Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:03:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716685.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_SRR9716685 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716685.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716685.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,505,268
Mapped reads	1,319,565 / 87.66%
Unmapped reads	185,703 / 12.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,003 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	31,181 / 2.07%
Duplication rate	1.61%
Clipped reads	1,320,061 / 87.7%

2.2. ACGT Content

Number/percentage of A's	19,163,349 / 25.6%
Number/percentage of C's	14,487,964 / 19.36%
Number/percentage of T's	22,518,284 / 30.09%
Number/percentage of G's	18,674,849 / 24.95%
Number/percentage of N's	477 / 0%
GC Percentage	44.31%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2174

2.4. Mapping Quality

Mean Mapping Quality	41.84

2.5. Mismatches and indels

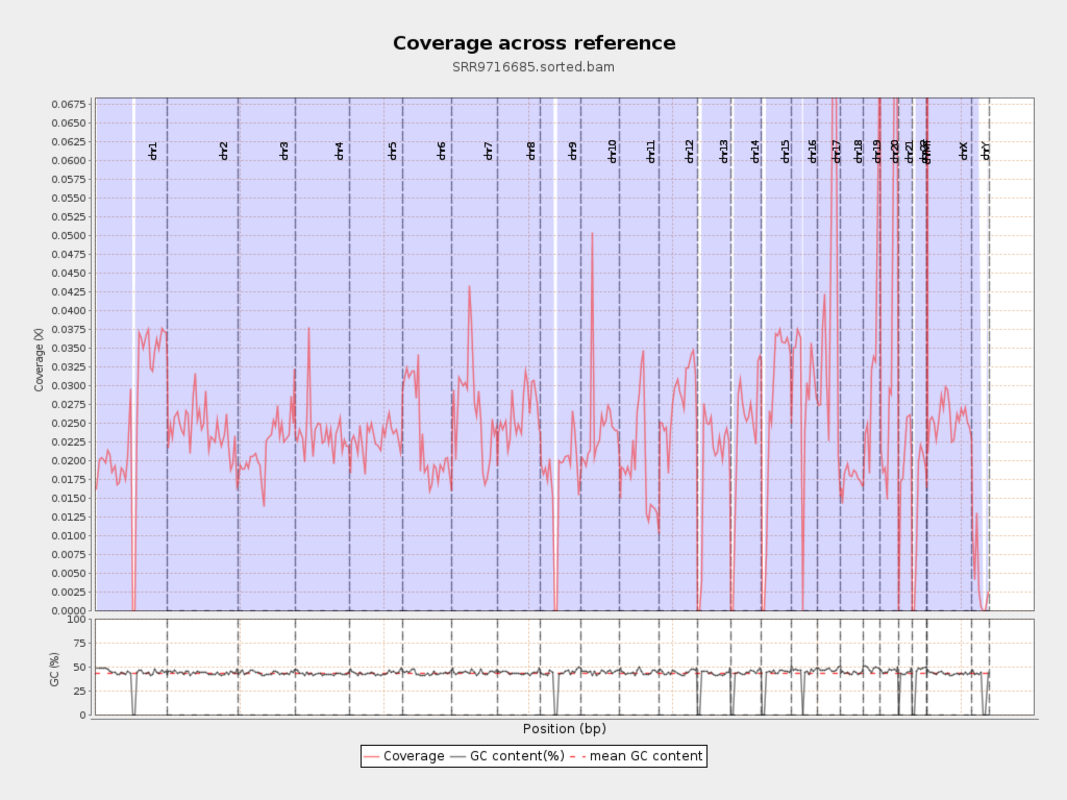
General error rate	0.54%
Mismatches	392,153
Insertions	5,738
Mapped reads with at least one insertion	0.43%
Deletions	13,768
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.69%

2.6. Chromosome stats

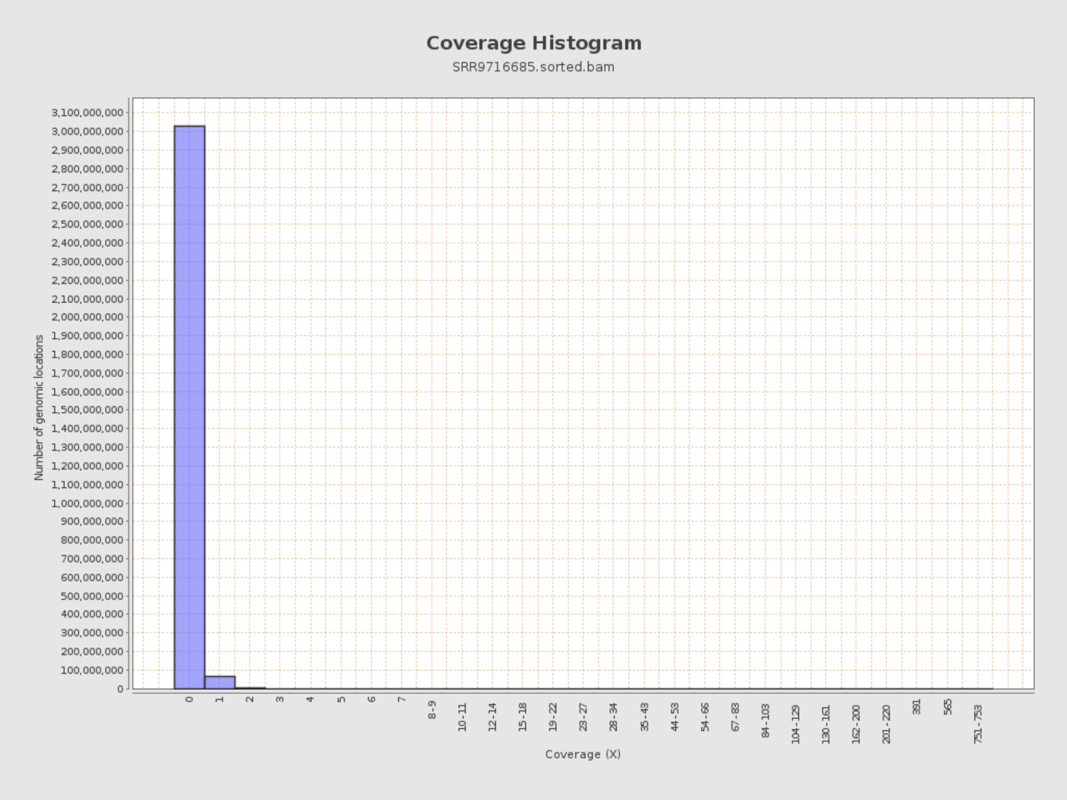
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6280595	0.0252	0.2443
chr2	243199373	5873356	0.0242	0.3438
chr3	198022430	4316527	0.0218	0.1647
chr4	191154276	4528918	0.0237	0.1779
chr5	180915260	4183308	0.0231	0.1624
chr6	171115067	3970973	0.0232	0.1933
chr7	159138663	4276501	0.0269	0.2994

chr8	146364022	3848832	0.0263	0.204
chr9	141213431	2491866	0.0176	0.1633
chr10	135534747	3334545	0.0246	0.277
chr11	135006516	2656469	0.0197	0.1758
chr12	133851895	3761312	0.0281	0.1815
chr13	115169878	2237371	0.0194	0.1487
chr14	107349540	2496423	0.0233	0.1678
chr15	102531392	2763951	0.027	0.1793
chr16	90354753	2633165	0.0291	0.1952
chr17	81195210	3427245	0.0422	0.2302
chr18	78077248	1380815	0.0177	0.2447
chr19	59128983	2054466	0.0347	0.2625
chr20	63025520	2396128	0.038	0.2186
chr21	48129895	944604	0.0196	0.1609
chr22	51304566	728523	0.0142	0.1294
chrMT	16571	63796	3.8499	3.1841
chrX	155270560	3987136	0.0257	0.1837
chrY	59373566	230020	0.0039	0.1151

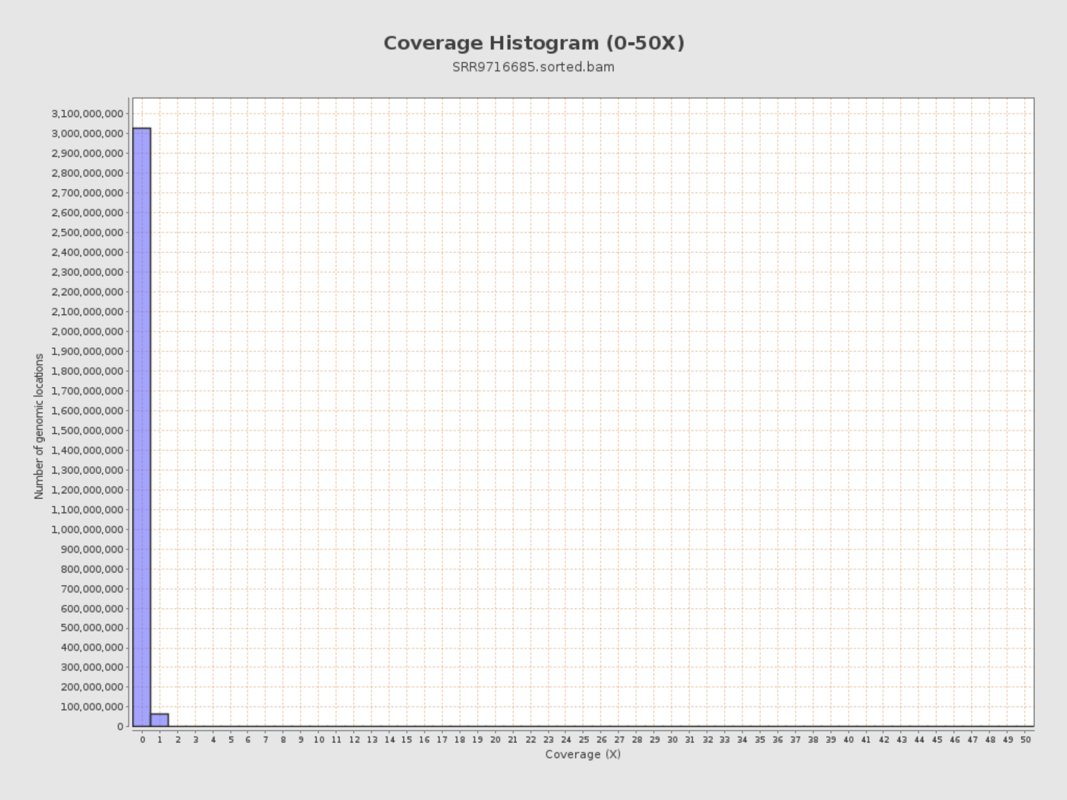
3. Results : Coverage across reference



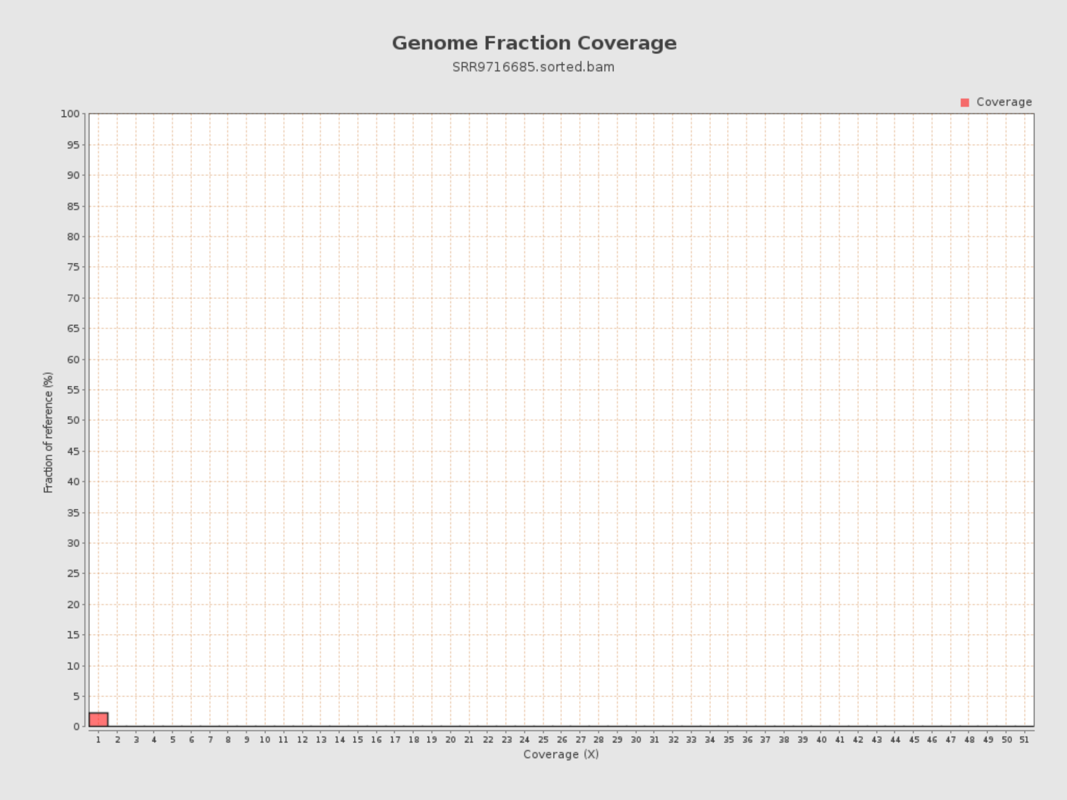
4. Results : Coverage Histogram



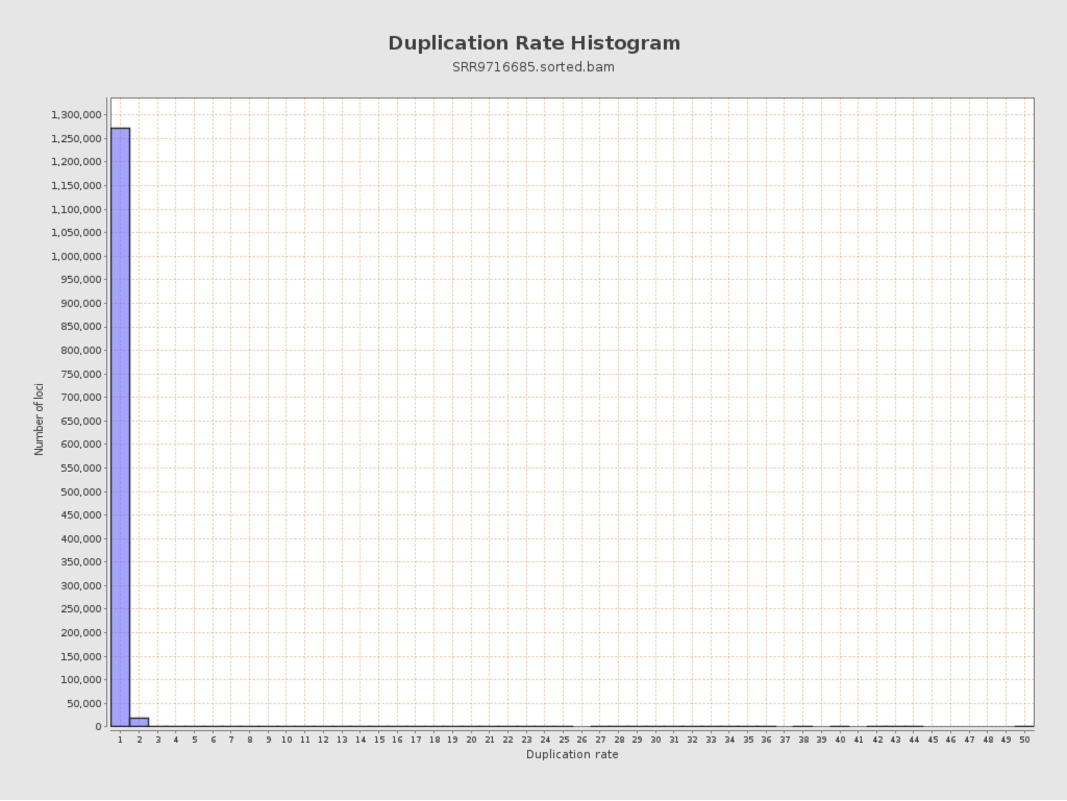
5. Results : Coverage Histogram (0-50X)



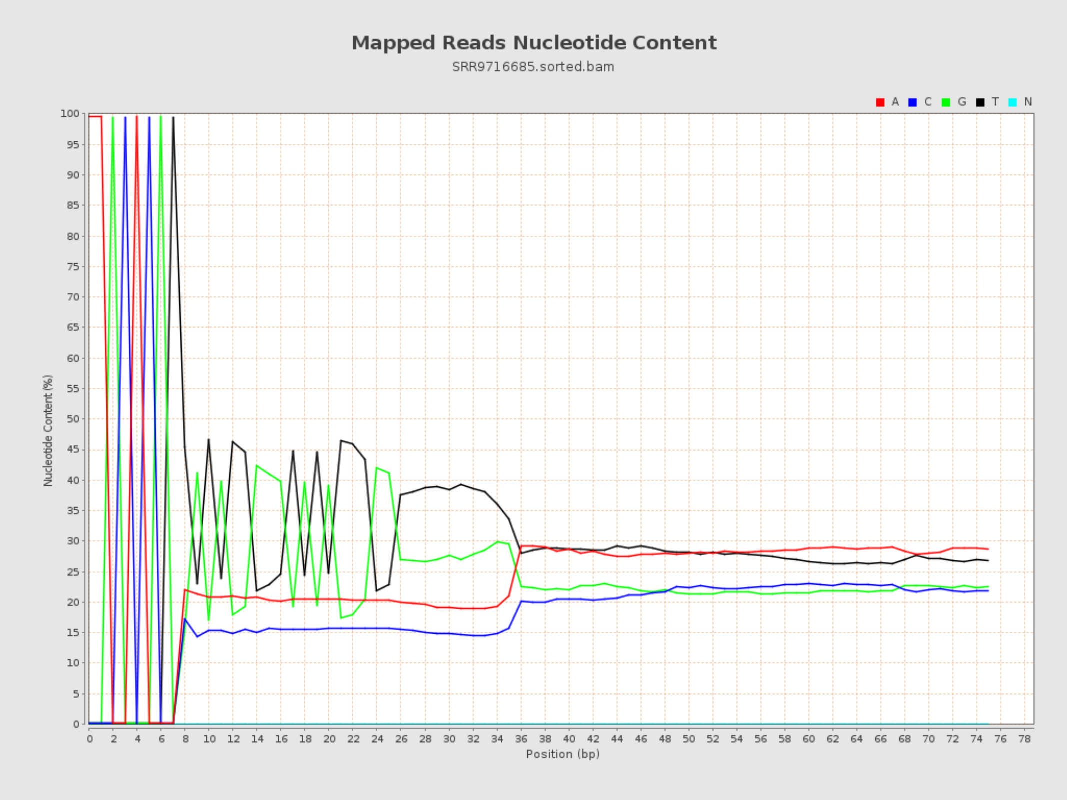
6. Results : Genome Fraction Coverage



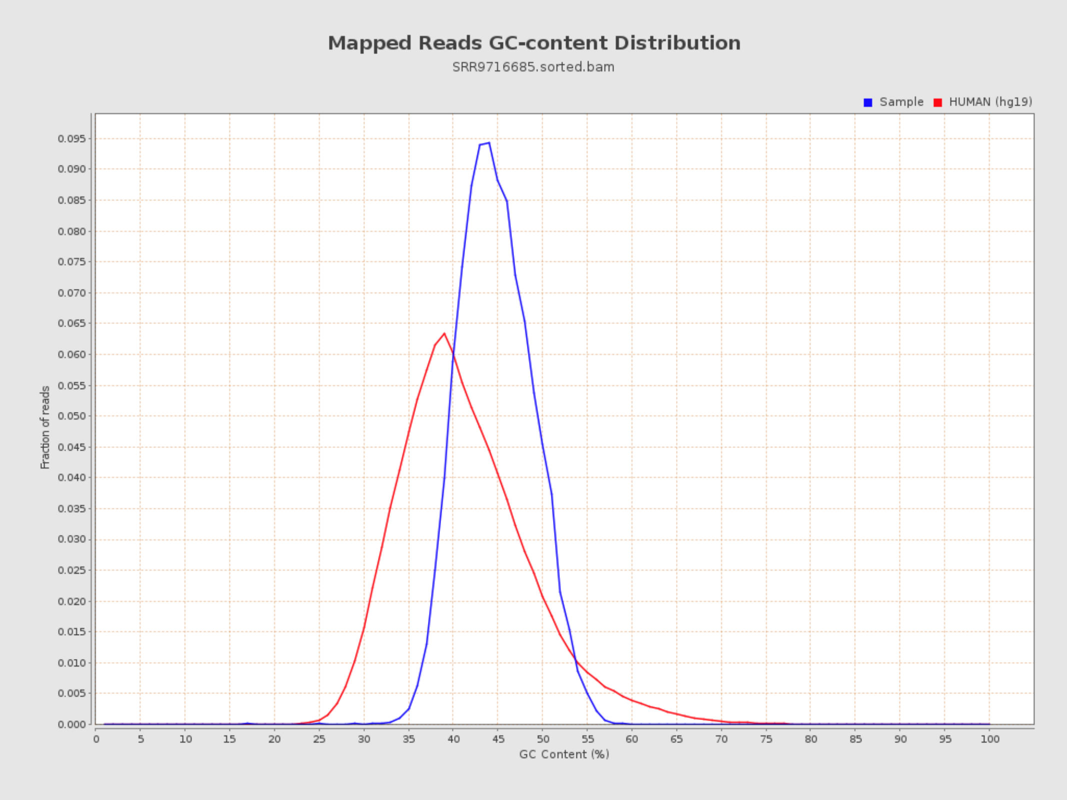
7. Results : Duplication Rate Histogram



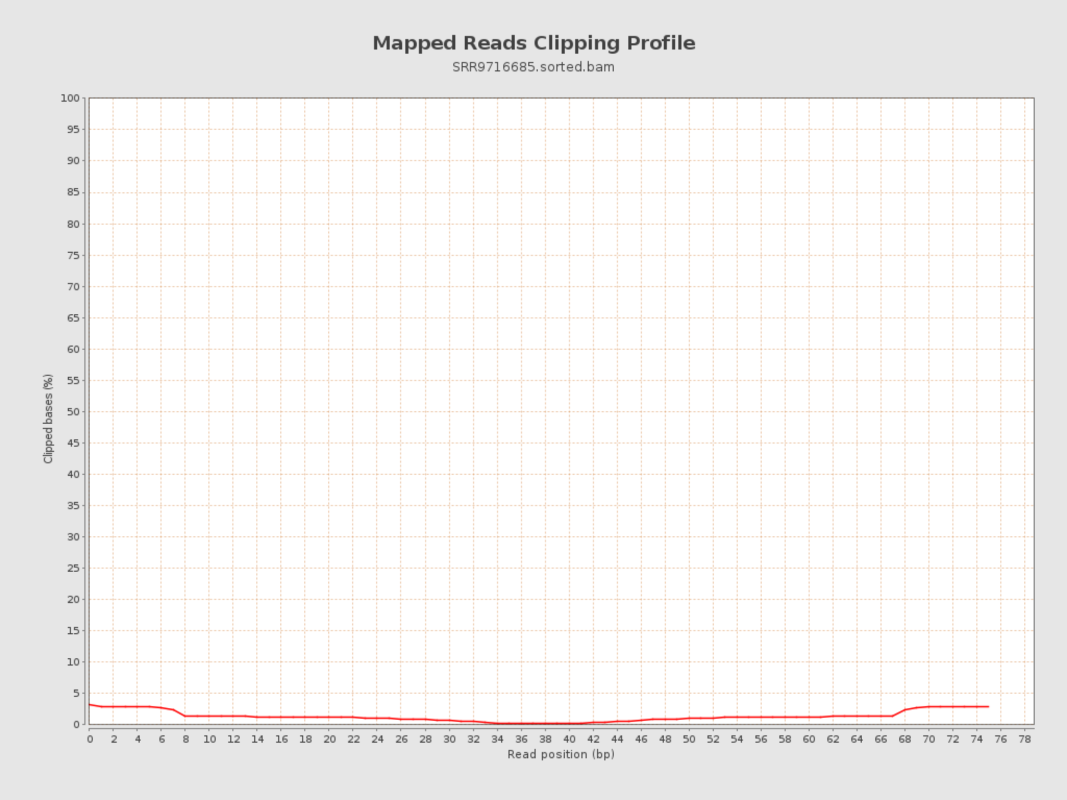
8. Results : Mapped Reads Nucleotide Content



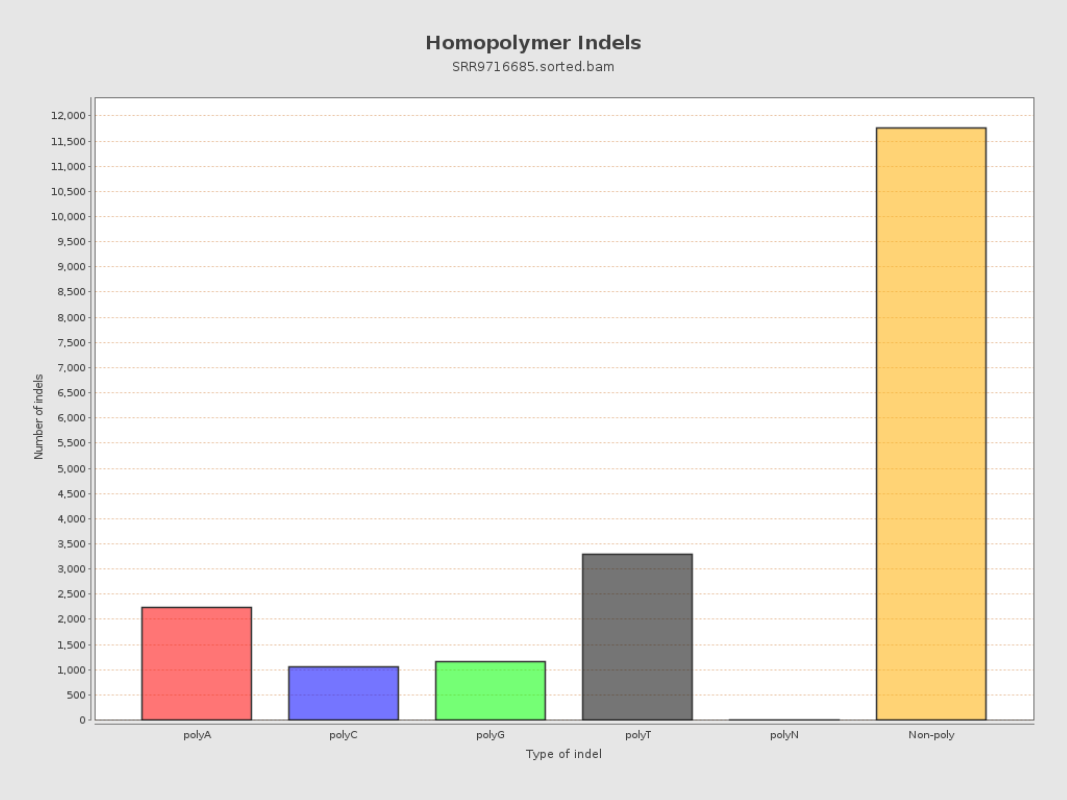
9. Results : Mapped Reads GC-content Distribution



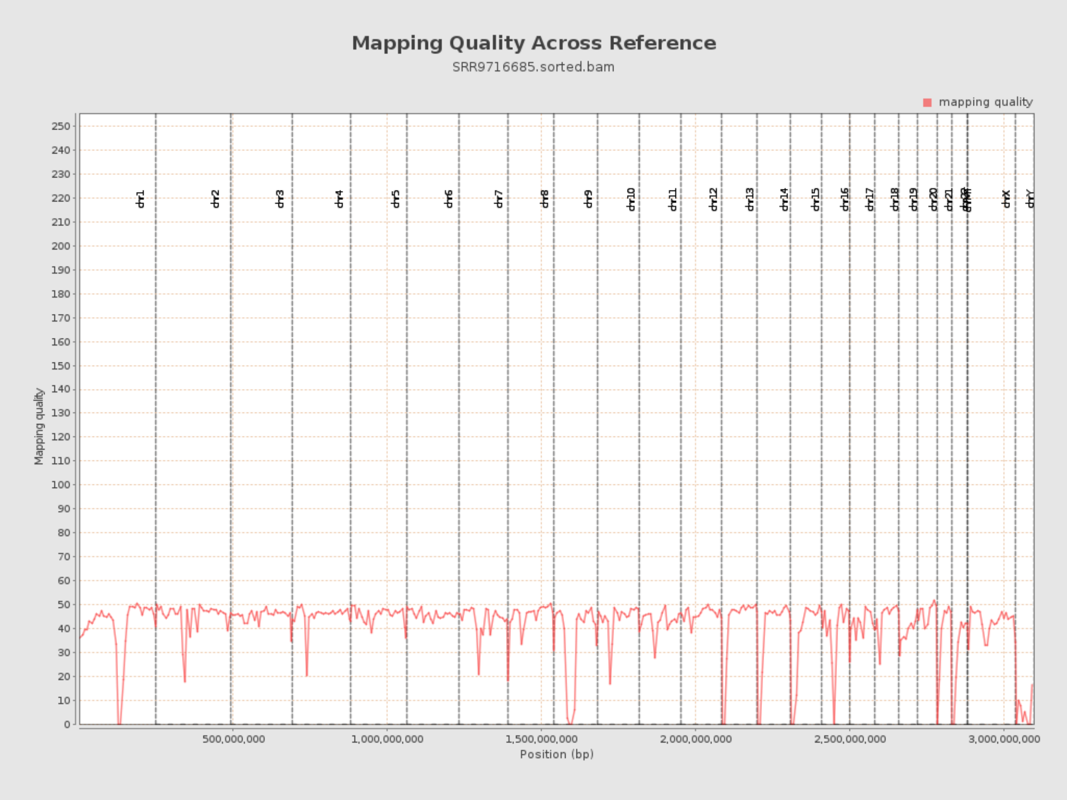
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram