Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:44:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524952.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_SRR10524952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:44:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,308,270
Mapped reads	2,138,672 / 92.65%
Unmapped reads	169,598 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,310 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	78,697 / 3.41%
Duplication rate	2.62%
Clipped reads	2,138,526 / 92.65%

2.2. ACGT Content

Number/percentage of A's	31,013,319 / 24.92%
Number/percentage of C's	22,944,910 / 18.44%
Number/percentage of T's	39,721,523 / 31.92%
Number/percentage of G's	30,750,630 / 24.71%
Number/percentage of N's	1,428 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3417

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

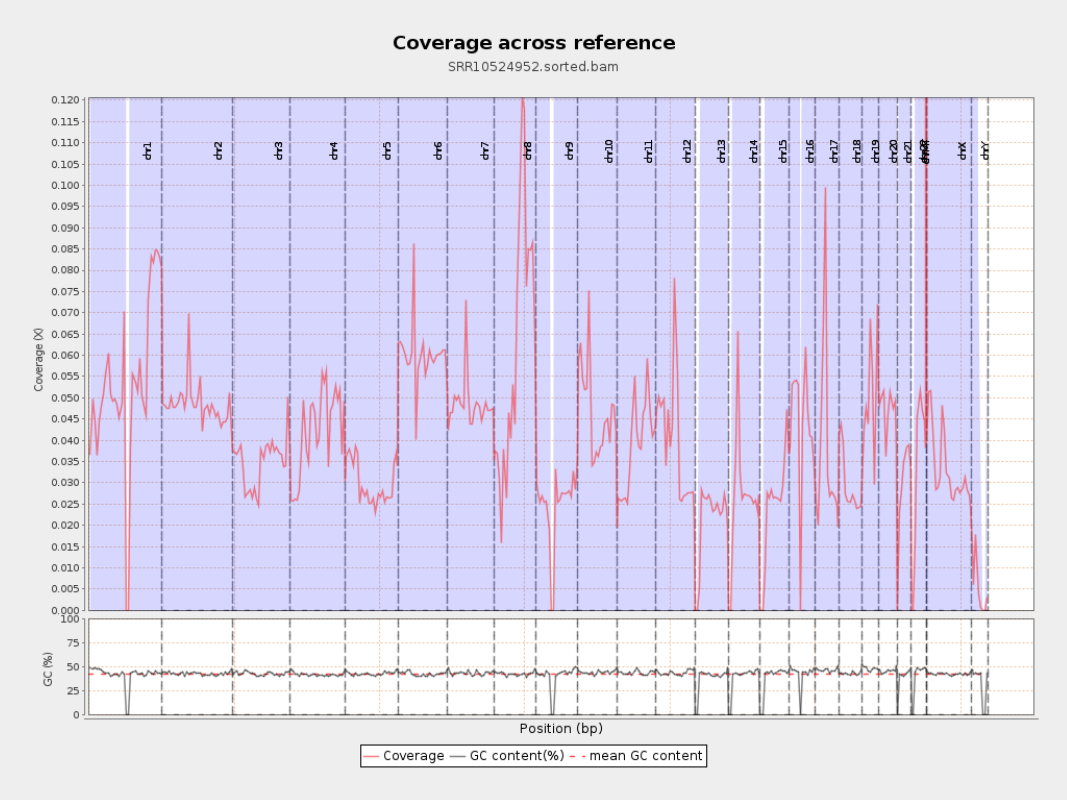
General error rate	0.49%
Mismatches	596,278
Insertions	7,997
Mapped reads with at least one insertion	0.37%
Deletions	23,879
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.66%

2.6. Chromosome stats

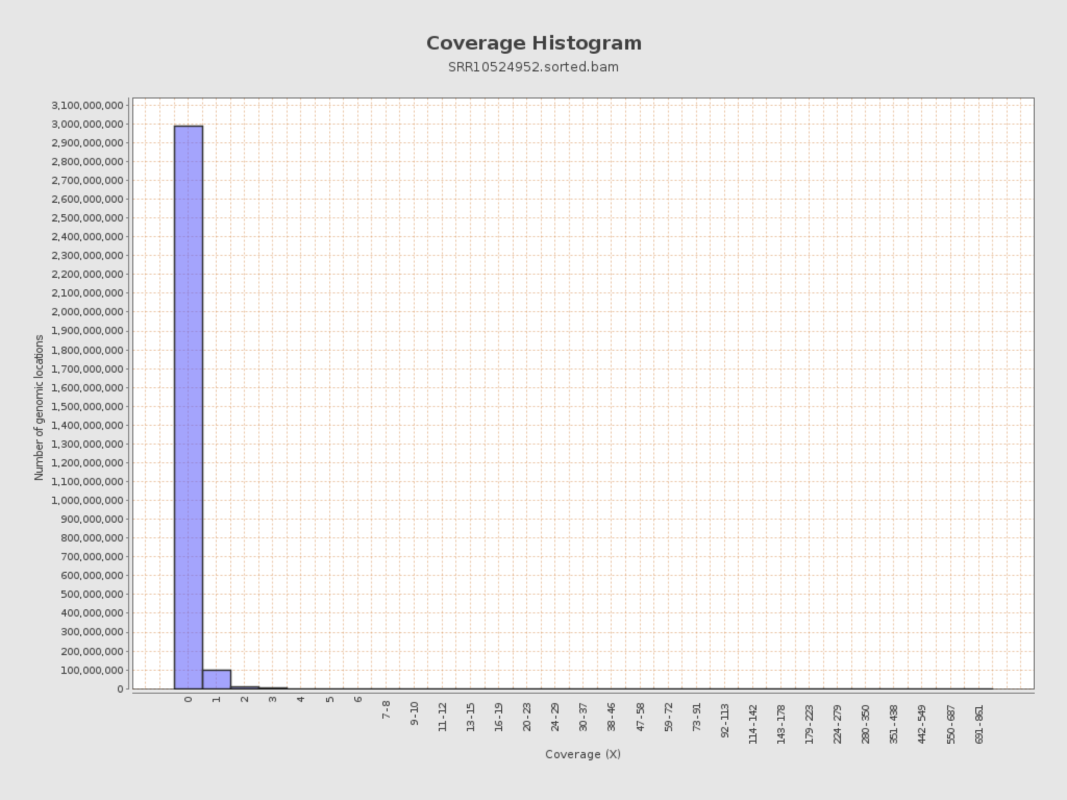
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13149677	0.0528	0.6532
chr2	243199373	11796293	0.0485	0.3949
chr3	198022430	6897196	0.0348	0.2094
chr4	191154276	8040627	0.0421	0.2501
chr5	180915260	5422619	0.03	0.1971
chr6	171115067	10287586	0.0601	0.3954
chr7	159138663	7754233	0.0487	0.483

chr8	146364022	9029721	0.0617	0.3484
chr9	141213431	3422012	0.0242	0.2587
chr10	135534747	6350086	0.0469	0.3388
chr11	135006516	5197371	0.0385	0.2979
chr12	133851895	5310545	0.0397	0.2234
chr13	115169878	2428938	0.0211	0.1651
chr14	107349540	2828210	0.0263	0.1868
chr15	102531392	2505776	0.0244	0.2041
chr16	90354753	3939631	0.0436	0.244
chr17	81195210	3146132	0.0387	0.3058
chr18	78077248	2304869	0.0295	0.3985
chr19	59128983	2991495	0.0506	0.3954
chr20	63025520	2968747	0.0471	0.2428
chr21	48129895	1429855	0.0297	0.2045
chr22	51304566	1659750	0.0324	0.1977
chrMT	16571	33164	2.0013	1.8789
chrX	155270560	5253578	0.0338	0.2426
chrY	59373566	324367	0.0055	0.1286

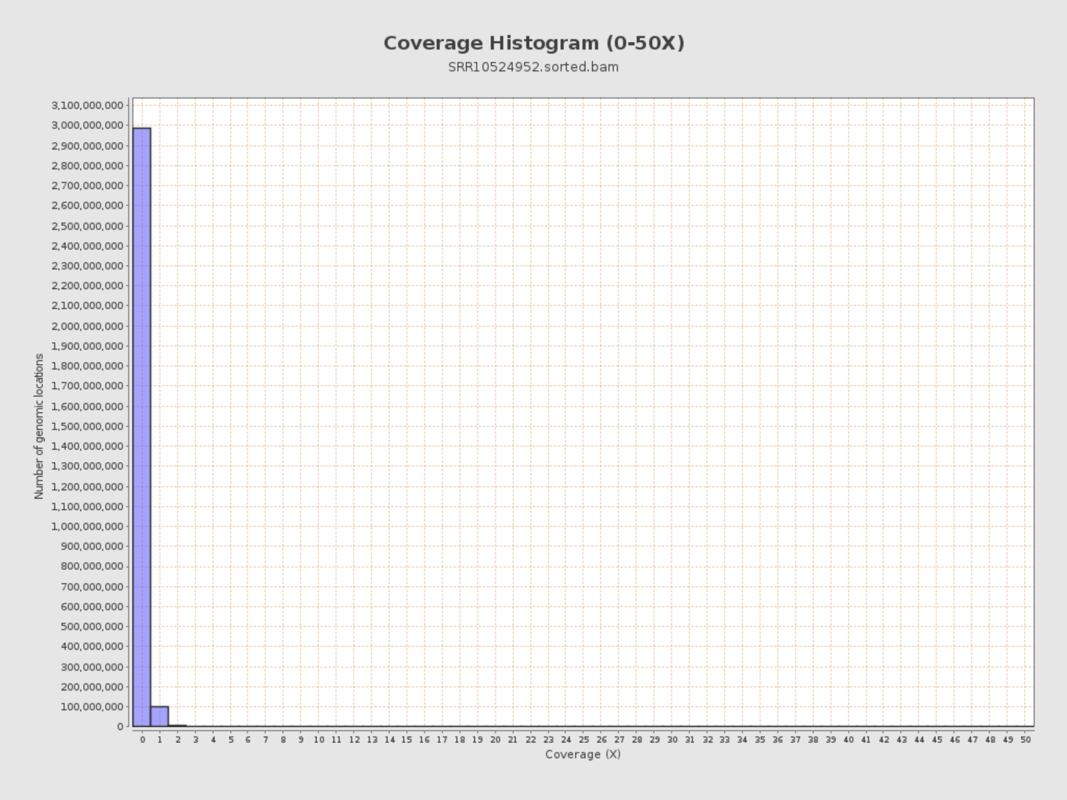
3. Results : Coverage across reference



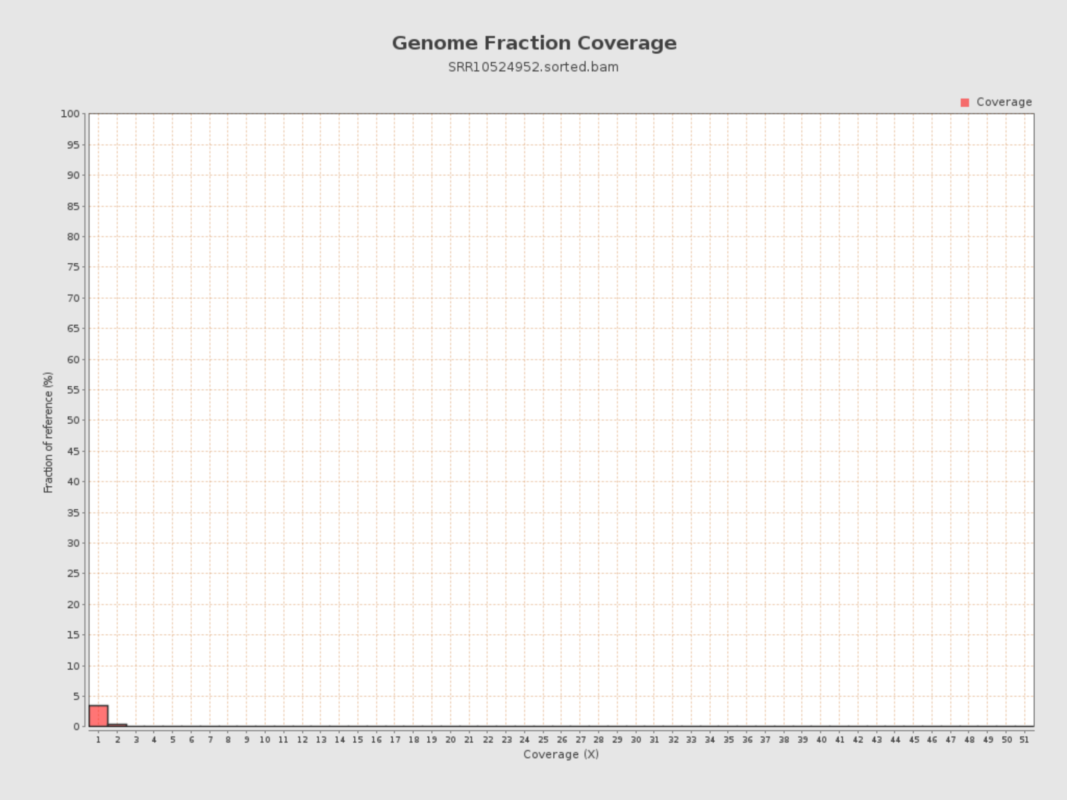
4. Results : Coverage Histogram



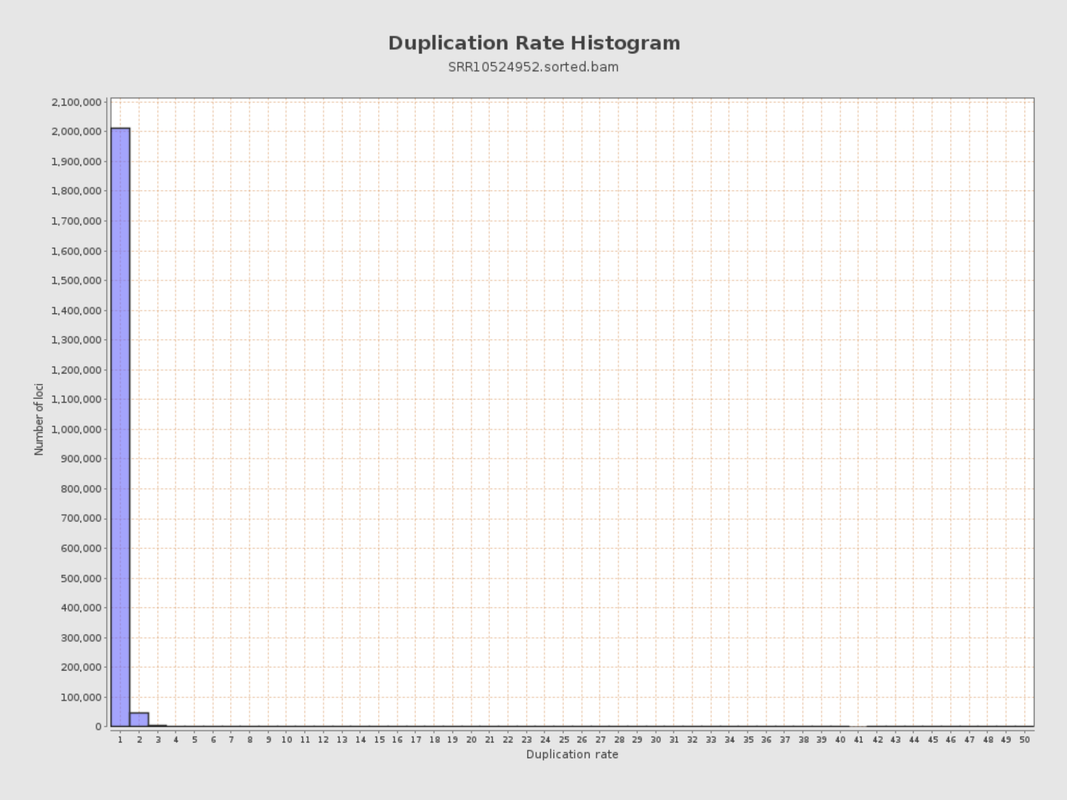
5. Results : Coverage Histogram (0-50X)



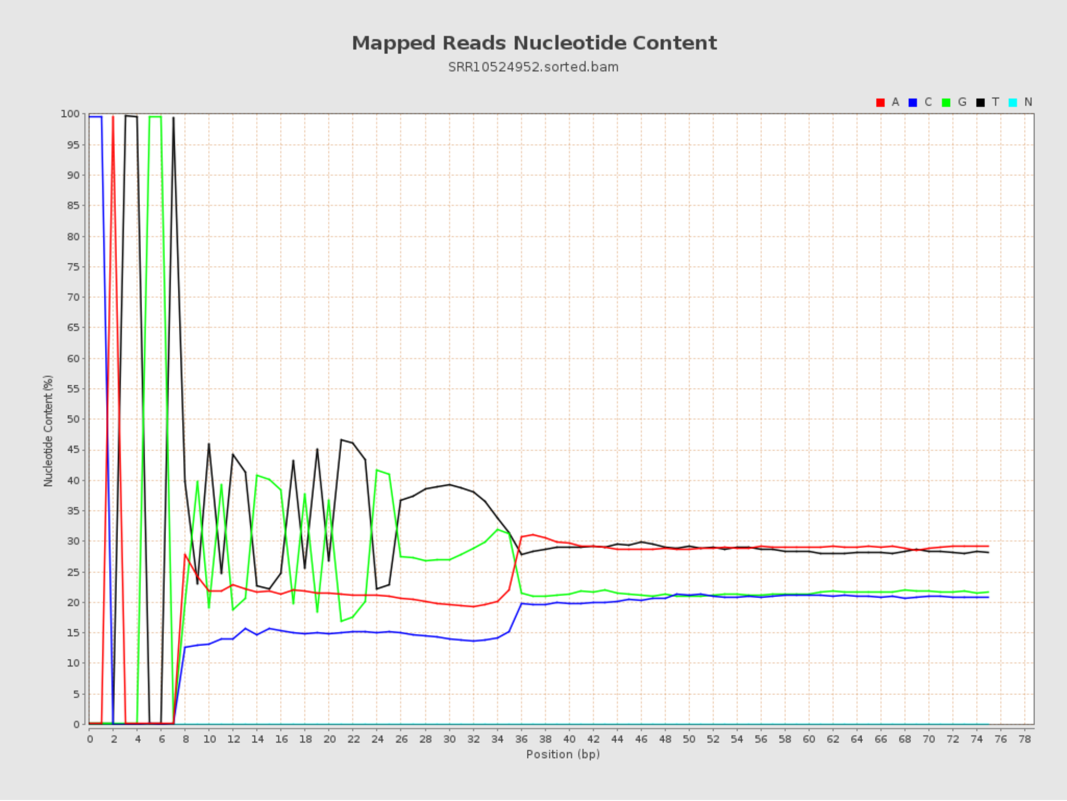
6. Results : Genome Fraction Coverage



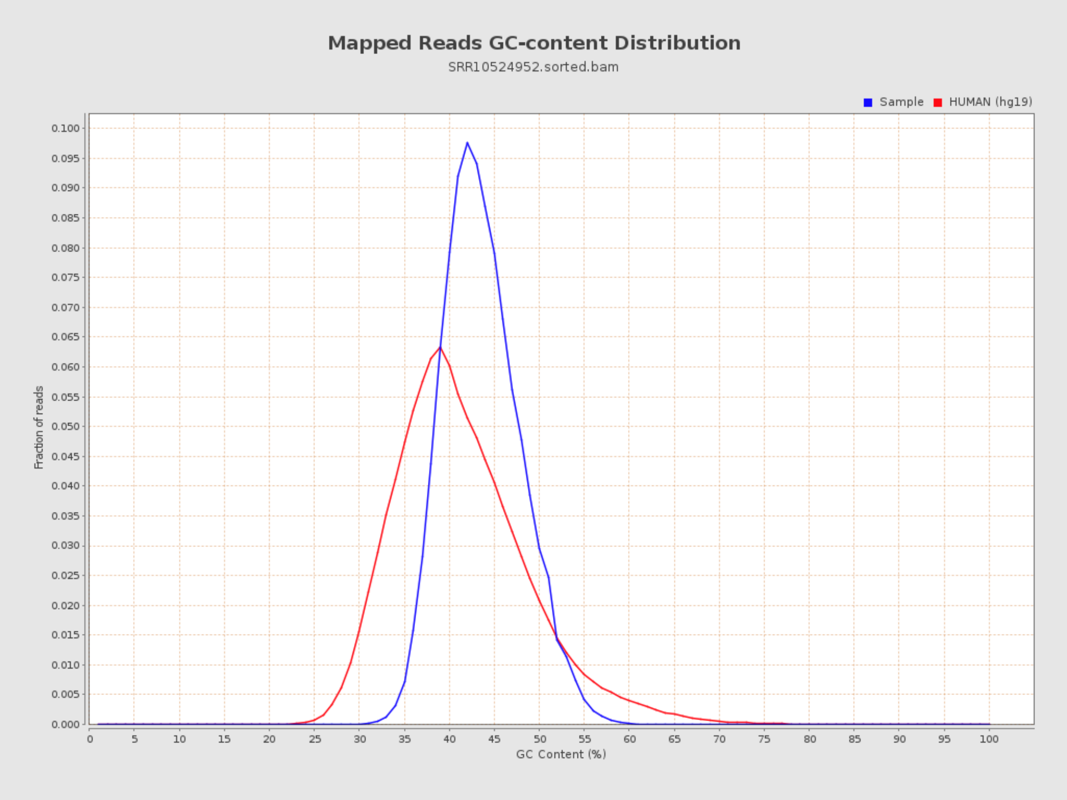
7. Results : Duplication Rate Histogram



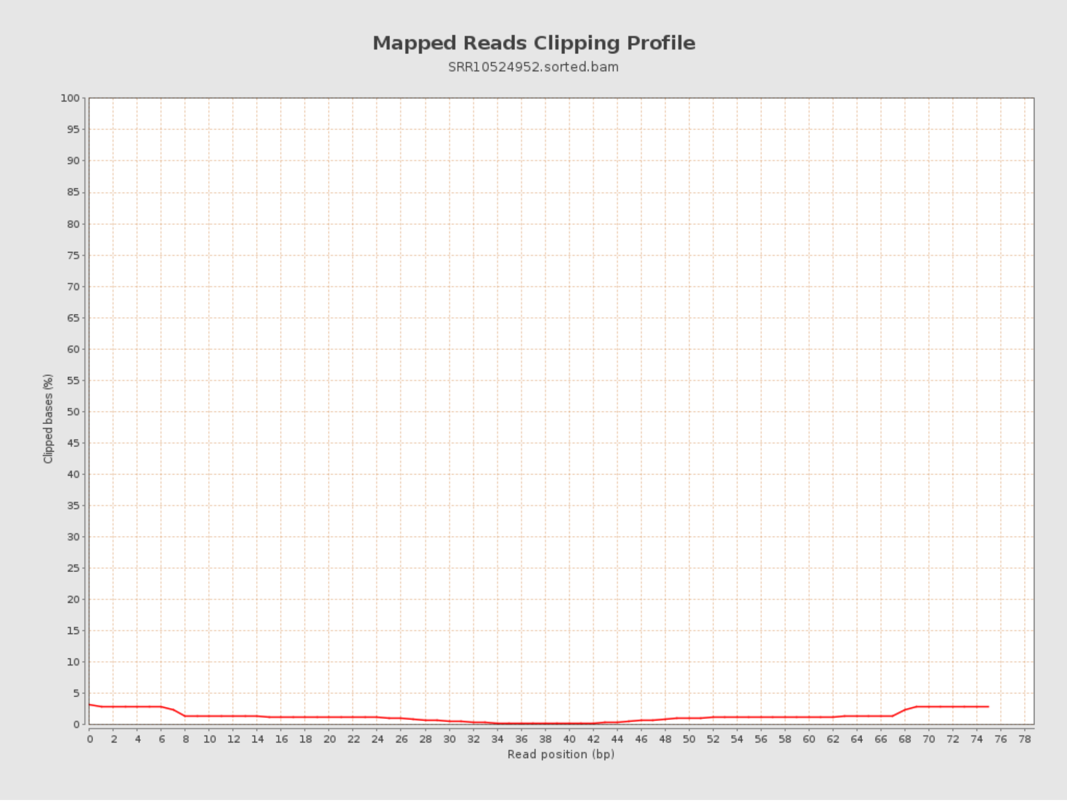
8. Results : Mapped Reads Nucleotide Content



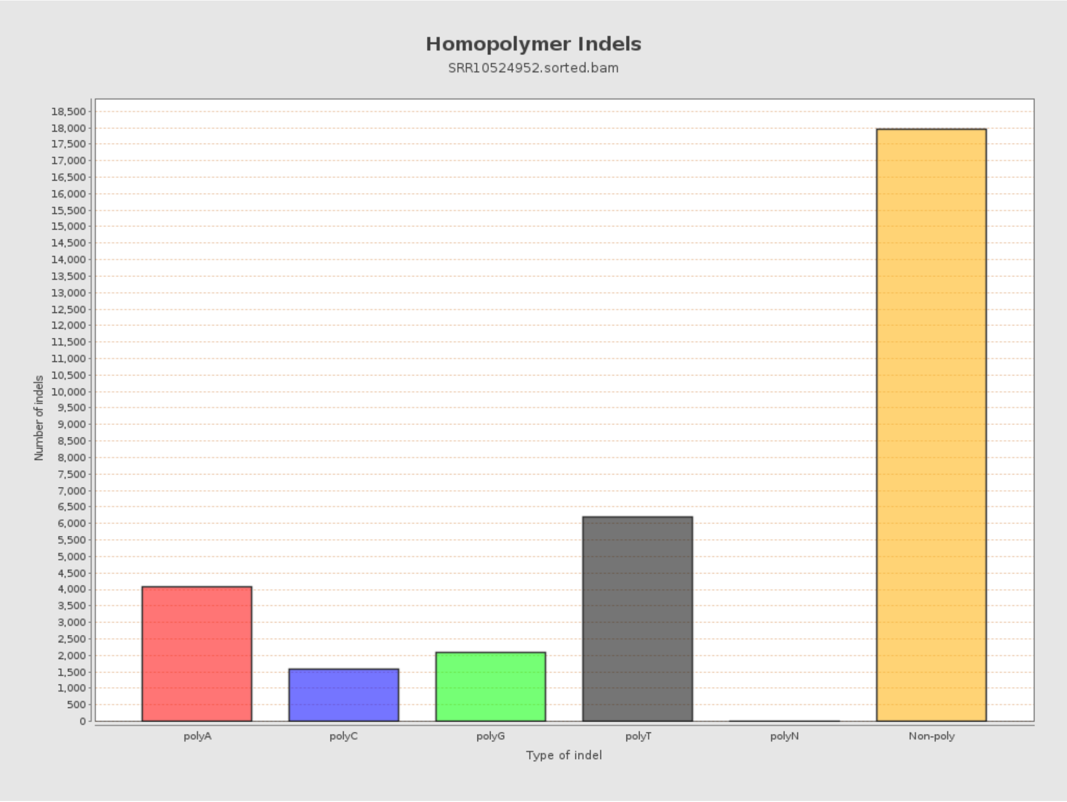
9. Results : Mapped Reads GC-content Distribution



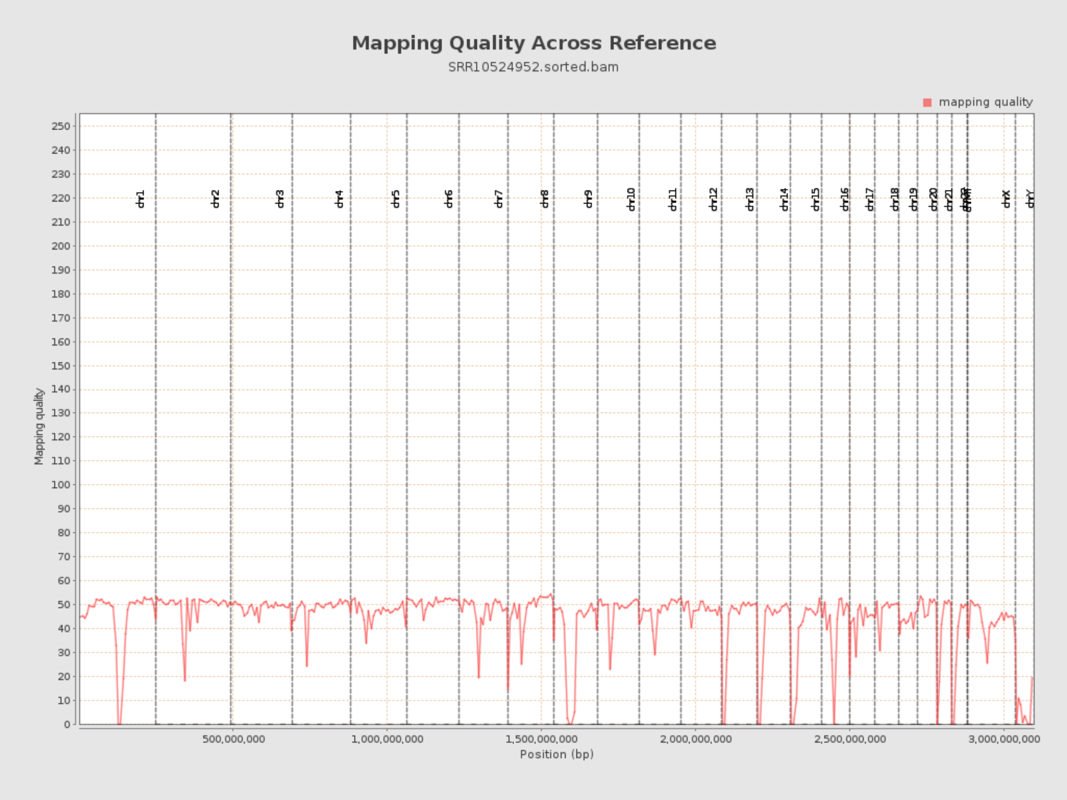
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram