Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:23:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716484.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_SRR9716484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716484.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:23:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	449,773
Mapped reads	405,711 / 90.2%
Unmapped reads	44,062 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,254 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,096 / 1.58%
Duplication rate	1.42%
Clipped reads	407,448 / 90.59%

2.2. ACGT Content

Number/percentage of A's	5,811,544 / 24.69%
Number/percentage of C's	4,750,701 / 20.19%
Number/percentage of T's	7,213,806 / 30.65%
Number/percentage of G's	5,757,254 / 24.46%
Number/percentage of N's	284 / 0%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.1007

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

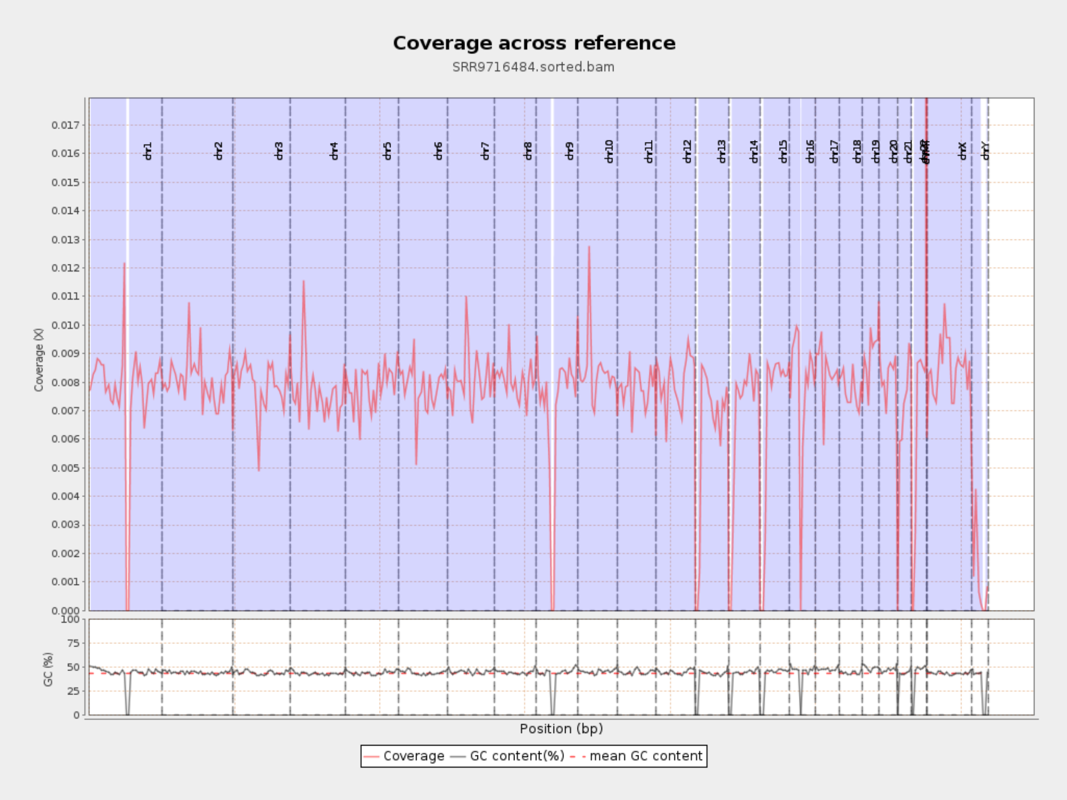
General error rate	0.51%
Mismatches	116,818
Insertions	1,510
Mapped reads with at least one insertion	0.37%
Deletions	4,339
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.24%

2.6. Chromosome stats

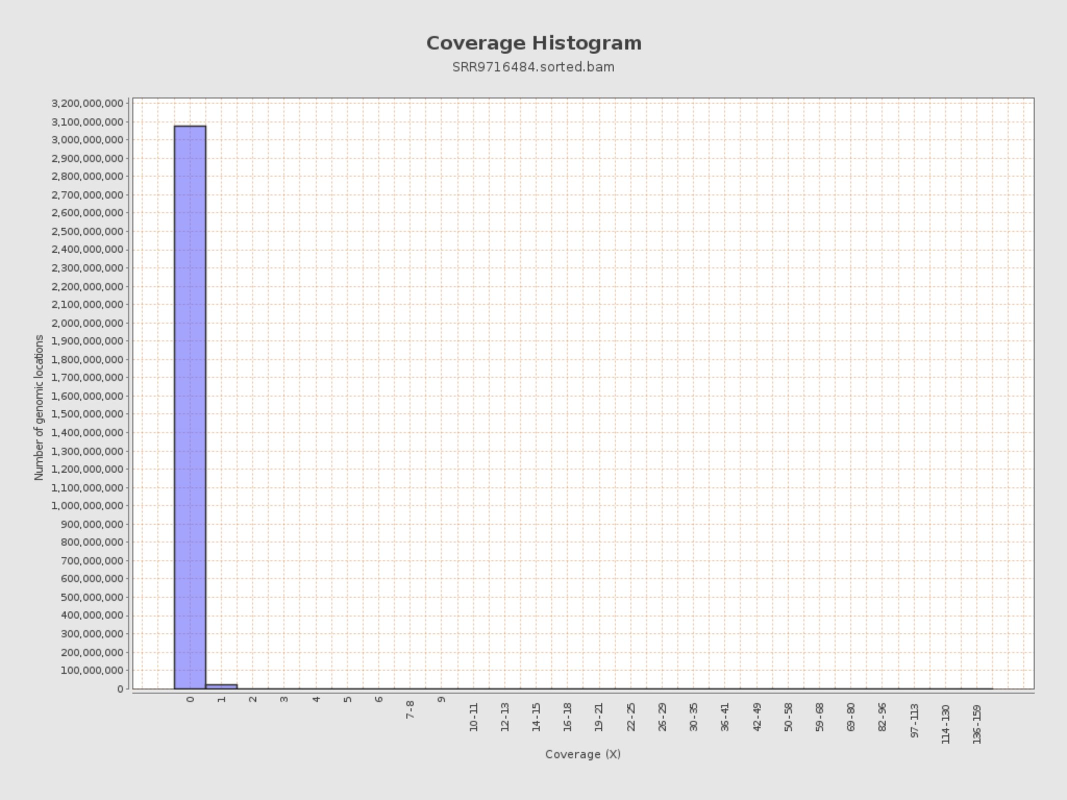
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1901758	0.0076	0.1407
chr2	243199373	1973292	0.0081	0.1157
chr3	198022430	1559097	0.0079	0.0915
chr4	191154276	1459501	0.0076	0.0921
chr5	180915260	1415935	0.0078	0.0916
chr6	171115067	1345702	0.0079	0.0949
chr7	159138663	1289762	0.0081	0.1086

chr8	146364022	1182091	0.0081	0.1006
chr9	141213431	978782	0.0069	0.0923
chr10	135534747	1136017	0.0084	0.1034
chr11	135006516	1057908	0.0078	0.0967
chr12	133851895	1078686	0.0081	0.0932
chr13	115169878	711256	0.0062	0.0813
chr14	107349540	710398	0.0066	0.0845
chr15	102531392	693336	0.0068	0.0852
chr16	90354753	705600	0.0078	0.0922
chr17	81195210	680439	0.0084	0.0964
chr18	78077248	604058	0.0077	0.1129
chr19	59128983	527666	0.0089	0.1167
chr20	63025520	513134	0.0081	0.0936
chr21	48129895	323672	0.0067	0.0862
chr22	51304566	304788	0.0059	0.0796
chrMT	16571	2808	0.1695	0.395
chrX	155270560	1312013	0.0084	0.0969
chrY	59373566	72831	0.0012	0.0458

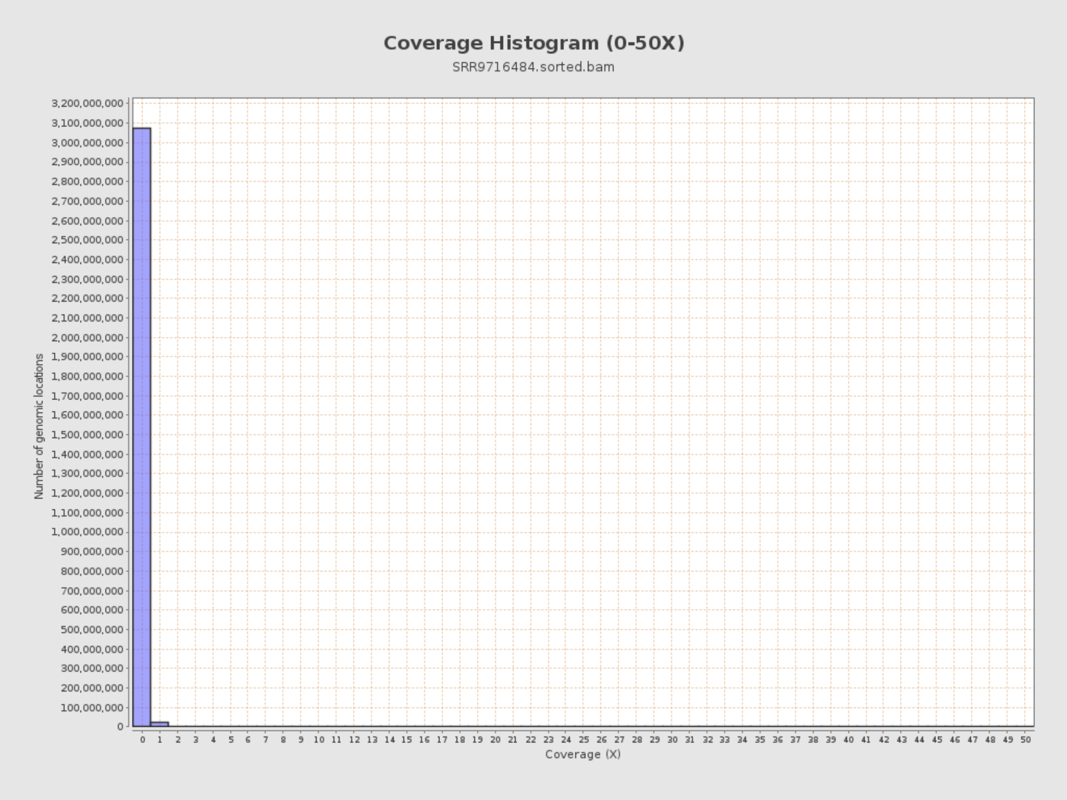
3. Results : Coverage across reference



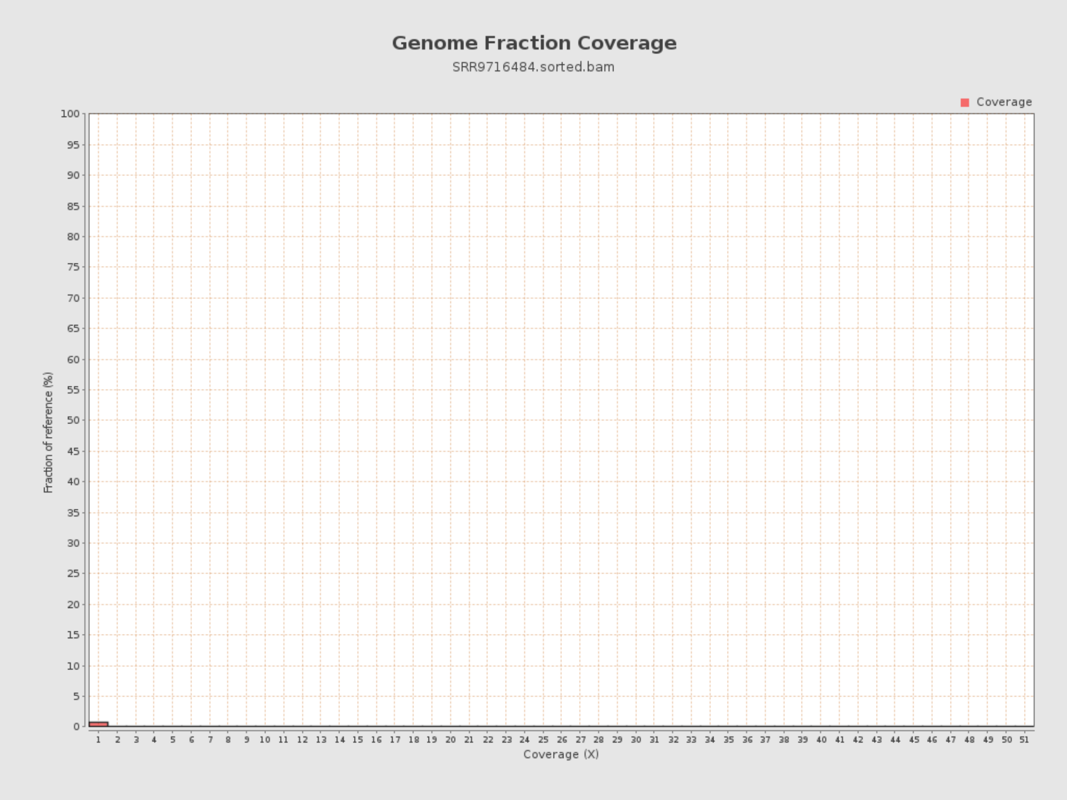
4. Results : Coverage Histogram



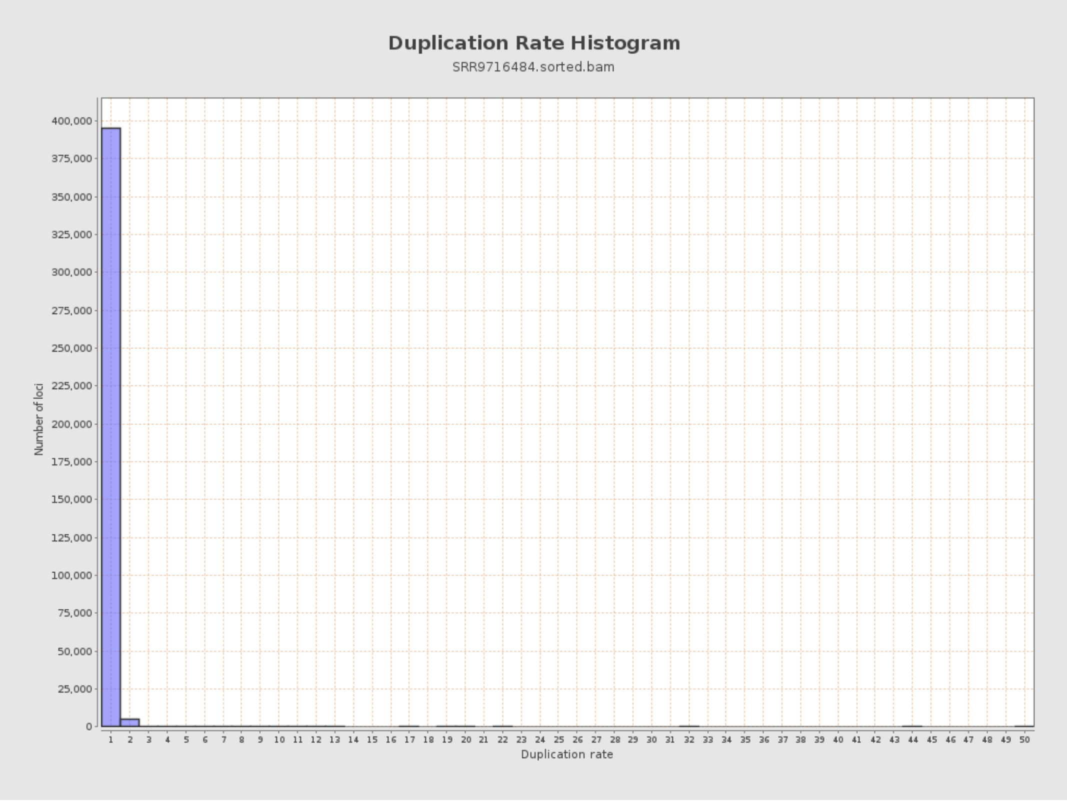
5. Results : Coverage Histogram (0-50X)



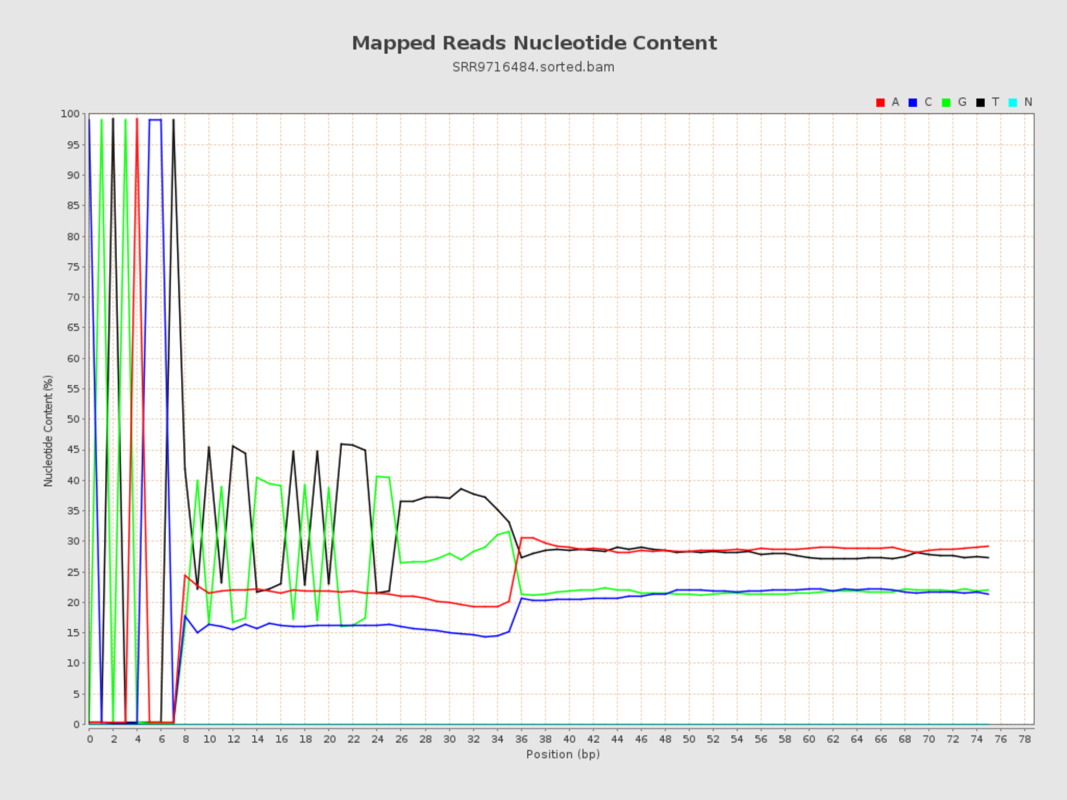
6. Results : Genome Fraction Coverage



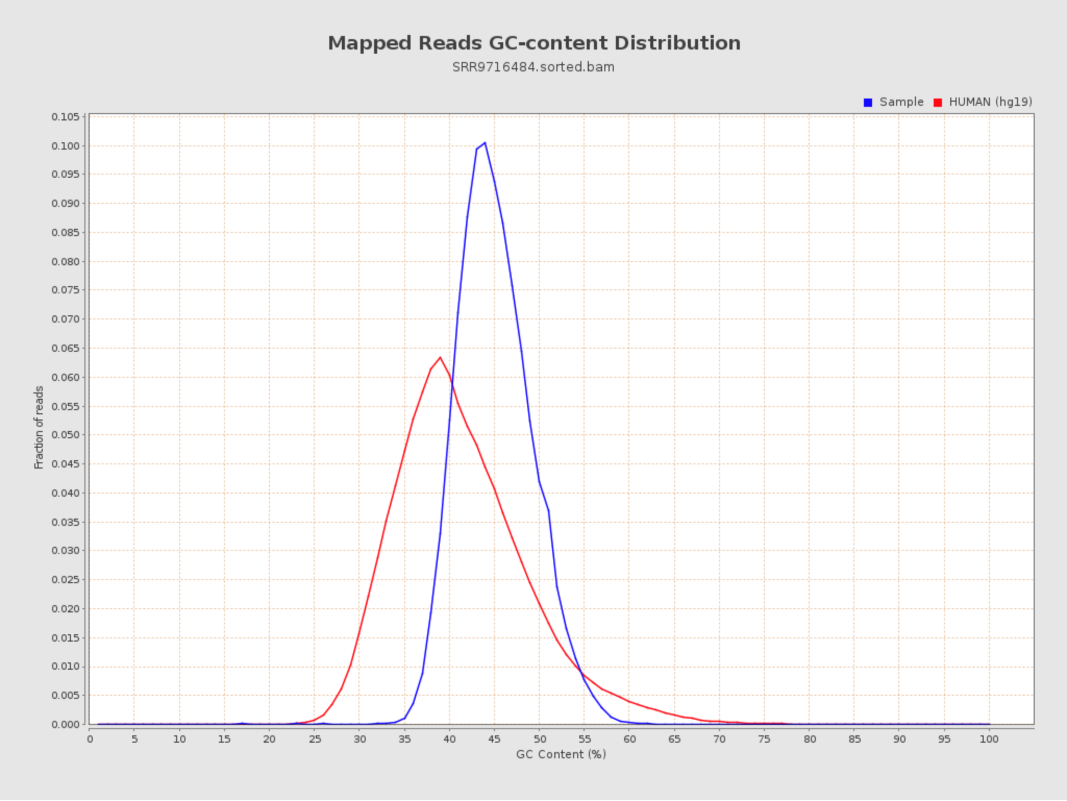
7. Results : Duplication Rate Histogram



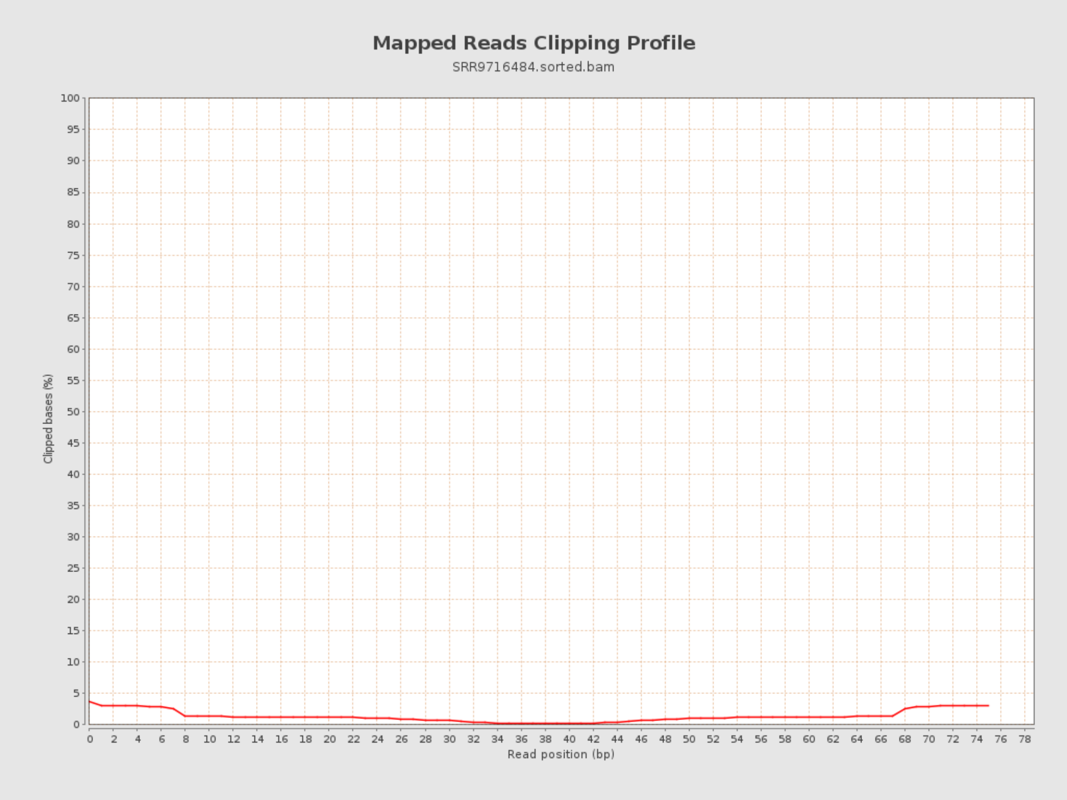
8. Results : Mapped Reads Nucleotide Content



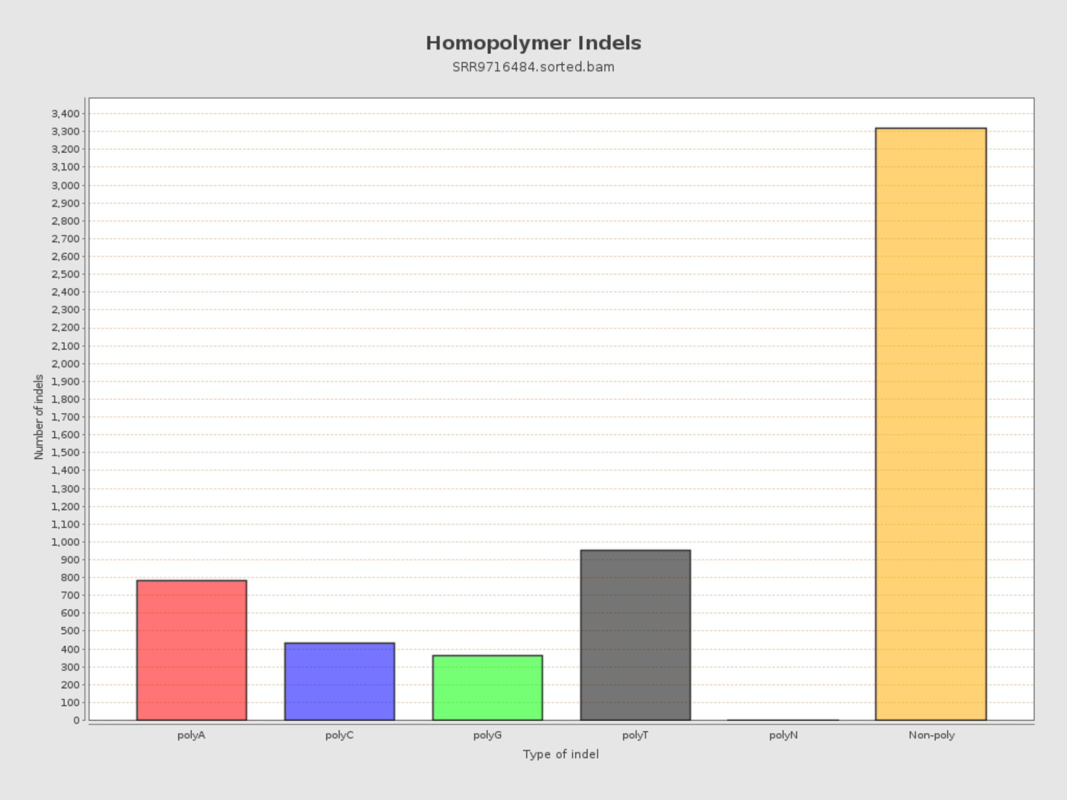
9. Results : Mapped Reads GC-content Distribution



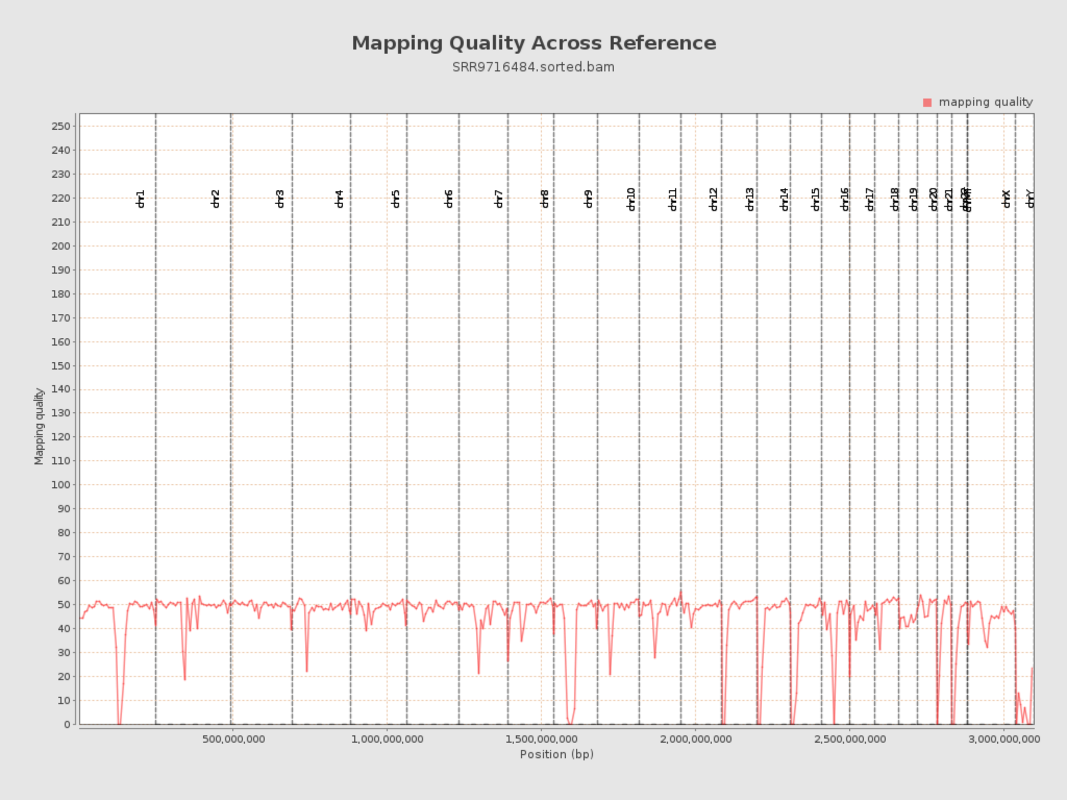
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram