Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:04:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525086.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_SRR10525086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,332,471
Mapped reads	1,613,358 / 69.17%
Unmapped reads	719,113 / 30.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,778 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	83,365 / 3.57%
Duplication rate	4.12%
Clipped reads	1,614,903 / 69.24%

2.2. ACGT Content

Number/percentage of A's	24,454,105 / 26.23%
Number/percentage of C's	16,383,974 / 17.58%
Number/percentage of T's	29,374,055 / 31.51%
Number/percentage of G's	22,997,237 / 24.67%
Number/percentage of N's	8,832 / 0.01%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2766

2.4. Mapping Quality

Mean Mapping Quality	45.57

2.5. Mismatches and indels

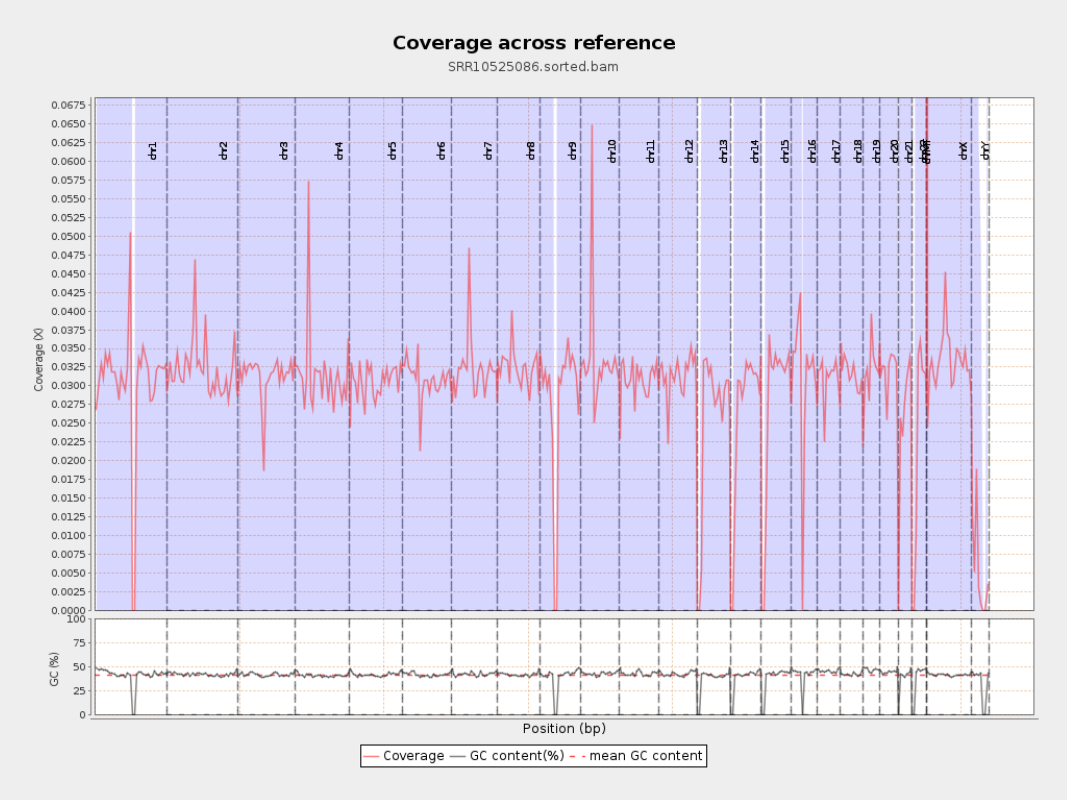
General error rate	0.49%
Mismatches	447,752
Insertions	6,524
Mapped reads with at least one insertion	0.4%
Deletions	17,503
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.19%

2.6. Chromosome stats

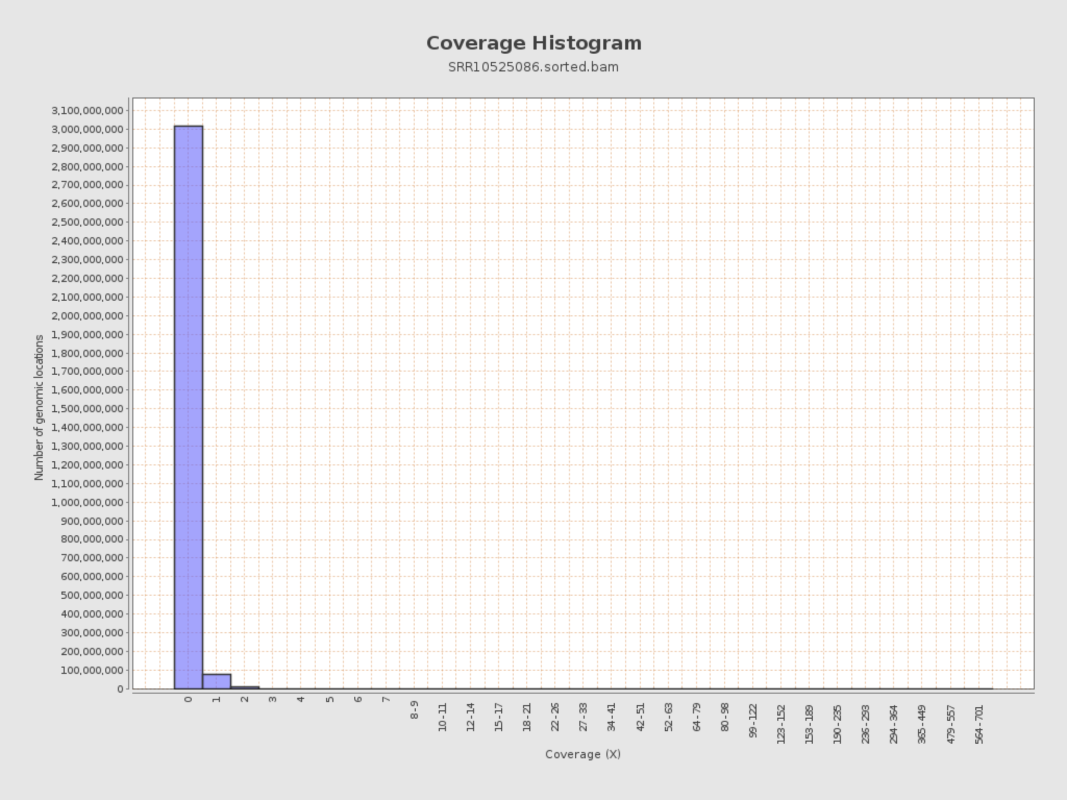
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7514474	0.0301	0.4977
chr2	243199373	7846520	0.0323	0.365
chr3	198022430	6176437	0.0312	0.1978
chr4	191154276	6031793	0.0316	0.2279
chr5	180915260	5565207	0.0308	0.1958
chr6	171115067	5281079	0.0309	0.2108
chr7	159138663	5149345	0.0324	0.3138

chr8	146364022	4740857	0.0324	0.2641
chr9	141213431	3936395	0.0279	0.2254
chr10	135534747	4559708	0.0336	0.3169
chr11	135006516	4185237	0.031	0.2296
chr12	133851895	4197482	0.0314	0.201
chr13	115169878	2898368	0.0252	0.1777
chr14	107349540	2780848	0.0259	0.1817
chr15	102531392	2782463	0.0271	0.1849
chr16	90354753	2755302	0.0305	0.2119
chr17	81195210	2514952	0.031	0.2031
chr18	78077248	2468431	0.0316	0.3531
chr19	59128983	1912913	0.0324	0.363
chr20	63025520	1999622	0.0317	0.2055
chr21	48129895	1251724	0.026	0.2041
chr22	51304566	1170002	0.0228	0.1676
chrMT	16571	20887	1.2605	1.3183
chrX	155270560	5197452	0.0335	0.2268
chrY	59373566	309212	0.0052	0.1609

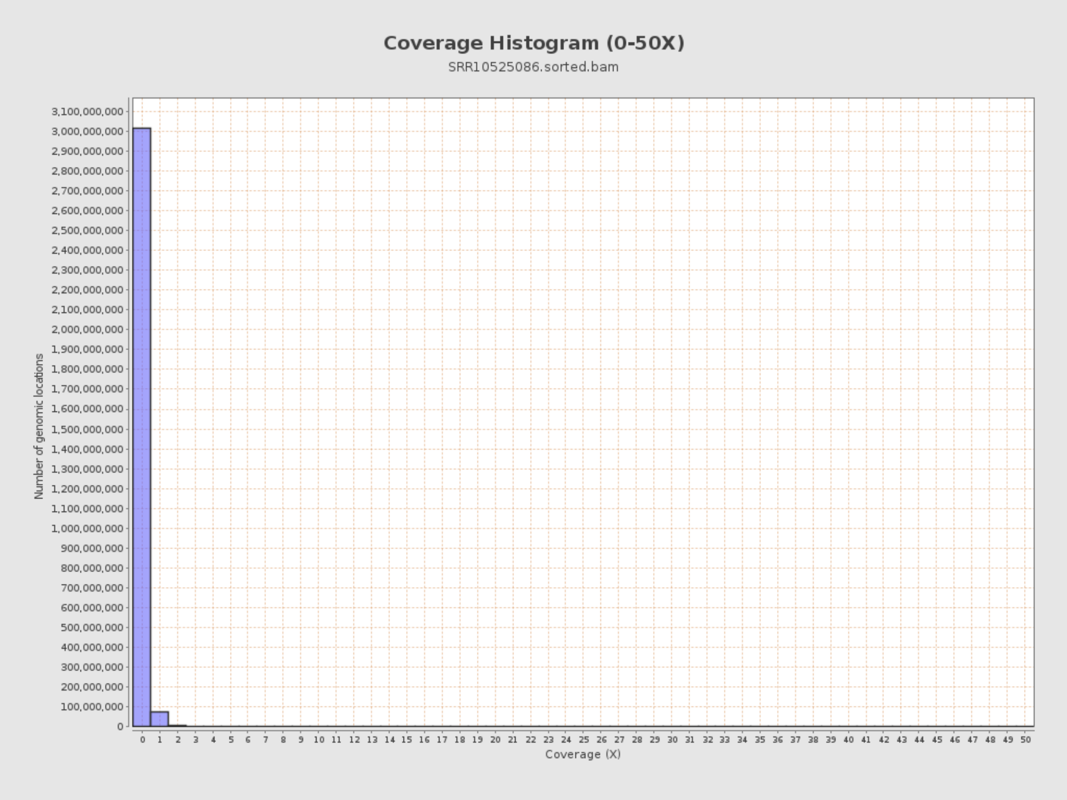
3. Results : Coverage across reference



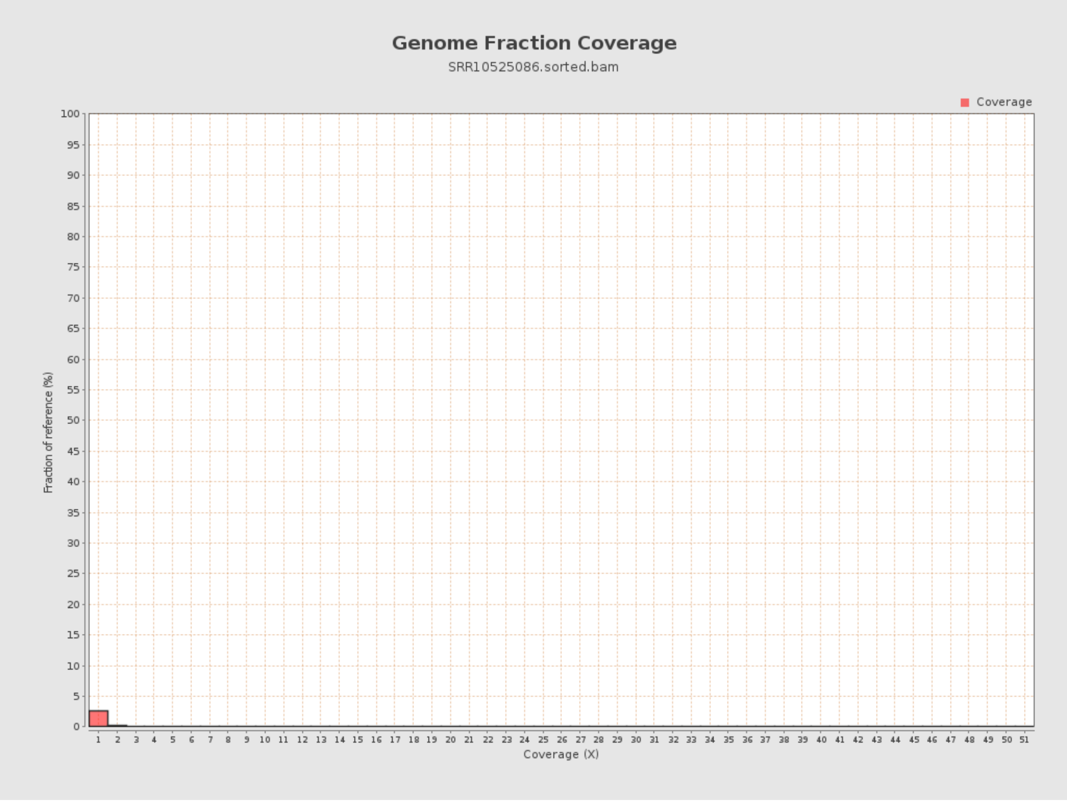
4. Results : Coverage Histogram



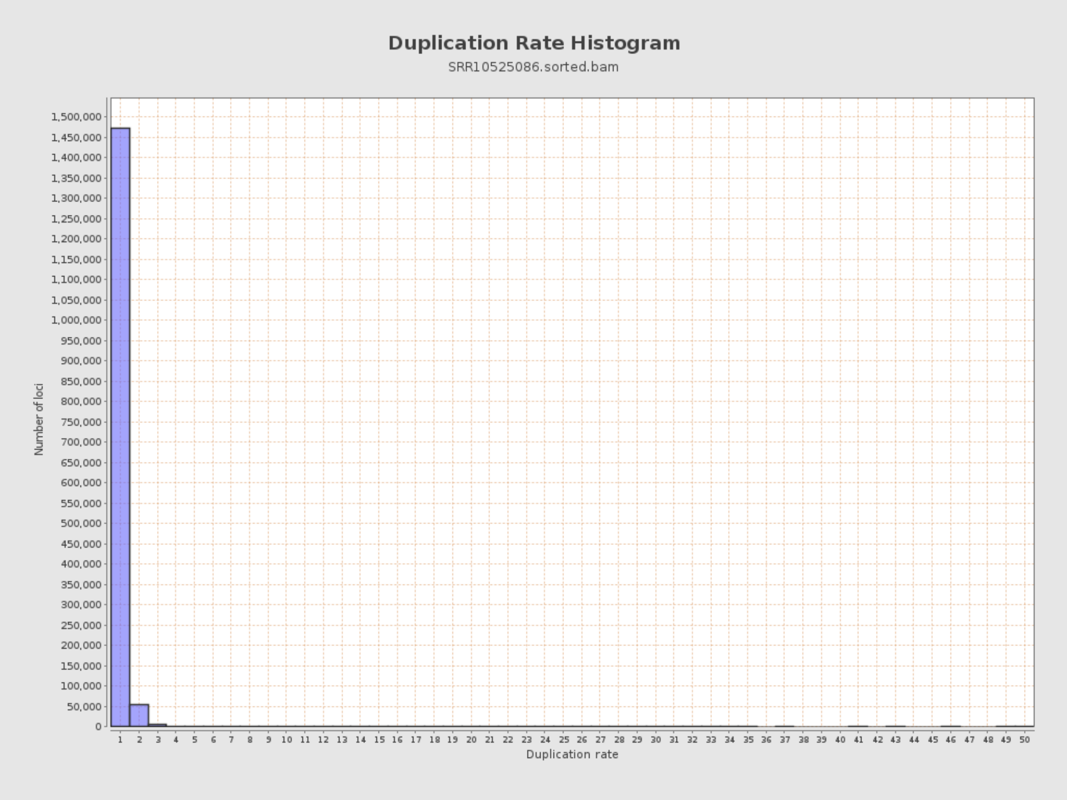
5. Results : Coverage Histogram (0-50X)



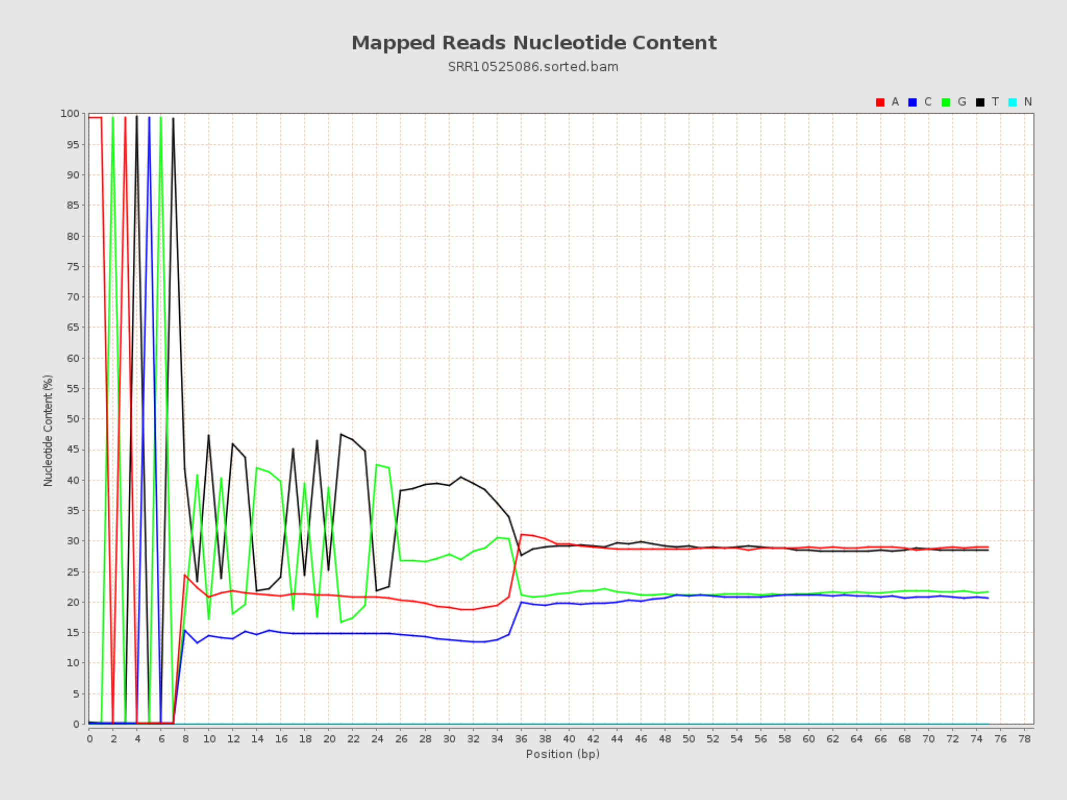
6. Results : Genome Fraction Coverage



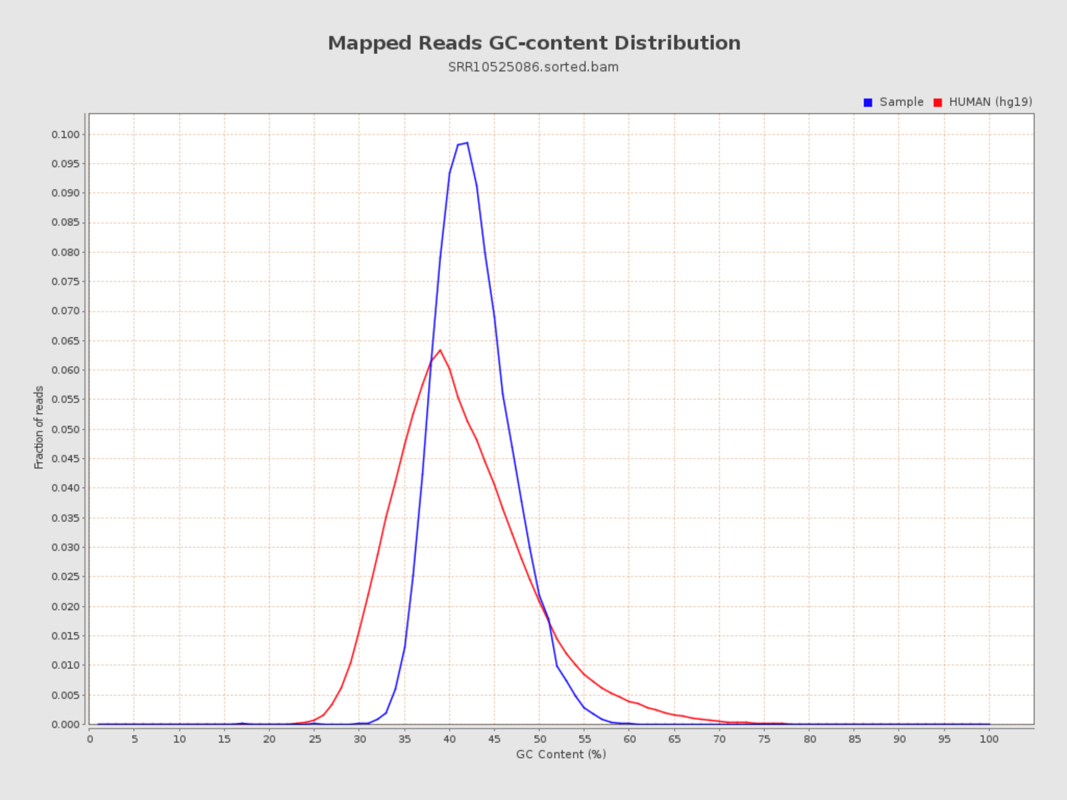
7. Results : Duplication Rate Histogram



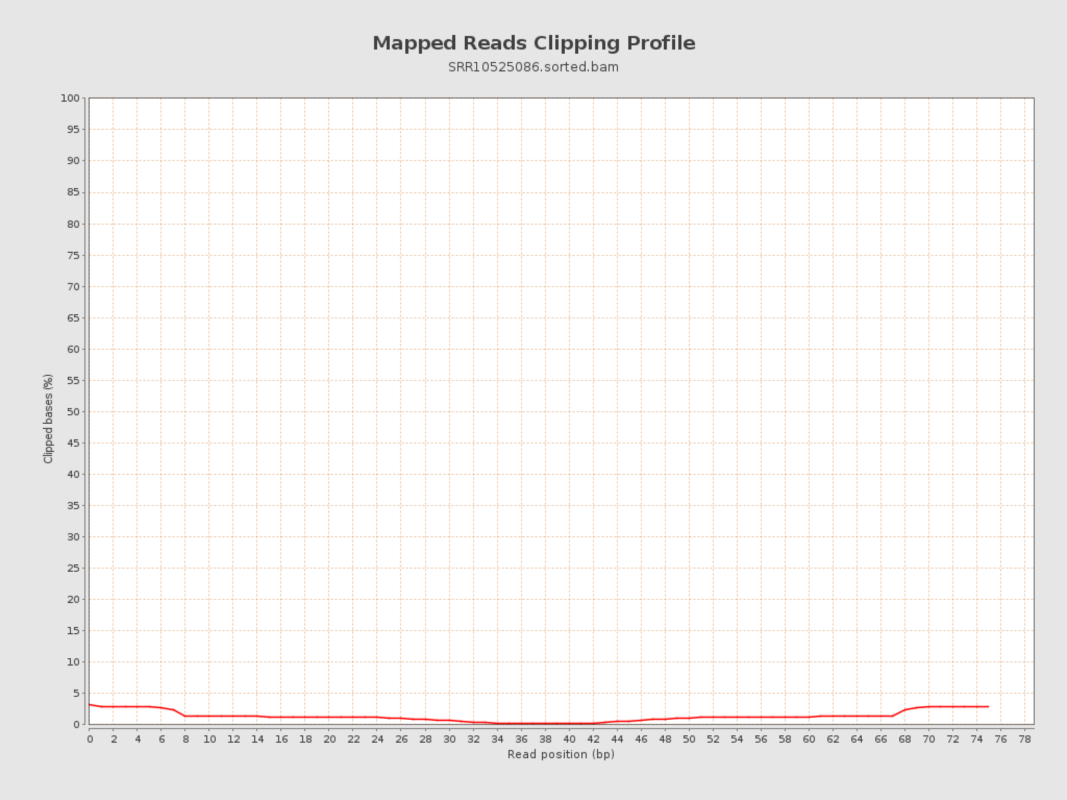
8. Results : Mapped Reads Nucleotide Content



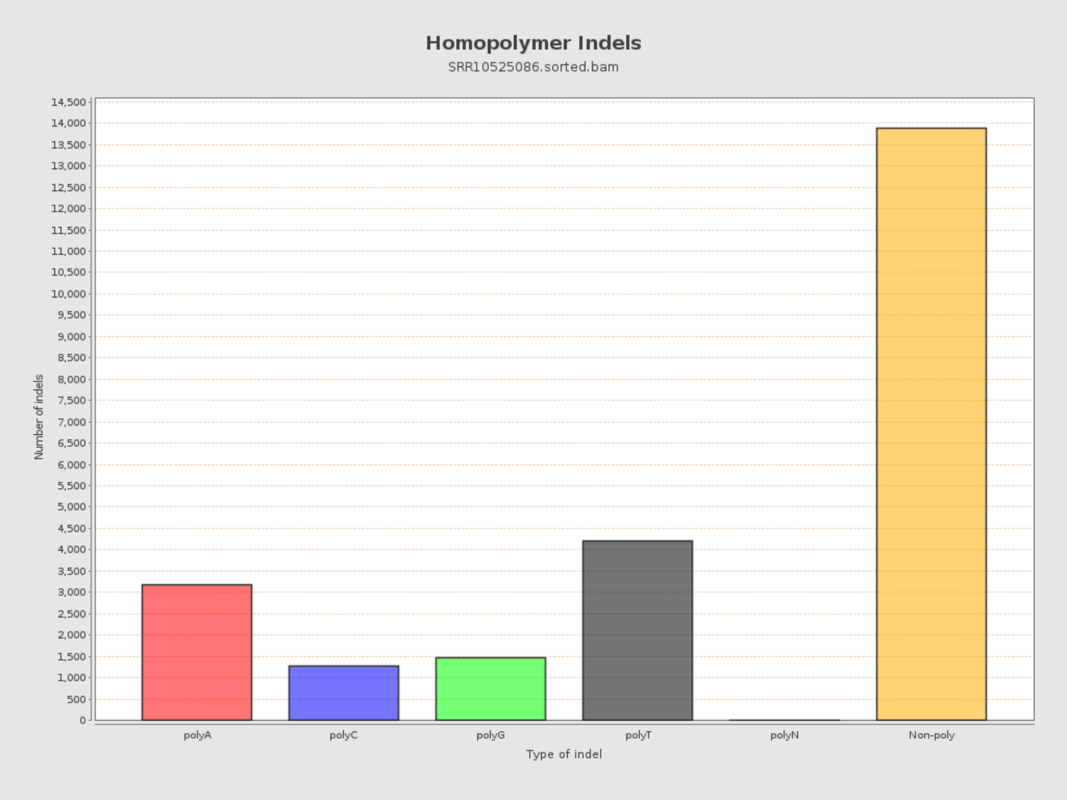
9. Results : Mapped Reads GC-content Distribution



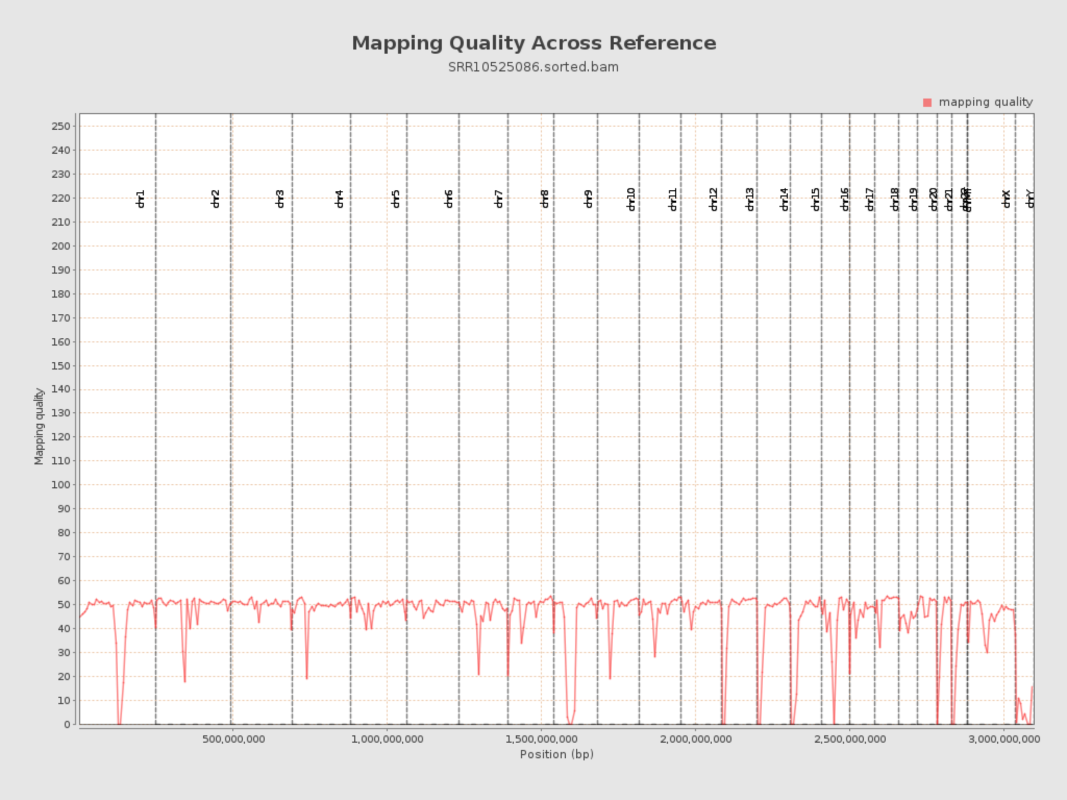
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram