Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:13:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524910.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_SRR10524910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524910.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:13:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,172,021
Mapped reads	6,644,064 / 92.64%
Unmapped reads	527,957 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,650 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	1,177,051 / 16.41%
Duplication rate	11.19%
Clipped reads	6,650,305 / 92.73%

2.2. ACGT Content

Number/percentage of A's	91,742,765 / 23.65%
Number/percentage of C's	76,242,966 / 19.66%
Number/percentage of T's	127,465,854 / 32.86%
Number/percentage of G's	92,446,169 / 23.83%
Number/percentage of N's	3,101 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.1253

Standard Deviation	0.9876

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

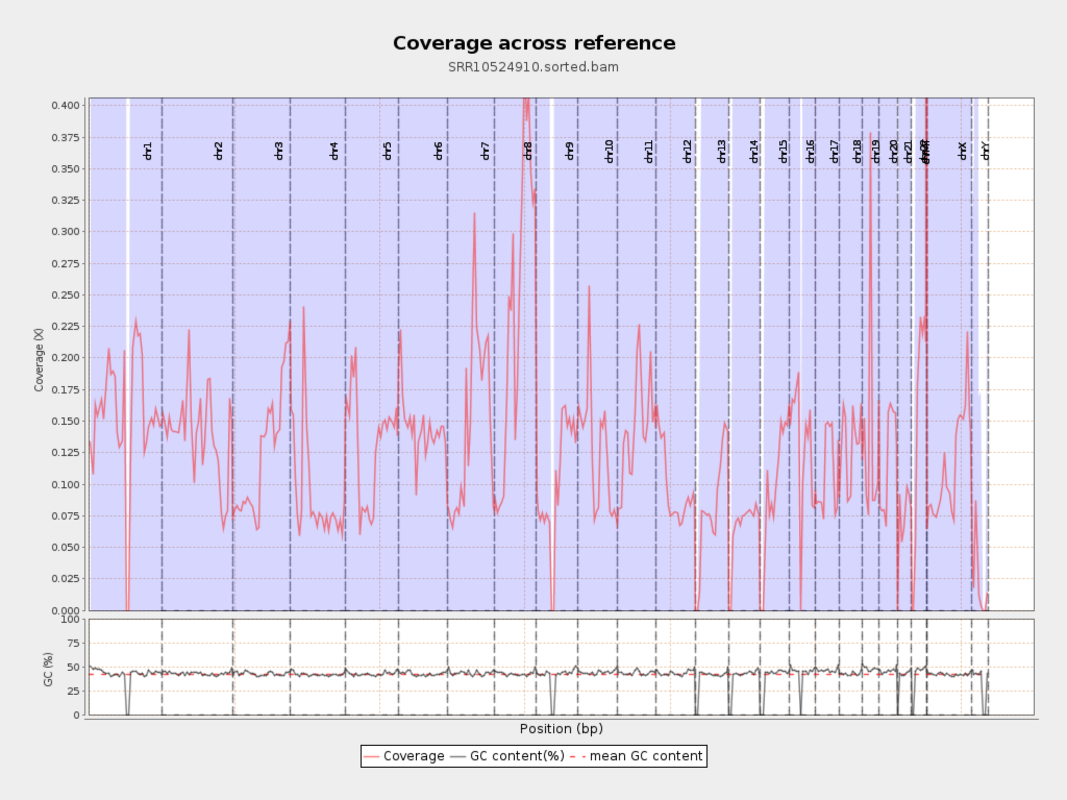
General error rate	0.52%
Mismatches	1,962,156
Insertions	27,254
Mapped reads with at least one insertion	0.41%
Deletions	73,609
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.5%

2.6. Chromosome stats

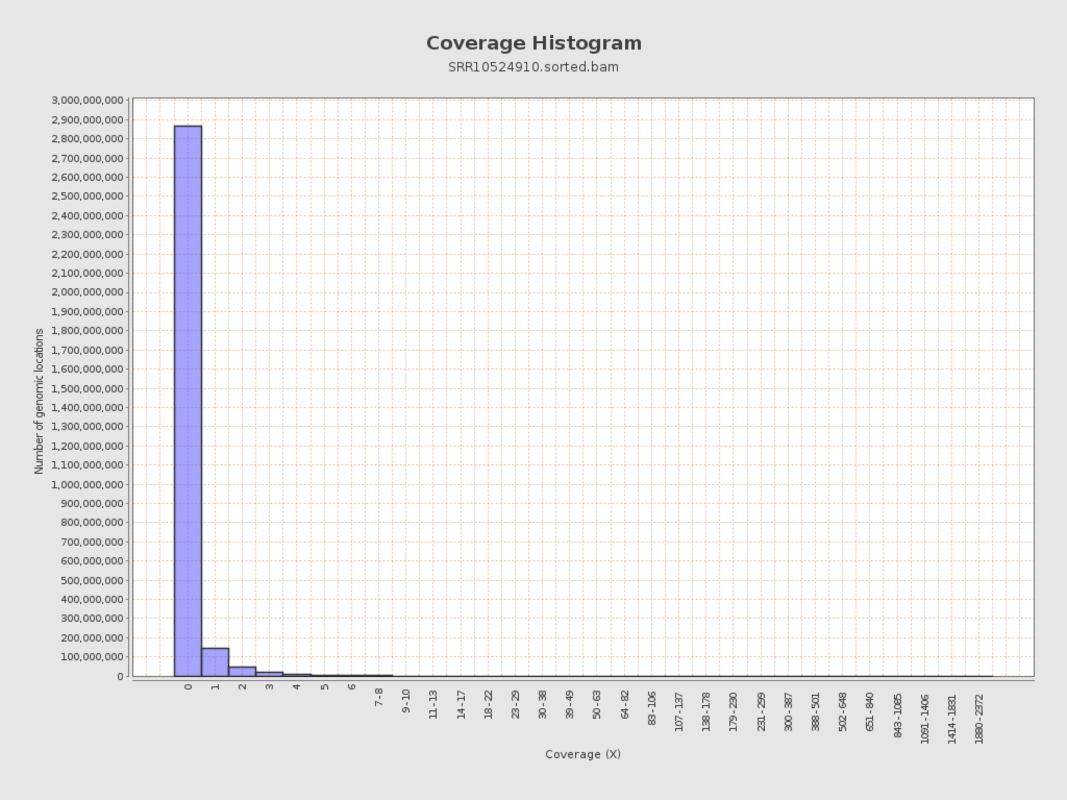
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38618627	0.1549	1.8093
chr2	243199373	33954442	0.1396	1.3594
chr3	198022430	24418725	0.1233	0.5561
chr4	191154276	17369952	0.0909	0.7969
chr5	180915260	23820990	0.1317	0.5753
chr6	171115067	24841970	0.1452	0.6659
chr7	159138663	23882277	0.1501	1.1939

chr8	146364022	34758373	0.2375	1.3379
chr9	141213431	14149596	0.1002	0.7774
chr10	135534747	17043800	0.1258	1.1549
chr11	135006516	19642028	0.1455	0.8057
chr12	133851895	12892845	0.0963	0.5186
chr13	115169878	9247329	0.0803	0.4542
chr14	107349540	6996894	0.0652	0.4366
chr15	102531392	9804331	0.0956	0.4942
chr16	90354753	11655727	0.129	0.6353
chr17	81195210	8873582	0.1093	0.5857
chr18	78077248	10355280	0.1326	1.3779
chr19	59128983	8226626	0.1391	1.3172
chr20	63025520	7555195	0.1199	0.6013
chr21	48129895	3502067	0.0728	0.7063
chr22	51304566	7505516	0.1463	0.6306
chrMT	16571	37494	2.2626	2.4506
chrX	155270560	17641741	0.1136	0.6341
chrY	59373566	1227740	0.0207	0.8026

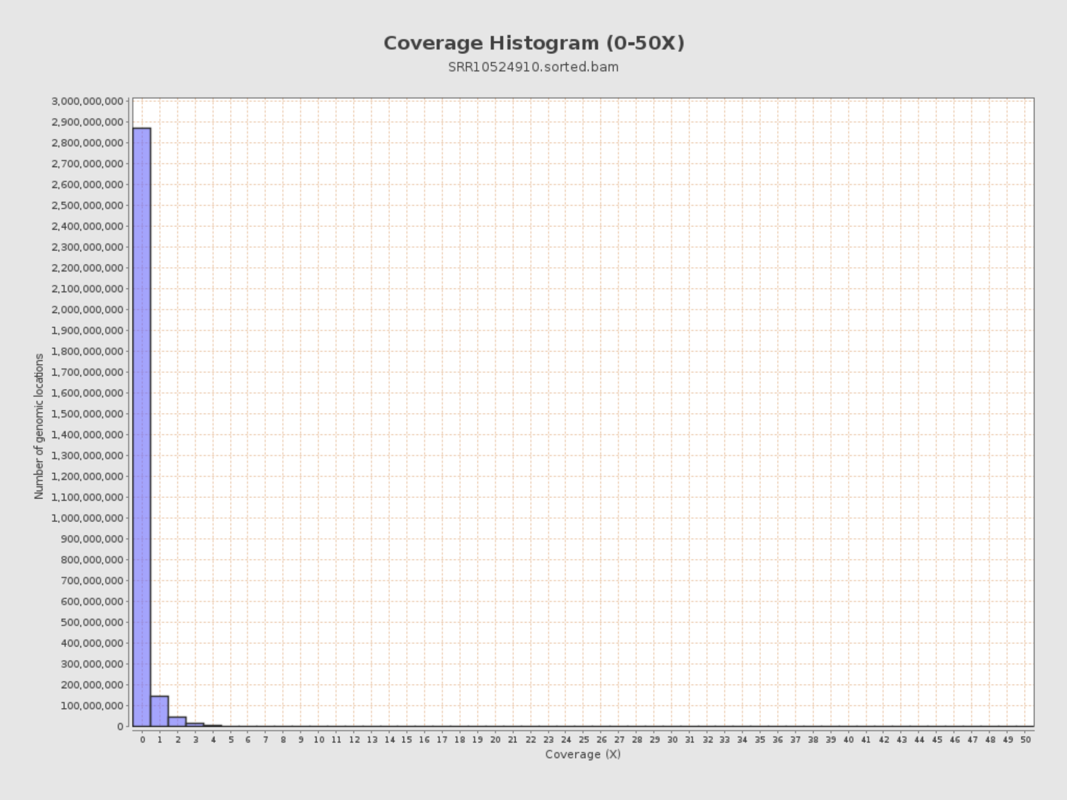
3. Results : Coverage across reference



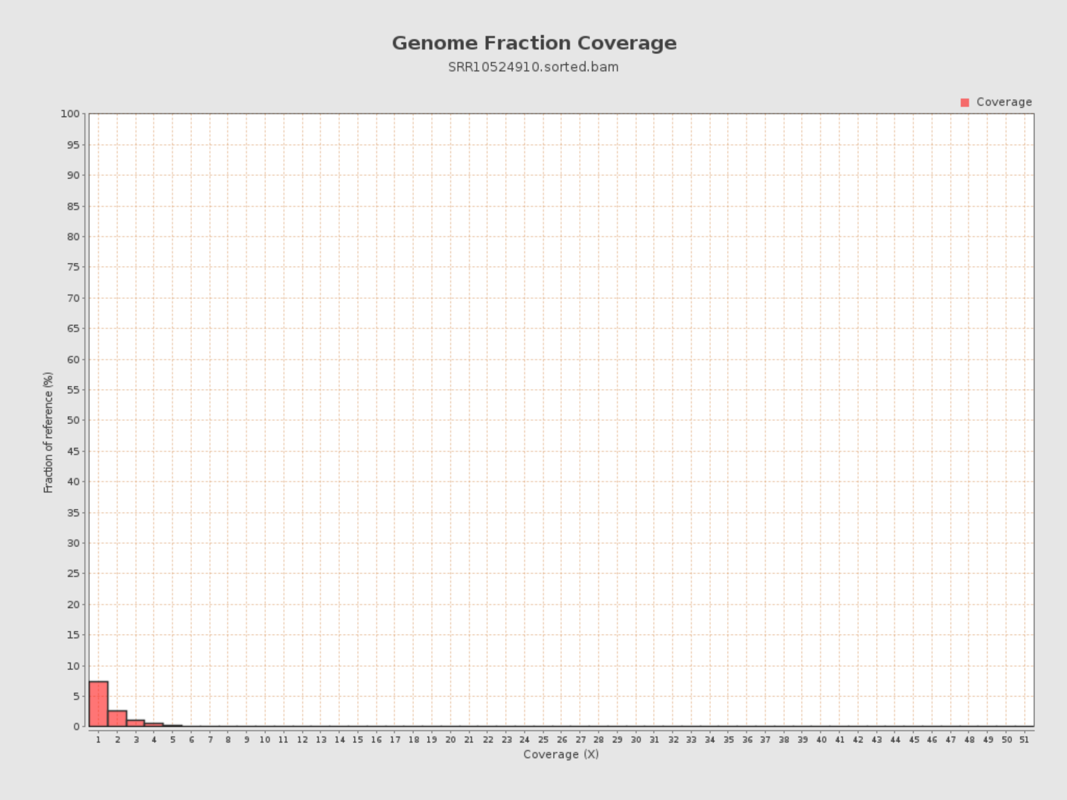
4. Results : Coverage Histogram



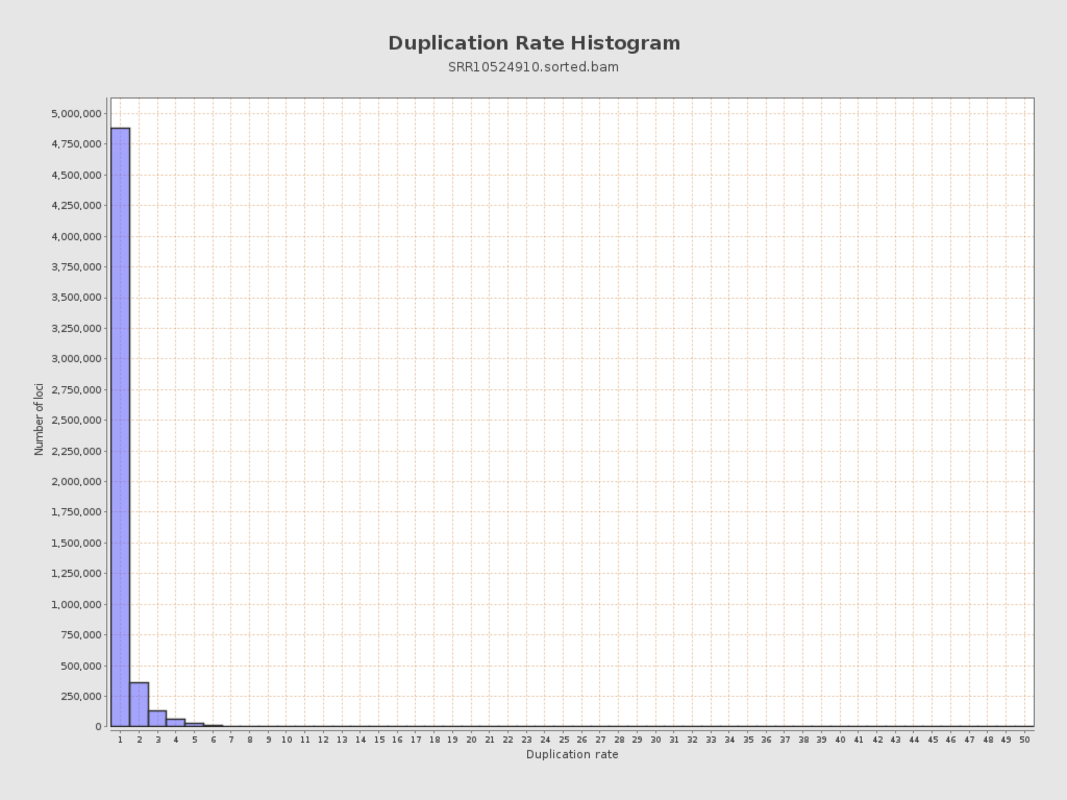
5. Results : Coverage Histogram (0-50X)



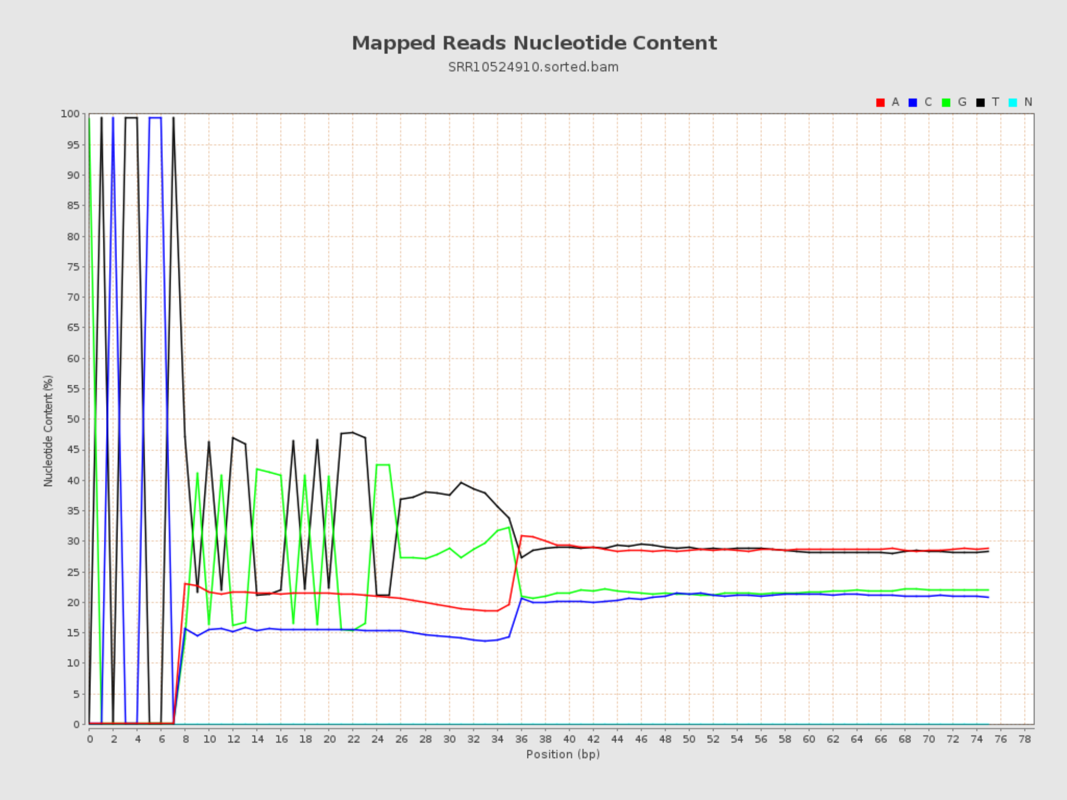
6. Results : Genome Fraction Coverage



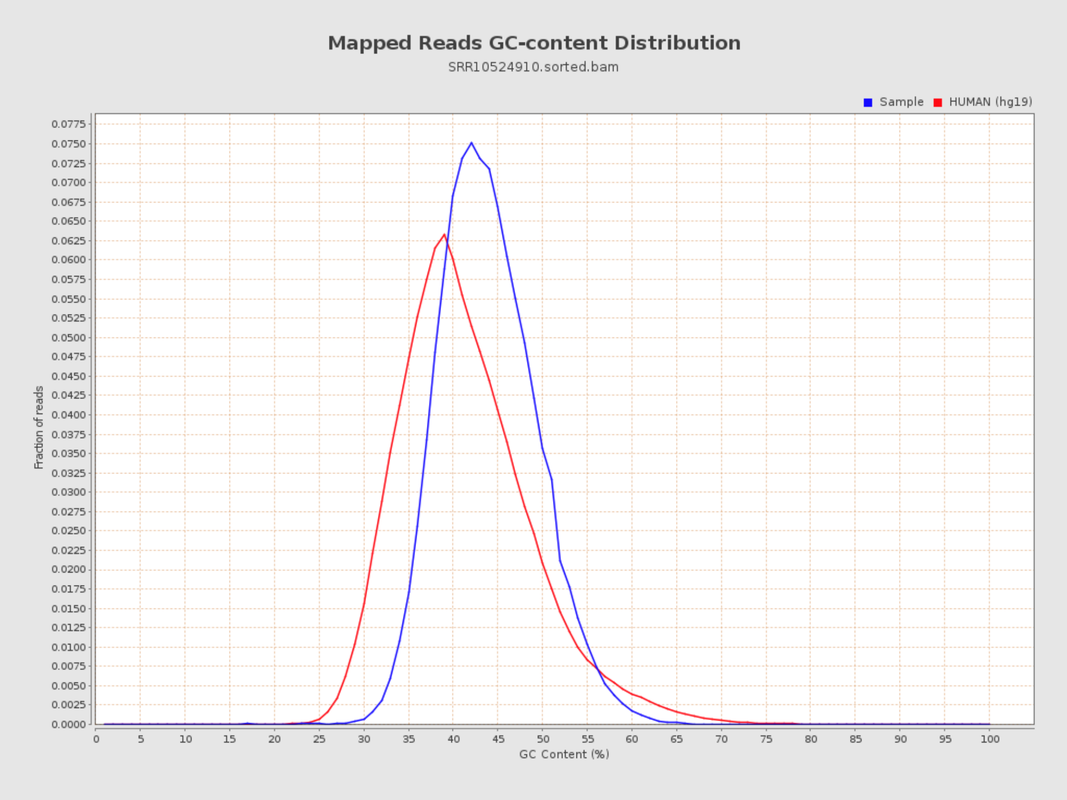
7. Results : Duplication Rate Histogram



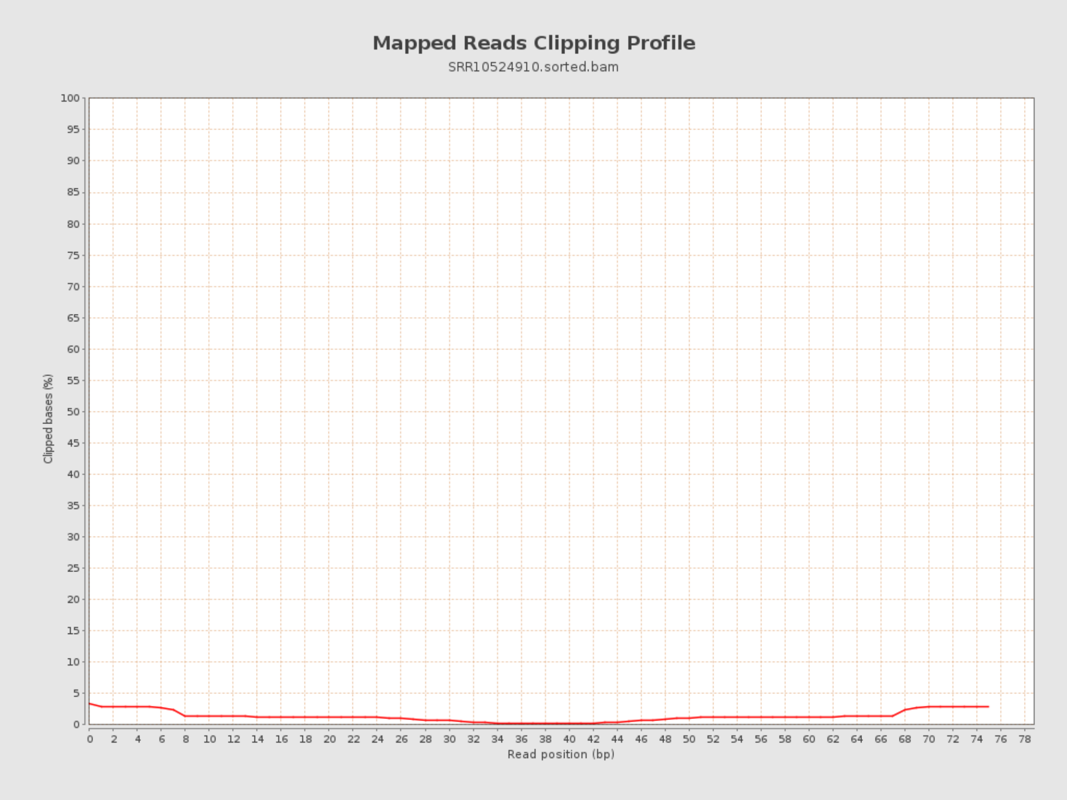
8. Results : Mapped Reads Nucleotide Content



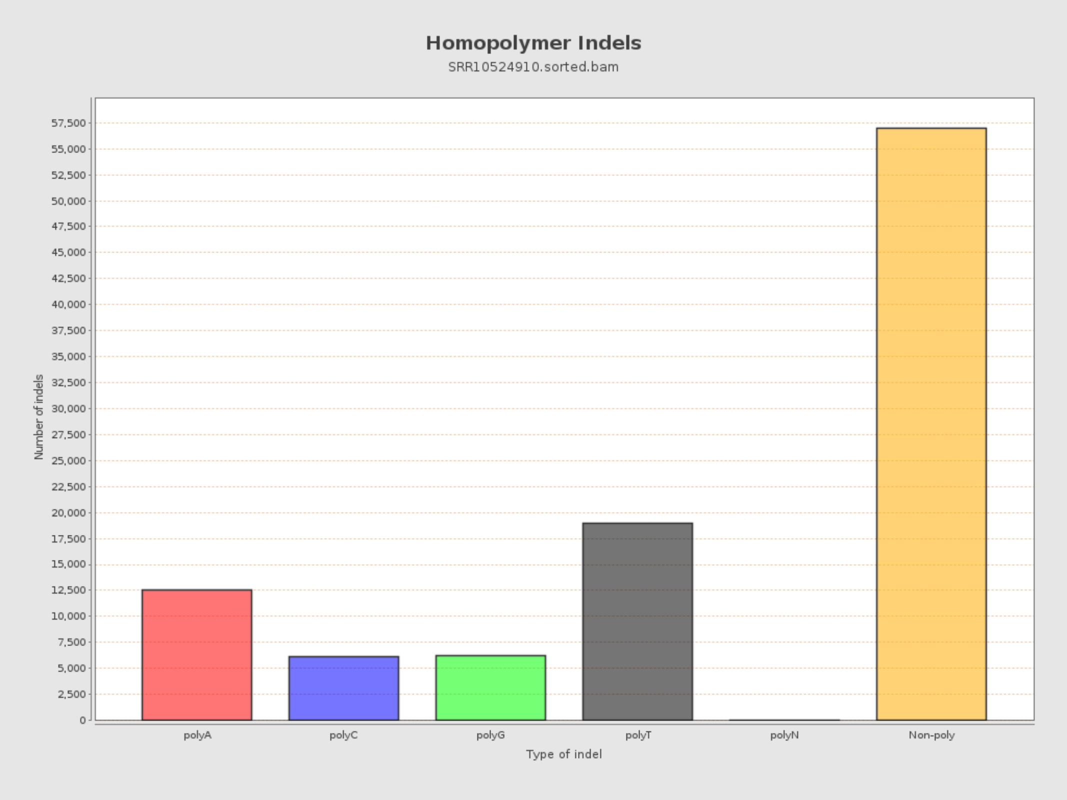
9. Results : Mapped Reads GC-content Distribution



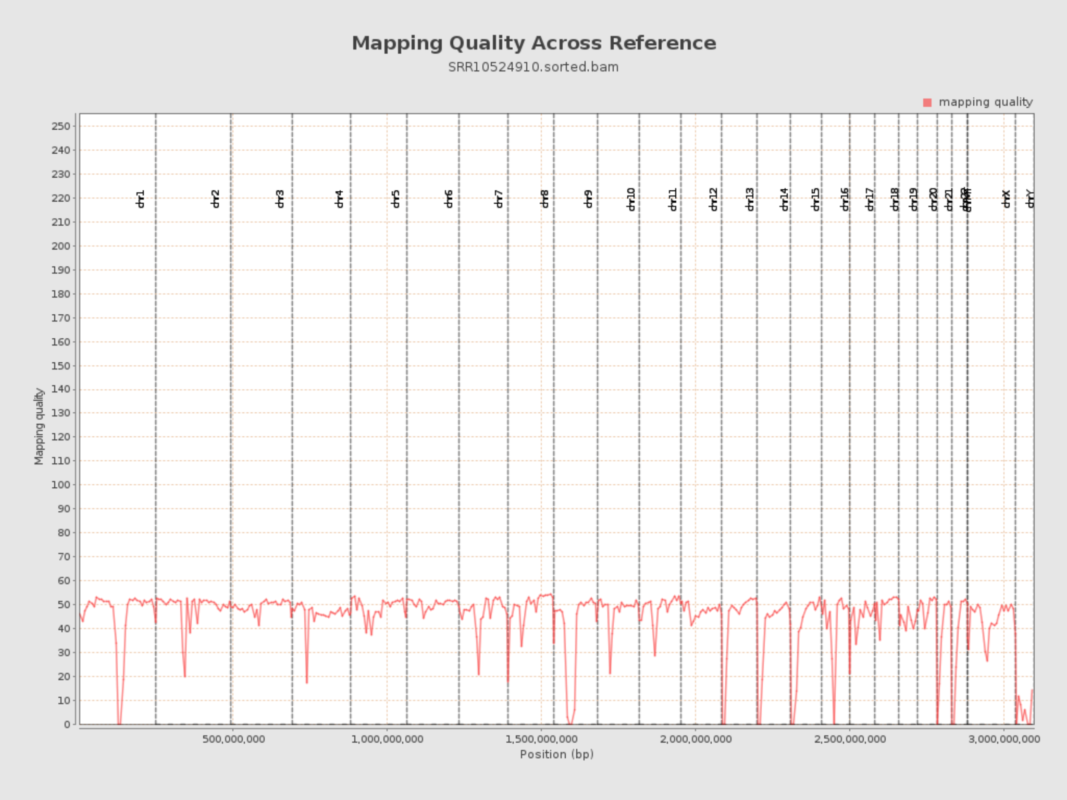
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram