Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:24:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524885.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_SRR10524885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524885.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:24:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,745,952
Mapped reads	2,529,434 / 92.12%
Unmapped reads	216,518 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,389 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	139,075 / 5.06%
Duplication rate	4.06%
Clipped reads	2,530,970 / 92.17%

2.2. ACGT Content

Number/percentage of A's	38,103,291 / 25.84%
Number/percentage of C's	27,115,319 / 18.39%
Number/percentage of T's	47,774,100 / 32.39%
Number/percentage of G's	34,466,306 / 23.37%
Number/percentage of N's	19,980 / 0.01%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.448

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

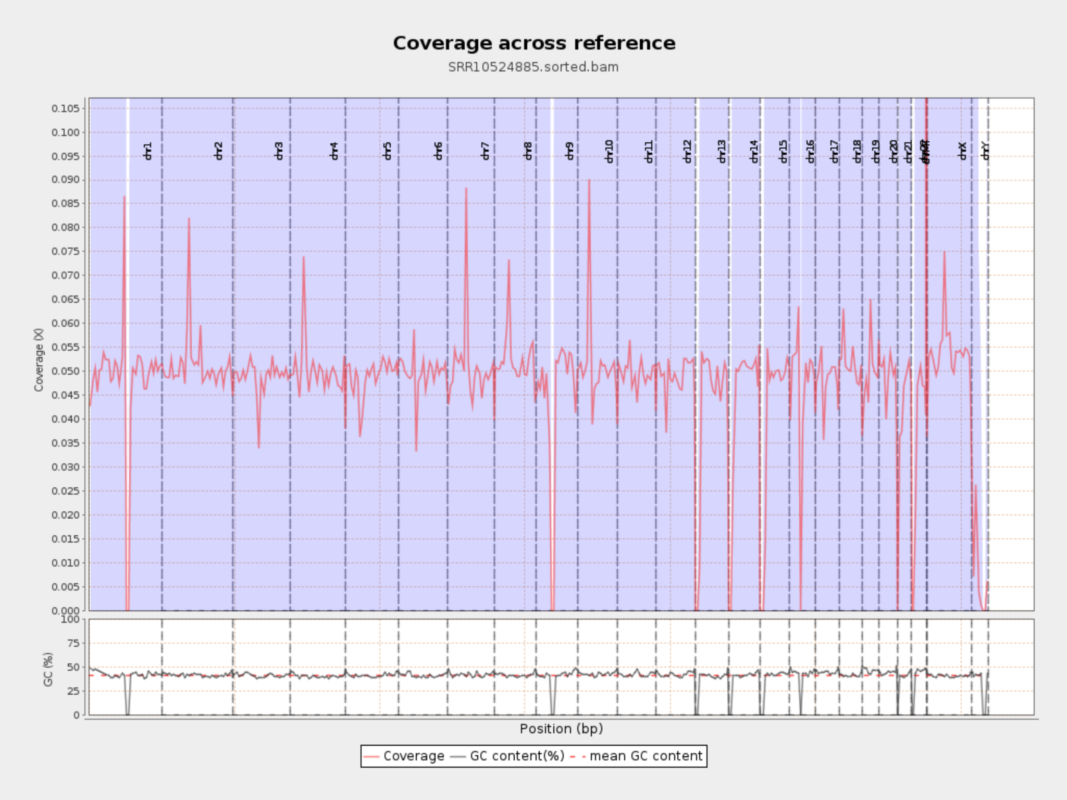
General error rate	0.51%
Mismatches	730,073
Insertions	10,476
Mapped reads with at least one insertion	0.41%
Deletions	27,949
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.06%

2.6. Chromosome stats

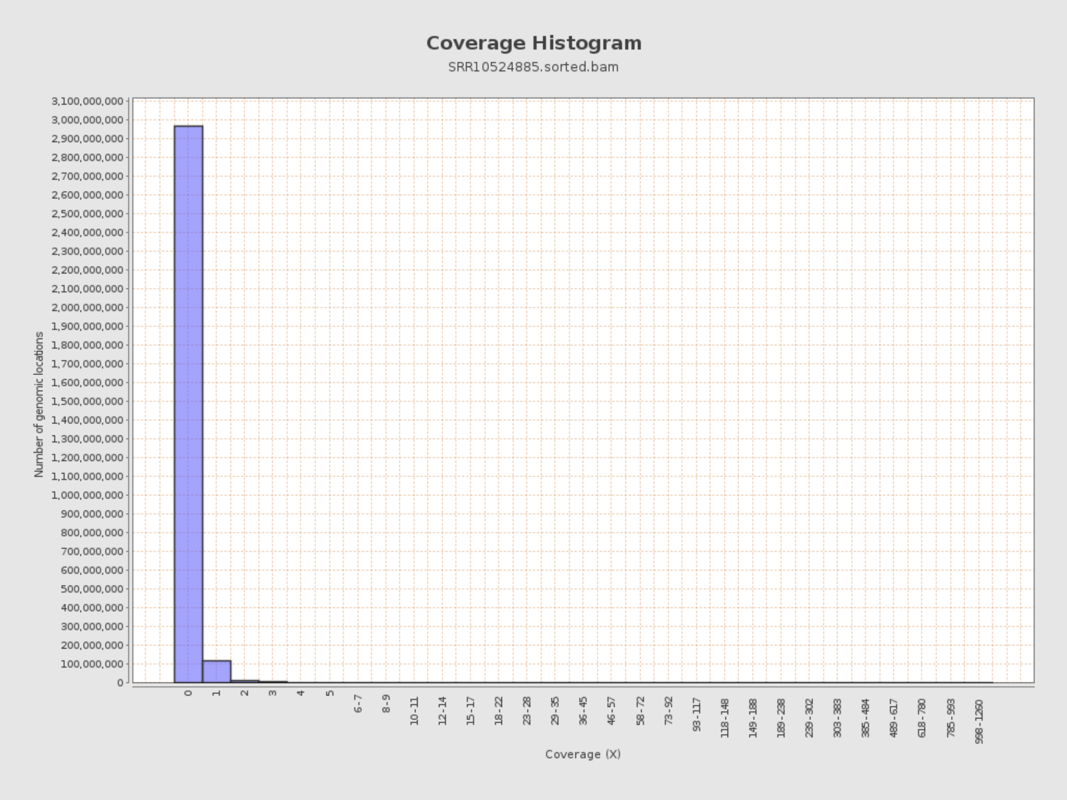
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11932732	0.0479	0.9262
chr2	243199373	12528216	0.0515	0.4759
chr3	198022430	9656448	0.0488	0.25
chr4	191154276	9587944	0.0502	0.2934
chr5	180915260	8848959	0.0489	0.2512
chr6	171115067	8497749	0.0497	0.2866
chr7	159138663	8136605	0.0511	0.6375

chr8	146364022	7701854	0.0526	0.4297
chr9	141213431	6184959	0.0438	0.3878
chr10	135534747	6991029	0.0516	0.4188
chr11	135006516	6685752	0.0495	0.4066
chr12	133851895	6593682	0.0493	0.264
chr13	115169878	4743432	0.0412	0.2281
chr14	107349540	4588868	0.0427	0.2557
chr15	102531392	4129141	0.0403	0.2282
chr16	90354753	4203404	0.0465	0.2789
chr17	81195210	3894508	0.048	0.2811
chr18	78077248	4060589	0.052	0.8026
chr19	59128983	2947057	0.0498	0.5808
chr20	63025520	3088618	0.049	0.2607
chr21	48129895	1957913	0.0407	0.2679
chr22	51304566	1713525	0.0334	0.2054
chrMT	16571	32964	1.9893	1.8447
chrX	155270560	8382891	0.054	0.3166
chrY	59373566	434336	0.0073	0.1877

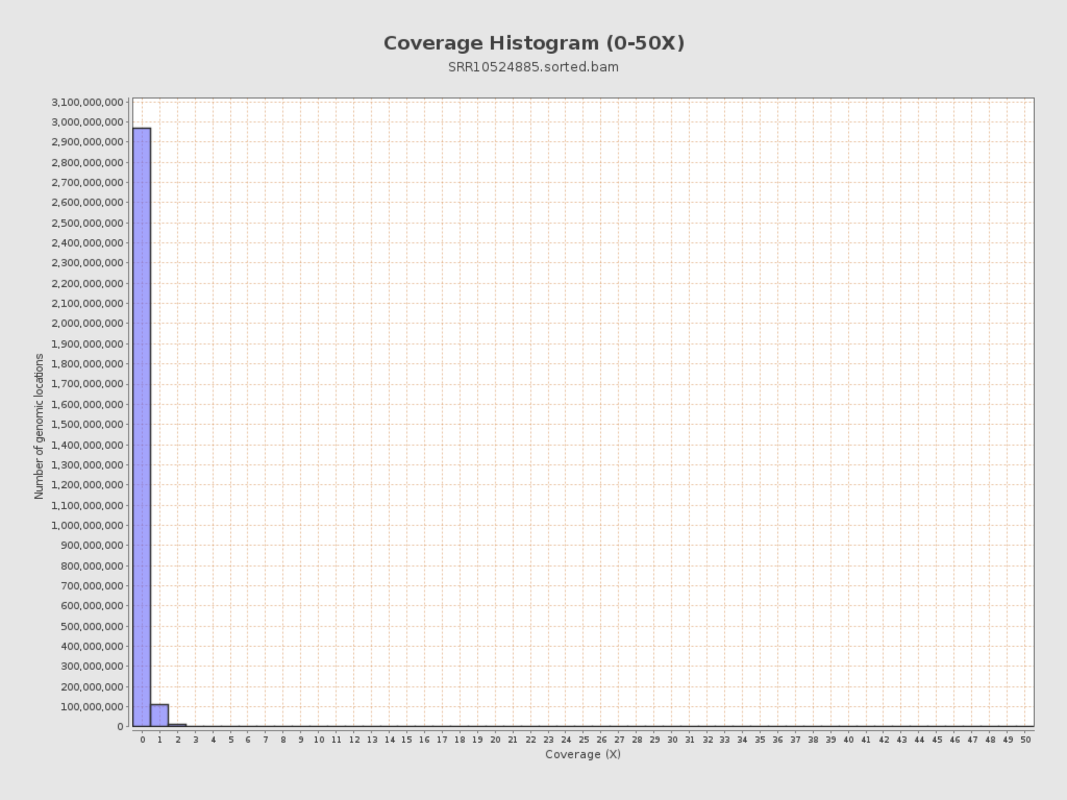
3. Results : Coverage across reference



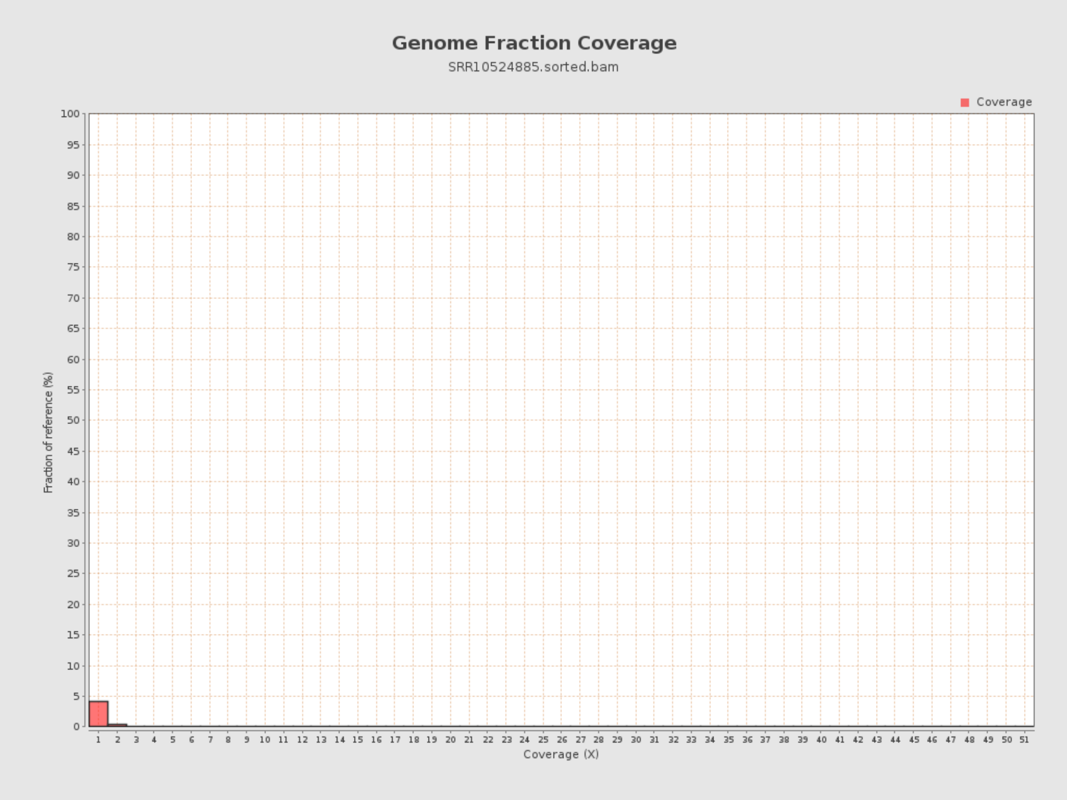
4. Results : Coverage Histogram



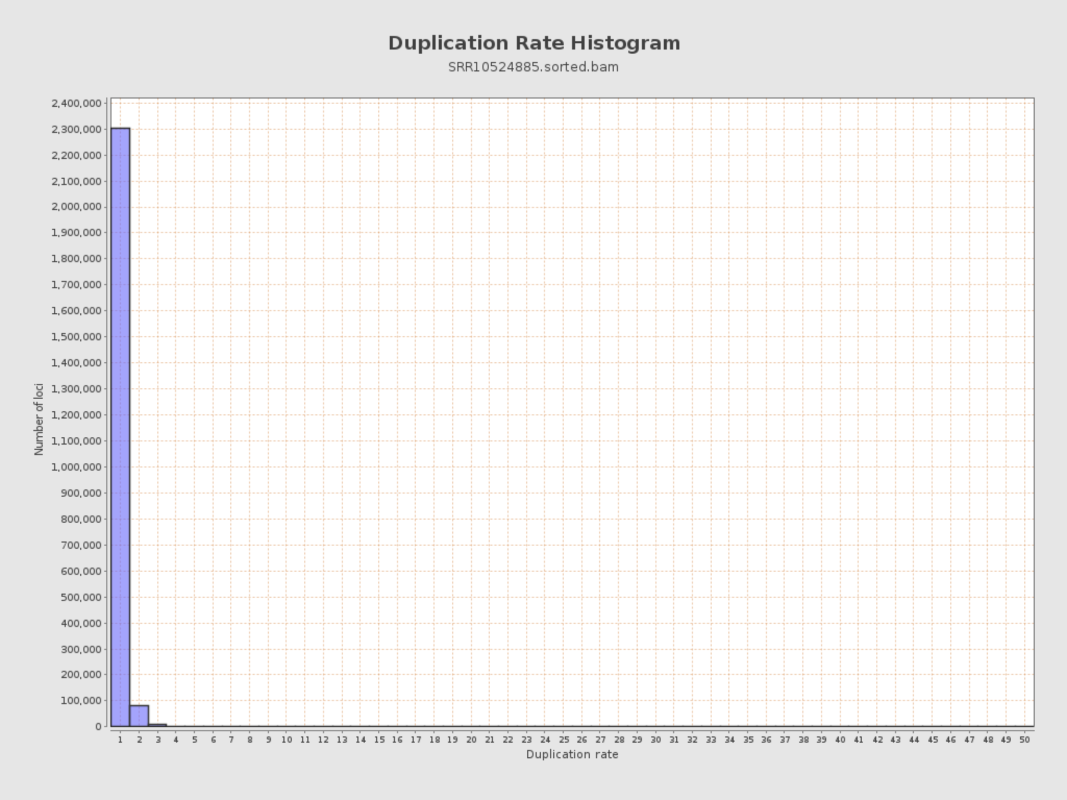
5. Results : Coverage Histogram (0-50X)



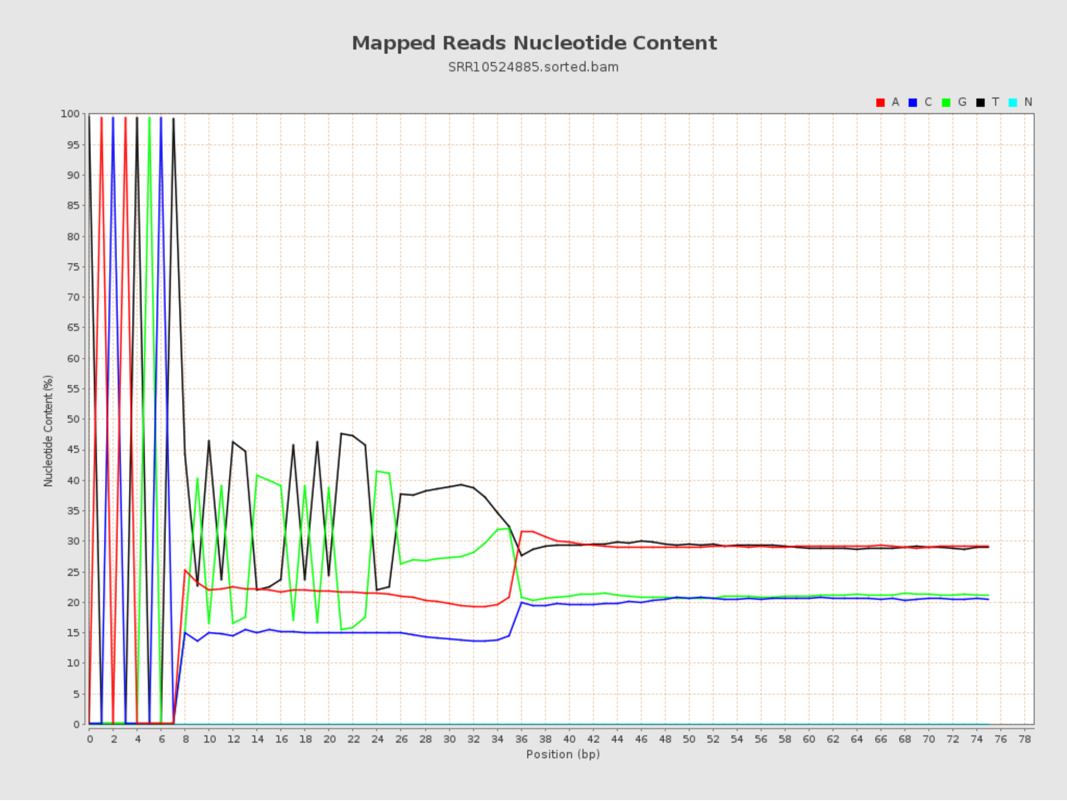
6. Results : Genome Fraction Coverage



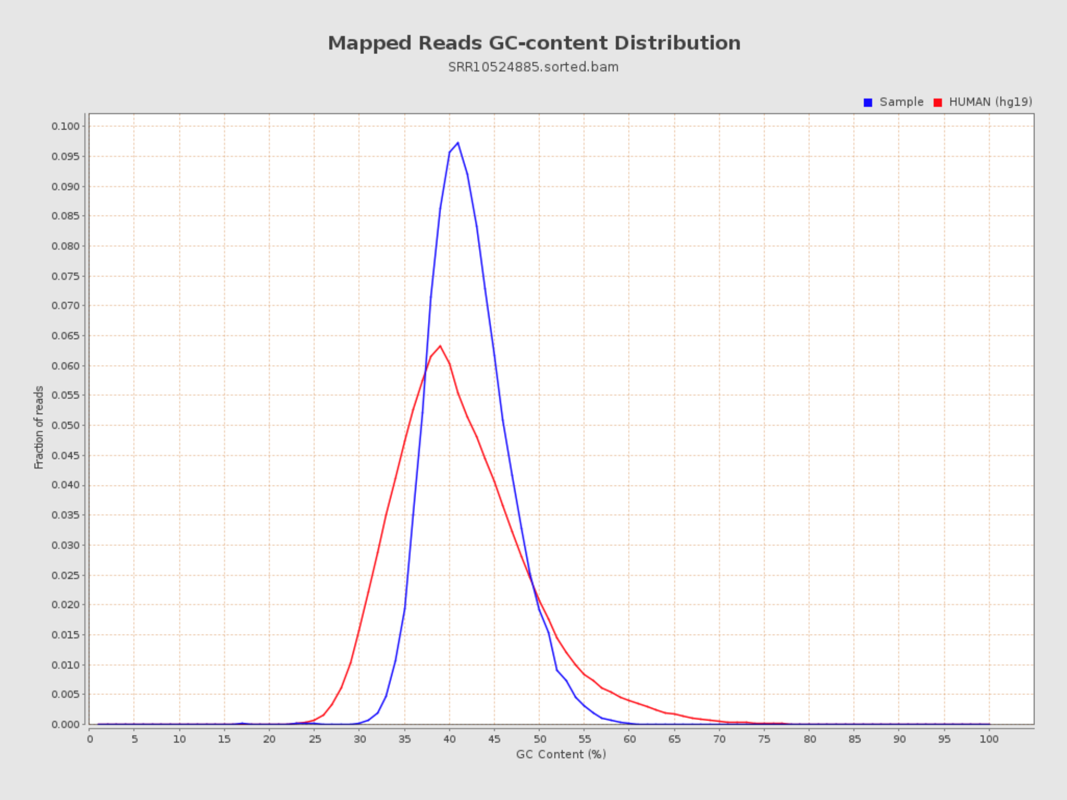
7. Results : Duplication Rate Histogram



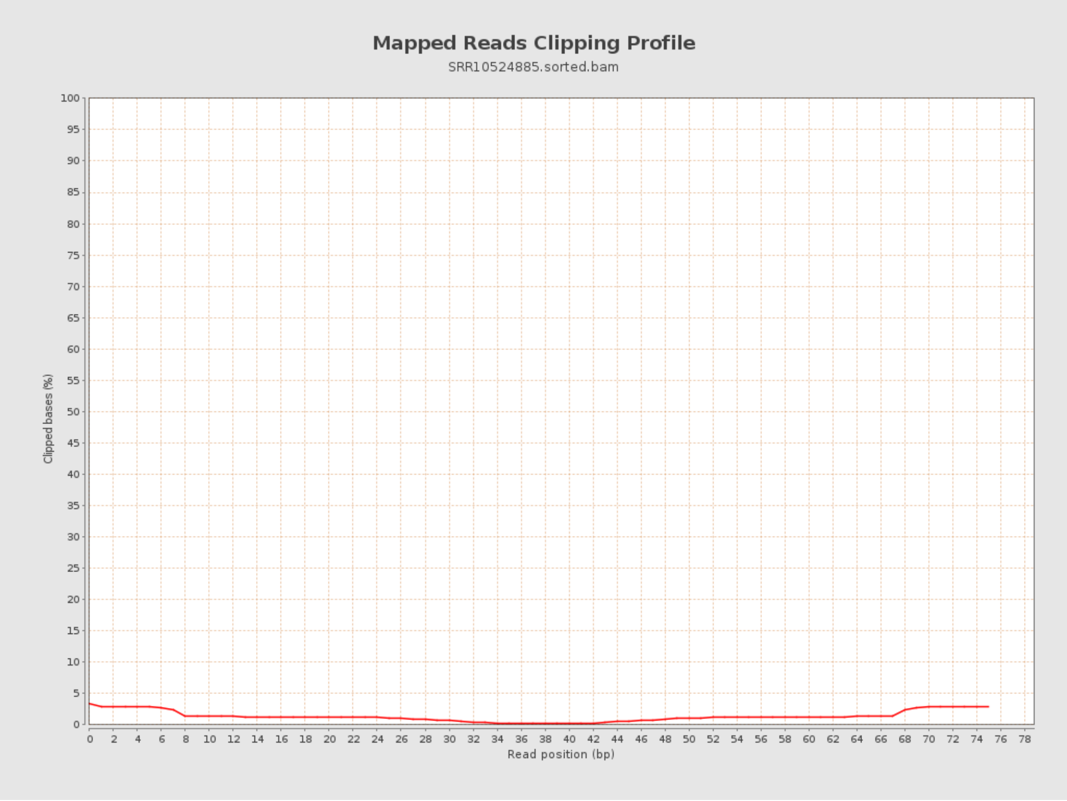
8. Results : Mapped Reads Nucleotide Content



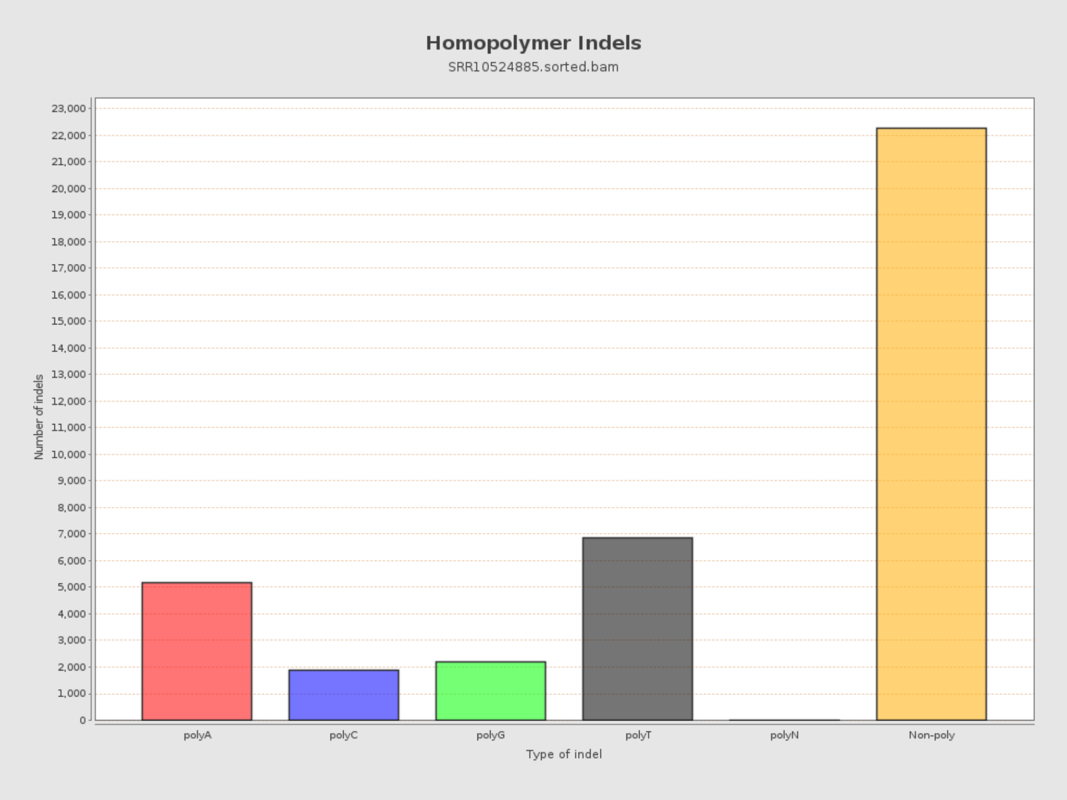
9. Results : Mapped Reads GC-content Distribution



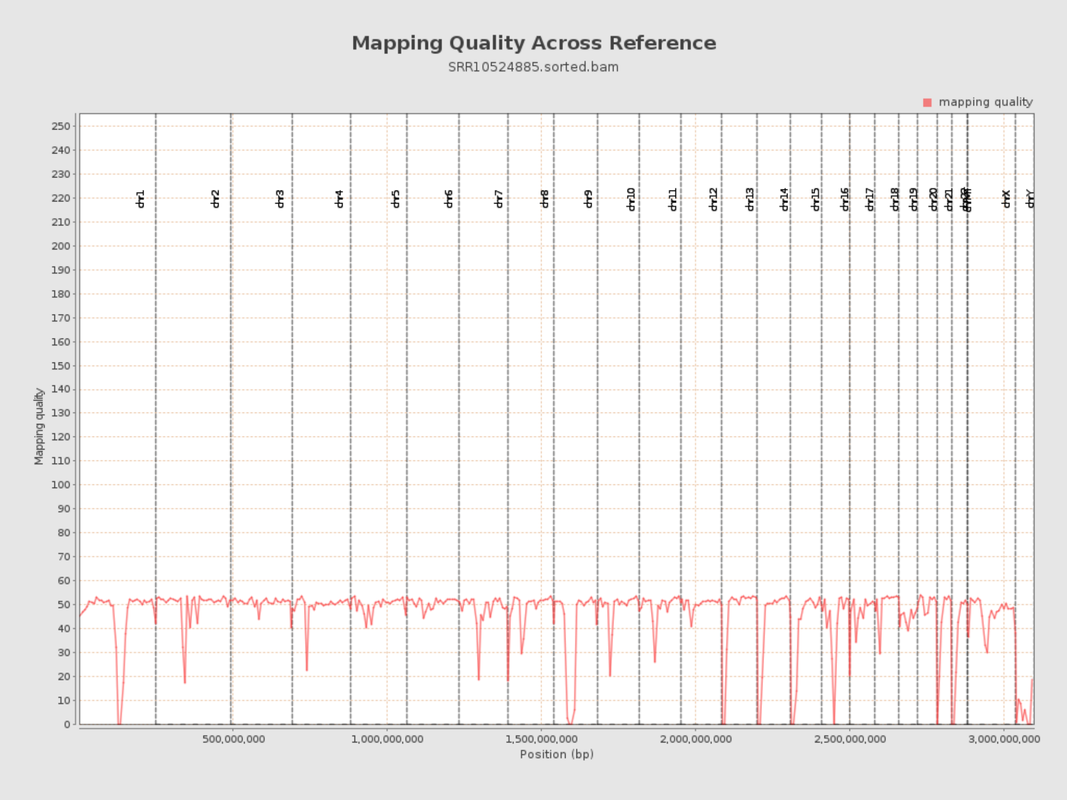
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram