Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:33:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525240.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_SRR10525240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:33:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,082,114
Mapped reads	993,187 / 91.78%
Unmapped reads	88,927 / 8.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,560 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	28,159 / 2.6%
Duplication rate	2.04%
Clipped reads	994,266 / 91.88%

2.2. ACGT Content

Number/percentage of A's	13,867,237 / 24.12%
Number/percentage of C's	10,365,119 / 18.03%
Number/percentage of T's	18,912,410 / 32.89%
Number/percentage of G's	14,352,350 / 24.96%
Number/percentage of N's	1,223 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.2081

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

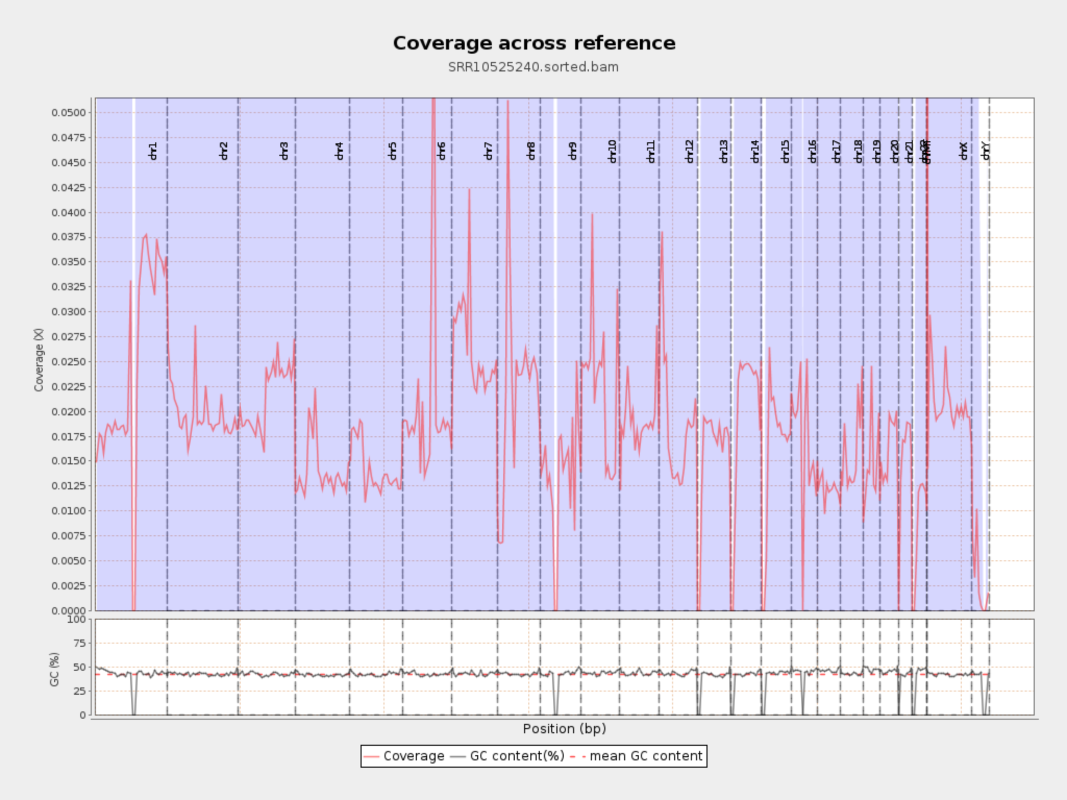
General error rate	0.51%
Mismatches	288,833
Insertions	3,937
Mapped reads with at least one insertion	0.39%
Deletions	12,000
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.38%

2.6. Chromosome stats

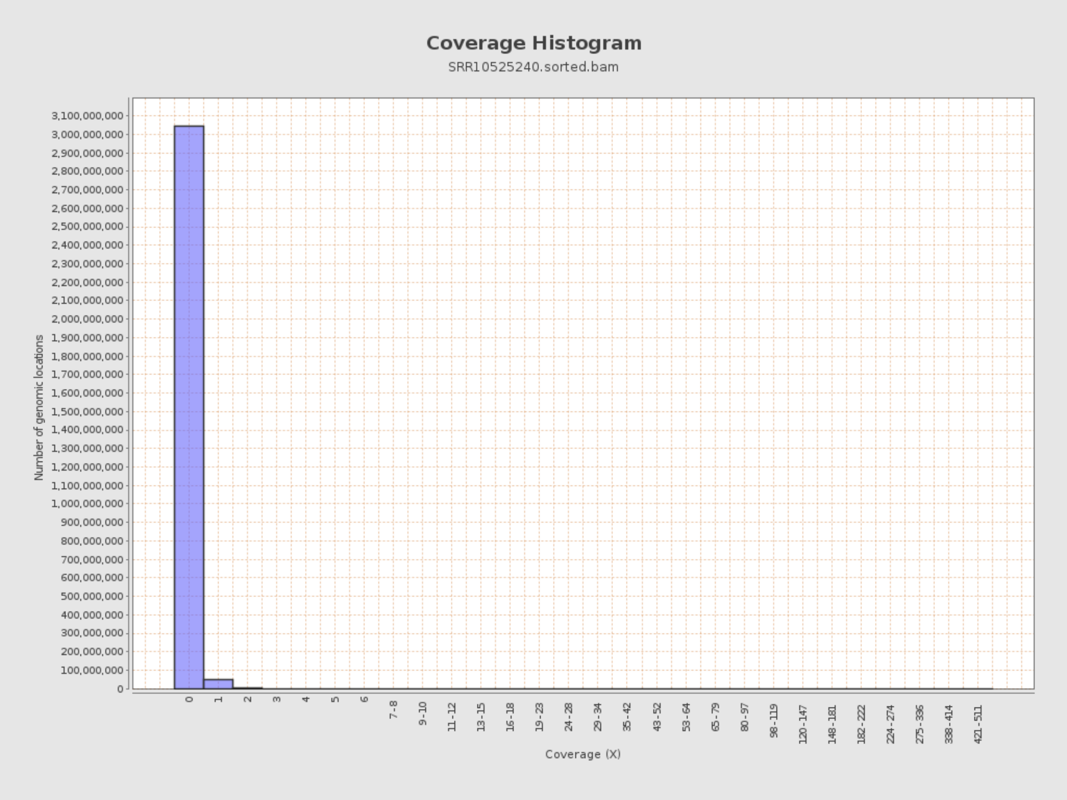
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6068168	0.0243	0.3817
chr2	243199373	4786911	0.0197	0.2468
chr3	198022430	4250699	0.0215	0.1567
chr4	191154276	2687151	0.0141	0.1309
chr5	180915260	2580125	0.0143	0.1262
chr6	171115067	3627651	0.0212	0.1668
chr7	159138663	4227825	0.0266	0.3428

chr8	146364022	3317293	0.0227	0.2175
chr9	141213431	1905909	0.0135	0.1469
chr10	135534747	3065783	0.0226	0.2164
chr11	135006516	2586669	0.0192	0.1684
chr12	133851895	2569636	0.0192	0.1482
chr13	115169878	1800226	0.0156	0.1342
chr14	107349540	2110641	0.0197	0.1501
chr15	102531392	1609180	0.0157	0.1334
chr16	90354753	1519078	0.0168	0.1482
chr17	81195210	991960	0.0122	0.1202
chr18	78077248	1239134	0.0159	0.2502
chr19	59128983	886097	0.015	0.243
chr20	63025520	1031984	0.0164	0.1378
chr21	48129895	735038	0.0153	0.1349
chr22	51304566	439982	0.0086	0.0969
chrMT	16571	60331	3.6408	2.6867
chrX	155270560	3247406	0.0209	0.161
chrY	59373566	172404	0.0029	0.0952

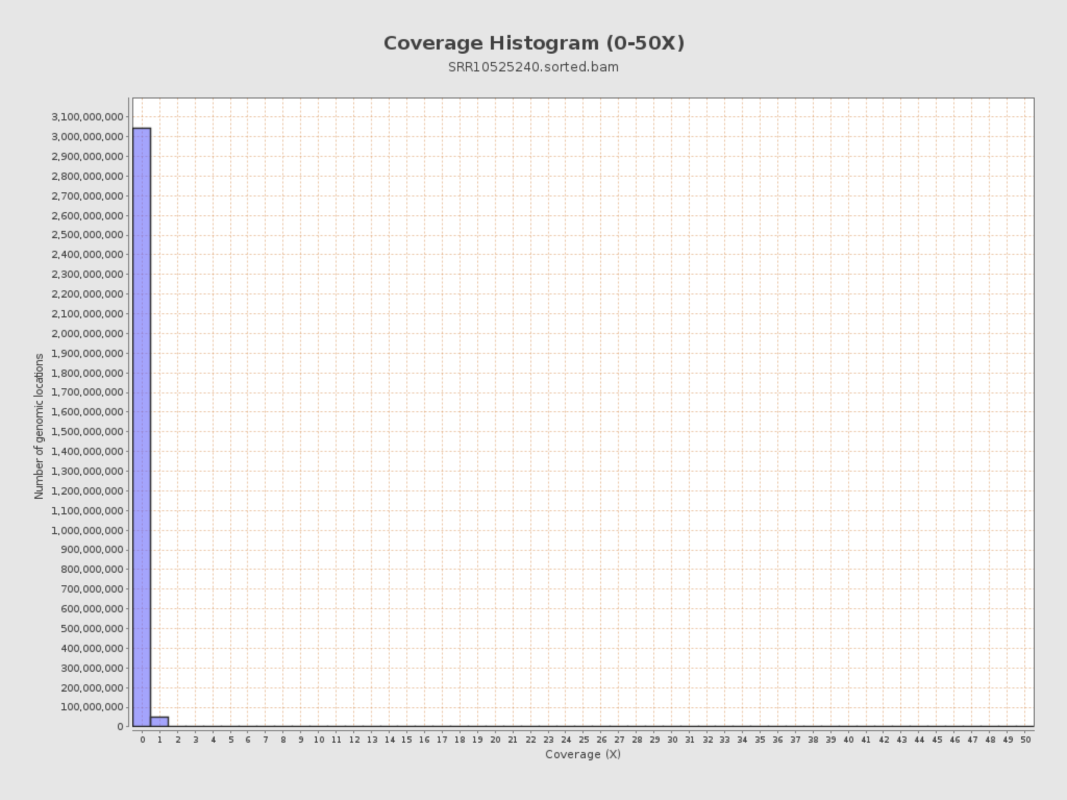
3. Results : Coverage across reference



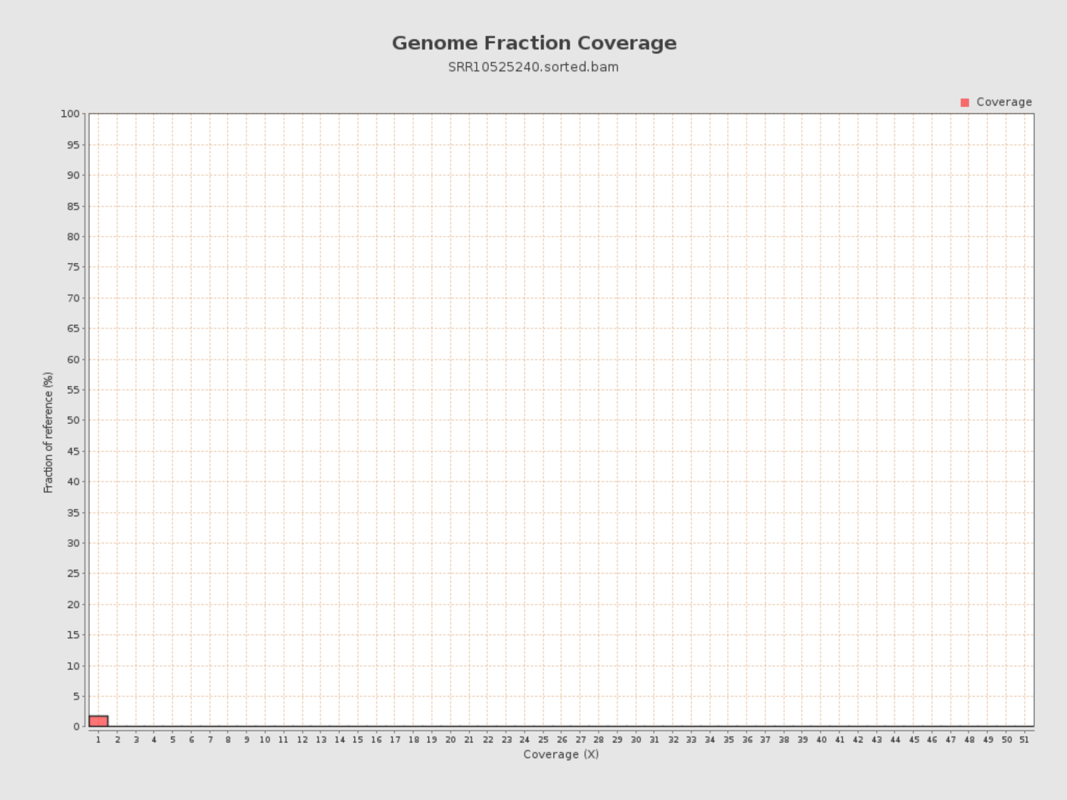
4. Results : Coverage Histogram



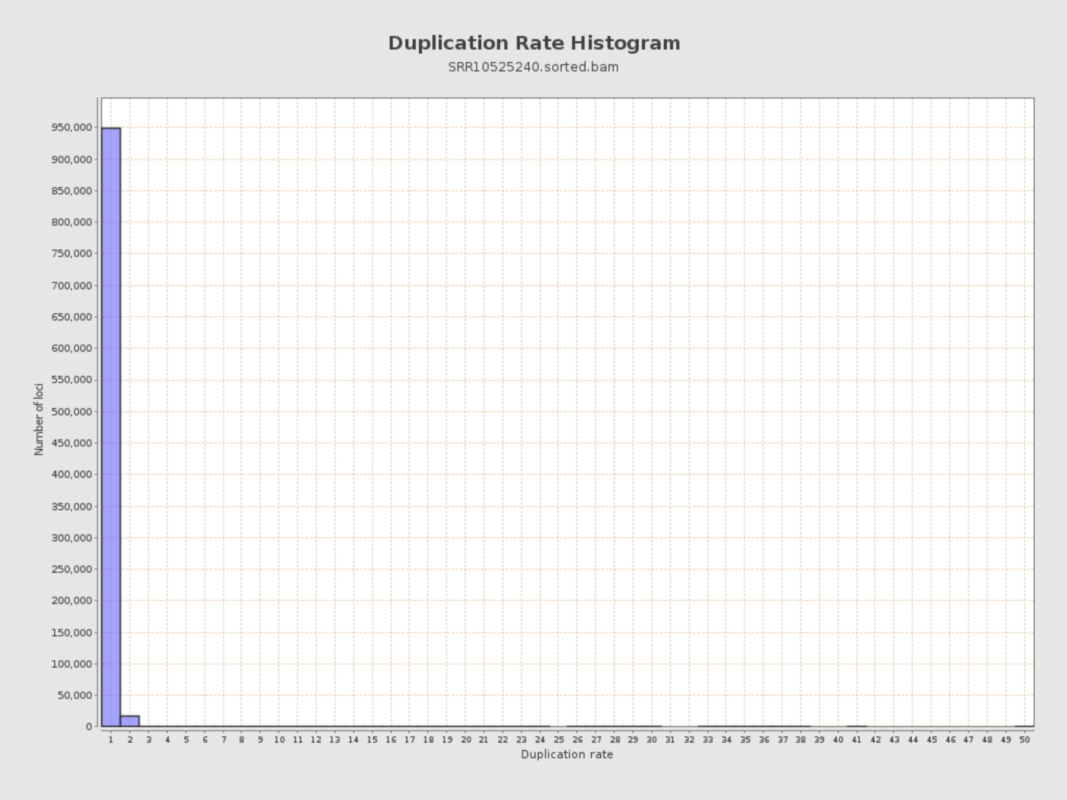
5. Results : Coverage Histogram (0-50X)



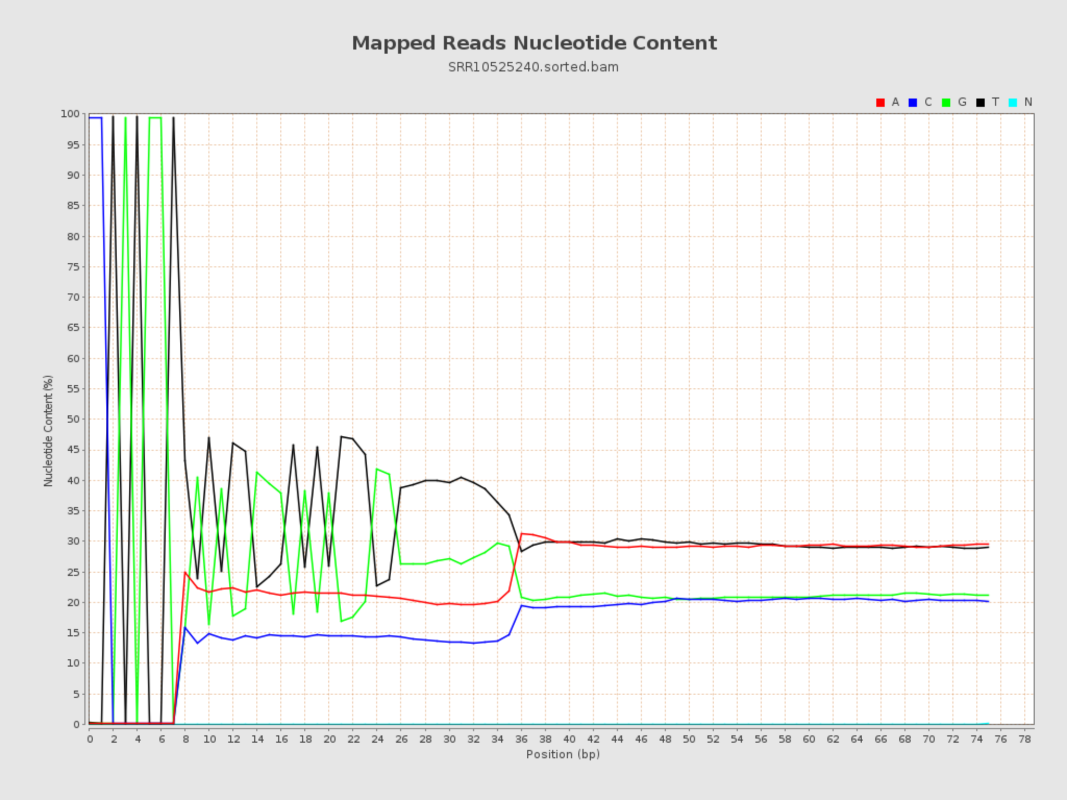
6. Results : Genome Fraction Coverage



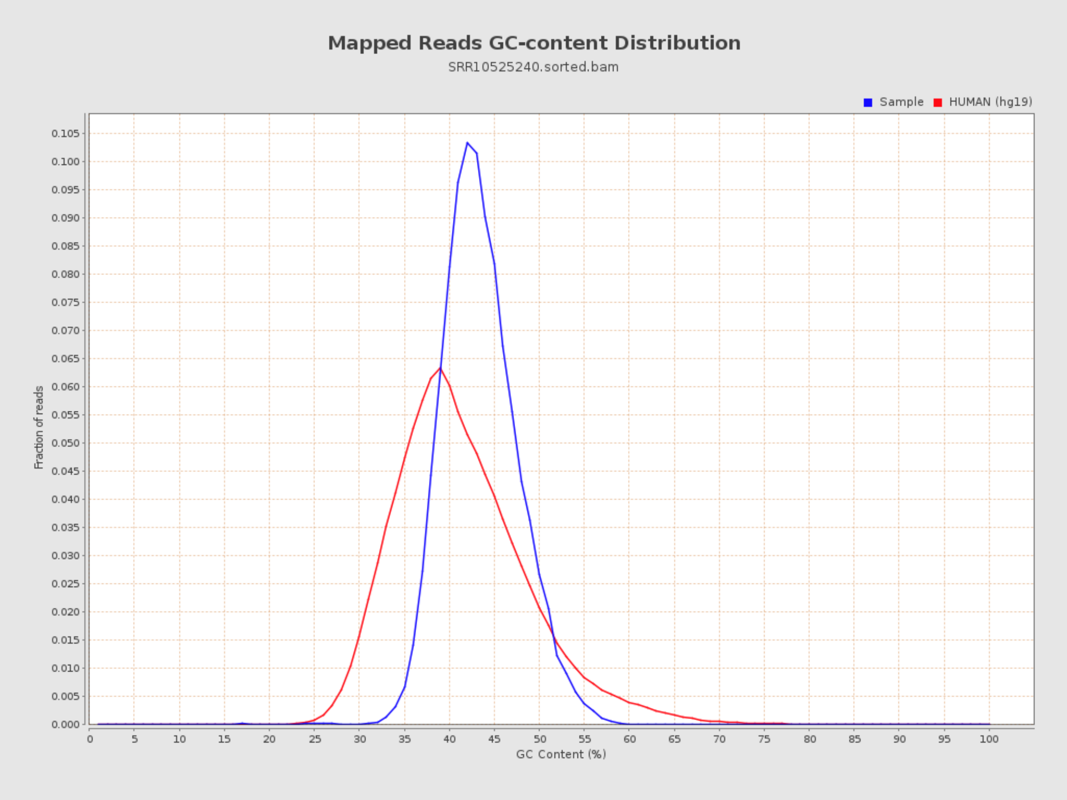
7. Results : Duplication Rate Histogram



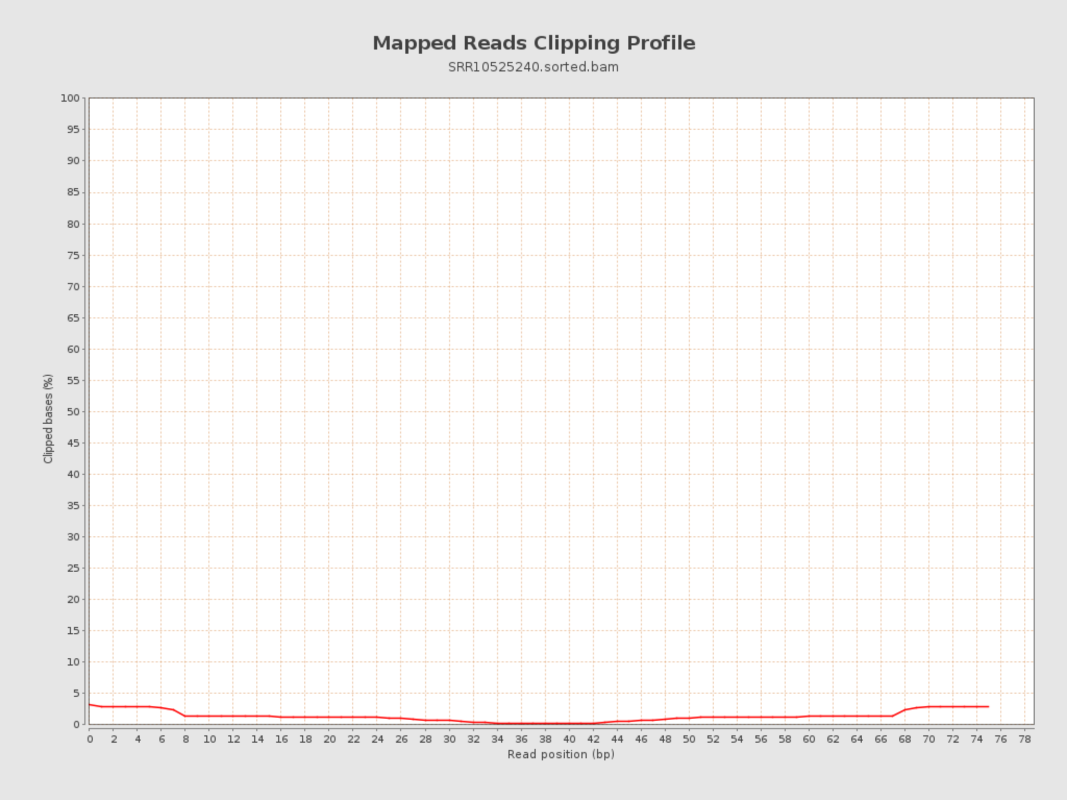
8. Results : Mapped Reads Nucleotide Content



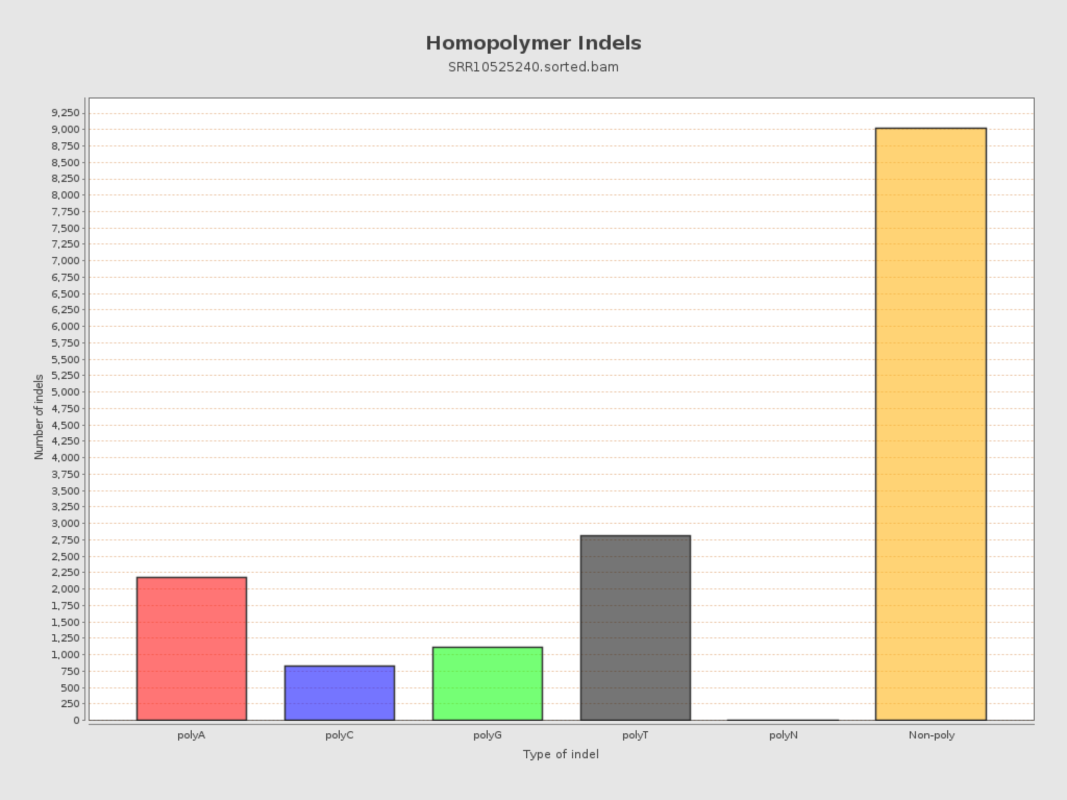
9. Results : Mapped Reads GC-content Distribution



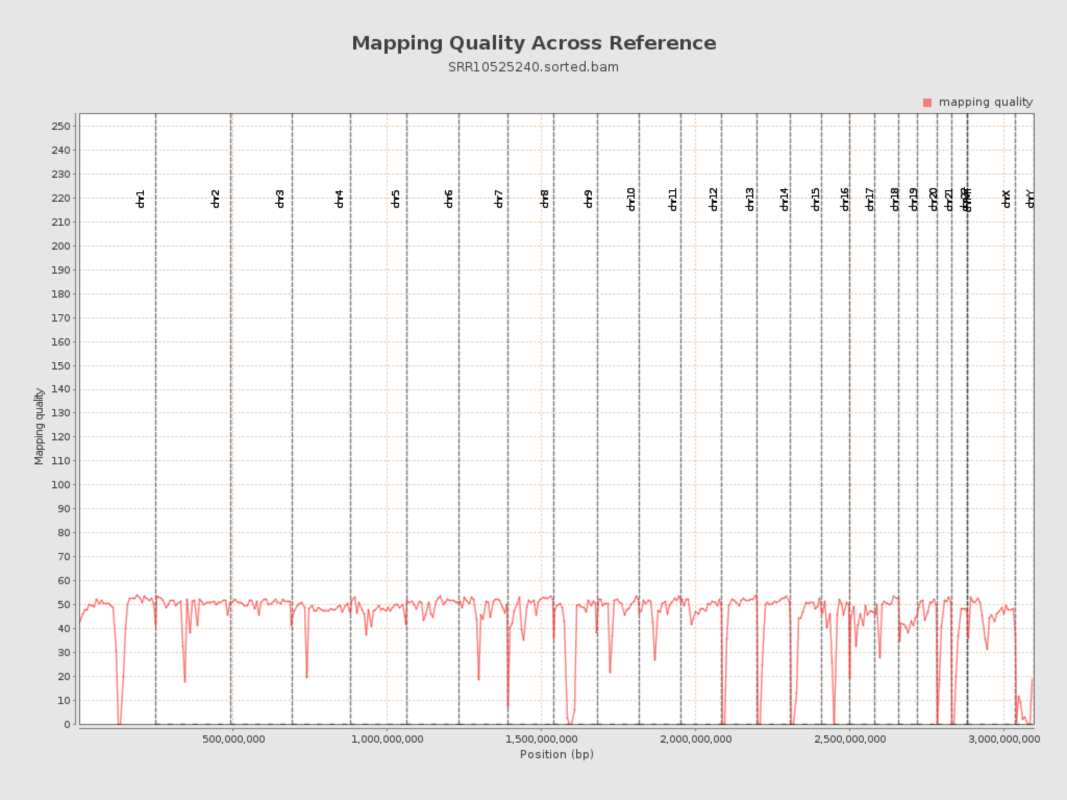
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram