Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:35:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524664.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_SRR10524664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:35:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,737,957
Mapped reads	1,605,252 / 92.36%
Unmapped reads	132,705 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,320 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	67,378 / 3.88%
Duplication rate	3.17%
Clipped reads	1,607,965 / 92.52%

2.2. ACGT Content

Number/percentage of A's	23,440,405 / 24.85%
Number/percentage of C's	16,887,978 / 17.9%
Number/percentage of T's	31,005,462 / 32.87%
Number/percentage of G's	22,973,736 / 24.36%
Number/percentage of N's	12,767 / 0.01%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.2759

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

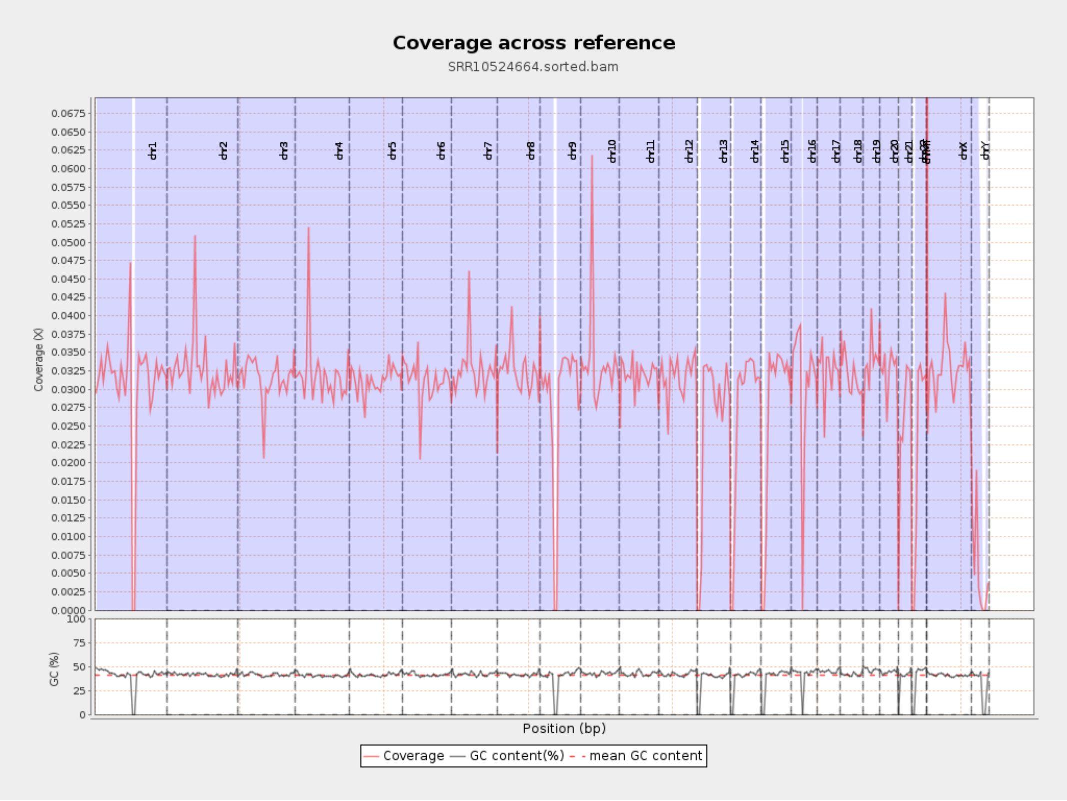
General error rate	0.52%
Mismatches	474,043
Insertions	6,991
Mapped reads with at least one insertion	0.43%
Deletions	17,238
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.98%

2.6. Chromosome stats

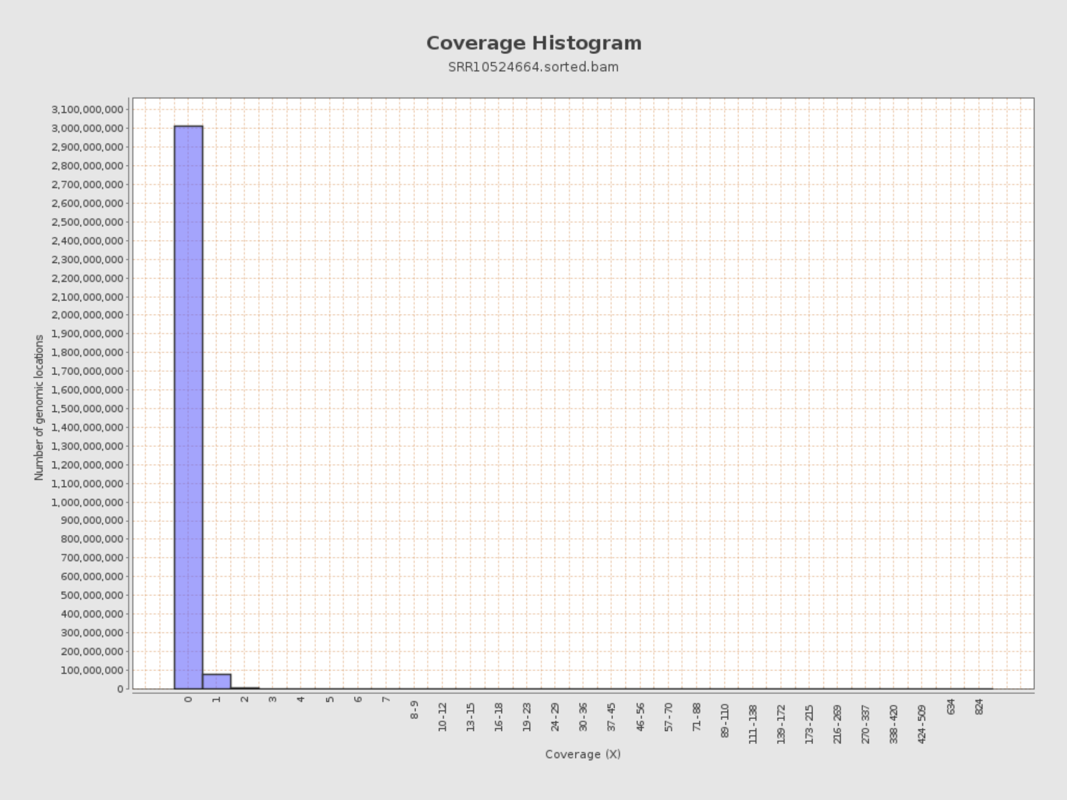
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7595135	0.0305	0.4404
chr2	243199373	7969846	0.0328	0.4029
chr3	198022430	6235757	0.0315	0.194
chr4	191154276	6129546	0.0321	0.2249
chr5	180915260	5660823	0.0313	0.1947
chr6	171115067	5327236	0.0311	0.2194
chr7	159138663	5227411	0.0328	0.3211

chr8	146364022	4768260	0.0326	0.2915
chr9	141213431	3989034	0.0282	0.2339
chr10	135534747	4590542	0.0339	0.3016
chr11	135006516	4325367	0.032	0.2443
chr12	133851895	4257171	0.0318	0.1986
chr13	115169878	2953773	0.0256	0.1755
chr14	107349540	2869008	0.0267	0.184
chr15	102531392	2755111	0.0269	0.1815
chr16	90354753	2731634	0.0302	0.2062
chr17	81195210	2641277	0.0325	0.2089
chr18	78077248	2495293	0.032	0.413
chr19	59128983	1997303	0.0338	0.3494
chr20	63025520	2041192	0.0324	0.2013
chr21	48129895	1235183	0.0257	0.1957
chr22	51304566	1133430	0.0221	0.1618
chrMT	16571	13439	0.811	1.0171
chrX	155270560	5095269	0.0328	0.2166
chrY	59373566	310110	0.0052	0.1766

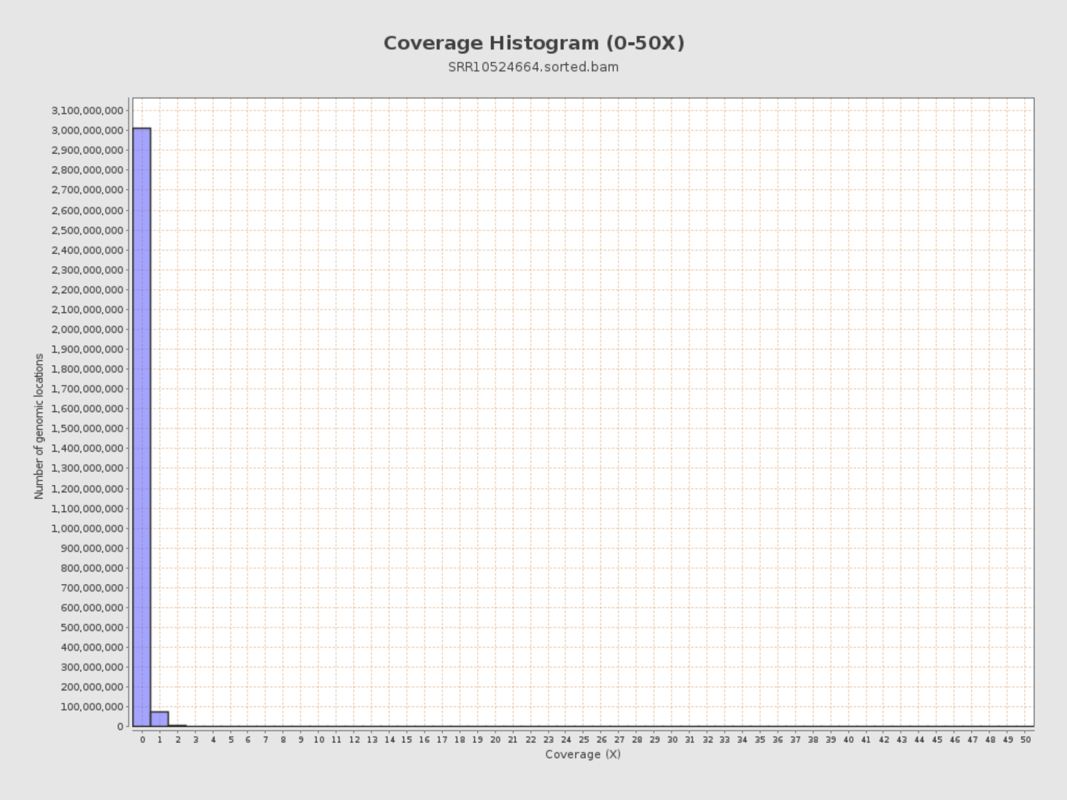
3. Results : Coverage across reference



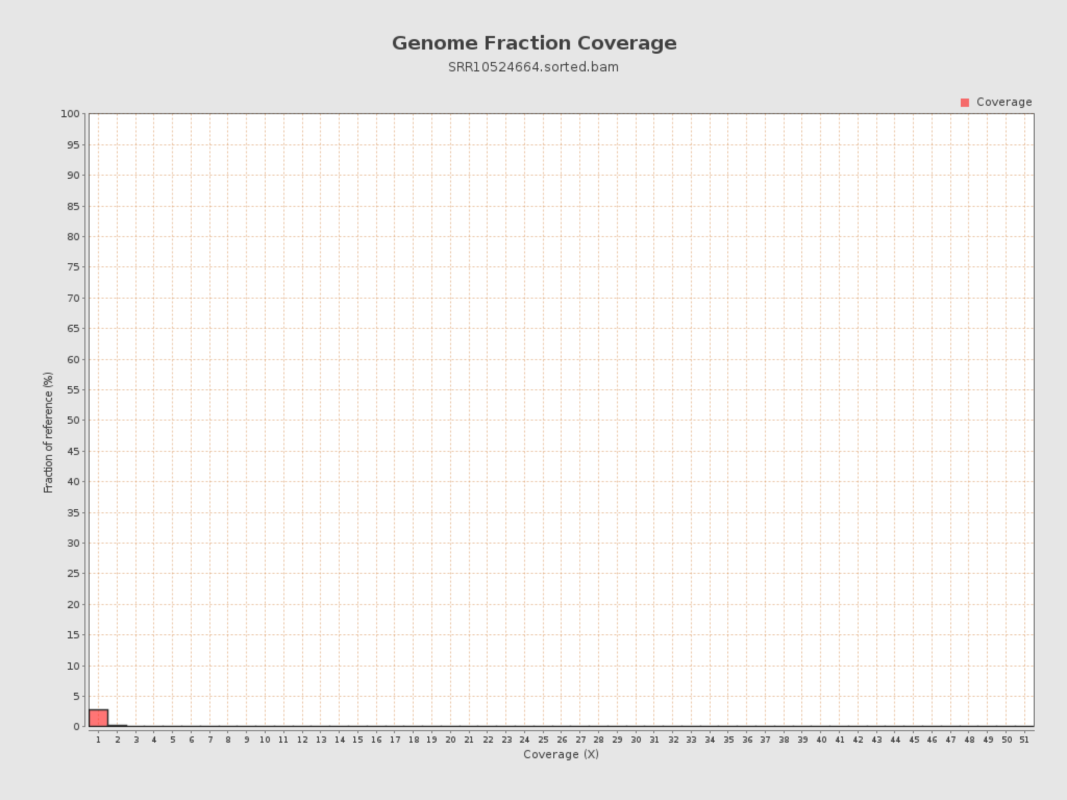
4. Results : Coverage Histogram



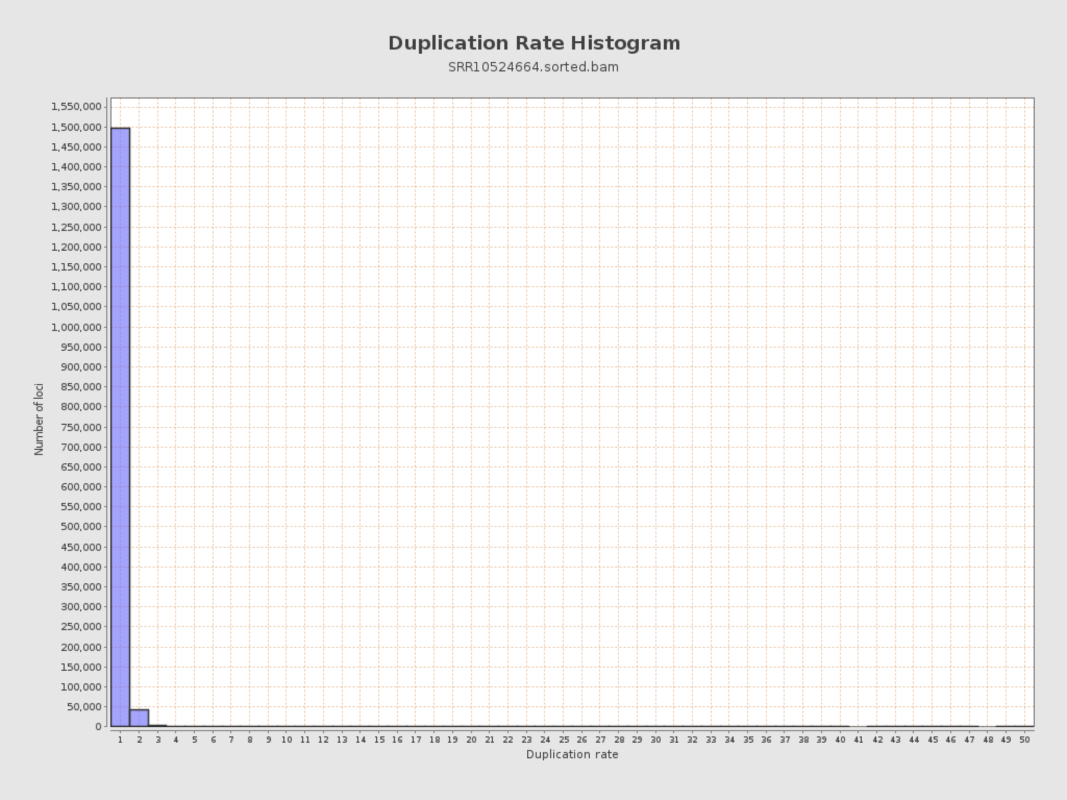
5. Results : Coverage Histogram (0-50X)



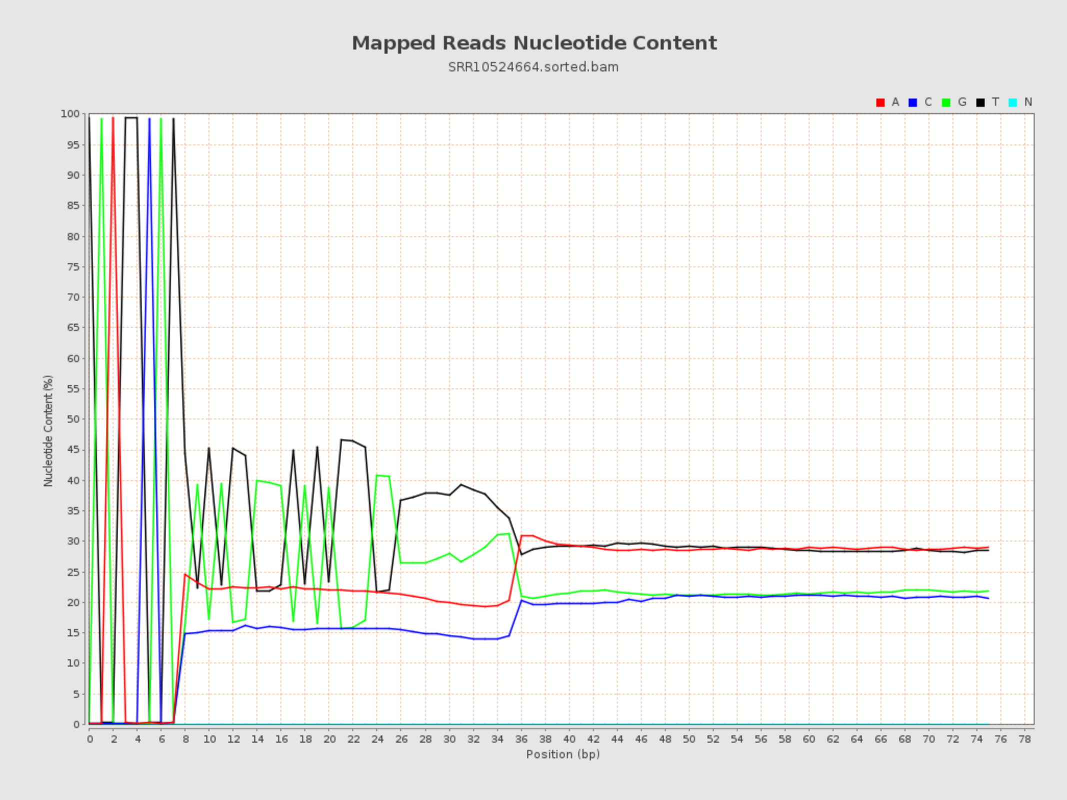
6. Results : Genome Fraction Coverage



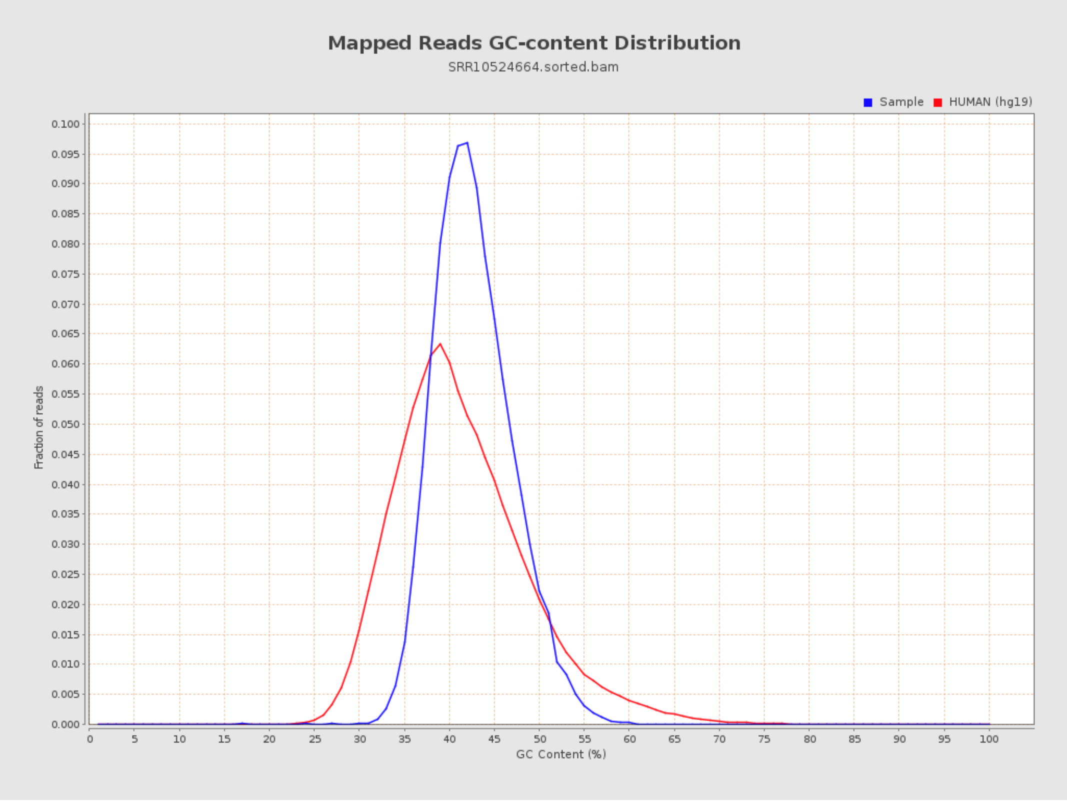
7. Results : Duplication Rate Histogram



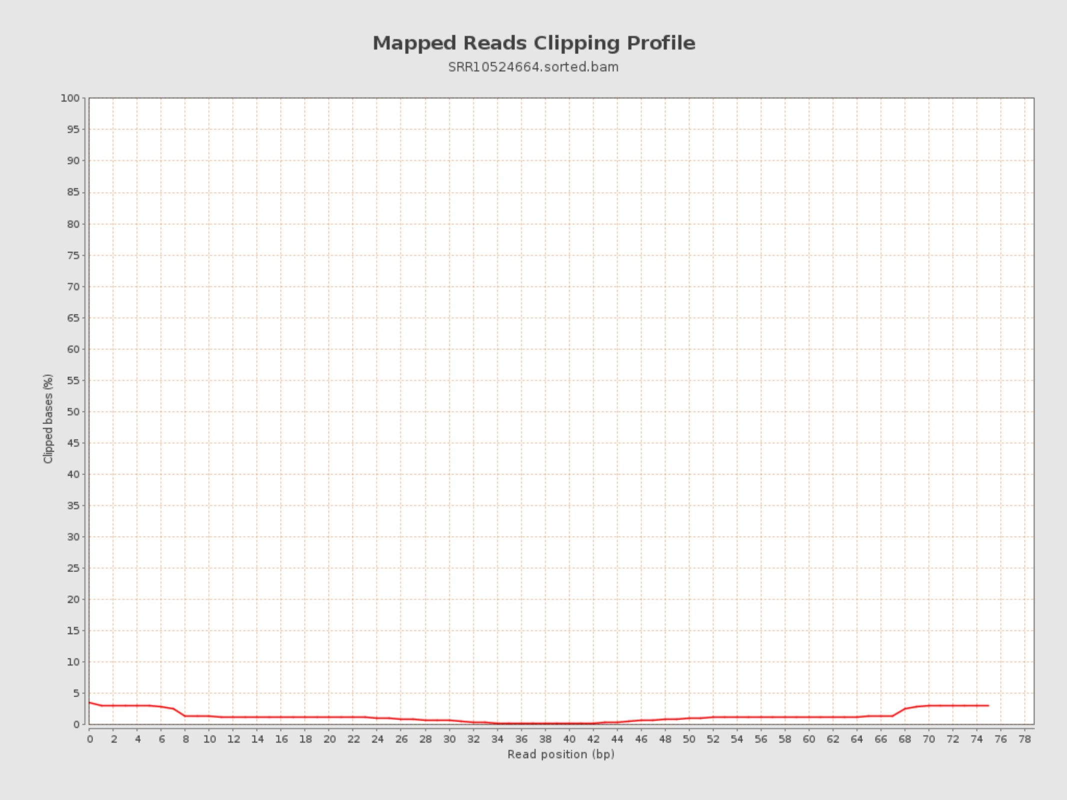
8. Results : Mapped Reads Nucleotide Content



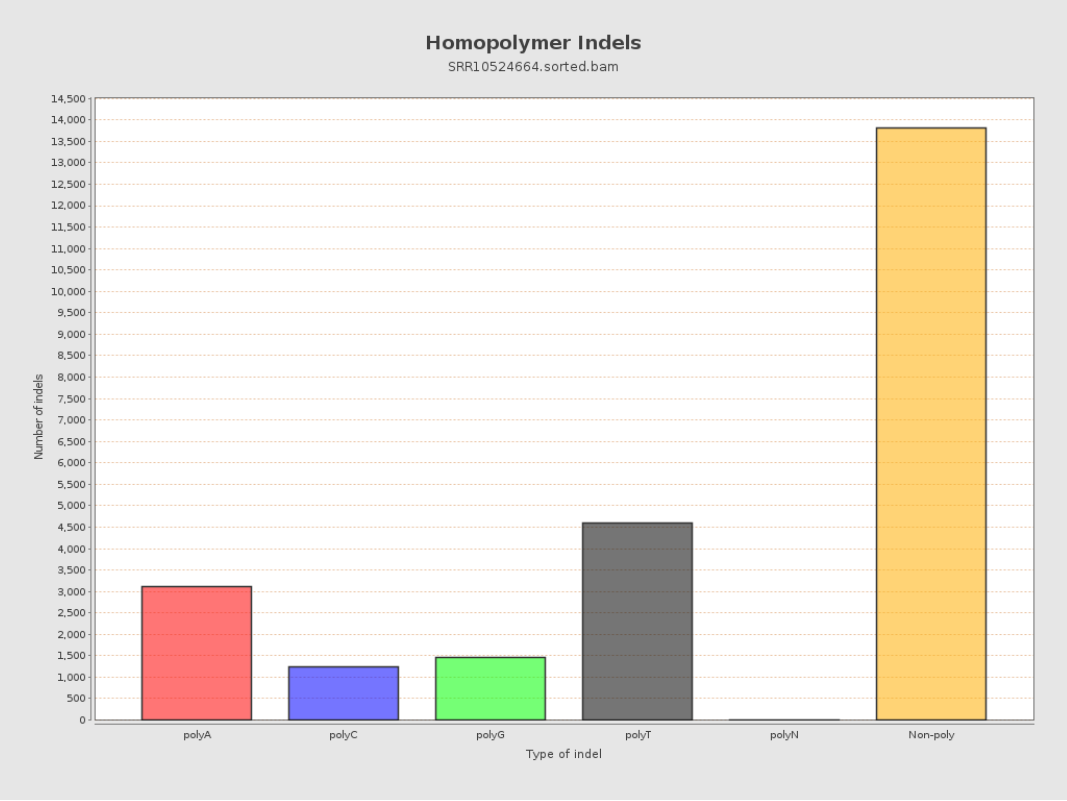
9. Results : Mapped Reads GC-content Distribution



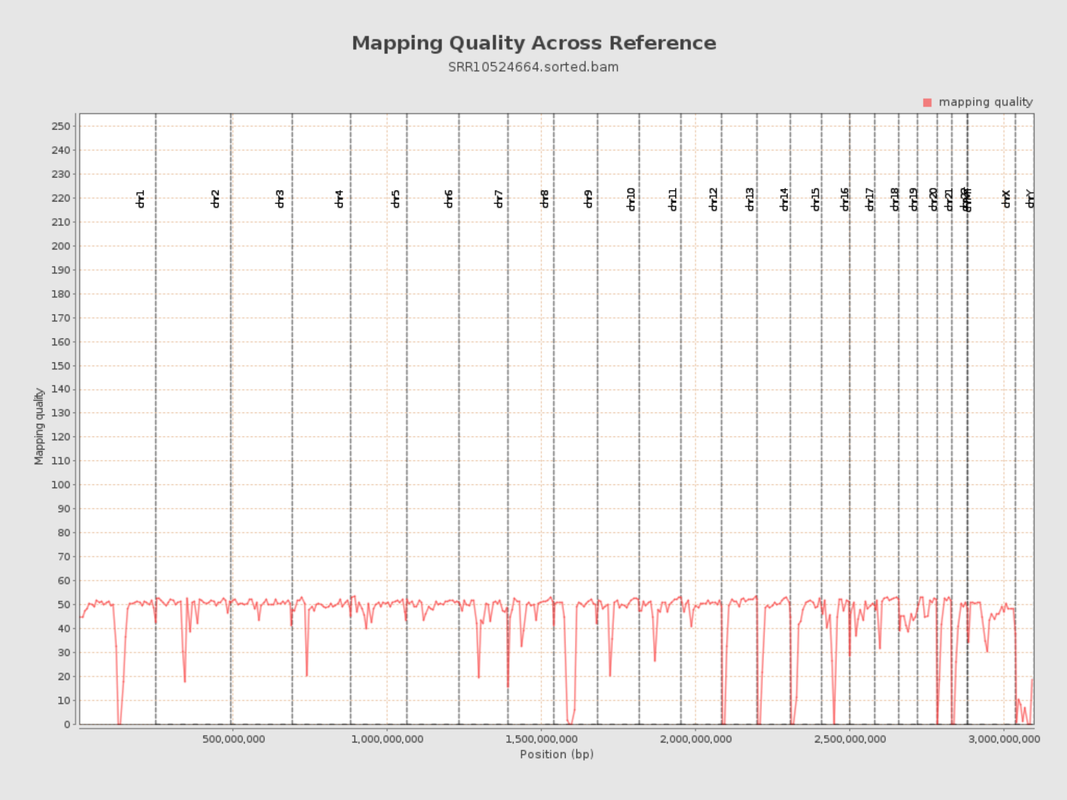
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram