Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:54:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524540.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_SRR10524540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:54:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,678,028
Mapped reads	5,170,660 / 91.06%
Unmapped reads	507,368 / 8.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,847 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	424,605 / 7.48%
Duplication rate	5.91%
Clipped reads	5,176,405 / 91.17%

2.2. ACGT Content

Number/percentage of A's	74,154,255 / 24.63%
Number/percentage of C's	61,740,870 / 20.51%
Number/percentage of T's	91,399,965 / 30.36%
Number/percentage of G's	73,757,727 / 24.5%
Number/percentage of N's	4,176 / 0%
GC Percentage	45.01%

2.3. Coverage

Mean	0.0973

Standard Deviation	0.7814

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

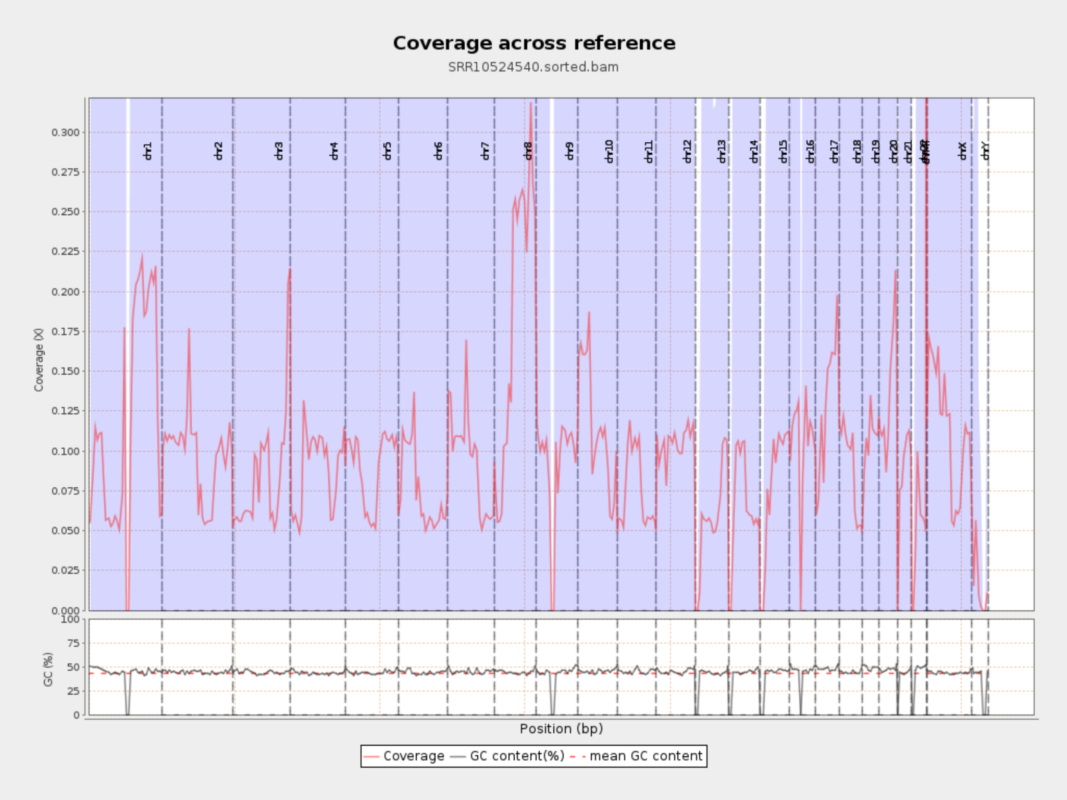
General error rate	0.53%
Mismatches	1,542,879
Insertions	20,058
Mapped reads with at least one insertion	0.39%
Deletions	57,986
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.53%

2.6. Chromosome stats

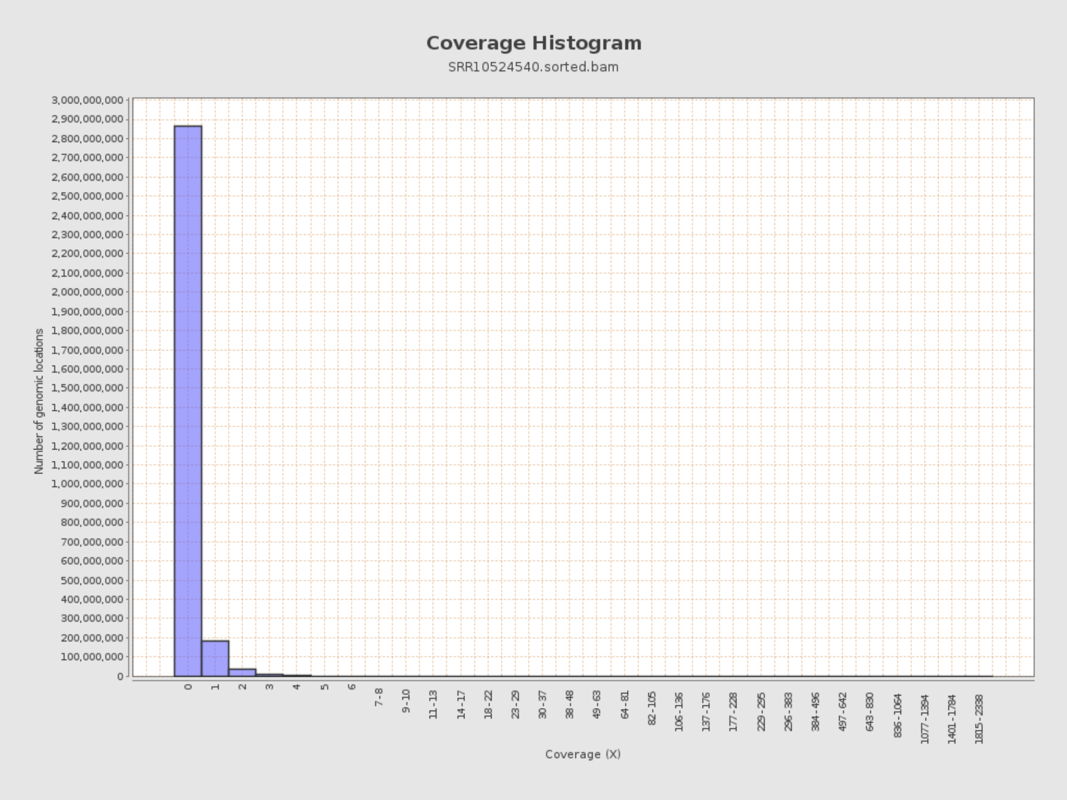
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29779562	0.1195	1.6605
chr2	243199373	23727973	0.0976	0.8927
chr3	198022430	16456699	0.0831	0.3737
chr4	191154276	16872714	0.0883	0.4752
chr5	180915260	16388669	0.0906	0.3866
chr6	171115067	12803426	0.0748	0.5601
chr7	159138663	15082169	0.0948	1.0498

chr8	146364022	27544838	0.1882	0.7544
chr9	141213431	12803968	0.0907	0.616
chr10	135534747	15893479	0.1173	0.7746
chr11	135006516	10261388	0.076	0.697
chr12	133851895	14059758	0.105	0.4184
chr13	115169878	6707010	0.0582	0.3108
chr14	107349540	7116797	0.0663	0.3445
chr15	102531392	8011539	0.0781	0.3756
chr16	90354753	9488354	0.105	0.491
chr17	81195210	10679494	0.1315	0.5211
chr18	78077248	7072349	0.0906	1.2872
chr19	59128983	6306040	0.1066	1.125
chr20	63025520	8655908	0.1373	0.4864
chr21	48129895	4136902	0.086	0.4501
chr22	51304566	2483808	0.0484	0.2783
chrMT	16571	26544	1.6018	1.8393
chrX	155270560	17830628	0.1148	0.5451
chrY	59373566	964129	0.0162	0.4296

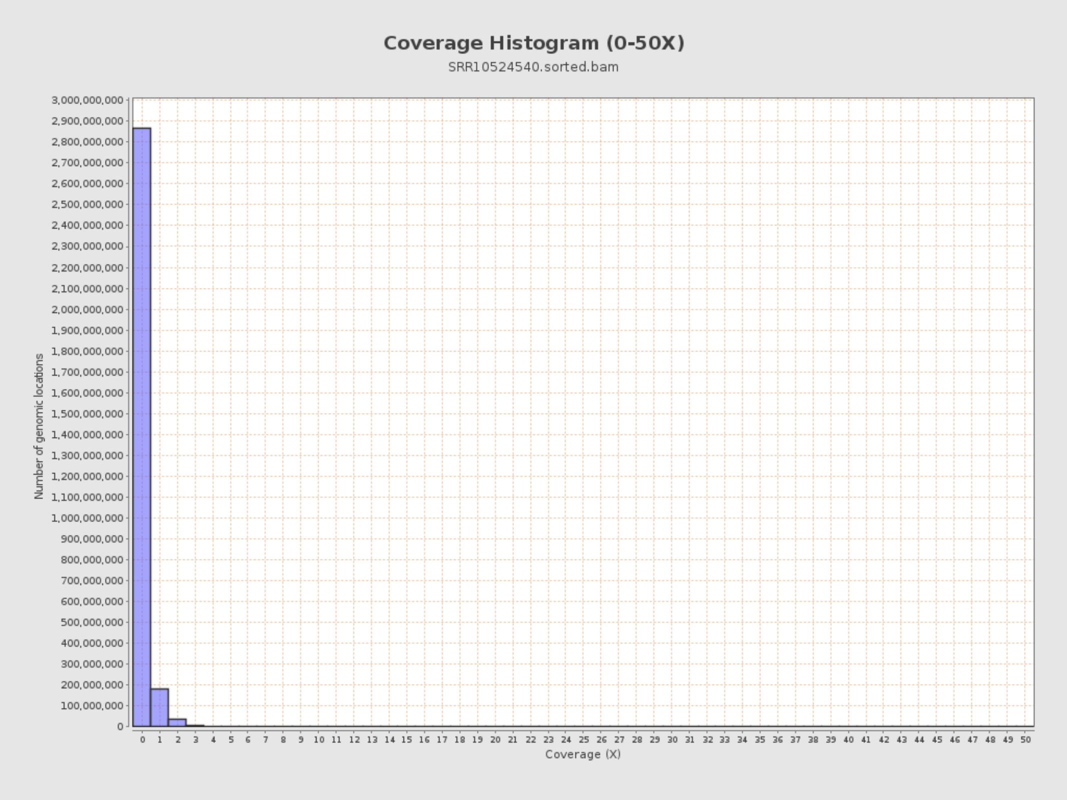
3. Results : Coverage across reference



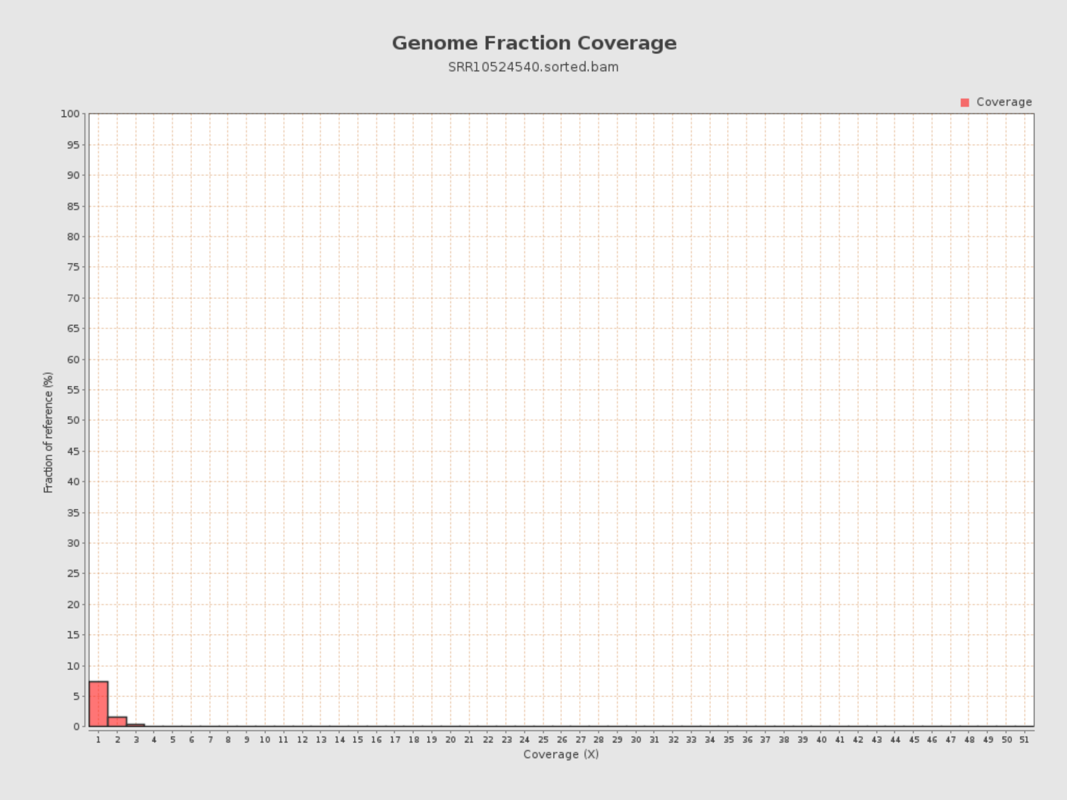
4. Results : Coverage Histogram



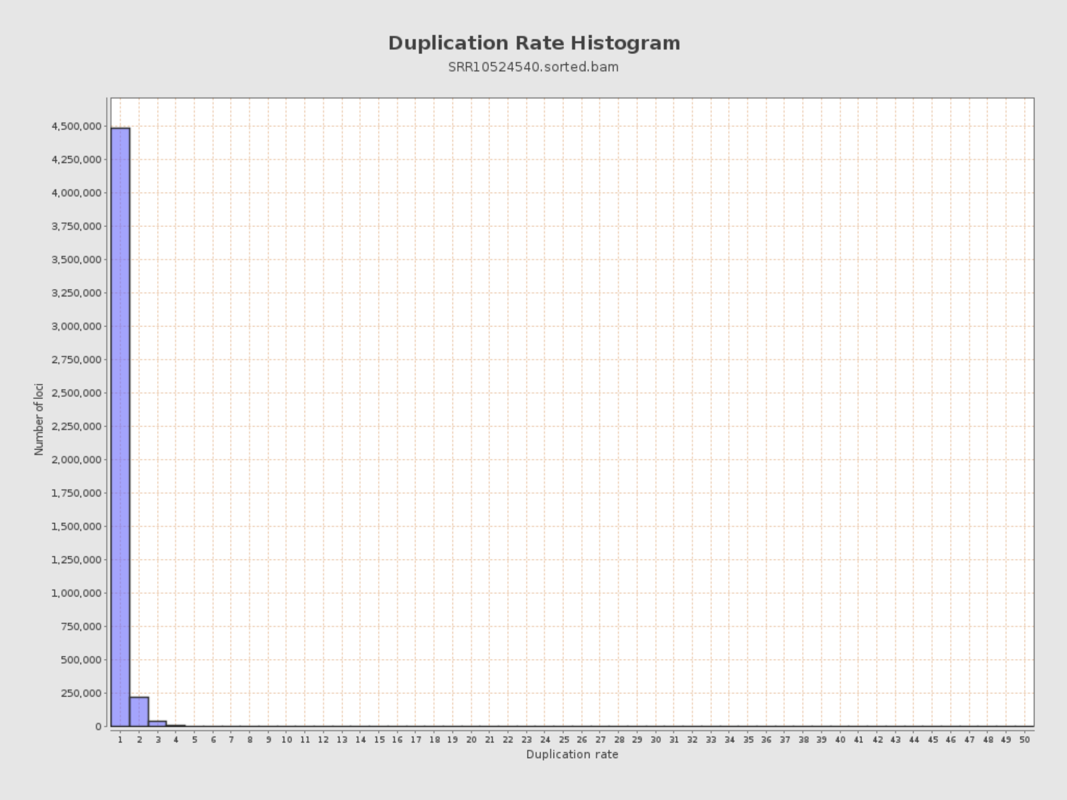
5. Results : Coverage Histogram (0-50X)



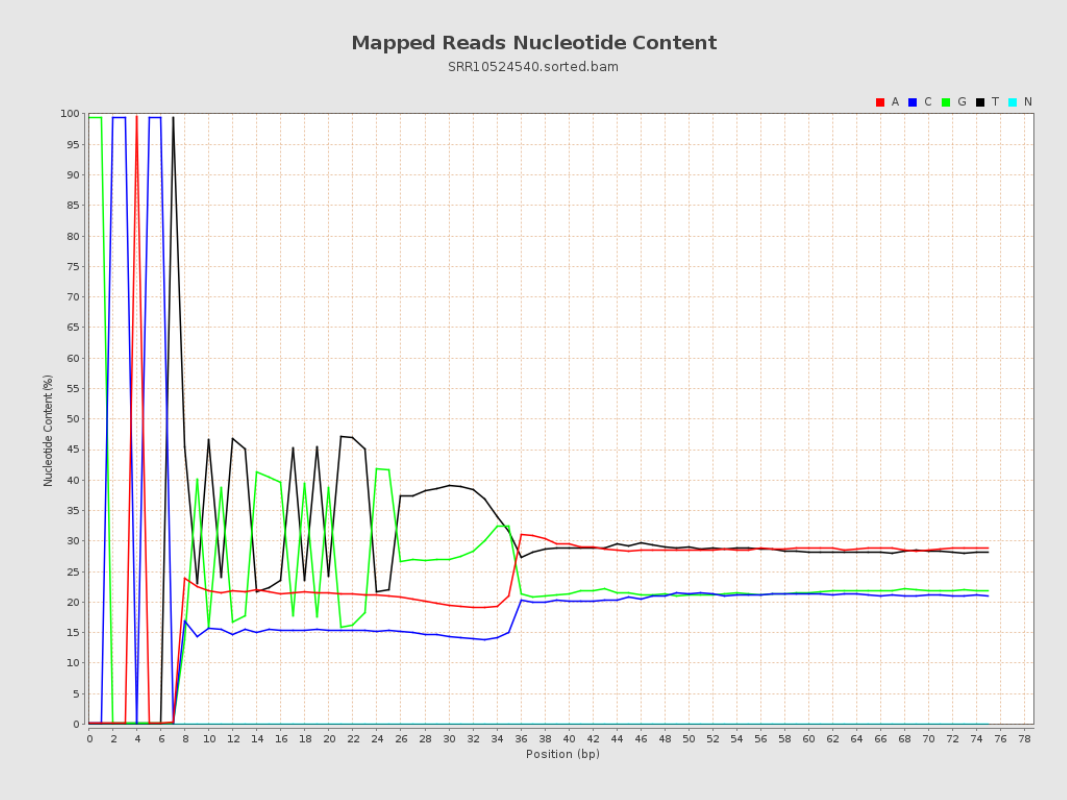
6. Results : Genome Fraction Coverage



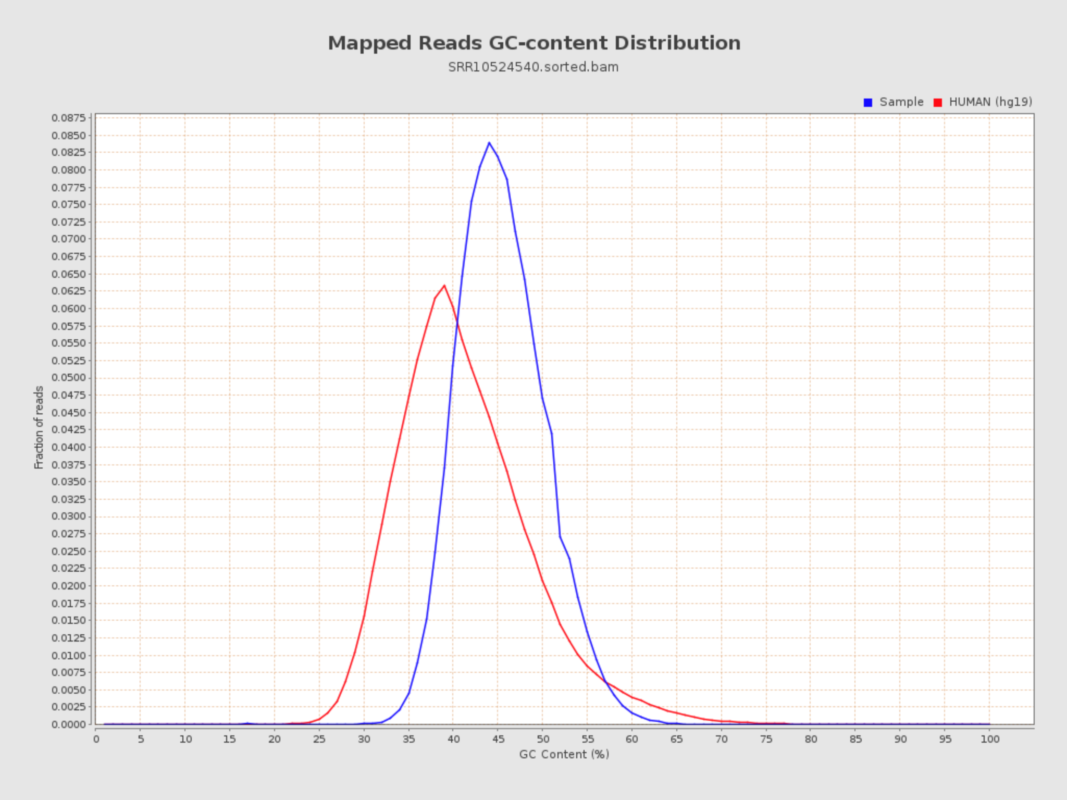
7. Results : Duplication Rate Histogram



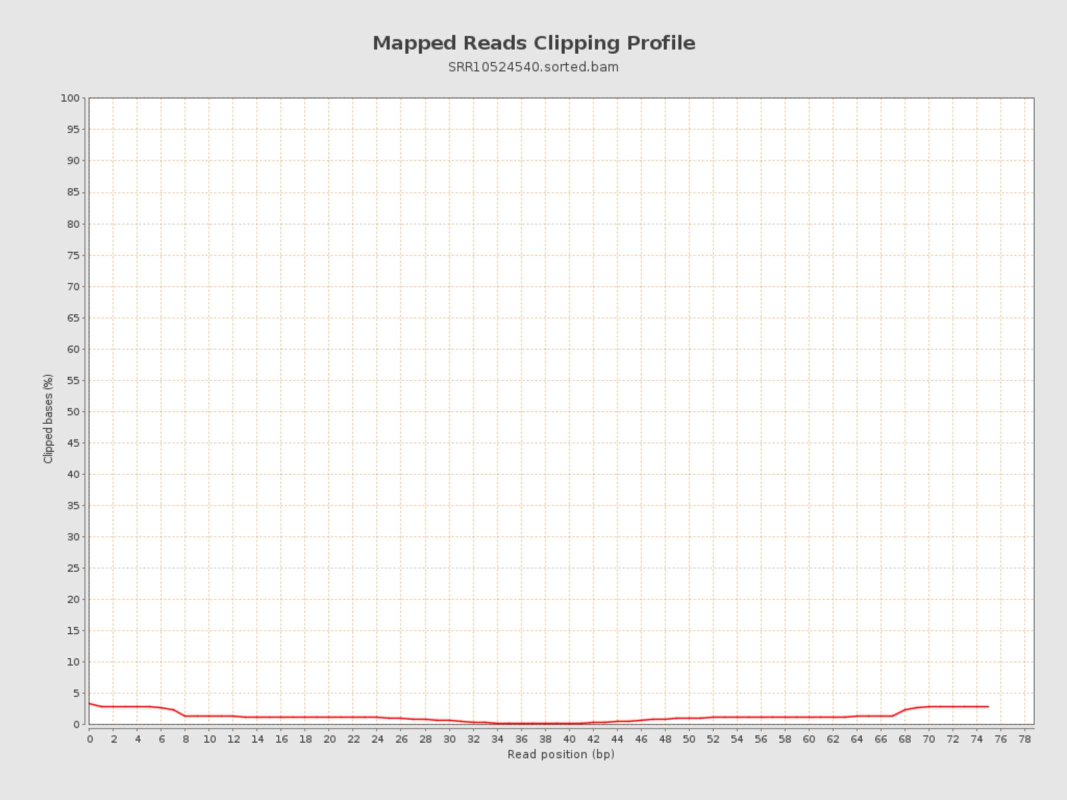
8. Results : Mapped Reads Nucleotide Content



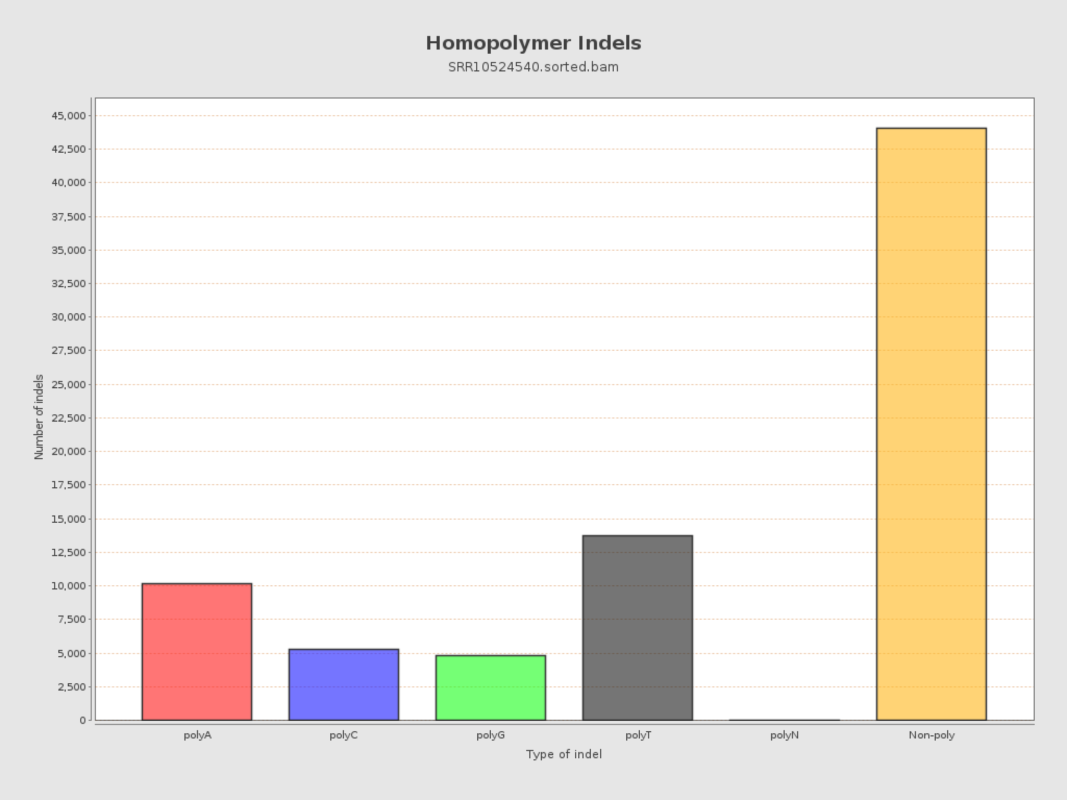
9. Results : Mapped Reads GC-content Distribution



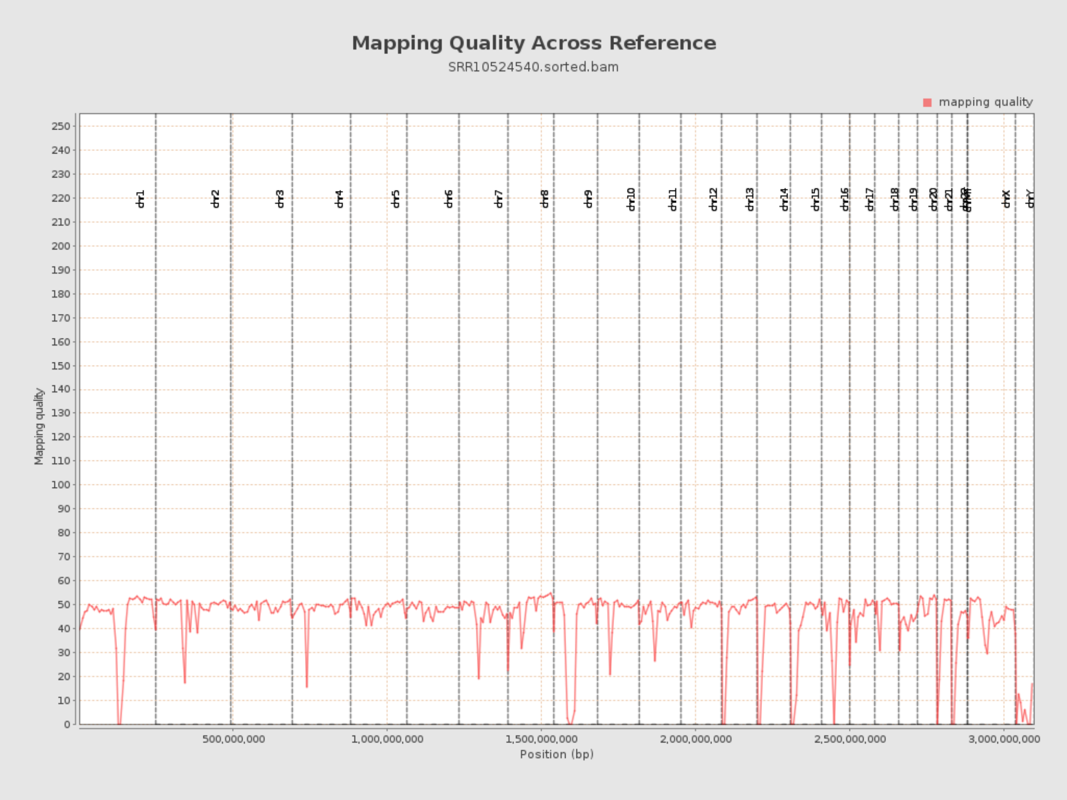
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram