Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:11:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524750.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_SRR10524750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:11:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,239,432
Mapped reads	1,131,513 / 91.29%
Unmapped reads	107,919 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,839 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	32,080 / 2.59%
Duplication rate	2.13%
Clipped reads	1,134,664 / 91.55%

2.2. ACGT Content

Number/percentage of A's	16,104,013 / 24.51%
Number/percentage of C's	12,932,401 / 19.68%
Number/percentage of T's	20,350,299 / 30.97%
Number/percentage of G's	16,318,565 / 24.83%
Number/percentage of N's	7,782 / 0.01%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.1962

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

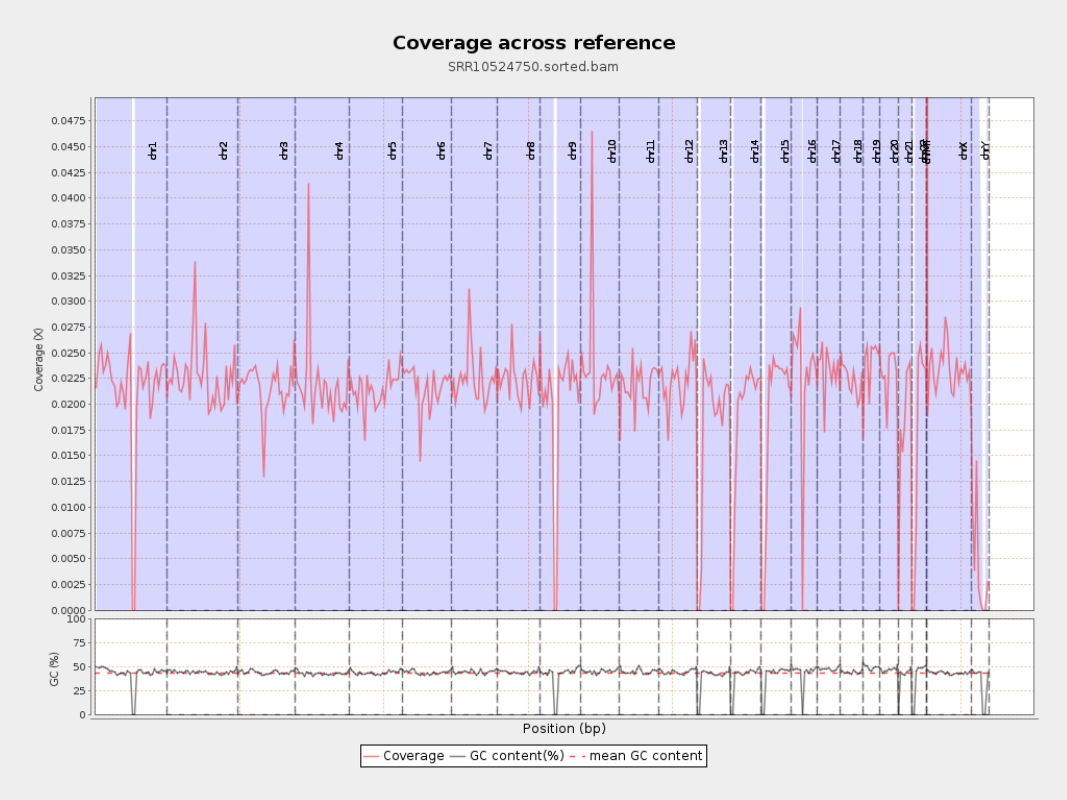
General error rate	0.51%
Mismatches	325,858
Insertions	3,907
Mapped reads with at least one insertion	0.34%
Deletions	12,376
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.64%

2.6. Chromosome stats

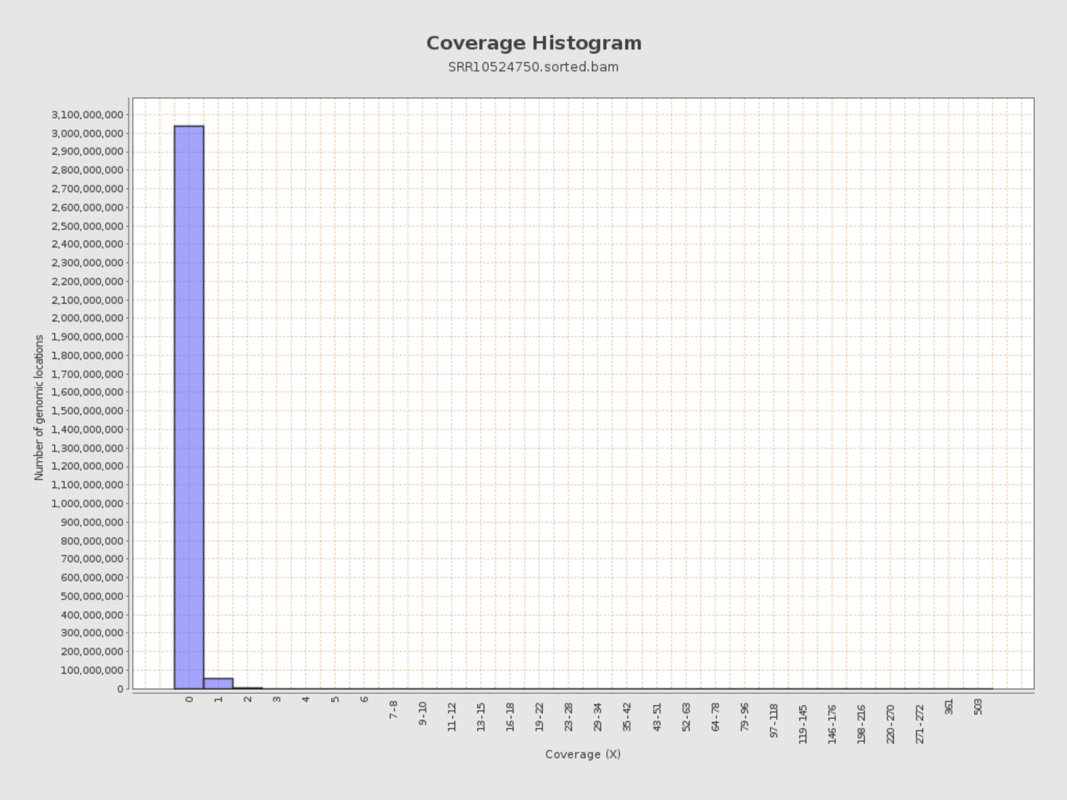
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5279551	0.0212	0.2406
chr2	243199373	5517381	0.0227	0.2872
chr3	198022430	4267354	0.0215	0.1598
chr4	191154276	4202443	0.022	0.1808
chr5	180915260	3891697	0.0215	0.1575
chr6	171115067	3702071	0.0216	0.1674
chr7	159138663	3595792	0.0226	0.2327

chr8	146364022	3282775	0.0224	0.1855
chr9	141213431	2798693	0.0198	0.1771
chr10	135534747	3211966	0.0237	0.2493
chr11	135006516	2957591	0.0219	0.1813
chr12	133851895	2982198	0.0223	0.1618
chr13	115169878	2030533	0.0176	0.1432
chr14	107349540	1962398	0.0183	0.1485
chr15	102531392	1922510	0.0188	0.1484
chr16	90354753	2018507	0.0223	0.1776
chr17	81195210	1896255	0.0234	0.1746
chr18	78077248	1741056	0.0223	0.2554
chr19	59128983	1431533	0.0242	0.2126
chr20	63025520	1435856	0.0228	0.169
chr21	48129895	867818	0.018	0.1604
chr22	51304566	858221	0.0167	0.1409
chrMT	16571	14127	0.8525	1.0017
chrX	155270560	3625554	0.0233	0.1736
chrY	59373566	239308	0.004	0.1185

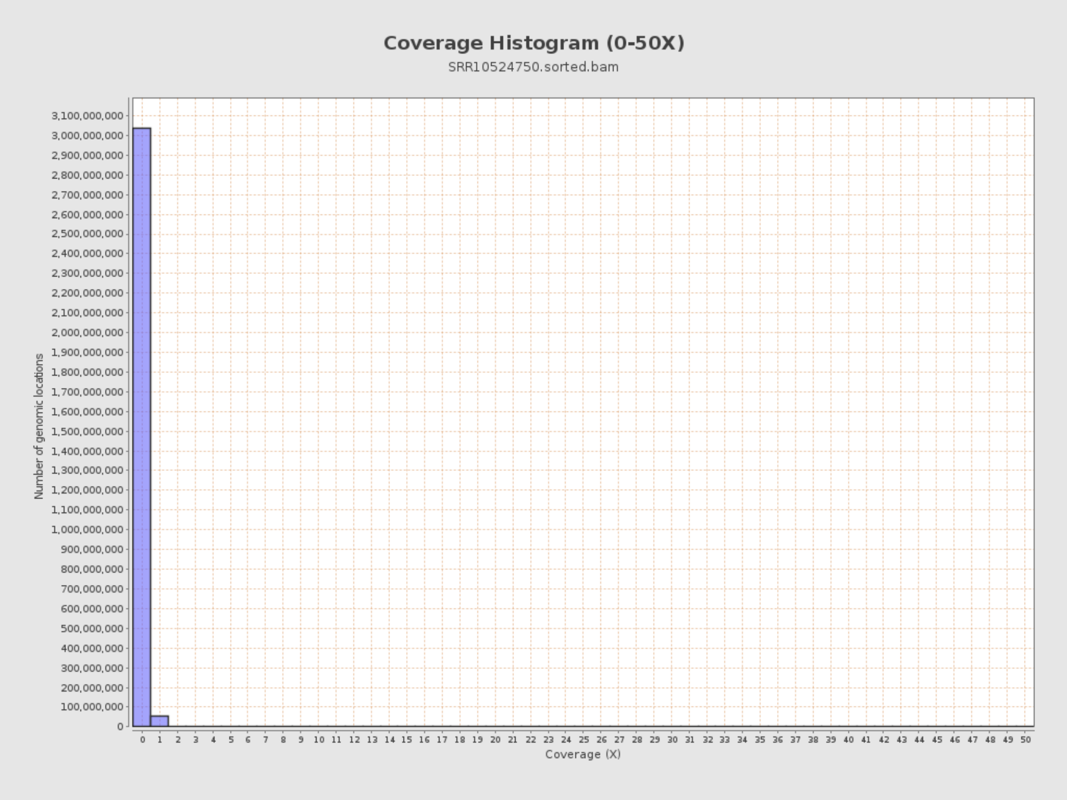
3. Results : Coverage across reference



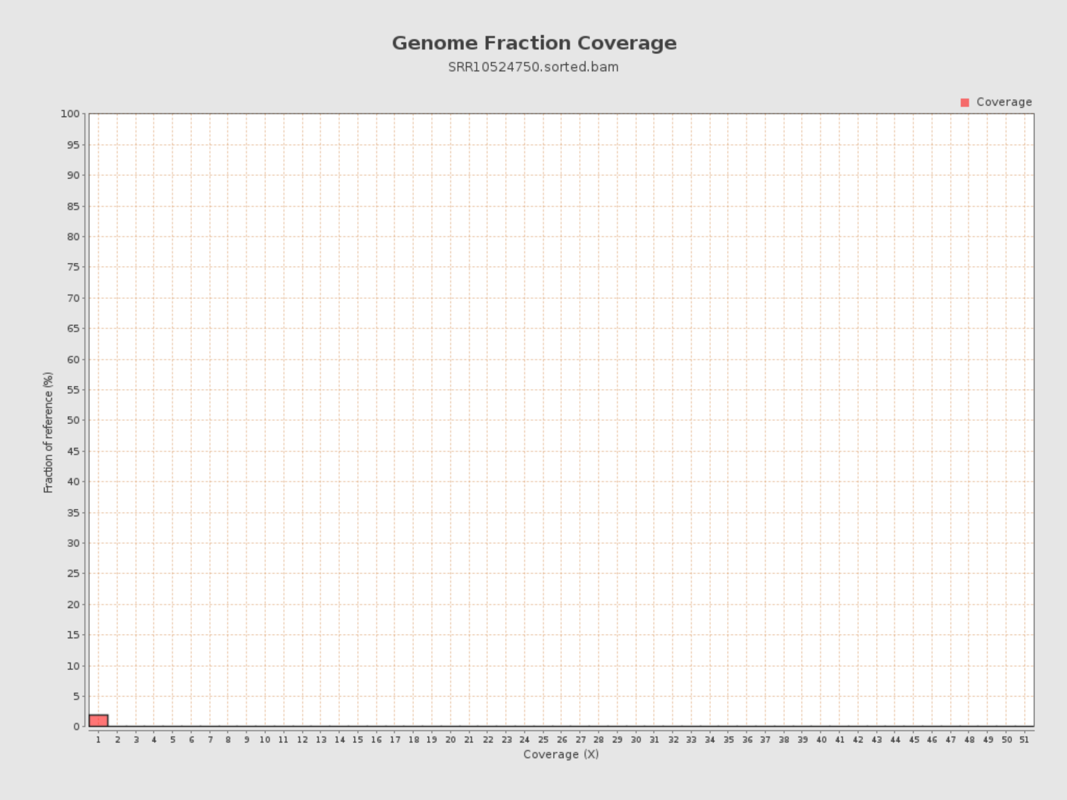
4. Results : Coverage Histogram



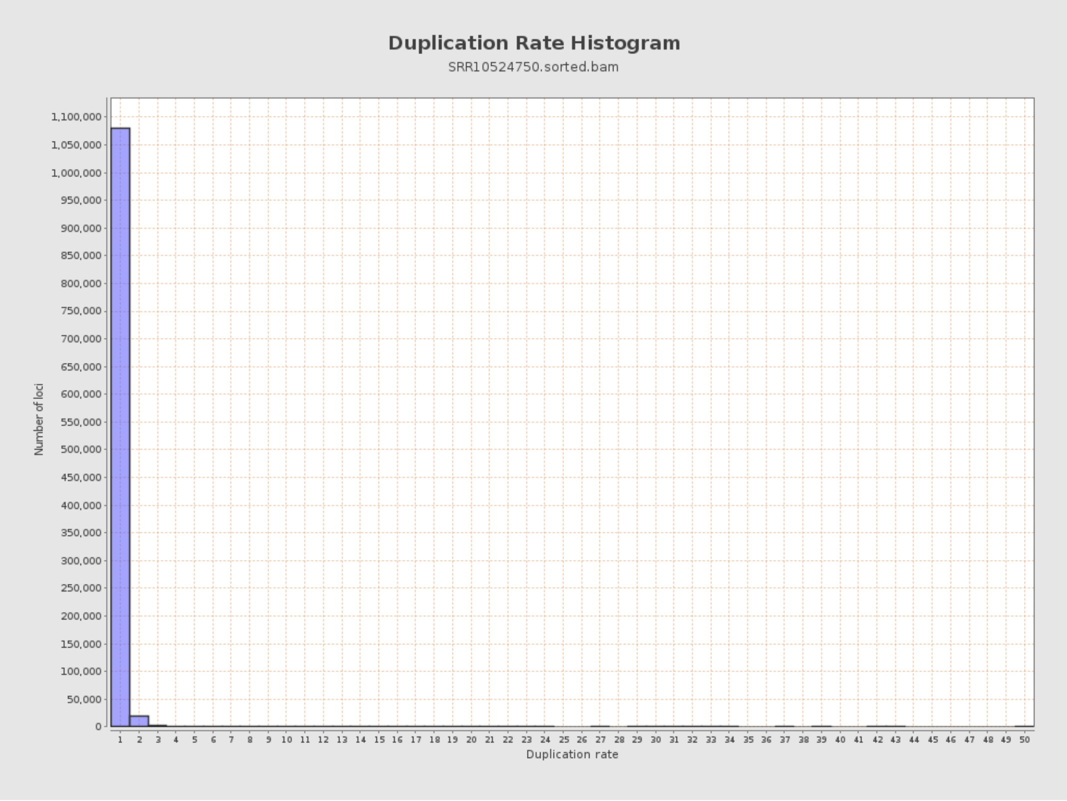
5. Results : Coverage Histogram (0-50X)



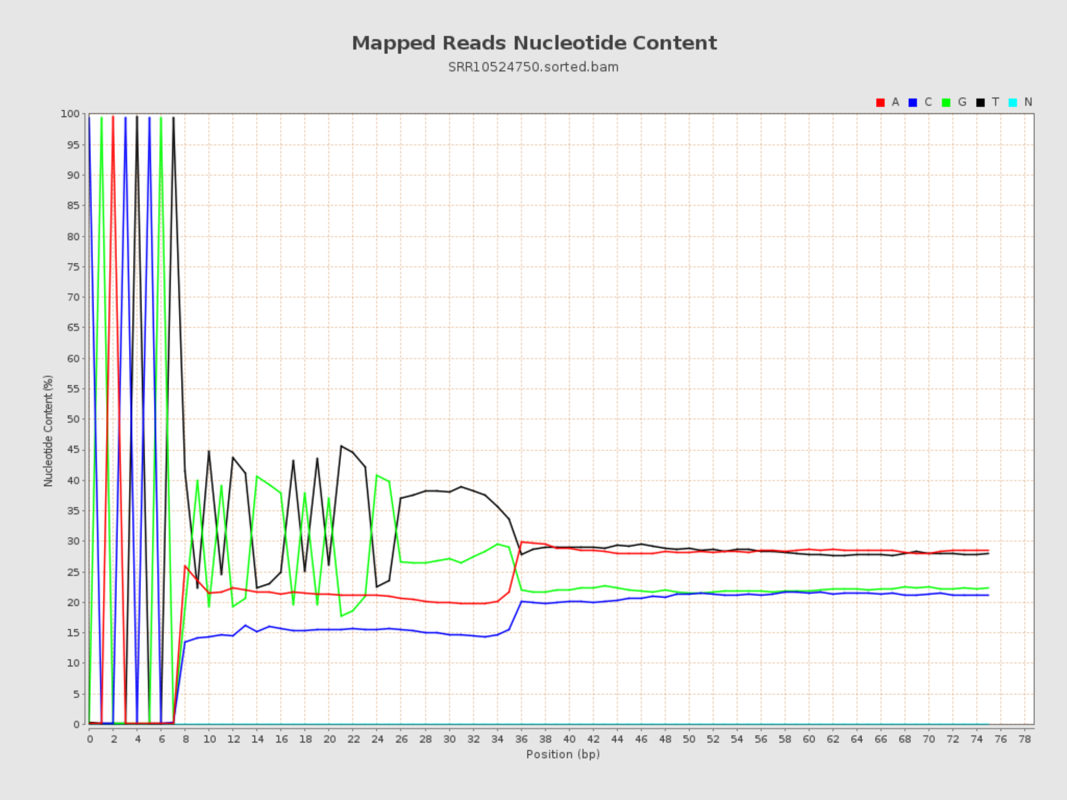
6. Results : Genome Fraction Coverage



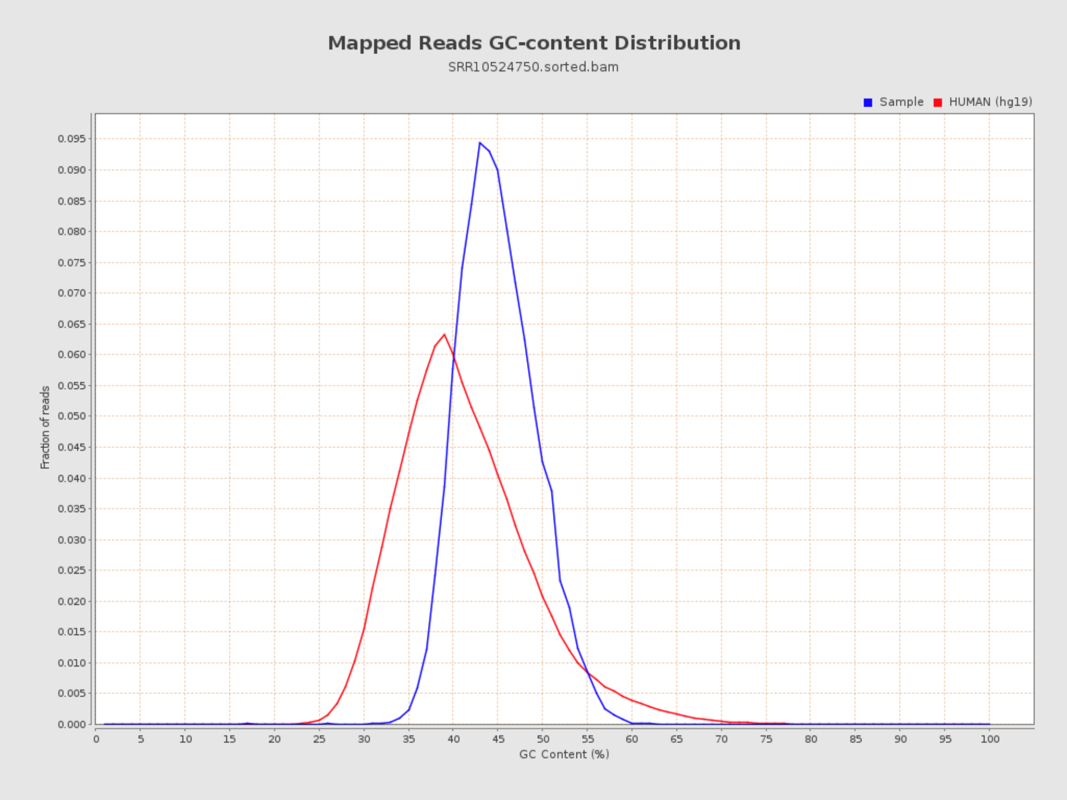
7. Results : Duplication Rate Histogram



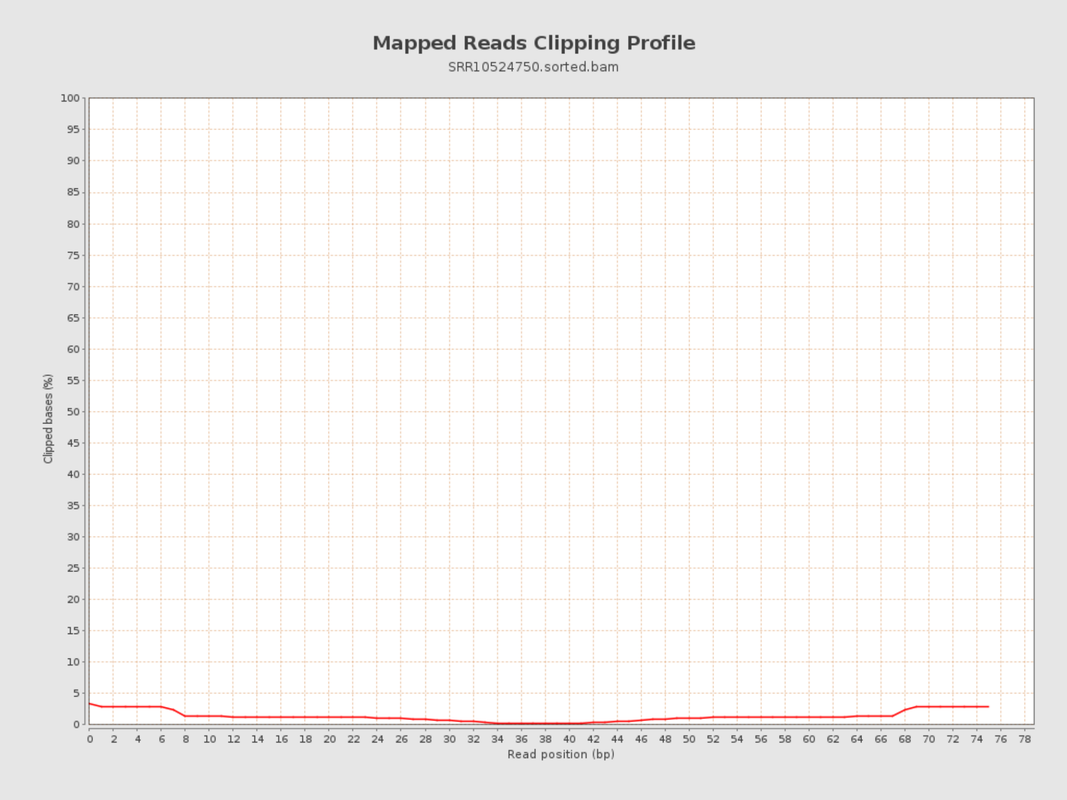
8. Results : Mapped Reads Nucleotide Content



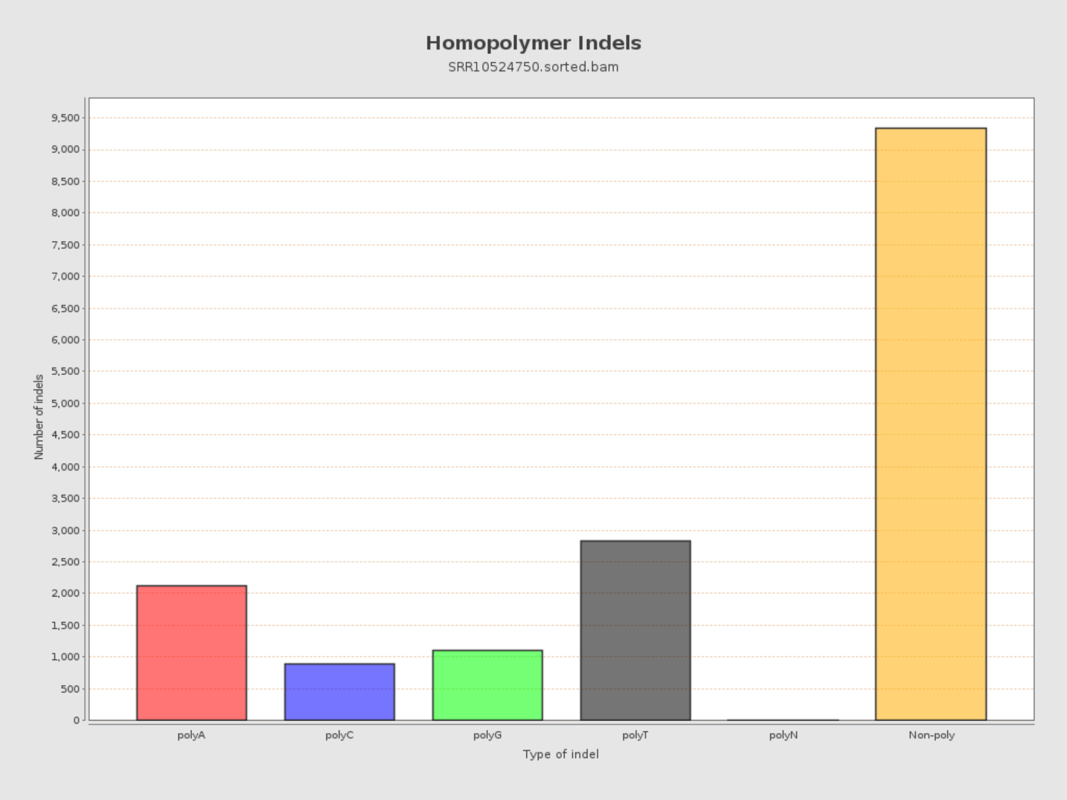
9. Results : Mapped Reads GC-content Distribution



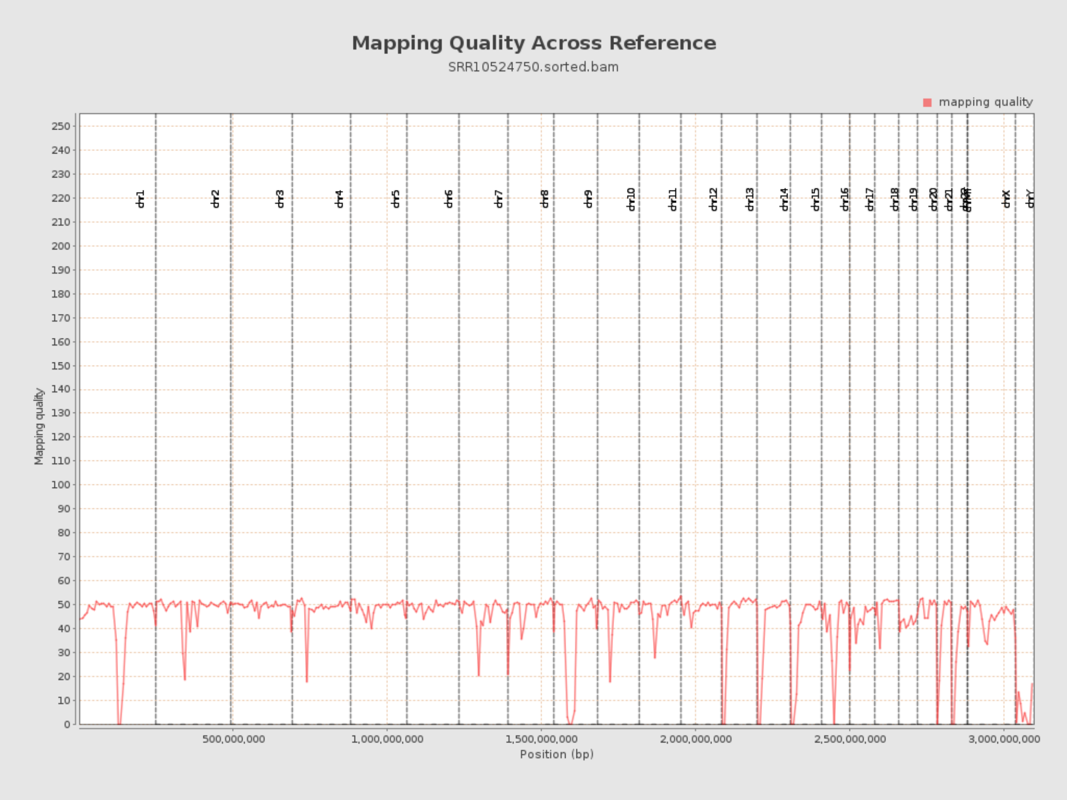
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram