Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:58:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525146.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_SRR10525146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:58:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,211,074
Mapped reads	1,075,430 / 88.8%
Unmapped reads	135,644 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,083 / 2.73%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	27,020 / 2.23%
Duplication rate	1.49%
Clipped reads	1,106,882 / 91.4%

2.2. ACGT Content

Number/percentage of A's	21,828,610 / 26.63%
Number/percentage of C's	15,894,654 / 19.39%
Number/percentage of T's	24,539,260 / 29.94%
Number/percentage of G's	19,701,122 / 24.04%
Number/percentage of N's	3,094 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2796

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

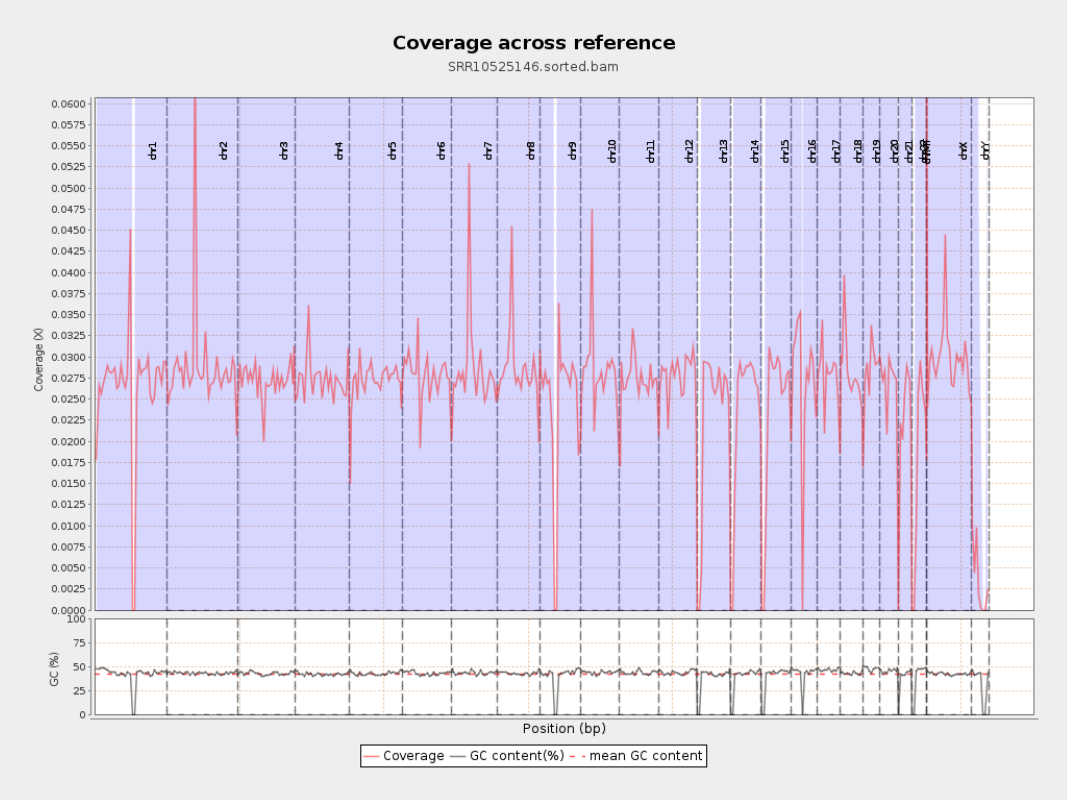
General error rate	0.75%
Mismatches	602,663
Insertions	7,687
Mapped reads with at least one insertion	0.7%
Deletions	19,387
Mapped reads with at least one deletion	1.78%
Homopolymer indels	41.45%

2.6. Chromosome stats

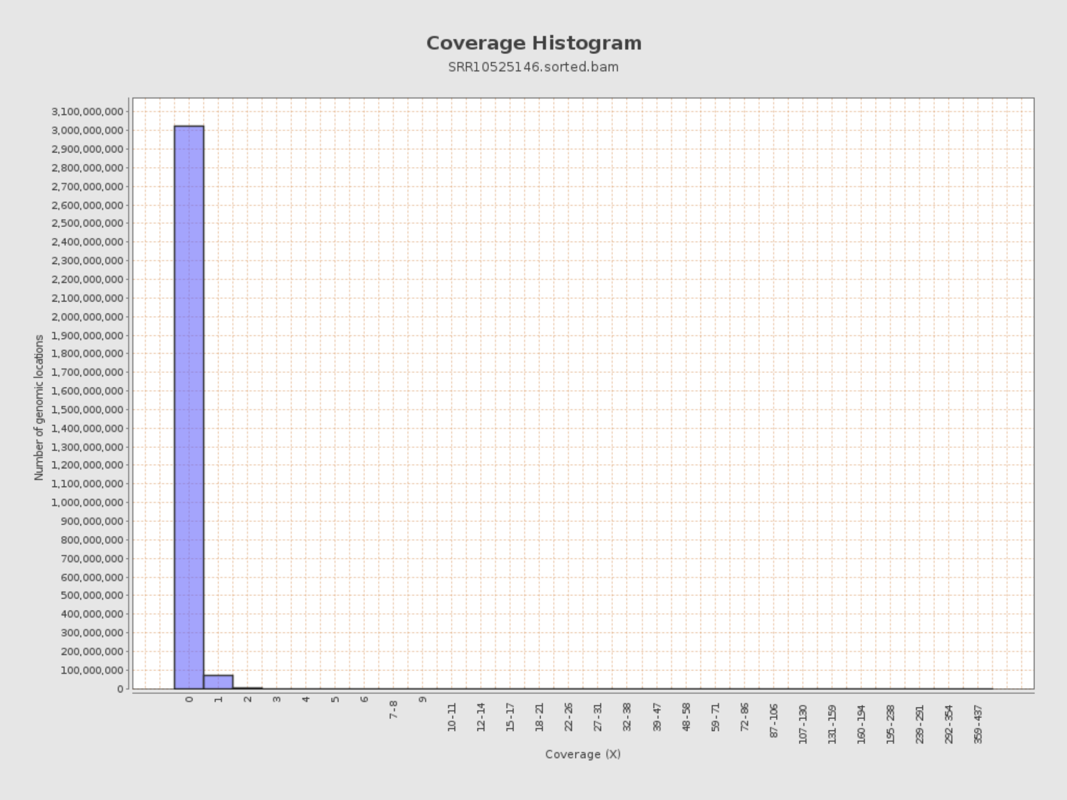
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6520377	0.0262	0.4076
chr2	243199373	7059353	0.029	0.4012
chr3	198022430	5390403	0.0272	0.1767
chr4	191154276	5238470	0.0274	0.1852
chr5	180915260	4969169	0.0275	0.1797
chr6	171115067	4745994	0.0277	0.1995
chr7	159138663	4560770	0.0287	0.41

chr8	146364022	4195511	0.0287	0.3669
chr9	141213431	3440462	0.0244	0.2769
chr10	135534747	3849756	0.0284	0.2803
chr11	135006516	3725287	0.0276	0.2808
chr12	133851895	3728787	0.0279	0.1798
chr13	115169878	2616937	0.0227	0.1602
chr14	107349540	2492691	0.0232	0.1857
chr15	102531392	2372133	0.0231	0.1627
chr16	90354753	2390252	0.0265	0.1877
chr17	81195210	2245693	0.0277	0.22
chr18	78077248	2214923	0.0284	0.4612
chr19	59128983	1703124	0.0288	0.3377
chr20	63025520	1689484	0.0268	0.1792
chr21	48129895	1066051	0.0221	0.1705
chr22	51304566	919214	0.0179	0.1433
chrMT	16571	1281	0.0773	0.2818
chrX	155270560	4664754	0.03	0.2322
chrY	59373566	199062	0.0034	0.0898

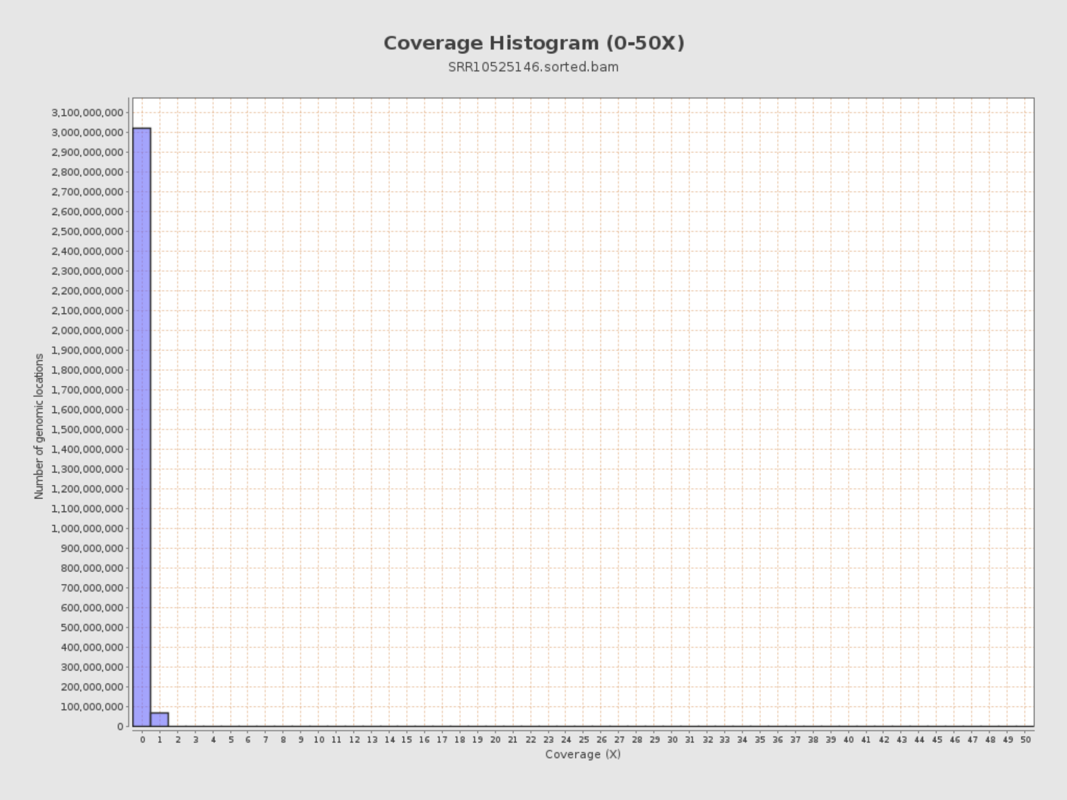
3. Results : Coverage across reference



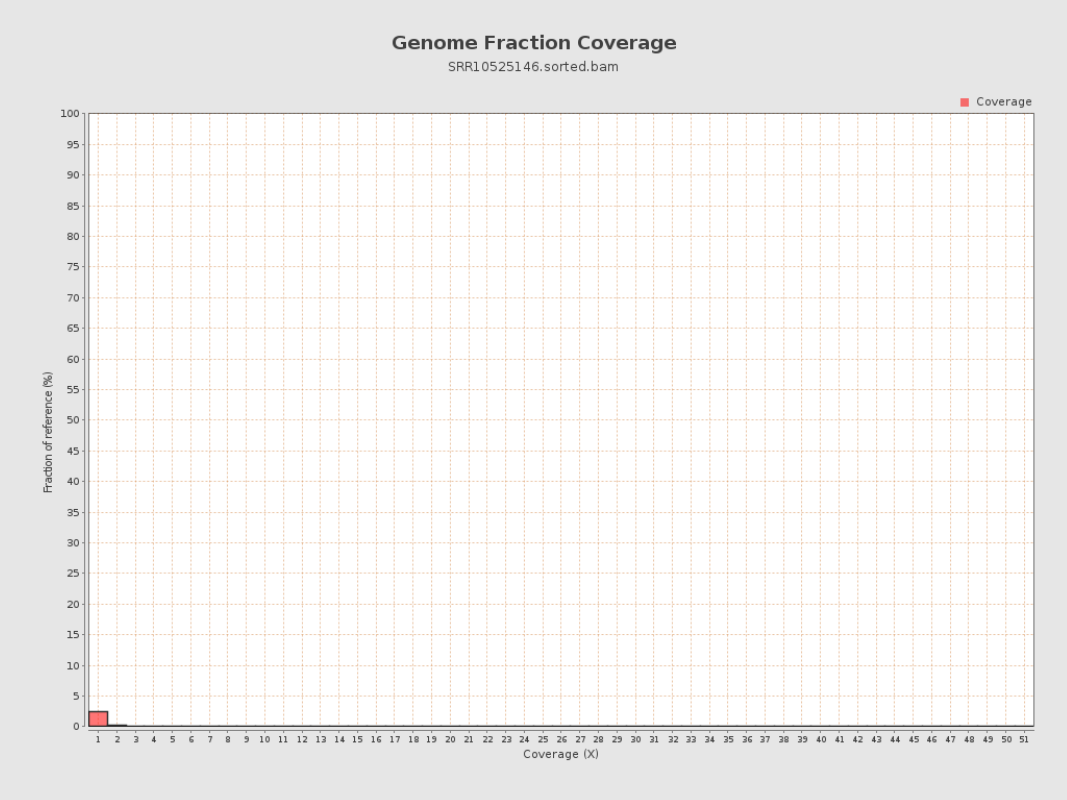
4. Results : Coverage Histogram



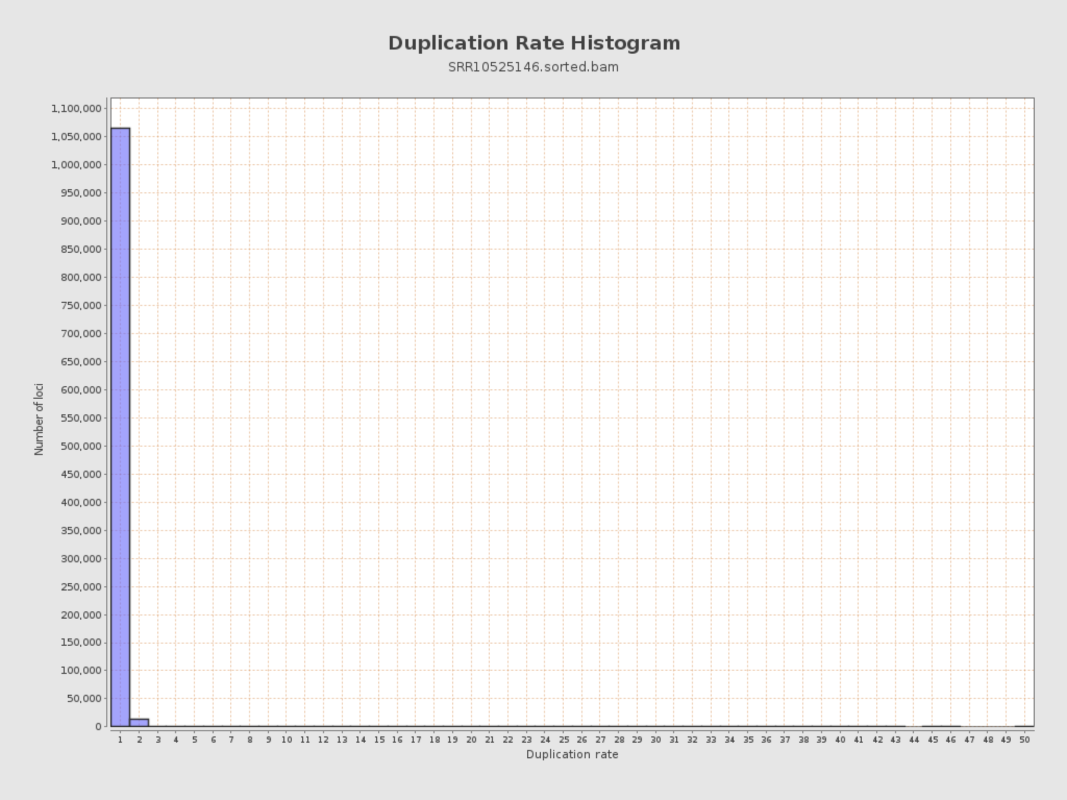
5. Results : Coverage Histogram (0-50X)



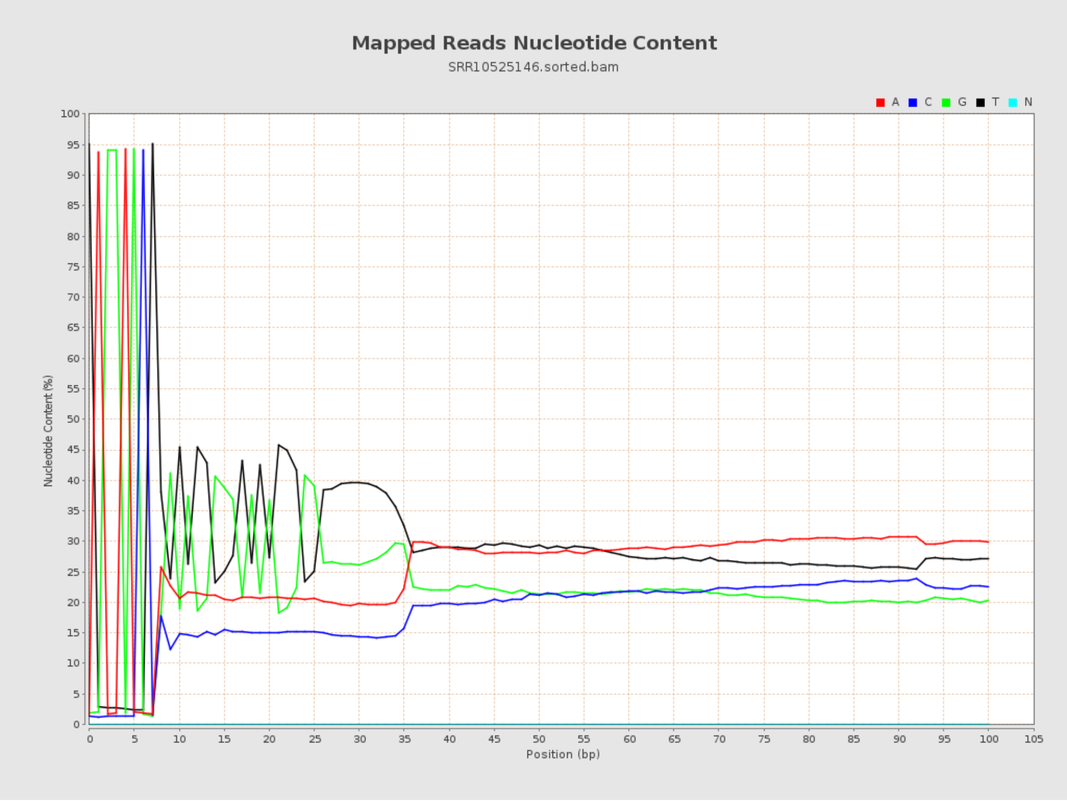
6. Results : Genome Fraction Coverage



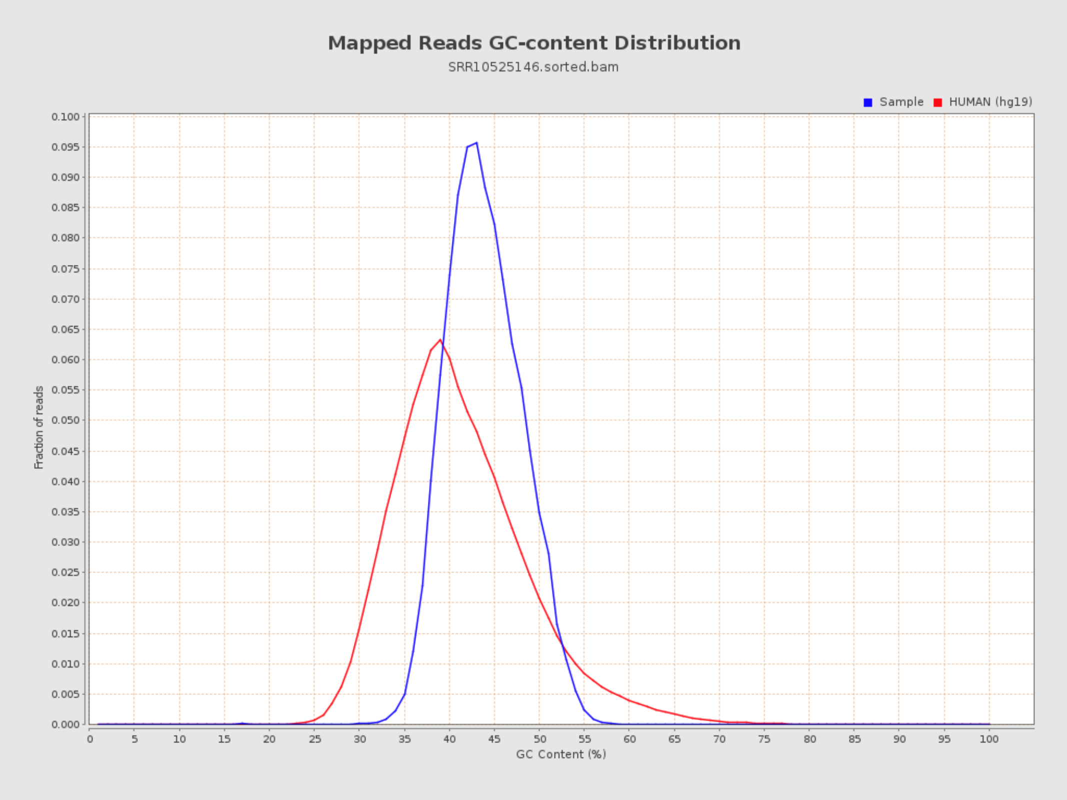
7. Results : Duplication Rate Histogram



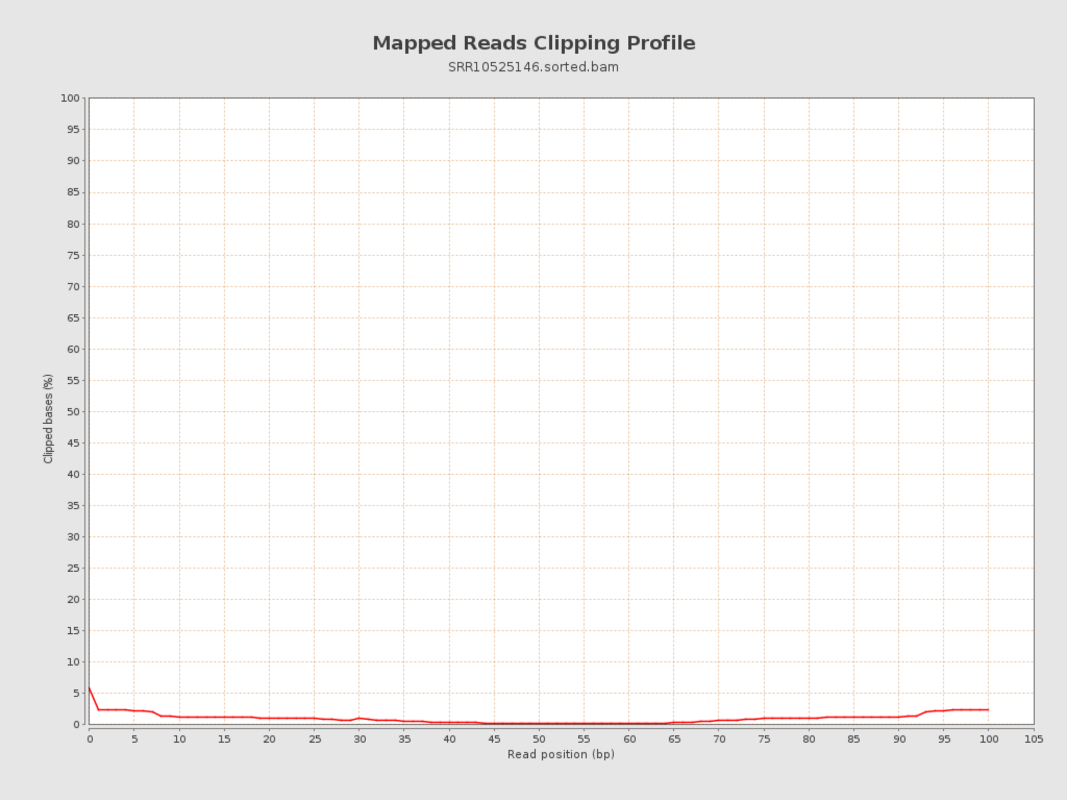
8. Results : Mapped Reads Nucleotide Content



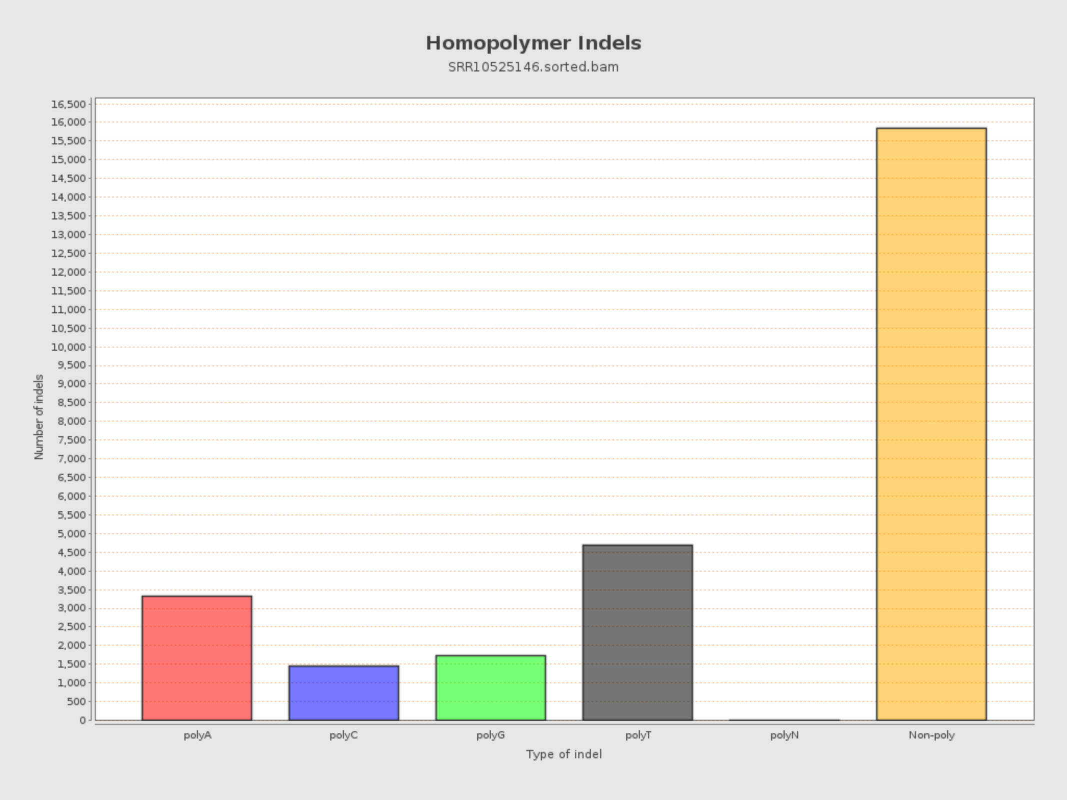
9. Results : Mapped Reads GC-content Distribution



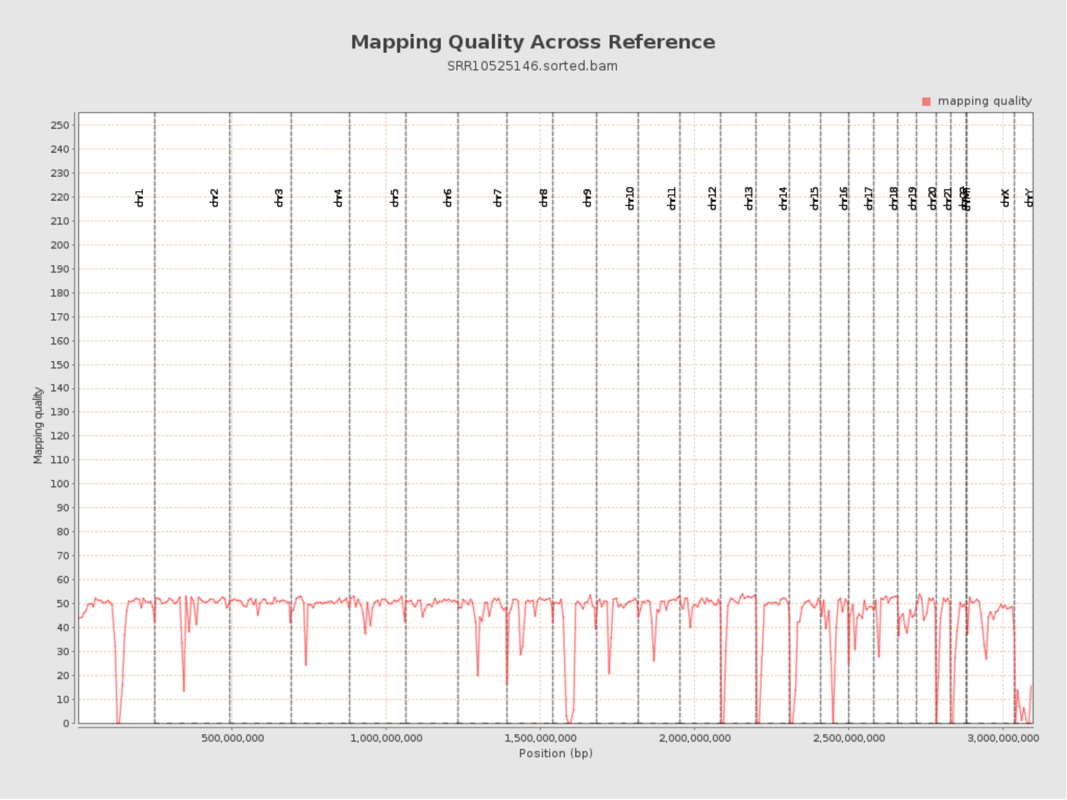
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram