Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:25:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524438.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_SRR10524438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524438.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:25:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,947,749
Mapped reads	2,709,527 / 91.92%
Unmapped reads	238,222 / 8.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,448 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	193,265 / 6.56%
Duplication rate	5.23%
Clipped reads	2,712,556 / 92.02%

2.2. ACGT Content

Number/percentage of A's	36,183,093 / 22.97%
Number/percentage of C's	33,111,807 / 21.02%
Number/percentage of T's	49,814,630 / 31.63%
Number/percentage of G's	38,382,915 / 24.37%
Number/percentage of N's	14,995 / 0.01%
GC Percentage	45.39%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.4839

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

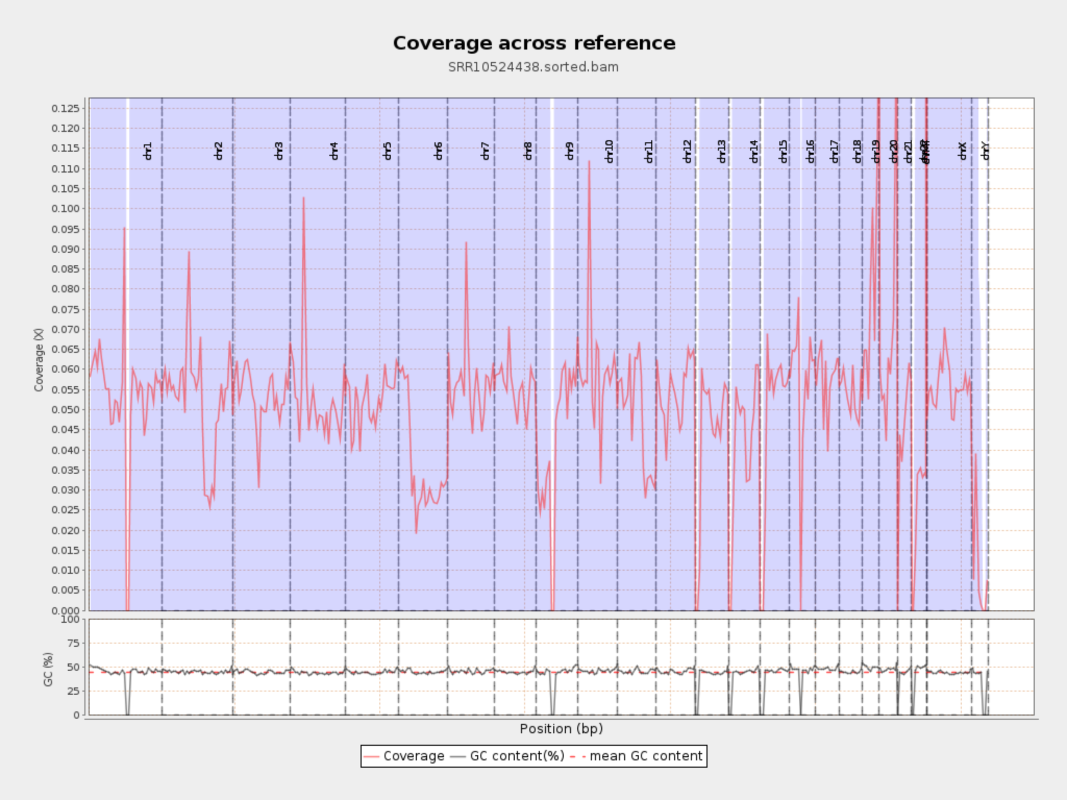
General error rate	0.52%
Mismatches	797,620
Insertions	11,690
Mapped reads with at least one insertion	0.43%
Deletions	26,536
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.04%

2.6. Chromosome stats

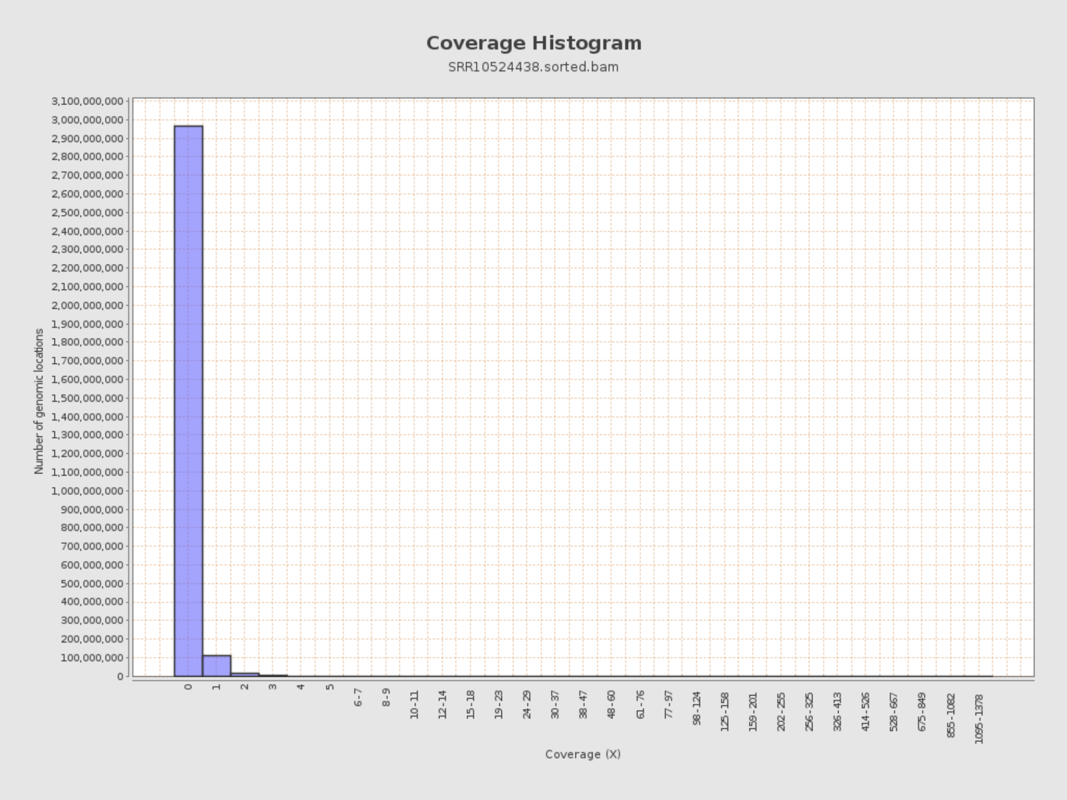
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13255250	0.0532	1.0237
chr2	243199373	12908414	0.0531	0.6643
chr3	198022430	10555546	0.0533	0.2769
chr4	191154276	10060166	0.0526	0.3749
chr5	180915260	9468454	0.0523	0.2701
chr6	171115067	6137916	0.0359	0.2513
chr7	159138663	9010906	0.0566	0.6475

chr8	146364022	8195944	0.056	0.3526
chr9	141213431	5761626	0.0408	0.3093
chr10	135534747	8077748	0.0596	0.5369
chr11	135006516	6507691	0.0482	0.3384
chr12	133851895	7331154	0.0548	0.2857
chr13	115169878	4933197	0.0428	0.245
chr14	107349540	4399826	0.041	0.252
chr15	102531392	4889264	0.0477	0.2615
chr16	90354753	5114590	0.0566	0.3135
chr17	81195210	4647117	0.0572	0.318
chr18	78077248	4206705	0.0539	0.5658
chr19	59128983	4882774	0.0826	0.6621
chr20	63025520	4484982	0.0712	0.3416
chr21	48129895	2154260	0.0448	0.3394
chr22	51304566	1230668	0.024	0.1869
chrMT	16571	33655	2.031	2.2137
chrX	155270560	8709999	0.0561	0.3133
chrY	59373566	593190	0.01	0.3477

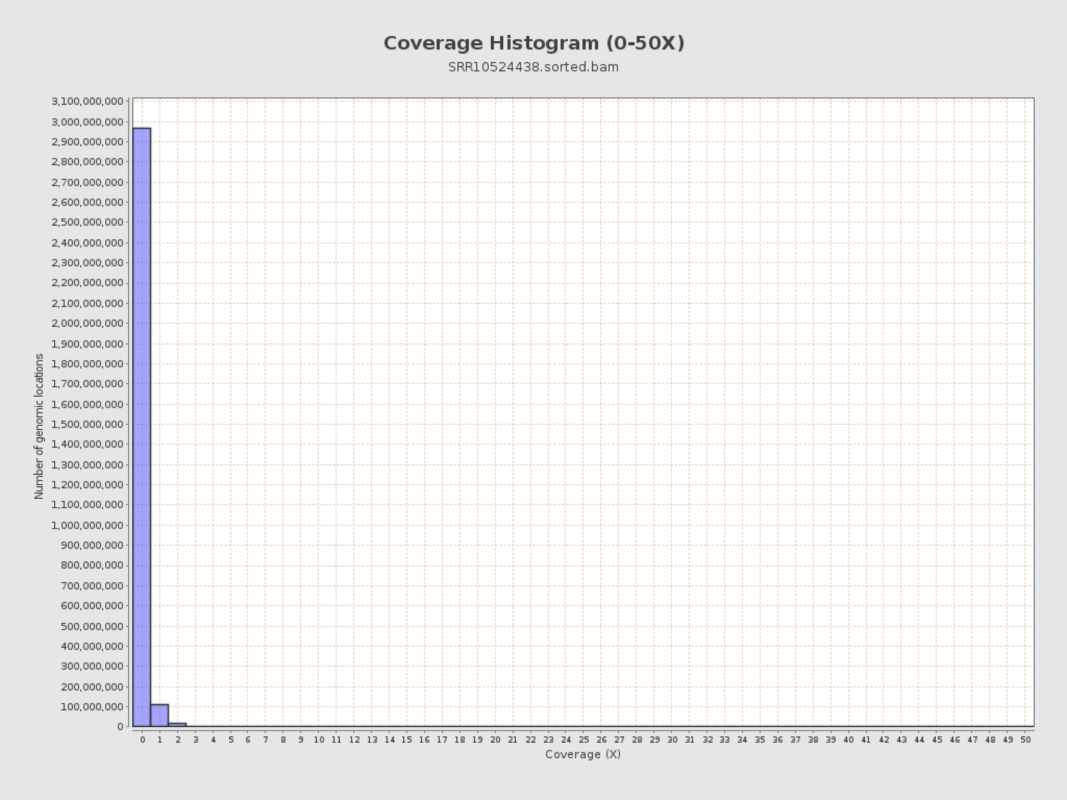
3. Results : Coverage across reference



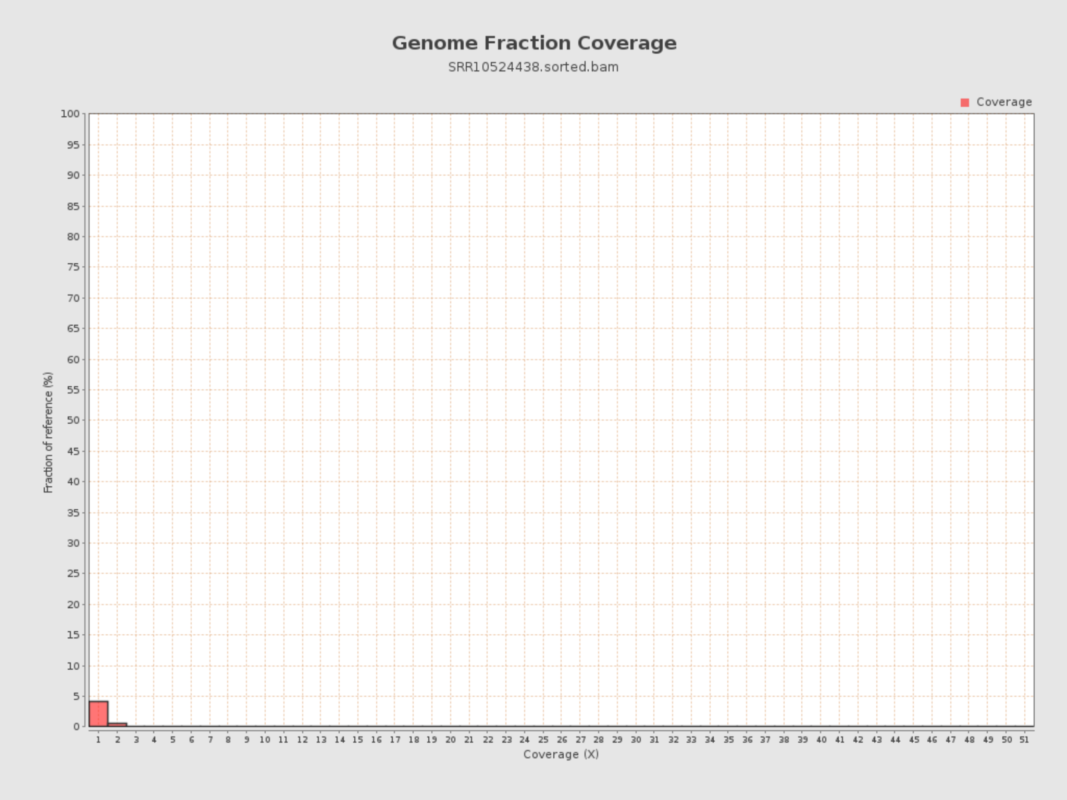
4. Results : Coverage Histogram



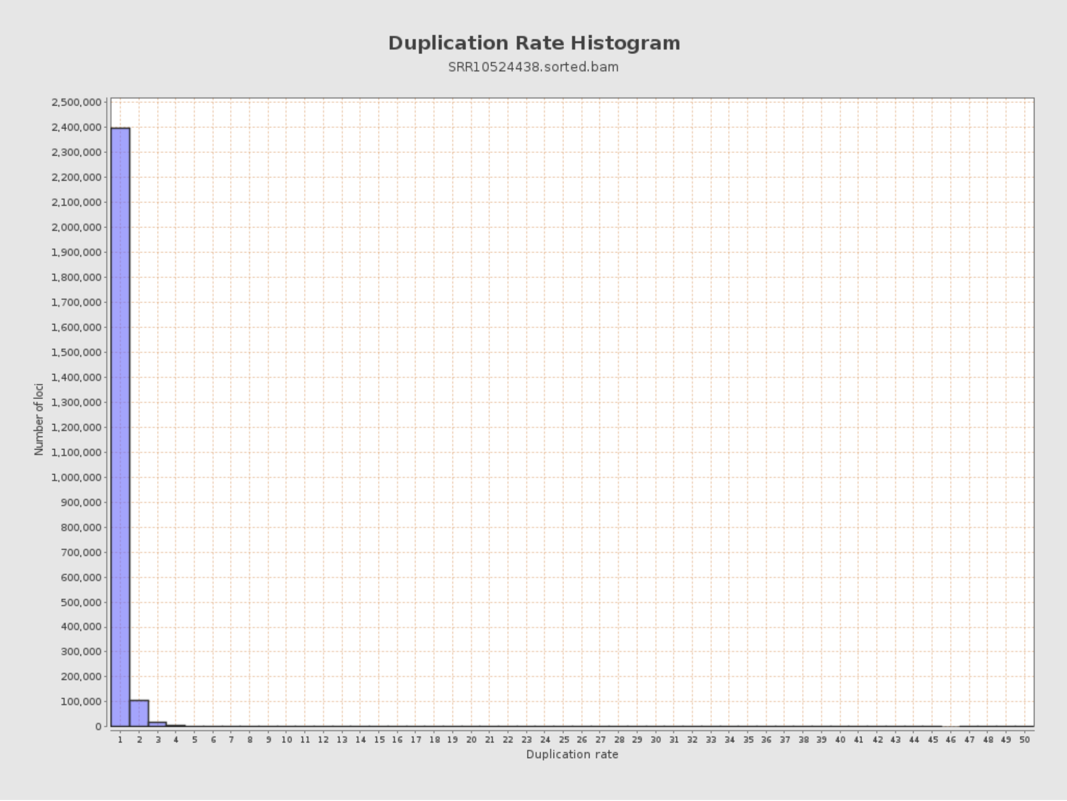
5. Results : Coverage Histogram (0-50X)



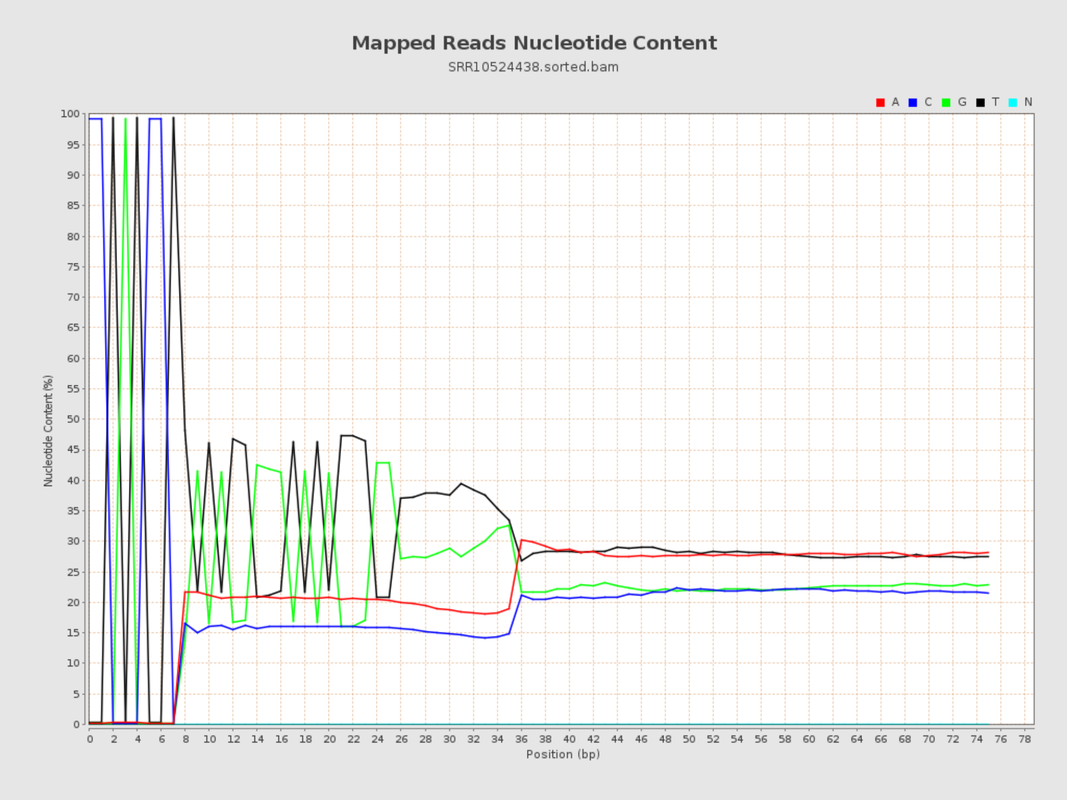
6. Results : Genome Fraction Coverage



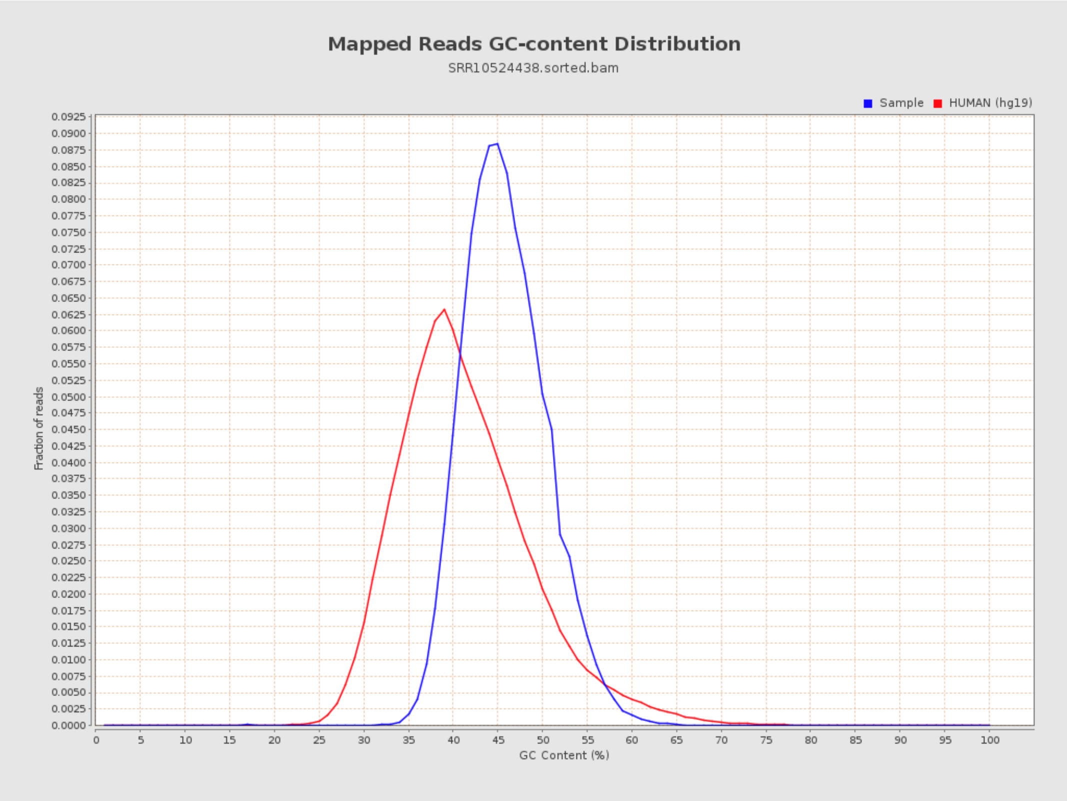
7. Results : Duplication Rate Histogram



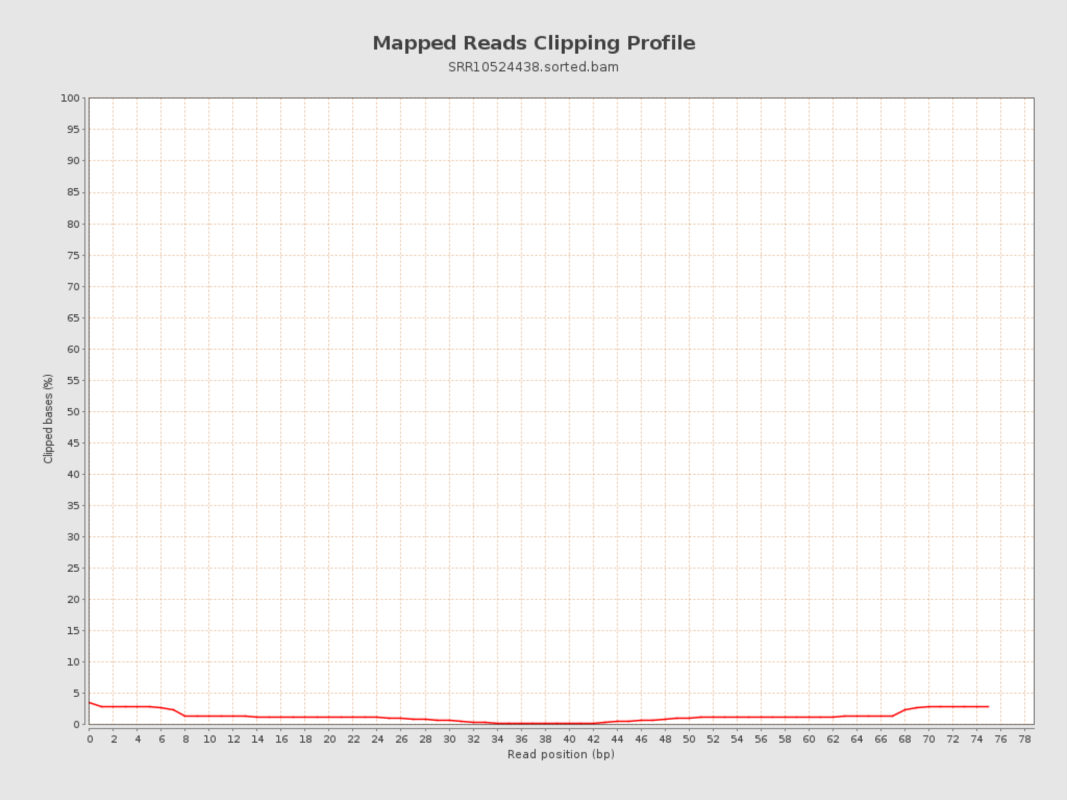
8. Results : Mapped Reads Nucleotide Content



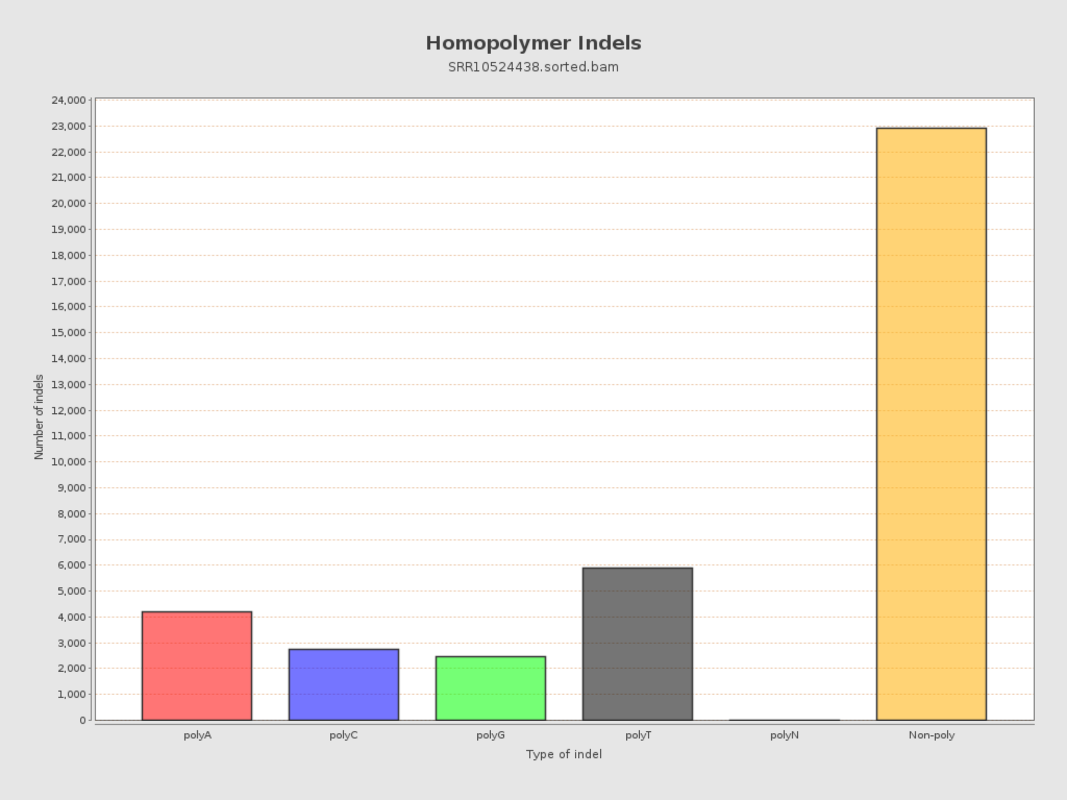
9. Results : Mapped Reads GC-content Distribution



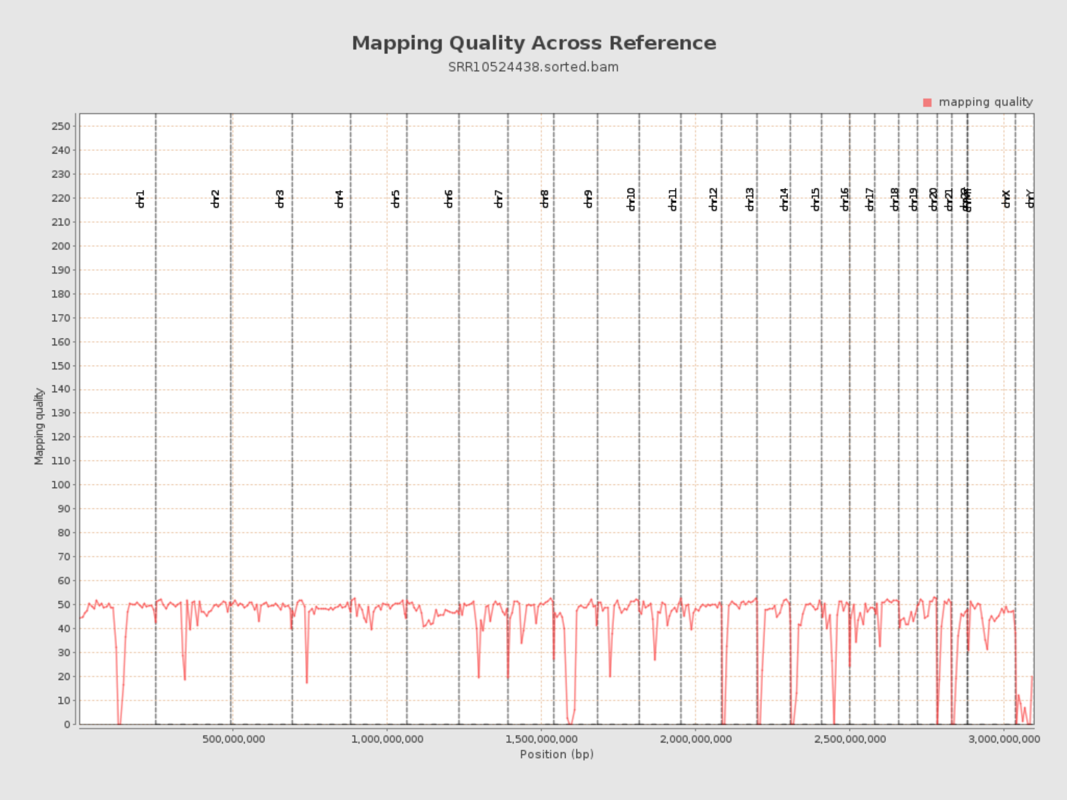
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram