Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:49:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124795.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_SRR3124795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:49:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	322,295
Mapped reads	318,271 / 98.75%
Unmapped reads	4,024 / 1.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	108,935 / 33.8%
Read min/max/mean length	30 / 151 / 173.68
Duplicated reads (estimated)	370,682 / 115.01%
Duplication rate	1.42%
Clipped reads	292,773 / 90.84%

2.2. ACGT Content

Number/percentage of A's	12,937,157 / 28.11%
Number/percentage of C's	8,230,841 / 17.88%
Number/percentage of T's	14,615,876 / 31.75%
Number/percentage of G's	10,245,299 / 22.26%
Number/percentage of N's	0 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0149

Standard Deviation	29.9531

2.4. Mapping Quality

Mean Mapping Quality	51.09

2.5. Mismatches and indels

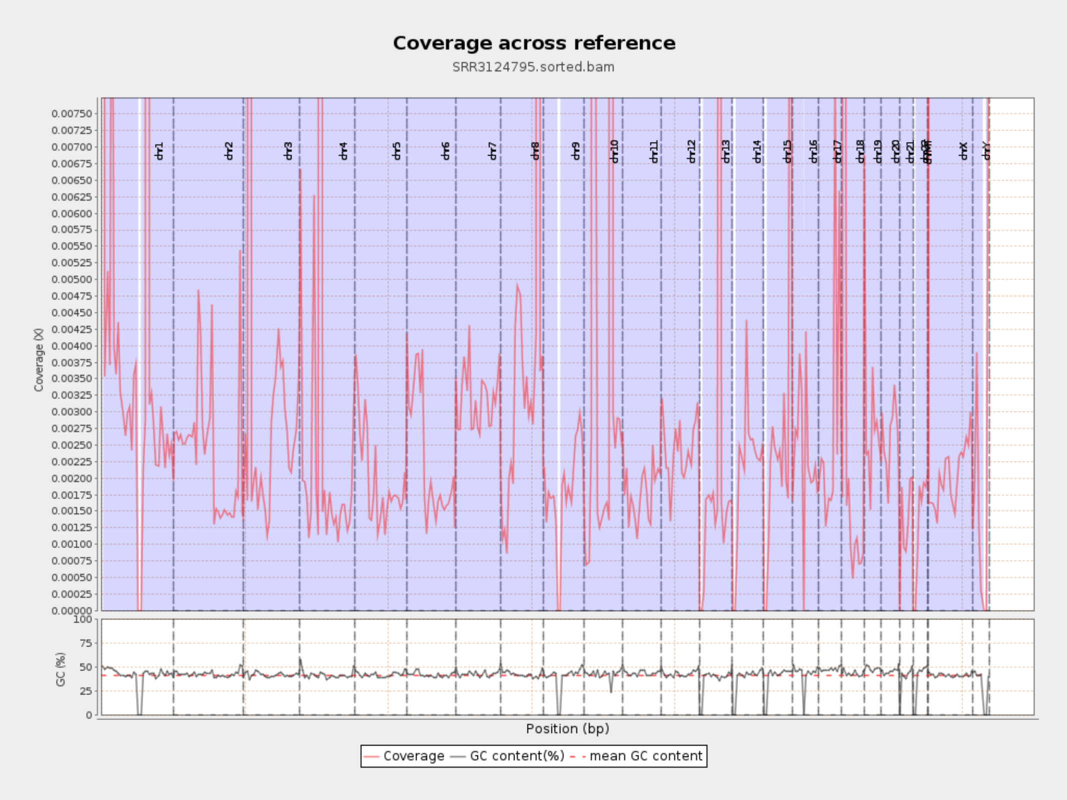
General error rate	0.97%
Mismatches	442,017
Insertions	3,016
Mapped reads with at least one insertion	0.91%
Deletions	67,352
Mapped reads with at least one deletion	20.92%
Homopolymer indels	84.65%

2.6. Chromosome stats

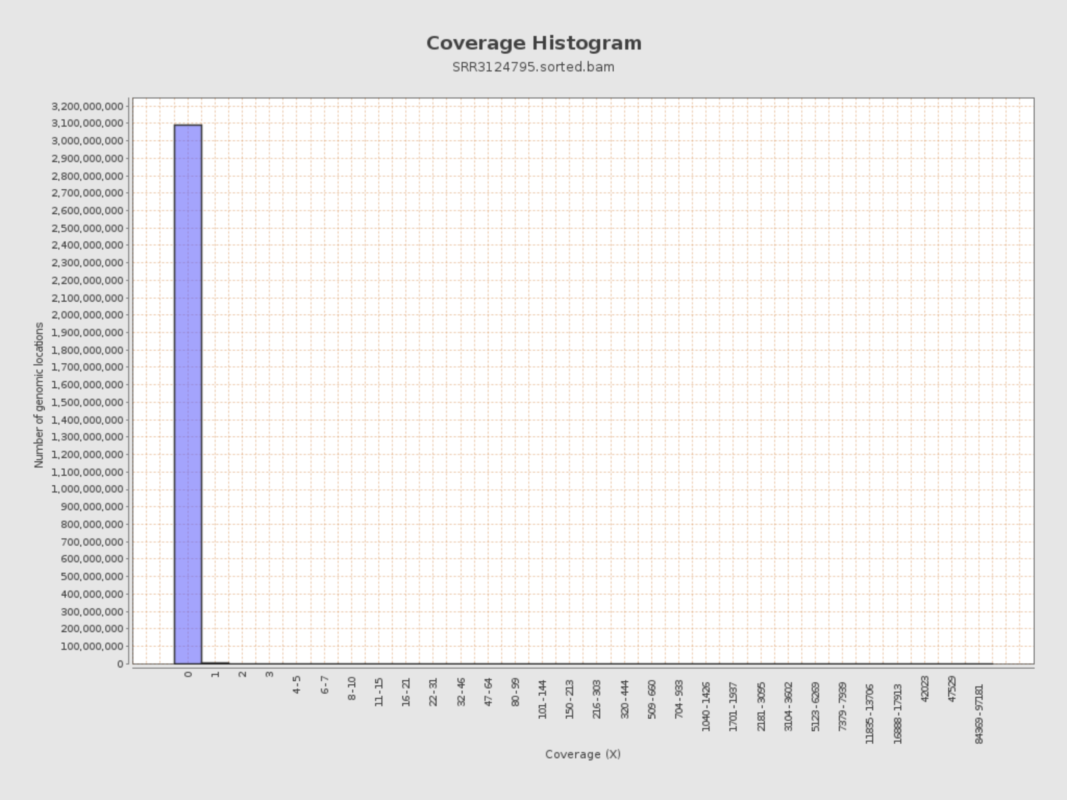
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3279075	0.0132	6.9014
chr2	243199373	594004	0.0024	0.1471
chr3	198022430	987289	0.005	2.9944
chr4	191154276	2011738	0.0105	9.2927
chr5	180915260	361170	0.002	0.0508
chr6	171115067	392524	0.0023	0.0497
chr7	159138663	510491	0.0032	0.0656

chr8	146364022	5868725	0.0401	25.5016
chr9	141213431	254956	0.0018	0.0433
chr10	135534747	28697339	0.2117	139.8635
chr11	135006516	242113	0.0018	0.0592
chr12	133851895	327804	0.0024	0.0543
chr13	115169878	392974	0.0034	2.0038
chr14	107349540	230978	0.0022	0.082
chr15	102531392	294620	0.0029	0.6984
chr16	90354753	218058	0.0024	0.1176
chr17	81195210	242365	0.003	0.4859
chr18	78077248	285183	0.0037	1.7101
chr19	59128983	163193	0.0028	0.1549
chr20	63025520	163495	0.0026	0.0751
chr21	48129895	64069	0.0013	0.04
chr22	51304566	67057	0.0013	0.0367
chrMT	16571	18150	1.0953	1.1862
chrX	155270560	313042	0.002	0.0465
chrY	59373566	124283	0.0021	0.0681

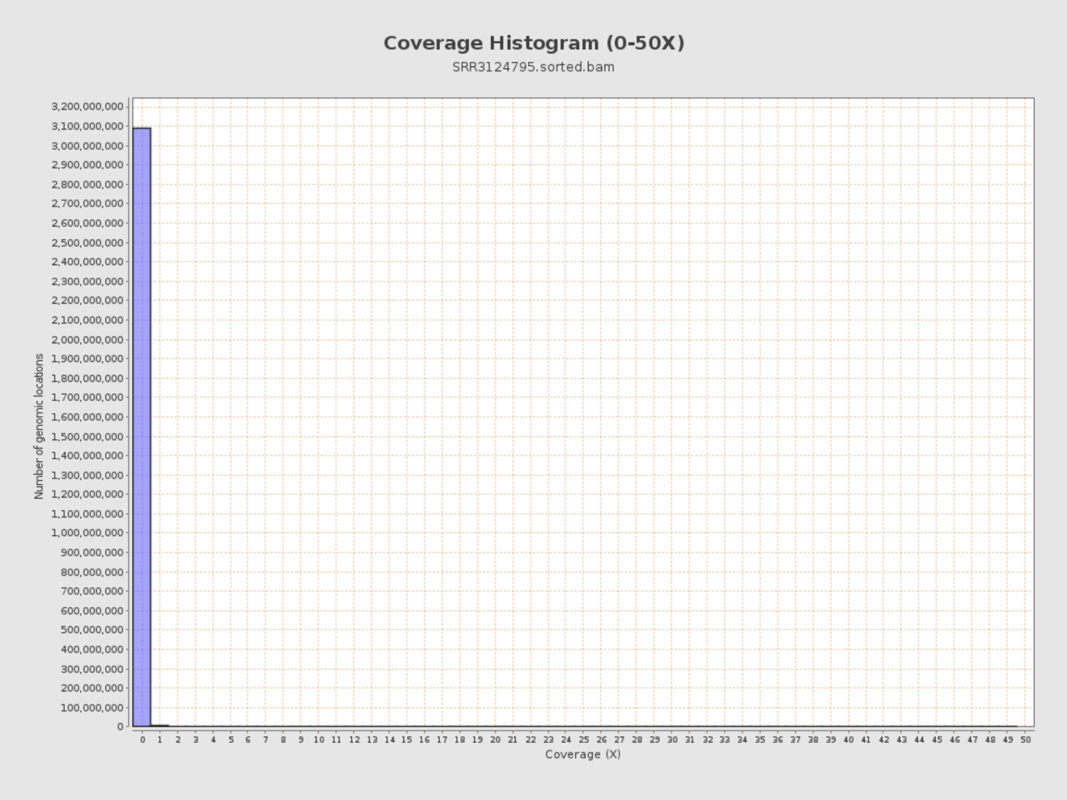
3. Results : Coverage across reference



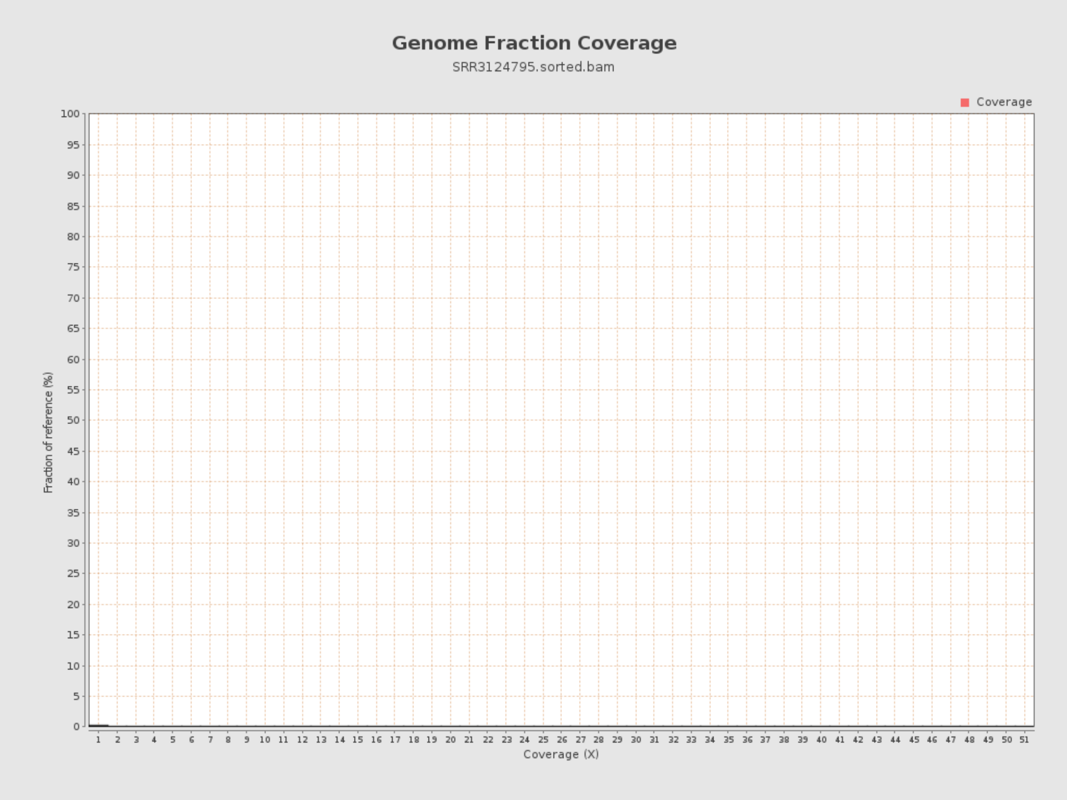
4. Results : Coverage Histogram



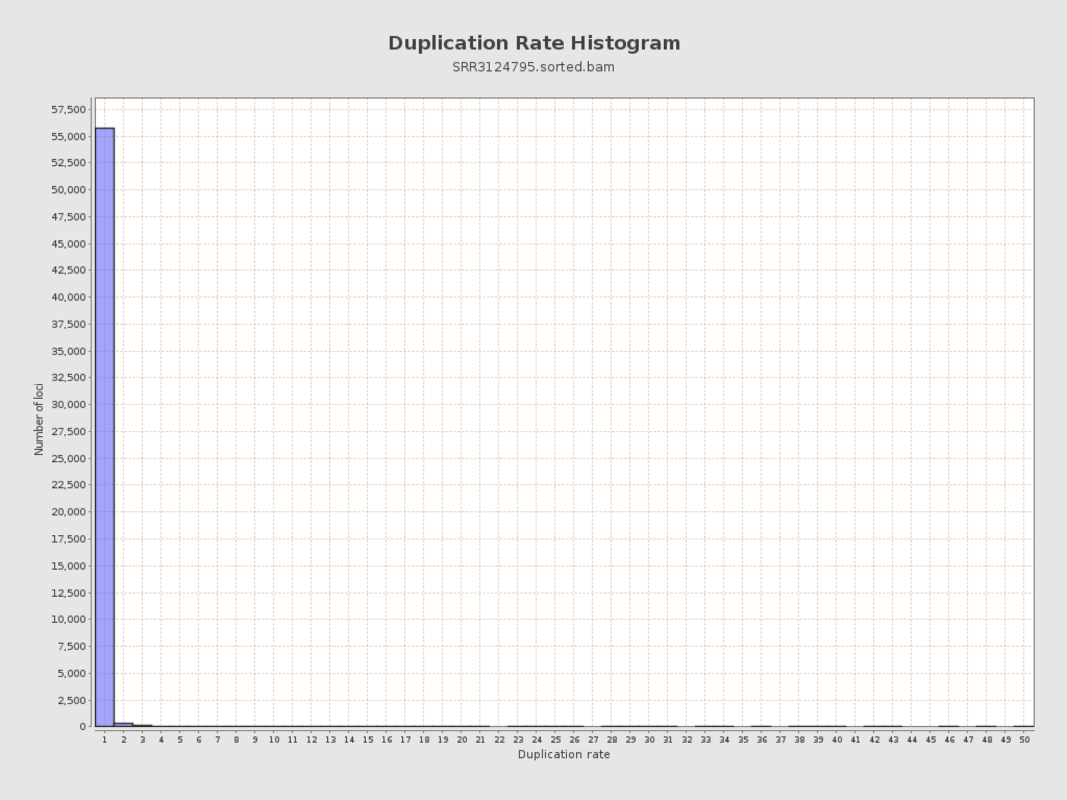
5. Results : Coverage Histogram (0-50X)



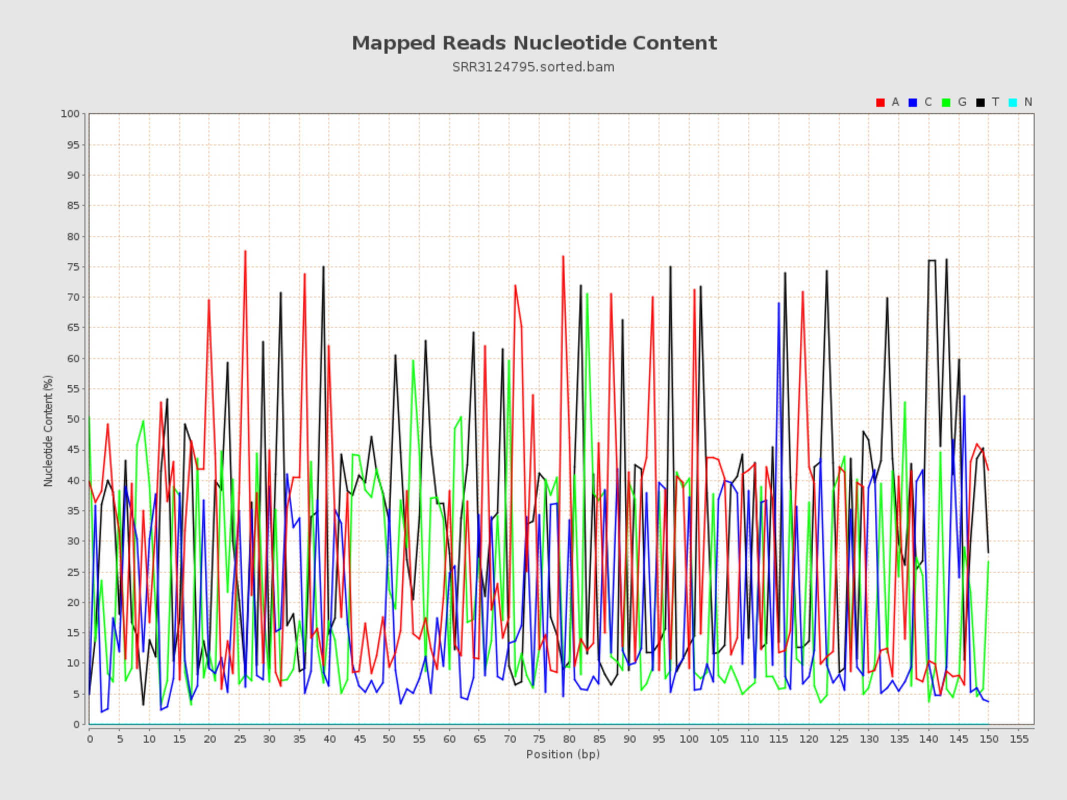
6. Results : Genome Fraction Coverage



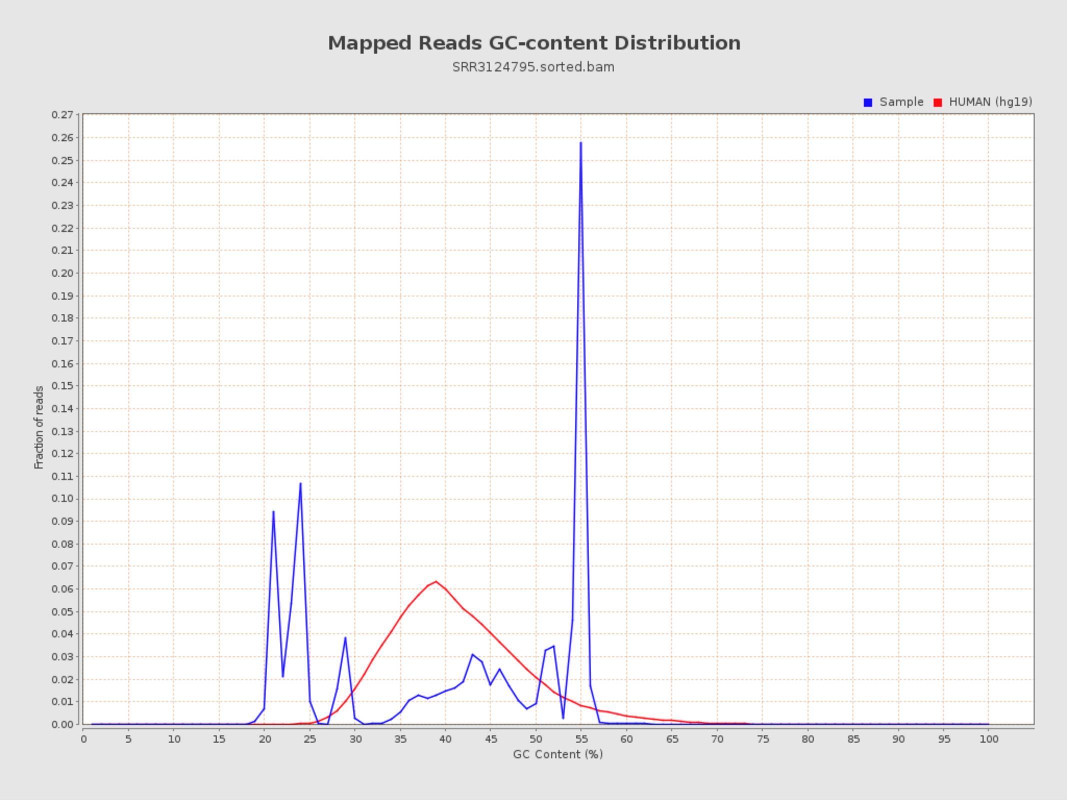
7. Results : Duplication Rate Histogram



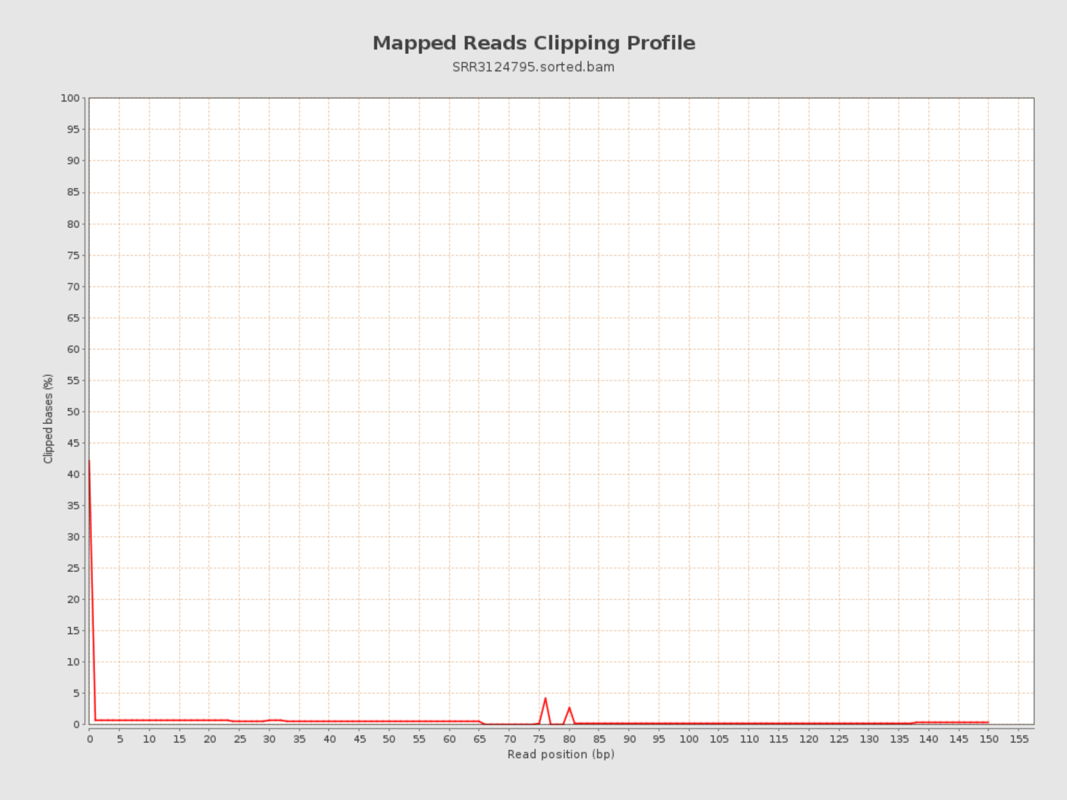
8. Results : Mapped Reads Nucleotide Content



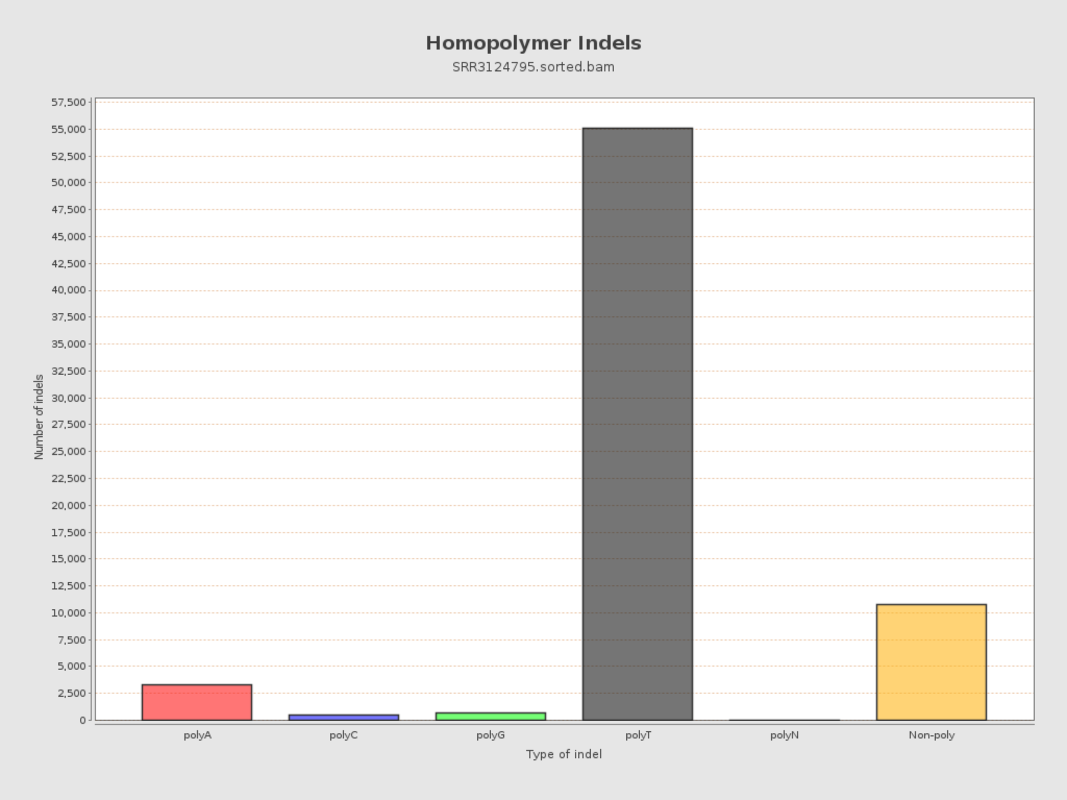
9. Results : Mapped Reads GC-content Distribution



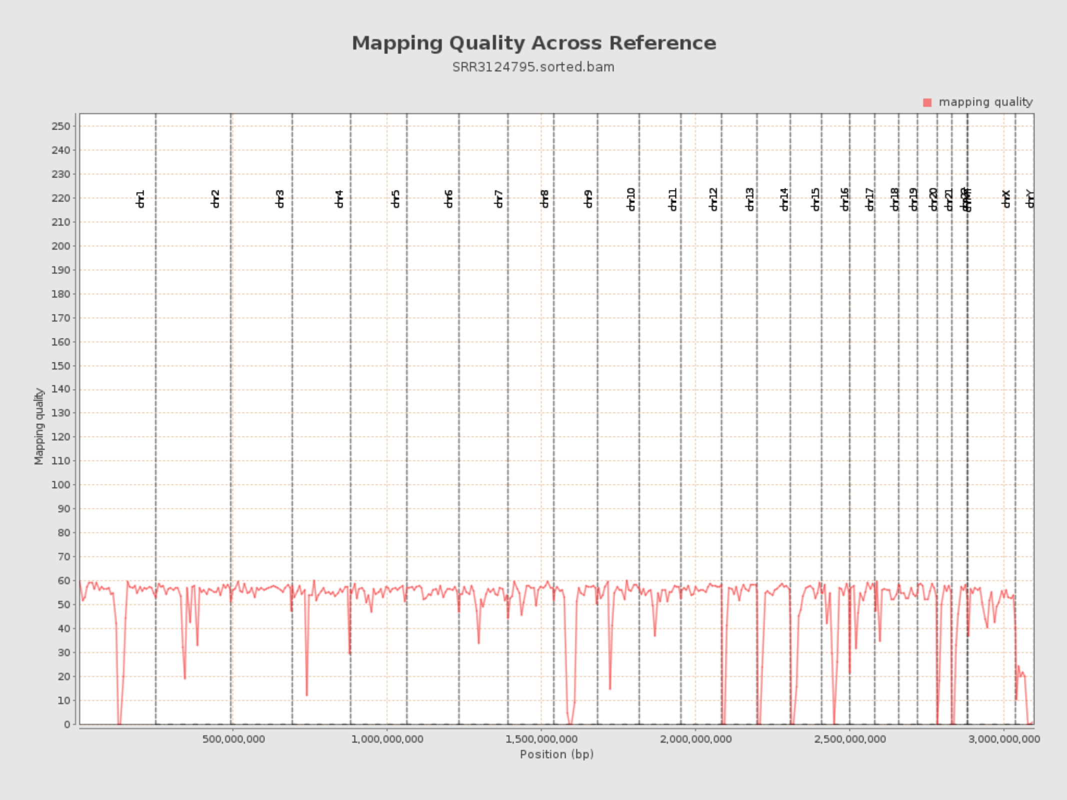
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram