Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:21:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524735.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_SRR10524735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:21:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	676,348
Mapped reads	583,105 / 86.21%
Unmapped reads	93,243 / 13.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,874 / 1.02%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	12,199 / 1.8%
Duplication rate	1.2%
Clipped reads	588,514 / 87.01%

2.2. ACGT Content

Number/percentage of A's	8,690,423 / 26.18%
Number/percentage of C's	6,052,493 / 18.23%
Number/percentage of T's	10,192,150 / 30.7%
Number/percentage of G's	8,261,260 / 24.88%
Number/percentage of N's	4,315 / 0.01%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1527

2.4. Mapping Quality

Mean Mapping Quality	39.89

2.5. Mismatches and indels

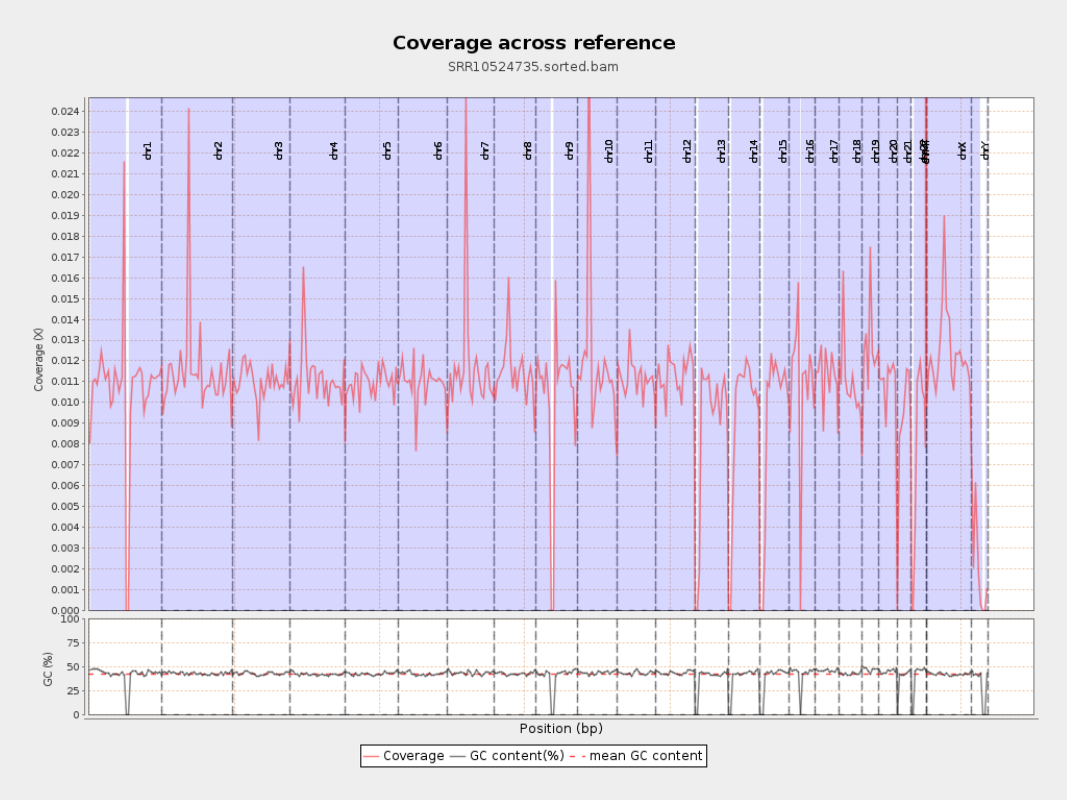
General error rate	0.51%
Mismatches	165,285
Insertions	2,657
Mapped reads with at least one insertion	0.45%
Deletions	5,390
Mapped reads with at least one deletion	0.92%
Homopolymer indels	39.44%

2.6. Chromosome stats

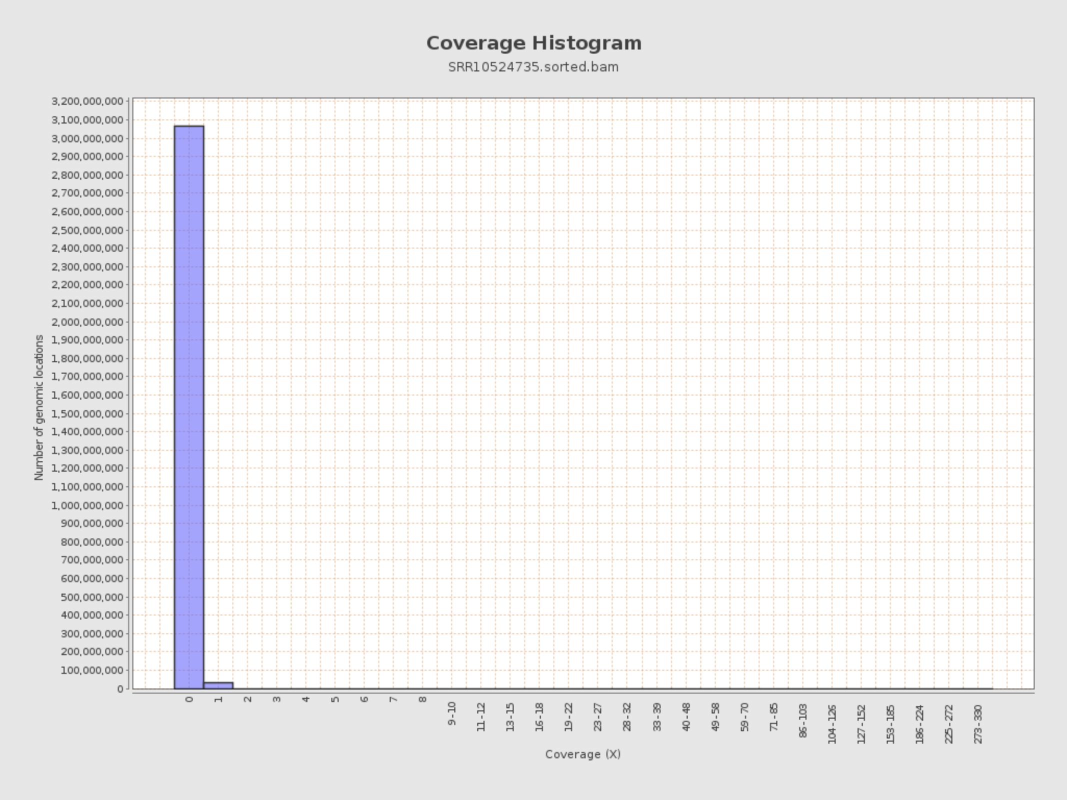
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2636940	0.0106	0.2709
chr2	243199373	2808848	0.0115	0.18
chr3	198022430	2179805	0.011	0.1102
chr4	191154276	2122046	0.0111	0.1126
chr5	180915260	1985098	0.011	0.1087
chr6	171115067	1874814	0.011	0.1117
chr7	159138663	1876053	0.0118	0.2039

chr8	146364022	1671941	0.0114	0.1415
chr9	141213431	1428374	0.0101	0.1385
chr10	135534747	1629913	0.012	0.1783
chr11	135006516	1497560	0.0111	0.1305
chr12	133851895	1516031	0.0113	0.1111
chr13	115169878	1009137	0.0088	0.0966
chr14	107349540	988269	0.0092	0.1024
chr15	102531392	927772	0.009	0.0994
chr16	90354753	977756	0.0108	0.1189
chr17	81195210	910933	0.0112	0.1135
chr18	78077248	866700	0.0111	0.2192
chr19	59128983	747097	0.0126	0.2123
chr20	63025520	683566	0.0108	0.1089
chr21	48129895	428849	0.0089	0.1027
chr22	51304566	384811	0.0075	0.0893
chrMT	16571	16041	0.968	1.1566
chrX	155270560	1925735	0.0124	0.1275
chrY	59373566	115253	0.0019	0.0586

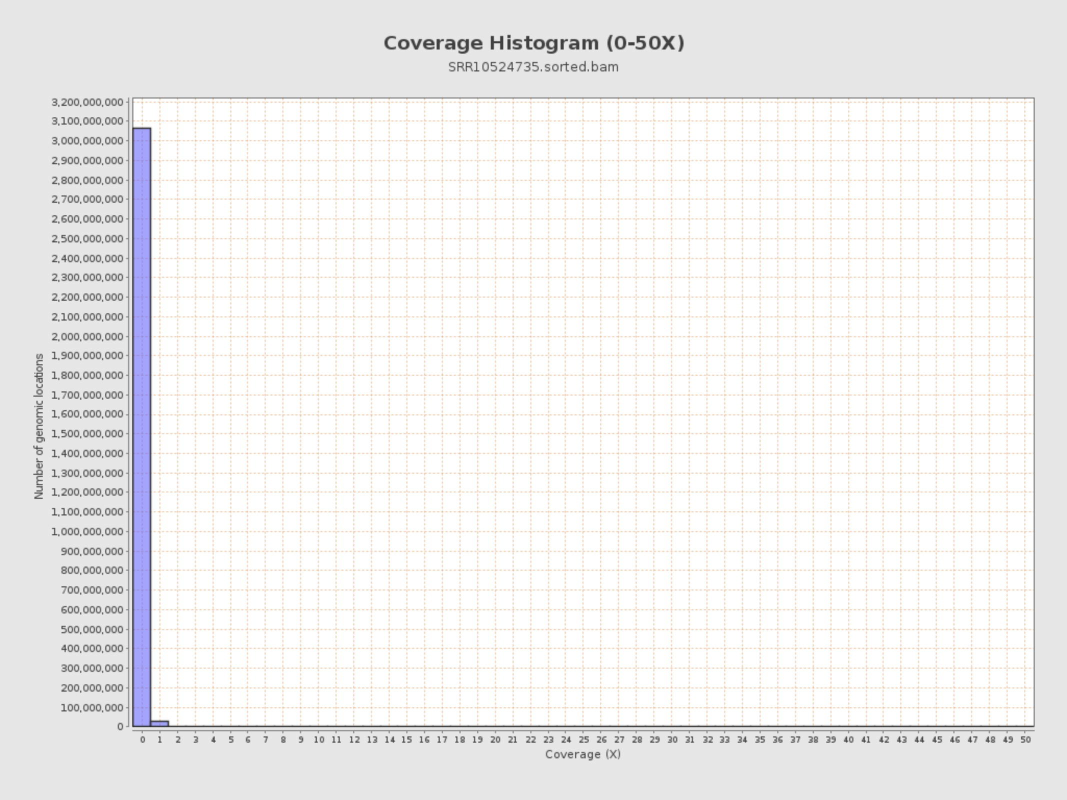
3. Results : Coverage across reference



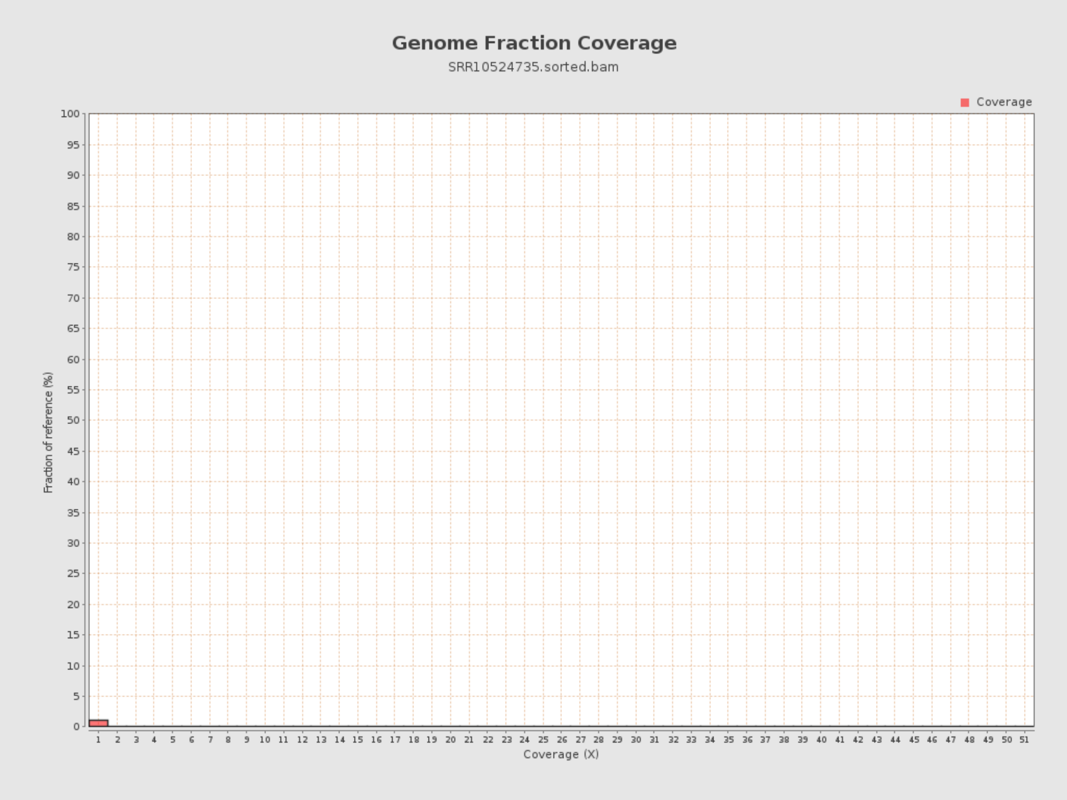
4. Results : Coverage Histogram



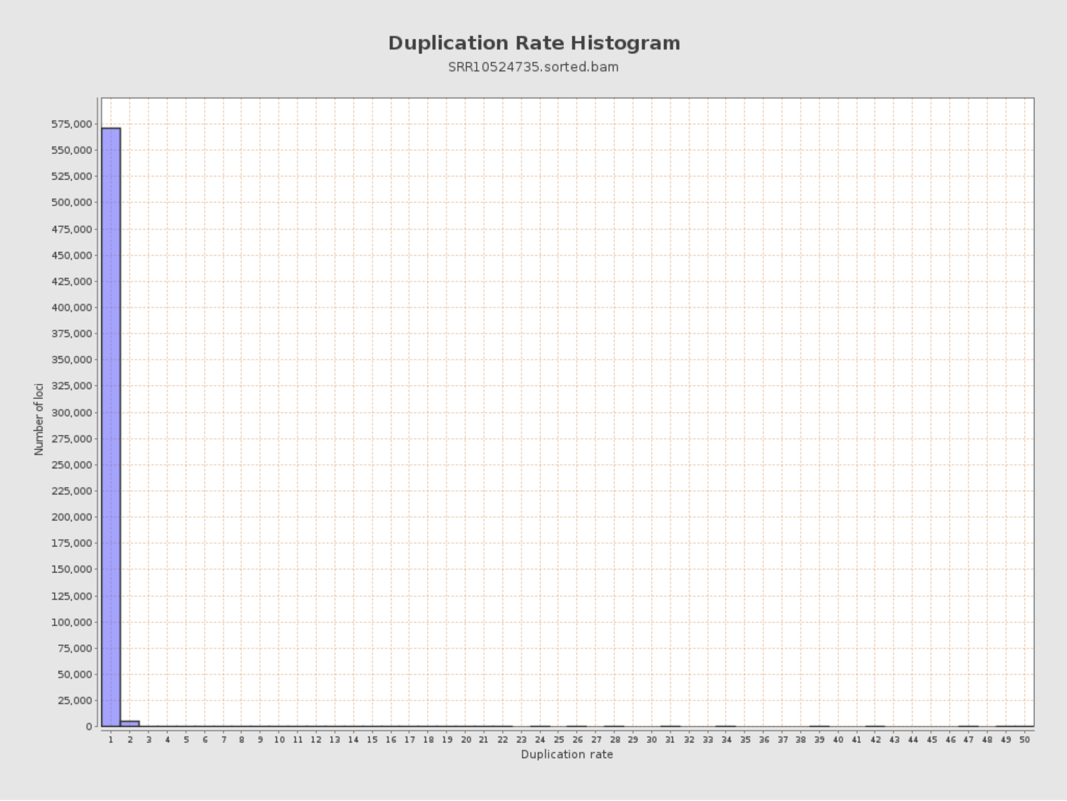
5. Results : Coverage Histogram (0-50X)



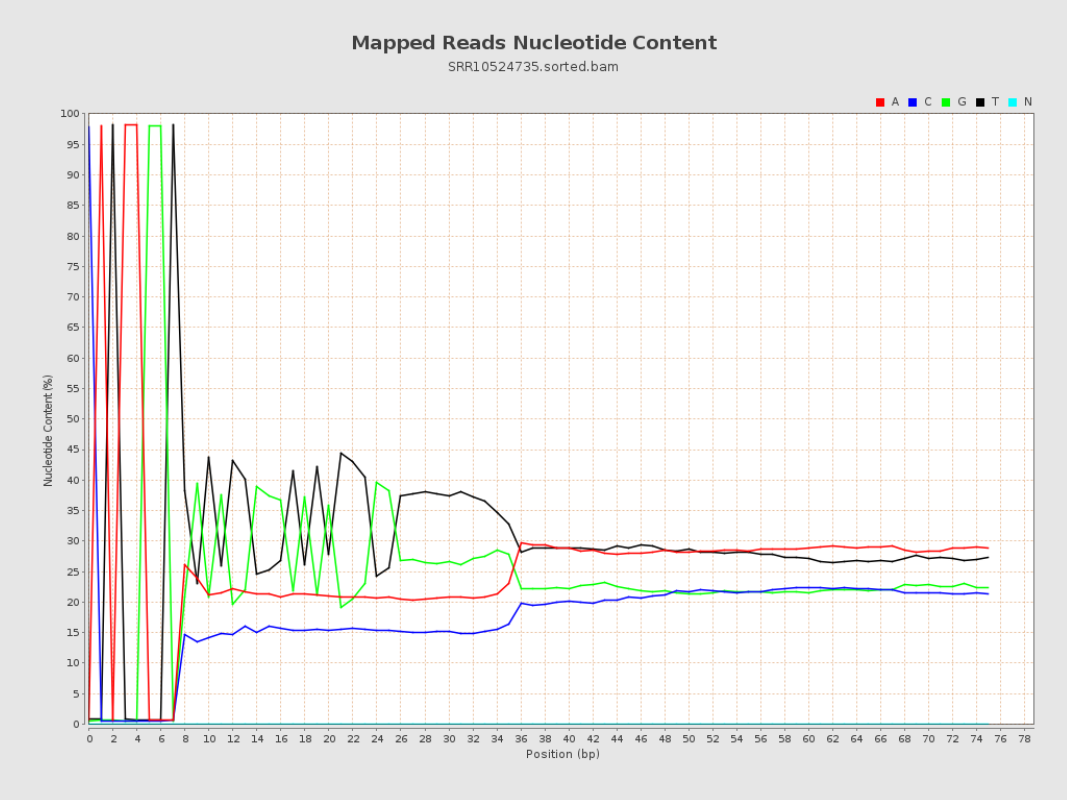
6. Results : Genome Fraction Coverage



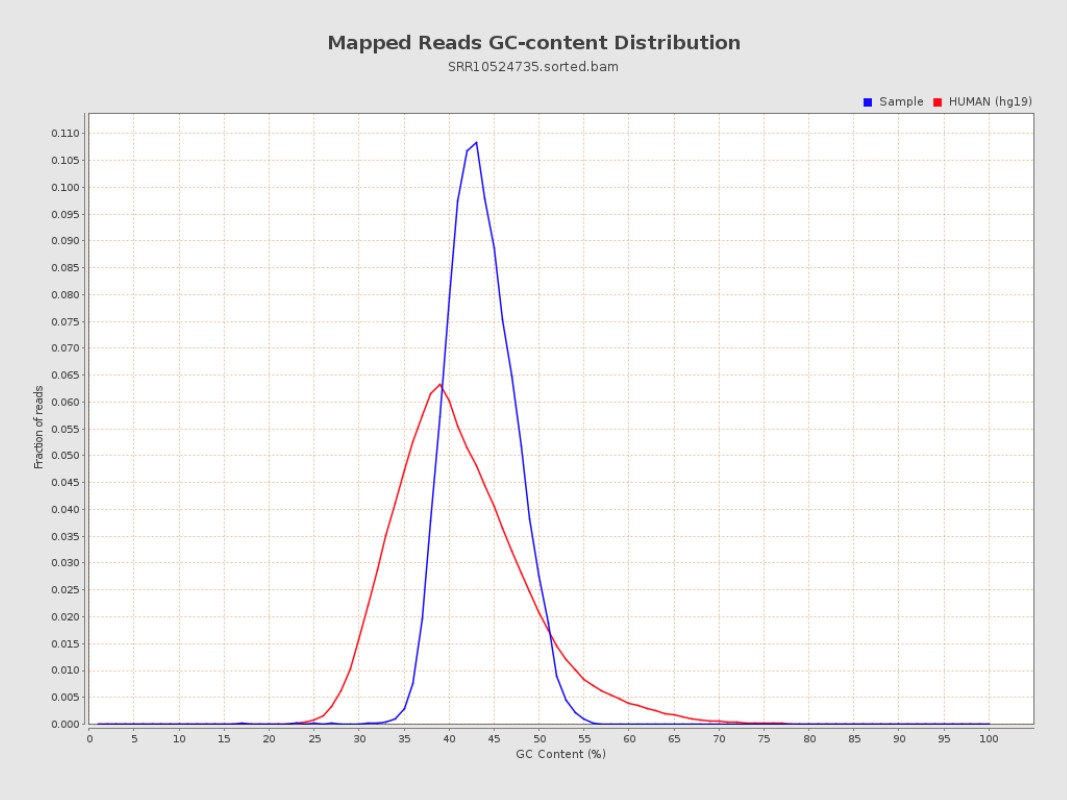
7. Results : Duplication Rate Histogram



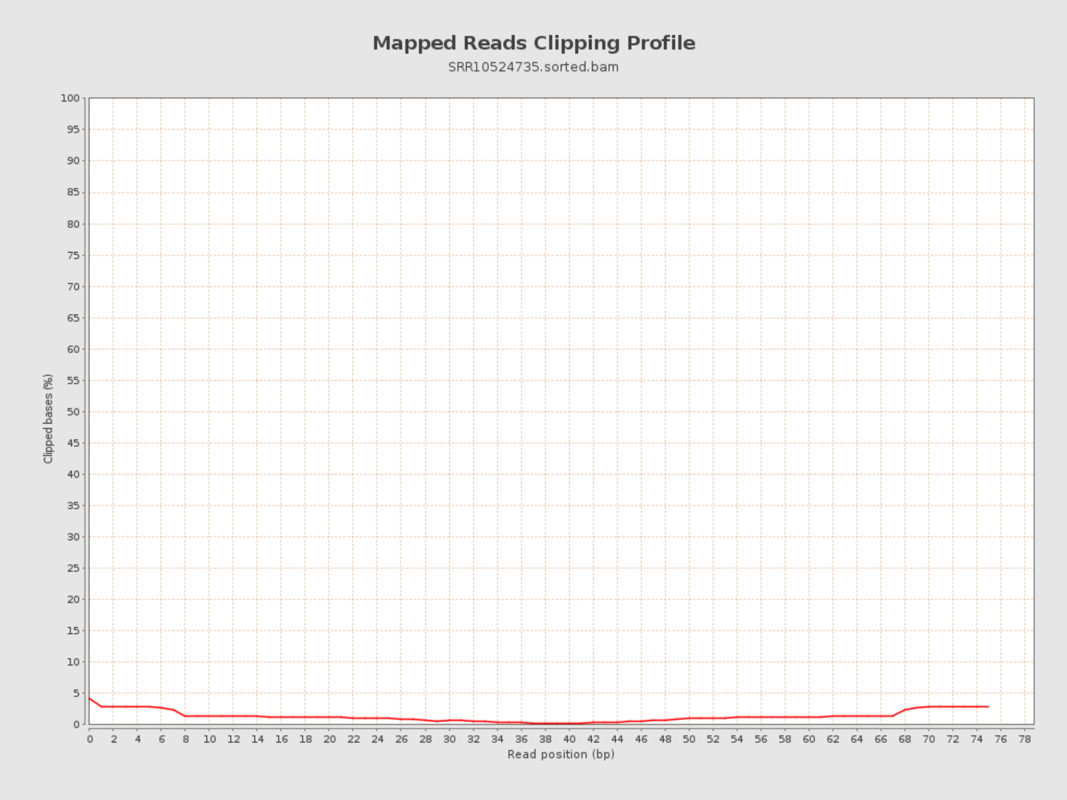
8. Results : Mapped Reads Nucleotide Content



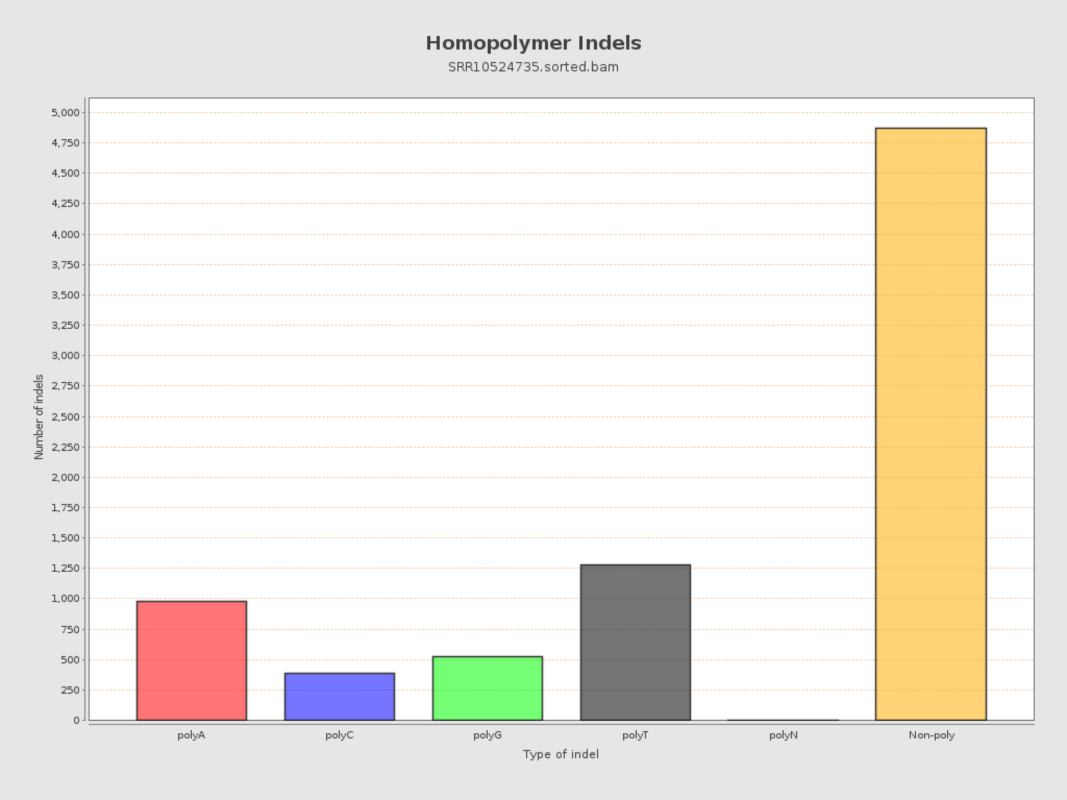
9. Results : Mapped Reads GC-content Distribution



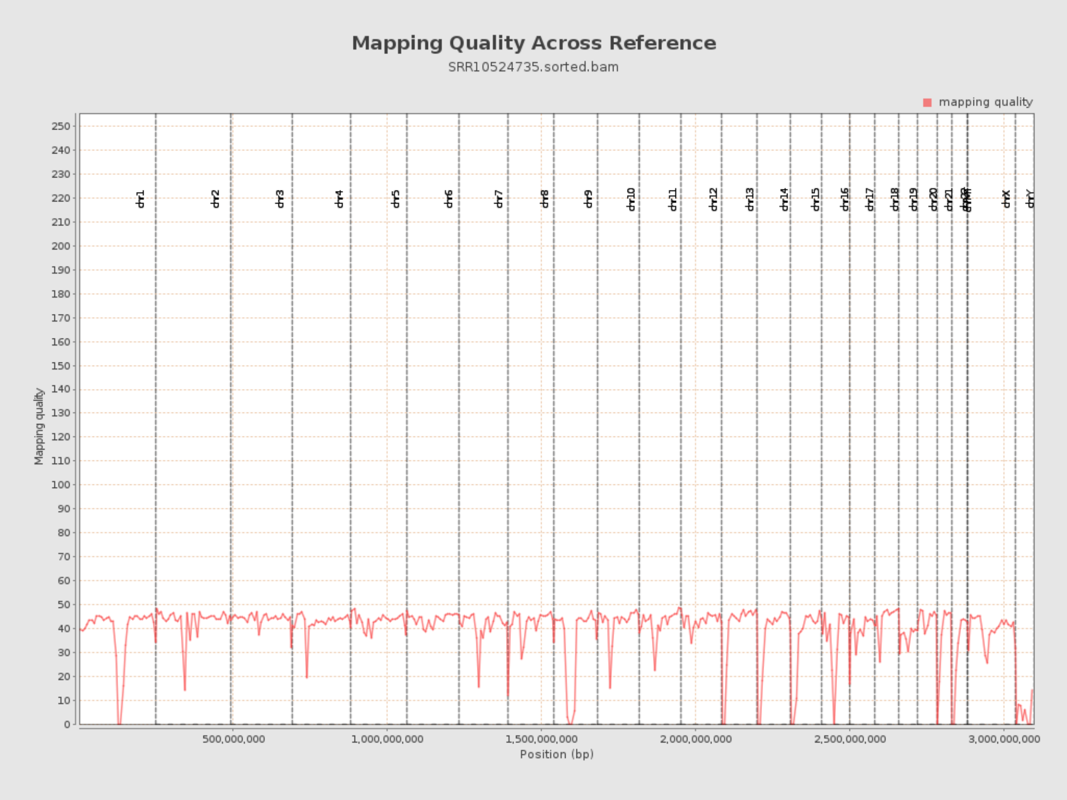
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram