Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:49:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524576.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_SRR10524576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,685,160
Mapped reads	1,526,227 / 90.57%
Unmapped reads	158,933 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,098 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	63,591 / 3.77%
Duplication rate	3.13%
Clipped reads	1,530,847 / 90.84%

2.2. ACGT Content

Number/percentage of A's	22,529,817 / 25.4%
Number/percentage of C's	17,448,881 / 19.67%
Number/percentage of T's	27,633,074 / 31.15%
Number/percentage of G's	21,087,278 / 23.77%
Number/percentage of N's	1,356 / 0%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2718

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

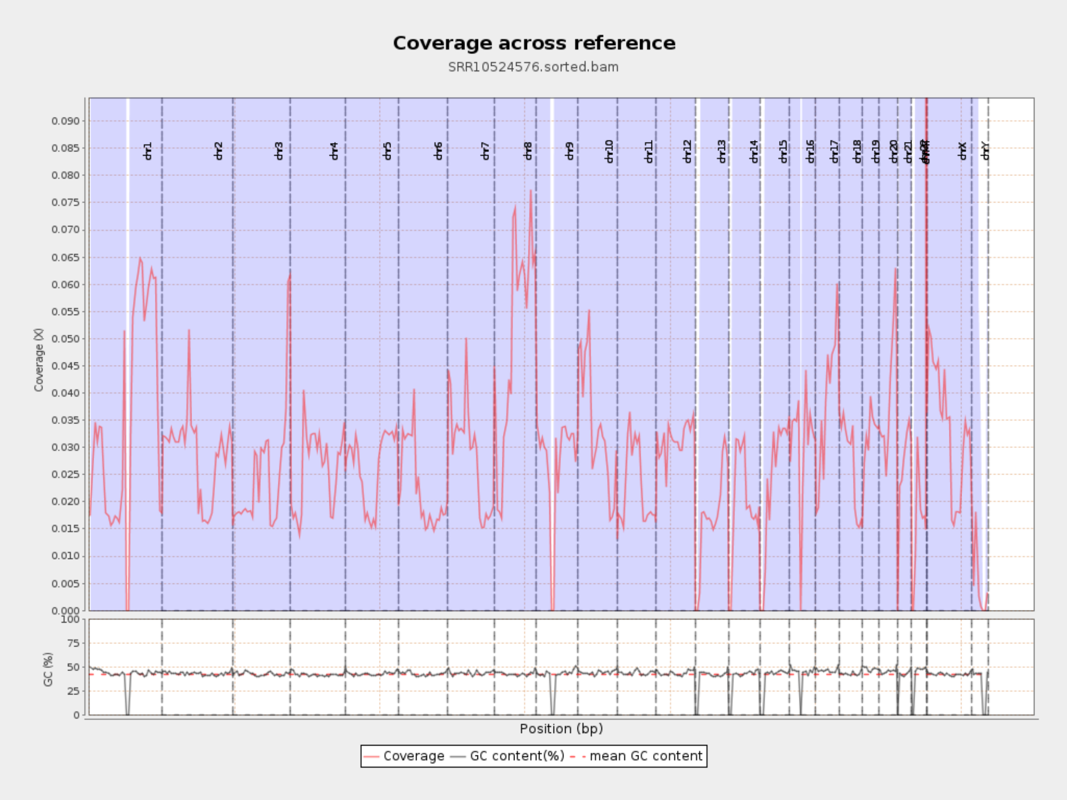
General error rate	0.53%
Mismatches	455,987
Insertions	5,054
Mapped reads with at least one insertion	0.33%
Deletions	16,164
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.4%

2.6. Chromosome stats

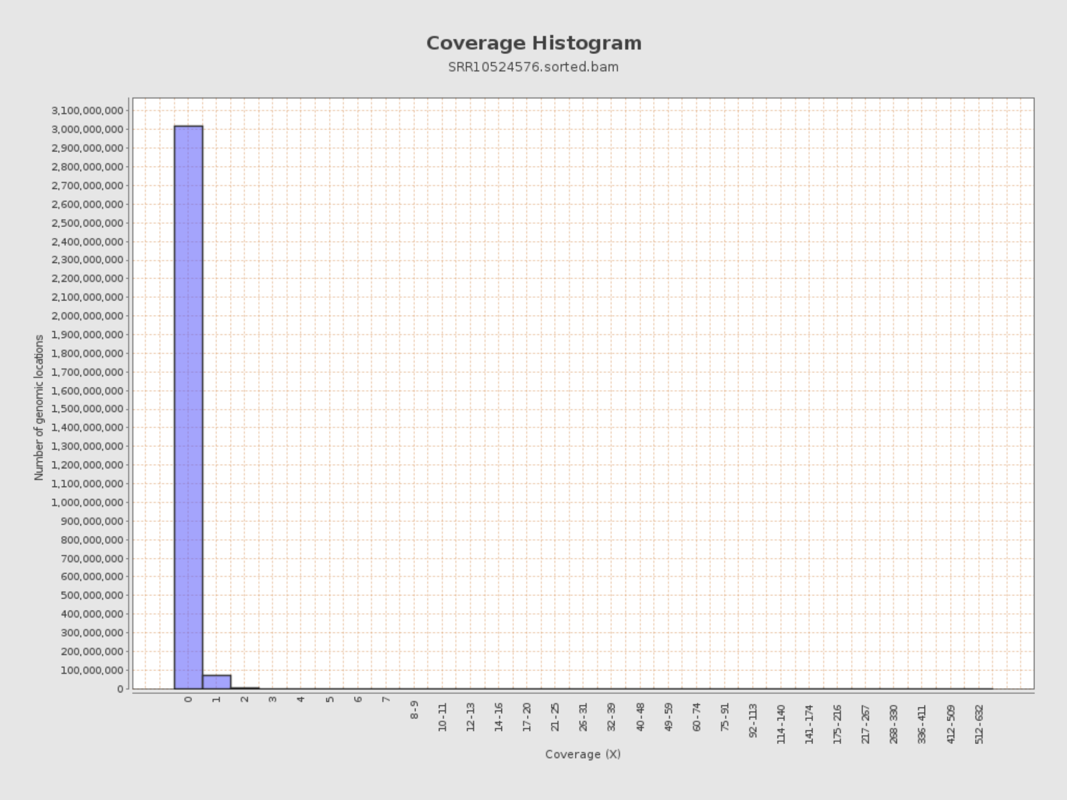
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8864778	0.0356	0.5082
chr2	243199373	7038499	0.0289	0.3129
chr3	198022430	4857681	0.0245	0.1742
chr4	191154276	5004150	0.0262	0.2011
chr5	180915260	4820613	0.0266	0.1807
chr6	171115067	3826676	0.0224	0.202
chr7	159138663	4561368	0.0287	0.335

chr8	146364022	7384680	0.0505	0.2968
chr9	141213431	3789570	0.0268	0.2311
chr10	135534747	4603614	0.034	0.274
chr11	135006516	3094084	0.0229	0.2491
chr12	133851895	4227460	0.0316	0.1964
chr13	115169878	1985434	0.0172	0.144
chr14	107349540	2130236	0.0198	0.1604
chr15	102531392	2413954	0.0235	0.1691
chr16	90354753	2798942	0.031	0.2053
chr17	81195210	3154112	0.0388	0.2312
chr18	78077248	2137680	0.0274	0.4145
chr19	59128983	1906614	0.0322	0.3399
chr20	63025520	2511342	0.0398	0.2209
chr21	48129895	1260464	0.0262	0.1926
chr22	51304566	762166	0.0149	0.1338
chrMT	16571	42590	2.5702	2.4096
chrX	155270560	5253999	0.0338	0.2272
chrY	59373566	296430	0.005	0.1458

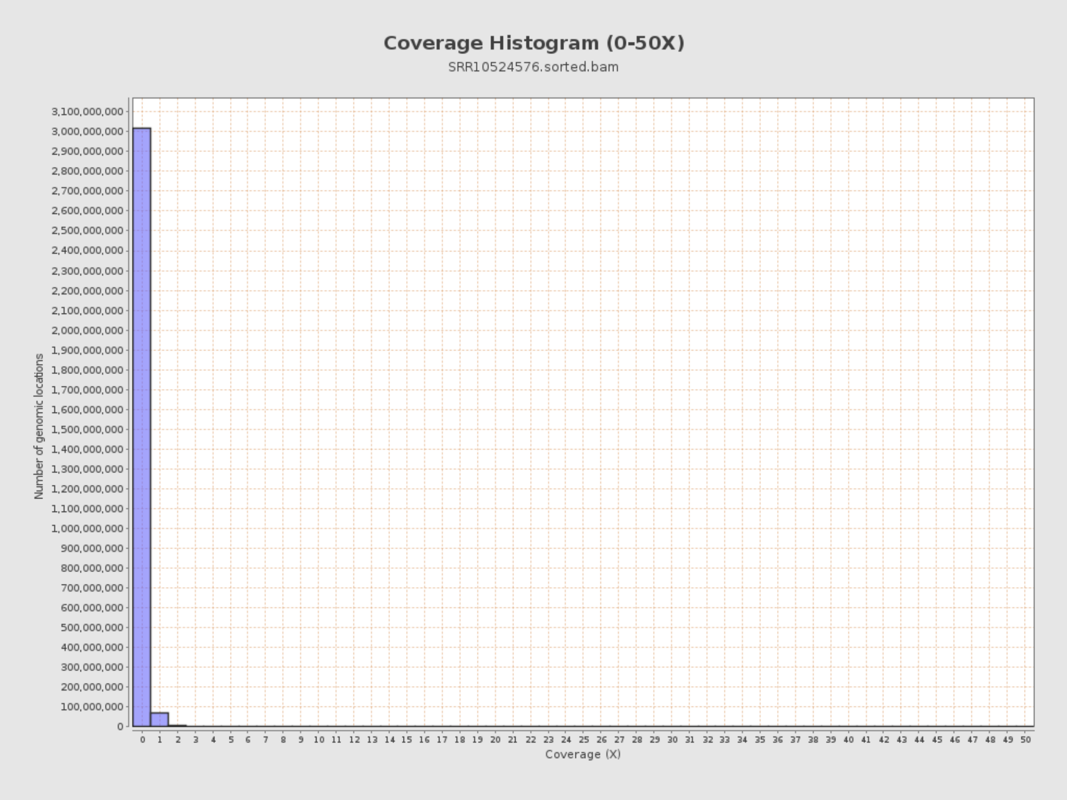
3. Results : Coverage across reference



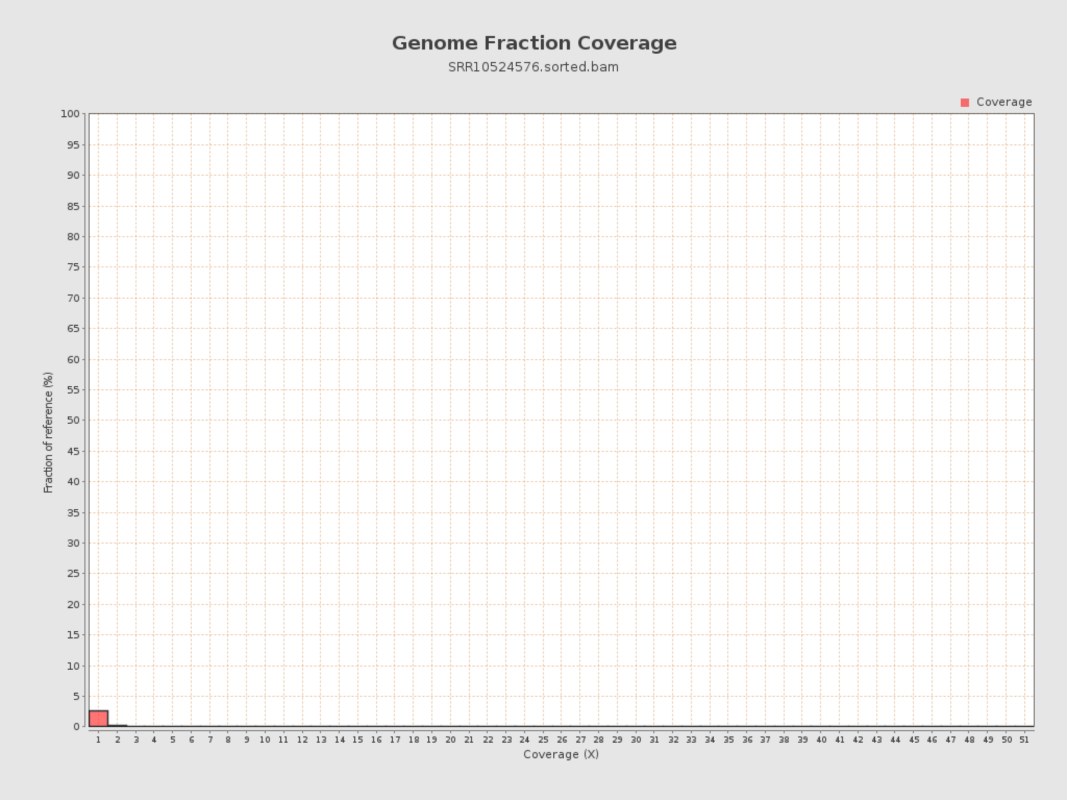
4. Results : Coverage Histogram



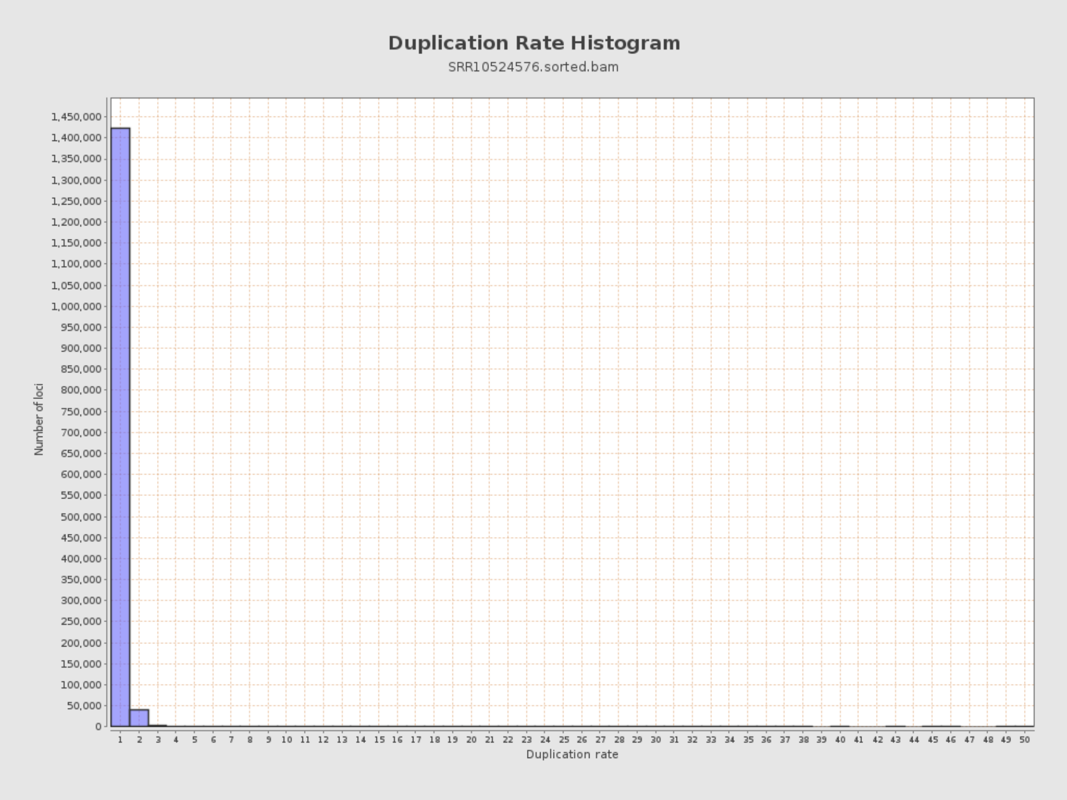
5. Results : Coverage Histogram (0-50X)



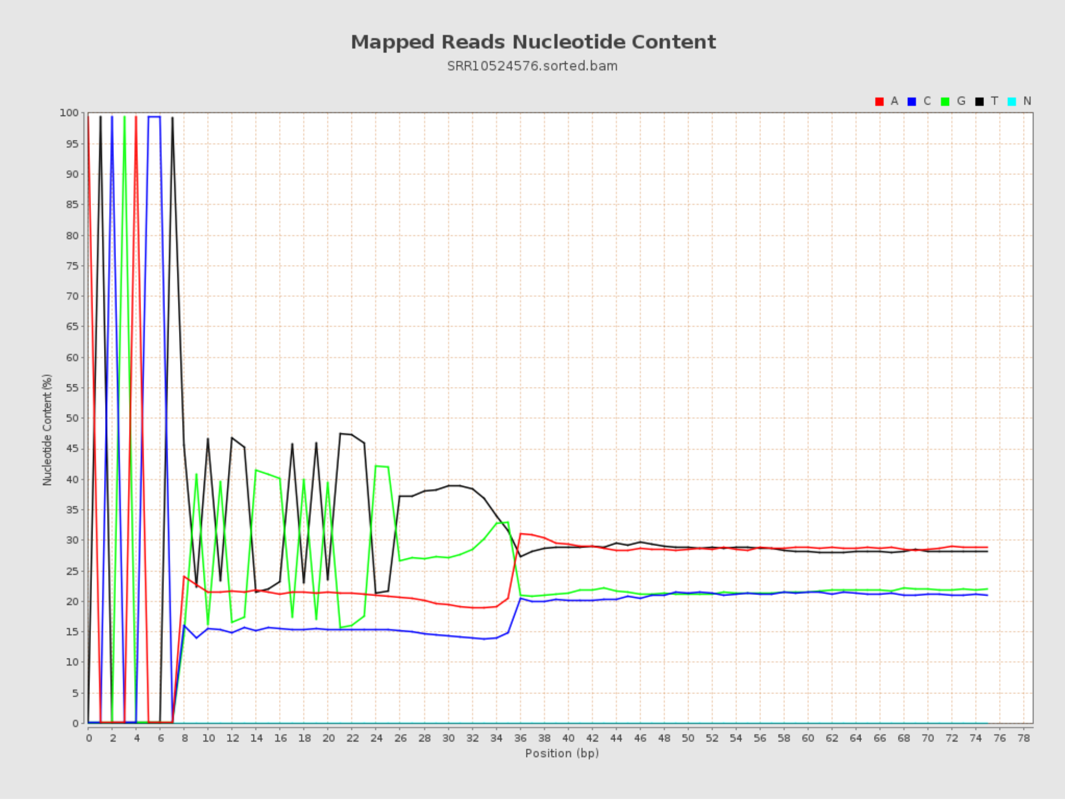
6. Results : Genome Fraction Coverage



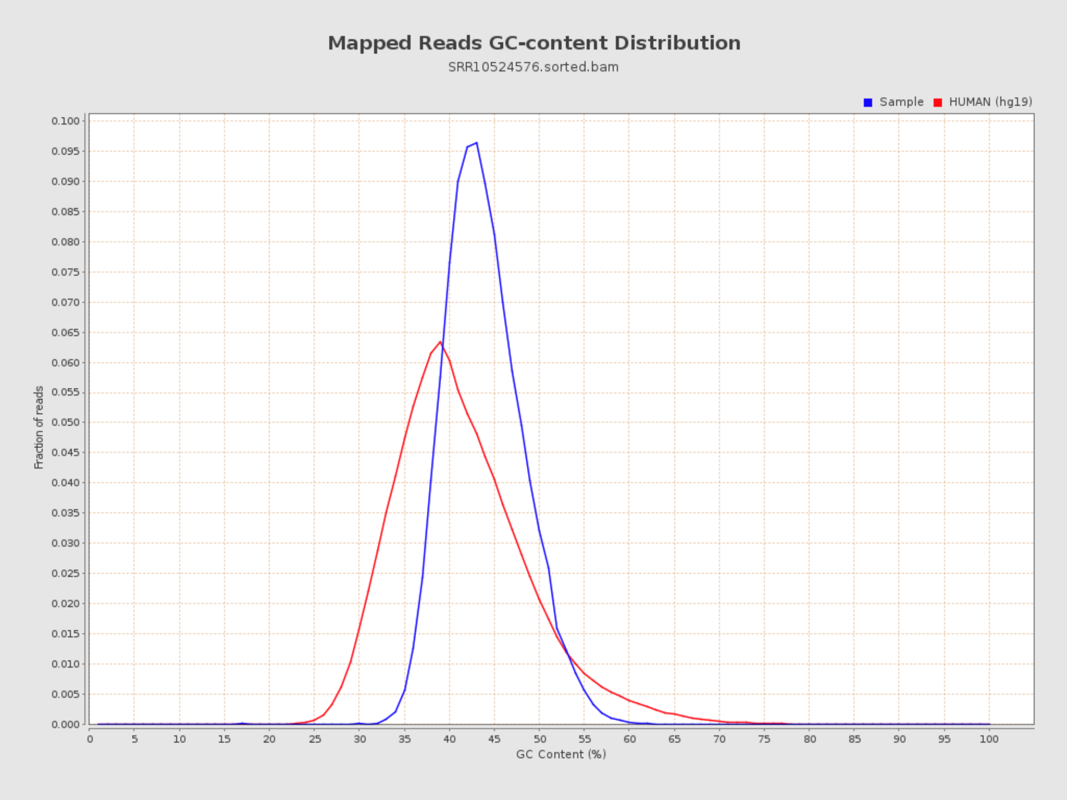
7. Results : Duplication Rate Histogram



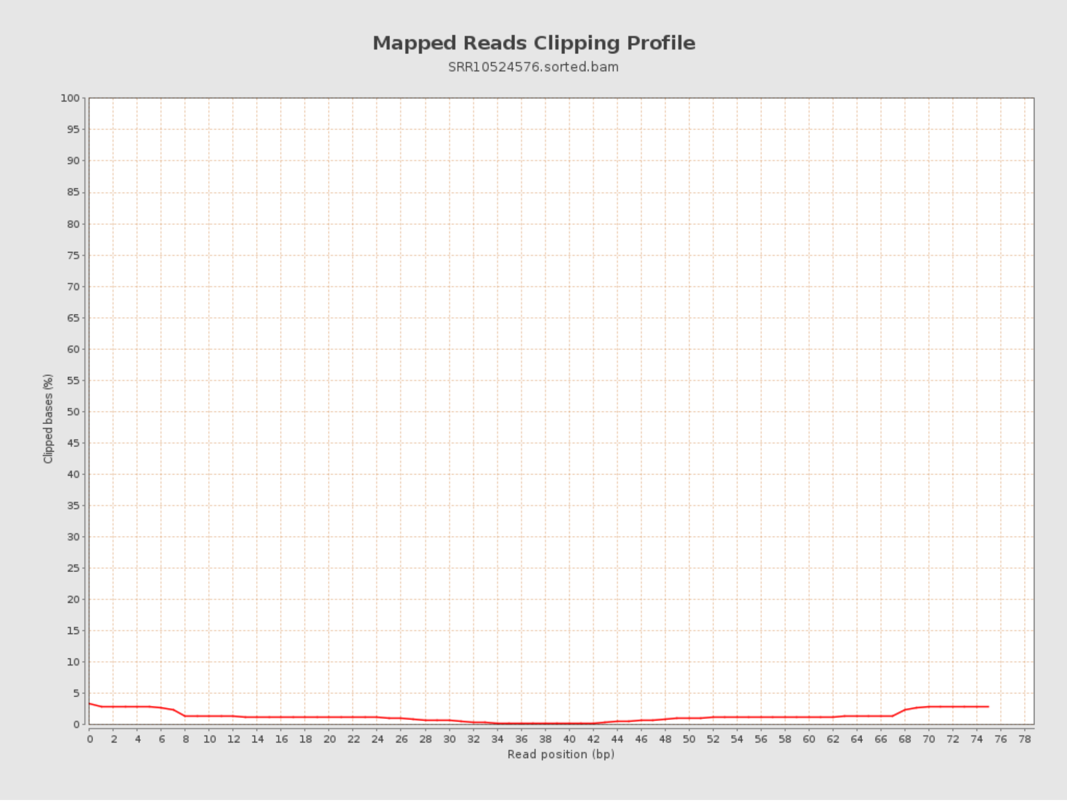
8. Results : Mapped Reads Nucleotide Content



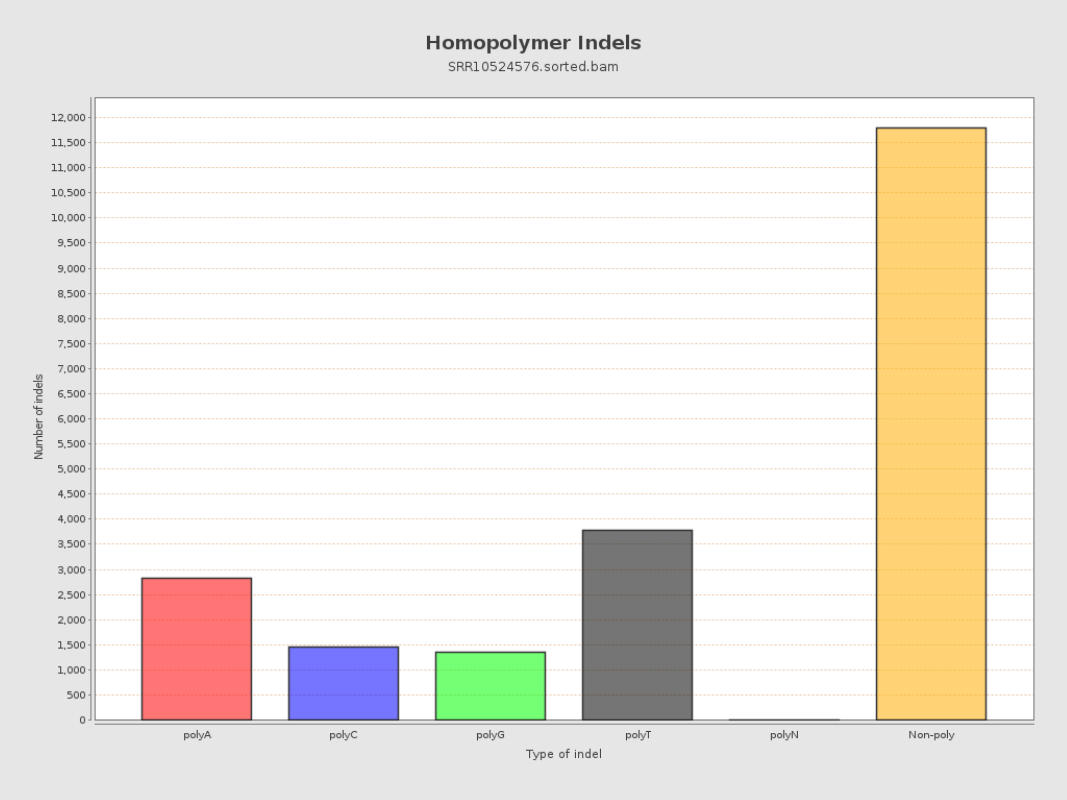
9. Results : Mapped Reads GC-content Distribution



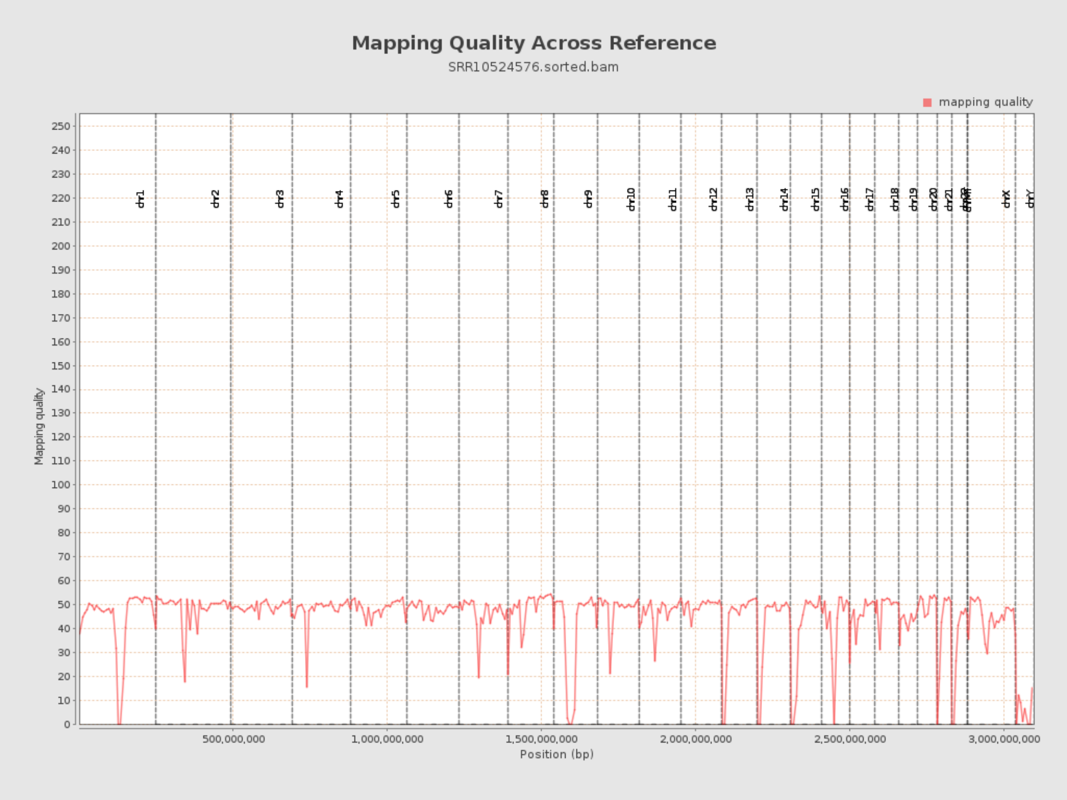
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram