Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:19:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524902.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_SRR10524902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:19:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,883,801
Mapped reads	1,711,326 / 90.84%
Unmapped reads	172,475 / 9.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,100 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	69,373 / 3.68%
Duplication rate	3.02%
Clipped reads	1,713,042 / 90.94%

2.2. ACGT Content

Number/percentage of A's	25,877,108 / 26.29%
Number/percentage of C's	17,745,109 / 18.03%
Number/percentage of T's	30,802,458 / 31.3%
Number/percentage of G's	23,985,087 / 24.37%
Number/percentage of N's	2,135 / 0%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.3046

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

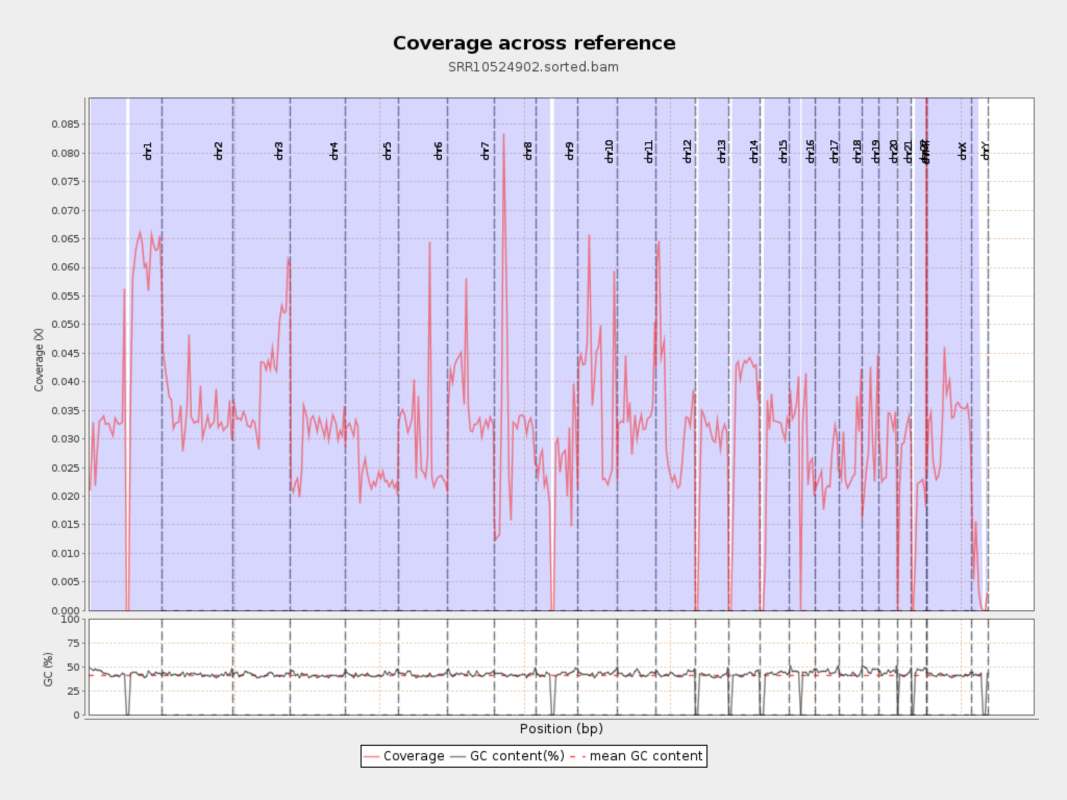
General error rate	0.53%
Mismatches	505,077
Insertions	7,920
Mapped reads with at least one insertion	0.46%
Deletions	21,151
Mapped reads with at least one deletion	1.23%
Homopolymer indels	43.54%

2.6. Chromosome stats

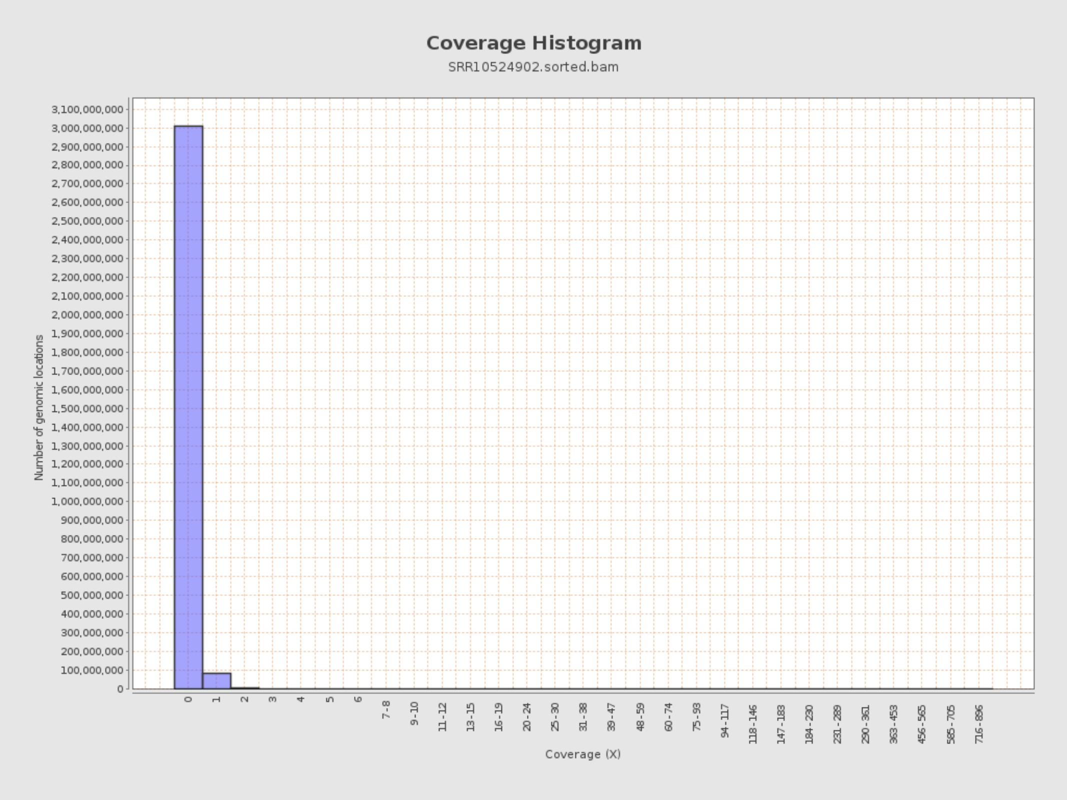
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10721704	0.043	0.5723
chr2	243199373	8429992	0.0347	0.4163
chr3	198022430	8009610	0.0404	0.222
chr4	191154276	5739111	0.03	0.2008
chr5	180915260	4545071	0.0251	0.174
chr6	171115067	5089494	0.0297	0.2215
chr7	159138663	5917084	0.0372	0.4292

chr8	146364022	4663950	0.0319	0.3079
chr9	141213431	3302883	0.0234	0.212
chr10	135534747	5397144	0.0398	0.3154
chr11	135006516	4640035	0.0344	0.2454
chr12	133851895	4535335	0.0339	0.2045
chr13	115169878	3152270	0.0274	0.1826
chr14	107349540	3769768	0.0351	0.2079
chr15	102531392	2734908	0.0267	0.1812
chr16	90354753	2622997	0.029	0.2049
chr17	81195210	1962876	0.0242	0.1755
chr18	78077248	2131517	0.0273	0.4062
chr19	59128983	1753278	0.0297	0.4243
chr20	63025520	1819856	0.0289	0.1893
chr21	48129895	1283396	0.0267	0.1888
chr22	51304566	789824	0.0154	0.1338
chrMT	16571	2267	0.1368	0.3805
chrX	155270560	5146955	0.0331	0.218
chrY	59373566	284292	0.0048	0.1421

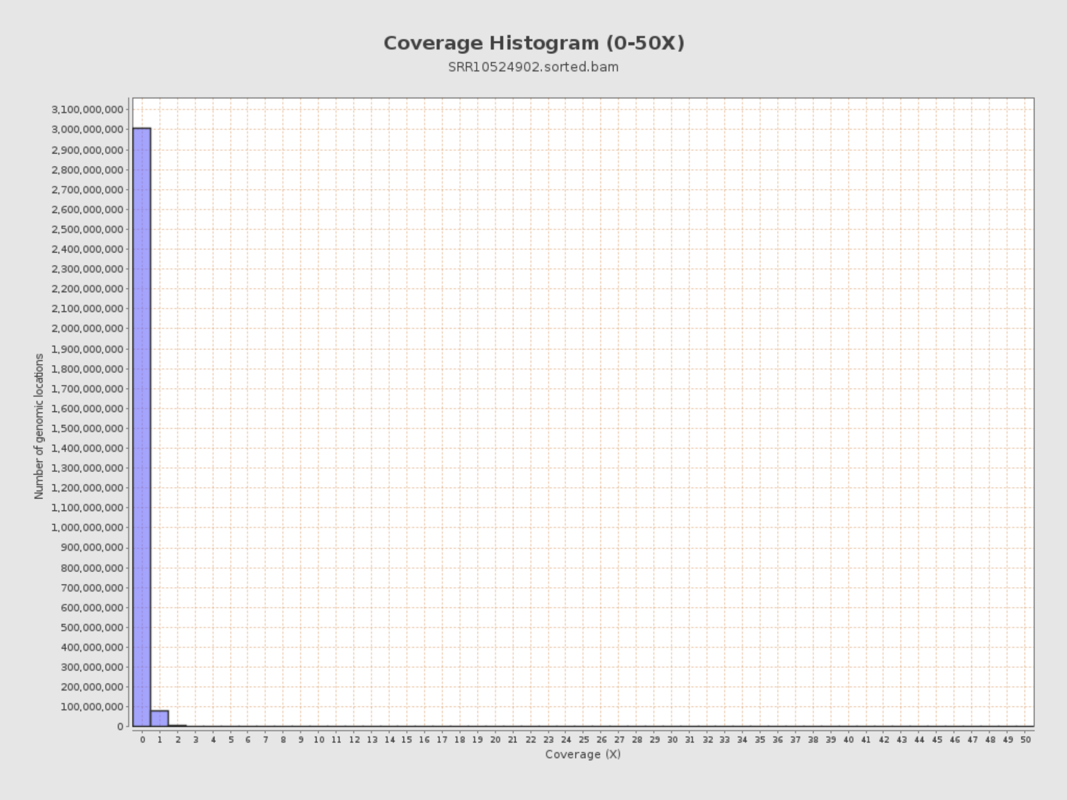
3. Results : Coverage across reference



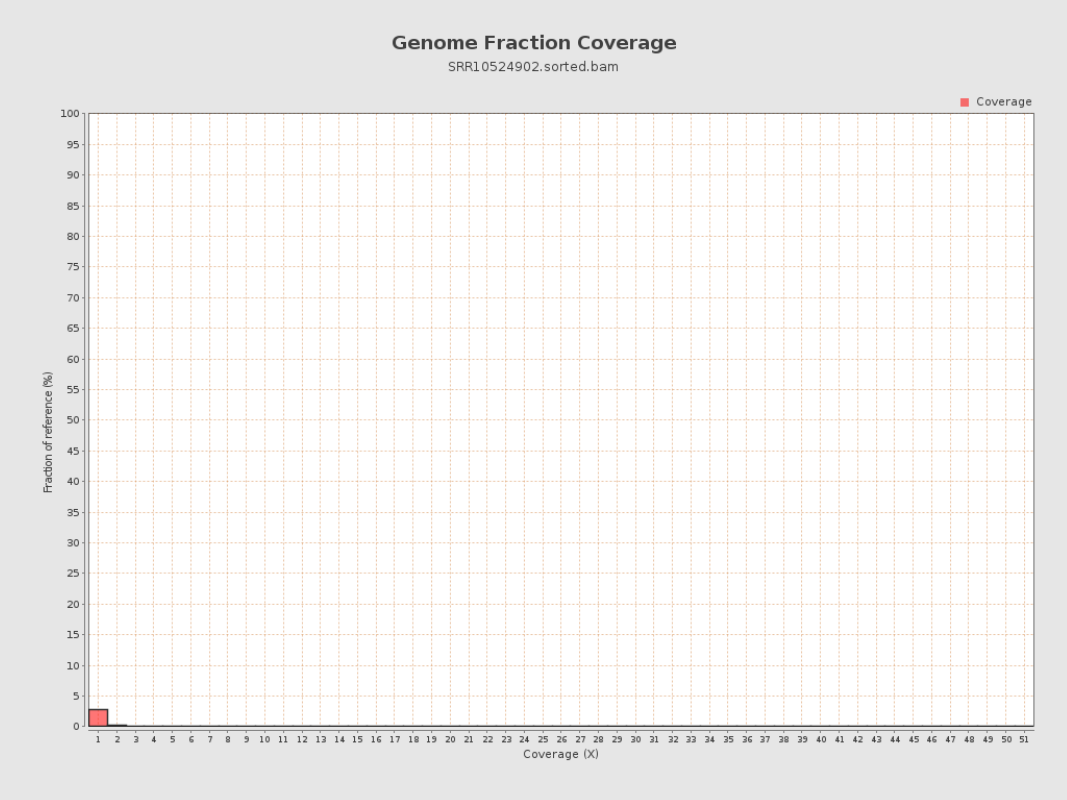
4. Results : Coverage Histogram



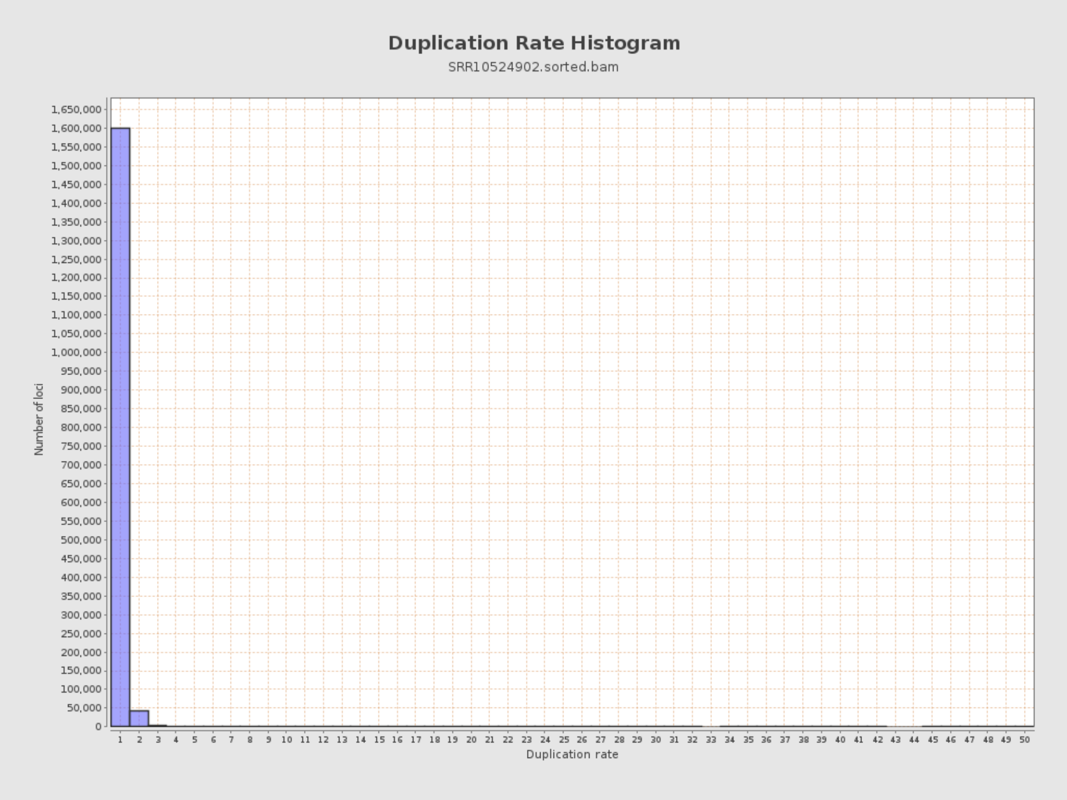
5. Results : Coverage Histogram (0-50X)



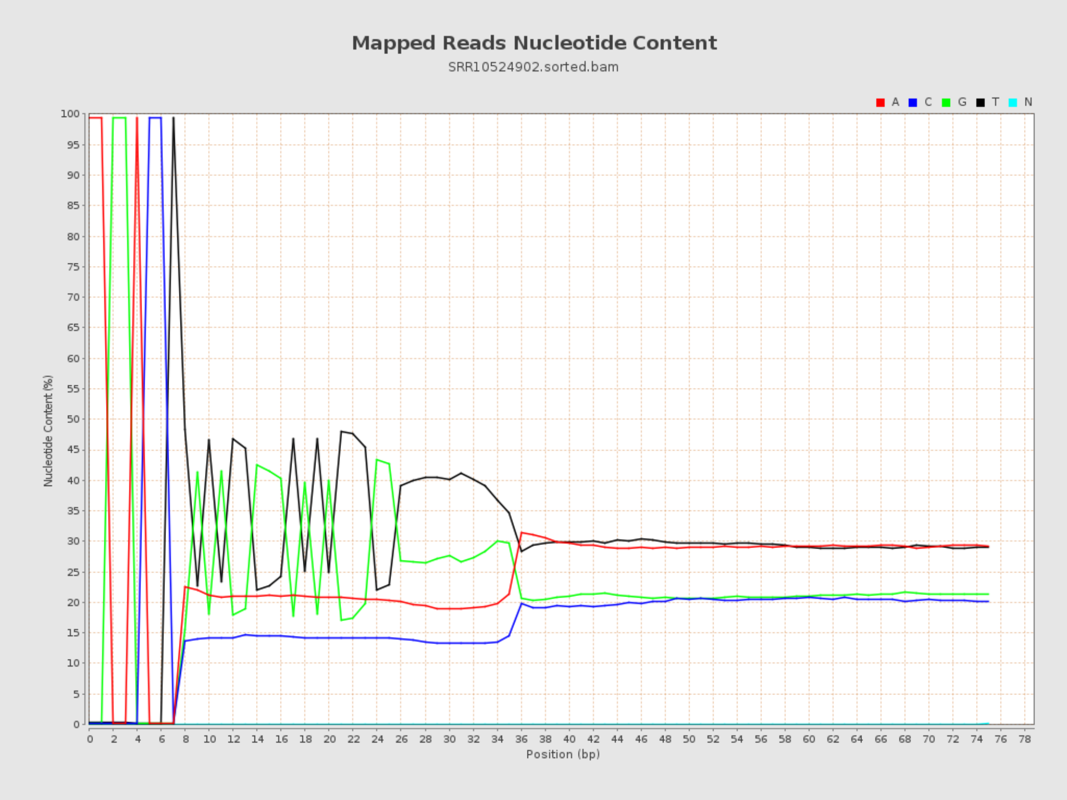
6. Results : Genome Fraction Coverage



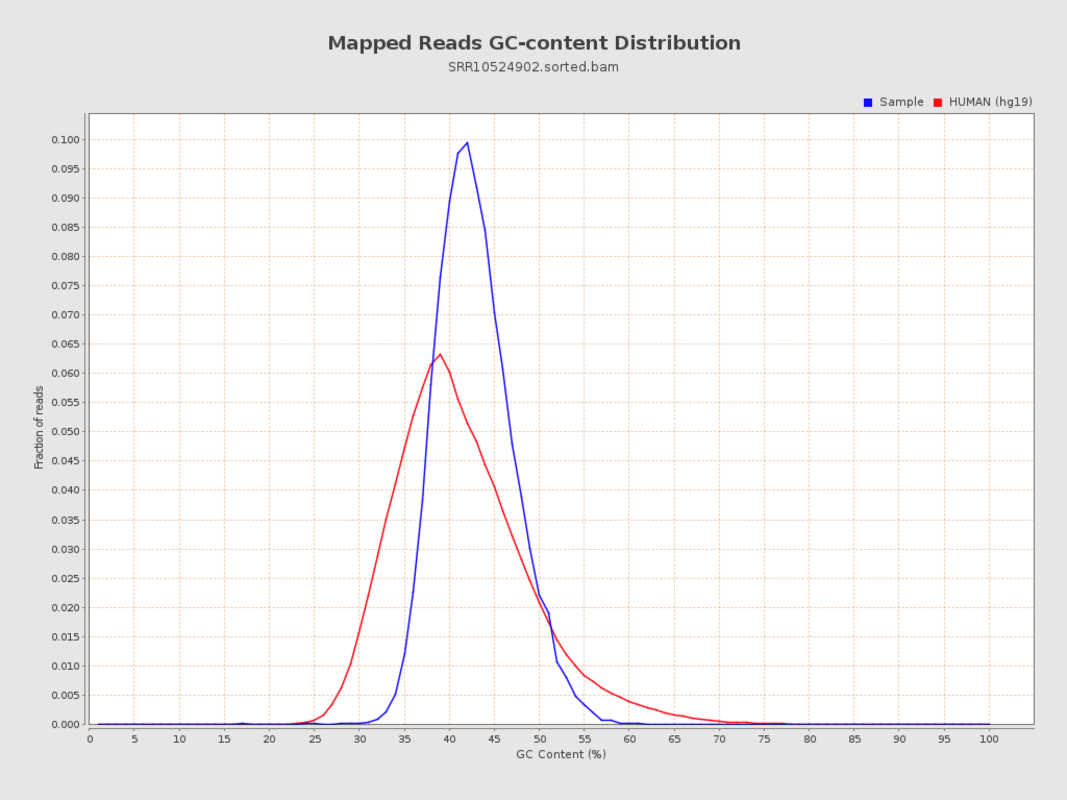
7. Results : Duplication Rate Histogram



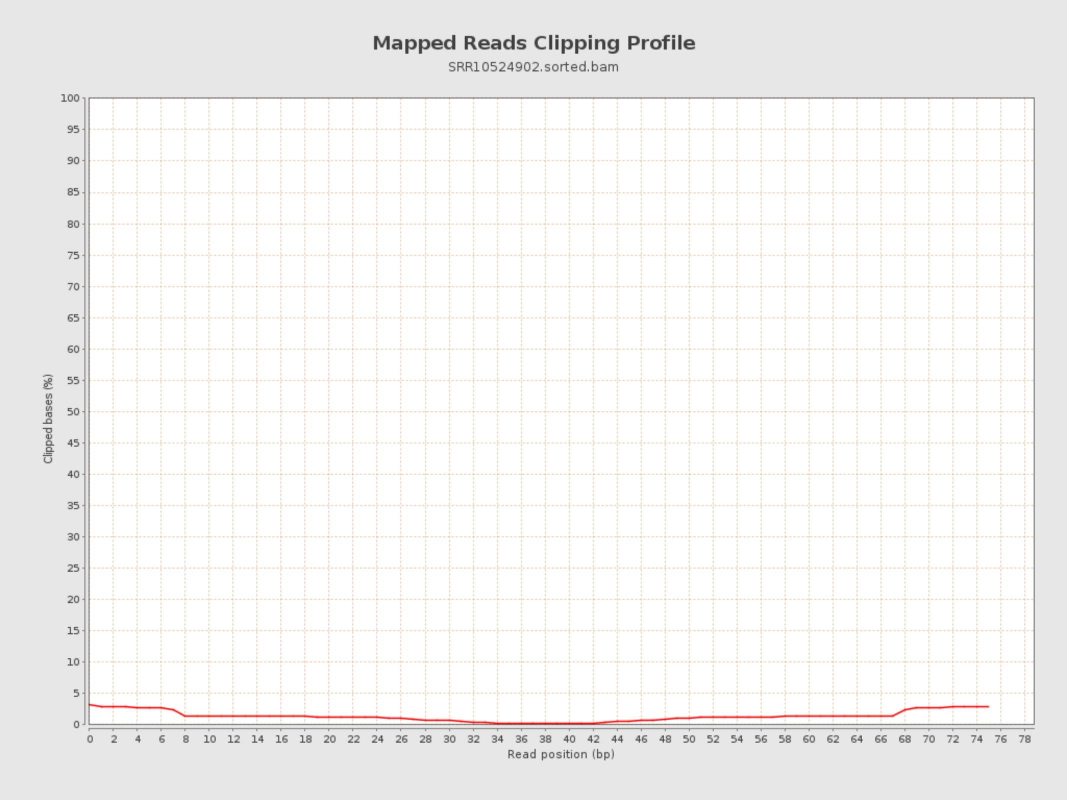
8. Results : Mapped Reads Nucleotide Content



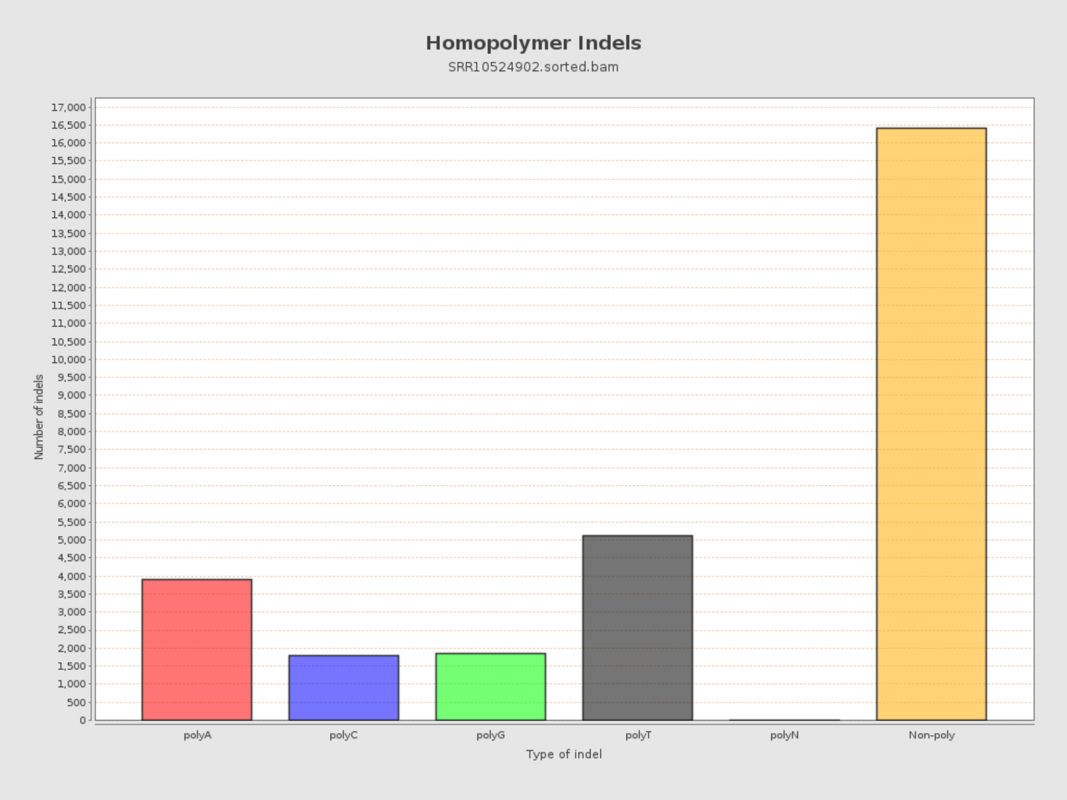
9. Results : Mapped Reads GC-content Distribution



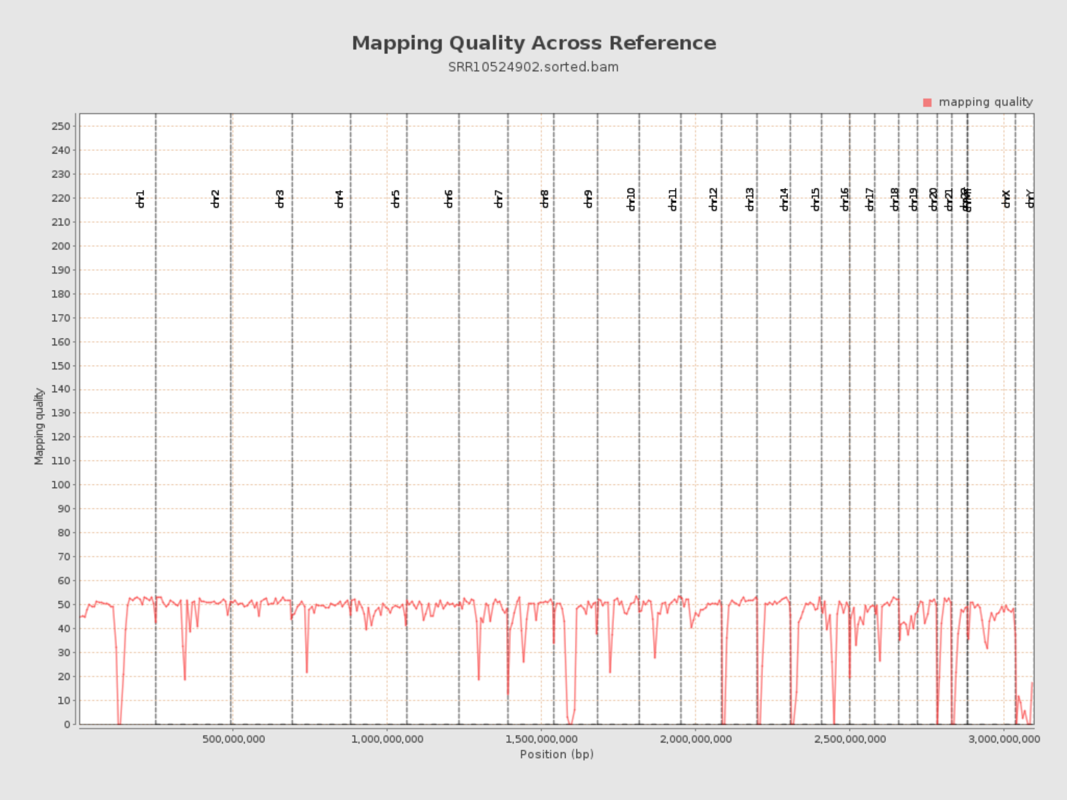
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram