Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524723.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_SRR10524723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:52:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	346,656
Mapped reads	318,028 / 91.74%
Unmapped reads	28,628 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,080 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	4,477 / 1.29%
Duplication rate	1.02%
Clipped reads	318,238 / 91.8%

2.2. ACGT Content

Number/percentage of A's	5,060,058 / 26.74%
Number/percentage of C's	3,394,445 / 17.94%
Number/percentage of T's	5,883,208 / 31.09%
Number/percentage of G's	4,581,823 / 24.21%
Number/percentage of N's	2,752 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0061

Standard Deviation	0.092

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

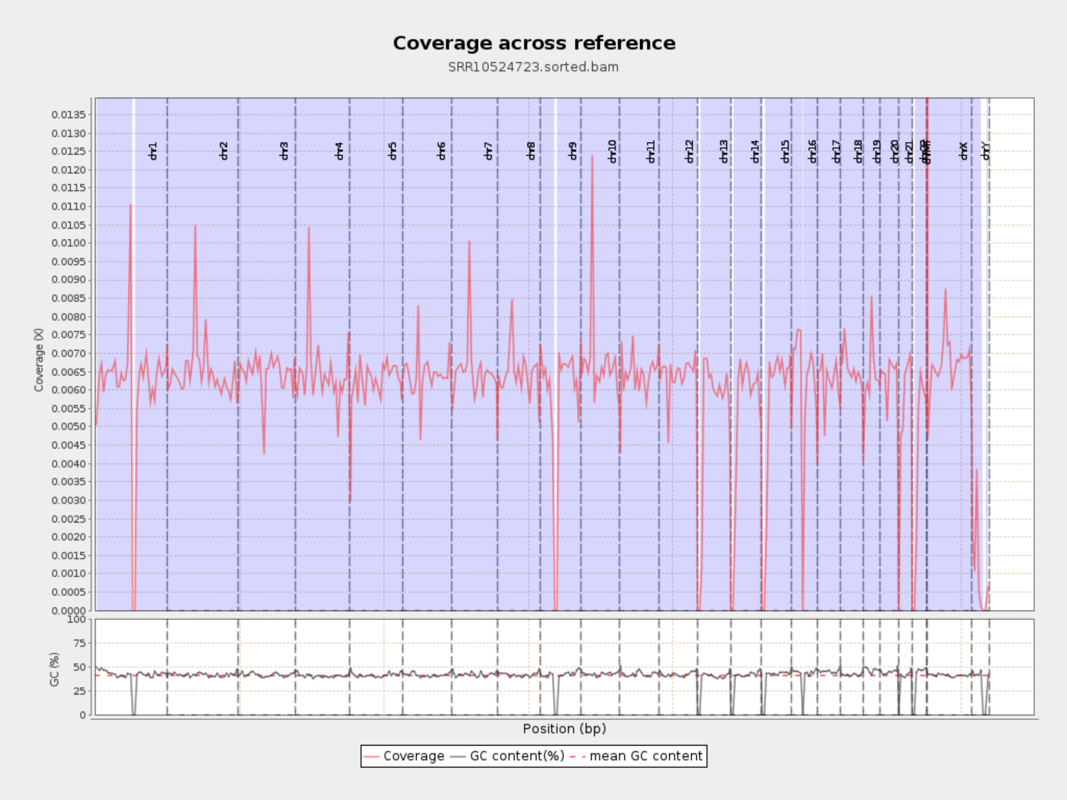
General error rate	0.51%
Mismatches	93,086
Insertions	1,519
Mapped reads with at least one insertion	0.47%
Deletions	3,675
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.84%

2.6. Chromosome stats

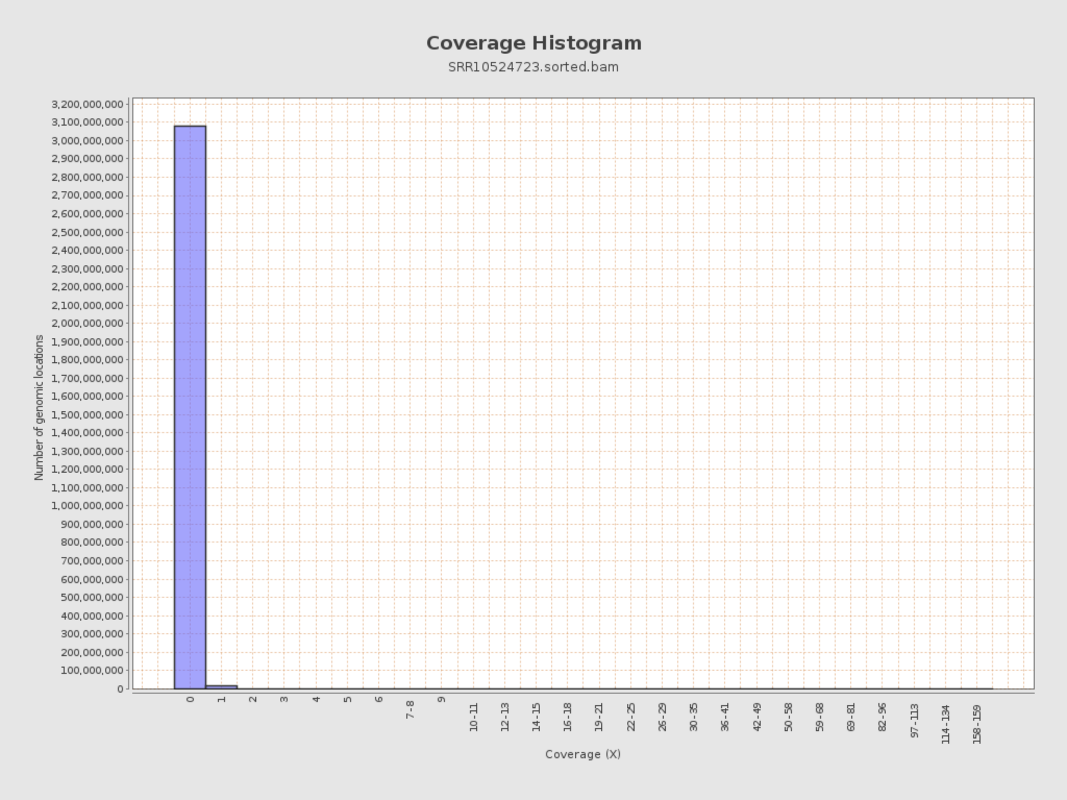
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1516960	0.0061	0.132
chr2	243199373	1586751	0.0065	0.1084
chr3	198022430	1274646	0.0064	0.0817
chr4	191154276	1234381	0.0065	0.0839
chr5	180915260	1142751	0.0063	0.0811
chr6	171115067	1098937	0.0064	0.0848
chr7	159138663	1042634	0.0066	0.1032

chr8	146364022	950869	0.0065	0.0955
chr9	141213431	800995	0.0057	0.0843
chr10	135534747	926232	0.0068	0.0959
chr11	135006516	869513	0.0064	0.086
chr12	133851895	858724	0.0064	0.0821
chr13	115169878	593830	0.0052	0.0733
chr14	107349540	559183	0.0052	0.0742
chr15	102531392	545096	0.0053	0.0742
chr16	90354753	544001	0.006	0.0814
chr17	81195210	508096	0.0063	0.0813
chr18	78077248	515131	0.0066	0.1111
chr19	59128983	380917	0.0064	0.107
chr20	63025520	400204	0.0063	0.0815
chr21	48129895	261986	0.0054	0.0771
chr22	51304566	209157	0.0041	0.0651
chrMT	16571	2759	0.1665	0.4042
chrX	155270560	1046358	0.0067	0.085
chrY	59373566	58066	0.001	0.0438

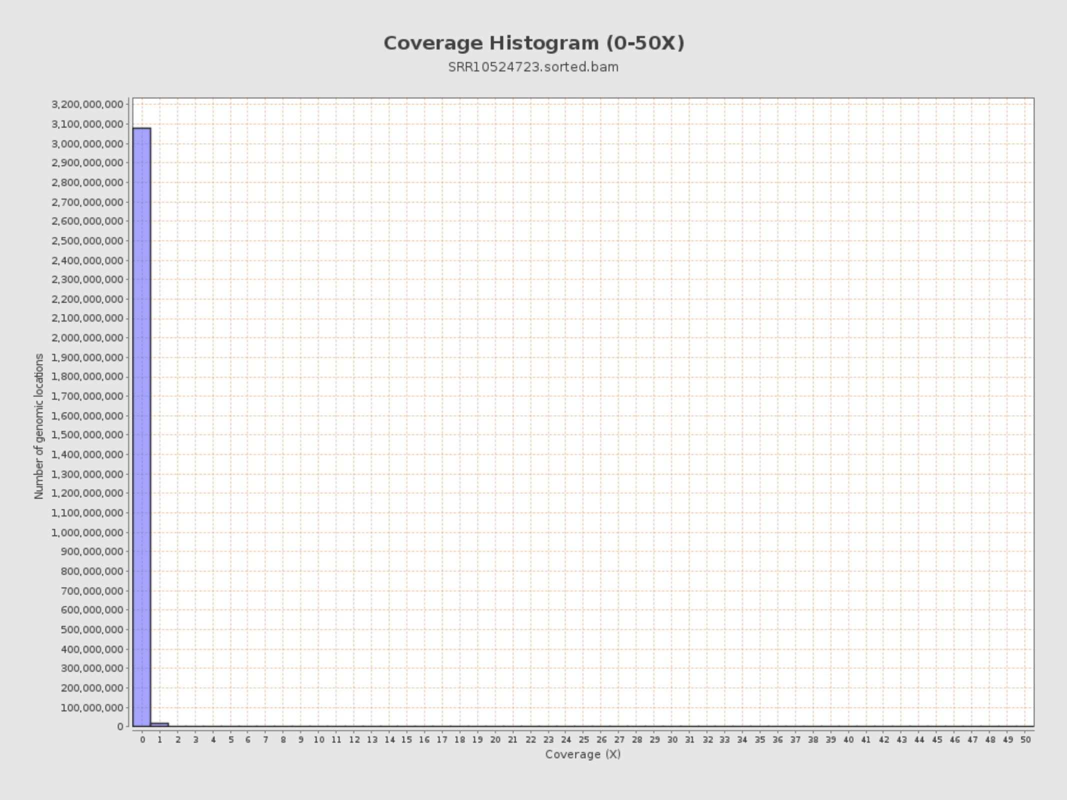
3. Results : Coverage across reference



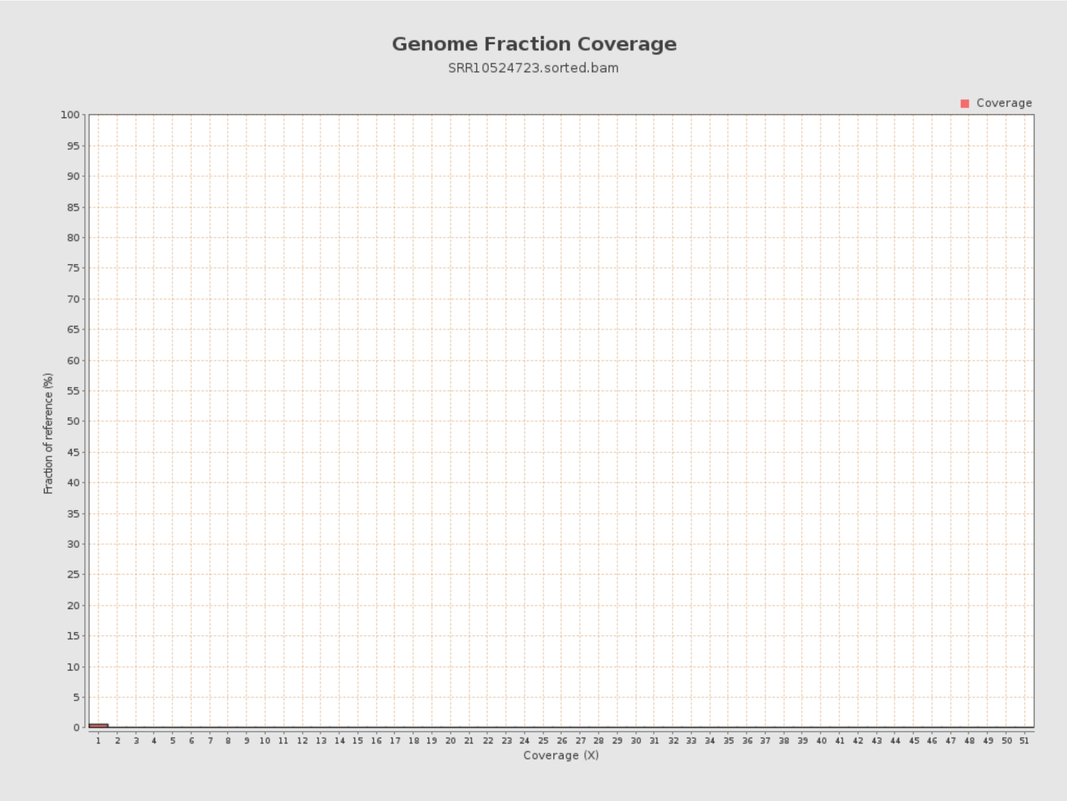
4. Results : Coverage Histogram



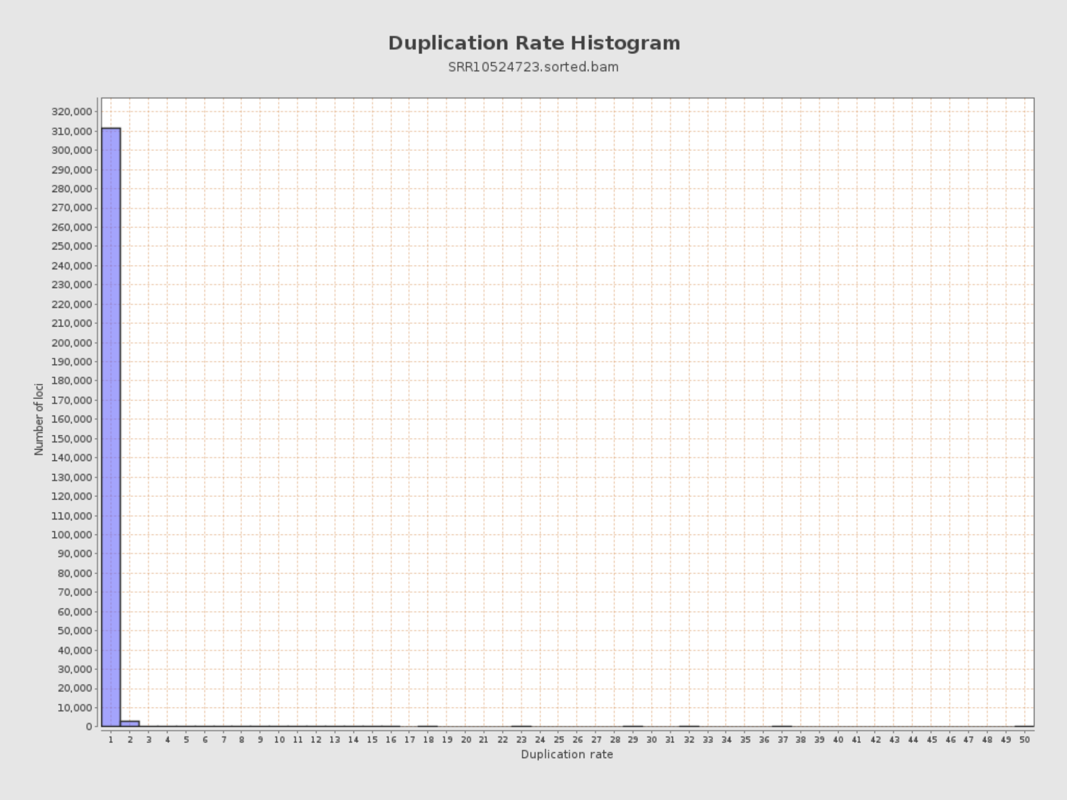
5. Results : Coverage Histogram (0-50X)



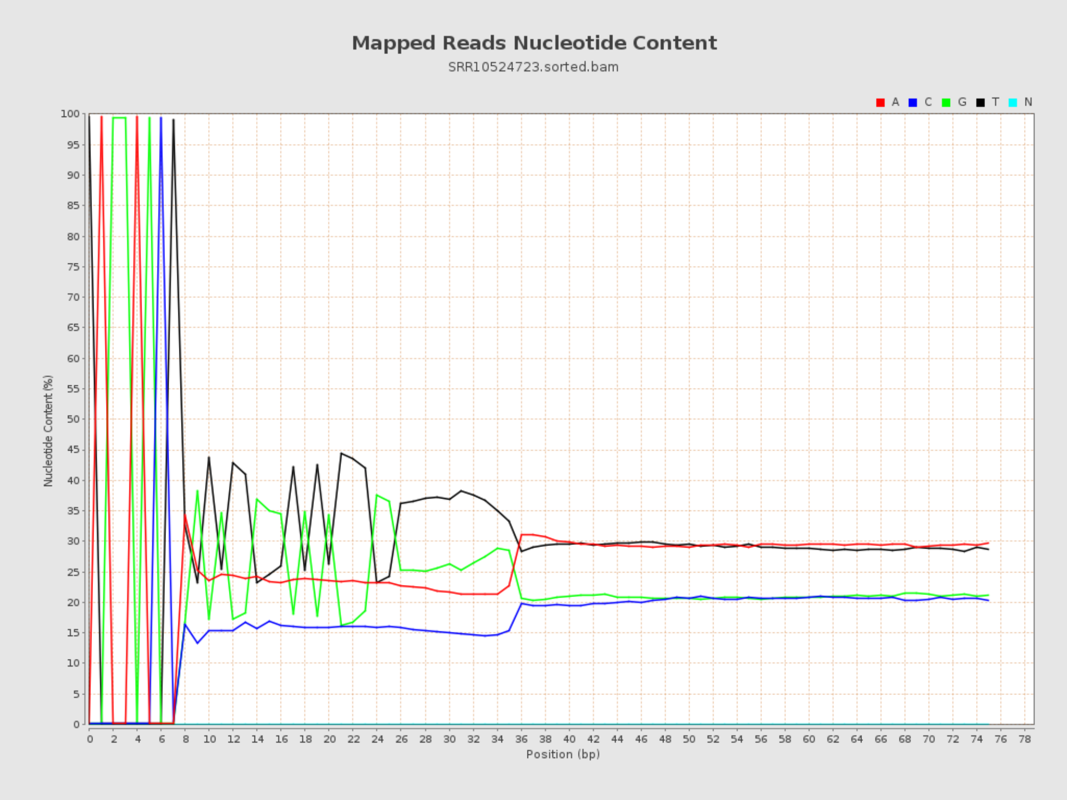
6. Results : Genome Fraction Coverage



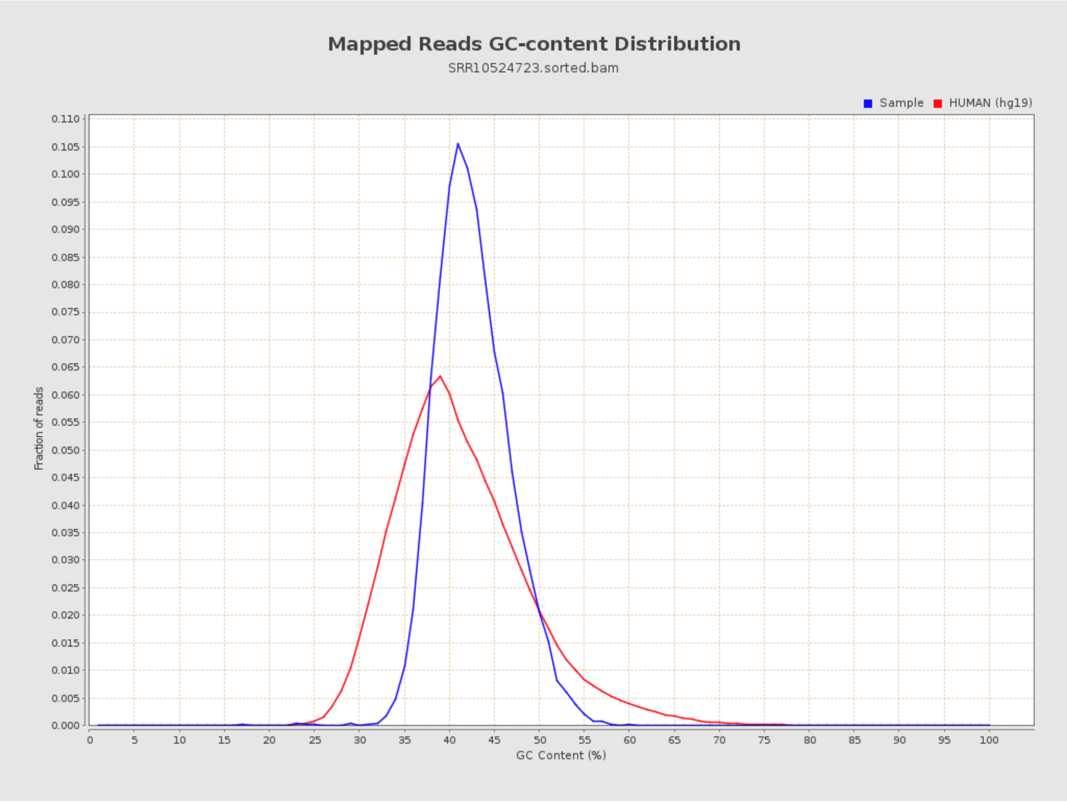
7. Results : Duplication Rate Histogram



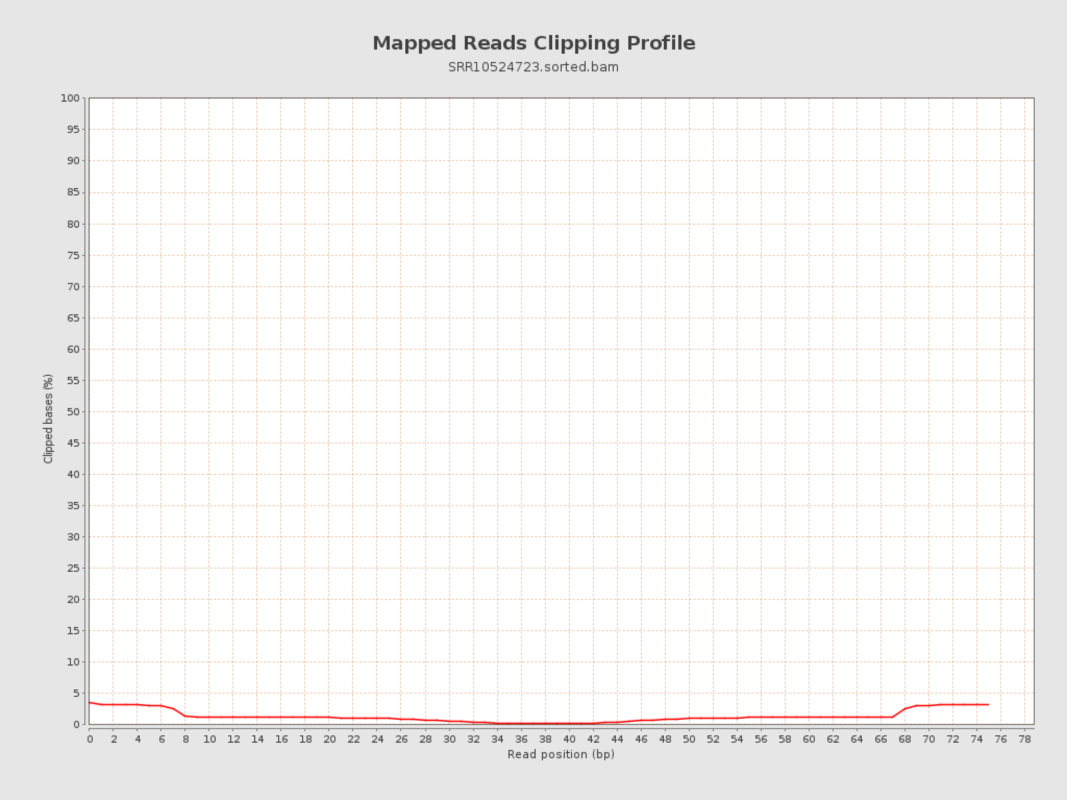
8. Results : Mapped Reads Nucleotide Content



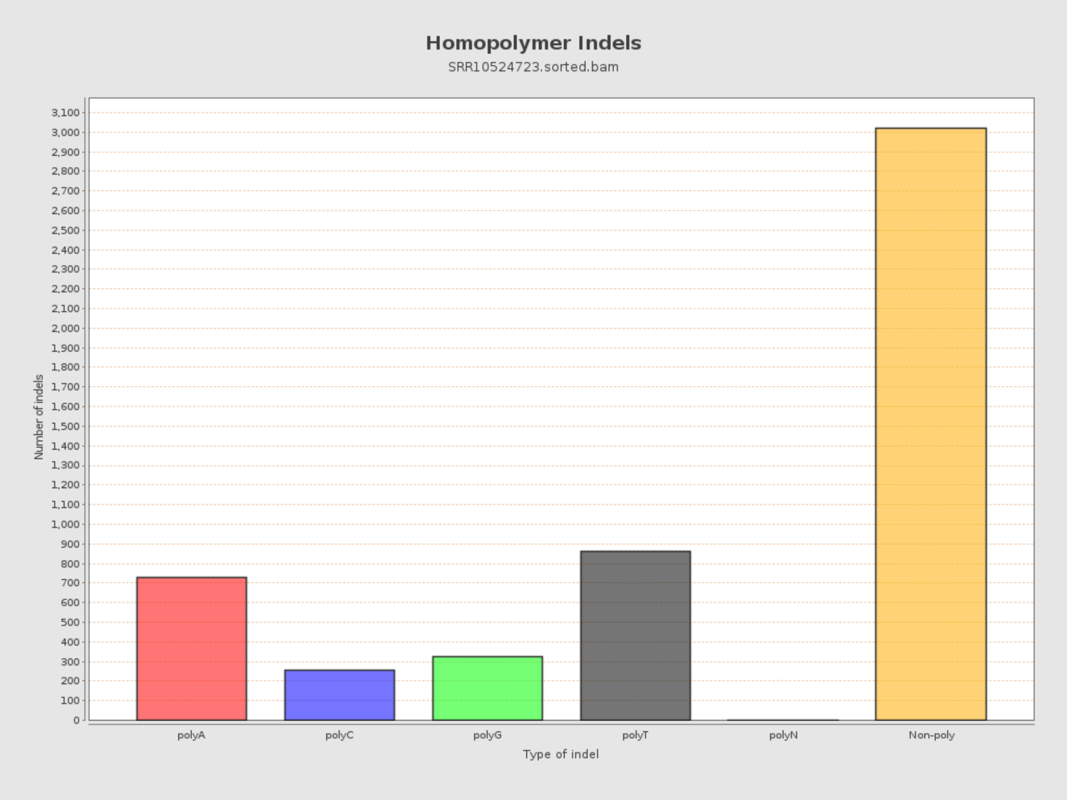
9. Results : Mapped Reads GC-content Distribution



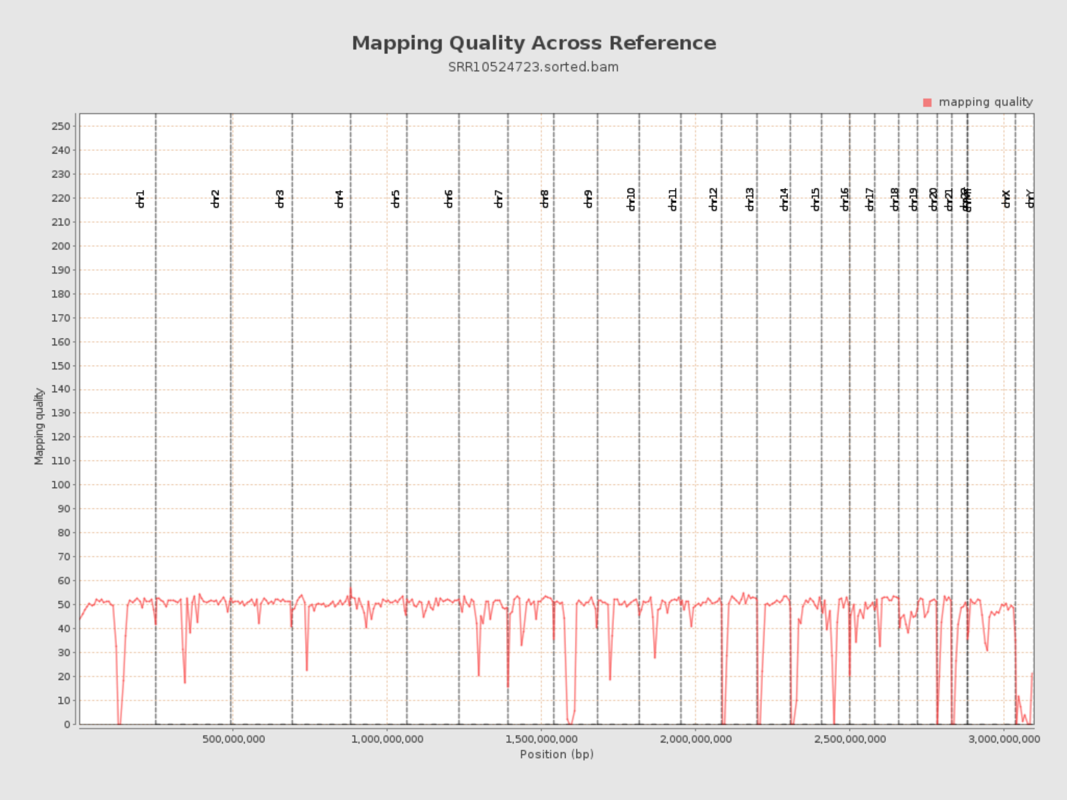
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram