Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:29:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524886.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_SRR10524886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524886.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:29:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,118,238
Mapped reads	2,858,273 / 91.66%
Unmapped reads	259,965 / 8.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,034 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	166,911 / 5.35%
Duplication rate	4.31%
Clipped reads	2,858,109 / 91.66%

2.2. ACGT Content

Number/percentage of A's	41,378,391 / 24.85%
Number/percentage of C's	33,488,284 / 20.11%
Number/percentage of T's	53,824,828 / 32.32%
Number/percentage of G's	37,809,412 / 22.71%
Number/percentage of N's	22,232 / 0.01%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0538

Standard Deviation	0.4956

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

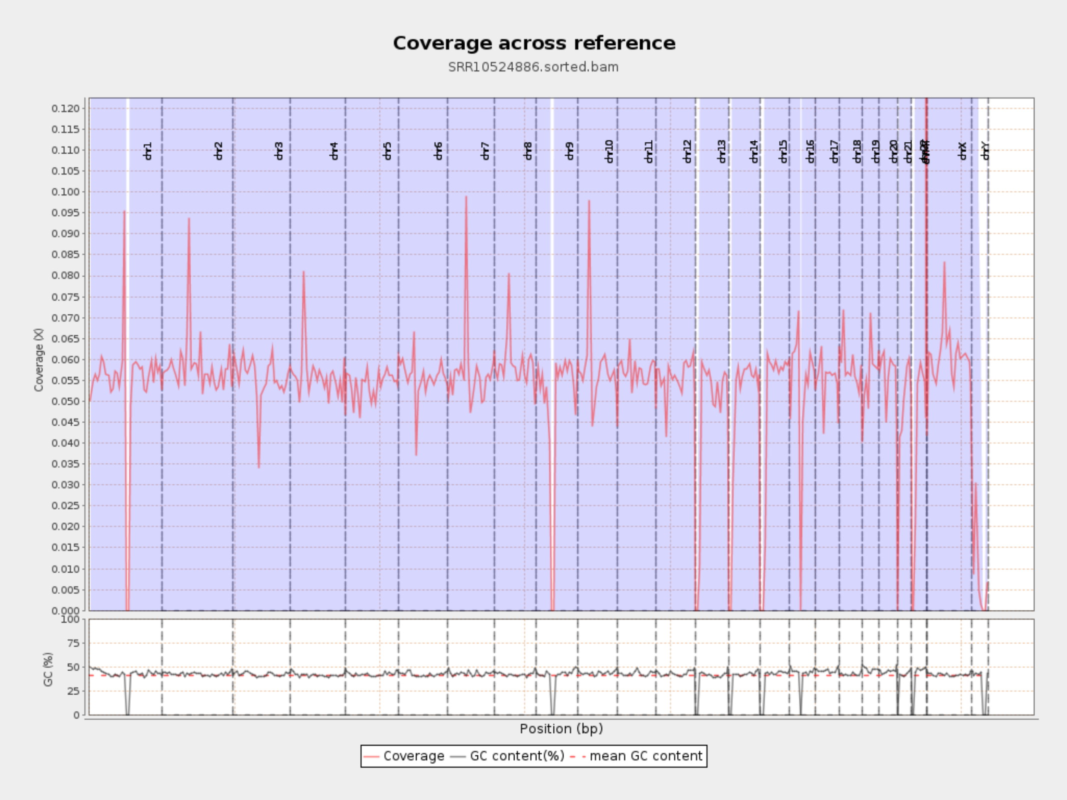
General error rate	0.51%
Mismatches	824,698
Insertions	13,967
Mapped reads with at least one insertion	0.49%
Deletions	31,609
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.82%

2.6. Chromosome stats

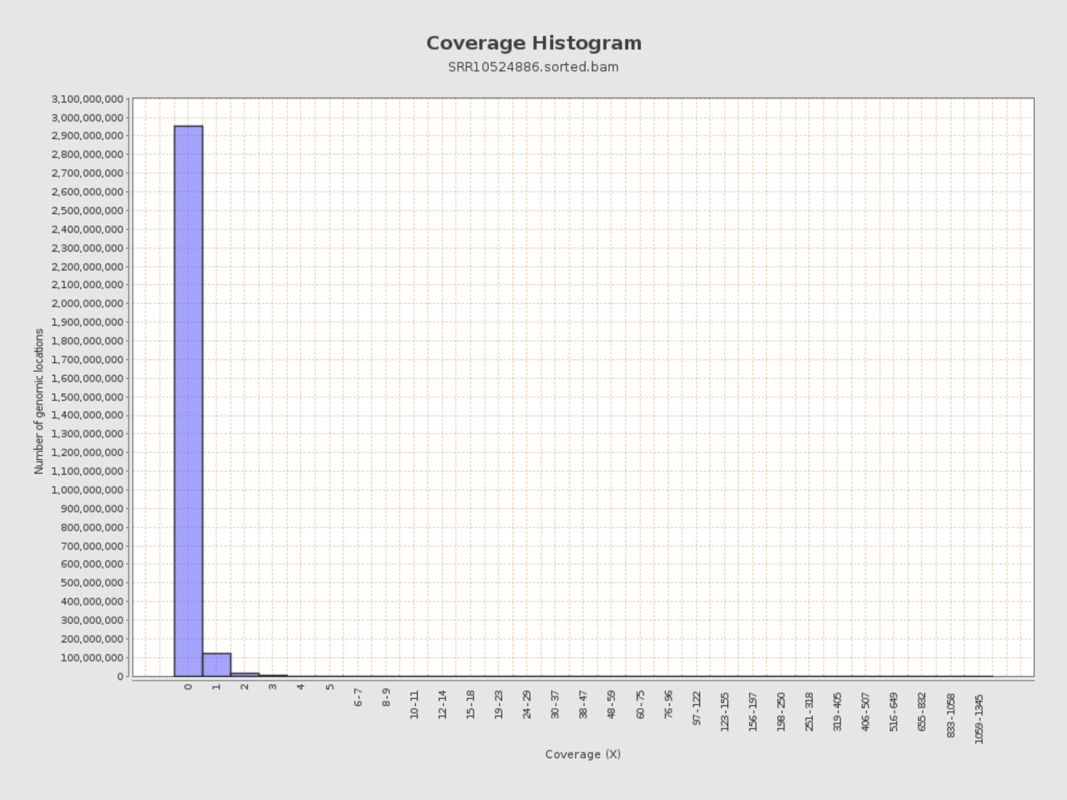
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13444252	0.0539	1.0325
chr2	243199373	14252887	0.0586	0.5477
chr3	198022430	11009315	0.0556	0.2692
chr4	191154276	10731894	0.0561	0.3165
chr5	180915260	9764832	0.054	0.2682
chr6	171115067	9564150	0.0559	0.3169
chr7	159138663	9075318	0.057	0.7128

chr8	146364022	8628732	0.059	0.4496
chr9	141213431	6899988	0.0489	0.4206
chr10	135534747	7892272	0.0582	0.4421
chr11	135006516	7697591	0.057	0.4357
chr12	133851895	7468600	0.0558	0.2813
chr13	115169878	5234098	0.0454	0.2451
chr14	107349540	5092895	0.0474	0.2743
chr15	102531392	4848359	0.0473	0.2554
chr16	90354753	4824567	0.0534	0.3057
chr17	81195210	4462250	0.055	0.3035
chr18	78077248	4565333	0.0585	0.9157
chr19	59128983	3349094	0.0566	0.6367
chr20	63025520	3570605	0.0567	0.2798
chr21	48129895	2219150	0.0461	0.2836
chr22	51304566	1994401	0.0389	0.2266
chrMT	16571	18081	1.0911	1.3017
chrX	155270560	9451209	0.0609	0.3459
chrY	59373566	513217	0.0086	0.2146

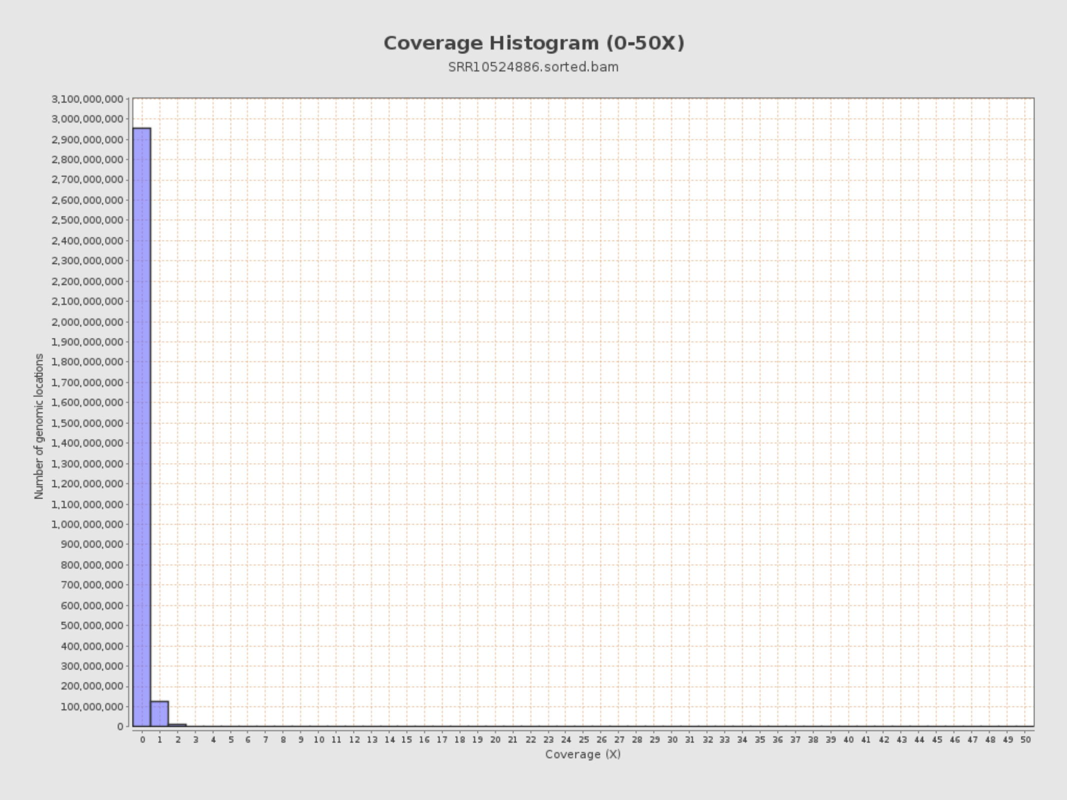
3. Results : Coverage across reference



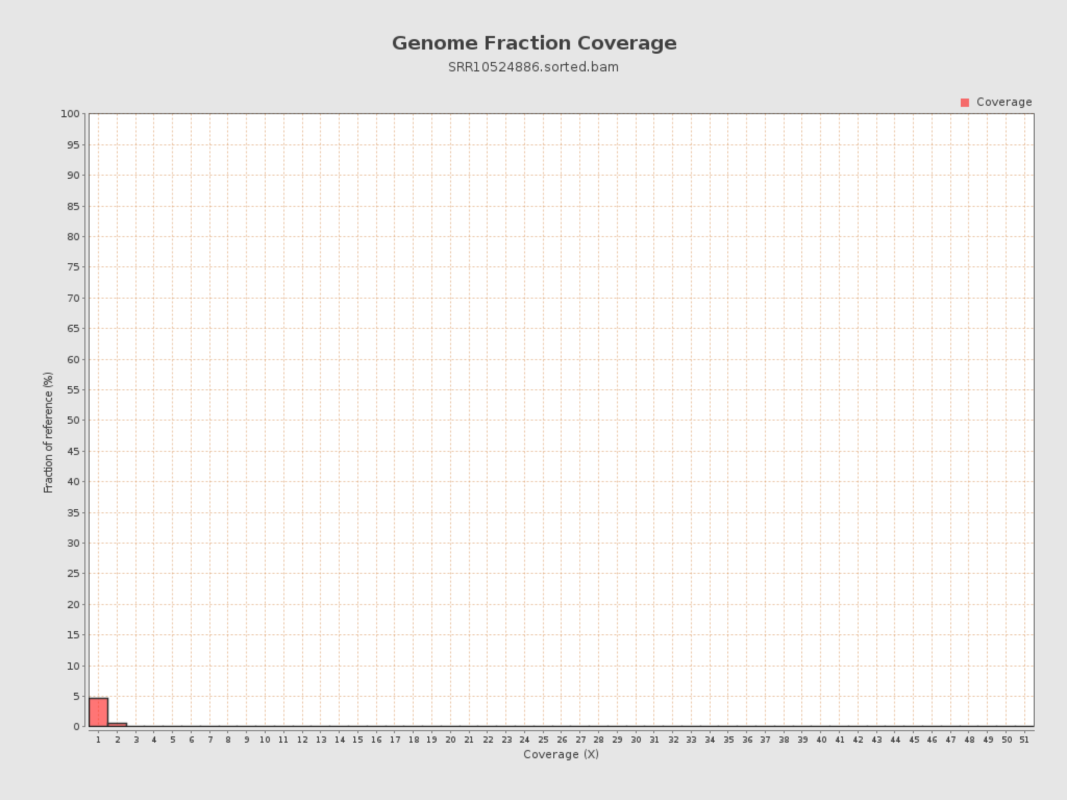
4. Results : Coverage Histogram



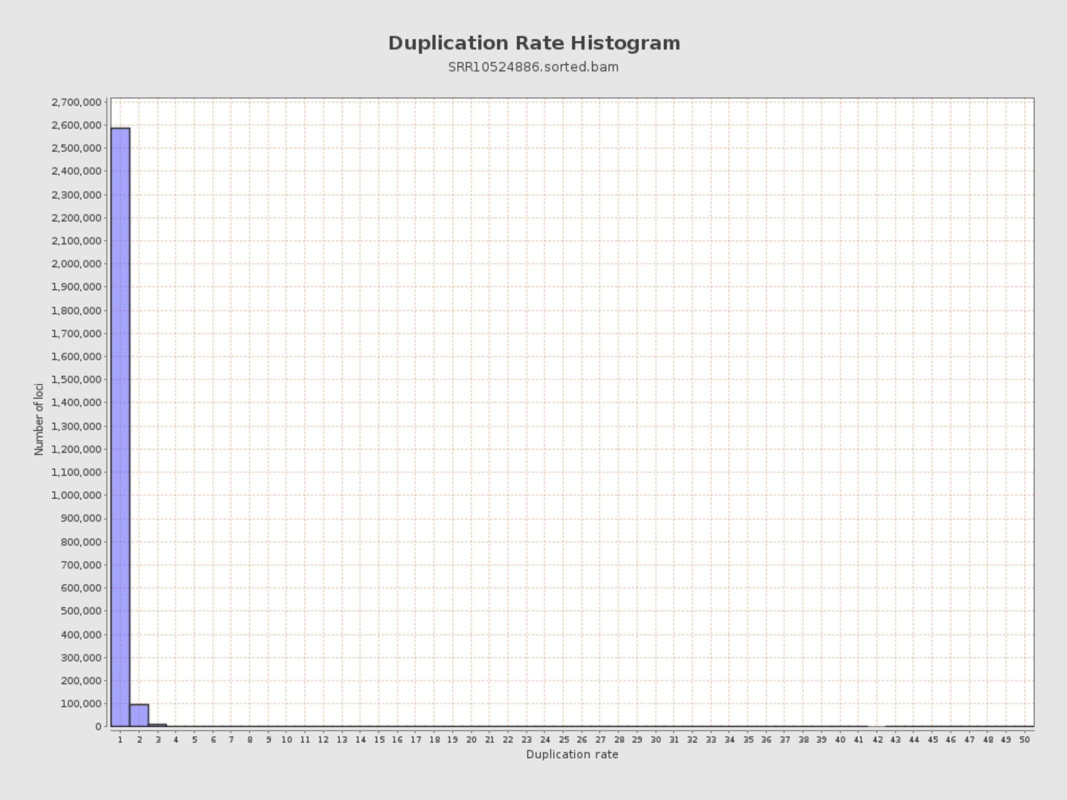
5. Results : Coverage Histogram (0-50X)



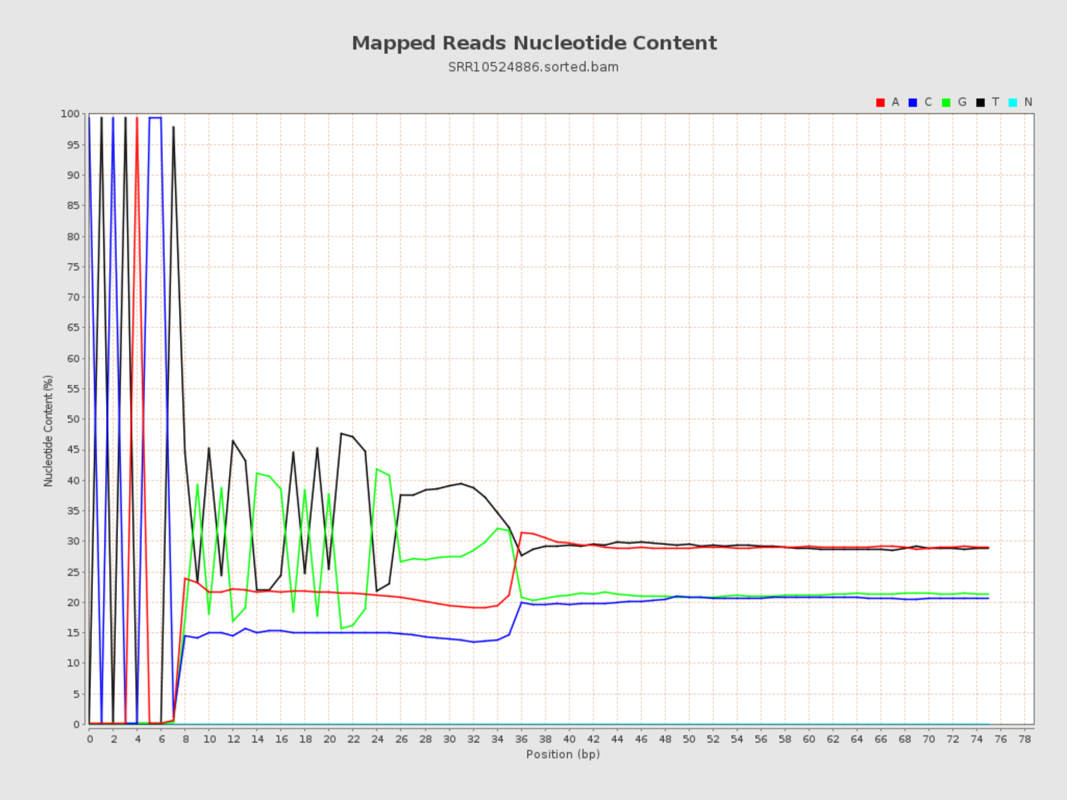
6. Results : Genome Fraction Coverage



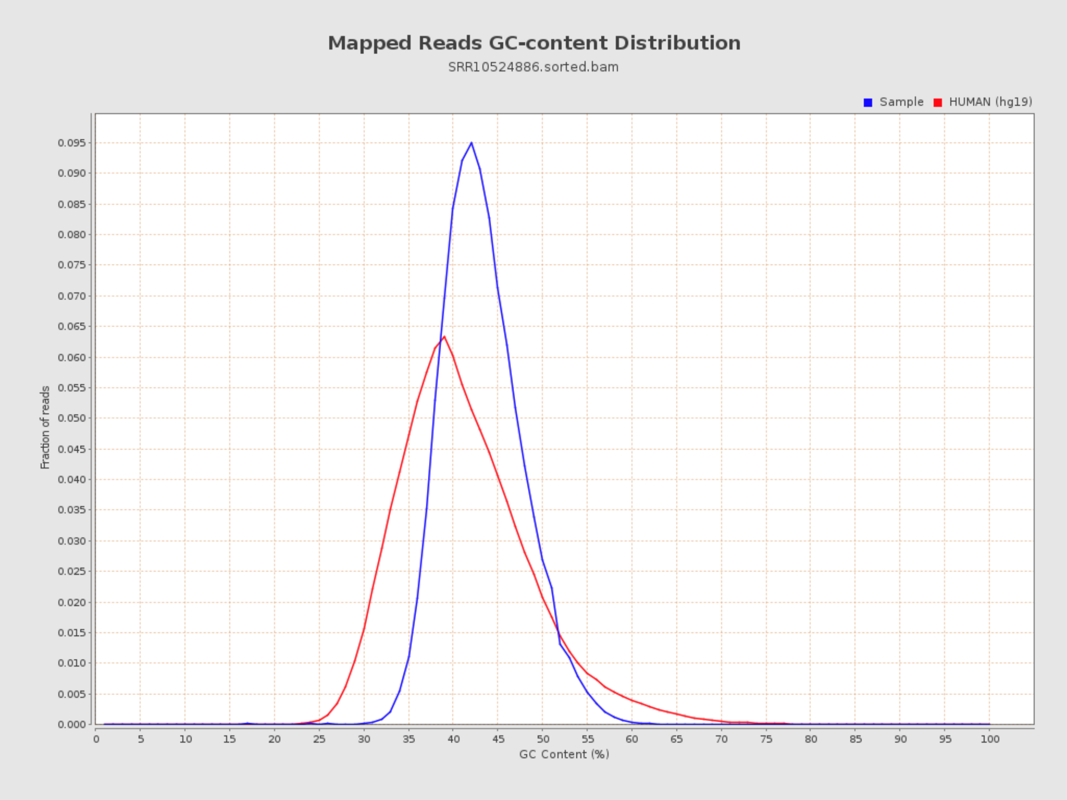
7. Results : Duplication Rate Histogram



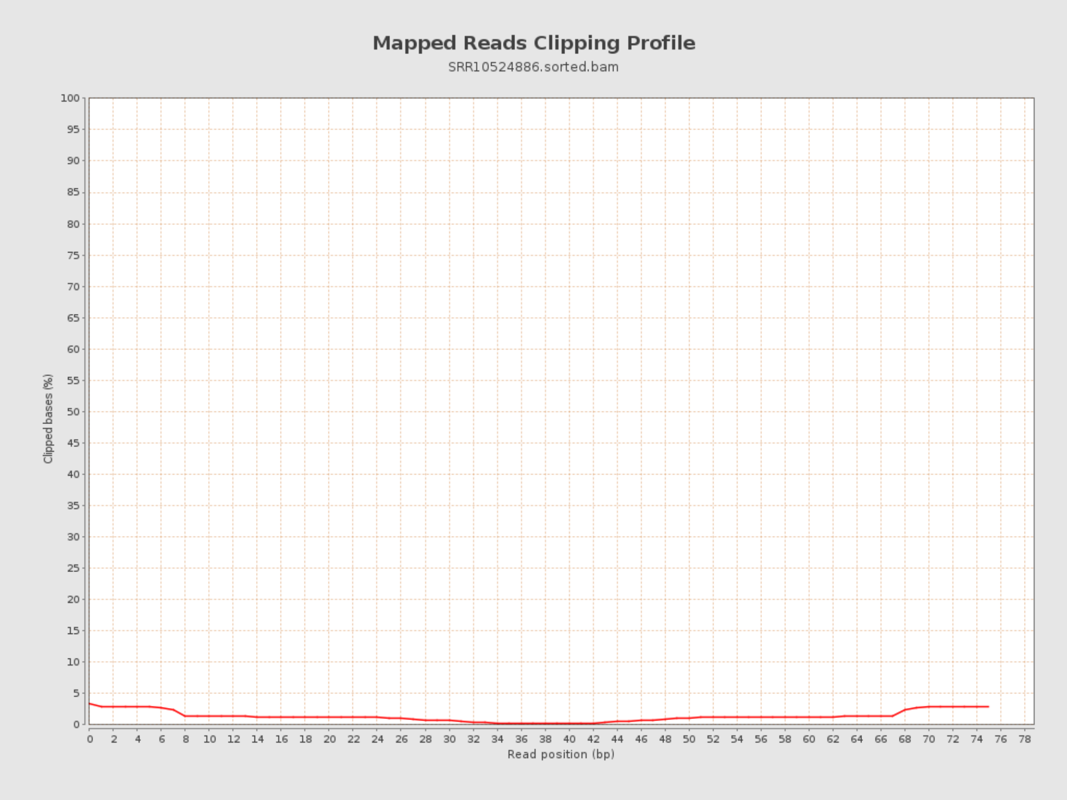
8. Results : Mapped Reads Nucleotide Content



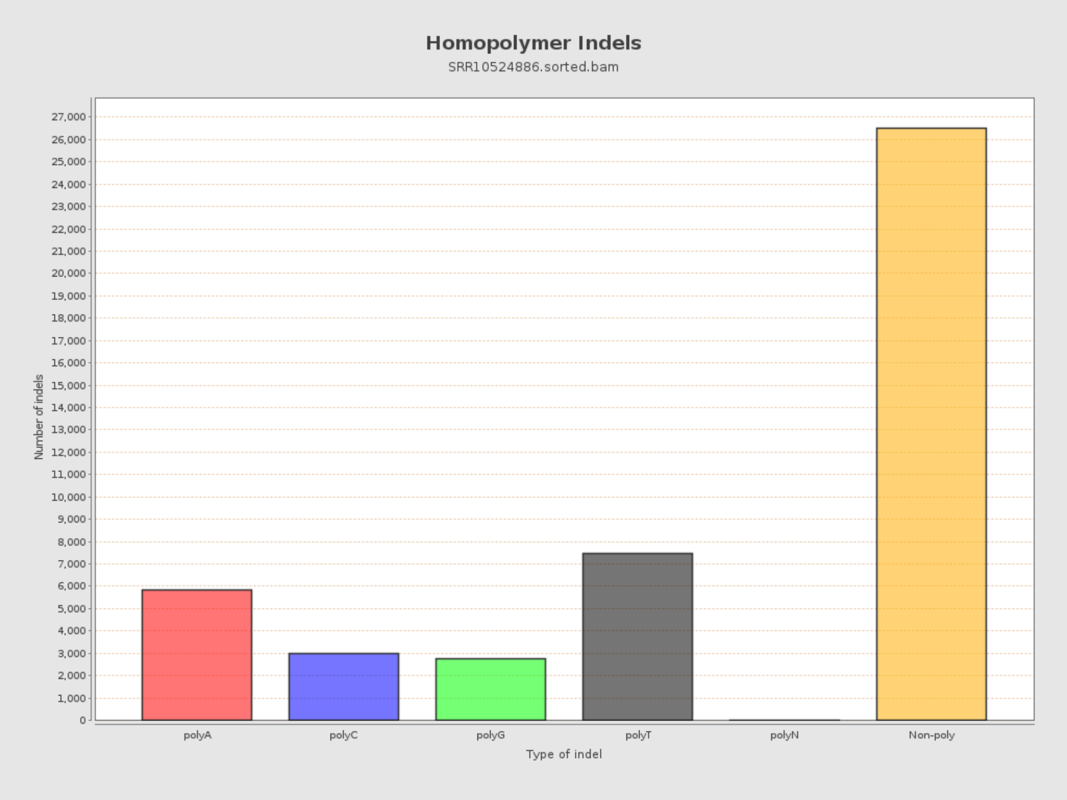
9. Results : Mapped Reads GC-content Distribution



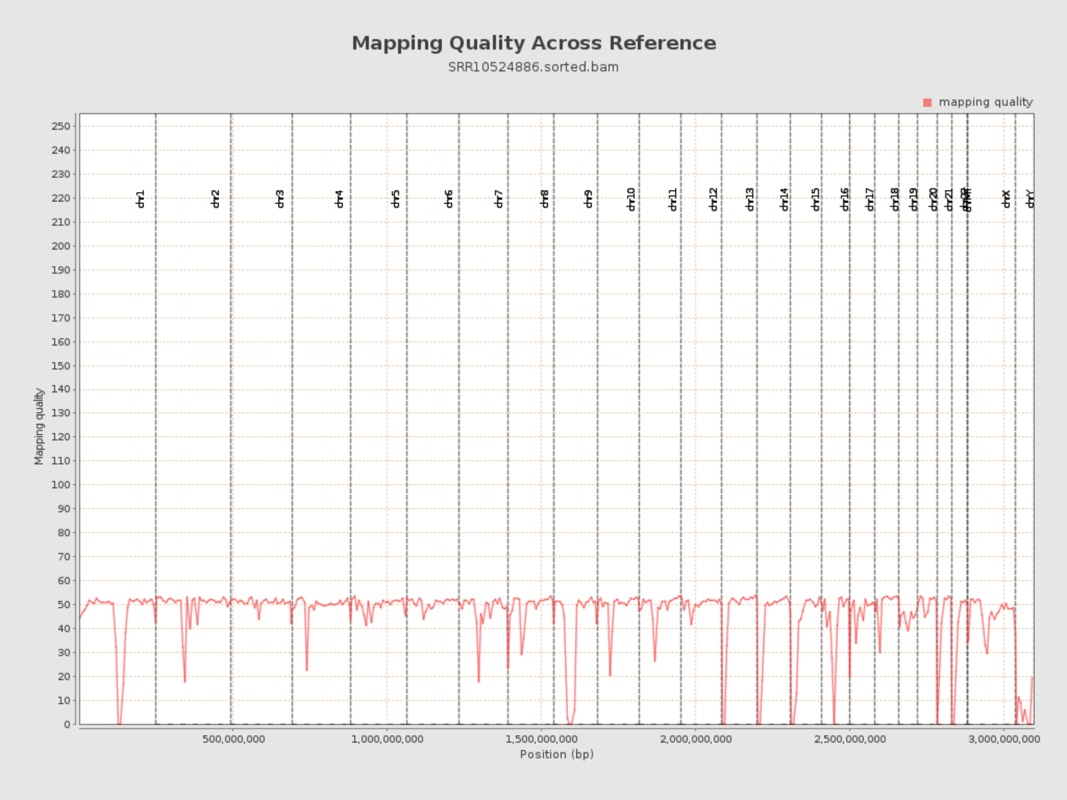
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram