Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:49:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716163.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_SRR9716163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:49:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,148,401
Mapped reads	3,723,752 / 89.76%
Unmapped reads	424,649 / 10.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,223 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	237,887 / 5.73%
Duplication rate	4.98%
Clipped reads	3,727,337 / 89.85%

2.2. ACGT Content

Number/percentage of A's	51,462,044 / 23.9%
Number/percentage of C's	39,380,917 / 18.29%
Number/percentage of T's	69,736,627 / 32.39%
Number/percentage of G's	54,707,848 / 25.41%
Number/percentage of N's	4,941 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0696

Standard Deviation	0.4748

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

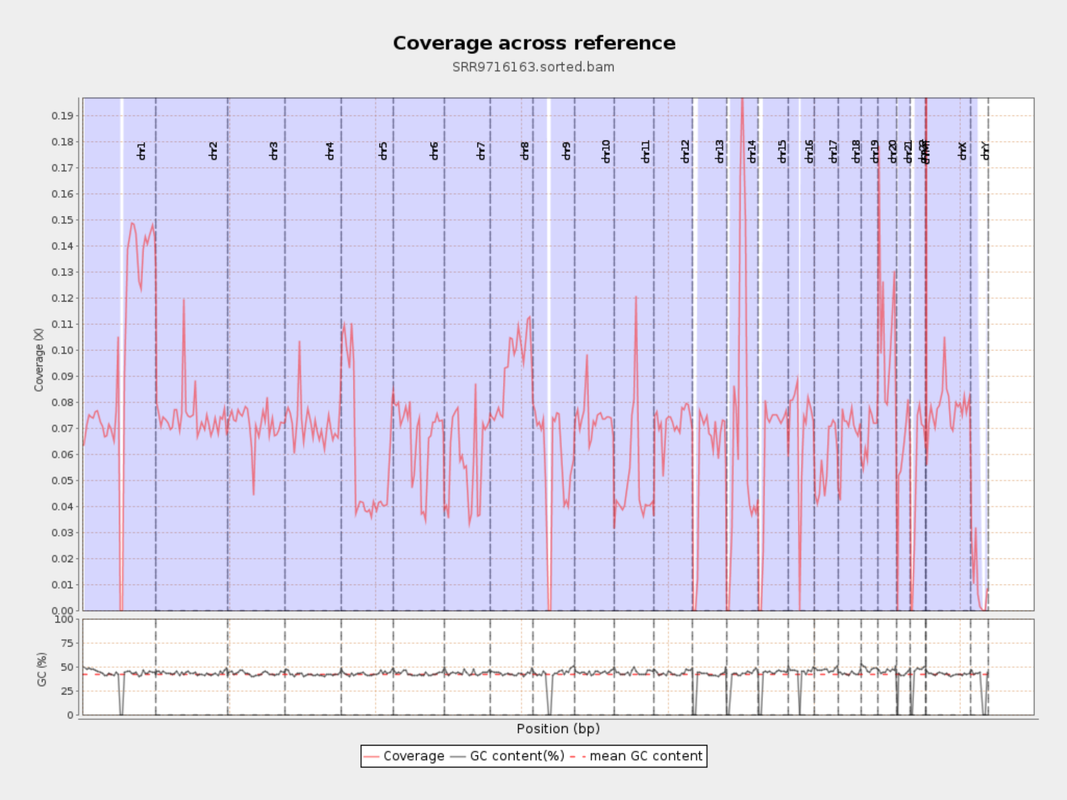
General error rate	0.49%
Mismatches	1,021,701
Insertions	13,733
Mapped reads with at least one insertion	0.37%
Deletions	33,119
Mapped reads with at least one deletion	0.88%
Homopolymer indels	42.2%

2.6. Chromosome stats

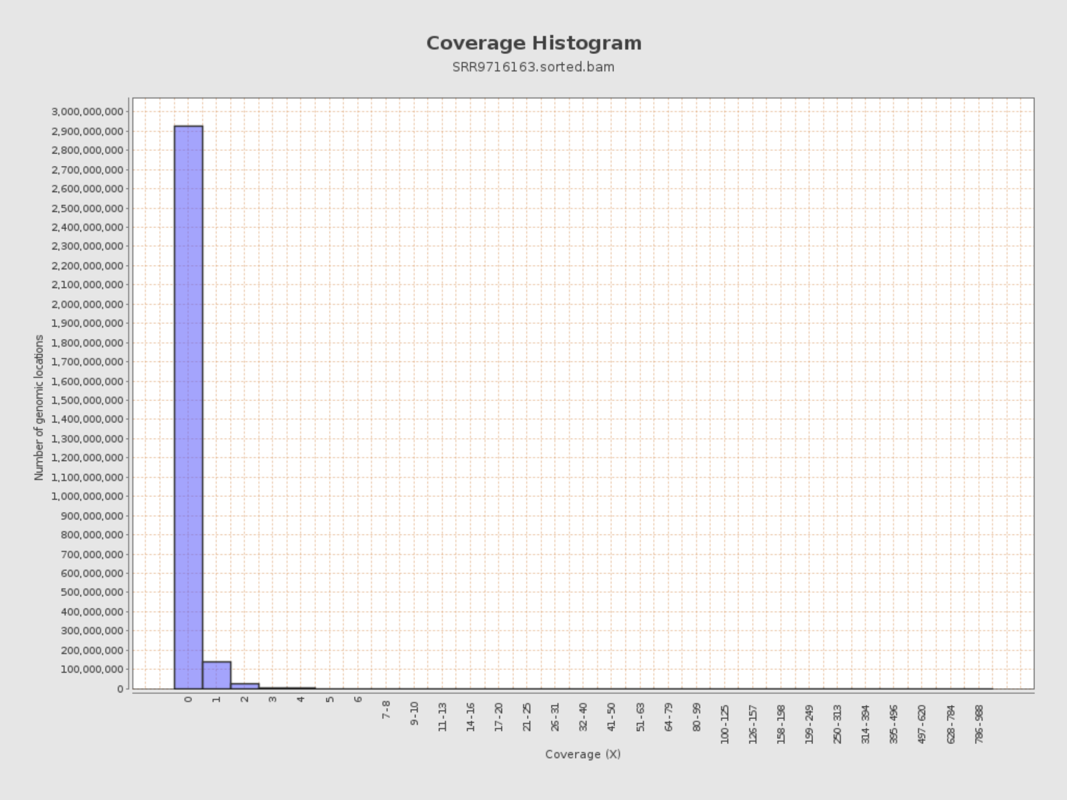
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24191385	0.0971	0.8357
chr2	243199373	18161317	0.0747	0.5364
chr3	198022430	14146533	0.0714	0.3259
chr4	191154276	13744881	0.0719	0.3686
chr5	180915260	10753725	0.0594	0.3037
chr6	171115067	11393769	0.0666	0.3569
chr7	159138663	9203368	0.0578	0.4085

chr8	146364022	13649011	0.0933	0.505
chr9	141213431	7881784	0.0558	0.4904
chr10	135534747	10028725	0.074	0.4398
chr11	135006516	6805633	0.0504	0.4511
chr12	133851895	9713841	0.0726	0.3383
chr13	115169878	6694800	0.0581	0.2905
chr14	107349540	7595926	0.0708	0.3624
chr15	102531392	6178630	0.0603	0.2991
chr16	90354753	6211706	0.0687	0.3606
chr17	81195210	4649934	0.0573	0.3193
chr18	78077248	5324185	0.0682	0.9919
chr19	59128983	3989768	0.0675	0.5952
chr20	63025520	6919195	0.1098	0.4238
chr21	48129895	2804710	0.0583	0.3434
chr22	51304566	2600438	0.0507	0.2725
chrMT	16571	13575	0.8192	1.1156
chrX	155270560	12095857	0.0779	0.4129
chrY	59373566	595266	0.01	0.2061

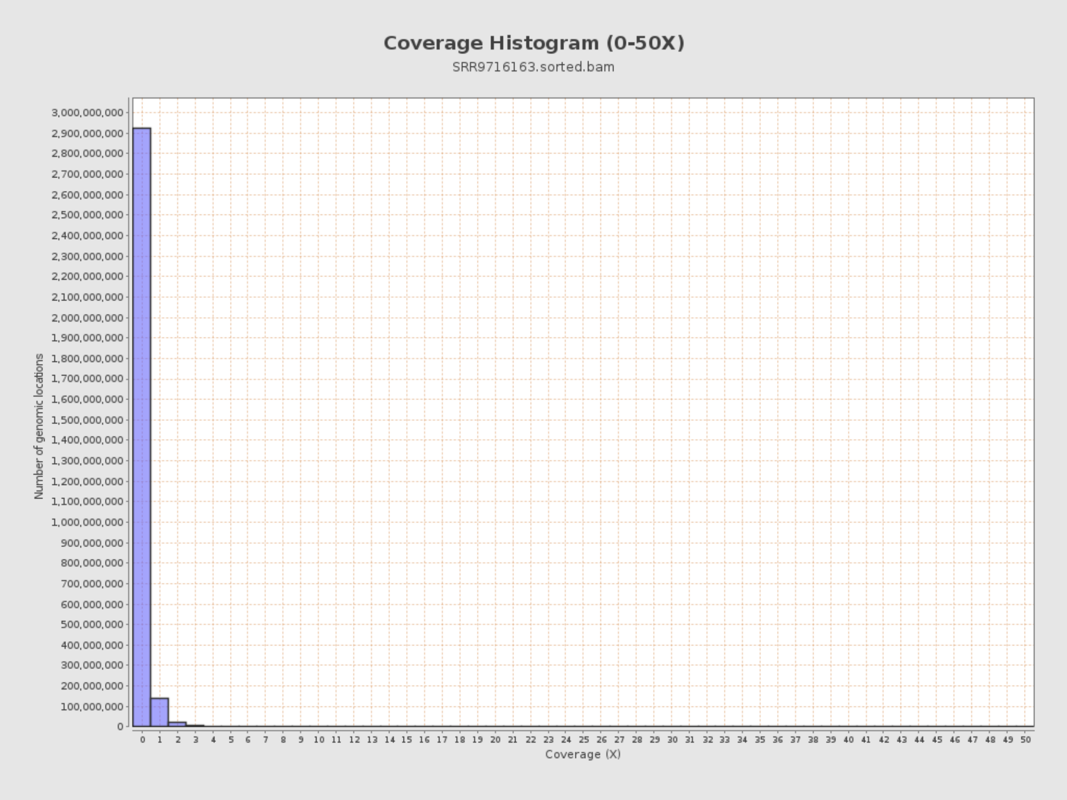
3. Results : Coverage across reference



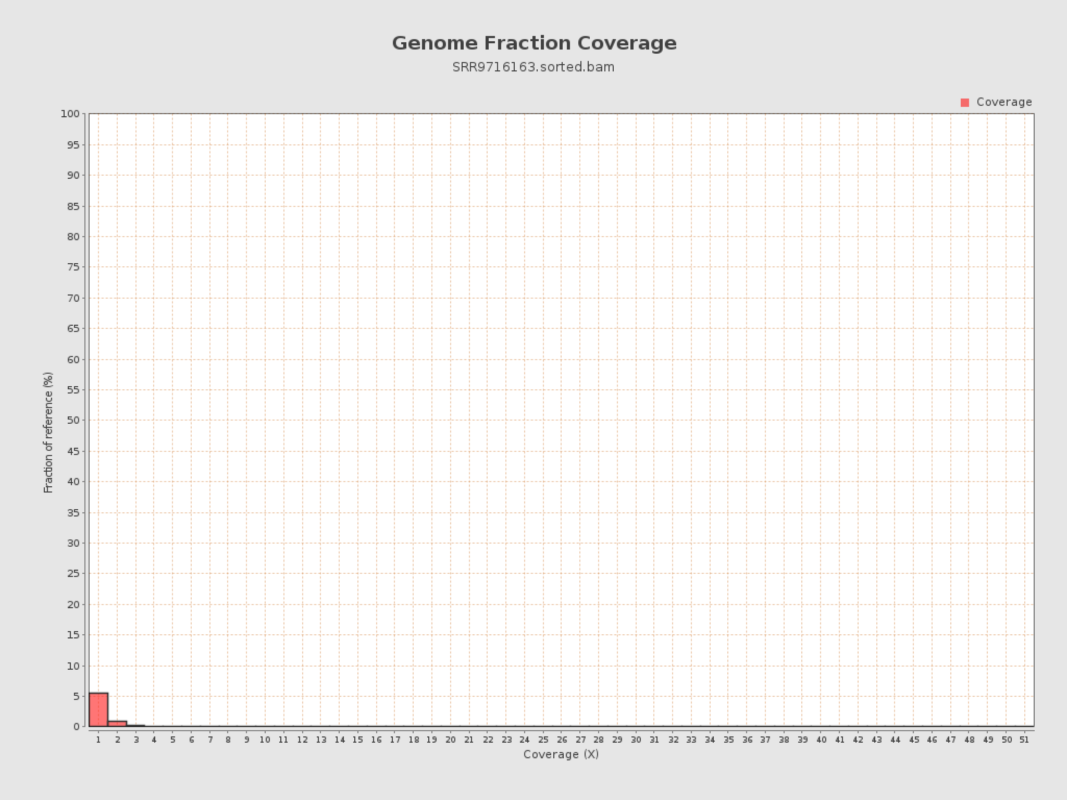
4. Results : Coverage Histogram



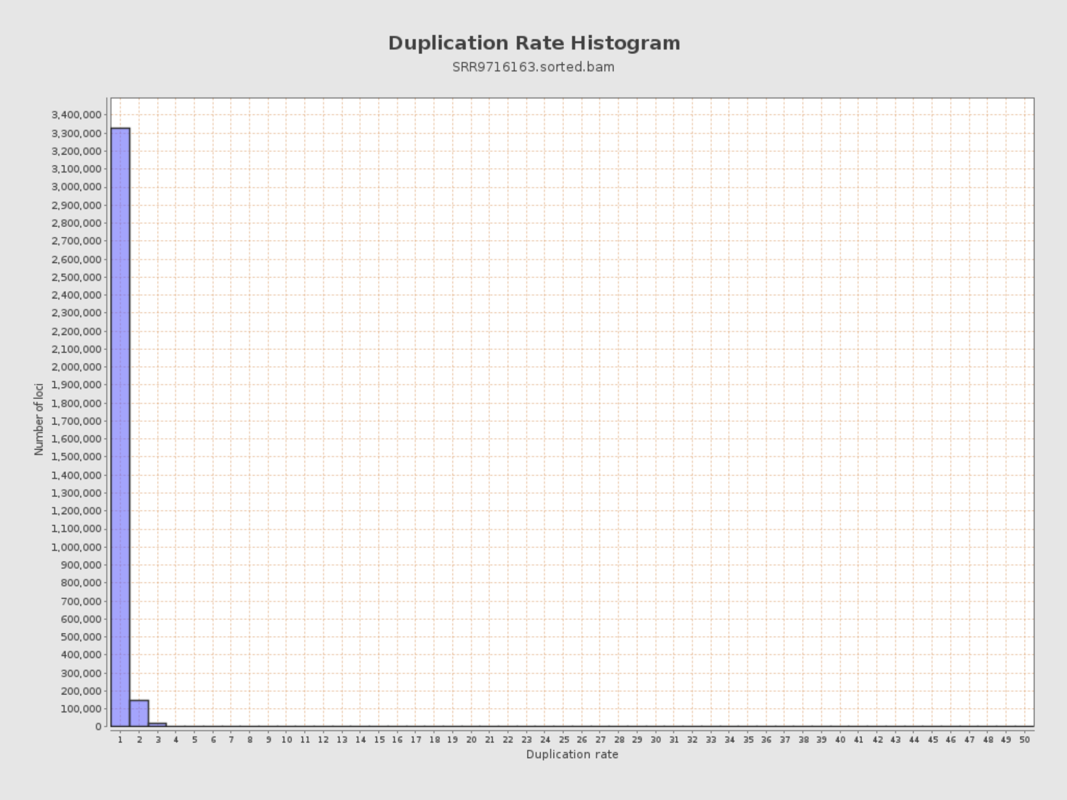
5. Results : Coverage Histogram (0-50X)



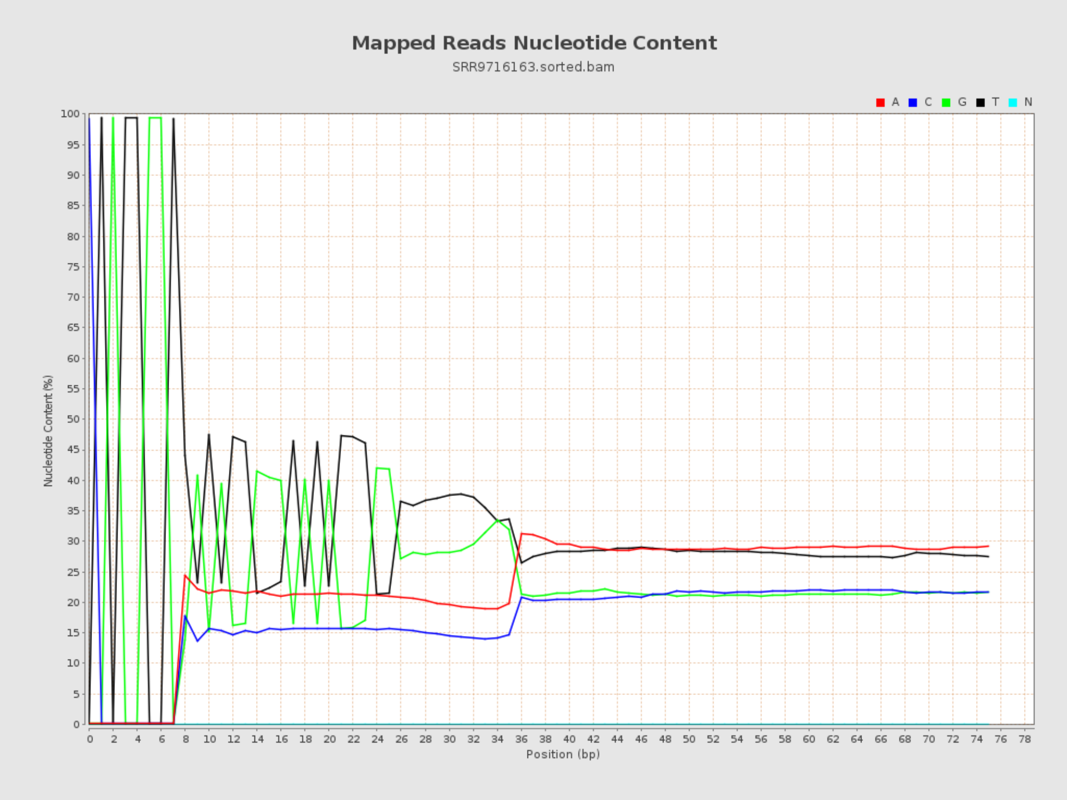
6. Results : Genome Fraction Coverage



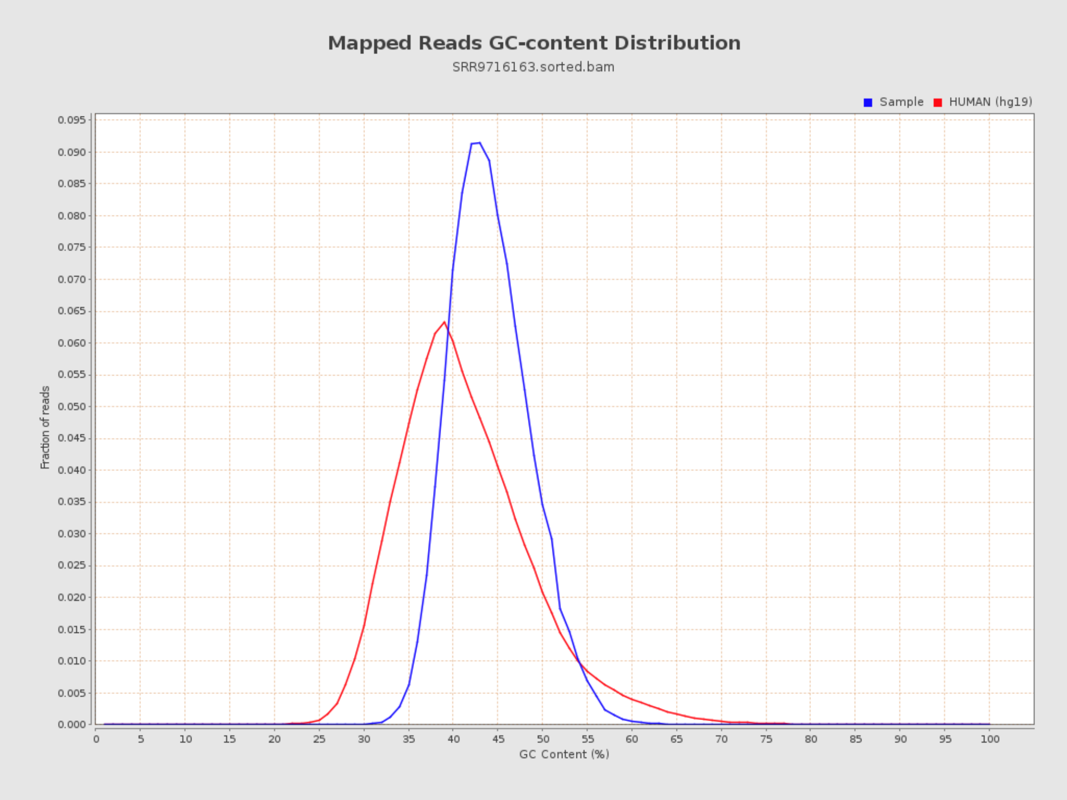
7. Results : Duplication Rate Histogram



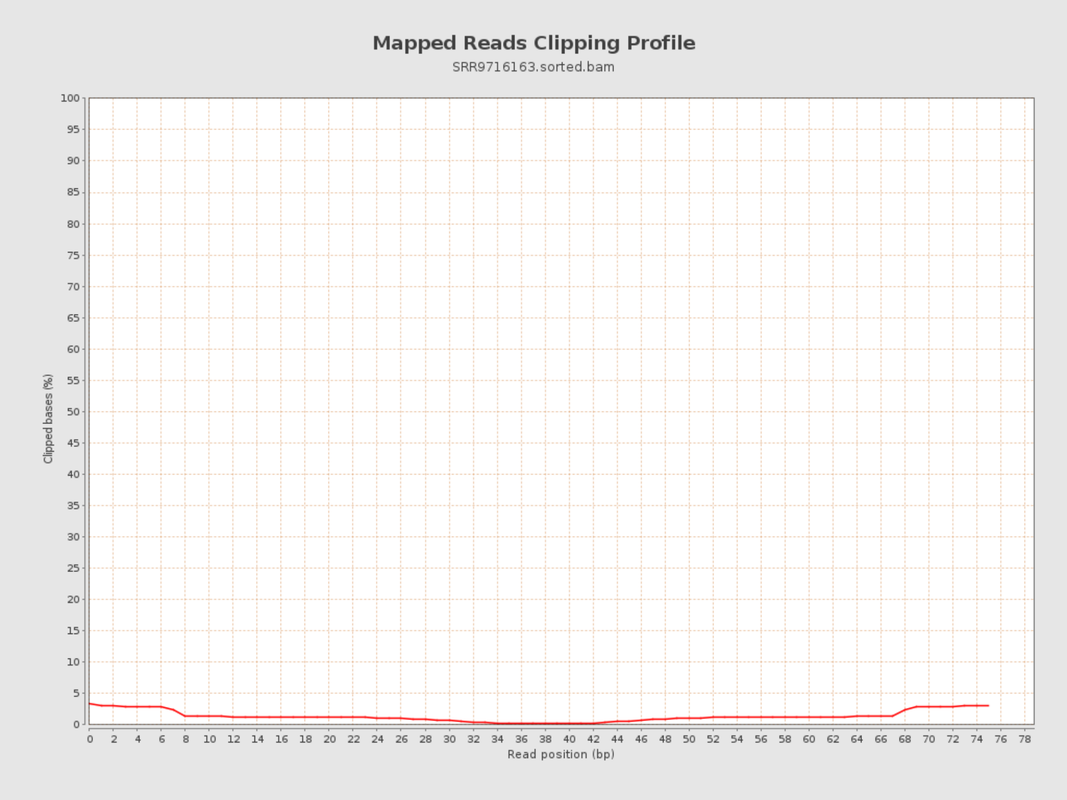
8. Results : Mapped Reads Nucleotide Content



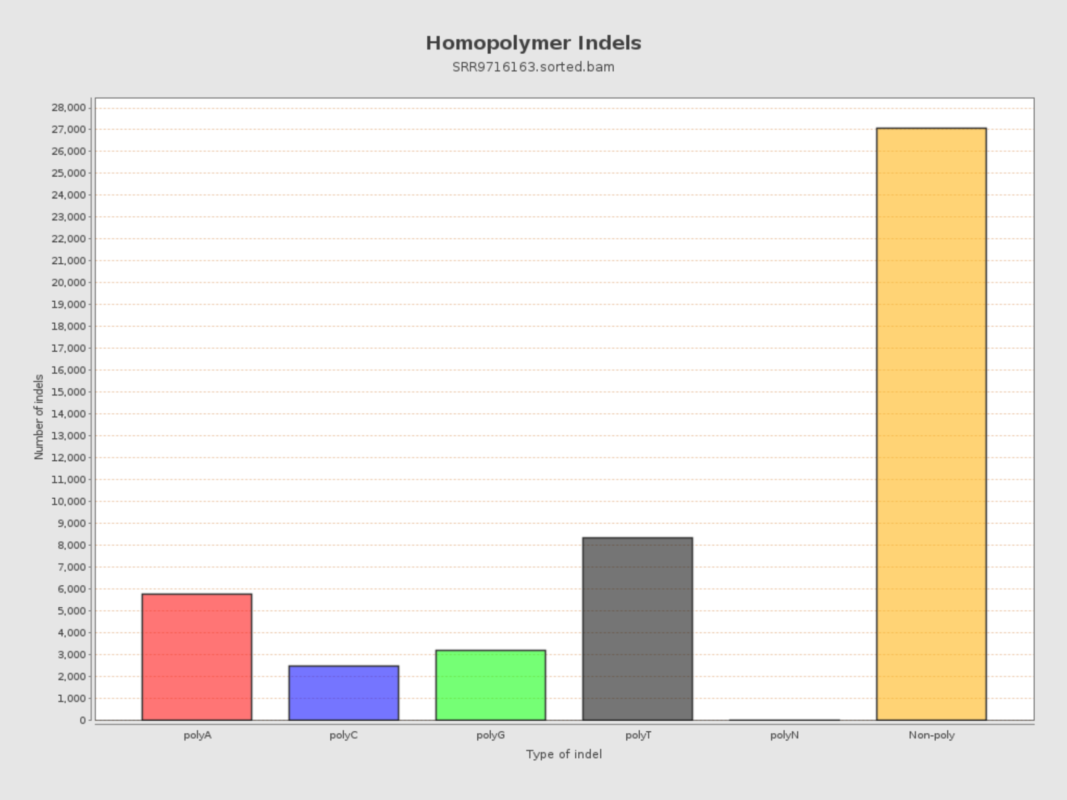
9. Results : Mapped Reads GC-content Distribution



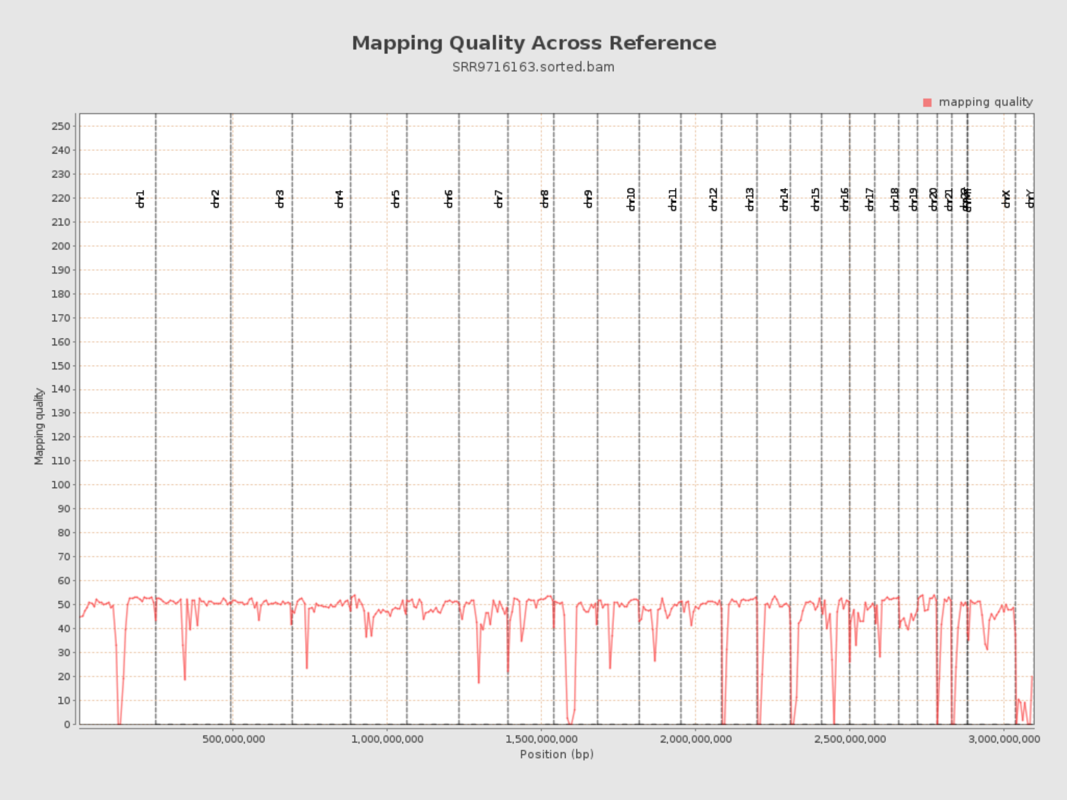
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram