Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:28:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716914.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_SRR9716914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716914.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:28:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	534,352
Mapped reads	478,326 / 89.52%
Unmapped reads	56,026 / 10.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,222 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	10,038 / 1.88%
Duplication rate	1.68%
Clipped reads	478,359 / 89.52%

2.2. ACGT Content

Number/percentage of A's	6,922,033 / 25.29%
Number/percentage of C's	4,968,208 / 18.15%
Number/percentage of T's	9,011,080 / 32.92%
Number/percentage of G's	6,471,444 / 23.64%
Number/percentage of N's	276 / 0%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1105

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

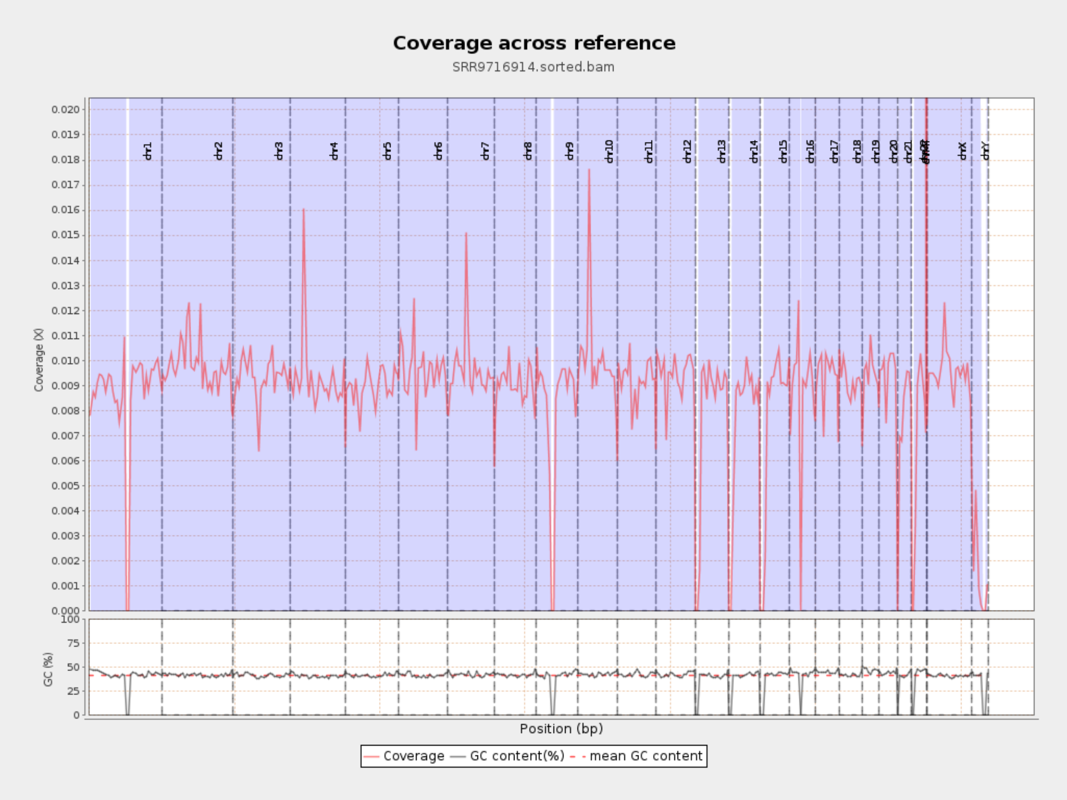
General error rate	0.52%
Mismatches	138,656
Insertions	1,949
Mapped reads with at least one insertion	0.41%
Deletions	5,732
Mapped reads with at least one deletion	1.19%
Homopolymer indels	42.48%

2.6. Chromosome stats

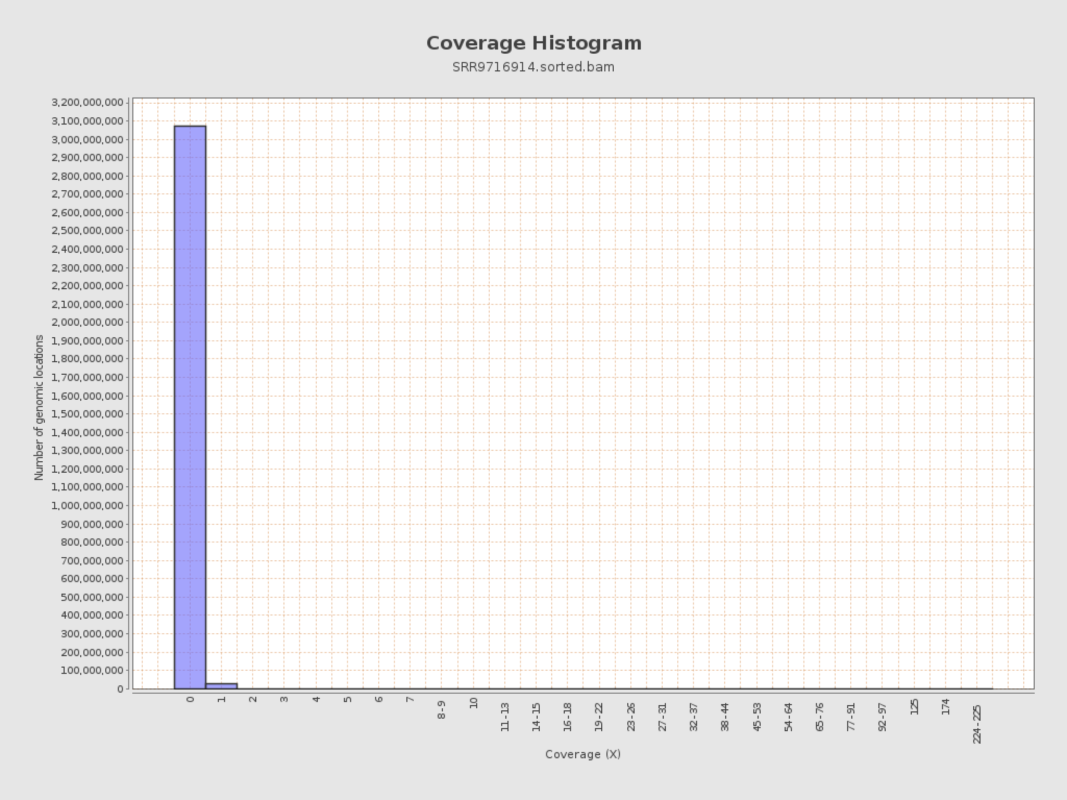
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2140265	0.0086	0.1224
chr2	243199373	2397691	0.0099	0.1418
chr3	198022430	1842149	0.0093	0.1002
chr4	191154276	1773615	0.0093	0.1042
chr5	180915260	1624460	0.009	0.0982
chr6	171115067	1641667	0.0096	0.1089
chr7	159138663	1544439	0.0097	0.1366

chr8	146364022	1319207	0.009	0.1146
chr9	141213431	1117813	0.0079	0.0996
chr10	135534747	1372297	0.0101	0.1224
chr11	135006516	1234521	0.0091	0.1079
chr12	133851895	1262769	0.0094	0.1008
chr13	115169878	881390	0.0077	0.0906
chr14	107349540	799784	0.0075	0.09
chr15	102531392	765474	0.0075	0.0899
chr16	90354753	782903	0.0087	0.1019
chr17	81195210	757887	0.0093	0.1022
chr18	78077248	719107	0.0092	0.1408
chr19	59128983	560764	0.0095	0.1162
chr20	63025520	594059	0.0094	0.1017
chr21	48129895	360995	0.0075	0.0937
chr22	51304566	325629	0.0063	0.0824
chrMT	16571	5227	0.3154	0.5875
chrX	155270560	1475770	0.0095	0.1049
chrY	59373566	82211	0.0014	0.0505

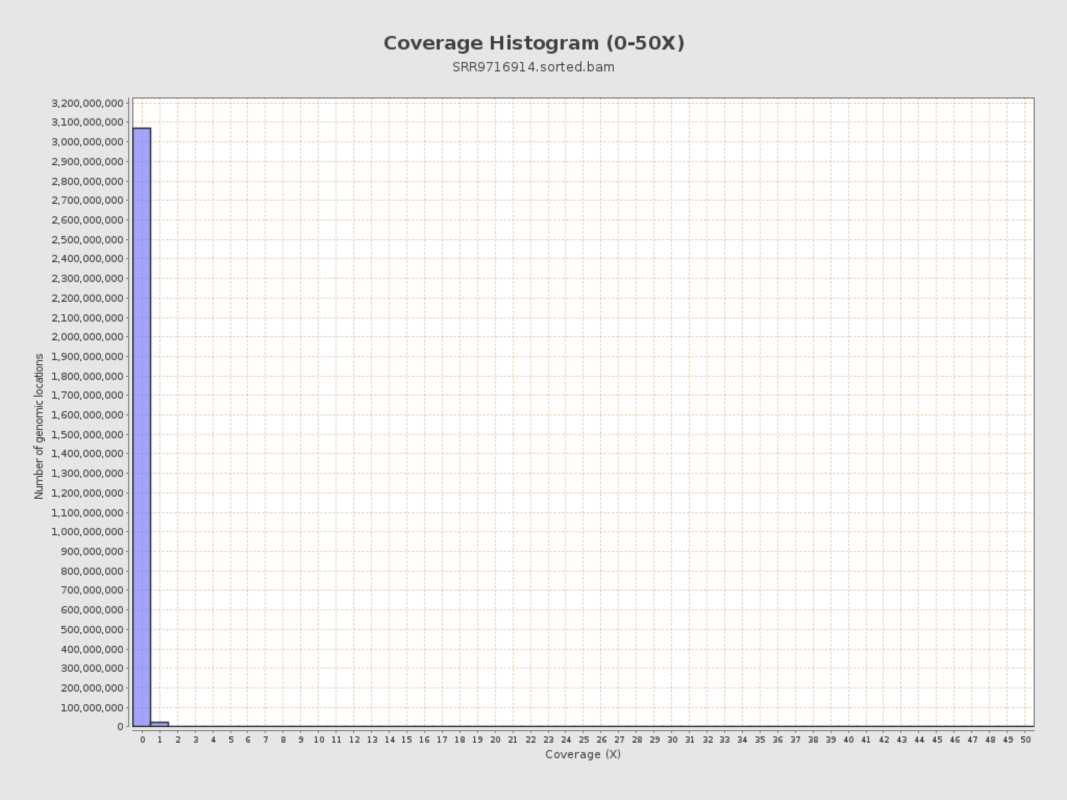
3. Results : Coverage across reference



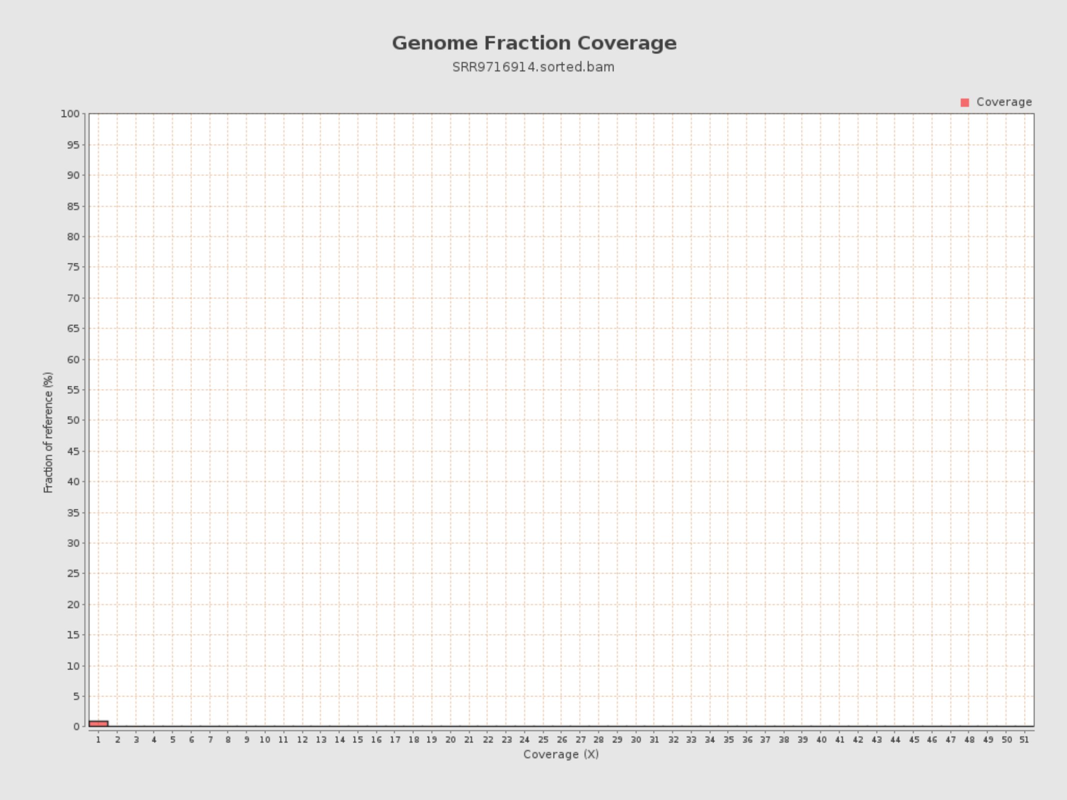
4. Results : Coverage Histogram



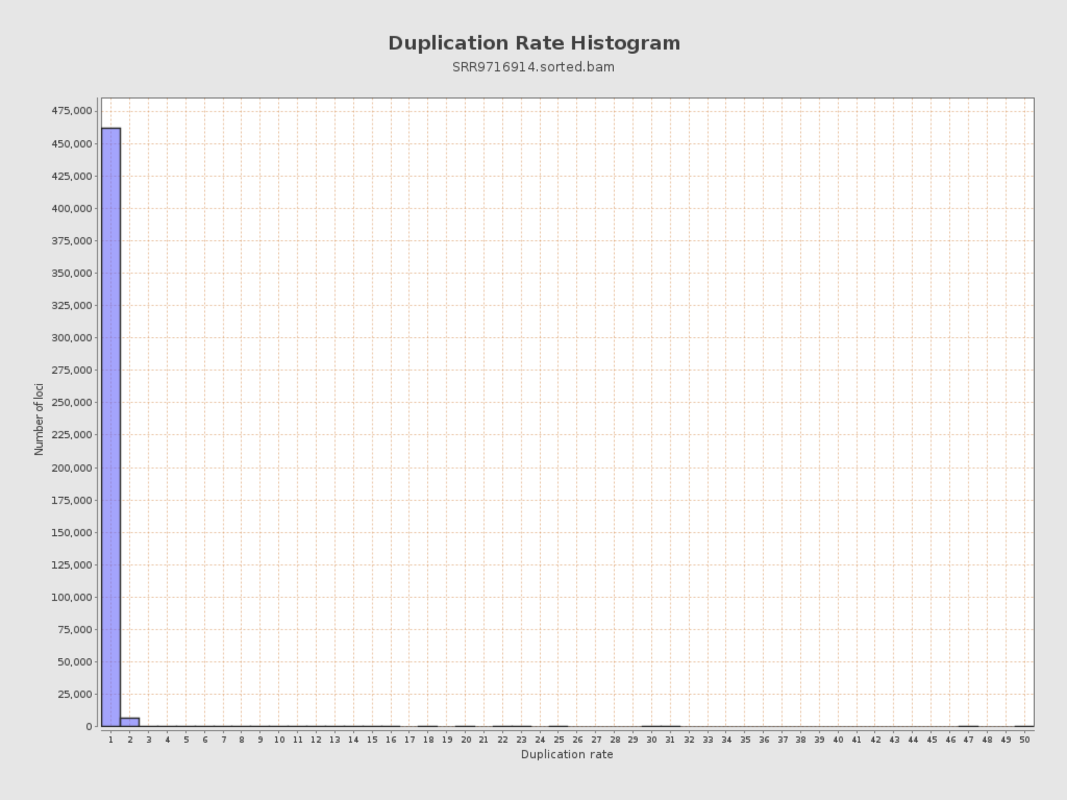
5. Results : Coverage Histogram (0-50X)



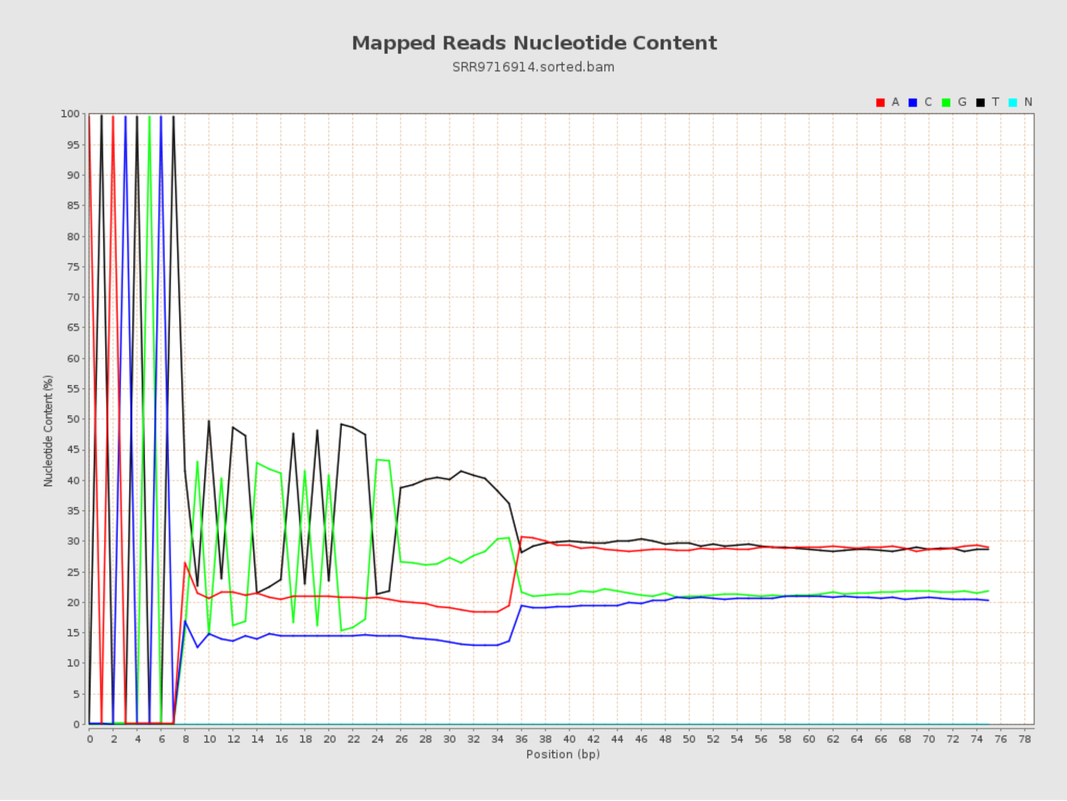
6. Results : Genome Fraction Coverage



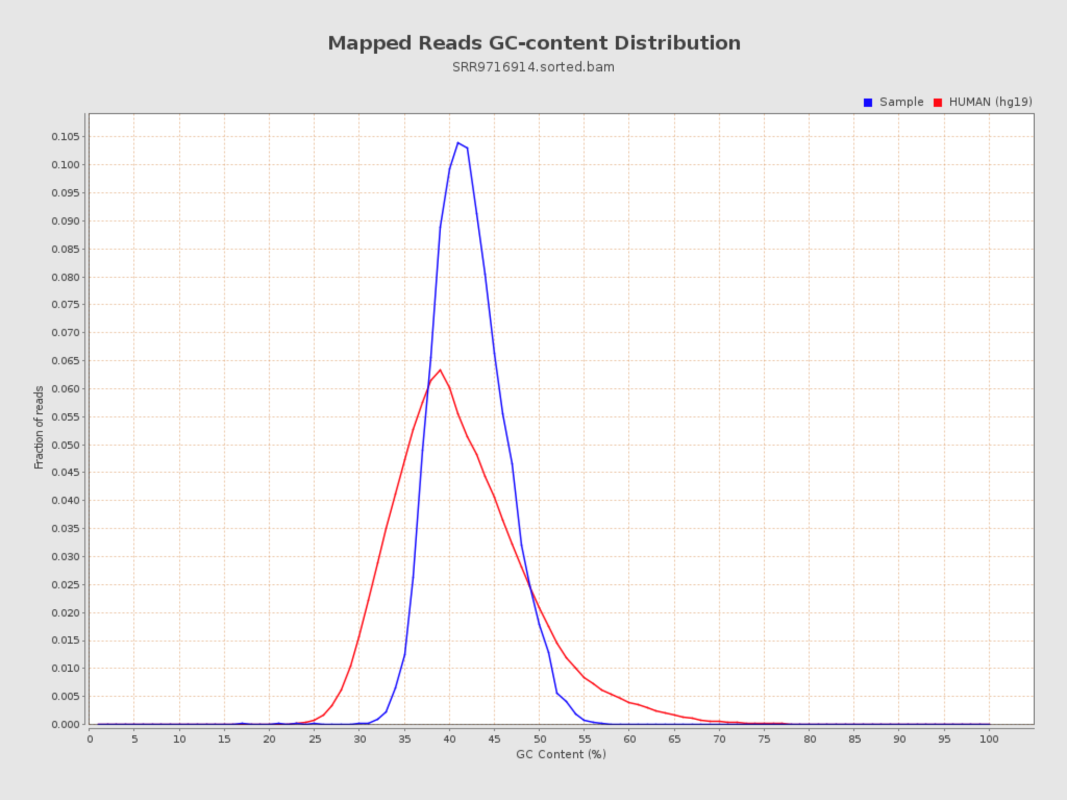
7. Results : Duplication Rate Histogram



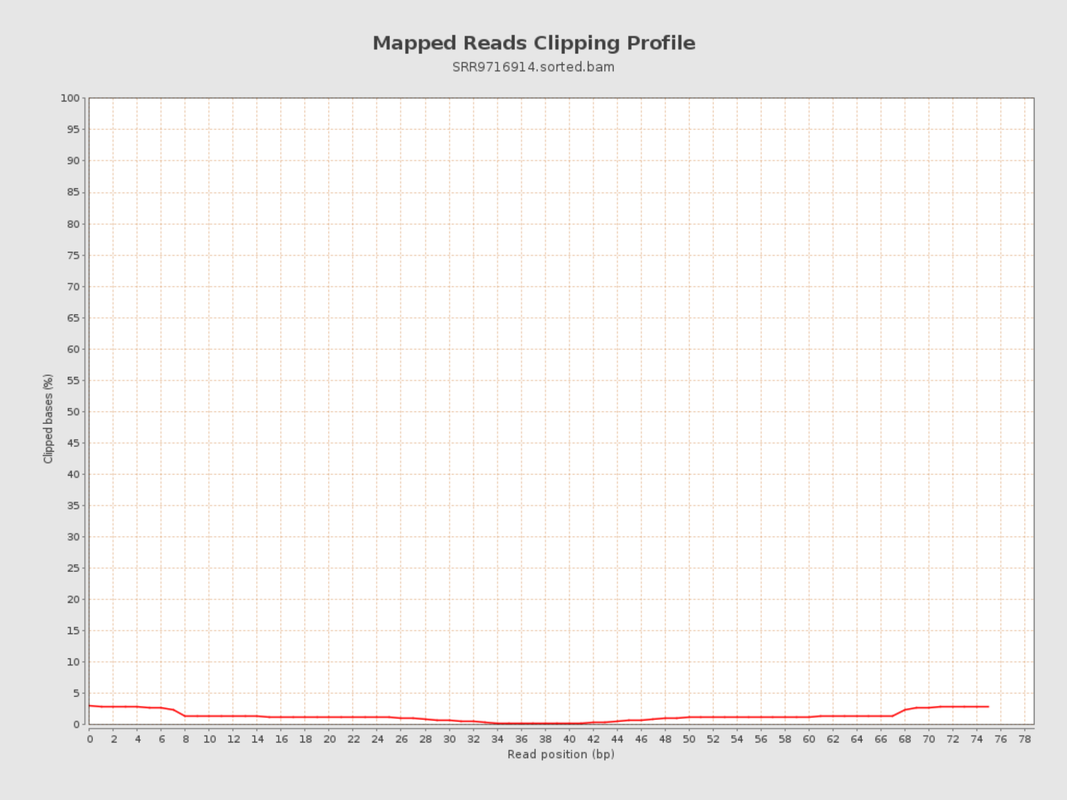
8. Results : Mapped Reads Nucleotide Content



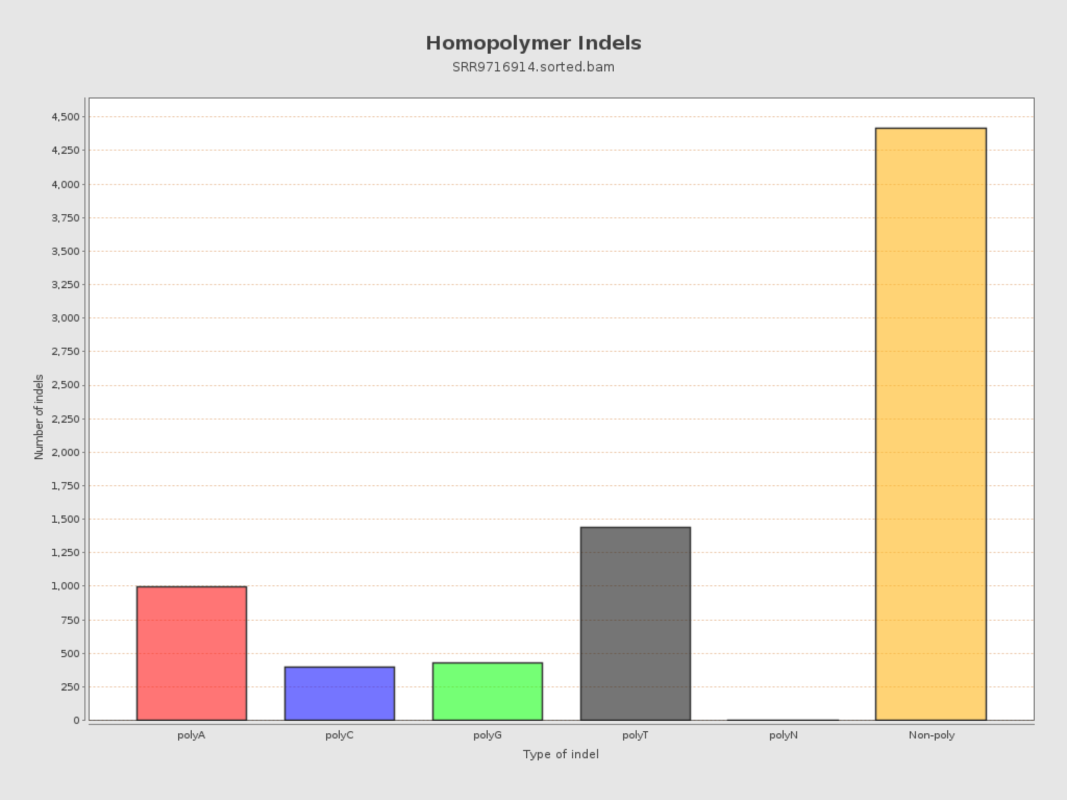
9. Results : Mapped Reads GC-content Distribution



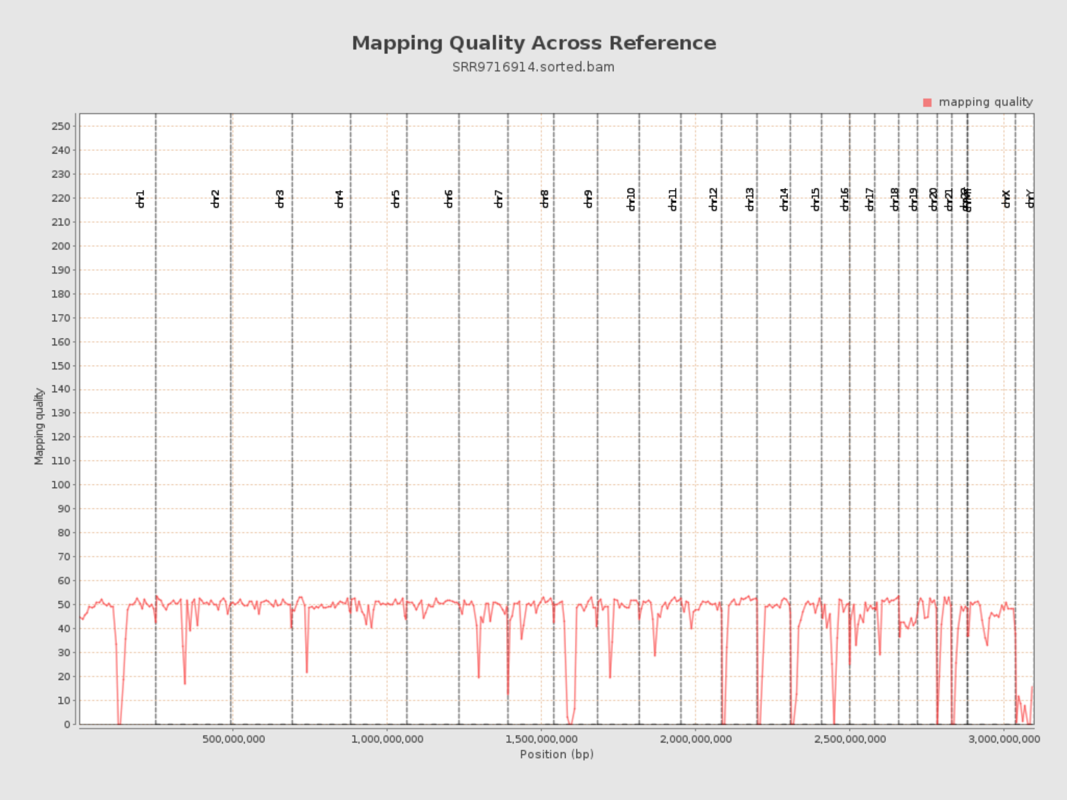
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram