Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:47:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716639.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_SRR9716639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:47:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	504,757
Mapped reads	463,298 / 91.79%
Unmapped reads	41,459 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,550 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	8,383 / 1.66%
Duplication rate	1.23%
Clipped reads	464,409 / 92.01%

2.2. ACGT Content

Number/percentage of A's	6,806,182 / 25.41%
Number/percentage of C's	4,961,414 / 18.52%
Number/percentage of T's	8,209,217 / 30.65%
Number/percentage of G's	6,808,388 / 25.42%
Number/percentage of N's	523 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.1147

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Mismatches and indels

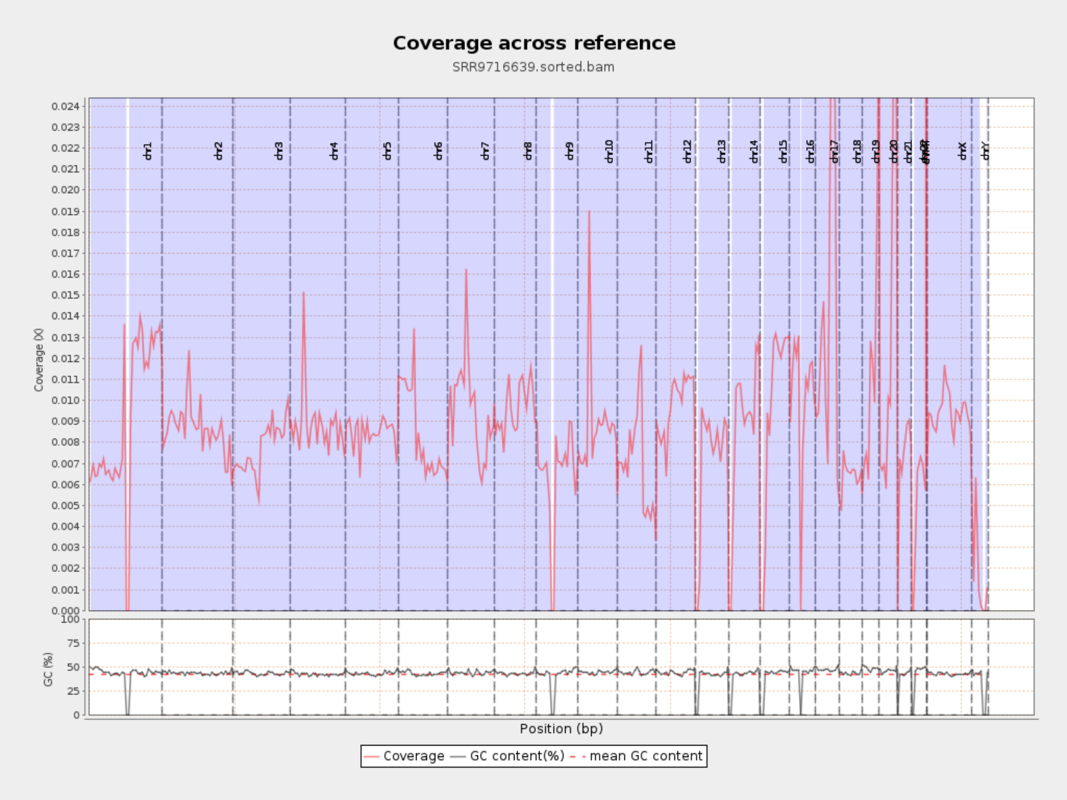
General error rate	0.52%
Mismatches	136,612
Insertions	1,762
Mapped reads with at least one insertion	0.38%
Deletions	5,216
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.79%

2.6. Chromosome stats

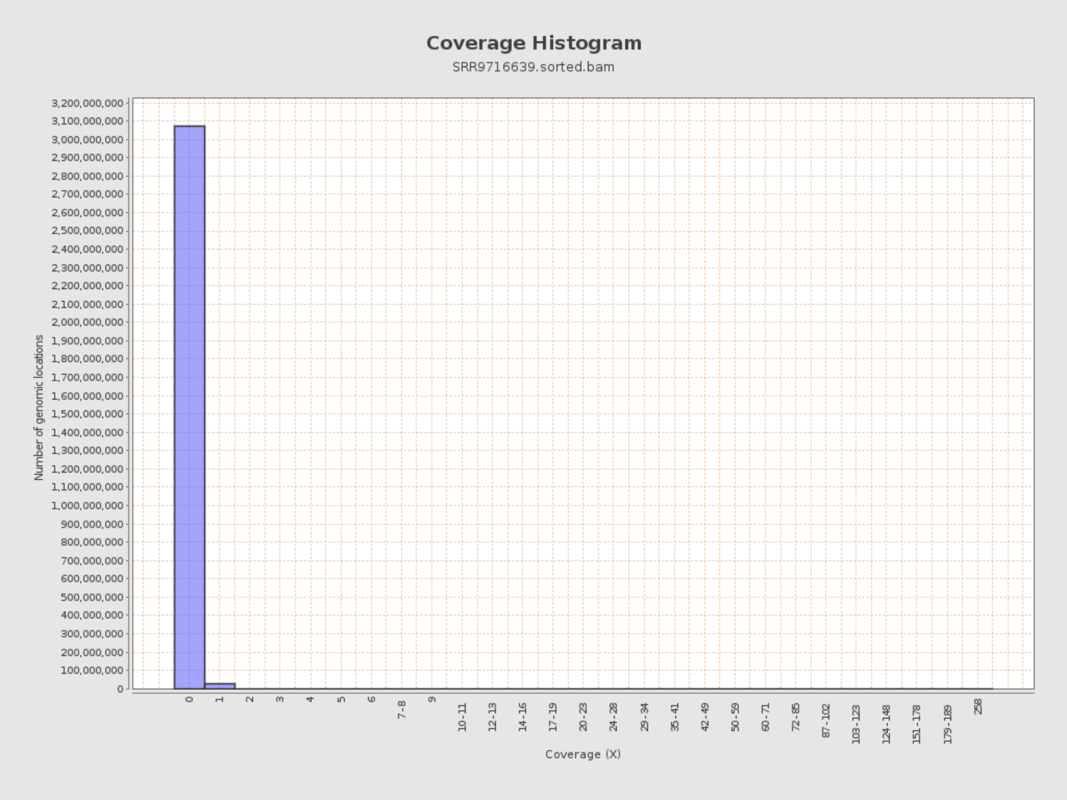
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2255287	0.009	0.1612
chr2	243199373	2109265	0.0087	0.1425
chr3	198022430	1529080	0.0077	0.0912
chr4	191154276	1681479	0.0088	0.1022
chr5	180915260	1527566	0.0084	0.0943
chr6	171115067	1441304	0.0084	0.1017
chr7	159138663	1534581	0.0096	0.1347

chr8	146364022	1411756	0.0096	0.1281
chr9	141213431	891541	0.0063	0.0905
chr10	135534747	1193201	0.0088	0.1223
chr11	135006516	947570	0.007	0.0989
chr12	133851895	1310833	0.0098	0.1018
chr13	115169878	808232	0.007	0.0873
chr14	107349540	913507	0.0085	0.0959
chr15	102531392	965084	0.0094	0.0998
chr16	90354753	914998	0.0101	0.1073
chr17	81195210	1158856	0.0143	0.1248
chr18	78077248	500869	0.0064	0.1231
chr19	59128983	689976	0.0117	0.1398
chr20	63025520	863447	0.0137	0.1217
chr21	48129895	343065	0.0071	0.0946
chr22	51304566	243798	0.0048	0.0712
chrMT	16571	4465	0.2694	0.5437
chrX	155270560	1457522	0.0094	0.1028
chrY	59373566	96879	0.0016	0.0704

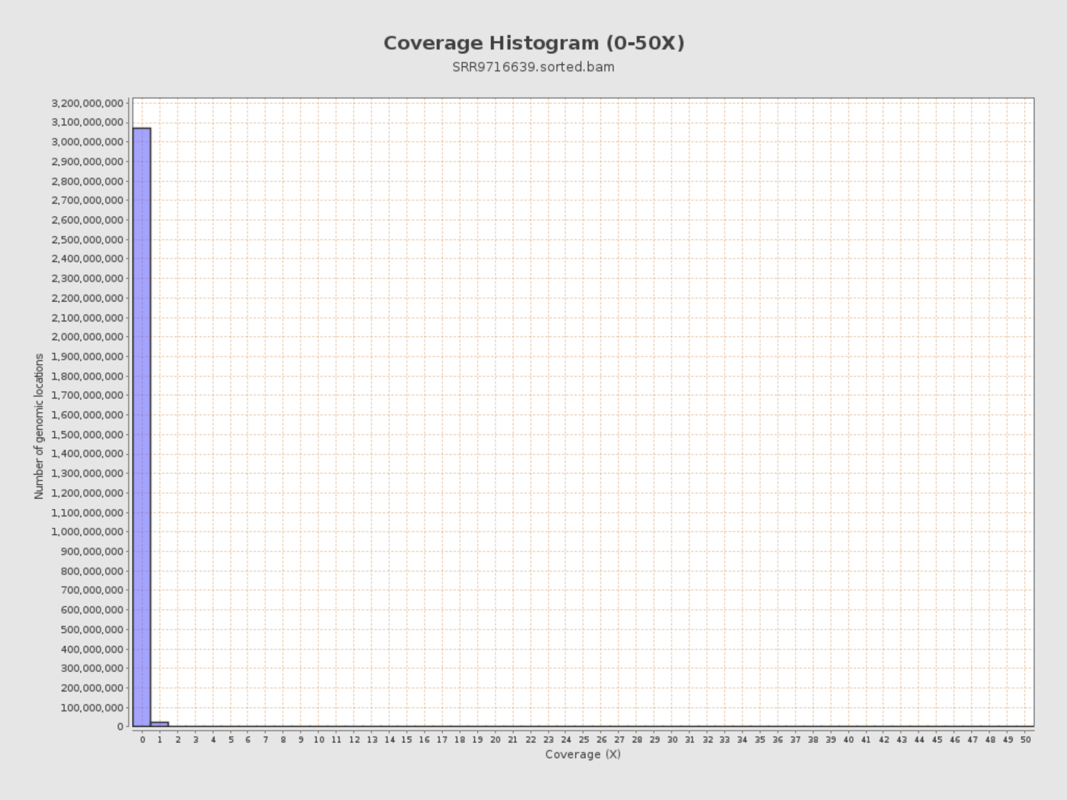
3. Results : Coverage across reference



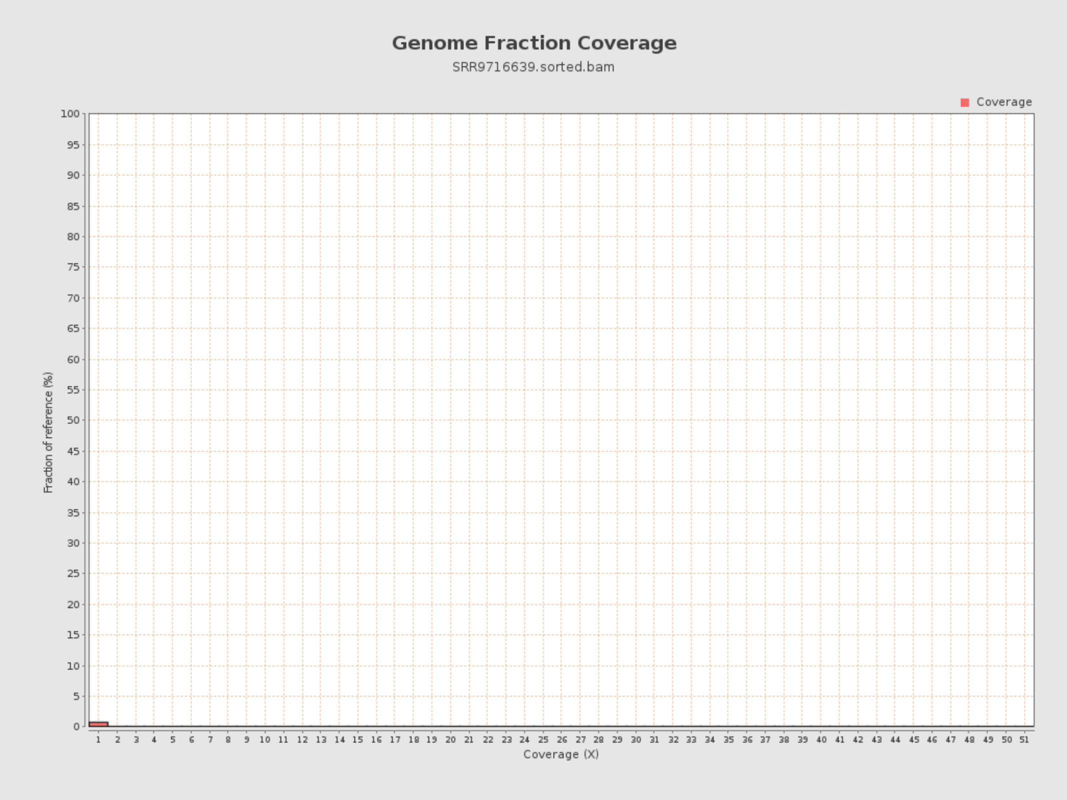
4. Results : Coverage Histogram



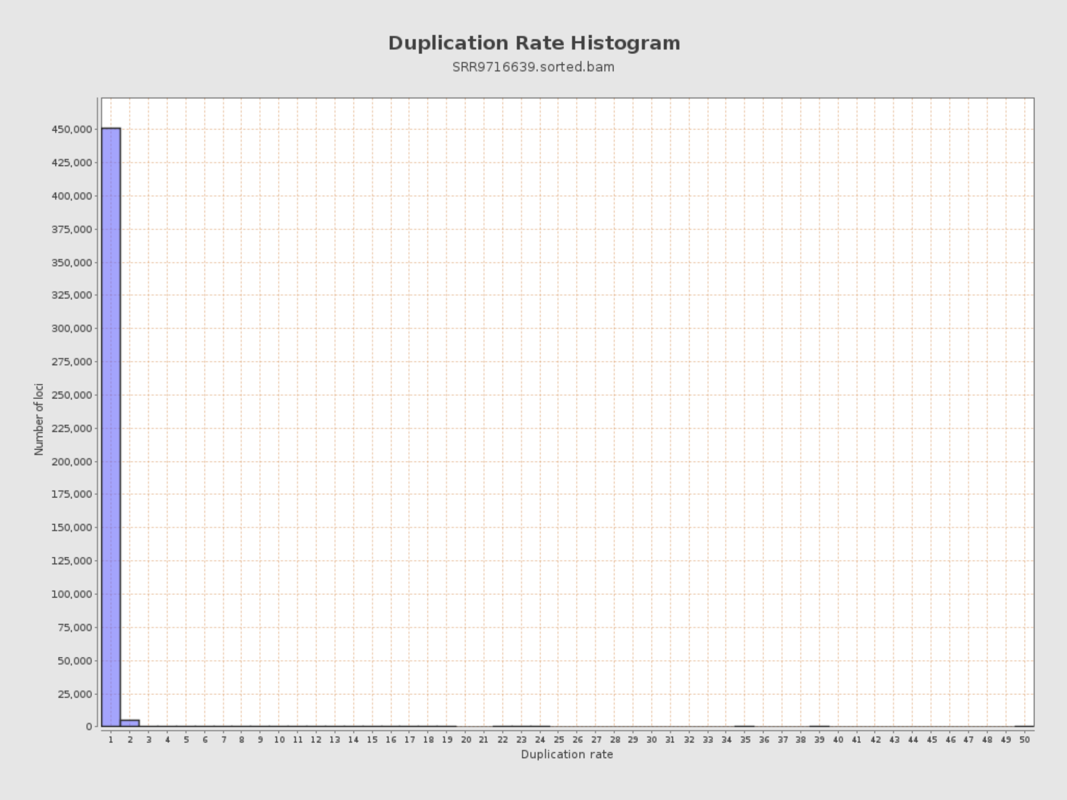
5. Results : Coverage Histogram (0-50X)



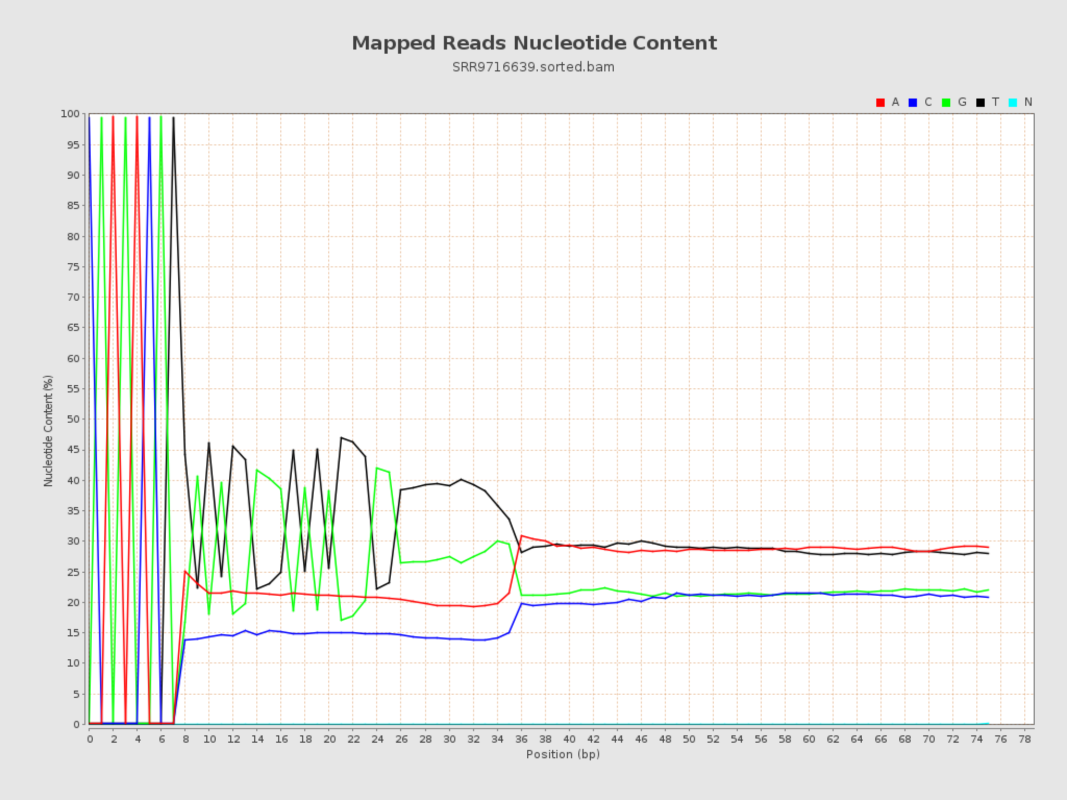
6. Results : Genome Fraction Coverage



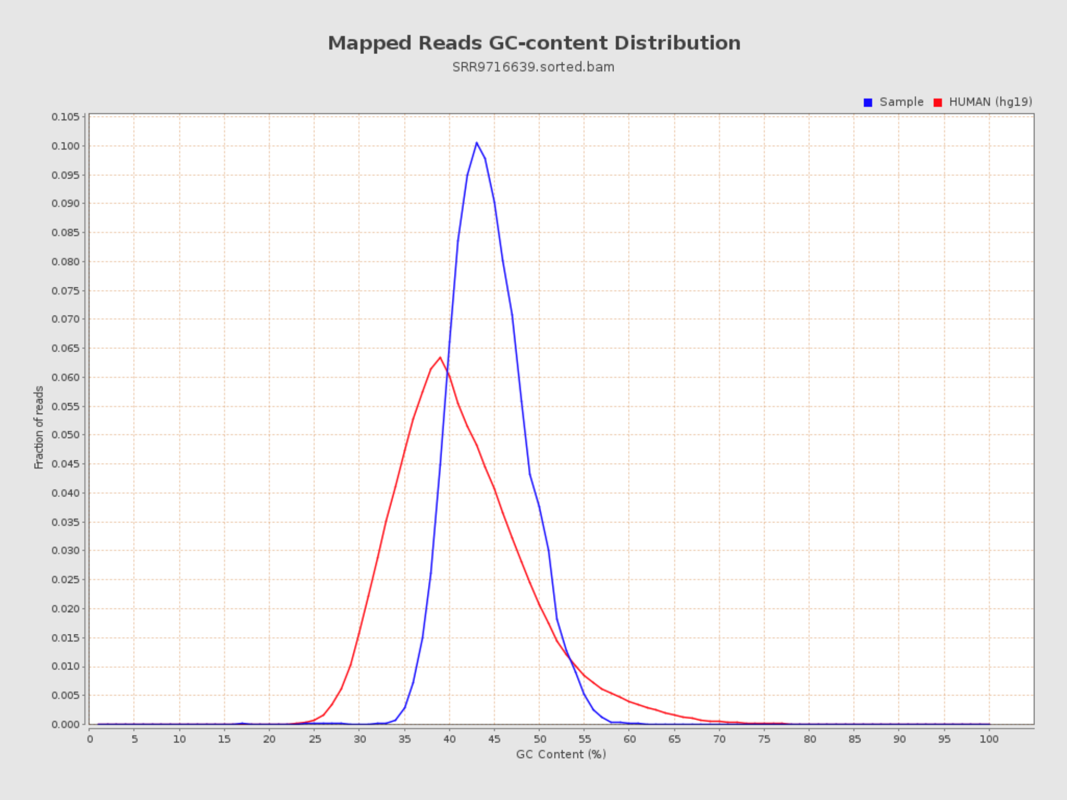
7. Results : Duplication Rate Histogram



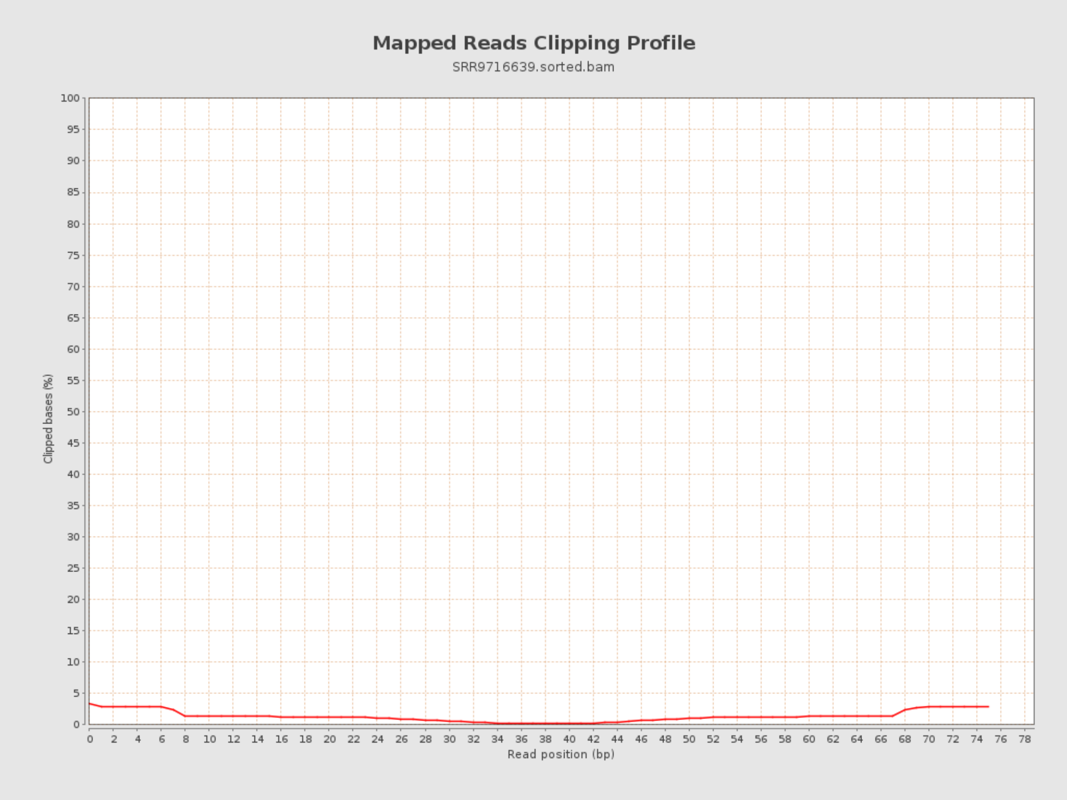
8. Results : Mapped Reads Nucleotide Content



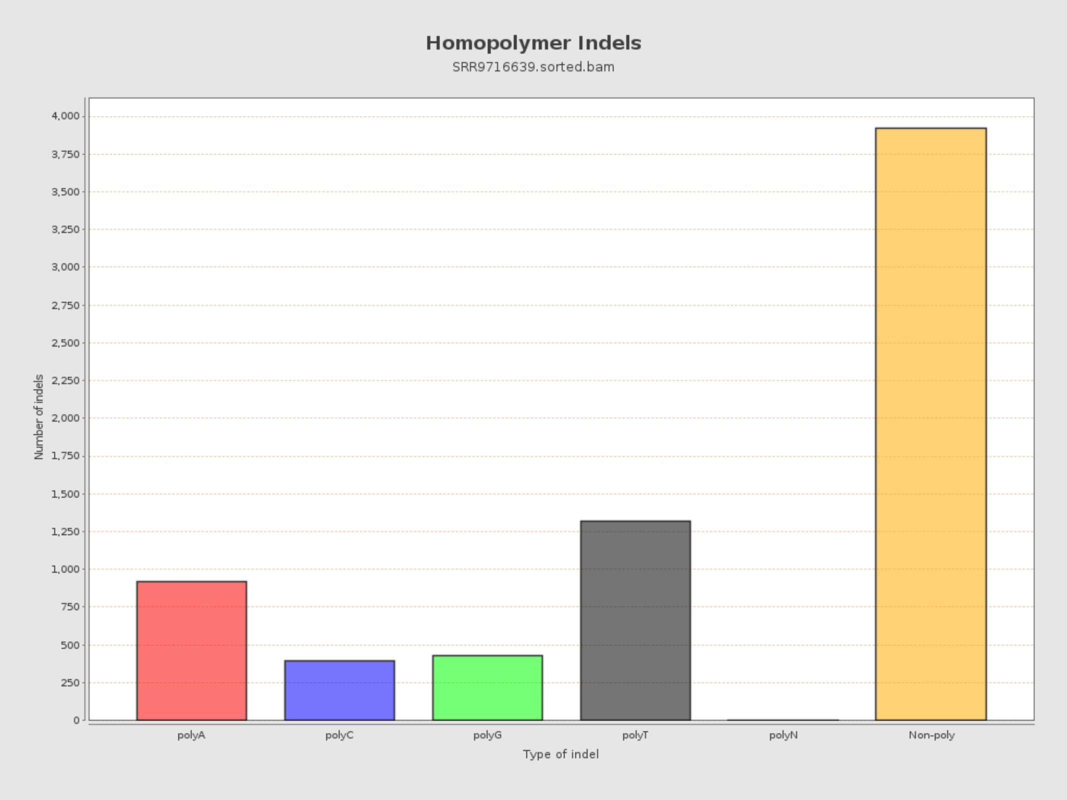
9. Results : Mapped Reads GC-content Distribution



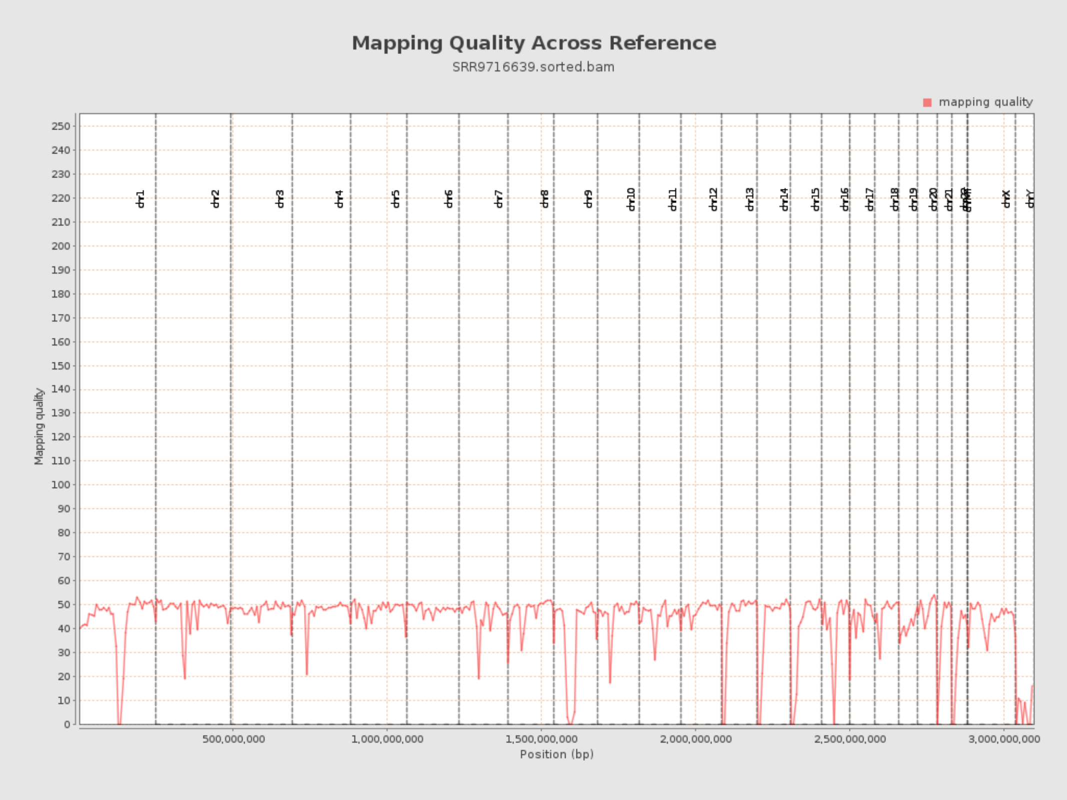
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram