Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:12:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716262.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_SRR9716262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:12:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	515,225
Mapped reads	422,499 / 82%
Unmapped reads	92,726 / 18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,110 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	6,786 / 1.32%
Duplication rate	1.28%
Clipped reads	423,941 / 82.28%

2.2. ACGT Content

Number/percentage of A's	6,165,490 / 25.36%
Number/percentage of C's	4,725,722 / 19.44%
Number/percentage of T's	7,598,741 / 31.26%
Number/percentage of G's	5,818,974 / 23.94%
Number/percentage of N's	360 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1031

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

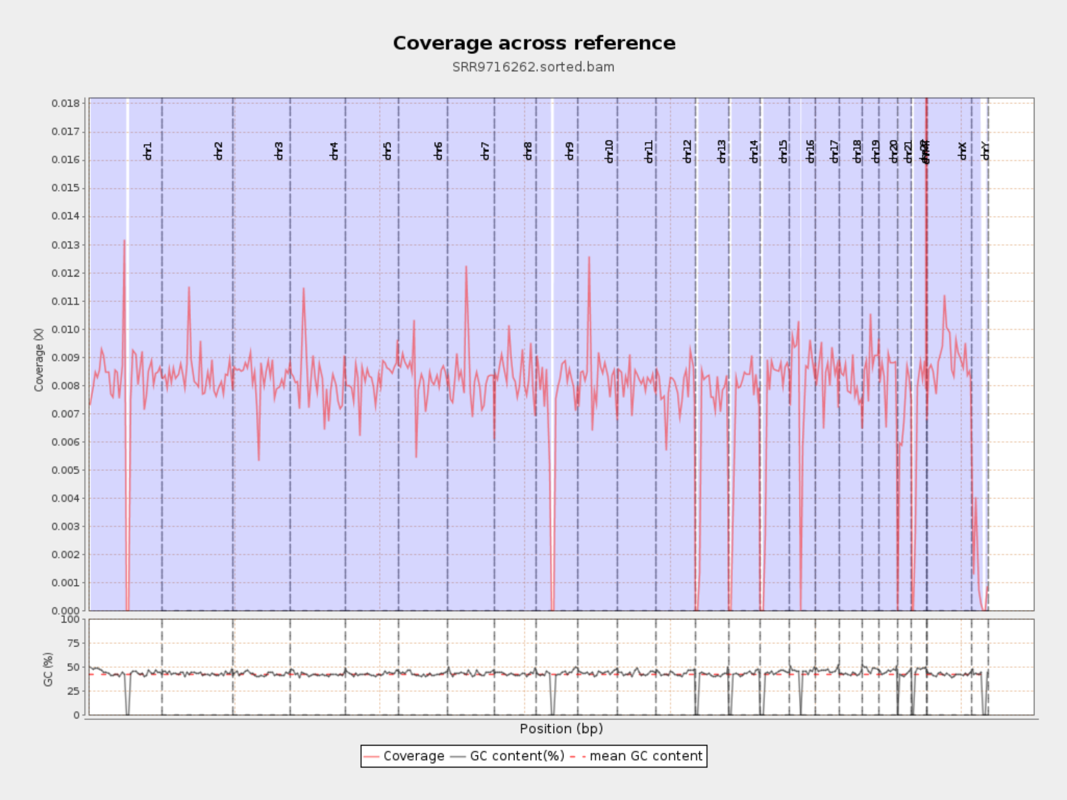
General error rate	0.5%
Mismatches	118,853
Insertions	1,484
Mapped reads with at least one insertion	0.35%
Deletions	4,240
Mapped reads with at least one deletion	1%
Homopolymer indels	41.7%

2.6. Chromosome stats

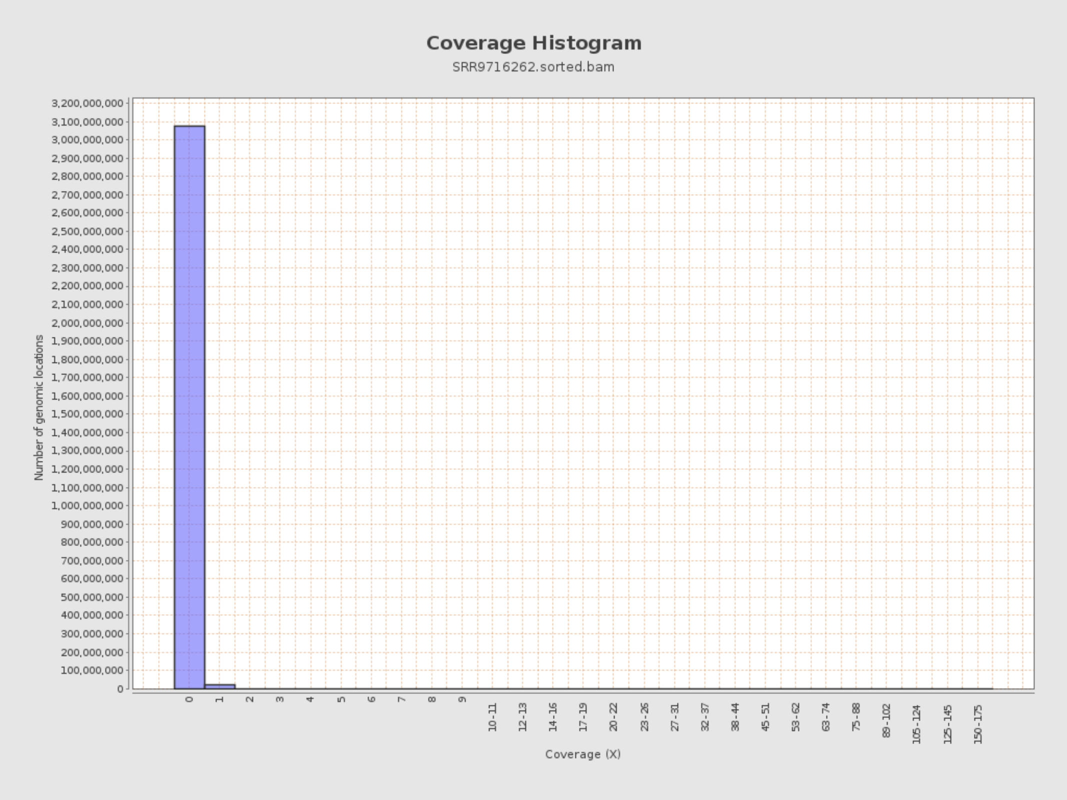
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1986309	0.008	0.1466
chr2	243199373	2039010	0.0084	0.1196
chr3	198022430	1635185	0.0083	0.0941
chr4	191154276	1552266	0.0081	0.0946
chr5	180915260	1488807	0.0082	0.0936
chr6	171115067	1420238	0.0083	0.0988
chr7	159138663	1317945	0.0083	0.112

chr8	146364022	1230358	0.0084	0.1027
chr9	141213431	1004701	0.0071	0.0929
chr10	135534747	1134220	0.0084	0.1017
chr11	135006516	1097660	0.0081	0.0993
chr12	133851895	1056241	0.0079	0.0919
chr13	115169878	758025	0.0066	0.0836
chr14	107349540	732358	0.0068	0.0875
chr15	102531392	706784	0.0069	0.0865
chr16	90354753	727134	0.008	0.0936
chr17	81195210	679176	0.0084	0.0955
chr18	78077248	633473	0.0081	0.1189
chr19	59128983	519826	0.0088	0.1186
chr20	63025520	525071	0.0083	0.0947
chr21	48129895	311191	0.0065	0.0844
chr22	51304566	298954	0.0058	0.0789
chrMT	16571	1391	0.0839	0.2956
chrX	155270560	1387316	0.0089	0.0995
chrY	59373566	72123	0.0012	0.0414

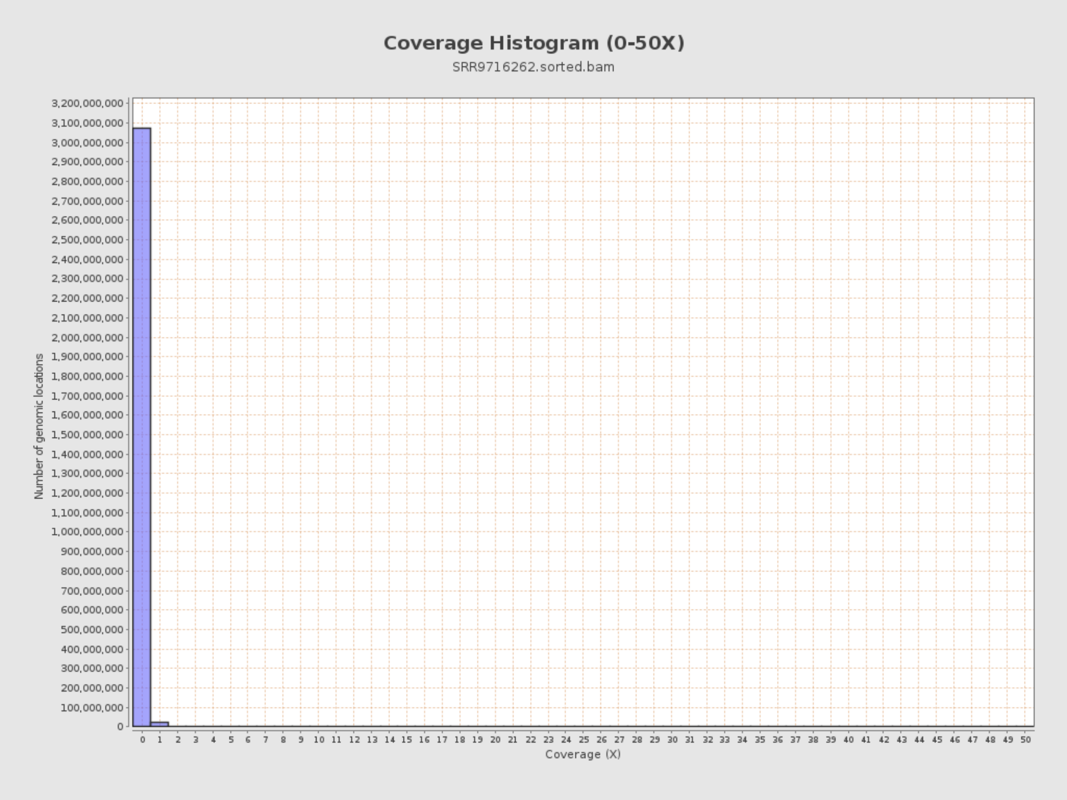
3. Results : Coverage across reference



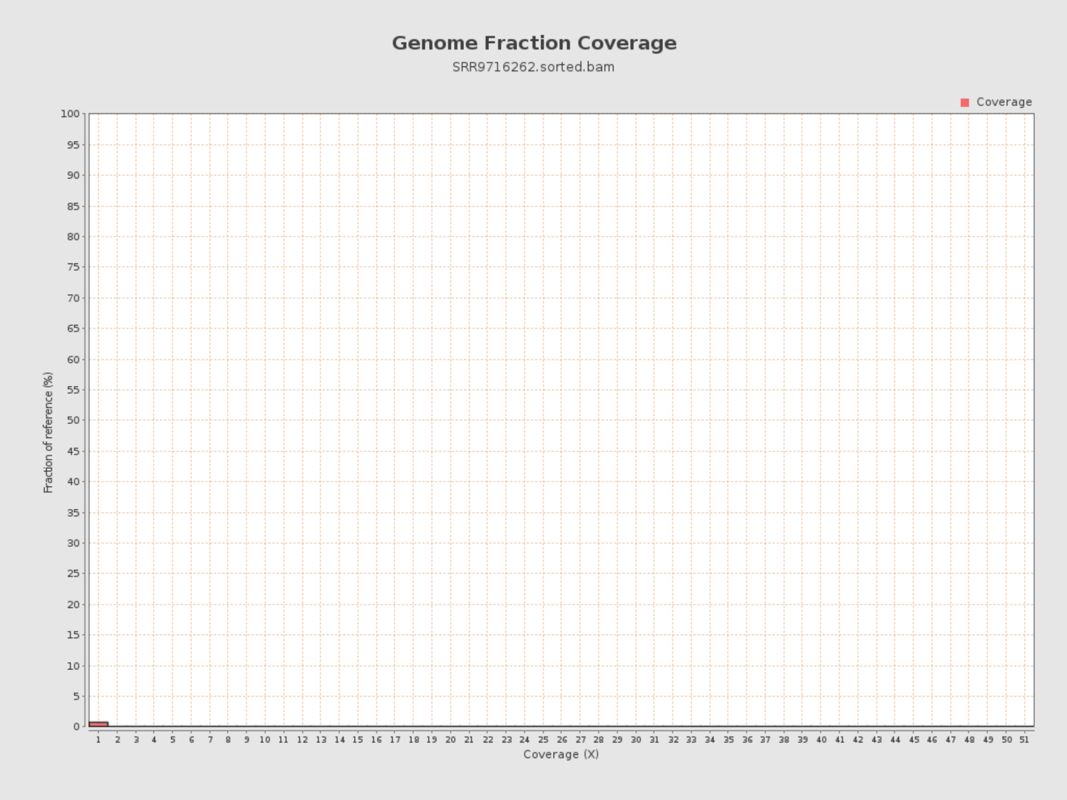
4. Results : Coverage Histogram



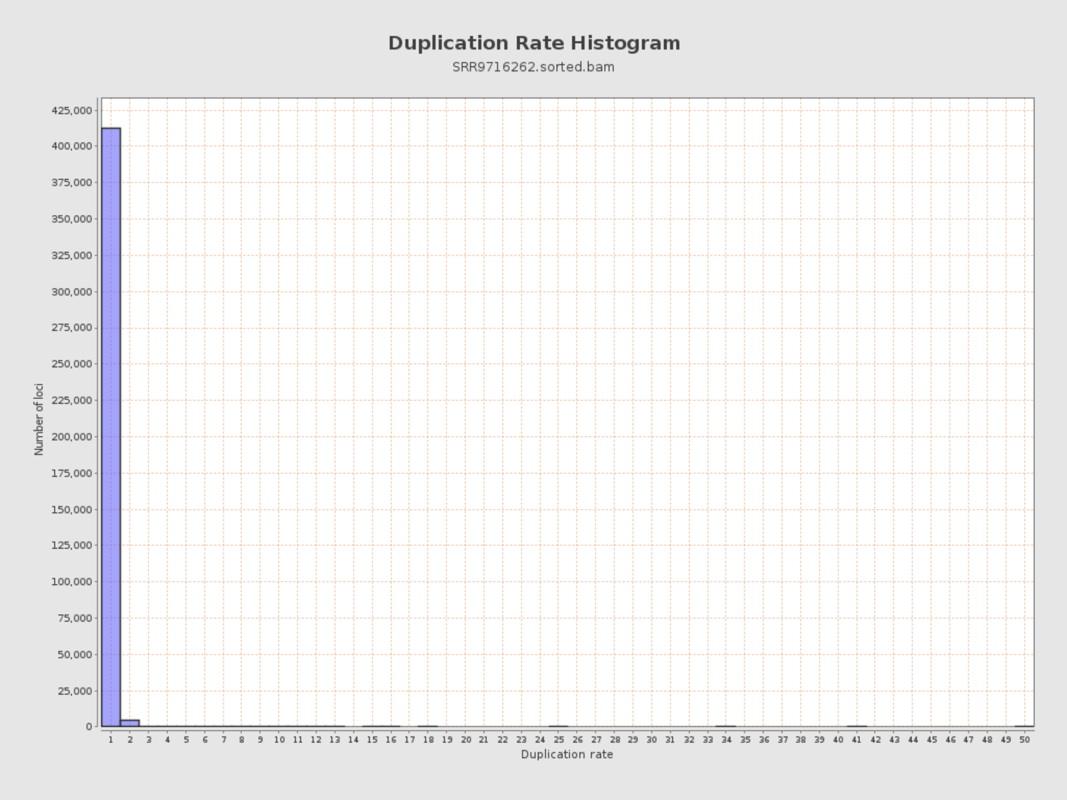
5. Results : Coverage Histogram (0-50X)



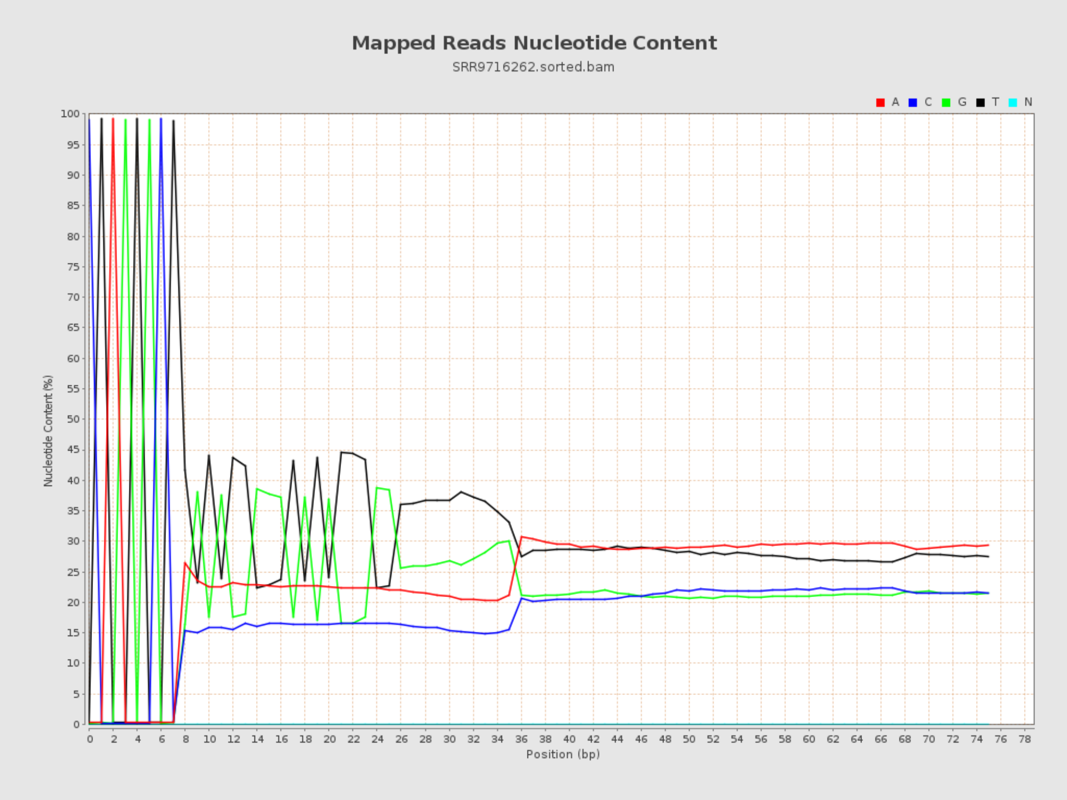
6. Results : Genome Fraction Coverage



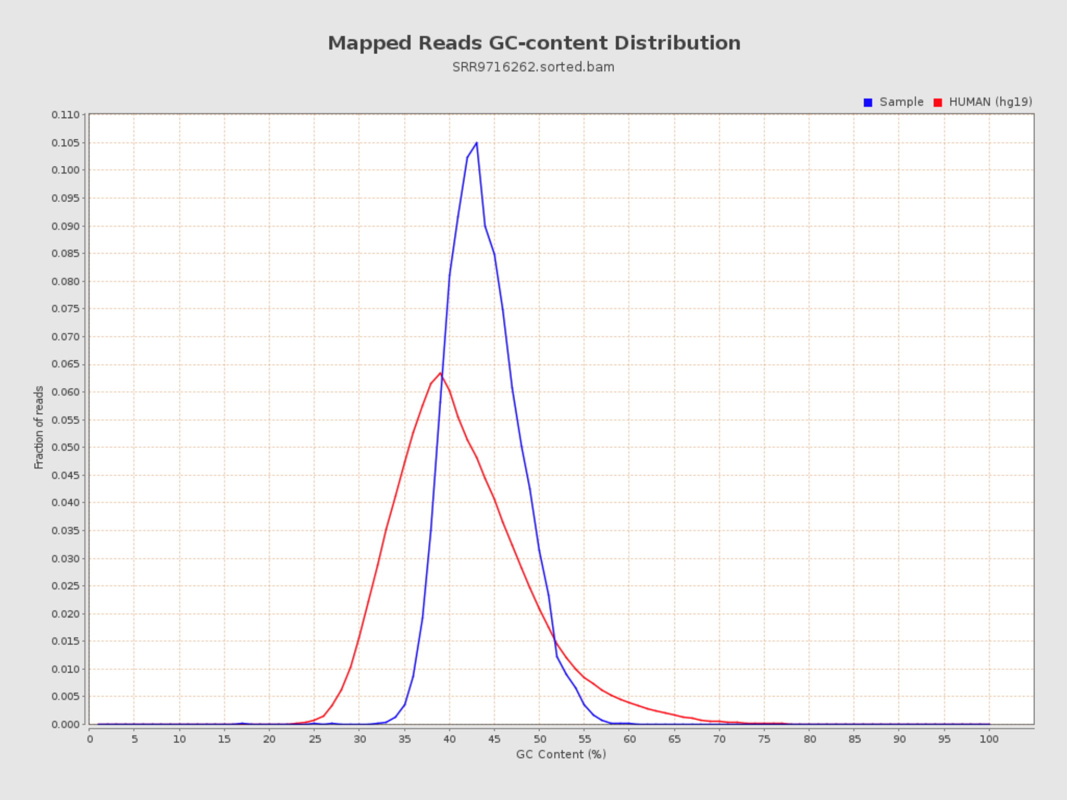
7. Results : Duplication Rate Histogram



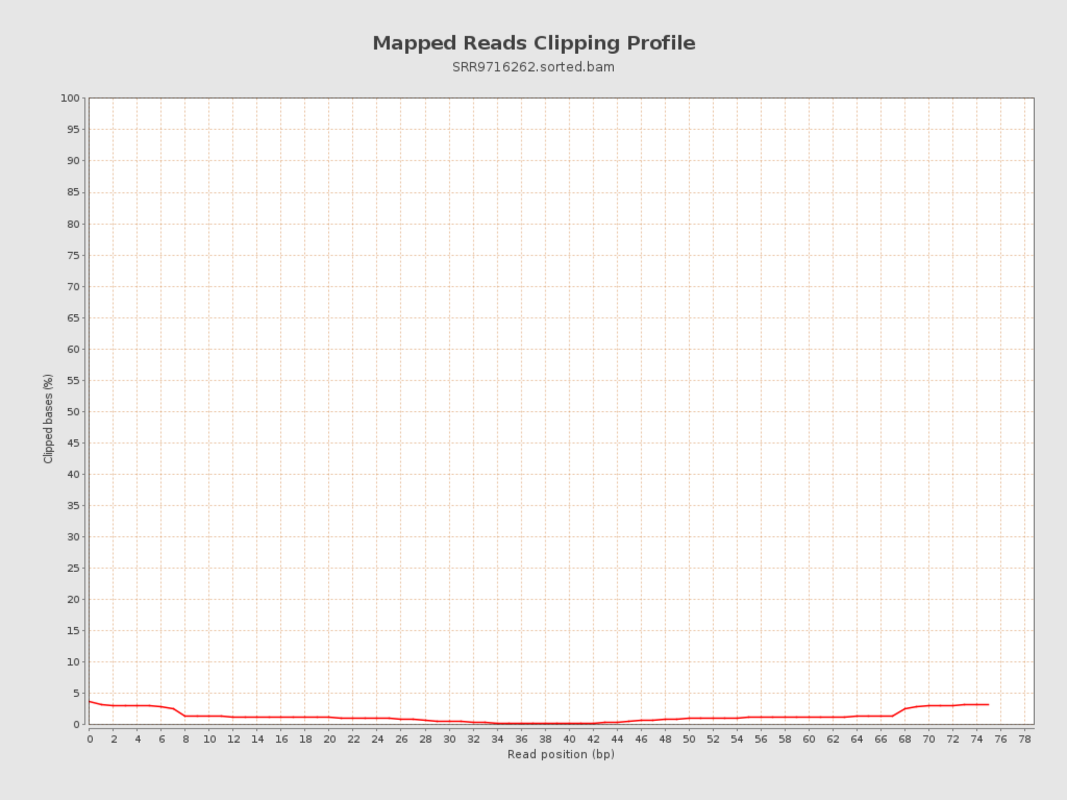
8. Results : Mapped Reads Nucleotide Content



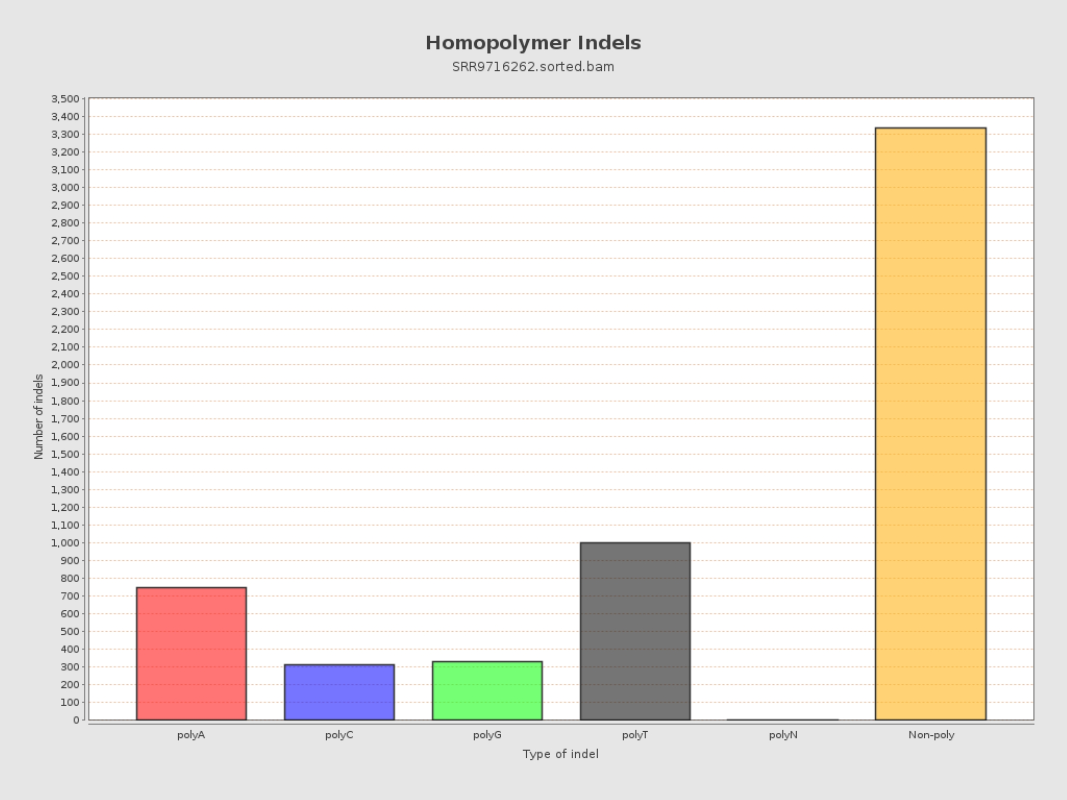
9. Results : Mapped Reads GC-content Distribution



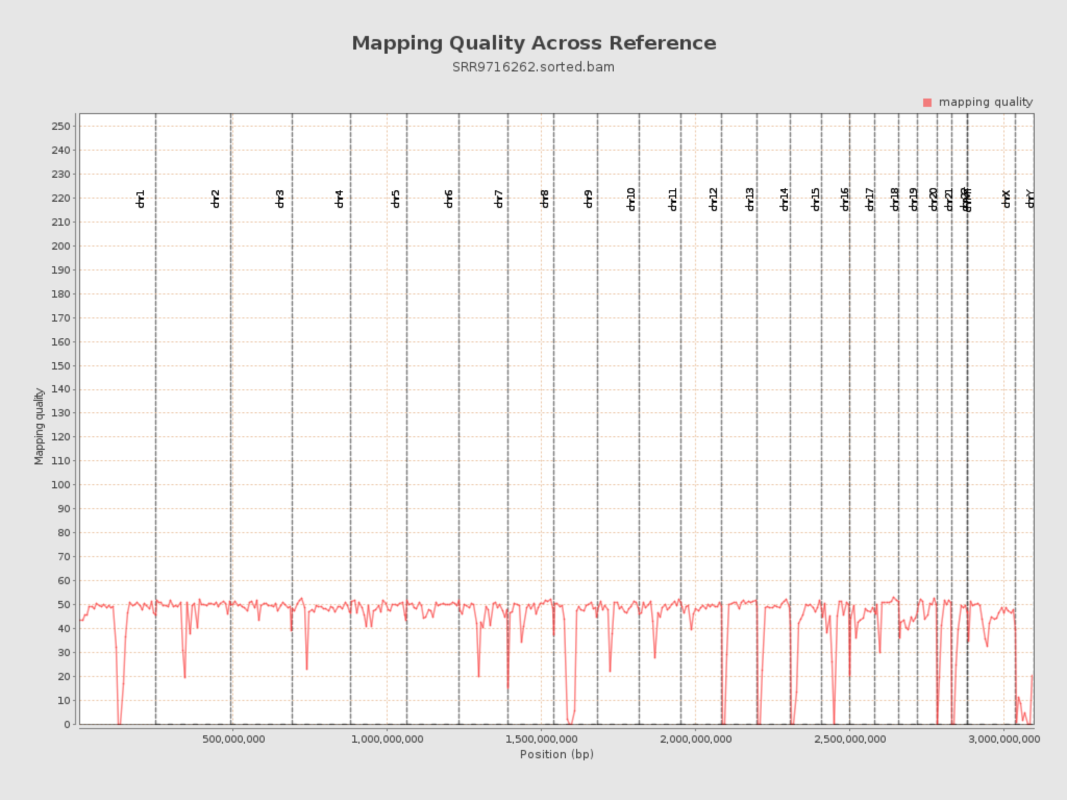
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram