Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:30:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524662.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_SRR10524662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:30:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,193,954
Mapped reads	1,102,078 / 92.3%
Unmapped reads	91,876 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,957 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	35,985 / 3.01%
Duplication rate	2.43%
Clipped reads	1,103,827 / 92.45%

2.2. ACGT Content

Number/percentage of A's	16,890,459 / 25.95%
Number/percentage of C's	12,744,813 / 19.58%
Number/percentage of T's	20,313,099 / 31.2%
Number/percentage of G's	15,143,101 / 23.26%
Number/percentage of N's	9,283 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.021

Standard Deviation	0.213

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

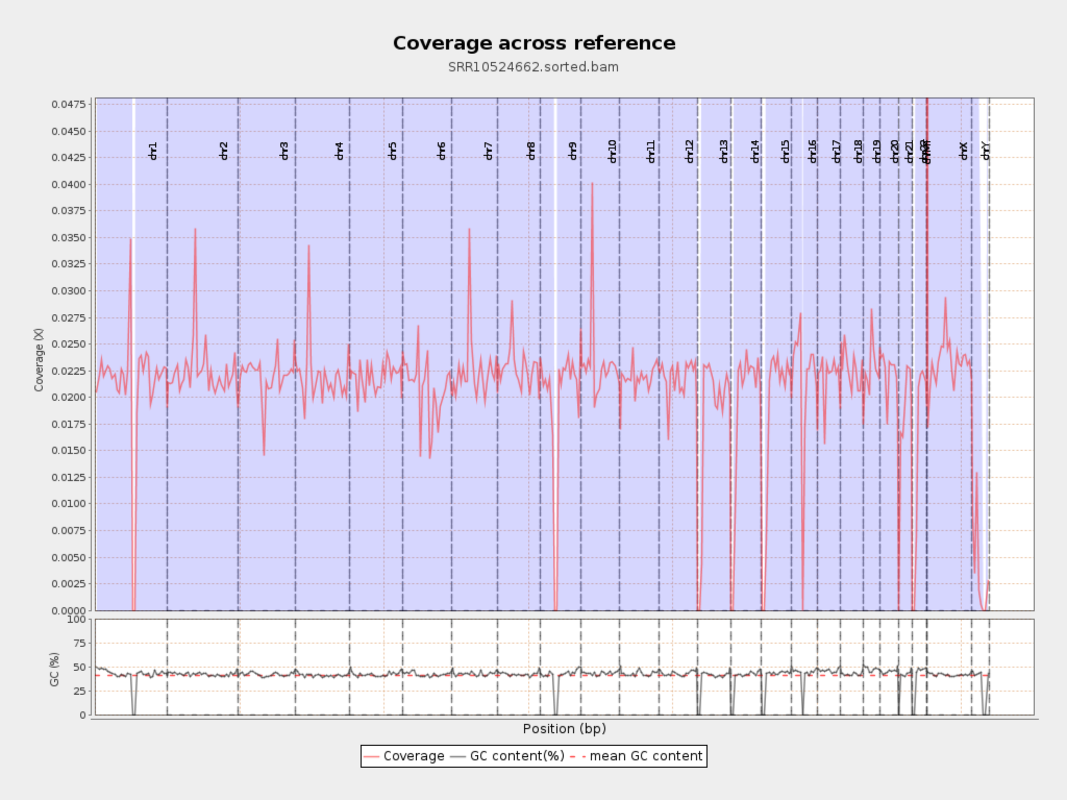
General error rate	0.52%
Mismatches	327,904
Insertions	4,530
Mapped reads with at least one insertion	0.41%
Deletions	12,531
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.98%

2.6. Chromosome stats

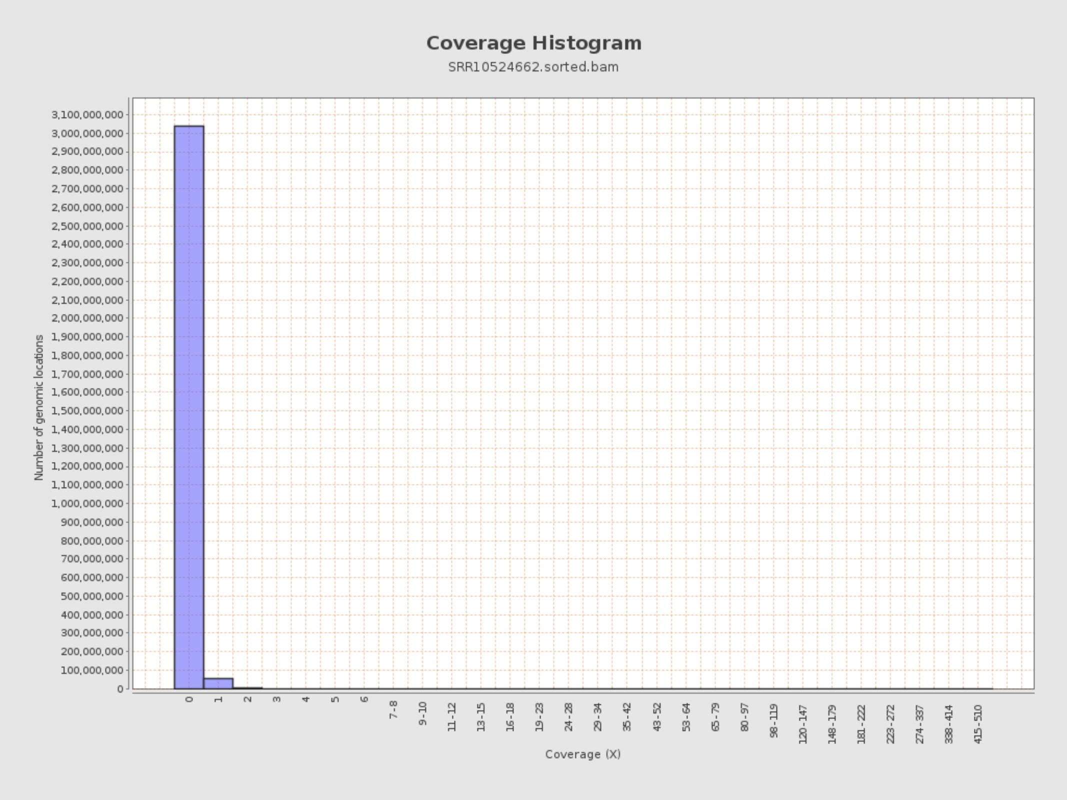
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5246300	0.021	0.3538
chr2	243199373	5478506	0.0225	0.2779
chr3	198022430	4339585	0.0219	0.1579
chr4	191154276	4218211	0.0221	0.1718
chr5	180915260	3978177	0.022	0.1581
chr6	171115067	3548473	0.0207	0.1678
chr7	159138663	3600940	0.0226	0.2613

chr8	146364022	3345562	0.0229	0.2244
chr9	141213431	2718183	0.0192	0.1797
chr10	135534747	3157505	0.0233	0.2198
chr11	135006516	2958704	0.0219	0.1896
chr12	133851895	2915801	0.0218	0.1586
chr13	115169878	2048675	0.0178	0.1442
chr14	107349540	1994166	0.0186	0.1517
chr15	102531392	1868168	0.0182	0.1438
chr16	90354753	1913788	0.0212	0.1645
chr17	81195210	1780562	0.0219	0.165
chr18	78077248	1763143	0.0226	0.3144
chr19	59128983	1351313	0.0229	0.266
chr20	63025520	1398048	0.0222	0.162
chr21	48129895	854702	0.0178	0.1539
chr22	51304566	766433	0.0149	0.1305
chrMT	16571	42984	2.5939	2.2136
chrX	155270560	3618445	0.0233	0.1734
chrY	59373566	214373	0.0036	0.1256

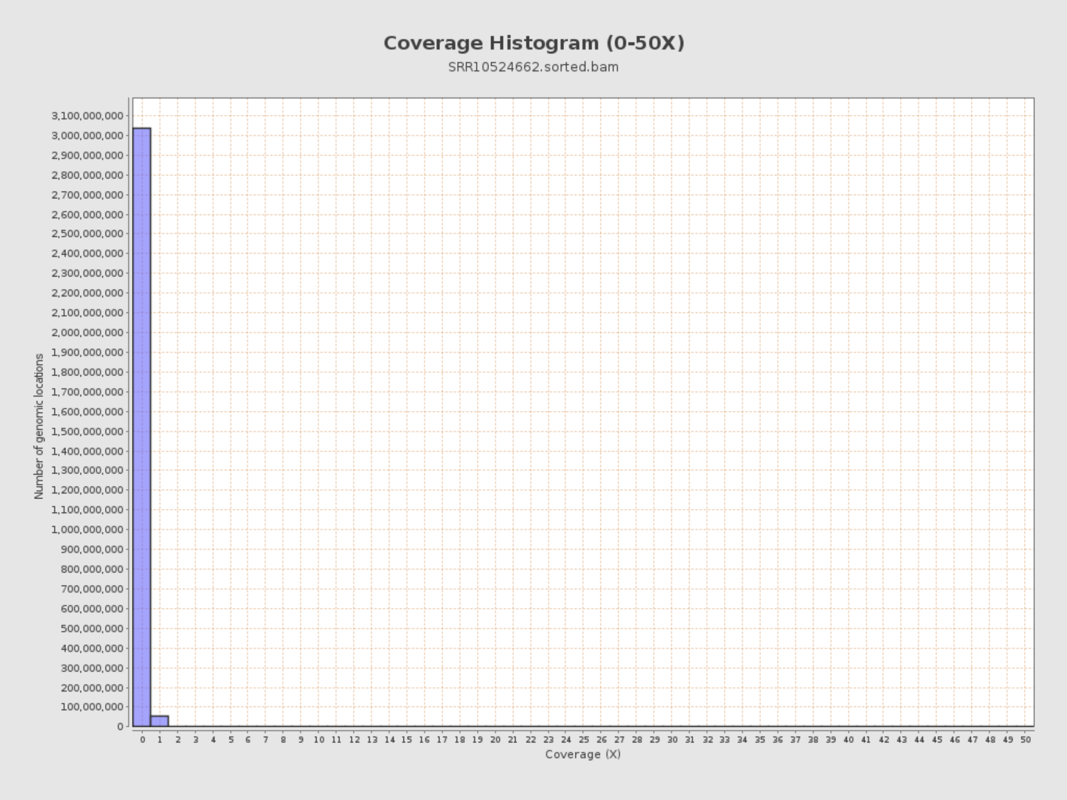
3. Results : Coverage across reference



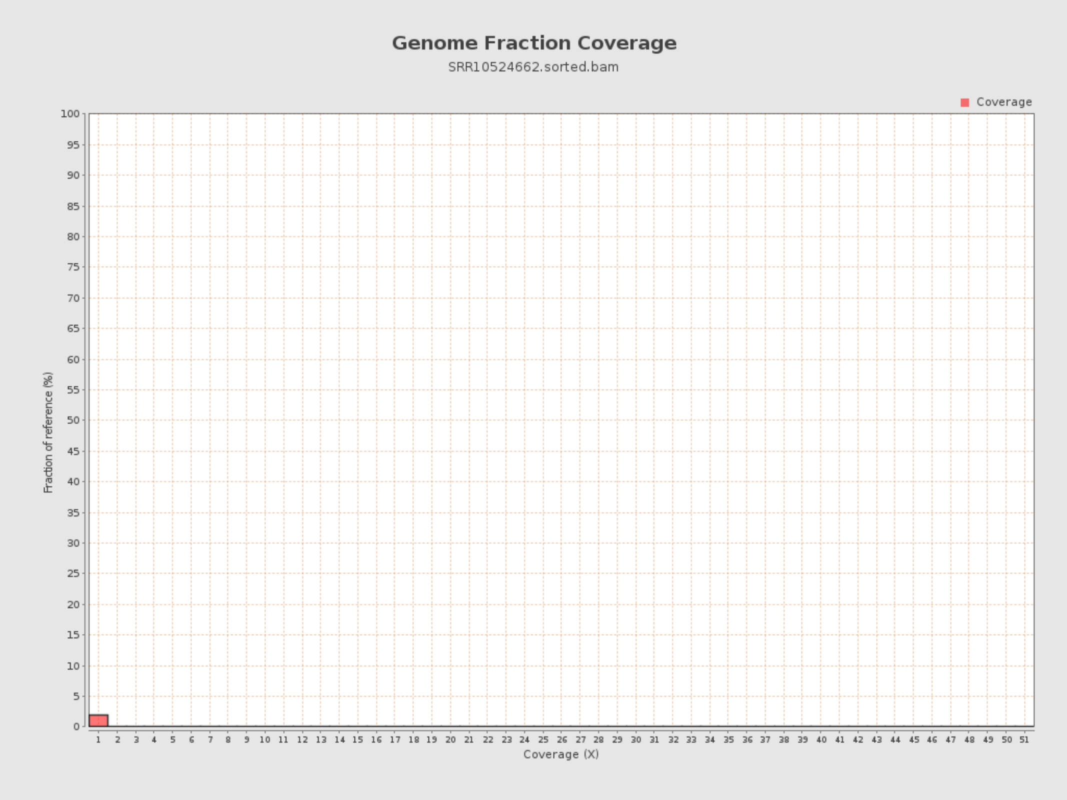
4. Results : Coverage Histogram



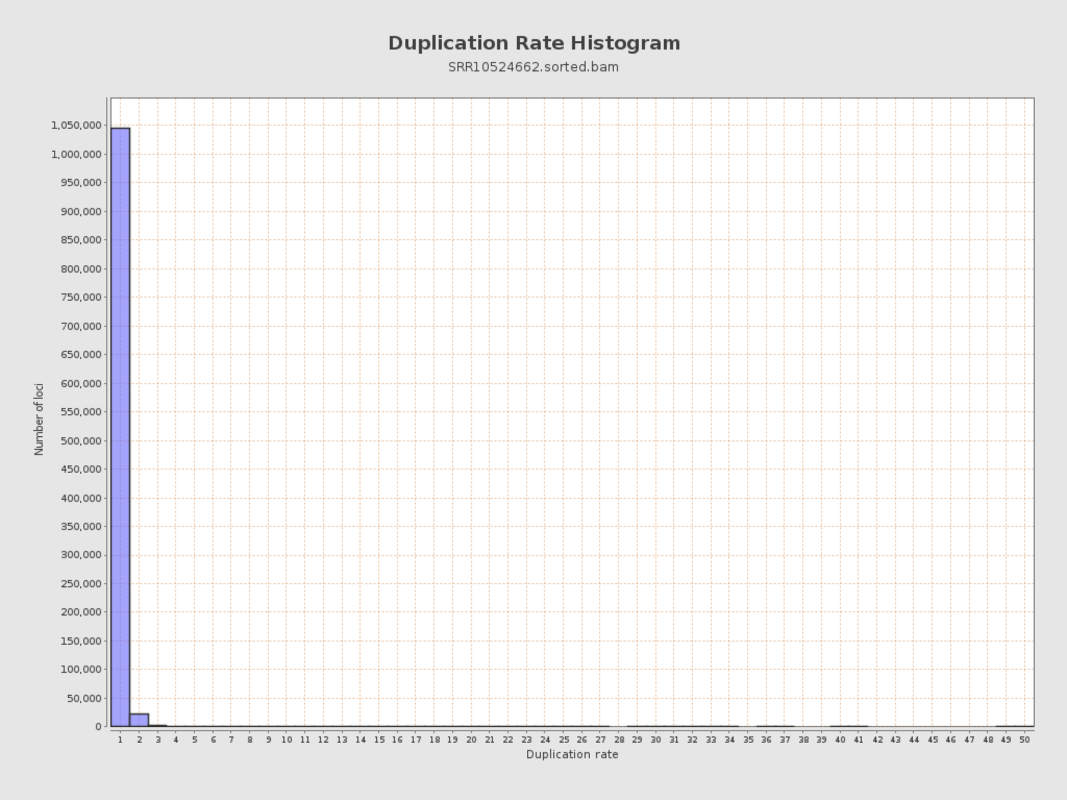
5. Results : Coverage Histogram (0-50X)



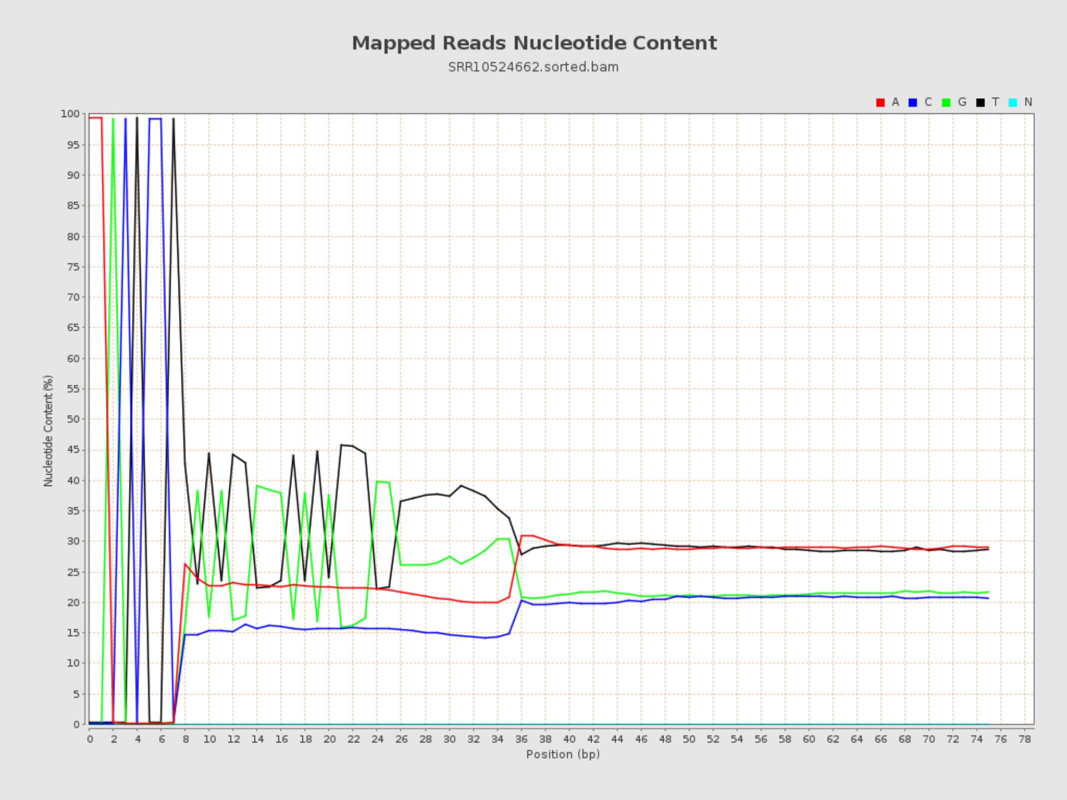
6. Results : Genome Fraction Coverage



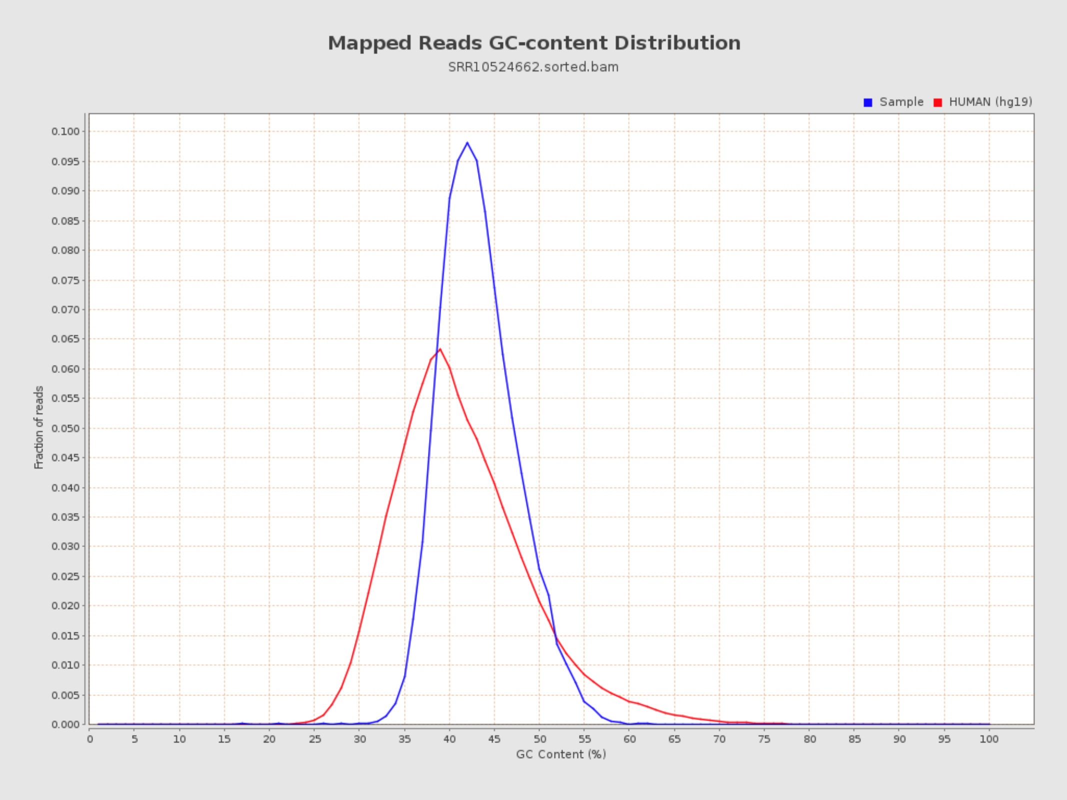
7. Results : Duplication Rate Histogram



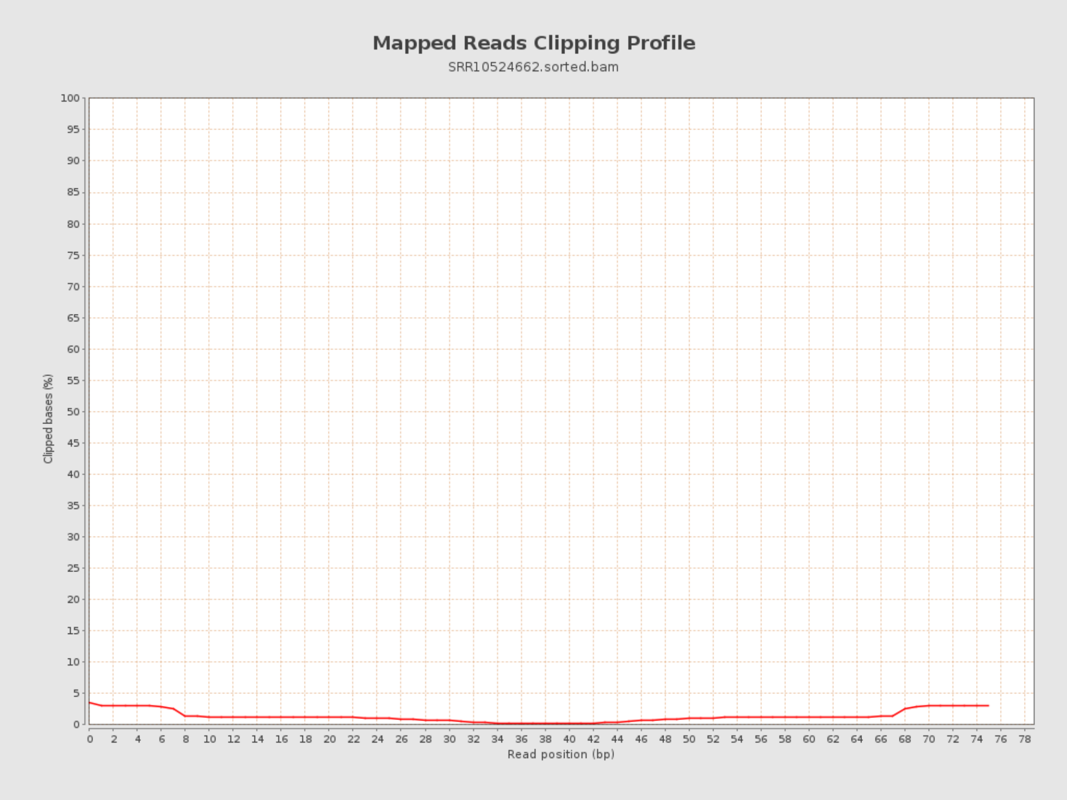
8. Results : Mapped Reads Nucleotide Content



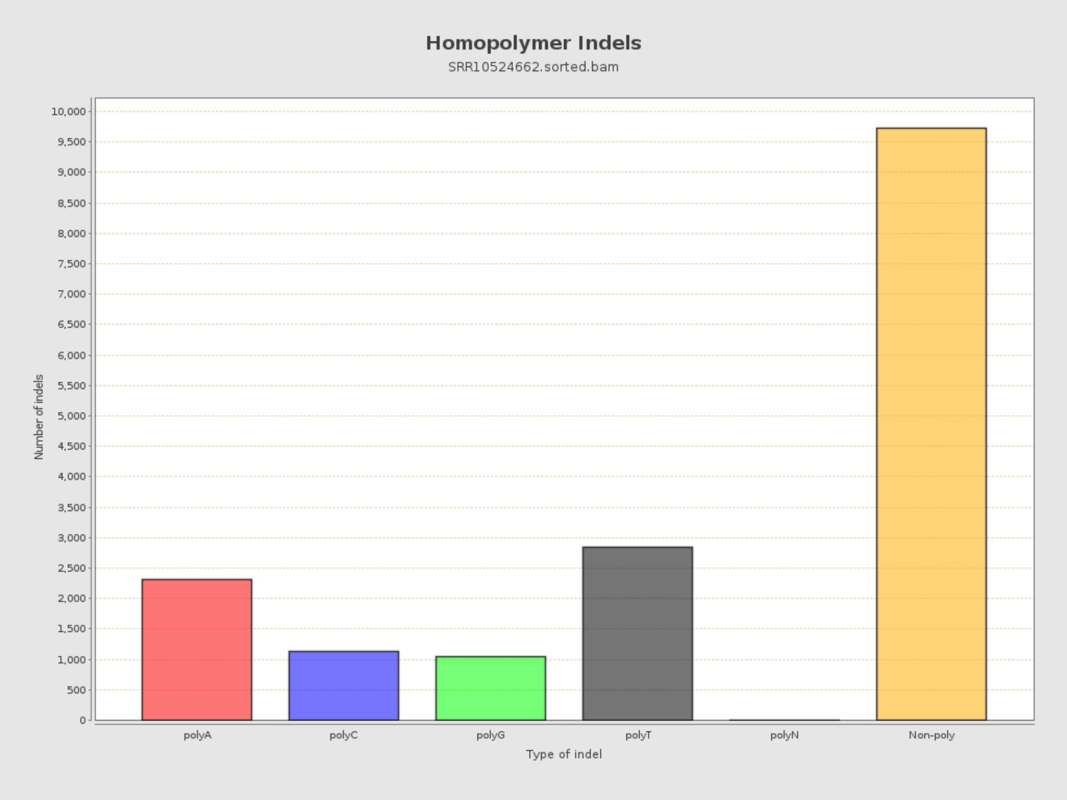
9. Results : Mapped Reads GC-content Distribution



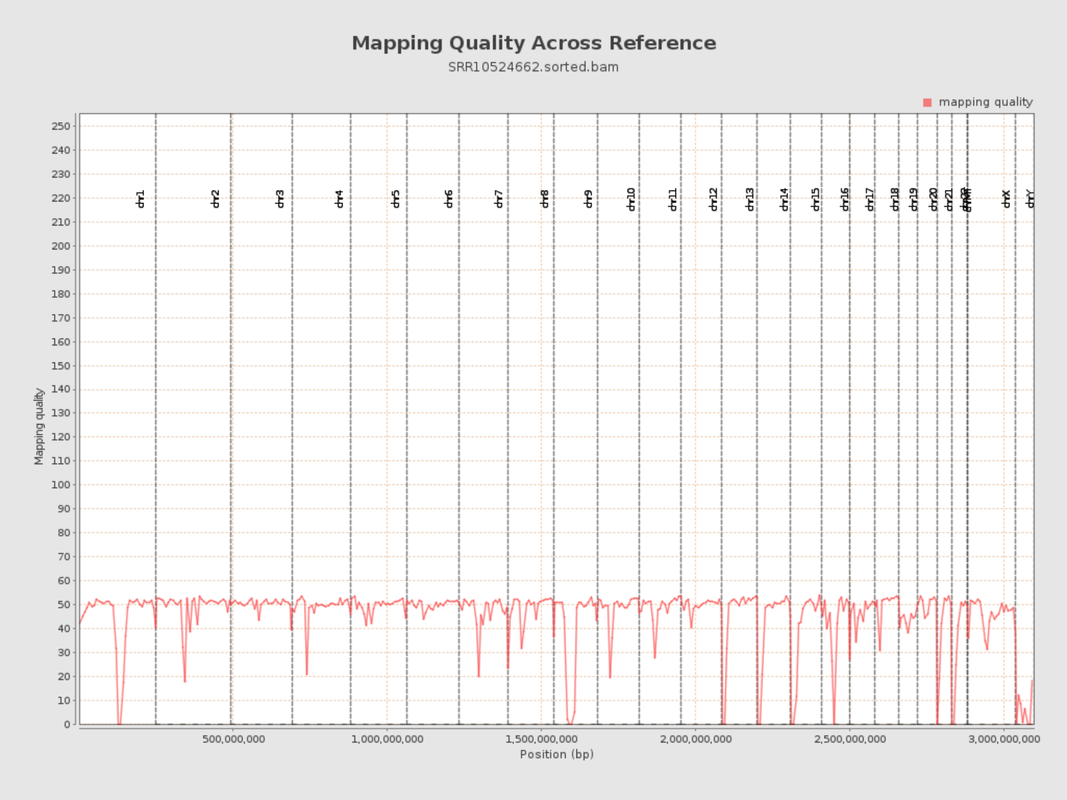
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram