Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:34:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525195.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_SRR10525195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:34:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	916,811
Mapped reads	859,088 / 93.7%
Unmapped reads	57,723 / 6.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,392 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	19,066 / 2.08%
Duplication rate	1.51%
Clipped reads	860,860 / 93.9%

2.2. ACGT Content

Number/percentage of A's	12,929,504 / 24.99%
Number/percentage of C's	9,931,078 / 19.2%
Number/percentage of T's	16,216,693 / 31.35%
Number/percentage of G's	12,653,297 / 24.46%
Number/percentage of N's	1,277 / 0%
GC Percentage	43.66%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.1986

2.4. Mapping Quality

Mean Mapping Quality	45.57

2.5. Mismatches and indels

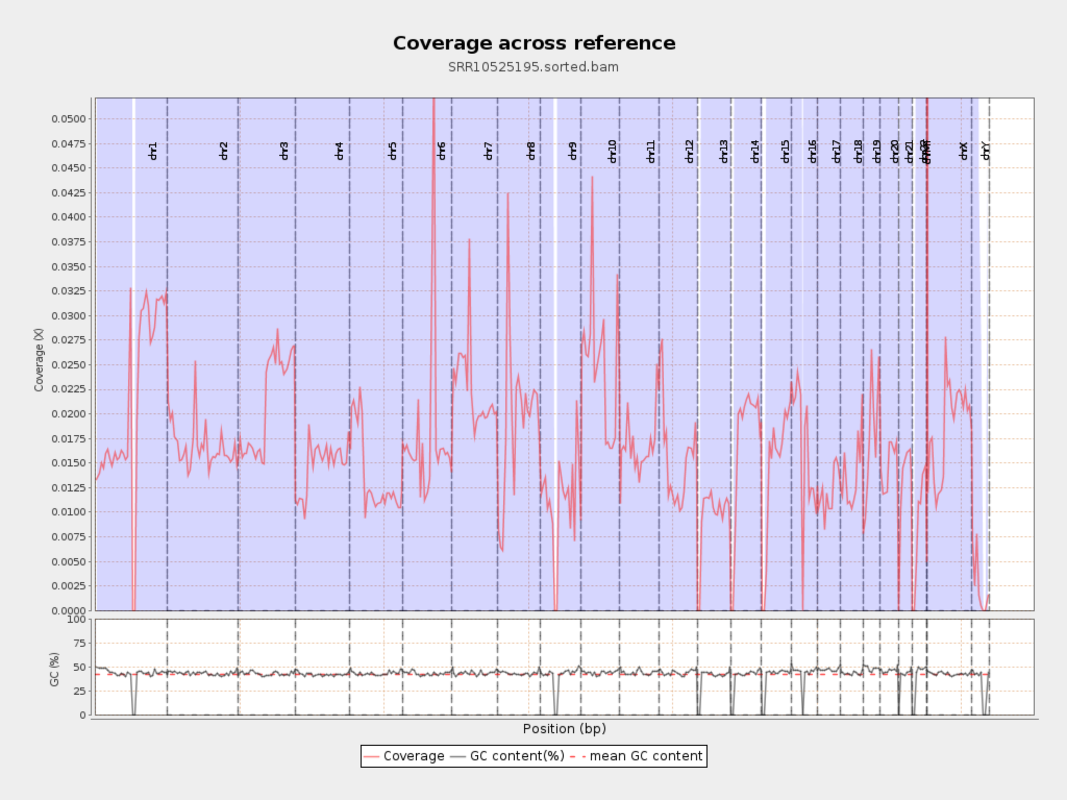
General error rate	0.5%
Mismatches	254,393
Insertions	2,970
Mapped reads with at least one insertion	0.34%
Deletions	10,425
Mapped reads with at least one deletion	1.2%
Homopolymer indels	46.27%

2.6. Chromosome stats

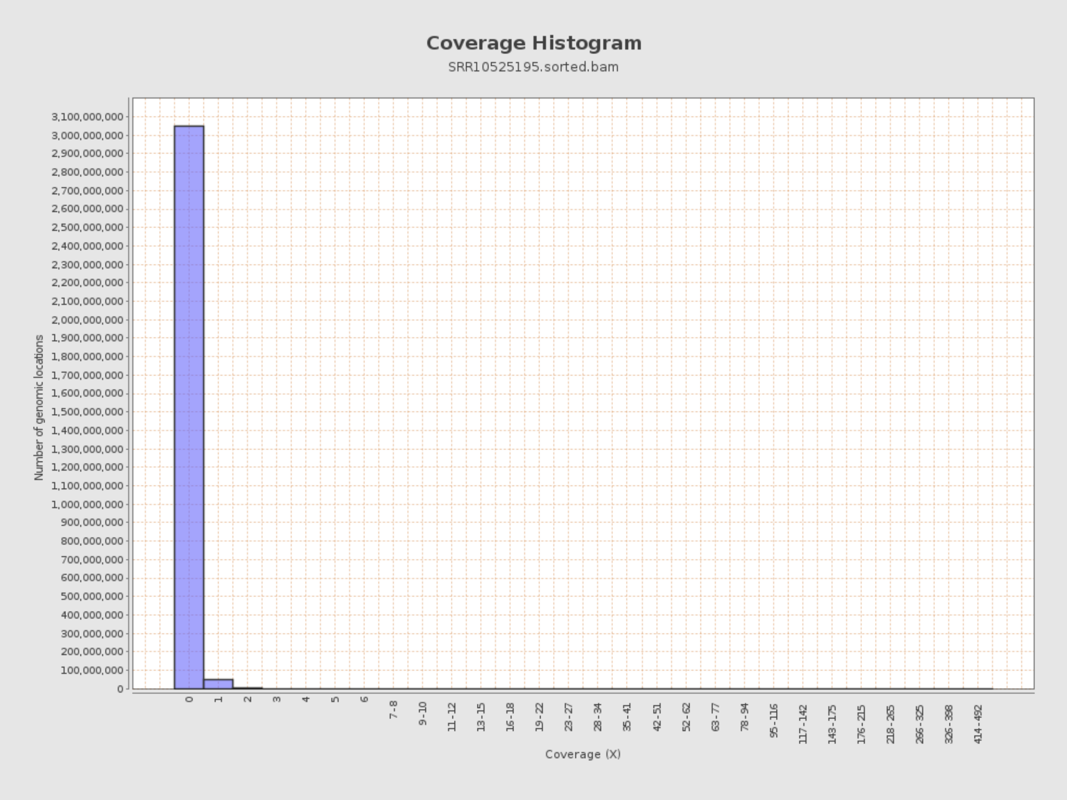
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5285500	0.0212	0.3949
chr2	243199373	4066393	0.0167	0.2071
chr3	198022430	4172679	0.0211	0.1525
chr4	191154276	2840120	0.0149	0.1314
chr5	180915260	2479671	0.0137	0.122
chr6	171115067	3113879	0.0182	0.1515
chr7	159138663	3591704	0.0226	0.3093

chr8	146364022	2865117	0.0196	0.1712
chr9	141213431	1582625	0.0112	0.1343
chr10	135534747	3415484	0.0252	0.2363
chr11	135006516	2247374	0.0166	0.1533
chr12	133851895	2075664	0.0155	0.1316
chr13	115169878	1092986	0.0095	0.1031
chr14	107349540	1825814	0.017	0.1376
chr15	102531392	1463354	0.0143	0.1245
chr16	90354753	1468404	0.0163	0.1428
chr17	81195210	982654	0.0121	0.1178
chr18	78077248	1054560	0.0135	0.2245
chr19	59128983	1057758	0.0179	0.2955
chr20	63025520	919175	0.0146	0.1269
chr21	48129895	629649	0.0131	0.123
chr22	51304566	438574	0.0085	0.0966
chrMT	16571	27772	1.6759	1.5046
chrX	155270560	2906870	0.0187	0.1497
chrY	59373566	144772	0.0024	0.0763

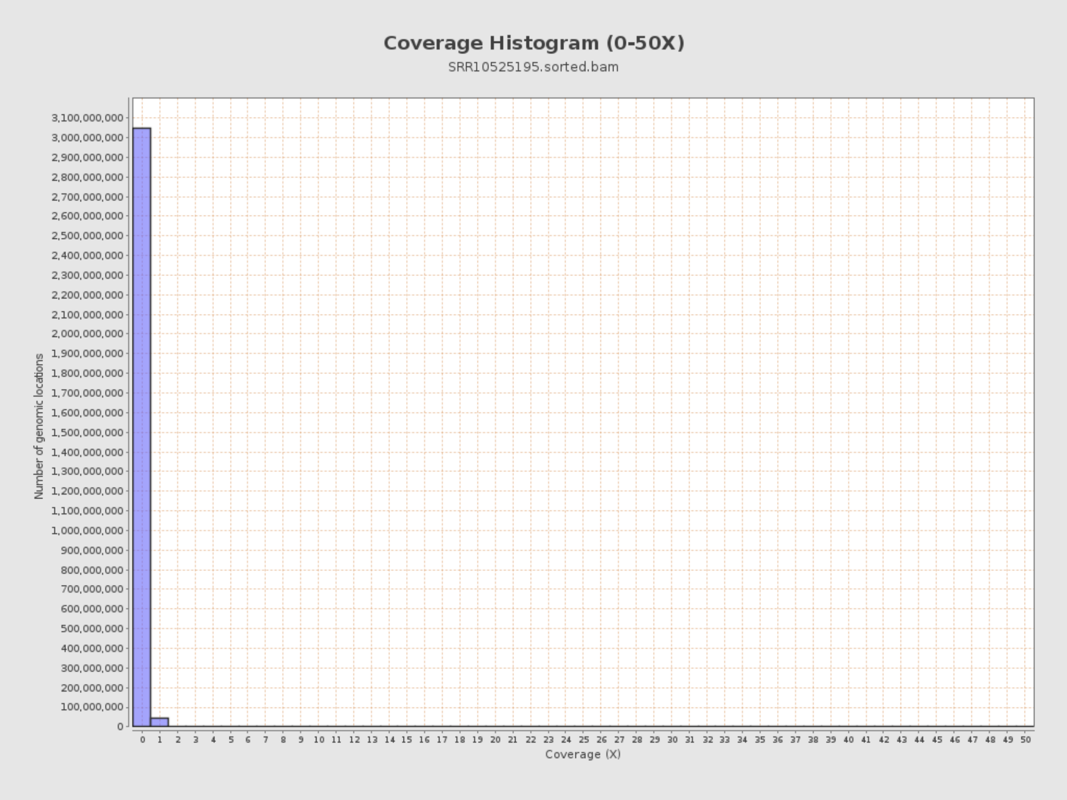
3. Results : Coverage across reference



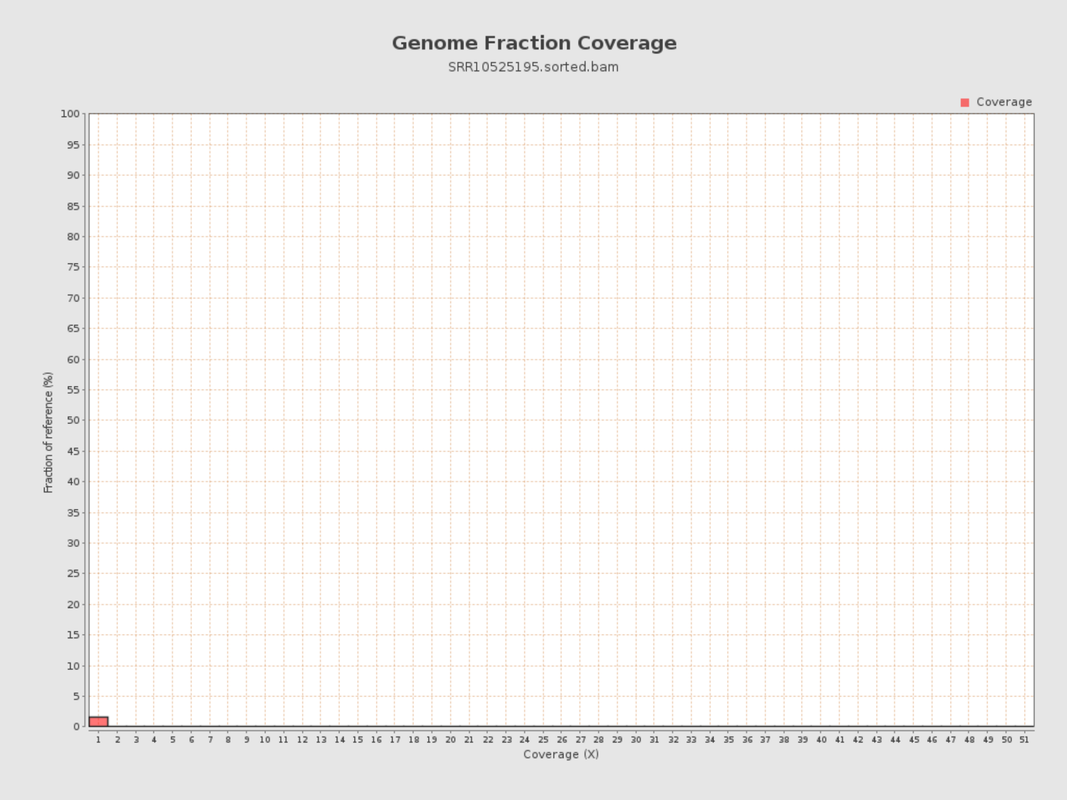
4. Results : Coverage Histogram



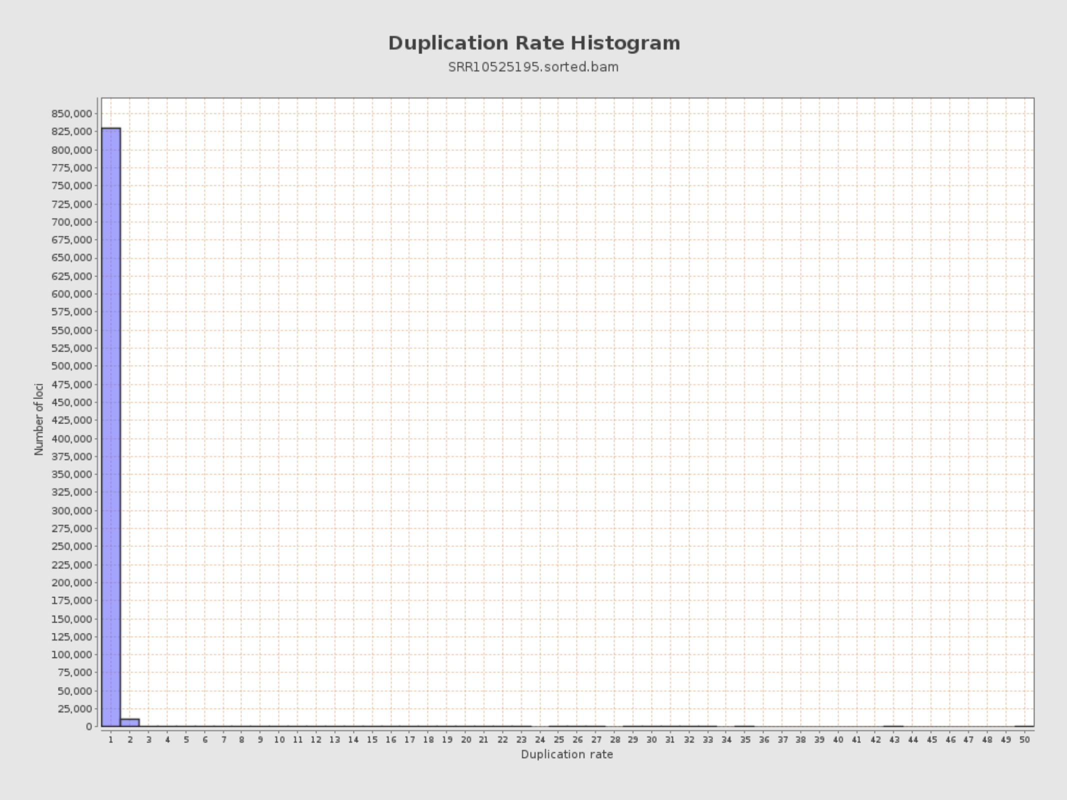
5. Results : Coverage Histogram (0-50X)



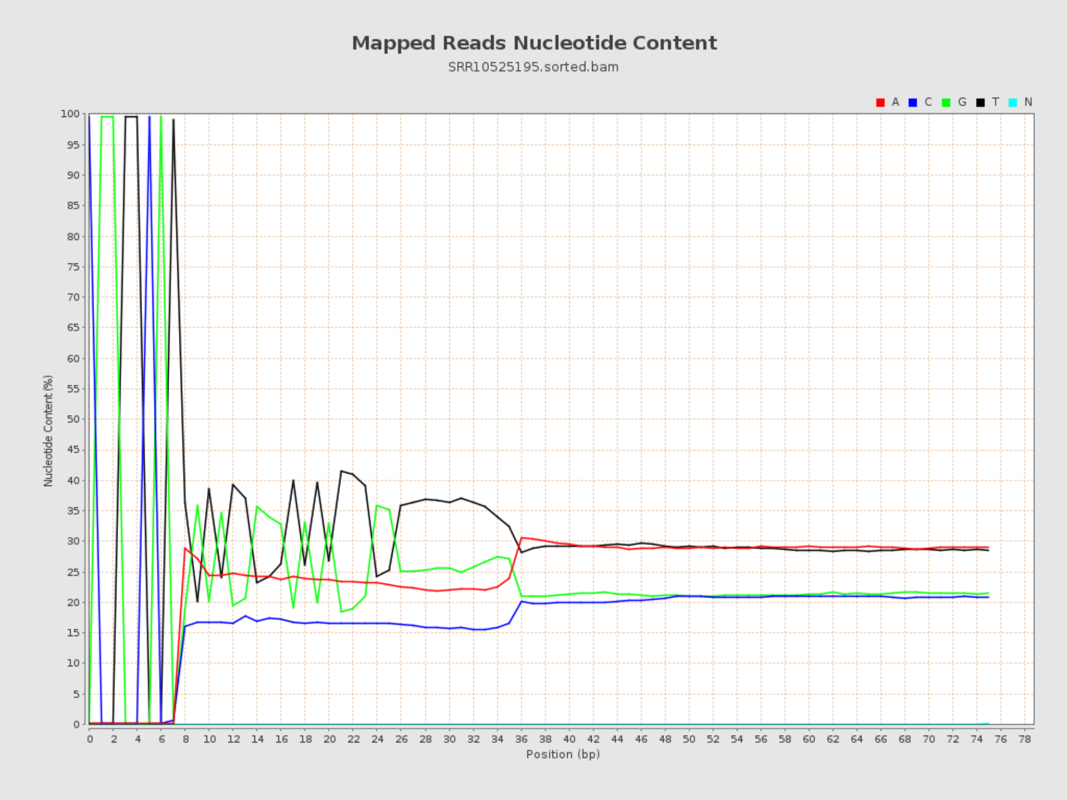
6. Results : Genome Fraction Coverage



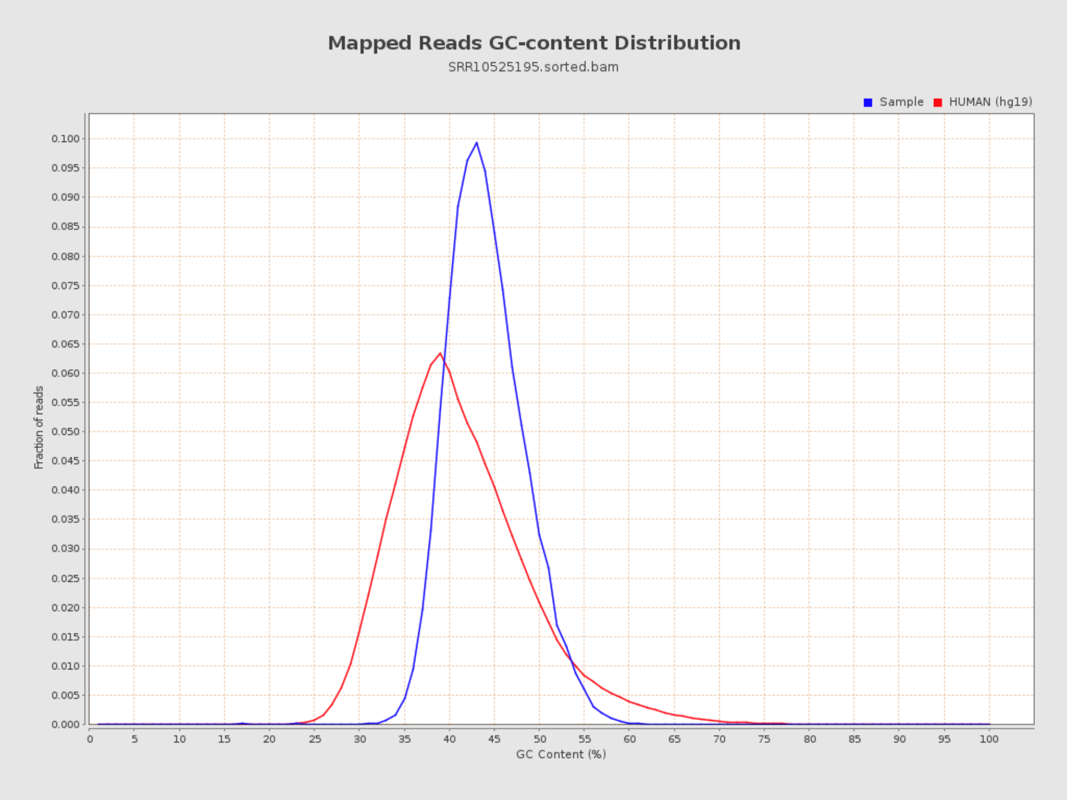
7. Results : Duplication Rate Histogram



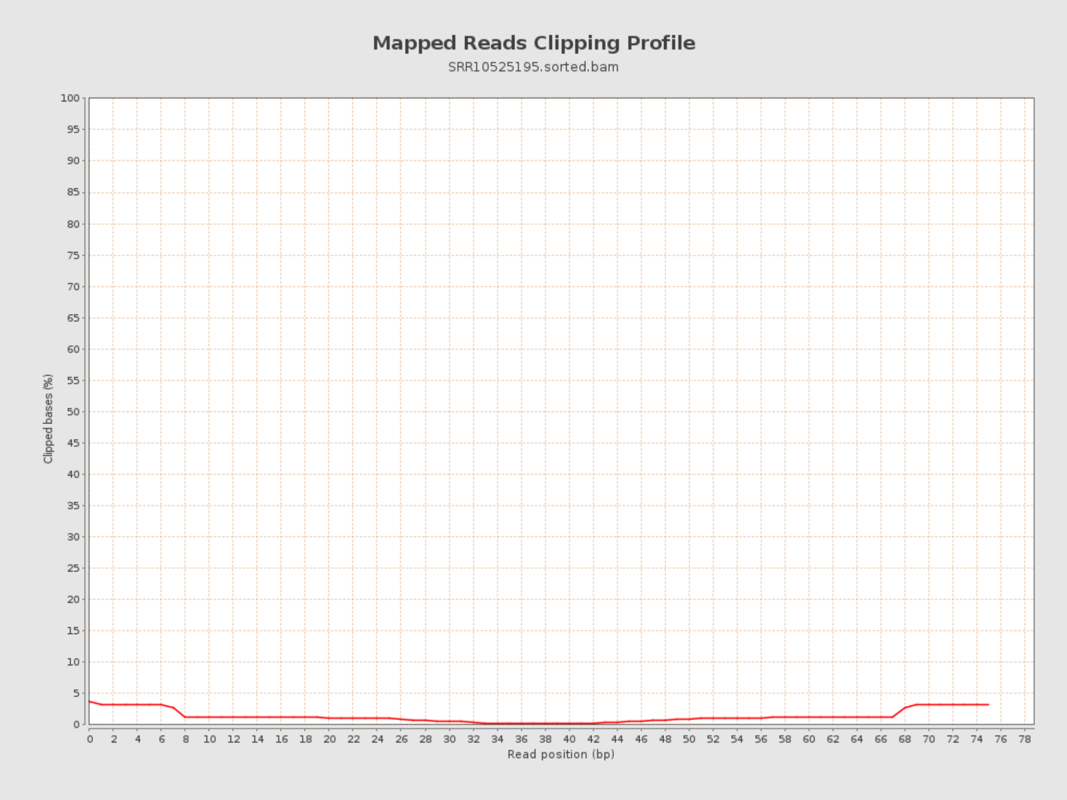
8. Results : Mapped Reads Nucleotide Content



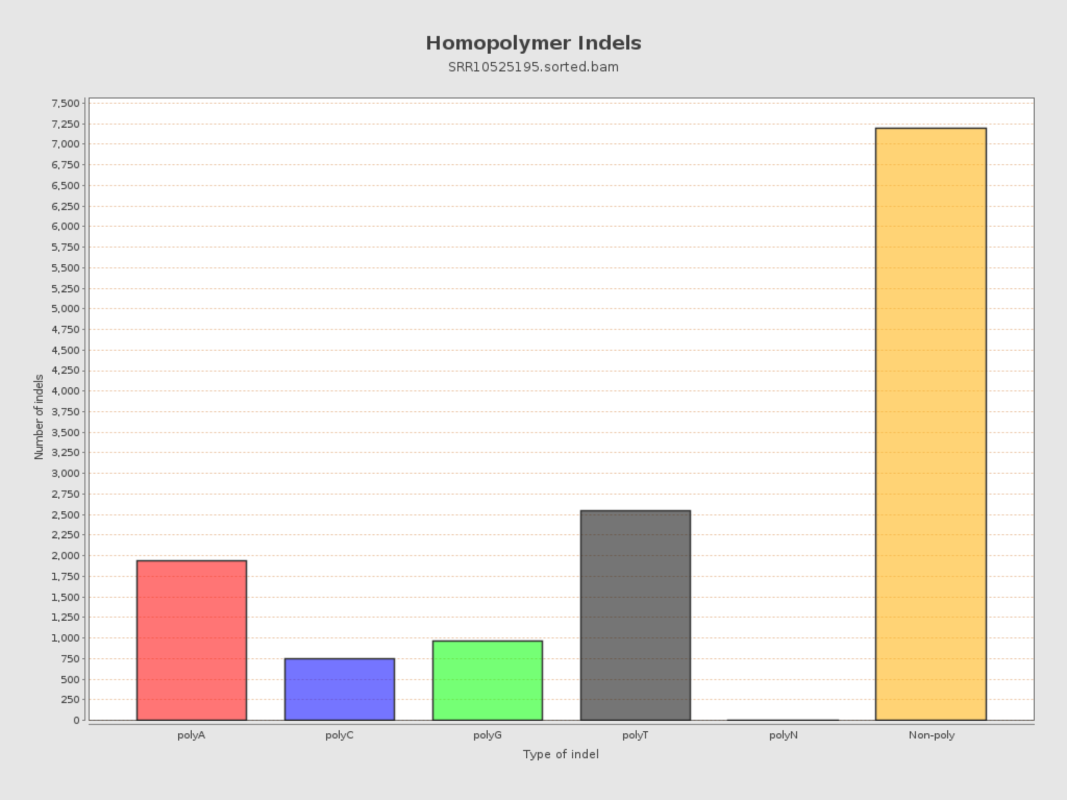
9. Results : Mapped Reads GC-content Distribution



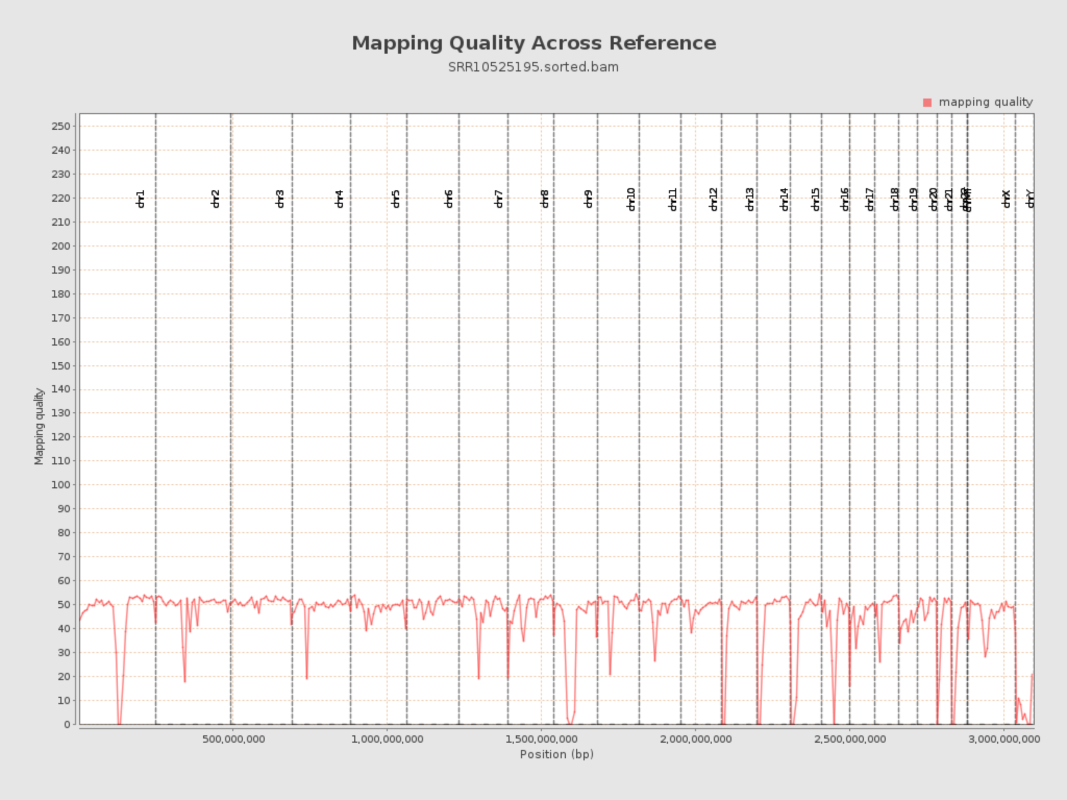
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram