Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:18:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716554.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_SRR9716554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716554.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:18:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,075,750
Mapped reads	2,722,323 / 88.51%
Unmapped reads	353,427 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,205 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	95,069 / 3.09%
Duplication rate	2.47%
Clipped reads	2,723,930 / 88.56%

2.2. ACGT Content

Number/percentage of A's	39,052,528 / 25.21%
Number/percentage of C's	31,192,654 / 20.14%
Number/percentage of T's	47,769,262 / 30.84%
Number/percentage of G's	36,863,417 / 23.8%
Number/percentage of N's	1,139 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.05

Standard Deviation	0.372

2.4. Mapping Quality

Mean Mapping Quality	42.35

2.5. Mismatches and indels

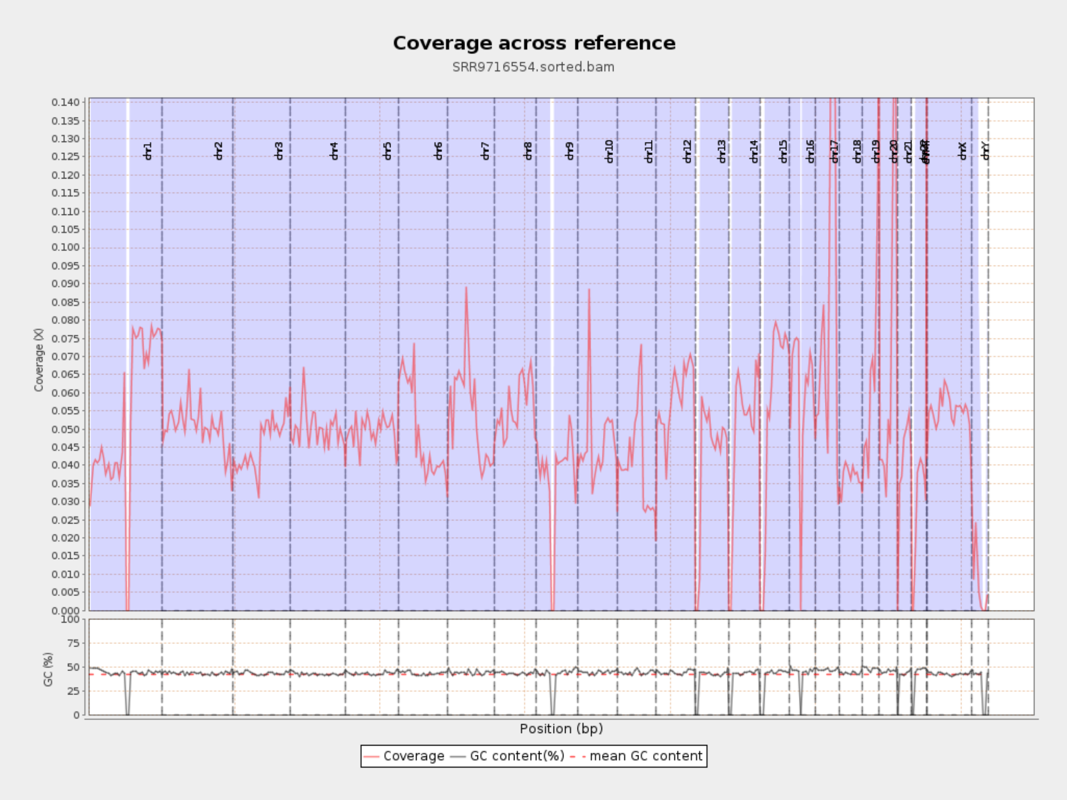
General error rate	0.53%
Mismatches	801,710
Insertions	12,881
Mapped reads with at least one insertion	0.47%
Deletions	28,680
Mapped reads with at least one deletion	1.05%
Homopolymer indels	38.83%

2.6. Chromosome stats

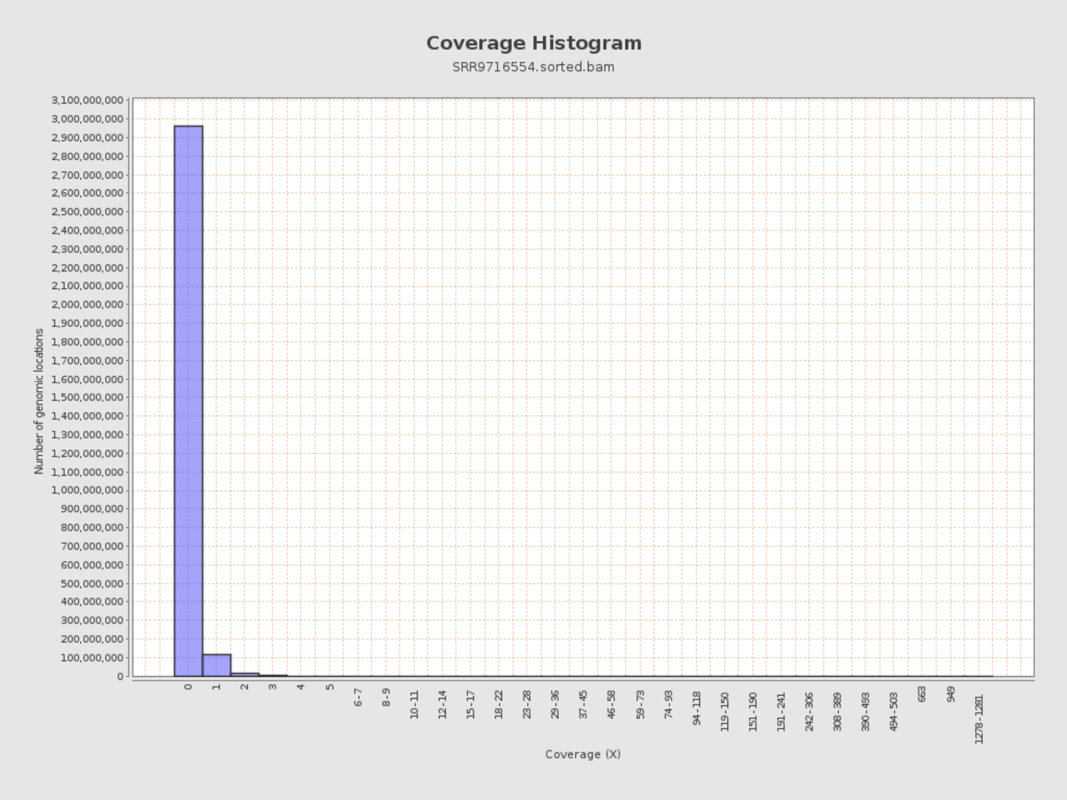
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13162669	0.0528	0.4848
chr2	243199373	12338254	0.0507	0.5793
chr3	198022430	9061578	0.0458	0.2499
chr4	191154276	9584710	0.0501	0.2743
chr5	180915260	8954860	0.0495	0.2517
chr6	171115067	8415894	0.0492	0.3221
chr7	159138663	8756187	0.055	0.575

chr8	146364022	8220464	0.0562	0.3573
chr9	141213431	5155055	0.0365	0.2721
chr10	135534747	6261729	0.0462	0.4614
chr11	135006516	5495379	0.0407	0.3057
chr12	133851895	7811784	0.0584	0.2773
chr13	115169878	4780953	0.0415	0.233
chr14	107349540	5254971	0.049	0.2745
chr15	102531392	5736919	0.056	0.2822
chr16	90354753	5388463	0.0596	0.3047
chr17	81195210	6860984	0.0845	0.3621
chr18	78077248	2890017	0.037	0.4678
chr19	59128983	3895761	0.0659	0.4619
chr20	63025520	4536576	0.072	0.3257
chr21	48129895	1956747	0.0407	0.2461
chr22	51304566	1394061	0.0272	0.1905
chrMT	16571	3109	0.1876	0.5106
chrX	155270560	8556806	0.0551	0.297
chrY	59373566	450134	0.0076	0.183

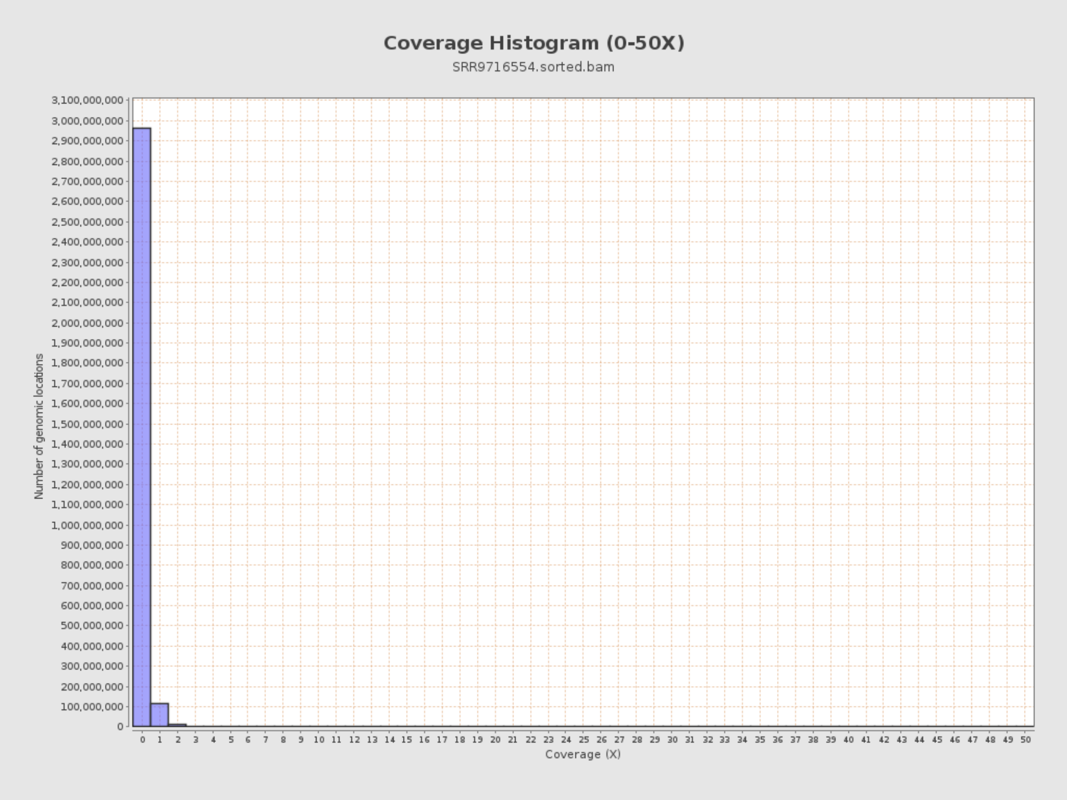
3. Results : Coverage across reference



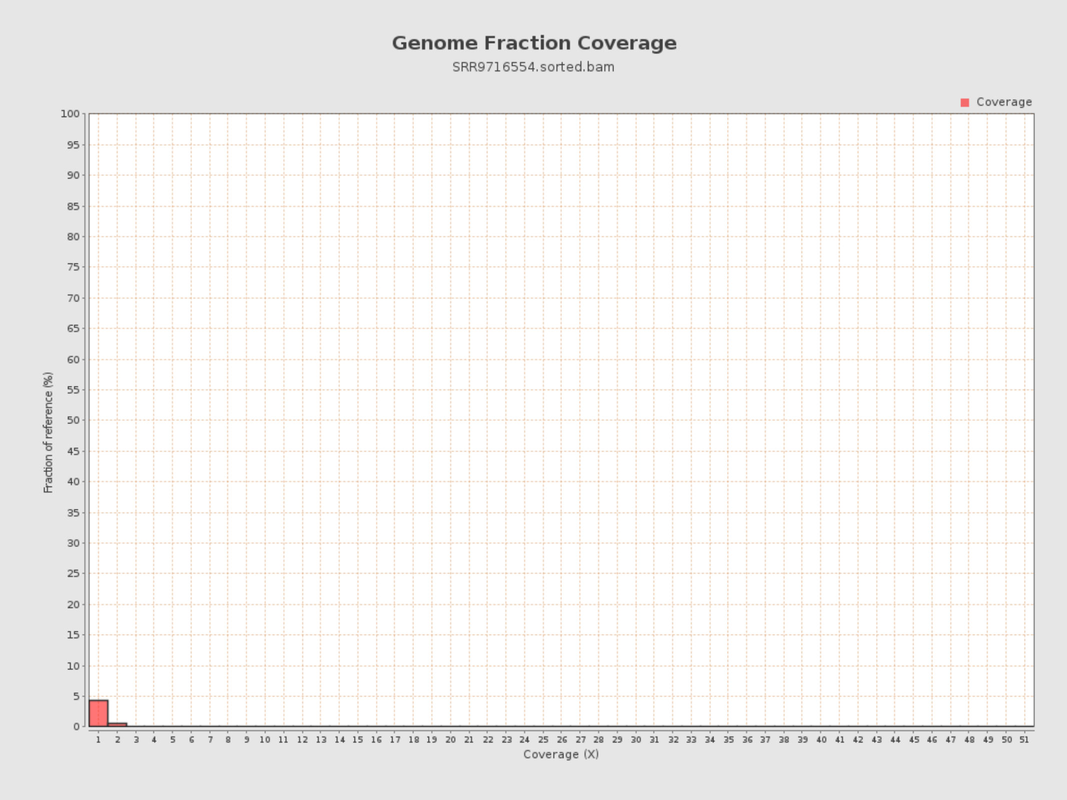
4. Results : Coverage Histogram



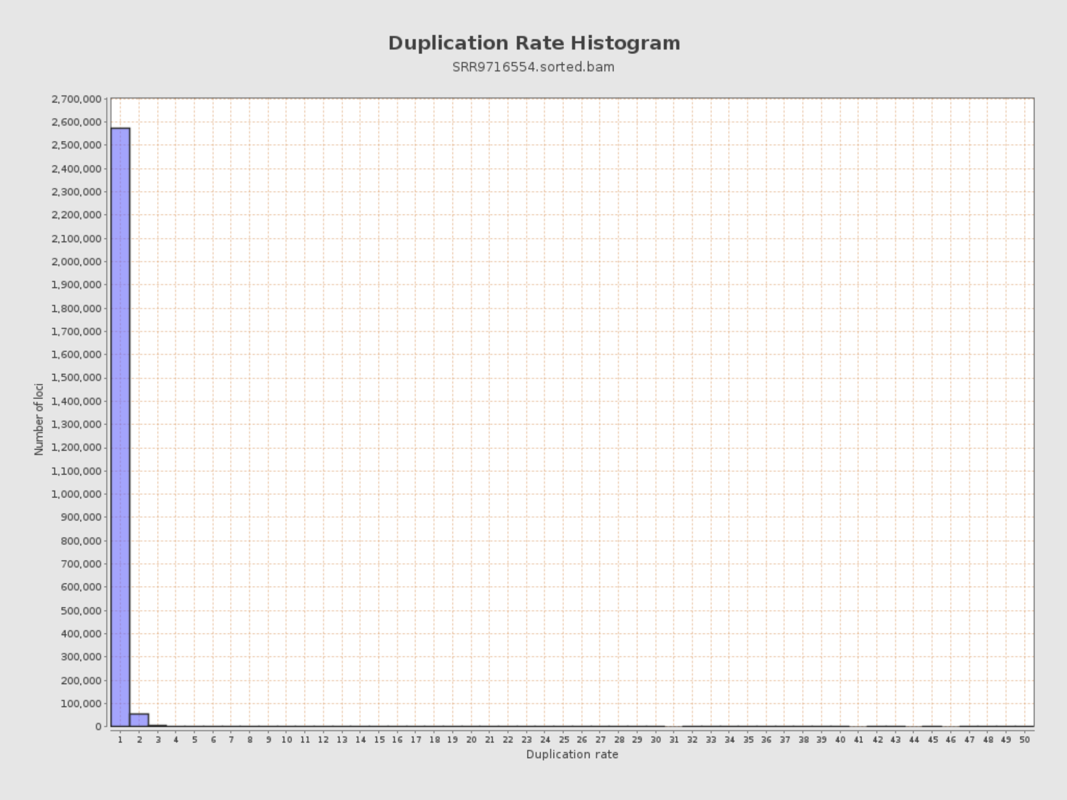
5. Results : Coverage Histogram (0-50X)



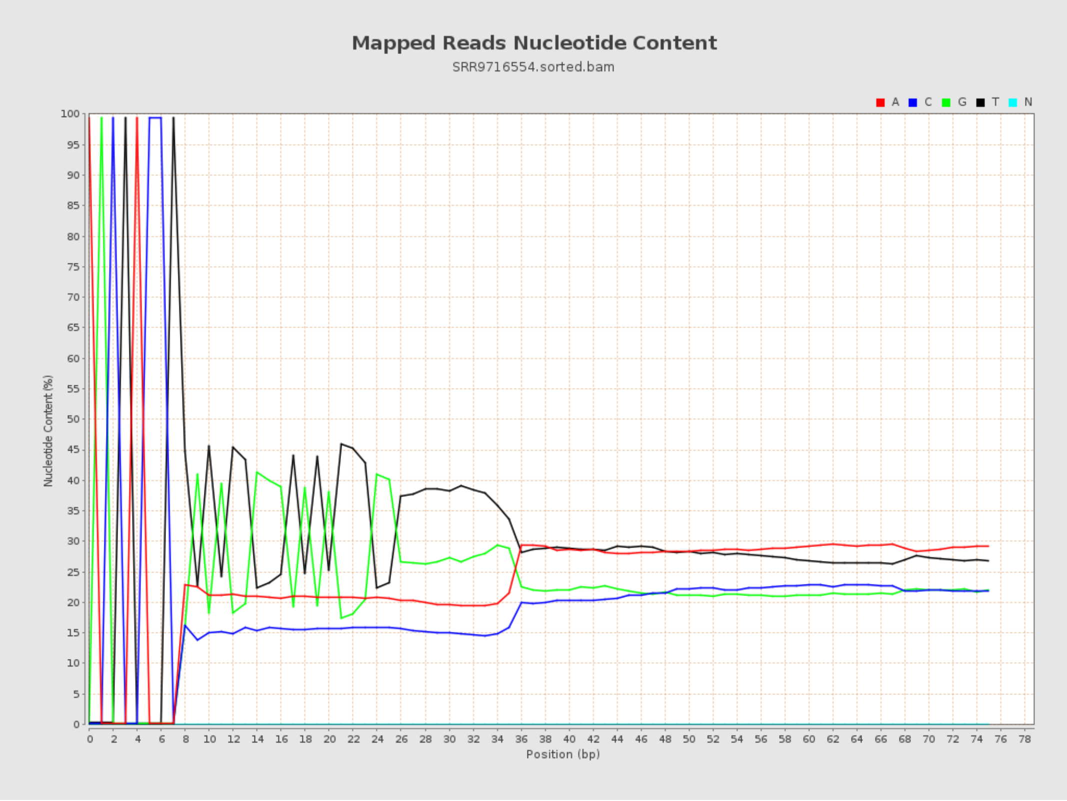
6. Results : Genome Fraction Coverage



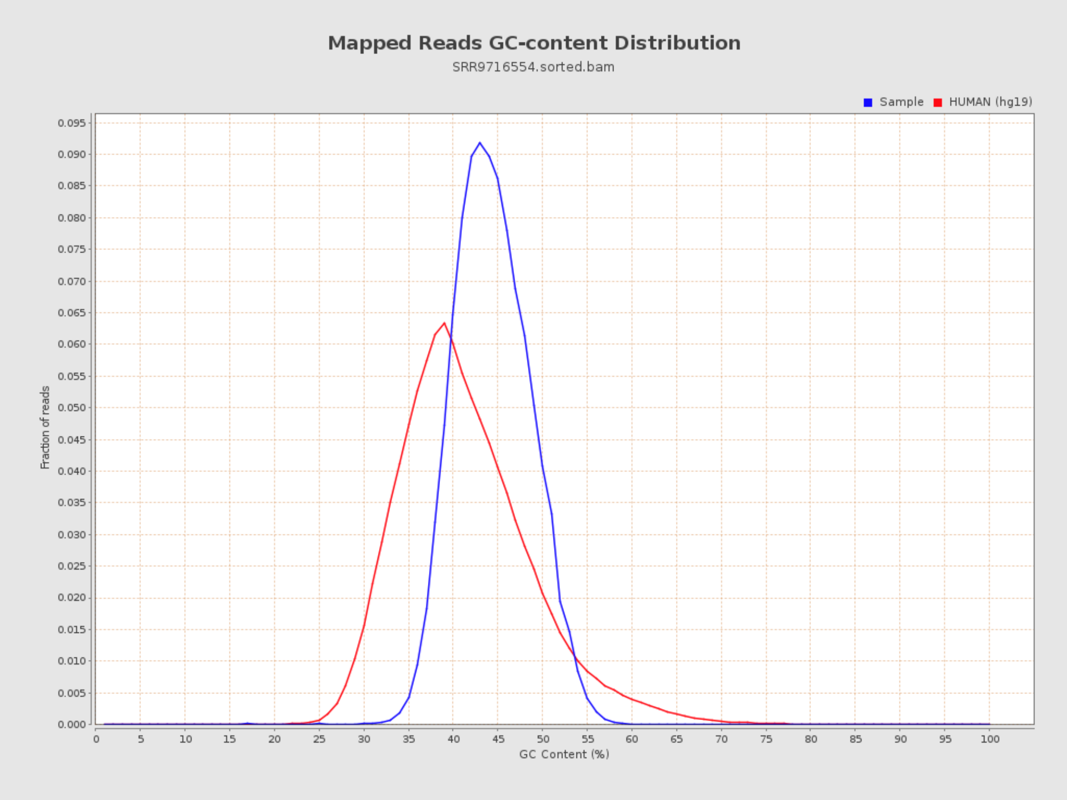
7. Results : Duplication Rate Histogram



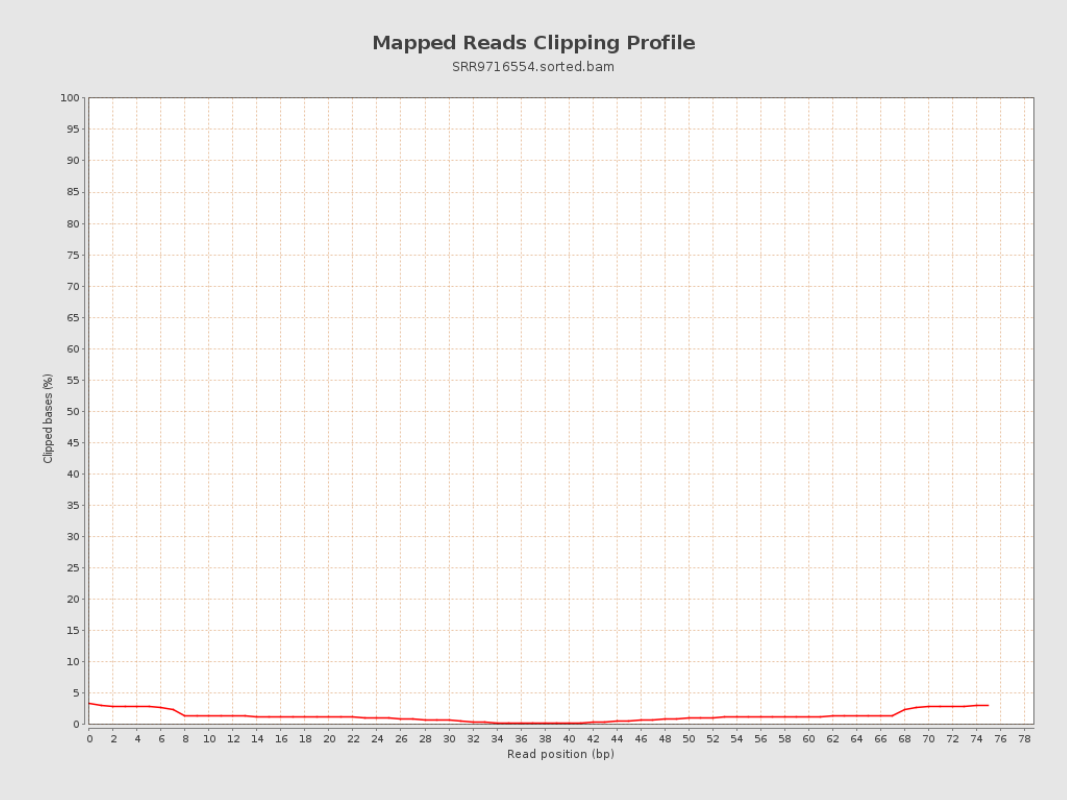
8. Results : Mapped Reads Nucleotide Content



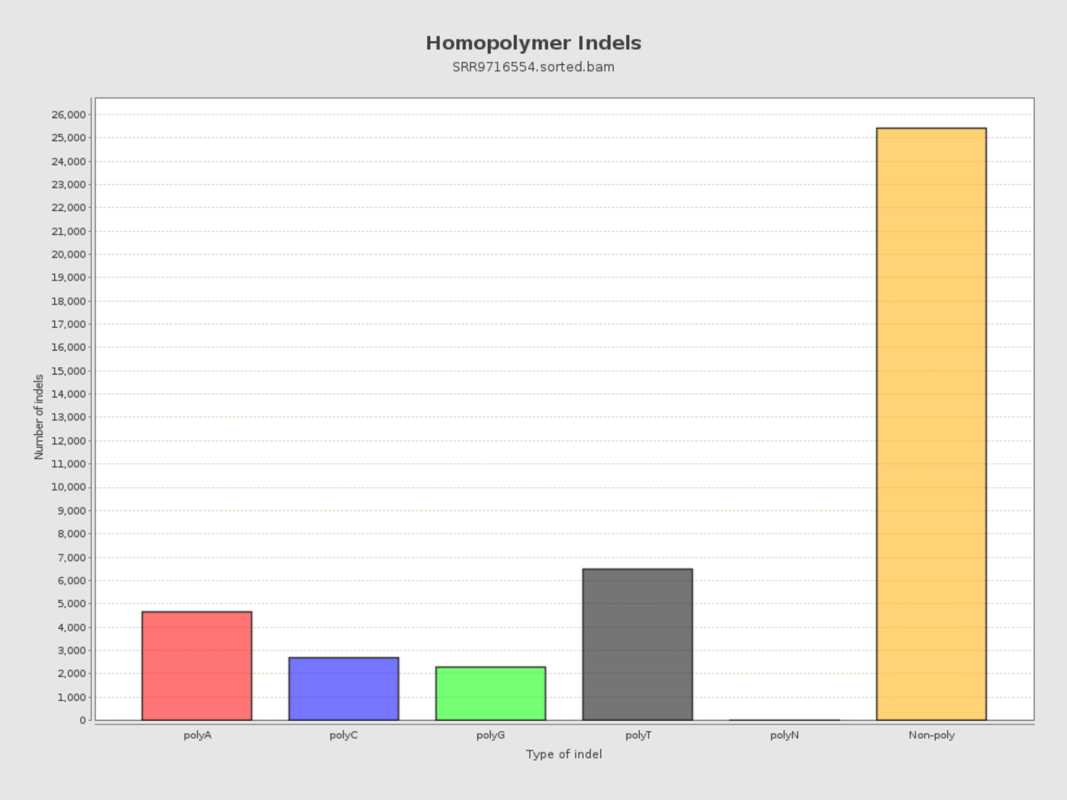
9. Results : Mapped Reads GC-content Distribution



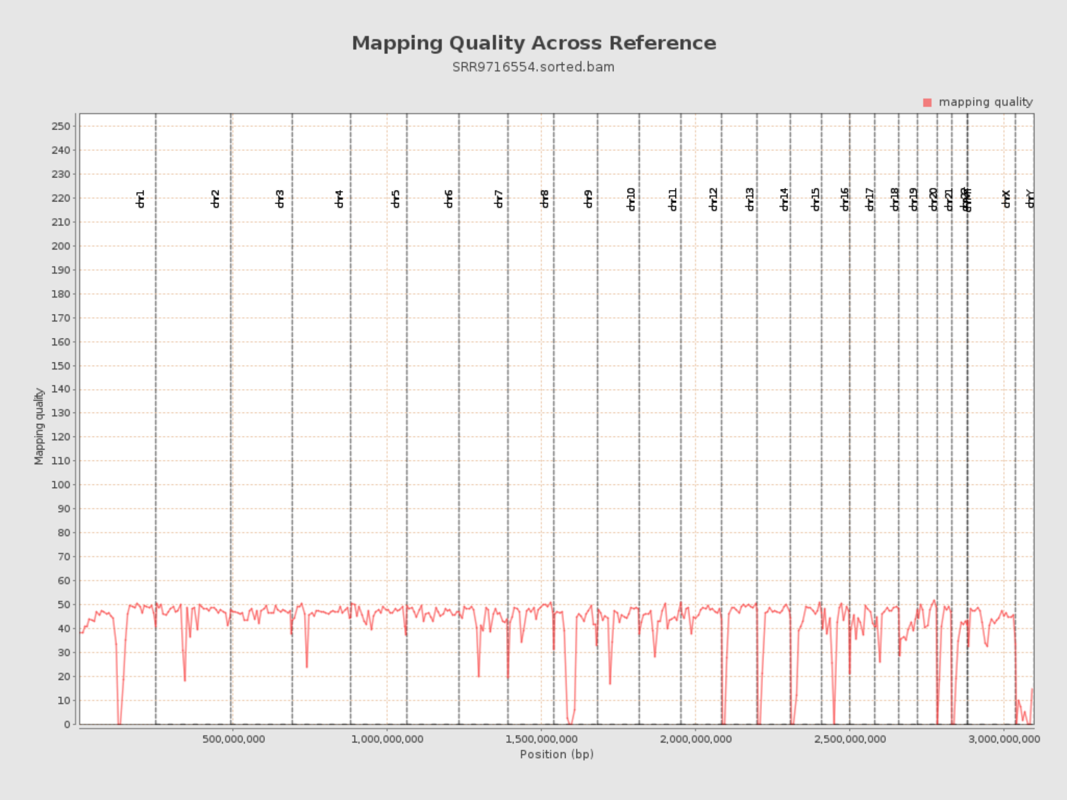
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram