Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:55:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525071.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_SRR10525071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:55:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,096,078
Mapped reads	954,667 / 87.1%
Unmapped reads	141,411 / 12.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,144 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	44,087 / 4.02%
Duplication rate	3.82%
Clipped reads	955,360 / 87.16%

2.2. ACGT Content

Number/percentage of A's	13,928,275 / 25.23%
Number/percentage of C's	10,715,041 / 19.41%
Number/percentage of T's	17,375,061 / 31.47%
Number/percentage of G's	13,181,746 / 23.88%
Number/percentage of N's	5,493 / 0.01%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1841

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

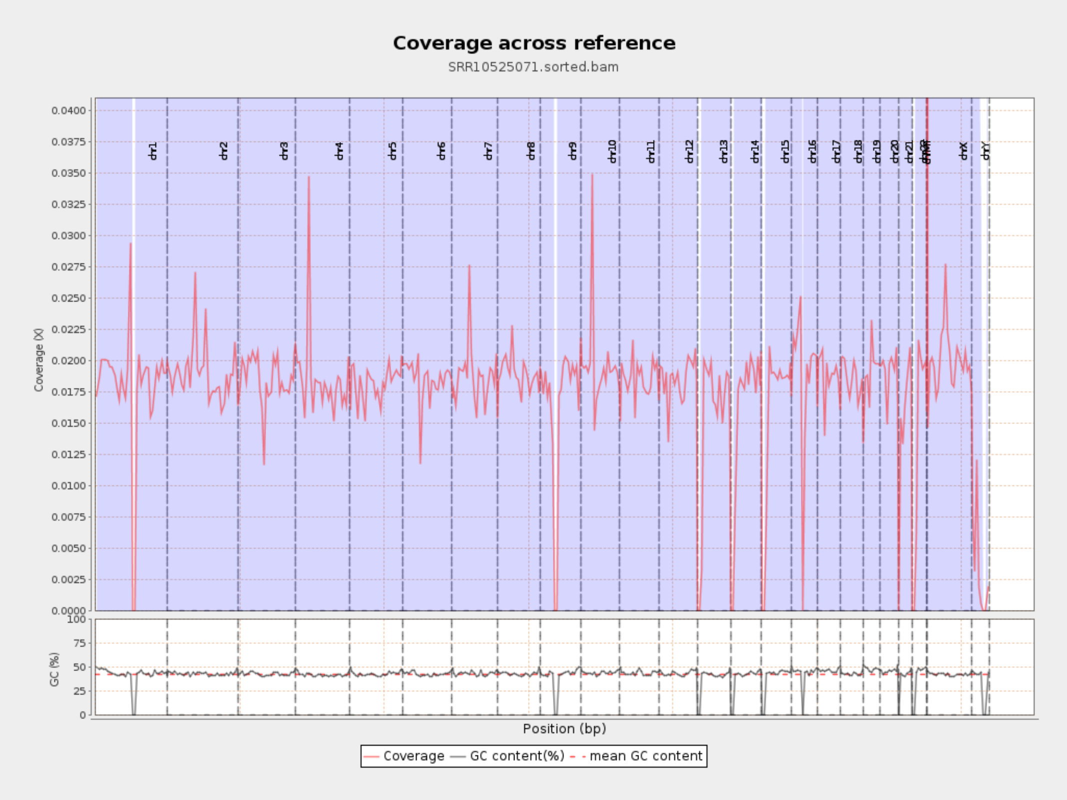
General error rate	0.48%
Mismatches	259,708
Insertions	3,719
Mapped reads with at least one insertion	0.39%
Deletions	10,668
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.5%

2.6. Chromosome stats

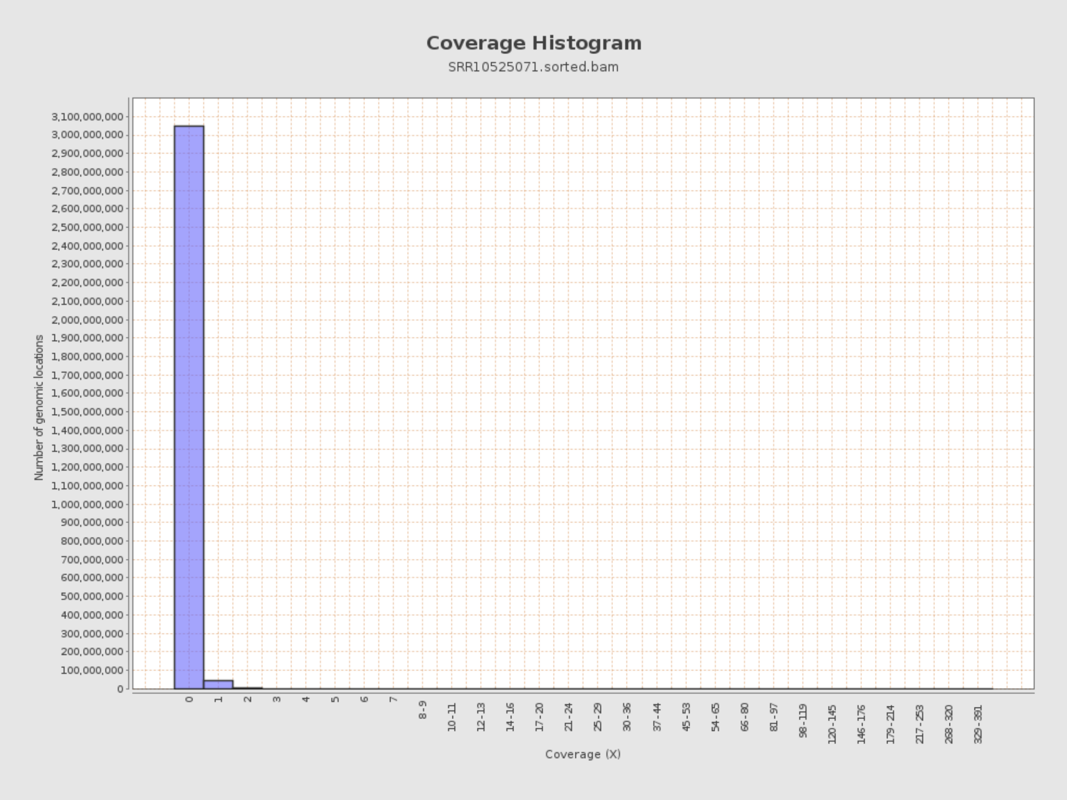
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4444252	0.0178	0.3031
chr2	243199373	4622924	0.019	0.2208
chr3	198022430	3659634	0.0185	0.1479
chr4	191154276	3553996	0.0186	0.1614
chr5	180915260	3298518	0.0182	0.1468
chr6	171115067	3152067	0.0184	0.1534
chr7	159138663	2999071	0.0188	0.2128

chr8	146364022	2777807	0.019	0.178
chr9	141213431	2296748	0.0163	0.1564
chr10	135534747	2667727	0.0197	0.2002
chr11	135006516	2521180	0.0187	0.1632
chr12	133851895	2477916	0.0185	0.1502
chr13	115169878	1726071	0.015	0.1335
chr14	107349540	1675085	0.0156	0.1378
chr15	102531392	1587552	0.0155	0.1365
chr16	90354753	1667110	0.0185	0.1533
chr17	81195210	1524833	0.0188	0.1529
chr18	78077248	1452429	0.0186	0.2297
chr19	59128983	1135376	0.0192	0.2238
chr20	63025520	1205632	0.0191	0.1538
chr21	48129895	747065	0.0155	0.1473
chr22	51304566	708611	0.0138	0.1282
chrMT	16571	13449	0.8116	1.1834
chrX	155270560	3115323	0.0201	0.1648
chrY	59373566	192174	0.0032	0.1167

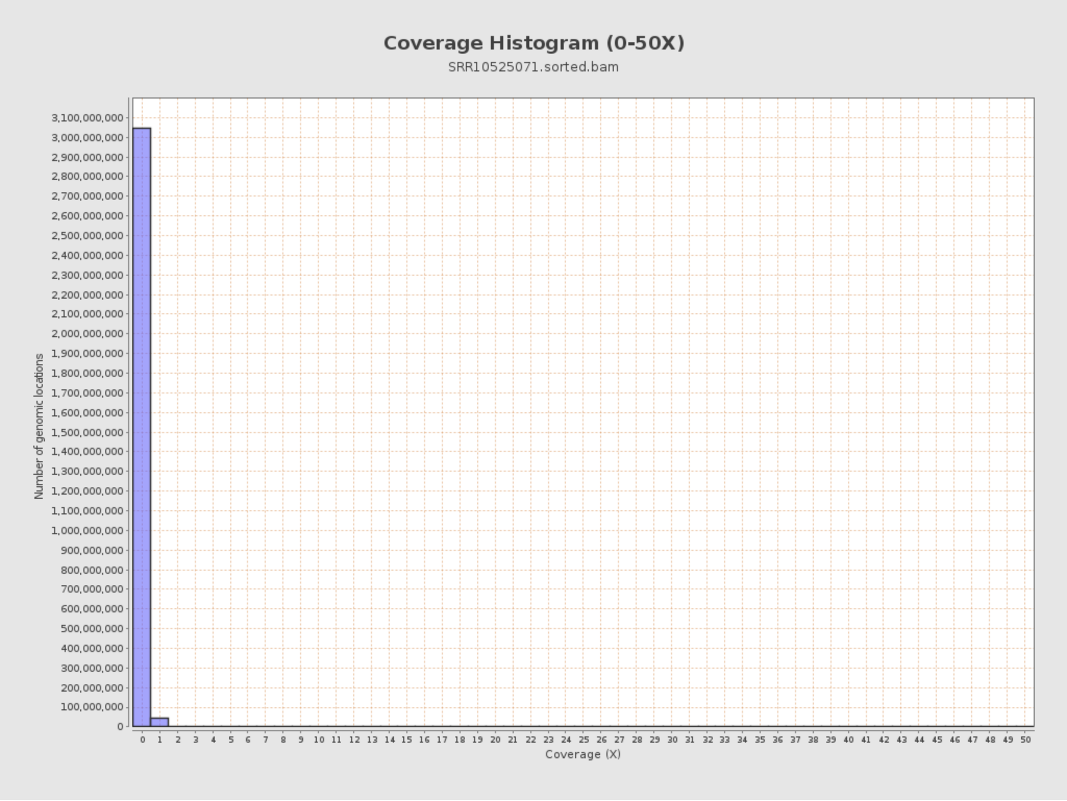
3. Results : Coverage across reference



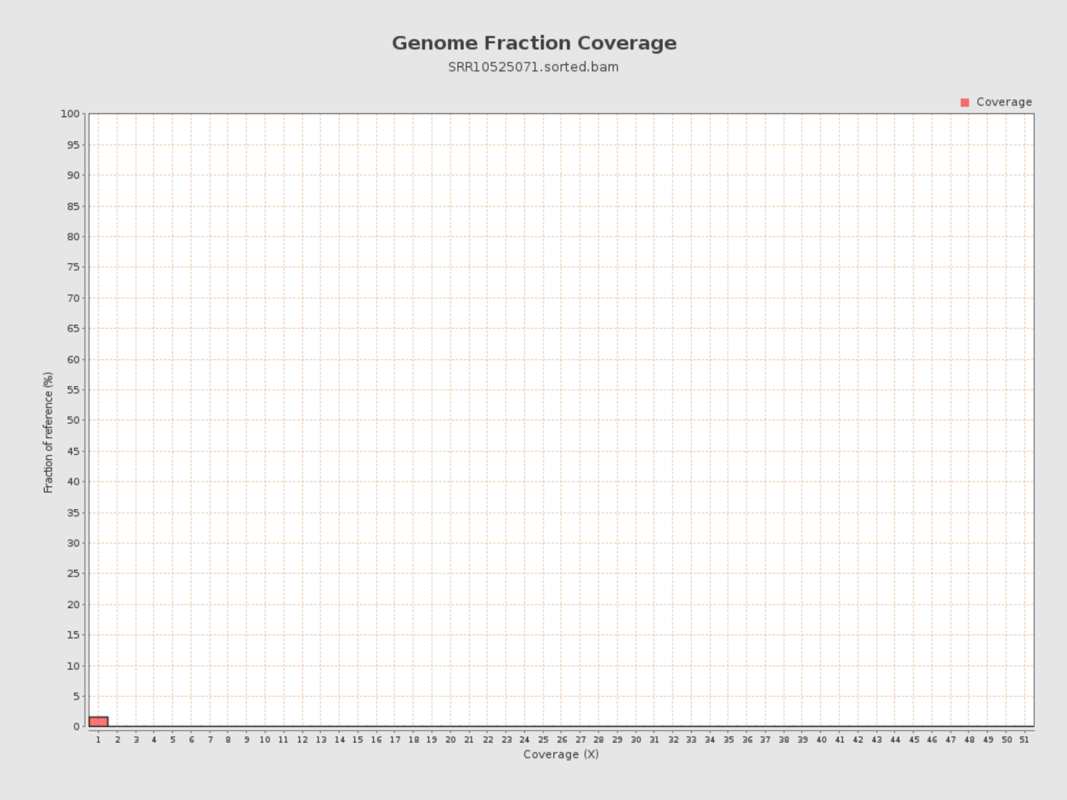
4. Results : Coverage Histogram



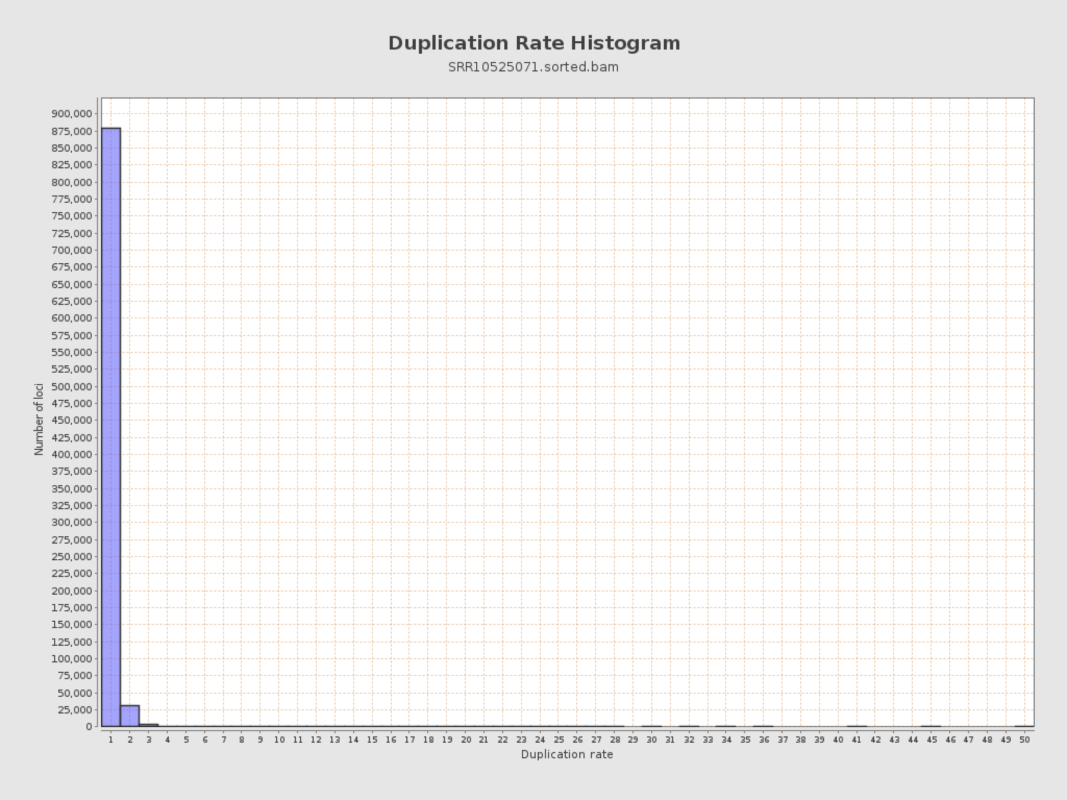
5. Results : Coverage Histogram (0-50X)



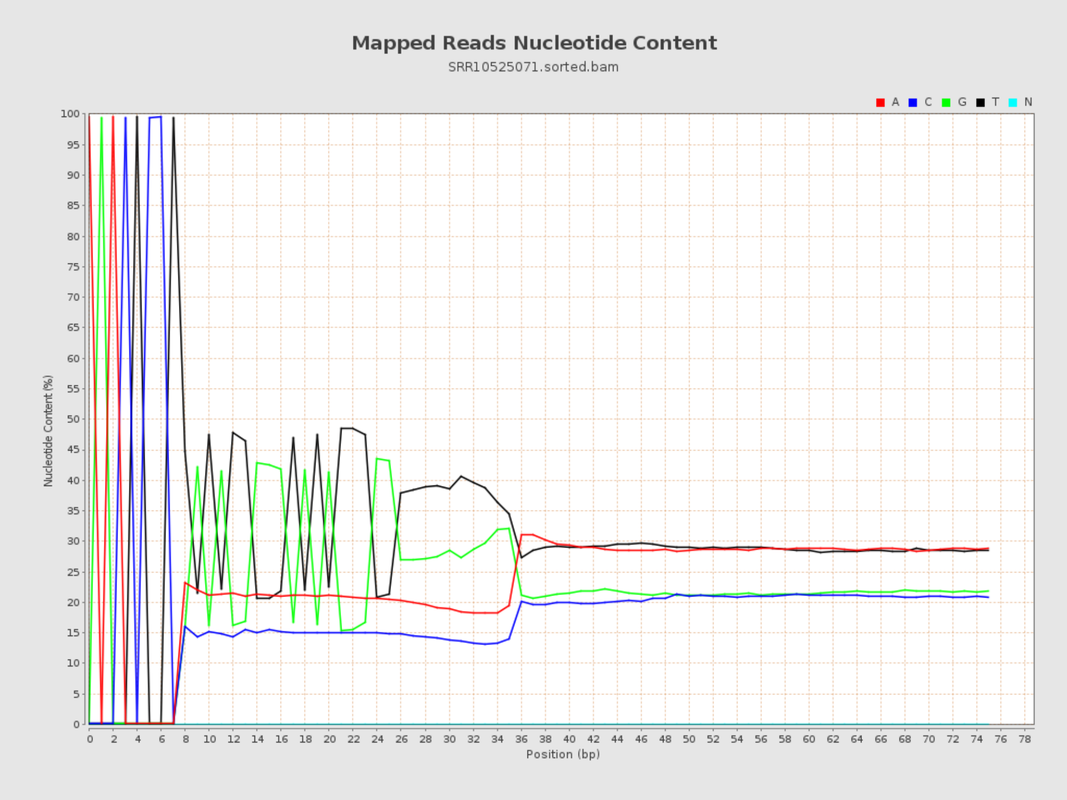
6. Results : Genome Fraction Coverage



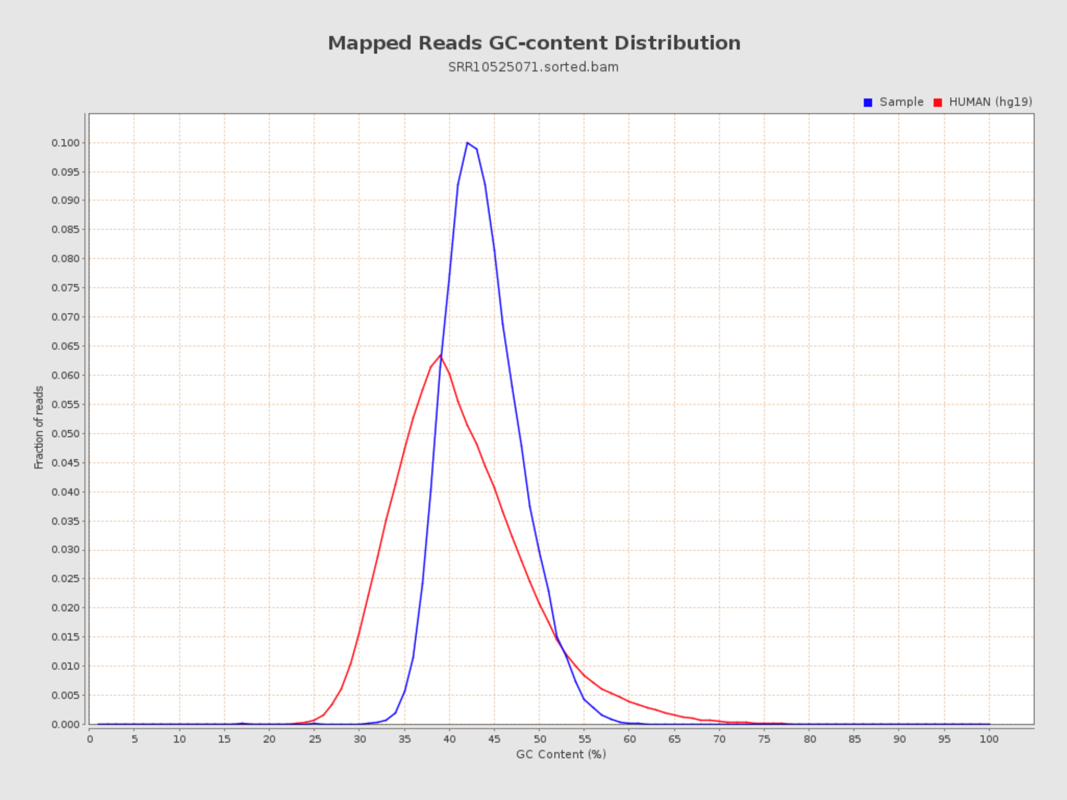
7. Results : Duplication Rate Histogram



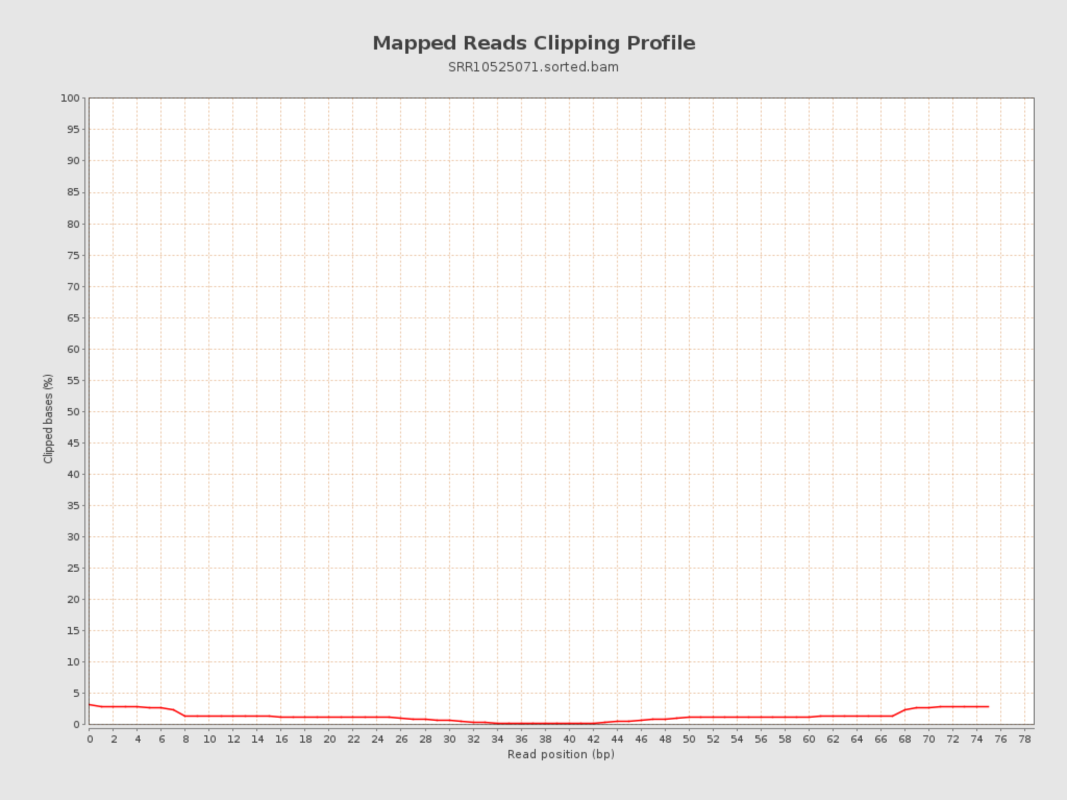
8. Results : Mapped Reads Nucleotide Content



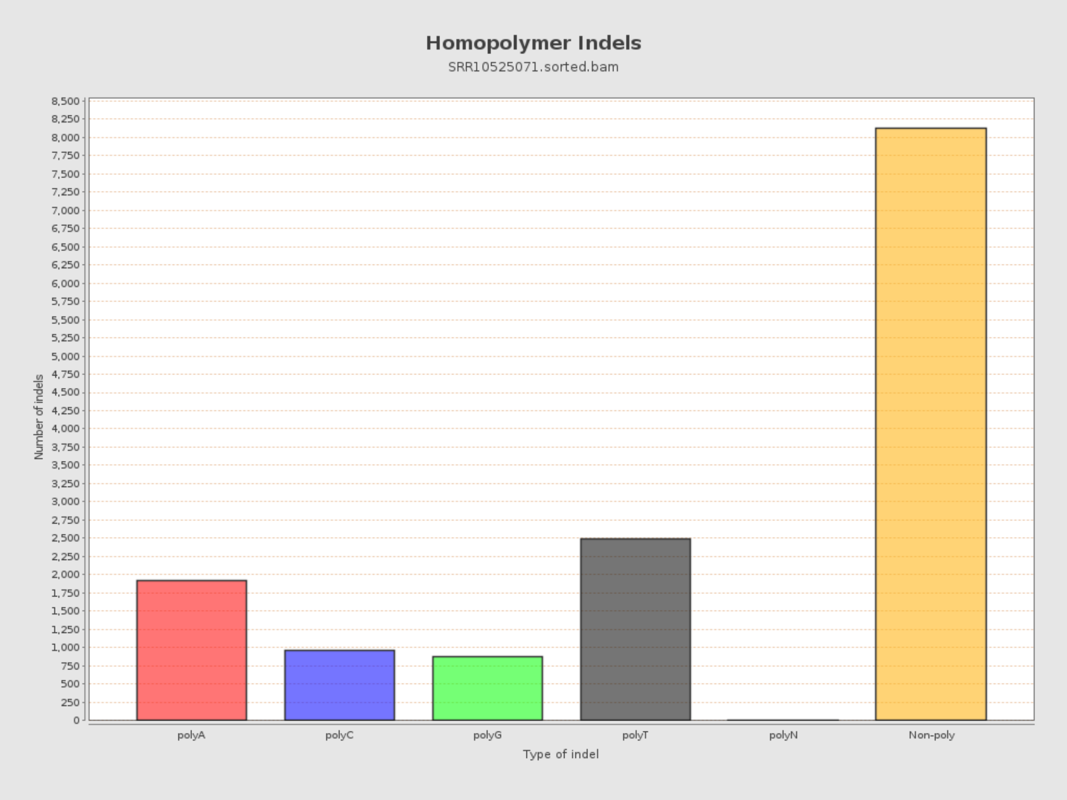
9. Results : Mapped Reads GC-content Distribution



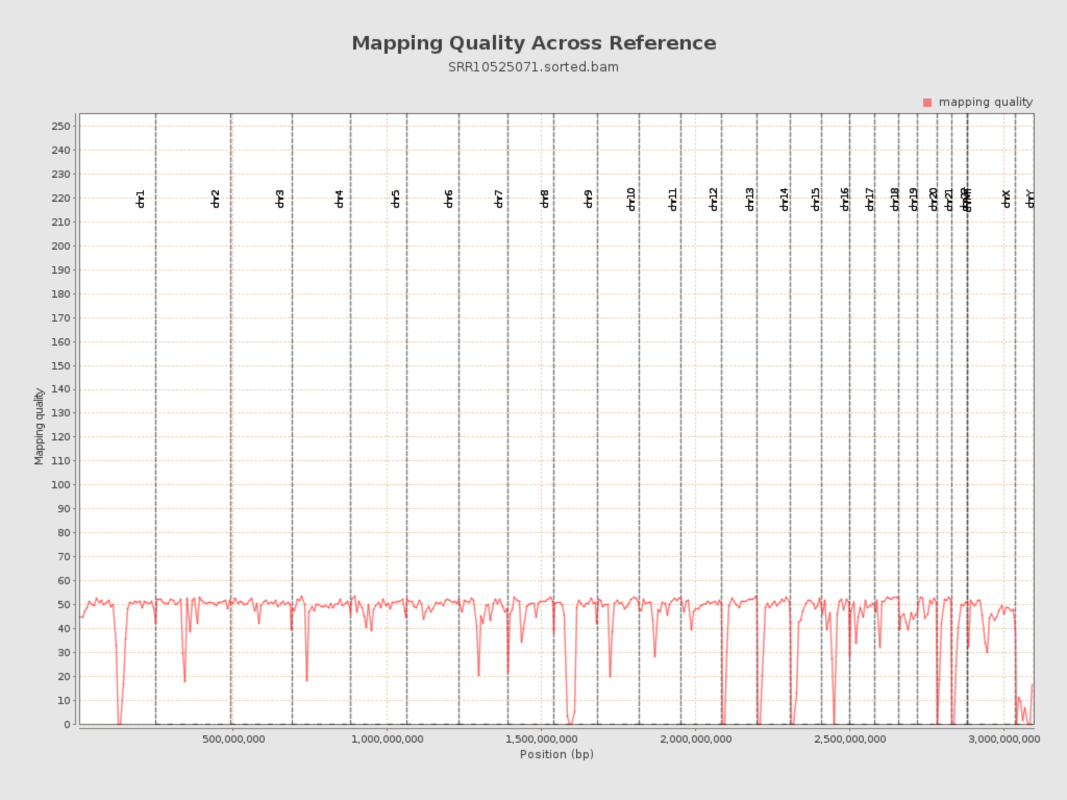
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram