Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716612.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_SRR9716612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716612.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:33:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,086,441
Mapped reads	997,800 / 91.84%
Unmapped reads	88,641 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,078 / 3.23%
Read min/max/mean length	30 / 101 / 102.17
Duplicated reads (estimated)	17,447 / 1.61%
Duplication rate	1.06%
Clipped reads	1,031,674 / 94.96%

2.2. ACGT Content

Number/percentage of A's	18,367,356 / 24.44%
Number/percentage of C's	15,638,703 / 20.81%
Number/percentage of T's	22,363,966 / 29.75%
Number/percentage of G's	18,785,845 / 24.99%
Number/percentage of N's	9,357 / 0.01%
GC Percentage	45.8%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2226

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Mismatches and indels

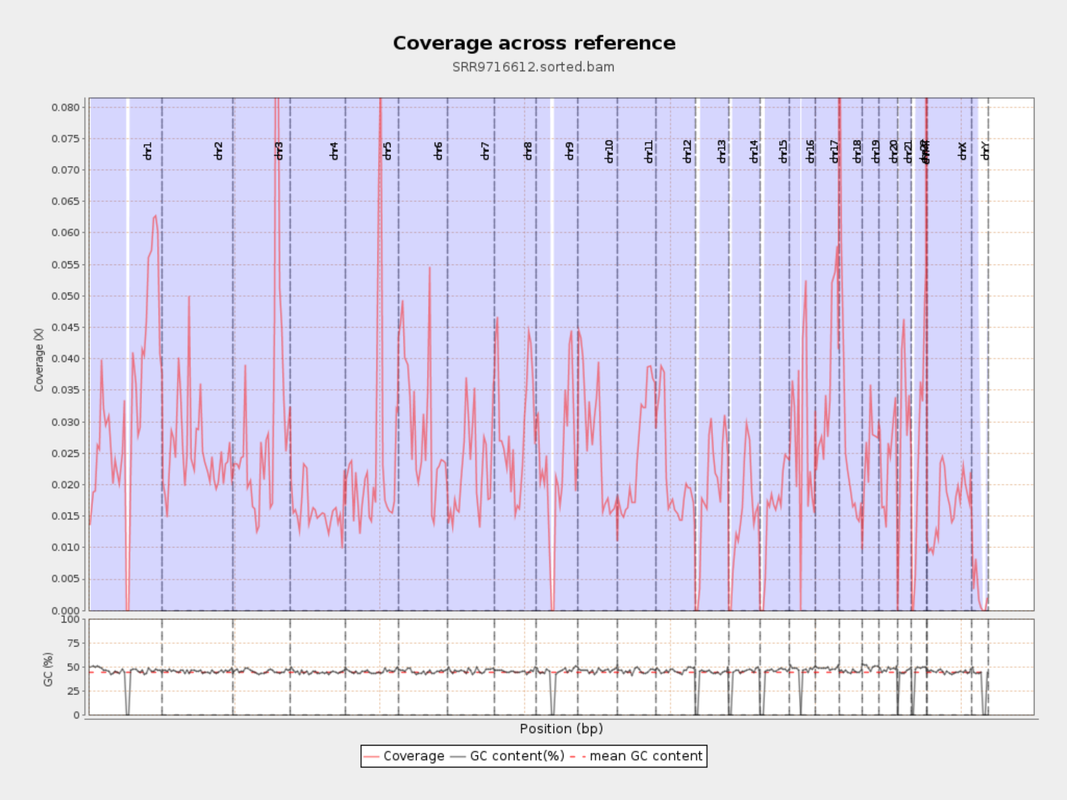
General error rate	0.76%
Mismatches	560,390
Insertions	6,236
Mapped reads with at least one insertion	0.62%
Deletions	15,694
Mapped reads with at least one deletion	1.55%
Homopolymer indels	40.26%

2.6. Chromosome stats

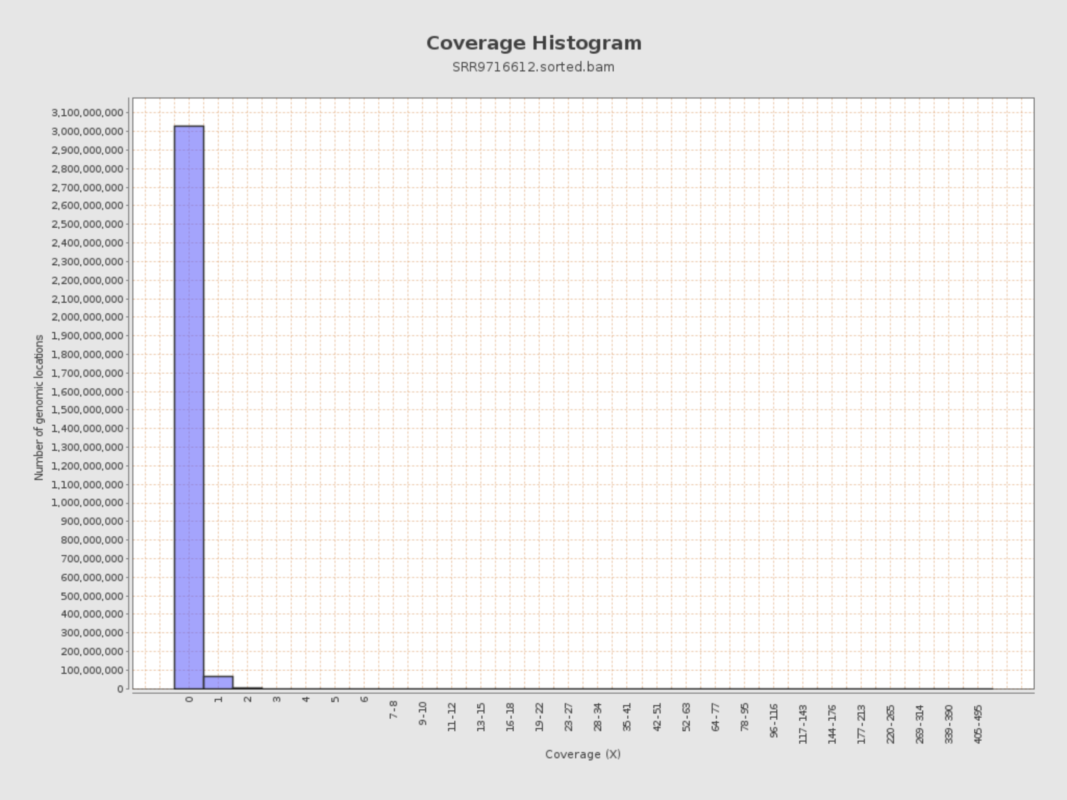
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8022337	0.0322	0.2503
chr2	243199373	6151861	0.0253	0.3732
chr3	198022430	5918200	0.0299	0.1883
chr4	191154276	3030779	0.0159	0.1393
chr5	180915260	4355530	0.0241	0.1666
chr6	171115067	5118766	0.0299	0.204
chr7	159138663	3625298	0.0228	0.2775

chr8	146364022	4259148	0.0291	0.2791
chr9	141213431	3209327	0.0227	0.206
chr10	135534747	3719012	0.0274	0.2087
chr11	135006516	3410944	0.0253	0.2067
chr12	133851895	2871488	0.0215	0.156
chr13	115169878	2244320	0.0195	0.1482
chr14	107349540	1603480	0.0149	0.1368
chr15	102531392	1592119	0.0155	0.1325
chr16	90354753	2422929	0.0268	0.1891
chr17	81195210	2941985	0.0362	0.2192
chr18	78077248	2236118	0.0286	0.3663
chr19	59128983	1530302	0.0259	0.2291
chr20	63025520	1479500	0.0235	0.1718
chr21	48129895	1415772	0.0294	0.1882
chr22	51304566	1220509	0.0238	0.1687
chrMT	16571	35282	2.1291	2.2574
chrX	155270560	2611343	0.0168	0.1534
chrY	59373566	166601	0.0028	0.0828

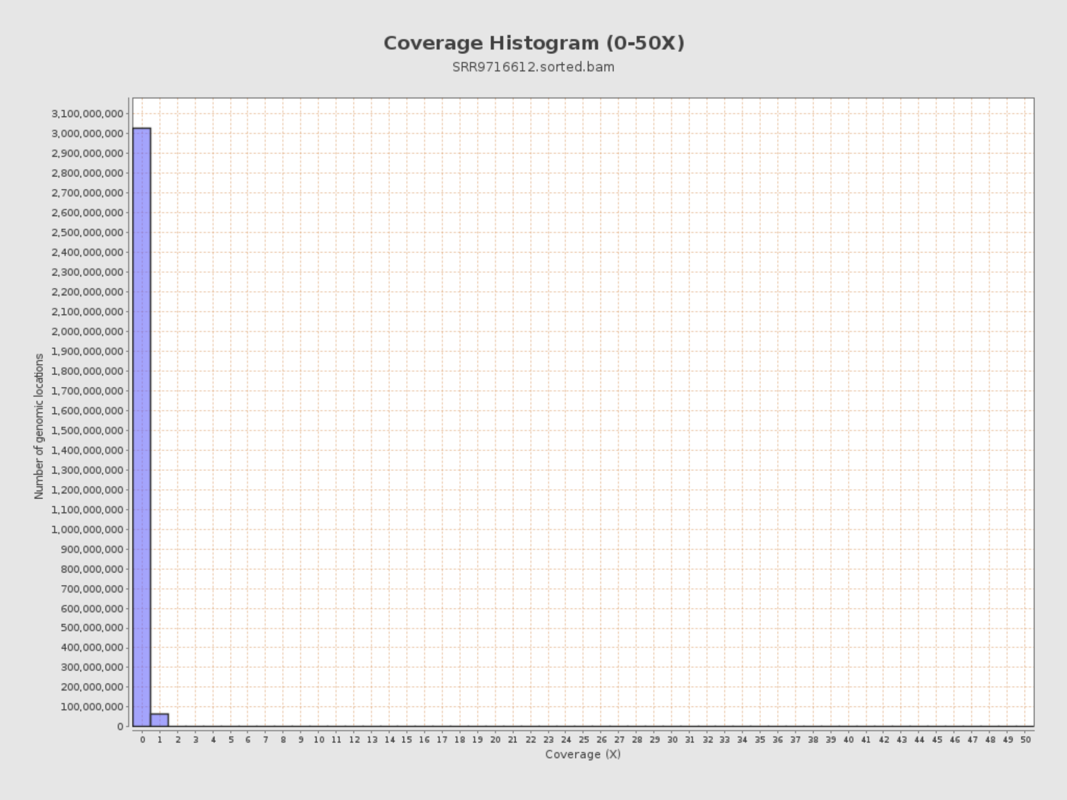
3. Results : Coverage across reference



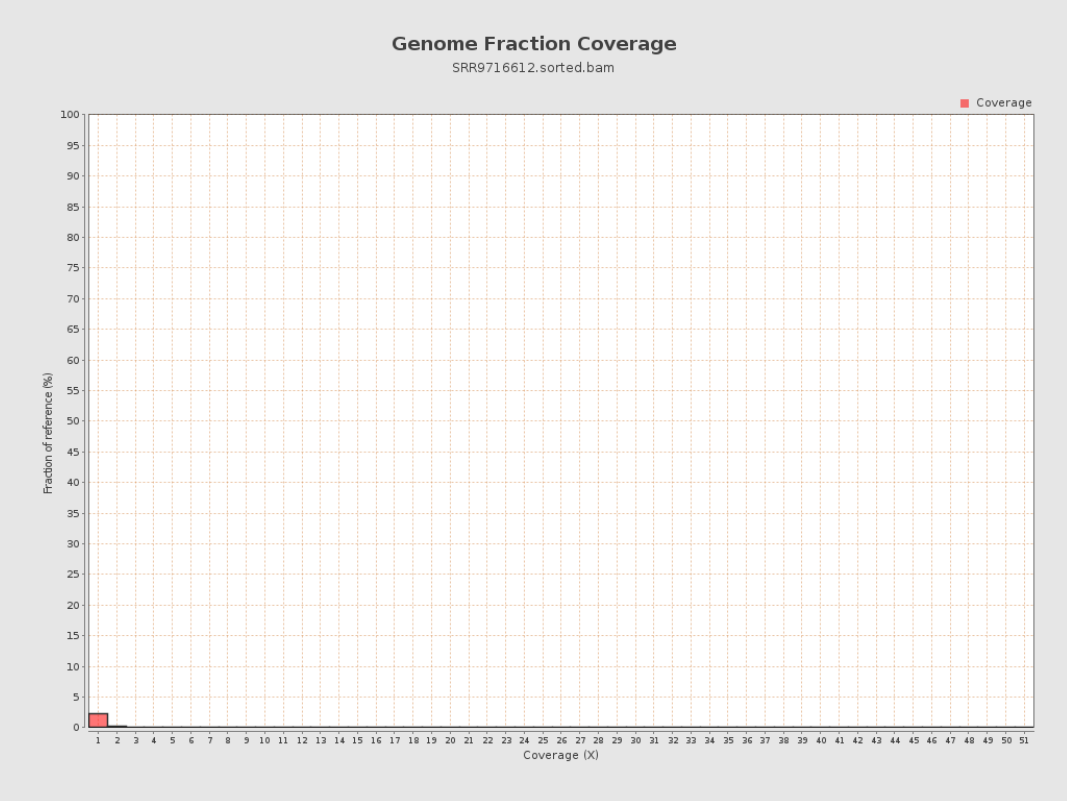
4. Results : Coverage Histogram



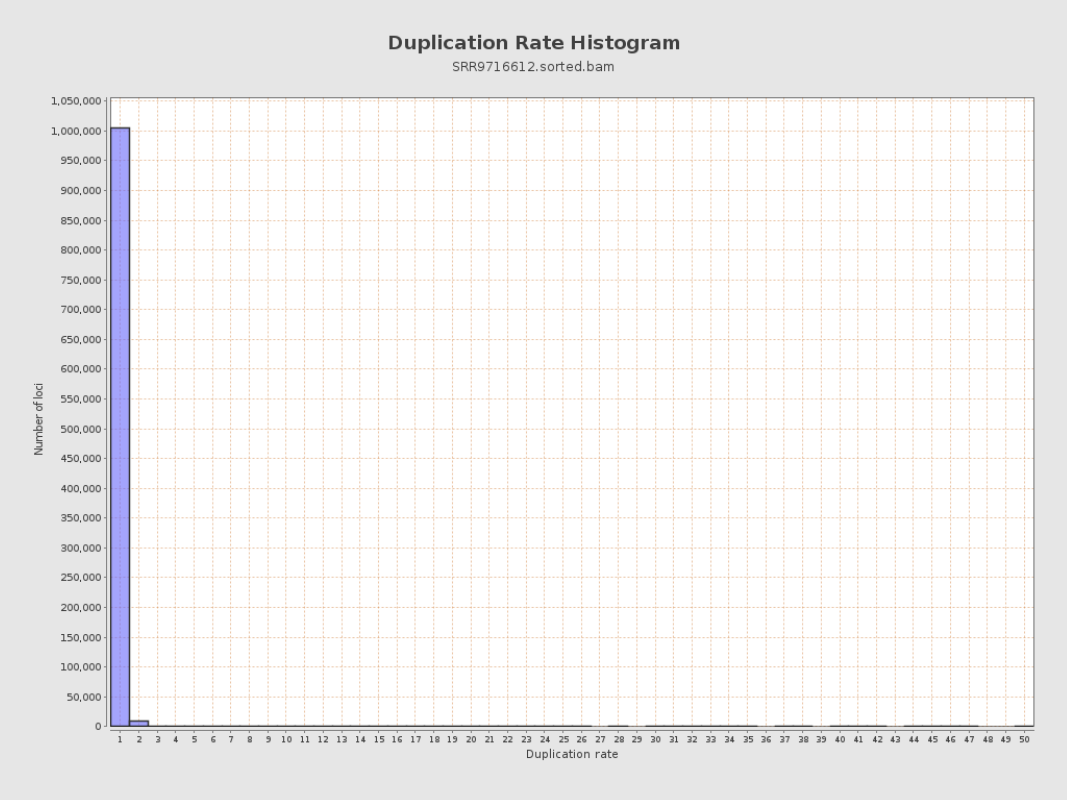
5. Results : Coverage Histogram (0-50X)



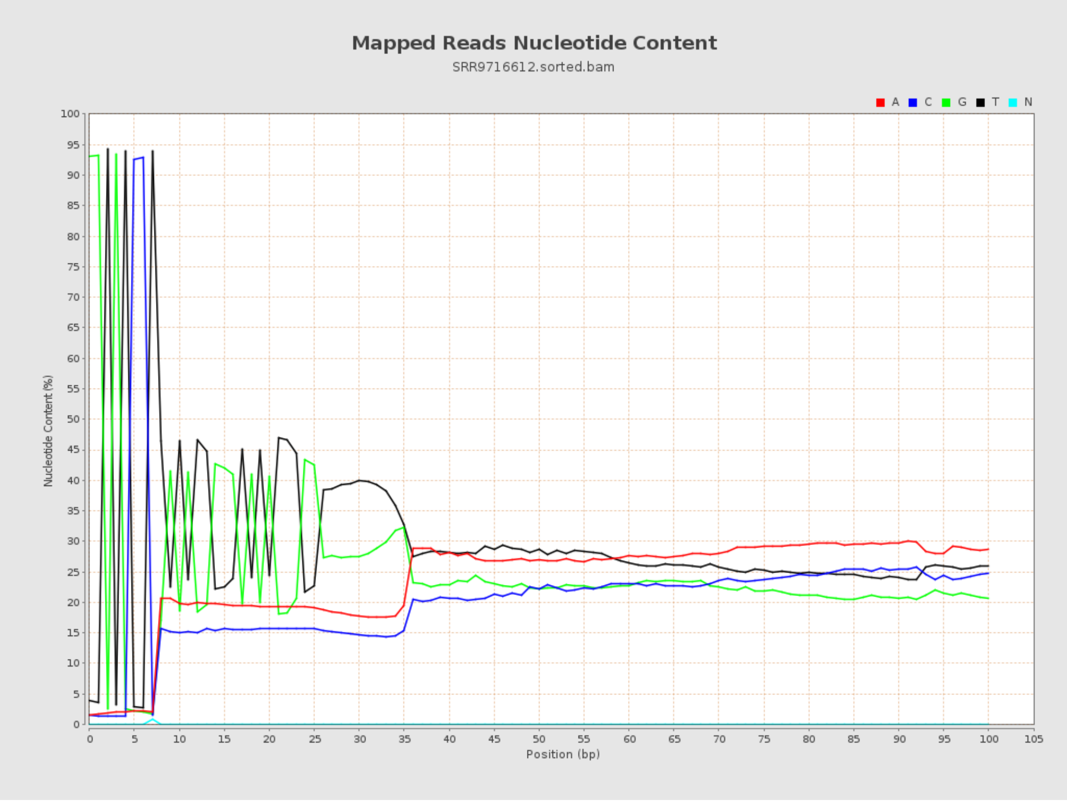
6. Results : Genome Fraction Coverage



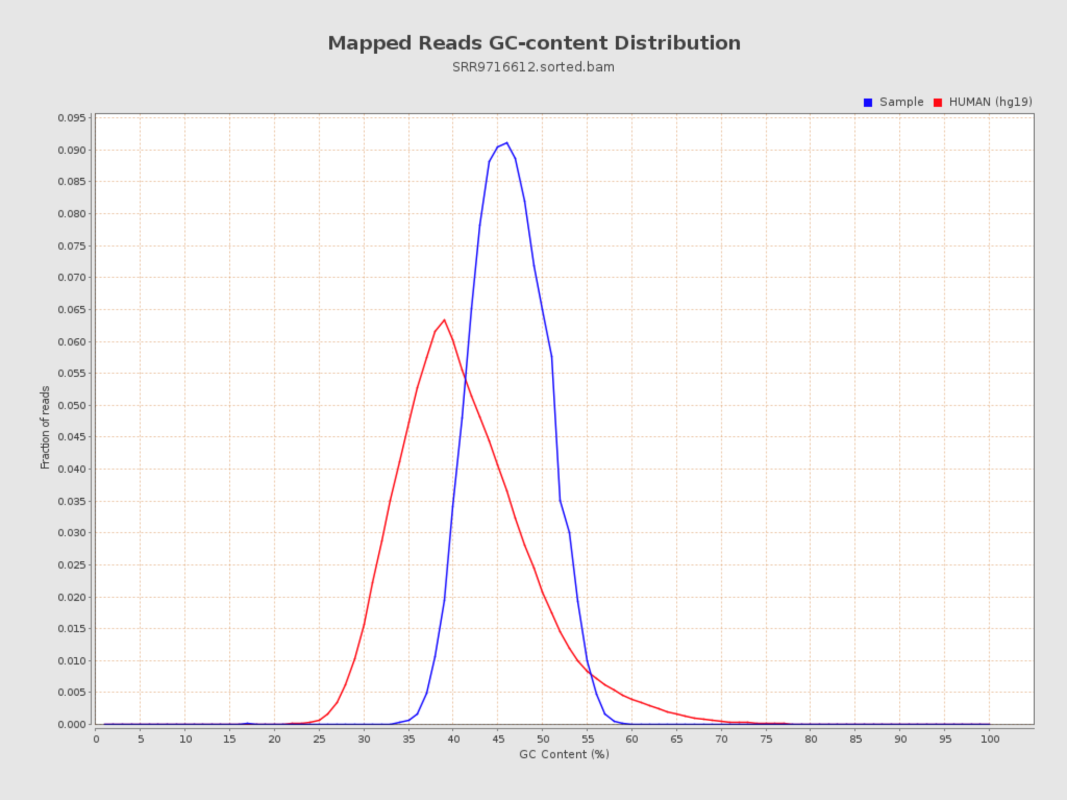
7. Results : Duplication Rate Histogram



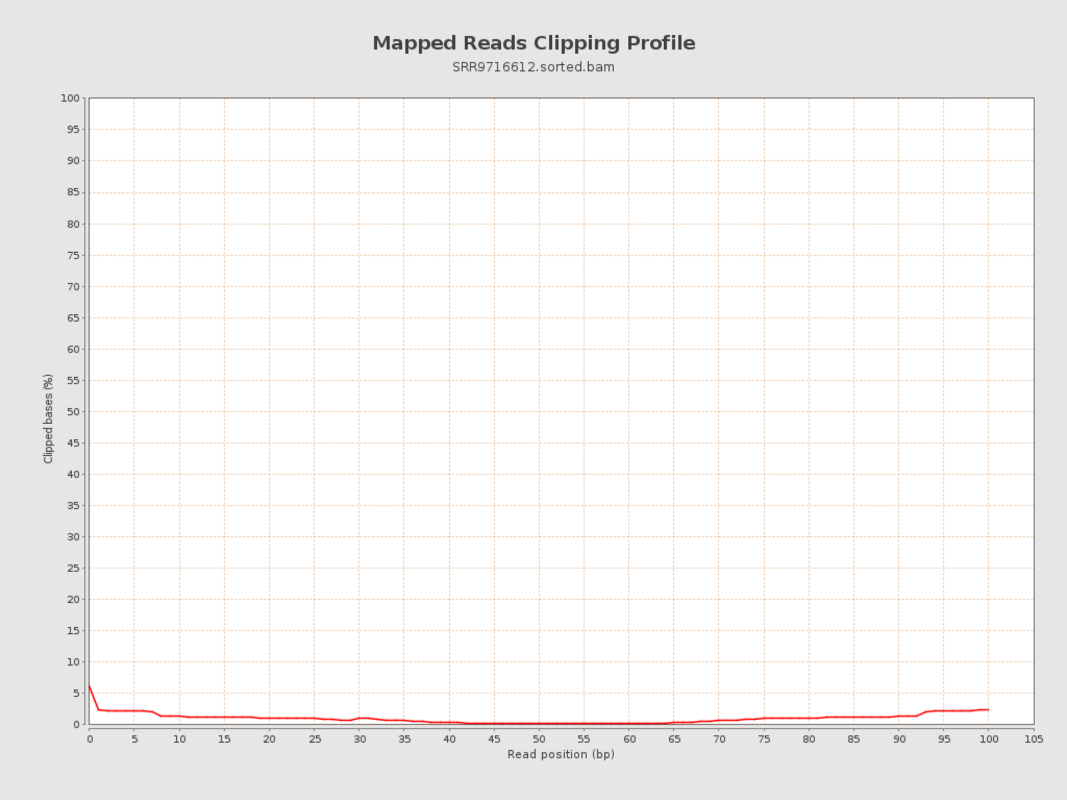
8. Results : Mapped Reads Nucleotide Content



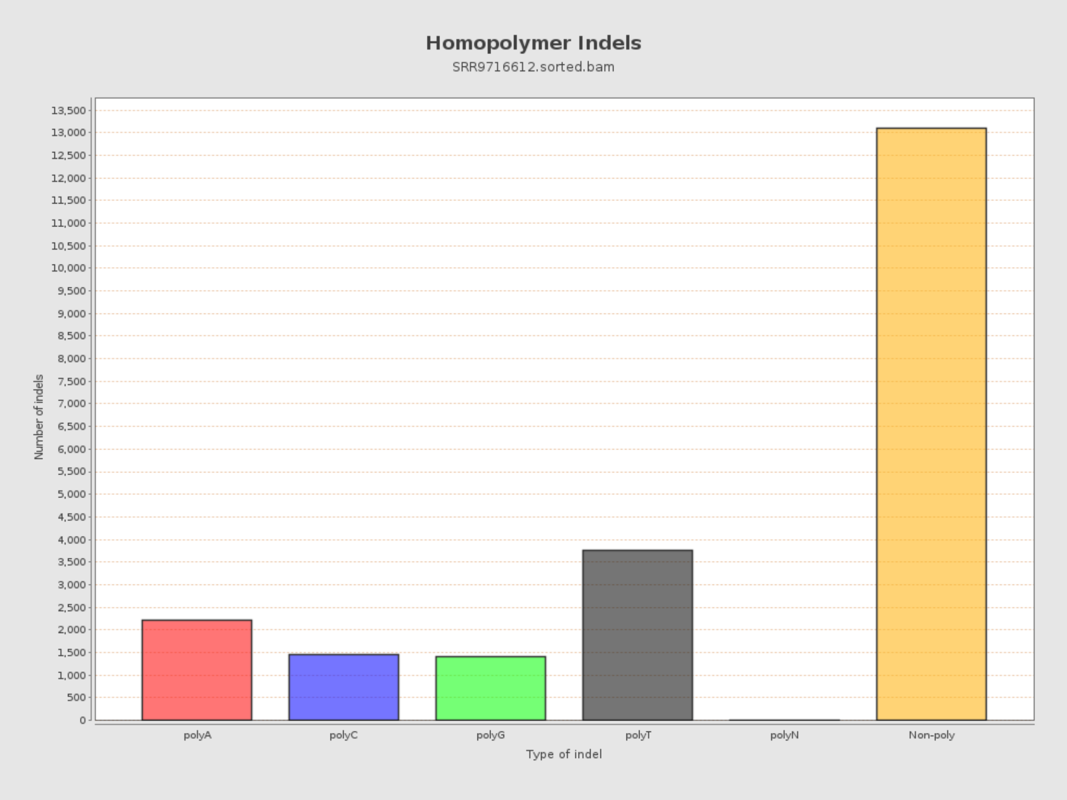
9. Results : Mapped Reads GC-content Distribution



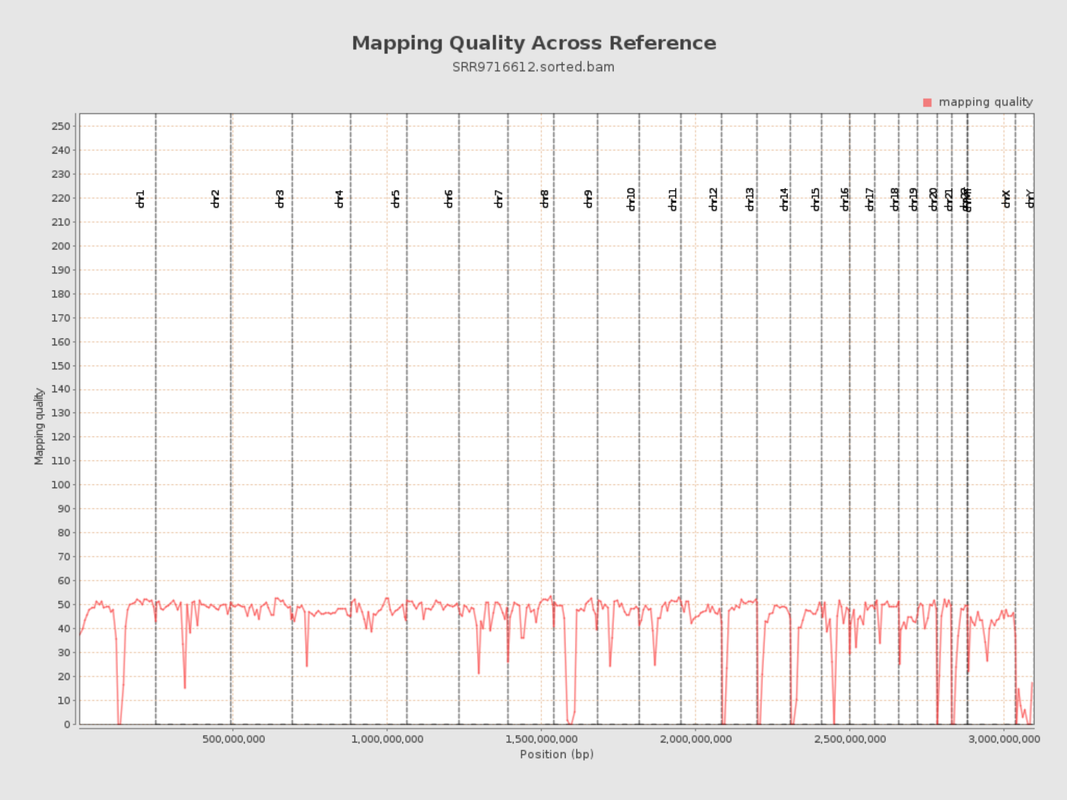
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram