Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:08:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716517.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_SRR9716517 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716517.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:08:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716517.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	952,131
Mapped reads	754,260 / 79.22%
Unmapped reads	197,871 / 20.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,861 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,414 / 1.51%
Duplication rate	1.35%
Clipped reads	755,490 / 79.35%

2.2. ACGT Content

Number/percentage of A's	9,592,221 / 23.16%
Number/percentage of C's	8,859,480 / 21.39%
Number/percentage of T's	12,776,883 / 30.85%
Number/percentage of G's	10,186,788 / 24.6%
Number/percentage of N's	1,131 / 0%
GC Percentage	45.99%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1397

2.4. Mapping Quality

Mean Mapping Quality	38.29

2.5. Mismatches and indels

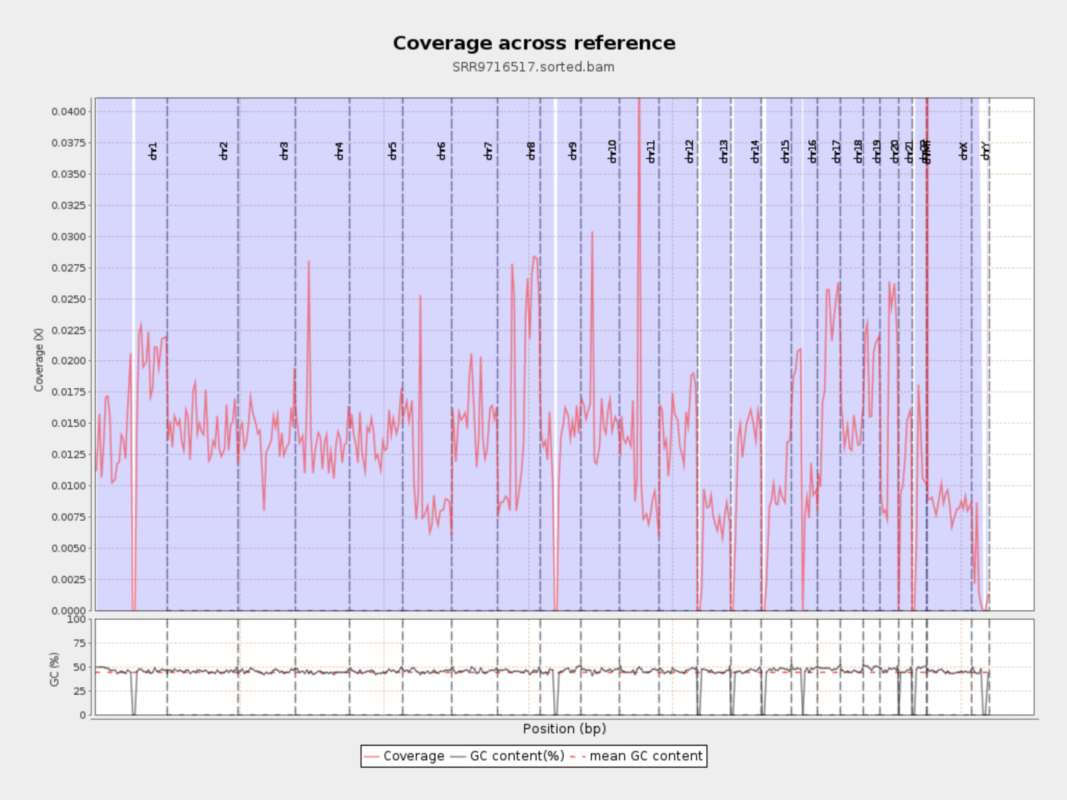
General error rate	0.57%
Mismatches	228,548
Insertions	3,141
Mapped reads with at least one insertion	0.41%
Deletions	7,089
Mapped reads with at least one deletion	0.93%
Homopolymer indels	34.96%

2.6. Chromosome stats

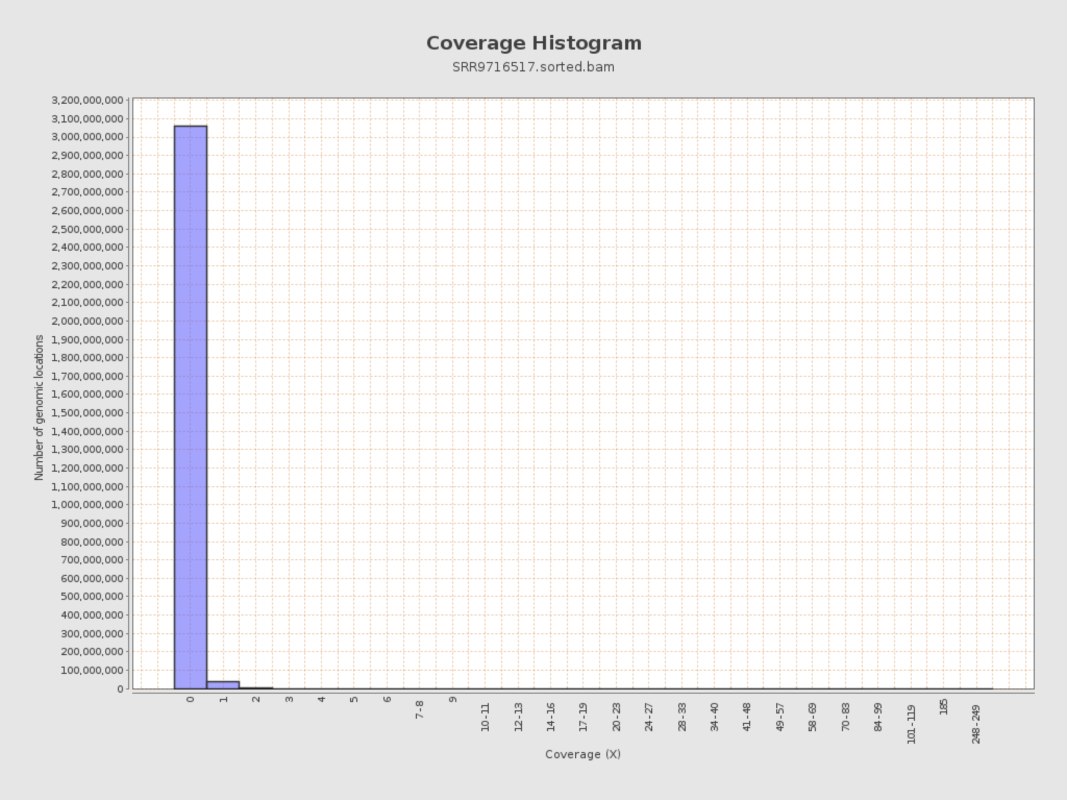
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3947716	0.0158	0.1601
chr2	243199373	3533469	0.0145	0.1748
chr3	198022430	2767491	0.014	0.1287
chr4	191154276	2673940	0.014	0.1394
chr5	180915260	2536450	0.014	0.1275
chr6	171115067	1804749	0.0105	0.1117
chr7	159138663	2449829	0.0154	0.1569

chr8	146364022	2506156	0.0171	0.147
chr9	141213431	1767864	0.0125	0.1276
chr10	135534747	2162036	0.016	0.1907
chr11	135006516	1731967	0.0128	0.1398
chr12	133851895	2016456	0.0151	0.1322
chr13	115169878	752285	0.0065	0.0868
chr14	107349540	1294471	0.0121	0.1194
chr15	102531392	824166	0.008	0.0963
chr16	90354753	1123927	0.0124	0.1279
chr17	81195210	1662119	0.0205	0.1589
chr18	78077248	1109180	0.0142	0.1503
chr19	59128983	1172660	0.0198	0.1708
chr20	63025520	1071993	0.017	0.1456
chr21	48129895	560746	0.0117	0.128
chr22	51304566	474730	0.0093	0.1041
chrMT	16571	22761	1.3735	1.6004
chrX	155270560	1324611	0.0085	0.1061
chrY	59373566	136635	0.0023	0.0778

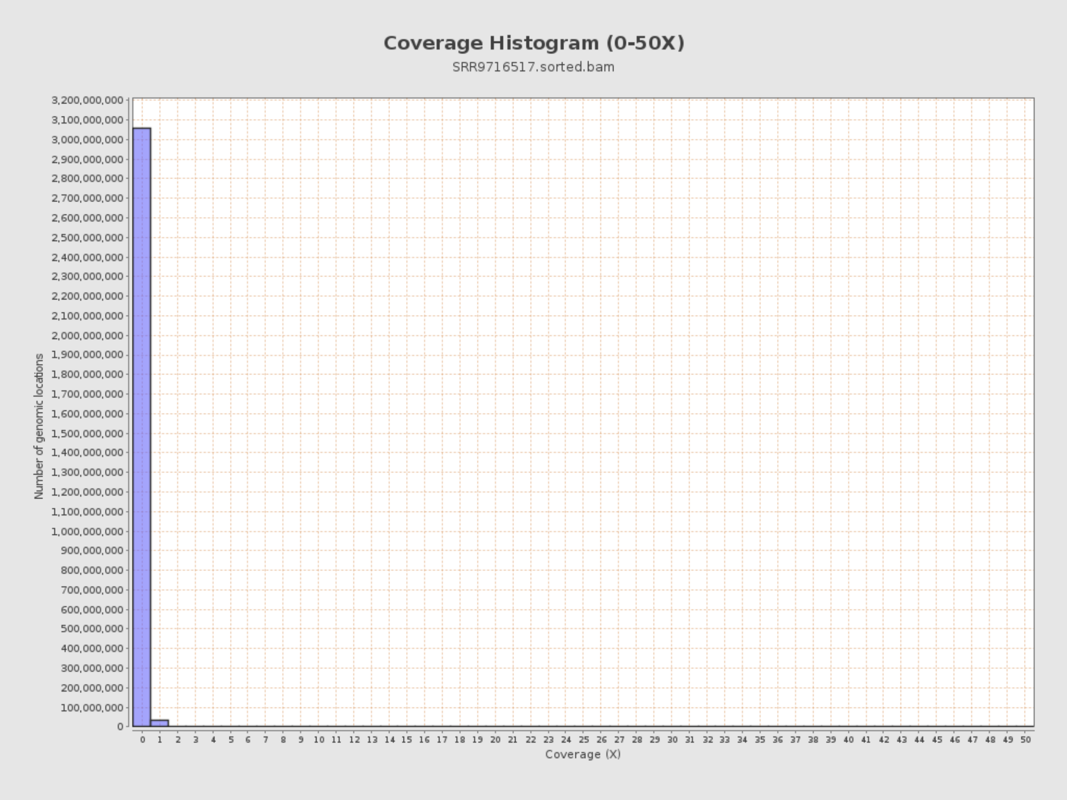
3. Results : Coverage across reference



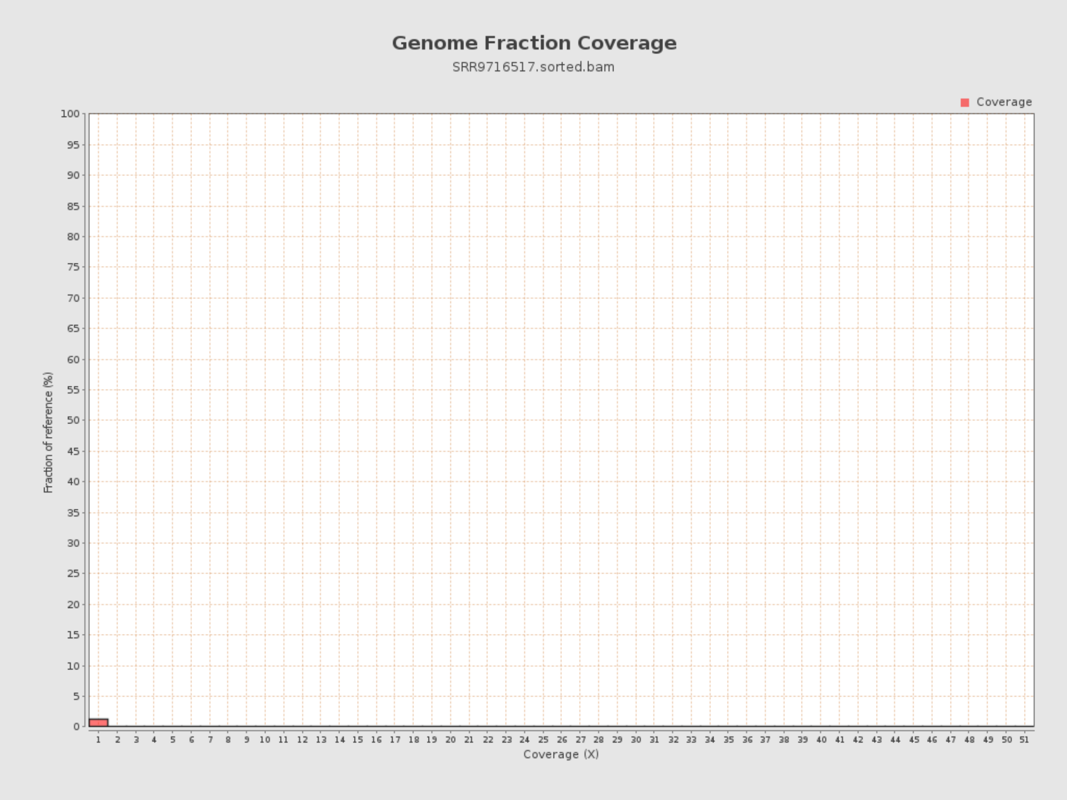
4. Results : Coverage Histogram



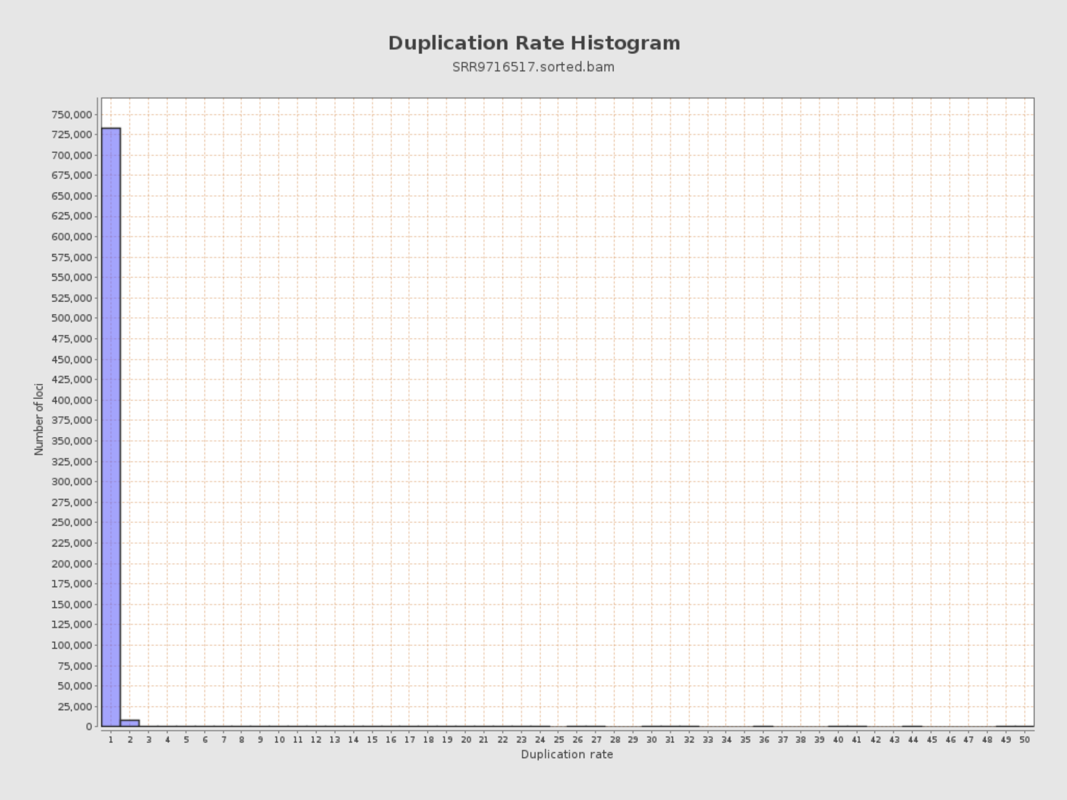
5. Results : Coverage Histogram (0-50X)



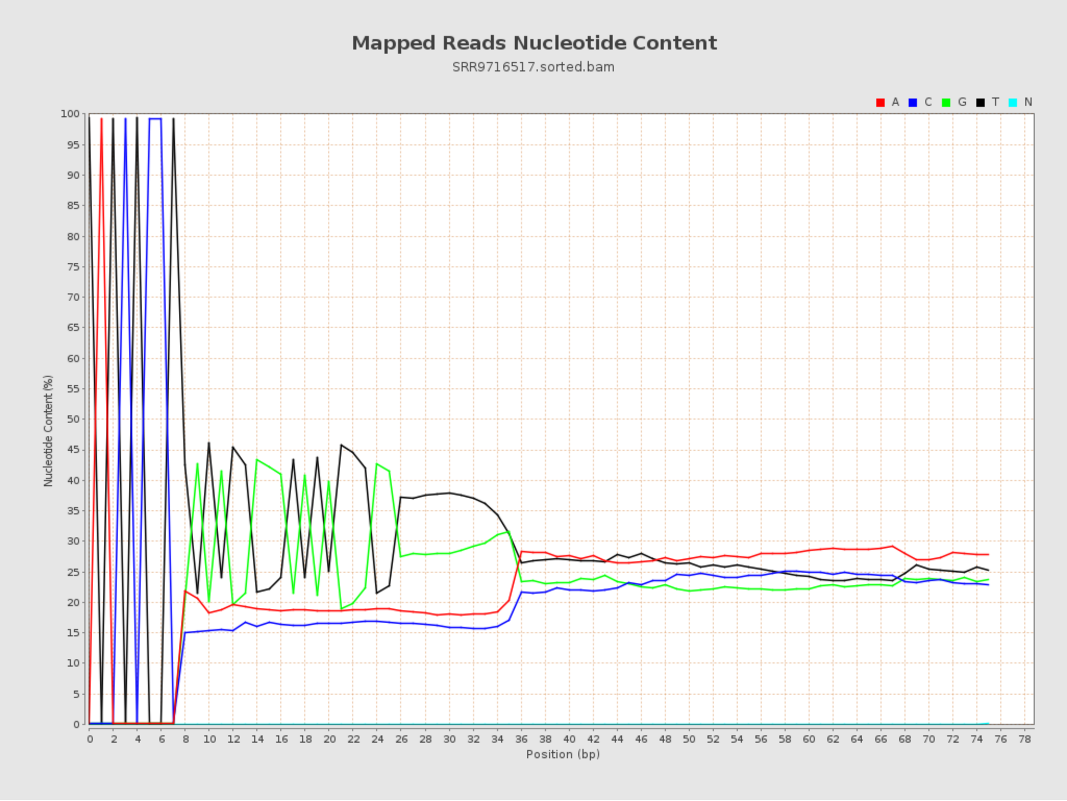
6. Results : Genome Fraction Coverage



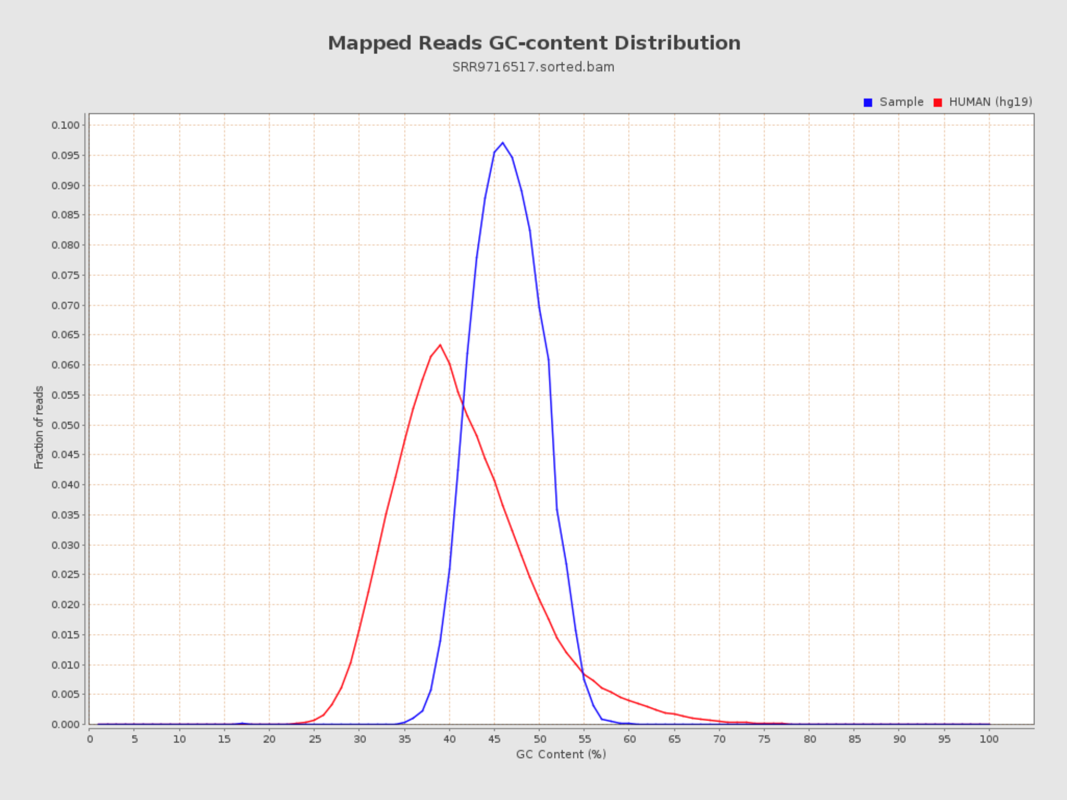
7. Results : Duplication Rate Histogram



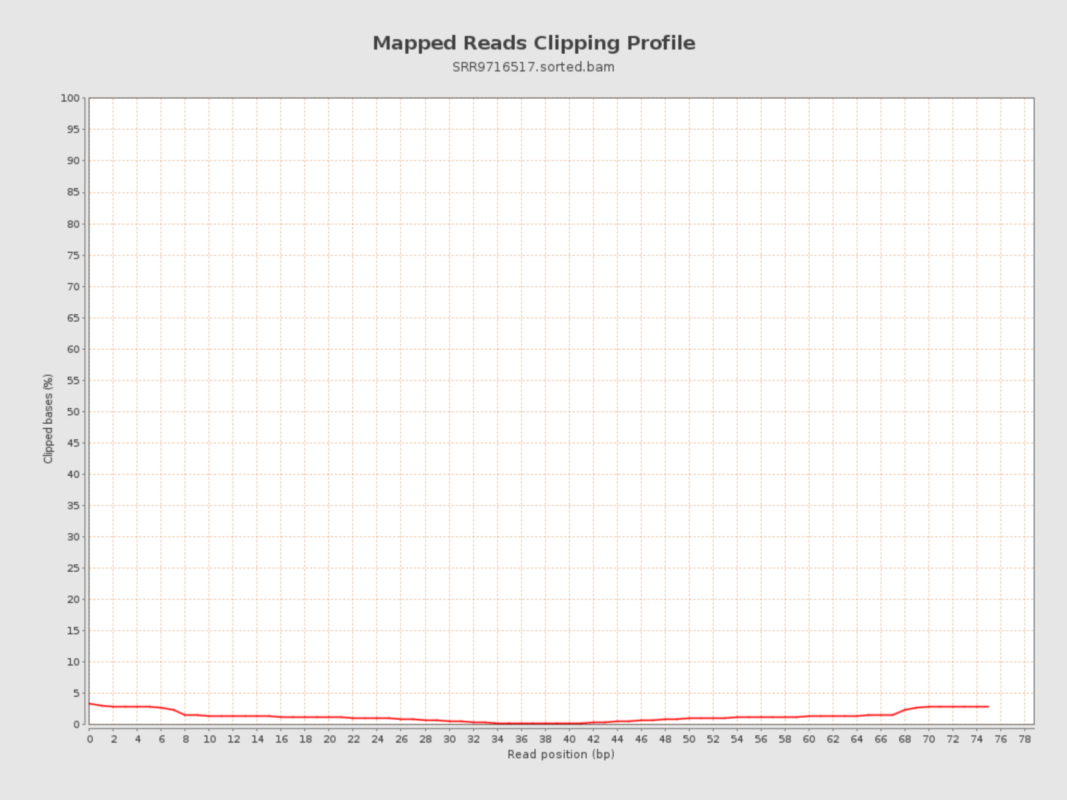
8. Results : Mapped Reads Nucleotide Content



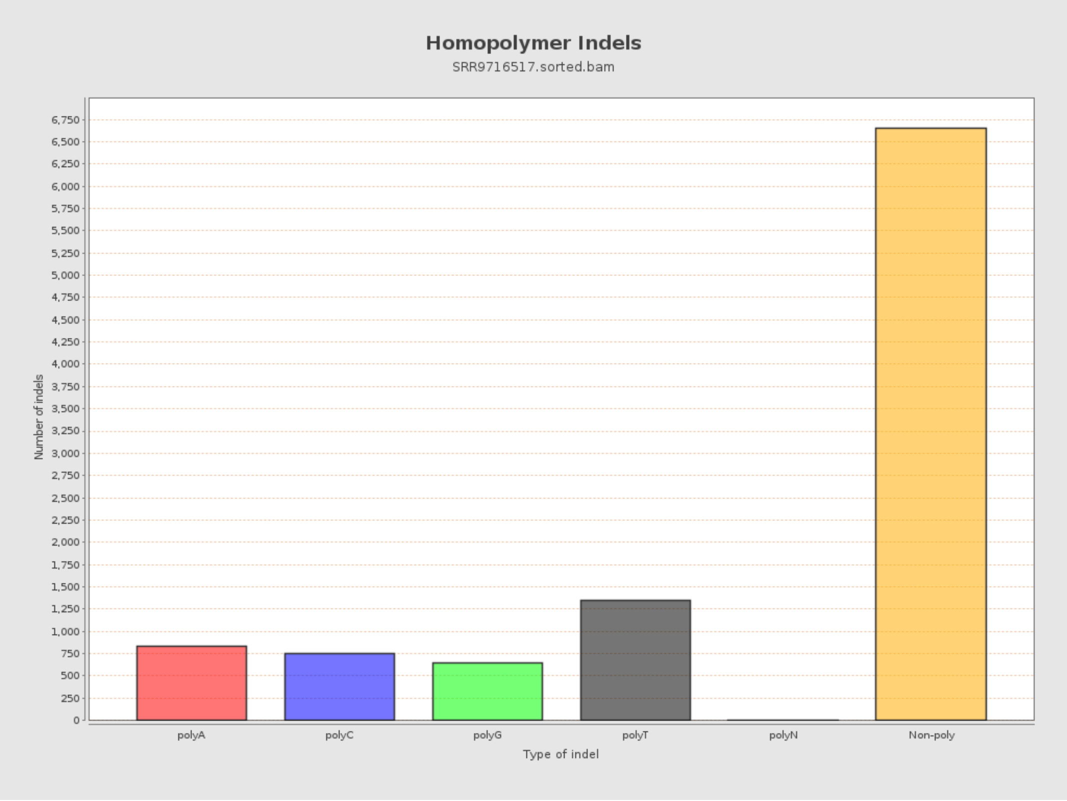
9. Results : Mapped Reads GC-content Distribution



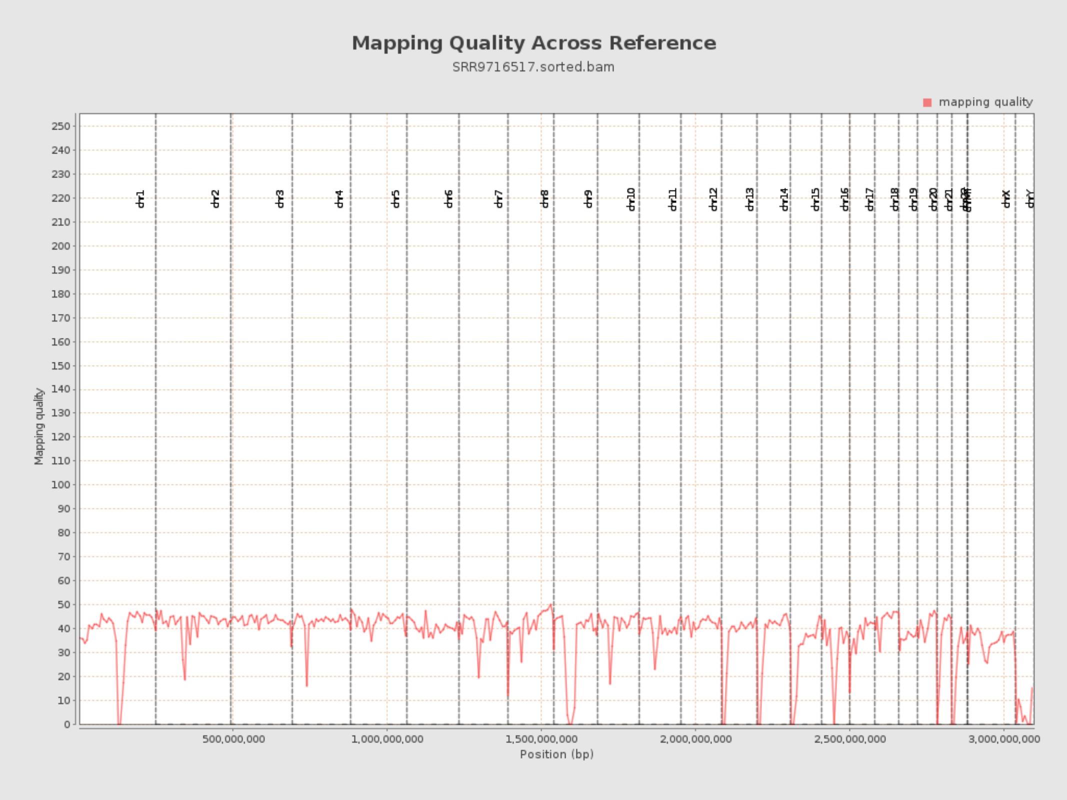
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram