Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:32:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524497.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_SRR10524497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524497.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:32:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	629,504
Mapped reads	581,506 / 92.38%
Unmapped reads	47,998 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,322 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	14,891 / 2.37%
Duplication rate	2.04%
Clipped reads	582,266 / 92.5%

2.2. ACGT Content

Number/percentage of A's	8,653,624 / 25.54%
Number/percentage of C's	6,596,544 / 19.47%
Number/percentage of T's	10,568,784 / 31.19%
Number/percentage of G's	8,064,263 / 23.8%
Number/percentage of N's	670 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1318

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

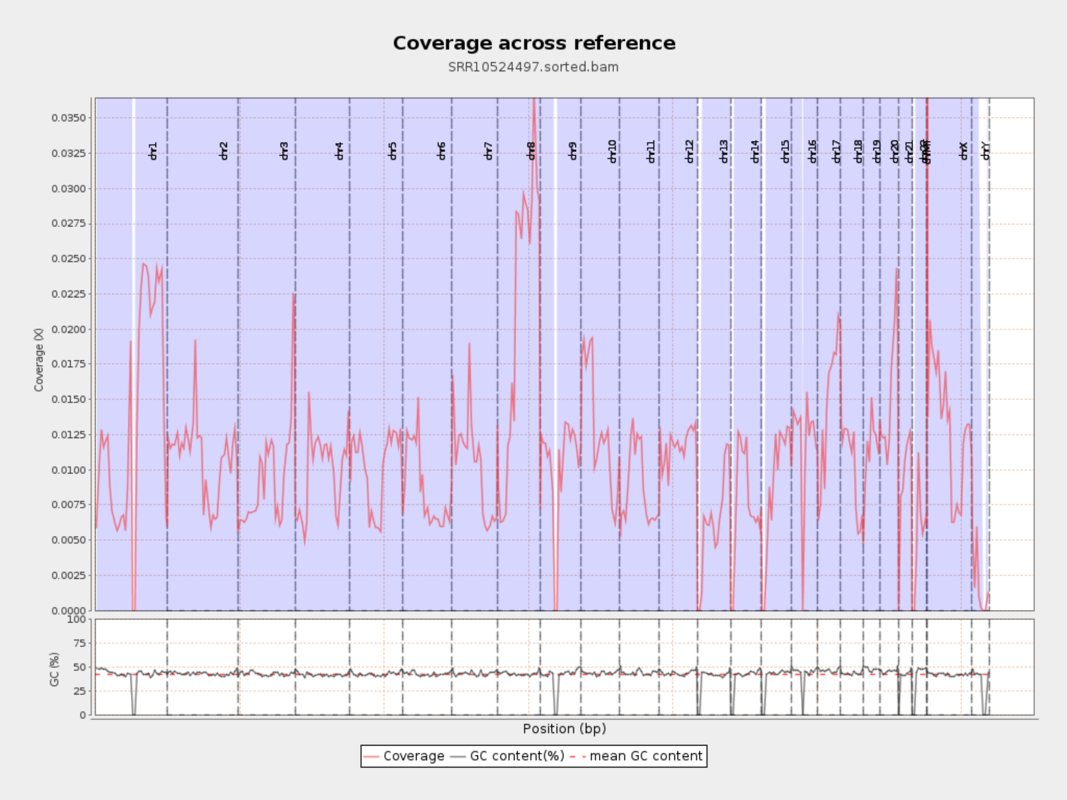
General error rate	0.48%
Mismatches	158,105
Insertions	1,830
Mapped reads with at least one insertion	0.31%
Deletions	6,097
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.54%

2.6. Chromosome stats

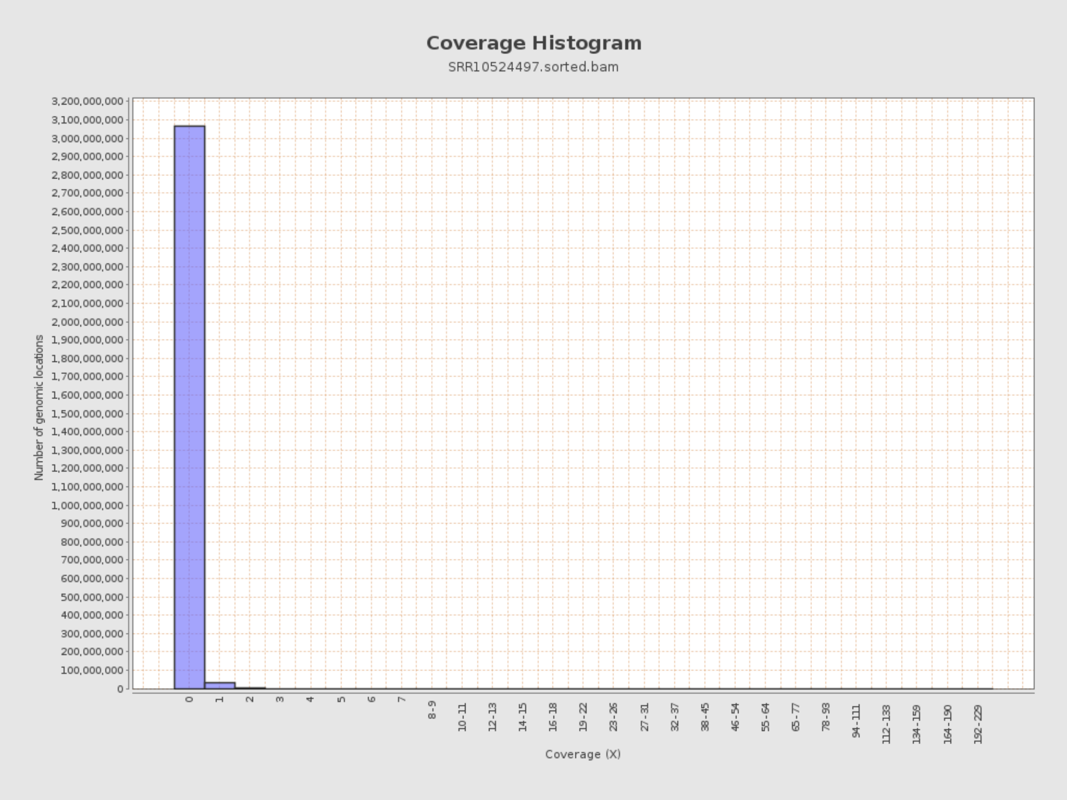
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3350241	0.0134	0.2097
chr2	243199373	2653759	0.0109	0.1401
chr3	198022430	1859397	0.0094	0.1017
chr4	191154276	1896117	0.0099	0.1103
chr5	180915260	1856229	0.0103	0.1064
chr6	171115067	1476115	0.0086	0.1082
chr7	159138663	1669450	0.0105	0.1558

chr8	146364022	3096676	0.0212	0.1627
chr9	141213431	1439953	0.0102	0.1188
chr10	135534747	1780882	0.0131	0.1357
chr11	135006516	1186193	0.0088	0.1221
chr12	133851895	1573311	0.0118	0.1144
chr13	115169878	725203	0.0063	0.0834
chr14	107349540	813856	0.0076	0.0925
chr15	102531392	913387	0.0089	0.1001
chr16	90354753	1067052	0.0118	0.1159
chr17	81195210	1180607	0.0145	0.1299
chr18	78077248	792703	0.0102	0.1659
chr19	59128983	687706	0.0116	0.16
chr20	63025520	979922	0.0155	0.1315
chr21	48129895	458753	0.0095	0.1063
chr22	51304566	273732	0.0053	0.076
chrMT	16571	11682	0.705	0.9451
chrX	155270560	2046004	0.0132	0.1259
chrY	59373566	105519	0.0018	0.0584

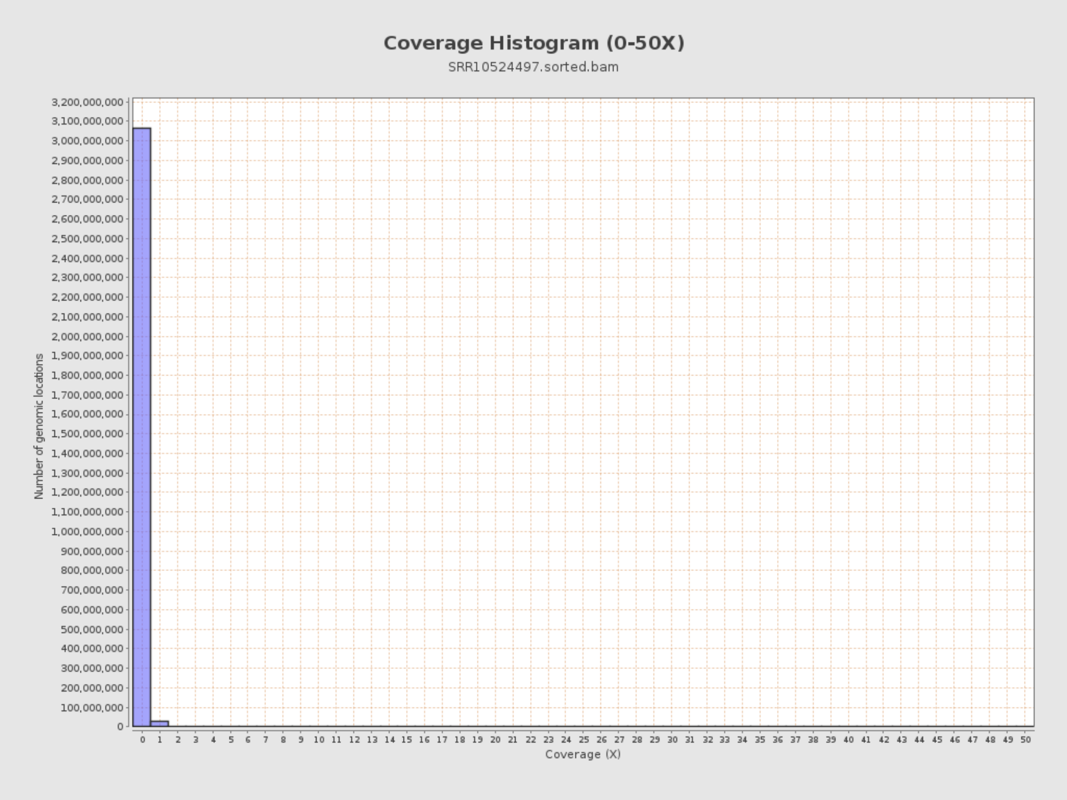
3. Results : Coverage across reference



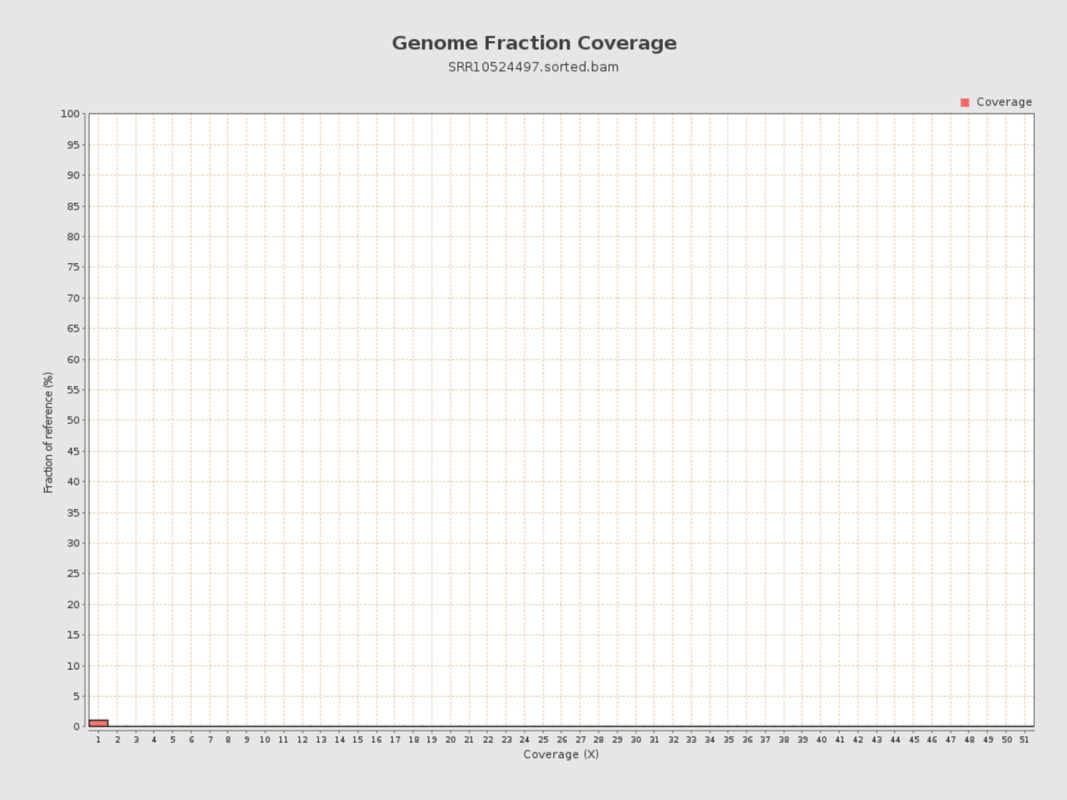
4. Results : Coverage Histogram



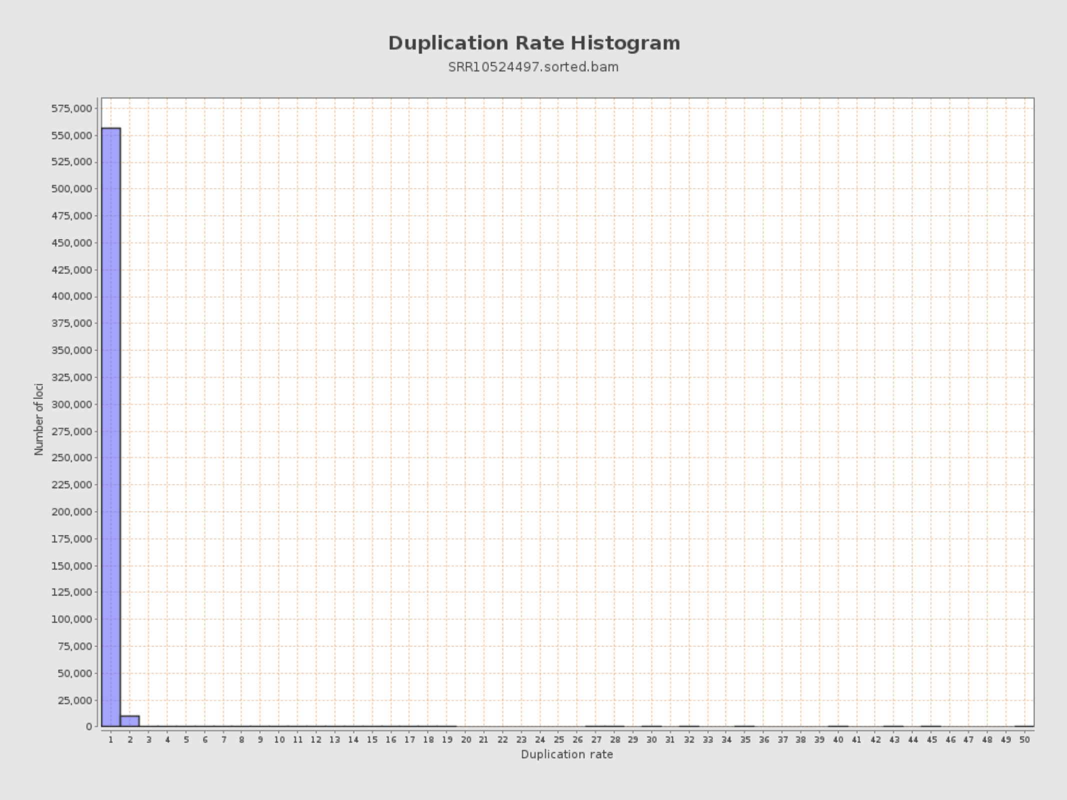
5. Results : Coverage Histogram (0-50X)



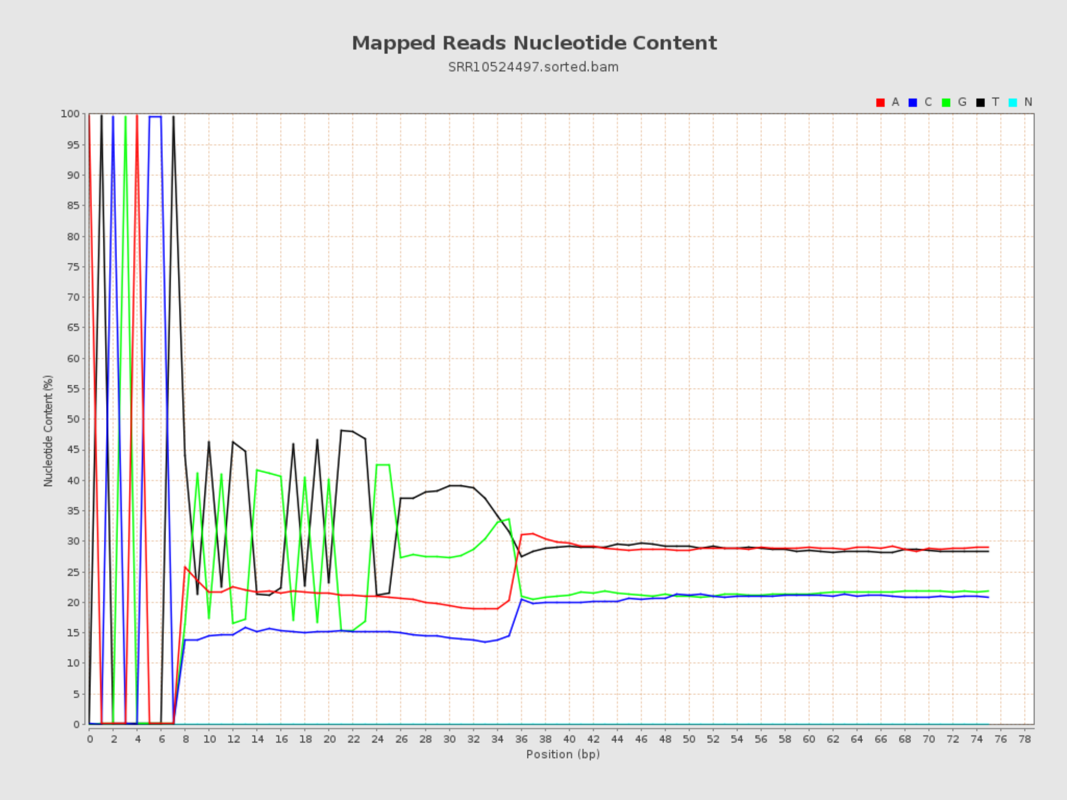
6. Results : Genome Fraction Coverage



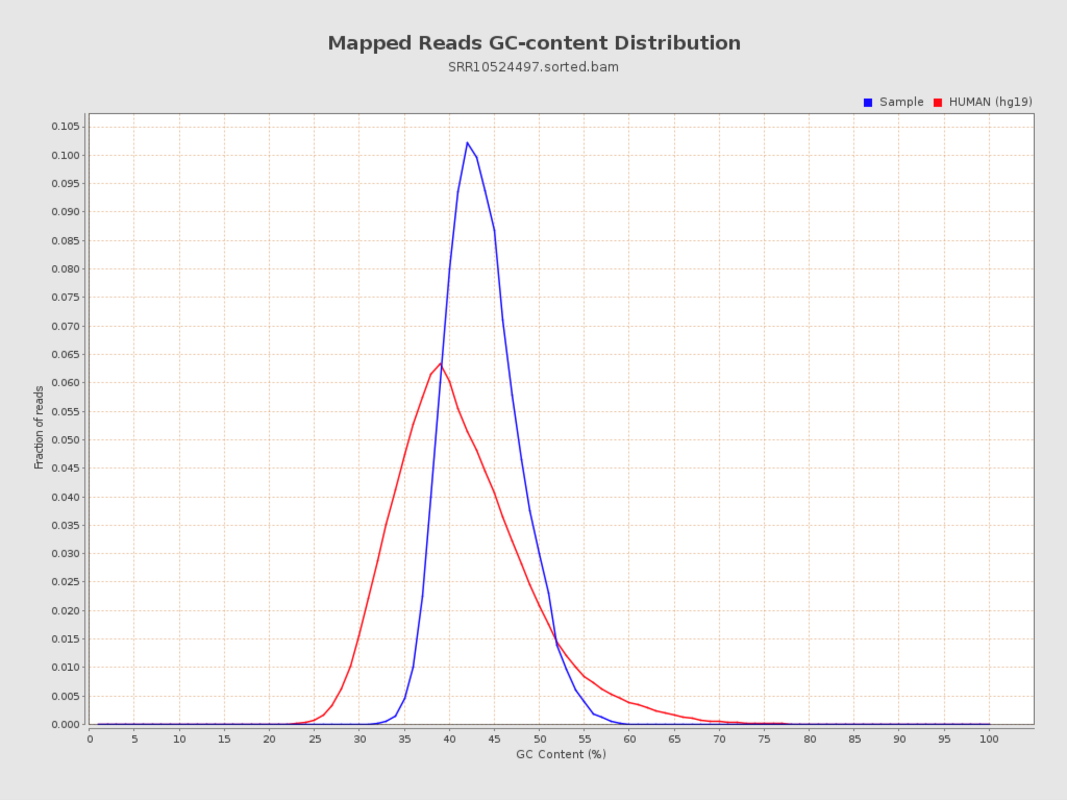
7. Results : Duplication Rate Histogram



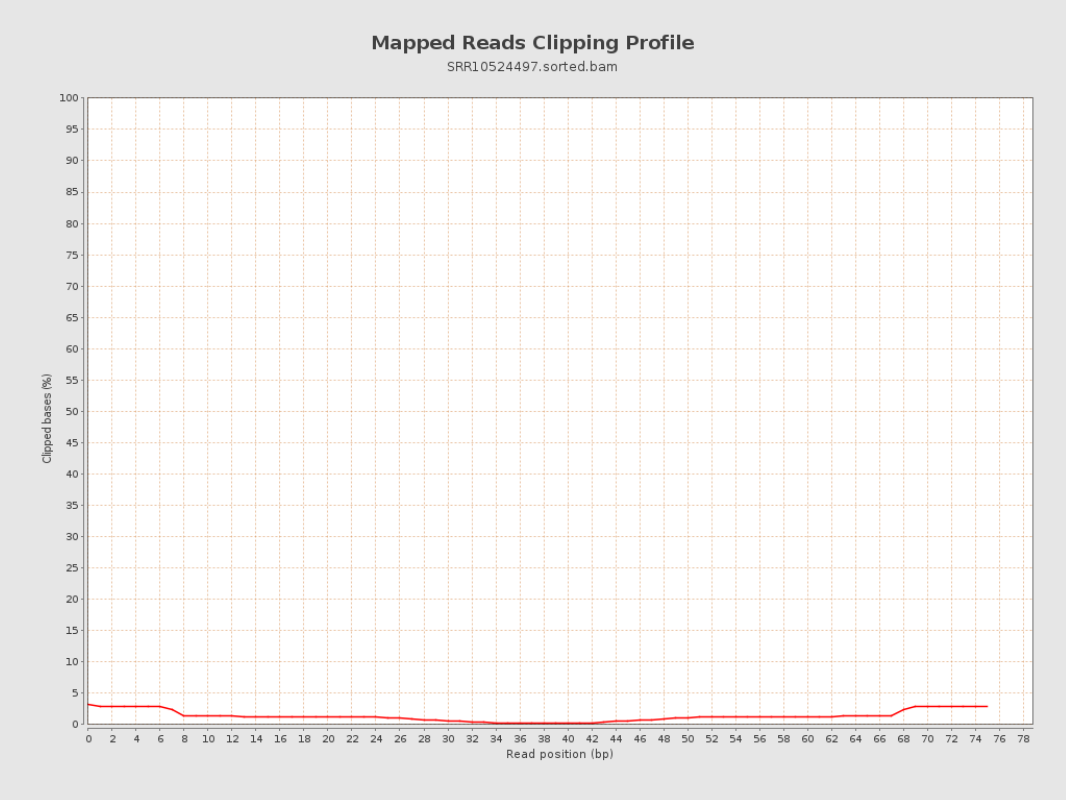
8. Results : Mapped Reads Nucleotide Content



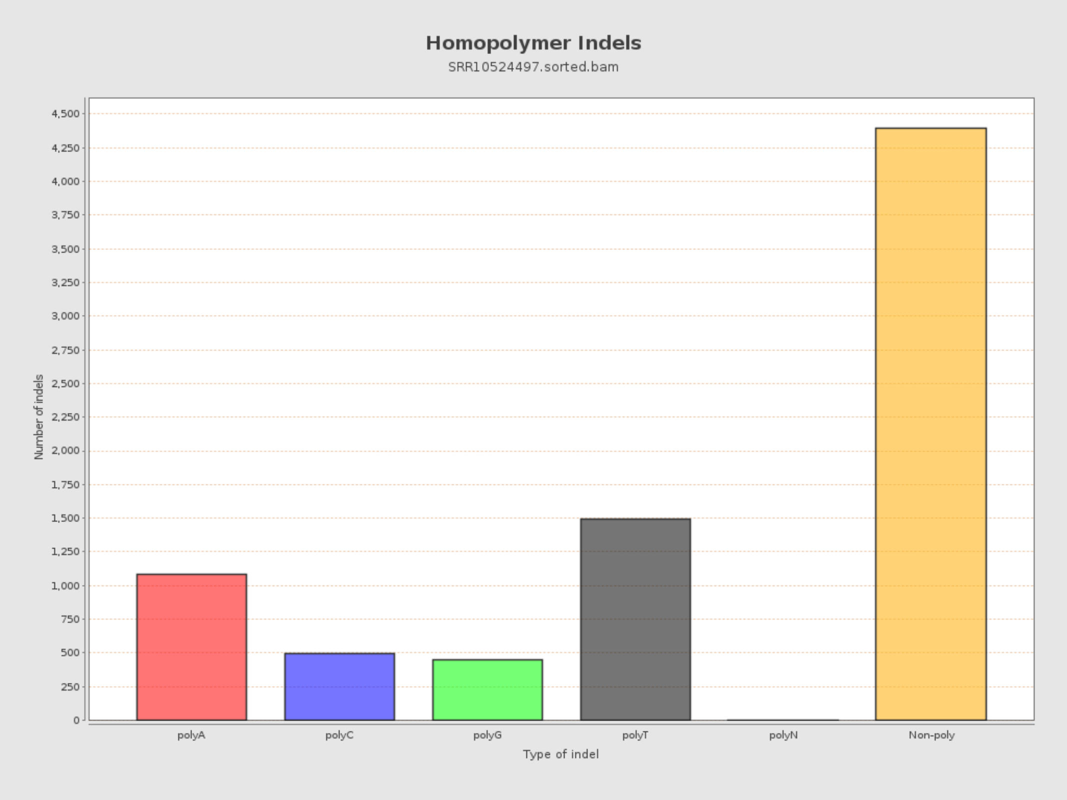
9. Results : Mapped Reads GC-content Distribution



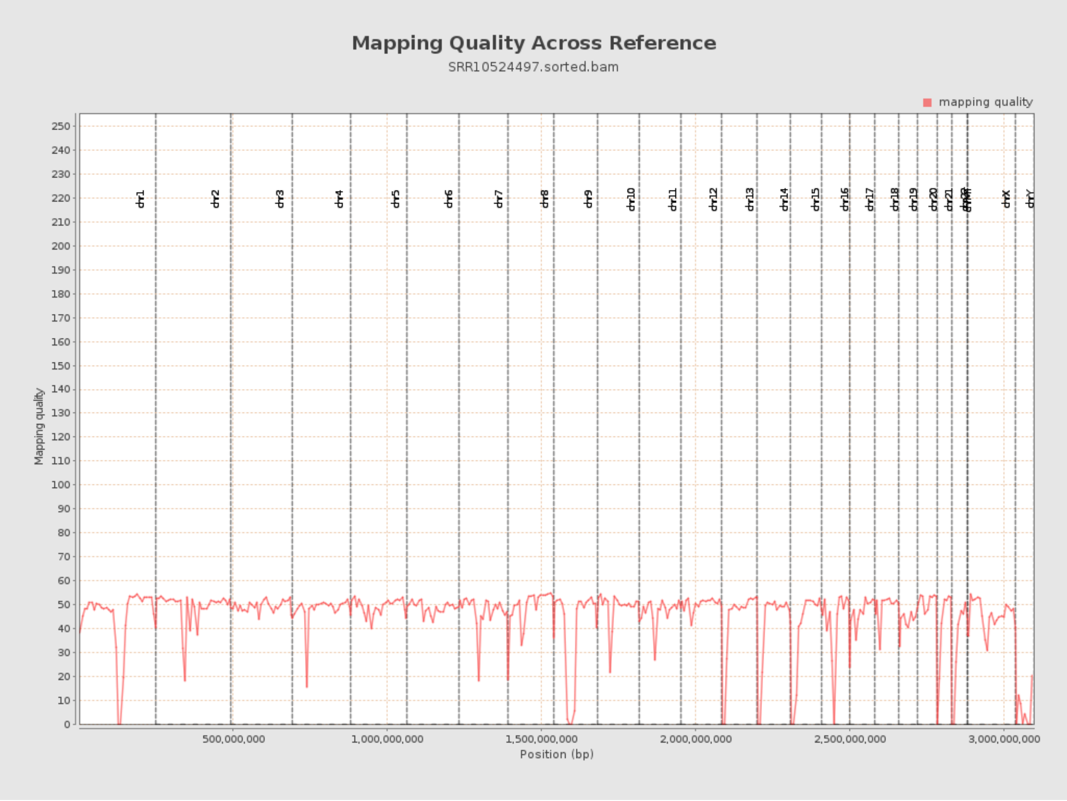
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram