Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:14:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524971.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_SRR10524971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524971.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:14:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	743,013
Mapped reads	690,971 / 93%
Unmapped reads	52,042 / 7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,757 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	13,170 / 1.77%
Duplication rate	1.37%
Clipped reads	691,905 / 93.12%

2.2. ACGT Content

Number/percentage of A's	10,616,022 / 26.08%
Number/percentage of C's	7,613,712 / 18.7%
Number/percentage of T's	12,191,016 / 29.95%
Number/percentage of G's	10,283,752 / 25.26%
Number/percentage of N's	447 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0132

Standard Deviation	0.1472

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

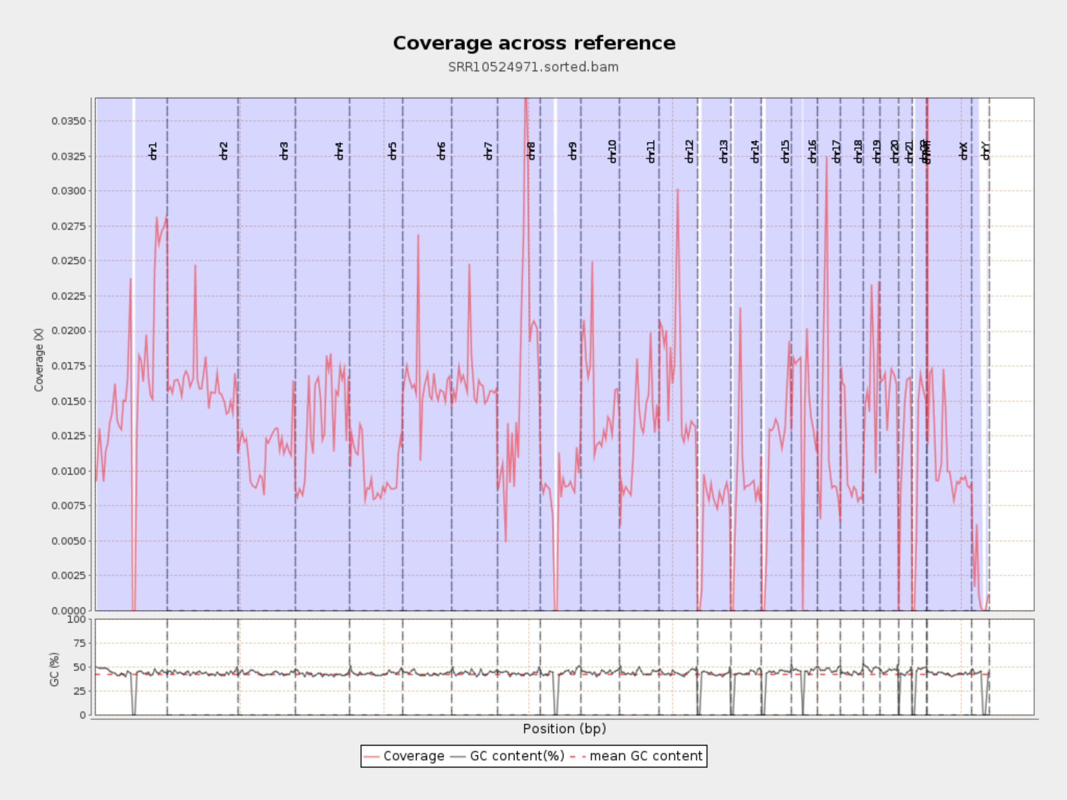
General error rate	0.5%
Mismatches	196,925
Insertions	2,420
Mapped reads with at least one insertion	0.35%
Deletions	7,936
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.86%

2.6. Chromosome stats

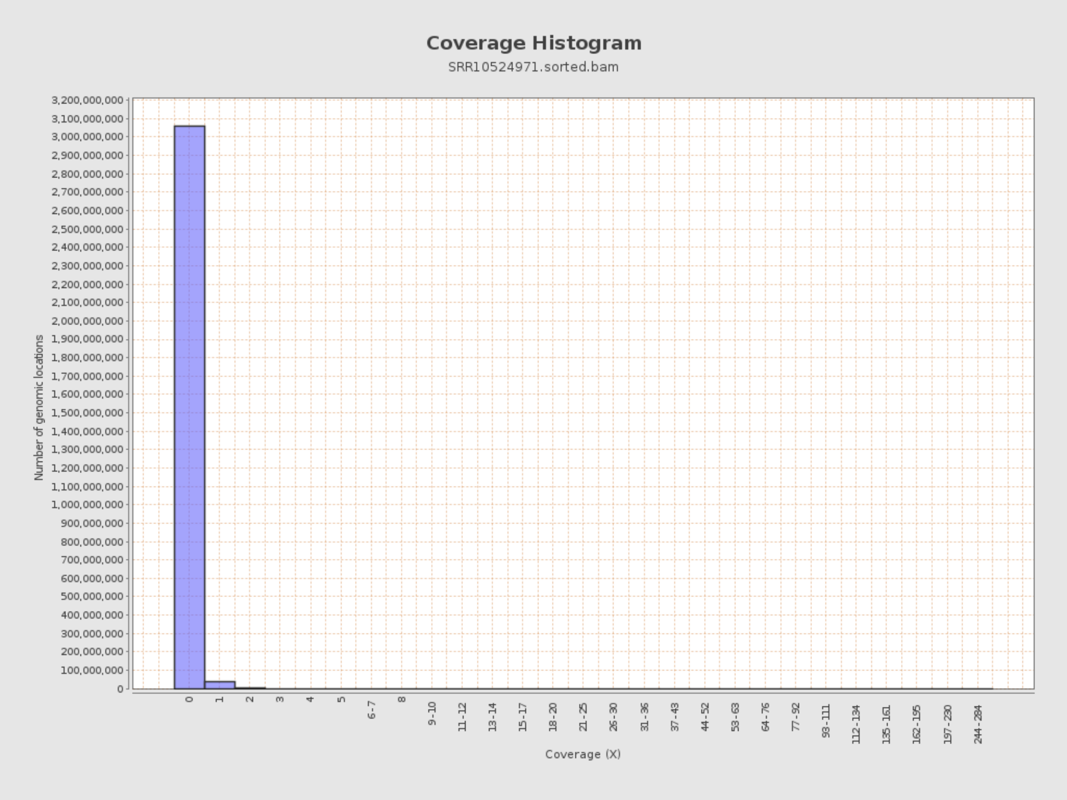
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4022681	0.0161	0.236
chr2	243199373	3932660	0.0162	0.1676
chr3	198022430	2264158	0.0114	0.1113
chr4	191154276	2650210	0.0139	0.1257
chr5	180915260	1781278	0.0098	0.1034
chr6	171115067	2776916	0.0162	0.1667
chr7	159138663	2602774	0.0164	0.1877

chr8	146364022	2465316	0.0168	0.1516
chr9	141213431	1151208	0.0082	0.1175
chr10	135534747	2067316	0.0153	0.1512
chr11	135006516	1720373	0.0127	0.1373
chr12	133851895	2247927	0.0168	0.135
chr13	115169878	802232	0.007	0.0878
chr14	107349540	939428	0.0088	0.0983
chr15	102531392	1147013	0.0112	0.1111
chr16	90354753	1309064	0.0145	0.129
chr17	81195210	1055233	0.013	0.1369
chr18	78077248	809258	0.0104	0.1666
chr19	59128983	994745	0.0168	0.1831
chr20	63025520	996093	0.0158	0.1312
chr21	48129895	598608	0.0124	0.1171
chr22	51304566	552751	0.0108	0.1073
chrMT	16571	7388	0.4458	0.7181
chrX	155270560	1718562	0.0111	0.1194
chrY	59373566	105462	0.0018	0.056

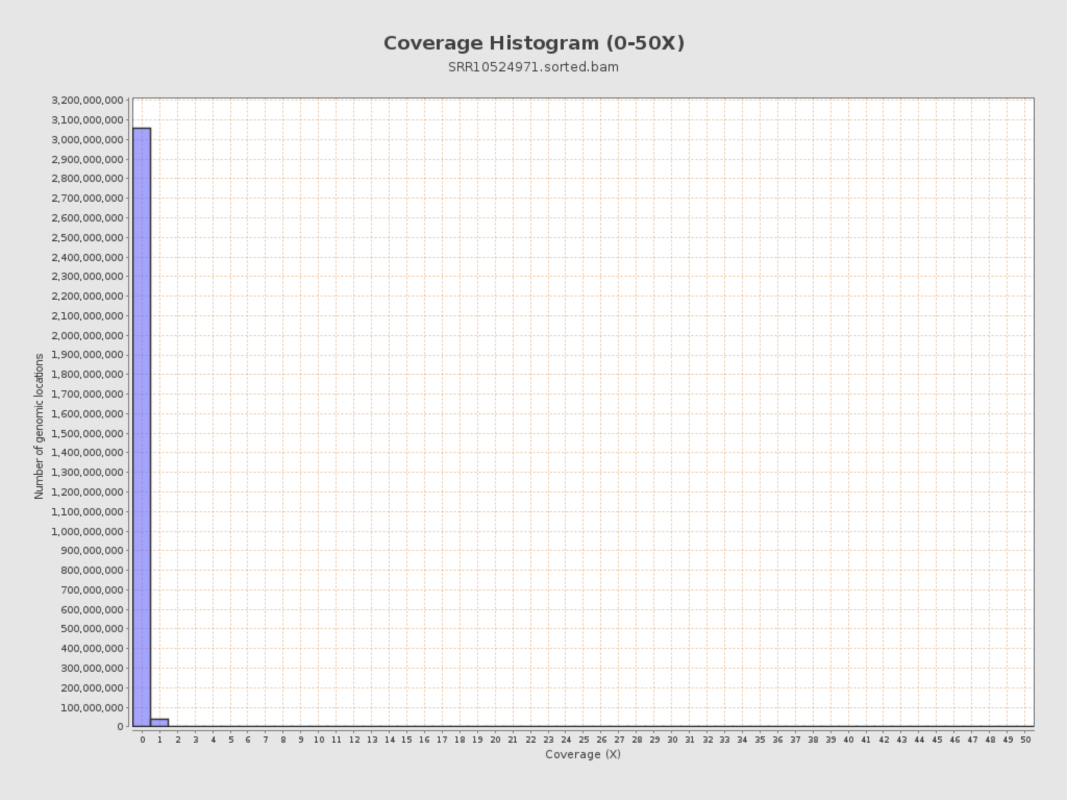
3. Results : Coverage across reference



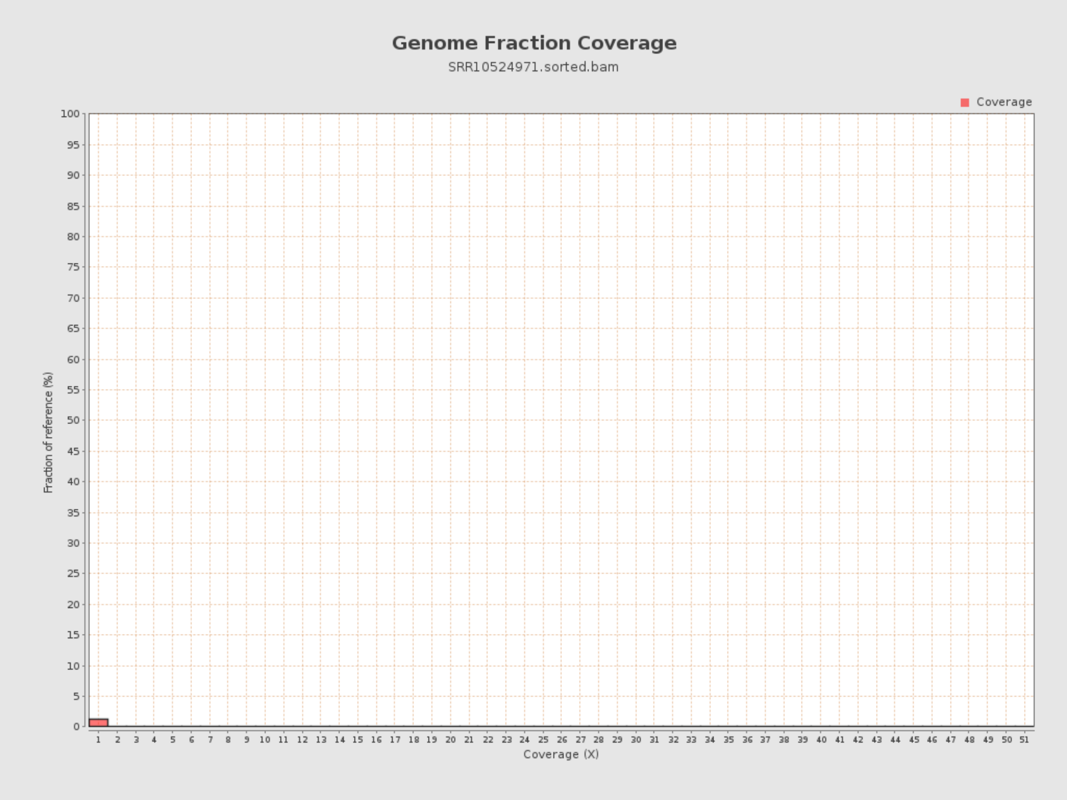
4. Results : Coverage Histogram



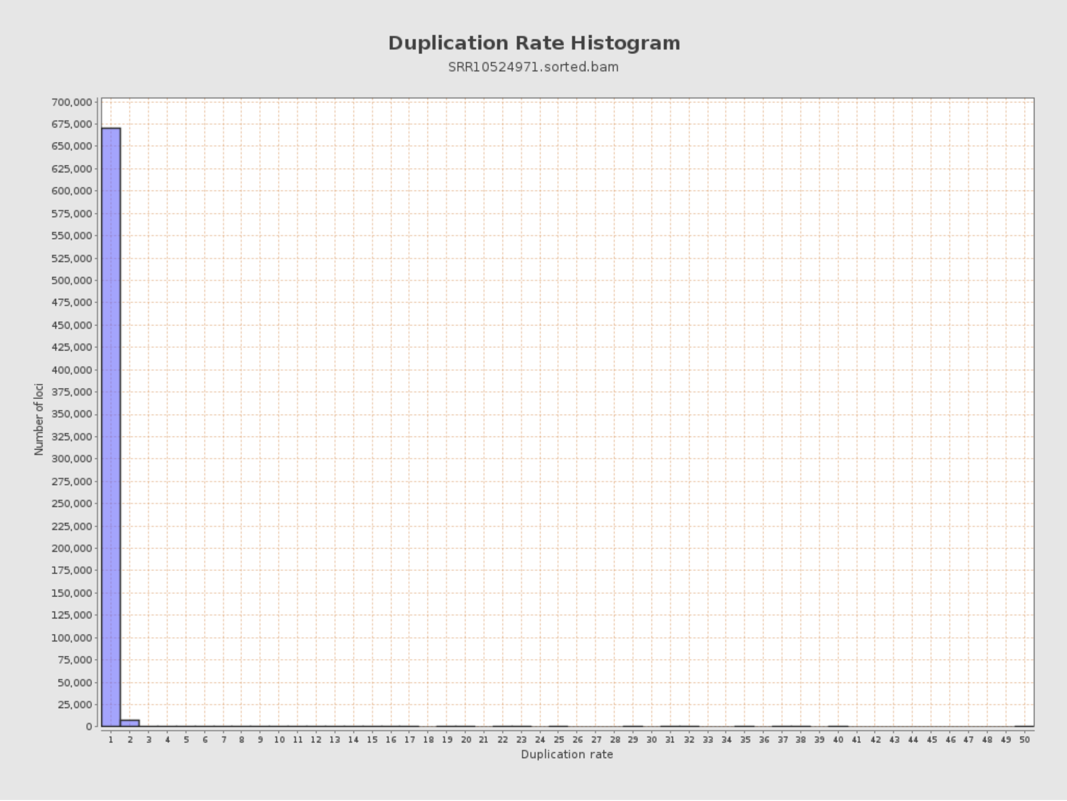
5. Results : Coverage Histogram (0-50X)



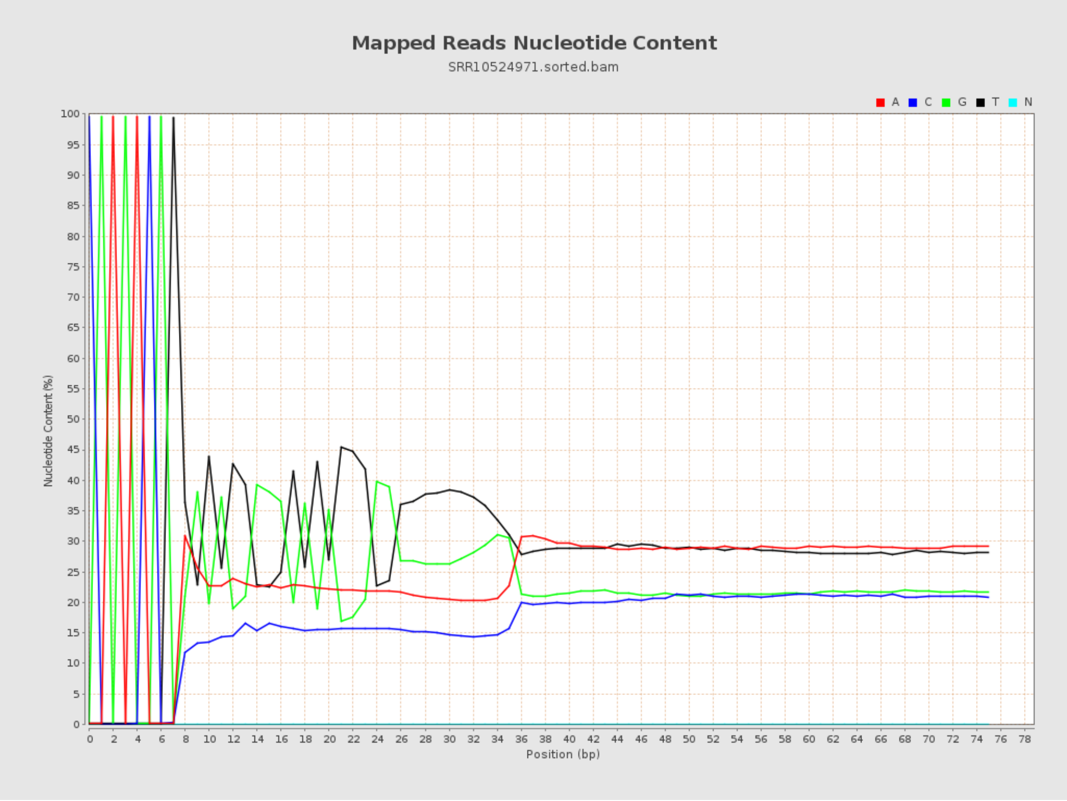
6. Results : Genome Fraction Coverage



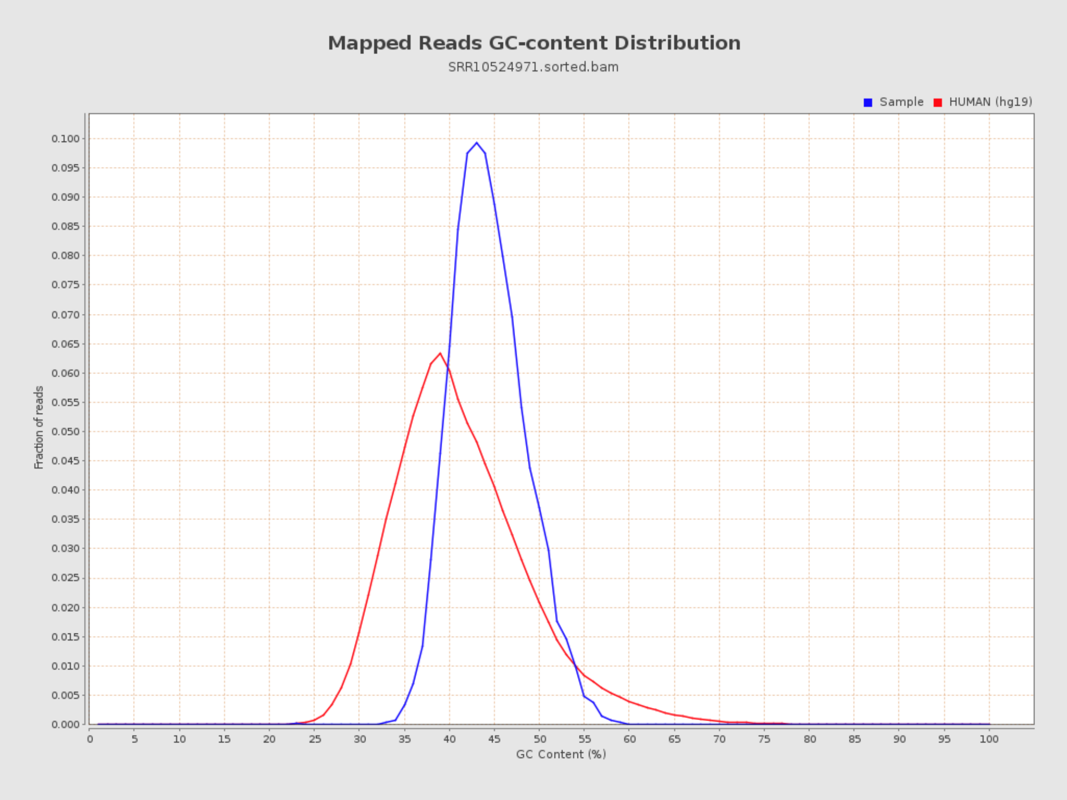
7. Results : Duplication Rate Histogram



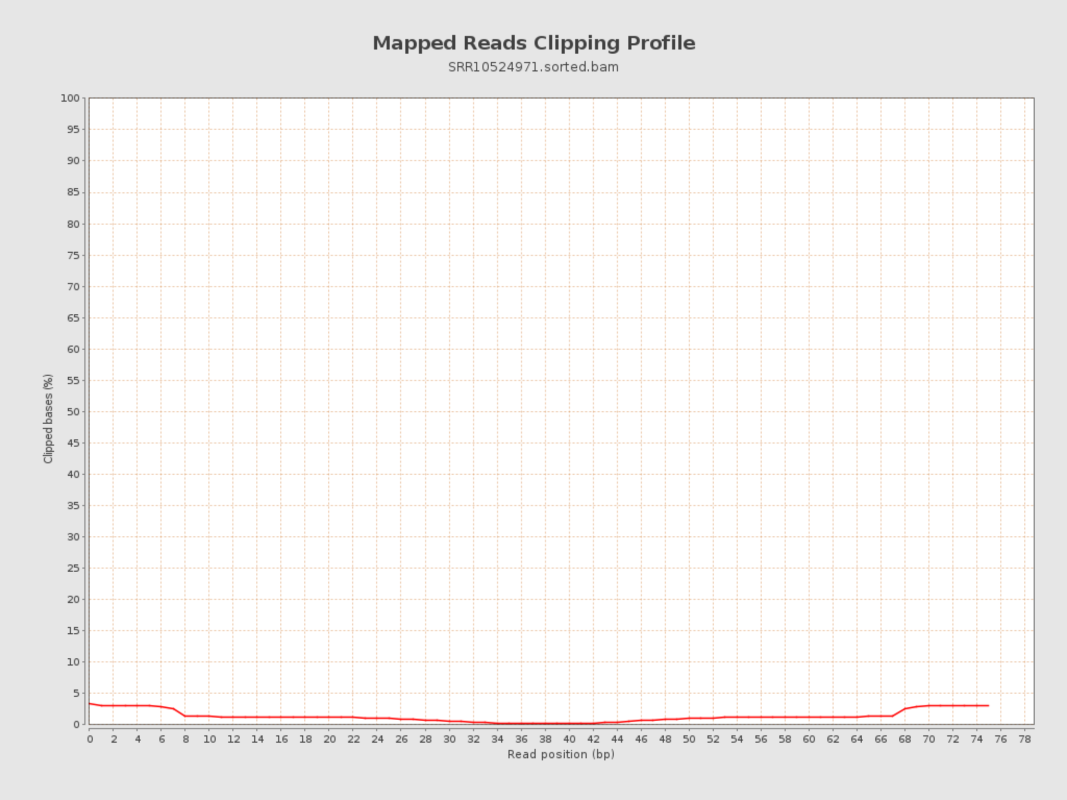
8. Results : Mapped Reads Nucleotide Content



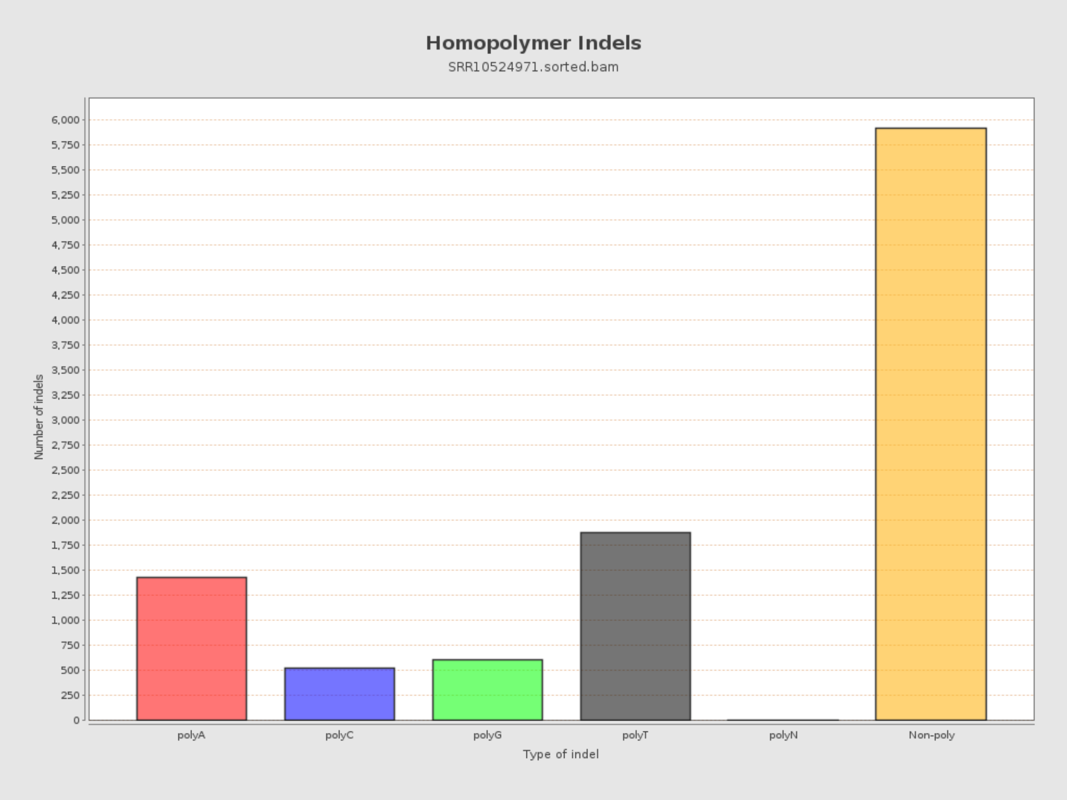
9. Results : Mapped Reads GC-content Distribution



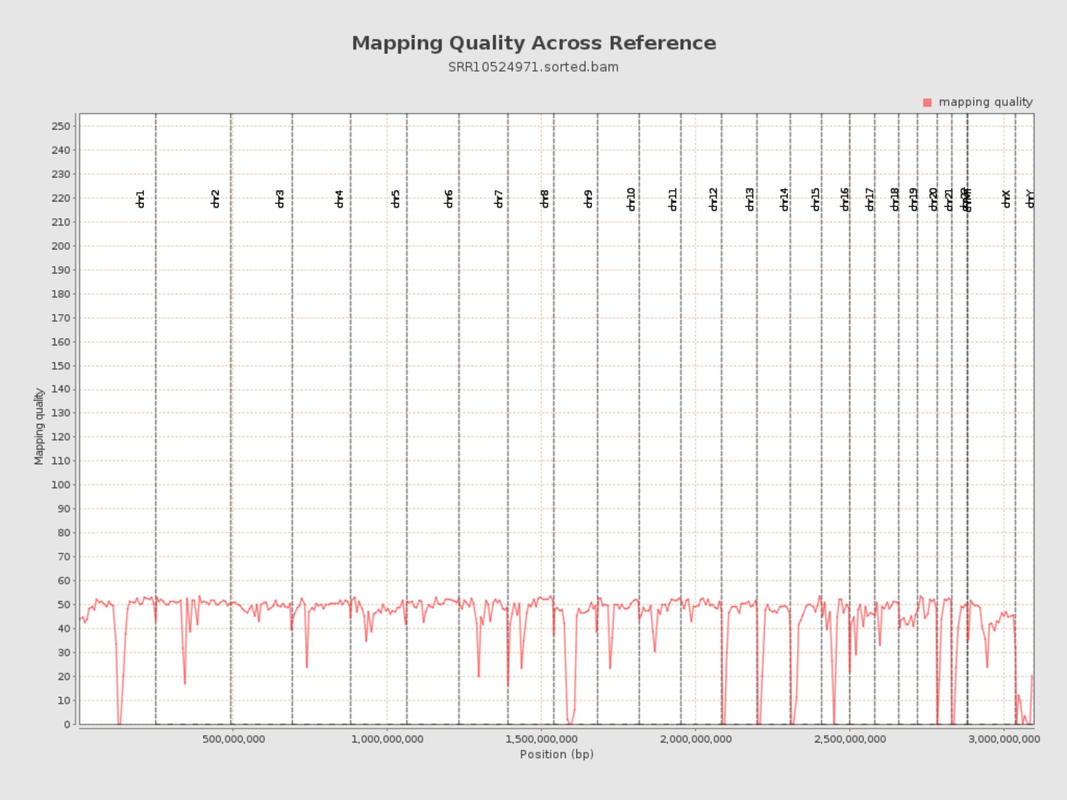
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram