Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:34:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716438.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_SRR9716438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716438.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:34:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,254,193
Mapped reads	23,654,904 / 97.53%
Unmapped reads	599,289 / 2.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,777 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	1,177,752 / 4.86%
Duplication rate	1.64%
Clipped reads	23,540,967 / 97.06%

2.2. ACGT Content

Number/percentage of A's	443,374,868 / 27.63%
Number/percentage of C's	355,986,361 / 22.19%
Number/percentage of T's	465,239,882 / 29%
Number/percentage of G's	339,630,049 / 21.17%
Number/percentage of N's	239,644 / 0.01%
GC Percentage	43.35%

2.3. Coverage

Mean	0.5184

Standard Deviation	5.7018

2.4. Mapping Quality

Mean Mapping Quality	48.73

2.5. Mismatches and indels

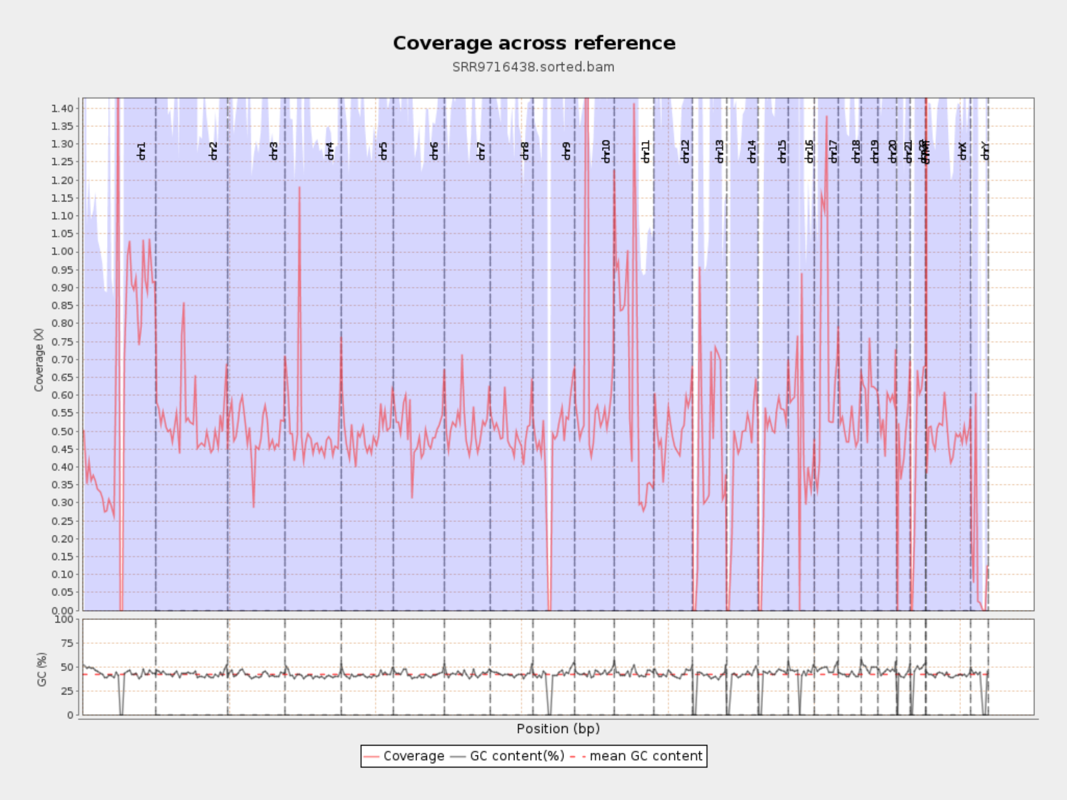
General error rate	0.38%
Mismatches	5,870,017
Insertions	137,240
Mapped reads with at least one insertion	0.58%
Deletions	140,708
Mapped reads with at least one deletion	0.59%
Homopolymer indels	35.87%

2.6. Chromosome stats

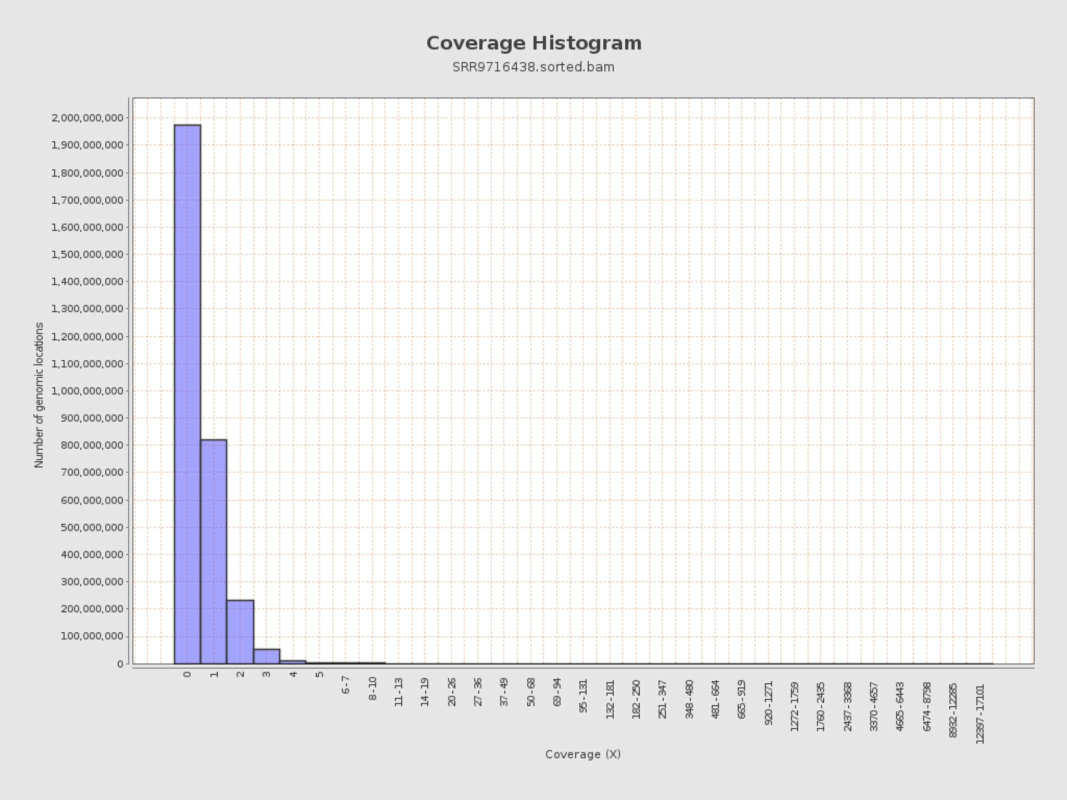
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	154063836	0.6181	15.1088
chr2	243199373	129214287	0.5313	3.5298
chr3	198022430	98247836	0.4961	2.0315
chr4	191154276	97521457	0.5102	3.1671
chr5	180915260	90041015	0.4977	0.8848
chr6	171115067	84724989	0.4951	1.5839
chr7	159138663	83276300	0.5233	3.5649

chr8	146364022	72797526	0.4974	2.2876
chr9	141213431	63956418	0.4529	2.0288
chr10	135534747	84559603	0.6239	11.942
chr11	135006516	89328463	0.6617	2.8617
chr12	133851895	68057711	0.5085	0.9698
chr13	115169878	51432467	0.4466	0.7866
chr14	107349540	45776636	0.4264	0.9438
chr15	102531392	45294304	0.4418	0.7496
chr16	90354753	44716319	0.4949	3.4106
chr17	81195210	56944782	0.7013	2.1476
chr18	78077248	40584606	0.5198	5.1509
chr19	59128983	36705307	0.6208	9.9888
chr20	63025520	35155019	0.5578	1.3168
chr21	48129895	21889061	0.4548	2.9293
chr22	51304566	22731032	0.4431	0.9178
chrMT	16571	4109618	248.0006	75.2564
chrX	155270560	76010374	0.4895	1.4987
chrY	59373566	7610522	0.1282	5.5266

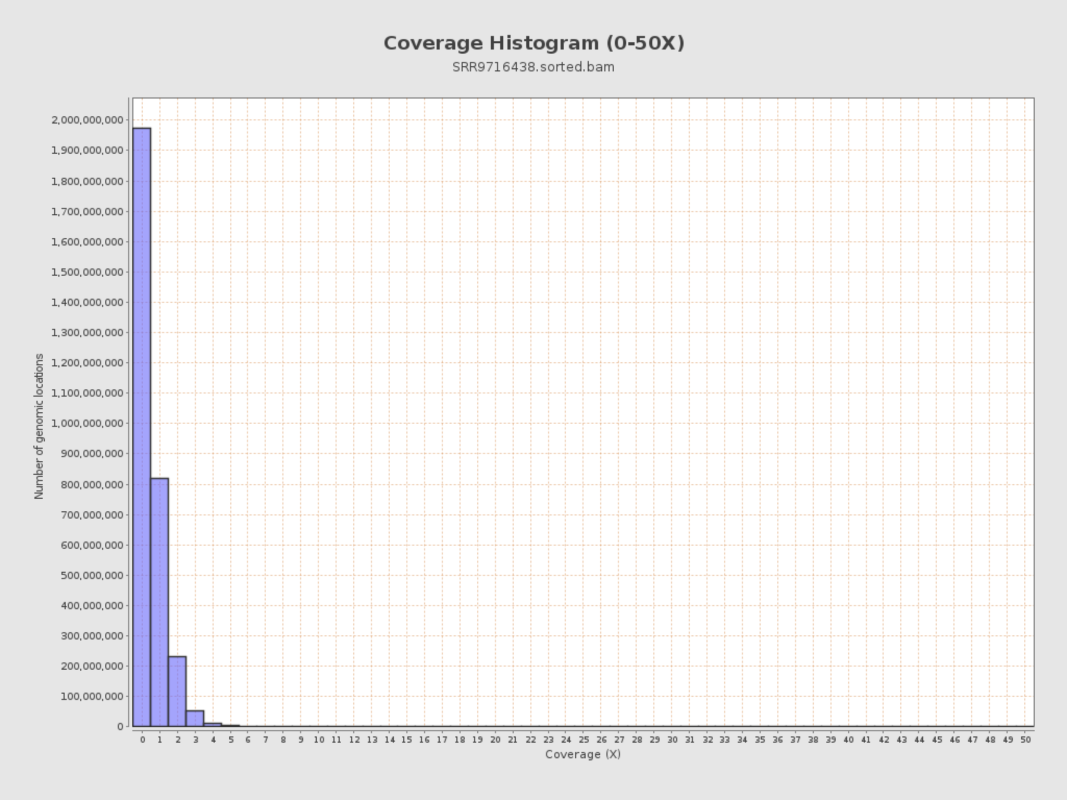
3. Results : Coverage across reference



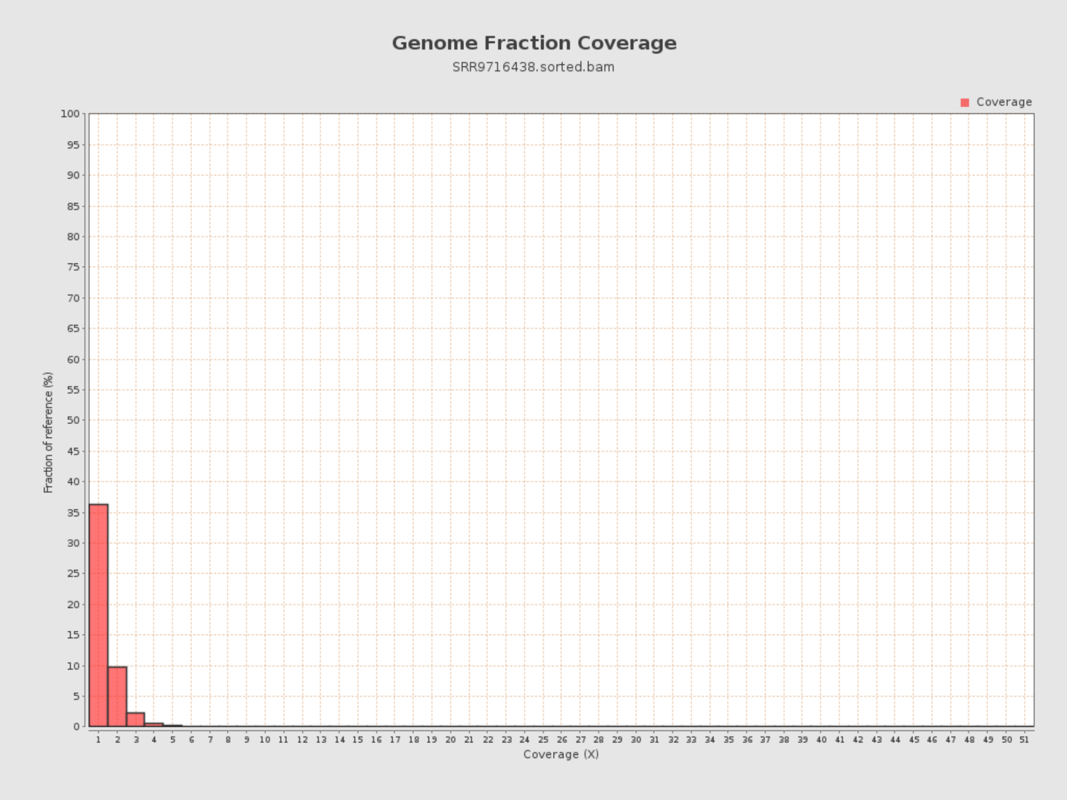
4. Results : Coverage Histogram



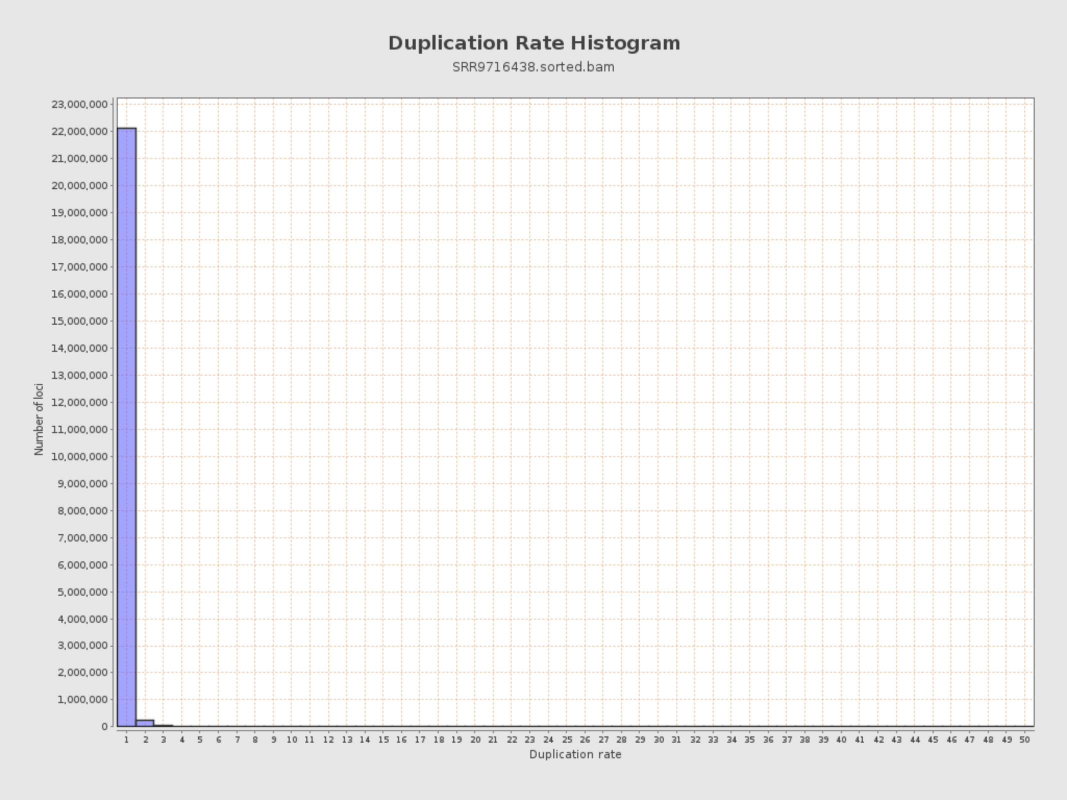
5. Results : Coverage Histogram (0-50X)



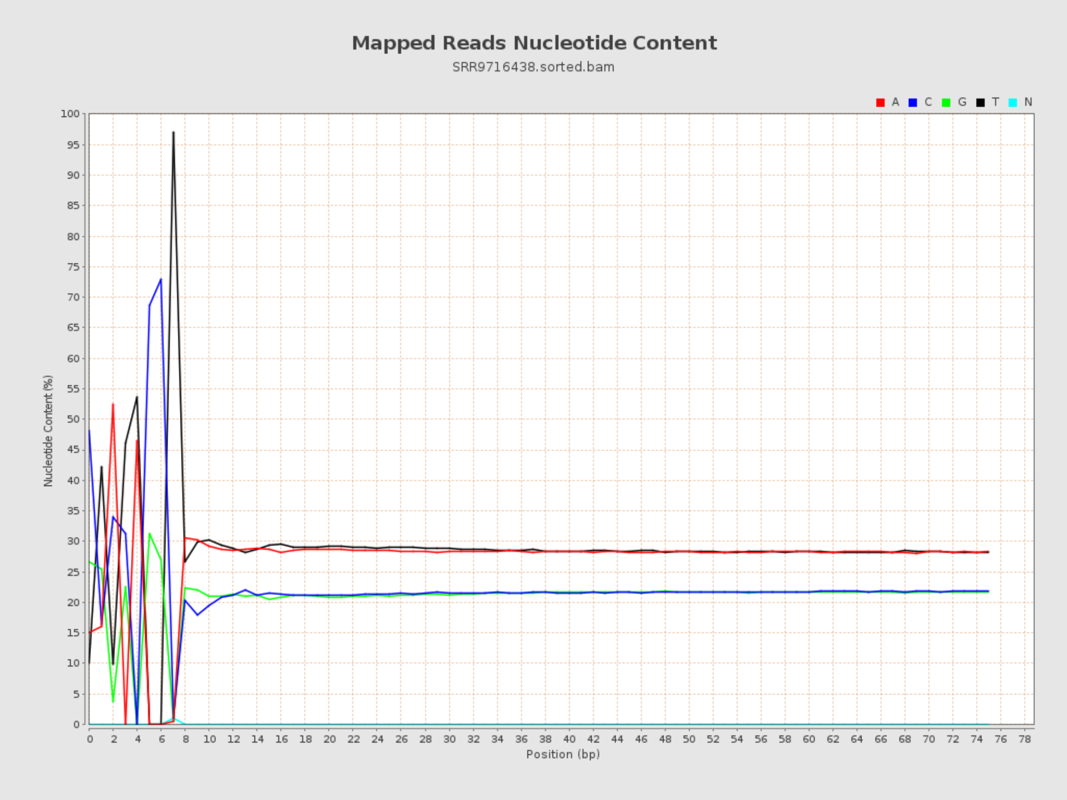
6. Results : Genome Fraction Coverage



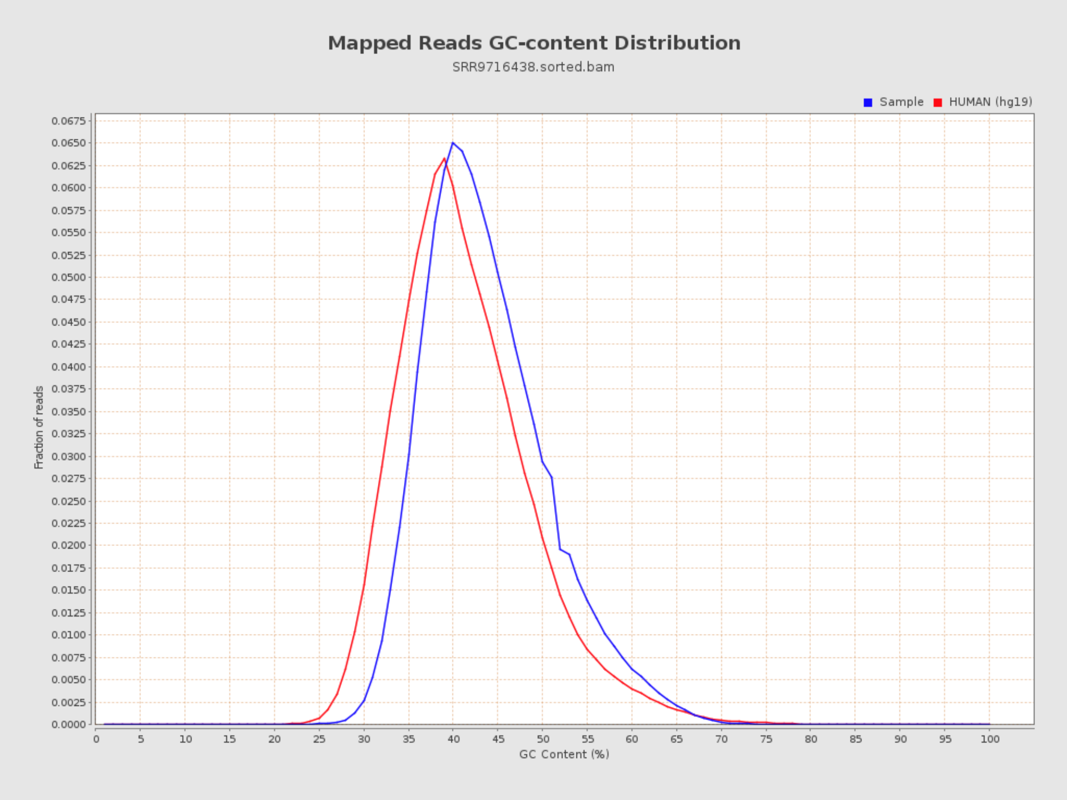
7. Results : Duplication Rate Histogram



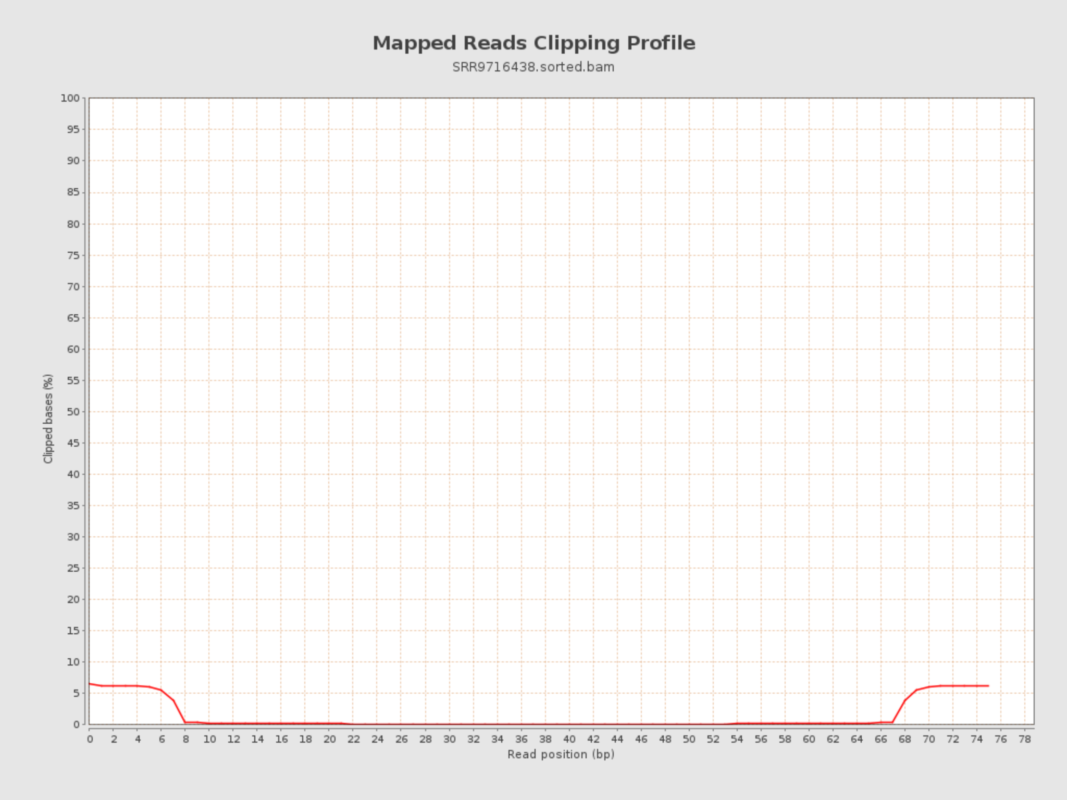
8. Results : Mapped Reads Nucleotide Content



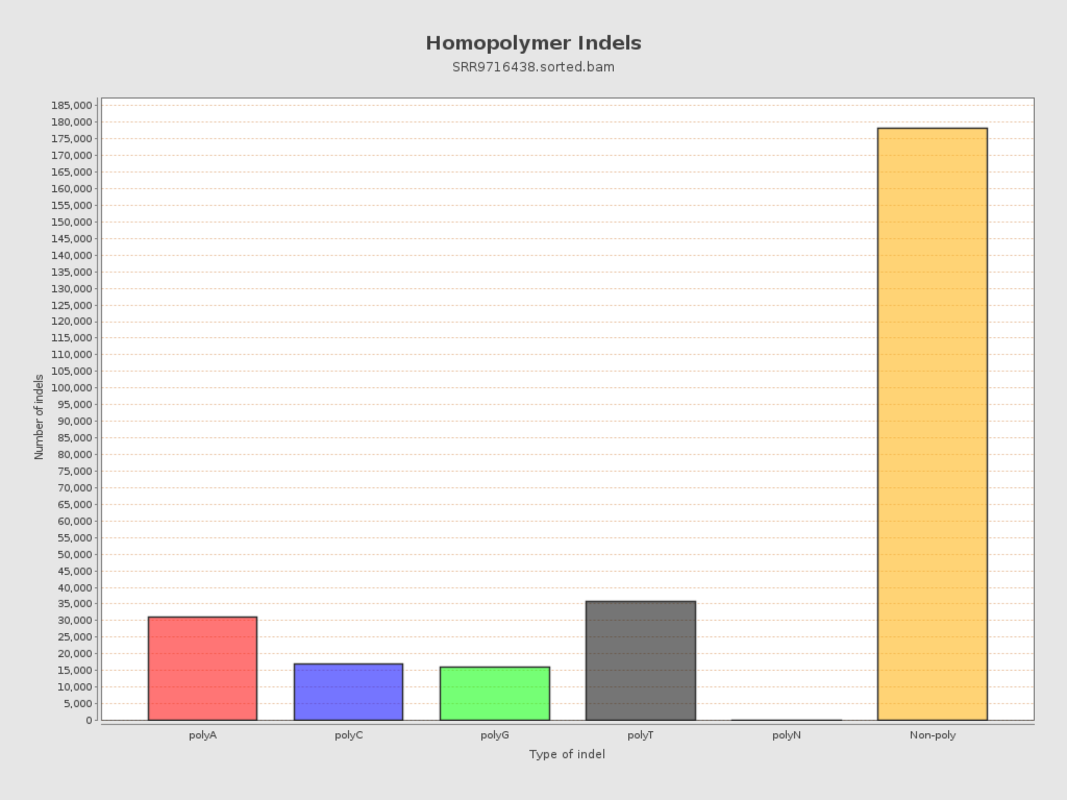
9. Results : Mapped Reads GC-content Distribution



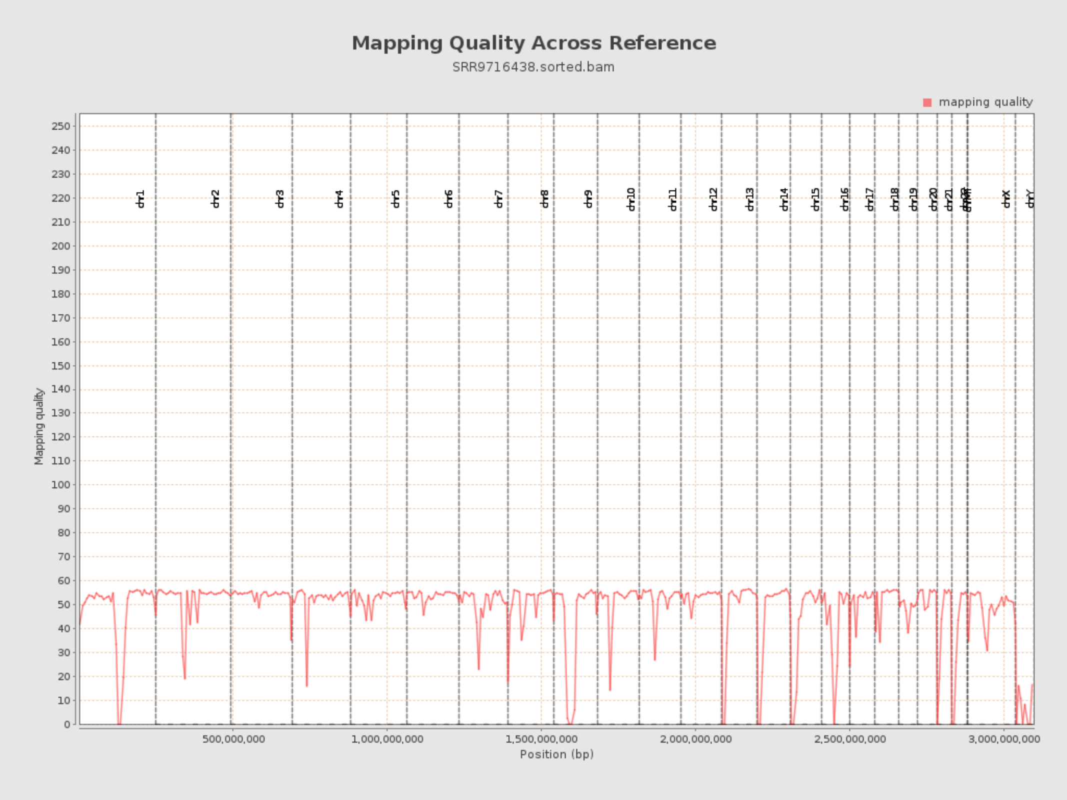
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram