Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:22:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524570.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_SRR10524570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:22:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,861,182
Mapped reads	2,607,960 / 91.15%
Unmapped reads	253,222 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,435 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	144,813 / 5.06%
Duplication rate	4.15%
Clipped reads	2,610,716 / 91.25%

2.2. ACGT Content

Number/percentage of A's	38,271,951 / 25.33%
Number/percentage of C's	28,218,280 / 18.68%
Number/percentage of T's	48,666,364 / 32.21%
Number/percentage of G's	35,934,641 / 23.78%
Number/percentage of N's	2,335 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.4165

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

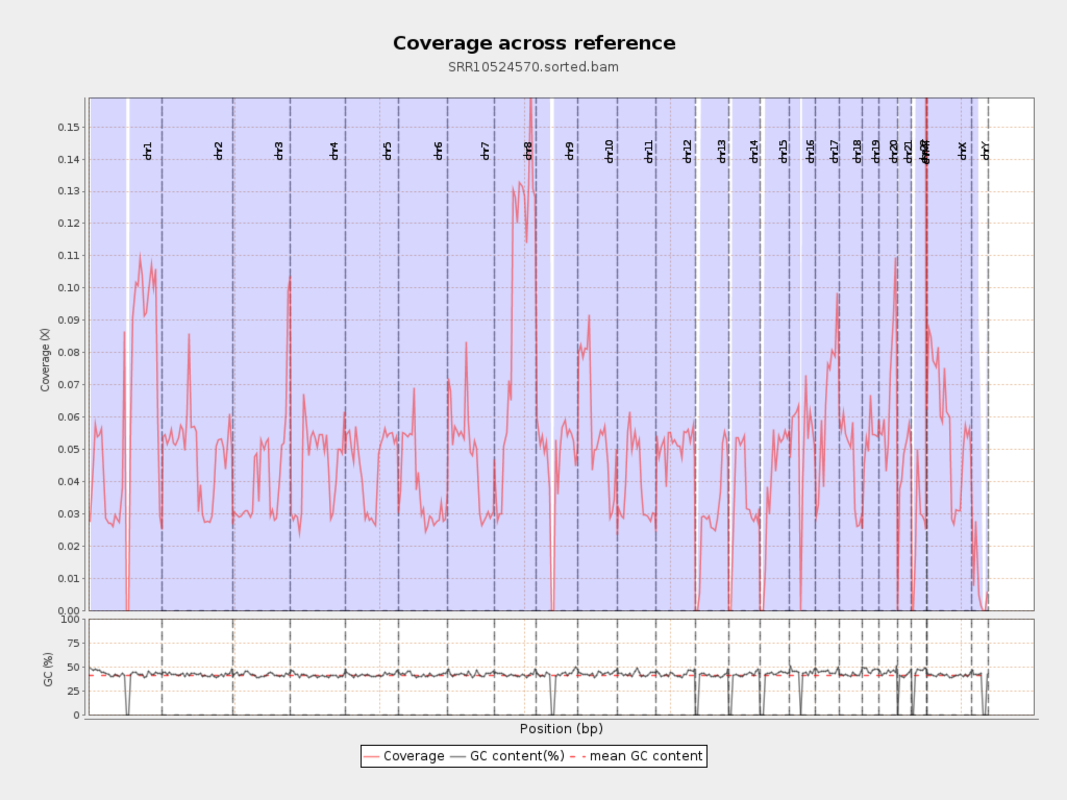
General error rate	0.52%
Mismatches	770,668
Insertions	9,754
Mapped reads with at least one insertion	0.37%
Deletions	28,858
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.49%

2.6. Chromosome stats

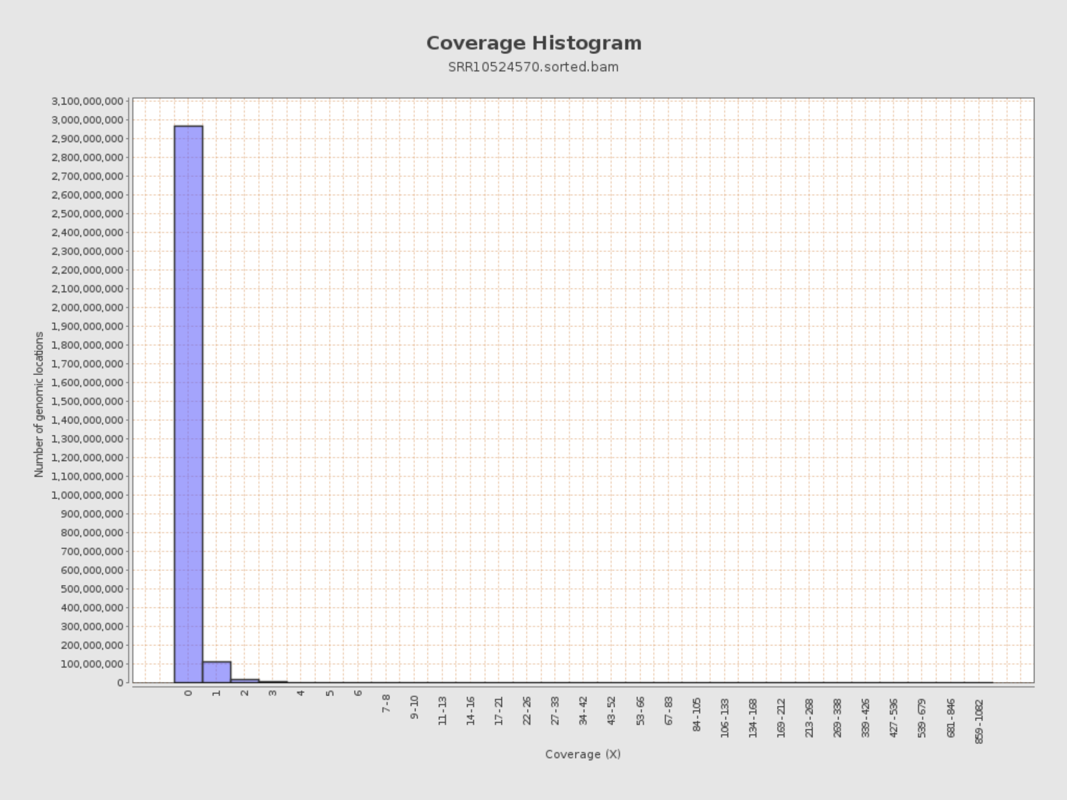
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14789460	0.0593	0.8205
chr2	243199373	11916704	0.049	0.4834
chr3	198022430	8232275	0.0416	0.2399
chr4	191154276	8590630	0.0449	0.2921
chr5	180915260	8272925	0.0457	0.2468
chr6	171115067	6481155	0.0379	0.3066
chr7	159138663	7600893	0.0478	0.5397

chr8	146364022	13901478	0.095	0.4338
chr9	141213431	6438659	0.0456	0.3501
chr10	135534747	7891621	0.0582	0.4216
chr11	135006516	5263865	0.039	0.397
chr12	133851895	6955479	0.052	0.2652
chr13	115169878	3366122	0.0292	0.199
chr14	107349540	3617687	0.0337	0.2195
chr15	102531392	3969654	0.0387	0.2389
chr16	90354753	4755333	0.0526	0.2918
chr17	81195210	5235744	0.0645	0.3166
chr18	78077248	3586651	0.0459	0.6385
chr19	59128983	3120889	0.0528	0.5302
chr20	63025520	4314424	0.0685	0.3085
chr21	48129895	2093588	0.0435	0.2712
chr22	51304566	1241521	0.0242	0.1784
chrMT	16571	105987	6.3959	4.2679
chrX	155270560	8913673	0.0574	0.322
chrY	59373566	484953	0.0082	0.2221

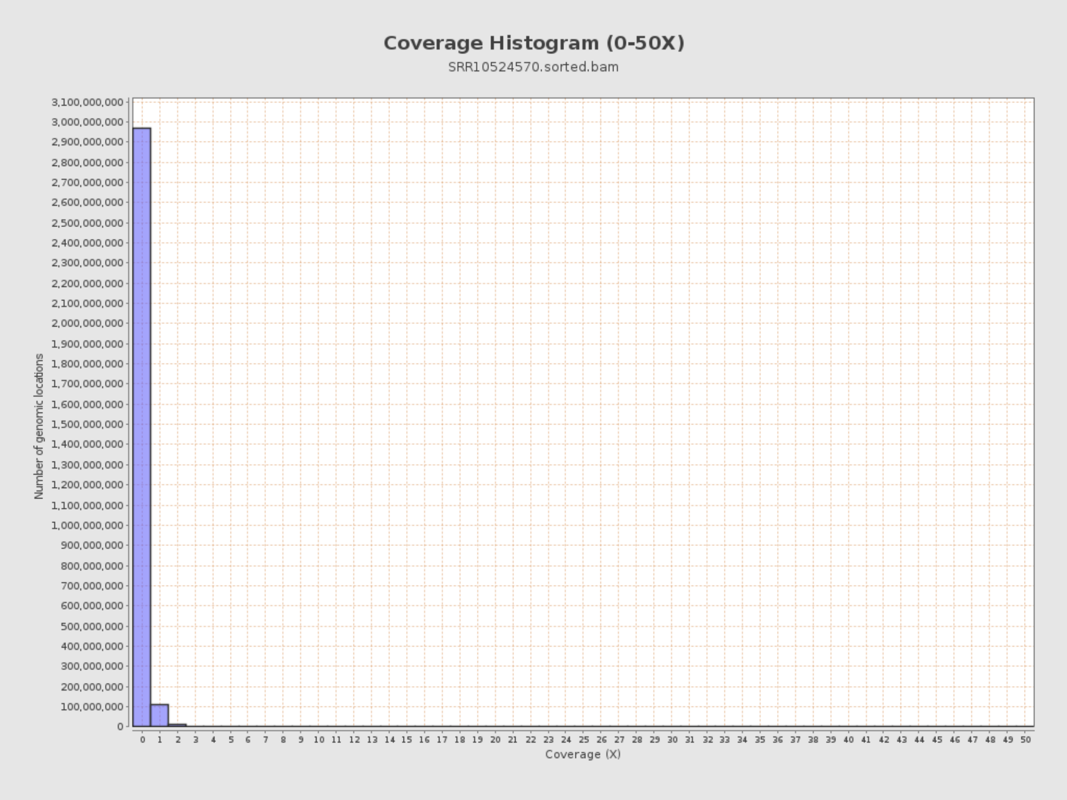
3. Results : Coverage across reference



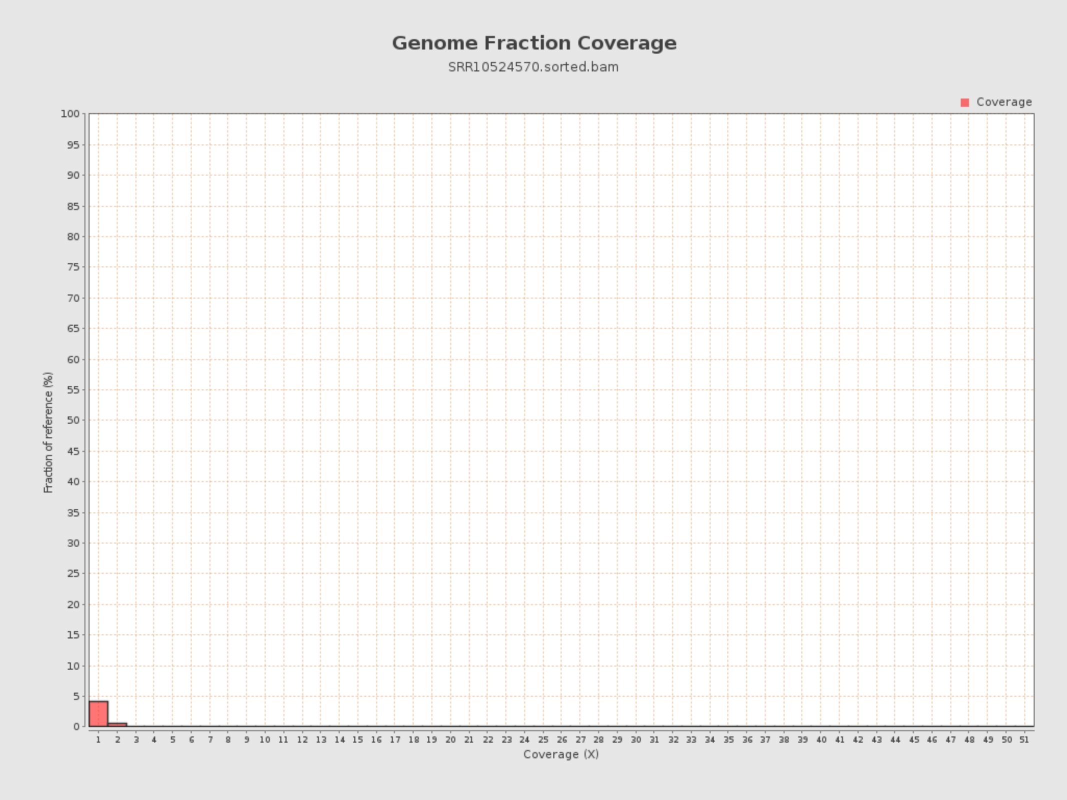
4. Results : Coverage Histogram



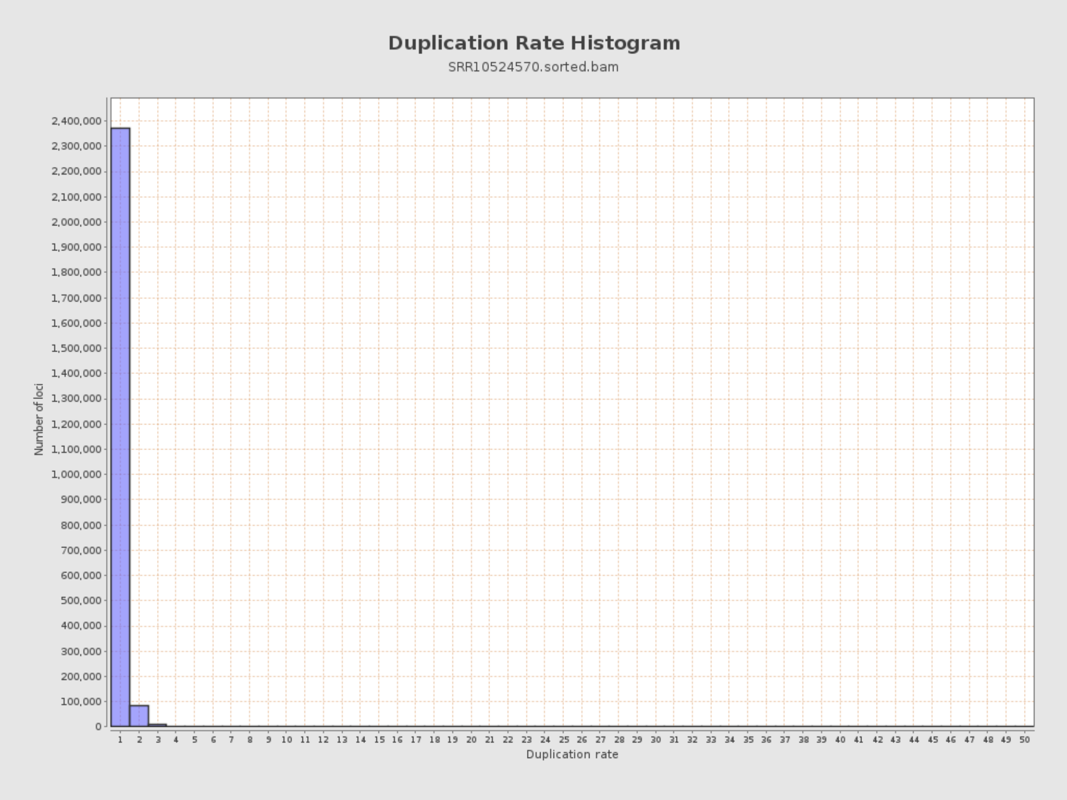
5. Results : Coverage Histogram (0-50X)



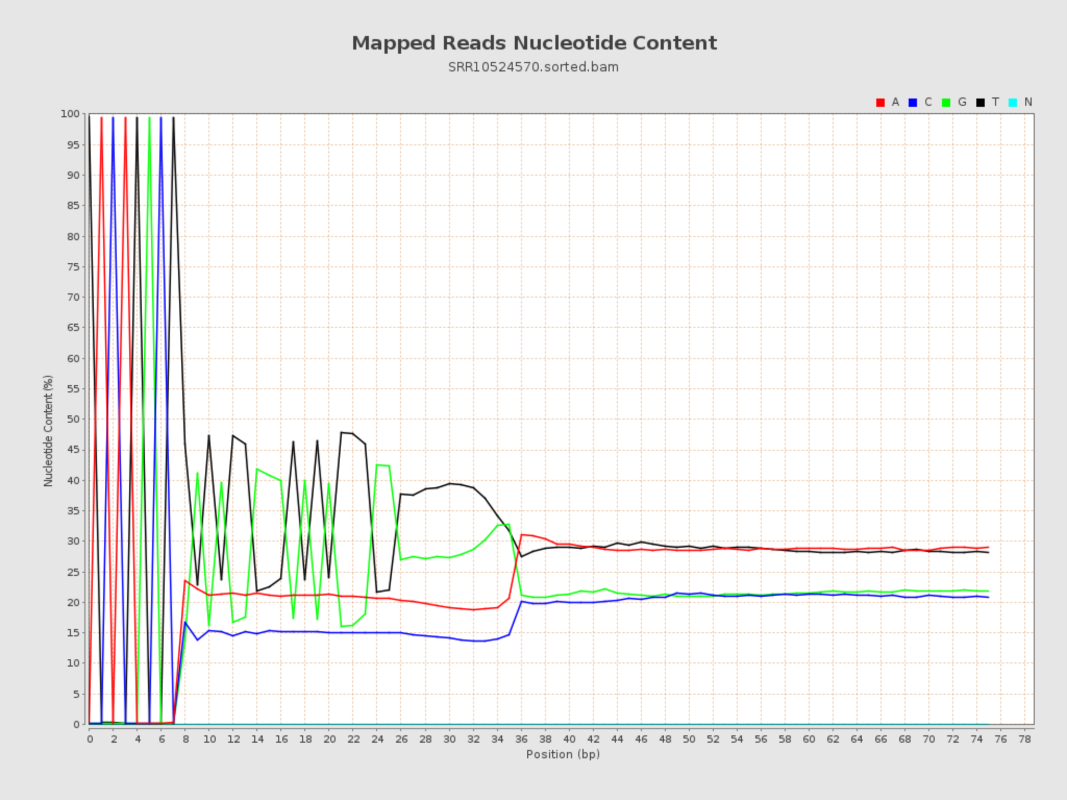
6. Results : Genome Fraction Coverage



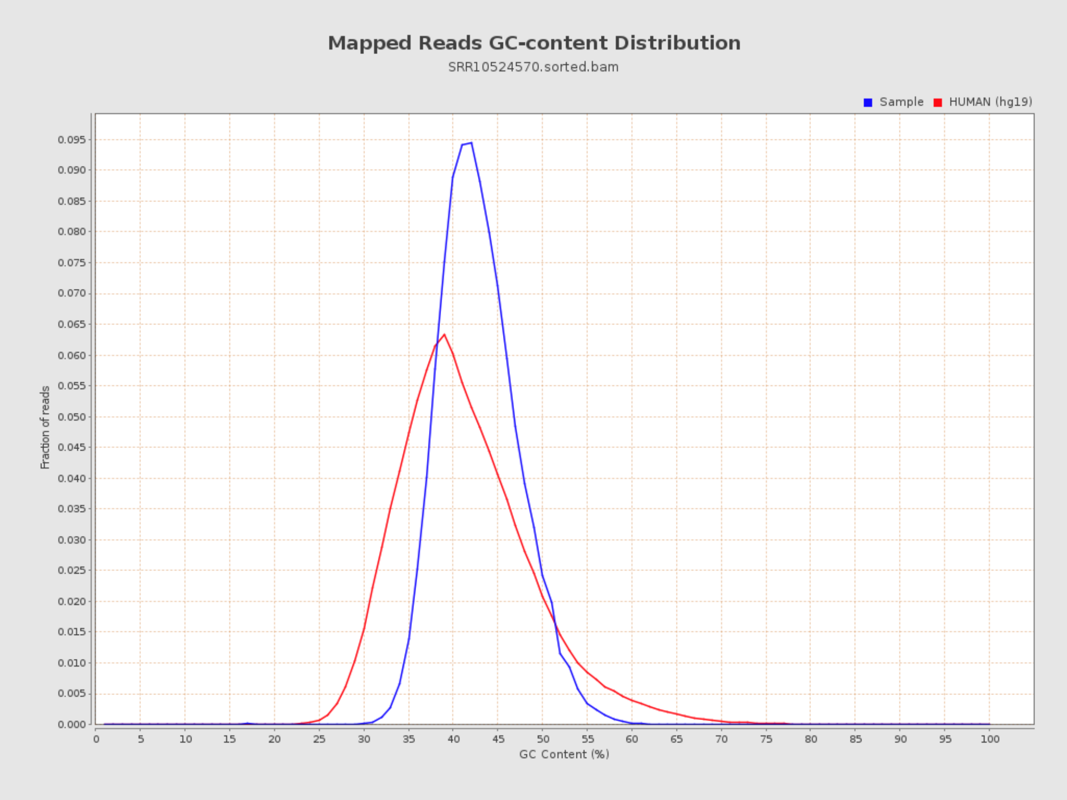
7. Results : Duplication Rate Histogram



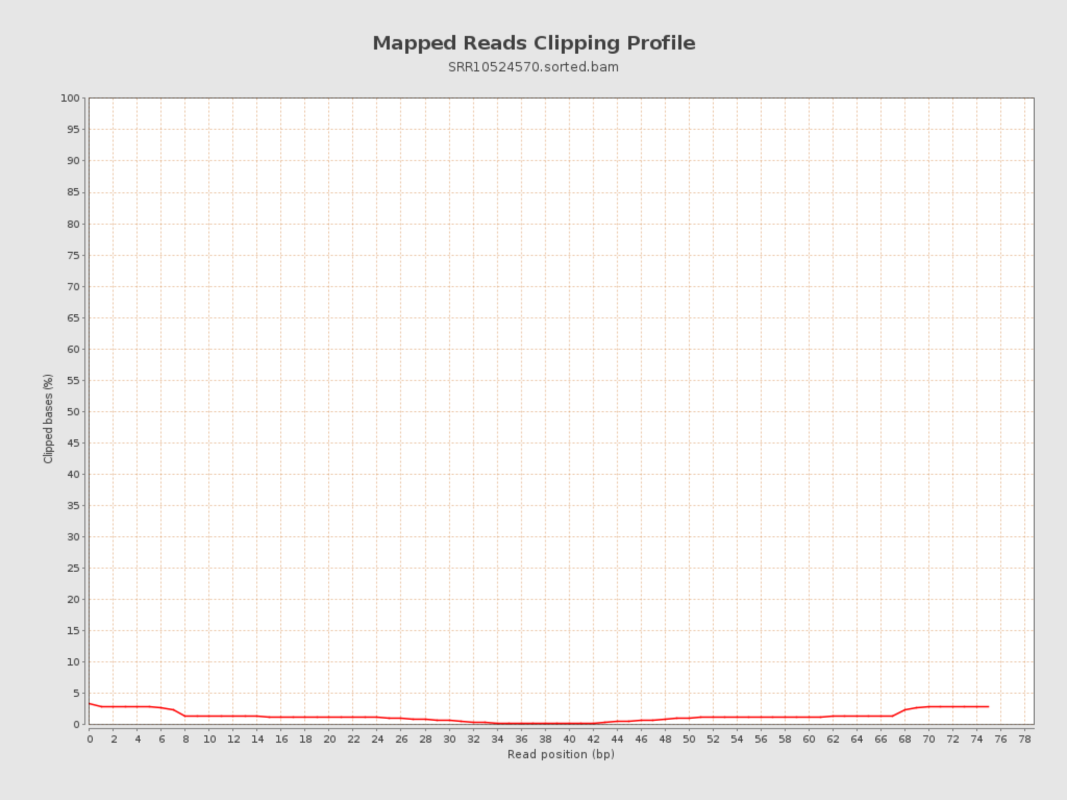
8. Results : Mapped Reads Nucleotide Content



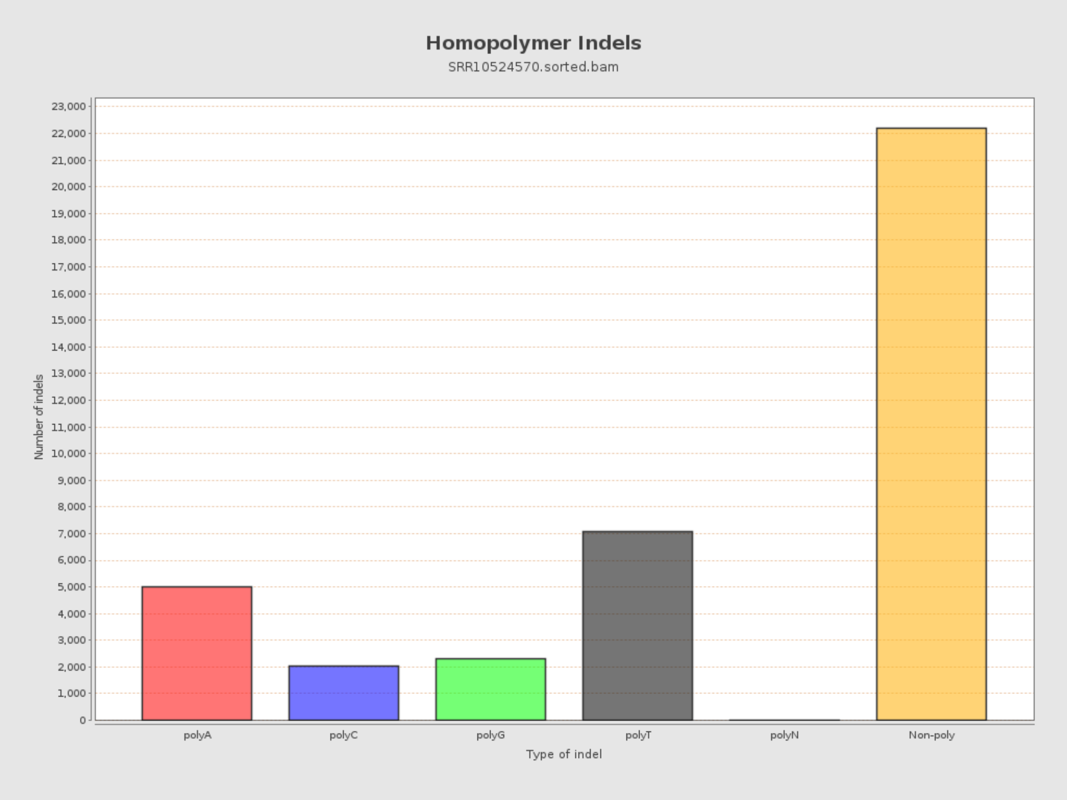
9. Results : Mapped Reads GC-content Distribution



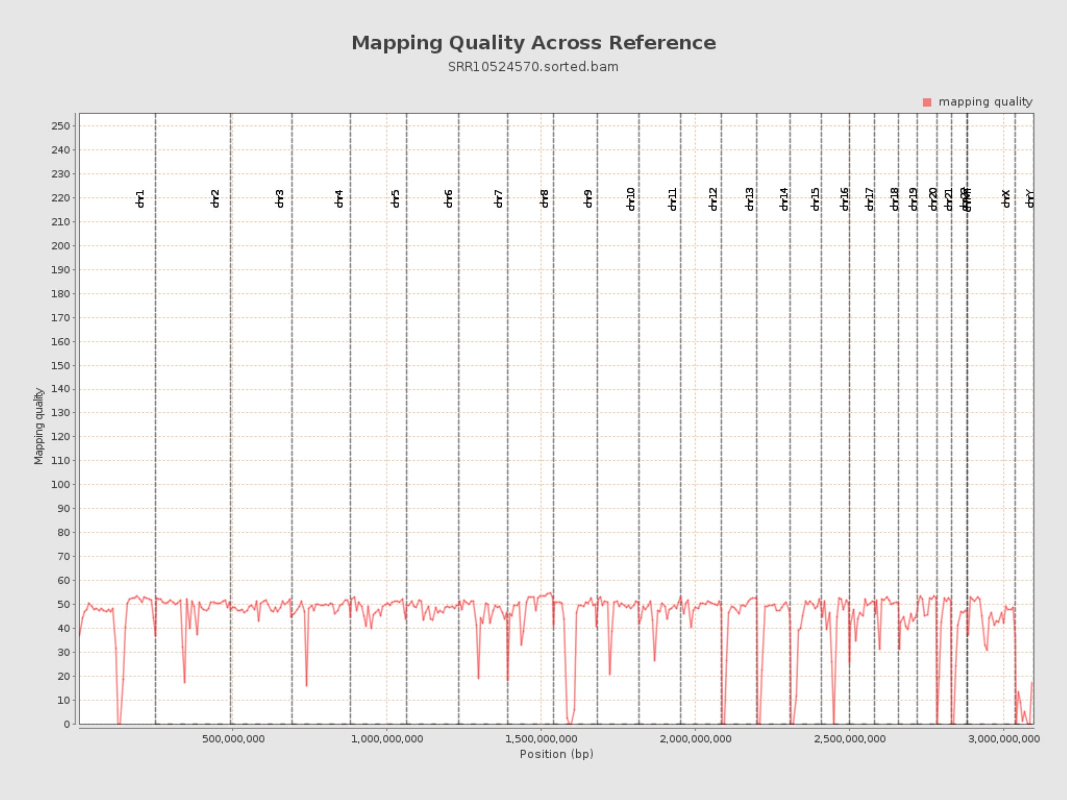
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram