Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:53:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525099.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_SRR10525099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:53:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,660,028
Mapped reads	1,531,682 / 92.27%
Unmapped reads	128,346 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,520 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	55,335 / 3.33%
Duplication rate	2.56%
Clipped reads	1,532,798 / 92.34%

2.2. ACGT Content

Number/percentage of A's	21,285,092 / 23.81%
Number/percentage of C's	15,994,545 / 17.89%
Number/percentage of T's	29,512,107 / 33.01%
Number/percentage of G's	22,597,675 / 25.28%
Number/percentage of N's	1,796 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2725

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

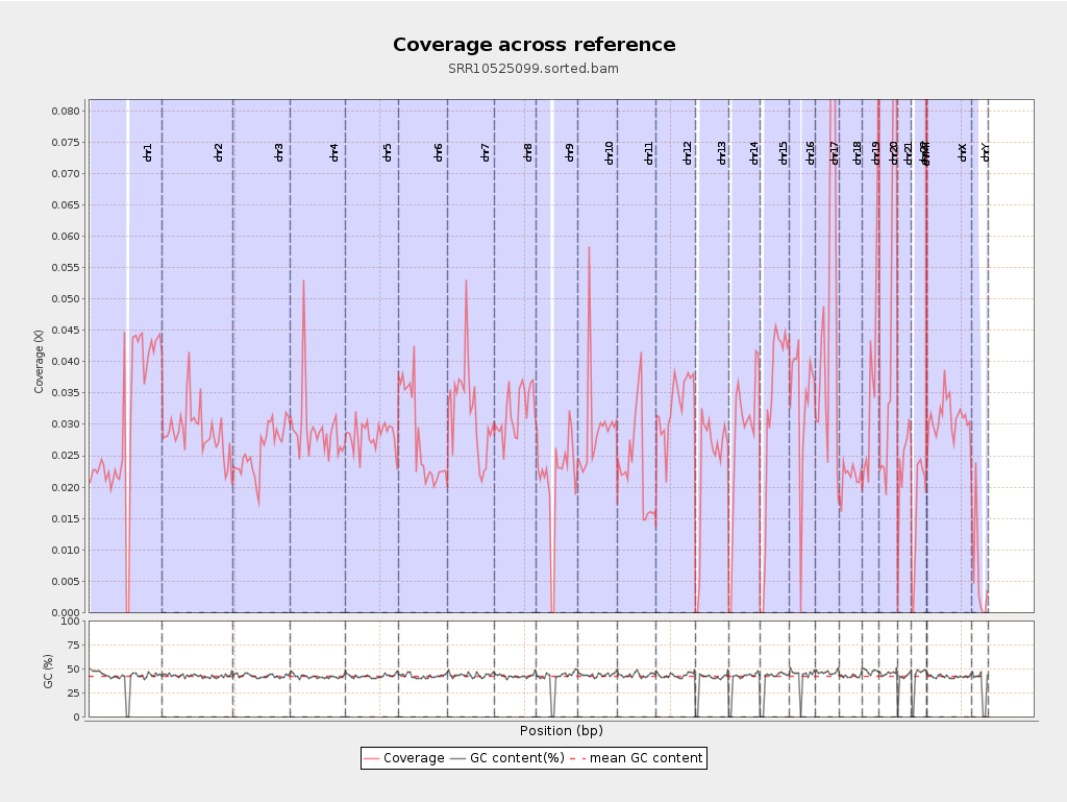
General error rate	0.52%
Mismatches	454,820
Insertions	6,824
Mapped reads with at least one insertion	0.44%
Deletions	17,517
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.29%

2.6. Chromosome stats

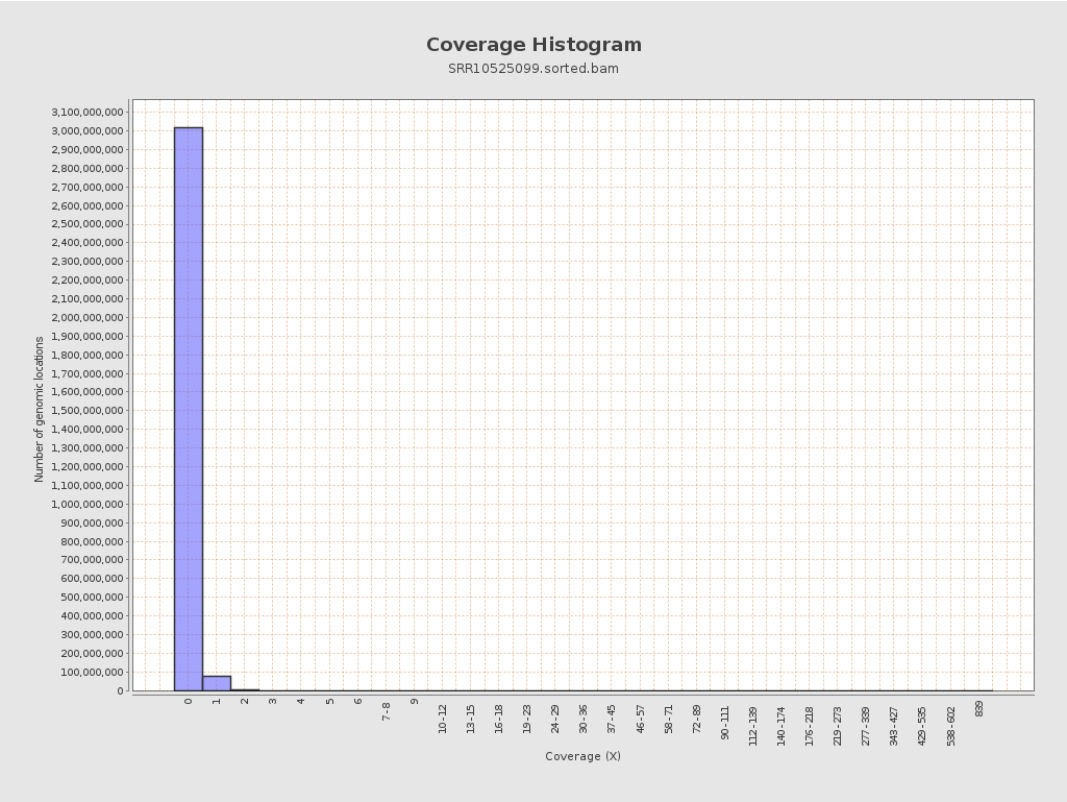
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7515691	0.0302	0.4321
chr2	243199373	7007623	0.0288	0.3878
chr3	198022430	5143308	0.026	0.1756
chr4	191154276	5540711	0.029	0.2204
chr5	180915260	5101145	0.0282	0.1818
chr6	171115067	4733308	0.0277	0.212
chr7	159138663	5101439	0.0321	0.3519

chr8	146364022	4688525	0.032	0.3413
chr9	141213431	2988485	0.0212	0.1942
chr10	135534747	3935217	0.029	0.2889
chr11	135006516	3166861	0.0235	0.2157
chr12	133851895	4450932	0.0333	0.1985
chr13	115169878	2704450	0.0235	0.1666
chr14	107349540	3014369	0.0281	0.185
chr15	102531392	3296277	0.0321	0.1964
chr16	90354753	3068540	0.034	0.2104
chr17	81195210	3914335	0.0482	0.2486
chr18	78077248	1681197	0.0215	0.3209
chr19	59128983	2307005	0.039	0.3472
chr20	63025520	2941483	0.0467	0.2441
chr21	48129895	1132286	0.0235	0.2089
chr22	51304566	830324	0.0162	0.138
chrMT	16571	13740	0.8292	0.9646
chrX	155270560	4808260	0.031	0.2064
chrY	59373566	333996	0.0056	0.2609

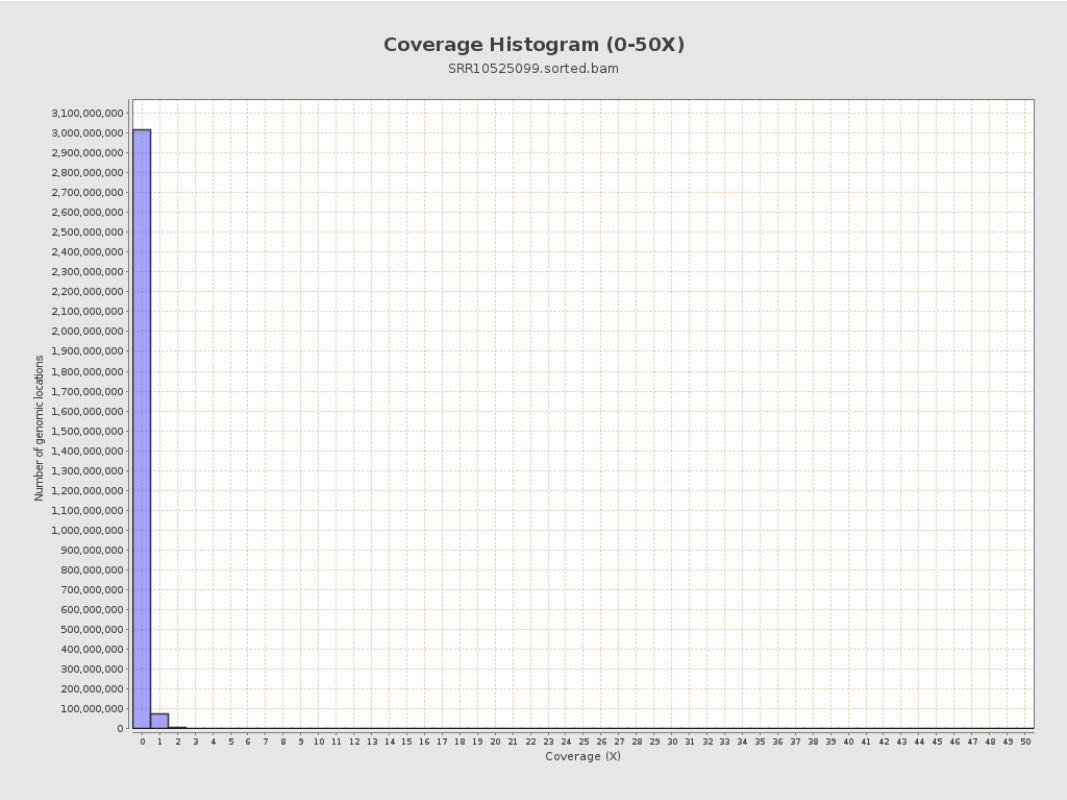
3. Results : Coverage across reference



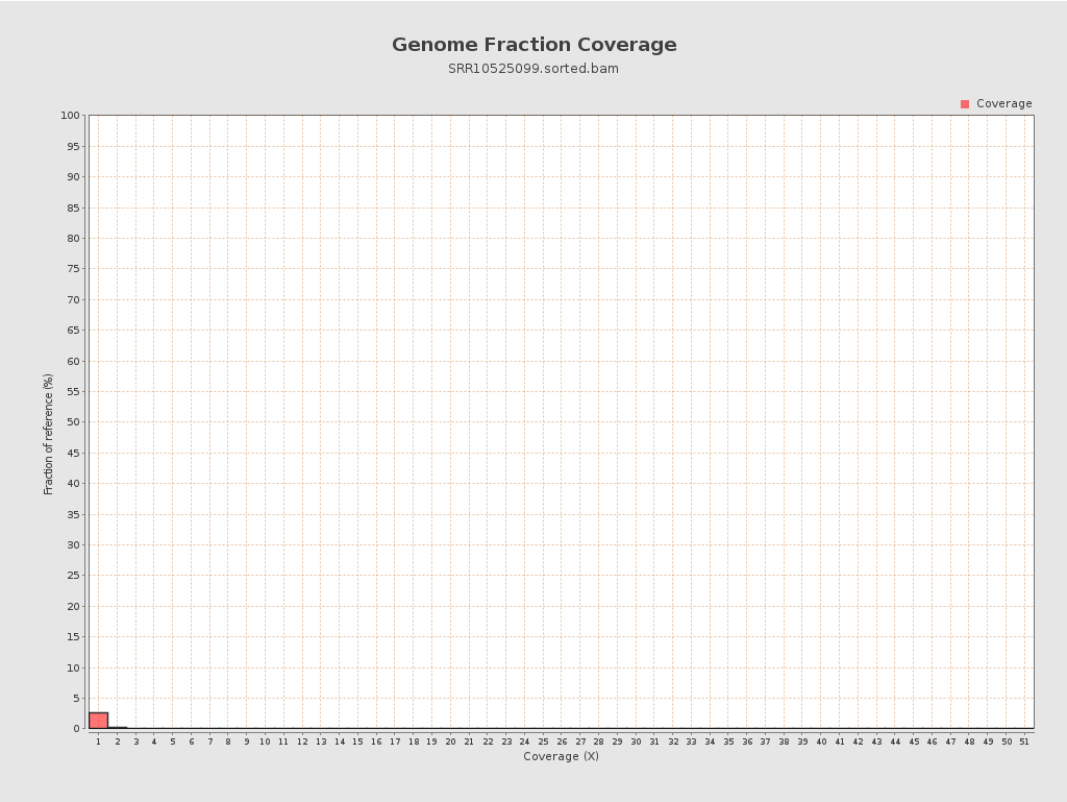
4. Results : Coverage Histogram



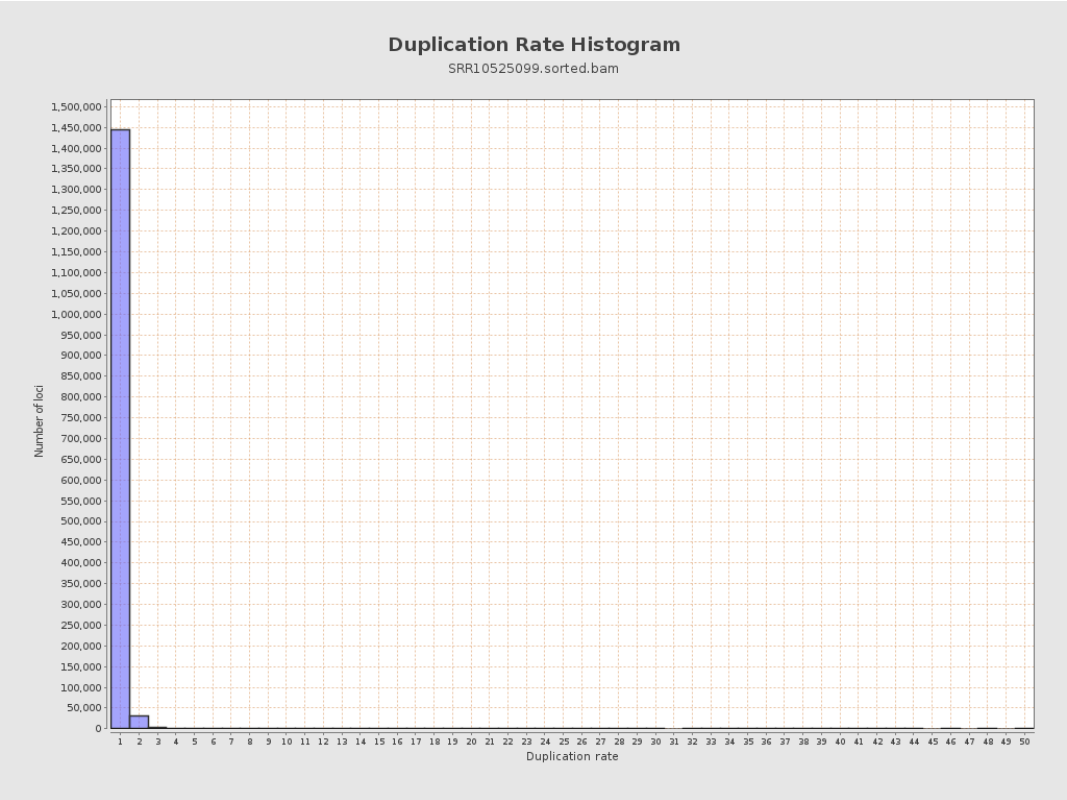
5. Results : Coverage Histogram (0-50X)



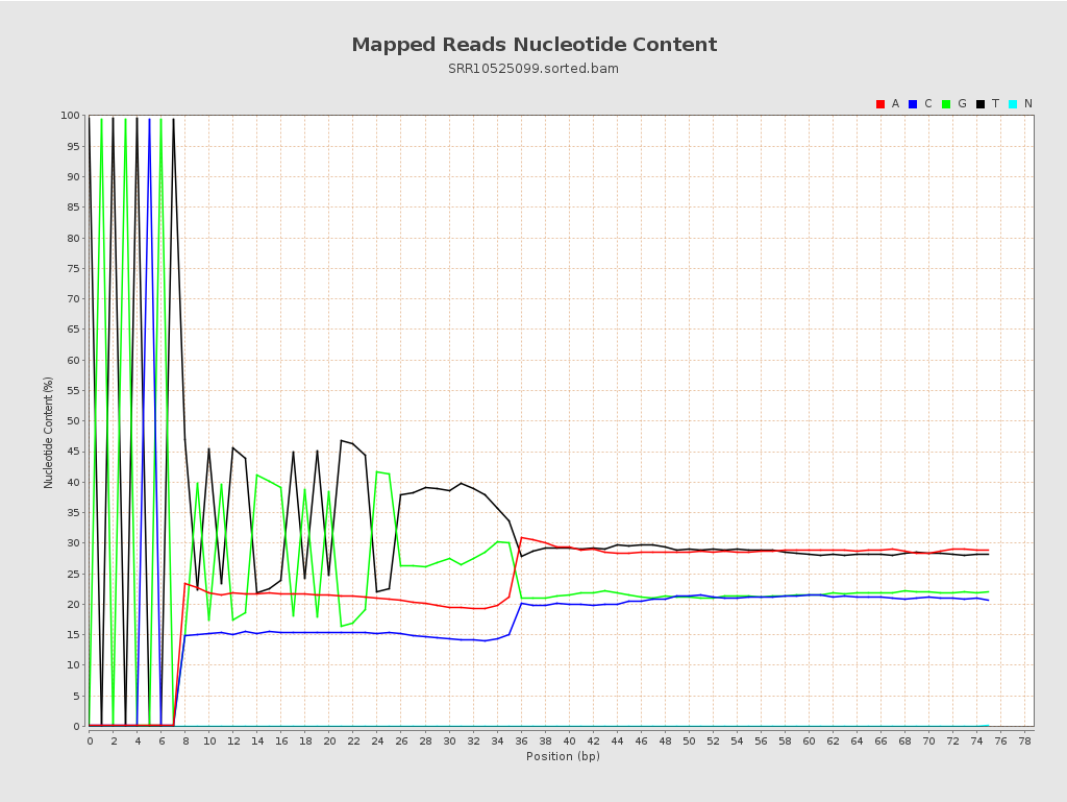
6. Results : Genome Fraction Coverage



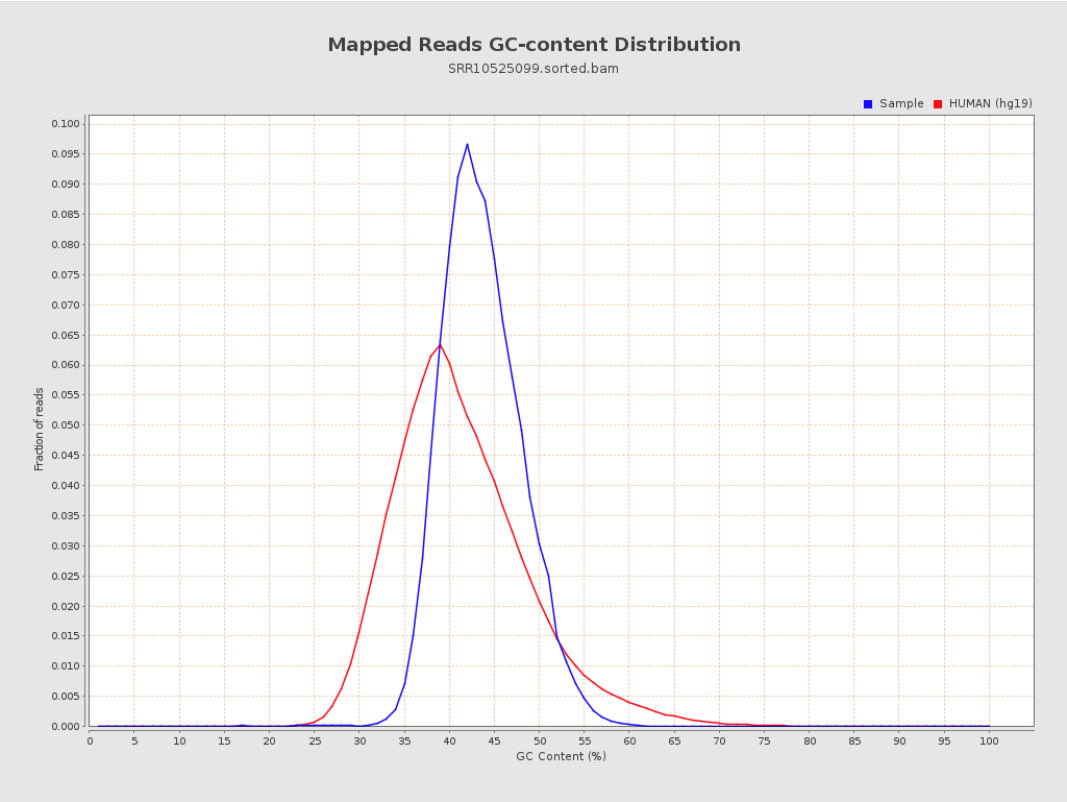
7. Results : Duplication Rate Histogram



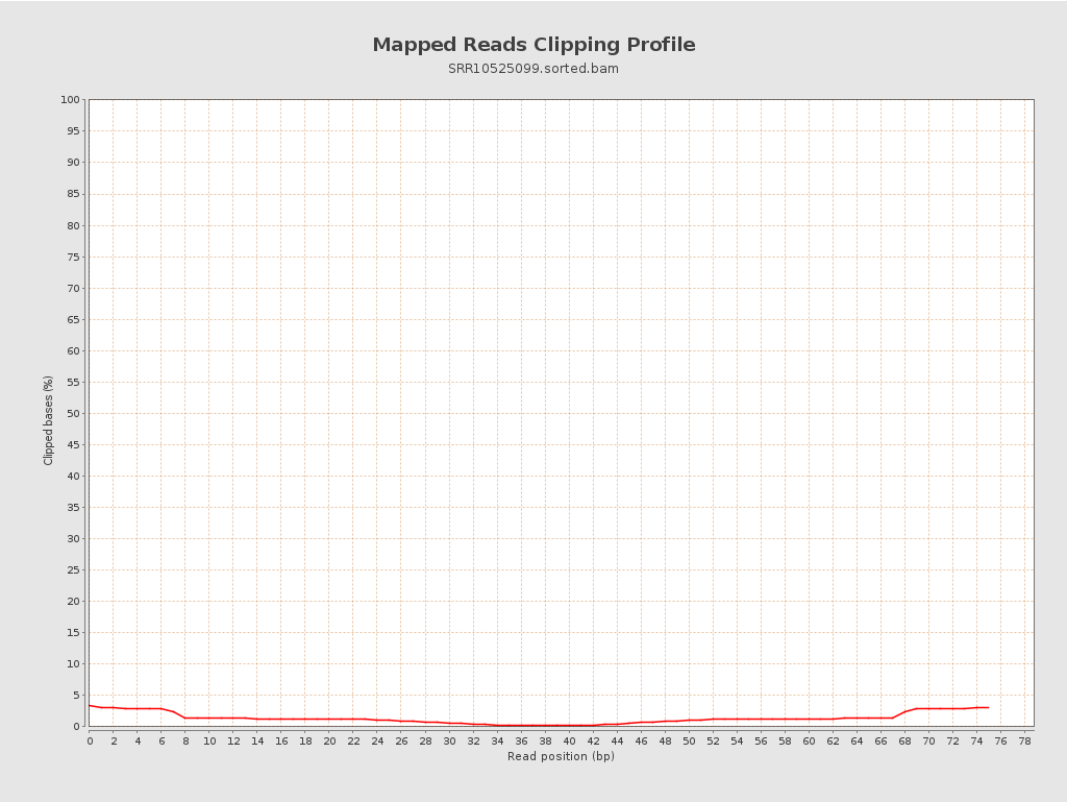
8. Results : Mapped Reads Nucleotide Content



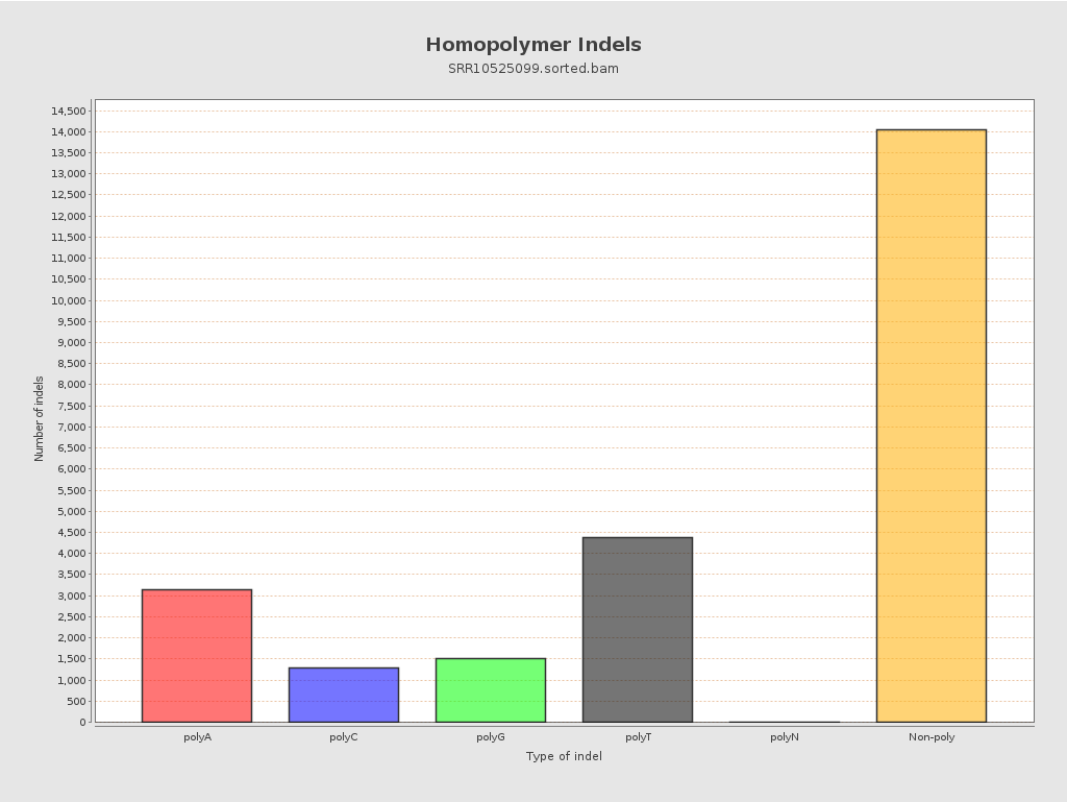
9. Results : Mapped Reads GC-content Distribution



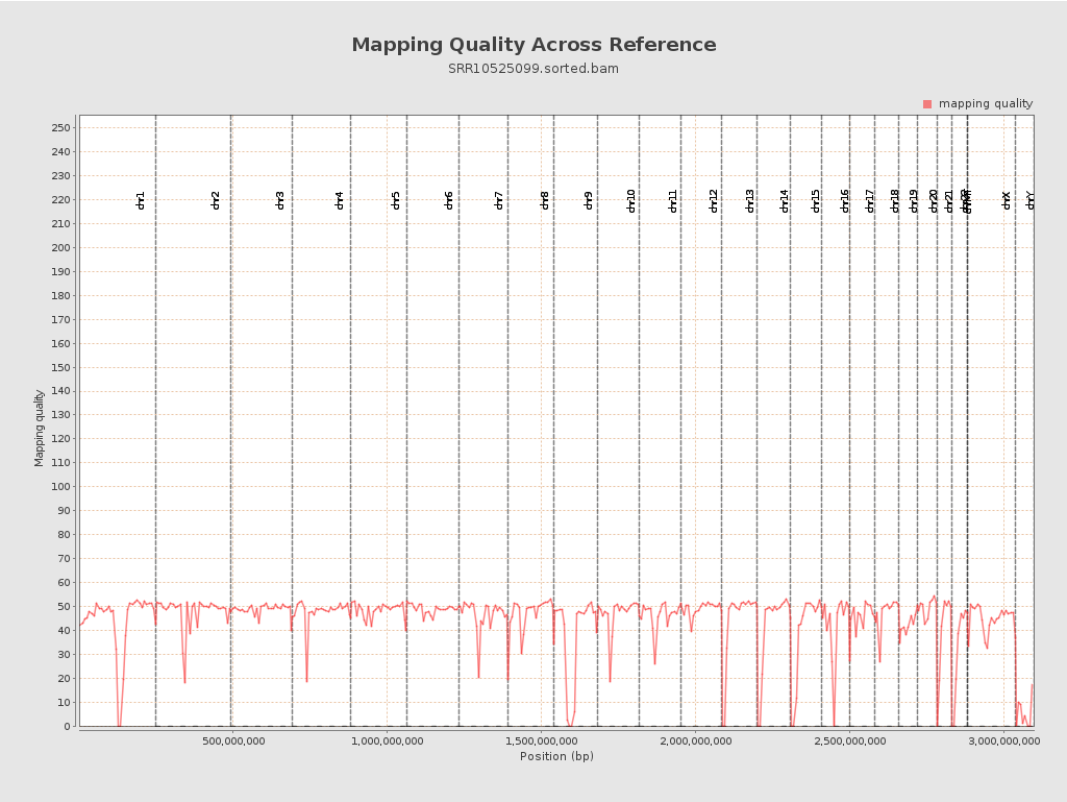
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram