Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:55:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716429.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_SRR9716429 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716429.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716429.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,747,534
Mapped reads	1,607,624 / 91.99%
Unmapped reads	139,910 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,682 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	59,786 / 3.42%
Duplication rate	2.66%
Clipped reads	1,610,362 / 92.15%

2.2. ACGT Content

Number/percentage of A's	21,959,071 / 23.48%
Number/percentage of C's	17,508,657 / 18.72%
Number/percentage of T's	30,137,795 / 32.23%
Number/percentage of G's	23,906,354 / 25.56%
Number/percentage of N's	1,945 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.2805

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

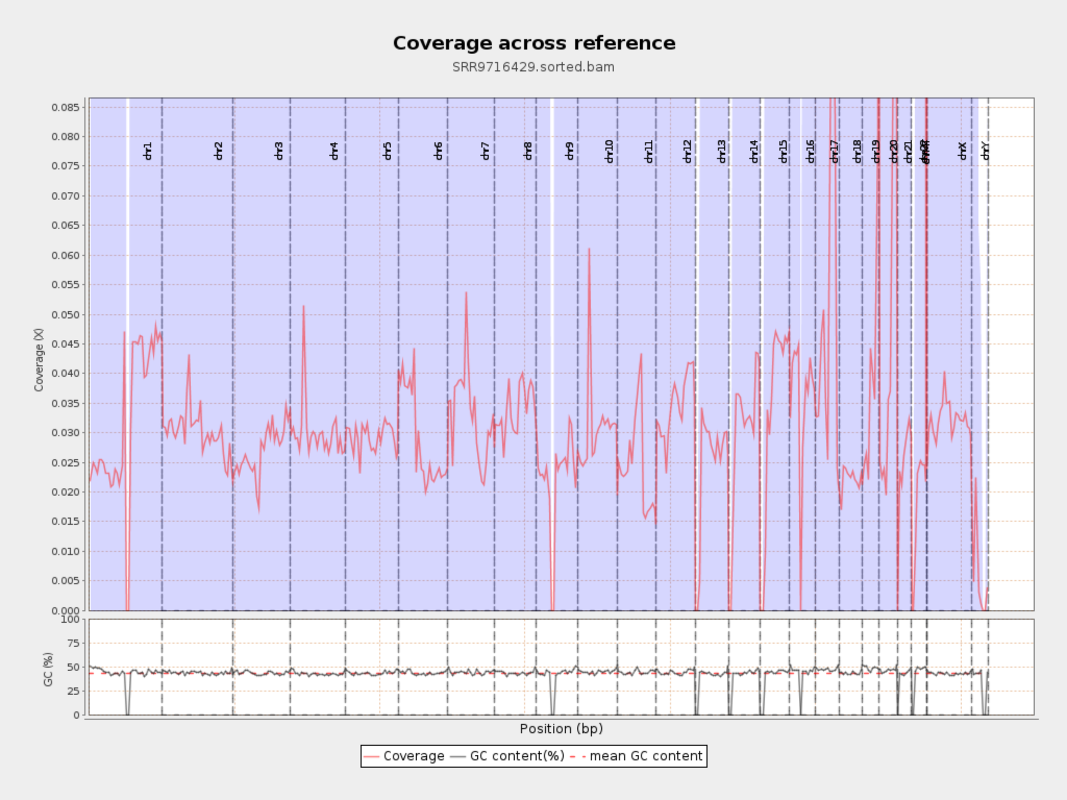
General error rate	0.52%
Mismatches	469,657
Insertions	6,307
Mapped reads with at least one insertion	0.39%
Deletions	19,016
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.28%

2.6. Chromosome stats

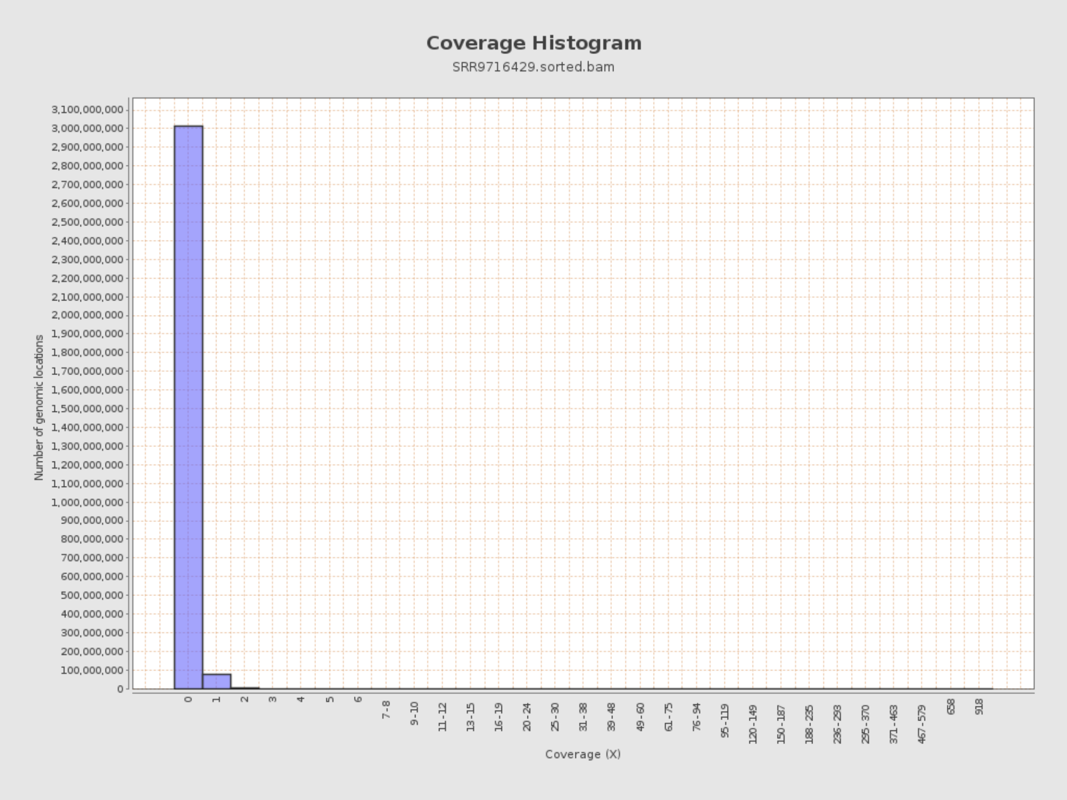
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7878157	0.0316	0.4435
chr2	243199373	7375276	0.0303	0.4178
chr3	198022430	5332527	0.0269	0.1799
chr4	191154276	5705857	0.0298	0.2223
chr5	180915260	5283068	0.0292	0.1851
chr6	171115067	4957517	0.029	0.2205
chr7	159138663	5280116	0.0332	0.3618

chr8	146364022	4973506	0.034	0.3465
chr9	141213431	3107020	0.022	0.2042
chr10	135534747	4177131	0.0308	0.2962
chr11	135006516	3349536	0.0248	0.2193
chr12	133851895	4640778	0.0347	0.204
chr13	115169878	2792905	0.0243	0.1711
chr14	107349540	3156160	0.0294	0.1914
chr15	102531392	3438960	0.0335	0.2016
chr16	90354753	3239792	0.0359	0.2155
chr17	81195210	4134157	0.0509	0.2563
chr18	78077248	1724393	0.0221	0.3121
chr19	59128983	2464890	0.0417	0.3604
chr20	63025520	3125804	0.0496	0.2541
chr21	48129895	1176968	0.0245	0.1955
chr22	51304566	874994	0.0171	0.141
chrMT	16571	21827	1.3172	1.4959
chrX	155270560	4997685	0.0322	0.2143
chrY	59373566	335466	0.0057	0.2229

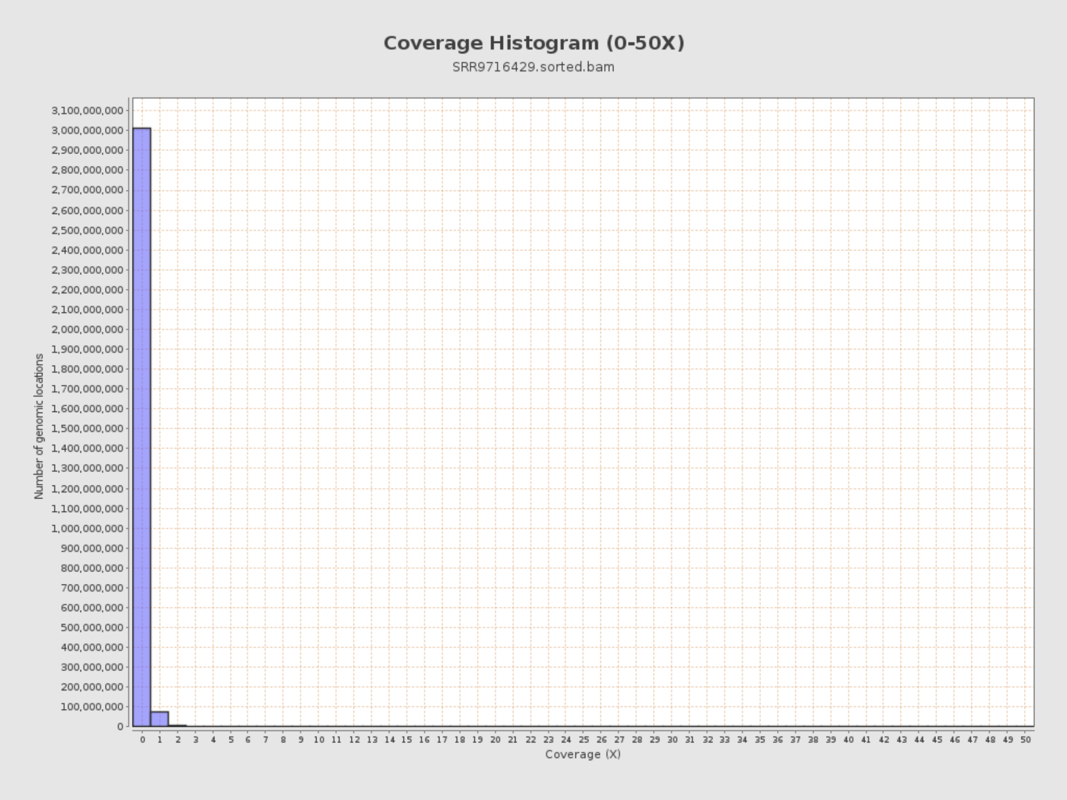
3. Results : Coverage across reference



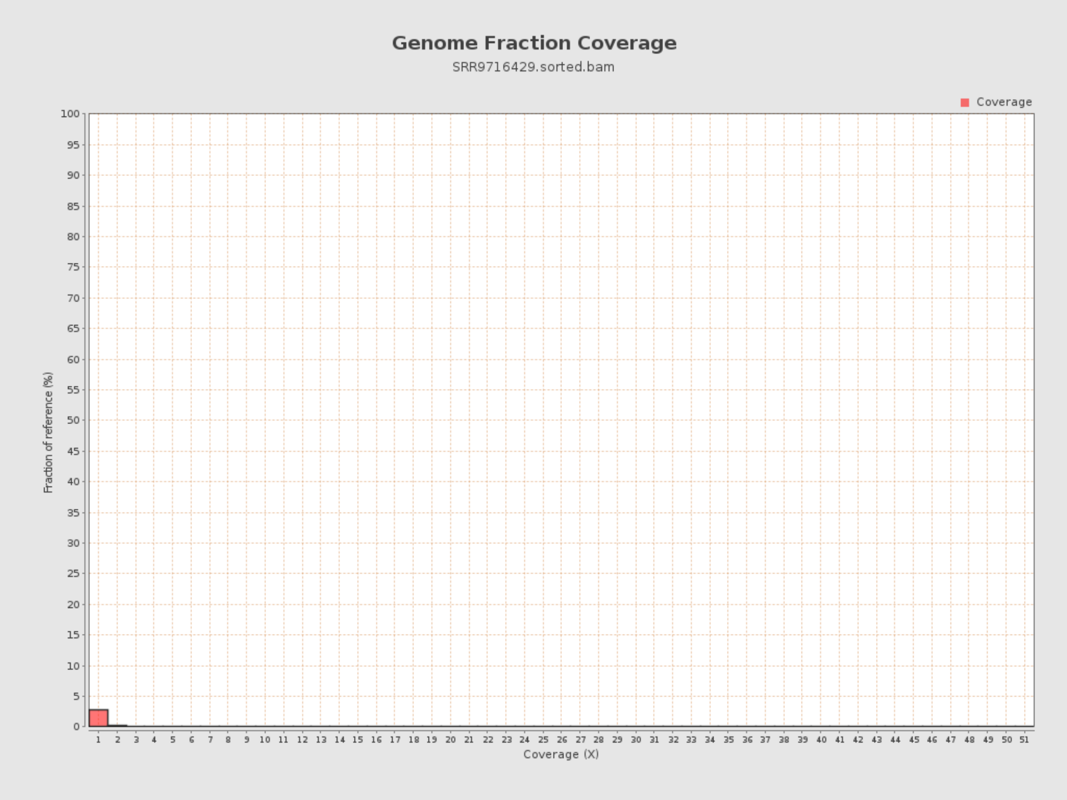
4. Results : Coverage Histogram



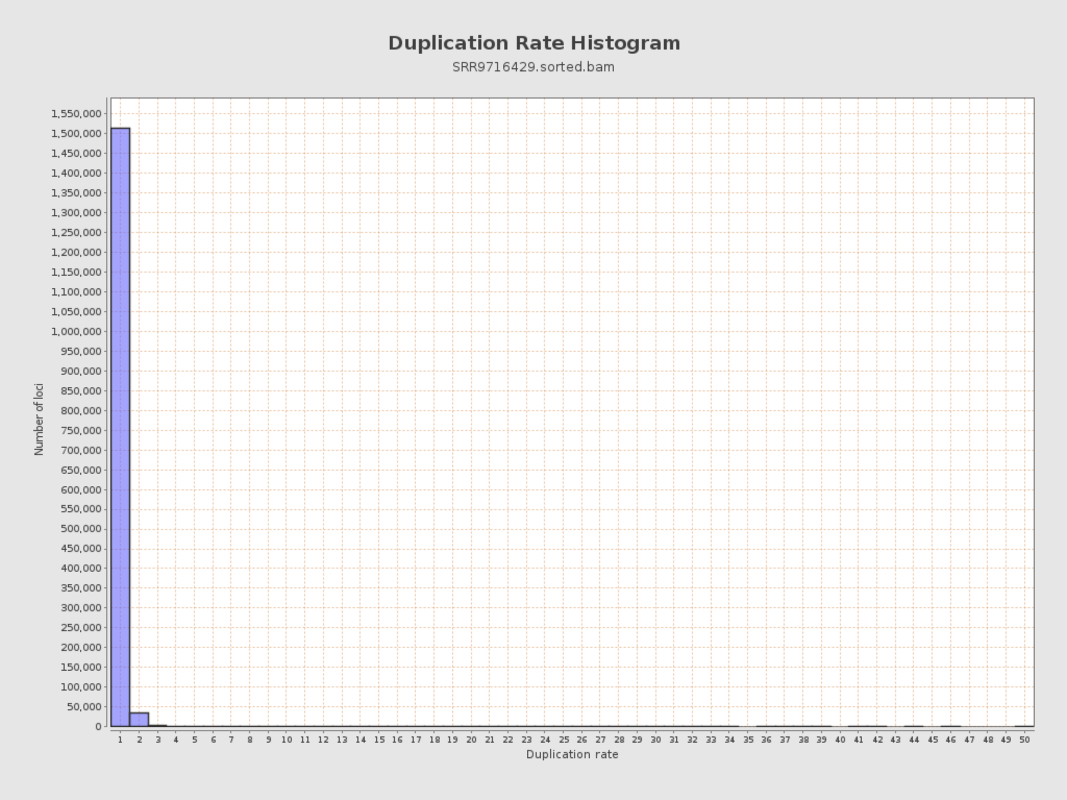
5. Results : Coverage Histogram (0-50X)



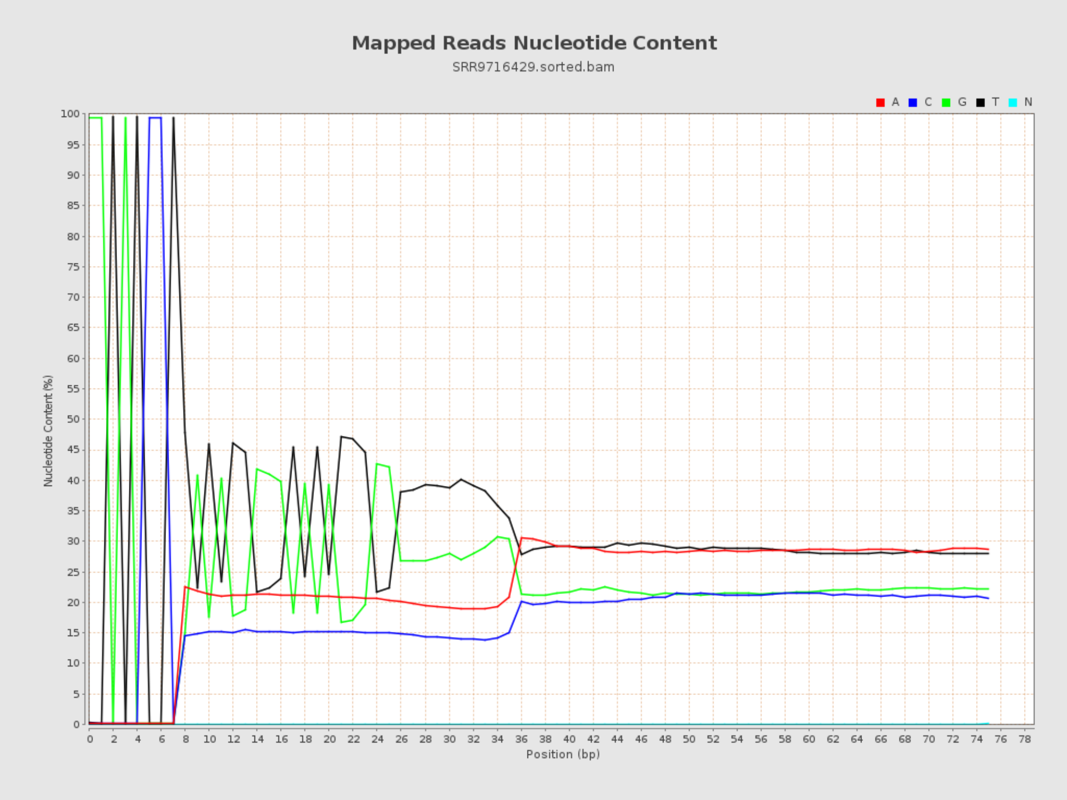
6. Results : Genome Fraction Coverage



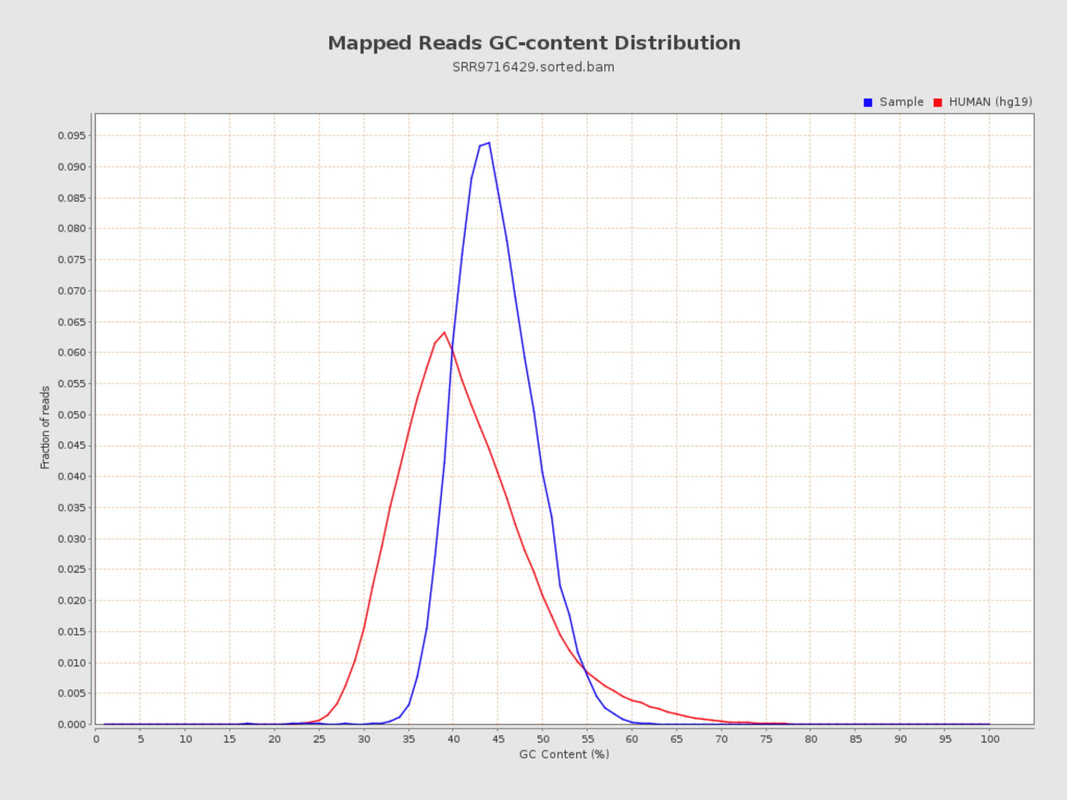
7. Results : Duplication Rate Histogram



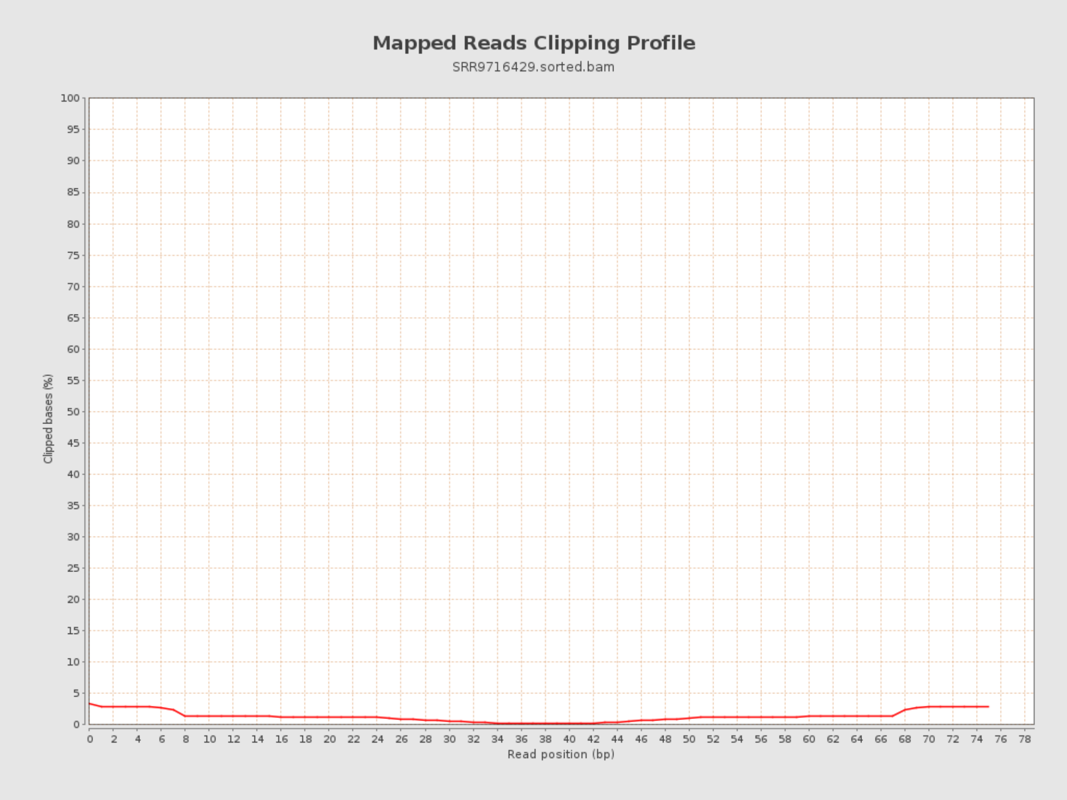
8. Results : Mapped Reads Nucleotide Content



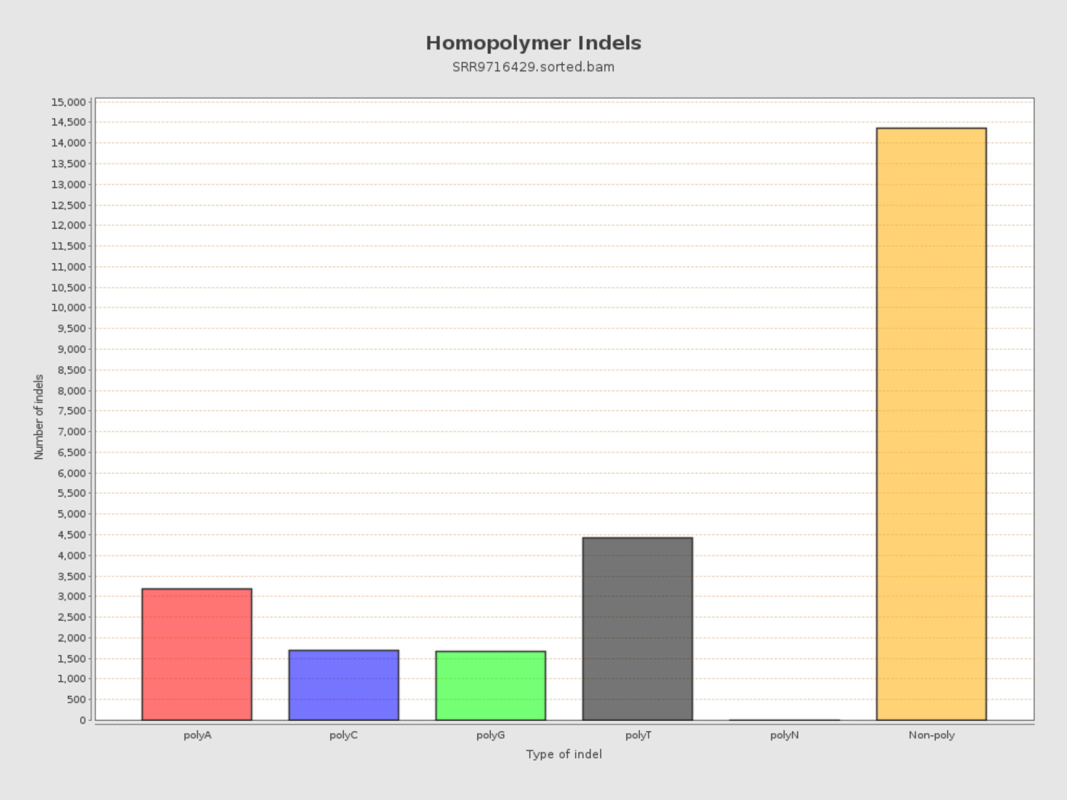
9. Results : Mapped Reads GC-content Distribution



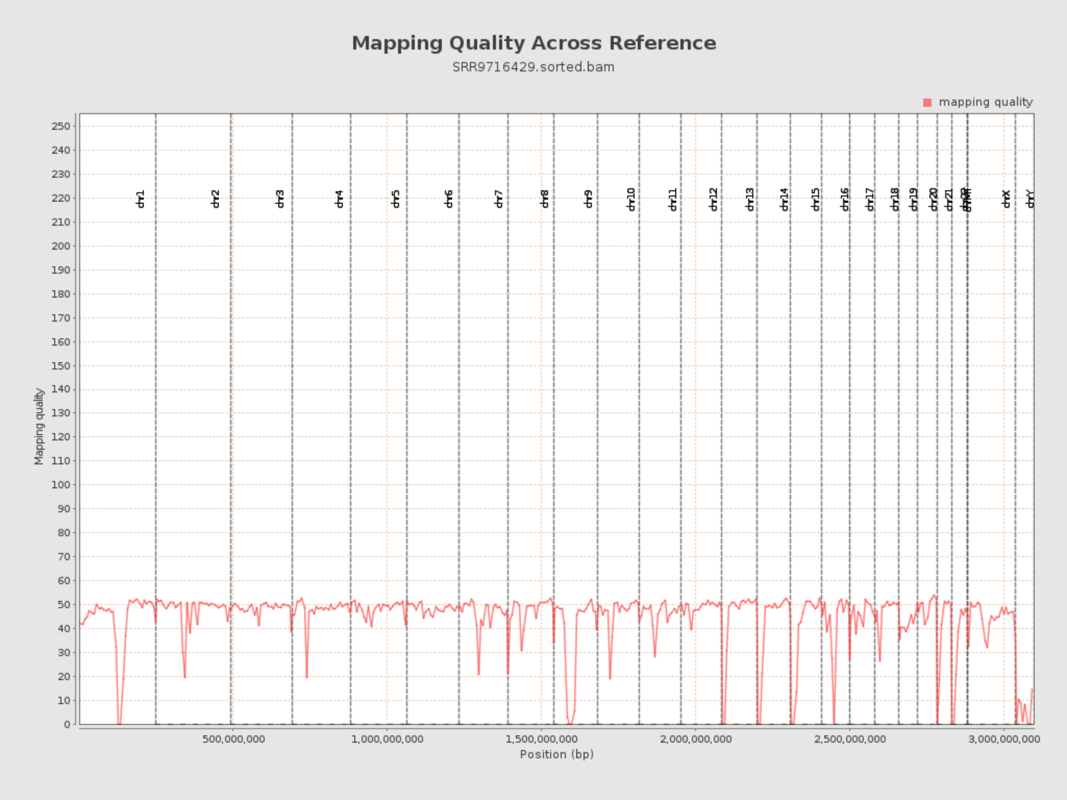
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram