Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:41:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524762.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_SRR10524762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,448,550
Mapped reads	1,322,491 / 91.3%
Unmapped reads	126,059 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,406 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	42,687 / 2.95%
Duplication rate	2.44%
Clipped reads	1,323,276 / 91.35%

2.2. ACGT Content

Number/percentage of A's	18,876,422 / 24.84%
Number/percentage of C's	13,517,183 / 17.79%
Number/percentage of T's	23,855,844 / 31.39%
Number/percentage of G's	19,735,563 / 25.97%
Number/percentage of N's	10,153 / 0.01%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2186

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

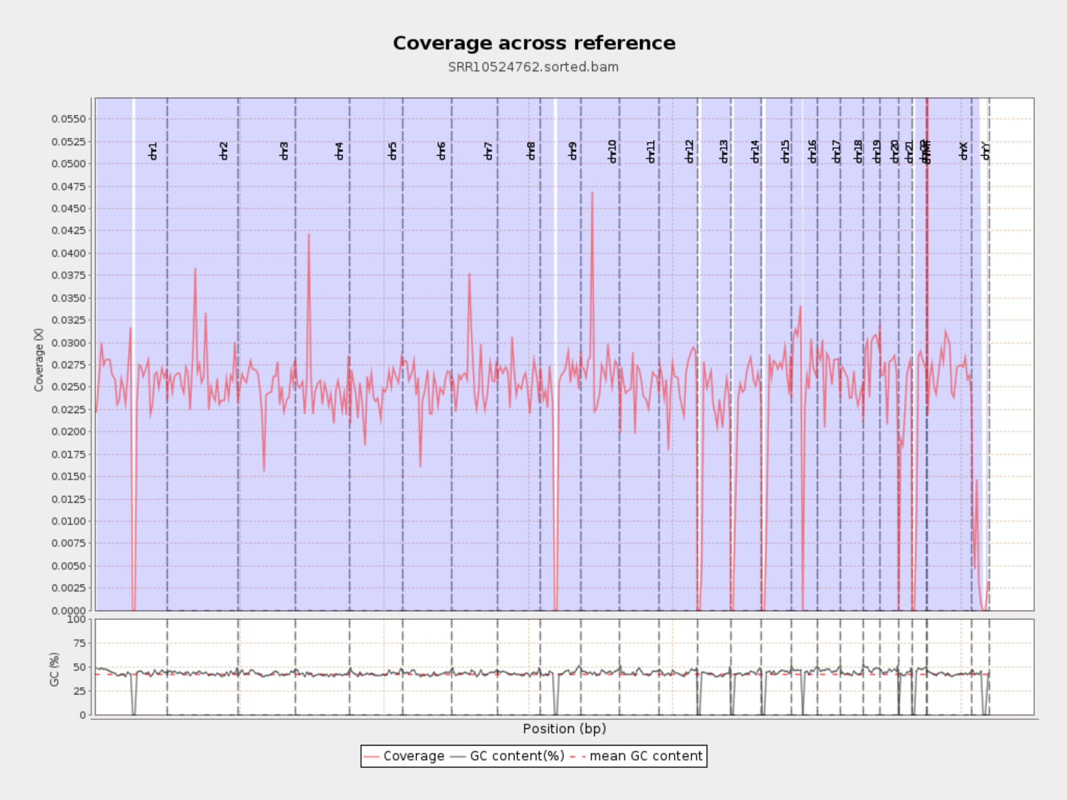
General error rate	0.52%
Mismatches	382,437
Insertions	5,368
Mapped reads with at least one insertion	0.4%
Deletions	14,997
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.56%

2.6. Chromosome stats

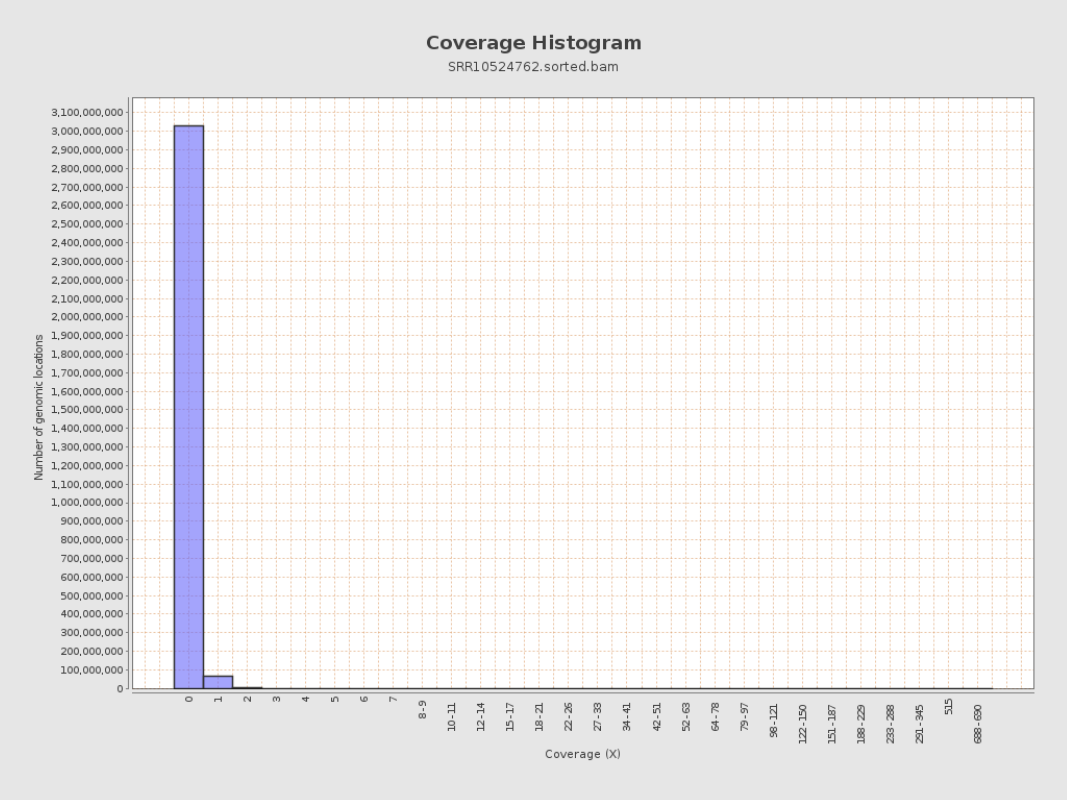
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6106280	0.0245	0.2726
chr2	243199373	6366416	0.0262	0.3437
chr3	198022430	4942587	0.025	0.174
chr4	191154276	4819943	0.0252	0.1905
chr5	180915260	4473655	0.0247	0.1709
chr6	171115067	4287368	0.0251	0.1859
chr7	159138663	4190131	0.0263	0.272

chr8	146364022	3786805	0.0259	0.2033
chr9	141213431	3260313	0.0231	0.1907
chr10	135534747	3740287	0.0276	0.2498
chr11	135006516	3396129	0.0252	0.2017
chr12	133851895	3434611	0.0257	0.1765
chr13	115169878	2317150	0.0201	0.1542
chr14	107349540	2296873	0.0214	0.1629
chr15	102531392	2252493	0.022	0.1652
chr16	90354753	2328984	0.0258	0.1885
chr17	81195210	2211917	0.0272	0.1853
chr18	78077248	1966682	0.0252	0.2847
chr19	59128983	1711047	0.0289	0.2382
chr20	63025520	1653083	0.0262	0.1813
chr21	48129895	1016358	0.0211	0.1713
chr22	51304566	990834	0.0193	0.1524
chrMT	16571	25408	1.5333	1.4925
chrX	155270560	4180439	0.0269	0.1916
chrY	59373566	263370	0.0044	0.1201

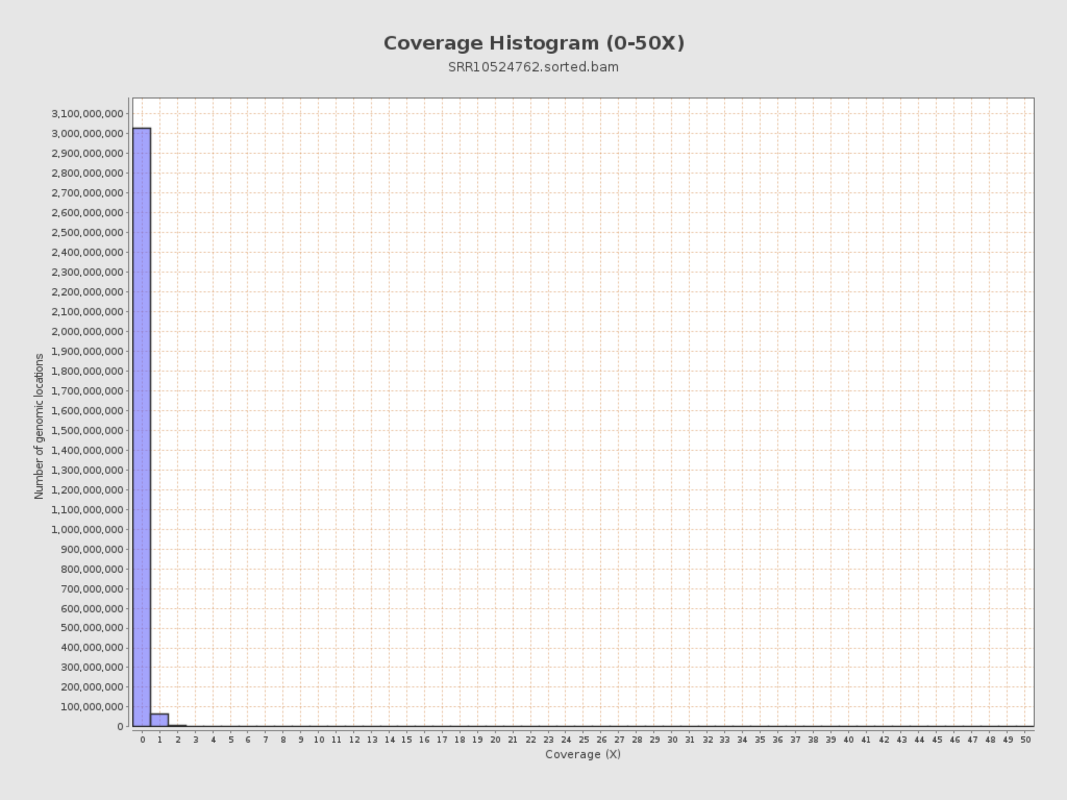
3. Results : Coverage across reference



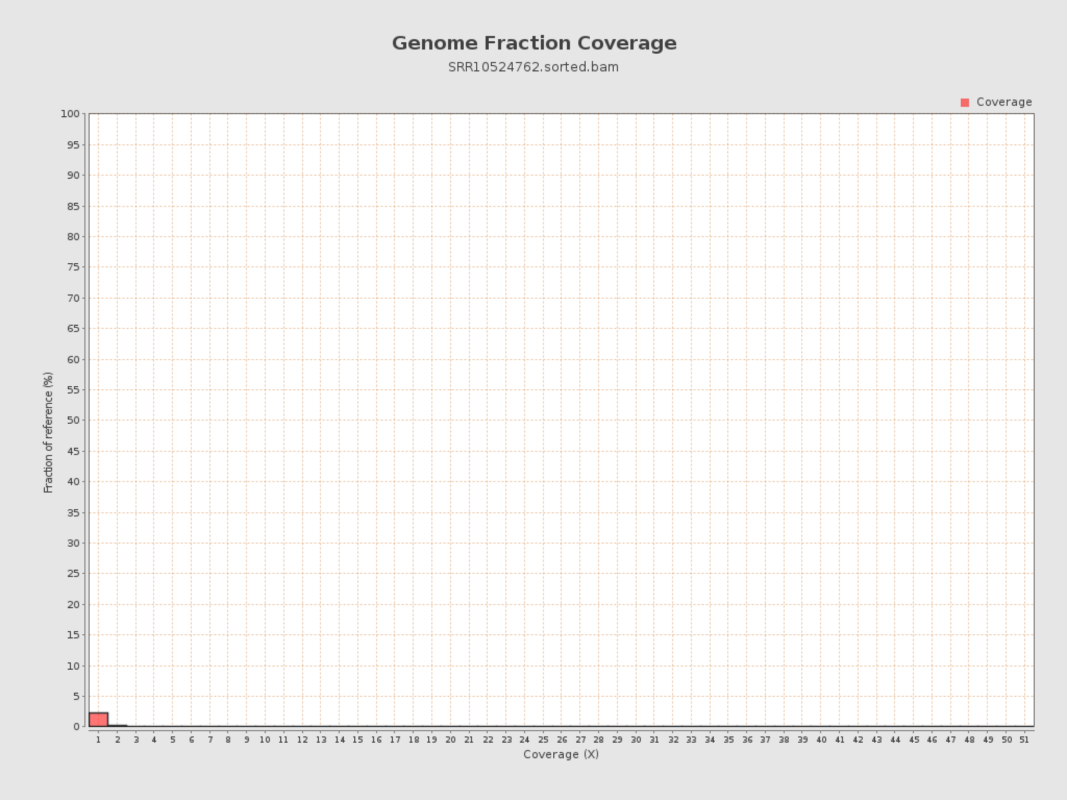
4. Results : Coverage Histogram



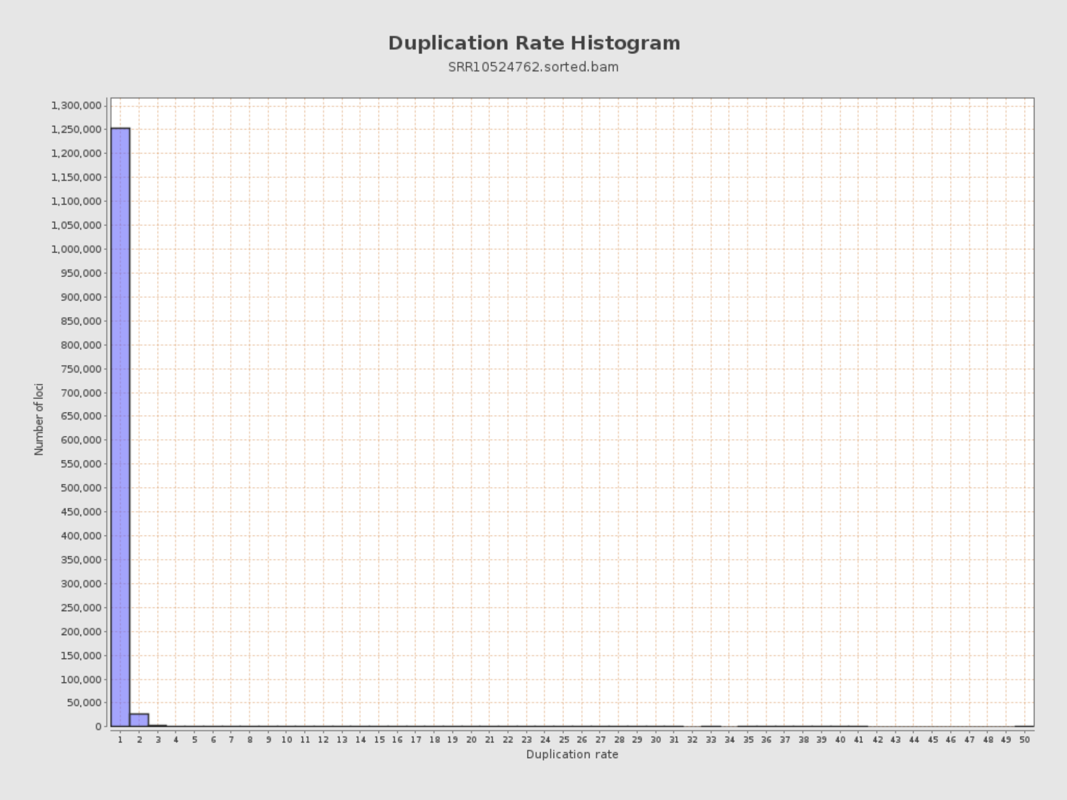
5. Results : Coverage Histogram (0-50X)



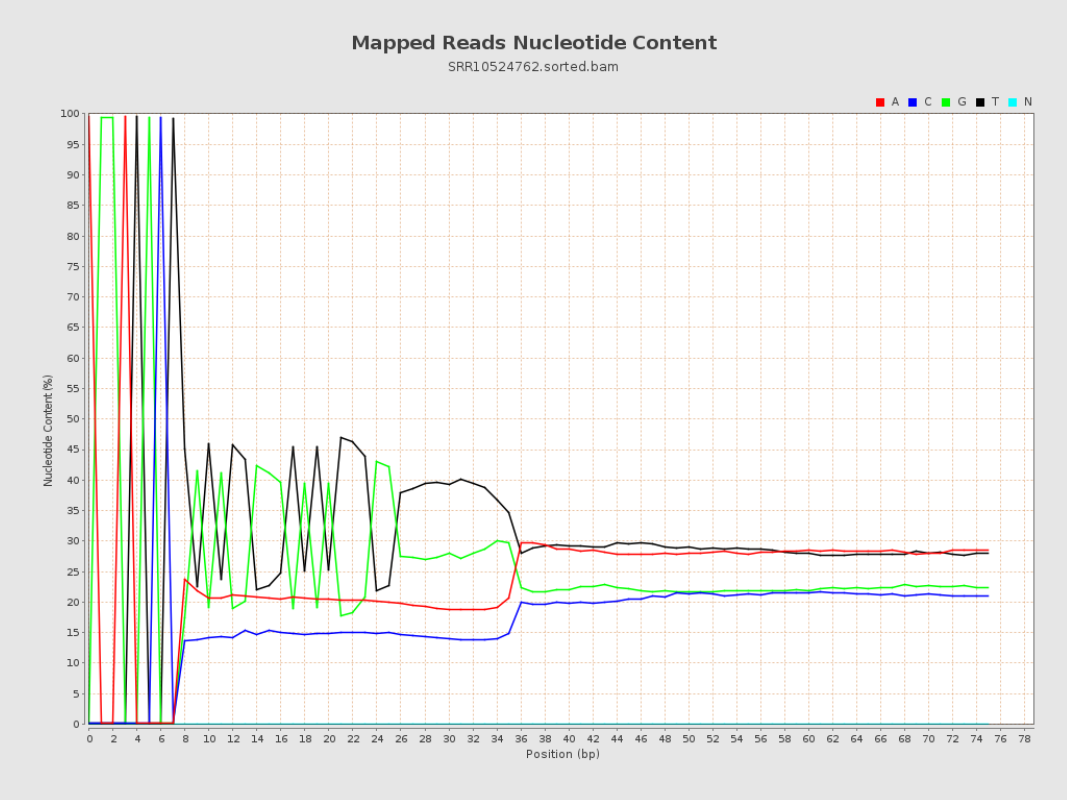
6. Results : Genome Fraction Coverage



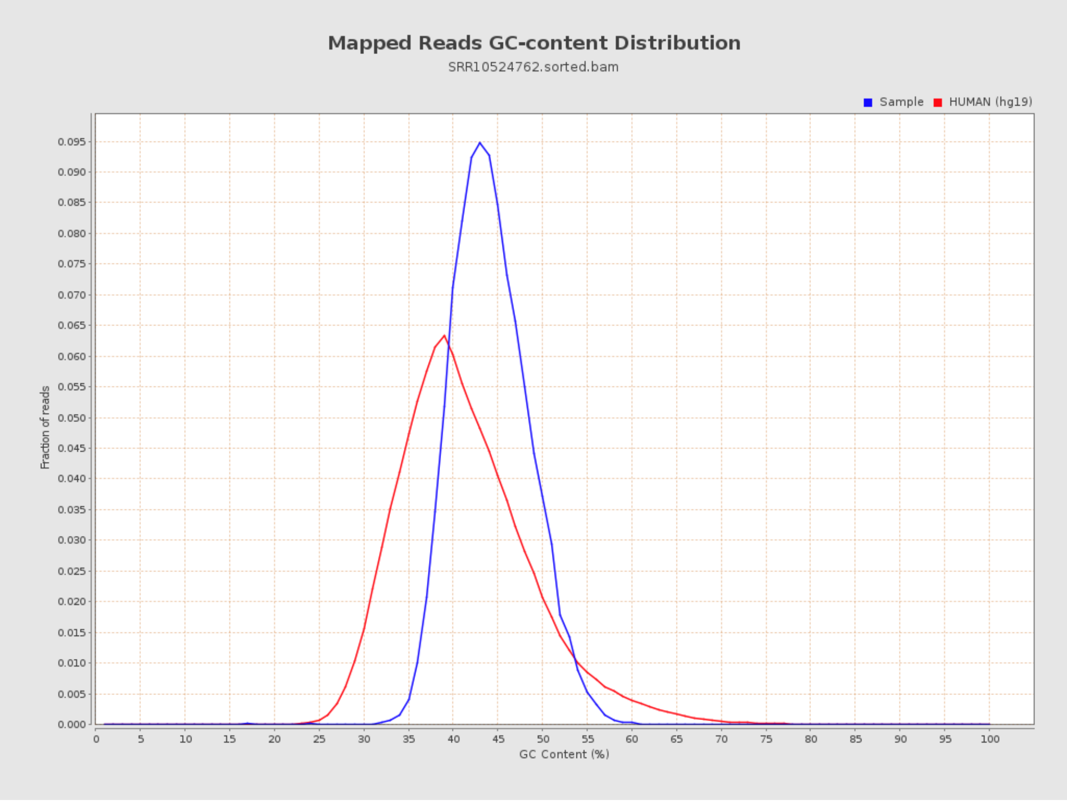
7. Results : Duplication Rate Histogram



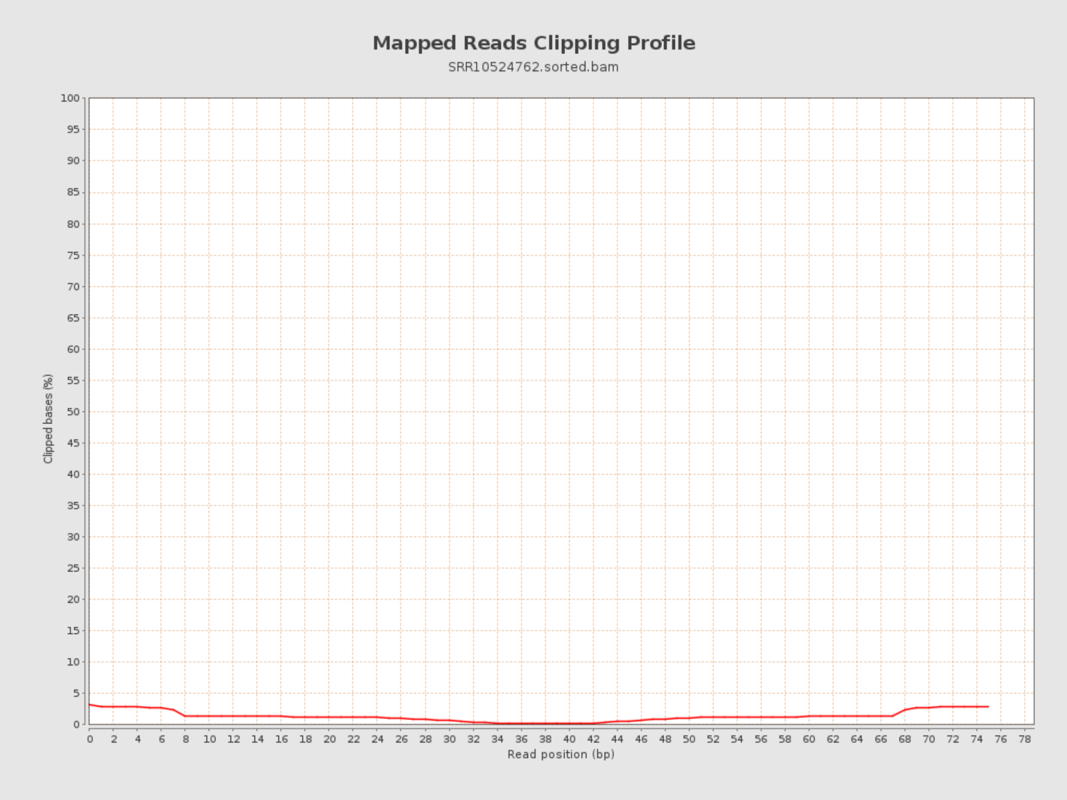
8. Results : Mapped Reads Nucleotide Content



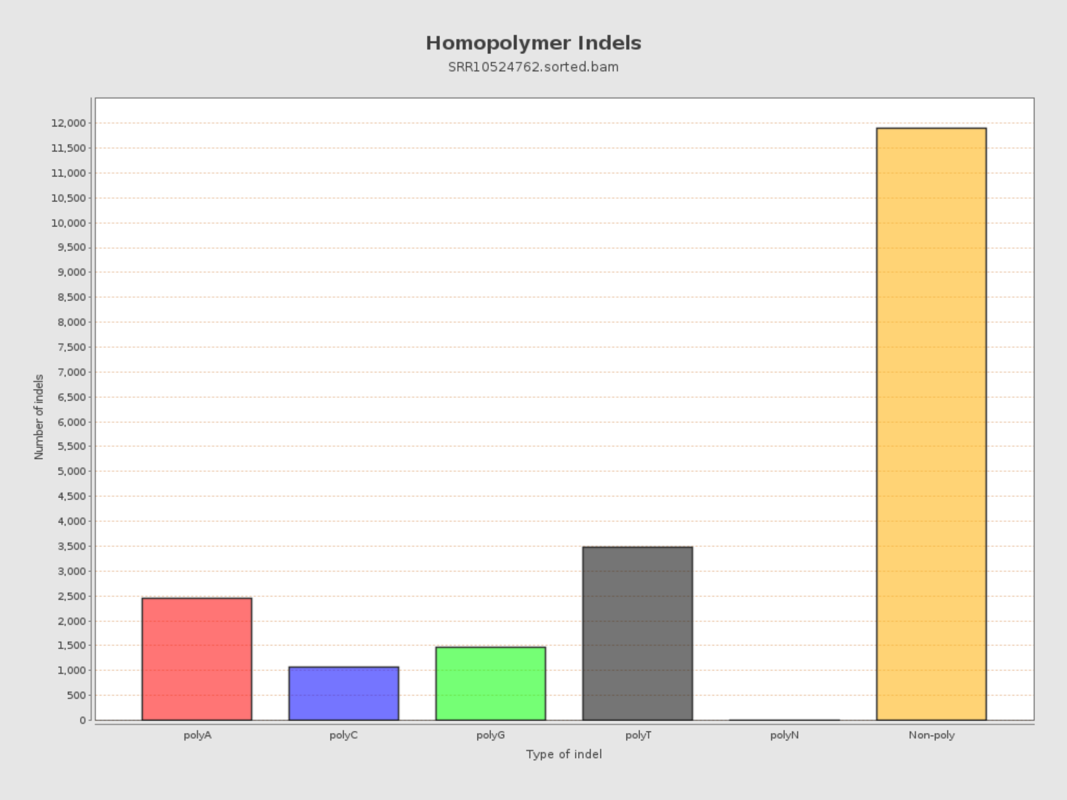
9. Results : Mapped Reads GC-content Distribution



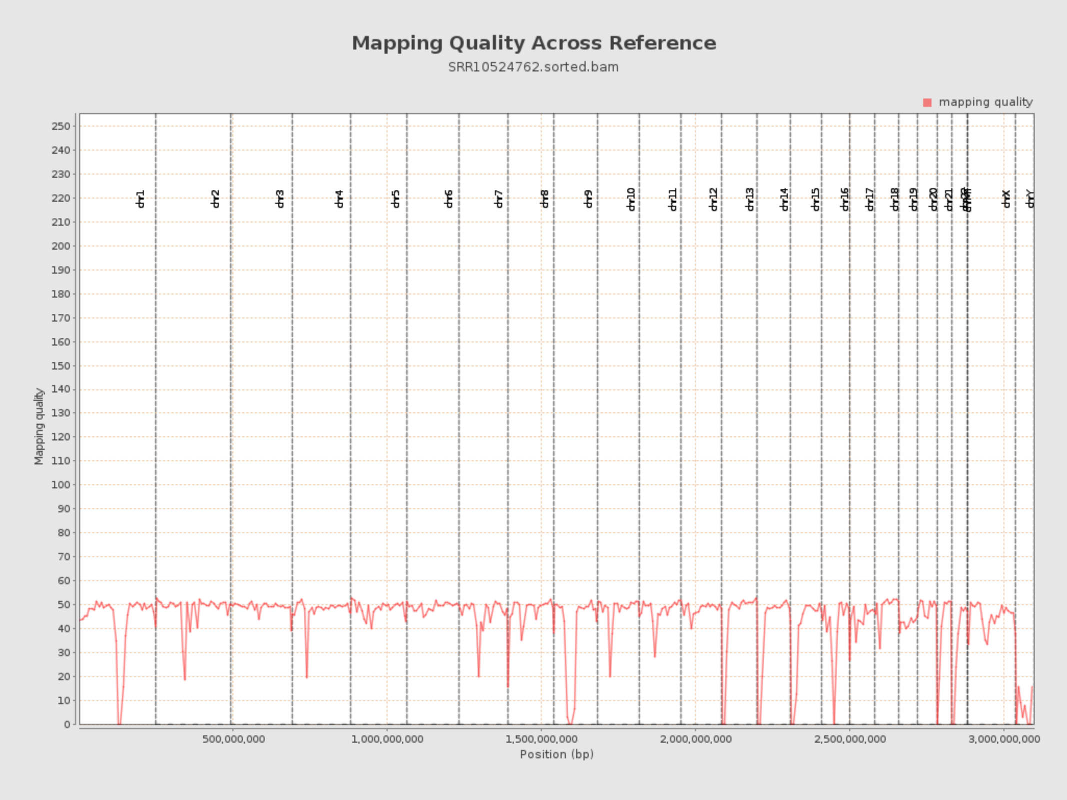
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram