Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:32:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716488.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_SRR9716488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716488.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:32:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	577,117
Mapped reads	405,755 / 70.31%
Unmapped reads	171,362 / 29.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,740 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	7,372 / 1.28%
Duplication rate	1.43%
Clipped reads	407,291 / 70.57%

2.2. ACGT Content

Number/percentage of A's	5,742,480 / 24.62%
Number/percentage of C's	4,662,775 / 19.99%
Number/percentage of T's	7,185,268 / 30.8%
Number/percentage of G's	5,738,203 / 24.6%
Number/percentage of N's	299 / 0%
GC Percentage	44.58%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.1021

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

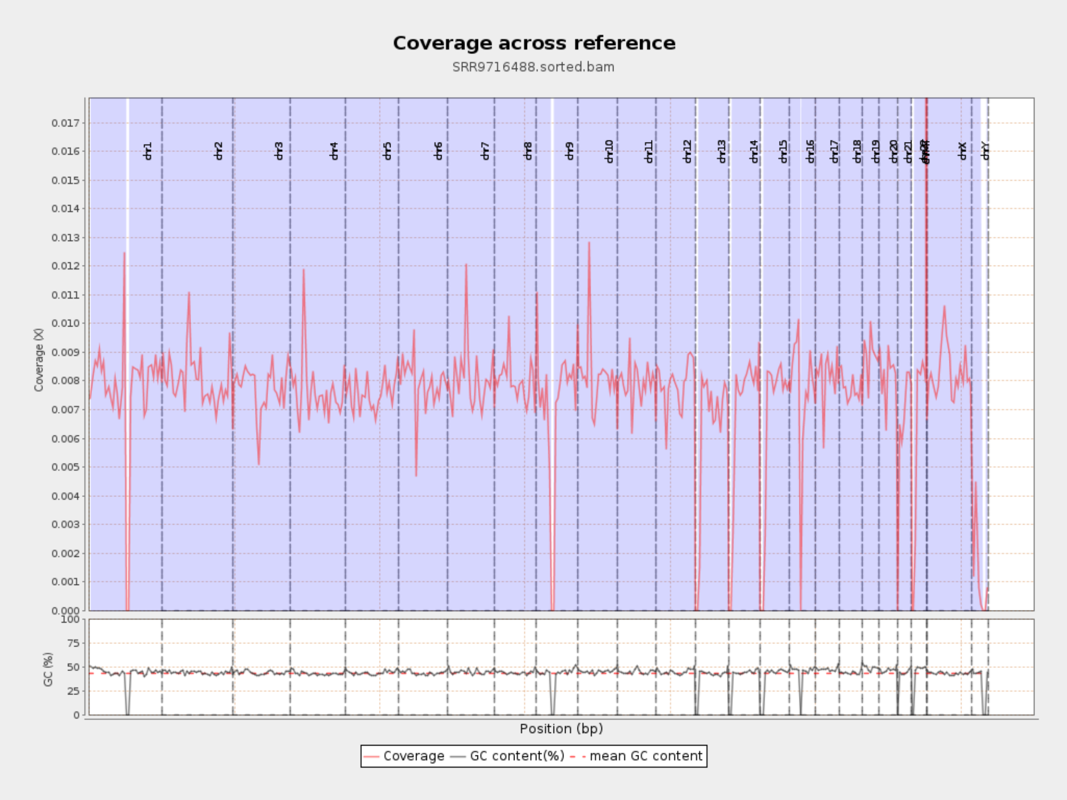
General error rate	0.51%
Mismatches	117,587
Insertions	1,307
Mapped reads with at least one insertion	0.32%
Deletions	4,208
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.38%

2.6. Chromosome stats

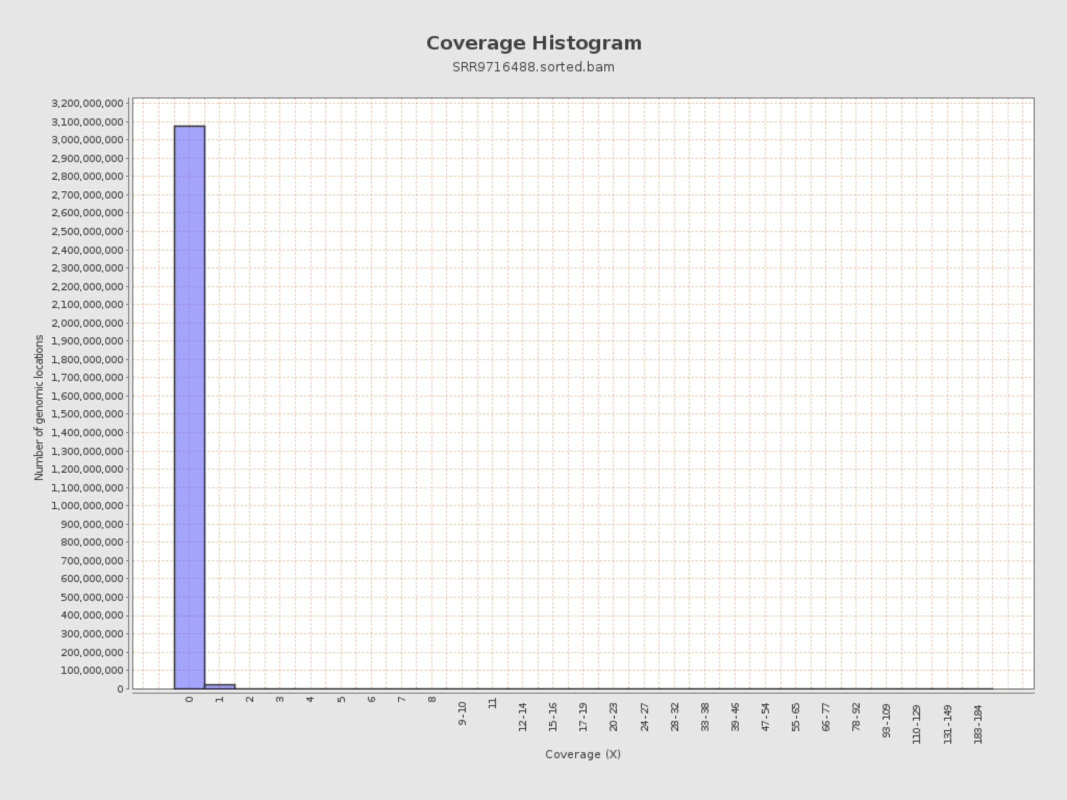
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1915811	0.0077	0.145
chr2	243199373	1967434	0.0081	0.1214
chr3	198022430	1536536	0.0078	0.0909
chr4	191154276	1458653	0.0076	0.0927
chr5	180915260	1371745	0.0076	0.09
chr6	171115067	1358294	0.0079	0.0977
chr7	159138663	1285524	0.0081	0.115

chr8	146364022	1171297	0.008	0.1012
chr9	141213431	967469	0.0069	0.0918
chr10	135534747	1112028	0.0082	0.1029
chr11	135006516	1068525	0.0079	0.0967
chr12	133851895	1056665	0.0079	0.0919
chr13	115169878	710452	0.0062	0.0808
chr14	107349540	713193	0.0066	0.0858
chr15	102531392	669703	0.0065	0.0832
chr16	90354753	683207	0.0076	0.0914
chr17	81195210	665497	0.0082	0.0947
chr18	78077248	607682	0.0078	0.1153
chr19	59128983	524023	0.0089	0.1193
chr20	63025520	512558	0.0081	0.0933
chr21	48129895	313692	0.0065	0.0861
chr22	51304566	295063	0.0058	0.0781
chrMT	16571	3419	0.2063	0.4956
chrX	155270560	1292161	0.0083	0.0971
chrY	59373566	75226	0.0013	0.0467

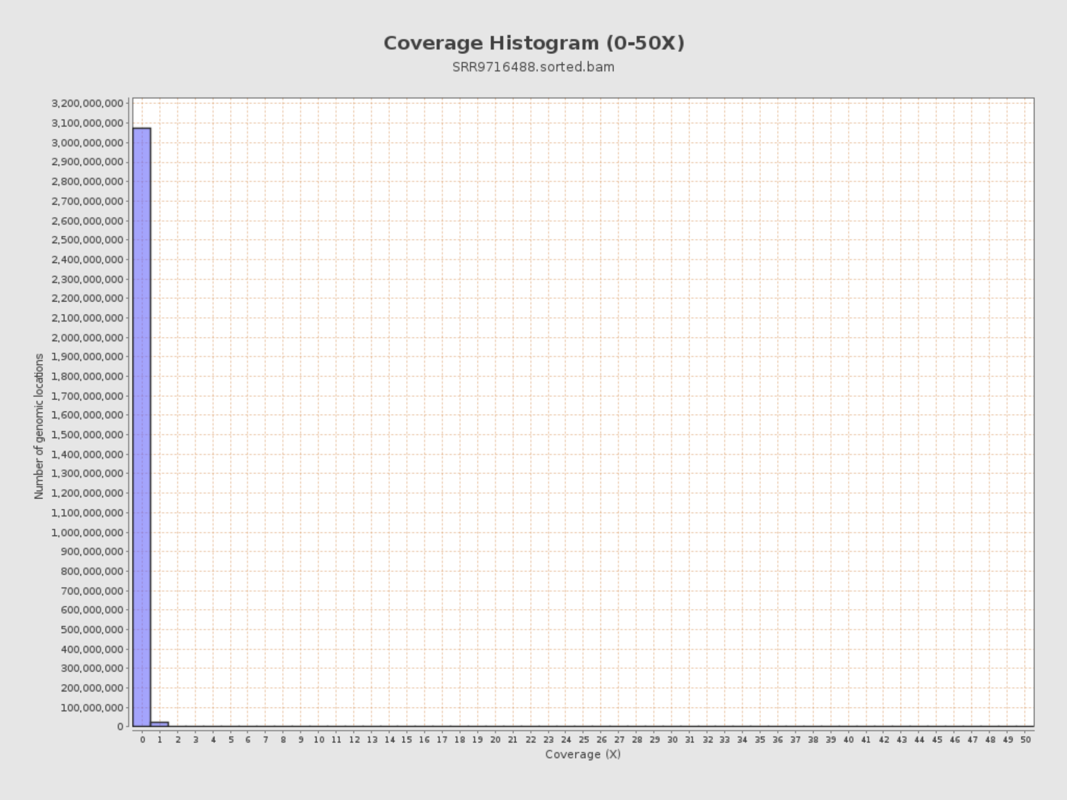
3. Results : Coverage across reference



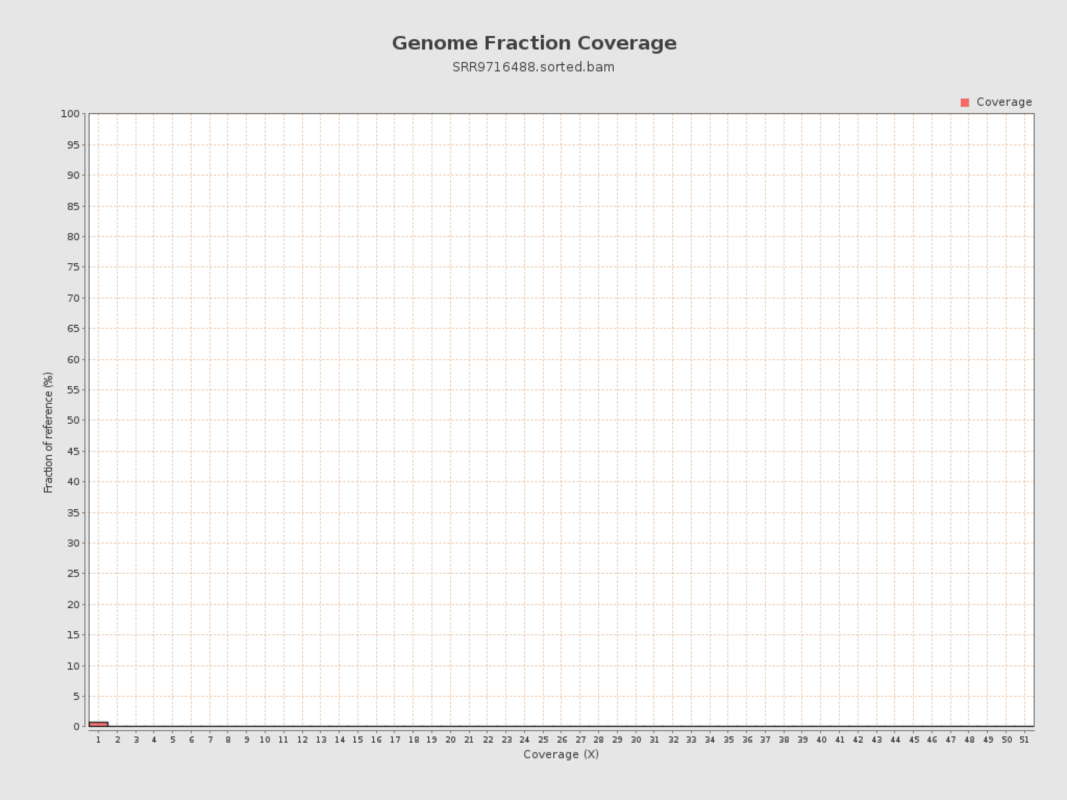
4. Results : Coverage Histogram



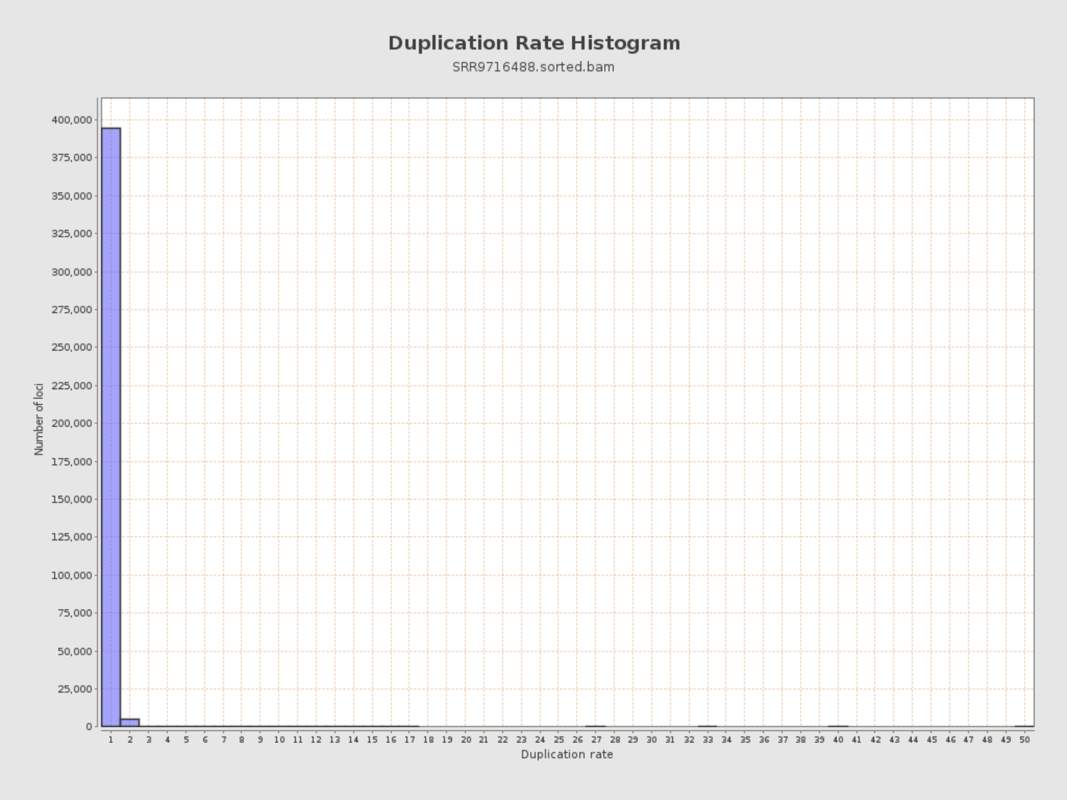
5. Results : Coverage Histogram (0-50X)



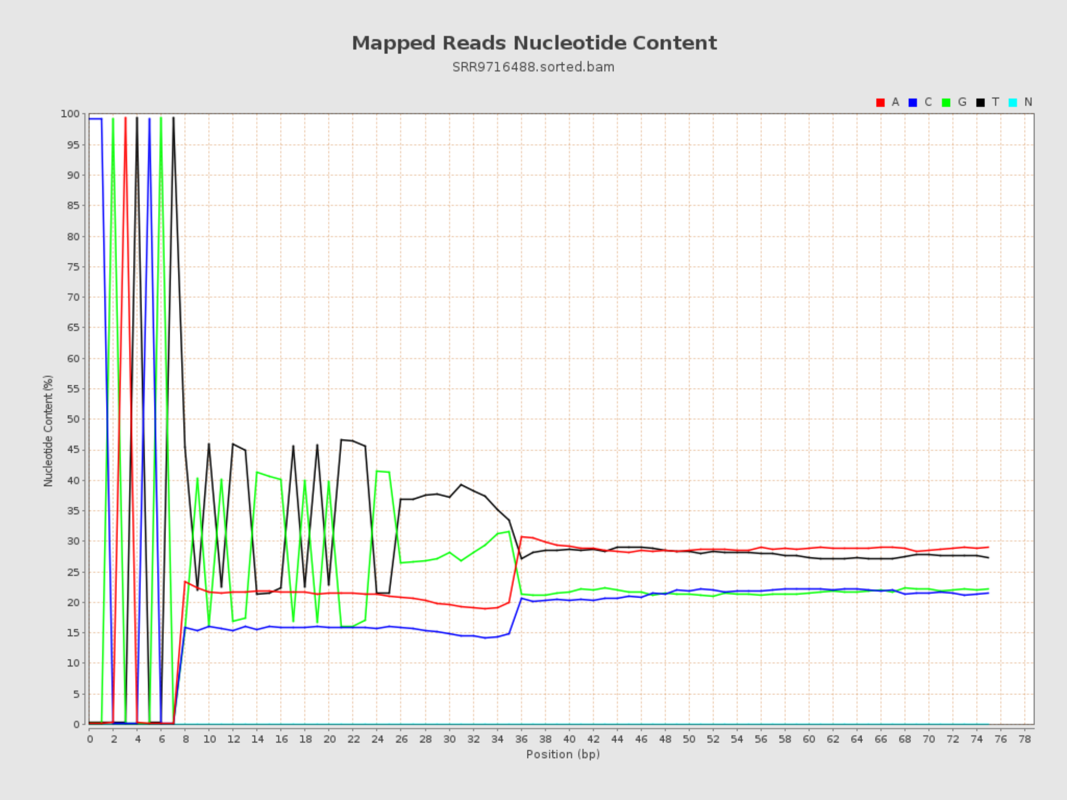
6. Results : Genome Fraction Coverage



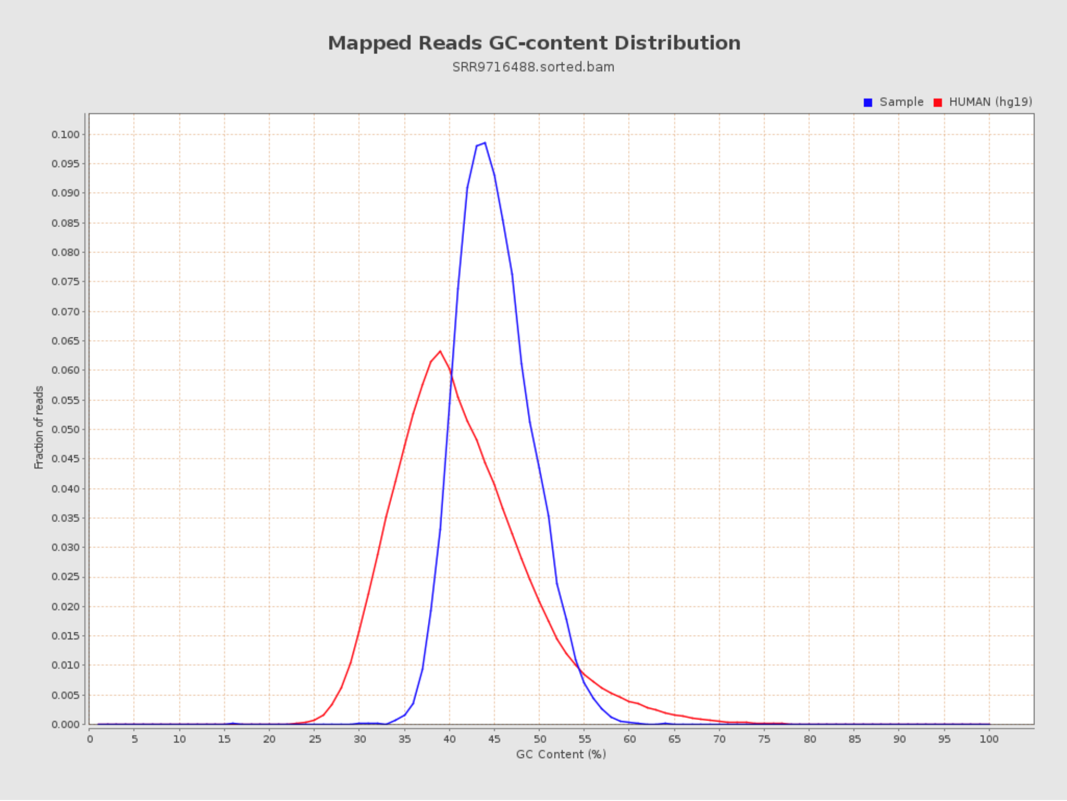
7. Results : Duplication Rate Histogram



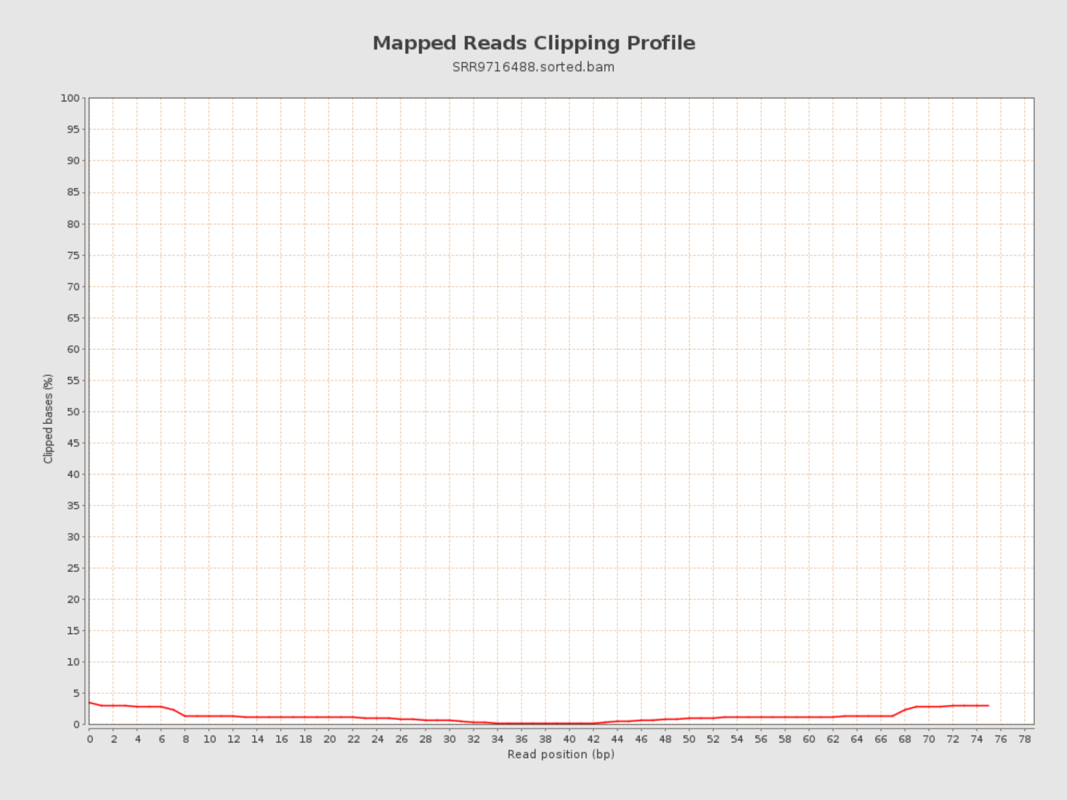
8. Results : Mapped Reads Nucleotide Content



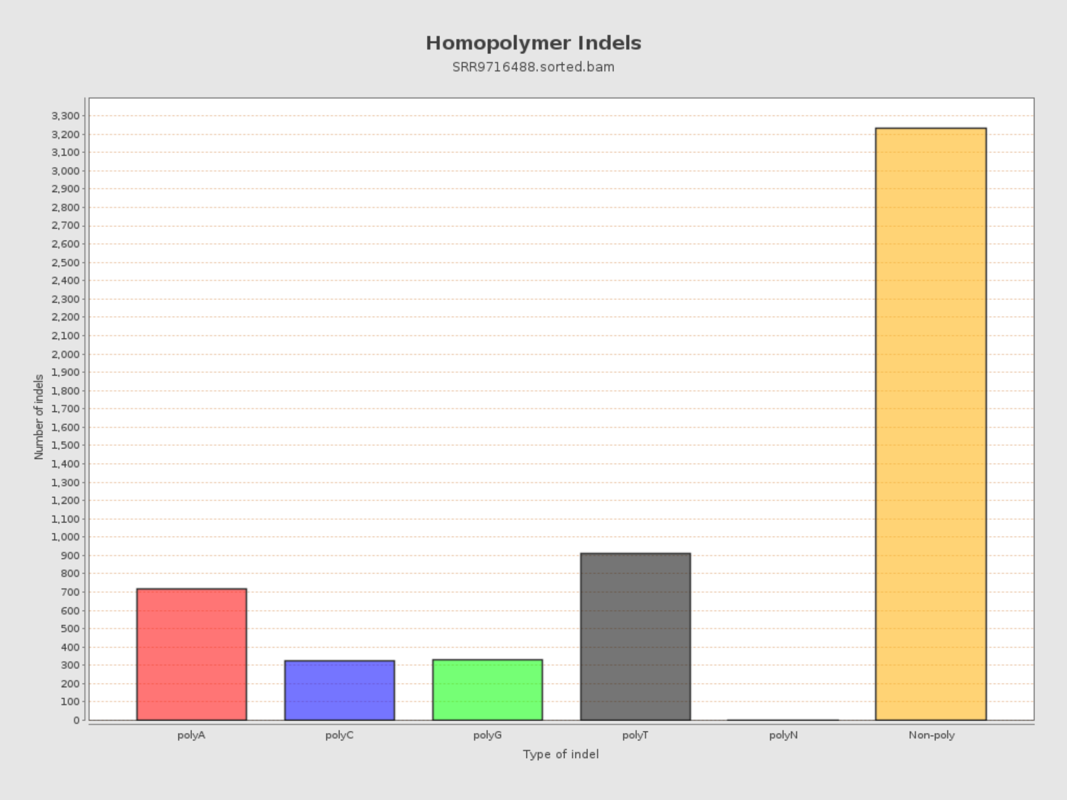
9. Results : Mapped Reads GC-content Distribution



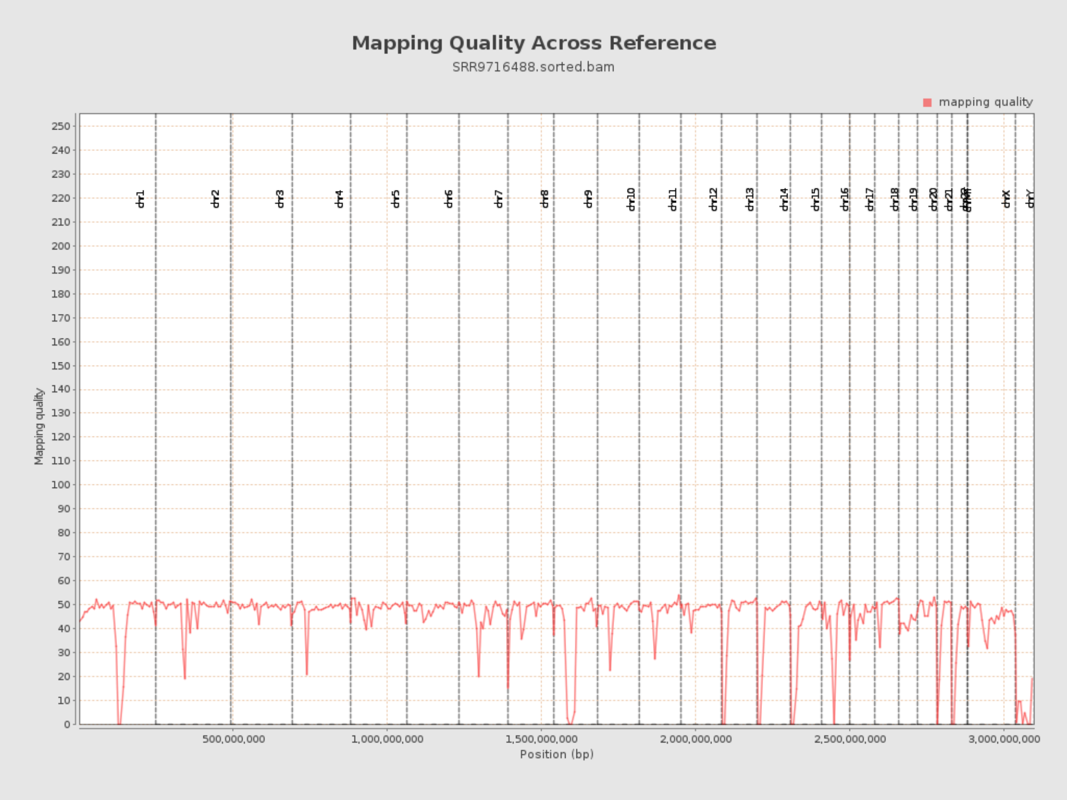
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram