Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:32:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524958.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_SRR10524958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:32:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	929,591
Mapped reads	851,485 / 91.6%
Unmapped reads	78,106 / 8.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,596 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	18,441 / 1.98%
Duplication rate	1.54%
Clipped reads	853,280 / 91.79%

2.2. ACGT Content

Number/percentage of A's	12,804,925 / 25.9%
Number/percentage of C's	9,986,990 / 20.2%
Number/percentage of T's	14,950,323 / 30.24%
Number/percentage of G's	11,700,361 / 23.66%
Number/percentage of N's	563 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.016

Standard Deviation	0.1698

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

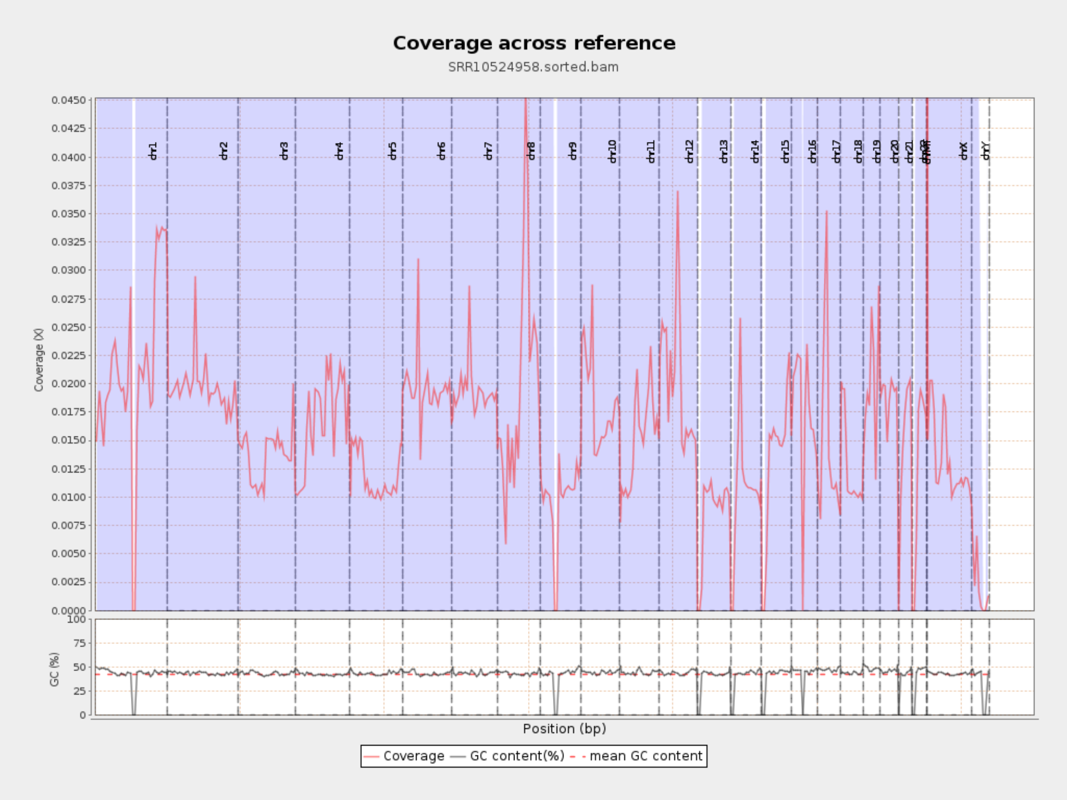
General error rate	0.5%
Mismatches	244,420
Insertions	2,725
Mapped reads with at least one insertion	0.32%
Deletions	9,320
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.78%

2.6. Chromosome stats

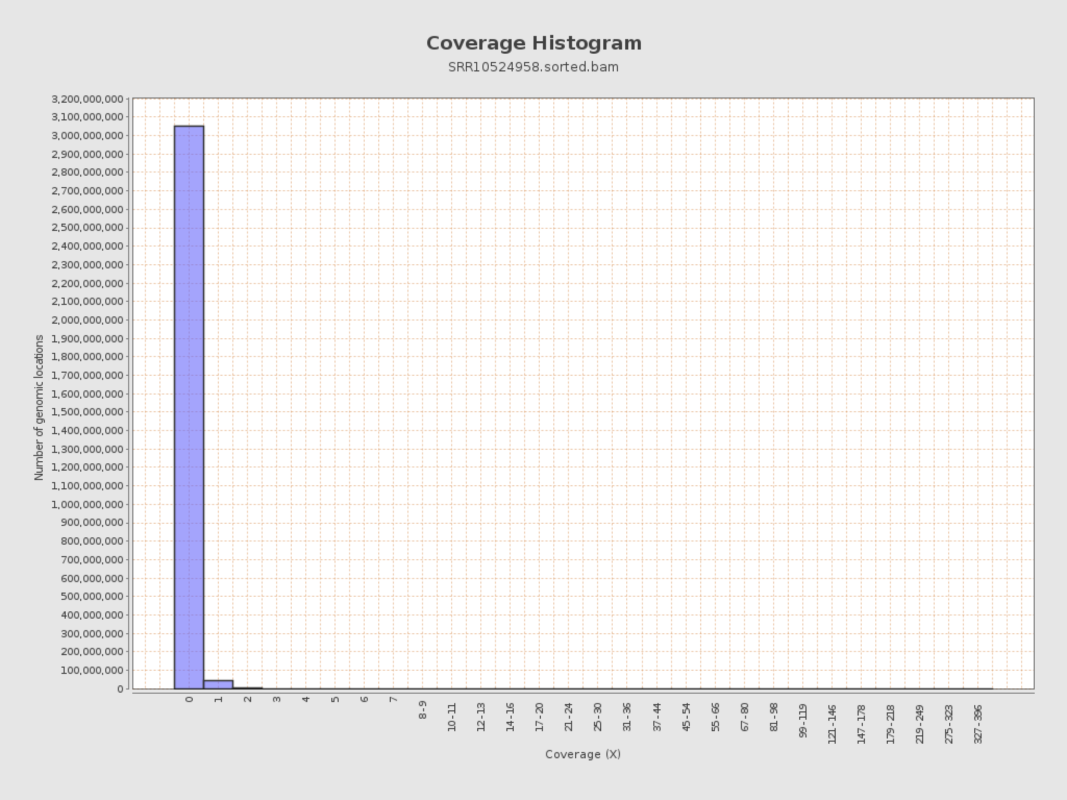
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5247449	0.0211	0.2957
chr2	243199373	4774893	0.0196	0.1959
chr3	198022430	2723564	0.0138	0.1225
chr4	191154276	3225297	0.0169	0.1396
chr5	180915260	2156521	0.0119	0.1158
chr6	171115067	3353079	0.0196	0.1925
chr7	159138663	3103210	0.0195	0.208

chr8	146364022	2986472	0.0204	0.1782
chr9	141213431	1361528	0.0096	0.1296
chr10	135534747	2513314	0.0185	0.1684
chr11	135006516	2069361	0.0153	0.1558
chr12	133851895	2708229	0.0202	0.1487
chr13	115169878	978056	0.0085	0.0973
chr14	107349540	1141451	0.0106	0.1103
chr15	102531392	1368815	0.0134	0.1301
chr16	90354753	1561714	0.0173	0.1419
chr17	81195210	1238471	0.0153	0.1516
chr18	78077248	981808	0.0126	0.1915
chr19	59128983	1198319	0.0203	0.1886
chr20	63025520	1174042	0.0186	0.1425
chr21	48129895	715039	0.0149	0.1293
chr22	51304566	644945	0.0126	0.1166
chrMT	16571	16886	1.019	1.2303
chrX	155270560	2090821	0.0135	0.1347
chrY	59373566	125947	0.0021	0.0617

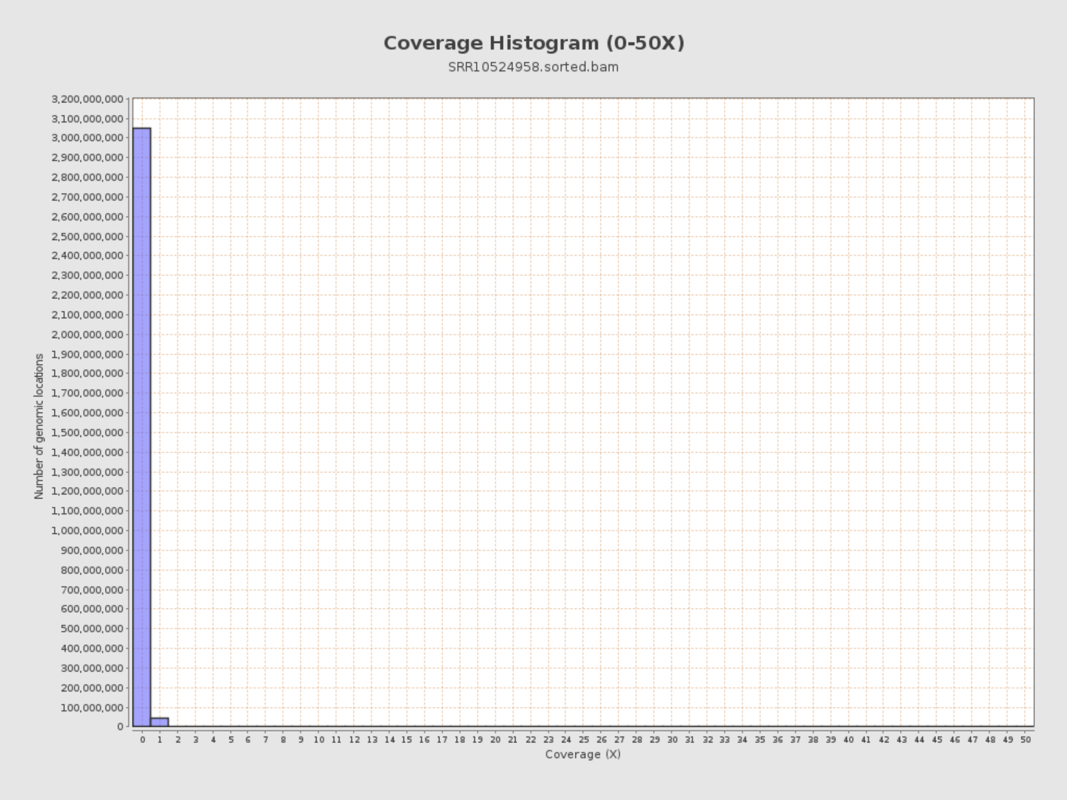
3. Results : Coverage across reference



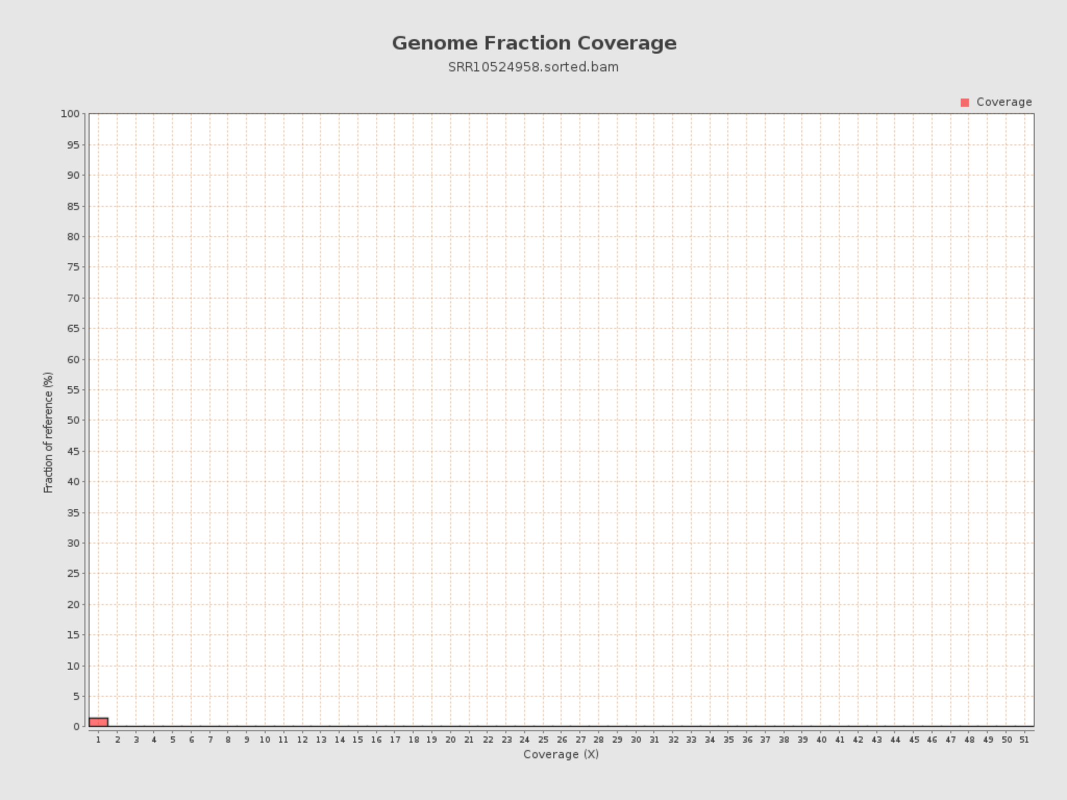
4. Results : Coverage Histogram



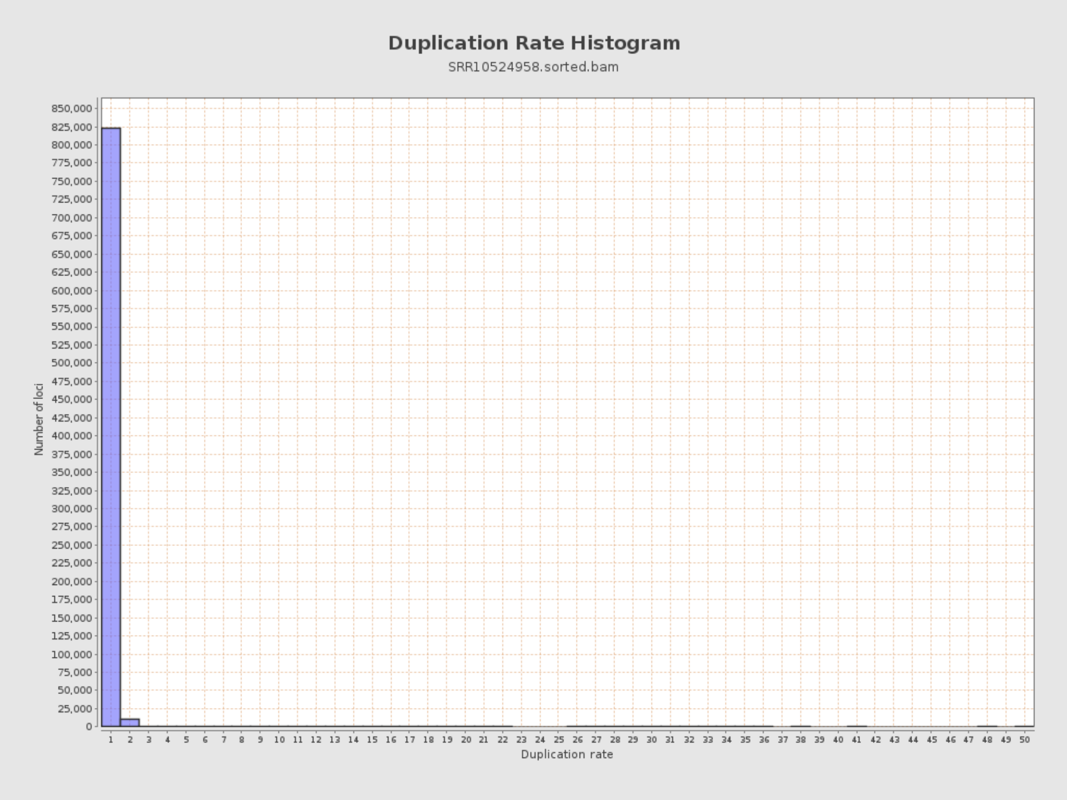
5. Results : Coverage Histogram (0-50X)



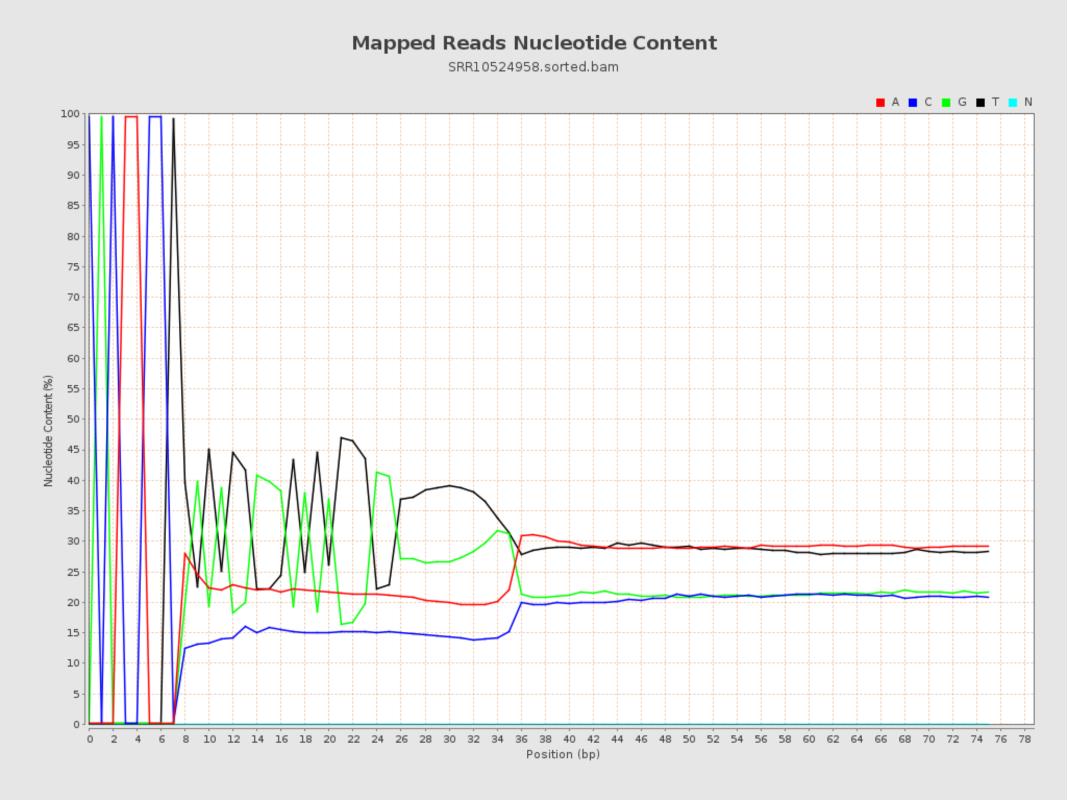
6. Results : Genome Fraction Coverage



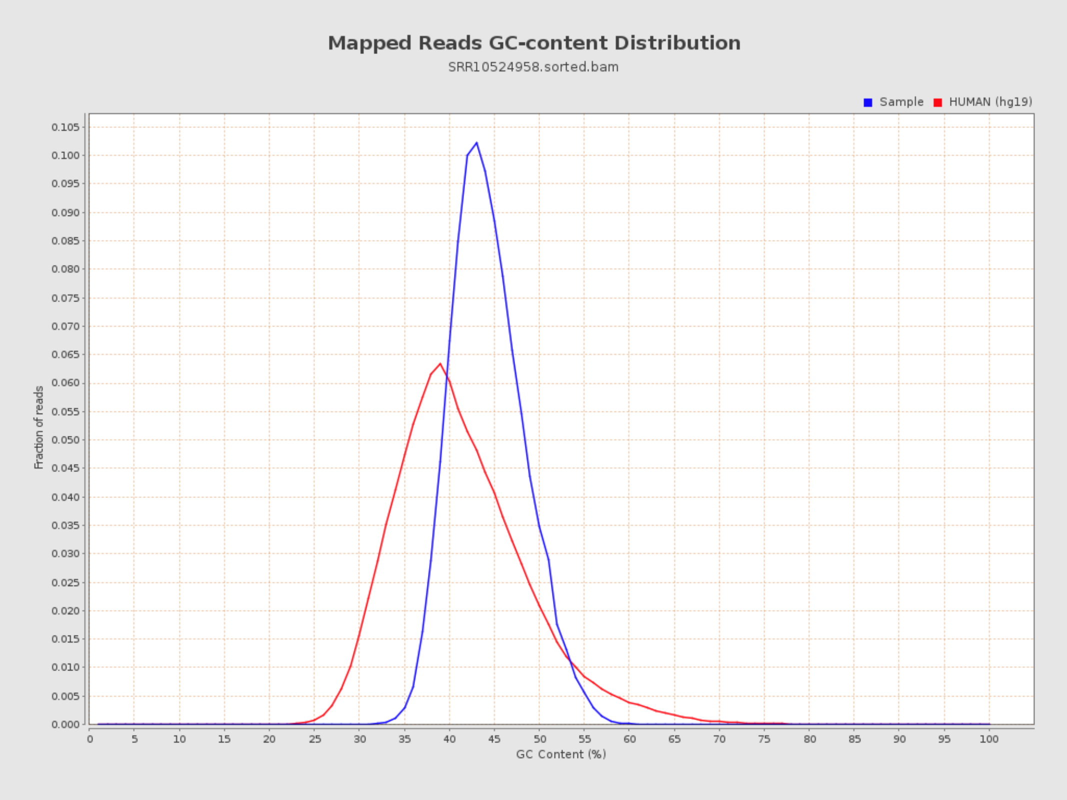
7. Results : Duplication Rate Histogram



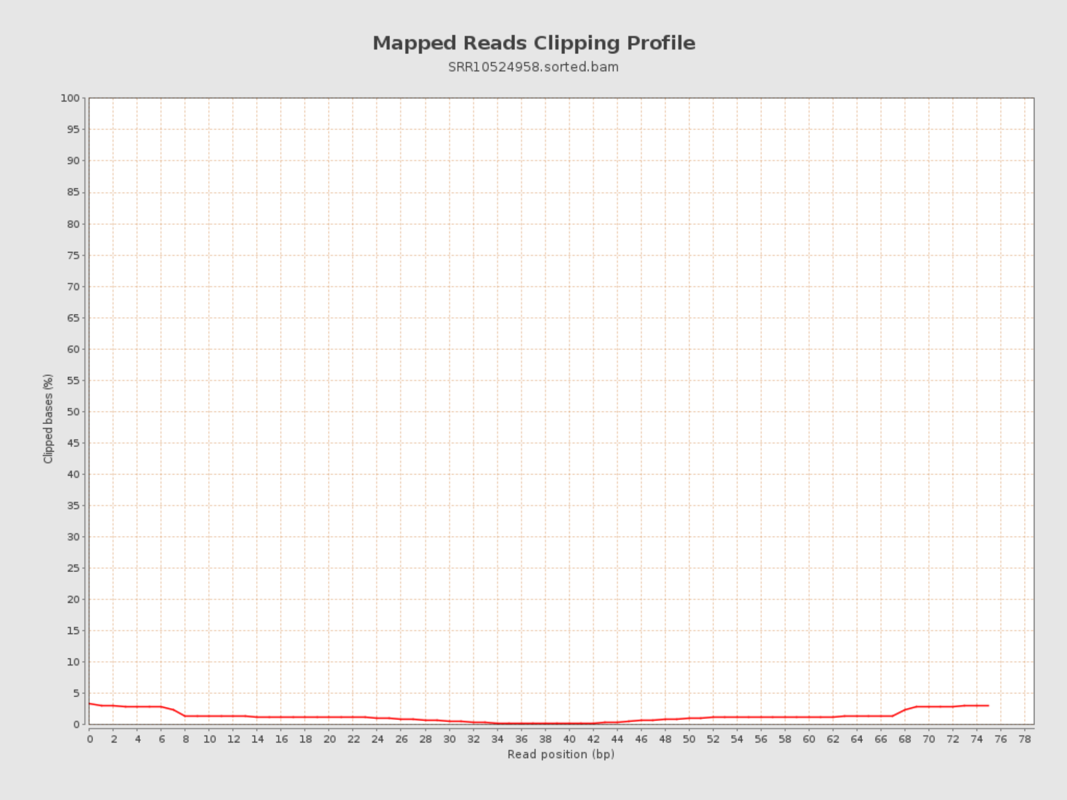
8. Results : Mapped Reads Nucleotide Content



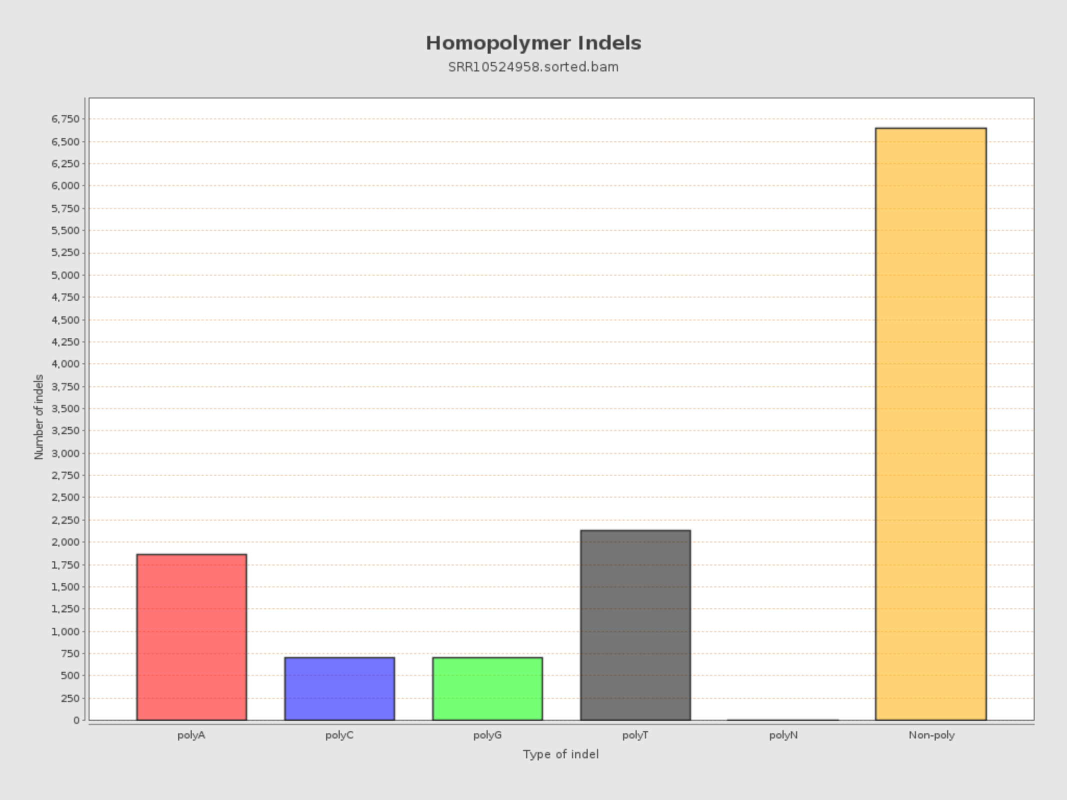
9. Results : Mapped Reads GC-content Distribution



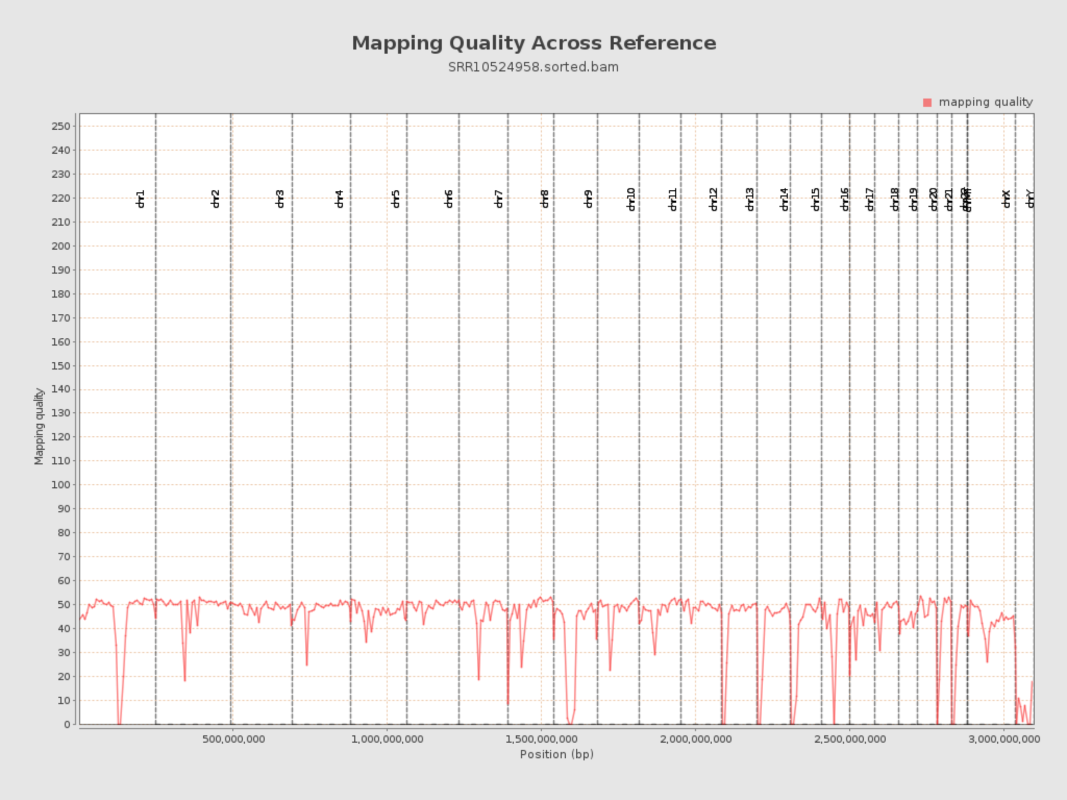
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram