Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:59:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716514.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_SRR9716514 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716514.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:59:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716514.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,962,696
Mapped reads	2,711,711 / 91.53%
Unmapped reads	250,985 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,681 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	117,595 / 3.97%
Duplication rate	3.01%
Clipped reads	2,726,931 / 92.04%

2.2. ACGT Content

Number/percentage of A's	39,793,157 / 25.16%
Number/percentage of C's	31,936,846 / 20.2%
Number/percentage of T's	48,242,304 / 30.51%
Number/percentage of G's	38,164,830 / 24.13%
Number/percentage of N's	2,098 / 0%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0511

Standard Deviation	0.4677

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

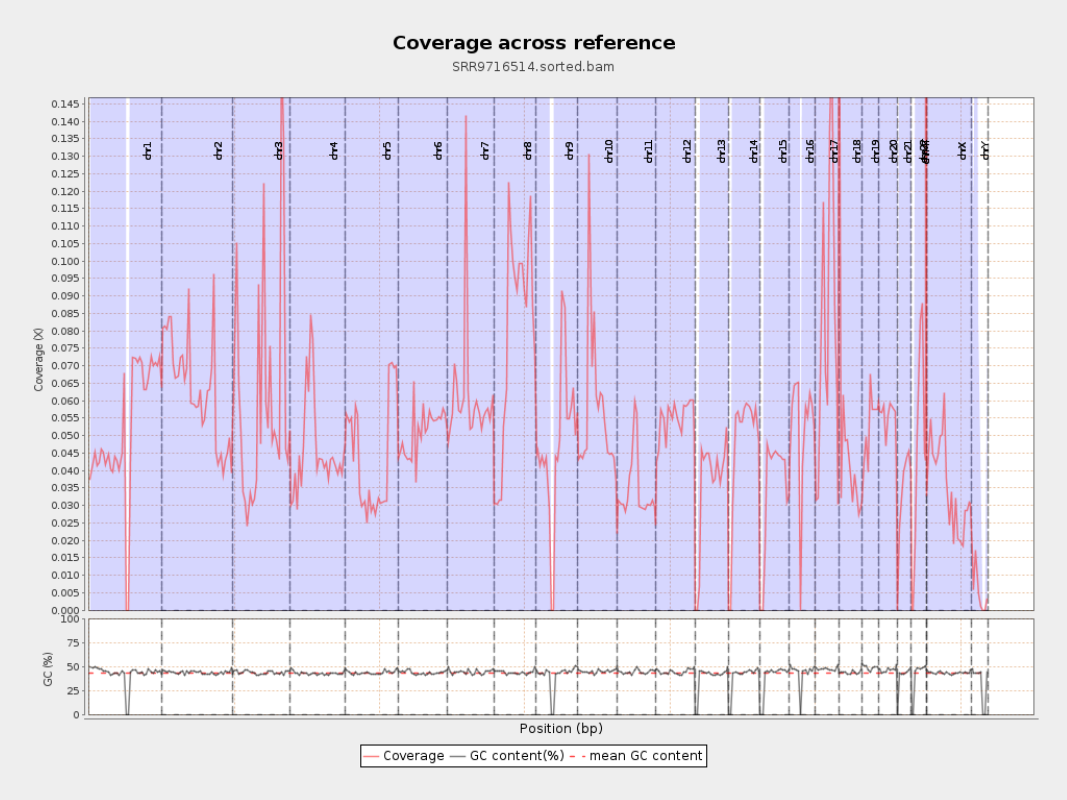
General error rate	0.51%
Mismatches	788,616
Insertions	8,307
Mapped reads with at least one insertion	0.3%
Deletions	28,294
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.92%

2.6. Chromosome stats

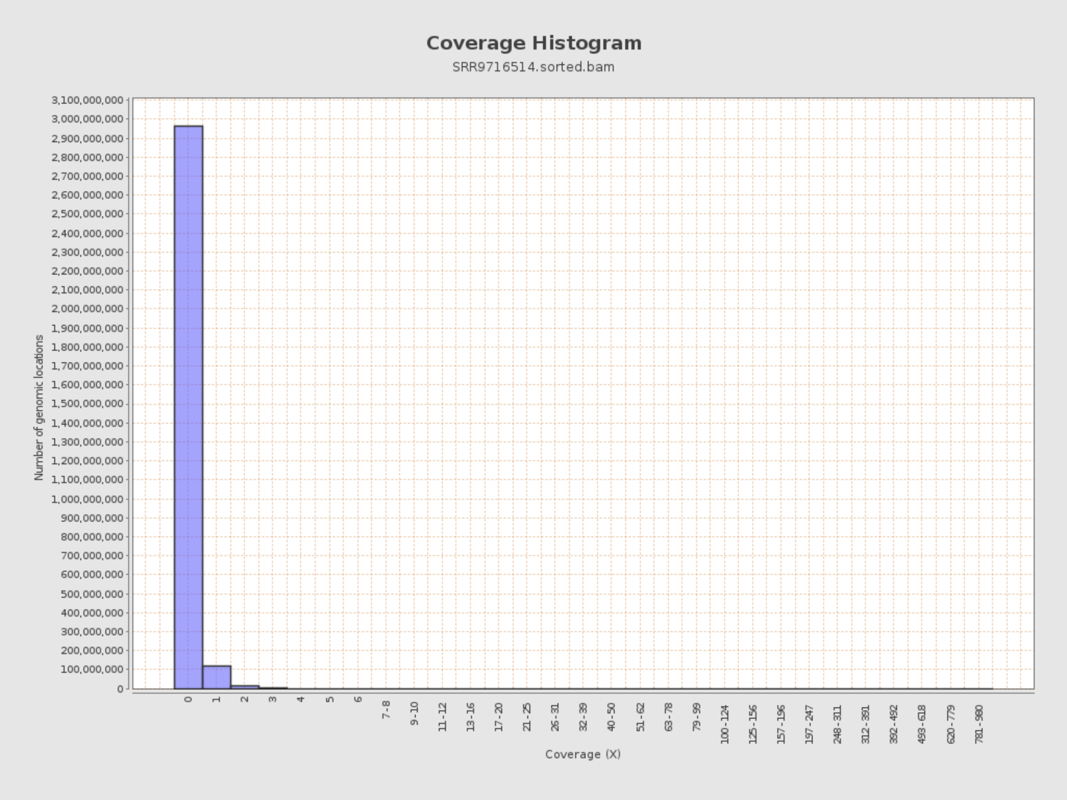
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12928964	0.0519	0.6332
chr2	243199373	15493879	0.0637	0.5277
chr3	198022430	12095995	0.0611	0.3131
chr4	191154276	8826931	0.0462	0.2675
chr5	180915260	7907017	0.0437	0.2402
chr6	171115067	8751838	0.0511	0.2886
chr7	159138663	9809191	0.0616	1.1919

chr8	146364022	11706329	0.08	0.4816
chr9	141213431	6609030	0.0468	0.3137
chr10	135534747	7761288	0.0573	0.6194
chr11	135006516	4622467	0.0342	0.2986
chr12	133851895	7327001	0.0547	0.3092
chr13	115169878	4102491	0.0356	0.2139
chr14	107349540	5055231	0.0471	0.2571
chr15	102531392	3572475	0.0348	0.2287
chr16	90354753	4751602	0.0526	0.2797
chr17	81195210	6593638	0.0812	0.3467
chr18	78077248	3687832	0.0472	0.5255
chr19	59128983	3092451	0.0523	0.567
chr20	63025520	3487802	0.0553	0.294
chr21	48129895	1618523	0.0336	0.2206
chr22	51304566	2301155	0.0449	0.2422
chrMT	16571	163261	9.8522	6.0495
chrX	155270560	5585008	0.036	0.27
chrY	59373566	332220	0.0056	0.1294

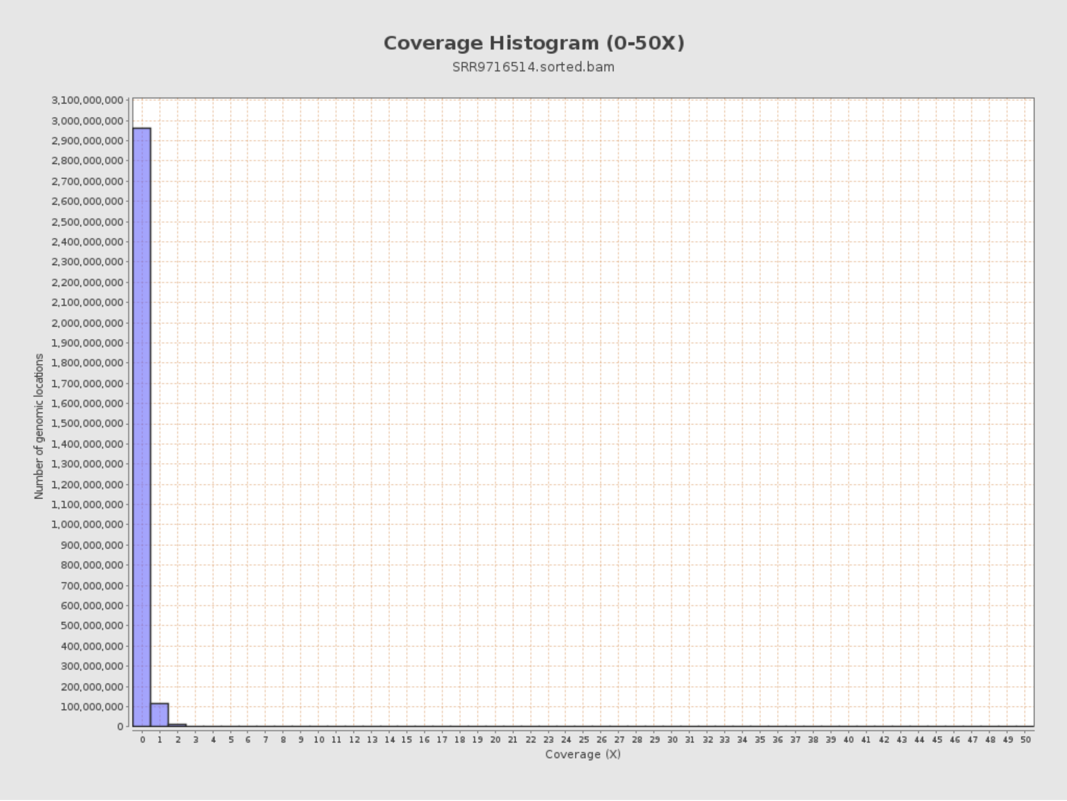
3. Results : Coverage across reference



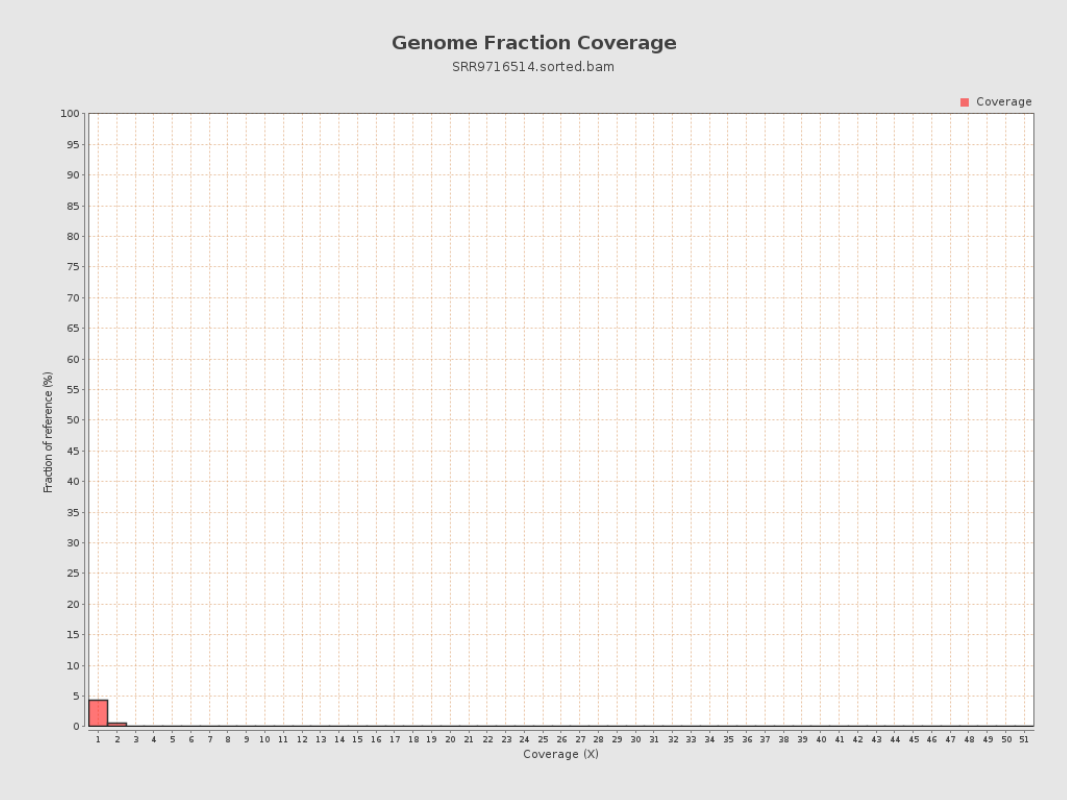
4. Results : Coverage Histogram



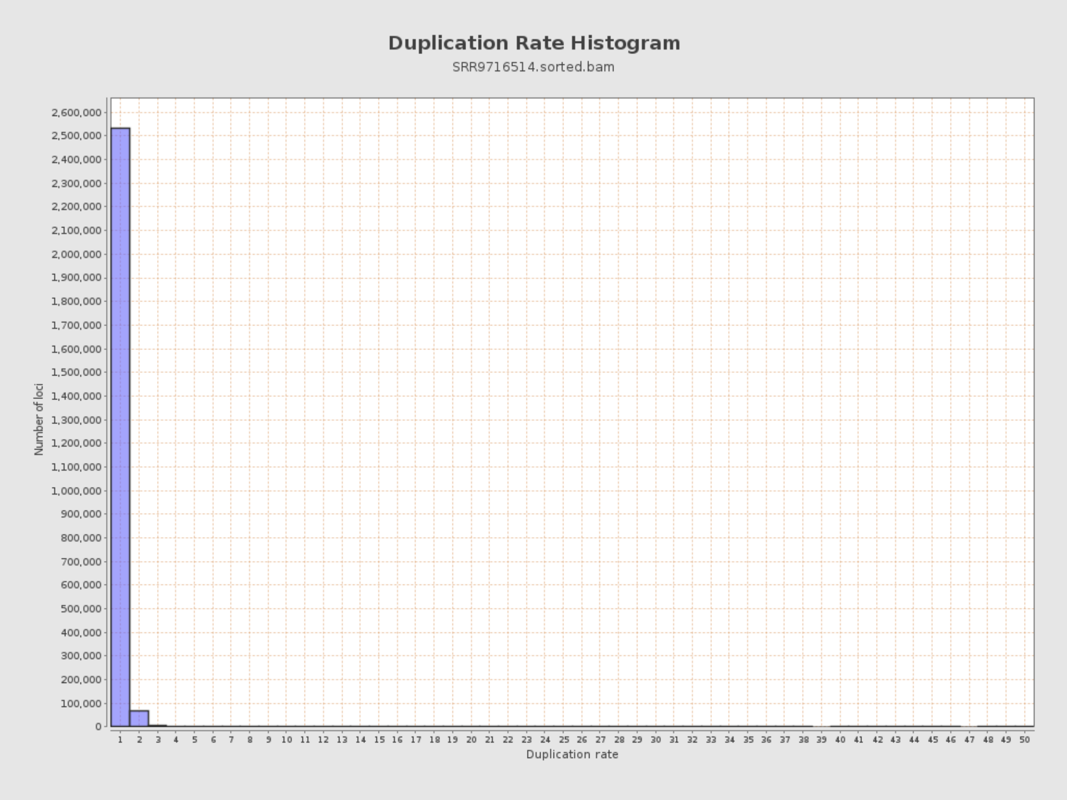
5. Results : Coverage Histogram (0-50X)



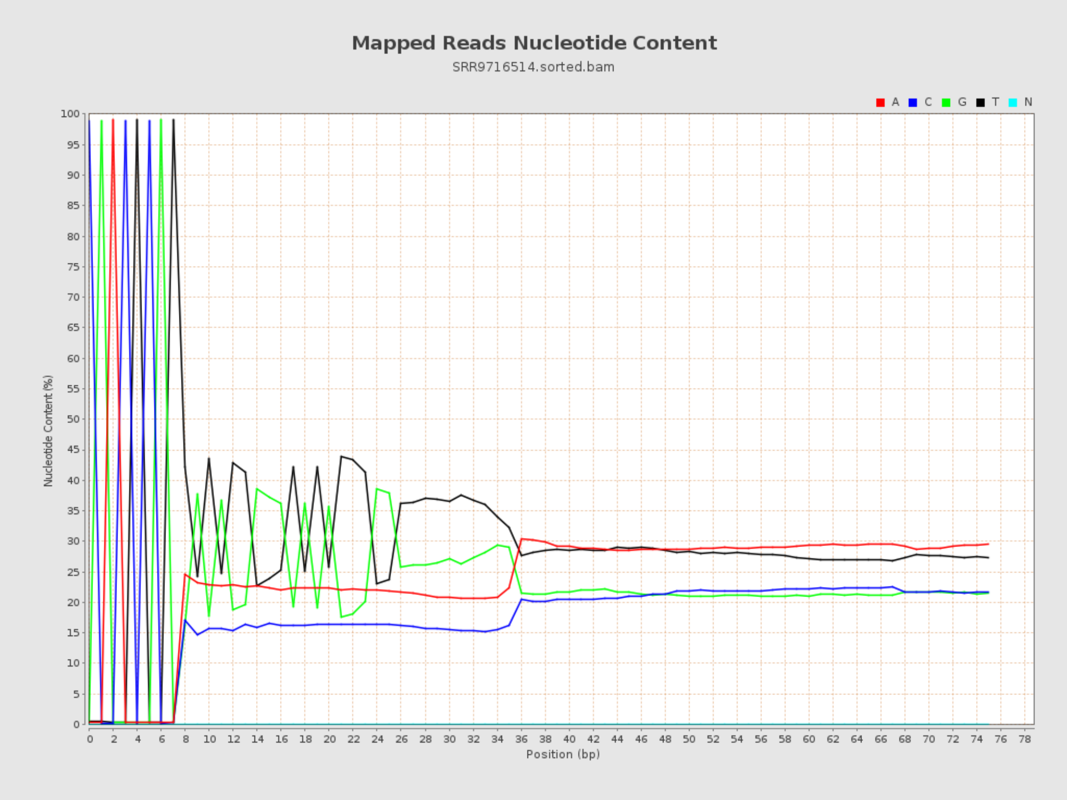
6. Results : Genome Fraction Coverage



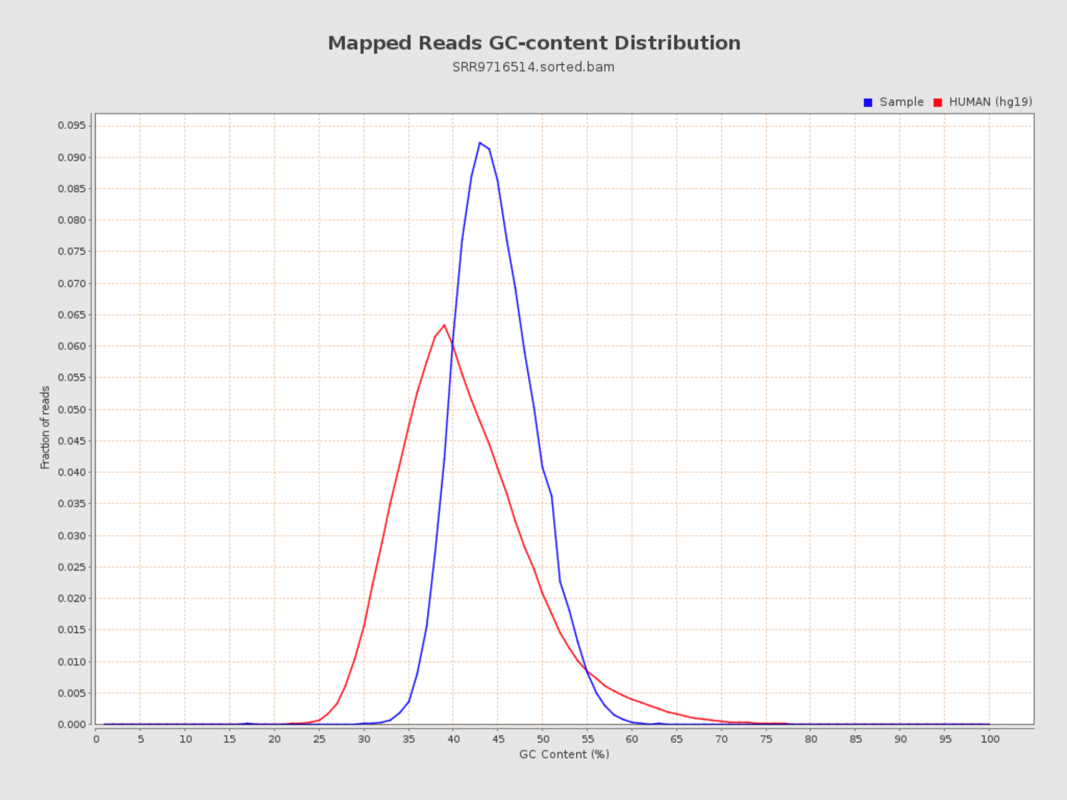
7. Results : Duplication Rate Histogram



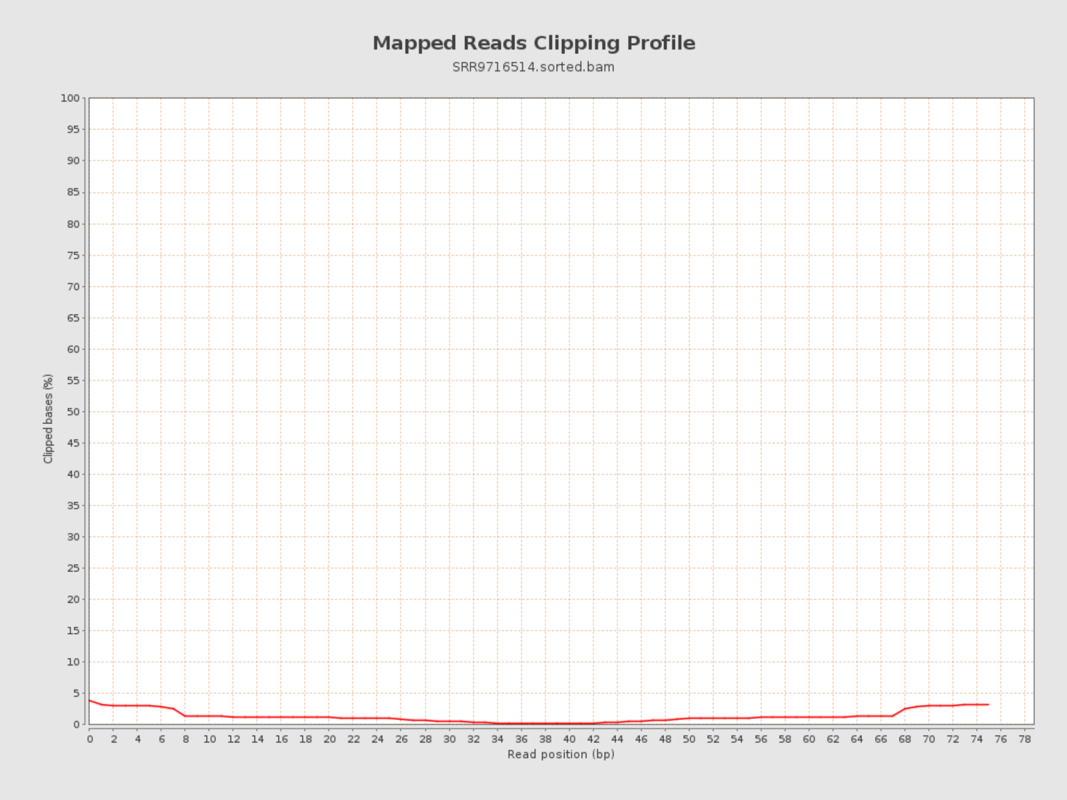
8. Results : Mapped Reads Nucleotide Content



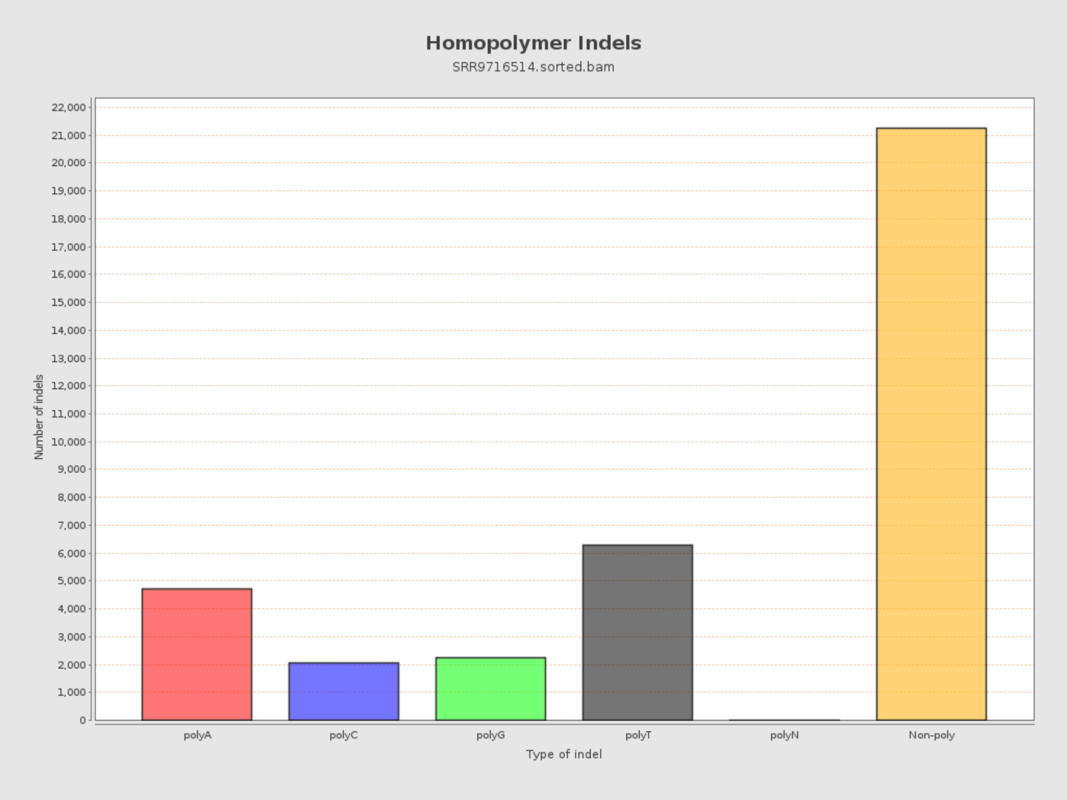
9. Results : Mapped Reads GC-content Distribution



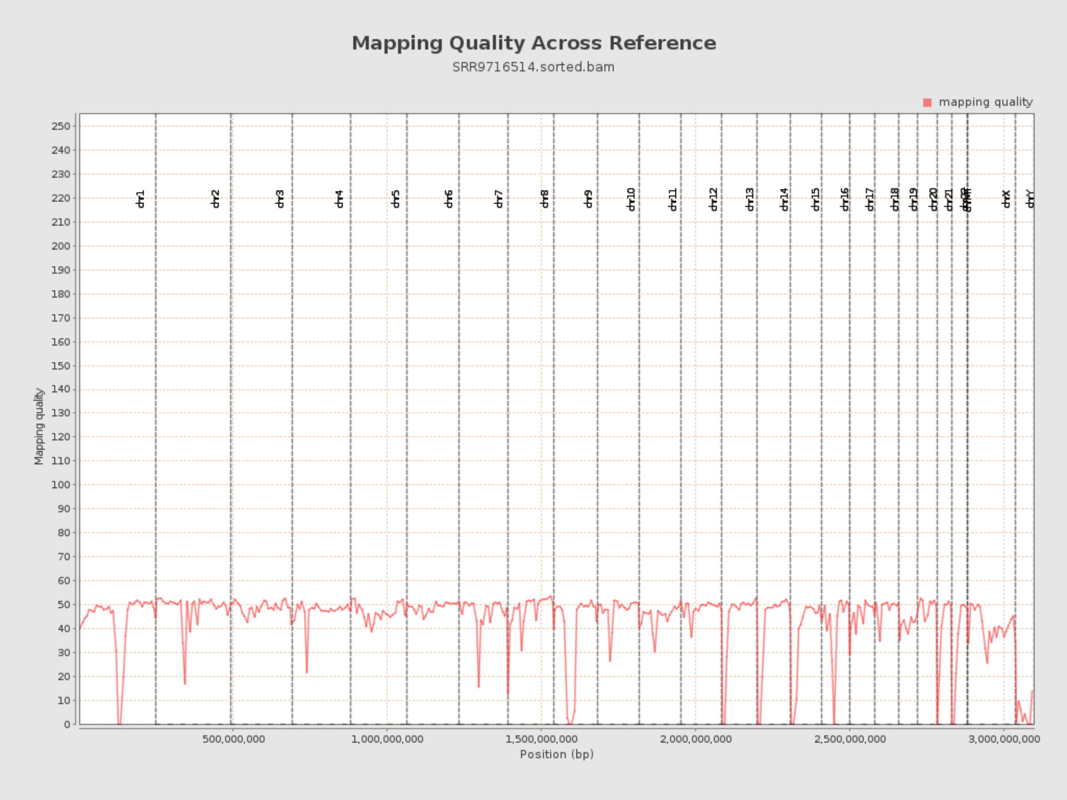
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram