Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:00:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716621.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_SRR9716621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716621.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,354
Mapped reads	496,925 / 90.62%
Unmapped reads	51,429 / 9.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,910 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	6,463 / 1.18%
Duplication rate	1.02%
Clipped reads	498,557 / 90.92%

2.2. ACGT Content

Number/percentage of A's	6,693,198 / 23.59%
Number/percentage of C's	5,533,480 / 19.5%
Number/percentage of T's	8,853,878 / 31.21%
Number/percentage of G's	7,290,801 / 25.7%
Number/percentage of N's	608 / 0%
GC Percentage	45.2%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1068

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

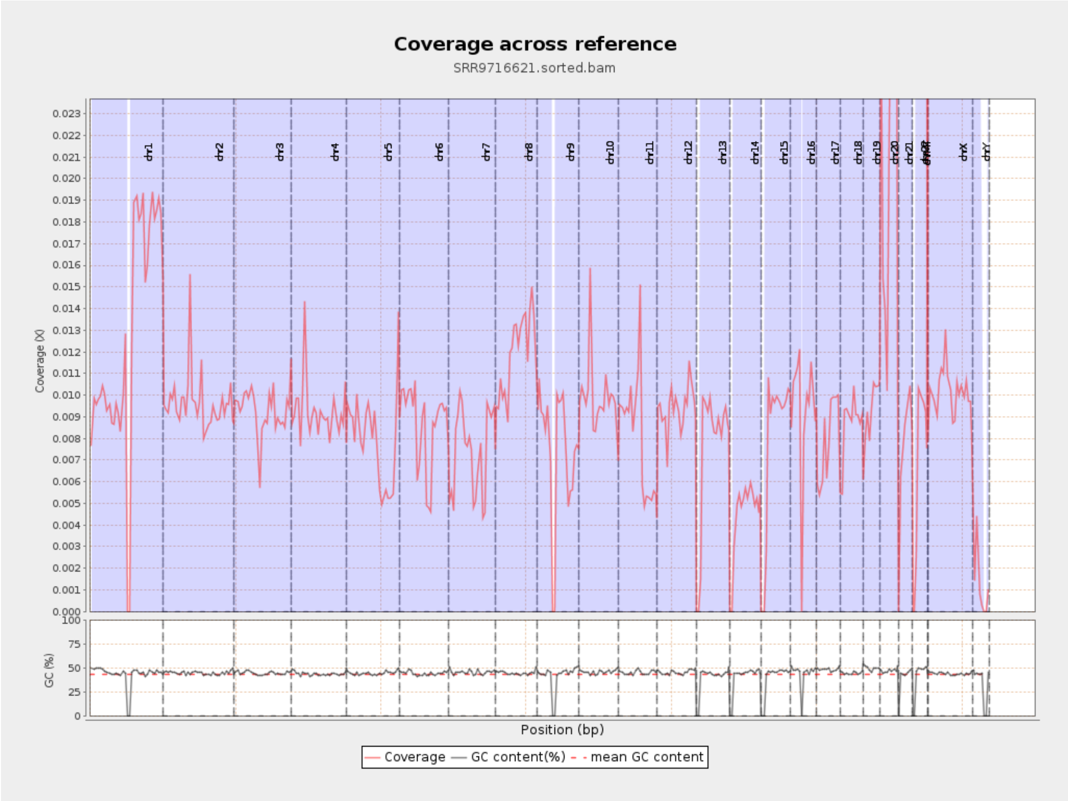
General error rate	0.5%
Mismatches	139,648
Insertions	1,491
Mapped reads with at least one insertion	0.3%
Deletions	4,586
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.52%

2.6. Chromosome stats

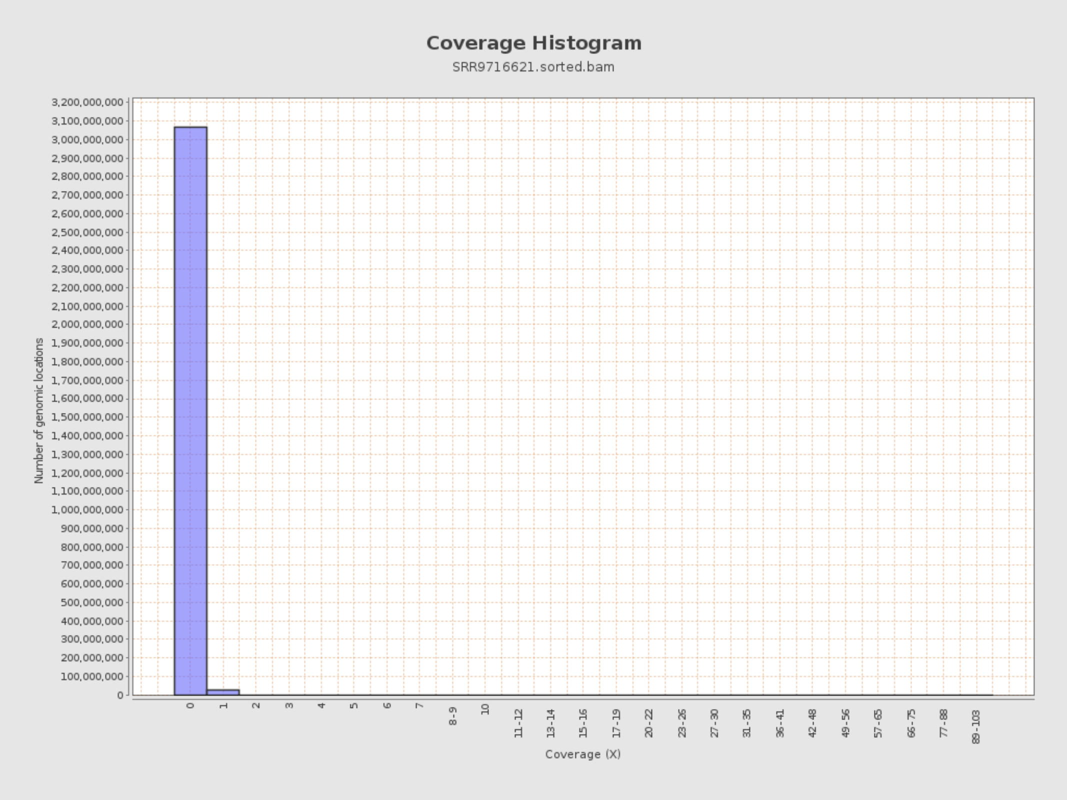
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3139518	0.0126	0.1375
chr2	243199373	2349123	0.0097	0.1167
chr3	198022430	1824162	0.0092	0.0991
chr4	191154276	1763175	0.0092	0.1015
chr5	180915260	1423669	0.0079	0.0916
chr6	171115067	1474266	0.0086	0.0981
chr7	159138663	1176062	0.0074	0.0935

chr8	146364022	1751083	0.012	0.1173
chr9	141213431	1037044	0.0073	0.103
chr10	135534747	1344848	0.0099	0.1164
chr11	135006516	1099641	0.0081	0.1009
chr12	133851895	1260087	0.0094	0.1003
chr13	115169878	867101	0.0075	0.0888
chr14	107349540	473026	0.0044	0.0722
chr15	102531392	809802	0.0079	0.0915
chr16	90354753	844618	0.0093	0.1023
chr17	81195210	646383	0.008	0.0923
chr18	78077248	677550	0.0087	0.1473
chr19	59128983	550187	0.0093	0.1118
chr20	63025520	1503160	0.0239	0.1613
chr21	48129895	369566	0.0077	0.0927
chr22	51304566	338742	0.0066	0.0835
chrMT	16571	1304	0.0787	0.2814
chrX	155270560	1575457	0.0101	0.1082
chrY	59373566	80222	0.0014	0.0452

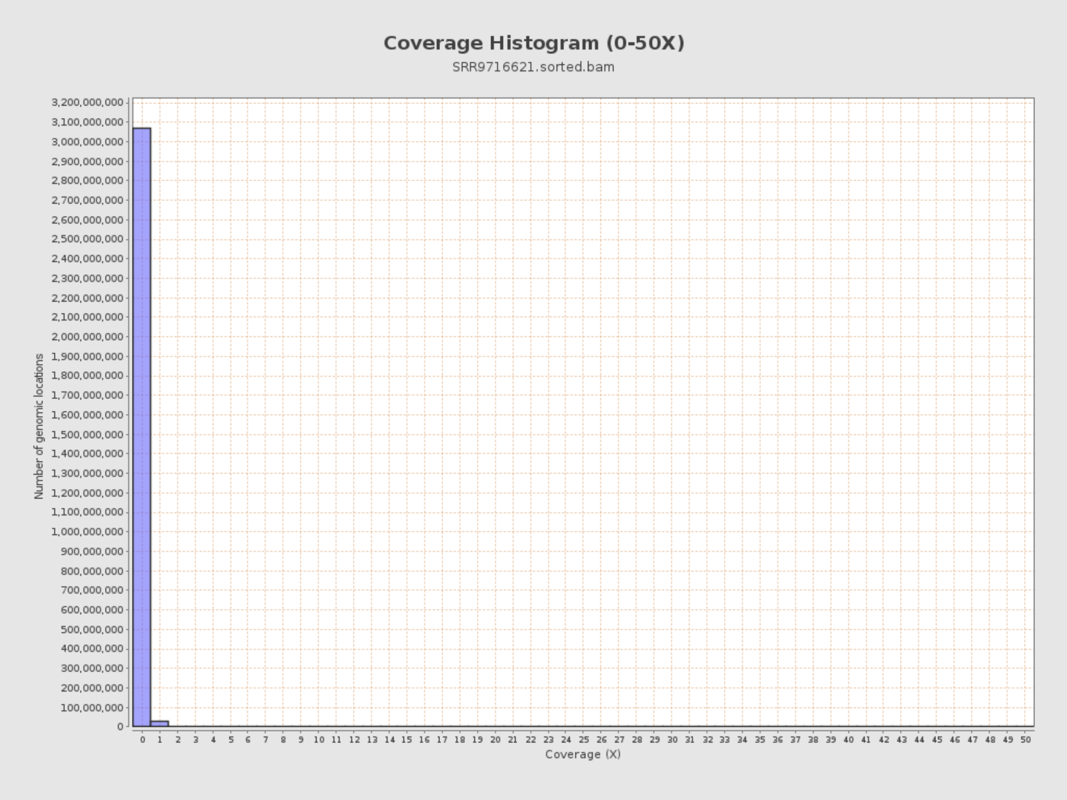
3. Results : Coverage across reference



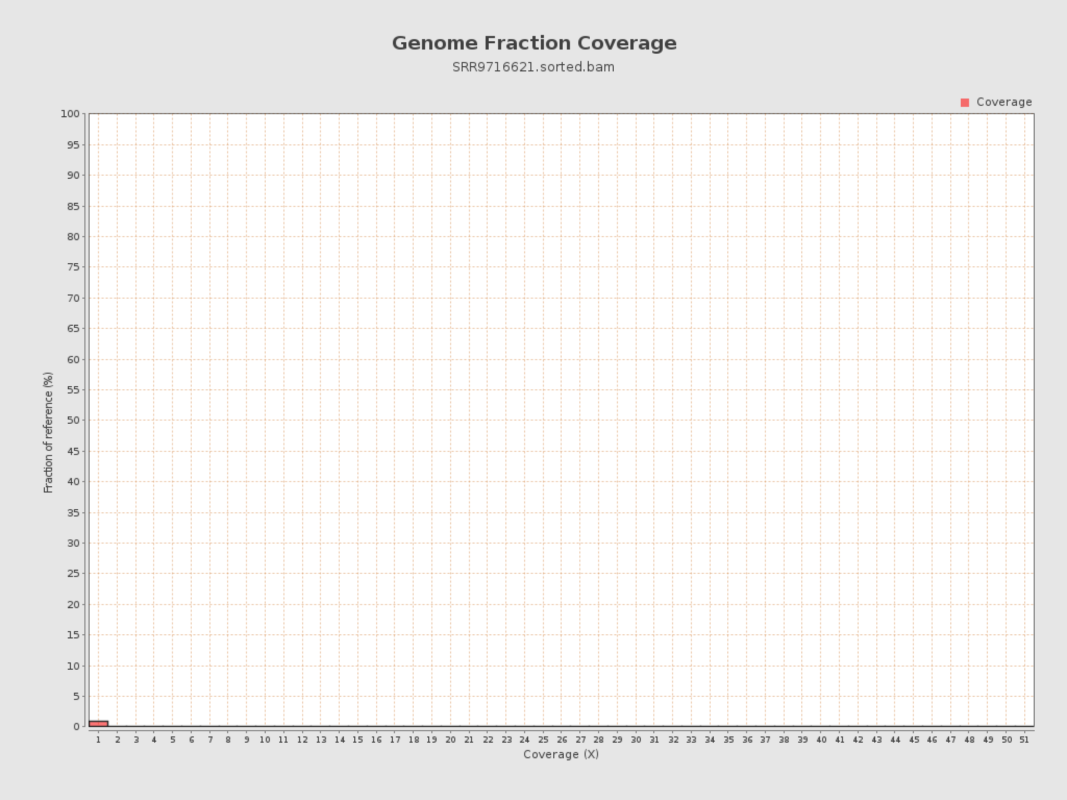
4. Results : Coverage Histogram



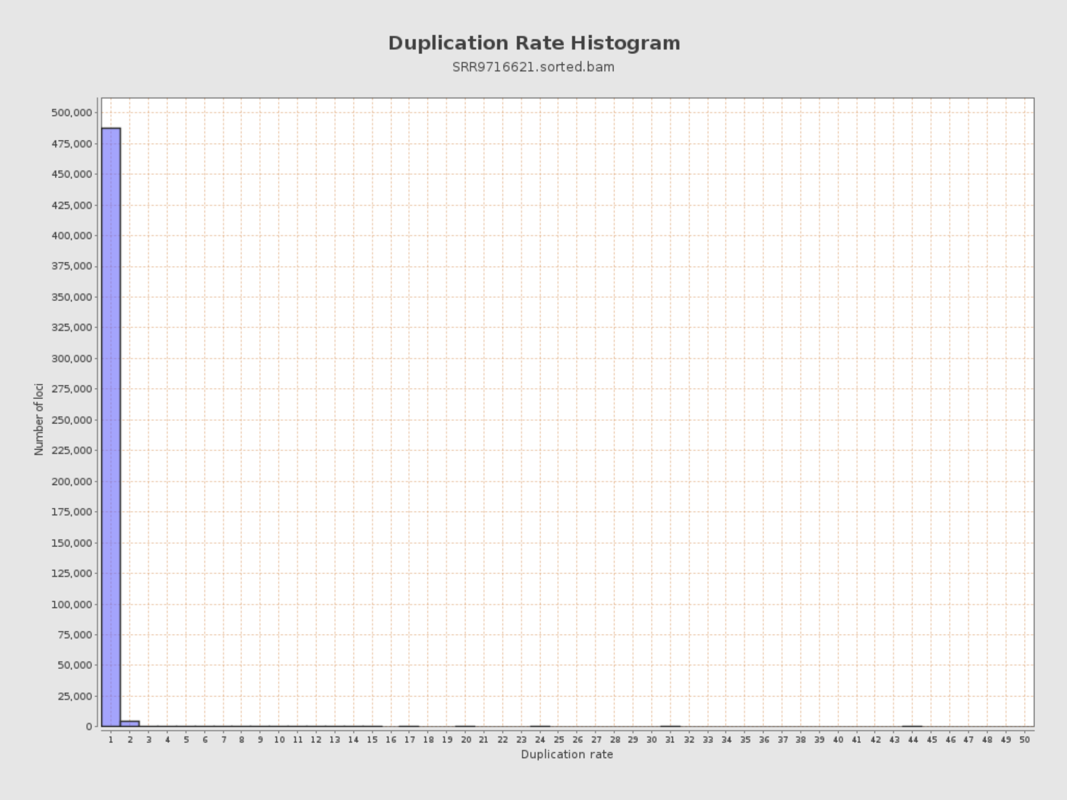
5. Results : Coverage Histogram (0-50X)



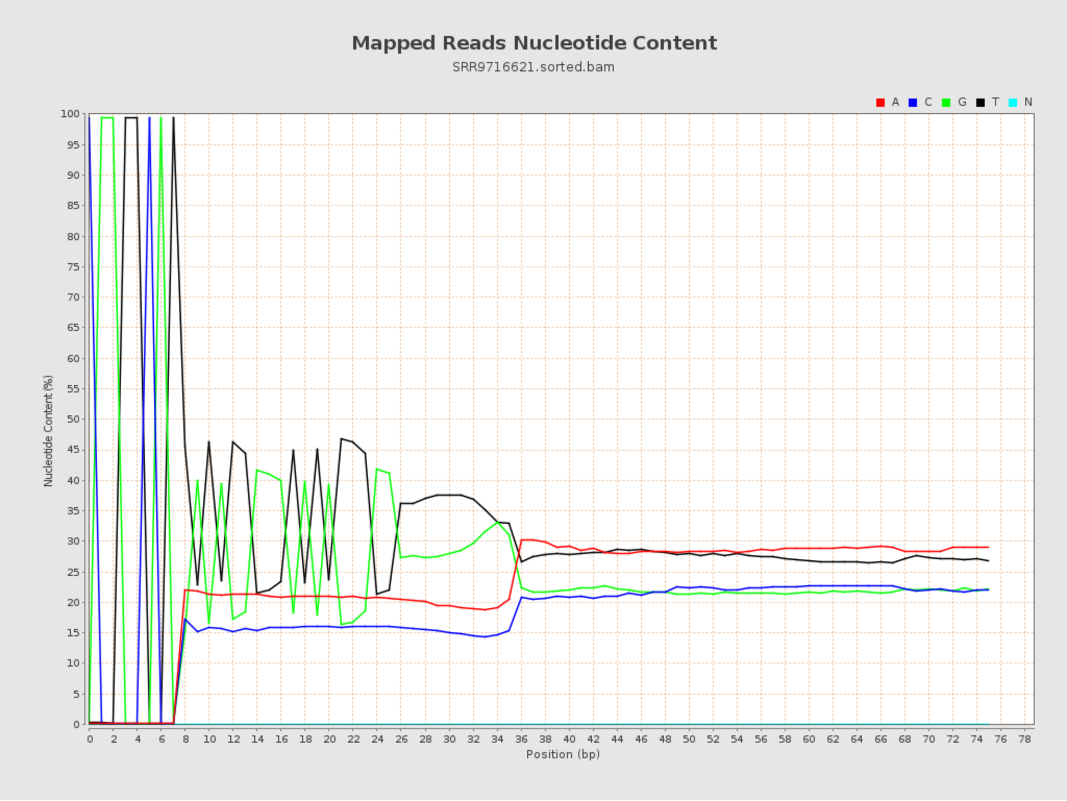
6. Results : Genome Fraction Coverage



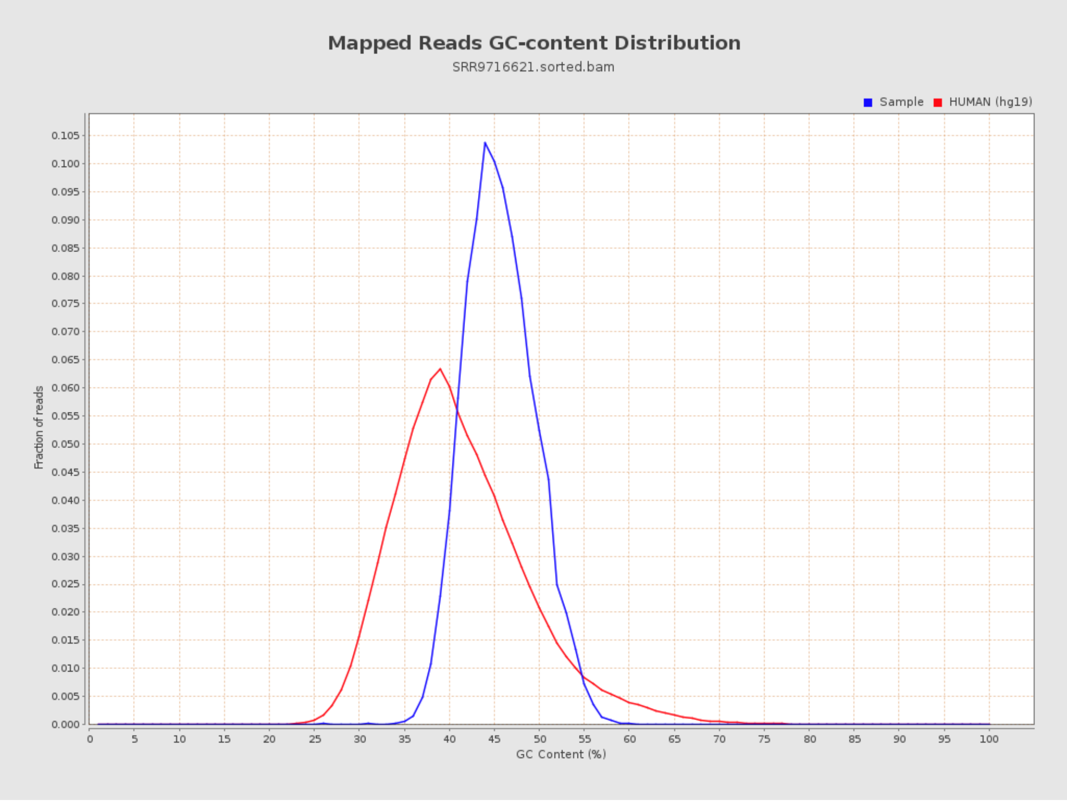
7. Results : Duplication Rate Histogram



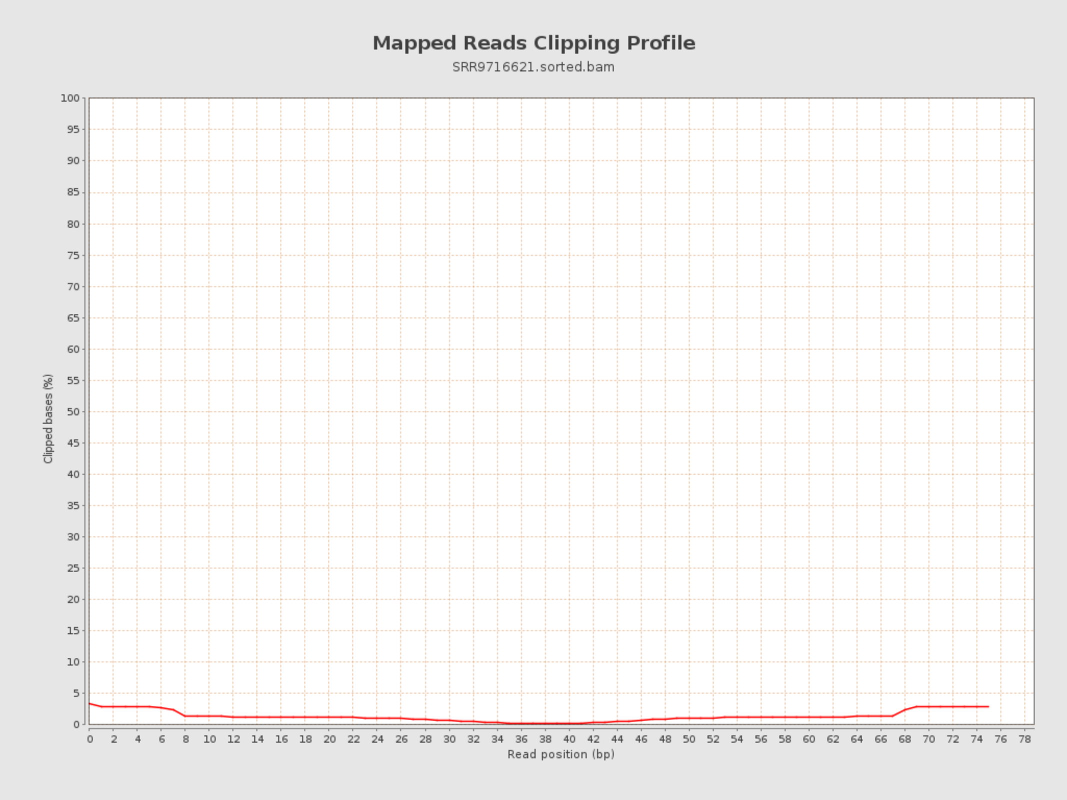
8. Results : Mapped Reads Nucleotide Content



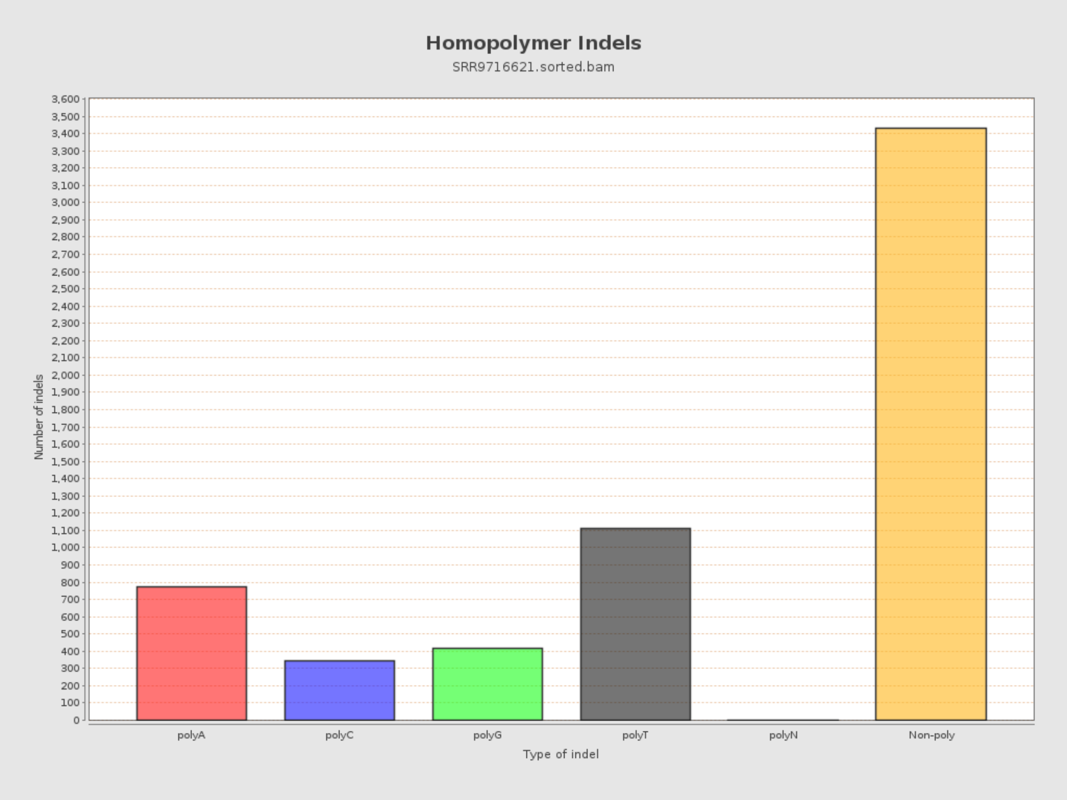
9. Results : Mapped Reads GC-content Distribution



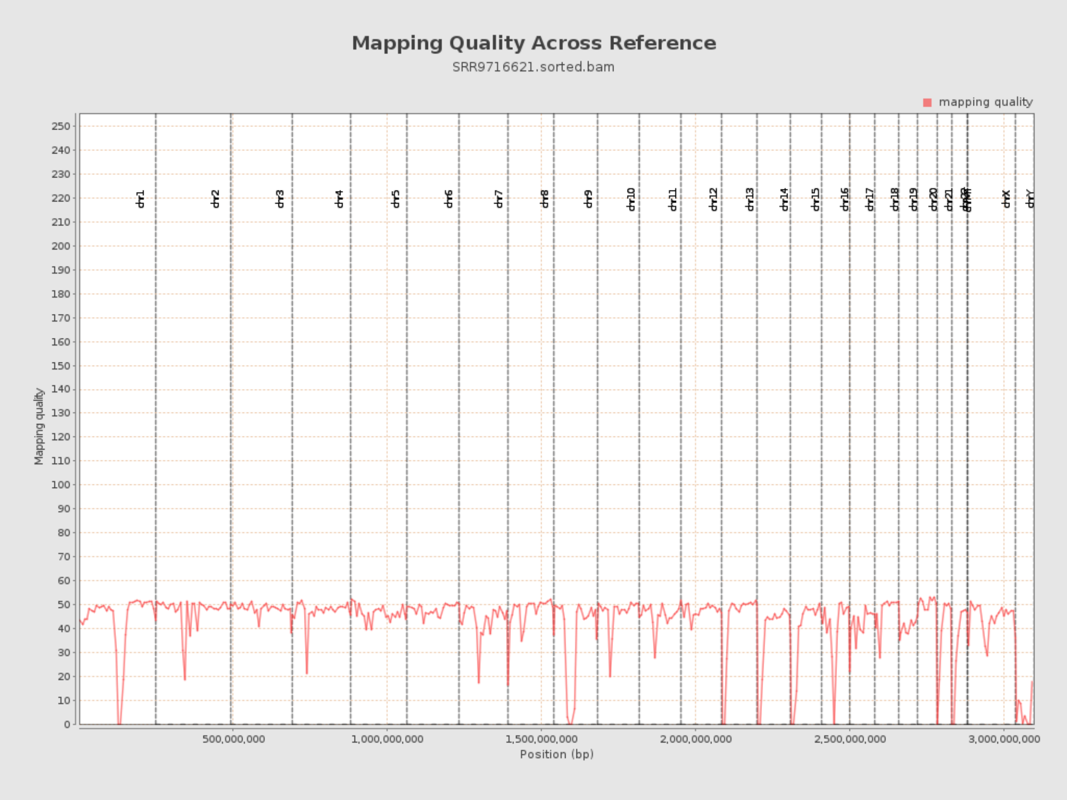
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram