Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:30:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525193.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_SRR10525193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:30:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,386,213
Mapped reads	1,268,980 / 91.54%
Unmapped reads	117,233 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,422 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	35,299 / 2.55%
Duplication rate	2.07%
Clipped reads	1,273,127 / 91.84%

2.2. ACGT Content

Number/percentage of A's	18,491,808 / 25.36%
Number/percentage of C's	13,322,816 / 18.27%
Number/percentage of T's	22,491,057 / 30.85%
Number/percentage of G's	18,606,933 / 25.52%
Number/percentage of N's	2,296 / 0%
GC Percentage	43.79%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.2197

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

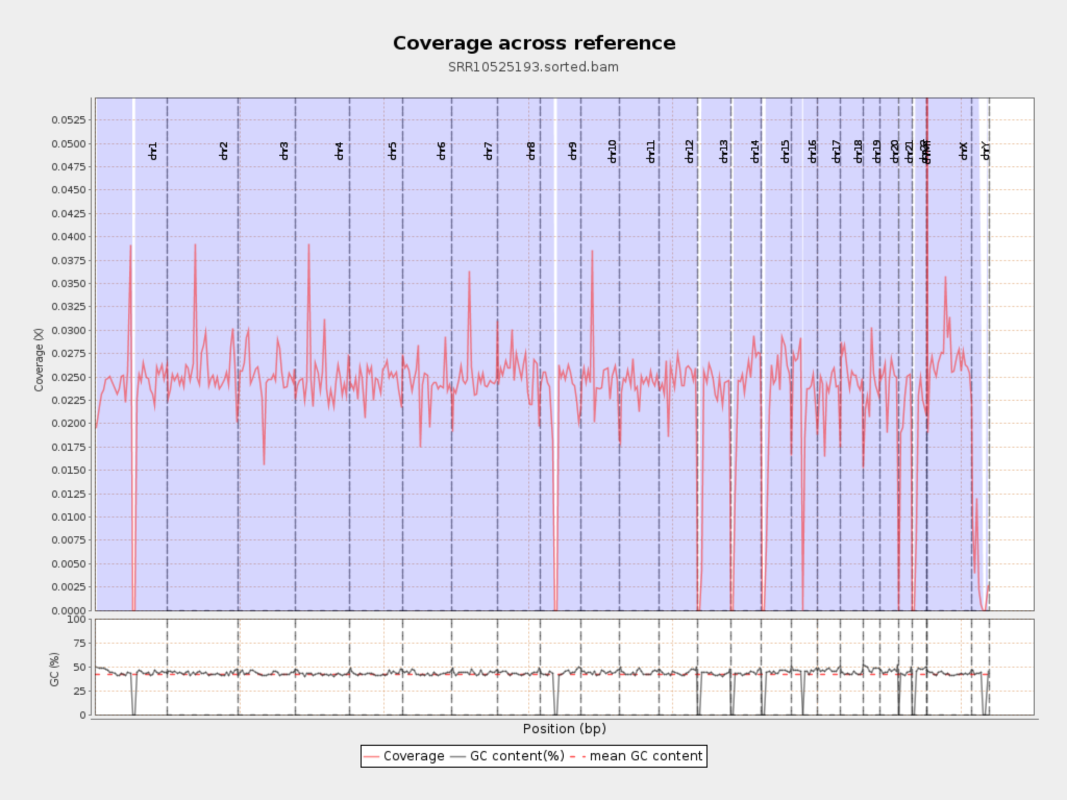
General error rate	0.5%
Mismatches	358,494
Insertions	3,914
Mapped reads with at least one insertion	0.31%
Deletions	11,499
Mapped reads with at least one deletion	0.9%
Homopolymer indels	43.89%

2.6. Chromosome stats

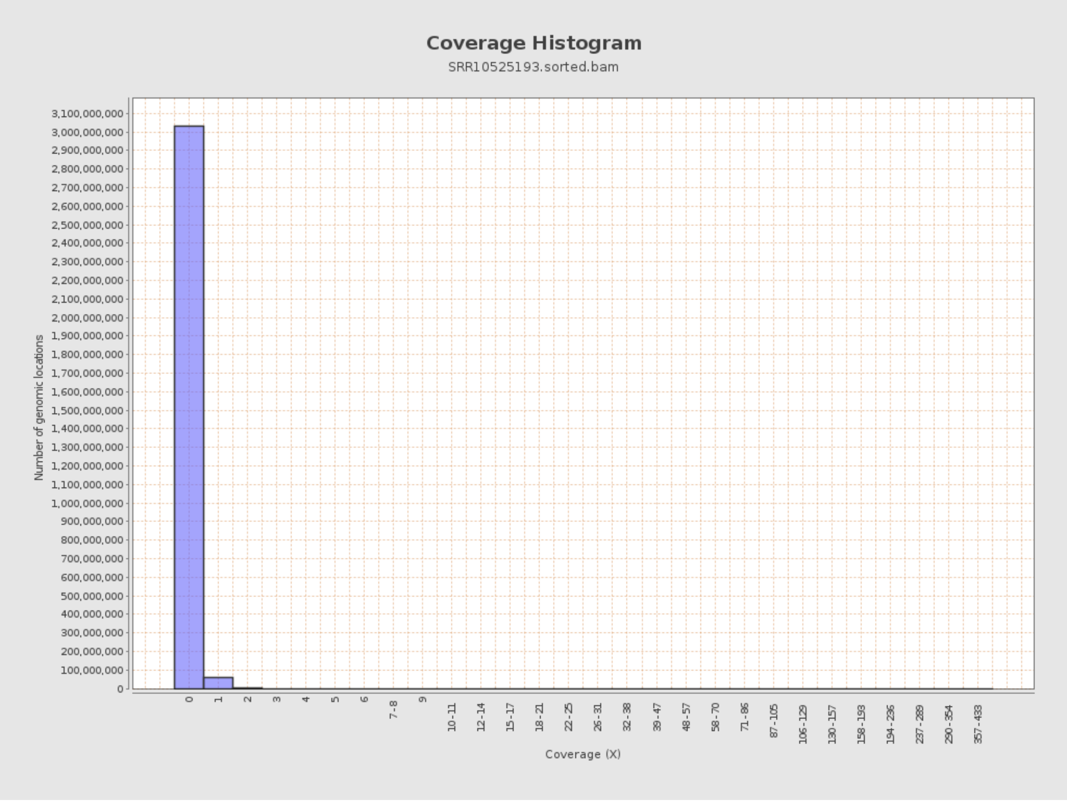
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5778061	0.0232	0.3715
chr2	243199373	6269651	0.0258	0.2293
chr3	198022430	4981026	0.0252	0.1698
chr4	191154276	4790139	0.0251	0.1839
chr5	180915260	4446437	0.0246	0.1696
chr6	171115067	4199532	0.0245	0.1802
chr7	159138663	3961645	0.0249	0.2526

chr8	146364022	3718425	0.0254	0.2477
chr9	141213431	3035158	0.0215	0.206
chr10	135534747	3407070	0.0251	0.2147
chr11	135006516	3286285	0.0243	0.2158
chr12	133851895	3301206	0.0247	0.1725
chr13	115169878	2336067	0.0203	0.1526
chr14	107349540	2333196	0.0217	0.169
chr15	102531392	2111959	0.0206	0.1545
chr16	90354753	1996238	0.0221	0.1689
chr17	81195210	1876062	0.0231	0.1714
chr18	78077248	1993196	0.0255	0.3371
chr19	59128983	1397101	0.0236	0.2901
chr20	63025520	1524614	0.0242	0.1707
chr21	48129895	968865	0.0201	0.1669
chr22	51304566	818838	0.016	0.1353
chrMT	16571	1867	0.1127	0.3372
chrX	155270560	4185050	0.027	0.1959
chrY	59373566	216426	0.0036	0.0914

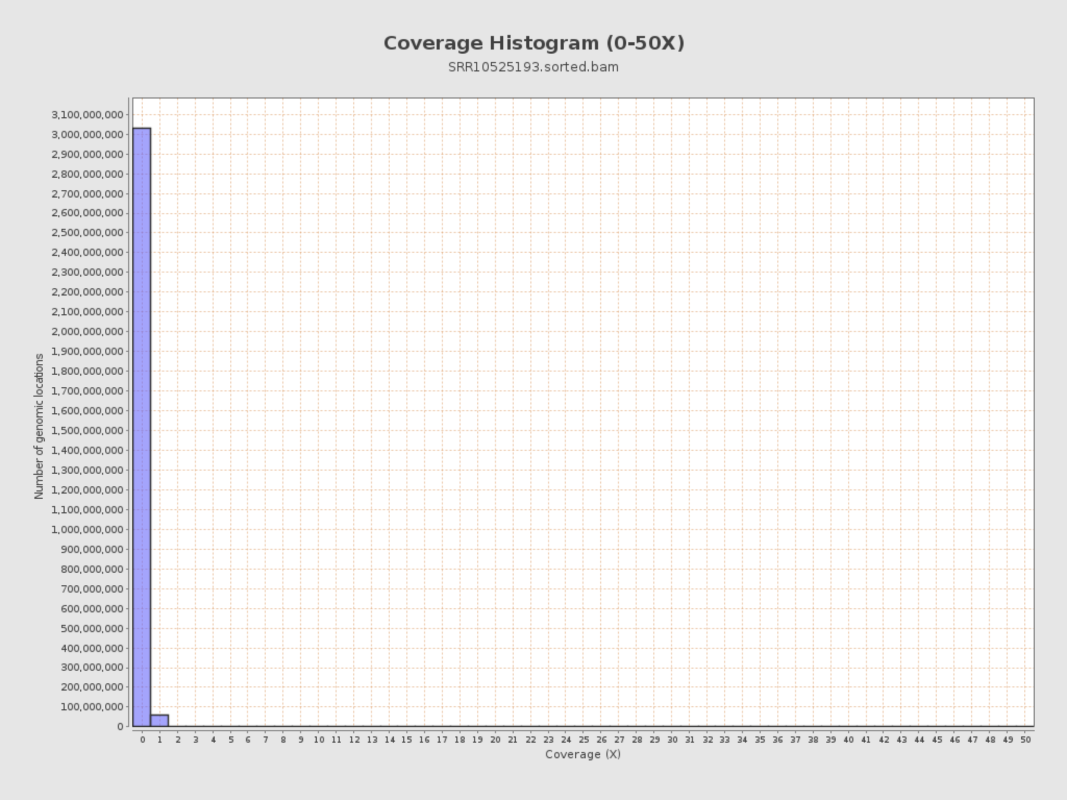
3. Results : Coverage across reference



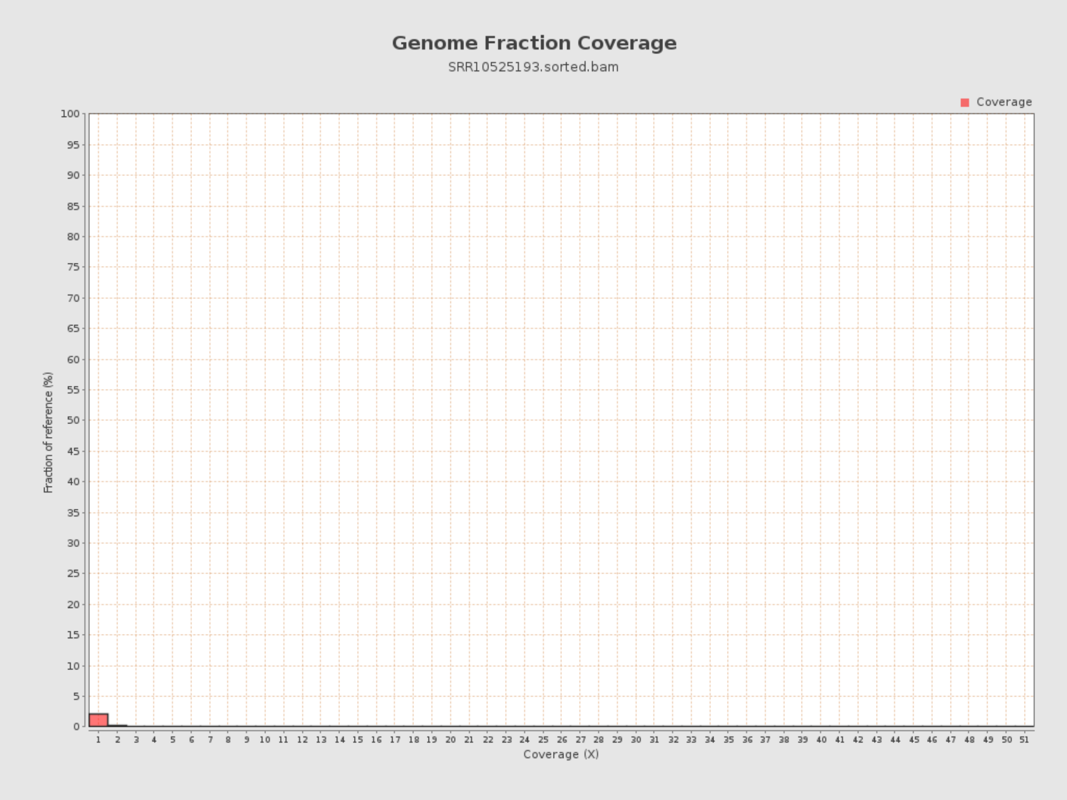
4. Results : Coverage Histogram



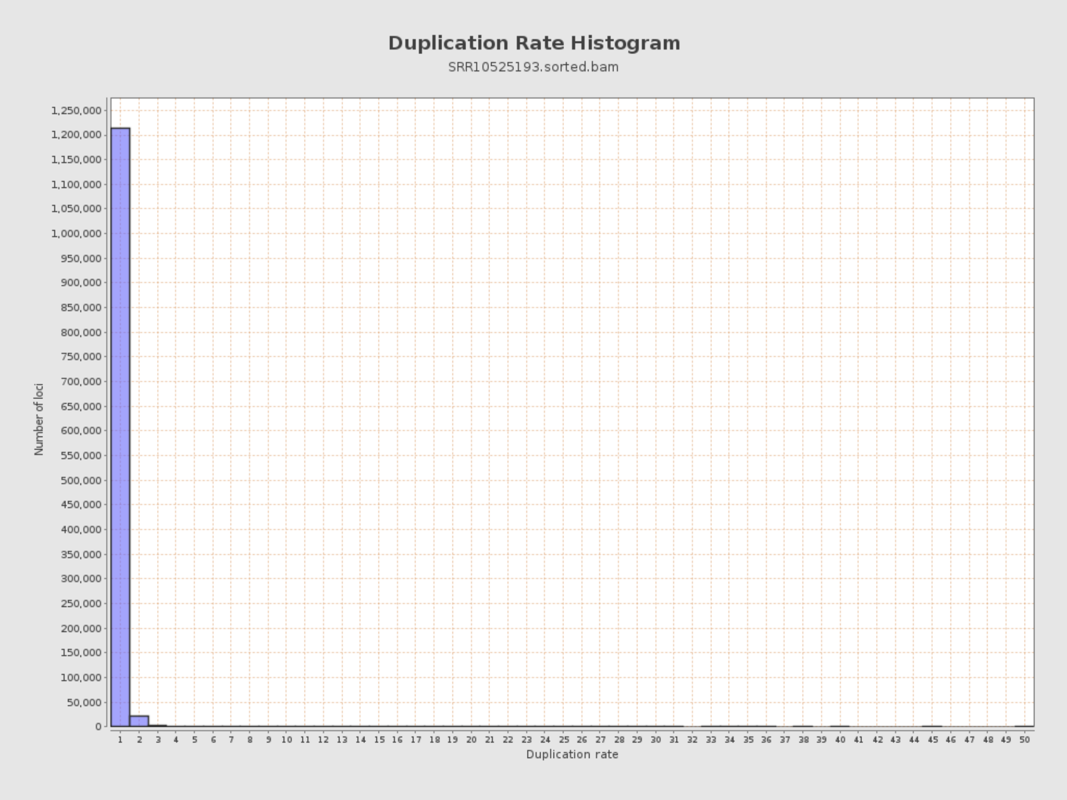
5. Results : Coverage Histogram (0-50X)



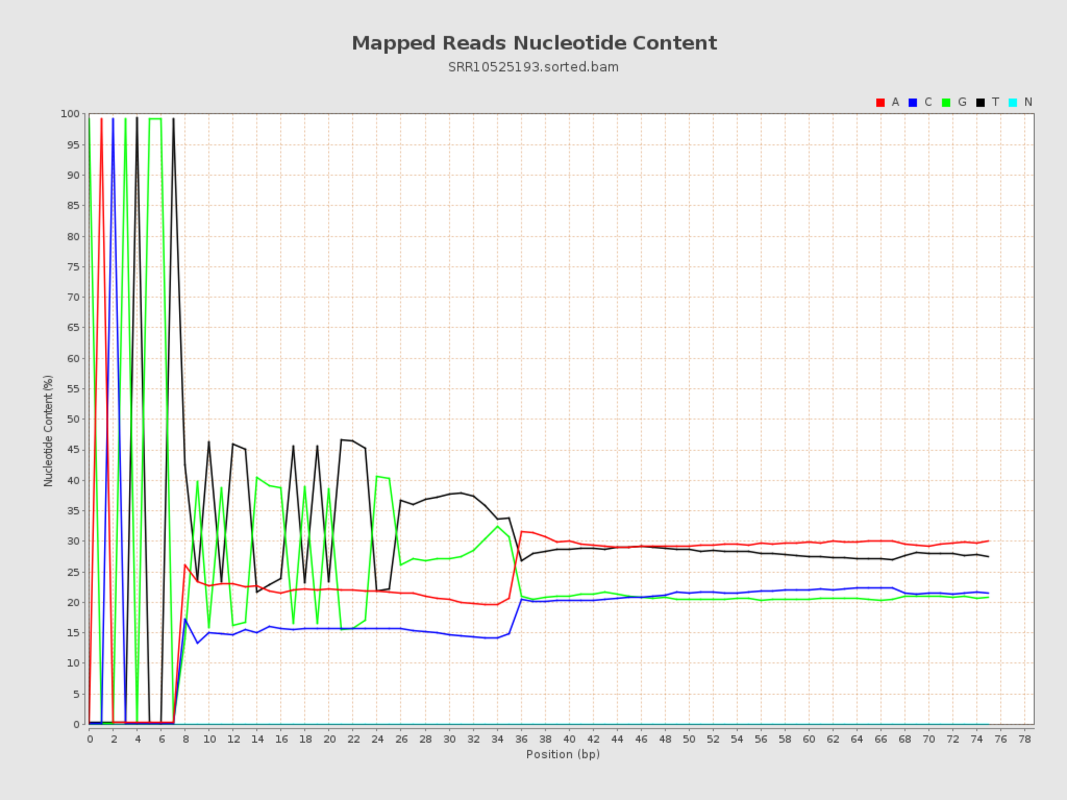
6. Results : Genome Fraction Coverage



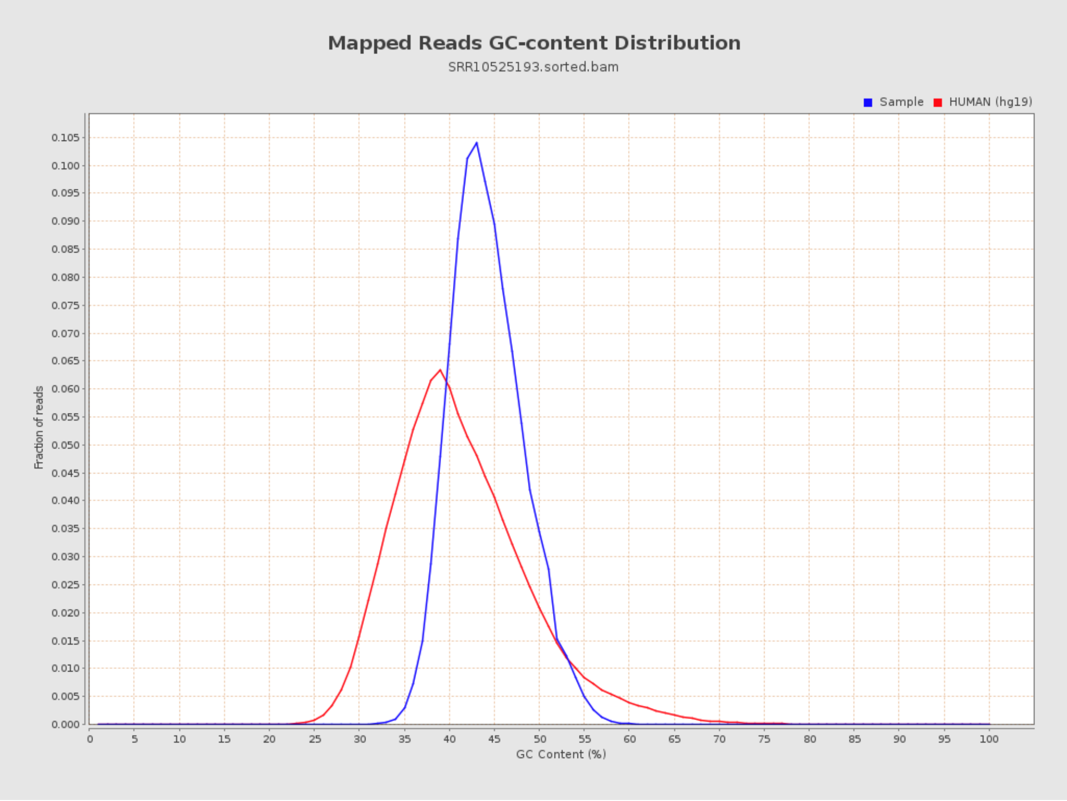
7. Results : Duplication Rate Histogram



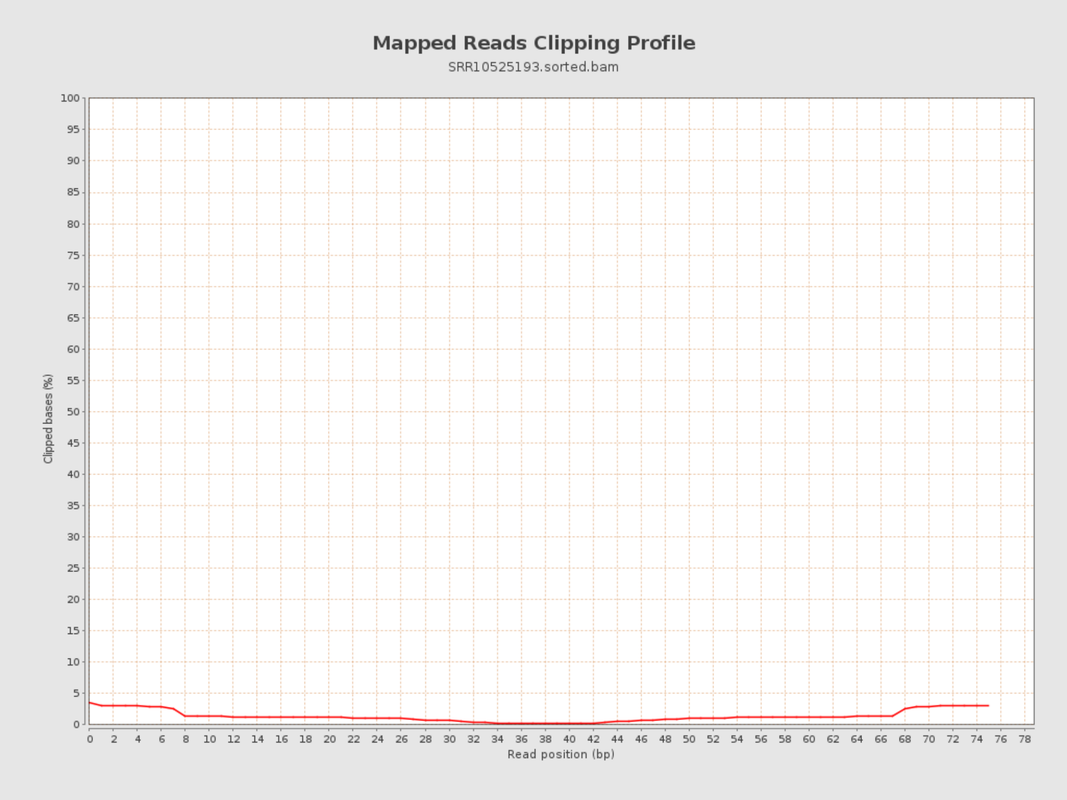
8. Results : Mapped Reads Nucleotide Content



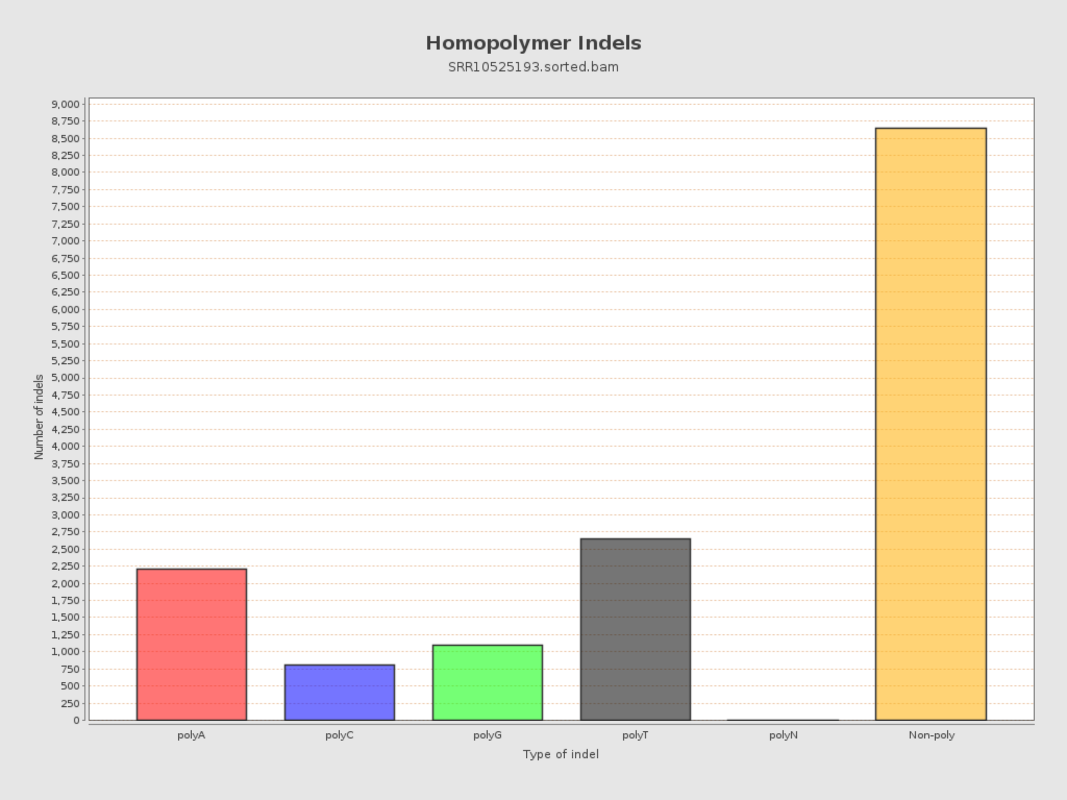
9. Results : Mapped Reads GC-content Distribution



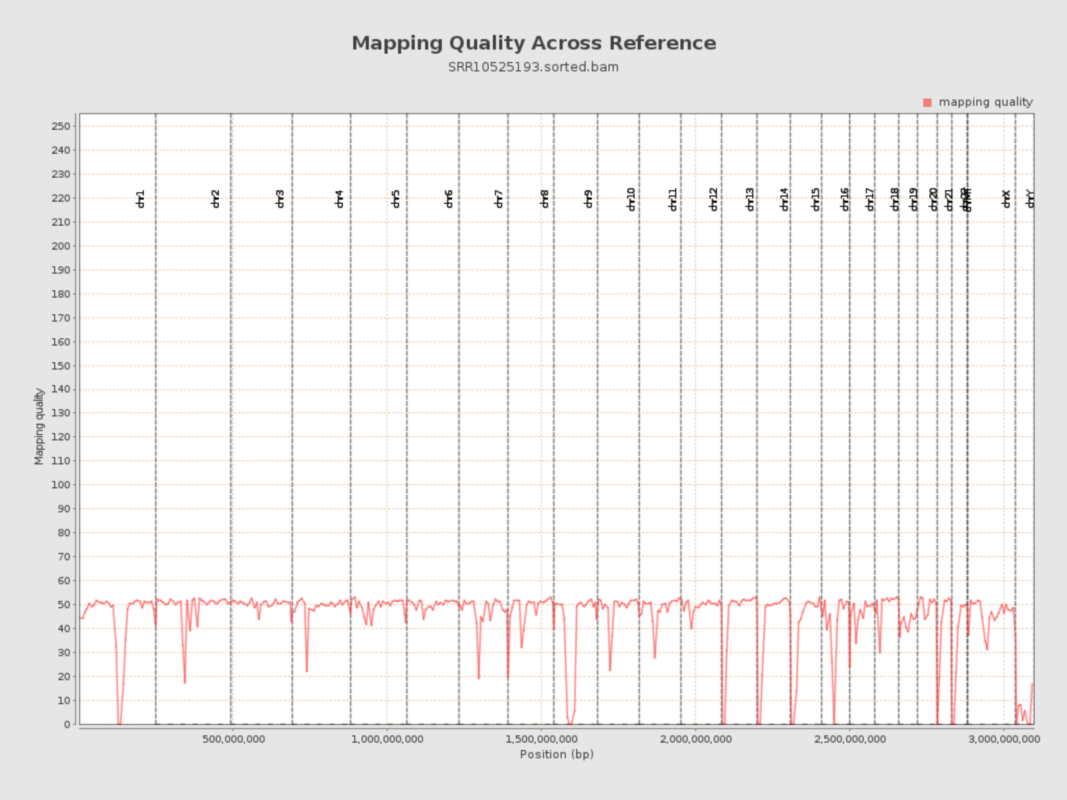
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram