Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:03:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524374.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_SRR10524374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524374.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,146,510
Mapped reads	1,046,997 / 91.32%
Unmapped reads	99,513 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,904 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	28,548 / 2.49%
Duplication rate	1.97%
Clipped reads	1,047,927 / 91.4%

2.2. ACGT Content

Number/percentage of A's	15,888,955 / 25.89%
Number/percentage of C's	11,440,068 / 18.64%
Number/percentage of T's	19,613,532 / 31.96%
Number/percentage of G's	14,411,900 / 23.49%
Number/percentage of N's	7,982 / 0.01%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.2162

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

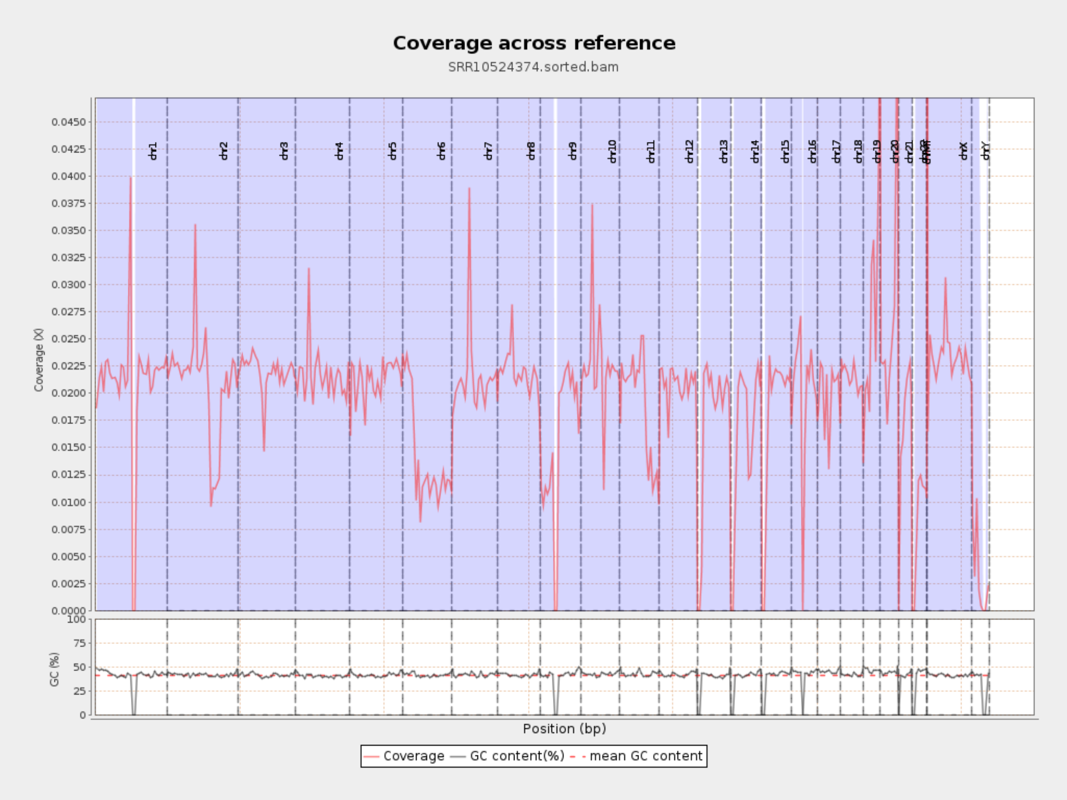
General error rate	0.5%
Mismatches	295,407
Insertions	4,847
Mapped reads with at least one insertion	0.46%
Deletions	10,963
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.03%

2.6. Chromosome stats

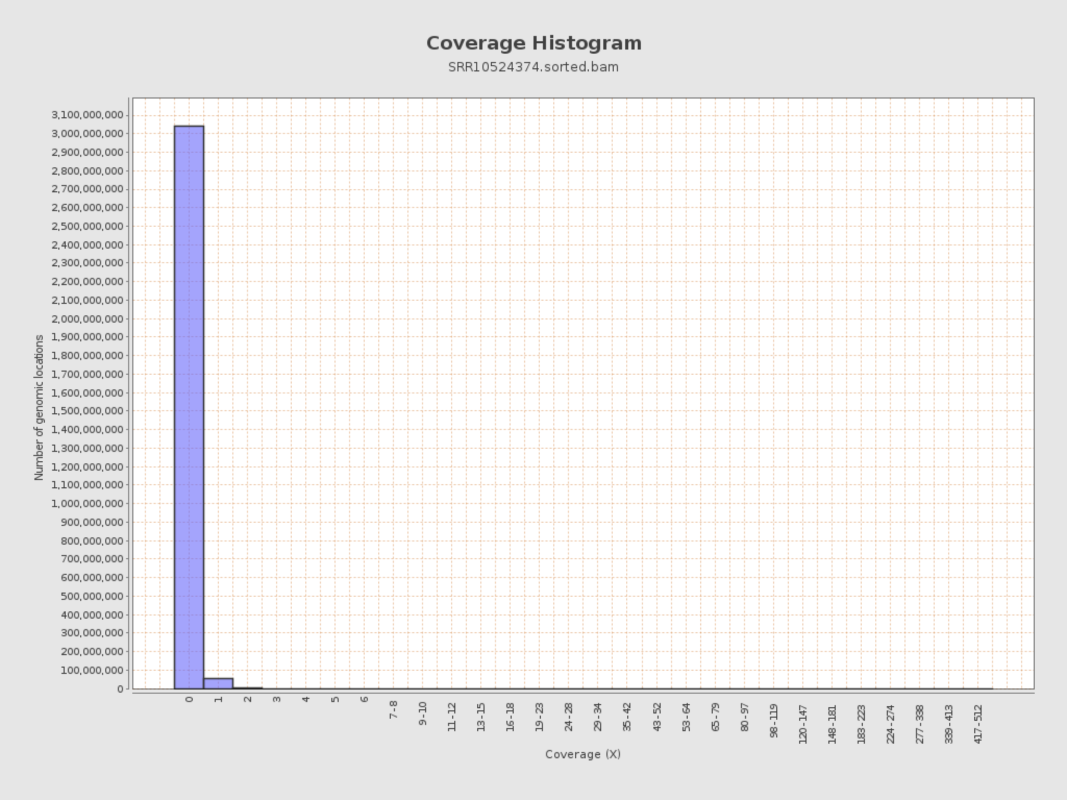
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5207286	0.0209	0.4335
chr2	243199373	5069266	0.0208	0.2314
chr3	198022430	4348871	0.022	0.1562
chr4	191154276	4136385	0.0216	0.1655
chr5	180915260	3889523	0.0215	0.1541
chr6	171115067	2394616	0.014	0.1342
chr7	159138663	3431401	0.0216	0.2991

chr8	146364022	3224981	0.022	0.2027
chr9	141213431	2160662	0.0153	0.1578
chr10	135534747	3064471	0.0226	0.2034
chr11	135006516	2568426	0.019	0.1739
chr12	133851895	2793204	0.0209	0.1543
chr13	115169878	1981171	0.0172	0.1377
chr14	107349540	1733014	0.0161	0.1378
chr15	102531392	1820332	0.0178	0.1405
chr16	90354753	1791281	0.0198	0.1553
chr17	81195210	1615323	0.0199	0.1599
chr18	78077248	1682326	0.0215	0.262
chr19	59128983	1670612	0.0283	0.3232
chr20	63025520	1721217	0.0273	0.178
chr21	48129895	824154	0.0171	0.147
chr22	51304566	431402	0.0084	0.0966
chrMT	16571	9830	0.5932	0.8836
chrX	155270560	3625193	0.0233	0.1727
chrY	59373566	184968	0.0031	0.0889

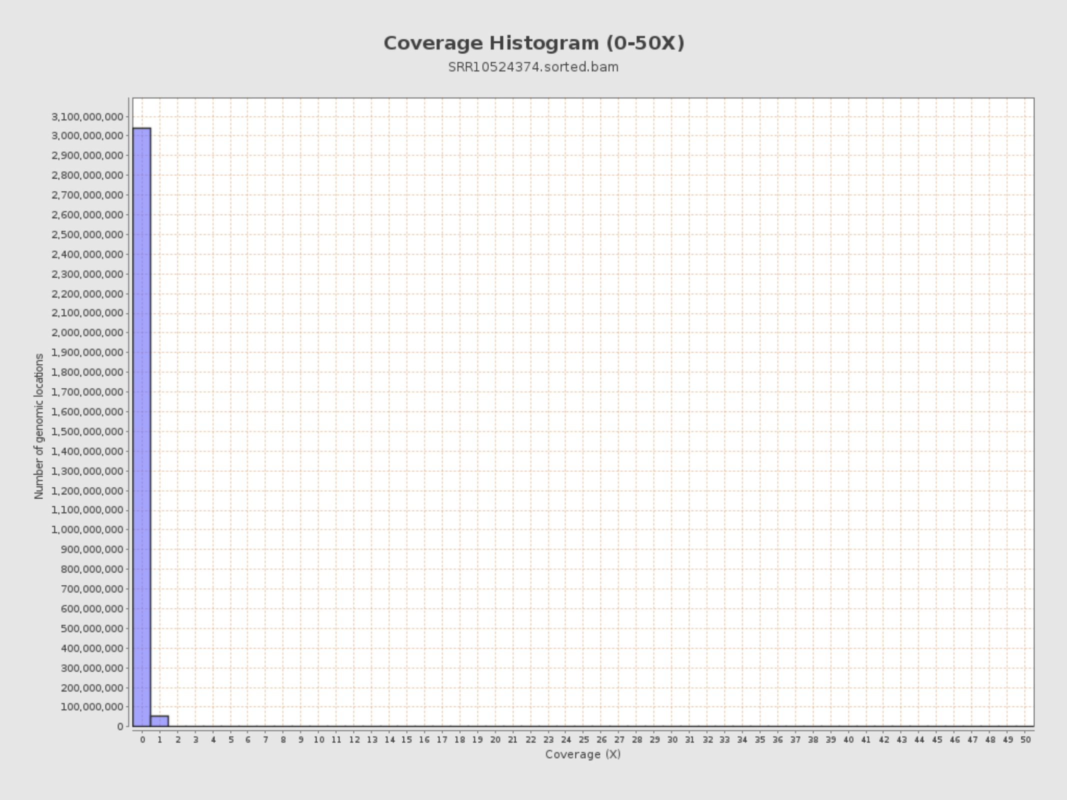
3. Results : Coverage across reference



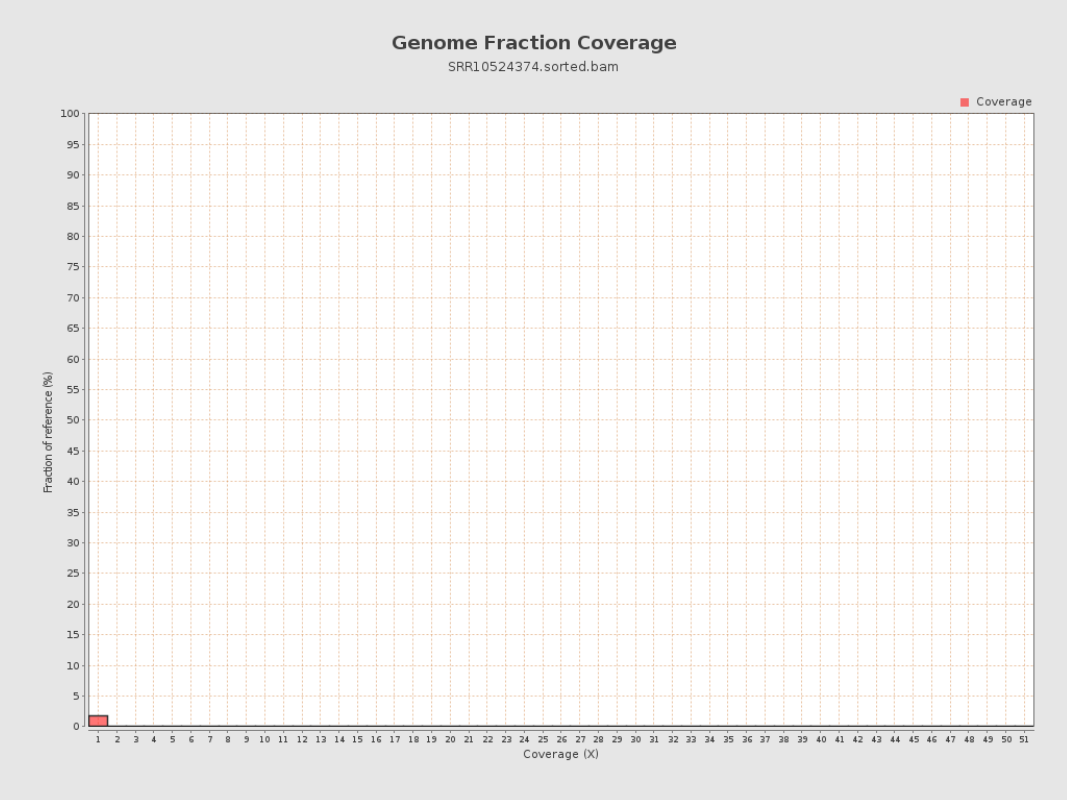
4. Results : Coverage Histogram



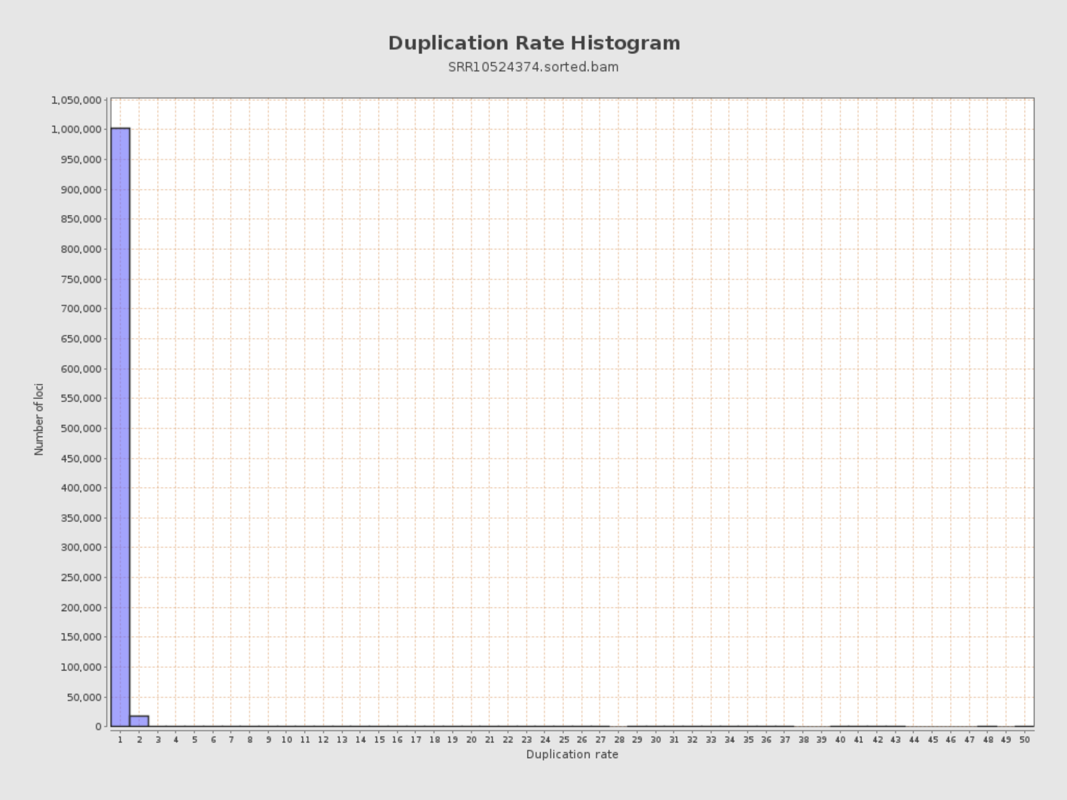
5. Results : Coverage Histogram (0-50X)



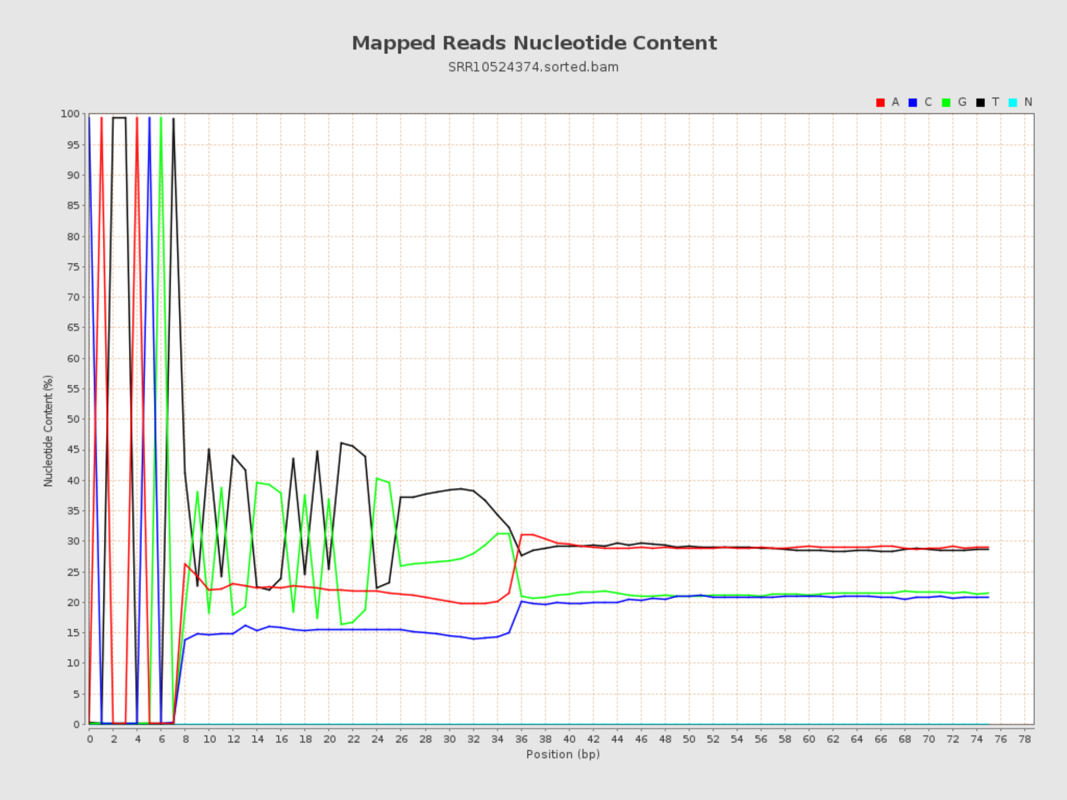
6. Results : Genome Fraction Coverage



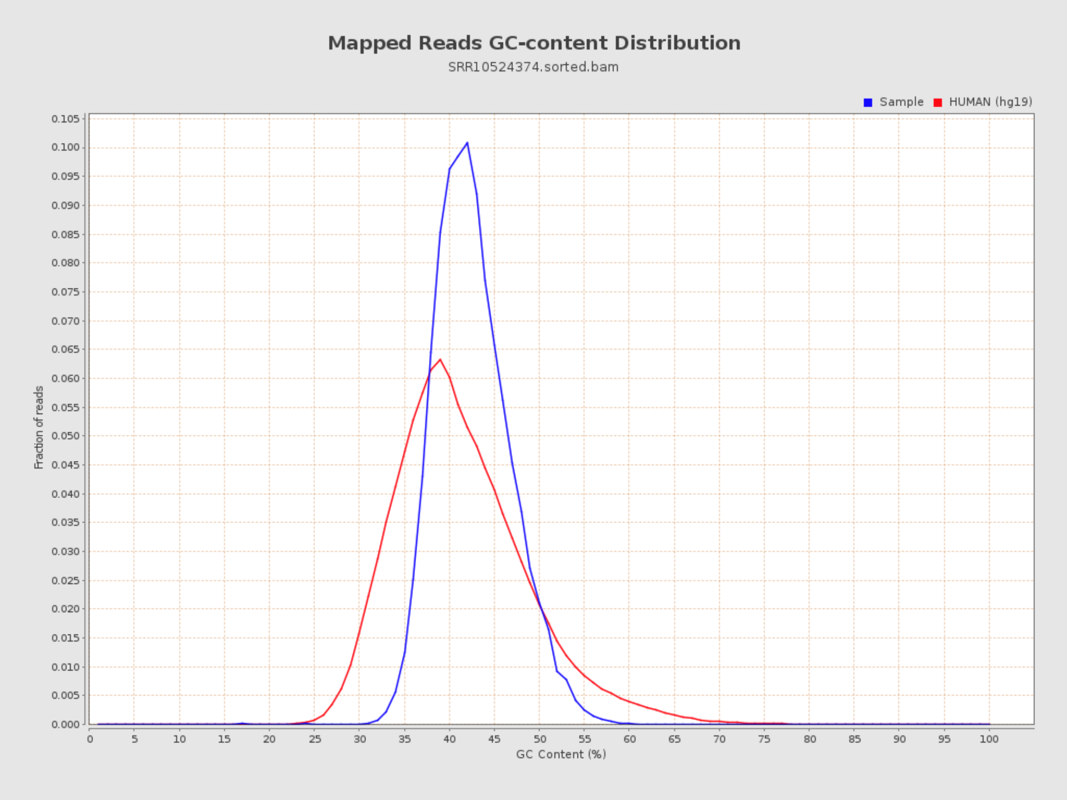
7. Results : Duplication Rate Histogram



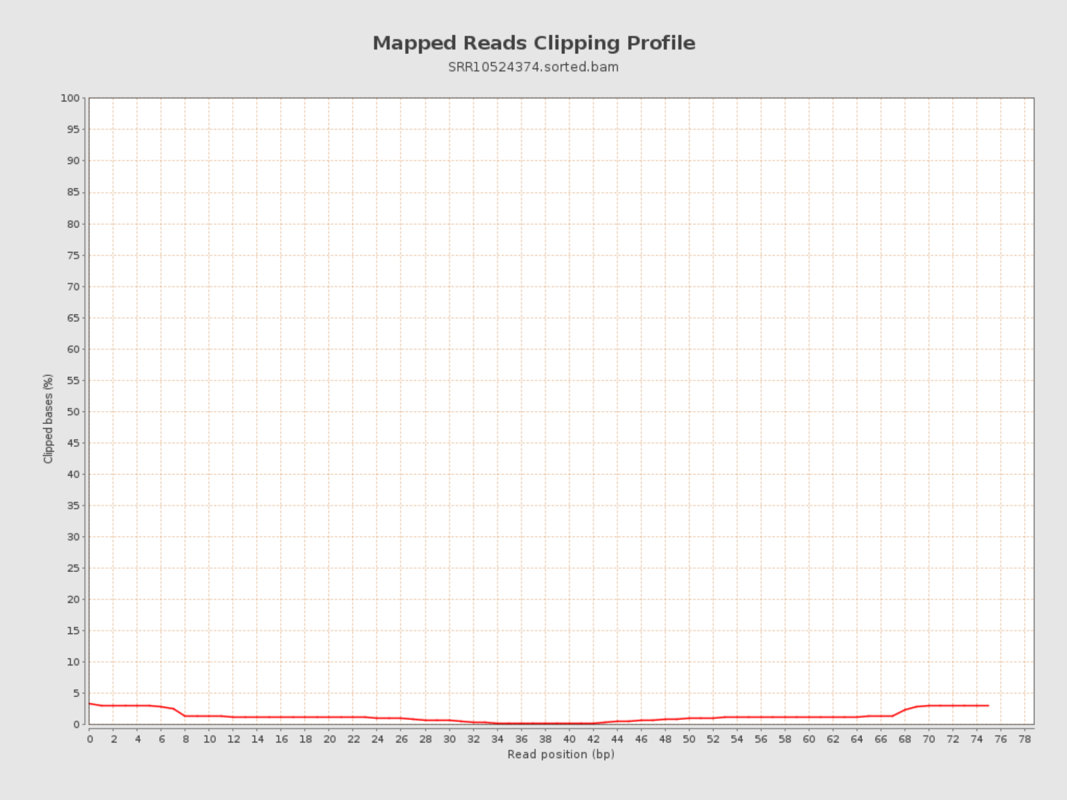
8. Results : Mapped Reads Nucleotide Content



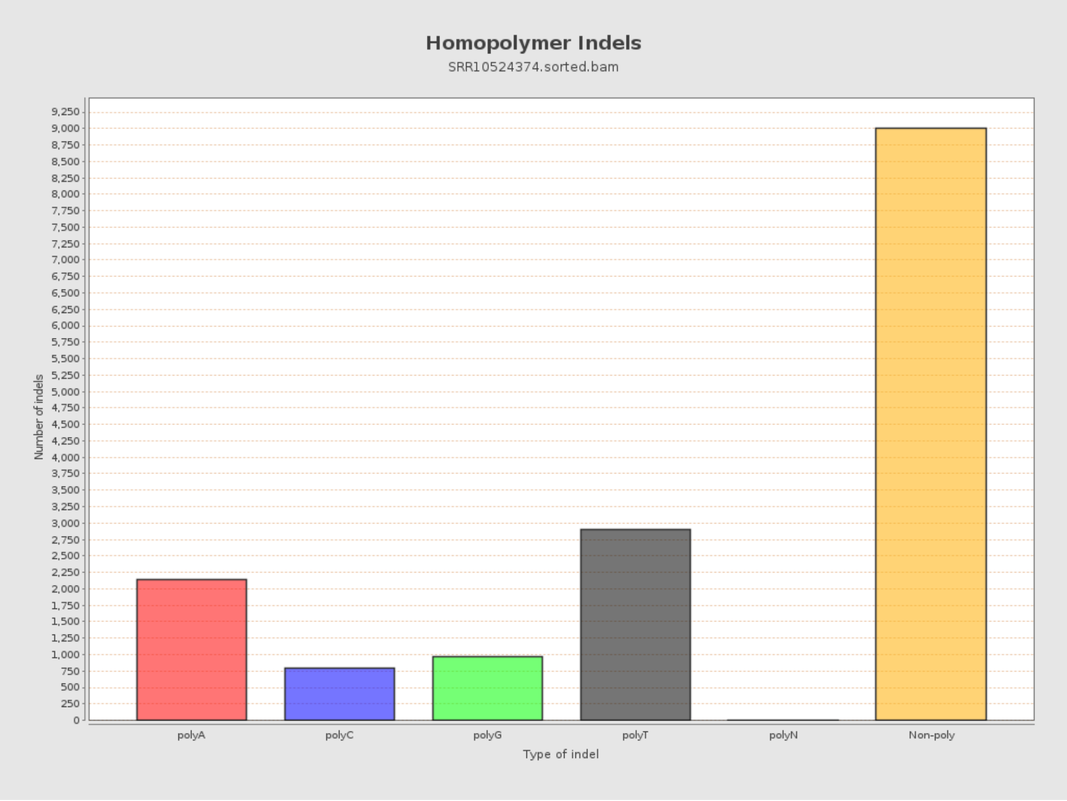
9. Results : Mapped Reads GC-content Distribution



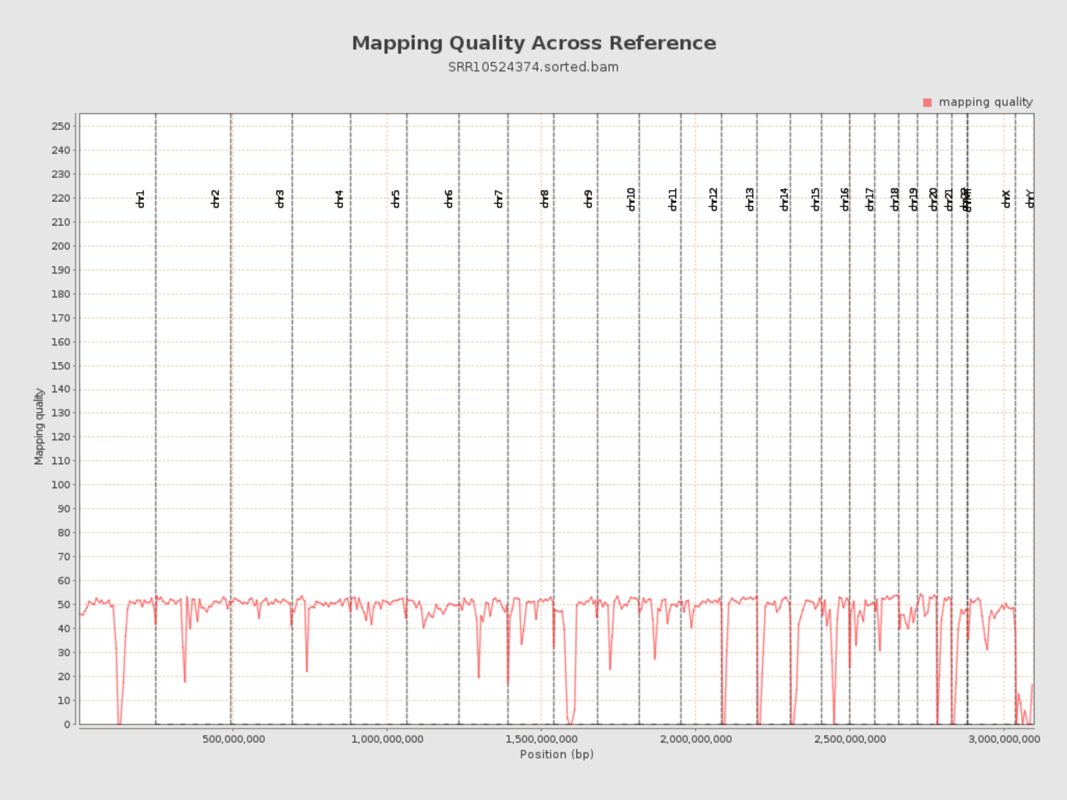
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram