Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:17:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524625.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_SRR10524625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524625.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:17:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	636,655
Mapped reads	579,056 / 90.95%
Unmapped reads	57,599 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,928 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,346 / 4.3%
Duplication rate	3.98%
Clipped reads	579,526 / 91.03%

2.2. ACGT Content

Number/percentage of A's	8,270,687 / 25.05%
Number/percentage of C's	5,728,273 / 17.35%
Number/percentage of T's	10,492,097 / 31.78%
Number/percentage of G's	8,525,013 / 25.82%
Number/percentage of N's	185 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1315

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

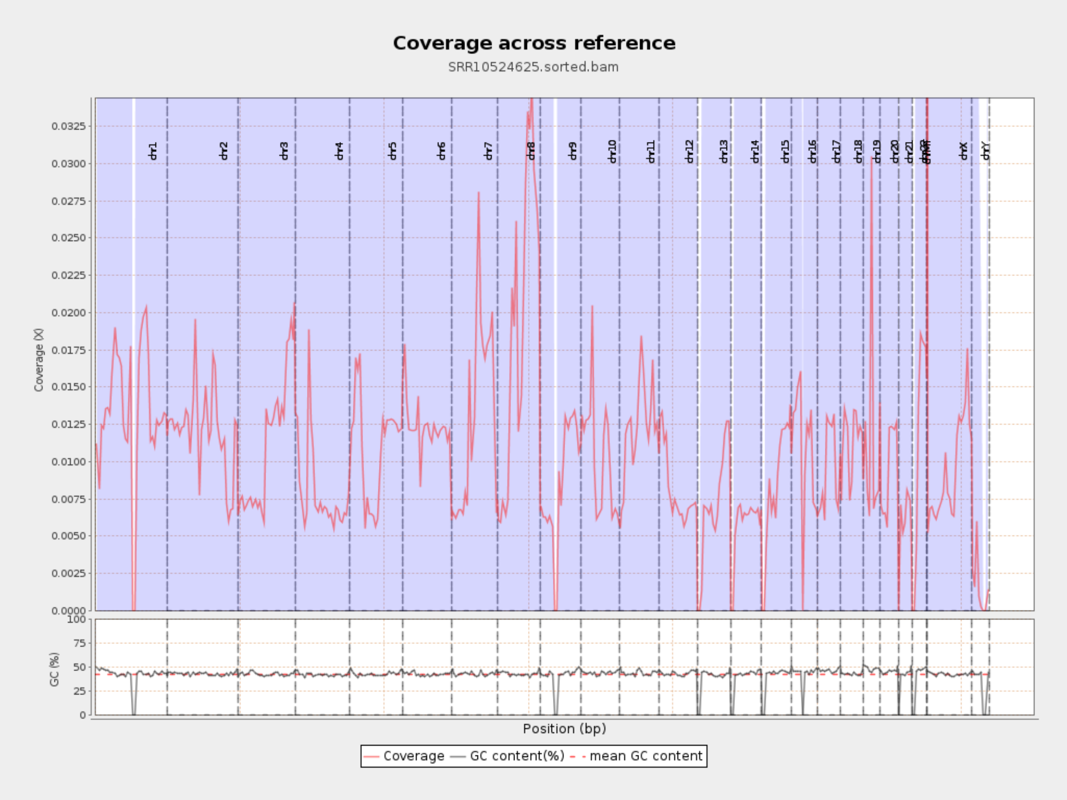
General error rate	0.58%
Mismatches	186,386
Insertions	2,000
Mapped reads with at least one insertion	0.34%
Deletions	10,447
Mapped reads with at least one deletion	1.79%
Homopolymer indels	42.24%

2.6. Chromosome stats

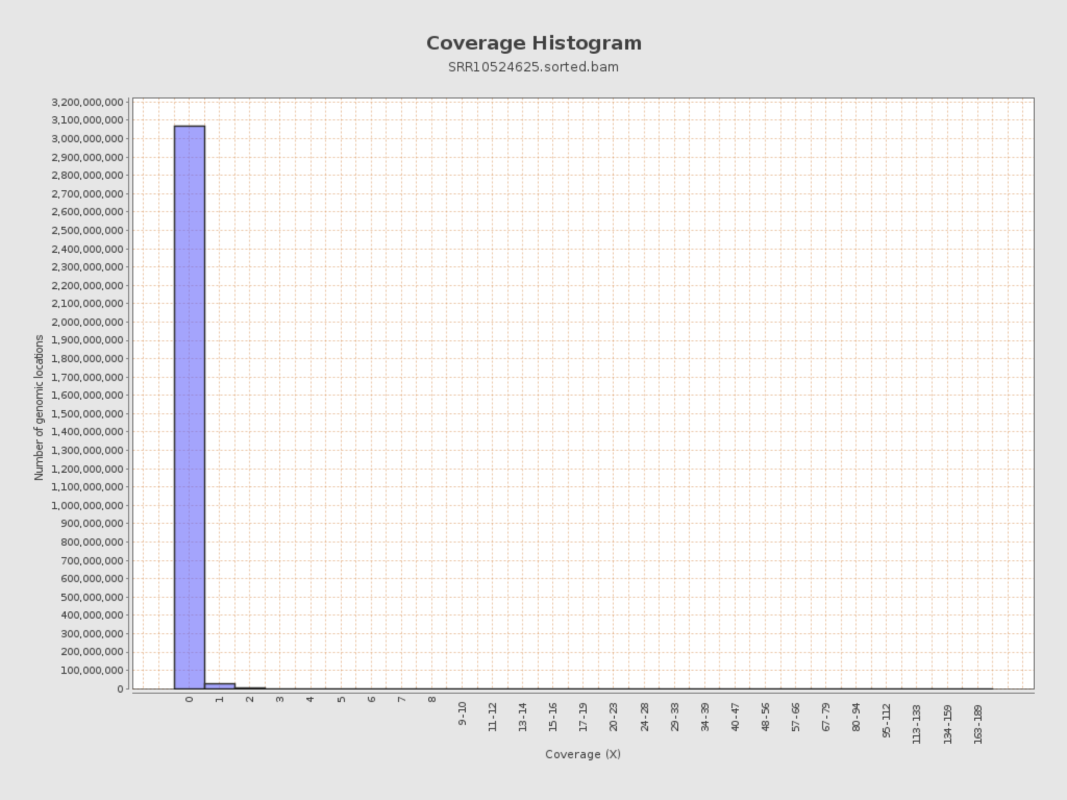
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3311542	0.0133	0.1898
chr2	243199373	2945476	0.0121	0.1525
chr3	198022430	2201136	0.0111	0.1166
chr4	191154276	1540402	0.0081	0.1079
chr5	180915260	1997721	0.011	0.1164
chr6	171115067	2109407	0.0123	0.1256
chr7	159138663	2093639	0.0132	0.1535

chr8	146364022	2866005	0.0196	0.178
chr9	141213431	1186956	0.0084	0.1135
chr10	135534747	1413081	0.0104	0.1342
chr11	135006516	1673669	0.0124	0.1338
chr12	133851895	1088877	0.0081	0.1006
chr13	115169878	811977	0.0071	0.0929
chr14	107349540	605350	0.0056	0.084
chr15	102531392	841104	0.0082	0.1008
chr16	90354753	973187	0.0108	0.1167
chr17	81195210	762038	0.0094	0.1088
chr18	78077248	884035	0.0113	0.1564
chr19	59128983	674644	0.0114	0.1531
chr20	63025520	594330	0.0094	0.1091
chr21	48129895	286459	0.006	0.0907
chr22	51304566	591049	0.0115	0.119
chrMT	16571	20675	1.2477	1.3804
chrX	155270560	1467616	0.0095	0.1121
chrY	59373566	93364	0.0016	0.0617

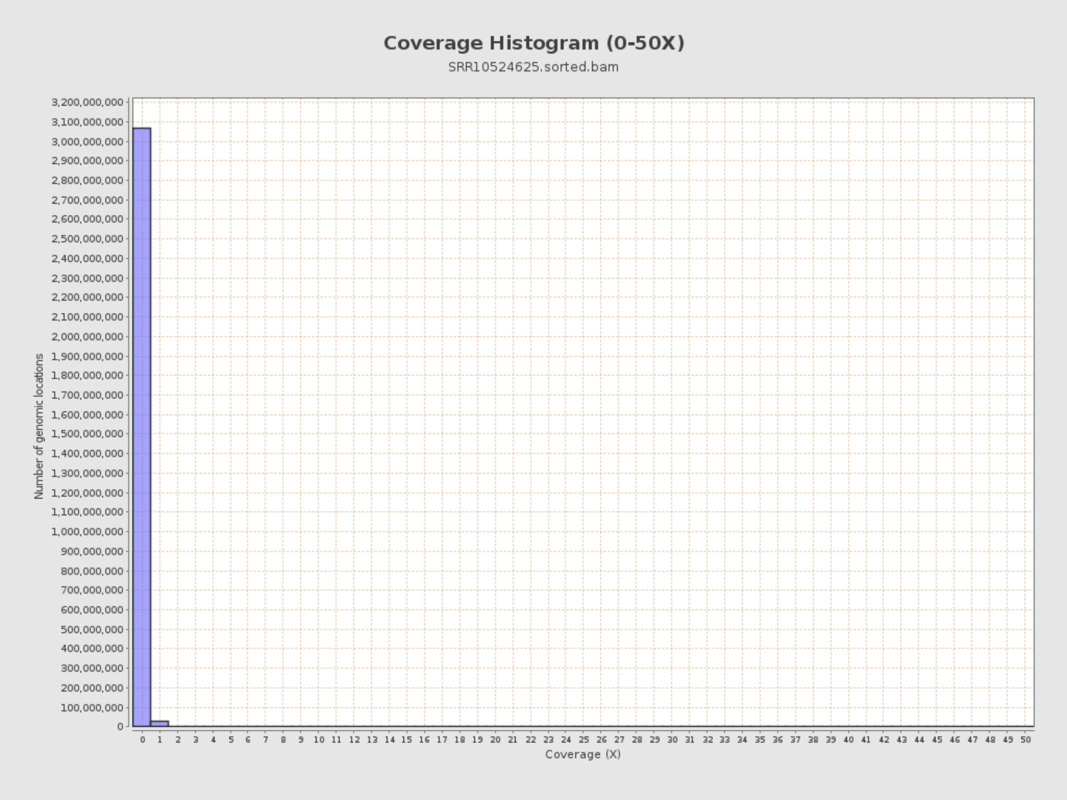
3. Results : Coverage across reference



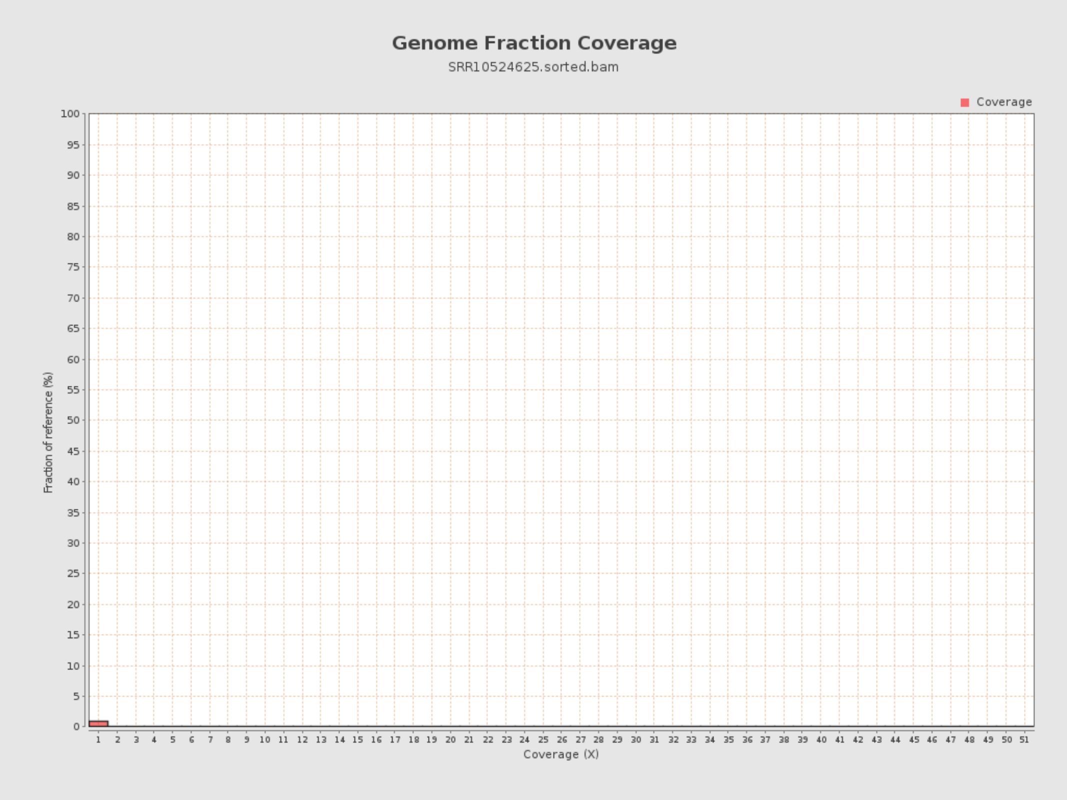
4. Results : Coverage Histogram



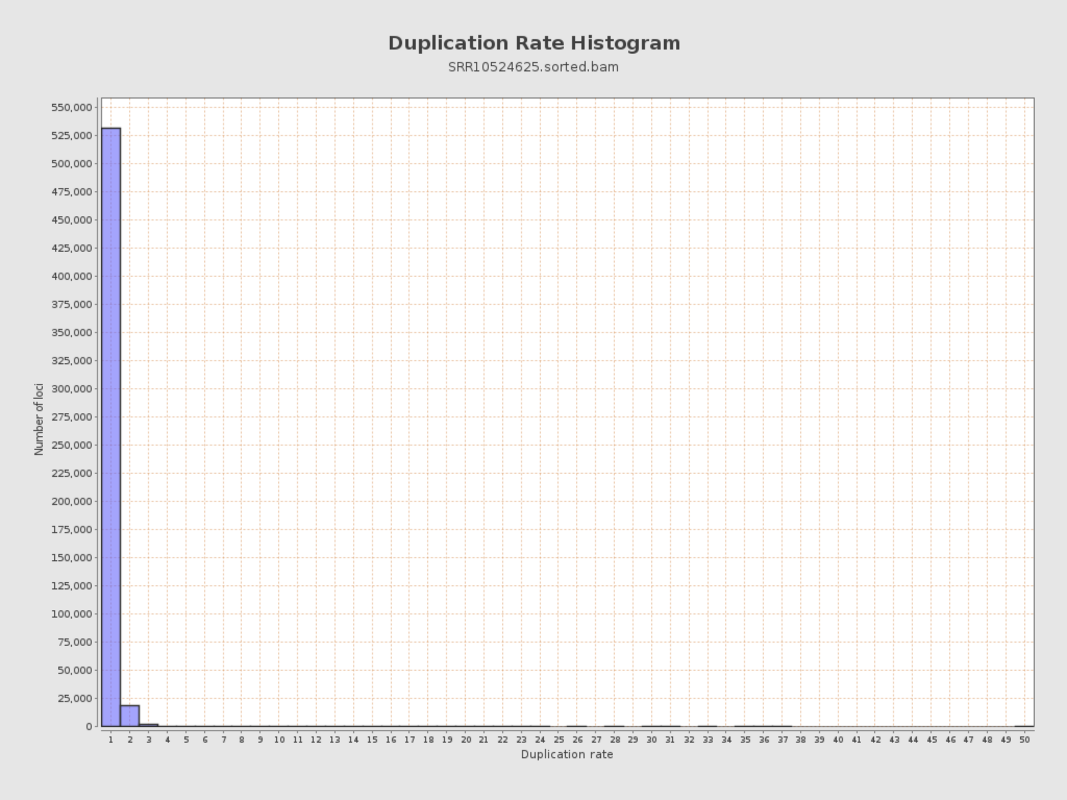
5. Results : Coverage Histogram (0-50X)



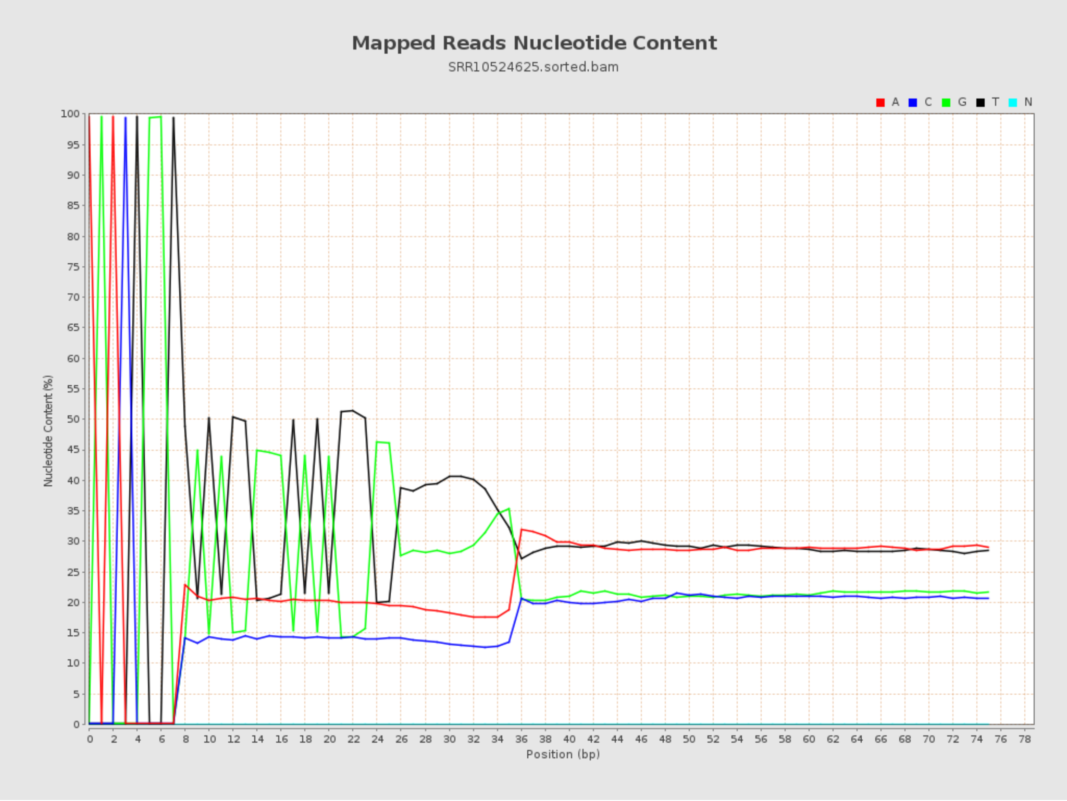
6. Results : Genome Fraction Coverage



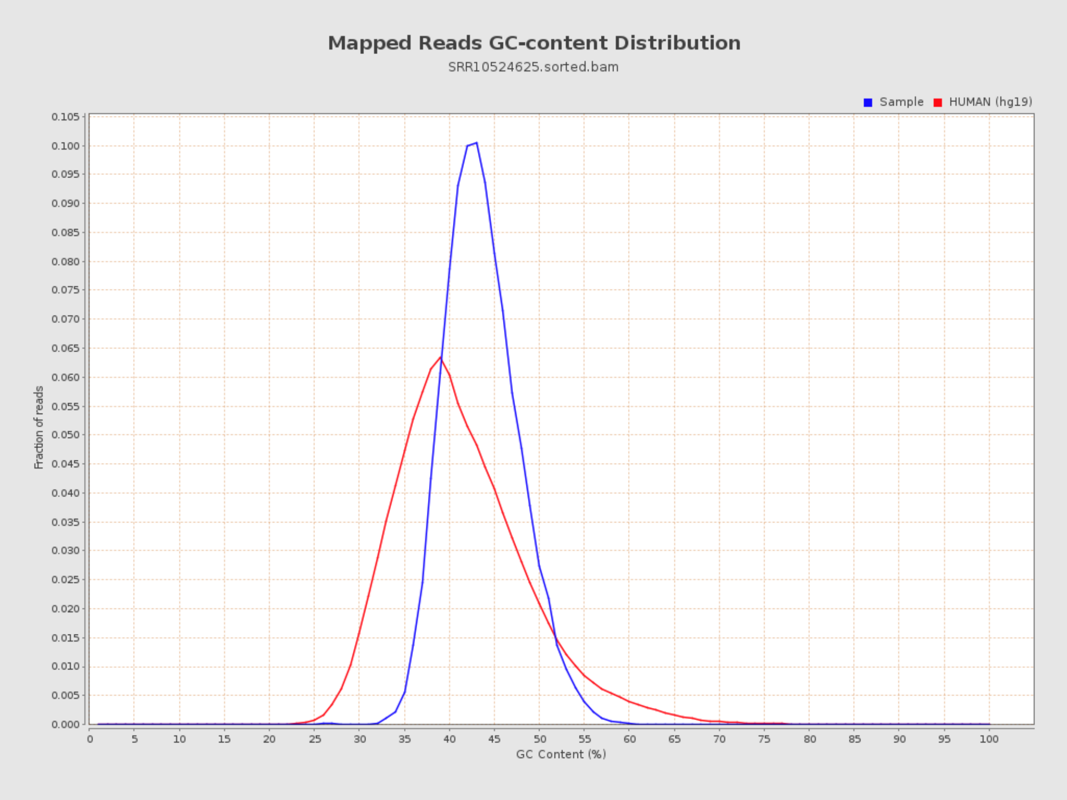
7. Results : Duplication Rate Histogram



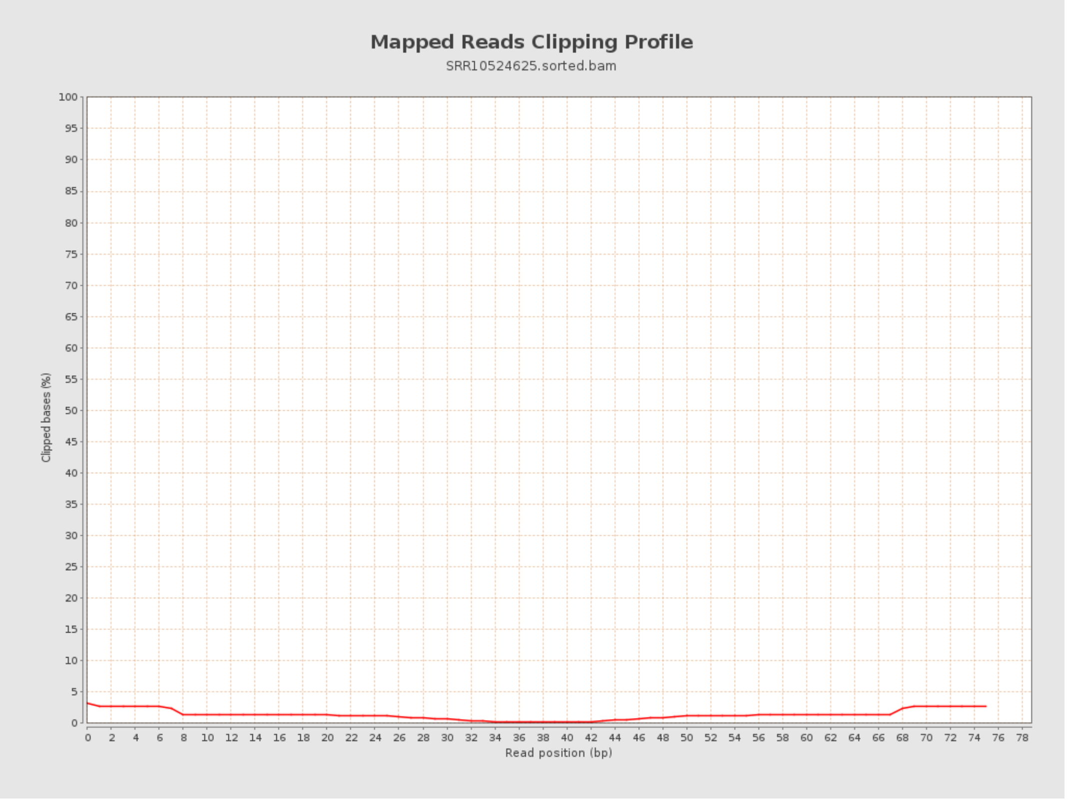
8. Results : Mapped Reads Nucleotide Content



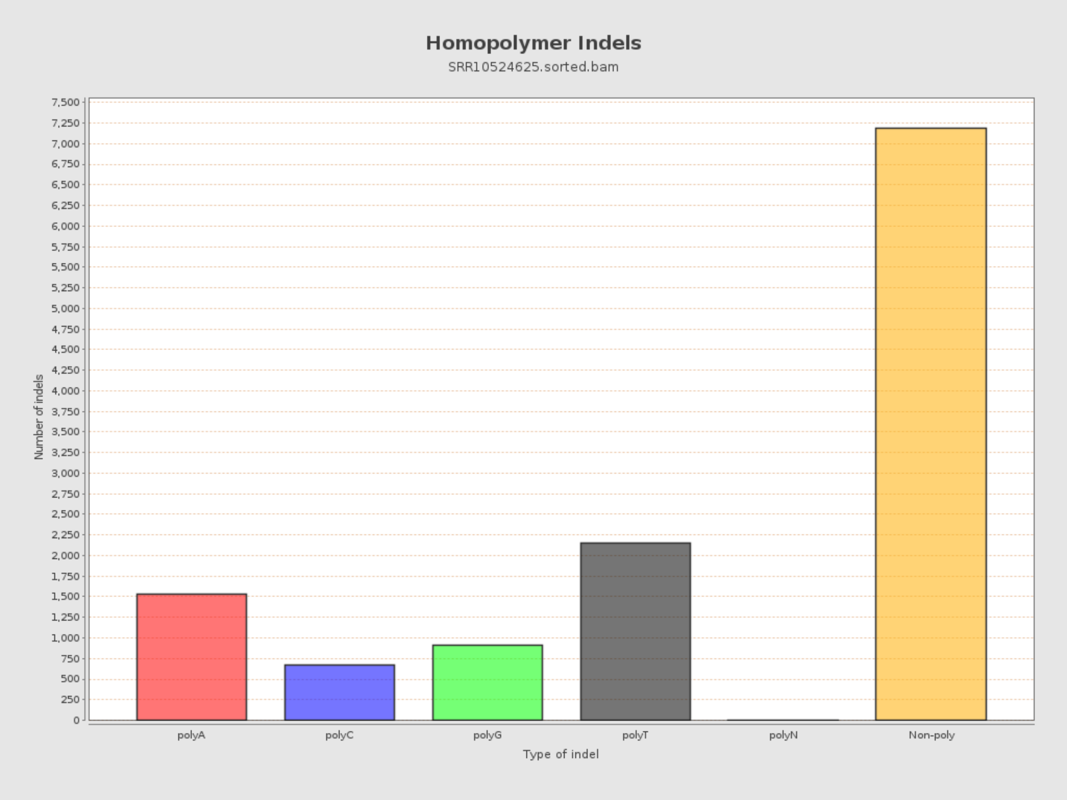
9. Results : Mapped Reads GC-content Distribution



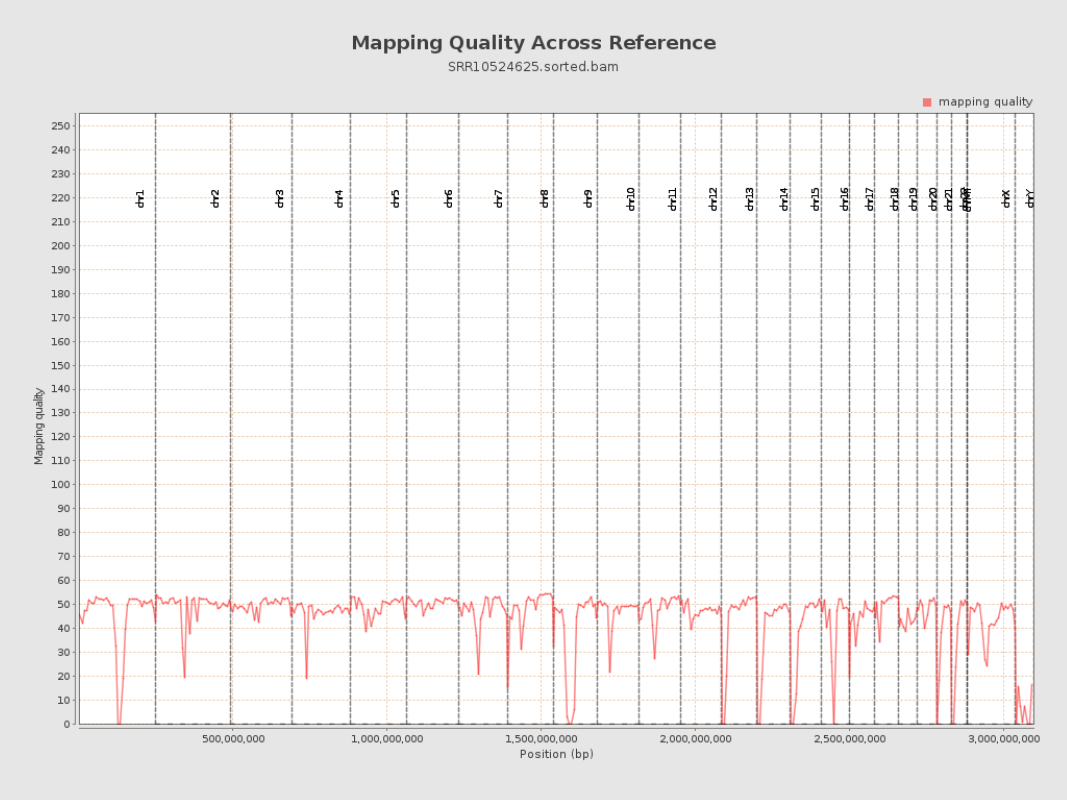
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram