Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:30:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525158.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_SRR10525158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:30:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	941,326
Mapped reads	662,841 / 70.42%
Unmapped reads	278,485 / 29.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,477 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	11,966 / 1.27%
Duplication rate	1.33%
Clipped reads	661,753 / 70.3%

2.2. ACGT Content

Number/percentage of A's	11,288,103 / 27.89%
Number/percentage of C's	7,650,457 / 18.9%
Number/percentage of T's	11,997,536 / 29.65%
Number/percentage of G's	9,532,634 / 23.55%
Number/percentage of N's	1,120 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1514

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

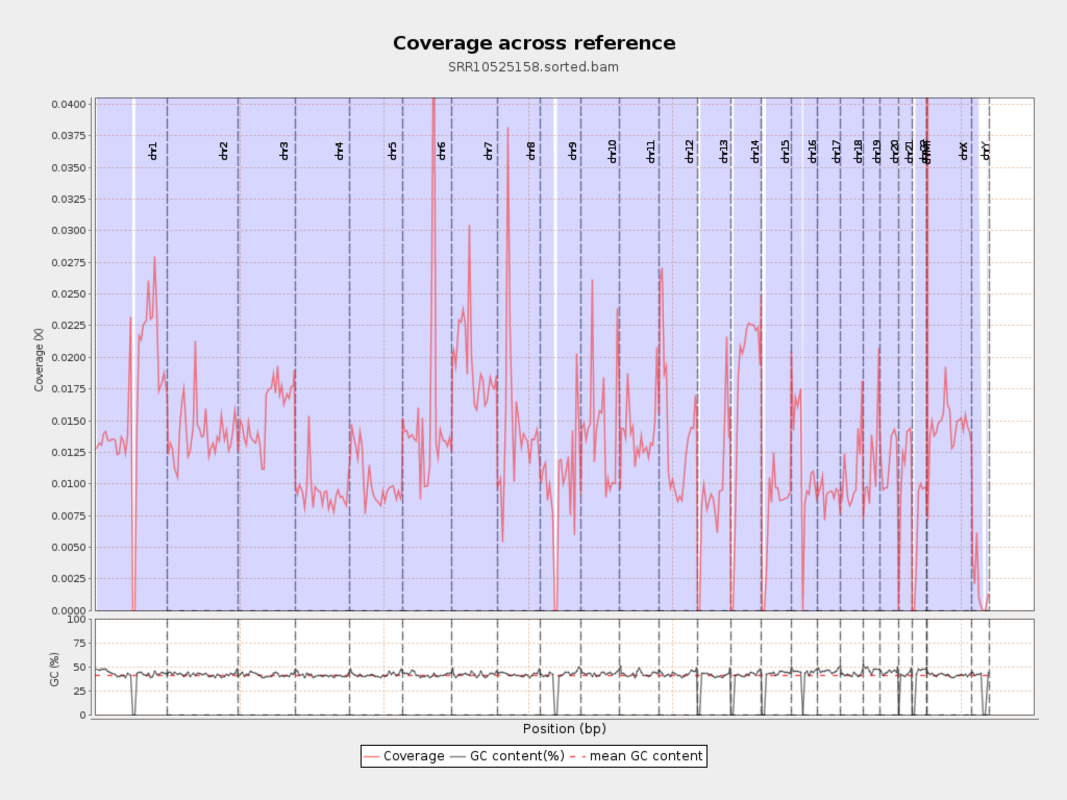
General error rate	0.5%
Mismatches	193,705
Insertions	3,783
Mapped reads with at least one insertion	0.57%
Deletions	7,943
Mapped reads with at least one deletion	1.19%
Homopolymer indels	41.32%

2.6. Chromosome stats

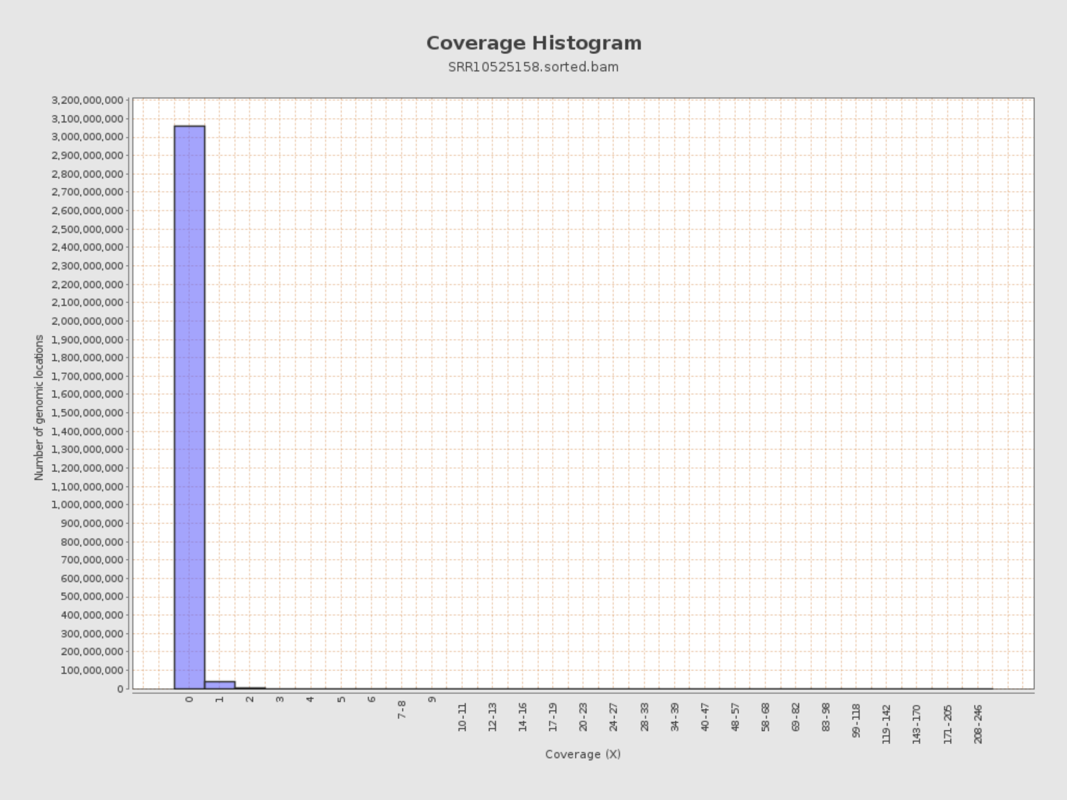
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4062668	0.0163	0.236
chr2	243199373	3401844	0.014	0.1673
chr3	198022430	3077054	0.0155	0.1295
chr4	191154276	1789940	0.0094	0.1046
chr5	180915260	1869575	0.0103	0.1051
chr6	171115067	2639700	0.0154	0.1337
chr7	159138663	3128515	0.0197	0.2514

chr8	146364022	2149755	0.0147	0.1449
chr9	141213431	1405114	0.01	0.1174
chr10	135534747	1978508	0.0146	0.1613
chr11	135006516	1888398	0.014	0.1363
chr12	133851895	1889290	0.0141	0.1237
chr13	115169878	1082635	0.0094	0.1005
chr14	107349540	1890682	0.0176	0.1393
chr15	102531392	786062	0.0077	0.0907
chr16	90354753	1051741	0.0116	0.1174
chr17	81195210	744674	0.0092	0.1016
chr18	78077248	840112	0.0108	0.1957
chr19	59128983	704018	0.0119	0.1711
chr20	63025520	734145	0.0116	0.1125
chr21	48129895	542046	0.0113	0.1134
chr22	51304566	344201	0.0067	0.0843
chrMT	16571	113274	6.8357	4.5533
chrX	155270560	2264325	0.0146	0.1282
chrY	59373566	104332	0.0018	0.0614

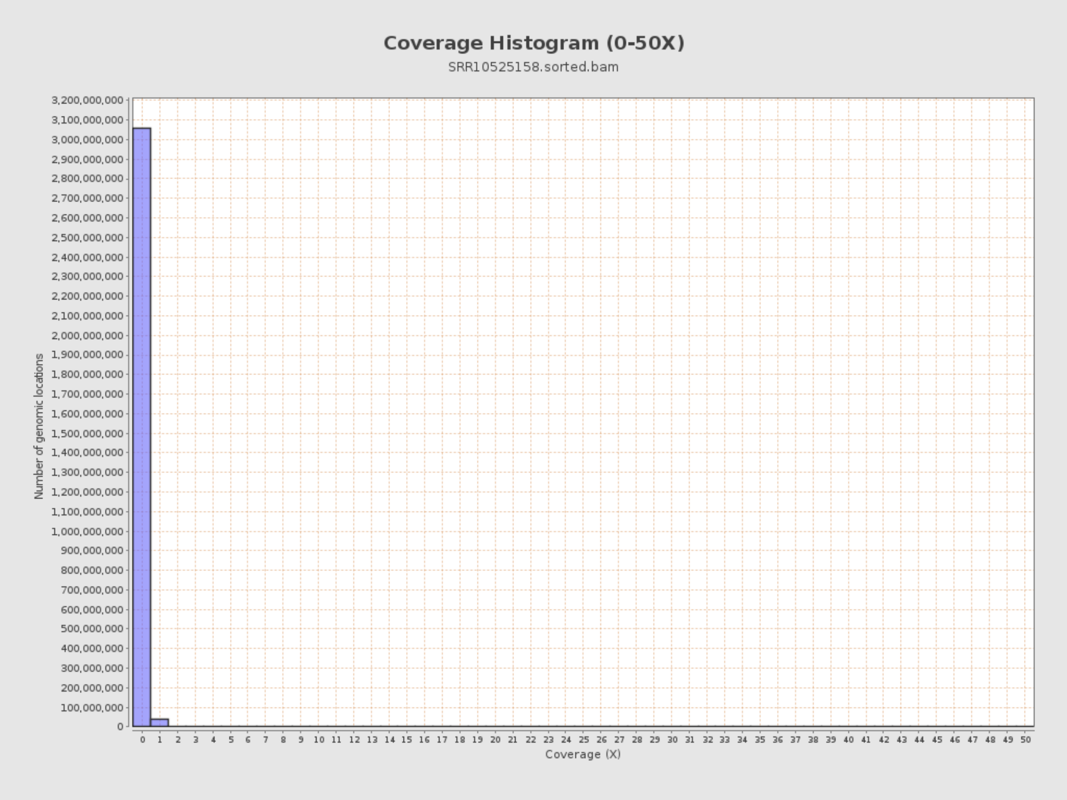
3. Results : Coverage across reference



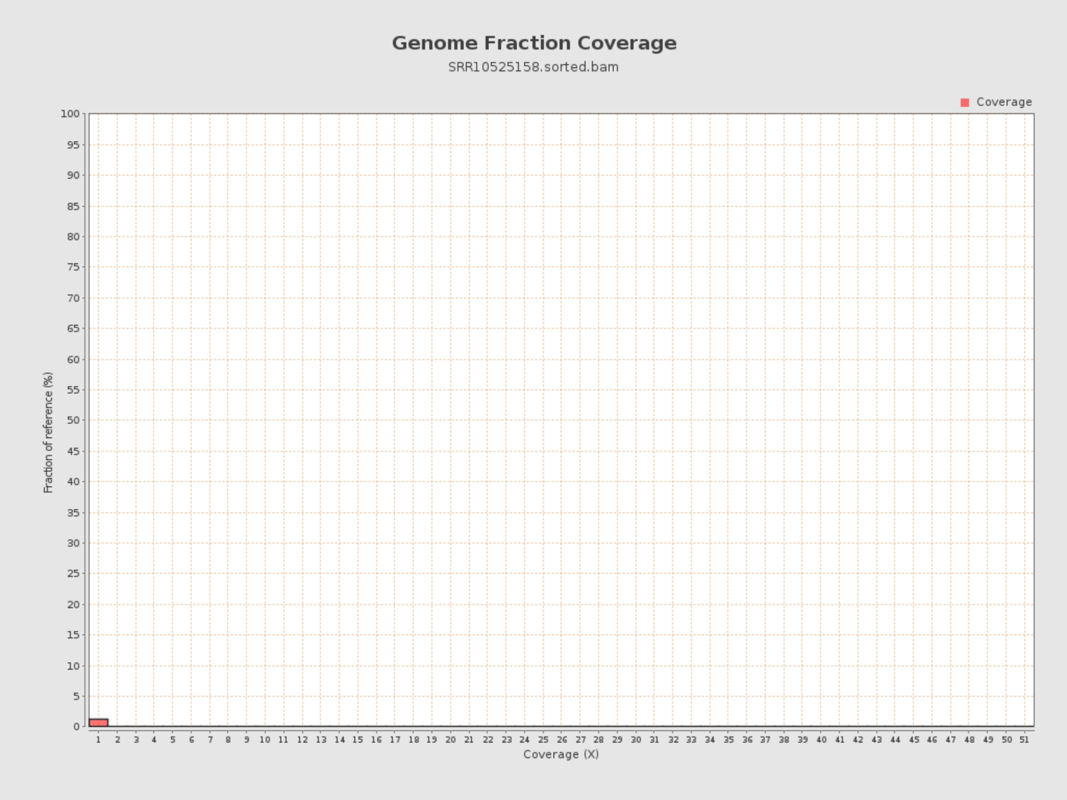
4. Results : Coverage Histogram



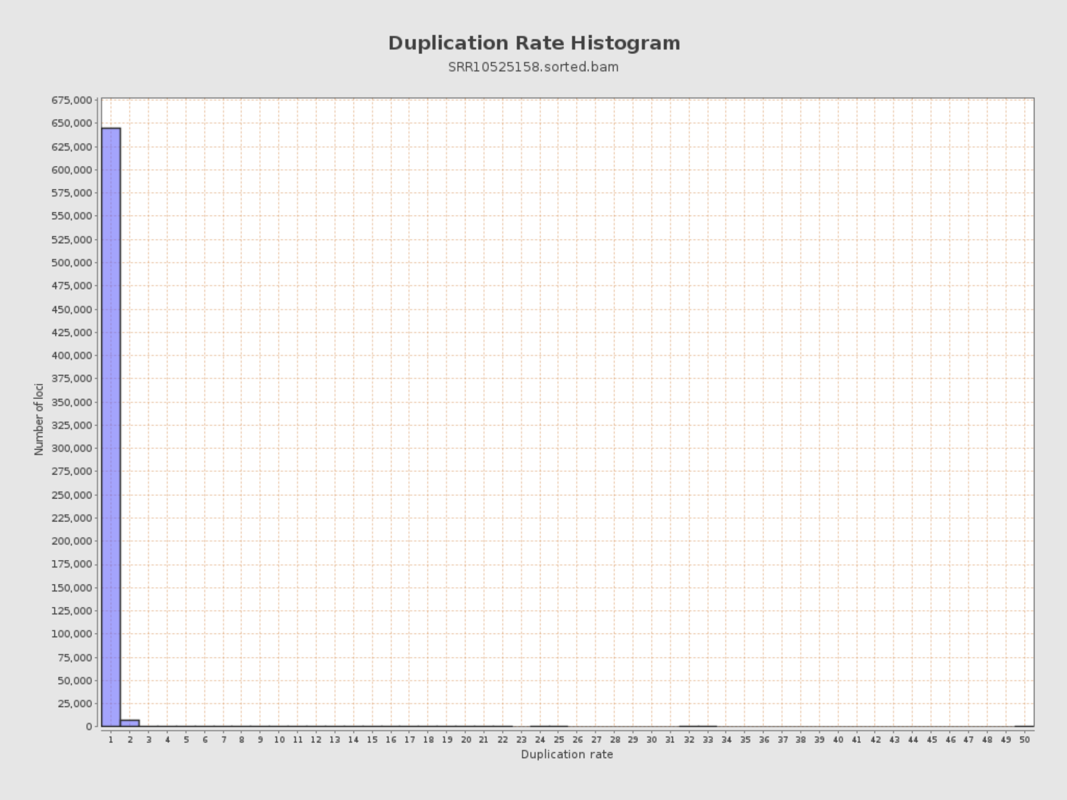
5. Results : Coverage Histogram (0-50X)



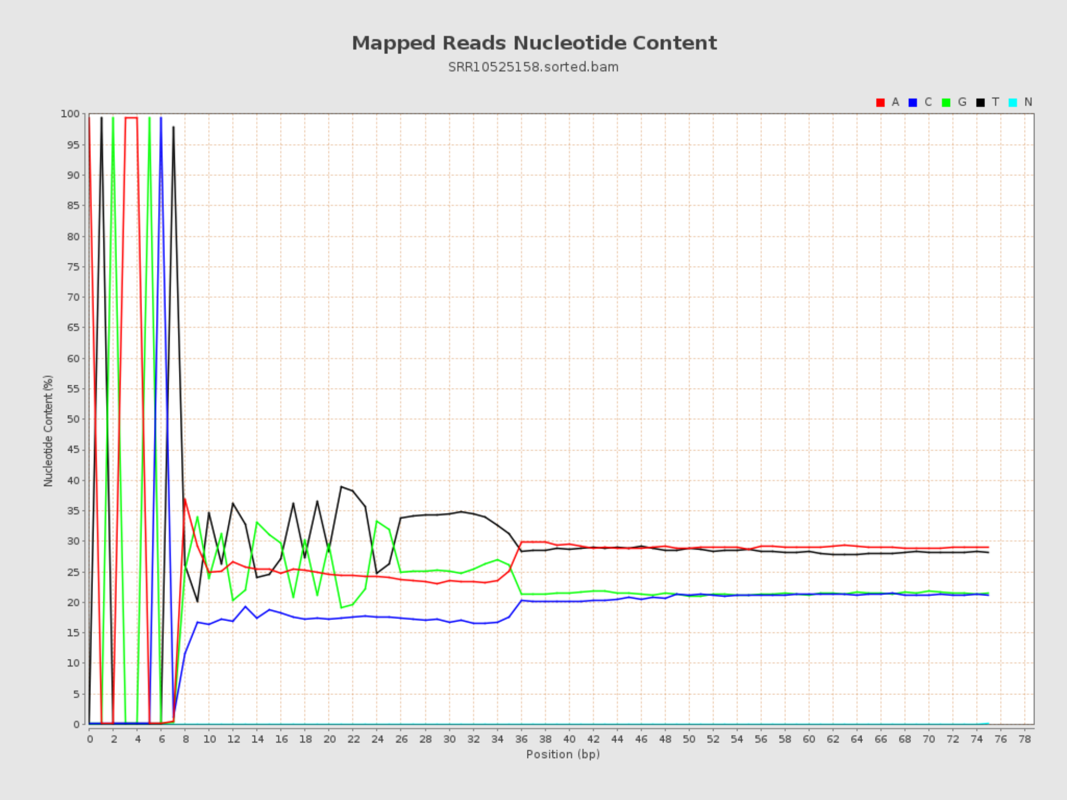
6. Results : Genome Fraction Coverage



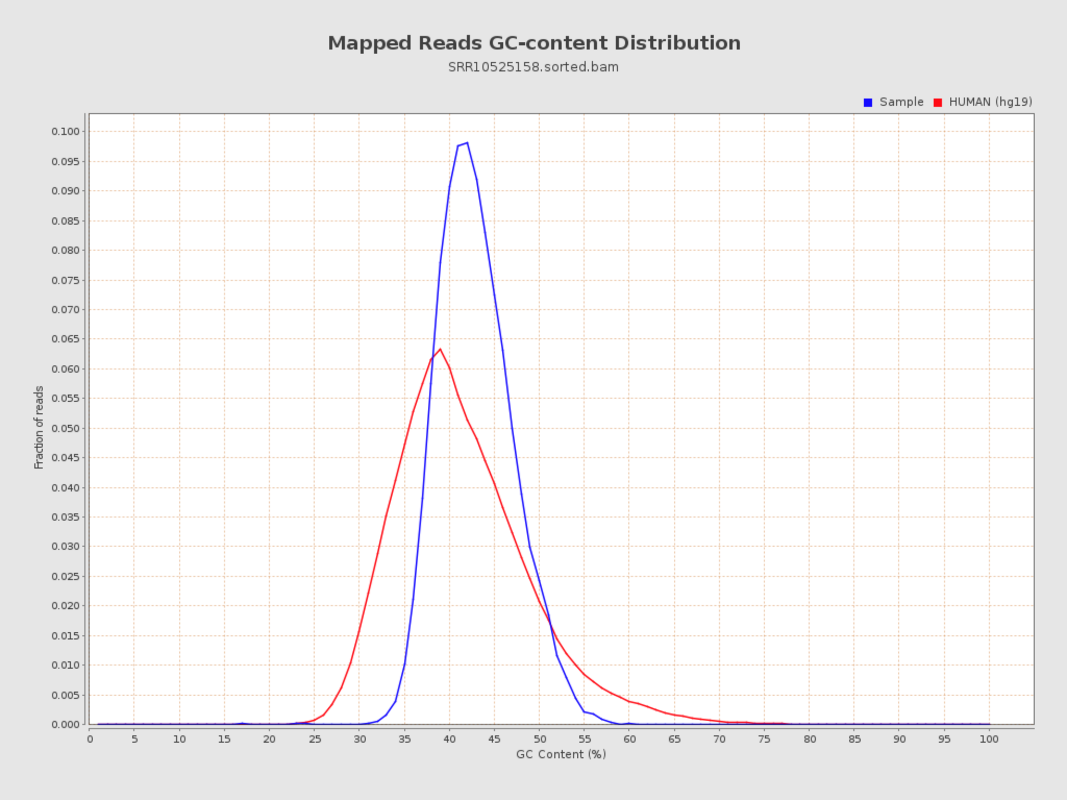
7. Results : Duplication Rate Histogram



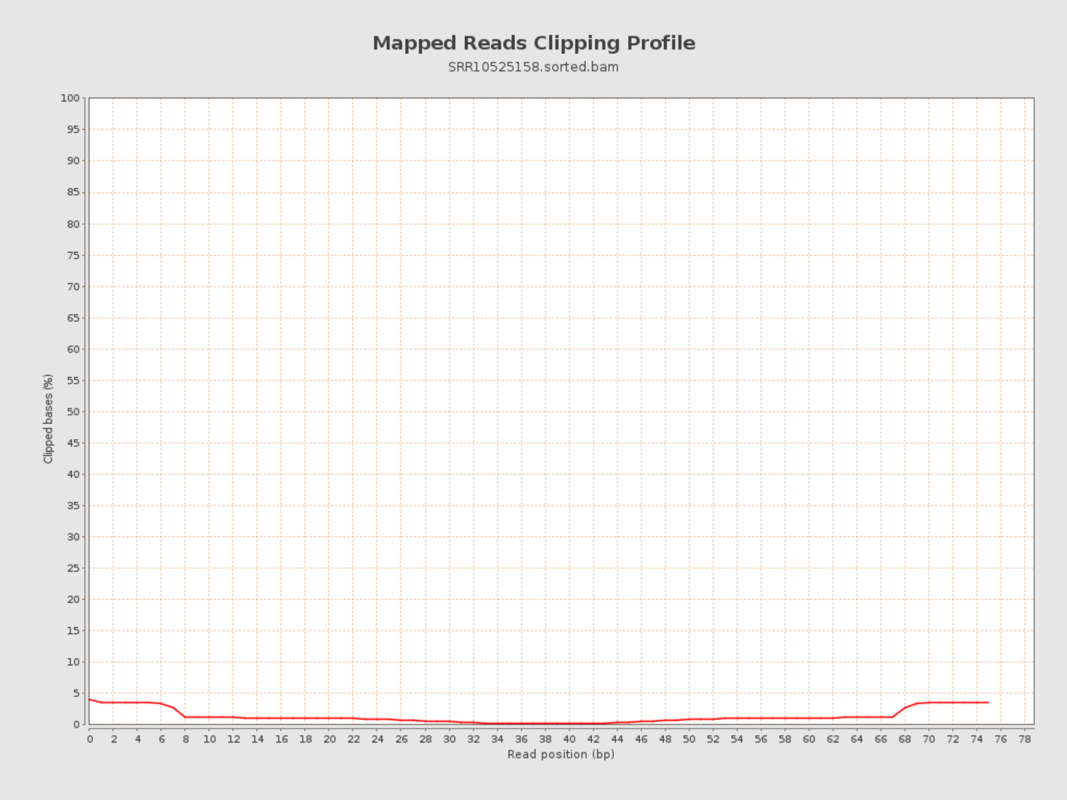
8. Results : Mapped Reads Nucleotide Content



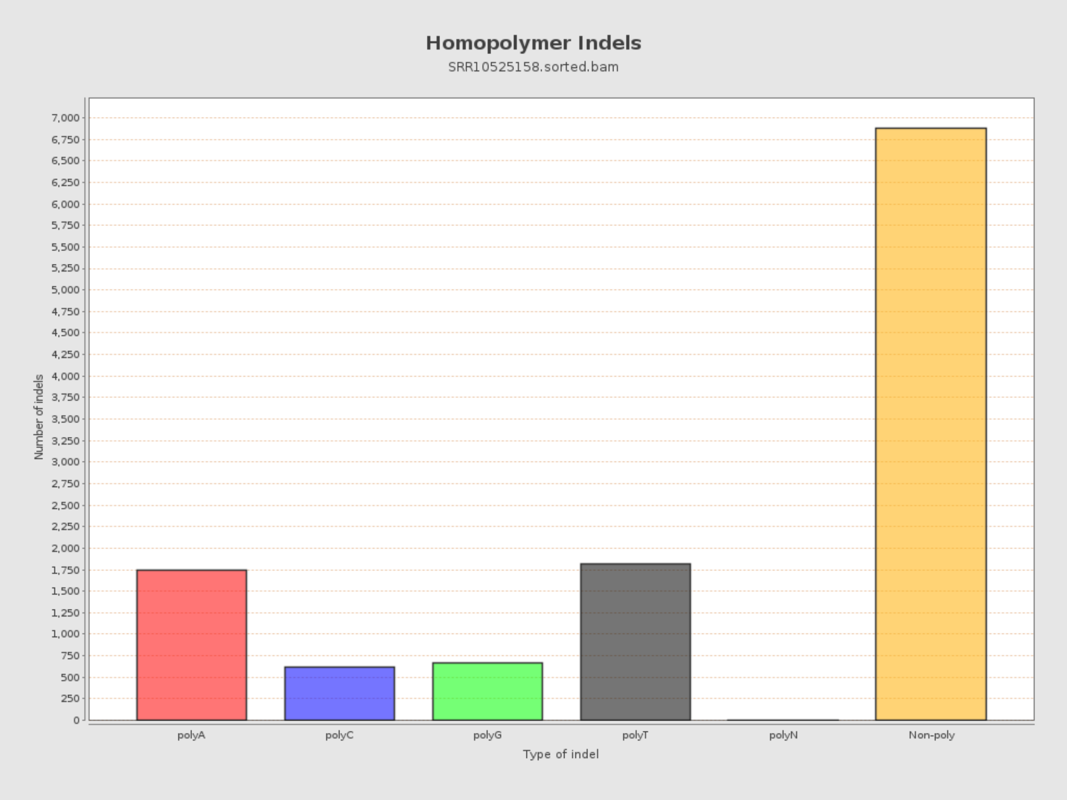
9. Results : Mapped Reads GC-content Distribution



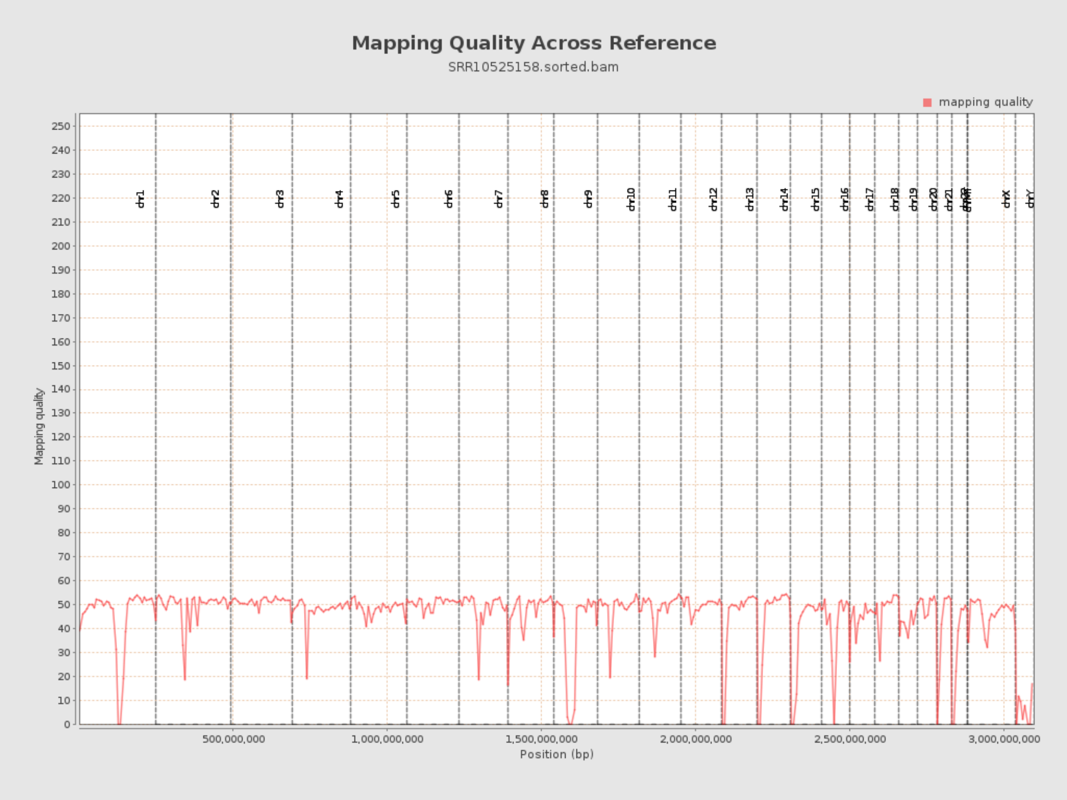
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram