Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:59:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525184.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_SRR10525184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:59:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,645,042
Mapped reads	2,446,212 / 92.48%
Unmapped reads	198,830 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,122 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	104,915 / 3.97%
Duplication rate	3.03%
Clipped reads	2,446,067 / 92.48%

2.2. ACGT Content

Number/percentage of A's	37,048,492 / 25.88%
Number/percentage of C's	25,063,185 / 17.51%
Number/percentage of T's	45,155,320 / 31.54%
Number/percentage of G's	35,898,592 / 25.07%
Number/percentage of N's	3,572 / 0%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.4299

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

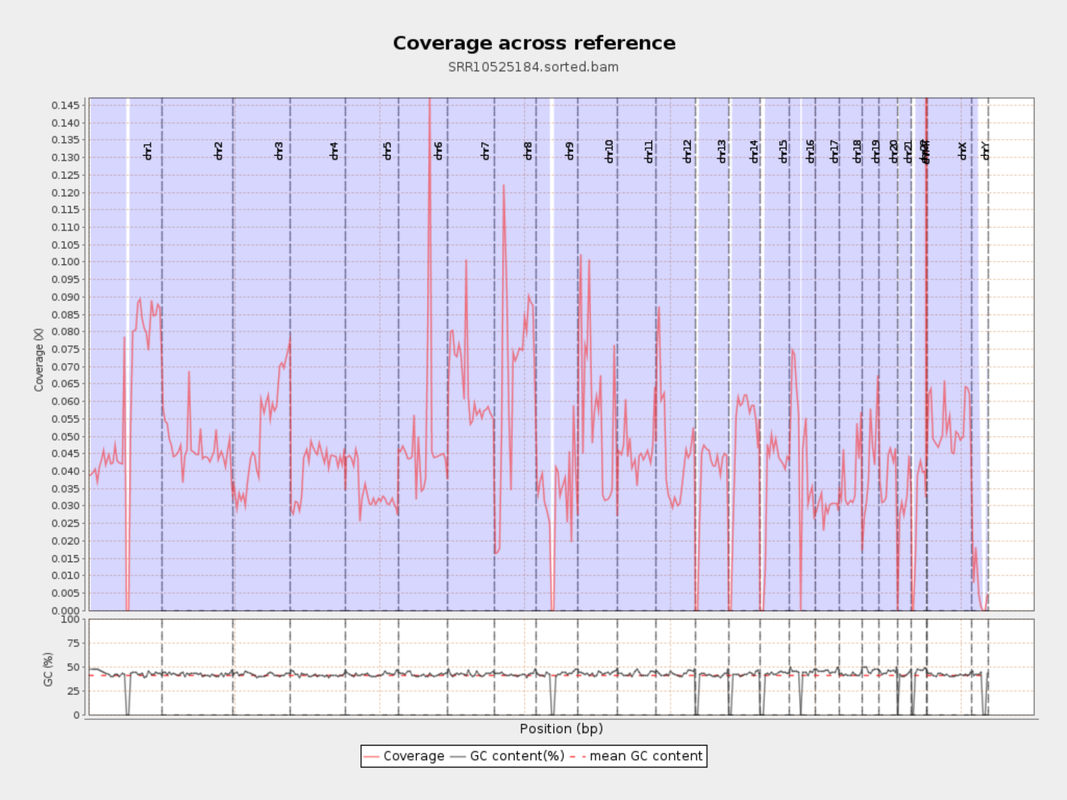
General error rate	0.51%
Mismatches	713,957
Insertions	9,612
Mapped reads with at least one insertion	0.39%
Deletions	27,799
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.92%

2.6. Chromosome stats

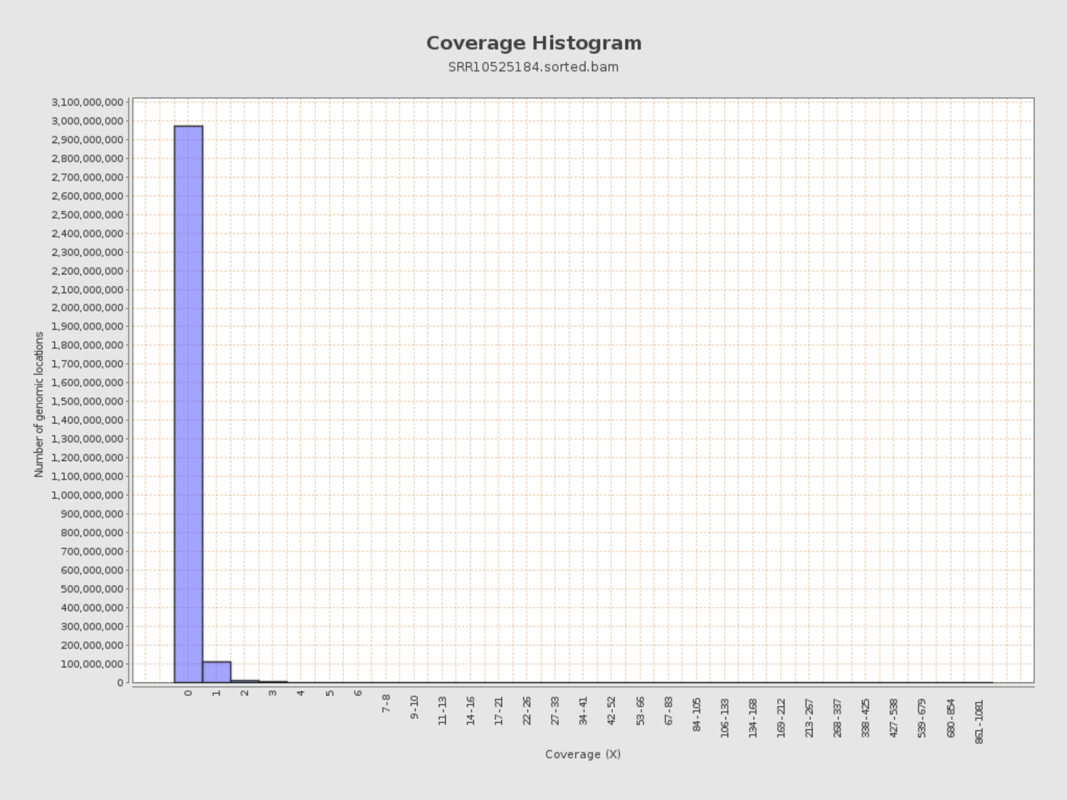
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14472270	0.0581	0.7874
chr2	243199373	11375750	0.0468	0.5228
chr3	198022430	10060317	0.0508	0.2613
chr4	191154276	7876482	0.0412	0.2403
chr5	180915260	6243315	0.0345	0.2107
chr6	171115067	8537402	0.0499	0.2902
chr7	159138663	10357322	0.0651	0.7619

chr8	146364022	9777277	0.0668	0.3995
chr9	141213431	4498509	0.0319	0.2913
chr10	135534747	7967669	0.0588	0.4862
chr11	135006516	6218666	0.0461	0.3348
chr12	133851895	6084146	0.0455	0.2421
chr13	115169878	4343464	0.0377	0.2206
chr14	107349540	5145084	0.0479	0.2561
chr15	102531392	3713704	0.0362	0.2172
chr16	90354753	4098339	0.0454	0.2768
chr17	81195210	2402528	0.0296	0.2086
chr18	78077248	2978039	0.0381	0.6432
chr19	59128983	2558497	0.0433	0.5245
chr20	63025520	2429241	0.0385	0.2234
chr21	48129895	1432190	0.0298	0.2046
chr22	51304566	1425549	0.0278	0.1853
chrMT	16571	542879	32.7608	18.4434
chrX	155270560	8293386	0.0534	0.2904
chrY	59373566	380936	0.0064	0.1369

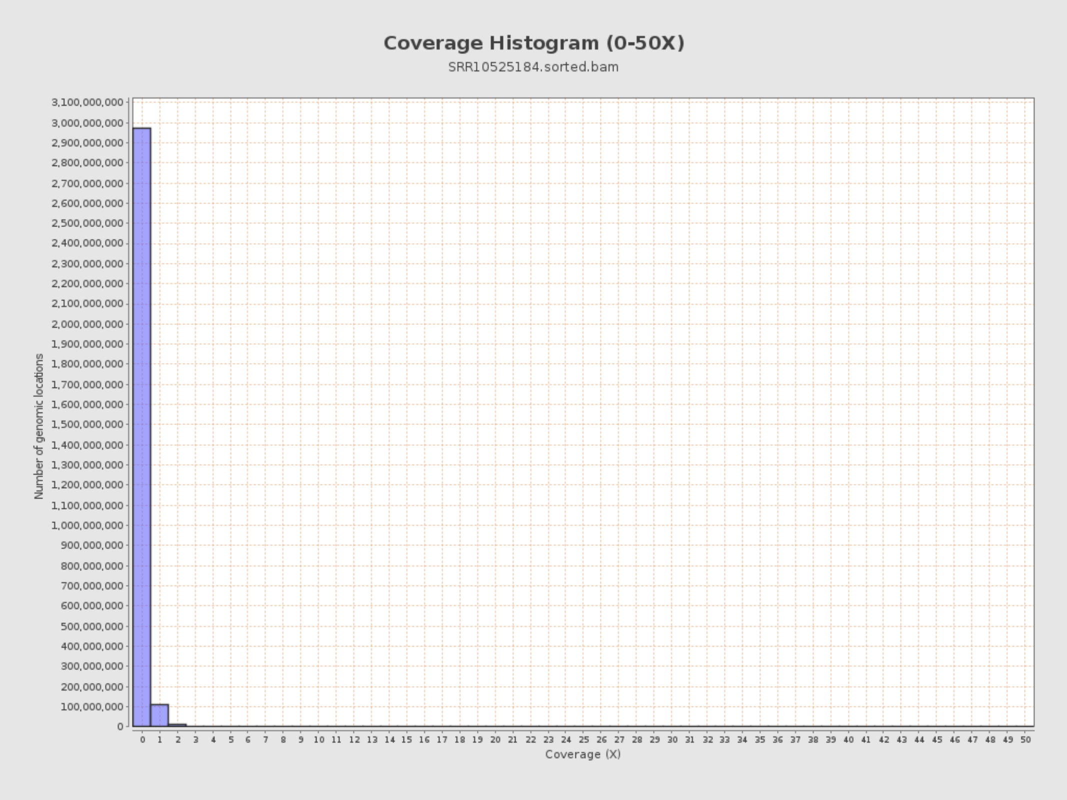
3. Results : Coverage across reference



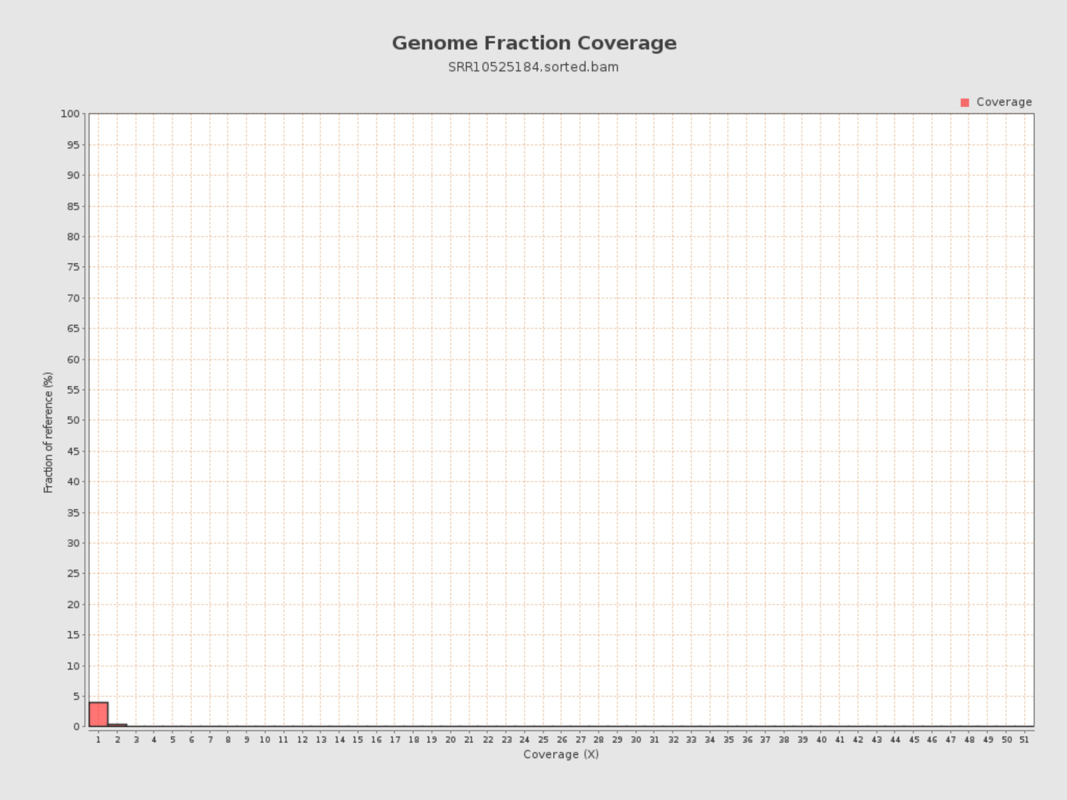
4. Results : Coverage Histogram



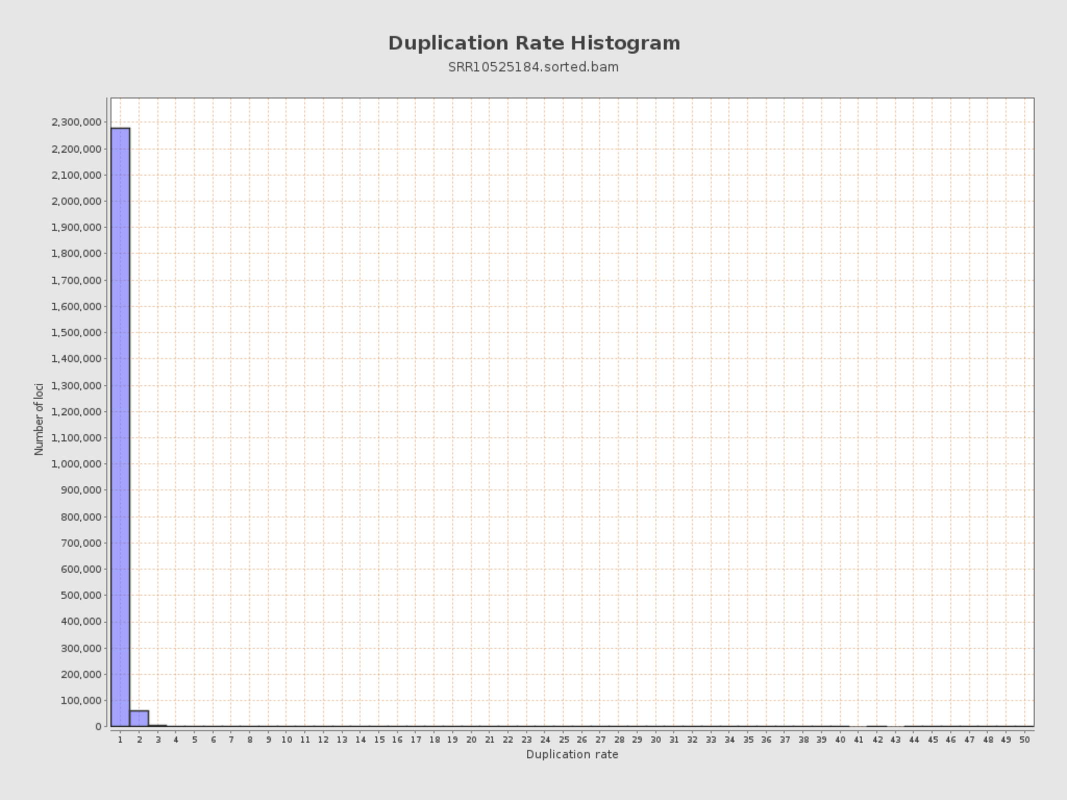
5. Results : Coverage Histogram (0-50X)



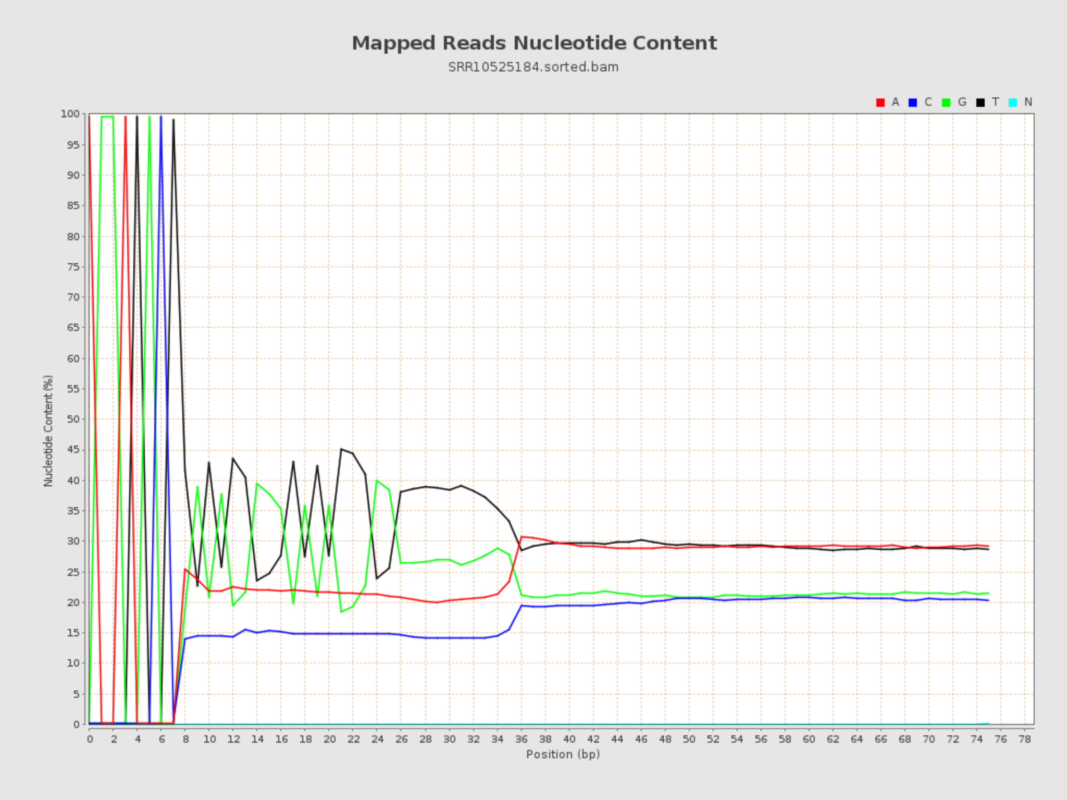
6. Results : Genome Fraction Coverage



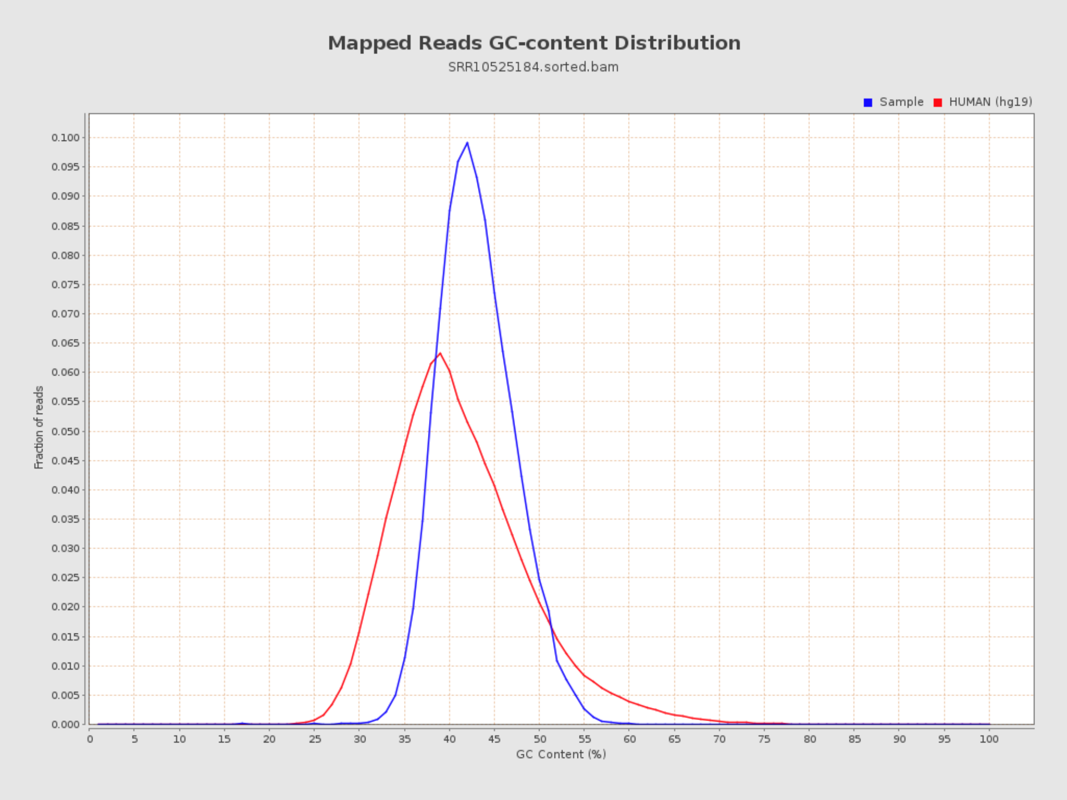
7. Results : Duplication Rate Histogram



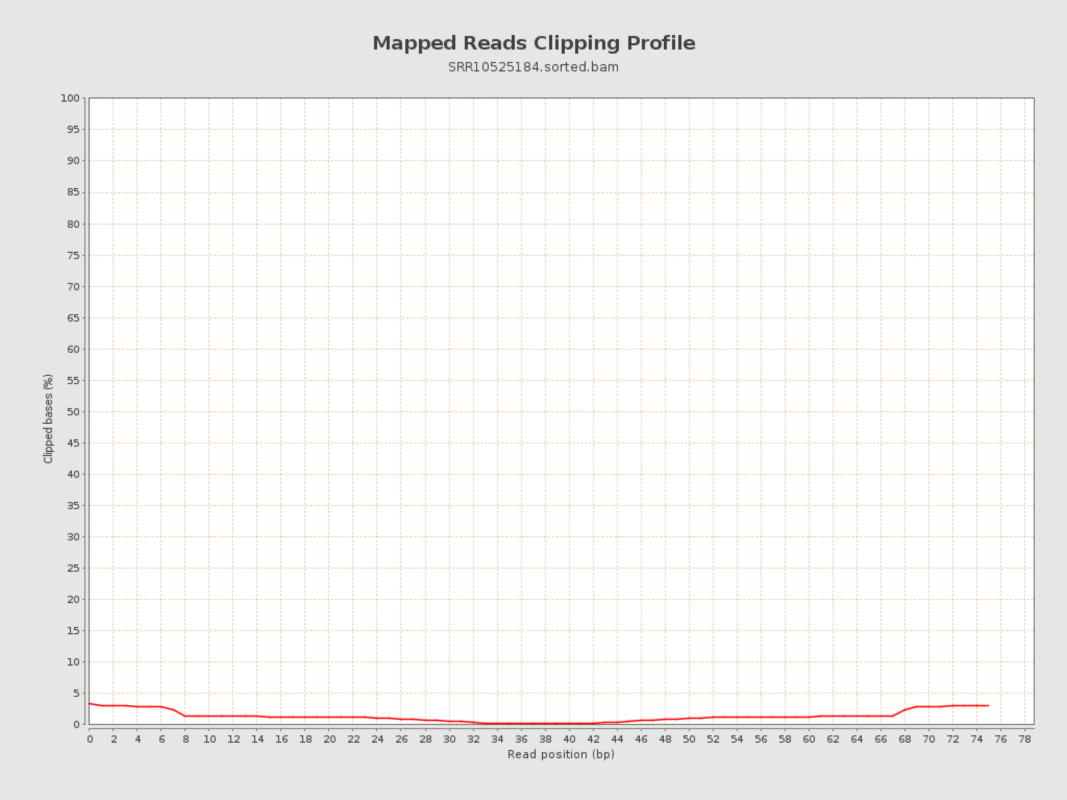
8. Results : Mapped Reads Nucleotide Content



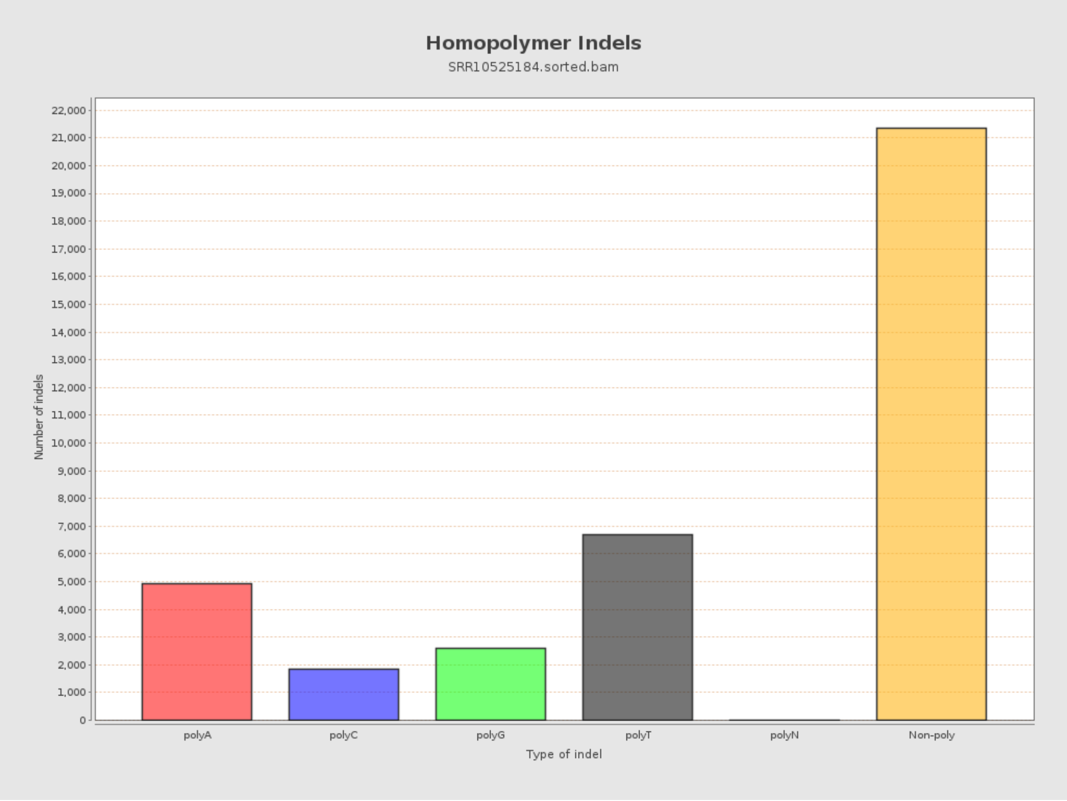
9. Results : Mapped Reads GC-content Distribution



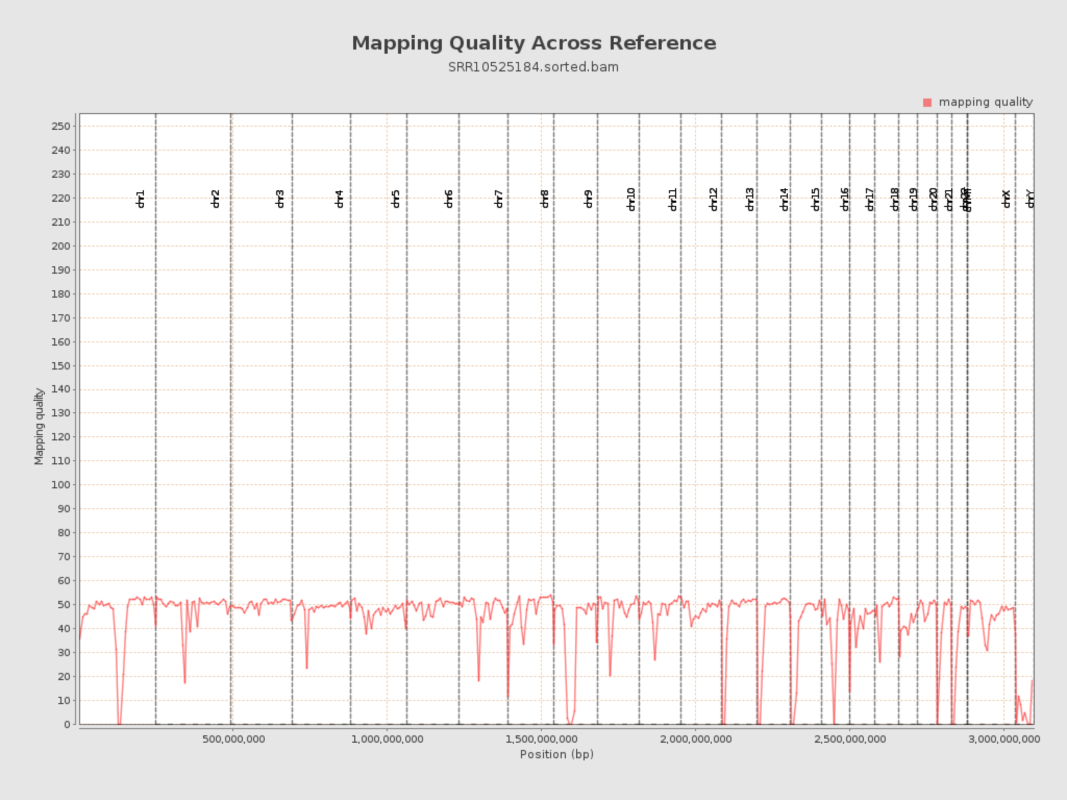
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram