Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:39:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525044.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_SRR10525044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:39:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,083,936
Mapped reads	989,433 / 91.28%
Unmapped reads	94,503 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,312 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,138 / 2.04%
Duplication rate	1.67%
Clipped reads	991,265 / 91.45%

2.2. ACGT Content

Number/percentage of A's	15,009,668 / 26.23%
Number/percentage of C's	11,276,167 / 19.7%
Number/percentage of T's	17,730,751 / 30.98%
Number/percentage of G's	13,215,947 / 23.09%
Number/percentage of N's	1,645 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.18

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

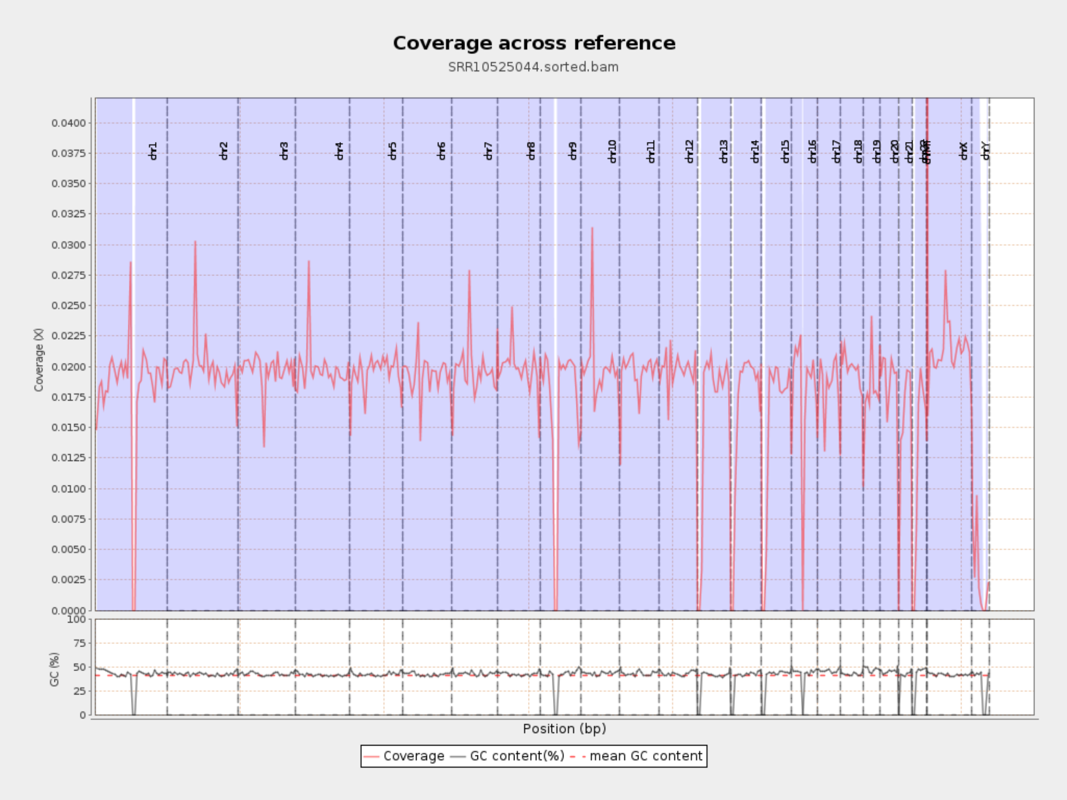
General error rate	0.49%
Mismatches	272,109
Insertions	3,905
Mapped reads with at least one insertion	0.39%
Deletions	8,662
Mapped reads with at least one deletion	0.87%
Homopolymer indels	41.71%

2.6. Chromosome stats

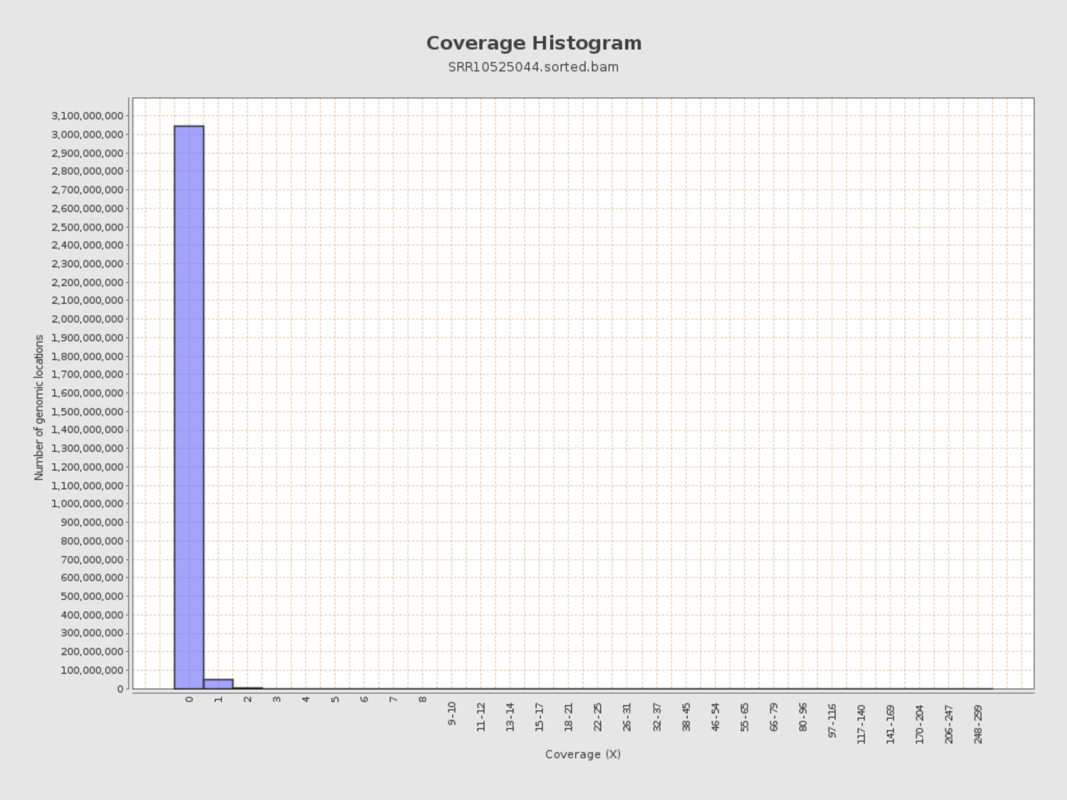
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4532683	0.0182	0.2783
chr2	243199373	4839567	0.0199	0.1918
chr3	198022430	3896853	0.0197	0.148
chr4	191154276	3789052	0.0198	0.1565
chr5	180915260	3561421	0.0197	0.1485
chr6	171115067	3305570	0.0193	0.1534
chr7	159138663	3130296	0.0197	0.1957

chr8	146364022	2898224	0.0198	0.2169
chr9	141213431	2396672	0.017	0.1754
chr10	135534747	2704754	0.02	0.1845
chr11	135006516	2647682	0.0196	0.1753
chr12	133851895	2632705	0.0197	0.1512
chr13	115169878	1847809	0.016	0.1331
chr14	107349540	1738457	0.0162	0.1407
chr15	102531392	1560466	0.0152	0.1301
chr16	90354753	1593275	0.0176	0.1467
chr17	81195210	1484892	0.0183	0.1494
chr18	78077248	1555516	0.0199	0.266
chr19	59128983	1074501	0.0182	0.227
chr20	63025520	1186747	0.0188	0.1472
chr21	48129895	736948	0.0153	0.1404
chr22	51304566	633668	0.0124	0.1171
chrMT	16571	4846	0.2924	0.5903
chrX	155270560	3326190	0.0214	0.165
chrY	59373566	169475	0.0029	0.0786

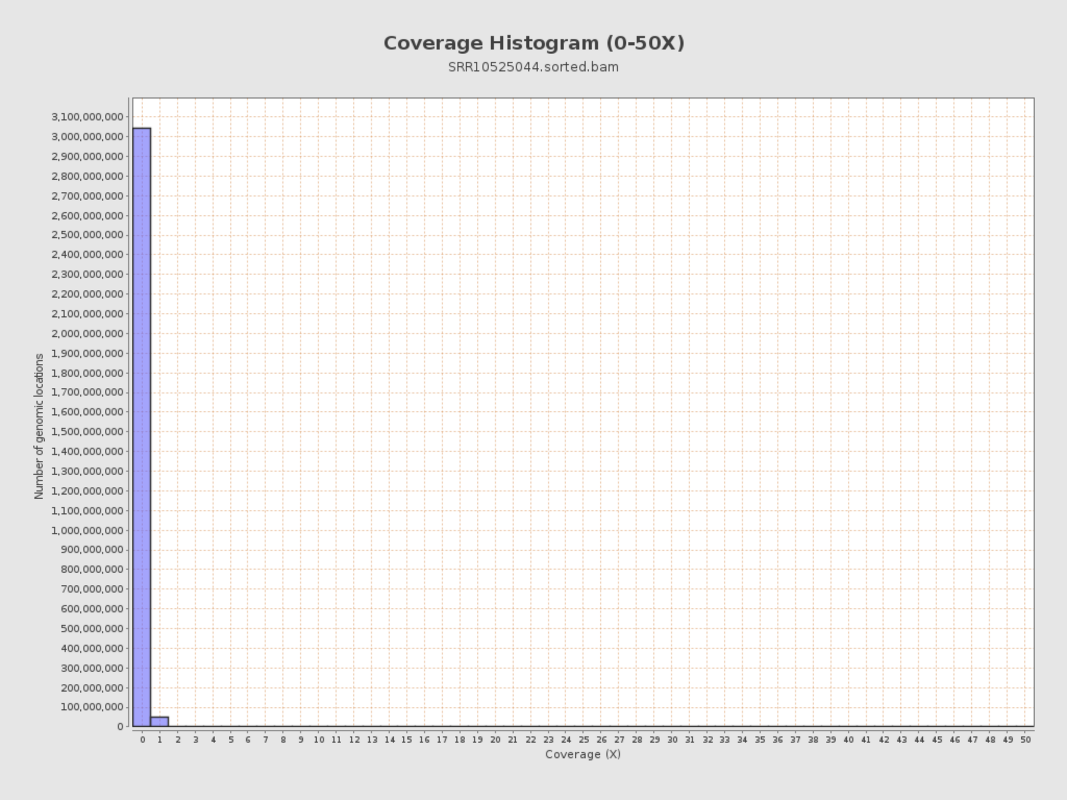
3. Results : Coverage across reference



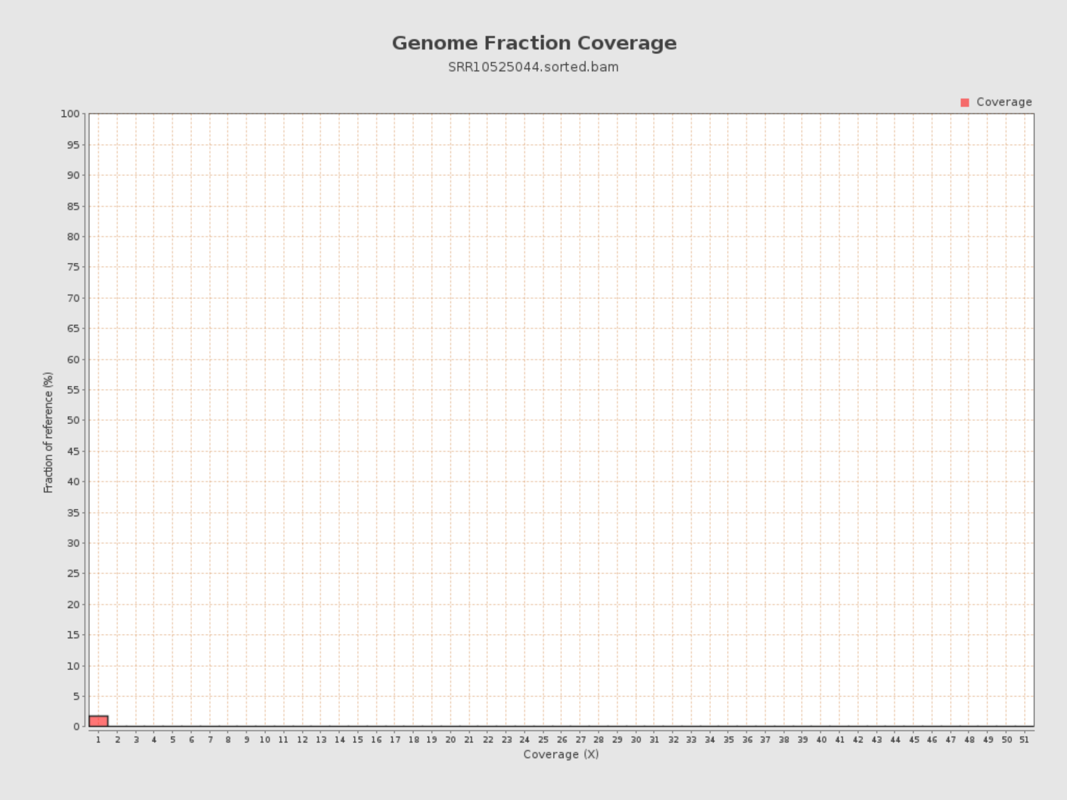
4. Results : Coverage Histogram



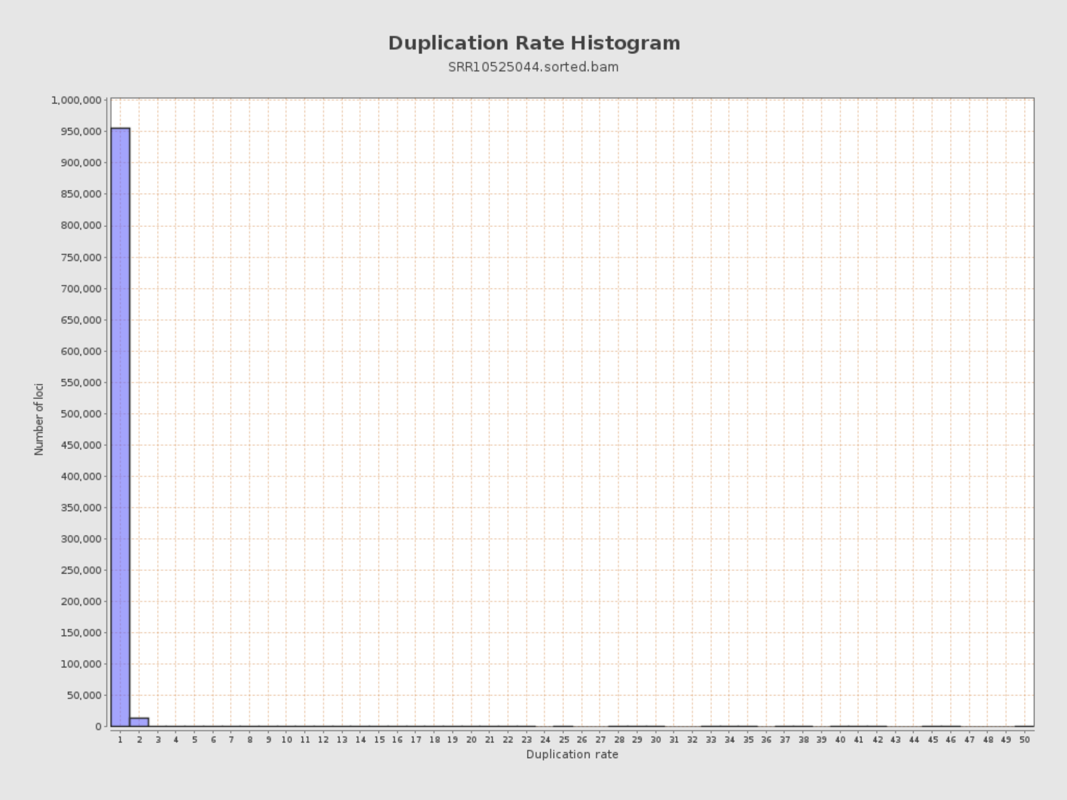
5. Results : Coverage Histogram (0-50X)



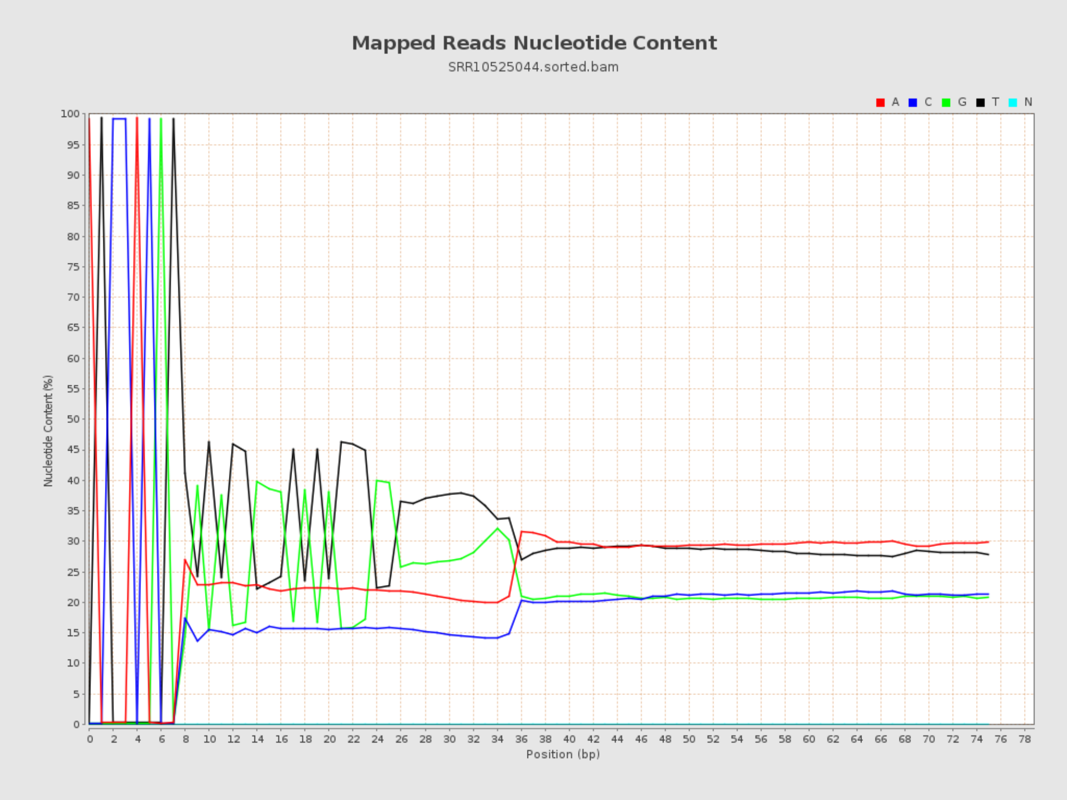
6. Results : Genome Fraction Coverage



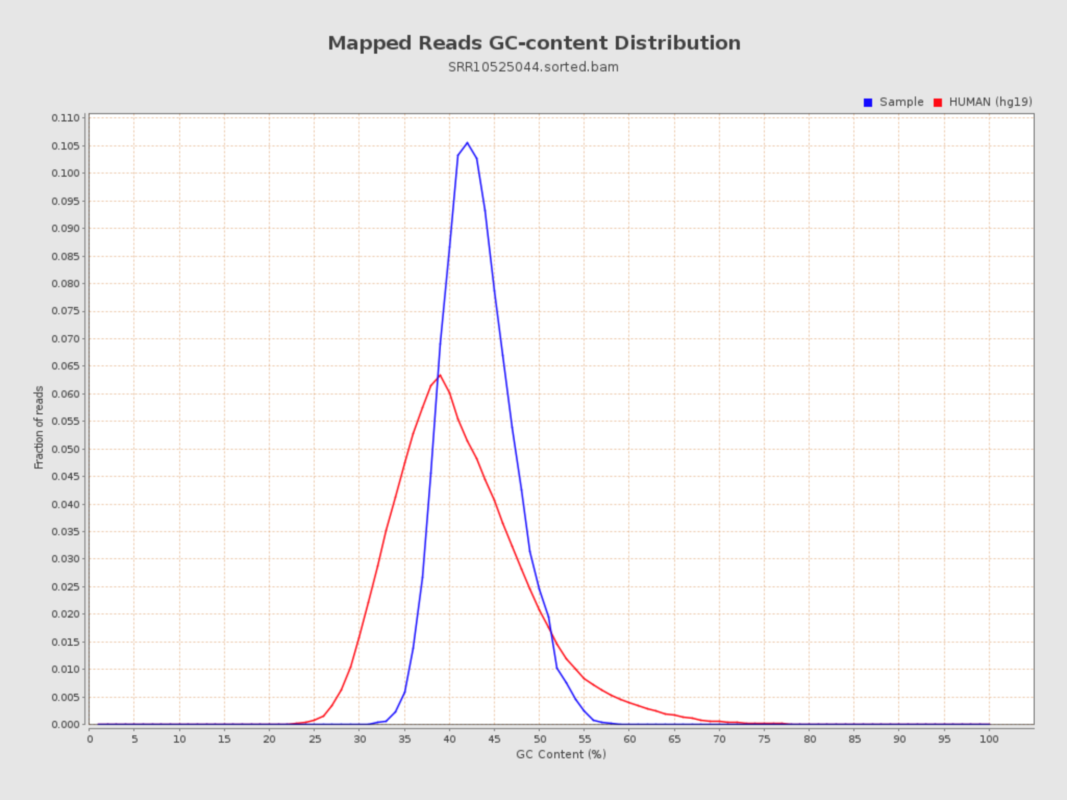
7. Results : Duplication Rate Histogram



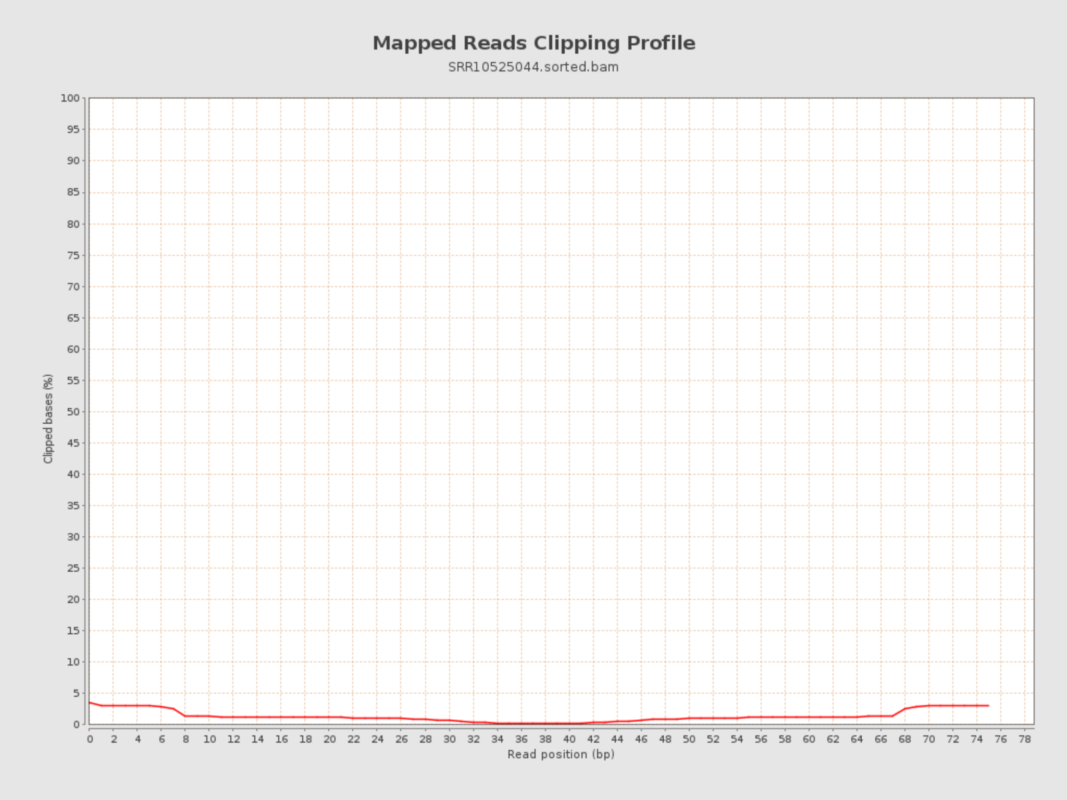
8. Results : Mapped Reads Nucleotide Content



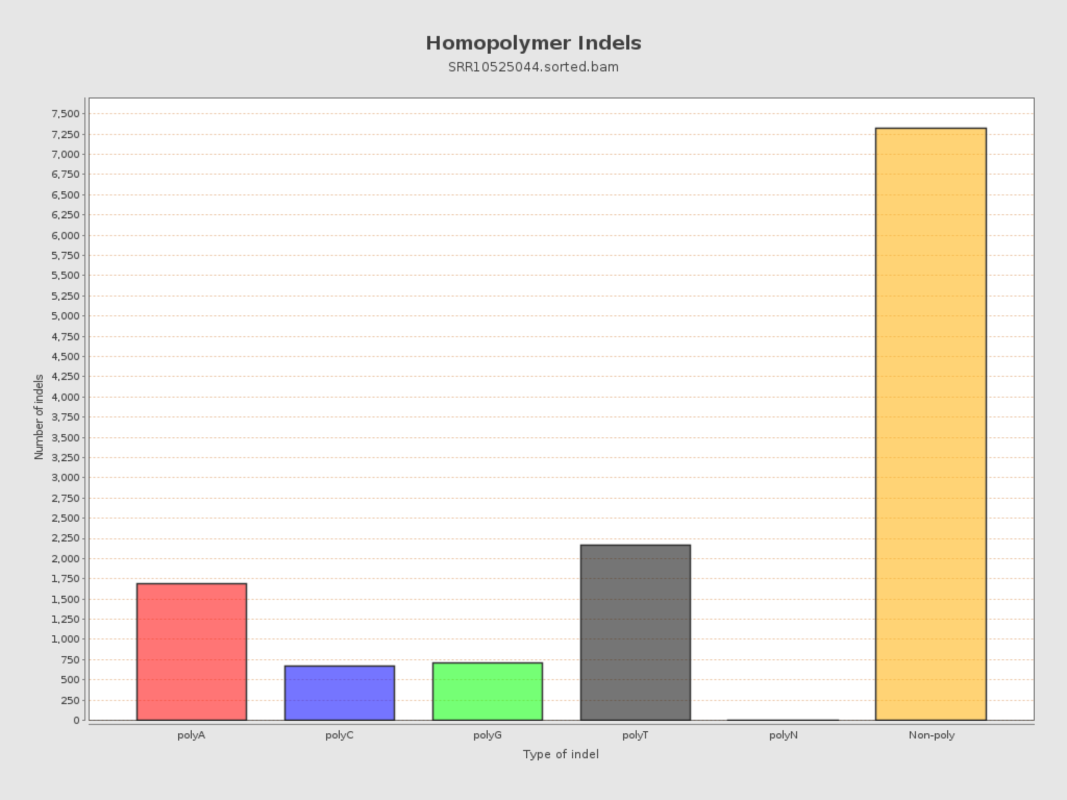
9. Results : Mapped Reads GC-content Distribution



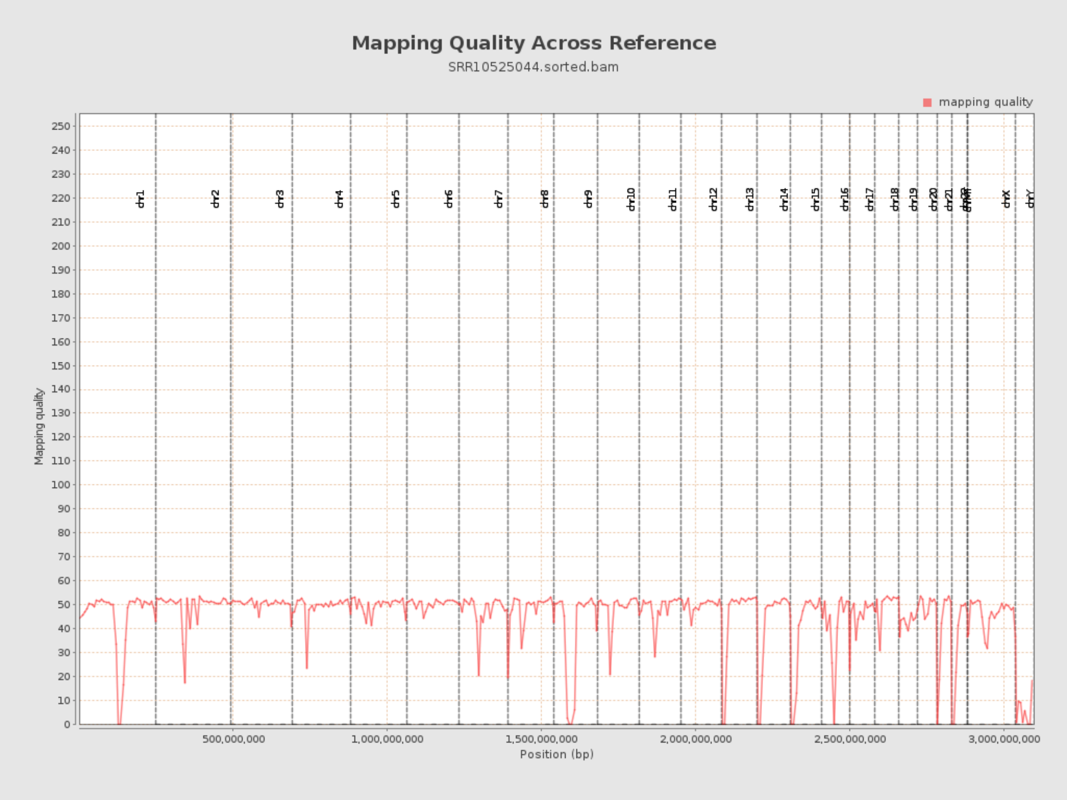
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram