Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:19:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524883.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_SRR10524883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:19:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,561,901
Mapped reads	1,444,510 / 92.48%
Unmapped reads	117,391 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,472 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	53,915 / 3.45%
Duplication rate	2.71%
Clipped reads	1,448,163 / 92.72%

2.2. ACGT Content

Number/percentage of A's	20,535,140 / 24.31%
Number/percentage of C's	14,864,348 / 17.59%
Number/percentage of T's	27,965,095 / 33.1%
Number/percentage of G's	21,108,905 / 24.99%
Number/percentage of N's	10,629 / 0.01%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2763

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

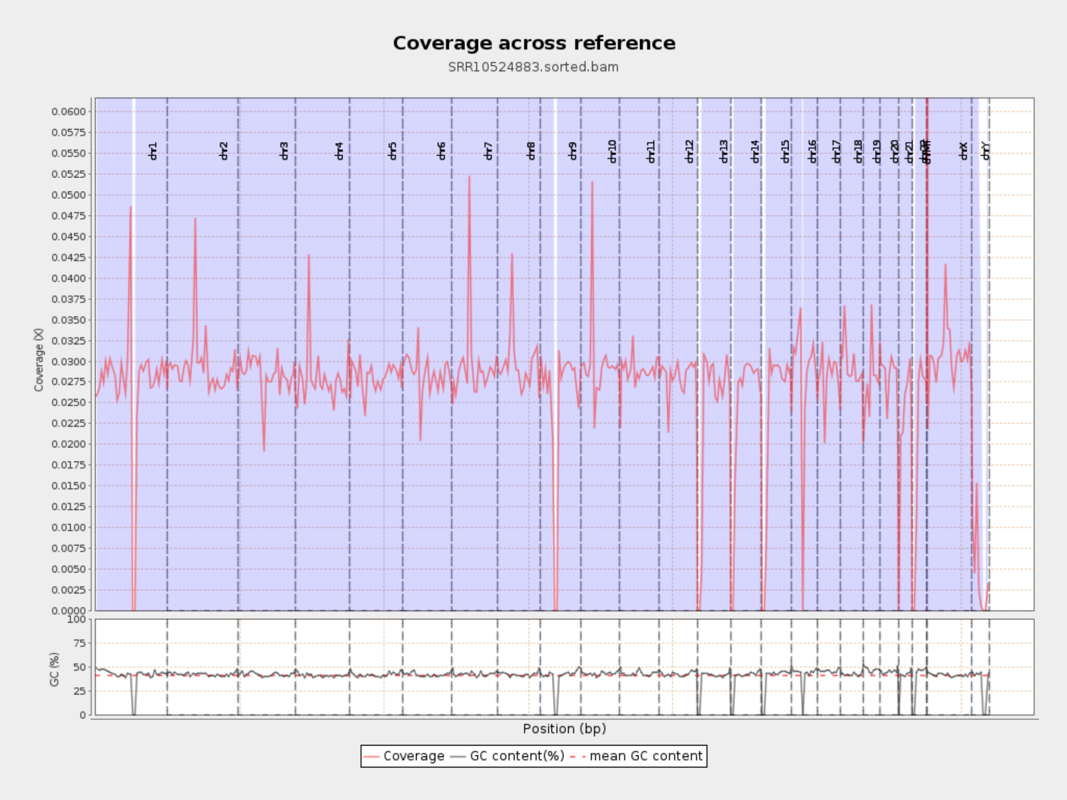
General error rate	0.5%
Mismatches	411,835
Insertions	4,940
Mapped reads with at least one insertion	0.34%
Deletions	15,712
Mapped reads with at least one deletion	1.08%
Homopolymer indels	46.4%

2.6. Chromosome stats

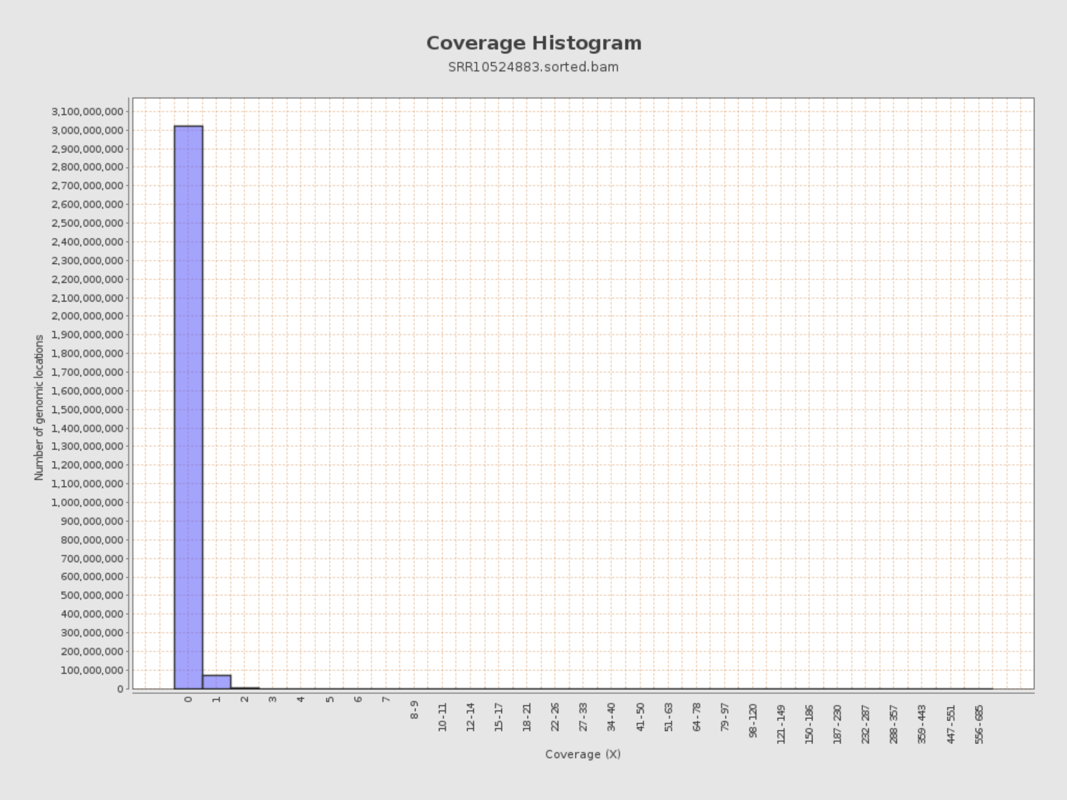
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6755090	0.0271	0.5258
chr2	243199373	7155718	0.0294	0.2881
chr3	198022430	5612230	0.0283	0.1813
chr4	191154276	5338688	0.0279	0.1994
chr5	180915260	5114501	0.0283	0.182
chr6	171115067	4868818	0.0285	0.1971
chr7	159138663	4700696	0.0295	0.3806

chr8	146364022	4359448	0.0298	0.2788
chr9	141213431	3525558	0.025	0.2353
chr10	135534747	4050638	0.0299	0.2577
chr11	135006516	3902013	0.0289	0.2504
chr12	133851895	3766944	0.0281	0.1846
chr13	115169878	2712451	0.0236	0.1652
chr14	107349540	2574147	0.024	0.176
chr15	102531392	2405469	0.0235	0.1653
chr16	90354753	2493153	0.0276	0.193
chr17	81195210	2281249	0.0281	0.1939
chr18	78077248	2313807	0.0296	0.5024
chr19	59128983	1643198	0.0278	0.3648
chr20	63025520	1780222	0.0282	0.1834
chr21	48129895	1098813	0.0228	0.1809
chr22	51304566	1008771	0.0197	0.1501
chrMT	16571	9545	0.576	0.9564
chrX	155270560	4781740	0.0308	0.215
chrY	59373566	256217	0.0043	0.1238

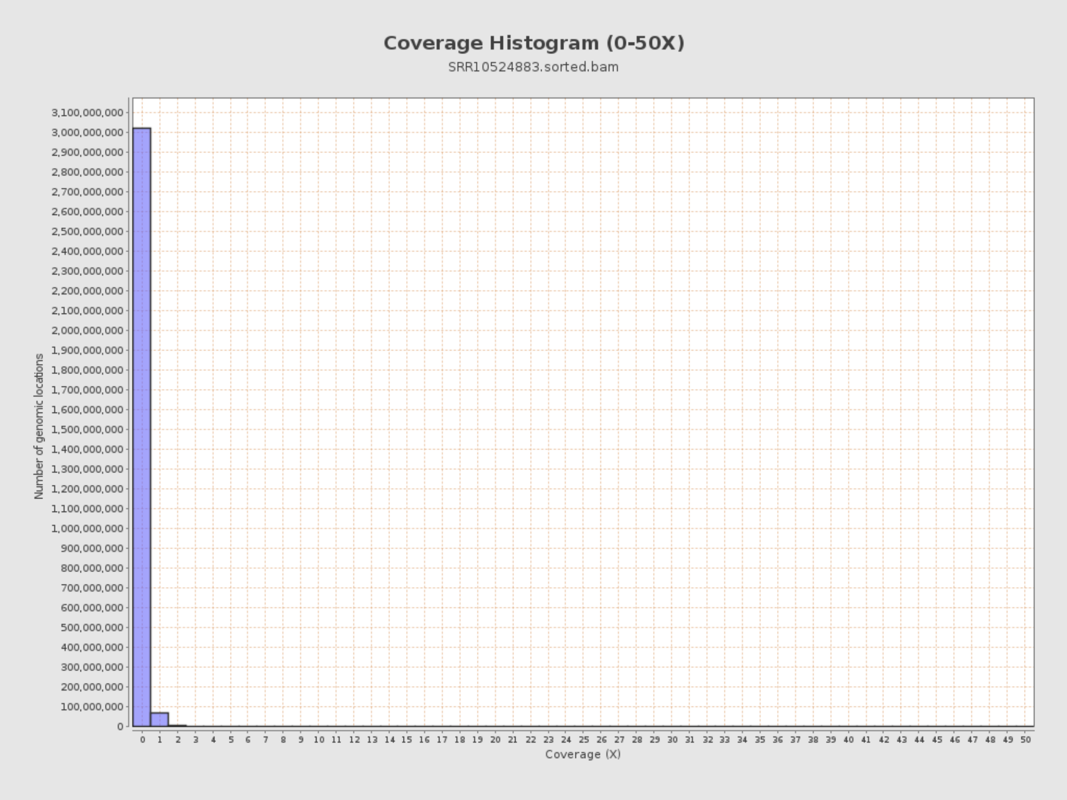
3. Results : Coverage across reference



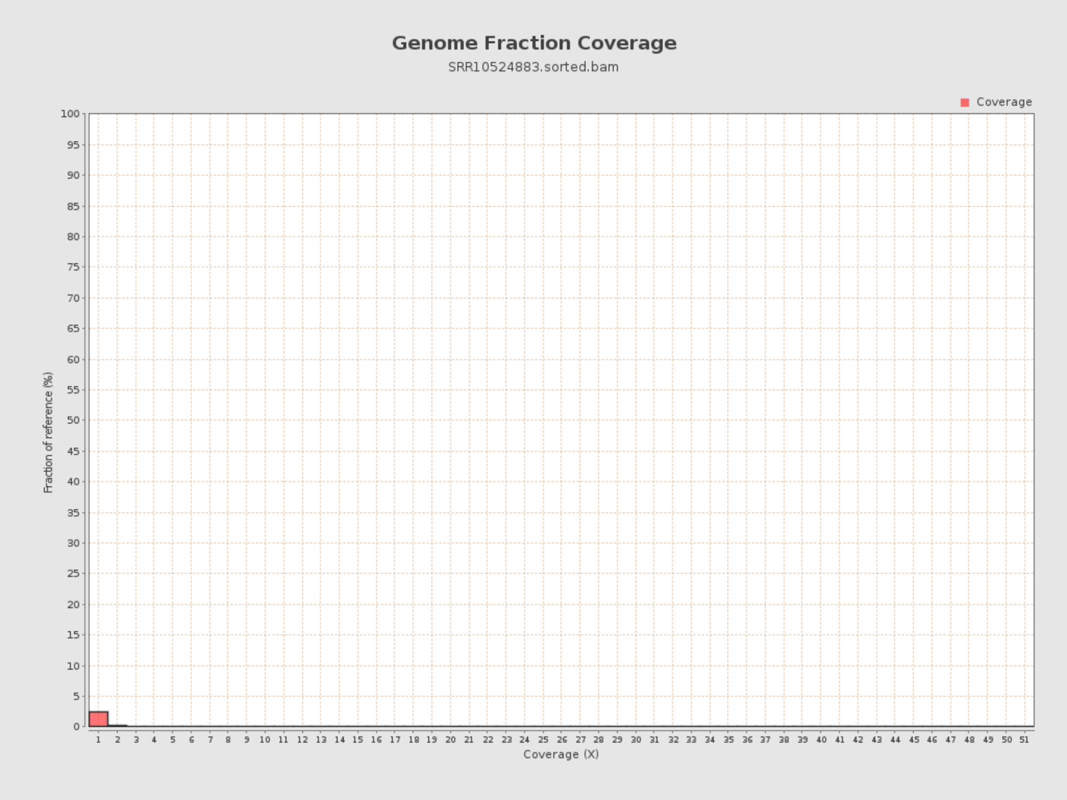
4. Results : Coverage Histogram



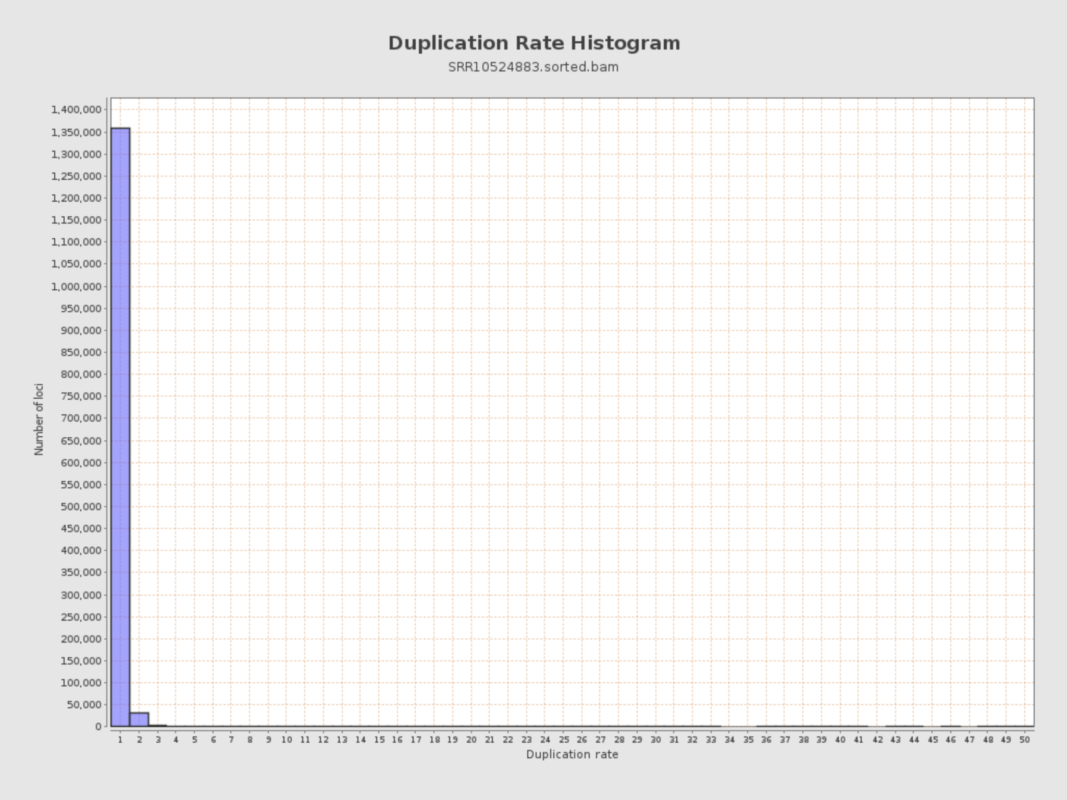
5. Results : Coverage Histogram (0-50X)



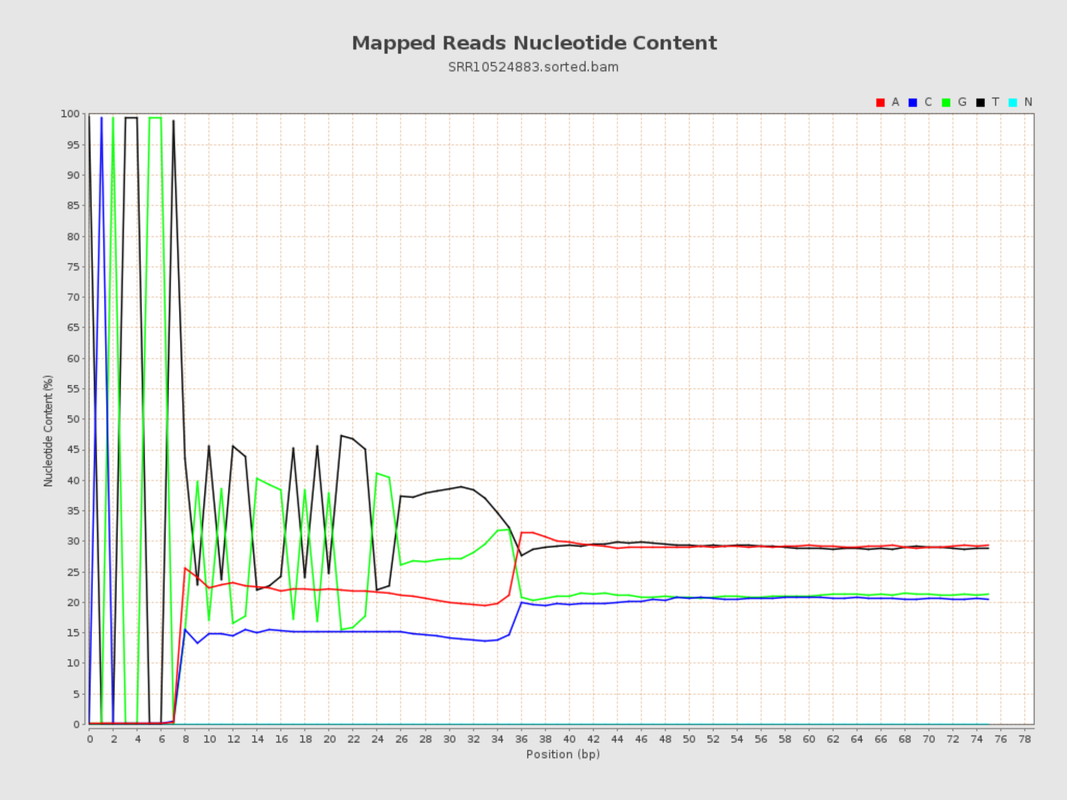
6. Results : Genome Fraction Coverage



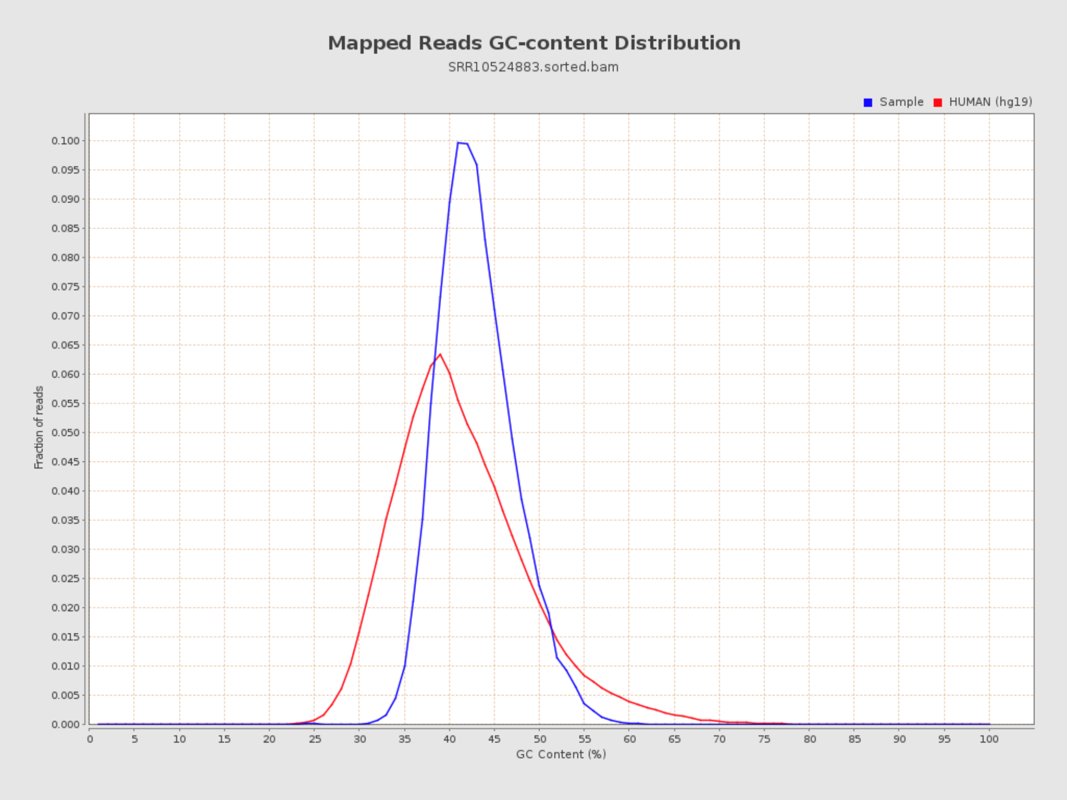
7. Results : Duplication Rate Histogram



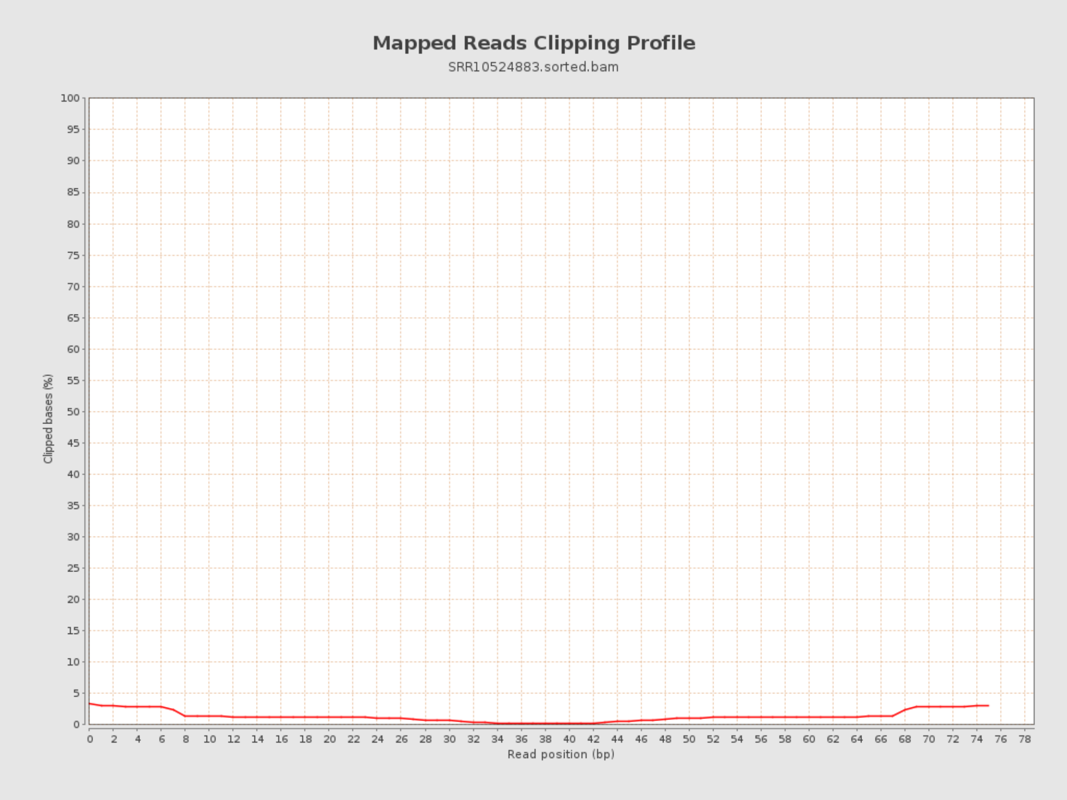
8. Results : Mapped Reads Nucleotide Content



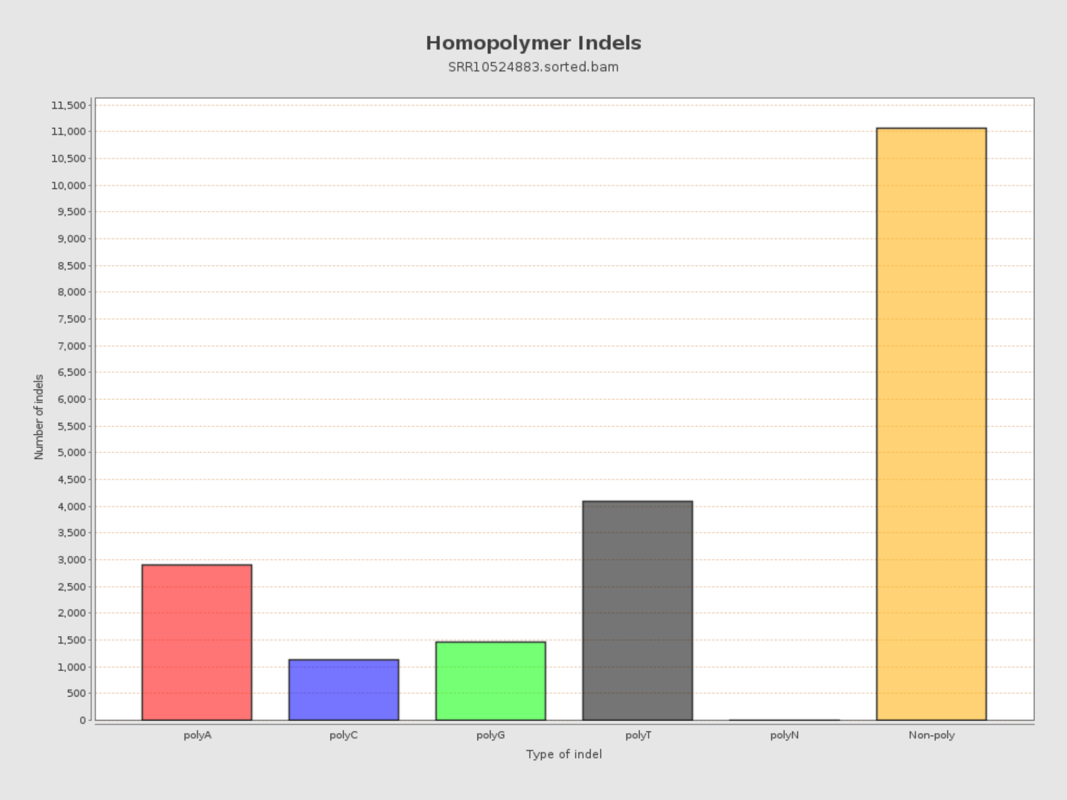
9. Results : Mapped Reads GC-content Distribution



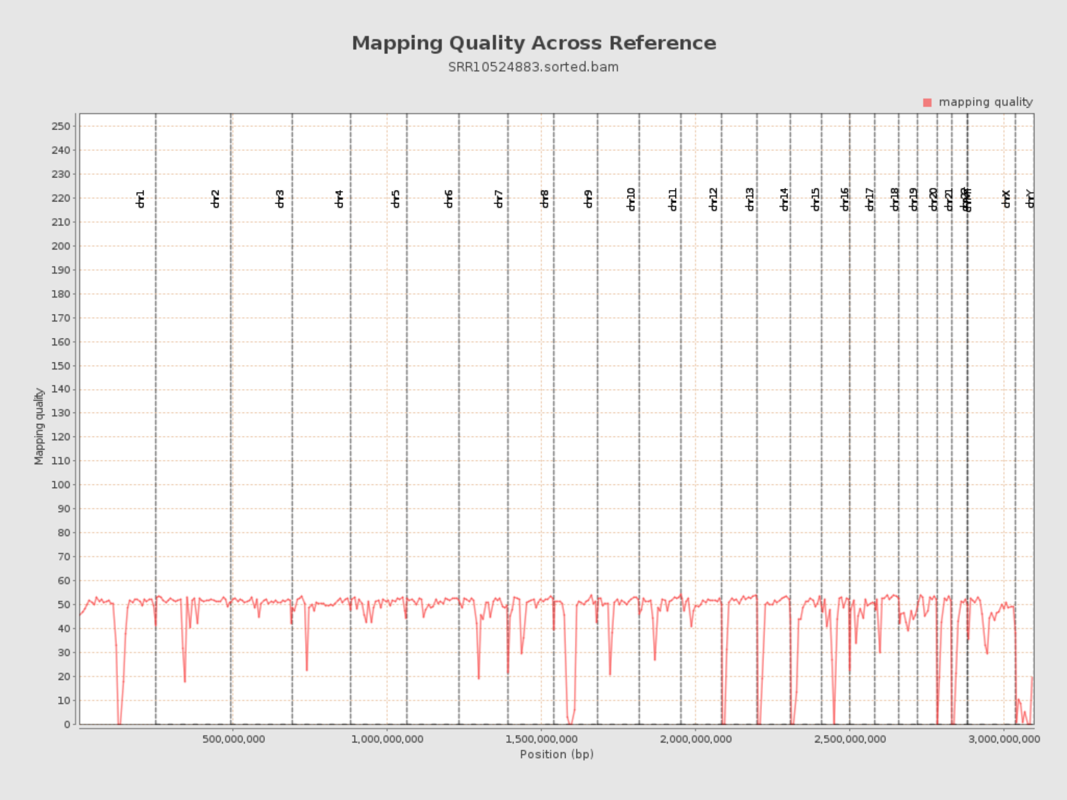
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram