Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:57:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716803.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_SRR9716803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:57:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	757,280
Mapped reads	690,419 / 91.17%
Unmapped reads	66,861 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,193 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	16,270 / 2.15%
Duplication rate	1.88%
Clipped reads	692,947 / 91.5%

2.2. ACGT Content

Number/percentage of A's	10,420,450 / 25.71%
Number/percentage of C's	8,172,847 / 20.16%
Number/percentage of T's	12,396,383 / 30.58%
Number/percentage of G's	9,541,221 / 23.54%
Number/percentage of N's	525 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1408

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

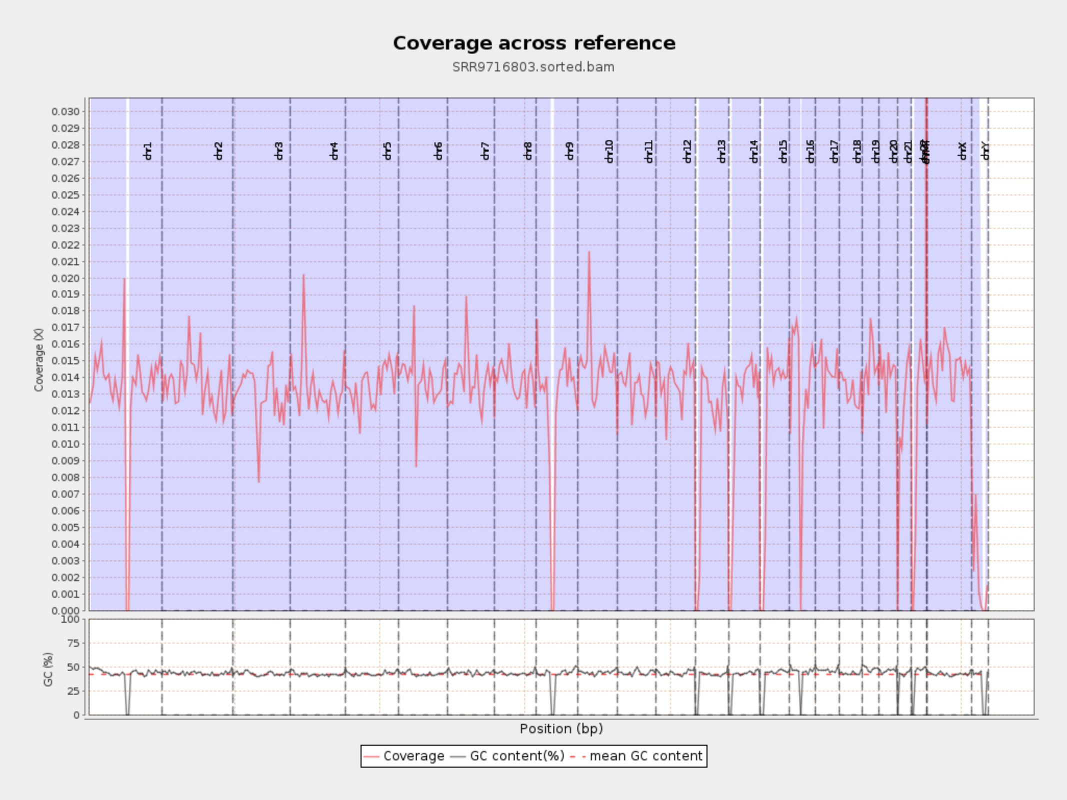
General error rate	0.49%
Mismatches	194,829
Insertions	2,381
Mapped reads with at least one insertion	0.34%
Deletions	7,074
Mapped reads with at least one deletion	1.02%
Homopolymer indels	44.32%

2.6. Chromosome stats

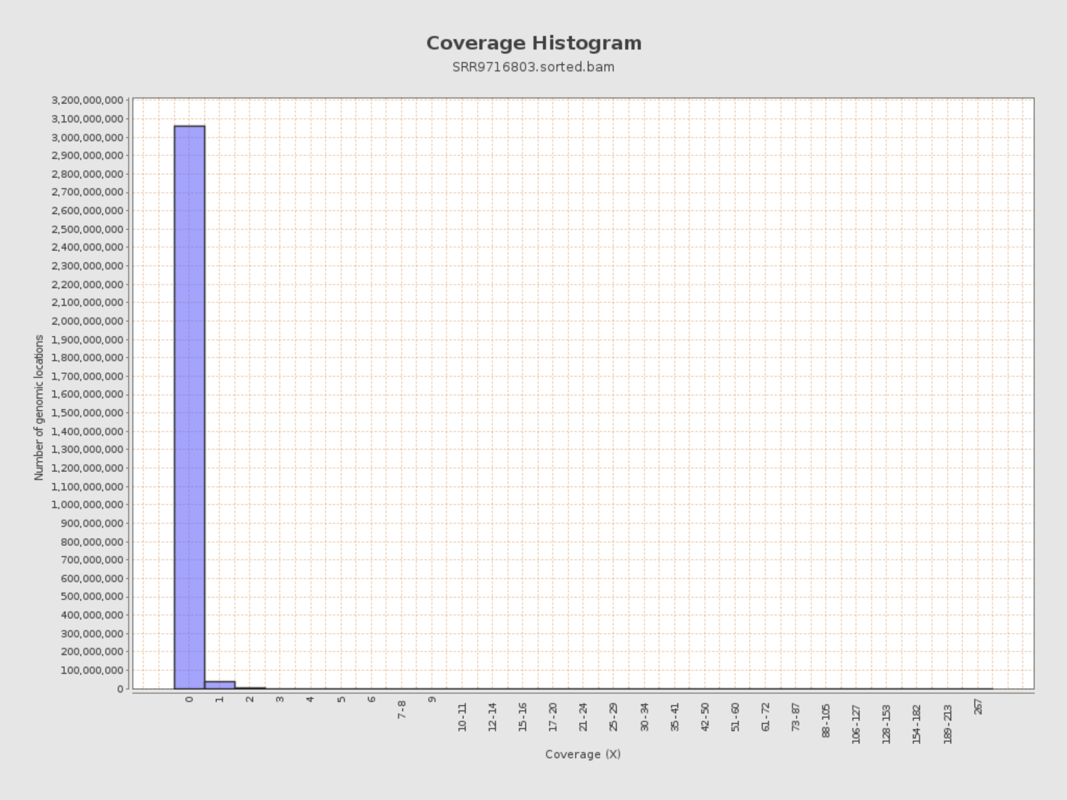
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3292956	0.0132	0.203
chr2	243199373	3320012	0.0137	0.1687
chr3	198022430	2576778	0.013	0.1202
chr4	191154276	2565146	0.0134	0.1277
chr5	180915260	2447447	0.0135	0.1226
chr6	171115067	2372384	0.0139	0.1331
chr7	159138663	2216081	0.0139	0.153

chr8	146364022	2037401	0.0139	0.1382
chr9	141213431	1706996	0.0121	0.1247
chr10	135534747	2004987	0.0148	0.148
chr11	135006516	1828489	0.0135	0.1361
chr12	133851895	1853160	0.0138	0.1249
chr13	115169878	1231076	0.0107	0.1091
chr14	107349540	1244941	0.0116	0.1153
chr15	102531392	1199236	0.0117	0.1147
chr16	90354753	1202915	0.0133	0.1243
chr17	81195210	1171366	0.0144	0.1294
chr18	78077248	1033710	0.0132	0.1736
chr19	59128983	869315	0.0147	0.1675
chr20	63025520	897749	0.0142	0.127
chr21	48129895	555044	0.0115	0.1176
chr22	51304566	514635	0.01	0.1056
chrMT	16571	23225	1.4015	1.4521
chrX	155270560	2253309	0.0145	0.1317
chrY	59373566	124004	0.0021	0.0648

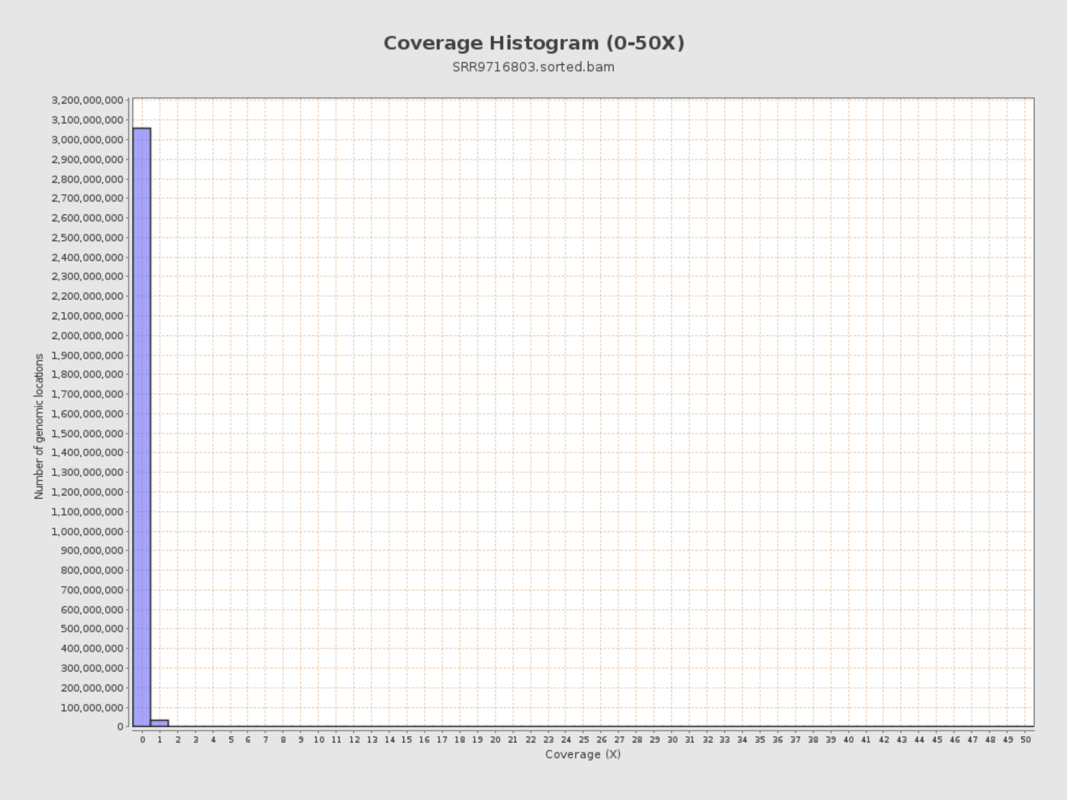
3. Results : Coverage across reference



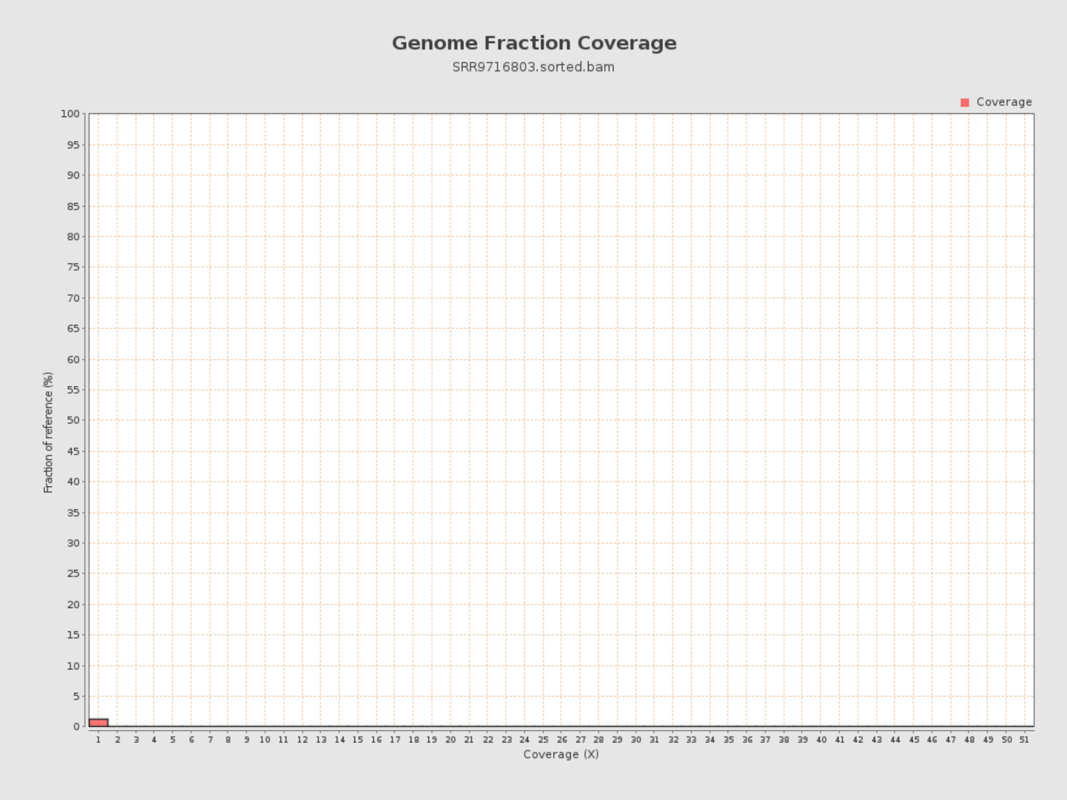
4. Results : Coverage Histogram



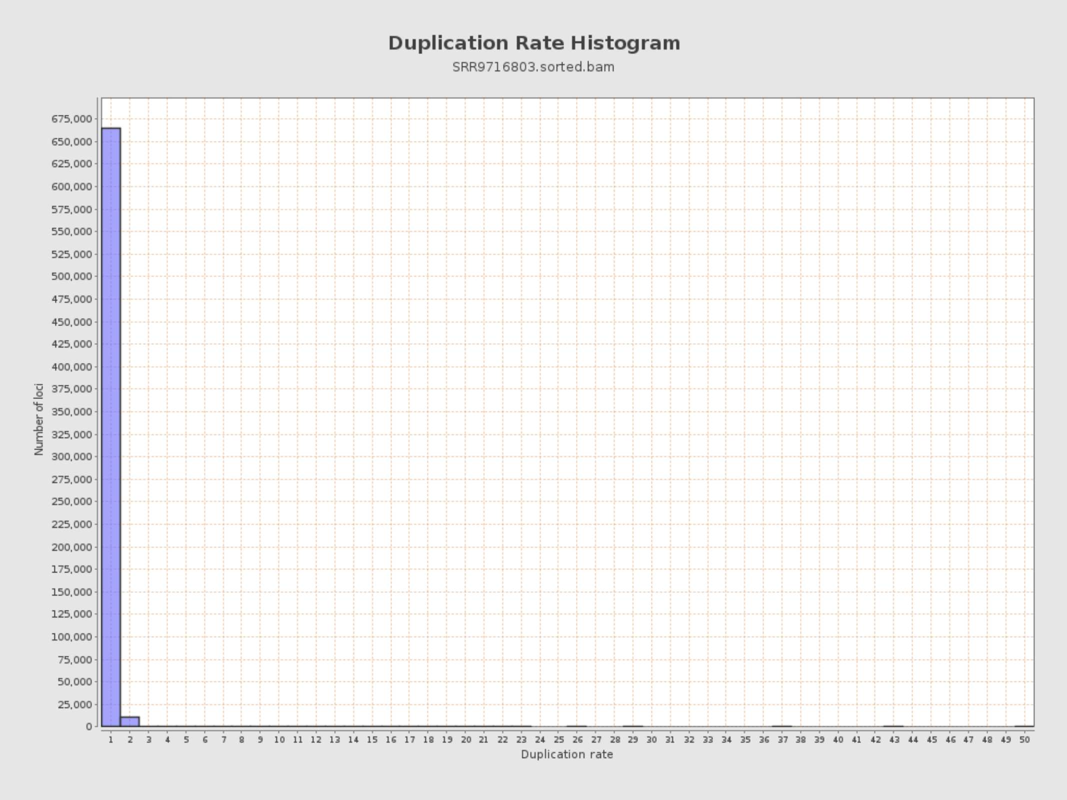
5. Results : Coverage Histogram (0-50X)



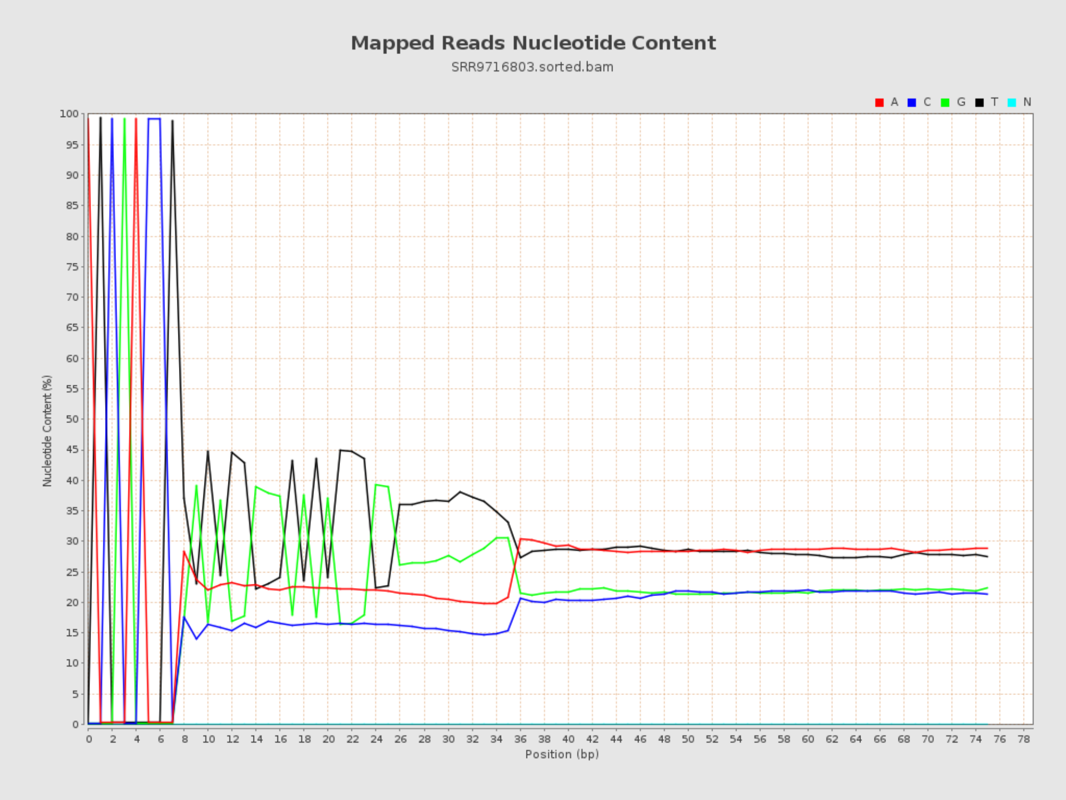
6. Results : Genome Fraction Coverage



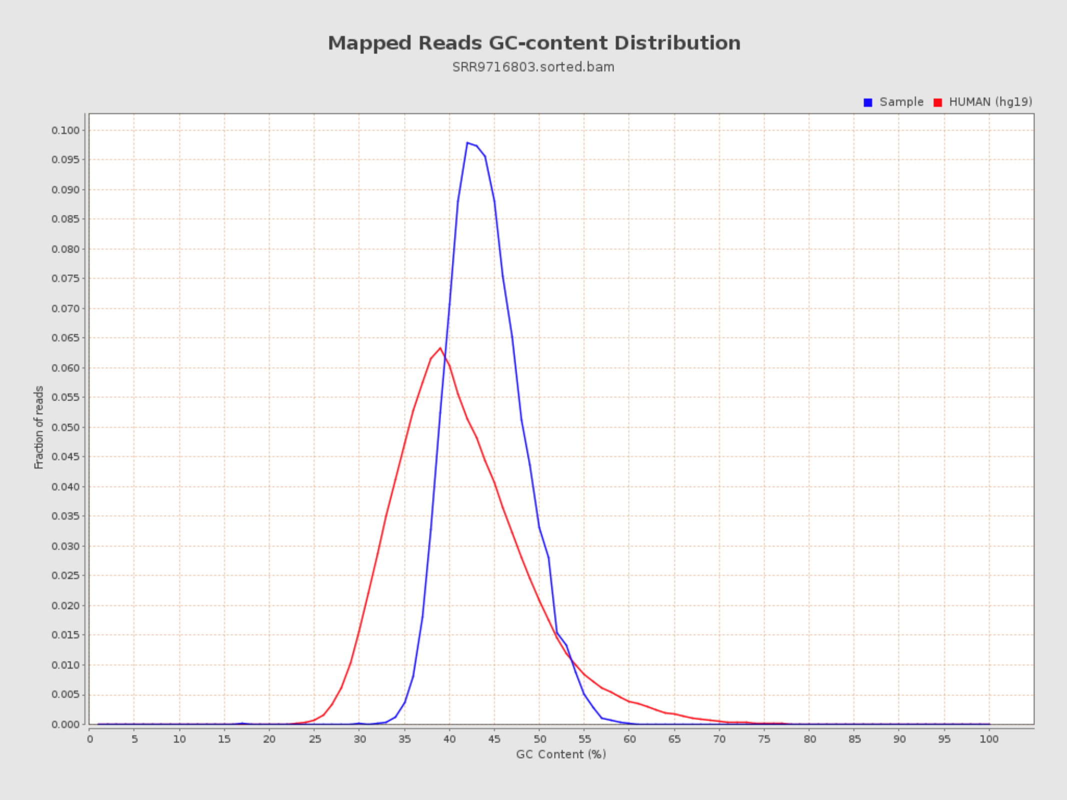
7. Results : Duplication Rate Histogram



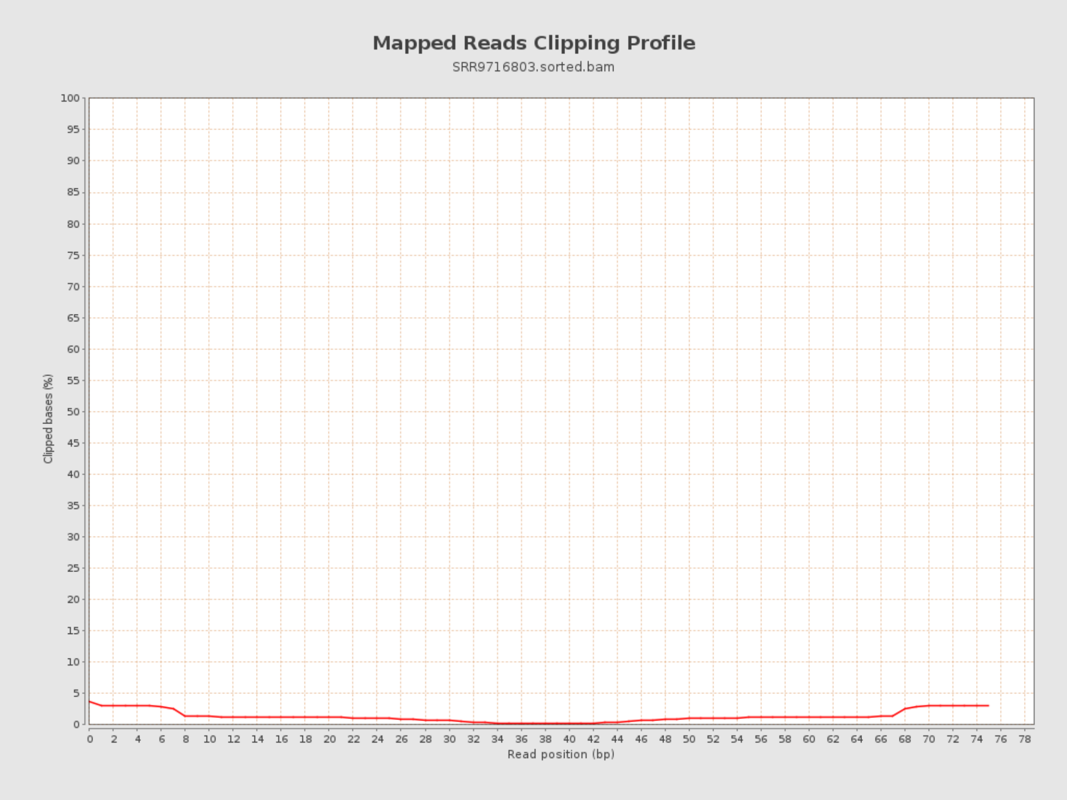
8. Results : Mapped Reads Nucleotide Content



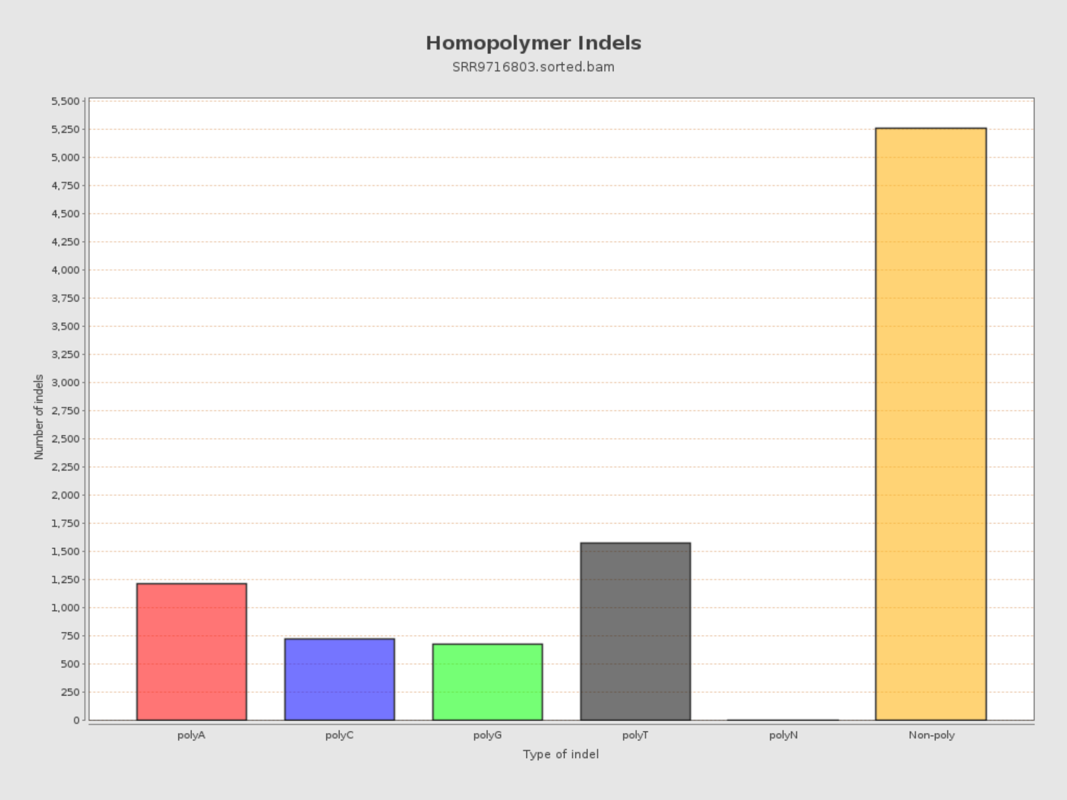
9. Results : Mapped Reads GC-content Distribution



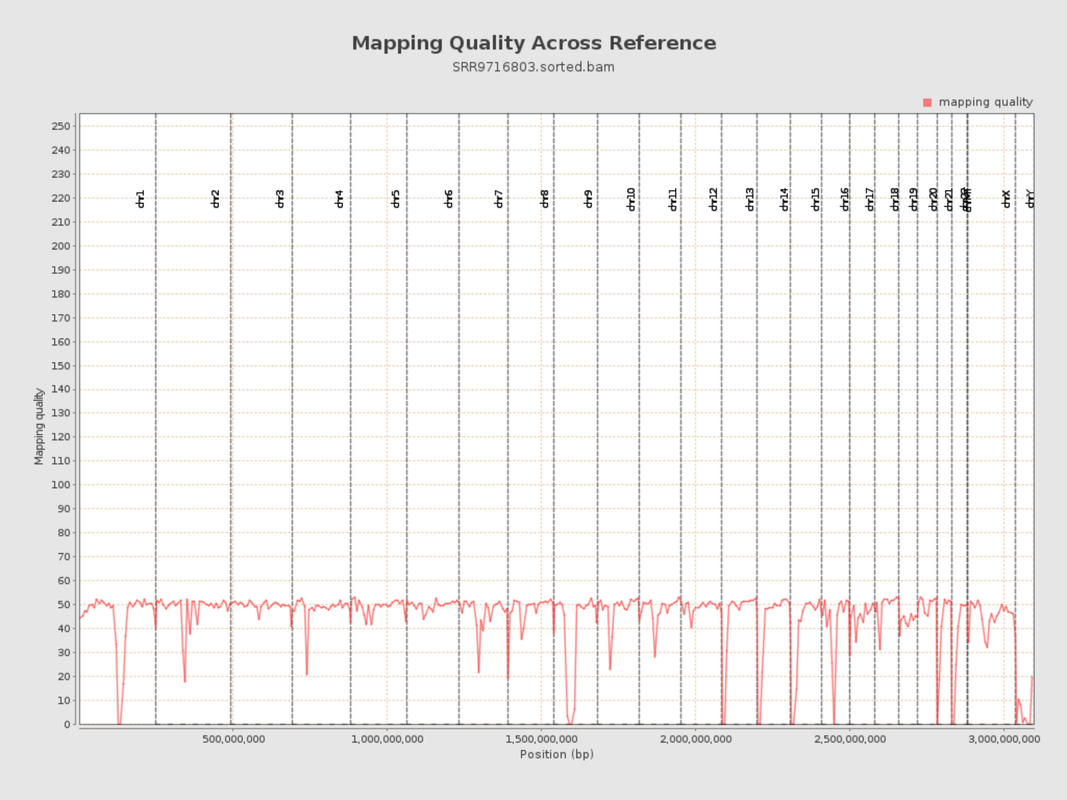
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram