Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:32:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716706.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_SRR9716706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716706.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:32:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,713,575
Mapped reads	3,152,632 / 84.89%
Unmapped reads	560,943 / 15.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,763 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	168,238 / 4.53%
Duplication rate	3.98%
Clipped reads	3,153,379 / 84.91%

2.2. ACGT Content

Number/percentage of A's	44,344,494 / 24.64%
Number/percentage of C's	33,887,979 / 18.83%
Number/percentage of T's	57,816,552 / 32.13%
Number/percentage of G's	43,895,056 / 24.39%
Number/percentage of N's	2,844 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0581

Standard Deviation	0.4343

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Mismatches and indels

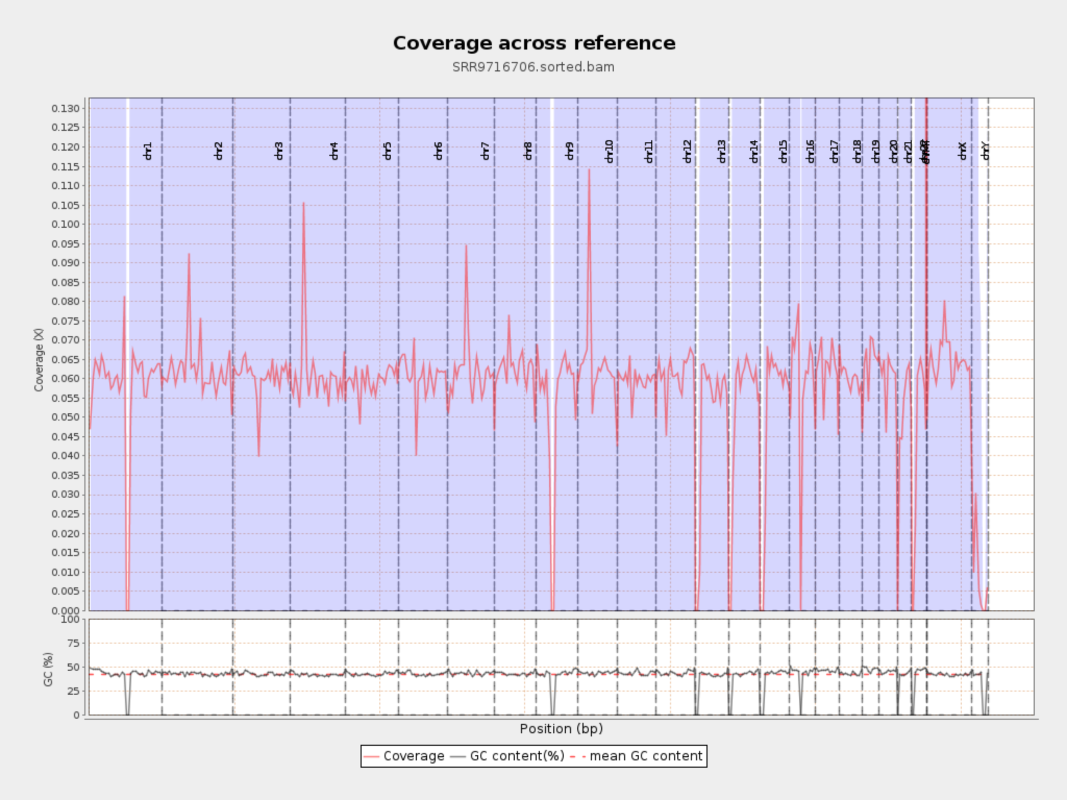
General error rate	0.53%
Mismatches	923,123
Insertions	13,026
Mapped reads with at least one insertion	0.41%
Deletions	36,168
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.62%

2.6. Chromosome stats

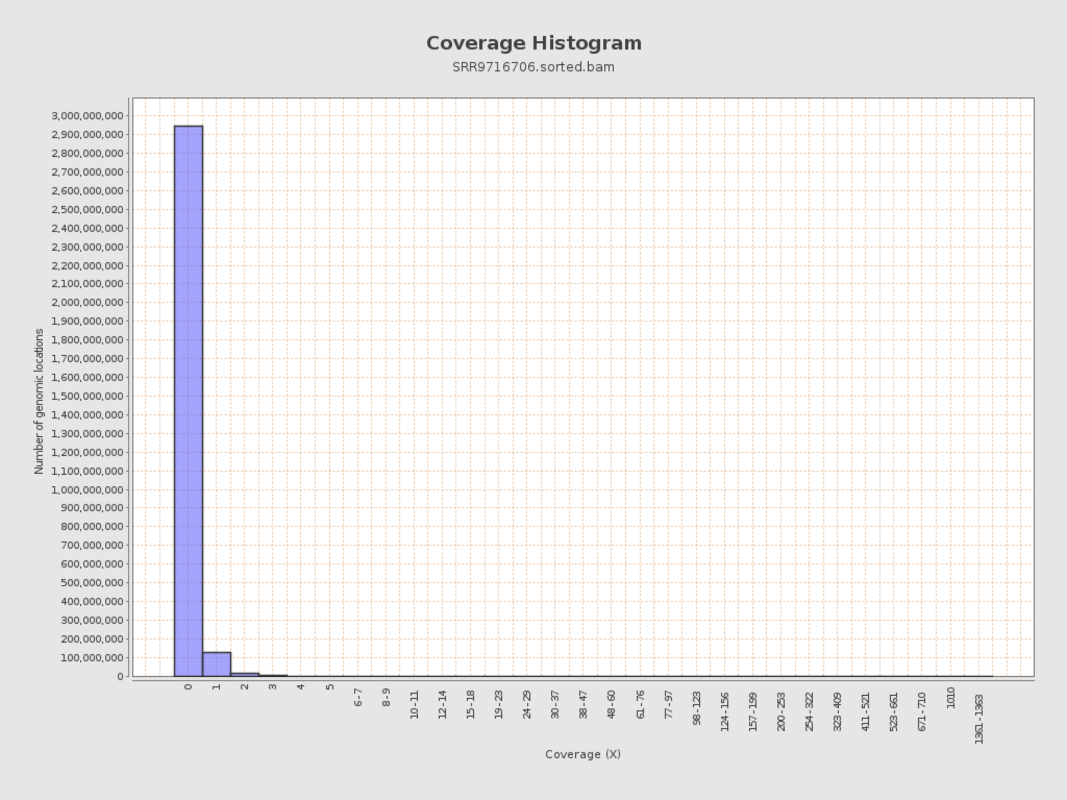
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14348801	0.0576	0.6177
chr2	243199373	15237745	0.0627	0.6729
chr3	198022430	11989696	0.0605	0.2935
chr4	191154276	11661135	0.061	0.3547
chr5	180915260	10769348	0.0595	0.2873
chr6	171115067	10363641	0.0606	0.3501
chr7	159138663	9927620	0.0624	0.6323

chr8	146364022	9144169	0.0625	0.4121
chr9	141213431	7430095	0.0526	0.3497
chr10	135534747	8722026	0.0644	0.5173
chr11	135006516	8018428	0.0594	0.3857
chr12	133851895	8204899	0.0613	0.296
chr13	115169878	5617743	0.0488	0.263
chr14	107349540	5524299	0.0515	0.2854
chr15	102531392	5196028	0.0507	0.2715
chr16	90354753	5367639	0.0594	0.3345
chr17	81195210	5061295	0.0623	0.3339
chr18	78077248	4726553	0.0605	0.6382
chr19	59128983	3818175	0.0646	0.5381
chr20	63025520	3795705	0.0602	0.305
chr21	48129895	2346101	0.0487	0.3063
chr22	51304566	2163128	0.0422	0.2432
chrMT	16571	24041	1.4508	1.6217
chrX	155270560	10002582	0.0644	0.3449
chrY	59373566	543913	0.0092	0.2317

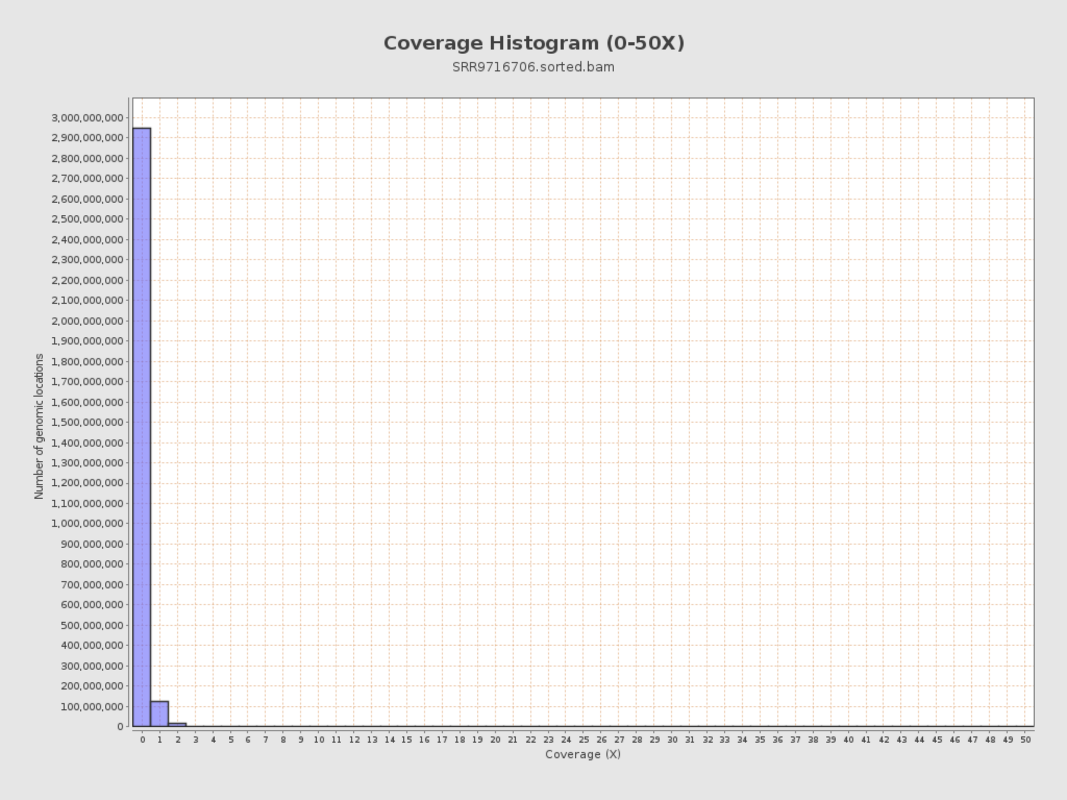
3. Results : Coverage across reference



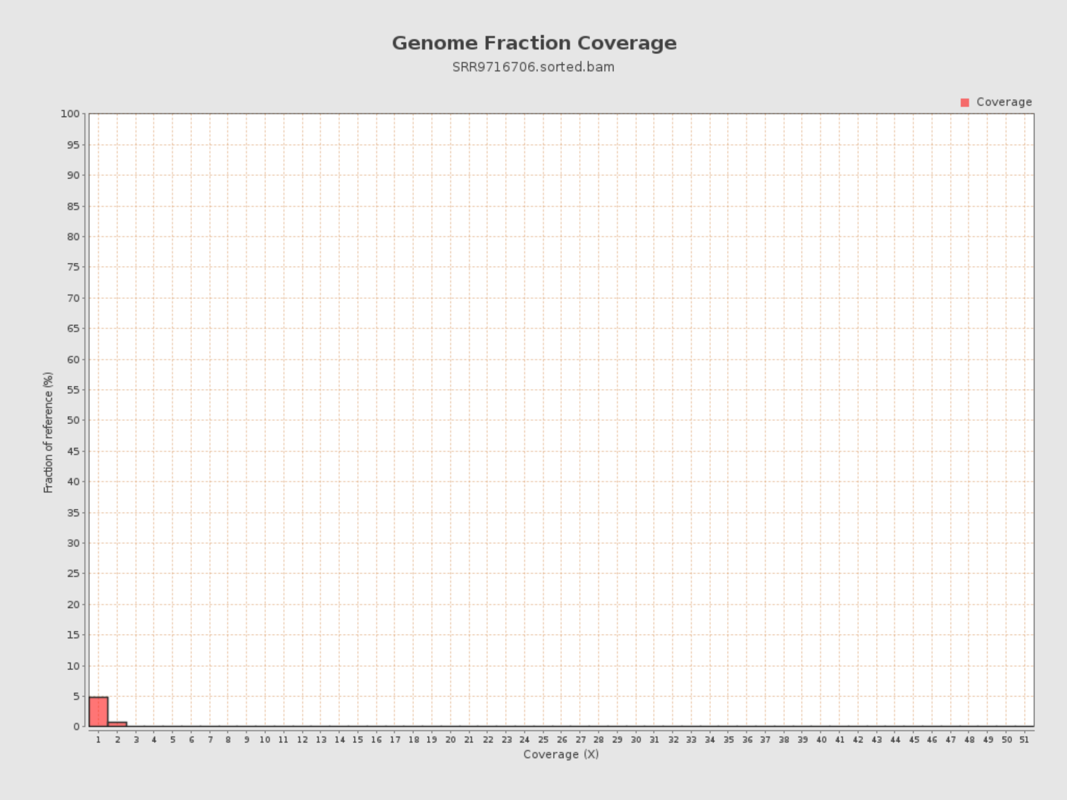
4. Results : Coverage Histogram



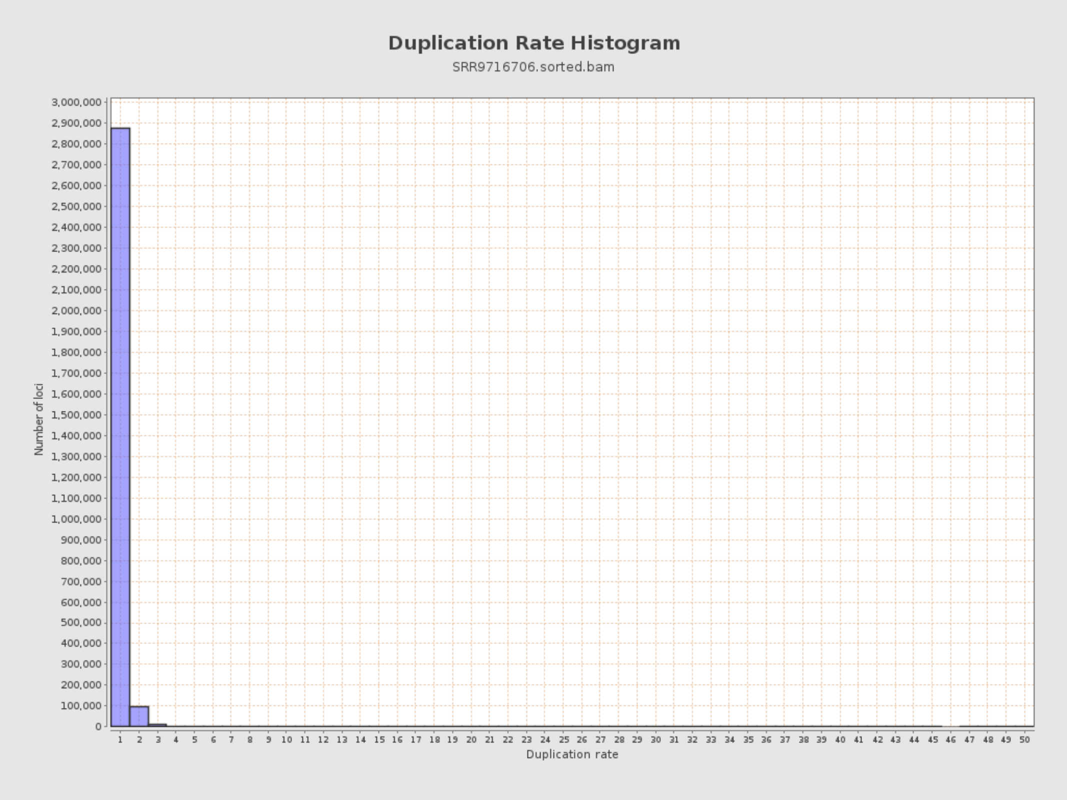
5. Results : Coverage Histogram (0-50X)



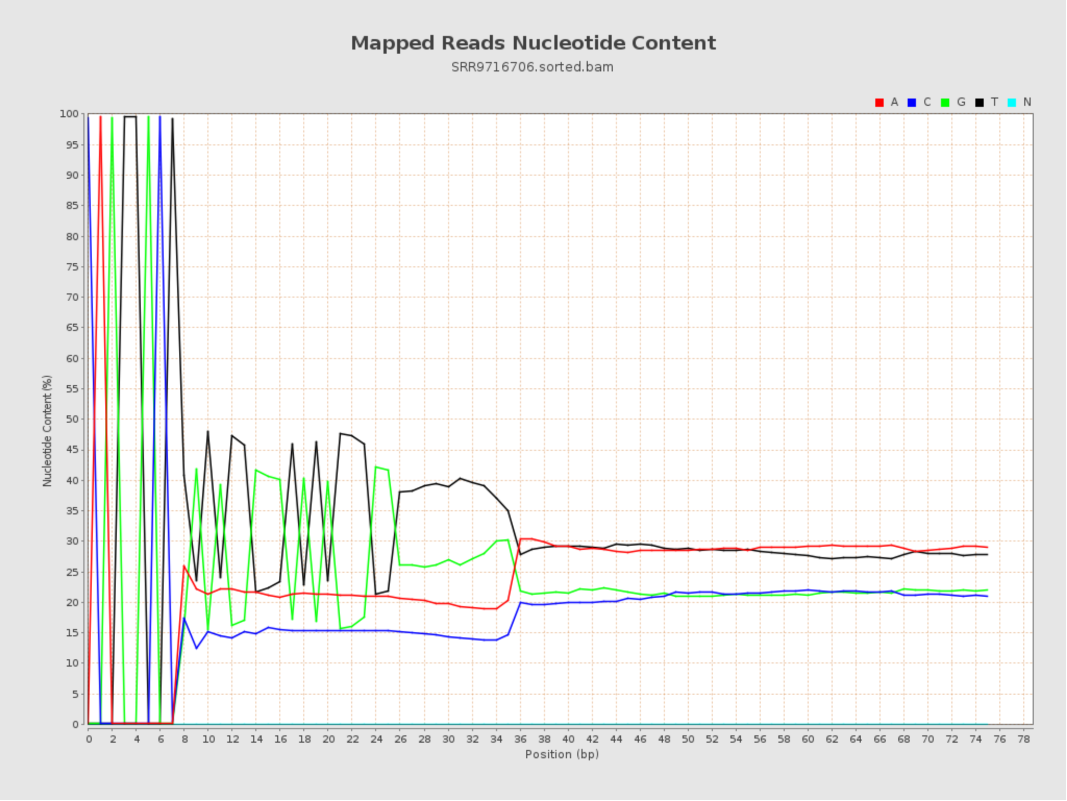
6. Results : Genome Fraction Coverage



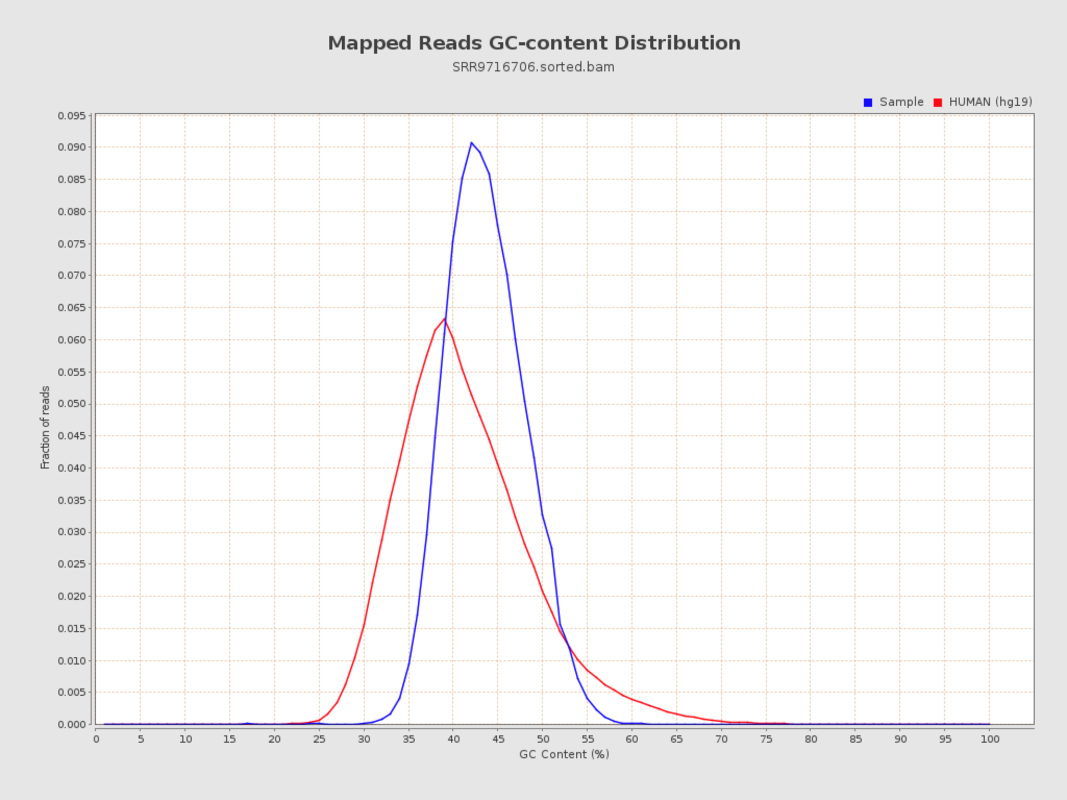
7. Results : Duplication Rate Histogram



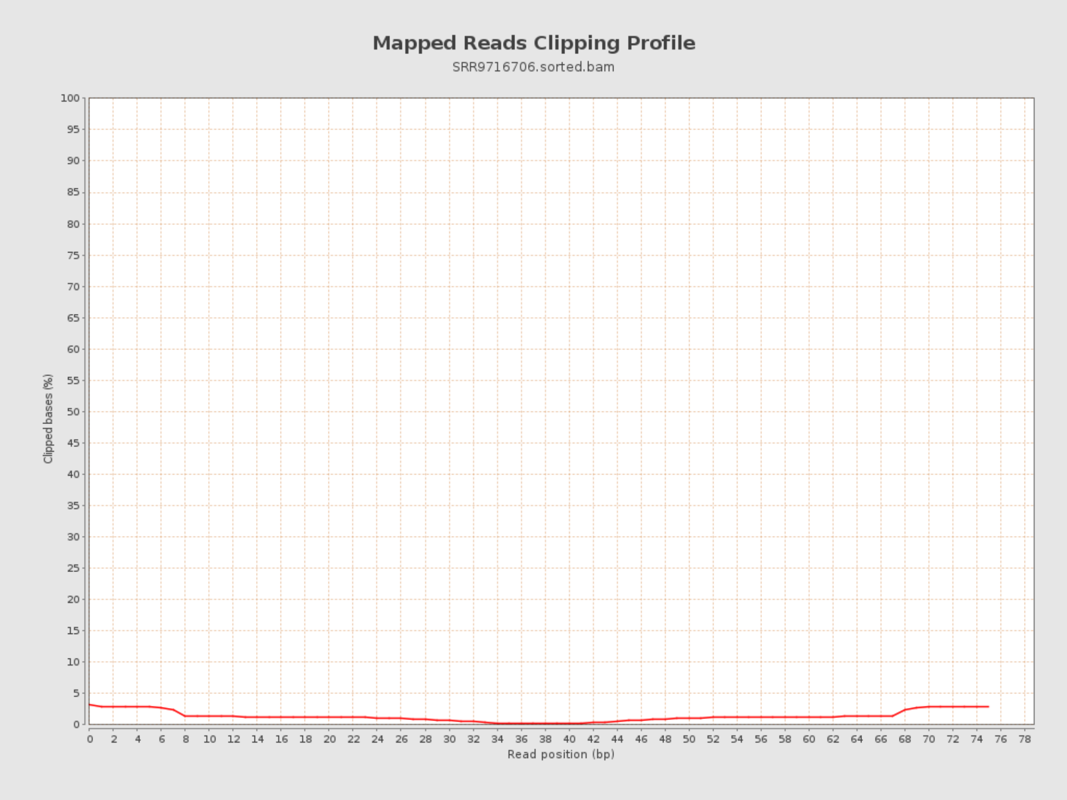
8. Results : Mapped Reads Nucleotide Content



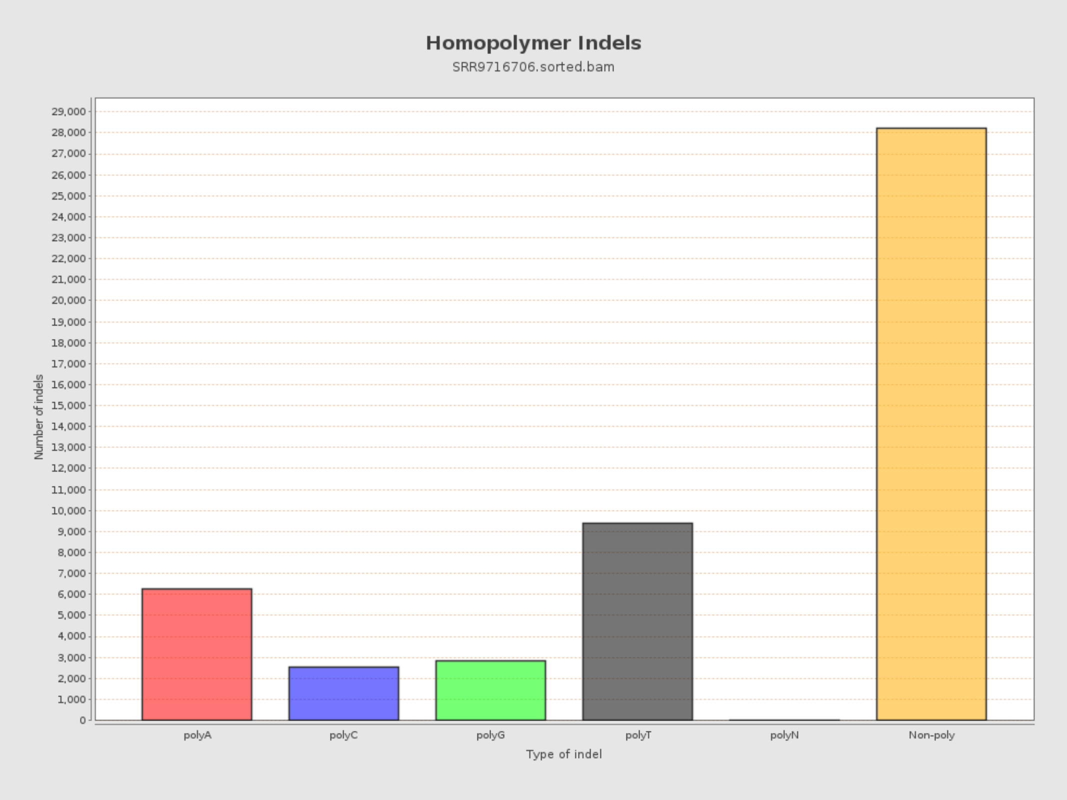
9. Results : Mapped Reads GC-content Distribution



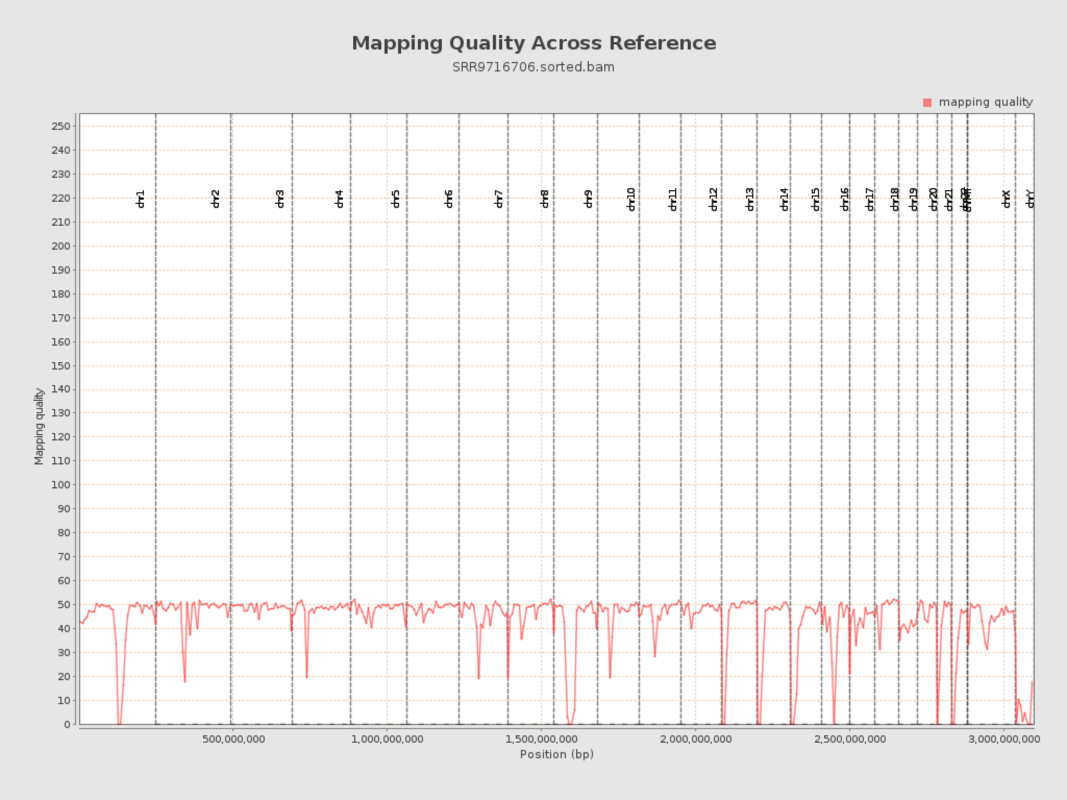
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram