Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:19:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716223.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_SRR9716223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:19:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,122,279
Mapped reads	1,010,151 / 90.01%
Unmapped reads	112,128 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,645 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,143 / 2.15%
Duplication rate	1.79%
Clipped reads	1,011,111 / 90.09%

2.2. ACGT Content

Number/percentage of A's	15,057,813 / 25.63%
Number/percentage of C's	11,350,358 / 19.32%
Number/percentage of T's	17,649,805 / 30.05%
Number/percentage of G's	14,685,939 / 25%
Number/percentage of N's	450 / 0%
GC Percentage	44.32%

2.3. Coverage

Mean	0.019

Standard Deviation	0.1783

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

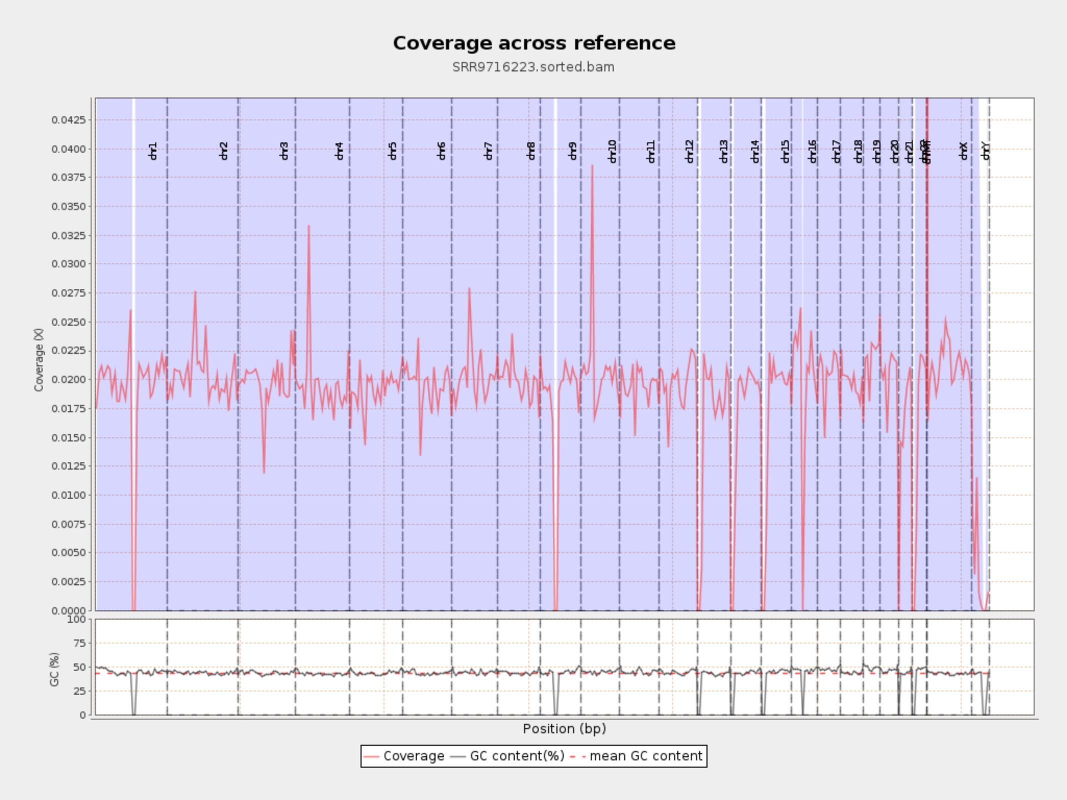
General error rate	0.53%
Mismatches	301,595
Insertions	4,389
Mapped reads with at least one insertion	0.43%
Deletions	11,727
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.2%

2.6. Chromosome stats

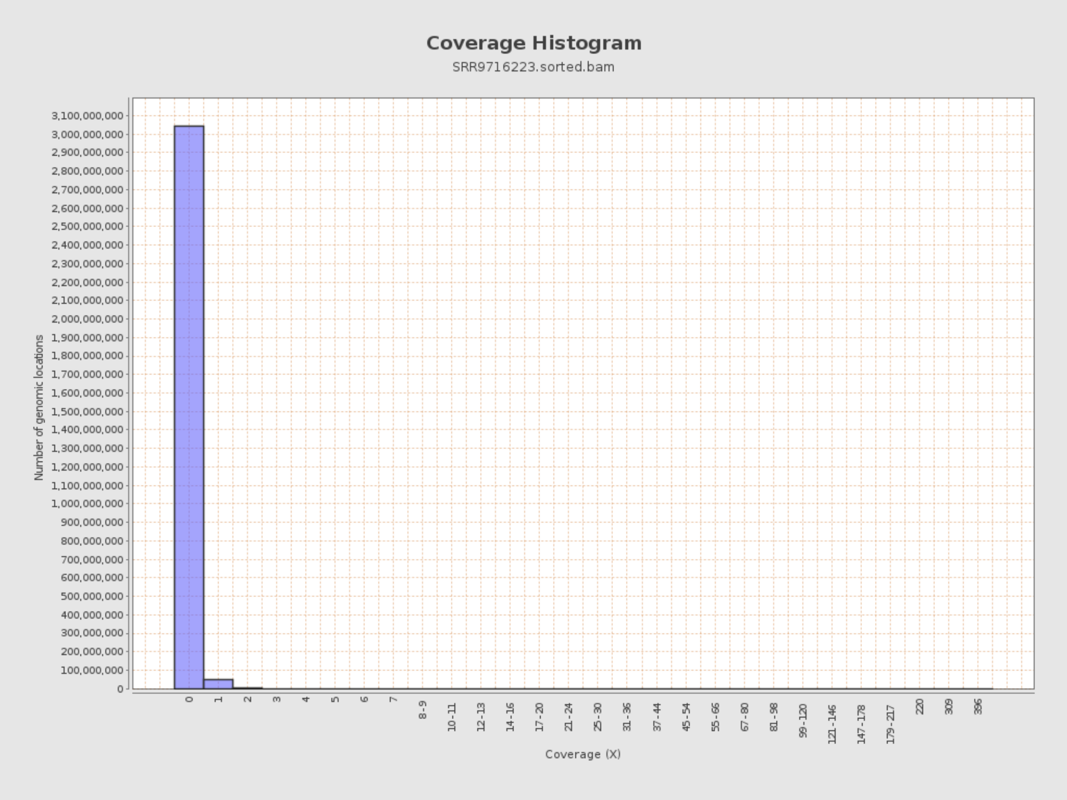
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4725447	0.019	0.2258
chr2	243199373	4948414	0.0203	0.2383
chr3	198022430	3910974	0.0198	0.1505
chr4	191154276	3738989	0.0196	0.1616
chr5	180915260	3475980	0.0192	0.1472
chr6	171115067	3348450	0.0196	0.1623
chr7	159138663	3245553	0.0204	0.2113

chr8	146364022	2914131	0.0199	0.1866
chr9	141213431	2466177	0.0175	0.1602
chr10	135534747	2858119	0.0211	0.2152
chr11	135006516	2637821	0.0195	0.1661
chr12	133851895	2643983	0.0198	0.1508
chr13	115169878	1844421	0.016	0.1353
chr14	107349540	1773370	0.0165	0.1394
chr15	102531392	1699775	0.0166	0.1382
chr16	90354753	1771272	0.0196	0.158
chr17	81195210	1661492	0.0205	0.1556
chr18	78077248	1542003	0.0197	0.2334
chr19	59128983	1290910	0.0218	0.2001
chr20	63025520	1276805	0.0203	0.1544
chr21	48129895	766464	0.0159	0.145
chr22	51304566	744583	0.0145	0.1286
chrMT	16571	5028	0.3034	0.5801
chrX	155270560	3288125	0.0212	0.1622
chrY	59373566	185360	0.0031	0.1036

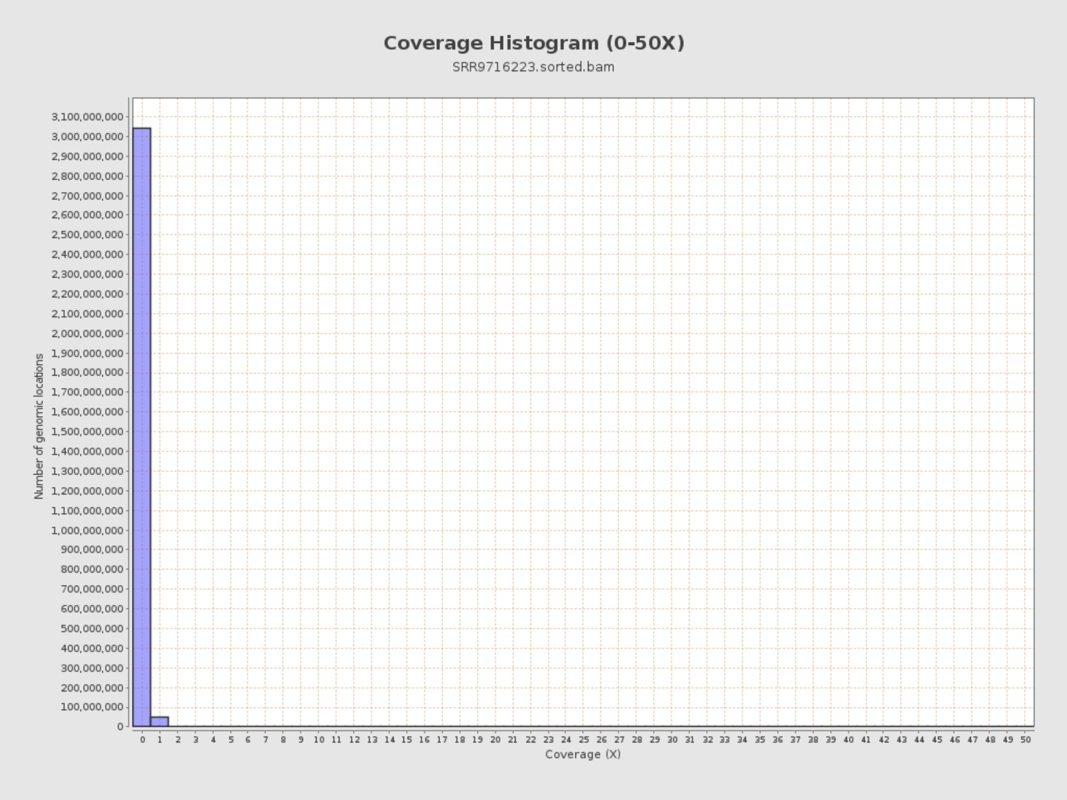
3. Results : Coverage across reference



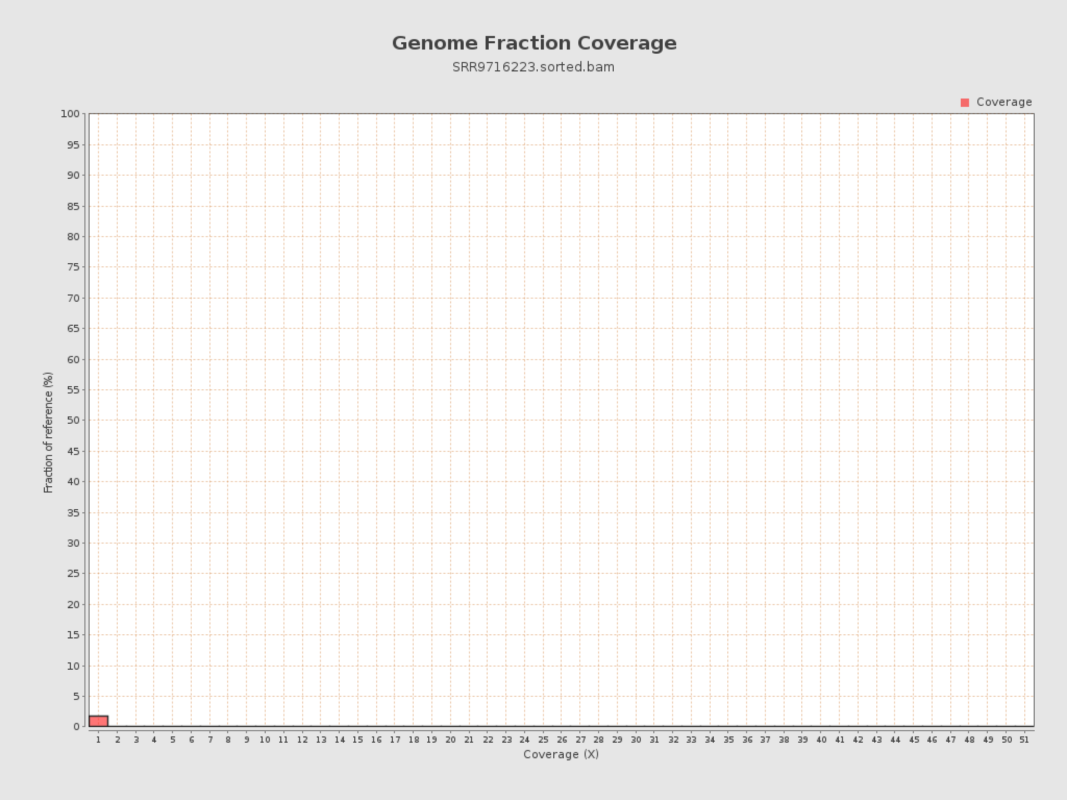
4. Results : Coverage Histogram



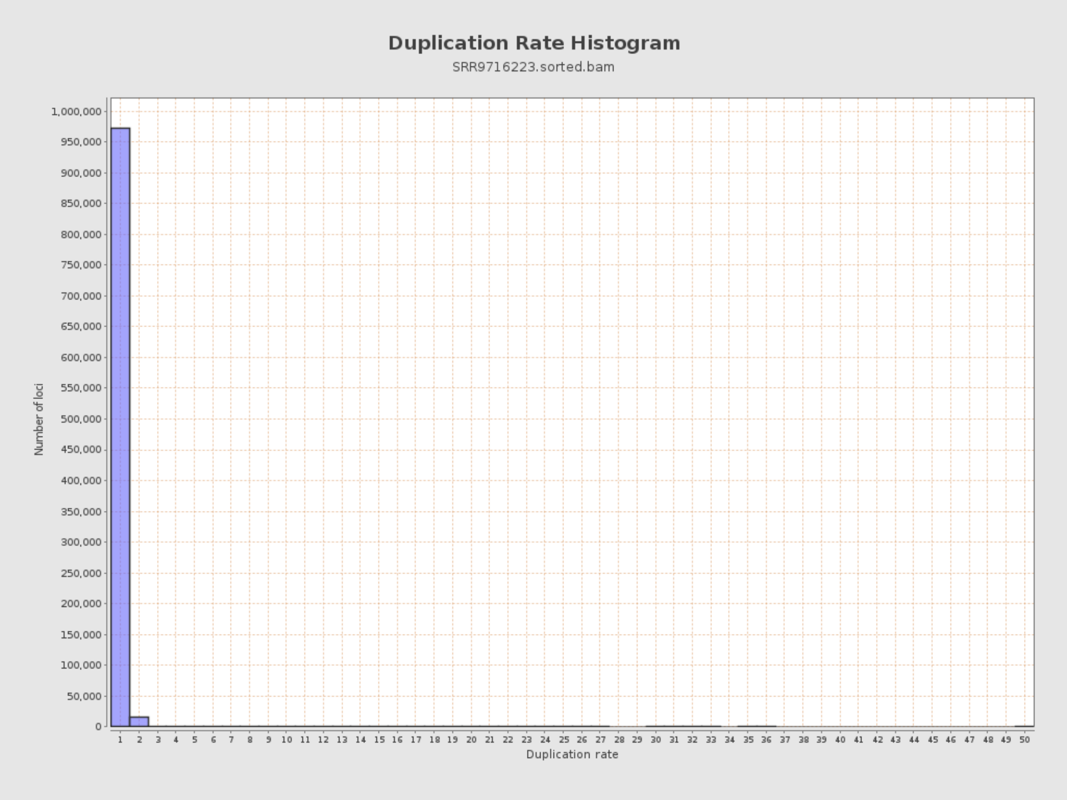
5. Results : Coverage Histogram (0-50X)



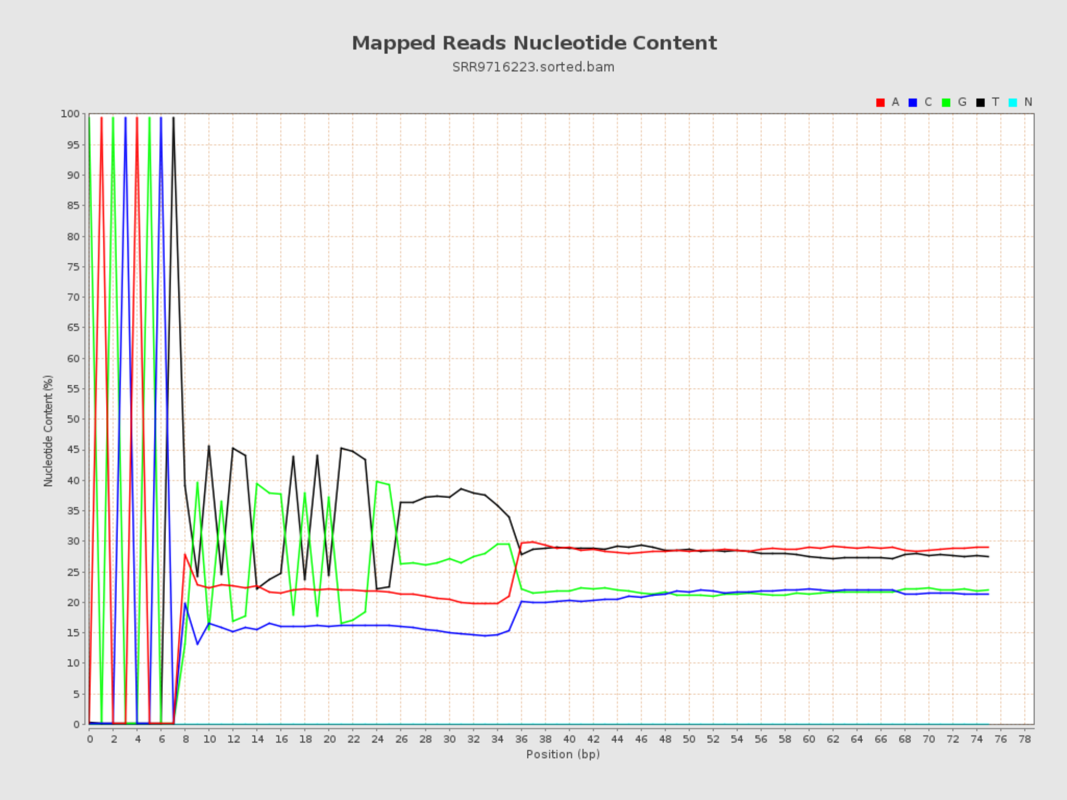
6. Results : Genome Fraction Coverage



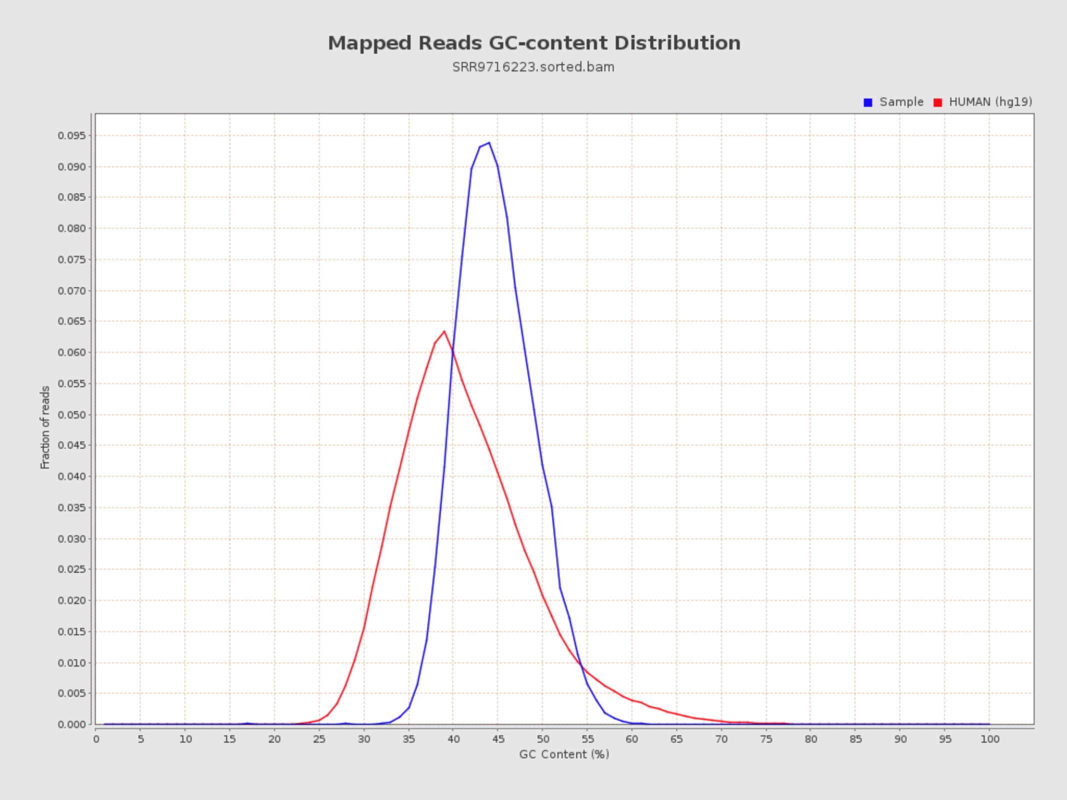
7. Results : Duplication Rate Histogram



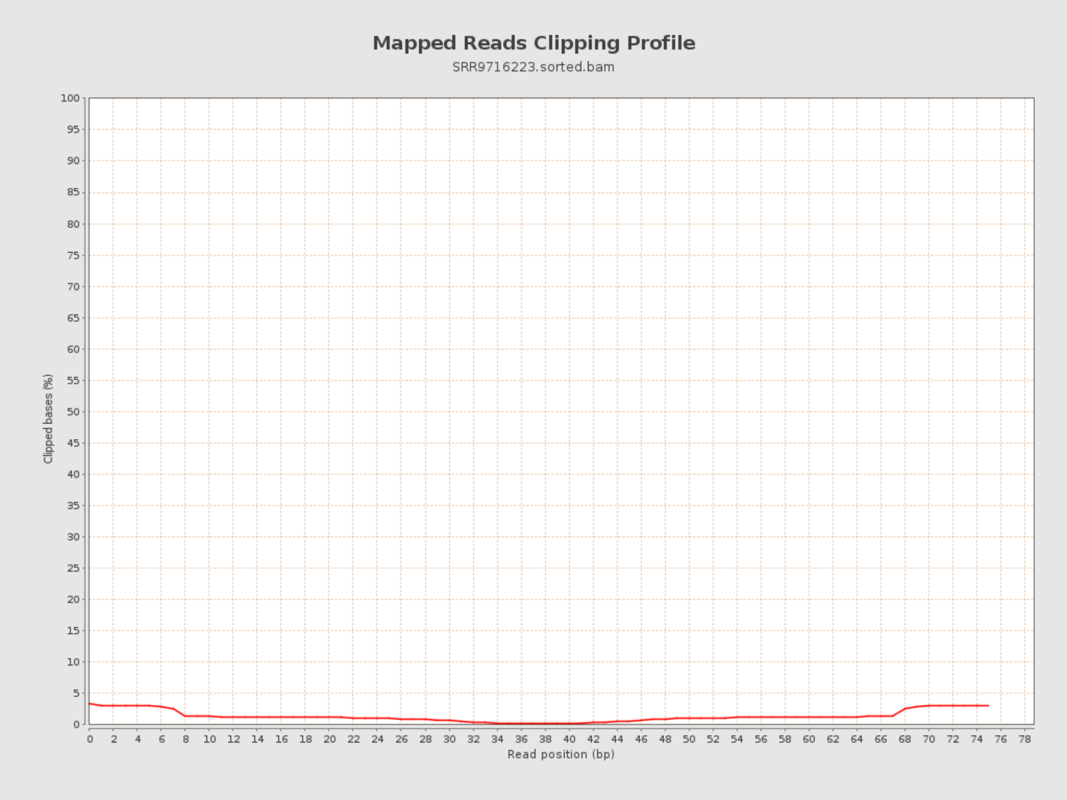
8. Results : Mapped Reads Nucleotide Content



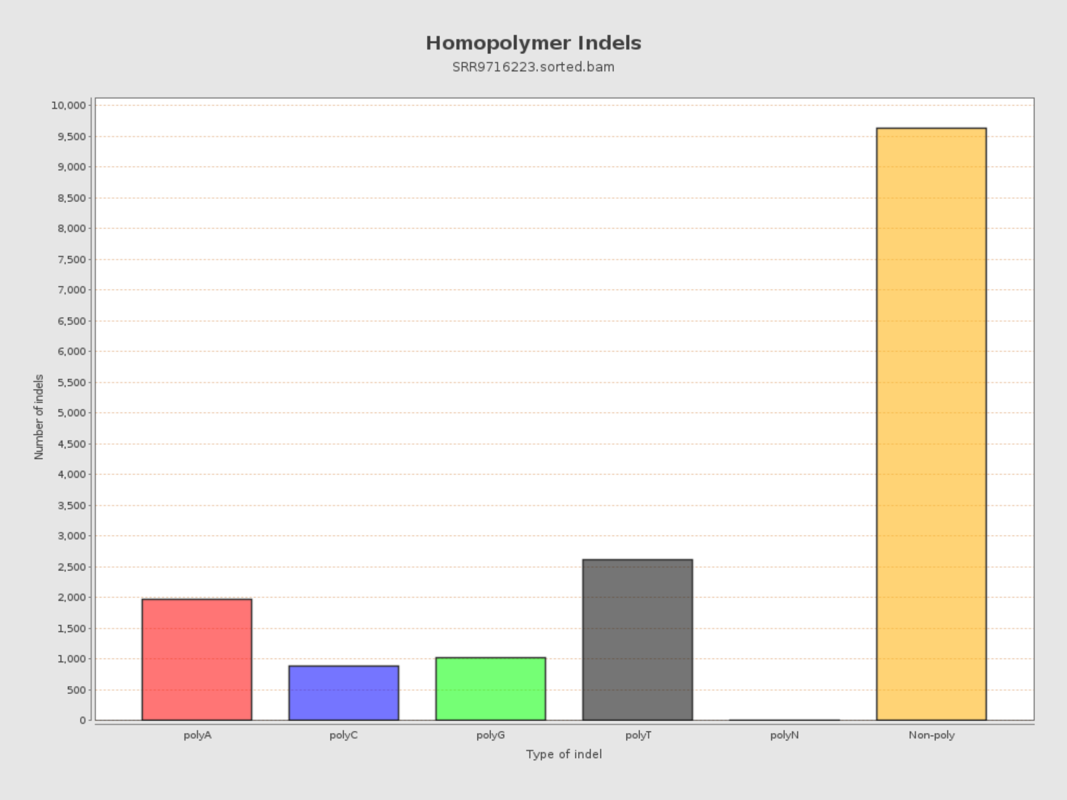
9. Results : Mapped Reads GC-content Distribution



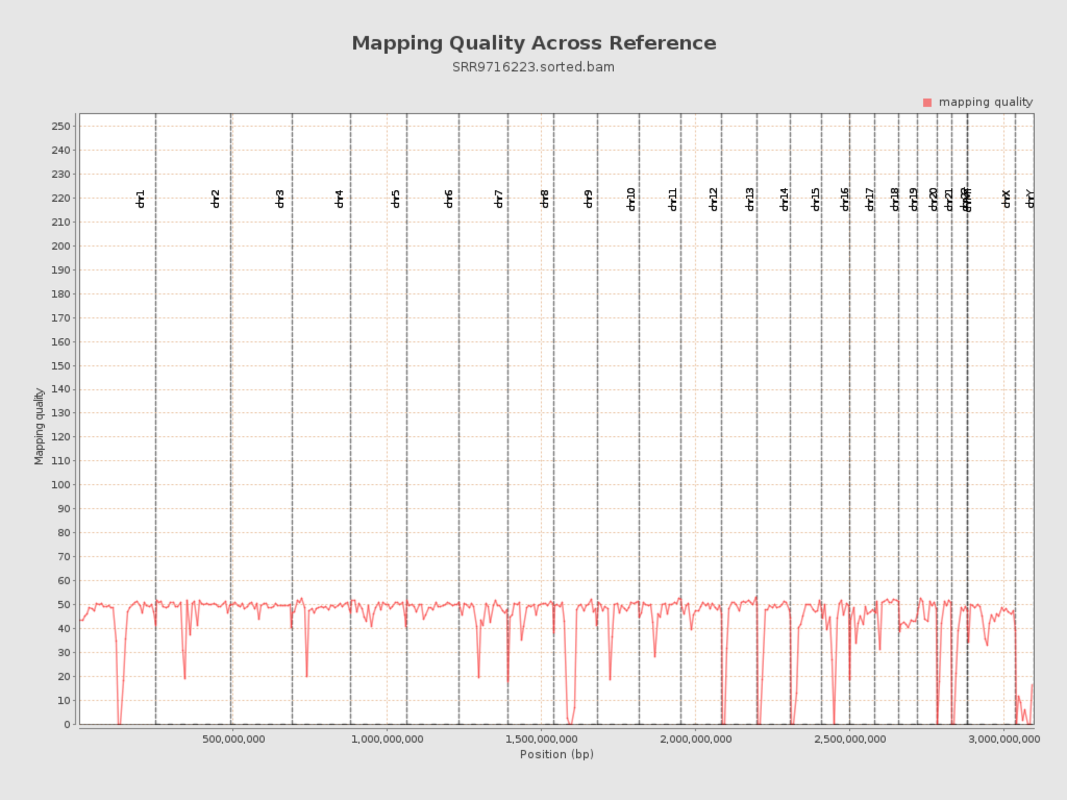
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram