Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:33:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524663.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_SRR10524663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:33:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,406,660
Mapped reads	1,295,676 / 92.11%
Unmapped reads	110,984 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,086 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	46,869 / 3.33%
Duplication rate	2.64%
Clipped reads	1,297,494 / 92.24%

2.2. ACGT Content

Number/percentage of A's	19,689,751 / 25.82%
Number/percentage of C's	14,870,240 / 19.5%
Number/percentage of T's	23,862,112 / 31.3%
Number/percentage of G's	17,813,005 / 23.36%
Number/percentage of N's	10,391 / 0.01%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2484

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

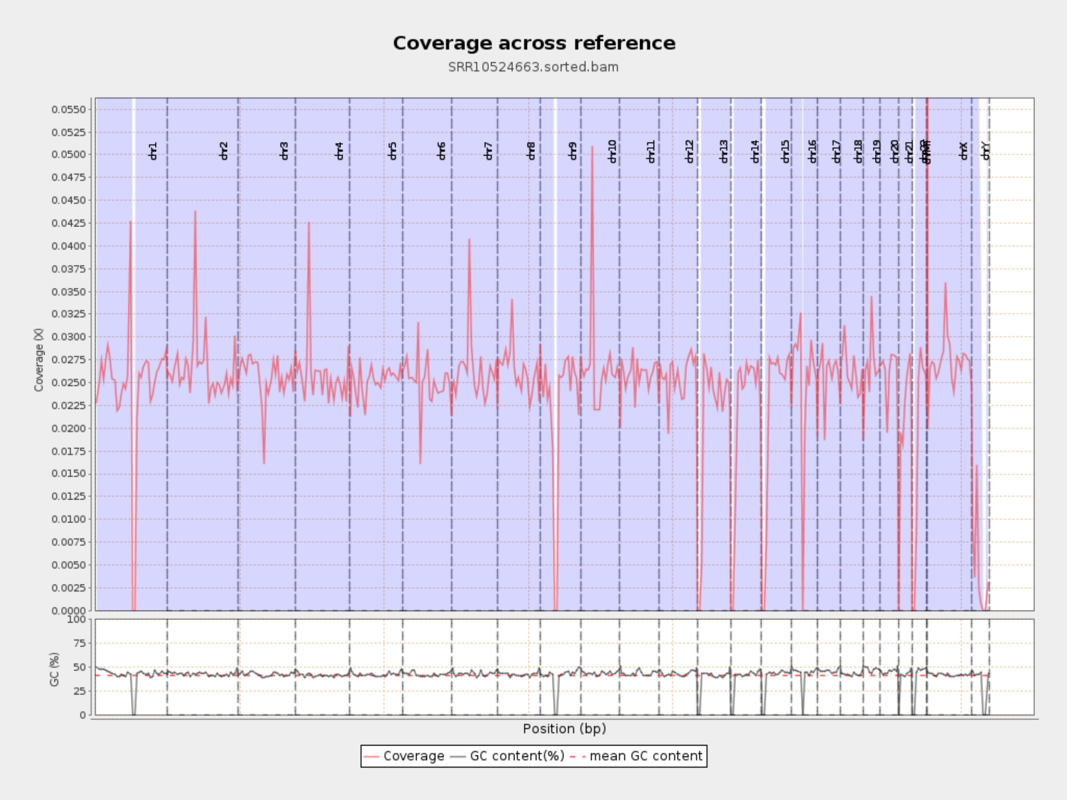
General error rate	0.52%
Mismatches	383,331
Insertions	5,640
Mapped reads with at least one insertion	0.43%
Deletions	14,608
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.84%

2.6. Chromosome stats

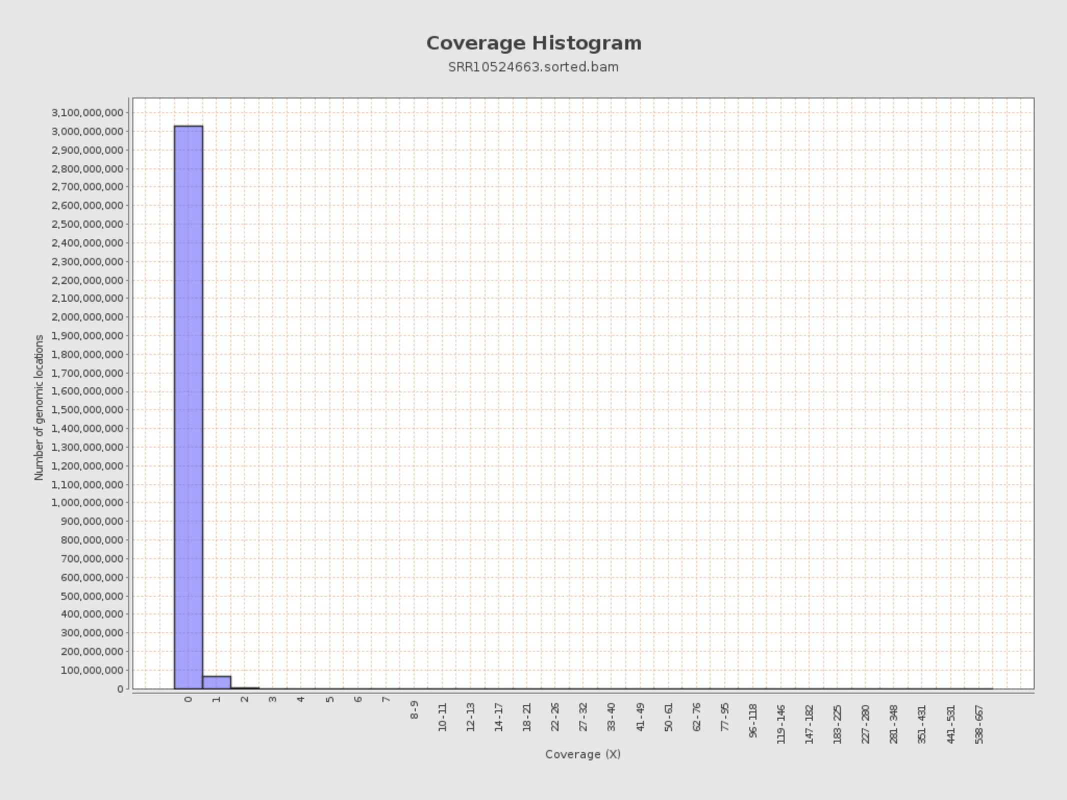
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6101031	0.0245	0.4409
chr2	243199373	6457735	0.0266	0.3415
chr3	198022430	5059838	0.0256	0.1721
chr4	191154276	4975567	0.026	0.1944
chr5	180915260	4588342	0.0254	0.1714
chr6	171115067	4294860	0.0251	0.1888
chr7	159138663	4211673	0.0265	0.2773

chr8	146364022	3866245	0.0264	0.2537
chr9	141213431	3143234	0.0223	0.2068
chr10	135534747	3659334	0.027	0.2487
chr11	135006516	3504248	0.026	0.2175
chr12	133851895	3436924	0.0257	0.1747
chr13	115169878	2386135	0.0207	0.1567
chr14	107349540	2293692	0.0214	0.1603
chr15	102531392	2218001	0.0216	0.1609
chr16	90354753	2230014	0.0247	0.1821
chr17	81195210	2108503	0.026	0.1812
chr18	78077248	2047104	0.0262	0.3745
chr19	59128983	1596461	0.027	0.333
chr20	63025520	1637682	0.026	0.1751
chr21	48129895	1005095	0.0209	0.176
chr22	51304566	936324	0.0183	0.1443
chrMT	16571	14695	0.8868	1.0919
chrX	155270560	4248485	0.0274	0.1914
chrY	59373566	247593	0.0042	0.1563

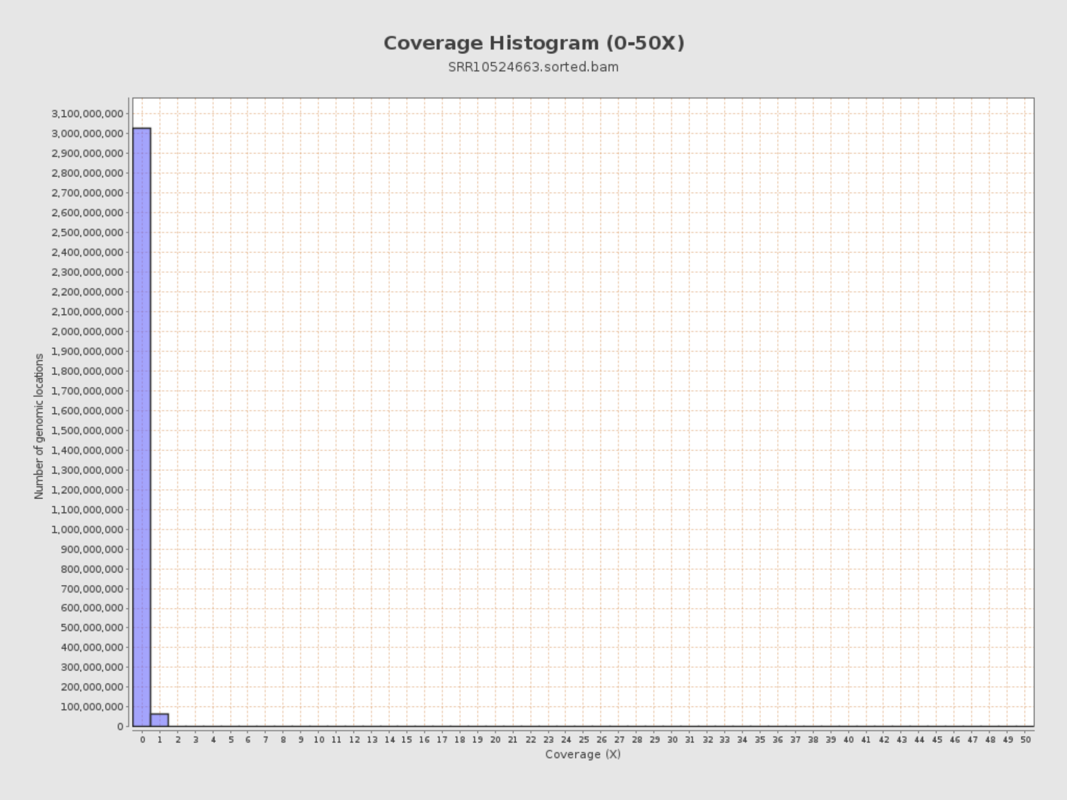
3. Results : Coverage across reference



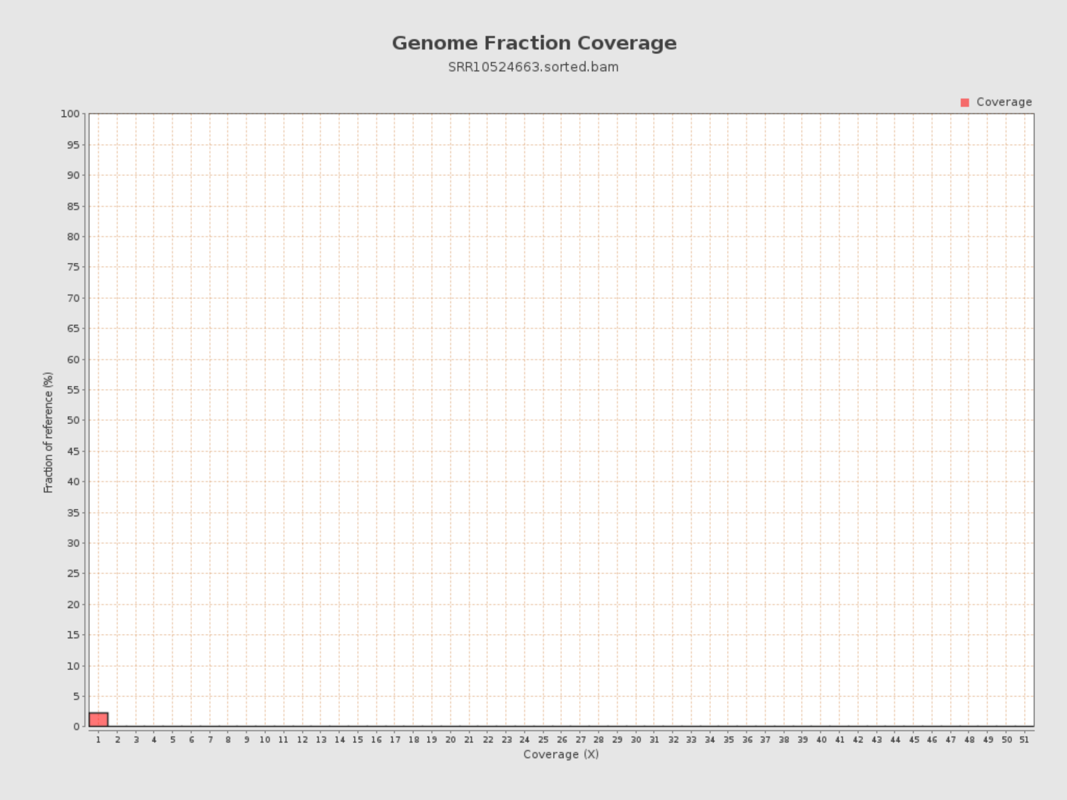
4. Results : Coverage Histogram



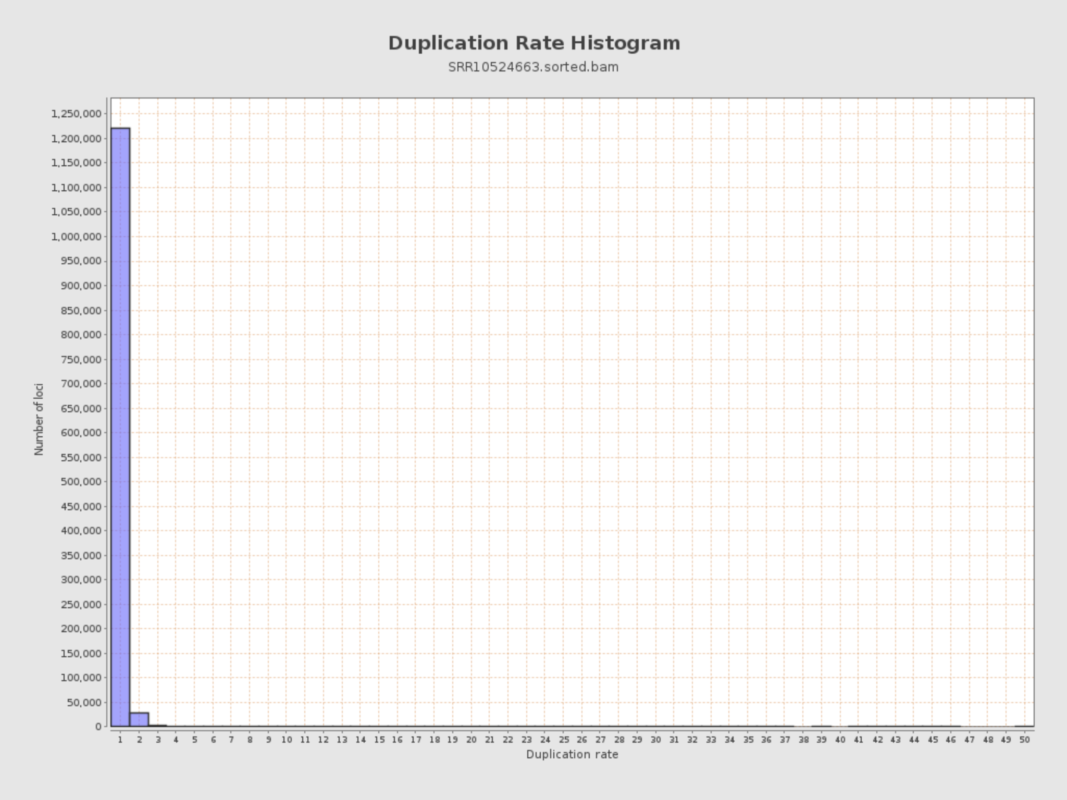
5. Results : Coverage Histogram (0-50X)



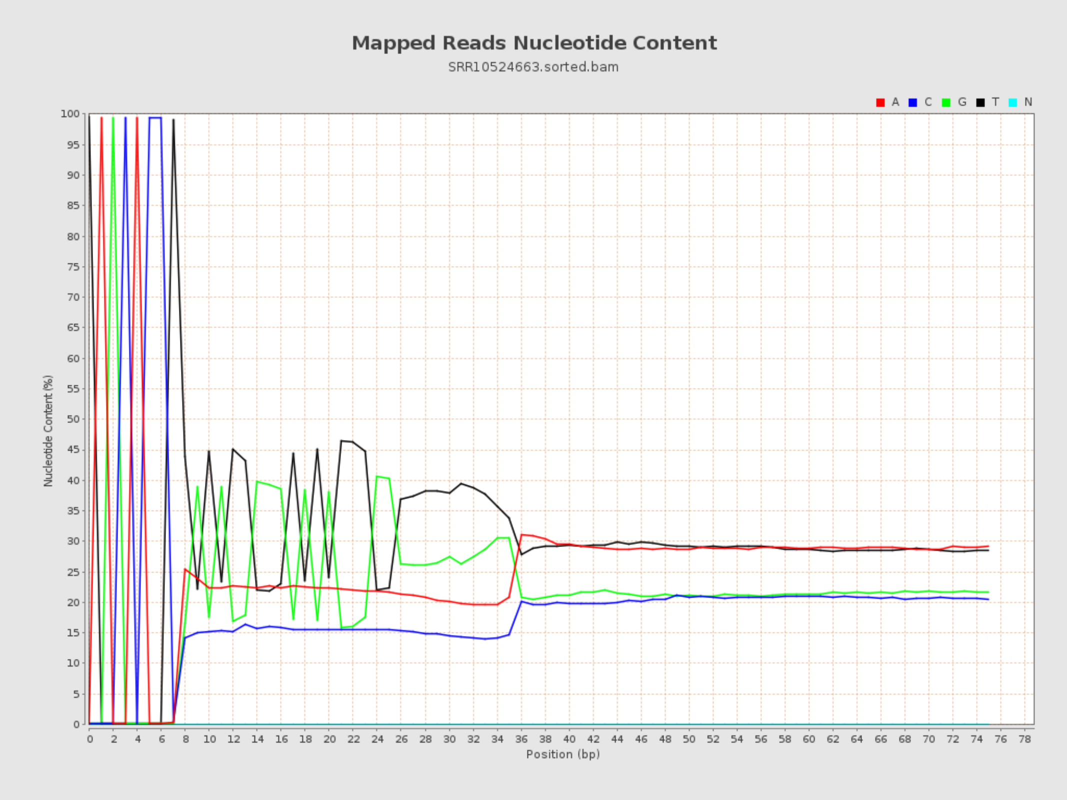
6. Results : Genome Fraction Coverage



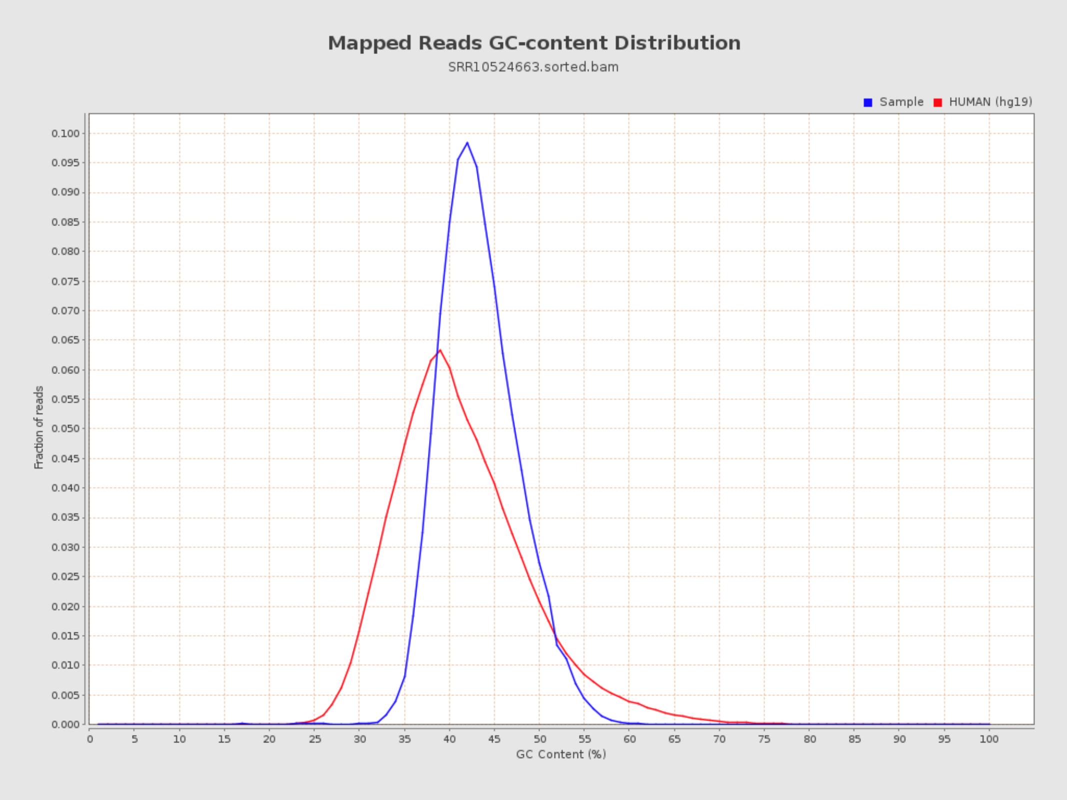
7. Results : Duplication Rate Histogram



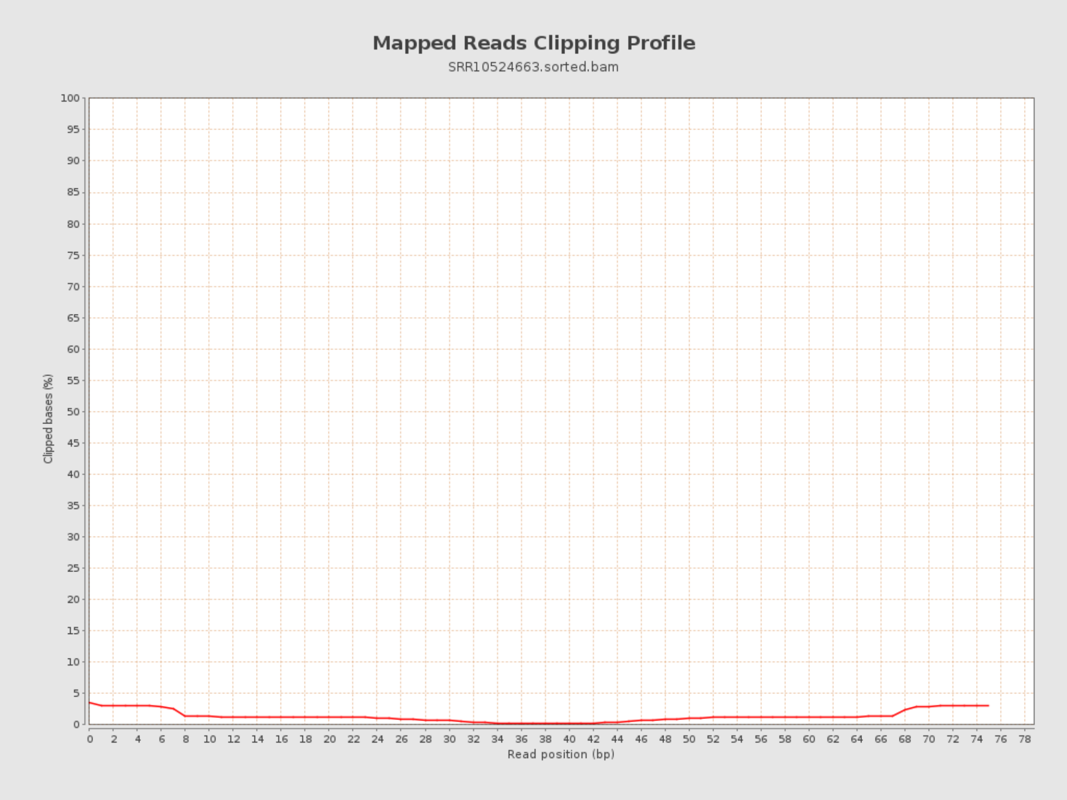
8. Results : Mapped Reads Nucleotide Content



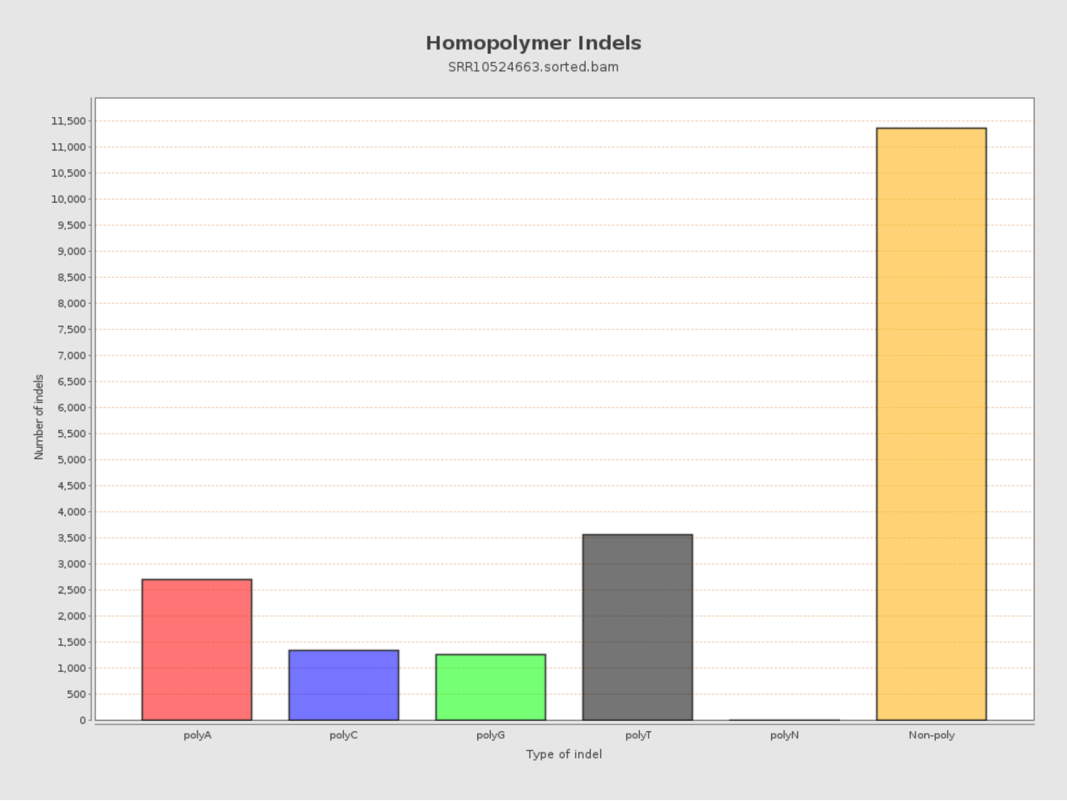
9. Results : Mapped Reads GC-content Distribution



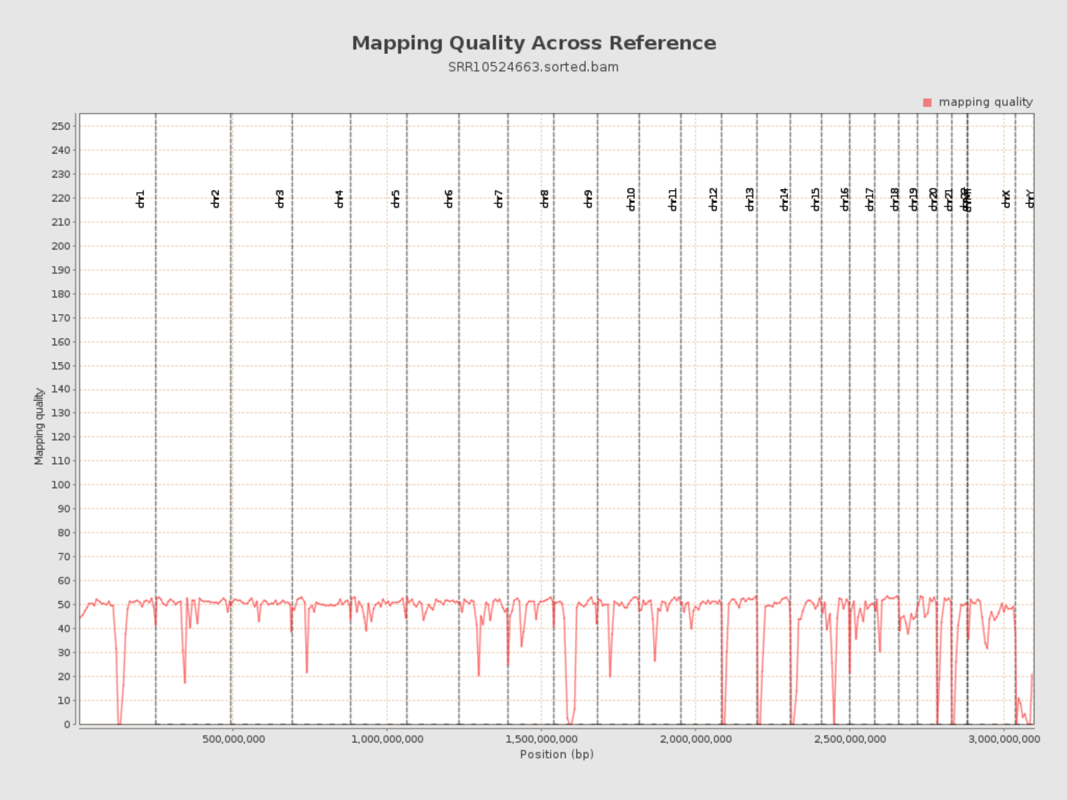
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram