Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524957.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_SRR10524957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:26:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	699,623
Mapped reads	647,646 / 92.57%
Unmapped reads	51,977 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,624 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	11,844 / 1.69%
Duplication rate	1.31%
Clipped reads	646,931 / 92.47%

2.2. ACGT Content

Number/percentage of A's	9,836,141 / 25.92%
Number/percentage of C's	7,381,193 / 19.45%
Number/percentage of T's	11,746,914 / 30.96%
Number/percentage of G's	8,977,263 / 23.66%
Number/percentage of N's	391 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0123

Standard Deviation	0.1419

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

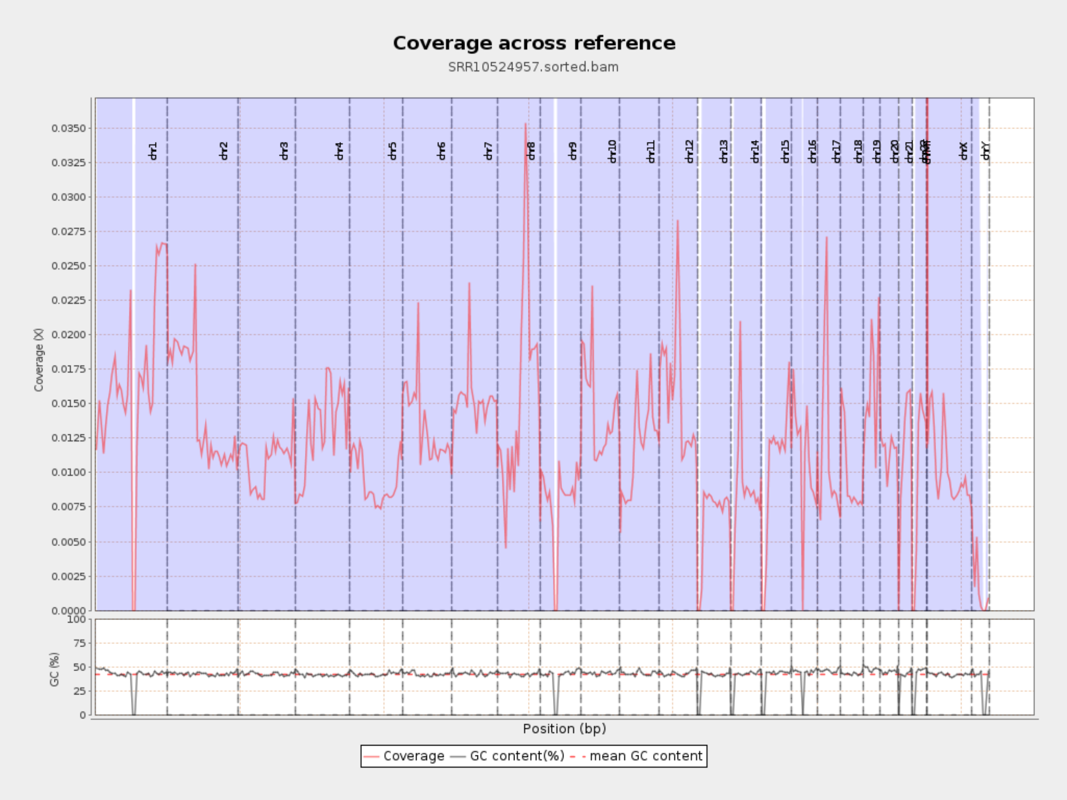
General error rate	0.51%
Mismatches	187,277
Insertions	3,020
Mapped reads with at least one insertion	0.46%
Deletions	7,432
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.29%

2.6. Chromosome stats

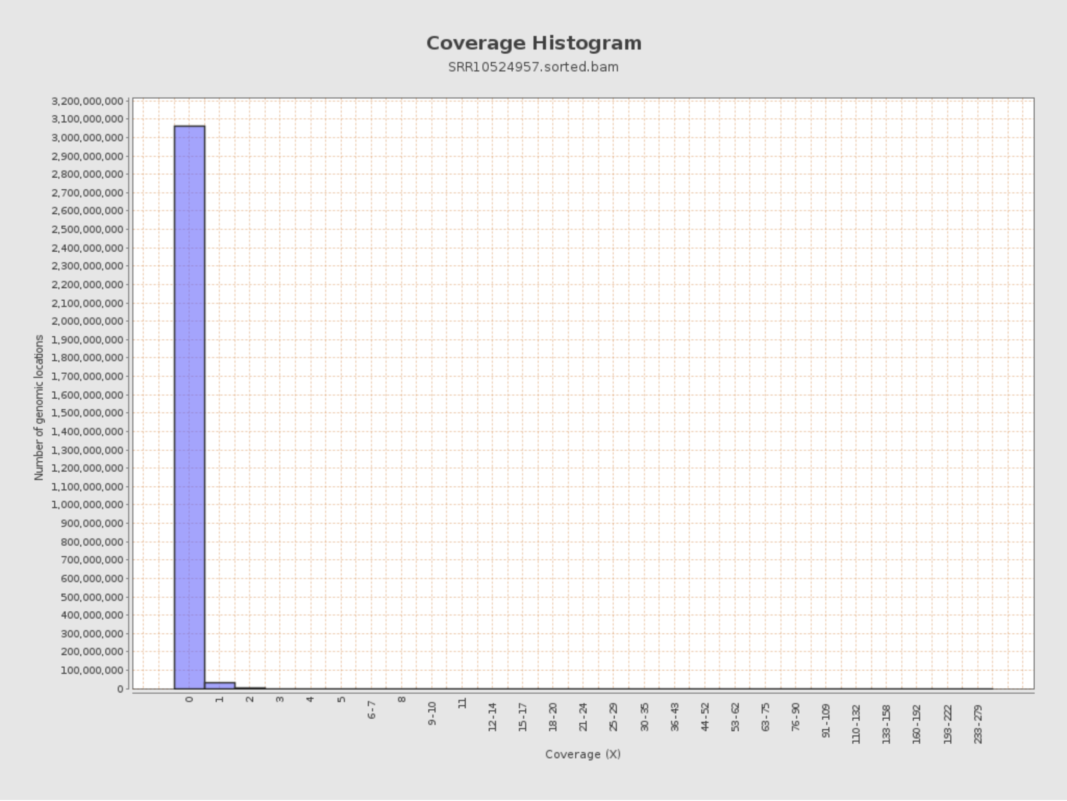
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4133866	0.0166	0.2424
chr2	243199373	3570342	0.0147	0.1573
chr3	198022430	2158507	0.0109	0.1083
chr4	191154276	2535077	0.0133	0.122
chr5	180915260	1702802	0.0094	0.1009
chr6	171115067	2300026	0.0134	0.1454
chr7	159138663	2446885	0.0154	0.1843

chr8	146364022	2340607	0.016	0.1497
chr9	141213431	1114536	0.0079	0.1103
chr10	135534747	1985218	0.0146	0.145
chr11	135006516	1616479	0.012	0.1283
chr12	133851895	2119372	0.0158	0.1303
chr13	115169878	766596	0.0067	0.0854
chr14	107349540	894576	0.0083	0.0965
chr15	102531392	1074672	0.0105	0.1106
chr16	90354753	990879	0.011	0.1119
chr17	81195210	960279	0.0118	0.1281
chr18	78077248	759620	0.0097	0.1496
chr19	59128983	959970	0.0162	0.1764
chr20	63025520	720876	0.0114	0.1114
chr21	48129895	566650	0.0118	0.1138
chr22	51304566	503345	0.0098	0.1018
chrMT	16571	6844	0.413	0.6604
chrX	155270560	1625698	0.0105	0.115
chrY	59373566	100661	0.0017	0.0503

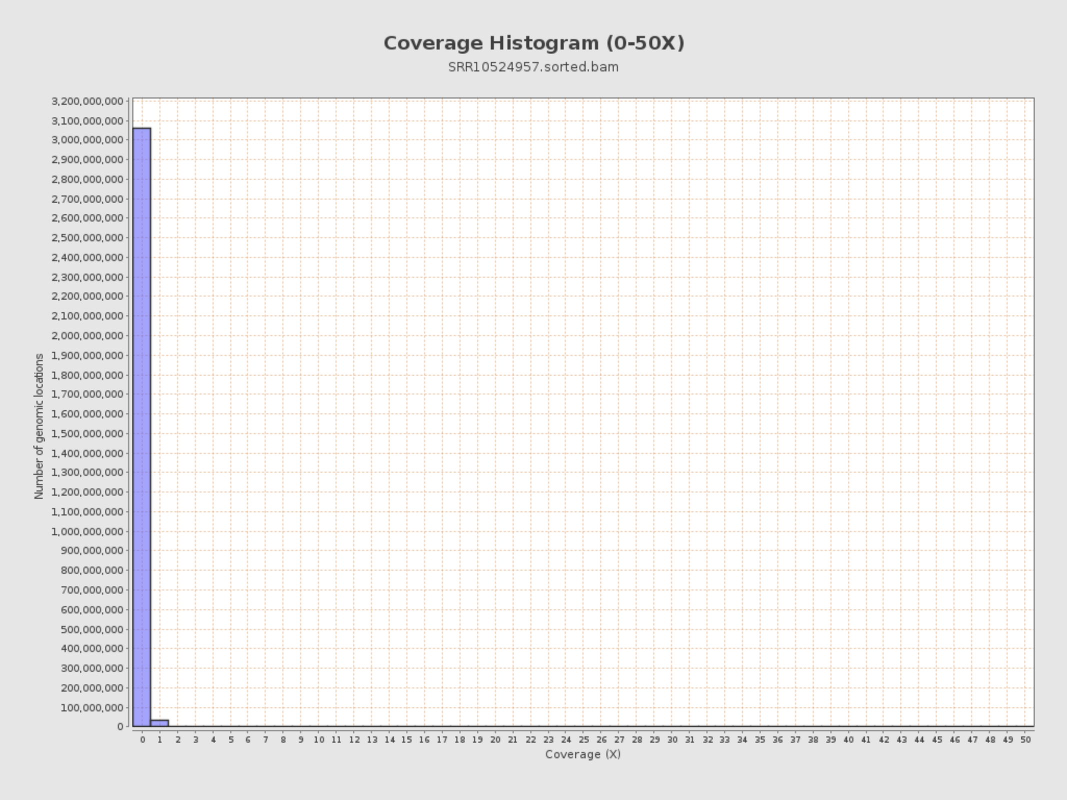
3. Results : Coverage across reference



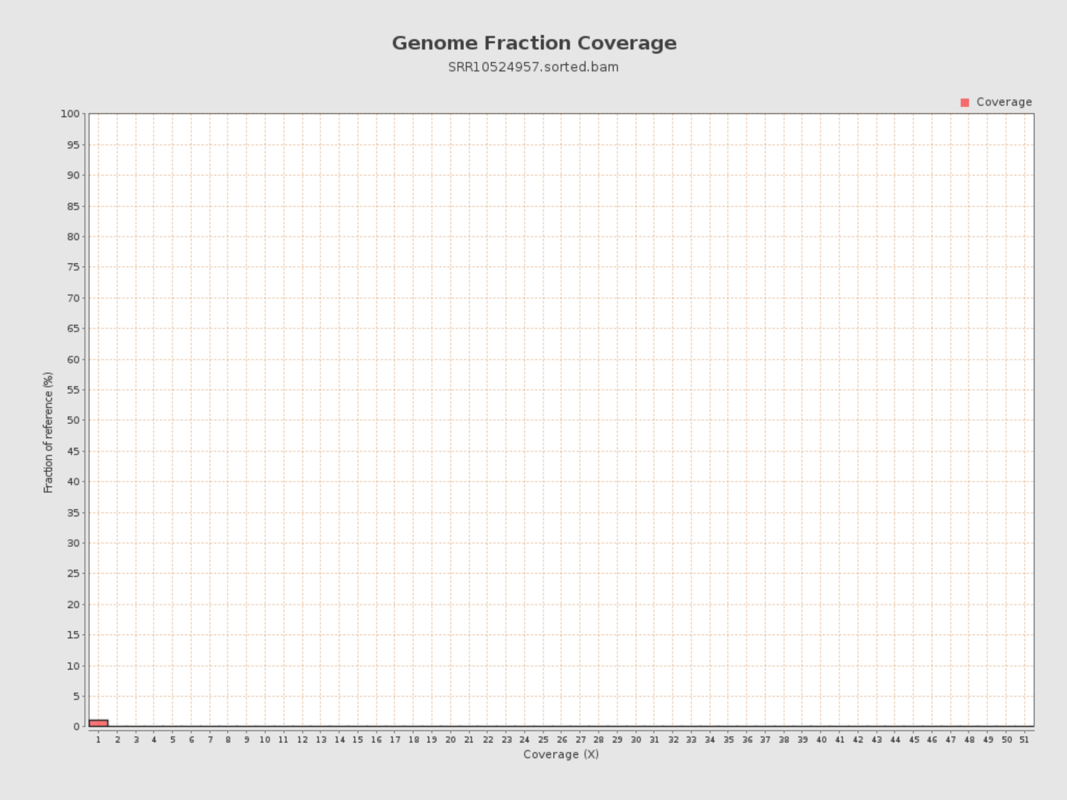
4. Results : Coverage Histogram



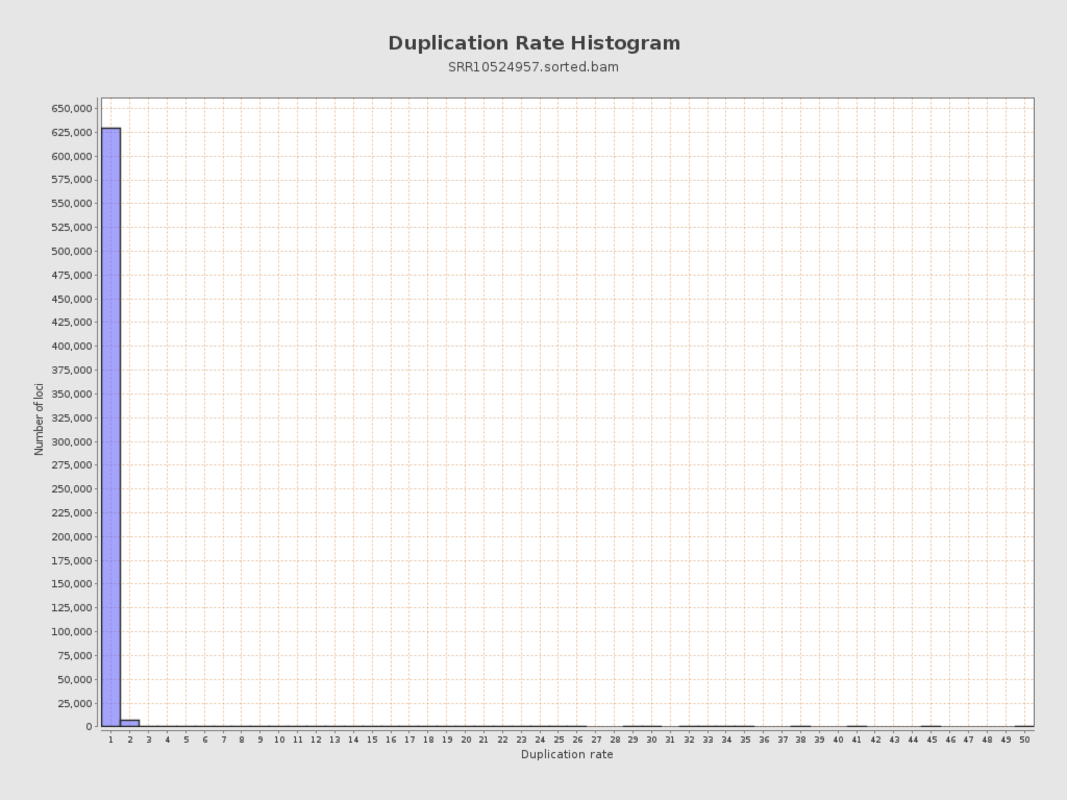
5. Results : Coverage Histogram (0-50X)



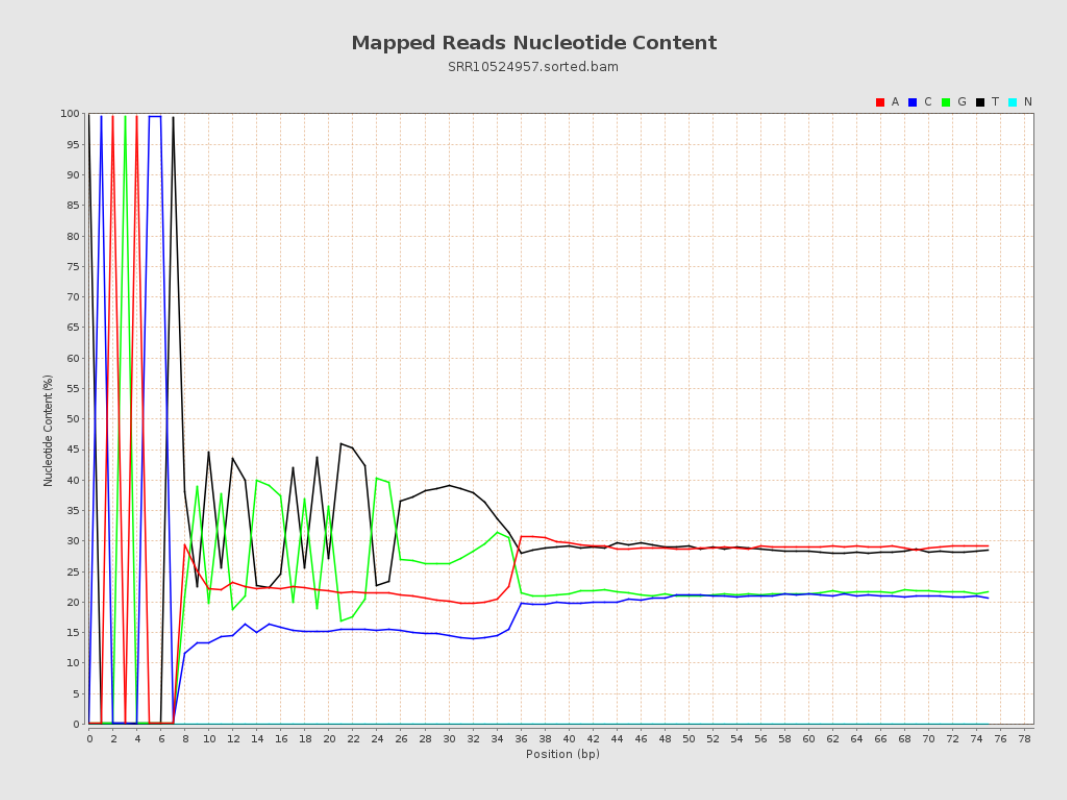
6. Results : Genome Fraction Coverage



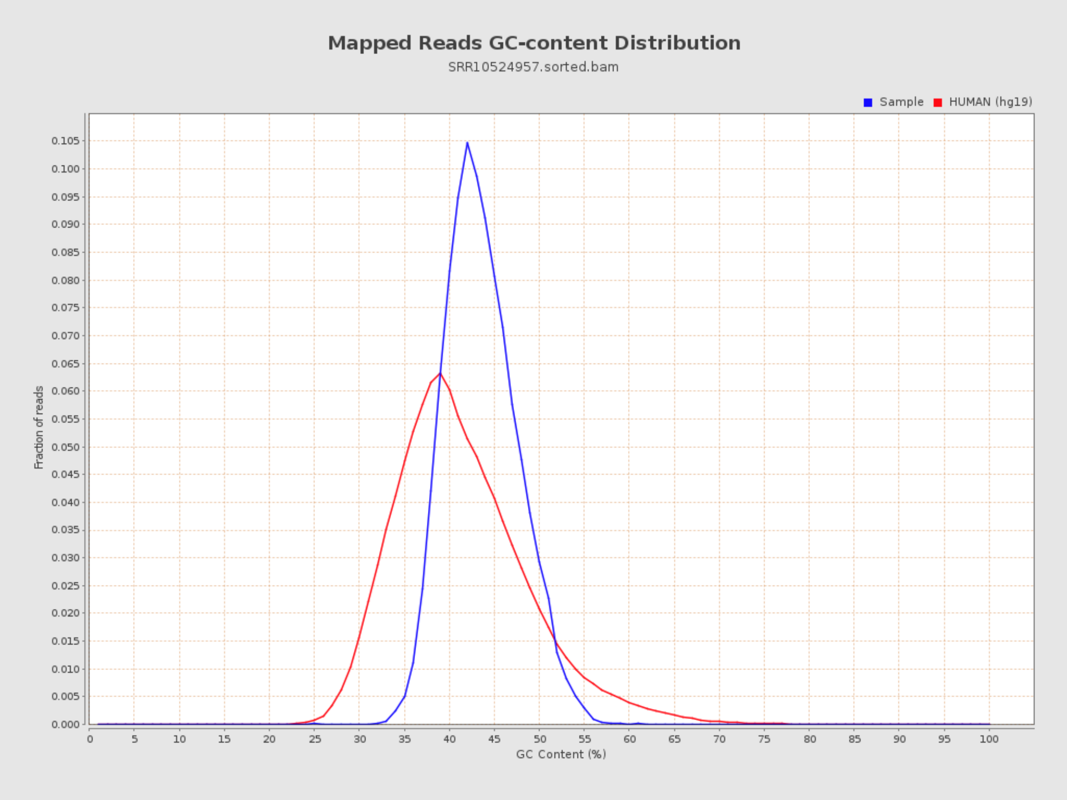
7. Results : Duplication Rate Histogram



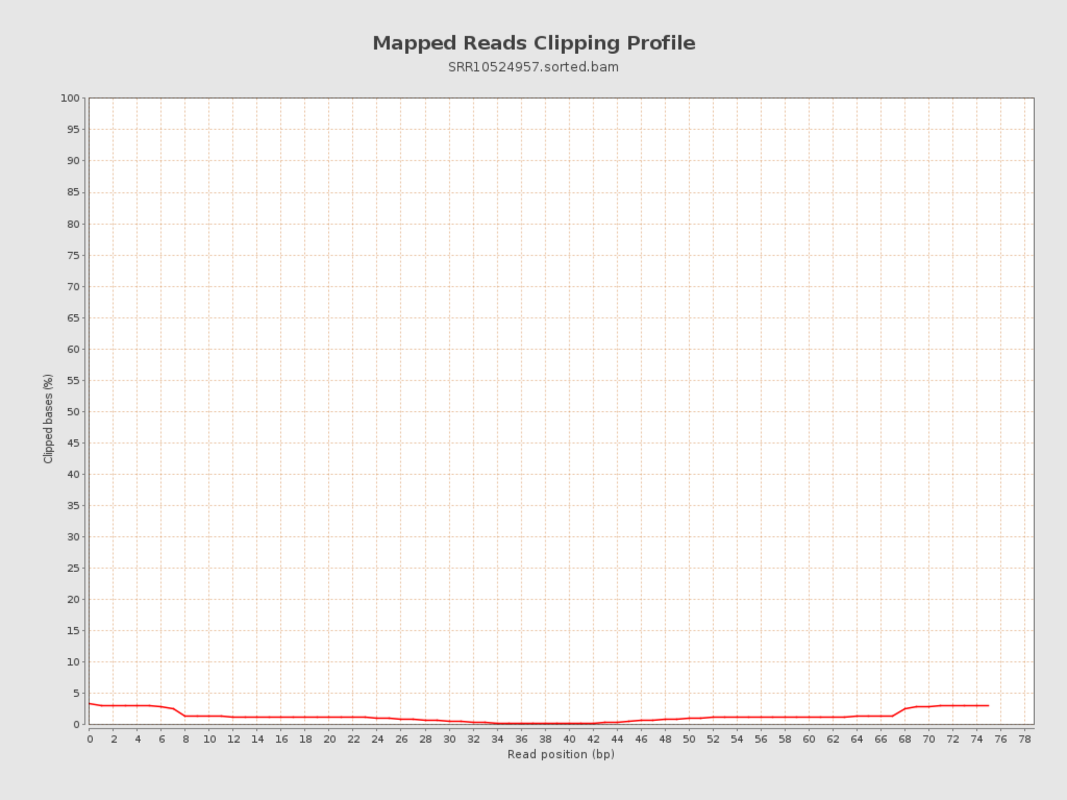
8. Results : Mapped Reads Nucleotide Content



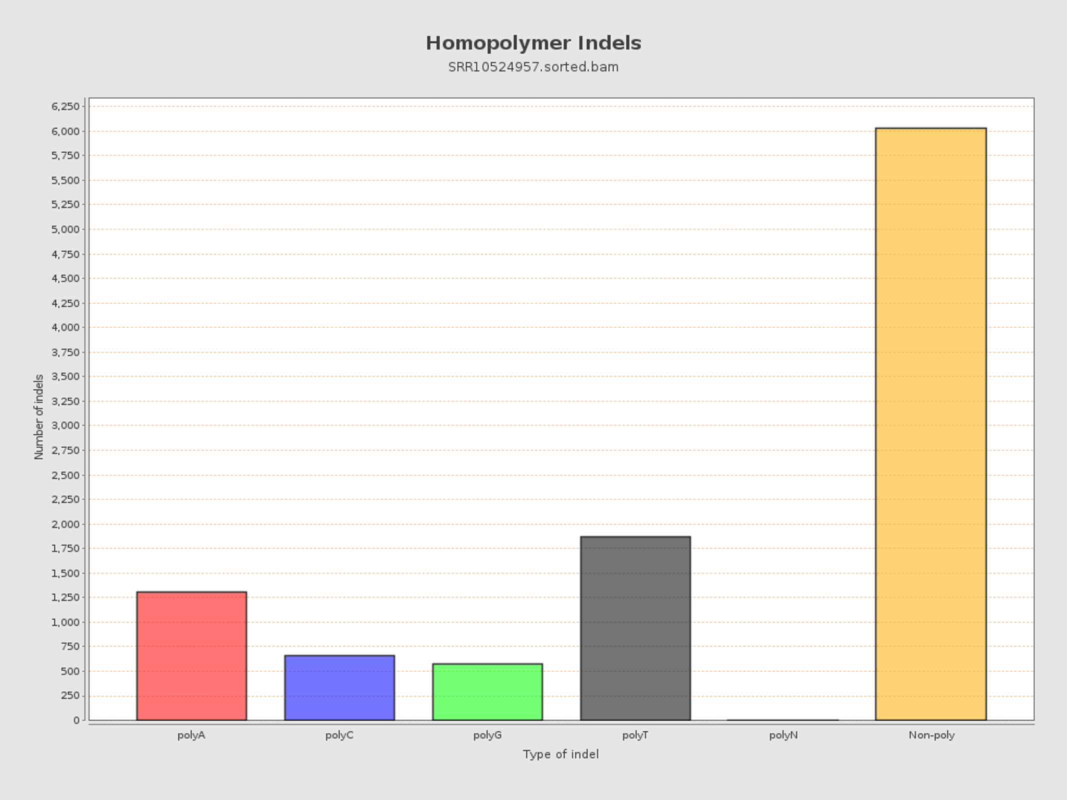
9. Results : Mapped Reads GC-content Distribution



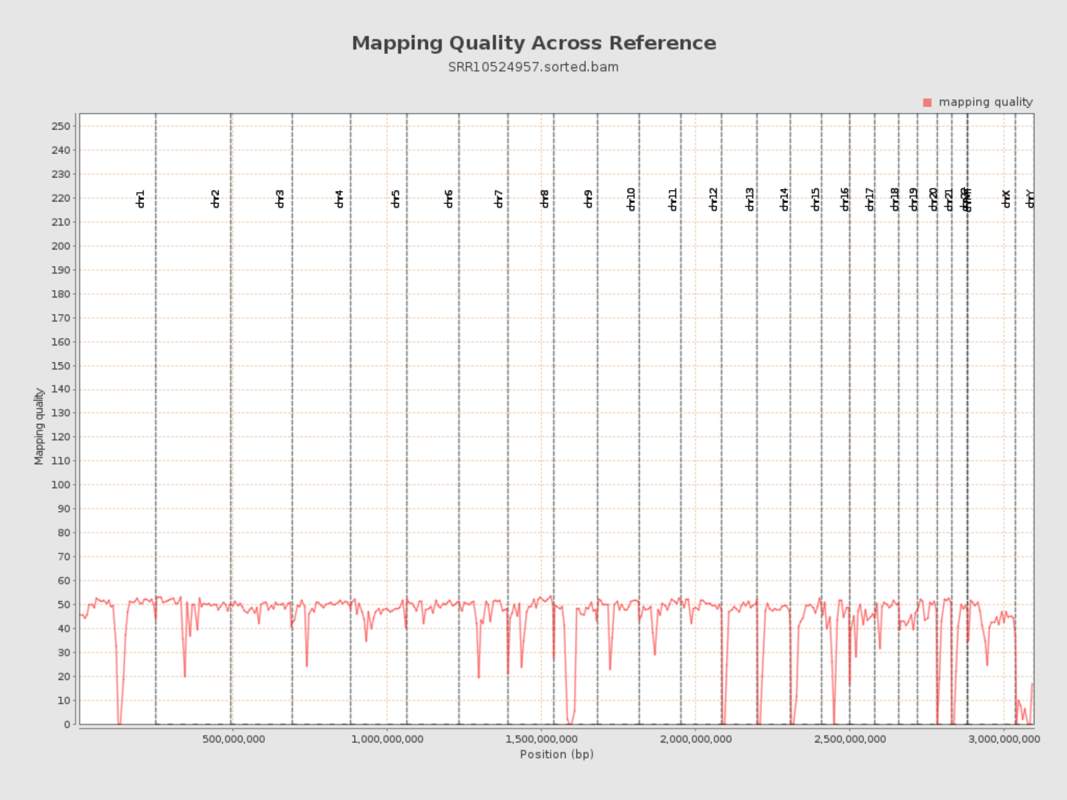
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram