Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:05:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524773.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_SRR10524773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:05:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,254,612
Mapped reads	1,125,968 / 89.75%
Unmapped reads	128,644 / 10.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,859 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,709 / 3.32%
Duplication rate	2.86%
Clipped reads	1,126,438 / 89.78%

2.2. ACGT Content

Number/percentage of A's	16,321,099 / 25.53%
Number/percentage of C's	11,685,002 / 18.28%
Number/percentage of T's	19,845,254 / 31.04%
Number/percentage of G's	16,070,600 / 25.14%
Number/percentage of N's	7,721 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2021

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

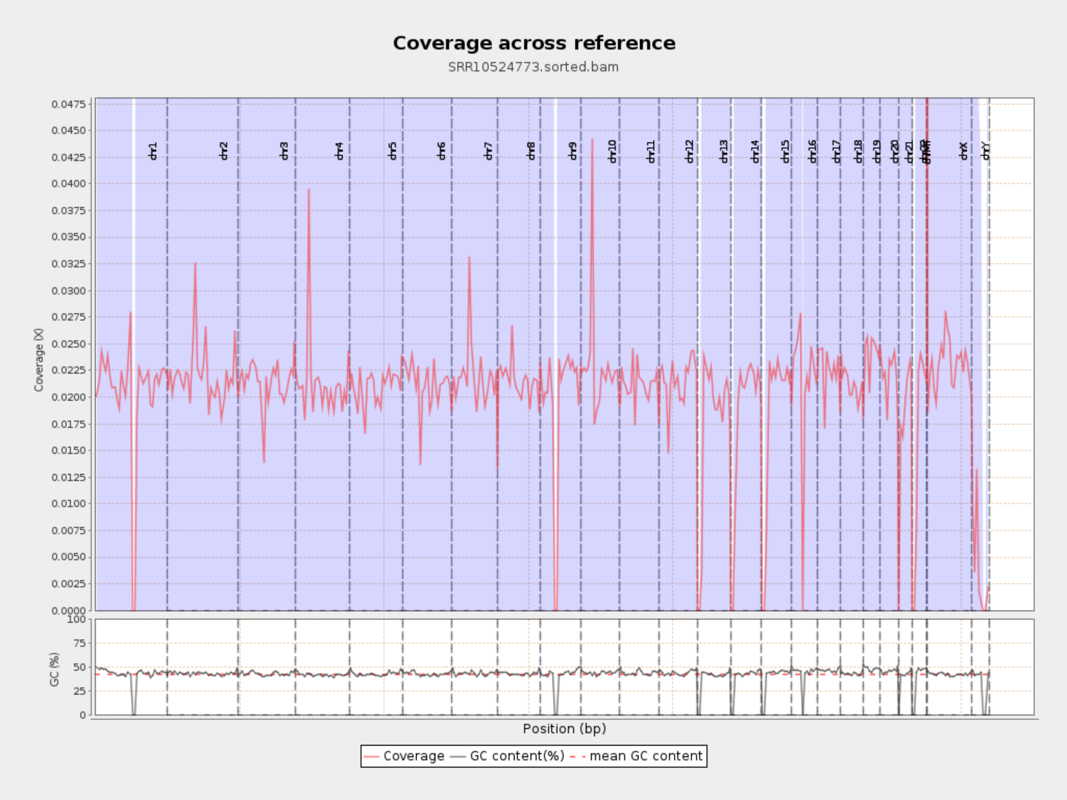
General error rate	0.53%
Mismatches	328,312
Insertions	5,341
Mapped reads with at least one insertion	0.47%
Deletions	12,809
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.64%

2.6. Chromosome stats

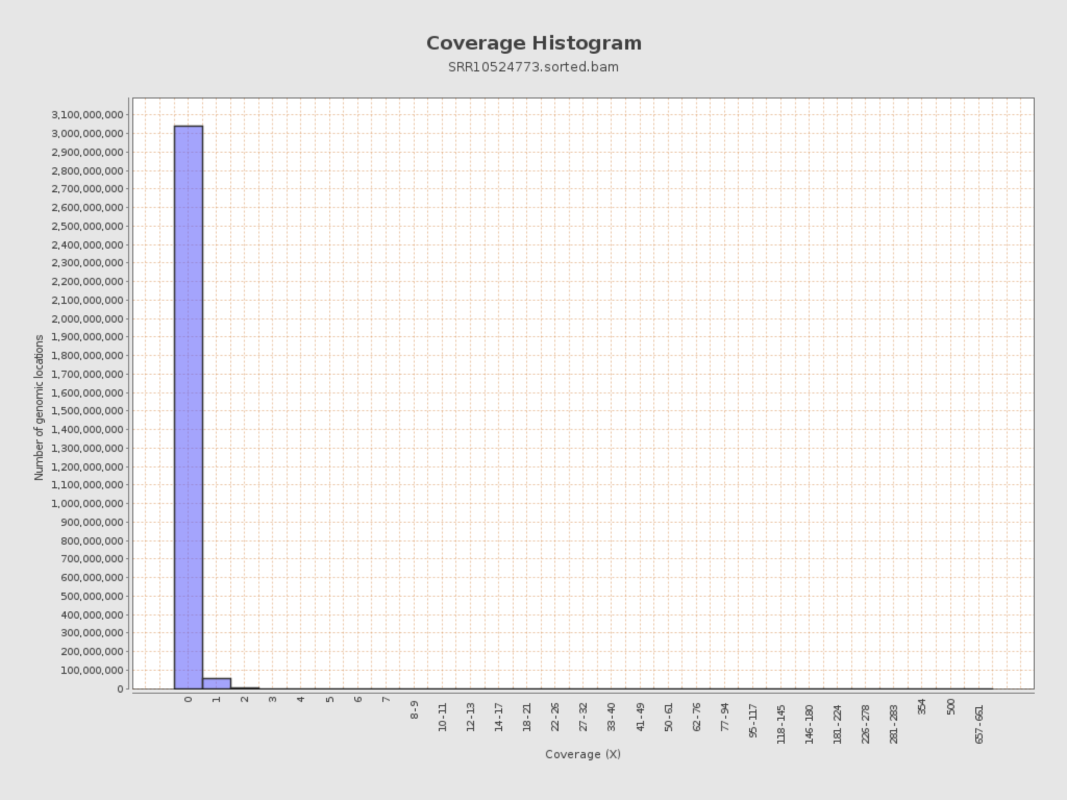
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5082446	0.0204	0.2632
chr2	243199373	5356008	0.022	0.3208
chr3	198022430	4217751	0.0213	0.1608
chr4	191154276	4089700	0.0214	0.1767
chr5	180915260	3799111	0.021	0.1574
chr6	171115067	3632704	0.0212	0.1725
chr7	159138663	3510000	0.0221	0.2318

chr8	146364022	3156509	0.0216	0.1907
chr9	141213431	2755309	0.0195	0.1775
chr10	135534747	3111742	0.023	0.2369
chr11	135006516	2881154	0.0213	0.1785
chr12	133851895	2884376	0.0215	0.1615
chr13	115169878	1987926	0.0173	0.1434
chr14	107349540	1933387	0.018	0.1506
chr15	102531392	1841466	0.018	0.146
chr16	90354753	1910435	0.0211	0.1719
chr17	81195210	1833999	0.0226	0.1677
chr18	78077248	1650213	0.0211	0.2551
chr19	59128983	1421868	0.024	0.2307
chr20	63025520	1389424	0.022	0.1662
chr21	48129895	866687	0.018	0.1585
chr22	51304566	809404	0.0158	0.138
chrMT	16571	20266	1.223	1.3801
chrX	155270560	3588191	0.0231	0.1757
chrY	59373566	220316	0.0037	0.1102

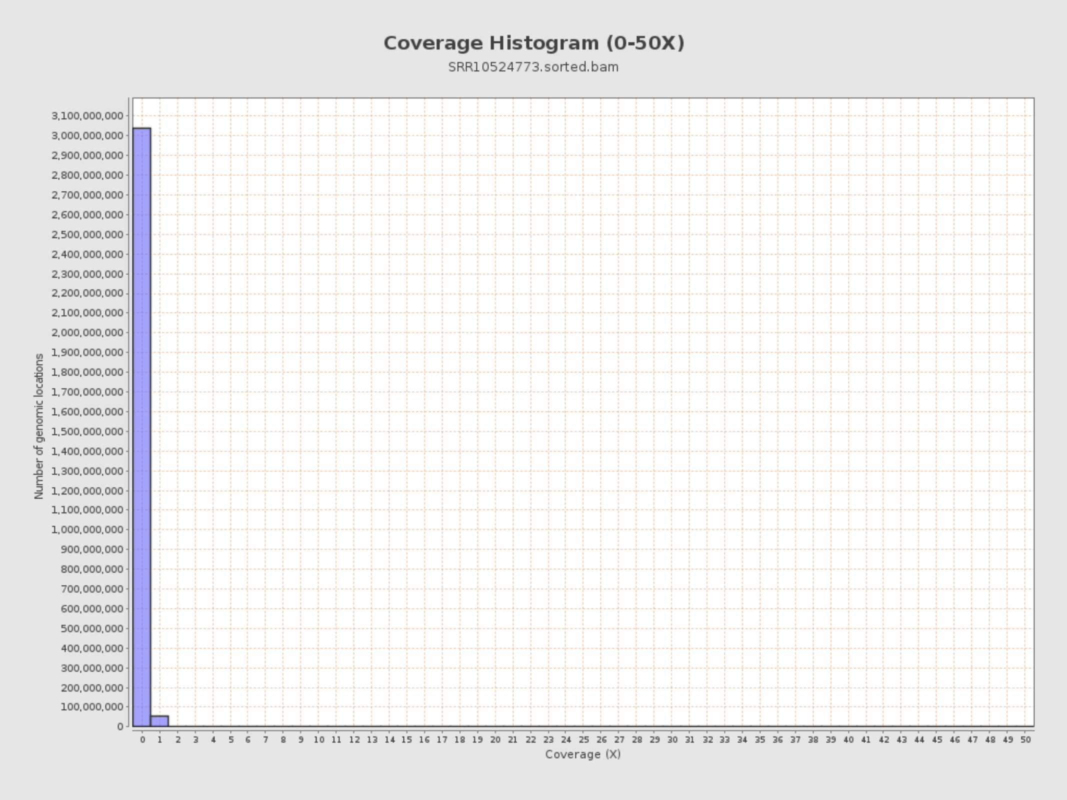
3. Results : Coverage across reference



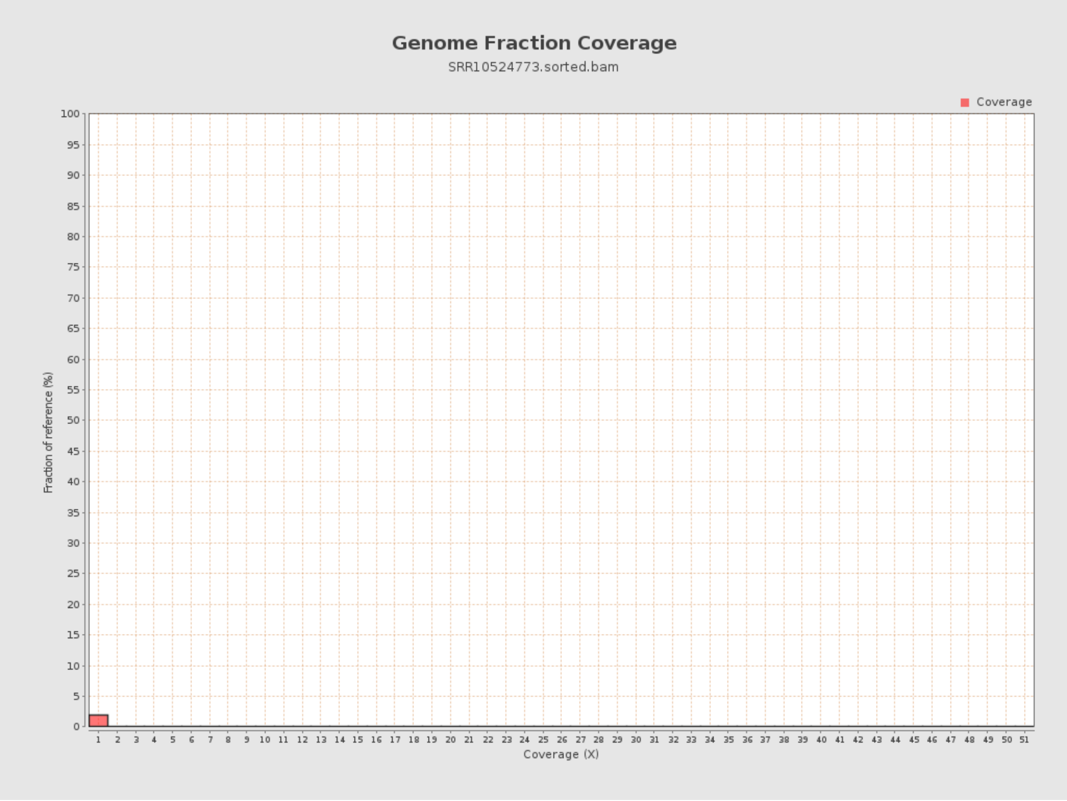
4. Results : Coverage Histogram



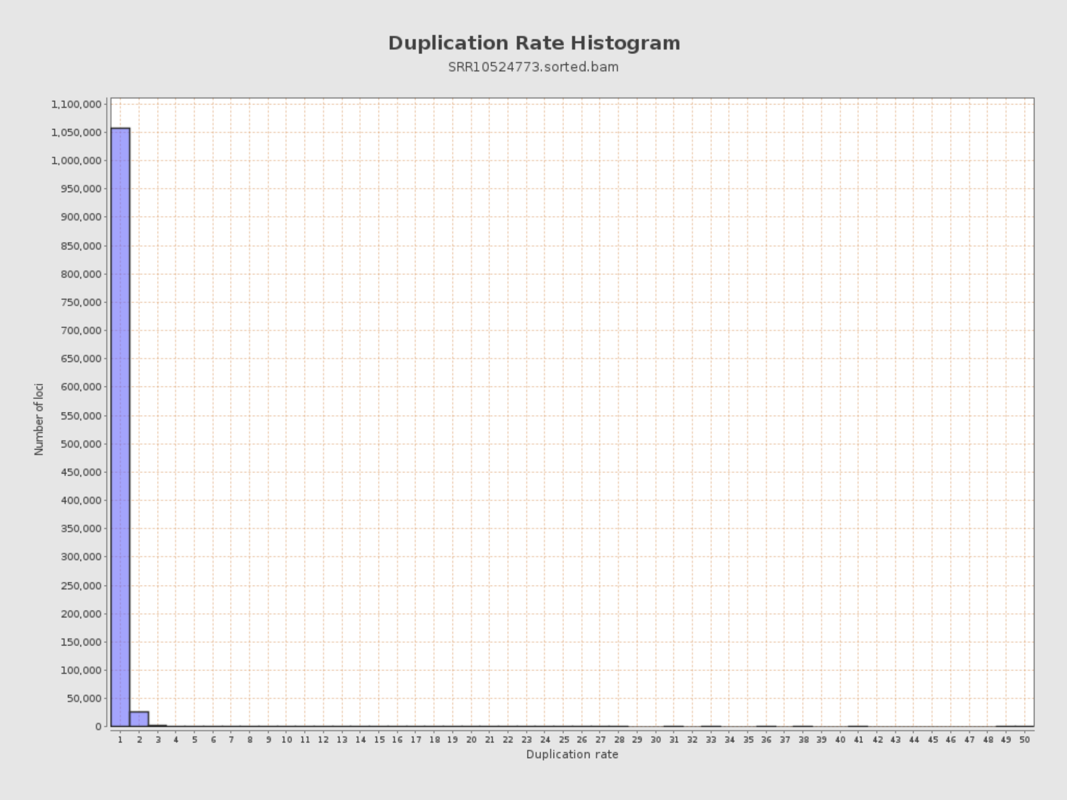
5. Results : Coverage Histogram (0-50X)



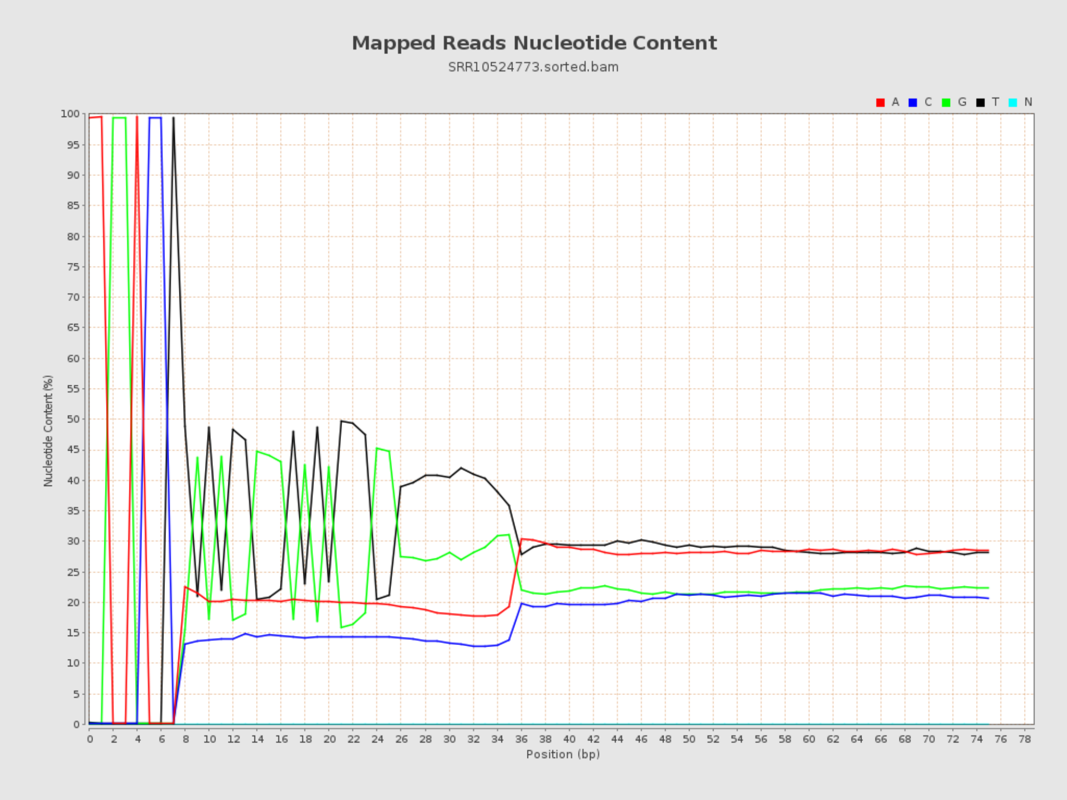
6. Results : Genome Fraction Coverage



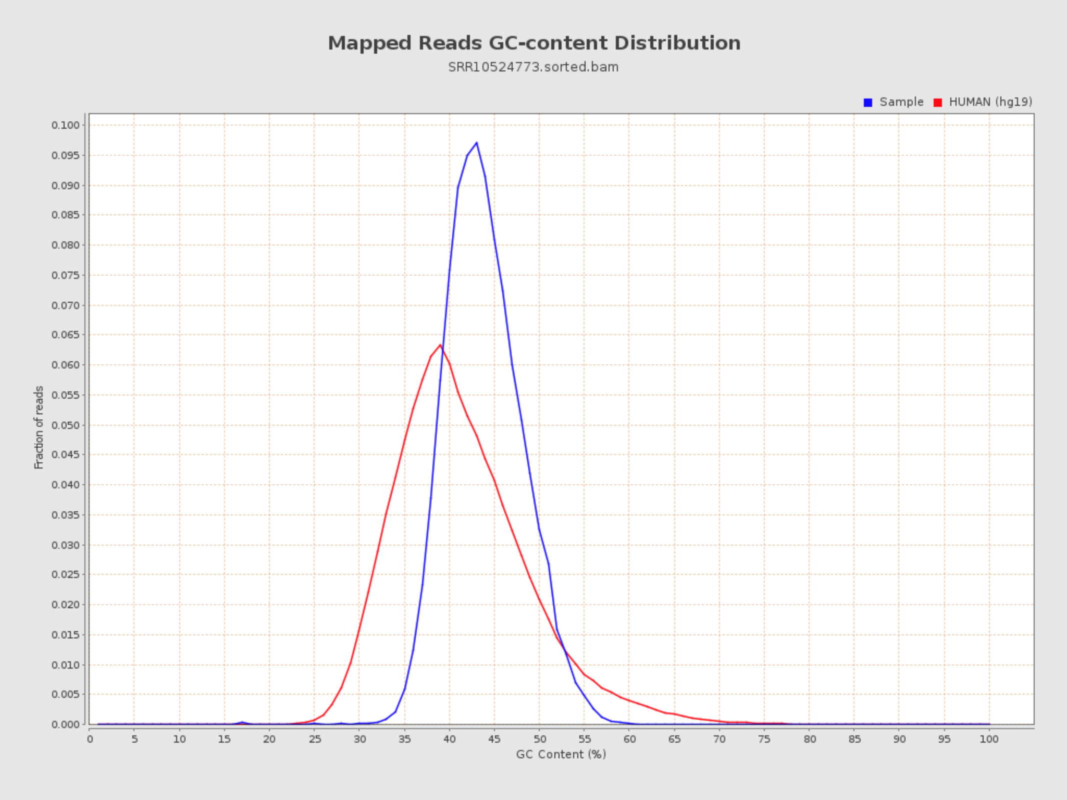
7. Results : Duplication Rate Histogram



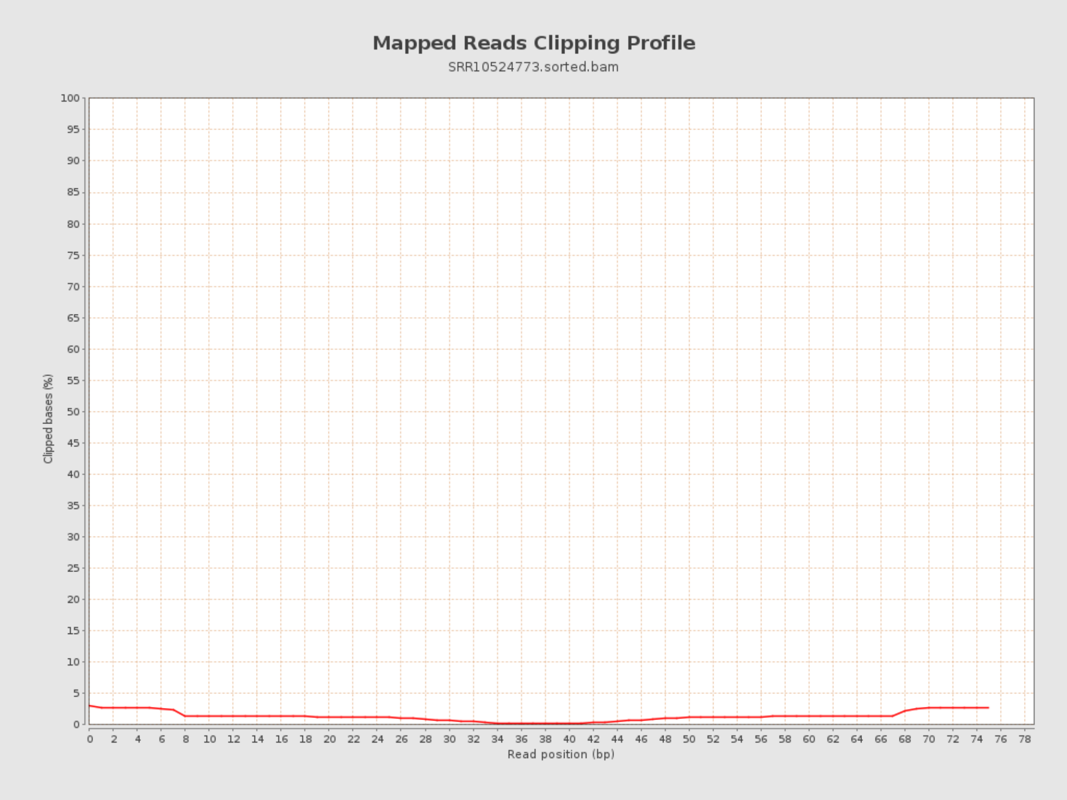
8. Results : Mapped Reads Nucleotide Content



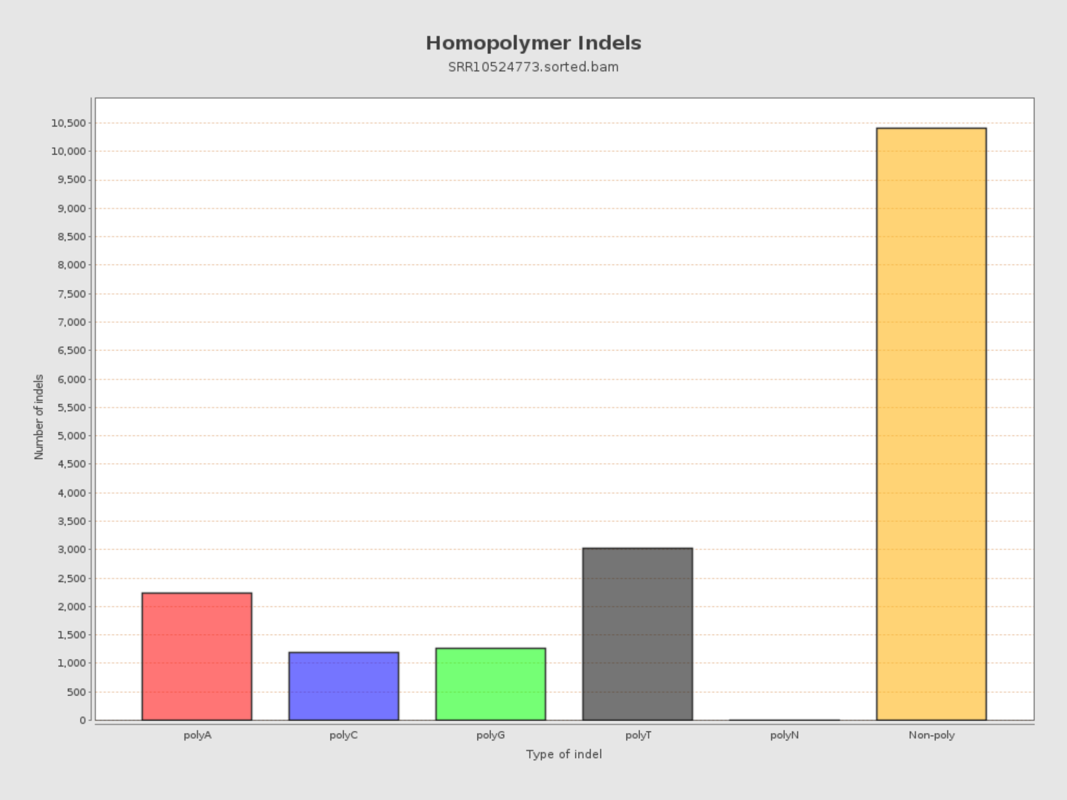
9. Results : Mapped Reads GC-content Distribution



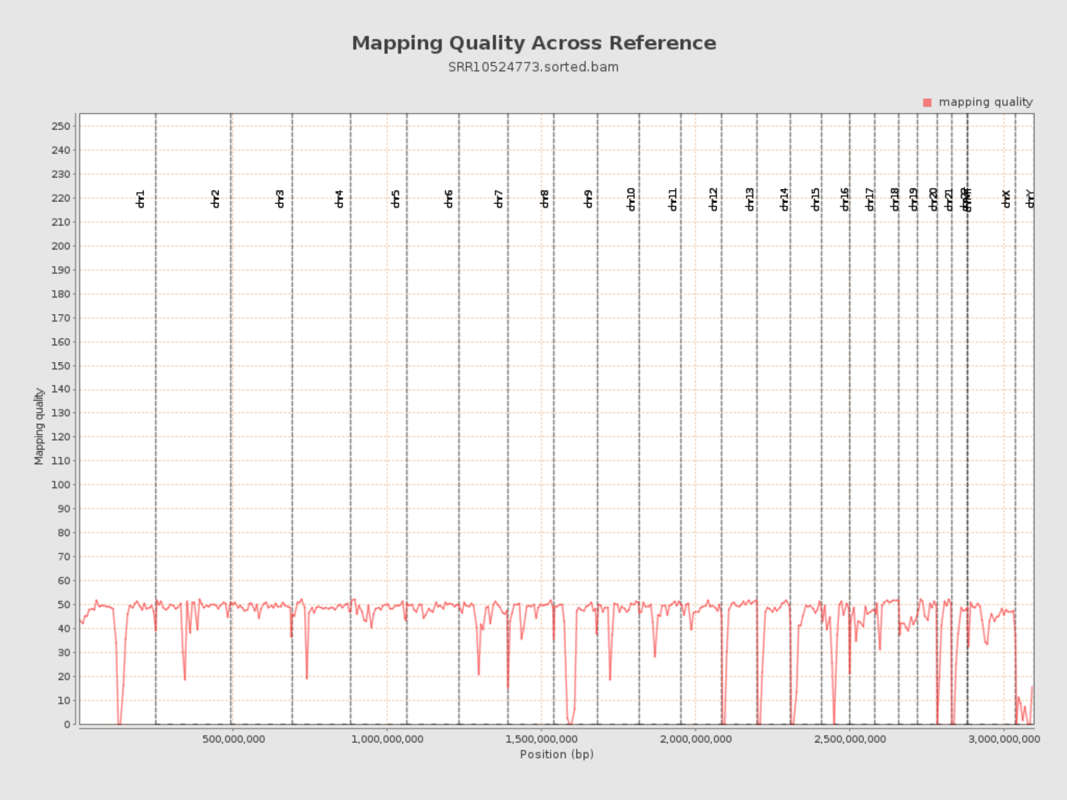
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram