Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:10:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716319.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_SRR9716319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:10:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	460,998
Mapped reads	422,713 / 91.7%
Unmapped reads	38,285 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,049 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	6,935 / 1.5%
Duplication rate	1.24%
Clipped reads	424,283 / 92.04%

2.2. ACGT Content

Number/percentage of A's	5,955,610 / 24.23%
Number/percentage of C's	4,590,254 / 18.68%
Number/percentage of T's	7,910,524 / 32.19%
Number/percentage of G's	6,119,170 / 24.9%
Number/percentage of N's	646 / 0%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1063

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

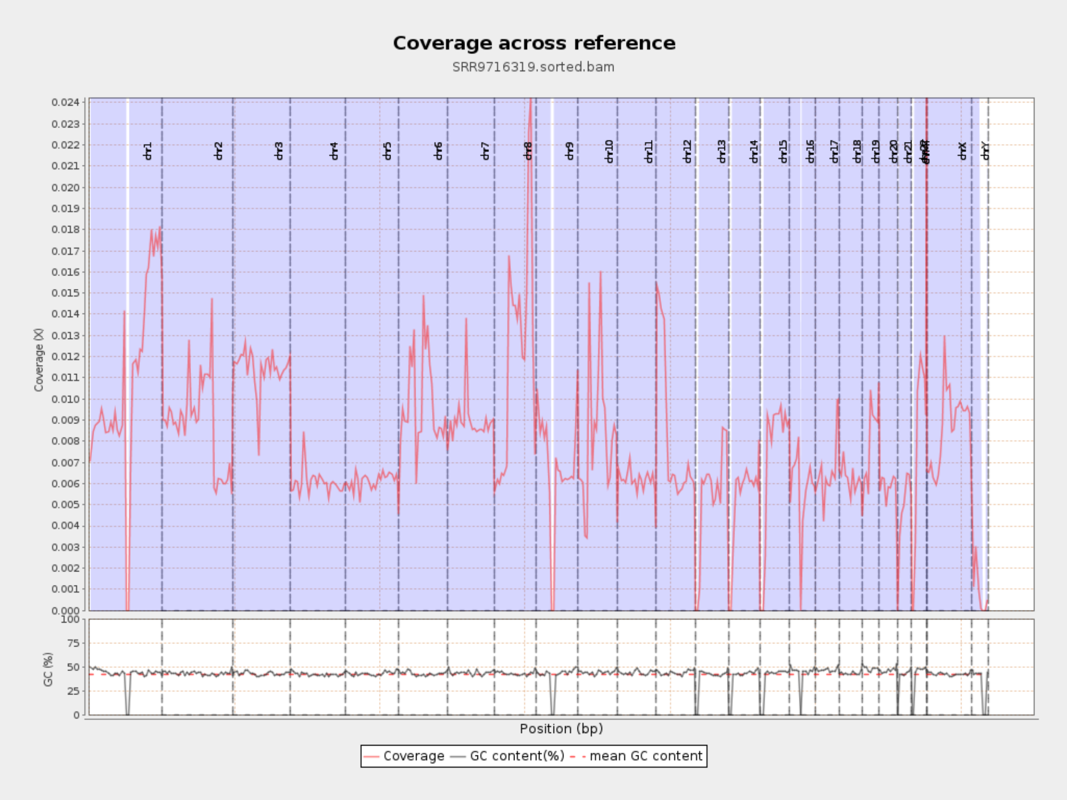
General error rate	0.5%
Mismatches	120,723
Insertions	1,383
Mapped reads with at least one insertion	0.33%
Deletions	4,307
Mapped reads with at least one deletion	1.01%
Homopolymer indels	44.02%

2.6. Chromosome stats

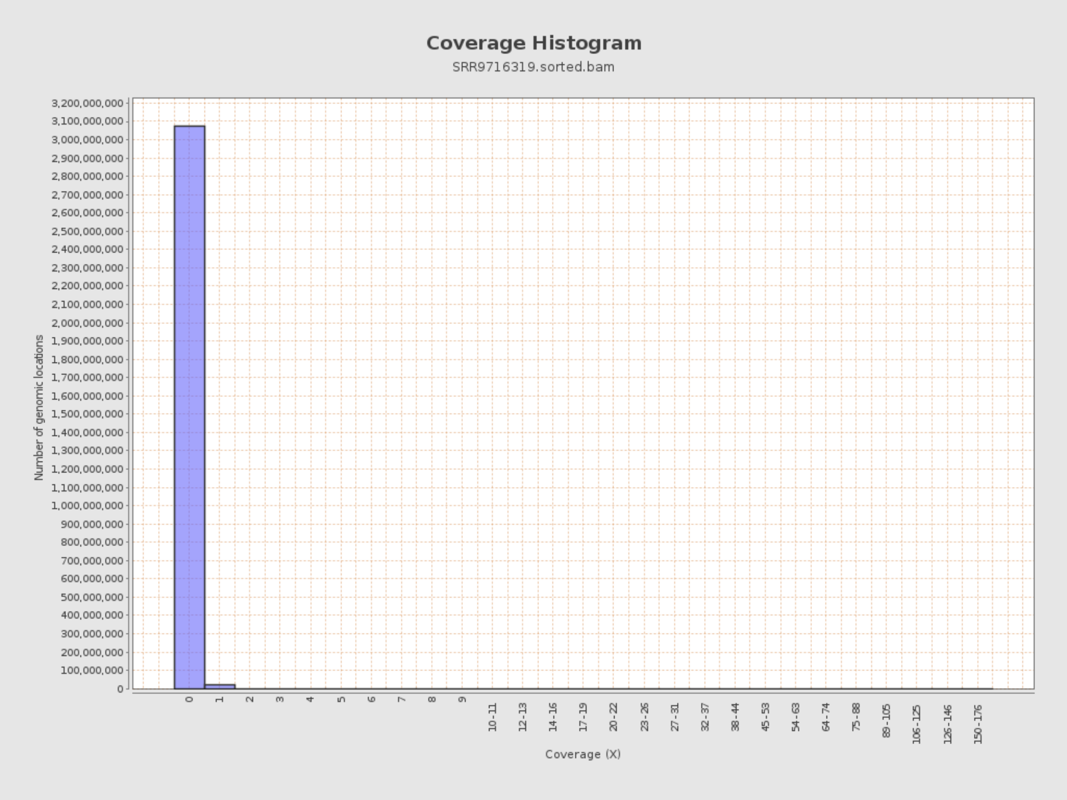
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2688741	0.0108	0.1661
chr2	243199373	2158206	0.0089	0.1218
chr3	198022430	2258234	0.0114	0.1102
chr4	191154276	1154336	0.006	0.0812
chr5	180915260	1109891	0.0061	0.0805
chr6	171115067	1673658	0.0098	0.1145
chr7	159138663	1435139	0.009	0.1194

chr8	146364022	1799961	0.0123	0.118
chr9	141213431	917963	0.0065	0.0918
chr10	135534747	1128348	0.0083	0.1136
chr11	135006516	833688	0.0062	0.0893
chr12	133851895	1102666	0.0082	0.094
chr13	115169878	622803	0.0054	0.076
chr14	107349540	549807	0.0051	0.0754
chr15	102531392	742139	0.0072	0.0874
chr16	90354753	521390	0.0058	0.0816
chr17	81195210	534773	0.0066	0.0841
chr18	78077248	489919	0.0063	0.1214
chr19	59128983	467776	0.0079	0.1176
chr20	63025520	367332	0.0058	0.0784
chr21	48129895	227888	0.0047	0.0724
chr22	51304566	390181	0.0076	0.0895
chrMT	16571	541	0.0326	0.1936
chrX	155270560	1344081	0.0087	0.0997
chrY	59373566	63455	0.0011	0.0382

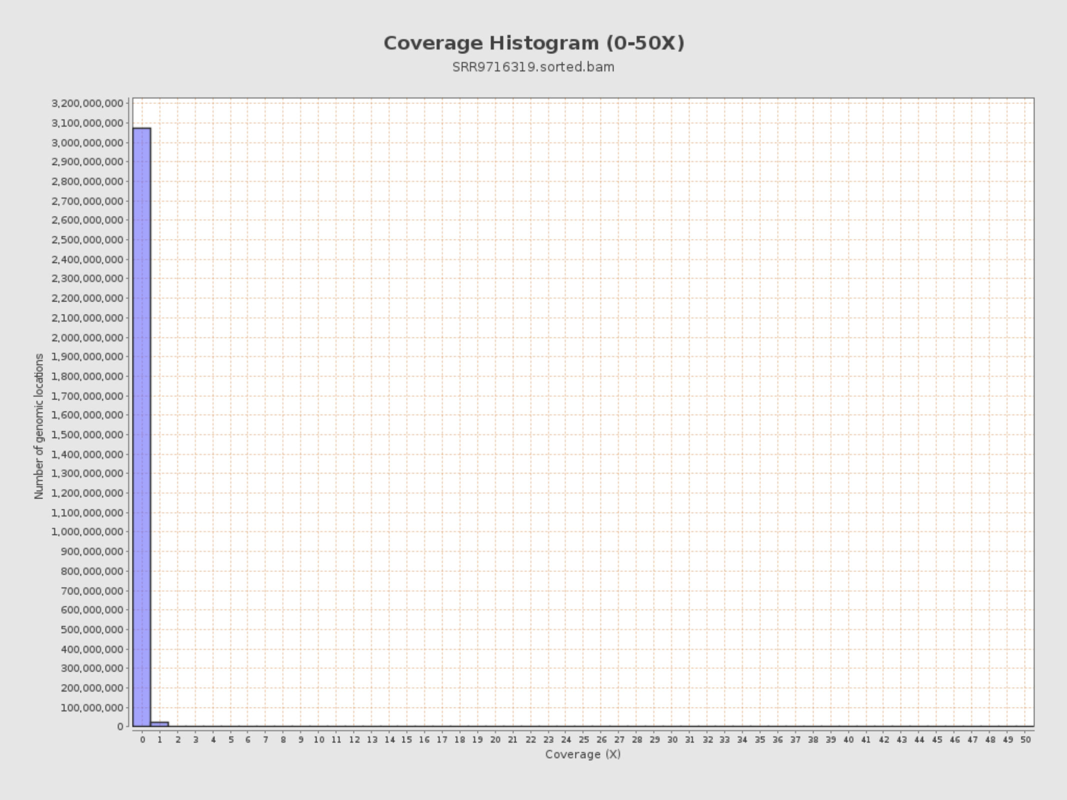
3. Results : Coverage across reference



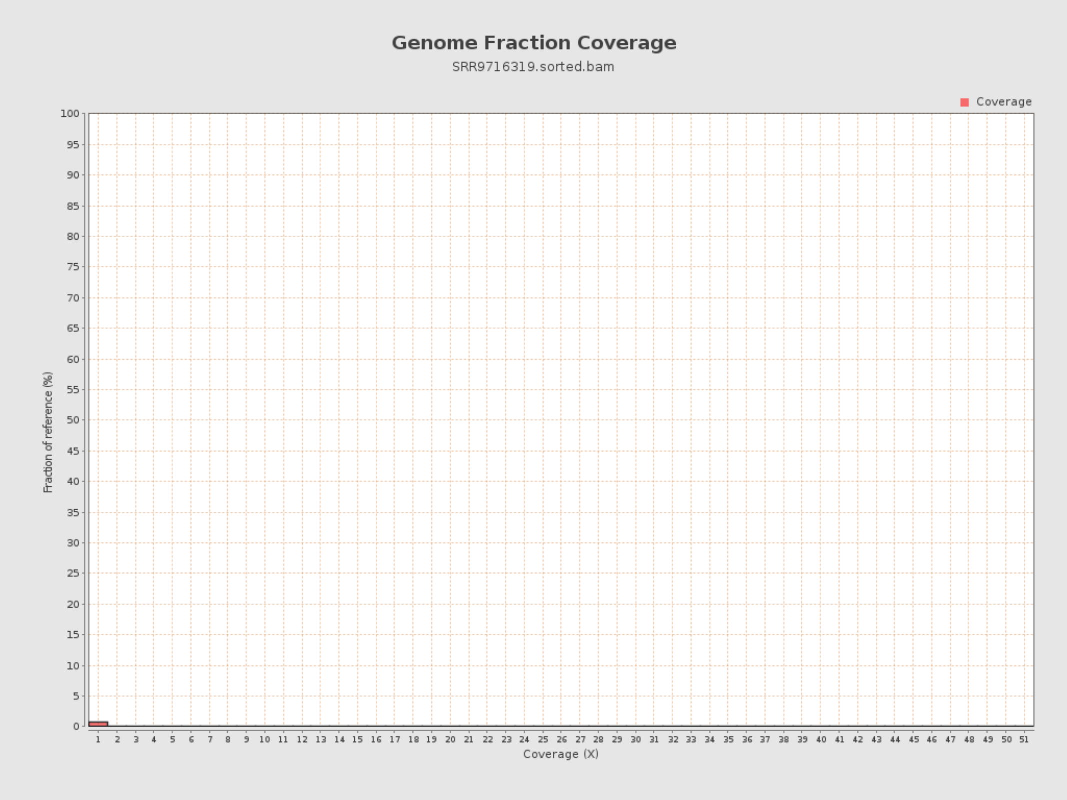
4. Results : Coverage Histogram



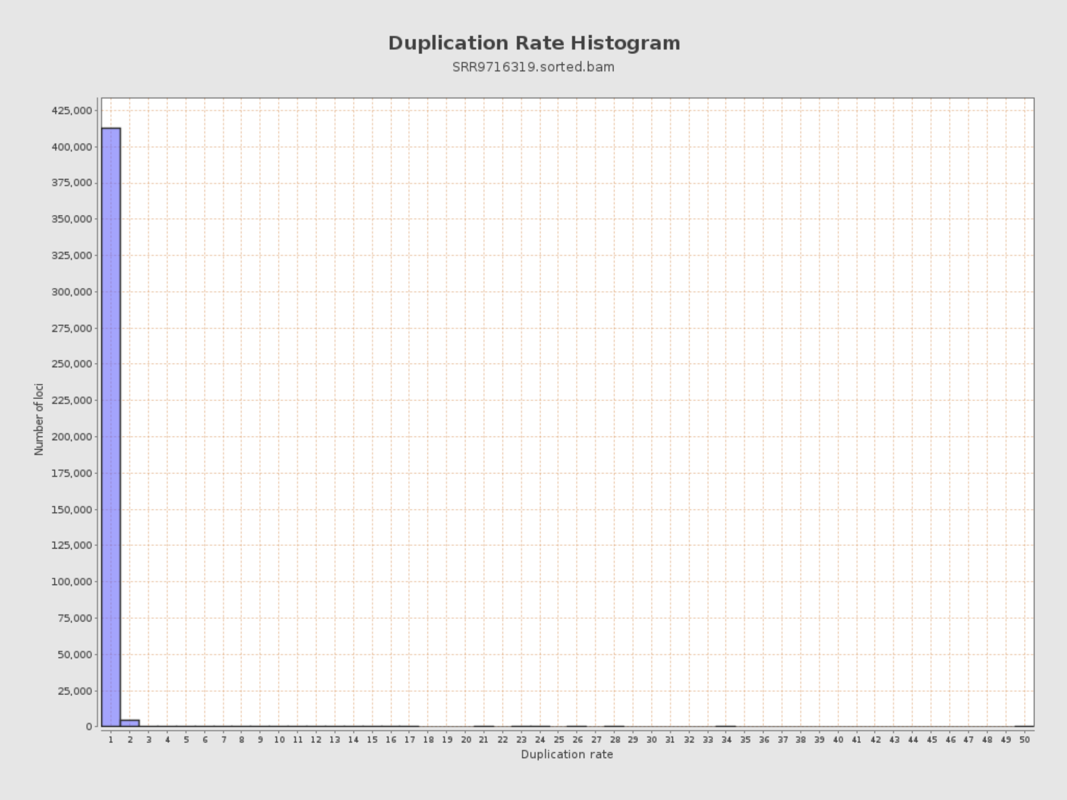
5. Results : Coverage Histogram (0-50X)



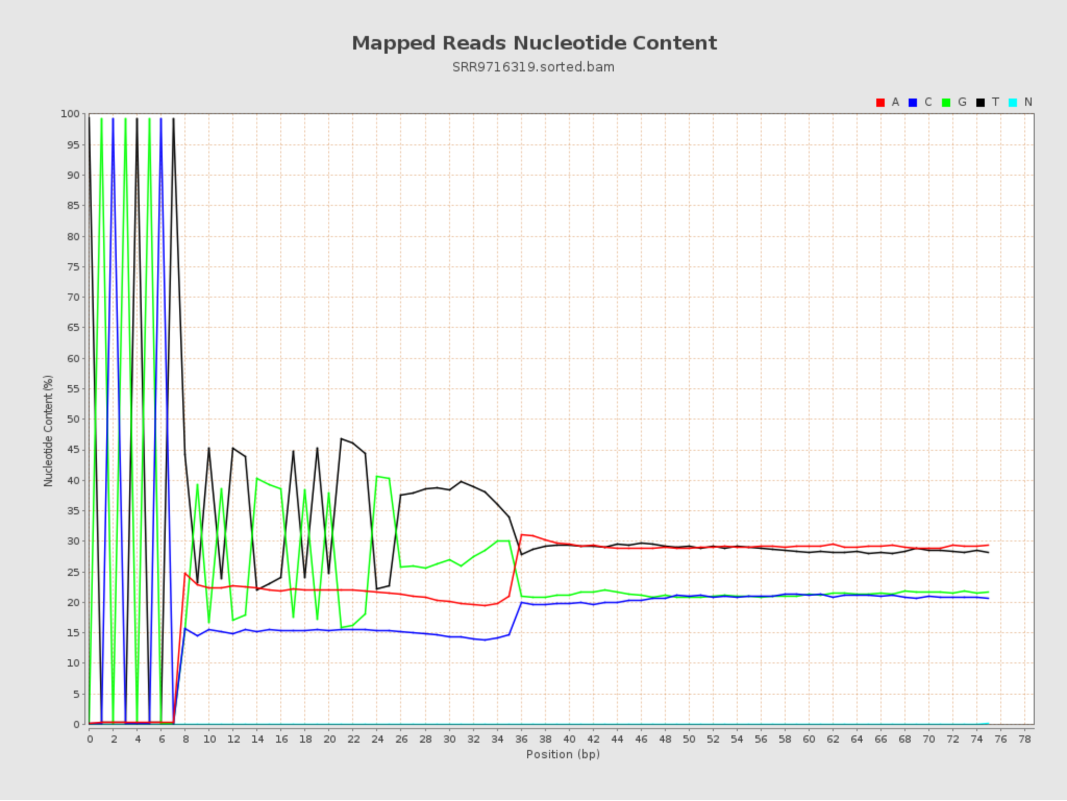
6. Results : Genome Fraction Coverage



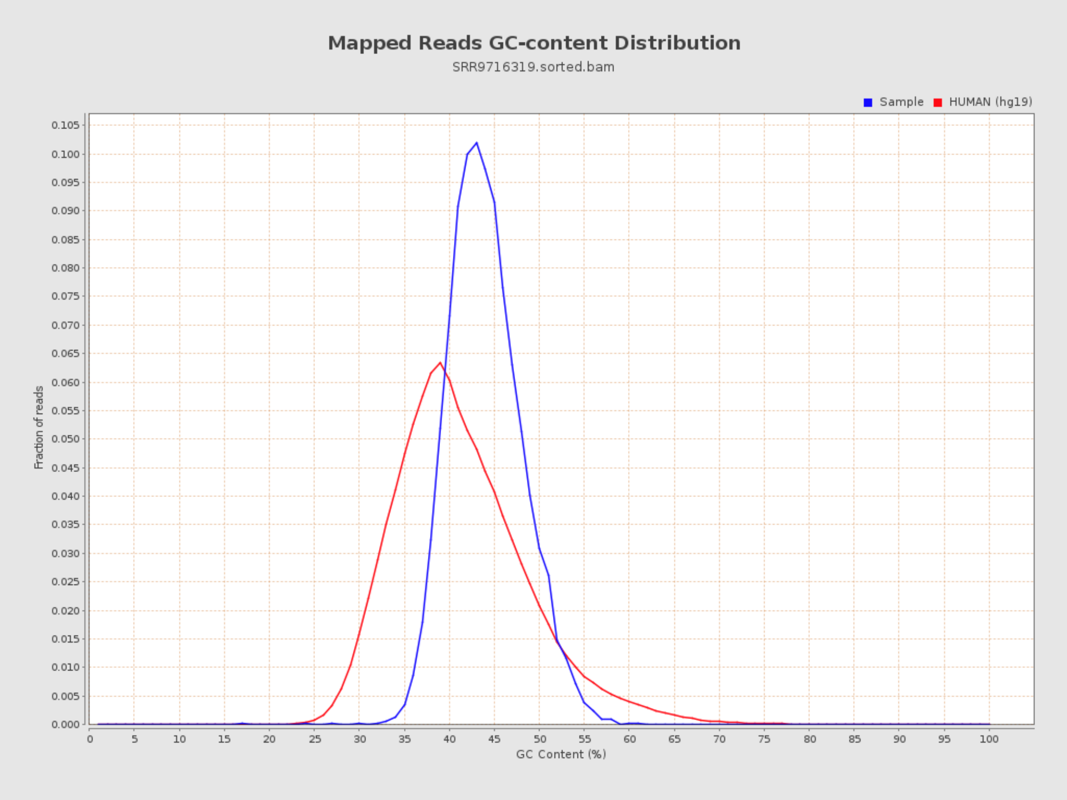
7. Results : Duplication Rate Histogram



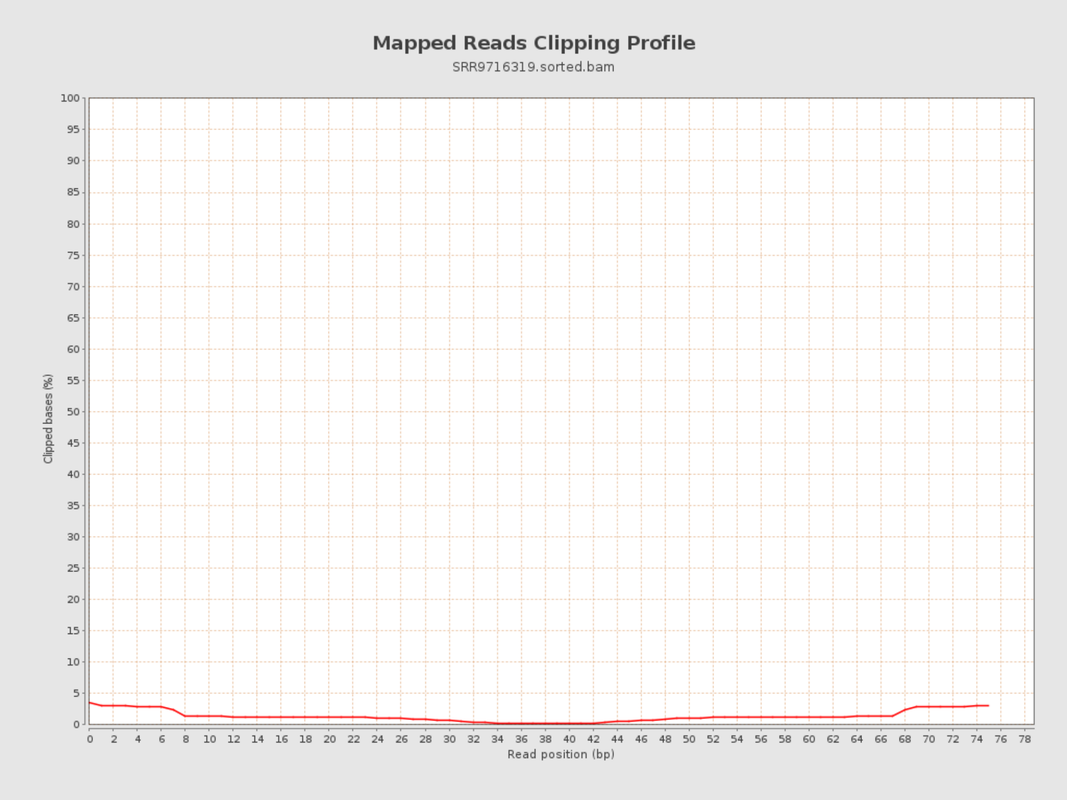
8. Results : Mapped Reads Nucleotide Content



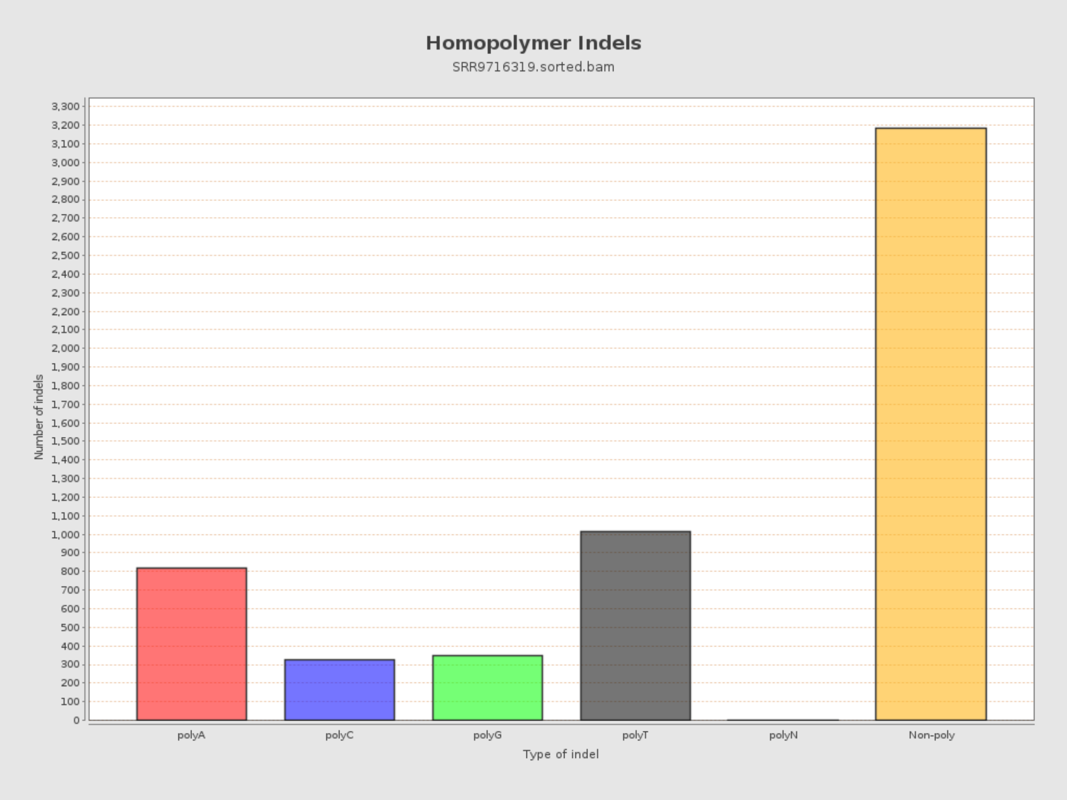
9. Results : Mapped Reads GC-content Distribution



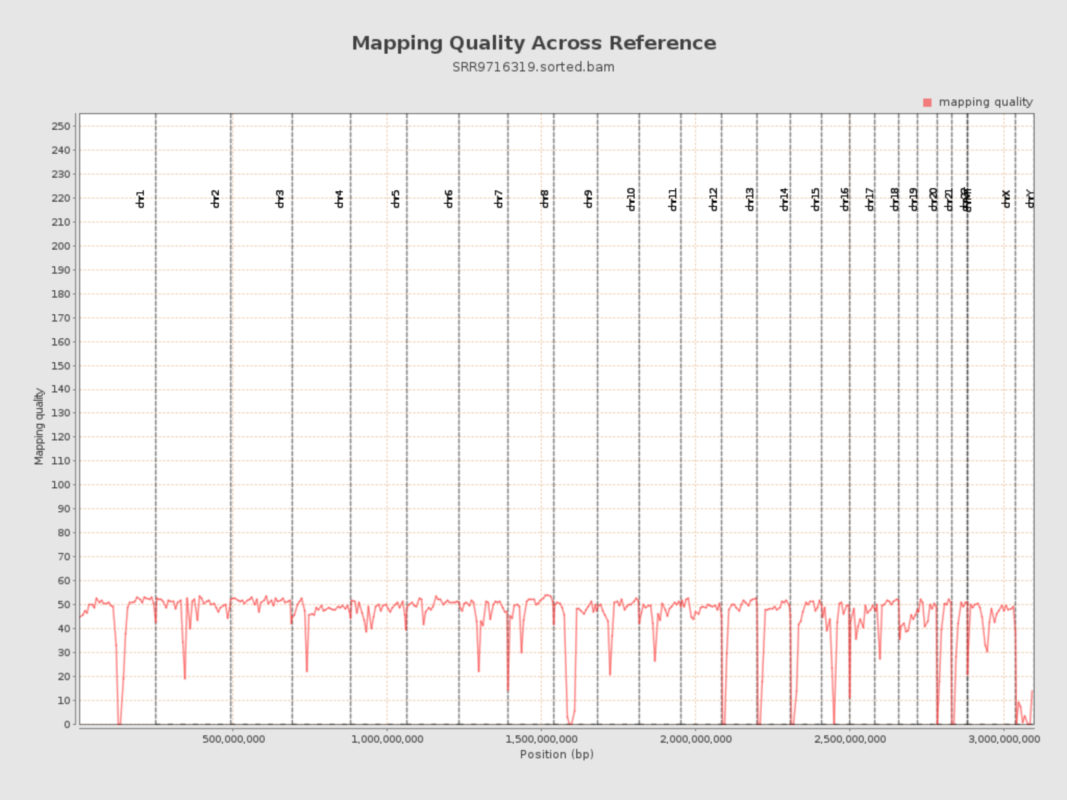
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram