Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:56:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716187.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_SRR9716187 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:56:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,955,576
Mapped reads	1,702,626 / 87.07%
Unmapped reads	252,950 / 12.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,594 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	45,365 / 2.32%
Duplication rate	1.82%
Clipped reads	1,704,635 / 87.17%

2.2. ACGT Content

Number/percentage of A's	24,140,945 / 25.08%
Number/percentage of C's	18,712,859 / 19.44%
Number/percentage of T's	30,254,693 / 31.43%
Number/percentage of G's	23,153,541 / 24.05%
Number/percentage of N's	867 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2645

2.4. Mapping Quality

Mean Mapping Quality	41.74

2.5. Mismatches and indels

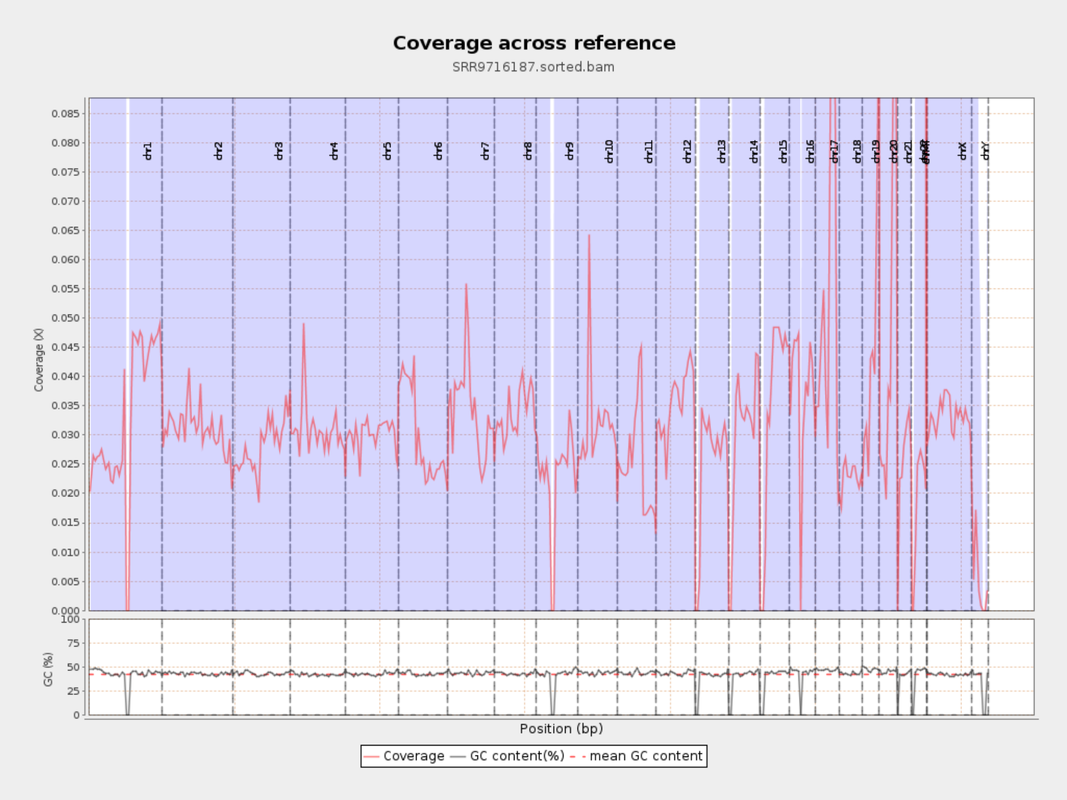
General error rate	0.55%
Mismatches	513,182
Insertions	7,064
Mapped reads with at least one insertion	0.41%
Deletions	18,272
Mapped reads with at least one deletion	1.06%
Homopolymer indels	40.85%

2.6. Chromosome stats

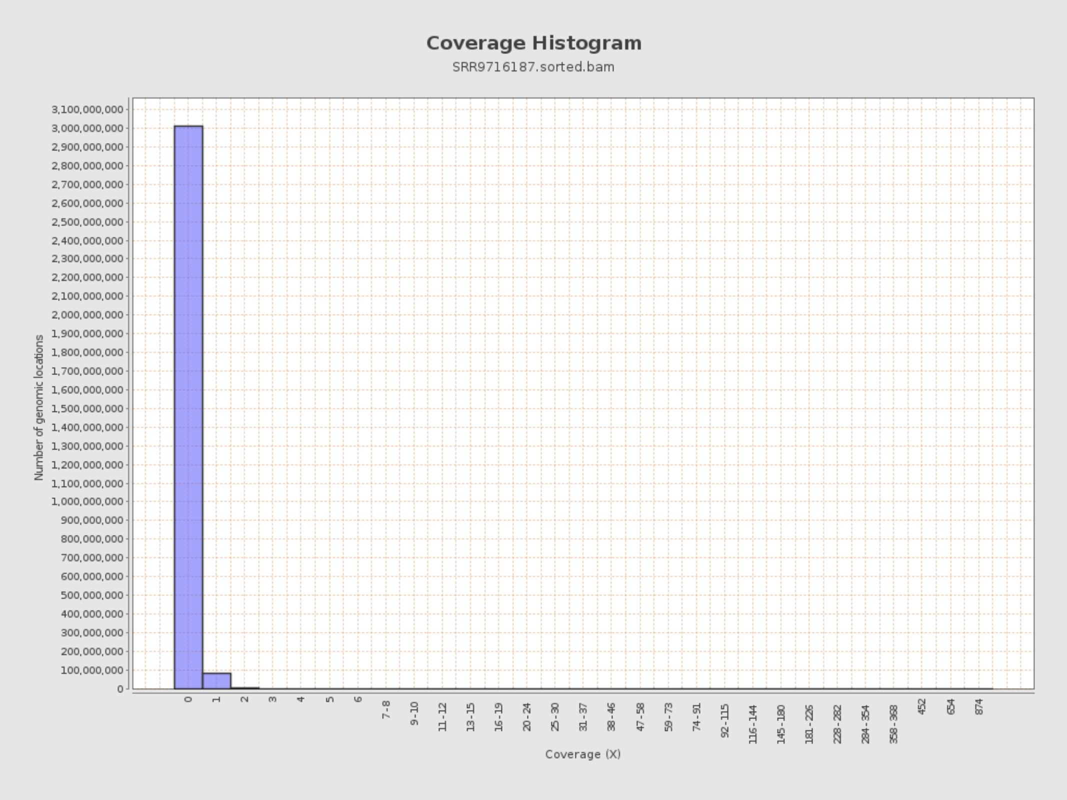
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8088286	0.0325	0.3509
chr2	243199373	7551120	0.031	0.4017
chr3	198022430	5559276	0.0281	0.1872
chr4	191154276	5896943	0.0308	0.2101
chr5	180915260	5456727	0.0302	0.1889
chr6	171115067	5124892	0.0299	0.2234
chr7	159138663	5493209	0.0345	0.3693

chr8	146364022	4951195	0.0338	0.2588
chr9	141213431	3195005	0.0226	0.1957
chr10	135534747	4310136	0.0318	0.3334
chr11	135006516	3401781	0.0252	0.2213
chr12	133851895	4754745	0.0355	0.2064
chr13	115169878	2883734	0.025	0.1718
chr14	107349540	3210610	0.0299	0.2007
chr15	102531392	3561728	0.0347	0.2098
chr16	90354753	3354693	0.0371	0.2264
chr17	81195210	4342105	0.0535	0.2669
chr18	78077248	1780968	0.0228	0.3102
chr19	59128983	2632232	0.0445	0.3231
chr20	63025520	3102155	0.0492	0.2558
chr21	48129895	1219261	0.0253	0.1887
chr22	51304566	907818	0.0177	0.1452
chrMT	16571	52095	3.1437	2.7642
chrX	155270560	5153503	0.0332	0.2114
chrY	59373566	307828	0.0052	0.1487

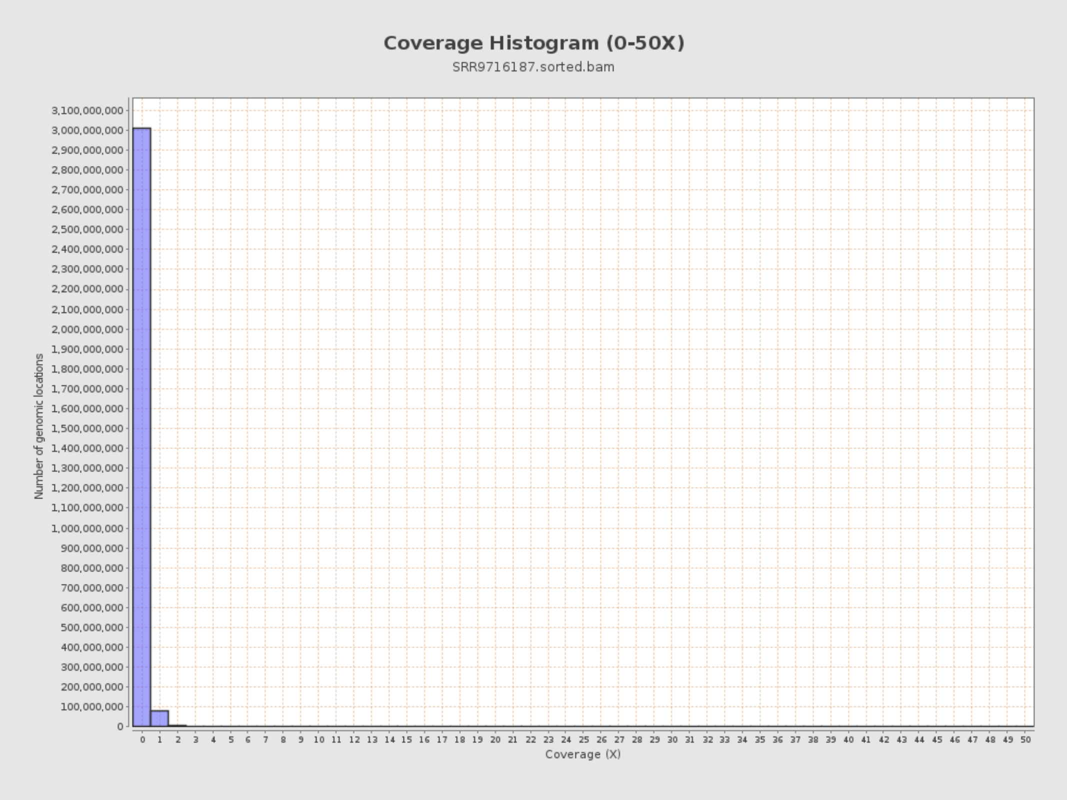
3. Results : Coverage across reference



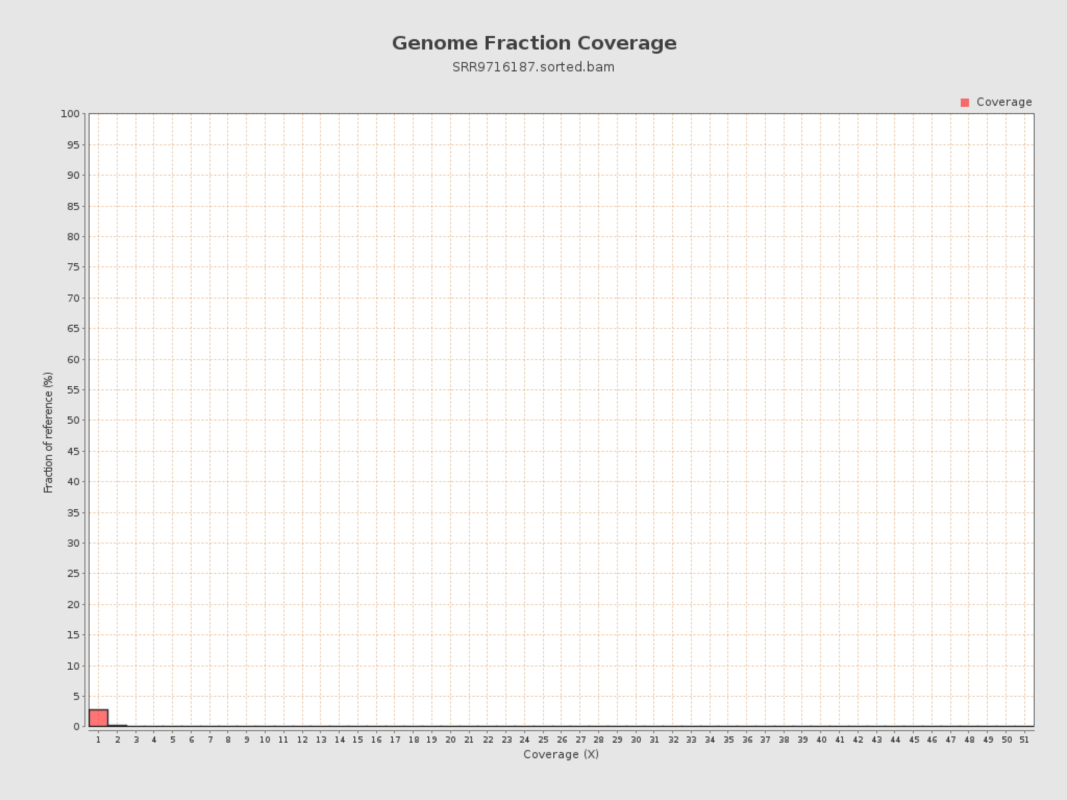
4. Results : Coverage Histogram



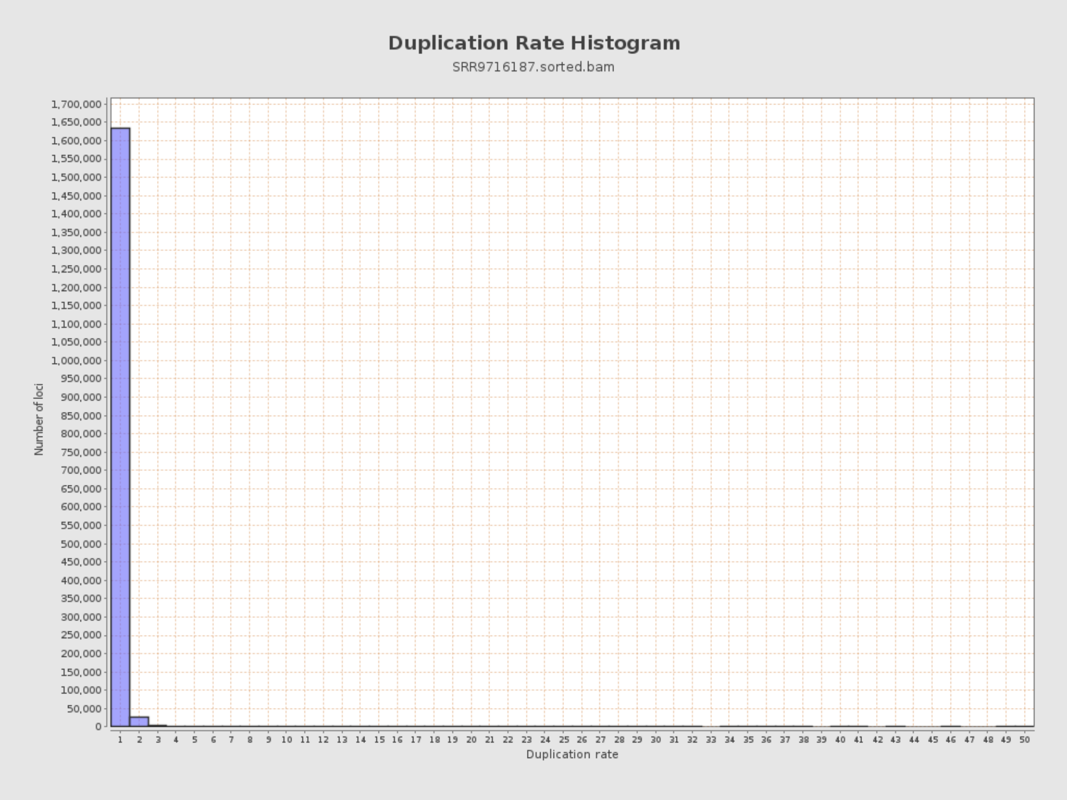
5. Results : Coverage Histogram (0-50X)



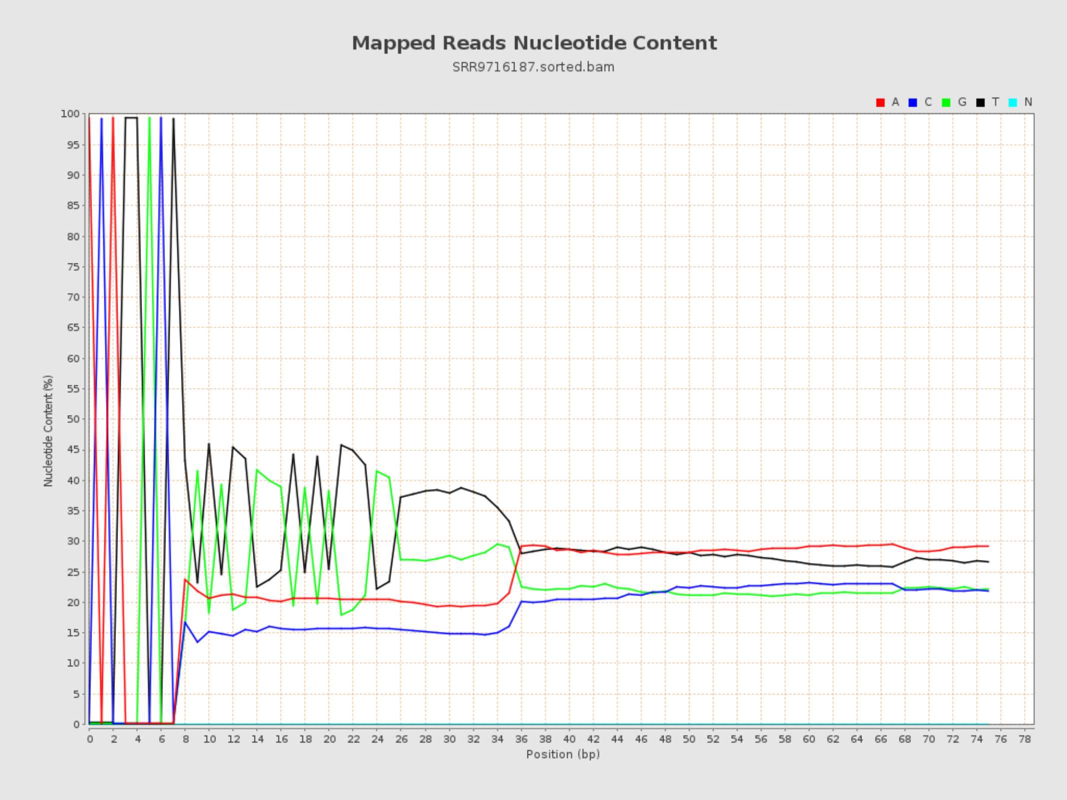
6. Results : Genome Fraction Coverage



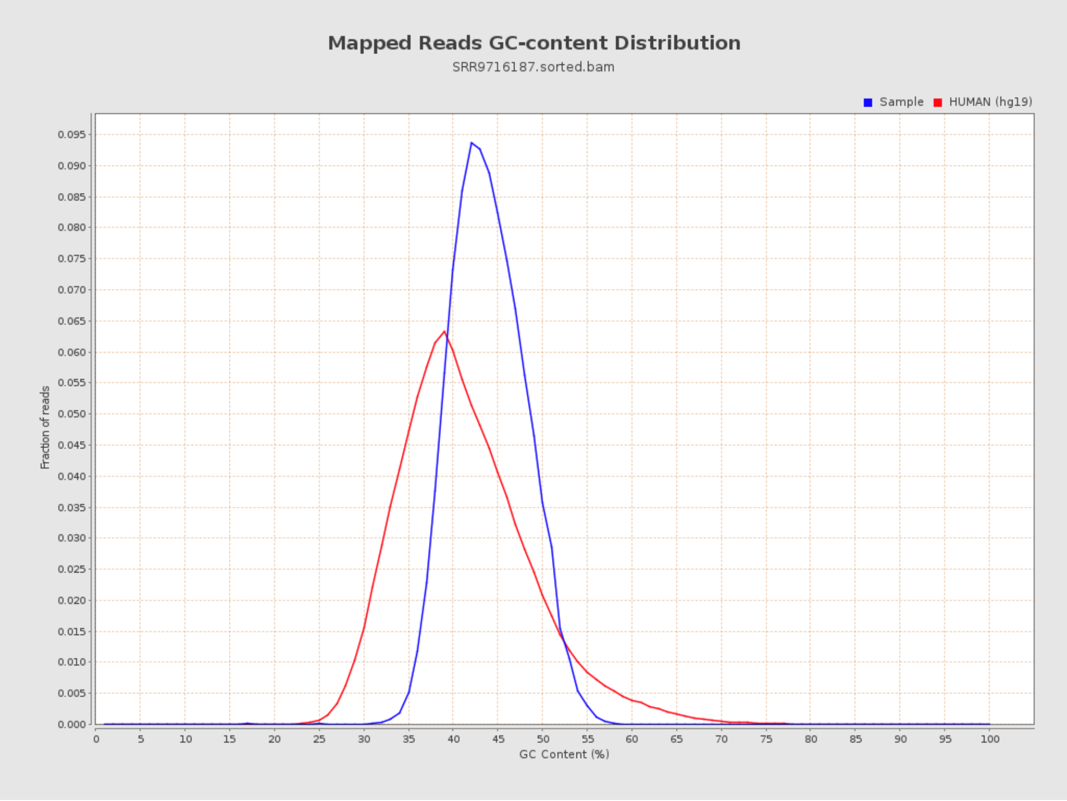
7. Results : Duplication Rate Histogram



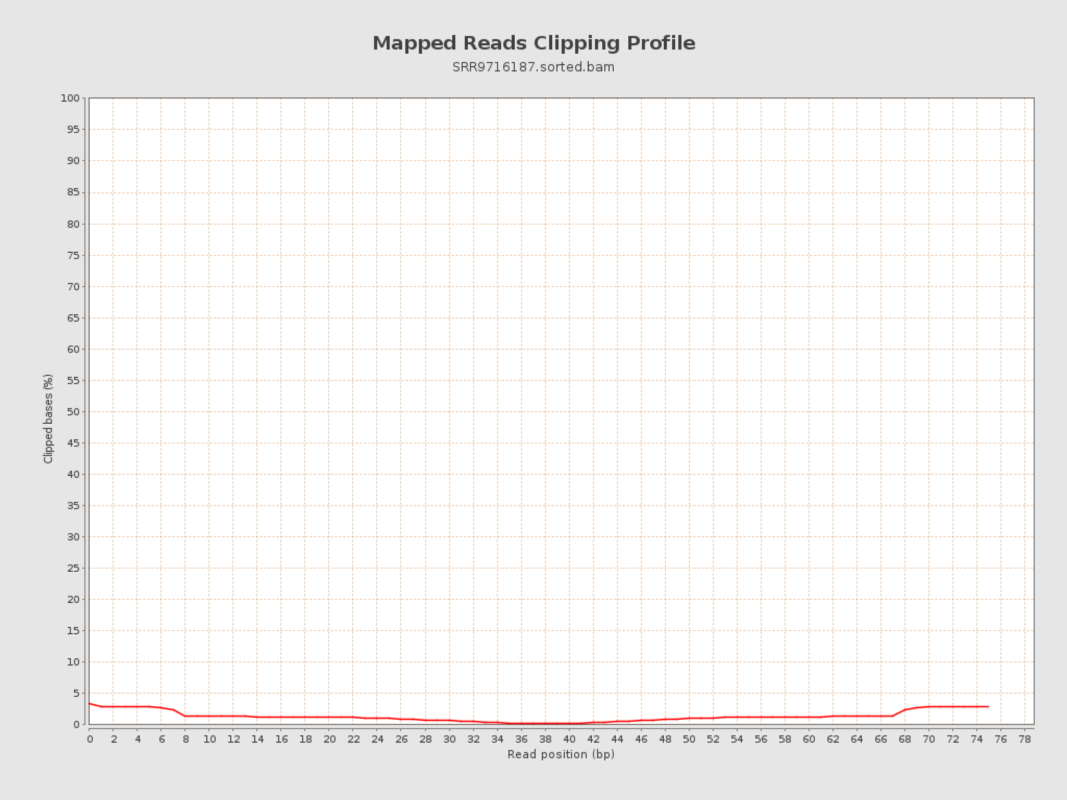
8. Results : Mapped Reads Nucleotide Content



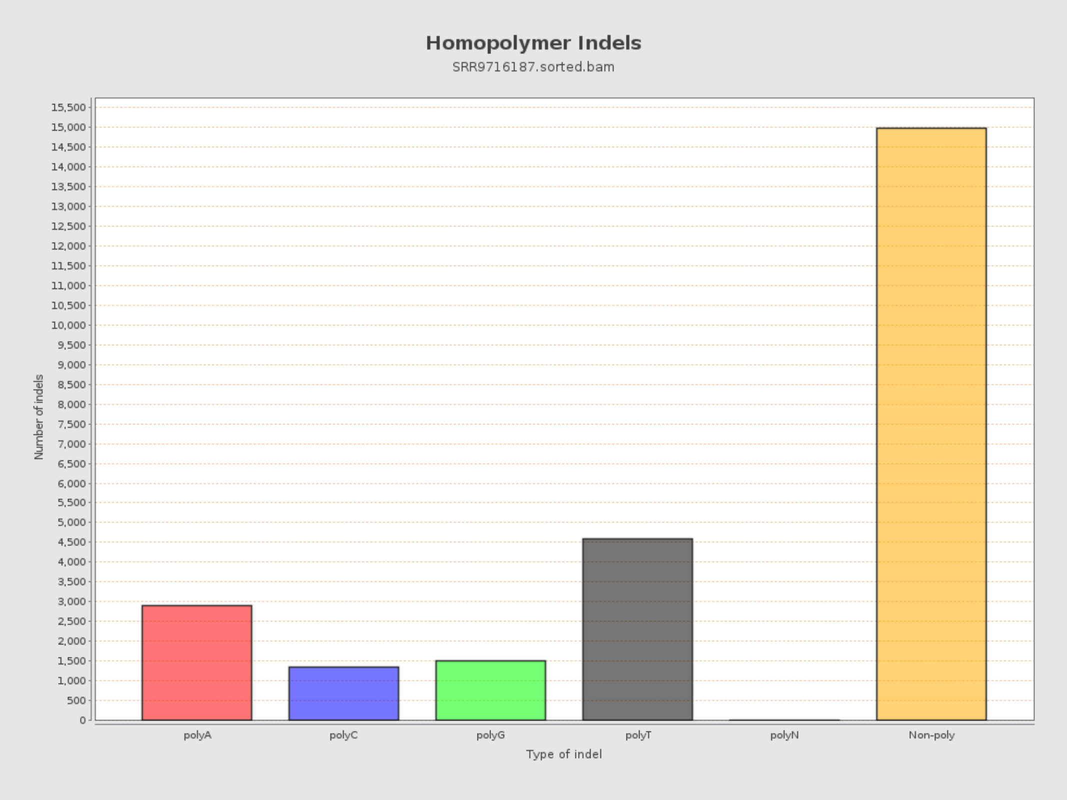
9. Results : Mapped Reads GC-content Distribution



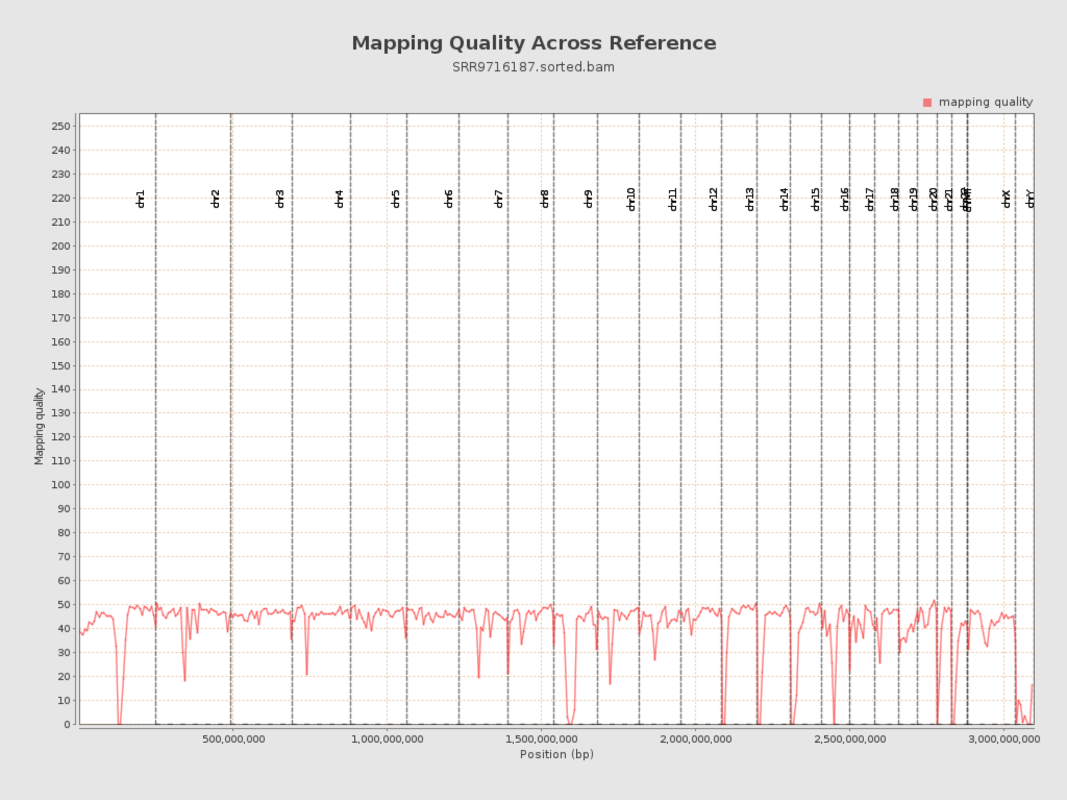
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram