Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:32:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716159.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_SRR9716159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:32:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,268,879
Mapped reads	6,627,117 / 91.17%
Unmapped reads	641,762 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,967 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	659,462 / 9.07%
Duplication rate	7.44%
Clipped reads	6,639,233 / 91.34%

2.2. ACGT Content

Number/percentage of A's	93,712,954 / 24.5%
Number/percentage of C's	79,242,511 / 20.72%
Number/percentage of T's	120,769,175 / 31.58%
Number/percentage of G's	88,749,333 / 23.2%
Number/percentage of N's	8,709 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.1236

Standard Deviation	0.8307

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

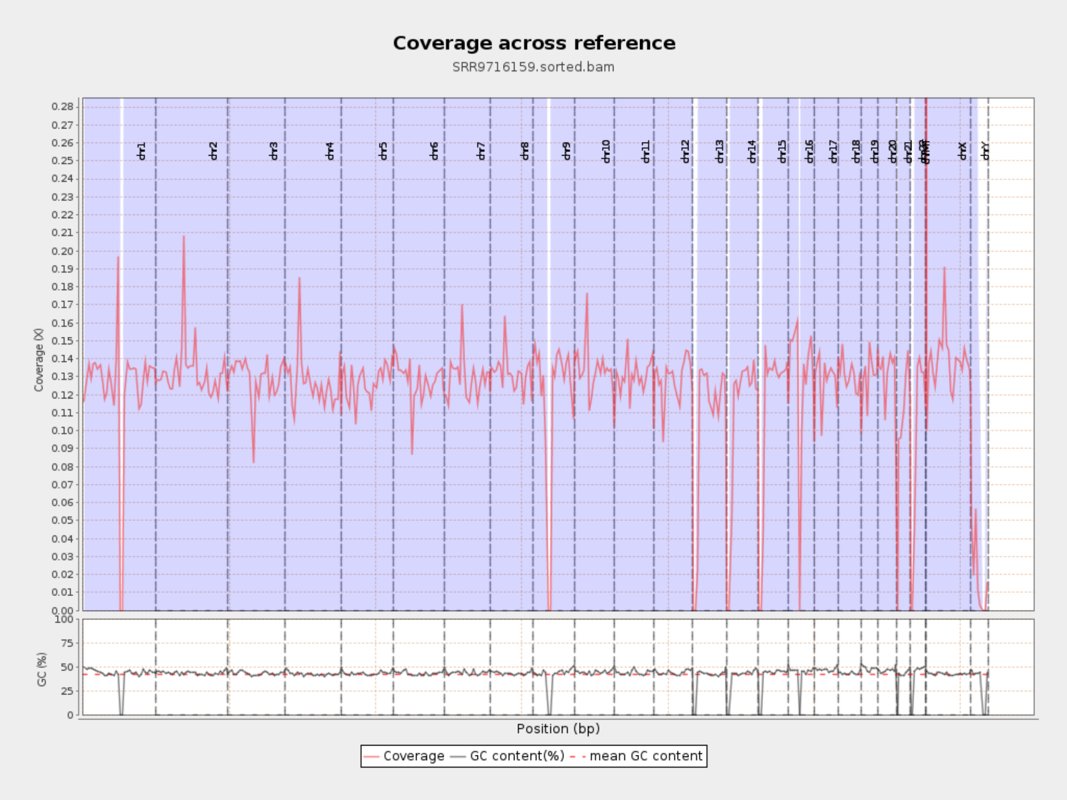
General error rate	0.5%
Mismatches	1,854,041
Insertions	22,986
Mapped reads with at least one insertion	0.35%
Deletions	59,655
Mapped reads with at least one deletion	0.89%
Homopolymer indels	42.6%

2.6. Chromosome stats

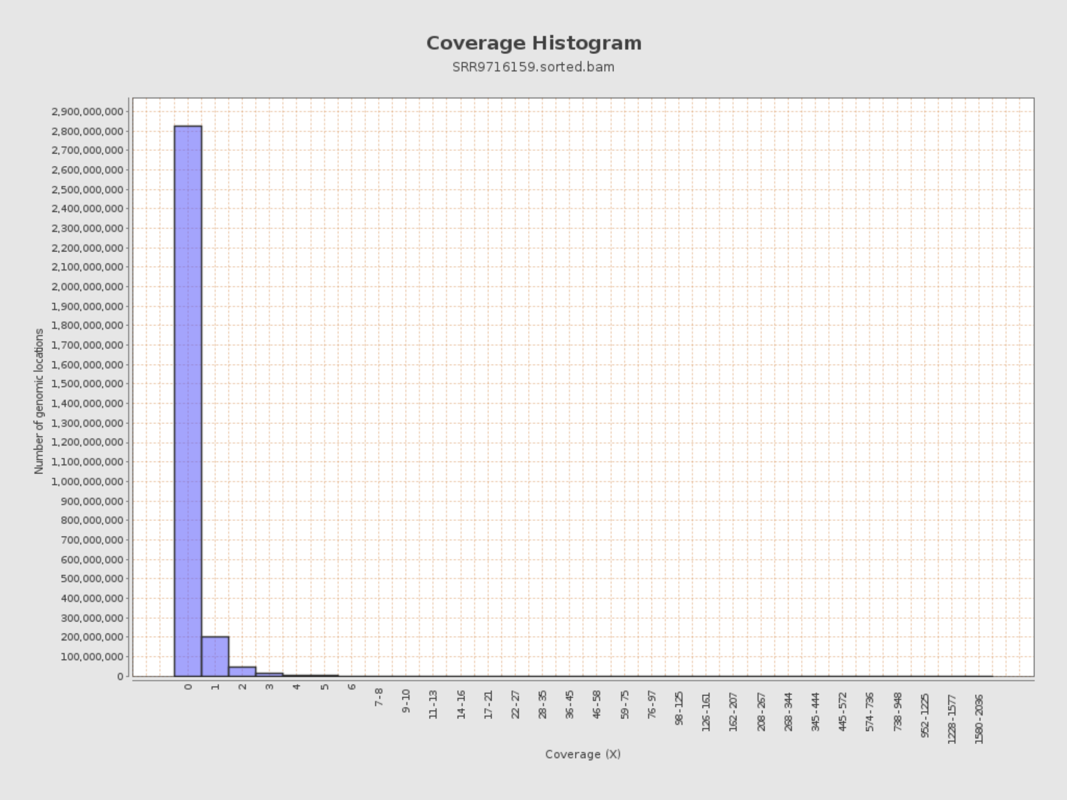
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30831712	0.1237	1.6358
chr2	243199373	32340607	0.133	0.918
chr3	198022430	25527866	0.1289	0.4865
chr4	191154276	24325427	0.1273	0.5869
chr5	180915260	23013350	0.1272	0.4975
chr6	171115067	21851624	0.1277	0.5656
chr7	159138663	20621258	0.1296	0.9376

chr8	146364022	19297766	0.1318	0.7609
chr9	141213431	16567096	0.1173	0.8455
chr10	135534747	18150189	0.1339	0.7105
chr11	135006516	17518980	0.1298	0.8484
chr12	133851895	17327212	0.1295	0.5036
chr13	115169878	11869067	0.1031	0.4318
chr14	107349540	11504109	0.1072	0.4995
chr15	102531392	11168045	0.1089	0.4533
chr16	90354753	11413325	0.1263	0.5644
chr17	81195210	10531017	0.1297	0.5654
chr18	78077248	10232735	0.1311	1.6688
chr19	59128983	7728829	0.1307	1.0678
chr20	63025520	8319143	0.132	0.5292
chr21	48129895	5071735	0.1054	0.5435
chr22	51304566	4742389	0.0924	0.417
chrMT	16571	20955	1.2646	1.4952
chrX	155270560	21529715	0.1387	0.666
chrY	59373566	1078907	0.0182	0.3505

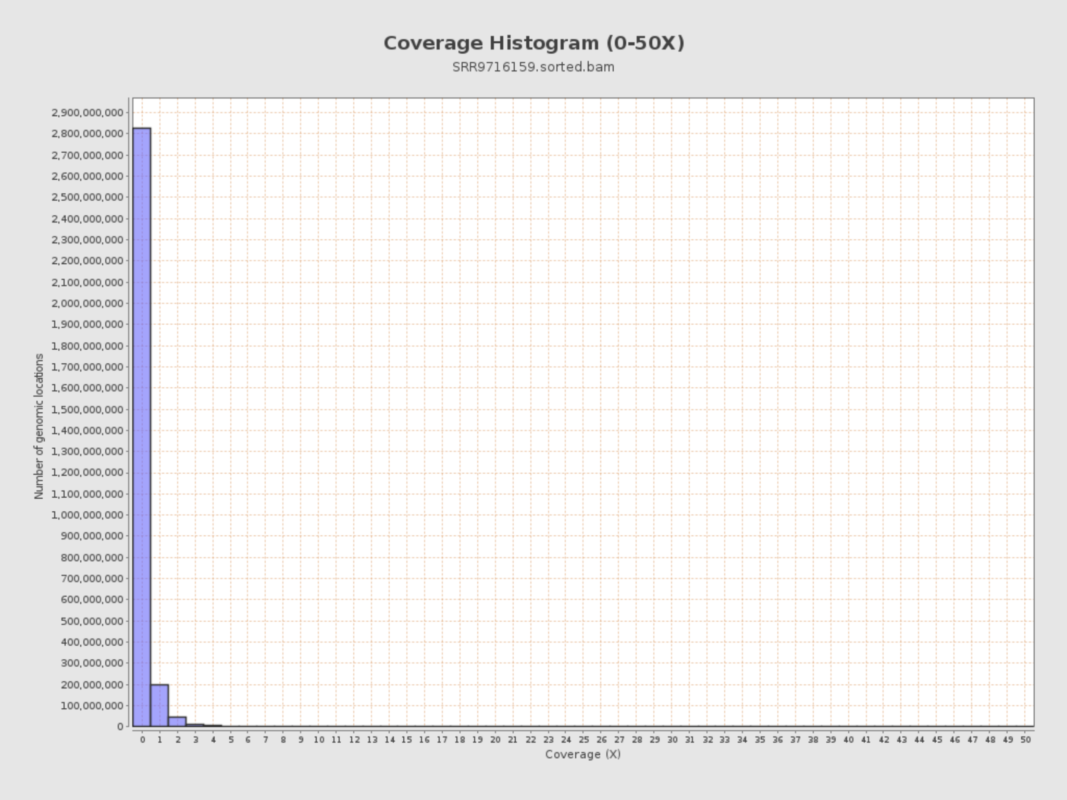
3. Results : Coverage across reference



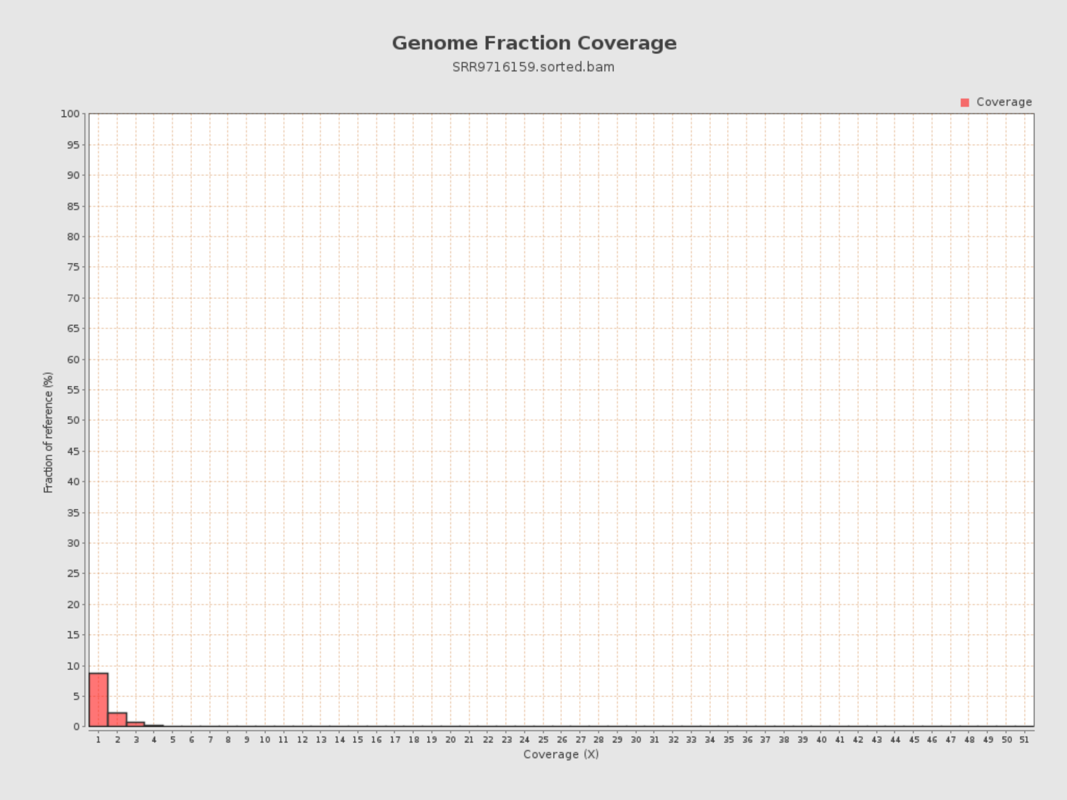
4. Results : Coverage Histogram



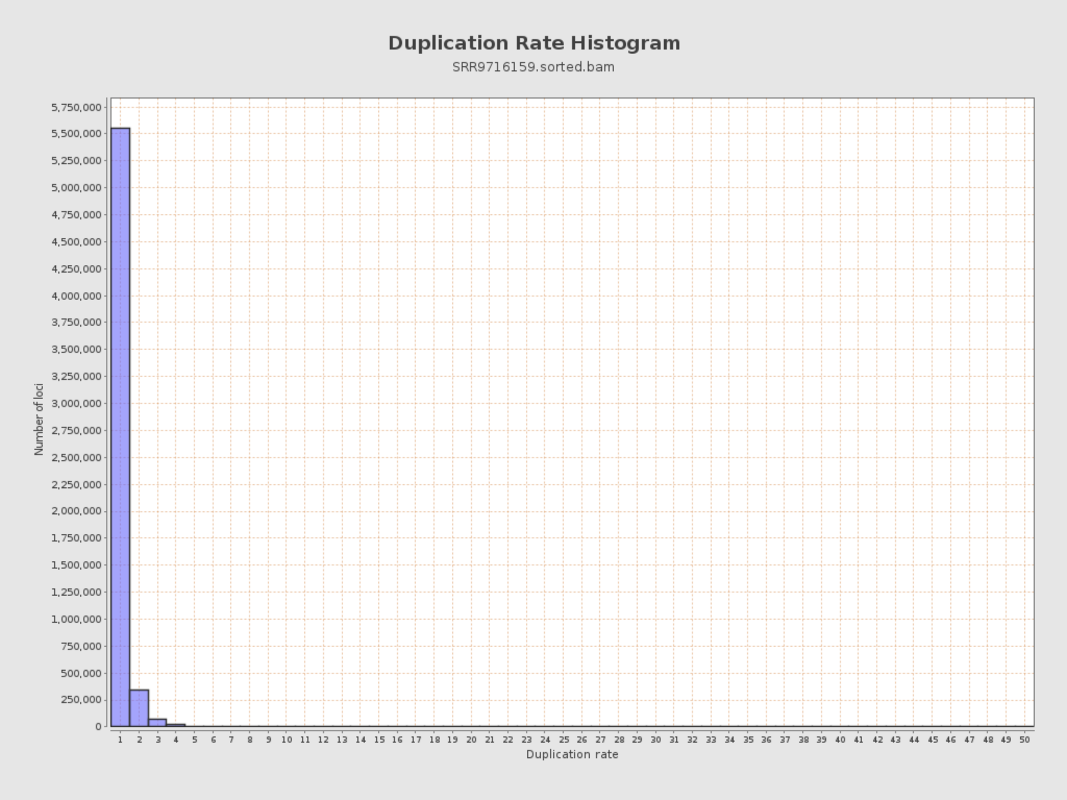
5. Results : Coverage Histogram (0-50X)



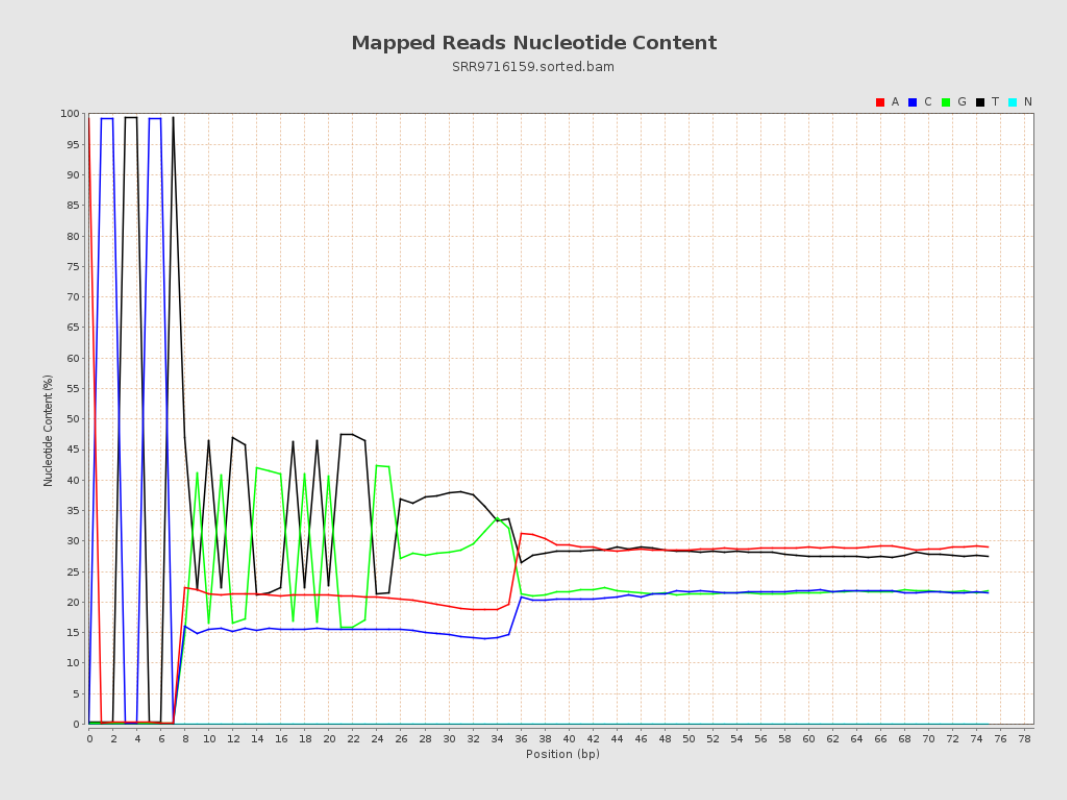
6. Results : Genome Fraction Coverage



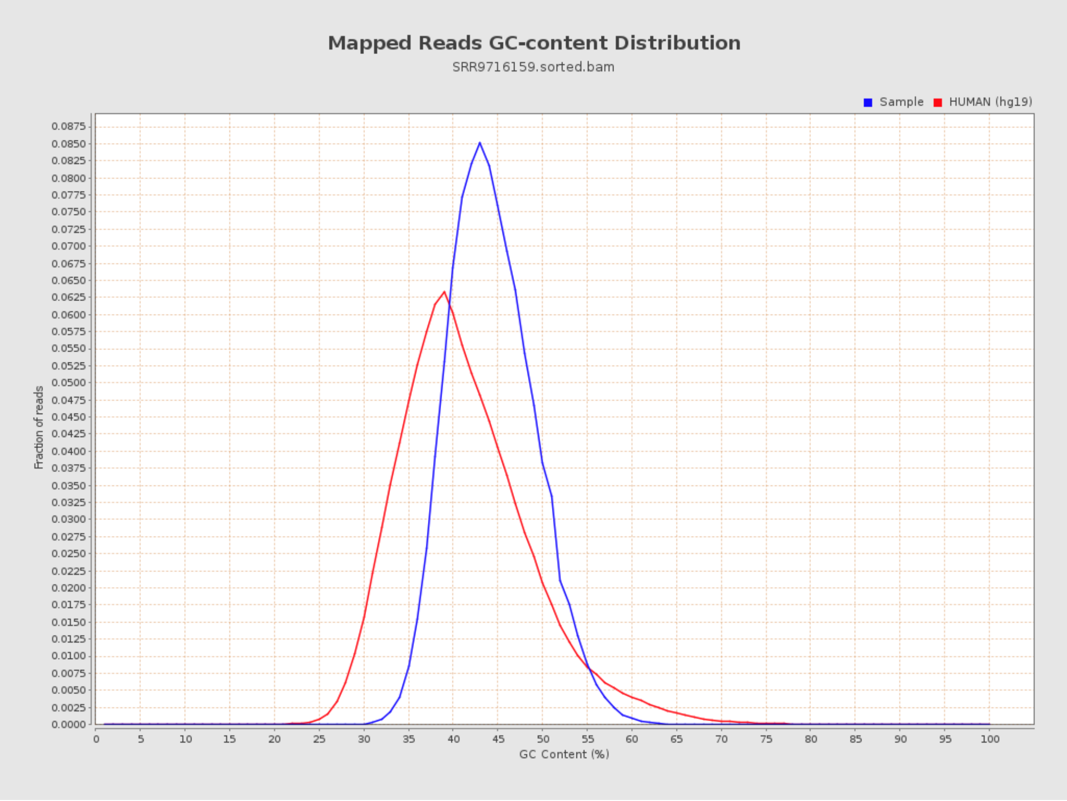
7. Results : Duplication Rate Histogram



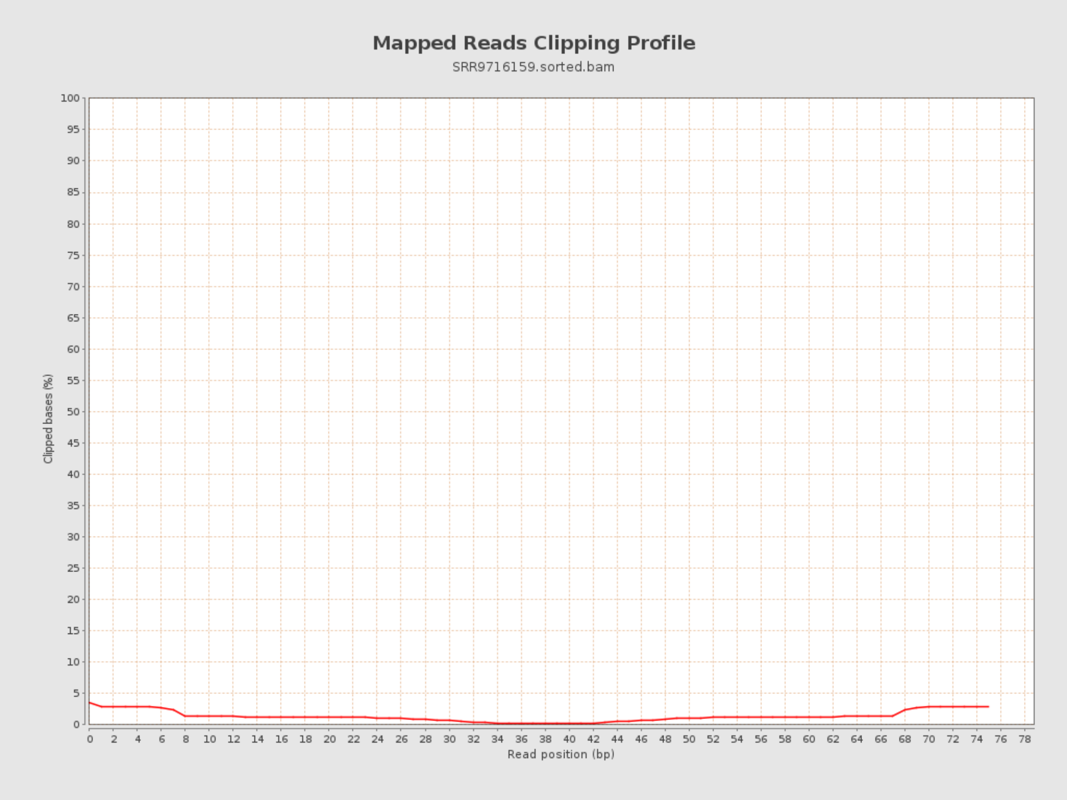
8. Results : Mapped Reads Nucleotide Content



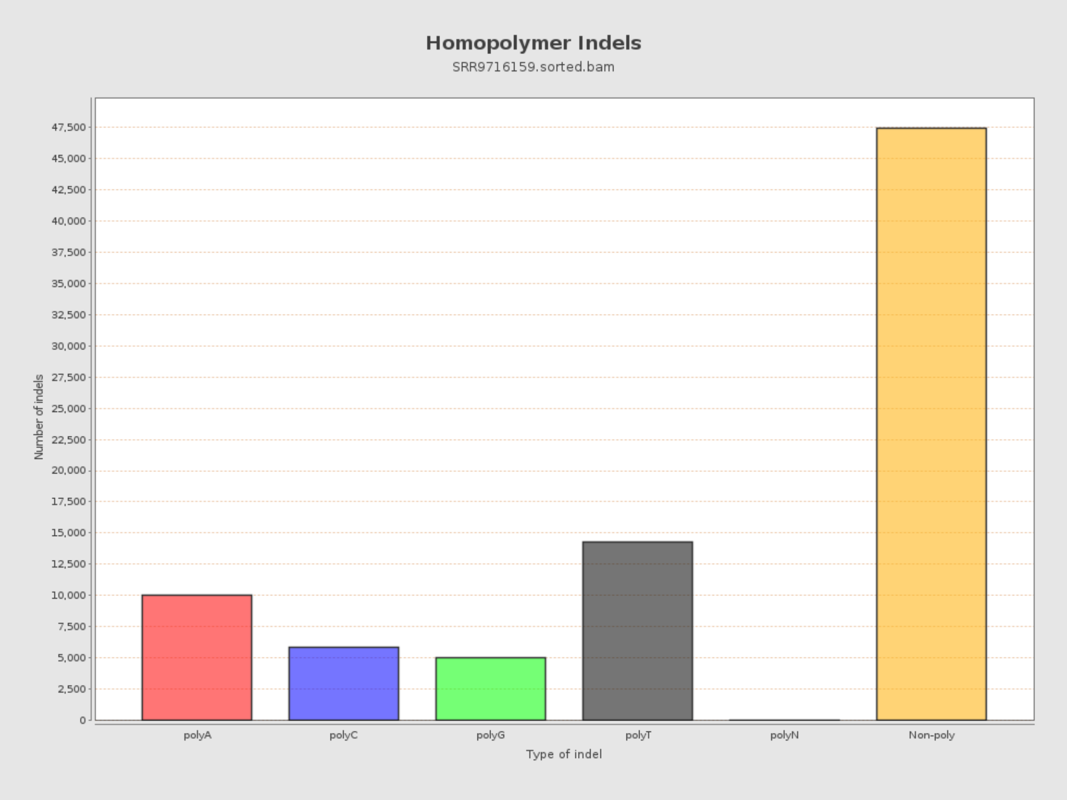
9. Results : Mapped Reads GC-content Distribution



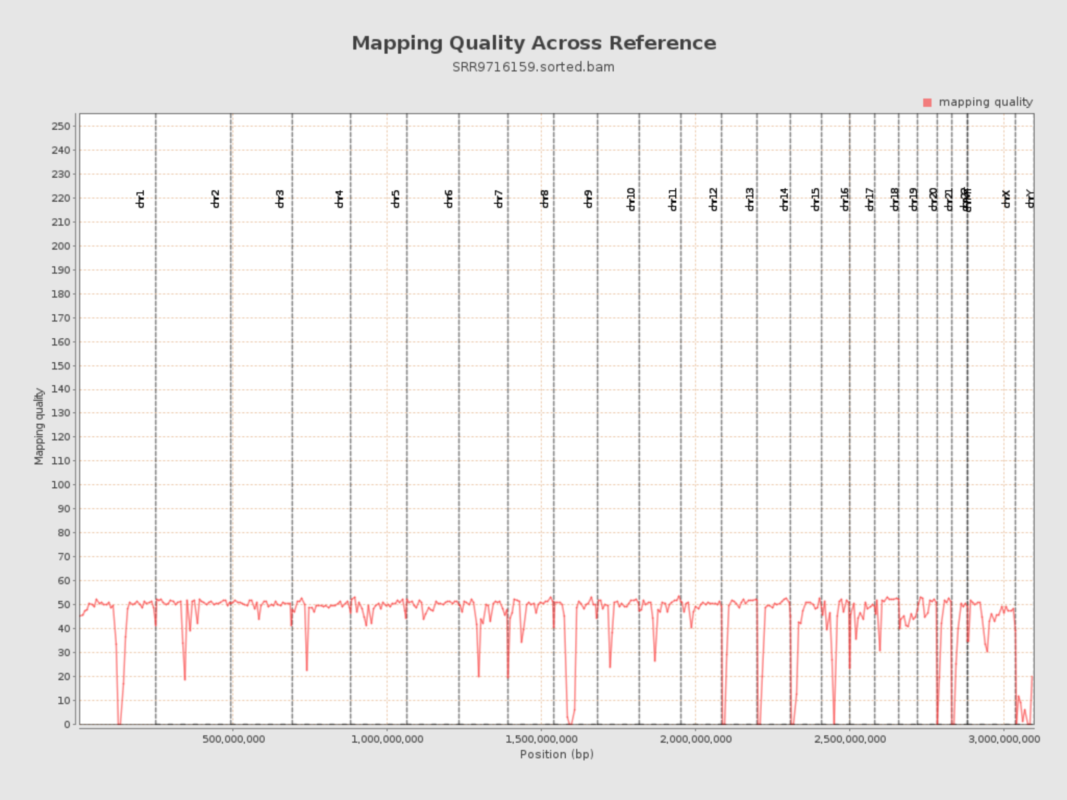
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram