Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:47:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524745.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_SRR10524745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:47:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,855,365
Mapped reads	1,686,619 / 90.9%
Unmapped reads	168,746 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,475 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	67,217 / 3.62%
Duplication rate	2.96%
Clipped reads	1,688,809 / 91.02%

2.2. ACGT Content

Number/percentage of A's	24,169,157 / 25.04%
Number/percentage of C's	17,011,965 / 17.62%
Number/percentage of T's	30,490,155 / 31.58%
Number/percentage of G's	24,854,394 / 25.75%
Number/percentage of N's	12,145 / 0.01%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.2713

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

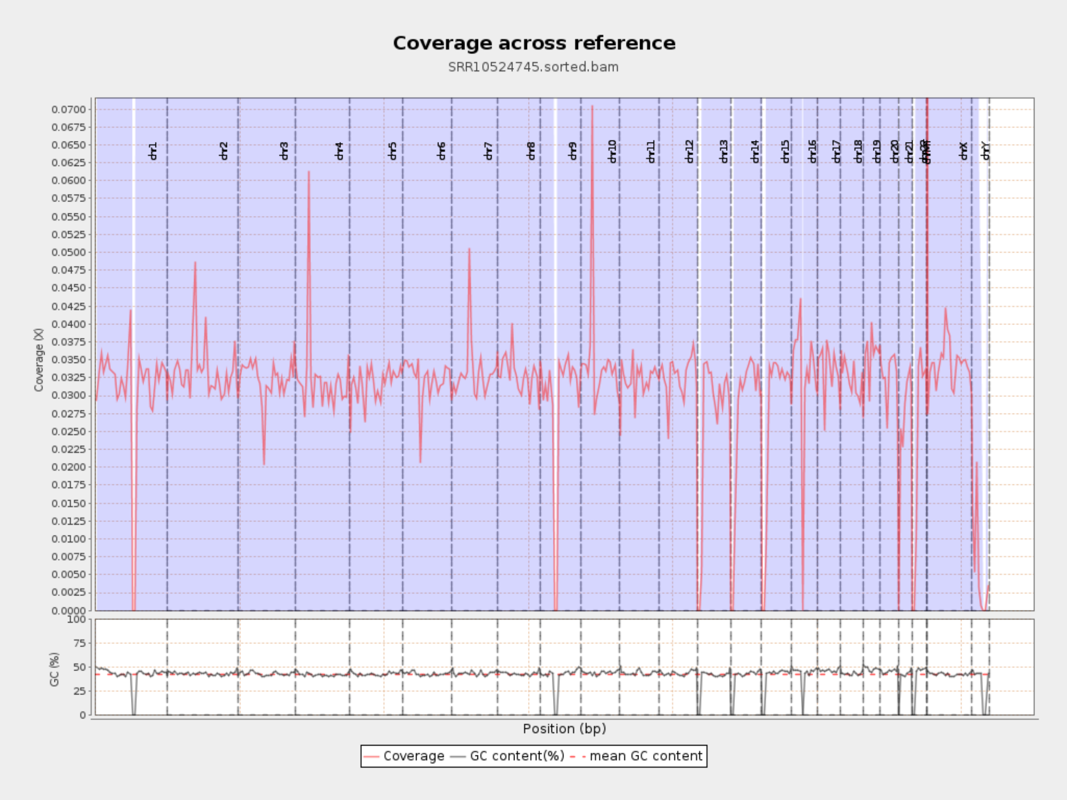
General error rate	0.52%
Mismatches	493,700
Insertions	6,629
Mapped reads with at least one insertion	0.39%
Deletions	19,649
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.1%

2.6. Chromosome stats

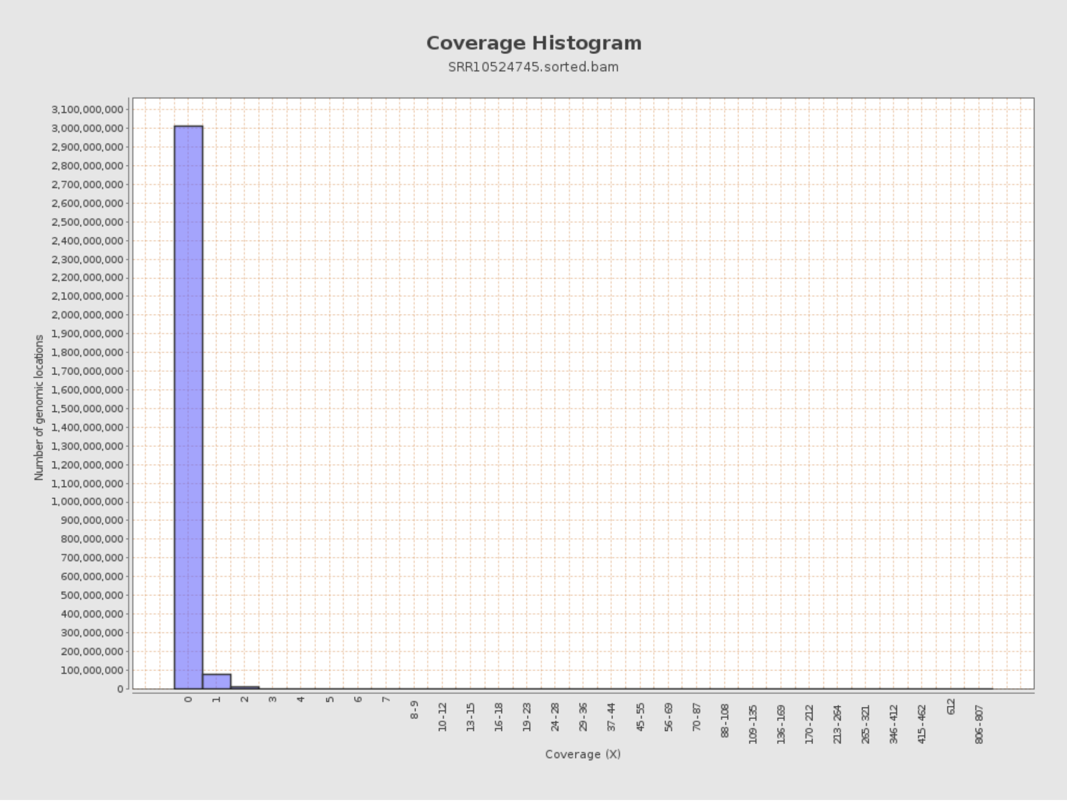
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7661394	0.0307	0.3799
chr2	243199373	8140616	0.0335	0.4115
chr3	198022430	6376813	0.0322	0.2011
chr4	191154276	6216018	0.0325	0.241
chr5	180915260	5782698	0.032	0.1978
chr6	171115067	5515501	0.0322	0.2193
chr7	159138663	5311045	0.0334	0.3359

chr8	146364022	4821724	0.0329	0.2483
chr9	141213431	4074008	0.0289	0.2286
chr10	135534747	4760256	0.0351	0.3514
chr11	135006516	4368273	0.0324	0.2418
chr12	133851895	4384099	0.0328	0.203
chr13	115169878	3000352	0.0261	0.1792
chr14	107349540	2893017	0.0269	0.1897
chr15	102531392	2761150	0.0269	0.1816
chr16	90354753	2908371	0.0322	0.2247
chr17	81195210	2737367	0.0337	0.2147
chr18	78077248	2520910	0.0323	0.3734
chr19	59128983	2100711	0.0355	0.3125
chr20	63025520	2051555	0.0326	0.2091
chr21	48129895	1260085	0.0262	0.204
chr22	51304566	1202021	0.0234	0.172
chrMT	16571	34515	2.0829	1.9142
chrX	155270560	5353772	0.0345	0.2239
chrY	59373566	333220	0.0056	0.1608

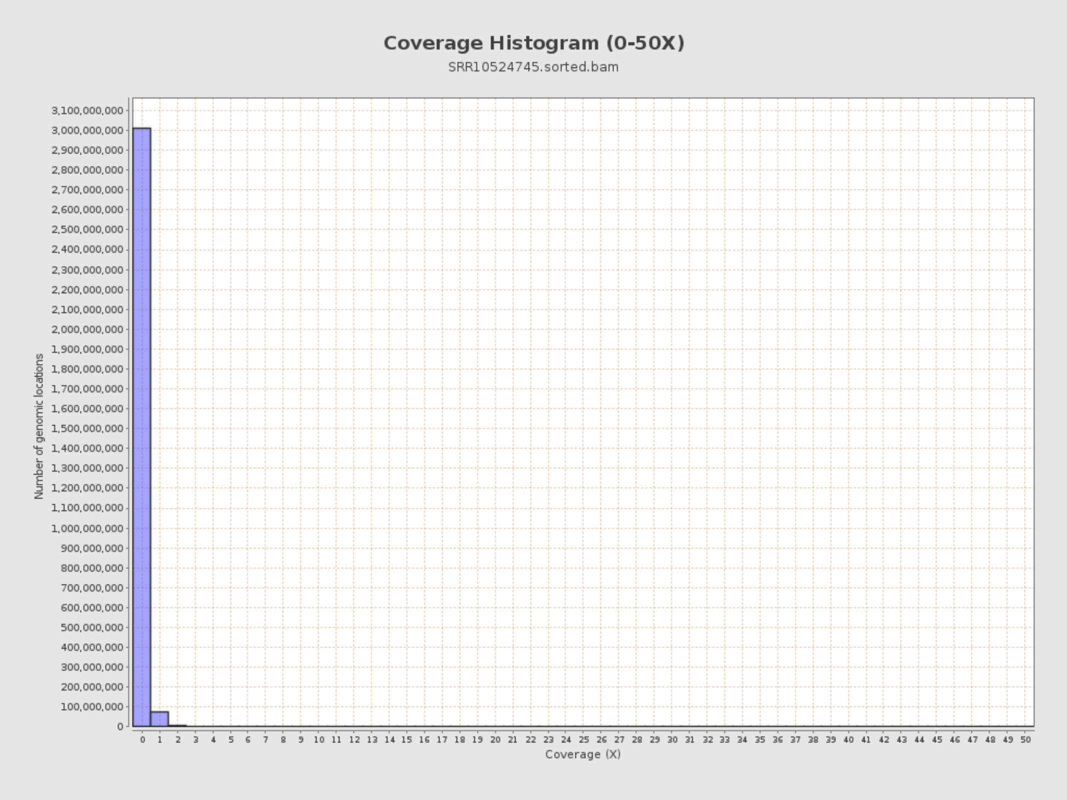
3. Results : Coverage across reference



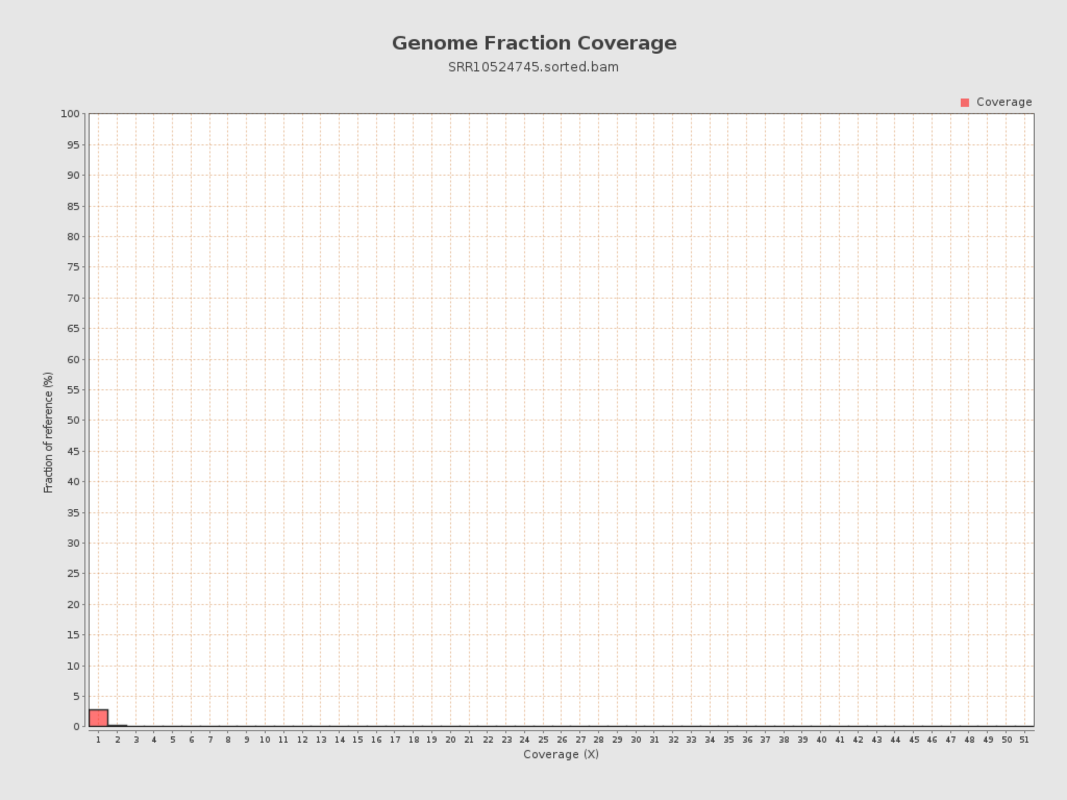
4. Results : Coverage Histogram



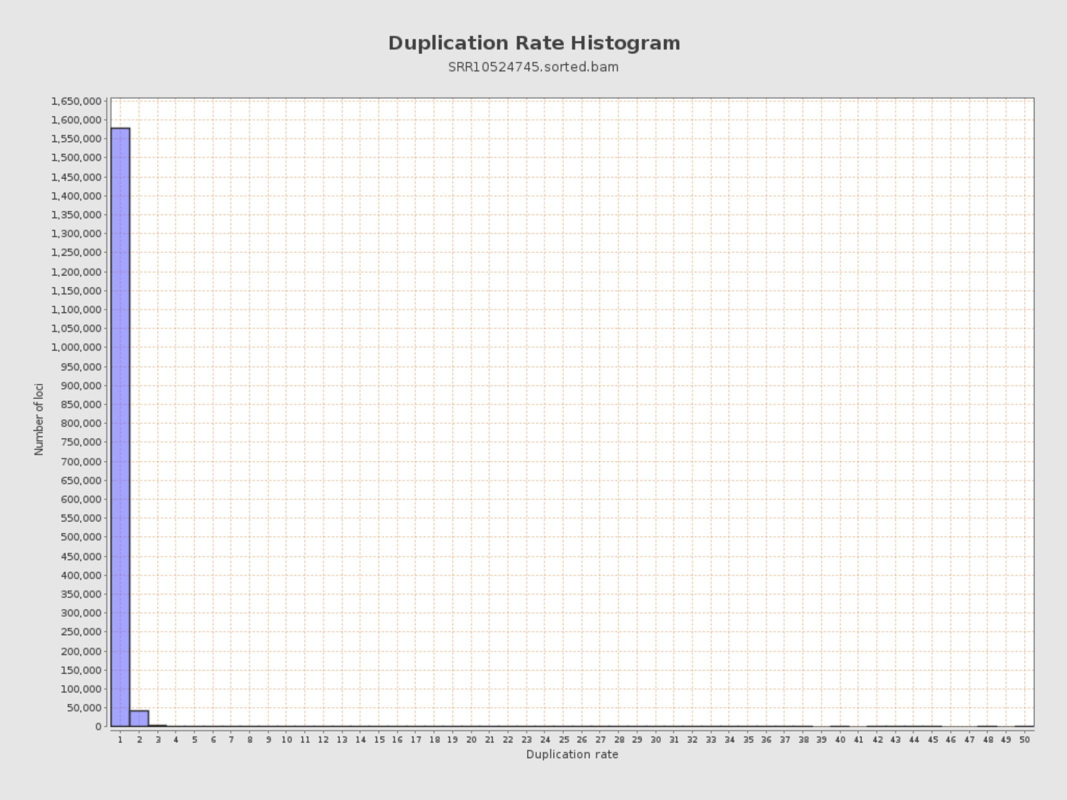
5. Results : Coverage Histogram (0-50X)



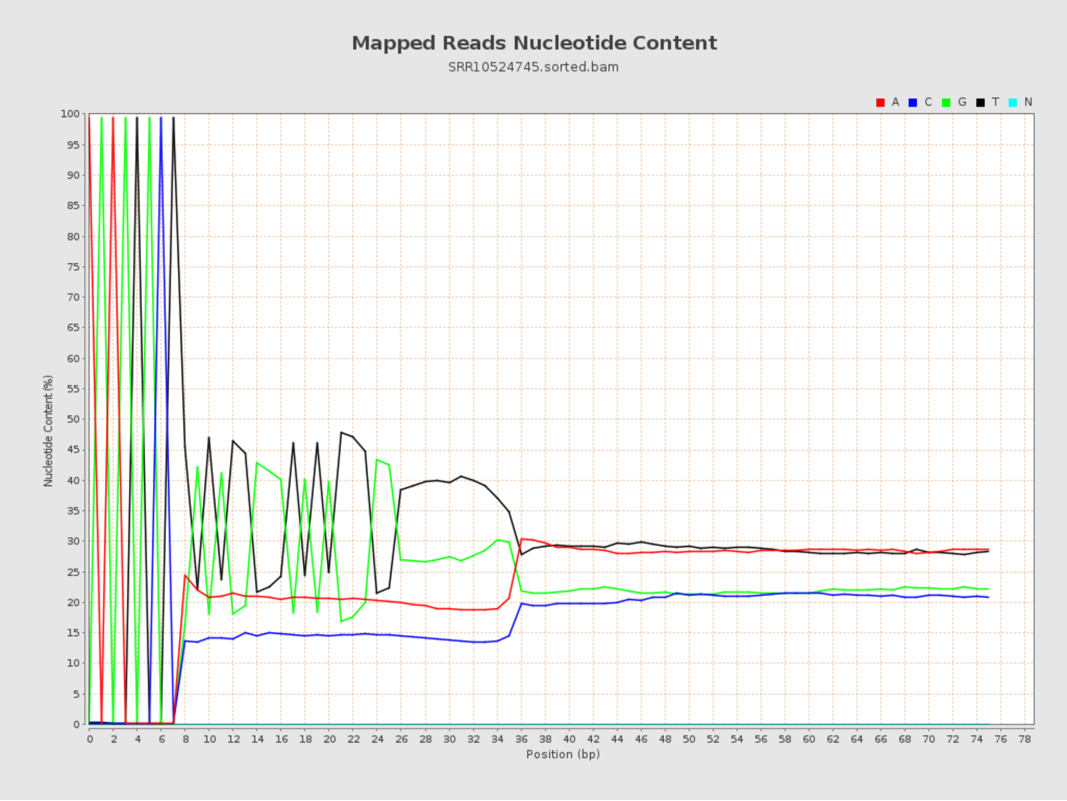
6. Results : Genome Fraction Coverage



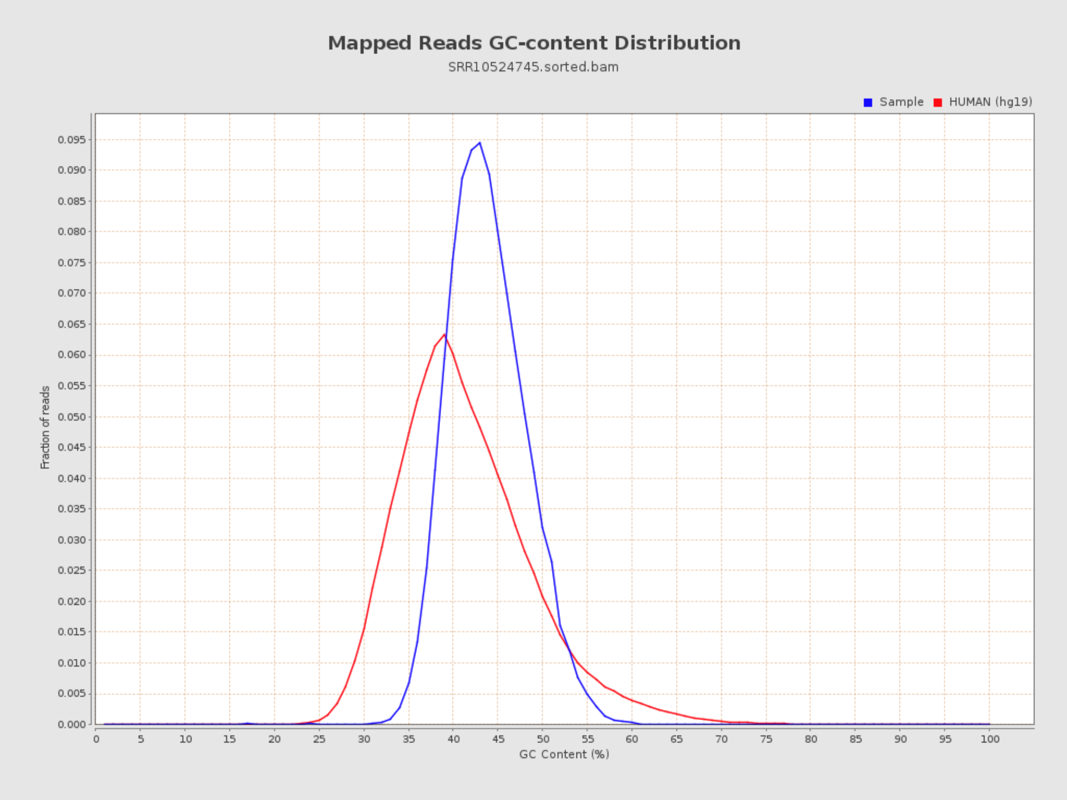
7. Results : Duplication Rate Histogram



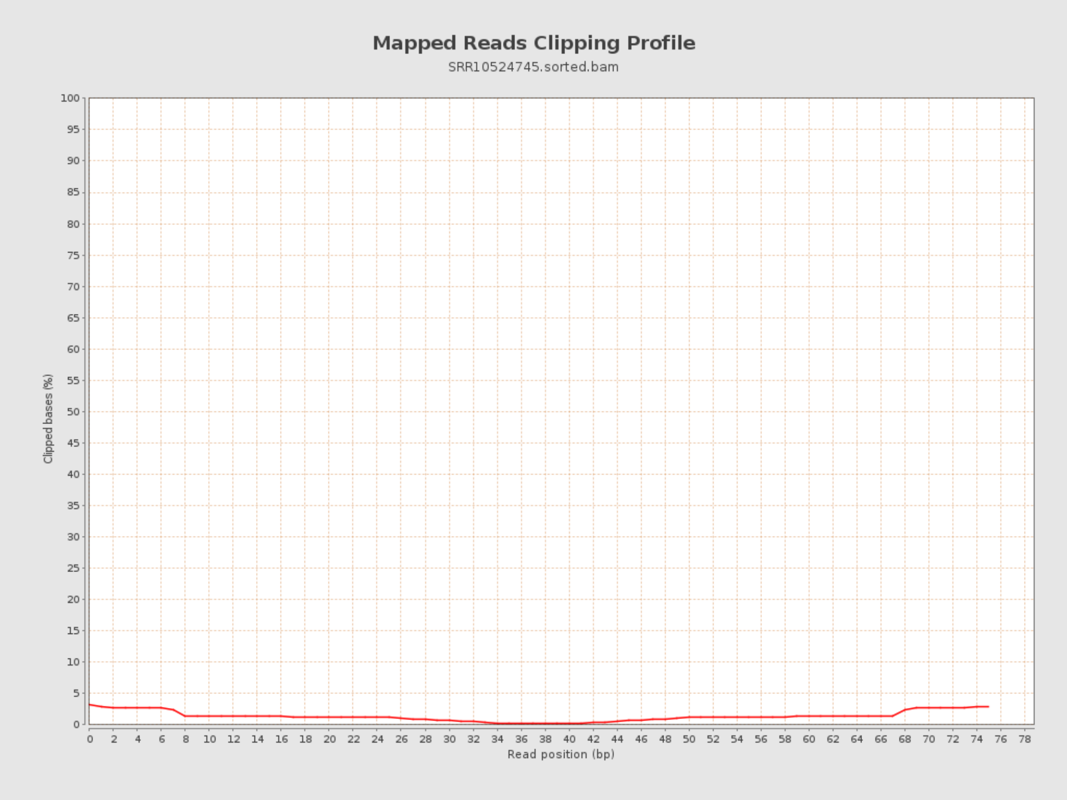
8. Results : Mapped Reads Nucleotide Content



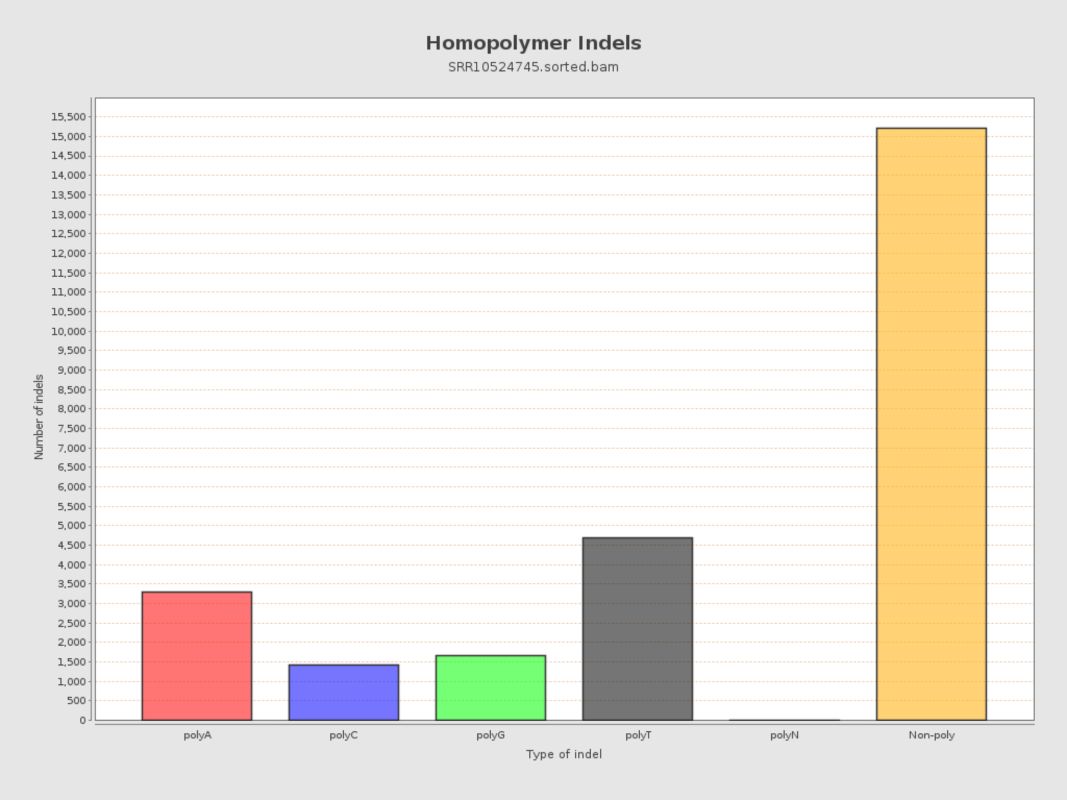
9. Results : Mapped Reads GC-content Distribution



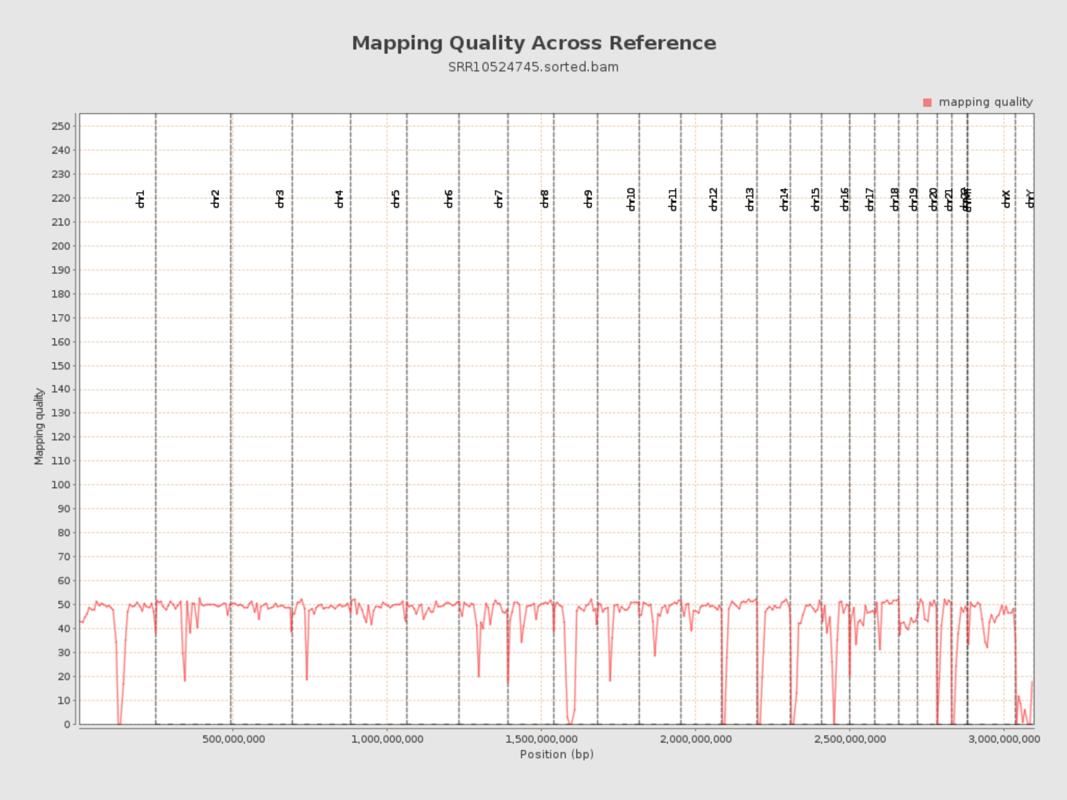
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram