Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:57:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525166.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_SRR10525166 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525166.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:57:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525166.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	492,150
Mapped reads	435,312 / 88.45%
Unmapped reads	56,838 / 11.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,487 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	6,581 / 1.34%
Duplication rate	1.14%
Clipped reads	435,087 / 88.41%

2.2. ACGT Content

Number/percentage of A's	7,359,821 / 27.23%
Number/percentage of C's	5,240,112 / 19.39%
Number/percentage of T's	7,936,288 / 29.36%
Number/percentage of G's	6,494,082 / 24.02%
Number/percentage of N's	670 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.1175

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

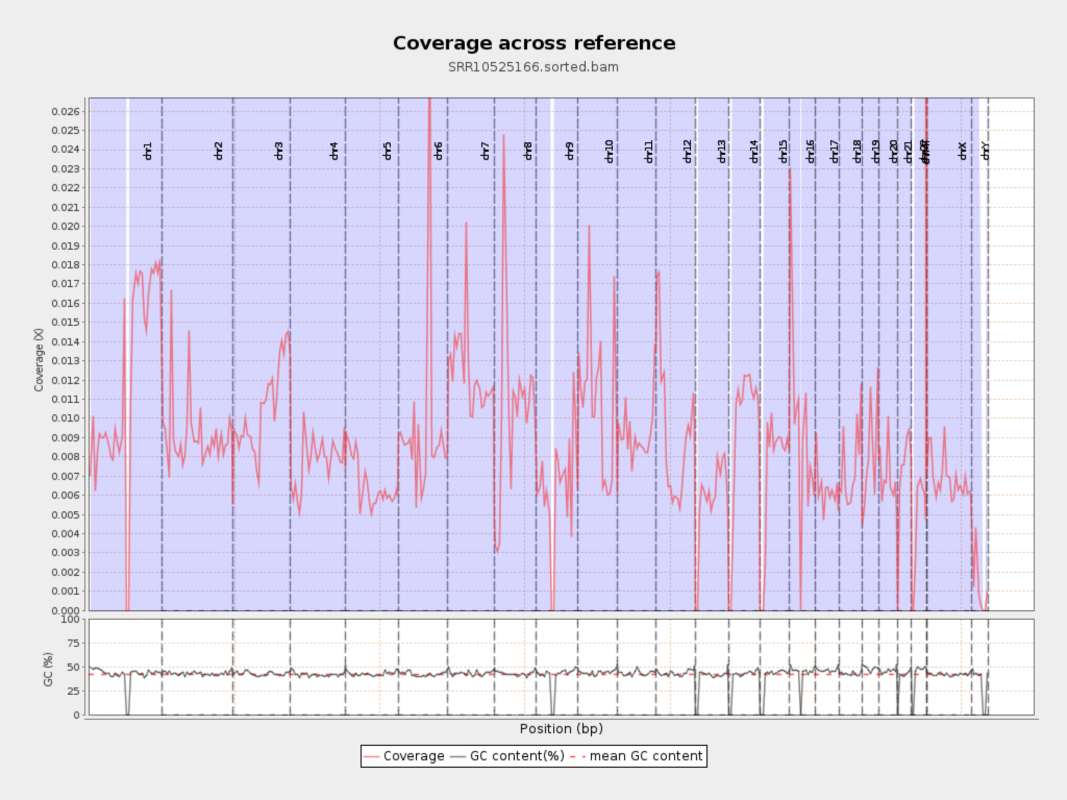
General error rate	0.49%
Mismatches	129,884
Insertions	1,966
Mapped reads with at least one insertion	0.45%
Deletions	5,679
Mapped reads with at least one deletion	1.29%
Homopolymer indels	42.51%

2.6. Chromosome stats

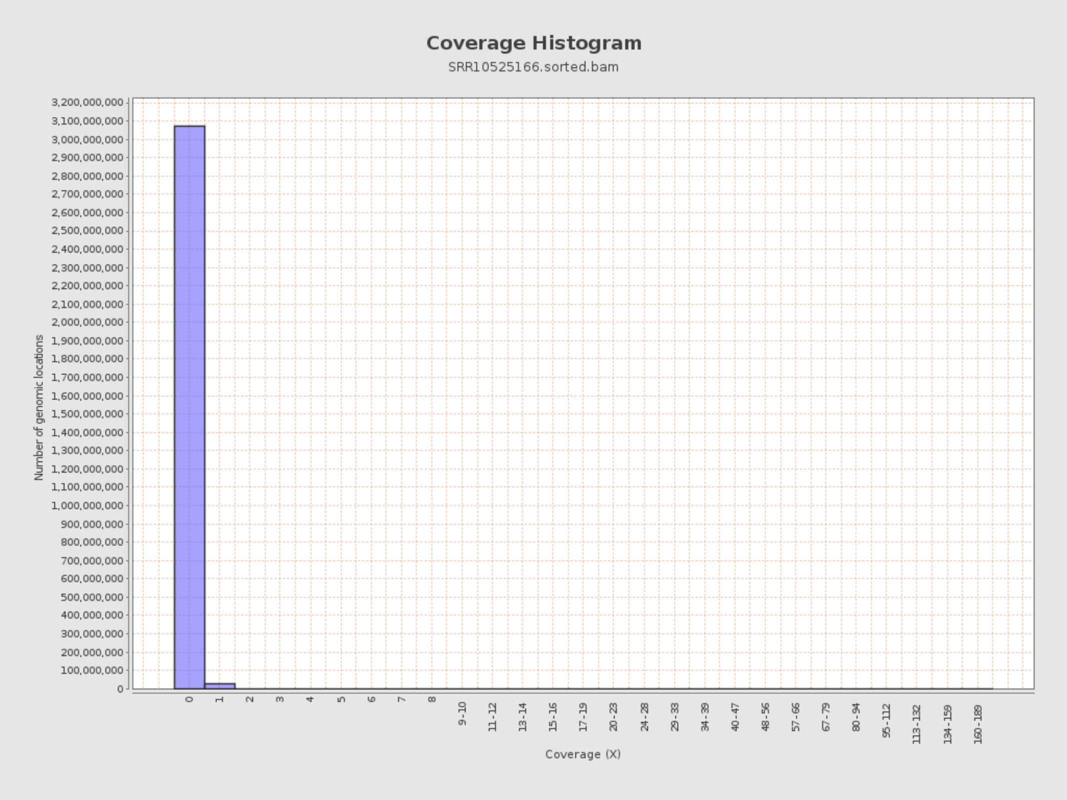
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2937452	0.0118	0.1917
chr2	243199373	2225913	0.0092	0.1178
chr3	198022430	2071950	0.0105	0.1052
chr4	191154276	1481108	0.0077	0.0925
chr5	180915260	1191548	0.0066	0.0832
chr6	171115067	1666923	0.0097	0.1053
chr7	159138663	1987003	0.0125	0.1843

chr8	146364022	1537176	0.0105	0.1121
chr9	141213431	898292	0.0064	0.0908
chr10	135534747	1495910	0.011	0.1295
chr11	135006516	1241037	0.0092	0.1061
chr12	133851895	1224075	0.0091	0.0984
chr13	115169878	665922	0.0058	0.0776
chr14	107349540	1016385	0.0095	0.1007
chr15	102531392	736612	0.0072	0.0869
chr16	90354753	841685	0.0093	0.1022
chr17	81195210	513902	0.0063	0.0829
chr18	78077248	582999	0.0075	0.1451
chr19	59128983	487608	0.0082	0.137
chr20	63025520	438934	0.007	0.0857
chr21	48129895	349846	0.0073	0.0894
chr22	51304566	227689	0.0044	0.0681
chrMT	16571	73341	4.4259	3.1597
chrX	155270560	1072766	0.0069	0.0872
chrY	59373566	74221	0.0013	0.0479

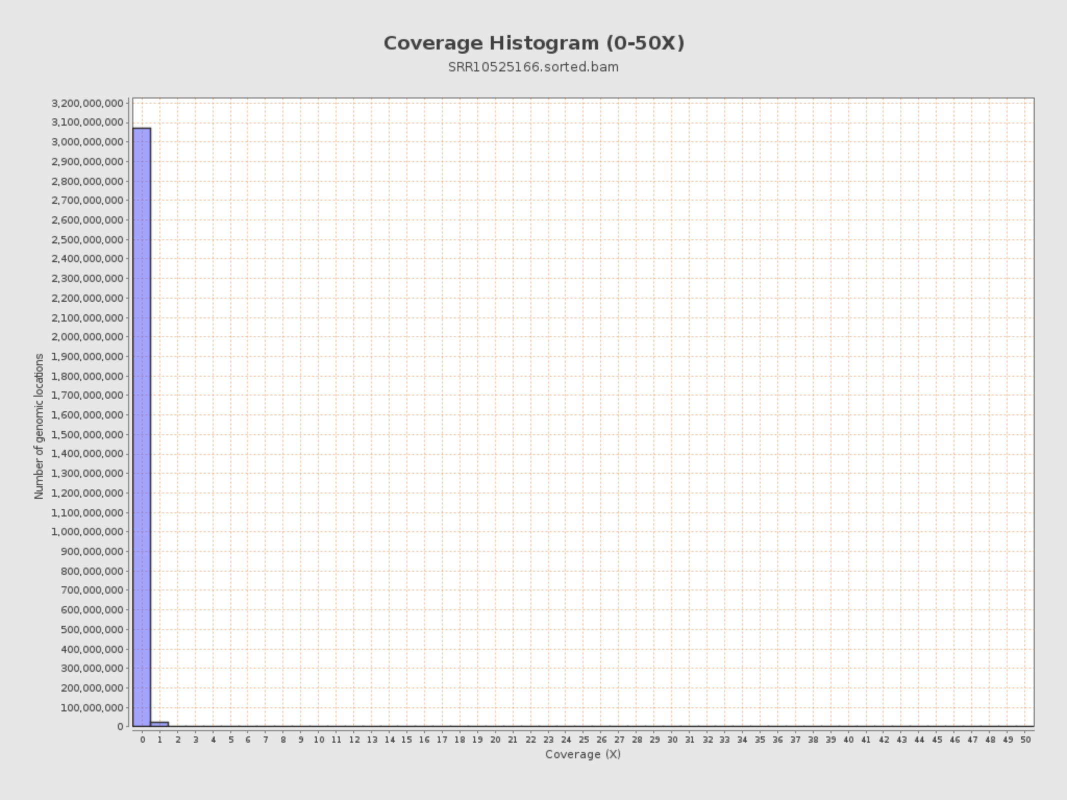
3. Results : Coverage across reference



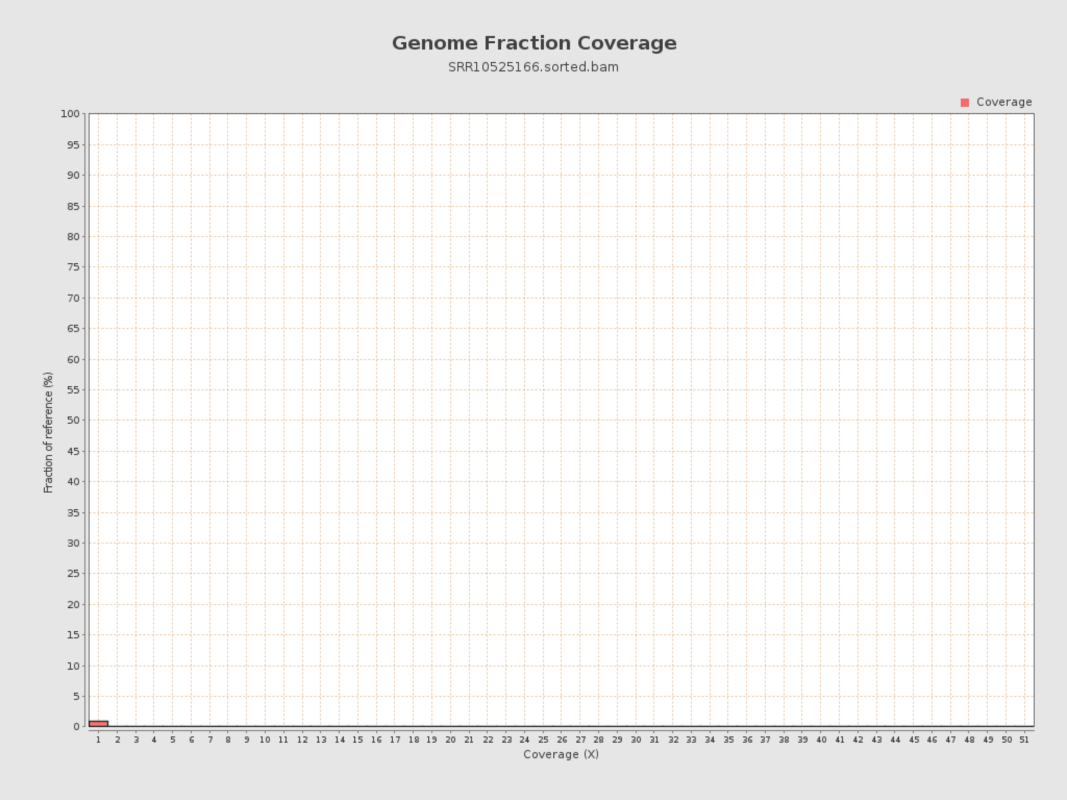
4. Results : Coverage Histogram



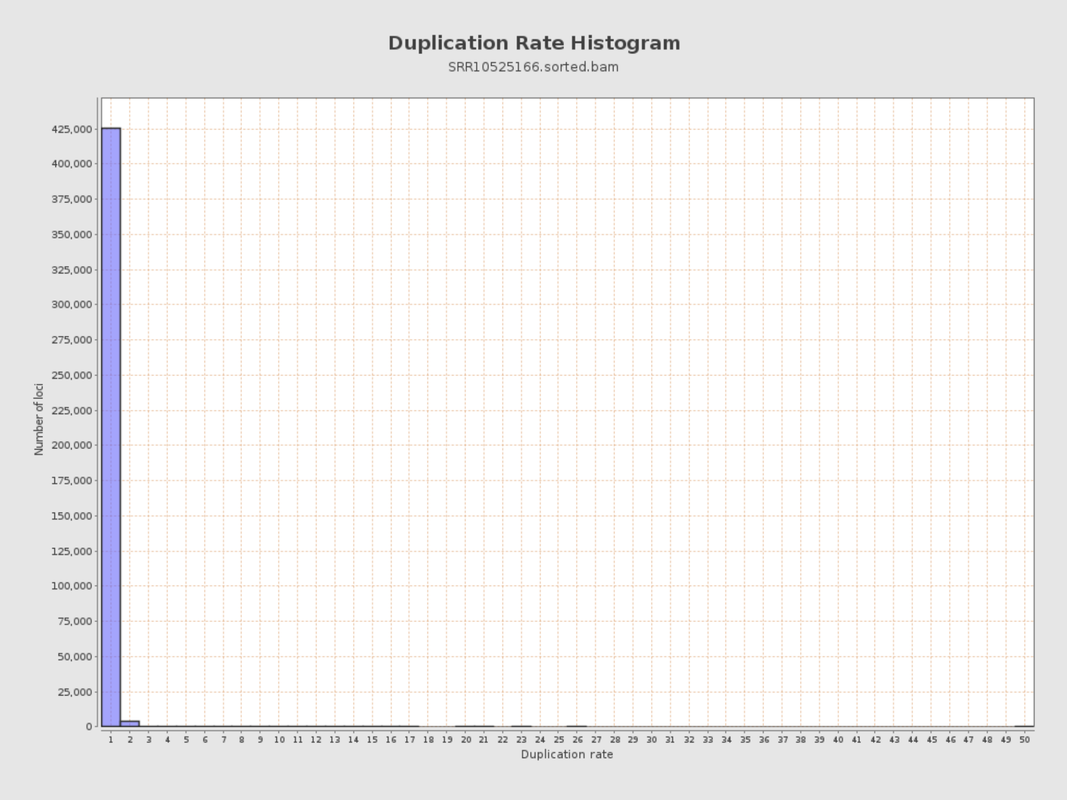
5. Results : Coverage Histogram (0-50X)



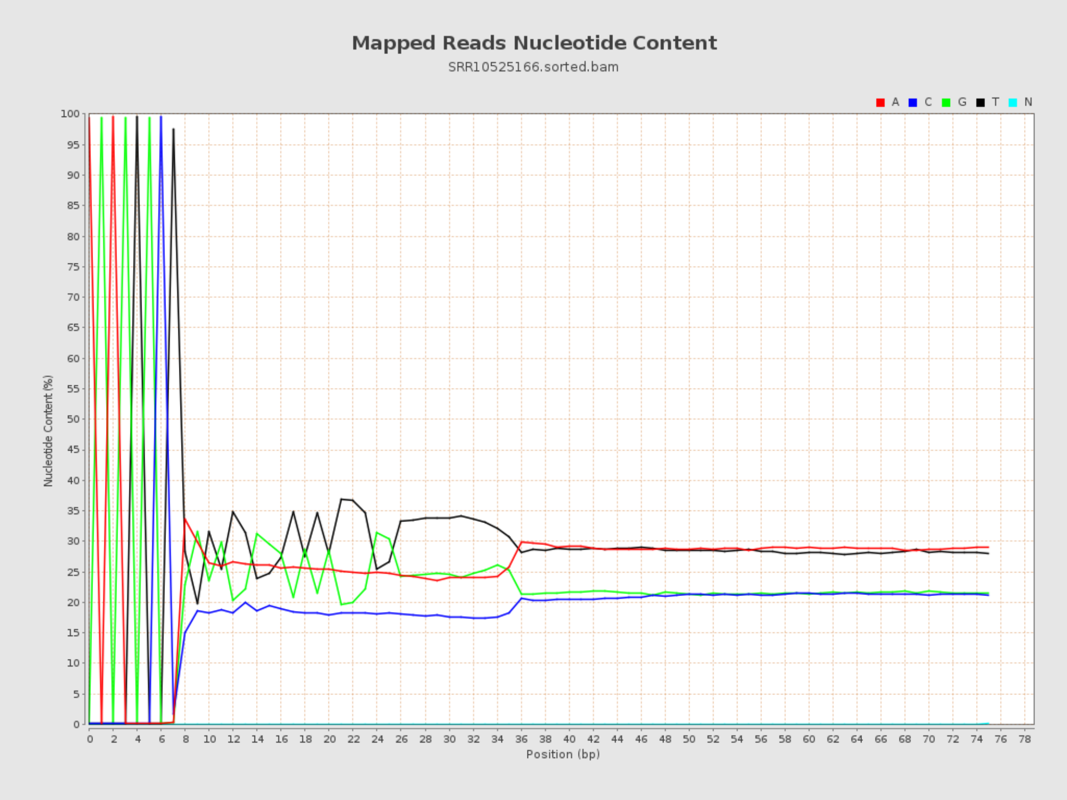
6. Results : Genome Fraction Coverage



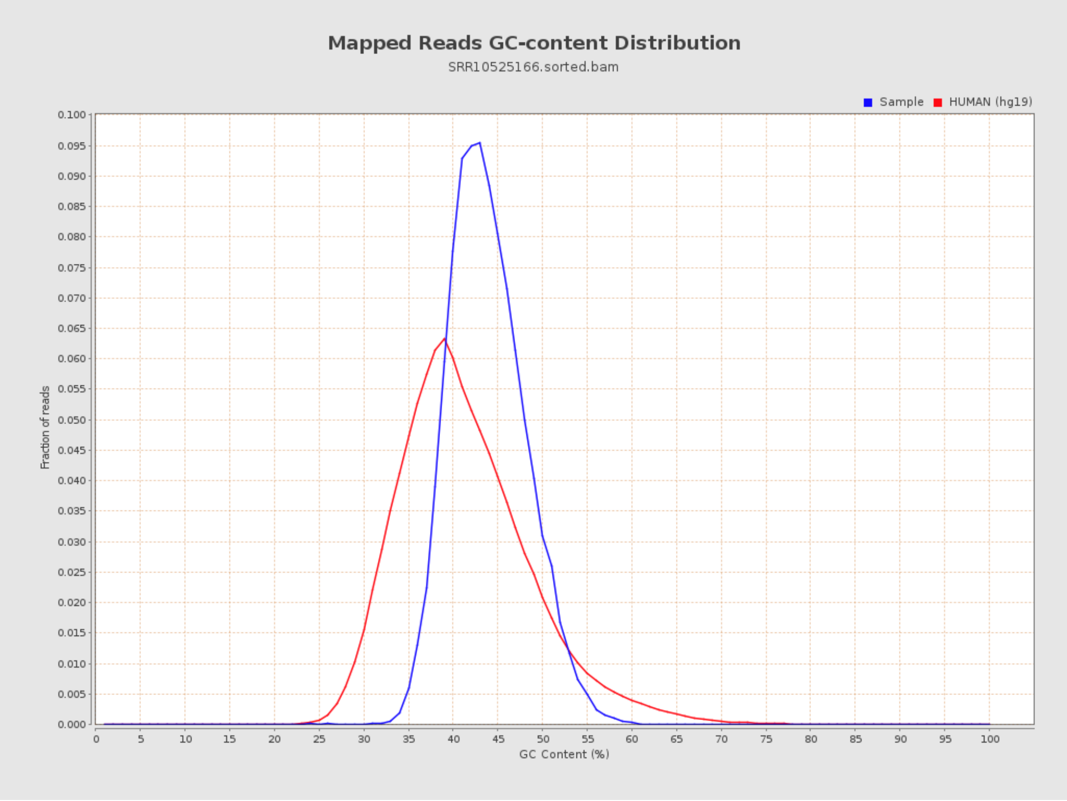
7. Results : Duplication Rate Histogram



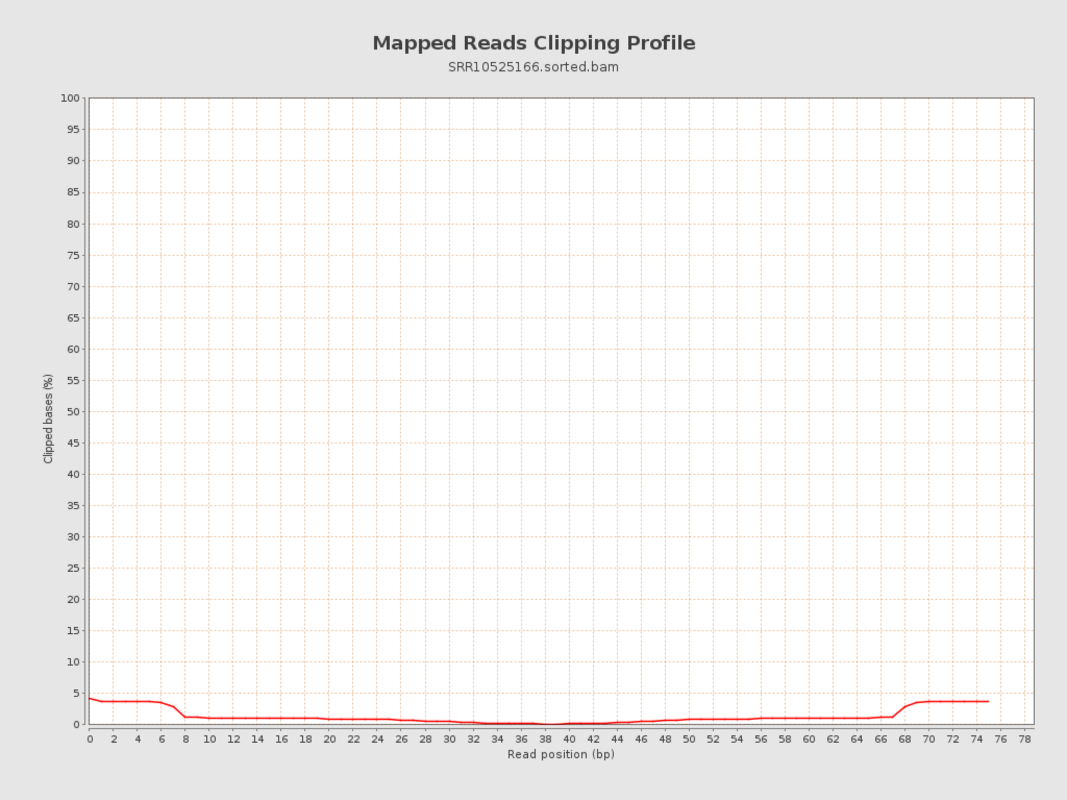
8. Results : Mapped Reads Nucleotide Content



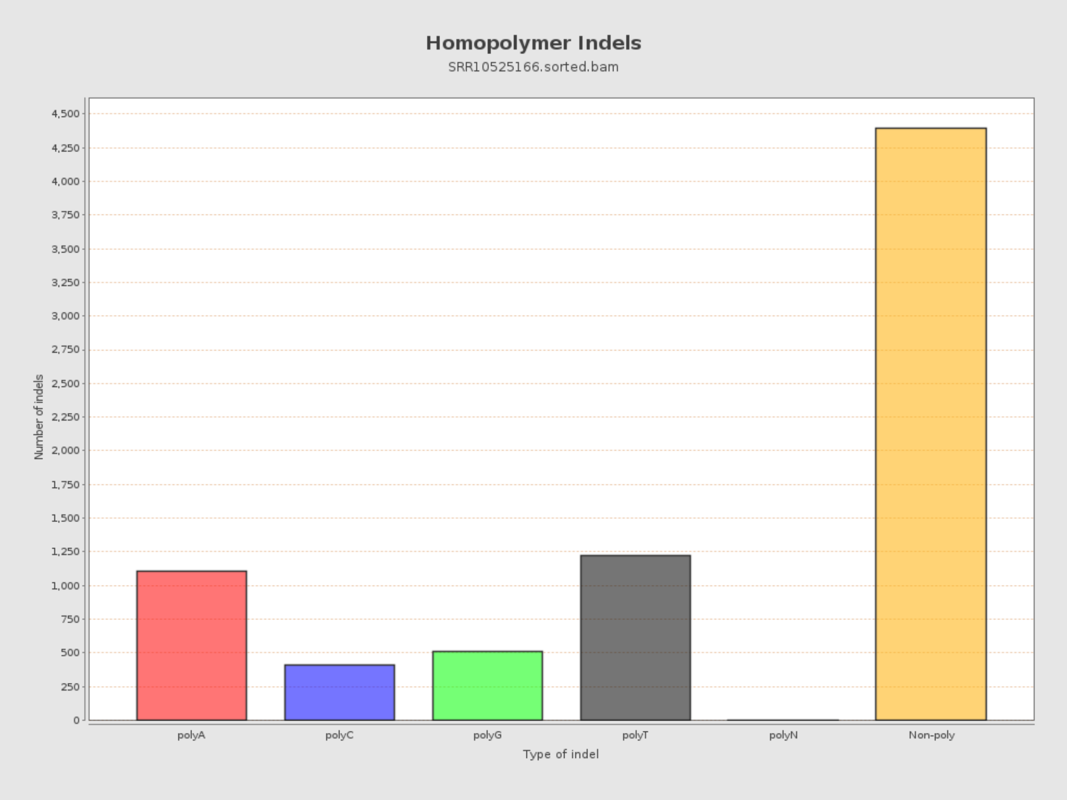
9. Results : Mapped Reads GC-content Distribution



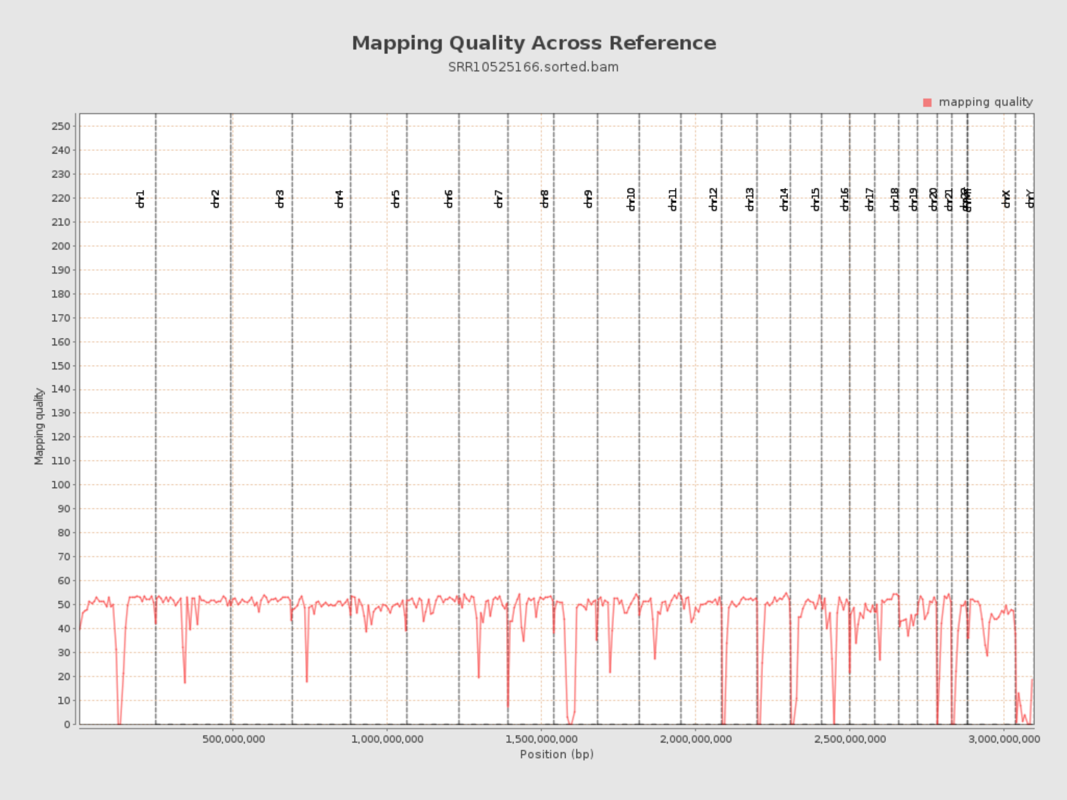
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram