Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:51:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716618.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_SRR9716618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:51:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	972,395
Mapped reads	868,030 / 89.27%
Unmapped reads	104,365 / 10.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,428 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,649 / 2.74%
Duplication rate	2.36%
Clipped reads	868,839 / 89.35%

2.2. ACGT Content

Number/percentage of A's	12,352,514 / 24.74%
Number/percentage of C's	10,057,560 / 20.15%
Number/percentage of T's	16,151,316 / 32.35%
Number/percentage of G's	11,359,445 / 22.75%
Number/percentage of N's	1,386 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.1766

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

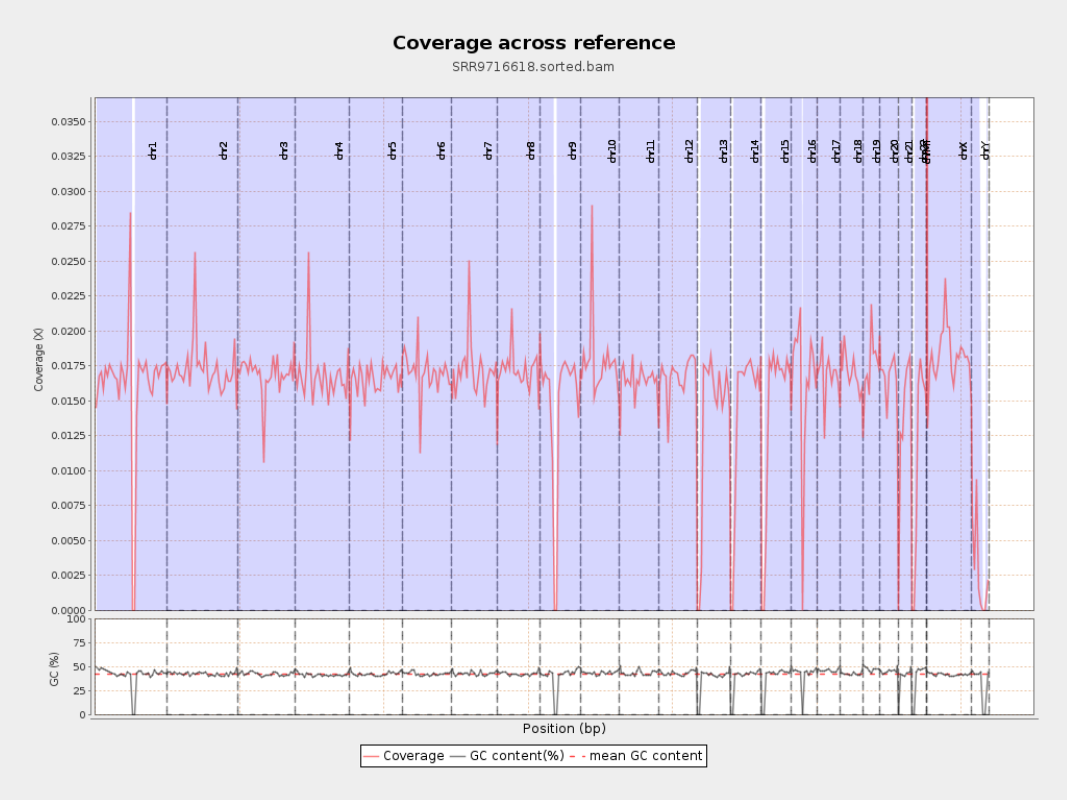
General error rate	0.53%
Mismatches	257,939
Insertions	3,417
Mapped reads with at least one insertion	0.39%
Deletions	9,687
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.71%

2.6. Chromosome stats

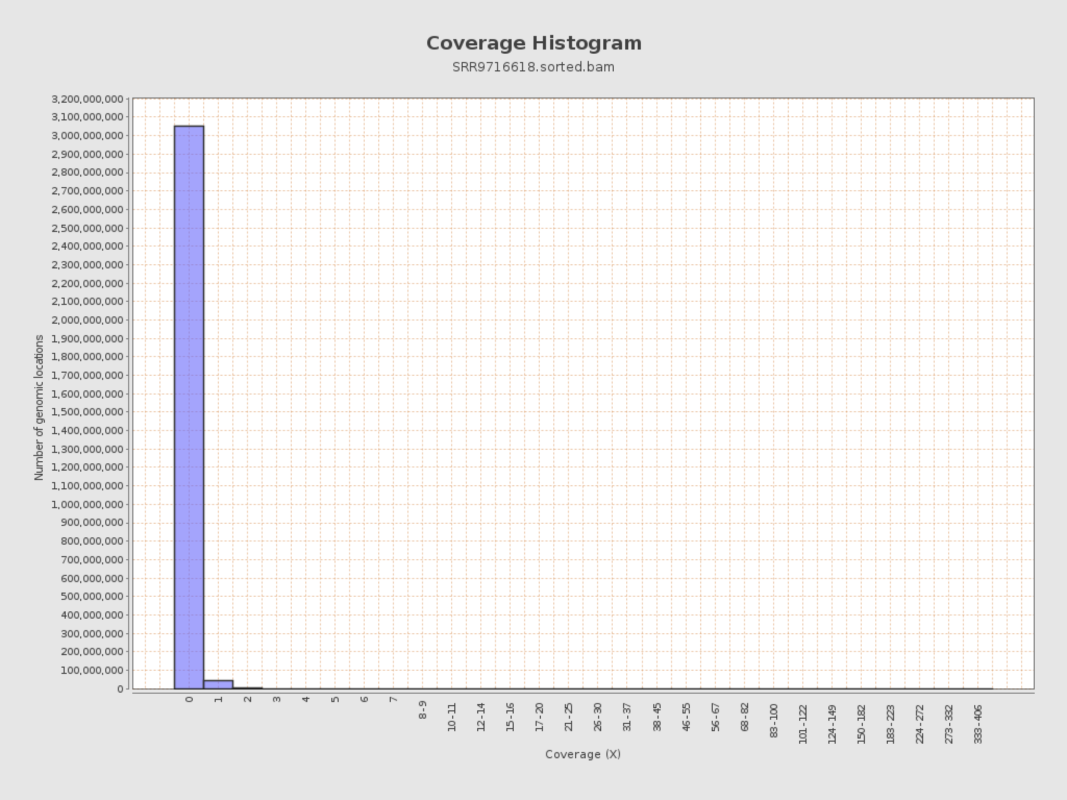
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4000031	0.016	0.3026
chr2	243199373	4208983	0.0173	0.2231
chr3	198022430	3334433	0.0168	0.1379
chr4	191154276	3222544	0.0169	0.1444
chr5	180915260	3011230	0.0166	0.1373
chr6	171115067	2913646	0.017	0.1567
chr7	159138663	2743990	0.0172	0.1953

chr8	146364022	2515823	0.0172	0.1721
chr9	141213431	2061536	0.0146	0.151
chr10	135534747	2417551	0.0178	0.1738
chr11	135006516	2236361	0.0166	0.1552
chr12	133851895	2239504	0.0167	0.1395
chr13	115169878	1570459	0.0136	0.1241
chr14	107349540	1512705	0.0141	0.1289
chr15	102531392	1447735	0.0141	0.1262
chr16	90354753	1444902	0.016	0.14
chr17	81195210	1360910	0.0168	0.1432
chr18	78077248	1333170	0.0171	0.2377
chr19	59128983	1044343	0.0177	0.2182
chr20	63025520	1044973	0.0166	0.1382
chr21	48129895	667546	0.0139	0.1315
chr22	51304566	582618	0.0114	0.1131
chrMT	16571	24880	1.5014	1.4353
chrX	155270560	2836874	0.0183	0.1544
chrY	59373566	160804	0.0027	0.0795

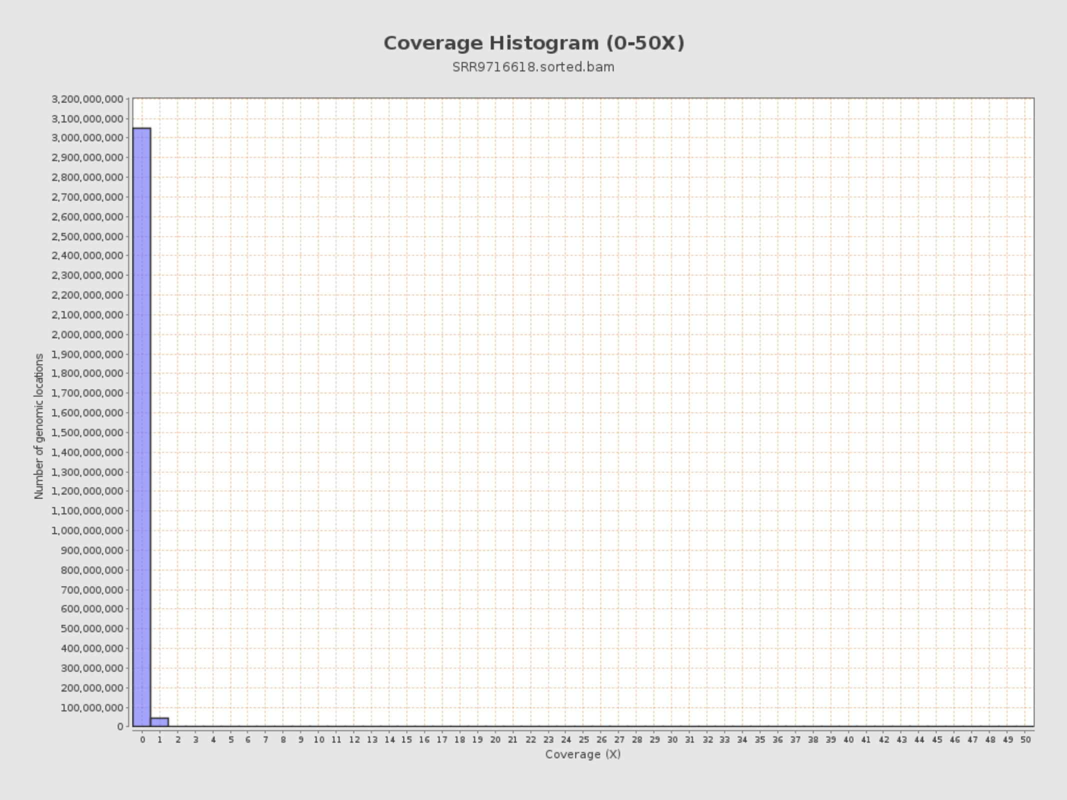
3. Results : Coverage across reference



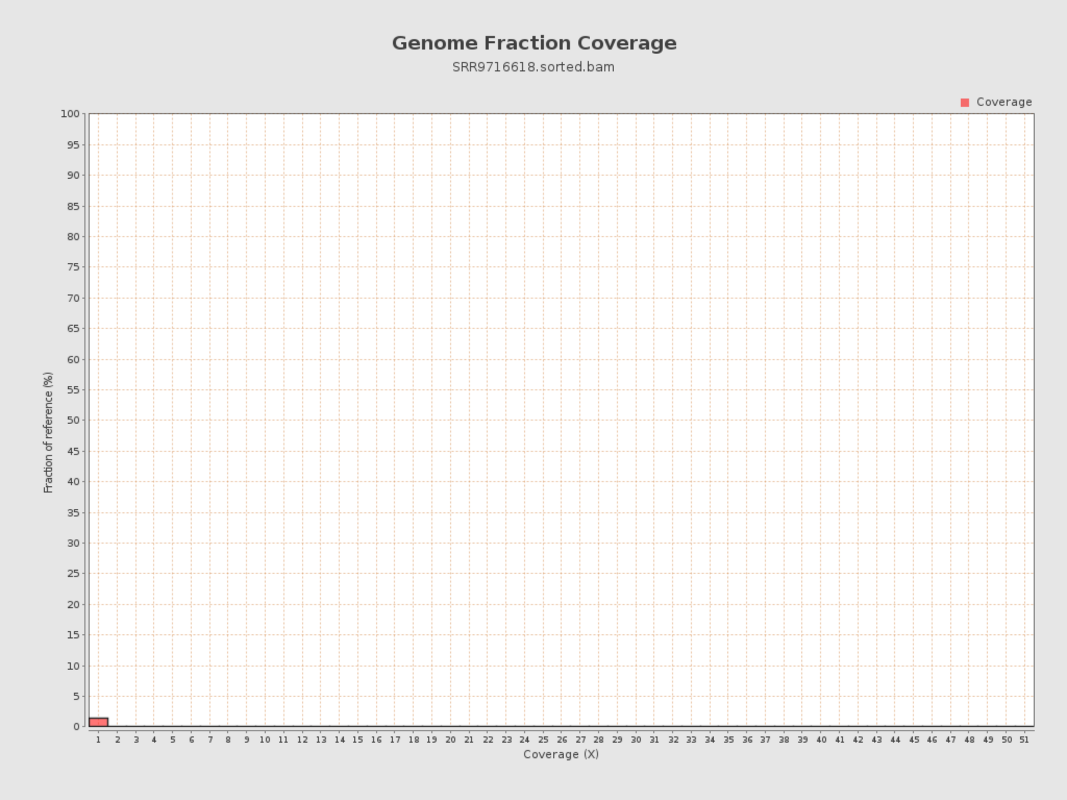
4. Results : Coverage Histogram



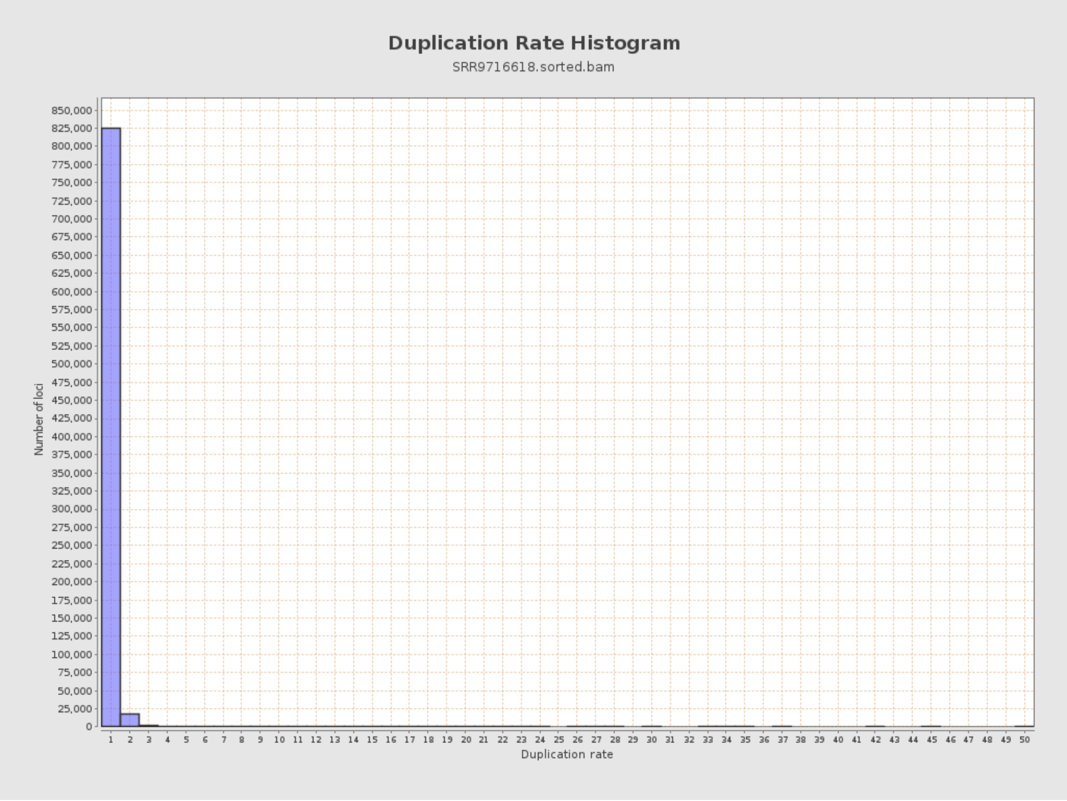
5. Results : Coverage Histogram (0-50X)



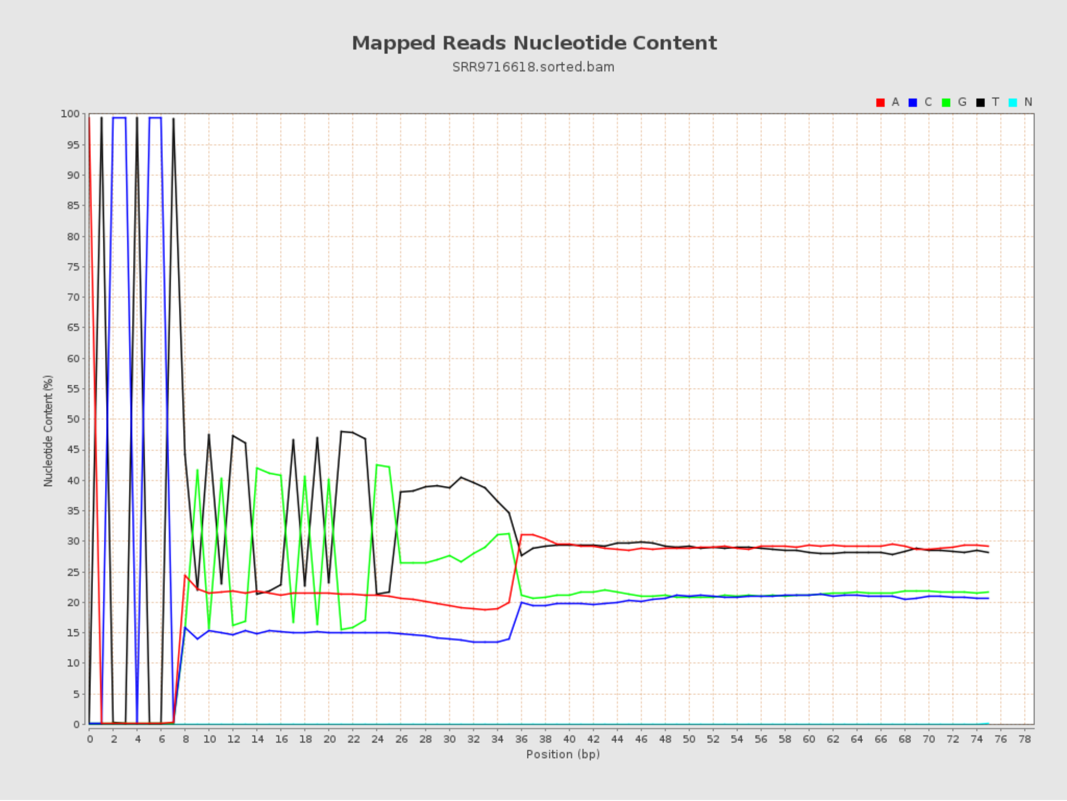
6. Results : Genome Fraction Coverage



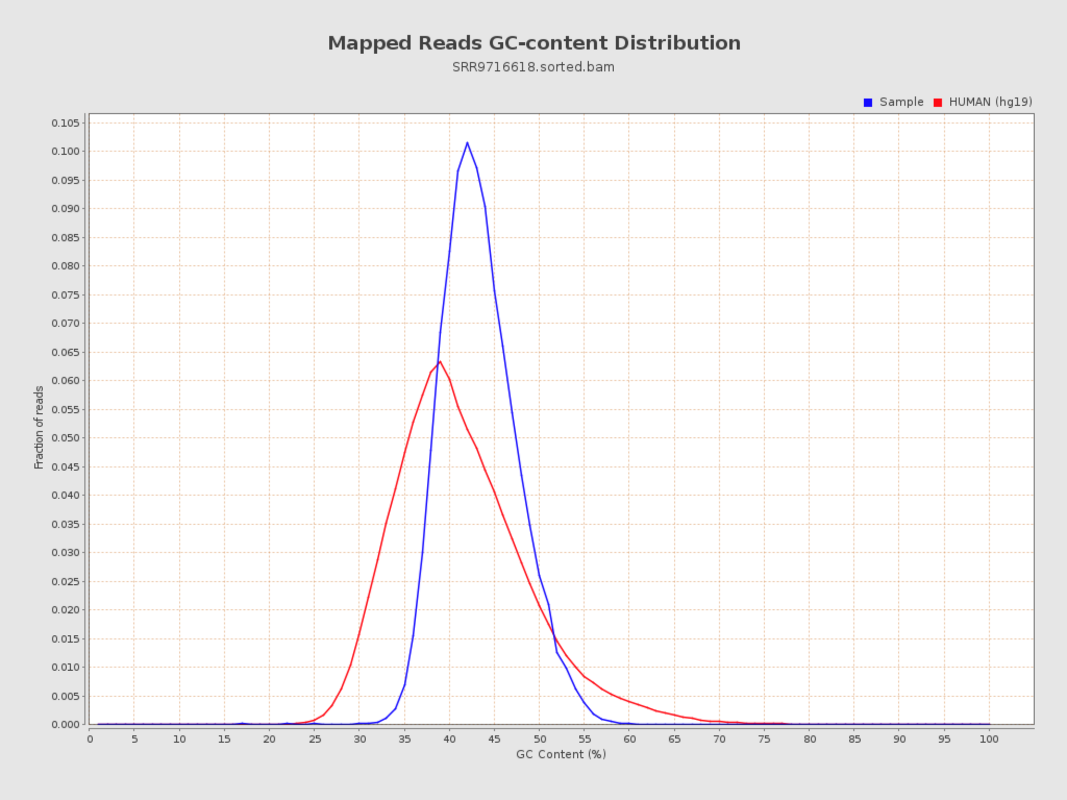
7. Results : Duplication Rate Histogram



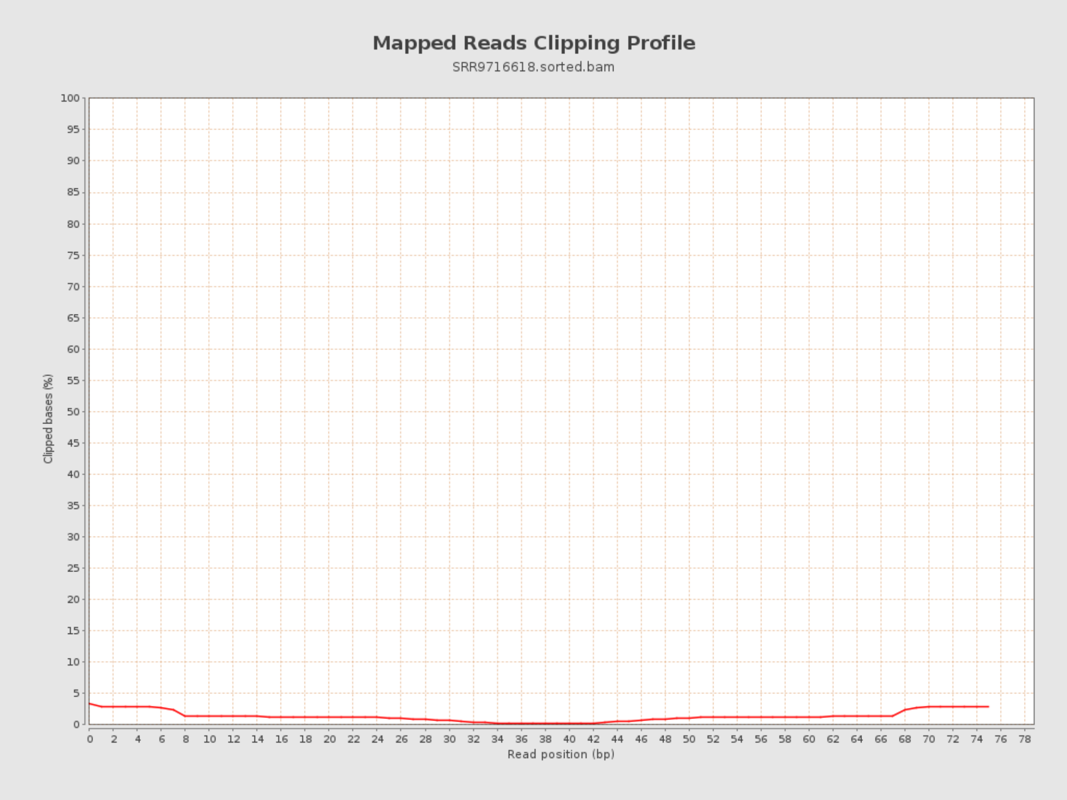
8. Results : Mapped Reads Nucleotide Content



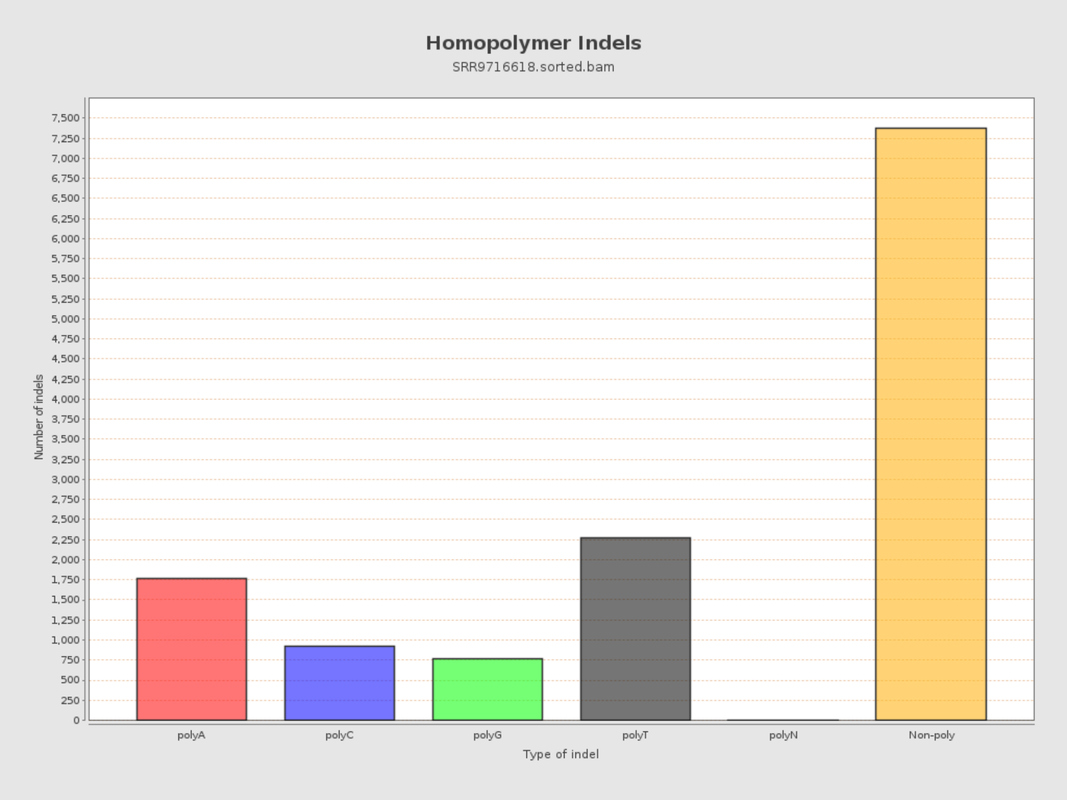
9. Results : Mapped Reads GC-content Distribution



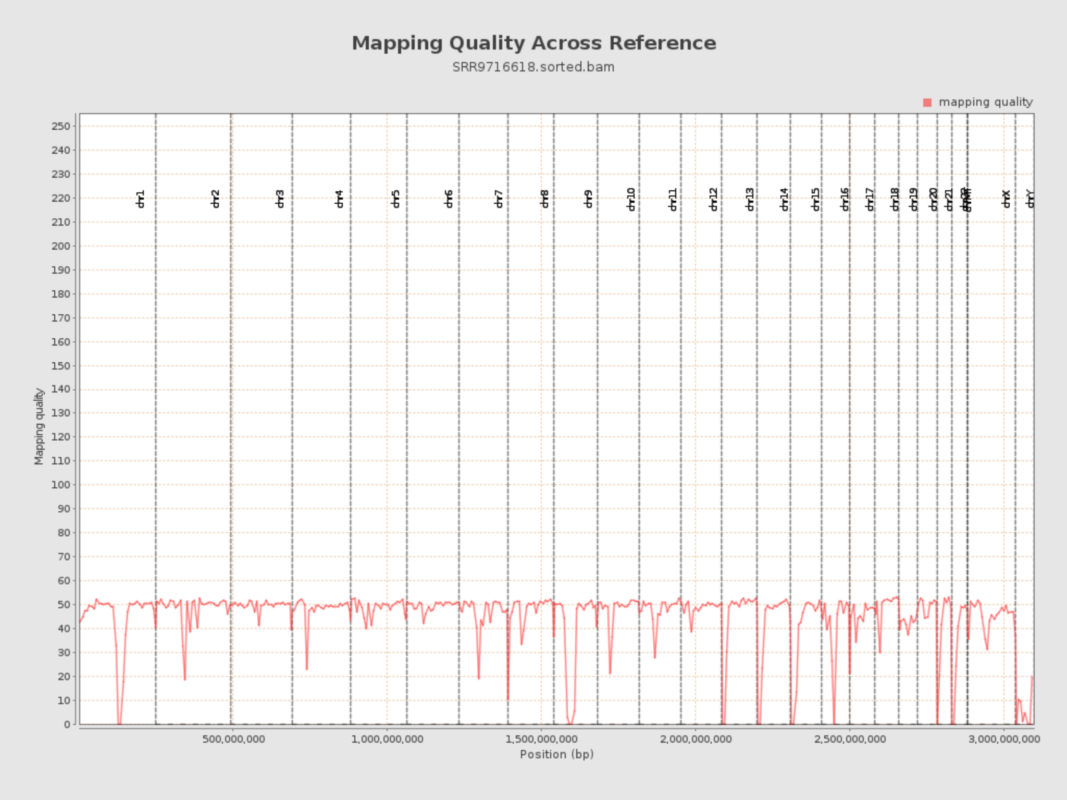
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram