Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:43:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525046.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_SRR10525046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:43:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,239,867
Mapped reads	1,141,629 / 92.08%
Unmapped reads	98,238 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,471 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	61,103 / 4.93%
Duplication rate	4.37%
Clipped reads	1,143,782 / 92.25%

2.2. ACGT Content

Number/percentage of A's	17,517,251 / 26.18%
Number/percentage of C's	12,298,344 / 18.38%
Number/percentage of T's	20,579,628 / 30.76%
Number/percentage of G's	16,501,663 / 24.66%
Number/percentage of N's	6,750 / 0.01%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2287

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

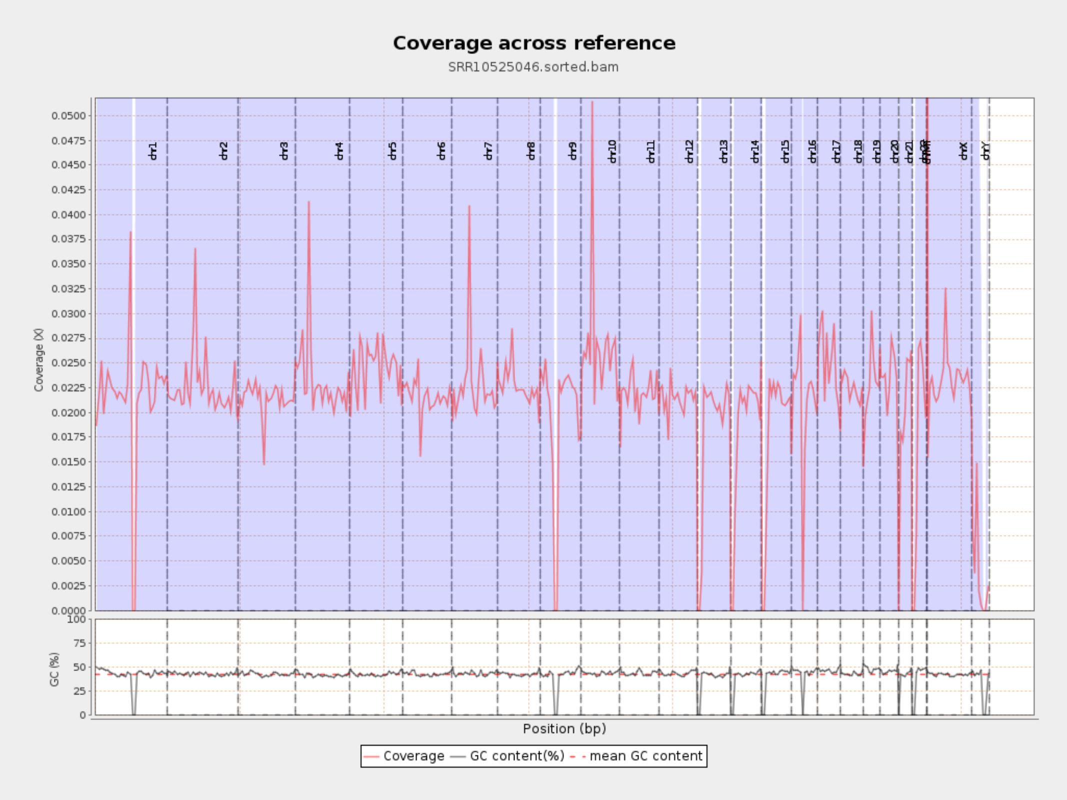
General error rate	0.5%
Mismatches	323,956
Insertions	4,421
Mapped reads with at least one insertion	0.39%
Deletions	13,528
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.76%

2.6. Chromosome stats

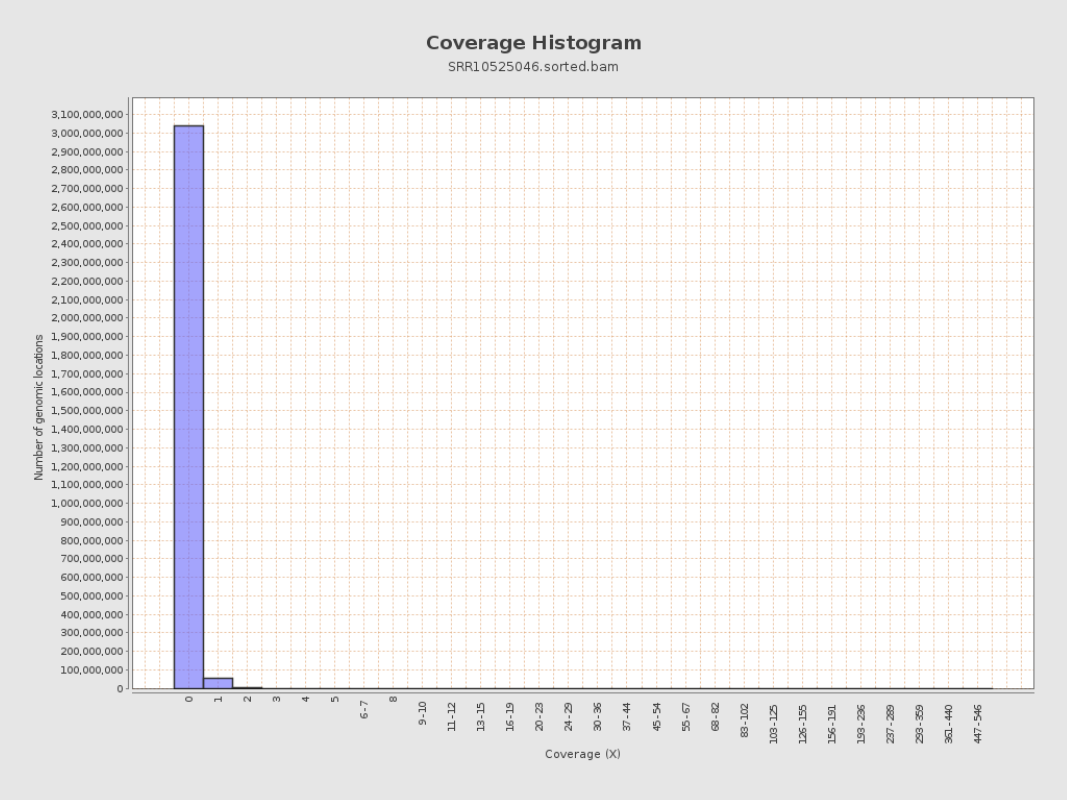
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5360391	0.0215	0.4087
chr2	243199373	5507387	0.0226	0.2741
chr3	198022430	4230859	0.0214	0.1608
chr4	191154276	4469885	0.0234	0.1866
chr5	180915260	4470552	0.0247	0.1728
chr6	171115067	3695735	0.0216	0.1731
chr7	159138663	3664032	0.023	0.2767

chr8	146364022	3324566	0.0227	0.2674
chr9	141213431	2776511	0.0197	0.1838
chr10	135534747	3622217	0.0267	0.2577
chr11	135006516	2982683	0.0221	0.1861
chr12	133851895	2869191	0.0214	0.1647
chr13	115169878	2044287	0.0178	0.1468
chr14	107349540	1918529	0.0179	0.1512
chr15	102531392	1831088	0.0179	0.1471
chr16	90354753	1848229	0.0205	0.1677
chr17	81195210	2048116	0.0252	0.1838
chr18	78077248	1754536	0.0225	0.2868
chr19	59128983	1369402	0.0232	0.303
chr20	63025520	1470792	0.0233	0.1736
chr21	48129895	944926	0.0196	0.171
chr22	51304566	863205	0.0168	0.1422
chrMT	16571	6733	0.4063	0.702
chrX	155270560	3625470	0.0233	0.1823
chrY	59373566	226114	0.0038	0.1401

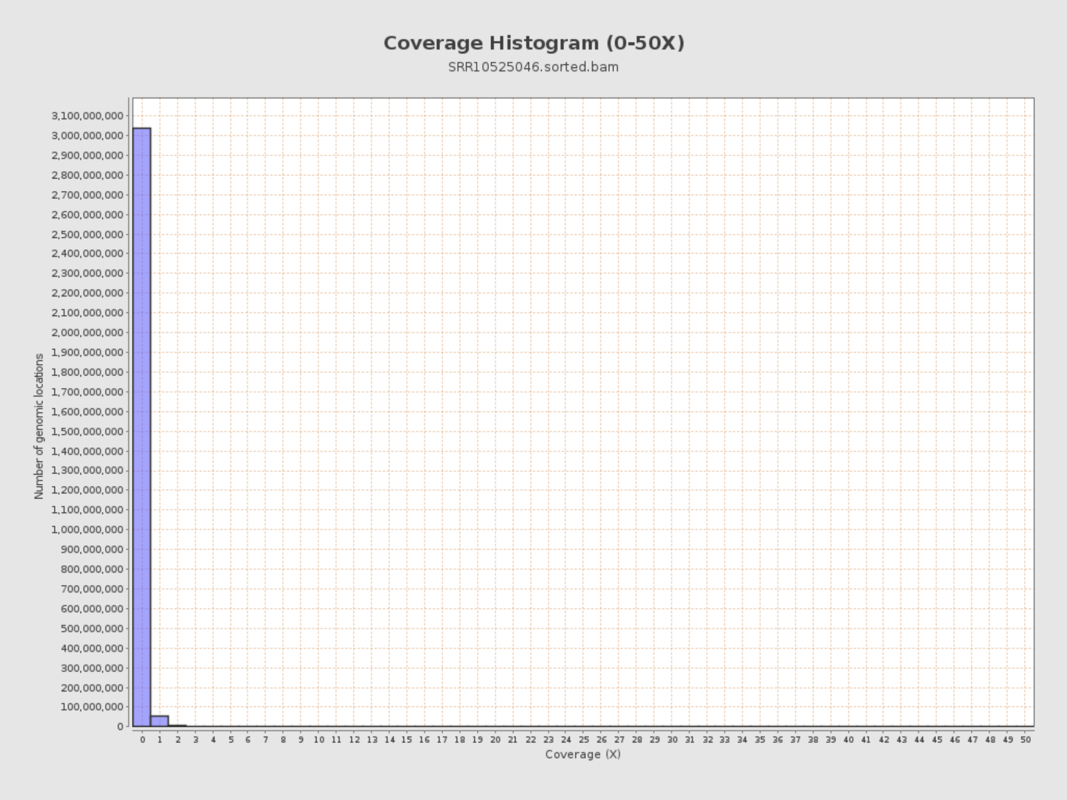
3. Results : Coverage across reference



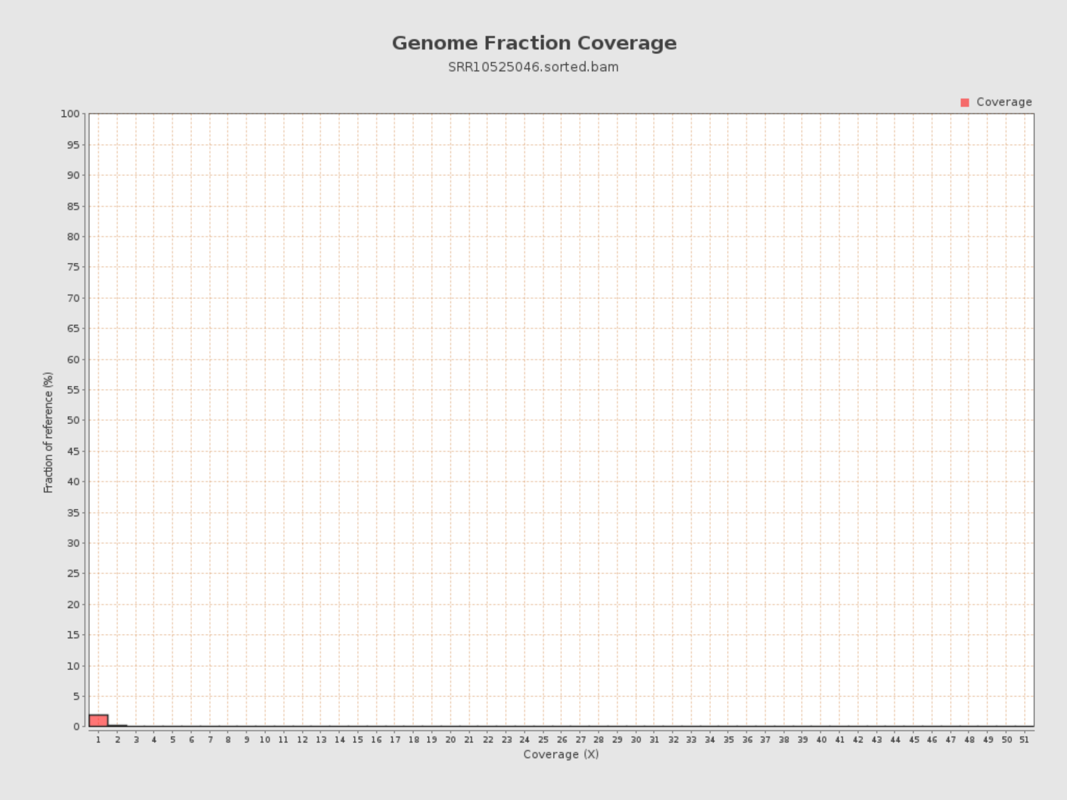
4. Results : Coverage Histogram



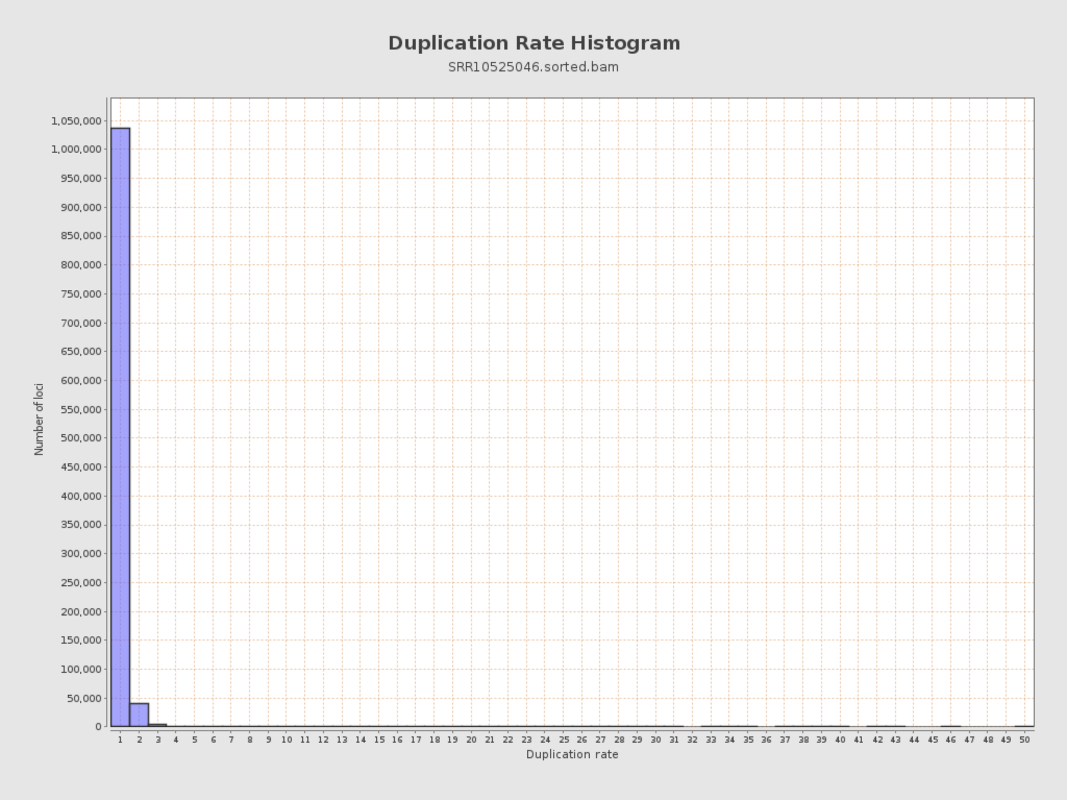
5. Results : Coverage Histogram (0-50X)



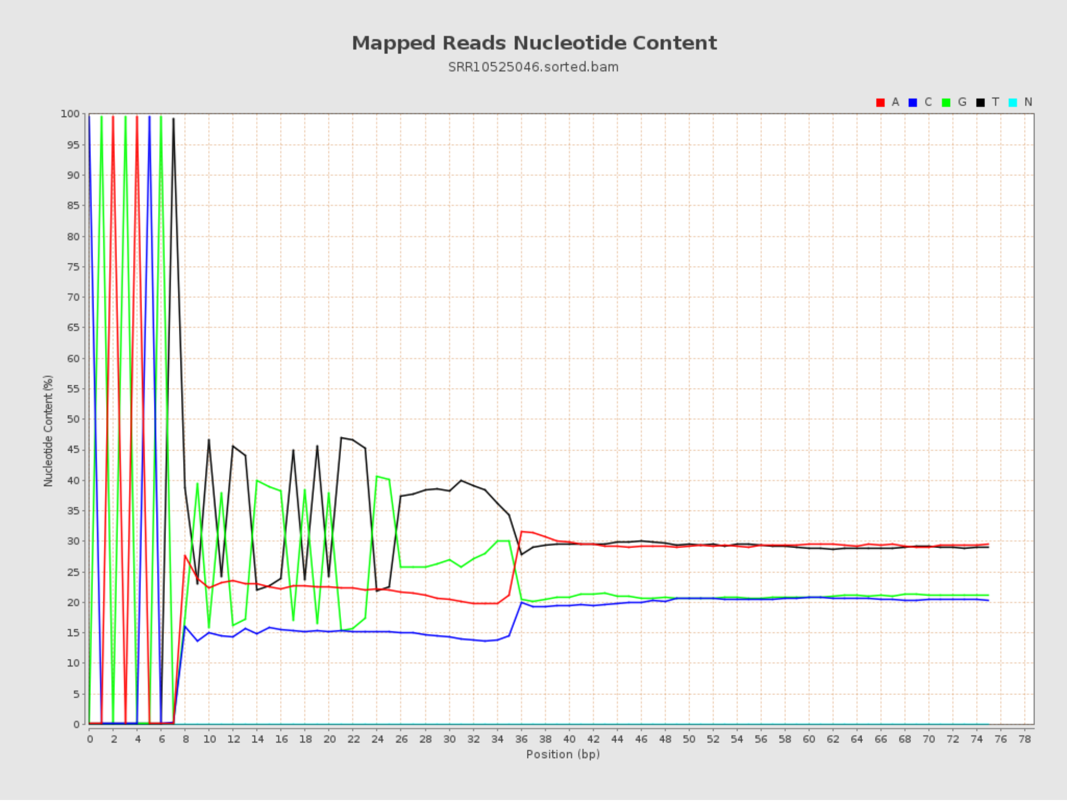
6. Results : Genome Fraction Coverage



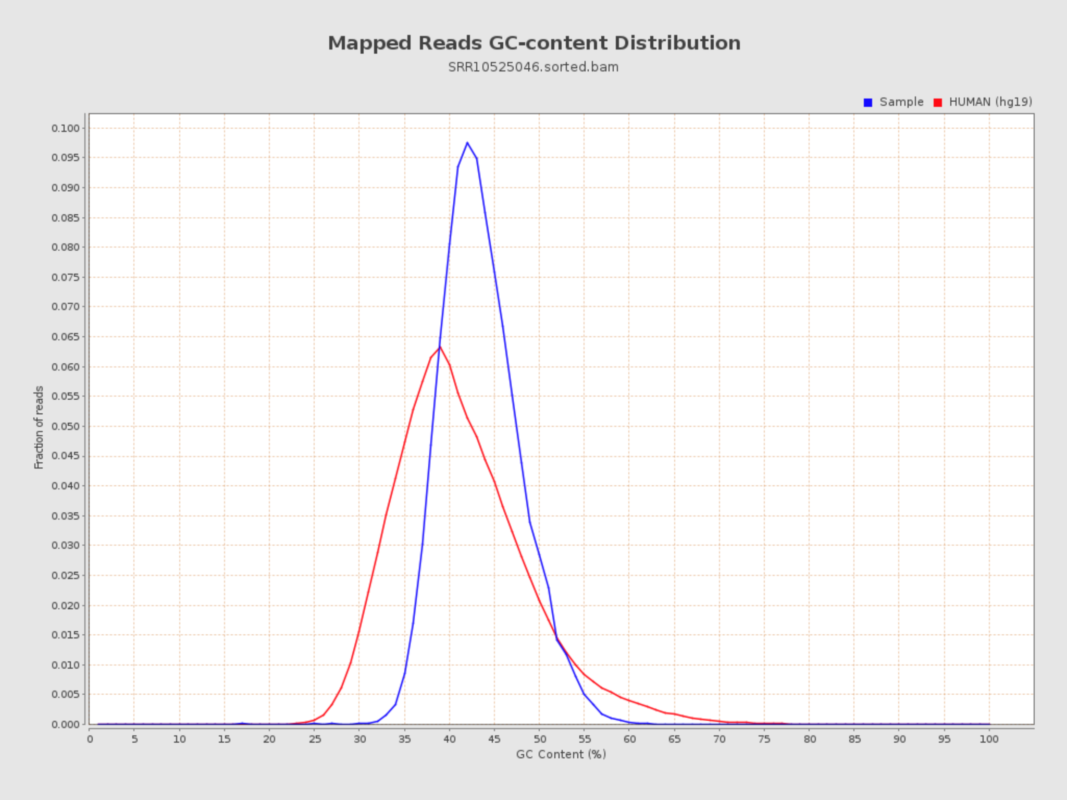
7. Results : Duplication Rate Histogram



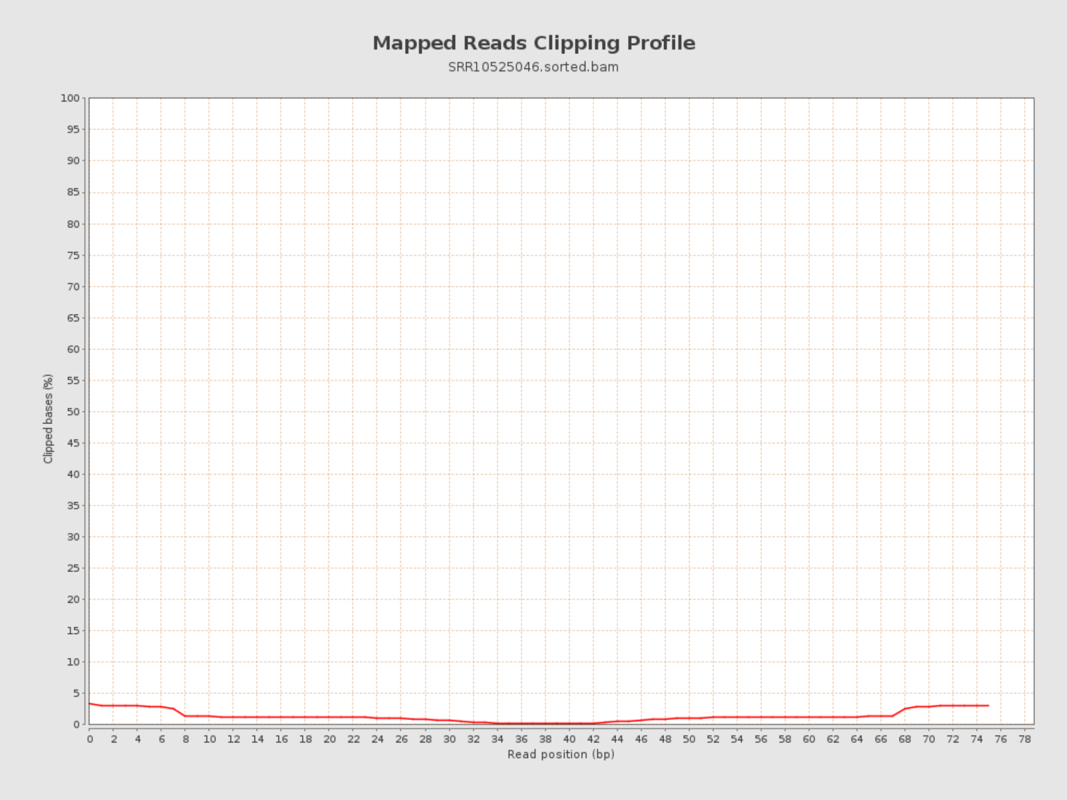
8. Results : Mapped Reads Nucleotide Content



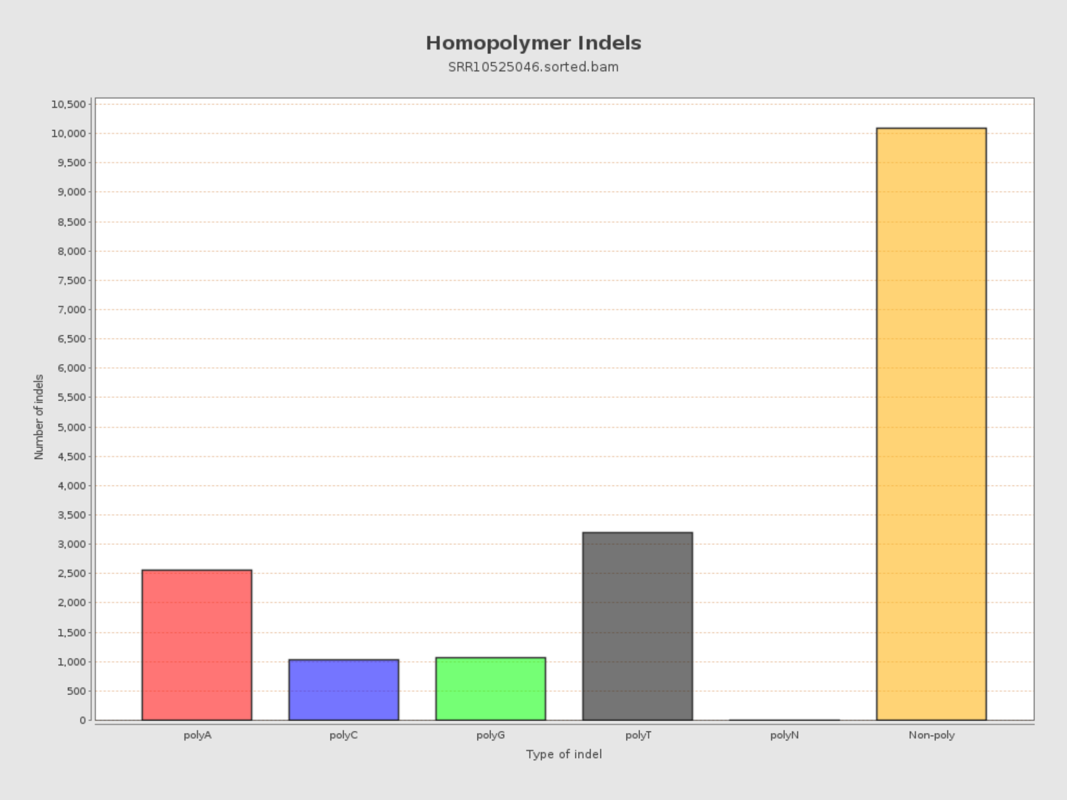
9. Results : Mapped Reads GC-content Distribution



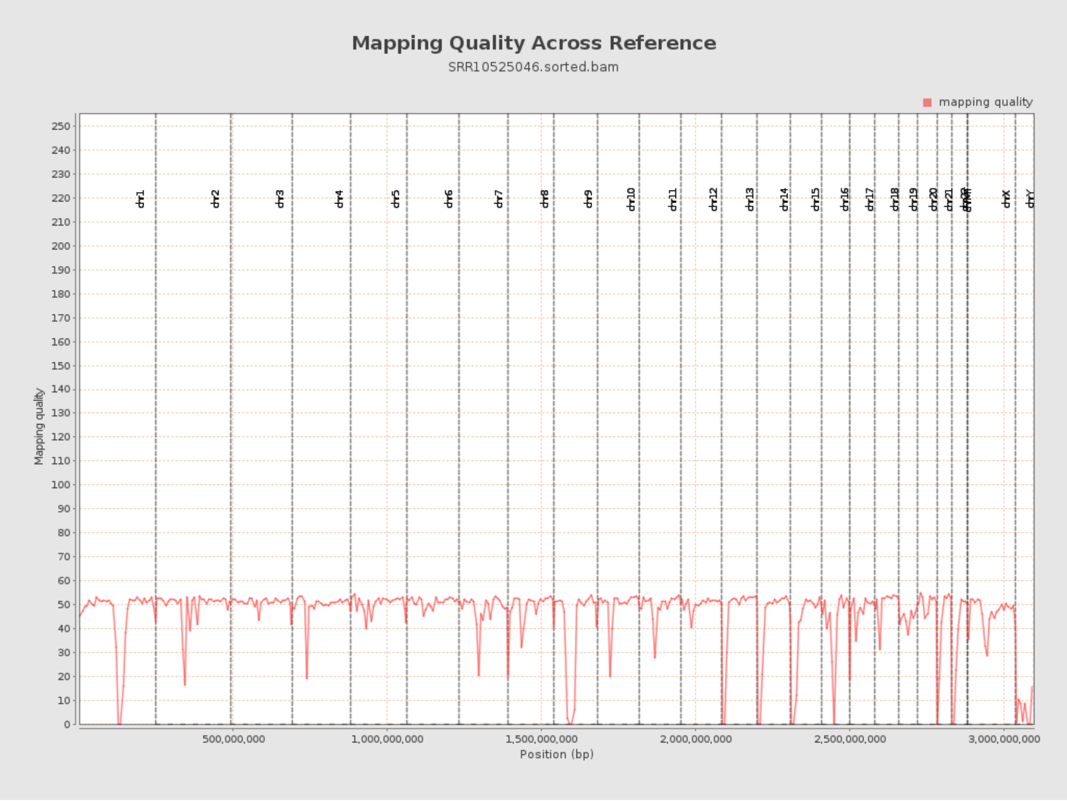
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram