Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:22:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524316.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_SRR10524316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524316.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:22:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,274,638
Mapped reads	2,079,422 / 91.42%
Unmapped reads	195,216 / 8.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,171 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	90,624 / 3.98%
Duplication rate	3.12%
Clipped reads	2,086,399 / 91.72%

2.2. ACGT Content

Number/percentage of A's	29,440,191 / 24.32%
Number/percentage of C's	24,031,633 / 19.86%
Number/percentage of T's	37,536,222 / 31.01%
Number/percentage of G's	30,006,947 / 24.79%
Number/percentage of N's	16,672 / 0.01%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3591

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Mismatches and indels

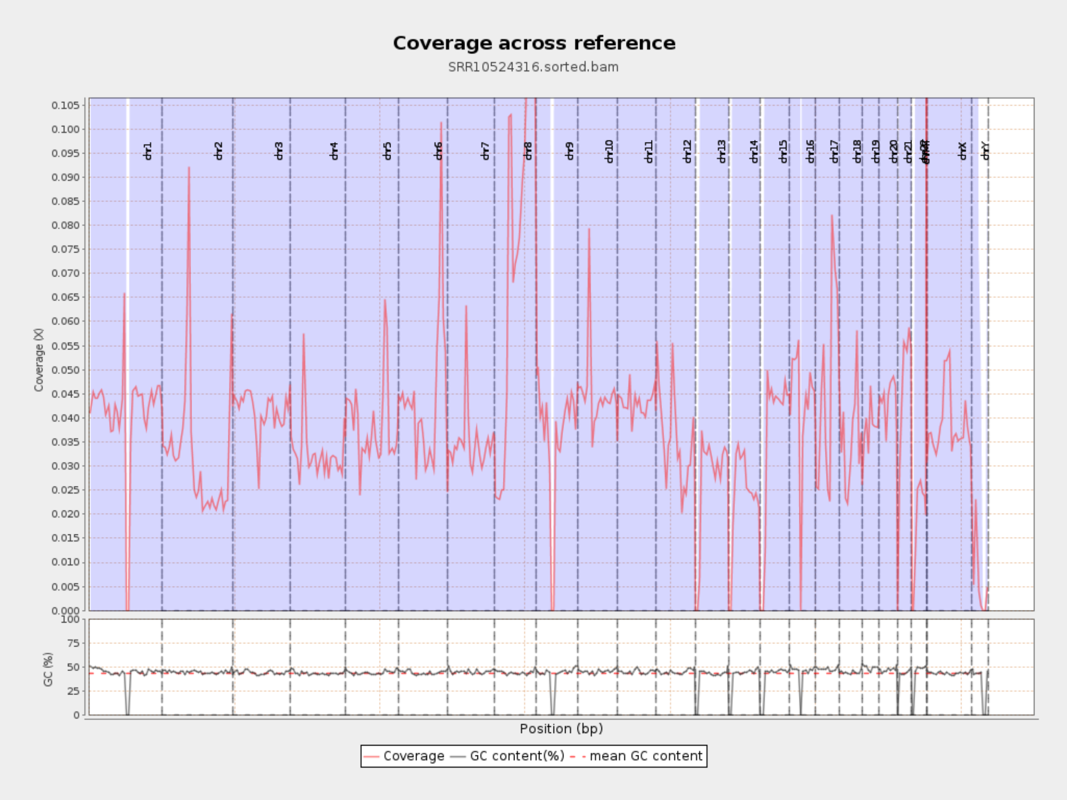
General error rate	0.53%
Mismatches	629,225
Insertions	6,789
Mapped reads with at least one insertion	0.32%
Deletions	20,648
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.91%

2.6. Chromosome stats

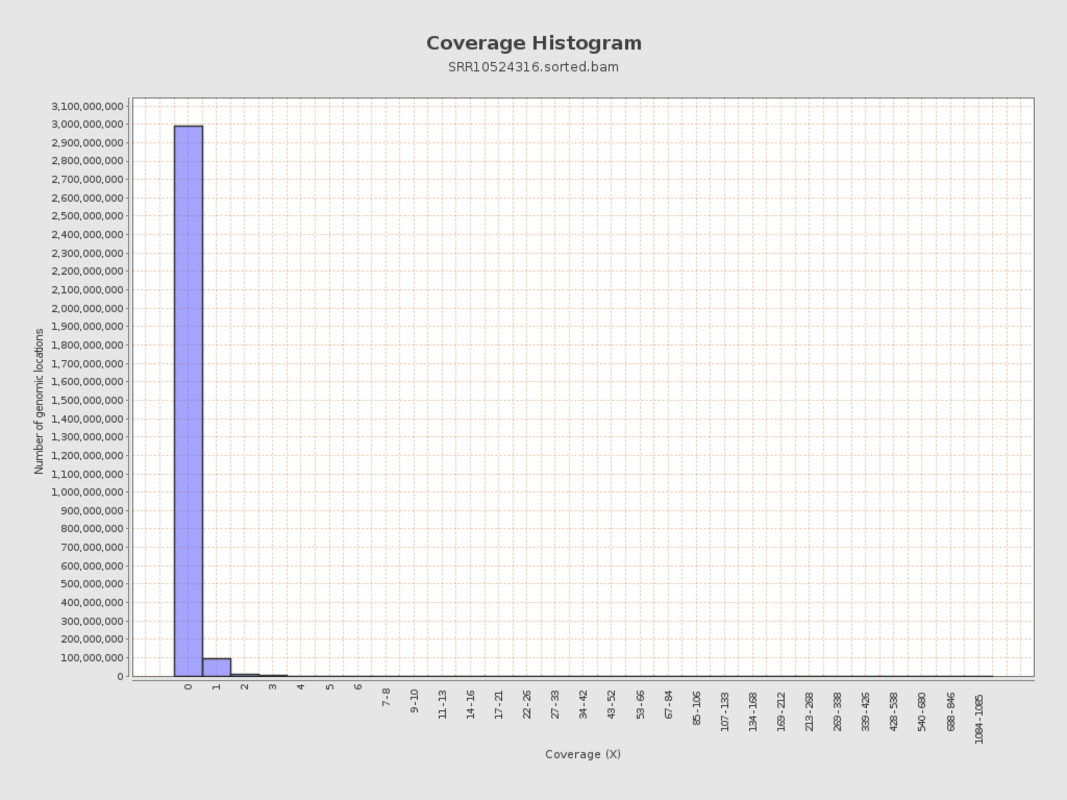
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10184529	0.0409	0.6532
chr2	243199373	7859005	0.0323	0.4984
chr3	198022430	8182040	0.0413	0.2313
chr4	191154276	6220111	0.0325	0.2386
chr5	180915260	7003843	0.0387	0.2217
chr6	171115067	7568954	0.0442	0.2584
chr7	159138663	5577372	0.035	0.4677

chr8	146364022	12443381	0.085	0.4585
chr9	141213431	5028104	0.0356	0.2792
chr10	135534747	6140536	0.0453	0.3682
chr11	135006516	5806356	0.043	0.3101
chr12	133851895	4764370	0.0356	0.2169
chr13	115169878	3085642	0.0268	0.1854
chr14	107349540	2548462	0.0237	0.1859
chr15	102531392	3716441	0.0362	0.2136
chr16	90354753	3907857	0.0433	0.2542
chr17	81195210	3748249	0.0462	0.2723
chr18	78077248	2835657	0.0363	0.5095
chr19	59128983	2256351	0.0382	0.4385
chr20	63025520	2772240	0.044	0.2452
chr21	48129895	2132840	0.0443	0.2645
chr22	51304566	906806	0.0177	0.1497
chrMT	16571	4196	0.2532	0.5571
chrX	155270560	5993713	0.0386	0.2533
chrY	59373566	377268	0.0064	0.1707

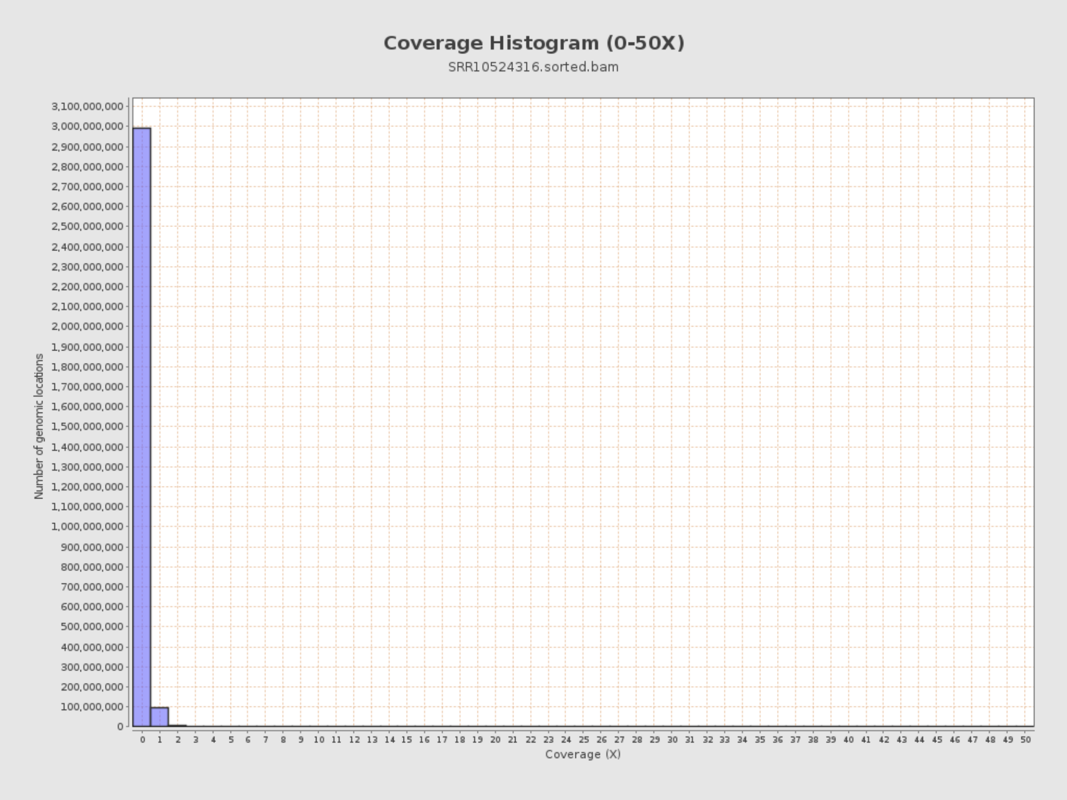
3. Results : Coverage across reference



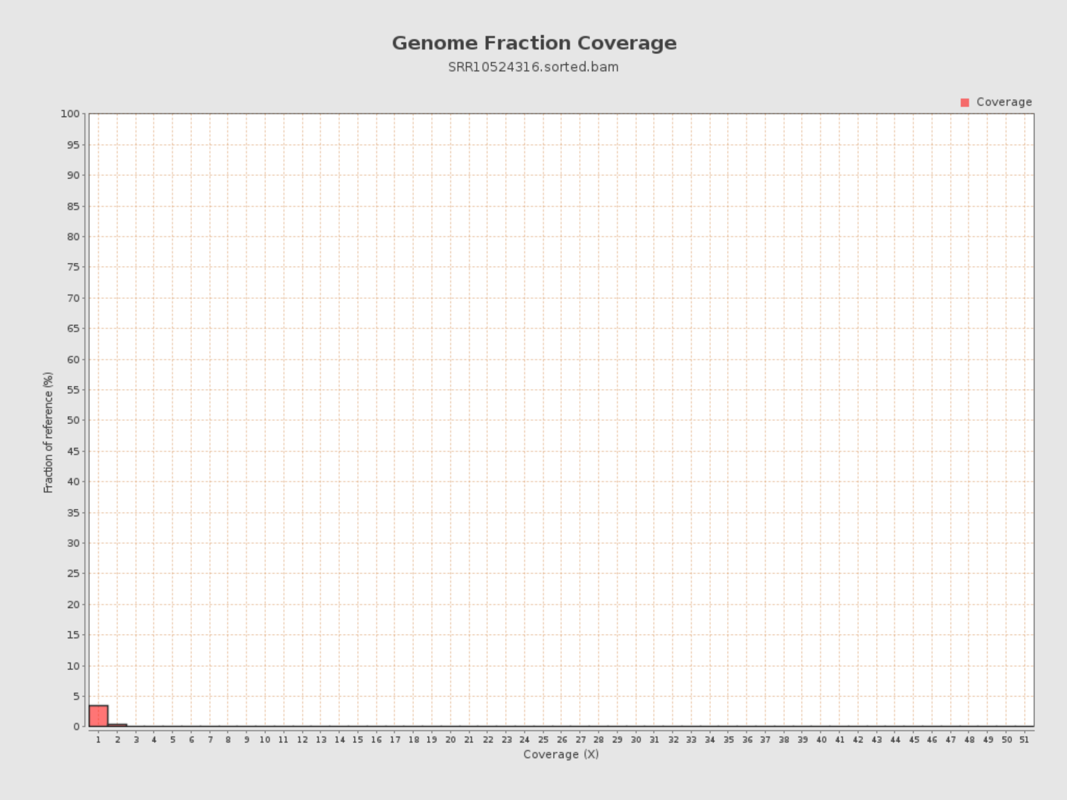
4. Results : Coverage Histogram



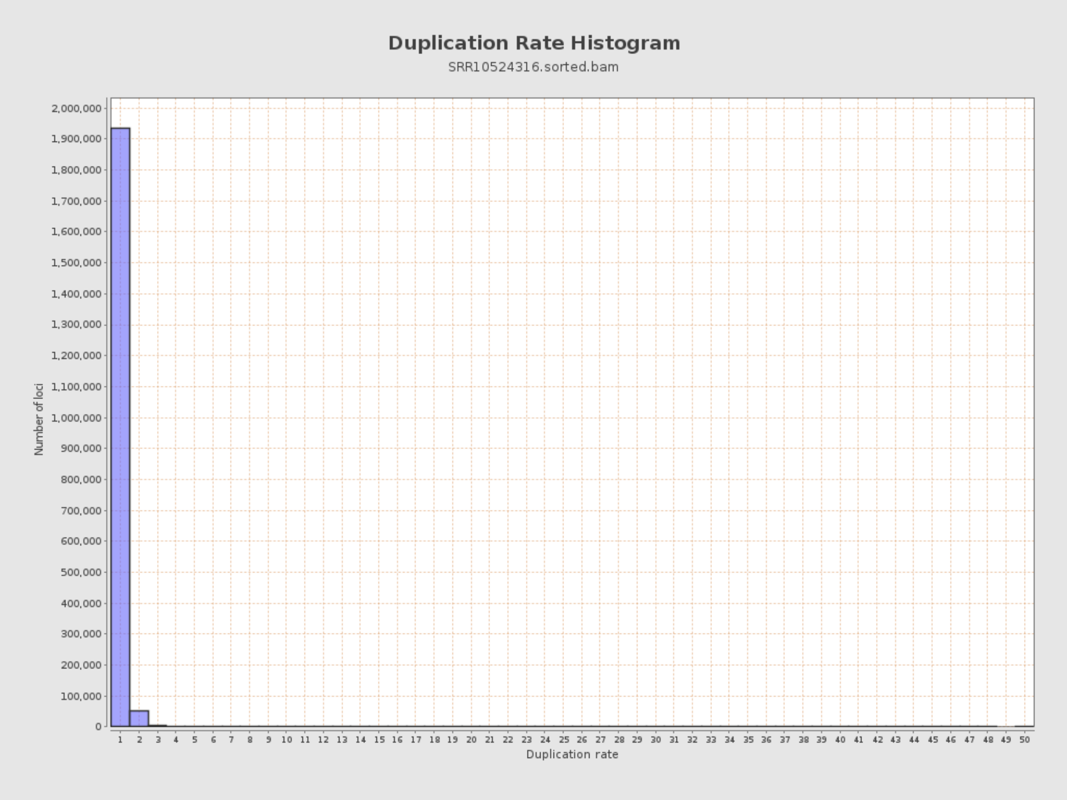
5. Results : Coverage Histogram (0-50X)



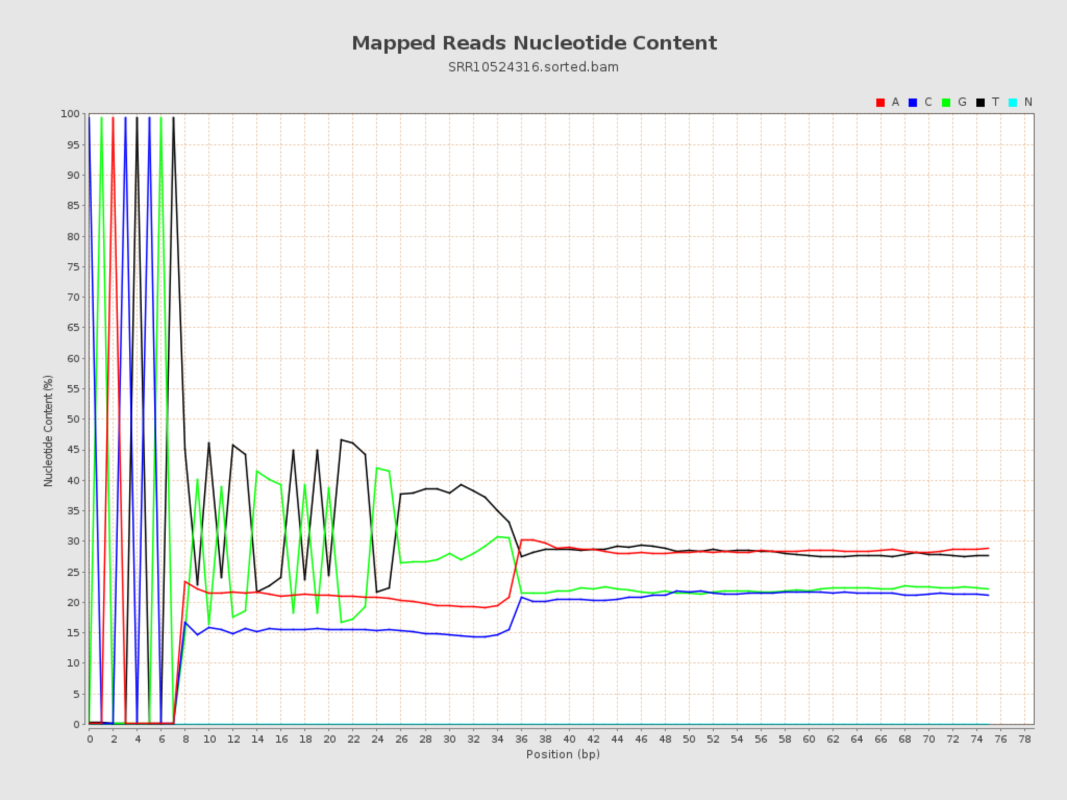
6. Results : Genome Fraction Coverage



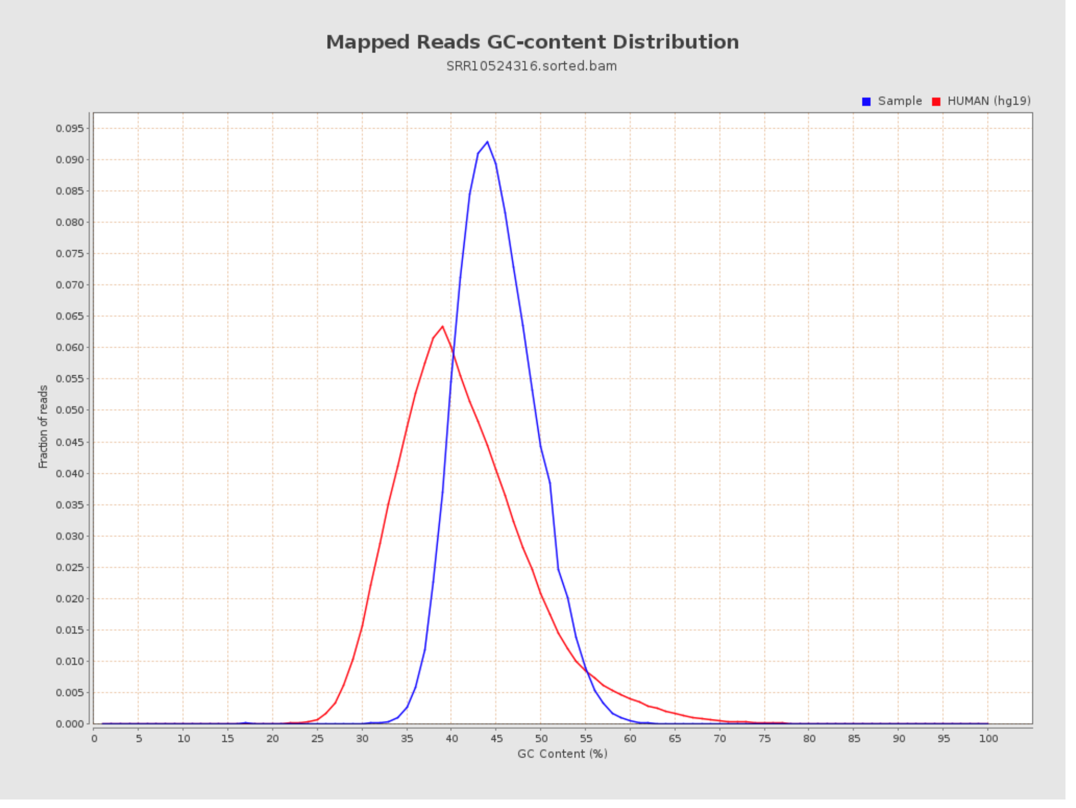
7. Results : Duplication Rate Histogram



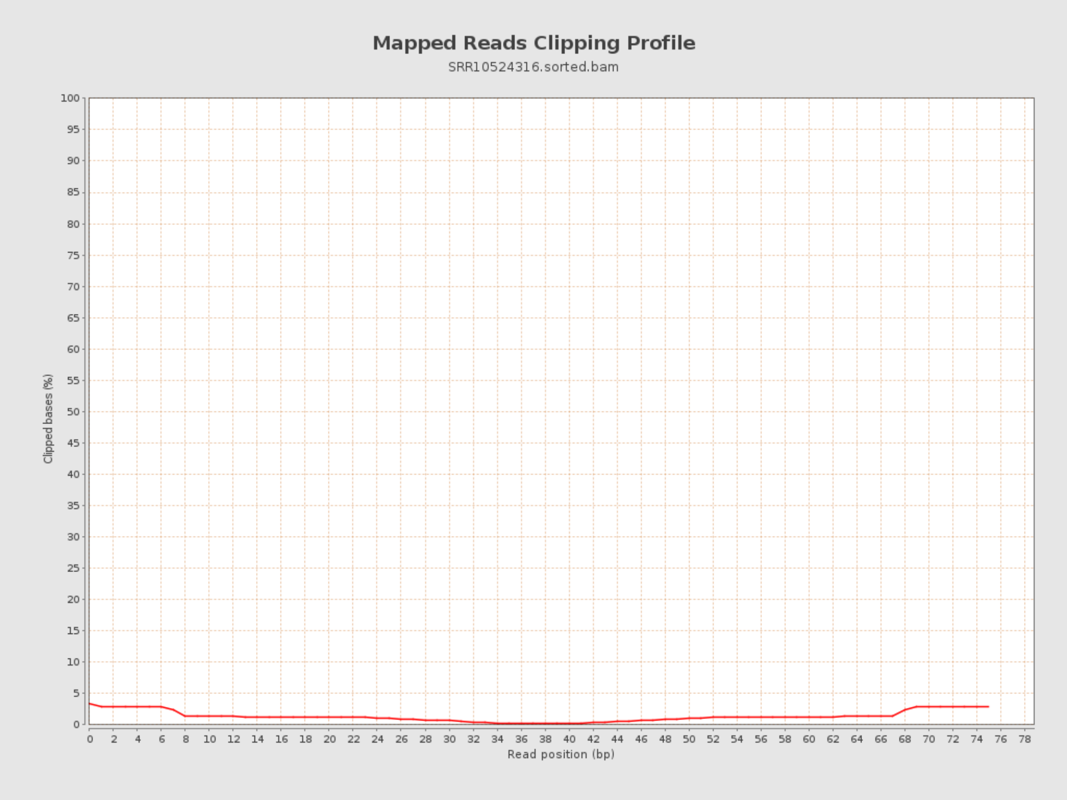
8. Results : Mapped Reads Nucleotide Content



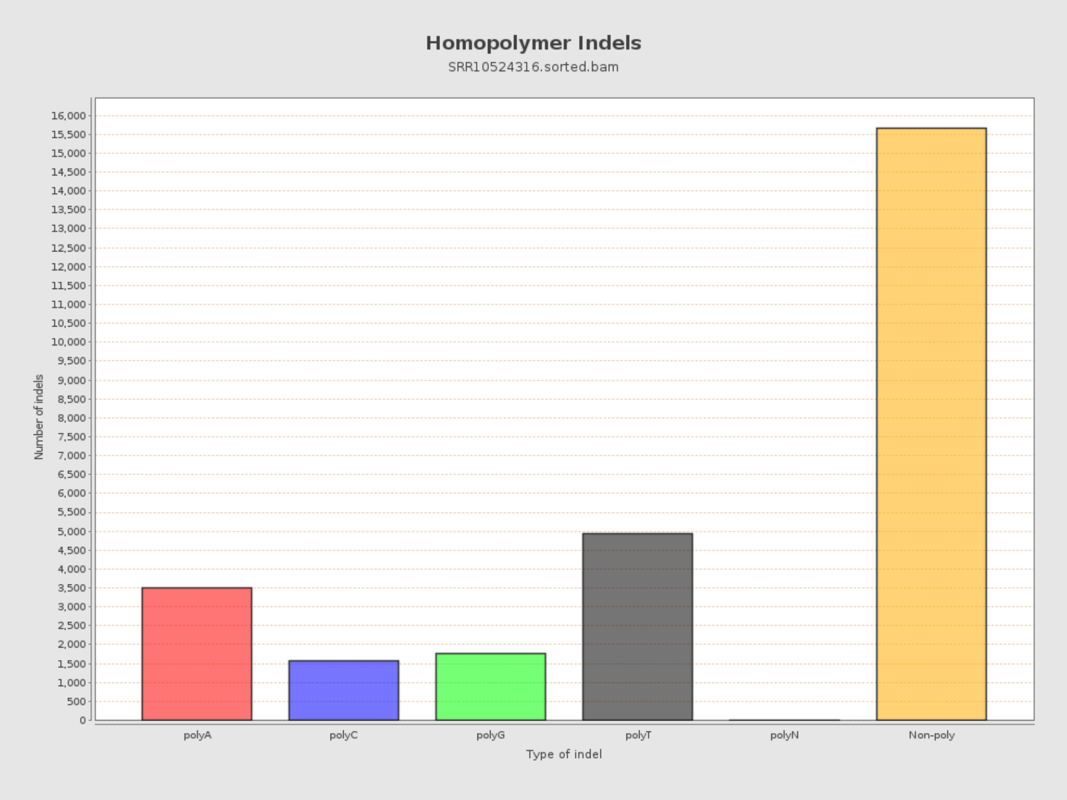
9. Results : Mapped Reads GC-content Distribution



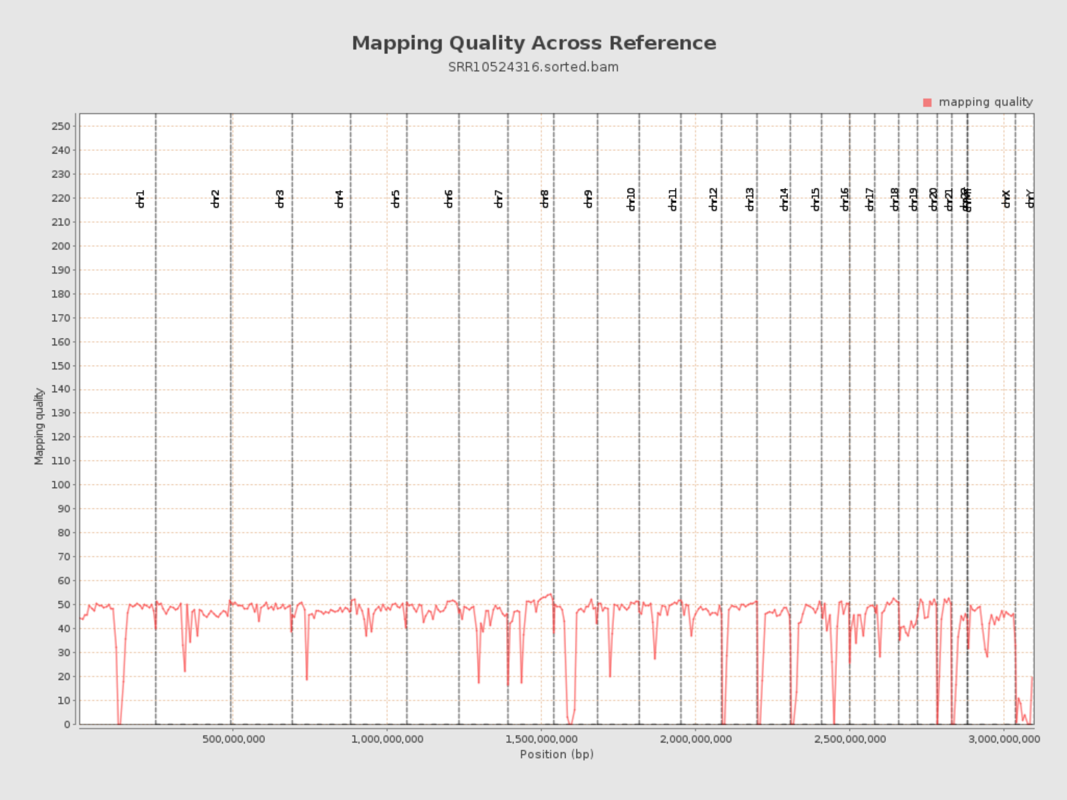
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram