Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:06:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524420.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_SRR10524420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524420.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:06:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,839,724
Mapped reads	2,618,178 / 92.2%
Unmapped reads	221,546 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,548 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	190,337 / 6.7%
Duplication rate	5.29%
Clipped reads	2,625,789 / 92.47%

2.2. ACGT Content

Number/percentage of A's	37,882,198 / 24.78%
Number/percentage of C's	29,729,043 / 19.45%
Number/percentage of T's	45,572,324 / 29.81%
Number/percentage of G's	39,670,564 / 25.95%
Number/percentage of N's	14,765 / 0.01%
GC Percentage	45.4%

2.3. Coverage

Mean	0.0494

Standard Deviation	0.4604

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

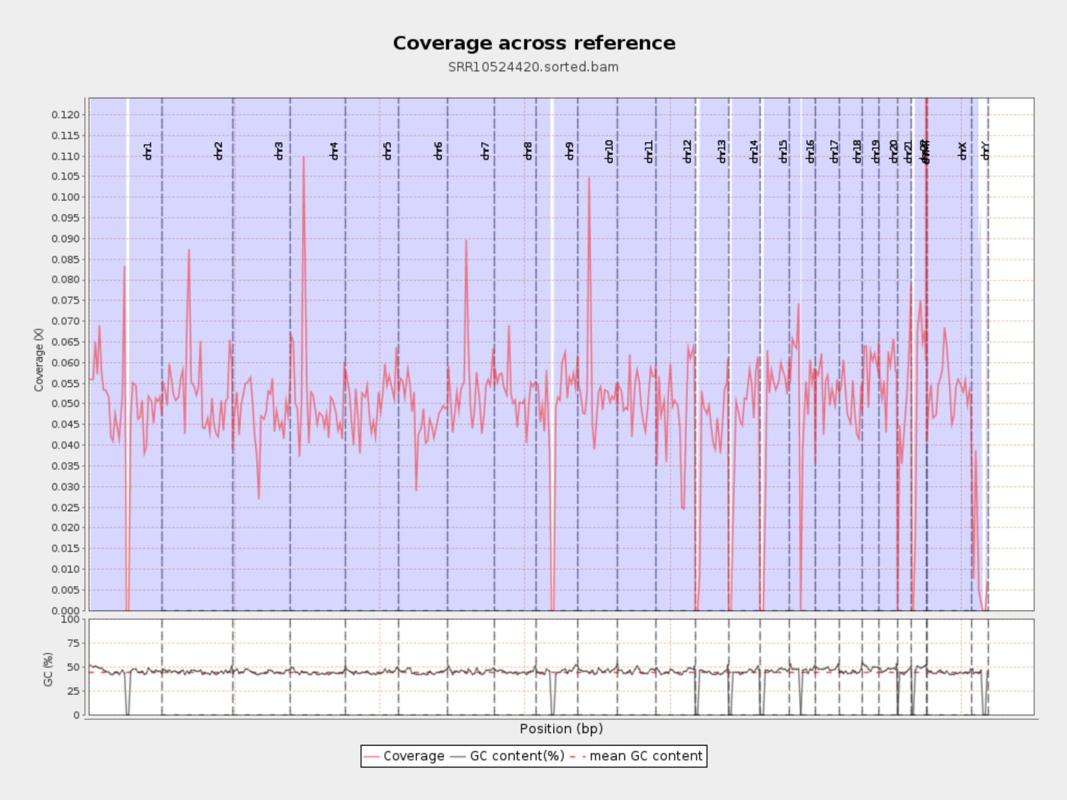
General error rate	0.52%
Mismatches	774,413
Insertions	10,049
Mapped reads with at least one insertion	0.38%
Deletions	25,309
Mapped reads with at least one deletion	0.96%
Homopolymer indels	40.85%

2.6. Chromosome stats

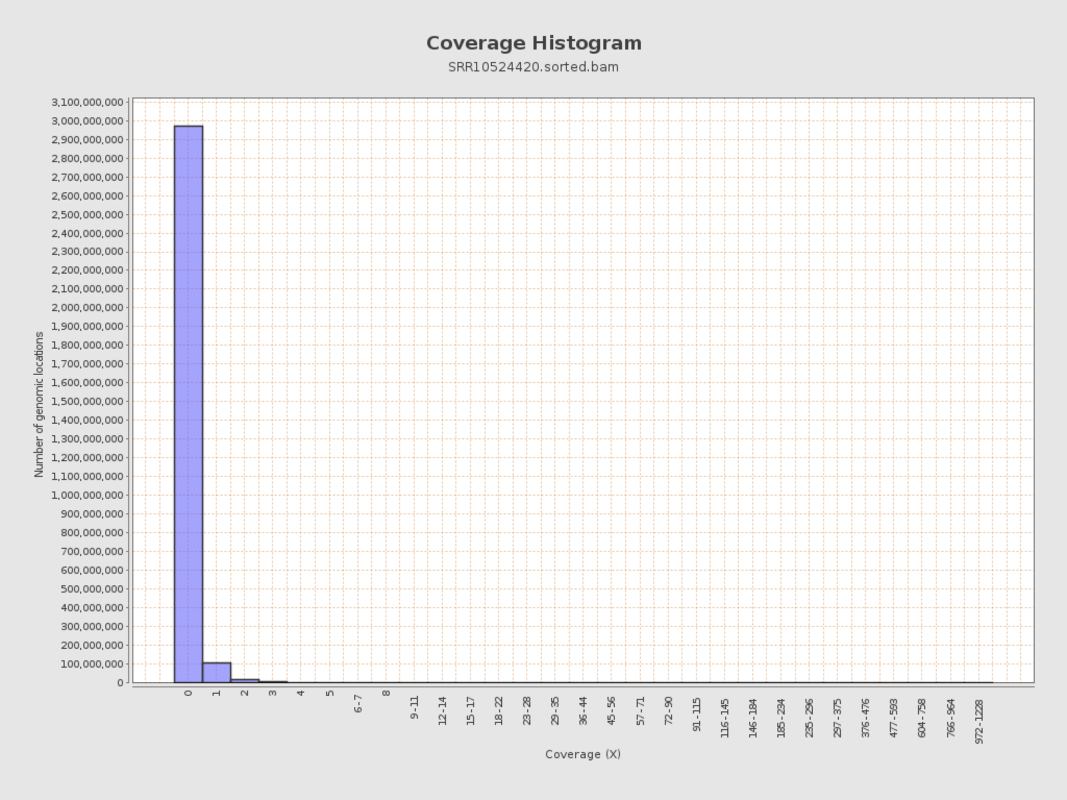
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12069307	0.0484	0.875
chr2	243199373	12933777	0.0532	0.6516
chr3	198022430	9424277	0.0476	0.2619
chr4	191154276	9844940	0.0515	0.4008
chr5	180915260	9176516	0.0507	0.2664
chr6	171115067	8158896	0.0477	0.29
chr7	159138663	8575065	0.0539	0.6153

chr8	146364022	7755429	0.053	0.3555
chr9	141213431	6598419	0.0467	0.3377
chr10	135534747	7224877	0.0533	0.537
chr11	135006516	7024536	0.052	0.3851
chr12	133851895	6468340	0.0483	0.2686
chr13	115169878	4538754	0.0394	0.2374
chr14	107349540	4633499	0.0432	0.2594
chr15	102531392	4739524	0.0462	0.2572
chr16	90354753	4802805	0.0532	0.3118
chr17	81195210	4390859	0.0541	0.3072
chr18	78077248	3922231	0.0502	0.6338
chr19	59128983	3530378	0.0597	0.5903
chr20	63025520	3567905	0.0566	0.3033
chr21	48129895	2231978	0.0464	0.3612
chr22	51304566	2392948	0.0466	0.2647
chrMT	16571	35467	2.1403	2.1215
chrX	155270560	8290139	0.0534	0.3133
chrY	59373566	579978	0.0098	0.34

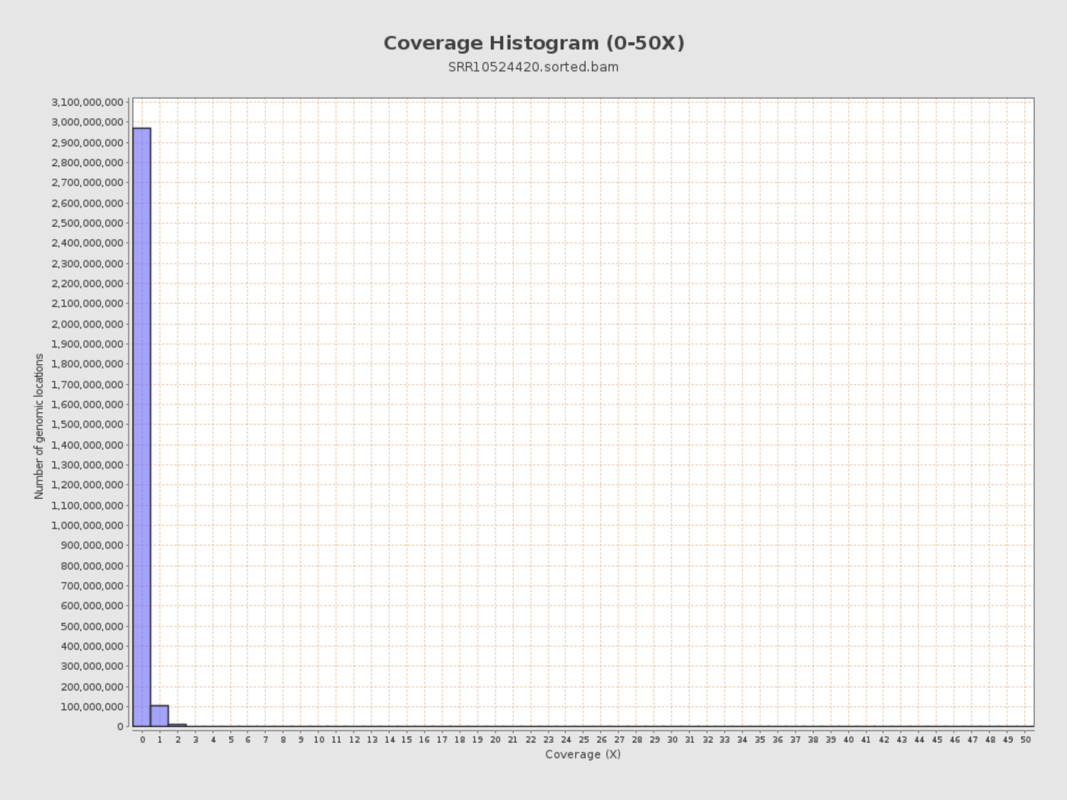
3. Results : Coverage across reference



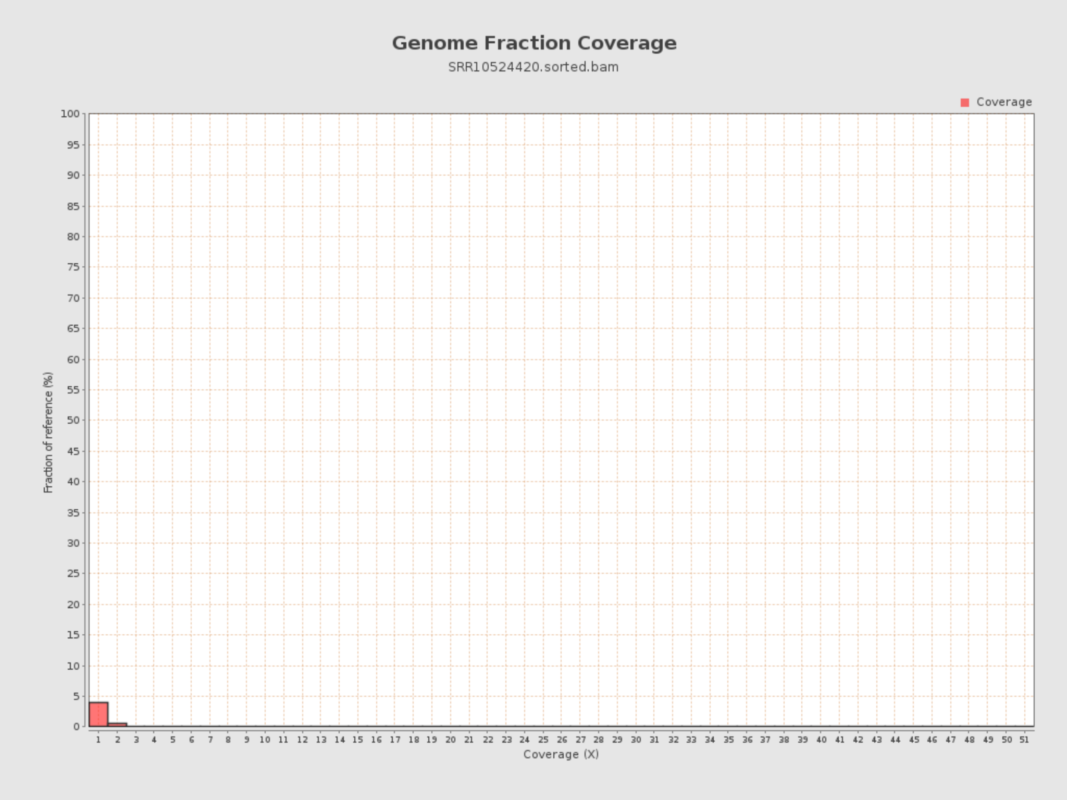
4. Results : Coverage Histogram



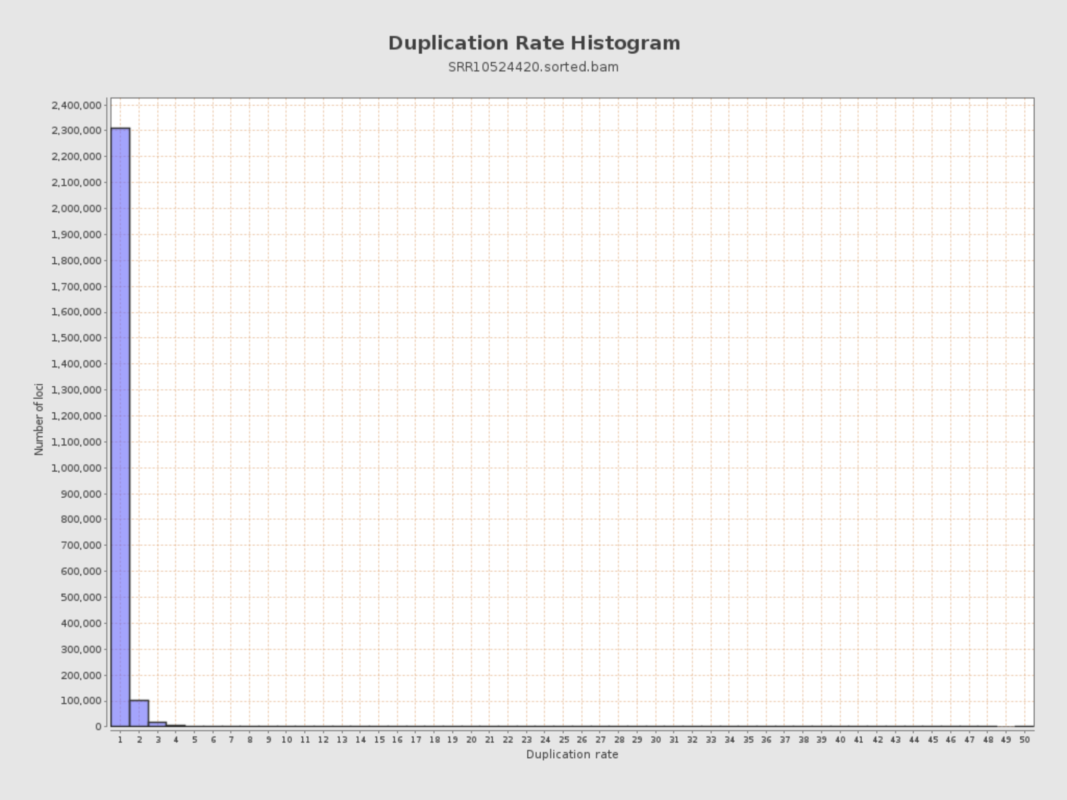
5. Results : Coverage Histogram (0-50X)



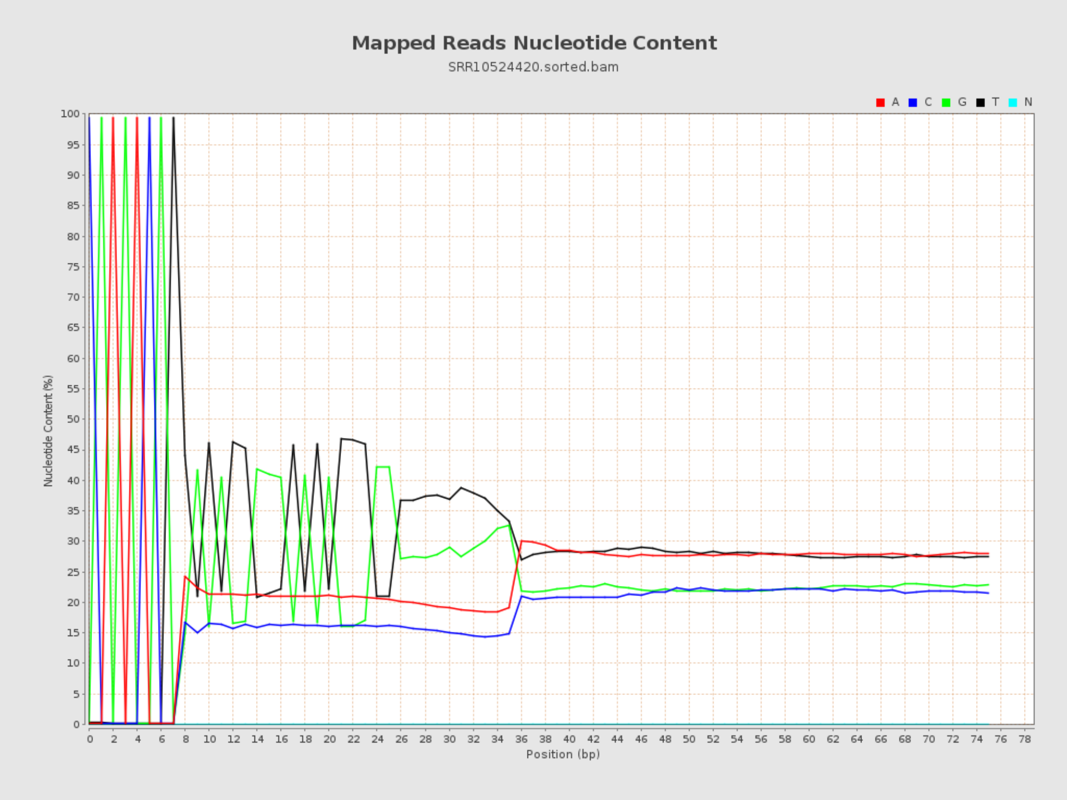
6. Results : Genome Fraction Coverage



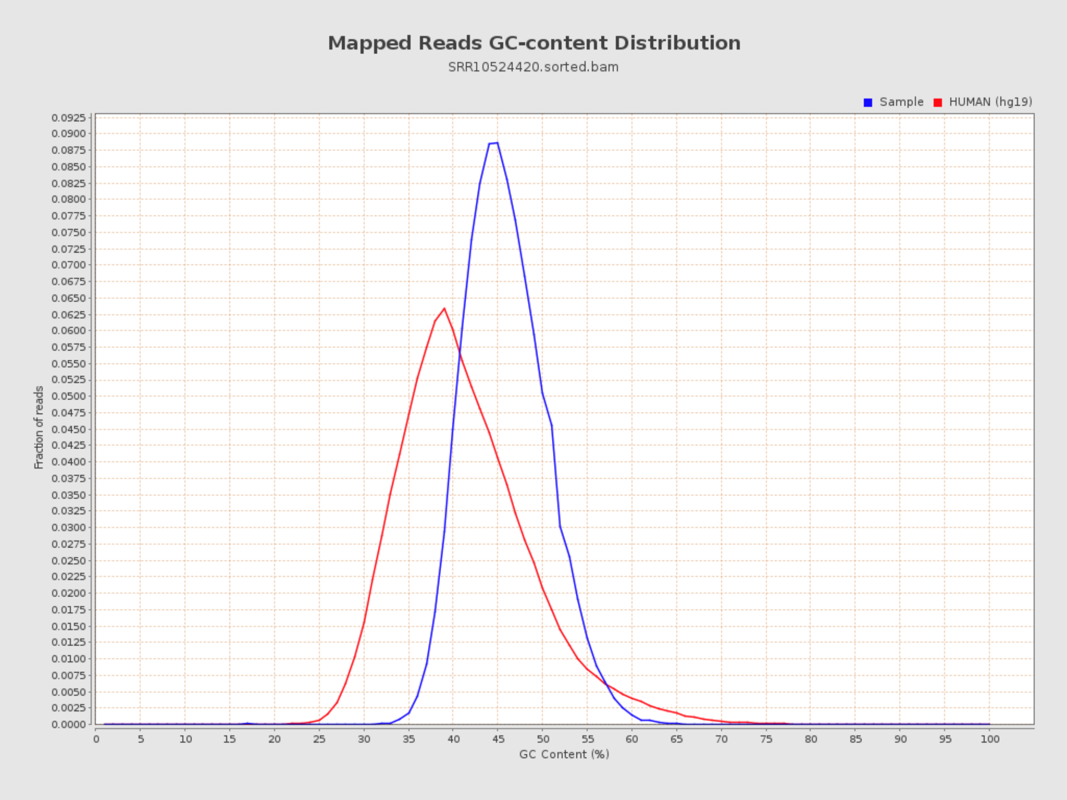
7. Results : Duplication Rate Histogram



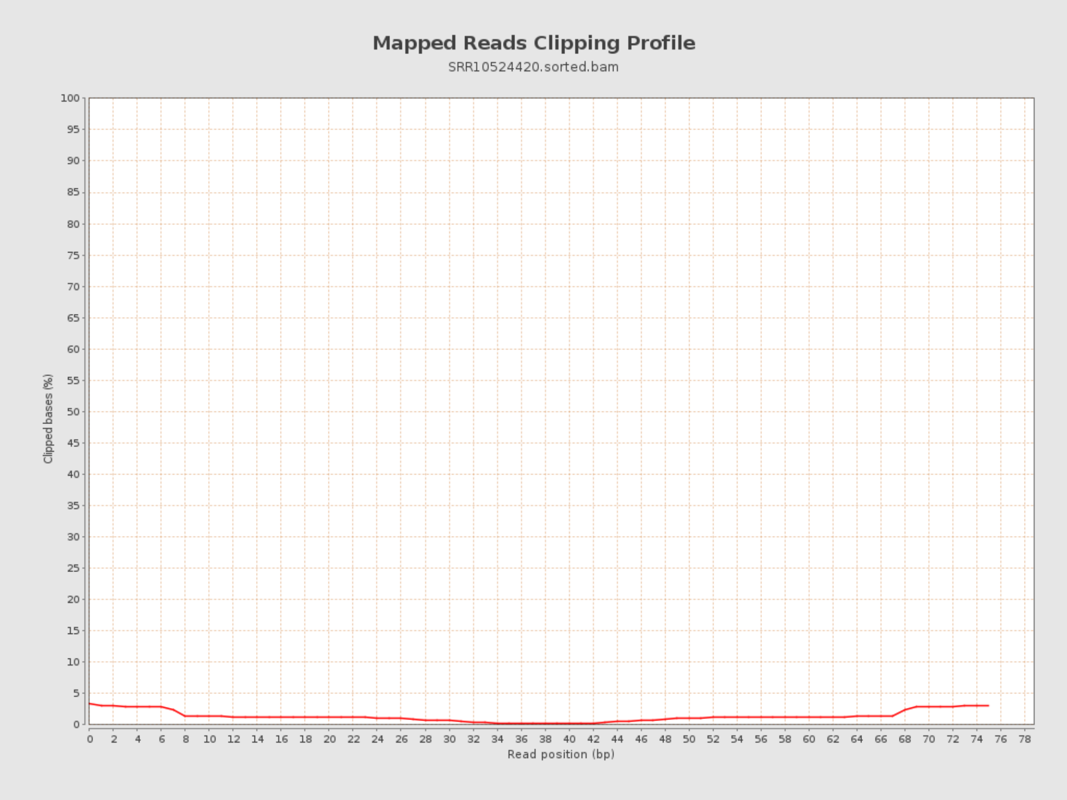
8. Results : Mapped Reads Nucleotide Content



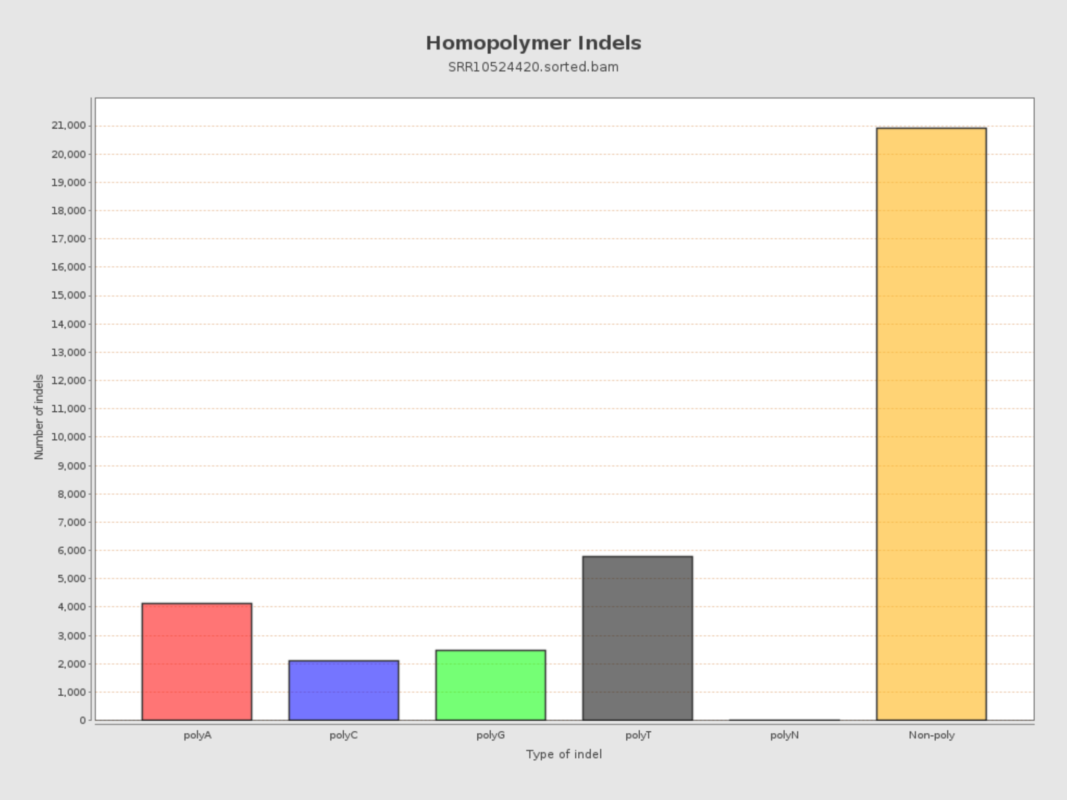
9. Results : Mapped Reads GC-content Distribution



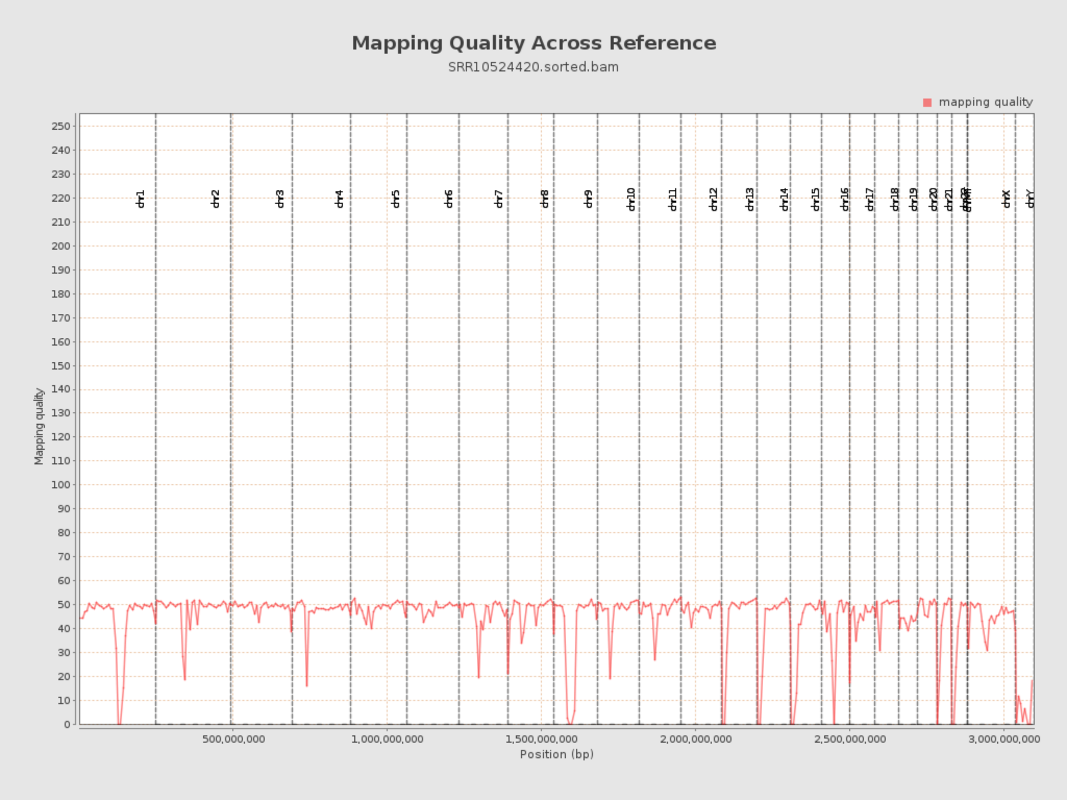
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram