Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:37:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525043.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_SRR10525043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:37:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	531,795
Mapped reads	490,682 / 92.27%
Unmapped reads	41,113 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,053 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	20,004 / 3.76%
Duplication rate	3.53%
Clipped reads	491,257 / 92.38%

2.2. ACGT Content

Number/percentage of A's	7,741,285 / 26.6%
Number/percentage of C's	5,385,579 / 18.5%
Number/percentage of T's	9,355,575 / 32.14%
Number/percentage of G's	6,621,698 / 22.75%
Number/percentage of N's	2,543 / 0.01%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1238

2.4. Mapping Quality

Mean Mapping Quality	46.47

2.5. Mismatches and indels

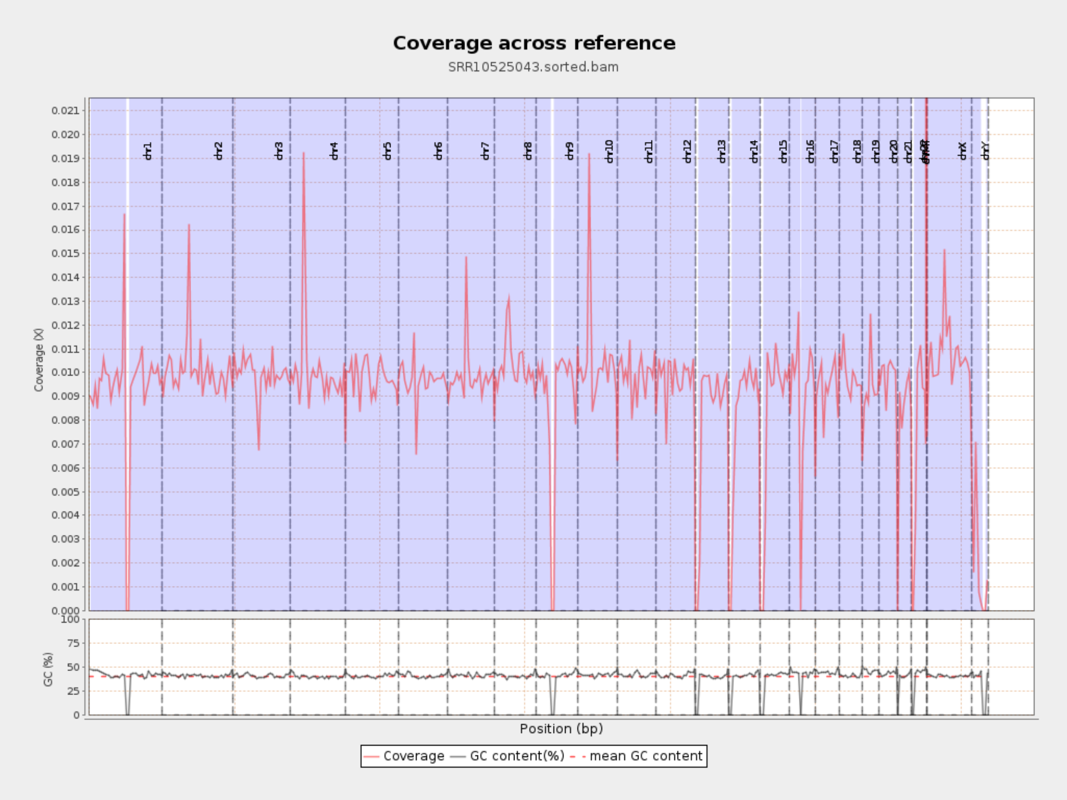
General error rate	0.5%
Mismatches	140,756
Insertions	2,460
Mapped reads with at least one insertion	0.5%
Deletions	6,170
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.93%

2.6. Chromosome stats

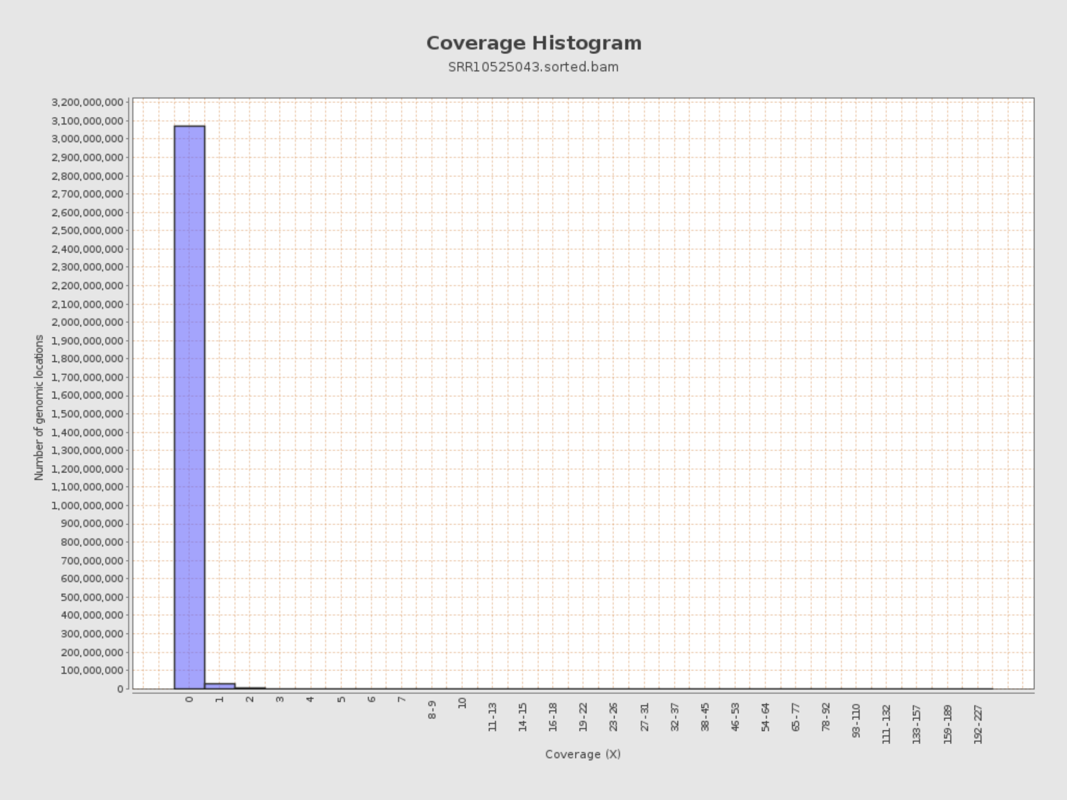
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2323634	0.0093	0.1787
chr2	243199373	2467285	0.0101	0.1413
chr3	198022430	1960642	0.0099	0.1054
chr4	191154276	1923707	0.0101	0.1146
chr5	180915260	1773306	0.0098	0.1052
chr6	171115067	1658660	0.0097	0.1071
chr7	159138663	1578725	0.0099	0.1291

chr8	146364022	1507499	0.0103	0.169
chr9	141213431	1226950	0.0087	0.1083
chr10	135534747	1417359	0.0105	0.1317
chr11	135006516	1330312	0.0099	0.1137
chr12	133851895	1304363	0.0097	0.1058
chr13	115169878	908124	0.0079	0.0938
chr14	107349540	856211	0.008	0.095
chr15	102531392	829488	0.0081	0.0954
chr16	90354753	821479	0.0091	0.1037
chr17	81195210	758895	0.0093	0.1043
chr18	78077248	774179	0.0099	0.1534
chr19	59128983	554703	0.0094	0.147
chr20	63025520	620821	0.0099	0.1074
chr21	48129895	390179	0.0081	0.1027
chr22	51304566	349685	0.0068	0.0871
chrMT	16571	13841	0.8353	1.125
chrX	155270560	1661578	0.0107	0.1134
chrY	59373566	104749	0.0018	0.0717

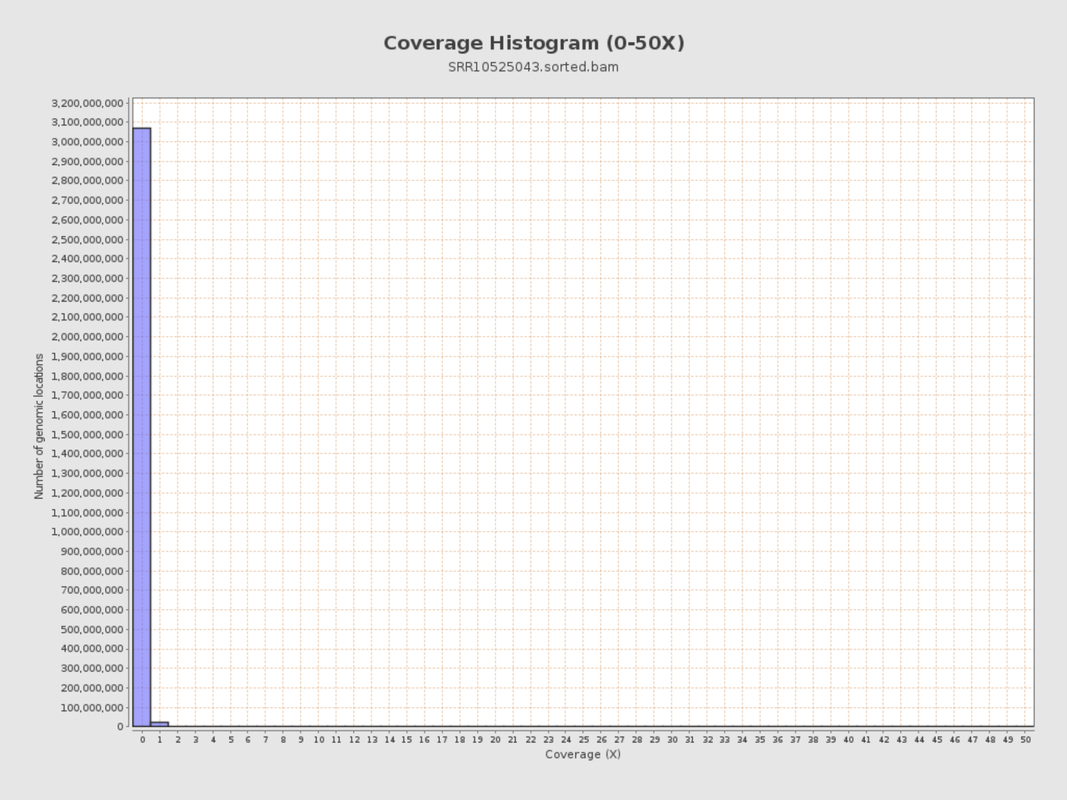
3. Results : Coverage across reference



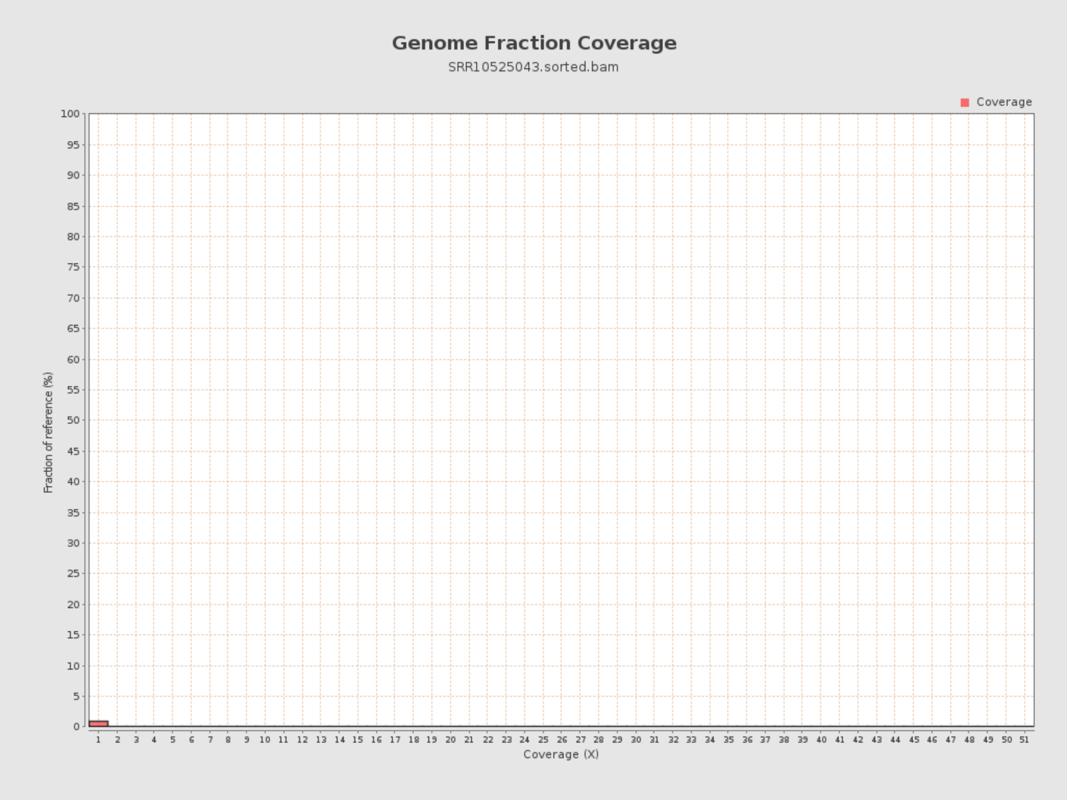
4. Results : Coverage Histogram



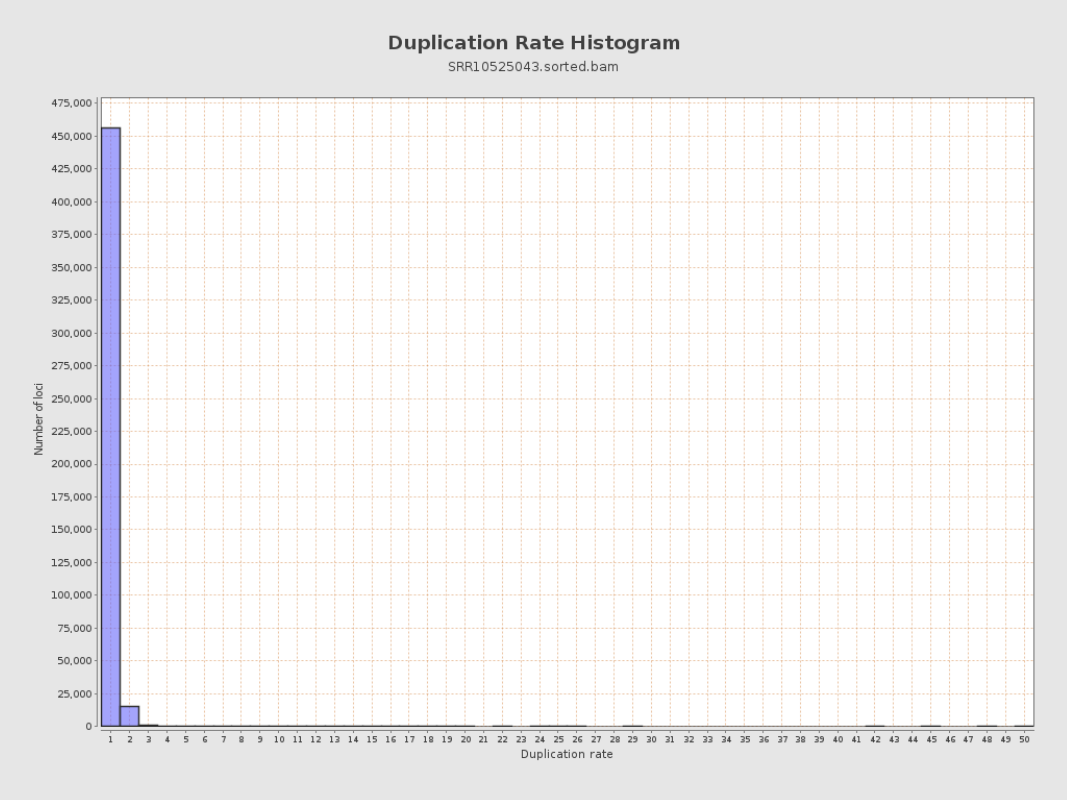
5. Results : Coverage Histogram (0-50X)



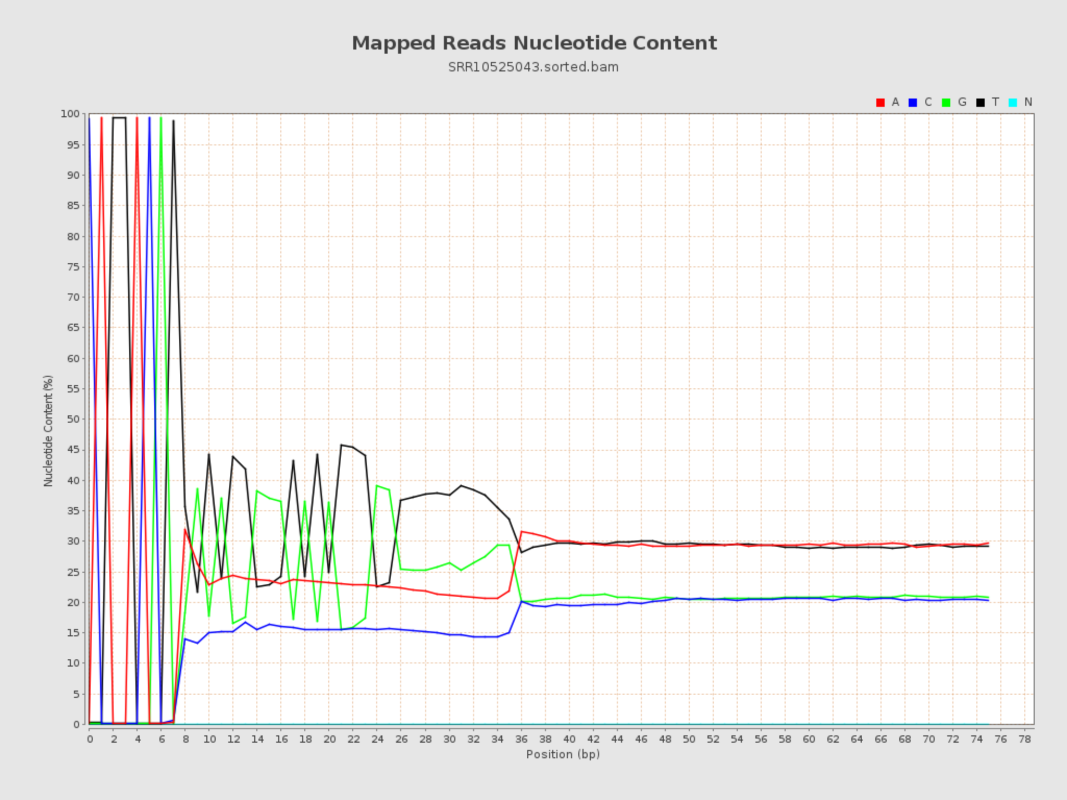
6. Results : Genome Fraction Coverage



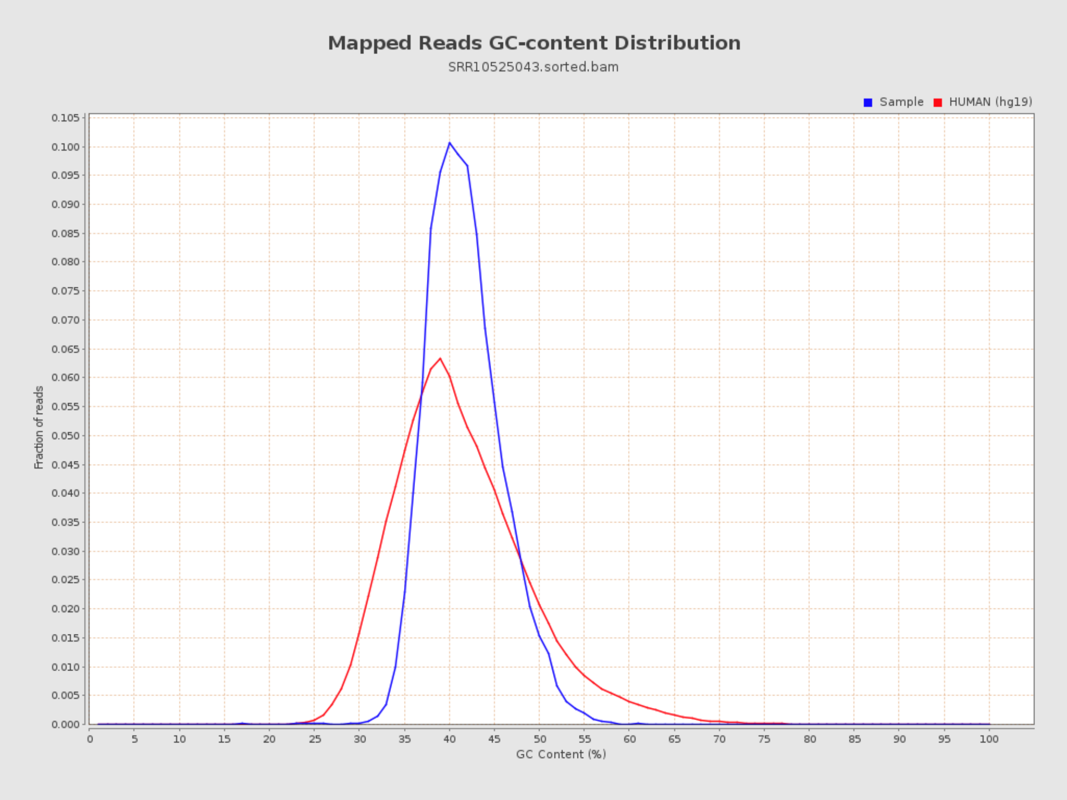
7. Results : Duplication Rate Histogram



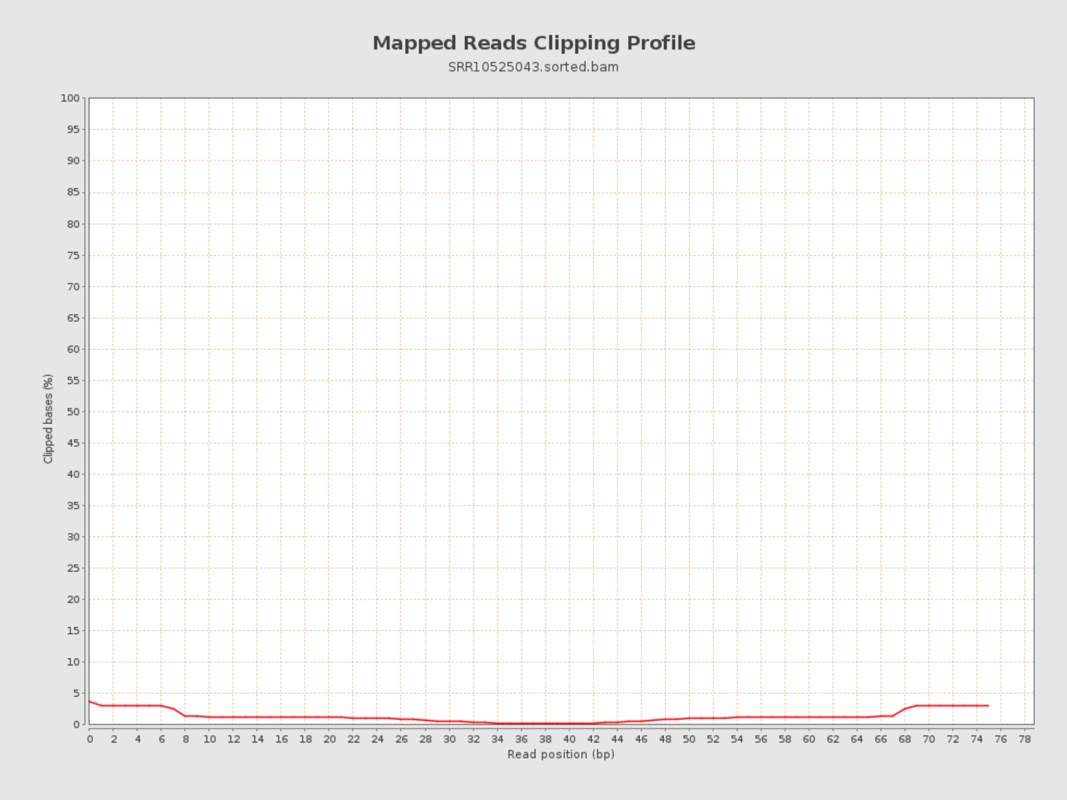
8. Results : Mapped Reads Nucleotide Content



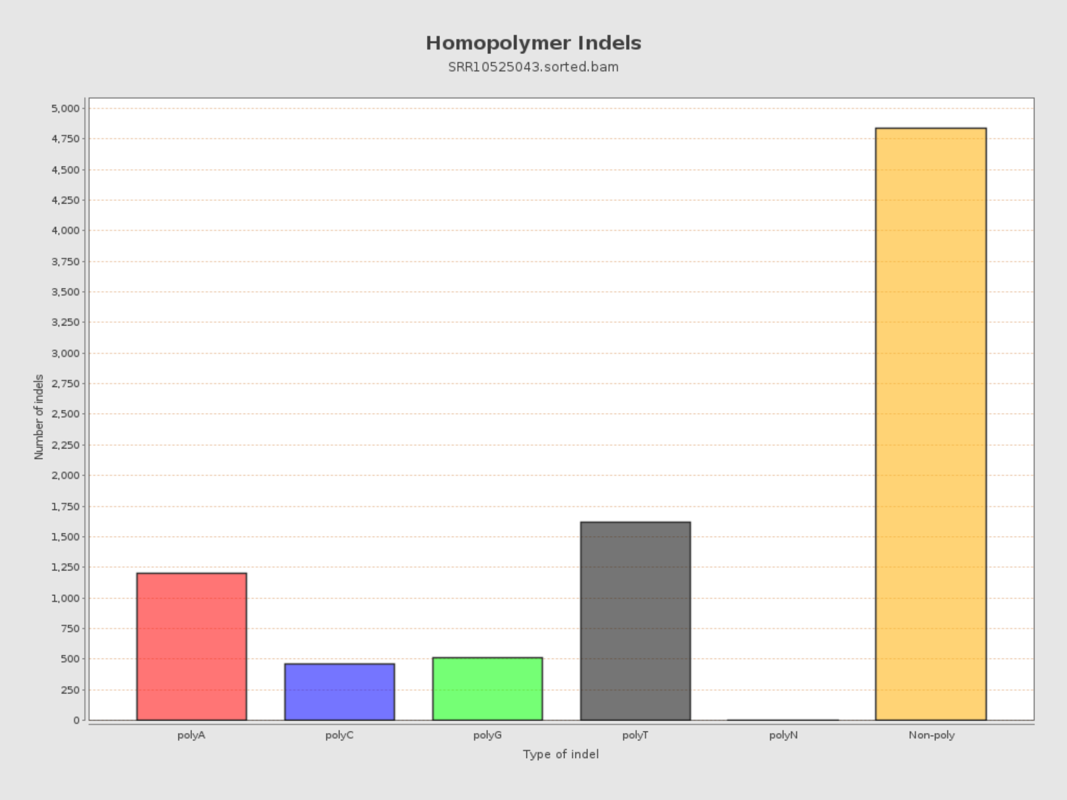
9. Results : Mapped Reads GC-content Distribution



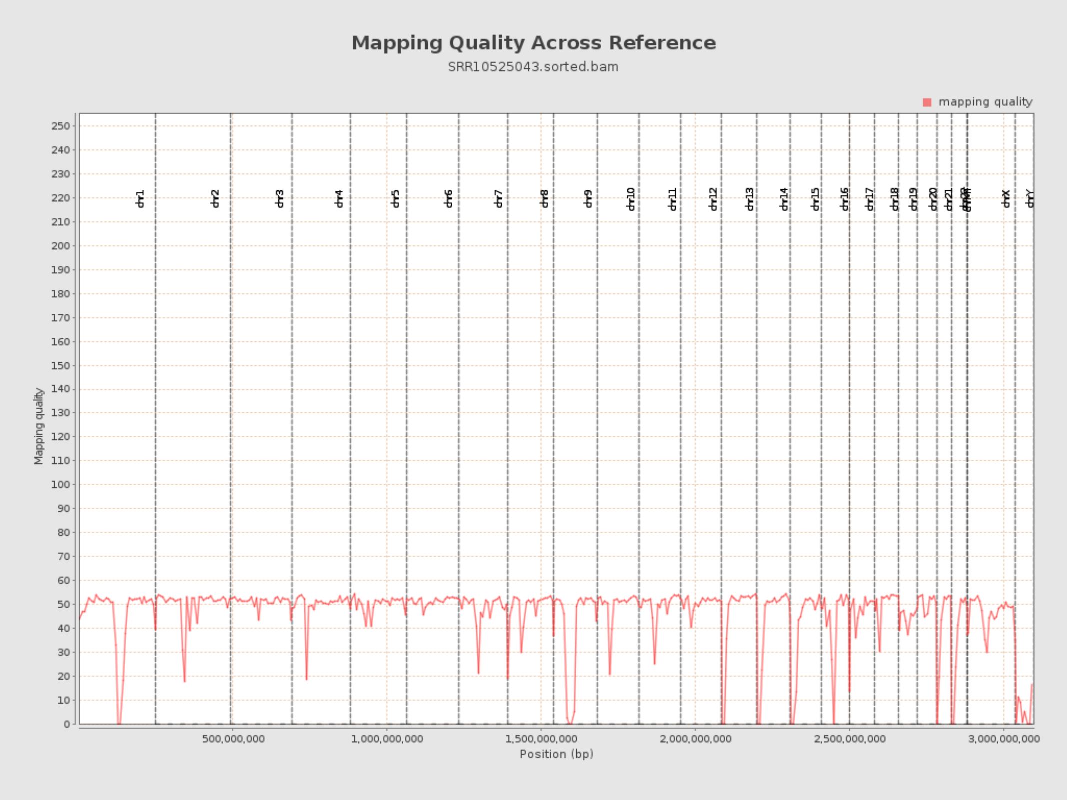
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram