Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:26:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716815.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_SRR9716815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:26:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	949,105
Mapped reads	767,128 / 80.83%
Unmapped reads	181,977 / 19.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,832 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,152 / 1.49%
Duplication rate	1.3%
Clipped reads	769,645 / 81.09%

2.2. ACGT Content

Number/percentage of A's	9,869,653 / 23.53%
Number/percentage of C's	8,274,935 / 19.73%
Number/percentage of T's	12,463,359 / 29.71%
Number/percentage of G's	11,339,909 / 27.03%
Number/percentage of N's	902 / 0%
GC Percentage	46.76%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1375

2.4. Mapping Quality

Mean Mapping Quality	38.84

2.5. Mismatches and indels

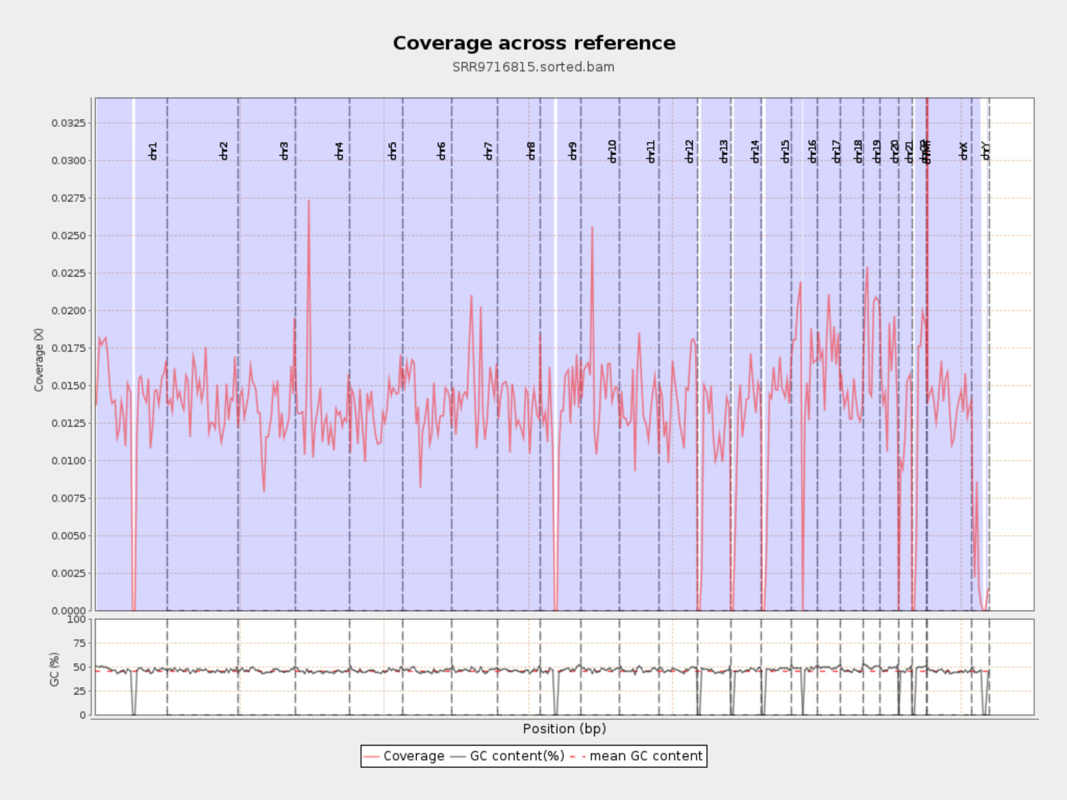
General error rate	0.54%
Mismatches	220,681
Insertions	2,763
Mapped reads with at least one insertion	0.36%
Deletions	7,103
Mapped reads with at least one deletion	0.92%
Homopolymer indels	36.07%

2.6. Chromosome stats

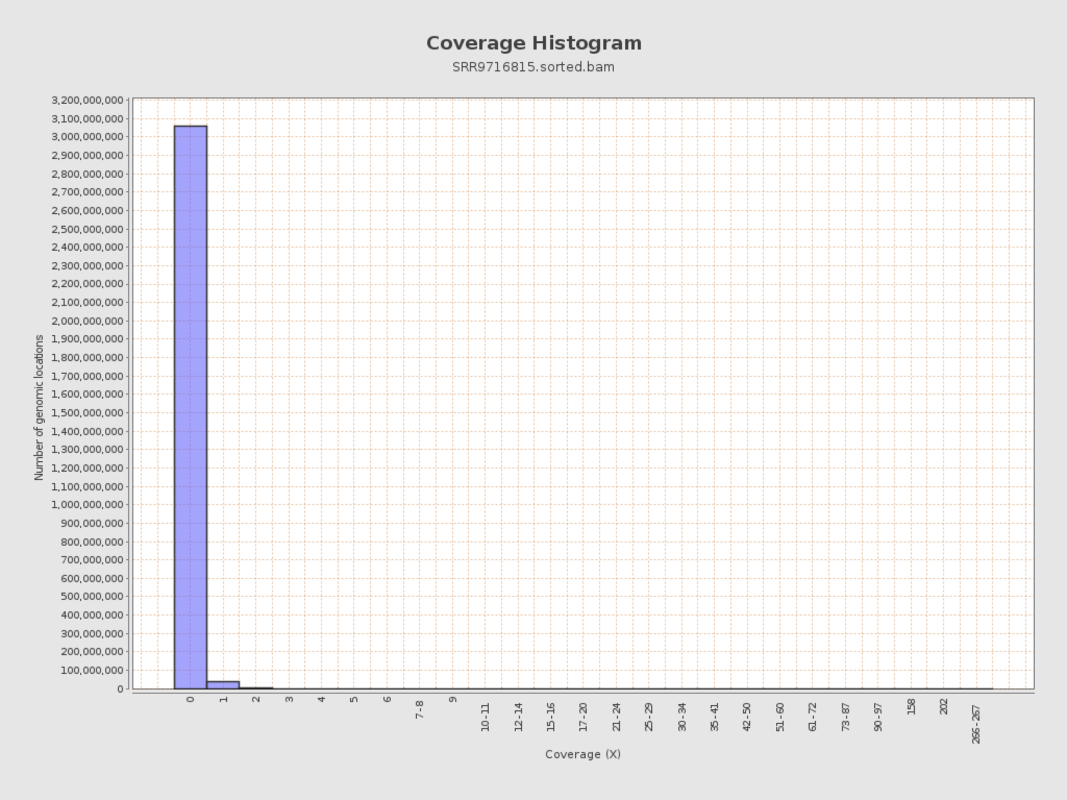
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3409119	0.0137	0.1413
chr2	243199373	3438131	0.0141	0.1733
chr3	198022430	2648507	0.0134	0.1278
chr4	191154276	2580553	0.0135	0.1373
chr5	180915260	2438937	0.0135	0.1245
chr6	171115067	2334074	0.0136	0.1273
chr7	159138663	2348248	0.0148	0.1493

chr8	146364022	1960075	0.0134	0.1289
chr9	141213431	1737980	0.0123	0.1256
chr10	135534747	2083247	0.0154	0.1649
chr11	135006516	1855220	0.0137	0.1384
chr12	133851895	1895593	0.0142	0.1278
chr13	115169878	1219300	0.0106	0.1113
chr14	107349540	1255757	0.0117	0.1189
chr15	102531392	1228500	0.012	0.1185
chr16	90354753	1411509	0.0156	0.1406
chr17	81195210	1415522	0.0174	0.1454
chr18	78077248	1080431	0.0138	0.1564
chr19	59128983	1130997	0.0191	0.1622
chr20	63025520	976480	0.0155	0.1357
chr21	48129895	549989	0.0114	0.1238
chr22	51304566	640527	0.0125	0.1221
chrMT	16571	5305	0.3201	0.6501
chrX	155270560	2167911	0.014	0.134
chrY	59373566	148929	0.0025	0.0812

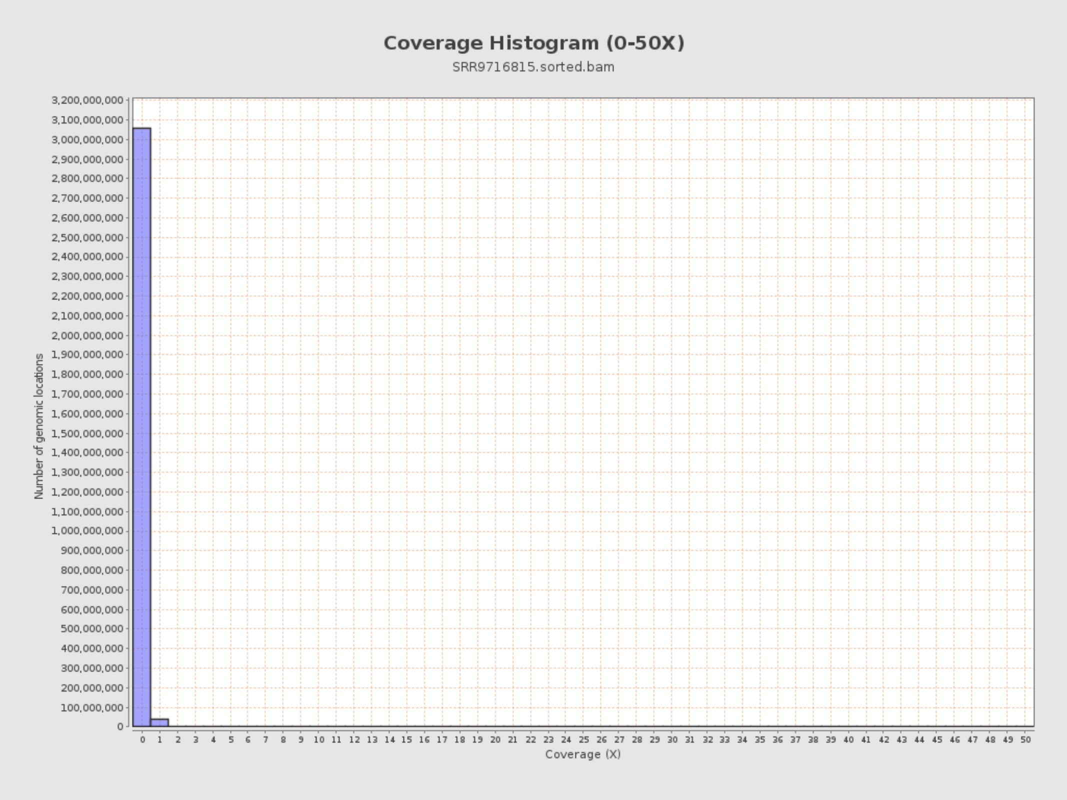
3. Results : Coverage across reference



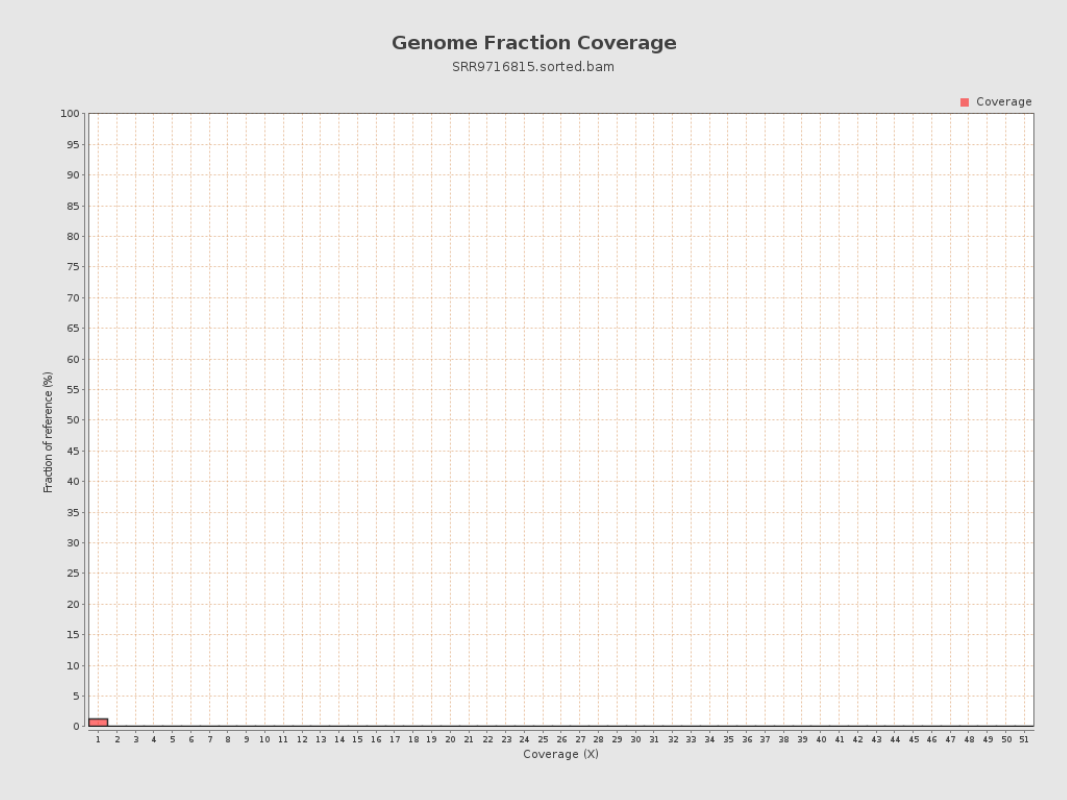
4. Results : Coverage Histogram



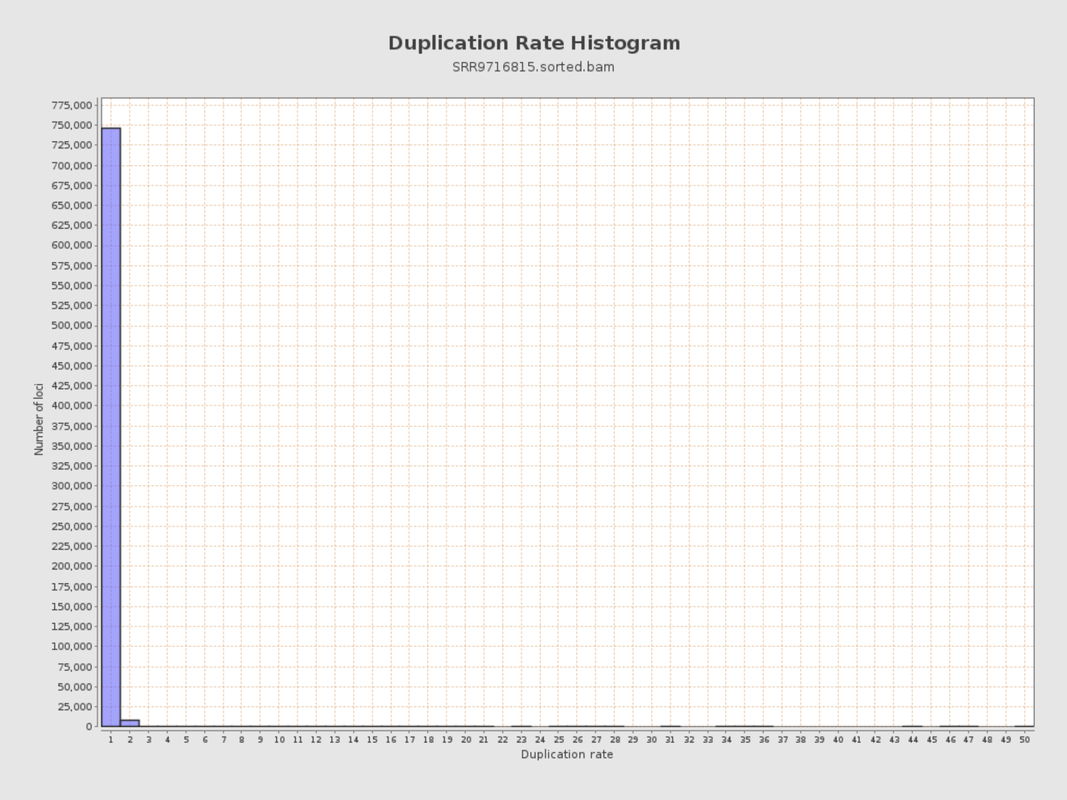
5. Results : Coverage Histogram (0-50X)



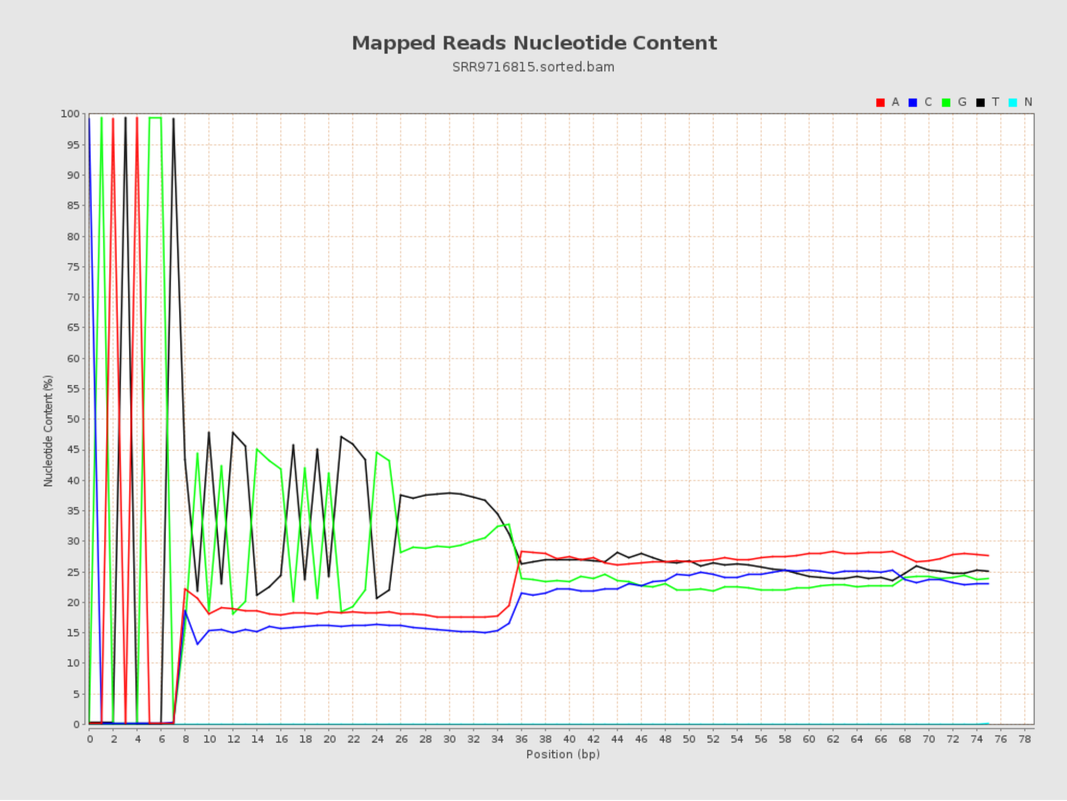
6. Results : Genome Fraction Coverage



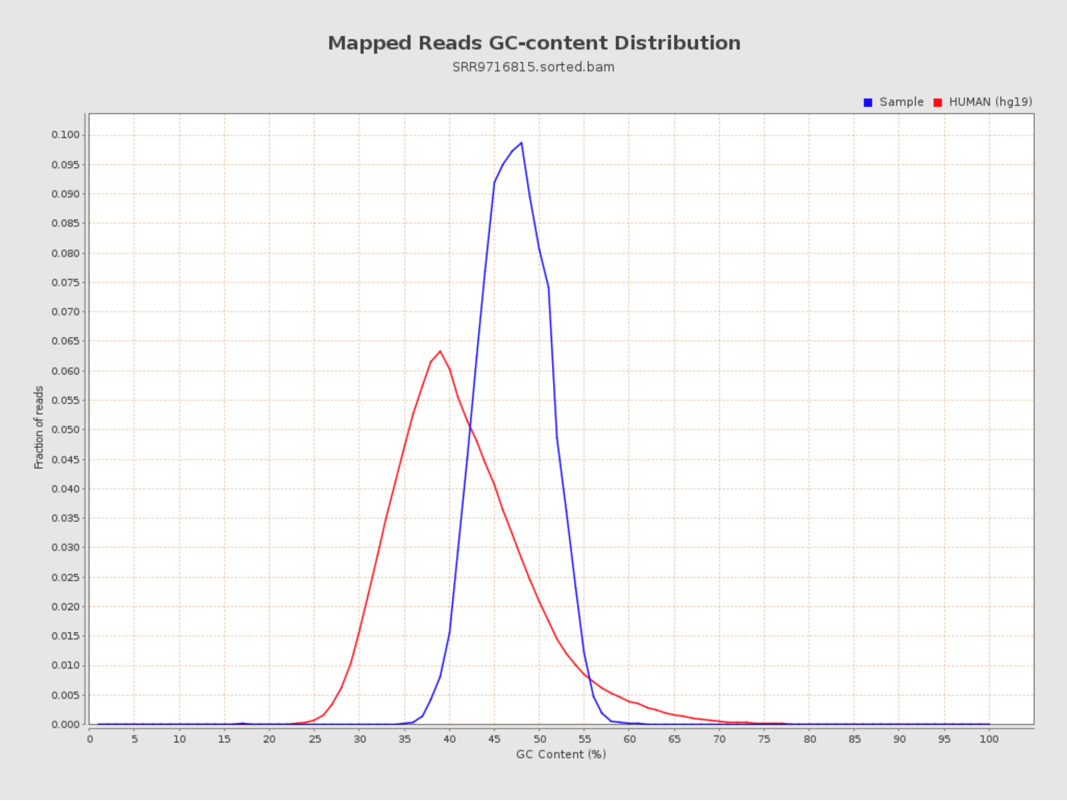
7. Results : Duplication Rate Histogram



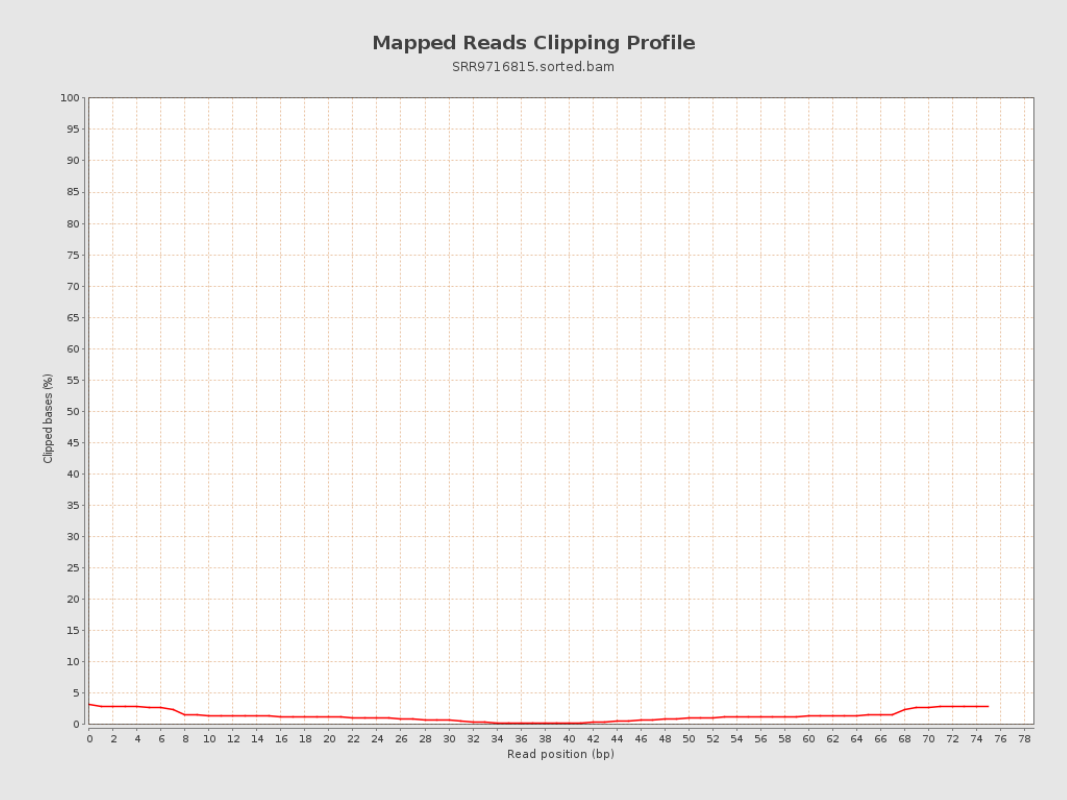
8. Results : Mapped Reads Nucleotide Content



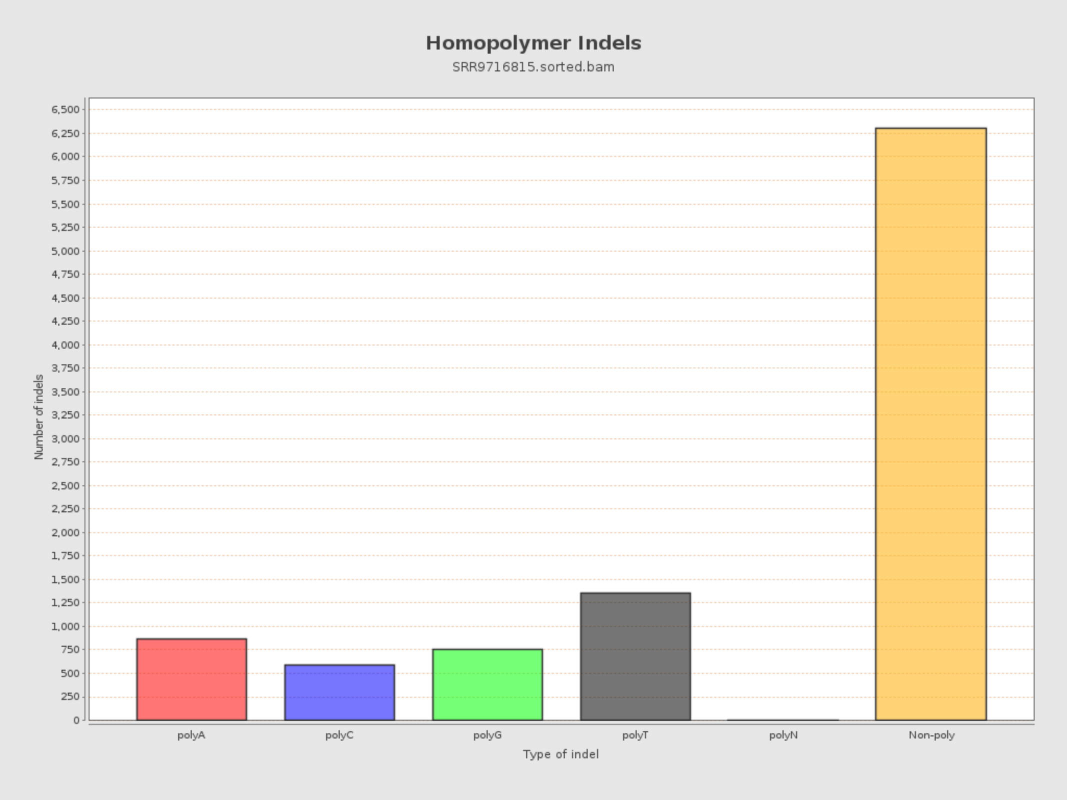
9. Results : Mapped Reads GC-content Distribution



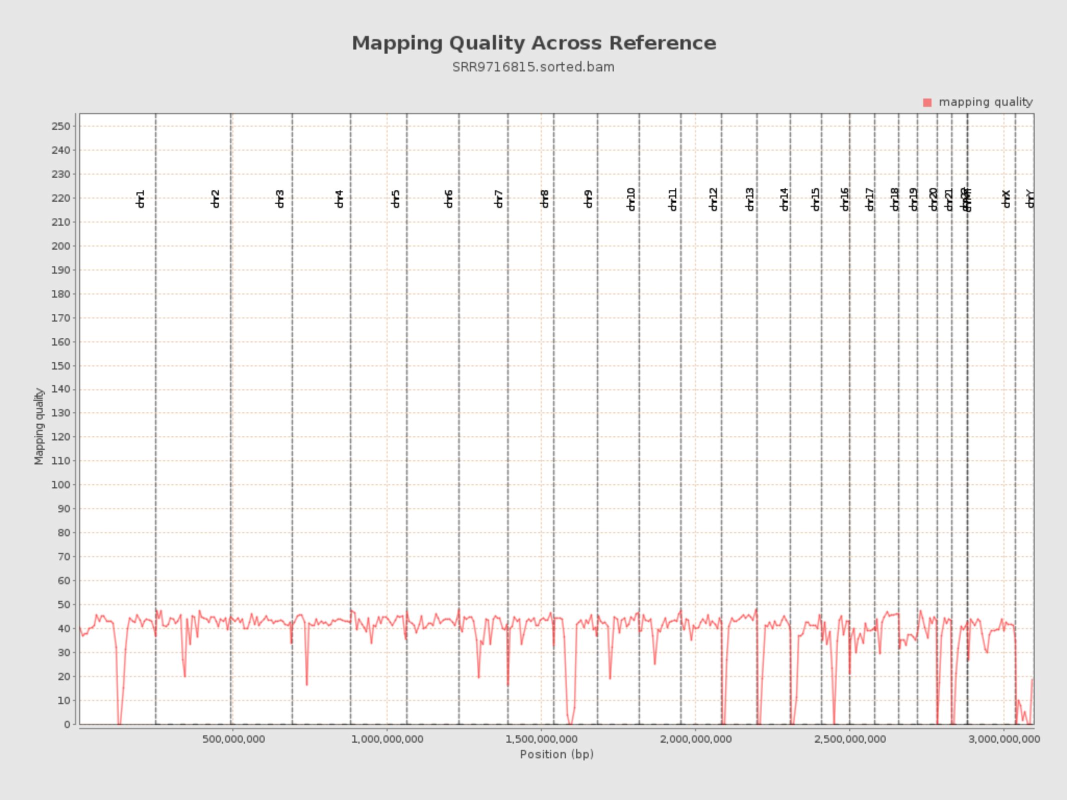
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram