Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:08:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004141.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_SRR6004141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:08:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,160,015
Mapped reads	1,635,586 / 75.72%
Unmapped reads	524,429 / 24.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,931 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	215,917 / 10%
Duplication rate	10.08%
Clipped reads	927,164 / 42.92%

2.2. ACGT Content

Number/percentage of A's	29,476,155 / 28.19%
Number/percentage of C's	18,135,543 / 17.34%
Number/percentage of T's	34,513,797 / 33.01%
Number/percentage of G's	22,371,792 / 21.4%
Number/percentage of N's	67,417 / 0.06%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0338

Standard Deviation	0.4191

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

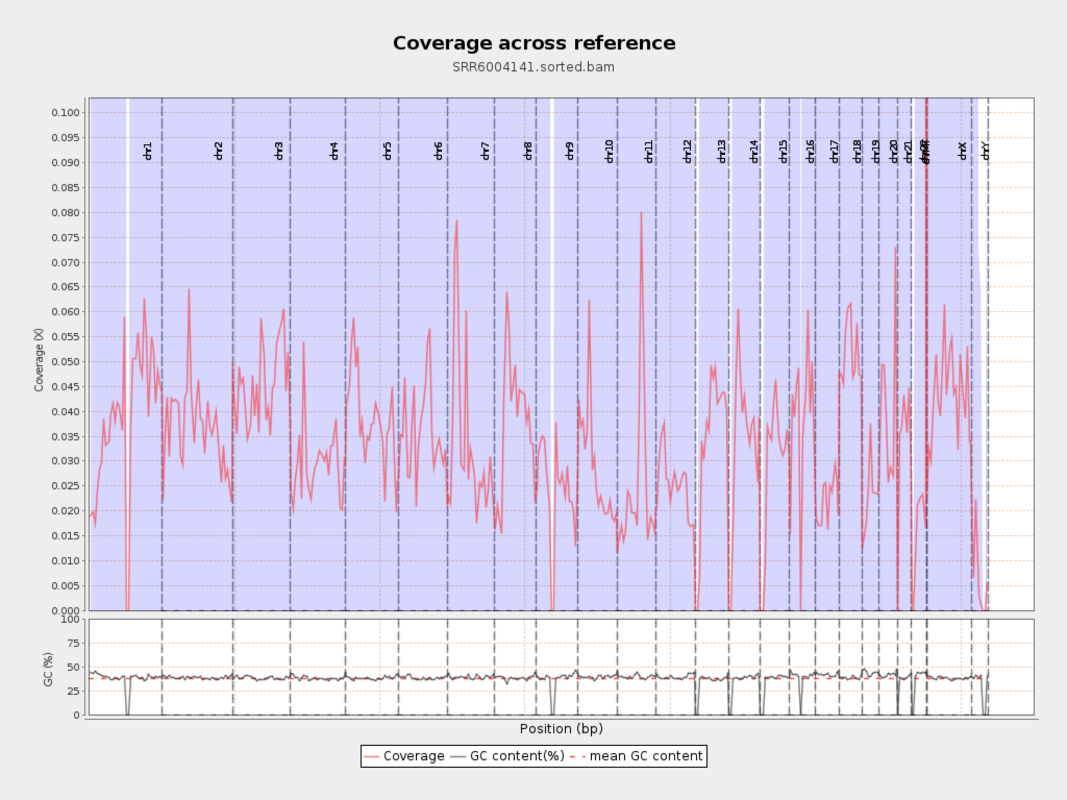
General error rate	1.03%
Mismatches	1,060,003
Insertions	8,324
Mapped reads with at least one insertion	0.51%
Deletions	38,921
Mapped reads with at least one deletion	2.35%
Homopolymer indels	43.66%

2.6. Chromosome stats

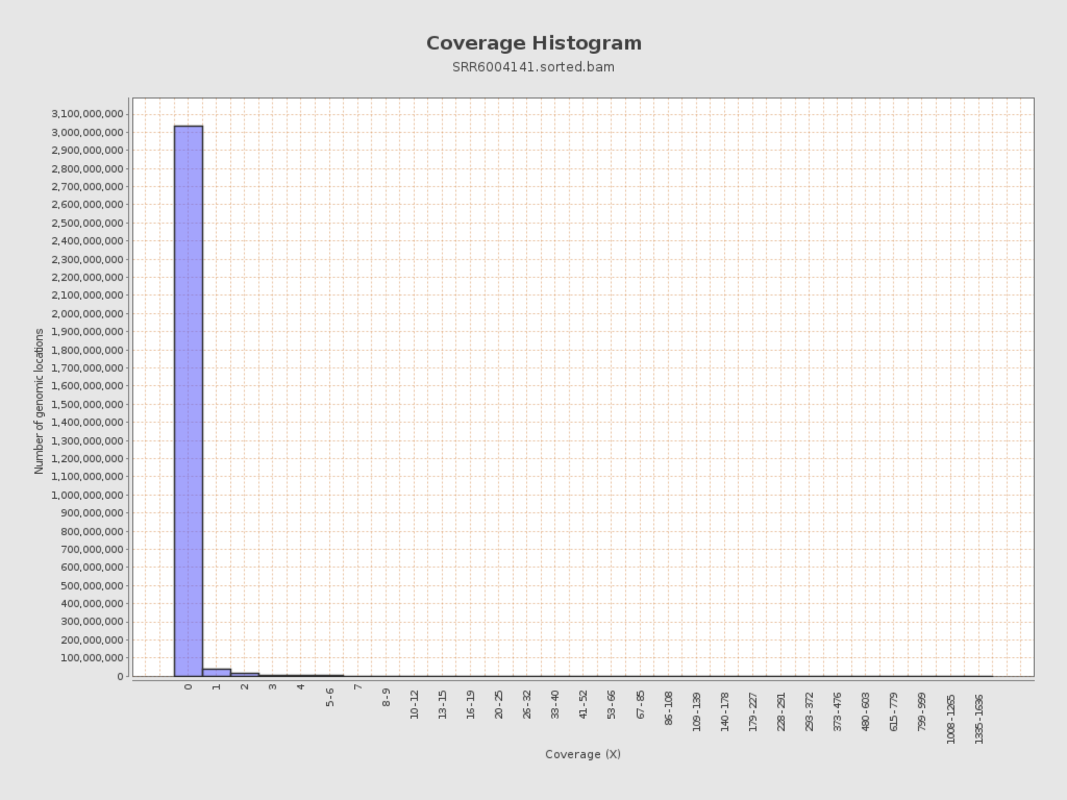
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9602991	0.0385	0.6354
chr2	243199373	8970693	0.0369	0.417
chr3	198022430	9024587	0.0456	0.3365
chr4	191154276	5579721	0.0292	0.2918
chr5	180915260	6963778	0.0385	0.3106
chr6	171115067	6168635	0.036	0.3172
chr7	159138663	5444499	0.0342	0.435

chr8	146364022	5477792	0.0374	0.9841
chr9	141213431	3375330	0.0239	0.2991
chr10	135534747	3882455	0.0286	0.334
chr11	135006516	3459774	0.0256	0.2675
chr12	133851895	3379153	0.0252	0.2504
chr13	115169878	3930516	0.0341	0.29
chr14	107349540	3596883	0.0335	0.2928
chr15	102531392	2962661	0.0289	0.2642
chr16	90354753	3474406	0.0385	0.3171
chr17	81195210	1807649	0.0223	0.2316
chr18	78077248	4048005	0.0518	0.5597
chr19	59128983	1374684	0.0232	0.4604
chr20	63025520	2581398	0.041	0.3274
chr21	48129895	1650957	0.0343	0.3027
chr22	51304566	780529	0.0152	0.1823
chrMT	16571	29132	1.758	2.2219
chrX	155270560	6690503	0.0431	0.3421
chrY	59373566	373494	0.0063	0.1861

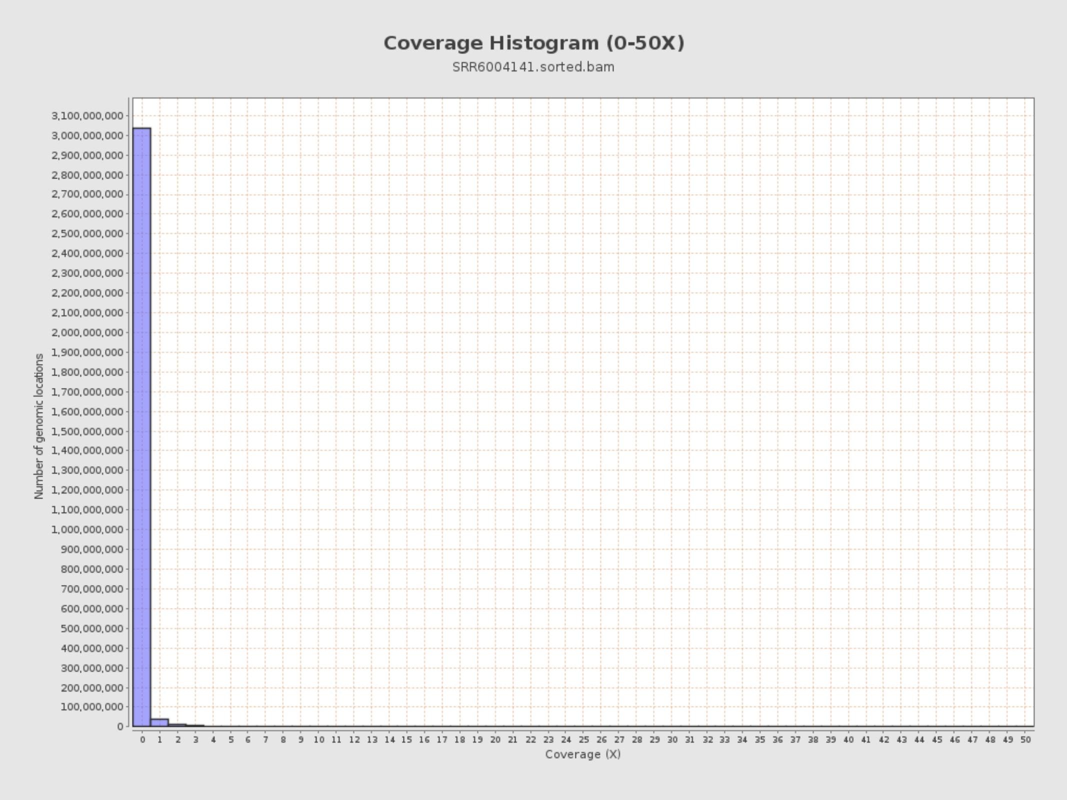
3. Results : Coverage across reference



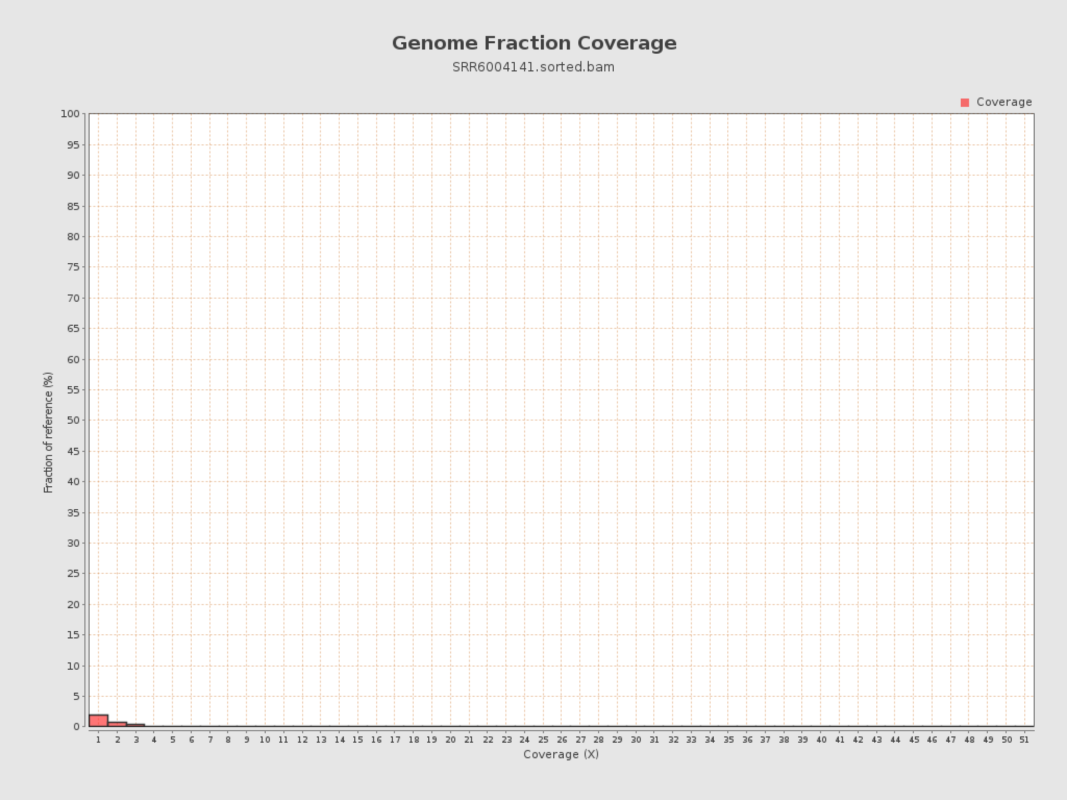
4. Results : Coverage Histogram



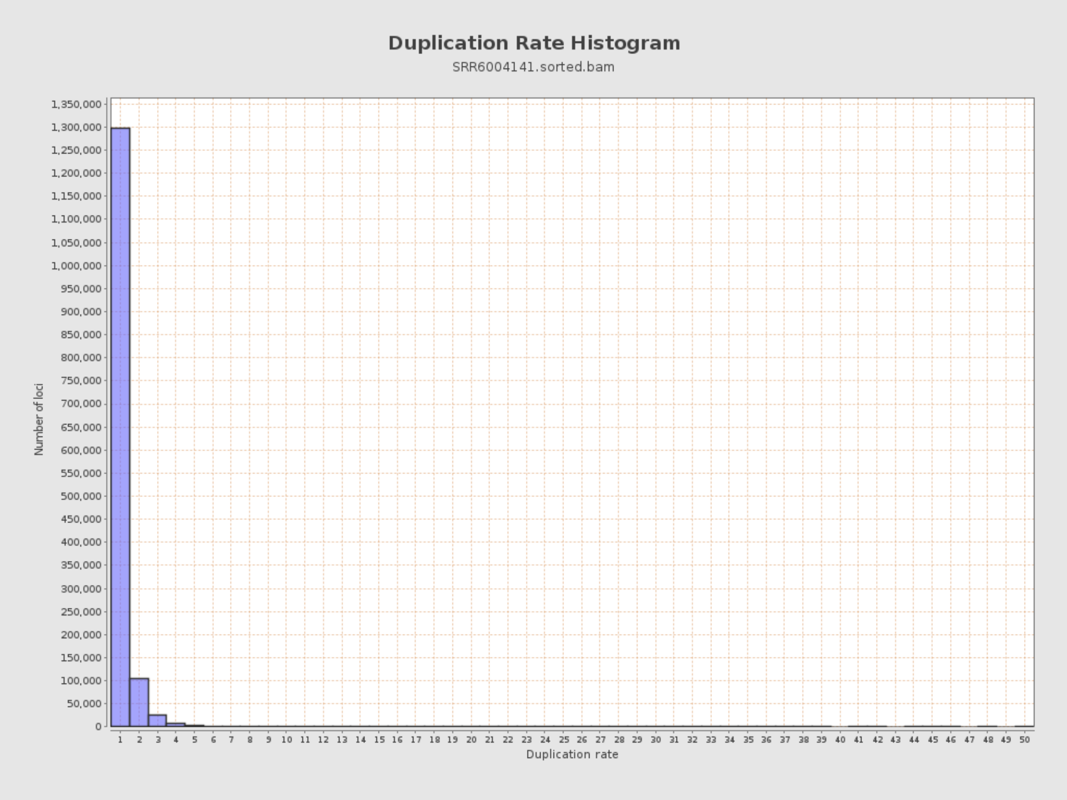
5. Results : Coverage Histogram (0-50X)



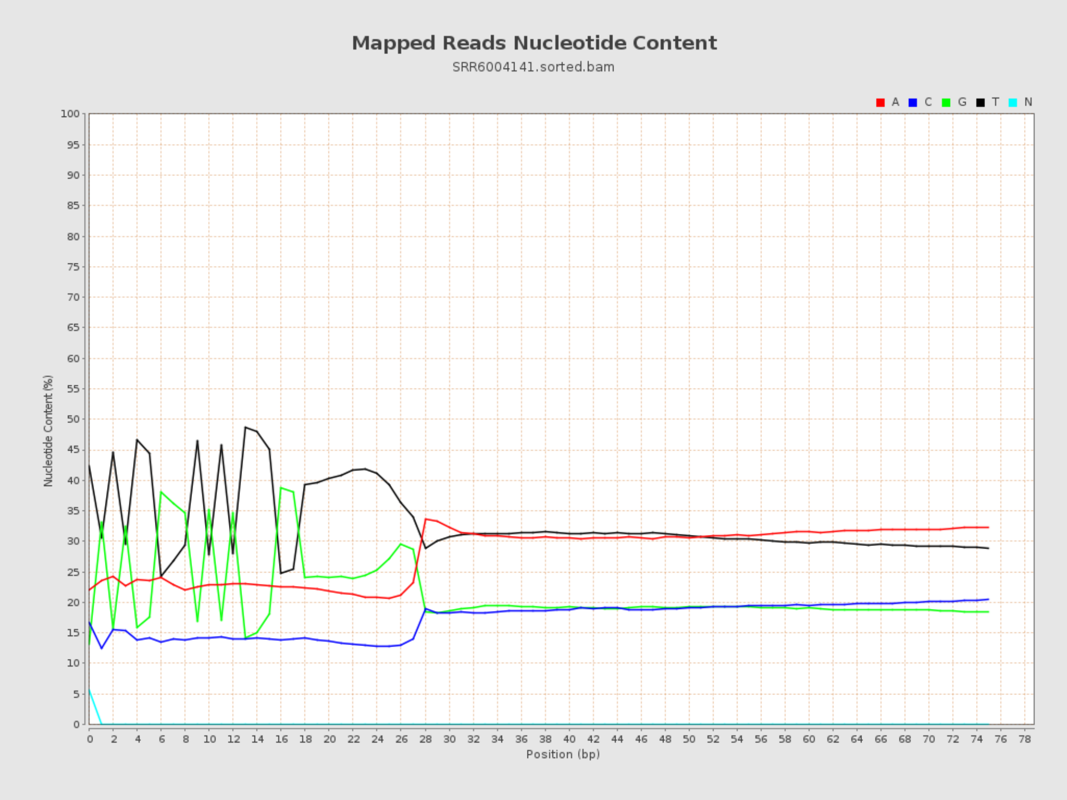
6. Results : Genome Fraction Coverage



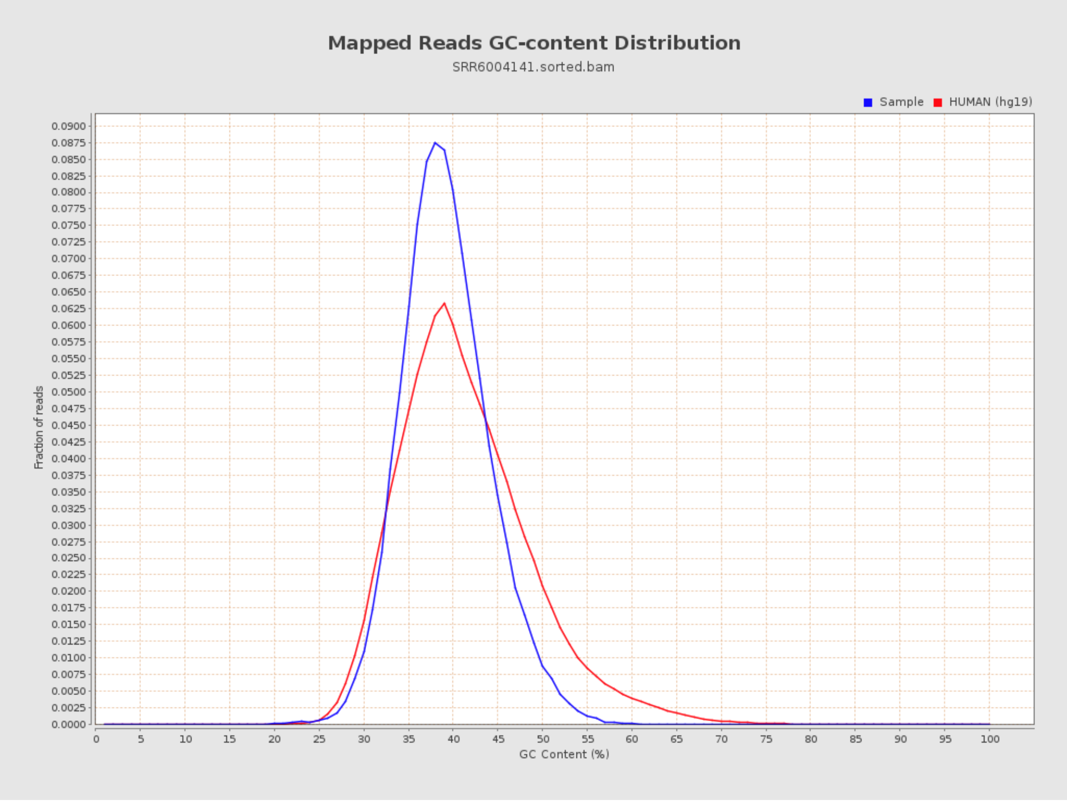
7. Results : Duplication Rate Histogram



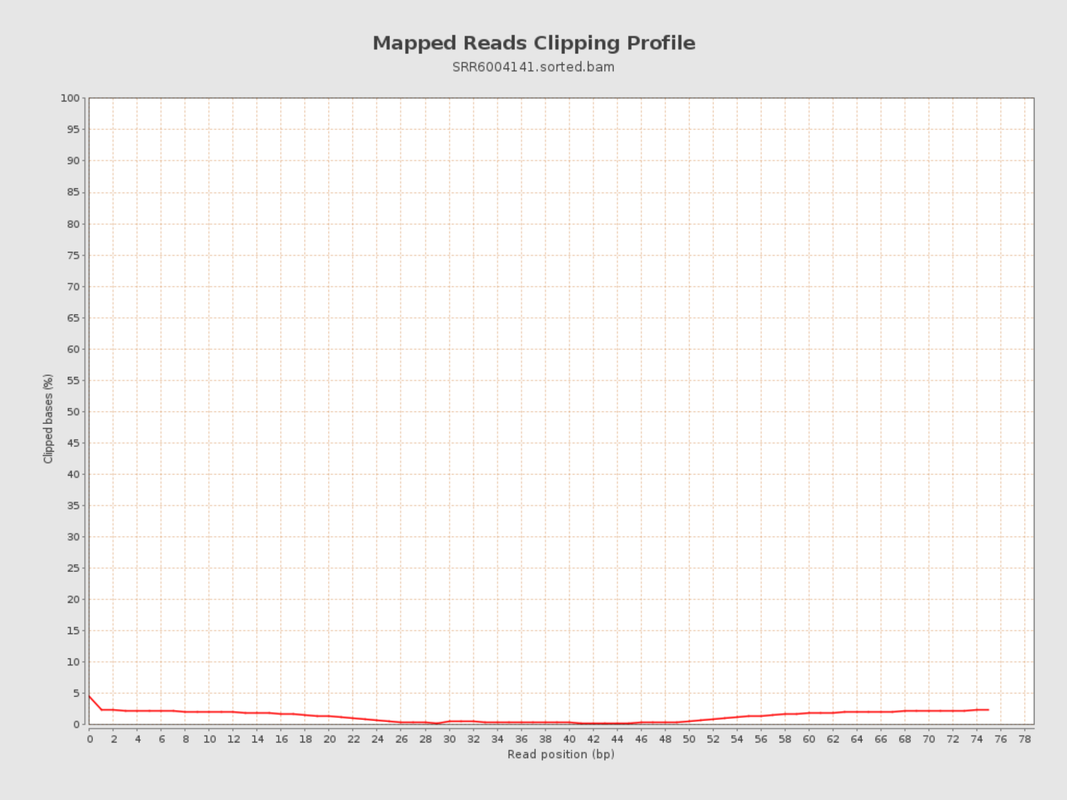
8. Results : Mapped Reads Nucleotide Content



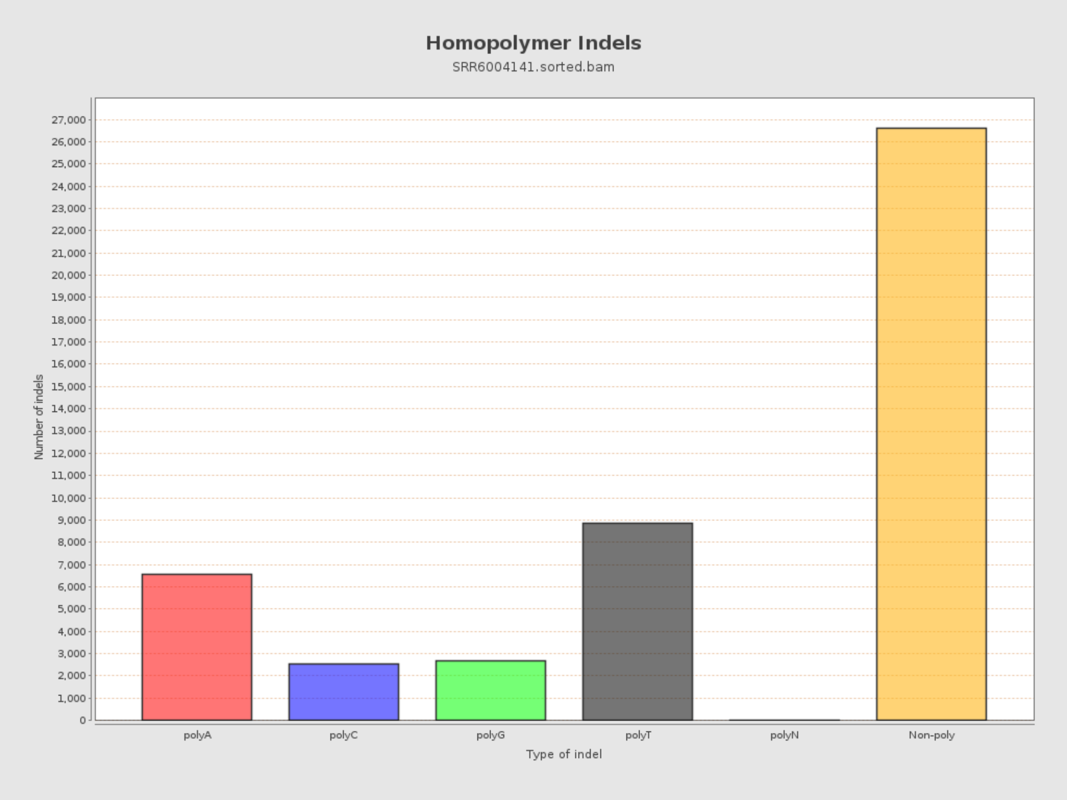
9. Results : Mapped Reads GC-content Distribution



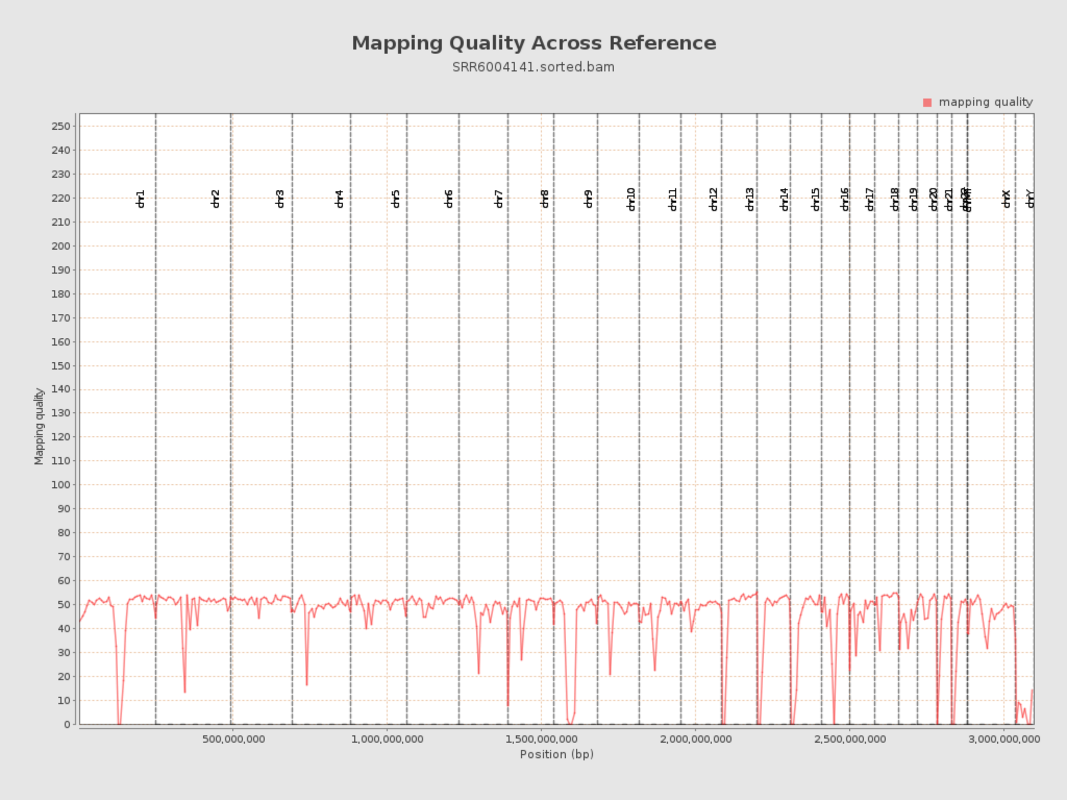
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram