Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:27:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716592.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_SRR9716592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716592.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:27:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	931,732
Mapped reads	701,650 / 75.31%
Unmapped reads	230,082 / 24.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,650 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	17,412 / 1.87%
Duplication rate	1.95%
Clipped reads	703,517 / 75.51%

2.2. ACGT Content

Number/percentage of A's	10,440,547 / 25.75%
Number/percentage of C's	7,761,484 / 19.15%
Number/percentage of T's	12,833,102 / 31.66%
Number/percentage of G's	9,504,473 / 23.44%
Number/percentage of N's	583 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1451

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

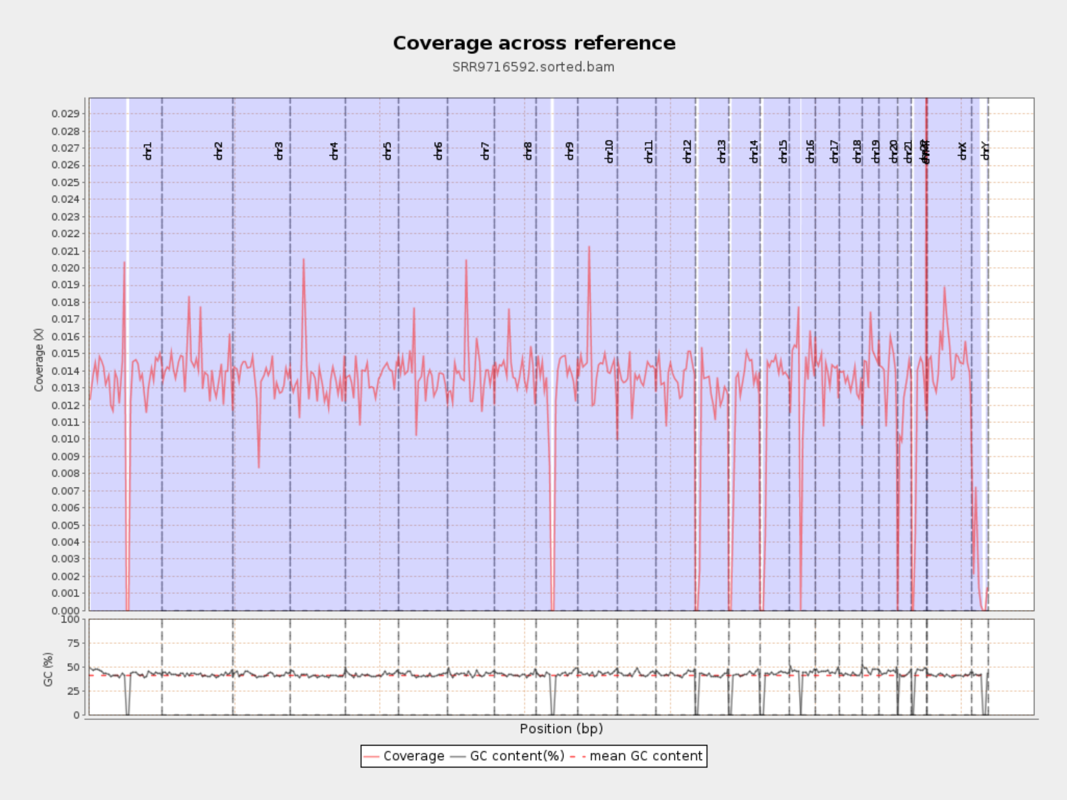
General error rate	0.51%
Mismatches	201,750
Insertions	3,150
Mapped reads with at least one insertion	0.45%
Deletions	7,319
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.99%

2.6. Chromosome stats

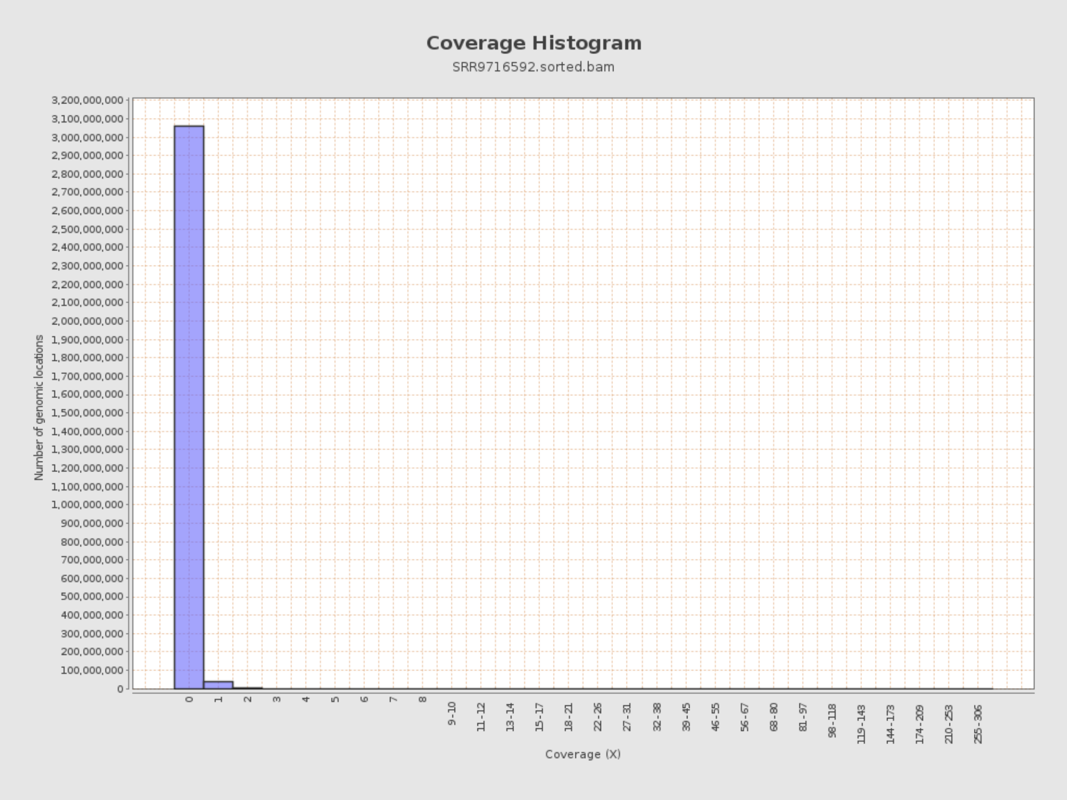
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3235289	0.013	0.2201
chr2	243199373	3449949	0.0142	0.1797
chr3	198022430	2676058	0.0135	0.1222
chr4	191154276	2580284	0.0135	0.1276
chr5	180915260	2453038	0.0136	0.1227
chr6	171115067	2356308	0.0138	0.1331
chr7	159138663	2213359	0.0139	0.1639

chr8	146364022	2062382	0.0141	0.1395
chr9	141213431	1700917	0.012	0.1289
chr10	135534747	1947549	0.0144	0.1449
chr11	135006516	1838491	0.0136	0.1377
chr12	133851895	1835670	0.0137	0.1242
chr13	115169878	1247878	0.0108	0.1092
chr14	107349540	1228433	0.0114	0.1167
chr15	102531392	1176374	0.0115	0.1136
chr16	90354753	1199229	0.0133	0.1251
chr17	81195210	1121297	0.0138	0.1272
chr18	78077248	1048459	0.0134	0.1826
chr19	59128983	869724	0.0147	0.1714
chr20	63025520	873808	0.0139	0.1254
chr21	48129895	536509	0.0111	0.116
chr22	51304566	492702	0.0096	0.1031
chrMT	16571	1367	0.0825	0.3349
chrX	155270560	2282288	0.0147	0.1345
chrY	59373566	124325	0.0021	0.0635

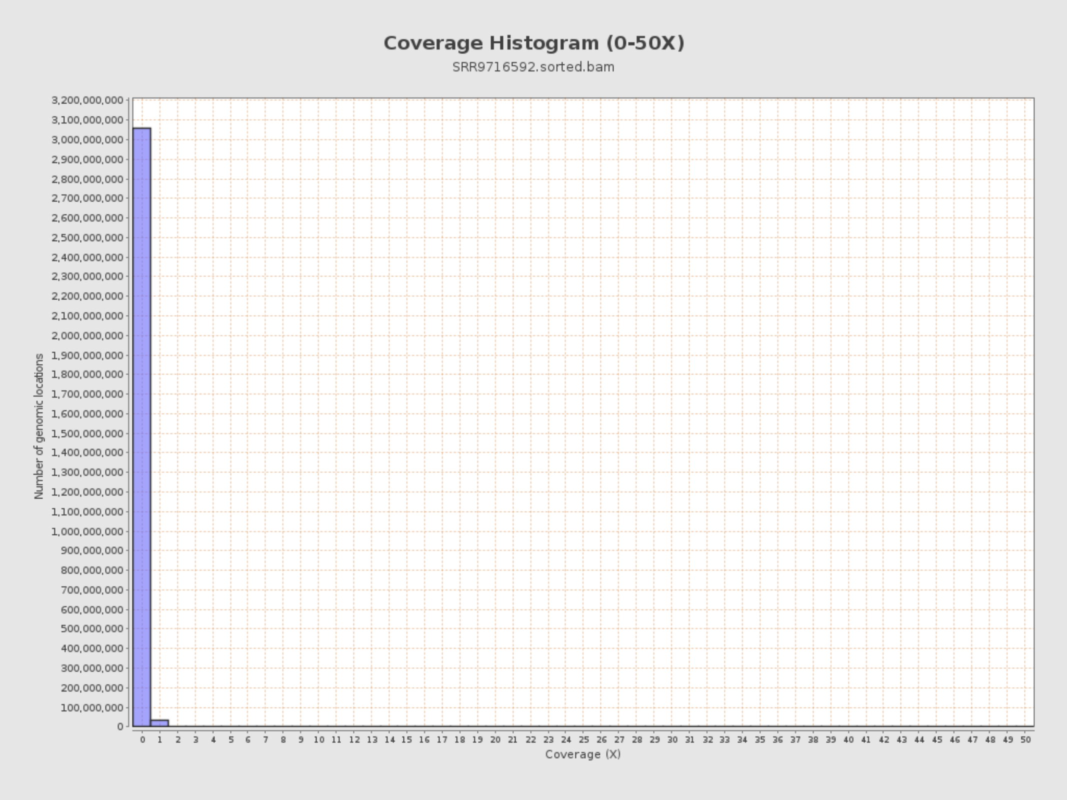
3. Results : Coverage across reference



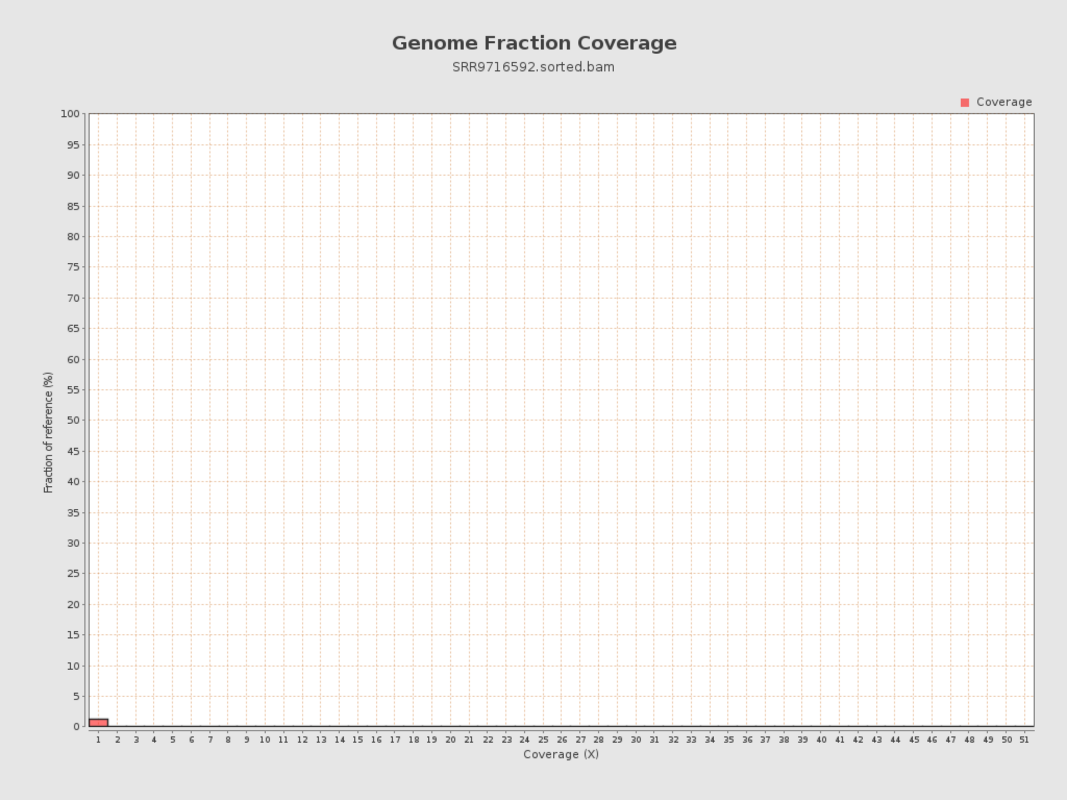
4. Results : Coverage Histogram



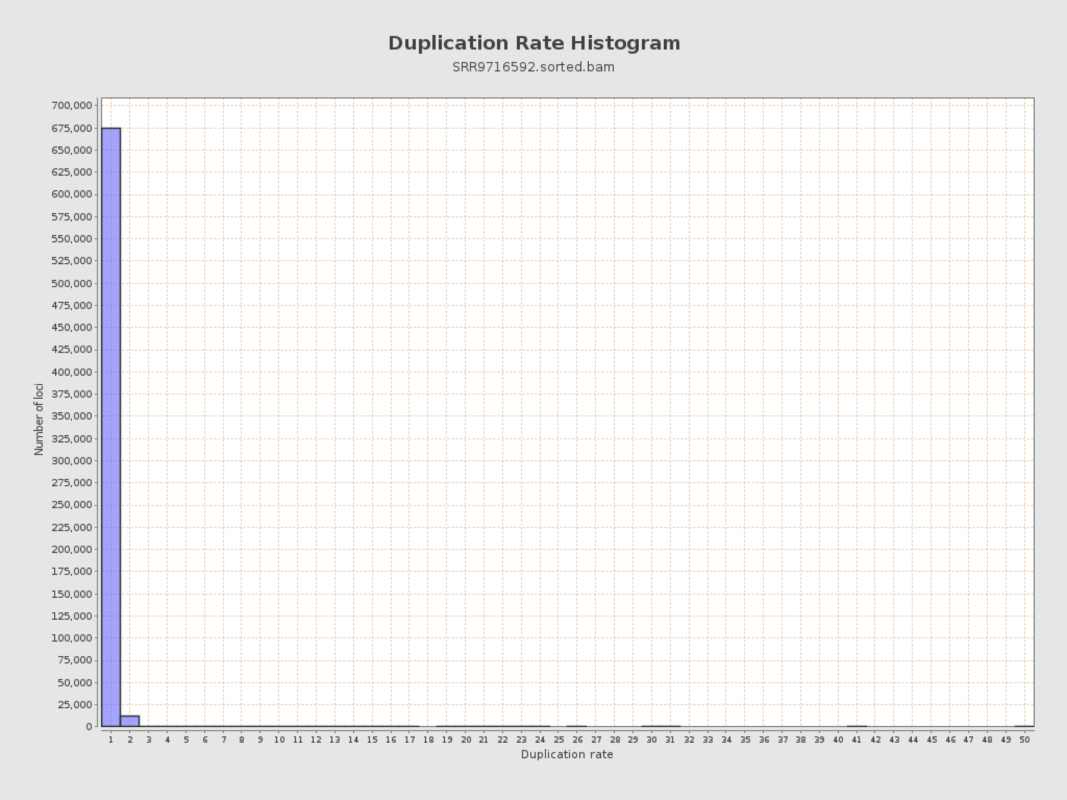
5. Results : Coverage Histogram (0-50X)



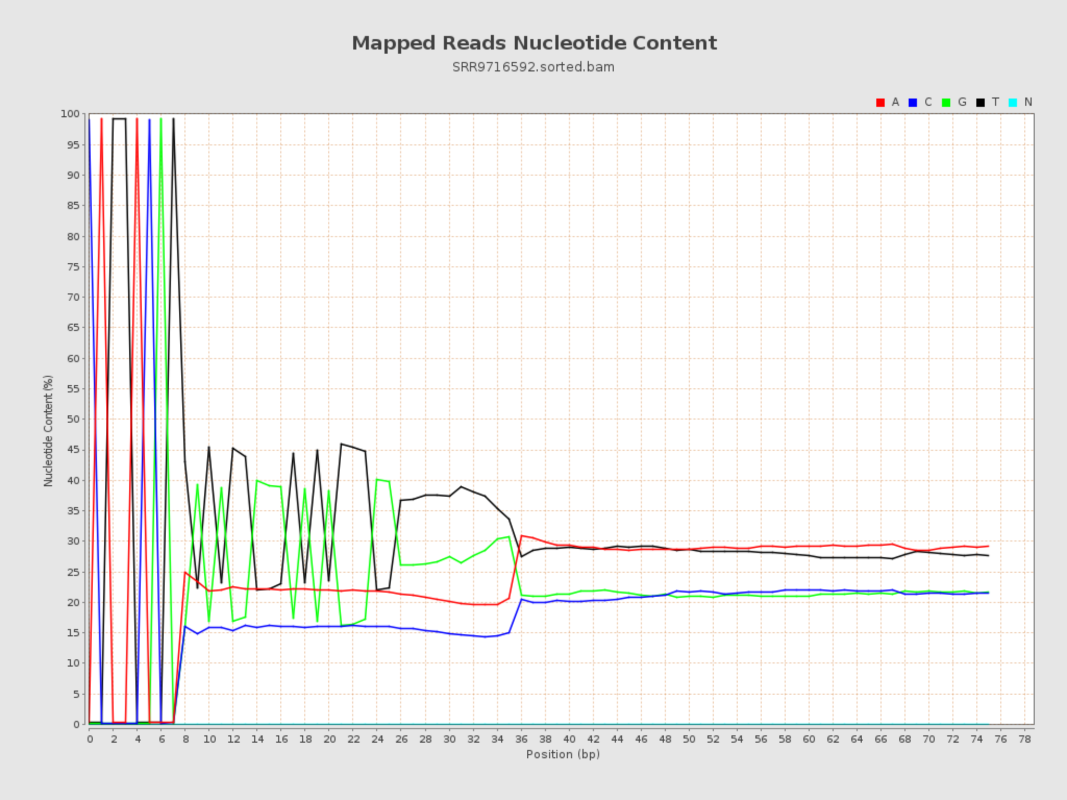
6. Results : Genome Fraction Coverage



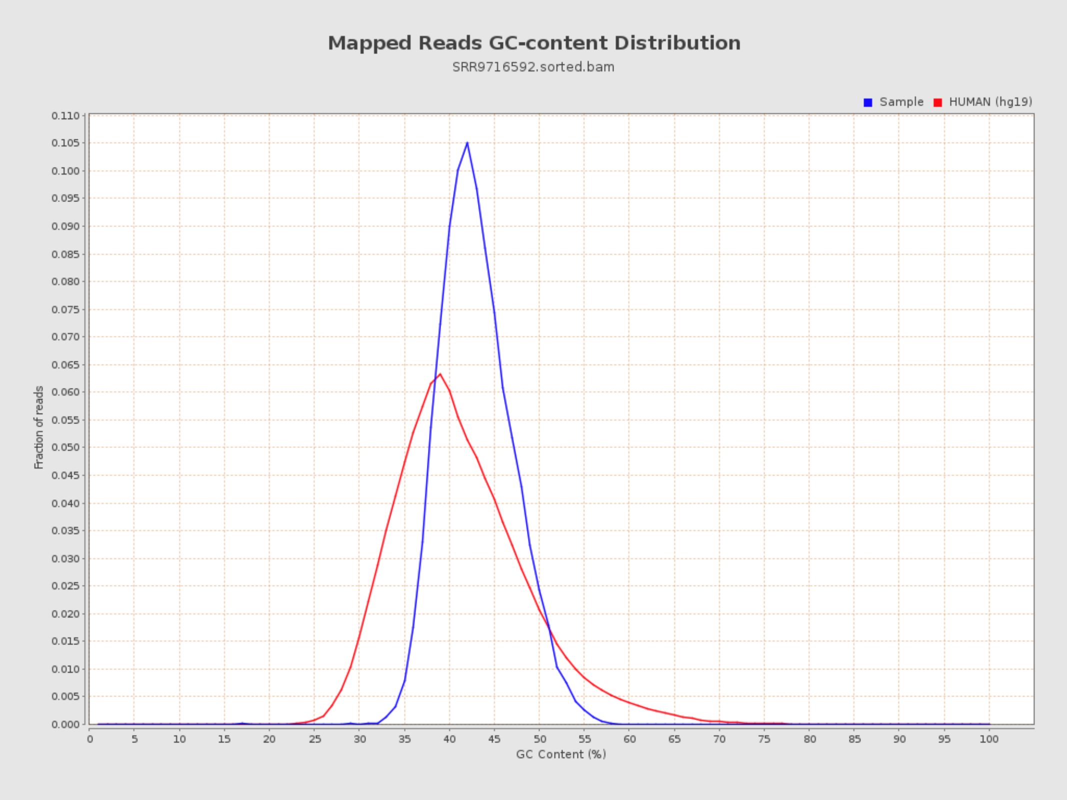
7. Results : Duplication Rate Histogram



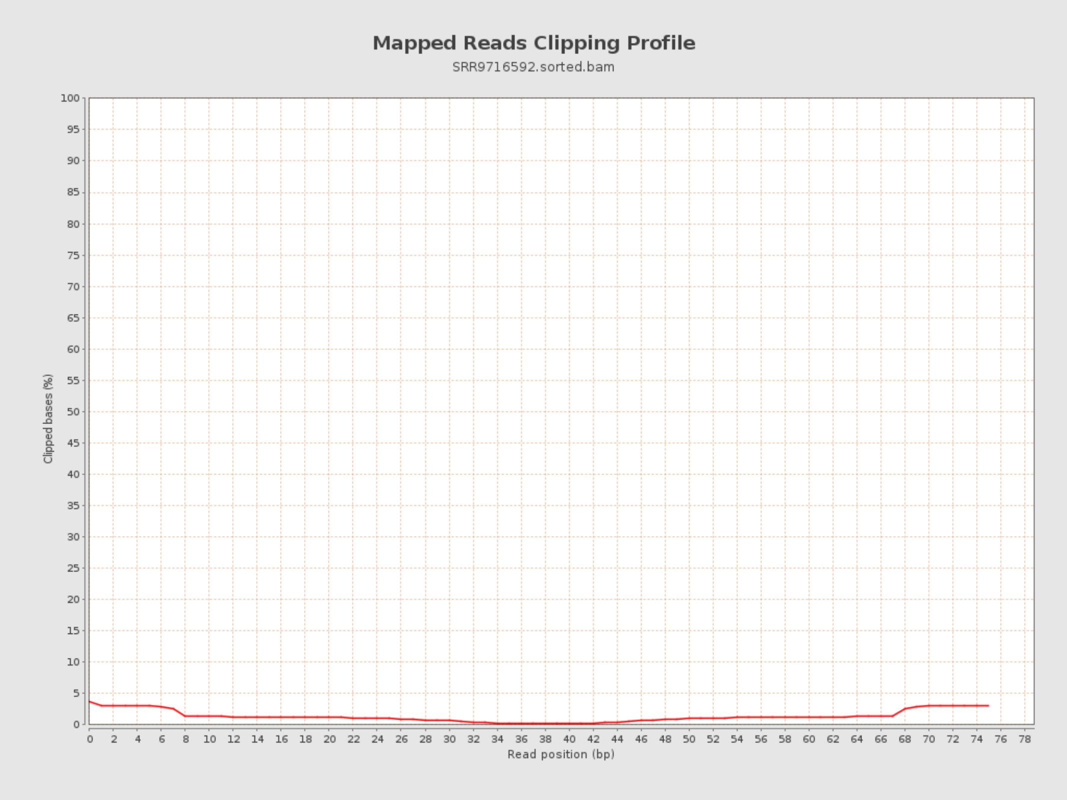
8. Results : Mapped Reads Nucleotide Content



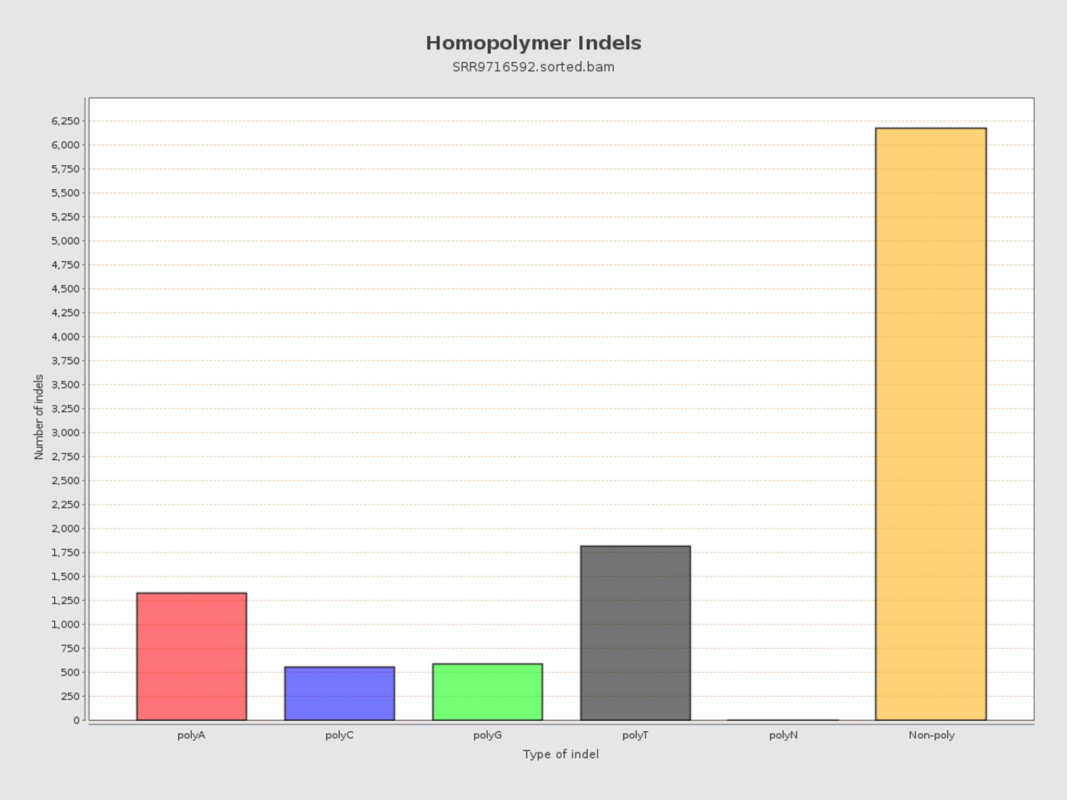
9. Results : Mapped Reads GC-content Distribution



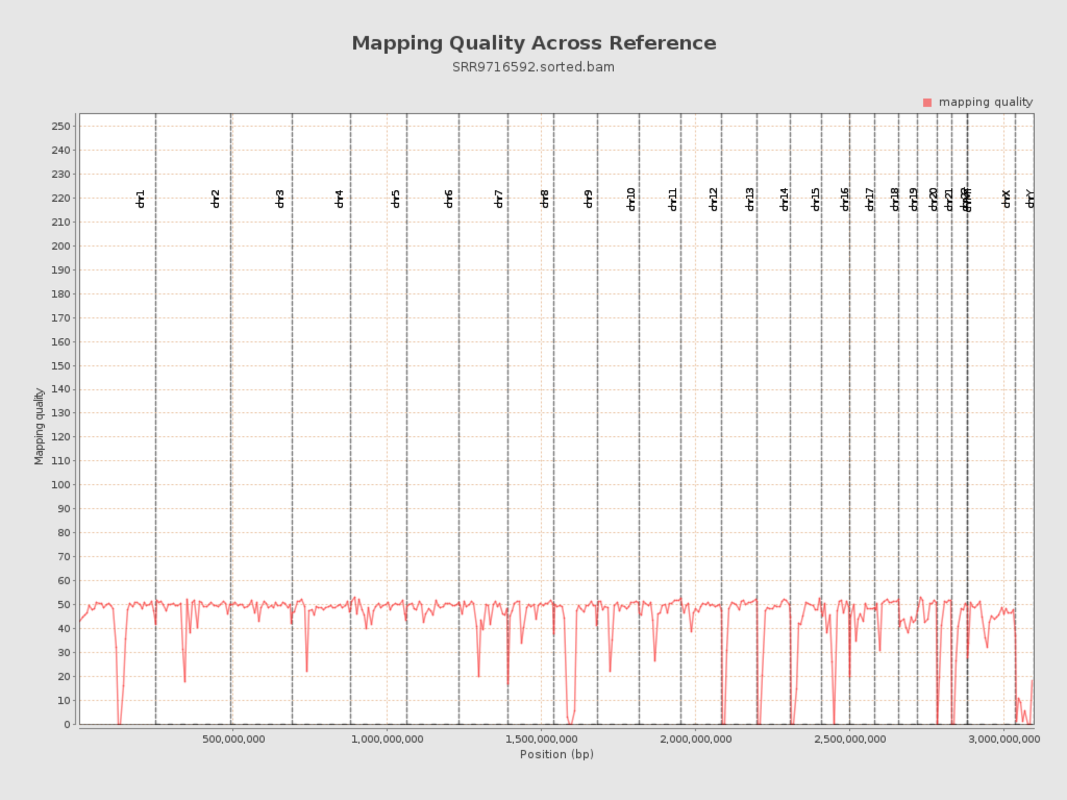
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram