Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:07:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524774.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_SRR10524774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524774.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:07:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,429,042
Mapped reads	1,314,900 / 92.01%
Unmapped reads	114,142 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,169 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	46,758 / 3.27%
Duplication rate	2.7%
Clipped reads	1,319,247 / 92.32%

2.2. ACGT Content

Number/percentage of A's	17,777,226 / 23.39%
Number/percentage of C's	14,261,092 / 18.76%
Number/percentage of T's	24,389,065 / 32.09%
Number/percentage of G's	19,564,171 / 25.74%
Number/percentage of N's	9,294 / 0.01%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2238

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

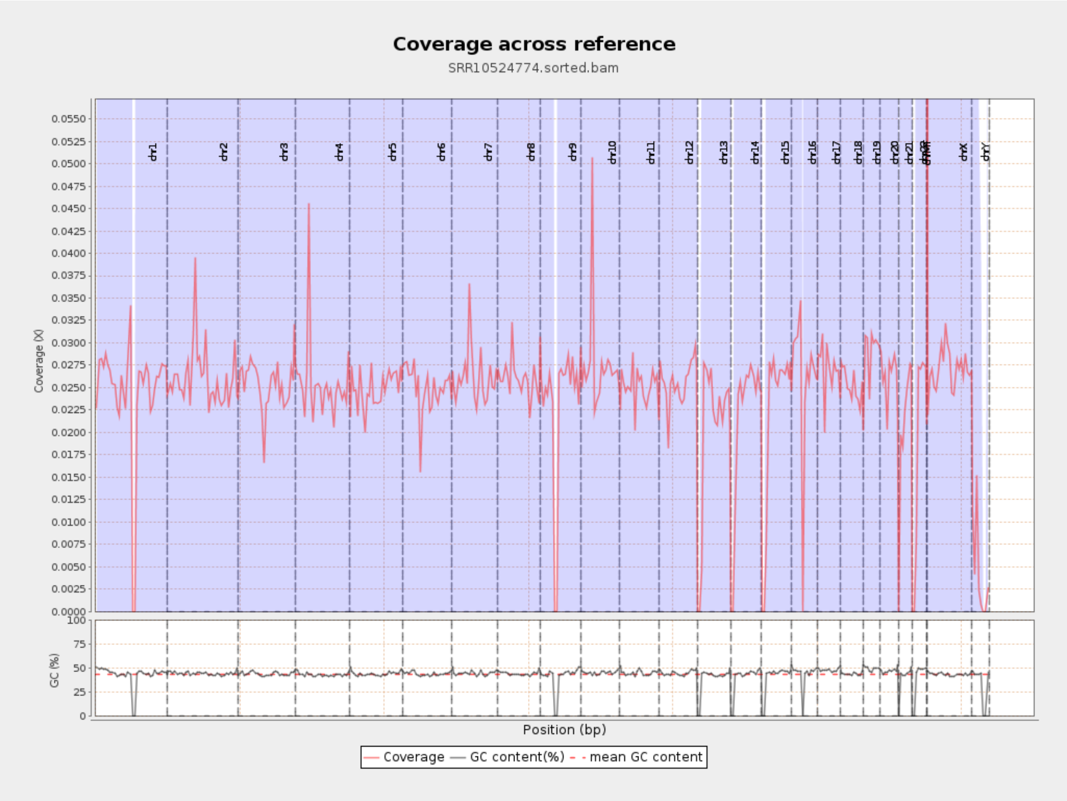
General error rate	0.51%
Mismatches	379,230
Insertions	4,530
Mapped reads with at least one insertion	0.34%
Deletions	14,702
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.13%

2.6. Chromosome stats

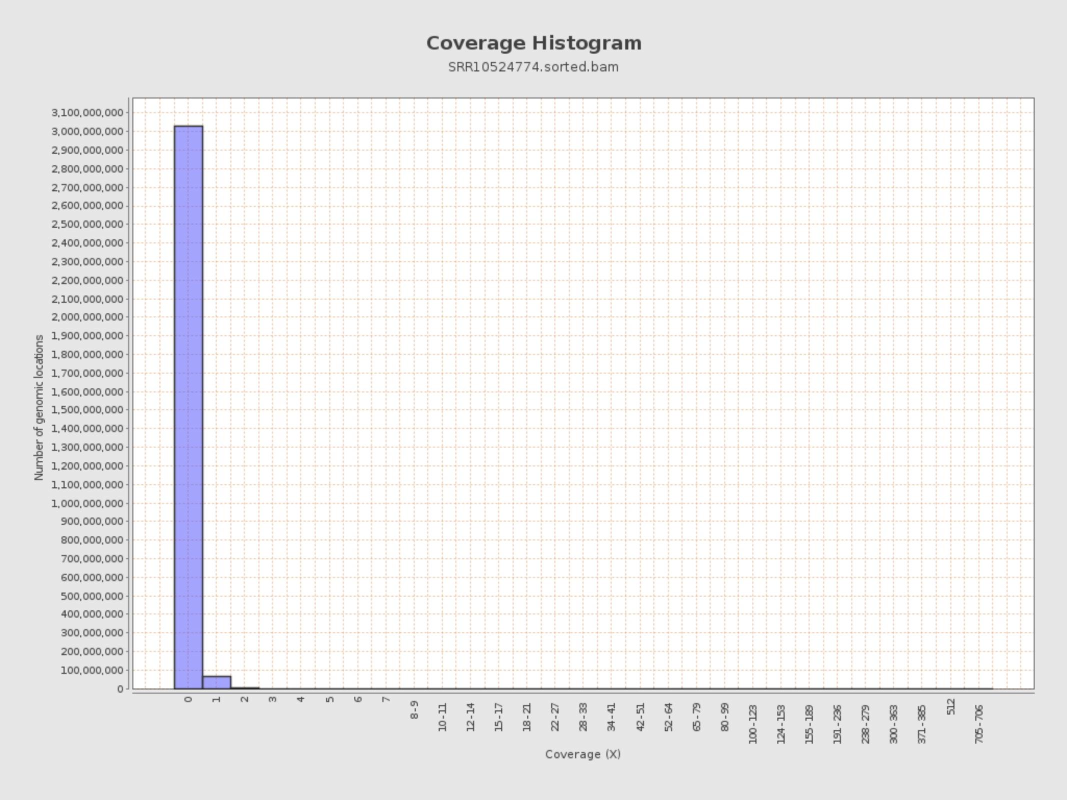
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6091156	0.0244	0.3051
chr2	243199373	6353066	0.0261	0.3495
chr3	198022430	5004514	0.0253	0.1746
chr4	191154276	4869360	0.0255	0.1972
chr5	180915260	4521148	0.025	0.1719
chr6	171115067	4263570	0.0249	0.1833
chr7	159138663	4170408	0.0262	0.2553

chr8	146364022	3792529	0.0259	0.2055
chr9	141213431	3243220	0.023	0.1926
chr10	135534747	3740801	0.0276	0.268
chr11	135006516	3409162	0.0253	0.1962
chr12	133851895	3419163	0.0255	0.1761
chr13	115169878	2321675	0.0202	0.1536
chr14	107349540	2280789	0.0212	0.1637
chr15	102531392	2213764	0.0216	0.1604
chr16	90354753	2330785	0.0258	0.1927
chr17	81195210	2201131	0.0271	0.1867
chr18	78077248	1968426	0.0252	0.2986
chr19	59128983	1715044	0.029	0.2575
chr20	63025520	1650587	0.0262	0.1834
chr21	48129895	1011090	0.021	0.1745
chr22	51304566	951386	0.0185	0.15
chrMT	16571	42743	2.5794	2.1373
chrX	155270560	4206952	0.0271	0.1903
chrY	59373566	252258	0.0042	0.1203

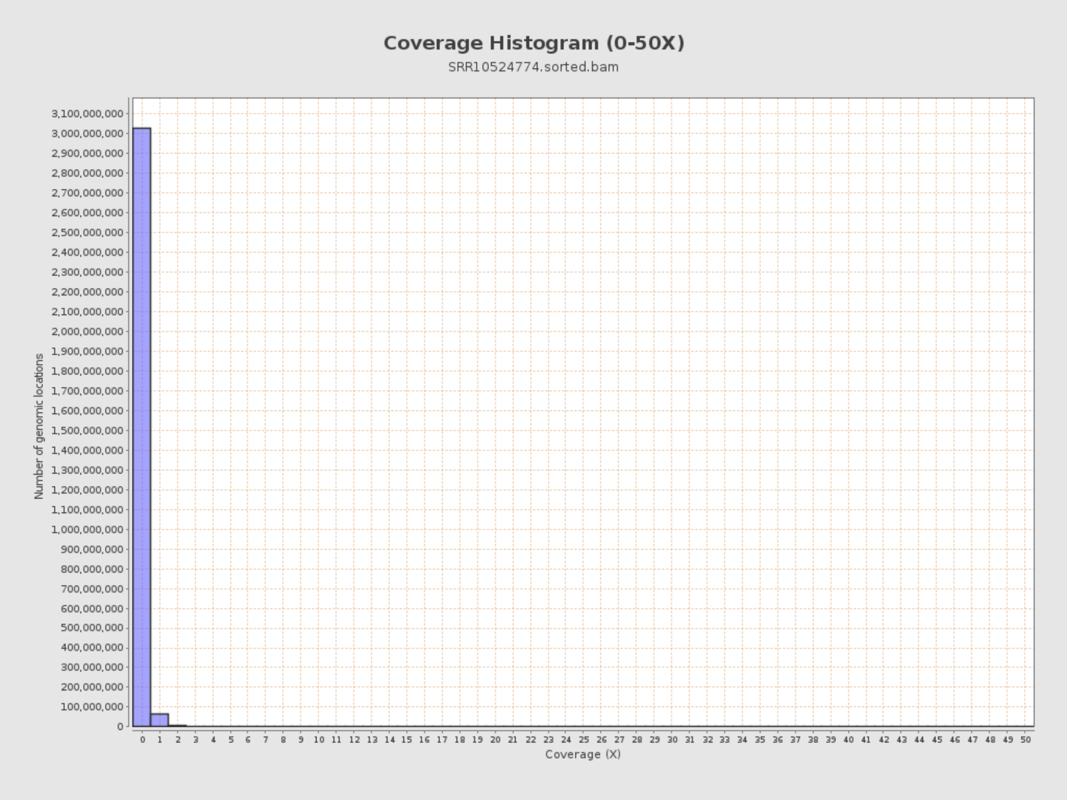
3. Results : Coverage across reference



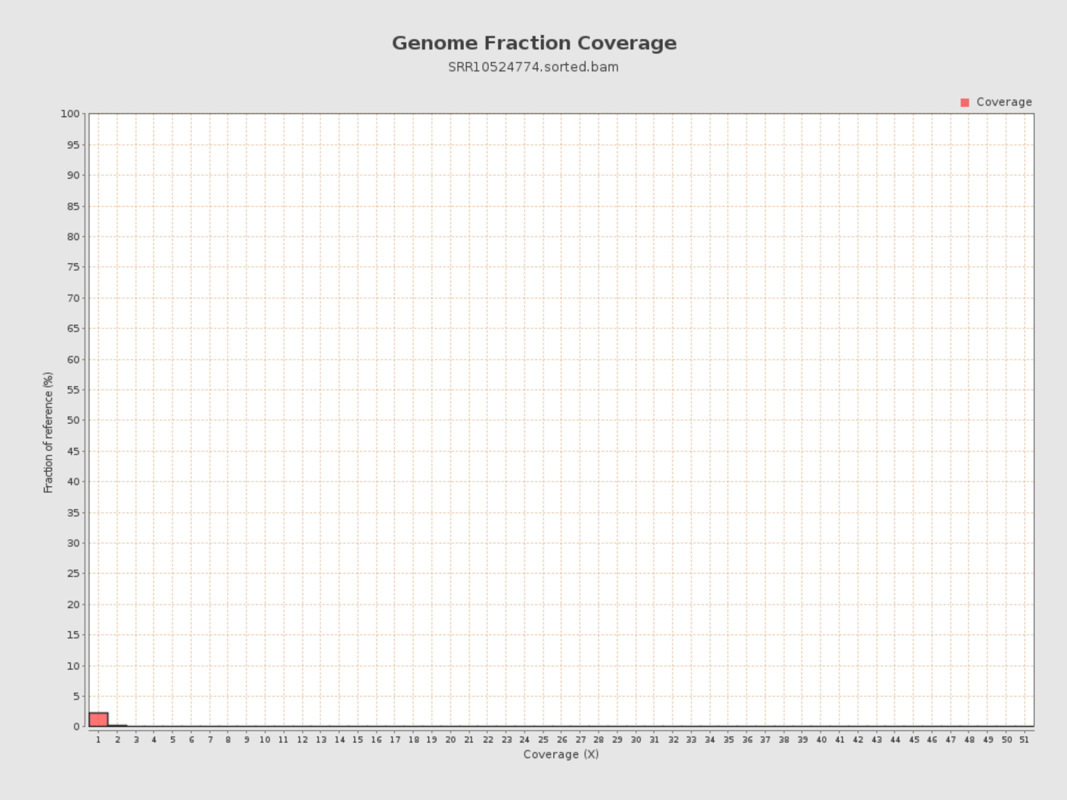
4. Results : Coverage Histogram



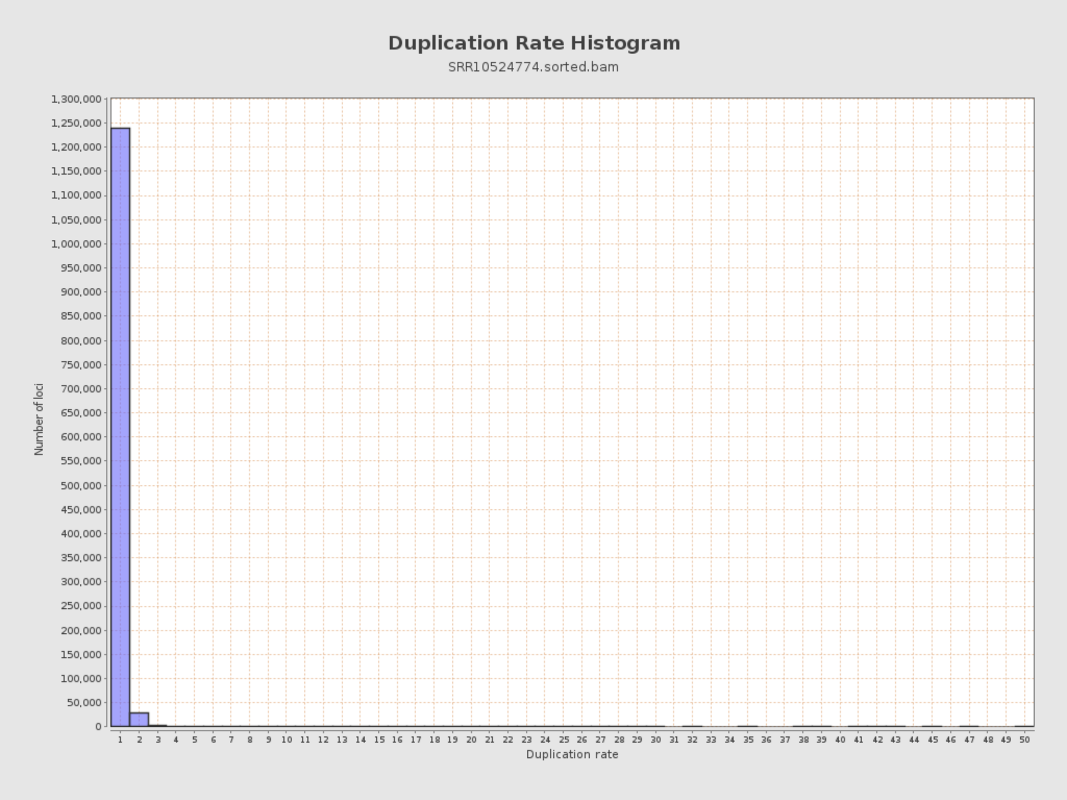
5. Results : Coverage Histogram (0-50X)



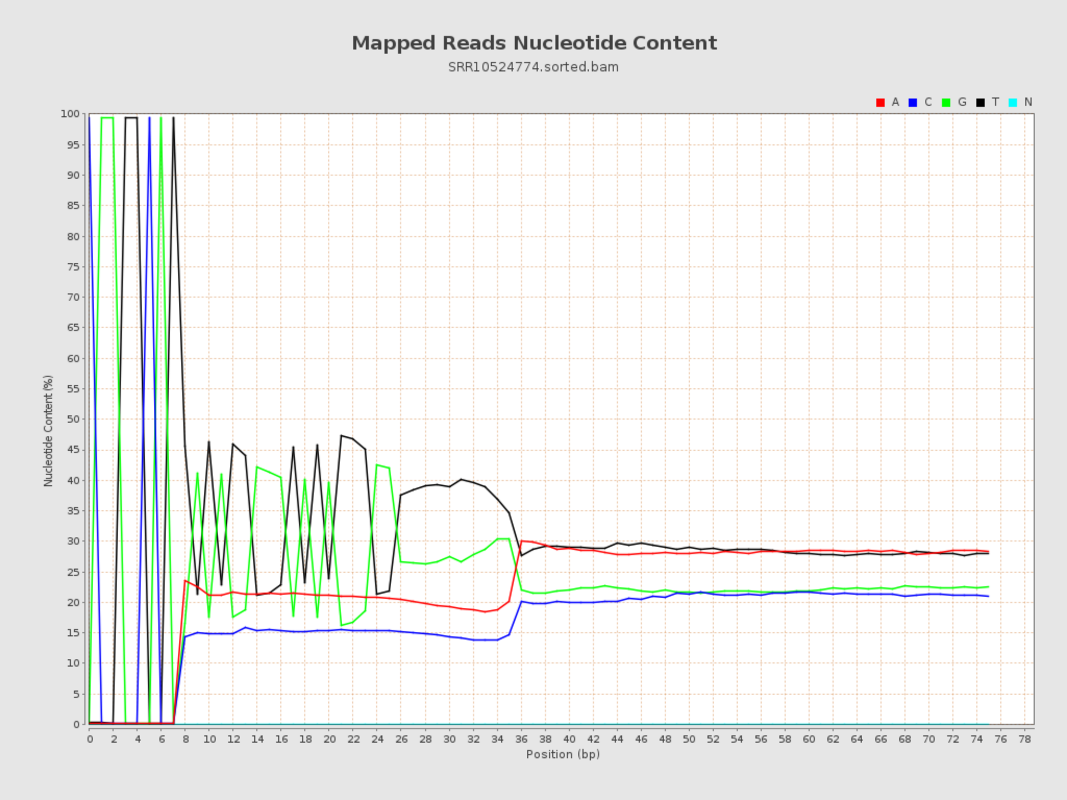
6. Results : Genome Fraction Coverage



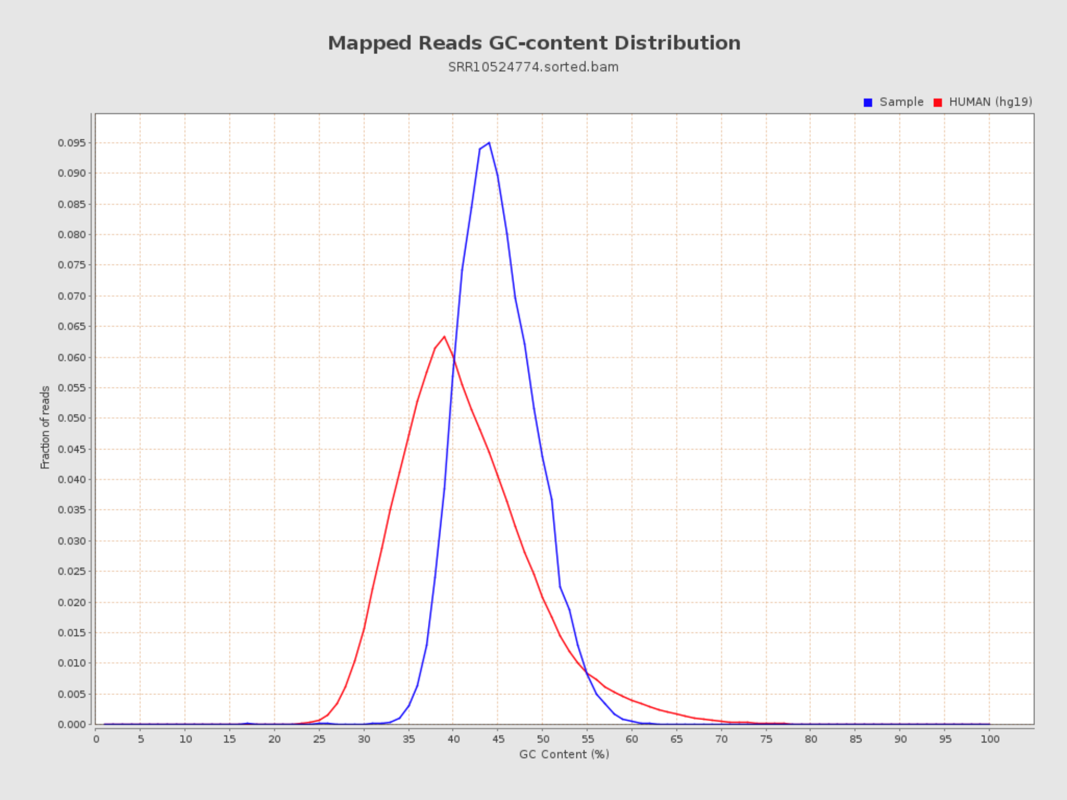
7. Results : Duplication Rate Histogram



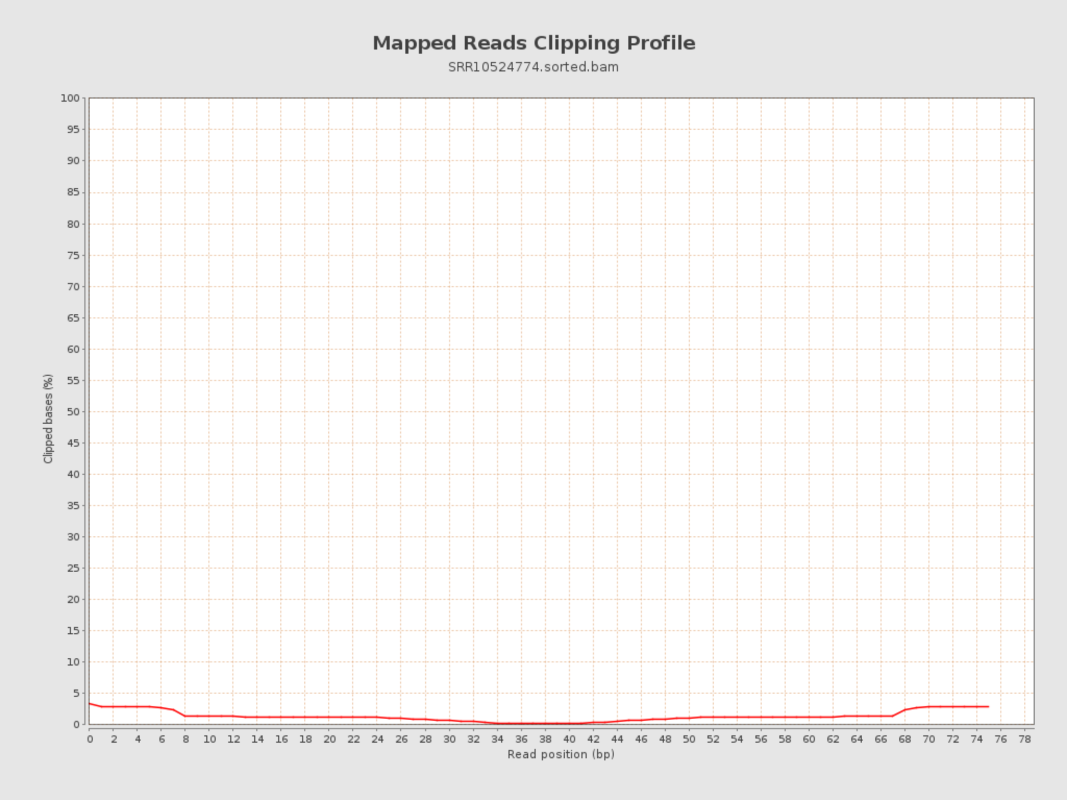
8. Results : Mapped Reads Nucleotide Content



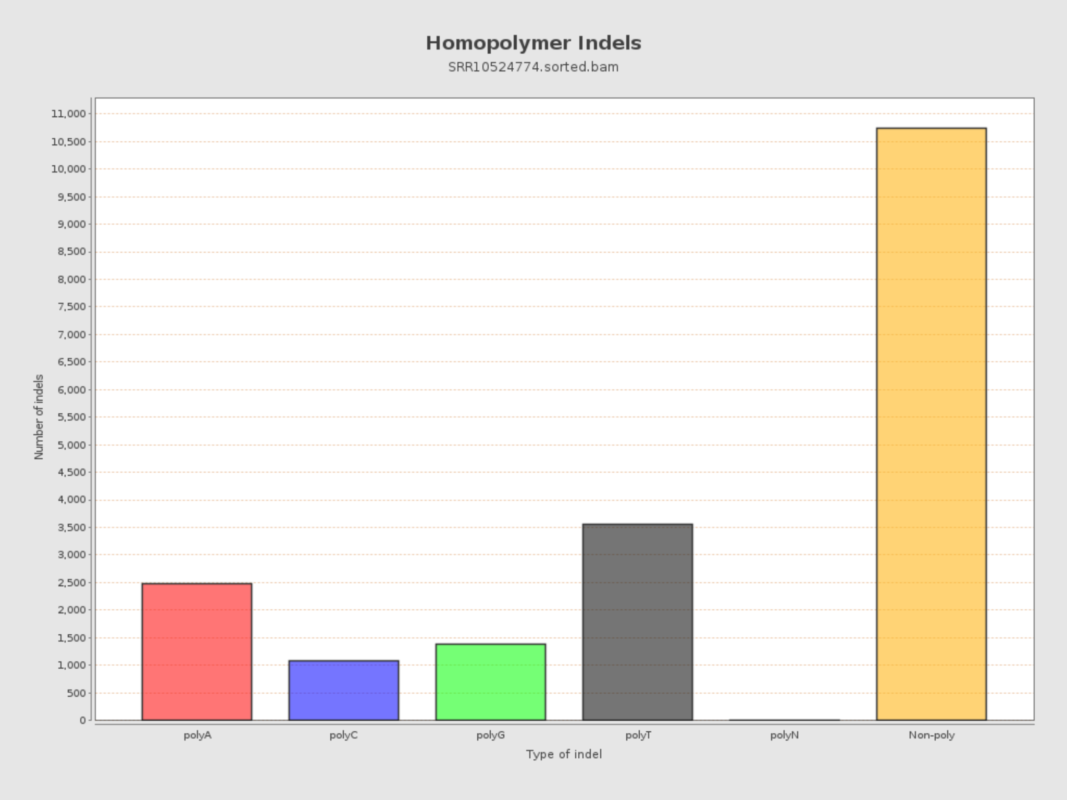
9. Results : Mapped Reads GC-content Distribution



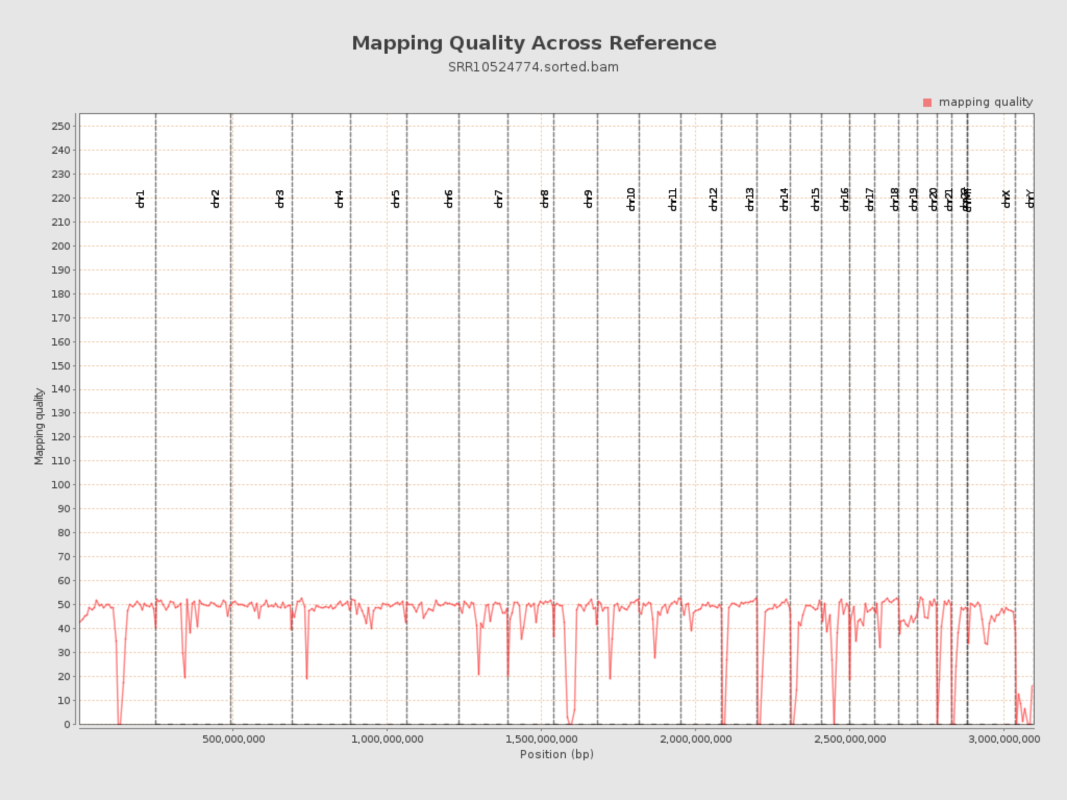
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram