Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:51:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716970.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_SRR9716970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:51:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,415,870
Mapped reads	2,110,716 / 87.37%
Unmapped reads	305,154 / 12.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,049 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	74,574 / 3.09%
Duplication rate	2.42%
Clipped reads	2,113,388 / 87.48%

2.2. ACGT Content

Number/percentage of A's	30,362,833 / 25.4%
Number/percentage of C's	23,521,100 / 19.68%
Number/percentage of T's	37,444,498 / 31.32%
Number/percentage of G's	28,214,189 / 23.6%
Number/percentage of N's	1,786 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3609

2.4. Mapping Quality

Mean Mapping Quality	42.93

2.5. Mismatches and indels

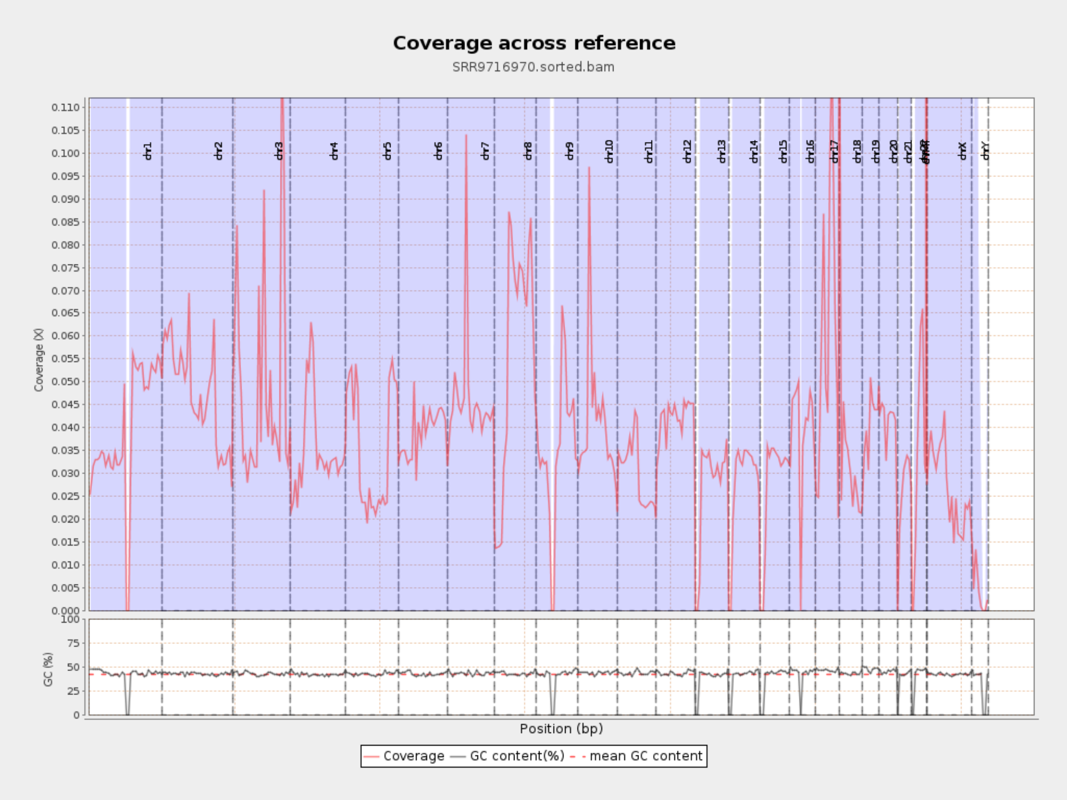
General error rate	0.52%
Mismatches	609,127
Insertions	8,333
Mapped reads with at least one insertion	0.39%
Deletions	22,459
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.89%

2.6. Chromosome stats

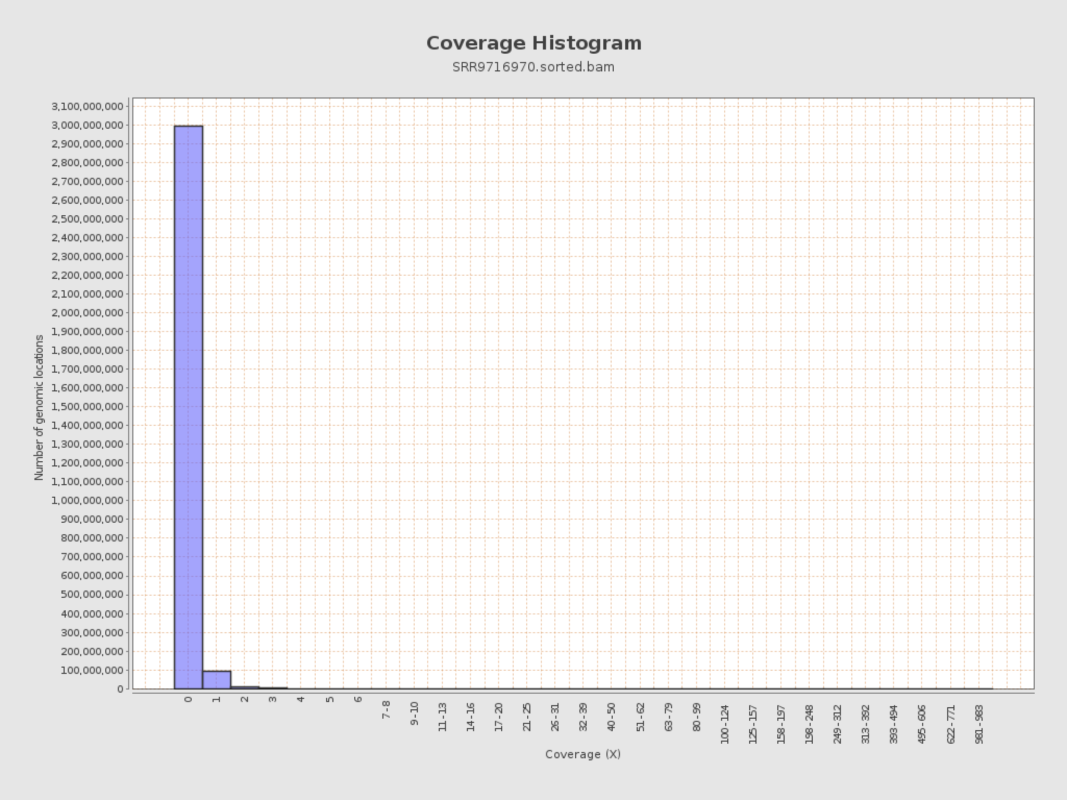
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9768675	0.0392	0.4281
chr2	243199373	11646946	0.0479	0.485
chr3	198022430	9844847	0.0497	0.2702
chr4	191154276	6736486	0.0352	0.217
chr5	180915260	6391269	0.0353	0.209
chr6	171115067	6664657	0.0389	0.2568
chr7	159138663	7428746	0.0467	0.8863

chr8	146364022	8309089	0.0568	0.3352
chr9	141213431	4897792	0.0347	0.2487
chr10	135534747	5596453	0.0413	0.4638
chr11	135006516	4022478	0.0298	0.2449
chr12	133851895	5609121	0.0419	0.2448
chr13	115169878	3113367	0.027	0.1832
chr14	107349540	2993794	0.0279	0.1934
chr15	102531392	2820021	0.0275	0.188
chr16	90354753	3570132	0.0395	0.2382
chr17	81195210	4895424	0.0603	0.2909
chr18	78077248	2779728	0.0356	0.3987
chr19	59128983	2403791	0.0407	0.4108
chr20	63025520	2600492	0.0413	0.236
chr21	48129895	1221031	0.0254	0.1845
chr22	51304566	1681496	0.0328	0.2033
chrMT	16571	66711	4.0258	3.2084
chrX	155270560	4257409	0.0274	0.2227
chrY	59373566	259527	0.0044	0.1055

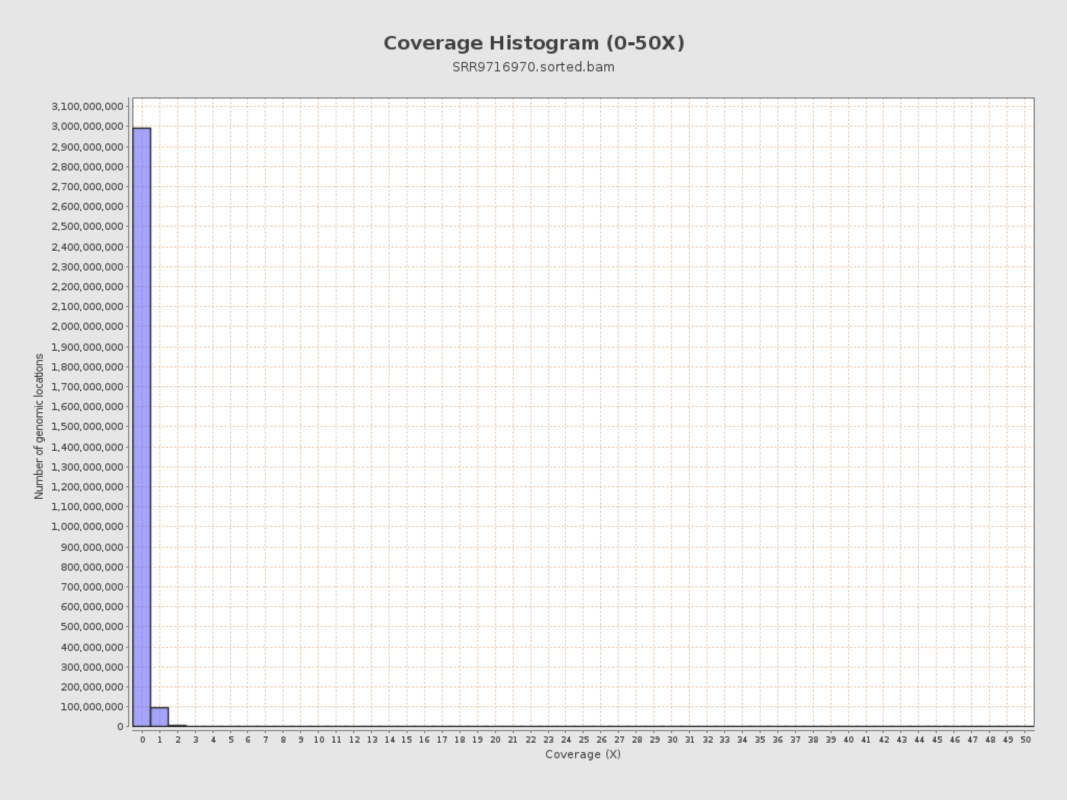
3. Results : Coverage across reference



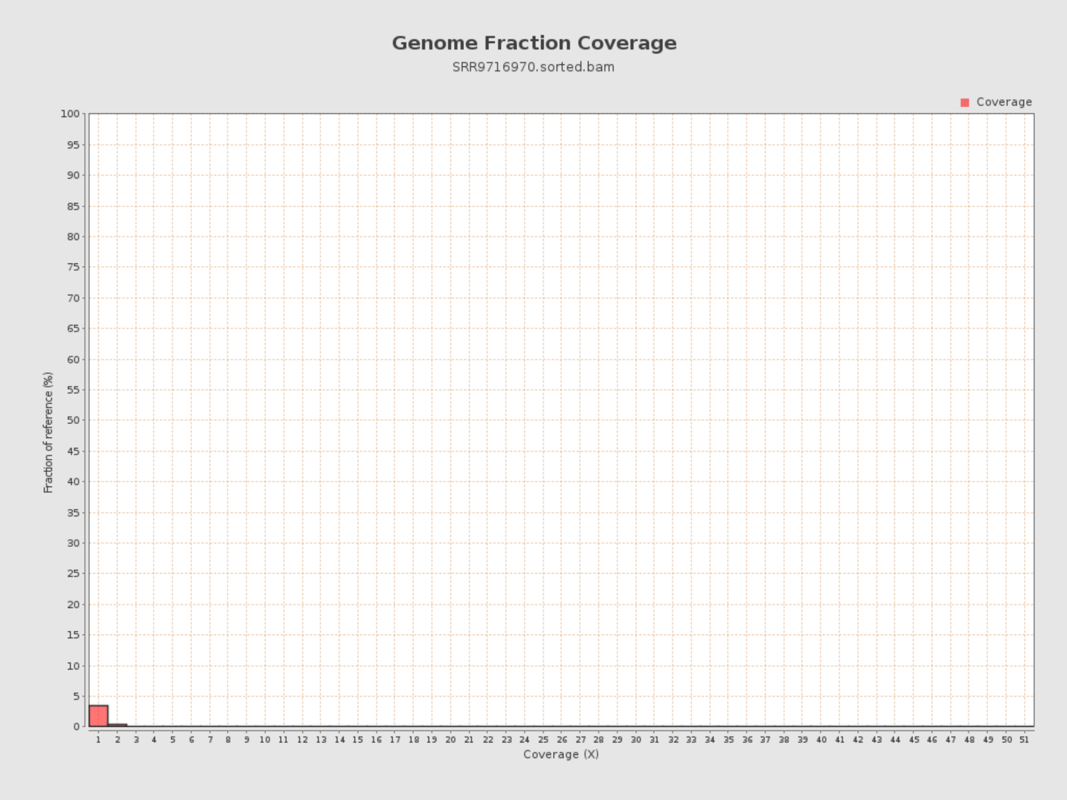
4. Results : Coverage Histogram



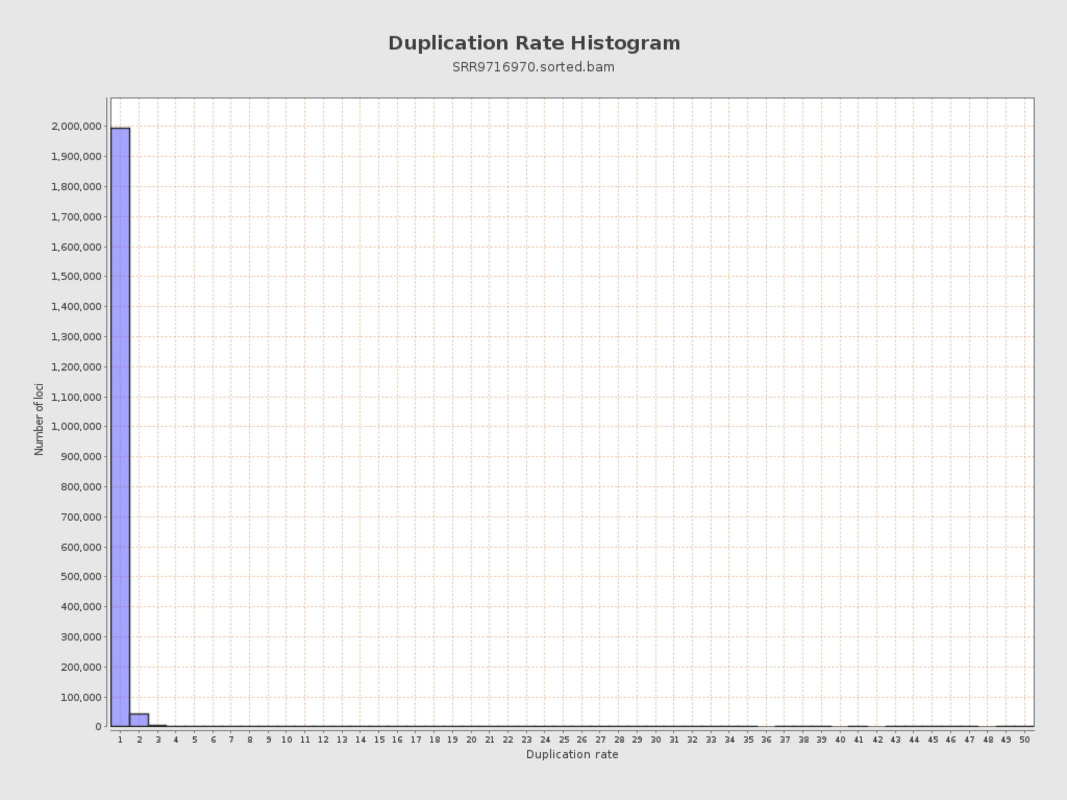
5. Results : Coverage Histogram (0-50X)



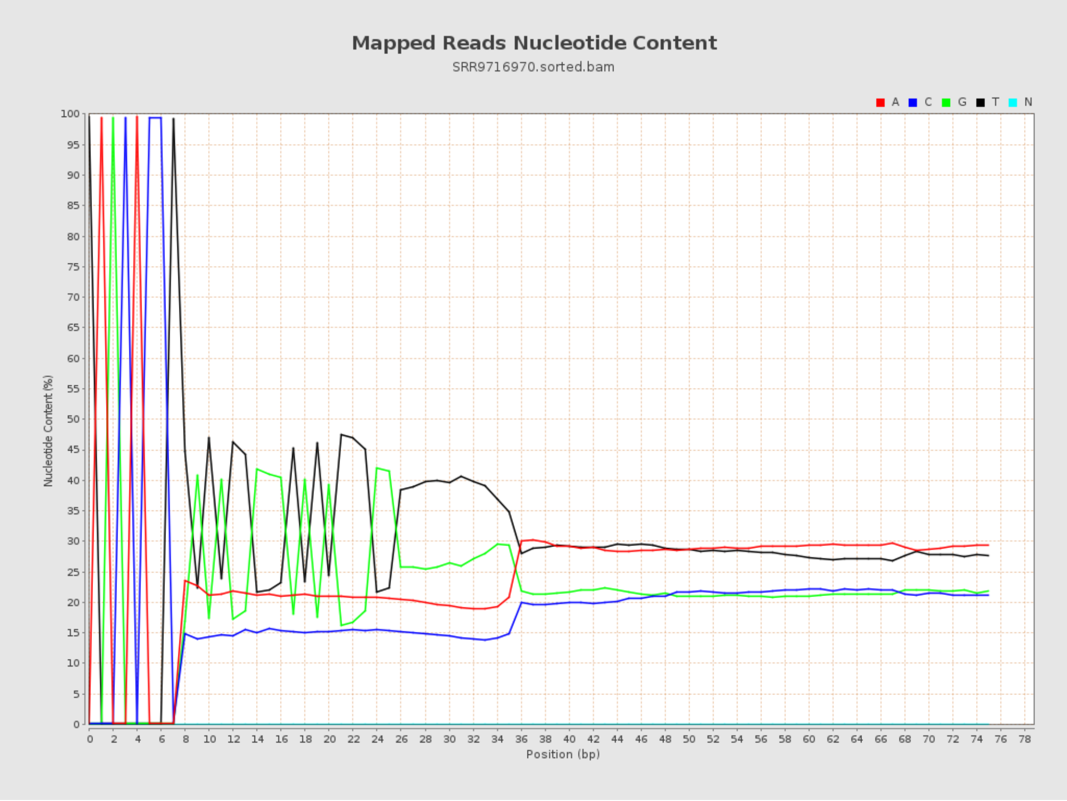
6. Results : Genome Fraction Coverage



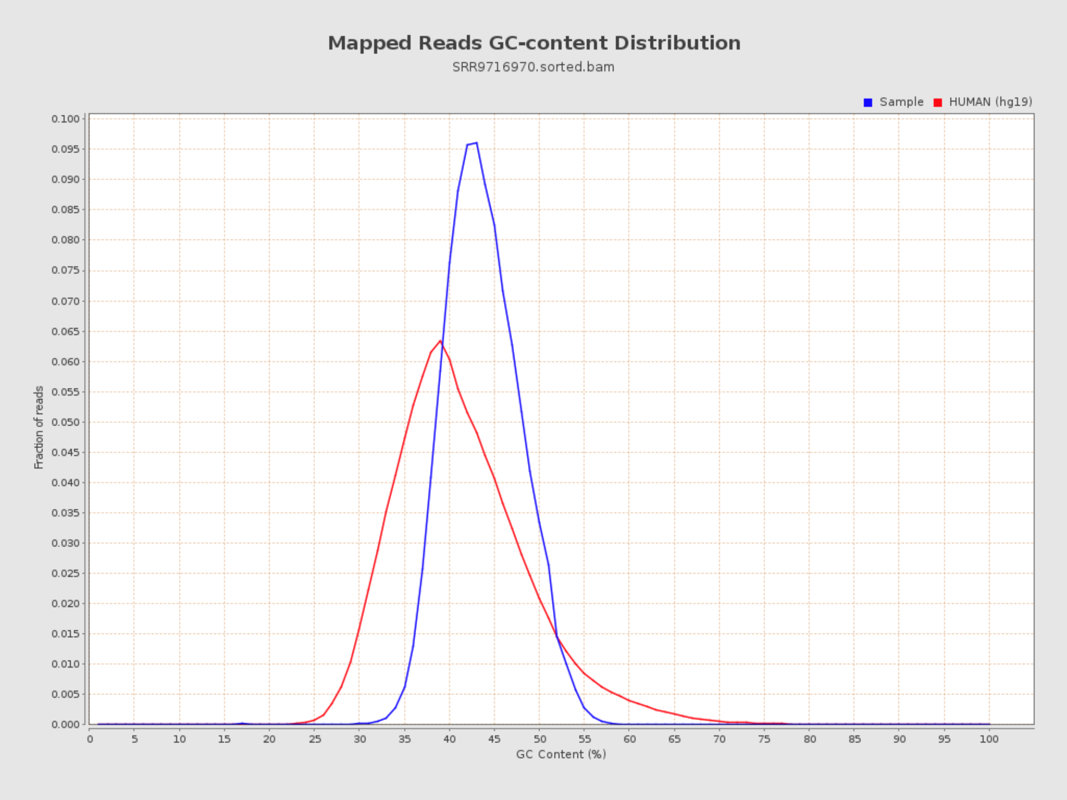
7. Results : Duplication Rate Histogram



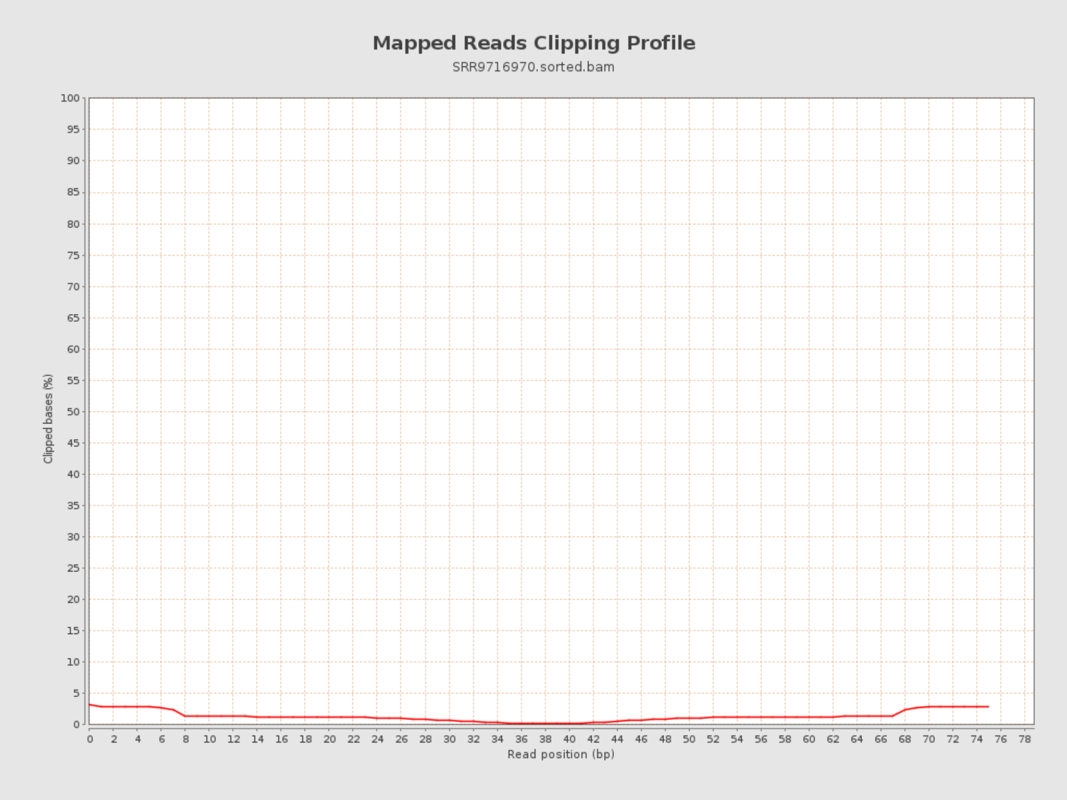
8. Results : Mapped Reads Nucleotide Content



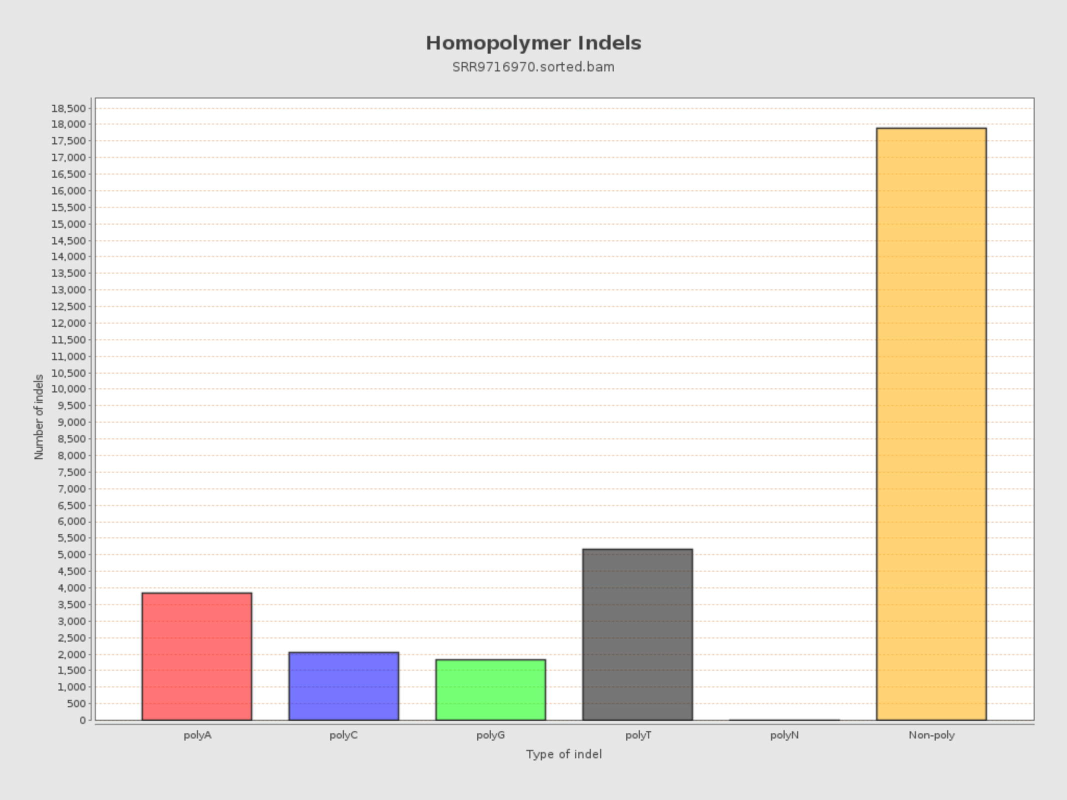
9. Results : Mapped Reads GC-content Distribution



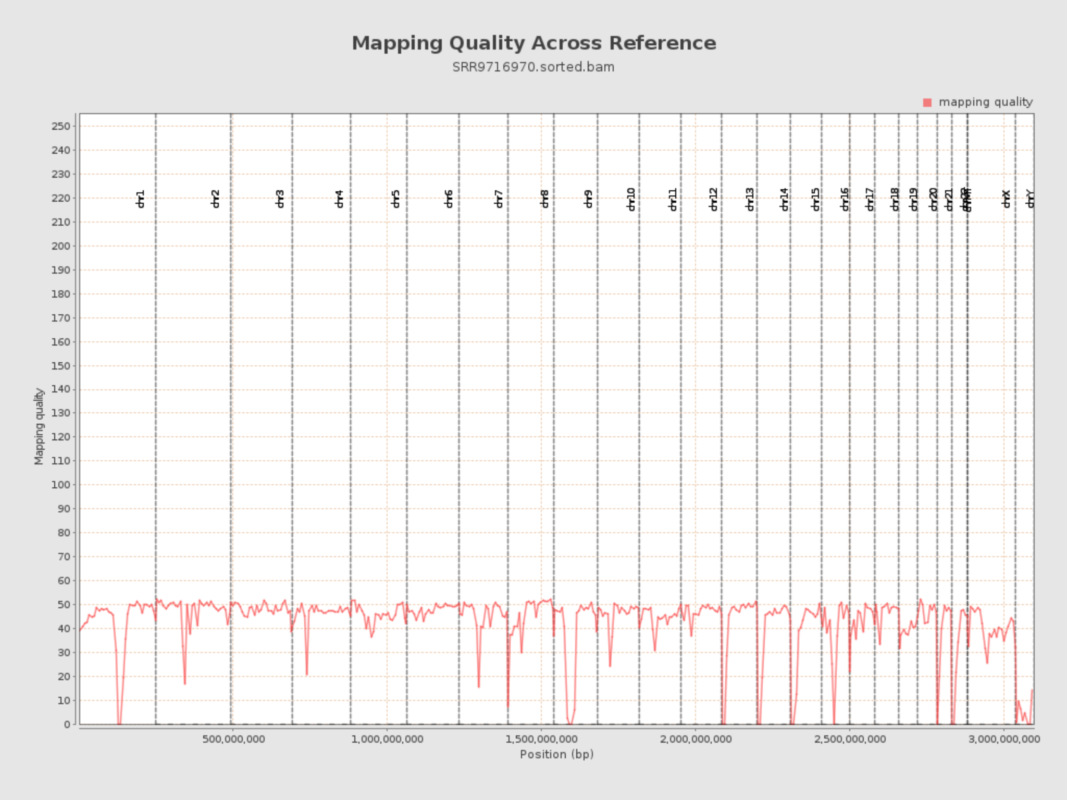
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram