Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:20:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716937.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_SRR9716937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716937.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:20:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	377,708
Mapped reads	282,719 / 74.85%
Unmapped reads	94,989 / 25.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	298 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	11,273 / 2.98%
Duplication rate	3.65%
Clipped reads	282,447 / 74.78%

2.2. ACGT Content

Number/percentage of A's	3,353,671 / 22.49%
Number/percentage of C's	2,643,890 / 17.73%
Number/percentage of T's	4,697,982 / 31.5%
Number/percentage of G's	4,218,979 / 28.29%
Number/percentage of N's	272 / 0%
GC Percentage	46.01%

2.3. Coverage

Mean	0.0048

Standard Deviation	0.0774

2.4. Mapping Quality

Mean Mapping Quality	42.67

2.5. Mismatches and indels

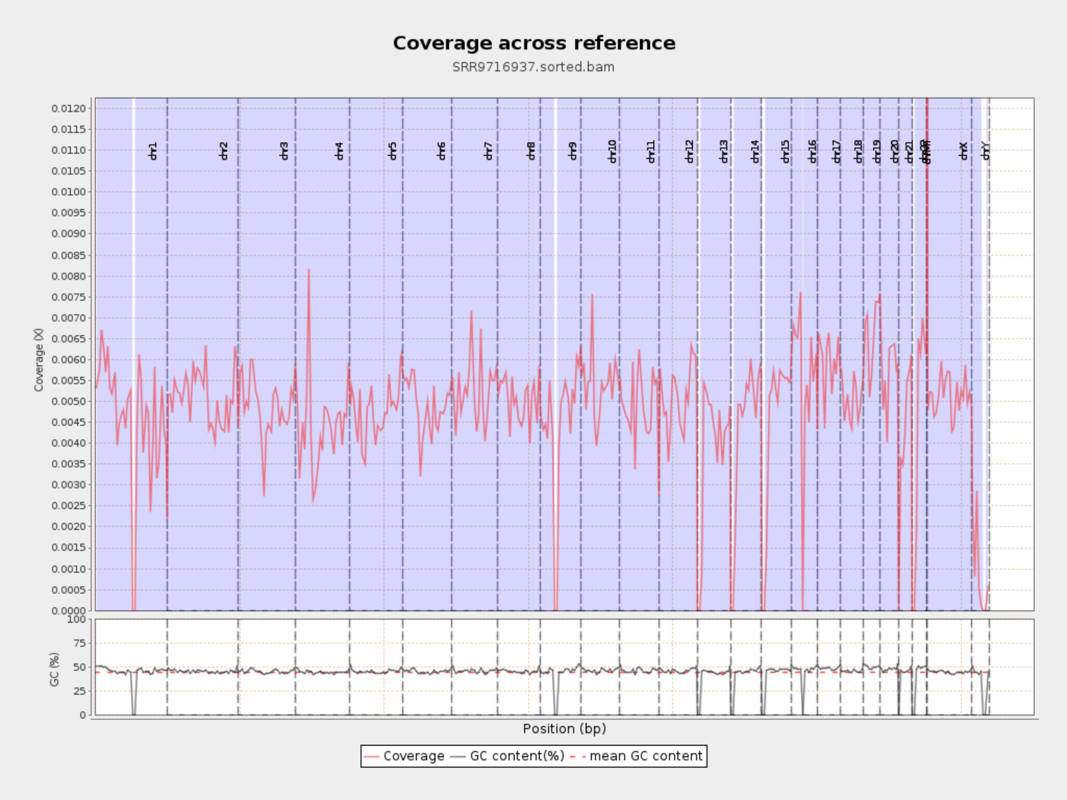
General error rate	0.67%
Mismatches	98,550
Insertions	964
Mapped reads with at least one insertion	0.34%
Deletions	2,392
Mapped reads with at least one deletion	0.84%
Homopolymer indels	41.6%

2.6. Chromosome stats

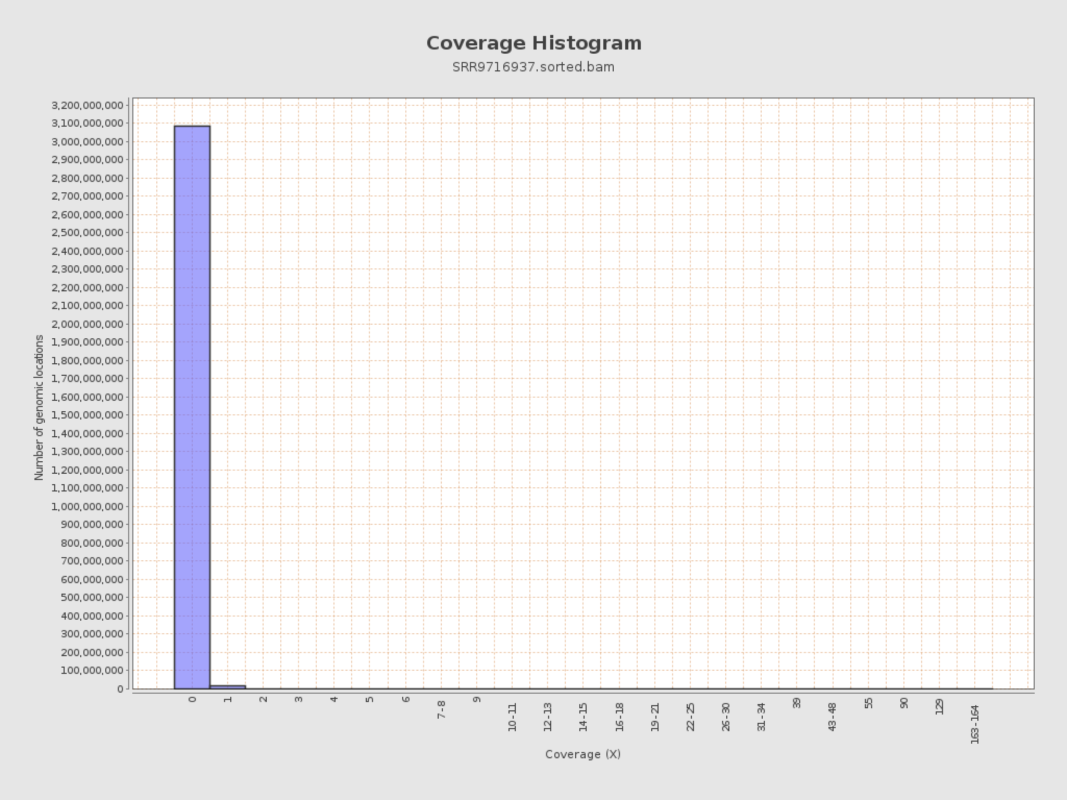
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1137271	0.0046	0.0753
chr2	243199373	1243998	0.0051	0.0995
chr3	198022430	961764	0.0049	0.0741
chr4	191154276	857470	0.0045	0.0722
chr5	180915260	861408	0.0048	0.0732
chr6	171115067	833465	0.0049	0.0792
chr7	159138663	836685	0.0053	0.08

chr8	146364022	738631	0.005	0.0758
chr9	141213431	616210	0.0044	0.0713
chr10	135534747	734556	0.0054	0.0819
chr11	135006516	669758	0.005	0.0762
chr12	133851895	680654	0.0051	0.0755
chr13	115169878	435772	0.0038	0.0651
chr14	107349540	461237	0.0043	0.0698
chr15	102531392	446872	0.0044	0.0704
chr16	90354753	499079	0.0055	0.0826
chr17	81195210	484351	0.006	0.083
chr18	78077248	391278	0.005	0.0796
chr19	59128983	387078	0.0065	0.0913
chr20	63025520	358097	0.0057	0.0809
chr21	48129895	205016	0.0043	0.0705
chr22	51304566	226790	0.0044	0.0714
chrMT	16571	1778	0.1073	0.3282
chrX	155270560	799139	0.0051	0.0767
chrY	59373566	50586	0.0009	0.0359

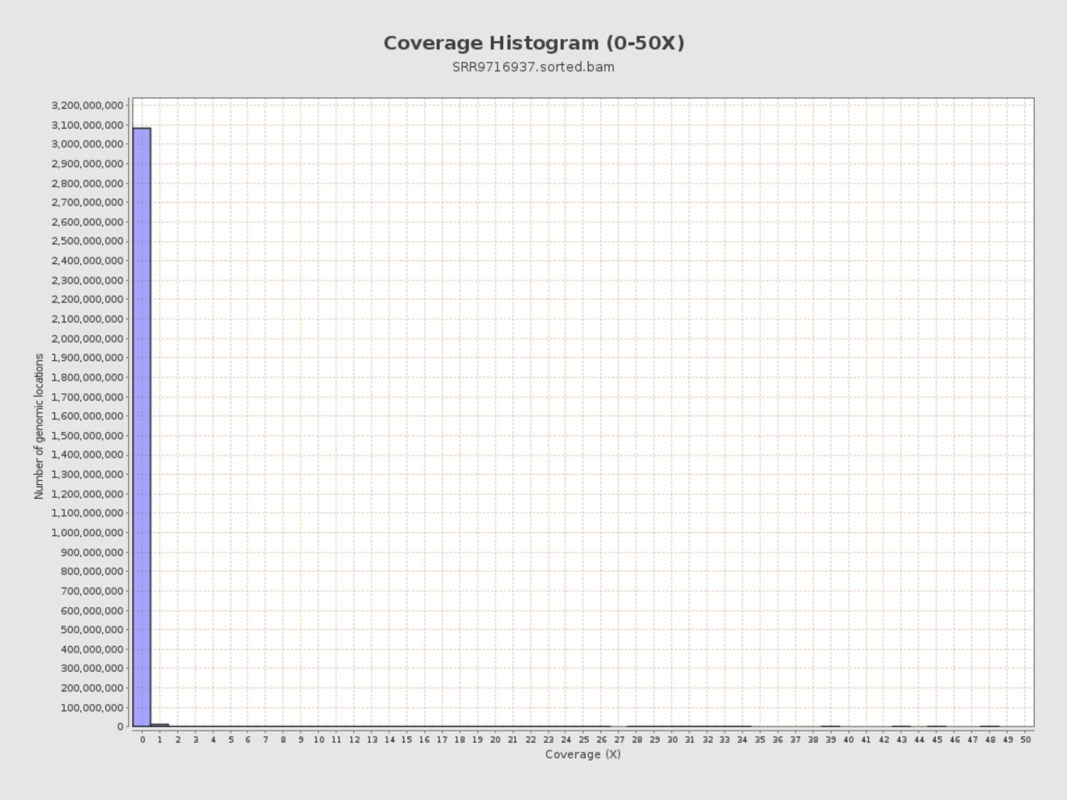
3. Results : Coverage across reference



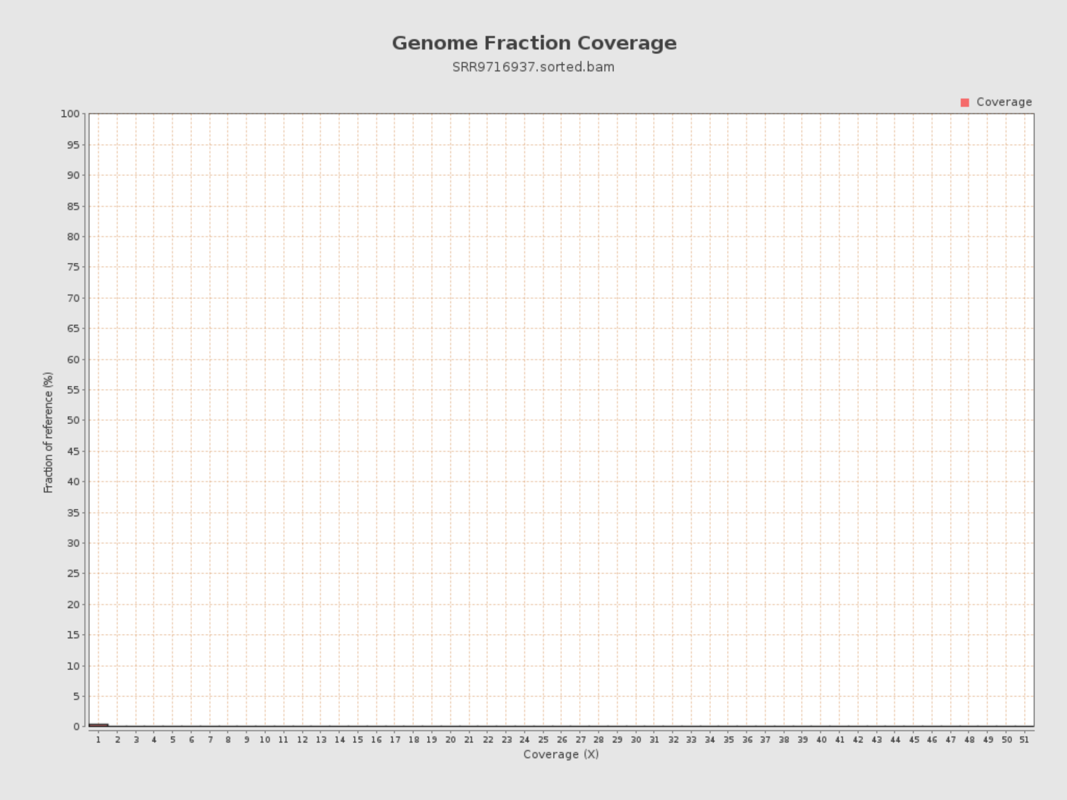
4. Results : Coverage Histogram



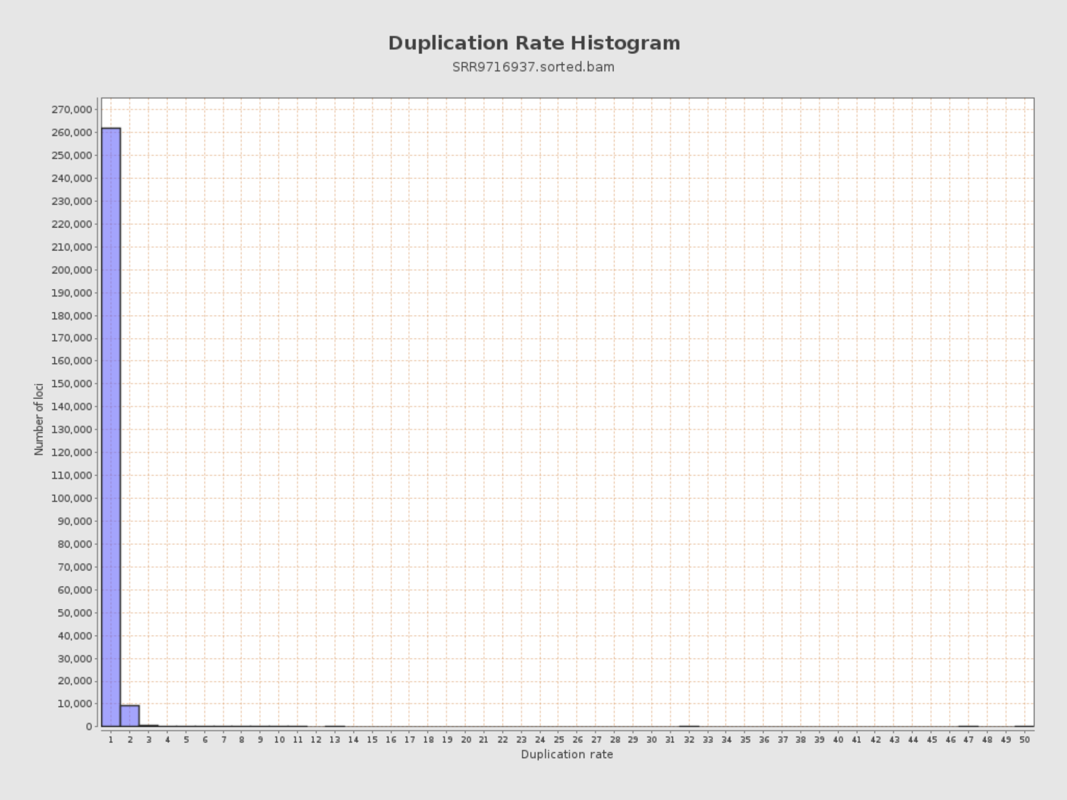
5. Results : Coverage Histogram (0-50X)



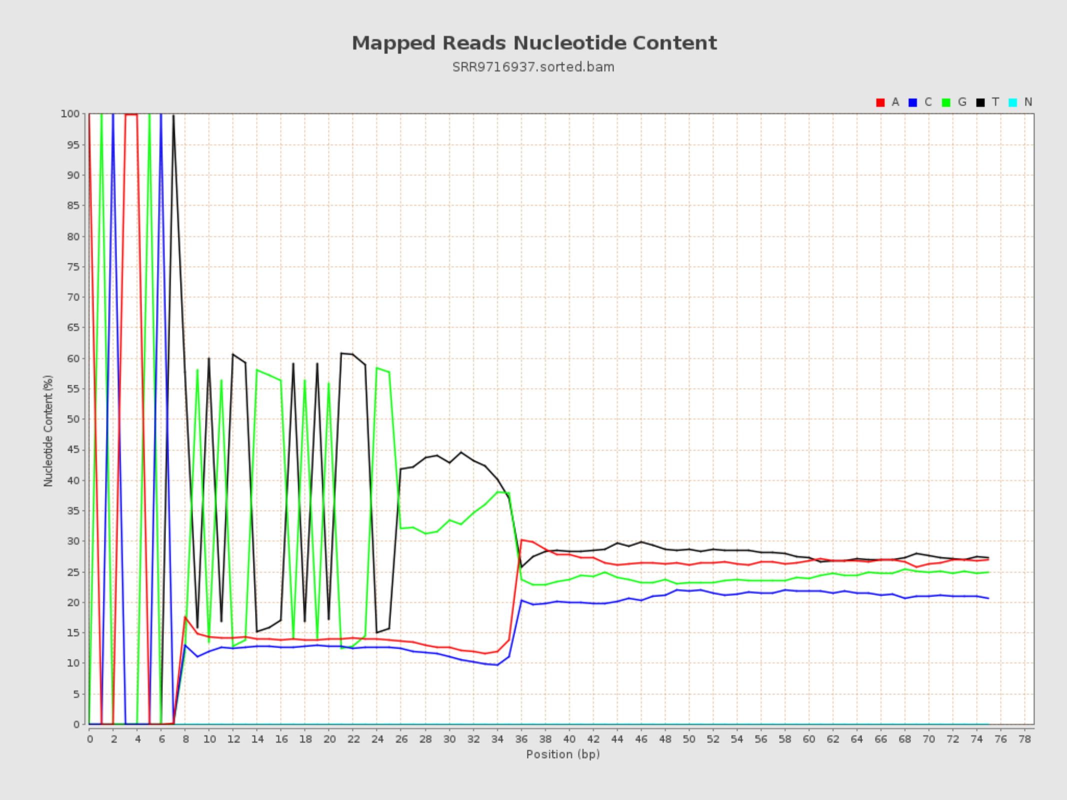
6. Results : Genome Fraction Coverage



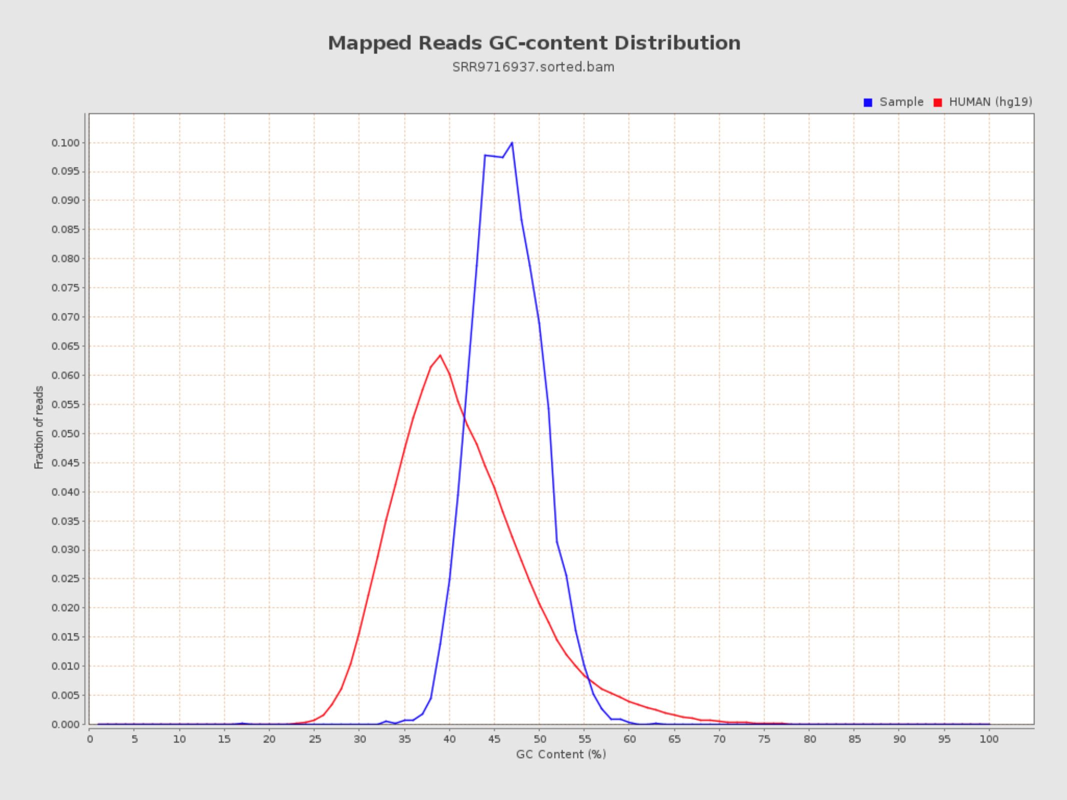
7. Results : Duplication Rate Histogram



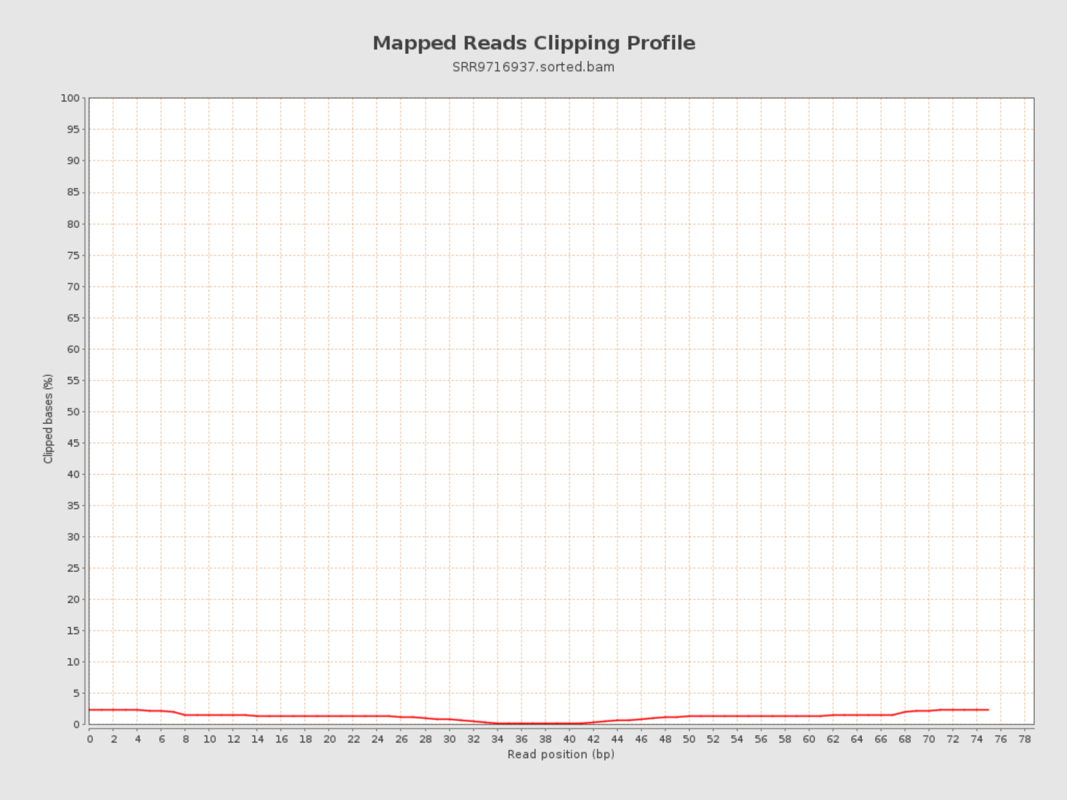
8. Results : Mapped Reads Nucleotide Content



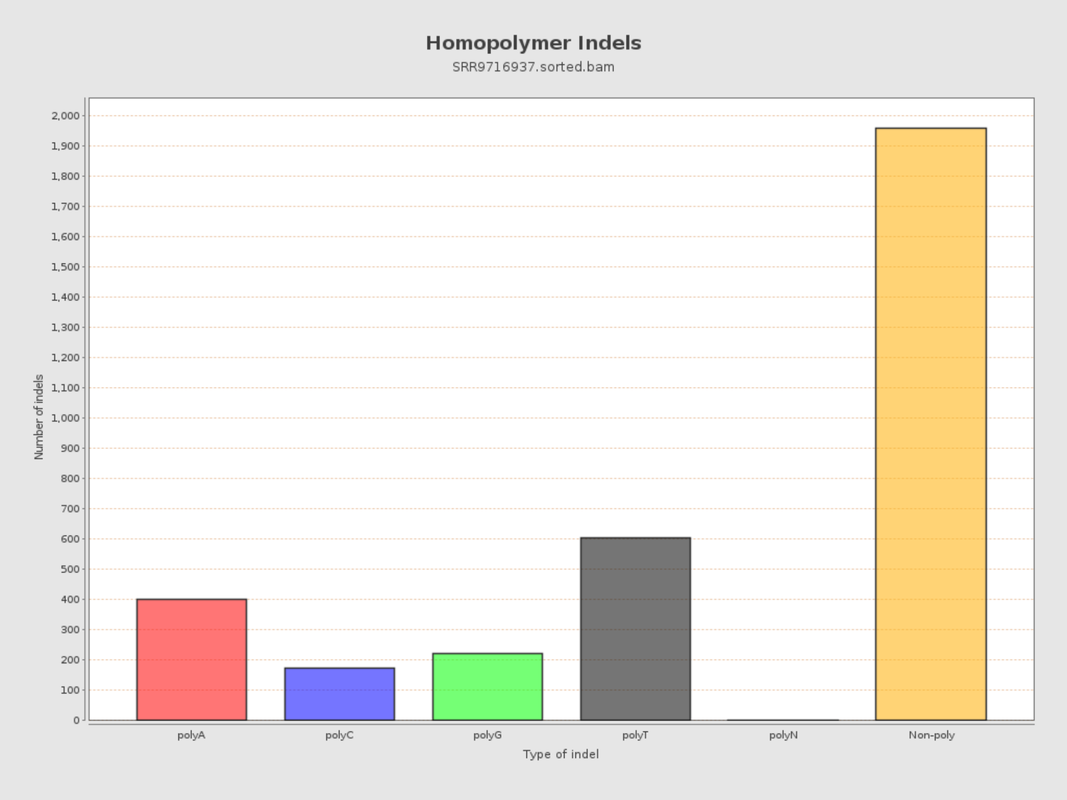
9. Results : Mapped Reads GC-content Distribution



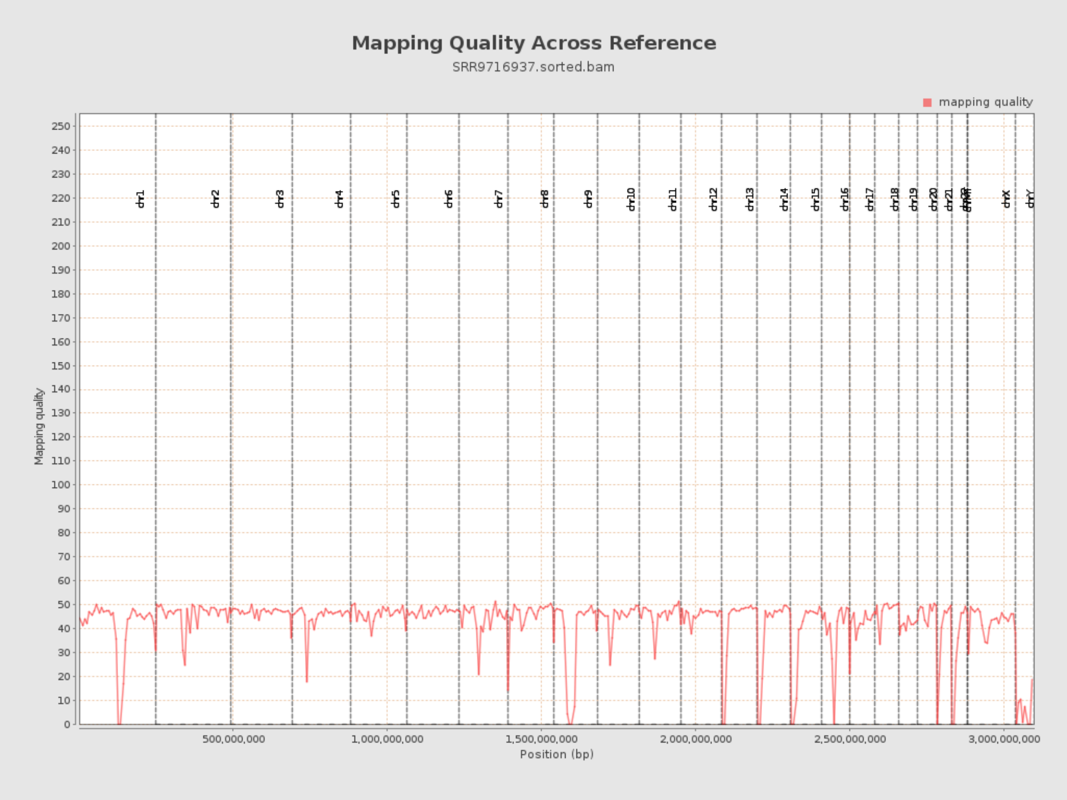
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram