Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:21:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716589.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_SRR9716589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716589.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:21:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	453,007
Mapped reads	386,095 / 85.23%
Unmapped reads	66,912 / 14.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,013 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	6,195 / 1.37%
Duplication rate	1.22%
Clipped reads	386,461 / 85.31%

2.2. ACGT Content

Number/percentage of A's	5,536,804 / 25.07%
Number/percentage of C's	4,042,937 / 18.3%
Number/percentage of T's	7,177,163 / 32.49%
Number/percentage of G's	5,332,291 / 24.14%
Number/percentage of N's	279 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0071

Standard Deviation	0.0987

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

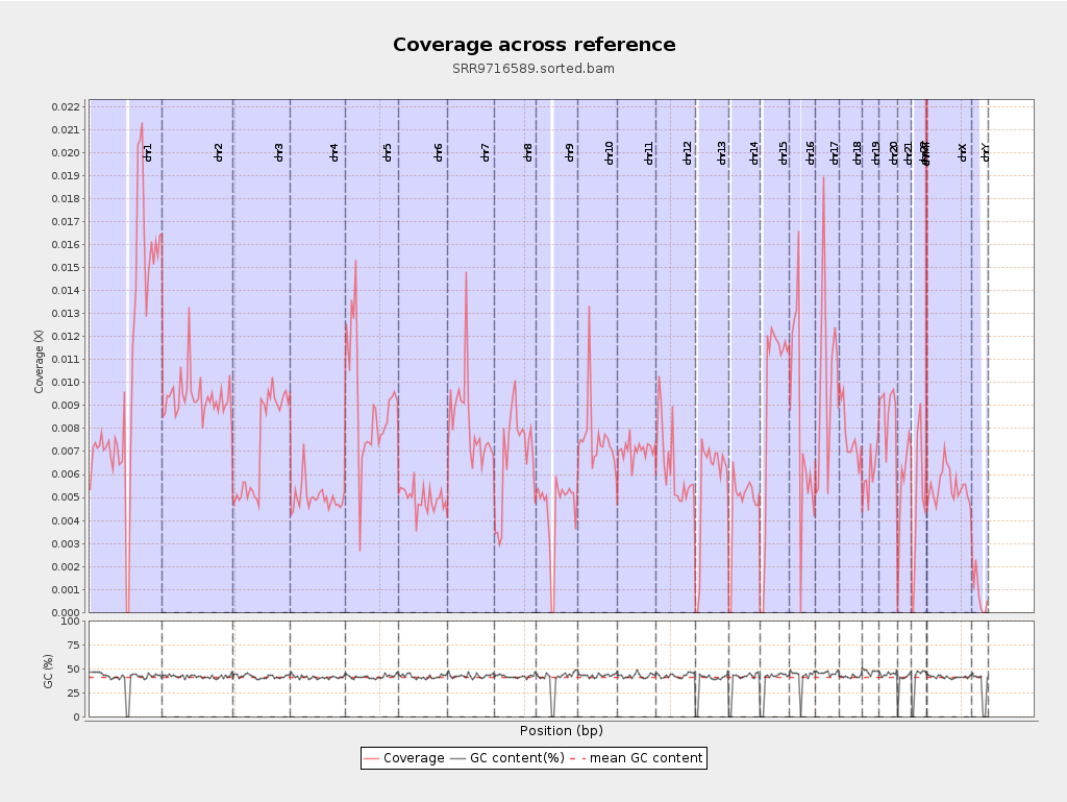
General error rate	0.52%
Mismatches	112,762
Insertions	1,354
Mapped reads with at least one insertion	0.35%
Deletions	4,222
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.61%

2.6. Chromosome stats

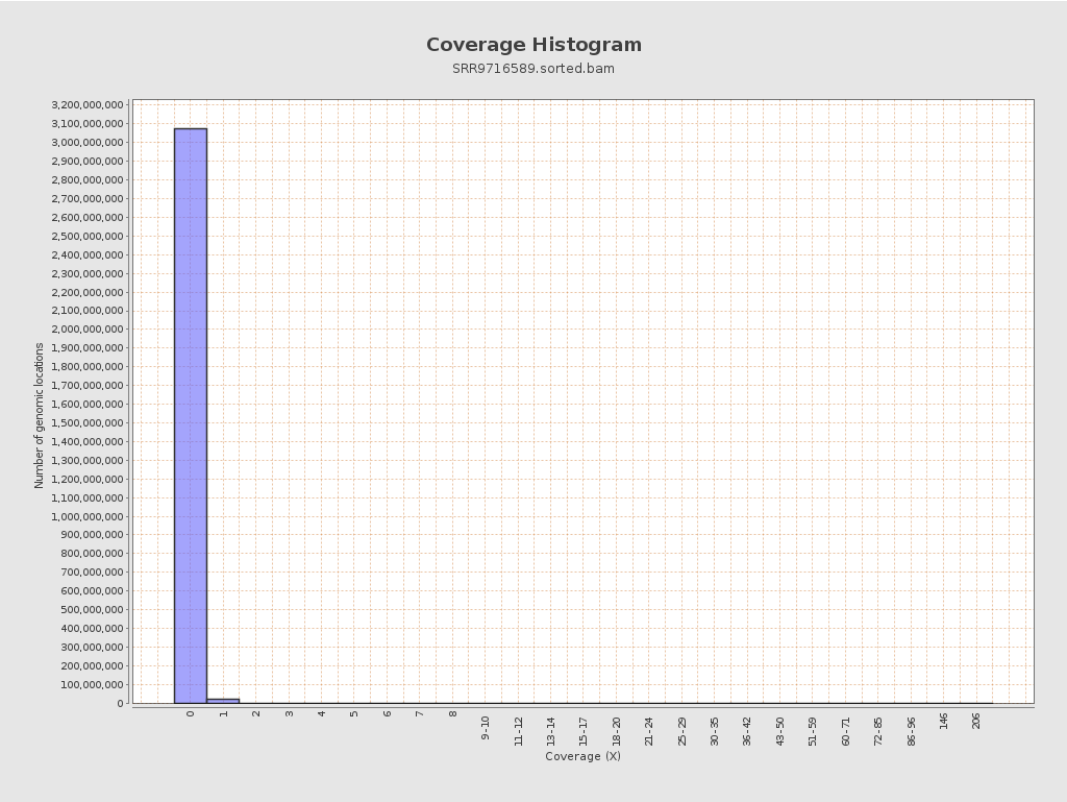
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2600644	0.0104	0.126
chr2	243199373	2280784	0.0094	0.1324
chr3	198022430	1441998	0.0073	0.088
chr4	191154276	952699	0.005	0.0735
chr5	180915260	1633271	0.009	0.0975
chr6	171115067	845944	0.0049	0.0758
chr7	159138663	1314650	0.0083	0.1368

chr8	146364022	991364	0.0068	0.0894
chr9	141213431	629804	0.0045	0.0784
chr10	135534747	1024259	0.0076	0.1044
chr11	135006516	948040	0.007	0.0939
chr12	133851895	840554	0.0063	0.0815
chr13	115169878	644468	0.0056	0.0769
chr14	107349540	492122	0.0046	0.0704
chr15	102531392	964705	0.0094	0.0998
chr16	90354753	729009	0.0081	0.0947
chr17	81195210	830791	0.0102	0.1066
chr18	78077248	601006	0.0077	0.1285
chr19	59128983	361582	0.0061	0.1039
chr20	63025520	551223	0.0087	0.0964
chr21	48129895	274266	0.0057	0.0782
chr22	51304566	240222	0.0047	0.07
chrMT	16571	7444	0.4492	0.6801
chrX	155270560	848180	0.0055	0.0806
chrY	59373566	47102	0.0008	0.0324

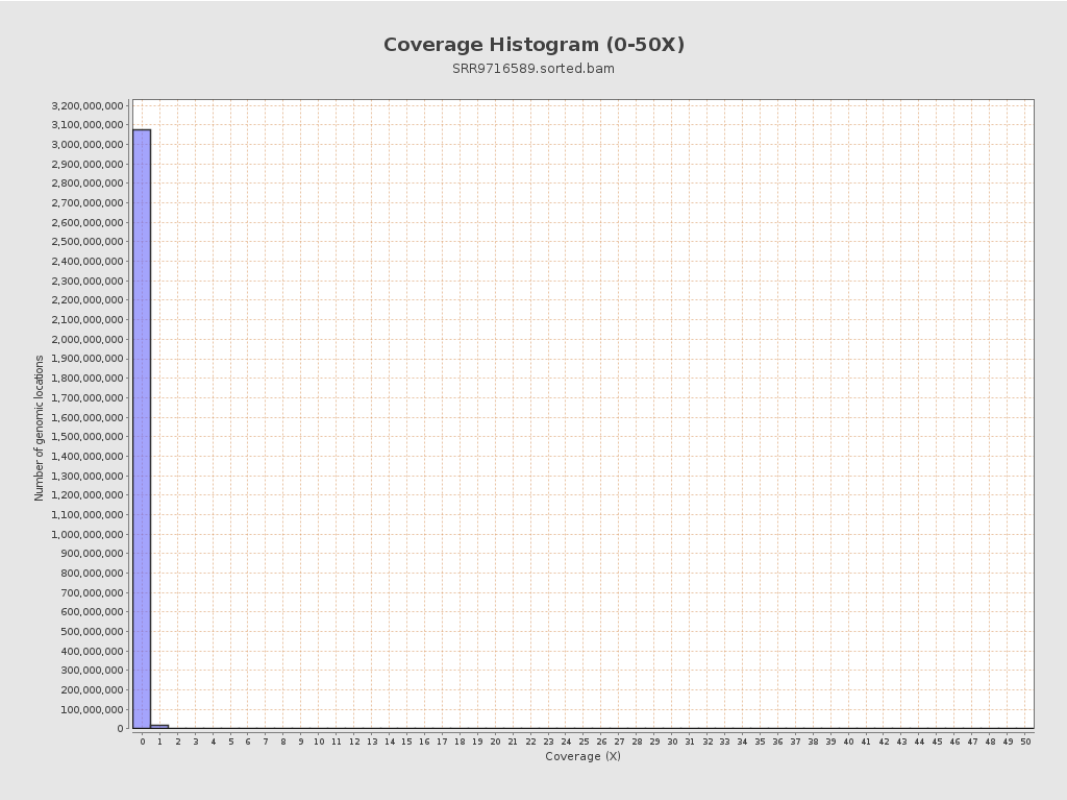
3. Results : Coverage across reference



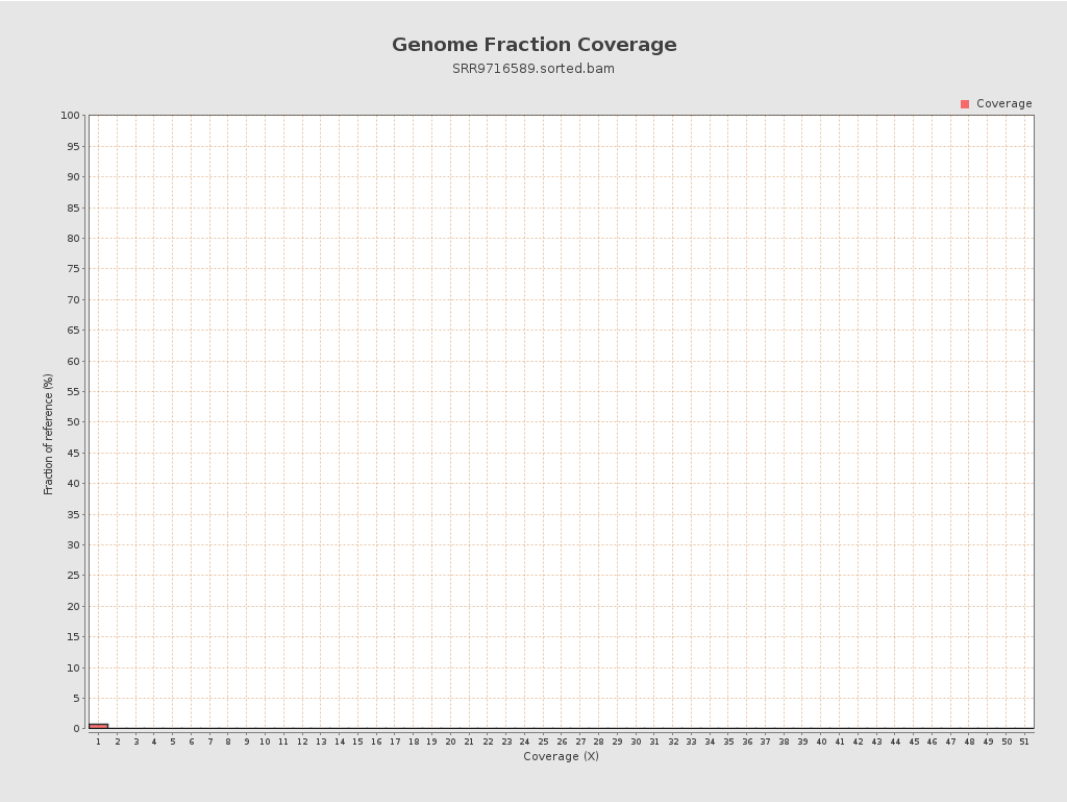
4. Results : Coverage Histogram



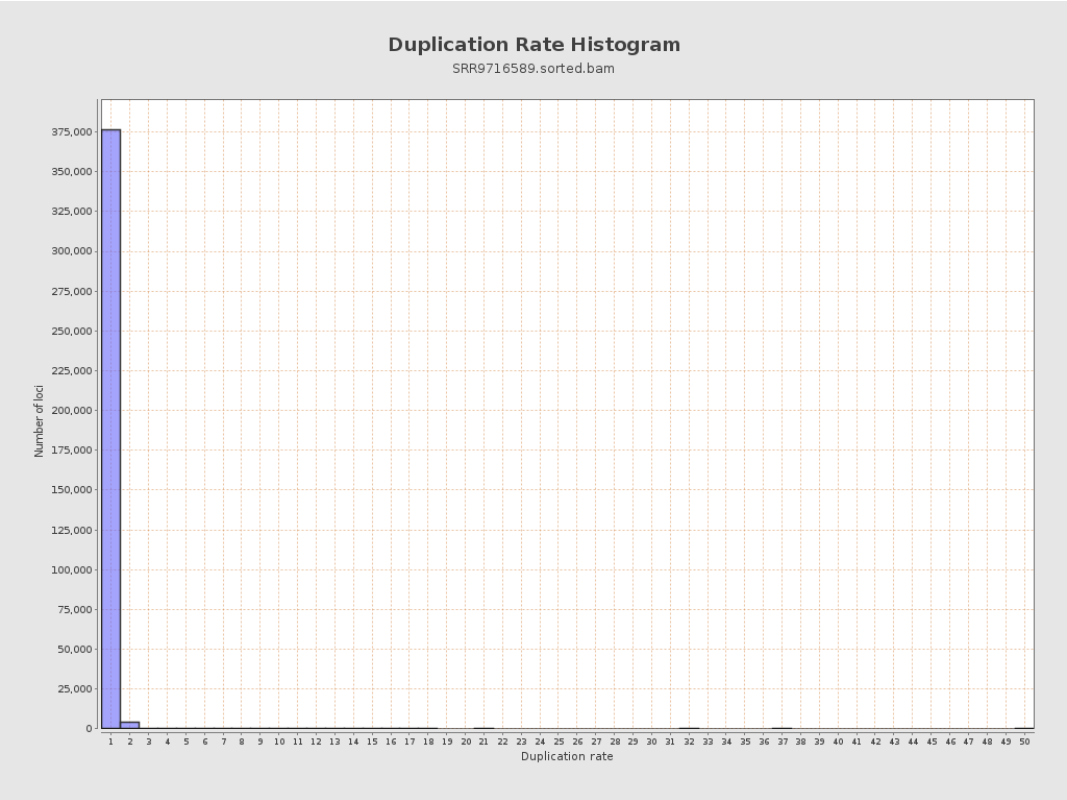
5. Results : Coverage Histogram (0-50X)



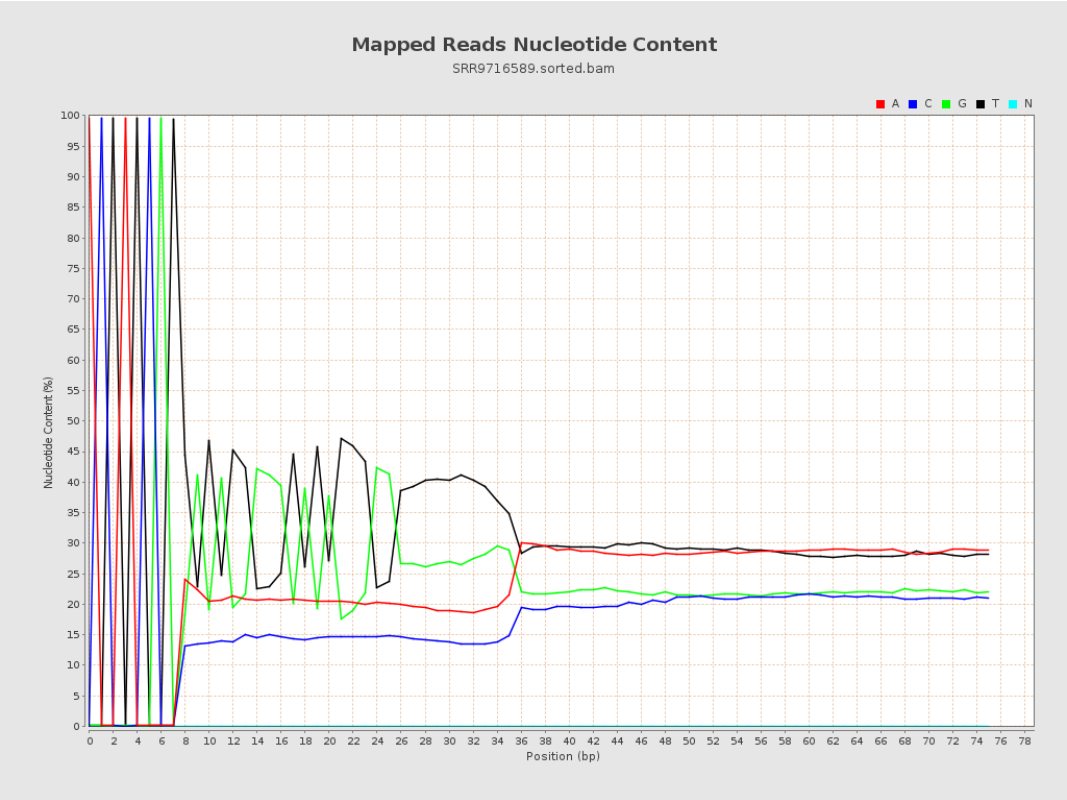
6. Results : Genome Fraction Coverage



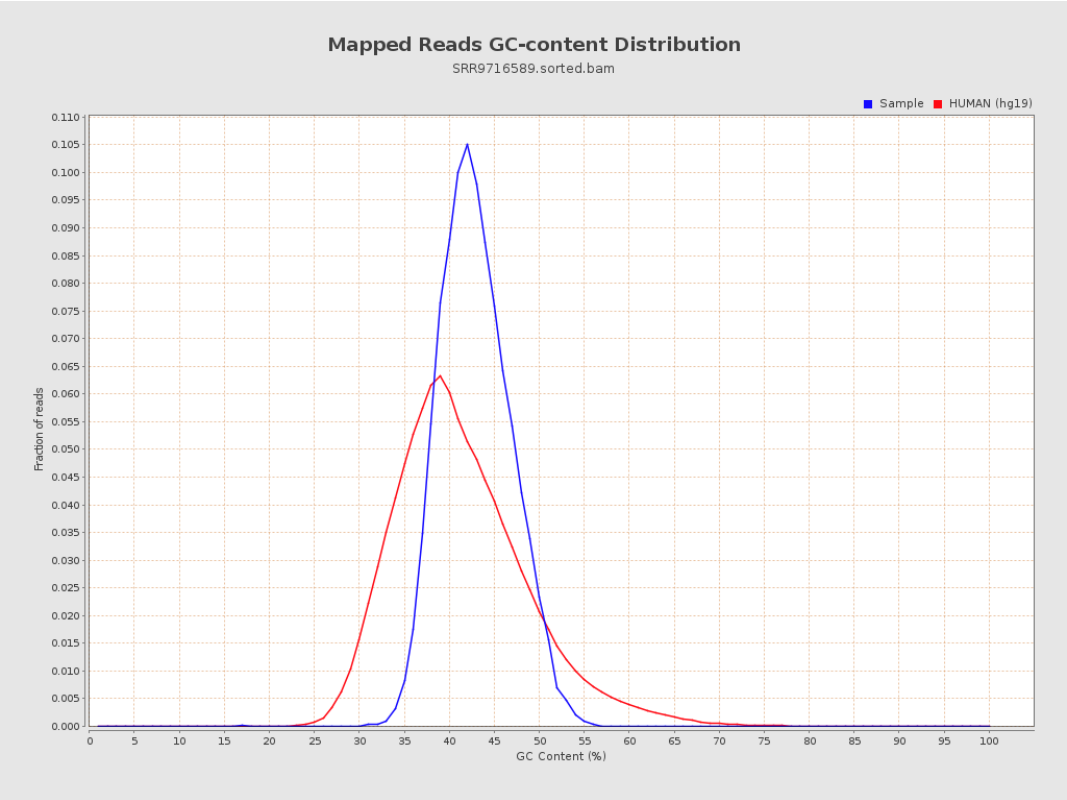
7. Results : Duplication Rate Histogram



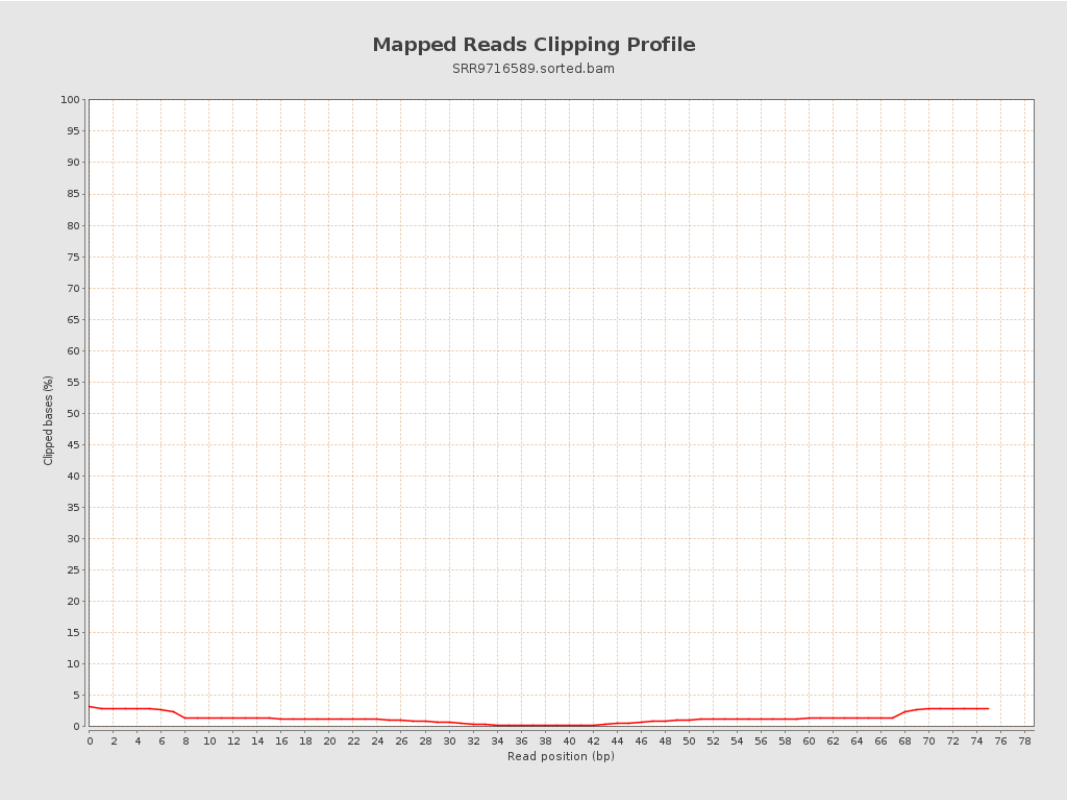
8. Results : Mapped Reads Nucleotide Content



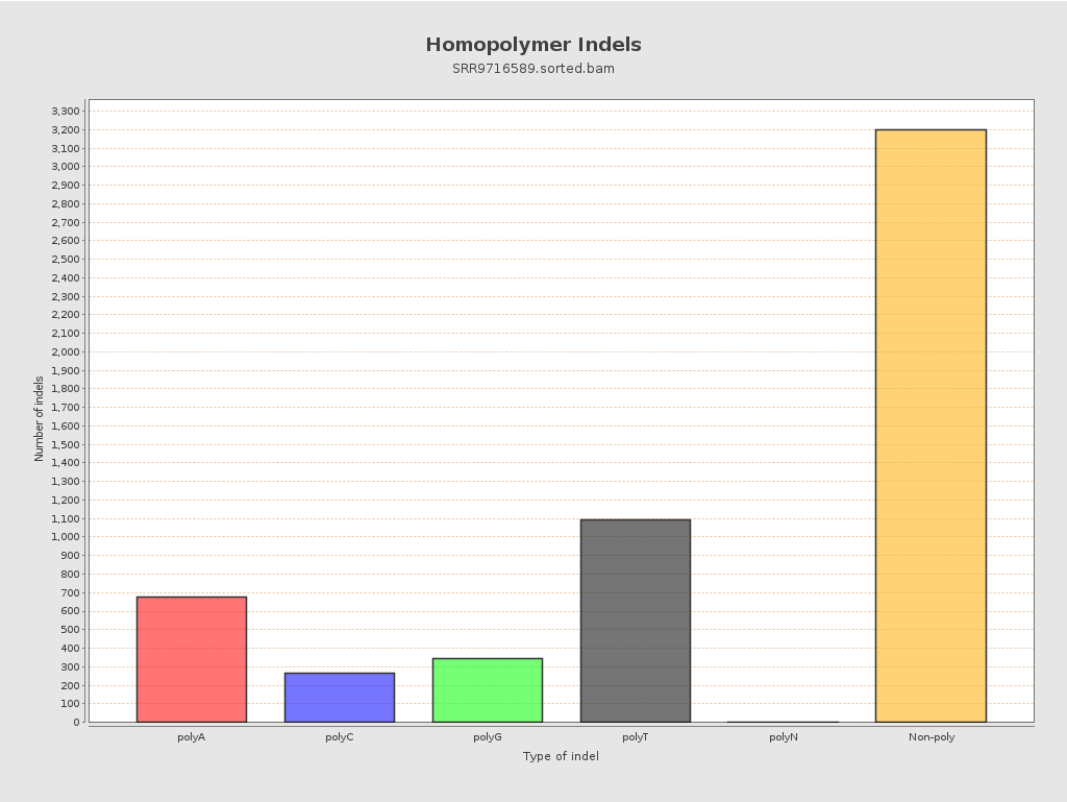
9. Results : Mapped Reads GC-content Distribution



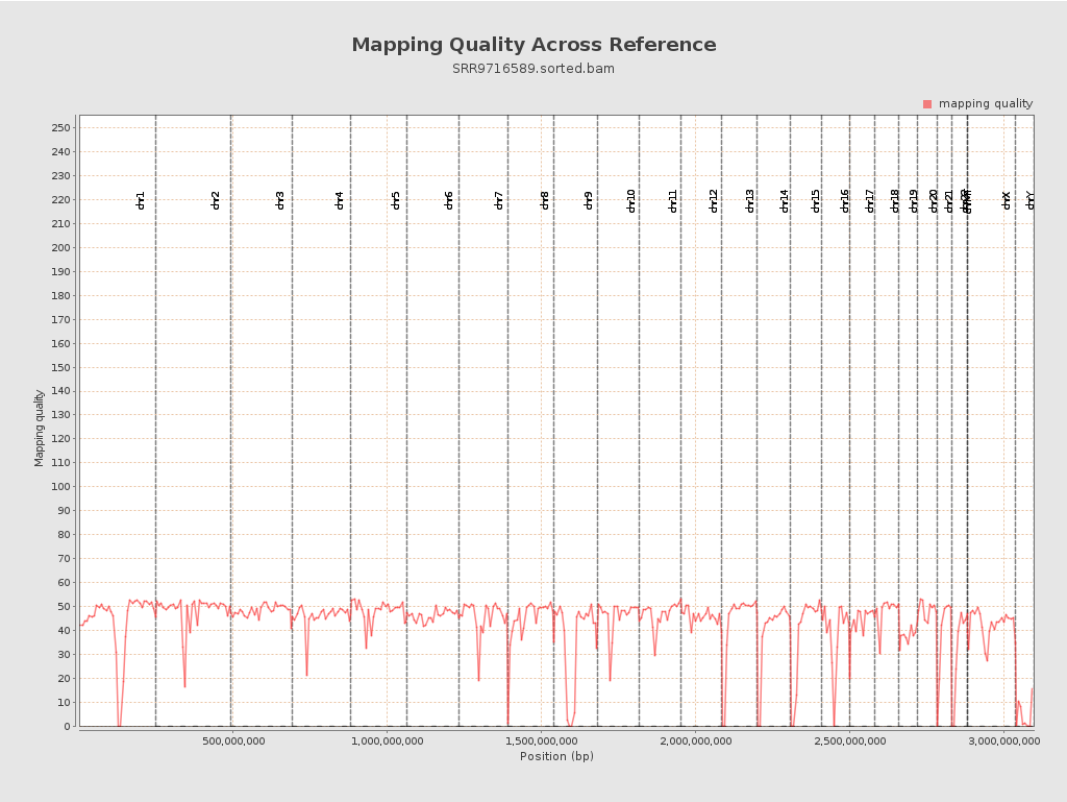
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram