Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:48:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524765.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_SRR10524765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524765.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:48:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,183,639
Mapped reads	1,066,296 / 90.09%
Unmapped reads	117,343 / 9.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,637 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	32,646 / 2.76%
Duplication rate	2.28%
Clipped reads	1,067,381 / 90.18%

2.2. ACGT Content

Number/percentage of A's	14,994,932 / 24.75%
Number/percentage of C's	11,645,212 / 19.22%
Number/percentage of T's	19,216,339 / 31.72%
Number/percentage of G's	14,719,530 / 24.3%
Number/percentage of N's	7,551 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.1935

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

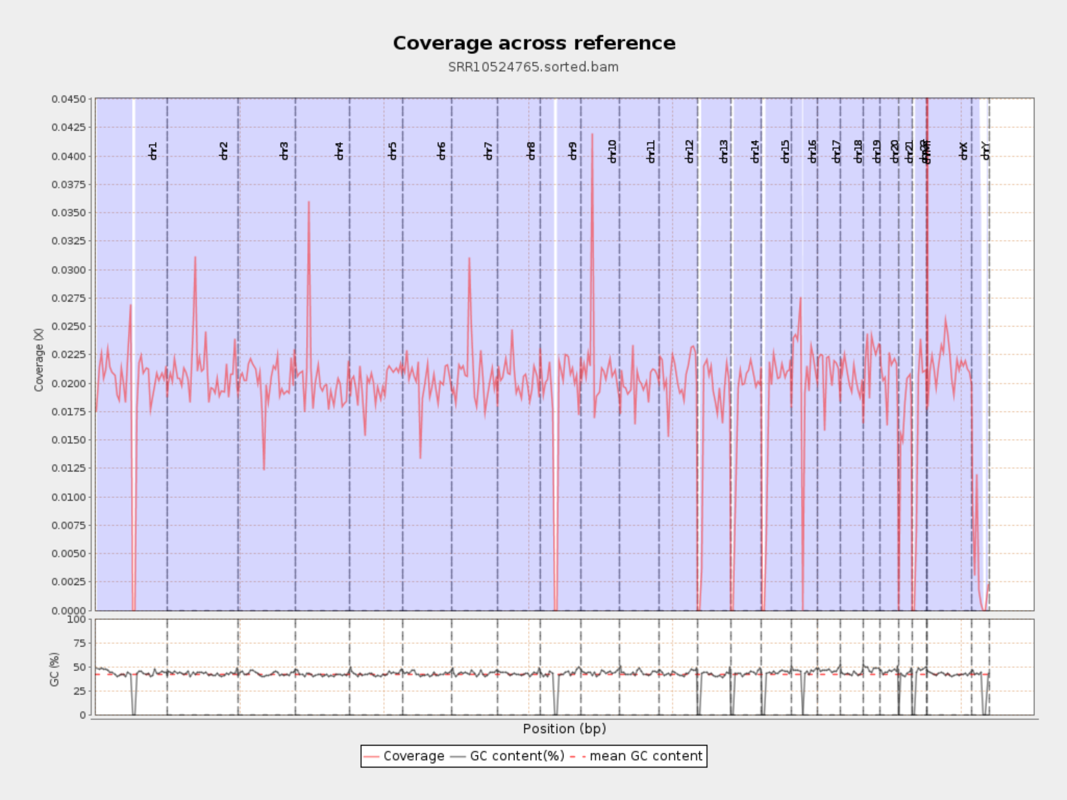
General error rate	0.53%
Mismatches	314,119
Insertions	4,098
Mapped reads with at least one insertion	0.38%
Deletions	12,054
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.54%

2.6. Chromosome stats

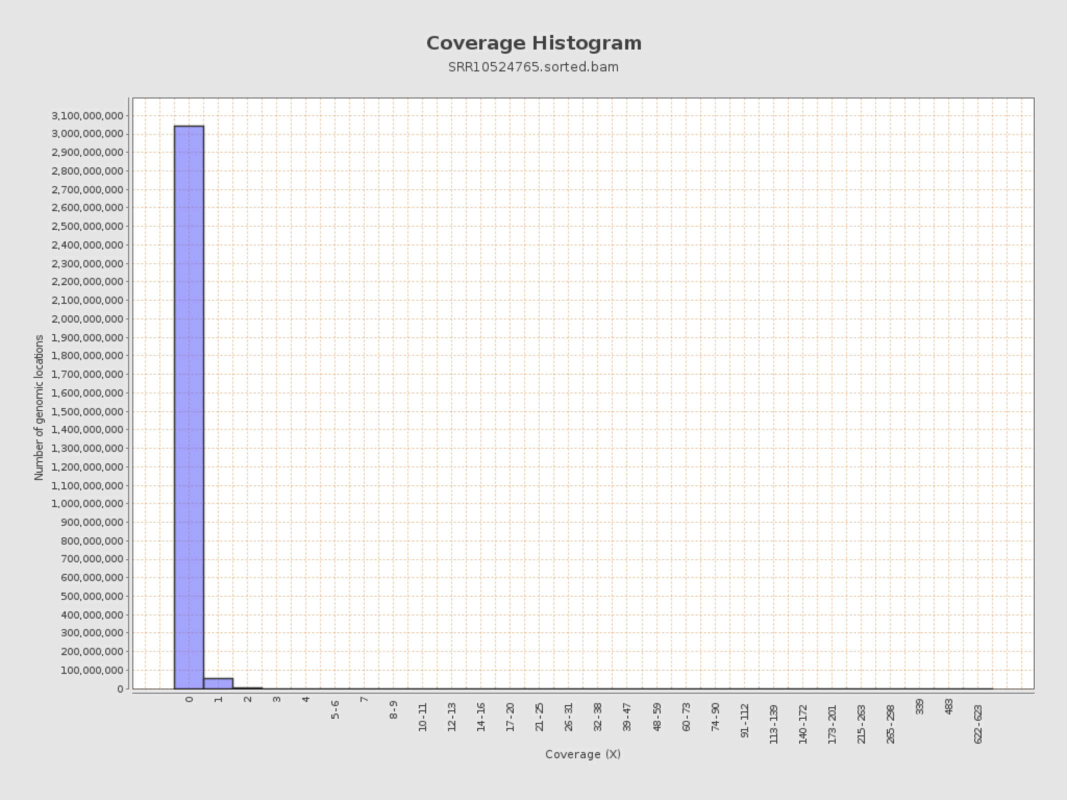
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4838052	0.0194	0.2523
chr2	243199373	5106644	0.021	0.3034
chr3	198022430	3972929	0.0201	0.1526
chr4	191154276	3895139	0.0204	0.1696
chr5	180915260	3621781	0.02	0.1515
chr6	171115067	3446314	0.0201	0.1623
chr7	159138663	3313666	0.0208	0.2307

chr8	146364022	3002815	0.0205	0.1837
chr9	141213431	2586232	0.0183	0.1701
chr10	135534747	2947866	0.0217	0.2226
chr11	135006516	2707772	0.0201	0.1726
chr12	133851895	2776287	0.0207	0.1564
chr13	115169878	1912343	0.0166	0.1381
chr14	107349540	1826248	0.017	0.1425
chr15	102531392	1749386	0.0171	0.1413
chr16	90354753	1841911	0.0204	0.1664
chr17	81195210	1713965	0.0211	0.1607
chr18	78077248	1598312	0.0205	0.2548
chr19	59128983	1323120	0.0224	0.2127
chr20	63025520	1301997	0.0207	0.1573
chr21	48129895	788367	0.0164	0.1471
chr22	51304566	759740	0.0148	0.1312
chrMT	16571	7912	0.4775	0.7525
chrX	155270560	3362719	0.0217	0.1685
chrY	59373566	201363	0.0034	0.1015

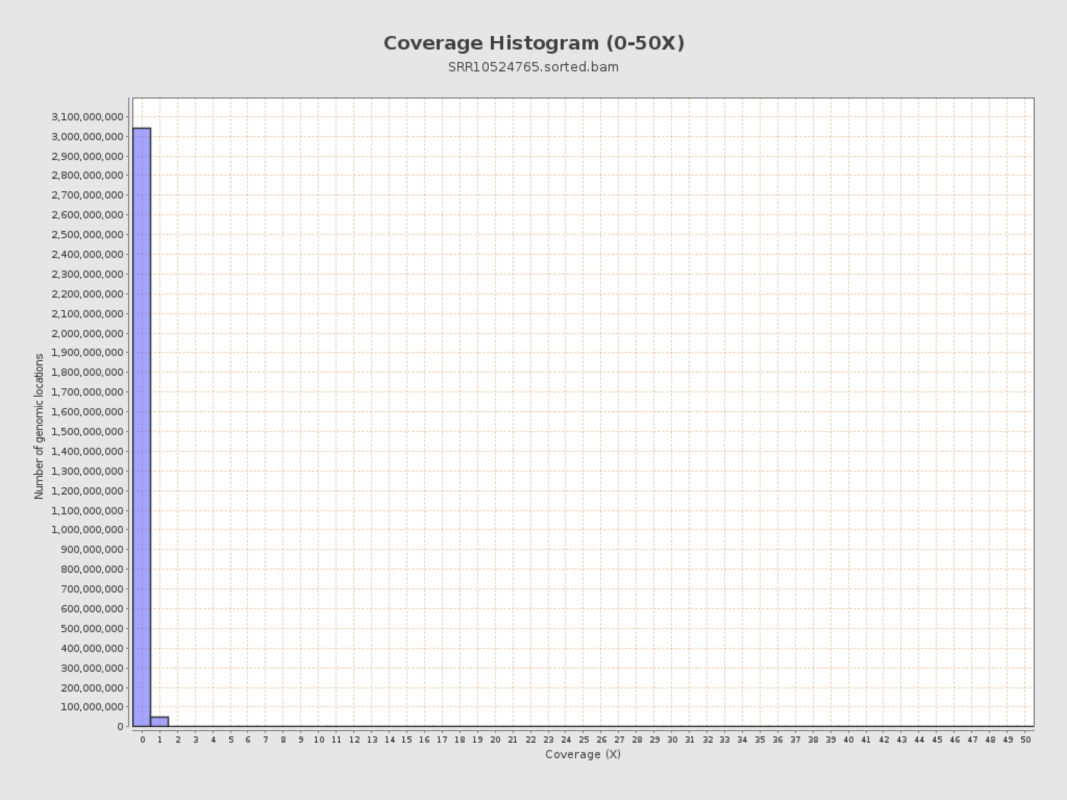
3. Results : Coverage across reference



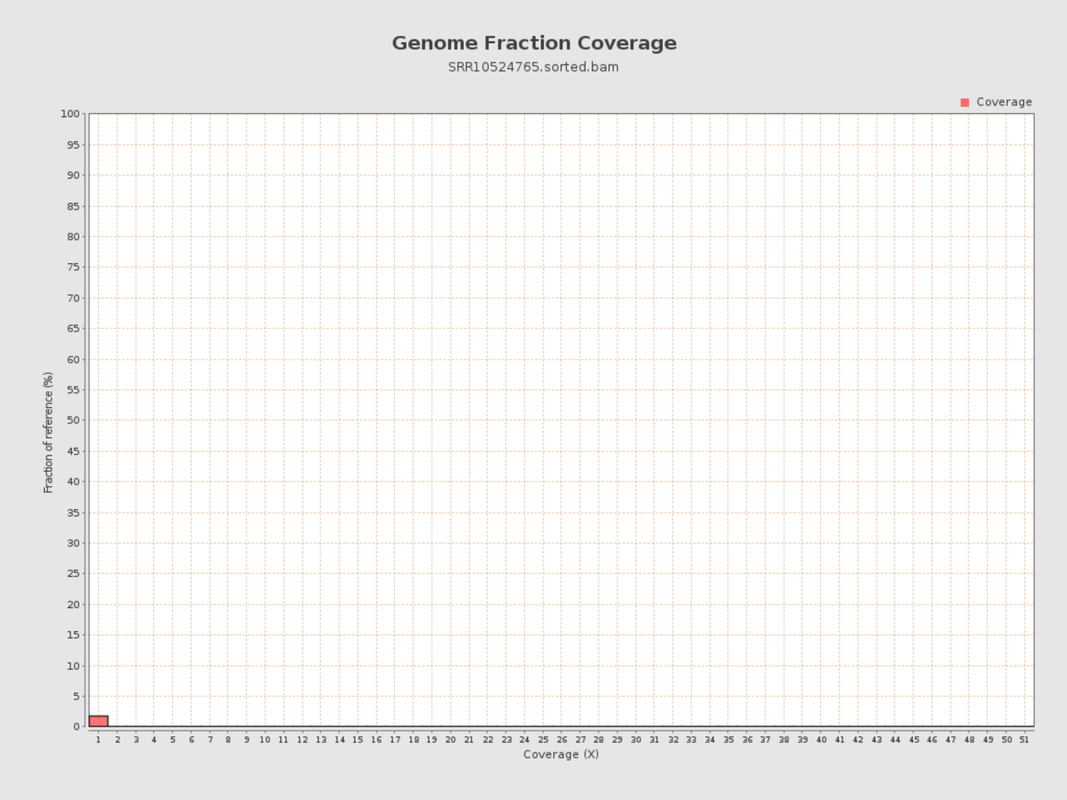
4. Results : Coverage Histogram



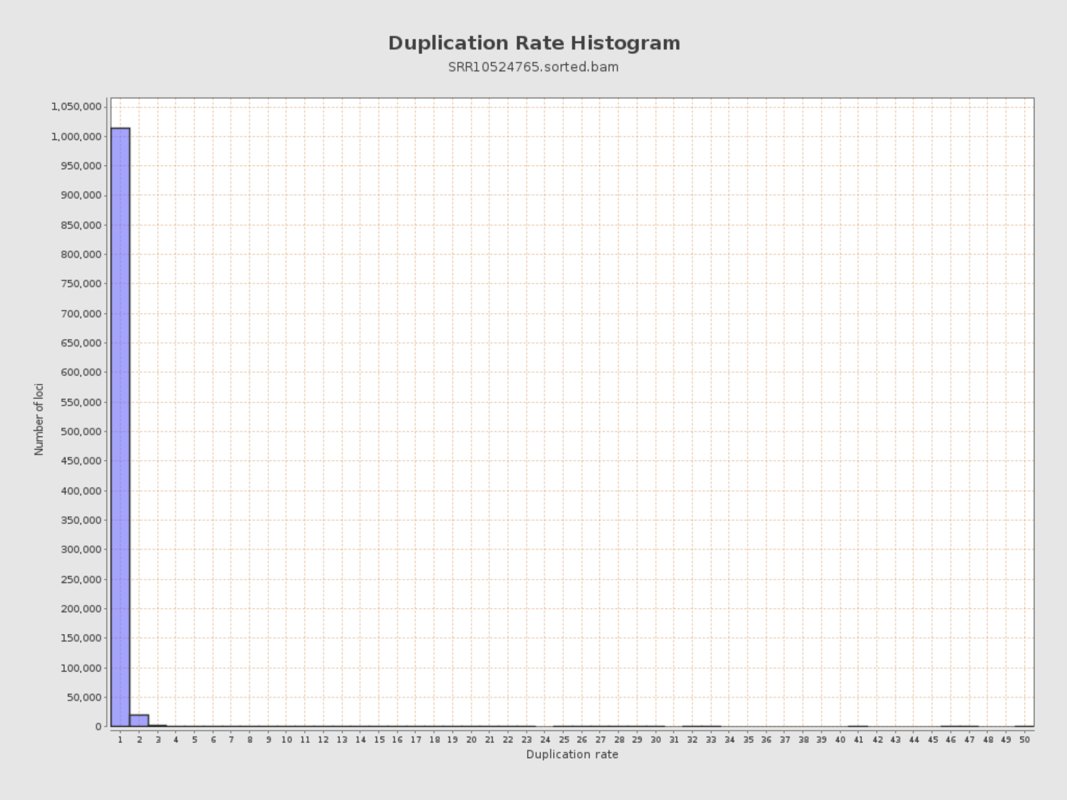
5. Results : Coverage Histogram (0-50X)



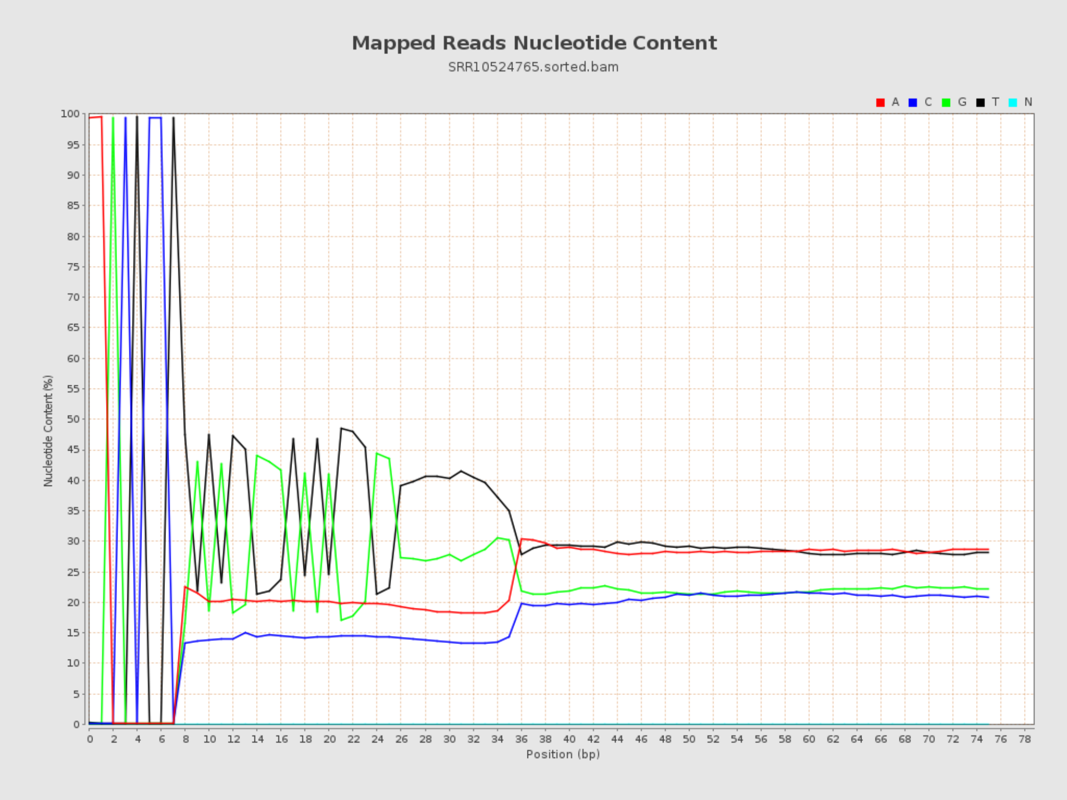
6. Results : Genome Fraction Coverage



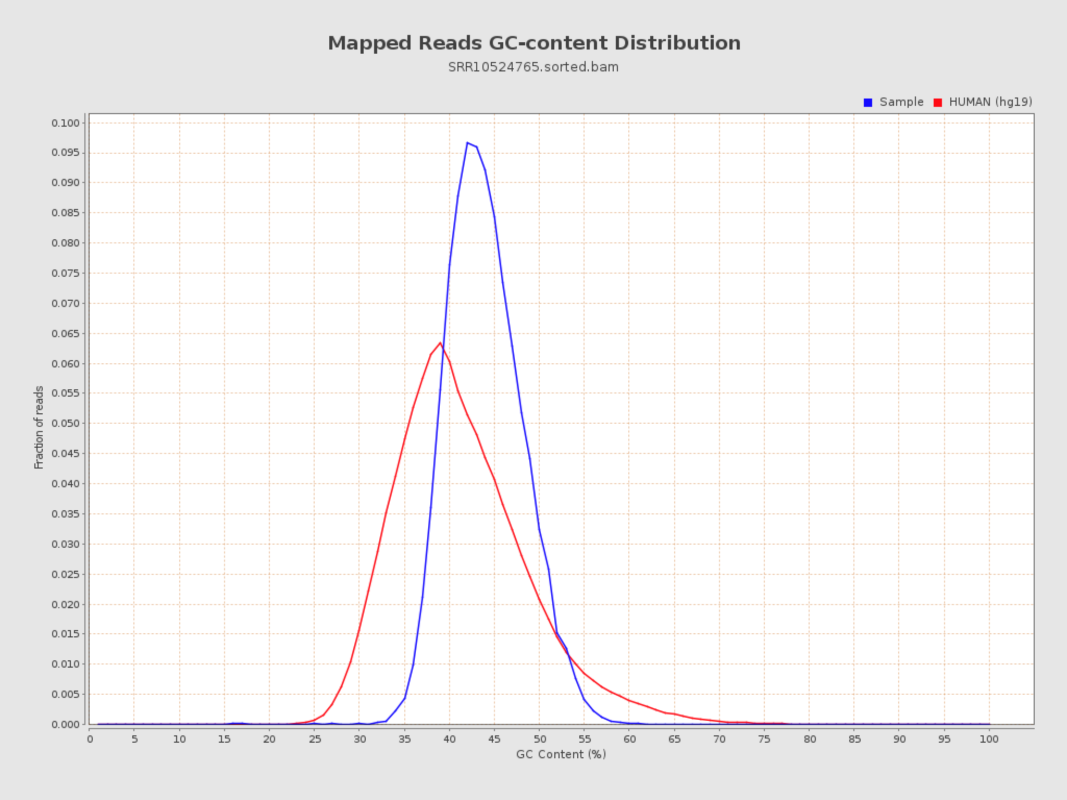
7. Results : Duplication Rate Histogram



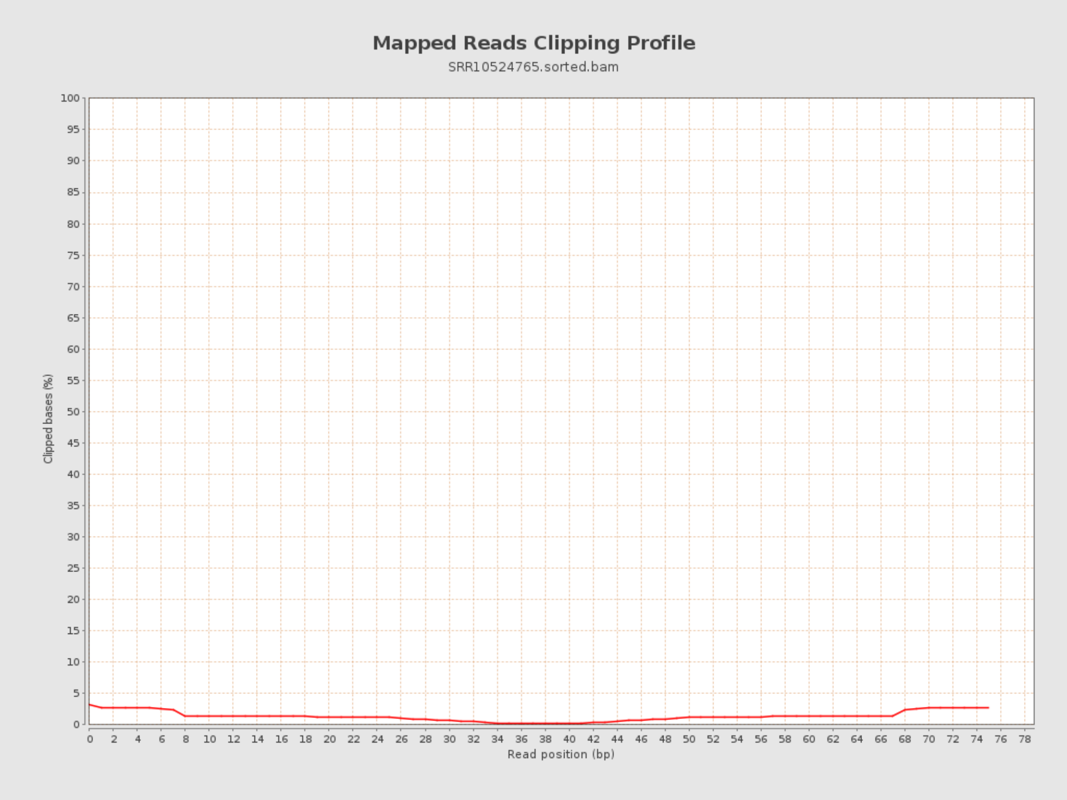
8. Results : Mapped Reads Nucleotide Content



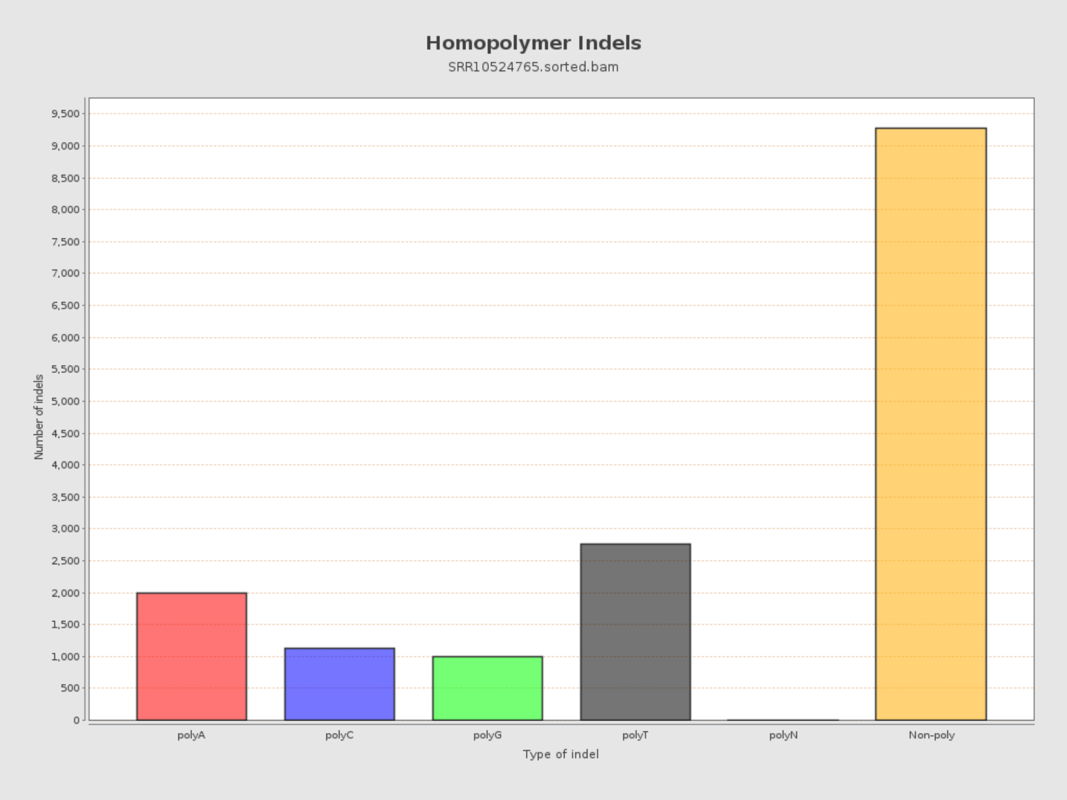
9. Results : Mapped Reads GC-content Distribution



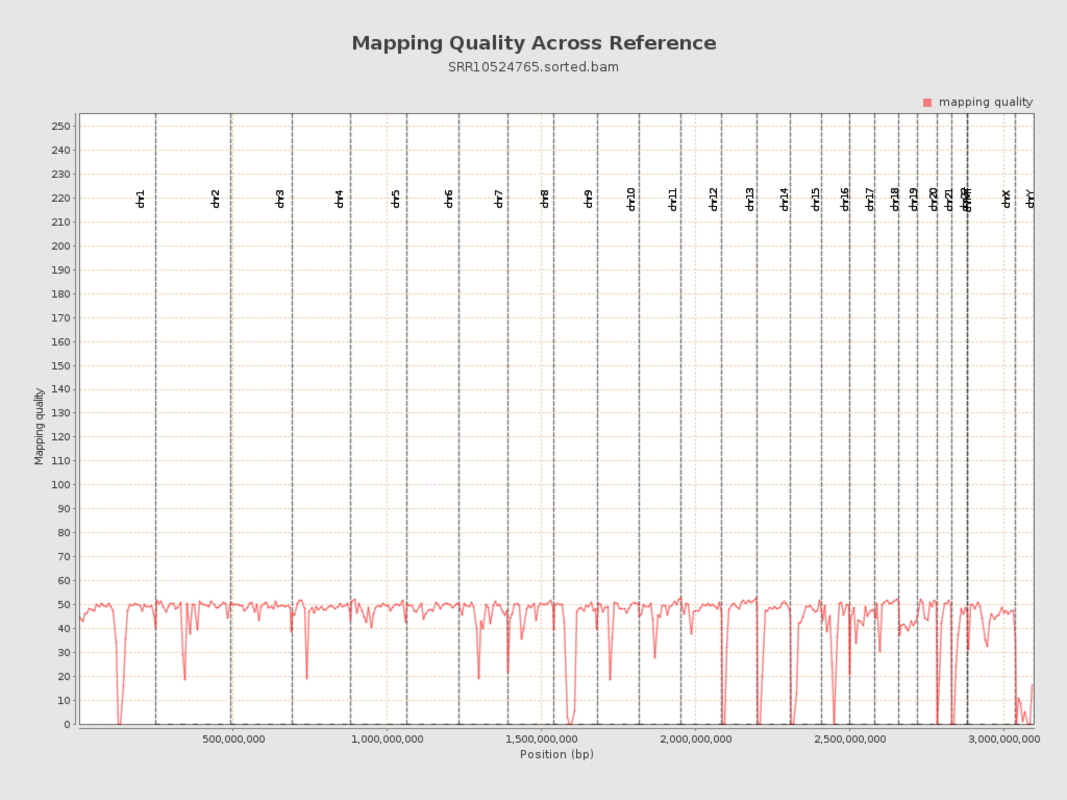
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram