Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:26:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524639.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_SRR10524639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524639.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:26:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,799,759
Mapped reads	1,640,482 / 91.15%
Unmapped reads	159,277 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,789 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	97,666 / 5.43%
Duplication rate	4.59%
Clipped reads	1,642,761 / 91.28%

2.2. ACGT Content

Number/percentage of A's	22,780,690 / 23.84%
Number/percentage of C's	17,869,467 / 18.7%
Number/percentage of T's	30,789,250 / 32.22%
Number/percentage of G's	24,127,660 / 25.25%
Number/percentage of N's	731 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.3022

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

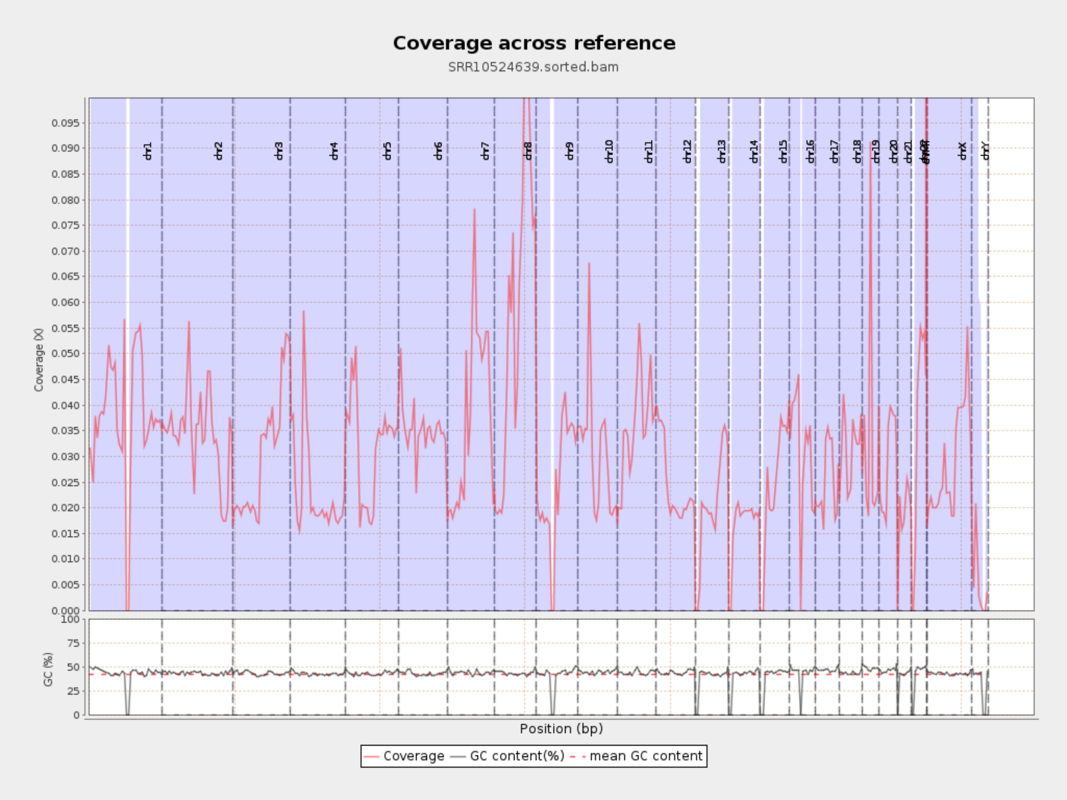
General error rate	0.52%
Mismatches	484,033
Insertions	6,329
Mapped reads with at least one insertion	0.38%
Deletions	19,065
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.05%

2.6. Chromosome stats

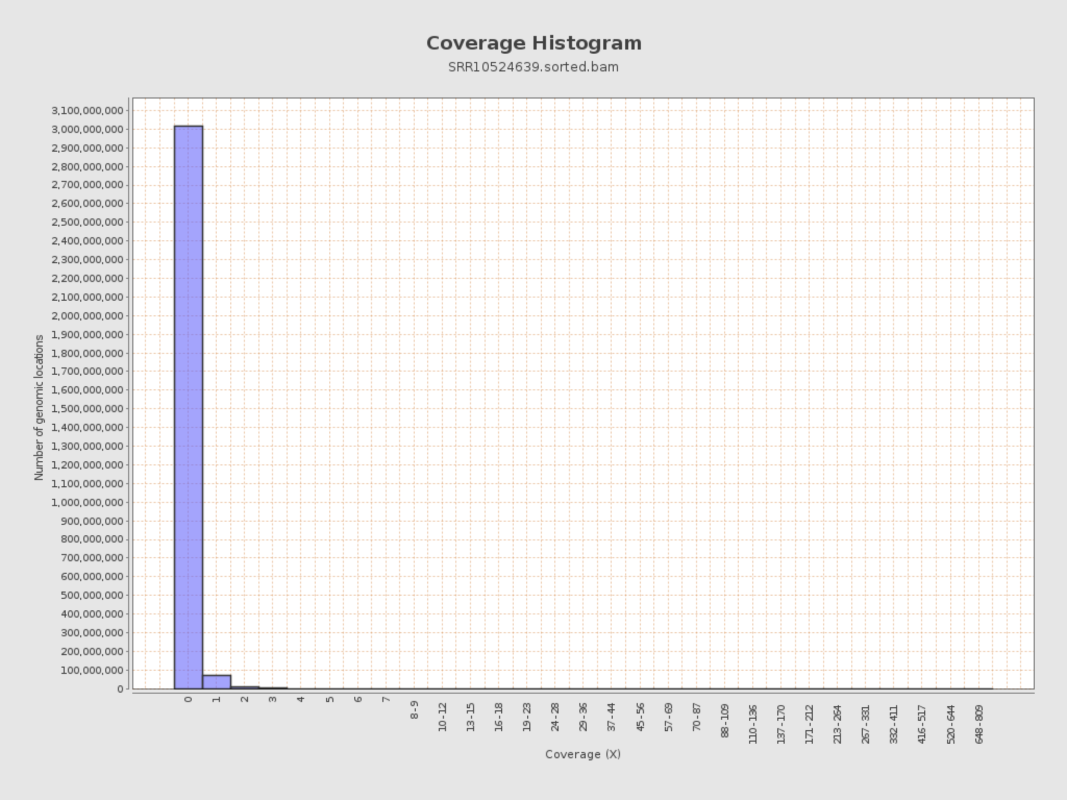
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9447495	0.0379	0.5871
chr2	243199373	8390895	0.0345	0.3517
chr3	198022430	5994500	0.0303	0.1978
chr4	191154276	4418362	0.0231	0.2251
chr5	180915260	5786394	0.032	0.2023
chr6	171115067	6036563	0.0353	0.2265
chr7	159138663	6107280	0.0384	0.3572

chr8	146364022	8553088	0.0584	0.4014
chr9	141213431	3448212	0.0244	0.2248
chr10	135534747	4117637	0.0304	0.3343
chr11	135006516	4874577	0.0361	0.2536
chr12	133851895	3231737	0.0241	0.1852
chr13	115169878	2336520	0.0203	0.1617
chr14	107349540	1772636	0.0165	0.1536
chr15	102531392	2465974	0.0241	0.177
chr16	90354753	2784514	0.0308	0.2125
chr17	81195210	2051484	0.0253	0.1869
chr18	78077248	2507318	0.0321	0.4061
chr19	59128983	1974638	0.0334	0.3795
chr20	63025520	1825476	0.029	0.2033
chr21	48129895	902927	0.0188	0.1985
chr22	51304566	1774303	0.0346	0.2126
chrMT	16571	11881	0.717	0.91
chrX	155270560	4486076	0.0289	0.2119
chrY	59373566	299255	0.005	0.2047

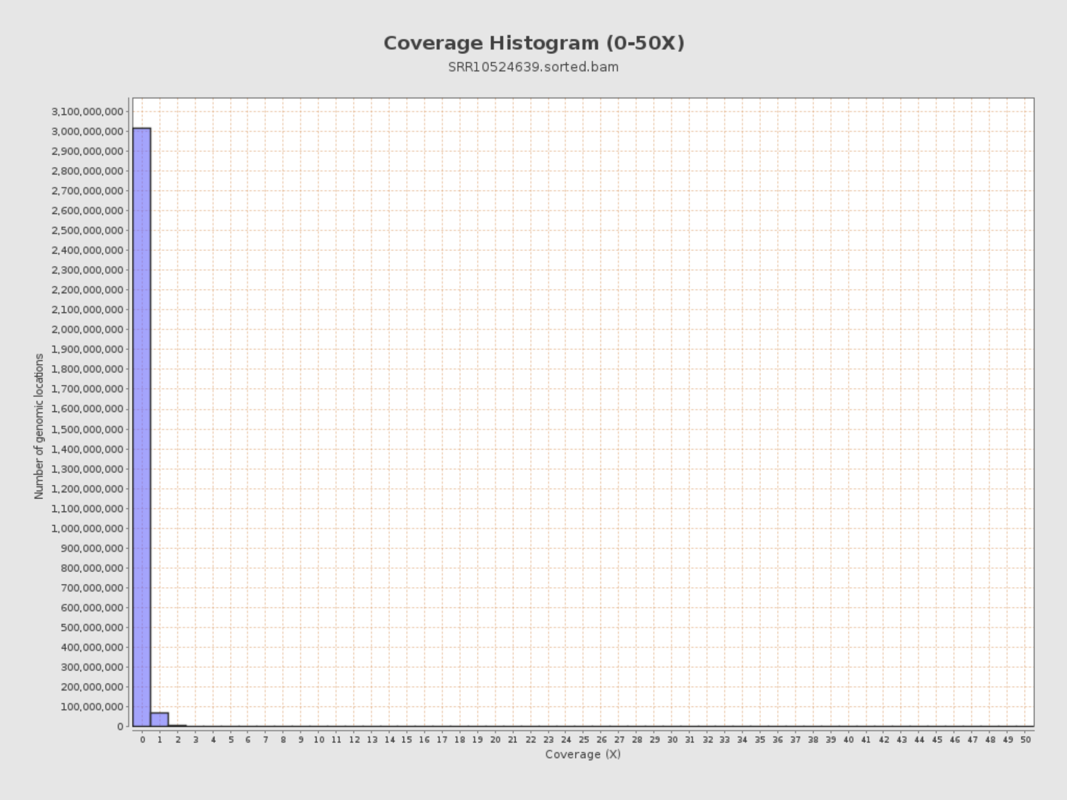
3. Results : Coverage across reference



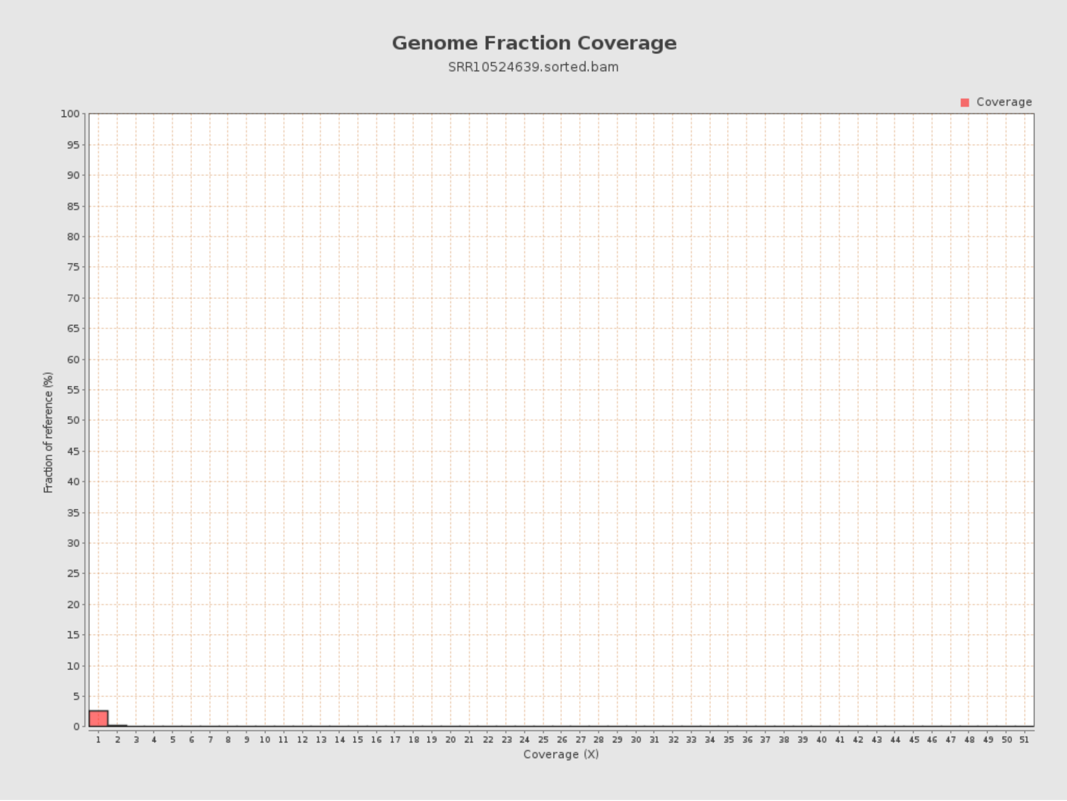
4. Results : Coverage Histogram



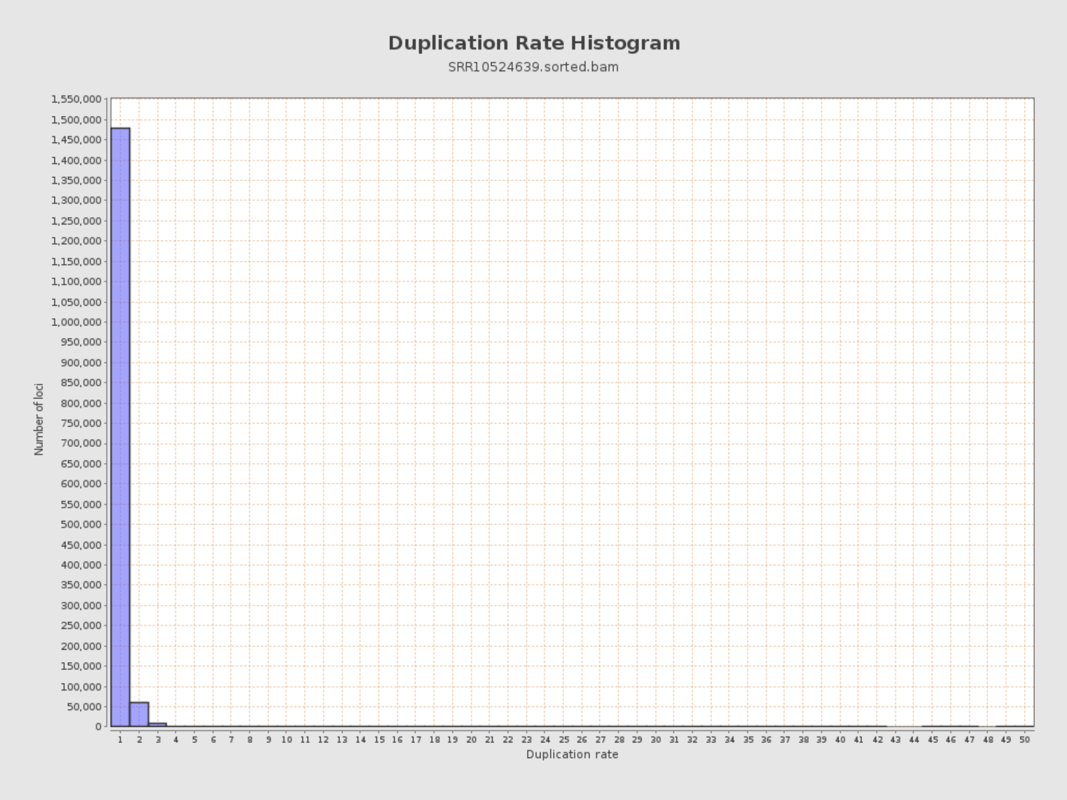
5. Results : Coverage Histogram (0-50X)



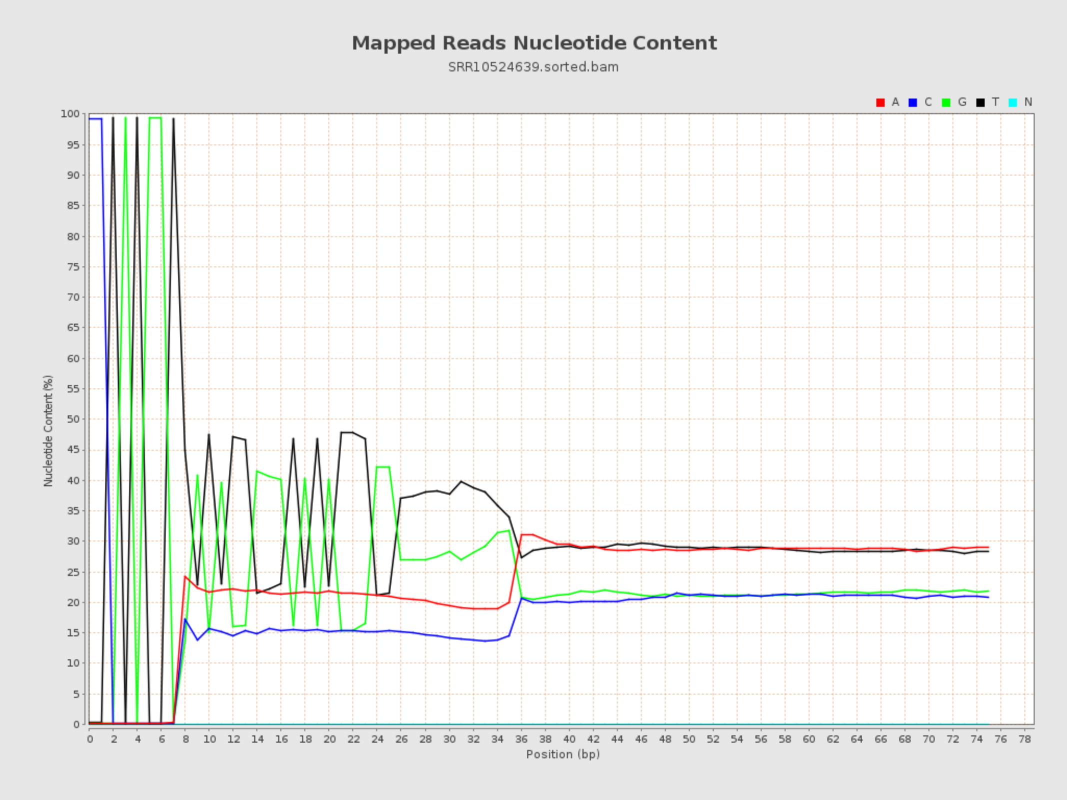
6. Results : Genome Fraction Coverage



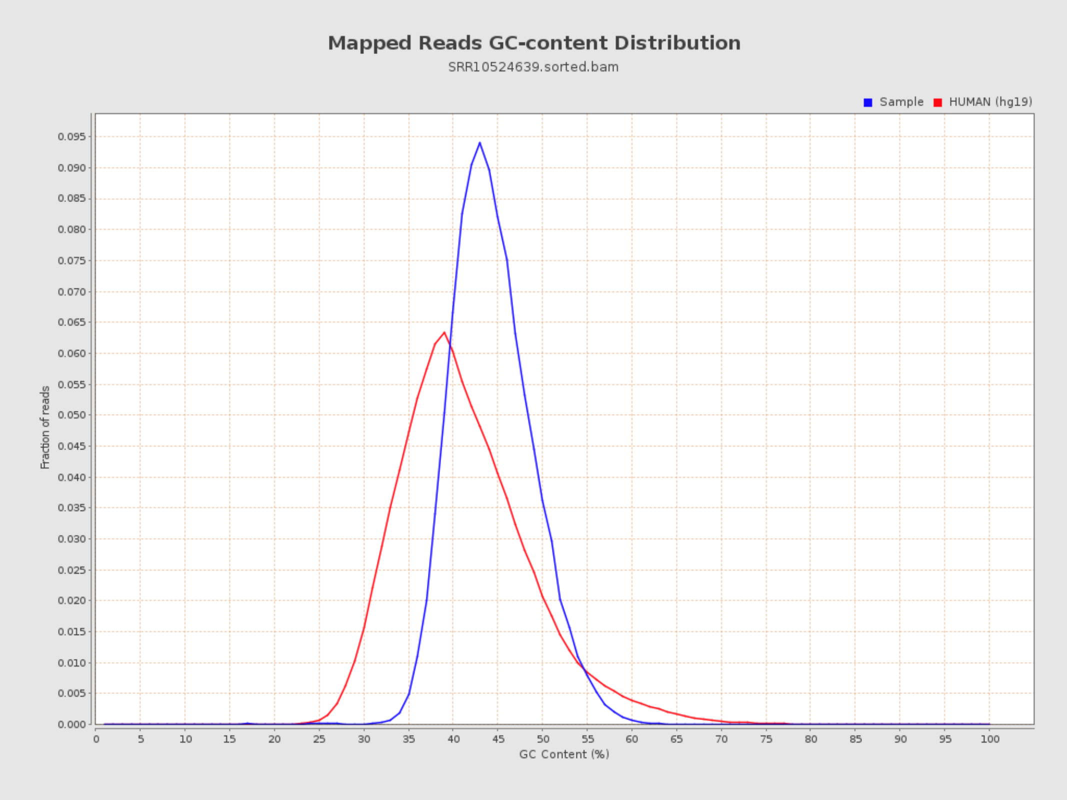
7. Results : Duplication Rate Histogram



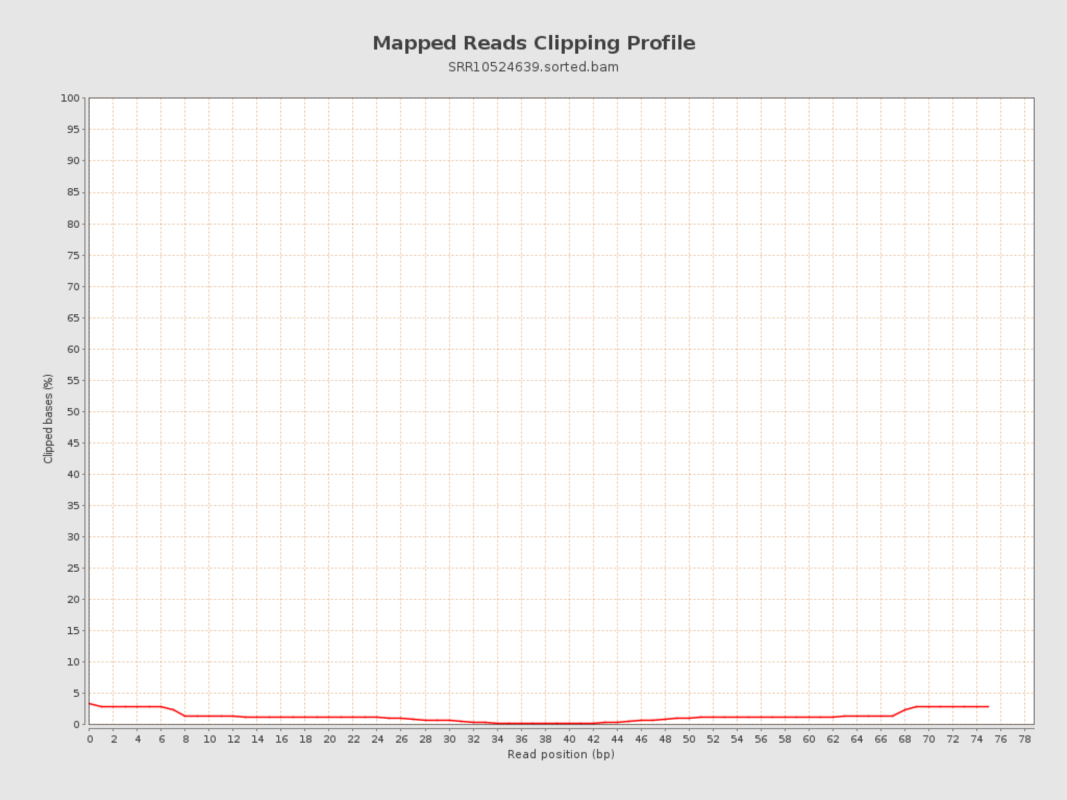
8. Results : Mapped Reads Nucleotide Content



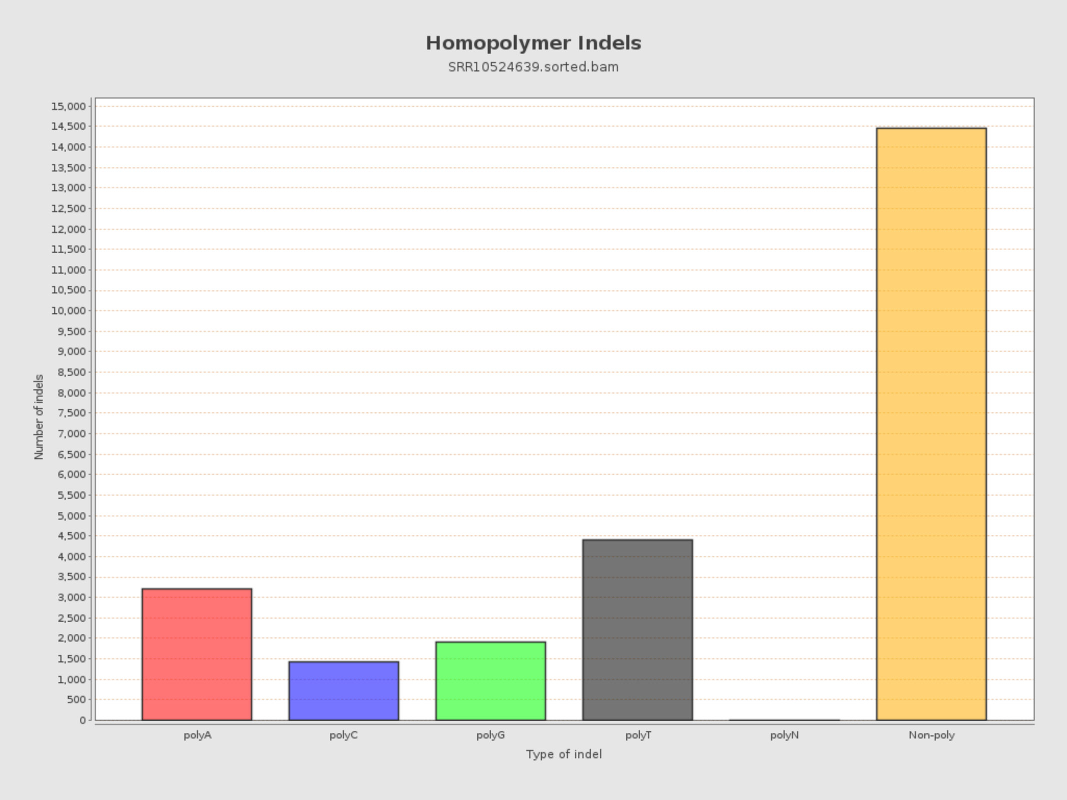
9. Results : Mapped Reads GC-content Distribution



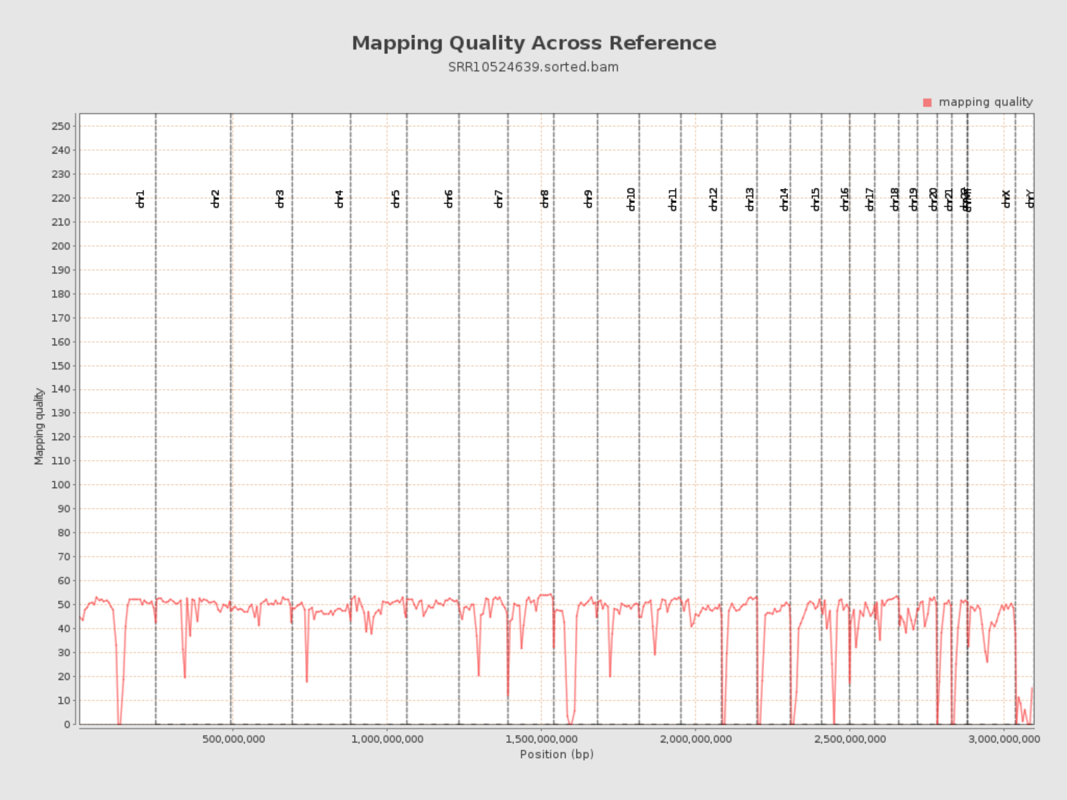
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram