Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:41:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716454.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_SRR9716454 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716454.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:41:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716454.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,467,814
Mapped reads	31,507,004 / 97.04%
Unmapped reads	960,810 / 2.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,475 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	1,795,101 / 5.53%
Duplication rate	2.52%
Clipped reads	31,376,899 / 96.64%

2.2. ACGT Content

Number/percentage of A's	619,957,919 / 28.99%
Number/percentage of C's	452,717,692 / 21.17%
Number/percentage of T's	637,795,633 / 29.83%
Number/percentage of G's	427,573,173 / 20%
Number/percentage of N's	334,193 / 0.02%
GC Percentage	41.17%

2.3. Coverage

Mean	0.6909

Standard Deviation	6.3009

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

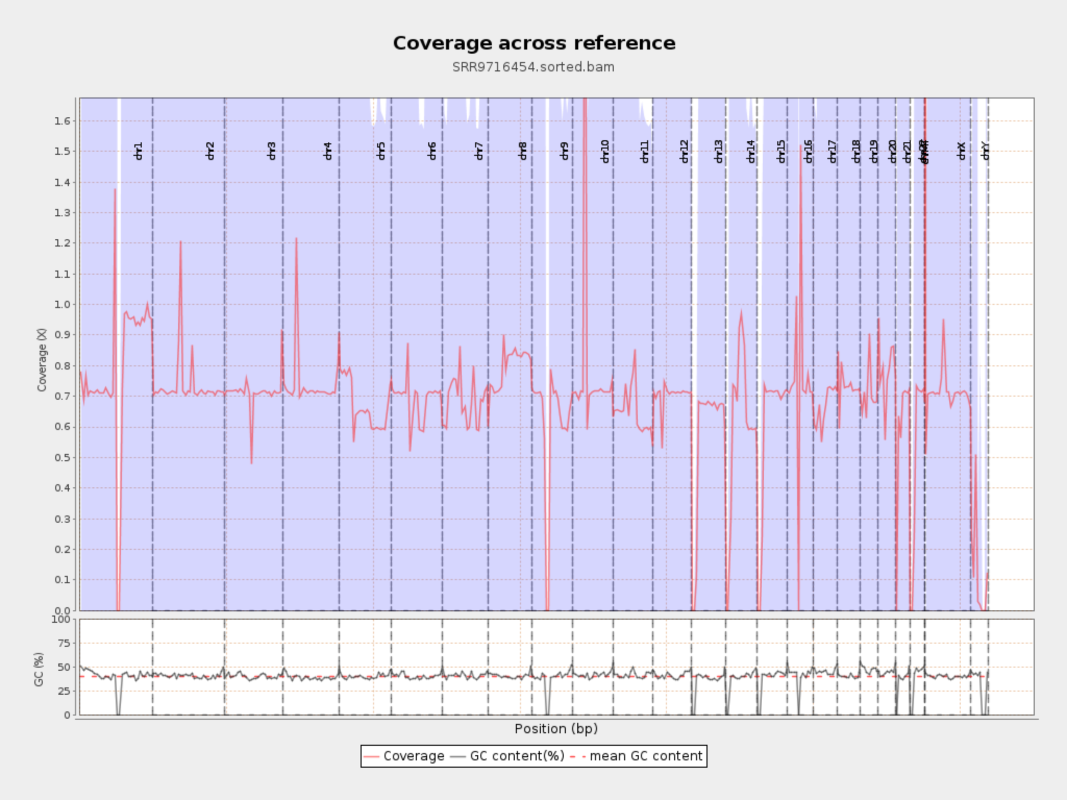
General error rate	0.36%
Mismatches	7,368,184
Insertions	179,309
Mapped reads with at least one insertion	0.57%
Deletions	203,168
Mapped reads with at least one deletion	0.64%
Homopolymer indels	39.7%

2.6. Chromosome stats

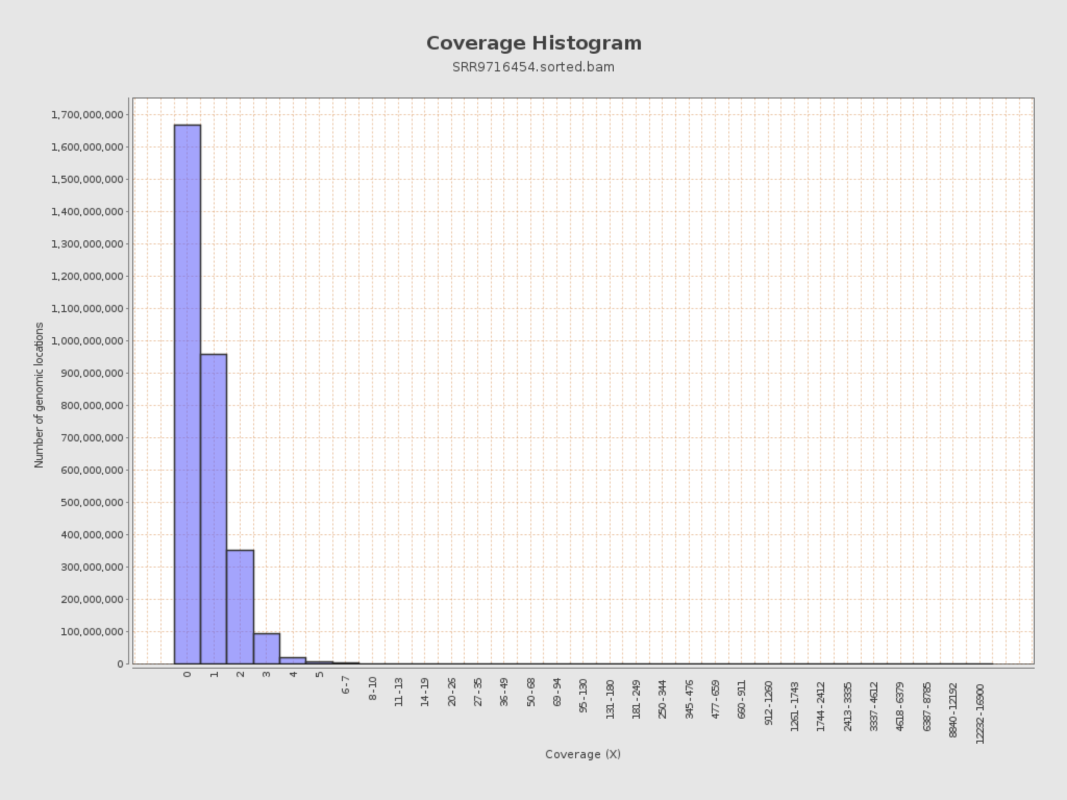
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	197359413	0.7918	14.8998
chr2	243199373	179759513	0.7391	4.1654
chr3	198022430	140226934	0.7081	2.6028
chr4	191154276	141080439	0.738	2.6445
chr5	180915260	120941603	0.6685	1.2238
chr6	171115067	118247872	0.691	2.2138
chr7	159138663	108696329	0.683	3.8272

chr8	146364022	117243854	0.801	4.6508
chr9	141213431	84775614	0.6003	3.7246
chr10	135534747	110740282	0.8171	15.1484
chr11	135006516	88606799	0.6563	2.7641
chr12	133851895	94242282	0.7041	1.3019
chr13	115169878	64805606	0.5627	0.8548
chr14	107349540	64026631	0.5964	1.6293
chr15	102531392	59231762	0.5777	0.883
chr16	90354753	68470580	0.7578	6.0023
chr17	81195210	54059530	0.6658	1.7471
chr18	78077248	56836794	0.728	8.6848
chr19	59128983	41724604	0.7057	10.1377
chr20	63025520	49392957	0.7837	1.4463
chr21	48129895	29374252	0.6103	2.6285
chr22	51304566	25725322	0.5014	1.0144
chrMT	16571	4992969	301.3076	66.0136
chrX	155270560	110794891	0.7136	2.2646
chrY	59373566	7401945	0.1247	3.9115

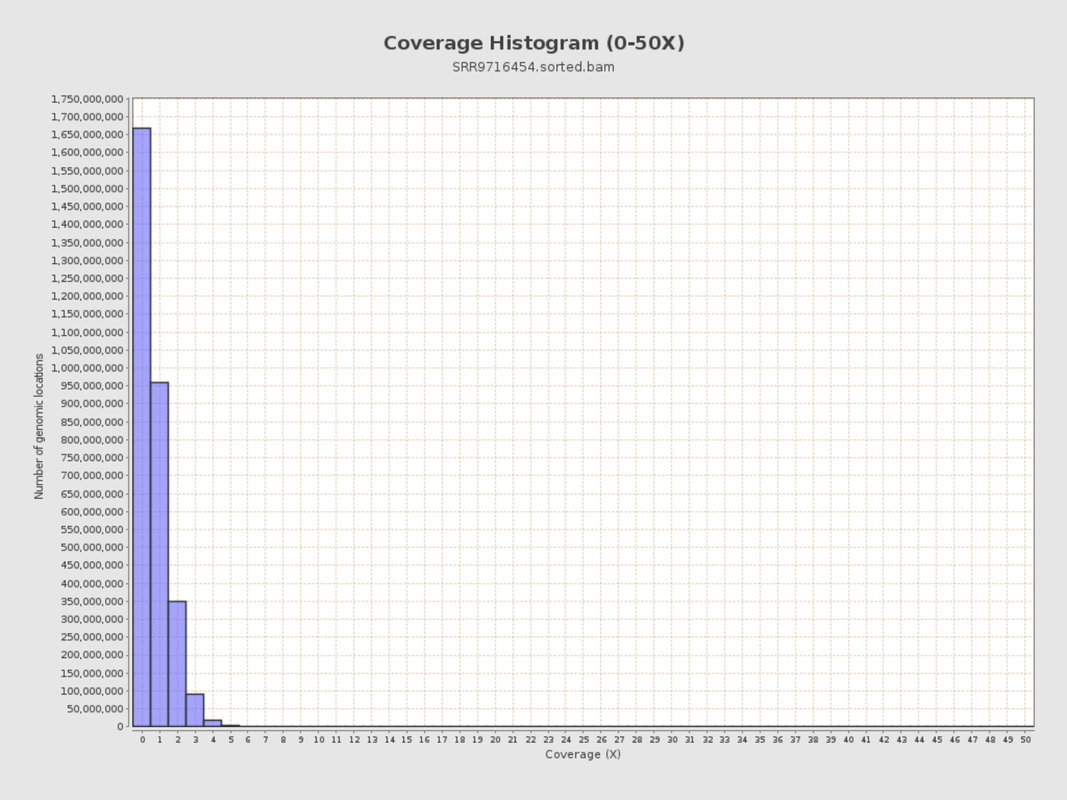
3. Results : Coverage across reference



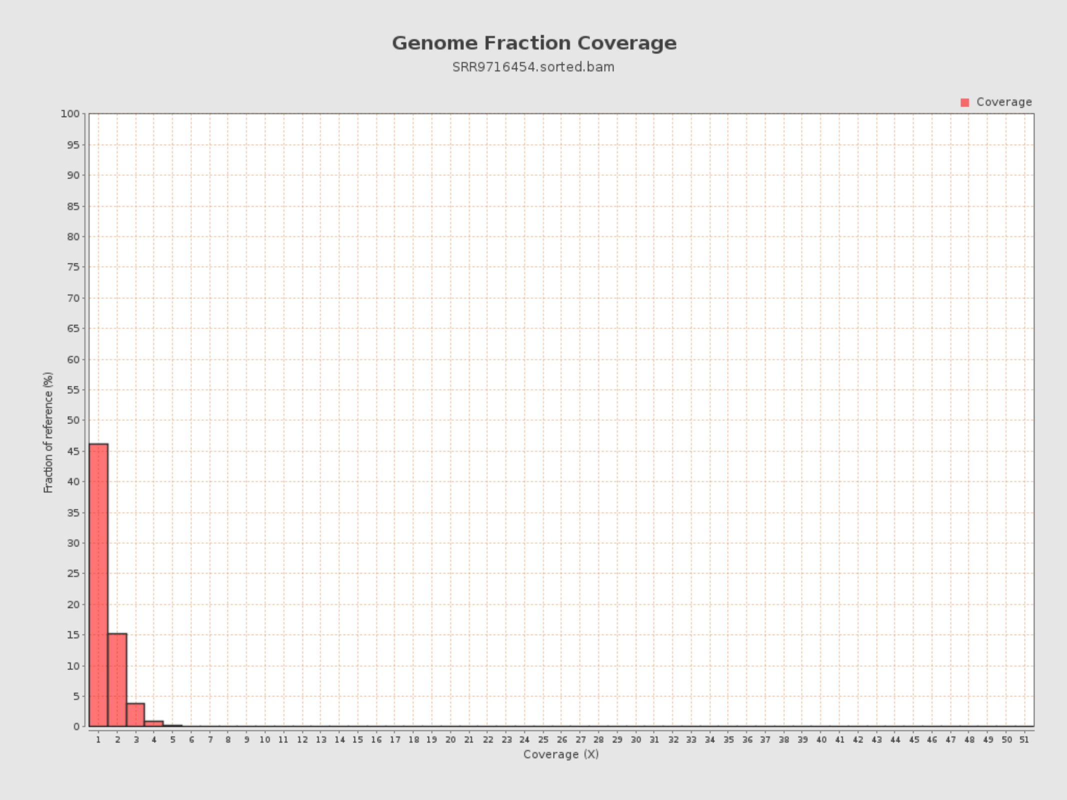
4. Results : Coverage Histogram



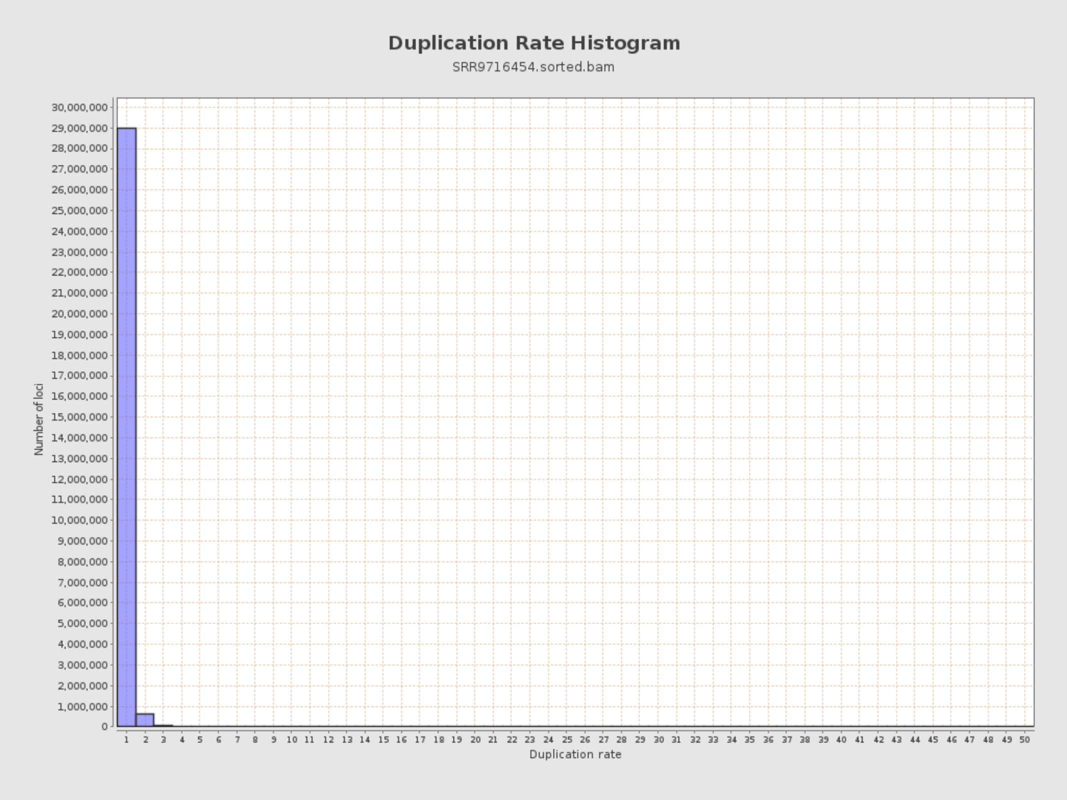
5. Results : Coverage Histogram (0-50X)



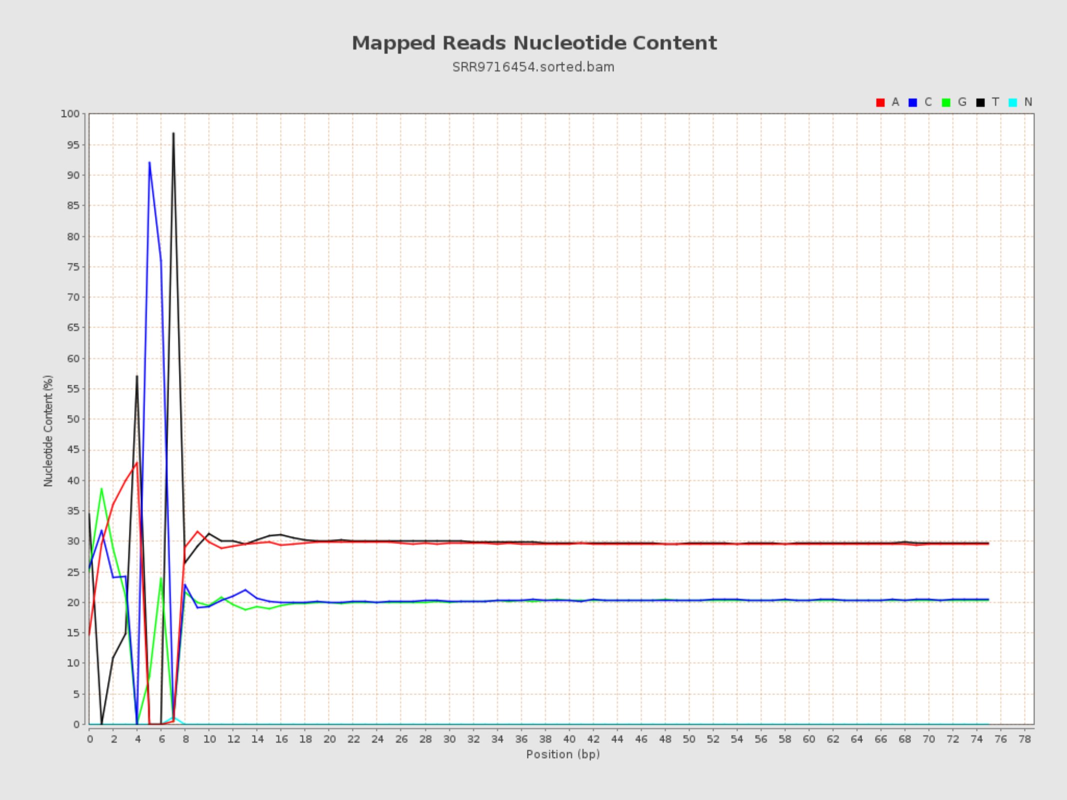
6. Results : Genome Fraction Coverage



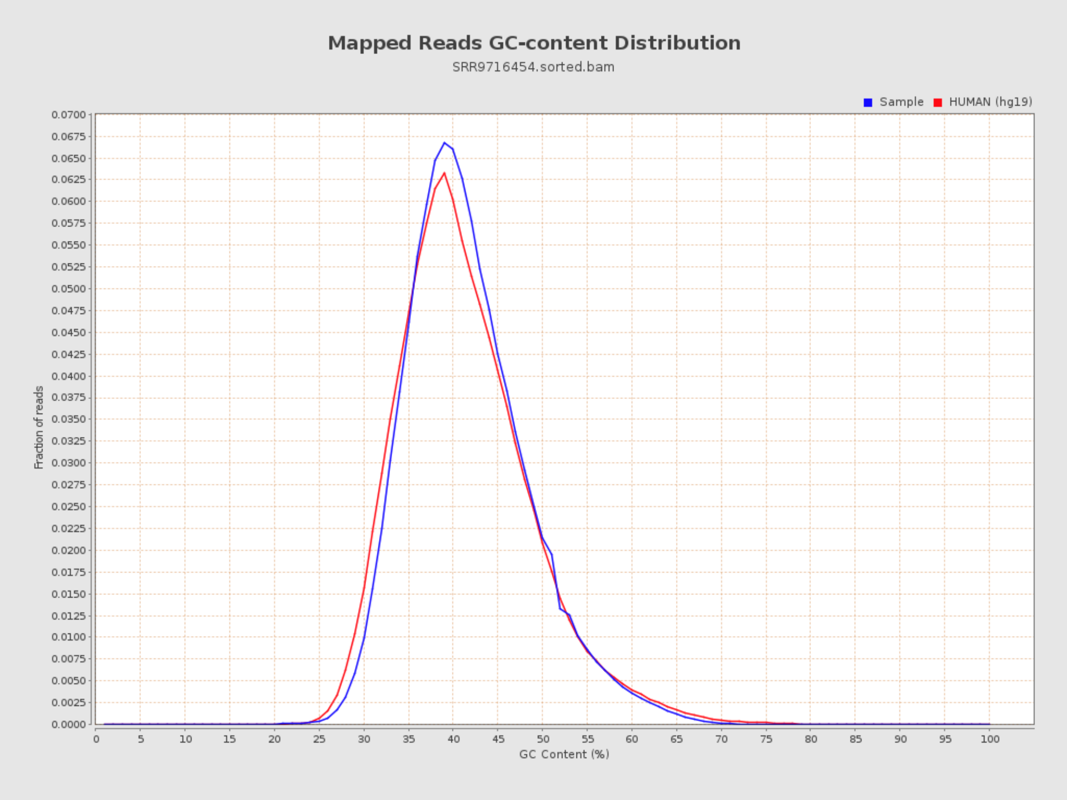
7. Results : Duplication Rate Histogram



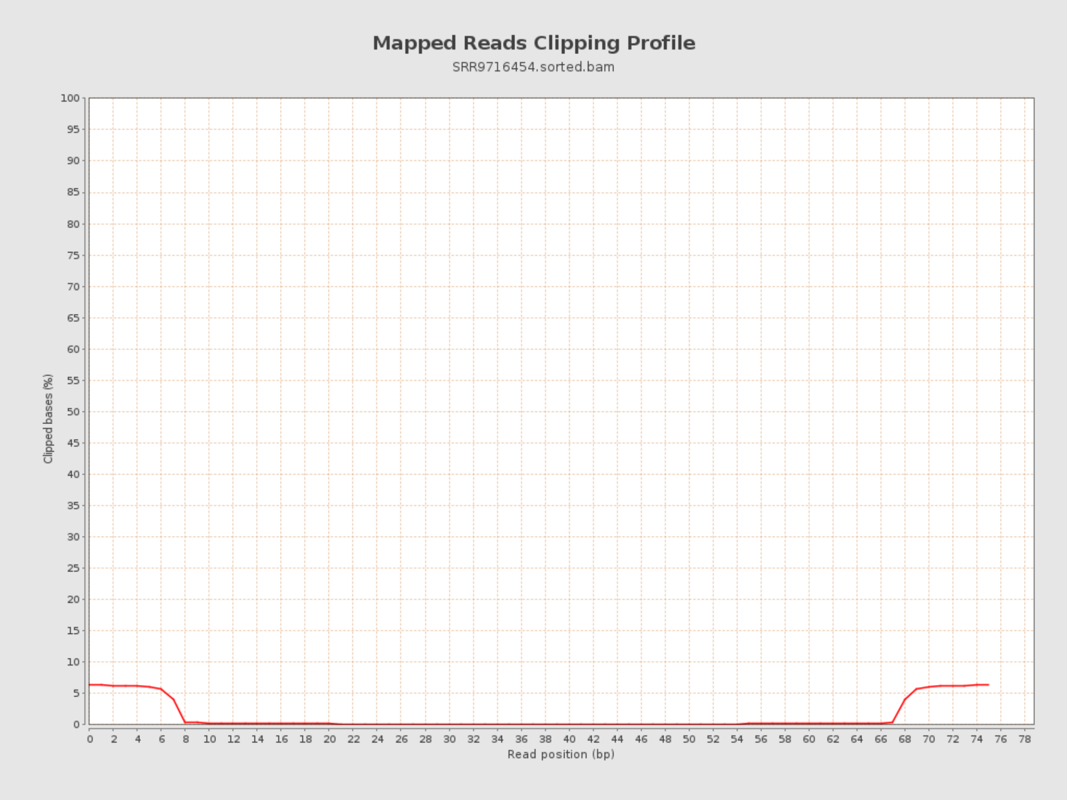
8. Results : Mapped Reads Nucleotide Content



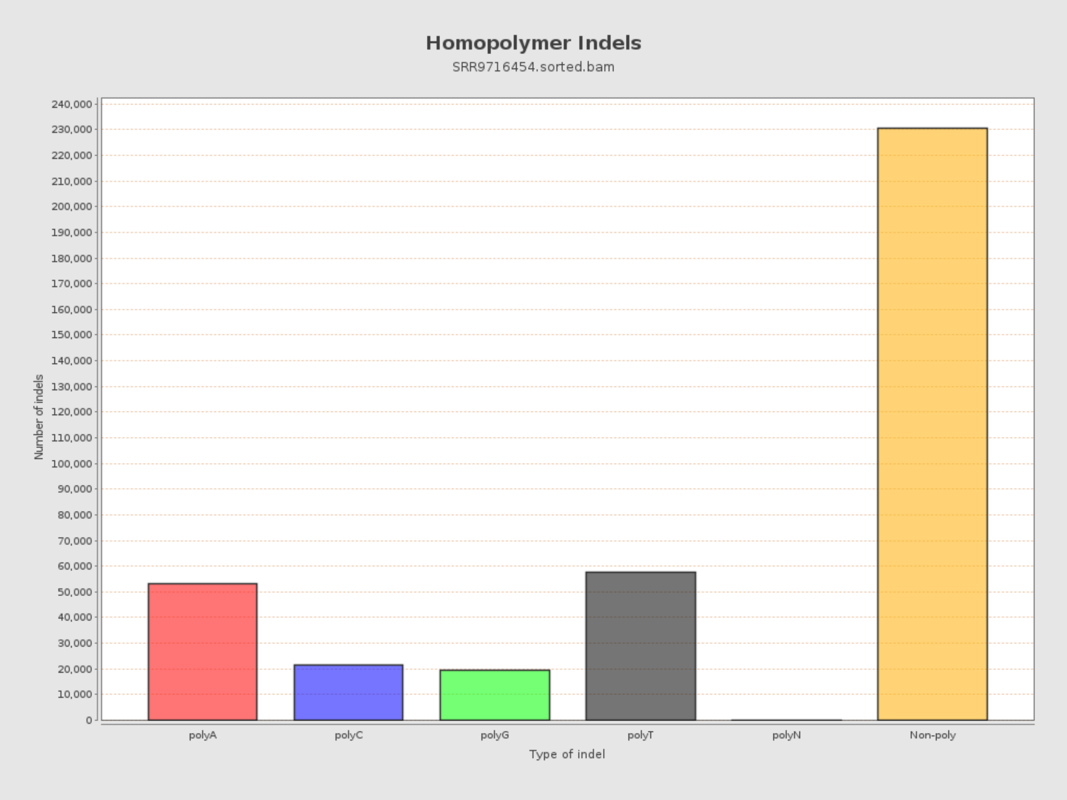
9. Results : Mapped Reads GC-content Distribution



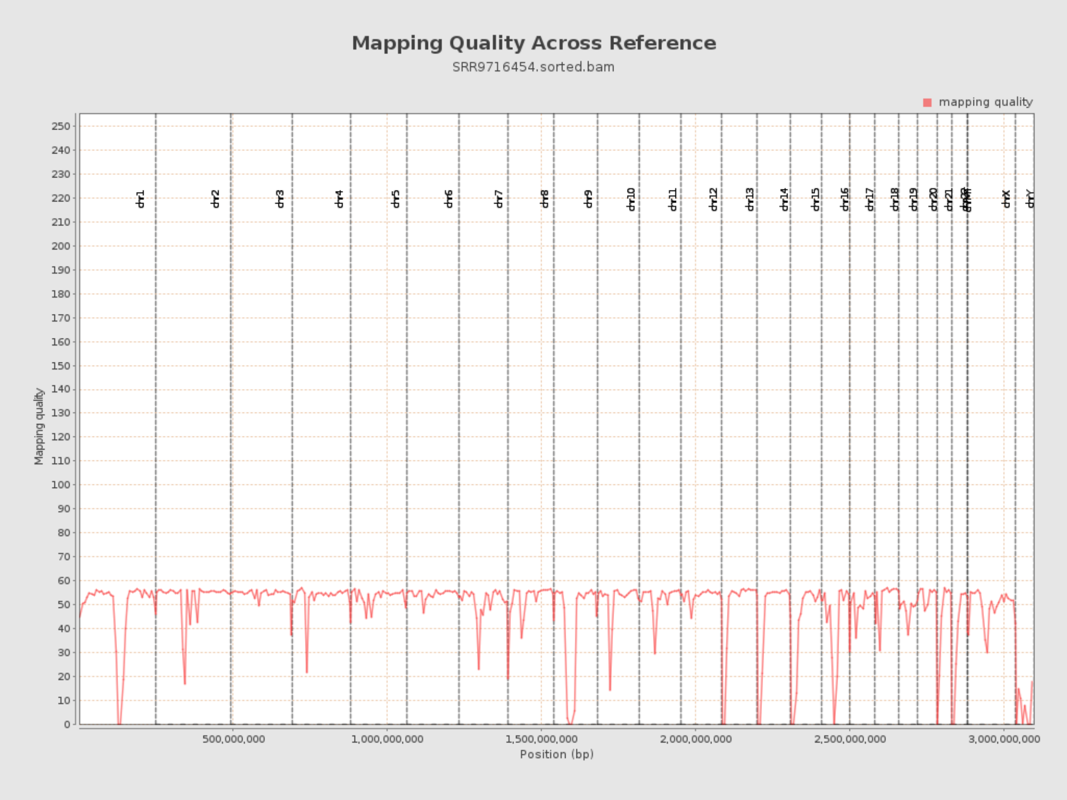
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram