Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:55:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525165.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_SRR10525165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525165.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:55:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,402,054
Mapped reads	2,201,873 / 91.67%
Unmapped reads	200,181 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,770 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	102,481 / 4.27%
Duplication rate	3.47%
Clipped reads	2,204,360 / 91.77%

2.2. ACGT Content

Number/percentage of A's	29,871,022 / 23.49%
Number/percentage of C's	23,332,337 / 18.35%
Number/percentage of T's	41,326,985 / 32.5%
Number/percentage of G's	32,623,853 / 25.66%
Number/percentage of N's	2,656 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0411

Standard Deviation	0.3689

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

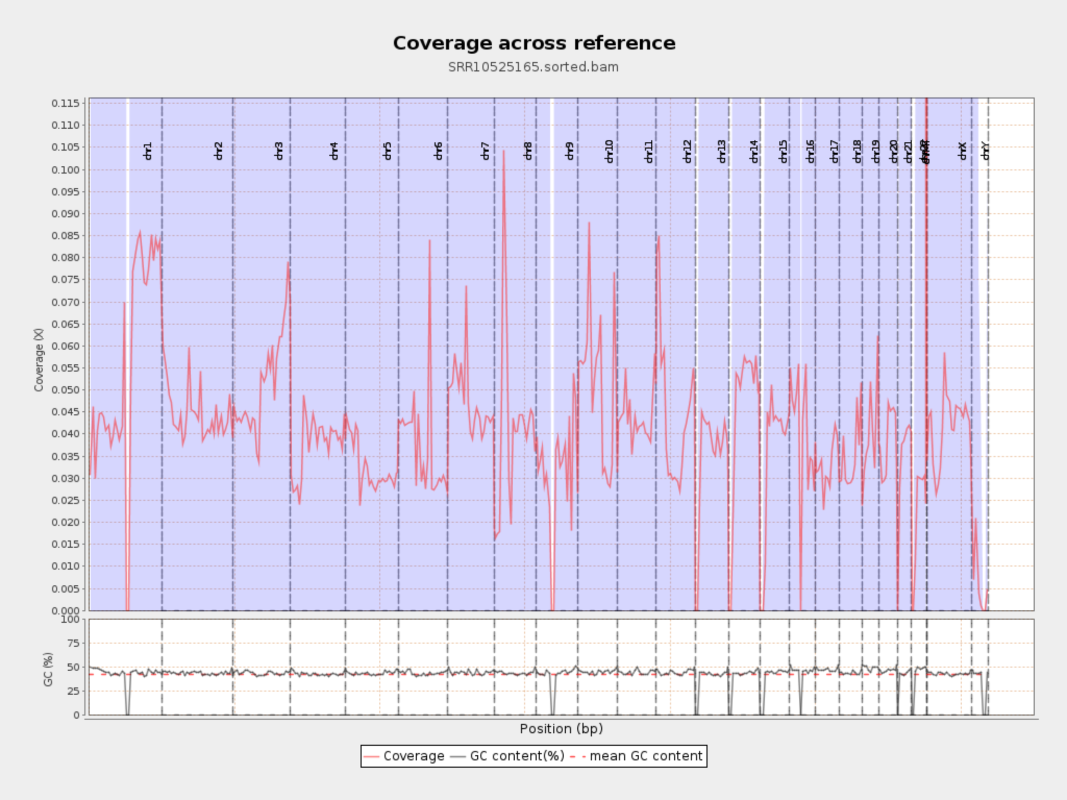
General error rate	0.53%
Mismatches	659,295
Insertions	8,147
Mapped reads with at least one insertion	0.37%
Deletions	24,827
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.92%

2.6. Chromosome stats

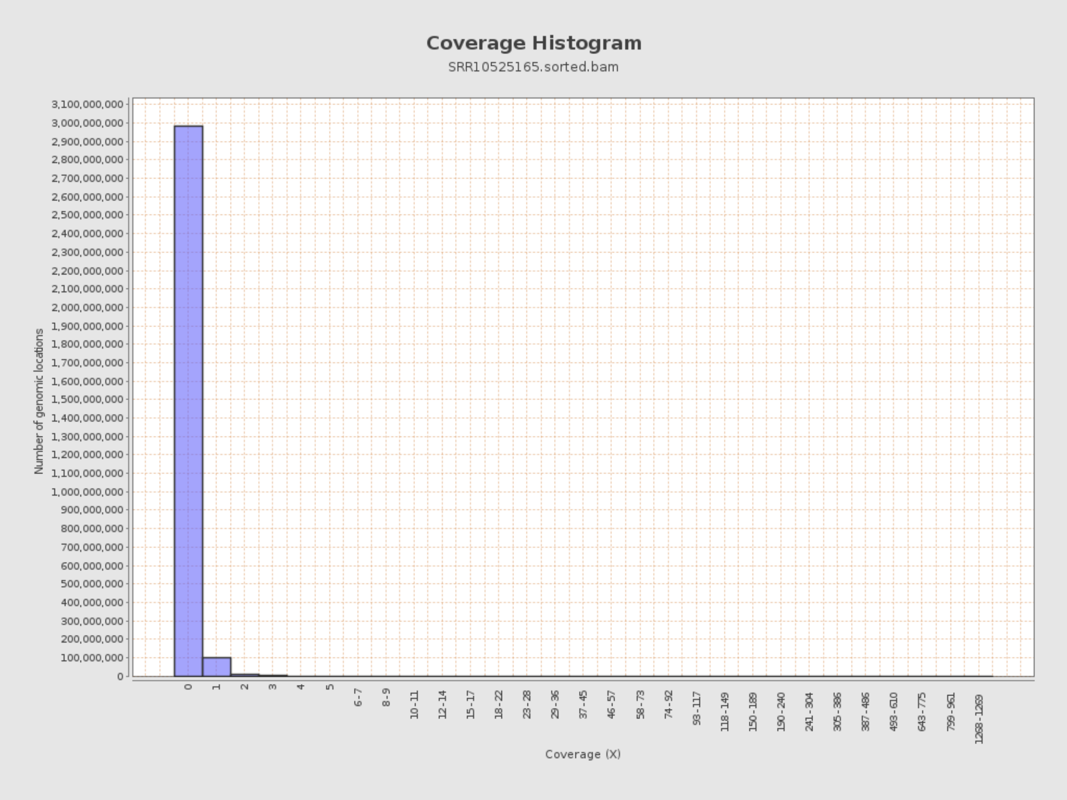
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13839485	0.0555	0.6653
chr2	243199373	10910401	0.0449	0.5546
chr3	198022430	10157377	0.0513	0.2573
chr4	191154276	7180521	0.0376	0.2323
chr5	180915260	5863070	0.0324	0.2017
chr6	171115067	6431743	0.0376	0.2656
chr7	159138663	7622321	0.0479	0.5491

chr8	146364022	6029228	0.0412	0.3091
chr9	141213431	4351259	0.0308	0.2609
chr10	135534747	7046095	0.052	0.4093
chr11	135006516	5914091	0.0438	0.3088
chr12	133851895	5967023	0.0446	0.24
chr13	115169878	3985294	0.0346	0.2116
chr14	107349540	4836240	0.0451	0.2452
chr15	102531392	3574669	0.0349	0.2123
chr16	90354753	3533796	0.0391	0.2503
chr17	81195210	2671322	0.0329	0.2127
chr18	78077248	2720524	0.0348	0.5048
chr19	59128983	2409086	0.0407	0.4591
chr20	63025520	2423988	0.0385	0.2246
chr21	48129895	1652015	0.0343	0.2222
chr22	51304566	1070166	0.0209	0.1599
chrMT	16571	119835	7.2316	4.5161
chrX	155270560	6510279	0.0419	0.2573
chrY	59373566	376698	0.0063	0.1761

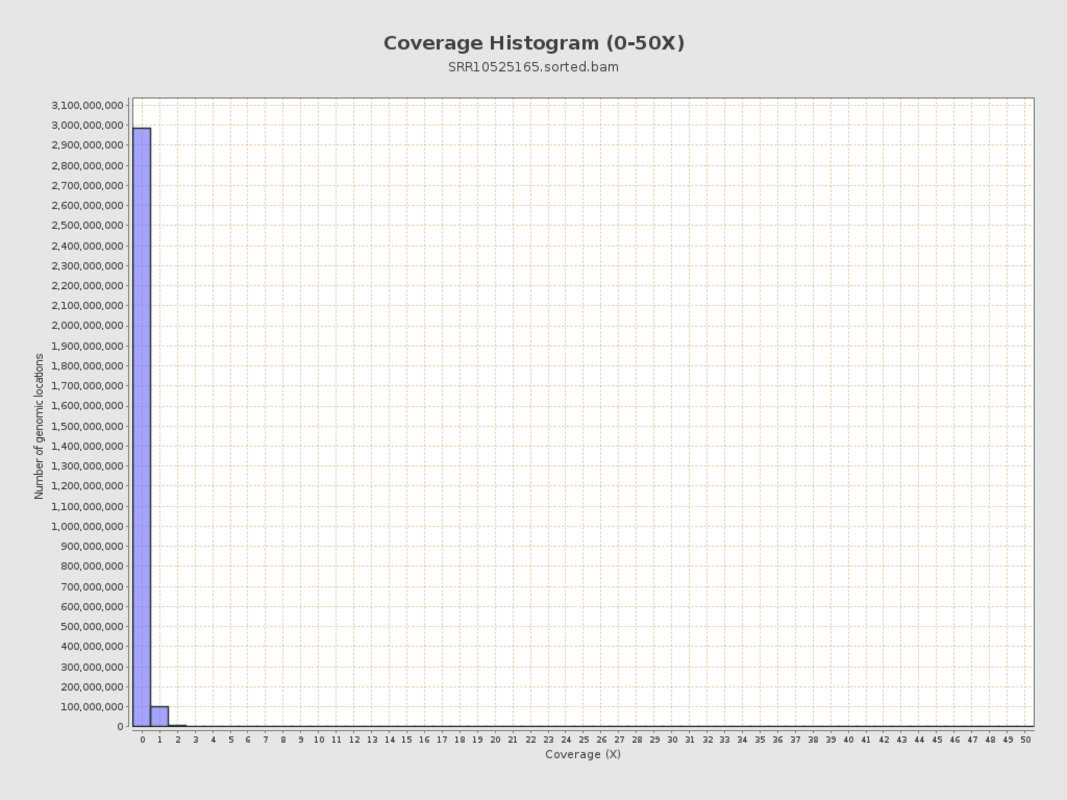
3. Results : Coverage across reference



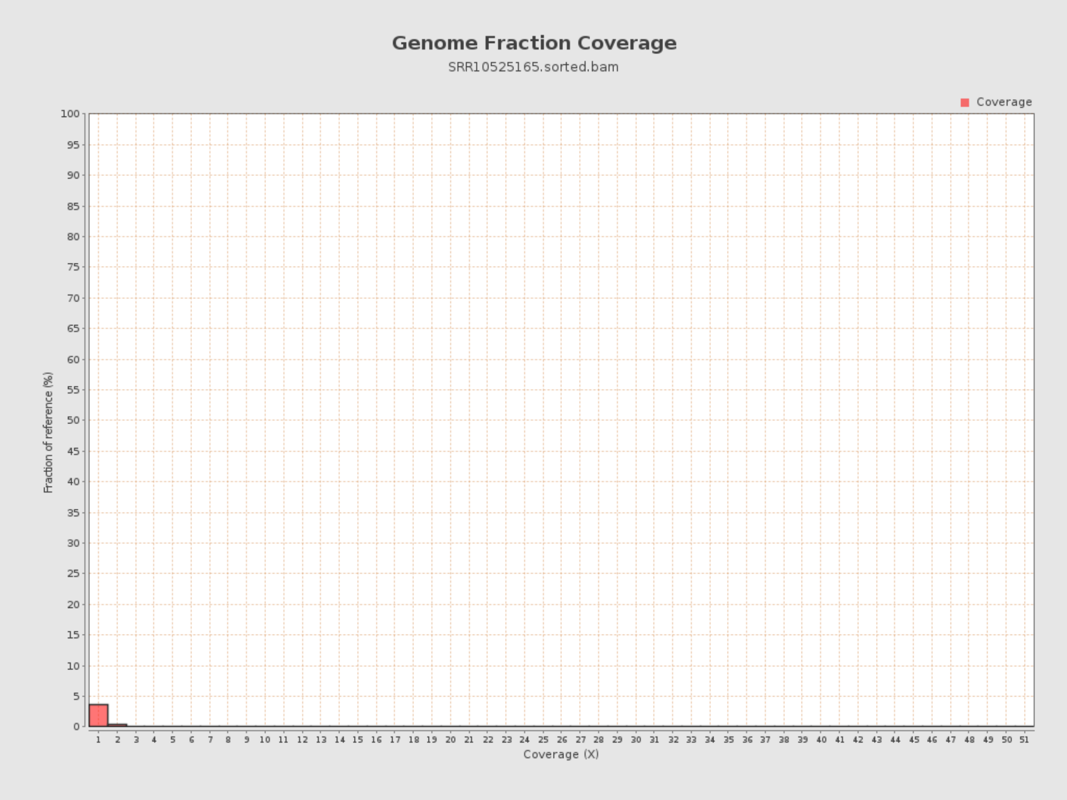
4. Results : Coverage Histogram



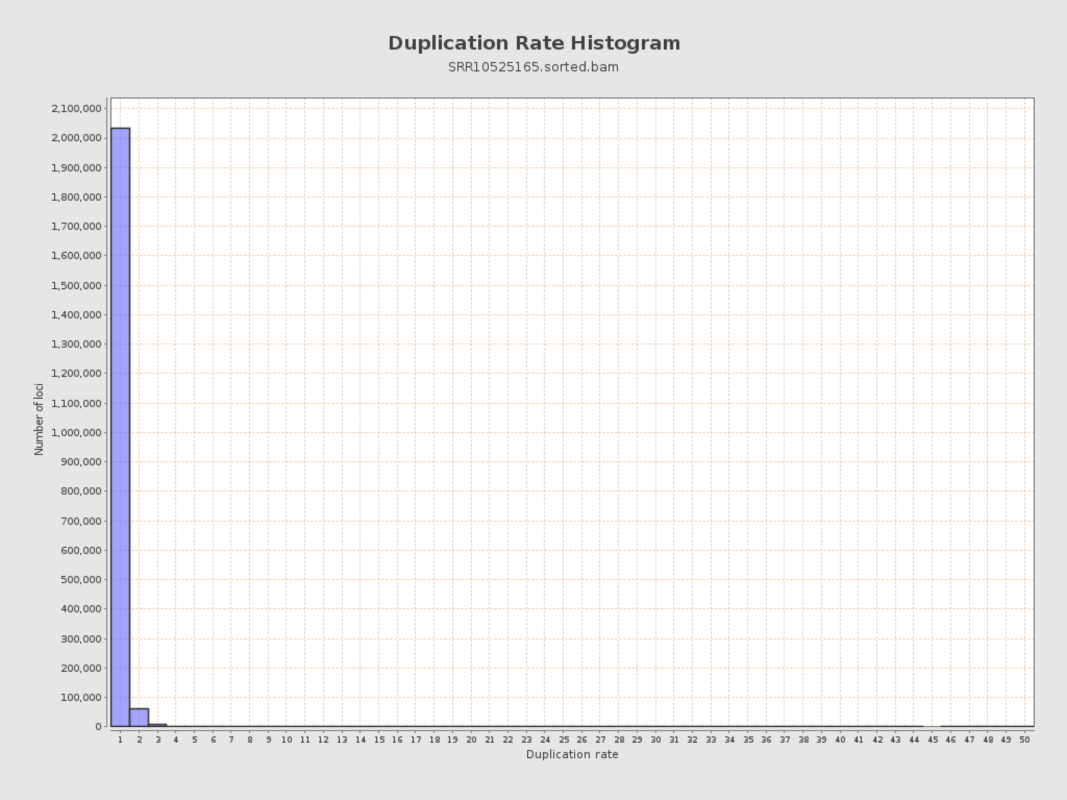
5. Results : Coverage Histogram (0-50X)



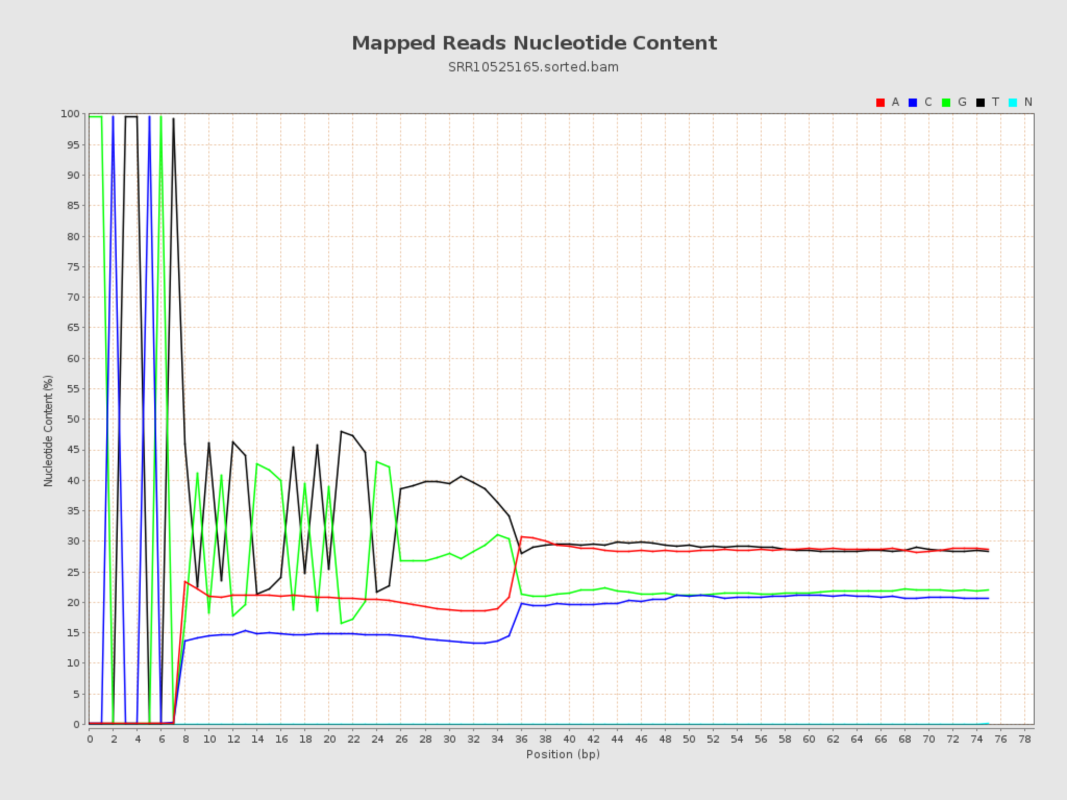
6. Results : Genome Fraction Coverage



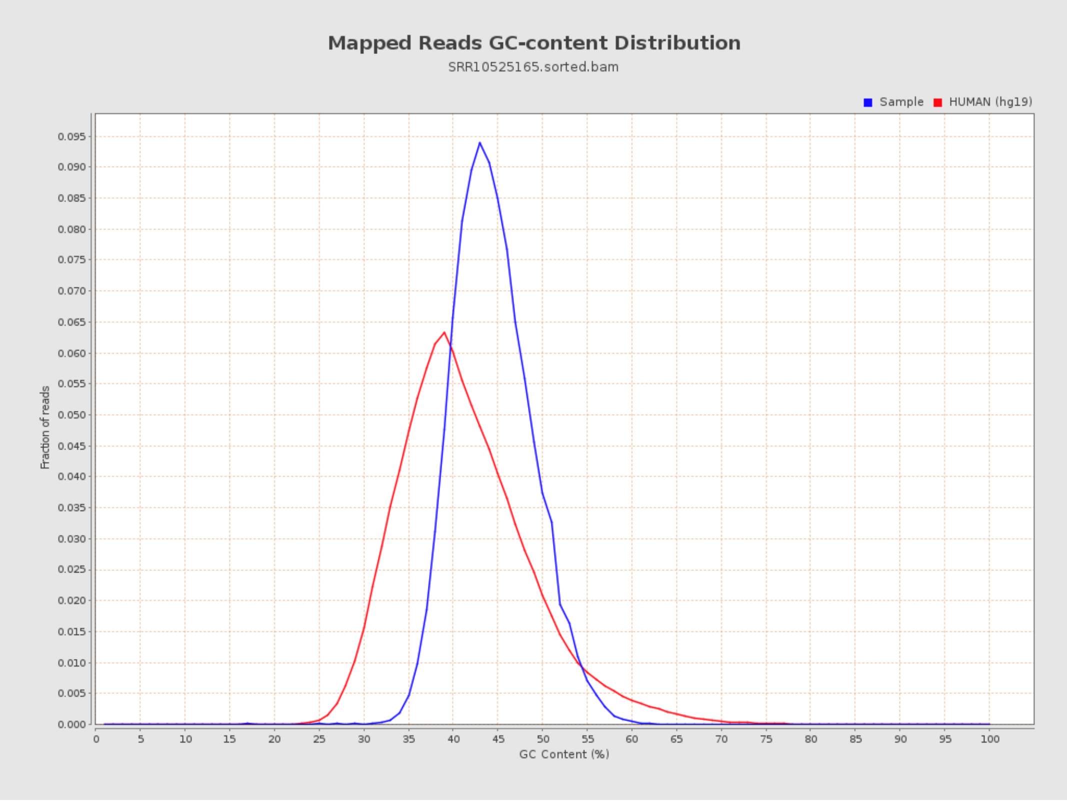
7. Results : Duplication Rate Histogram



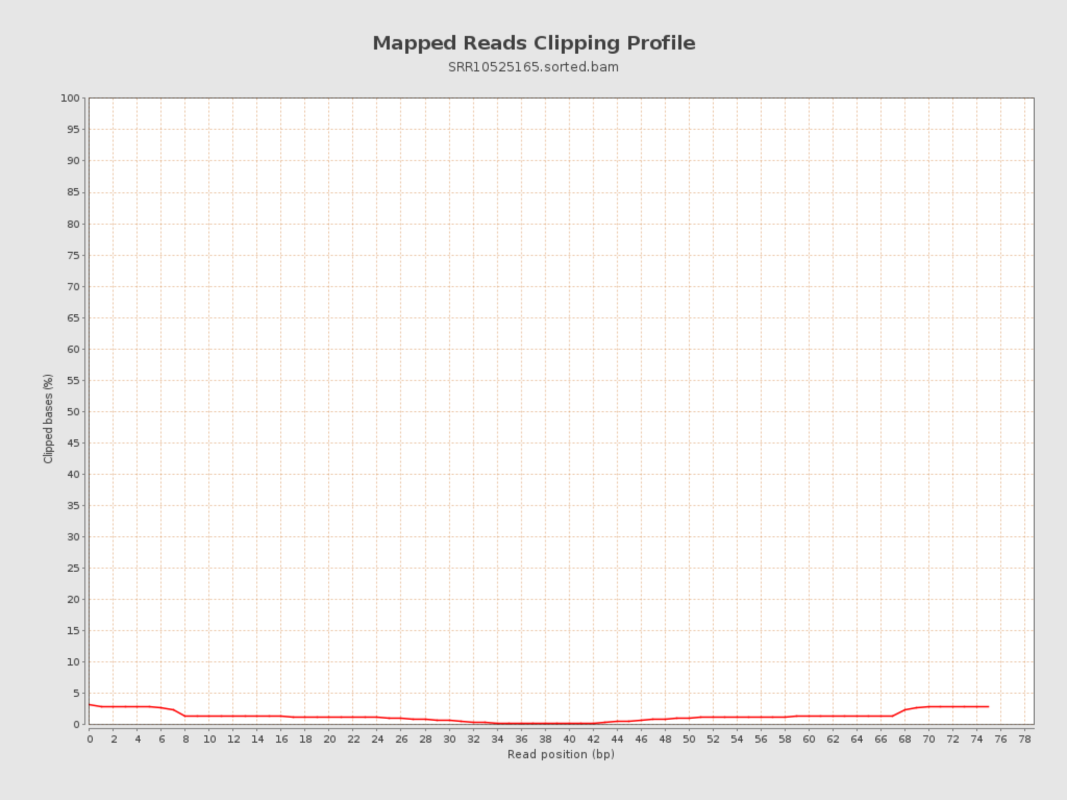
8. Results : Mapped Reads Nucleotide Content



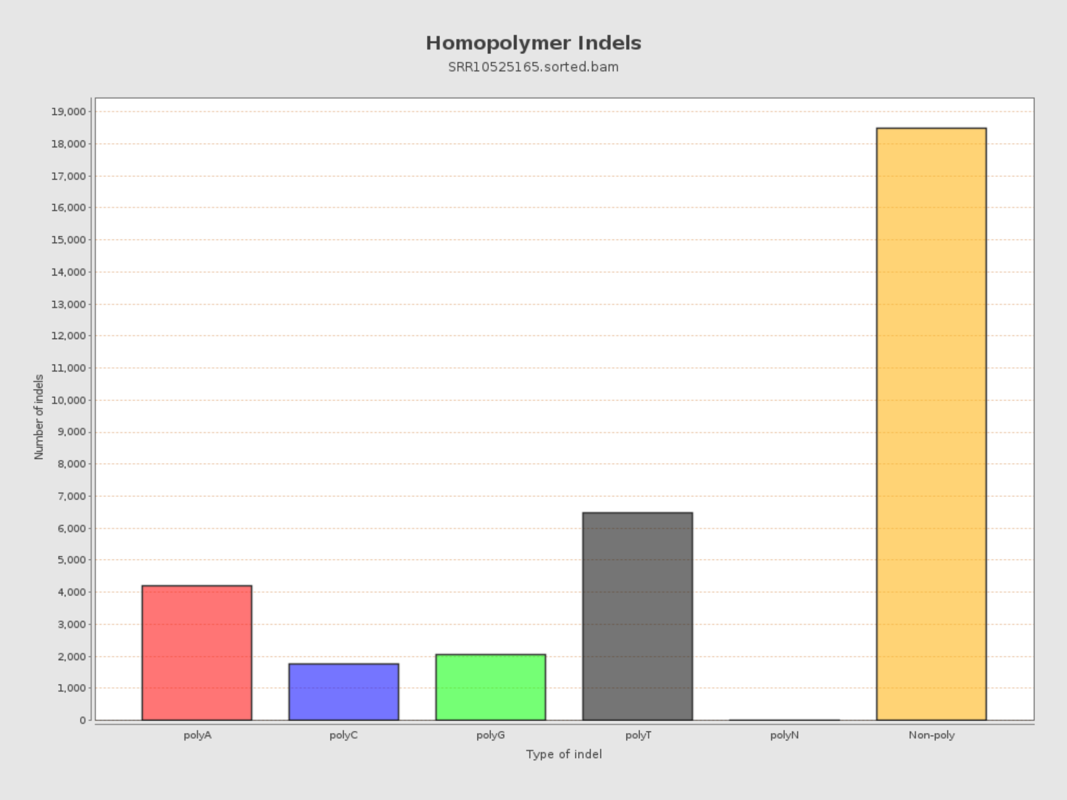
9. Results : Mapped Reads GC-content Distribution



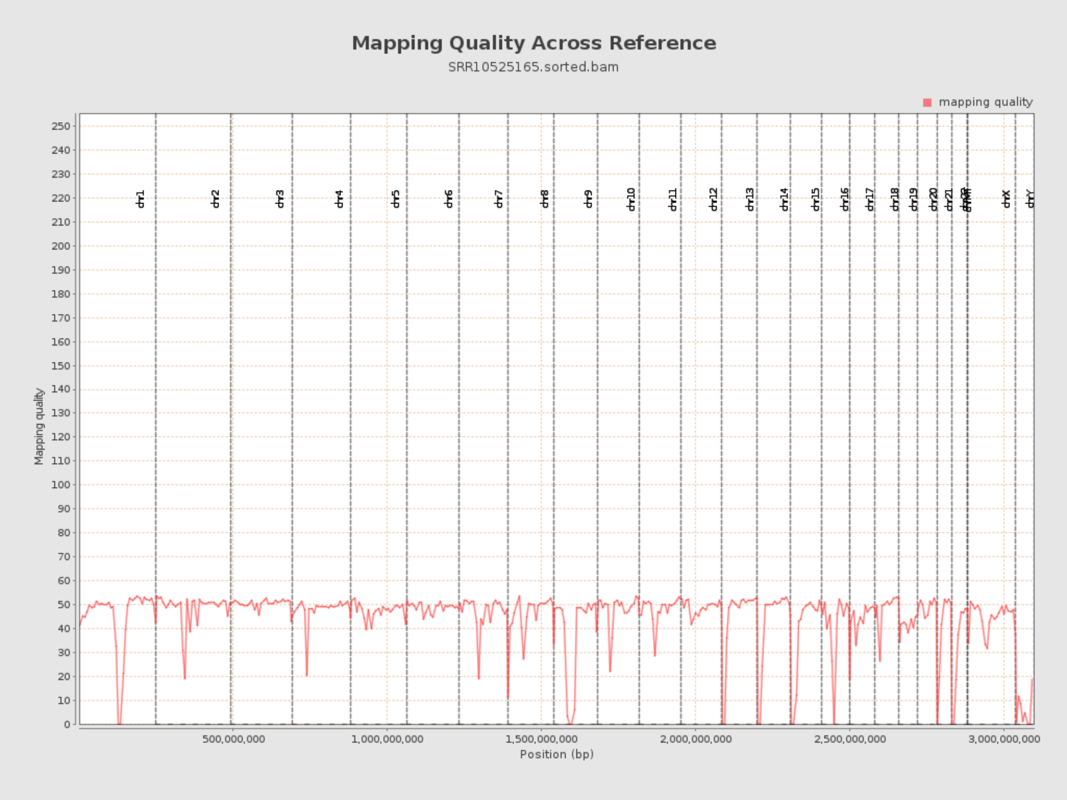
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram