Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:59:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525225.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_SRR10525225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:59:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	559,898
Mapped reads	514,843 / 91.95%
Unmapped reads	45,055 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,220 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	11,124 / 1.99%
Duplication rate	1.64%
Clipped reads	514,986 / 91.98%

2.2. ACGT Content

Number/percentage of A's	7,214,181 / 24.26%
Number/percentage of C's	5,335,351 / 17.94%
Number/percentage of T's	9,248,728 / 31.1%
Number/percentage of G's	7,943,313 / 26.71%
Number/percentage of N's	661 / 0%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1245

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

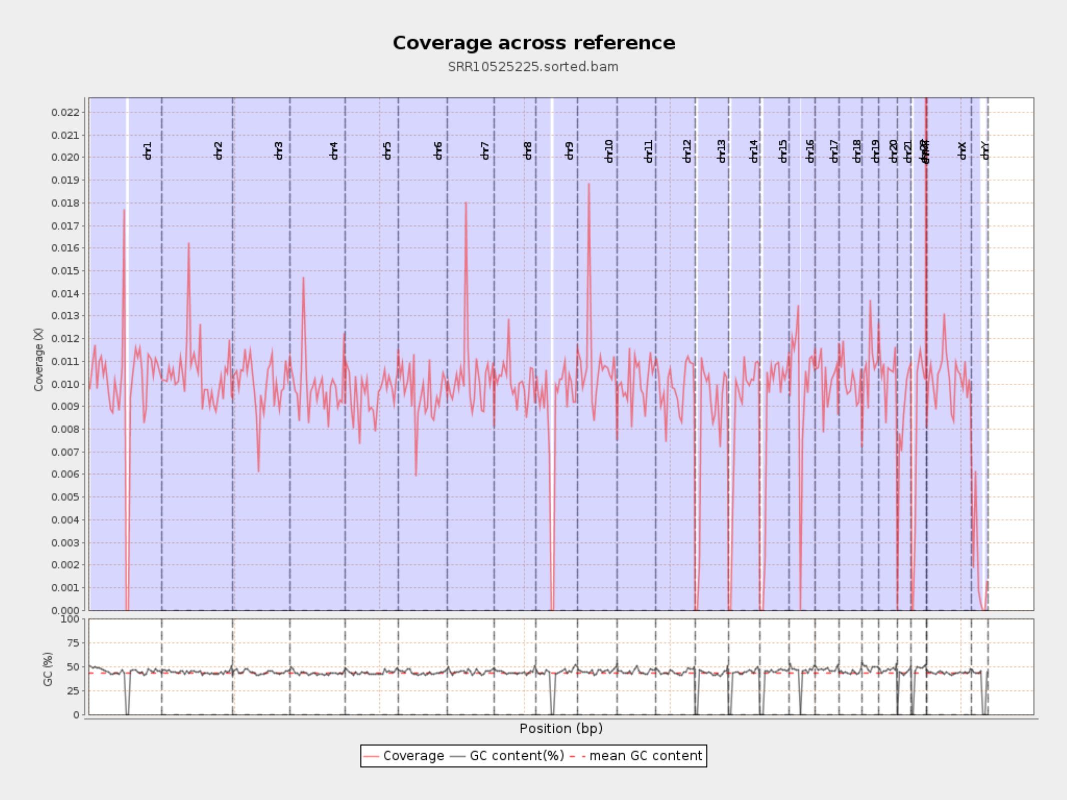
General error rate	0.53%
Mismatches	152,892
Insertions	2,044
Mapped reads with at least one insertion	0.4%
Deletions	5,874
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.82%

2.6. Chromosome stats

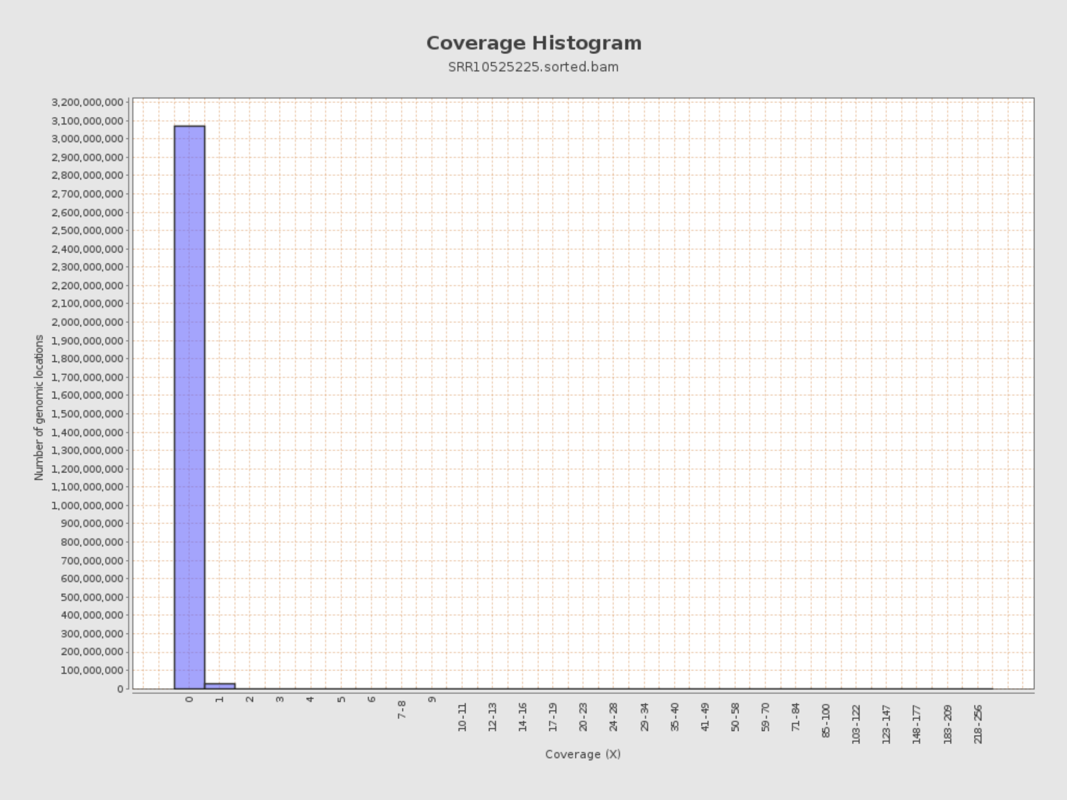
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2472399	0.0099	0.2029
chr2	243199373	2545247	0.0105	0.1478
chr3	198022430	1978716	0.01	0.1035
chr4	191154276	1891830	0.0099	0.1067
chr5	180915260	1727841	0.0096	0.101
chr6	171115067	1648493	0.0096	0.1059
chr7	159138663	1651751	0.0104	0.1534

chr8	146364022	1479594	0.0101	0.1125
chr9	141213431	1212315	0.0086	0.1048
chr10	135534747	1469353	0.0108	0.1258
chr11	135006516	1356153	0.01	0.1137
chr12	133851895	1324654	0.0099	0.1034
chr13	115169878	928598	0.0081	0.0933
chr14	107349540	914052	0.0085	0.0966
chr15	102531392	855283	0.0083	0.0945
chr16	90354753	903201	0.01	0.1081
chr17	81195210	820296	0.0101	0.1049
chr18	78077248	796884	0.0102	0.1599
chr19	59128983	643351	0.0109	0.1532
chr20	63025520	658697	0.0105	0.1065
chr21	48129895	396880	0.0082	0.0969
chr22	51304566	380531	0.0074	0.089
chrMT	16571	5238	0.3161	0.6609
chrX	155270560	1587884	0.0102	0.1081
chrY	59373566	102413	0.0017	0.0634

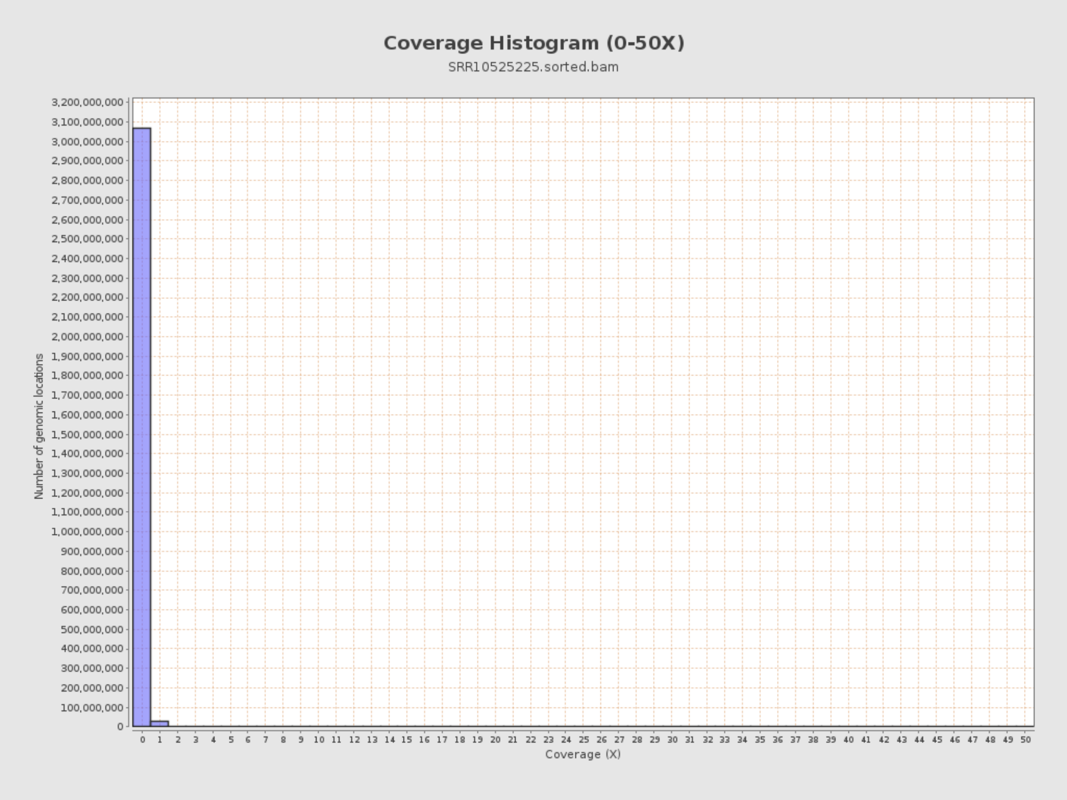
3. Results : Coverage across reference



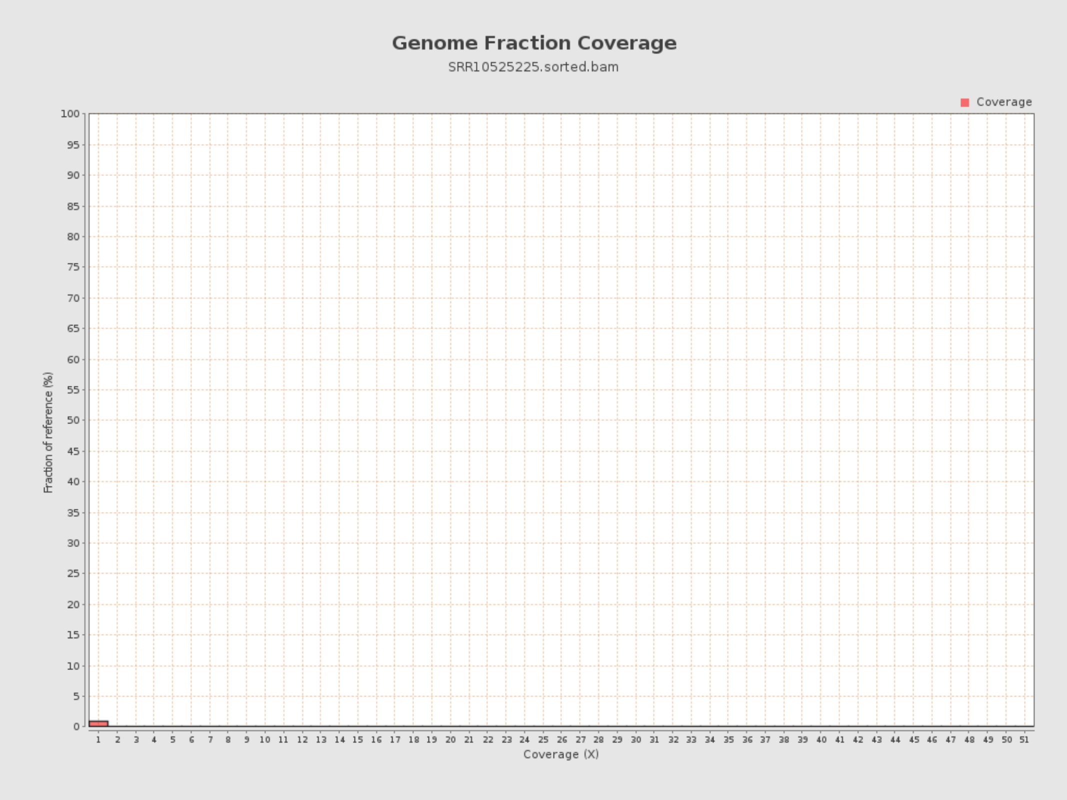
4. Results : Coverage Histogram



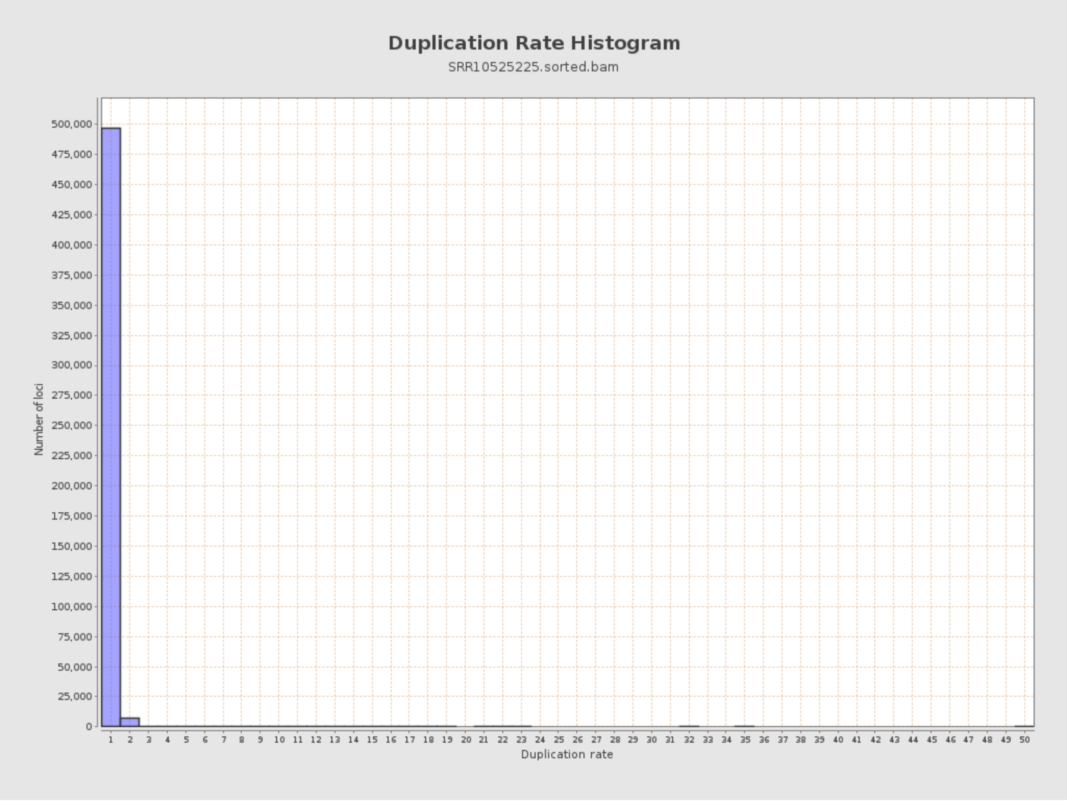
5. Results : Coverage Histogram (0-50X)



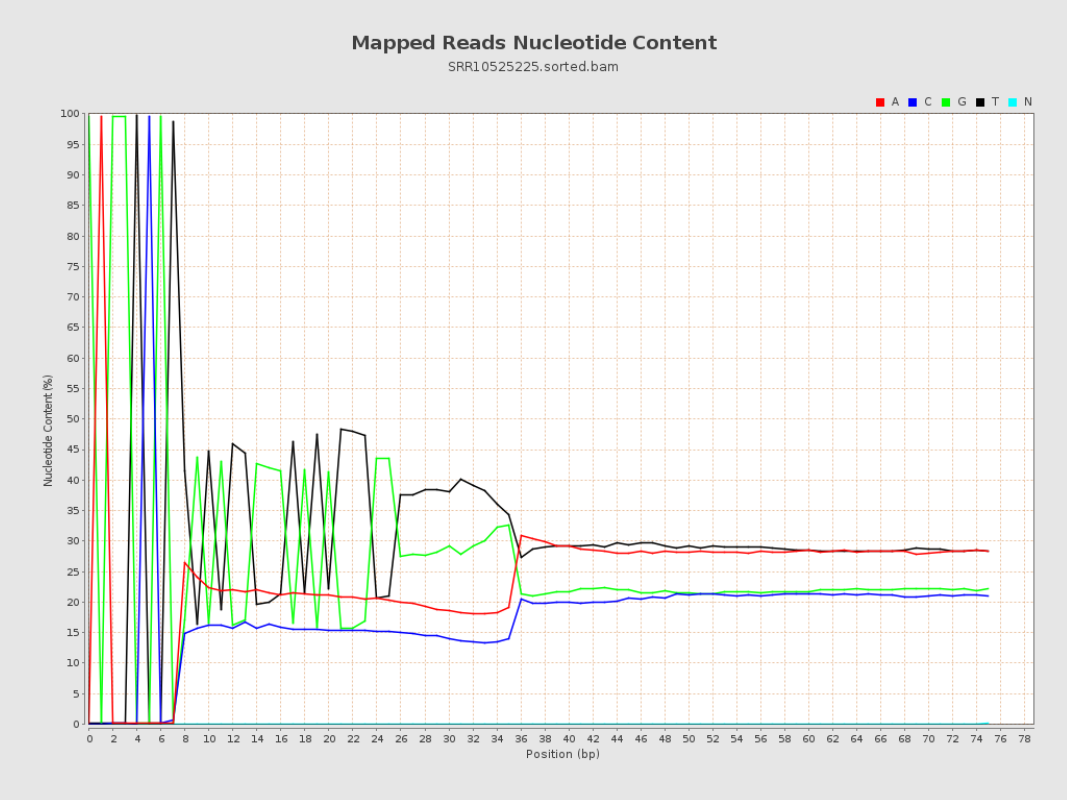
6. Results : Genome Fraction Coverage



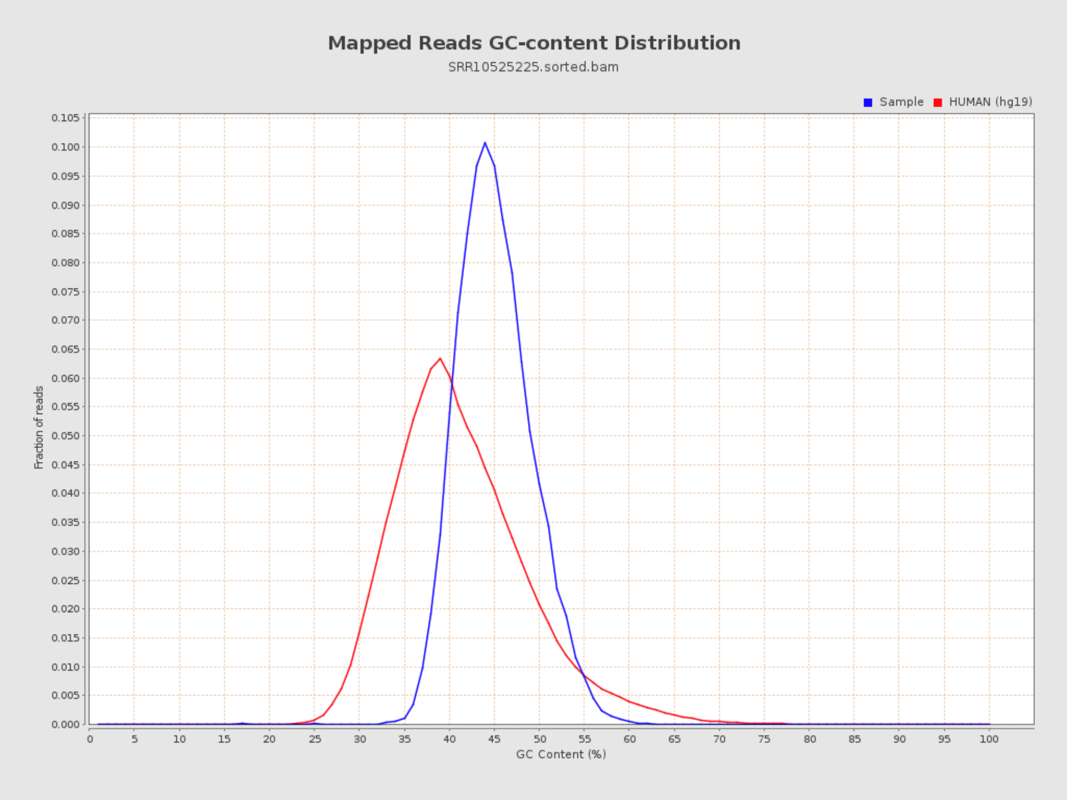
7. Results : Duplication Rate Histogram



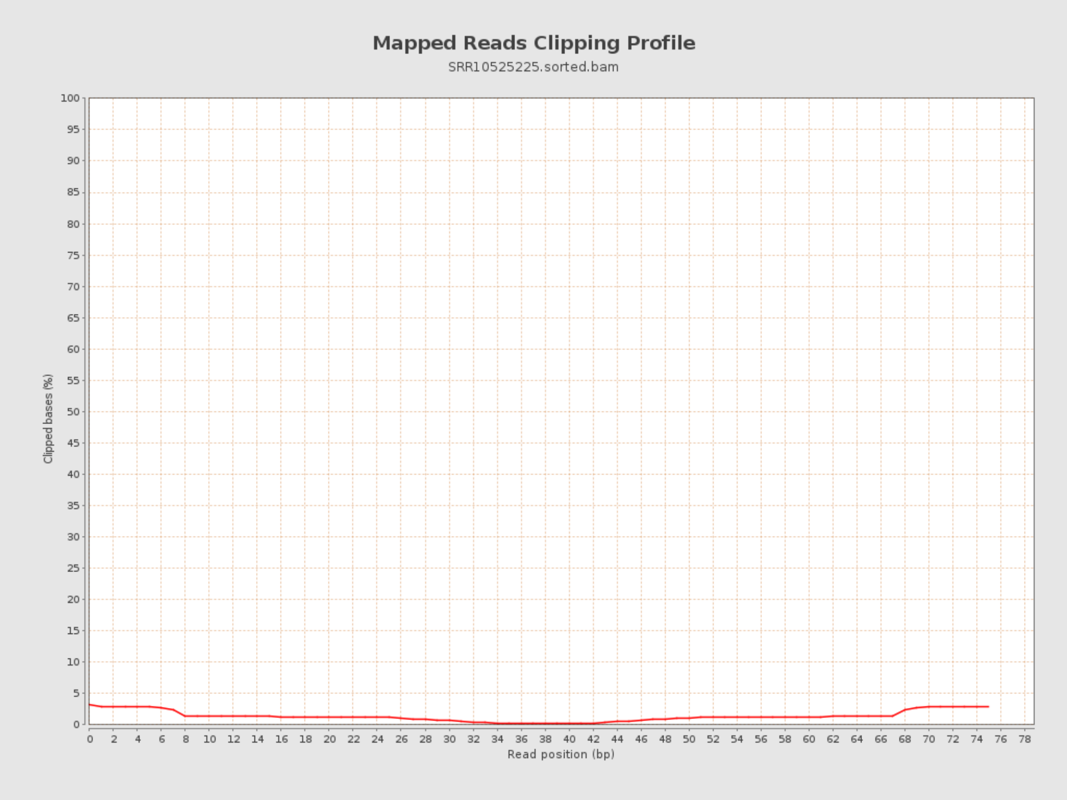
8. Results : Mapped Reads Nucleotide Content



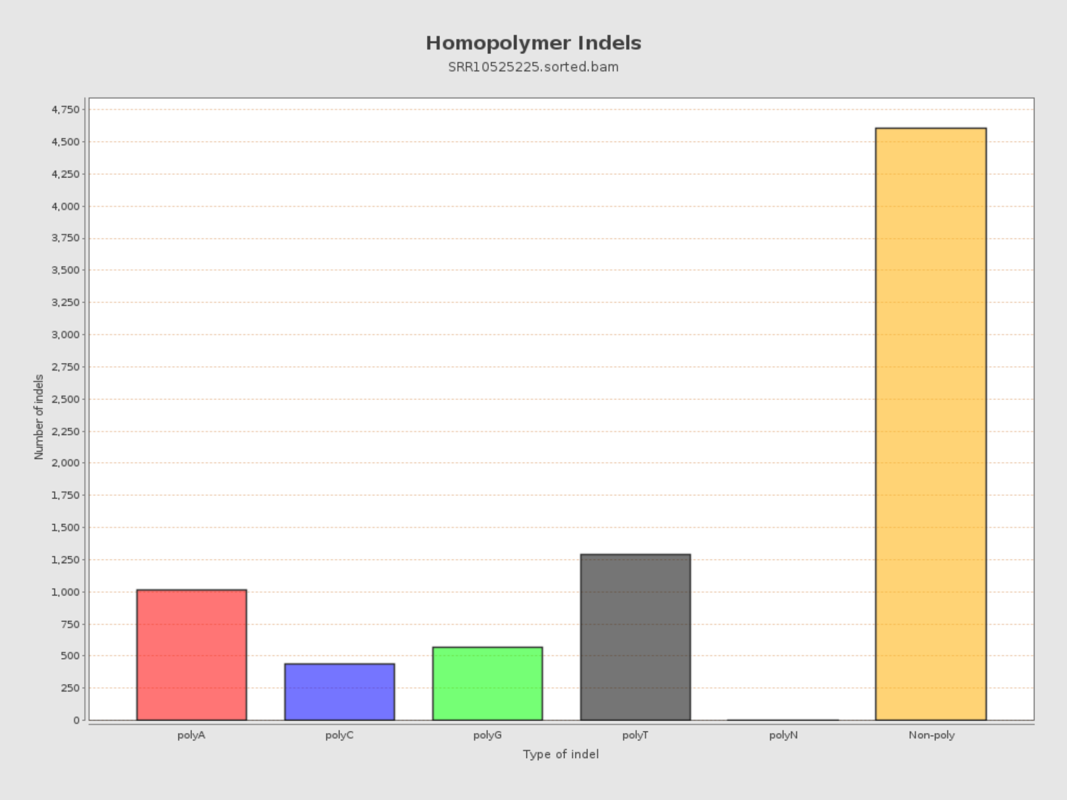
9. Results : Mapped Reads GC-content Distribution



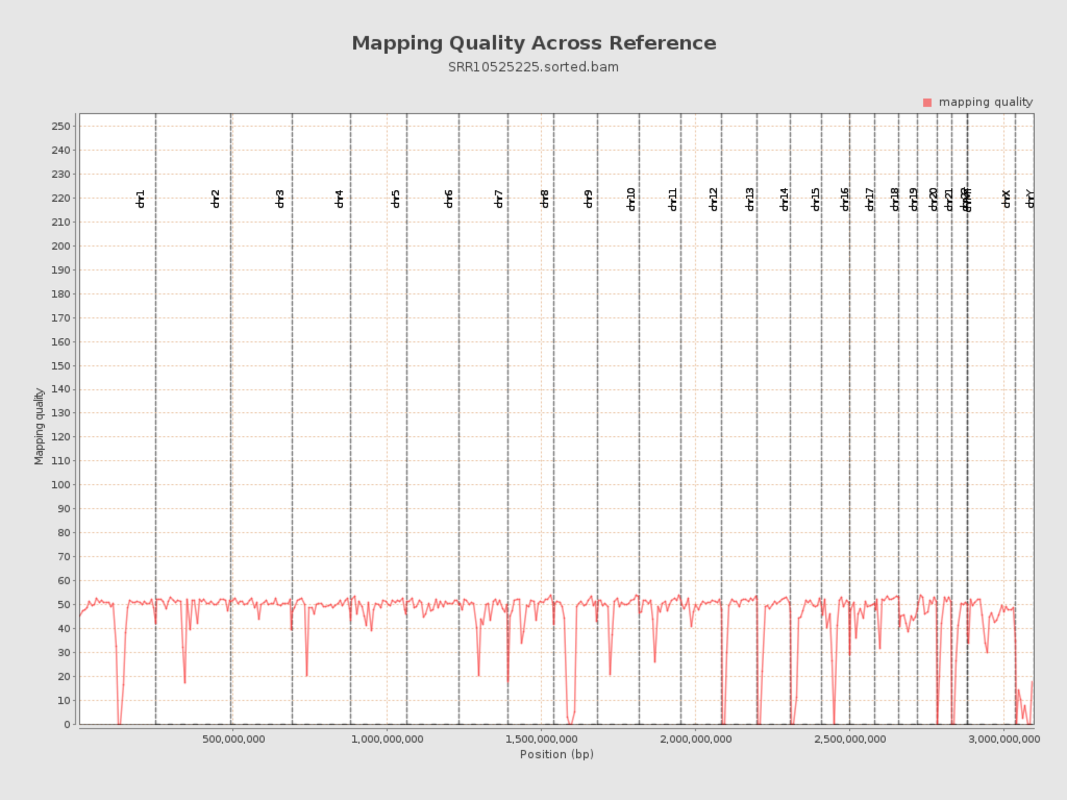
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram