Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:03:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525055.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_SRR10525055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,152,096
Mapped reads	1,058,493 / 91.88%
Unmapped reads	93,603 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,708 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	23,799 / 2.07%
Duplication rate	1.69%
Clipped reads	1,062,105 / 92.19%

2.2. ACGT Content

Number/percentage of A's	15,106,174 / 24.69%
Number/percentage of C's	11,038,530 / 18.04%
Number/percentage of T's	19,904,902 / 32.54%
Number/percentage of G's	15,128,336 / 24.73%
Number/percentage of N's	1,889 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.1856

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

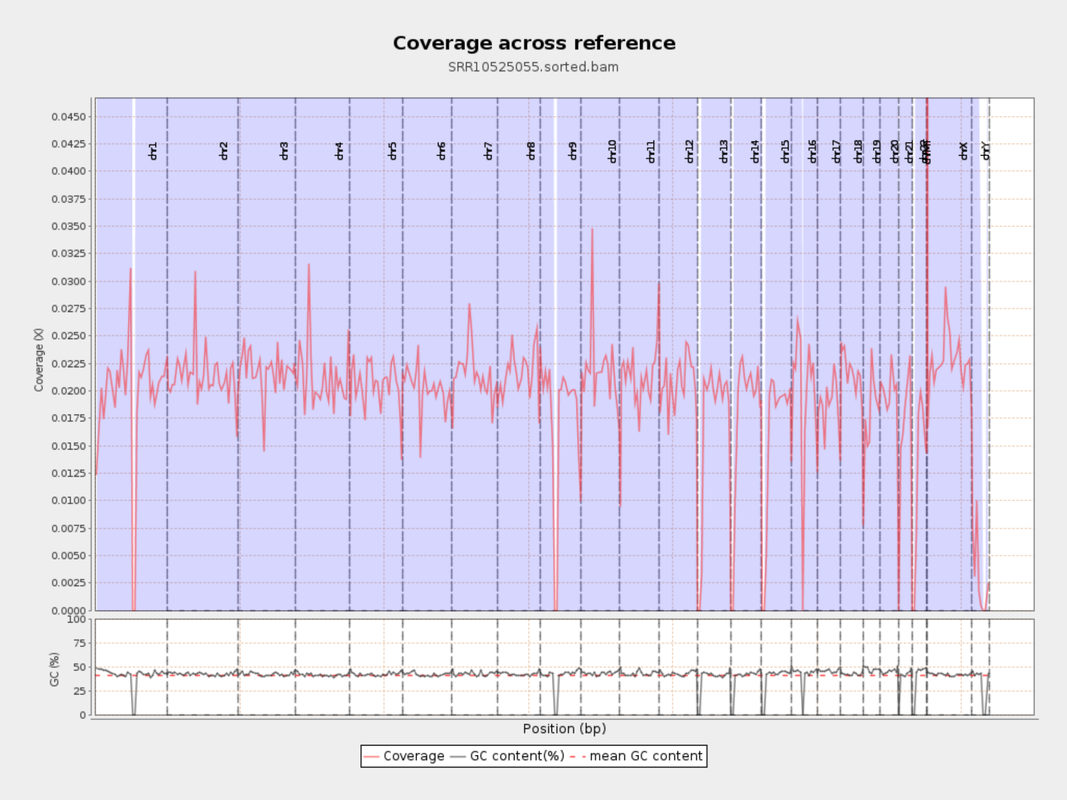
General error rate	0.48%
Mismatches	287,432
Insertions	3,206
Mapped reads with at least one insertion	0.3%
Deletions	9,667
Mapped reads with at least one deletion	0.91%
Homopolymer indels	44.89%

2.6. Chromosome stats

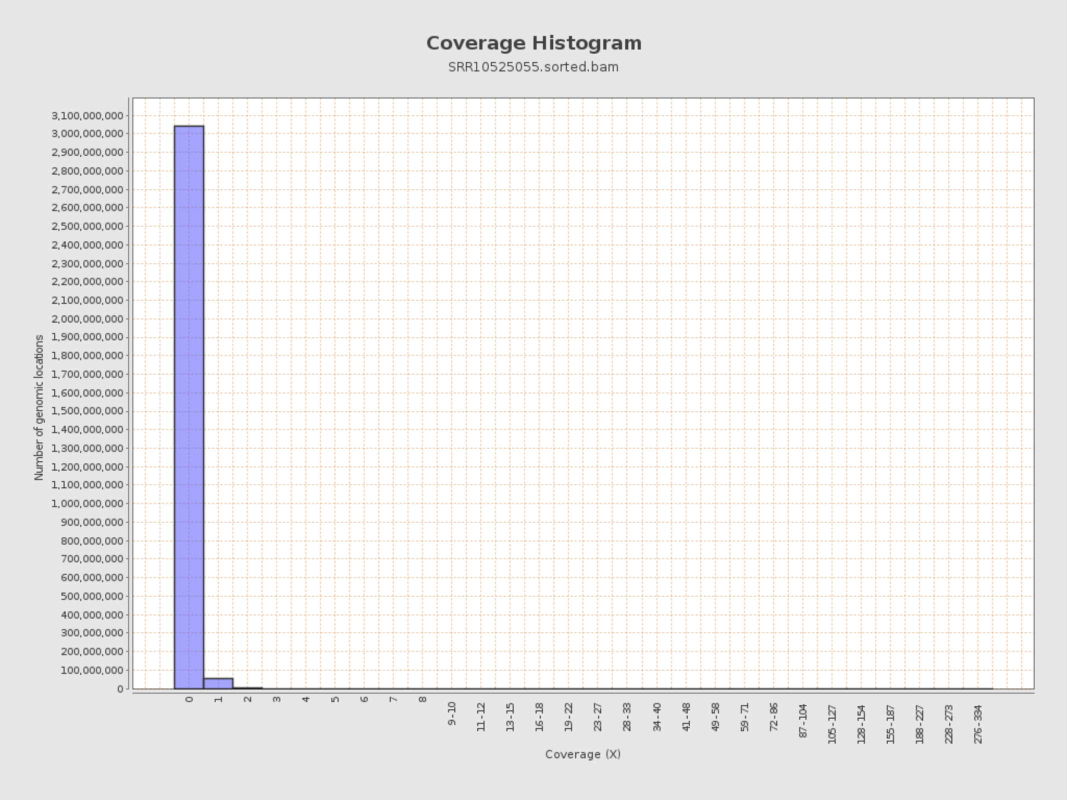
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4878461	0.0196	0.2963
chr2	243199373	5203365	0.0214	0.1974
chr3	198022430	4308499	0.0218	0.156
chr4	191154276	4055219	0.0212	0.1662
chr5	180915260	3748881	0.0207	0.1528
chr6	171115067	3459048	0.0202	0.1598
chr7	159138663	3423622	0.0215	0.2026

chr8	146364022	3169611	0.0217	0.1968
chr9	141213431	2483598	0.0176	0.1774
chr10	135534747	2974571	0.0219	0.1983
chr11	135006516	2834369	0.021	0.1801
chr12	133851895	2781894	0.0208	0.1549
chr13	115169878	1943510	0.0169	0.1369
chr14	107349540	1879408	0.0175	0.1453
chr15	102531392	1617927	0.0158	0.1329
chr16	90354753	1748463	0.0194	0.1523
chr17	81195210	1524348	0.0188	0.15
chr18	78077248	1701607	0.0218	0.271
chr19	59128983	1071526	0.0181	0.2253
chr20	63025520	1247848	0.0198	0.1535
chr21	48129895	788865	0.0164	0.1446
chr22	51304566	634497	0.0124	0.1174
chrMT	16571	4185	0.2525	0.5193
chrX	155270560	3537244	0.0228	0.1704
chrY	59373566	175723	0.003	0.082

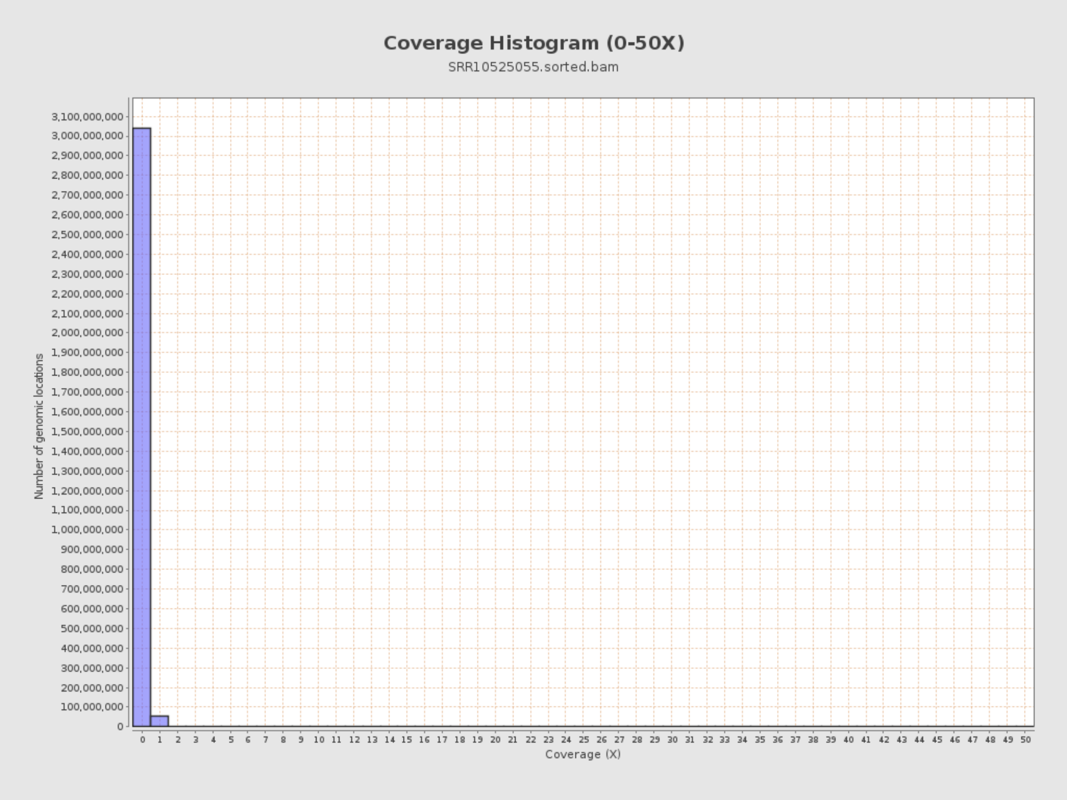
3. Results : Coverage across reference



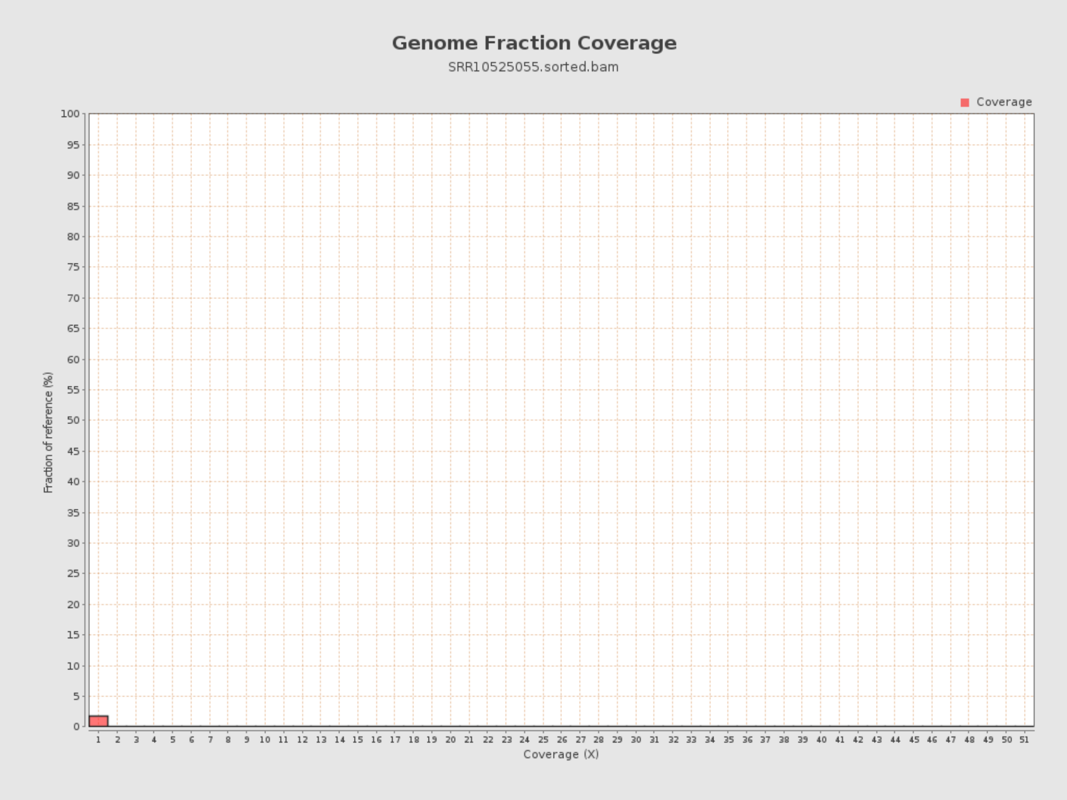
4. Results : Coverage Histogram



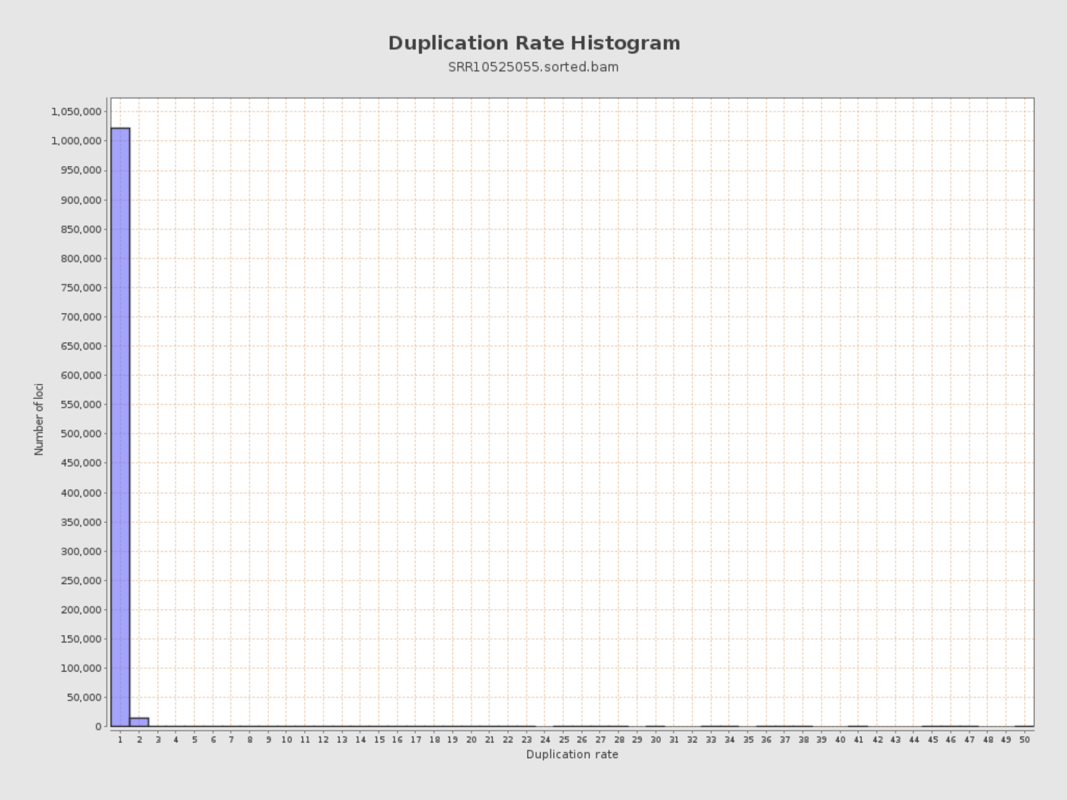
5. Results : Coverage Histogram (0-50X)



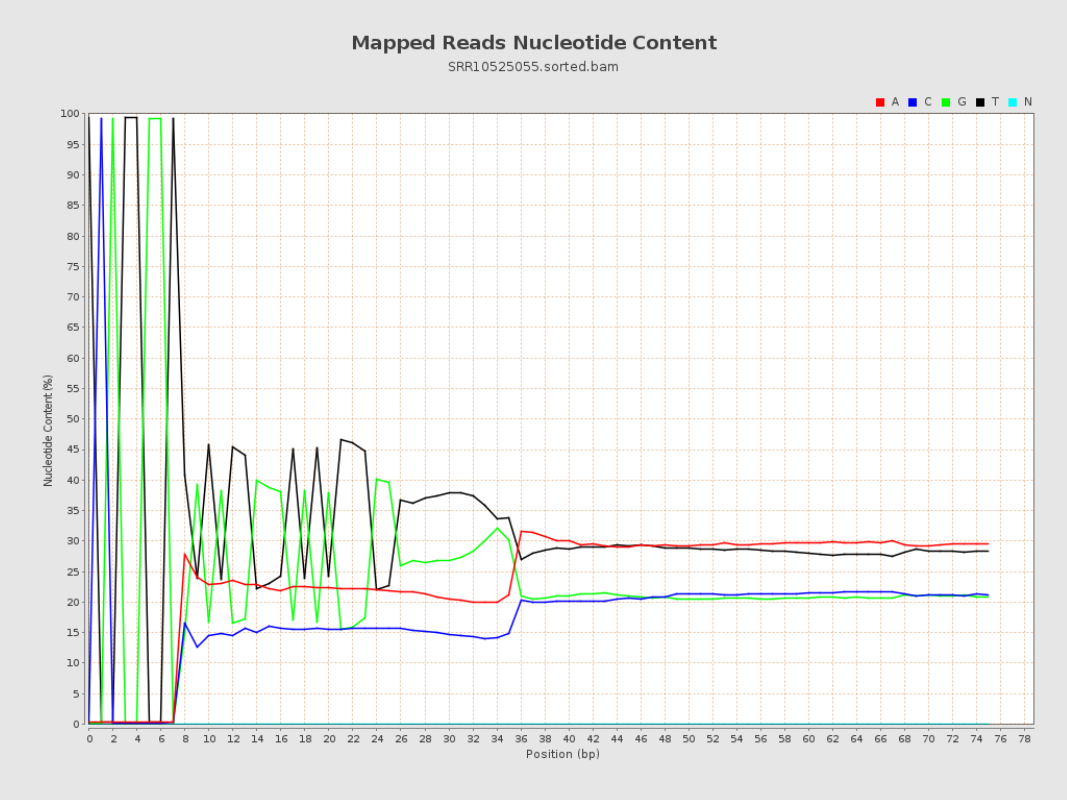
6. Results : Genome Fraction Coverage



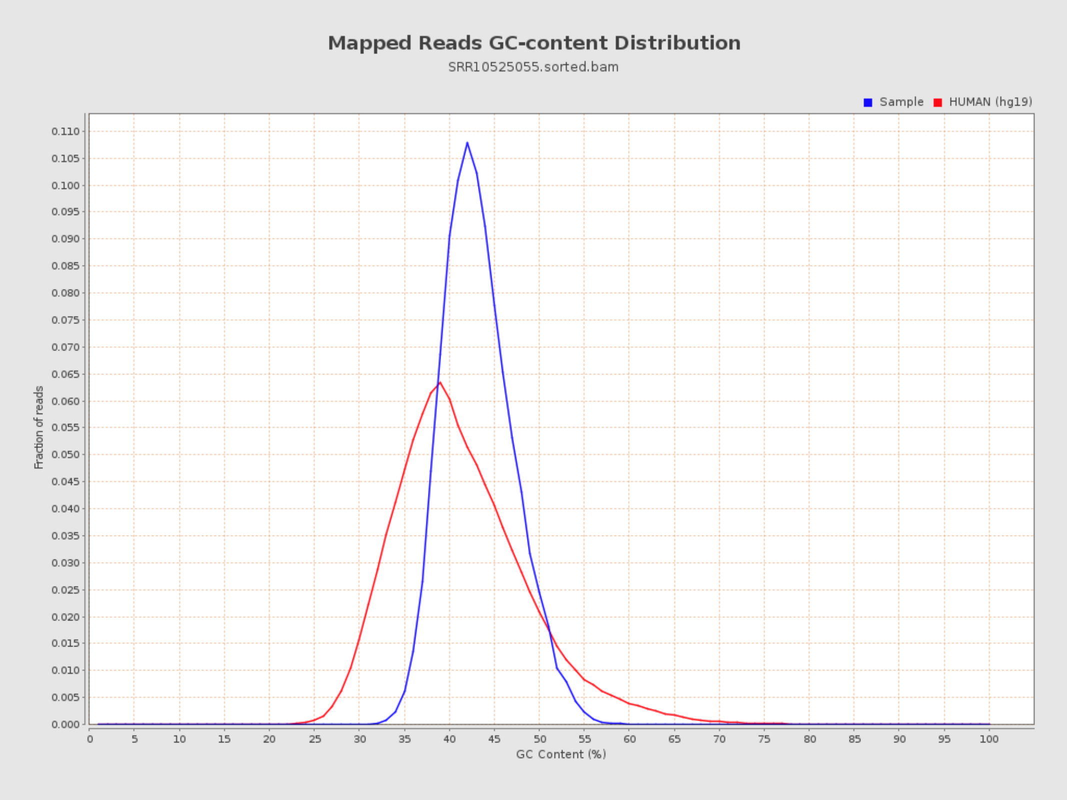
7. Results : Duplication Rate Histogram



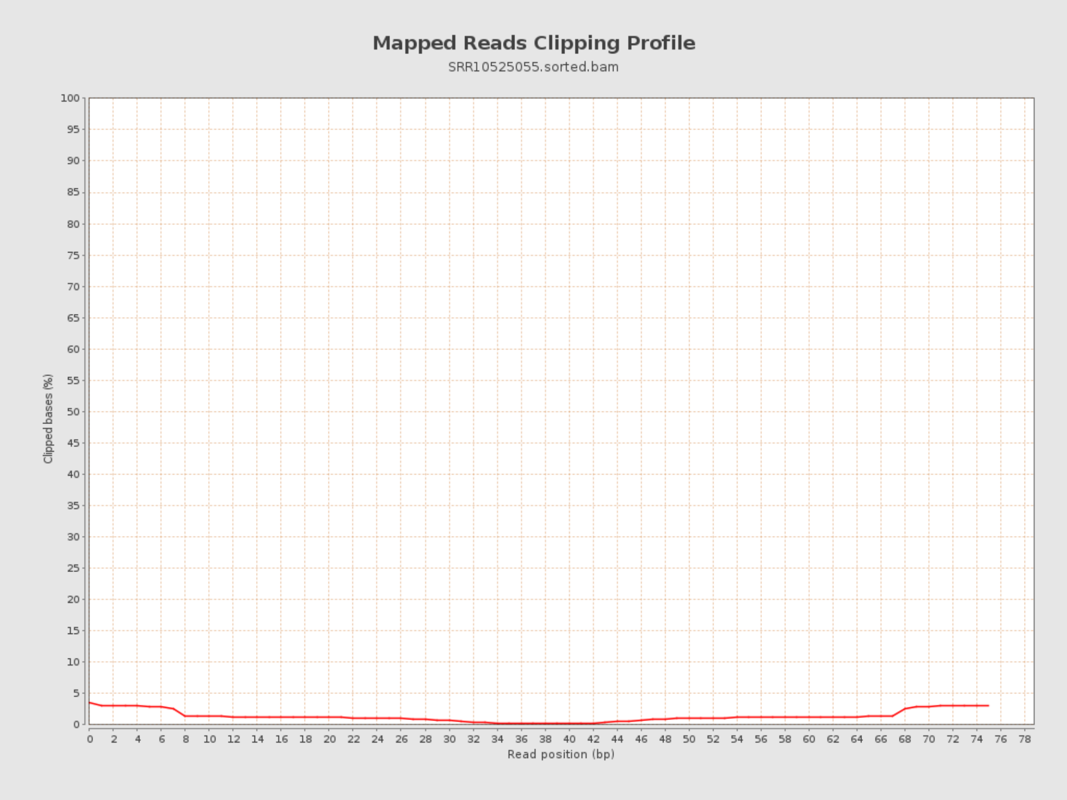
8. Results : Mapped Reads Nucleotide Content



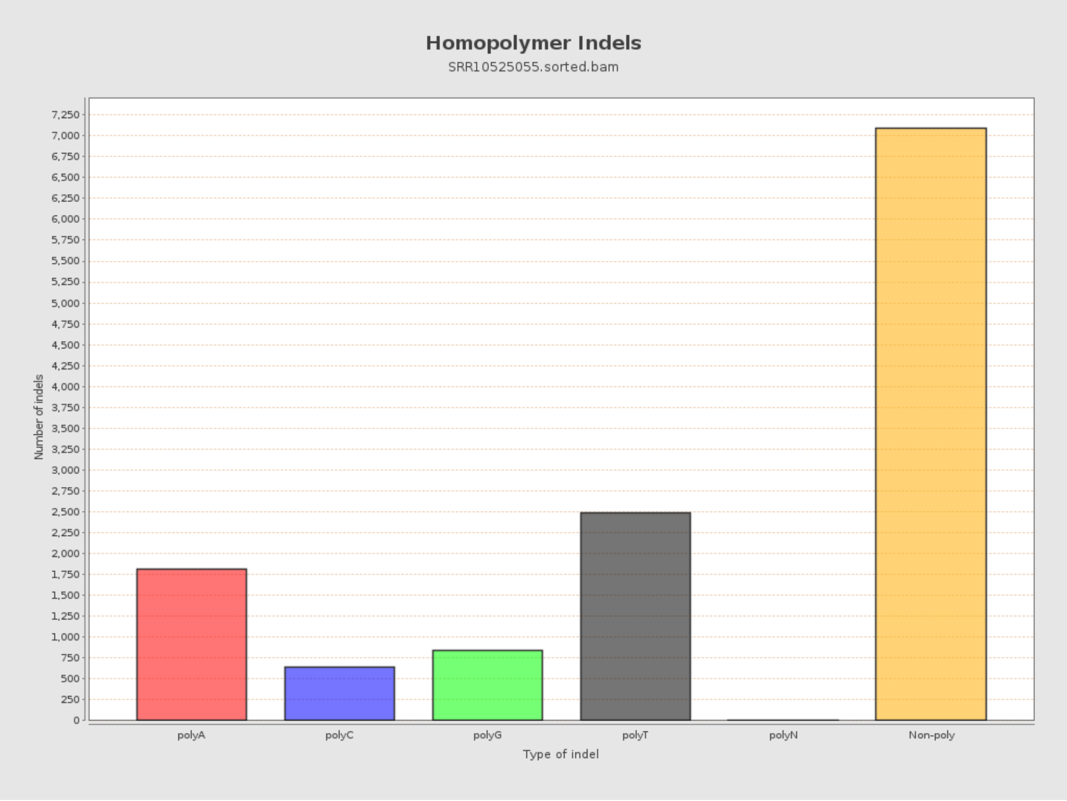
9. Results : Mapped Reads GC-content Distribution



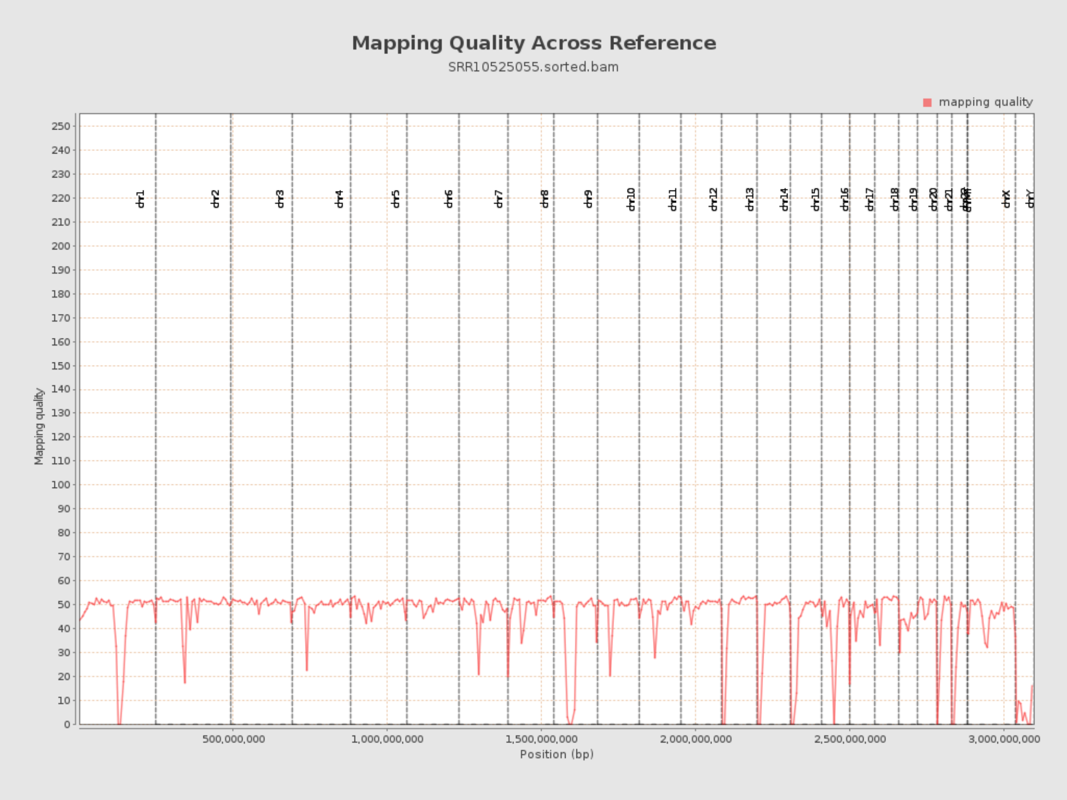
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram