Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:17:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084797.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_SRR3084797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:17:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,823,882
Mapped reads	1,637,109 / 89.76%
Unmapped reads	186,773 / 10.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,765 / 1.19%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	72,473 / 3.97%
Duplication rate	3.74%
Clipped reads	750,573 / 41.15%

2.2. ACGT Content

Number/percentage of A's	29,845,165 / 27.38%
Number/percentage of C's	20,451,391 / 18.76%
Number/percentage of T's	34,162,409 / 31.35%
Number/percentage of G's	24,511,787 / 22.49%
Number/percentage of N's	16,354 / 0.02%
GC Percentage	41.26%

2.3. Coverage

Mean	0.0352

Standard Deviation	0.2711

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

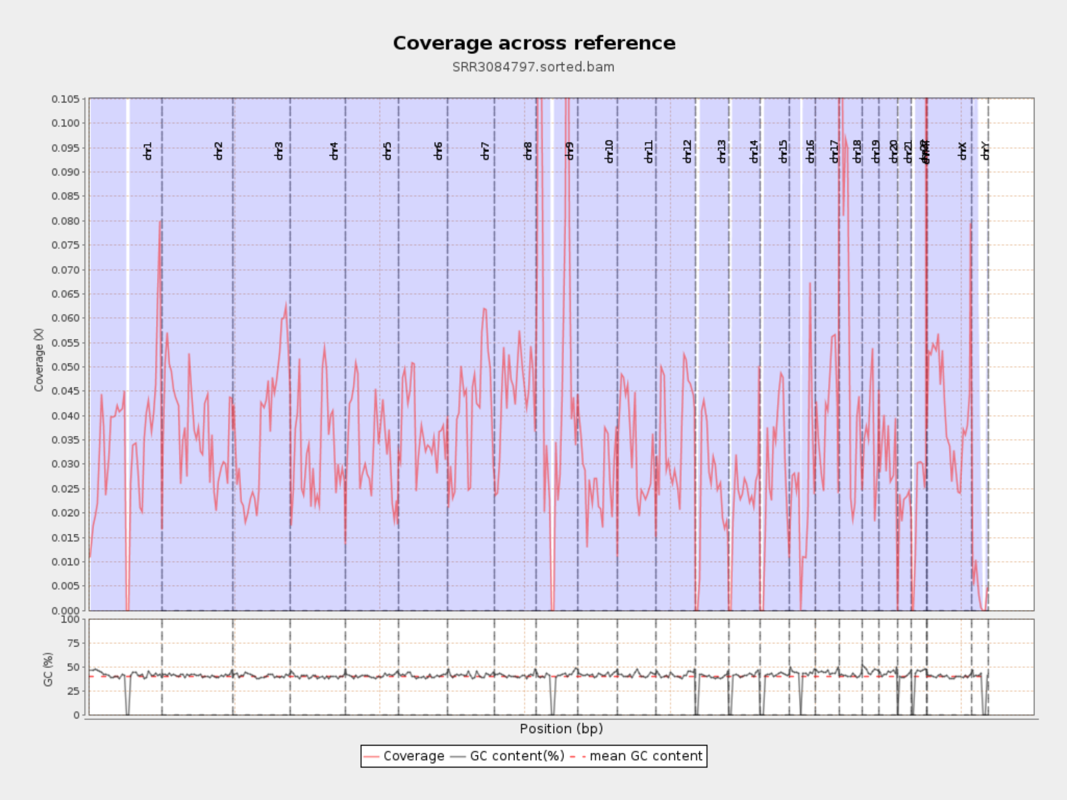
General error rate	0.79%
Mismatches	844,133
Insertions	8,949
Mapped reads with at least one insertion	0.54%
Deletions	25,426
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.63%

2.6. Chromosome stats

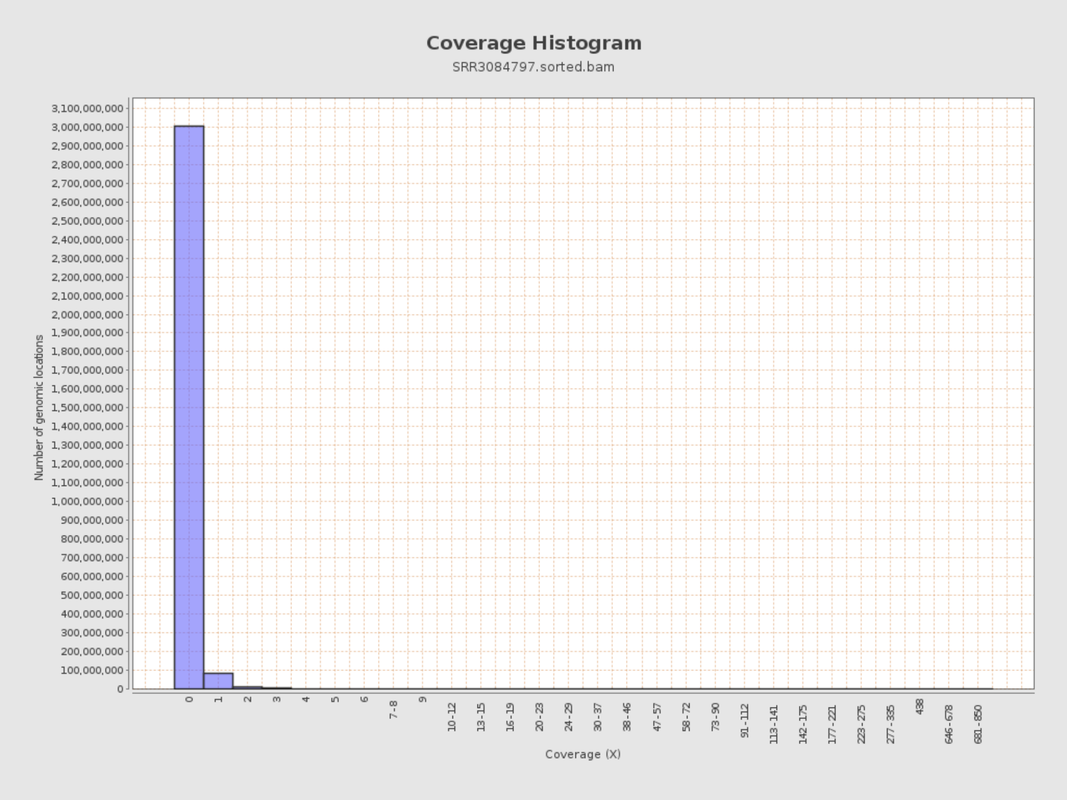
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8396670	0.0337	0.3144
chr2	243199373	9076922	0.0373	0.4507
chr3	198022430	7417537	0.0375	0.2211
chr4	191154276	6233499	0.0326	0.2101
chr5	180915260	6116938	0.0338	0.2112
chr6	171115067	6379798	0.0373	0.2396
chr7	159138663	6578198	0.0413	0.2756

chr8	146364022	6443055	0.044	0.334
chr9	141213431	7970905	0.0564	0.3294
chr10	135534747	3718574	0.0274	0.2129
chr11	135006516	4388836	0.0325	0.2346
chr12	133851895	4921295	0.0368	0.2233
chr13	115169878	2742729	0.0238	0.1778
chr14	107349540	2346374	0.0219	0.1783
chr15	102531392	2855574	0.0279	0.1939
chr16	90354753	2287243	0.0253	0.1952
chr17	81195210	3309992	0.0408	0.2343
chr18	78077248	4961171	0.0635	0.4291
chr19	59128983	2163021	0.0366	0.2703
chr20	63025520	2032163	0.0322	0.2105
chr21	48129895	969171	0.0201	0.1676
chr22	51304566	1046299	0.0204	0.1617
chrMT	16571	24027	1.4499	1.4687
chrX	155270560	6411727	0.0413	0.2502
chrY	59373566	236958	0.004	0.091

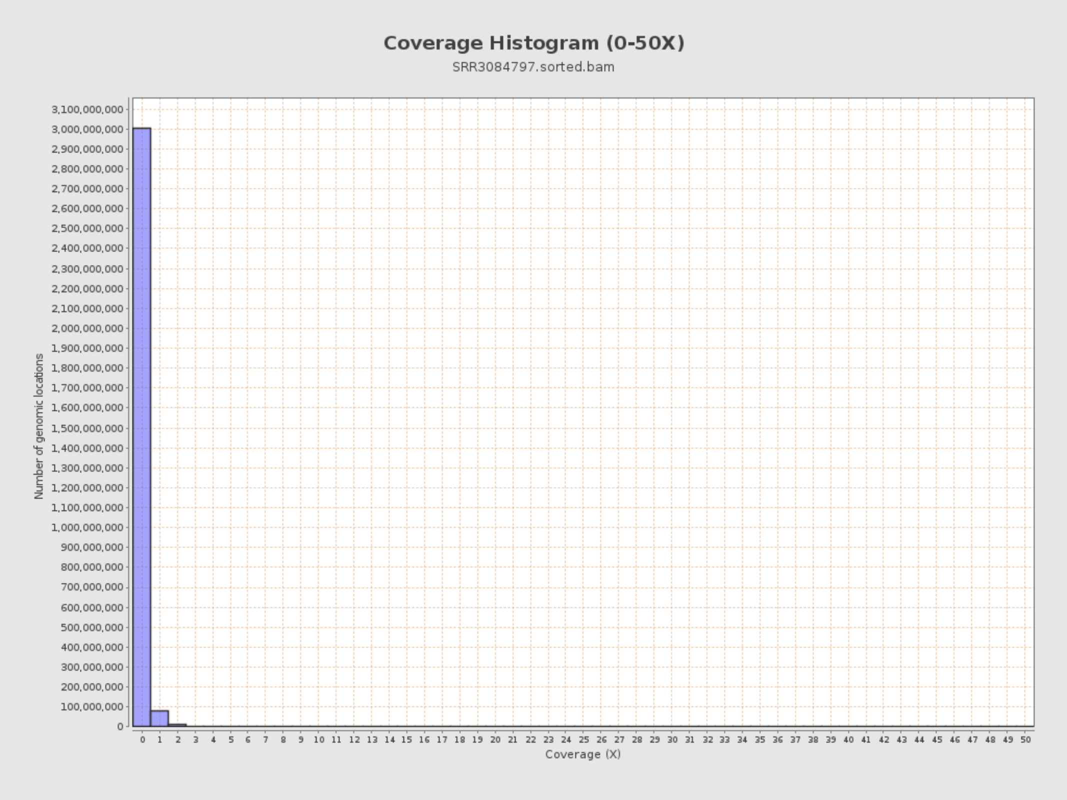
3. Results : Coverage across reference



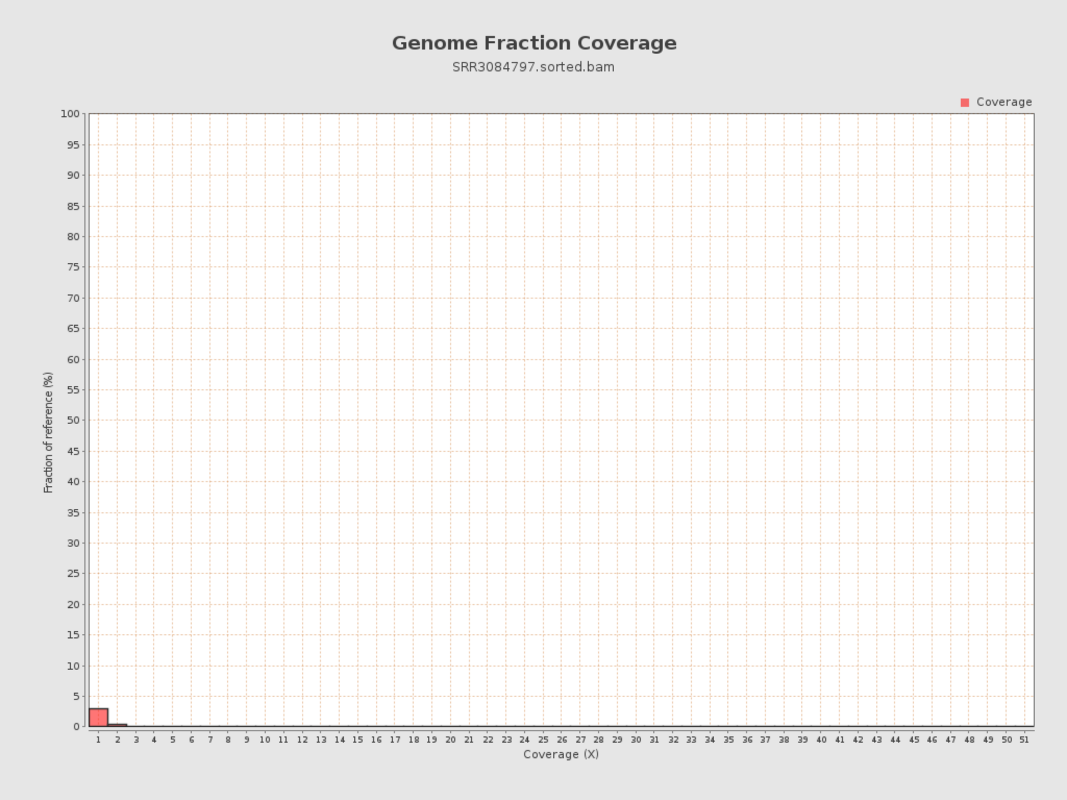
4. Results : Coverage Histogram



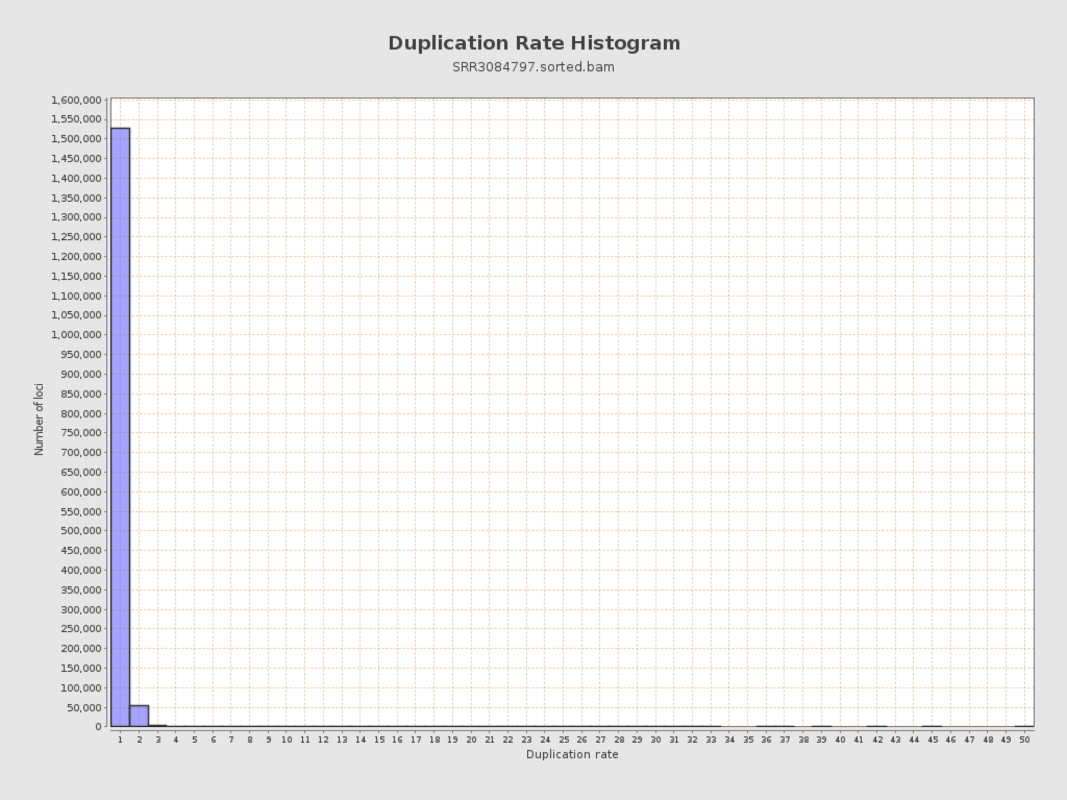
5. Results : Coverage Histogram (0-50X)



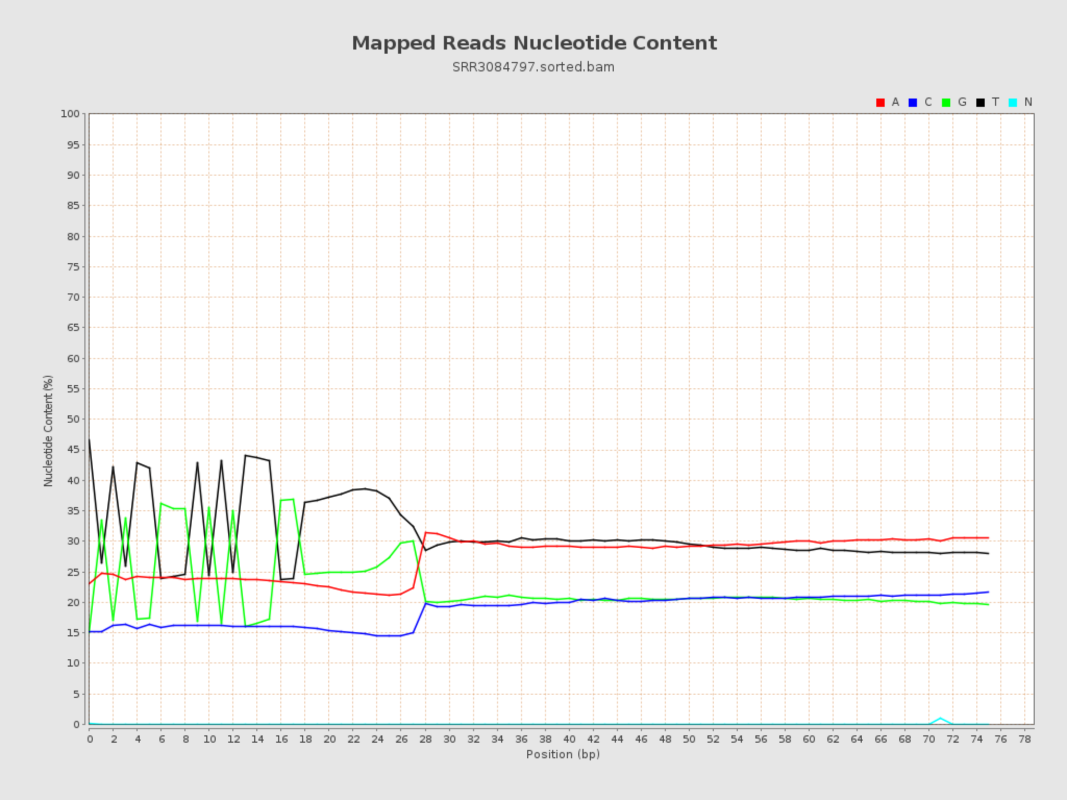
6. Results : Genome Fraction Coverage



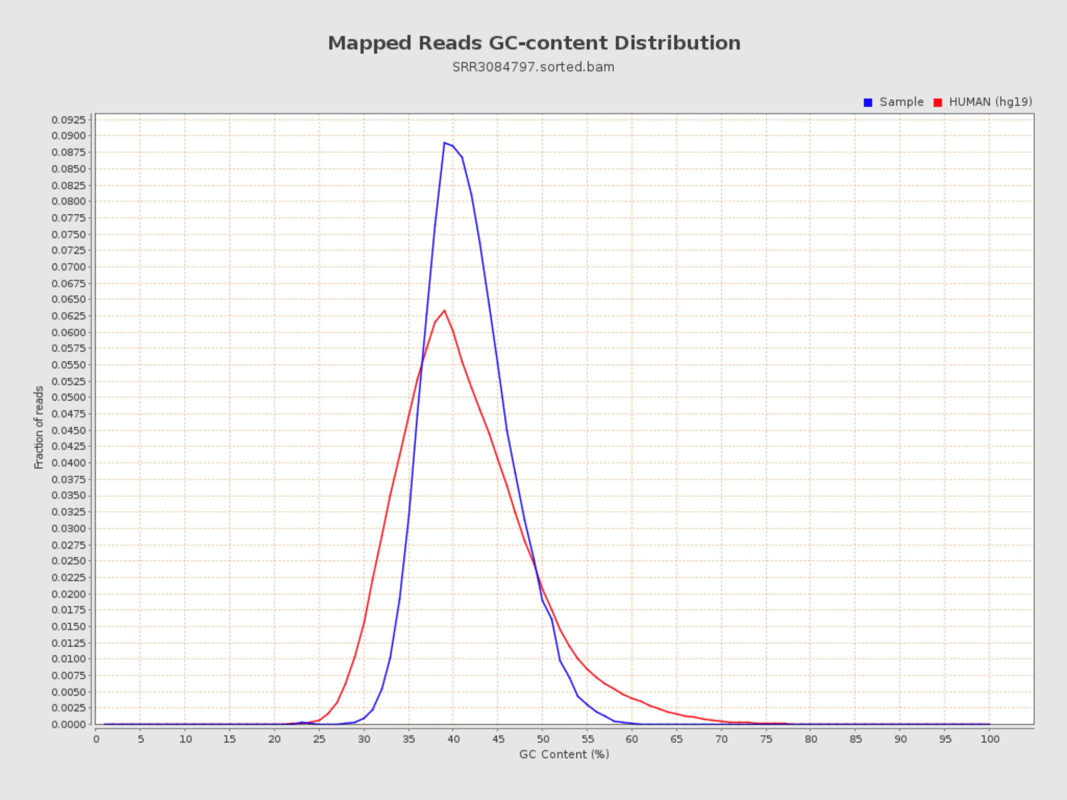
7. Results : Duplication Rate Histogram



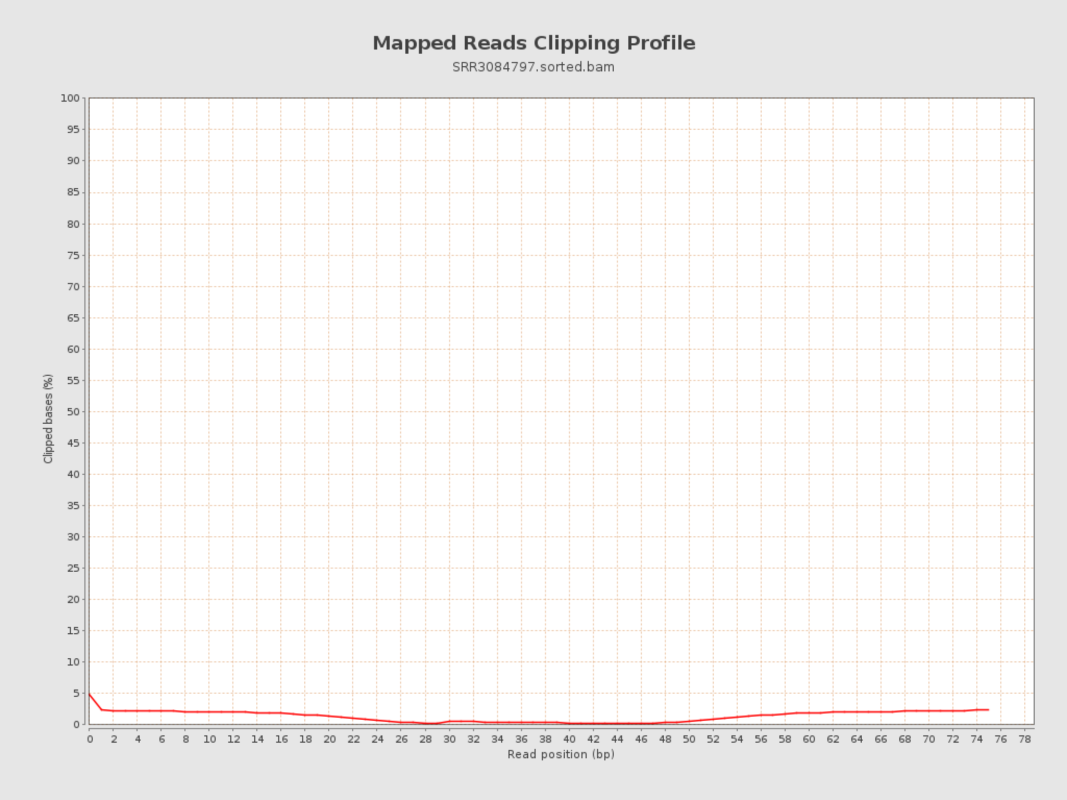
8. Results : Mapped Reads Nucleotide Content



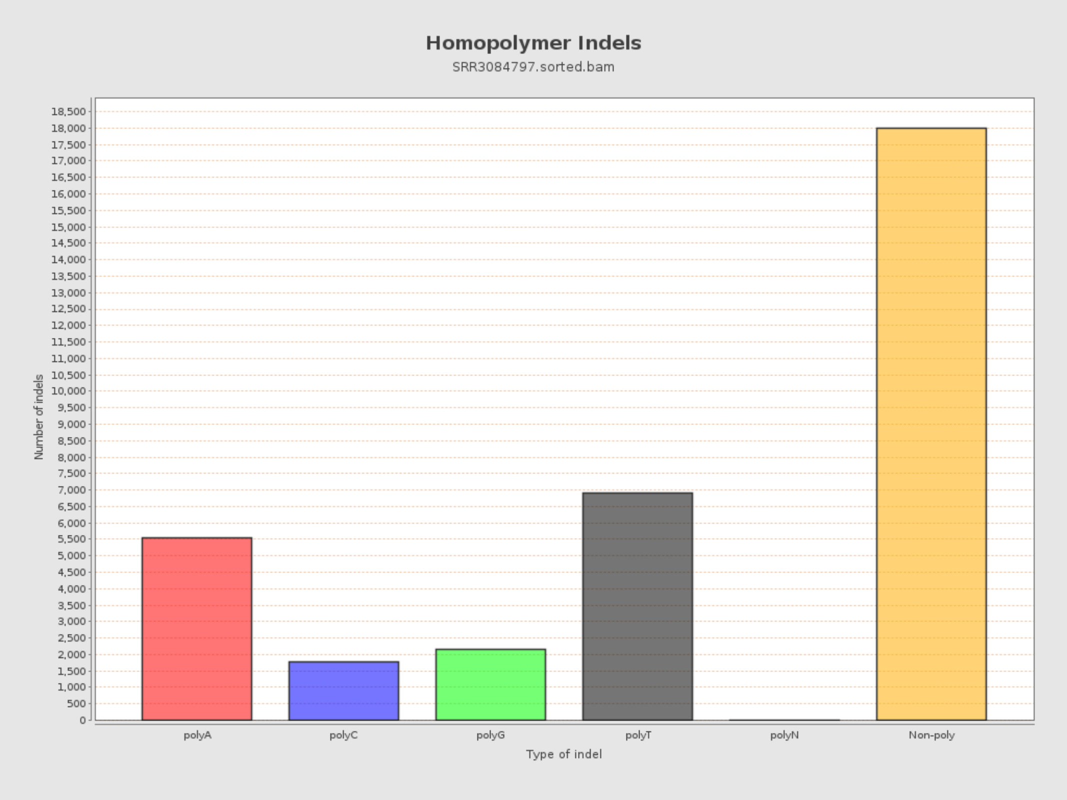
9. Results : Mapped Reads GC-content Distribution



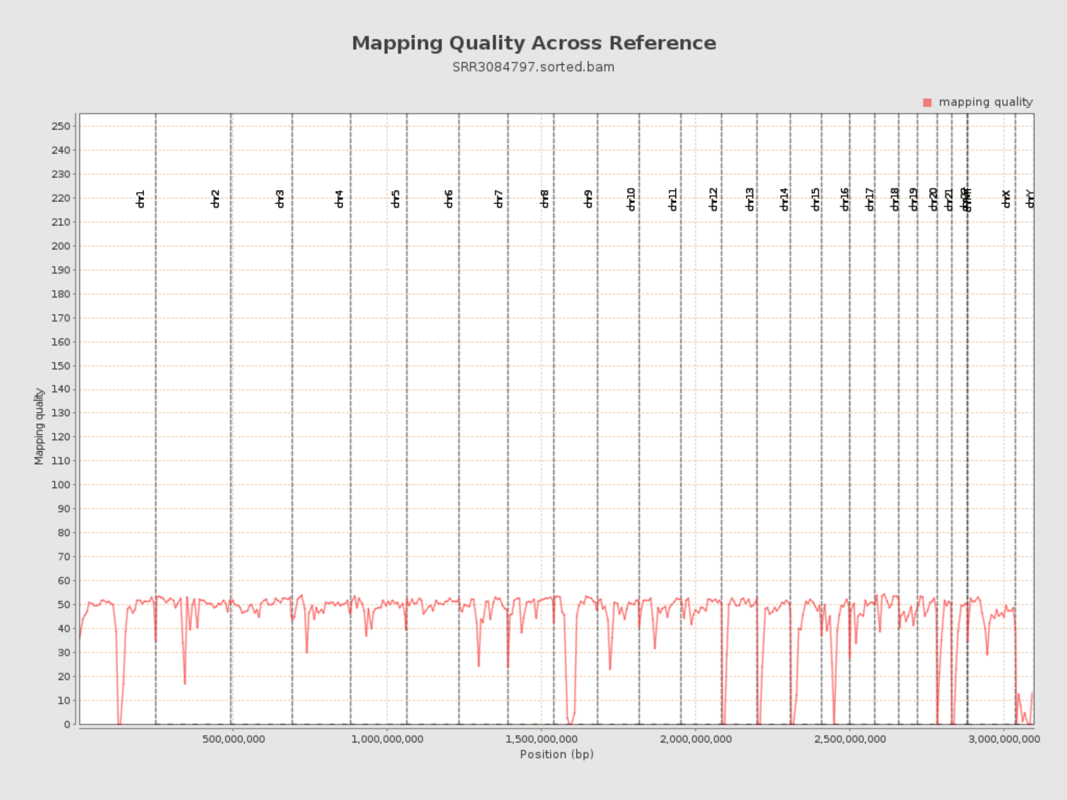
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram