Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:00:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524992.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_SRR10524992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:00:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	979,703
Mapped reads	908,055 / 92.69%
Unmapped reads	71,648 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,126 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	23,994 / 2.45%
Duplication rate	1.98%
Clipped reads	907,848 / 92.67%

2.2. ACGT Content

Number/percentage of A's	13,777,826 / 26.01%
Number/percentage of C's	9,331,380 / 17.62%
Number/percentage of T's	16,565,667 / 31.28%
Number/percentage of G's	13,287,658 / 25.09%
Number/percentage of N's	560 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1736

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

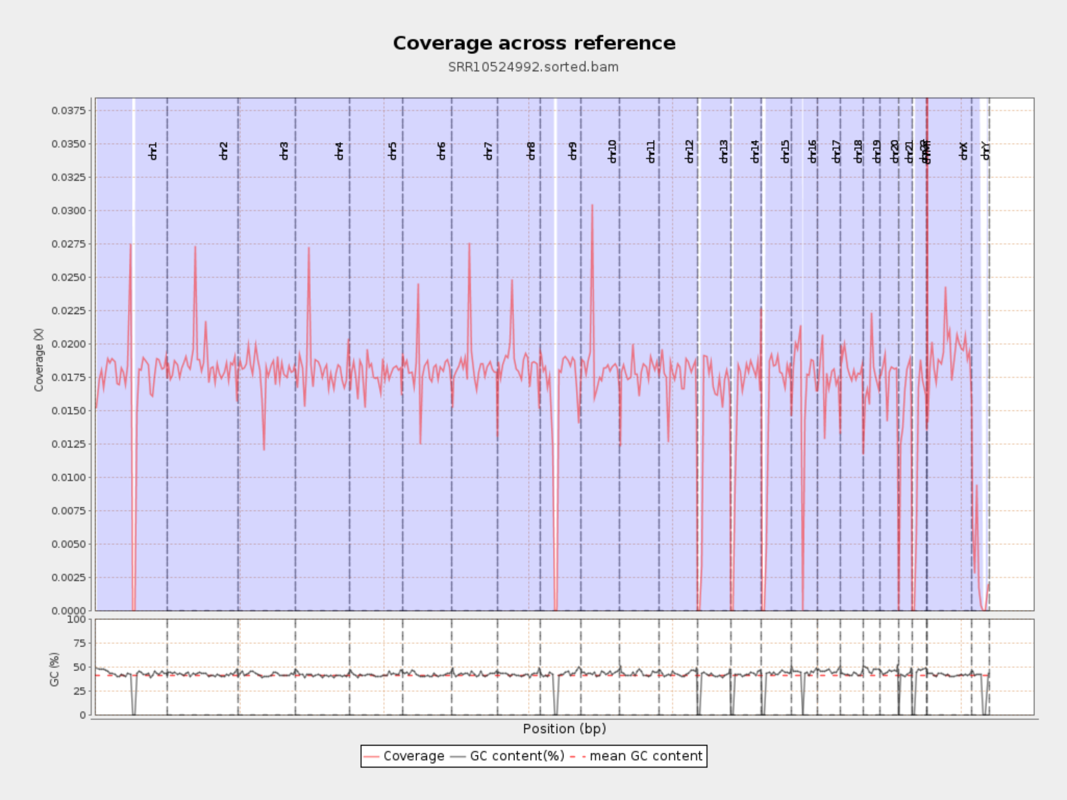
General error rate	0.49%
Mismatches	253,784
Insertions	3,604
Mapped reads with at least one insertion	0.4%
Deletions	10,368
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.98%

2.6. Chromosome stats

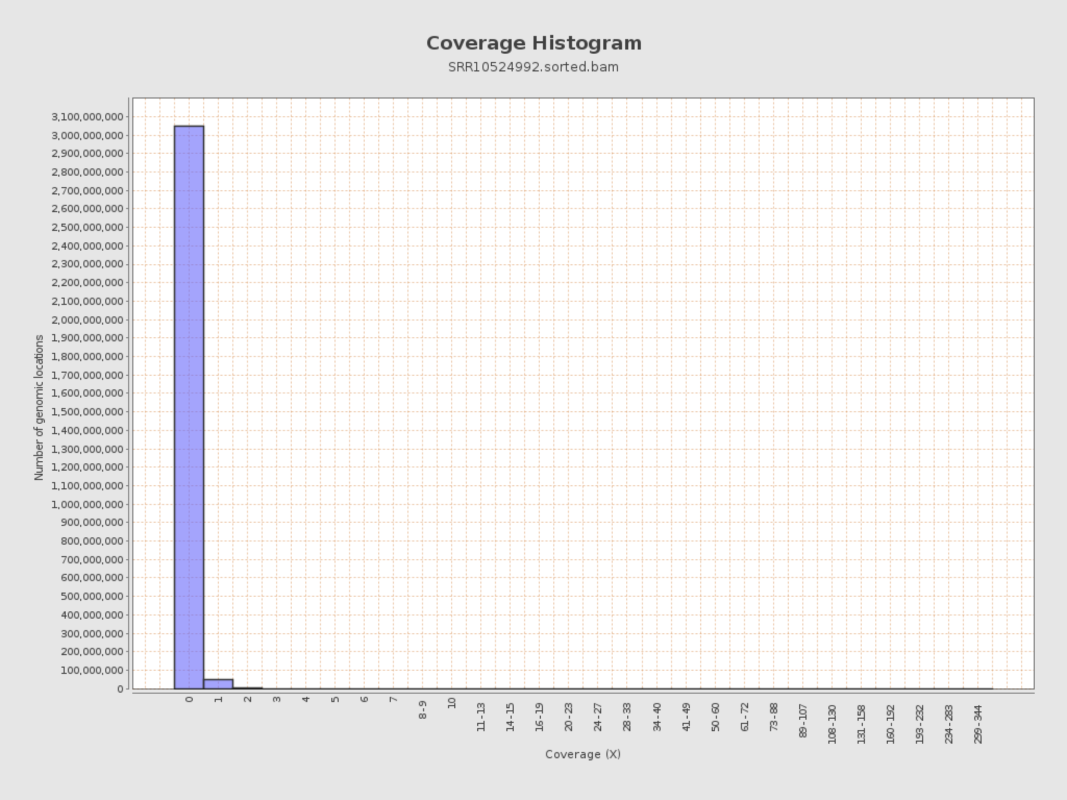
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4231221	0.017	0.2735
chr2	243199373	4516154	0.0186	0.1939
chr3	198022430	3553576	0.0179	0.1421
chr4	191154276	3482414	0.0182	0.1525
chr5	180915260	3218013	0.0178	0.1408
chr6	171115067	3100785	0.0181	0.1636
chr7	159138663	2937952	0.0185	0.2037

chr8	146364022	2732649	0.0187	0.1841
chr9	141213431	2214335	0.0157	0.1576
chr10	135534747	2530296	0.0187	0.1794
chr11	135006516	2420250	0.0179	0.171
chr12	133851895	2368369	0.0177	0.1414
chr13	115169878	1676070	0.0146	0.1274
chr14	107349540	1613358	0.015	0.1324
chr15	102531392	1500534	0.0146	0.1355
chr16	90354753	1494427	0.0165	0.141
chr17	81195210	1398863	0.0172	0.1496
chr18	78077248	1421877	0.0182	0.2292
chr19	59128983	1019003	0.0172	0.2063
chr20	63025520	1100743	0.0175	0.1408
chr21	48129895	696169	0.0145	0.1339
chr22	51304566	604887	0.0118	0.114
chrMT	16571	1360	0.0821	0.2952
chrX	155270560	2988832	0.0192	0.1558
chrY	59373566	158675	0.0027	0.0836

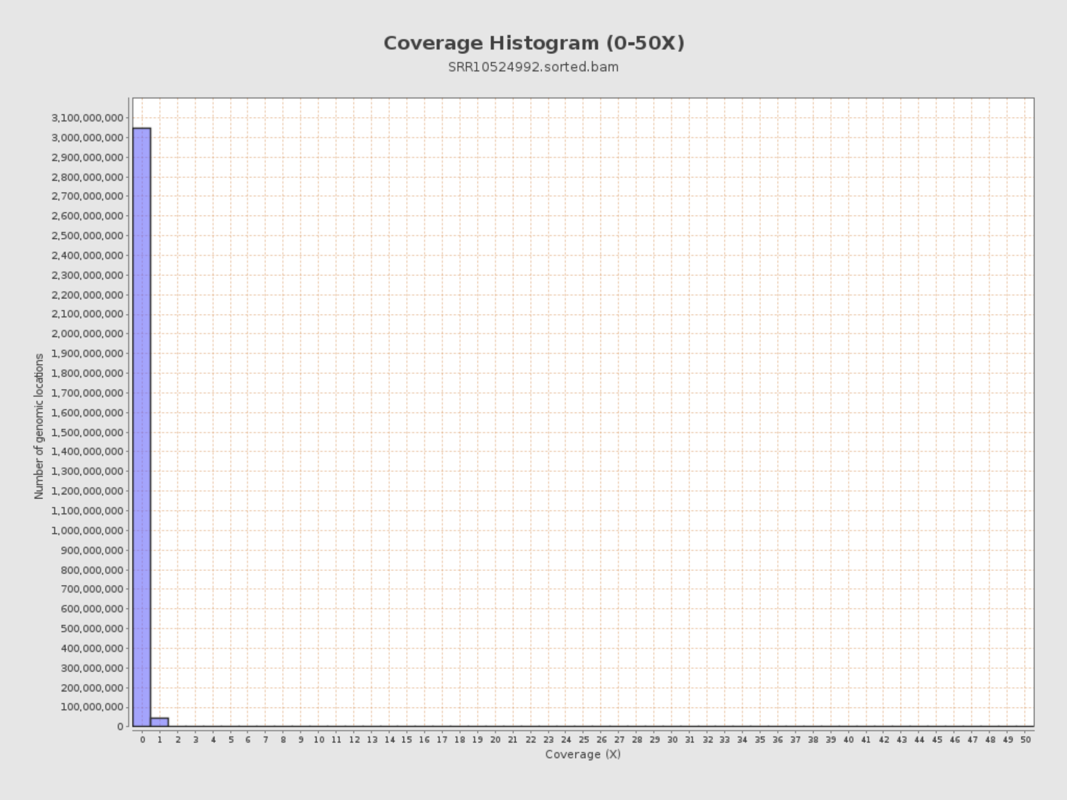
3. Results : Coverage across reference



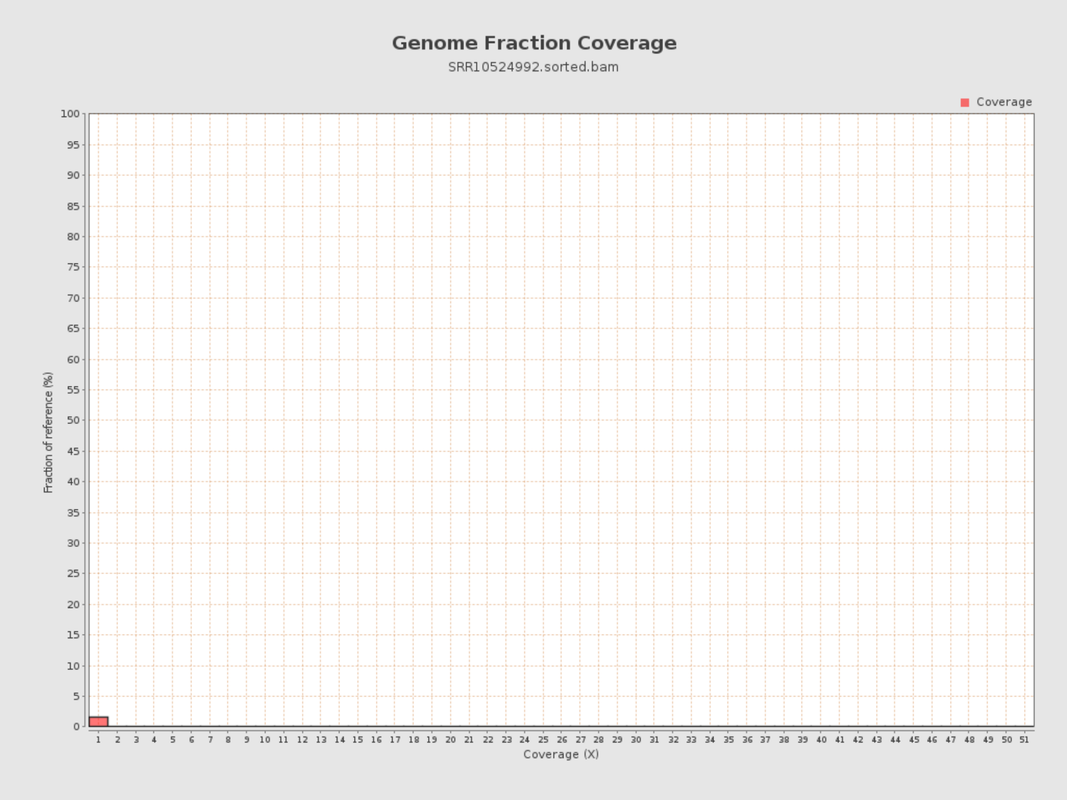
4. Results : Coverage Histogram



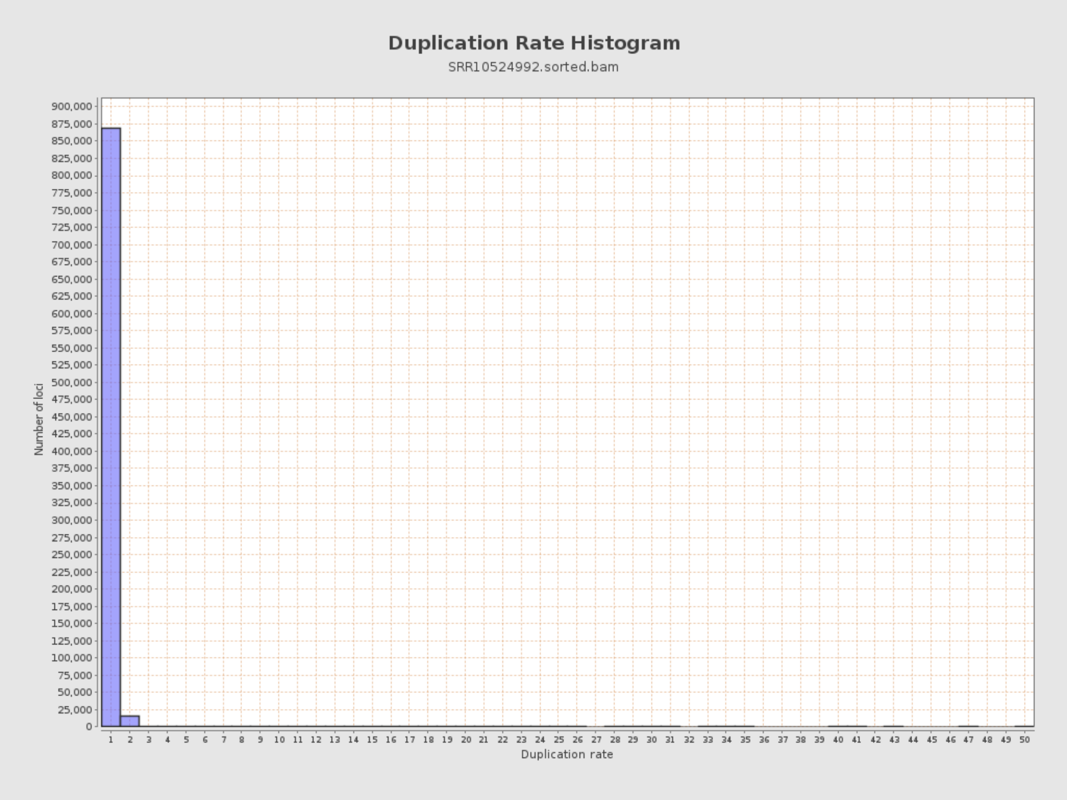
5. Results : Coverage Histogram (0-50X)



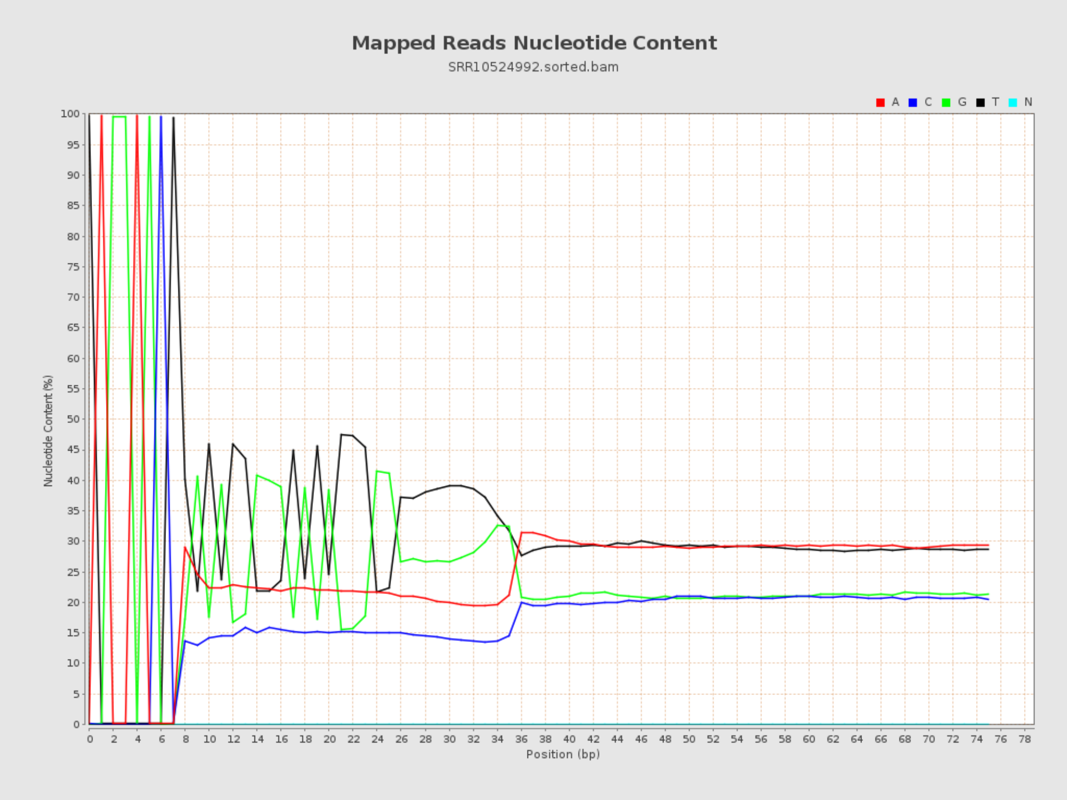
6. Results : Genome Fraction Coverage



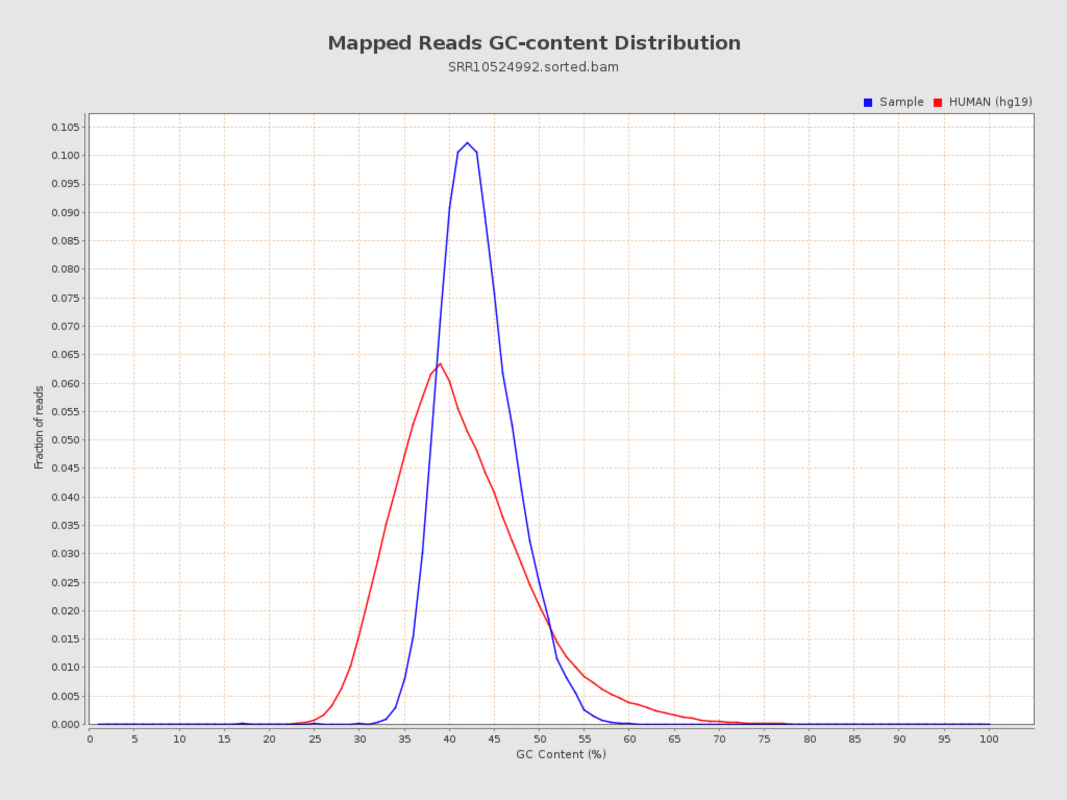
7. Results : Duplication Rate Histogram



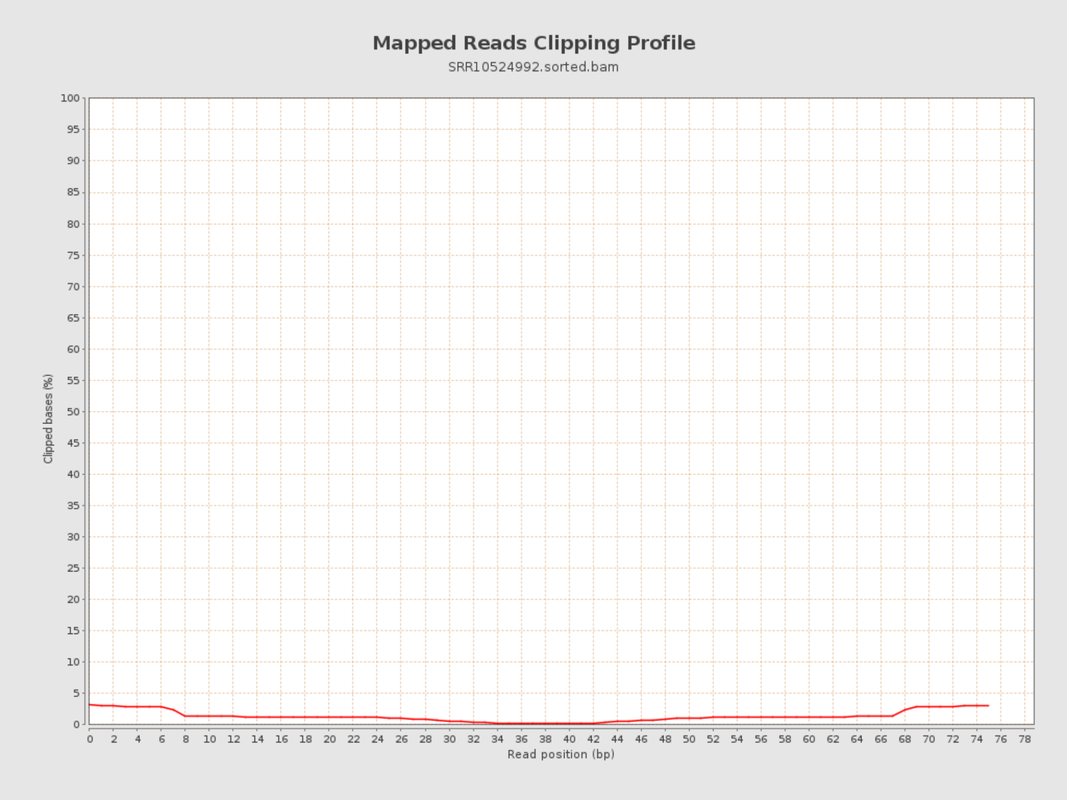
8. Results : Mapped Reads Nucleotide Content



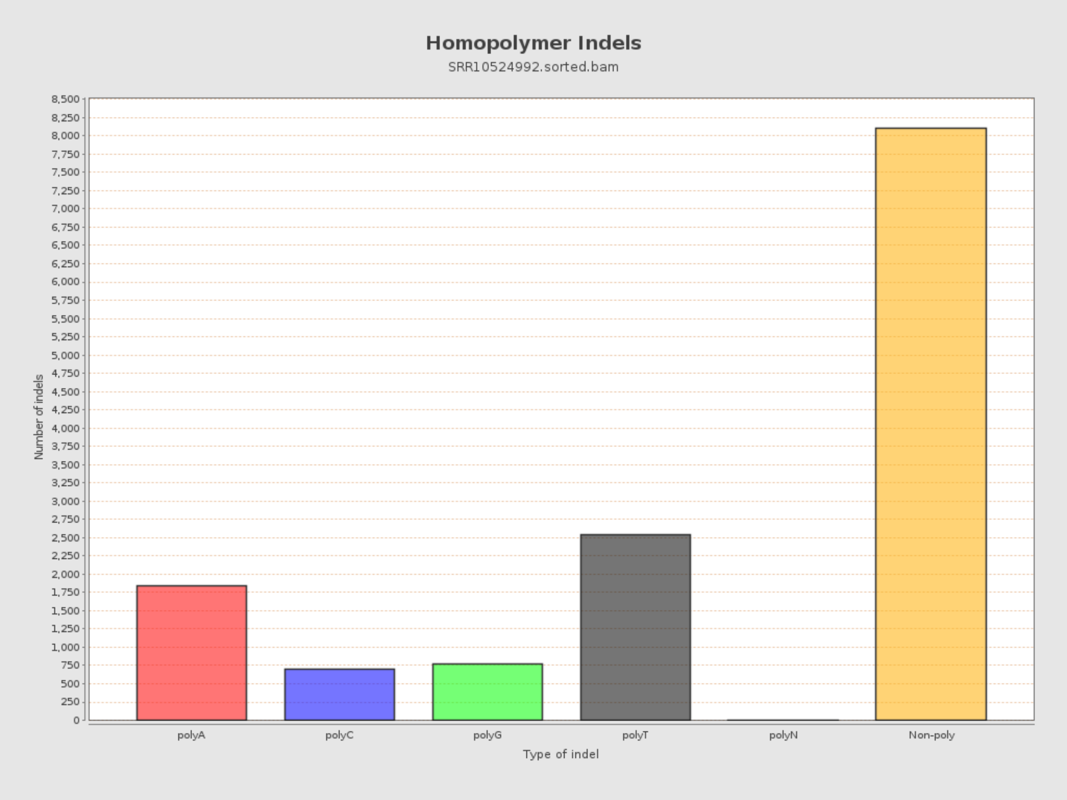
9. Results : Mapped Reads GC-content Distribution



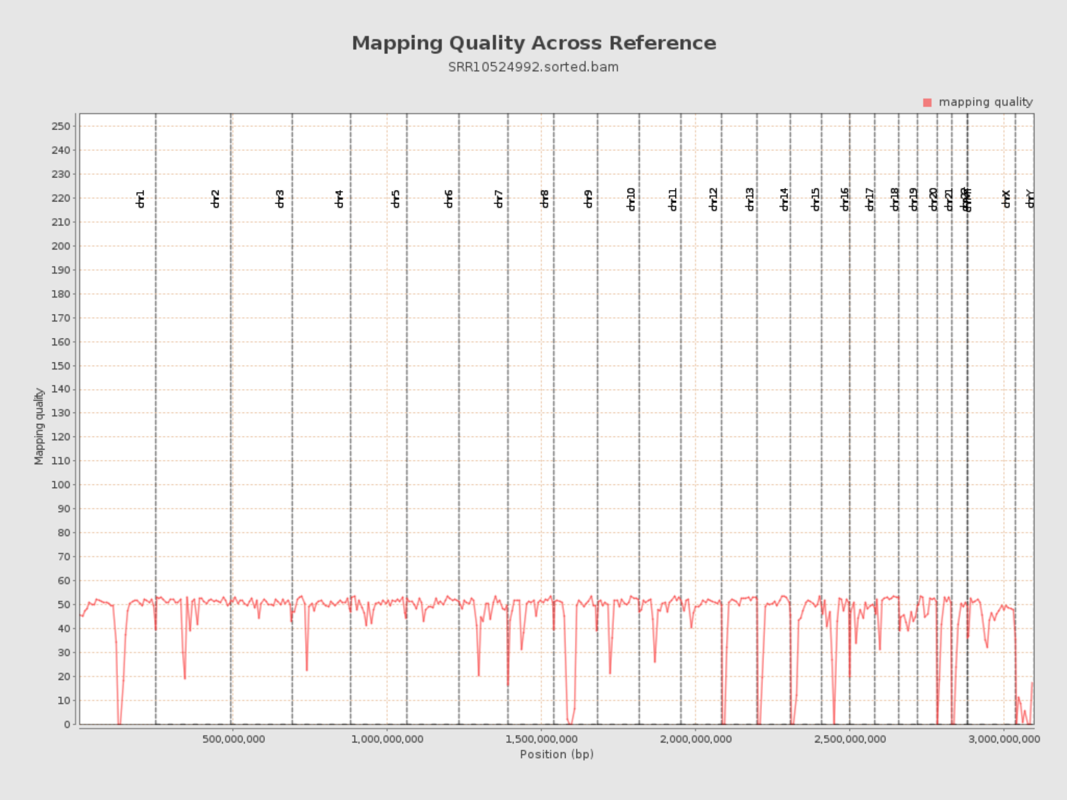
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram