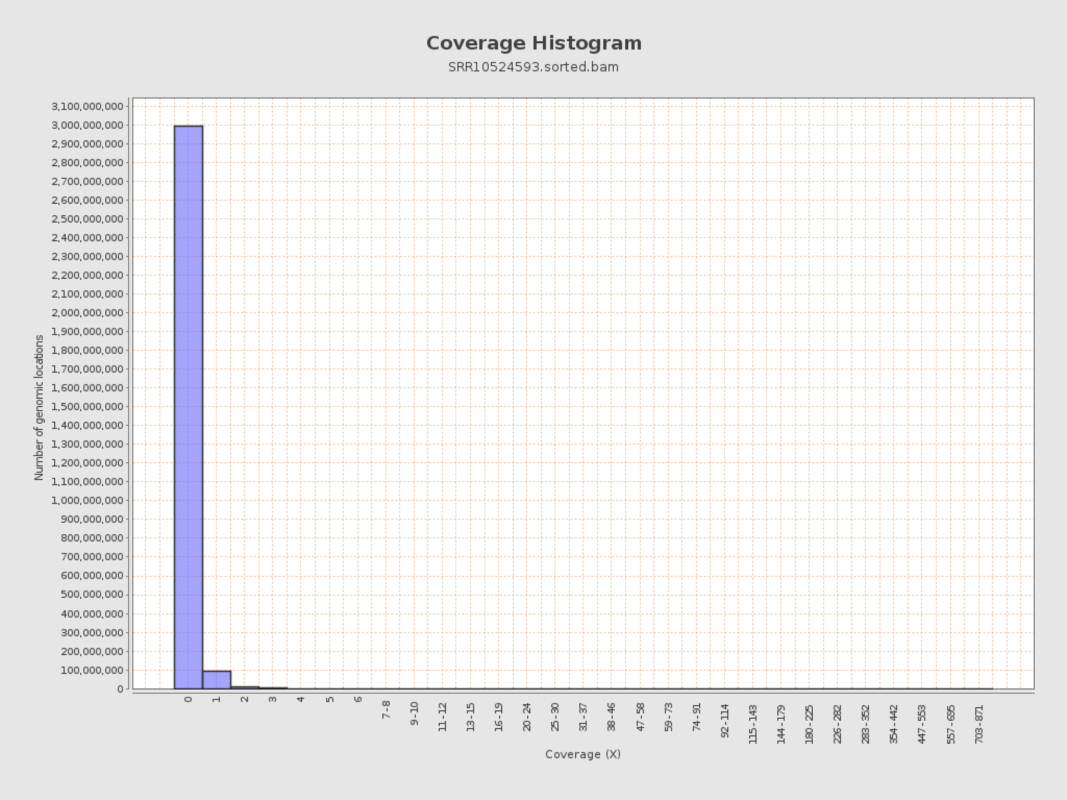
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12695108	0.0509	0.6393
chr2	243199373	10942036	0.045	0.4077
chr3	198022430	7927595	0.04	0.2326
chr4	191154276	5582893	0.0292	0.2335
chr5	180915260	7712335	0.0426	0.2379
chr6	171115067	8087323	0.0473	0.2744
chr7	159138663	7571905	0.0476	0.4521

chr8	146364022	11087843	0.0758	0.4583
chr9	141213431	4421923	0.0313	0.3061
chr10	135534747	5328432	0.0393	0.3402
chr11	135006516	6327976	0.0469	0.3209
chr12	133851895	3814283	0.0285	0.2026
chr13	115169878	3092449	0.0269	0.1928
chr14	107349540	2258472	0.021	0.1759
chr15	102531392	3195100	0.0312	0.2109
chr16	90354753	3643519	0.0403	0.248
chr17	81195210	2708590	0.0334	0.2199
chr18	78077248	3327983	0.0426	0.5086
chr19	59128983	2401987	0.0406	0.4279
chr20	63025520	2280164	0.0362	0.2213
chr21	48129895	1098238	0.0228	0.1994
chr22	51304566	2296982	0.0448	0.2451
chrMT	16571	6652	0.4014	0.6751
chrX	155270560	5651793	0.0364	0.2555
chrY	59373566	299644	0.005	0.1397

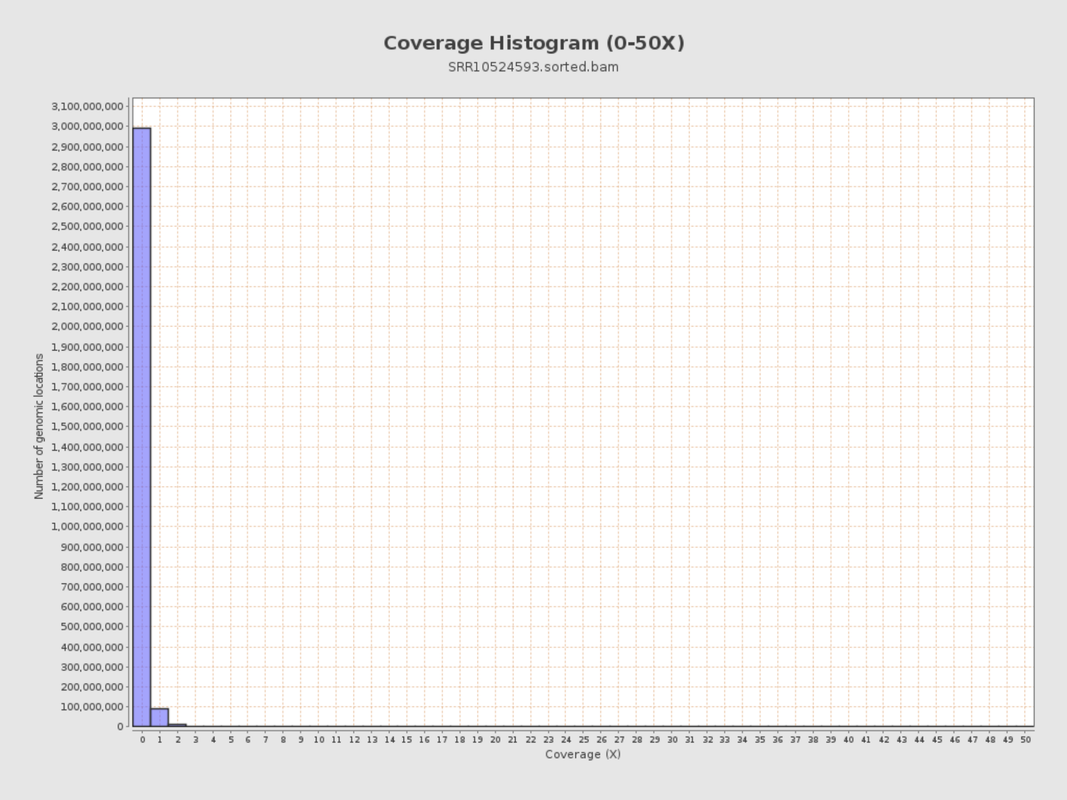
3. Results : Coverage across reference



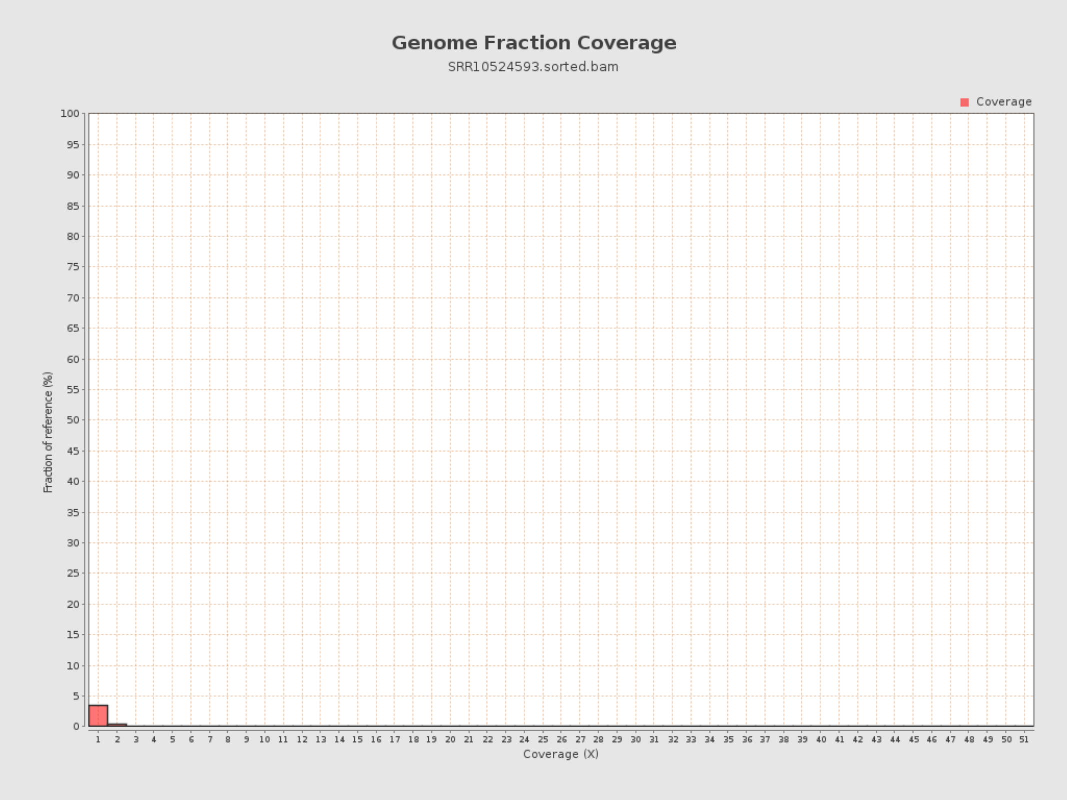
4. Results : Coverage Histogram



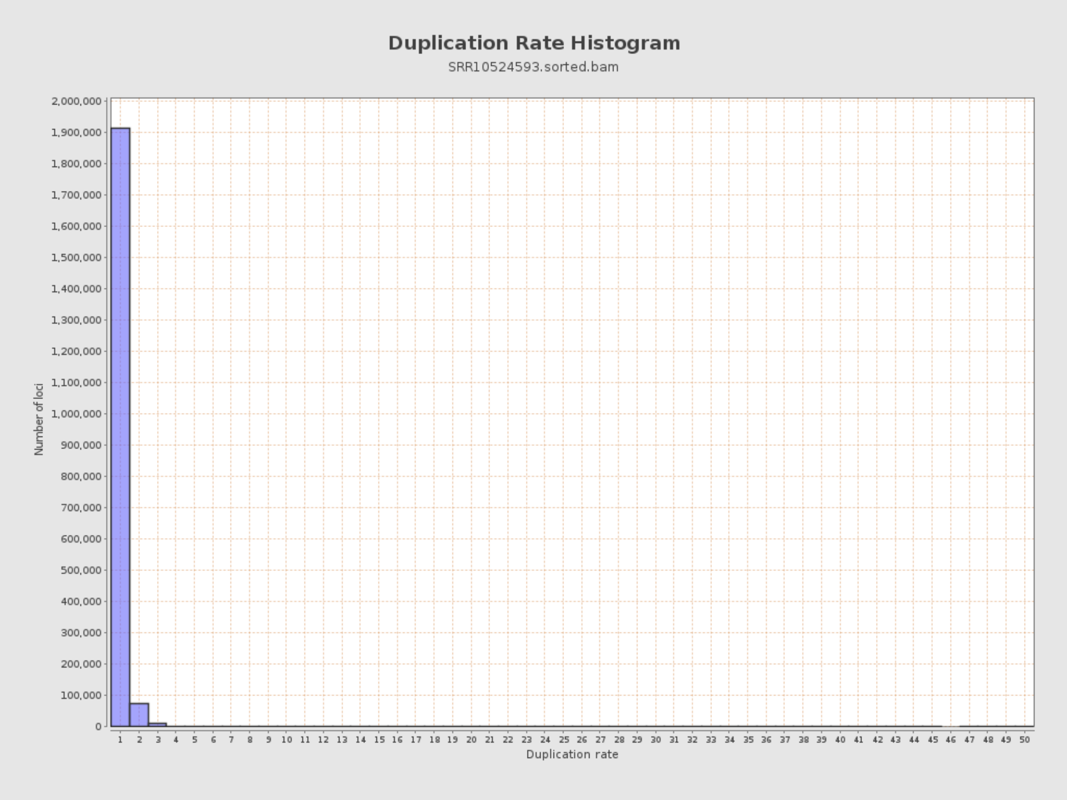
5. Results : Coverage Histogram (0-50X)



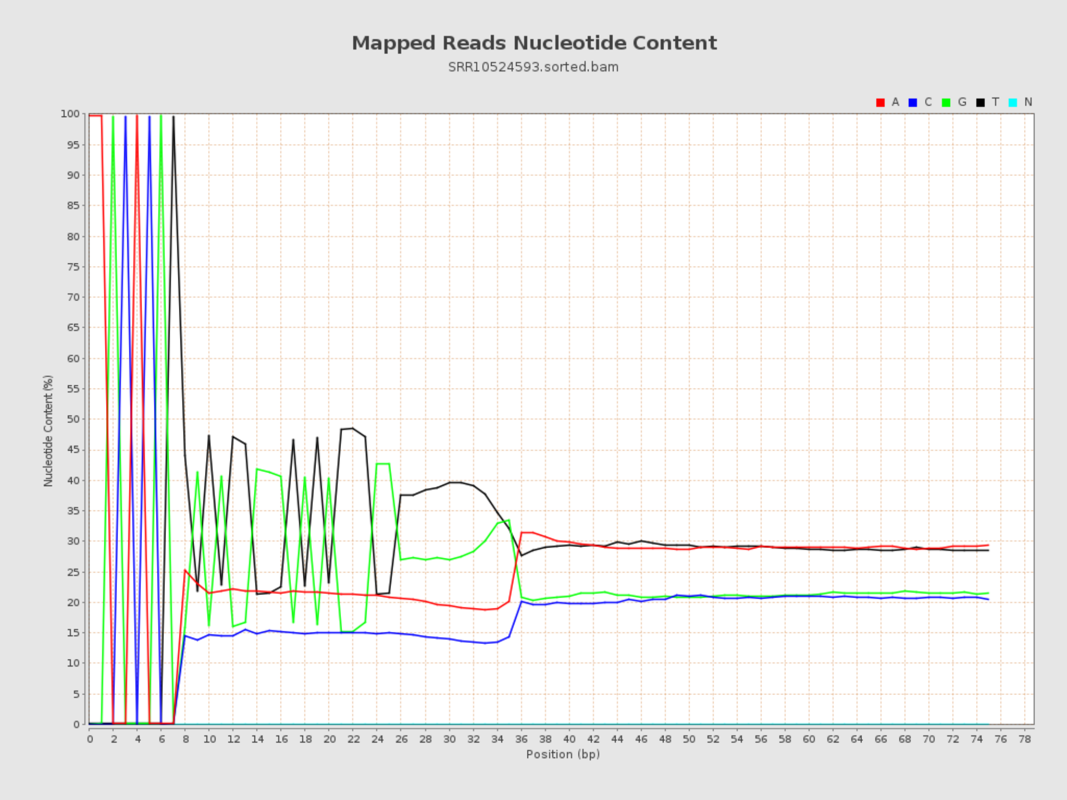
6. Results : Genome Fraction Coverage



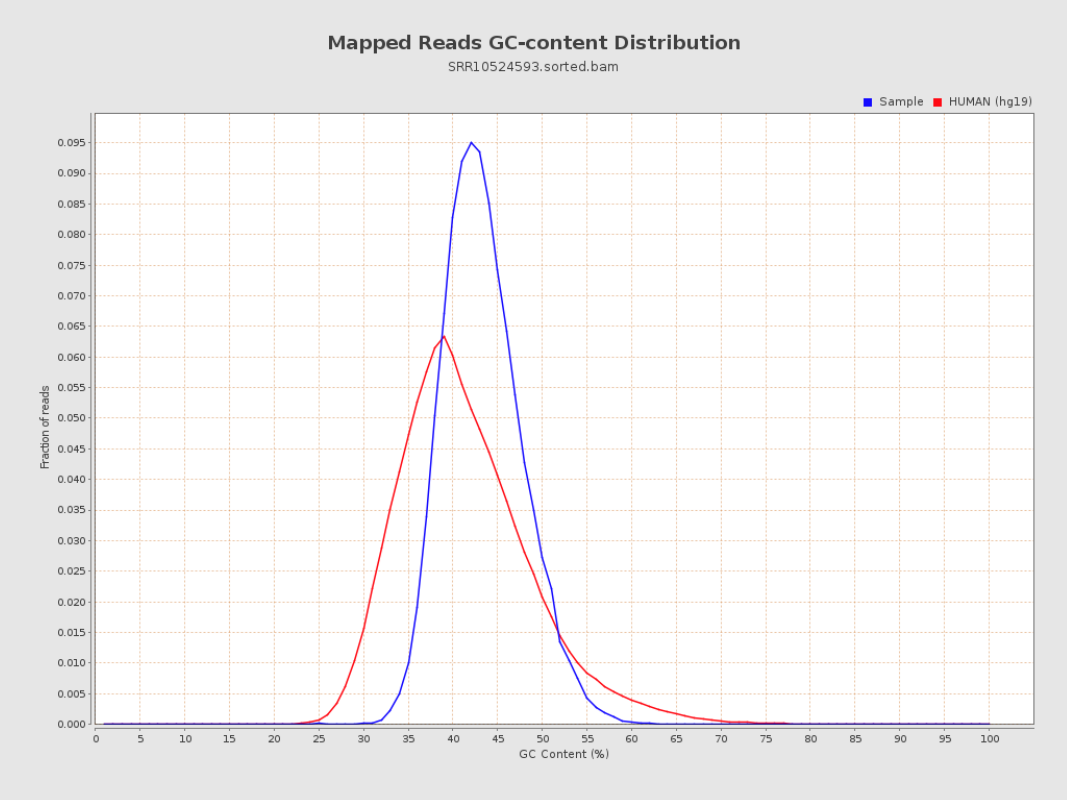
7. Results : Duplication Rate Histogram



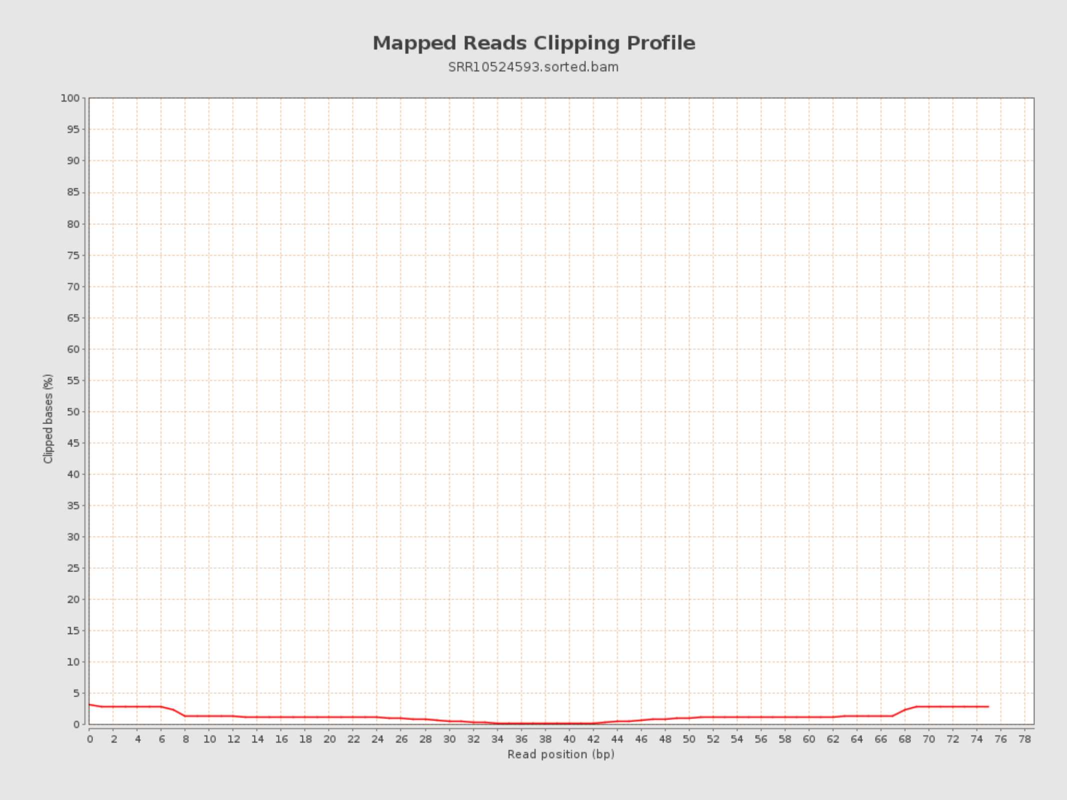
8. Results : Mapped Reads Nucleotide Content



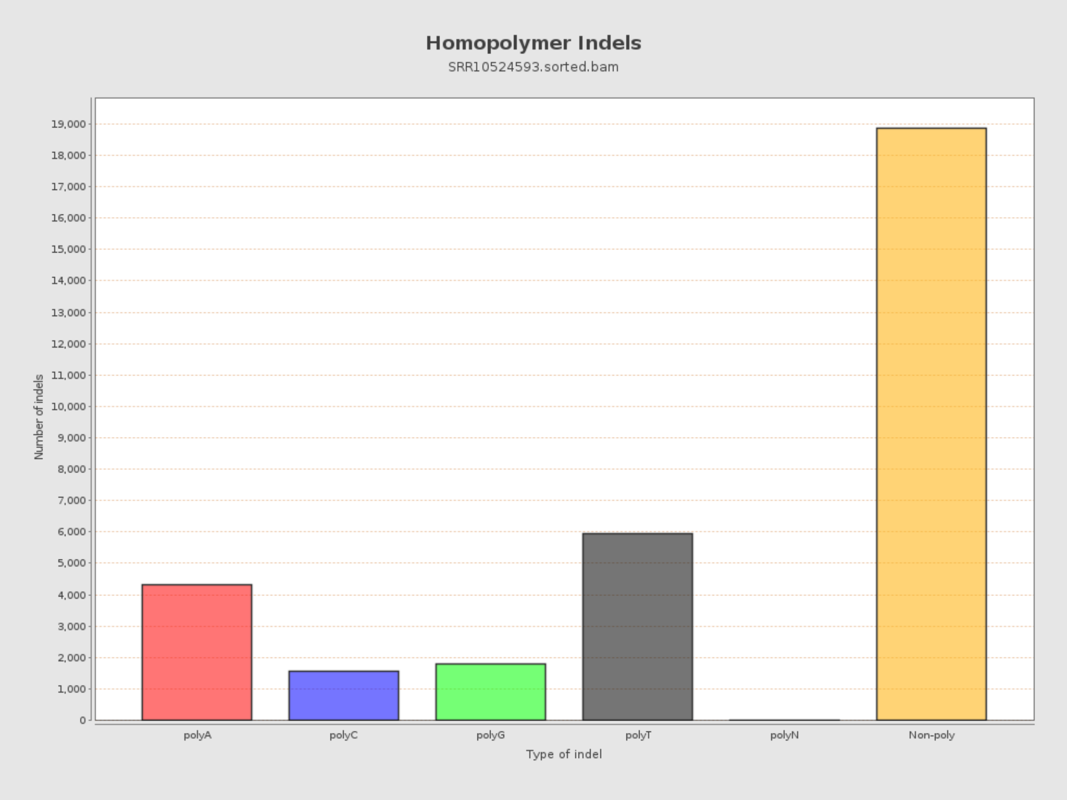
9. Results : Mapped Reads GC-content Distribution



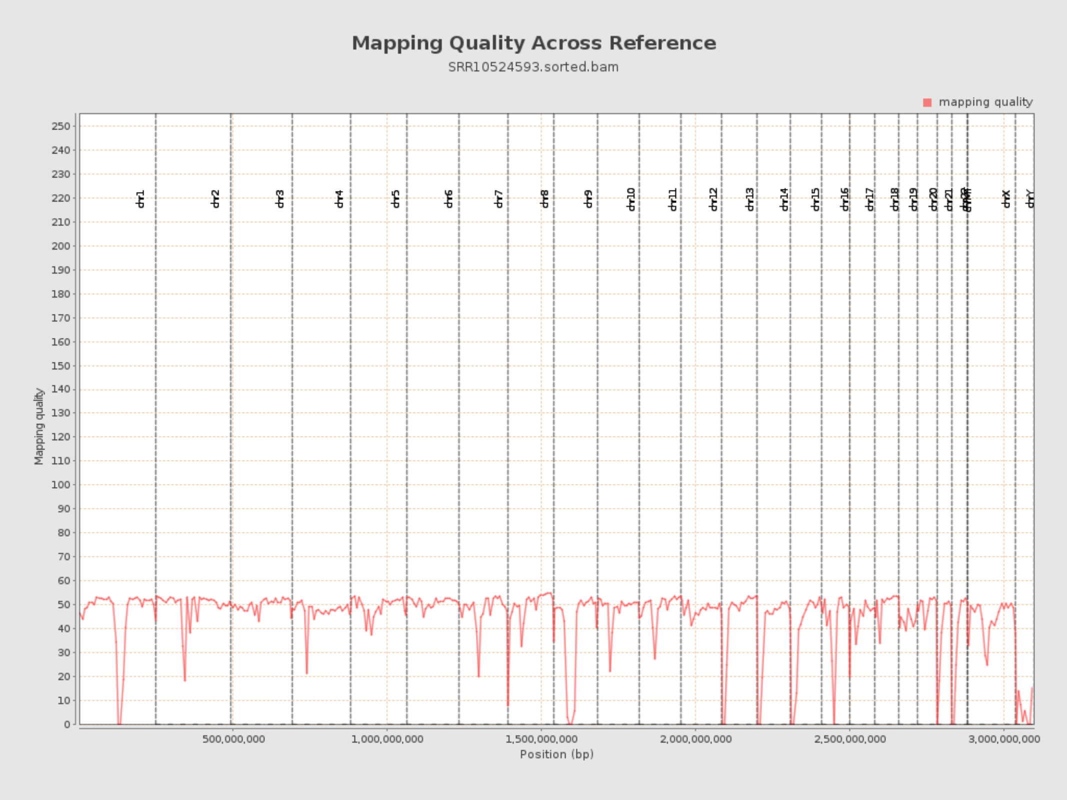
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram