Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:58:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716430.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_SRR9716430 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716430.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:58:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716430.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,696,081
Mapped reads	1,558,400 / 91.88%
Unmapped reads	137,681 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,541 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,288 / 3.44%
Duplication rate	2.64%
Clipped reads	1,559,680 / 91.96%

2.2. ACGT Content

Number/percentage of A's	22,920,711 / 25.31%
Number/percentage of C's	16,129,099 / 17.81%
Number/percentage of T's	28,552,804 / 31.52%
Number/percentage of G's	22,973,295 / 25.36%
Number/percentage of N's	1,706 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.2791

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

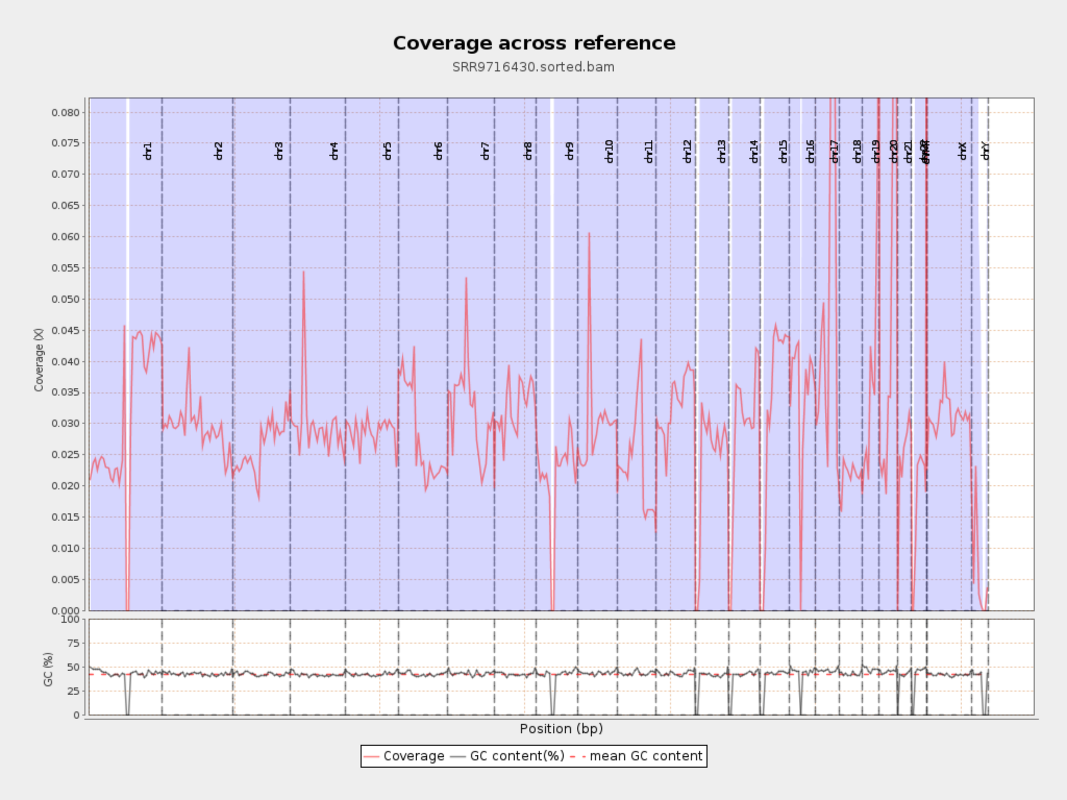
General error rate	0.52%
Mismatches	461,372
Insertions	6,626
Mapped reads with at least one insertion	0.42%
Deletions	18,416
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.5%

2.6. Chromosome stats

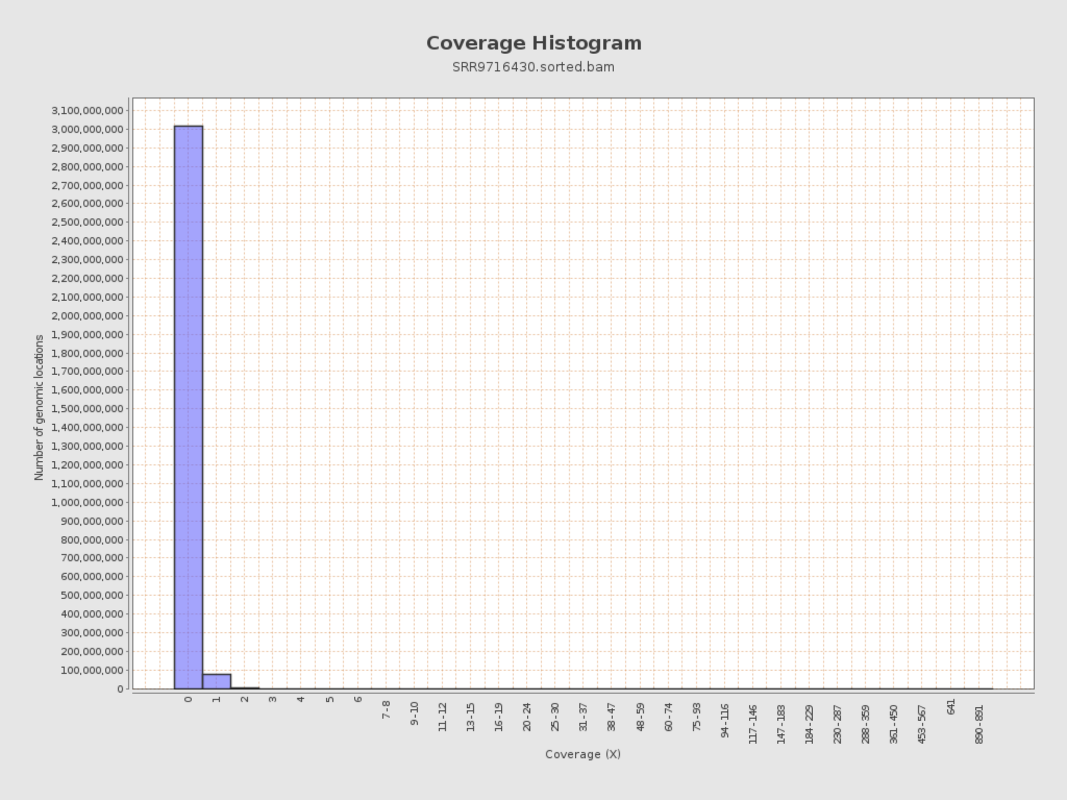
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7625064	0.0306	0.4395
chr2	243199373	7160892	0.0294	0.4078
chr3	198022430	5189861	0.0262	0.1766
chr4	191154276	5644408	0.0295	0.2254
chr5	180915260	5184970	0.0287	0.1835
chr6	171115067	4802822	0.0281	0.212
chr7	159138663	5138518	0.0323	0.3608

chr8	146364022	4787361	0.0327	0.3607
chr9	141213431	2987751	0.0212	0.1995
chr10	135534747	4035504	0.0298	0.302
chr11	135006516	3204338	0.0237	0.2096
chr12	133851895	4457581	0.0333	0.1998
chr13	115169878	2736339	0.0238	0.1659
chr14	107349540	3044826	0.0284	0.1864
chr15	102531392	3324114	0.0324	0.1963
chr16	90354753	3135038	0.0347	0.2125
chr17	81195210	3931053	0.0484	0.249
chr18	78077248	1689168	0.0216	0.334
chr19	59128983	2335899	0.0395	0.3598
chr20	63025520	2997122	0.0476	0.246
chr21	48129895	1166026	0.0242	0.2117
chr22	51304566	851601	0.0166	0.1414
chrMT	16571	3522	0.2125	0.4831
chrX	155270560	4841069	0.0312	0.2105
chrY	59373566	332614	0.0056	0.2438

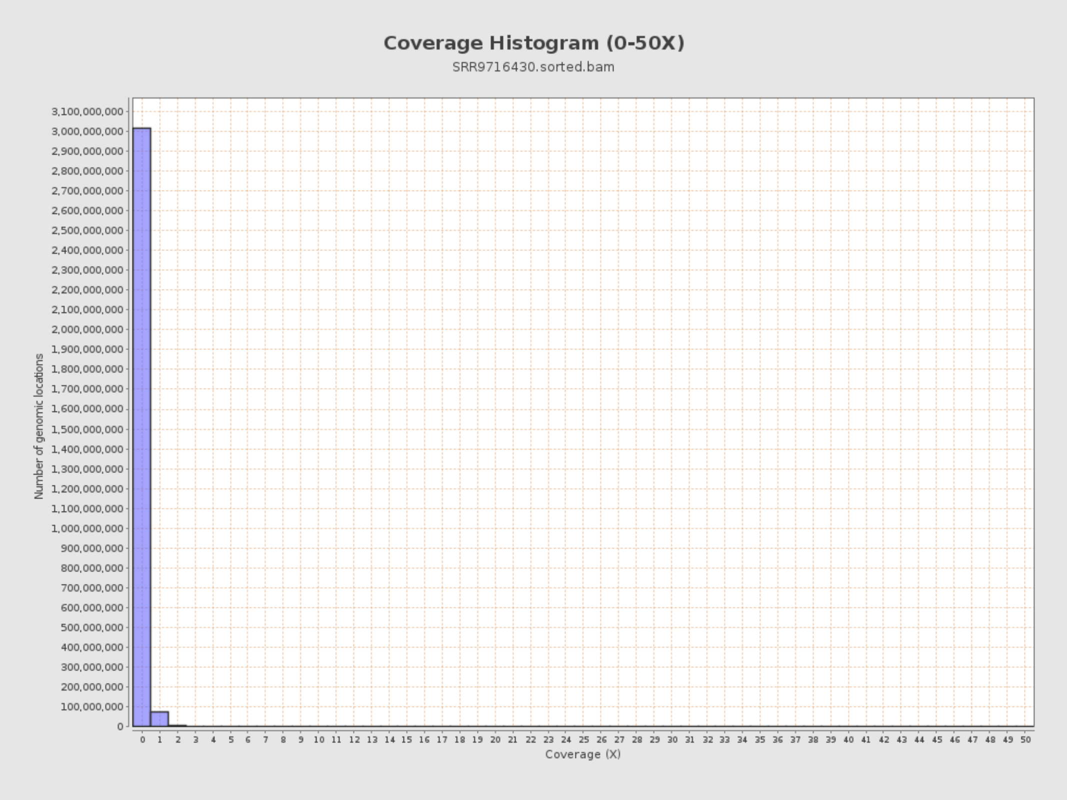
3. Results : Coverage across reference



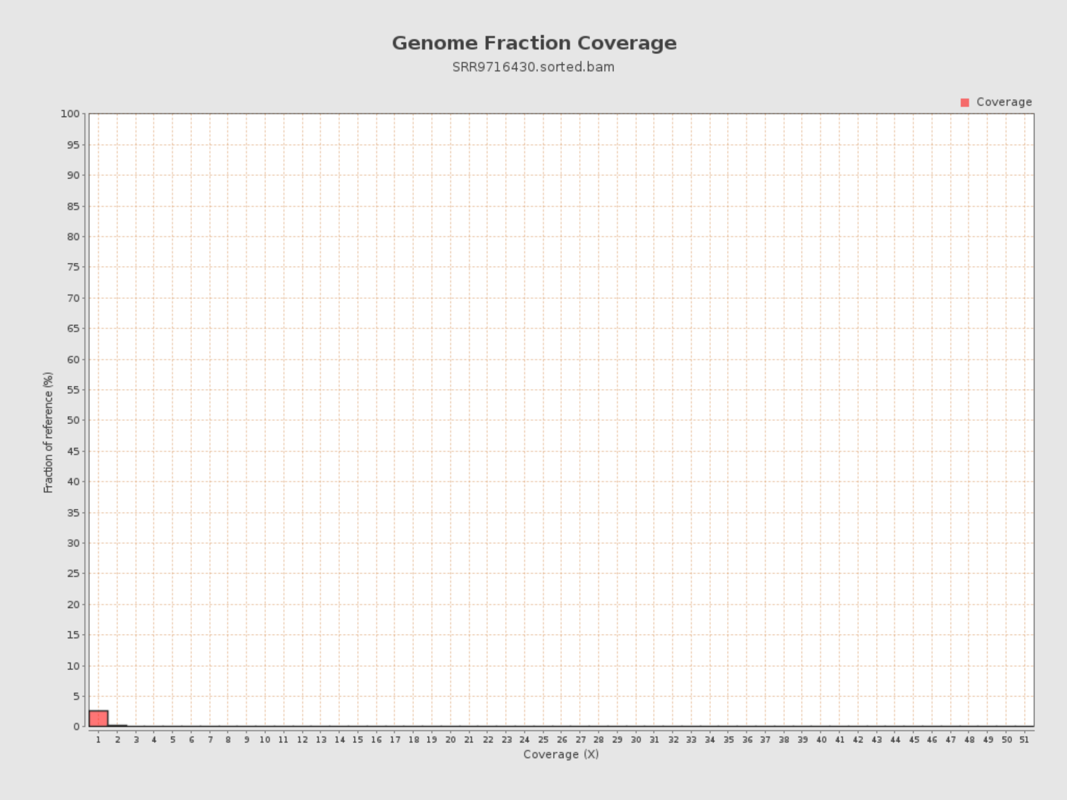
4. Results : Coverage Histogram



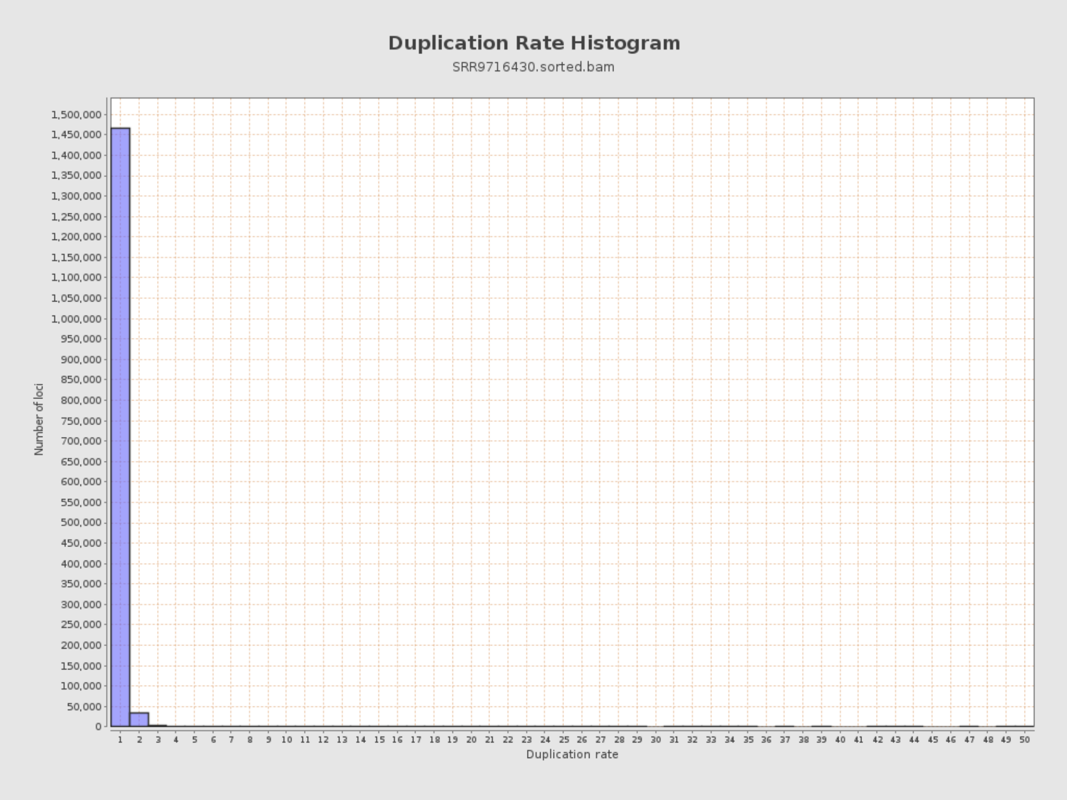
5. Results : Coverage Histogram (0-50X)



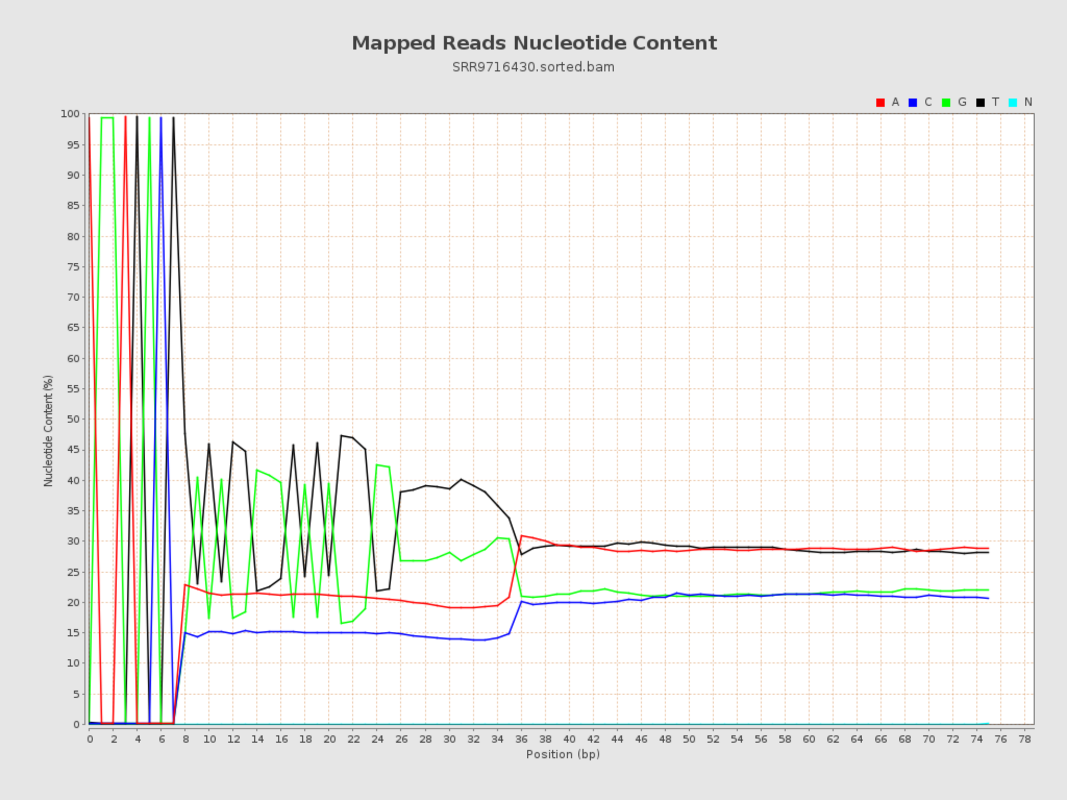
6. Results : Genome Fraction Coverage



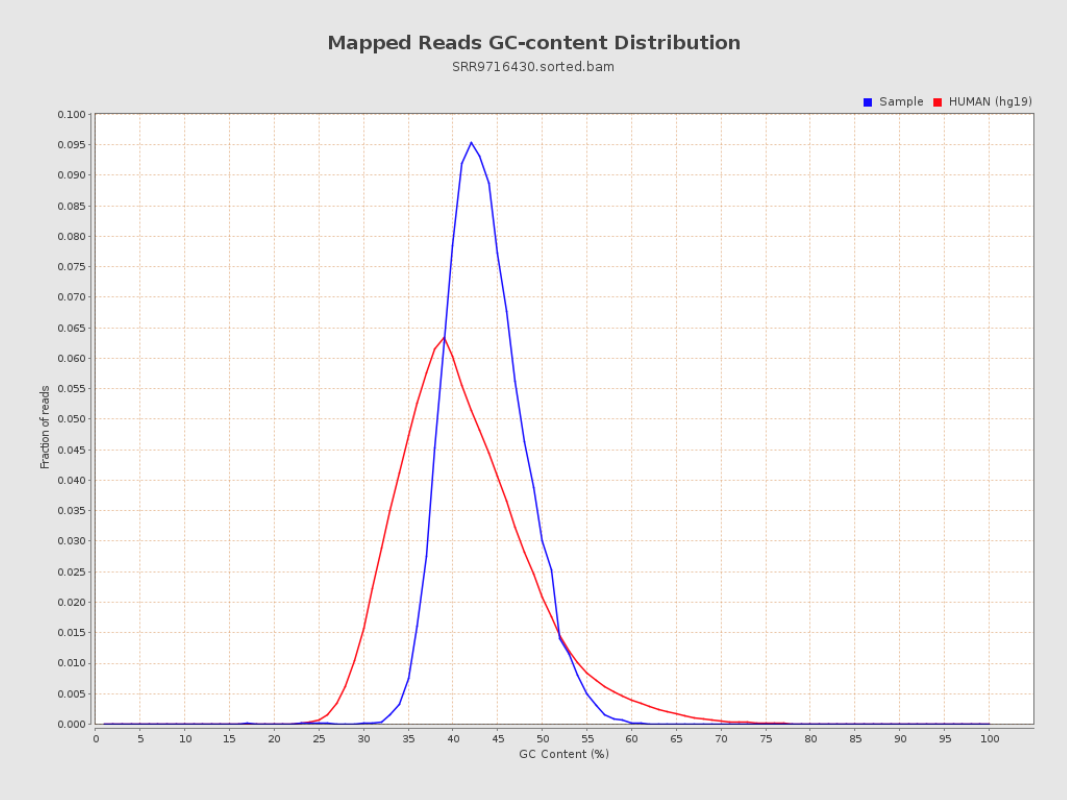
7. Results : Duplication Rate Histogram



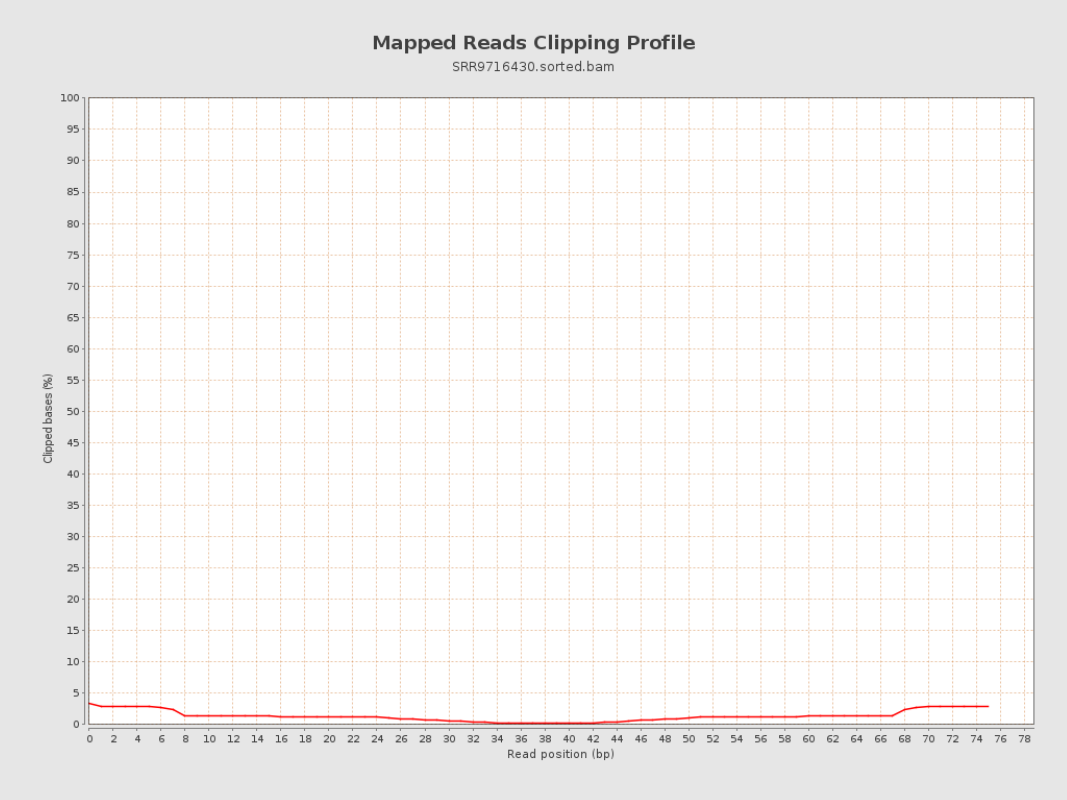
8. Results : Mapped Reads Nucleotide Content



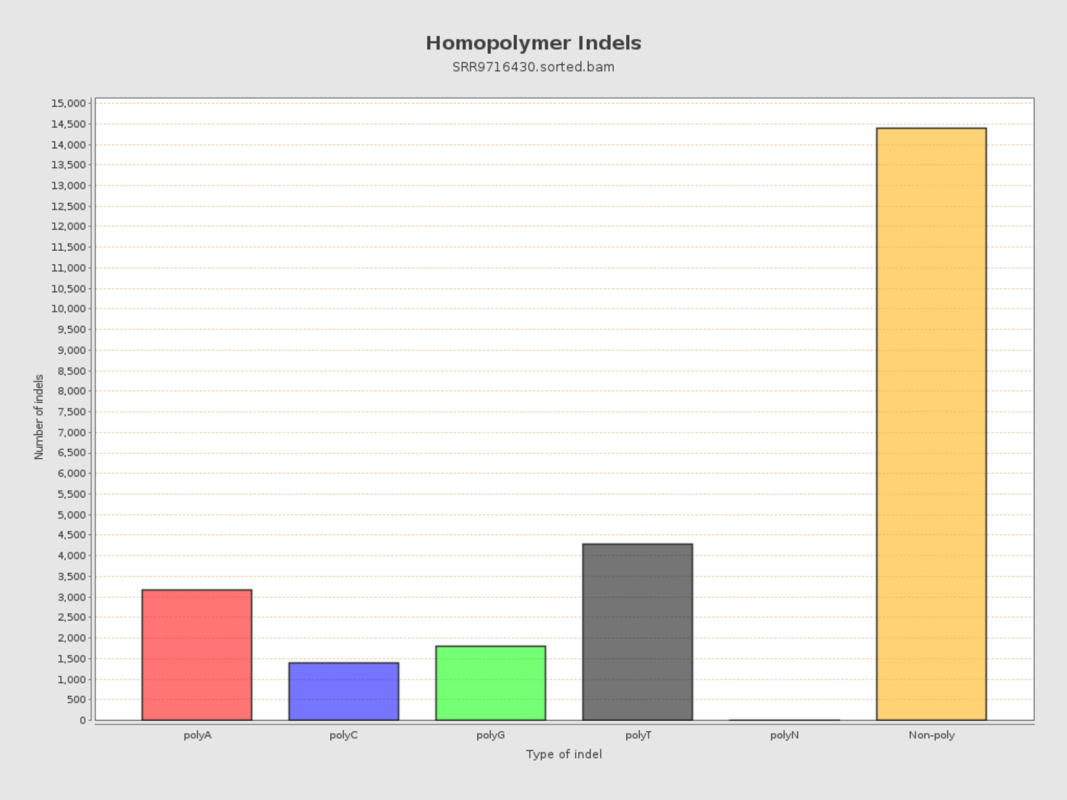
9. Results : Mapped Reads GC-content Distribution



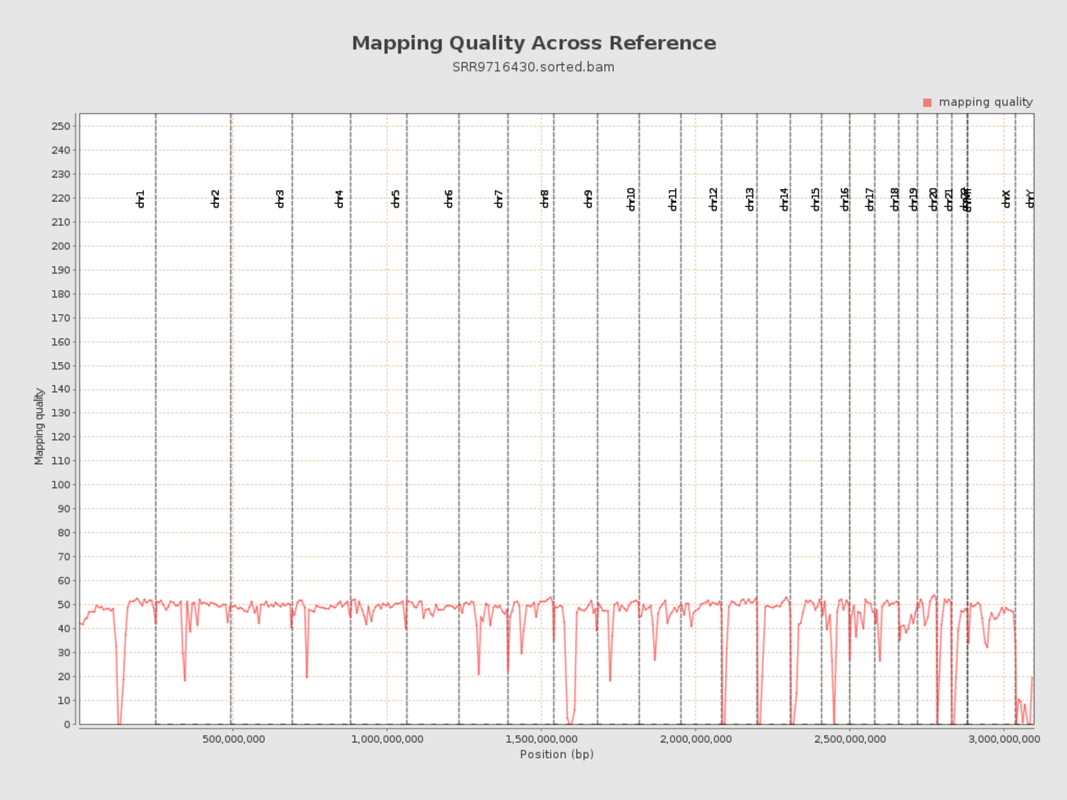
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram