Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:57:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525224.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_SRR10525224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:57:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,018,124
Mapped reads	956,606 / 93.96%
Unmapped reads	61,518 / 6.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,216 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	19,729 / 1.94%
Duplication rate	1.4%
Clipped reads	956,247 / 93.92%

2.2. ACGT Content

Number/percentage of A's	15,785,267 / 26.23%
Number/percentage of C's	13,067,865 / 21.71%
Number/percentage of T's	18,068,693 / 30.02%
Number/percentage of G's	13,260,980 / 22.03%
Number/percentage of N's	1,437 / 0%
GC Percentage	43.75%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2053

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

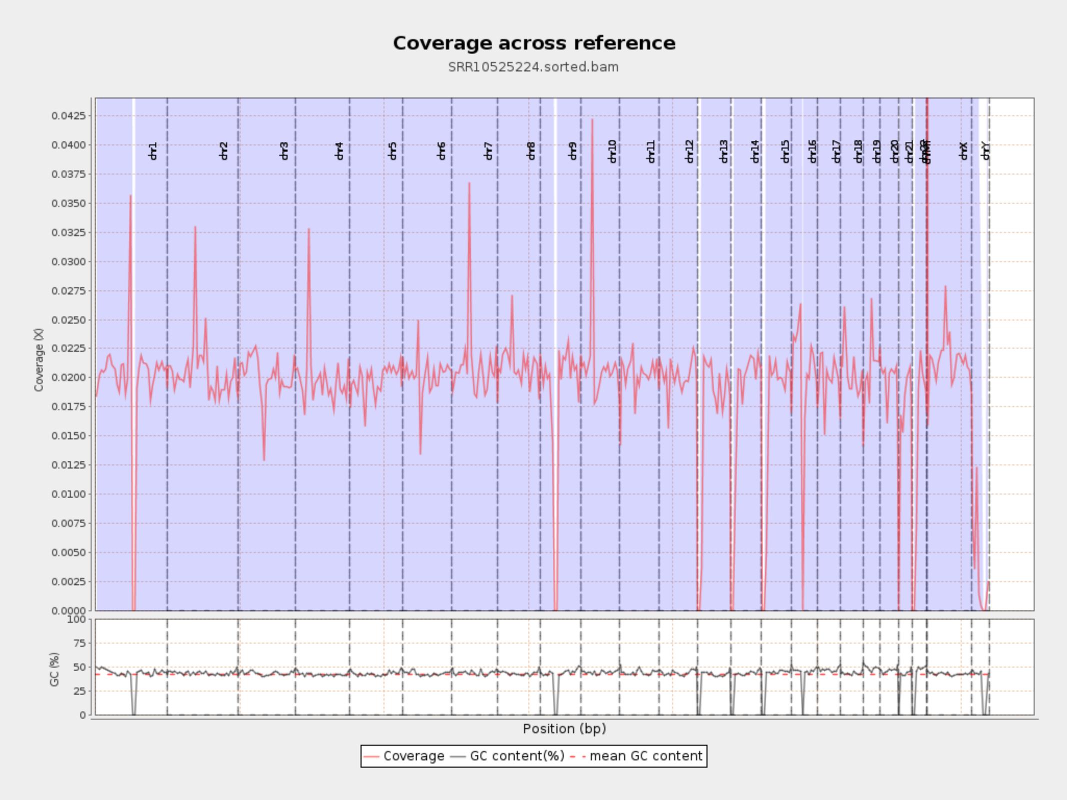
General error rate	0.5%
Mismatches	293,026
Insertions	4,774
Mapped reads with at least one insertion	0.5%
Deletions	13,721
Mapped reads with at least one deletion	1.42%
Homopolymer indels	42.21%

2.6. Chromosome stats

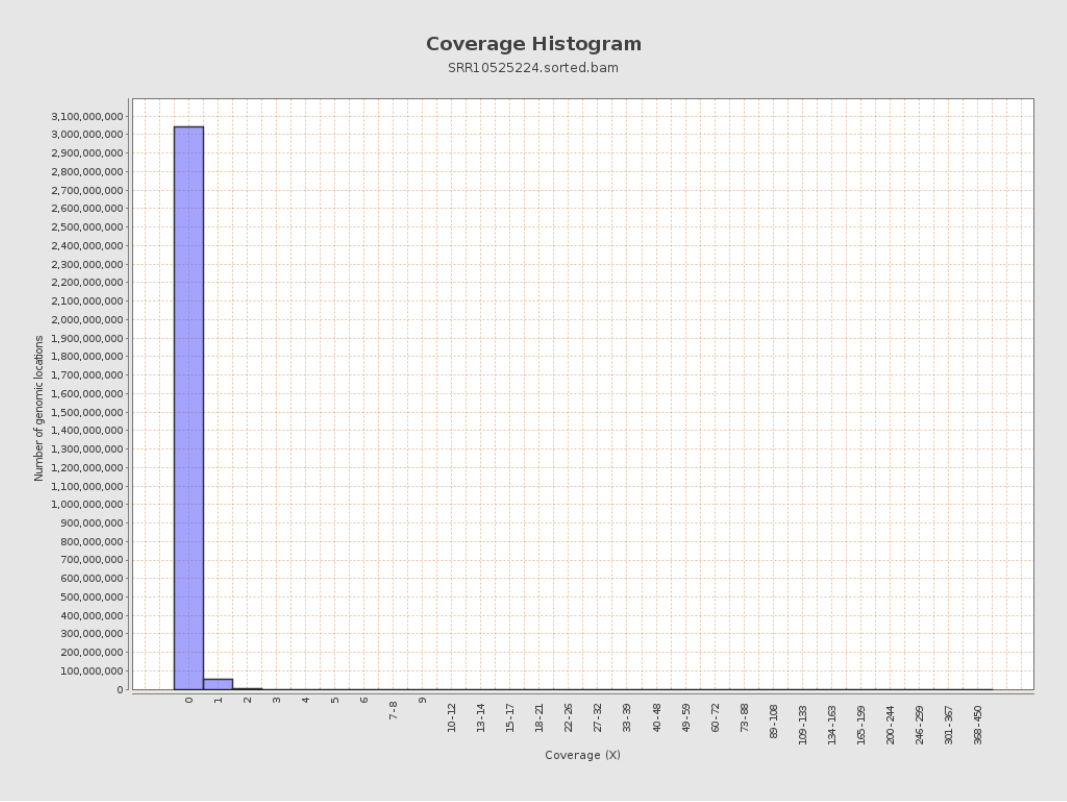
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4894782	0.0196	0.3706
chr2	243199373	5019601	0.0206	0.2107
chr3	198022430	3974780	0.0201	0.1497
chr4	191154276	3830835	0.02	0.1631
chr5	180915260	3594553	0.0199	0.1481
chr6	171115067	3450886	0.0202	0.1606
chr7	159138663	3381090	0.0212	0.2843

chr8	146364022	3097114	0.0212	0.1904
chr9	141213431	2569961	0.0182	0.1784
chr10	135534747	2922135	0.0216	0.2192
chr11	135006516	2750249	0.0204	0.1725
chr12	133851895	2706909	0.0202	0.1513
chr13	115169878	1888002	0.0164	0.134
chr14	107349540	1854406	0.0173	0.1421
chr15	102531392	1684723	0.0164	0.1348
chr16	90354753	1780060	0.0197	0.1599
chr17	81195210	1614927	0.0199	0.155
chr18	78077248	1603417	0.0205	0.3216
chr19	59128983	1240858	0.021	0.2752
chr20	63025520	1250658	0.0198	0.1511
chr21	48129895	798847	0.0166	0.148
chr22	51304566	712937	0.0139	0.1238
chrMT	16571	41103	2.4804	1.9873
chrX	155270560	3347826	0.0216	0.161
chrY	59373566	196395	0.0033	0.1186

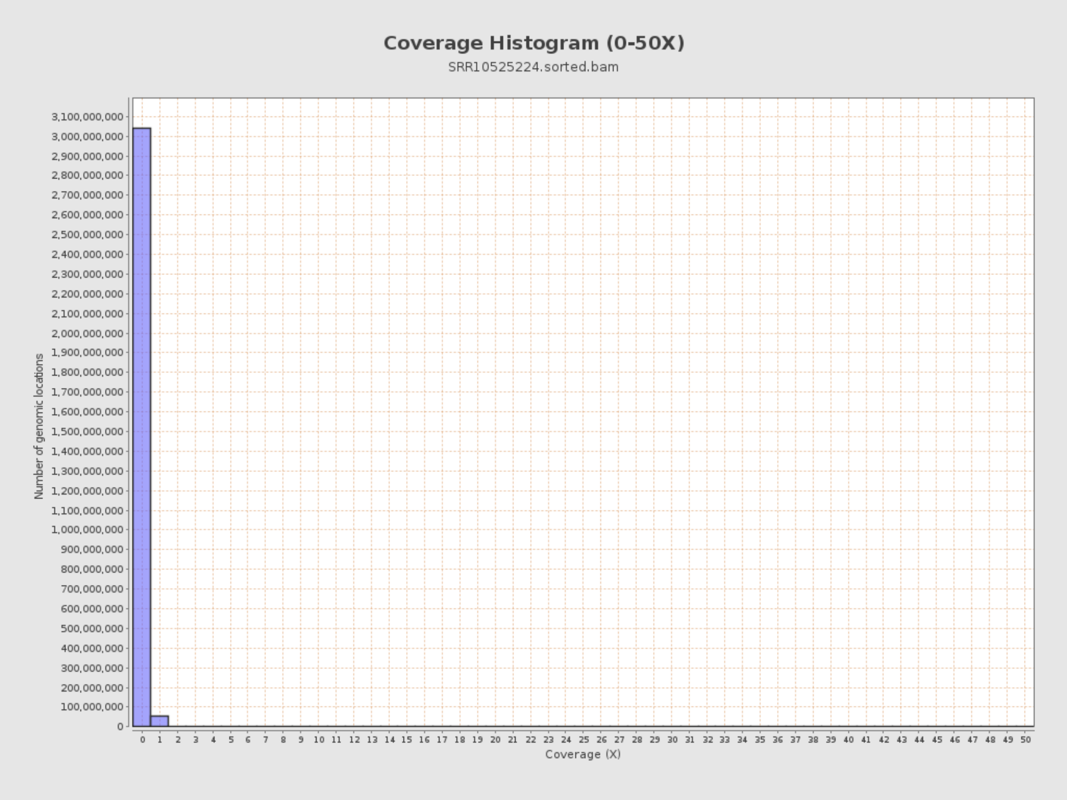
3. Results : Coverage across reference



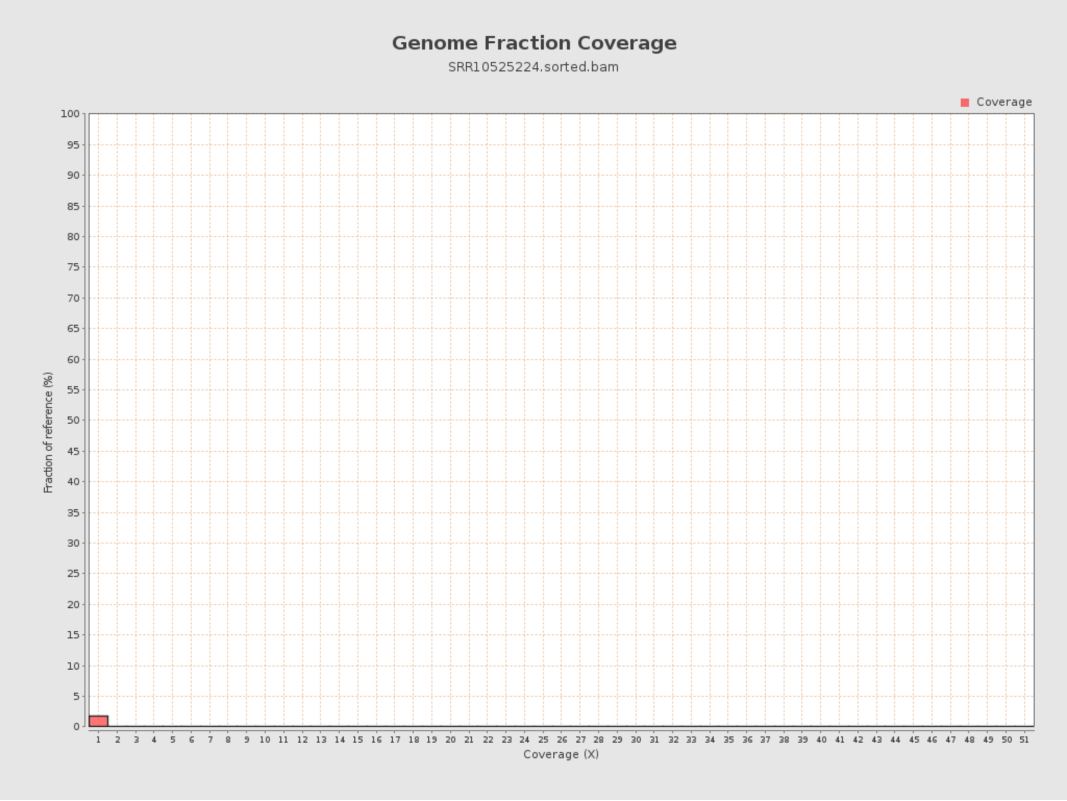
4. Results : Coverage Histogram



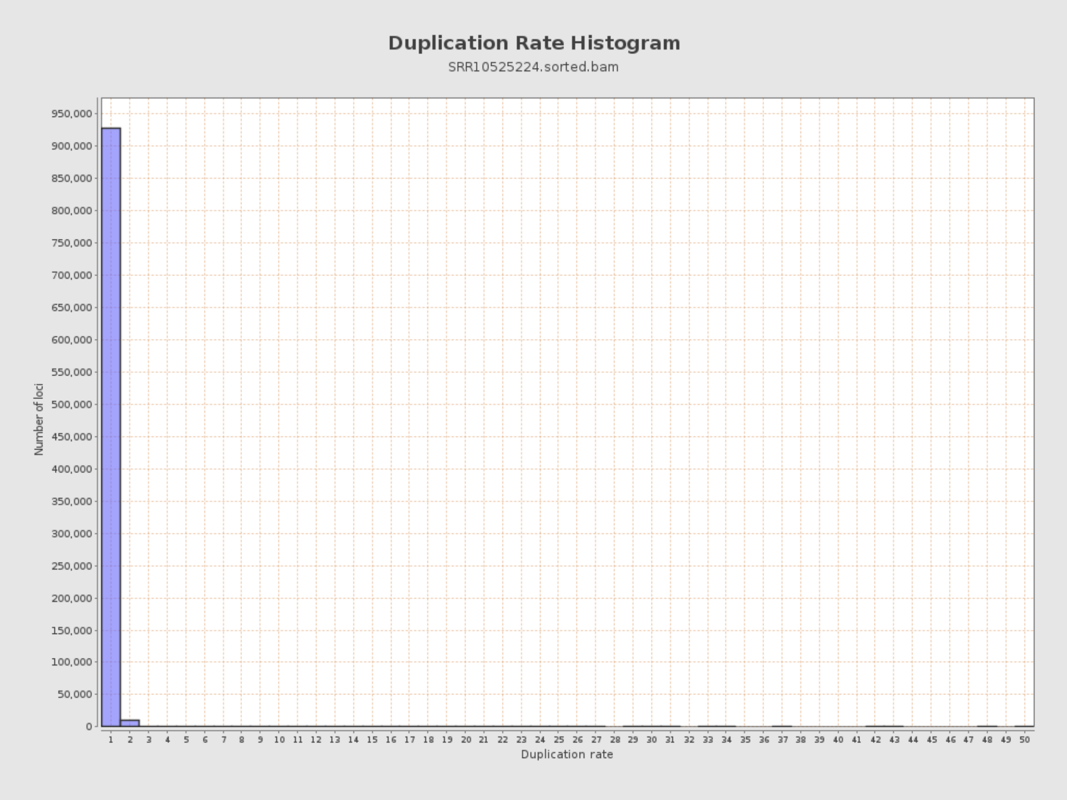
5. Results : Coverage Histogram (0-50X)



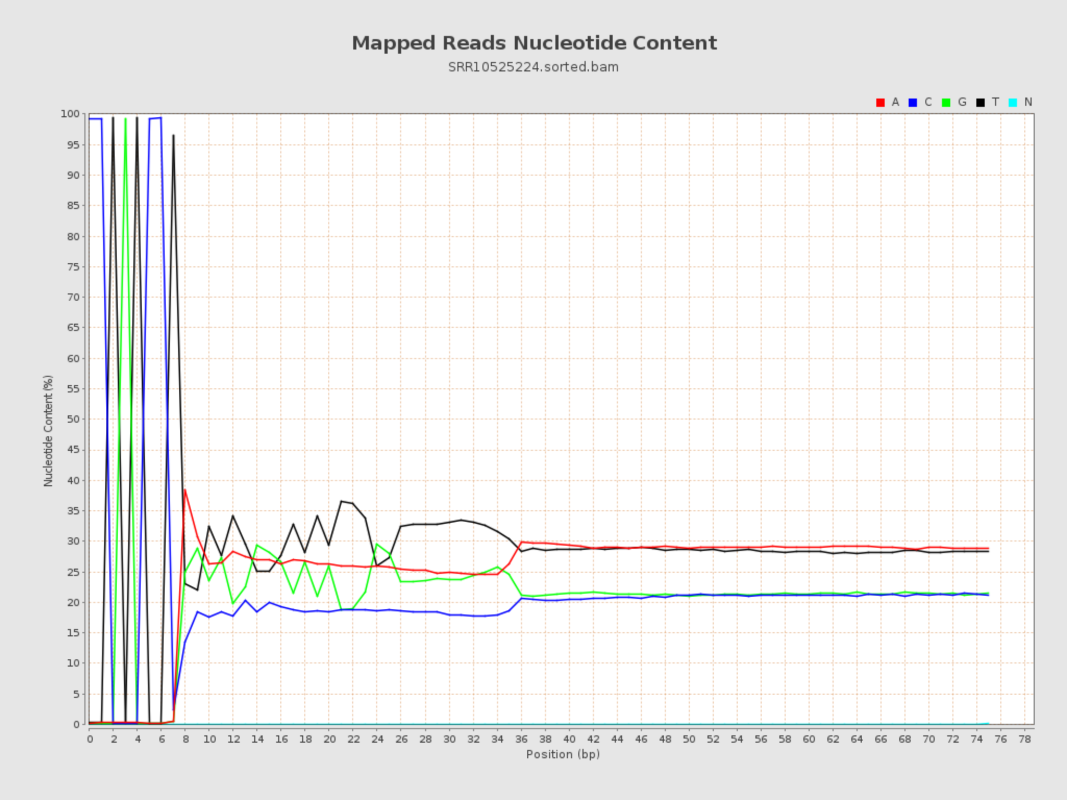
6. Results : Genome Fraction Coverage



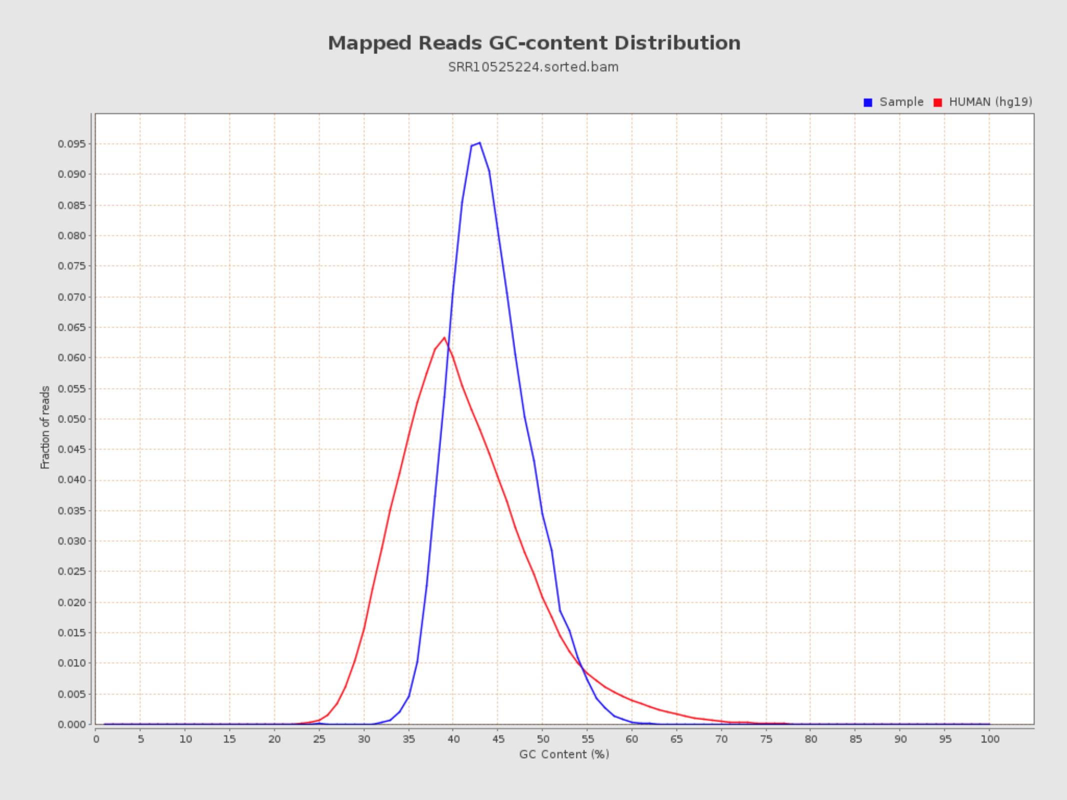
7. Results : Duplication Rate Histogram



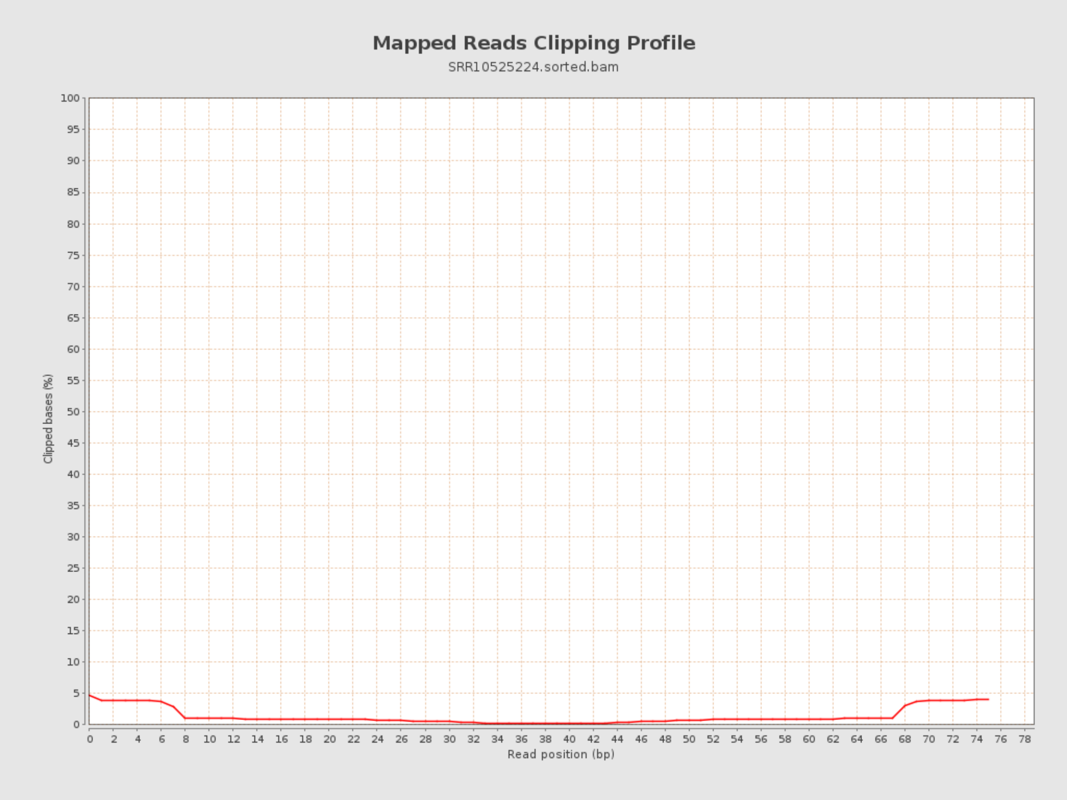
8. Results : Mapped Reads Nucleotide Content



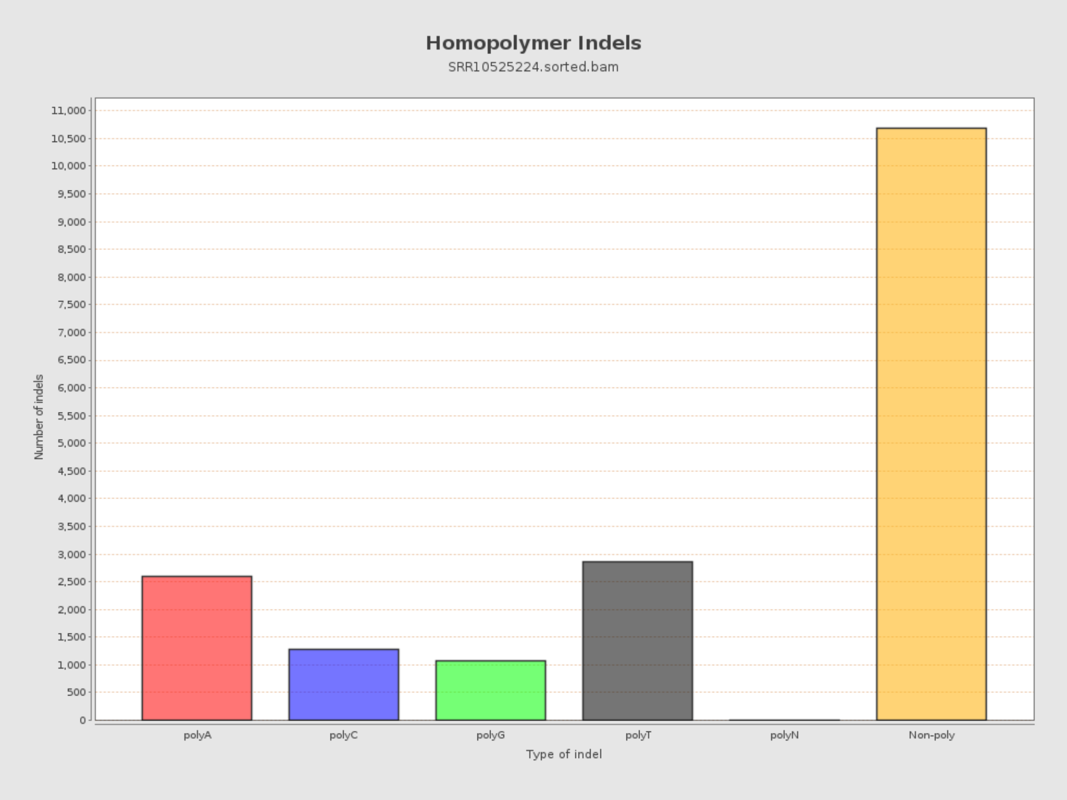
9. Results : Mapped Reads GC-content Distribution



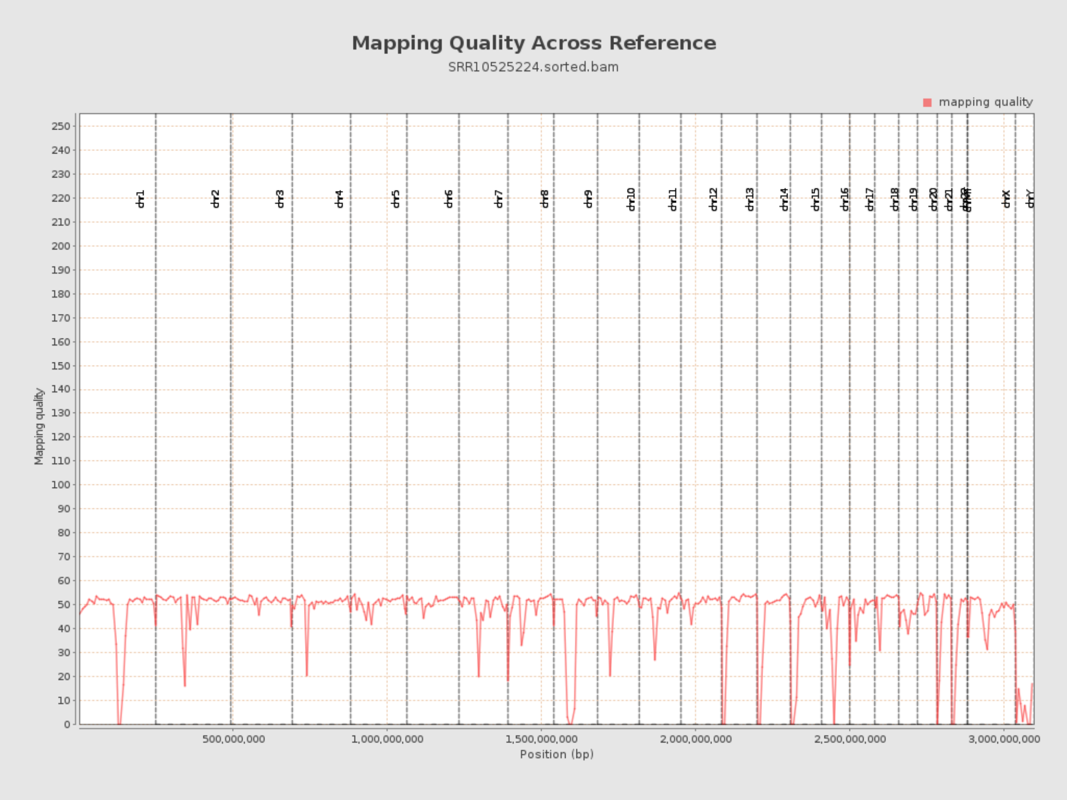
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram