Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:54:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524724.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_SRR10524724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:54:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	677,483
Mapped reads	623,248 / 91.99%
Unmapped reads	54,235 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,024 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,773 / 2.03%
Duplication rate	1.6%
Clipped reads	622,863 / 91.94%

2.2. ACGT Content

Number/percentage of A's	9,522,958 / 26.06%
Number/percentage of C's	6,760,539 / 18.5%
Number/percentage of T's	11,777,711 / 32.23%
Number/percentage of G's	8,475,352 / 23.19%
Number/percentage of N's	4,835 / 0.01%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.1419

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

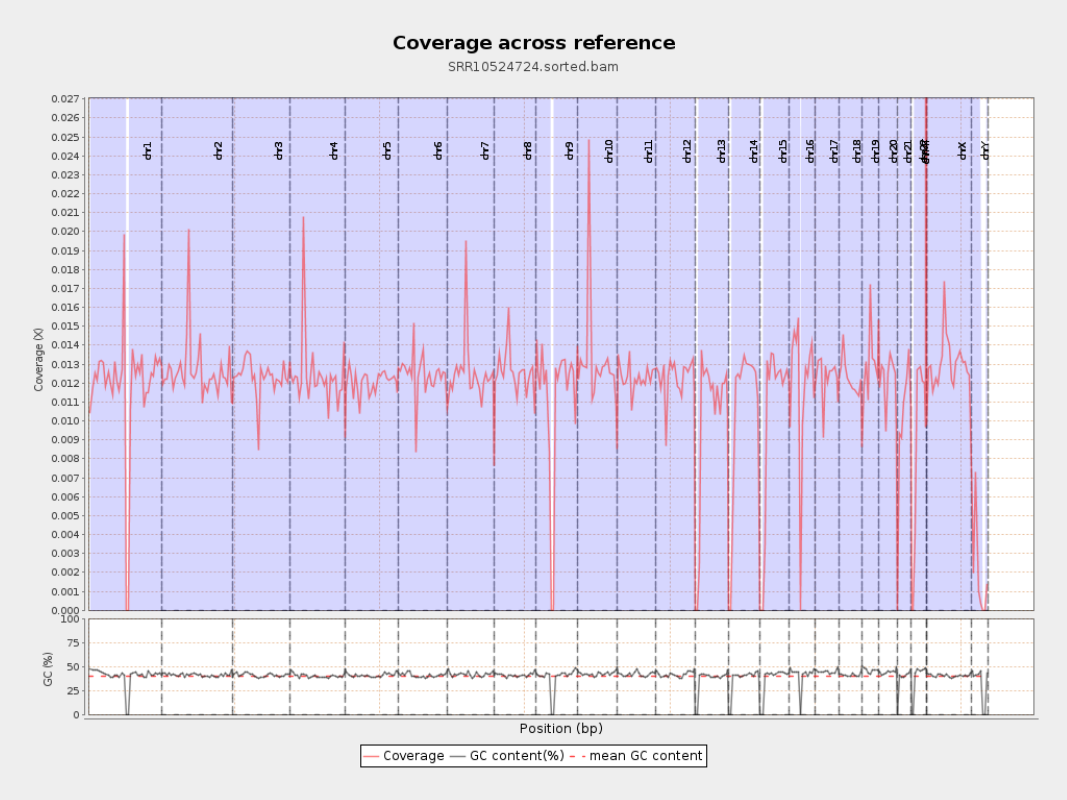
General error rate	0.52%
Mismatches	184,366
Insertions	3,257
Mapped reads with at least one insertion	0.52%
Deletions	7,087
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.85%

2.6. Chromosome stats

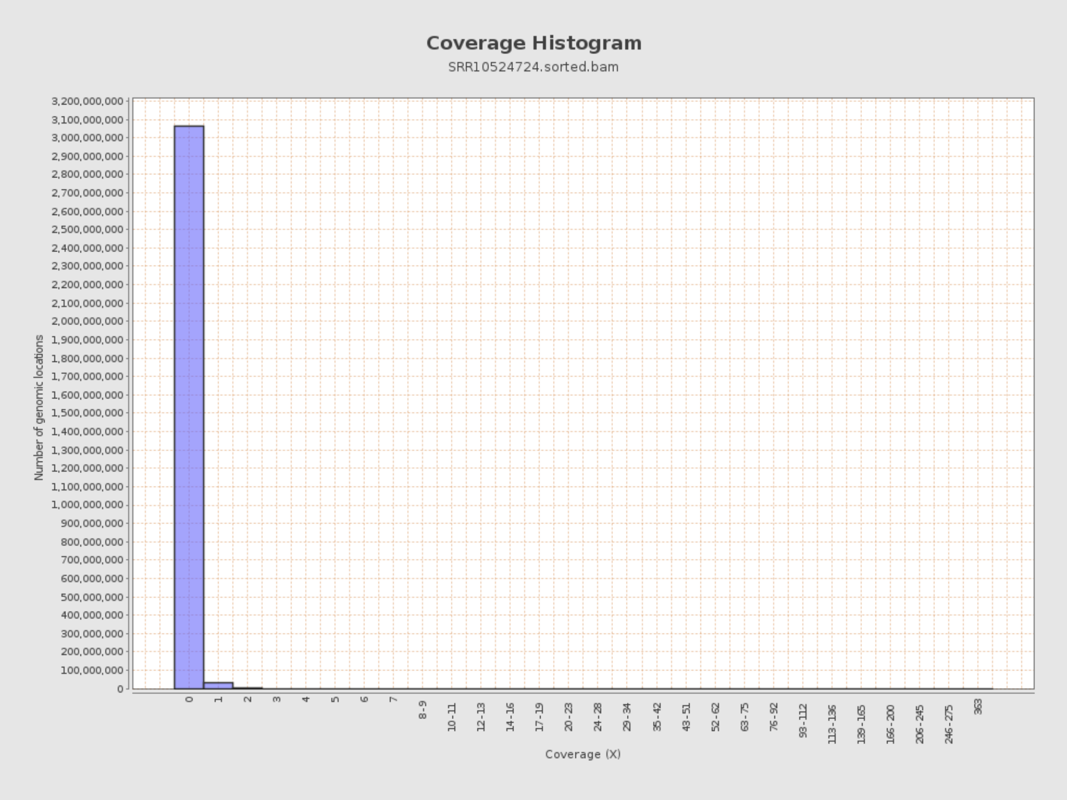
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2943725	0.0118	0.2093
chr2	243199373	3083530	0.0127	0.1914
chr3	198022430	2435135	0.0123	0.1156
chr4	191154276	2370840	0.0124	0.1229
chr5	180915260	2177808	0.012	0.1143
chr6	171115067	2128283	0.0124	0.1258
chr7	159138663	2004028	0.0126	0.1561

chr8	146364022	1840793	0.0126	0.1525
chr9	141213431	1538686	0.0109	0.1266
chr10	135534747	1789050	0.0132	0.1487
chr11	135006516	1653223	0.0122	0.1263
chr12	133851895	1646016	0.0123	0.1155
chr13	115169878	1152776	0.01	0.104
chr14	107349540	1120841	0.0104	0.1079
chr15	102531392	1045133	0.0102	0.105
chr16	90354753	1073904	0.0119	0.1173
chr17	81195210	995547	0.0123	0.1176
chr18	78077248	959885	0.0123	0.1904
chr19	59128983	768939	0.013	0.1805
chr20	63025520	767715	0.0122	0.1148
chr21	48129895	482637	0.01	0.1124
chr22	51304566	435083	0.0085	0.0956
chrMT	16571	10367	0.6256	0.8261
chrX	155270560	2009964	0.0129	0.1242
chrY	59373566	118898	0.002	0.0737

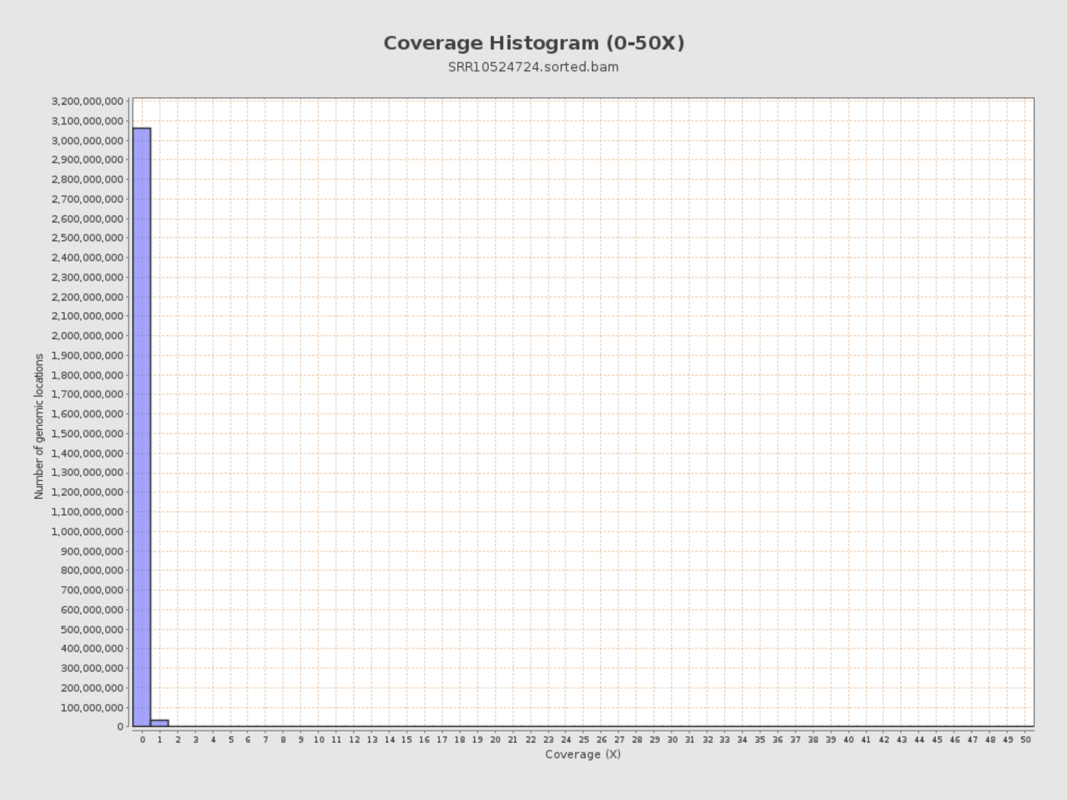
3. Results : Coverage across reference



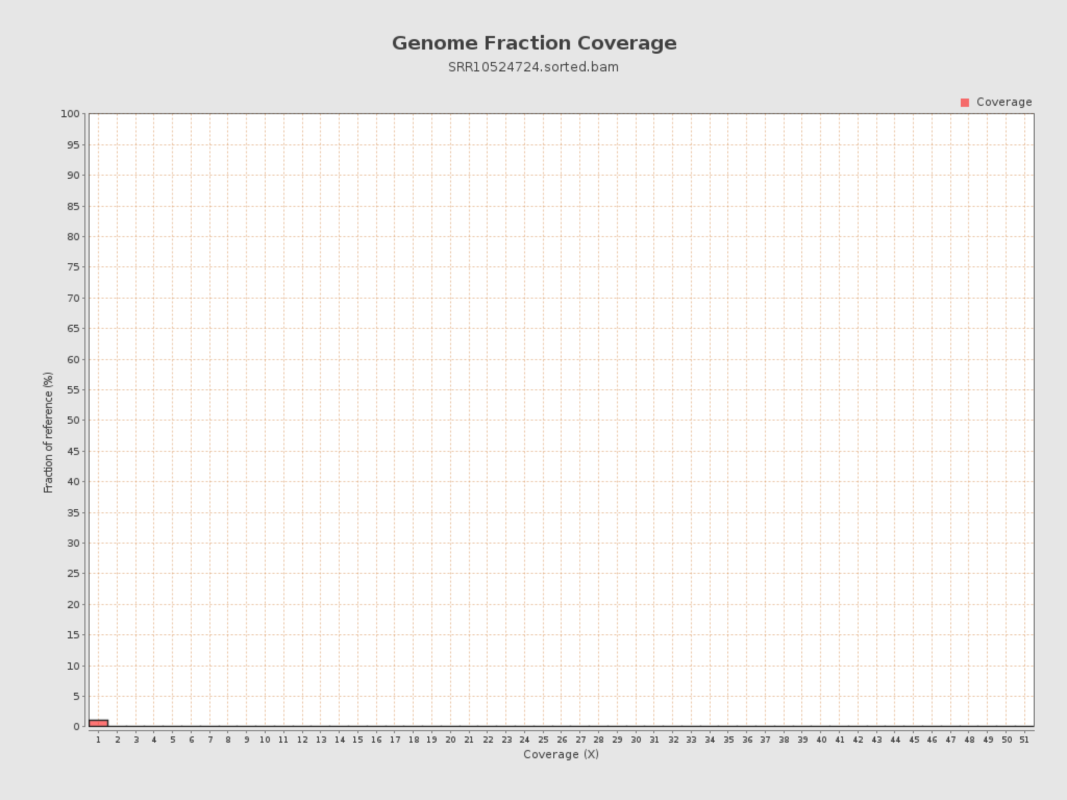
4. Results : Coverage Histogram



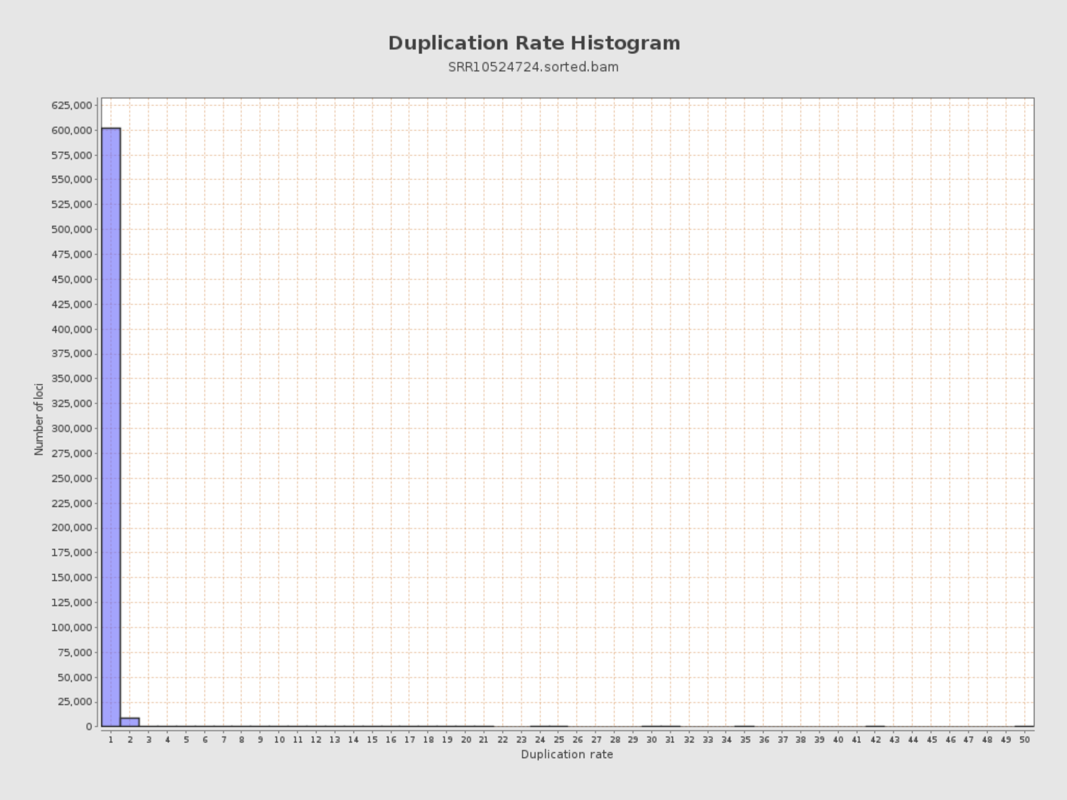
5. Results : Coverage Histogram (0-50X)



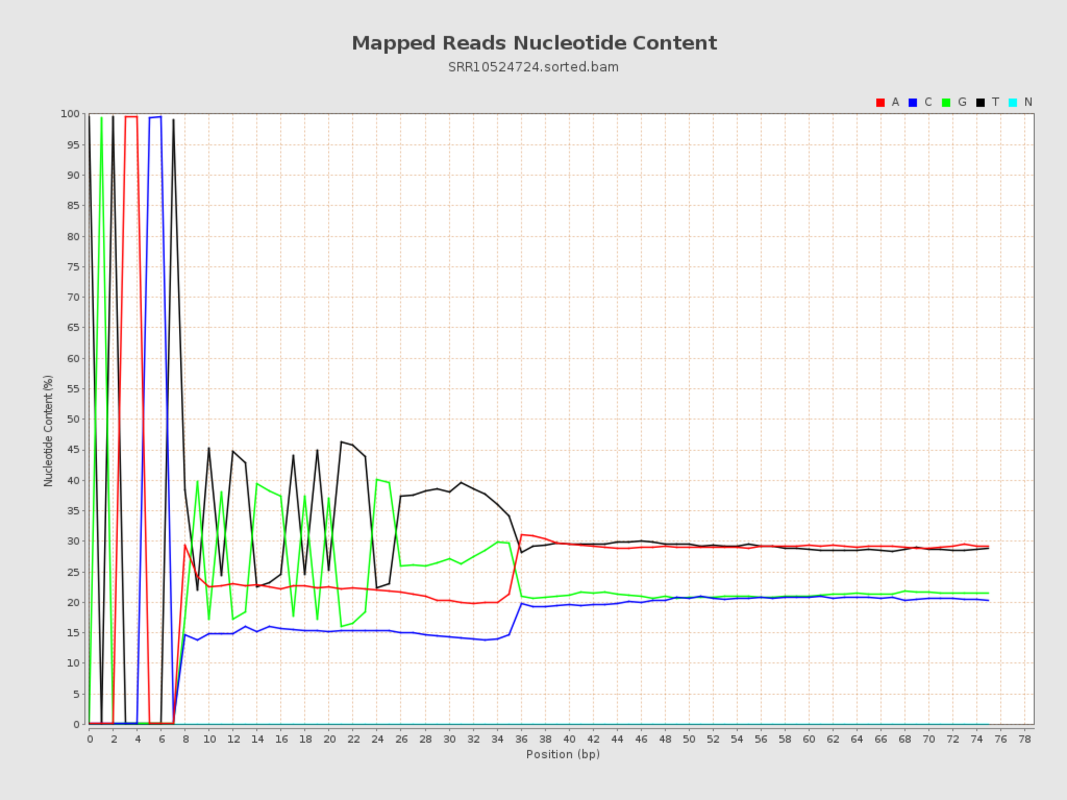
6. Results : Genome Fraction Coverage



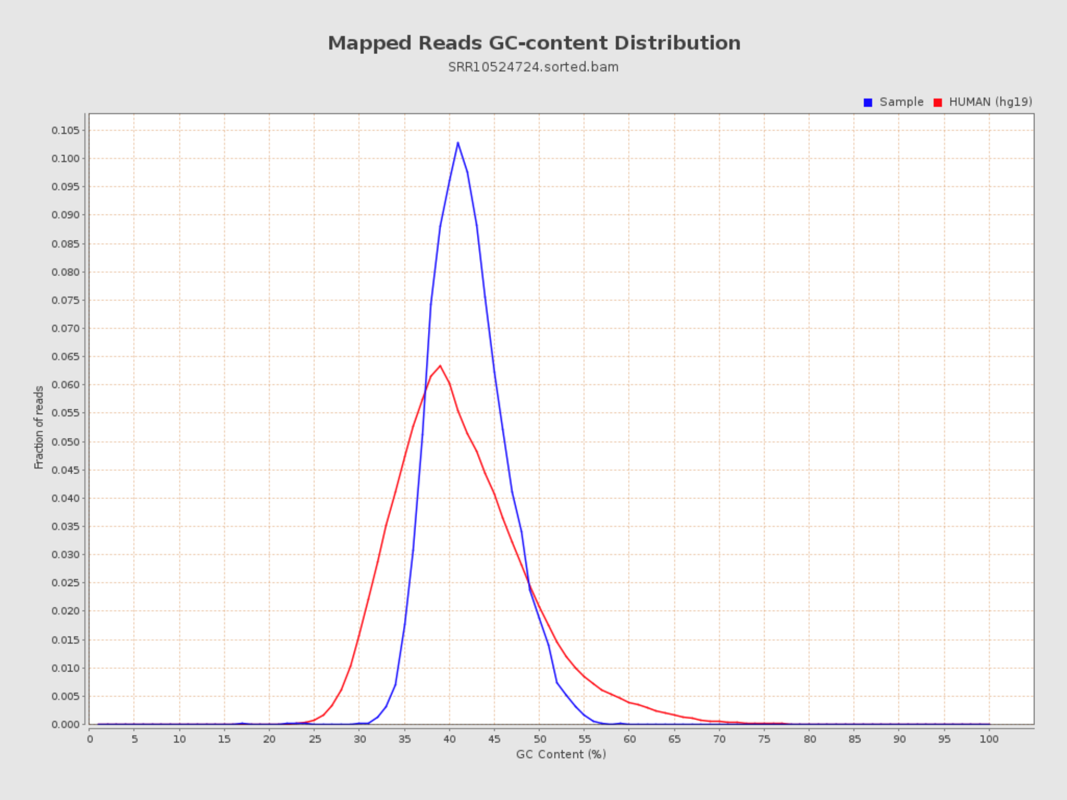
7. Results : Duplication Rate Histogram



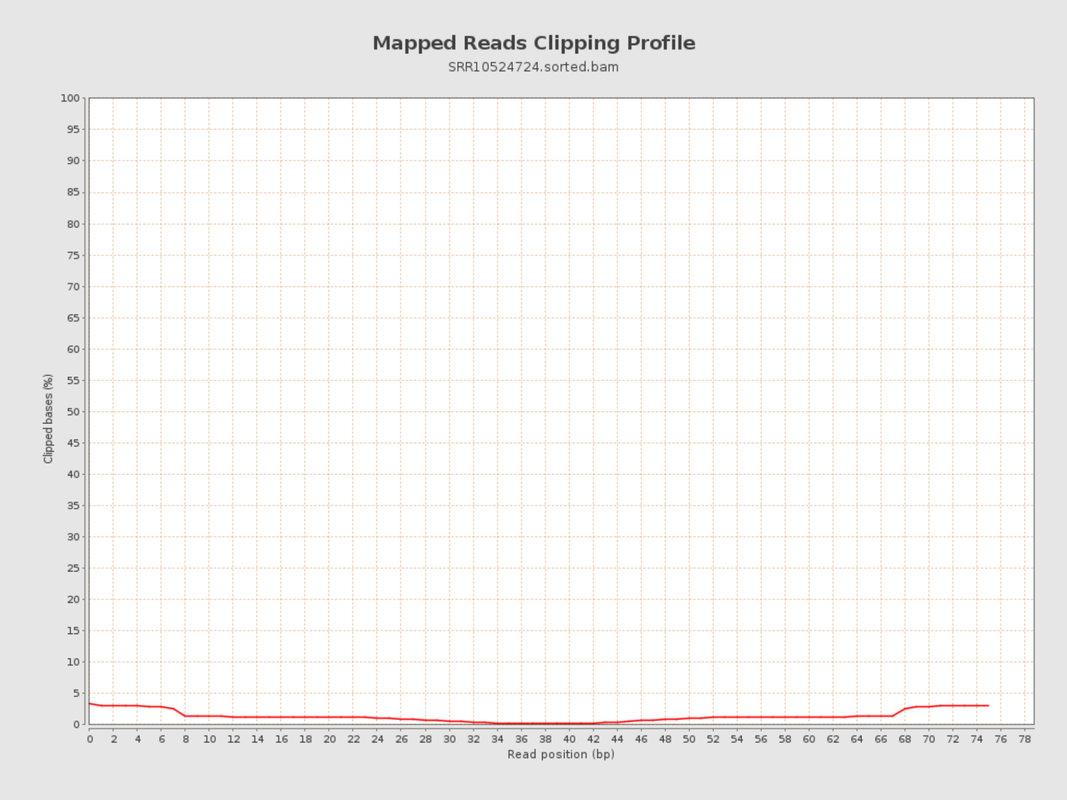
8. Results : Mapped Reads Nucleotide Content



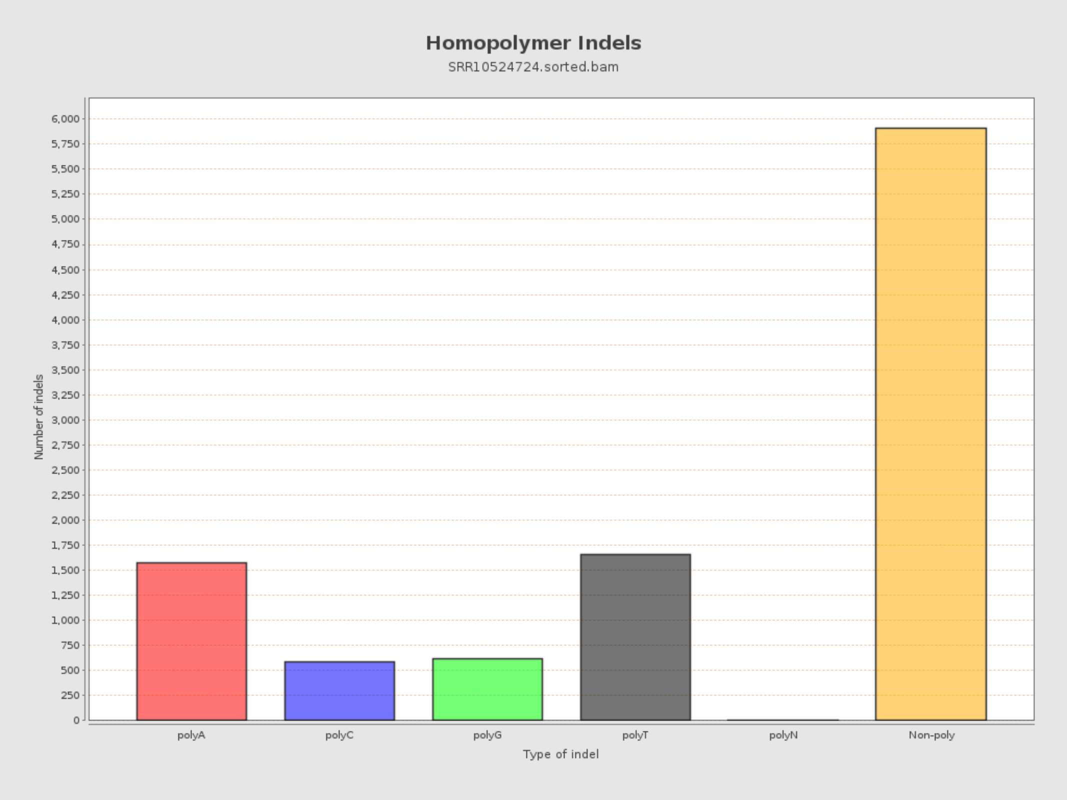
9. Results : Mapped Reads GC-content Distribution



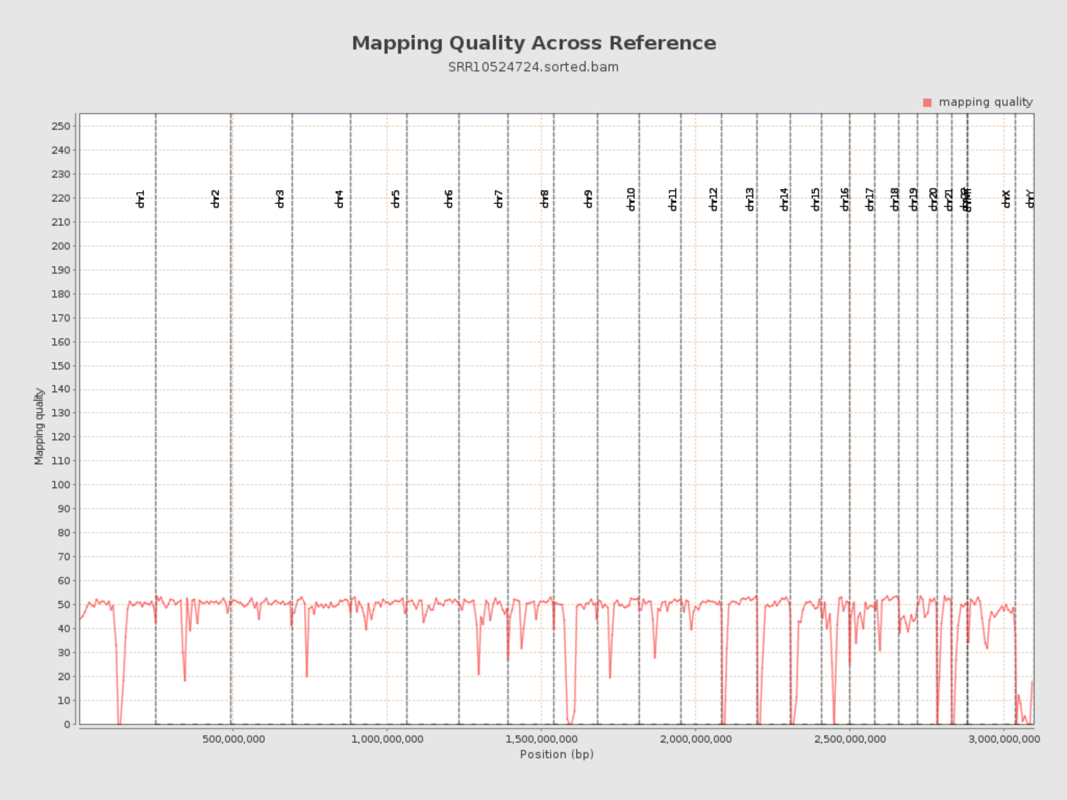
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram