Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:18:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525074.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_SRR10525074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:18:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	543,217
Mapped reads	503,000 / 92.6%
Unmapped reads	40,217 / 7.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,765 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,940 / 3.3%
Duplication rate	2.98%
Clipped reads	504,030 / 92.79%

2.2. ACGT Content

Number/percentage of A's	7,406,547 / 24.99%
Number/percentage of C's	5,623,311 / 18.97%
Number/percentage of T's	8,966,729 / 30.25%
Number/percentage of G's	7,641,300 / 25.78%
Number/percentage of N's	2,950 / 0.01%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1219

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

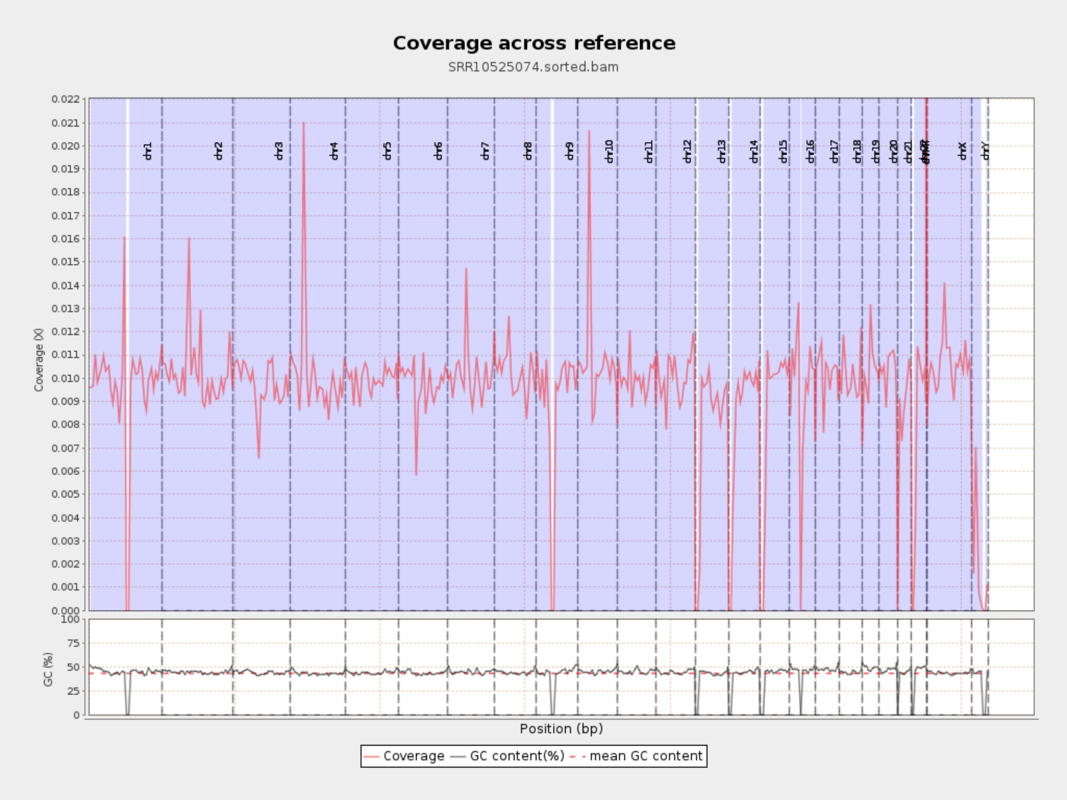
General error rate	0.49%
Mismatches	140,072
Insertions	1,854
Mapped reads with at least one insertion	0.37%
Deletions	5,702
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.23%

2.6. Chromosome stats

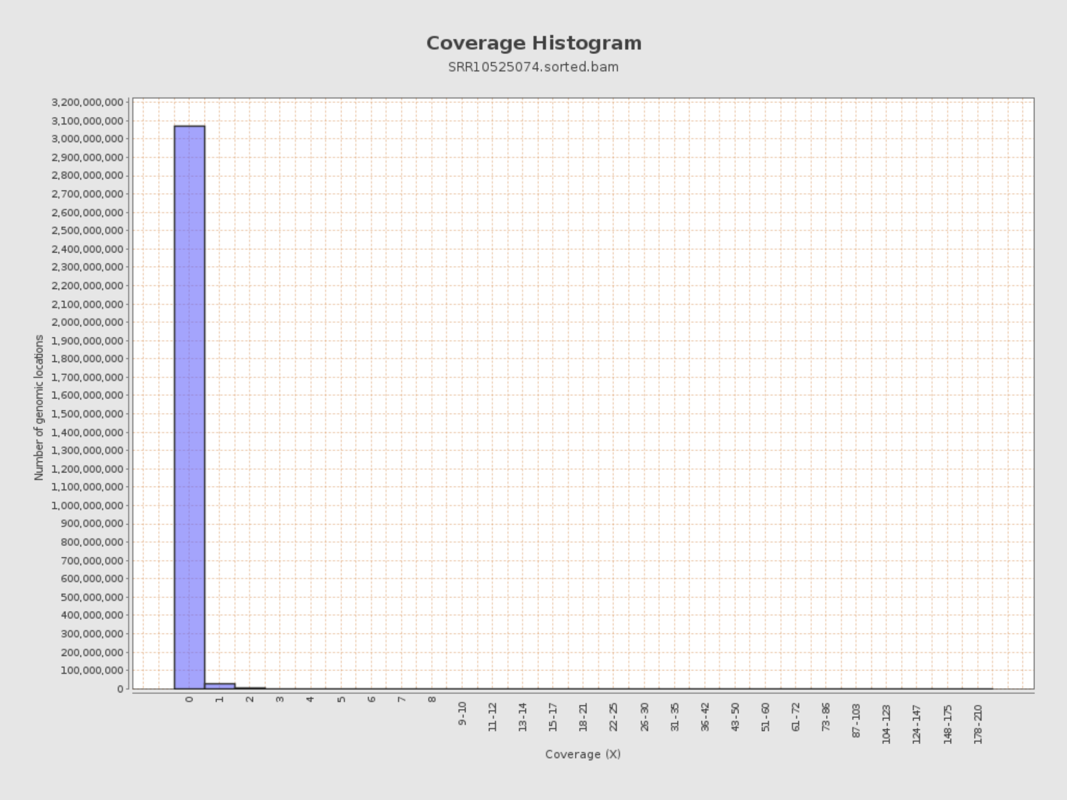
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2379820	0.0095	0.177
chr2	243199373	2502653	0.0103	0.1398
chr3	198022430	1929112	0.0097	0.1043
chr4	191154276	1943714	0.0102	0.1156
chr5	180915260	1803119	0.01	0.1054
chr6	171115067	1672621	0.0098	0.1076
chr7	159138663	1617311	0.0102	0.1326

chr8	146364022	1489832	0.0102	0.1262
chr9	141213431	1239596	0.0088	0.1098
chr10	135534747	1458896	0.0108	0.1349
chr11	135006516	1349391	0.01	0.1147
chr12	133851895	1351531	0.0101	0.1076
chr13	115169878	896848	0.0078	0.0929
chr14	107349540	873704	0.0081	0.0957
chr15	102531392	870885	0.0085	0.0974
chr16	90354753	855180	0.0095	0.1055
chr17	81195210	827749	0.0102	0.1092
chr18	78077248	788141	0.0101	0.1543
chr19	59128983	610969	0.0103	0.1472
chr20	63025520	654918	0.0104	0.1101
chr21	48129895	402398	0.0084	0.1083
chr22	51304566	370768	0.0072	0.0905
chrMT	16571	11432	0.6899	0.979
chrX	155270560	1645710	0.0106	0.1129
chrY	59373566	103740	0.0017	0.0744

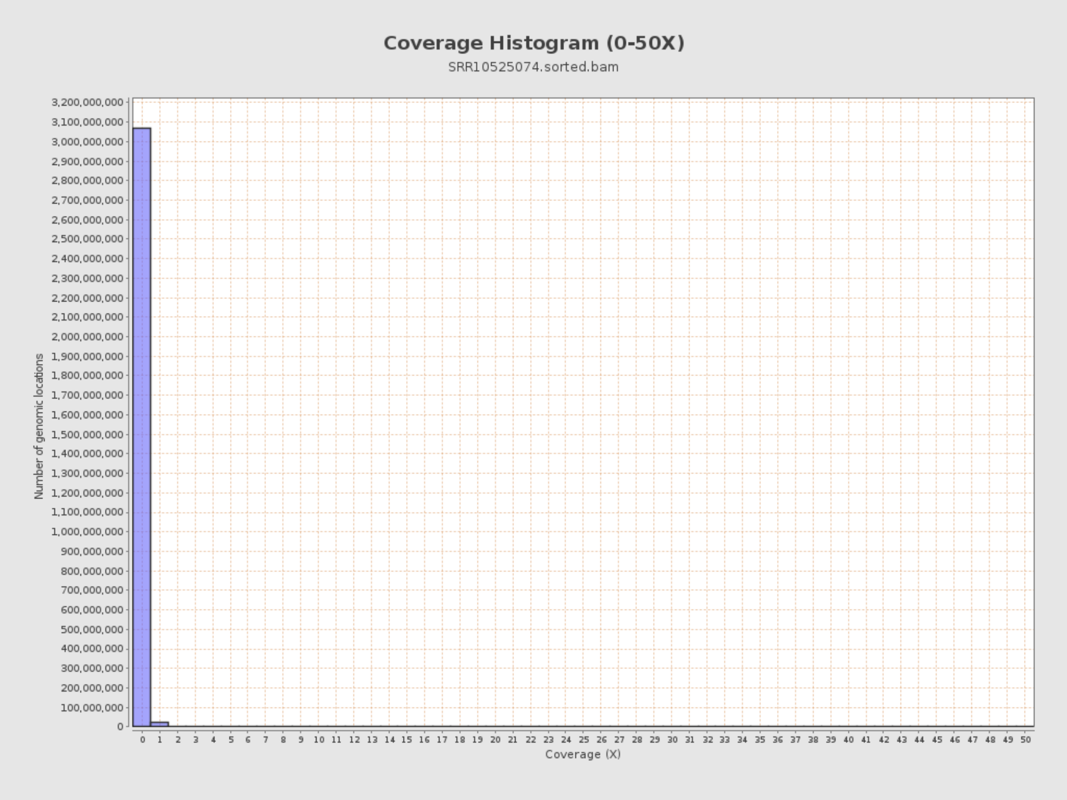
3. Results : Coverage across reference



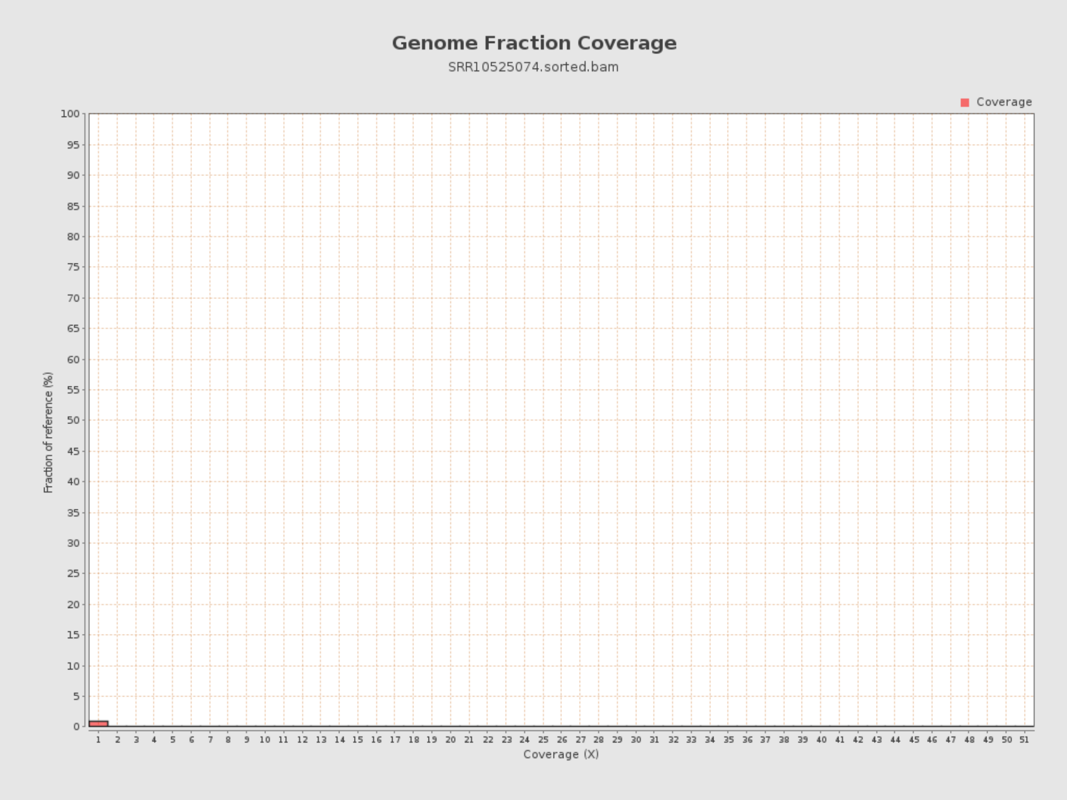
4. Results : Coverage Histogram



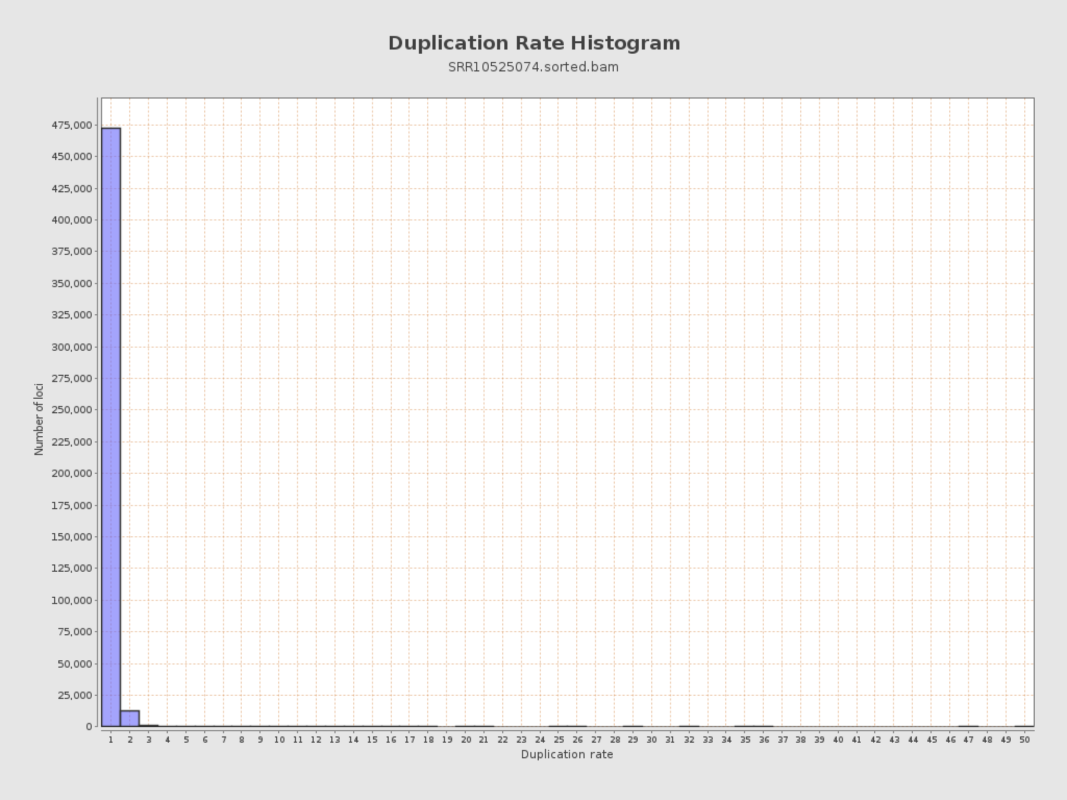
5. Results : Coverage Histogram (0-50X)



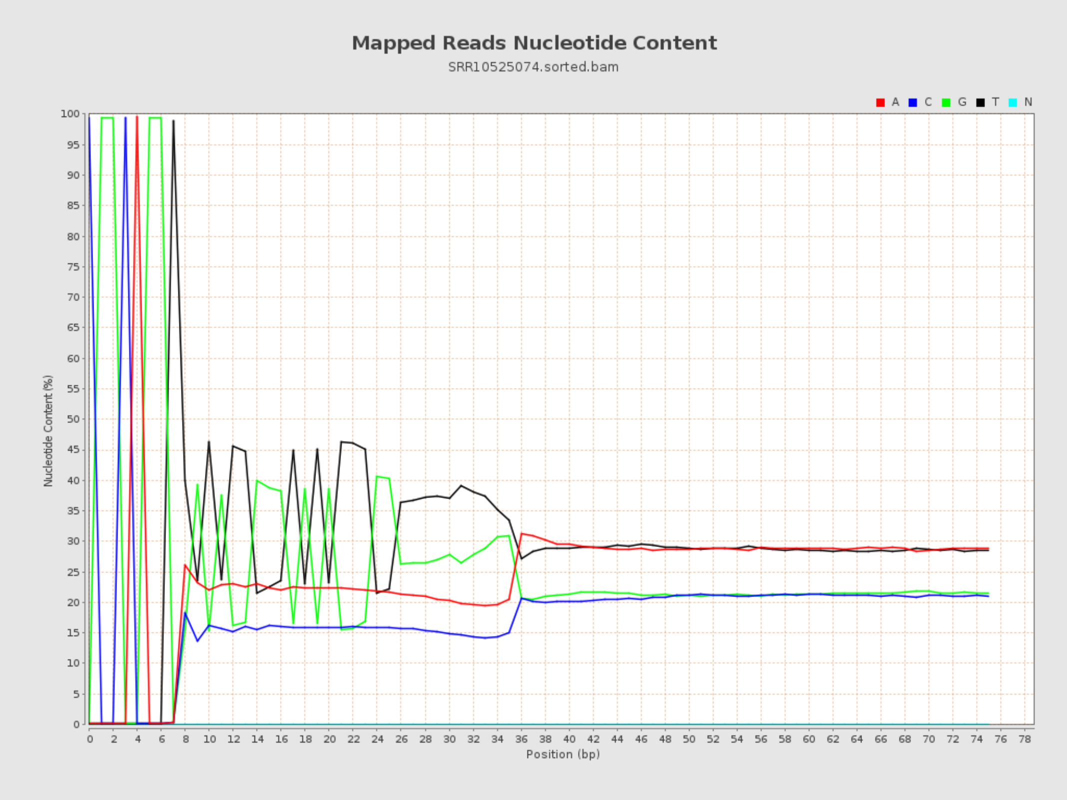
6. Results : Genome Fraction Coverage



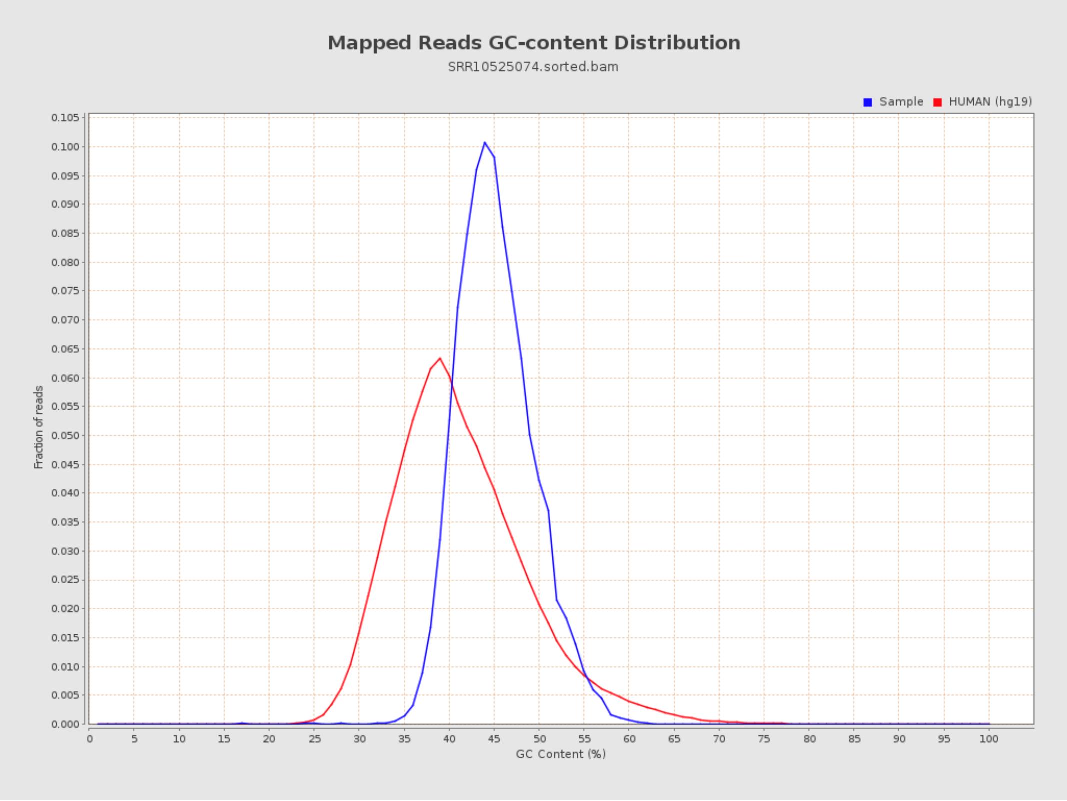
7. Results : Duplication Rate Histogram



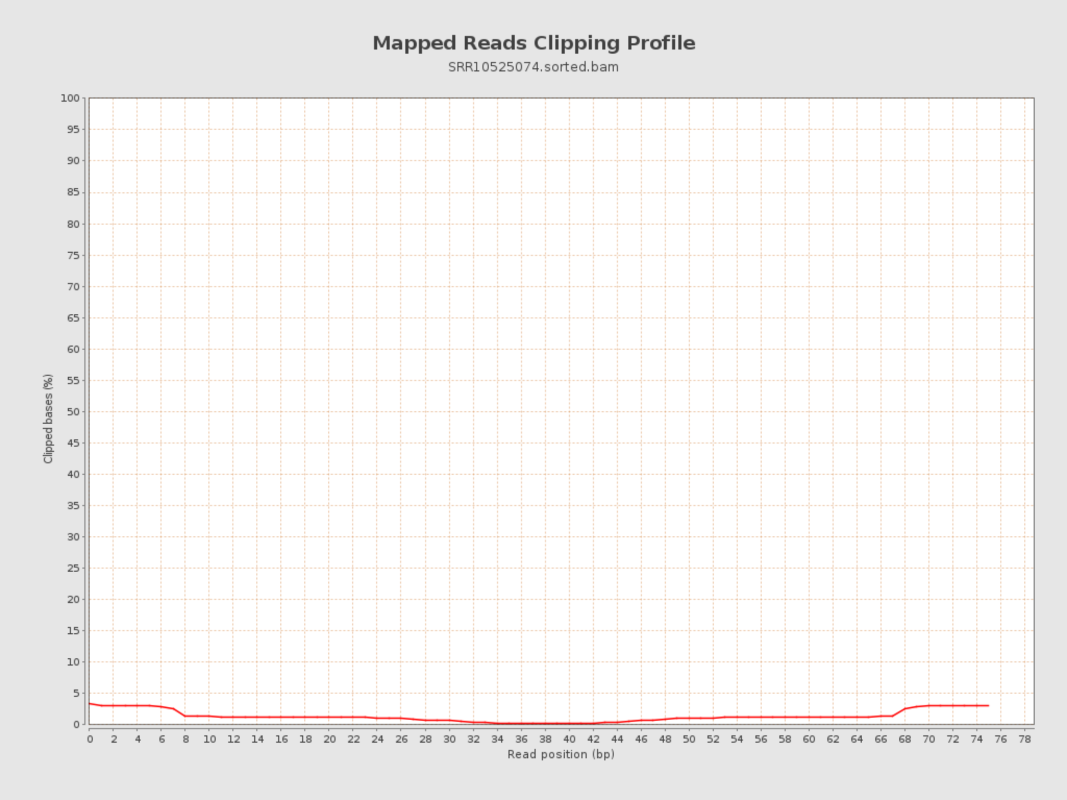
8. Results : Mapped Reads Nucleotide Content



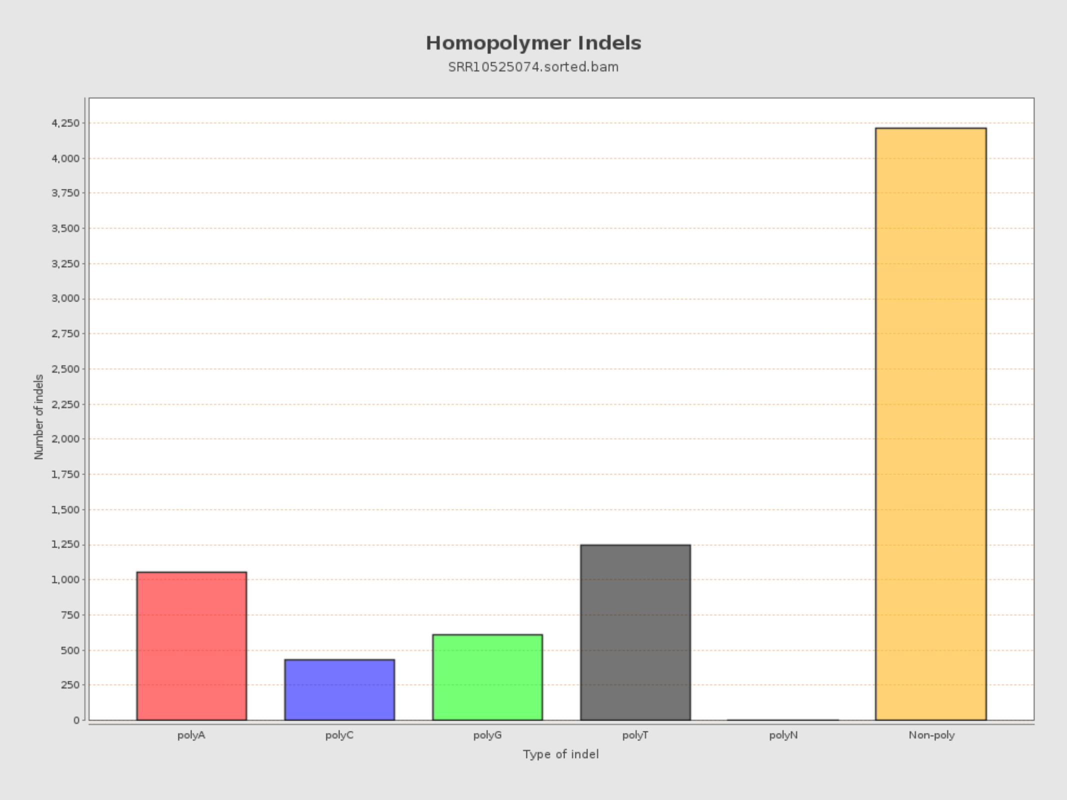
9. Results : Mapped Reads GC-content Distribution



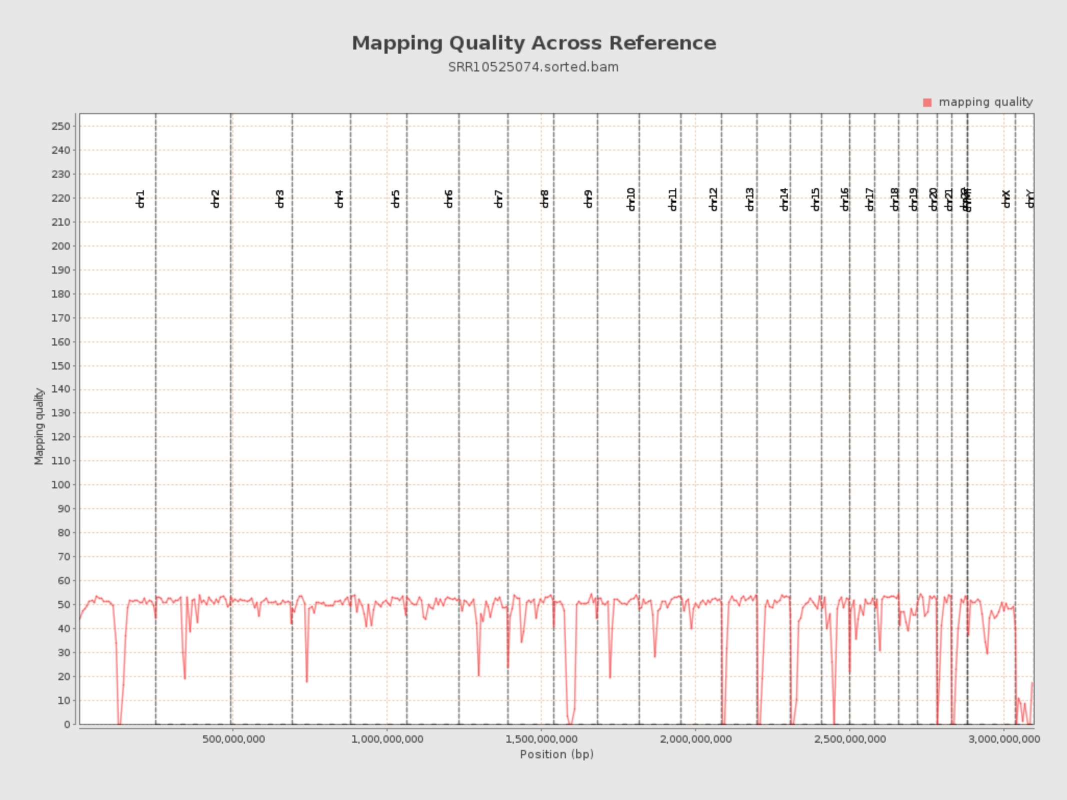
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram