Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:43:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524501.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_SRR10524501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524501.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:43:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,094,142
Mapped reads	1,003,401 / 91.71%
Unmapped reads	90,741 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,191 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	30,179 / 2.76%
Duplication rate	2.31%
Clipped reads	1,002,709 / 91.64%

2.2. ACGT Content

Number/percentage of A's	14,931,011 / 25.64%
Number/percentage of C's	10,730,294 / 18.42%
Number/percentage of T's	18,767,429 / 32.22%
Number/percentage of G's	13,813,722 / 23.72%
Number/percentage of N's	1,162 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.1866

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

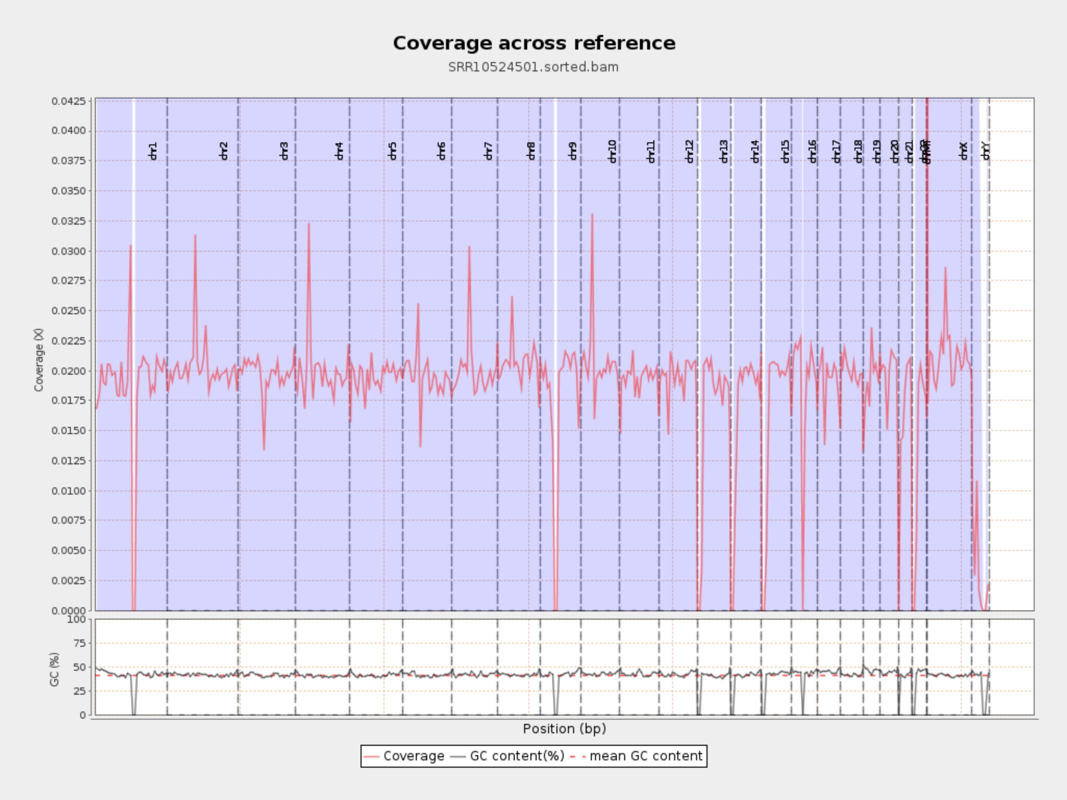
General error rate	0.48%
Mismatches	273,431
Insertions	3,587
Mapped reads with at least one insertion	0.36%
Deletions	11,055
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.04%

2.6. Chromosome stats

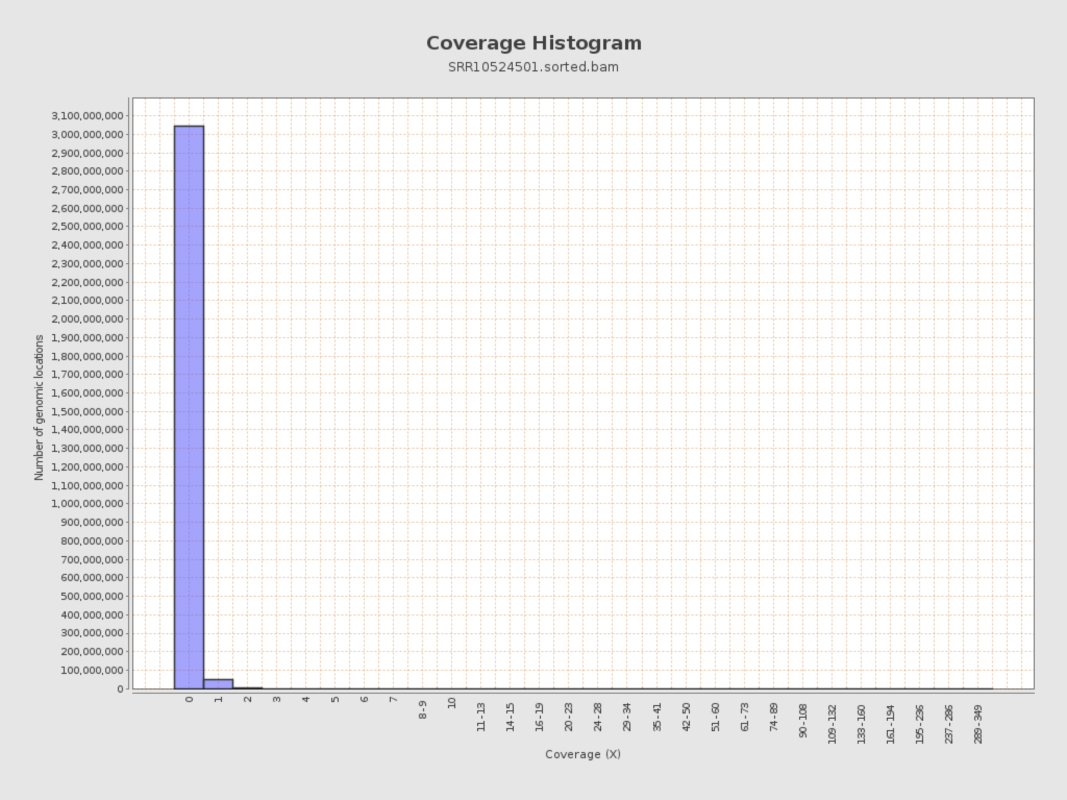
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4632805	0.0186	0.2961
chr2	243199373	4928259	0.0203	0.2064
chr3	198022430	3902326	0.0197	0.1493
chr4	191154276	3825878	0.02	0.162
chr5	180915260	3547140	0.0196	0.15
chr6	171115067	3338634	0.0195	0.1673
chr7	159138663	3192032	0.0201	0.235

chr8	146364022	3021024	0.0206	0.1819
chr9	141213431	2462554	0.0174	0.167
chr10	135534747	2808655	0.0207	0.1936
chr11	135006516	2625822	0.0194	0.188
chr12	133851895	2622449	0.0196	0.1499
chr13	115169878	1852777	0.0161	0.1358
chr14	107349540	1747433	0.0163	0.1389
chr15	102531392	1665484	0.0162	0.1424
chr16	90354753	1672444	0.0185	0.1516
chr17	81195210	1559603	0.0192	0.1528
chr18	78077248	1561980	0.02	0.2681
chr19	59128983	1141615	0.0193	0.2239
chr20	63025520	1237397	0.0196	0.1527
chr21	48129895	775308	0.0161	0.1403
chr22	51304566	667761	0.013	0.1209
chrMT	16571	8614	0.5198	0.8287
chrX	155270560	3279620	0.0211	0.1661
chrY	59373566	184516	0.0031	0.0926

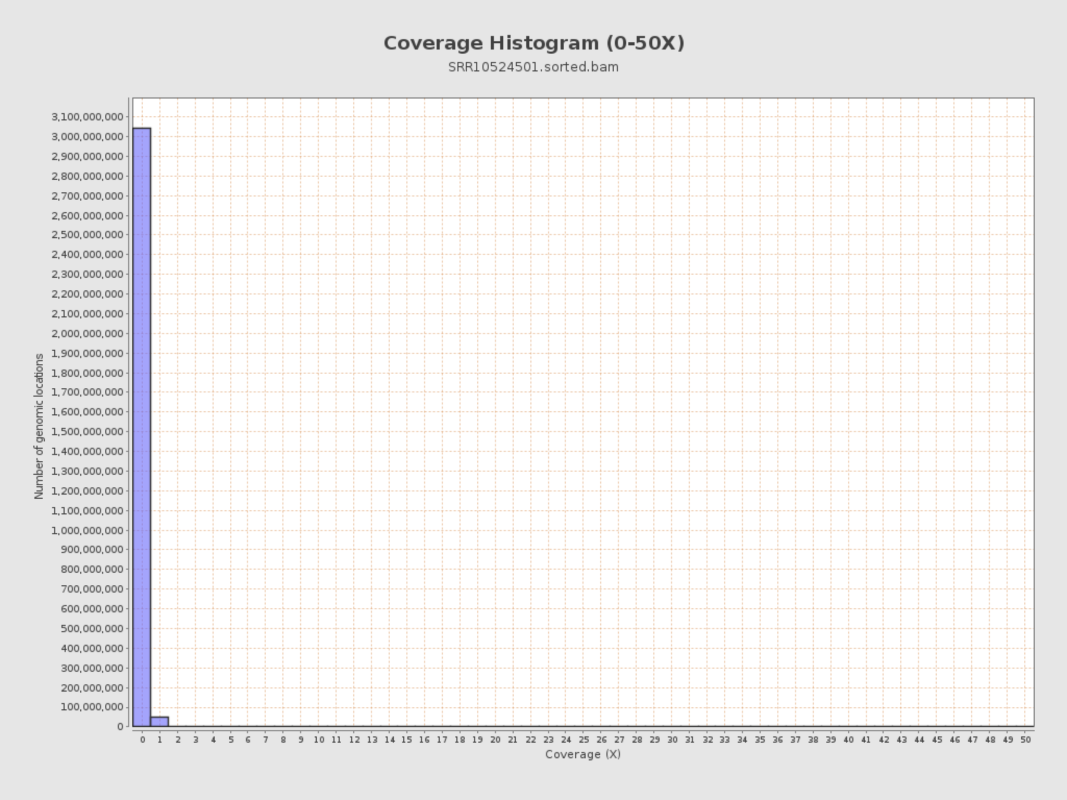
3. Results : Coverage across reference



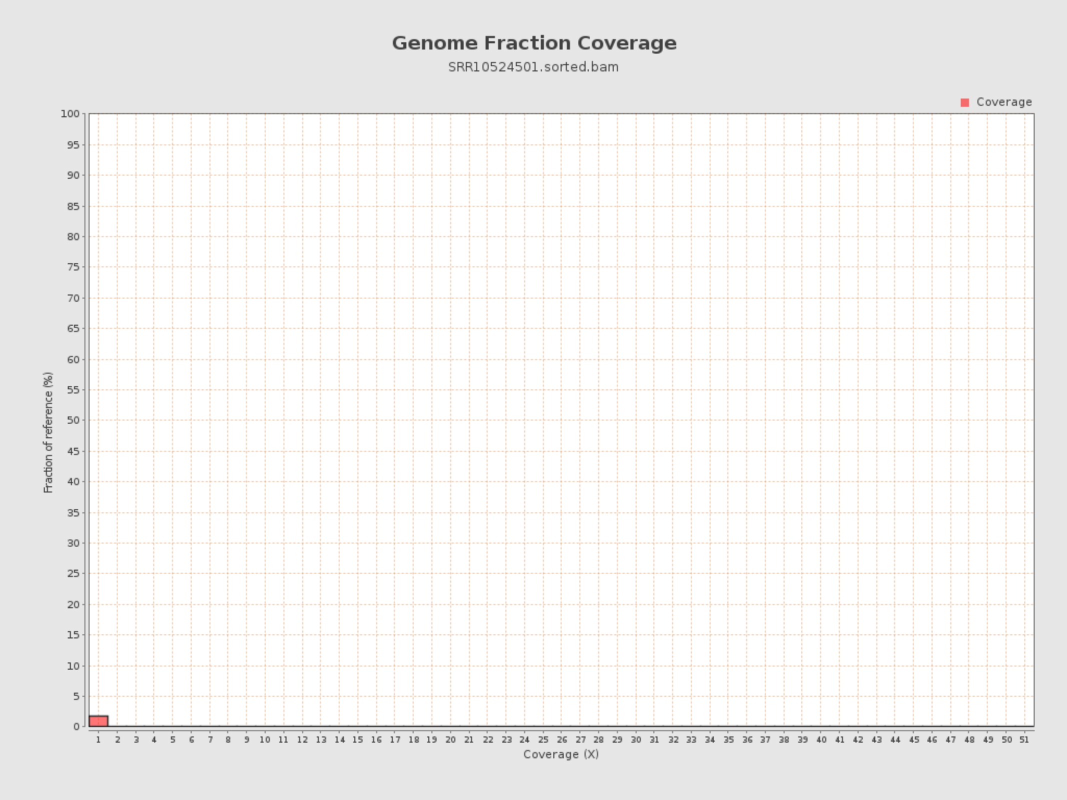
4. Results : Coverage Histogram



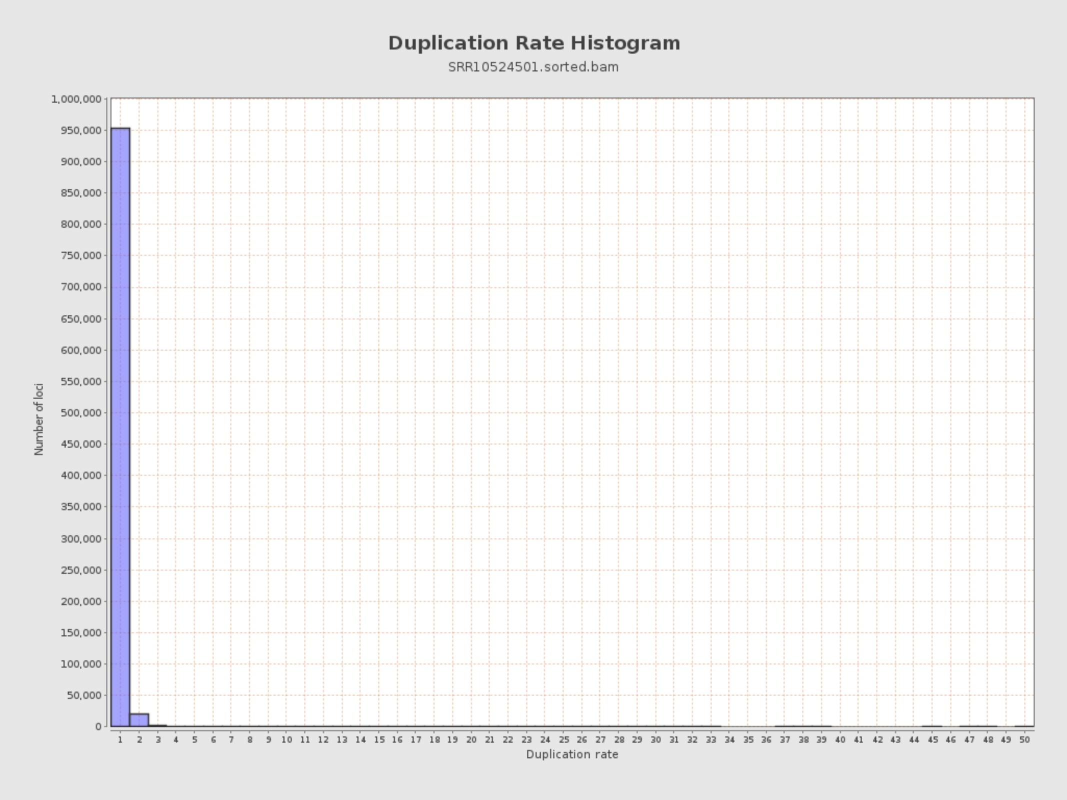
5. Results : Coverage Histogram (0-50X)



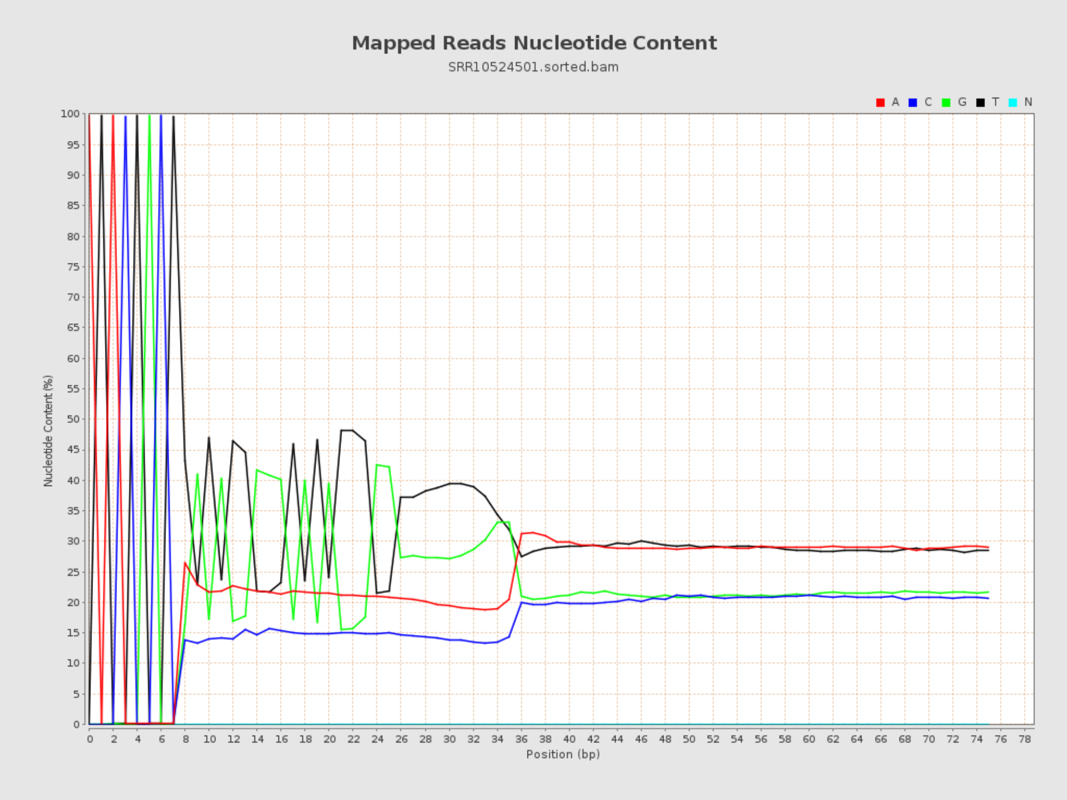
6. Results : Genome Fraction Coverage



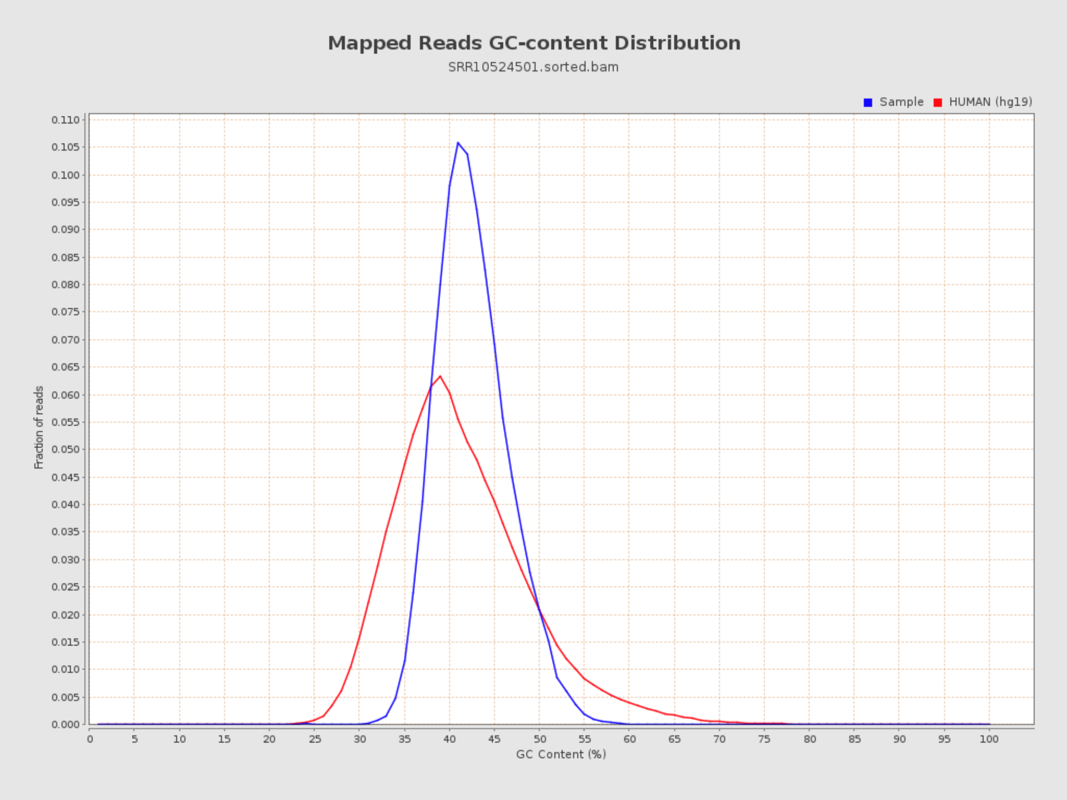
7. Results : Duplication Rate Histogram



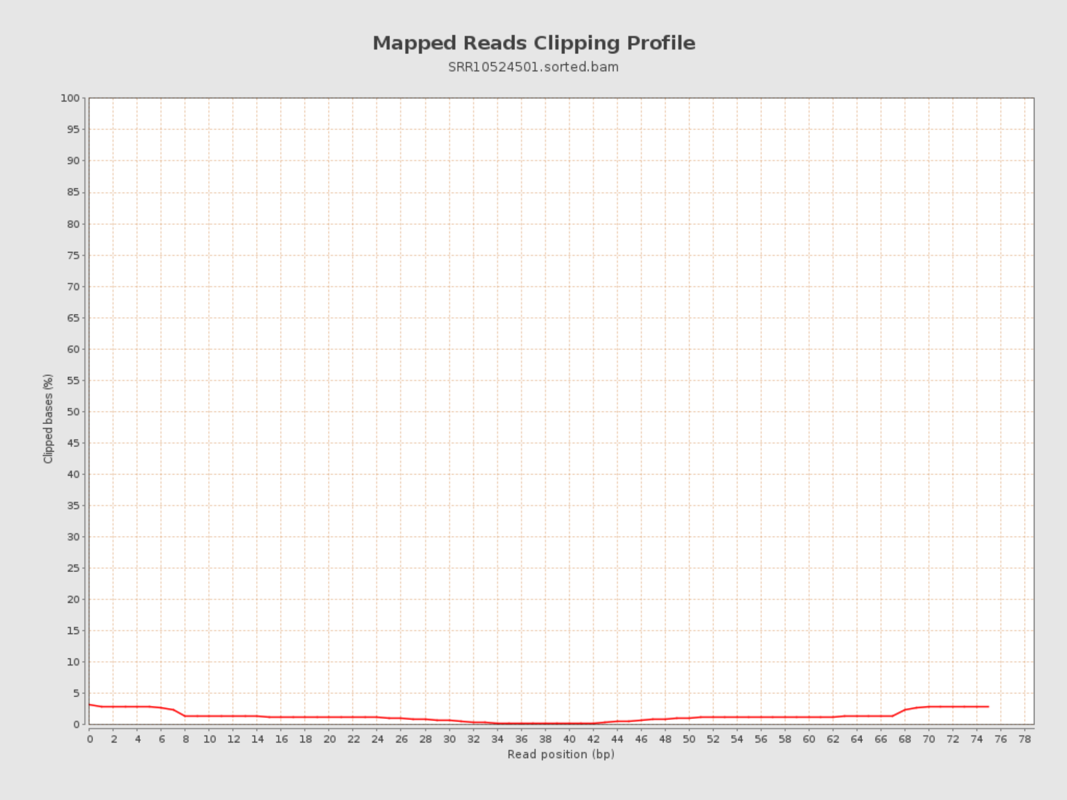
8. Results : Mapped Reads Nucleotide Content



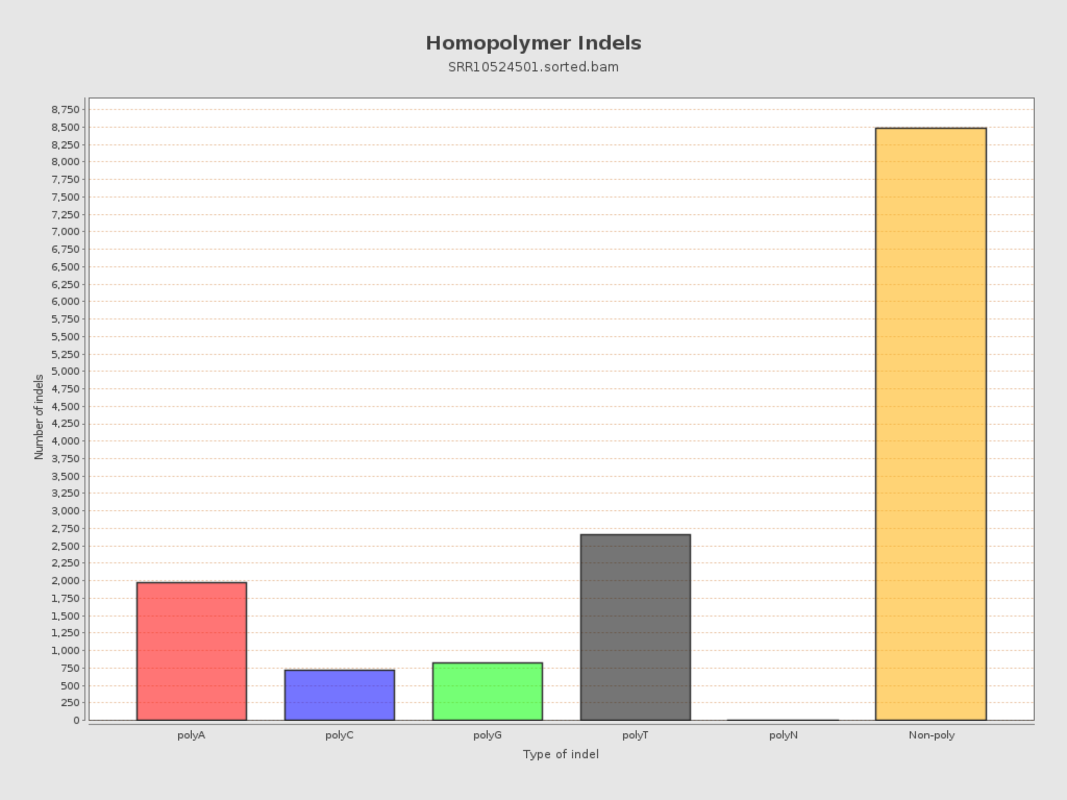
9. Results : Mapped Reads GC-content Distribution



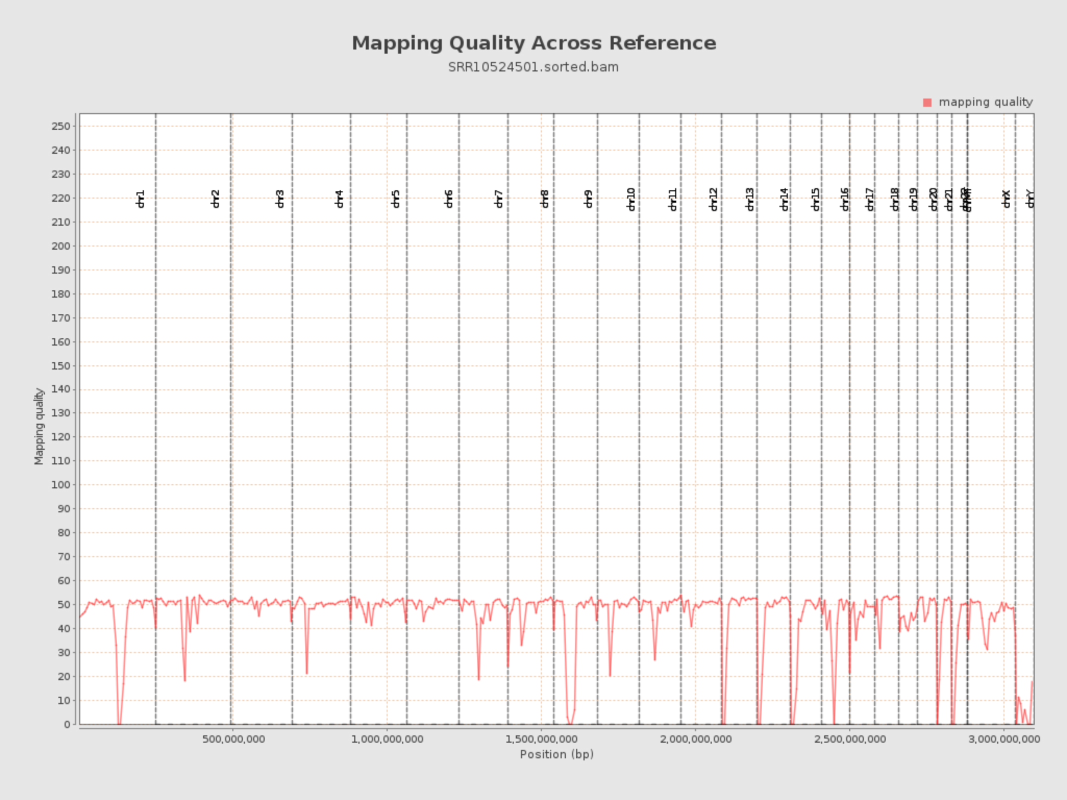
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram