Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:30:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525135.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_SRR10525135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:30:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,618,614
Mapped reads	1,446,435 / 89.36%
Unmapped reads	172,179 / 10.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,865 / 2.22%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	42,789 / 2.64%
Duplication rate	1.83%
Clipped reads	1,480,014 / 91.44%

2.2. ACGT Content

Number/percentage of A's	29,651,241 / 26.73%
Number/percentage of C's	21,185,293 / 19.1%
Number/percentage of T's	34,701,487 / 31.28%
Number/percentage of G's	25,378,219 / 22.88%
Number/percentage of N's	4,371 / 0%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.3526

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

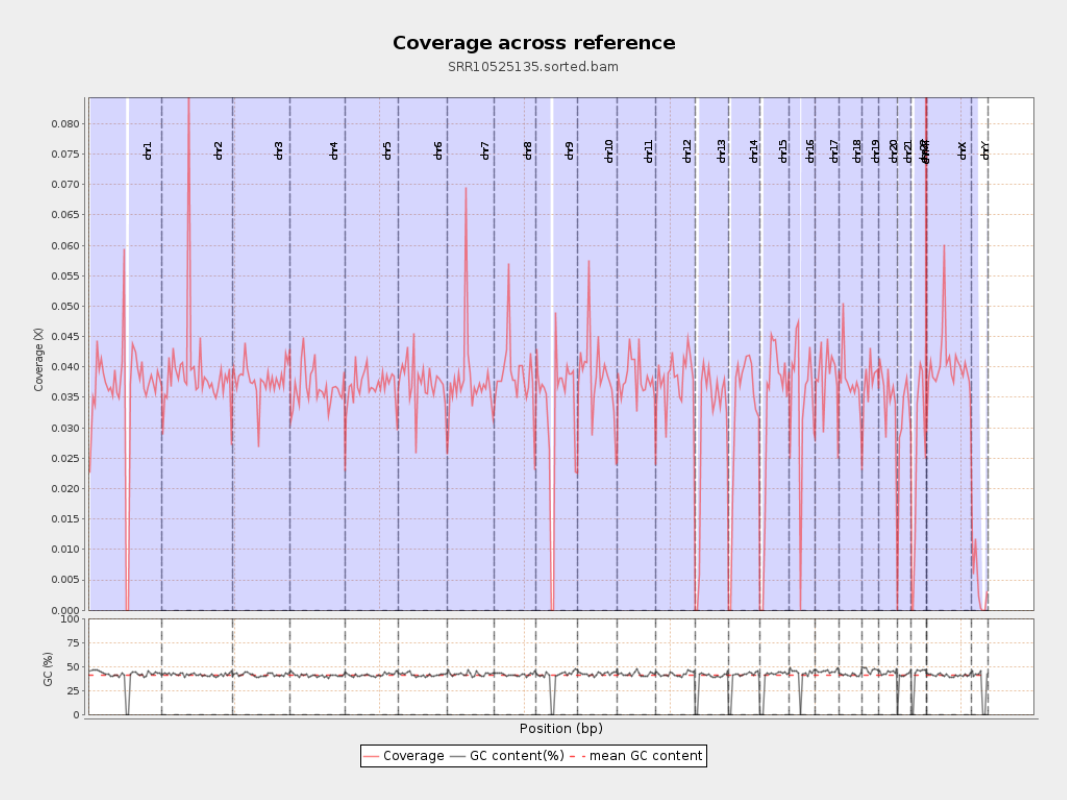
General error rate	0.76%
Mismatches	819,938
Insertions	9,529
Mapped reads with at least one insertion	0.65%
Deletions	24,803
Mapped reads with at least one deletion	1.69%
Homopolymer indels	42.61%

2.6. Chromosome stats

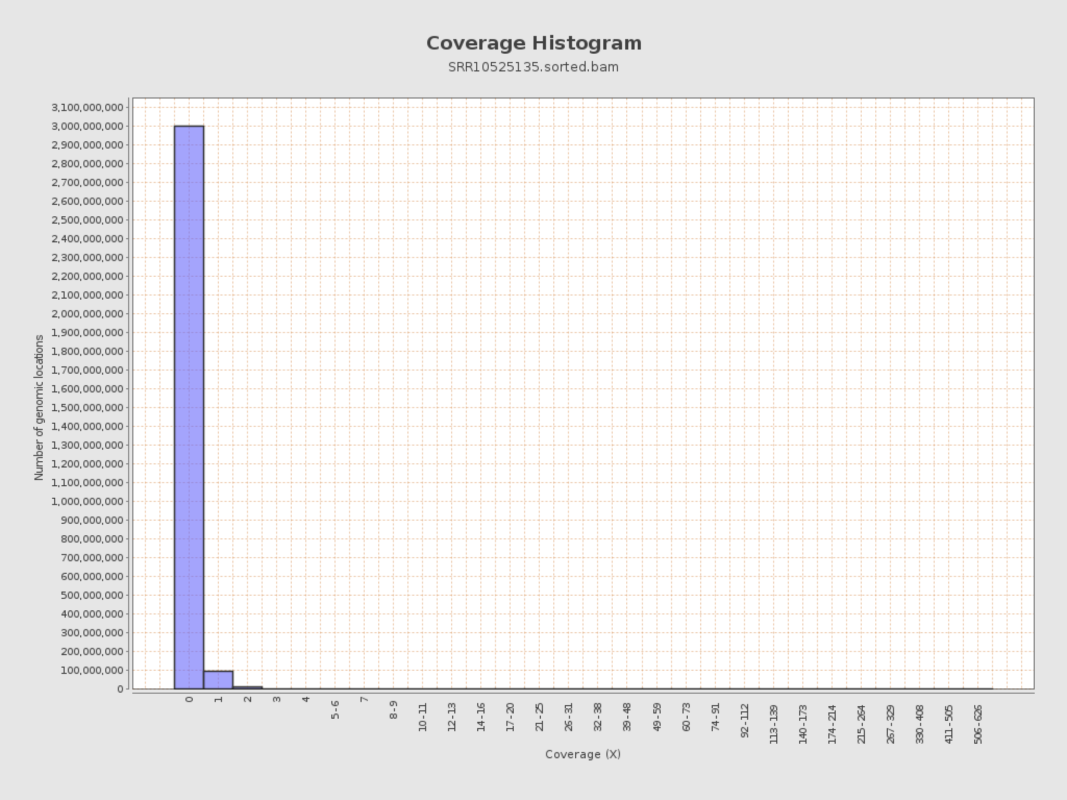
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8968748	0.036	0.4882
chr2	243199373	9567056	0.0393	0.5315
chr3	198022430	7516834	0.038	0.2133
chr4	191154276	6992058	0.0366	0.2186
chr5	180915260	6678767	0.0369	0.2129
chr6	171115067	6386612	0.0373	0.2451
chr7	159138663	6080413	0.0382	0.5593

chr8	146364022	5629774	0.0385	0.4702
chr9	141213431	4619020	0.0327	0.3474
chr10	135534747	5240743	0.0387	0.3499
chr11	135006516	5115696	0.0379	0.3462
chr12	133851895	5094385	0.0381	0.2149
chr13	115169878	3477344	0.0302	0.1881
chr14	107349540	3429213	0.0319	0.2252
chr15	102531392	3307315	0.0323	0.1961
chr16	90354753	3150870	0.0349	0.2257
chr17	81195210	3112477	0.0383	0.2685
chr18	78077248	2961162	0.0379	0.6039
chr19	59128983	2219318	0.0375	0.3909
chr20	63025520	2226085	0.0353	0.2125
chr21	48129895	1425355	0.0296	0.2011
chr22	51304566	1249886	0.0244	0.1702
chrMT	16571	4479	0.2703	0.594
chrX	155270560	6267695	0.0404	0.2964
chrY	59373566	241611	0.0041	0.102

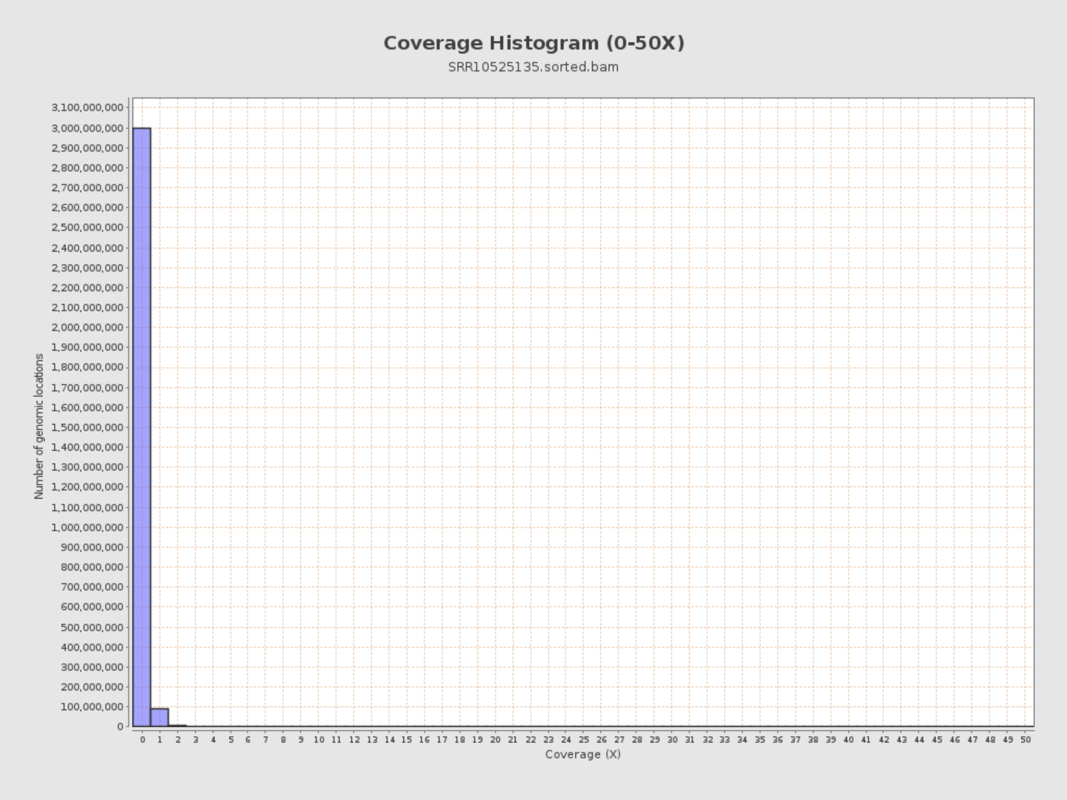
3. Results : Coverage across reference



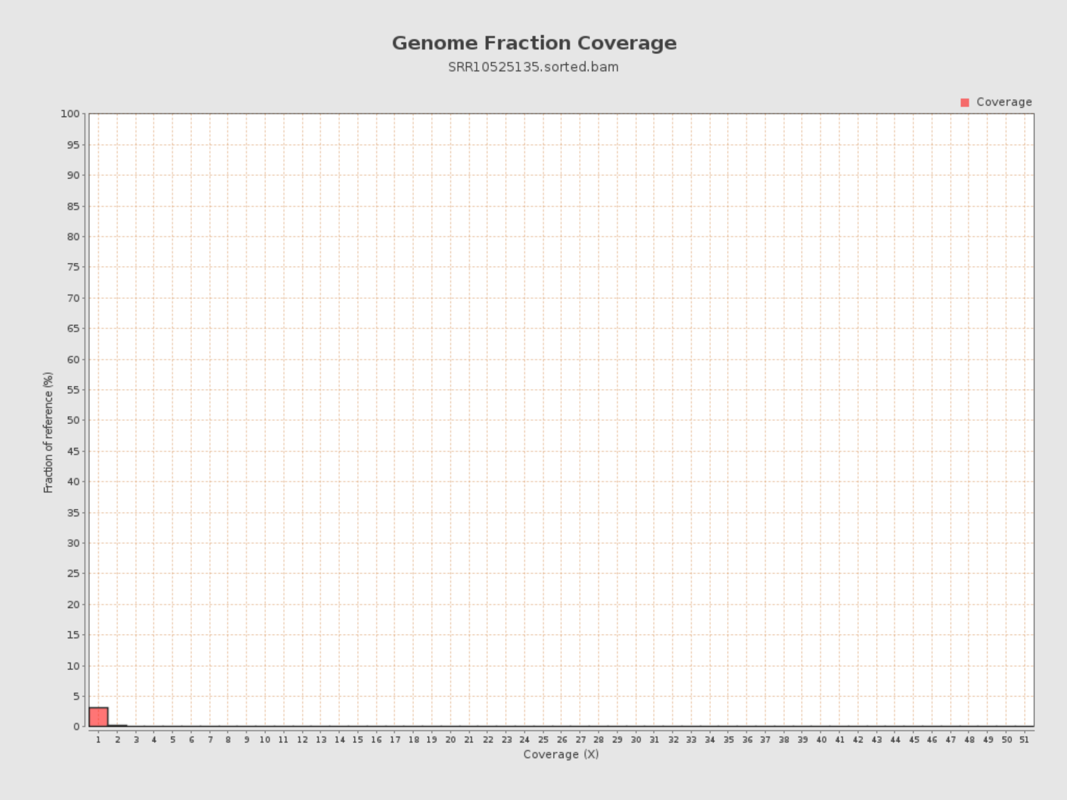
4. Results : Coverage Histogram



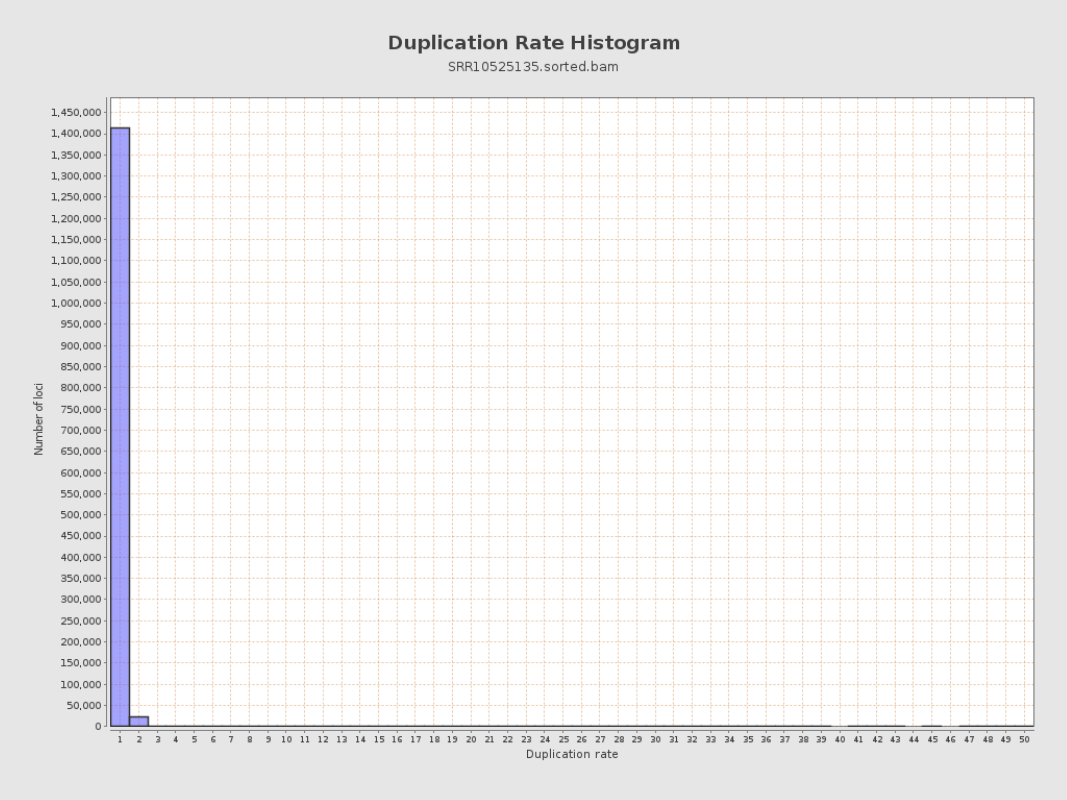
5. Results : Coverage Histogram (0-50X)



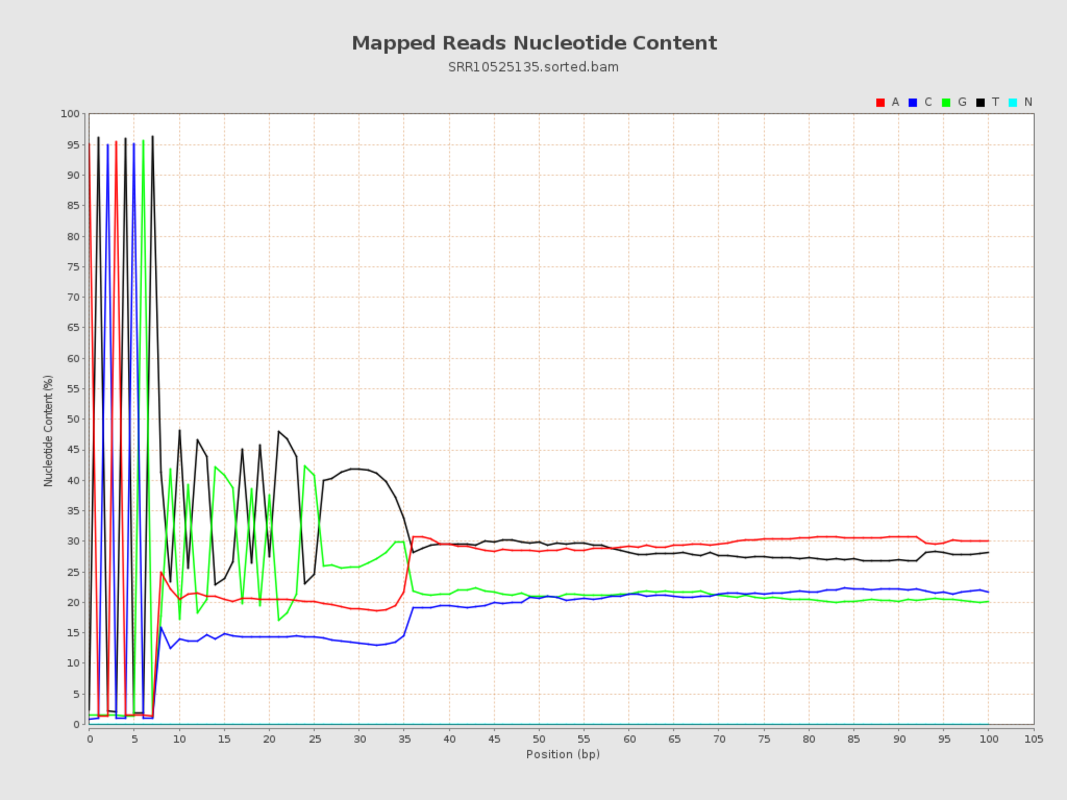
6. Results : Genome Fraction Coverage



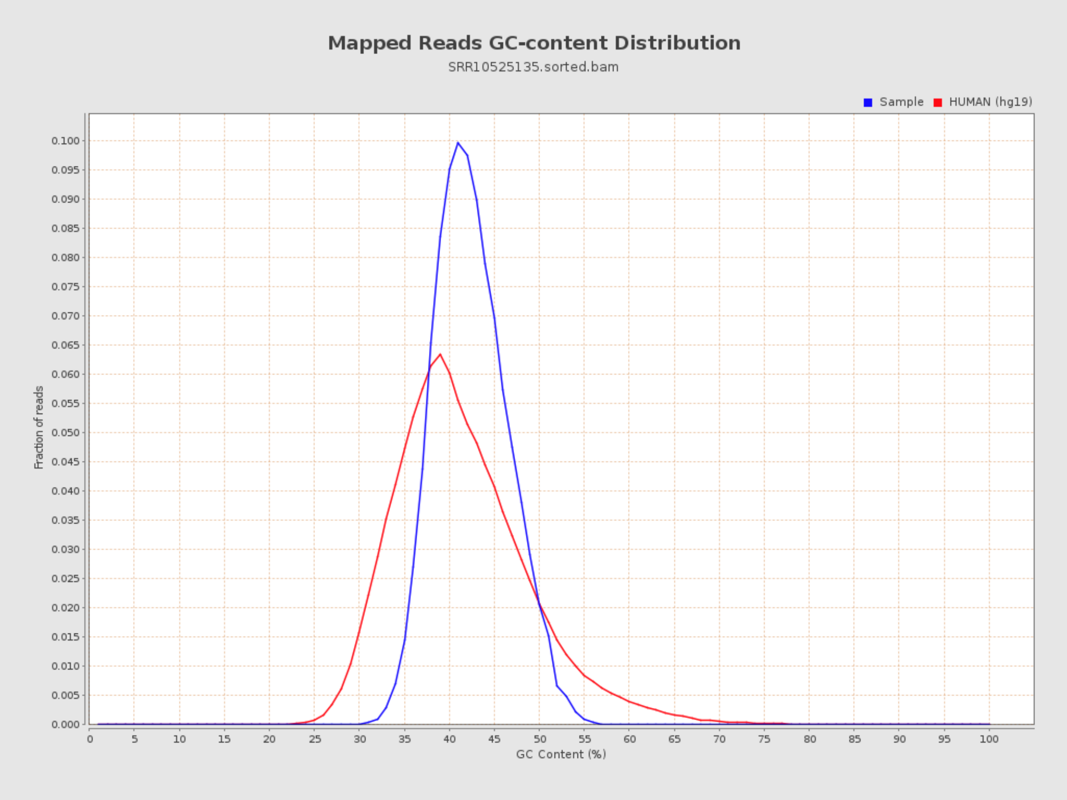
7. Results : Duplication Rate Histogram



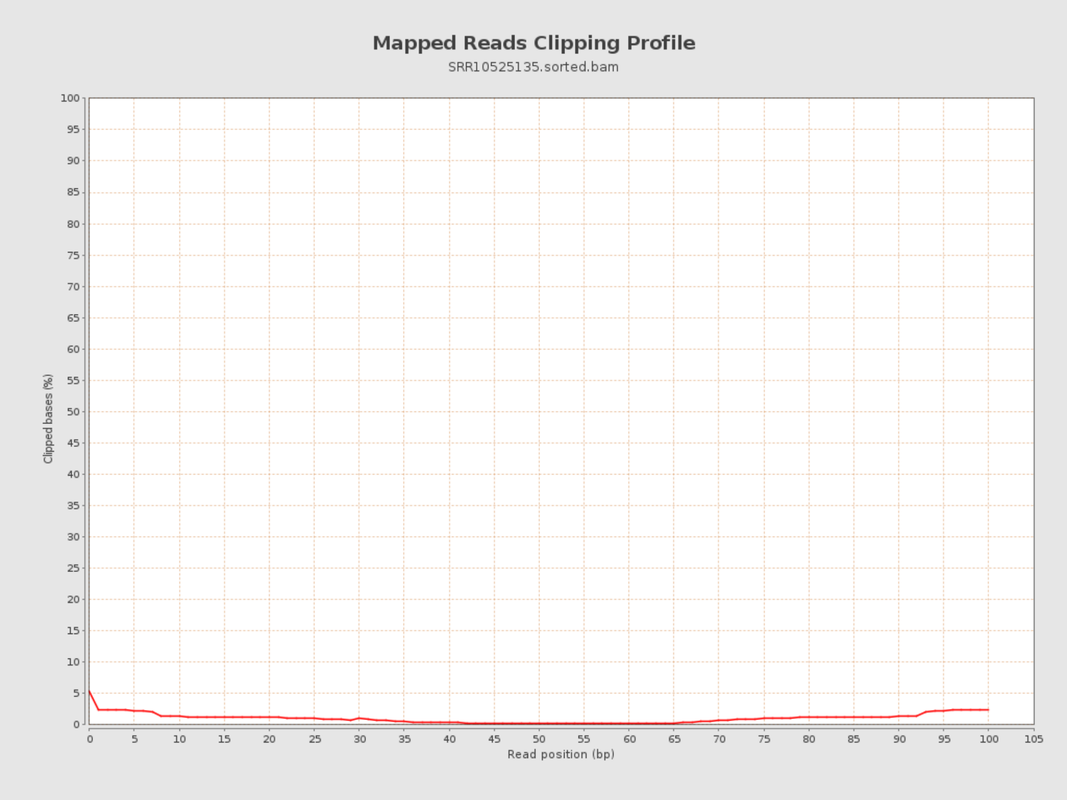
8. Results : Mapped Reads Nucleotide Content



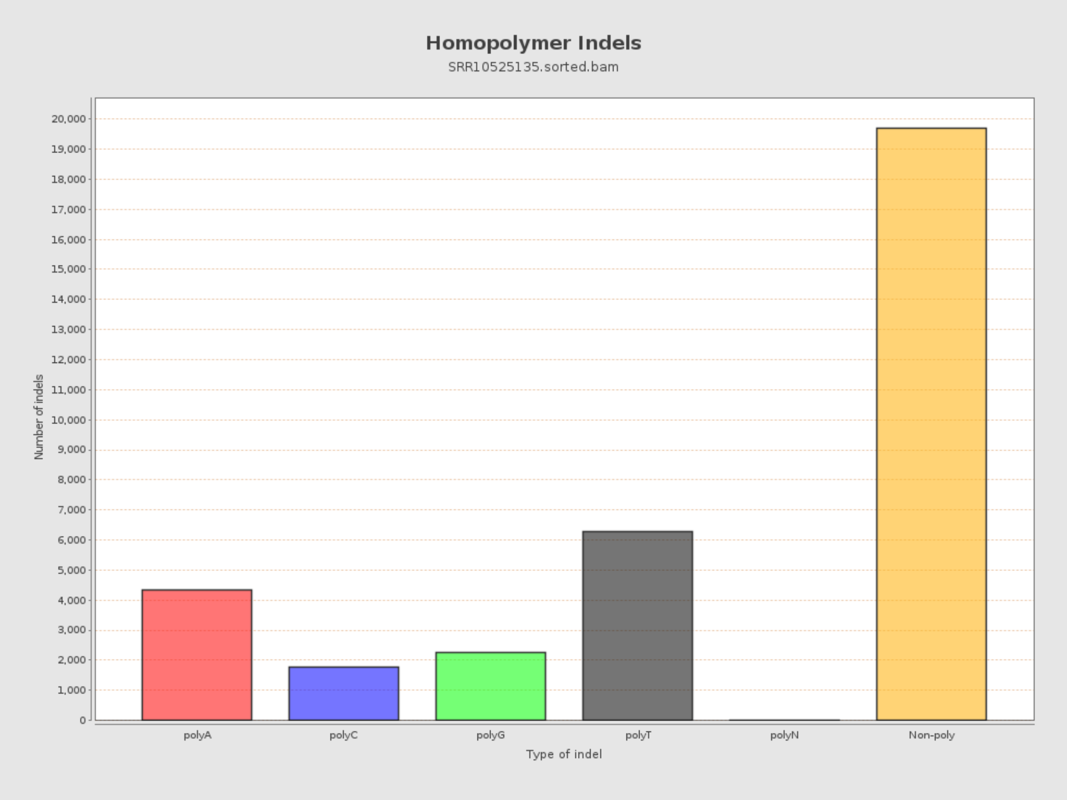
9. Results : Mapped Reads GC-content Distribution



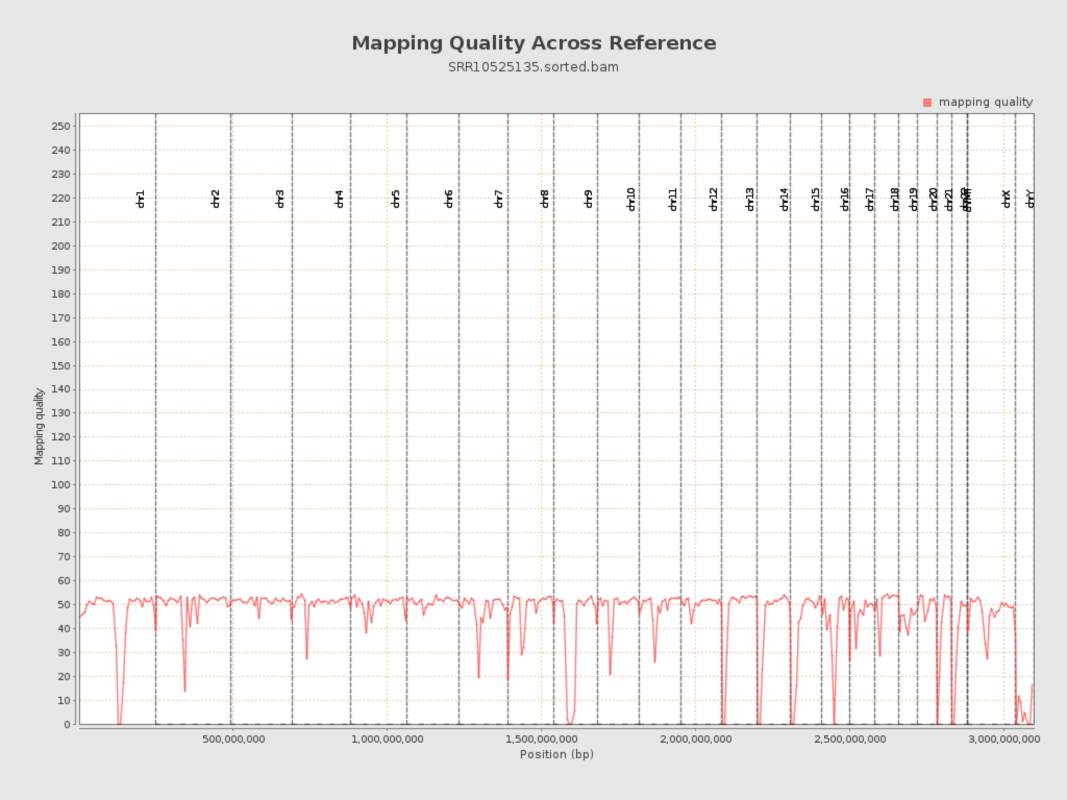
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram