Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:38:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716116.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_SRR9716116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:38:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,703,234
Mapped reads	1,286,378 / 75.53%
Unmapped reads	416,856 / 24.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,692 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	36,501 / 2.14%
Duplication rate	1.85%
Clipped reads	1,288,463 / 75.65%

2.2. ACGT Content

Number/percentage of A's	18,290,845 / 25.58%
Number/percentage of C's	13,535,703 / 18.93%
Number/percentage of T's	22,973,648 / 32.12%
Number/percentage of G's	16,717,191 / 23.37%
Number/percentage of N's	1,041 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.251

2.4. Mapping Quality

Mean Mapping Quality	41.85

2.5. Mismatches and indels

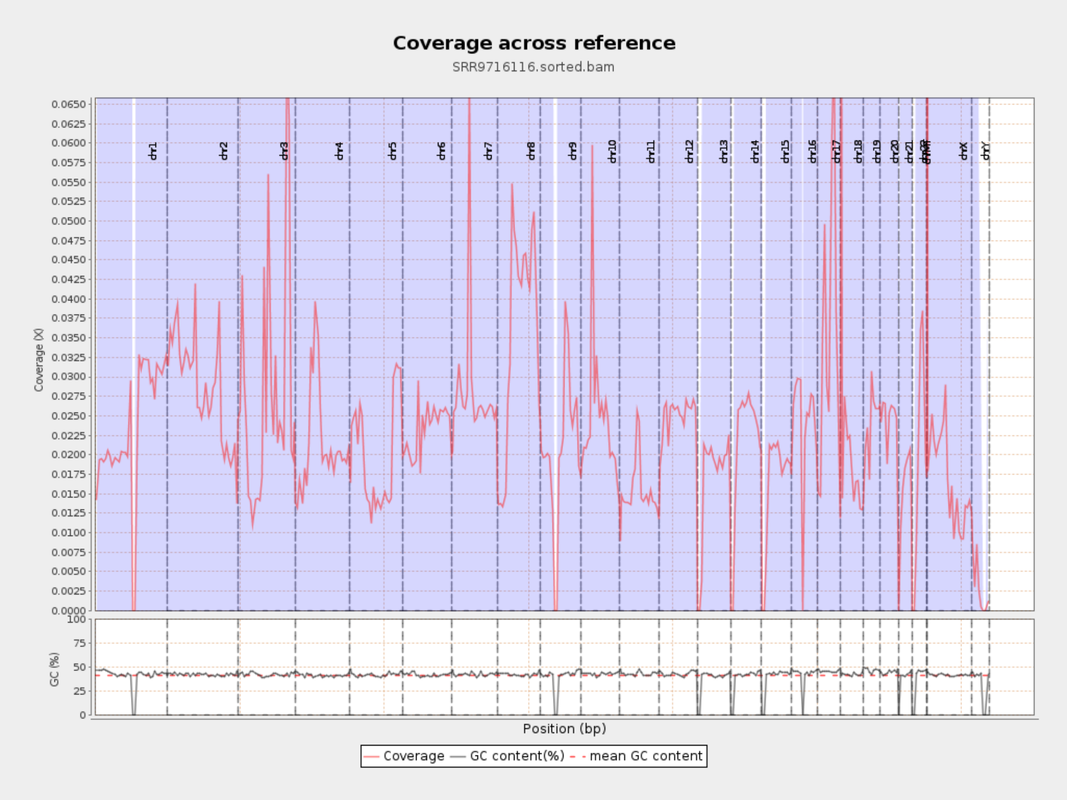
General error rate	0.55%
Mismatches	382,485
Insertions	5,221
Mapped reads with at least one insertion	0.4%
Deletions	13,755
Mapped reads with at least one deletion	1.06%
Homopolymer indels	38.79%

2.6. Chromosome stats

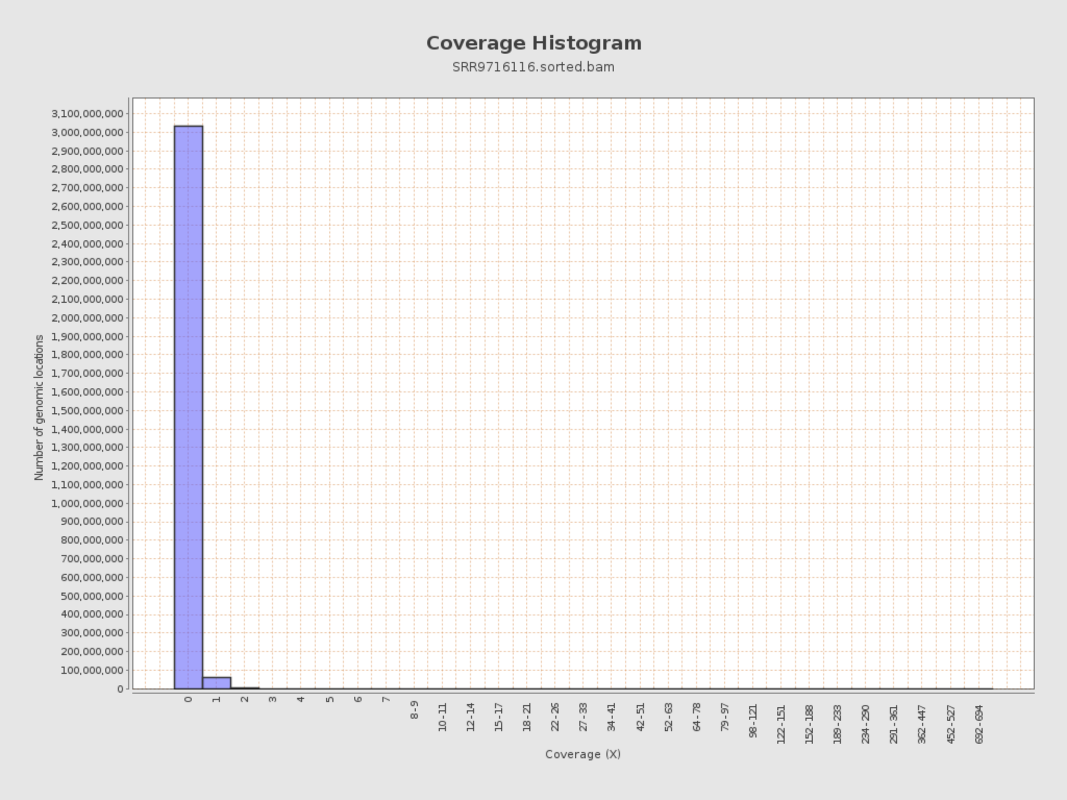
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5797584	0.0233	0.2872
chr2	243199373	6984551	0.0287	0.3392
chr3	198022430	5478018	0.0277	0.1908
chr4	191154276	4089335	0.0214	0.1626
chr5	180915260	3584257	0.0198	0.1513
chr6	171115067	3978383	0.0232	0.185
chr7	159138663	4504984	0.0283	0.6024

chr8	146364022	5306509	0.0363	0.2421
chr9	141213431	2912238	0.0206	0.178
chr10	135534747	3357095	0.0248	0.3117
chr11	135006516	2115027	0.0157	0.1631
chr12	133851895	3334394	0.0249	0.1805
chr13	115169878	1911438	0.0166	0.1388
chr14	107349540	2294845	0.0214	0.1595
chr15	102531392	1666309	0.0163	0.1401
chr16	90354753	2131165	0.0236	0.1751
chr17	81195210	2883715	0.0355	0.2093
chr18	78077248	1674754	0.0214	0.2669
chr19	59128983	1412814	0.0239	0.2759
chr20	63025520	1533325	0.0243	0.1704
chr21	48129895	731490	0.0152	0.1356
chr22	51304566	994814	0.0194	0.1507
chrMT	16571	59025	3.5619	2.981
chrX	155270560	2637830	0.017	0.1666
chrY	59373566	166237	0.0028	0.0752

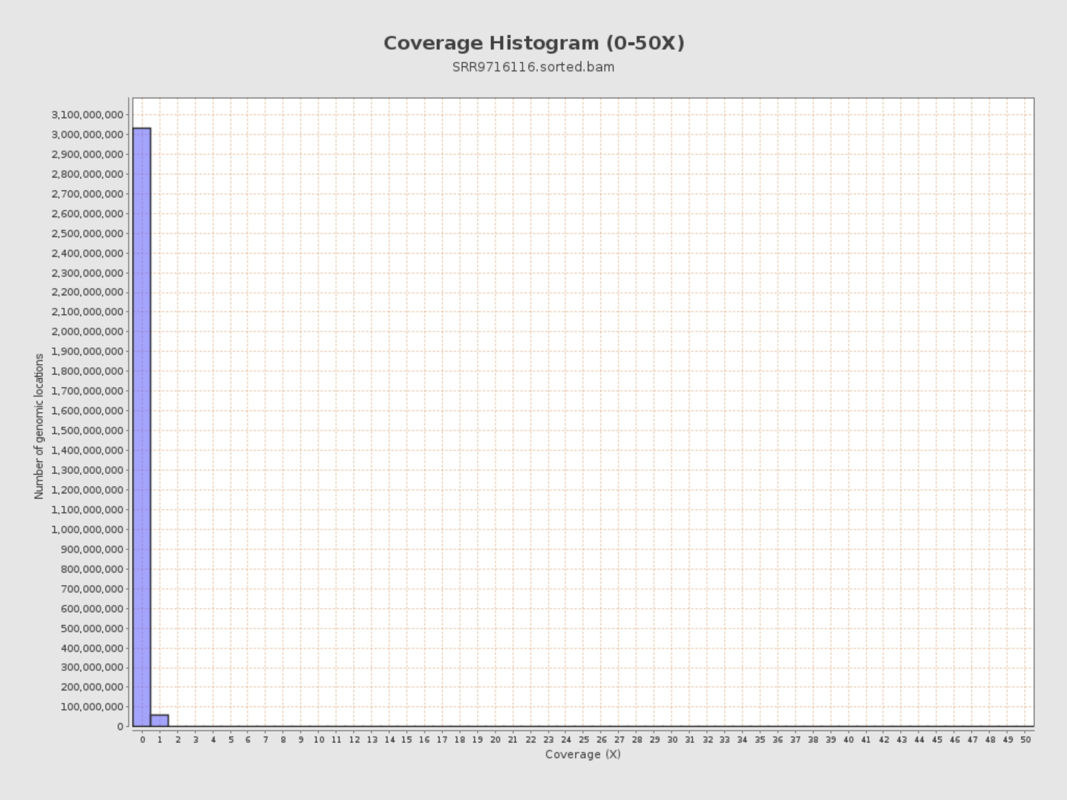
3. Results : Coverage across reference



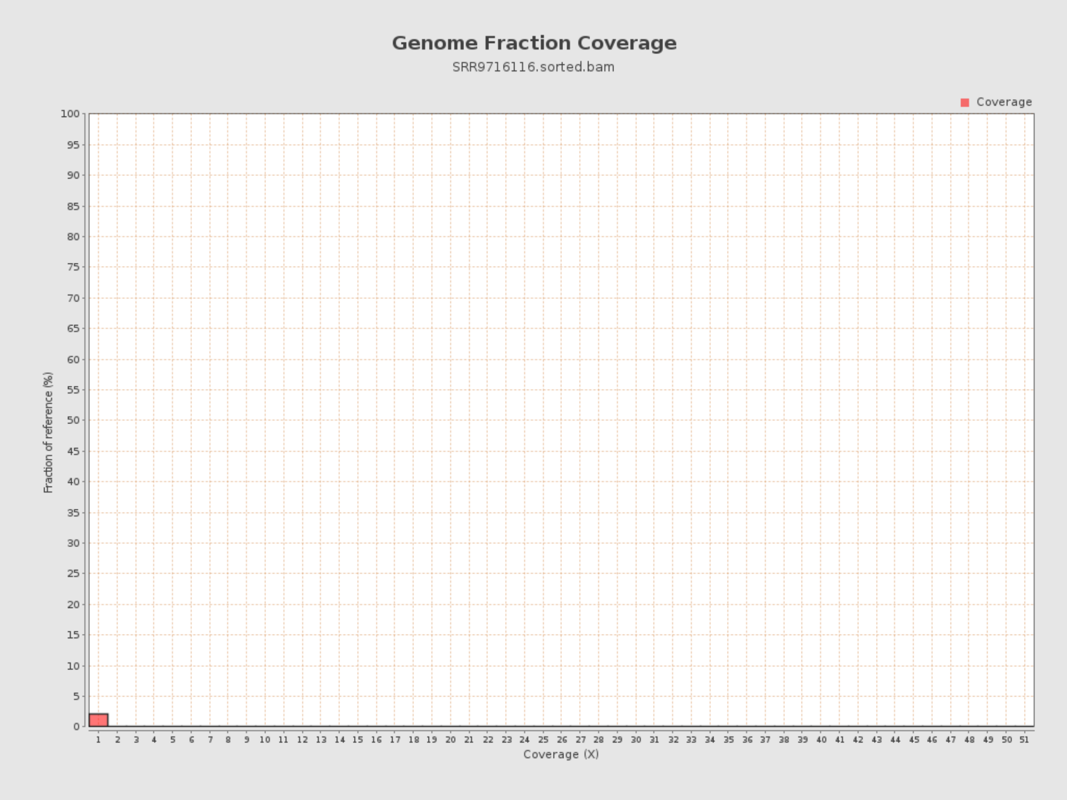
4. Results : Coverage Histogram



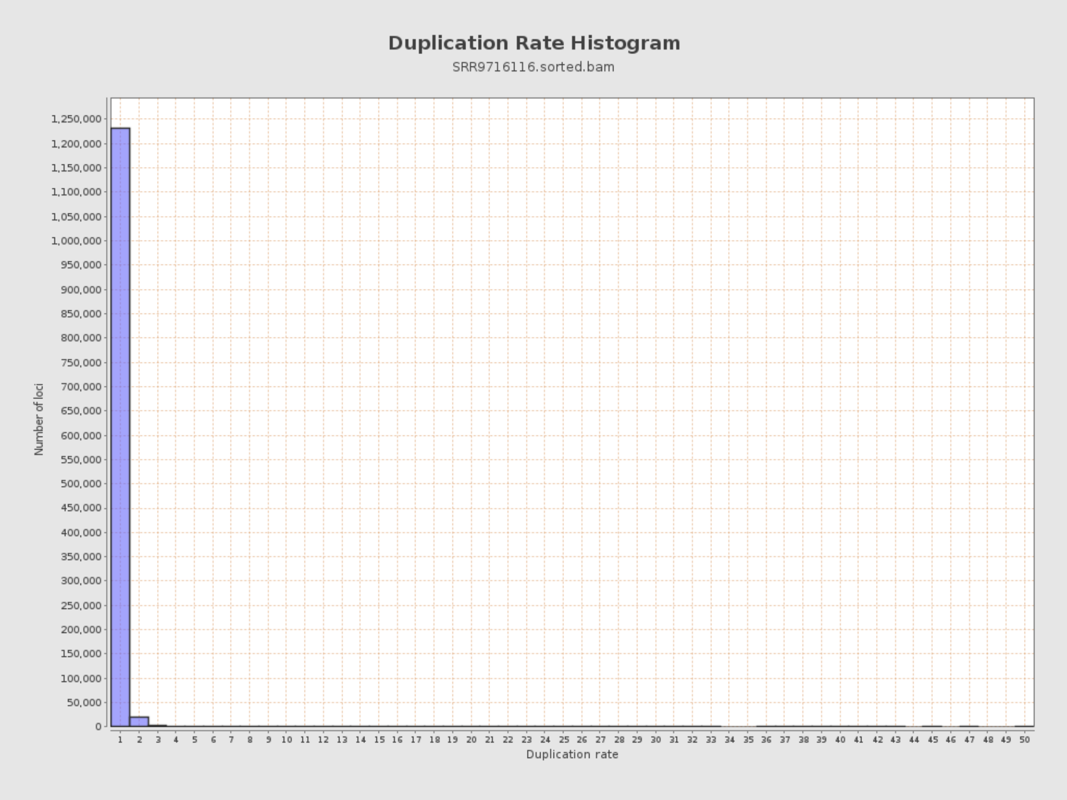
5. Results : Coverage Histogram (0-50X)



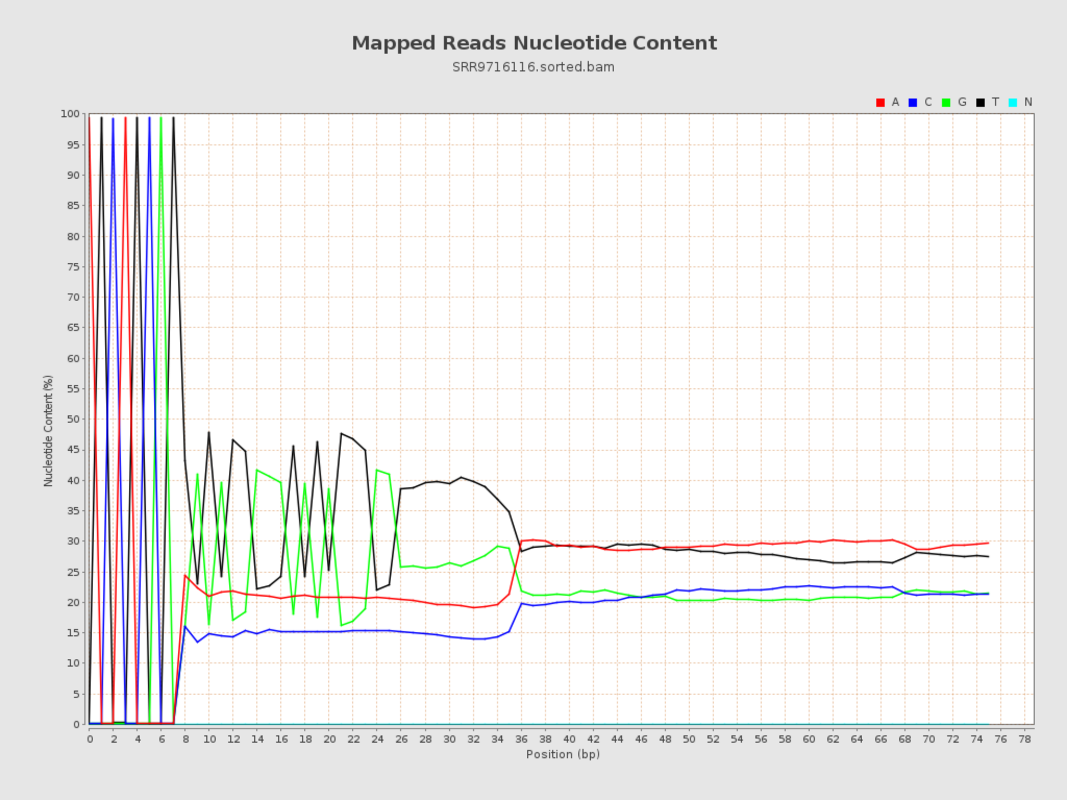
6. Results : Genome Fraction Coverage



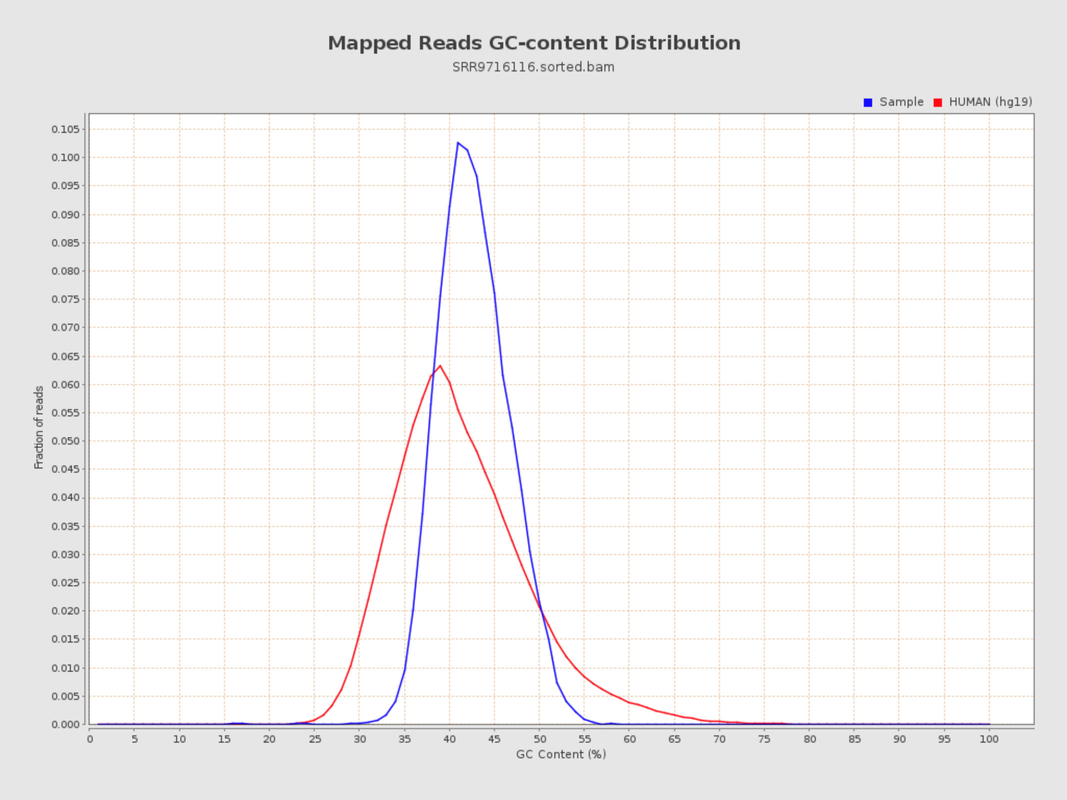
7. Results : Duplication Rate Histogram



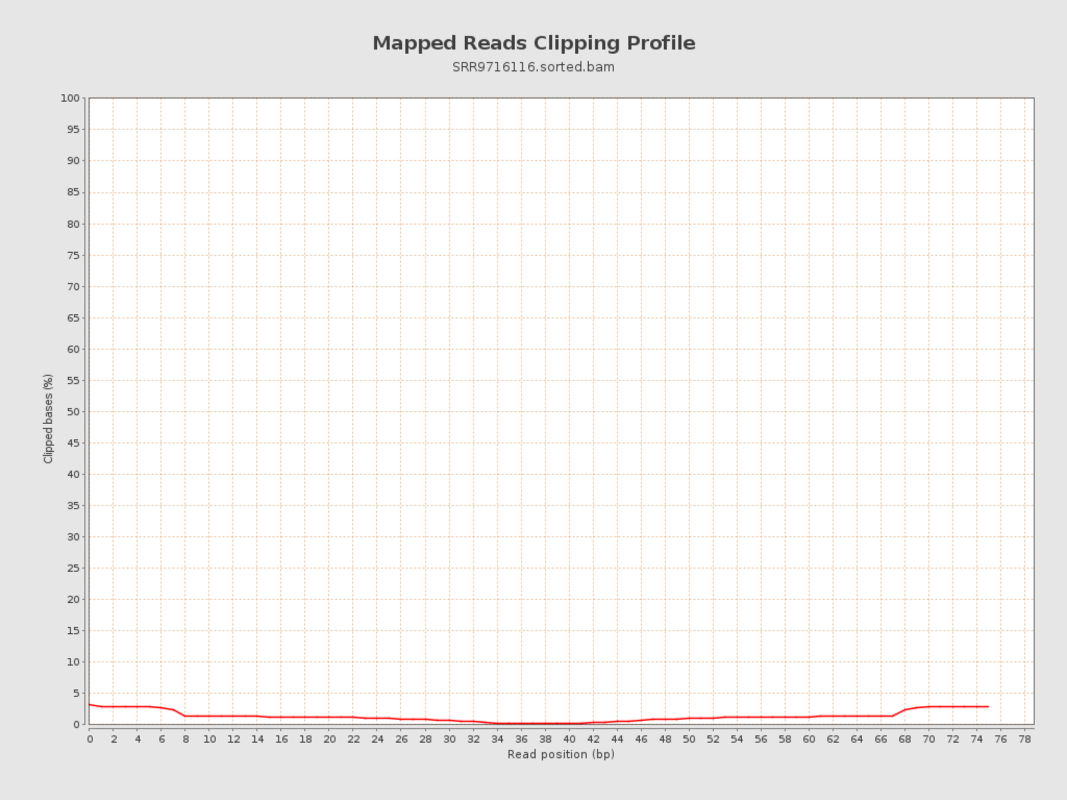
8. Results : Mapped Reads Nucleotide Content



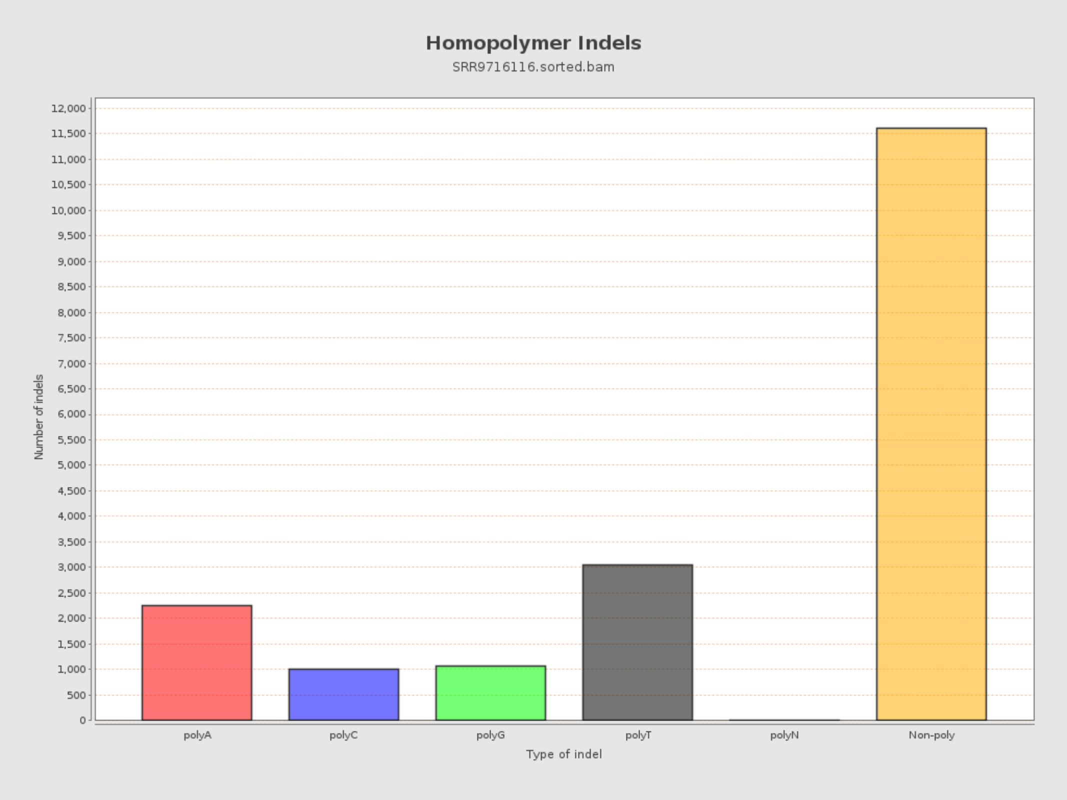
9. Results : Mapped Reads GC-content Distribution



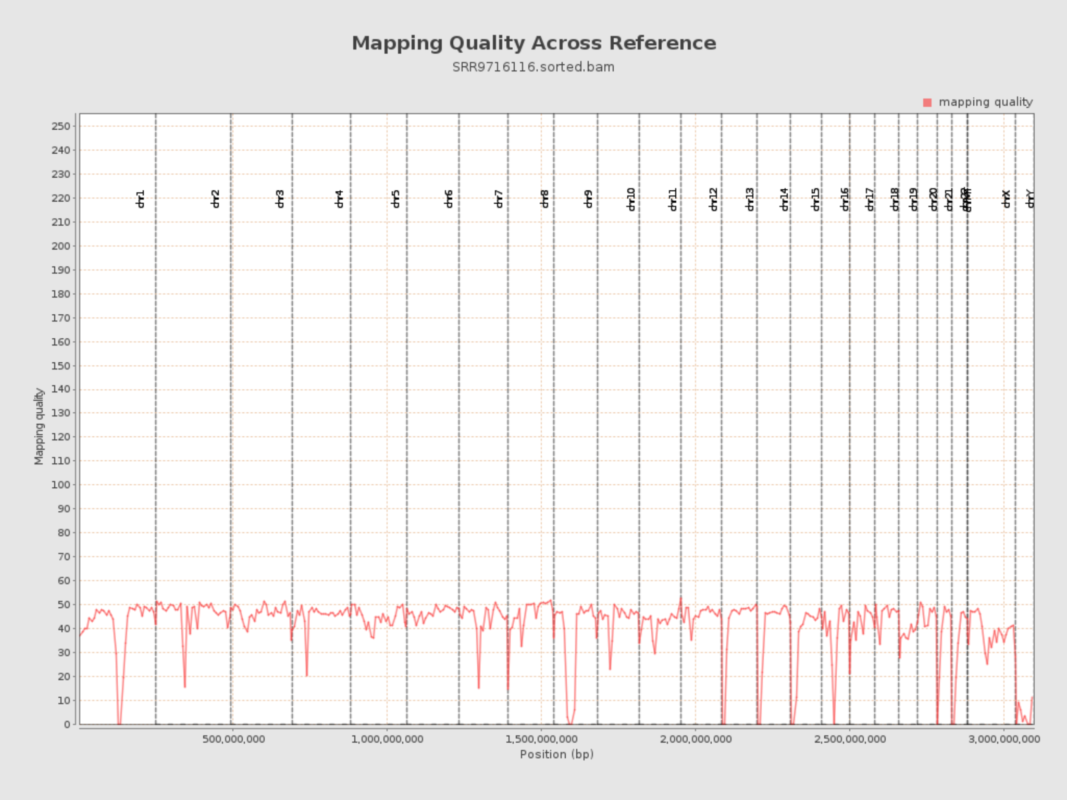
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram