Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:09:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525105.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_SRR10525105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:09:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,085,470
Mapped reads	990,375 / 91.24%
Unmapped reads	95,095 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,055 / 2.86%
Read min/max/mean length	30 / 101 / 102.06
Duplicated reads (estimated)	24,153 / 2.23%
Duplication rate	1.44%
Clipped reads	1,020,083 / 93.98%

2.2. ACGT Content

Number/percentage of A's	19,528,349 / 25.62%
Number/percentage of C's	15,403,047 / 20.2%
Number/percentage of T's	22,978,255 / 30.14%
Number/percentage of G's	18,322,894 / 24.03%
Number/percentage of N's	2,835 / 0%
GC Percentage	44.24%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2702

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

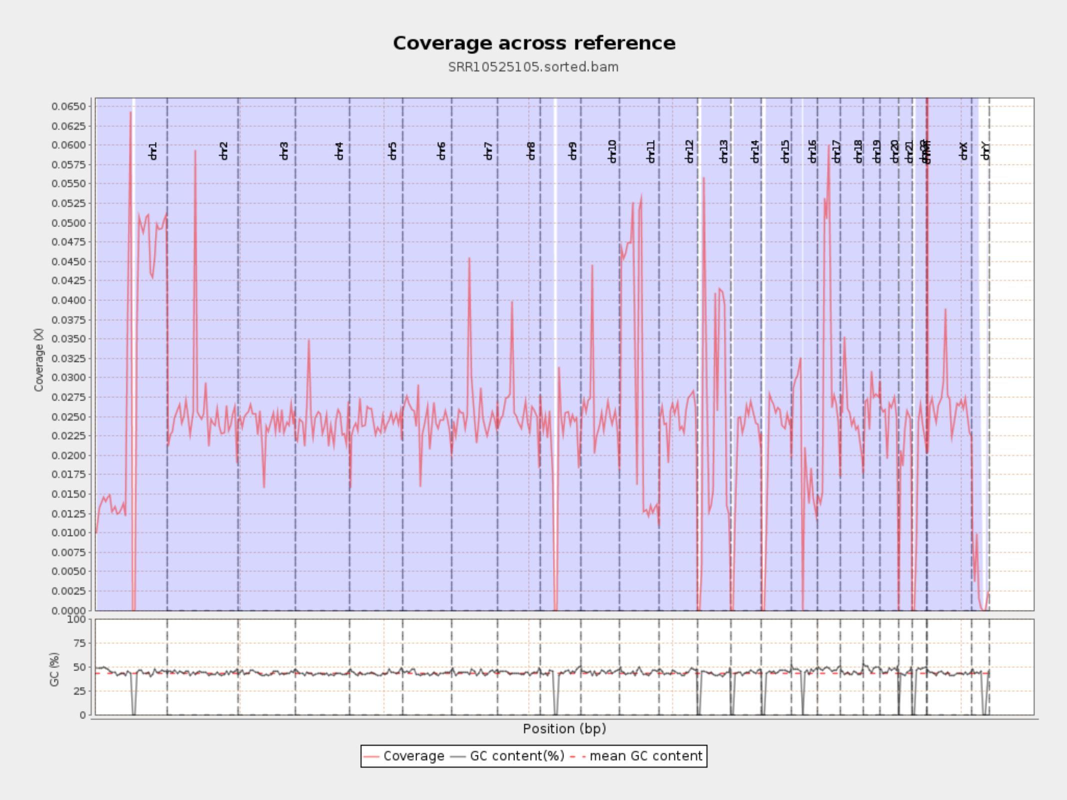
General error rate	0.77%
Mismatches	571,647
Insertions	6,658
Mapped reads with at least one insertion	0.66%
Deletions	17,484
Mapped reads with at least one deletion	1.74%
Homopolymer indels	43.06%

2.6. Chromosome stats

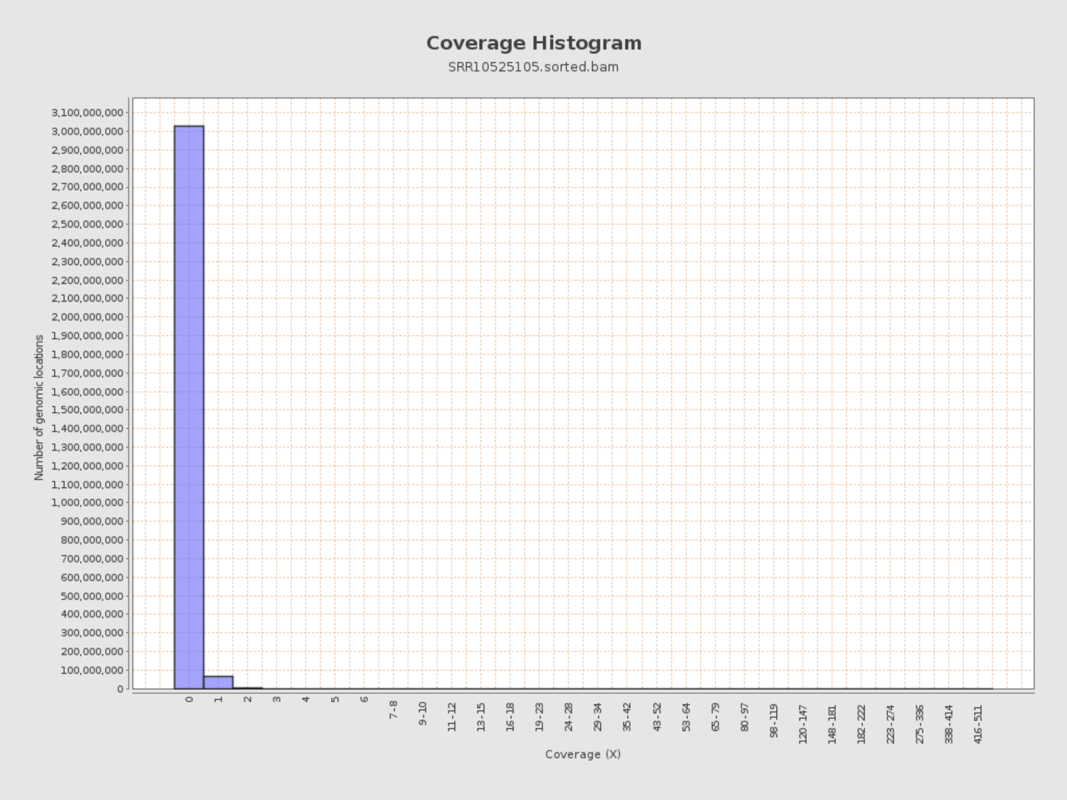
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7470596	0.03	0.4583
chr2	243199373	6233432	0.0256	0.3721
chr3	198022430	4786228	0.0242	0.1652
chr4	191154276	4642445	0.0243	0.1759
chr5	180915260	4405281	0.0243	0.1673
chr6	171115067	4199671	0.0245	0.1832
chr7	159138663	4093690	0.0257	0.3598

chr8	146364022	3776346	0.0258	0.3302
chr9	141213431	3043574	0.0216	0.2427
chr10	135534747	3489932	0.0257	0.2648
chr11	135006516	4191869	0.031	0.3164
chr12	133851895	3364192	0.0251	0.169
chr13	115169878	2689469	0.0234	0.1629
chr14	107349540	2211063	0.0206	0.1698
chr15	102531392	2128227	0.0208	0.1522
chr16	90354753	1788281	0.0198	0.1622
chr17	81195210	2485446	0.0306	0.2143
chr18	78077248	1971179	0.0252	0.4071
chr19	59128983	1593765	0.027	0.3349
chr20	63025520	1562259	0.0248	0.173
chr21	48129895	978786	0.0203	0.1604
chr22	51304566	851418	0.0166	0.136
chrMT	16571	7582	0.4575	0.7716
chrX	155270560	4112583	0.0265	0.2165
chrY	59373566	188311	0.0032	0.088

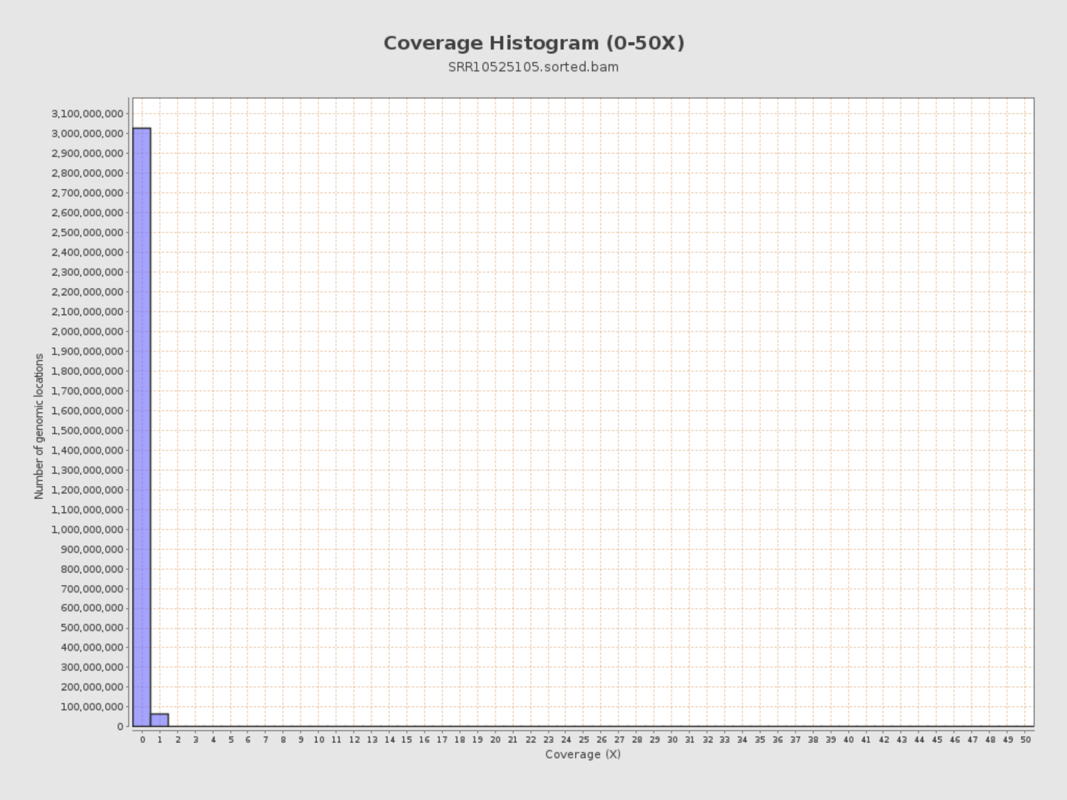
3. Results : Coverage across reference



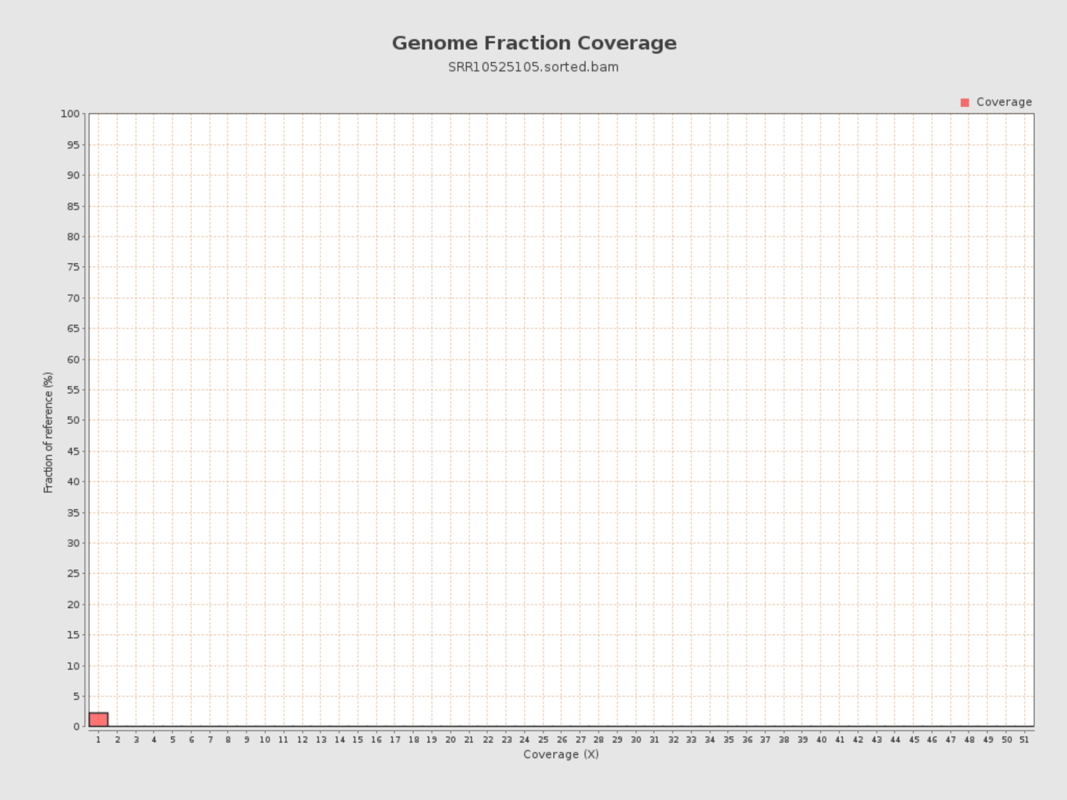
4. Results : Coverage Histogram



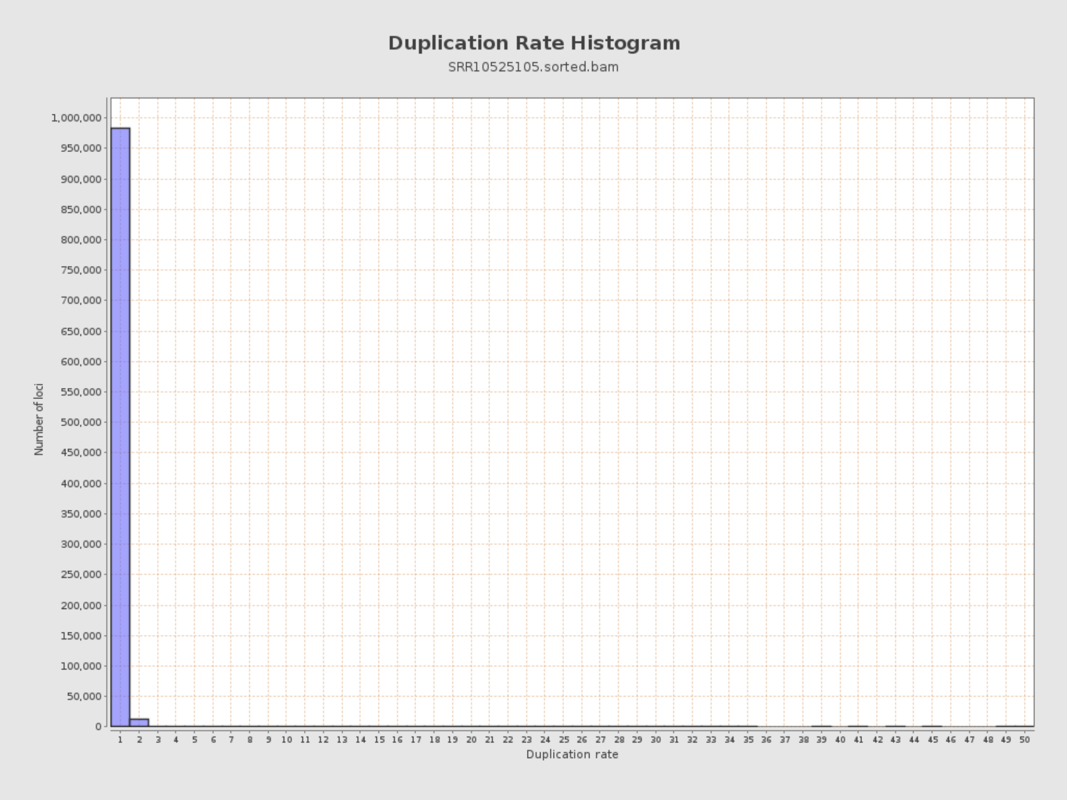
5. Results : Coverage Histogram (0-50X)



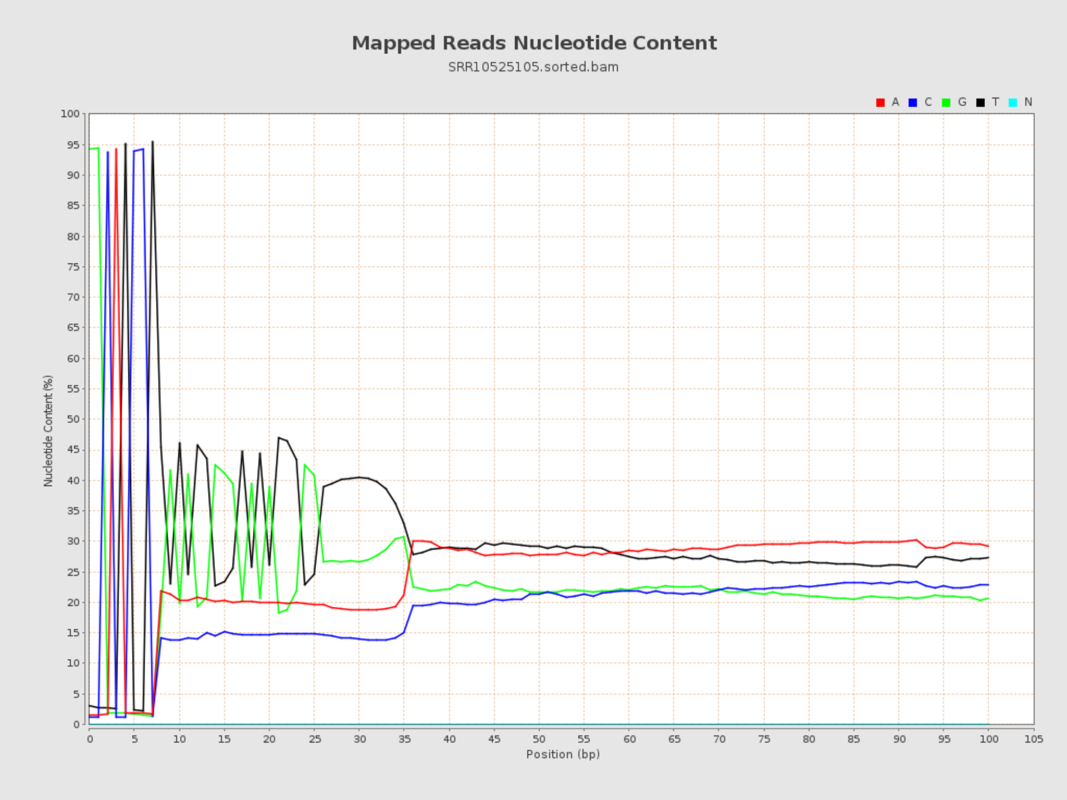
6. Results : Genome Fraction Coverage



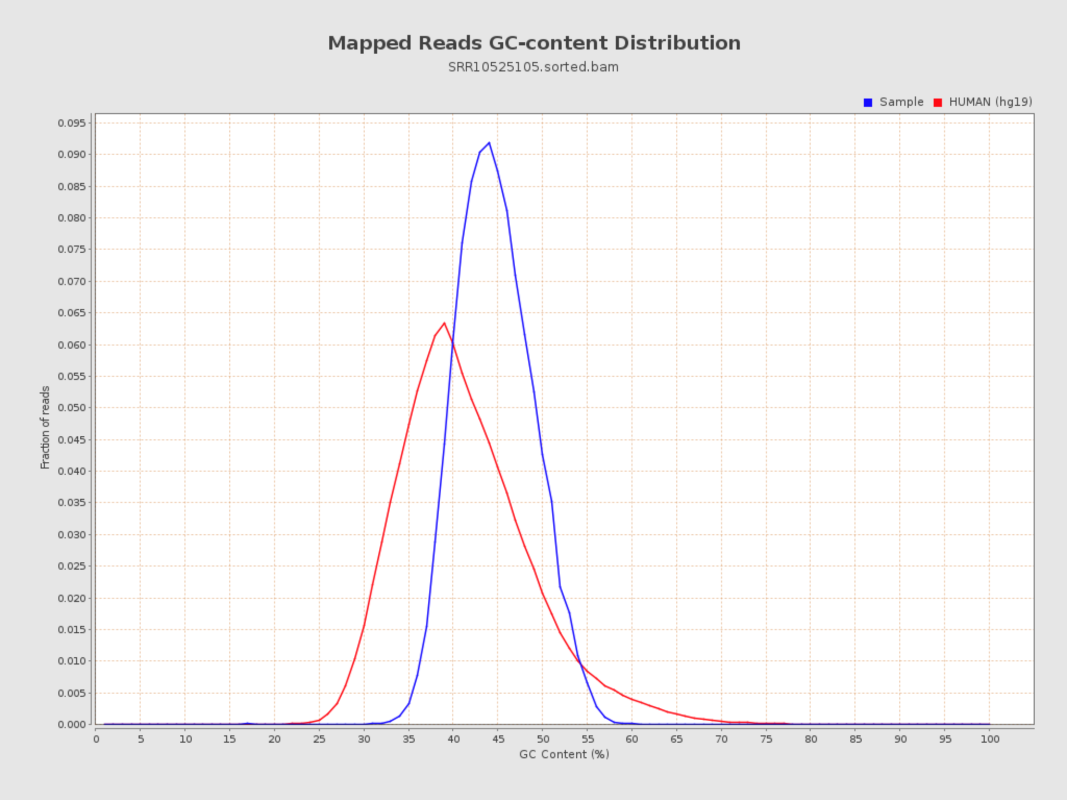
7. Results : Duplication Rate Histogram



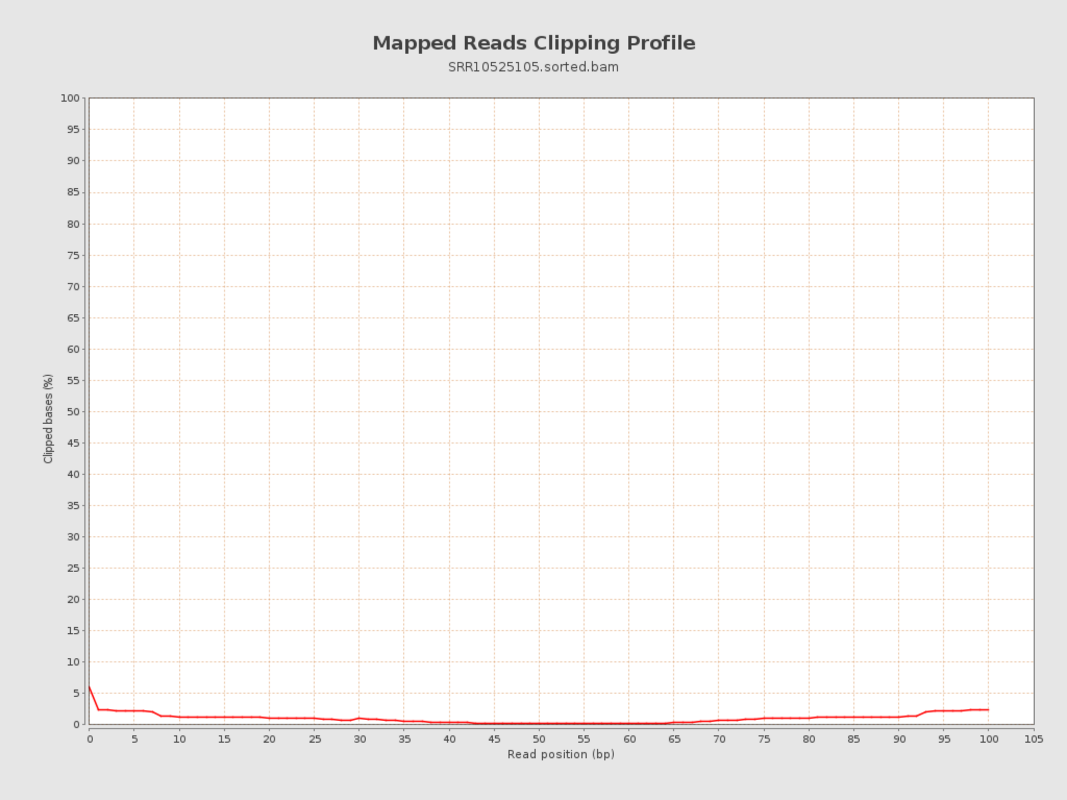
8. Results : Mapped Reads Nucleotide Content



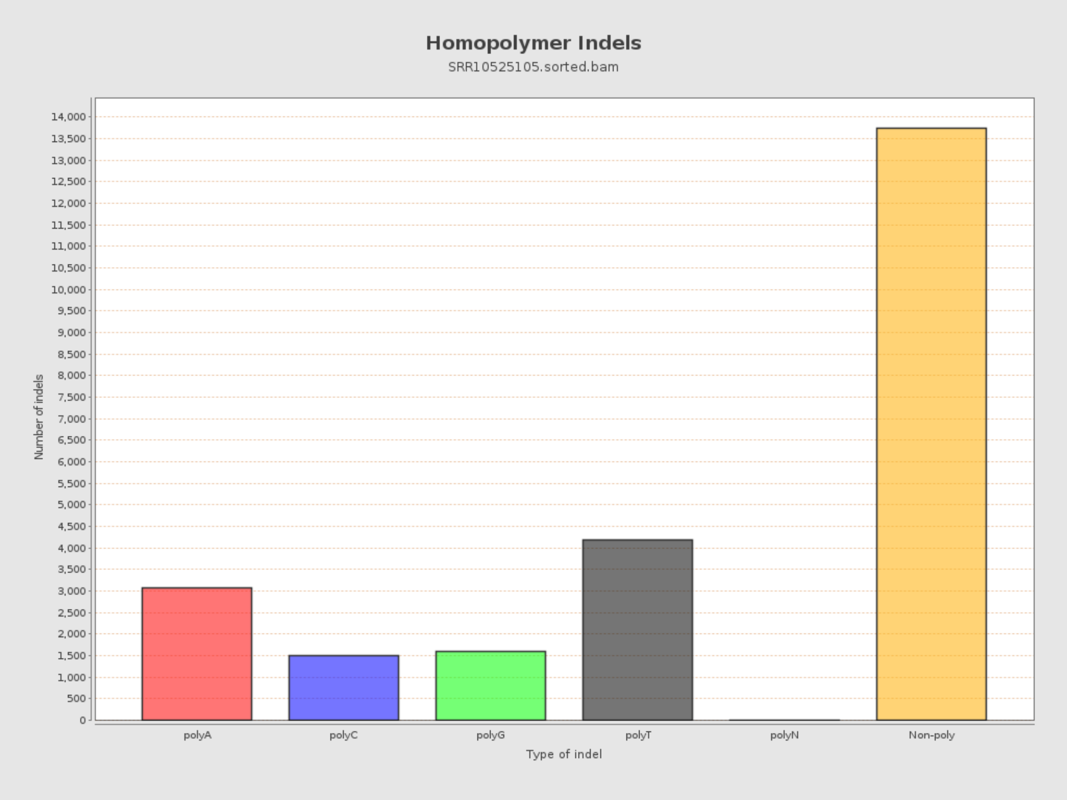
9. Results : Mapped Reads GC-content Distribution



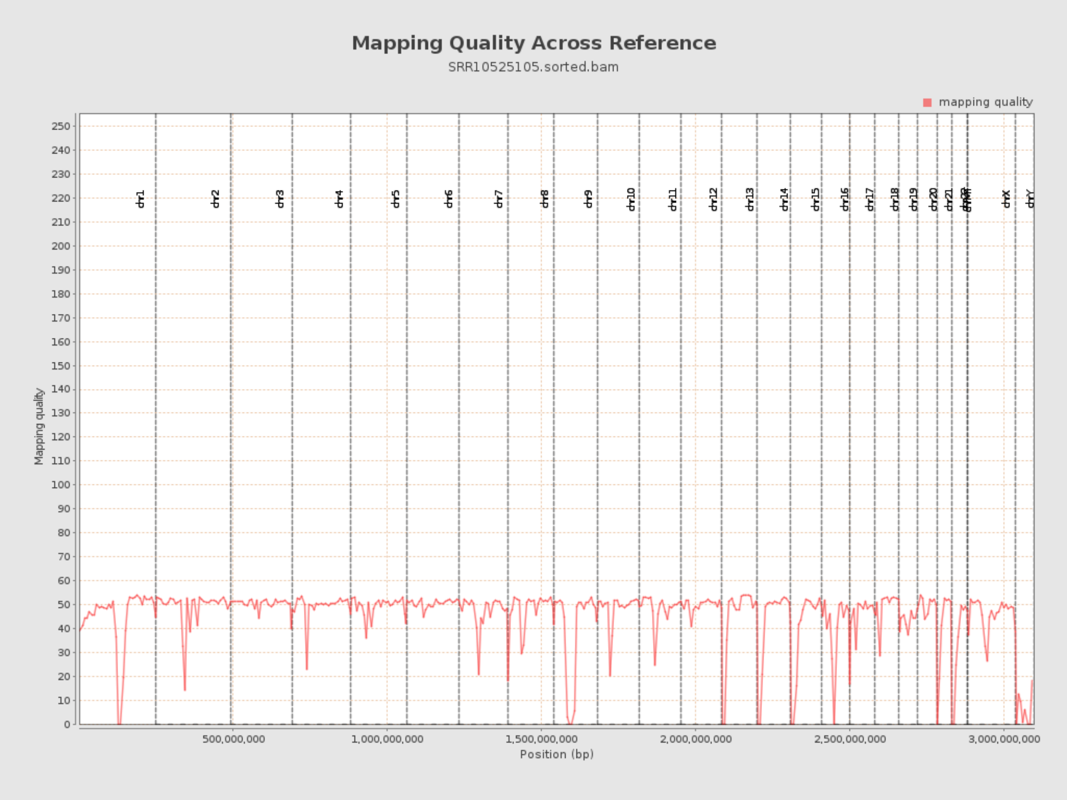
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram