Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:23:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525174.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_SRR10525174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:23:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,120,643
Mapped reads	1,030,531 / 91.96%
Unmapped reads	90,112 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,869 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	22,162 / 1.98%
Duplication rate	1.47%
Clipped reads	1,029,699 / 91.88%

2.2. ACGT Content

Number/percentage of A's	17,401,900 / 27.27%
Number/percentage of C's	13,292,197 / 20.83%
Number/percentage of T's	18,842,280 / 29.52%
Number/percentage of G's	14,286,692 / 22.38%
Number/percentage of N's	1,580 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0206

Standard Deviation	0.2212

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

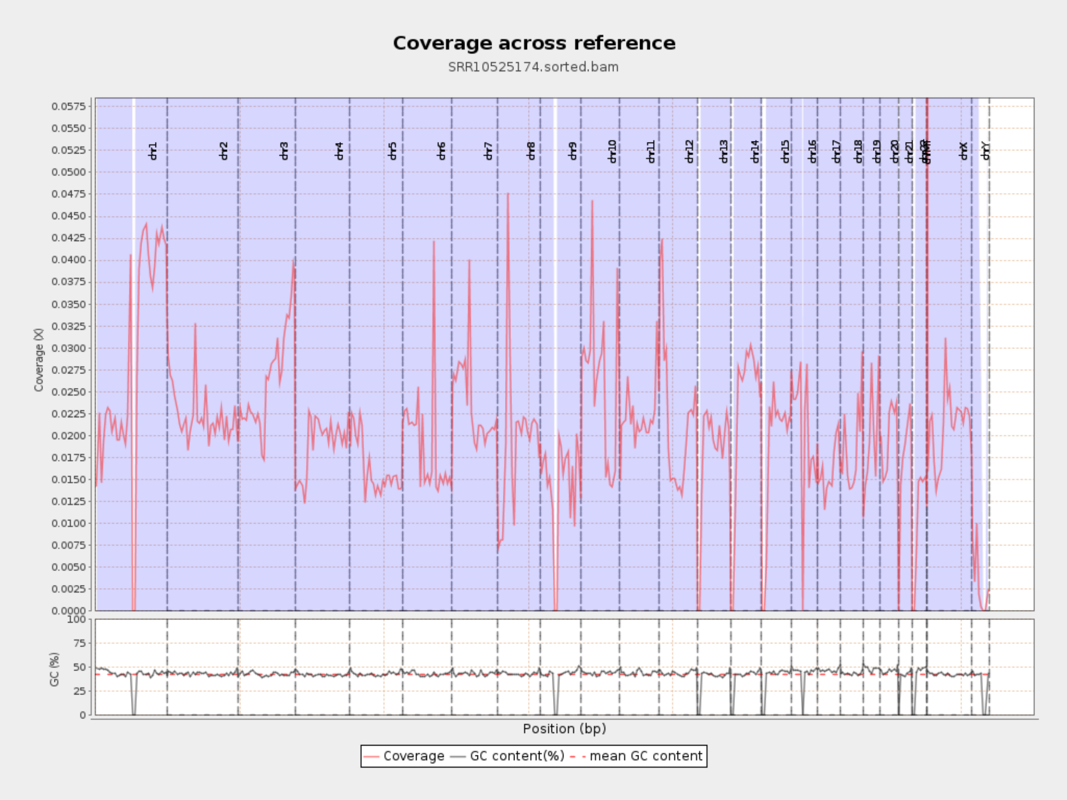
General error rate	0.5%
Mismatches	306,806
Insertions	5,645
Mapped reads with at least one insertion	0.55%
Deletions	13,151
Mapped reads with at least one deletion	1.27%
Homopolymer indels	41.52%

2.6. Chromosome stats

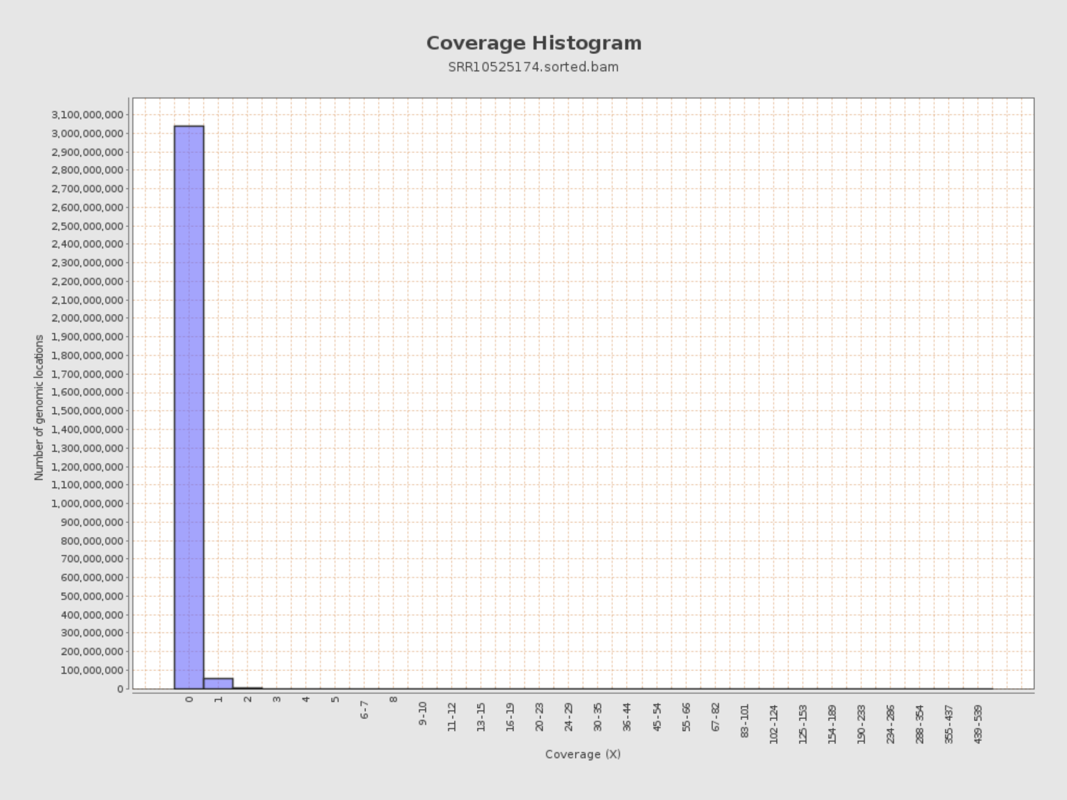
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7071616	0.0284	0.4449
chr2	243199373	5418896	0.0223	0.2222
chr3	198022430	5184007	0.0262	0.1711
chr4	191154276	3641304	0.019	0.1486
chr5	180915260	2948080	0.0163	0.1343
chr6	171115067	3246776	0.019	0.1595
chr7	159138663	3795060	0.0238	0.3218

chr8	146364022	2882492	0.0197	0.1743
chr9	141213431	2013184	0.0143	0.1574
chr10	135534747	3567965	0.0263	0.2456
chr11	135006516	2985246	0.0221	0.1825
chr12	133851895	2931408	0.0219	0.1568
chr13	115169878	2039900	0.0177	0.1395
chr14	107349540	2462679	0.0229	0.1635
chr15	102531392	1836370	0.0179	0.1398
chr16	90354753	1812098	0.0201	0.1634
chr17	81195210	1301328	0.016	0.1375
chr18	78077248	1420828	0.0182	0.3093
chr19	59128983	1173318	0.0198	0.3116
chr20	63025520	1233514	0.0196	0.1478
chr21	48129895	833198	0.0173	0.1466
chr22	51304566	537568	0.0105	0.107
chrMT	16571	35711	2.155	1.8126
chrX	155270560	3292387	0.0212	0.1623
chrY	59373566	180865	0.003	0.101

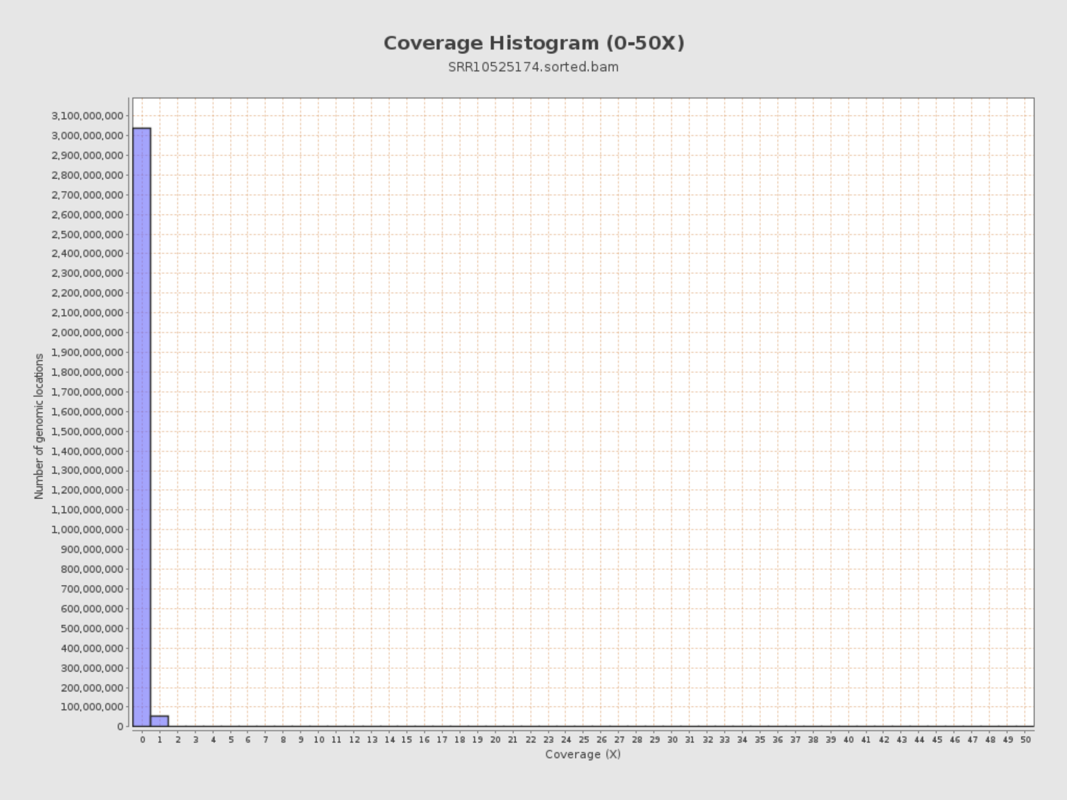
3. Results : Coverage across reference



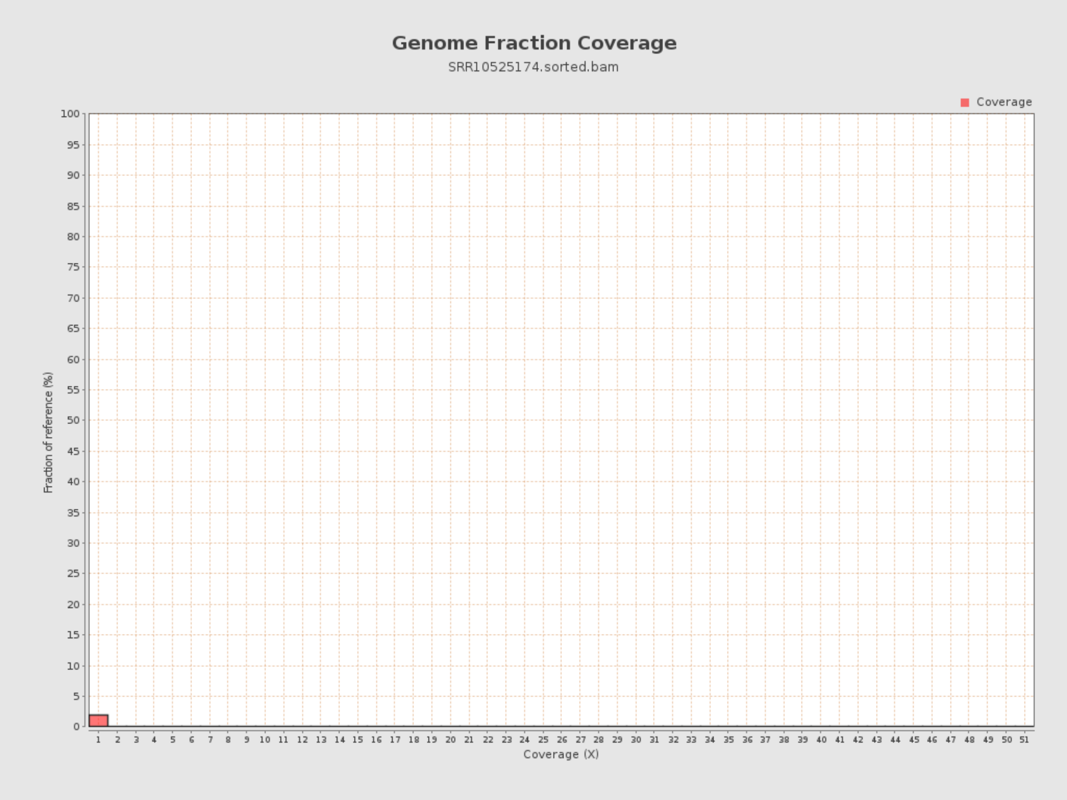
4. Results : Coverage Histogram



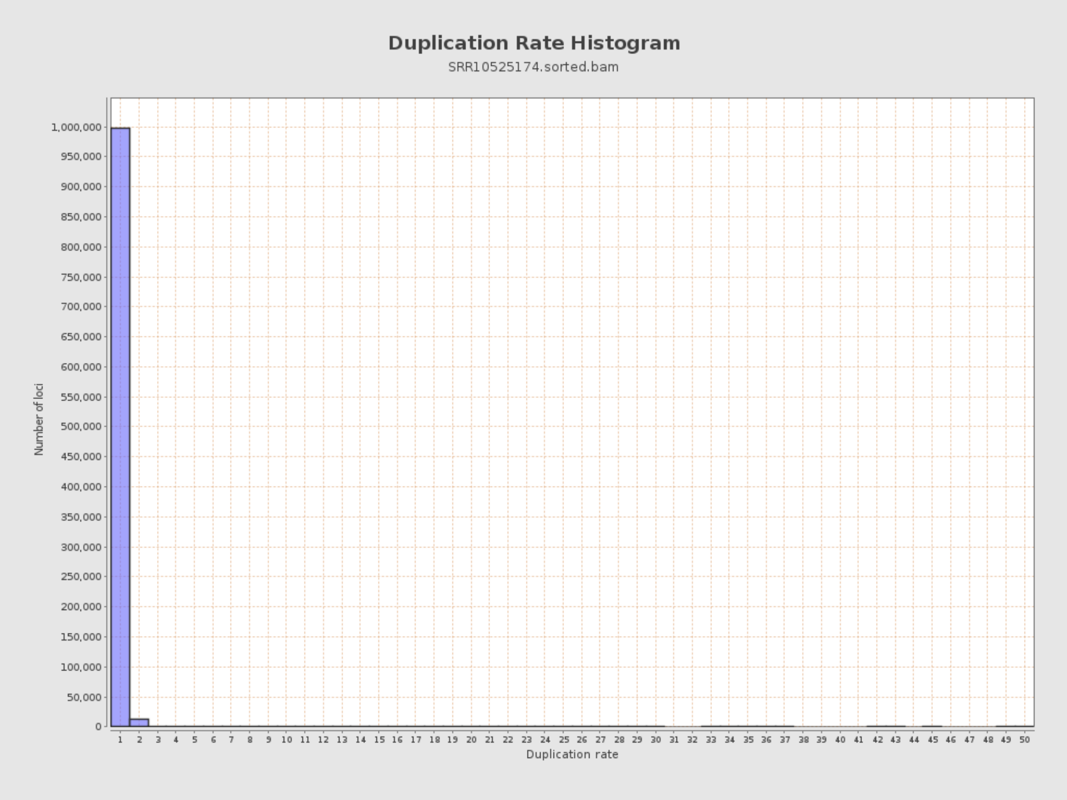
5. Results : Coverage Histogram (0-50X)



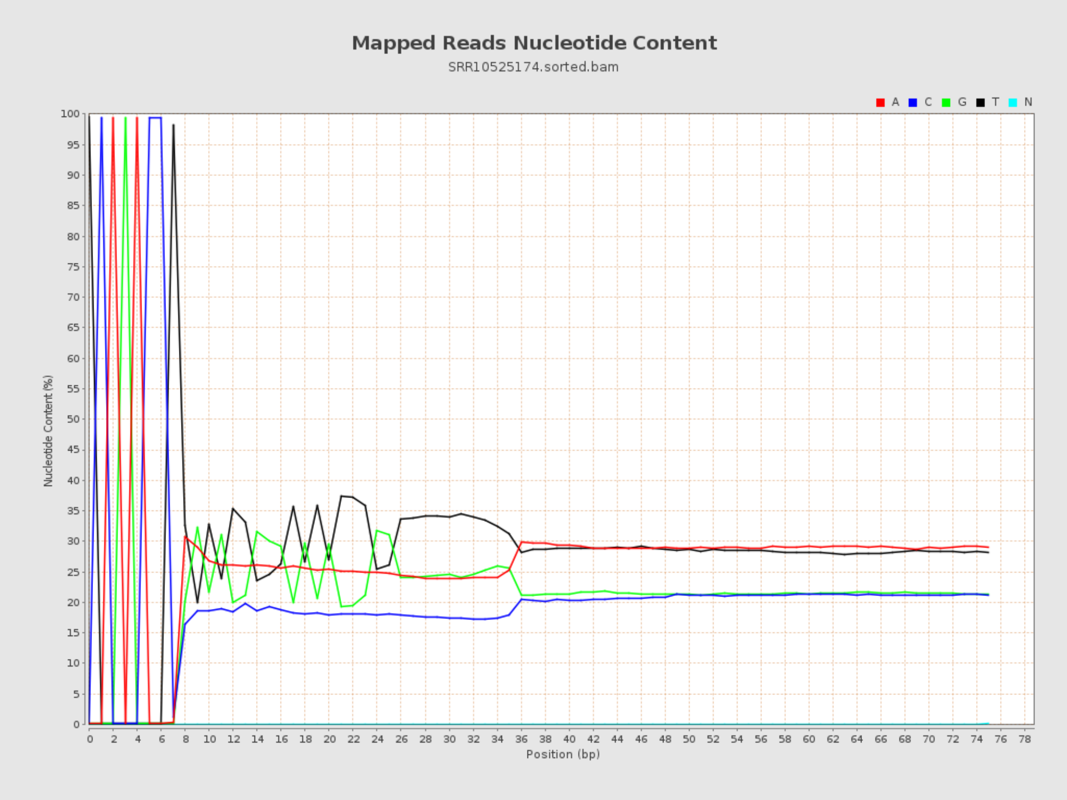
6. Results : Genome Fraction Coverage



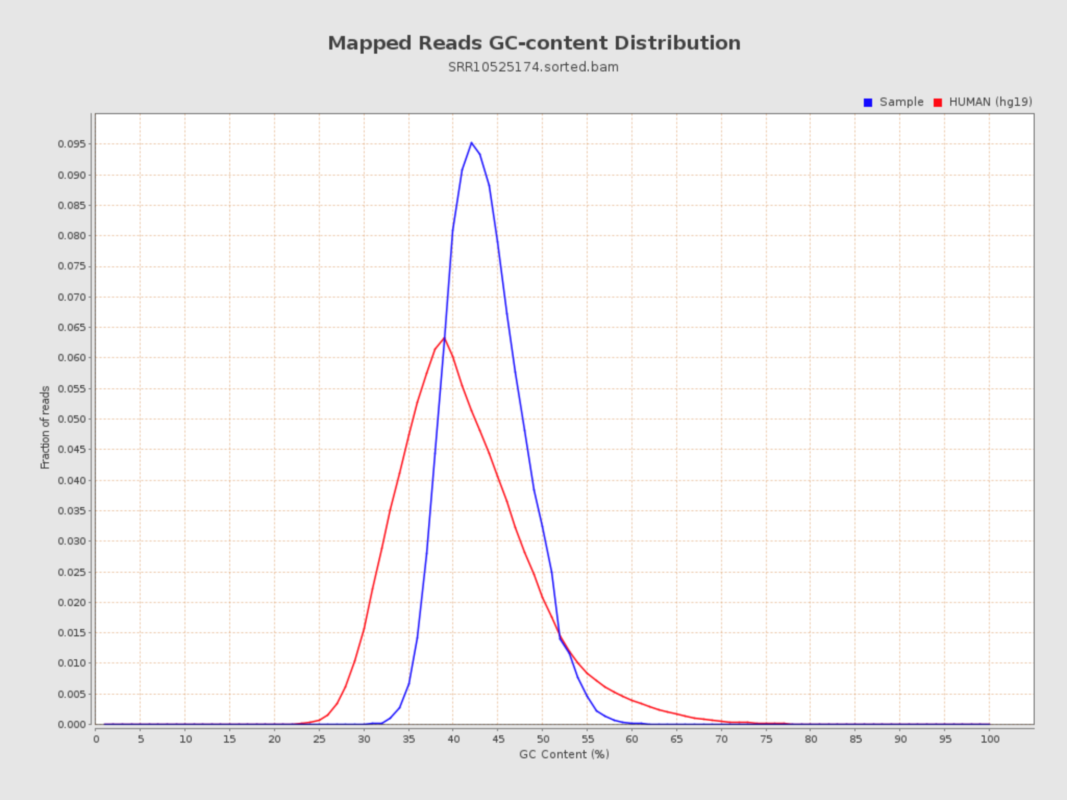
7. Results : Duplication Rate Histogram



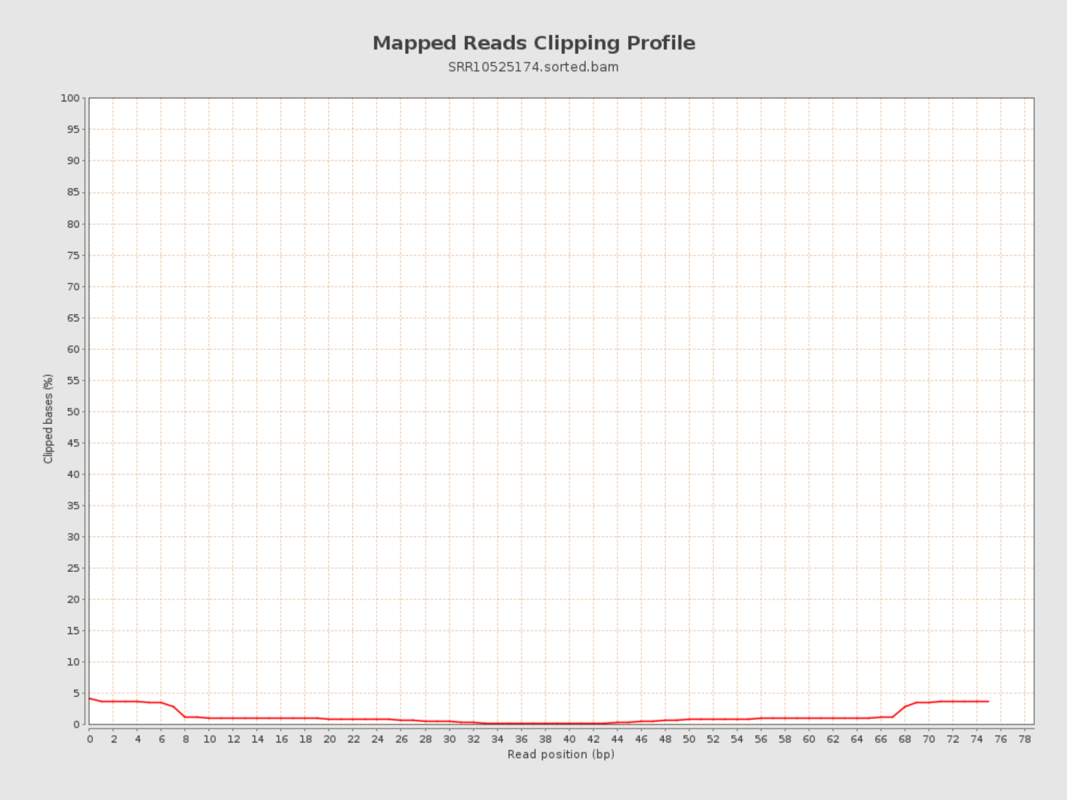
8. Results : Mapped Reads Nucleotide Content



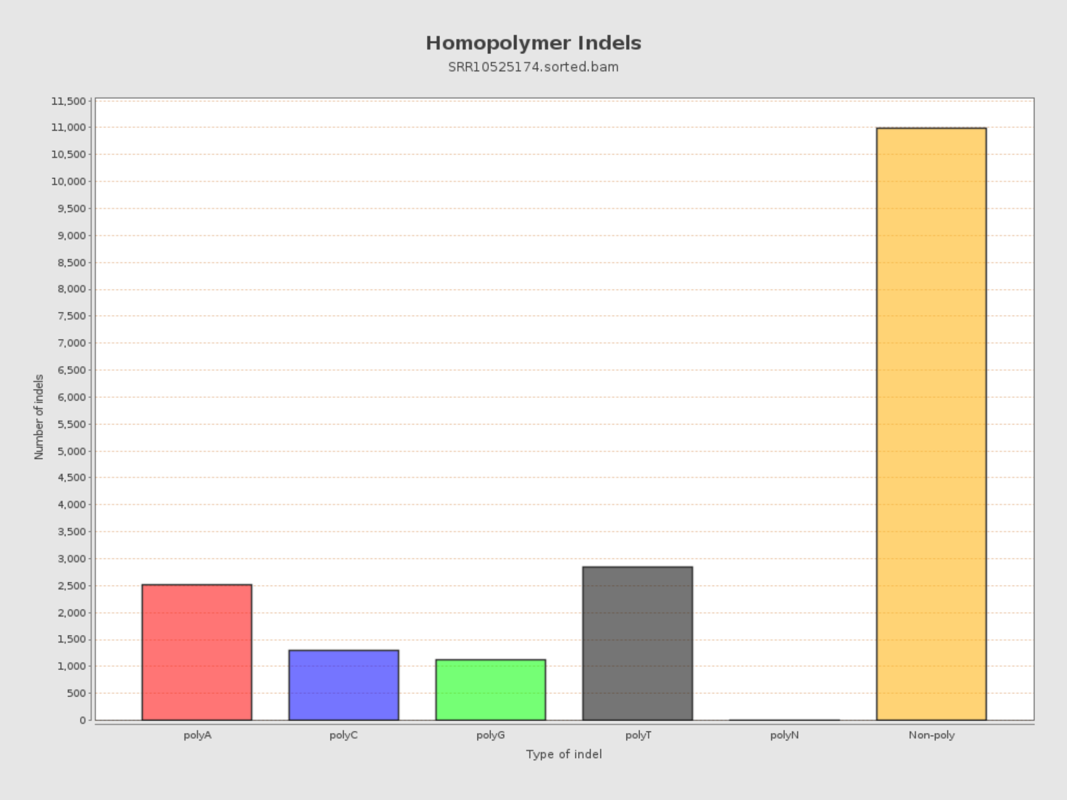
9. Results : Mapped Reads GC-content Distribution



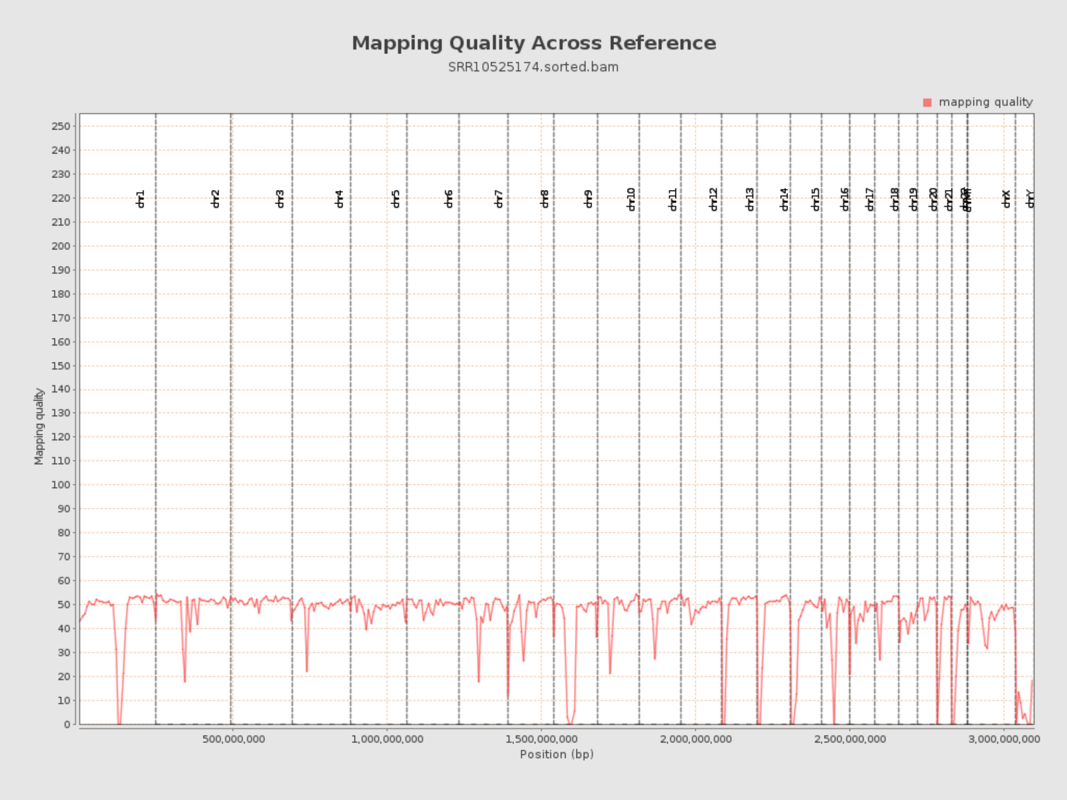
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram