Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:20:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525190.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_SRR10525190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:20:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,906,689
Mapped reads	1,759,630 / 92.29%
Unmapped reads	147,059 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,609 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	70,267 / 3.69%
Duplication rate	2.88%
Clipped reads	1,763,946 / 92.51%

2.2. ACGT Content

Number/percentage of A's	24,145,755 / 23.75%
Number/percentage of C's	19,387,282 / 19.07%
Number/percentage of T's	32,281,060 / 31.75%
Number/percentage of G's	25,869,238 / 25.44%
Number/percentage of N's	2,399 / 0%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3122

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

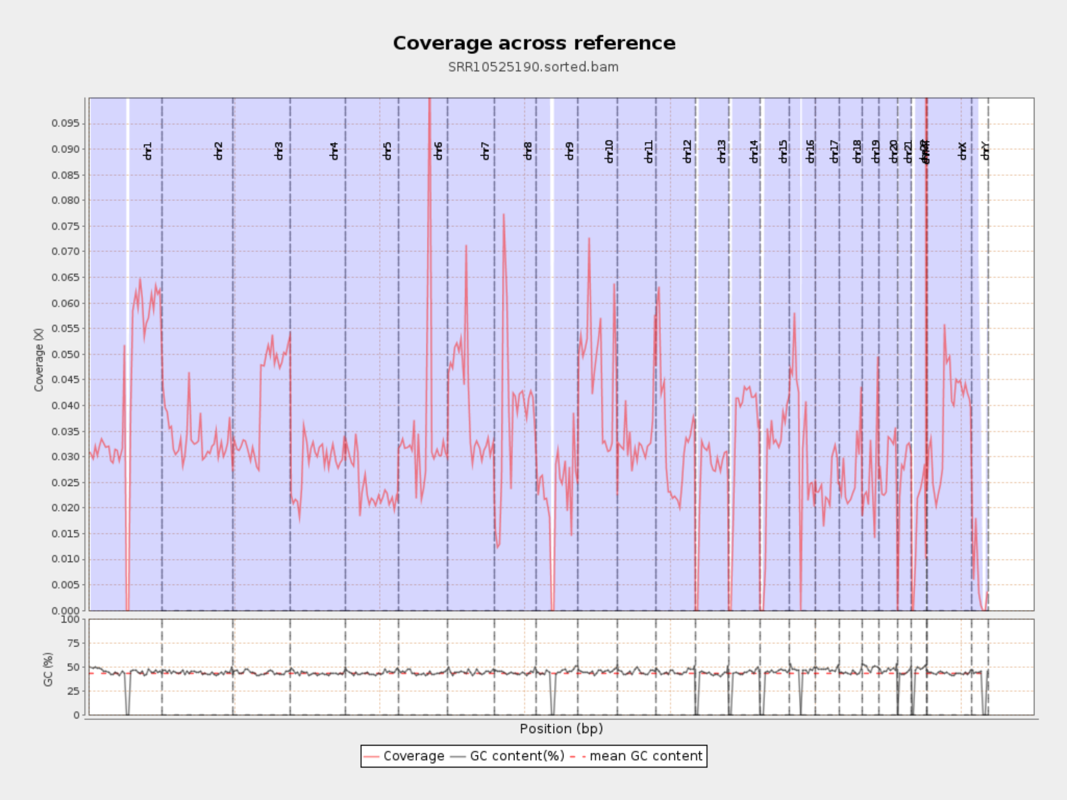
General error rate	0.52%
Mismatches	513,916
Insertions	5,773
Mapped reads with at least one insertion	0.33%
Deletions	20,261
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.44%

2.6. Chromosome stats

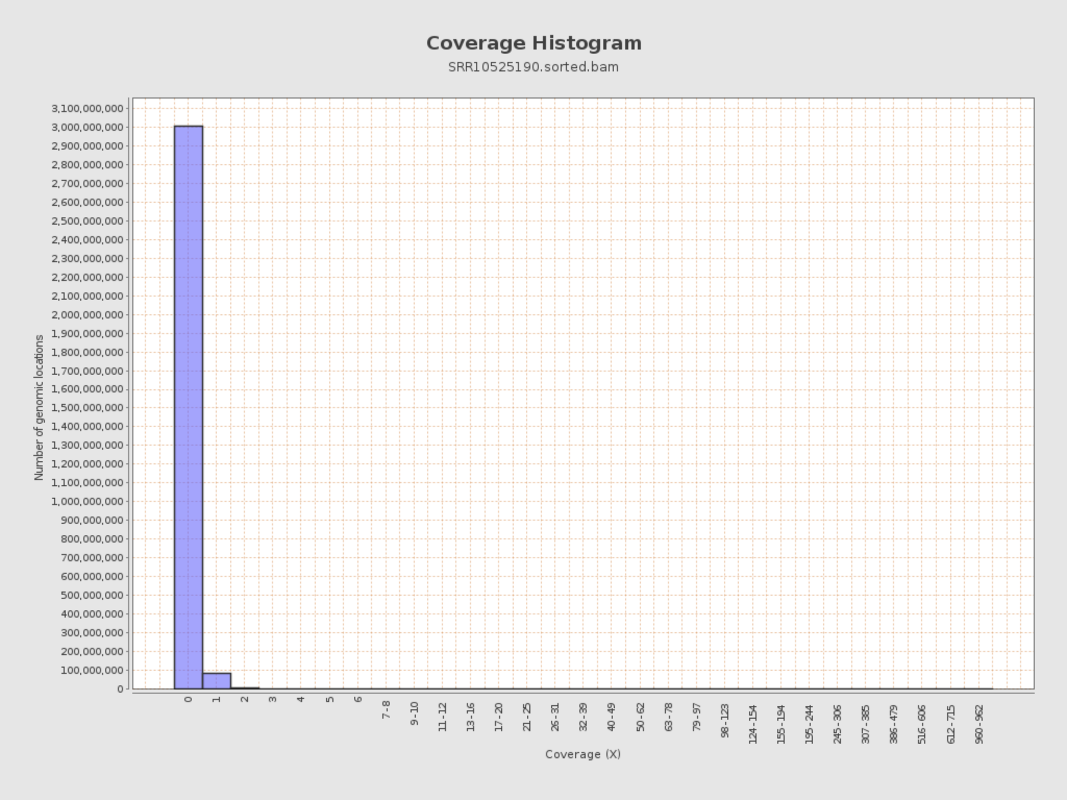
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10425739	0.0418	0.5106
chr2	243199373	8157396	0.0335	0.4373
chr3	198022430	8060883	0.0407	0.2236
chr4	191154276	5471061	0.0286	0.1977
chr5	180915260	4385759	0.0242	0.1716
chr6	171115067	6080711	0.0355	0.2325
chr7	159138663	6476362	0.0407	0.5321

chr8	146364022	5504054	0.0376	0.3078
chr9	141213431	3174393	0.0225	0.212
chr10	135534747	6395701	0.0472	0.328
chr11	135006516	4546743	0.0337	0.2588
chr12	133851895	4430279	0.0331	0.2022
chr13	115169878	2993139	0.026	0.1785
chr14	107349540	3678379	0.0343	0.2059
chr15	102531392	2902128	0.0283	0.1876
chr16	90354753	2990888	0.0331	0.2177
chr17	81195210	1980637	0.0244	0.1777
chr18	78077248	2078789	0.0266	0.3964
chr19	59128983	1552868	0.0263	0.3737
chr20	63025520	1809723	0.0287	0.1901
chr21	48129895	1260305	0.0262	0.1929
chr22	51304566	862932	0.0168	0.1424
chrMT	16571	344447	20.7861	11.3857
chrX	155270560	5837085	0.0376	0.2344
chrY	59373566	317428	0.0053	0.1651

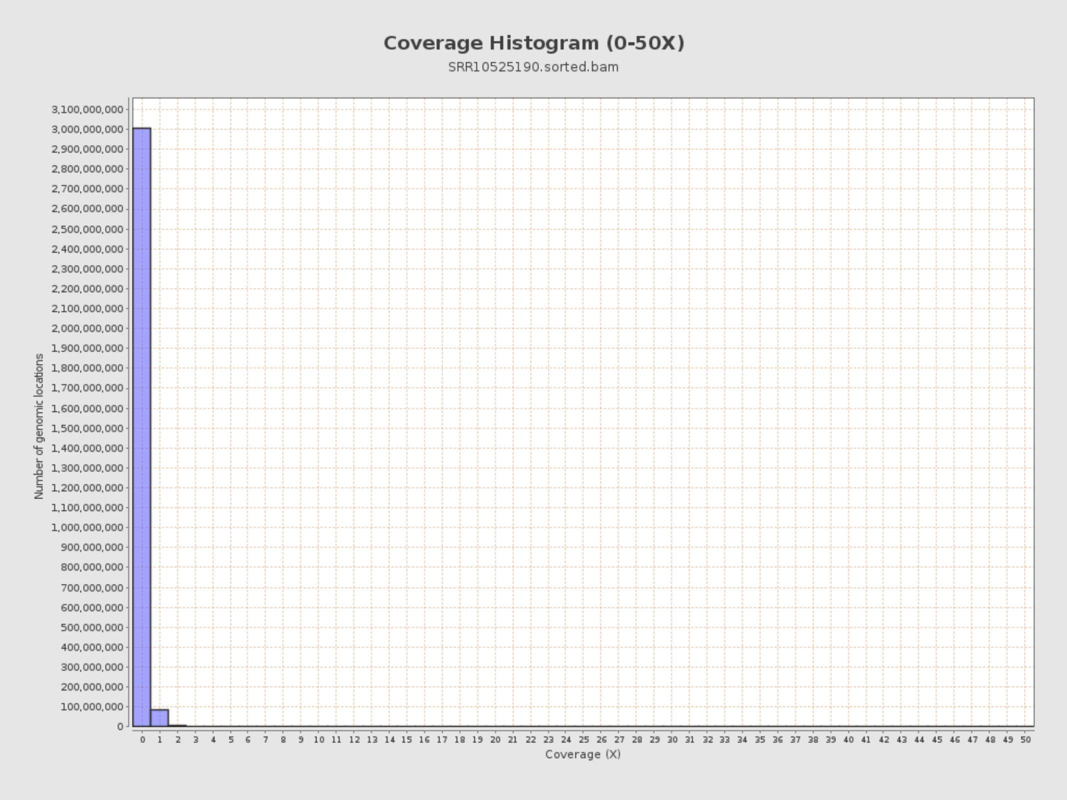
3. Results : Coverage across reference



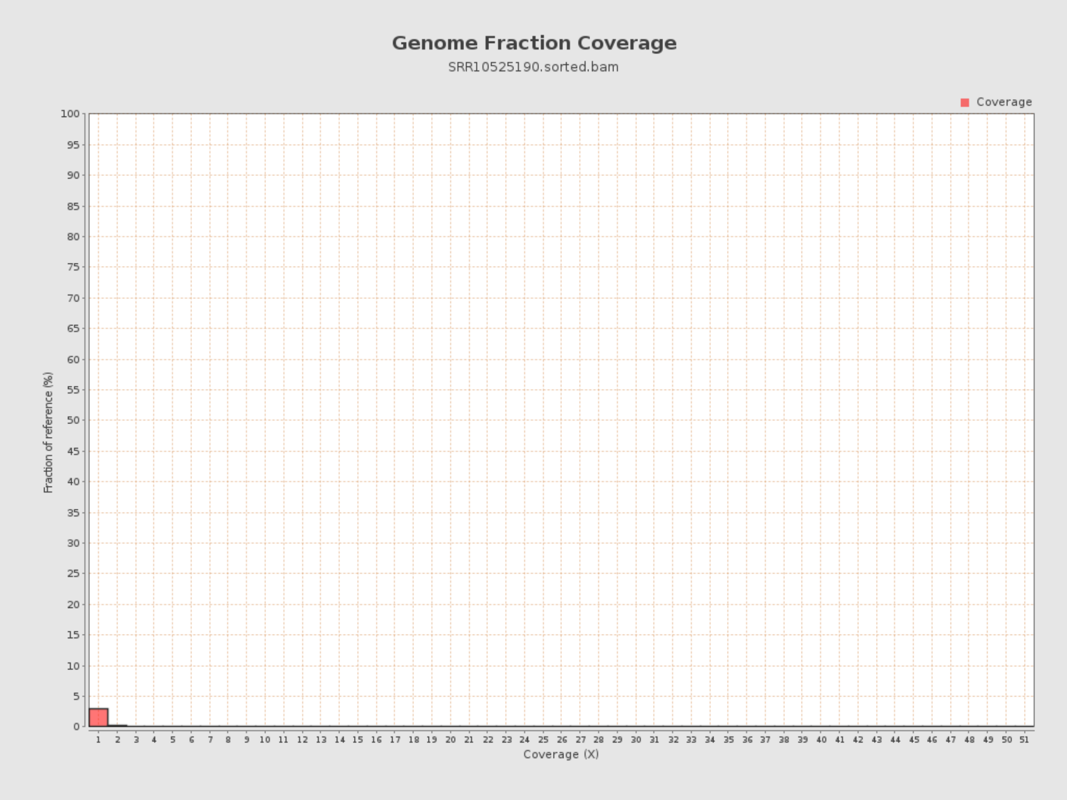
4. Results : Coverage Histogram



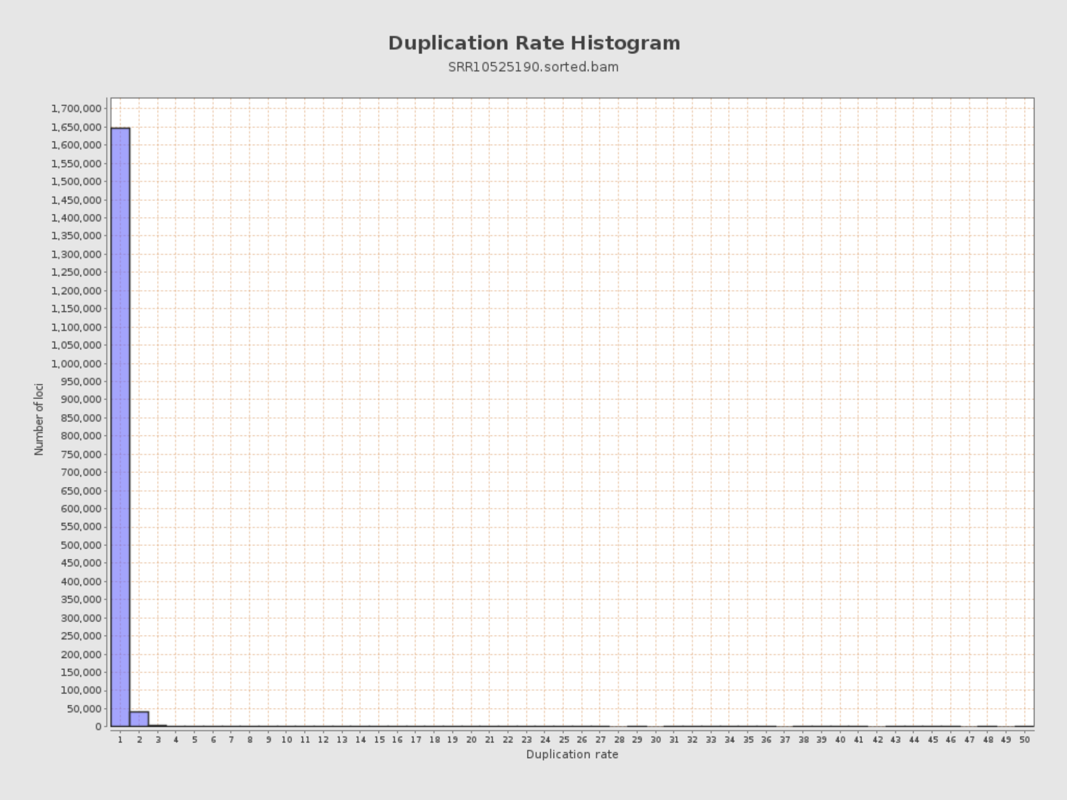
5. Results : Coverage Histogram (0-50X)



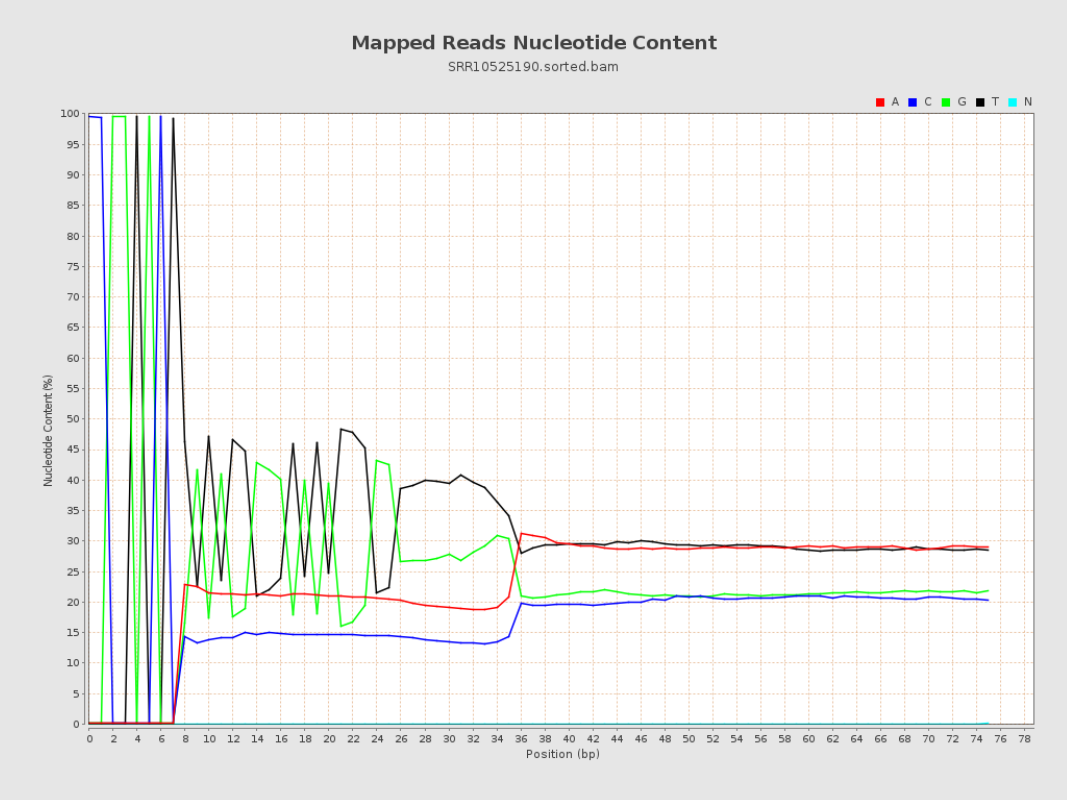
6. Results : Genome Fraction Coverage



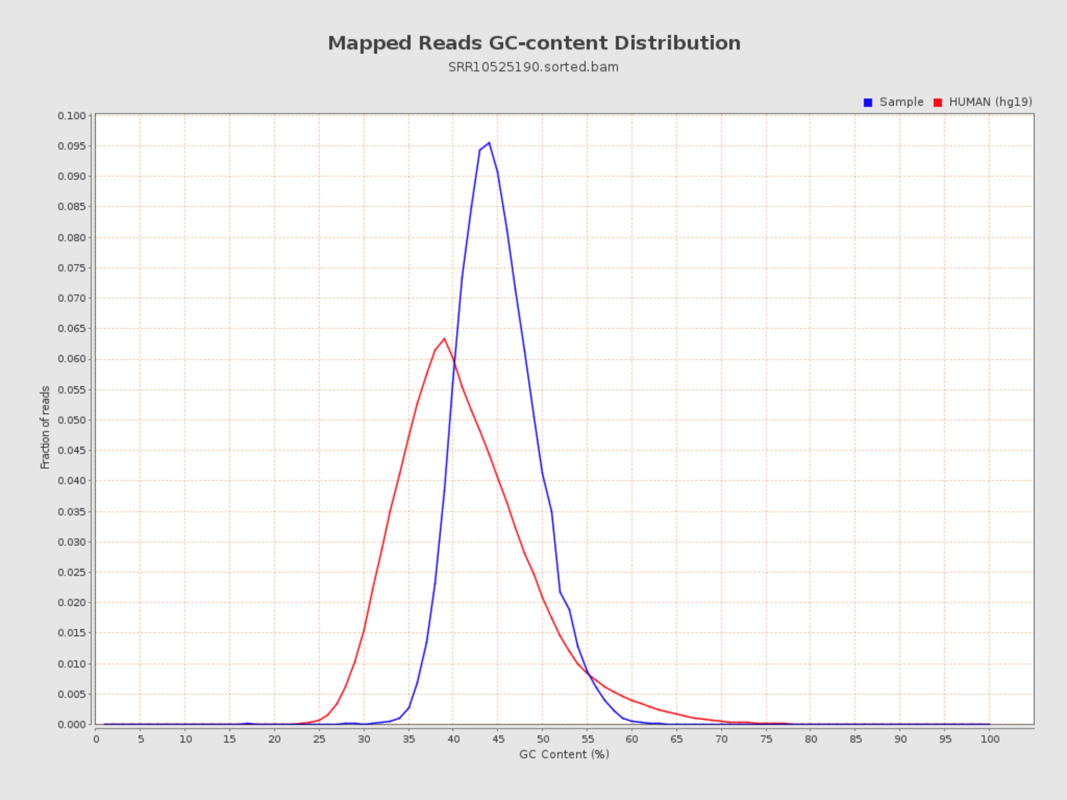
7. Results : Duplication Rate Histogram



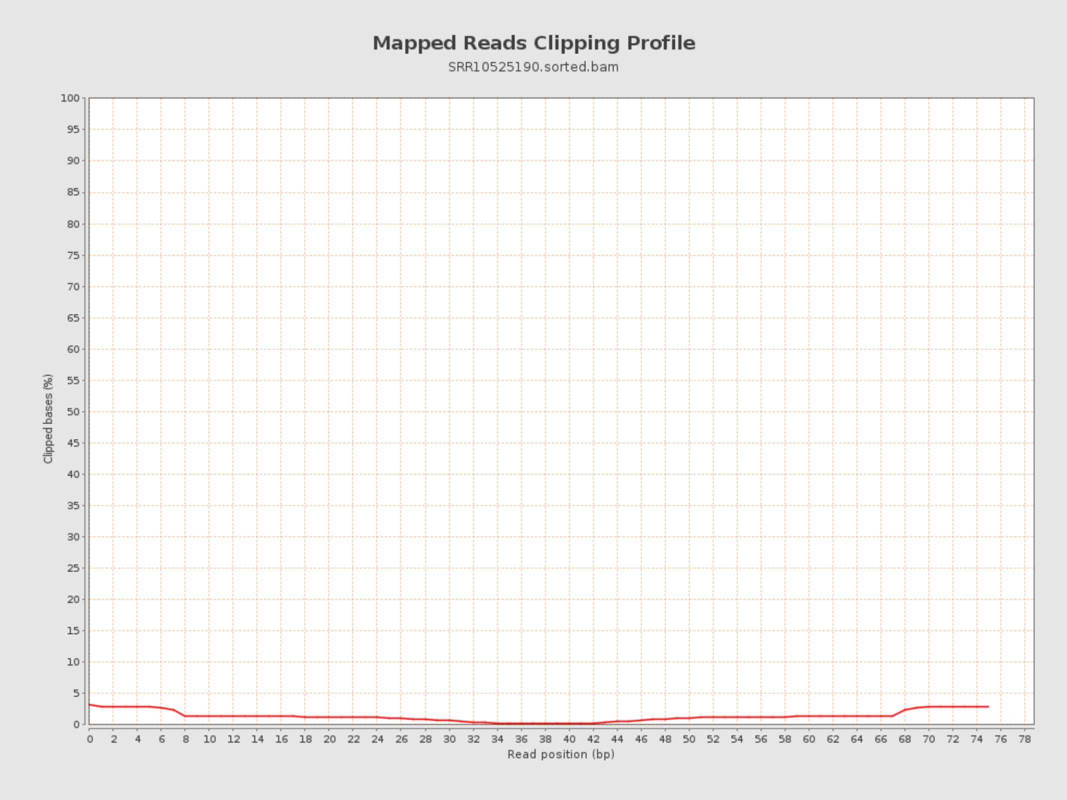
8. Results : Mapped Reads Nucleotide Content



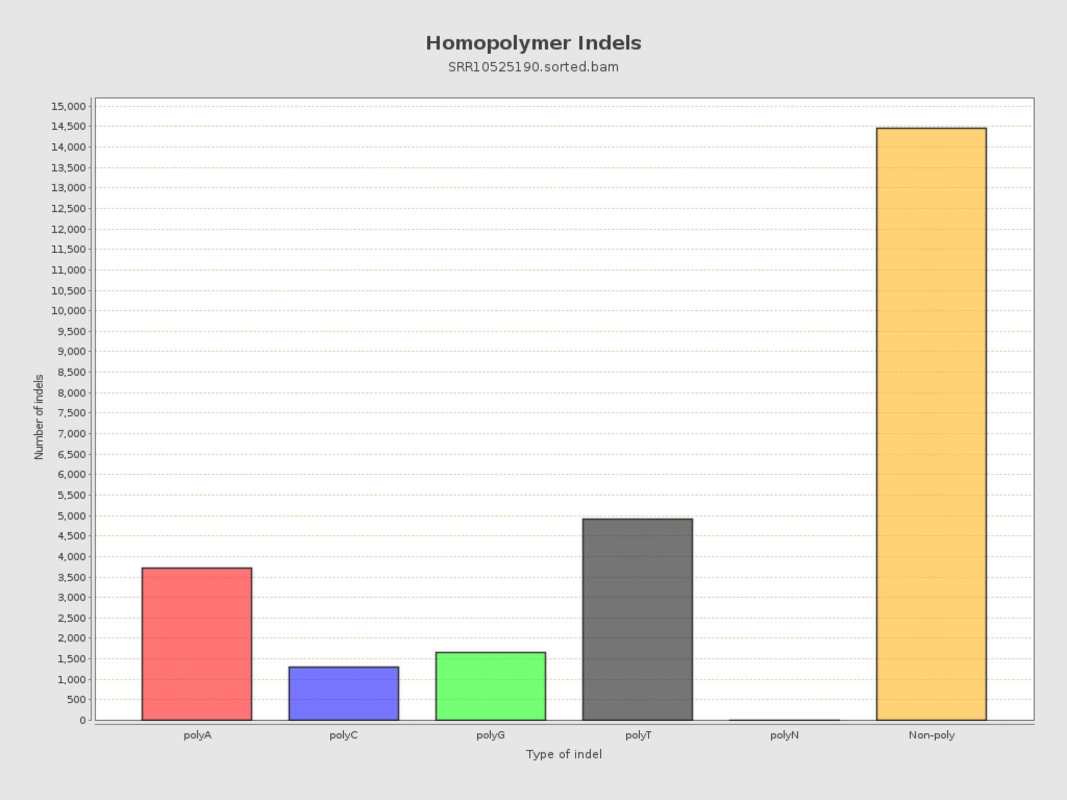
9. Results : Mapped Reads GC-content Distribution



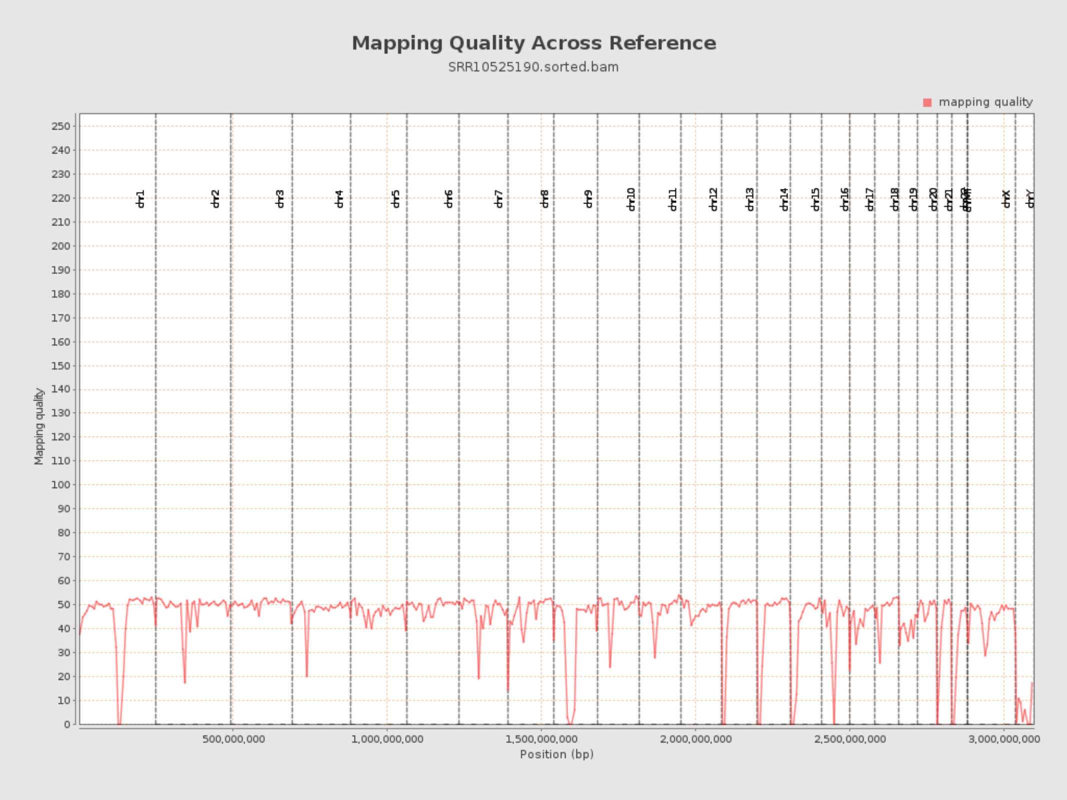
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram