Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:25:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716912.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_SRR9716912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716912.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:25:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,247,912
Mapped reads	1,095,982 / 87.83%
Unmapped reads	151,930 / 12.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,948 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	28,172 / 2.26%
Duplication rate	1.89%
Clipped reads	1,097,346 / 87.93%

2.2. ACGT Content

Number/percentage of A's	15,984,570 / 25.3%
Number/percentage of C's	11,666,057 / 18.46%
Number/percentage of T's	19,499,754 / 30.86%
Number/percentage of G's	16,031,174 / 25.37%
Number/percentage of N's	478 / 0%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.1908

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

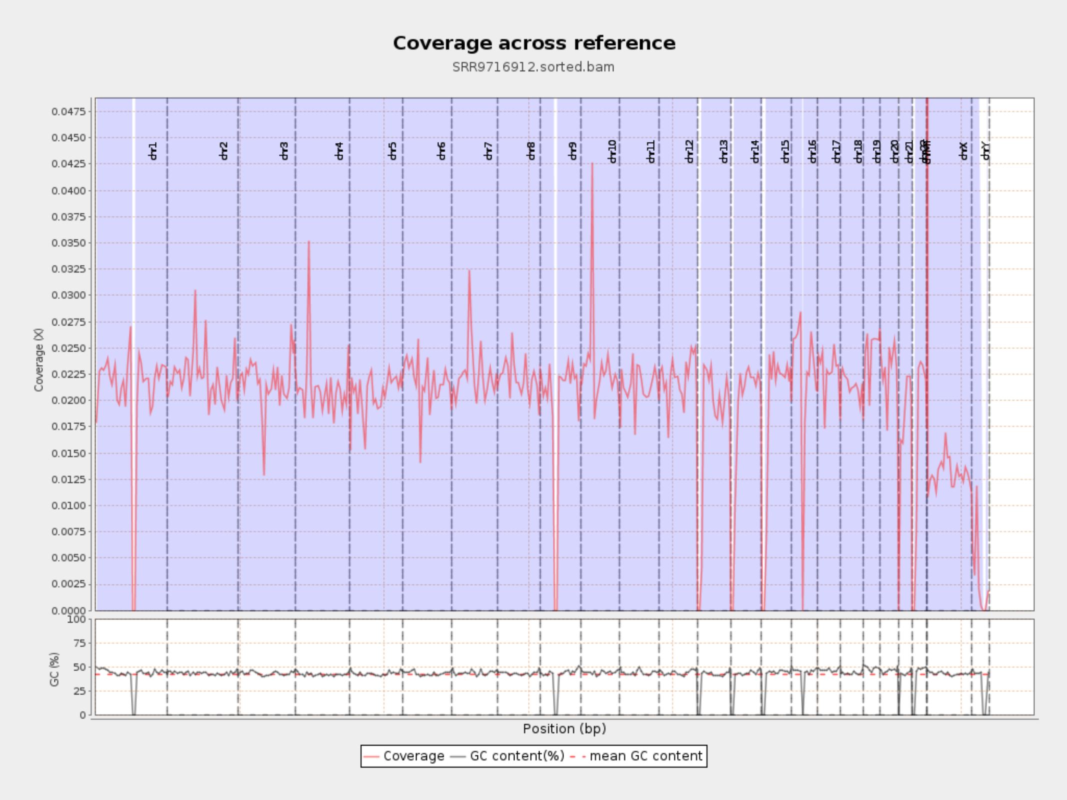
General error rate	0.54%
Mismatches	330,282
Insertions	4,611
Mapped reads with at least one insertion	0.42%
Deletions	12,355
Mapped reads with at least one deletion	1.12%
Homopolymer indels	40.6%

2.6. Chromosome stats

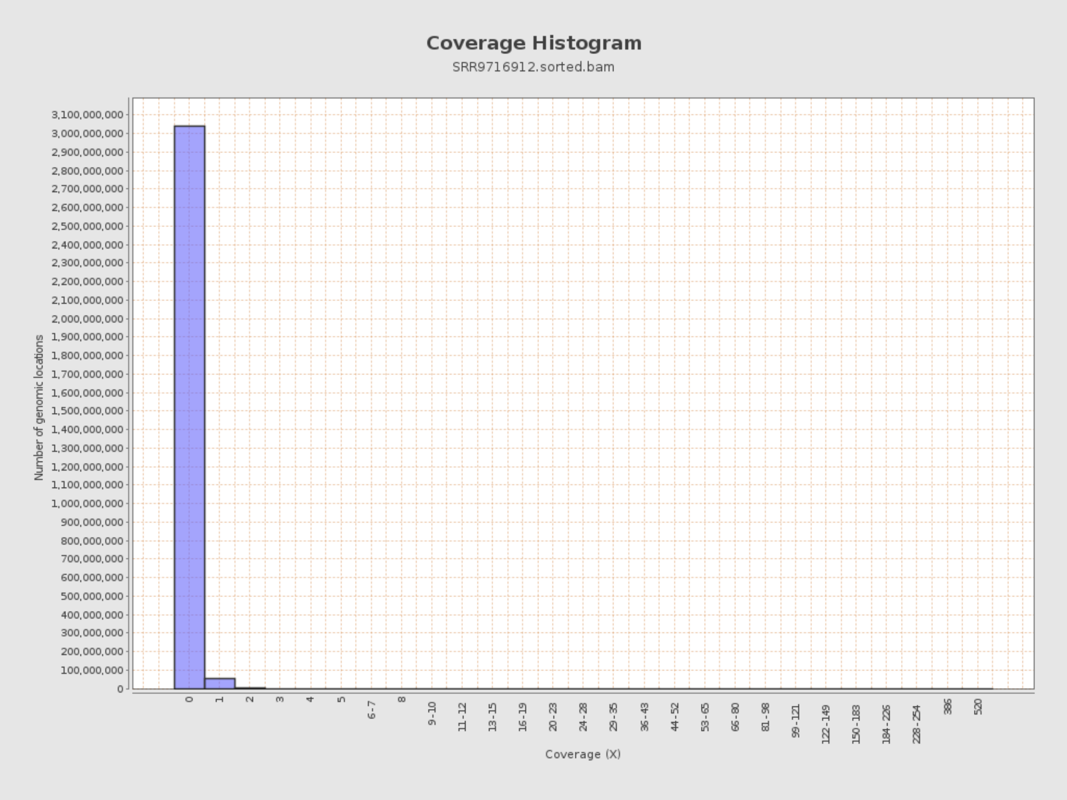
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5163728	0.0207	0.2349
chr2	243199373	5437876	0.0224	0.2775
chr3	198022430	4304831	0.0217	0.1594
chr4	191154276	4073637	0.0213	0.1704
chr5	180915260	3780922	0.0209	0.1543
chr6	171115067	3722587	0.0218	0.1747
chr7	159138663	3594157	0.0226	0.2336

chr8	146364022	3240479	0.0221	0.1886
chr9	141213431	2721653	0.0193	0.169
chr10	135534747	3180813	0.0235	0.232
chr11	135006516	2900601	0.0215	0.1834
chr12	133851895	2964516	0.0221	0.1597
chr13	115169878	1995576	0.0173	0.1409
chr14	107349540	1959783	0.0183	0.1502
chr15	102531392	1891123	0.0184	0.1485
chr16	90354753	1973766	0.0218	0.1687
chr17	81195210	1846766	0.0227	0.165
chr18	78077248	1677909	0.0215	0.2528
chr19	59128983	1453391	0.0246	0.2207
chr20	63025520	1429597	0.0227	0.1655
chr21	48129895	841945	0.0175	0.1533
chr22	51304566	807279	0.0157	0.135
chrMT	16571	21442	1.2939	1.4129
chrX	155270560	2034185	0.0131	0.134
chrY	59373566	183294	0.0031	0.1061

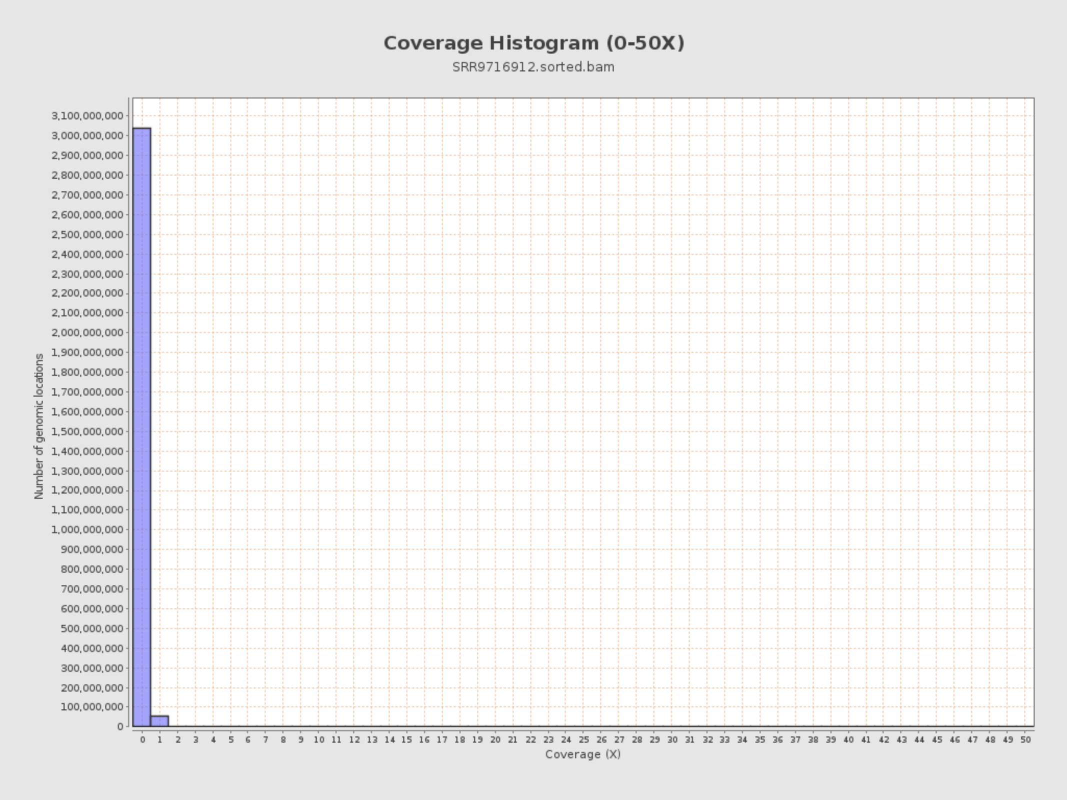
3. Results : Coverage across reference



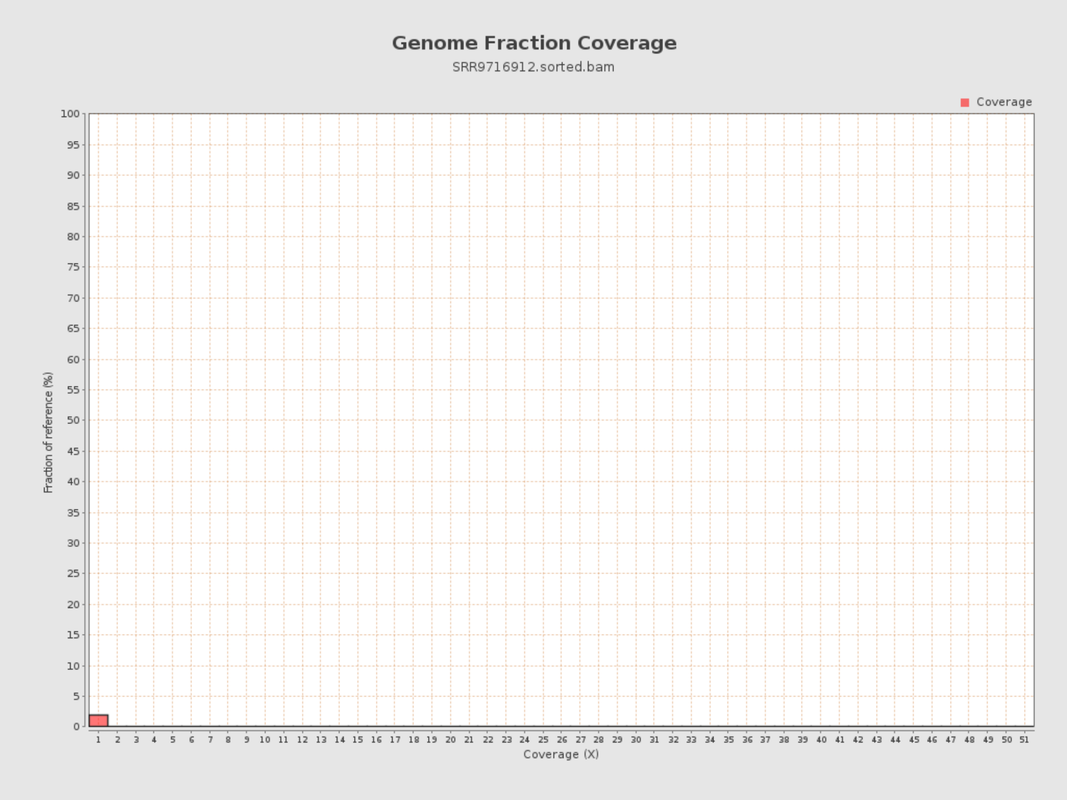
4. Results : Coverage Histogram



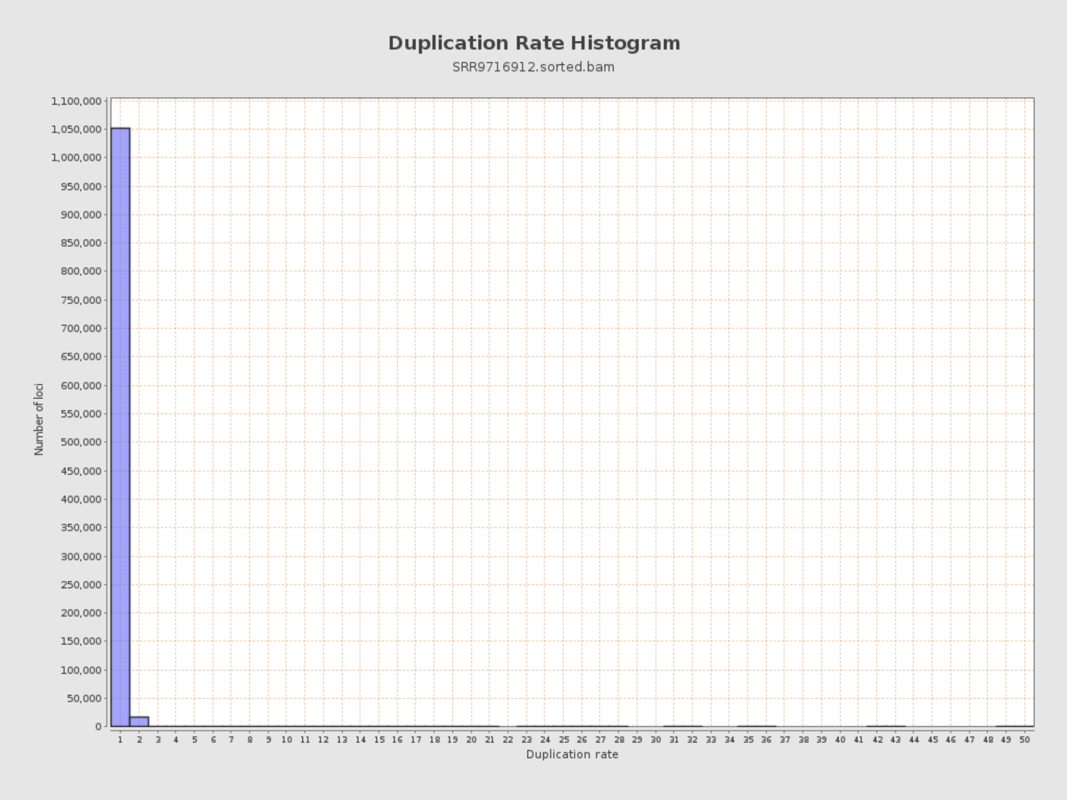
5. Results : Coverage Histogram (0-50X)



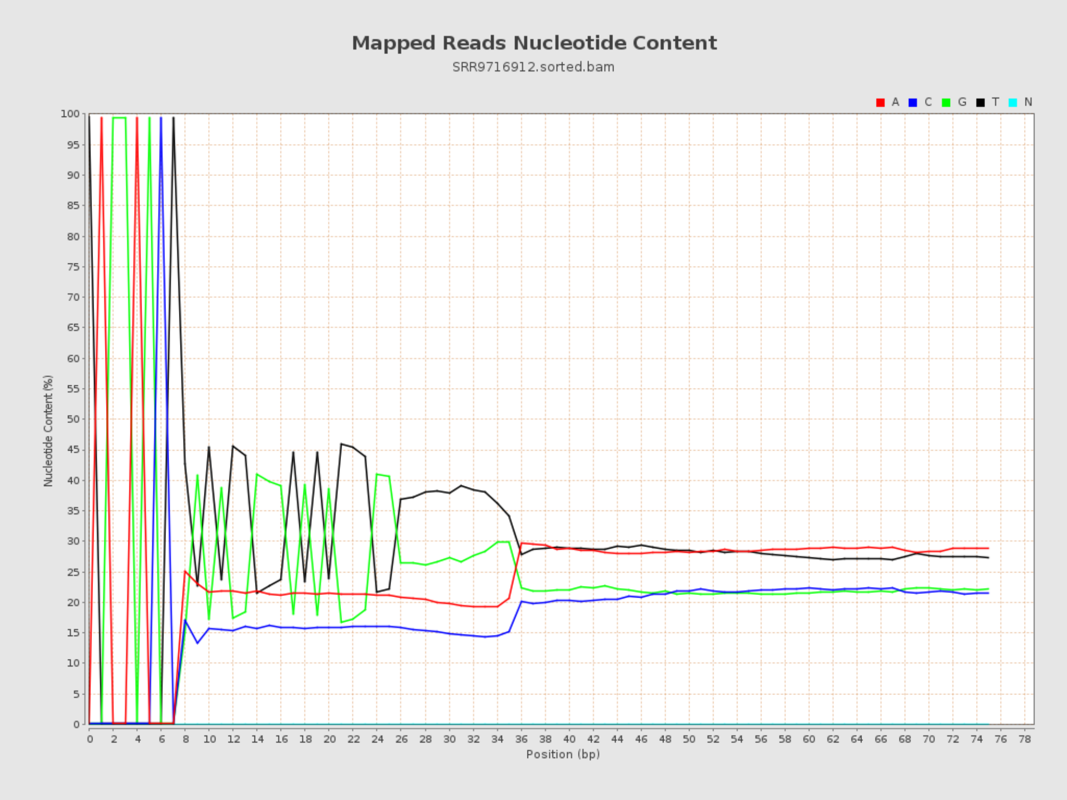
6. Results : Genome Fraction Coverage



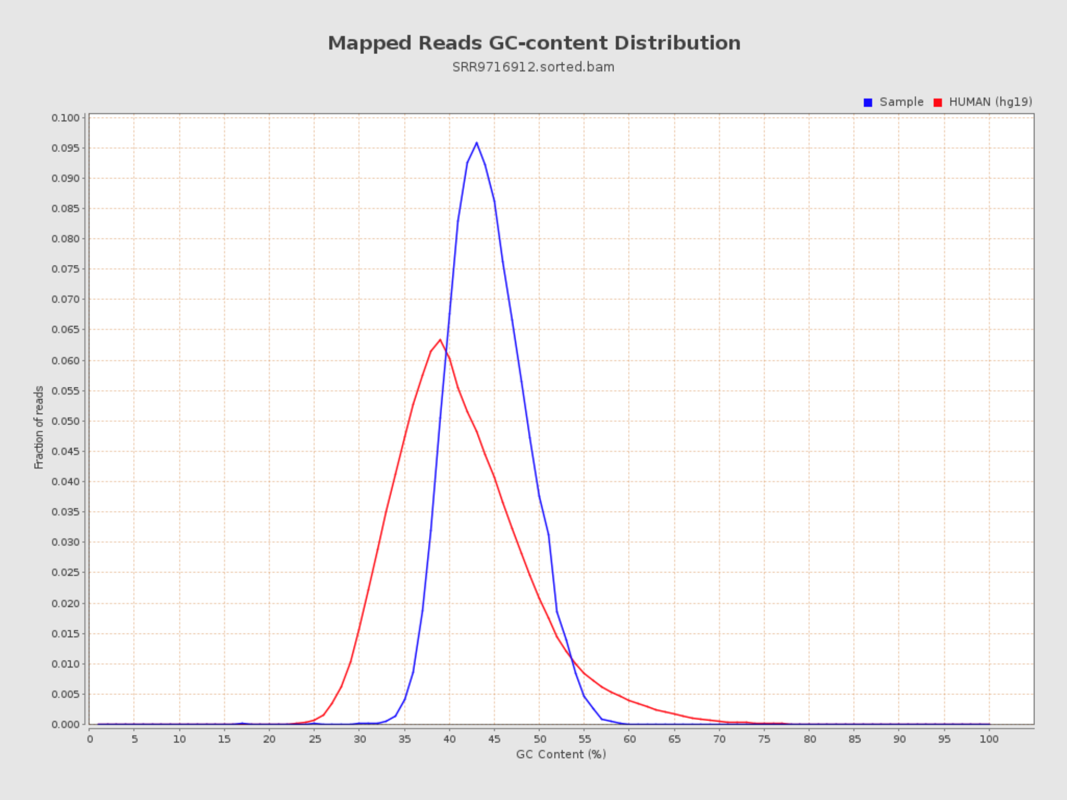
7. Results : Duplication Rate Histogram



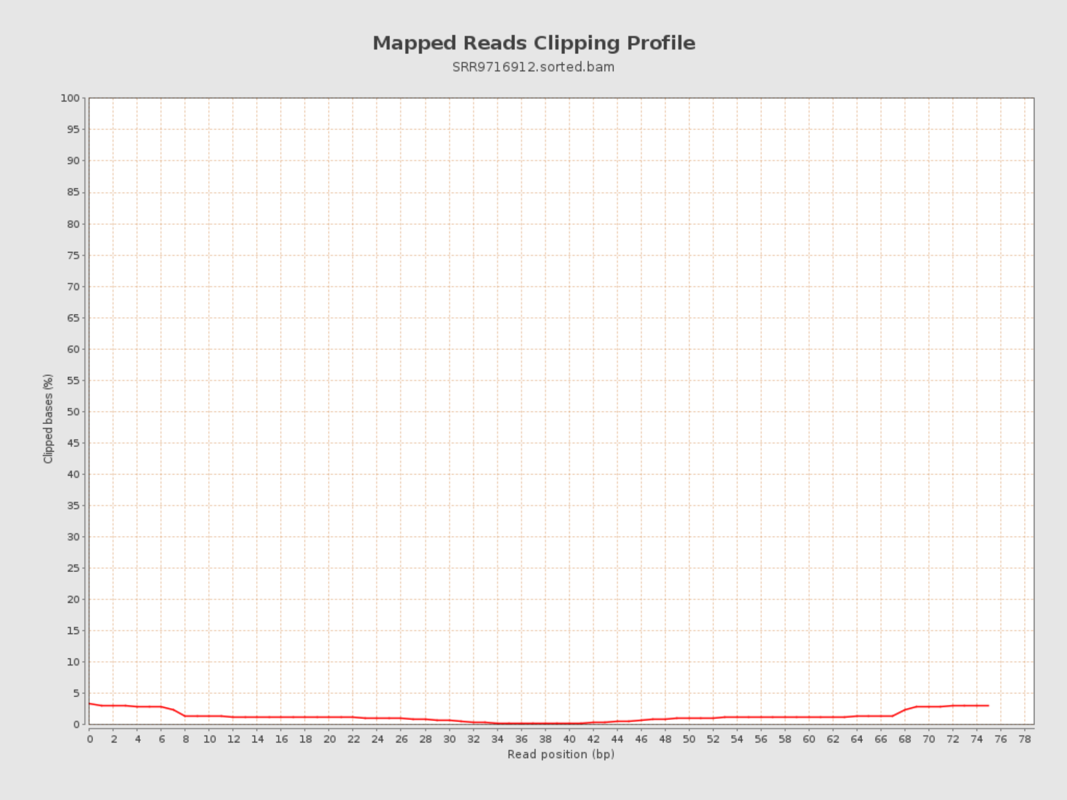
8. Results : Mapped Reads Nucleotide Content



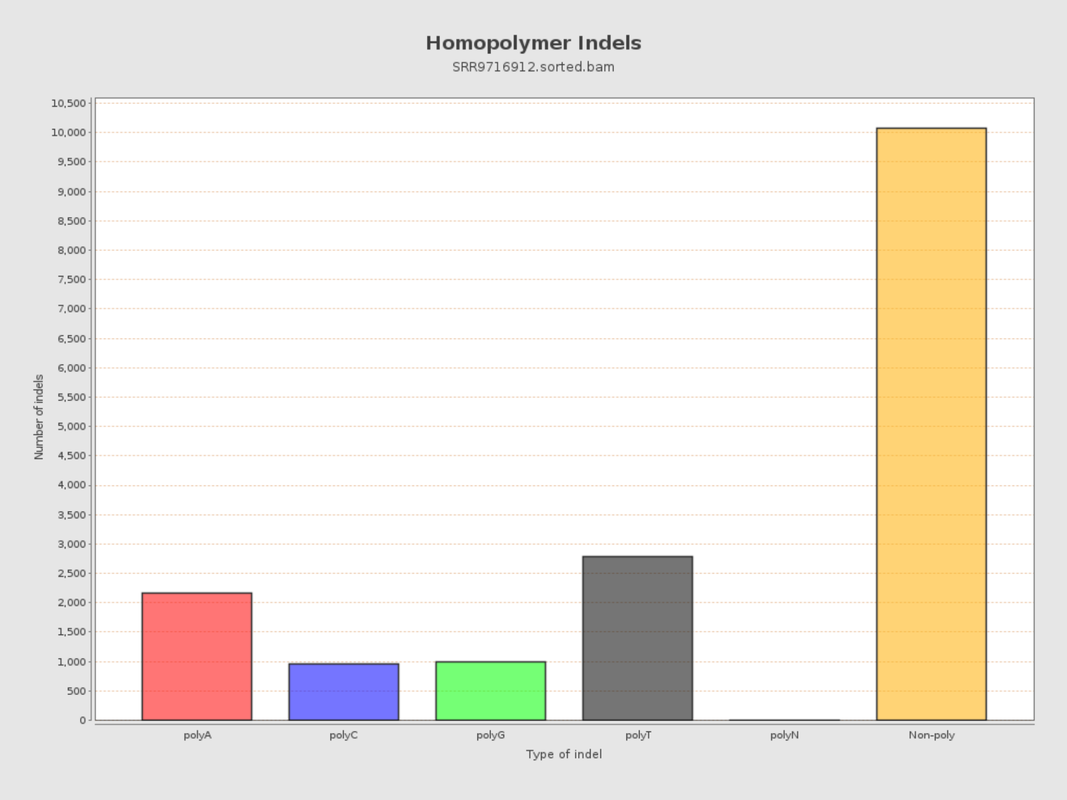
9. Results : Mapped Reads GC-content Distribution



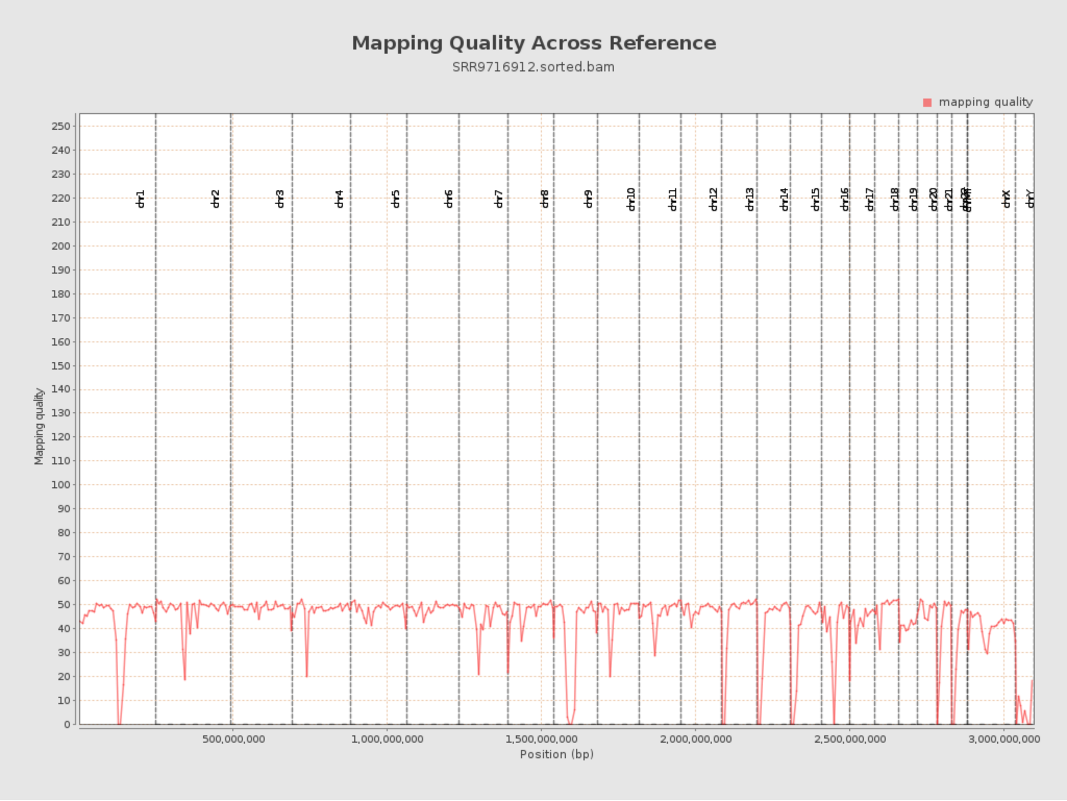
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram