Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:46:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124793.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_SRR3124793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124793.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:46:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,663
Mapped reads	404,446 / 98.01%
Unmapped reads	8,217 / 1.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	106,665 / 25.85%
Read min/max/mean length	30 / 151 / 167.28
Duplicated reads (estimated)	442,918 / 107.33%
Duplication rate	1.92%
Clipped reads	380,206 / 92.13%

2.2. ACGT Content

Number/percentage of A's	17,018,263 / 29.37%
Number/percentage of C's	10,731,861 / 18.52%
Number/percentage of T's	17,527,765 / 30.25%
Number/percentage of G's	12,671,517 / 21.87%
Number/percentage of N's	0 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0187

Standard Deviation	30.4044

2.4. Mapping Quality

Mean Mapping Quality	50.9

2.5. Mismatches and indels

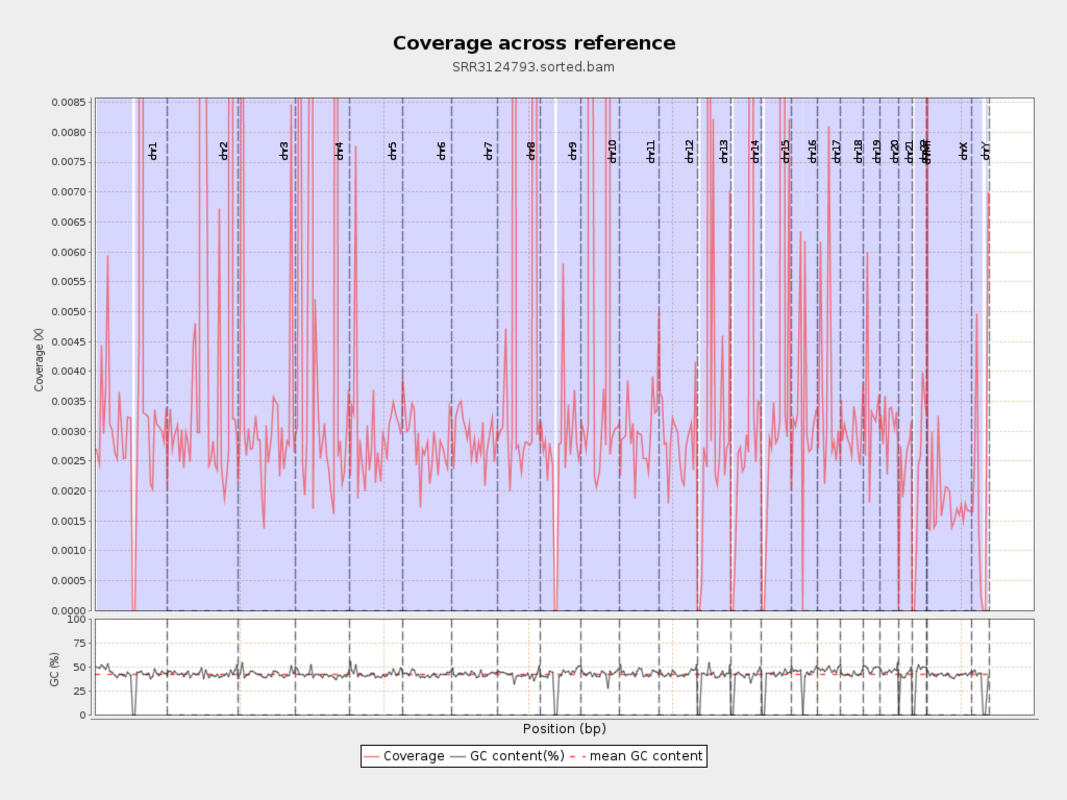
General error rate	1%
Mismatches	571,126
Insertions	5,893
Mapped reads with at least one insertion	1.41%
Deletions	32,740
Mapped reads with at least one deletion	8.01%
Homopolymer indels	68.6%

2.6. Chromosome stats

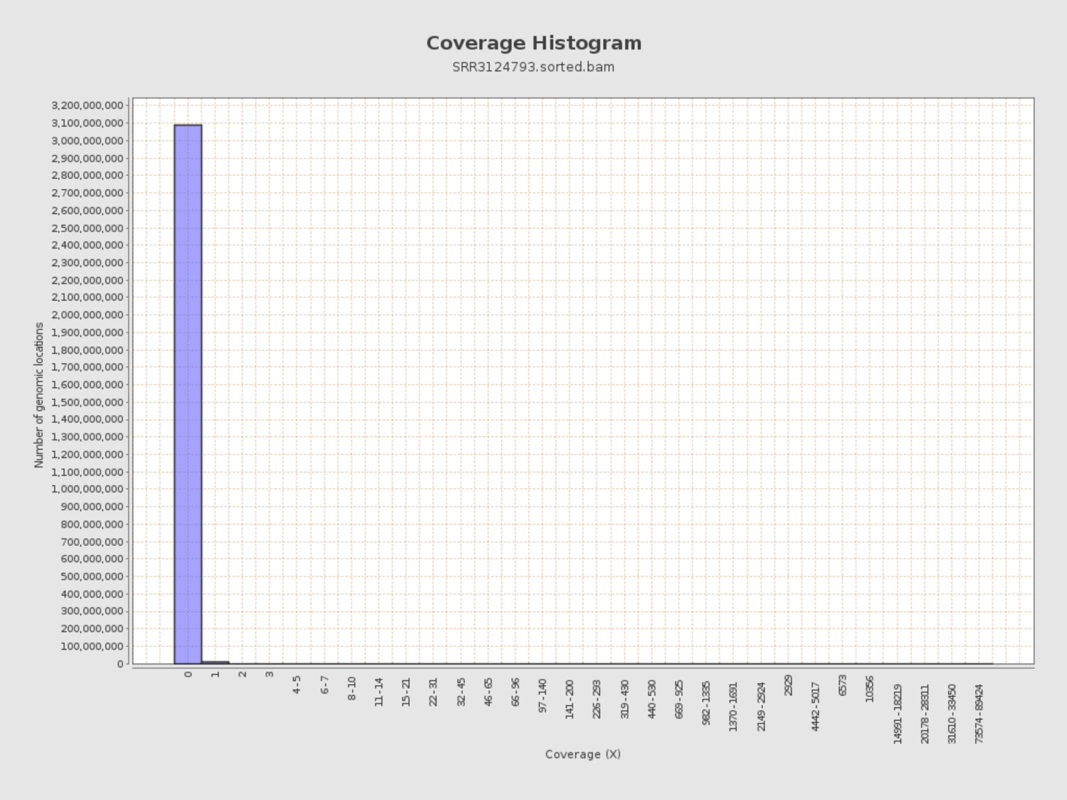
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10293683	0.0413	35.7524
chr2	243199373	6767703	0.0278	23.9016
chr3	198022430	705830	0.0036	0.8474
chr4	191154276	1224708	0.0064	2.0383
chr5	180915260	549516	0.003	0.1097
chr6	171115067	479473	0.0028	0.0602
chr7	159138663	457620	0.0029	0.0887

chr8	146364022	948059	0.0065	2.3295
chr9	141213431	376346	0.0027	0.1906
chr10	135534747	31925919	0.2356	133.1205
chr11	135006516	397466	0.0029	0.0734
chr12	133851895	383350	0.0029	0.055
chr13	115169878	443429	0.0039	0.785
chr14	107349540	467868	0.0044	1.4921
chr15	102531392	711240	0.0069	1.7713
chr16	90354753	296029	0.0033	0.0844
chr17	81195210	292978	0.0036	0.31
chr18	78077248	229529	0.0029	0.0645
chr19	59128983	200825	0.0034	0.1919
chr20	63025520	196015	0.0031	0.0687
chr21	48129895	112532	0.0023	0.0515
chr22	51304566	110214	0.0021	0.0951
chrMT	16571	5939	0.3584	0.6052
chrX	155270560	279215	0.0018	0.0871
chrY	59373566	132576	0.0022	0.0876

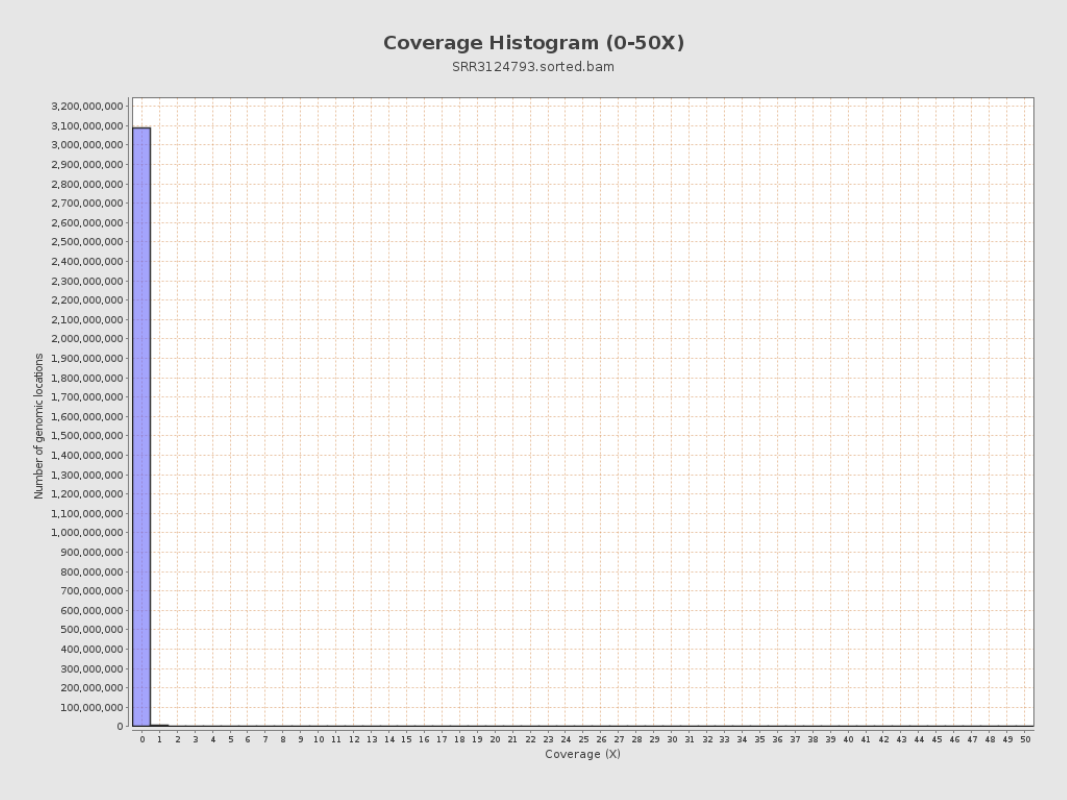
3. Results : Coverage across reference



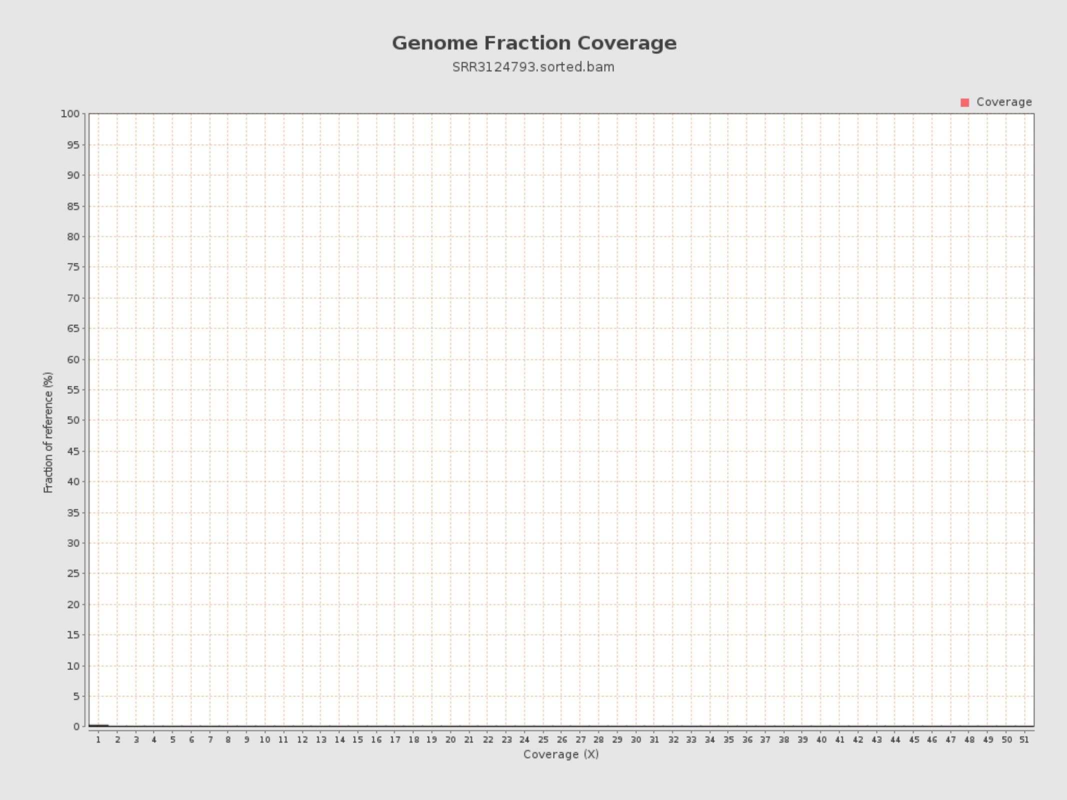
4. Results : Coverage Histogram



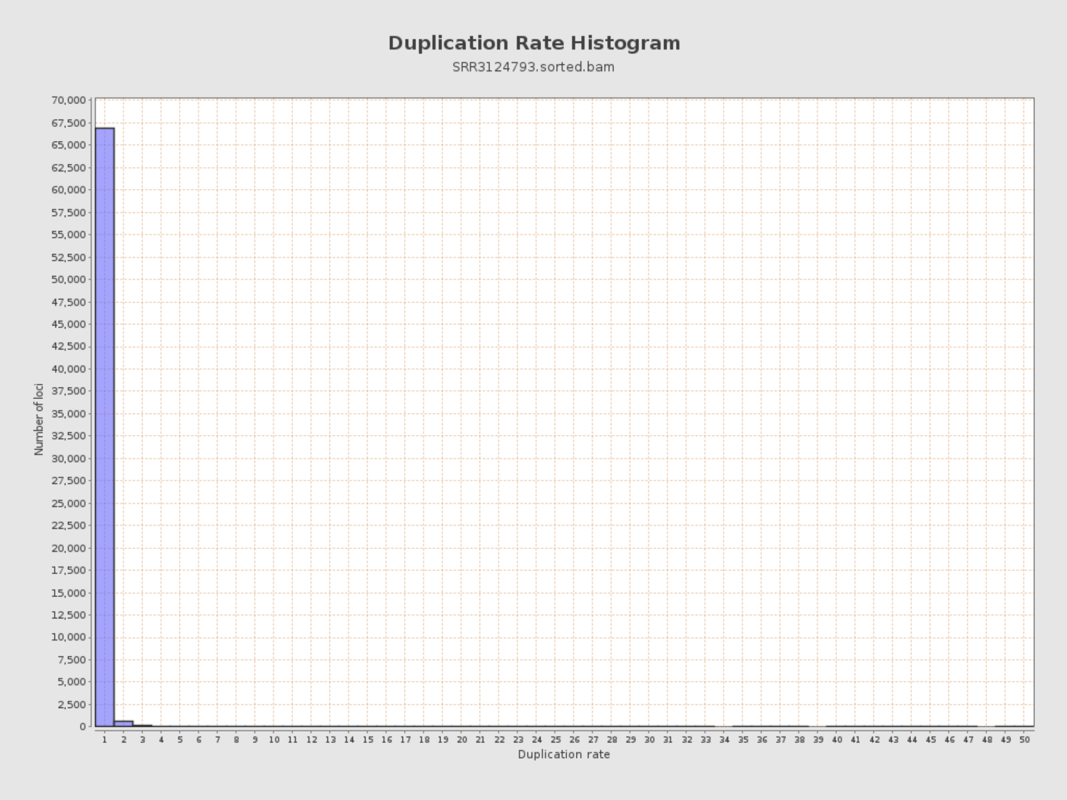
5. Results : Coverage Histogram (0-50X)



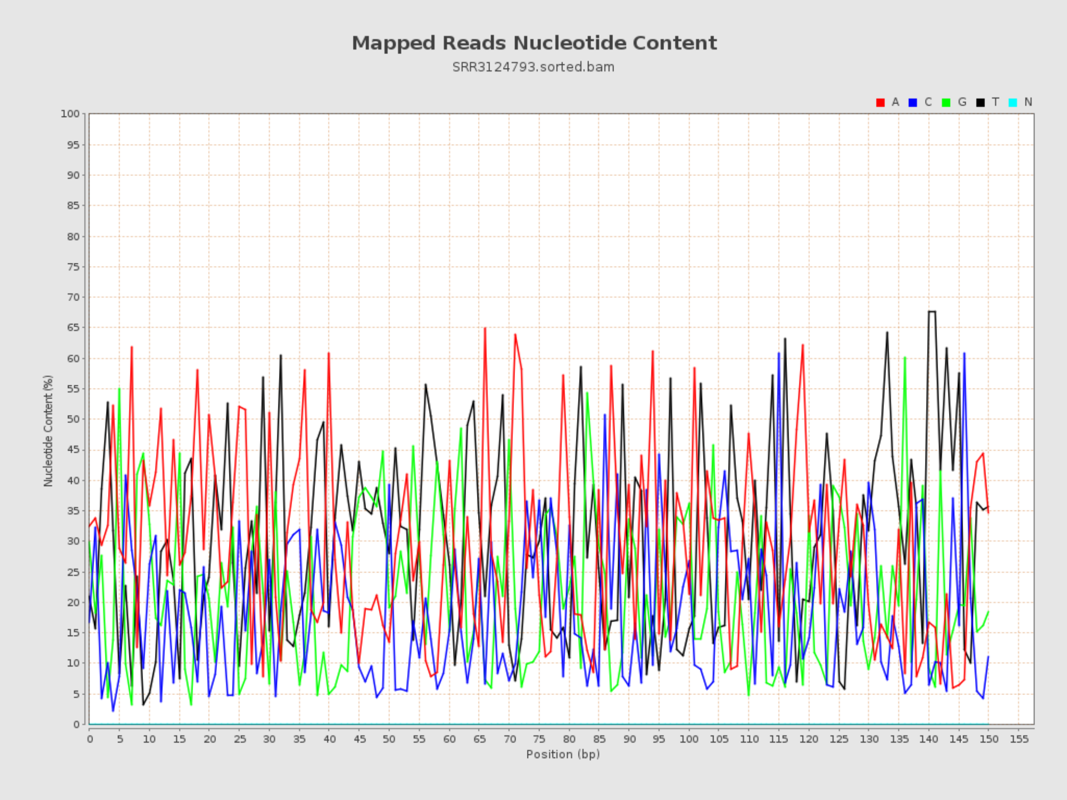
6. Results : Genome Fraction Coverage



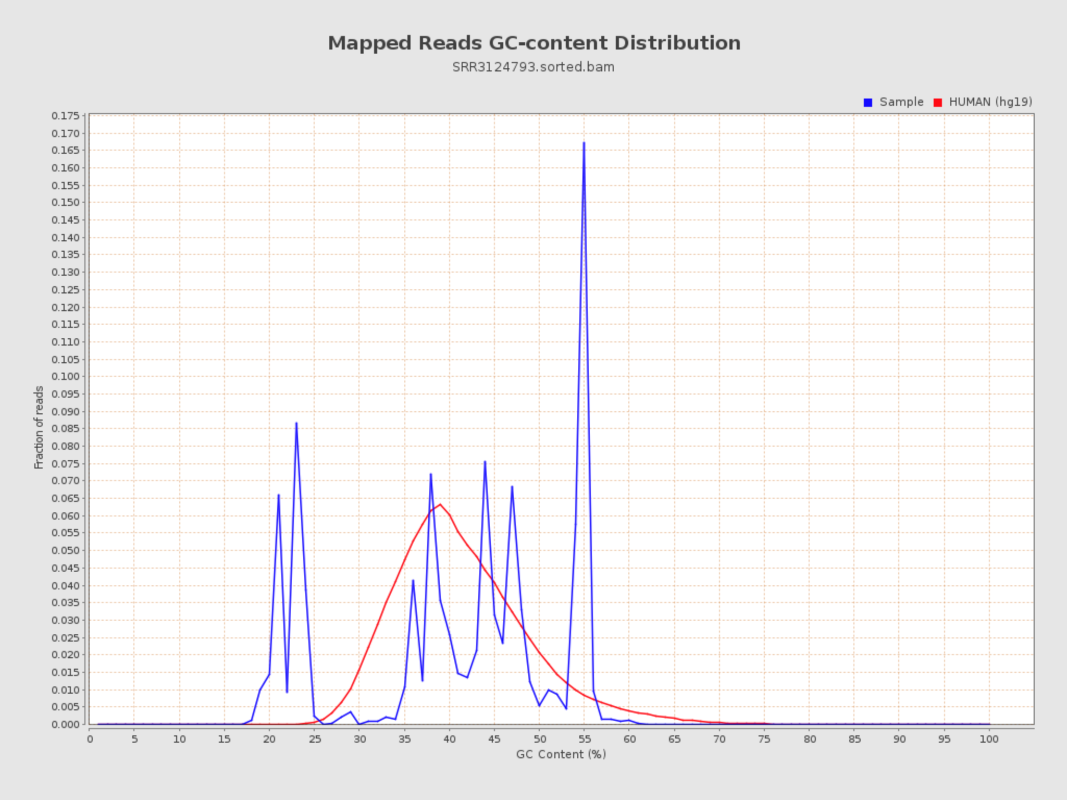
7. Results : Duplication Rate Histogram



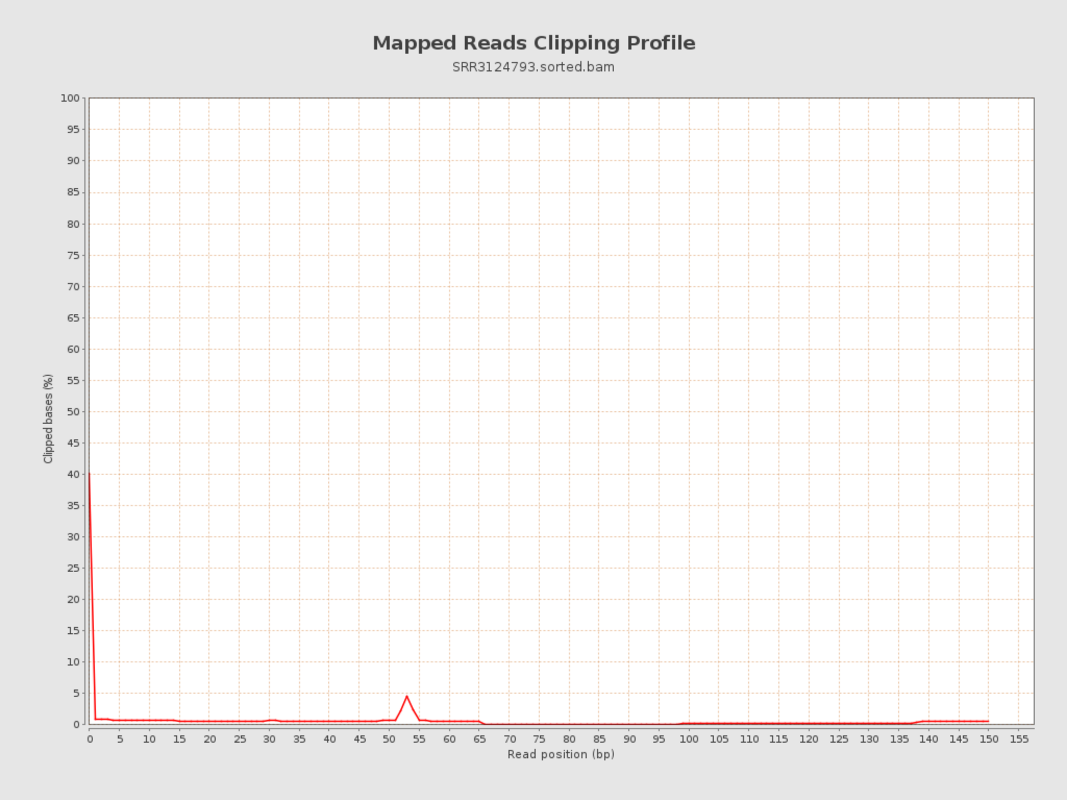
8. Results : Mapped Reads Nucleotide Content



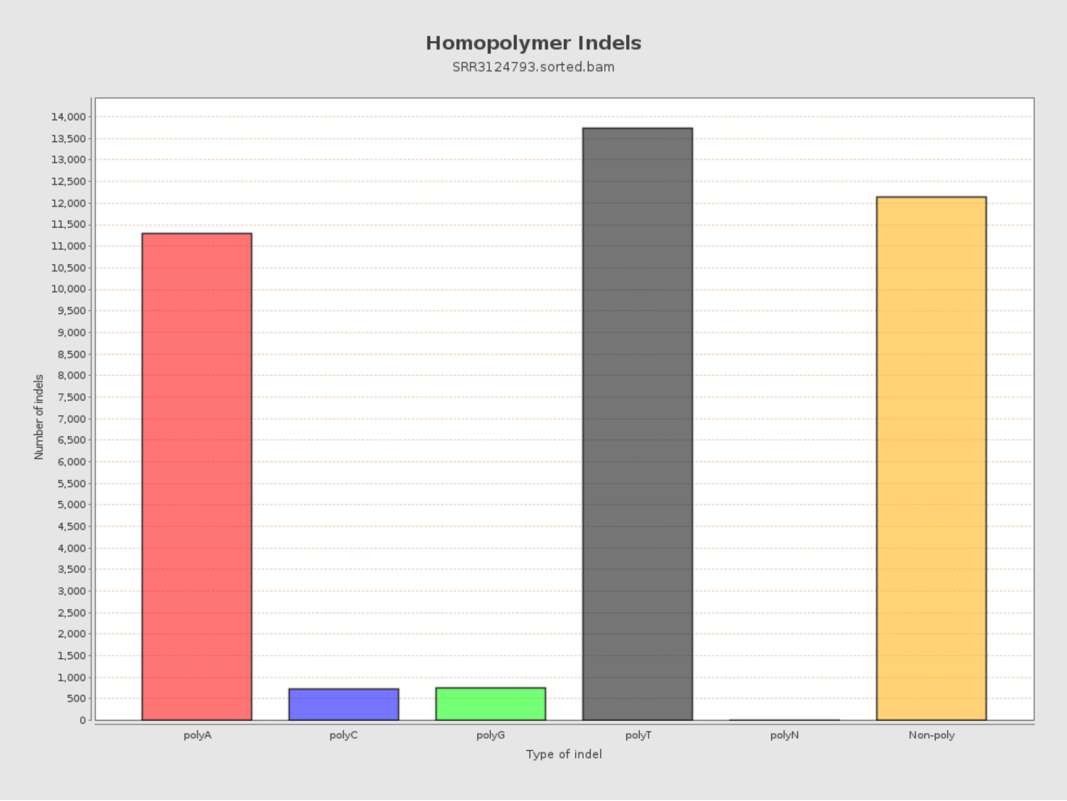
9. Results : Mapped Reads GC-content Distribution



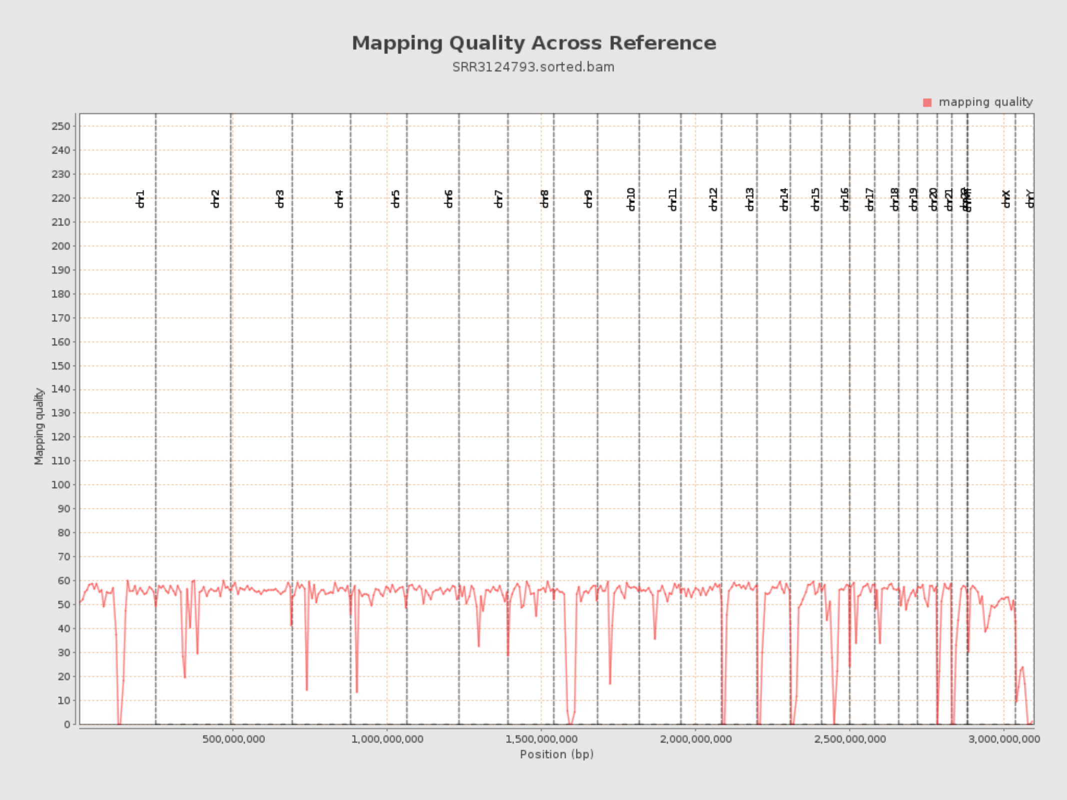
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram