Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:54:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525203.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_SRR10525203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:54:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,326,977
Mapped reads	2,157,695 / 92.73%
Unmapped reads	169,282 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,639 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	95,127 / 4.09%
Duplication rate	3.19%
Clipped reads	2,159,975 / 92.82%

2.2. ACGT Content

Number/percentage of A's	31,642,208 / 25.03%
Number/percentage of C's	24,672,394 / 19.51%
Number/percentage of T's	39,485,034 / 31.23%
Number/percentage of G's	30,632,398 / 24.23%
Number/percentage of N's	2,916 / 0%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.3803

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

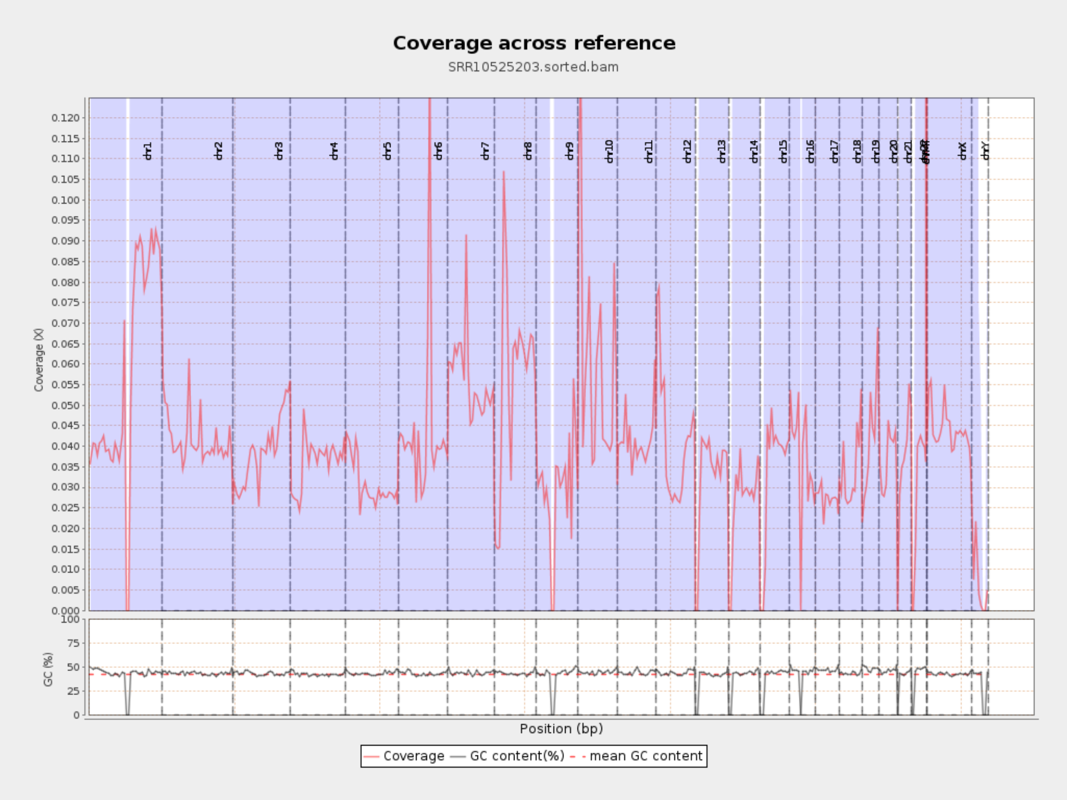
General error rate	0.52%
Mismatches	644,245
Insertions	8,906
Mapped reads with at least one insertion	0.41%
Deletions	26,804
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.57%

2.6. Chromosome stats

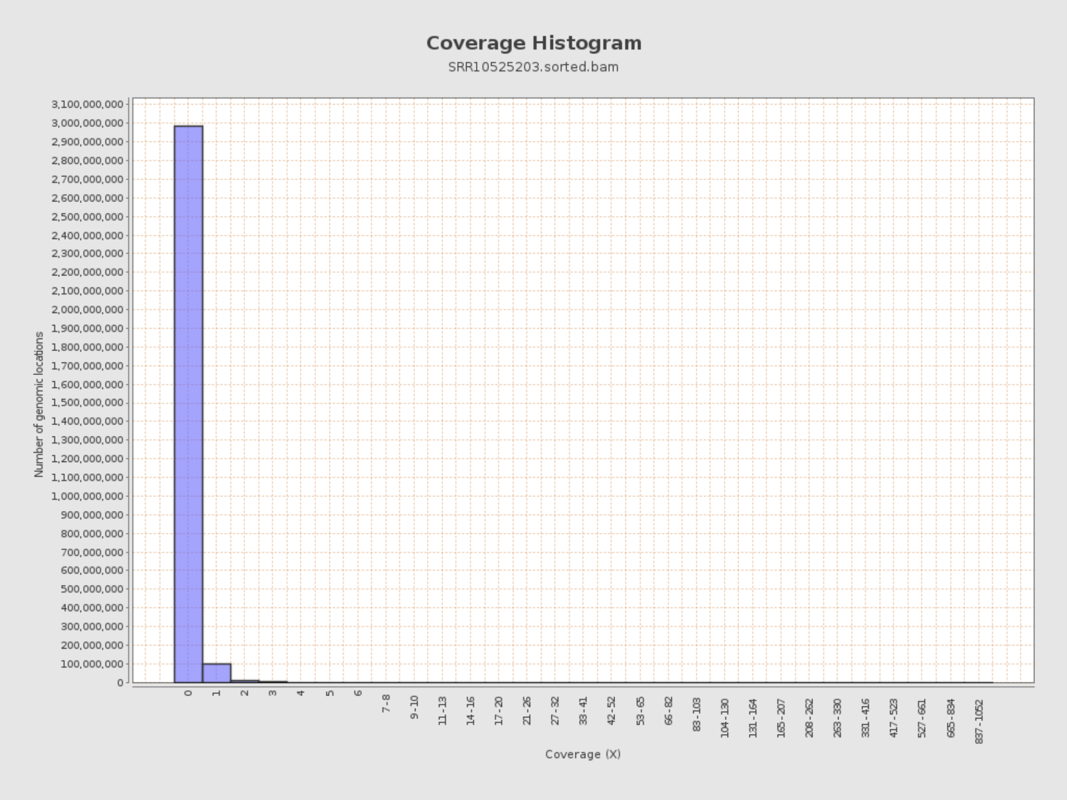
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14306723	0.0574	0.7078
chr2	243199373	10145158	0.0417	0.4945
chr3	198022430	7629602	0.0385	0.2192
chr4	191154276	6906387	0.0361	0.2323
chr5	180915260	5593949	0.0309	0.1957
chr6	171115067	7533663	0.044	0.2629
chr7	159138663	9042720	0.0568	0.6773

chr8	146364022	8194438	0.056	0.384
chr9	141213431	4131464	0.0293	0.2596
chr10	135534747	8304558	0.0613	0.3949
chr11	135006516	5602745	0.0415	0.2987
chr12	133851895	5529716	0.0413	0.2278
chr13	115169878	3770633	0.0327	0.2021
chr14	107349540	2830035	0.0264	0.1896
chr15	102531392	3425859	0.0334	0.2074
chr16	90354753	3307378	0.0366	0.2439
chr17	81195210	2207849	0.0272	0.1929
chr18	78077248	2655616	0.034	0.5513
chr19	59128983	2504769	0.0424	0.5041
chr20	63025520	2317010	0.0368	0.218
chr21	48129895	1766019	0.0367	0.2367
chr22	51304566	1444073	0.0281	0.1848
chrMT	16571	40797	2.462	2.113
chrX	155270560	6885758	0.0443	0.2558
chrY	59373566	401068	0.0068	0.1932

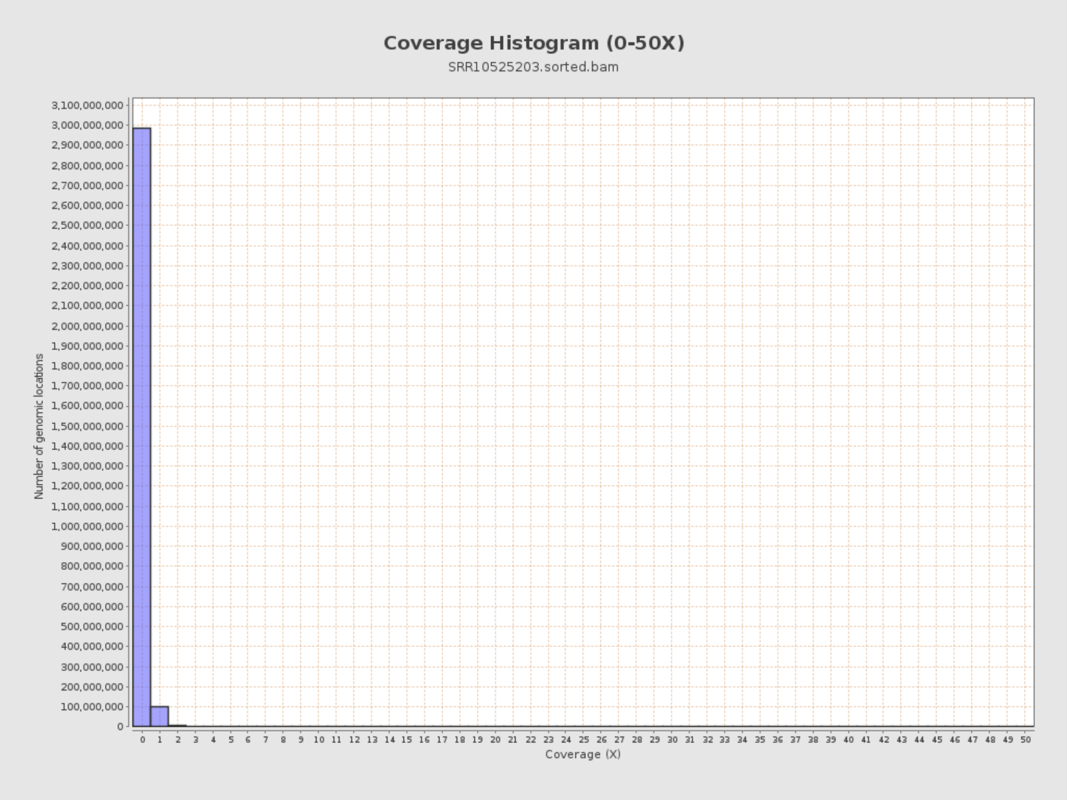
3. Results : Coverage across reference



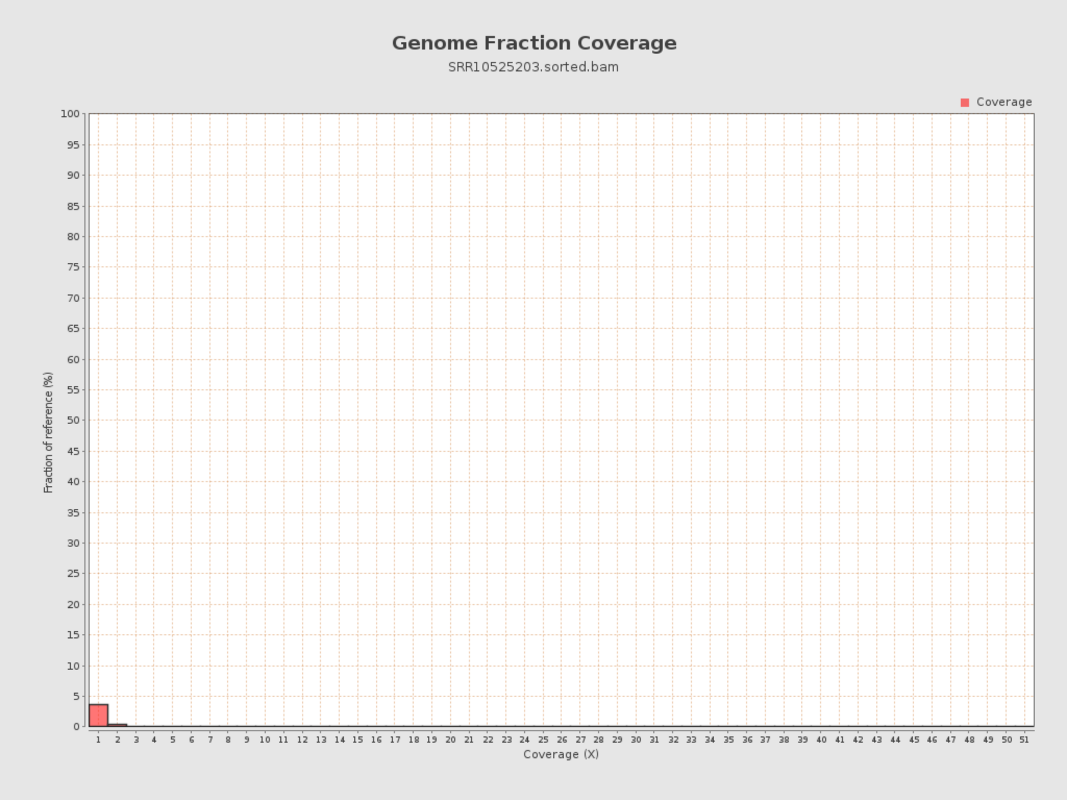
4. Results : Coverage Histogram



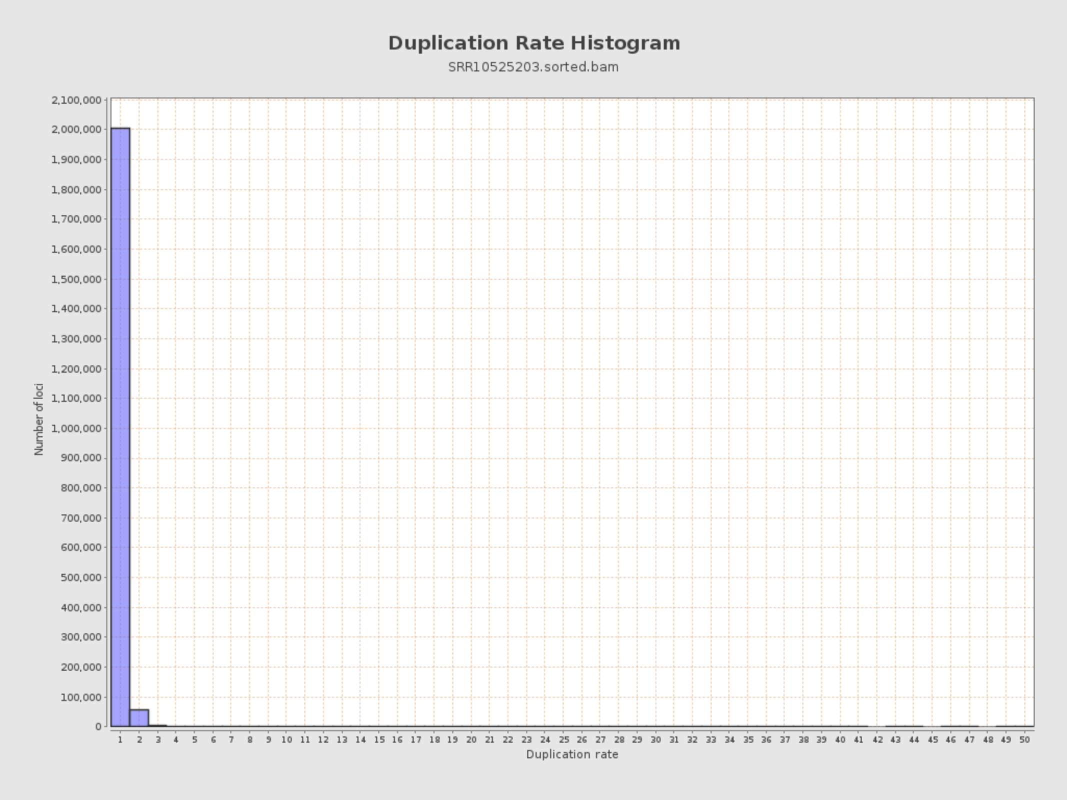
5. Results : Coverage Histogram (0-50X)



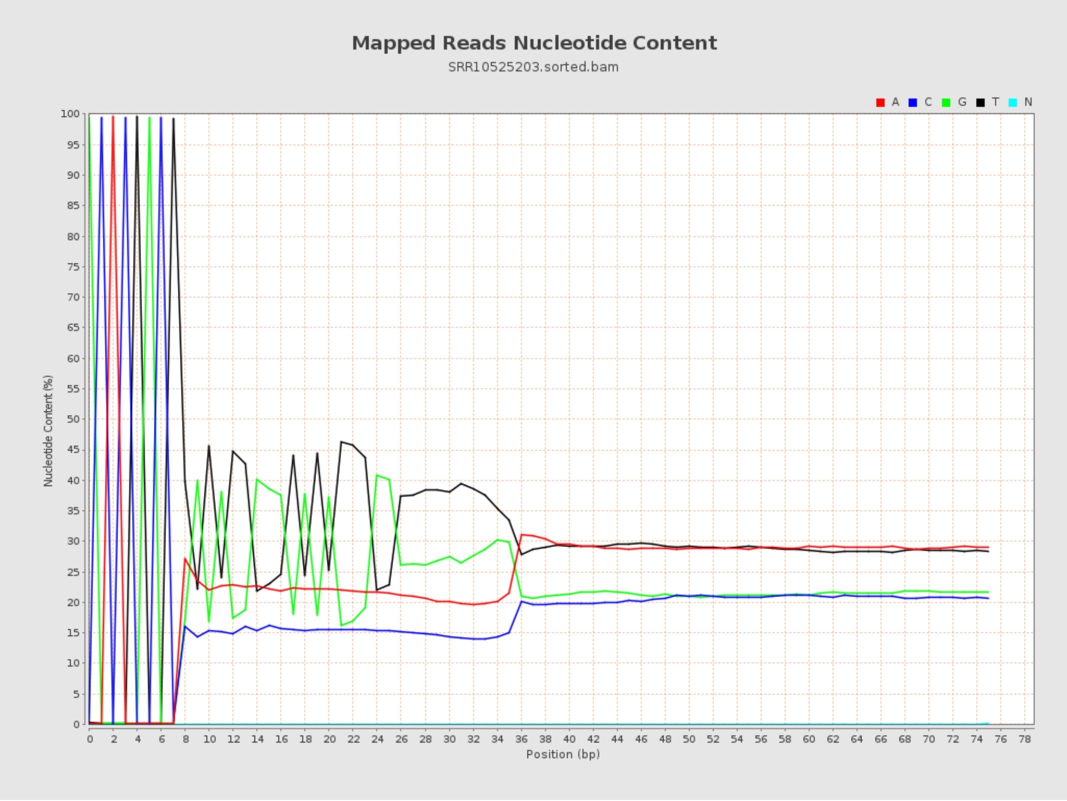
6. Results : Genome Fraction Coverage



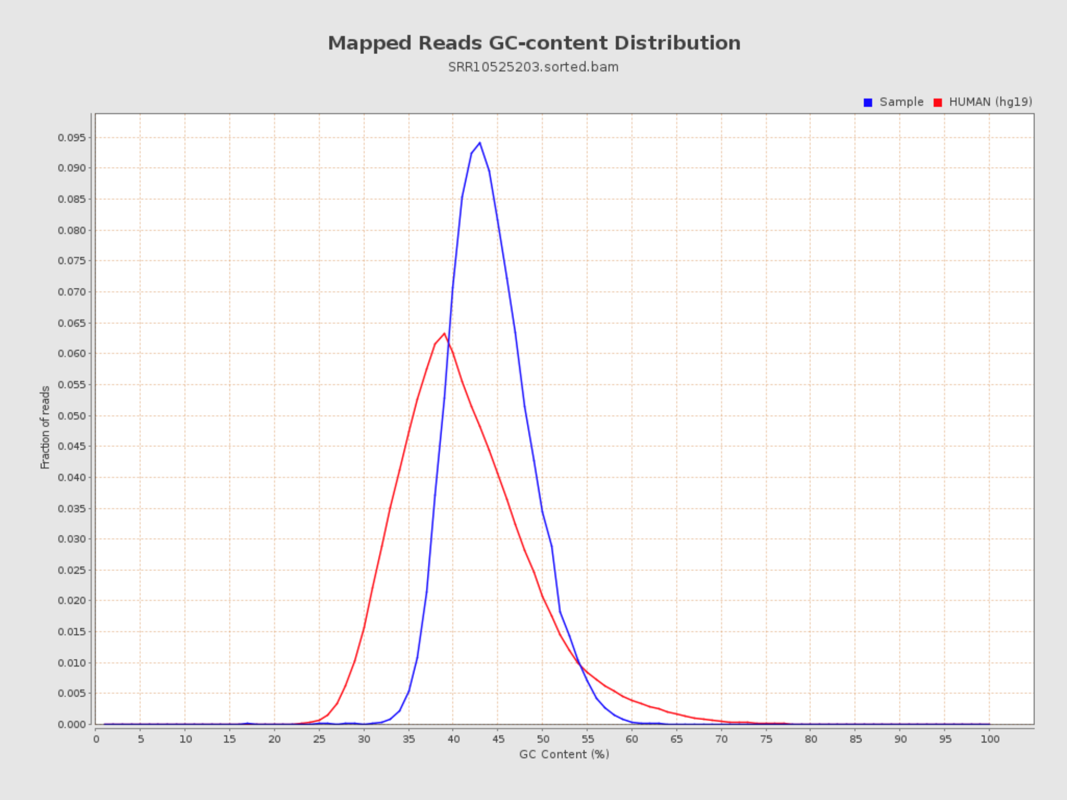
7. Results : Duplication Rate Histogram



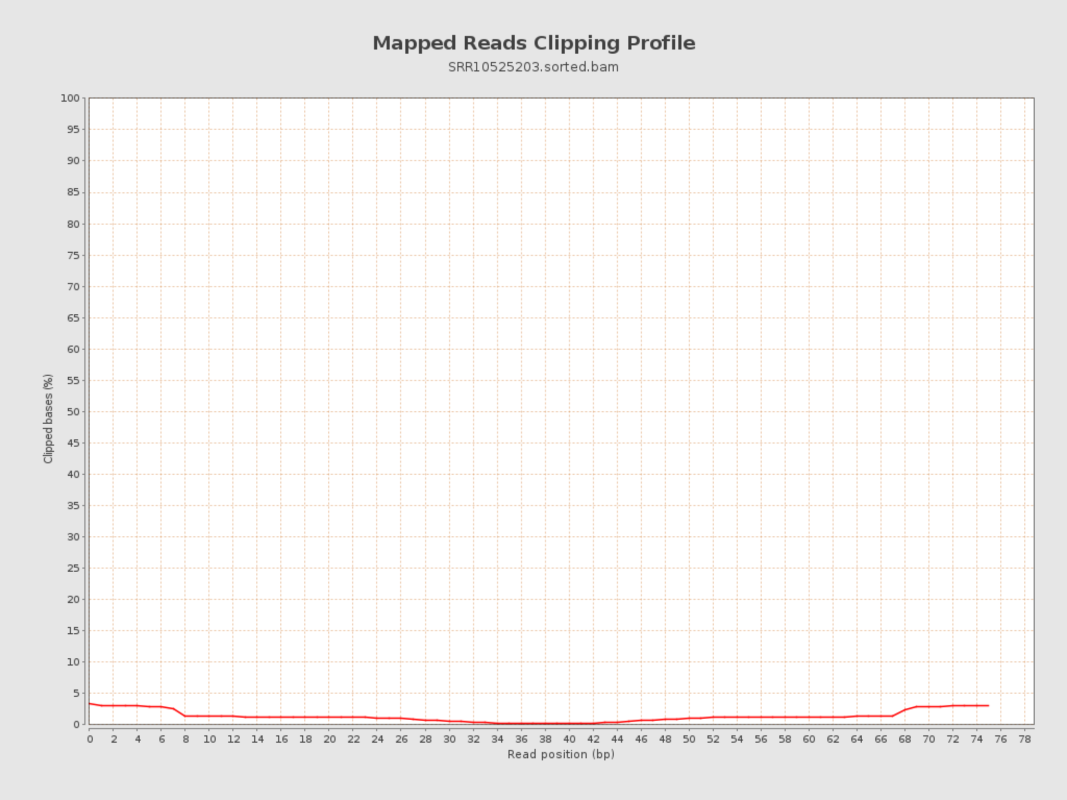
8. Results : Mapped Reads Nucleotide Content



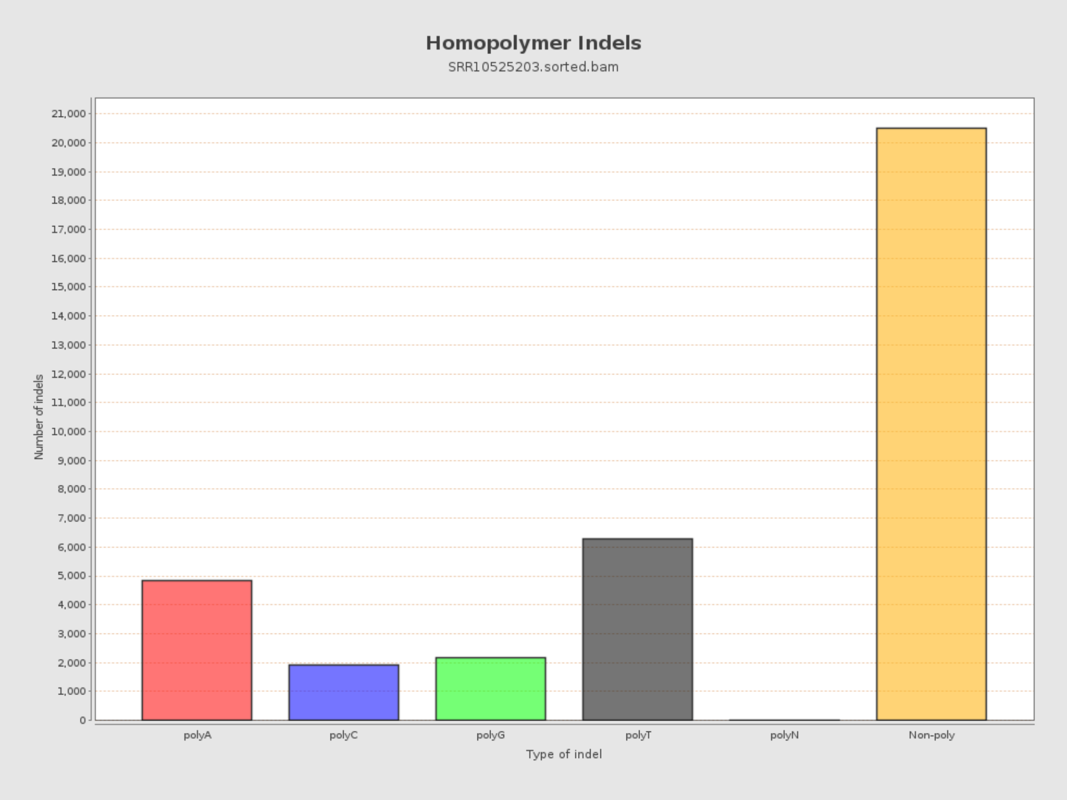
9. Results : Mapped Reads GC-content Distribution



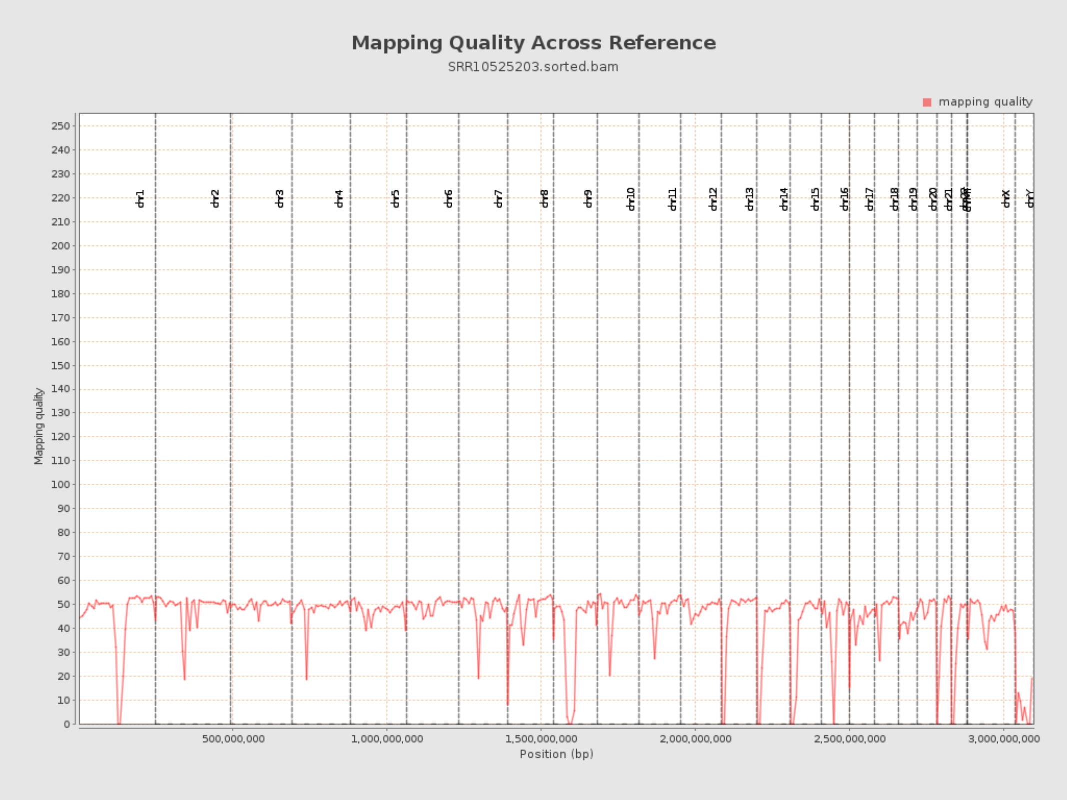
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram