Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:21:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524292.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_SRR10524292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:21:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,648,035
Mapped reads	1,533,713 / 93.06%
Unmapped reads	114,322 / 6.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,713 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	54,414 / 3.3%
Duplication rate	2.53%
Clipped reads	1,533,389 / 93.04%

2.2. ACGT Content

Number/percentage of A's	24,185,455 / 26.63%
Number/percentage of C's	16,682,914 / 18.37%
Number/percentage of T's	29,311,134 / 32.28%
Number/percentage of G's	20,612,951 / 22.7%
Number/percentage of N's	11,329 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.2963

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

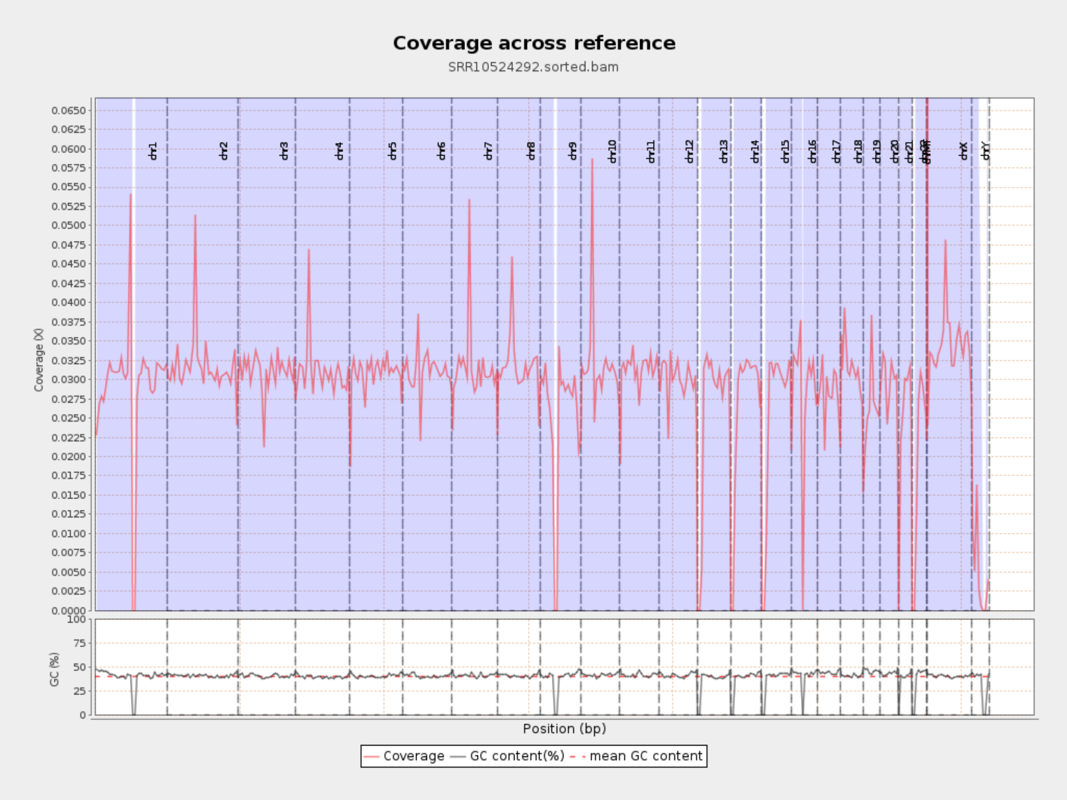
General error rate	0.5%
Mismatches	436,748
Insertions	7,687
Mapped reads with at least one insertion	0.5%
Deletions	17,614
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.61%

2.6. Chromosome stats

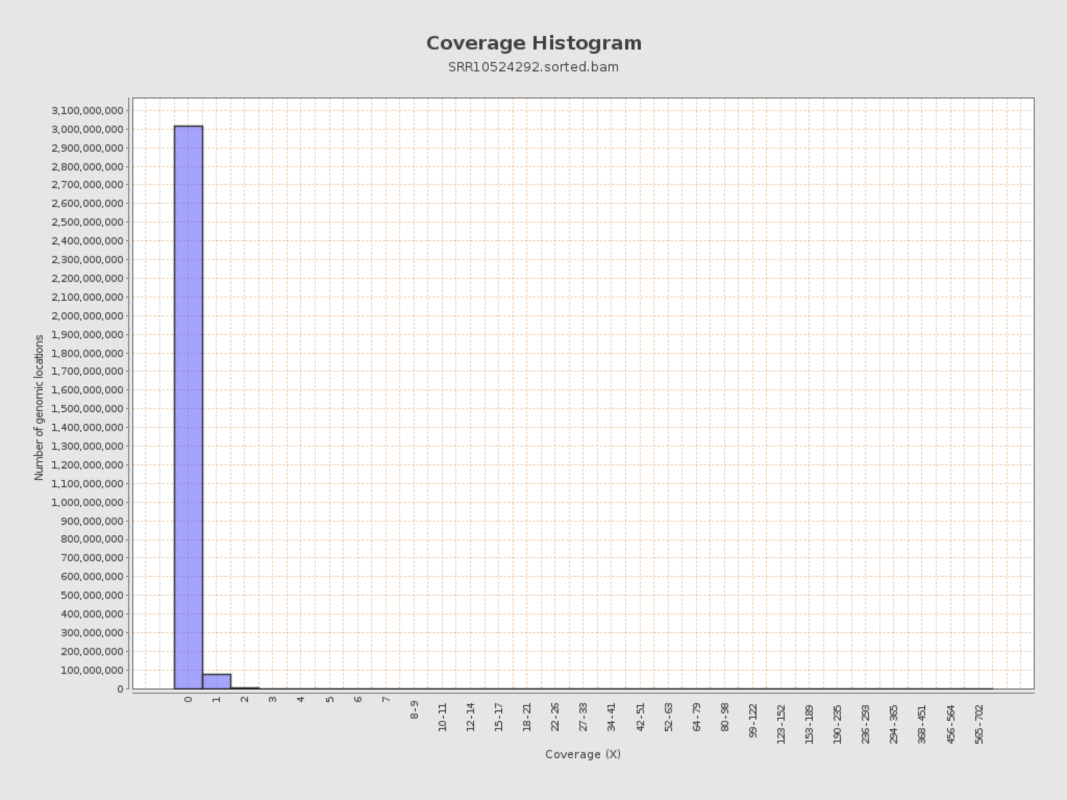
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7238752	0.029	0.588
chr2	243199373	7732808	0.0318	0.2945
chr3	198022430	6138883	0.031	0.1906
chr4	191154276	5946711	0.0311	0.2098
chr5	180915260	5634264	0.0311	0.1921
chr6	171115067	5328318	0.0311	0.2056
chr7	159138663	5037441	0.0317	0.4127

chr8	146364022	4688049	0.032	0.2861
chr9	141213431	3562078	0.0252	0.2582
chr10	135534747	4357388	0.0321	0.2849
chr11	135006516	4230140	0.0313	0.2705
chr12	133851895	4017180	0.03	0.1909
chr13	115169878	2941367	0.0255	0.174
chr14	107349540	2802791	0.0261	0.1859
chr15	102531392	2578595	0.0251	0.1709
chr16	90354753	2528474	0.028	0.2009
chr17	81195210	2286754	0.0282	0.202
chr18	78077248	2474384	0.0317	0.5077
chr19	59128983	1569357	0.0265	0.393
chr20	63025520	1863528	0.0296	0.1902
chr21	48129895	1202451	0.025	0.1937
chr22	51304566	1010123	0.0197	0.1498
chrMT	16571	18919	1.1417	1.2706
chrX	155270560	5365866	0.0346	0.2282
chrY	59373566	277021	0.0047	0.1252

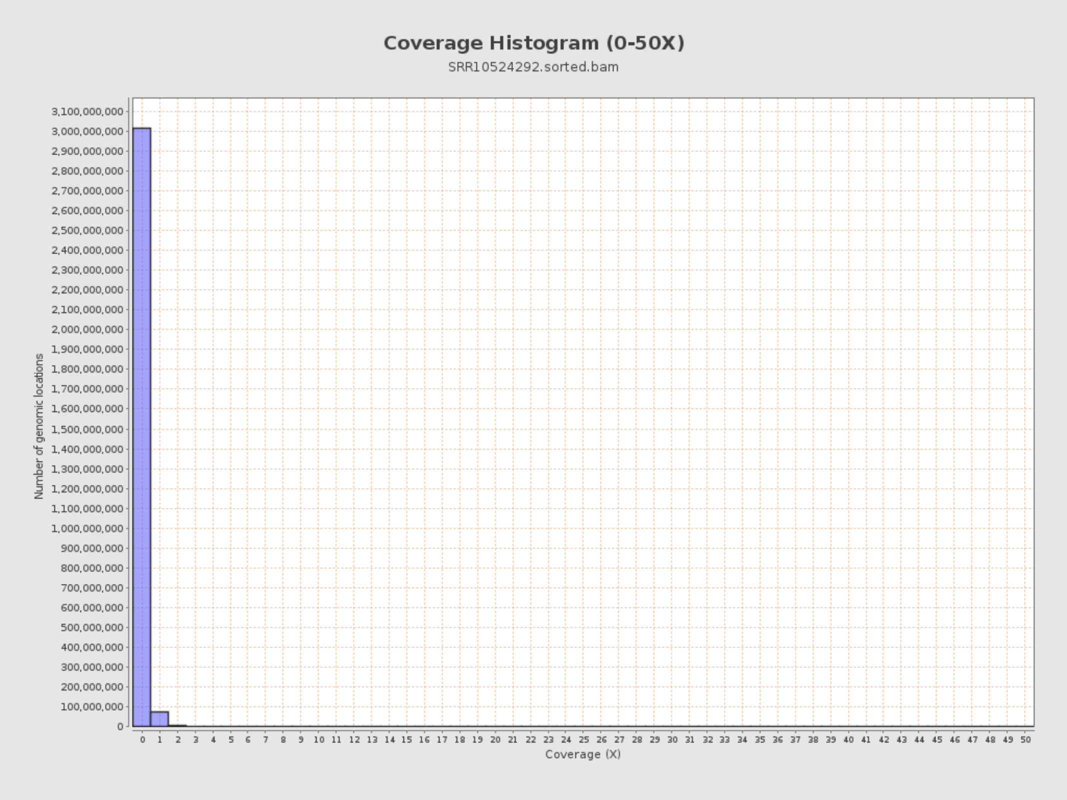
3. Results : Coverage across reference



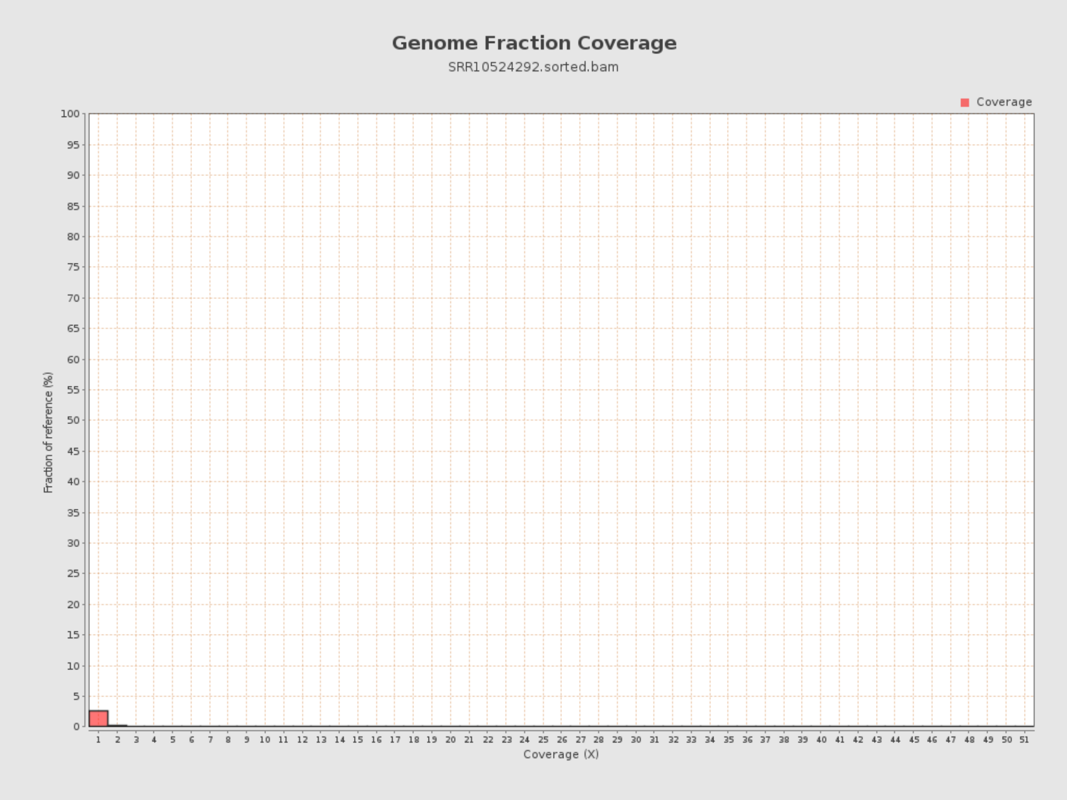
4. Results : Coverage Histogram



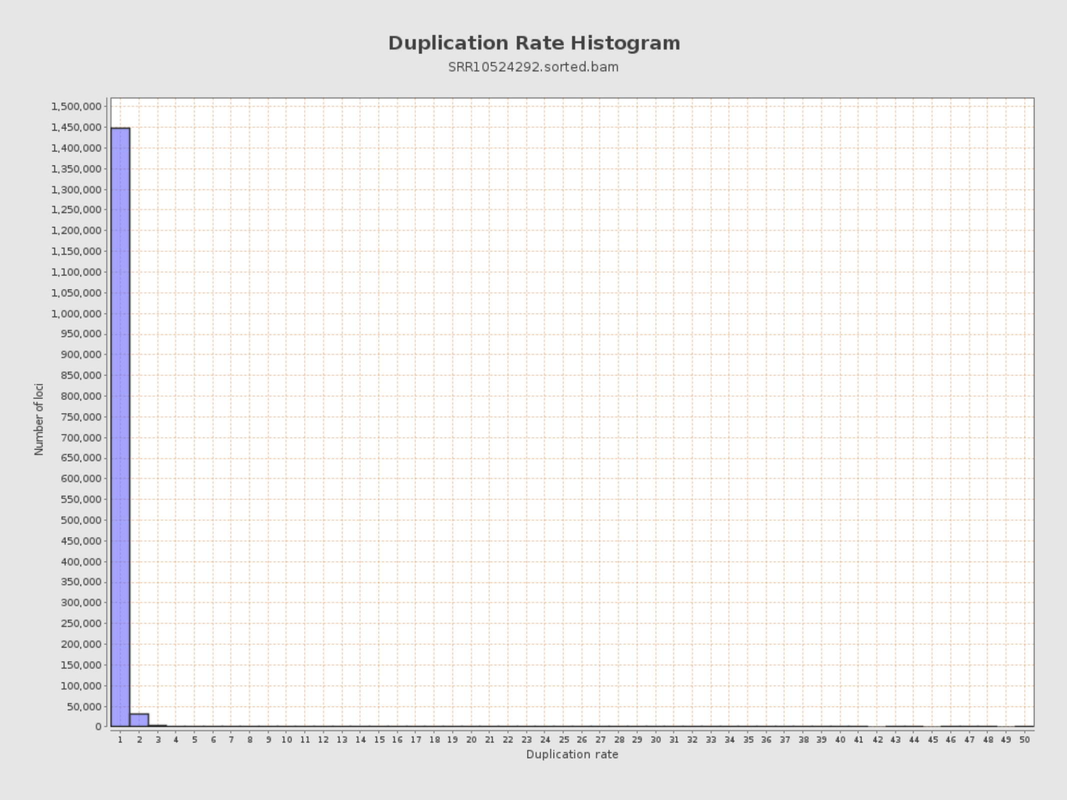
5. Results : Coverage Histogram (0-50X)



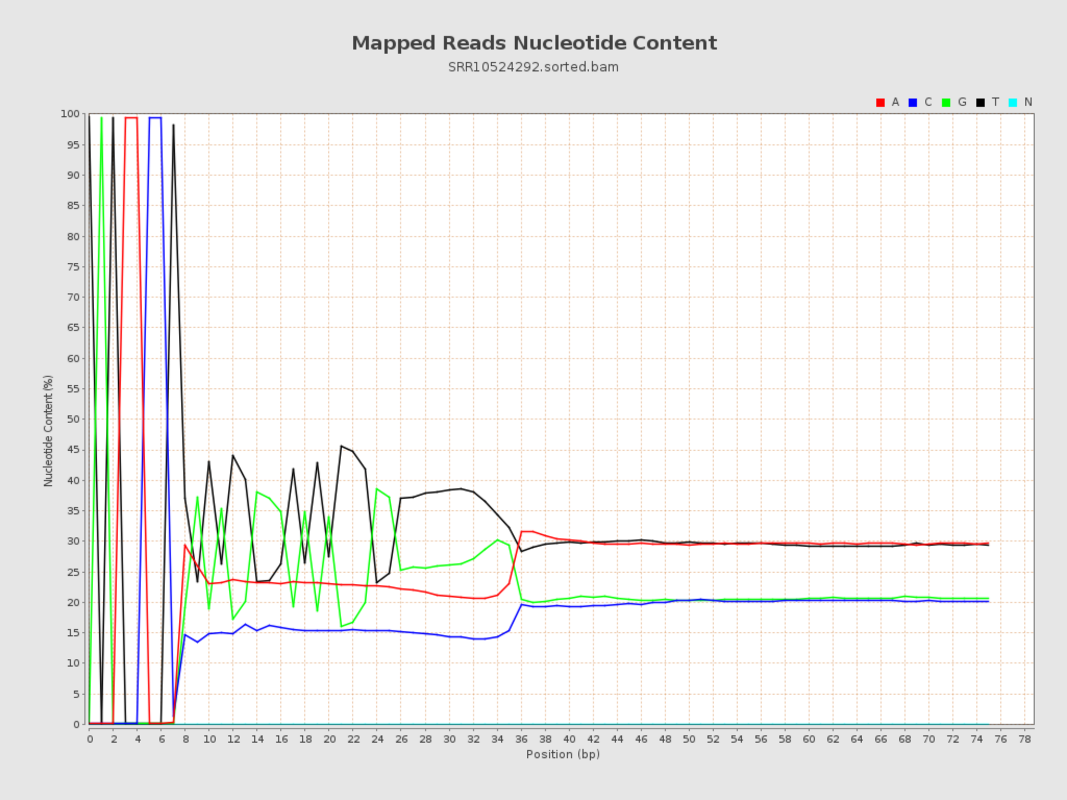
6. Results : Genome Fraction Coverage



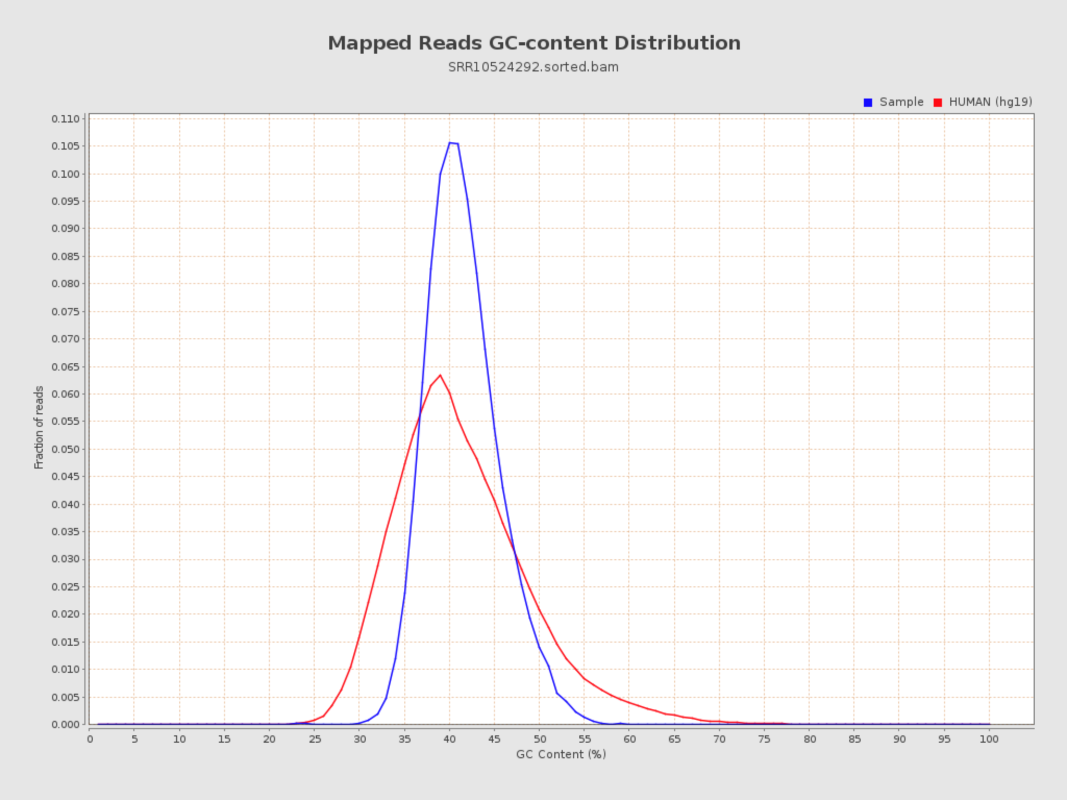
7. Results : Duplication Rate Histogram



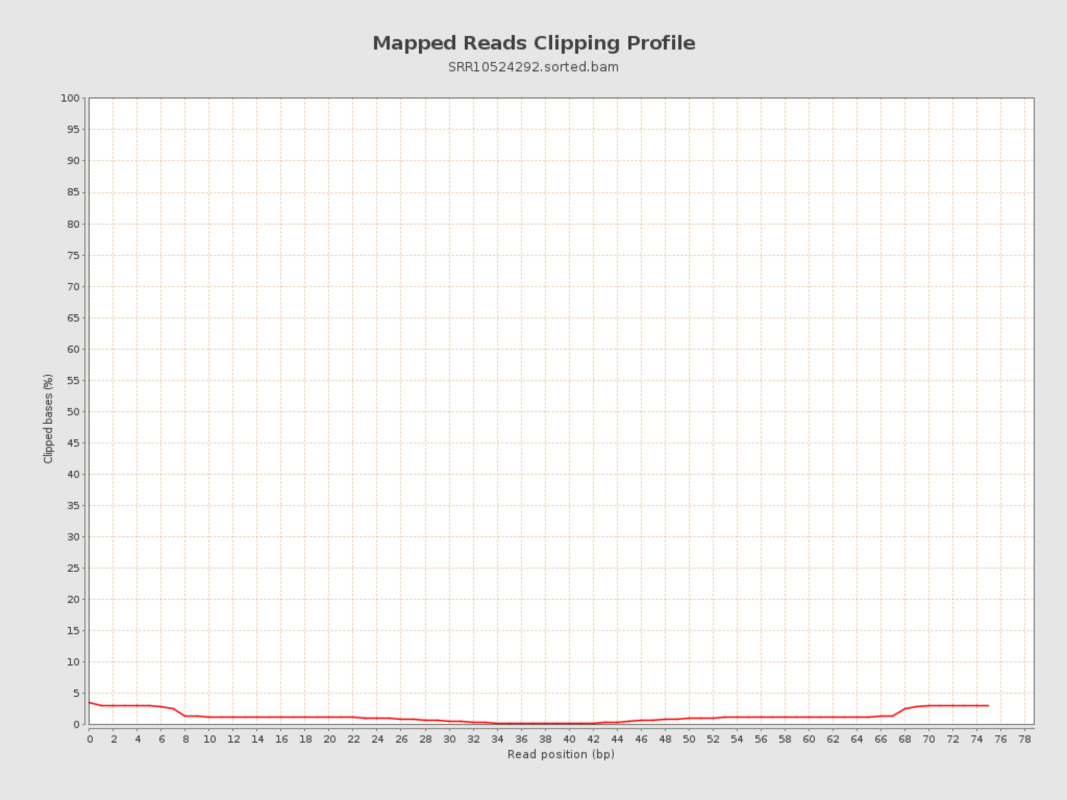
8. Results : Mapped Reads Nucleotide Content



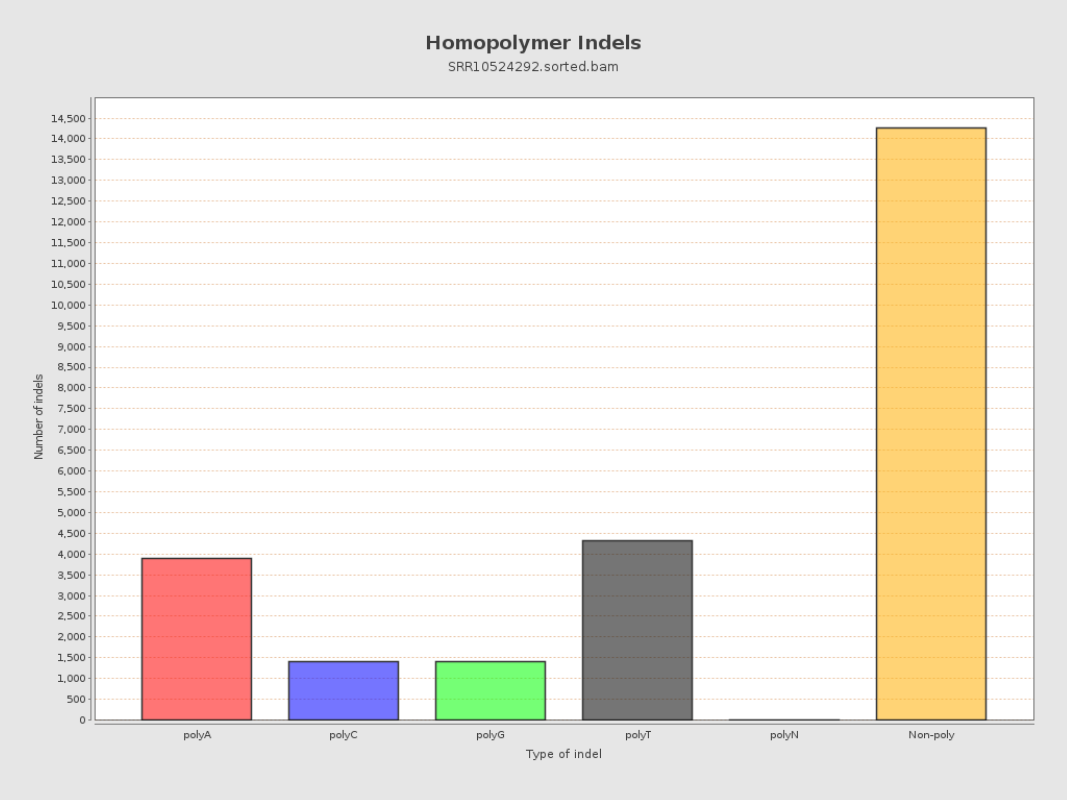
9. Results : Mapped Reads GC-content Distribution



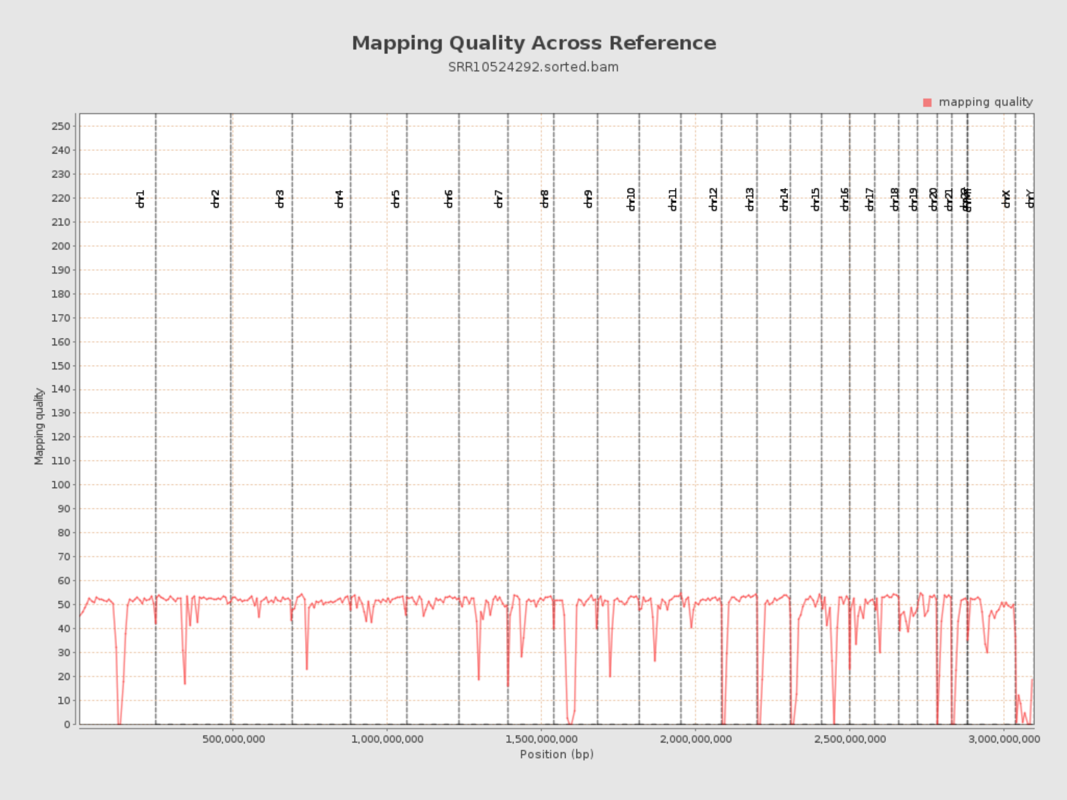
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram