Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:15:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716363.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_SRR9716363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716363.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:15:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,595,972
Mapped reads	1,466,109 / 91.86%
Unmapped reads	129,863 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,921 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	57,120 / 3.58%
Duplication rate	3.06%
Clipped reads	1,473,111 / 92.3%

2.2. ACGT Content

Number/percentage of A's	20,835,070 / 24.33%
Number/percentage of C's	16,502,537 / 19.27%
Number/percentage of T's	26,876,665 / 31.39%
Number/percentage of G's	21,418,208 / 25.01%
Number/percentage of N's	636 / 0%
GC Percentage	44.28%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2494

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

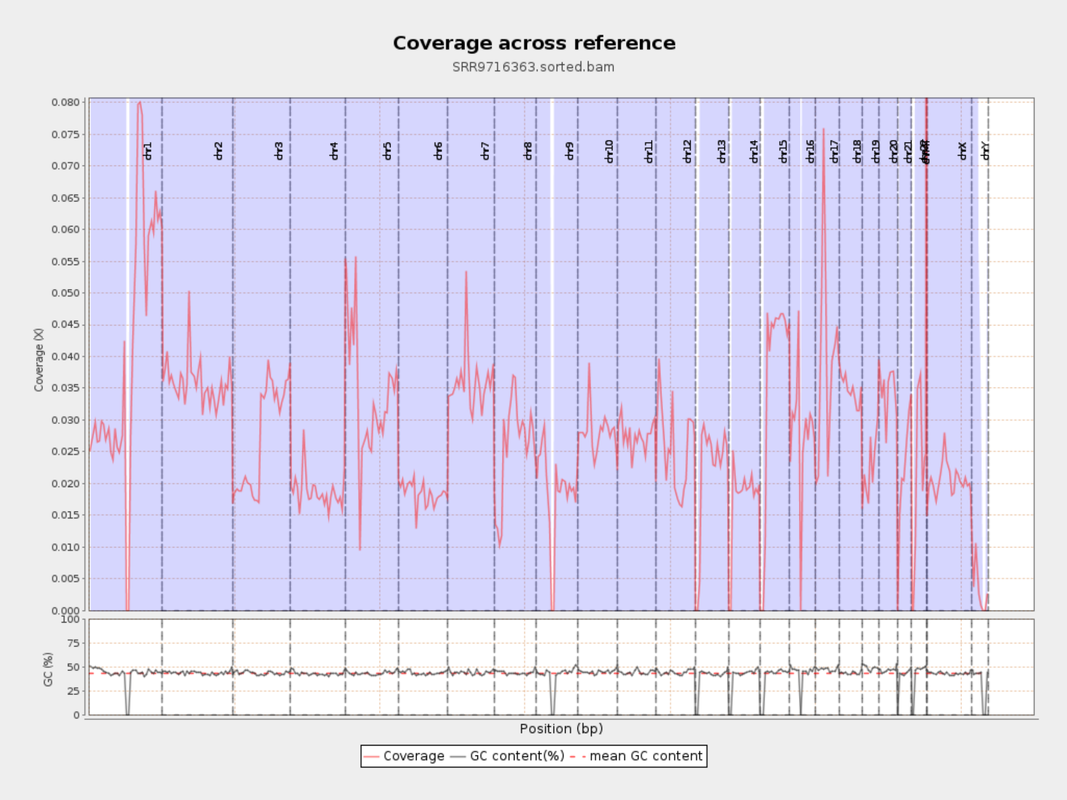
General error rate	0.49%
Mismatches	413,292
Insertions	4,663
Mapped reads with at least one insertion	0.32%
Deletions	14,192
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.97%

2.6. Chromosome stats

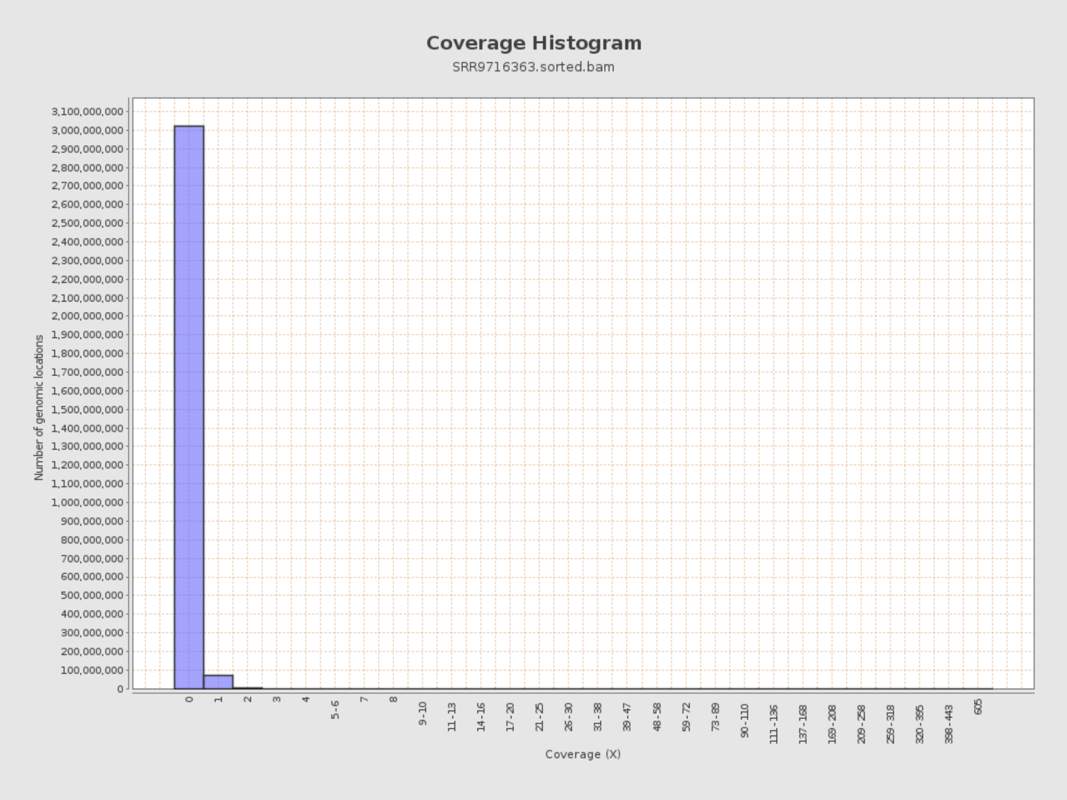
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10065381	0.0404	0.4029
chr2	243199373	8738800	0.0359	0.343
chr3	198022430	5371334	0.0271	0.1807
chr4	191154276	3562953	0.0186	0.1677
chr5	180915260	6094487	0.0337	0.2018
chr6	171115067	3166450	0.0185	0.1641
chr7	159138663	5732991	0.036	0.3838

chr8	146364022	3789692	0.0259	0.2289
chr9	141213431	2630807	0.0186	0.1945
chr10	135534747	3816941	0.0282	0.2183
chr11	135006516	3707861	0.0275	0.2299
chr12	133851895	3423164	0.0256	0.1777
chr13	115169878	2482120	0.0216	0.1616
chr14	107349540	1852006	0.0173	0.1521
chr15	102531392	3717102	0.0363	0.2094
chr16	90354753	2535303	0.0281	0.1911
chr17	81195210	3231580	0.0398	0.2344
chr18	78077248	2711924	0.0347	0.3885
chr19	59128983	1368403	0.0231	0.2953
chr20	63025520	2174493	0.0345	0.2065
chr21	48129895	1060865	0.022	0.1686
chr22	51304566	1018469	0.0199	0.1549
chrMT	16571	9582	0.5782	0.8122
chrX	155270560	3195416	0.0206	0.1742
chrY	59373566	197696	0.0033	0.0841

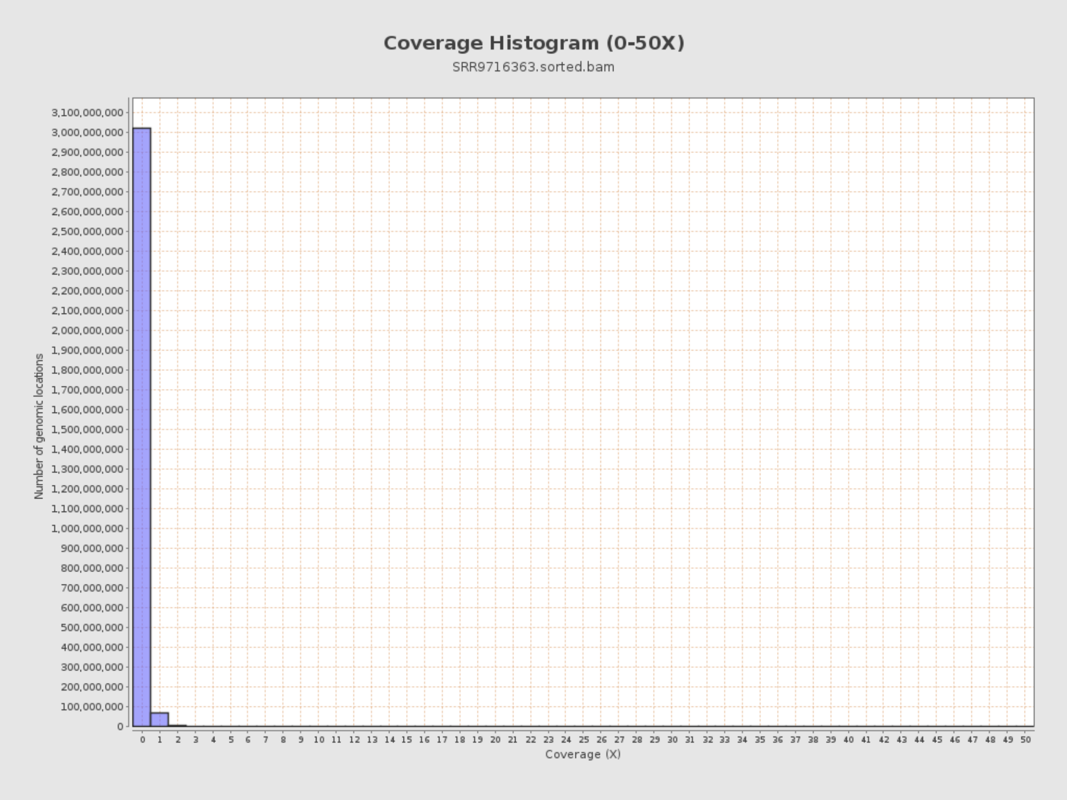
3. Results : Coverage across reference



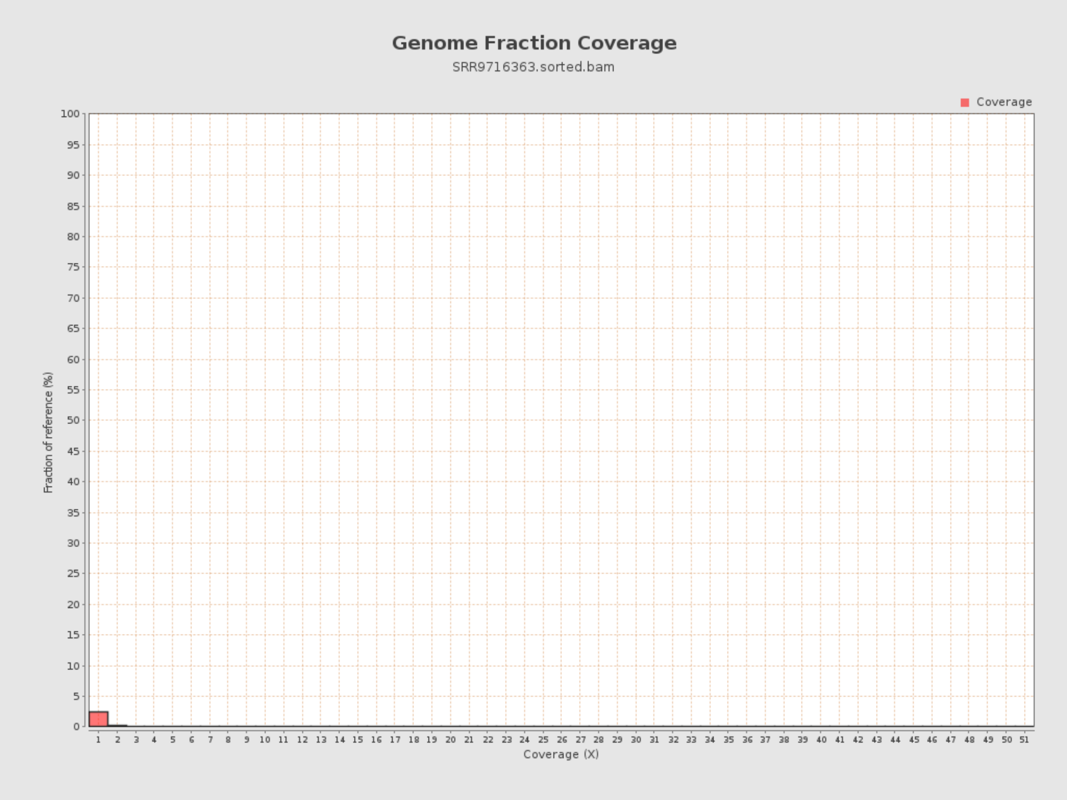
4. Results : Coverage Histogram



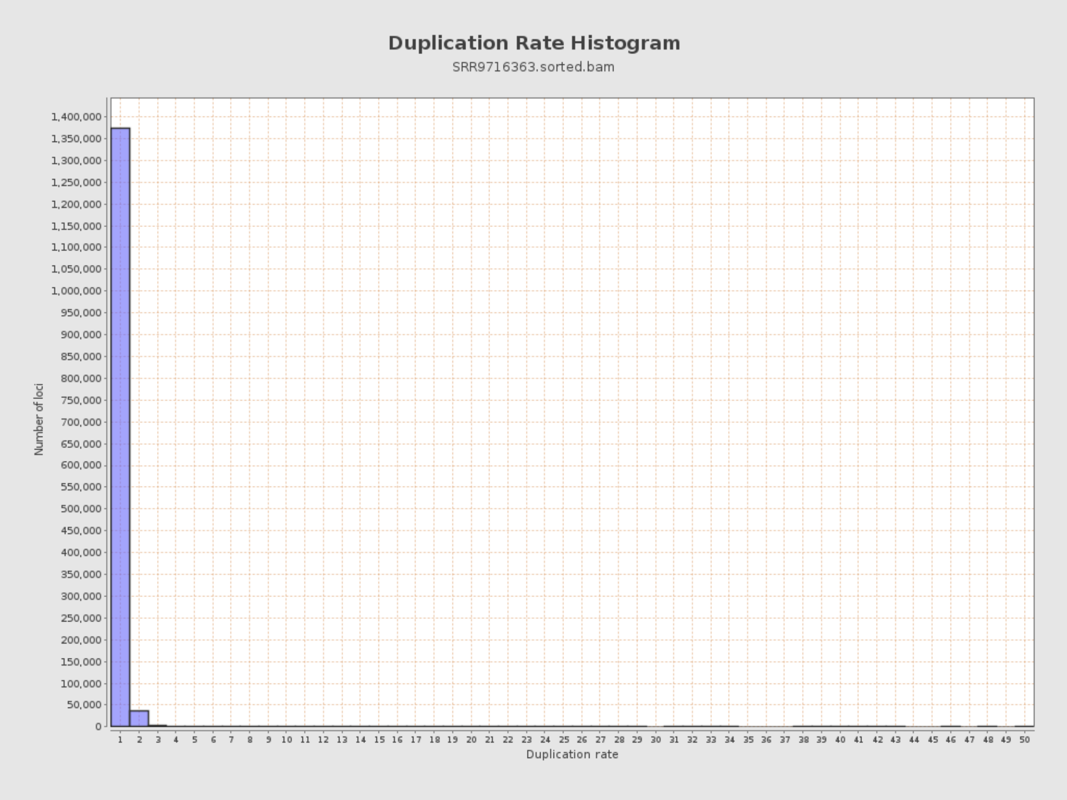
5. Results : Coverage Histogram (0-50X)



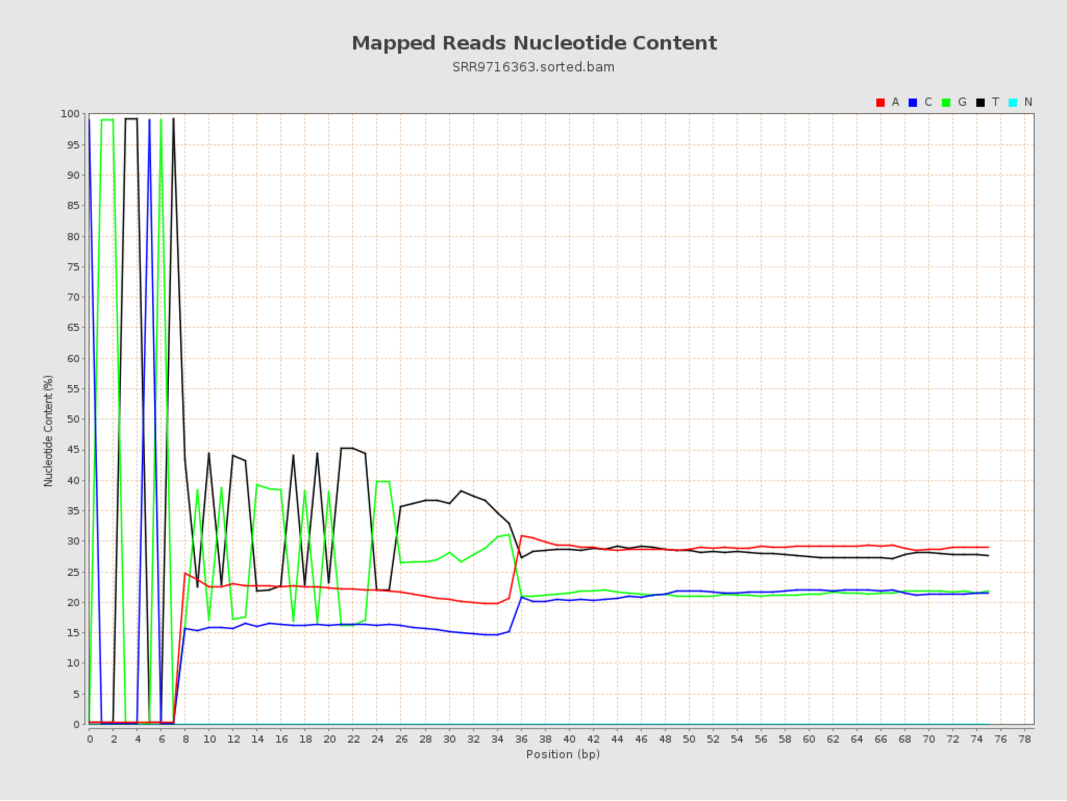
6. Results : Genome Fraction Coverage



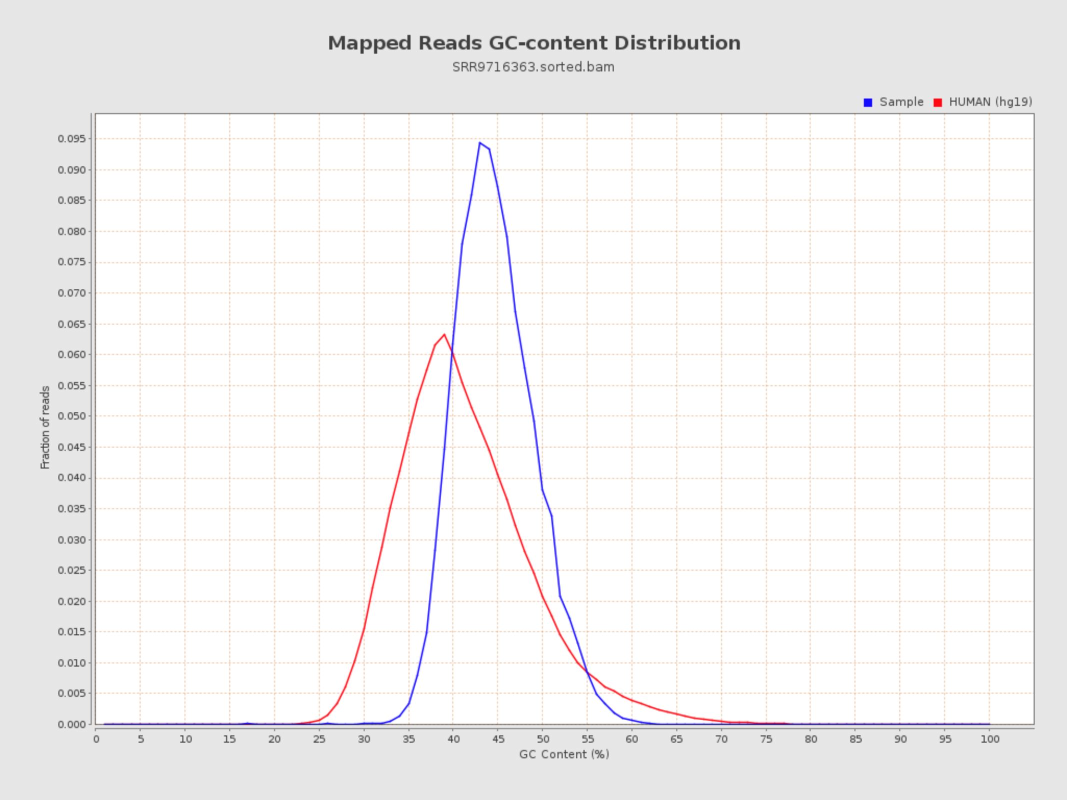
7. Results : Duplication Rate Histogram



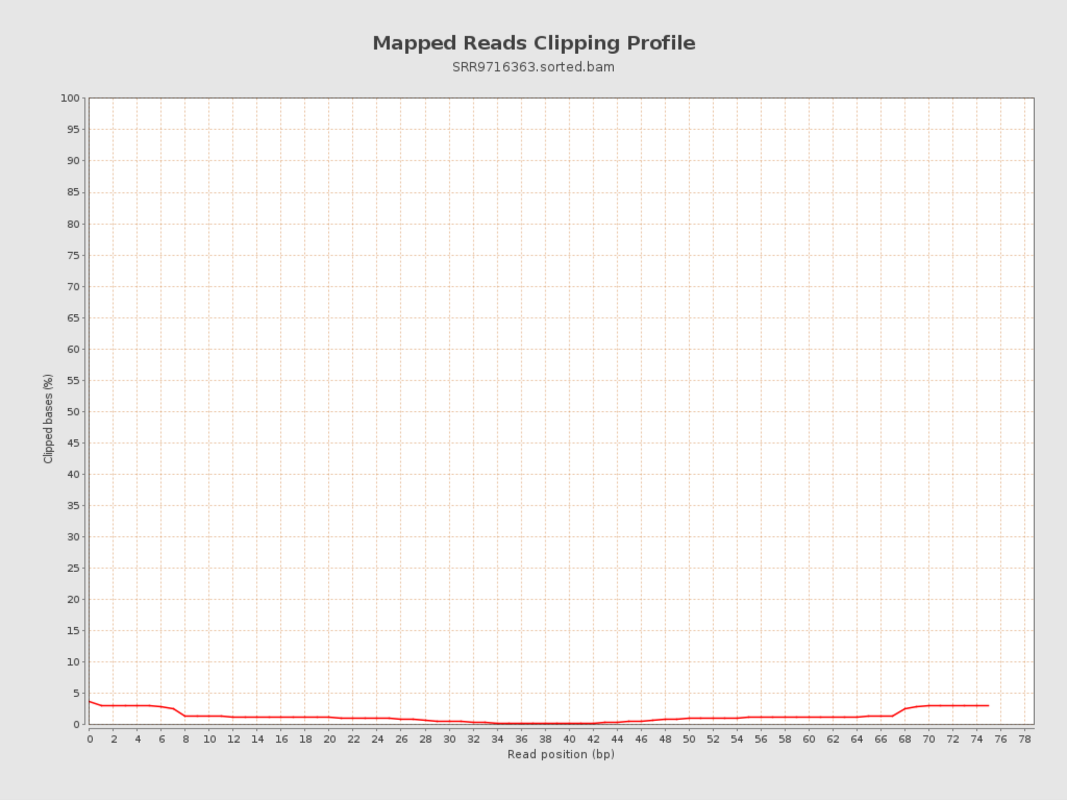
8. Results : Mapped Reads Nucleotide Content



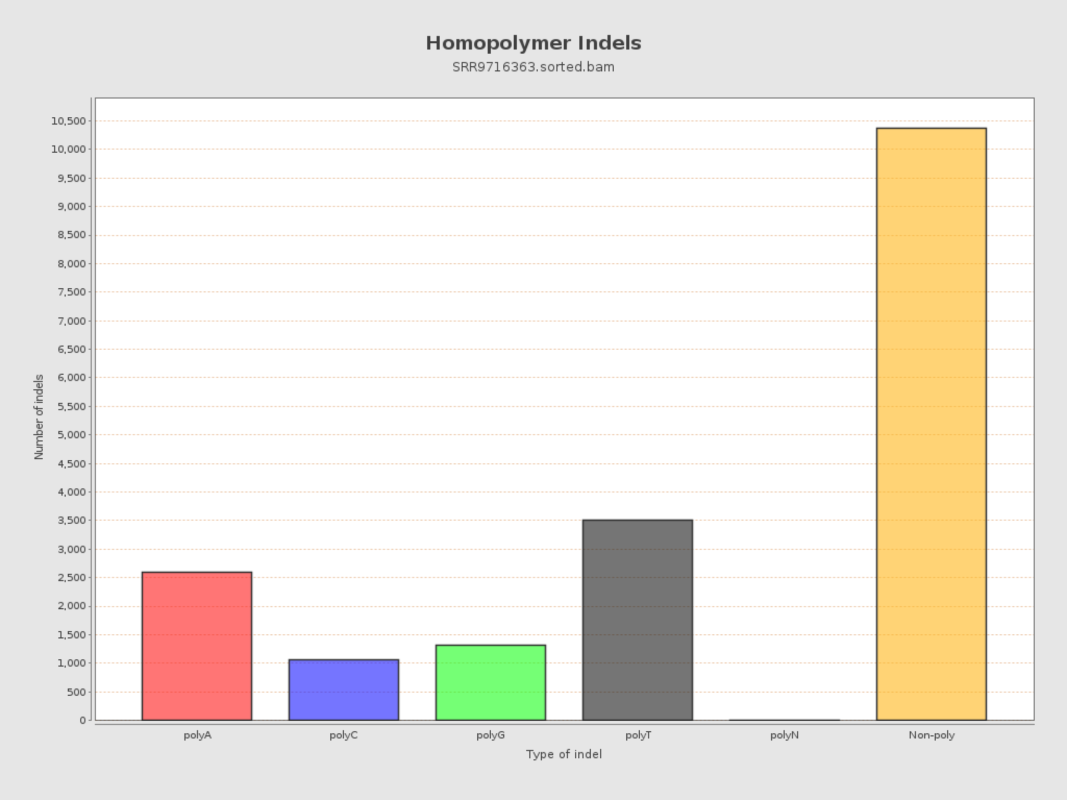
9. Results : Mapped Reads GC-content Distribution



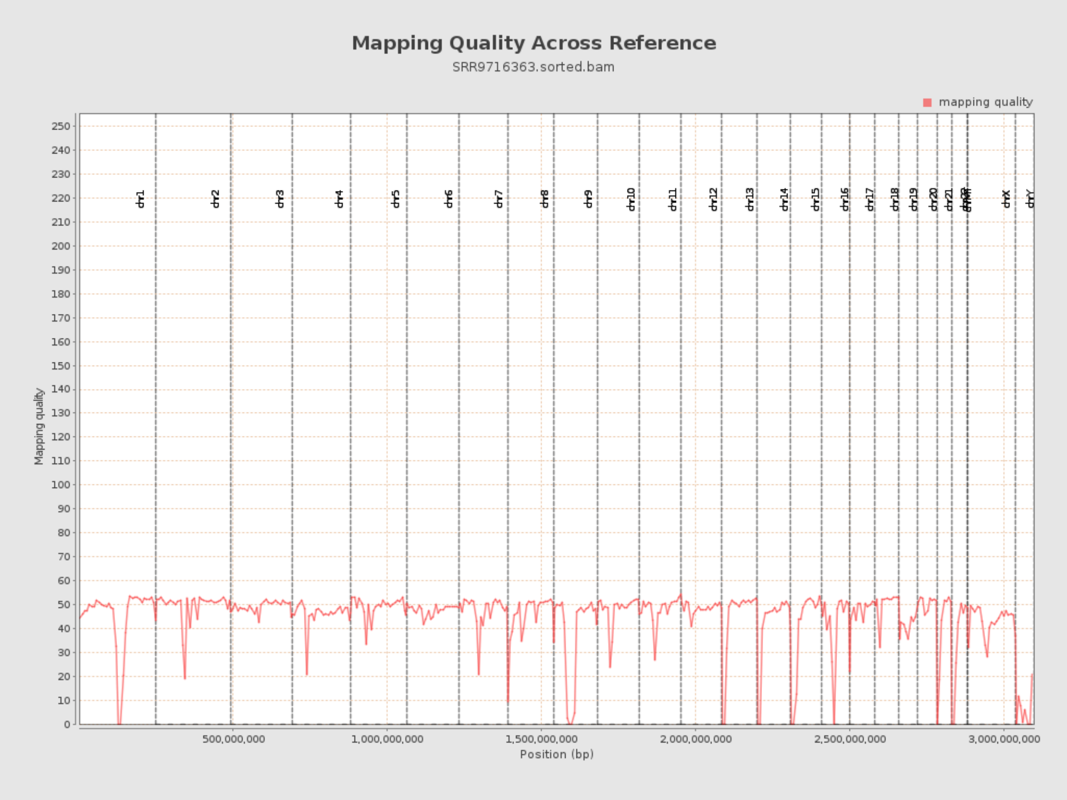
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram