Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:40:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524343.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_SRR10524343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:40:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,732,561
Mapped reads	1,588,893 / 91.71%
Unmapped reads	143,668 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,252 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	66,624 / 3.85%
Duplication rate	3%
Clipped reads	1,591,383 / 91.85%

2.2. ACGT Content

Number/percentage of A's	22,586,550 / 24.38%
Number/percentage of C's	18,405,815 / 19.86%
Number/percentage of T's	28,873,240 / 31.16%
Number/percentage of G's	22,778,499 / 24.58%
Number/percentage of N's	12,964 / 0.01%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.2962

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

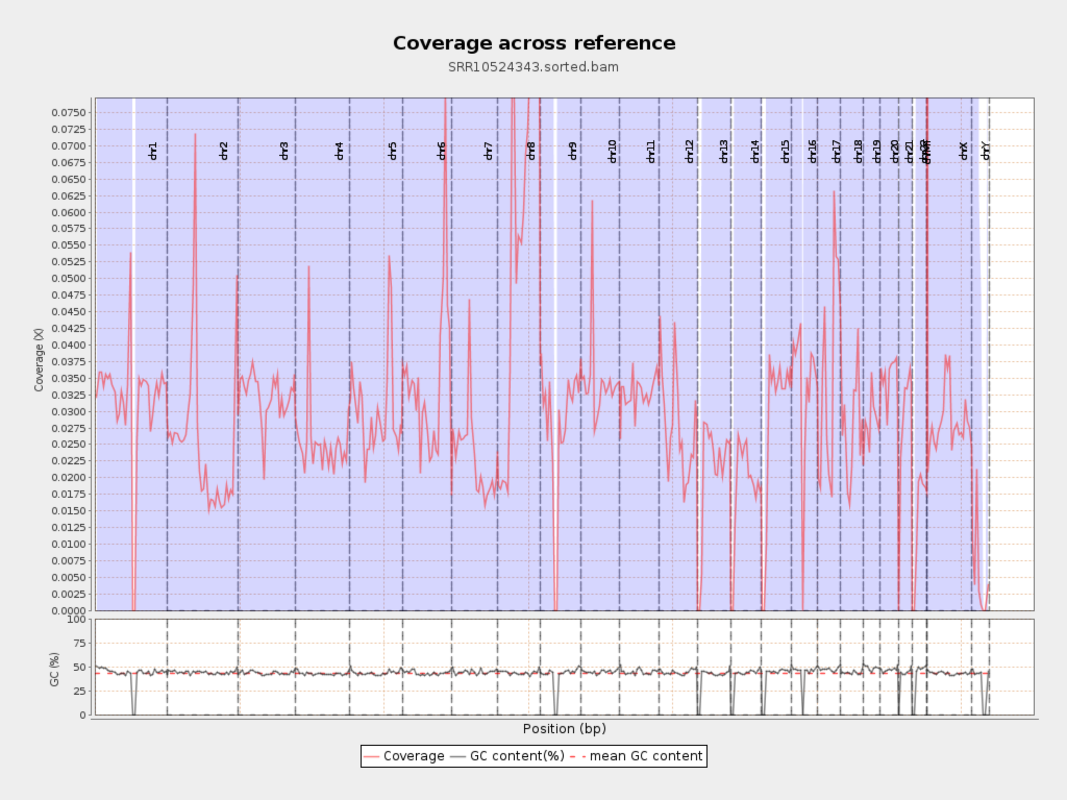
General error rate	0.53%
Mismatches	479,227
Insertions	6,405
Mapped reads with at least one insertion	0.4%
Deletions	16,734
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.3%

2.6. Chromosome stats

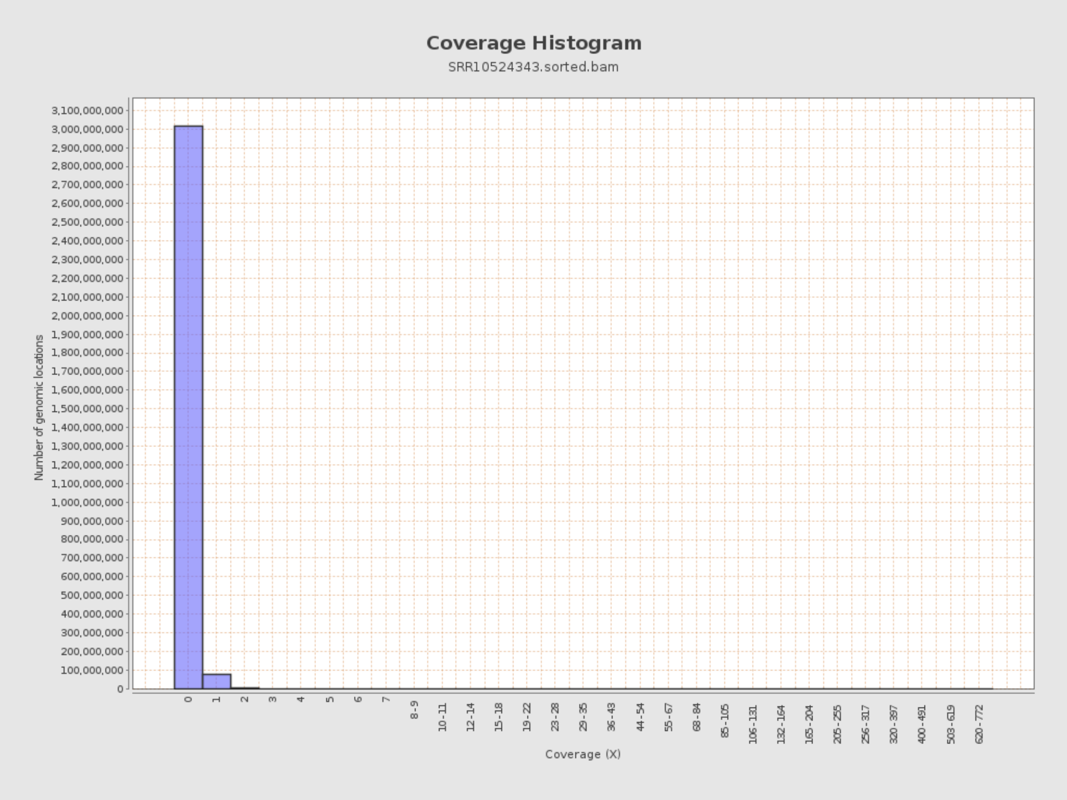
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7832086	0.0314	0.5646
chr2	243199373	6099533	0.0251	0.3754
chr3	198022430	6394080	0.0323	0.1952
chr4	191154276	4869870	0.0255	0.2212
chr5	180915260	5470107	0.0302	0.1909
chr6	171115067	5878230	0.0344	0.2168
chr7	159138663	3708994	0.0233	0.3438

chr8	146364022	9681501	0.0661	0.3894
chr9	141213431	3897036	0.0276	0.2376
chr10	135534747	4699495	0.0347	0.3053
chr11	135006516	4444748	0.0329	0.2456
chr12	133851895	3681147	0.0275	0.1857
chr13	115169878	2357784	0.0205	0.1578
chr14	107349540	1969354	0.0183	0.1541
chr15	102531392	2892853	0.0282	0.1822
chr16	90354753	3000363	0.0332	0.2095
chr17	81195210	2917727	0.0359	0.2259
chr18	78077248	2163217	0.0277	0.3903
chr19	59128983	1694767	0.0287	0.3687
chr20	63025520	2216847	0.0352	0.2085
chr21	48129895	1366257	0.0284	0.2214
chr22	51304566	702174	0.0137	0.1281
chrMT	16571	14827	0.8948	1.1591
chrX	155270560	4422196	0.0285	0.2086
chrY	59373566	308356	0.0052	0.1874

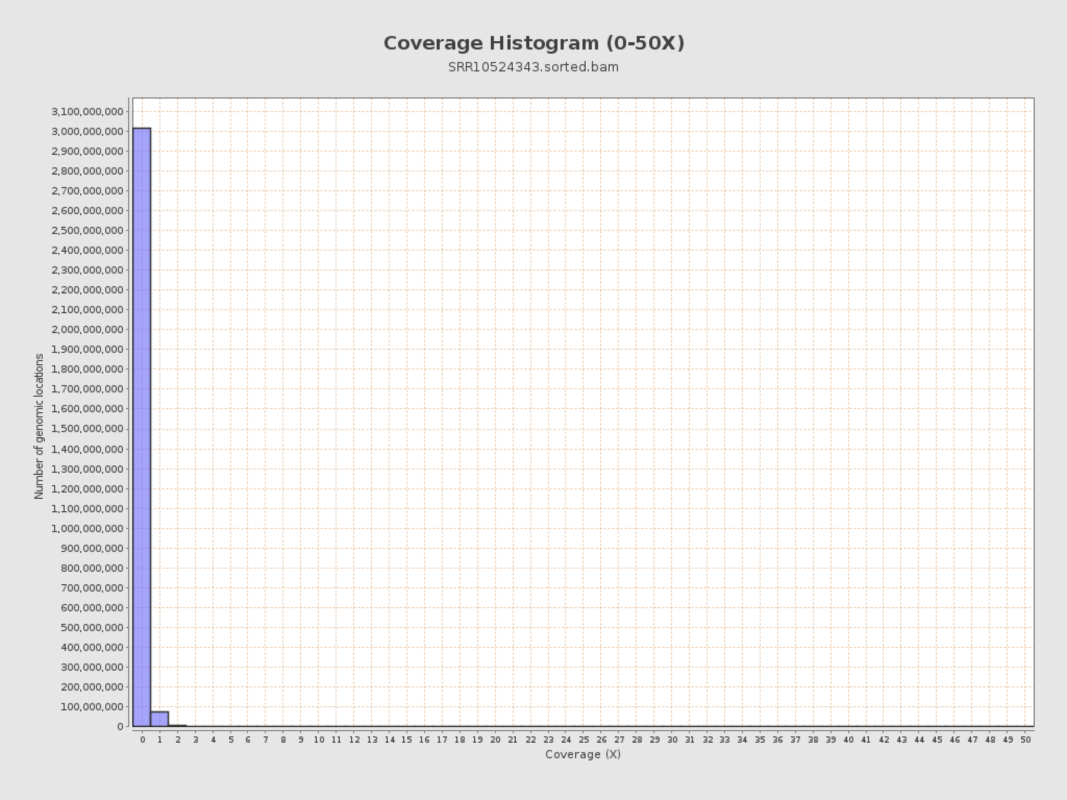
3. Results : Coverage across reference



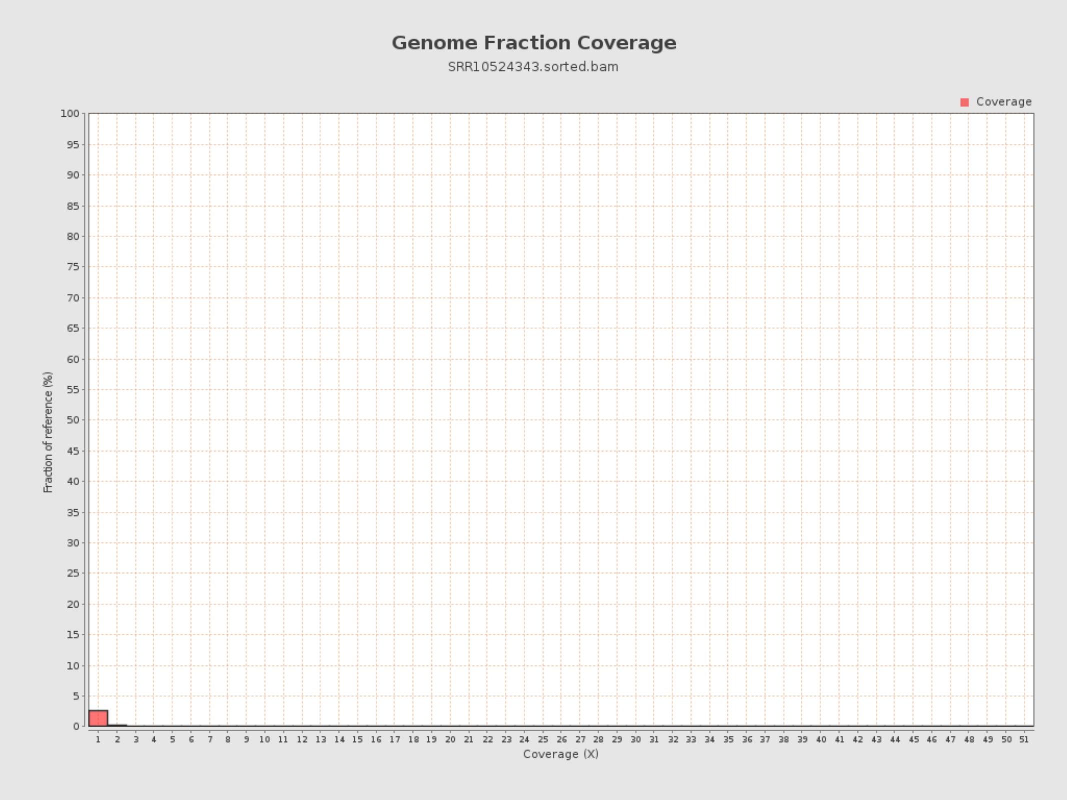
4. Results : Coverage Histogram



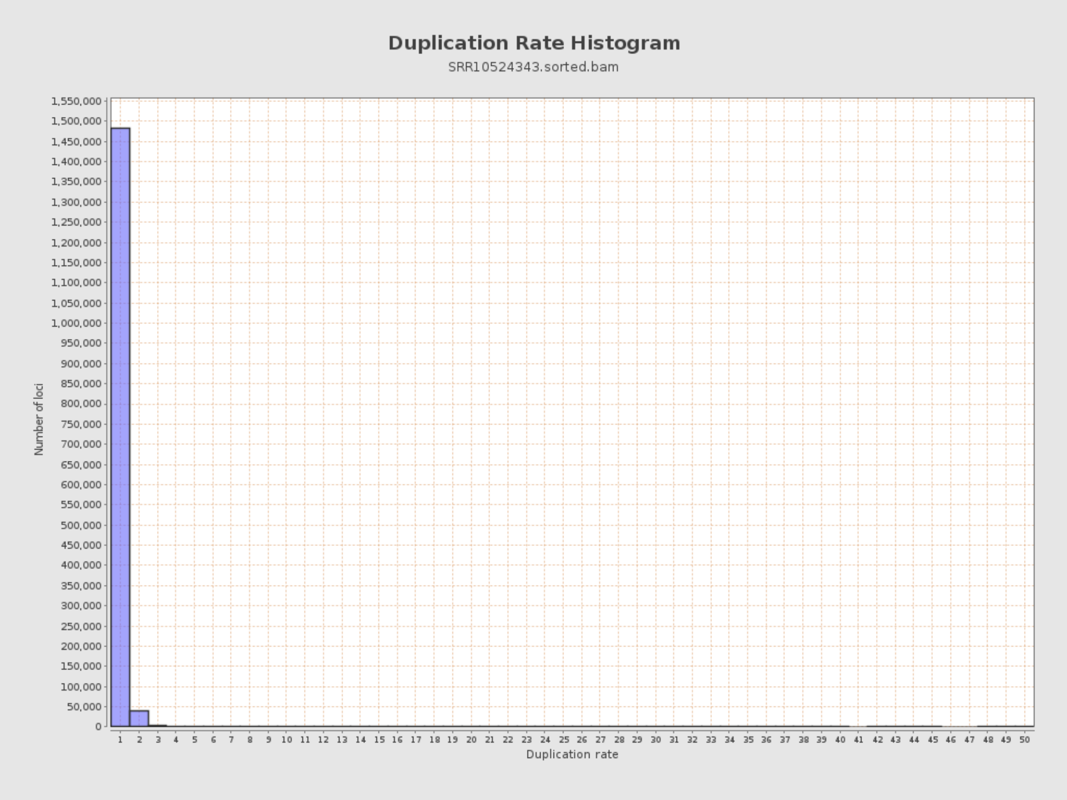
5. Results : Coverage Histogram (0-50X)



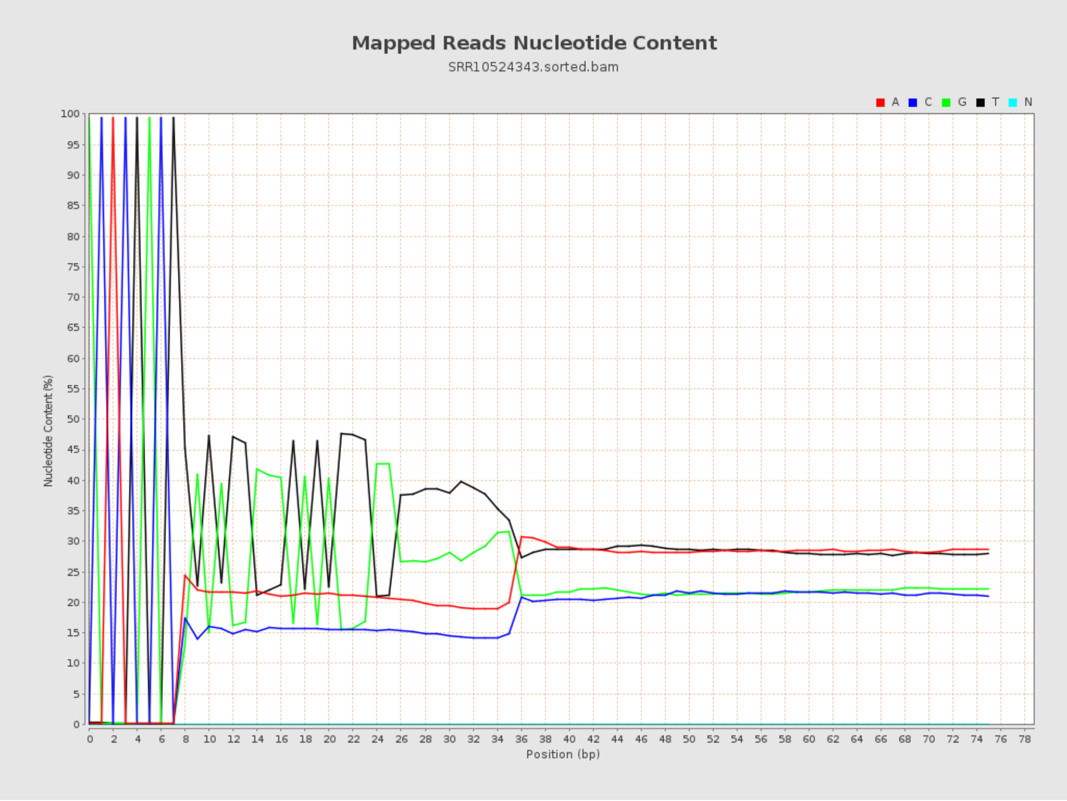
6. Results : Genome Fraction Coverage



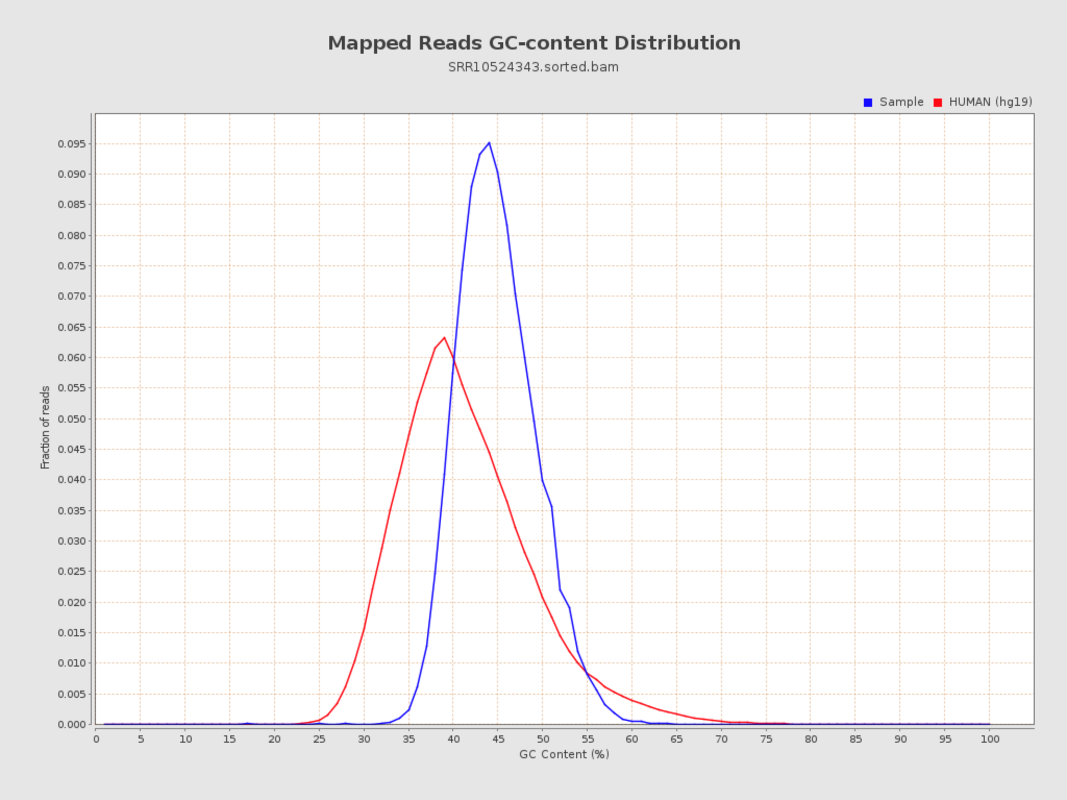
7. Results : Duplication Rate Histogram



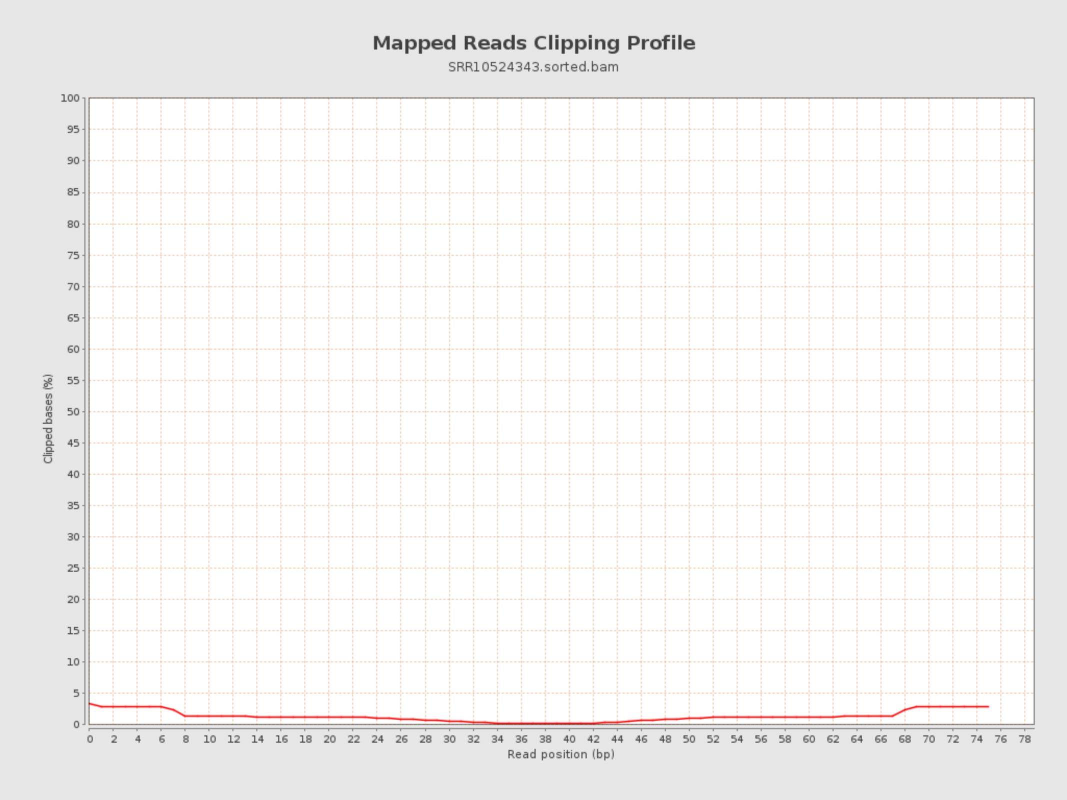
8. Results : Mapped Reads Nucleotide Content



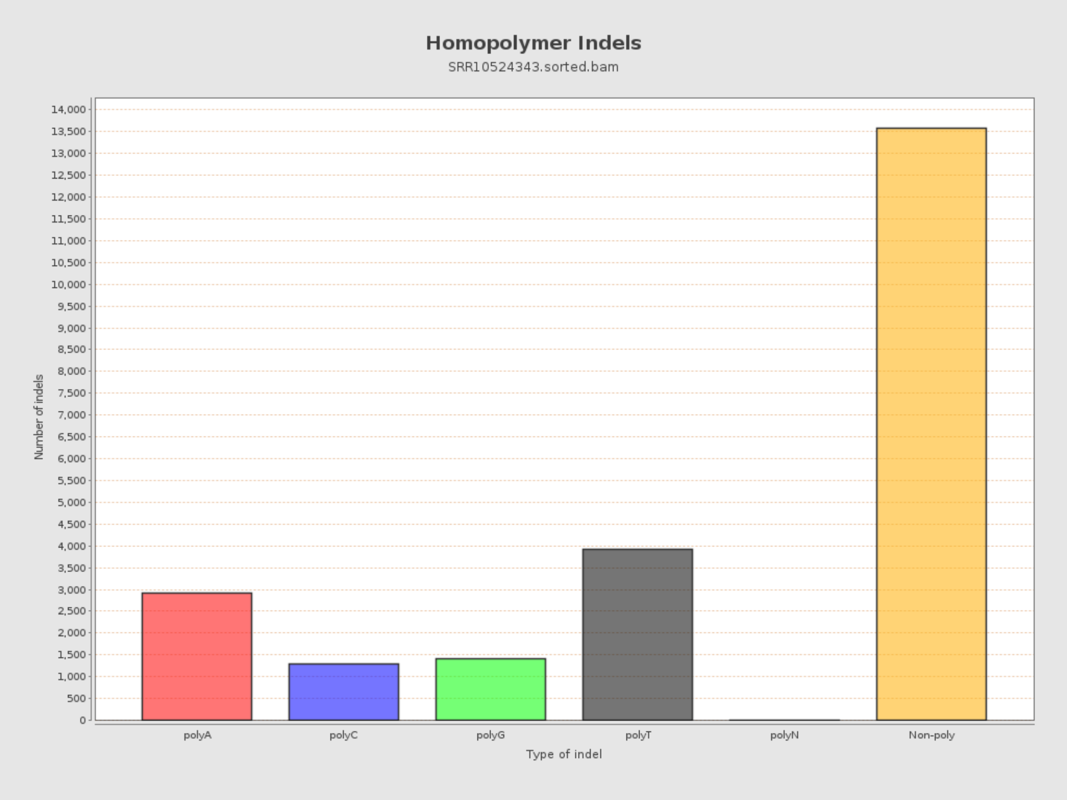
9. Results : Mapped Reads GC-content Distribution



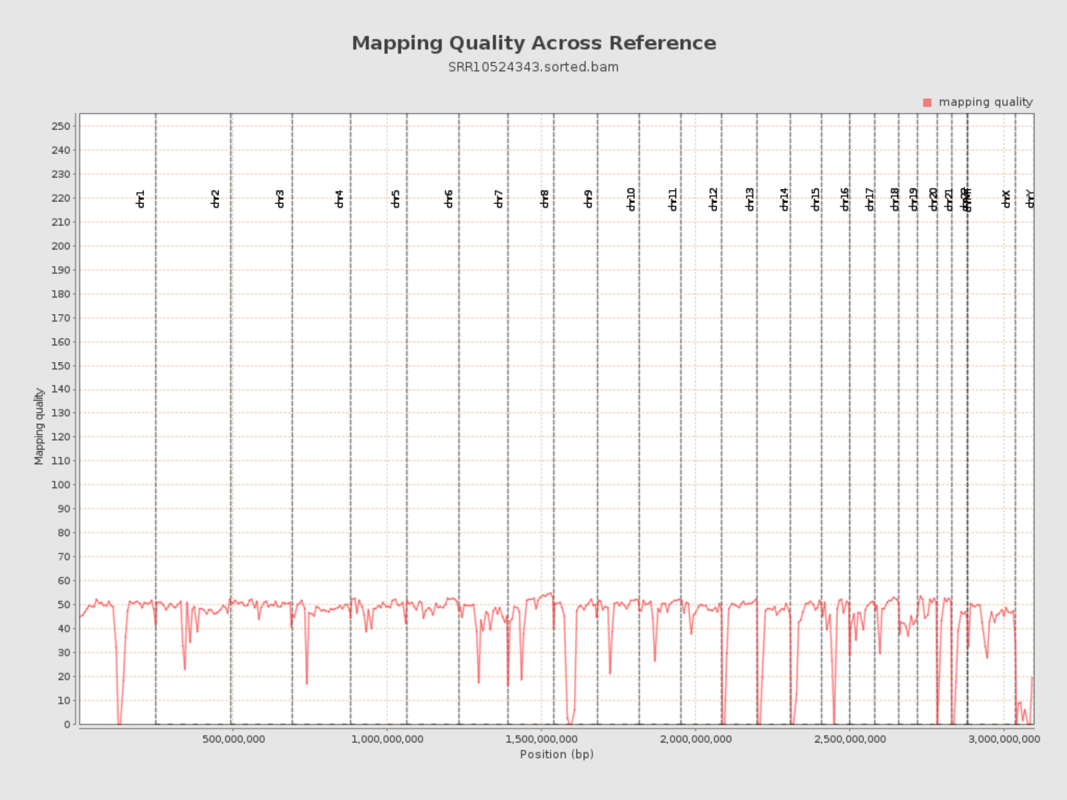
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram