Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:56:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525145.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_SRR10525145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:56:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,046,228
Mapped reads	937,065 / 89.57%
Unmapped reads	109,163 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,688 / 2.65%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	22,813 / 2.18%
Duplication rate	1.45%
Clipped reads	963,047 / 92.05%

2.2. ACGT Content

Number/percentage of A's	18,679,590 / 25.97%
Number/percentage of C's	14,405,816 / 20.03%
Number/percentage of T's	21,809,041 / 30.32%
Number/percentage of G's	17,021,331 / 23.67%
Number/percentage of N's	2,638 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2588

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

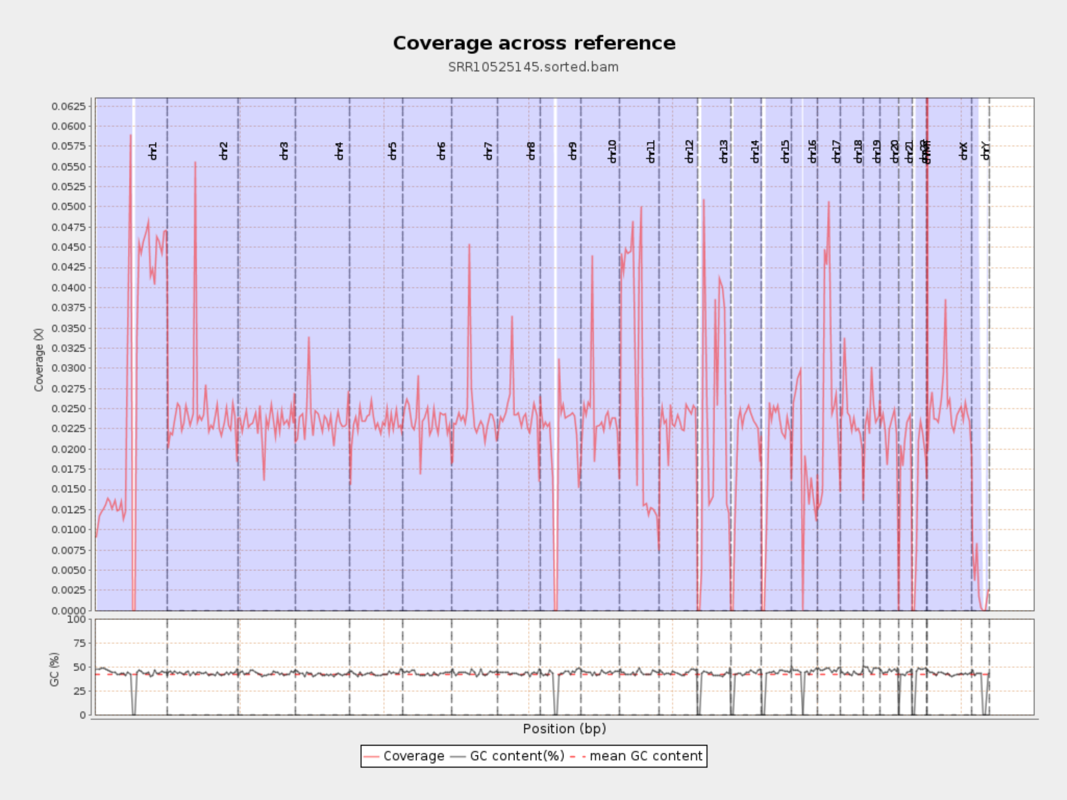
General error rate	0.77%
Mismatches	535,819
Insertions	7,070
Mapped reads with at least one insertion	0.75%
Deletions	16,409
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.24%

2.6. Chromosome stats

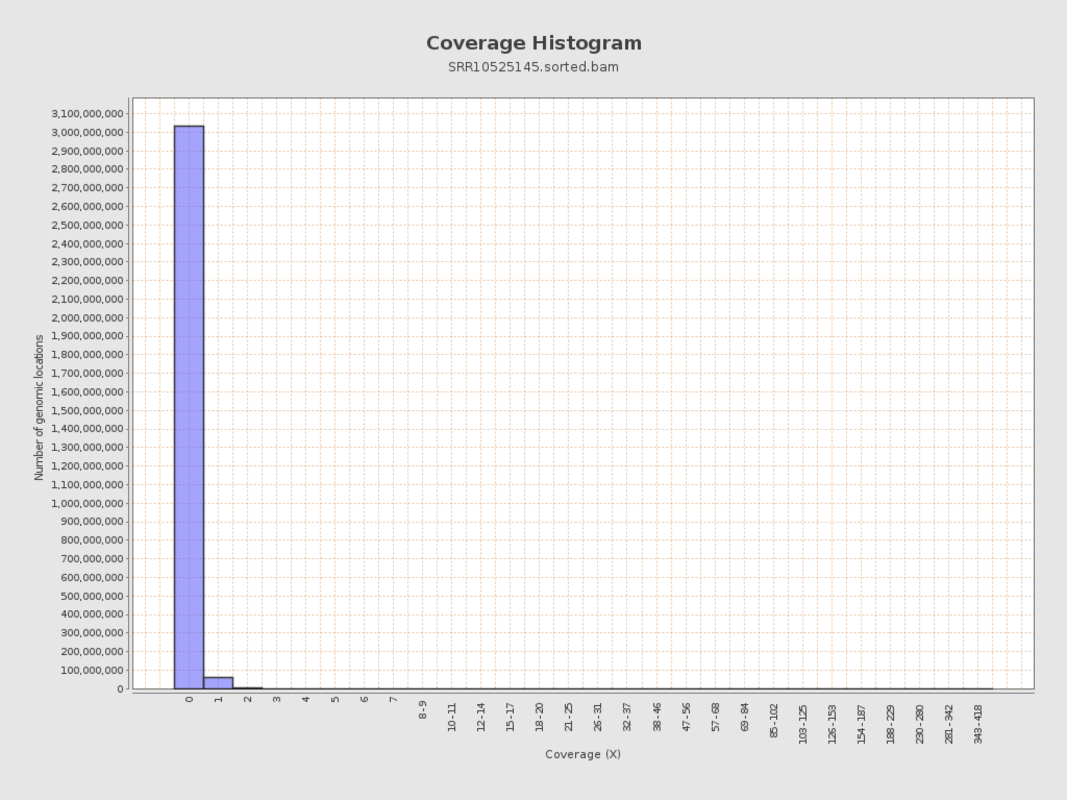
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6920058	0.0278	0.4173
chr2	243199373	5977694	0.0246	0.353
chr3	198022430	4590904	0.0232	0.1619
chr4	191154276	4542003	0.0238	0.1723
chr5	180915260	4225841	0.0234	0.1631
chr6	171115067	4023409	0.0235	0.1784
chr7	159138663	3869135	0.0243	0.369

chr8	146364022	3562669	0.0243	0.3154
chr9	141213431	2925362	0.0207	0.2458
chr10	135534747	3288291	0.0243	0.2803
chr11	135006516	3911058	0.029	0.2786
chr12	133851895	3143610	0.0235	0.1632
chr13	115169878	2568867	0.0223	0.1598
chr14	107349540	2104918	0.0196	0.1672
chr15	102531392	1980983	0.0193	0.1475
chr16	90354753	1646179	0.0182	0.1575
chr17	81195210	2197482	0.0271	0.199
chr18	78077248	1885460	0.0241	0.4078
chr19	59128983	1427473	0.0241	0.3035
chr20	63025520	1390909	0.0221	0.1638
chr21	48129895	914542	0.019	0.1568
chr22	51304566	747606	0.0146	0.128
chrMT	16571	19901	1.201	1.3257
chrX	155270560	3912815	0.0252	0.2106
chrY	59373566	169518	0.0029	0.074

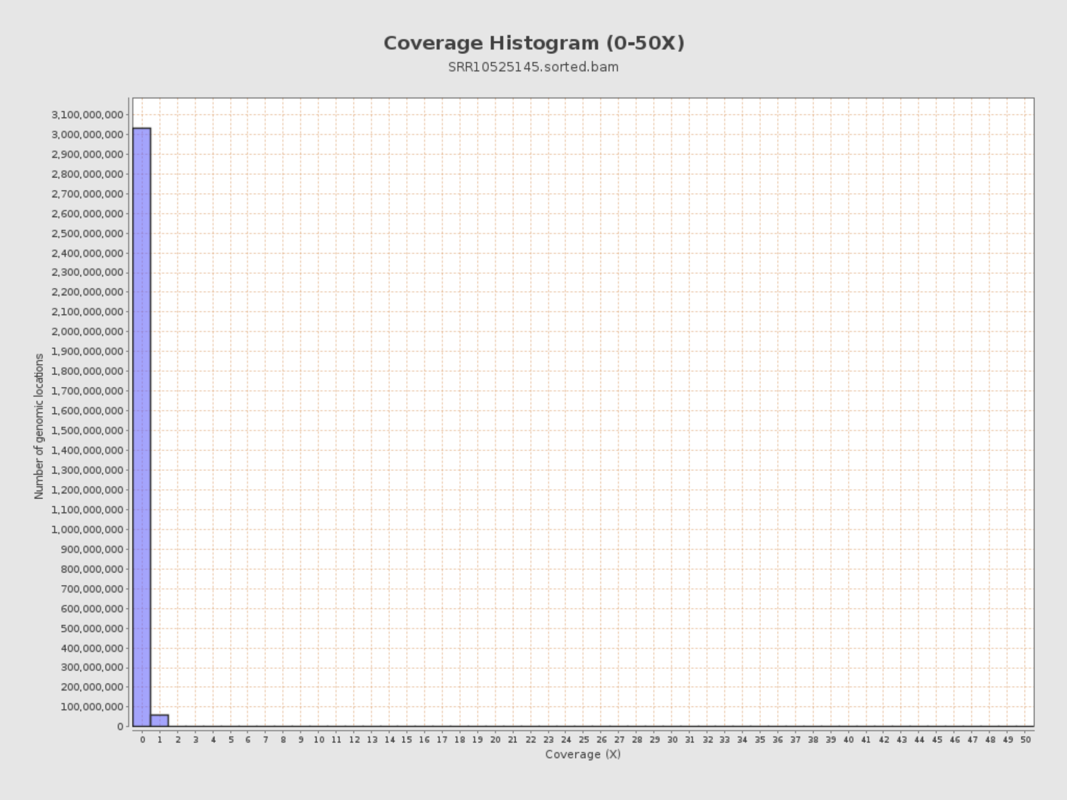
3. Results : Coverage across reference



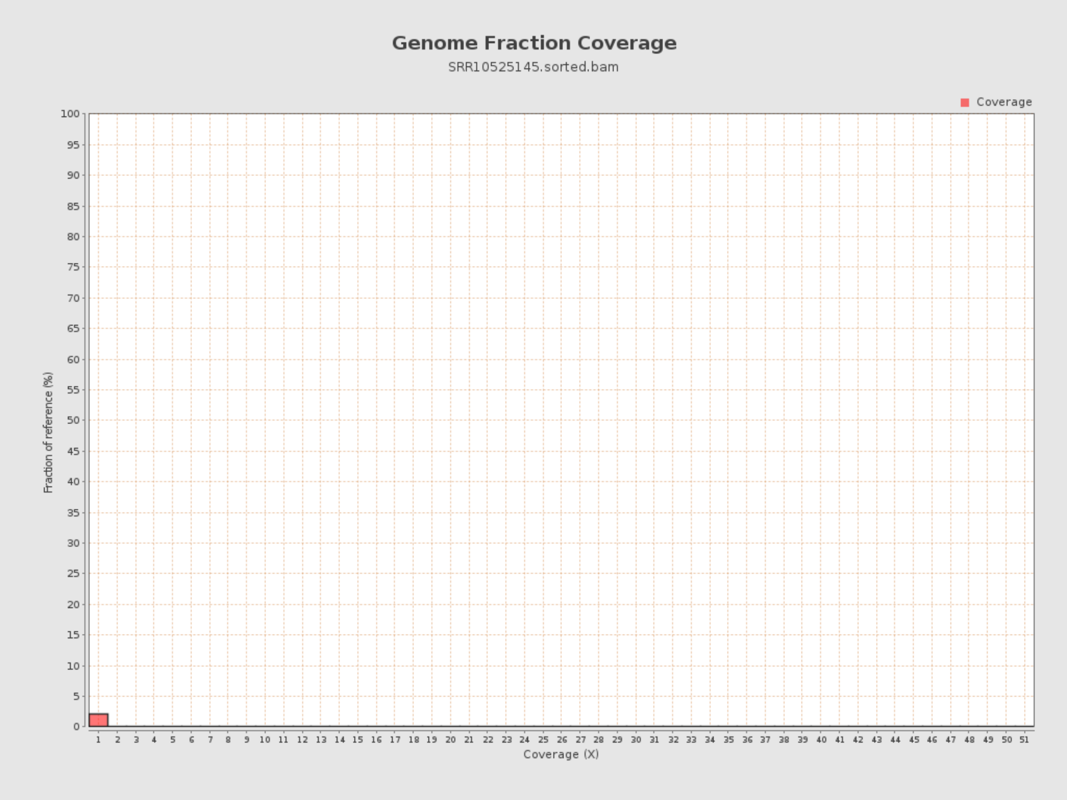
4. Results : Coverage Histogram



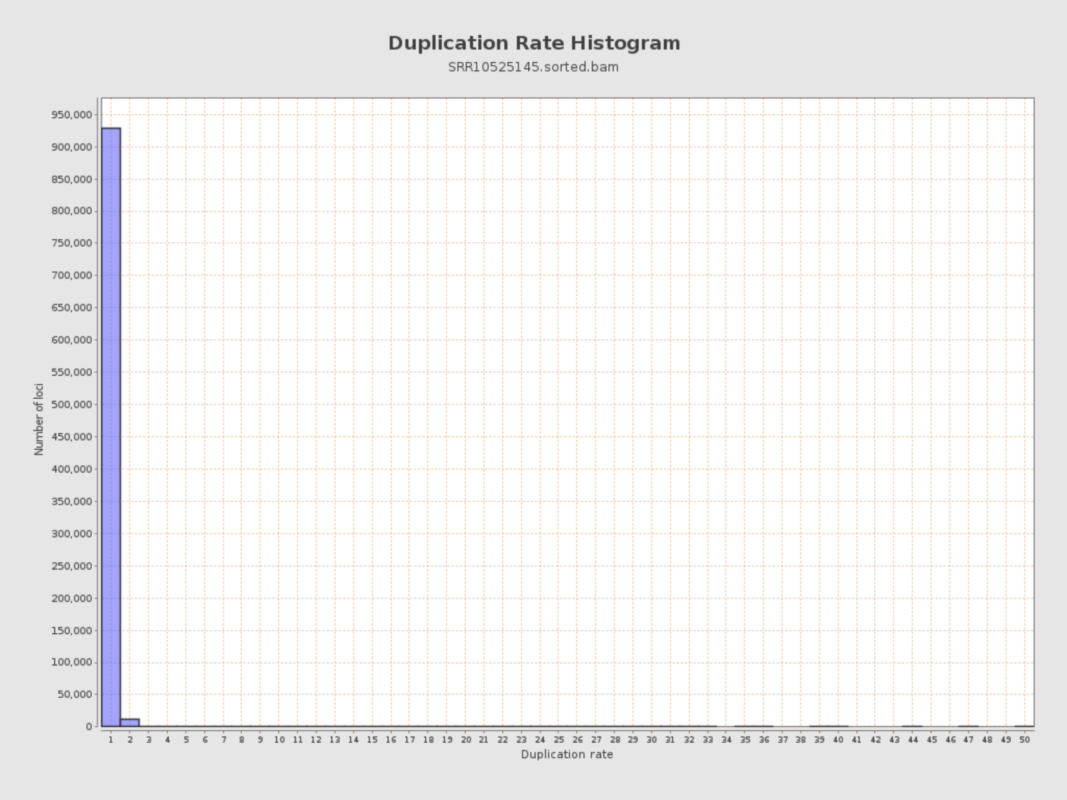
5. Results : Coverage Histogram (0-50X)



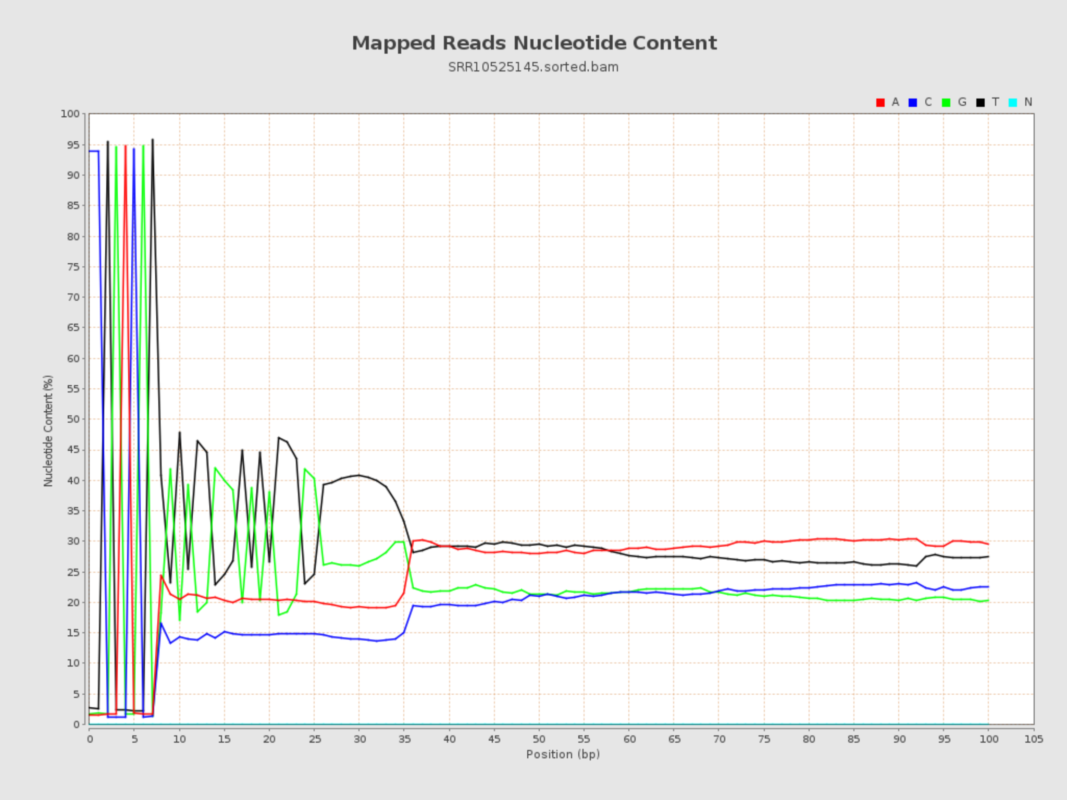
6. Results : Genome Fraction Coverage



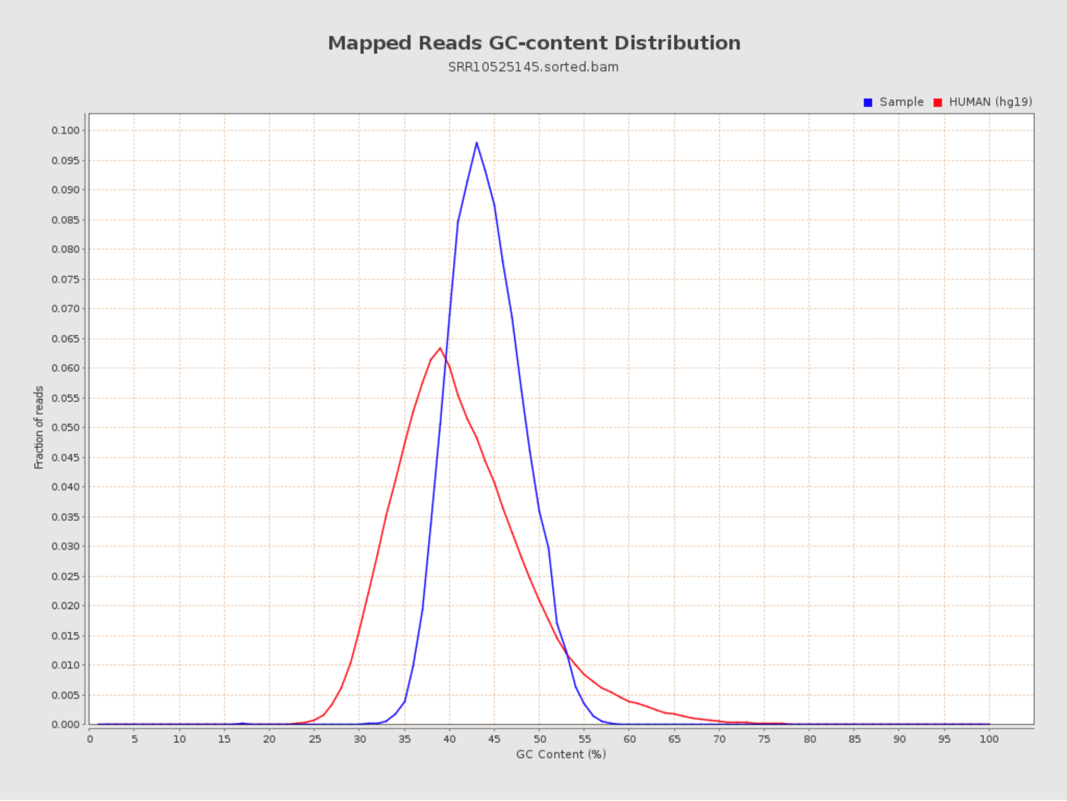
7. Results : Duplication Rate Histogram



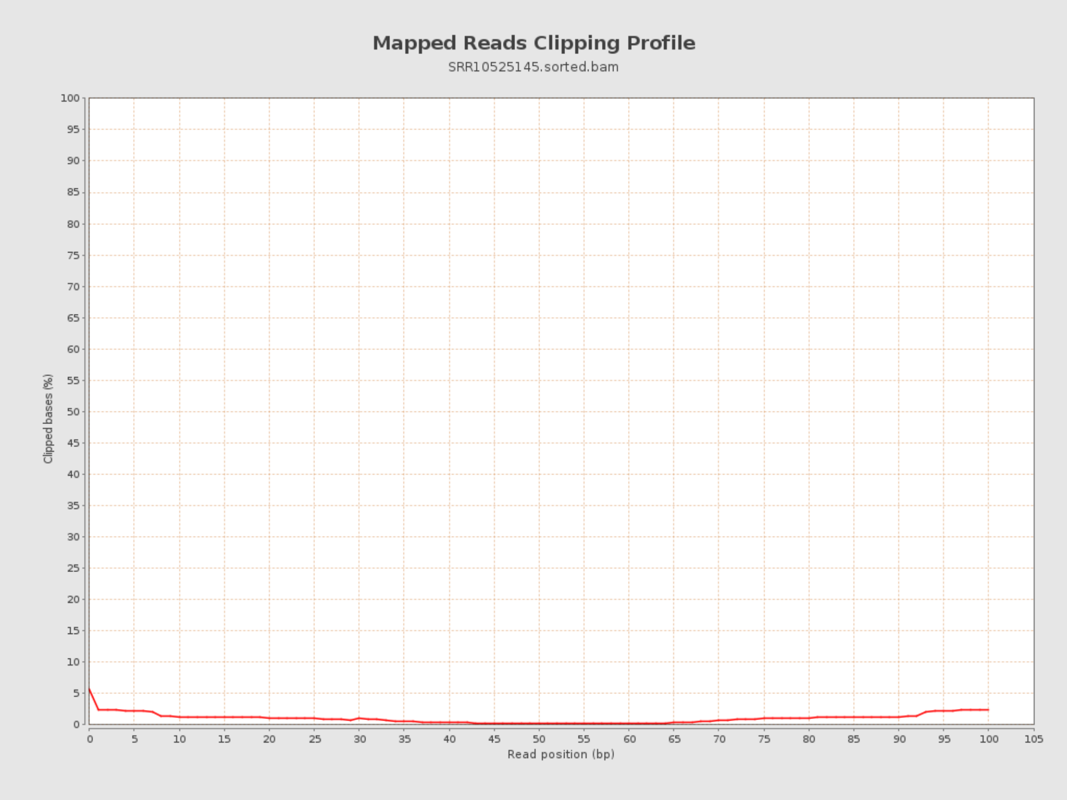
8. Results : Mapped Reads Nucleotide Content



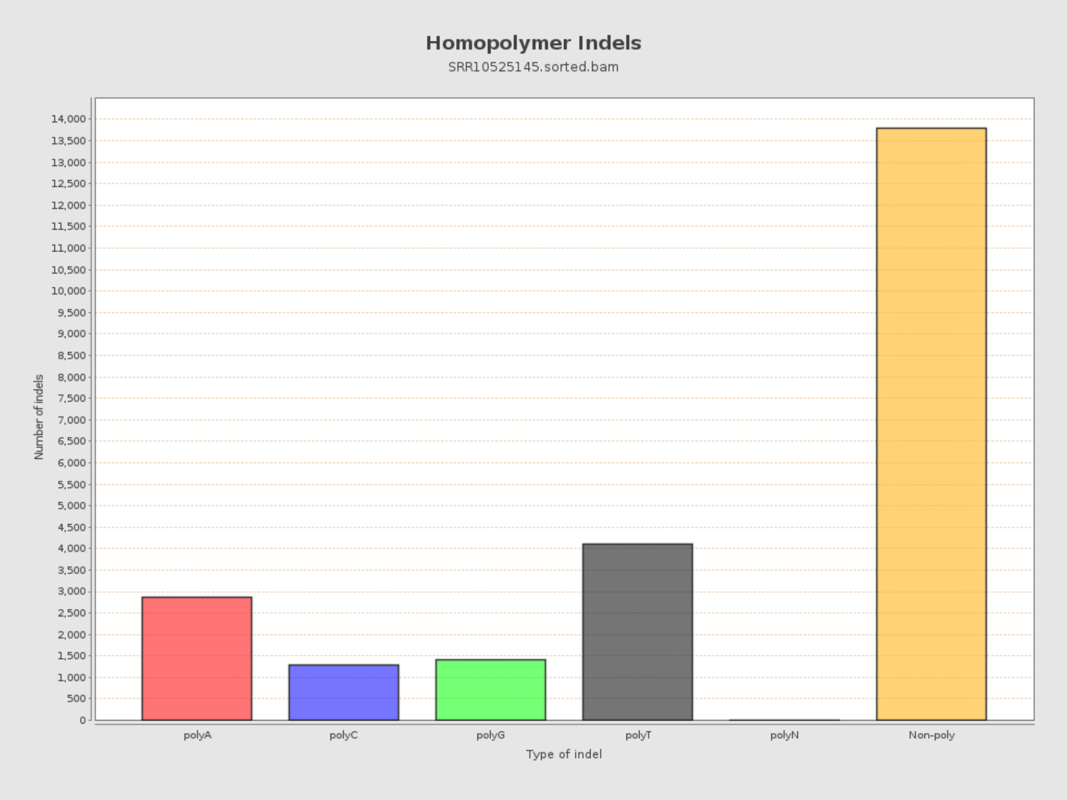
9. Results : Mapped Reads GC-content Distribution



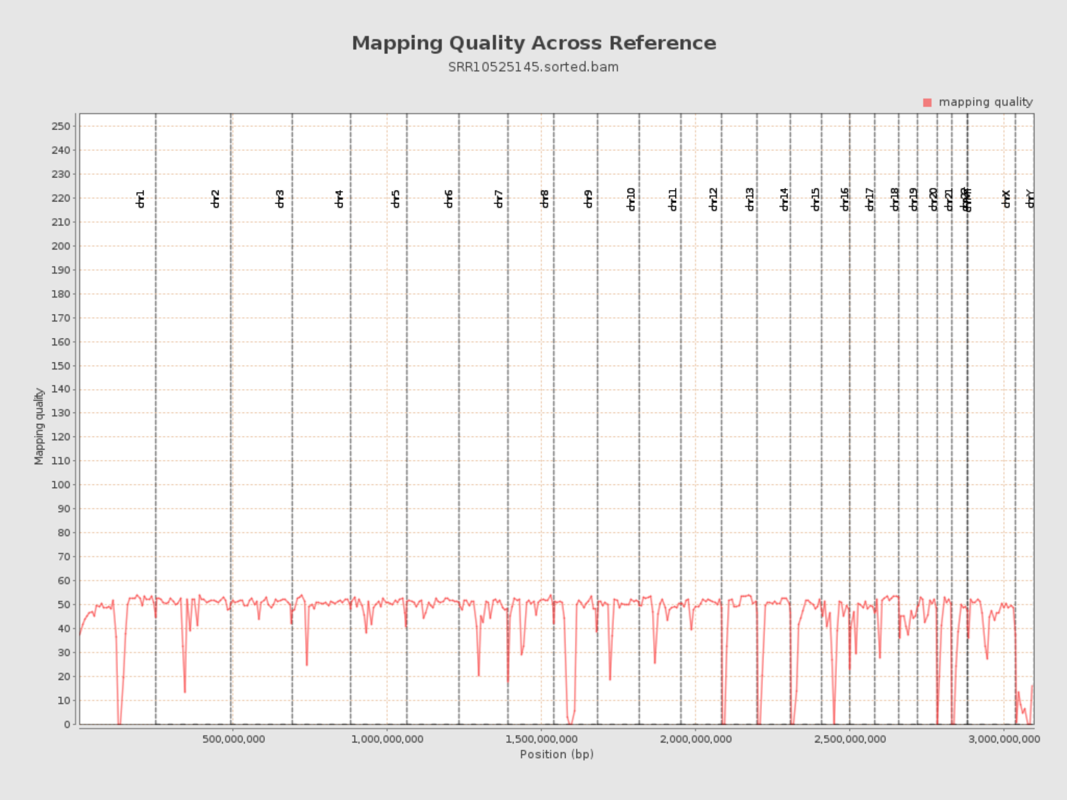
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram