Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:56:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524633.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_SRR10524633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:56:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,714,085
Mapped reads	1,567,427 / 91.44%
Unmapped reads	146,658 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,525 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	43,315 / 2.53%
Duplication rate	1.87%
Clipped reads	1,567,972 / 91.48%

2.2. ACGT Content

Number/percentage of A's	24,086,670 / 26.75%
Number/percentage of C's	18,372,276 / 20.41%
Number/percentage of T's	27,314,568 / 30.34%
Number/percentage of G's	20,254,545 / 22.5%
Number/percentage of N's	2,655 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2688

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

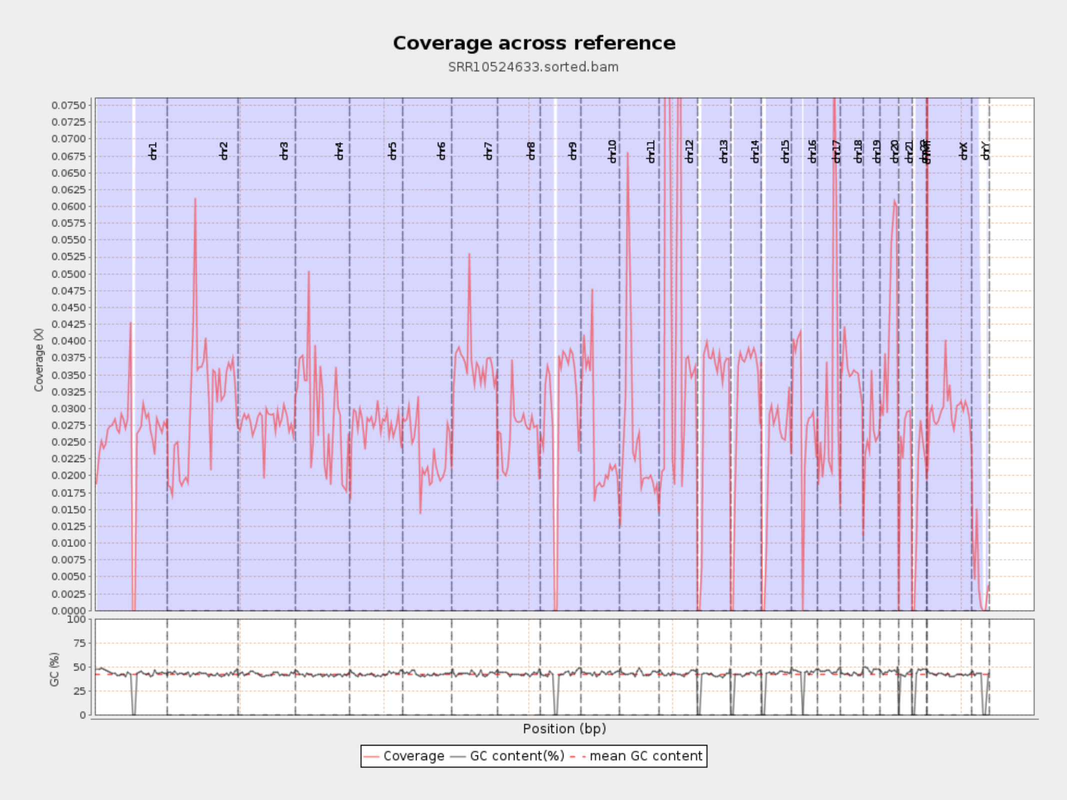
General error rate	0.49%
Mismatches	431,021
Insertions	6,767
Mapped reads with at least one insertion	0.43%
Deletions	14,289
Mapped reads with at least one deletion	0.91%
Homopolymer indels	40.95%

2.6. Chromosome stats

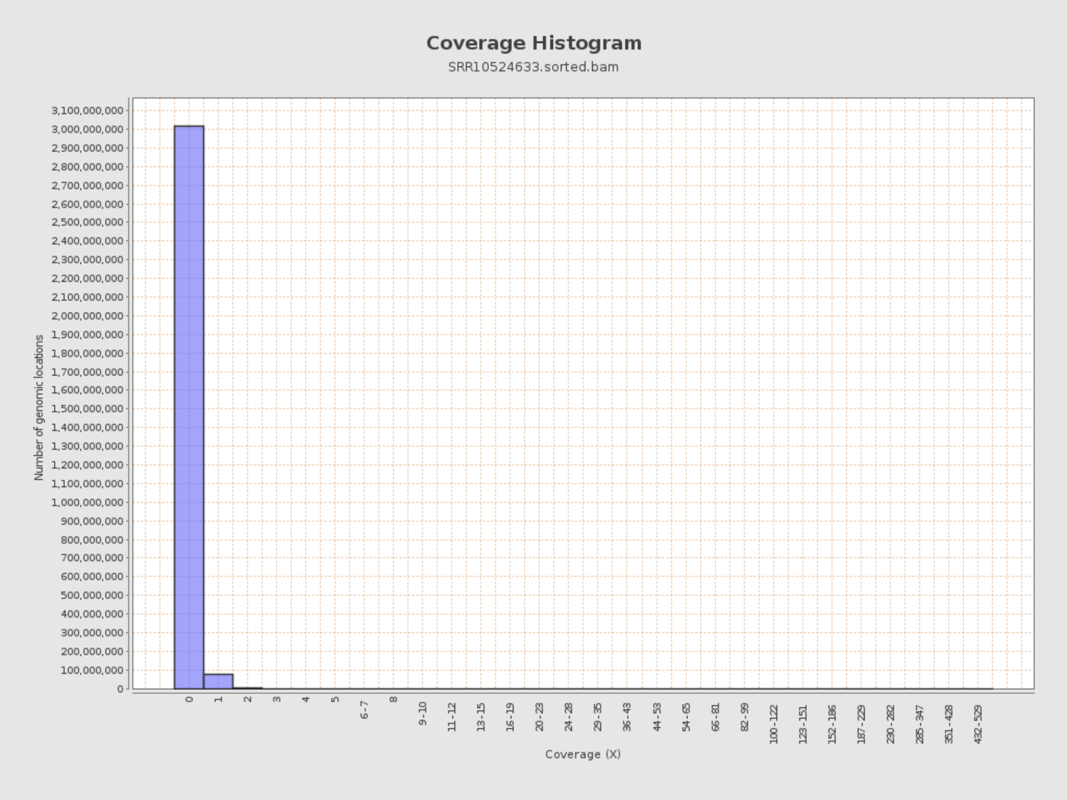
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6376825	0.0256	0.4256
chr2	243199373	7470099	0.0307	0.3062
chr3	198022430	5530147	0.0279	0.1786
chr4	191154276	5588626	0.0292	0.2032
chr5	180915260	5021691	0.0278	0.1808
chr6	171115067	4033425	0.0236	0.1807
chr7	159138663	5819948	0.0366	0.3699

chr8	146364022	3892635	0.0266	0.2459
chr9	141213431	4216431	0.0299	0.2894
chr10	135534747	3490197	0.0258	0.2634
chr11	135006516	3432496	0.0254	0.2229
chr12	133851895	6721821	0.0502	0.2707
chr13	115169878	3557381	0.0309	0.1887
chr14	107349540	3295024	0.0307	0.2058
chr15	102531392	2355257	0.023	0.1636
chr16	90354753	2592286	0.0287	0.1999
chr17	81195210	2691700	0.0332	0.2033
chr18	78077248	2784001	0.0357	0.5349
chr19	59128983	1528892	0.0259	0.3369
chr20	63025520	2714072	0.0431	0.2313
chr21	48129895	1163067	0.0242	0.1933
chr22	51304566	880515	0.0172	0.1396
chrMT	16571	6109	0.3687	0.6479
chrX	155270560	4626264	0.0298	0.2156
chrY	59373566	265782	0.0045	0.1121

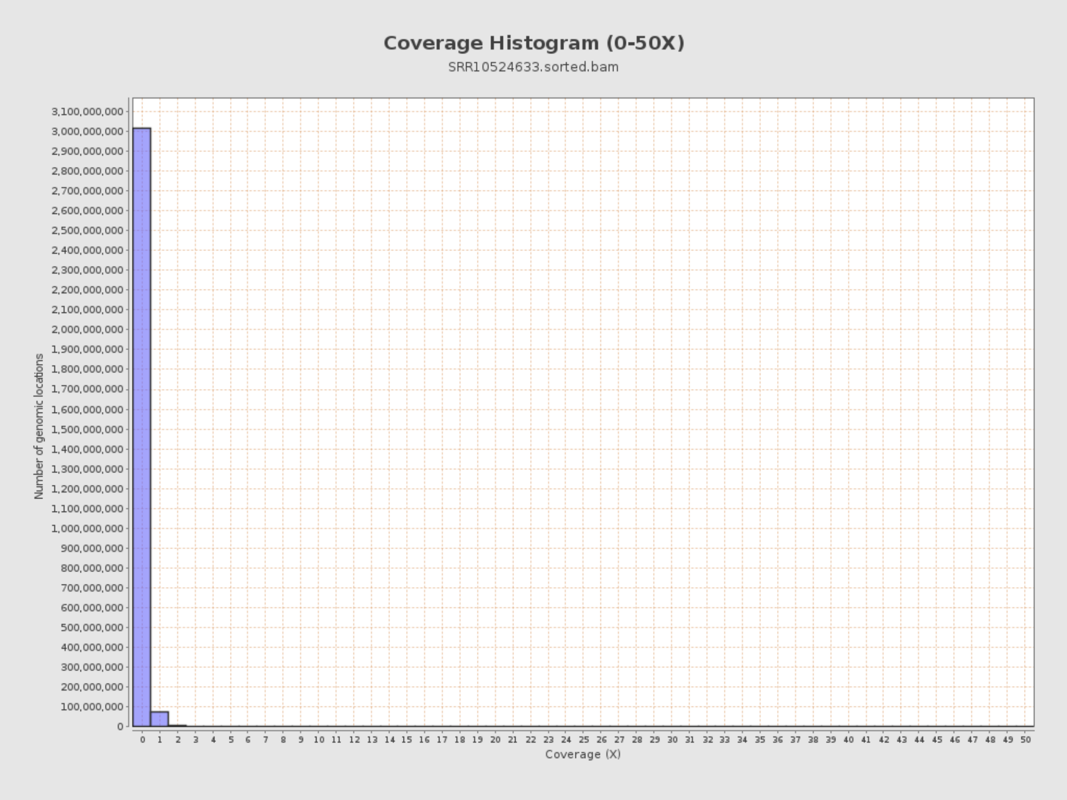
3. Results : Coverage across reference



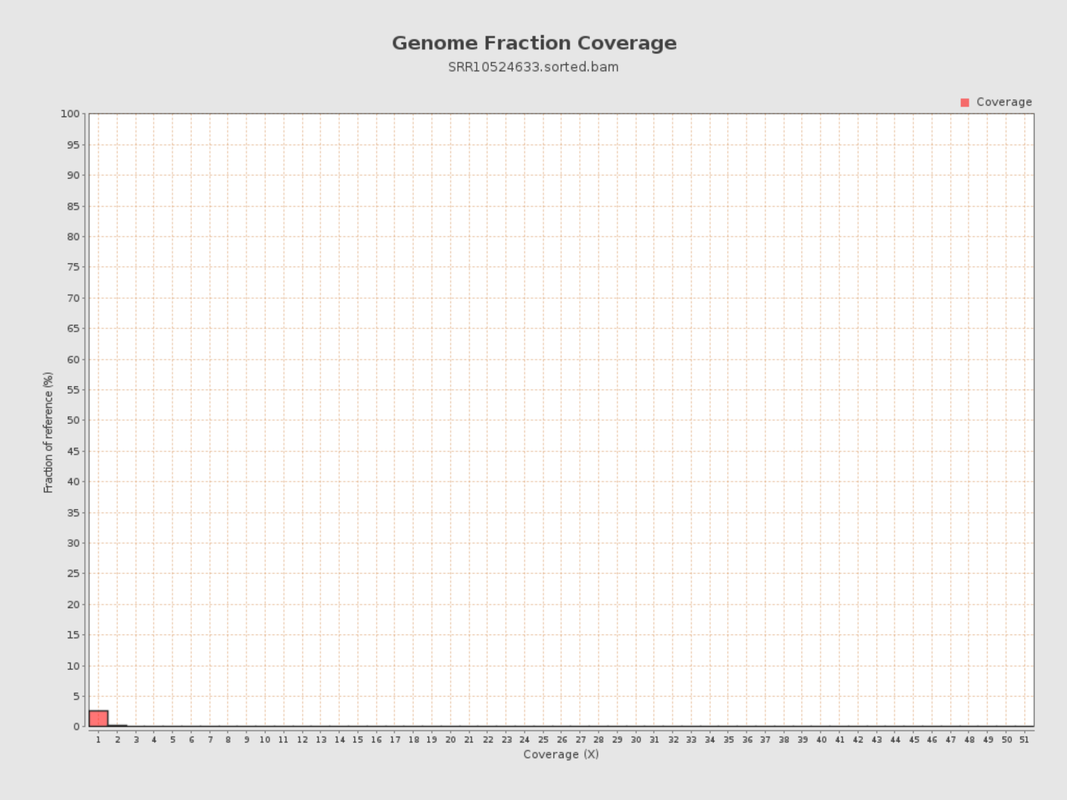
4. Results : Coverage Histogram



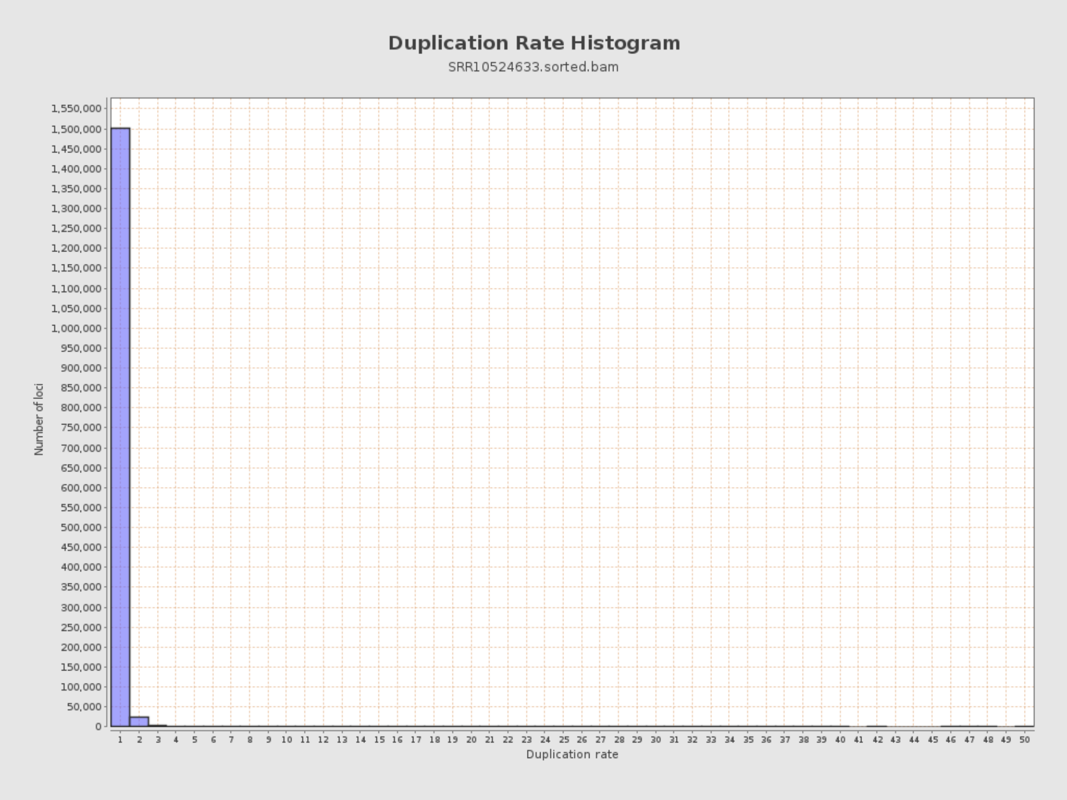
5. Results : Coverage Histogram (0-50X)



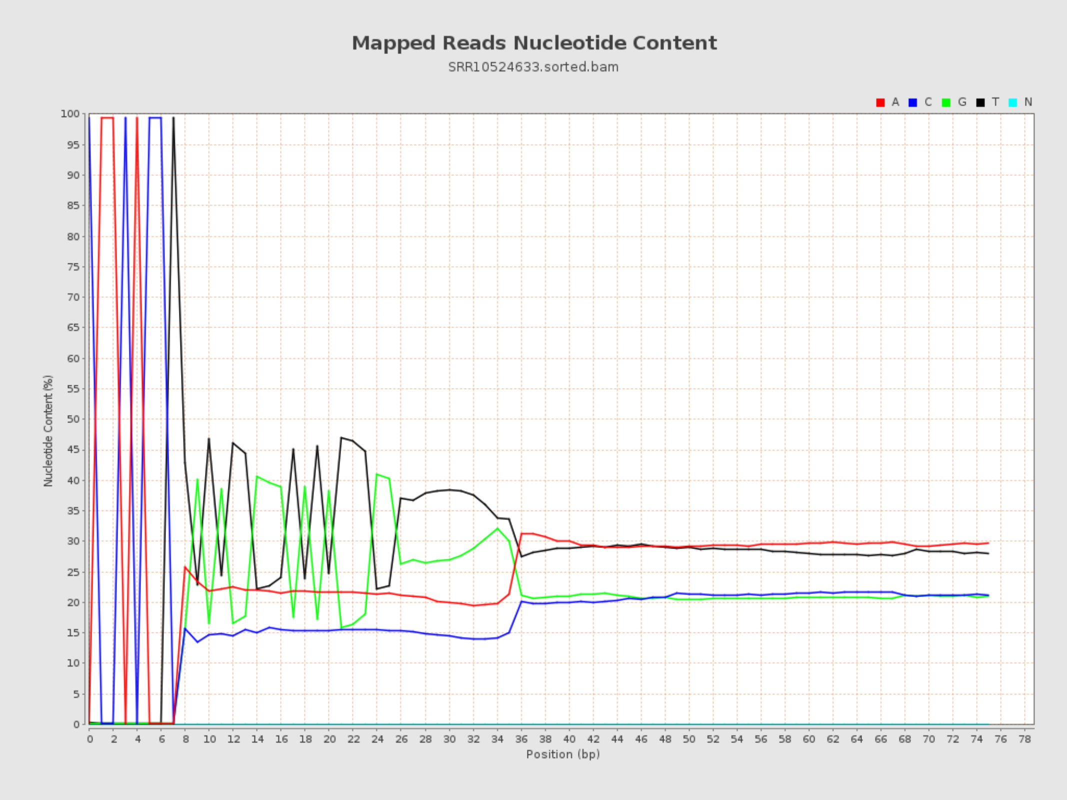
6. Results : Genome Fraction Coverage



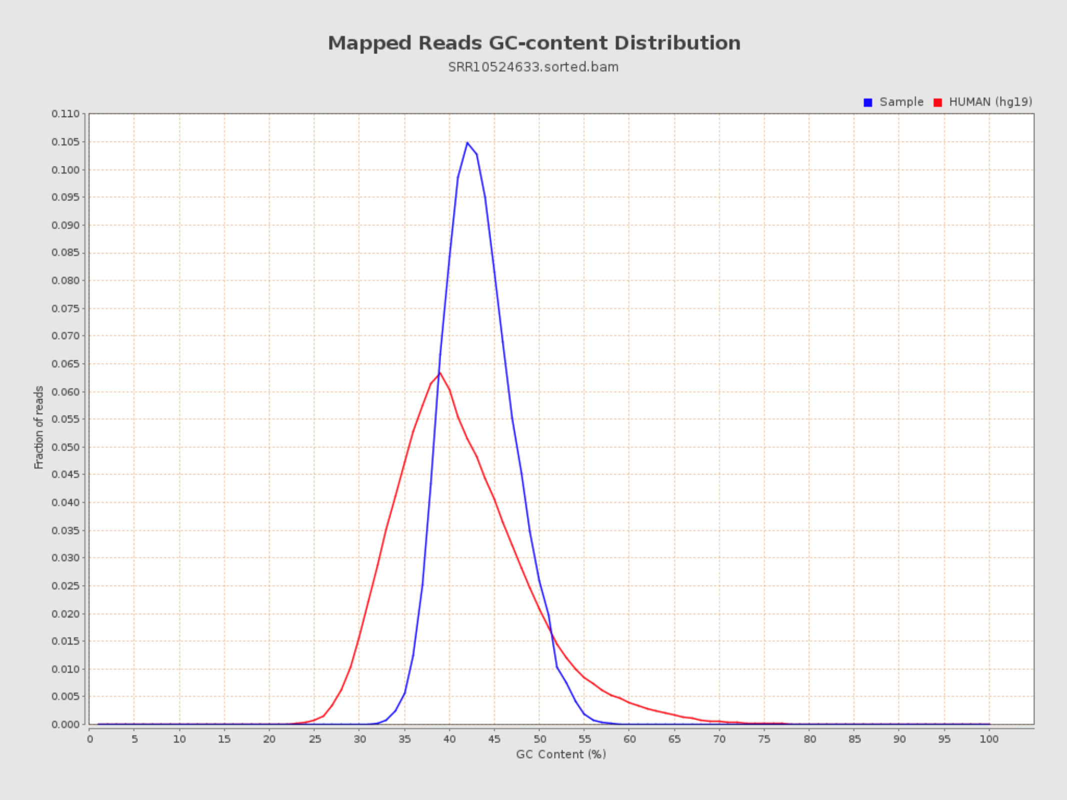
7. Results : Duplication Rate Histogram



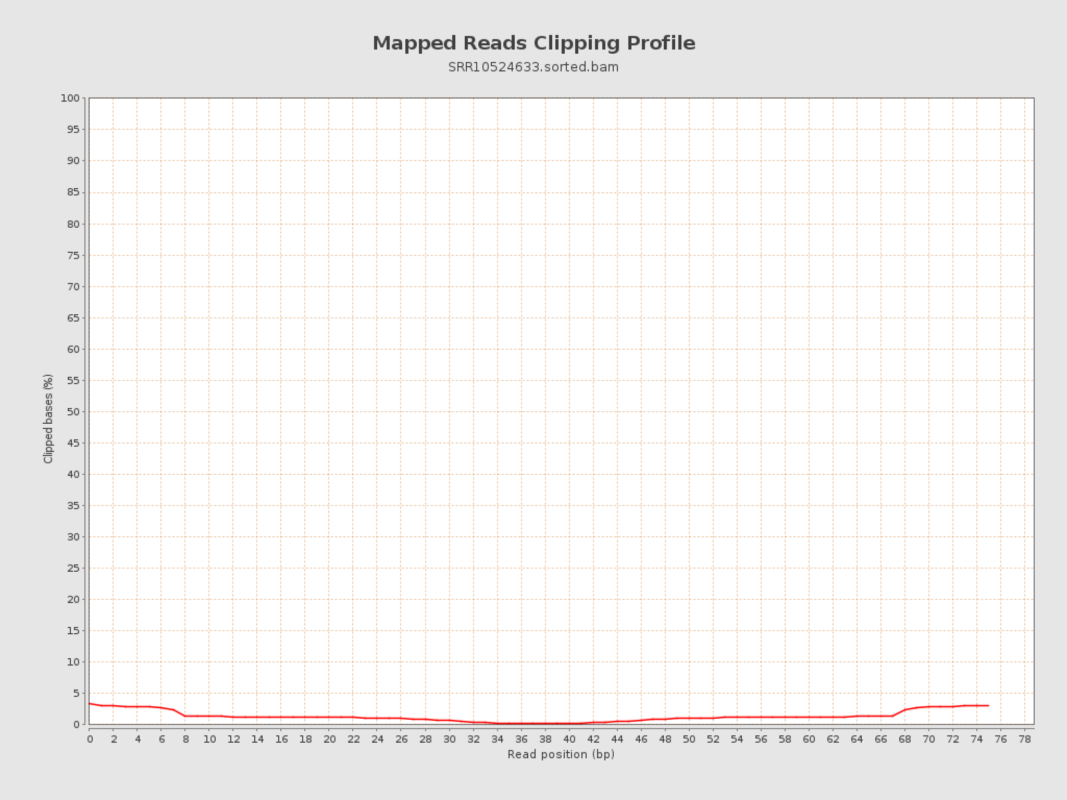
8. Results : Mapped Reads Nucleotide Content



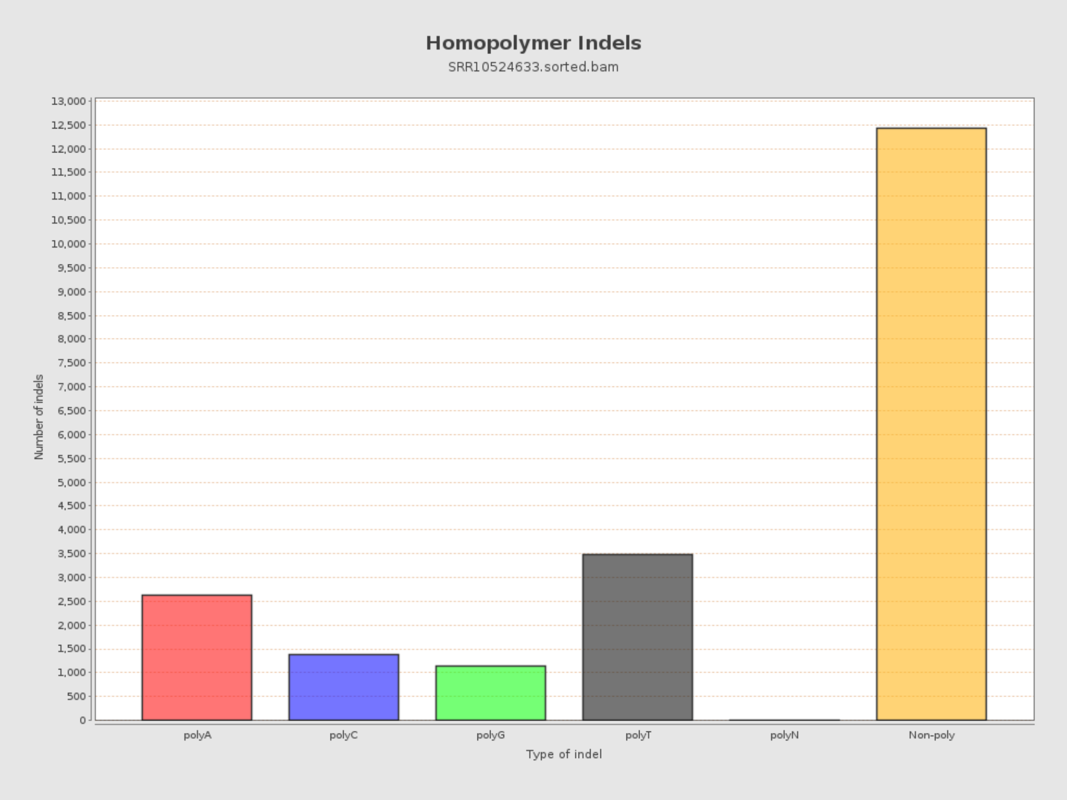
9. Results : Mapped Reads GC-content Distribution



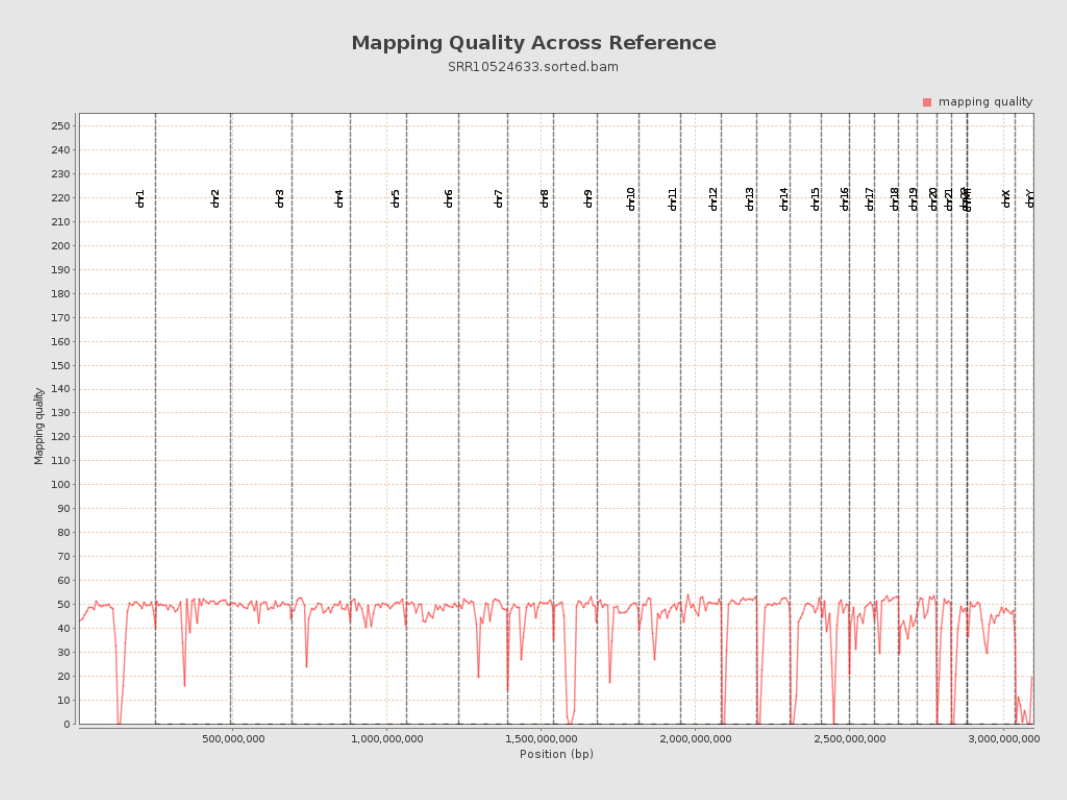
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram