Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:21:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524884.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_SRR10524884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524884.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:21:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,702,931
Mapped reads	1,573,065 / 92.37%
Unmapped reads	129,866 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,409 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	63,140 / 3.71%
Duplication rate	2.97%
Clipped reads	1,573,522 / 92.4%

2.2. ACGT Content

Number/percentage of A's	23,954,912 / 26.04%
Number/percentage of C's	15,342,975 / 16.68%
Number/percentage of T's	29,763,182 / 32.36%
Number/percentage of G's	22,902,122 / 24.9%
Number/percentage of N's	11,903 / 0.01%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.2946

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

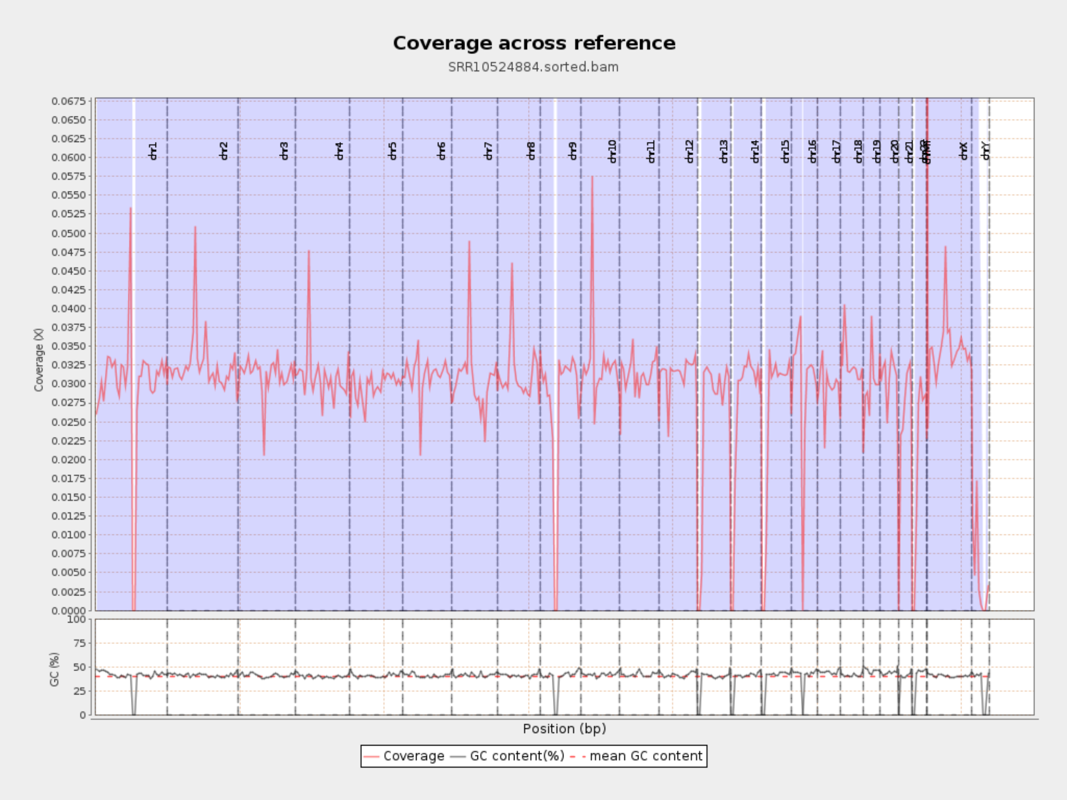
General error rate	0.5%
Mismatches	449,350
Insertions	6,881
Mapped reads with at least one insertion	0.44%
Deletions	17,696
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.2%

2.6. Chromosome stats

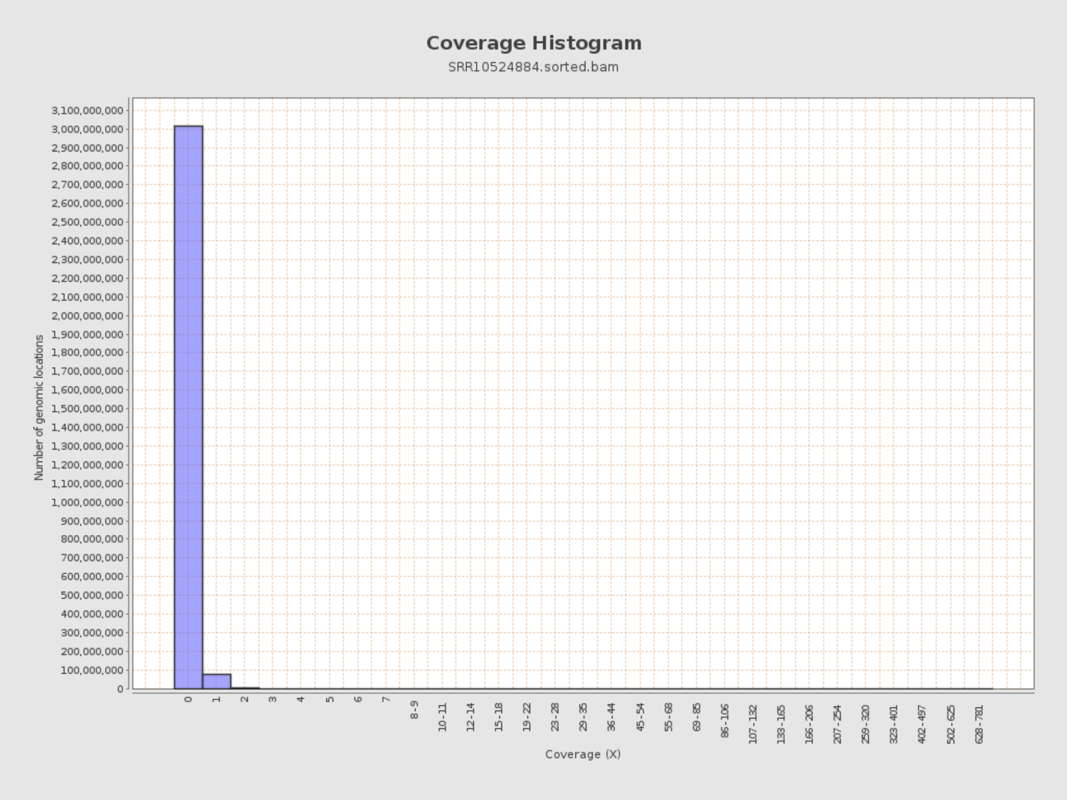
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7382592	0.0296	0.5844
chr2	243199373	7910061	0.0325	0.3108
chr3	198022430	6185173	0.0312	0.1909
chr4	191154276	5944049	0.0311	0.2128
chr5	180915260	5409629	0.0299	0.1891
chr6	171115067	5328433	0.0311	0.2083
chr7	159138663	4892891	0.0307	0.3623

chr8	146364022	4598035	0.0314	0.2902
chr9	141213431	3844873	0.0272	0.2562
chr10	135534747	4439583	0.0328	0.2781
chr11	135006516	4231035	0.0313	0.2699
chr12	133851895	4207746	0.0314	0.1946
chr13	115169878	2913055	0.0253	0.1737
chr14	107349540	2839885	0.0265	0.187
chr15	102531392	2634421	0.0257	0.1732
chr16	90354753	2659433	0.0294	0.2016
chr17	81195210	2396306	0.0295	0.2011
chr18	78077248	2554727	0.0327	0.528
chr19	59128983	1778079	0.0301	0.3823
chr20	63025520	1933018	0.0307	0.1943
chr21	48129895	1224251	0.0254	0.1924
chr22	51304566	1028431	0.02	0.153
chrMT	16571	6985	0.4215	0.7321
chrX	155270560	5376815	0.0346	0.2311
chrY	59373566	283599	0.0048	0.1349

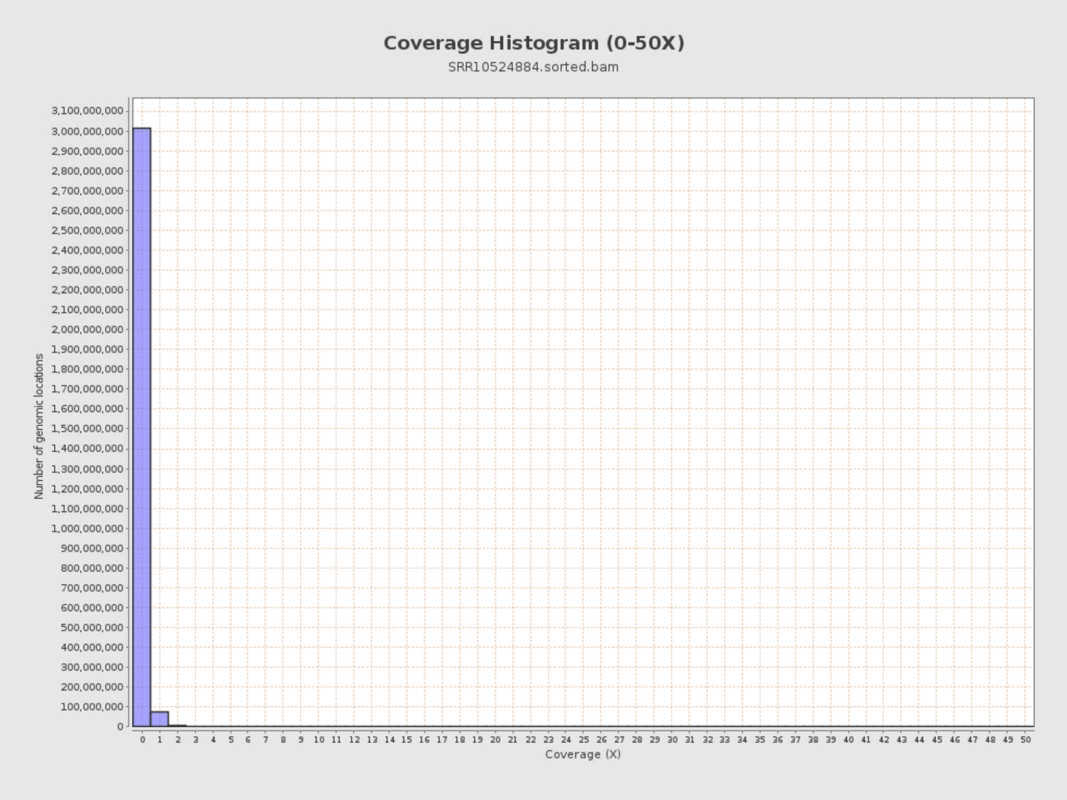
3. Results : Coverage across reference



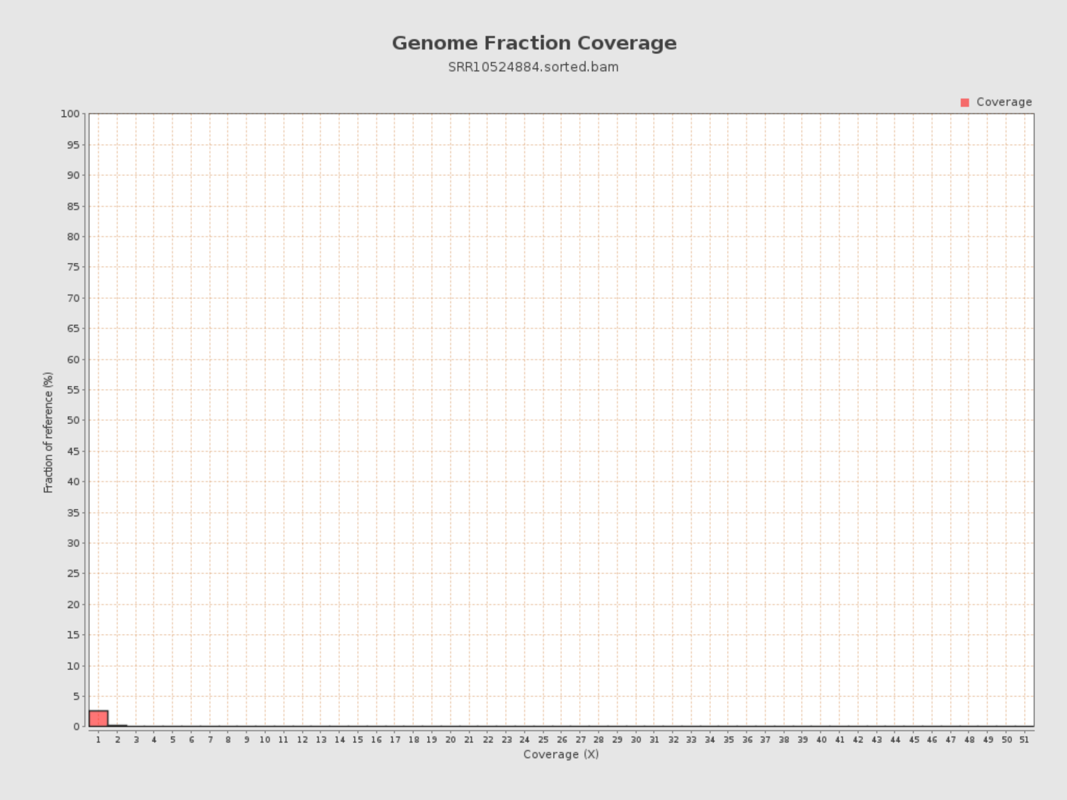
4. Results : Coverage Histogram



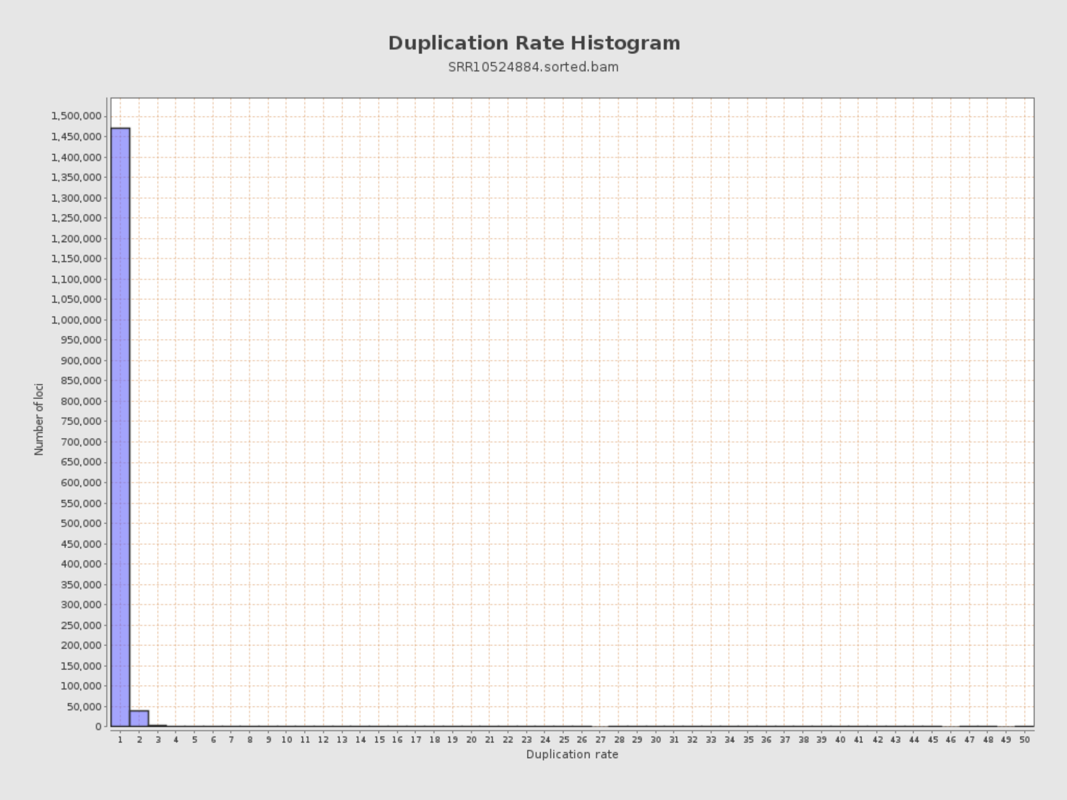
5. Results : Coverage Histogram (0-50X)



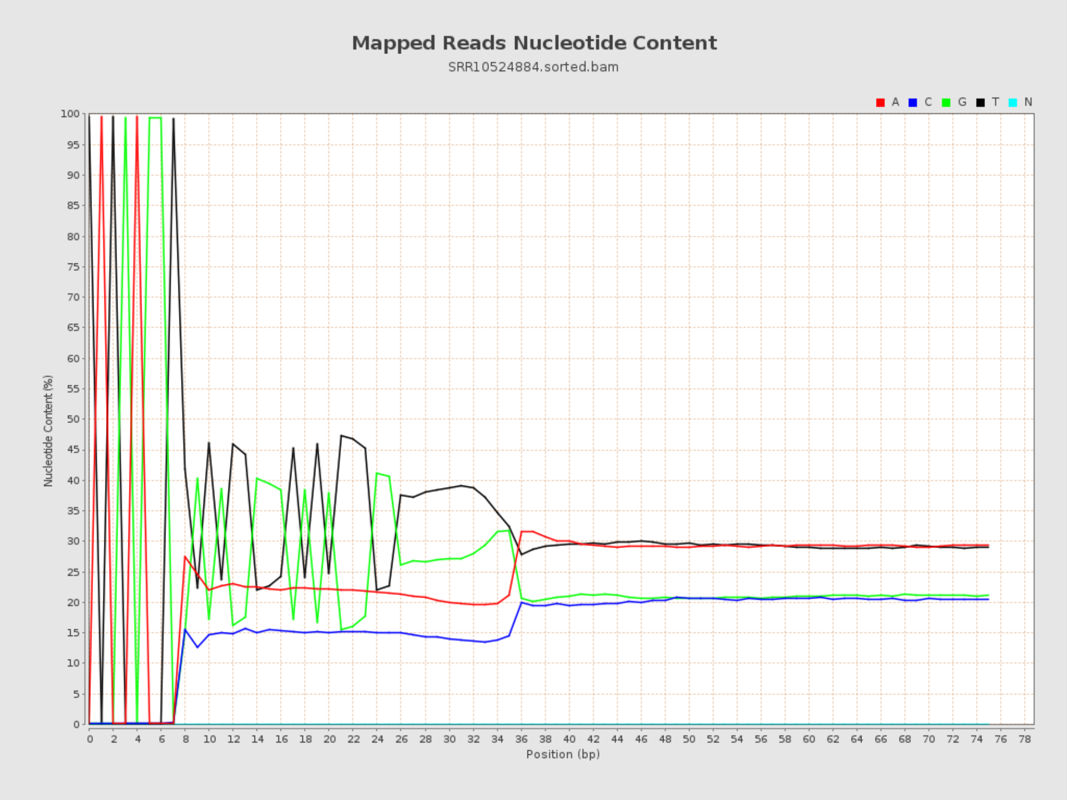
6. Results : Genome Fraction Coverage



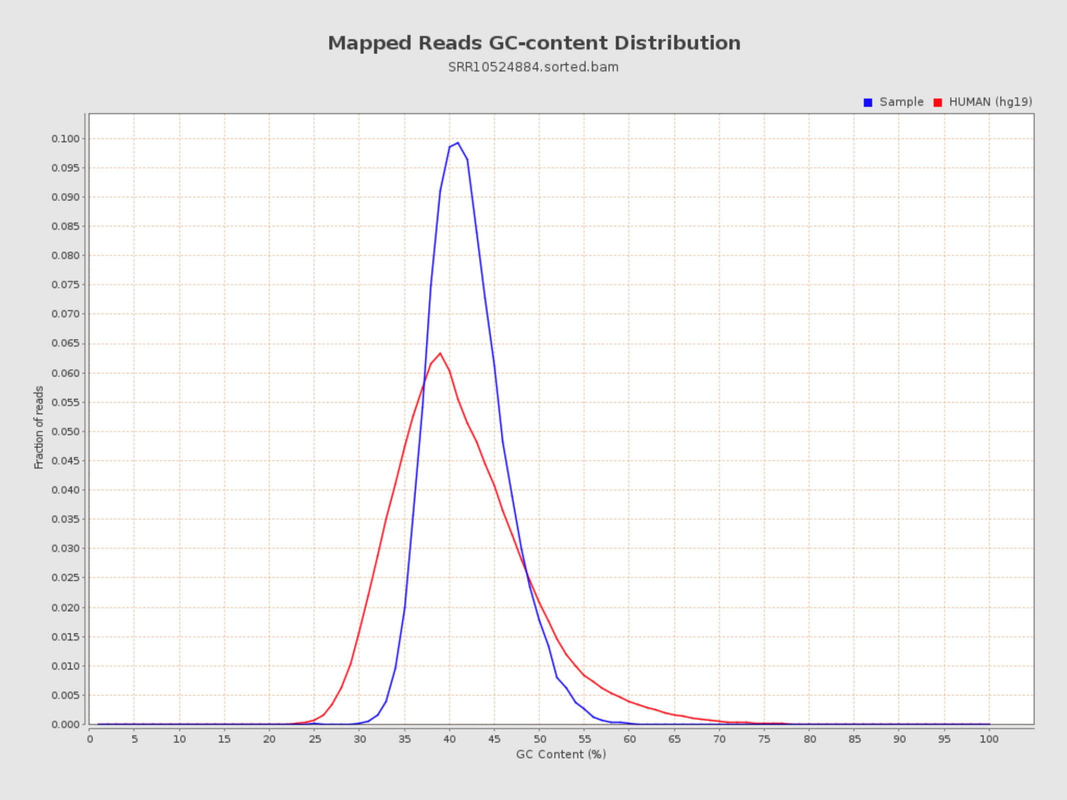
7. Results : Duplication Rate Histogram



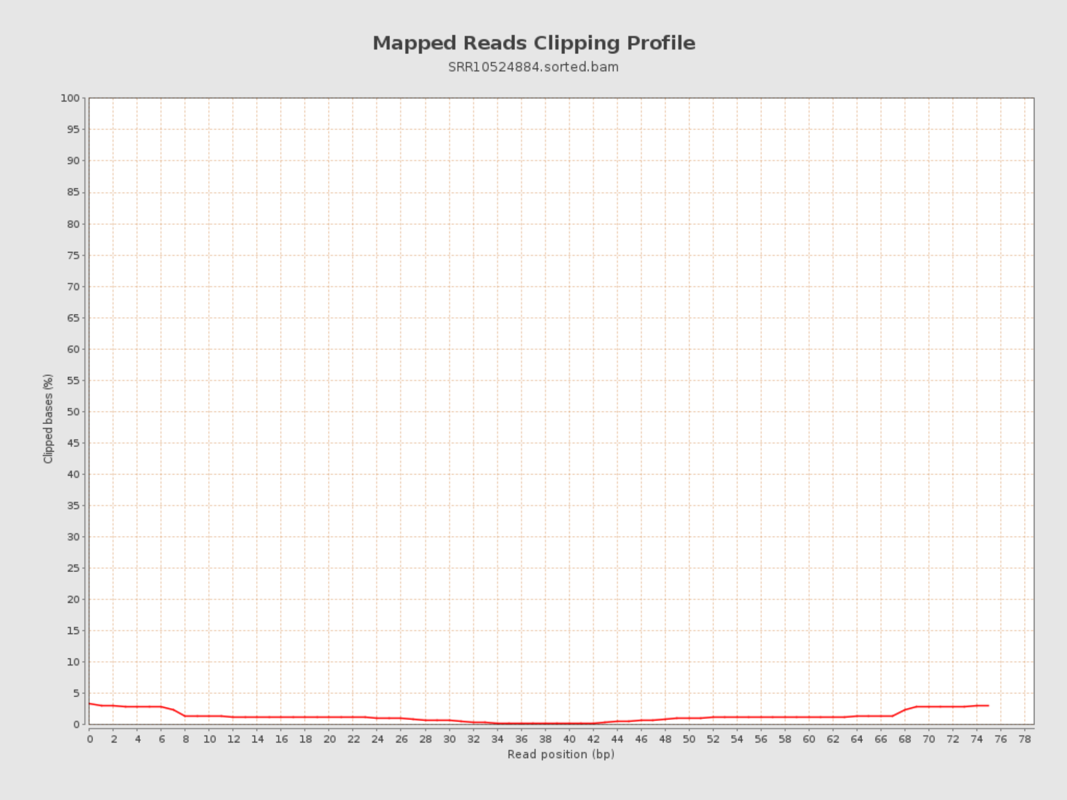
8. Results : Mapped Reads Nucleotide Content



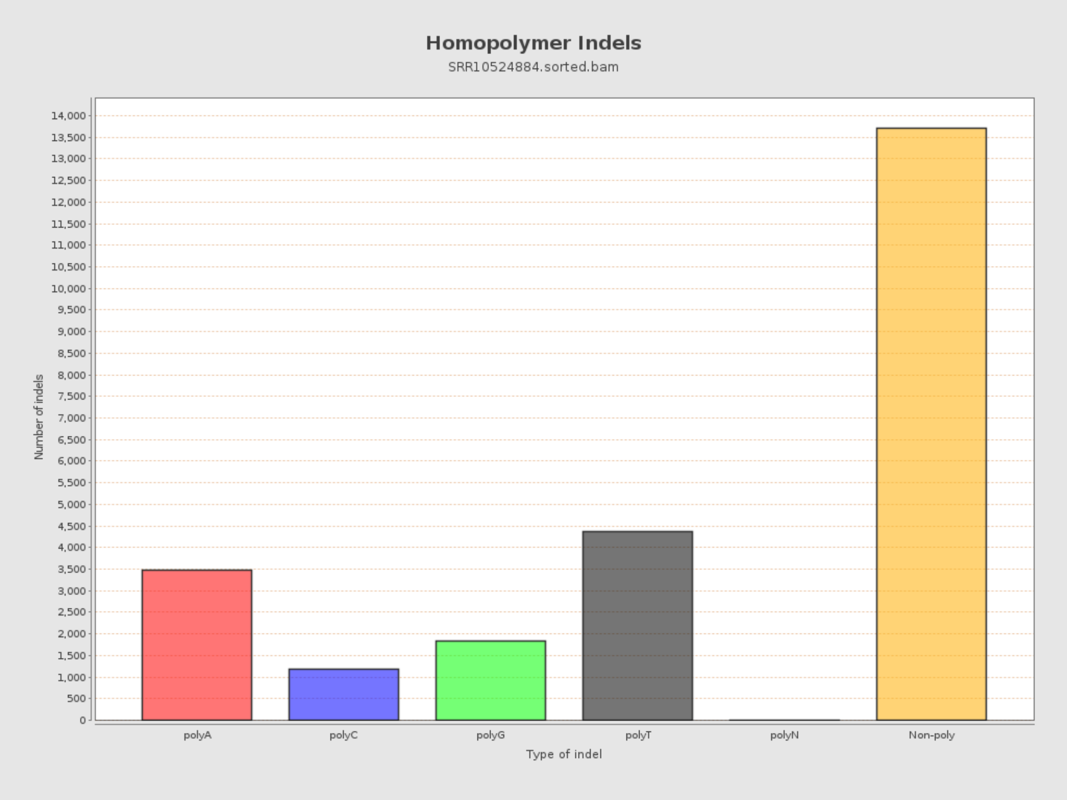
9. Results : Mapped Reads GC-content Distribution



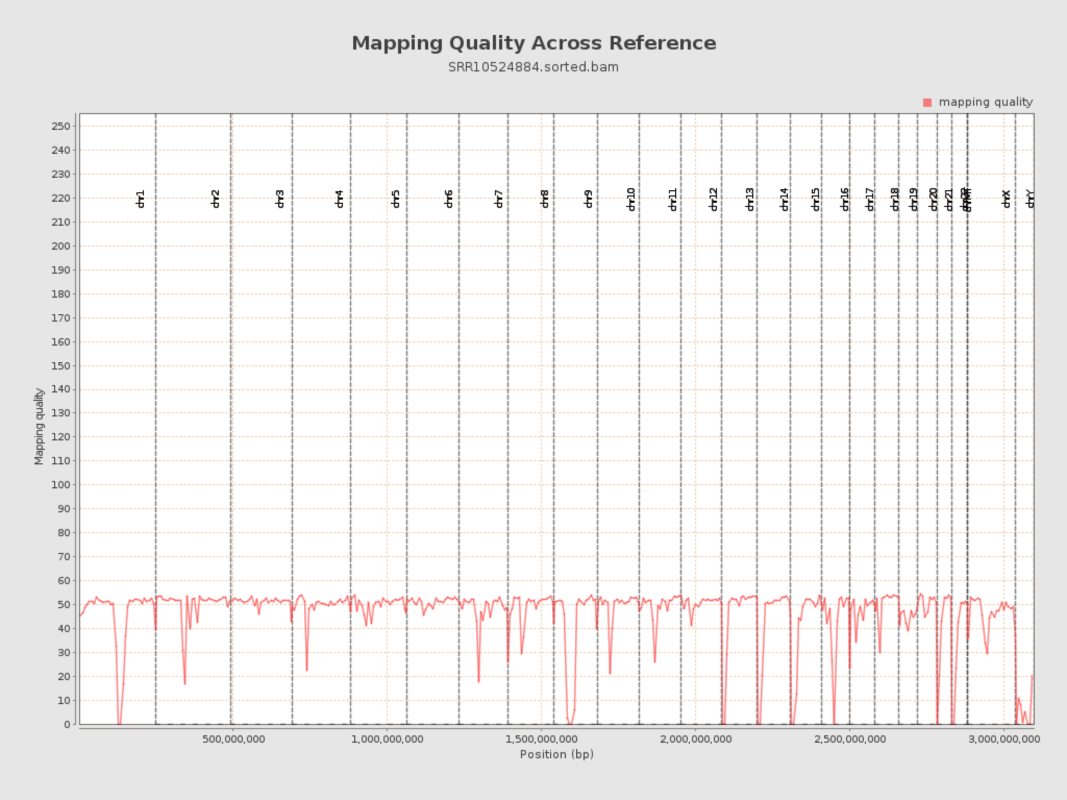
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram