Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524775.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_SRR10524775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:10:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,419,720
Mapped reads	1,268,766 / 89.37%
Unmapped reads	150,954 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,904 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	45,479 / 3.2%
Duplication rate	2.73%
Clipped reads	1,271,568 / 89.56%

2.2. ACGT Content

Number/percentage of A's	17,899,045 / 24.85%
Number/percentage of C's	13,157,569 / 18.26%
Number/percentage of T's	23,500,547 / 32.62%
Number/percentage of G's	17,473,673 / 24.26%
Number/percentage of N's	8,846 / 0.01%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2203

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

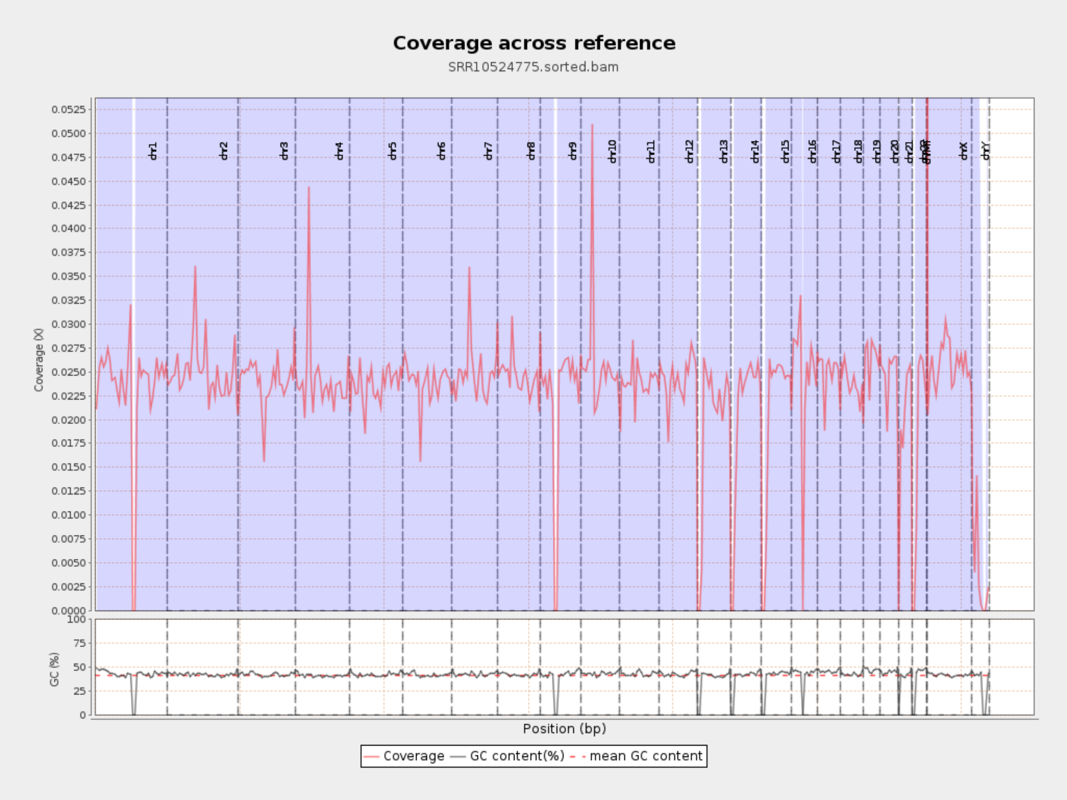
General error rate	0.53%
Mismatches	375,705
Insertions	4,756
Mapped reads with at least one insertion	0.37%
Deletions	14,352
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.49%

2.6. Chromosome stats

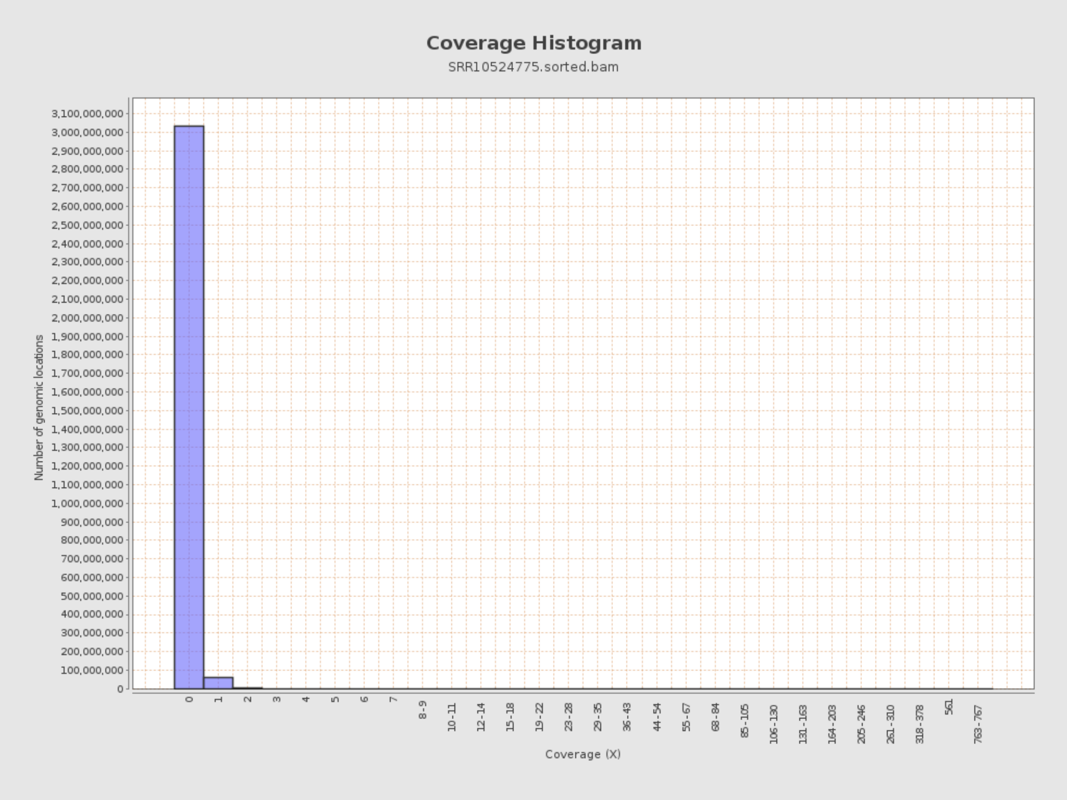
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5770283	0.0232	0.2851
chr2	243199373	6093483	0.0251	0.3632
chr3	198022430	4747057	0.024	0.1713
chr4	191154276	4635155	0.0242	0.1905
chr5	180915260	4304331	0.0238	0.1674
chr6	171115067	4093617	0.0239	0.1898
chr7	159138663	3958746	0.0249	0.2594

chr8	146364022	3589570	0.0245	0.2016
chr9	141213431	3091406	0.0219	0.1901
chr10	135534747	3521401	0.026	0.2611
chr11	135006516	3243475	0.024	0.1982
chr12	133851895	3253582	0.0243	0.1713
chr13	115169878	2215841	0.0192	0.1512
chr14	107349540	2186040	0.0204	0.1584
chr15	102531392	2077161	0.0203	0.1563
chr16	90354753	2171287	0.024	0.1879
chr17	81195210	2021798	0.0249	0.1784
chr18	78077248	1862213	0.0239	0.2776
chr19	59128983	1559146	0.0264	0.2395
chr20	63025520	1551838	0.0246	0.1767
chr21	48129895	954903	0.0198	0.1695
chr22	51304566	894638	0.0174	0.1445
chrMT	16571	28883	1.743	1.7606
chrX	155270560	4001776	0.0258	0.1863
chrY	59373566	235389	0.004	0.115

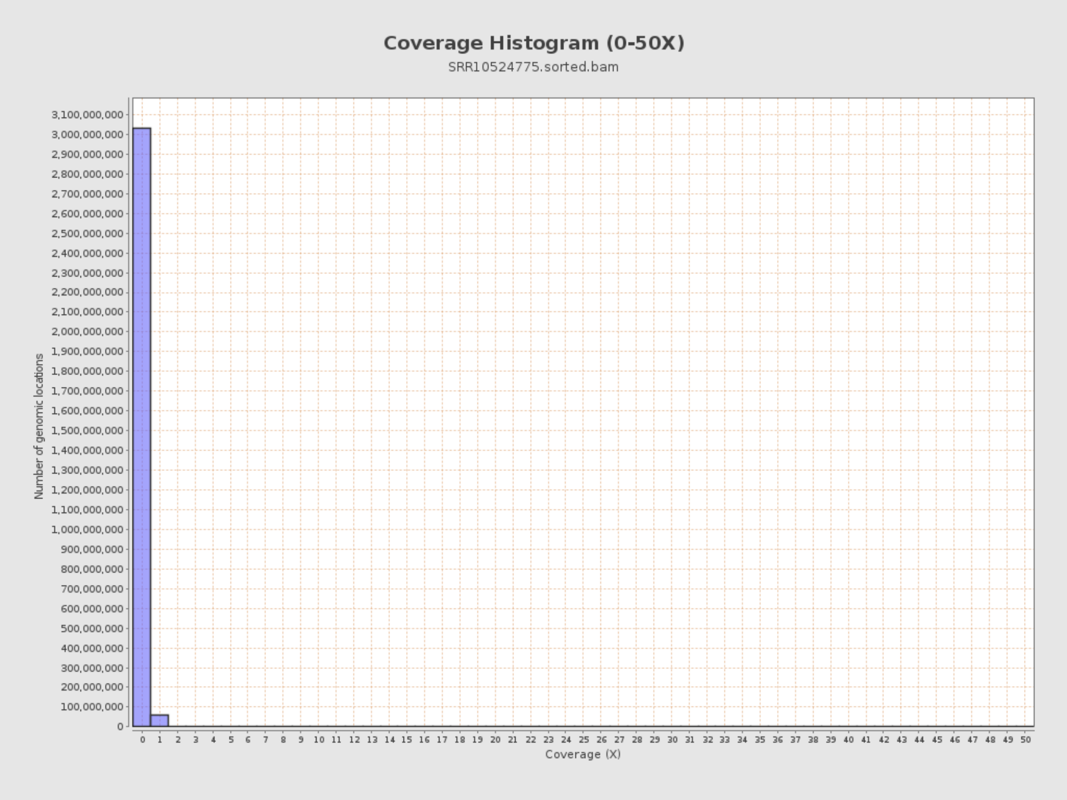
3. Results : Coverage across reference



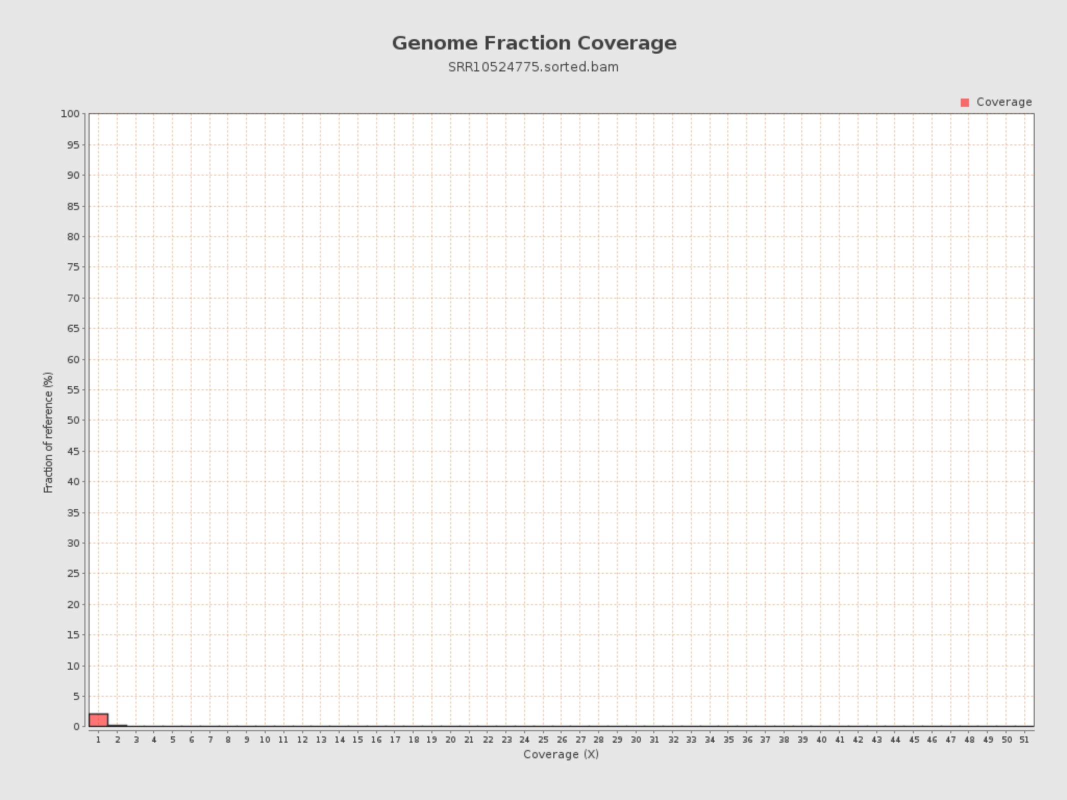
4. Results : Coverage Histogram



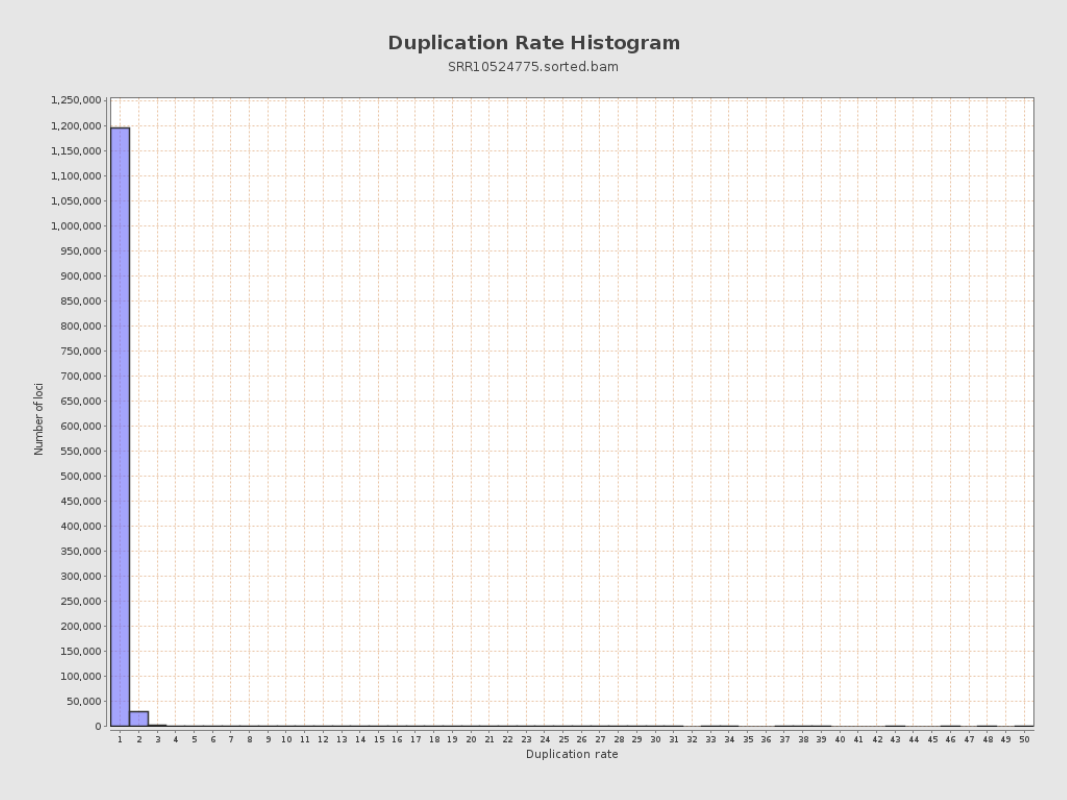
5. Results : Coverage Histogram (0-50X)



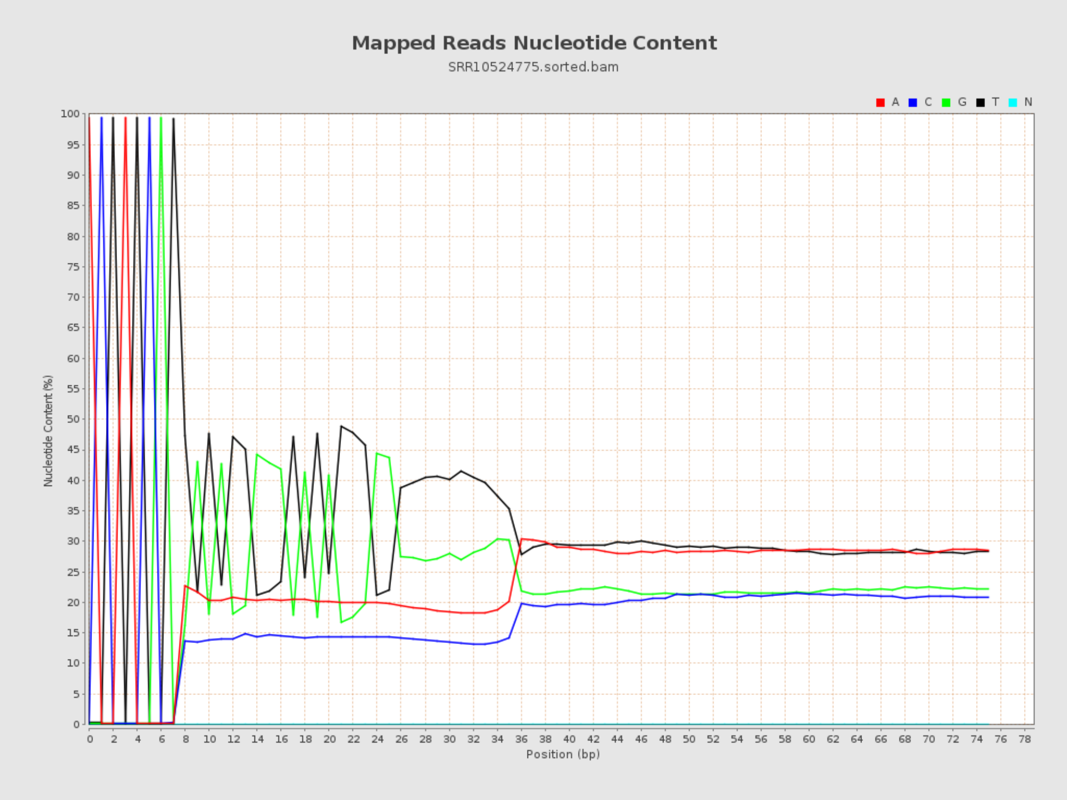
6. Results : Genome Fraction Coverage



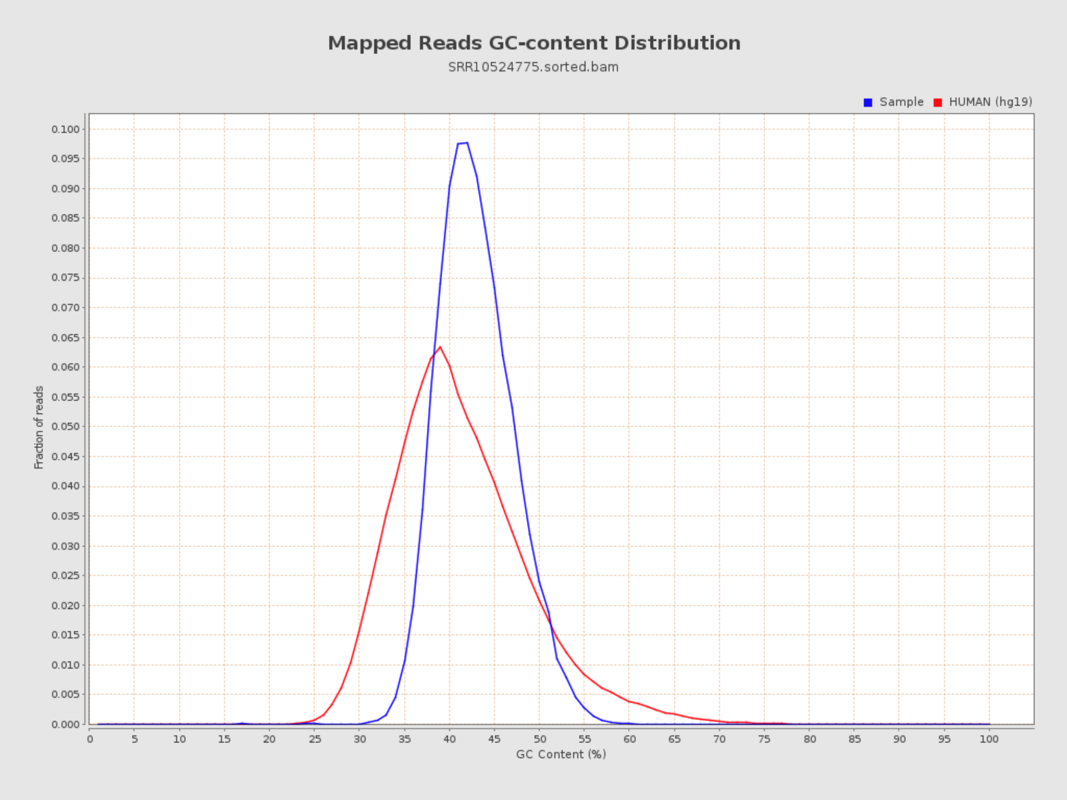
7. Results : Duplication Rate Histogram



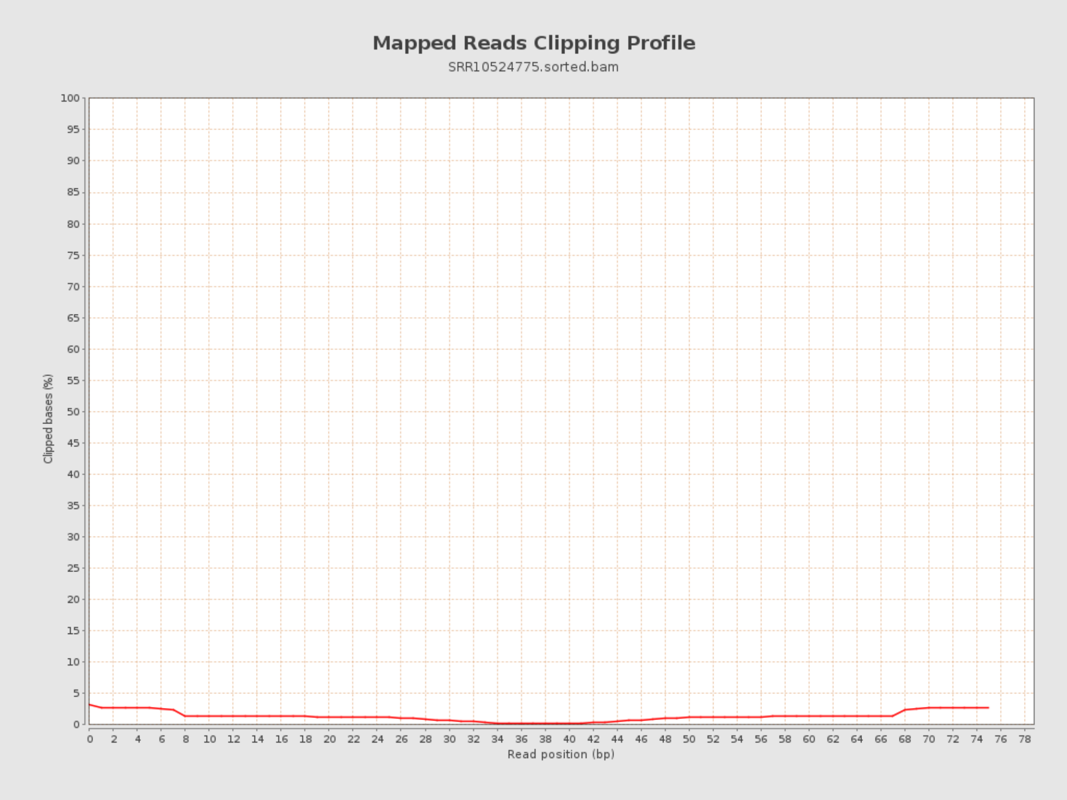
8. Results : Mapped Reads Nucleotide Content



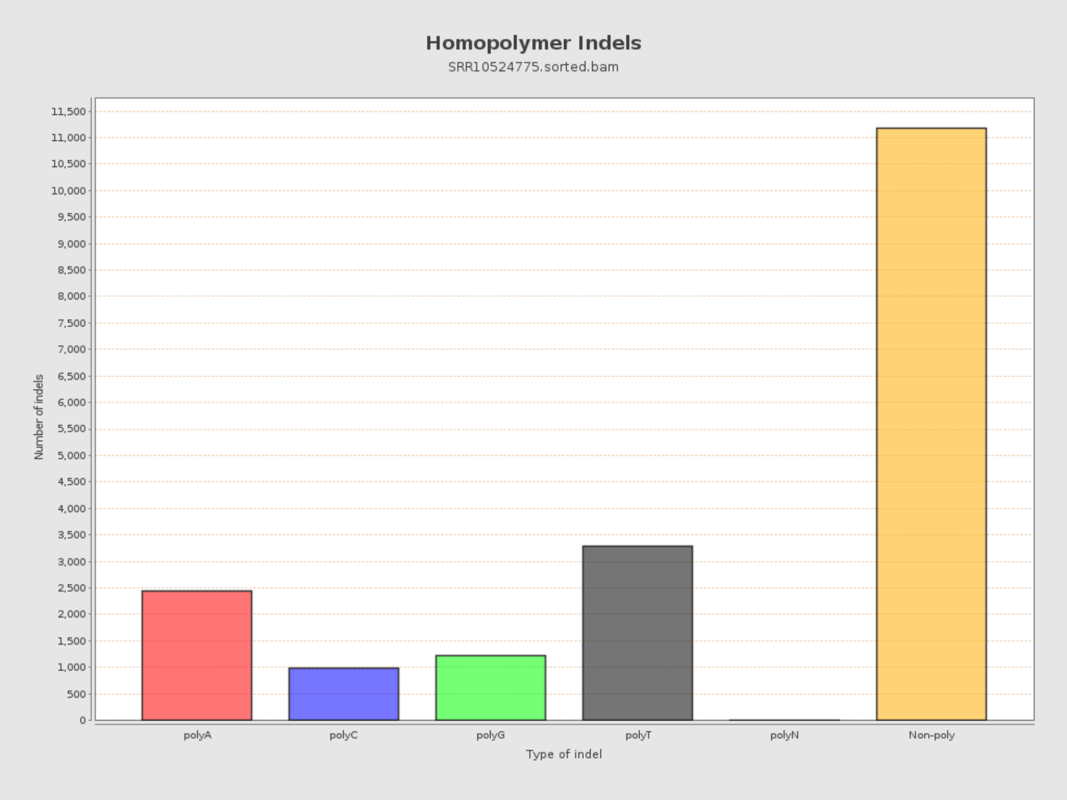
9. Results : Mapped Reads GC-content Distribution



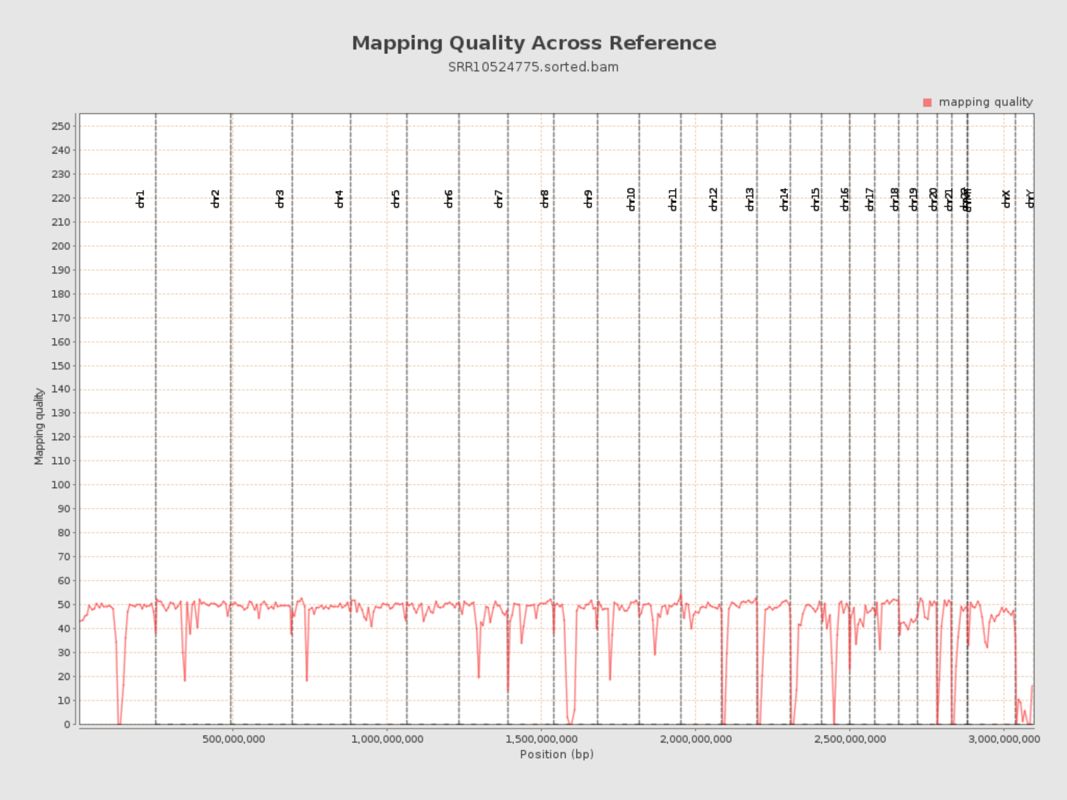
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram