Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084795.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_SRR3084795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:09:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,866,618
Mapped reads	1,696,207 / 90.87%
Unmapped reads	170,411 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,256 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	82,439 / 4.42%
Duplication rate	4.29%
Clipped reads	726,281 / 38.91%

2.2. ACGT Content

Number/percentage of A's	31,358,852 / 27.55%
Number/percentage of C's	21,194,603 / 18.62%
Number/percentage of T's	35,993,207 / 31.62%
Number/percentage of G's	25,267,299 / 22.2%
Number/percentage of N's	16,236 / 0.01%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.2587

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

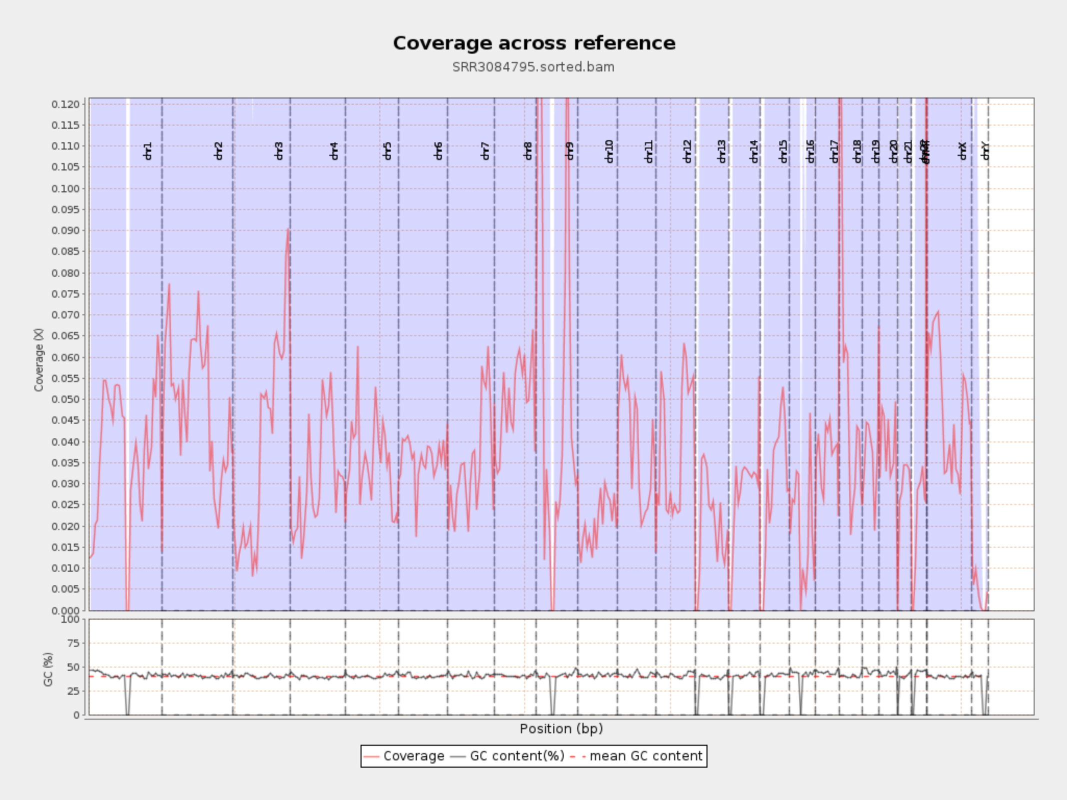
General error rate	0.74%
Mismatches	829,696
Insertions	9,010
Mapped reads with at least one insertion	0.53%
Deletions	26,321
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.39%

2.6. Chromosome stats

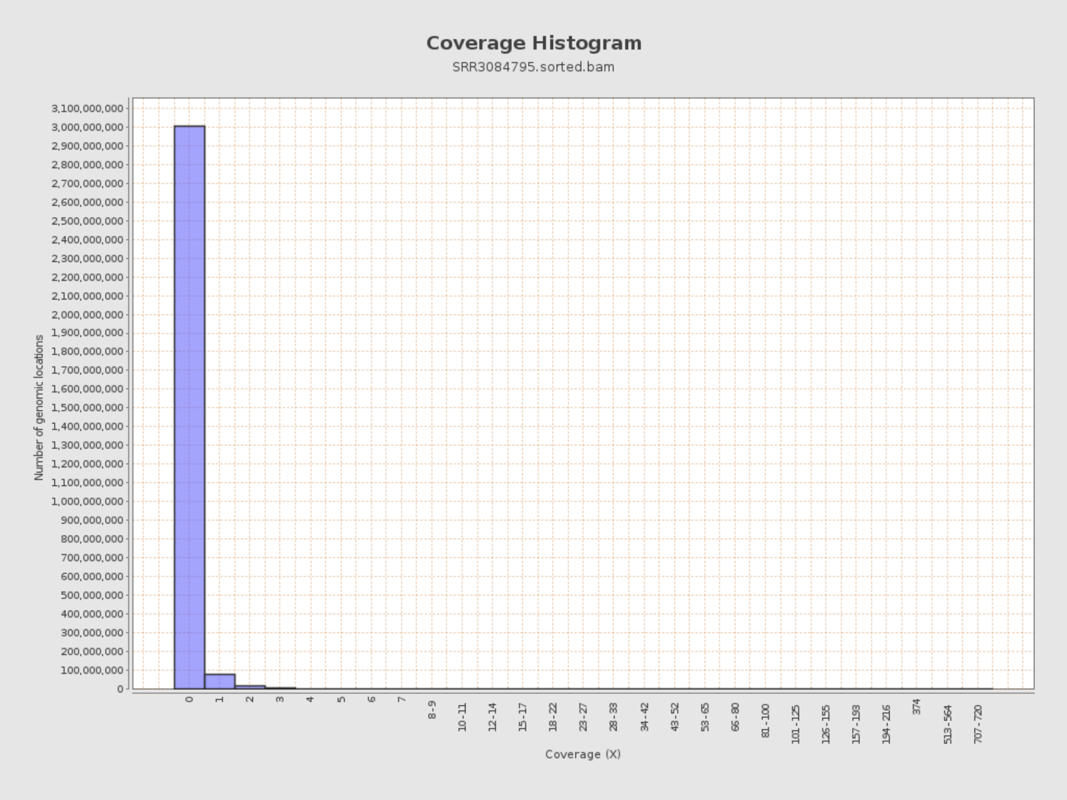
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9436525	0.0379	0.2796
chr2	243199373	12031434	0.0495	0.4063
chr3	198022430	7649386	0.0386	0.2371
chr4	191154276	6051291	0.0317	0.2147
chr5	180915260	6466694	0.0357	0.2277
chr6	171115067	6121841	0.0358	0.2407
chr7	159138663	5565608	0.035	0.2317

chr8	146364022	7265572	0.0496	0.2939
chr9	141213431	7919127	0.0561	0.3134
chr10	135534747	2815159	0.0208	0.1796
chr11	135006516	5285645	0.0392	0.261
chr12	133851895	5235390	0.0391	0.2373
chr13	115169878	2267121	0.0197	0.1702
chr14	107349540	2850912	0.0266	0.1965
chr15	102531392	3058125	0.0298	0.21
chr16	90354753	1775431	0.0196	0.1709
chr17	81195210	3023281	0.0372	0.2324
chr18	78077248	4163624	0.0533	0.3579
chr19	59128983	2222671	0.0376	0.2557
chr20	63025520	2492058	0.0395	0.2419
chr21	48129895	1342490	0.0279	0.2031
chr22	51304566	1060883	0.0207	0.1687
chrMT	16571	13852	0.8359	1.1009
chrX	155270560	7518645	0.0484	0.2699
chrY	59373566	240587	0.0041	0.085

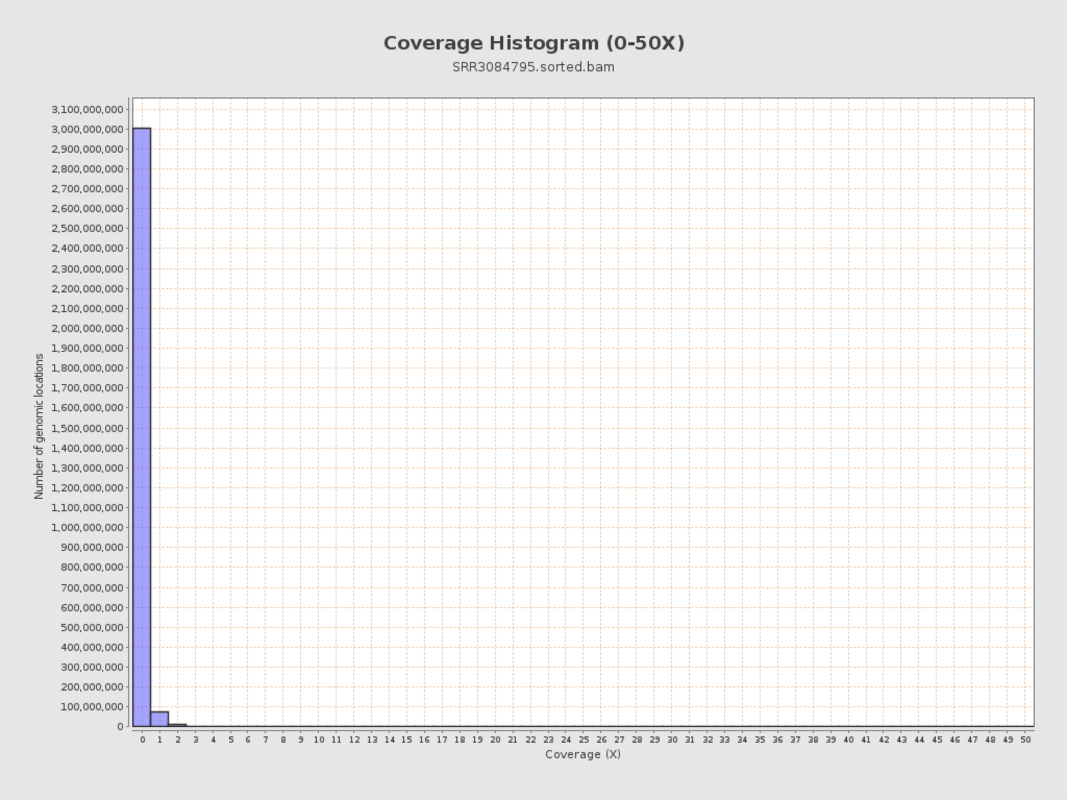
3. Results : Coverage across reference



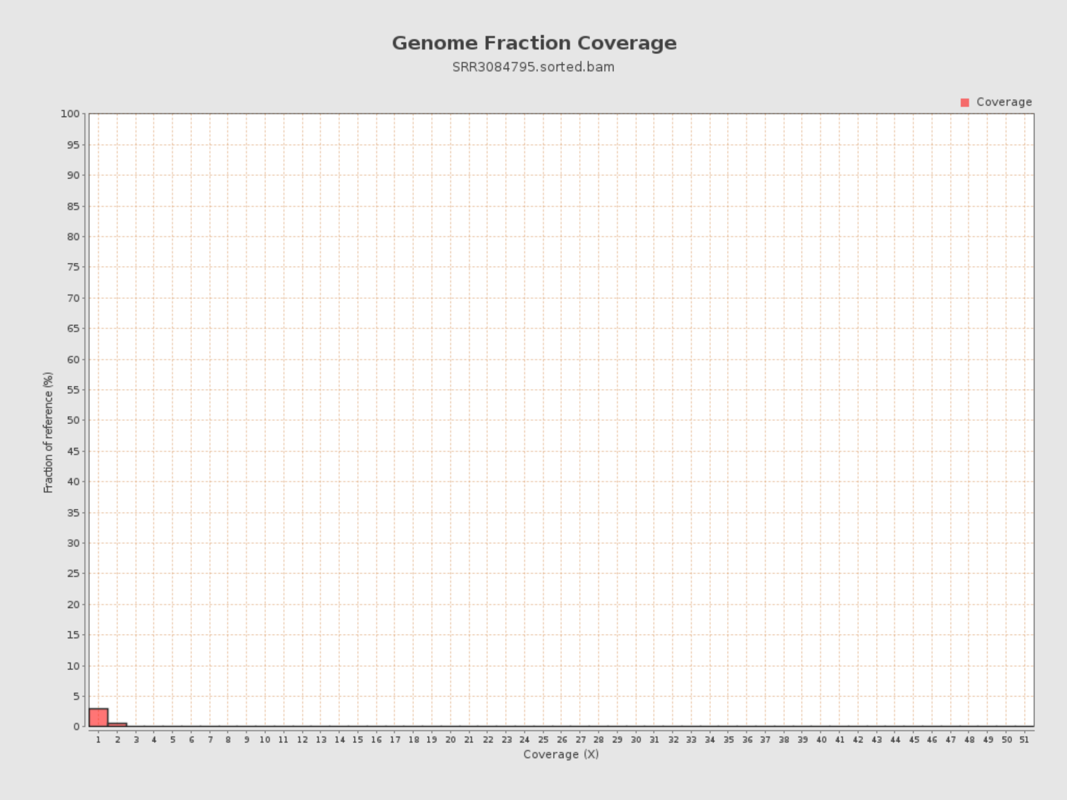
4. Results : Coverage Histogram



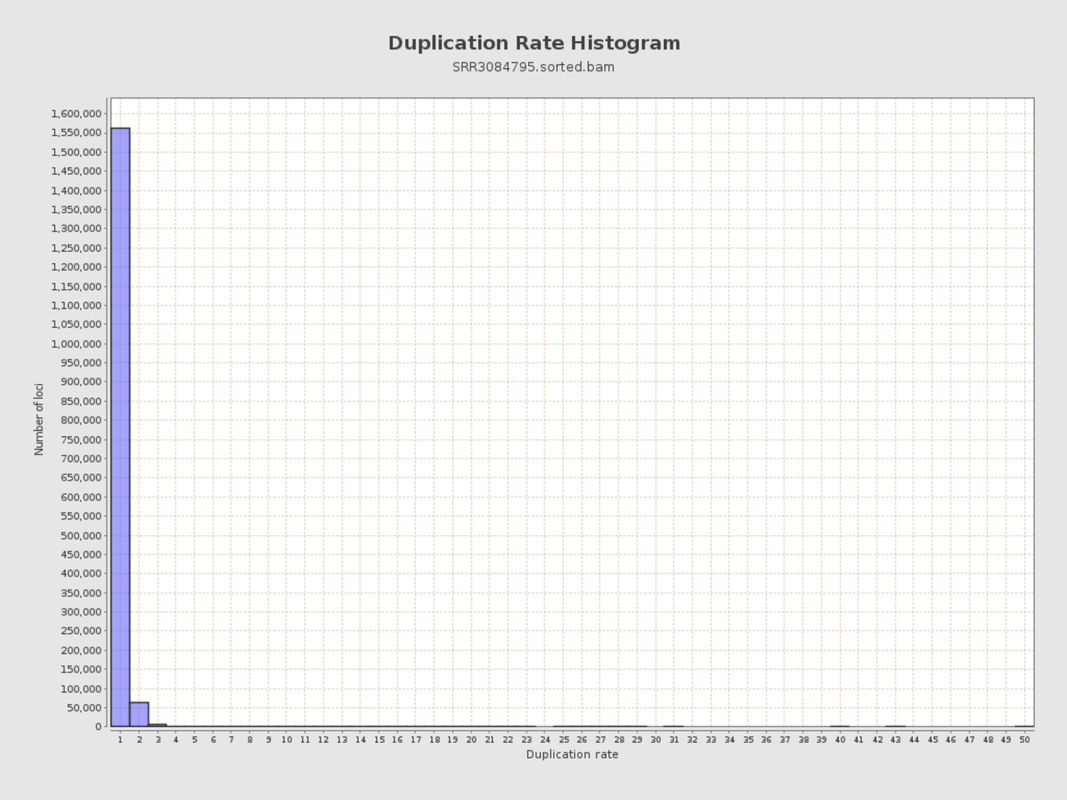
5. Results : Coverage Histogram (0-50X)



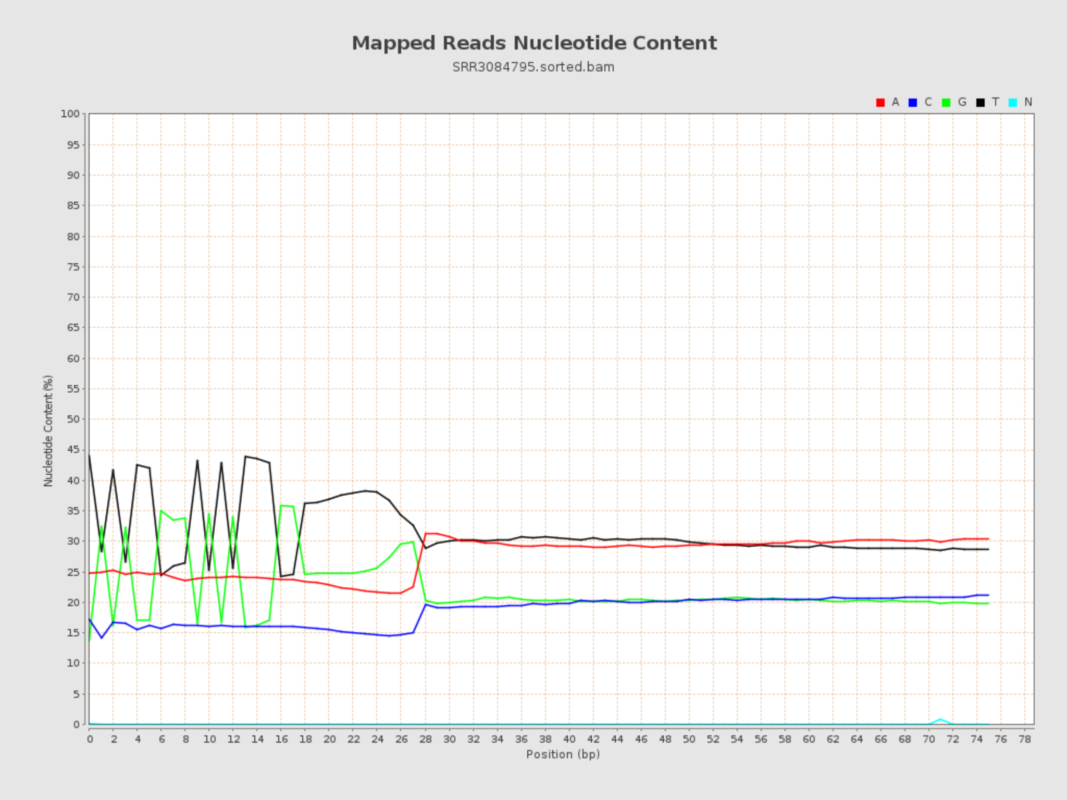
6. Results : Genome Fraction Coverage



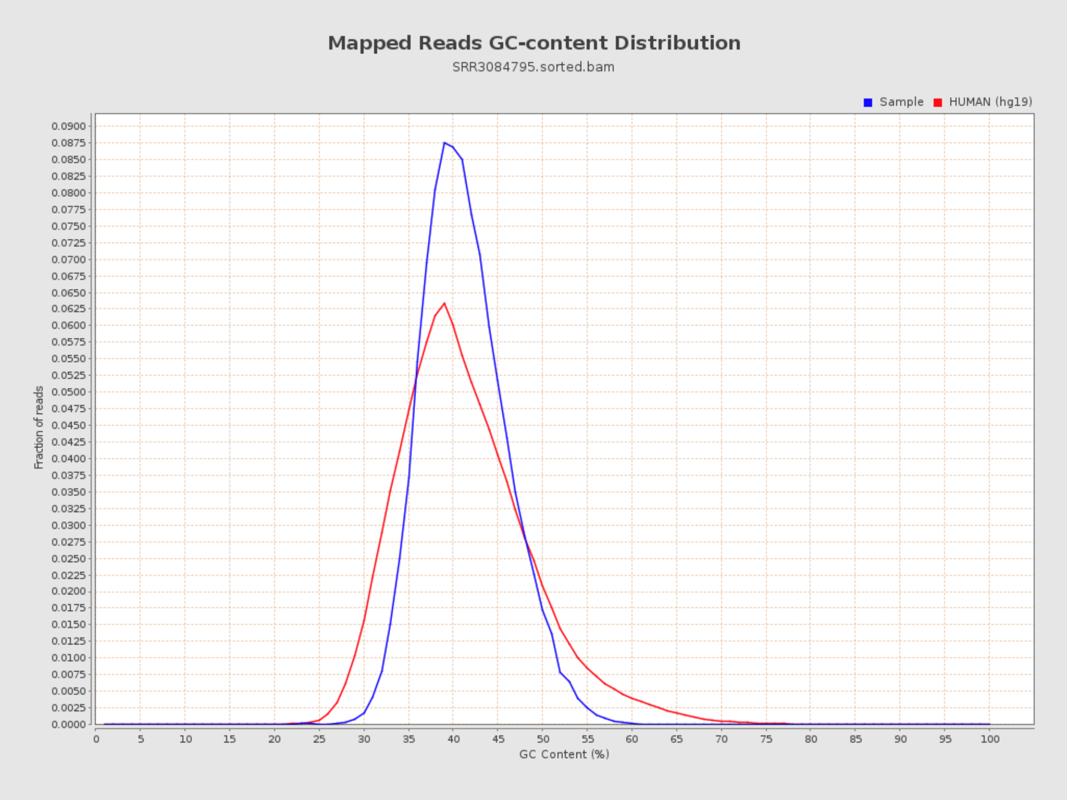
7. Results : Duplication Rate Histogram



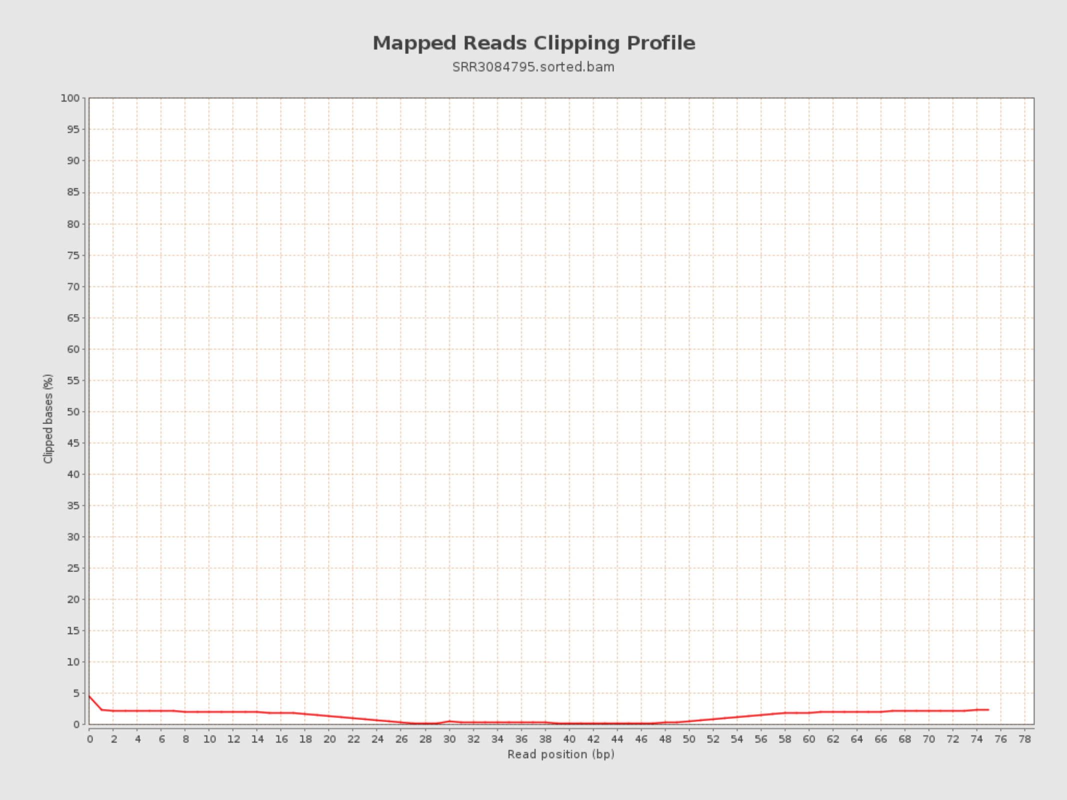
8. Results : Mapped Reads Nucleotide Content



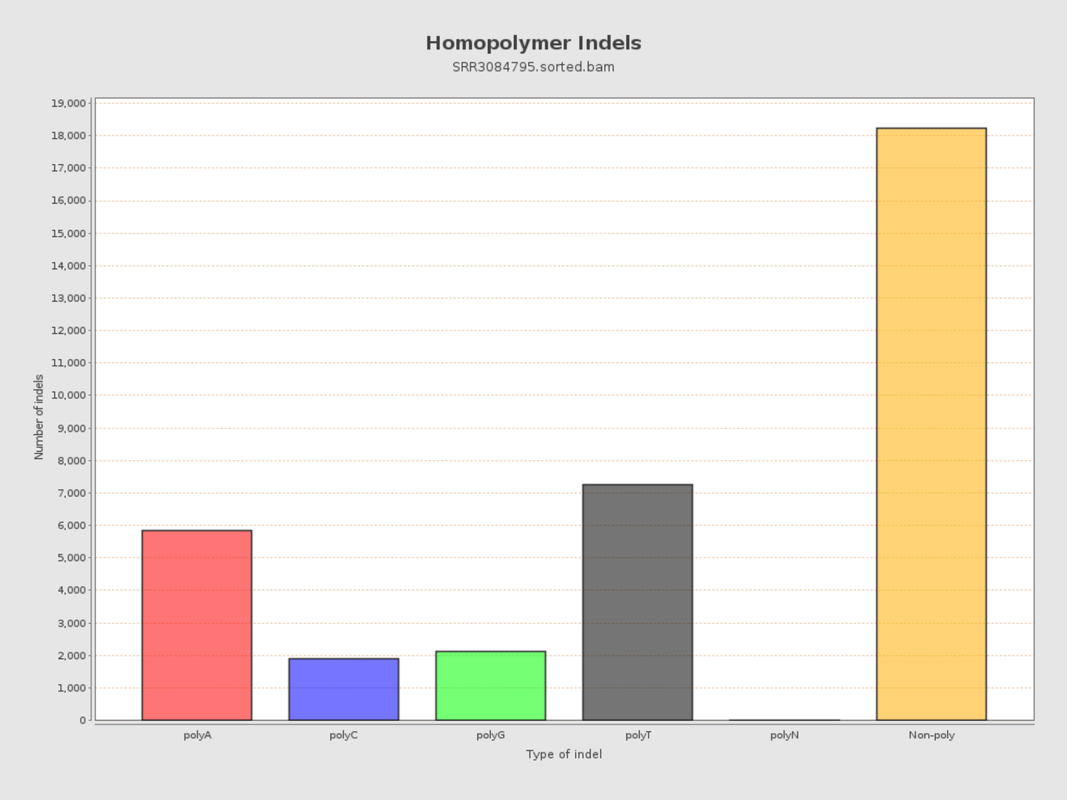
9. Results : Mapped Reads GC-content Distribution



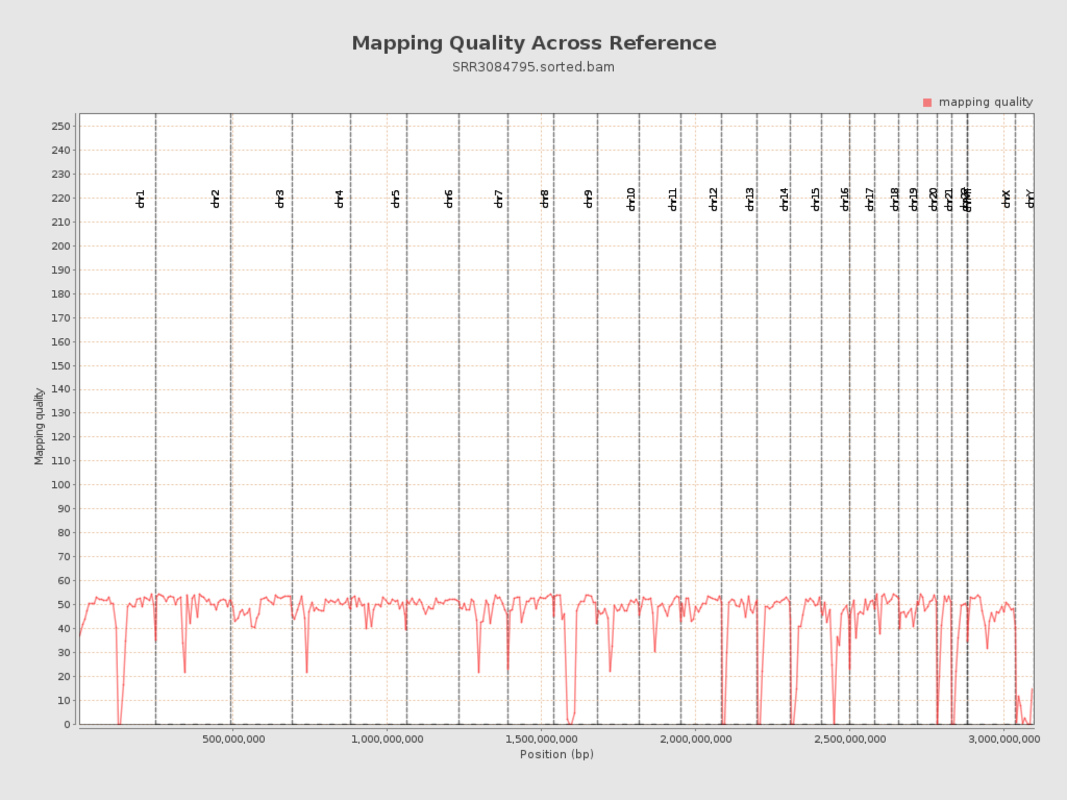
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram