Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:43:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525199.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_SRR10525199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:43:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,337,622
Mapped reads	943,732 / 70.55%
Unmapped reads	393,890 / 29.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,062 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	21,653 / 1.62%
Duplication rate	1.62%
Clipped reads	943,749 / 70.55%

2.2. ACGT Content

Number/percentage of A's	15,269,320 / 26.72%
Number/percentage of C's	11,111,448 / 19.44%
Number/percentage of T's	17,717,360 / 31%
Number/percentage of G's	13,055,330 / 22.84%
Number/percentage of N's	1,437 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.2001

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

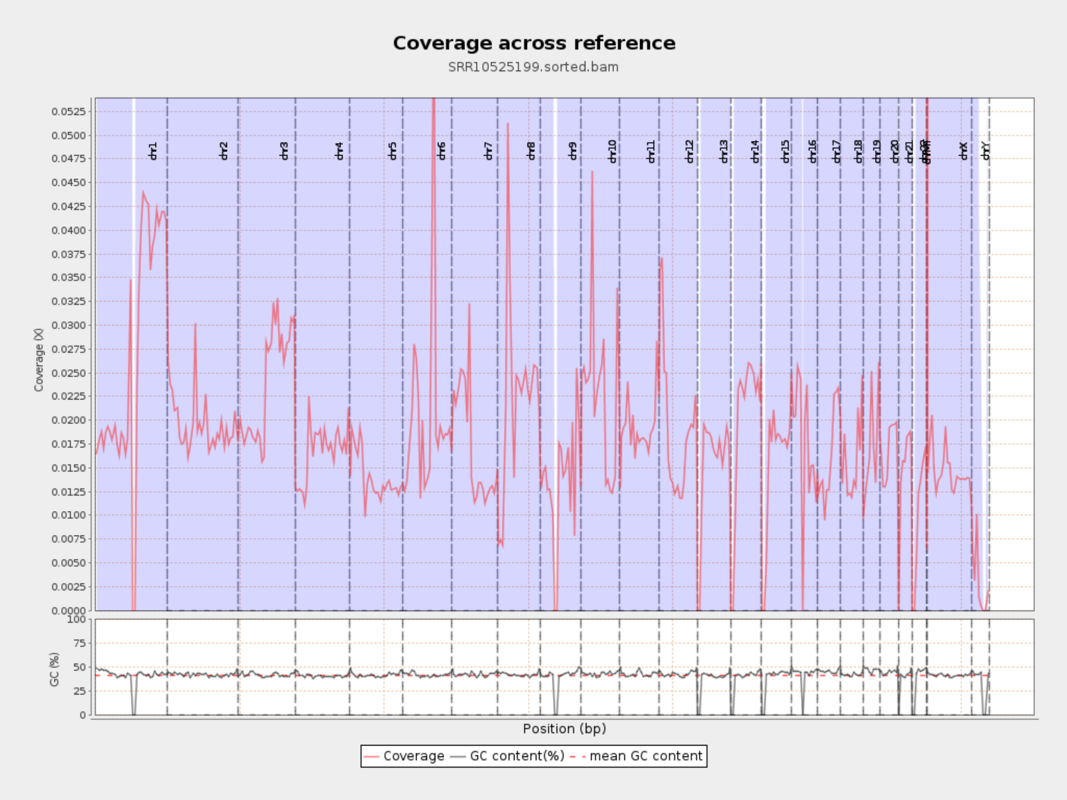
General error rate	0.5%
Mismatches	279,425
Insertions	4,537
Mapped reads with at least one insertion	0.48%
Deletions	11,887
Mapped reads with at least one deletion	1.25%
Homopolymer indels	41.78%

2.6. Chromosome stats

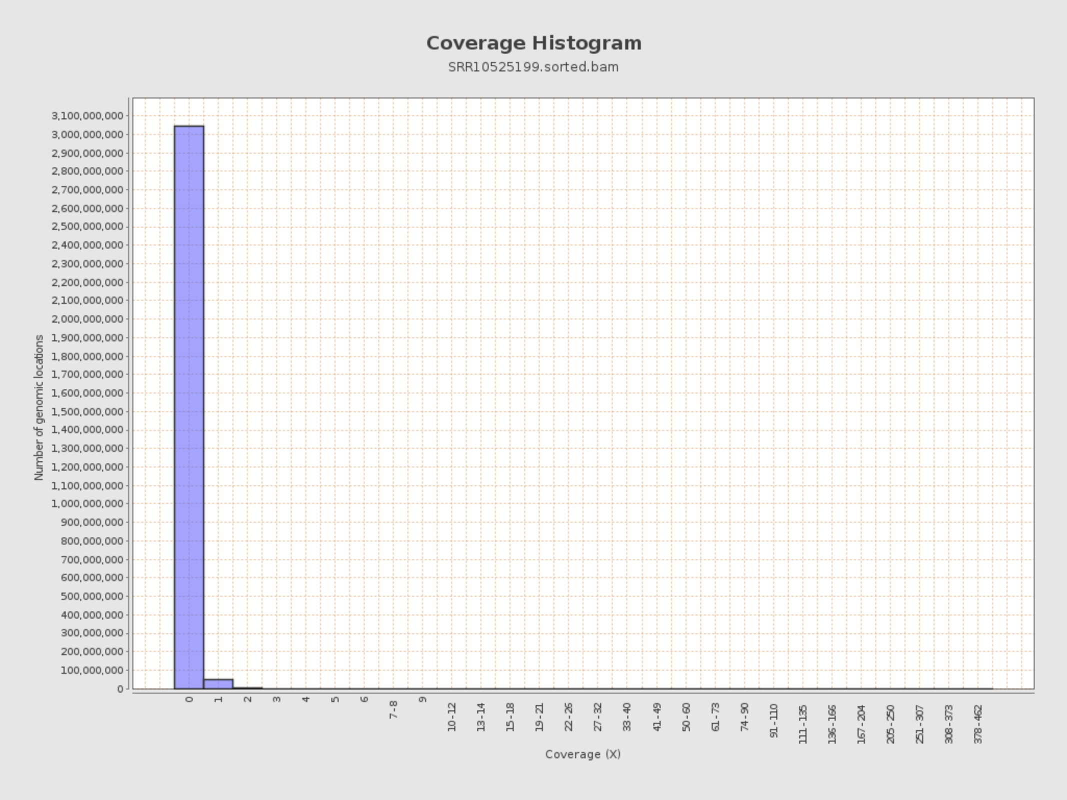
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6658875	0.0267	0.3747
chr2	243199373	4757208	0.0196	0.2181
chr3	198022430	4723363	0.0239	0.1631
chr4	191154276	3212166	0.0168	0.1428
chr5	180915260	2550633	0.0141	0.1242
chr6	171115067	3595162	0.021	0.1609
chr7	159138663	2785594	0.0175	0.2849

chr8	146364022	3296706	0.0225	0.1869
chr9	141213431	1908573	0.0135	0.1487
chr10	135534747	3120634	0.023	0.234
chr11	135006516	2590762	0.0192	0.1665
chr12	133851895	2563624	0.0192	0.1462
chr13	115169878	1757928	0.0153	0.1296
chr14	107349540	2137788	0.0199	0.1505
chr15	102531392	1532393	0.0149	0.1278
chr16	90354753	1589523	0.0176	0.1475
chr17	81195210	1322497	0.0163	0.1369
chr18	78077248	1205114	0.0154	0.2567
chr19	59128983	1027643	0.0174	0.271
chr20	63025520	1054669	0.0167	0.1364
chr21	48129895	719884	0.015	0.1358
chr22	51304566	508490	0.0099	0.1035
chrMT	16571	96308	5.8118	3.7884
chrX	155270560	2292057	0.0148	0.1338
chrY	59373566	166721	0.0028	0.1029

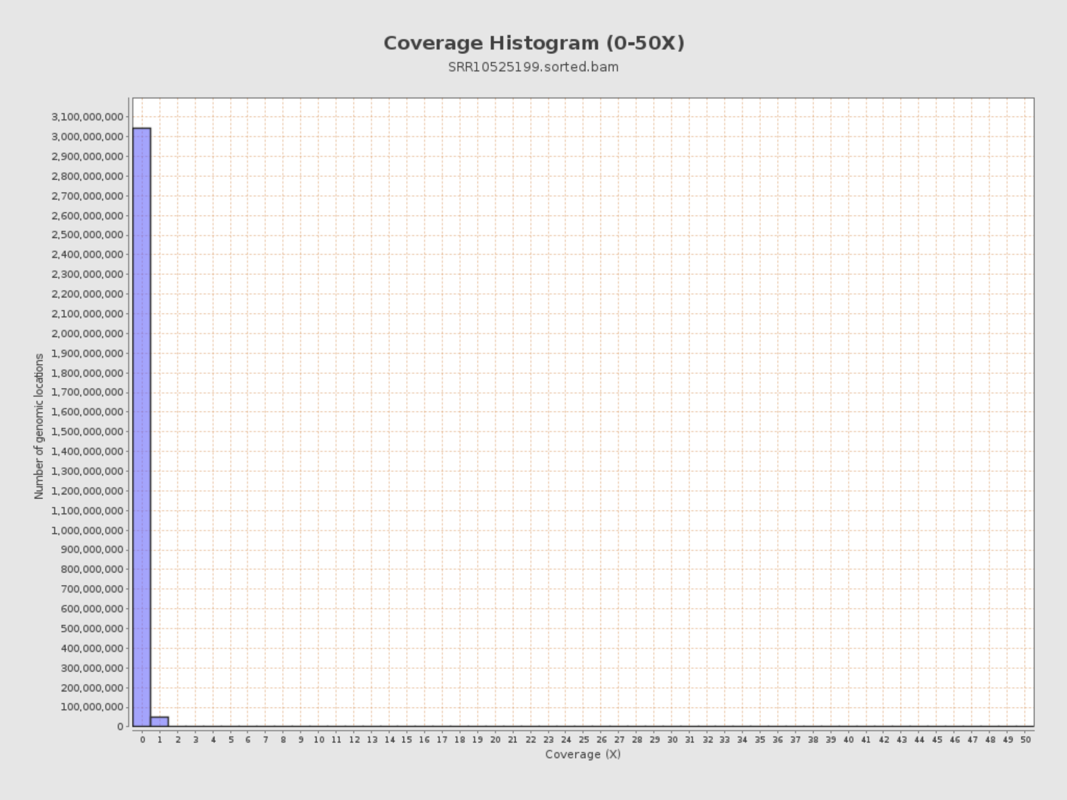
3. Results : Coverage across reference



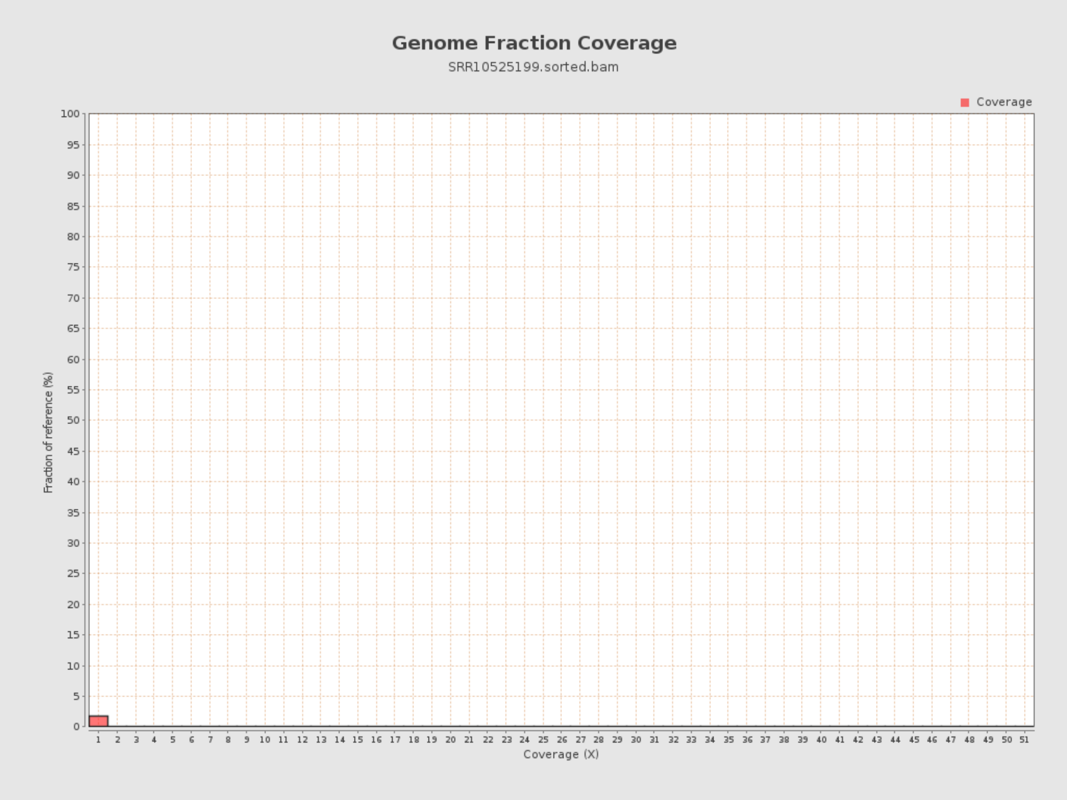
4. Results : Coverage Histogram



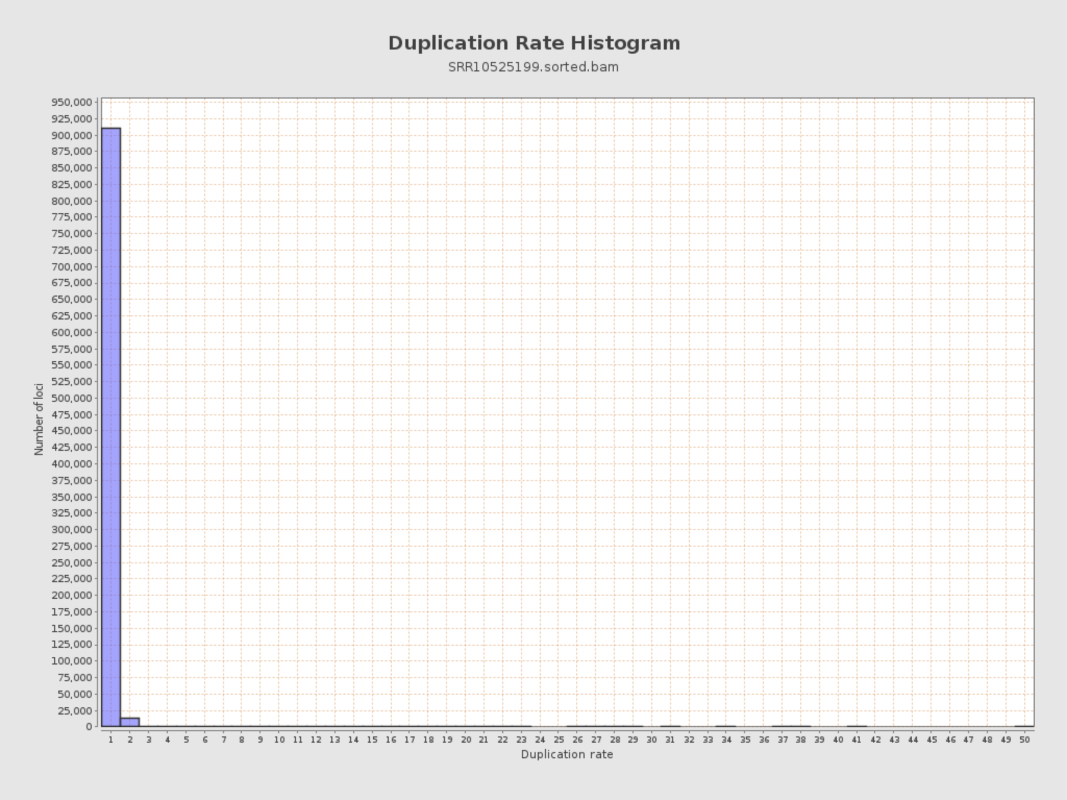
5. Results : Coverage Histogram (0-50X)



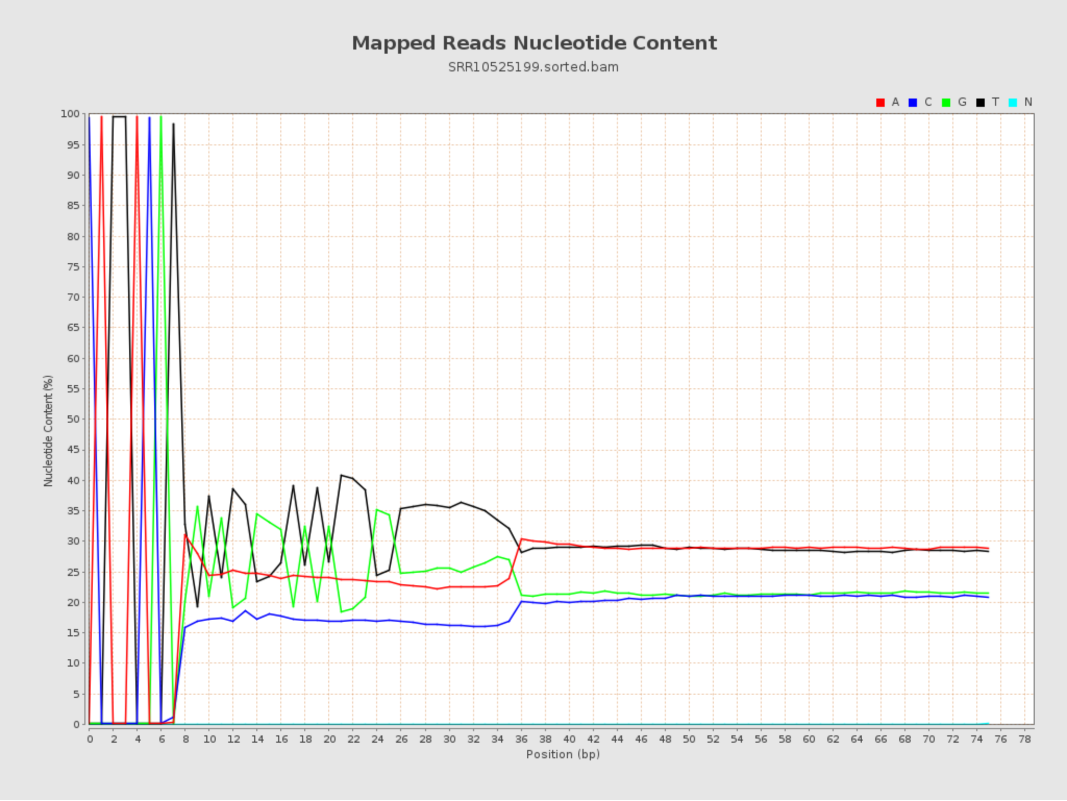
6. Results : Genome Fraction Coverage



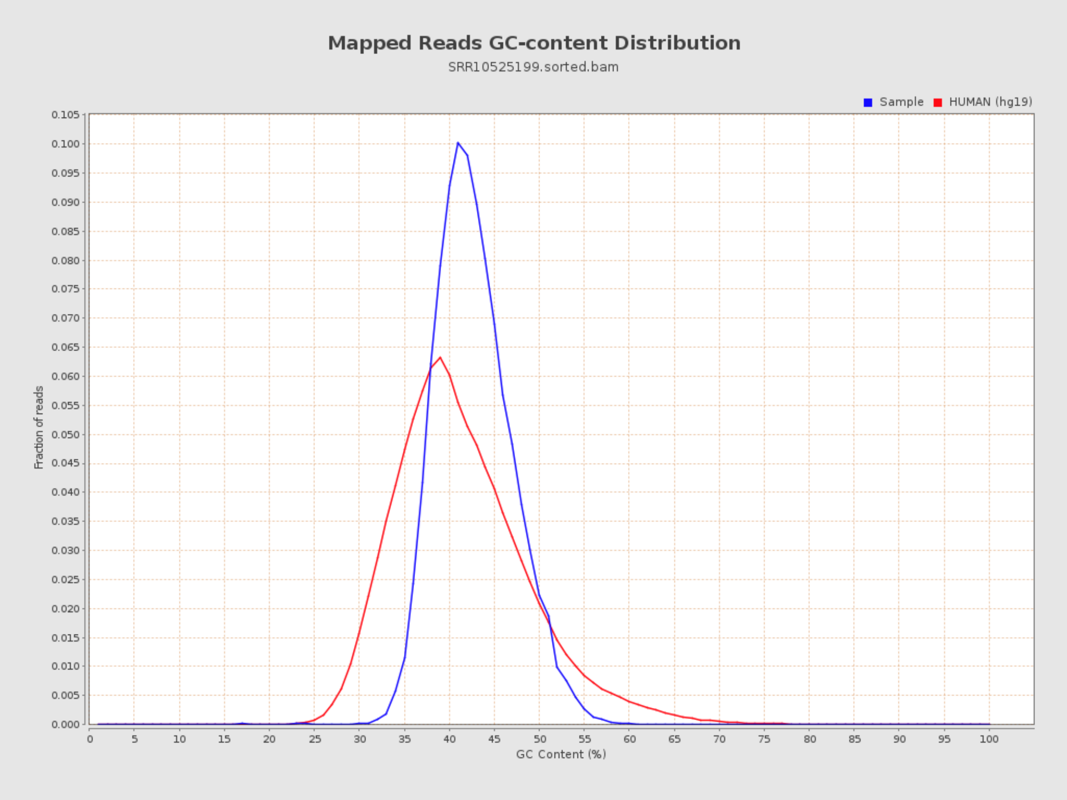
7. Results : Duplication Rate Histogram



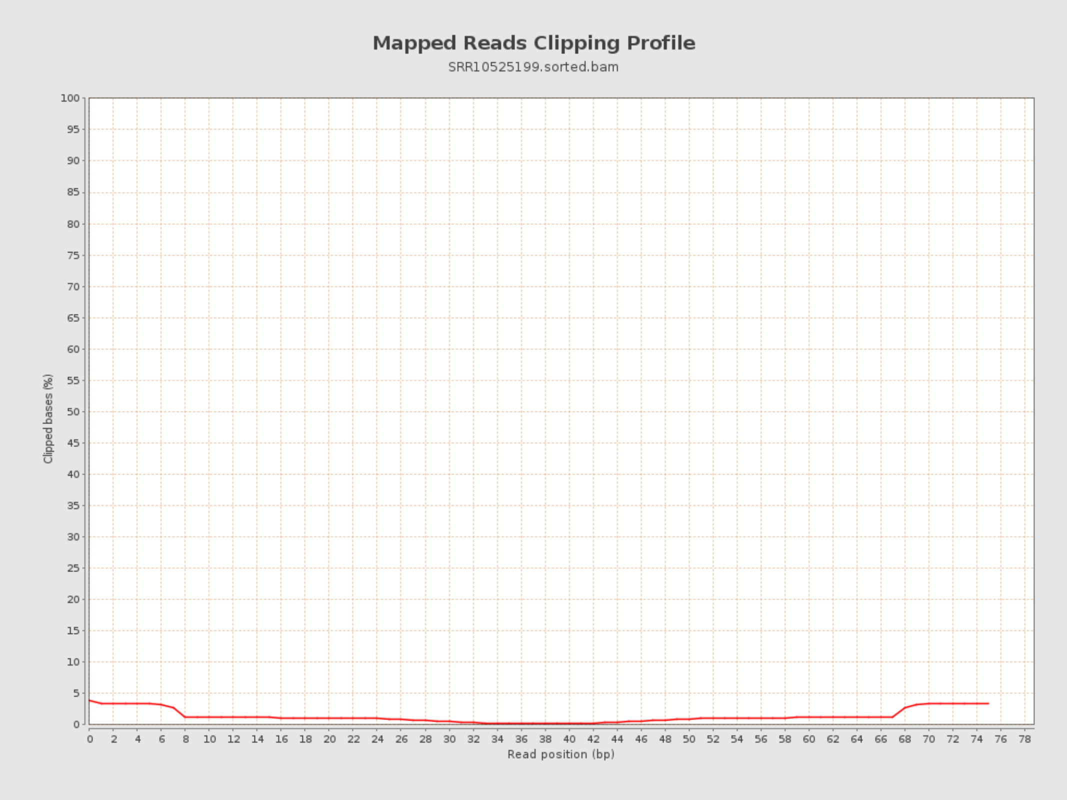
8. Results : Mapped Reads Nucleotide Content



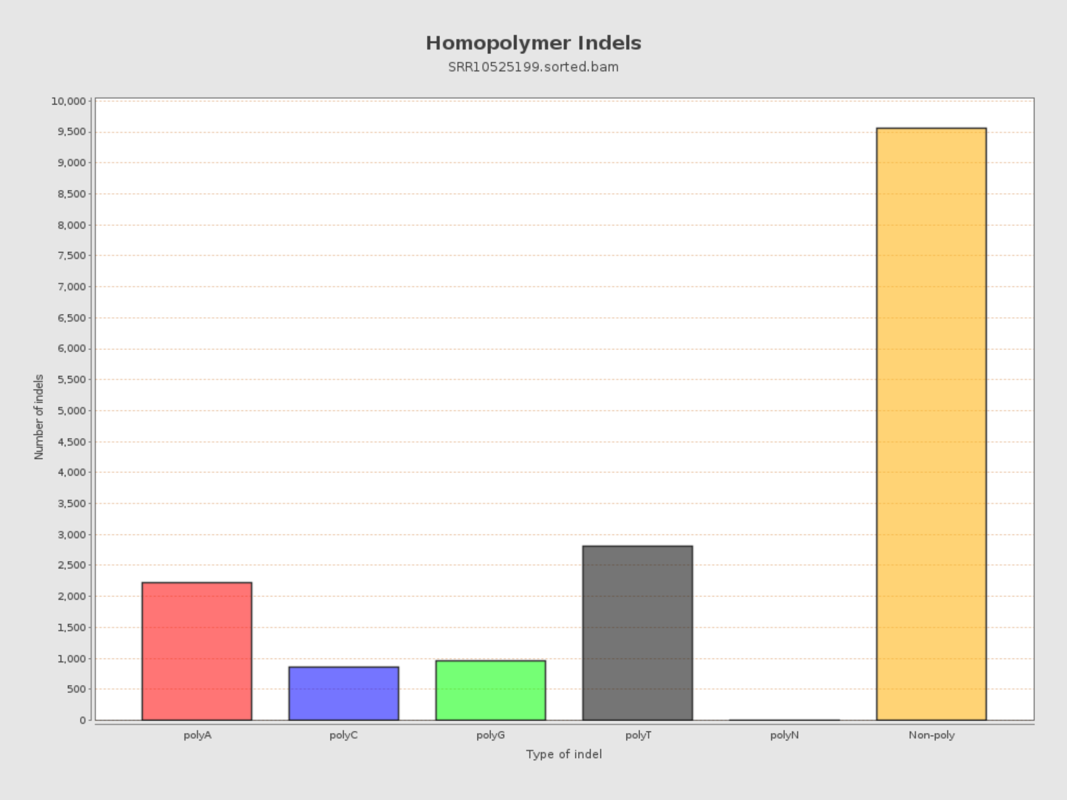
9. Results : Mapped Reads GC-content Distribution



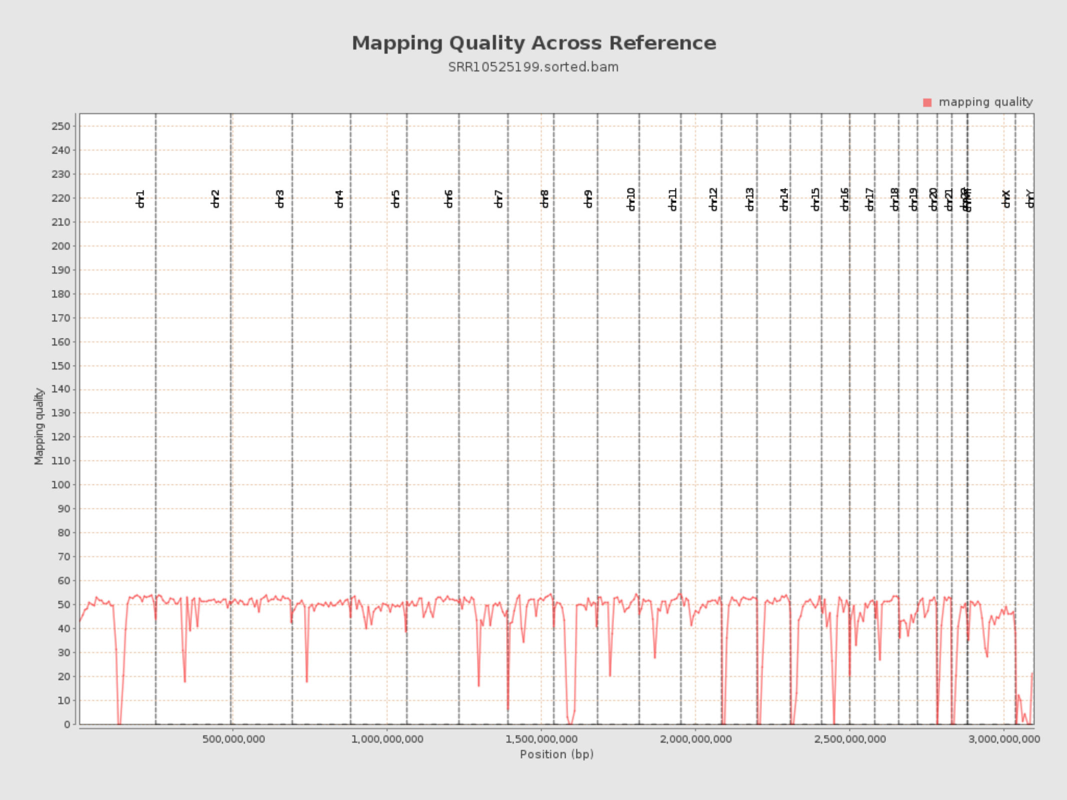
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram