

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:16:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716450.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_SRR9716450 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716450.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716450.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,687,282
Mapped reads	1,456,984 / 86.35%
Unmapped reads	230,298 / 13.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,768 / 1.29%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	63,707 / 3.78%
Duplication rate	2.84%
Clipped reads	1,476,520 / 87.51%

2.2. ACGT Content

Number/percentage of A's	27,979,517 / 24.66%
Number/percentage of C's	20,723,056 / 18.26%
Number/percentage of T's	36,511,775 / 32.18%
Number/percentage of G's	28,242,053 / 24.89%
Number/percentage of N's	6,448 / 0.01%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.4034
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2.4. Mapping Quality

Mean Mapping Quality	44.78
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2.5. Mismatches and indels

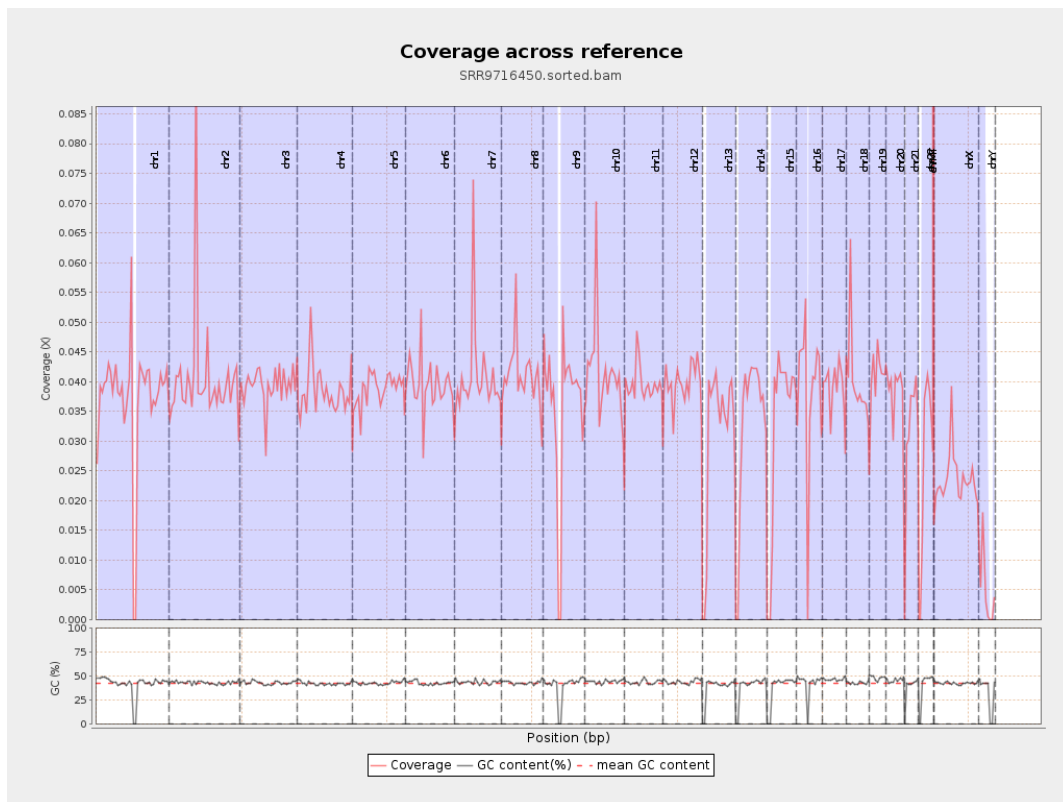
General error rate	0.88%
Mismatches	979,821
Insertions	10,175
Mapped reads with at least one insertion	0.69%
Deletions	28,038
Mapped reads with at least one deletion	1.9%
Homopolymer indels	44.45%

2.6. Chromosome stats

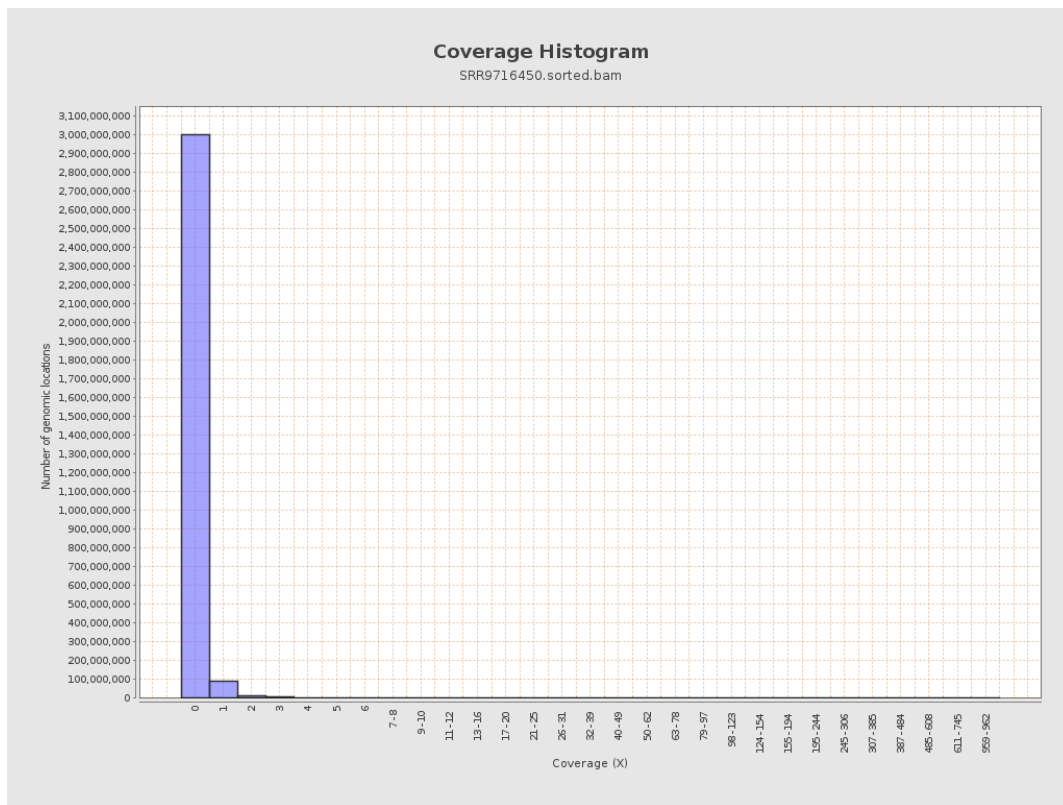
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9242418	0.0371	0.5965
chr2	243199373	9852897	0.0405	0.6327
chr3	198022430	7775879	0.0393	0.2227
chr4	191154276	7332621	0.0384	0.2428
chr5	180915260	7007399	0.0387	0.2266
chr6	171115067	6745297	0.0394	0.2836
chr7	159138663	6523125	0.041	0.5368

chr8	146364022	5985246	0.0409	0.5286
chr9	141213431	4981948	0.0353	0.4573
chr10	135534747	5609139	0.0414	0.3793
chr11	135006516	5294006	0.0392	0.406
chr12	133851895	5330230	0.0398	0.2298
chr13	115169878	3564105	0.0309	0.195
chr14	107349540	3530585	0.0329	0.2803
chr15	102531392	3338548	0.0326	0.2076
chr16	90354753	3466994	0.0384	0.2536
chr17	81195210	3144707	0.0387	0.2404
chr18	78077248	3158629	0.0405	0.8021
chr19	59128983	2438347	0.0412	0.4543
chr20	63025520	2396048	0.038	0.2323
chr21	48129895	1515084	0.0315	0.219
chr22	51304566	1320341	0.0257	0.1802
chrMT	16571	16192	0.9771	1.3843
chrX	155270560	3660338	0.0236	0.2459
chrY	59373566	281555	0.0047	0.1496

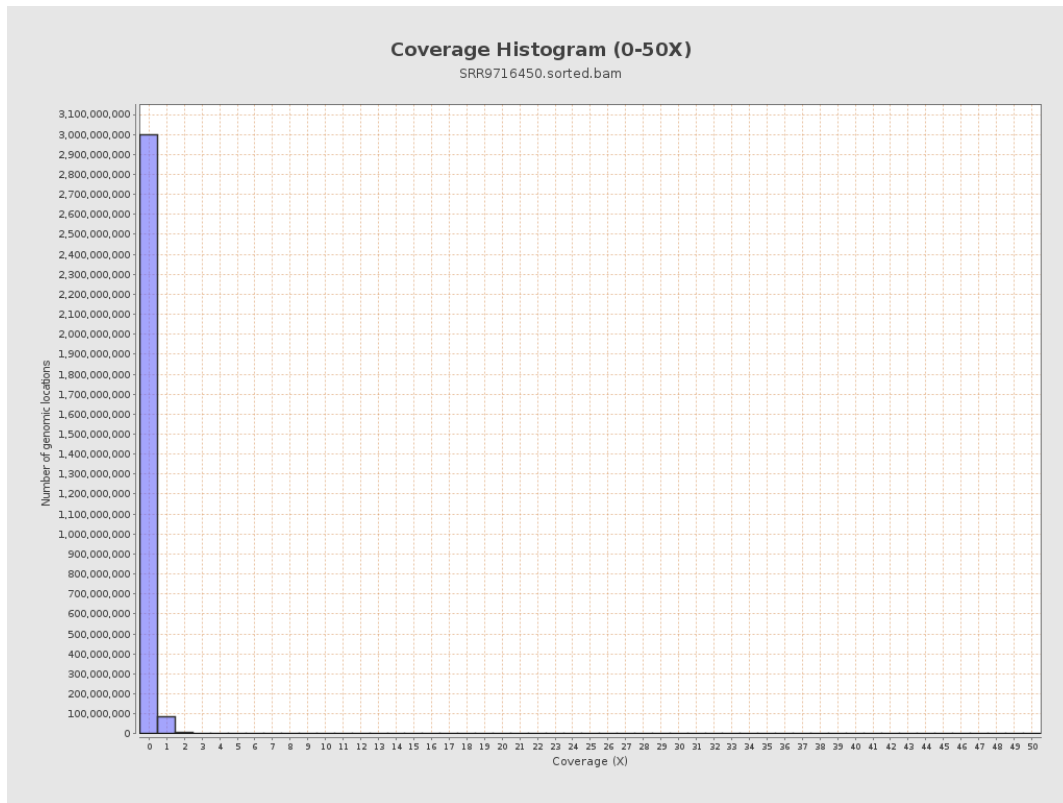
3. Results : Coverage across reference



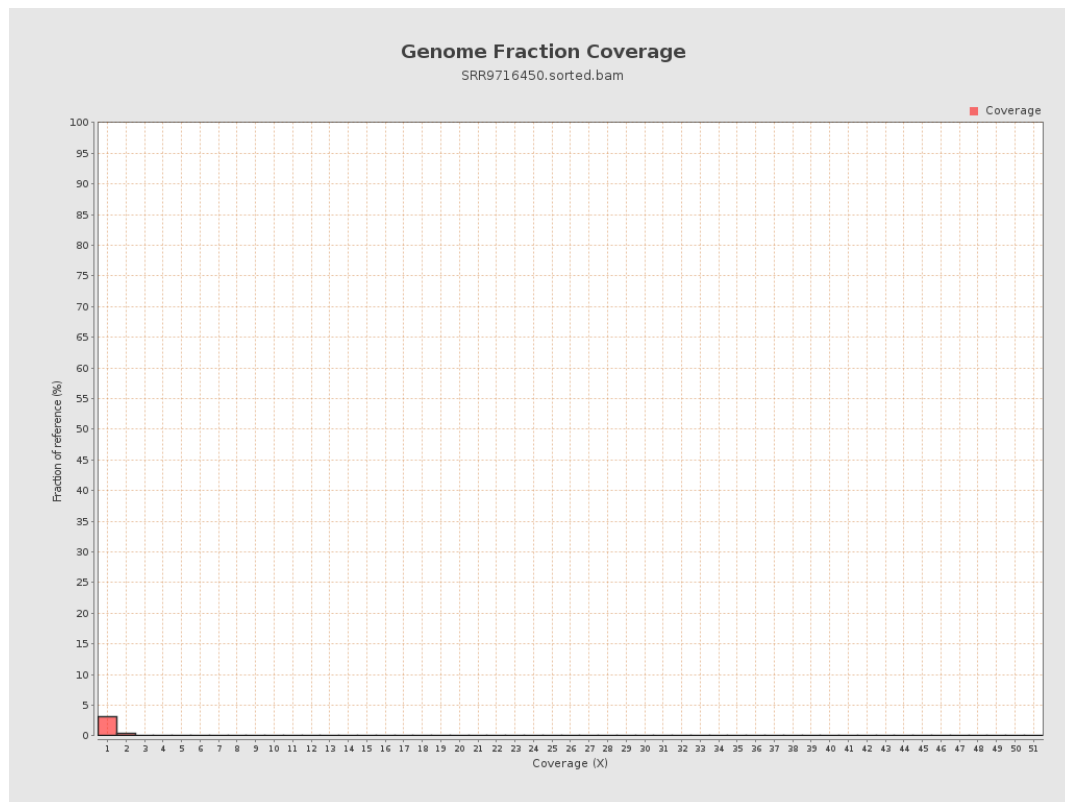
4. Results : Coverage Histogram



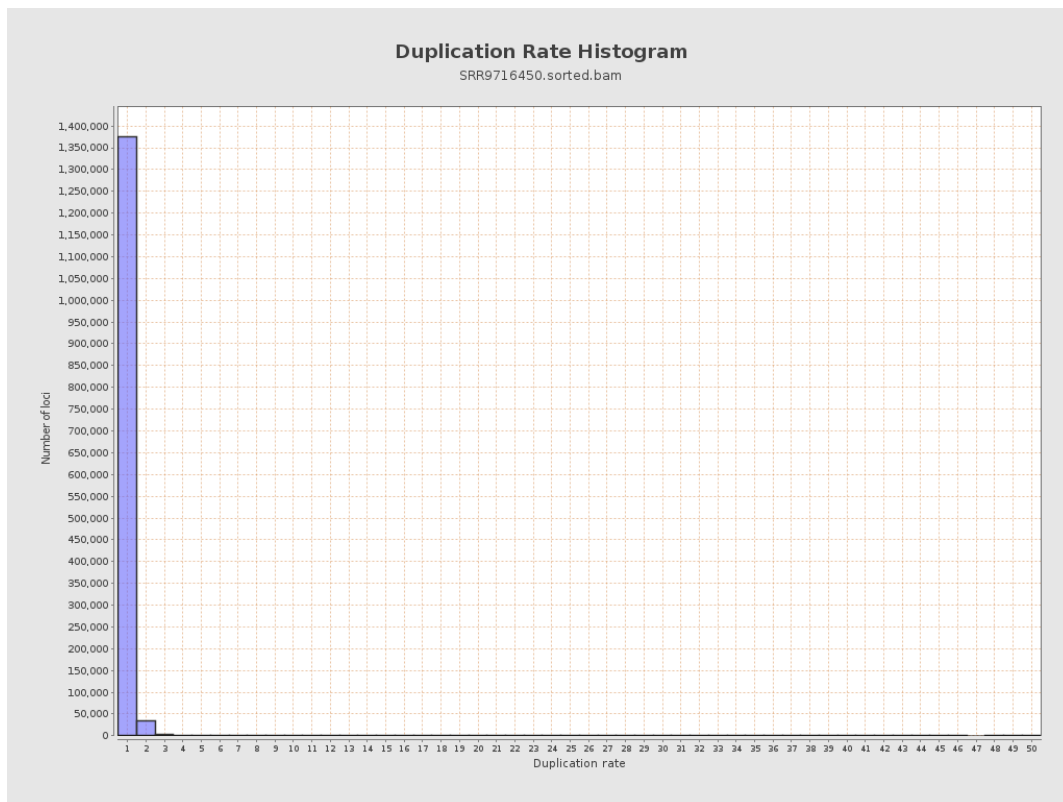
5. Results : Coverage Histogram (0-50X)



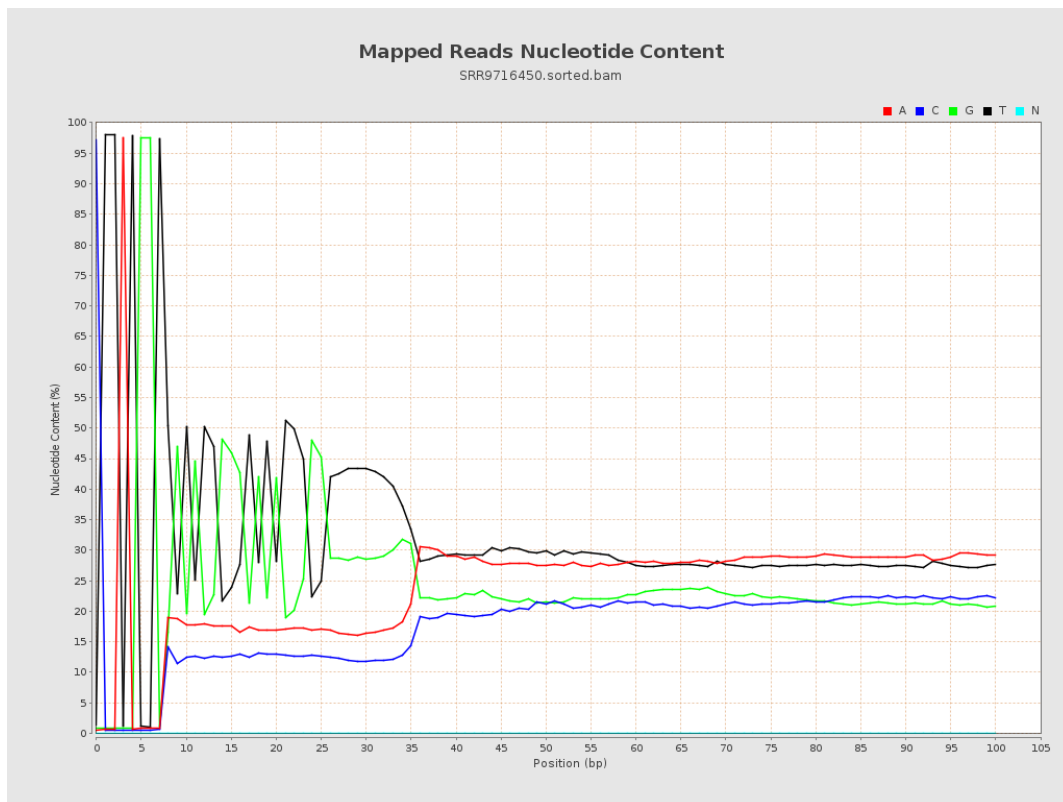
6. Results : Genome Fraction Coverage



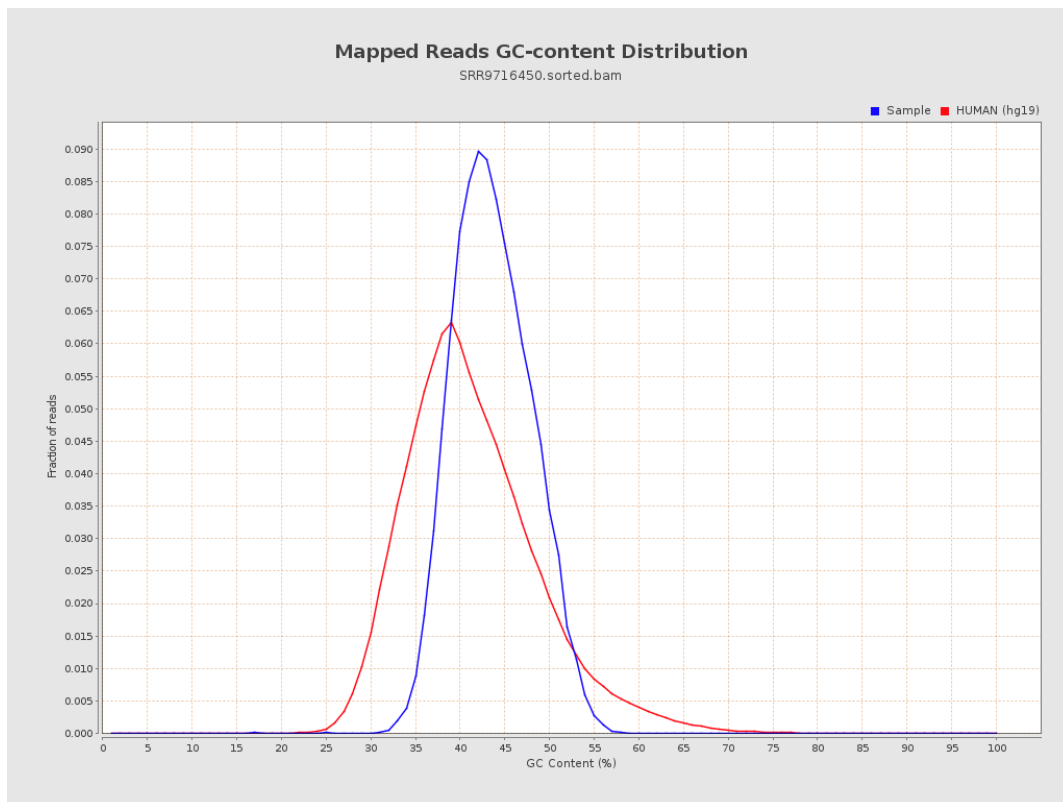
7. Results : Duplication Rate Histogram



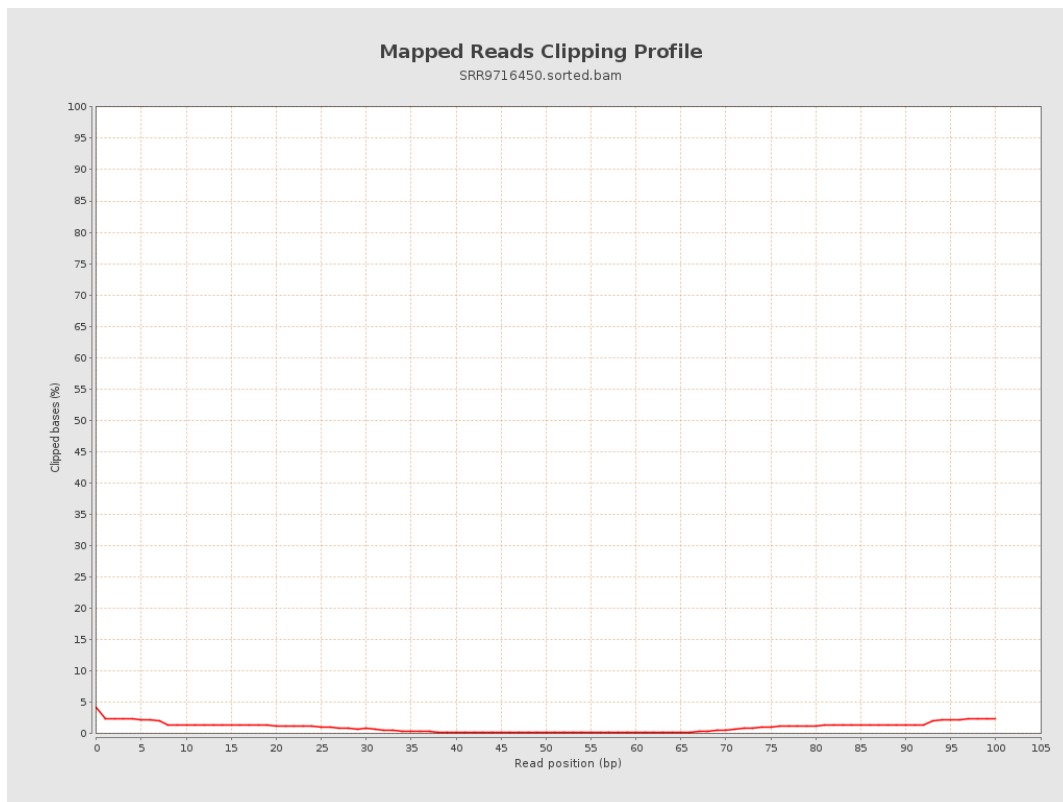
8. Results : Mapped Reads Nucleotide Content



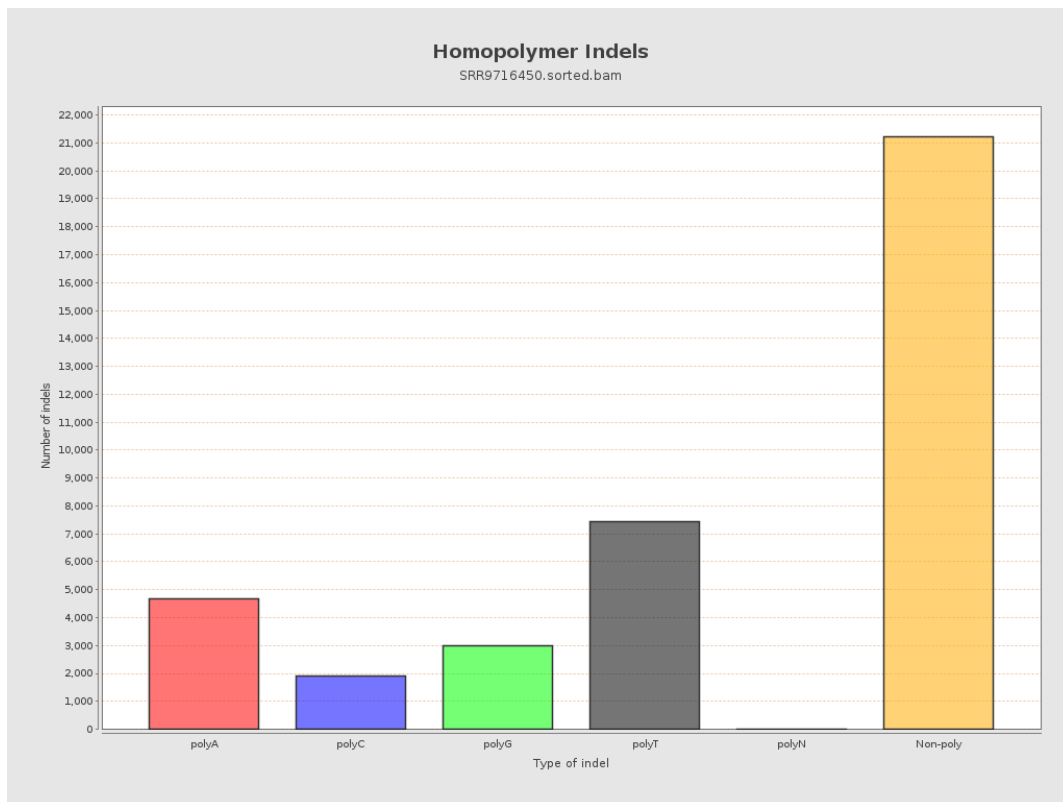
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

