Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:51:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525098.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_SRR10525098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:51:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,938,236
Mapped reads	1,787,546 / 92.23%
Unmapped reads	150,690 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,398 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	65,296 / 3.37%
Duplication rate	2.57%
Clipped reads	1,789,346 / 92.32%

2.2. ACGT Content

Number/percentage of A's	26,293,729 / 25.3%
Number/percentage of C's	18,485,768 / 17.78%
Number/percentage of T's	32,729,151 / 31.49%
Number/percentage of G's	26,435,356 / 25.43%
Number/percentage of N's	1,987 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.3055

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

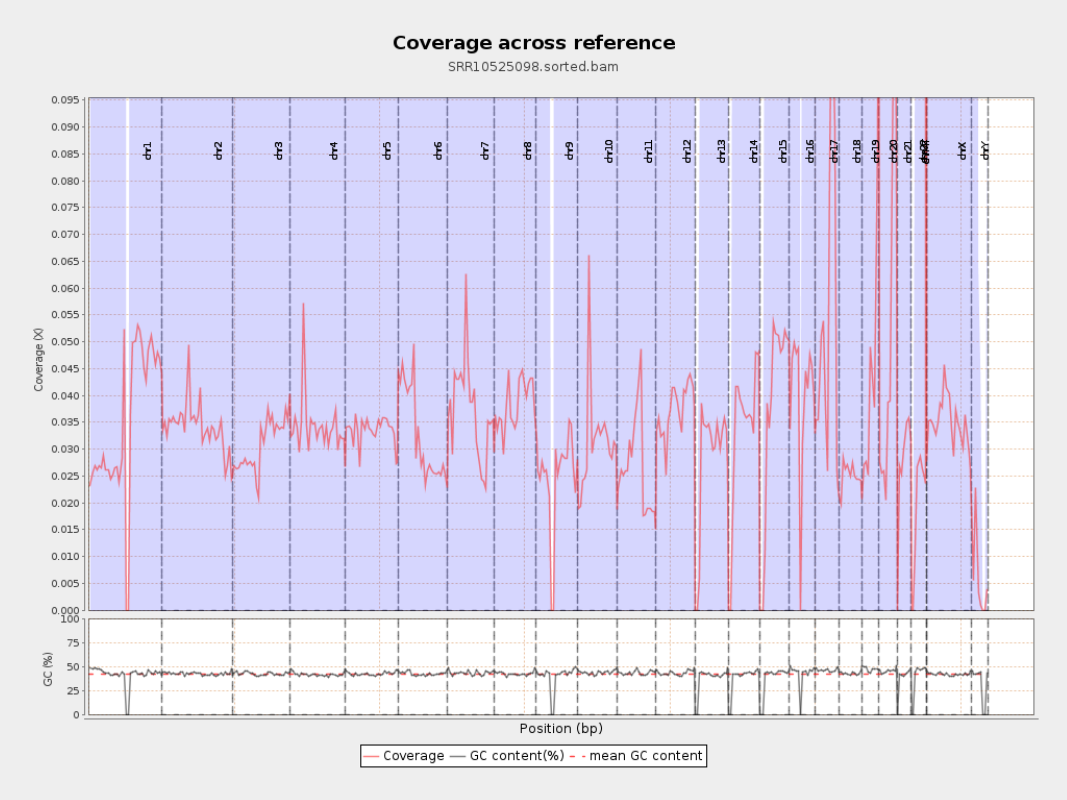
General error rate	0.52%
Mismatches	526,931
Insertions	7,244
Mapped reads with at least one insertion	0.4%
Deletions	20,831
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.92%

2.6. Chromosome stats

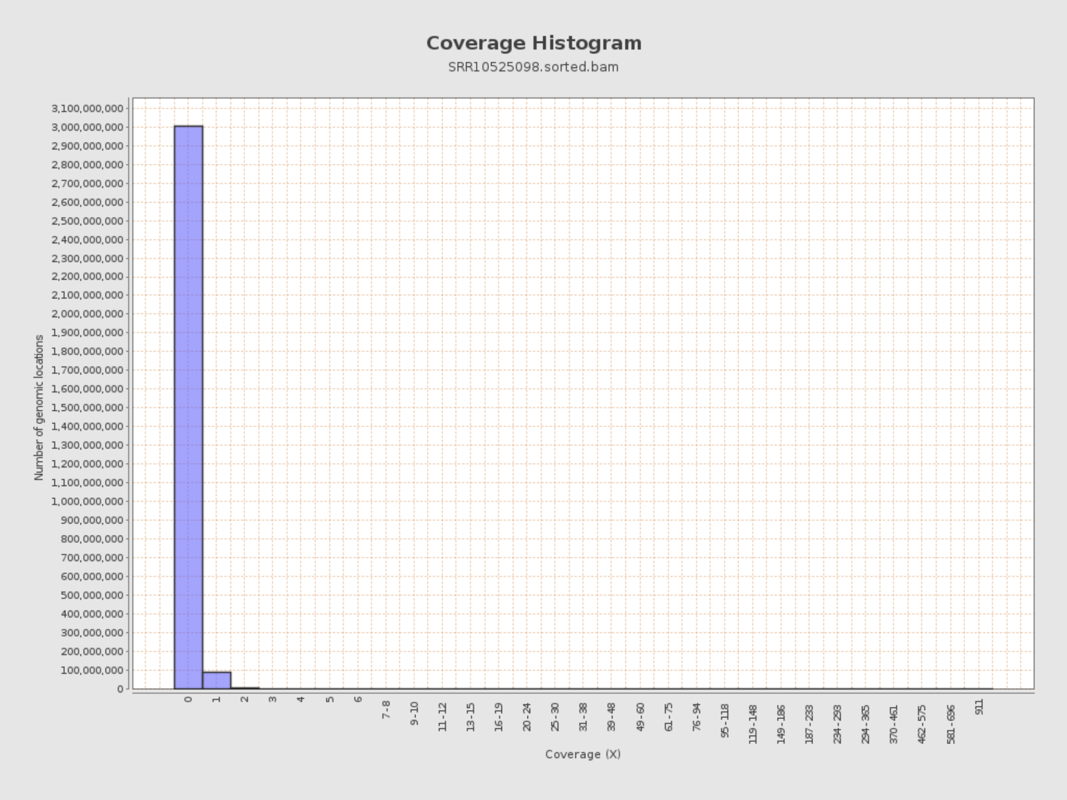
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8679978	0.0348	0.5015
chr2	243199373	8335045	0.0343	0.424
chr3	198022430	6075136	0.0307	0.1962
chr4	191154276	6532671	0.0342	0.2382
chr5	180915260	6065315	0.0335	0.2002
chr6	171115067	5581847	0.0326	0.2398
chr7	159138663	5944063	0.0374	0.4063

chr8	146364022	5620929	0.0384	0.3941
chr9	141213431	3449223	0.0244	0.2172
chr10	135534747	4239175	0.0313	0.319
chr11	135006516	3640002	0.027	0.2376
chr12	133851895	4997419	0.0373	0.2141
chr13	115169878	3218814	0.0279	0.1827
chr14	107349540	3548732	0.0331	0.2026
chr15	102531392	3860453	0.0377	0.2134
chr16	90354753	3611906	0.04	0.2336
chr17	81195210	4393841	0.0541	0.2699
chr18	78077248	1957930	0.0251	0.3795
chr19	59128983	2655112	0.0449	0.3854
chr20	63025520	3362592	0.0534	0.2652
chr21	48129895	1341200	0.0279	0.2197
chr22	51304566	958711	0.0187	0.1494
chrMT	16571	116427	7.0259	4.7257
chrX	155270560	5442841	0.0351	0.2229
chrY	59373566	350264	0.0059	0.2257

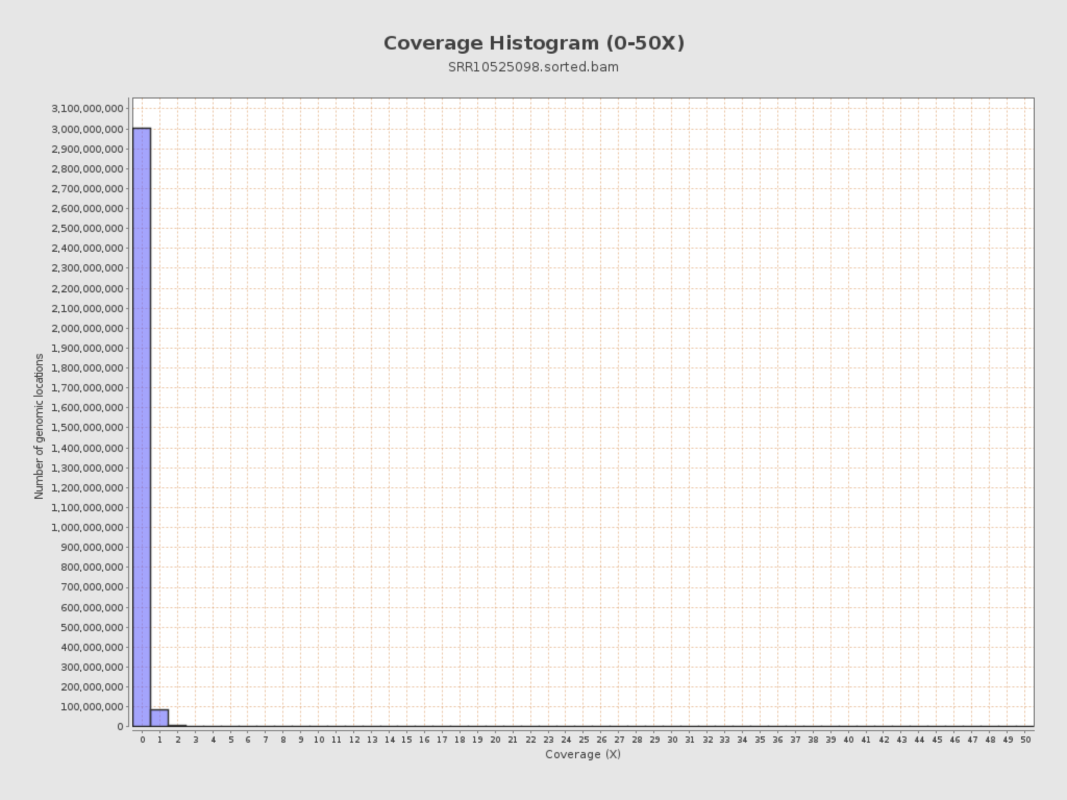
3. Results : Coverage across reference



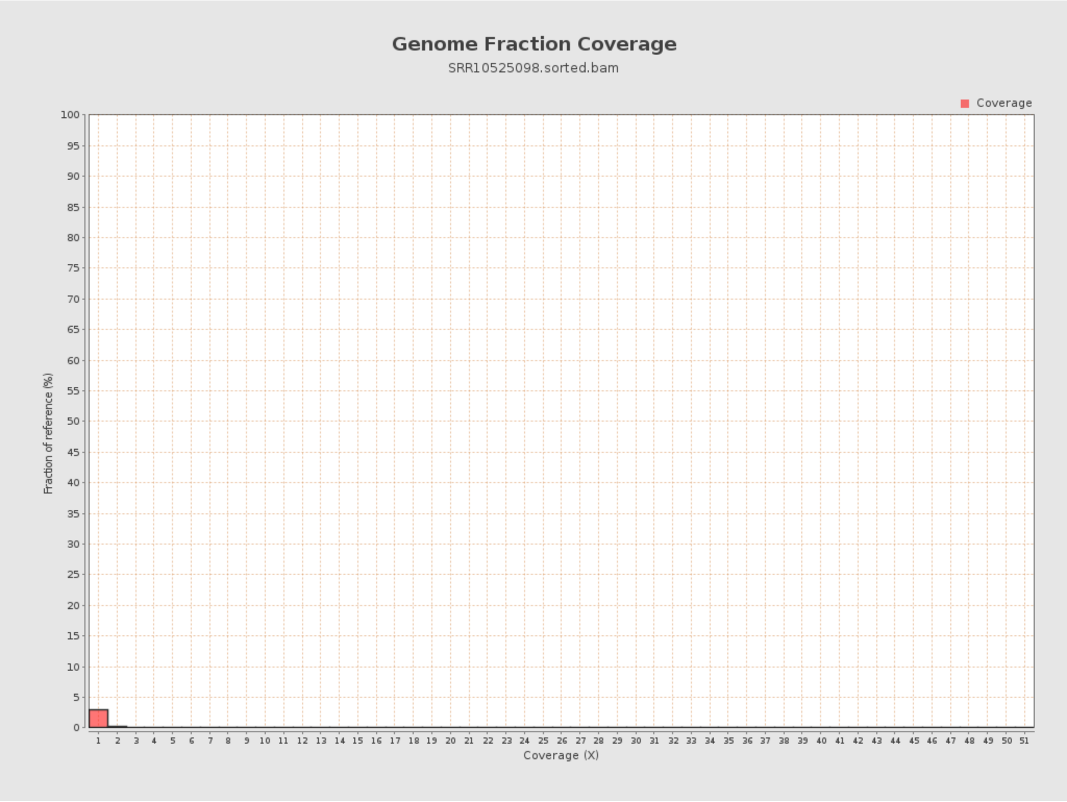
4. Results : Coverage Histogram



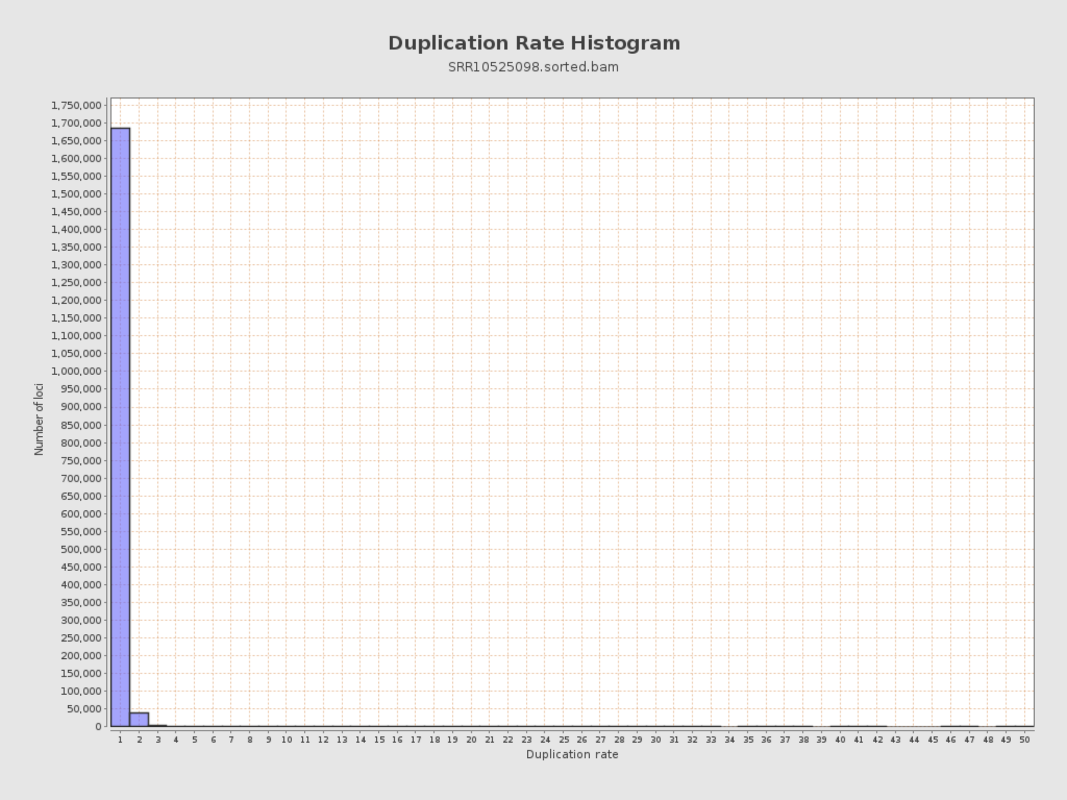
5. Results : Coverage Histogram (0-50X)



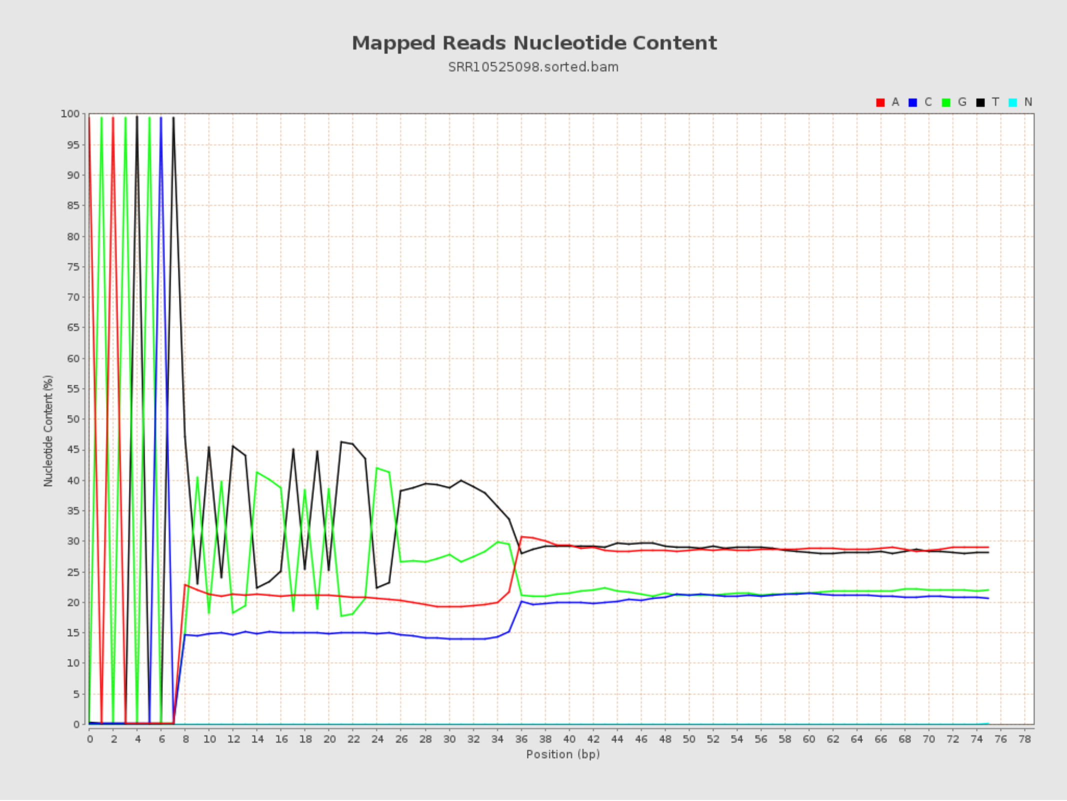
6. Results : Genome Fraction Coverage



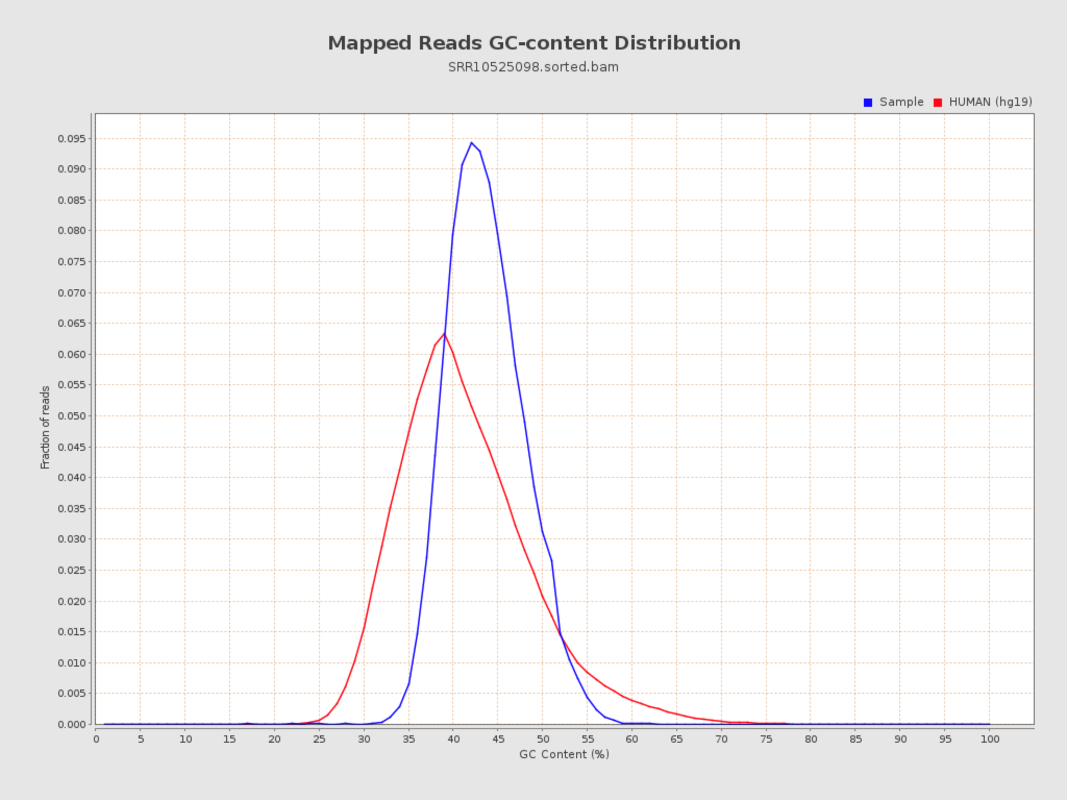
7. Results : Duplication Rate Histogram



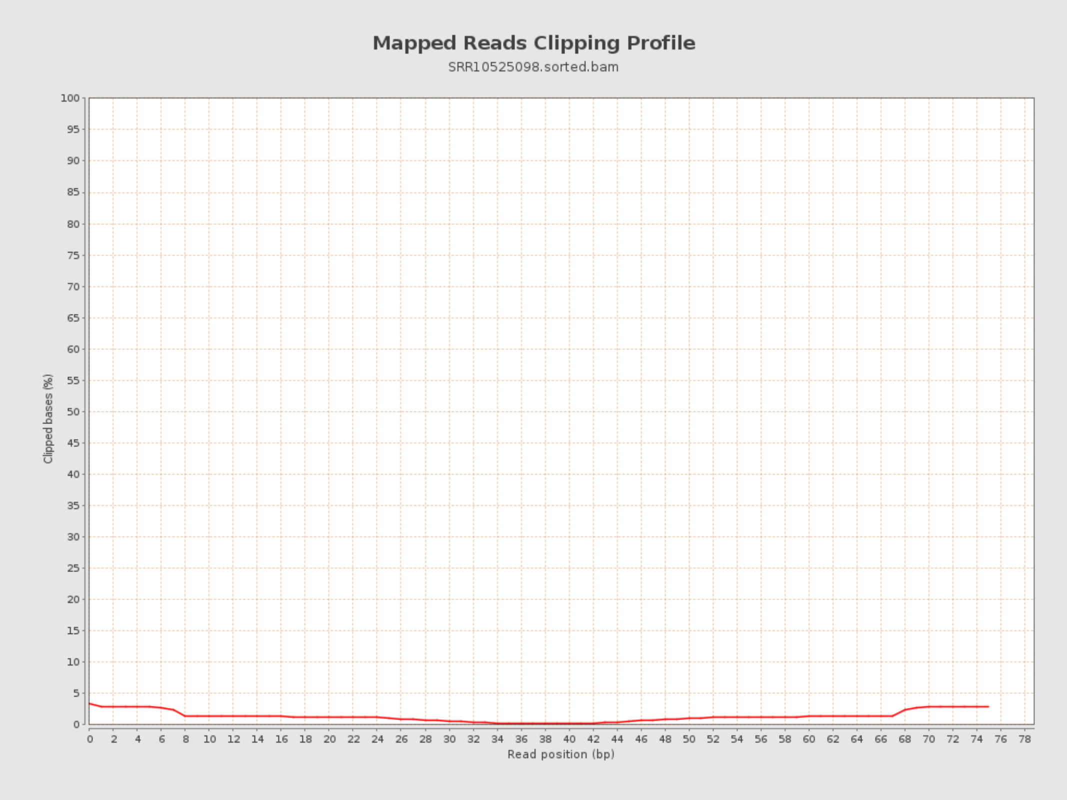
8. Results : Mapped Reads Nucleotide Content



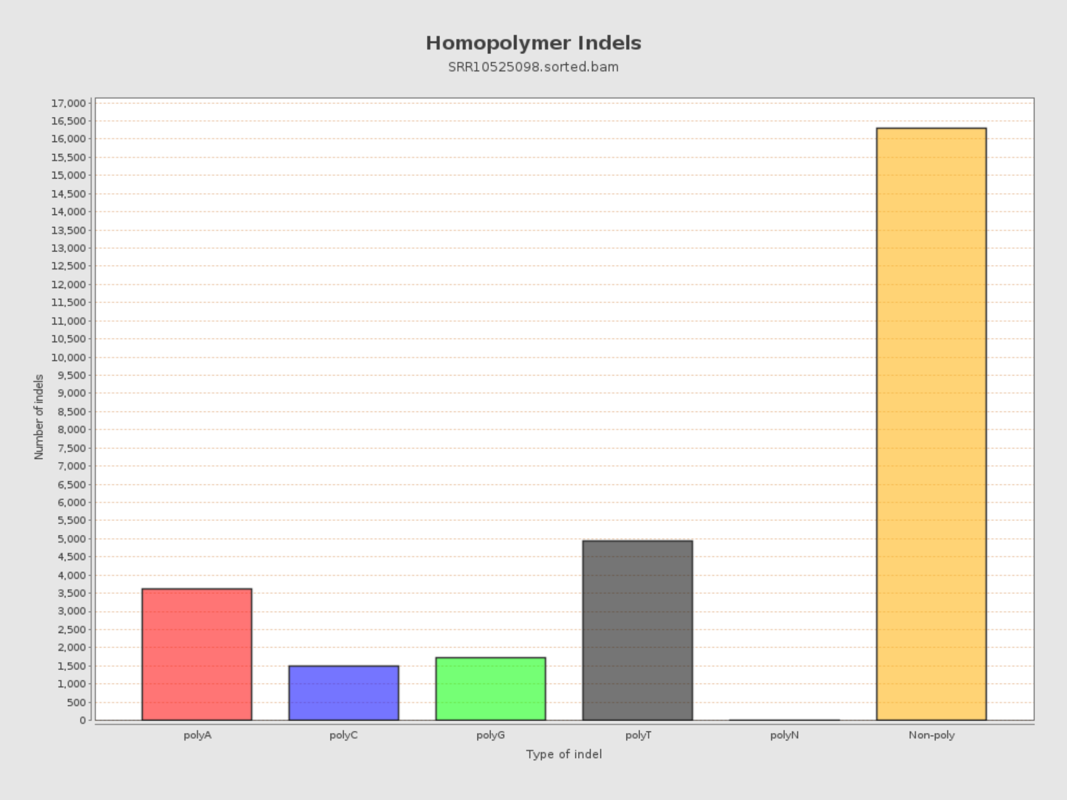
9. Results : Mapped Reads GC-content Distribution



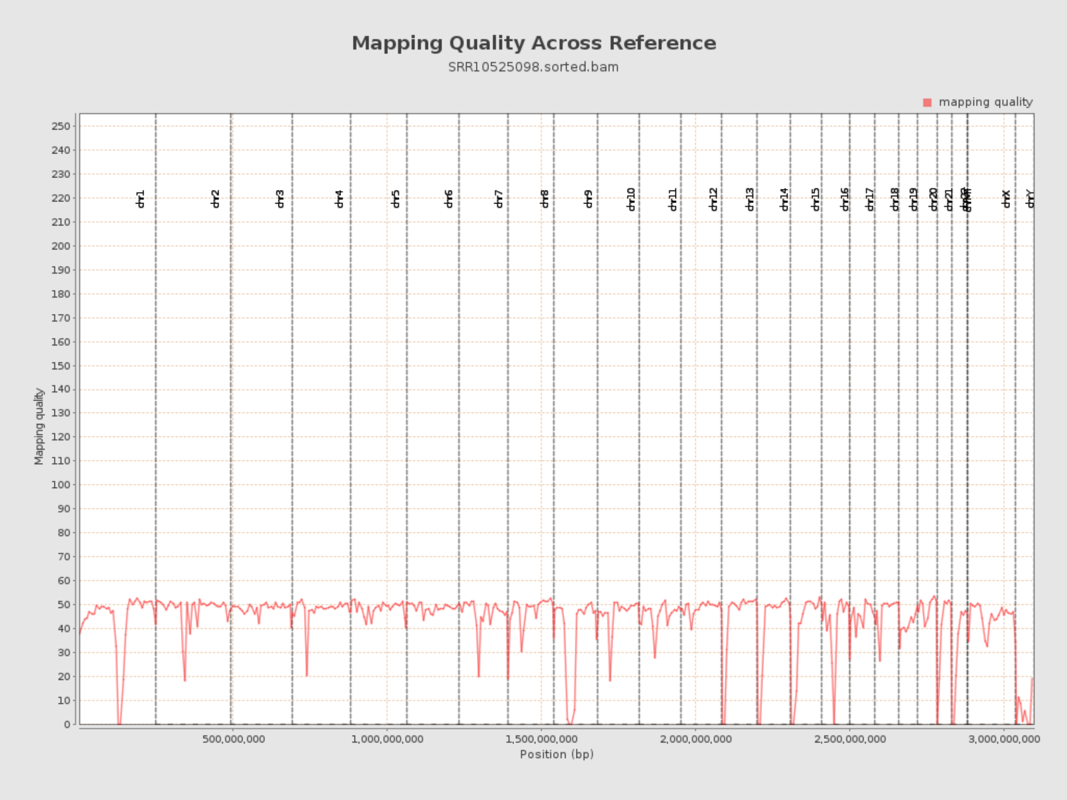
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram