Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:54:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524875.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_SRR10524875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524875.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:54:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,420,586
Mapped reads	1,306,864 / 91.99%
Unmapped reads	113,722 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,454 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	35,420 / 2.49%
Duplication rate	1.8%
Clipped reads	1,310,754 / 92.27%

2.2. ACGT Content

Number/percentage of A's	20,205,121 / 26.46%
Number/percentage of C's	14,551,938 / 19.06%
Number/percentage of T's	24,133,378 / 31.6%
Number/percentage of G's	17,459,333 / 22.86%
Number/percentage of N's	10,672 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2569

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

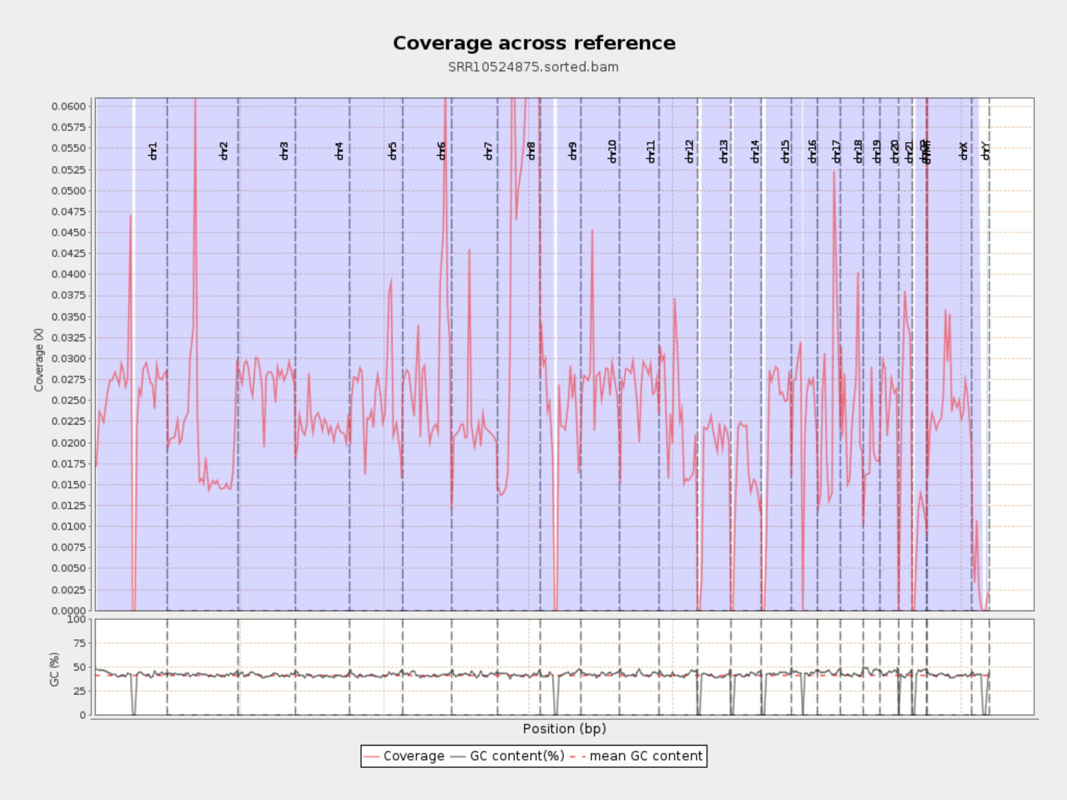
General error rate	0.5%
Mismatches	371,560
Insertions	5,258
Mapped reads with at least one insertion	0.4%
Deletions	14,737
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.34%

2.6. Chromosome stats

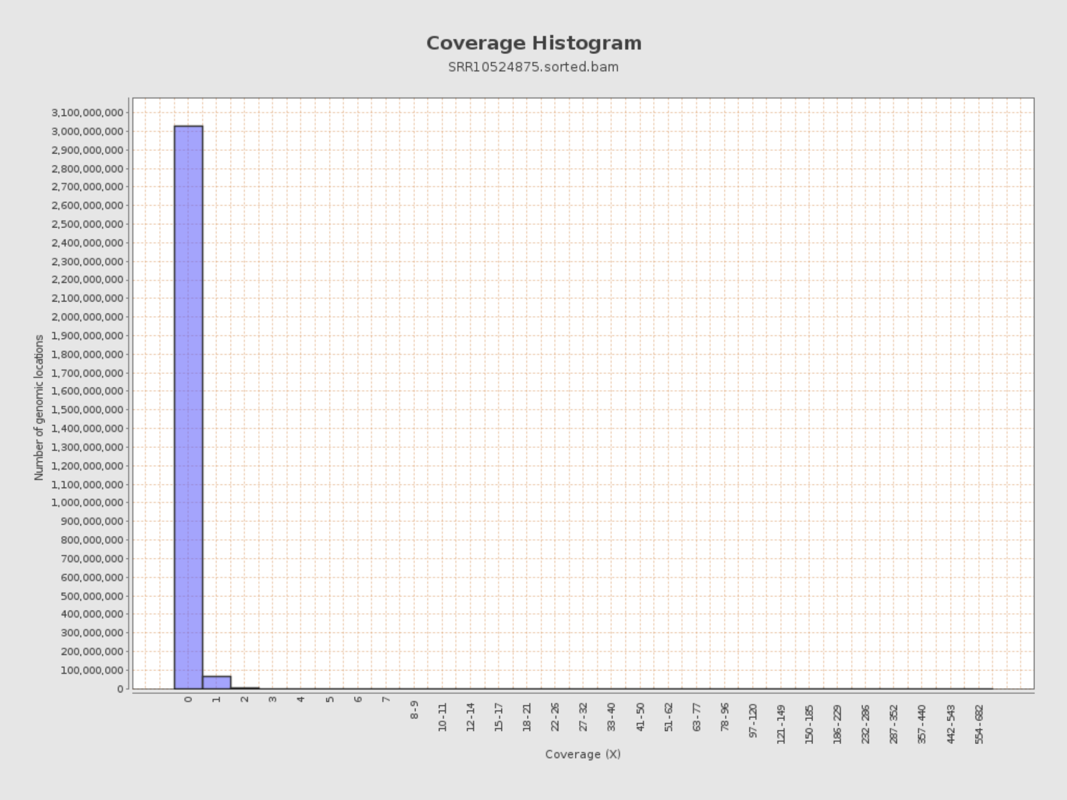
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6335184	0.0254	0.4992
chr2	243199373	4963985	0.0204	0.2509
chr3	198022430	5501896	0.0278	0.176
chr4	191154276	4192939	0.0219	0.1658
chr5	180915260	4590237	0.0254	0.1691
chr6	171115067	4982551	0.0291	0.1981
chr7	159138663	3511948	0.0221	0.3496

chr8	146364022	8301505	0.0567	0.3503
chr9	141213431	3133079	0.0222	0.2098
chr10	135534747	3771911	0.0278	0.2384
chr11	135006516	3648517	0.027	0.2332
chr12	133851895	3015242	0.0225	0.1616
chr13	115169878	2020928	0.0175	0.1395
chr14	107349540	1628690	0.0152	0.142
chr15	102531392	2242004	0.0219	0.1577
chr16	90354753	2148588	0.0238	0.179
chr17	81195210	2046852	0.0252	0.1902
chr18	78077248	1853211	0.0237	0.3897
chr19	59128983	1095056	0.0185	0.3377
chr20	63025520	1605718	0.0255	0.1699
chr21	48129895	1287772	0.0268	0.1807
chr22	51304566	450749	0.0088	0.0985
chrMT	16571	1603	0.0967	0.3136
chrX	155270560	3862577	0.0249	0.1888
chrY	59373566	190923	0.0032	0.0854

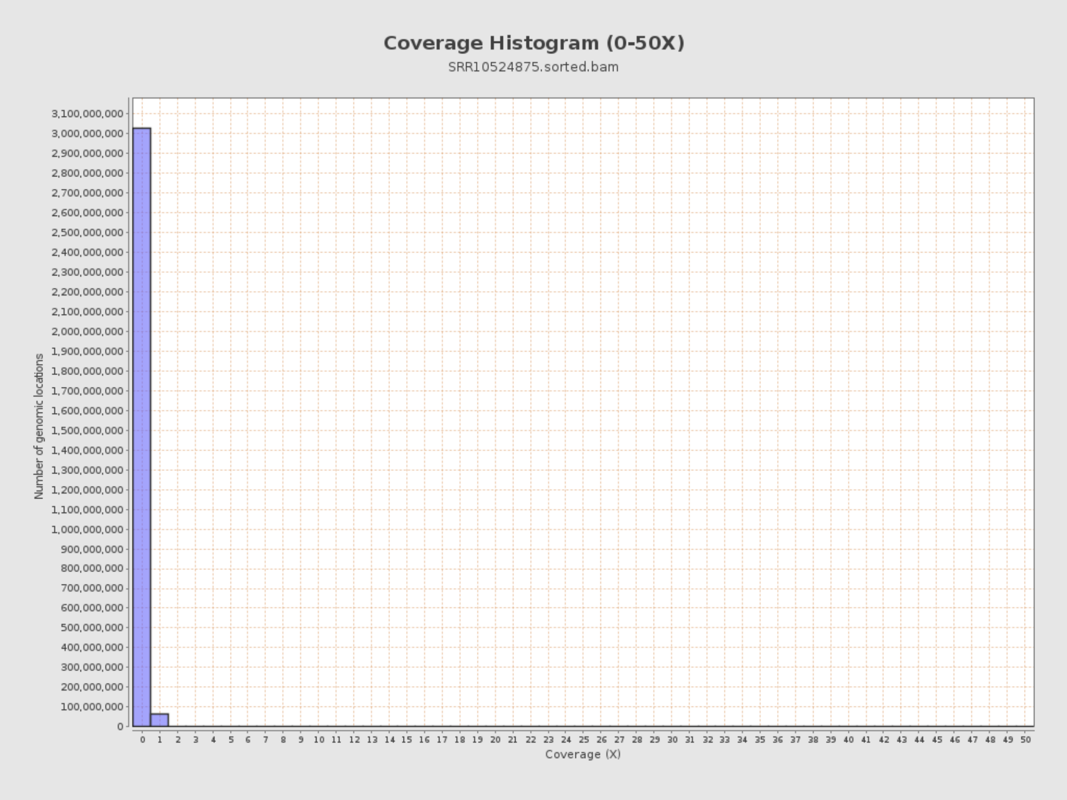
3. Results : Coverage across reference



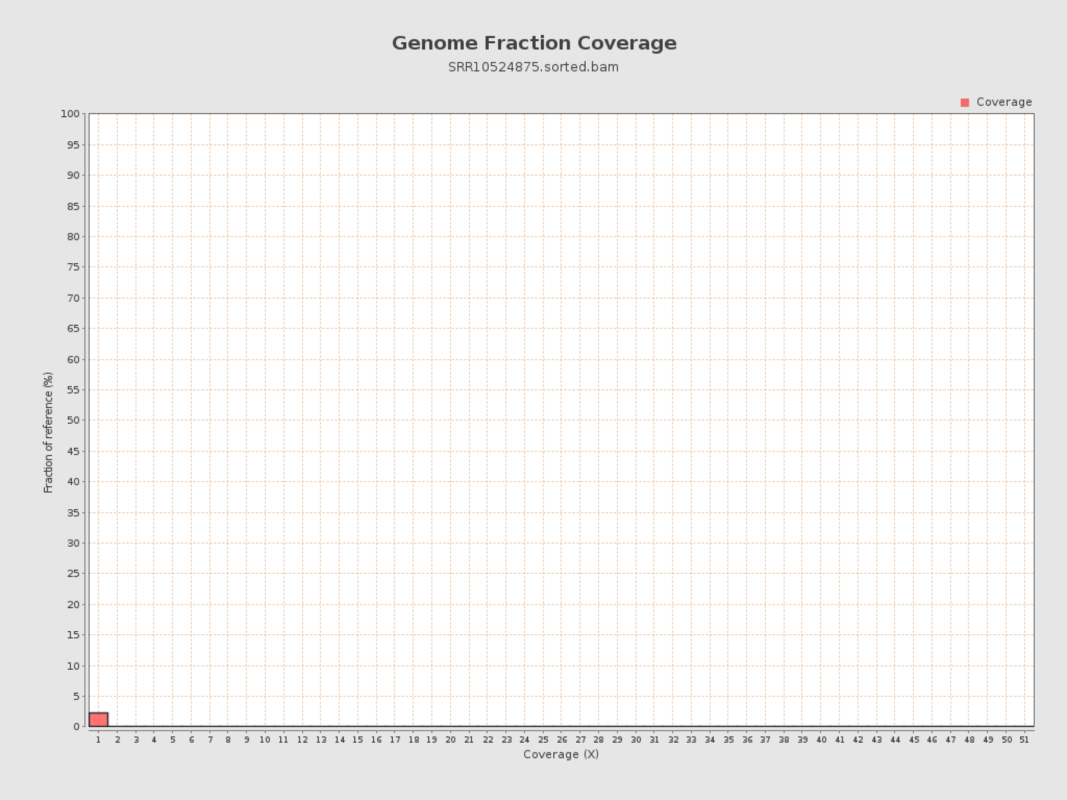
4. Results : Coverage Histogram



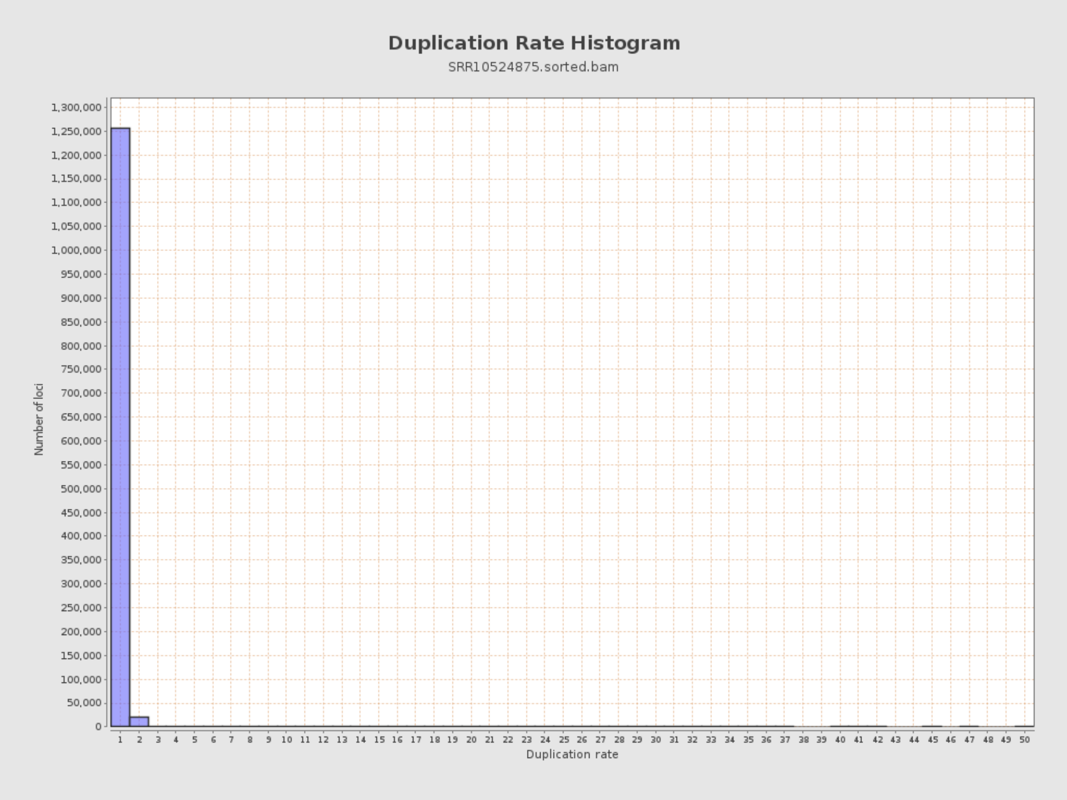
5. Results : Coverage Histogram (0-50X)



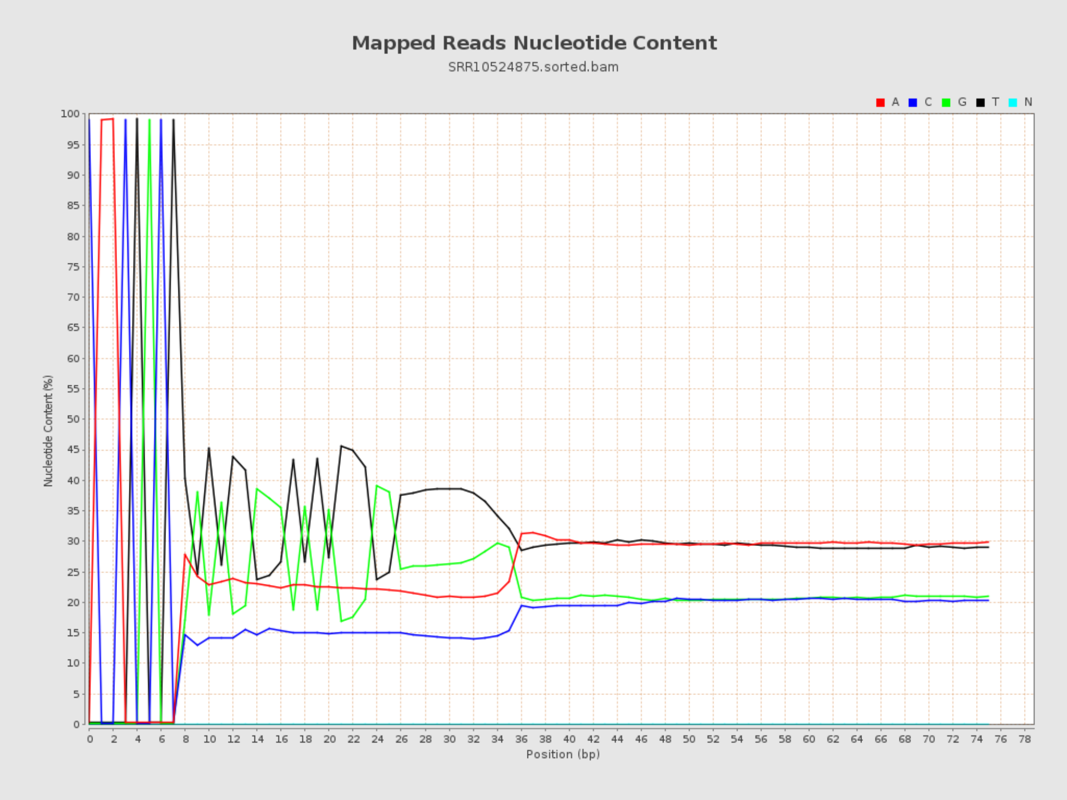
6. Results : Genome Fraction Coverage



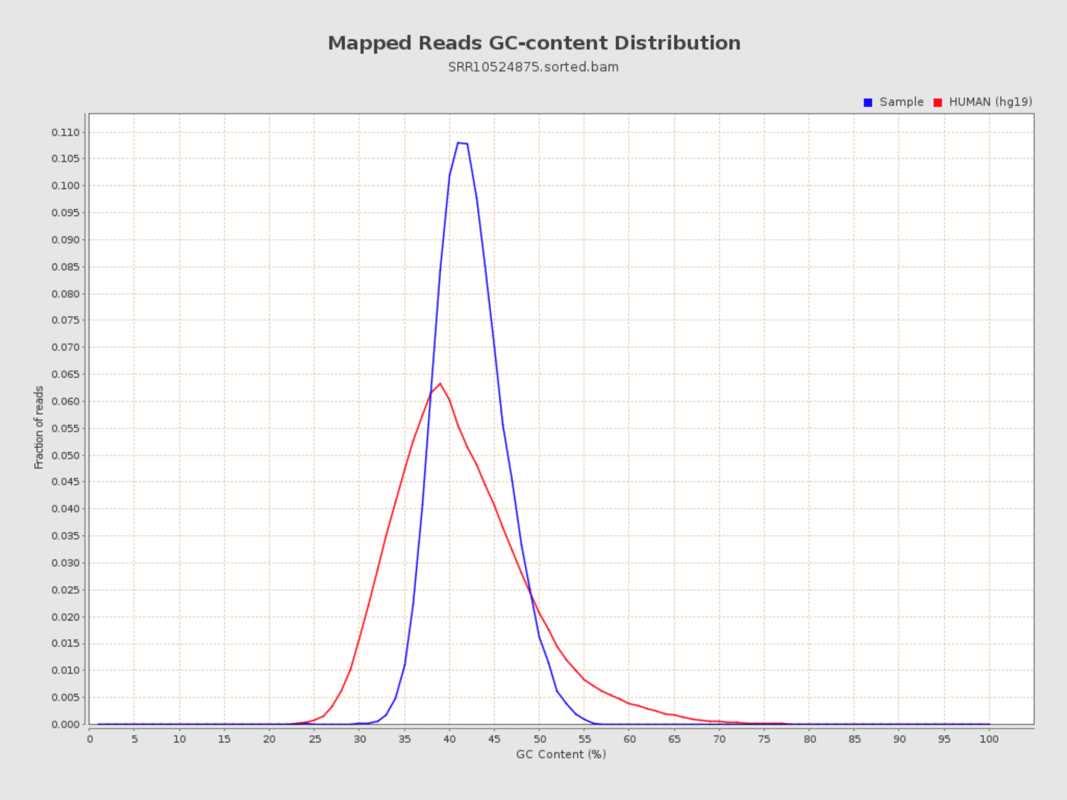
7. Results : Duplication Rate Histogram



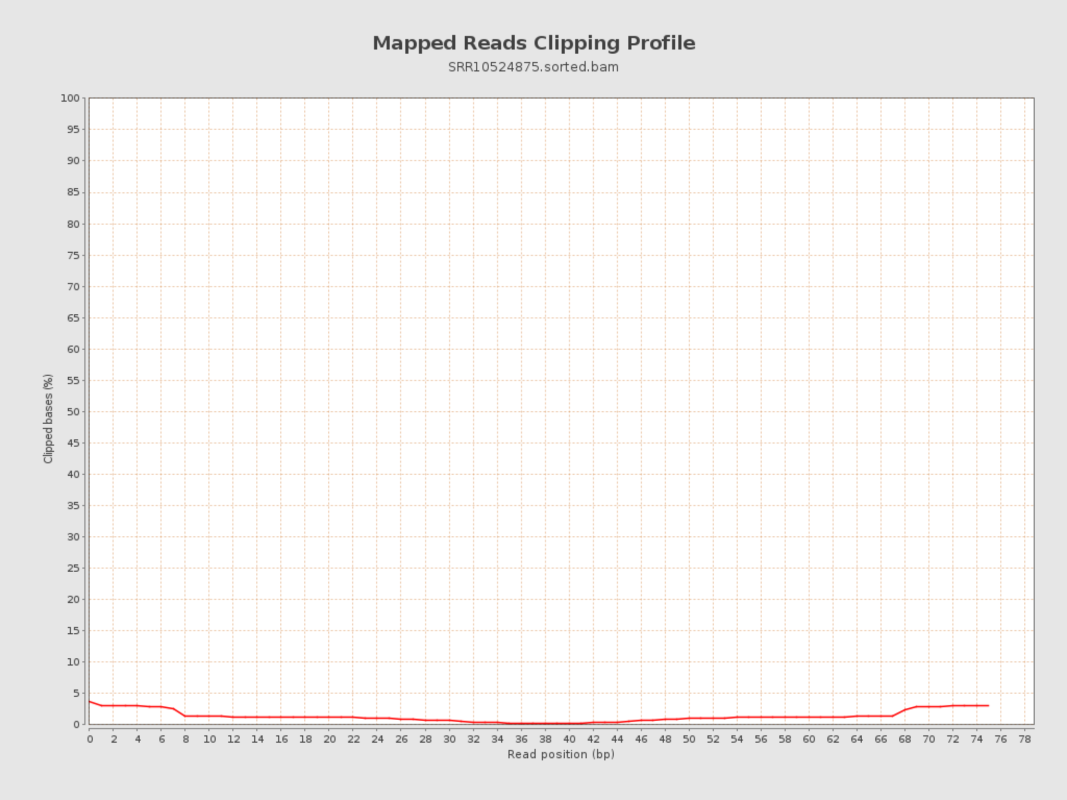
8. Results : Mapped Reads Nucleotide Content



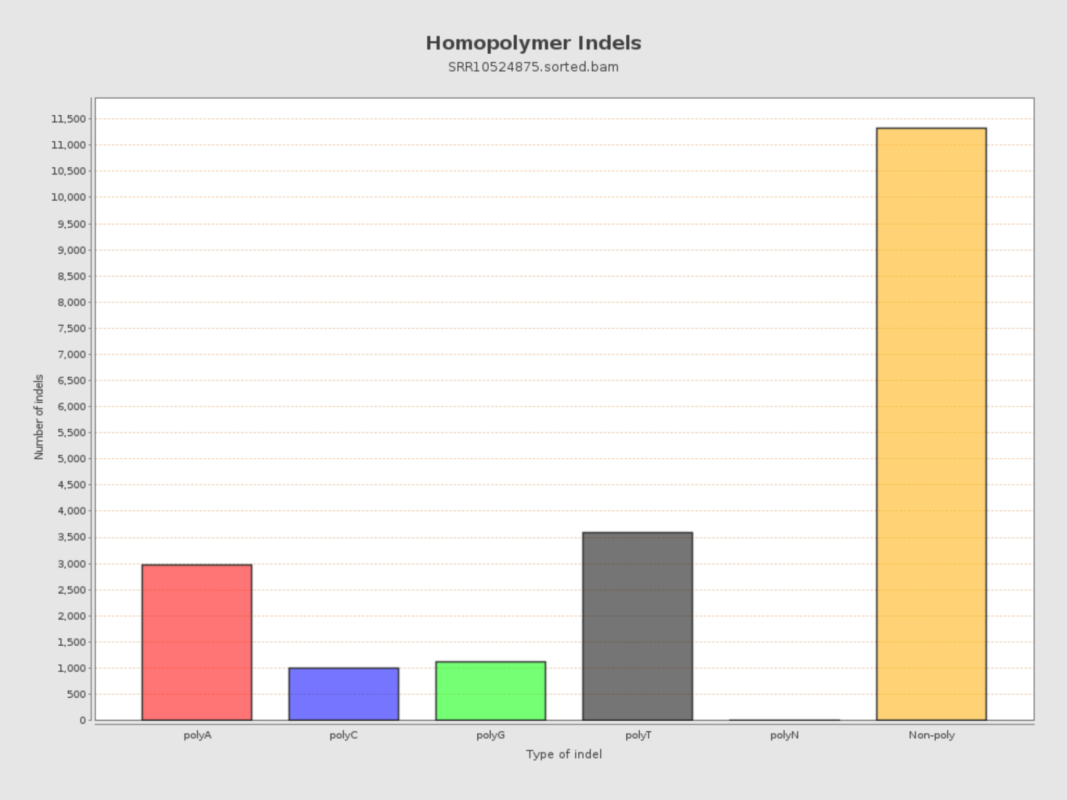
9. Results : Mapped Reads GC-content Distribution



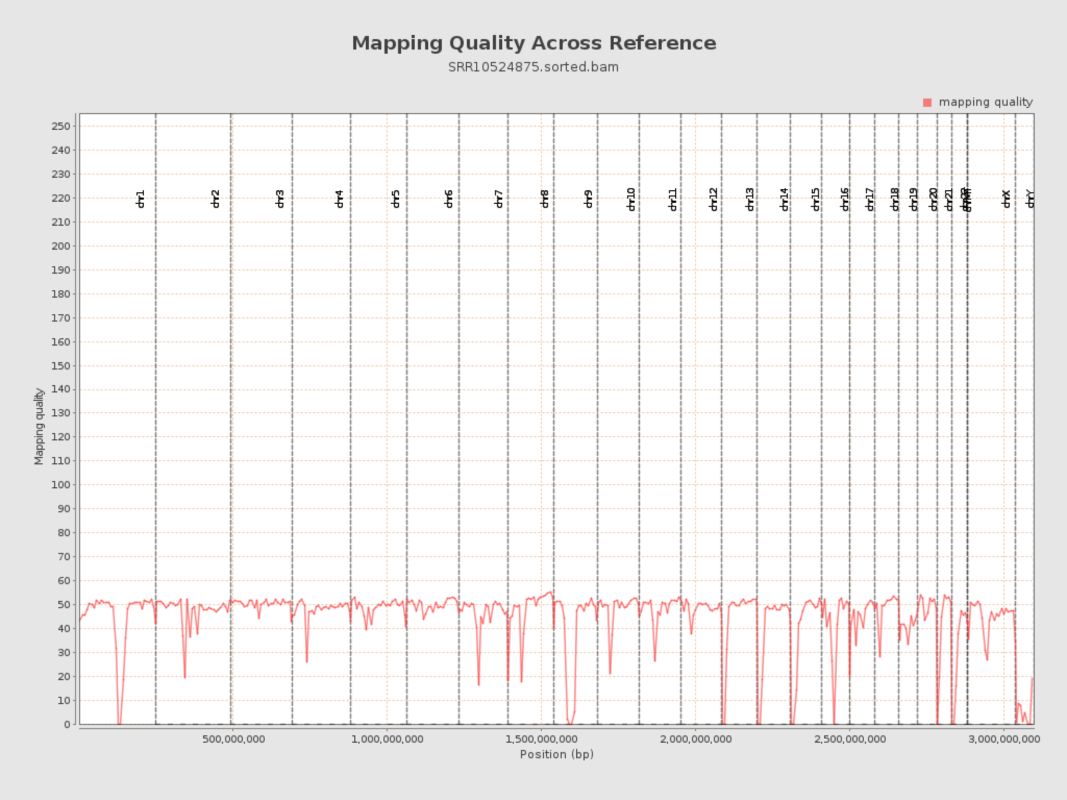
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram