Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524707.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_SRR10524707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,271,233
Mapped reads	1,163,815 / 91.55%
Unmapped reads	107,418 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,048 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	37,909 / 2.98%
Duplication rate	2.34%
Clipped reads	1,163,523 / 91.53%

2.2. ACGT Content

Number/percentage of A's	17,382,013 / 25.41%
Number/percentage of C's	13,202,986 / 19.3%
Number/percentage of T's	22,636,877 / 33.09%
Number/percentage of G's	15,176,773 / 22.19%
Number/percentage of N's	9,294 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2313

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

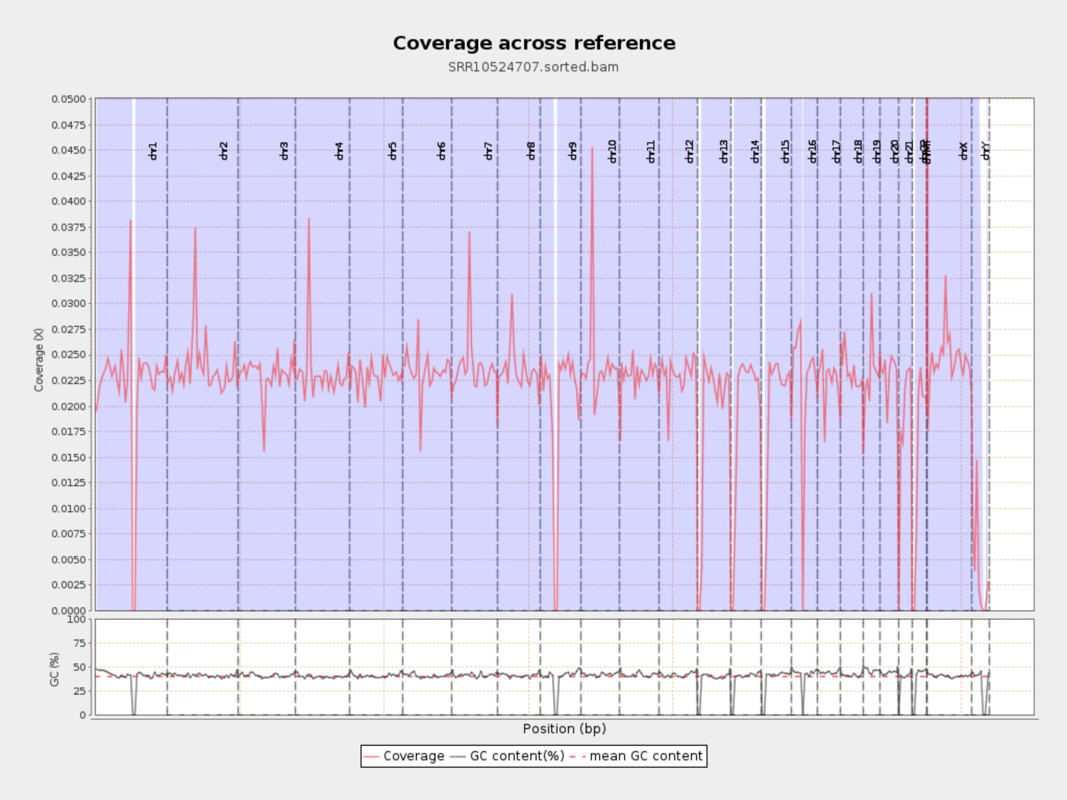
General error rate	0.53%
Mismatches	351,716
Insertions	4,975
Mapped reads with at least one insertion	0.42%
Deletions	13,410
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.21%

2.6. Chromosome stats

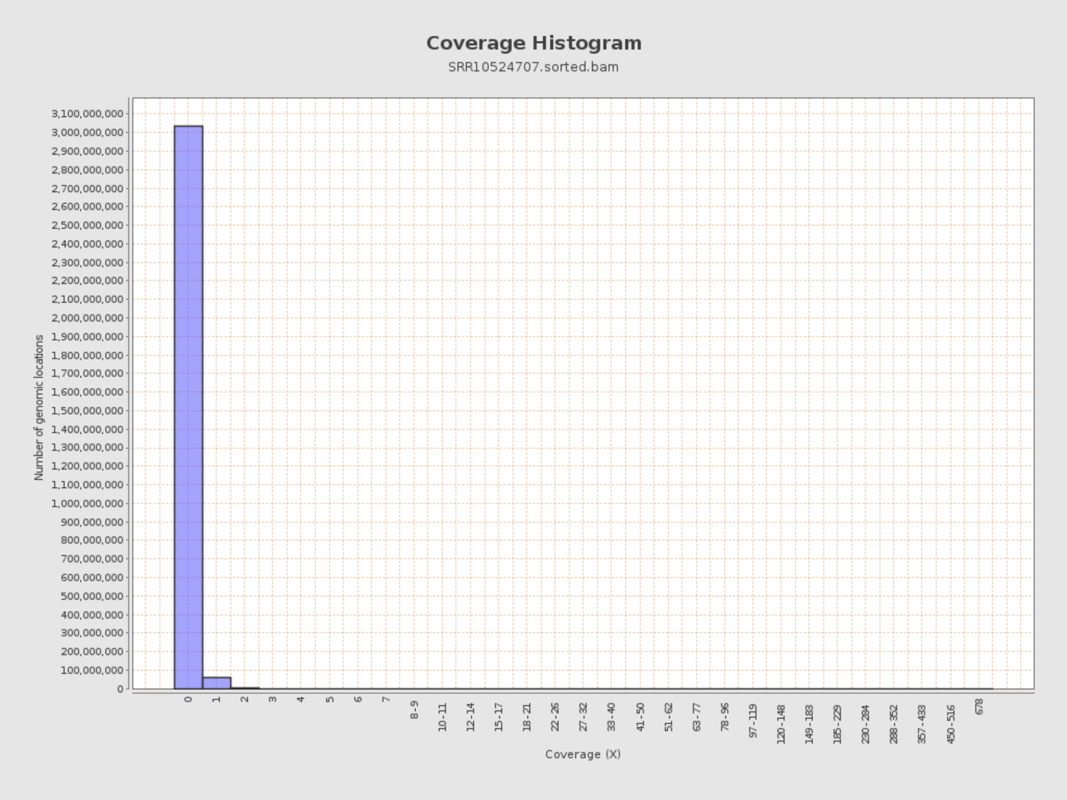
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5496649	0.0221	0.395
chr2	243199373	5801501	0.0239	0.3301
chr3	198022430	4562171	0.023	0.1629
chr4	191154276	4467495	0.0234	0.1803
chr5	180915260	4178647	0.0231	0.1624
chr6	171115067	3991980	0.0233	0.1821
chr7	159138663	3824682	0.024	0.2595

chr8	146364022	3457257	0.0236	0.2606
chr9	141213431	2861339	0.0203	0.1942
chr10	135534747	3290486	0.0243	0.2369
chr11	135006516	3127280	0.0232	0.1971
chr12	133851895	3086249	0.0231	0.1636
chr13	115169878	2156602	0.0187	0.1476
chr14	107349540	2036617	0.019	0.1497
chr15	102531392	1912548	0.0187	0.146
chr16	90354753	1979368	0.0219	0.1691
chr17	81195210	1825954	0.0225	0.167
chr18	78077248	1824663	0.0234	0.3269
chr19	59128983	1380727	0.0234	0.3012
chr20	63025520	1441905	0.0229	0.1641
chr21	48129895	895020	0.0186	0.1561
chr22	51304566	770238	0.015	0.1305
chrMT	16571	3984	0.2404	0.572
chrX	155270560	3824221	0.0246	0.1822
chrY	59373566	232007	0.0039	0.1479

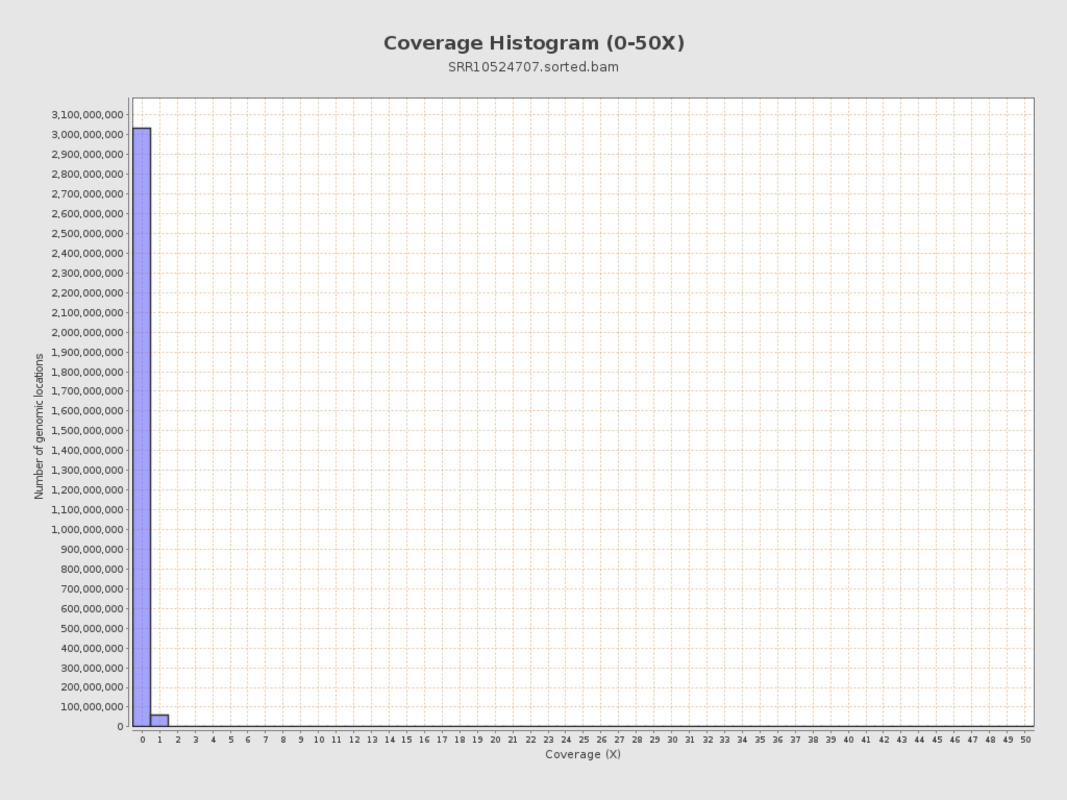
3. Results : Coverage across reference



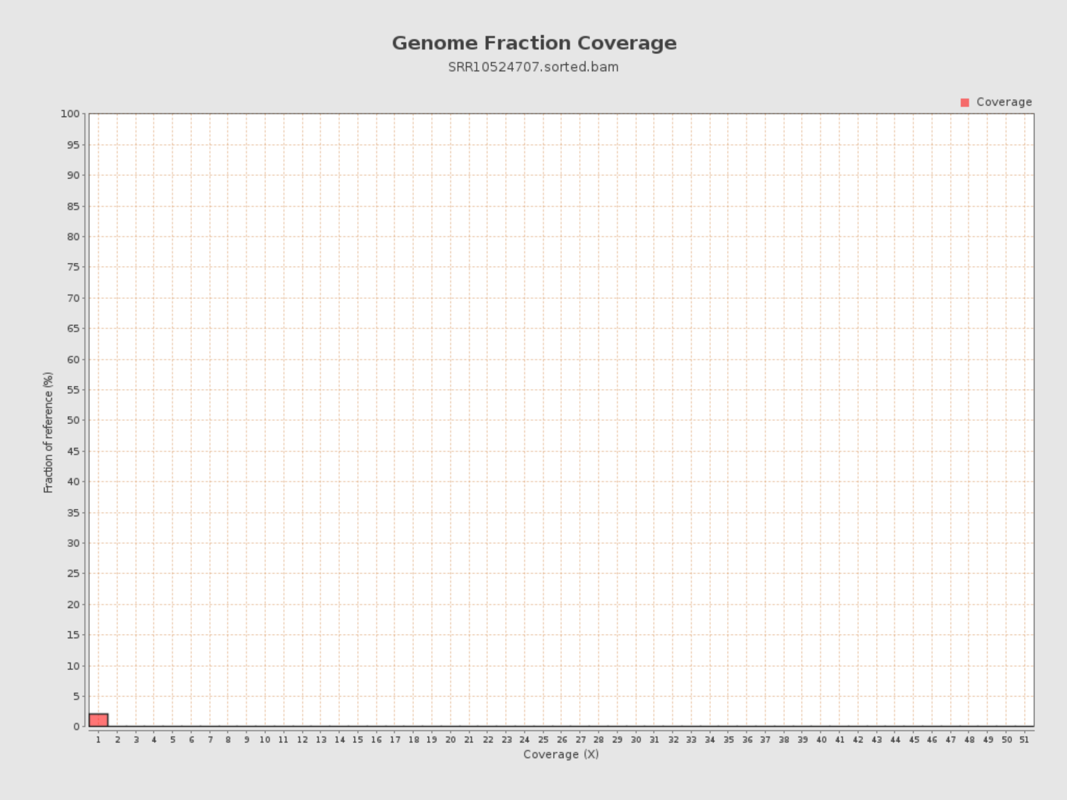
4. Results : Coverage Histogram



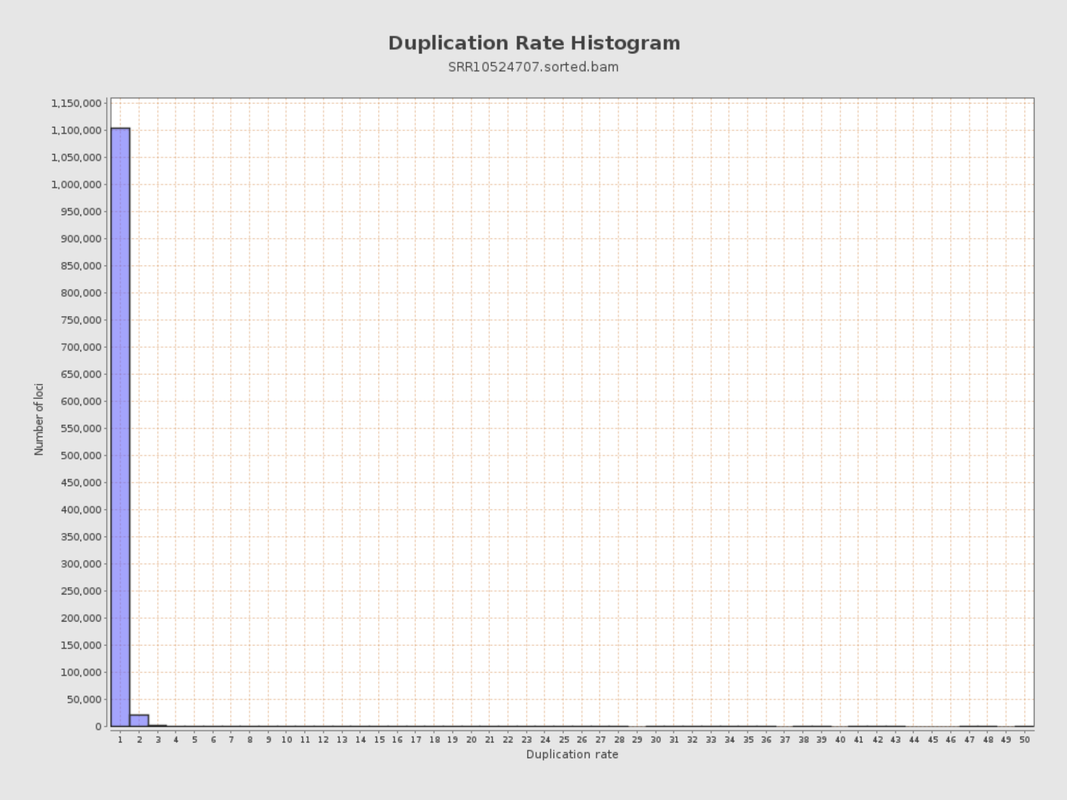
5. Results : Coverage Histogram (0-50X)



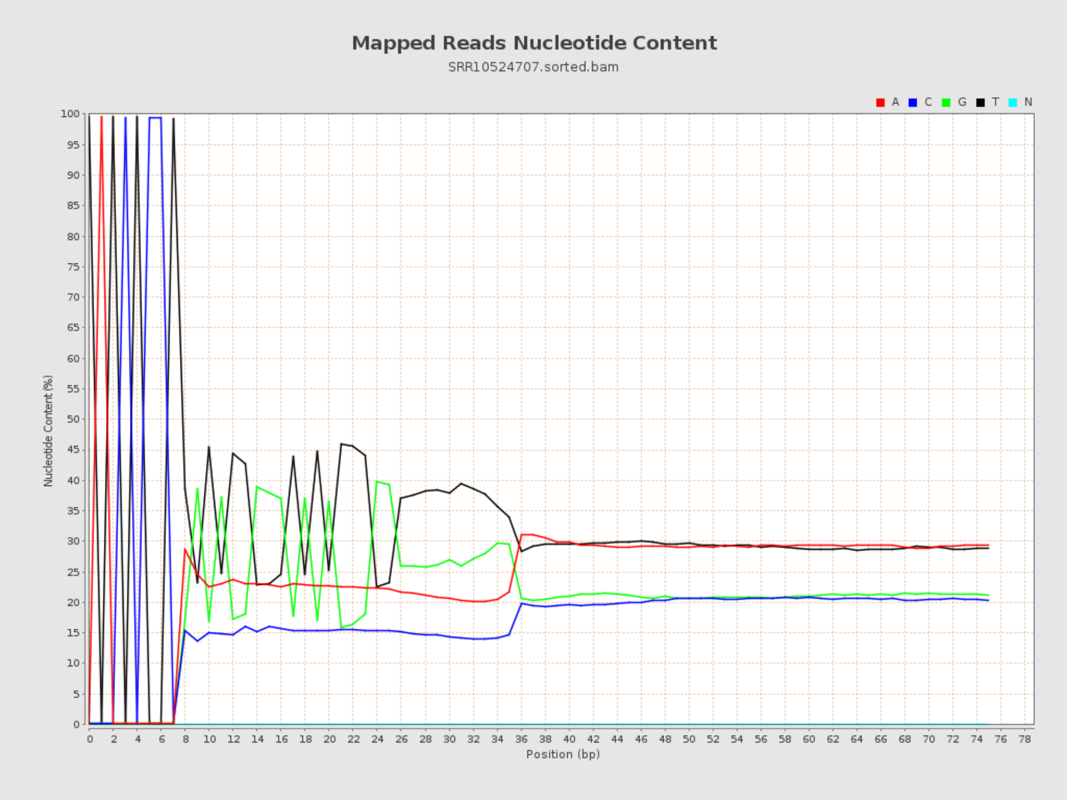
6. Results : Genome Fraction Coverage



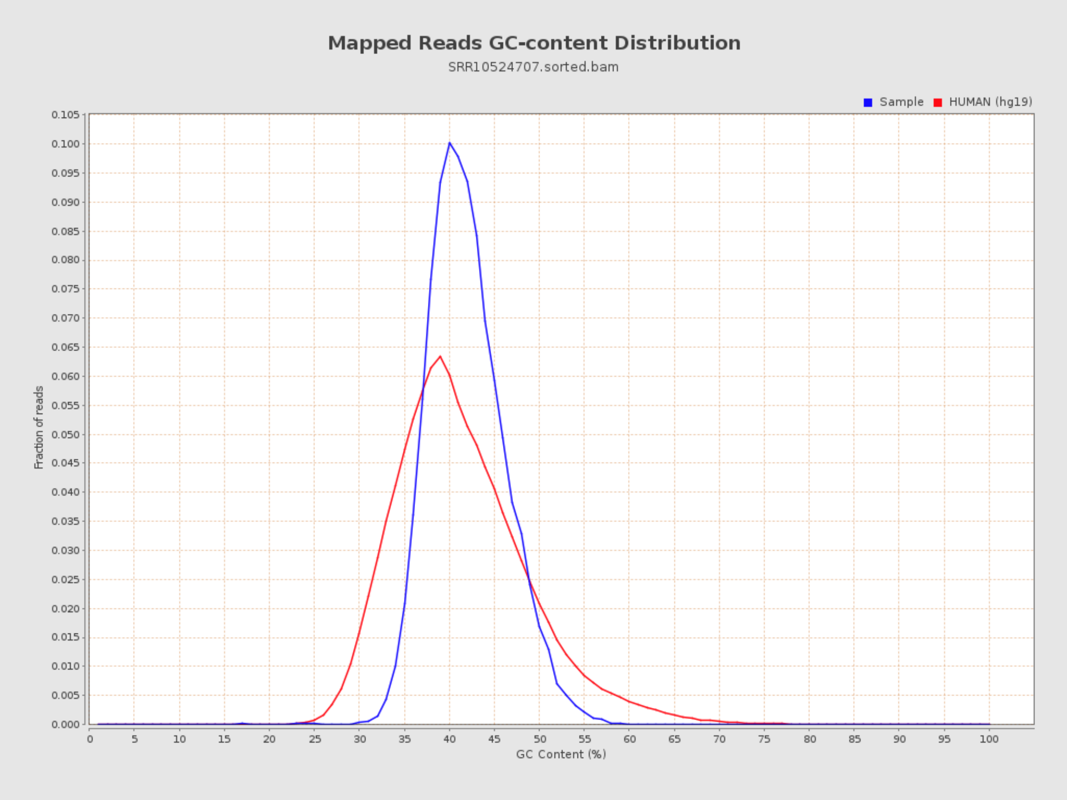
7. Results : Duplication Rate Histogram



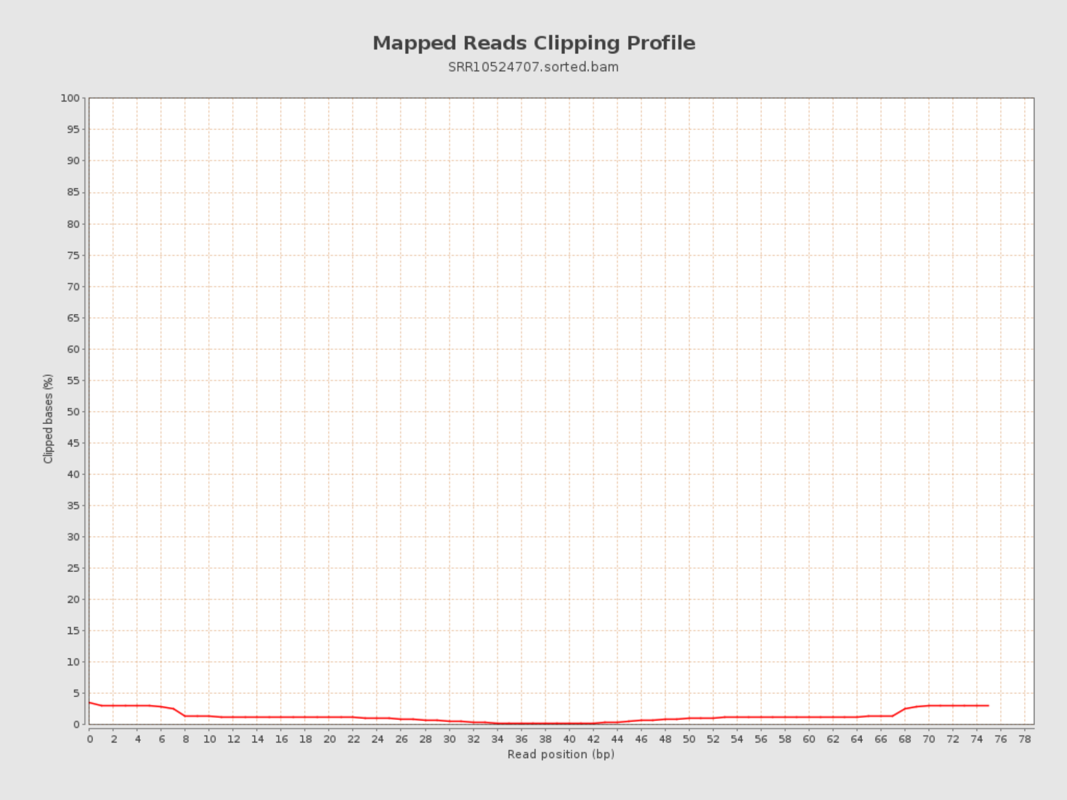
8. Results : Mapped Reads Nucleotide Content



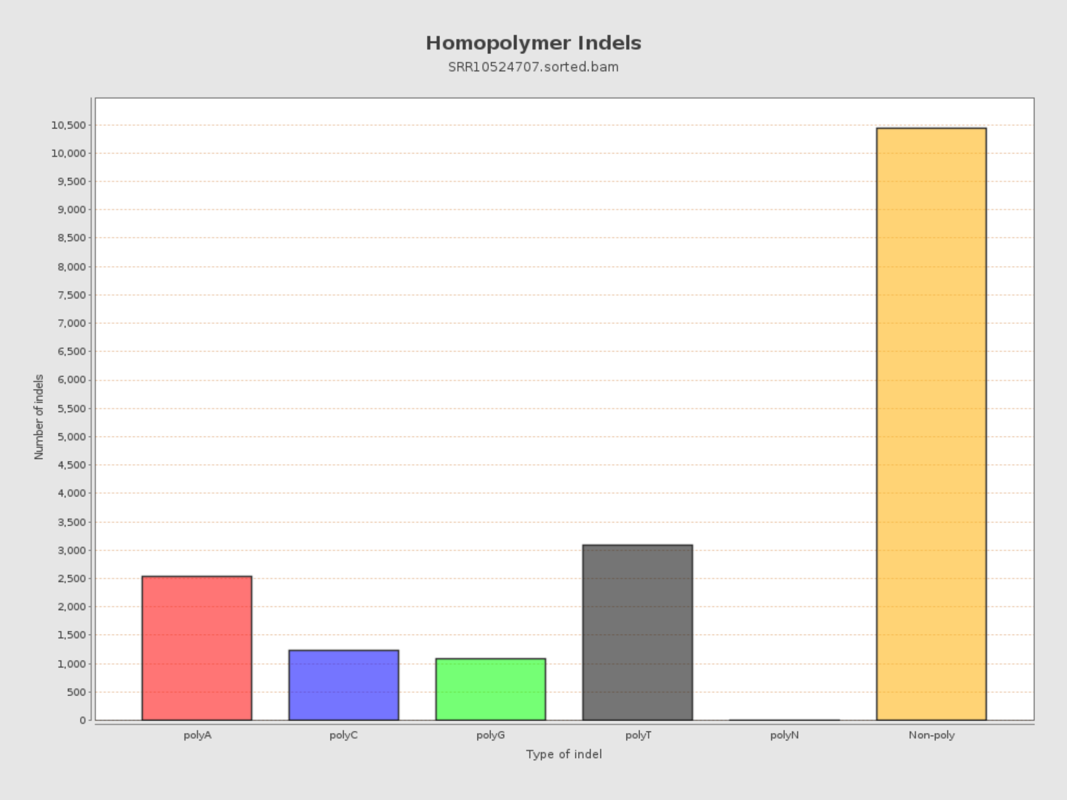
9. Results : Mapped Reads GC-content Distribution



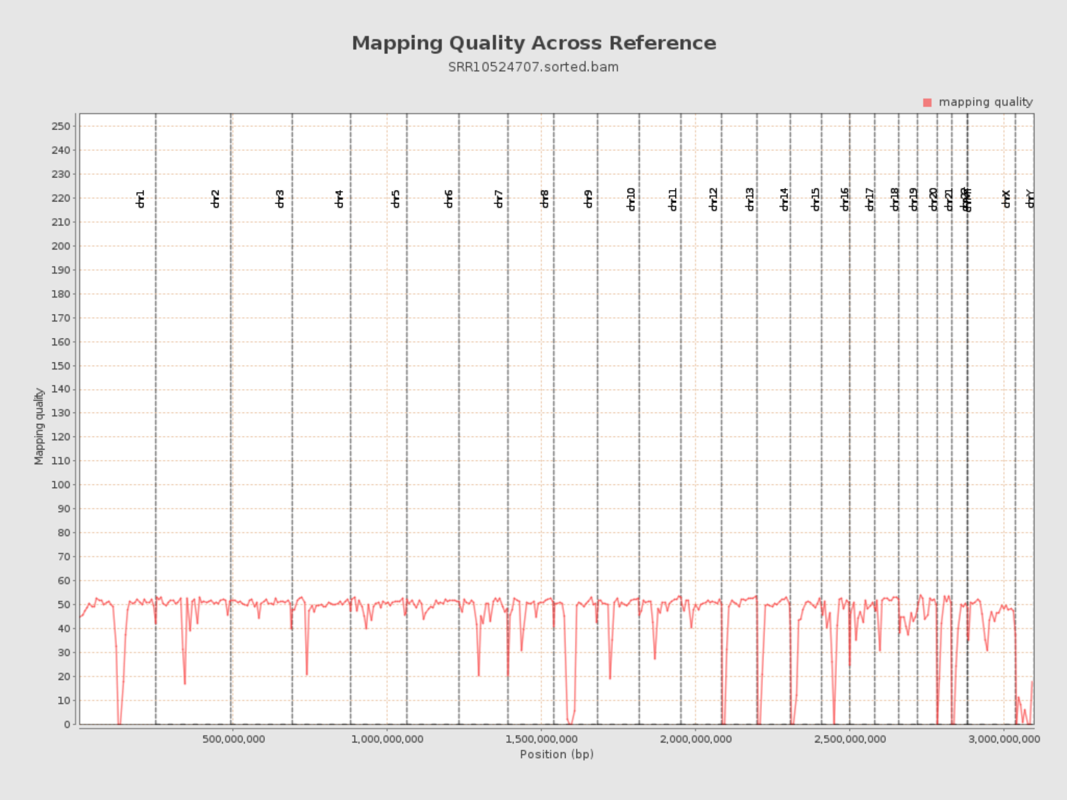
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram