Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:46:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524647.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_SRR10524647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524647.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:46:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,210,932
Mapped reads	1,122,955 / 92.73%
Unmapped reads	87,977 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,868 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	47,825 / 3.95%
Duplication rate	3.34%
Clipped reads	1,125,565 / 92.95%

2.2. ACGT Content

Number/percentage of A's	16,019,102 / 24.47%
Number/percentage of C's	12,883,386 / 19.68%
Number/percentage of T's	20,472,440 / 31.27%
Number/percentage of G's	16,096,553 / 24.59%
Number/percentage of N's	526 / 0%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.213

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

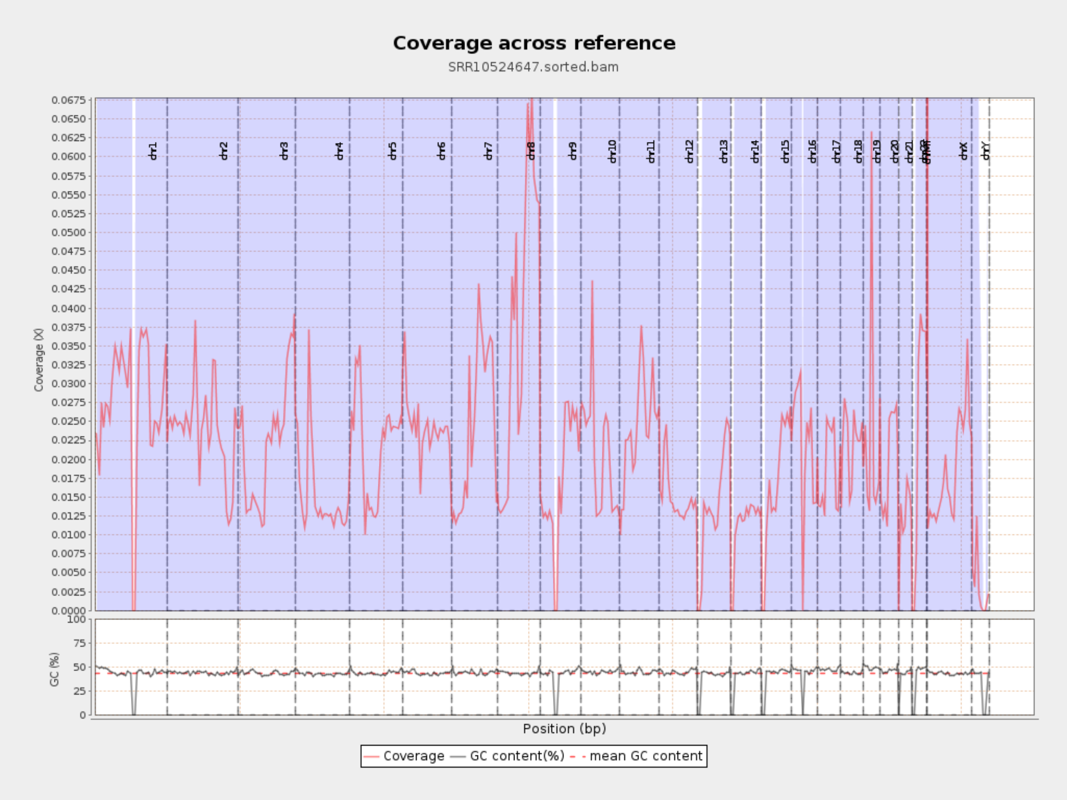
General error rate	0.51%
Mismatches	328,469
Insertions	4,083
Mapped reads with at least one insertion	0.36%
Deletions	12,927
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.28%

2.6. Chromosome stats

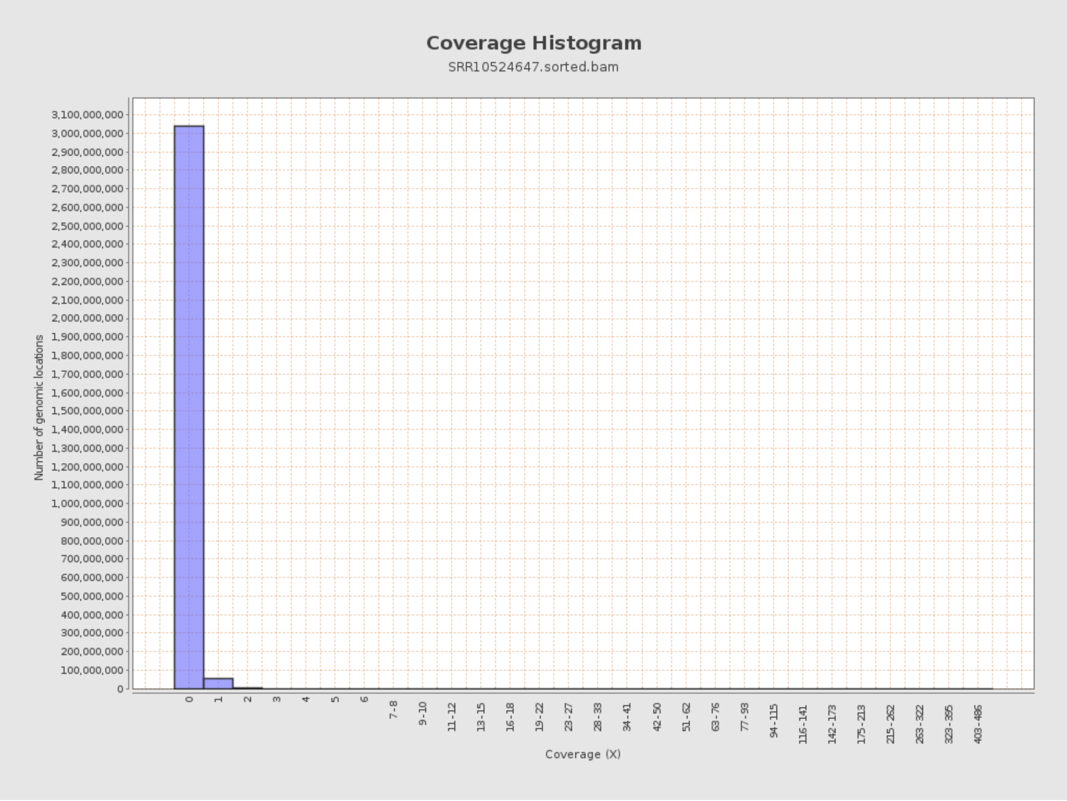
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6850273	0.0275	0.3816
chr2	243199373	5789359	0.0238	0.251
chr3	198022430	4343533	0.0219	0.1607
chr4	191154276	2961933	0.0155	0.1595
chr5	180915260	3991700	0.0221	0.1617
chr6	171115067	4165667	0.0243	0.177
chr7	159138663	3925153	0.0247	0.2459

chr8	146364022	5693428	0.0389	0.2815
chr9	141213431	2395759	0.017	0.1696
chr10	135534747	2871675	0.0212	0.2226
chr11	135006516	3297937	0.0244	0.196
chr12	133851895	2016757	0.0151	0.139
chr13	115169878	1585749	0.0138	0.1294
chr14	107349540	1189451	0.0111	0.1169
chr15	102531392	1678955	0.0164	0.14
chr16	90354753	1959221	0.0217	0.1679
chr17	81195210	1488119	0.0183	0.1525
chr18	78077248	1716272	0.022	0.273
chr19	59128983	1370592	0.0232	0.2712
chr20	63025520	1255208	0.0199	0.1575
chr21	48129895	593206	0.0123	0.1412
chr22	51304566	1256396	0.0245	0.1714
chrMT	16571	11792	0.7116	0.9751
chrX	155270560	2898376	0.0187	0.1588
chrY	59373566	187376	0.0032	0.1236

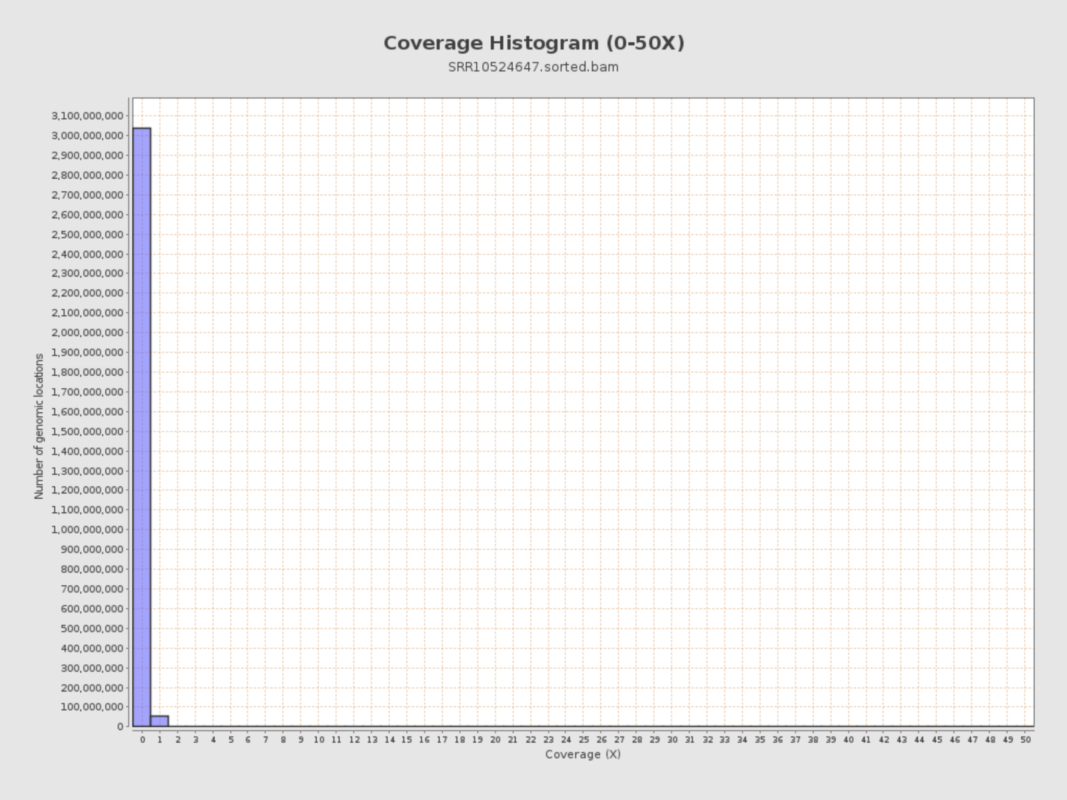
3. Results : Coverage across reference



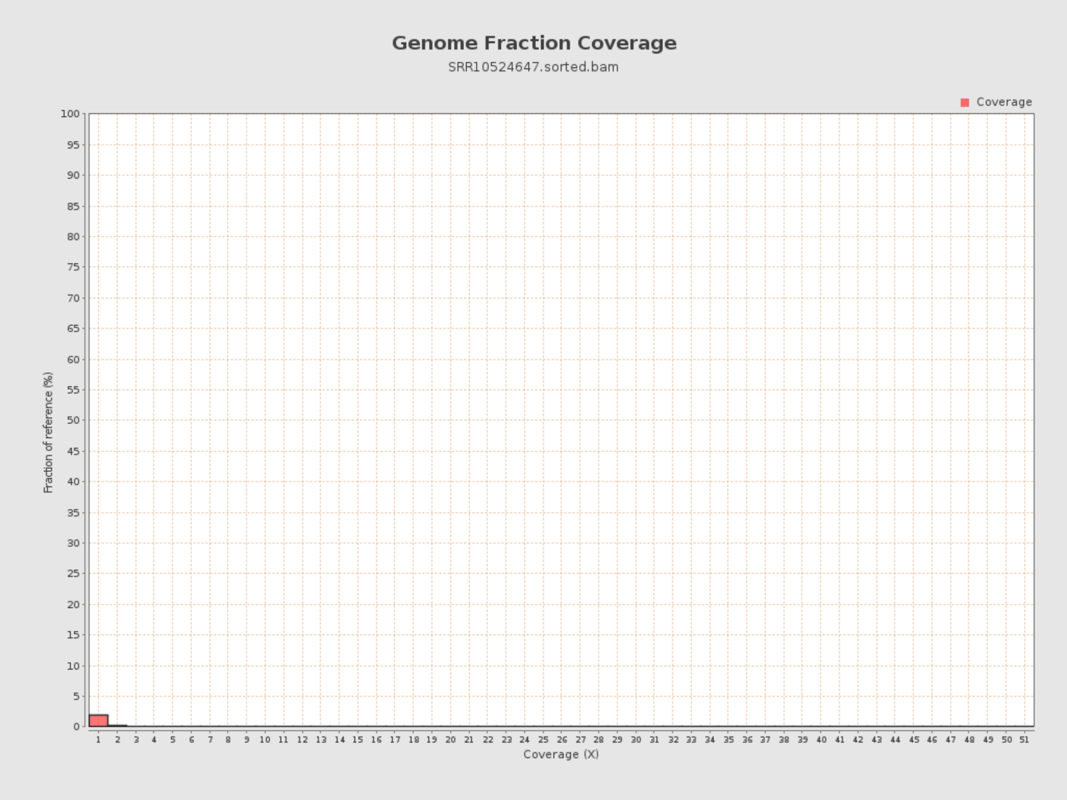
4. Results : Coverage Histogram



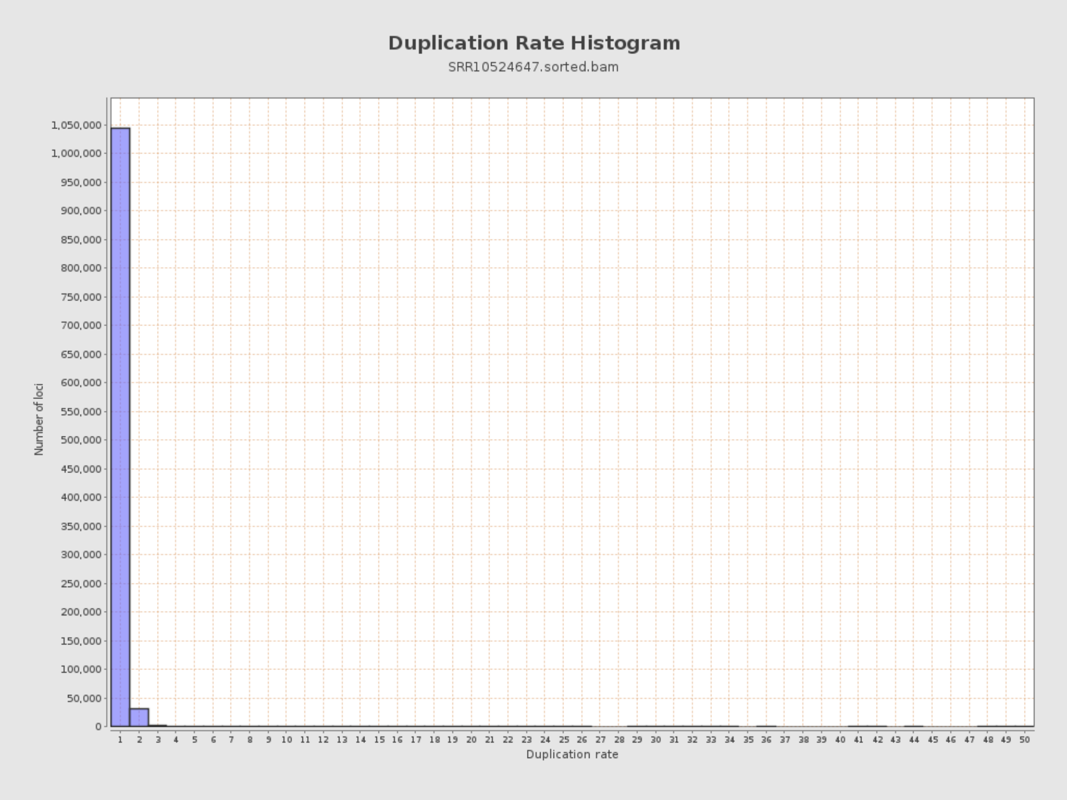
5. Results : Coverage Histogram (0-50X)



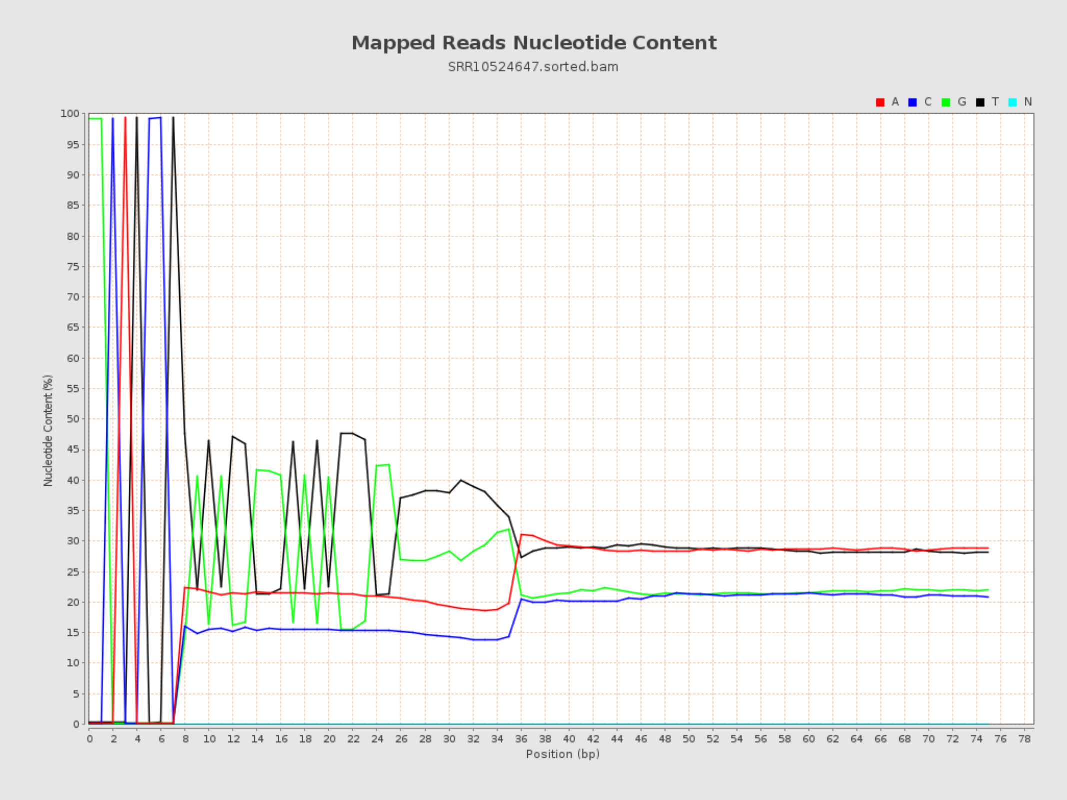
6. Results : Genome Fraction Coverage



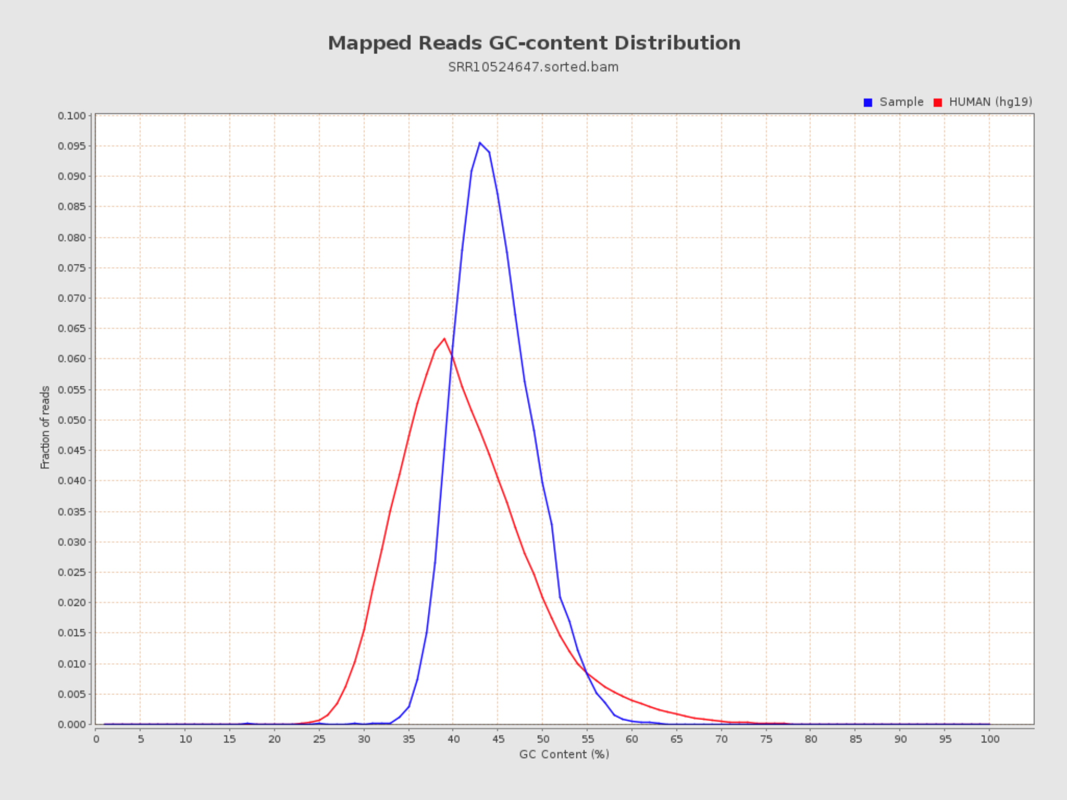
7. Results : Duplication Rate Histogram



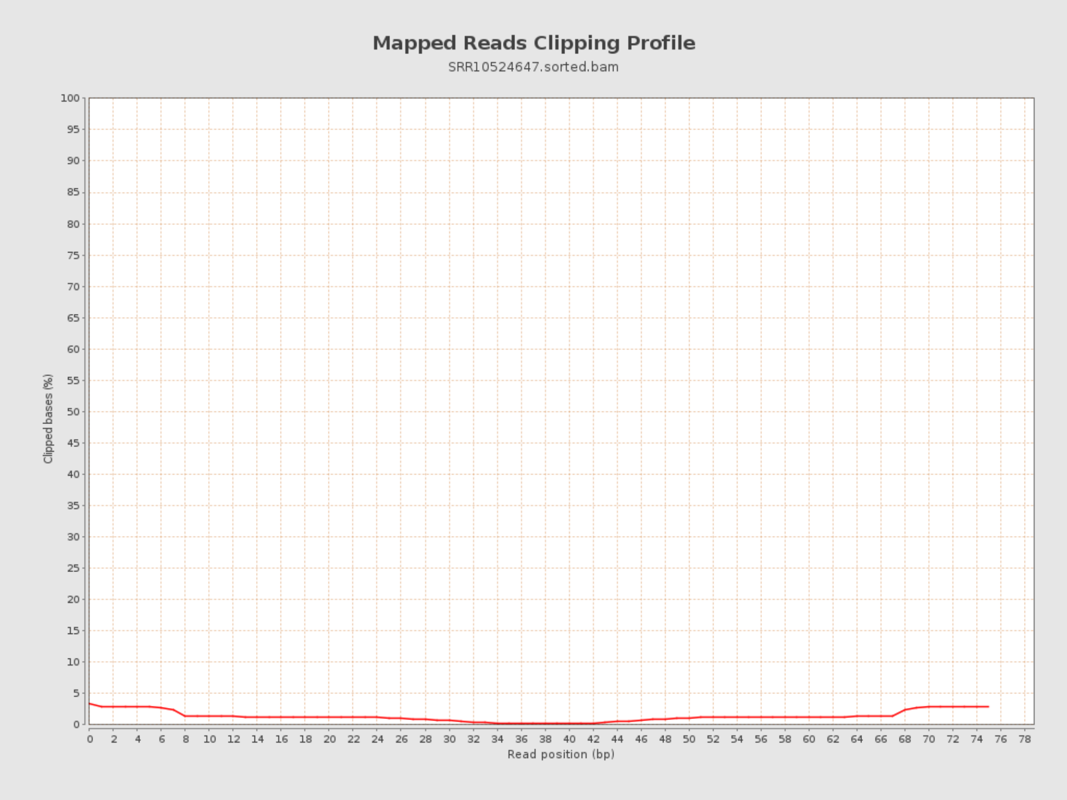
8. Results : Mapped Reads Nucleotide Content



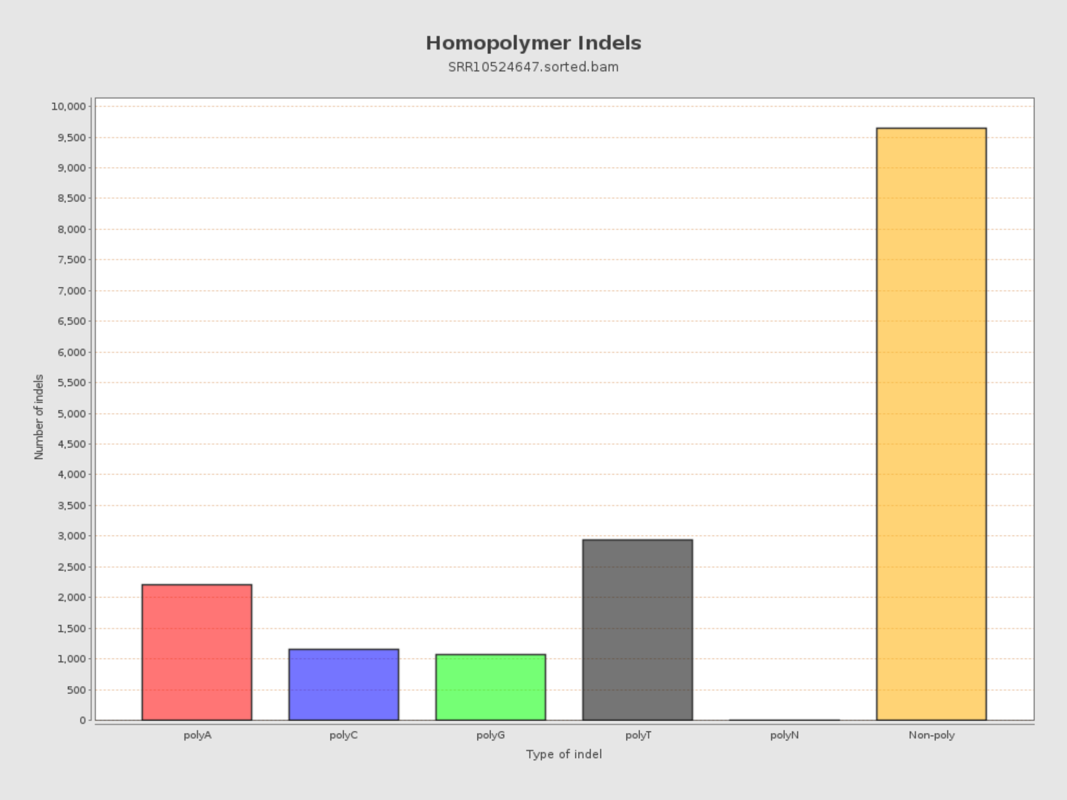
9. Results : Mapped Reads GC-content Distribution



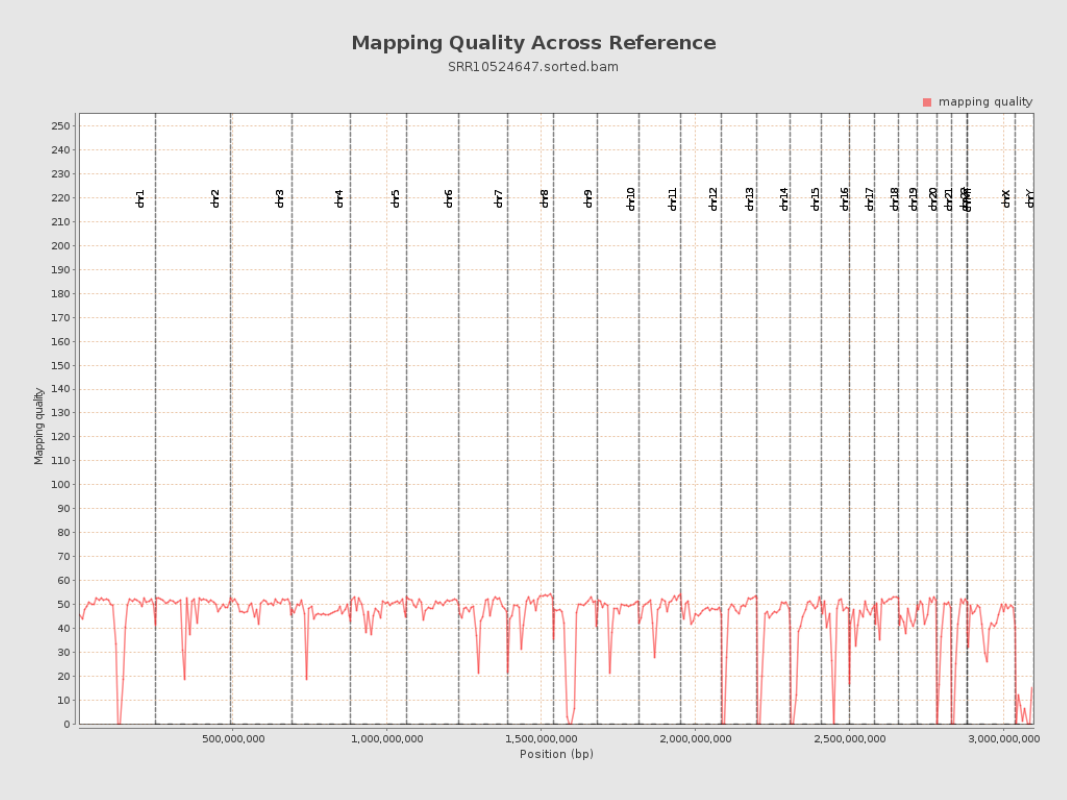
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram