Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:08:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525253.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_SRR10525253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525253.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:08:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,106,584
Mapped reads	1,010,079 / 91.28%
Unmapped reads	96,505 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,084 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,236 / 2.55%
Duplication rate	2.04%
Clipped reads	1,011,093 / 91.37%

2.2. ACGT Content

Number/percentage of A's	15,058,251 / 25.78%
Number/percentage of C's	10,544,317 / 18.06%
Number/percentage of T's	19,199,820 / 32.88%
Number/percentage of G's	13,597,355 / 23.28%
Number/percentage of N's	1,214 / 0%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.2007

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

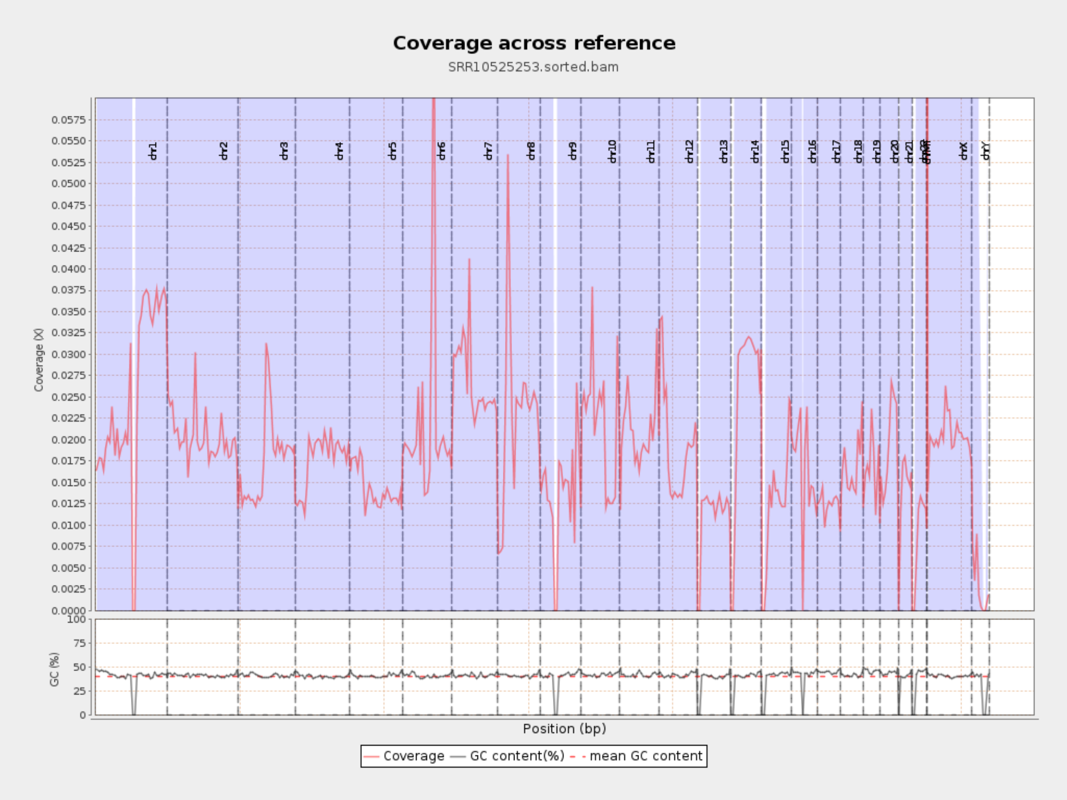
General error rate	0.52%
Mismatches	293,952
Insertions	4,696
Mapped reads with at least one insertion	0.46%
Deletions	12,229
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42%

2.6. Chromosome stats

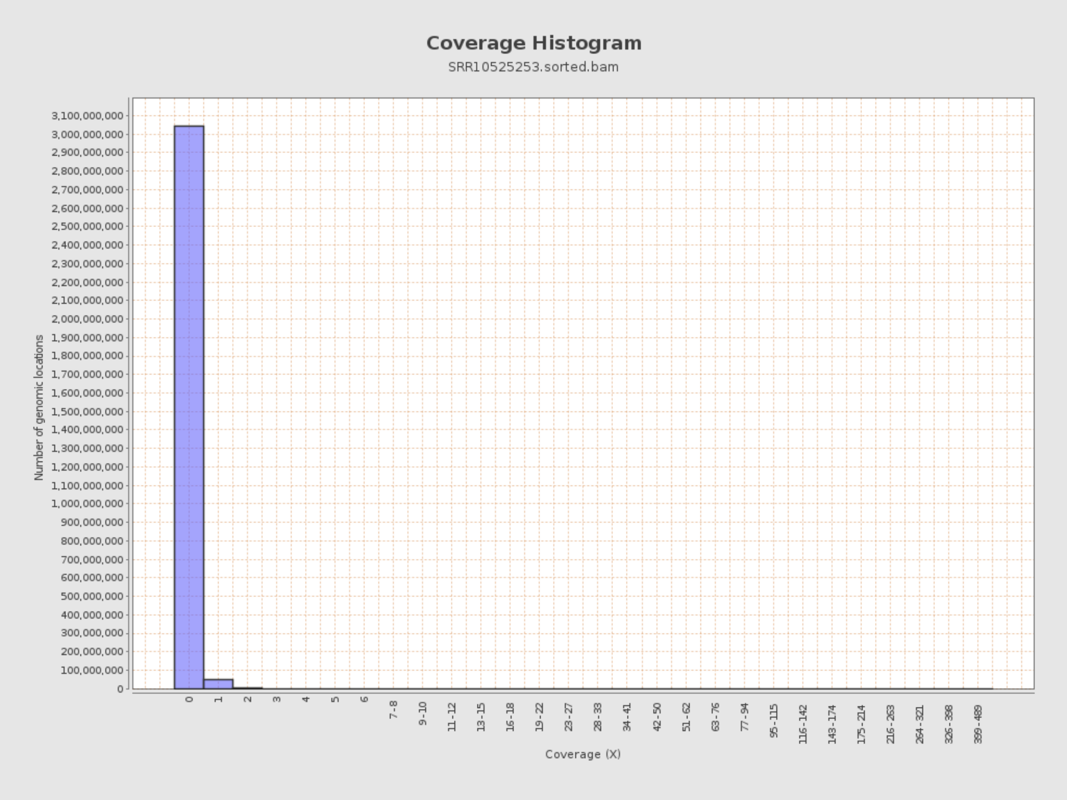
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6299666	0.0253	0.335
chr2	243199373	4935564	0.0203	0.2565
chr3	198022430	3462004	0.0175	0.1405
chr4	191154276	3386039	0.0177	0.1458
chr5	180915260	2597766	0.0144	0.1267
chr6	171115067	3848580	0.0225	0.1741
chr7	159138663	4292863	0.027	0.3236

chr8	146364022	3404414	0.0233	0.208
chr9	141213431	1932295	0.0137	0.1514
chr10	135534747	2995050	0.0221	0.2098
chr11	135006516	2840282	0.021	0.1782
chr12	133851895	2595085	0.0194	0.1481
chr13	115169878	1281595	0.0111	0.112
chr14	107349540	2704579	0.0252	0.1687
chr15	102531392	1267412	0.0124	0.1194
chr16	90354753	1480337	0.0164	0.1453
chr17	81195210	1010968	0.0125	0.1211
chr18	78077248	1308118	0.0168	0.2583
chr19	59128983	1001526	0.0169	0.2341
chr20	63025520	1218690	0.0193	0.1481
chr21	48129895	679646	0.0141	0.1285
chr22	51304566	449073	0.0088	0.0978
chrMT	16571	83938	5.0654	3.3386
chrX	155270560	3175575	0.0205	0.1599
chrY	59373566	169290	0.0029	0.0815

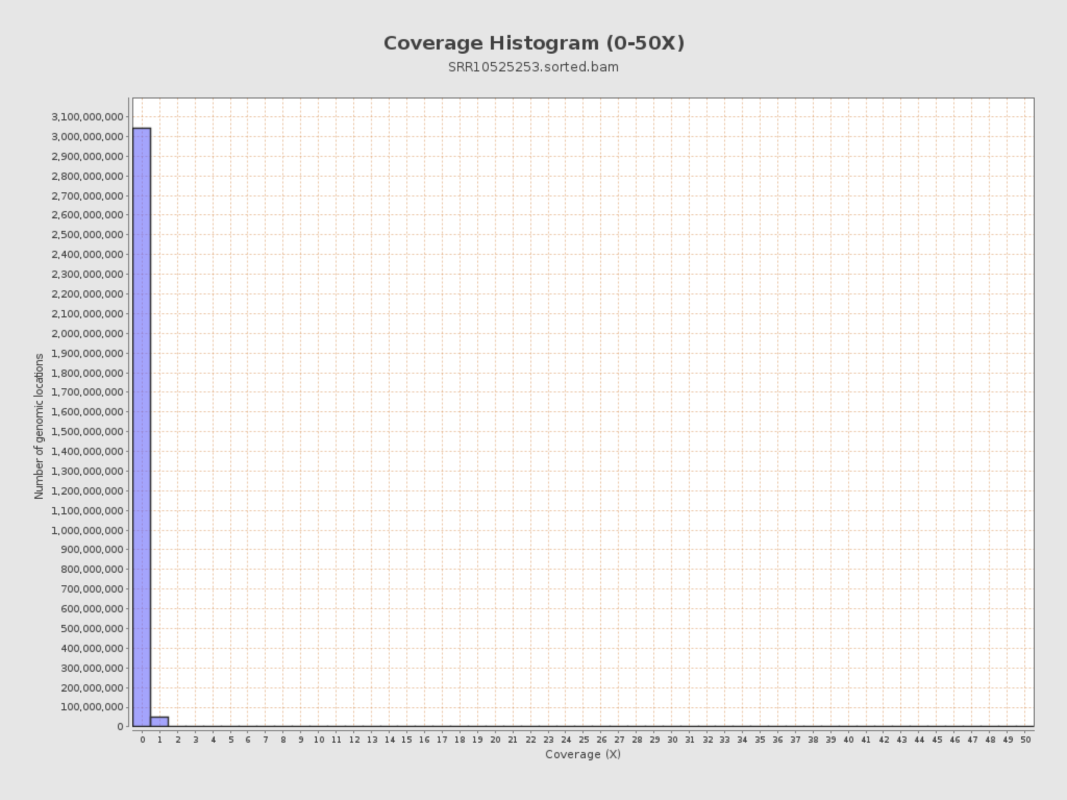
3. Results : Coverage across reference



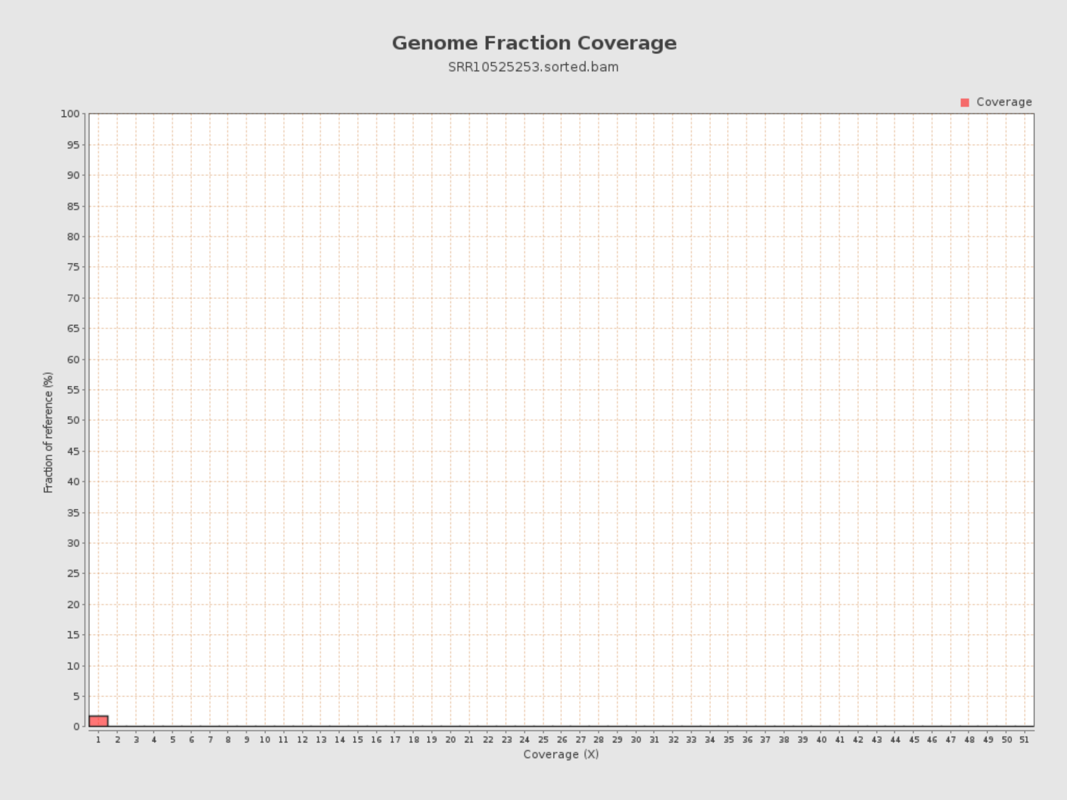
4. Results : Coverage Histogram



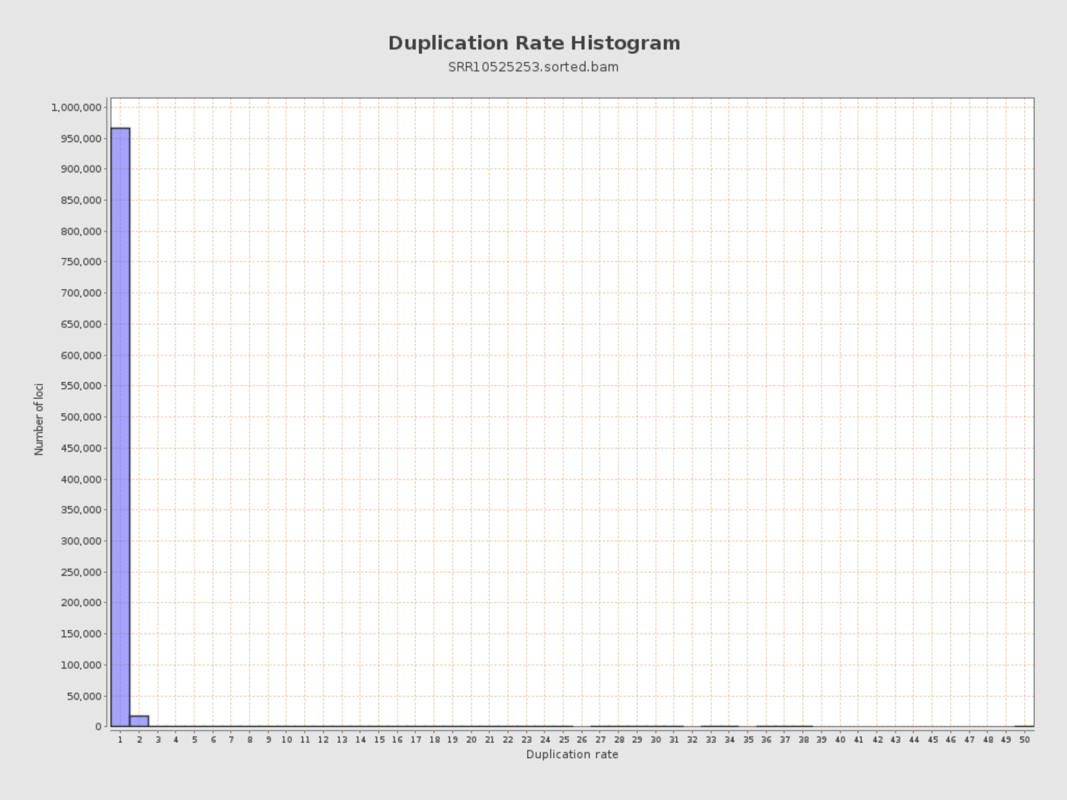
5. Results : Coverage Histogram (0-50X)



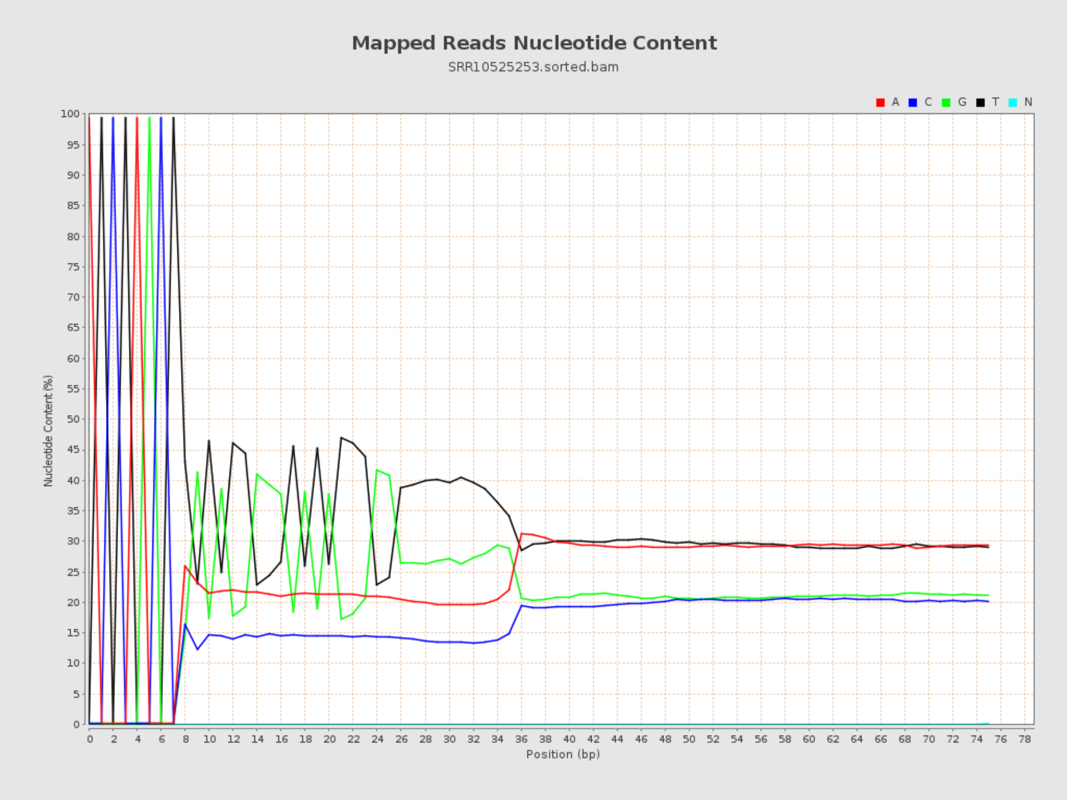
6. Results : Genome Fraction Coverage



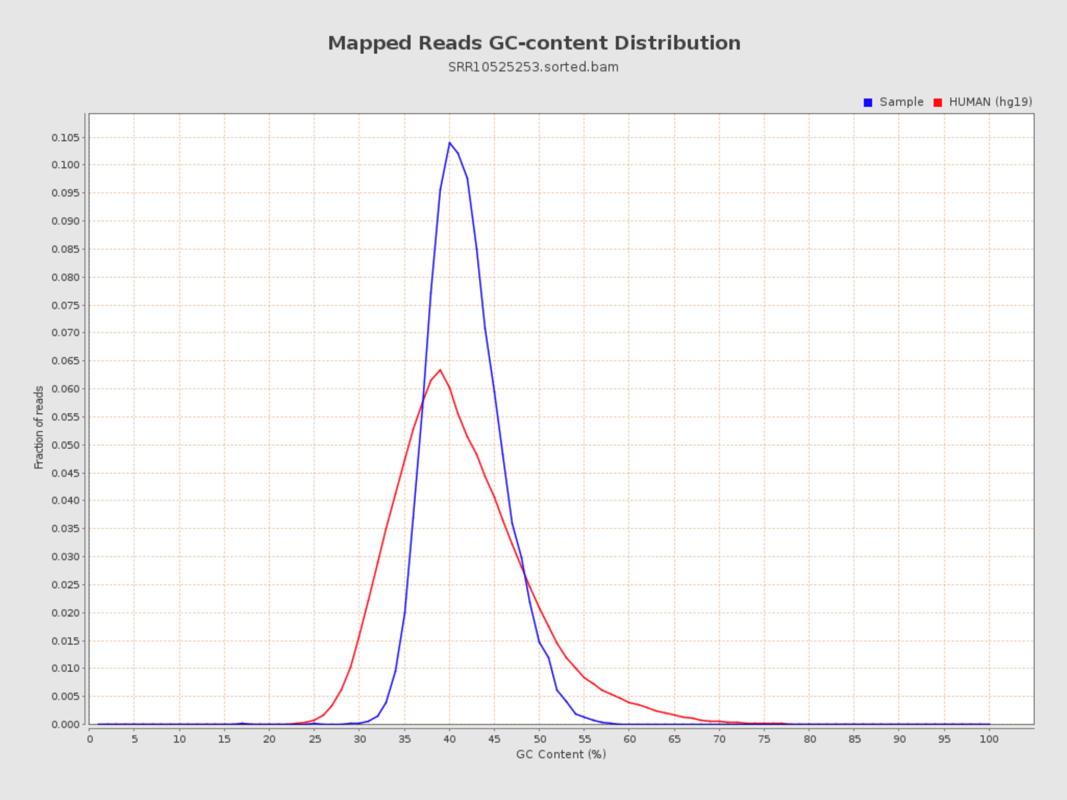
7. Results : Duplication Rate Histogram



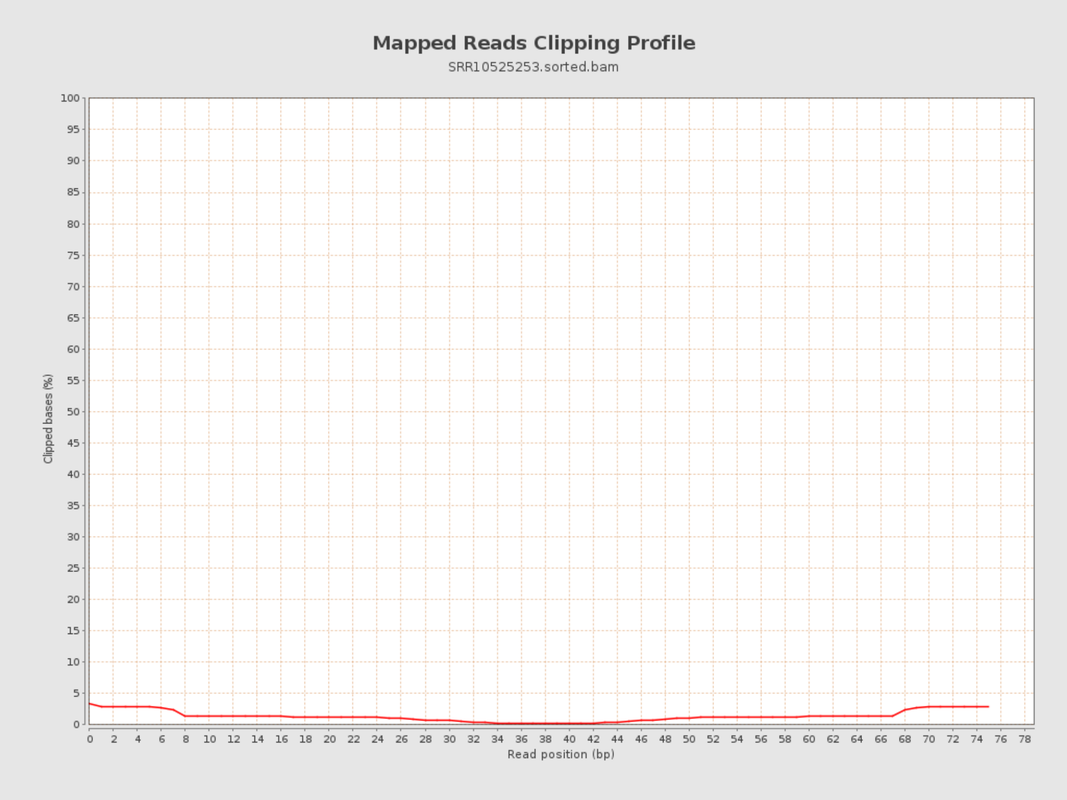
8. Results : Mapped Reads Nucleotide Content



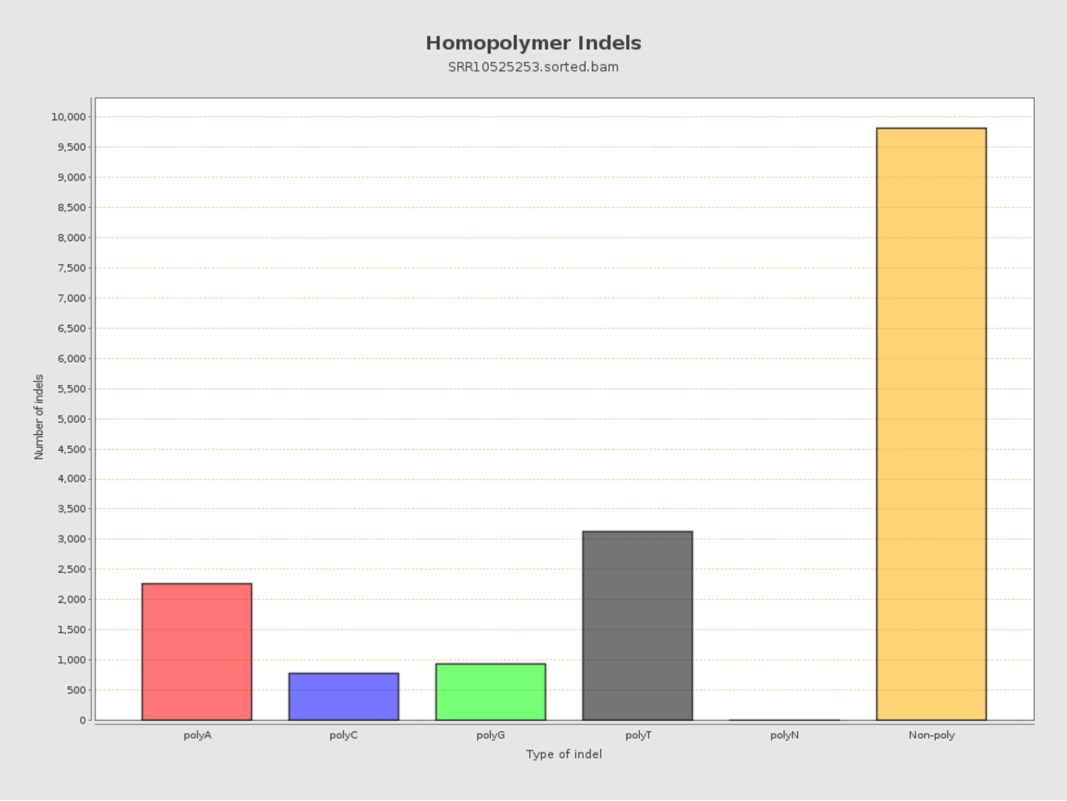
9. Results : Mapped Reads GC-content Distribution



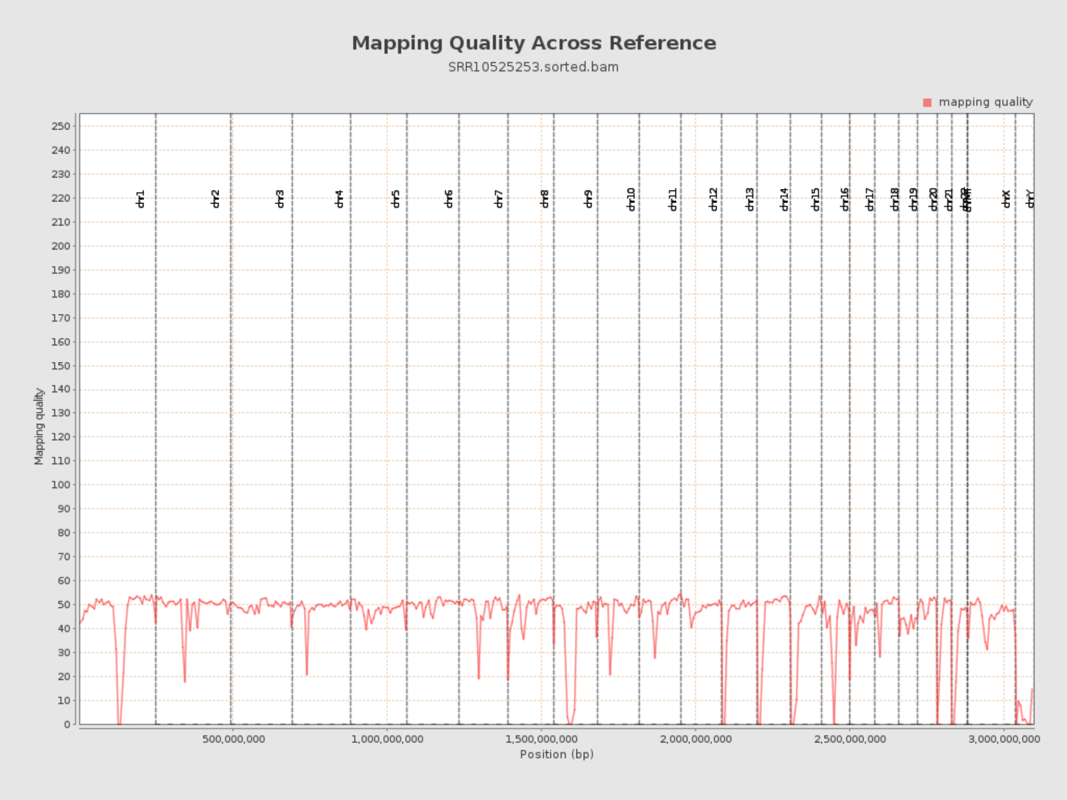
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram