Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:41:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524743.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_SRR10524743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,932,966
Mapped reads	1,762,095 / 91.16%
Unmapped reads	170,871 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,175 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	71,661 / 3.71%
Duplication rate	3.07%
Clipped reads	1,764,946 / 91.31%

2.2. ACGT Content

Number/percentage of A's	23,554,095 / 23.25%
Number/percentage of C's	18,902,409 / 18.66%
Number/percentage of T's	32,671,884 / 32.25%
Number/percentage of G's	26,167,117 / 25.83%
Number/percentage of N's	11,746 / 0.01%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.2755

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

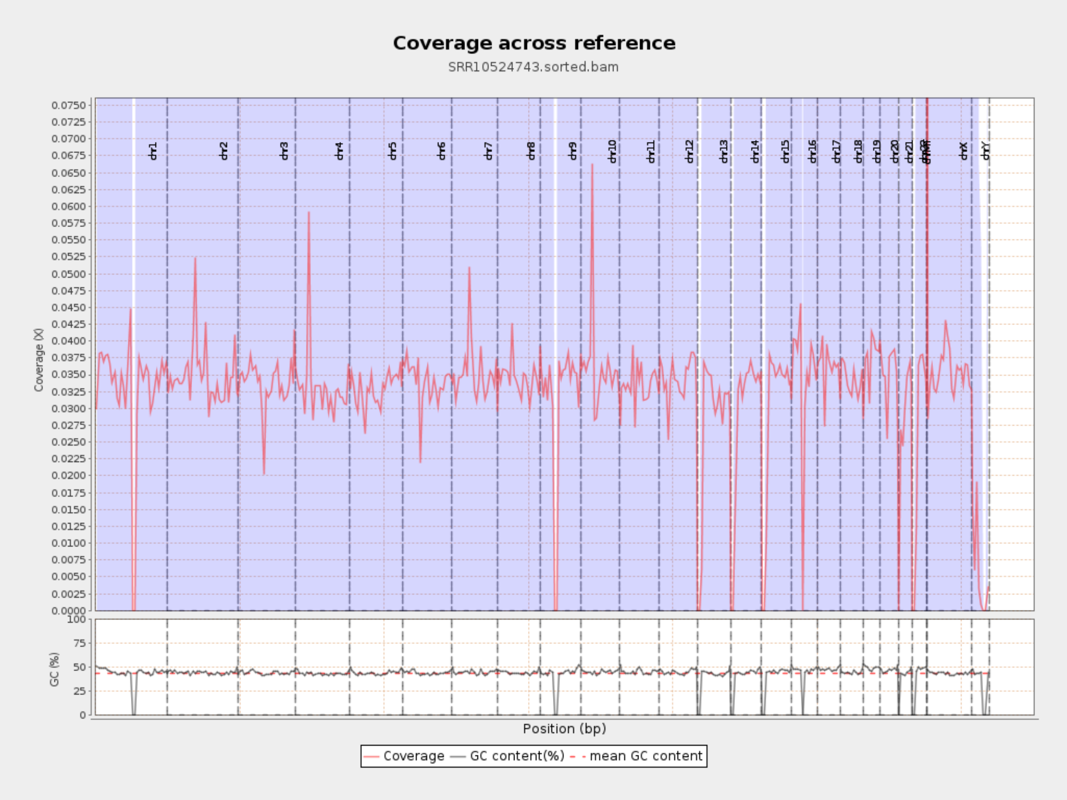
General error rate	0.53%
Mismatches	521,757
Insertions	6,598
Mapped reads with at least one insertion	0.37%
Deletions	20,992
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.39%

2.6. Chromosome stats

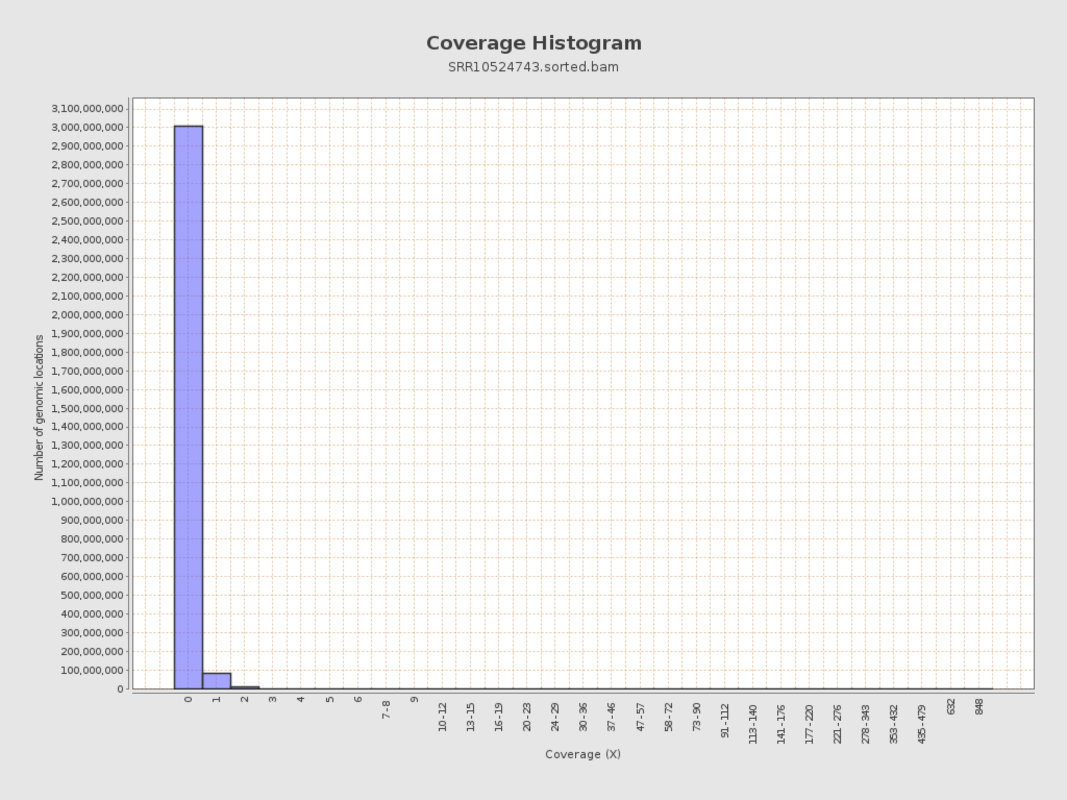
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8150976	0.0327	0.3851
chr2	243199373	8486972	0.0349	0.4286
chr3	198022430	6664952	0.0337	0.2067
chr4	191154276	6378838	0.0334	0.2324
chr5	180915260	5972937	0.033	0.2012
chr6	171115067	5793905	0.0339	0.224
chr7	159138663	5641472	0.0355	0.3382

chr8	146364022	5054488	0.0345	0.2577
chr9	141213431	4358968	0.0309	0.2438
chr10	135534747	4934888	0.0364	0.3296
chr11	135006516	4542137	0.0336	0.2474
chr12	133851895	4614892	0.0345	0.2098
chr13	115169878	3128825	0.0272	0.183
chr14	107349540	3074382	0.0286	0.1934
chr15	102531392	2944440	0.0287	0.1877
chr16	90354753	3072852	0.034	0.2259
chr17	81195210	2937376	0.0362	0.2243
chr18	78077248	2672557	0.0342	0.3784
chr19	59128983	2222882	0.0376	0.3164
chr20	63025520	2203769	0.035	0.2176
chr21	48129895	1348591	0.028	0.2074
chr22	51304566	1289718	0.0251	0.1768
chrMT	16571	15008	0.9057	1.0956
chrX	155270560	5503440	0.0354	0.228
chrY	59373566	331932	0.0056	0.1478

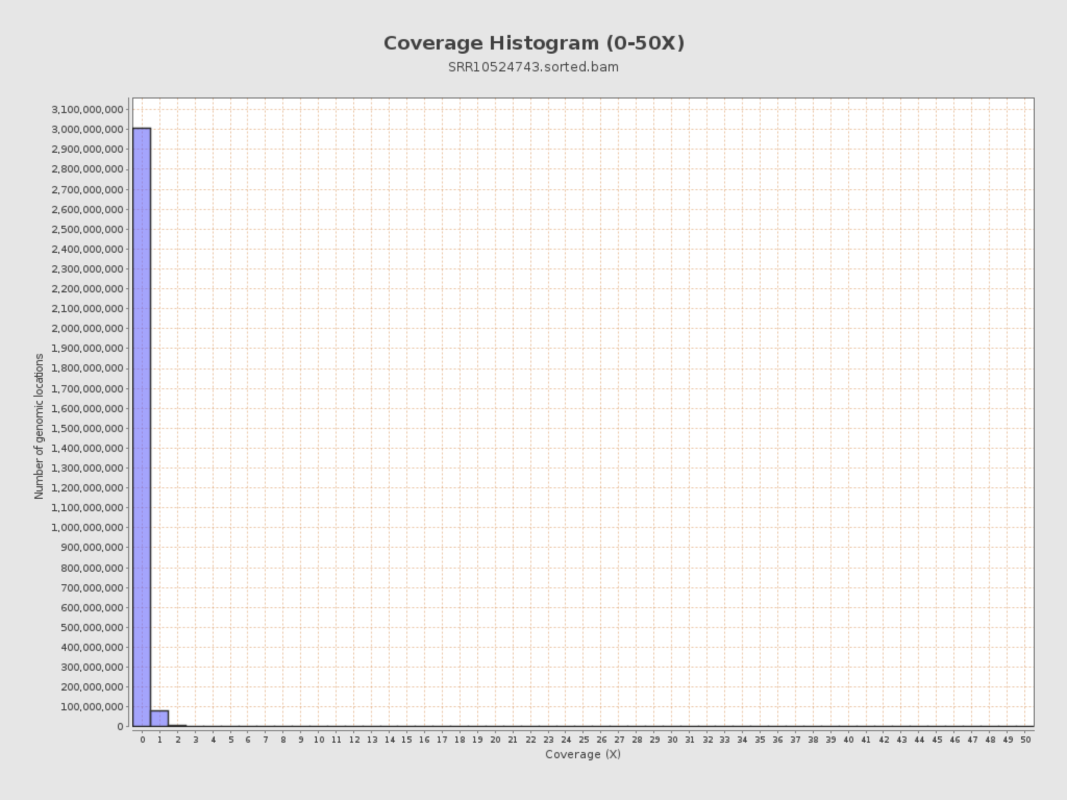
3. Results : Coverage across reference



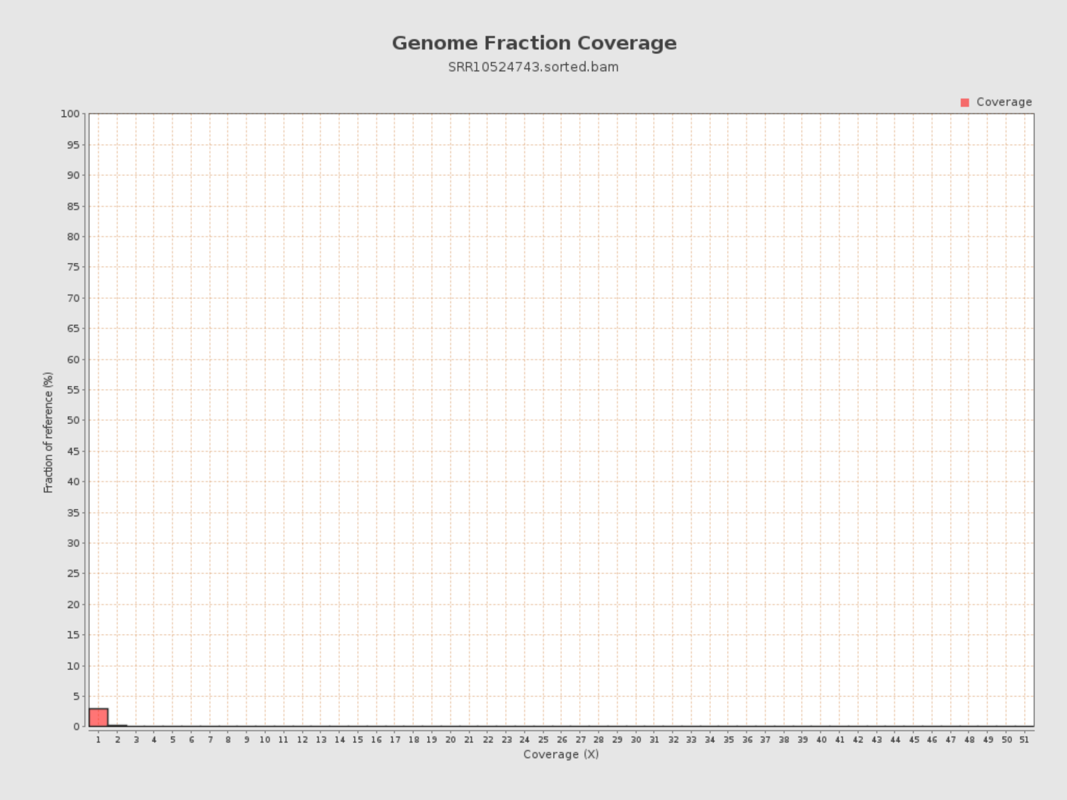
4. Results : Coverage Histogram



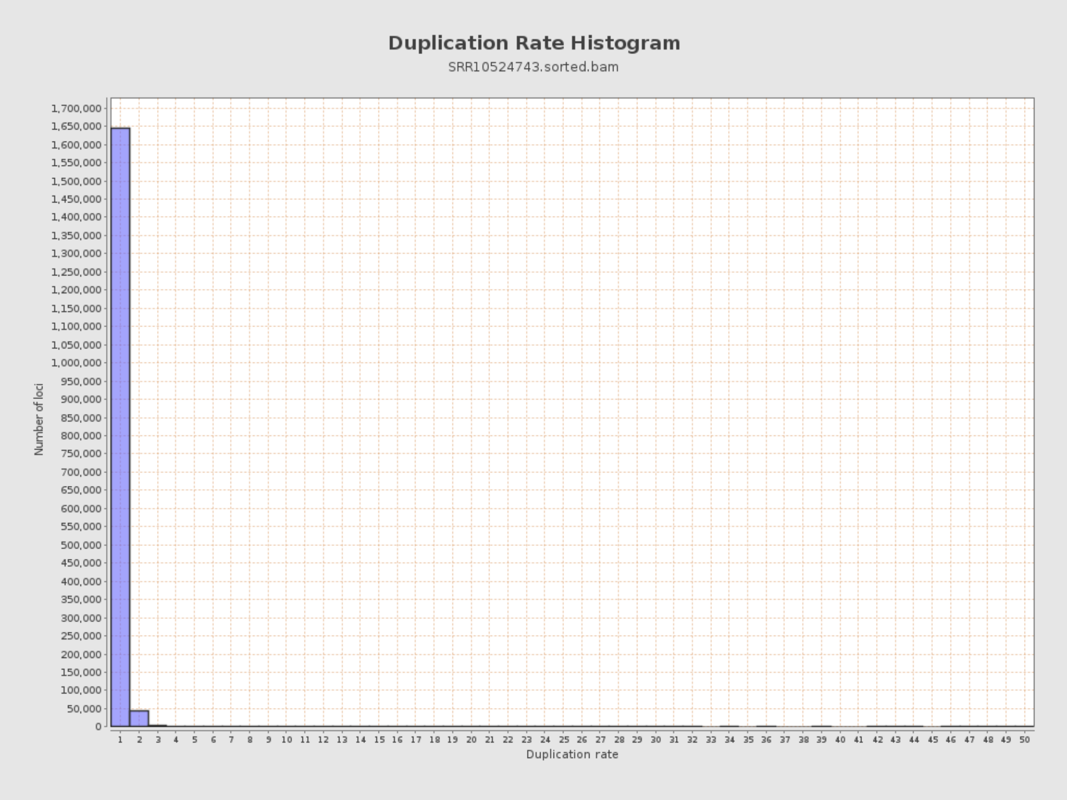
5. Results : Coverage Histogram (0-50X)



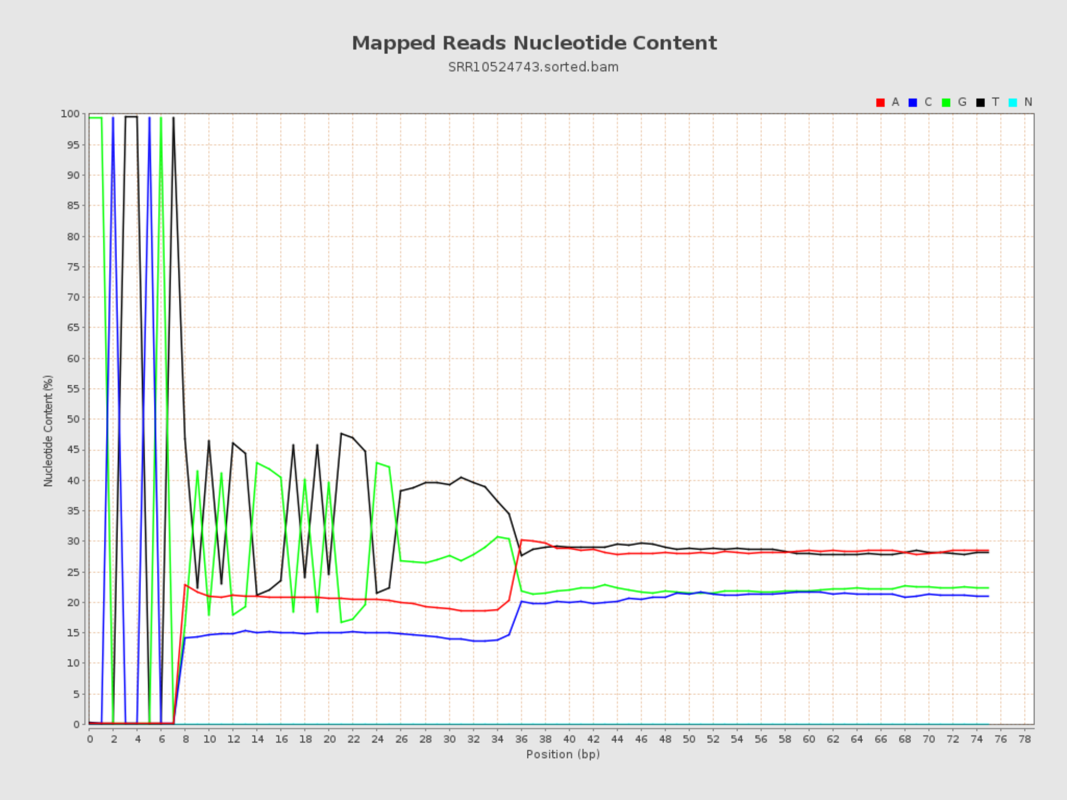
6. Results : Genome Fraction Coverage



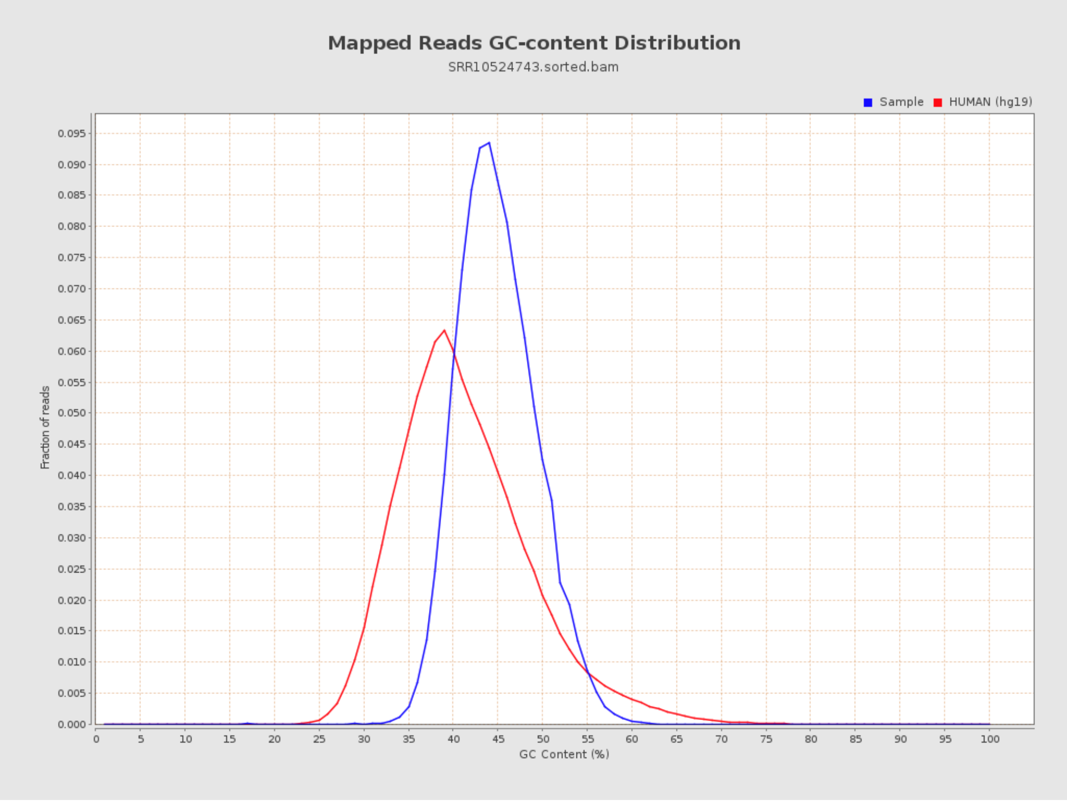
7. Results : Duplication Rate Histogram



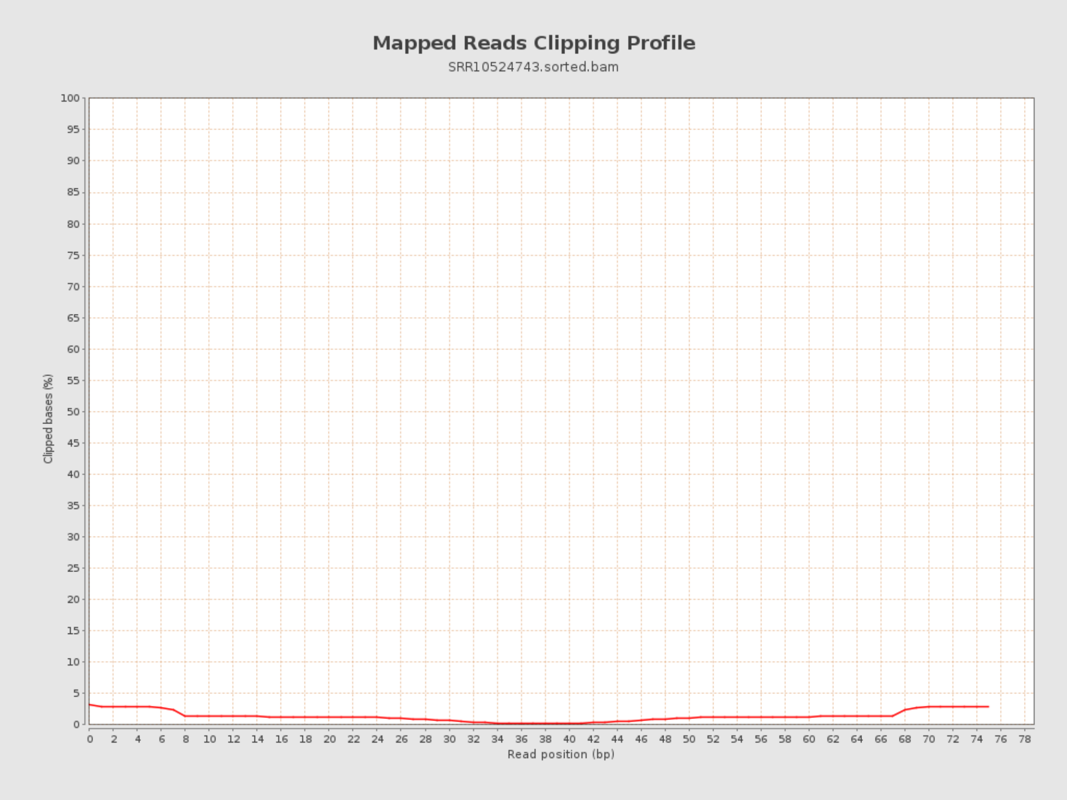
8. Results : Mapped Reads Nucleotide Content



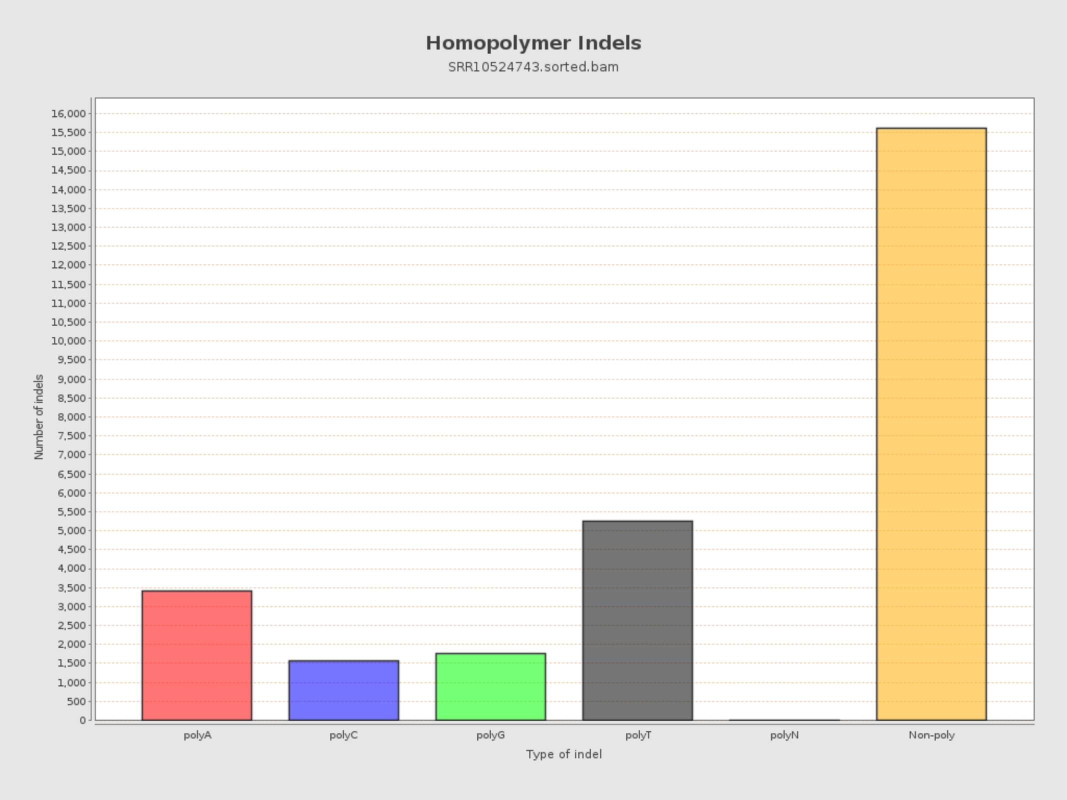
9. Results : Mapped Reads GC-content Distribution



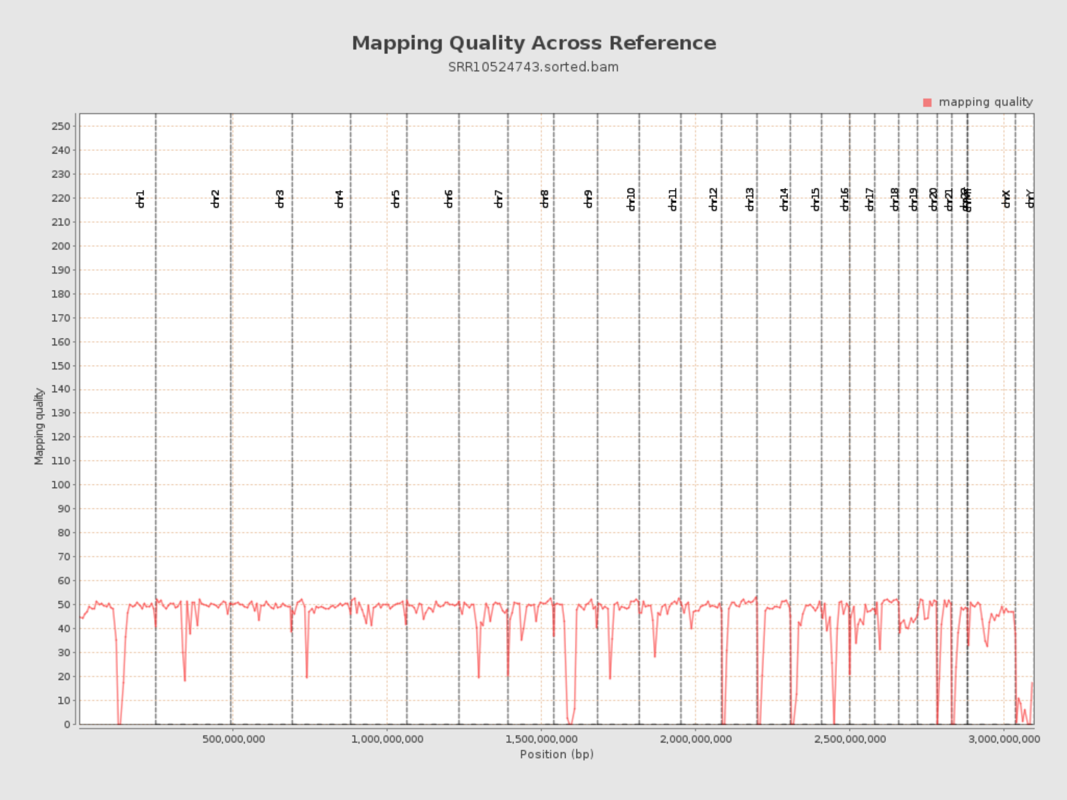
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram