Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:41:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716423.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_SRR9716423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716423.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:41:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,420,880
Mapped reads	1,308,277 / 92.08%
Unmapped reads	112,603 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,513 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	41,205 / 2.9%
Duplication rate	2.16%
Clipped reads	1,309,481 / 92.16%

2.2. ACGT Content

Number/percentage of A's	18,503,018 / 24.38%
Number/percentage of C's	14,107,603 / 18.59%
Number/percentage of T's	24,646,393 / 32.47%
Number/percentage of G's	18,649,559 / 24.57%
Number/percentage of N's	1,447 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2436

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

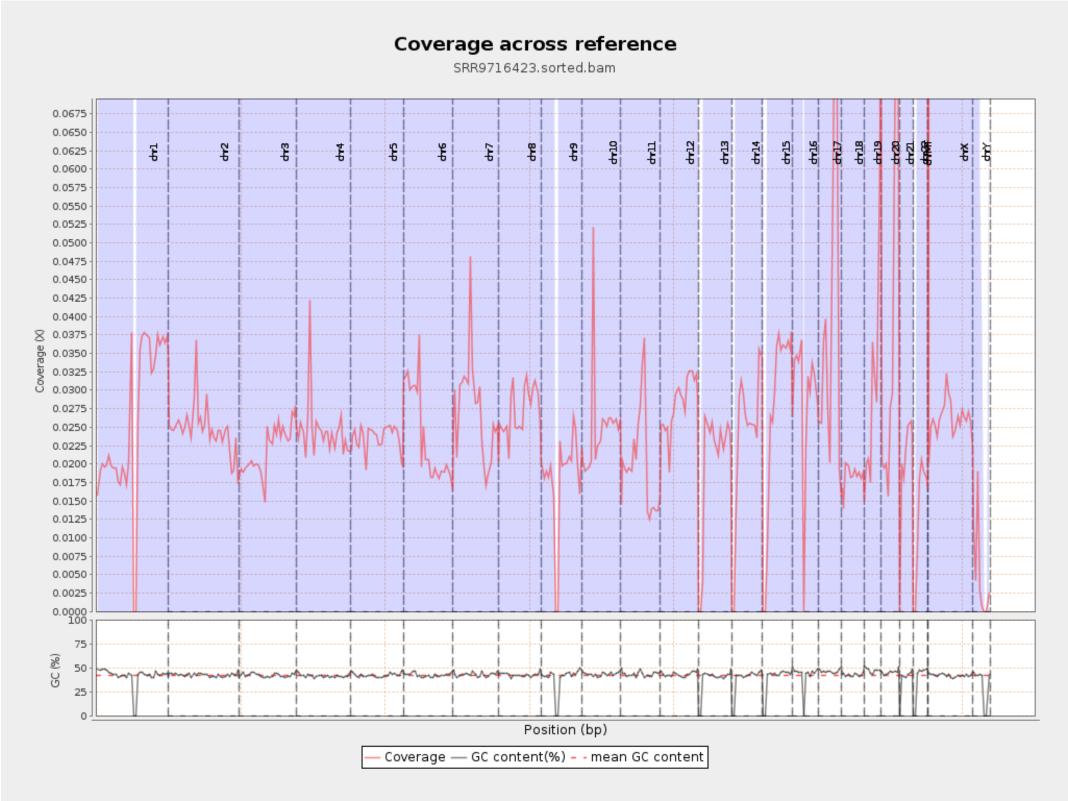
General error rate	0.52%
Mismatches	386,921
Insertions	5,242
Mapped reads with at least one insertion	0.4%
Deletions	15,080
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.1%

2.6. Chromosome stats

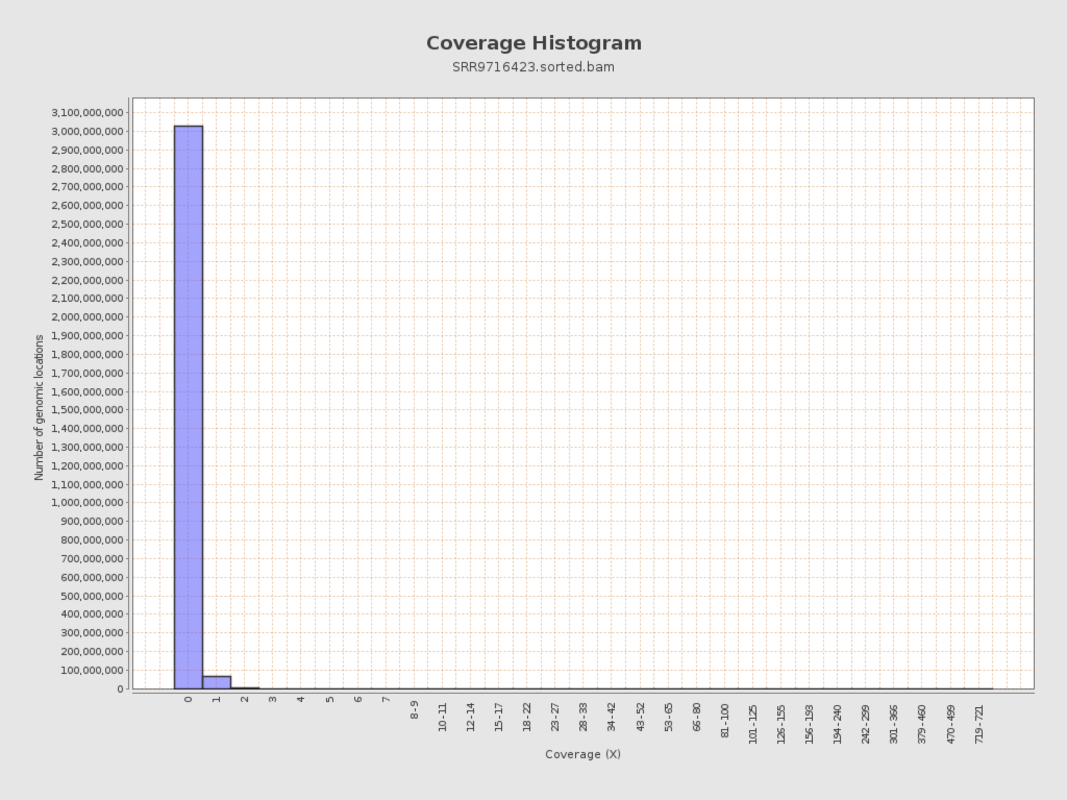
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6392337	0.0256	0.3795
chr2	243199373	6020923	0.0248	0.3376
chr3	198022430	4339691	0.0219	0.1592
chr4	191154276	4695762	0.0246	0.1903
chr5	180915260	4291191	0.0237	0.1648
chr6	171115067	4069785	0.0238	0.1924
chr7	159138663	4367888	0.0274	0.3382

chr8	146364022	3992717	0.0273	0.2958
chr9	141213431	2530199	0.0179	0.1753
chr10	135534747	3379370	0.0249	0.265
chr11	135006516	2732764	0.0202	0.1889
chr12	133851895	3764719	0.0281	0.1811
chr13	115169878	2311561	0.0201	0.1523
chr14	107349540	2554075	0.0238	0.1686
chr15	102531392	2770822	0.027	0.1781
chr16	90354753	2599241	0.0288	0.1921
chr17	81195210	3275448	0.0403	0.2243
chr18	78077248	1429479	0.0183	0.2971
chr19	59128983	1916637	0.0324	0.3171
chr20	63025520	2460164	0.039	0.2186
chr21	48129895	980846	0.0204	0.1794
chr22	51304566	684755	0.0133	0.1232
chrMT	16571	11734	0.7081	1.0332
chrX	155270560	4076513	0.0263	0.1855
chrY	59373566	283940	0.0048	0.2182

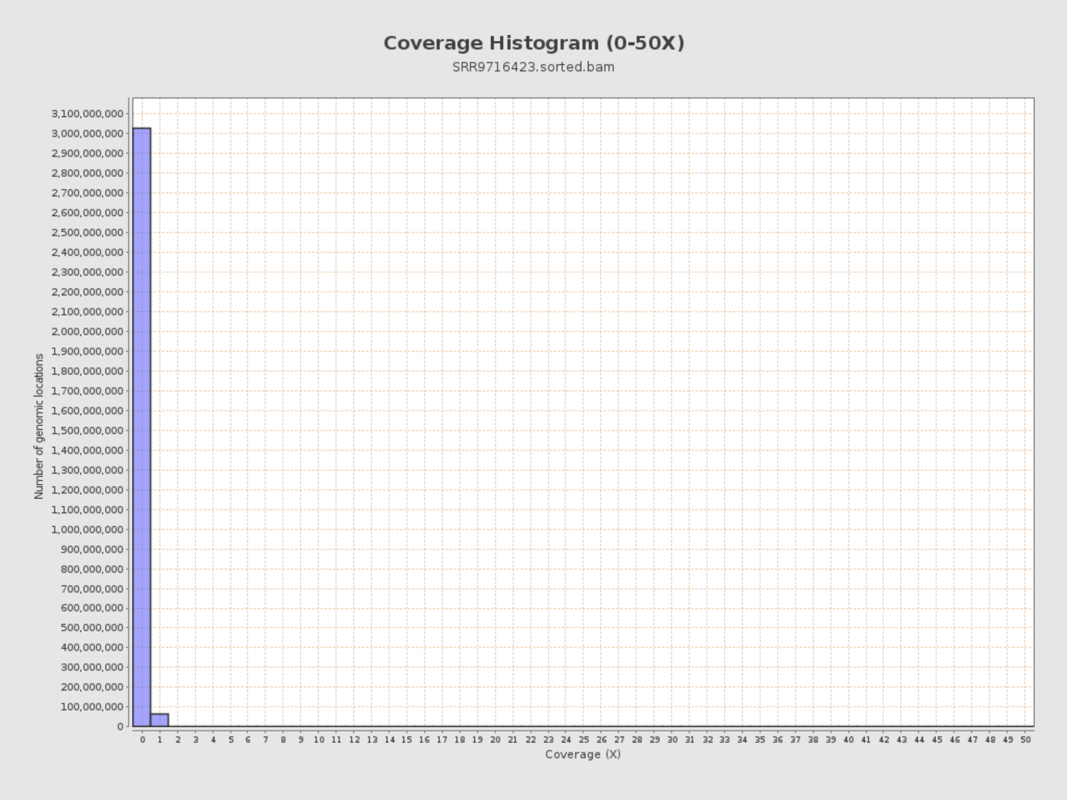
3. Results : Coverage across reference



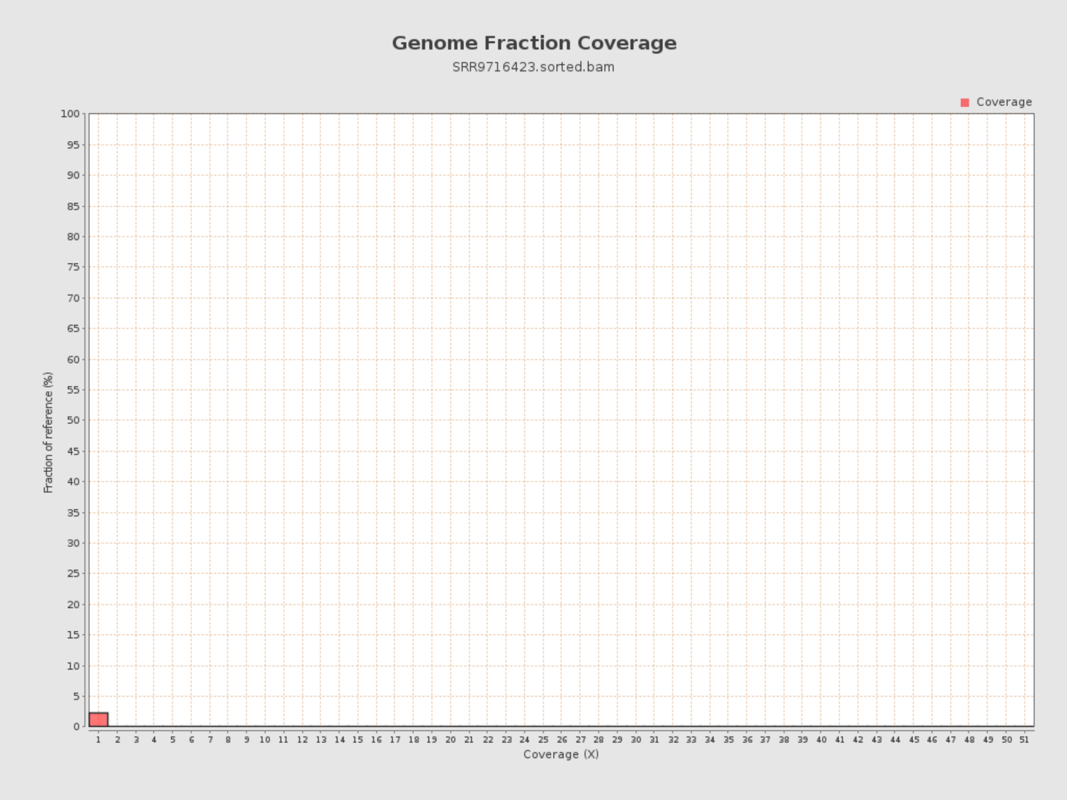
4. Results : Coverage Histogram



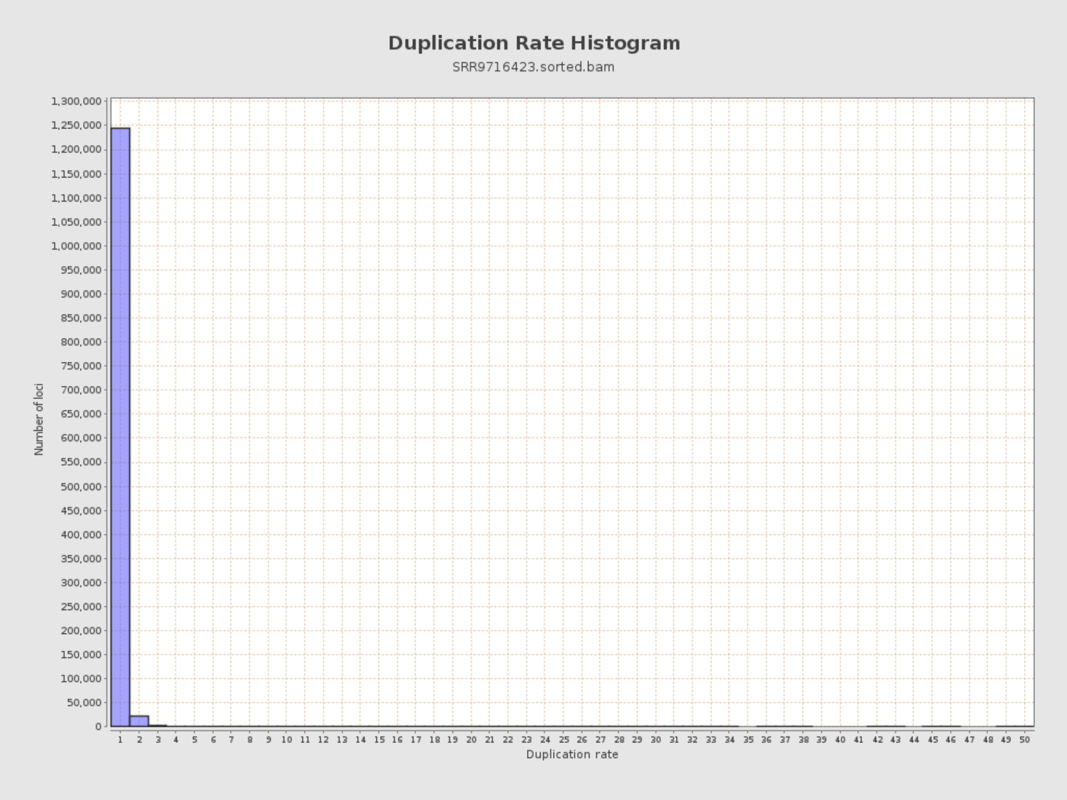
5. Results : Coverage Histogram (0-50X)



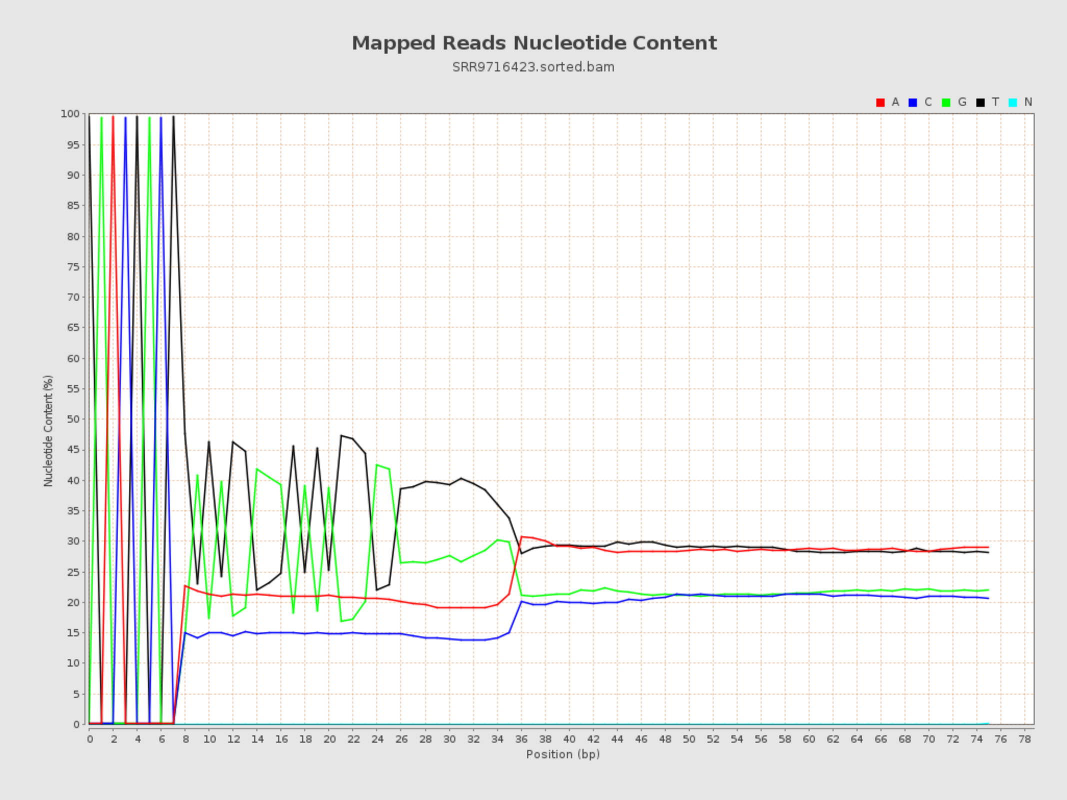
6. Results : Genome Fraction Coverage



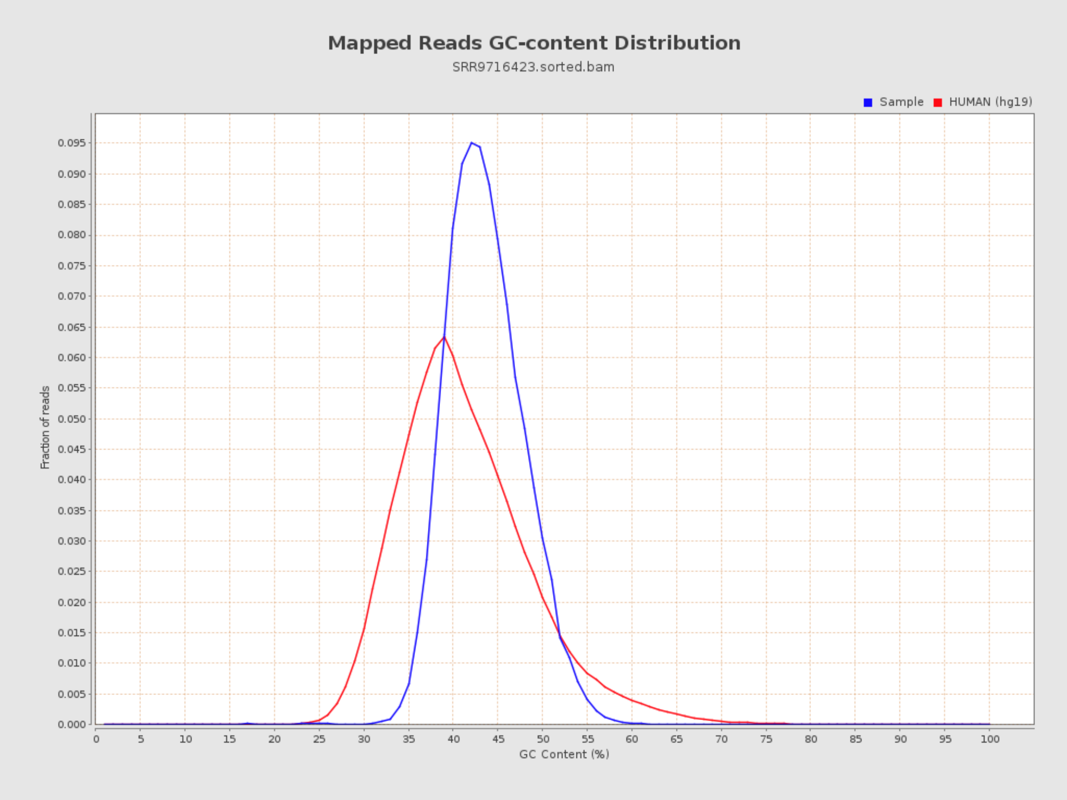
7. Results : Duplication Rate Histogram



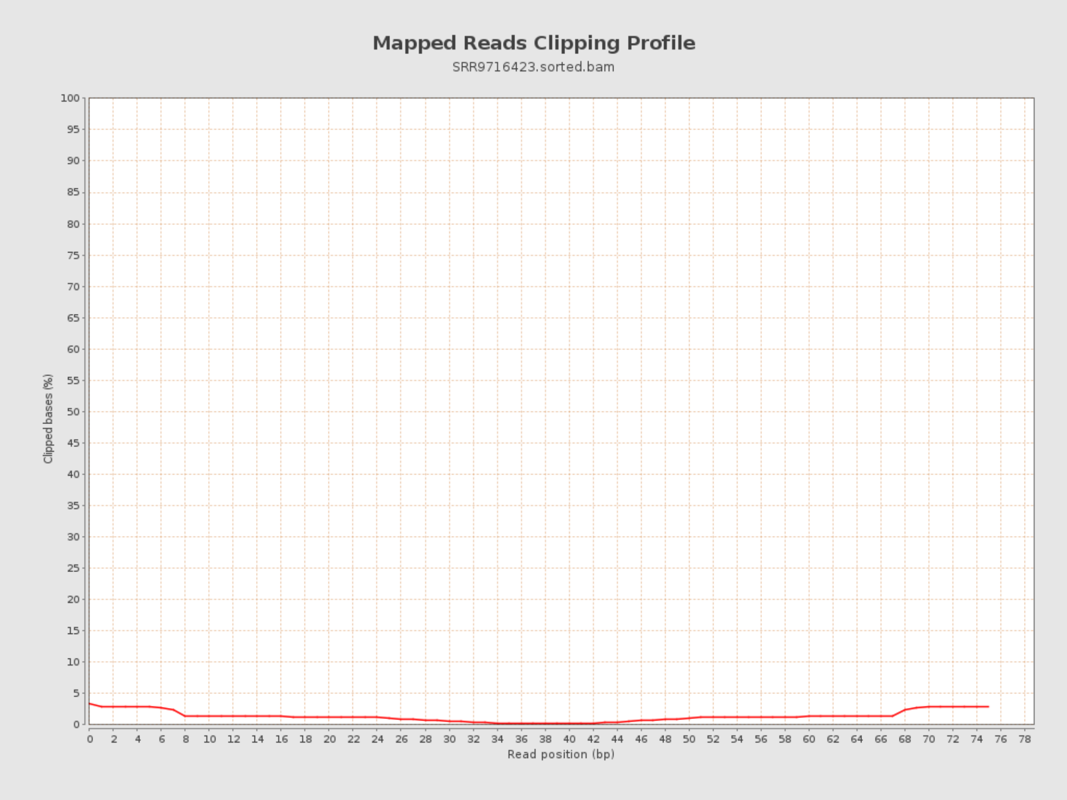
8. Results : Mapped Reads Nucleotide Content



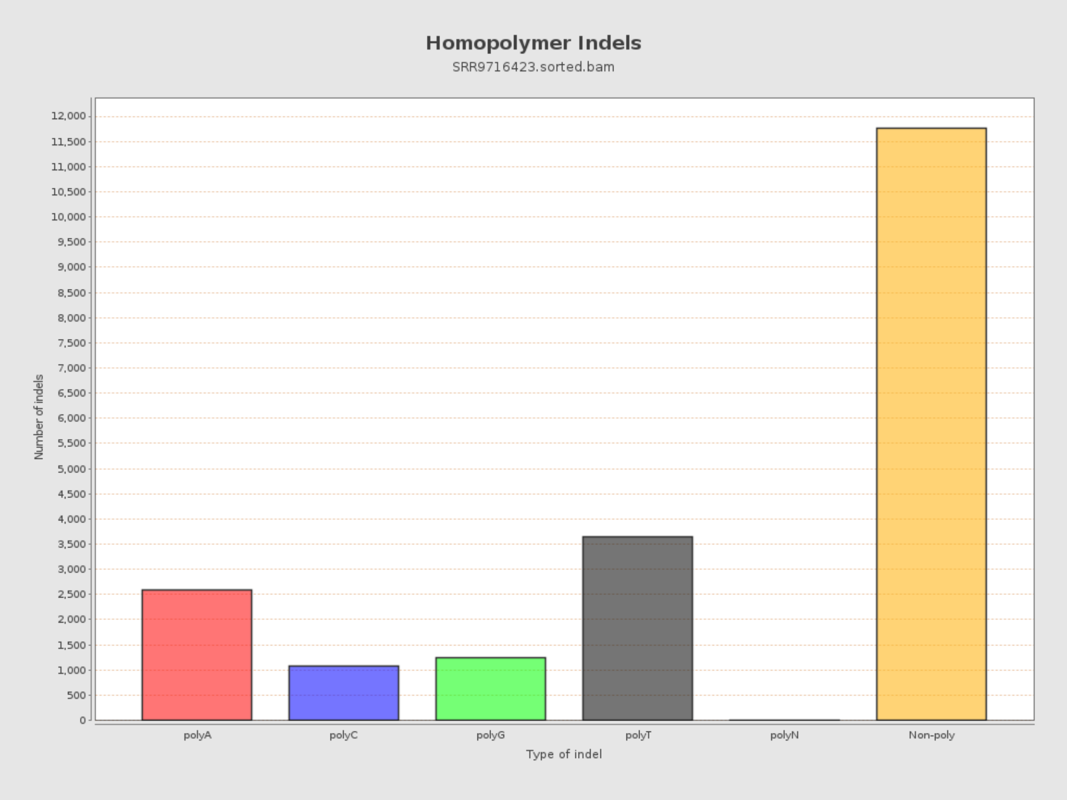
9. Results : Mapped Reads GC-content Distribution



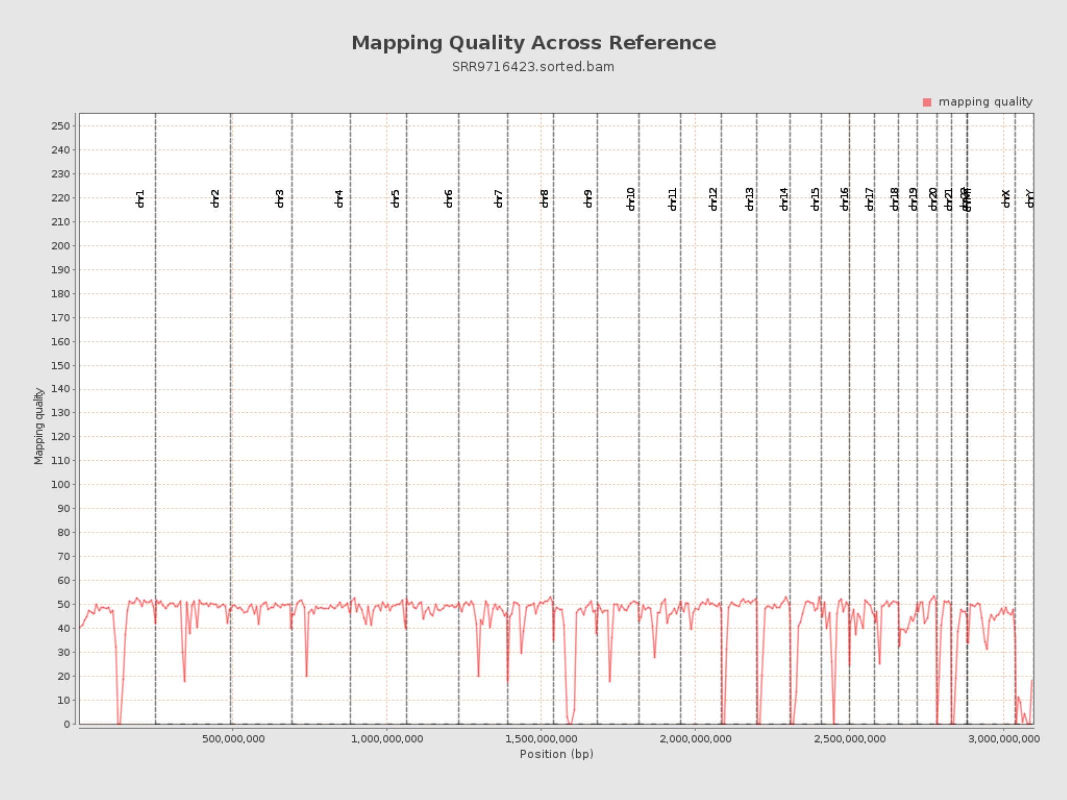
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram