Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:08:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524566.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_SRR10524566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524566.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:08:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,333,892
Mapped reads	1,234,084 / 92.52%
Unmapped reads	99,808 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,385 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	37,946 / 2.84%
Duplication rate	2.25%
Clipped reads	1,234,879 / 92.58%

2.2. ACGT Content

Number/percentage of A's	17,694,336 / 24.54%
Number/percentage of C's	13,485,962 / 18.7%
Number/percentage of T's	22,972,871 / 31.86%
Number/percentage of G's	17,946,423 / 24.89%
Number/percentage of N's	2,057 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2295

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

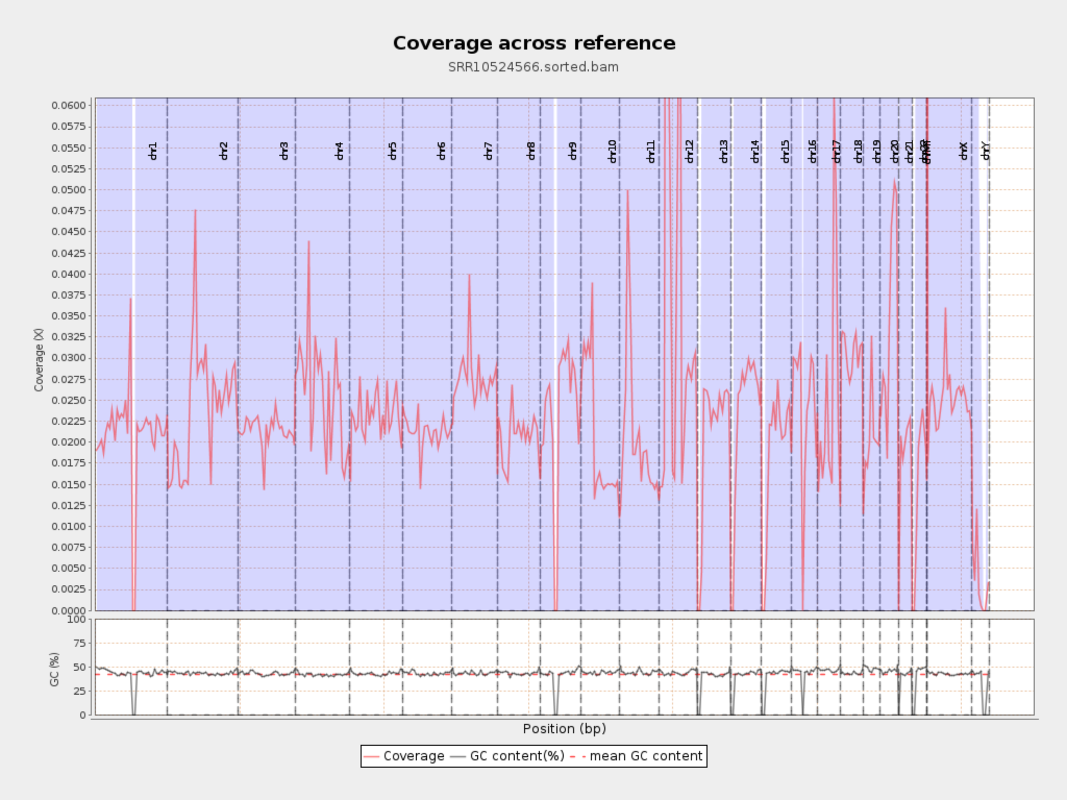
General error rate	0.49%
Mismatches	347,609
Insertions	4,681
Mapped reads with at least one insertion	0.38%
Deletions	11,548
Mapped reads with at least one deletion	0.93%
Homopolymer indels	44.53%

2.6. Chromosome stats

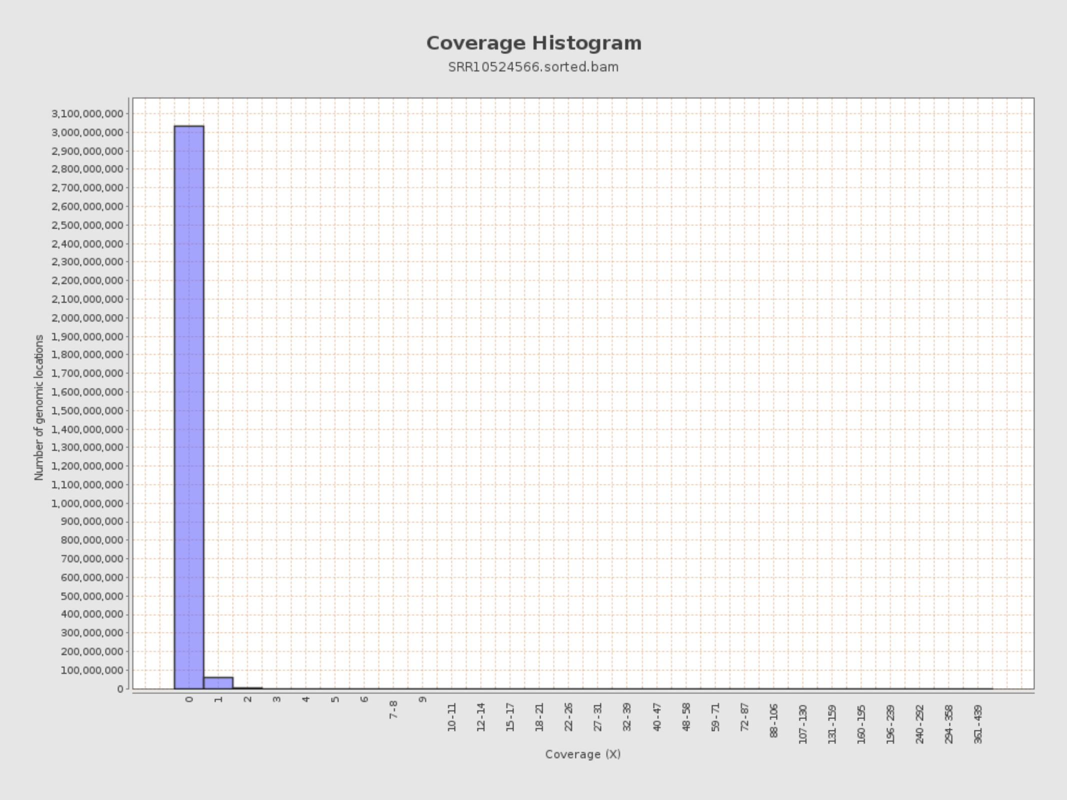
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5188506	0.0208	0.3906
chr2	243199373	5861824	0.0241	0.2445
chr3	198022430	4237344	0.0214	0.1561
chr4	191154276	4915761	0.0257	0.1885
chr5	180915260	4223394	0.0233	0.165
chr6	171115067	3622546	0.0212	0.1664
chr7	159138663	4427250	0.0278	0.2854

chr8	146364022	3034940	0.0207	0.2471
chr9	141213431	3283306	0.0233	0.2244
chr10	135534747	2779189	0.0205	0.2237
chr11	135006516	2776270	0.0206	0.1943
chr12	133851895	5202880	0.0389	0.232
chr13	115169878	2366159	0.0205	0.1536
chr14	107349540	2473721	0.023	0.1723
chr15	102531392	1893294	0.0185	0.1449
chr16	90354753	2142022	0.0237	0.1707
chr17	81195210	2093238	0.0258	0.1785
chr18	78077248	2398842	0.0307	0.395
chr19	59128983	1225178	0.0207	0.2777
chr20	63025520	2190805	0.0348	0.2048
chr21	48129895	884679	0.0184	0.1611
chr22	51304566	755698	0.0147	0.1291
chrMT	16571	18664	1.1263	1.2461
chrX	155270560	3918973	0.0252	0.191
chrY	59373566	206208	0.0035	0.0956

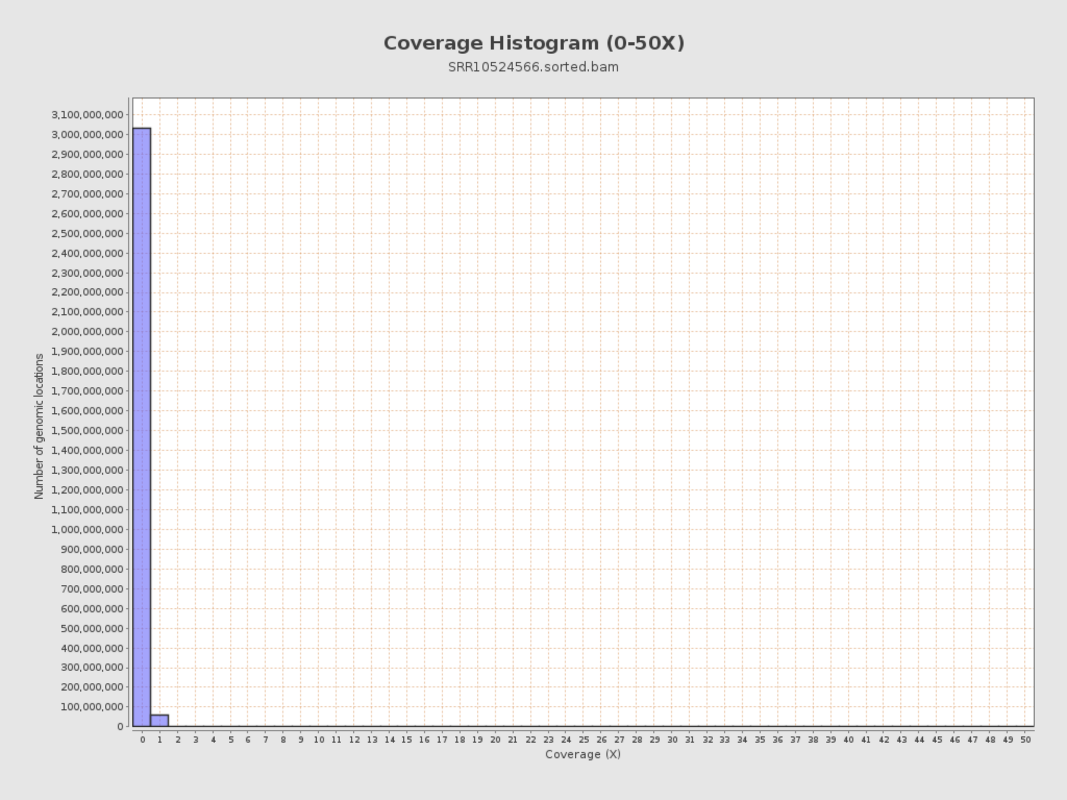
3. Results : Coverage across reference



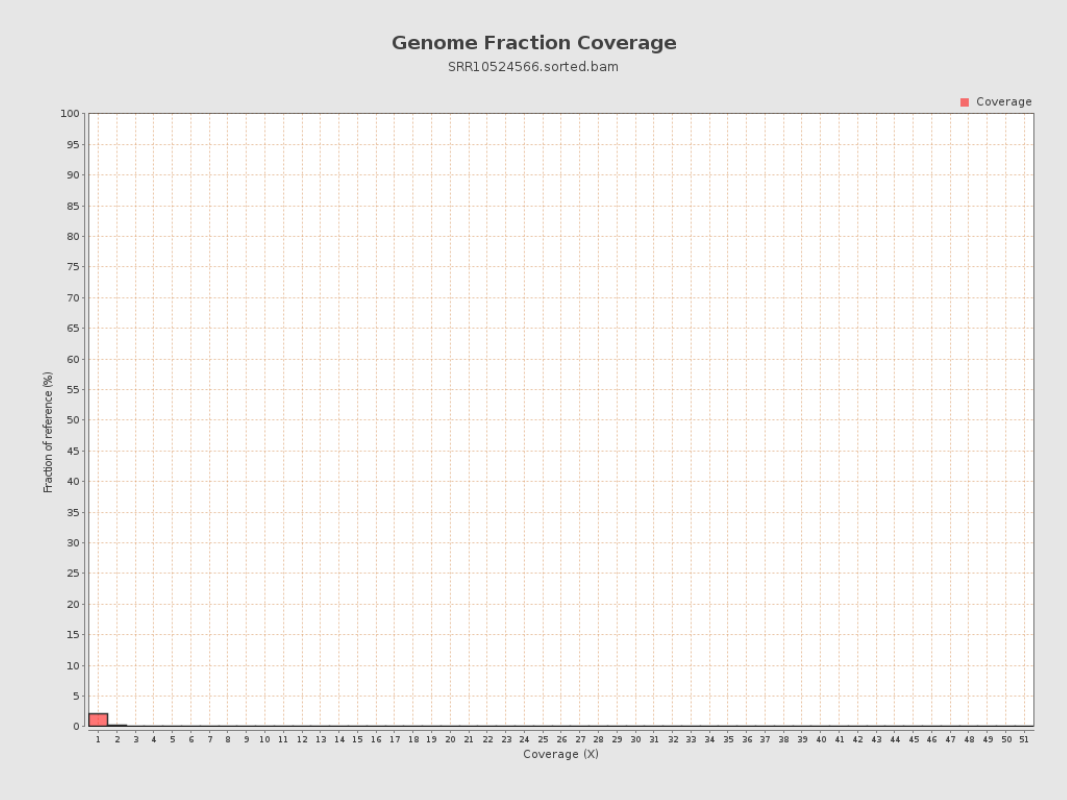
4. Results : Coverage Histogram



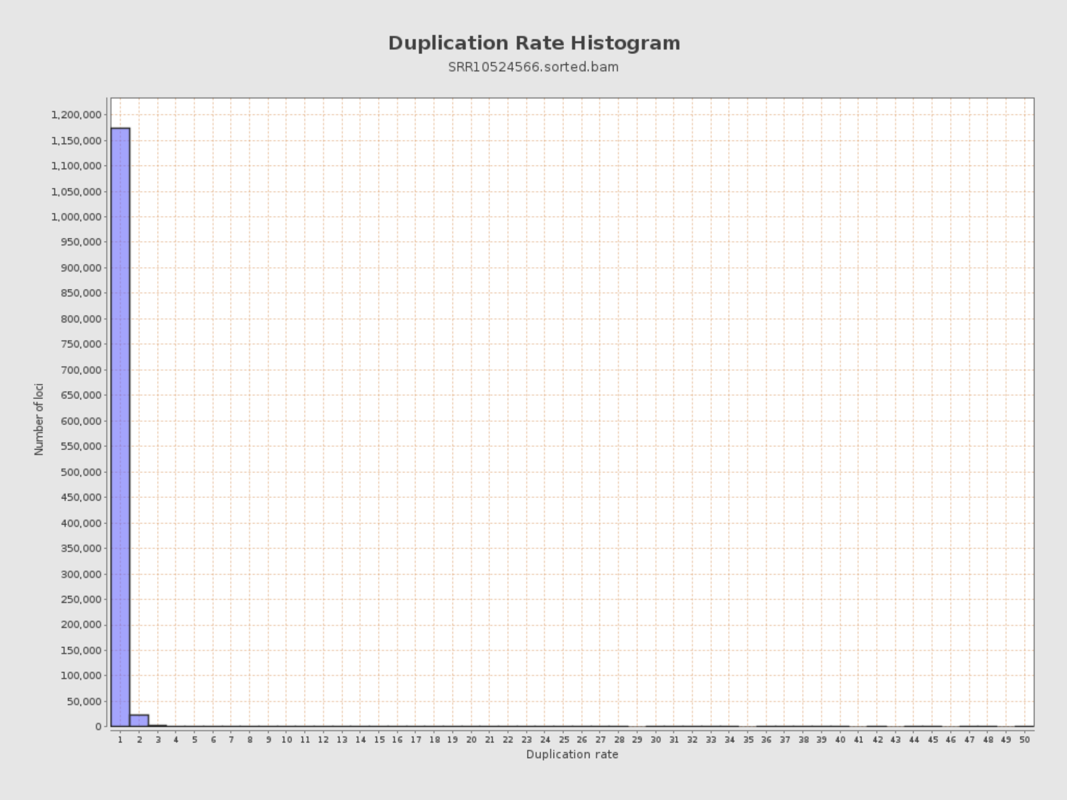
5. Results : Coverage Histogram (0-50X)



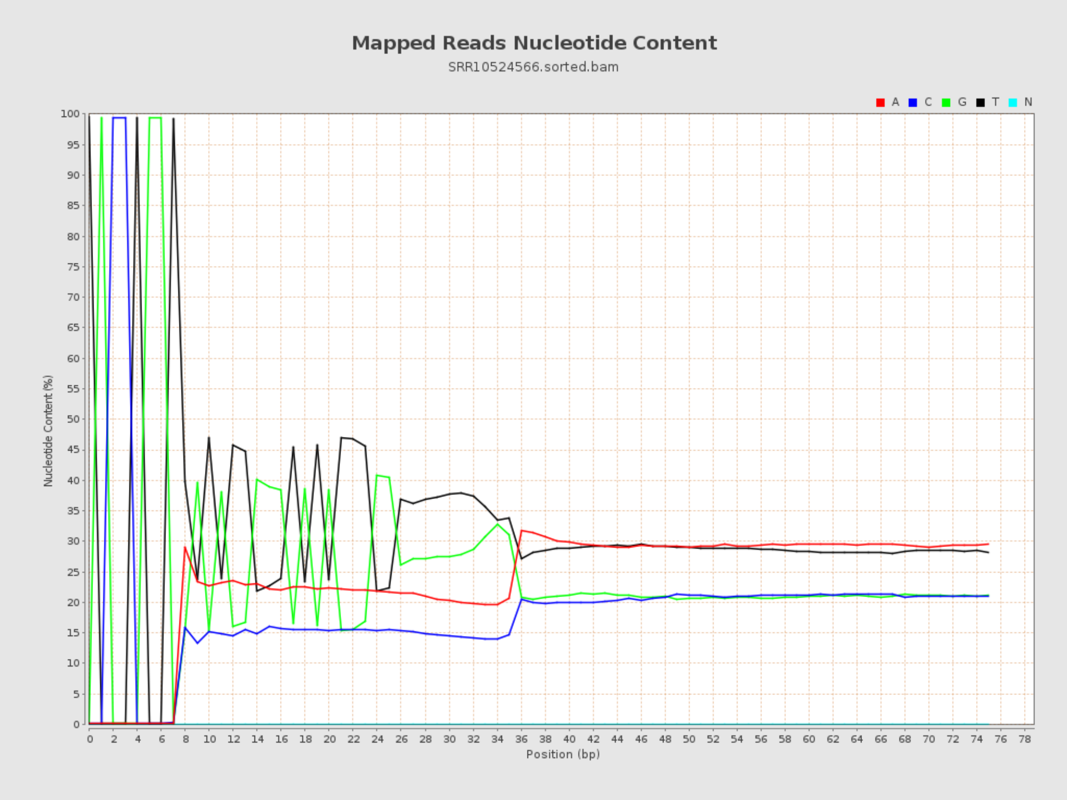
6. Results : Genome Fraction Coverage



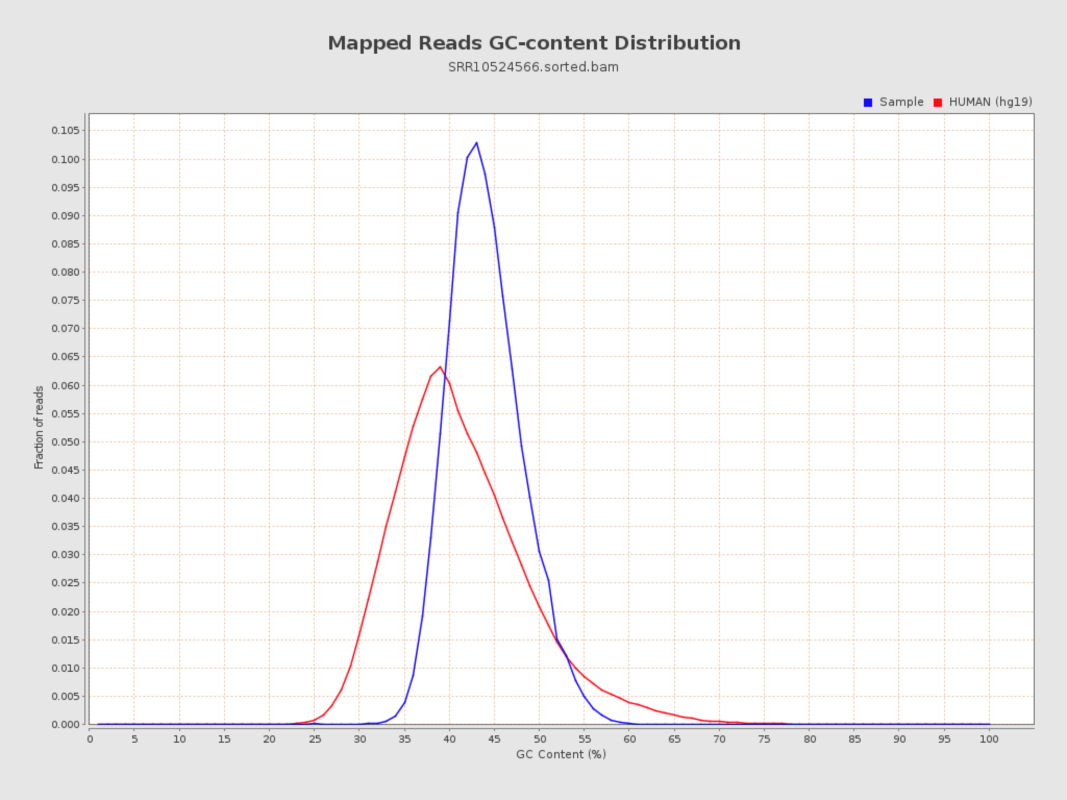
7. Results : Duplication Rate Histogram



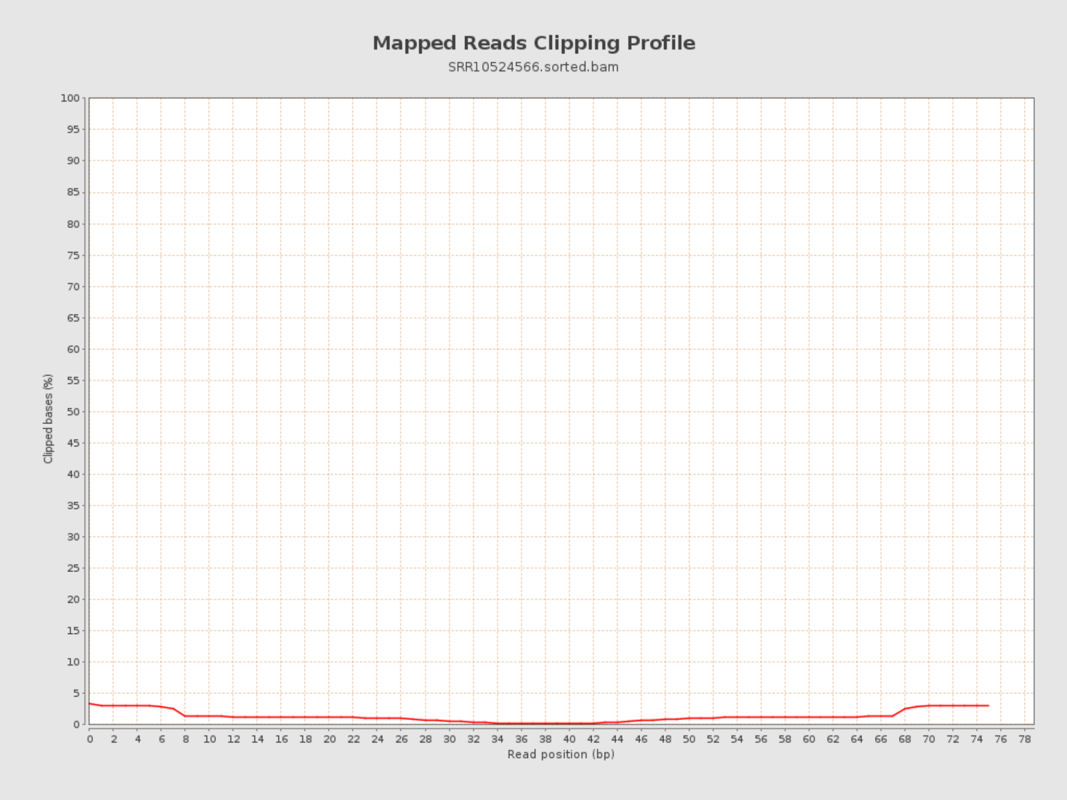
8. Results : Mapped Reads Nucleotide Content



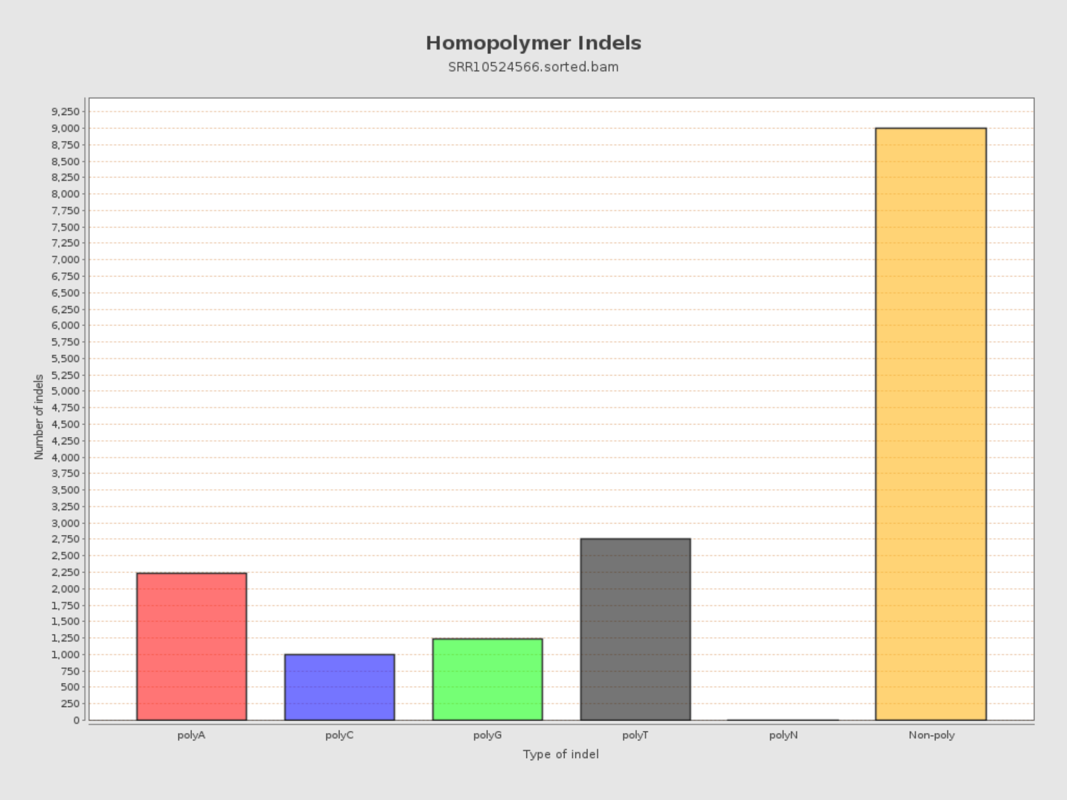
9. Results : Mapped Reads GC-content Distribution



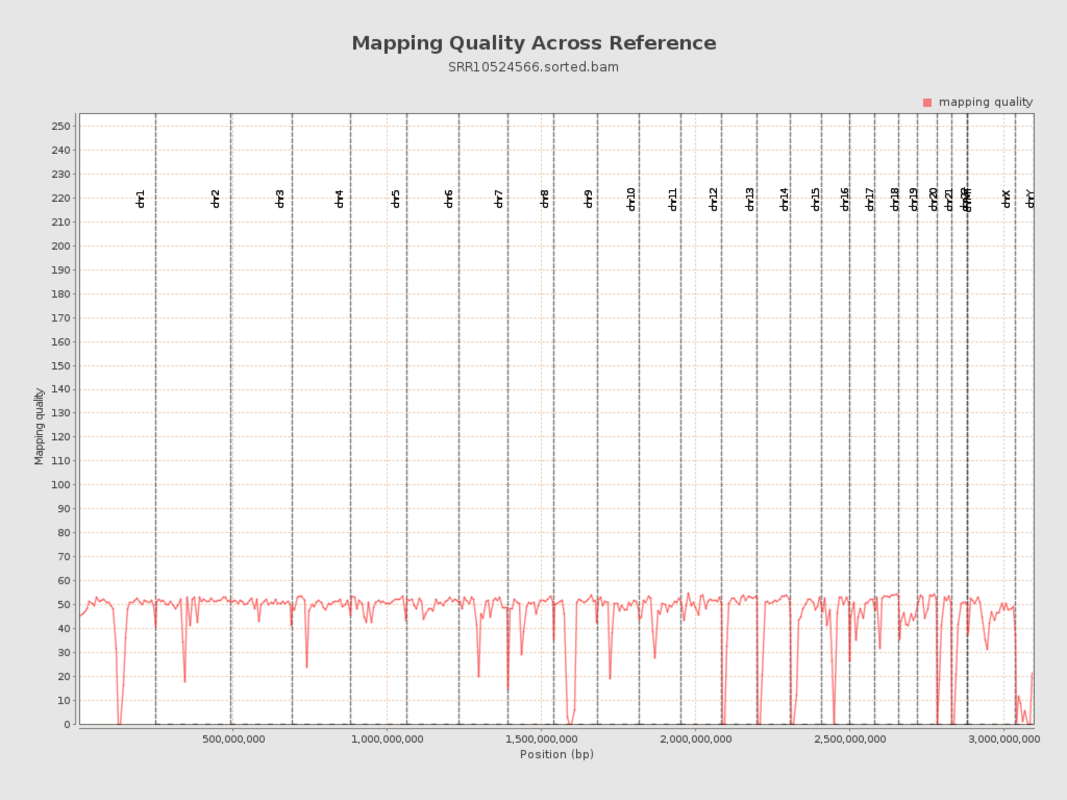
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram