Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:06:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524458.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_SRR10524458 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524458.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:06:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524458.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	521,628
Mapped reads	480,992 / 92.21%
Unmapped reads	40,636 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,087 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	10,481 / 2.01%
Duplication rate	1.7%
Clipped reads	480,556 / 92.13%

2.2. ACGT Content

Number/percentage of A's	7,171,857 / 25.61%
Number/percentage of C's	5,177,529 / 18.49%
Number/percentage of T's	9,018,055 / 32.2%
Number/percentage of G's	6,638,494 / 23.7%
Number/percentage of N's	584 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1161

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

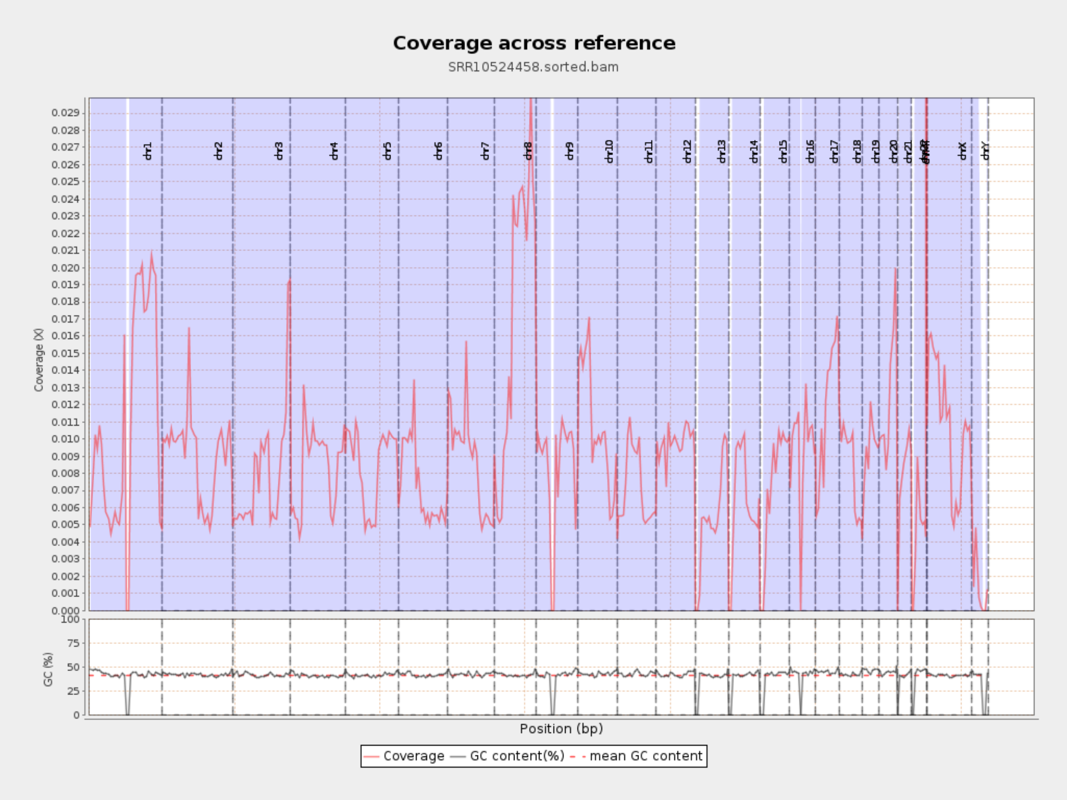
General error rate	0.48%
Mismatches	130,662
Insertions	1,997
Mapped reads with at least one insertion	0.41%
Deletions	5,325
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.51%

2.6. Chromosome stats

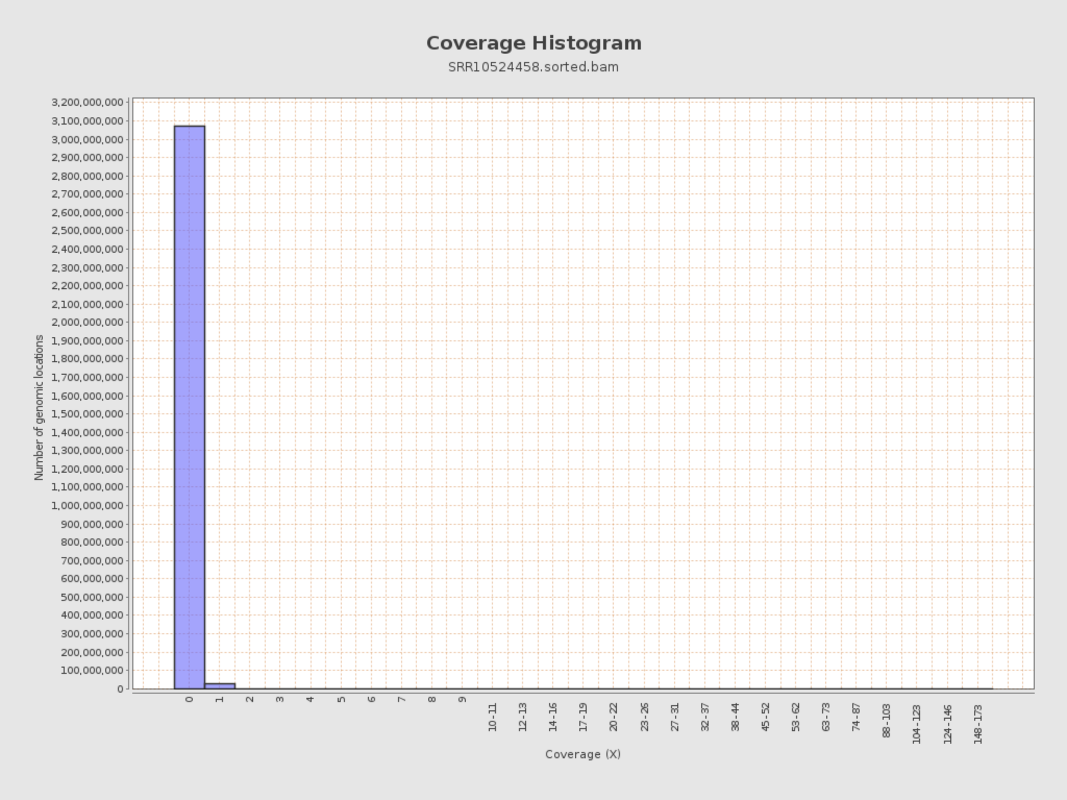
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2760436	0.0111	0.1726
chr2	243199373	2209478	0.0091	0.1248
chr3	198022430	1548521	0.0078	0.092
chr4	191154276	1589878	0.0083	0.0991
chr5	180915260	1540416	0.0085	0.0957
chr6	171115067	1238018	0.0072	0.0976
chr7	159138663	1393579	0.0088	0.1379

chr8	146364022	2567452	0.0175	0.1477
chr9	141213431	1162719	0.0082	0.1061
chr10	135534747	1473830	0.0109	0.1236
chr11	135006516	968454	0.0072	0.11
chr12	133851895	1314994	0.0098	0.103
chr13	115169878	621418	0.0054	0.0762
chr14	107349540	666165	0.0062	0.0825
chr15	102531392	734653	0.0072	0.0894
chr16	90354753	850151	0.0094	0.1033
chr17	81195210	977111	0.012	0.1169
chr18	78077248	664955	0.0085	0.1525
chr19	59128983	556755	0.0094	0.1291
chr20	63025520	793397	0.0126	0.1174
chr21	48129895	378289	0.0079	0.0934
chr22	51304566	221848	0.0043	0.068
chrMT	16571	4410	0.2661	0.5307
chrX	155270560	1691867	0.0109	0.1124
chrY	59373566	87023	0.0015	0.0512

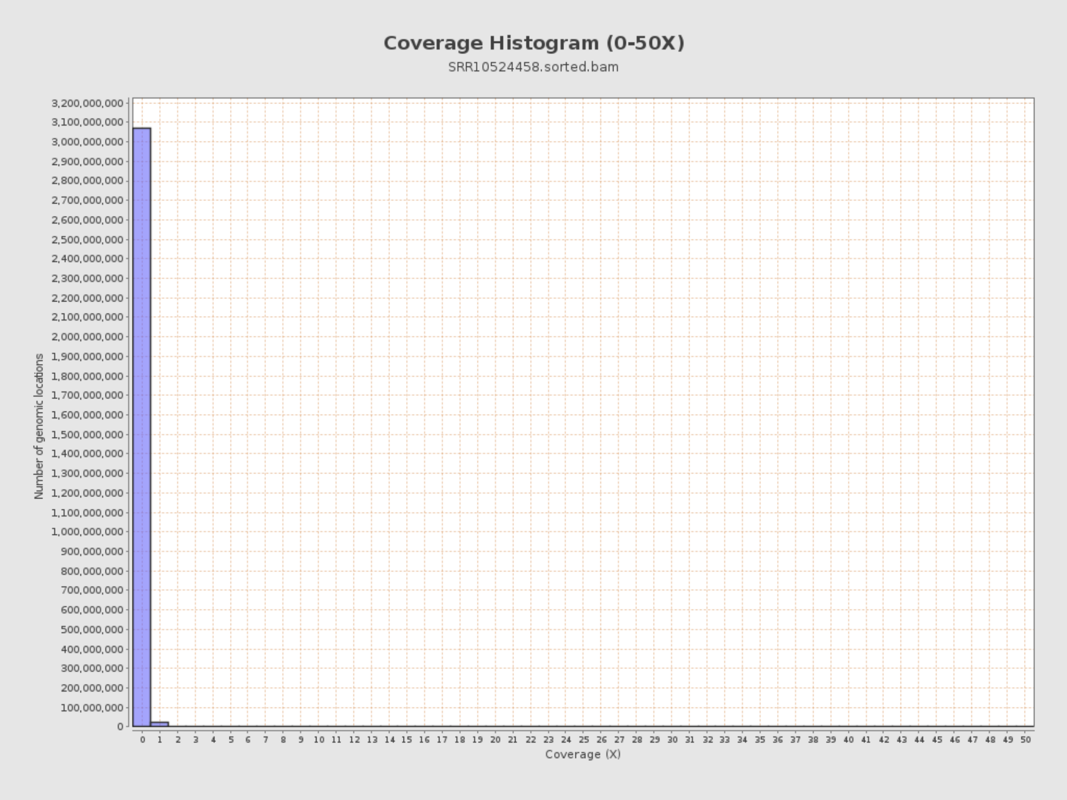
3. Results : Coverage across reference



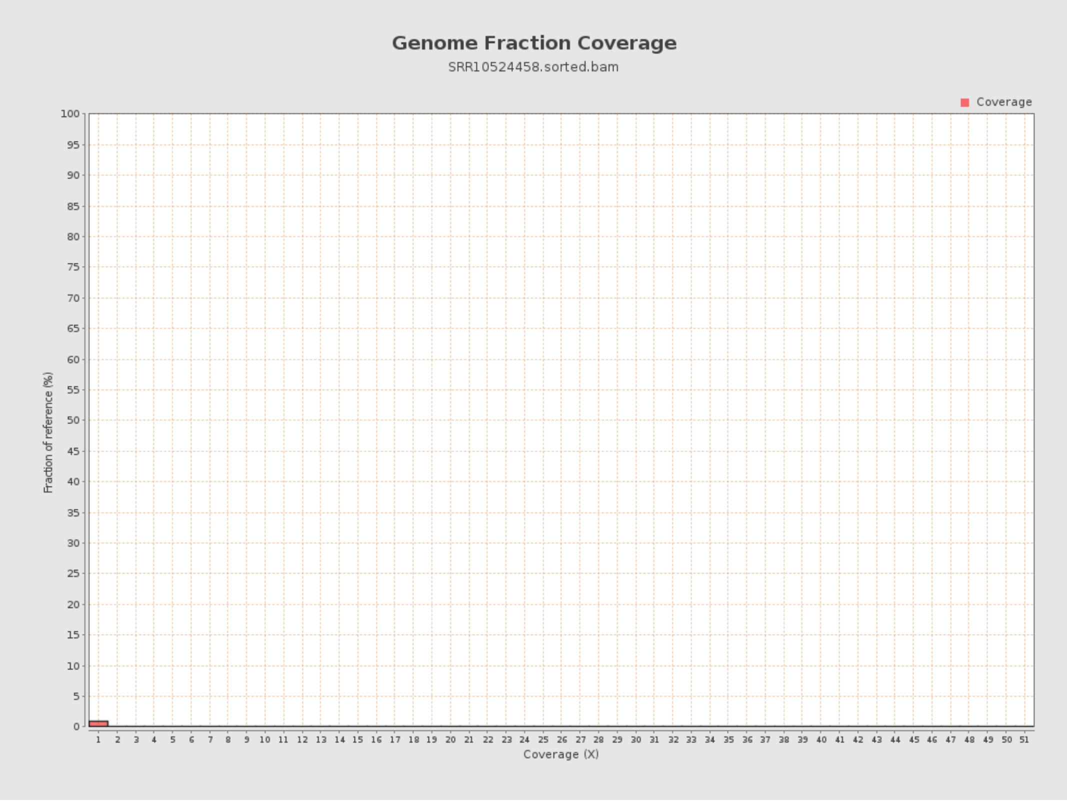
4. Results : Coverage Histogram



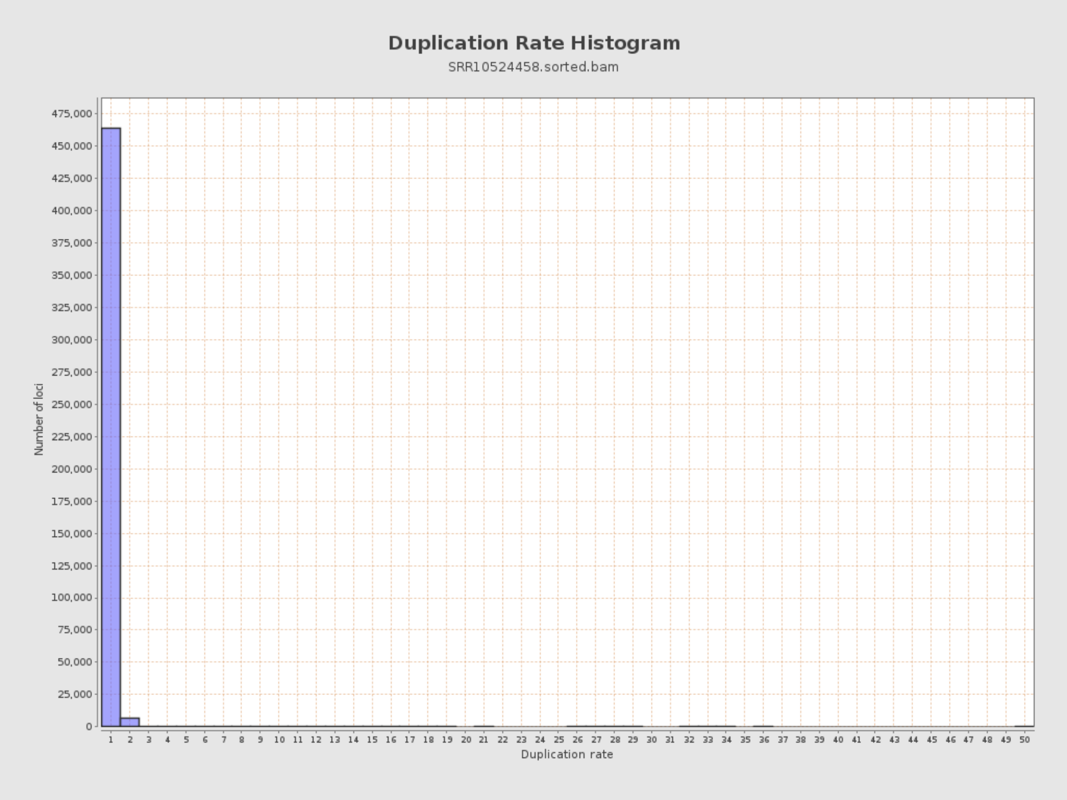
5. Results : Coverage Histogram (0-50X)



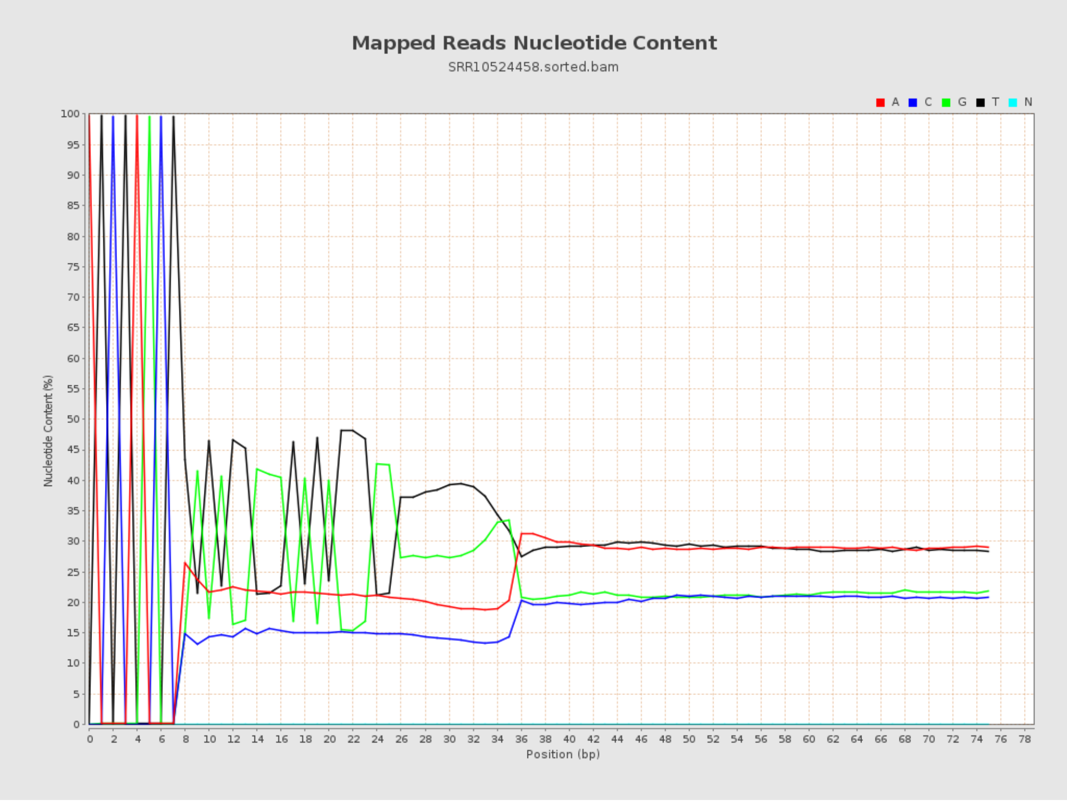
6. Results : Genome Fraction Coverage



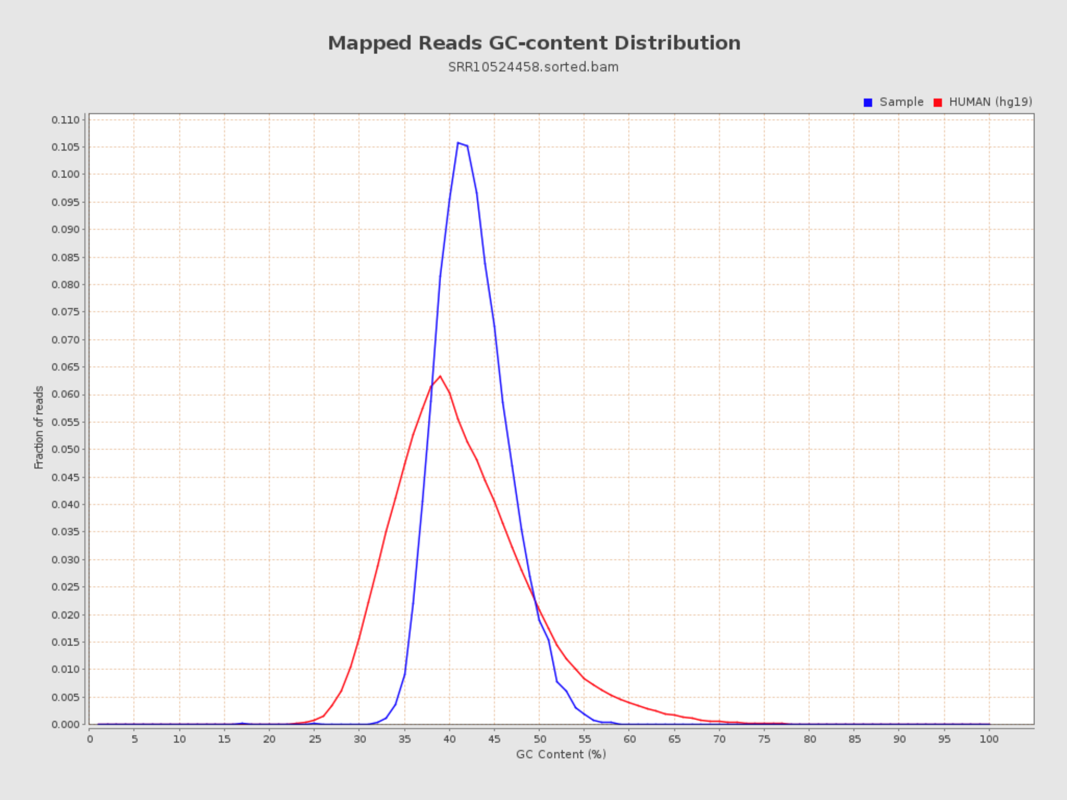
7. Results : Duplication Rate Histogram



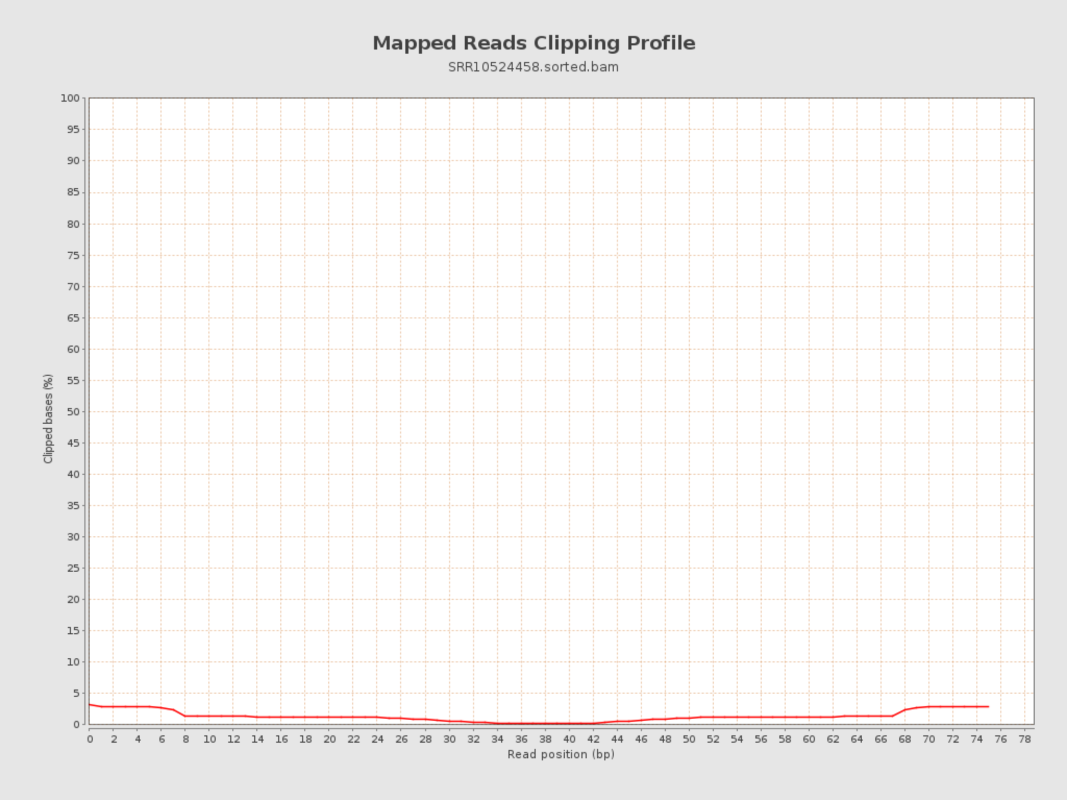
8. Results : Mapped Reads Nucleotide Content



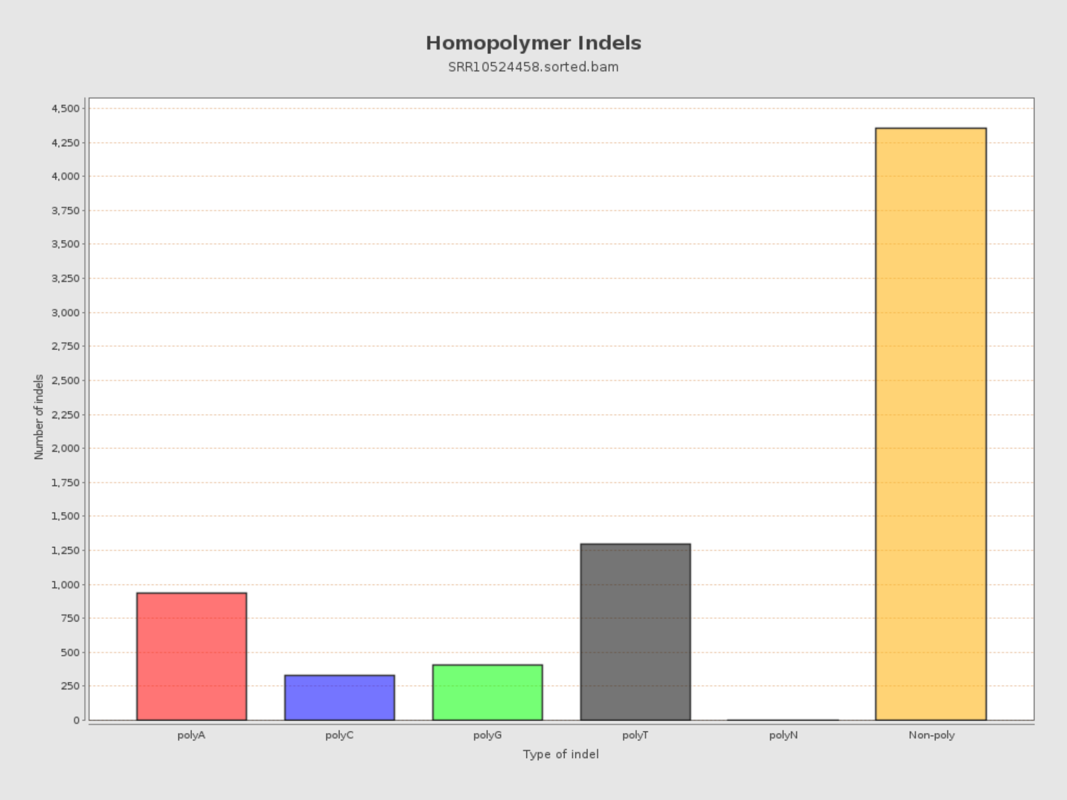
9. Results : Mapped Reads GC-content Distribution



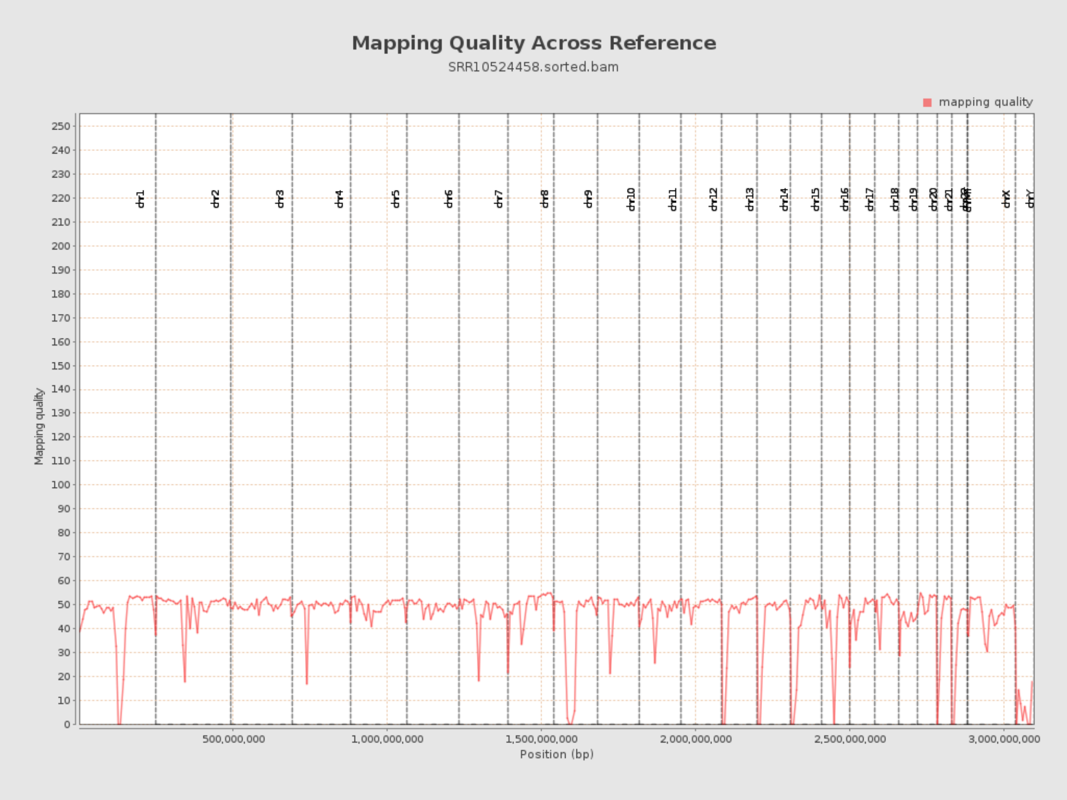
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram