Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:52:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716828.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_SRR9716828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:52:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	755,524
Mapped reads	571,064 / 75.59%
Unmapped reads	184,460 / 24.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	695 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	36,214 / 4.79%
Duplication rate	5.56%
Clipped reads	571,043 / 75.58%

2.2. ACGT Content

Number/percentage of A's	6,297,495 / 21.1%
Number/percentage of C's	5,431,902 / 18.2%
Number/percentage of T's	9,773,698 / 32.75%
Number/percentage of G's	8,339,434 / 27.94%
Number/percentage of N's	484 / 0%
GC Percentage	46.15%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1198

2.4. Mapping Quality

Mean Mapping Quality	42.65

2.5. Mismatches and indels

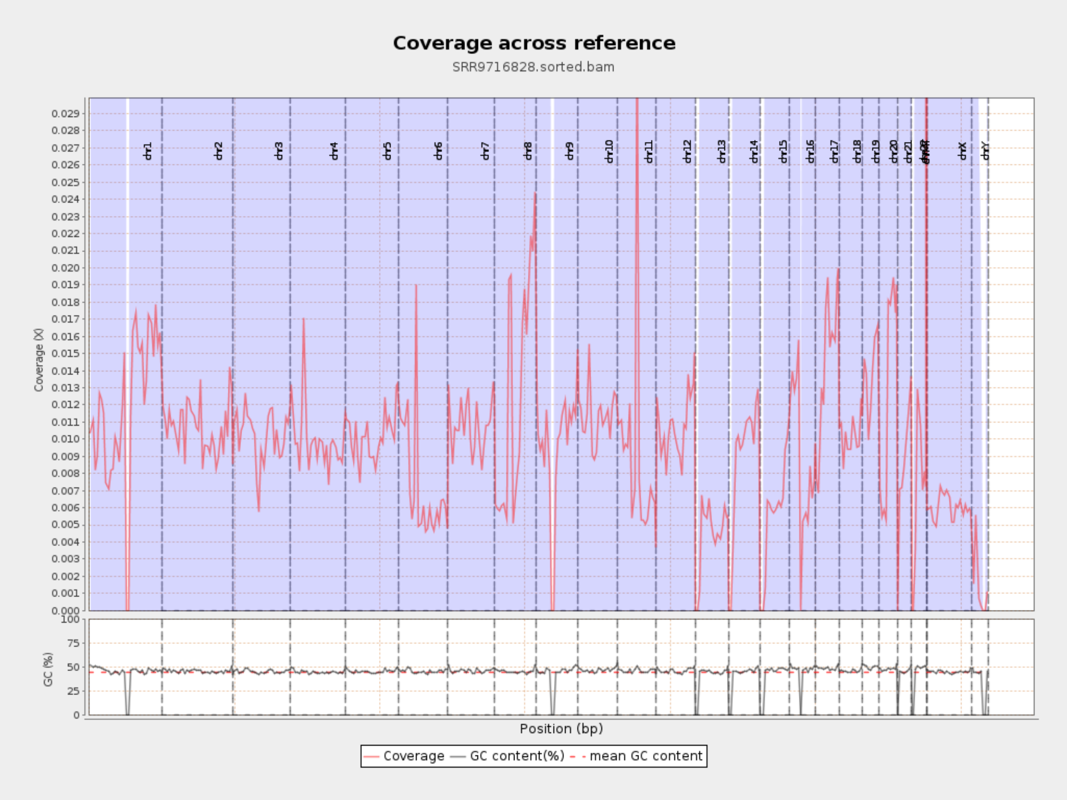
General error rate	0.68%
Mismatches	199,111
Insertions	1,710
Mapped reads with at least one insertion	0.3%
Deletions	4,439
Mapped reads with at least one deletion	0.77%
Homopolymer indels	40.84%

2.6. Chromosome stats

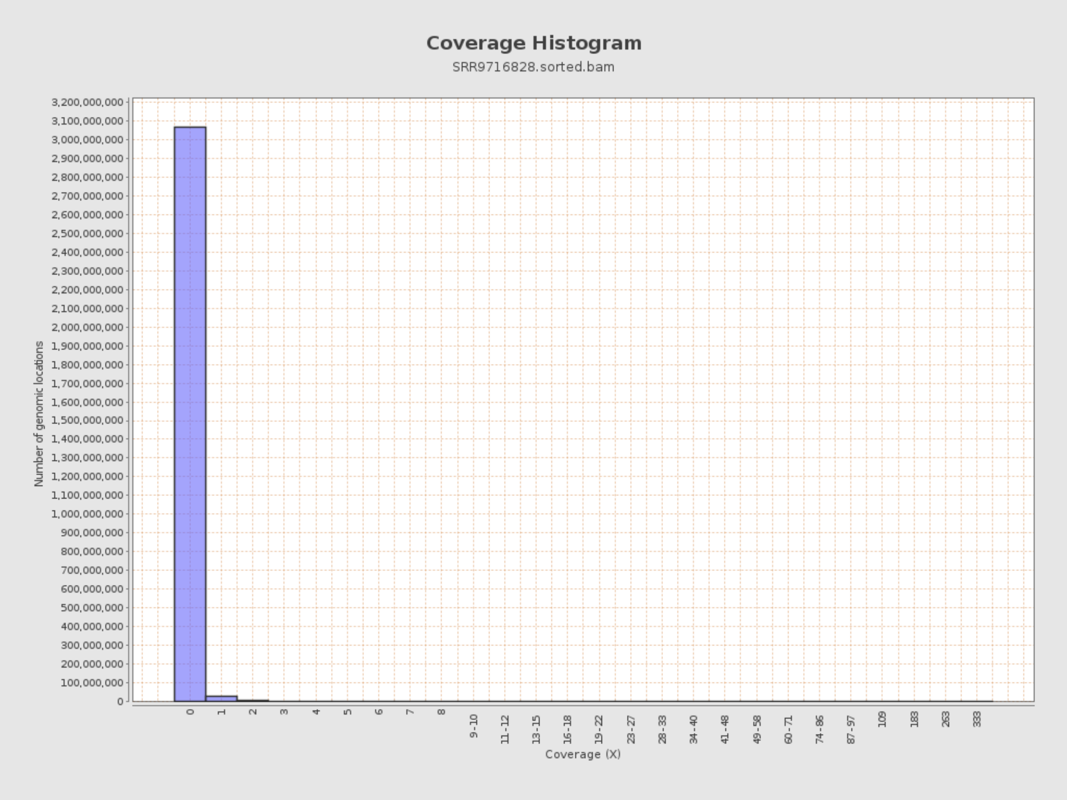
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2937119	0.0118	0.1365
chr2	243199373	2601711	0.0107	0.1741
chr3	198022430	2017372	0.0102	0.1125
chr4	191154276	1896299	0.0099	0.1124
chr5	180915260	1830824	0.0101	0.1109
chr6	171115067	1274945	0.0075	0.1087
chr7	159138663	1702278	0.0107	0.1248

chr8	146364022	1848035	0.0126	0.1278
chr9	141213431	1305839	0.0092	0.1096
chr10	135534747	1527606	0.0113	0.1284
chr11	135006516	1267365	0.0094	0.1136
chr12	133851895	1433176	0.0107	0.115
chr13	115169878	506017	0.0044	0.0743
chr14	107349540	948727	0.0088	0.1046
chr15	102531392	574416	0.0056	0.0822
chr16	90354753	796254	0.0088	0.1068
chr17	81195210	1191612	0.0147	0.1381
chr18	78077248	789857	0.0101	0.1206
chr19	59128983	806484	0.0136	0.146
chr20	63025520	792852	0.0126	0.1279
chr21	48129895	415605	0.0086	0.1089
chr22	51304566	342741	0.0067	0.0945
chrMT	16571	13823	0.8342	1.1641
chrX	155270560	940235	0.0061	0.0873
chrY	59373566	89400	0.0015	0.0525

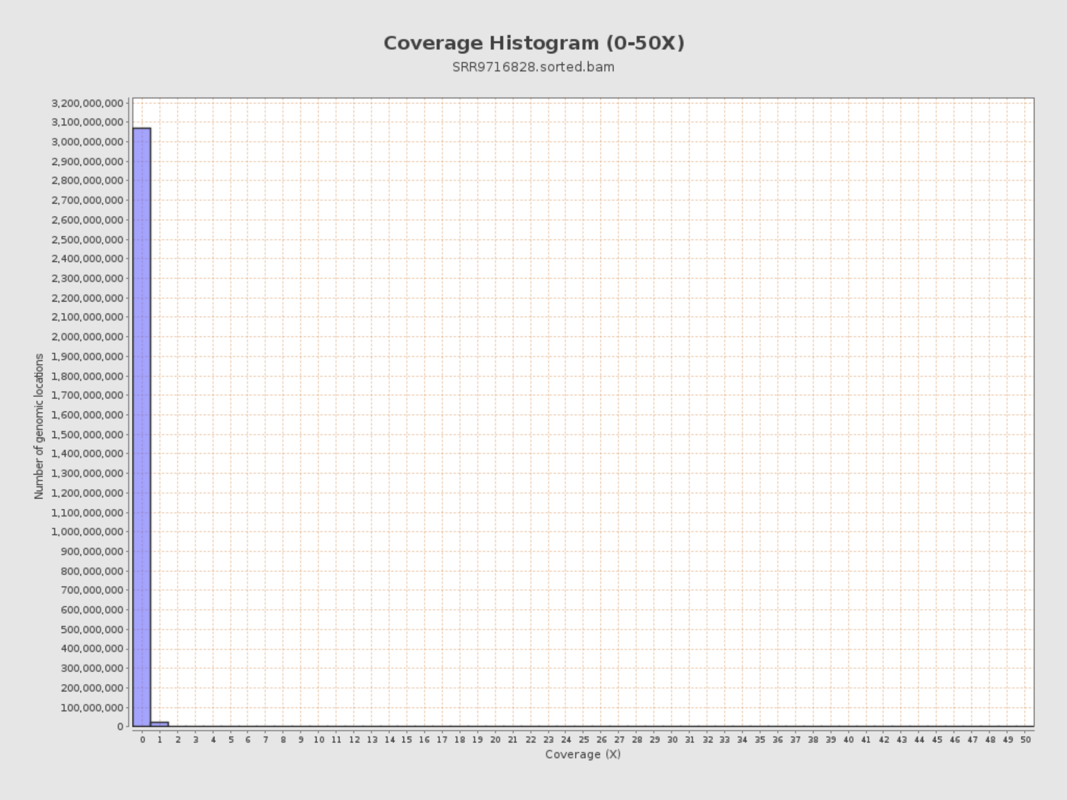
3. Results : Coverage across reference



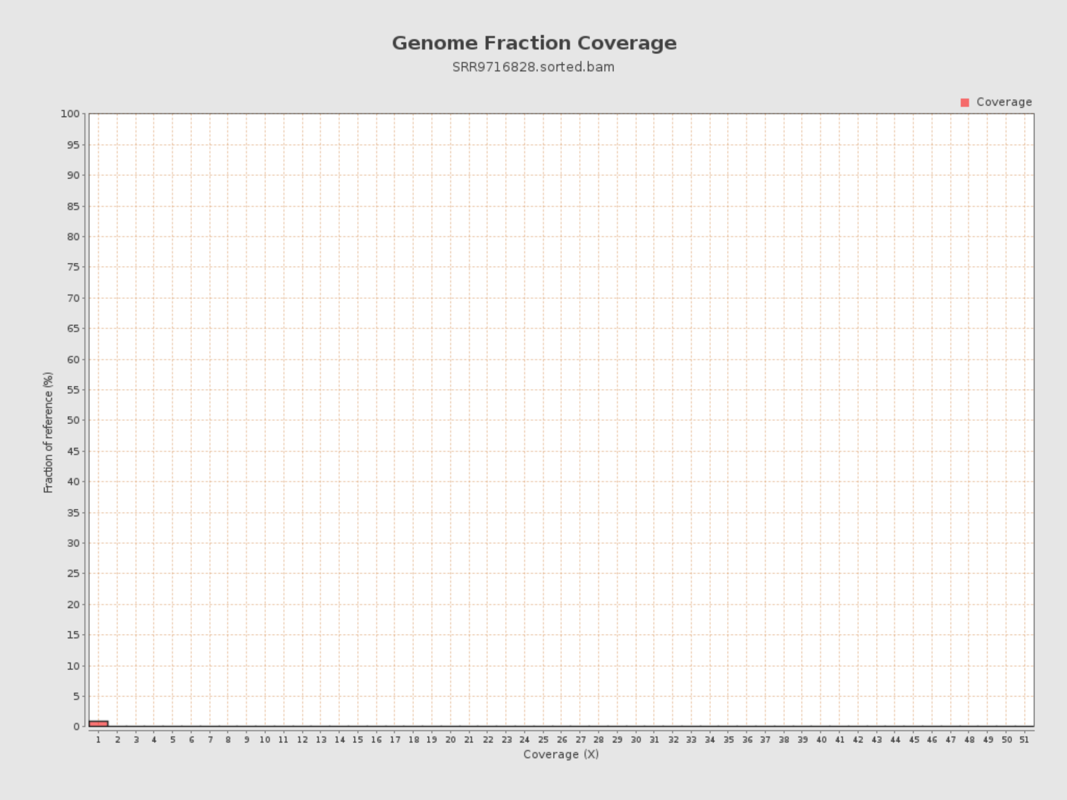
4. Results : Coverage Histogram



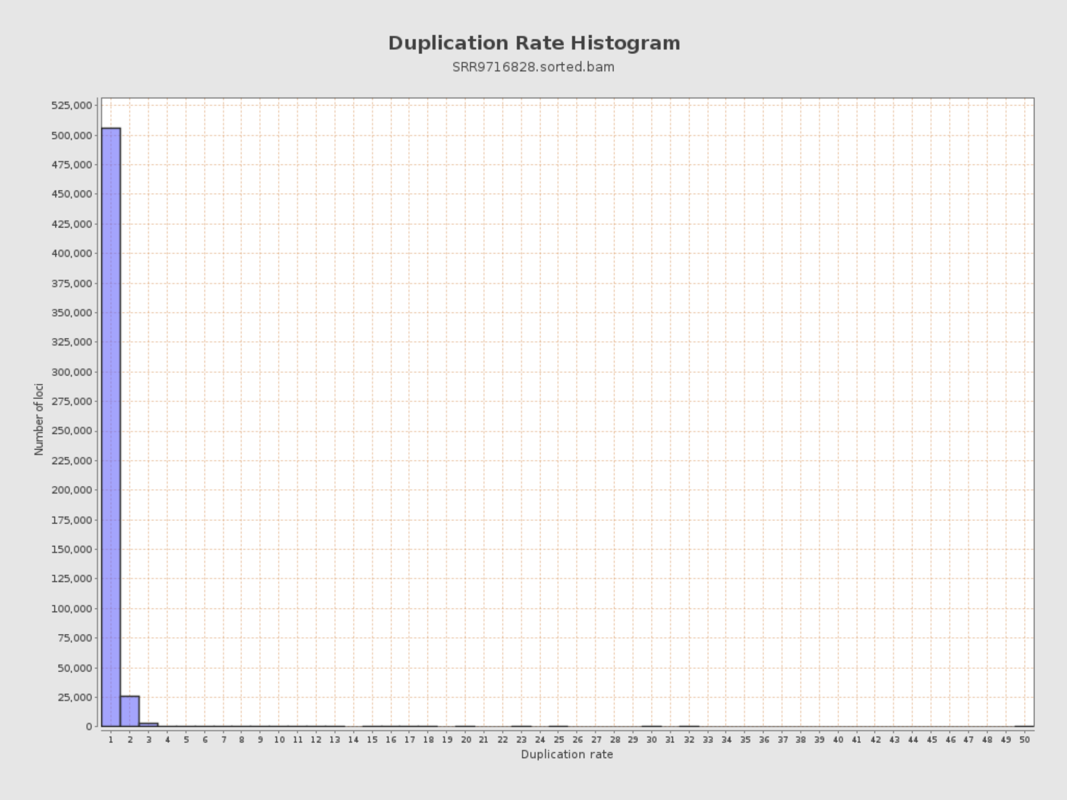
5. Results : Coverage Histogram (0-50X)



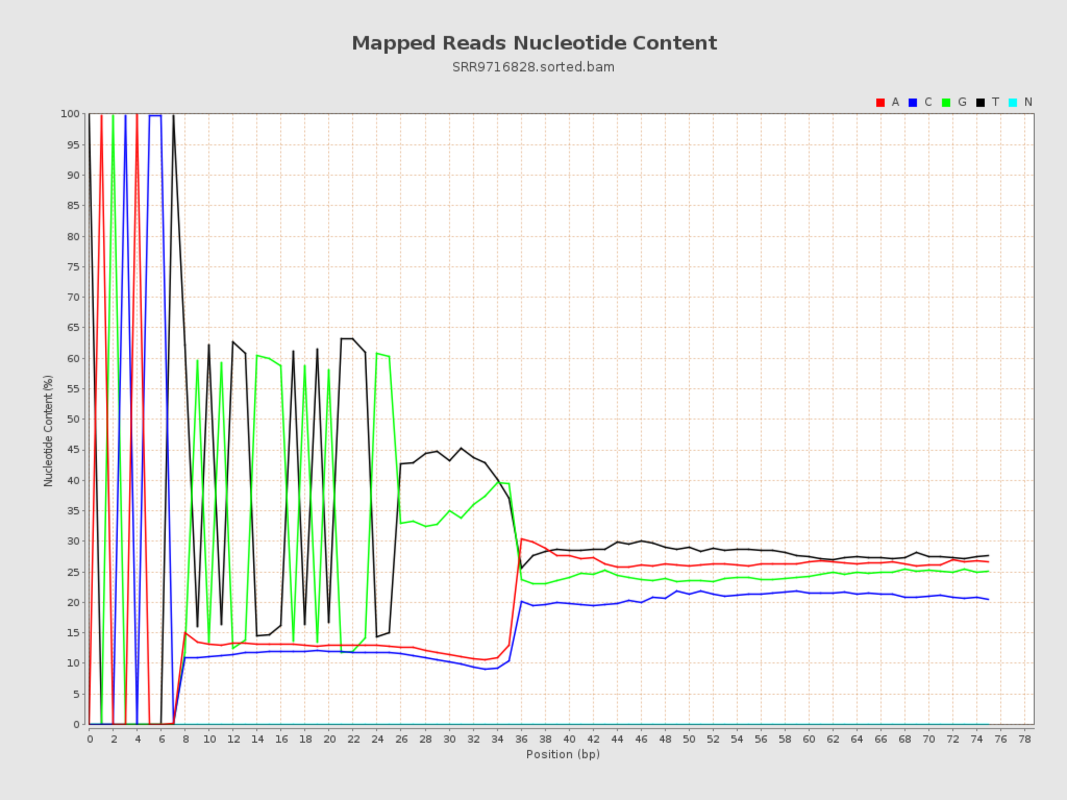
6. Results : Genome Fraction Coverage



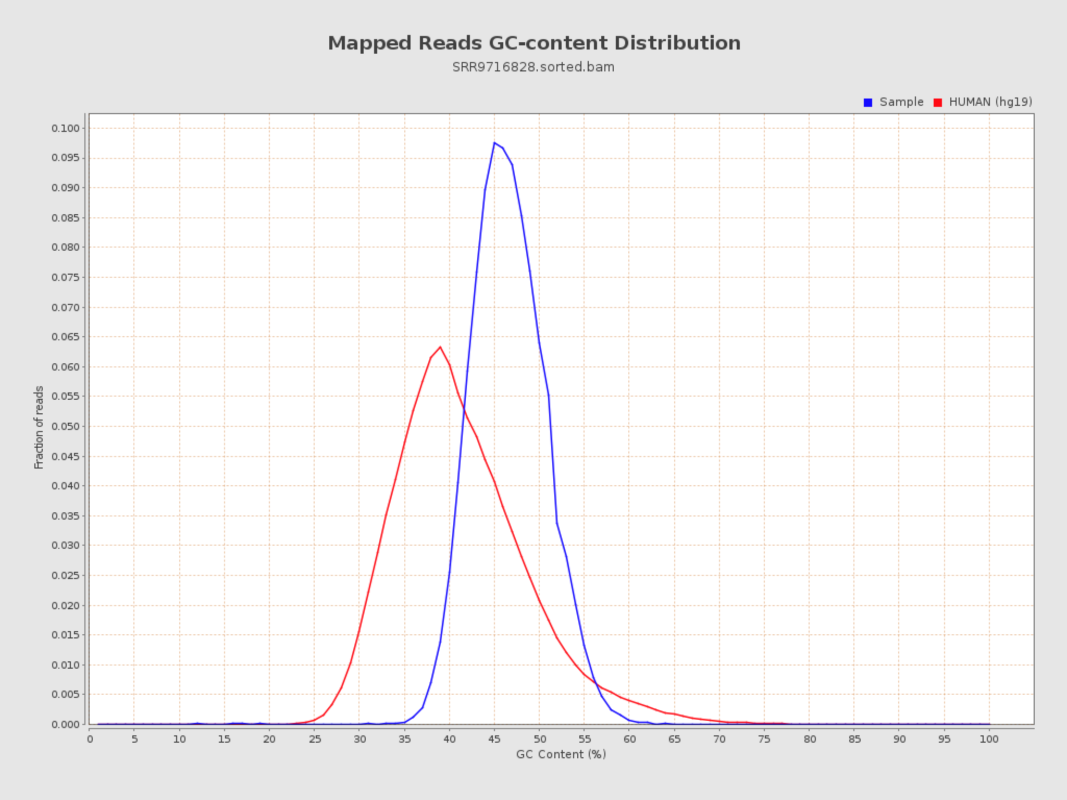
7. Results : Duplication Rate Histogram



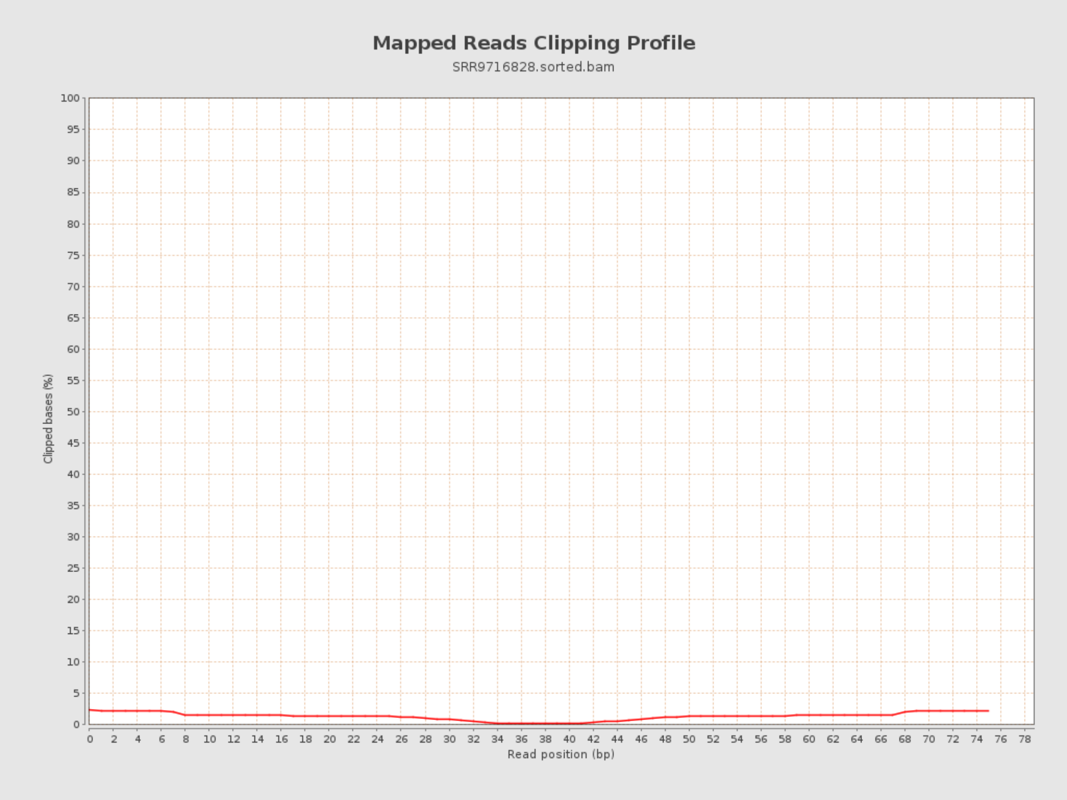
8. Results : Mapped Reads Nucleotide Content



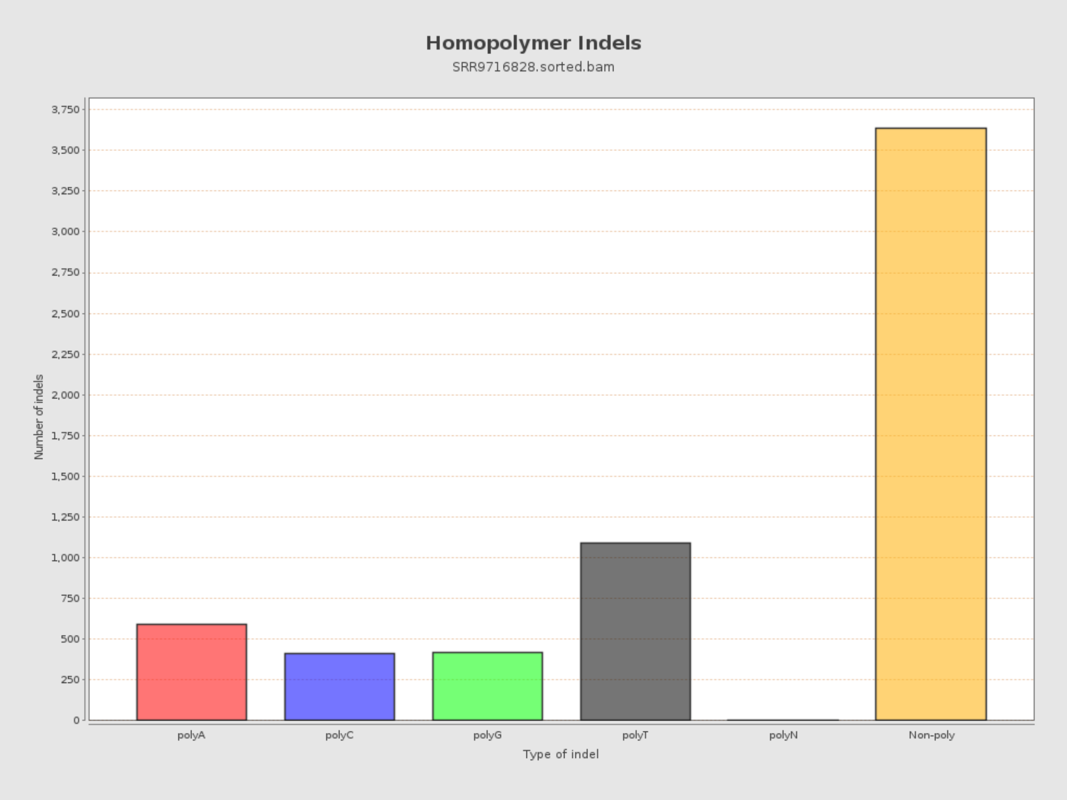
9. Results : Mapped Reads GC-content Distribution



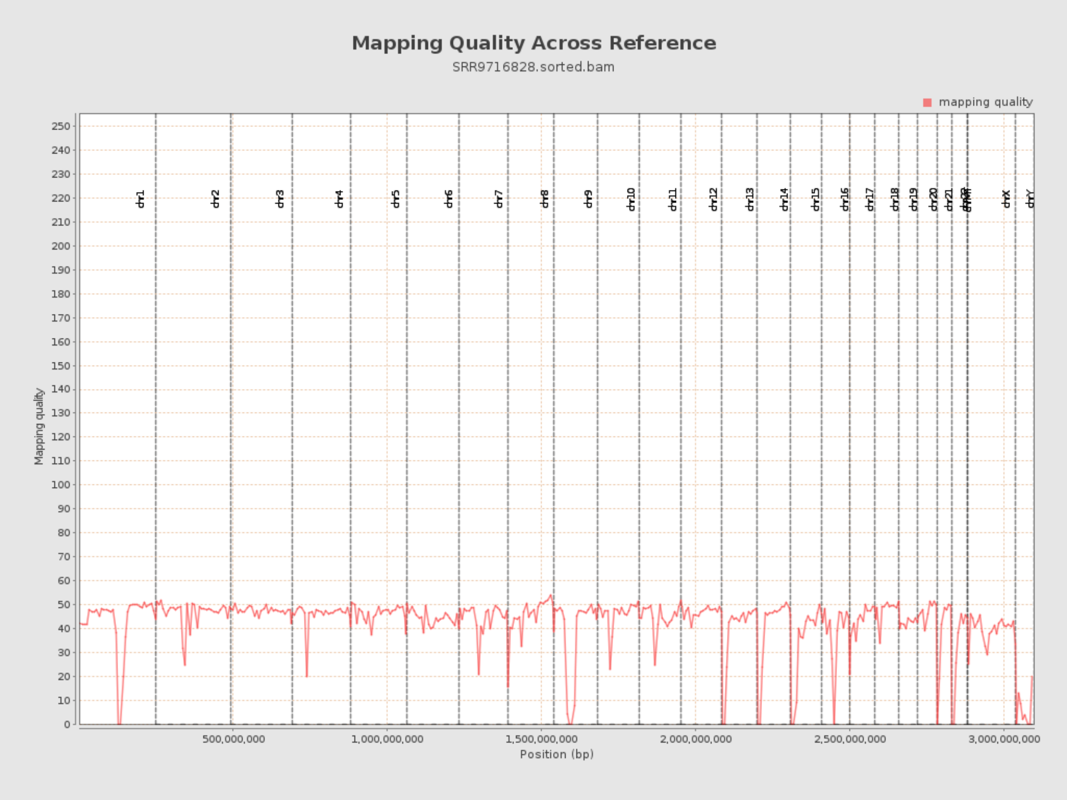
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram