Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:48:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716826.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_SRR9716826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:48:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	788,731
Mapped reads	648,402 / 82.21%
Unmapped reads	140,329 / 17.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	781 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	52,074 / 6.6%
Duplication rate	7%
Clipped reads	648,553 / 82.23%

2.2. ACGT Content

Number/percentage of A's	6,809,414 / 19.8%
Number/percentage of C's	6,062,427 / 17.63%
Number/percentage of T's	11,396,178 / 33.13%
Number/percentage of G's	10,127,002 / 29.44%
Number/percentage of N's	577 / 0%
GC Percentage	47.07%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1303

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

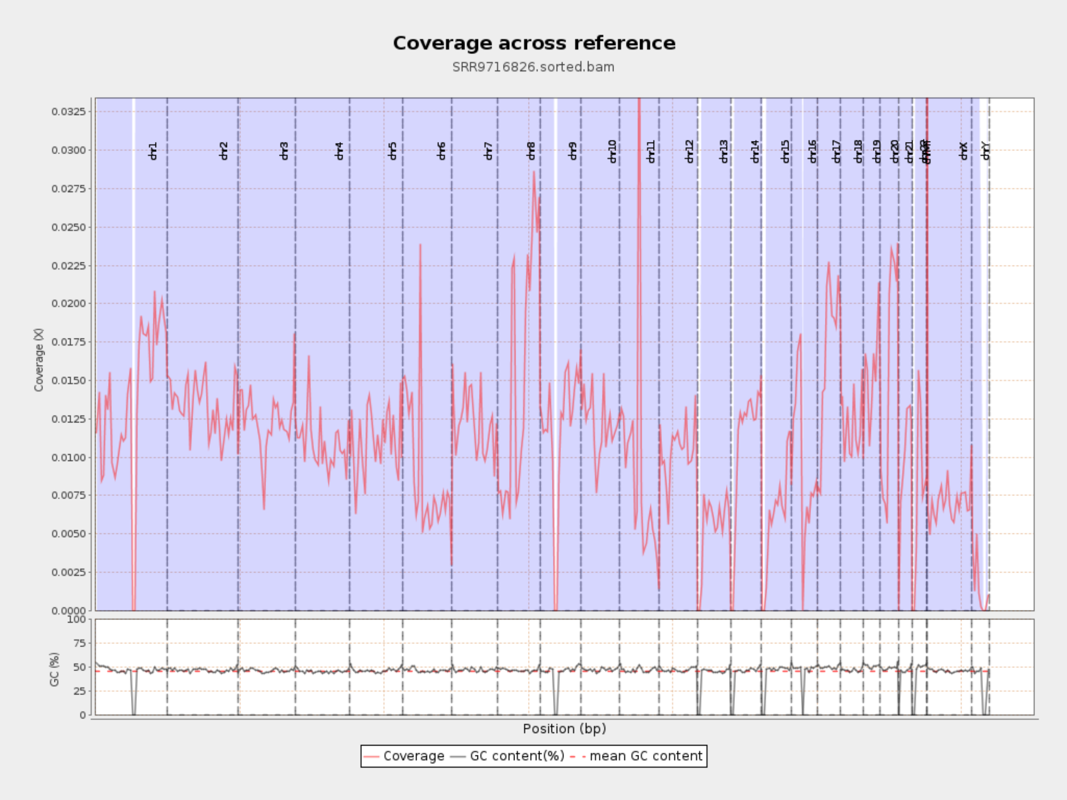
General error rate	0.63%
Mismatches	215,288
Insertions	1,690
Mapped reads with at least one insertion	0.26%
Deletions	4,807
Mapped reads with at least one deletion	0.74%
Homopolymer indels	41.9%

2.6. Chromosome stats

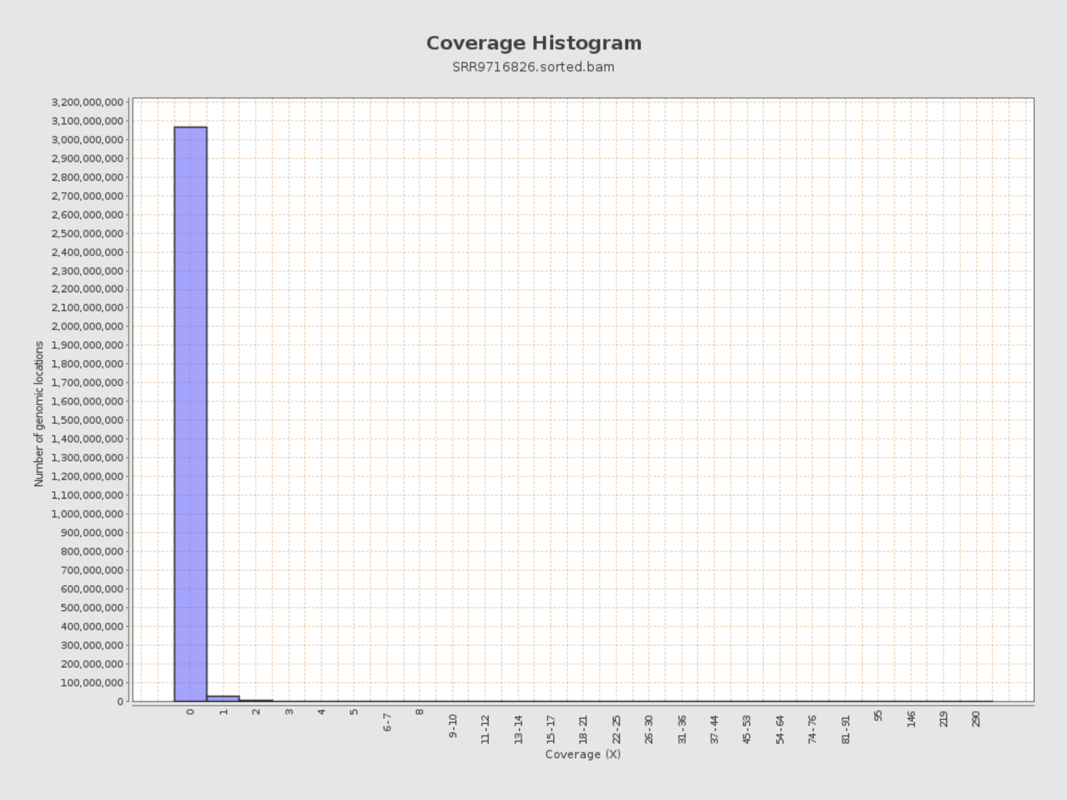
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3400630	0.0136	0.1431
chr2	243199373	3240431	0.0133	0.1767
chr3	198022430	2427248	0.0123	0.128
chr4	191154276	2091744	0.0109	0.1205
chr5	180915260	2014486	0.0111	0.1216
chr6	171115067	1537971	0.009	0.1176
chr7	159138663	1950501	0.0123	0.1374

chr8	146364022	2250020	0.0154	0.1464
chr9	141213431	1644993	0.0116	0.1298
chr10	135534747	1652662	0.0122	0.1359
chr11	135006516	1326689	0.0098	0.1219
chr12	133851895	1403984	0.0105	0.1174
chr13	115169878	618754	0.0054	0.0874
chr14	107349540	1158131	0.0108	0.1199
chr15	102531392	635718	0.0062	0.0909
chr16	90354753	830417	0.0092	0.117
chr17	81195210	1372112	0.0169	0.1545
chr18	78077248	935083	0.012	0.1371
chr19	59128983	909902	0.0154	0.1709
chr20	63025520	965992	0.0153	0.1481
chr21	48129895	468630	0.0097	0.1192
chr22	51304566	396712	0.0077	0.1046
chrMT	16571	1575	0.095	0.3497
chrX	155270560	1079686	0.007	0.0974
chrY	59373566	89828	0.0015	0.0506

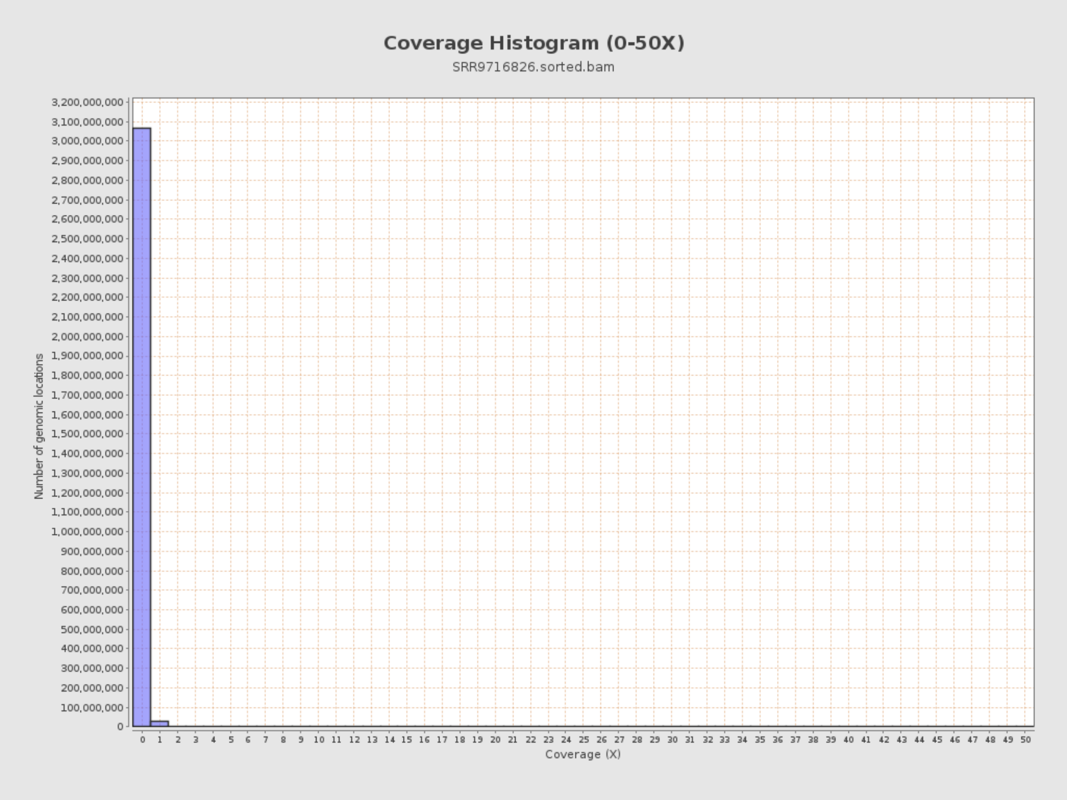
3. Results : Coverage across reference



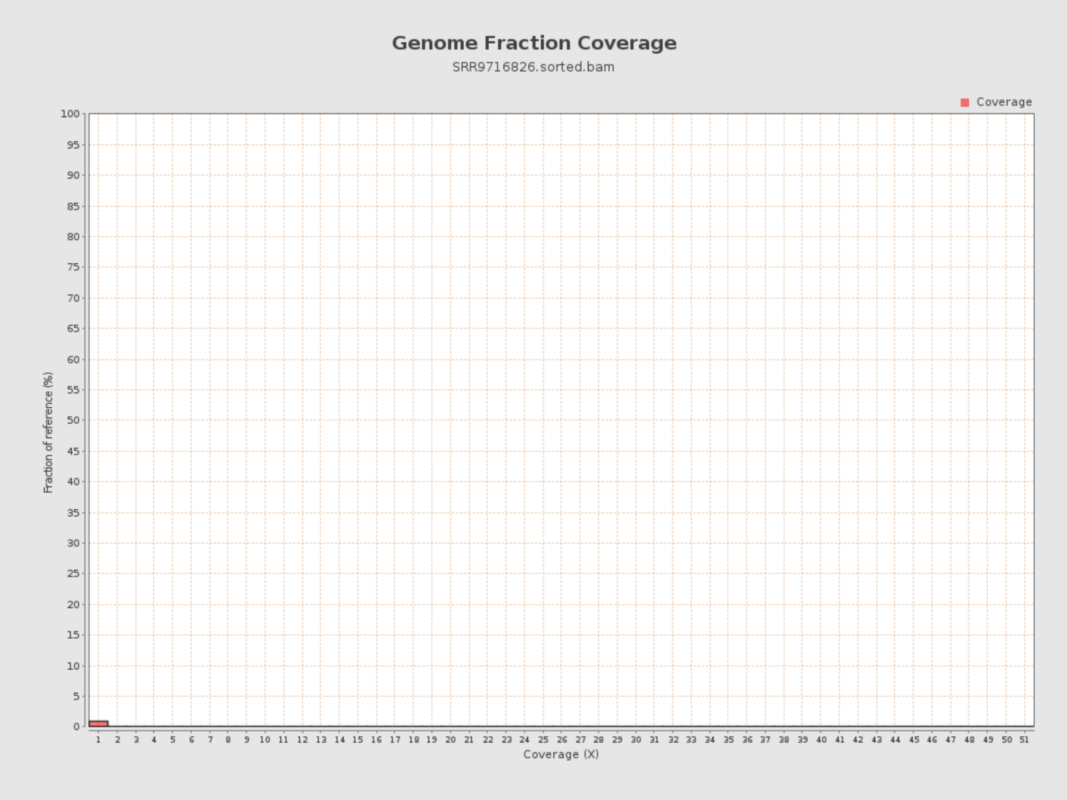
4. Results : Coverage Histogram



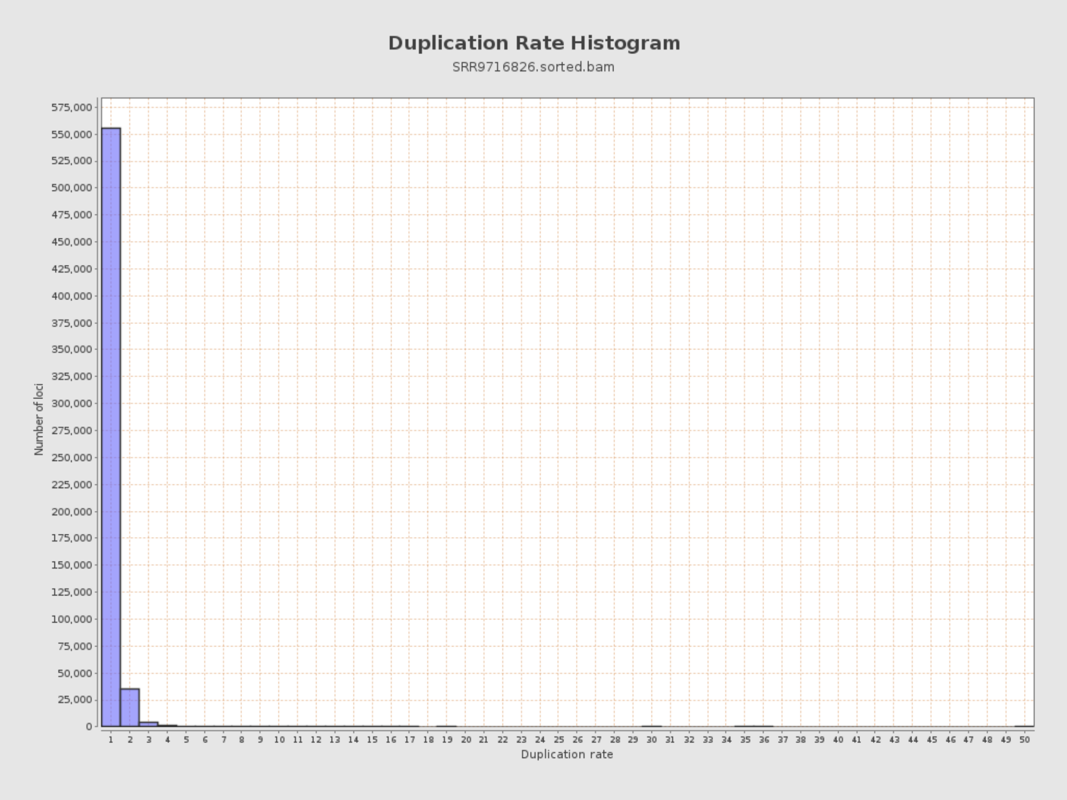
5. Results : Coverage Histogram (0-50X)



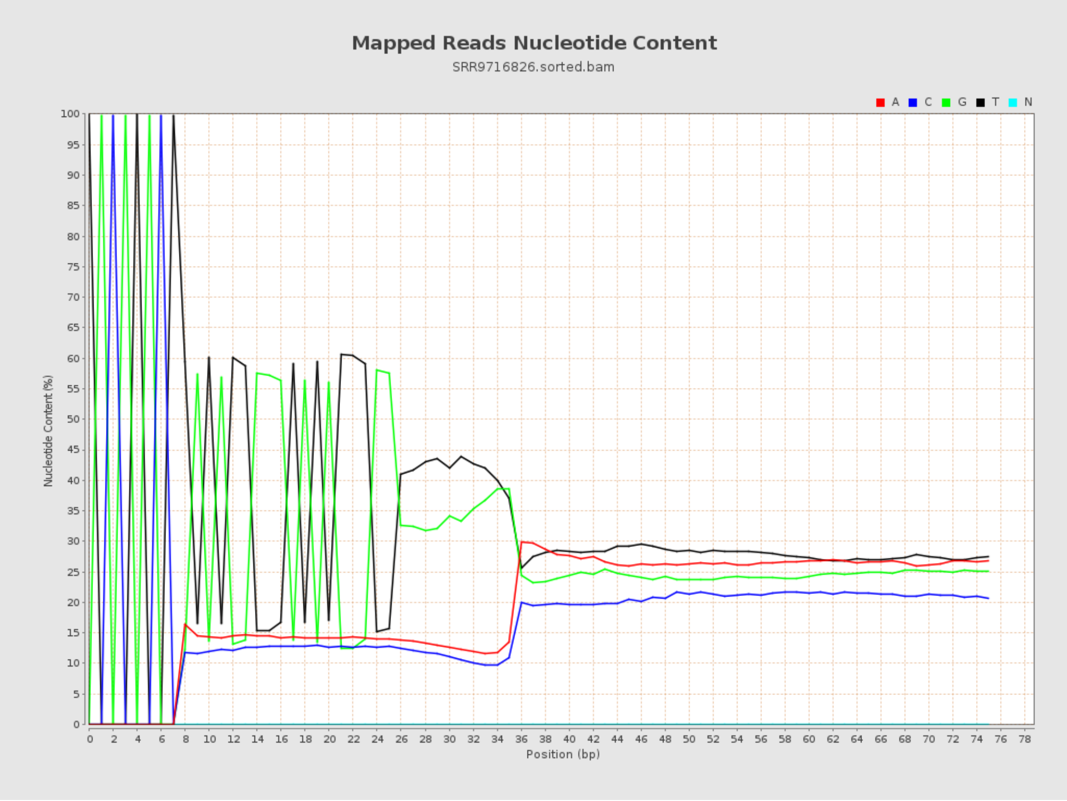
6. Results : Genome Fraction Coverage



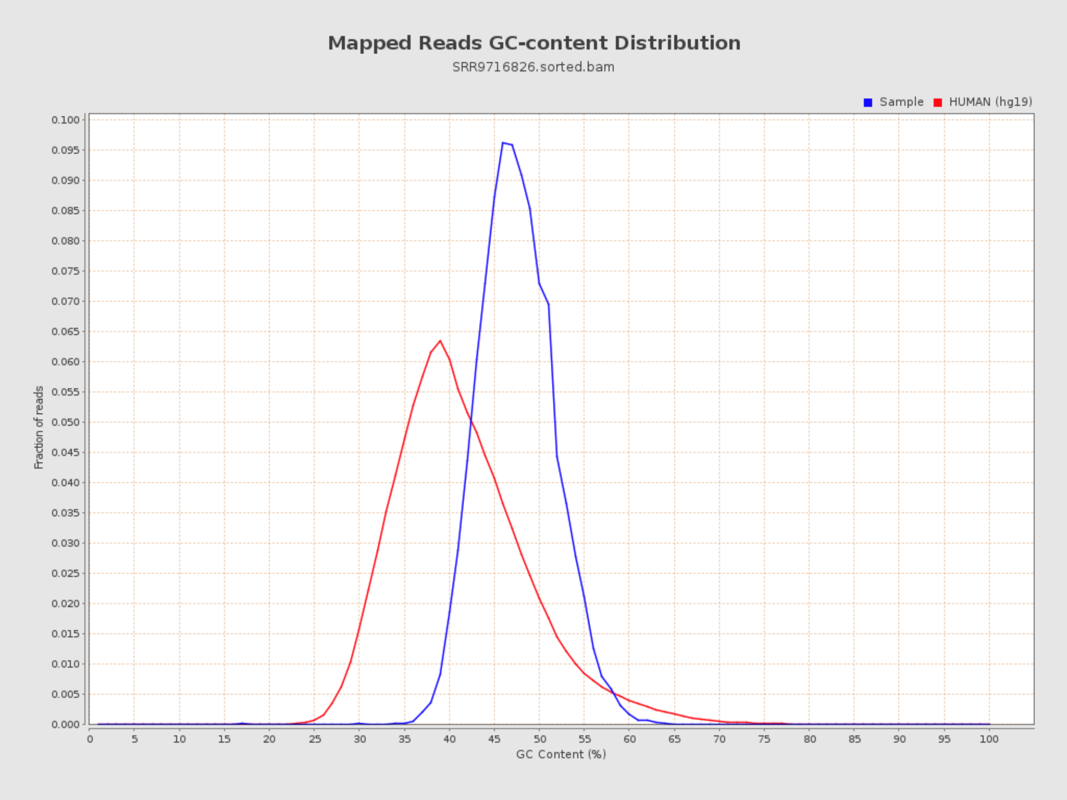
7. Results : Duplication Rate Histogram



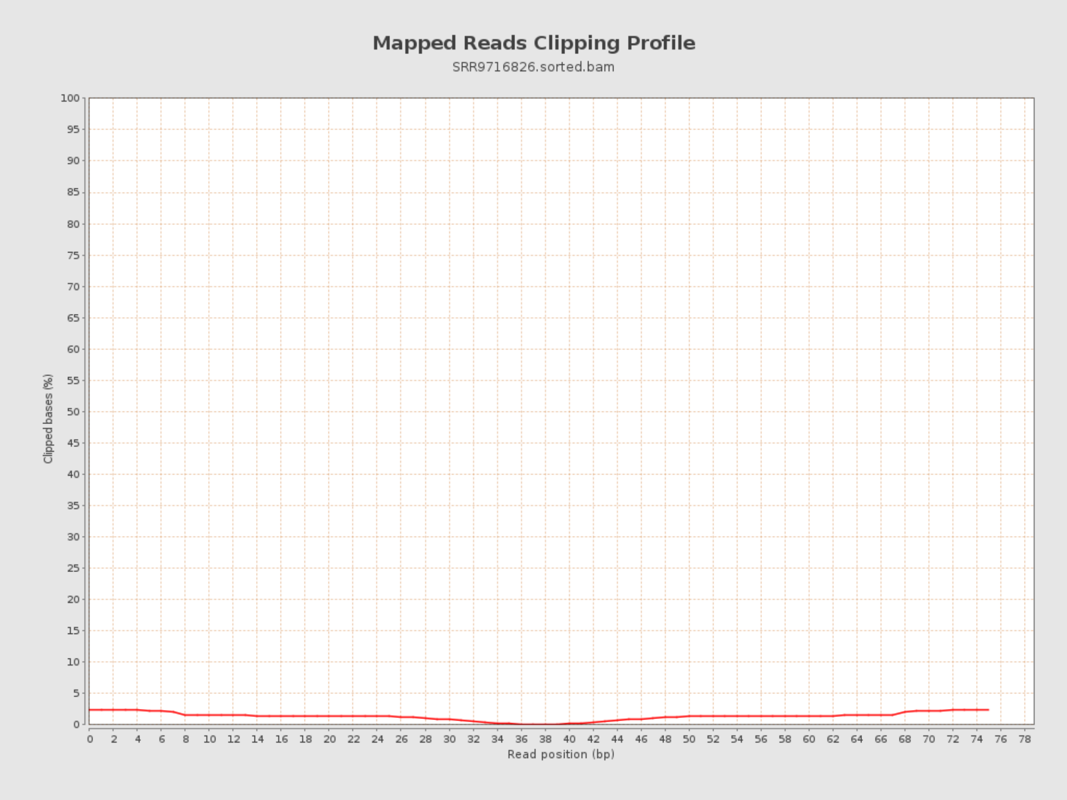
8. Results : Mapped Reads Nucleotide Content



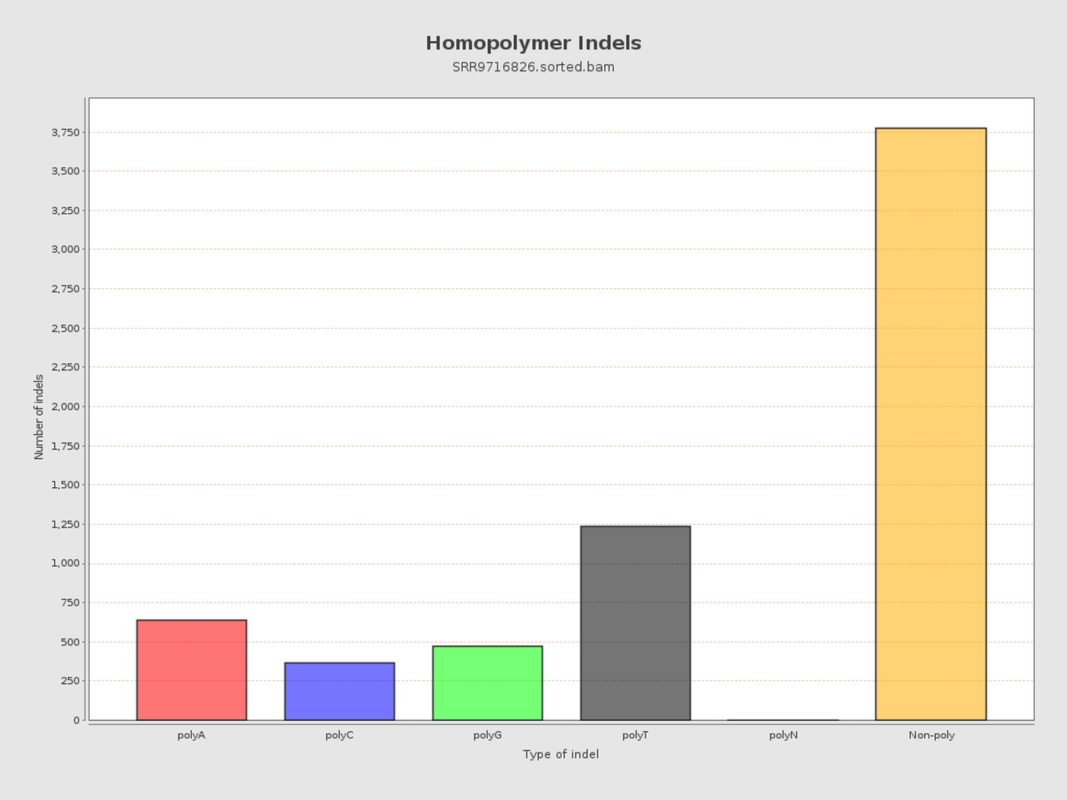
9. Results : Mapped Reads GC-content Distribution



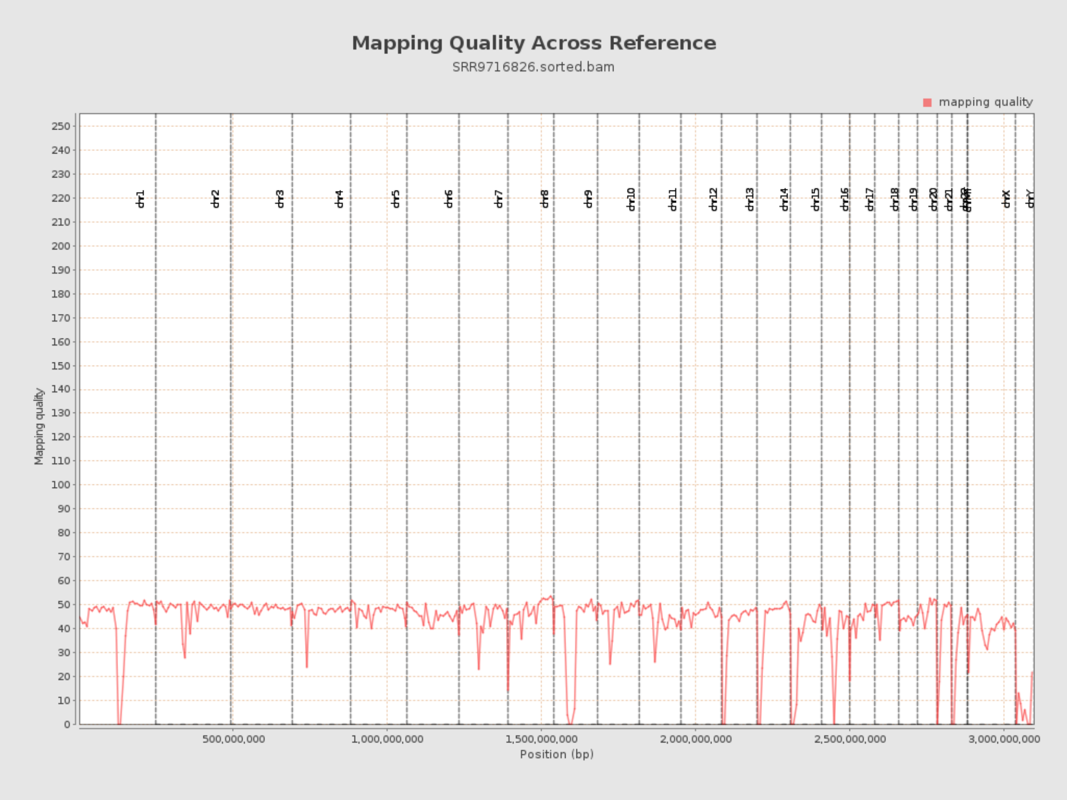
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram