Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:21:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716155.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_SRR9716155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:21:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	811,640
Mapped reads	734,320 / 90.47%
Unmapped reads	77,320 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,801 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	12,527 / 1.54%
Duplication rate	1.34%
Clipped reads	734,976 / 90.55%

2.2. ACGT Content

Number/percentage of A's	10,779,606 / 25.52%
Number/percentage of C's	8,180,031 / 19.37%
Number/percentage of T's	13,231,686 / 31.33%
Number/percentage of G's	10,044,760 / 23.78%
Number/percentage of N's	872 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1372

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

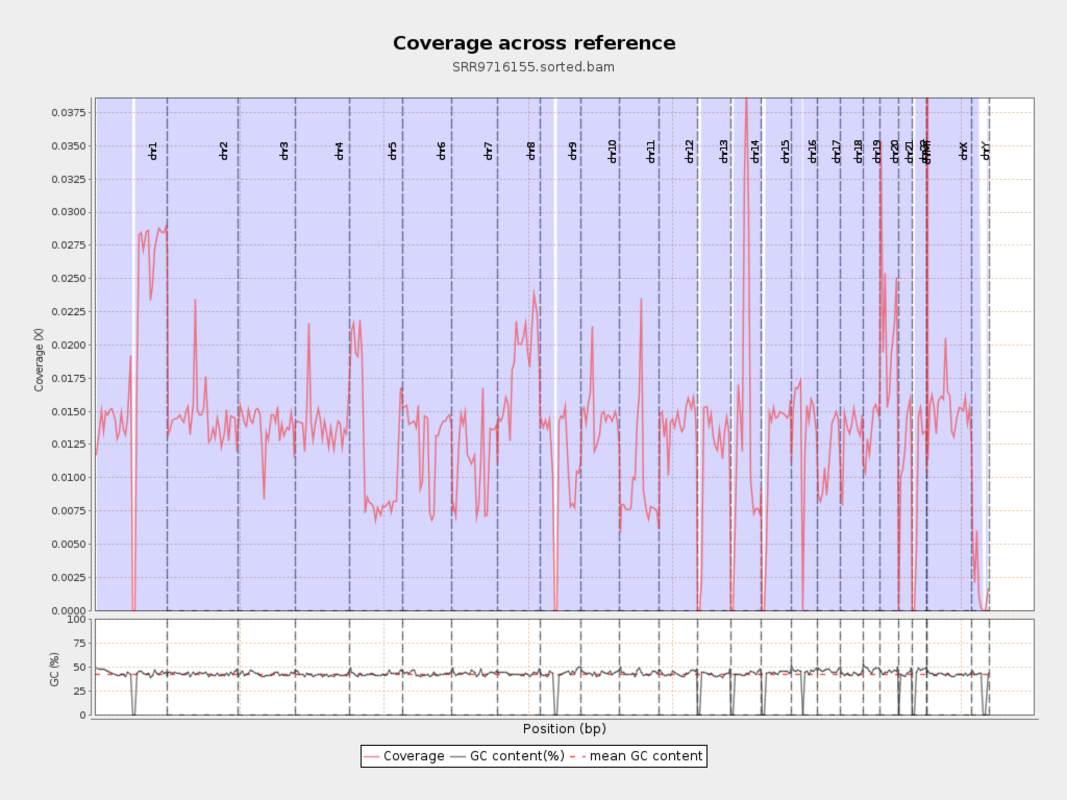
General error rate	0.49%
Mismatches	201,459
Insertions	2,953
Mapped reads with at least one insertion	0.4%
Deletions	6,693
Mapped reads with at least one deletion	0.9%
Homopolymer indels	39.17%

2.6. Chromosome stats

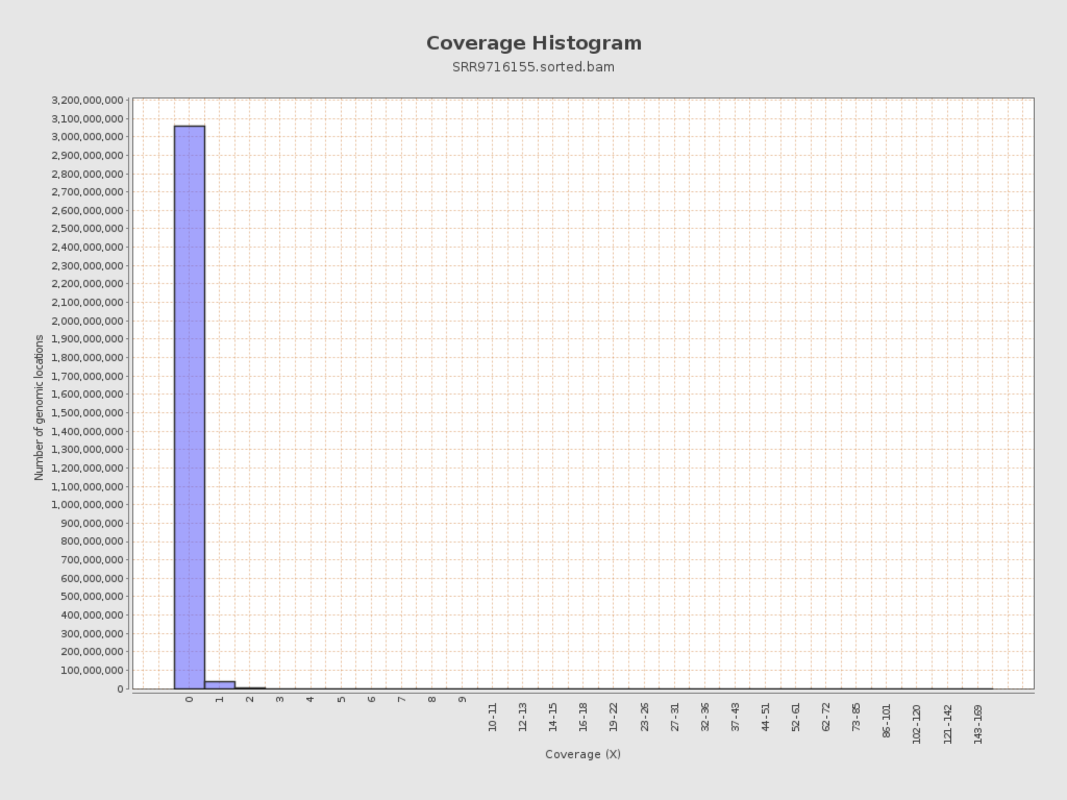
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4736645	0.019	0.1868
chr2	243199373	3532503	0.0145	0.1505
chr3	198022430	2760097	0.0139	0.1232
chr4	191154276	2689053	0.0141	0.1295
chr5	180915260	2131110	0.0118	0.114
chr6	171115067	2215855	0.0129	0.1228
chr7	159138663	1807692	0.0114	0.1217

chr8	146364022	2713218	0.0185	0.1522
chr9	141213431	1531445	0.0108	0.1336
chr10	135534747	1998233	0.0147	0.1445
chr11	135006516	1313224	0.0097	0.118
chr12	133851895	1914477	0.0143	0.126
chr13	115169878	1305034	0.0113	0.111
chr14	107349540	1496813	0.0139	0.1269
chr15	102531392	1221119	0.0119	0.114
chr16	90354753	1238872	0.0137	0.1269
chr17	81195210	925814	0.0114	0.1132
chr18	78077248	1032752	0.0132	0.2205
chr19	59128983	794408	0.0134	0.1434
chr20	63025520	1354514	0.0215	0.1557
chr21	48129895	553195	0.0115	0.1183
chr22	51304566	494393	0.0096	0.1024
chrMT	16571	3932	0.2373	0.5285
chrX	155270560	2367403	0.0152	0.1361
chrY	59373566	116510	0.002	0.0558

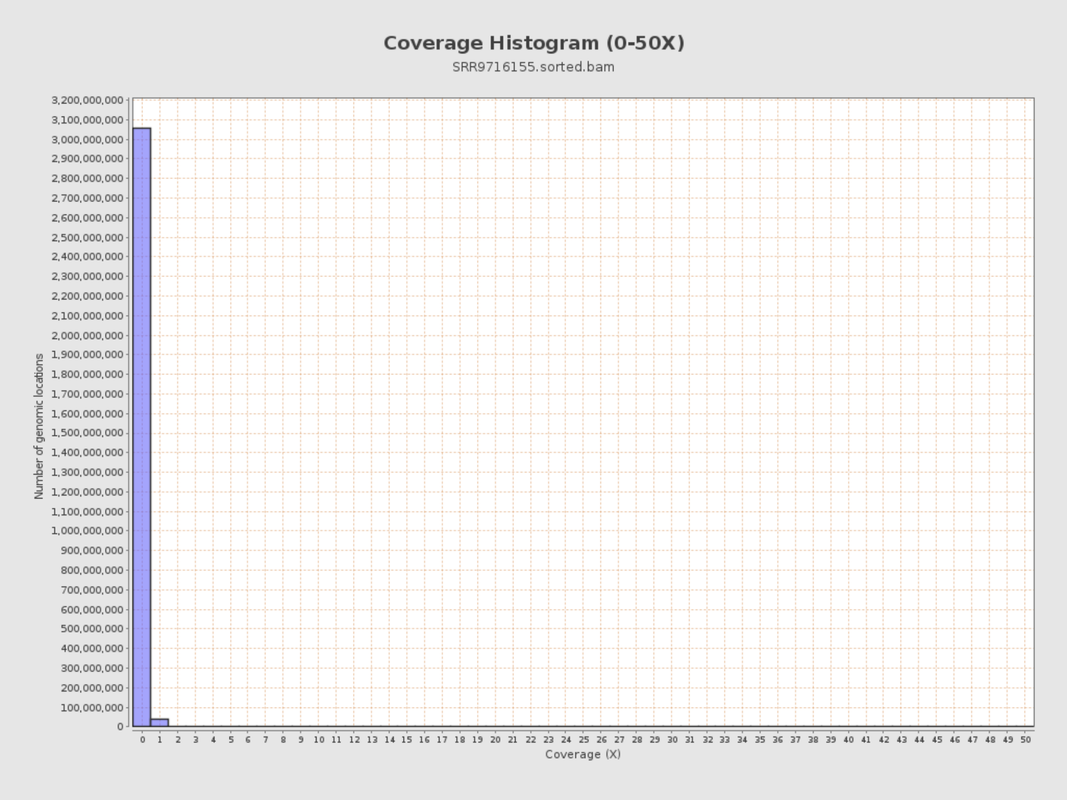
3. Results : Coverage across reference



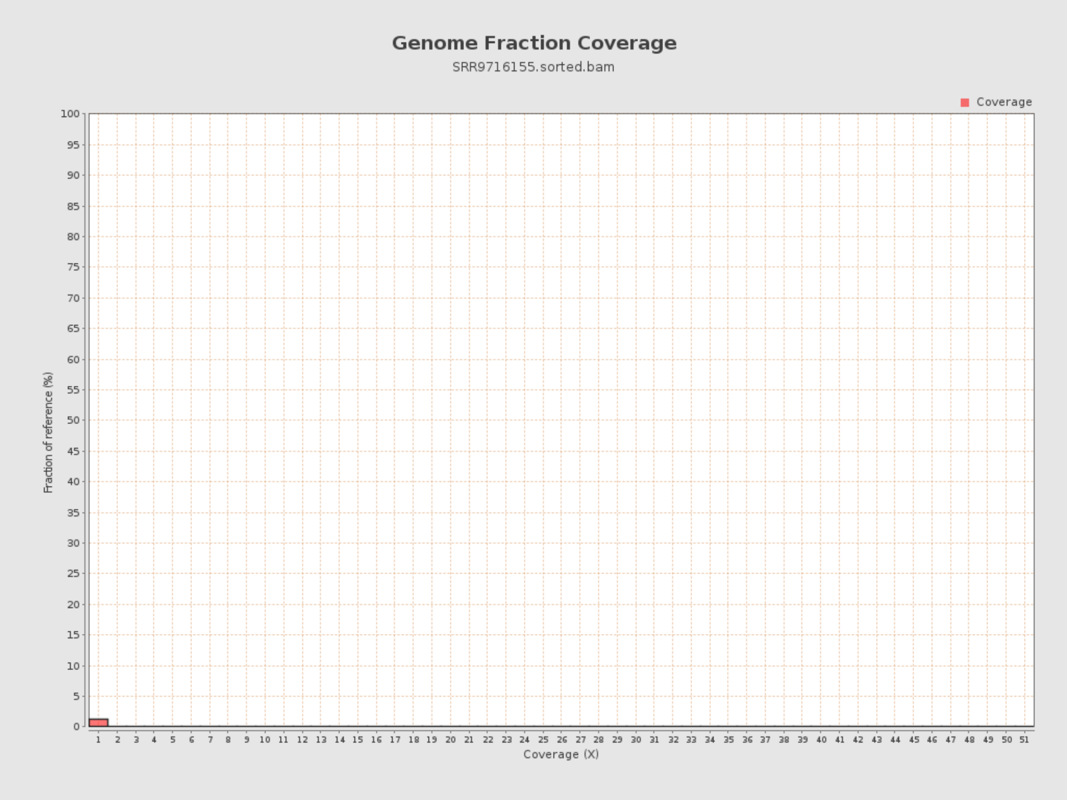
4. Results : Coverage Histogram



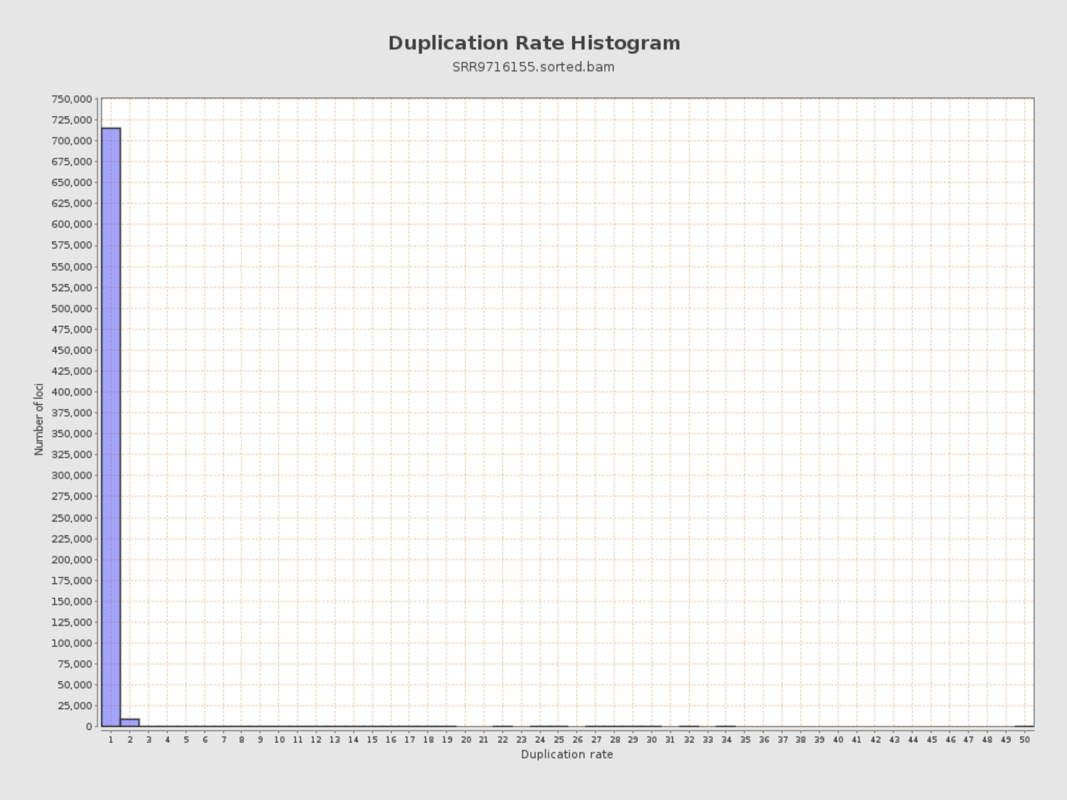
5. Results : Coverage Histogram (0-50X)



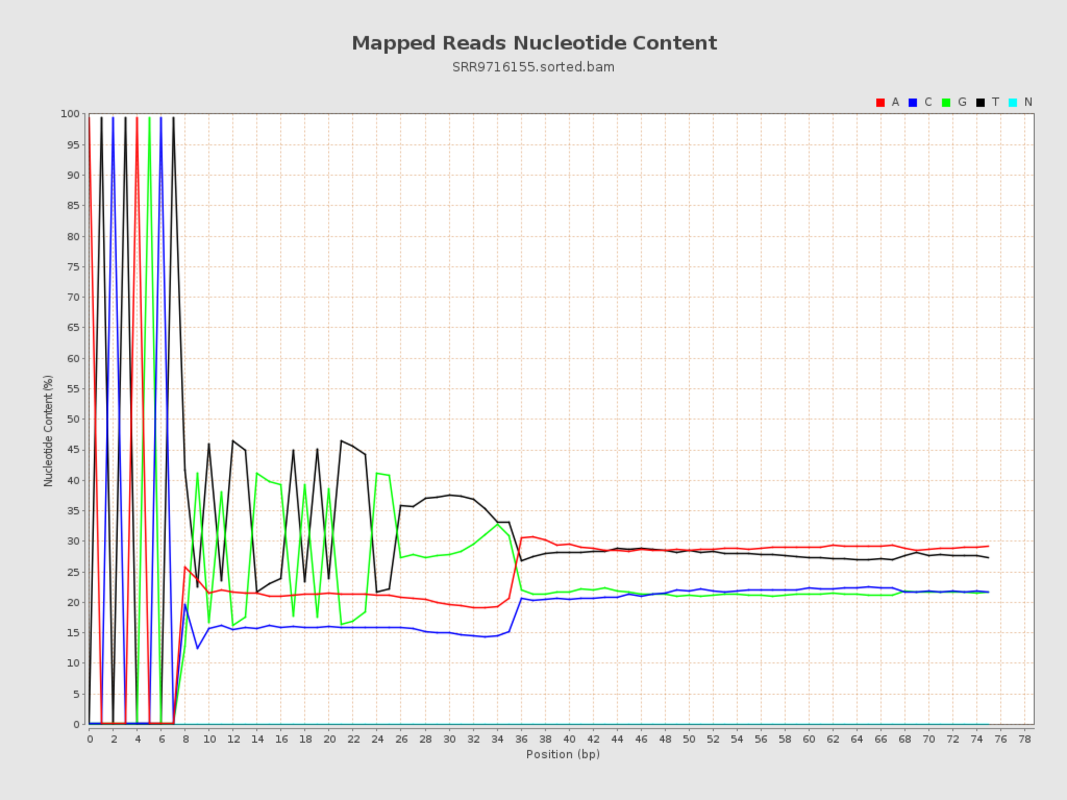
6. Results : Genome Fraction Coverage



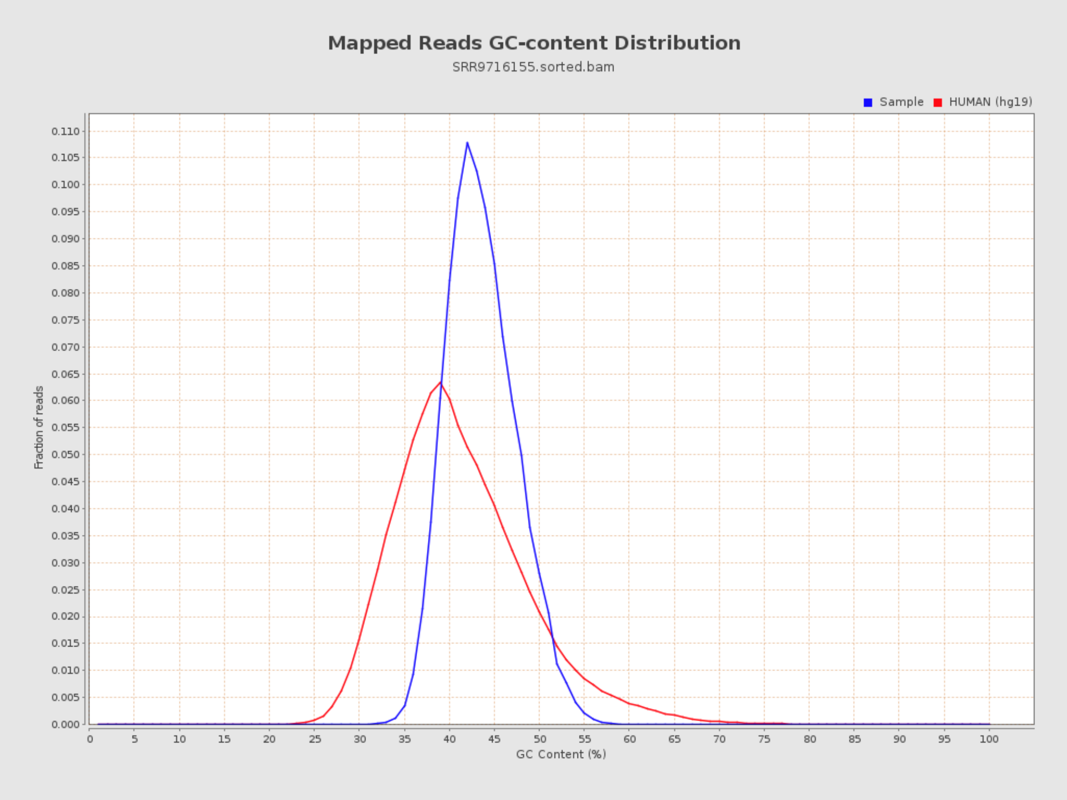
7. Results : Duplication Rate Histogram



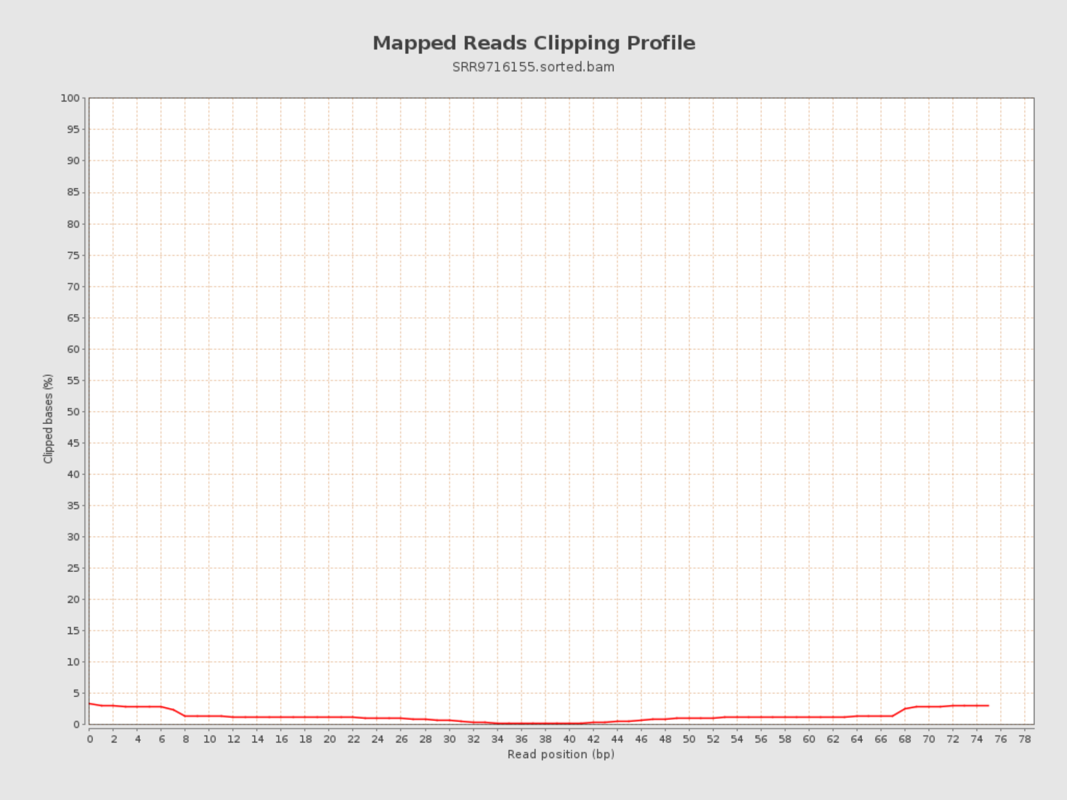
8. Results : Mapped Reads Nucleotide Content



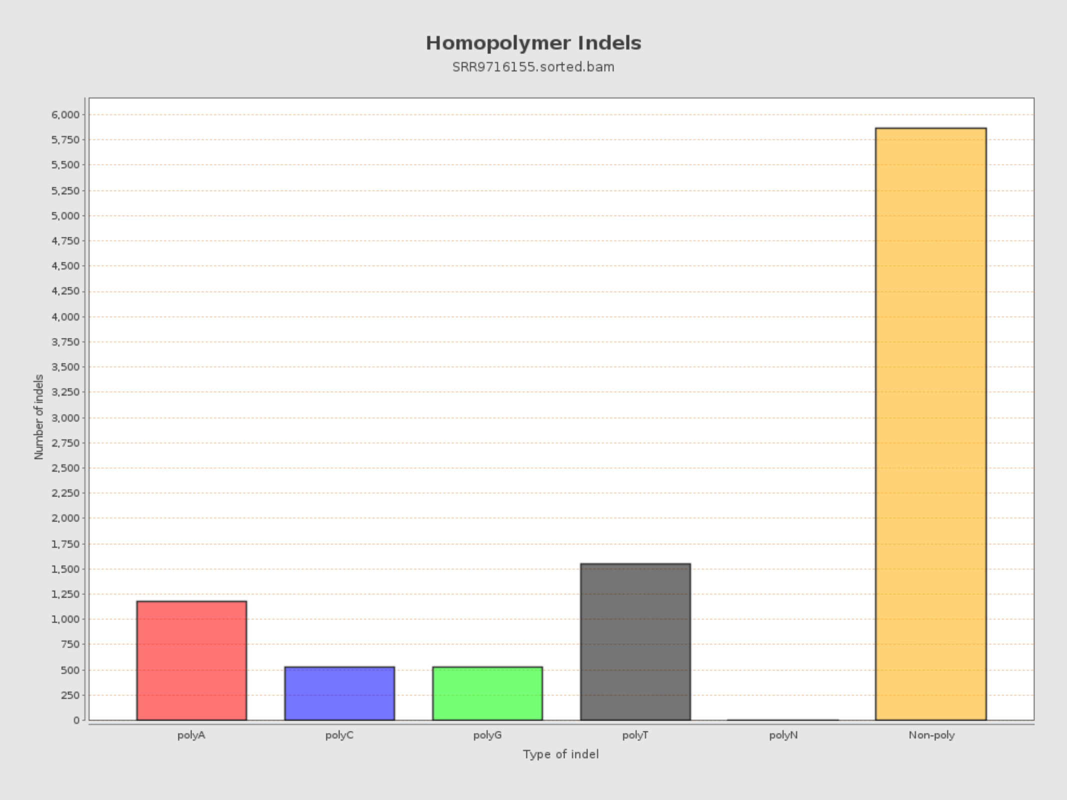
9. Results : Mapped Reads GC-content Distribution



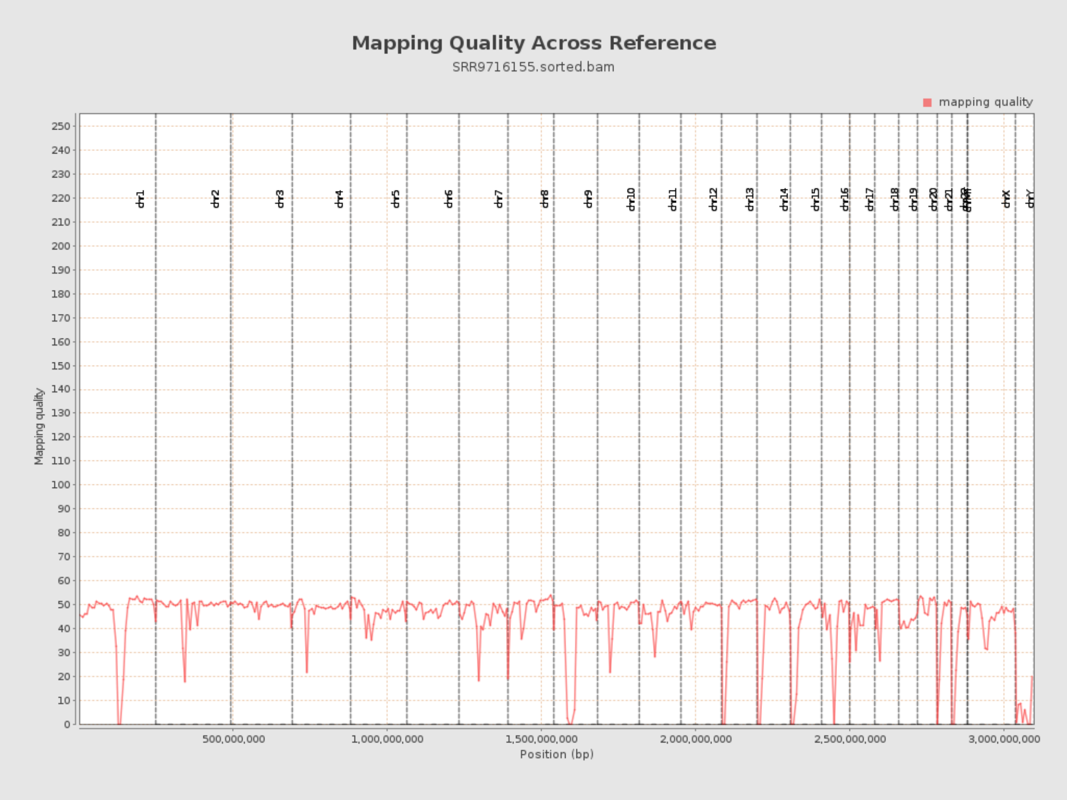
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram