Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716522.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_SRR9716522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716522.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:24:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	871,726
Mapped reads	717,961 / 82.36%
Unmapped reads	153,765 / 17.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,050 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	13,408 / 1.54%
Duplication rate	1.34%
Clipped reads	719,876 / 82.58%

2.2. ACGT Content

Number/percentage of A's	9,001,354 / 22.85%
Number/percentage of C's	8,087,847 / 20.53%
Number/percentage of T's	11,418,945 / 28.98%
Number/percentage of G's	10,889,623 / 27.64%
Number/percentage of N's	1,020 / 0%
GC Percentage	48.17%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1349

2.4. Mapping Quality

Mean Mapping Quality	38.19

2.5. Mismatches and indels

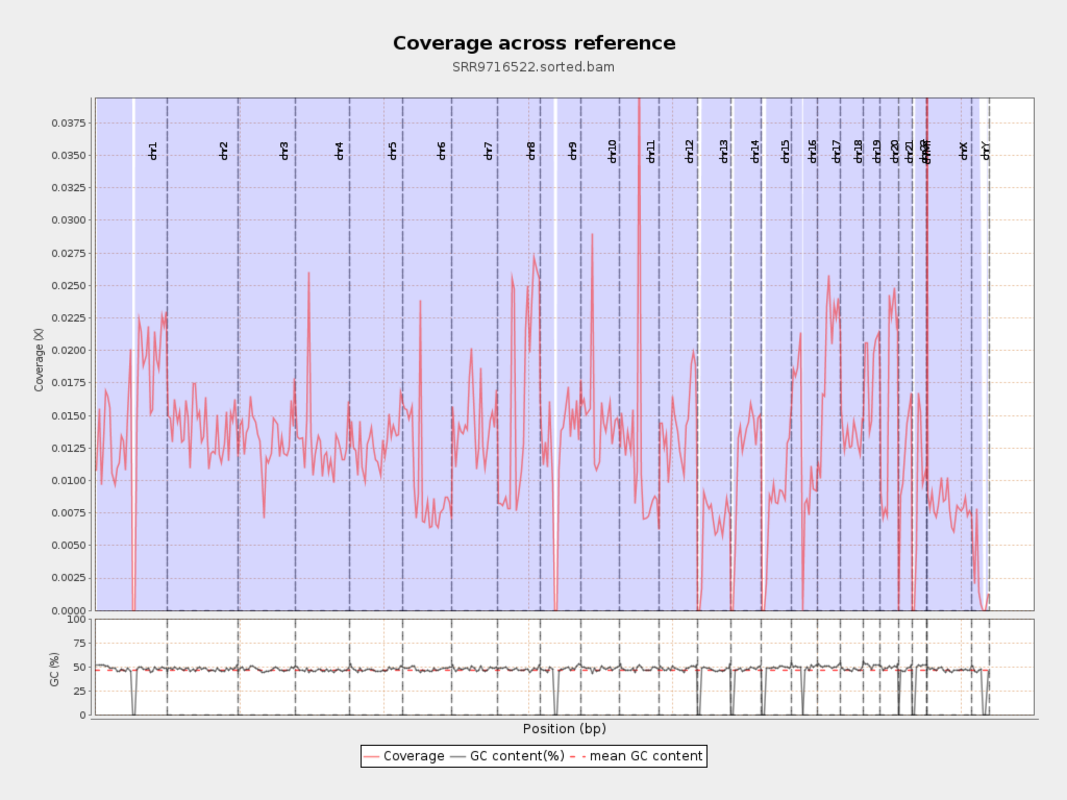
General error rate	0.56%
Mismatches	213,018
Insertions	3,024
Mapped reads with at least one insertion	0.42%
Deletions	6,568
Mapped reads with at least one deletion	0.91%
Homopolymer indels	33.27%

2.6. Chromosome stats

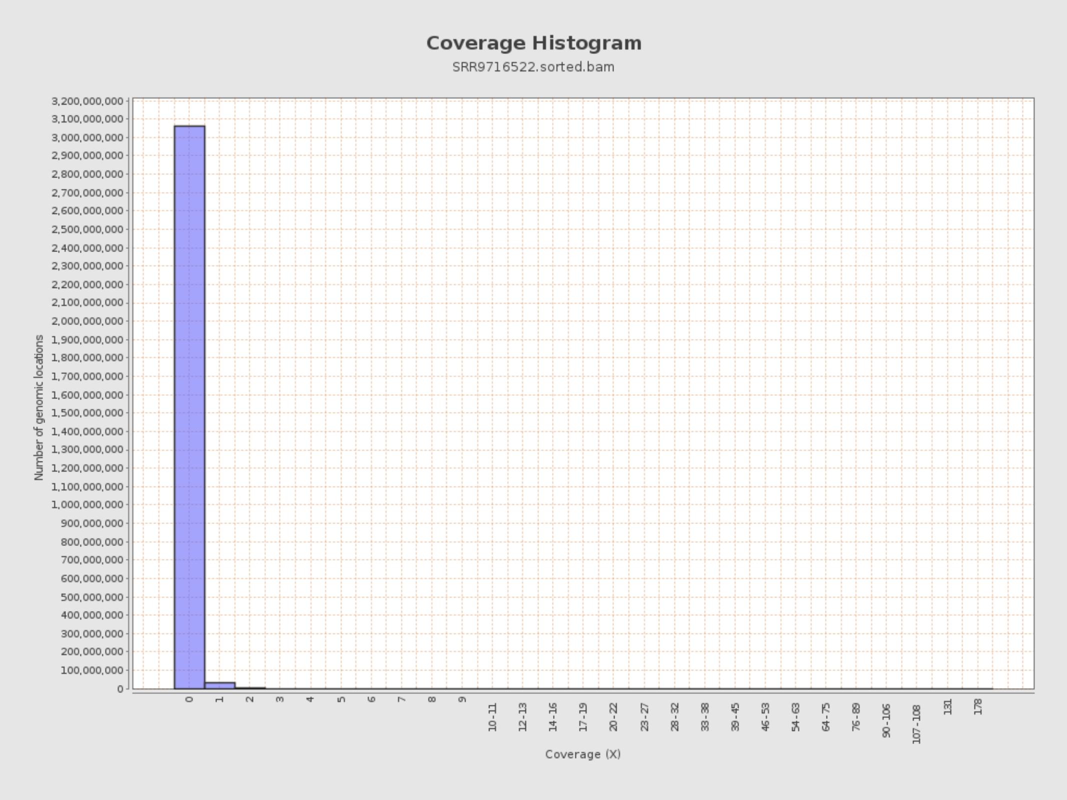
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3811815	0.0153	0.1548
chr2	243199373	3414946	0.014	0.1604
chr3	198022430	2613176	0.0132	0.1279
chr4	191154276	2493453	0.013	0.1352
chr5	180915260	2336500	0.0129	0.1223
chr6	171115067	1720394	0.0101	0.1087
chr7	159138663	2286495	0.0144	0.1516

chr8	146364022	2365789	0.0162	0.1414
chr9	141213431	1723926	0.0122	0.1261
chr10	135534747	2048764	0.0151	0.1819
chr11	135006516	1679028	0.0124	0.1406
chr12	133851895	1914118	0.0143	0.1295
chr13	115169878	712704	0.0062	0.0854
chr14	107349540	1242832	0.0116	0.1162
chr15	102531392	808352	0.0079	0.0983
chr16	90354753	1088868	0.0121	0.1256
chr17	81195210	1589091	0.0196	0.1545
chr18	78077248	1045977	0.0134	0.1437
chr19	59128983	1098275	0.0186	0.1659
chr20	63025520	1018865	0.0162	0.1425
chr21	48129895	555483	0.0115	0.1246
chr22	51304566	461394	0.009	0.1045
chrMT	16571	1768	0.1067	0.3281
chrX	155270560	1249148	0.008	0.1017
chrY	59373566	128903	0.0022	0.0731

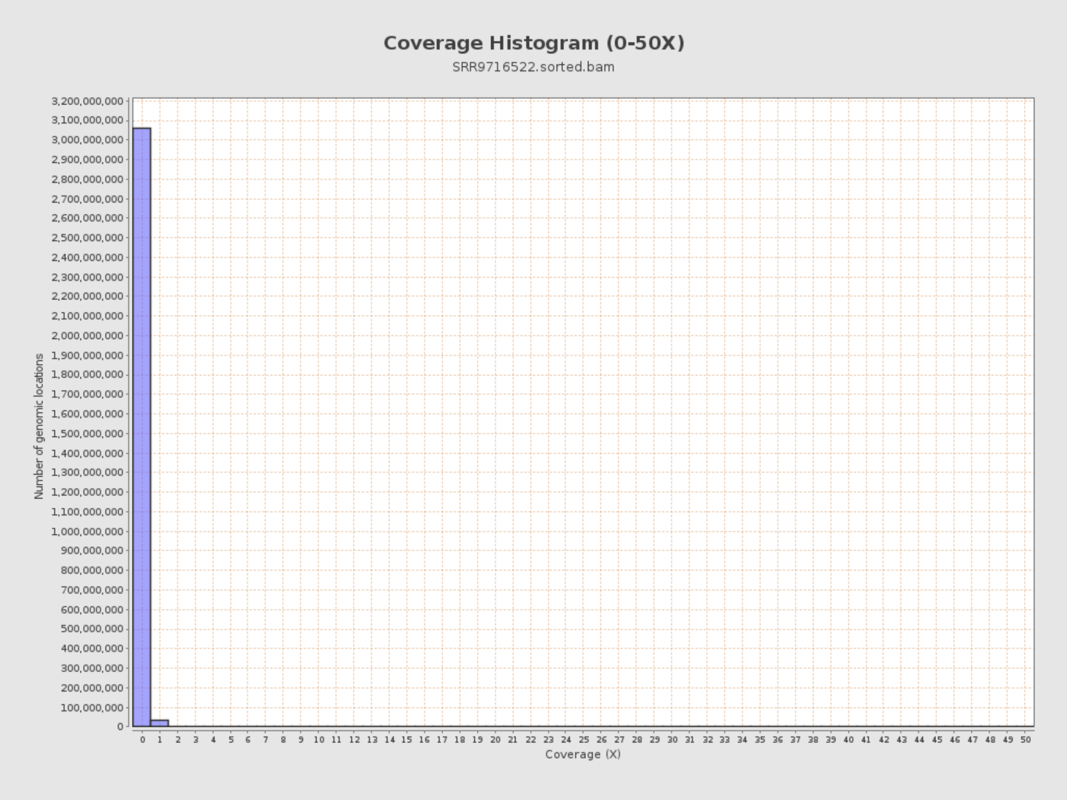
3. Results : Coverage across reference



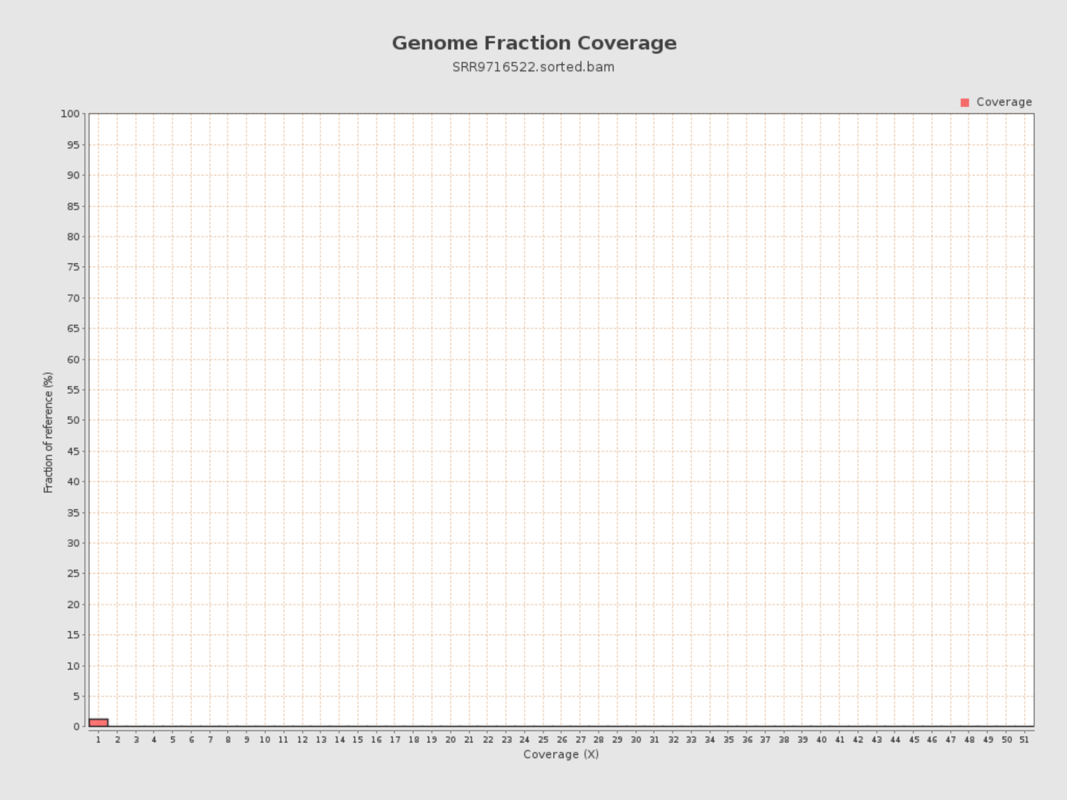
4. Results : Coverage Histogram



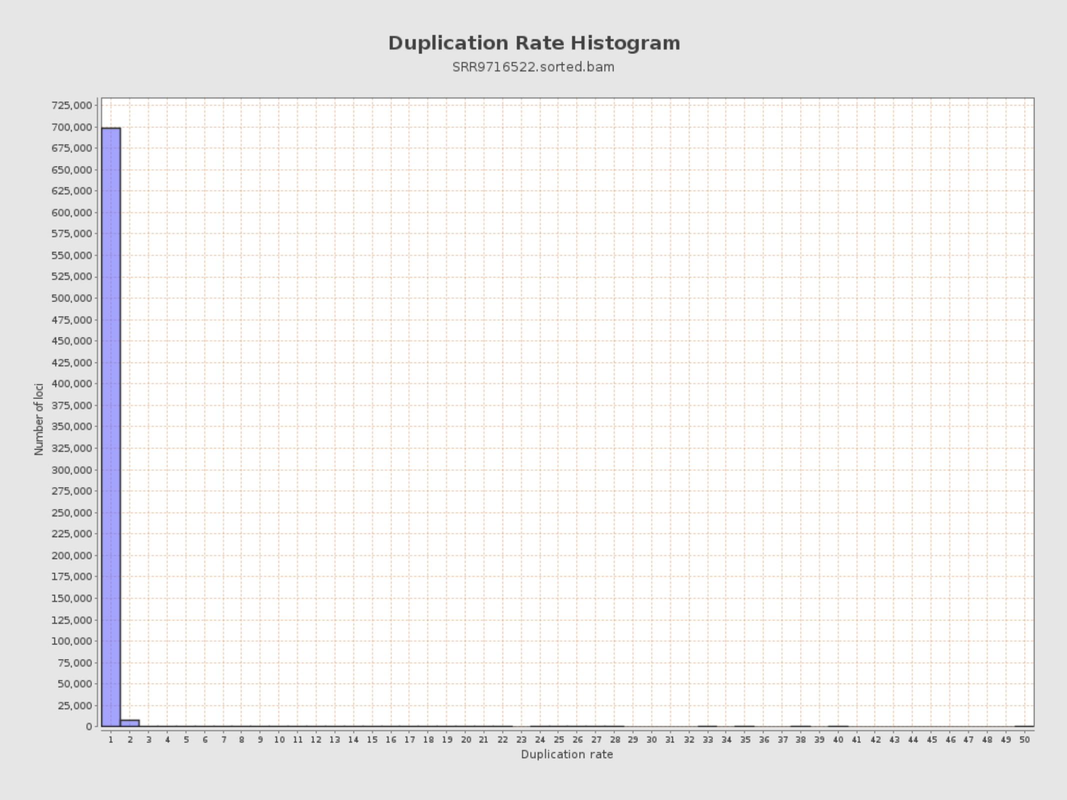
5. Results : Coverage Histogram (0-50X)



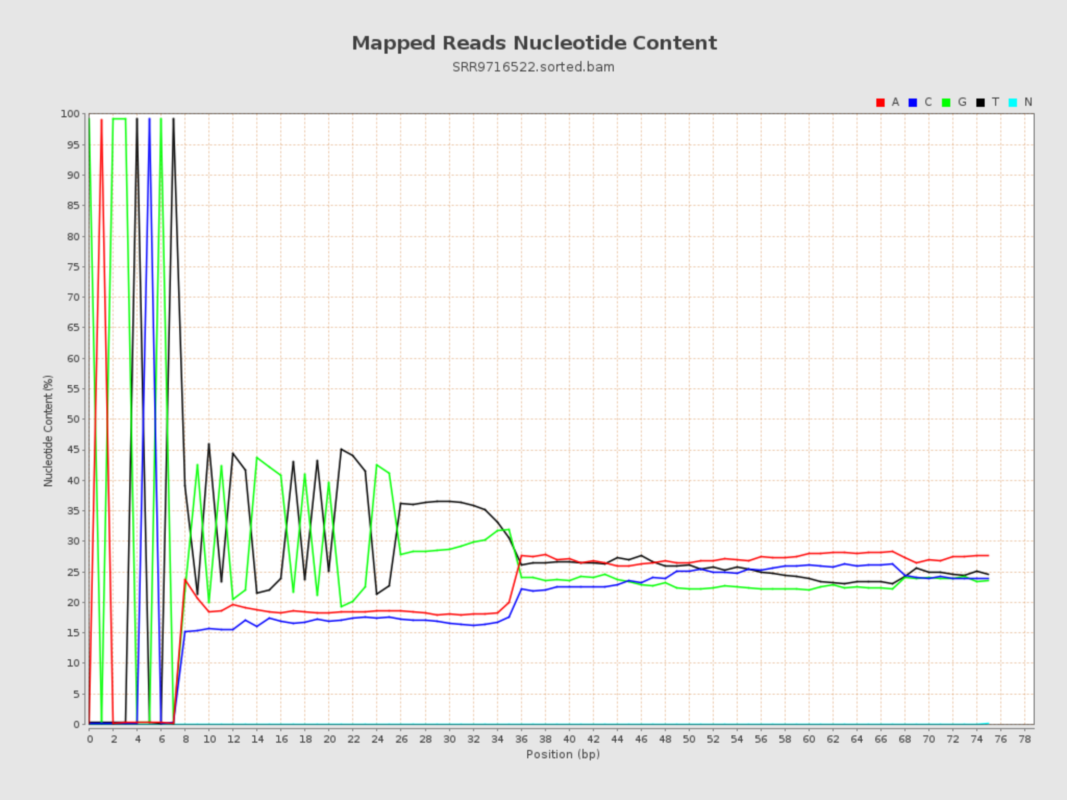
6. Results : Genome Fraction Coverage



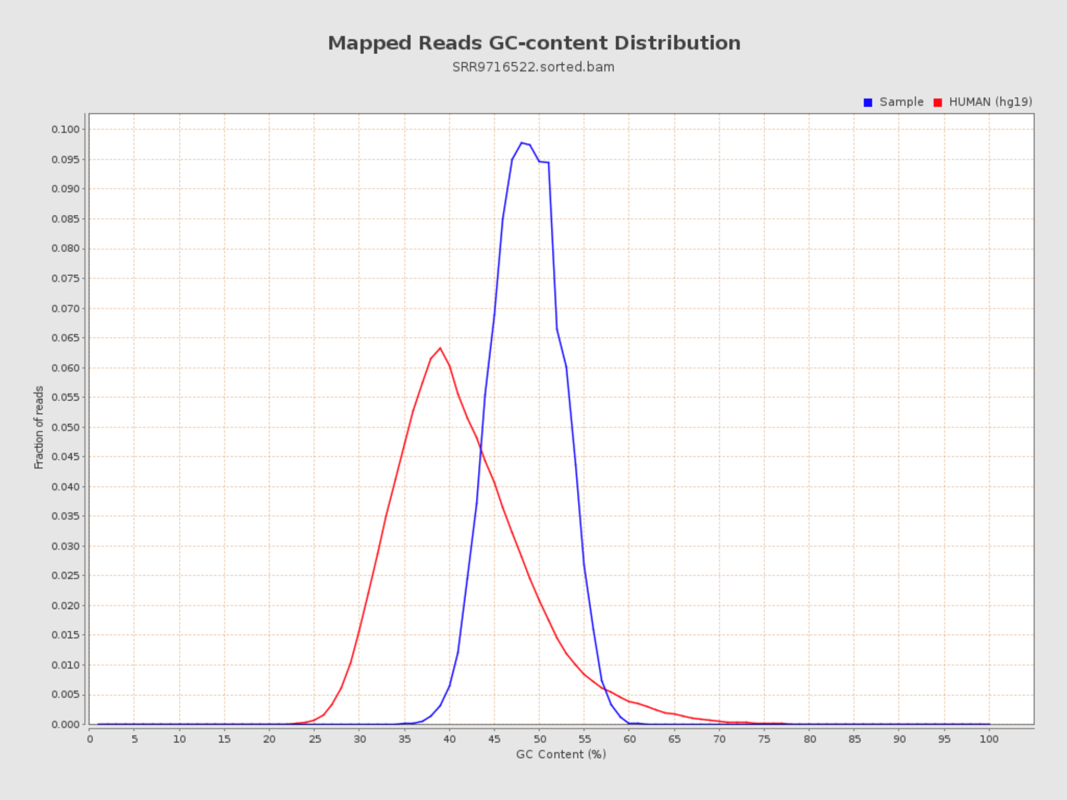
7. Results : Duplication Rate Histogram



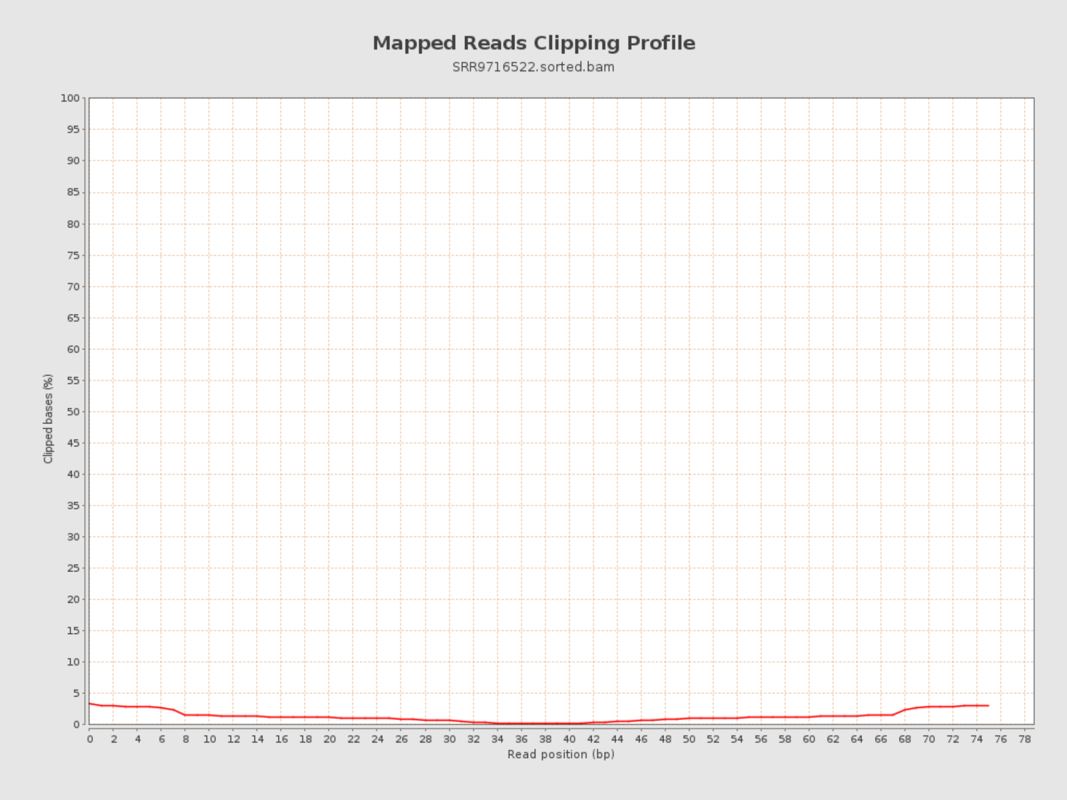
8. Results : Mapped Reads Nucleotide Content



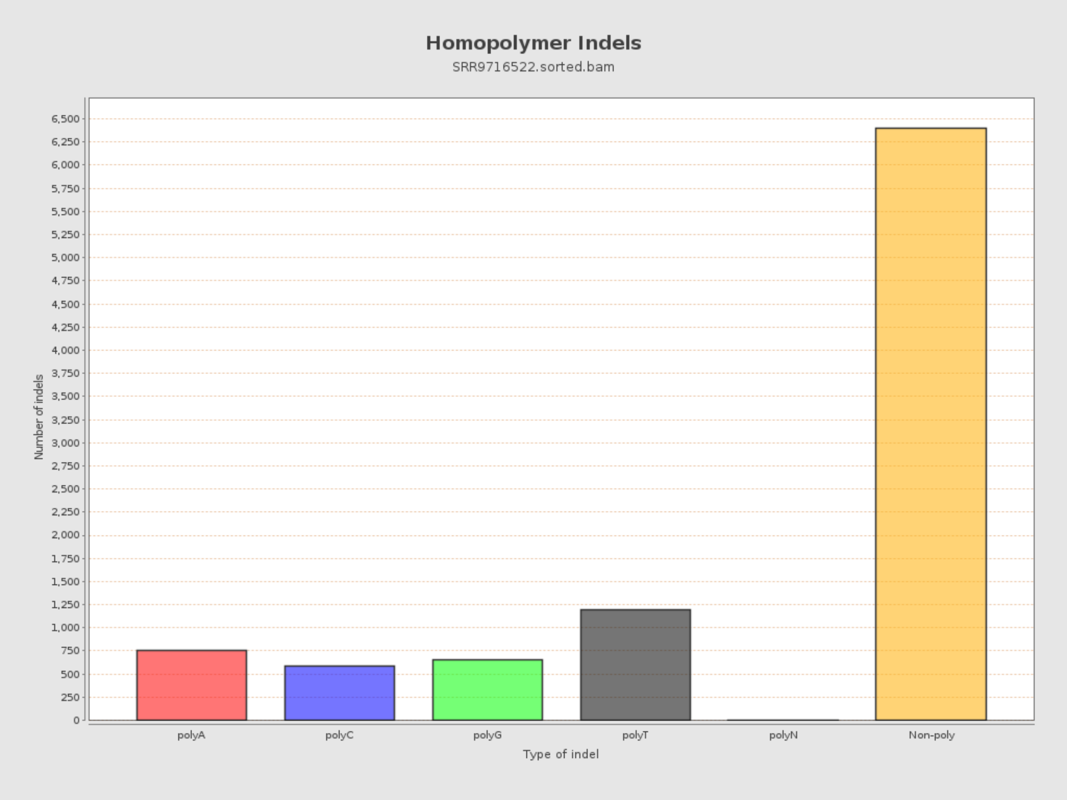
9. Results : Mapped Reads GC-content Distribution



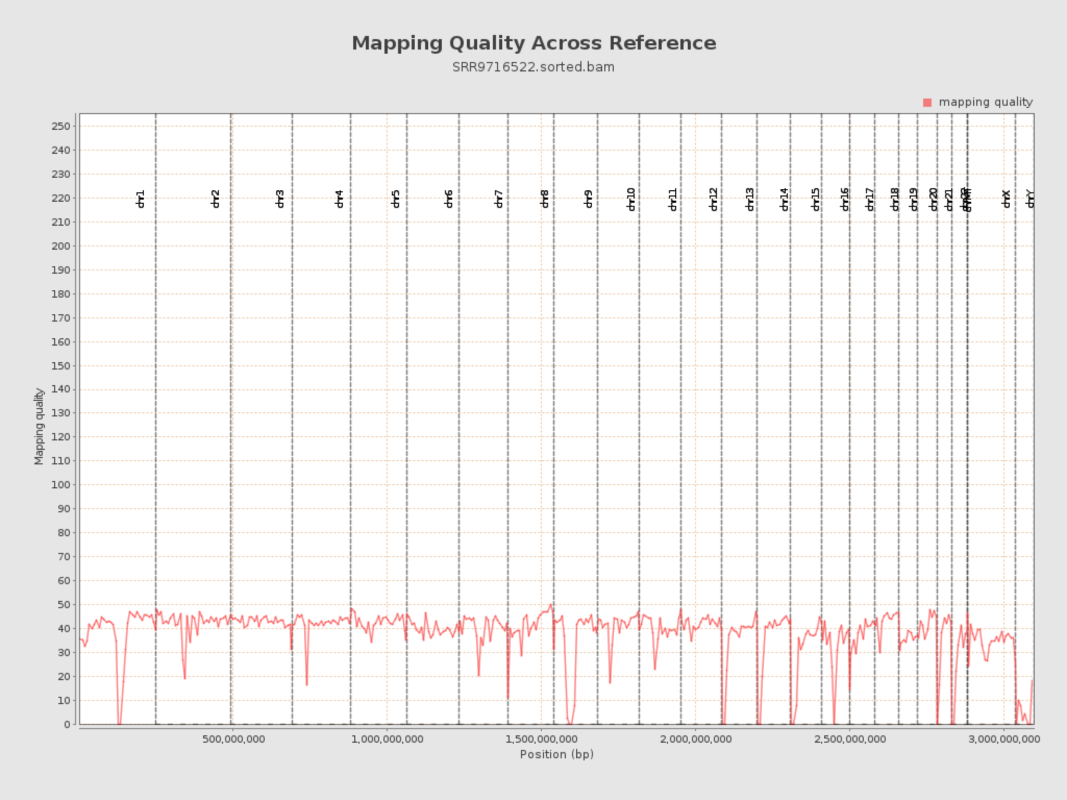
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram