Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:02:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525226.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_SRR10525226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525226.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:02:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,852,869
Mapped reads	2,640,222 / 92.55%
Unmapped reads	212,647 / 7.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,781 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	152,364 / 5.34%
Duplication rate	4.25%
Clipped reads	2,647,591 / 92.8%

2.2. ACGT Content

Number/percentage of A's	39,124,708 / 25.35%
Number/percentage of C's	31,657,465 / 20.51%
Number/percentage of T's	46,953,047 / 30.42%
Number/percentage of G's	36,606,344 / 23.72%
Number/percentage of N's	3,207 / 0%
GC Percentage	44.23%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4294

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

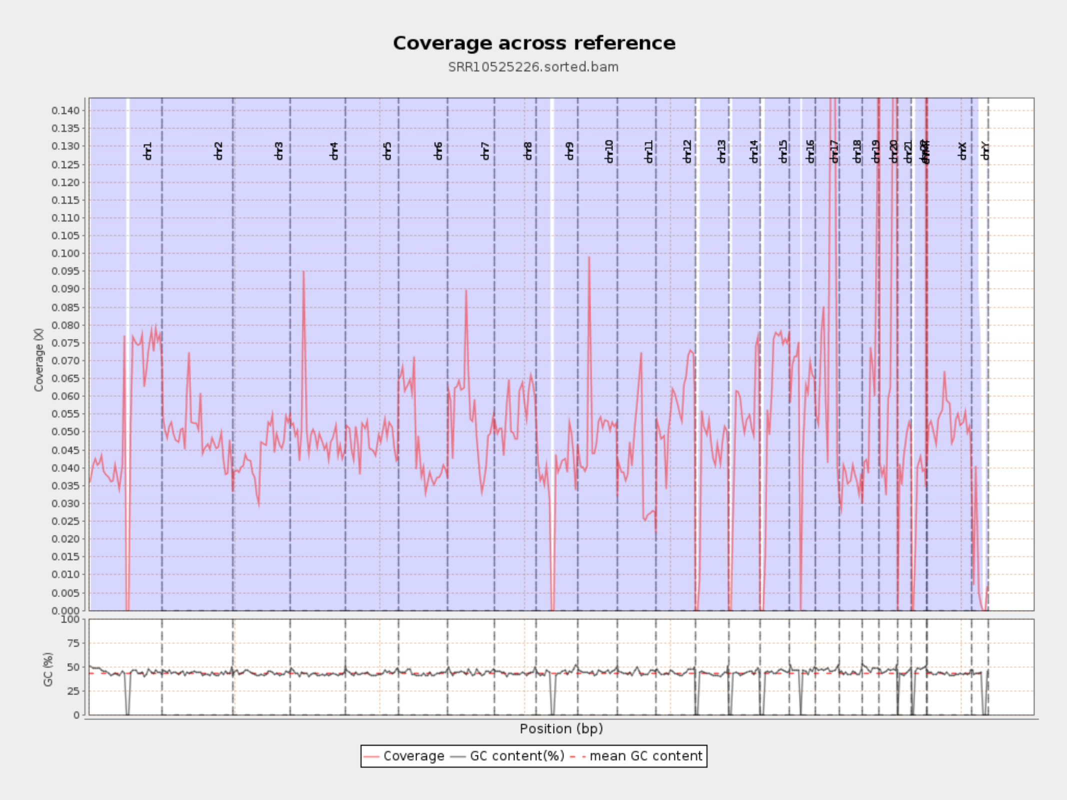
General error rate	0.5%
Mismatches	755,665
Insertions	10,476
Mapped reads with at least one insertion	0.39%
Deletions	29,439
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.32%

2.6. Chromosome stats

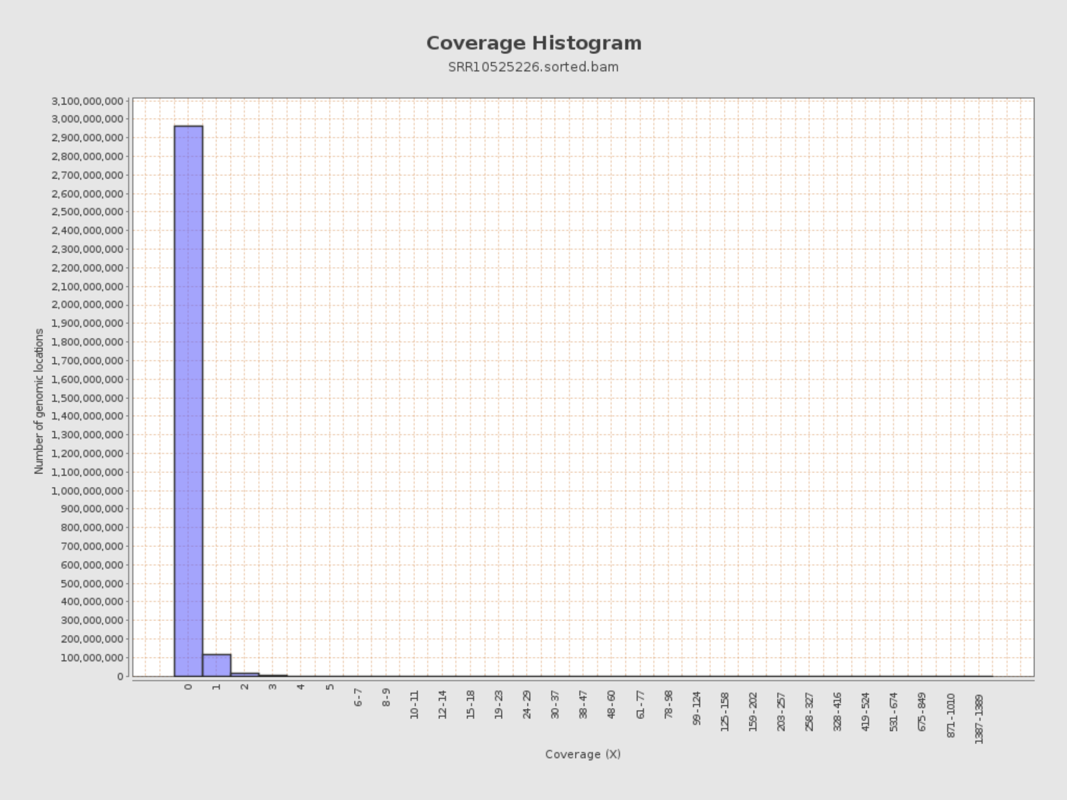
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13101948	0.0526	0.7117
chr2	243199373	12003578	0.0494	0.6339
chr3	198022430	8730792	0.0441	0.2425
chr4	191154276	9453204	0.0495	0.3432
chr5	180915260	8658730	0.0479	0.2495
chr6	171115067	8169367	0.0477	0.3082
chr7	159138663	8691673	0.0546	0.5684

chr8	146364022	8118748	0.0555	0.5733
chr9	141213431	5105837	0.0362	0.294
chr10	135534747	6849404	0.0505	0.4772
chr11	135006516	5447329	0.0403	0.3047
chr12	133851895	7694829	0.0575	0.2784
chr13	115169878	4627187	0.0402	0.2319
chr14	107349540	5258490	0.049	0.2586
chr15	102531392	5759584	0.0562	0.2732
chr16	90354753	5376702	0.0595	0.2968
chr17	81195210	6848770	0.0843	0.3574
chr18	78077248	2843401	0.0364	0.5312
chr19	59128983	4093672	0.0692	0.5706
chr20	63025520	5294195	0.084	0.3596
chr21	48129895	1968900	0.0409	0.3316
chr22	51304566	1450850	0.0283	0.1912
chrMT	16571	26561	1.6029	1.7231
chrX	155270560	8229551	0.053	0.2907
chrY	59373566	589601	0.0099	0.4129

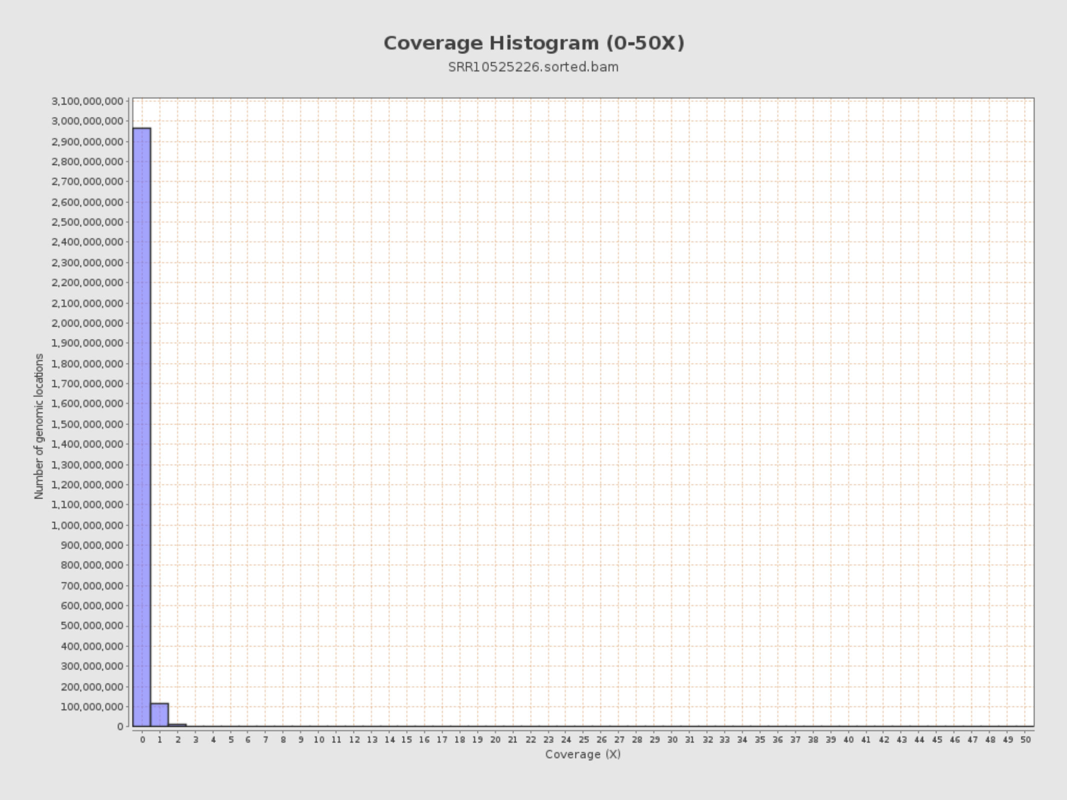
3. Results : Coverage across reference



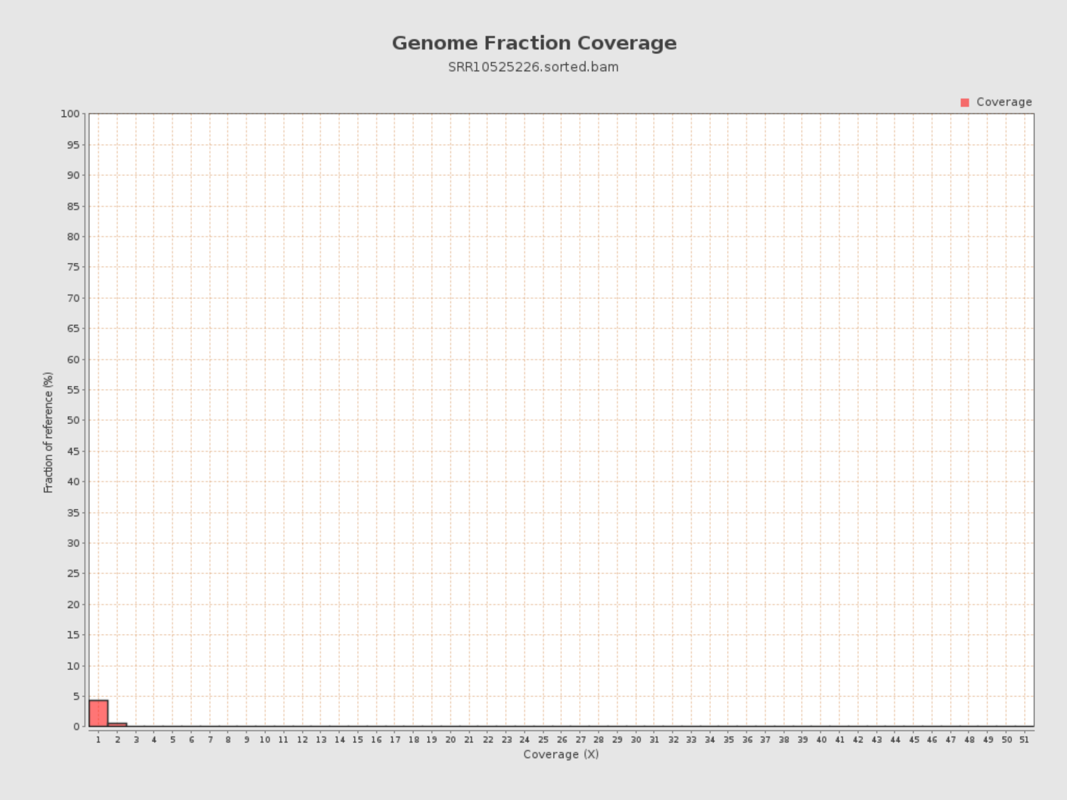
4. Results : Coverage Histogram



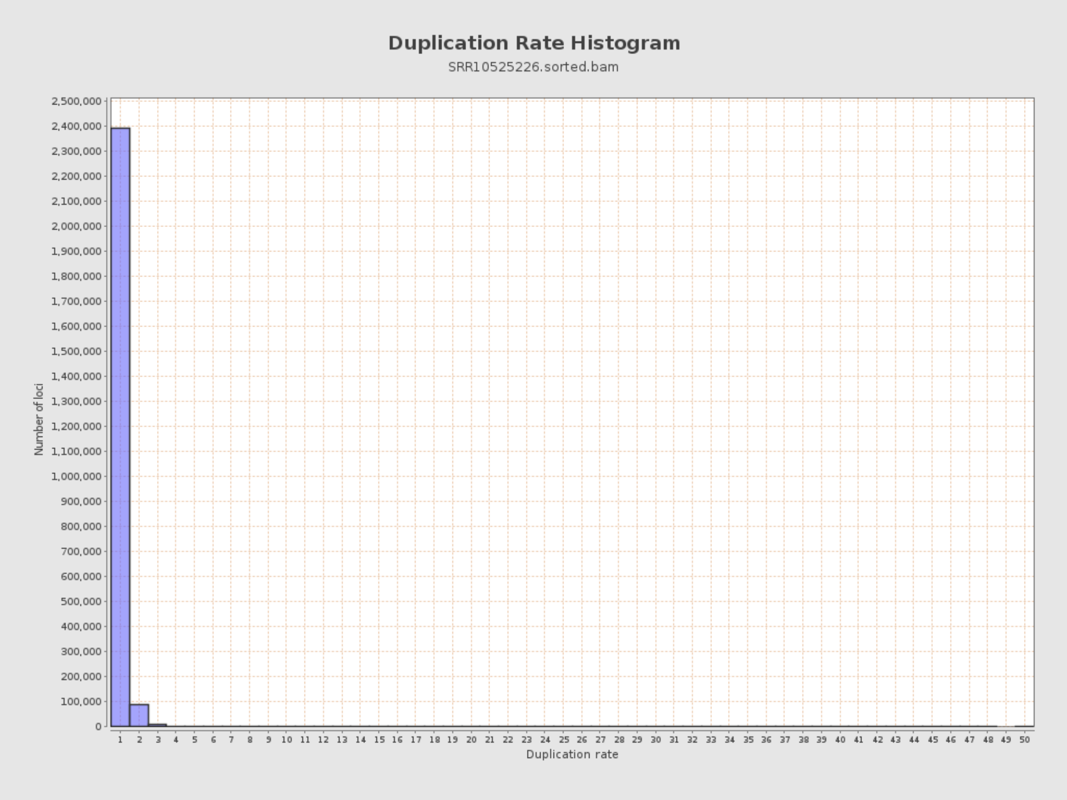
5. Results : Coverage Histogram (0-50X)



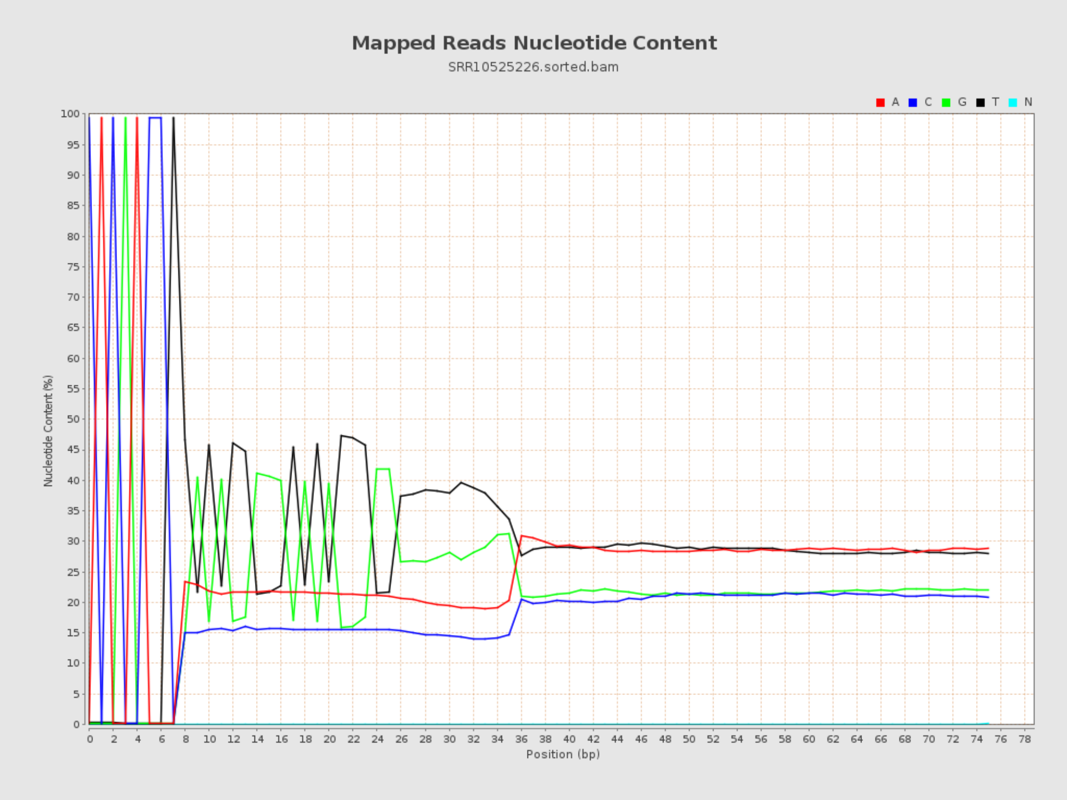
6. Results : Genome Fraction Coverage



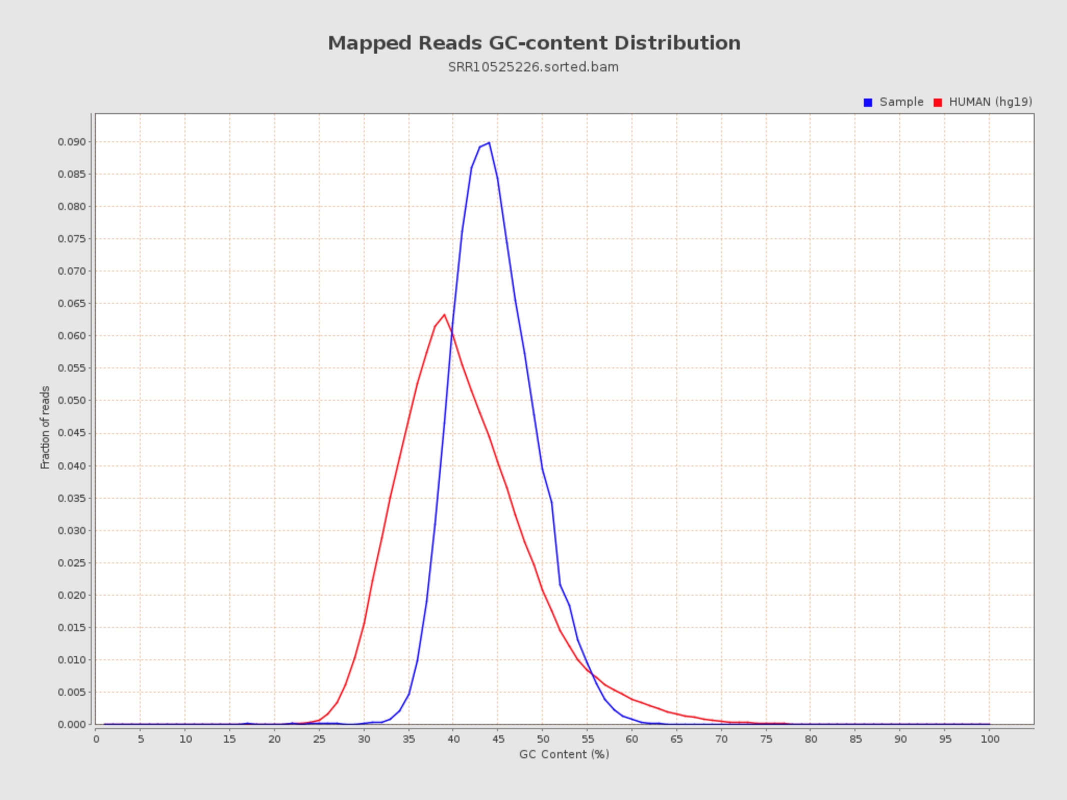
7. Results : Duplication Rate Histogram



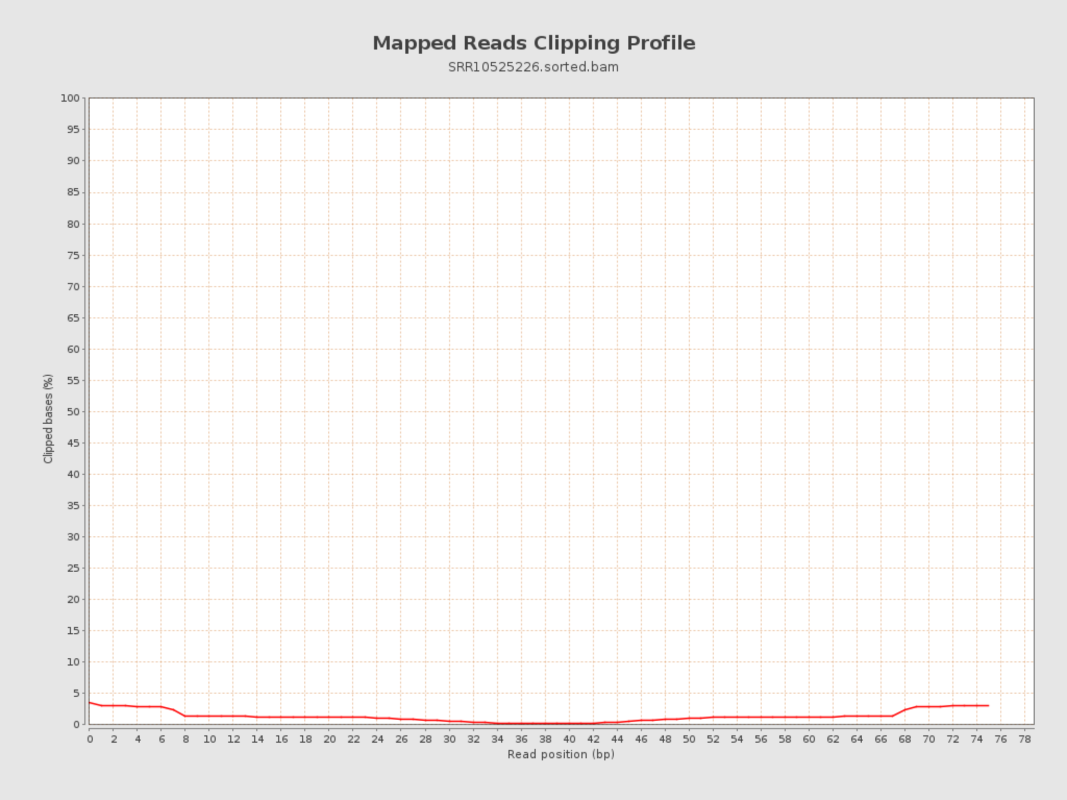
8. Results : Mapped Reads Nucleotide Content



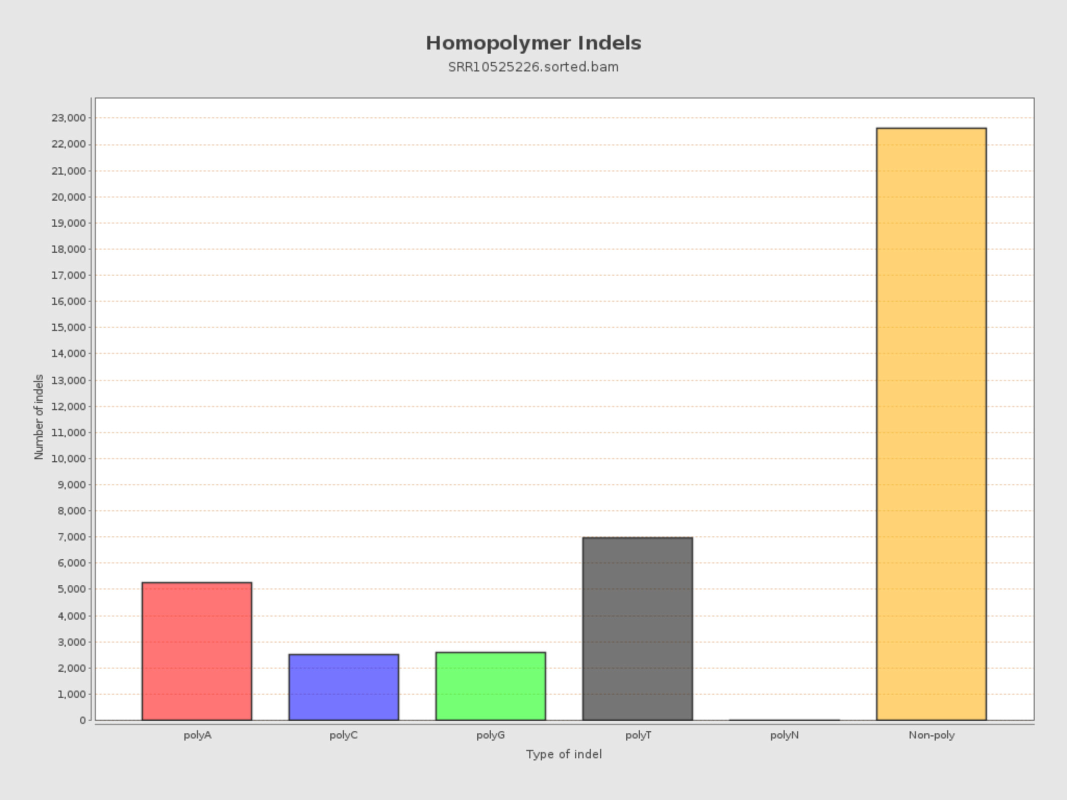
9. Results : Mapped Reads GC-content Distribution



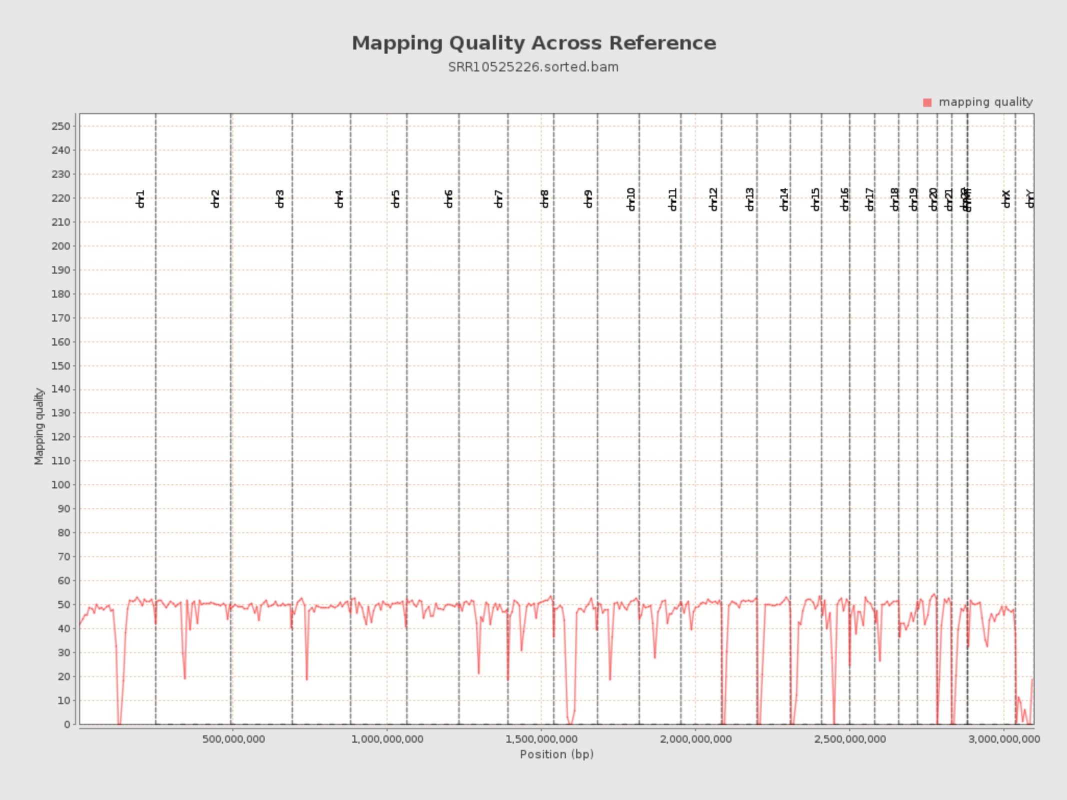
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram