Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:38:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524761.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_SRR10524761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:38:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,301,730
Mapped reads	1,191,773 / 91.55%
Unmapped reads	109,957 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,793 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	34,595 / 2.66%
Duplication rate	2.16%
Clipped reads	1,193,285 / 91.67%

2.2. ACGT Content

Number/percentage of A's	15,837,881 / 23.12%
Number/percentage of C's	12,837,461 / 18.74%
Number/percentage of T's	21,965,806 / 32.07%
Number/percentage of G's	17,850,102 / 26.06%
Number/percentage of N's	8,028 / 0.01%
GC Percentage	44.8%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2005

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

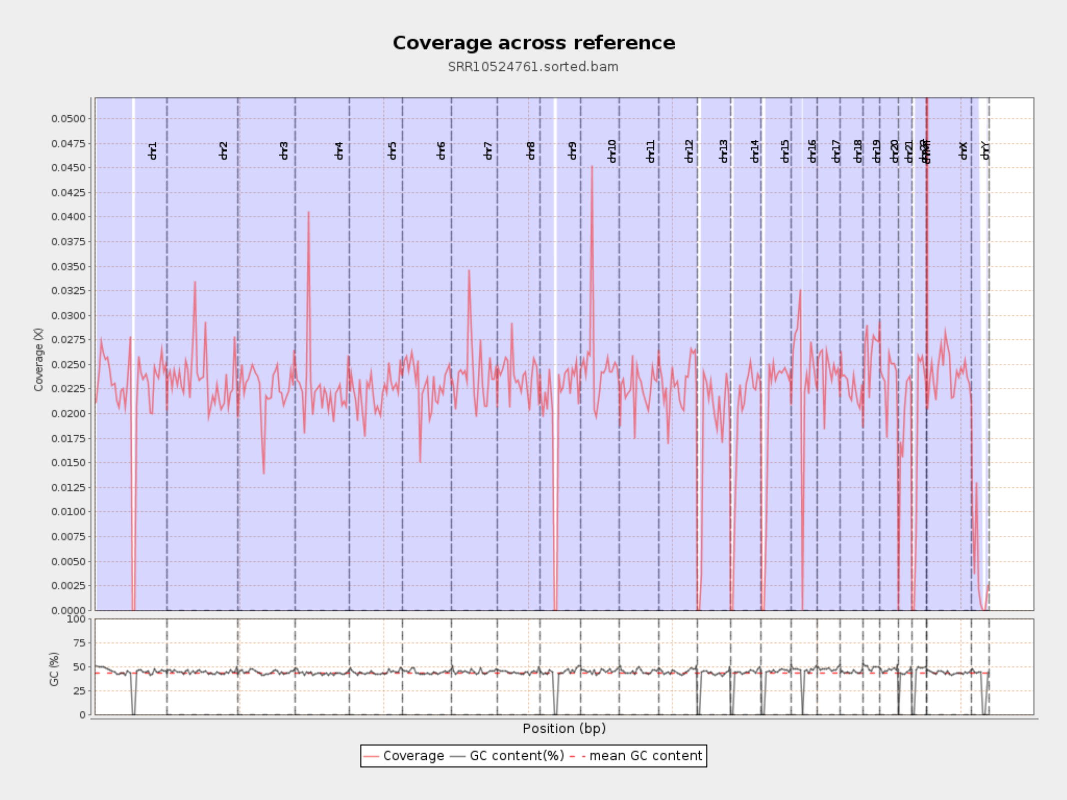
General error rate	0.51%
Mismatches	340,858
Insertions	4,544
Mapped reads with at least one insertion	0.38%
Deletions	13,370
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.65%

2.6. Chromosome stats

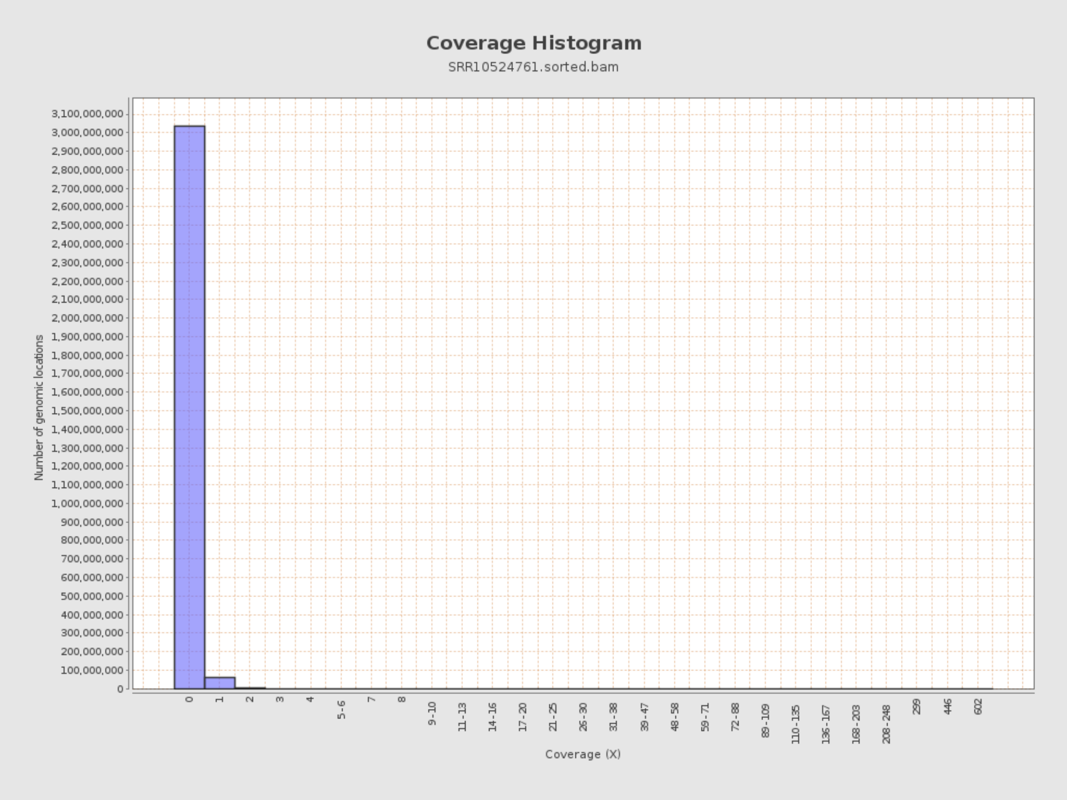
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5517848	0.0221	0.2414
chr2	243199373	5724850	0.0235	0.3052
chr3	198022430	4460120	0.0225	0.1636
chr4	191154276	4358022	0.0228	0.1805
chr5	180915260	4025781	0.0223	0.1609
chr6	171115067	3937283	0.023	0.1723
chr7	159138663	3826496	0.024	0.2449

chr8	146364022	3486685	0.0238	0.1881
chr9	141213431	2859323	0.0202	0.1806
chr10	135534747	3424561	0.0253	0.2366
chr11	135006516	3050606	0.0226	0.1896
chr12	133851895	3079903	0.023	0.1646
chr13	115169878	2058113	0.0179	0.1448
chr14	107349540	2027791	0.0189	0.1502
chr15	102531392	1999888	0.0195	0.151
chr16	90354753	2120862	0.0235	0.1827
chr17	81195210	1979399	0.0244	0.1743
chr18	78077248	1771799	0.0227	0.2563
chr19	59128983	1561166	0.0264	0.2216
chr20	63025520	1479455	0.0235	0.1716
chr21	48129895	890413	0.0185	0.1623
chr22	51304566	877862	0.0171	0.1434
chrMT	16571	23244	1.4027	1.3465
chrX	155270560	3755063	0.0242	0.1781
chrY	59373566	224565	0.0038	0.1059

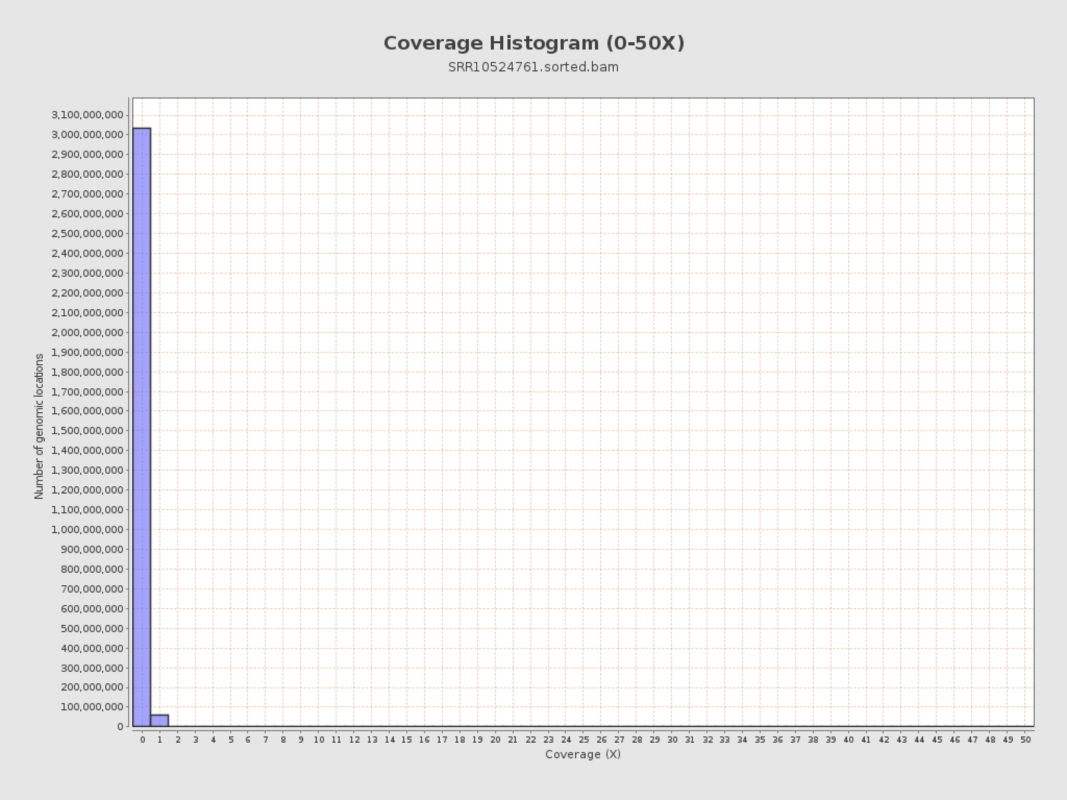
3. Results : Coverage across reference



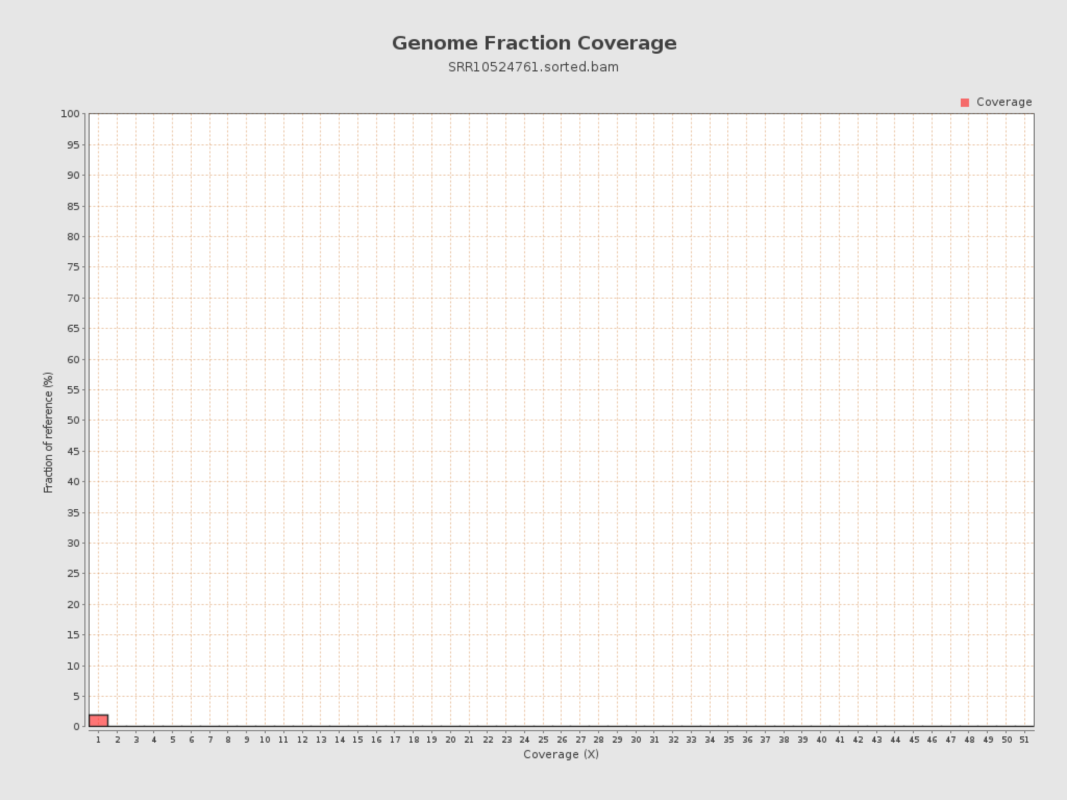
4. Results : Coverage Histogram



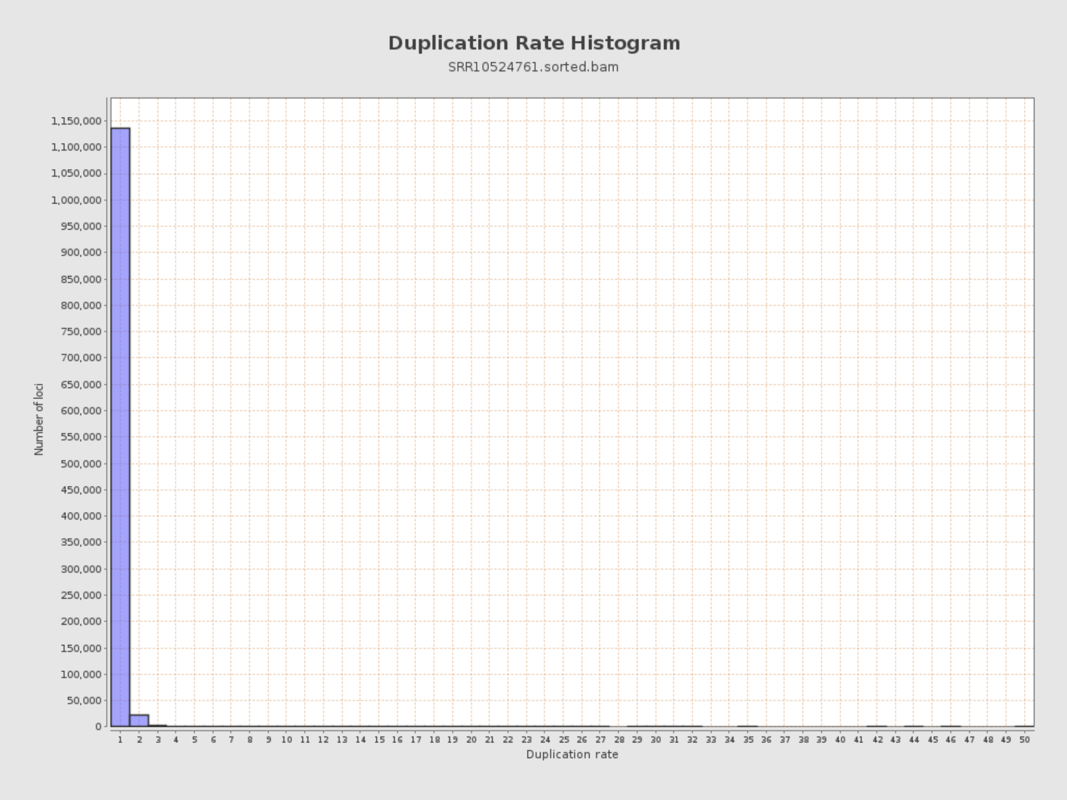
5. Results : Coverage Histogram (0-50X)



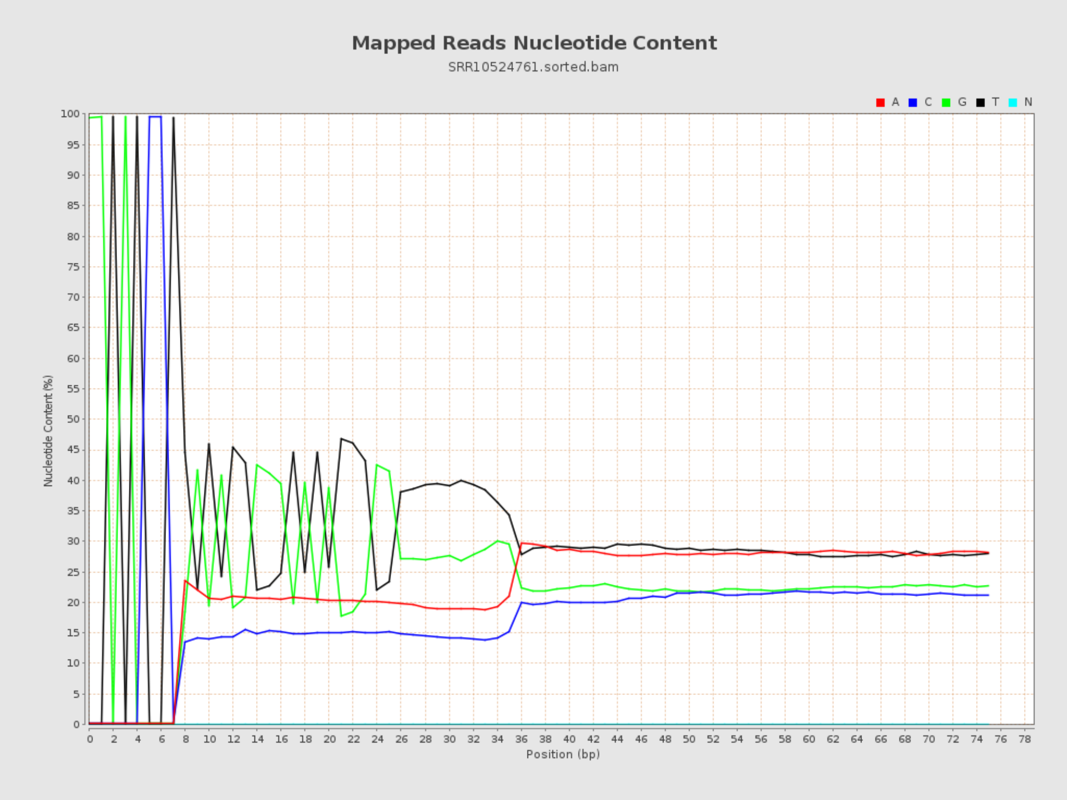
6. Results : Genome Fraction Coverage



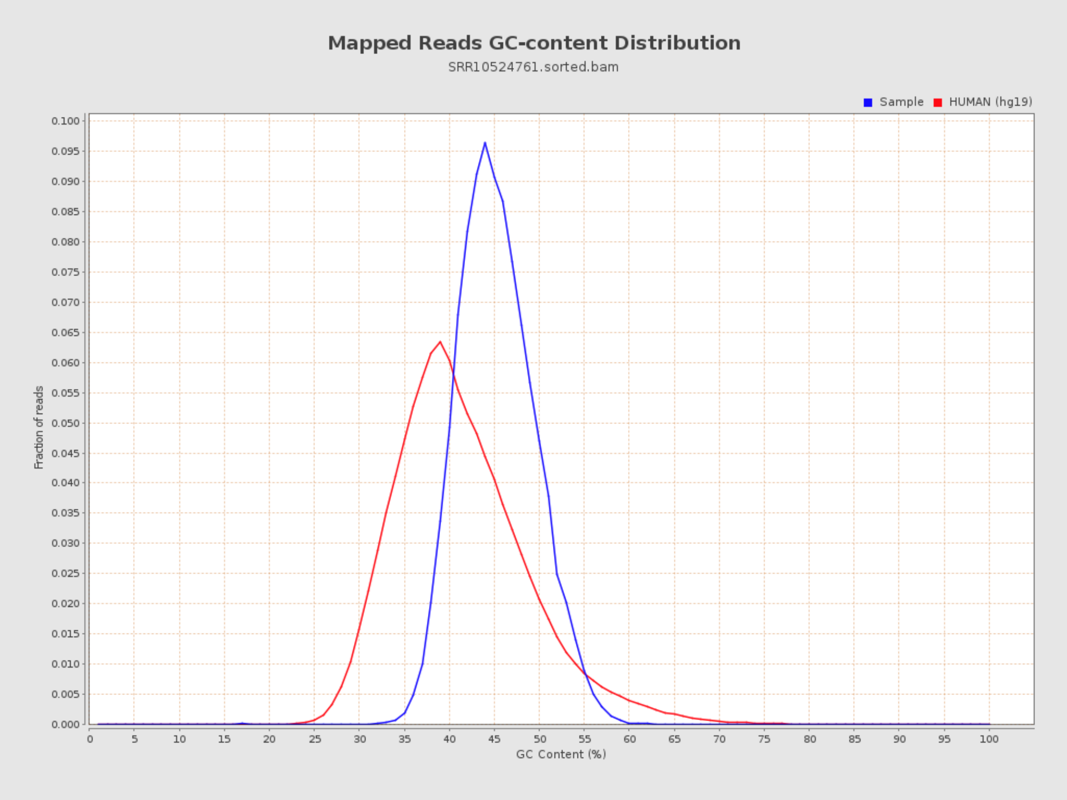
7. Results : Duplication Rate Histogram



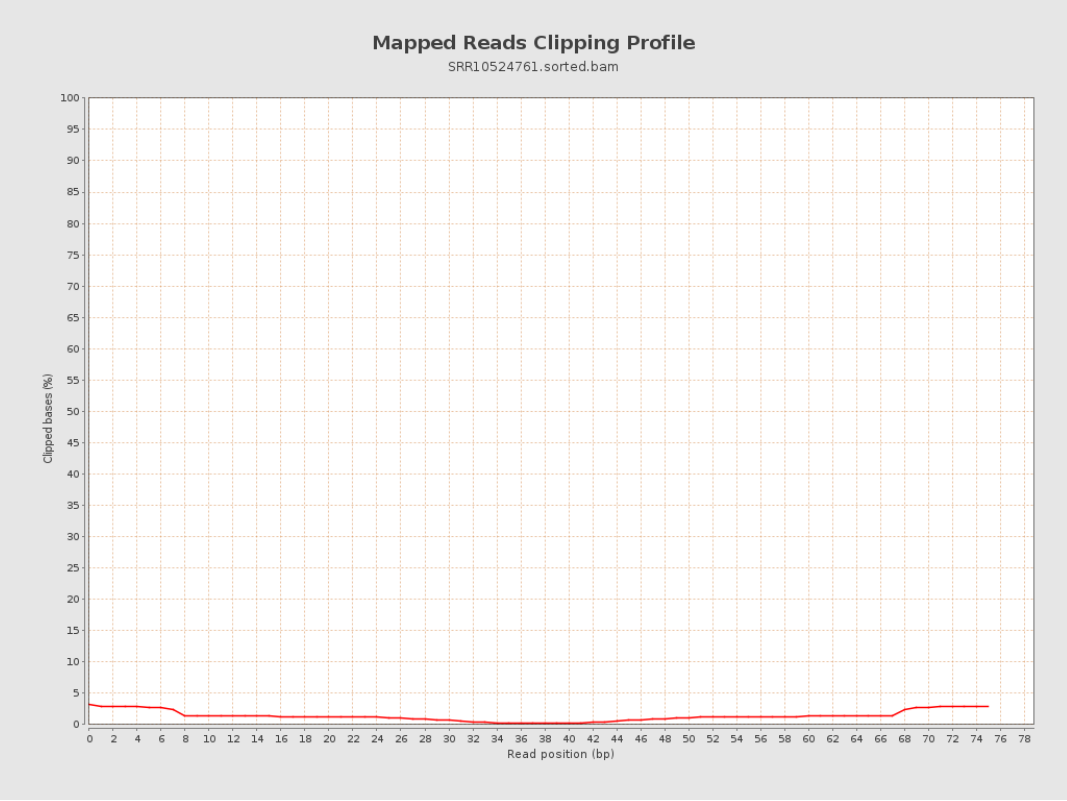
8. Results : Mapped Reads Nucleotide Content



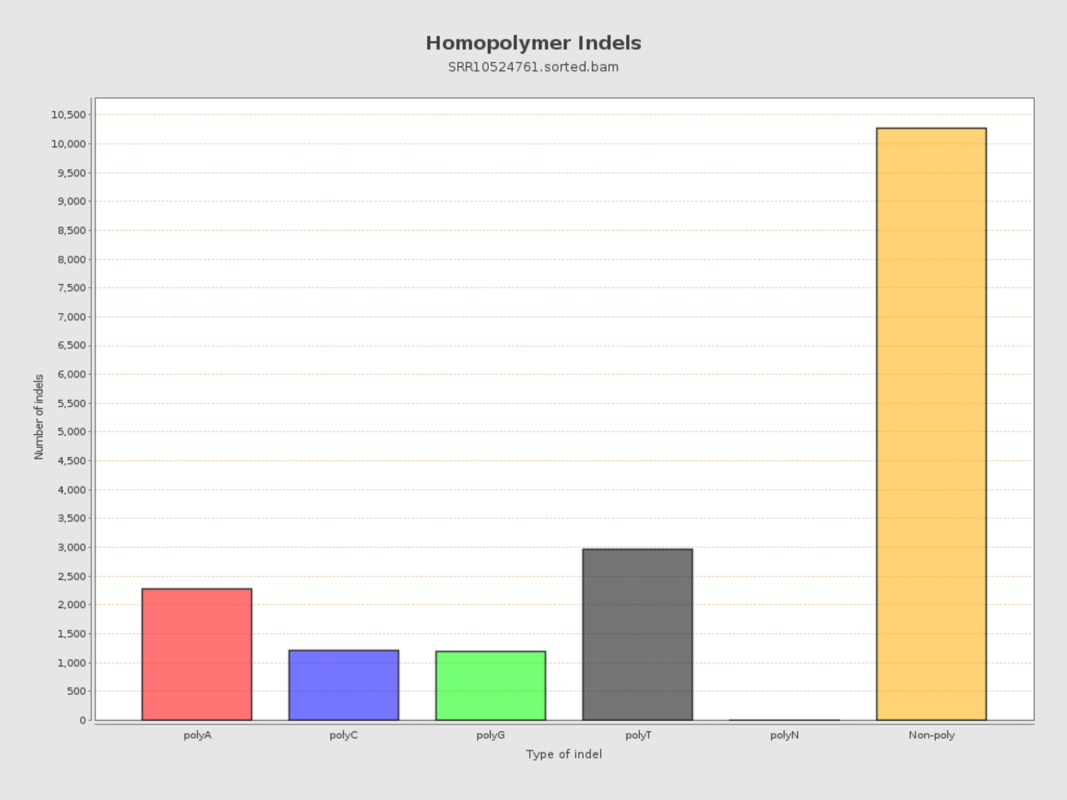
9. Results : Mapped Reads GC-content Distribution



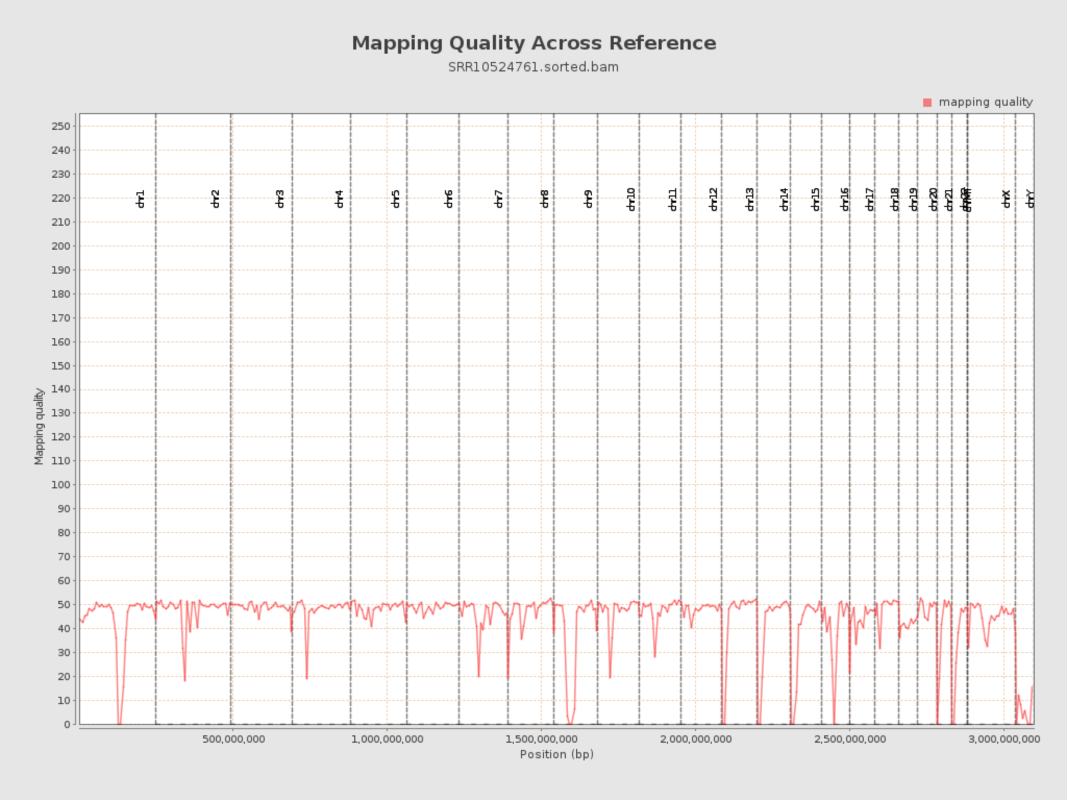
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram