Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:53:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525026.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_SRR10525026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:53:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,028,534
Mapped reads	941,964 / 91.58%
Unmapped reads	86,570 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,511 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	27,614 / 2.68%
Duplication rate	2.21%
Clipped reads	942,969 / 91.68%

2.2. ACGT Content

Number/percentage of A's	13,900,816 / 25.45%
Number/percentage of C's	10,618,416 / 19.44%
Number/percentage of T's	17,187,962 / 31.47%
Number/percentage of G's	12,908,219 / 23.63%
Number/percentage of N's	473 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.1825

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

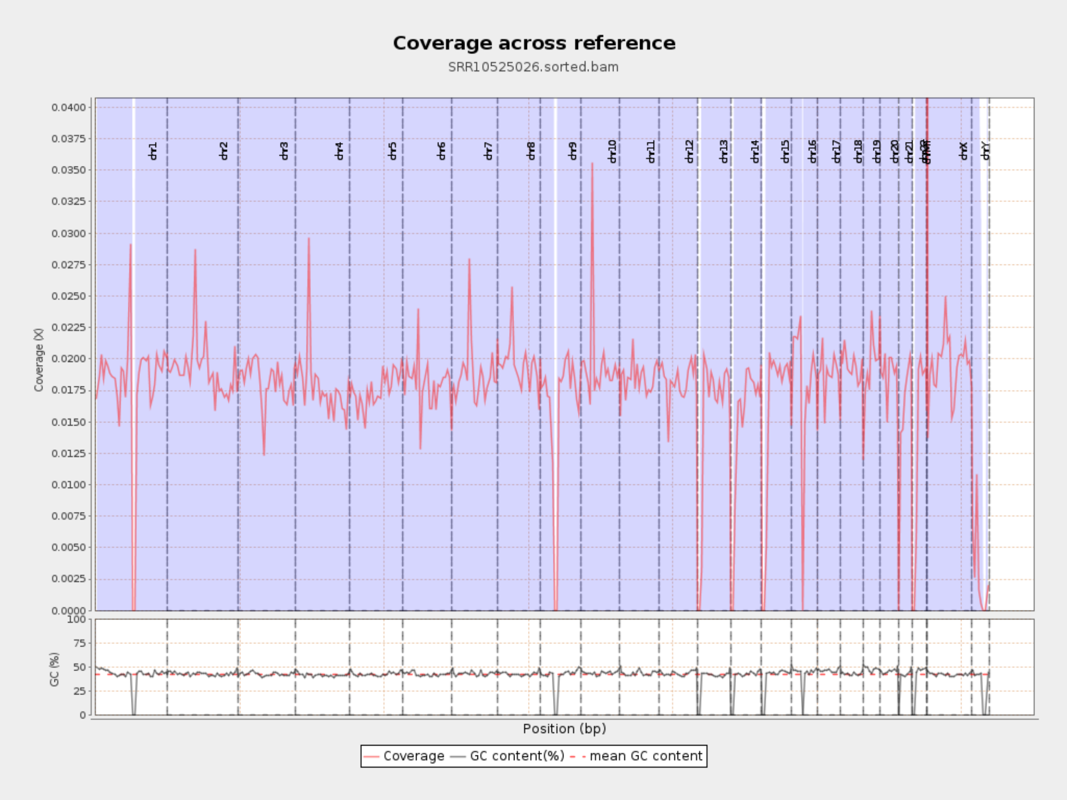
General error rate	0.51%
Mismatches	272,700
Insertions	3,952
Mapped reads with at least one insertion	0.42%
Deletions	10,254
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.52%

2.6. Chromosome stats

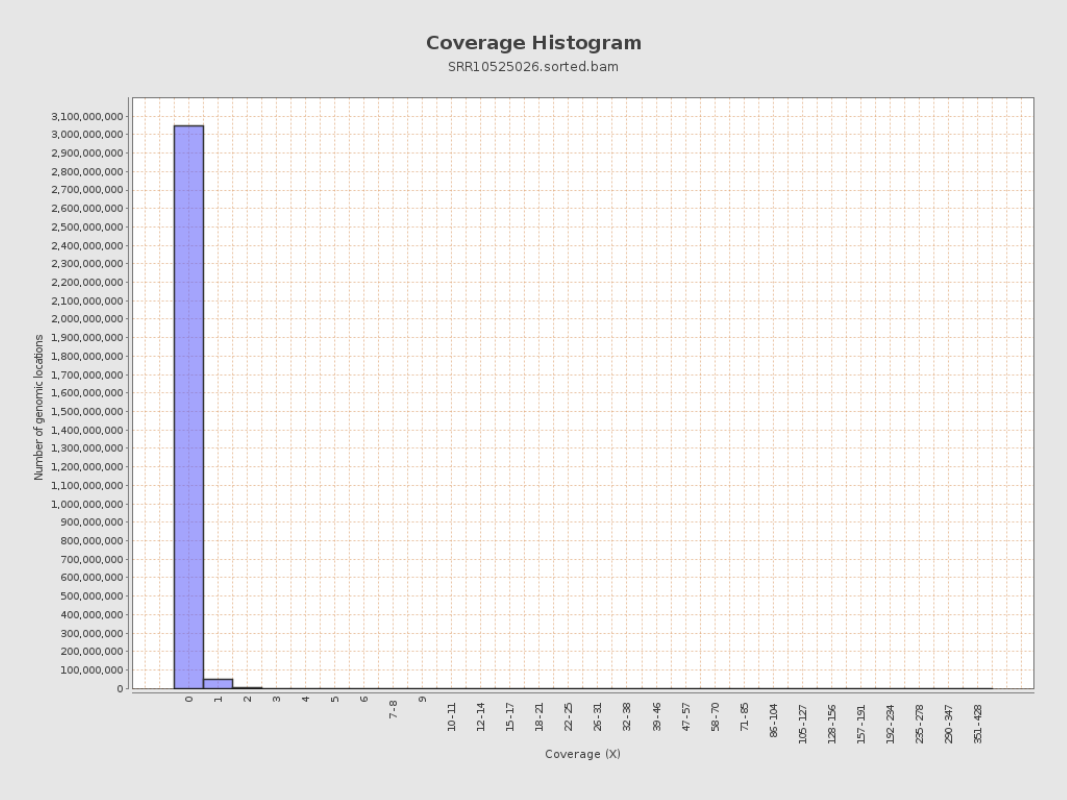
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4463308	0.0179	0.3066
chr2	243199373	4669601	0.0192	0.2064
chr3	198022430	3592458	0.0181	0.1439
chr4	191154276	3421668	0.0179	0.1556
chr5	180915260	3171260	0.0175	0.141
chr6	171115067	3091544	0.0181	0.1593
chr7	159138663	2990366	0.0188	0.2023

chr8	146364022	2865049	0.0196	0.1993
chr9	141213431	2237629	0.0158	0.1542
chr10	135534747	2669250	0.0197	0.1976
chr11	135006516	2496532	0.0185	0.172
chr12	133851895	2436874	0.0182	0.1447
chr13	115169878	1747671	0.0152	0.1312
chr14	107349540	1568210	0.0146	0.1303
chr15	102531392	1592094	0.0155	0.1335
chr16	90354753	1590582	0.0176	0.1464
chr17	81195210	1525143	0.0188	0.1553
chr18	78077248	1516482	0.0194	0.2511
chr19	59128983	1157117	0.0196	0.2165
chr20	63025520	1180378	0.0187	0.1466
chr21	48129895	750373	0.0156	0.1449
chr22	51304566	678013	0.0132	0.1215
chrMT	16571	10227	0.6172	0.9289
chrX	155270560	3040693	0.0196	0.1577
chrY	59373566	170451	0.0029	0.0982

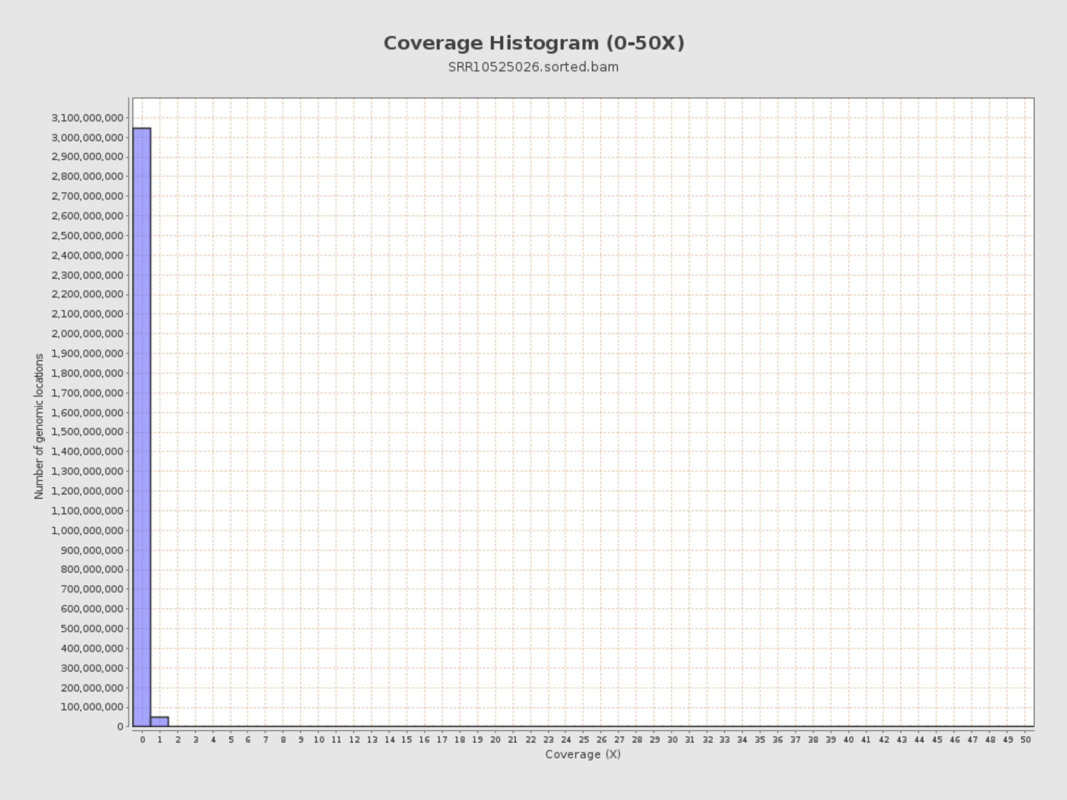
3. Results : Coverage across reference



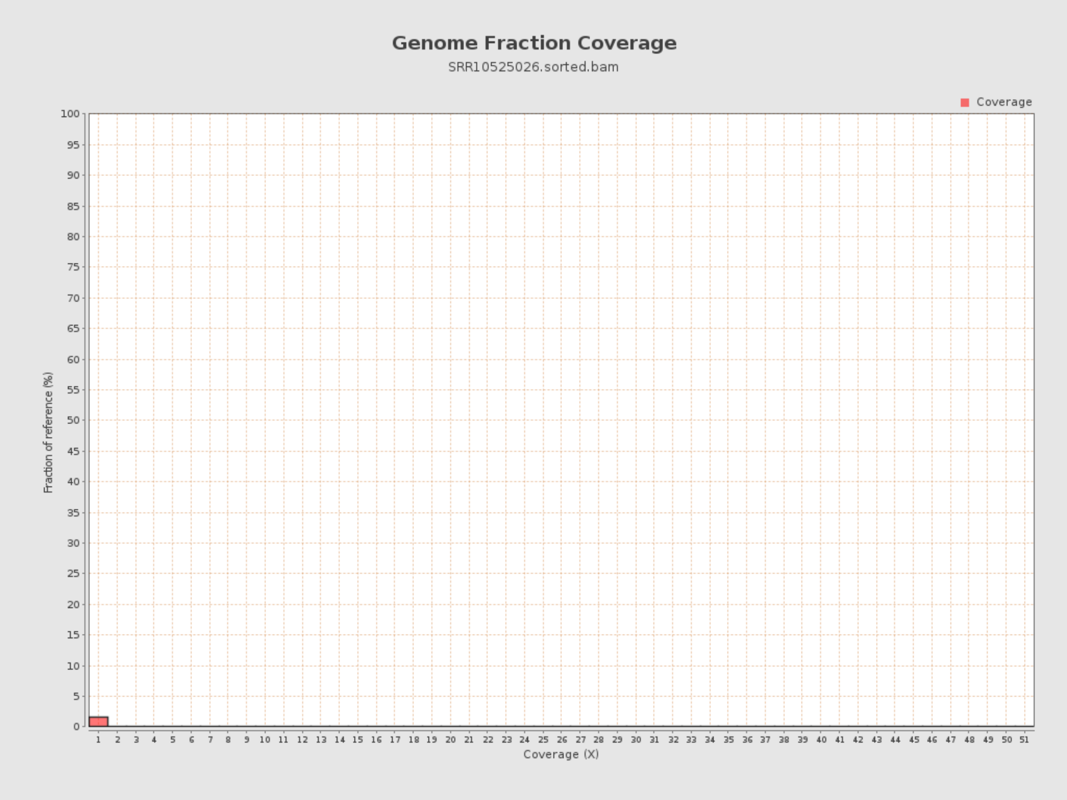
4. Results : Coverage Histogram



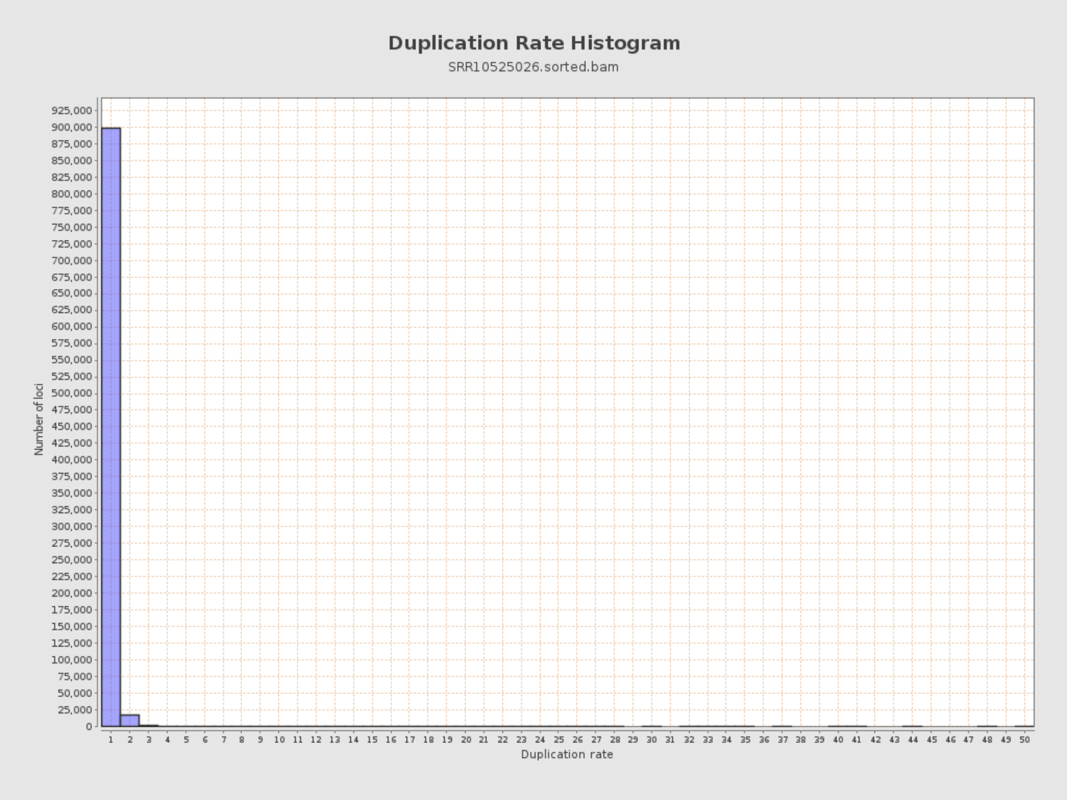
5. Results : Coverage Histogram (0-50X)



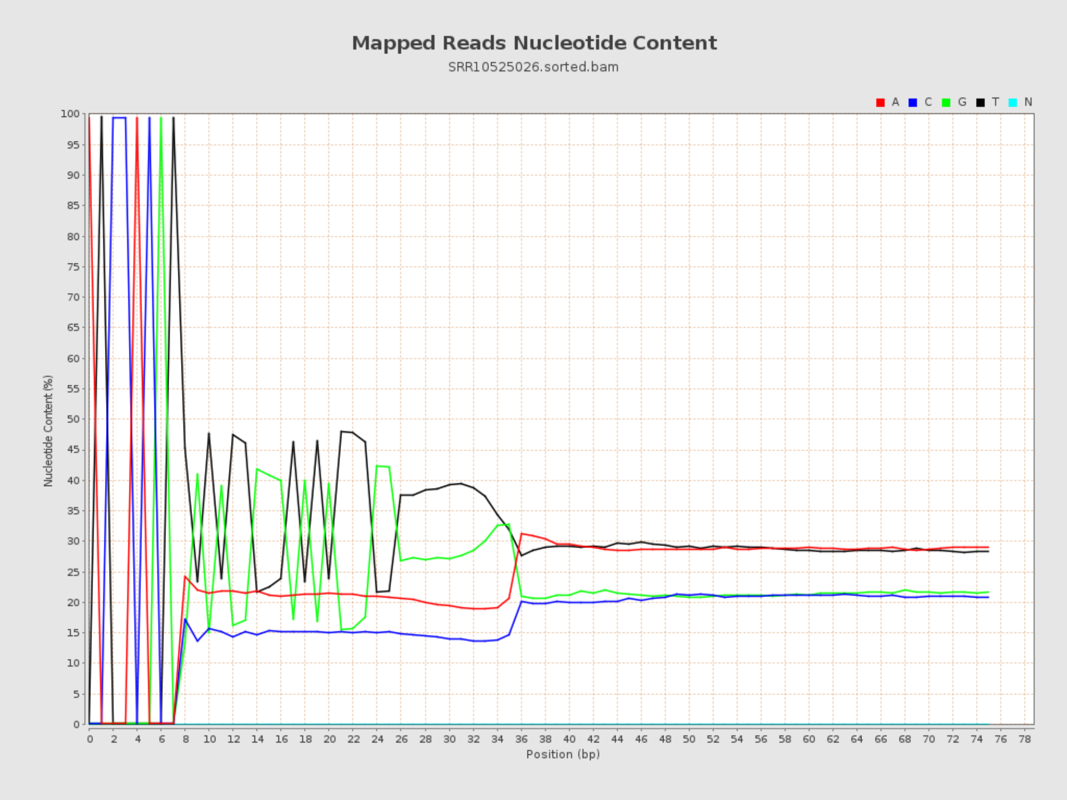
6. Results : Genome Fraction Coverage



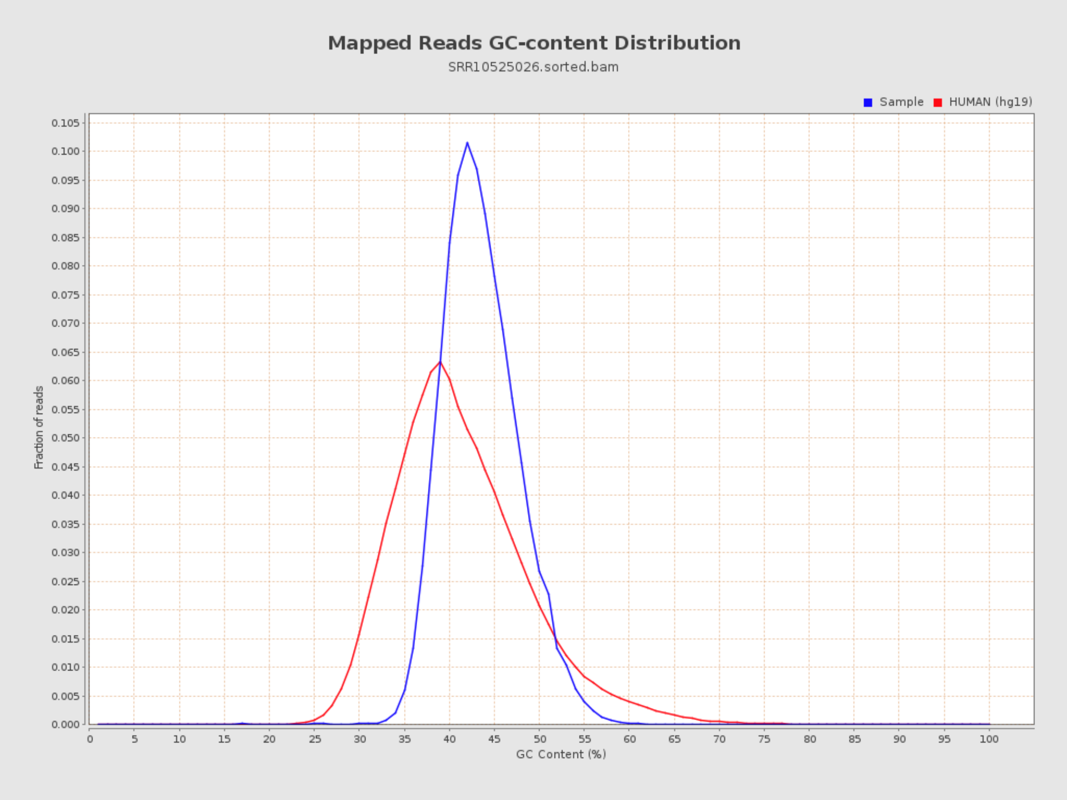
7. Results : Duplication Rate Histogram



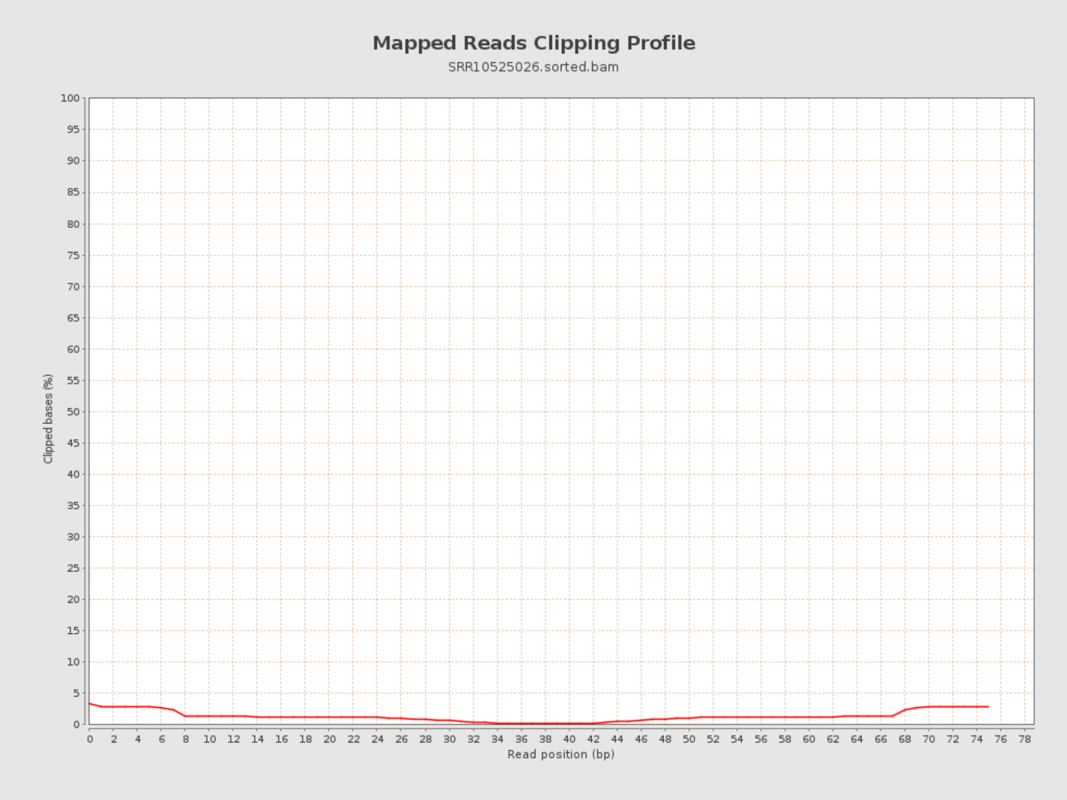
8. Results : Mapped Reads Nucleotide Content



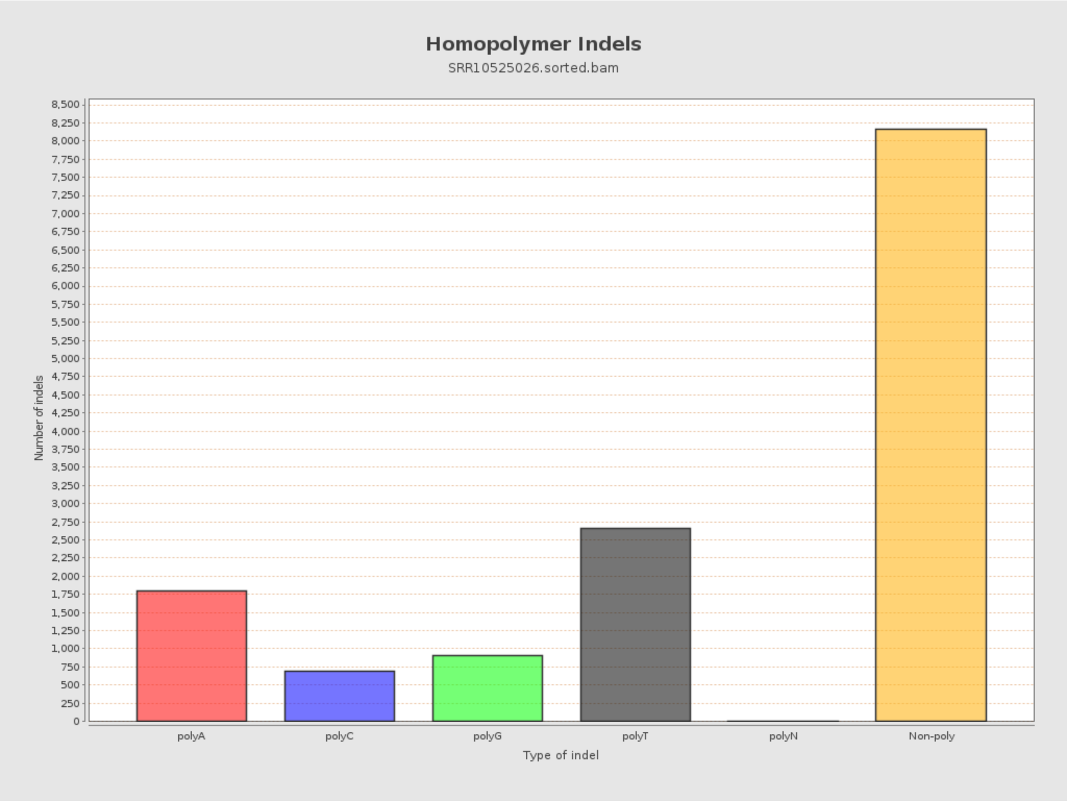
9. Results : Mapped Reads GC-content Distribution



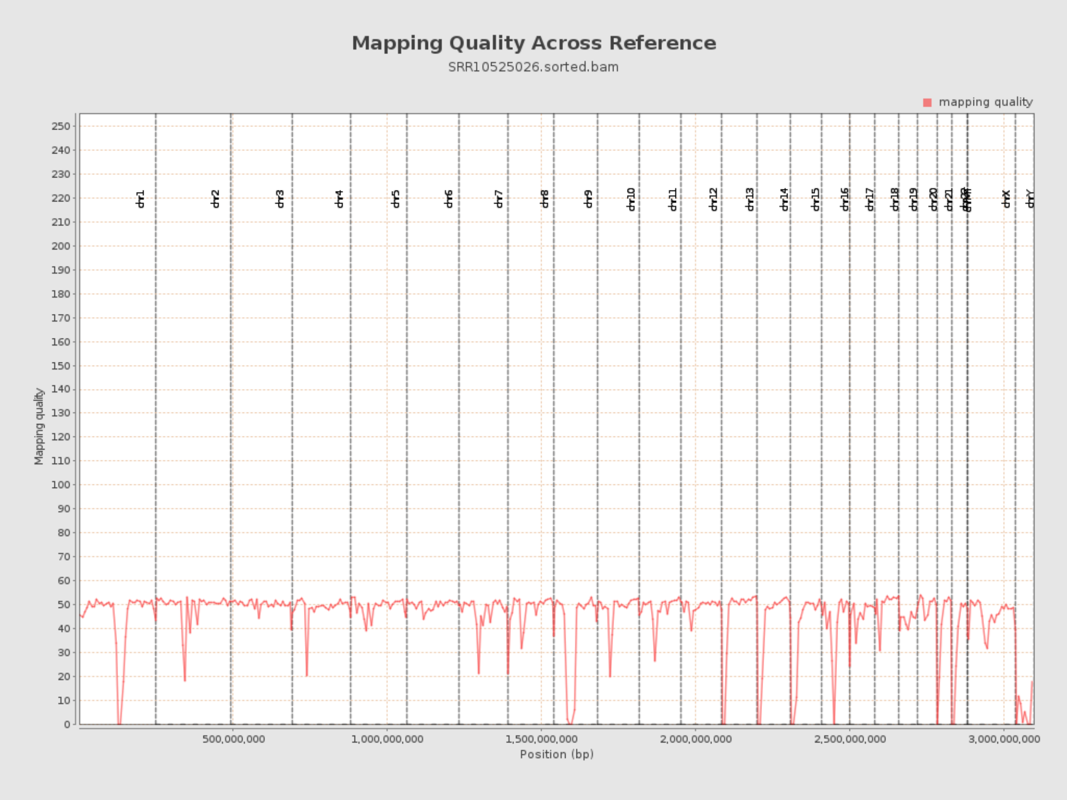
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram