Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524809.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_SRR10524809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:26:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,352,708
Mapped reads	1,240,375 / 91.7%
Unmapped reads	112,333 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,827 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	40,470 / 2.99%
Duplication rate	2.48%
Clipped reads	1,241,695 / 91.79%

2.2. ACGT Content

Number/percentage of A's	18,100,491 / 25.26%
Number/percentage of C's	13,415,262 / 18.72%
Number/percentage of T's	21,849,519 / 30.49%
Number/percentage of G's	18,296,311 / 25.53%
Number/percentage of N's	9,228 / 0.01%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2112

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

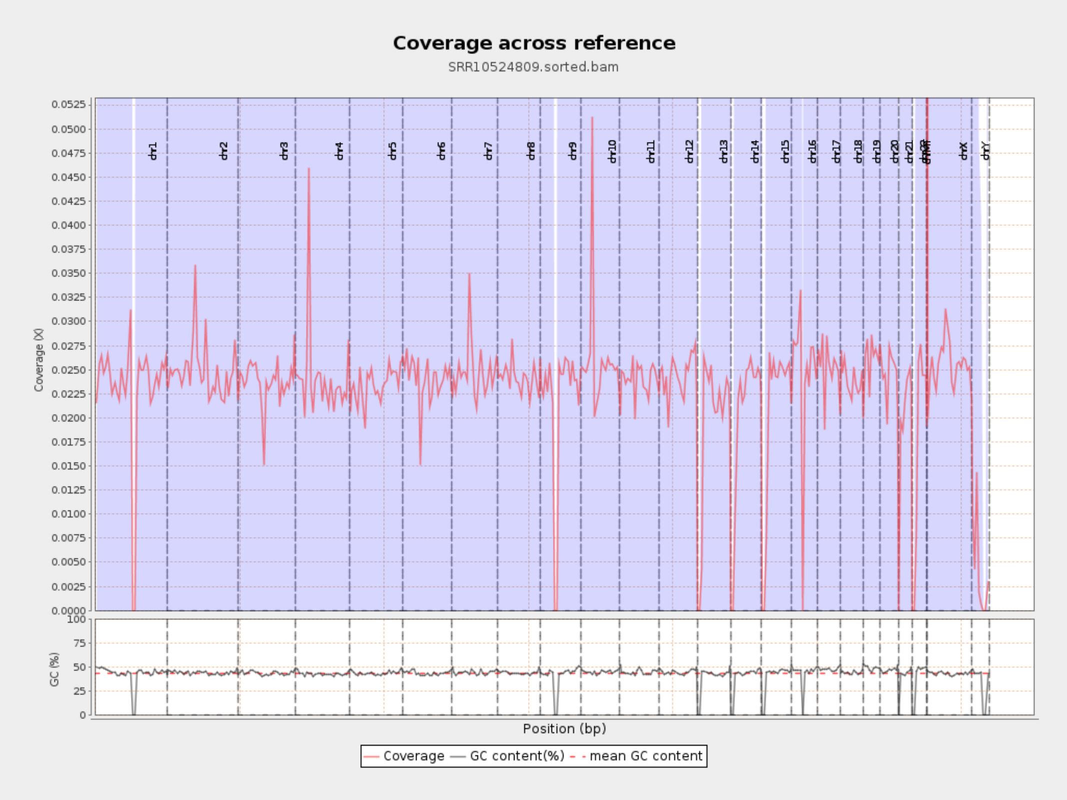
General error rate	0.52%
Mismatches	360,053
Insertions	5,442
Mapped reads with at least one insertion	0.44%
Deletions	14,662
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.84%

2.6. Chromosome stats

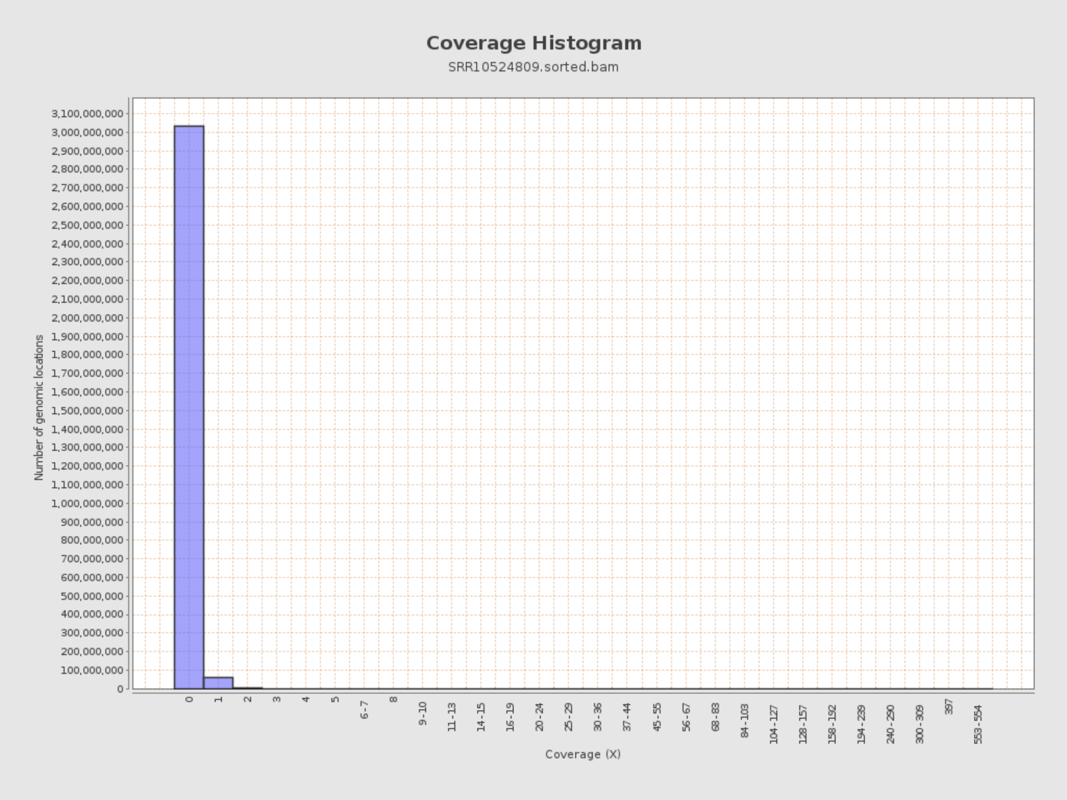
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5720345	0.023	0.281
chr2	243199373	6045991	0.0249	0.3046
chr3	198022430	4678526	0.0236	0.1673
chr4	191154276	4611963	0.0241	0.1938
chr5	180915260	4250873	0.0235	0.1652
chr6	171115067	4107993	0.024	0.1793
chr7	159138663	3950124	0.0248	0.2525

chr8	146364022	3528605	0.0241	0.1971
chr9	141213431	3030912	0.0215	0.1858
chr10	135534747	3544489	0.0262	0.2659
chr11	135006516	3252233	0.0241	0.1951
chr12	133851895	3269730	0.0244	0.1712
chr13	115169878	2206978	0.0192	0.1497
chr14	107349540	2142074	0.02	0.1557
chr15	102531392	2075286	0.0202	0.1549
chr16	90354753	2185817	0.0242	0.1844
chr17	81195210	2048689	0.0252	0.1811
chr18	78077248	1863661	0.0239	0.2824
chr19	59128983	1546854	0.0262	0.2308
chr20	63025520	1549323	0.0246	0.1754
chr21	48129895	958561	0.0199	0.1688
chr22	51304566	896001	0.0175	0.144
chrMT	16571	12650	0.7634	0.9915
chrX	155270560	3976092	0.0256	0.1825
chrY	59373566	240848	0.0041	0.124

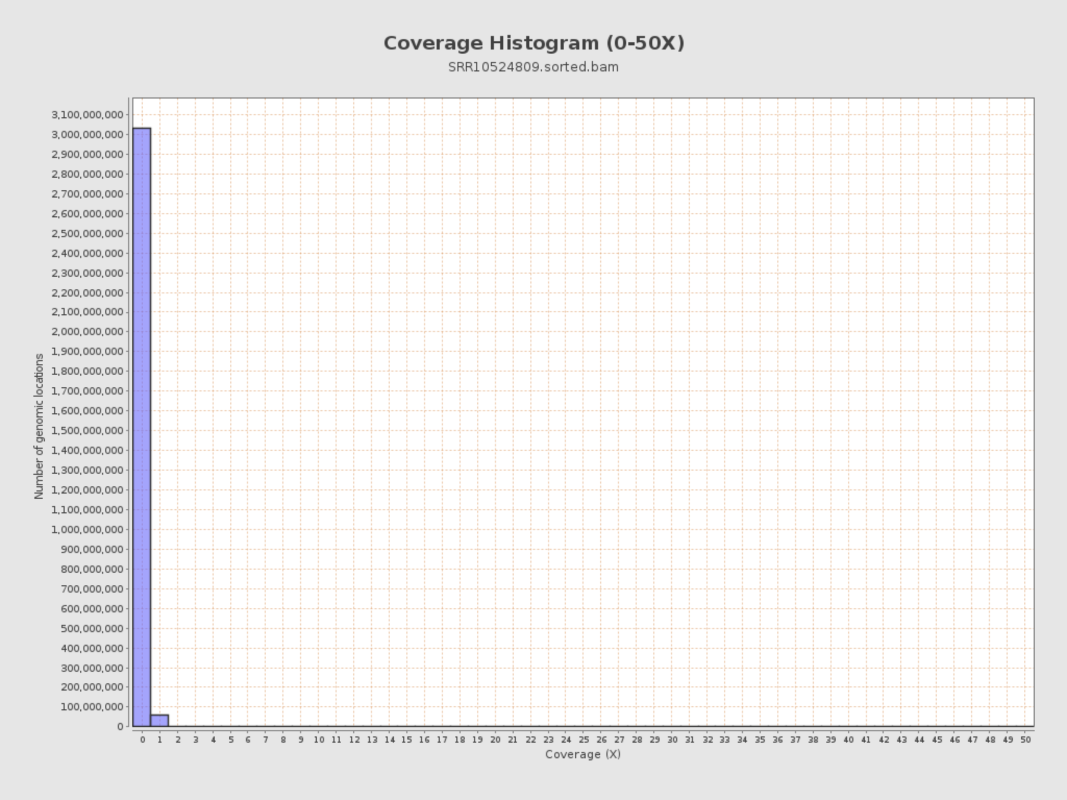
3. Results : Coverage across reference



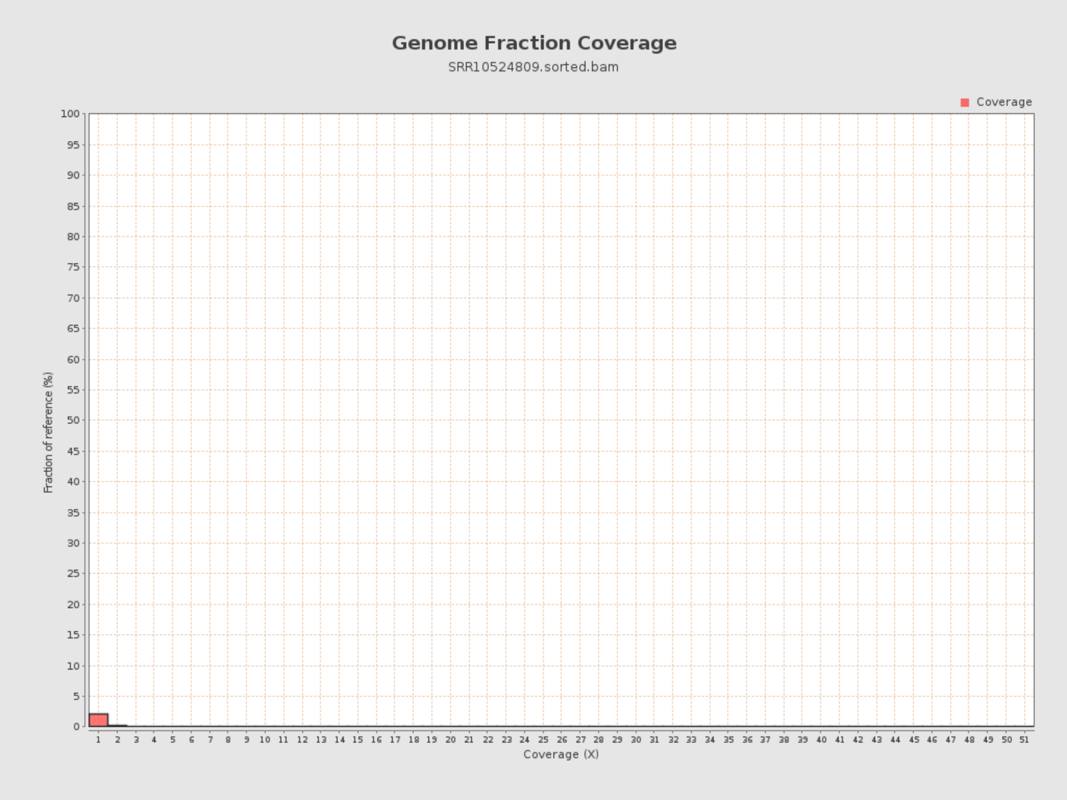
4. Results : Coverage Histogram



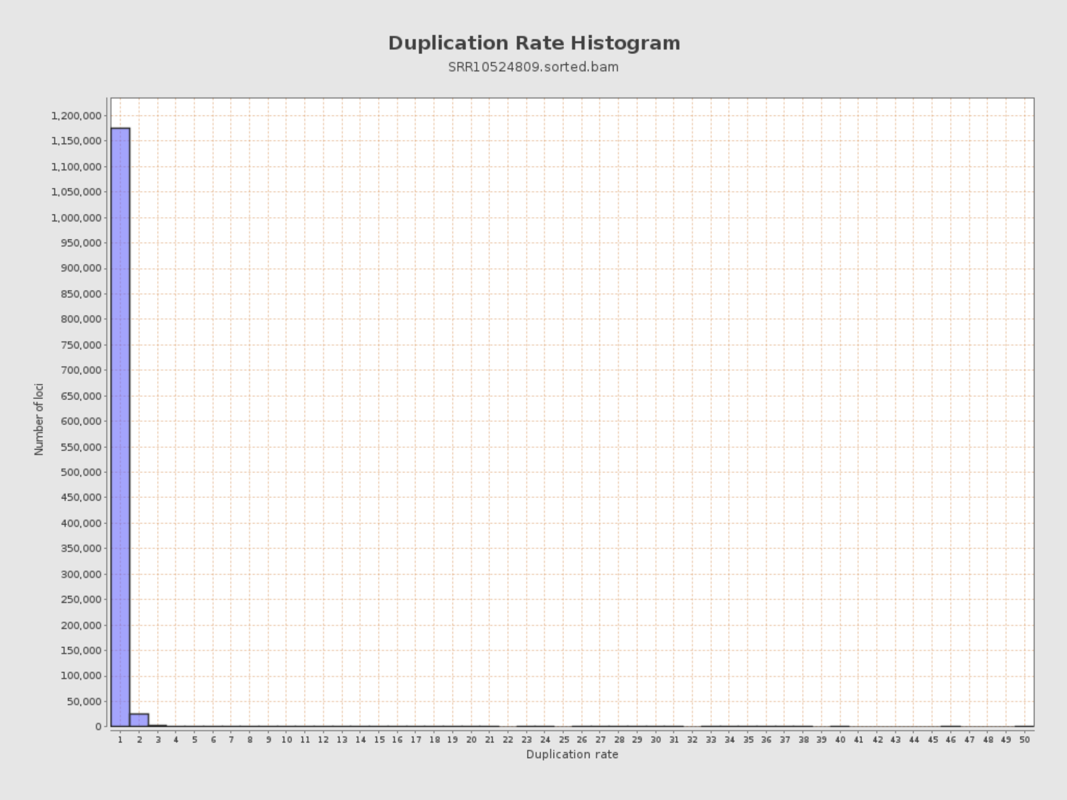
5. Results : Coverage Histogram (0-50X)



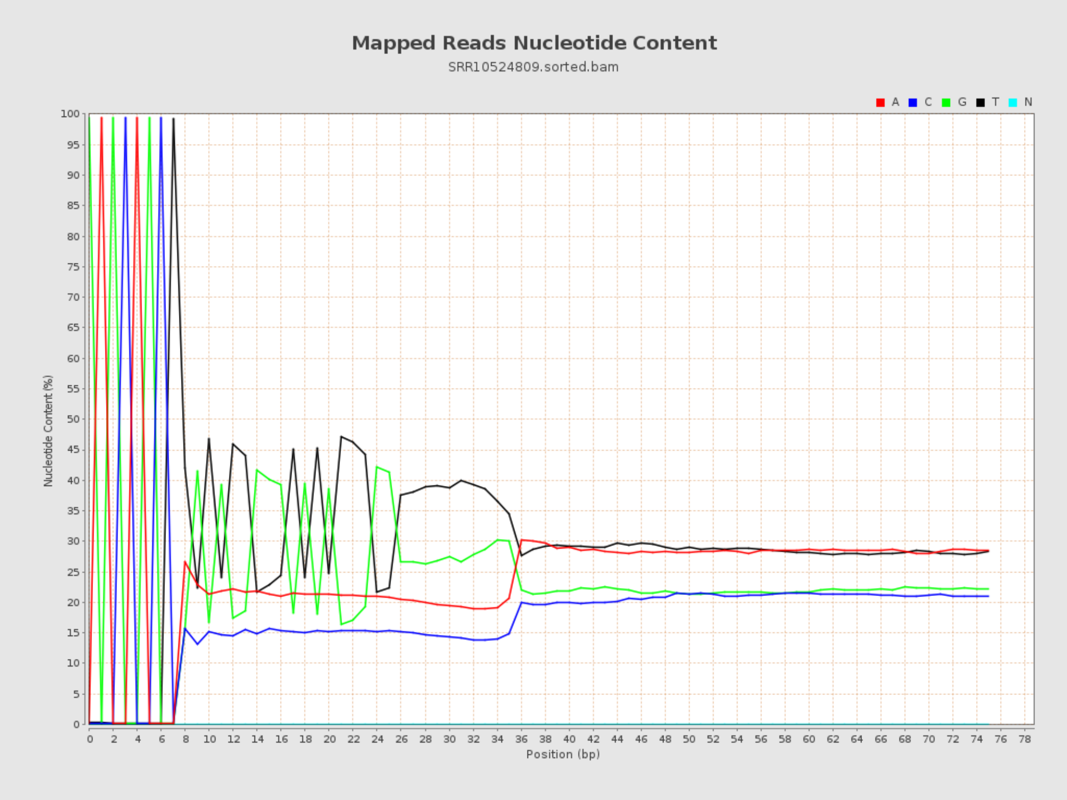
6. Results : Genome Fraction Coverage



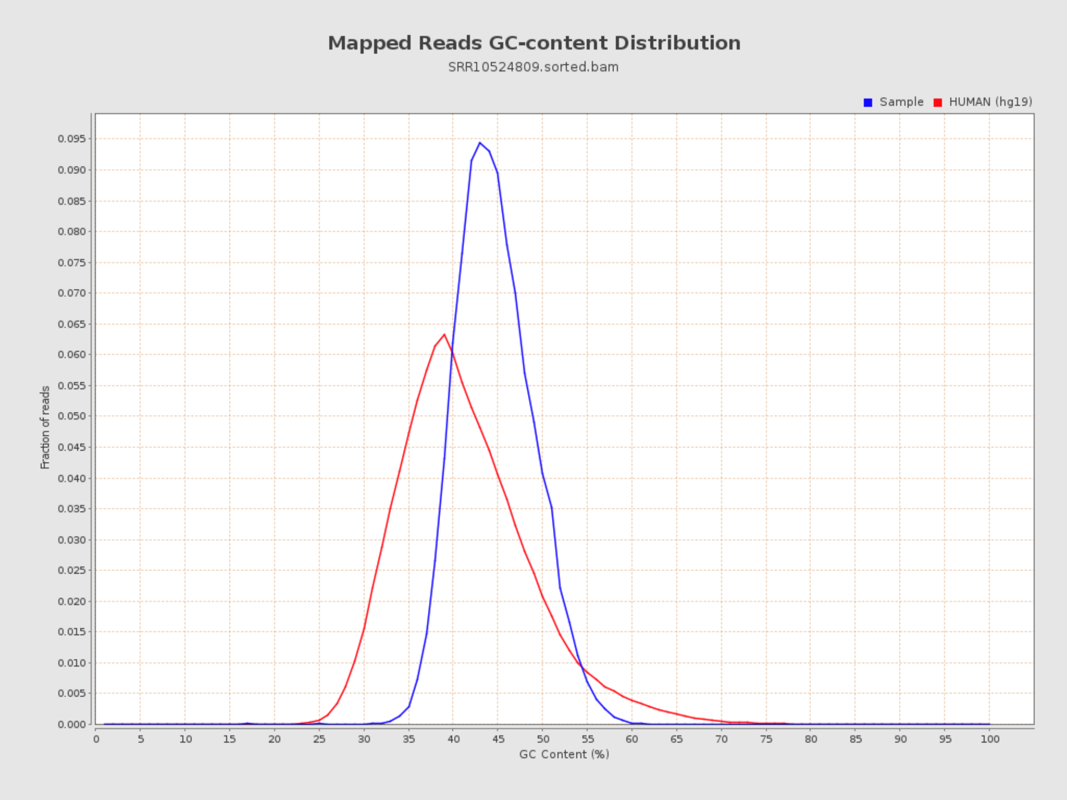
7. Results : Duplication Rate Histogram



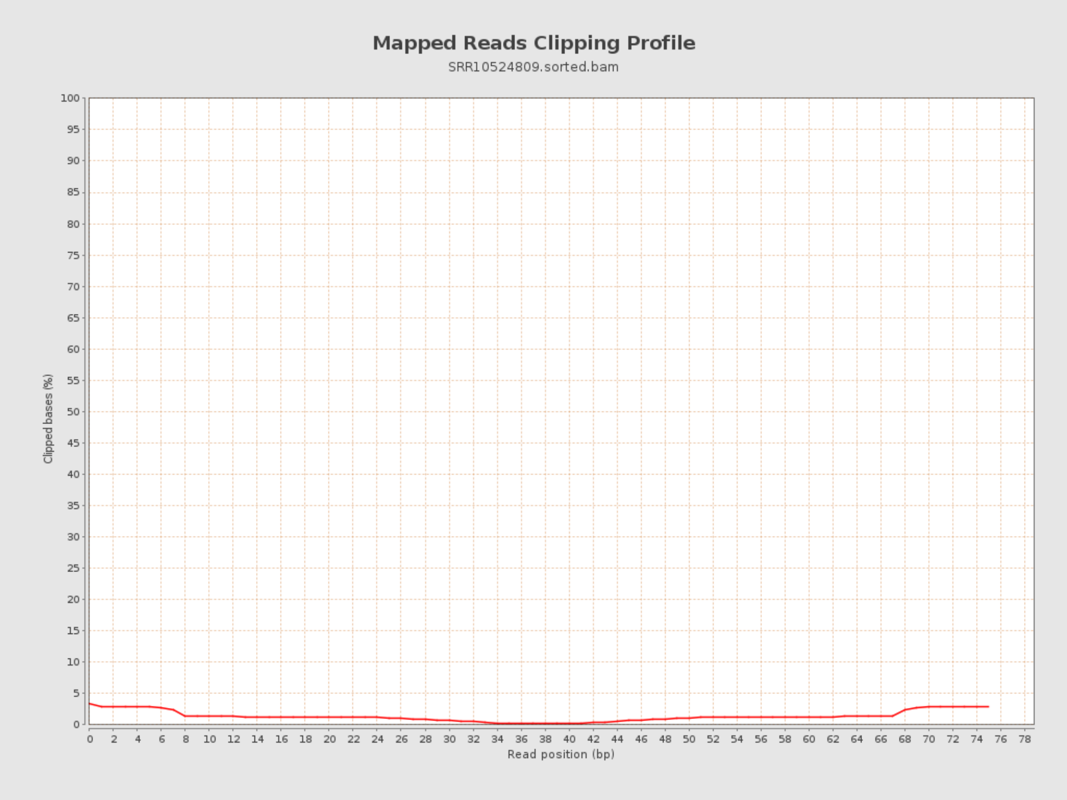
8. Results : Mapped Reads Nucleotide Content



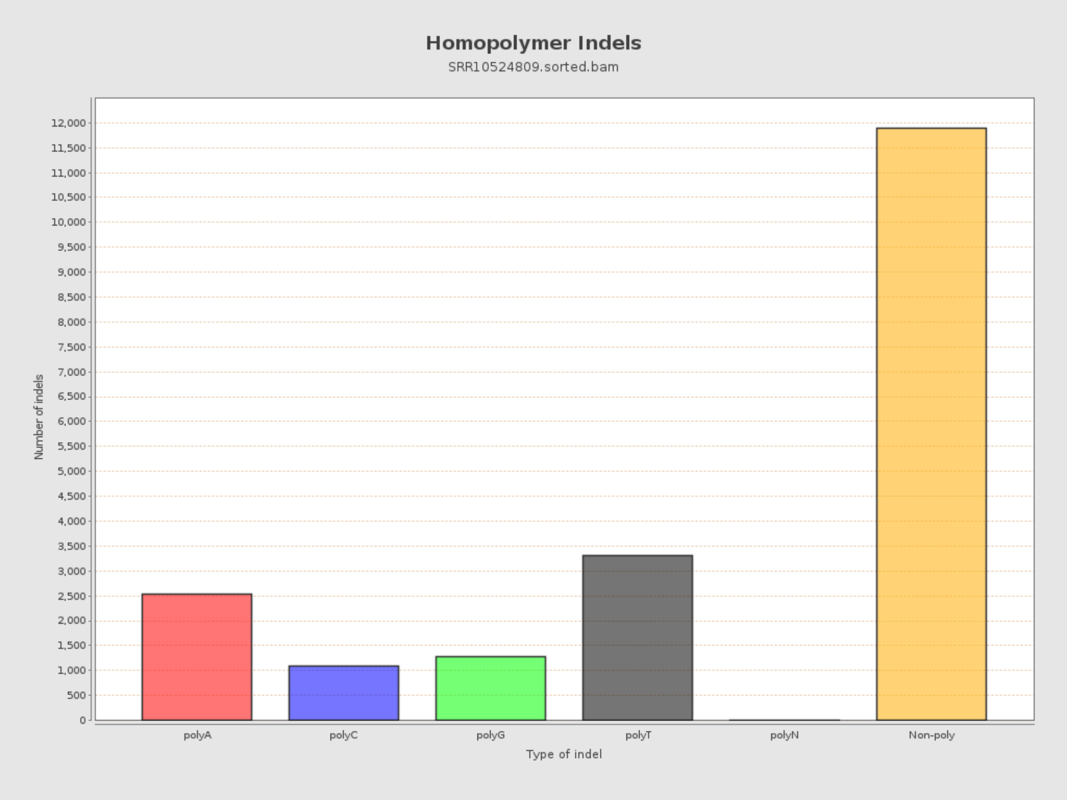
9. Results : Mapped Reads GC-content Distribution



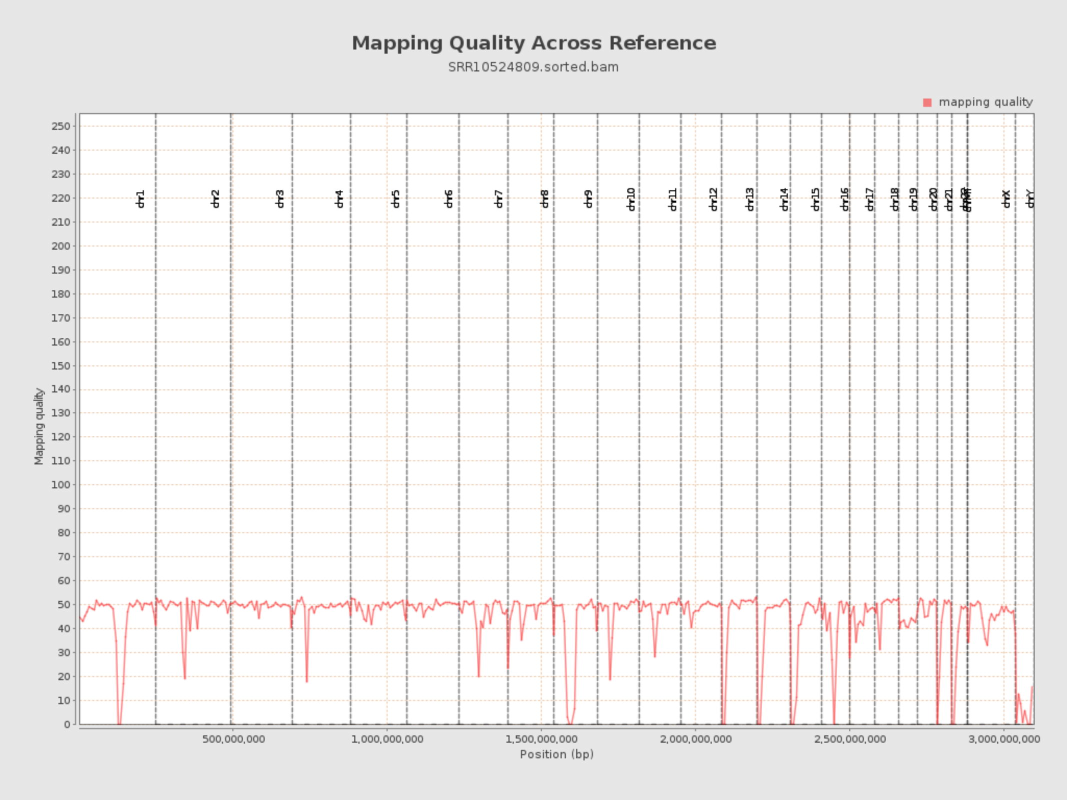
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram