Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:30:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716982.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_SRR9716982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:30:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,363,378
Mapped reads	2,168,626 / 91.76%
Unmapped reads	194,752 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,886 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	77,570 / 3.28%
Duplication rate	2.46%
Clipped reads	2,175,556 / 92.05%

2.2. ACGT Content

Number/percentage of A's	30,095,640 / 23.93%
Number/percentage of C's	24,085,223 / 19.15%
Number/percentage of T's	39,824,149 / 31.66%
Number/percentage of G's	31,778,504 / 25.26%
Number/percentage of N's	1,393 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.376

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

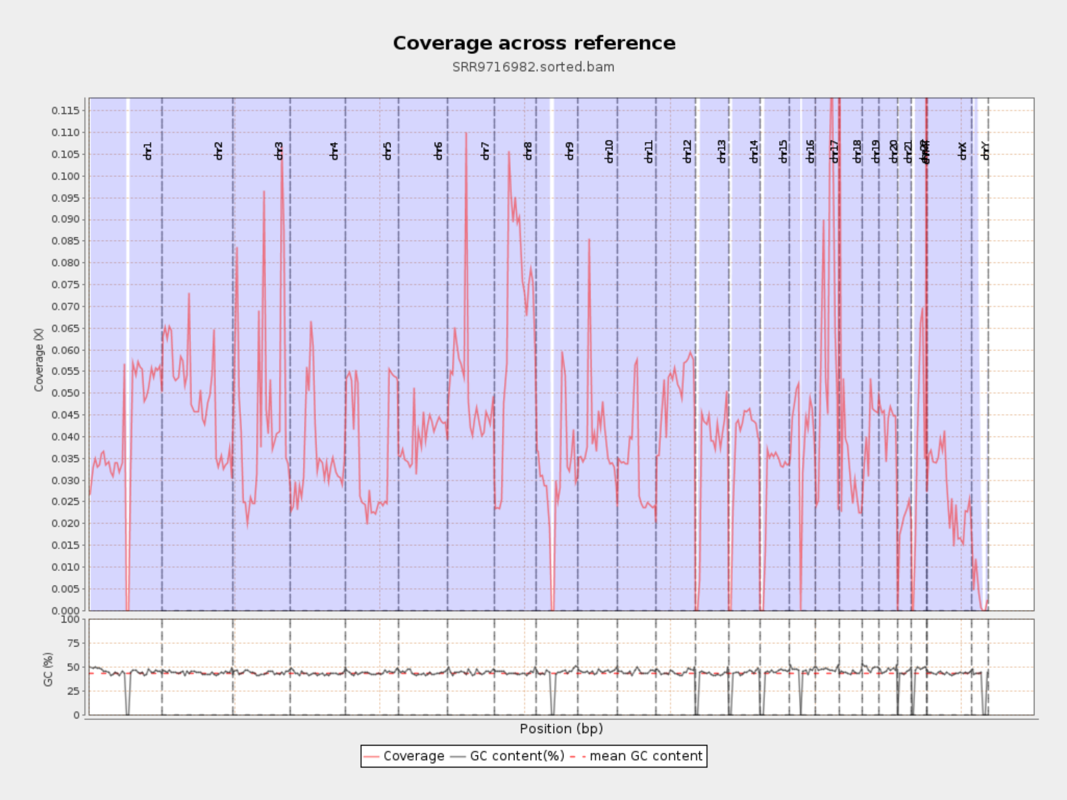
General error rate	0.51%
Mismatches	626,817
Insertions	7,604
Mapped reads with at least one insertion	0.35%
Deletions	23,369
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.62%

2.6. Chromosome stats

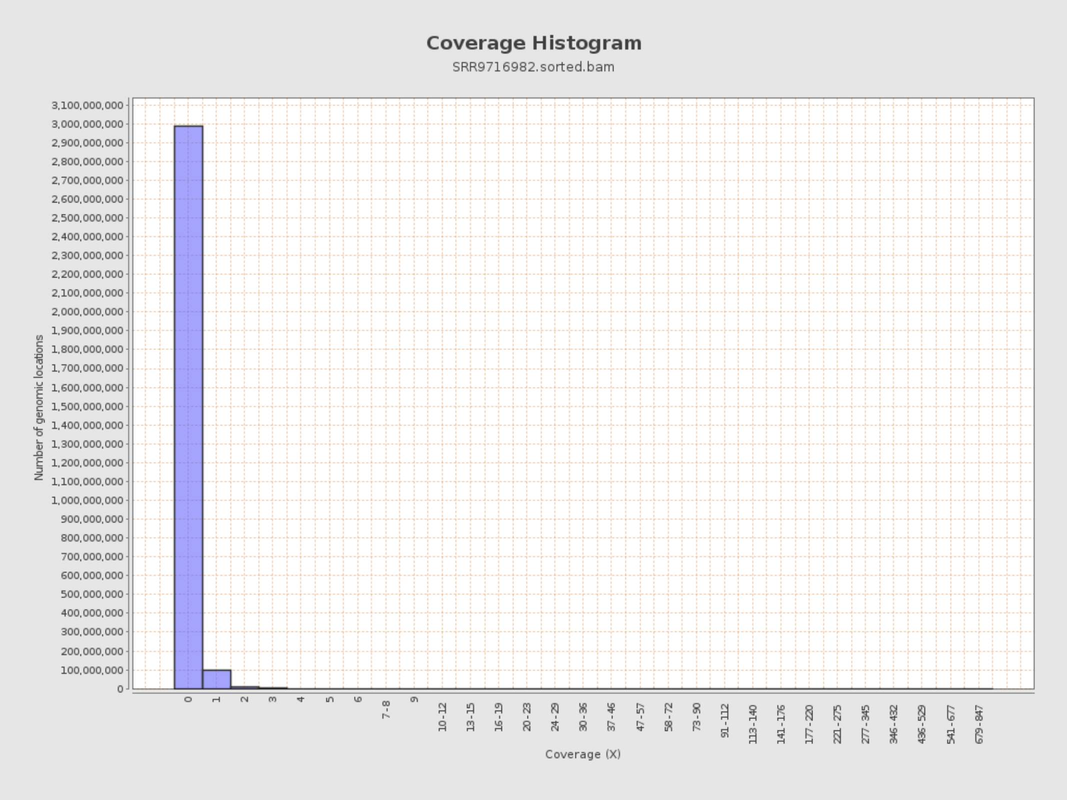
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10091430	0.0405	0.55
chr2	243199373	12093776	0.0497	0.4388
chr3	198022430	9176031	0.0463	0.2508
chr4	191154276	6769724	0.0354	0.2178
chr5	180915260	6664151	0.0368	0.2135
chr6	171115067	6853646	0.0401	0.2492
chr7	159138663	8269149	0.052	0.9076

chr8	146364022	9801548	0.067	0.3954
chr9	141213431	4275421	0.0303	0.2379
chr10	135534747	5474586	0.0404	0.4394
chr11	135006516	4410239	0.0327	0.2587
chr12	133851895	6818657	0.0509	0.2677
chr13	115169878	4066525	0.0353	0.2061
chr14	107349540	3935560	0.0367	0.2167
chr15	102531392	2904492	0.0283	0.1953
chr16	90354753	3649547	0.0404	0.2373
chr17	81195210	5118437	0.063	0.2944
chr18	78077248	2934588	0.0376	0.4242
chr19	59128983	2464162	0.0417	0.4707
chr20	63025520	2741762	0.0435	0.2411
chr21	48129895	930221	0.0193	0.1593
chr22	51304566	1828108	0.0356	0.2103
chrMT	16571	7111	0.4291	0.765
chrX	155270560	4294483	0.0277	0.2153
chrY	59373566	248063	0.0042	0.0877

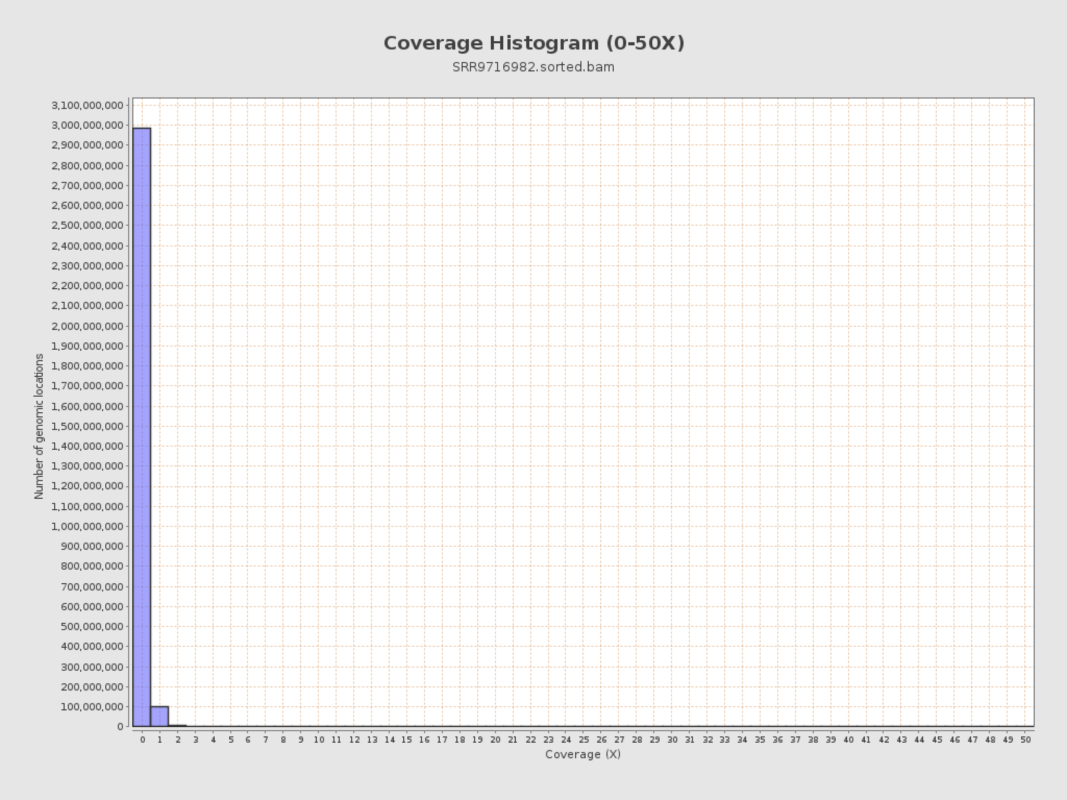
3. Results : Coverage across reference



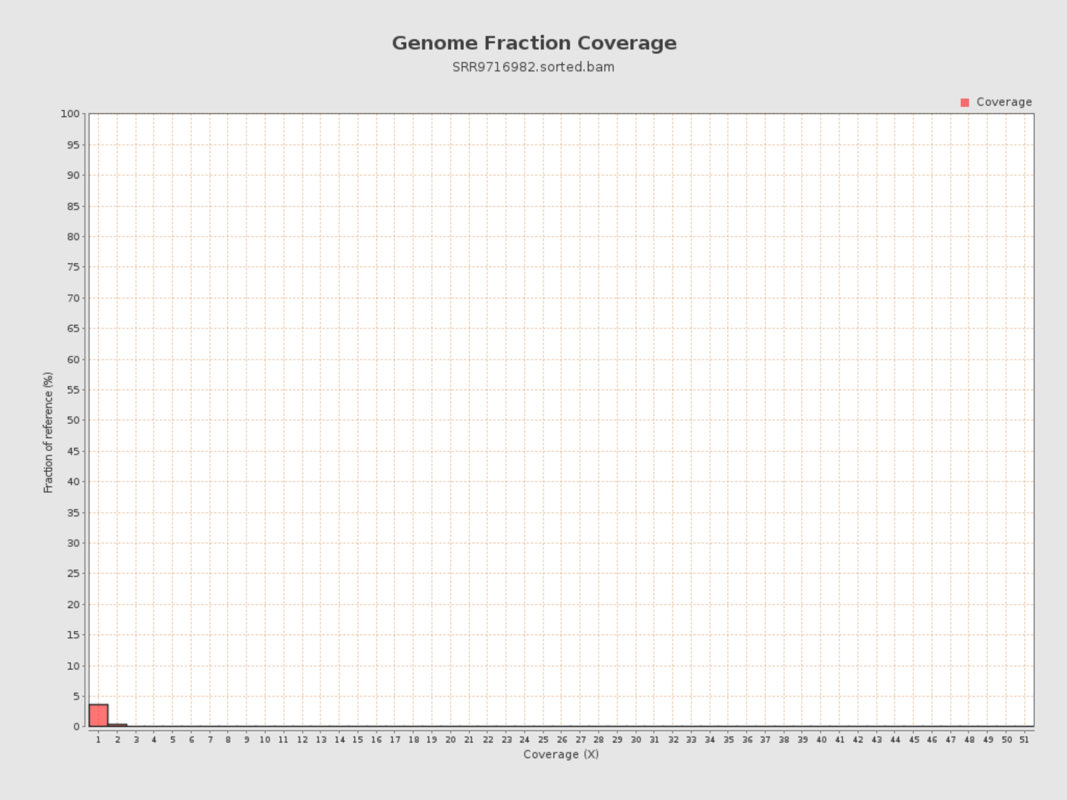
4. Results : Coverage Histogram



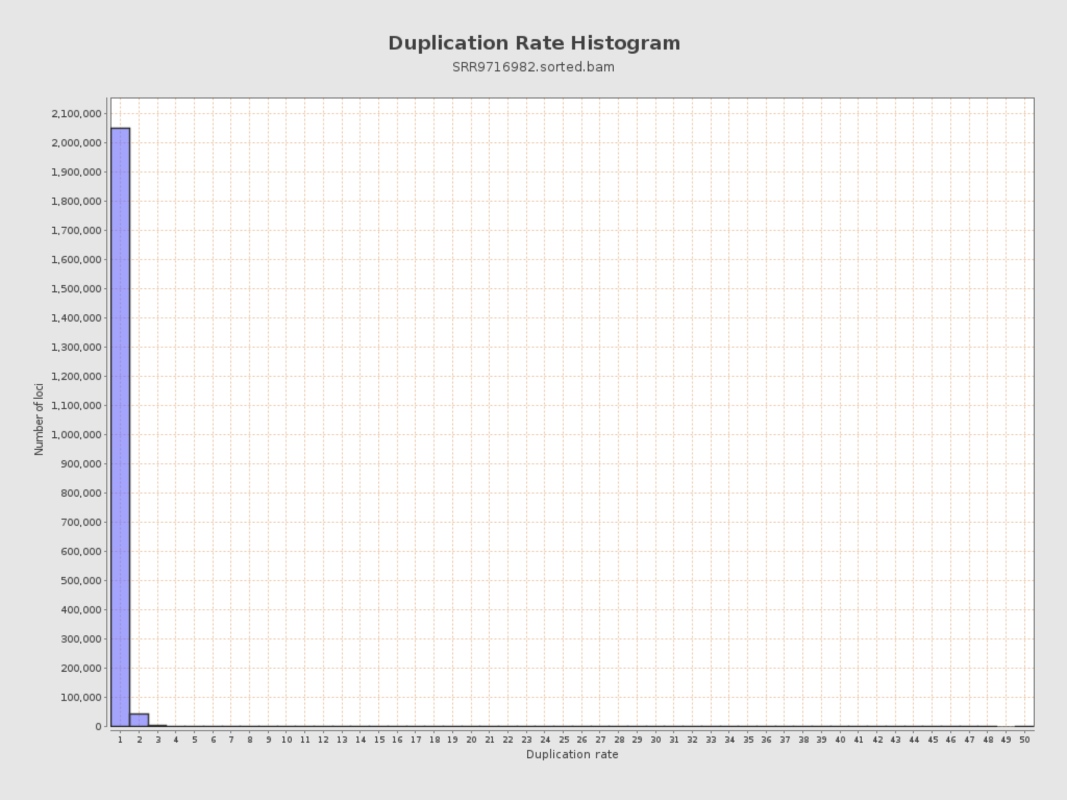
5. Results : Coverage Histogram (0-50X)



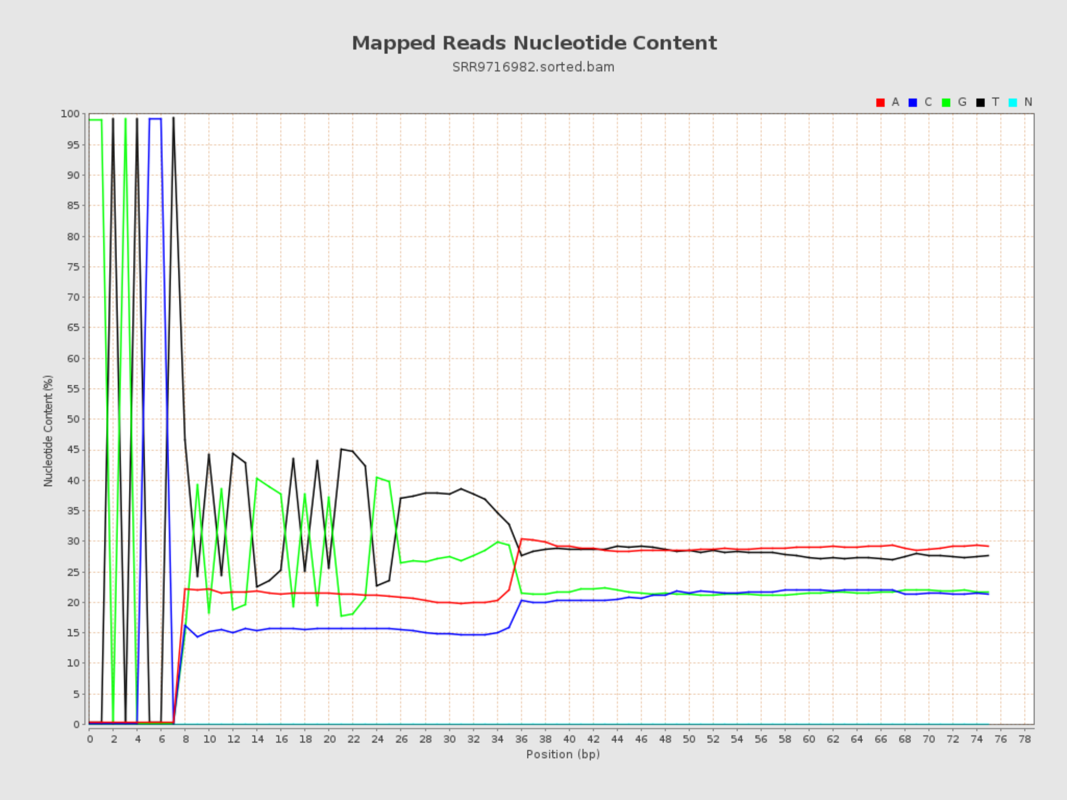
6. Results : Genome Fraction Coverage



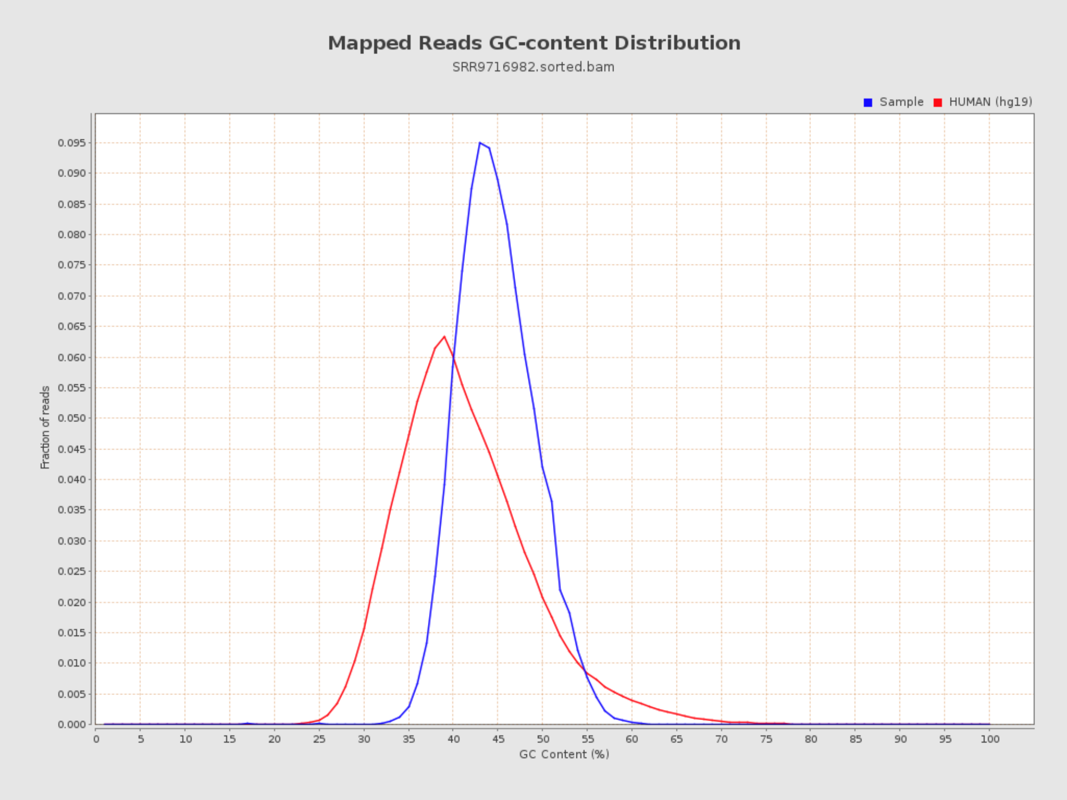
7. Results : Duplication Rate Histogram



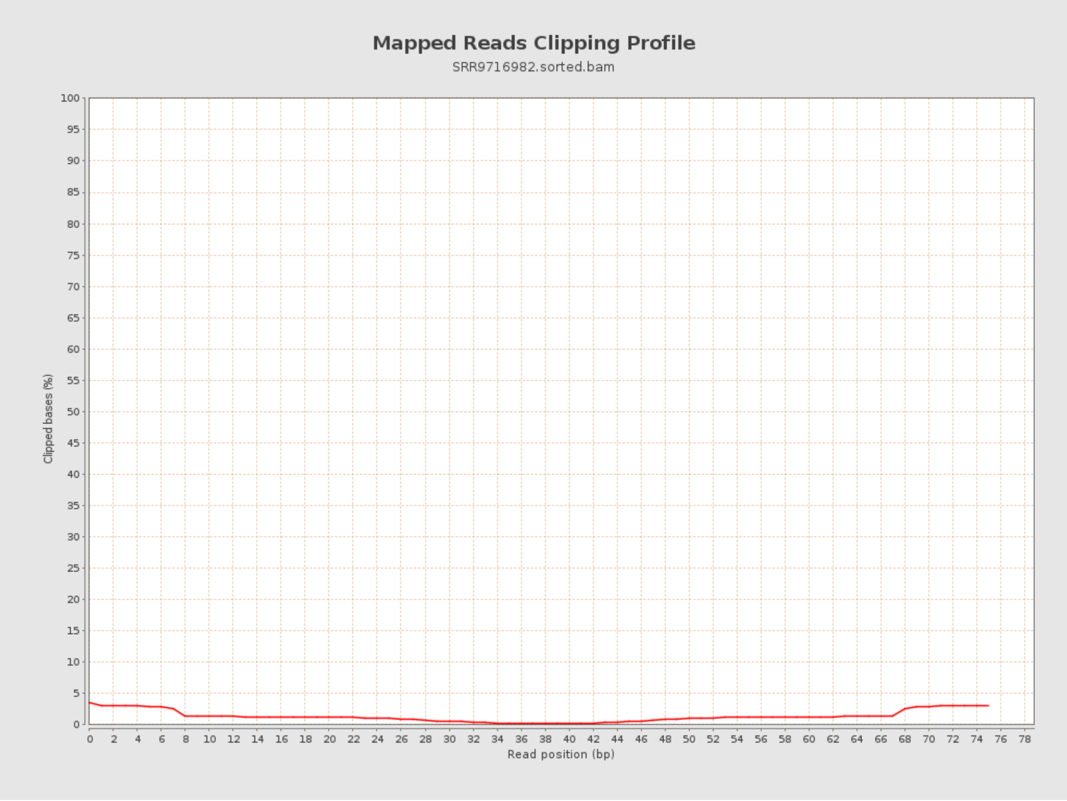
8. Results : Mapped Reads Nucleotide Content



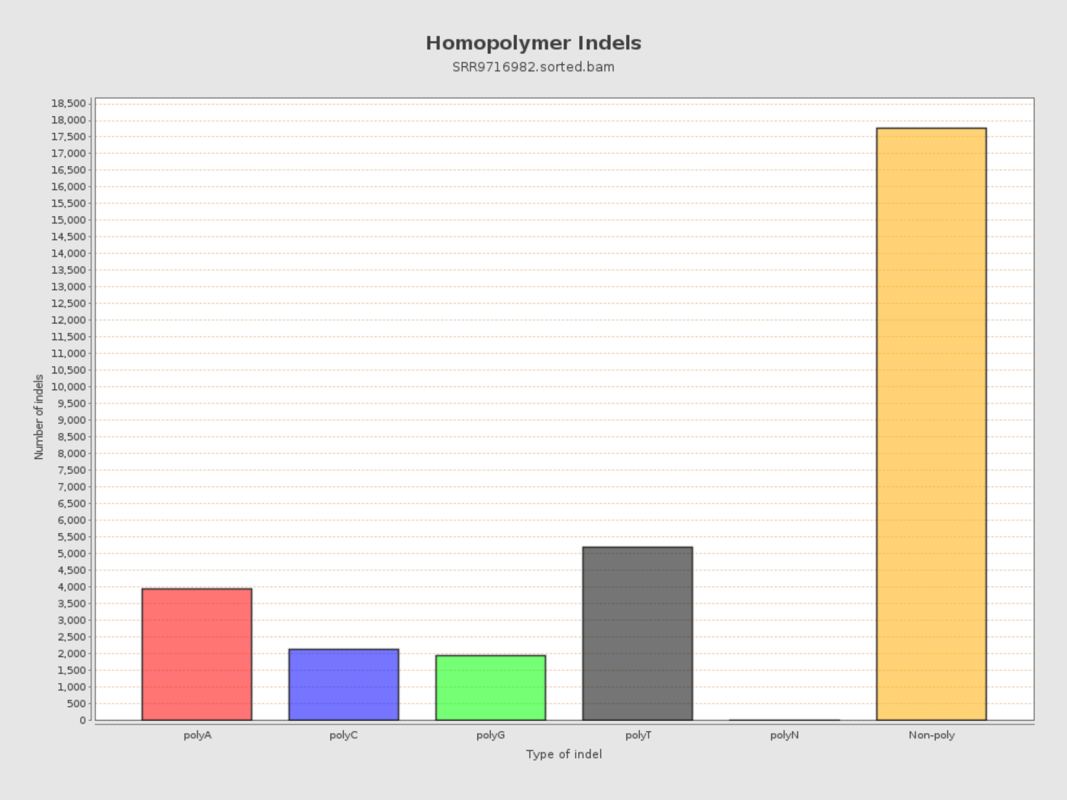
9. Results : Mapped Reads GC-content Distribution



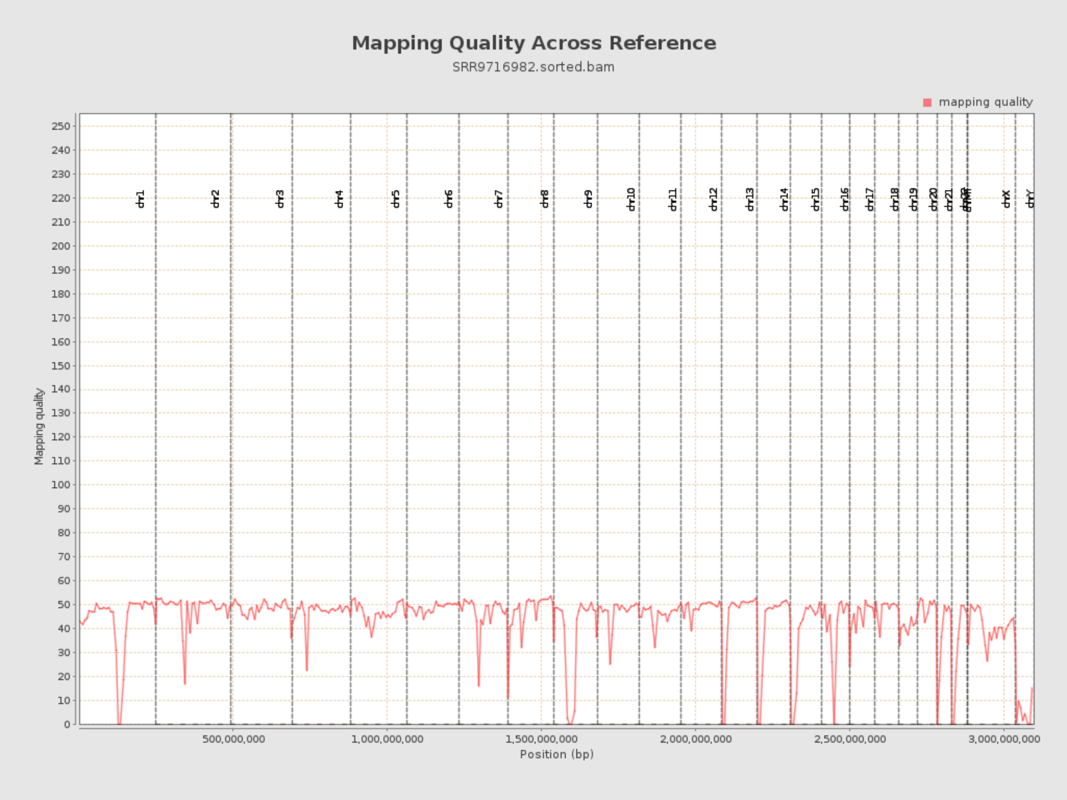
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram