Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:05:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524375.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_SRR10524375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524375.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,469,961
Mapped reads	1,356,085 / 92.25%
Unmapped reads	113,876 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,902 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	46,206 / 3.14%
Duplication rate	2.49%
Clipped reads	1,356,226 / 92.26%

2.2. ACGT Content

Number/percentage of A's	19,771,532 / 24.95%
Number/percentage of C's	16,070,497 / 20.28%
Number/percentage of T's	25,342,882 / 31.98%
Number/percentage of G's	18,050,287 / 22.78%
Number/percentage of N's	10,561 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.2561

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

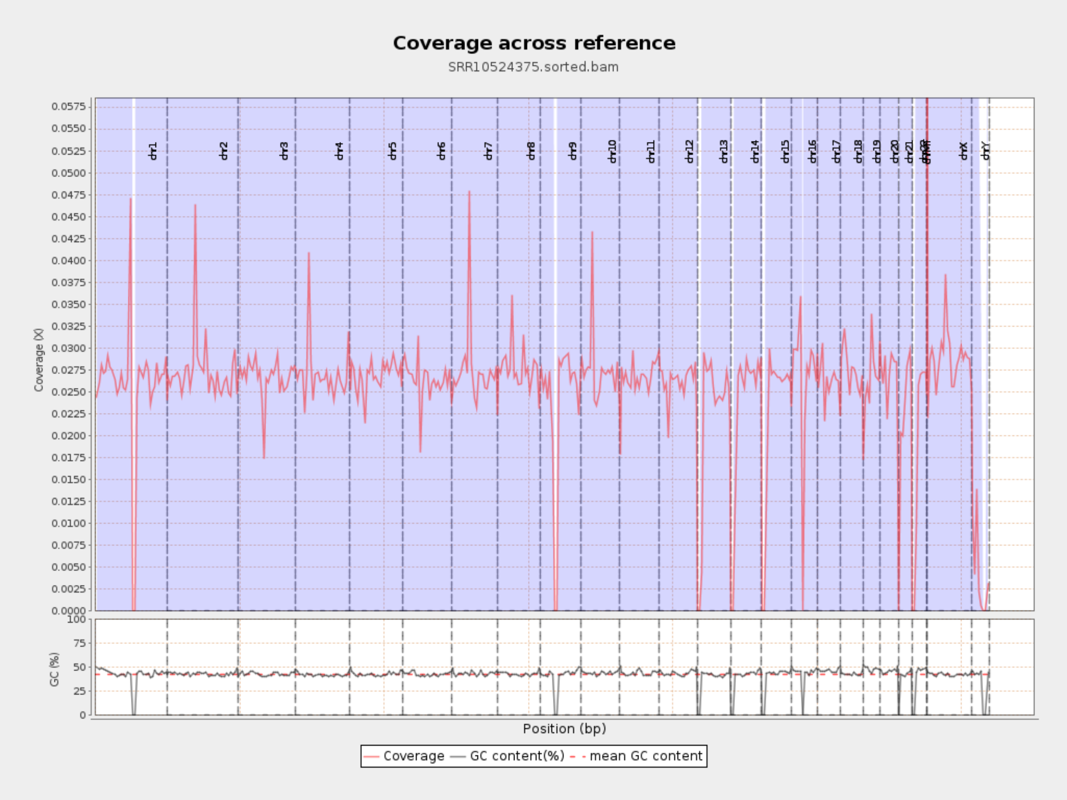
General error rate	0.5%
Mismatches	385,734
Insertions	6,183
Mapped reads with at least one insertion	0.45%
Deletions	14,655
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.02%

2.6. Chromosome stats

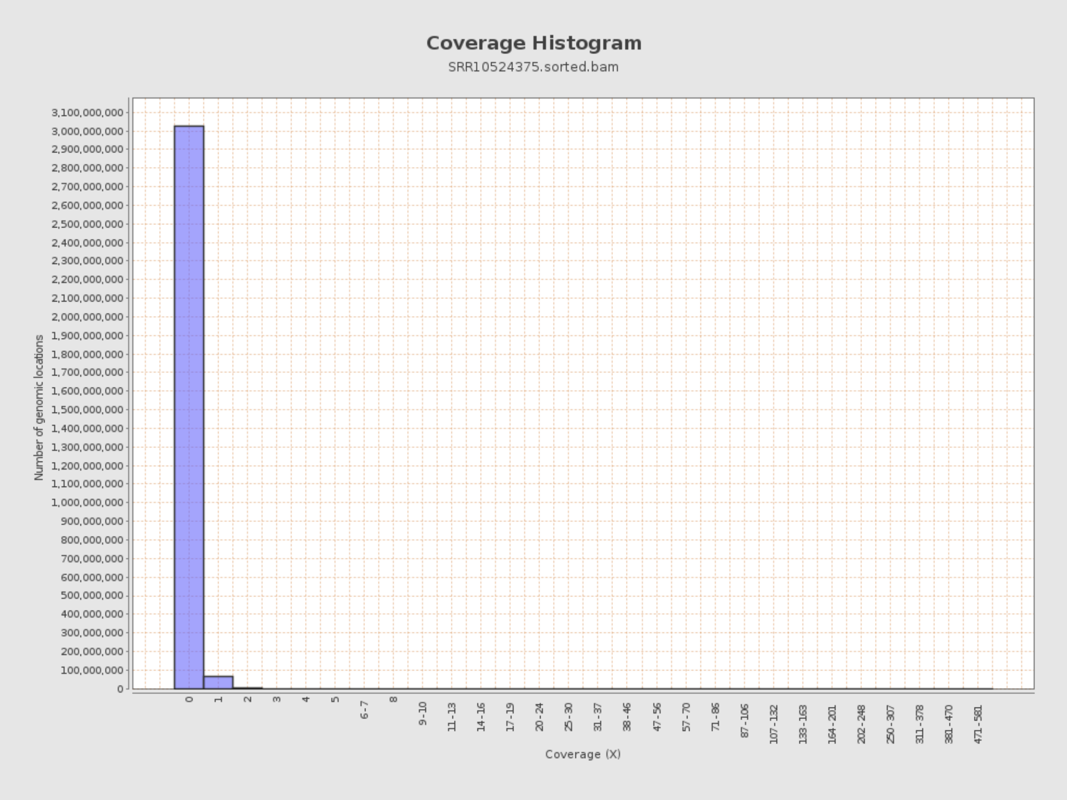
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6368860	0.0256	0.4831
chr2	243199373	6652124	0.0274	0.2859
chr3	198022430	5273134	0.0266	0.1752
chr4	191154276	5166367	0.027	0.1922
chr5	180915260	4872509	0.0269	0.177
chr6	171115067	4504966	0.0263	0.1915
chr7	159138663	4396687	0.0276	0.3724

chr8	146364022	4053143	0.0277	0.2313
chr9	141213431	3322857	0.0235	0.2132
chr10	135534747	3740796	0.0276	0.2325
chr11	135006516	3601626	0.0267	0.2375
chr12	133851895	3500299	0.0262	0.1782
chr13	115169878	2494298	0.0217	0.158
chr14	107349540	2428894	0.0226	0.1691
chr15	102531392	2265187	0.0221	0.1608
chr16	90354753	2343657	0.0259	0.1826
chr17	81195210	2123565	0.0262	0.1895
chr18	78077248	2147263	0.0275	0.396
chr19	59128983	1575838	0.0267	0.3131
chr20	63025520	1691084	0.0268	0.1817
chr21	48129895	1067975	0.0222	0.1766
chr22	51304566	951520	0.0185	0.1464
chrMT	16571	4434	0.2676	0.5577
chrX	155270560	4479932	0.0289	0.2034
chrY	59373566	241745	0.0041	0.1086

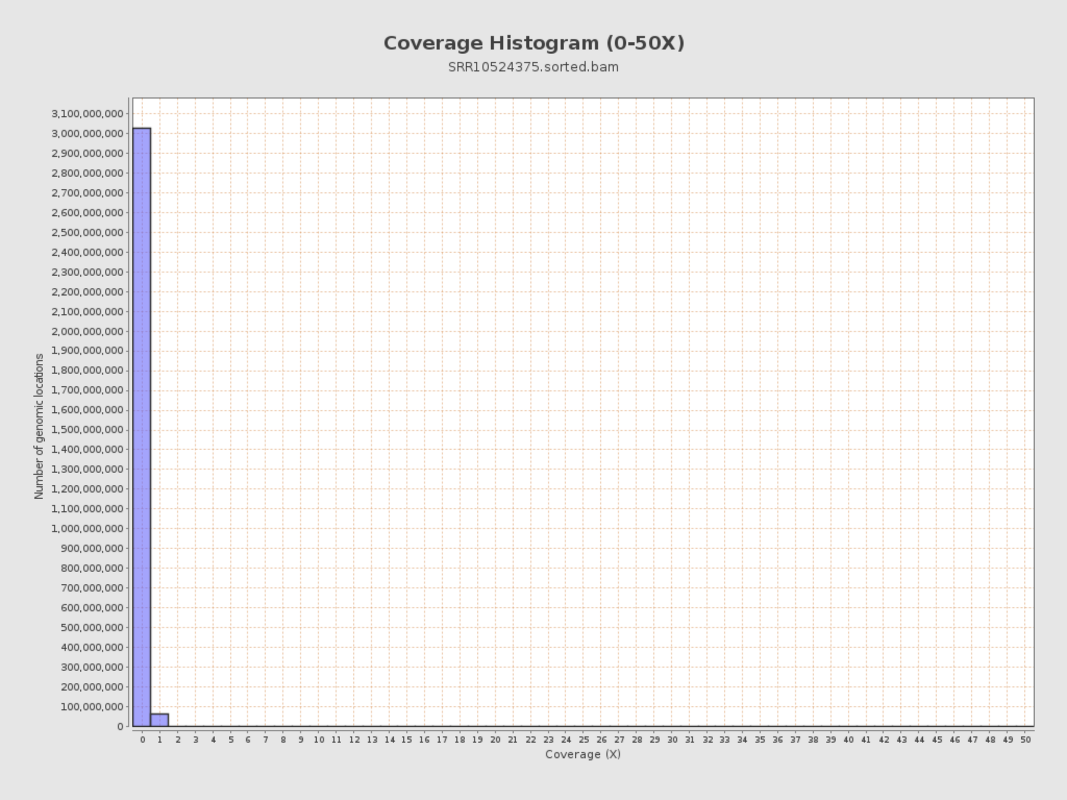
3. Results : Coverage across reference



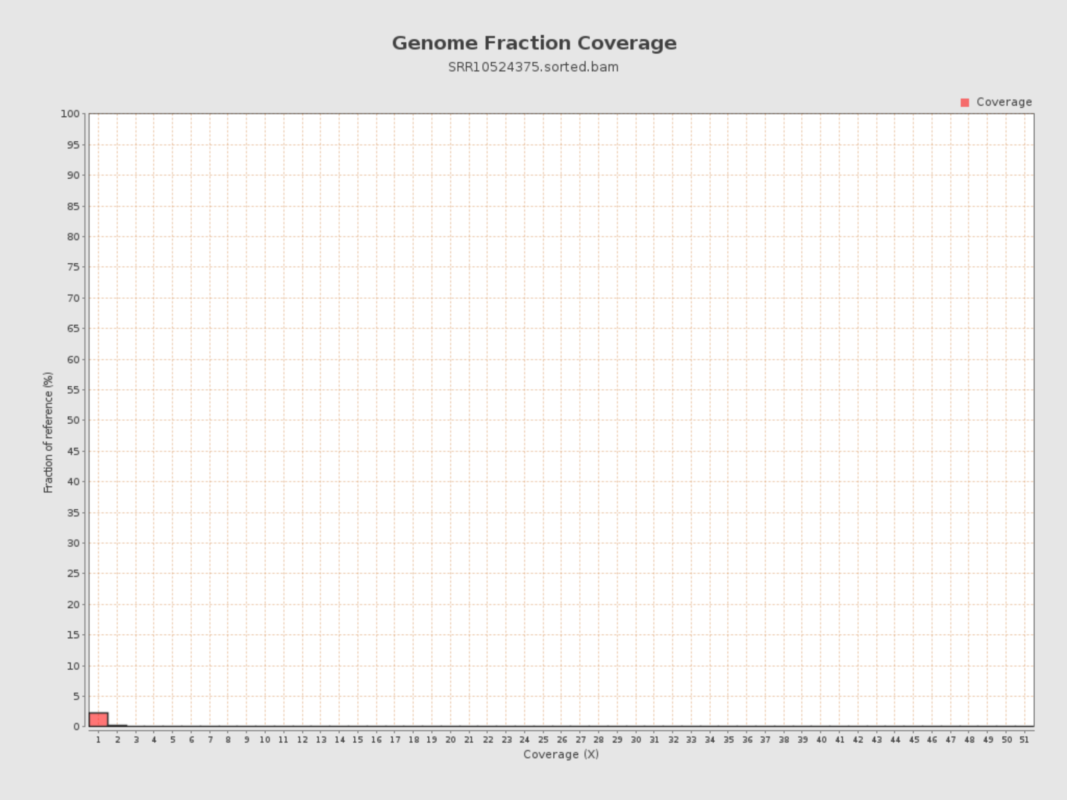
4. Results : Coverage Histogram



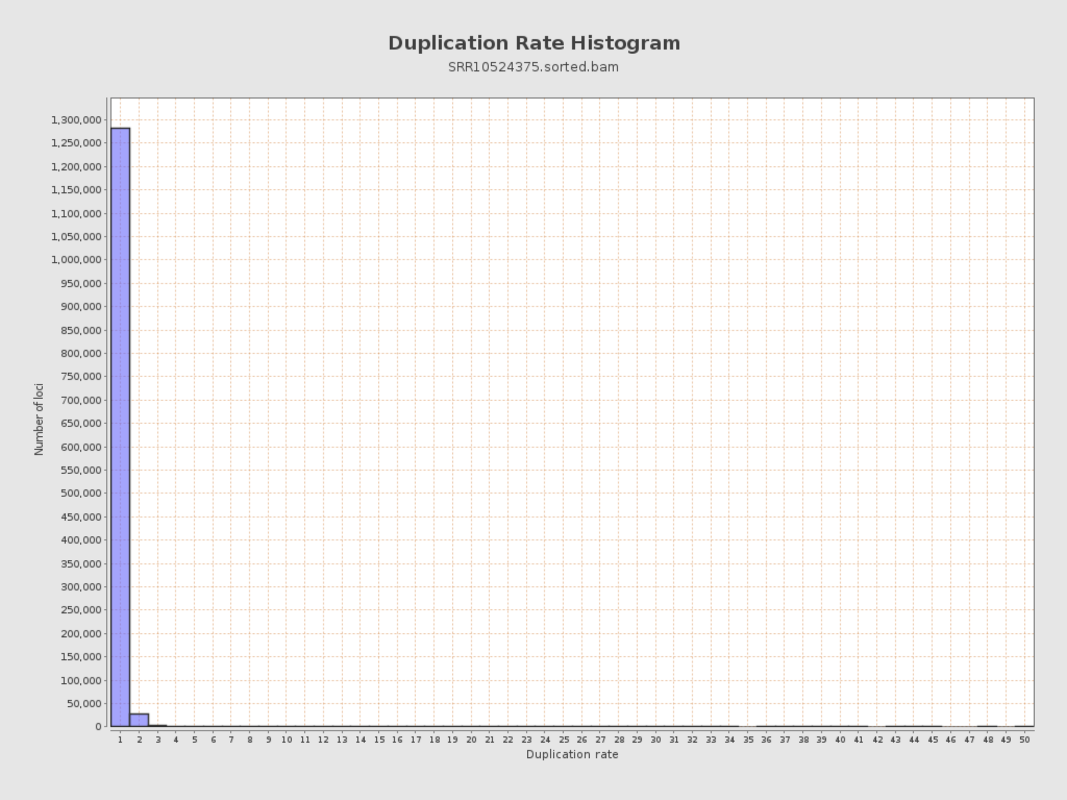
5. Results : Coverage Histogram (0-50X)



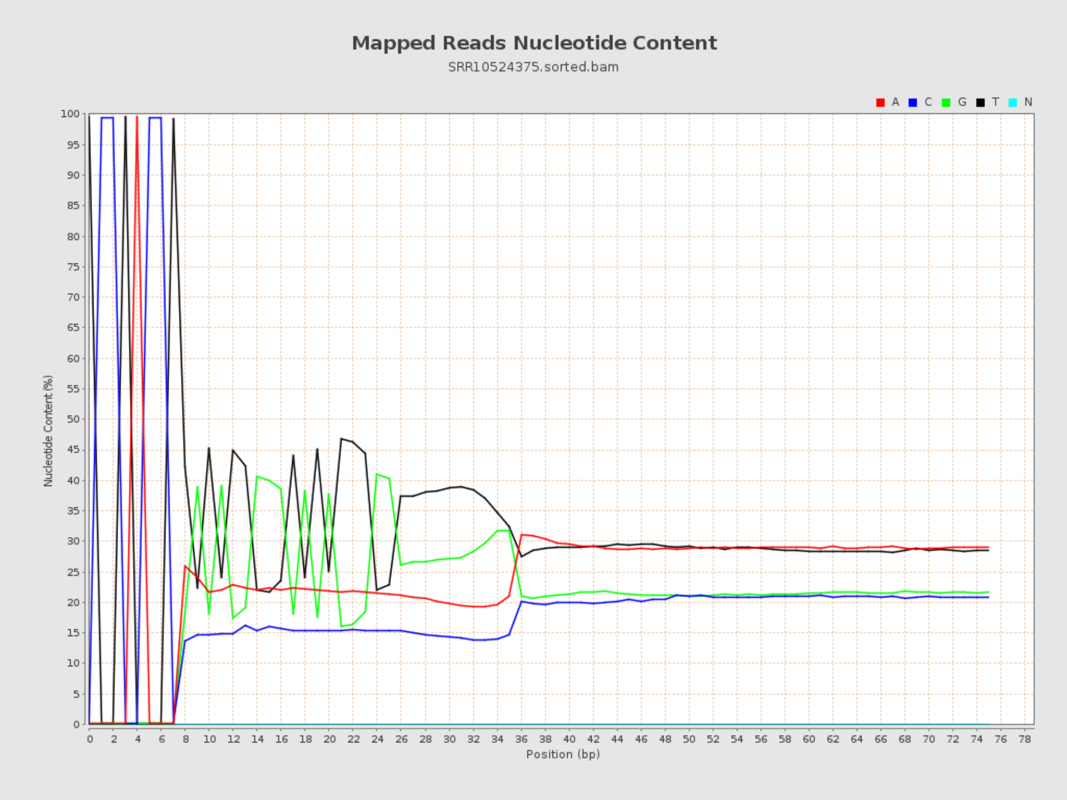
6. Results : Genome Fraction Coverage



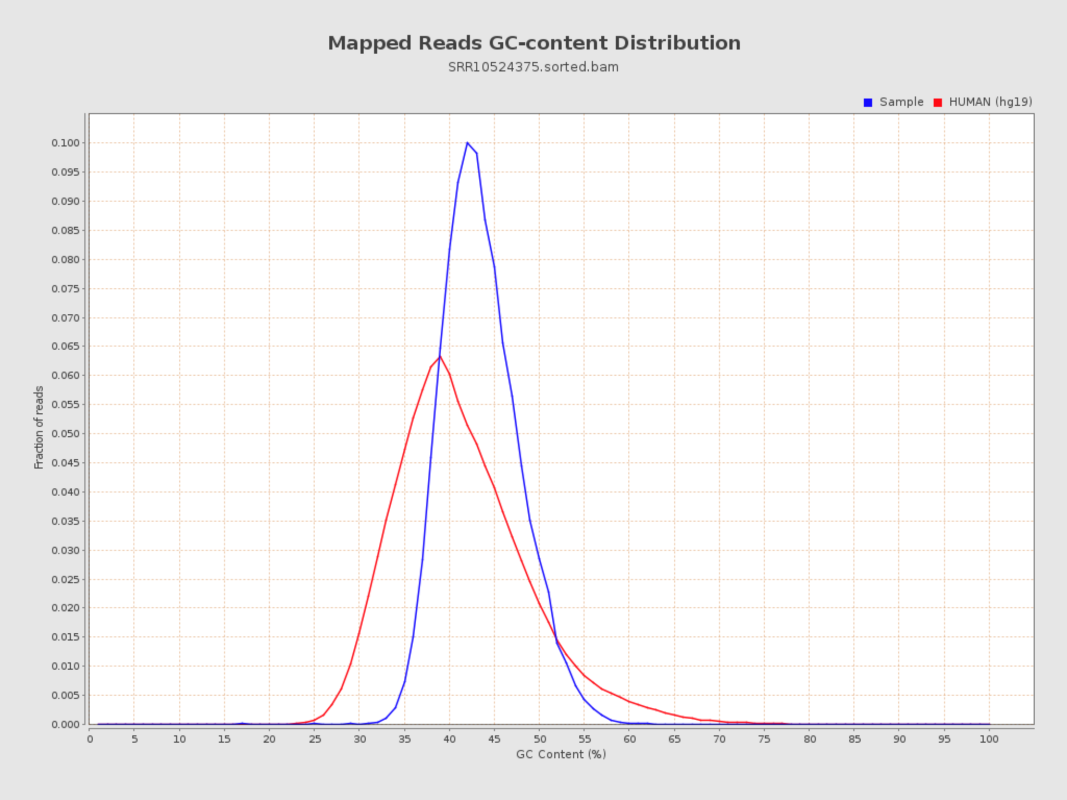
7. Results : Duplication Rate Histogram



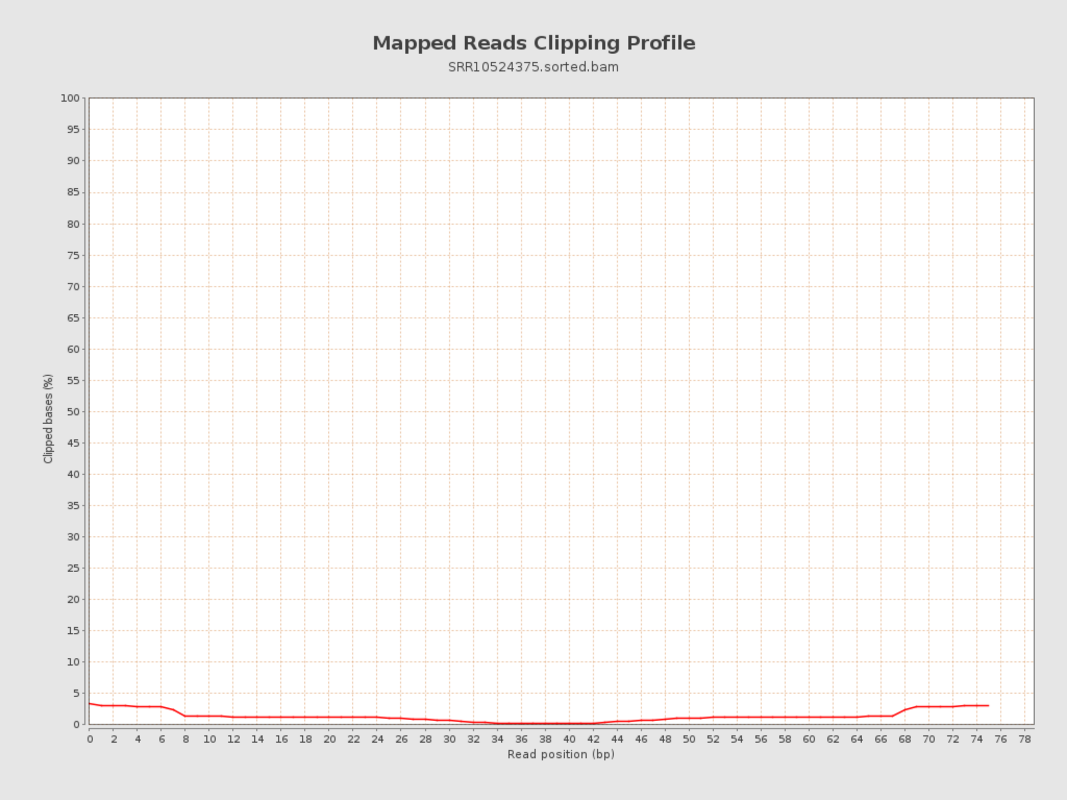
8. Results : Mapped Reads Nucleotide Content



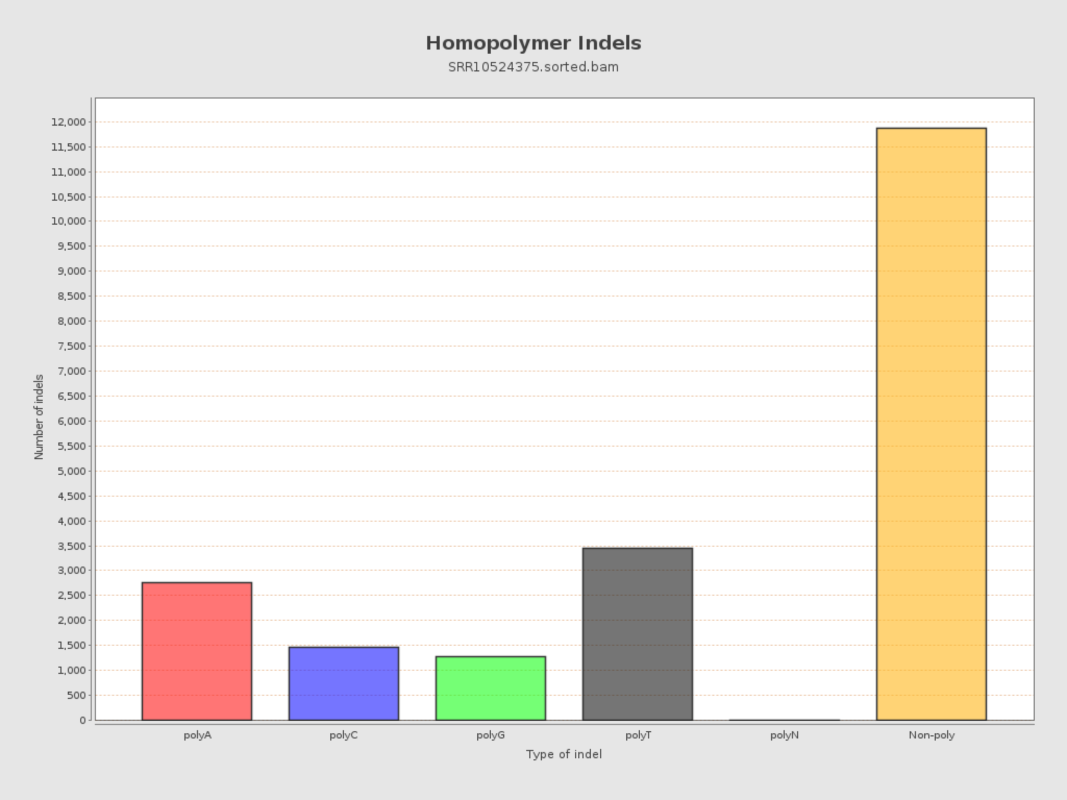
9. Results : Mapped Reads GC-content Distribution



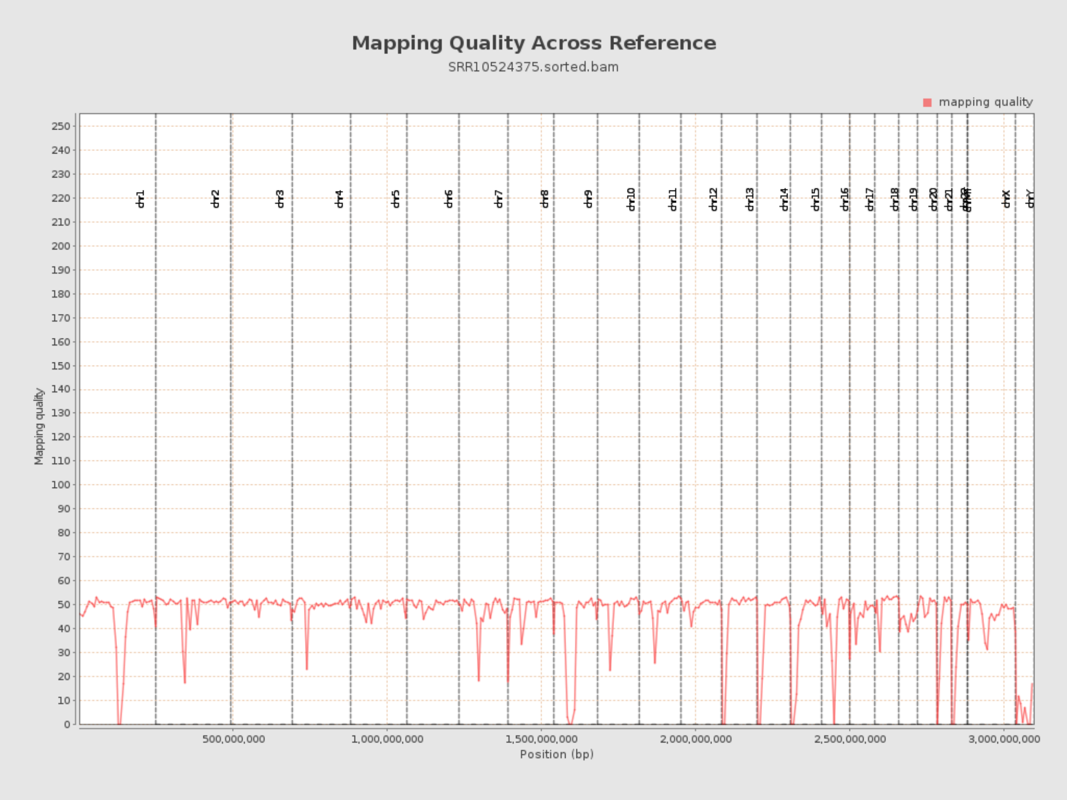
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram