Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:25:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525175.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_SRR10525175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:25:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	931,185
Mapped reads	842,348 / 90.46%
Unmapped reads	88,837 / 9.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,265 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	16,450 / 1.77%
Duplication rate	1.38%
Clipped reads	841,312 / 90.35%

2.2. ACGT Content

Number/percentage of A's	14,419,755 / 27.48%
Number/percentage of C's	11,026,950 / 21.02%
Number/percentage of T's	15,369,024 / 29.29%
Number/percentage of G's	11,652,354 / 22.21%
Number/percentage of N's	1,433 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.017

Standard Deviation	0.1864

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

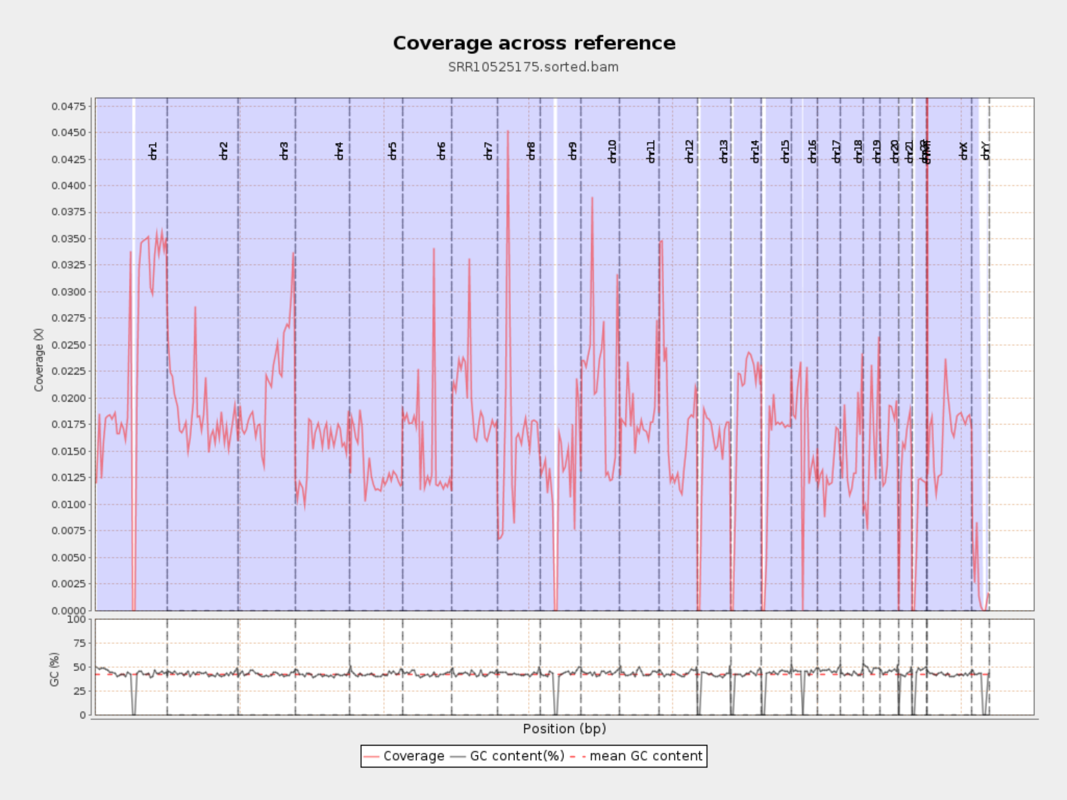
General error rate	0.5%
Mismatches	253,847
Insertions	4,612
Mapped reads with at least one insertion	0.55%
Deletions	11,494
Mapped reads with at least one deletion	1.36%
Homopolymer indels	41.96%

2.6. Chromosome stats

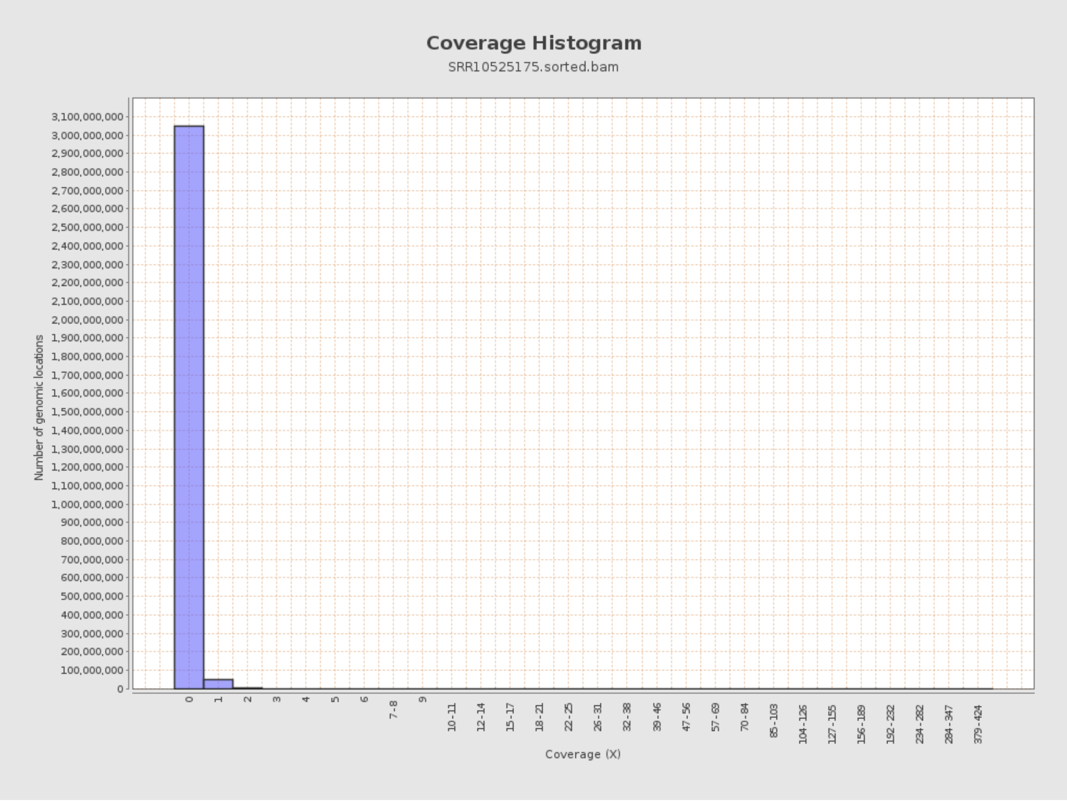
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5819796	0.0233	0.3528
chr2	243199373	4455598	0.0183	0.1896
chr3	198022430	4189666	0.0212	0.1522
chr4	191154276	2942734	0.0154	0.1328
chr5	180915260	2440089	0.0135	0.1212
chr6	171115067	2657757	0.0155	0.1397
chr7	159138663	3168215	0.0199	0.2624

chr8	146364022	2444657	0.0167	0.1536
chr9	141213431	1778610	0.0126	0.1457
chr10	135534747	2950490	0.0218	0.2105
chr11	135006516	2469475	0.0183	0.159
chr12	133851895	2430784	0.0182	0.1415
chr13	115169878	1686738	0.0146	0.126
chr14	107349540	2011102	0.0187	0.1469
chr15	102531392	1471950	0.0144	0.1254
chr16	90354753	1466225	0.0162	0.143
chr17	81195210	1076997	0.0133	0.1236
chr18	78077248	1168844	0.015	0.2667
chr19	59128983	920808	0.0156	0.2563
chr20	63025520	1006957	0.016	0.1331
chr21	48129895	687822	0.0143	0.1295
chr22	51304566	439052	0.0086	0.0967
chrMT	16571	3458	0.2087	0.5001
chrX	155270560	2654034	0.0171	0.1426
chrY	59373566	146185	0.0025	0.0831

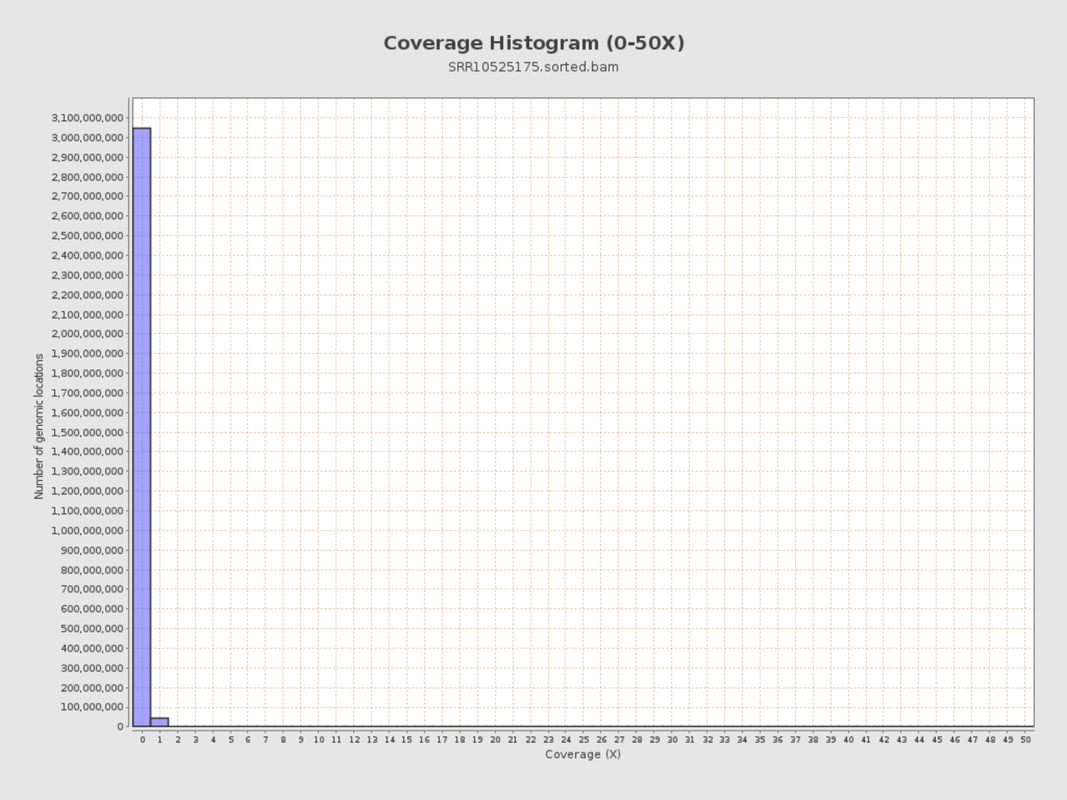
3. Results : Coverage across reference



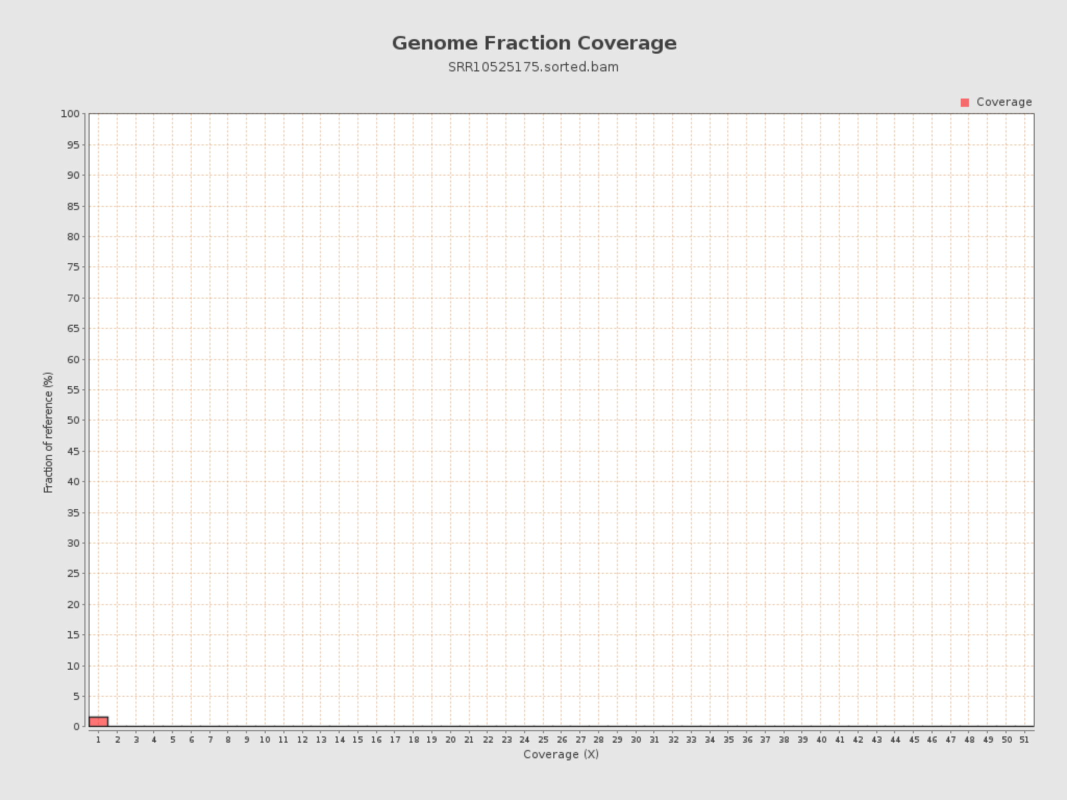
4. Results : Coverage Histogram



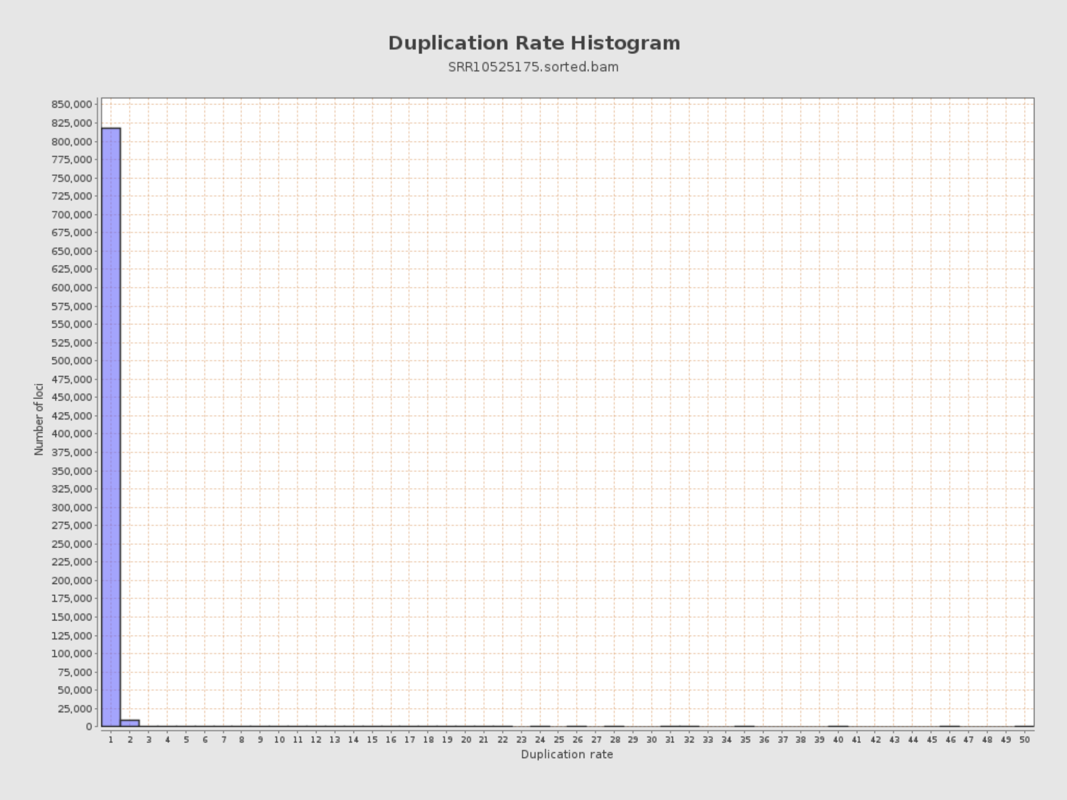
5. Results : Coverage Histogram (0-50X)



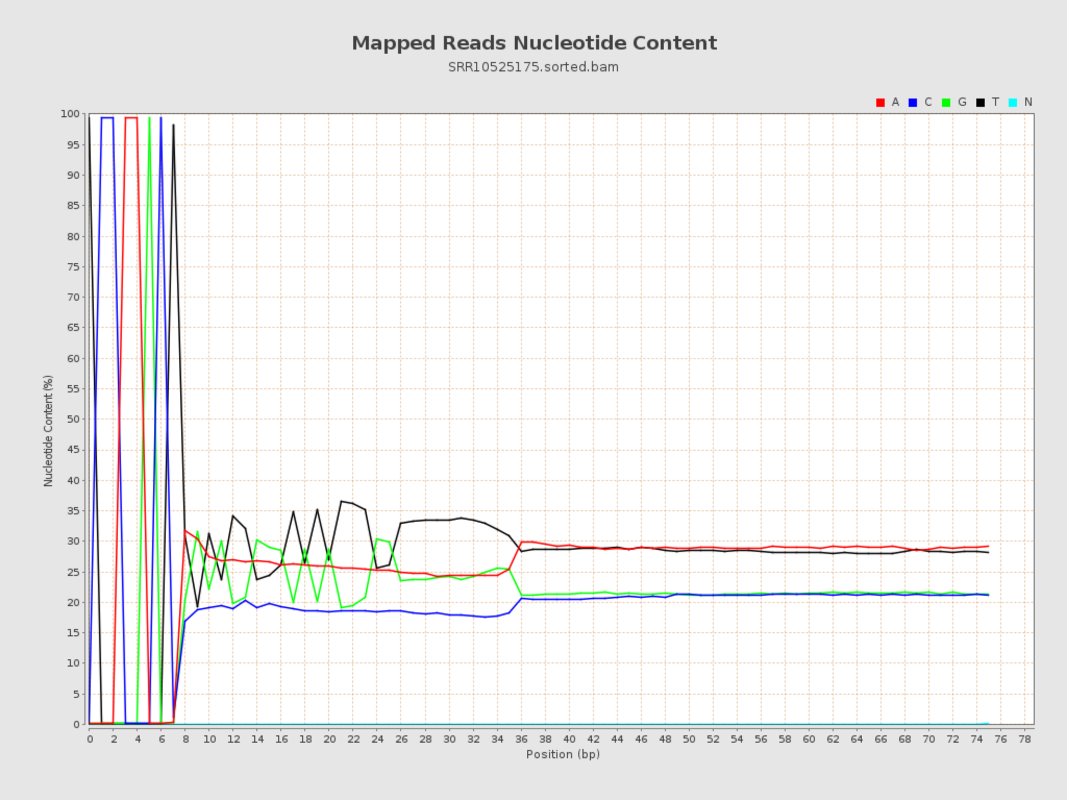
6. Results : Genome Fraction Coverage



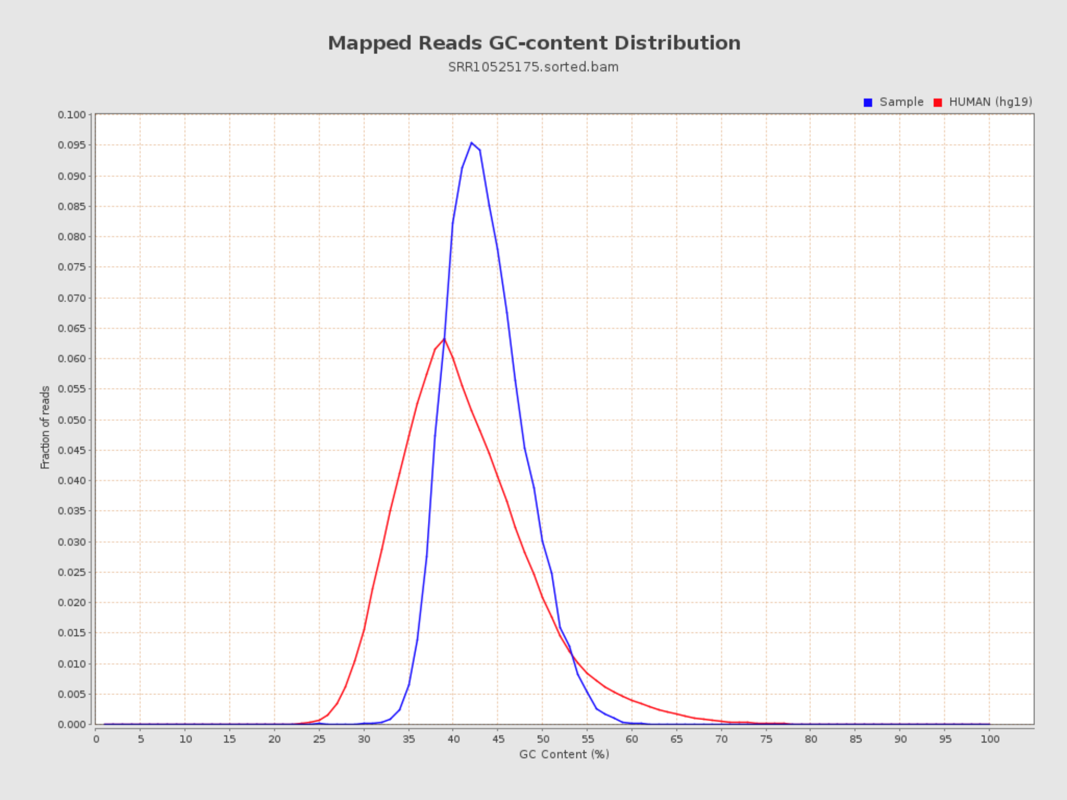
7. Results : Duplication Rate Histogram



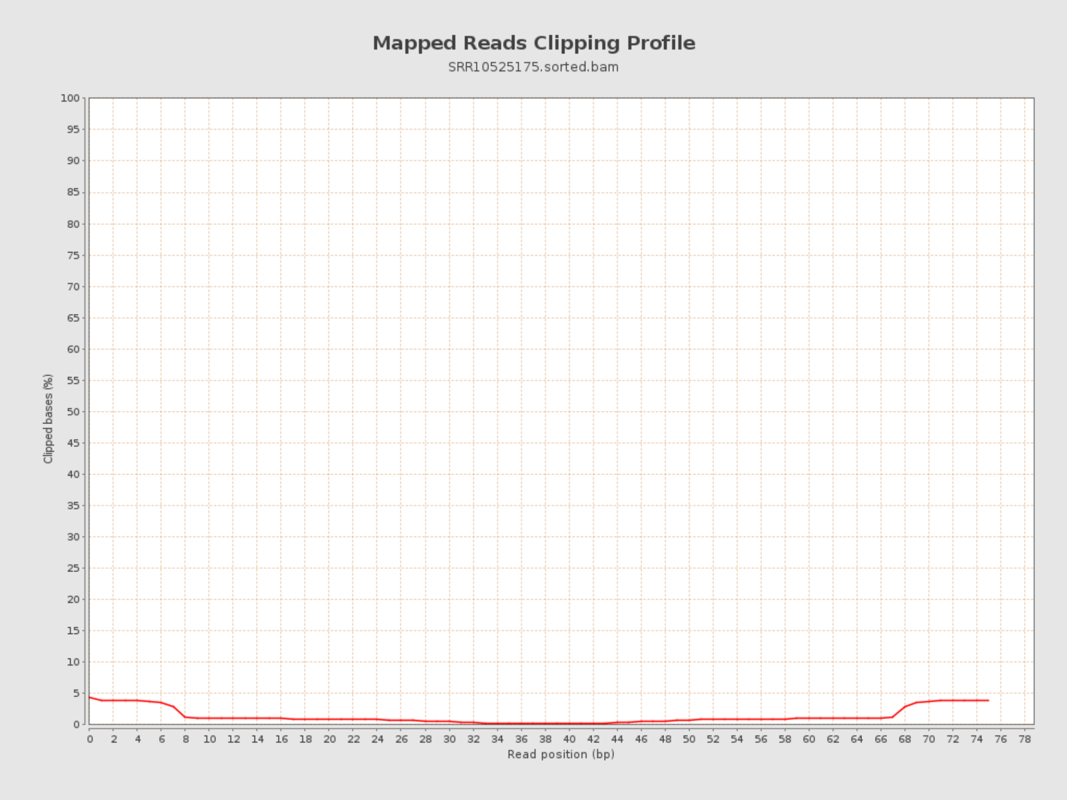
8. Results : Mapped Reads Nucleotide Content



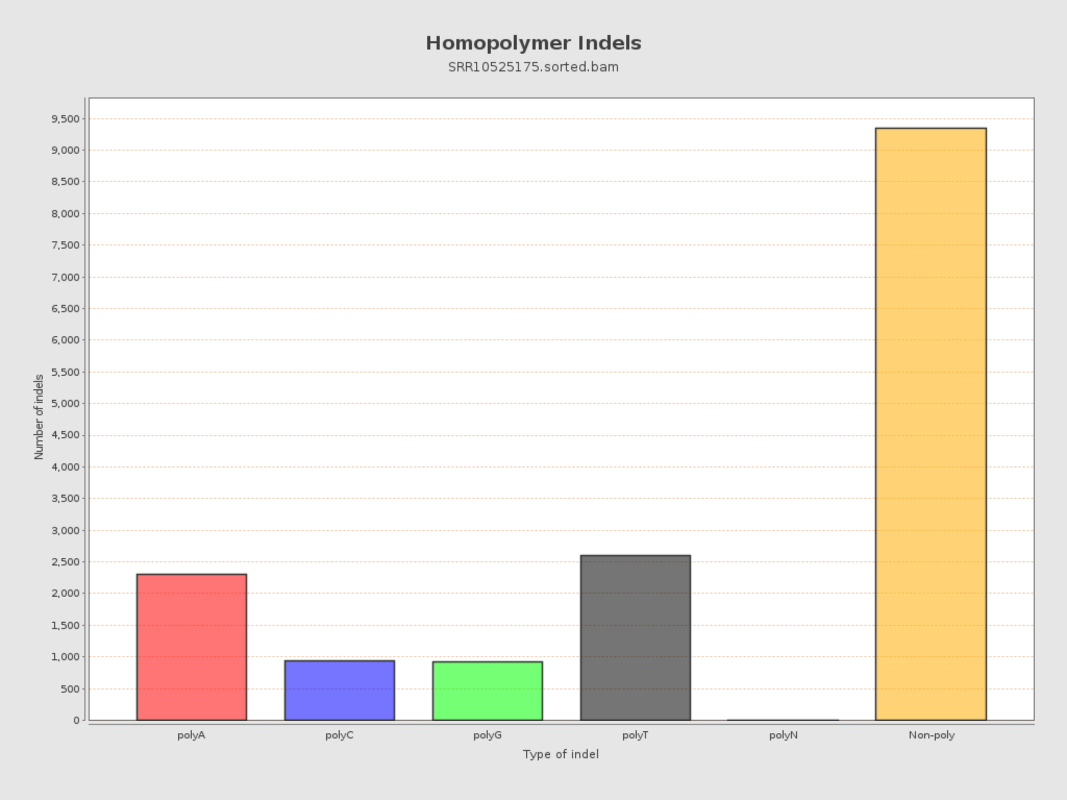
9. Results : Mapped Reads GC-content Distribution



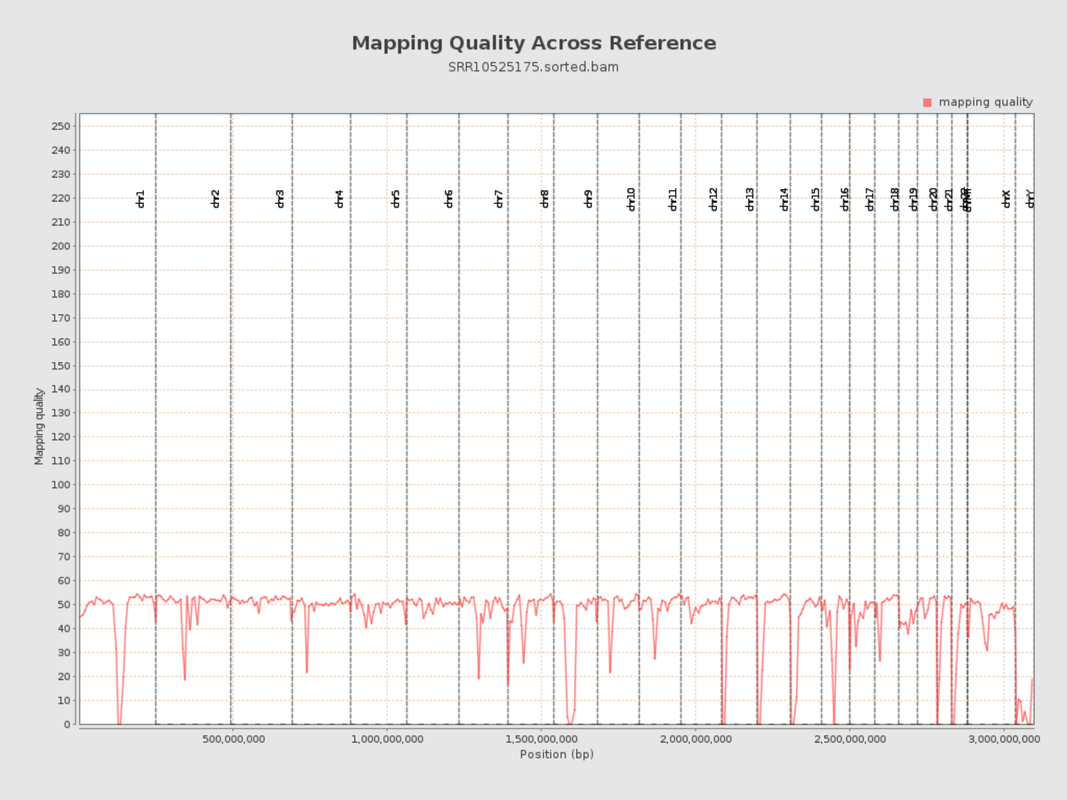
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram