Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:06:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084794.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_SRR3084794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:06:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,324,050
Mapped reads	1,176,241 / 88.84%
Unmapped reads	147,809 / 11.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,321 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	43,263 / 3.27%
Duplication rate	3.12%
Clipped reads	491,382 / 37.11%

2.2. ACGT Content

Number/percentage of A's	22,190,810 / 27.95%
Number/percentage of C's	14,940,794 / 18.82%
Number/percentage of T's	24,767,360 / 31.2%
Number/percentage of G's	17,468,843 / 22%
Number/percentage of N's	26,918 / 0.03%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2194

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

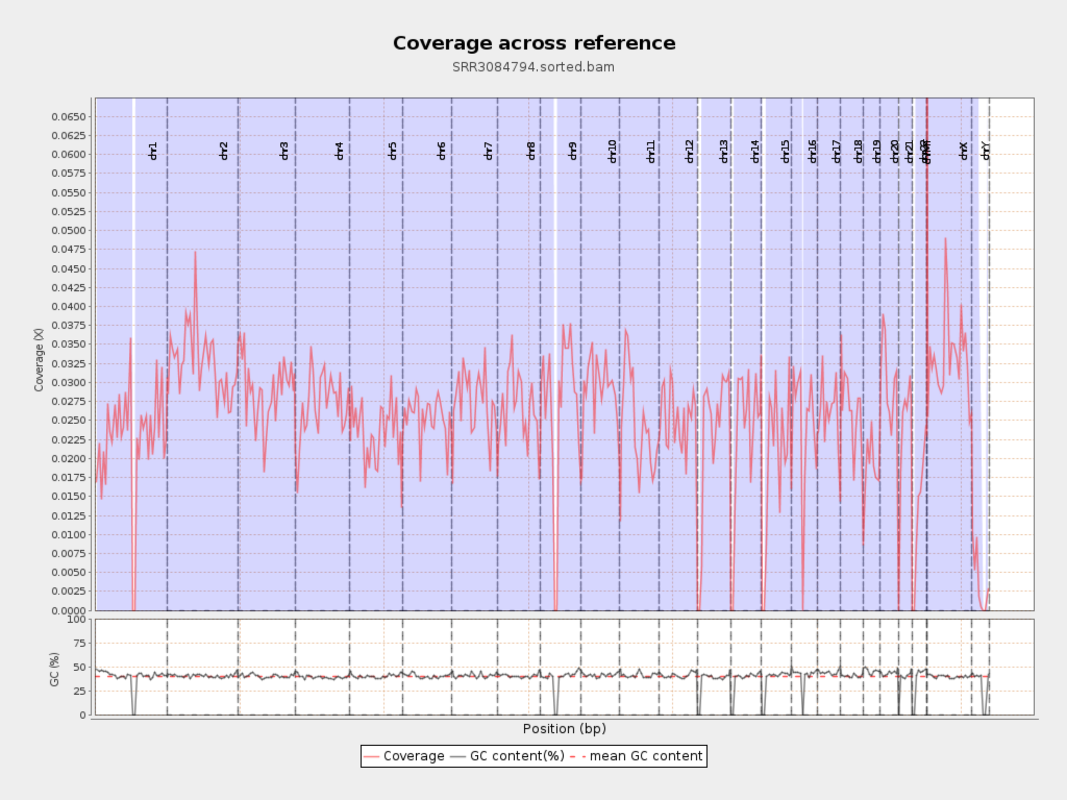
General error rate	0.82%
Mismatches	638,594
Insertions	5,888
Mapped reads with at least one insertion	0.5%
Deletions	18,180
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.58%

2.6. Chromosome stats

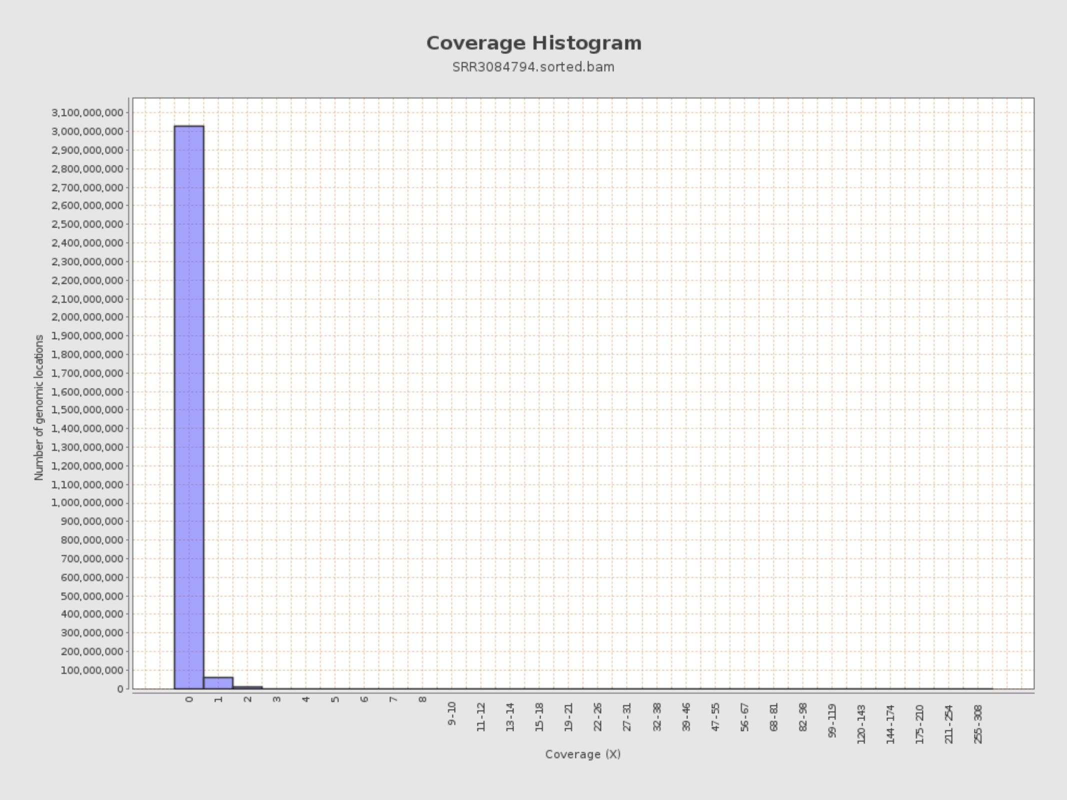
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5591024	0.0224	0.2863
chr2	243199373	7949469	0.0327	0.2731
chr3	198022430	5744946	0.029	0.1914
chr4	191154276	5168845	0.027	0.1889
chr5	180915260	4273085	0.0236	0.1733
chr6	171115067	4340674	0.0254	0.1916
chr7	159138663	4393846	0.0276	0.2211

chr8	146364022	3904361	0.0267	0.2653
chr9	141213431	3797117	0.0269	0.2256
chr10	135534747	3947212	0.0291	0.2196
chr11	135006516	3268051	0.0242	0.1989
chr12	133851895	3383193	0.0253	0.1808
chr13	115169878	2615500	0.0227	0.1704
chr14	107349540	2454297	0.0229	0.1794
chr15	102531392	2024125	0.0197	0.1594
chr16	90354753	2157925	0.0239	0.1847
chr17	81195210	2107062	0.026	0.1975
chr18	78077248	2052890	0.0263	0.3864
chr19	59128983	1135260	0.0192	0.2242
chr20	63025520	1882767	0.0299	0.2031
chr21	48129895	1139236	0.0237	0.1765
chr22	51304566	681120	0.0133	0.1284
chrMT	16571	2232	0.1347	0.4073
chrX	155270560	5201007	0.0335	0.2183
chrY	59373566	209326	0.0035	0.0818

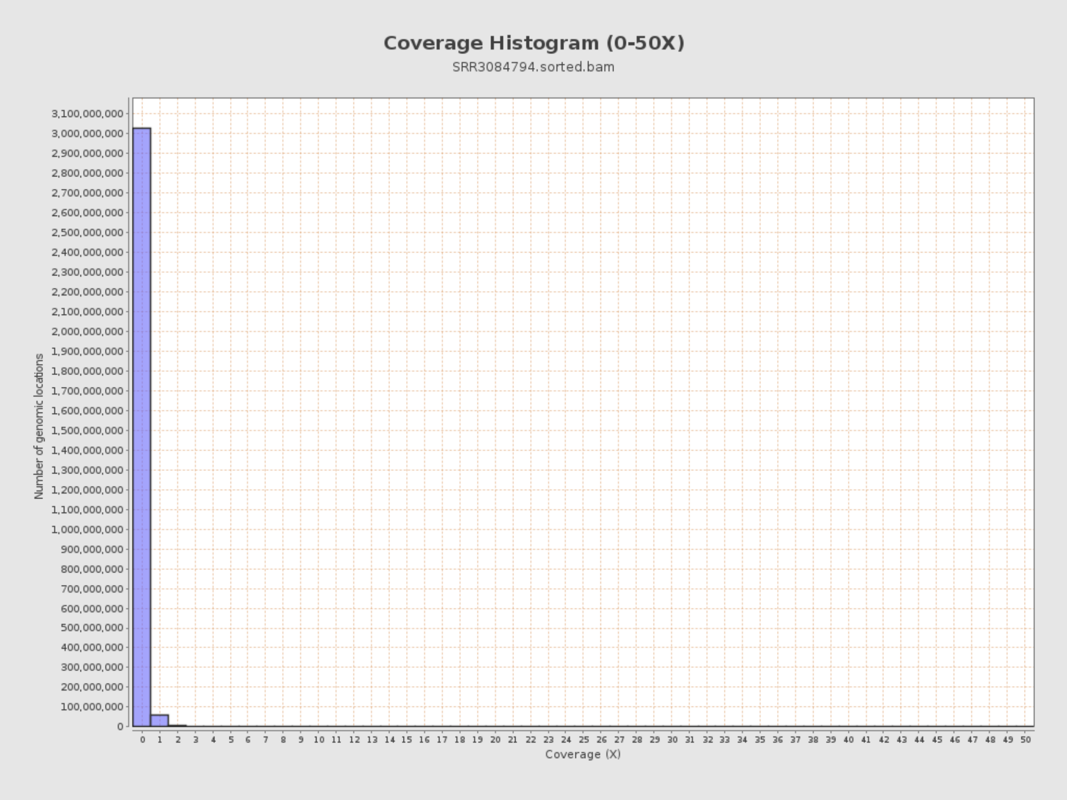
3. Results : Coverage across reference



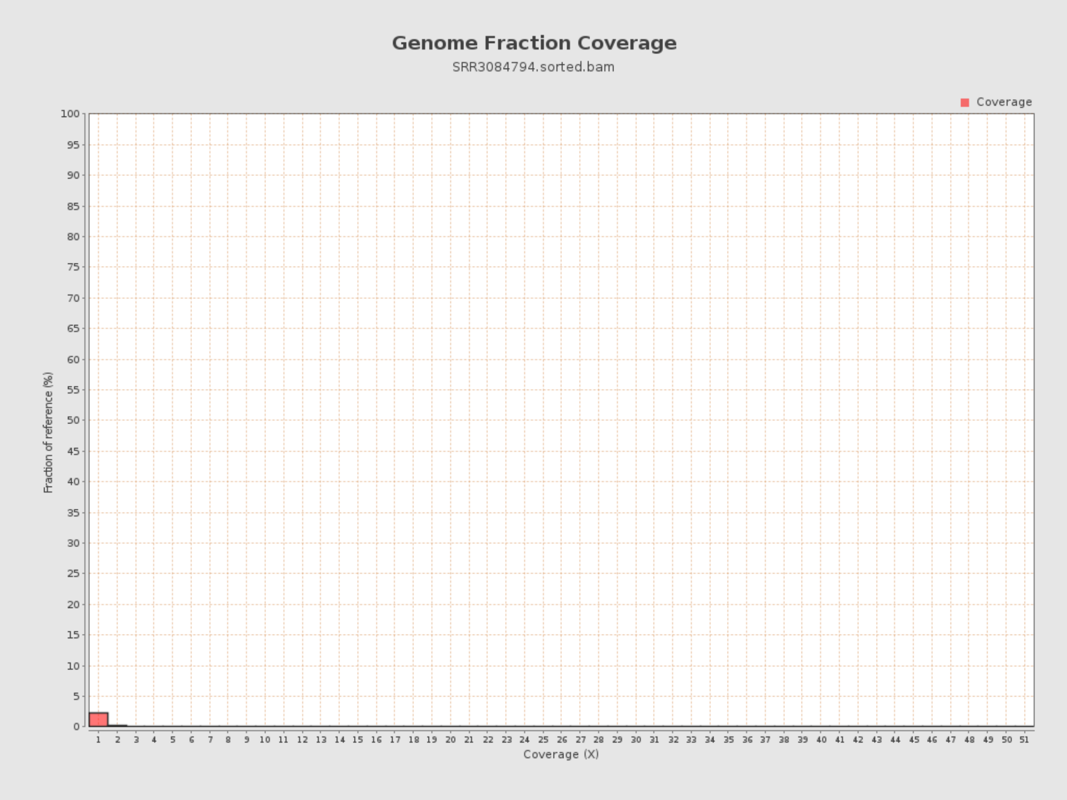
4. Results : Coverage Histogram



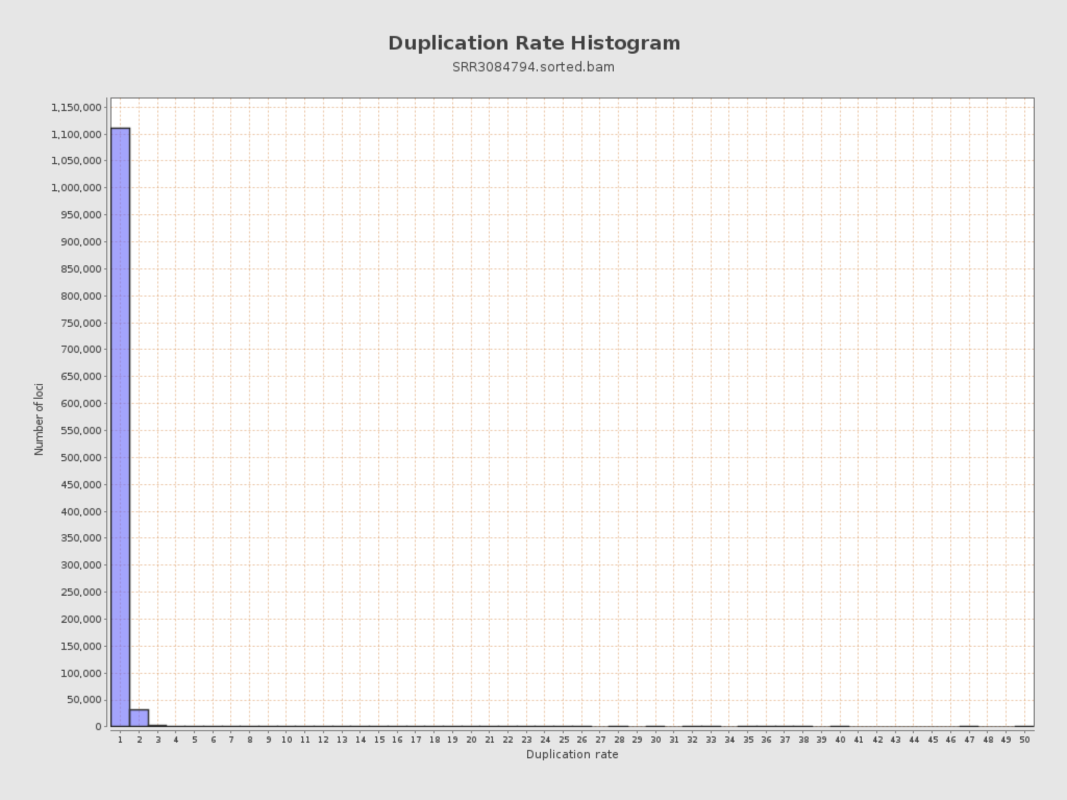
5. Results : Coverage Histogram (0-50X)



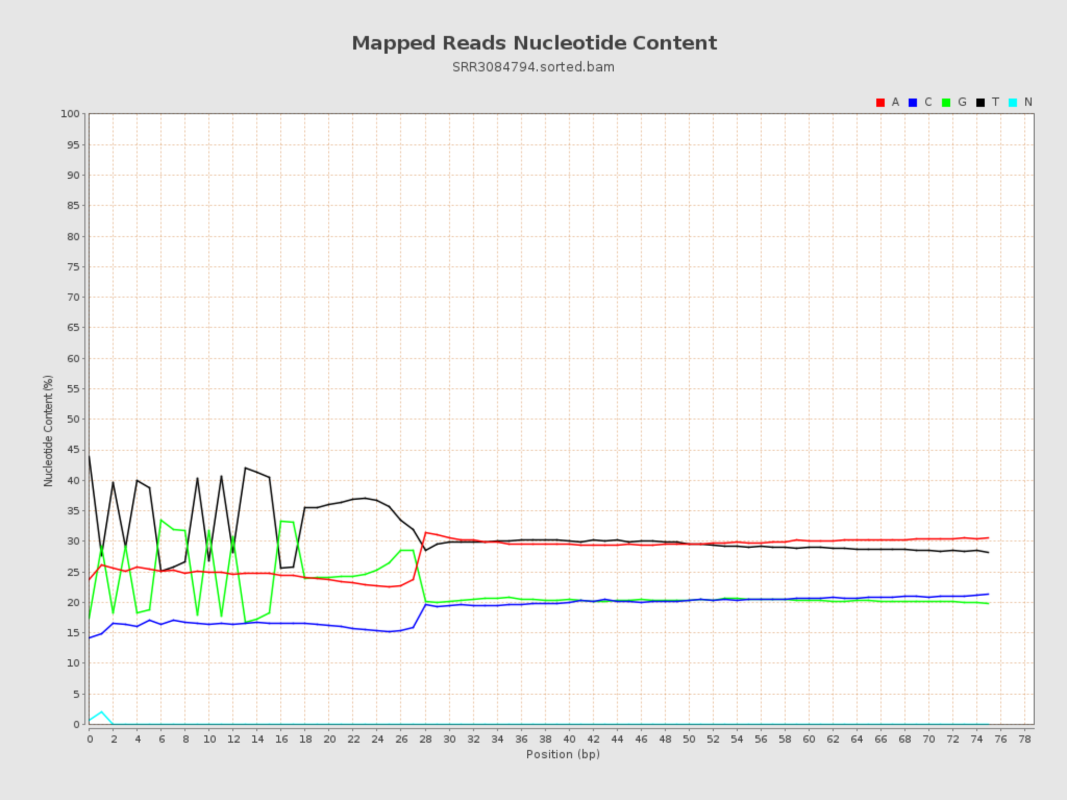
6. Results : Genome Fraction Coverage



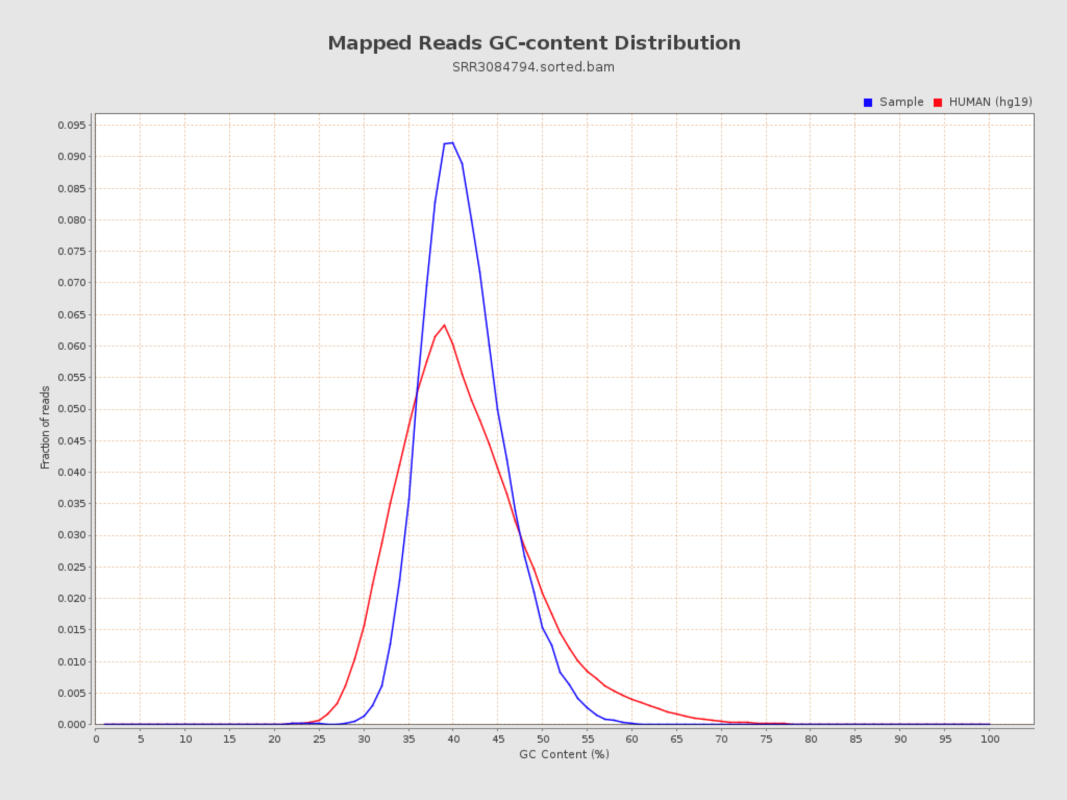
7. Results : Duplication Rate Histogram



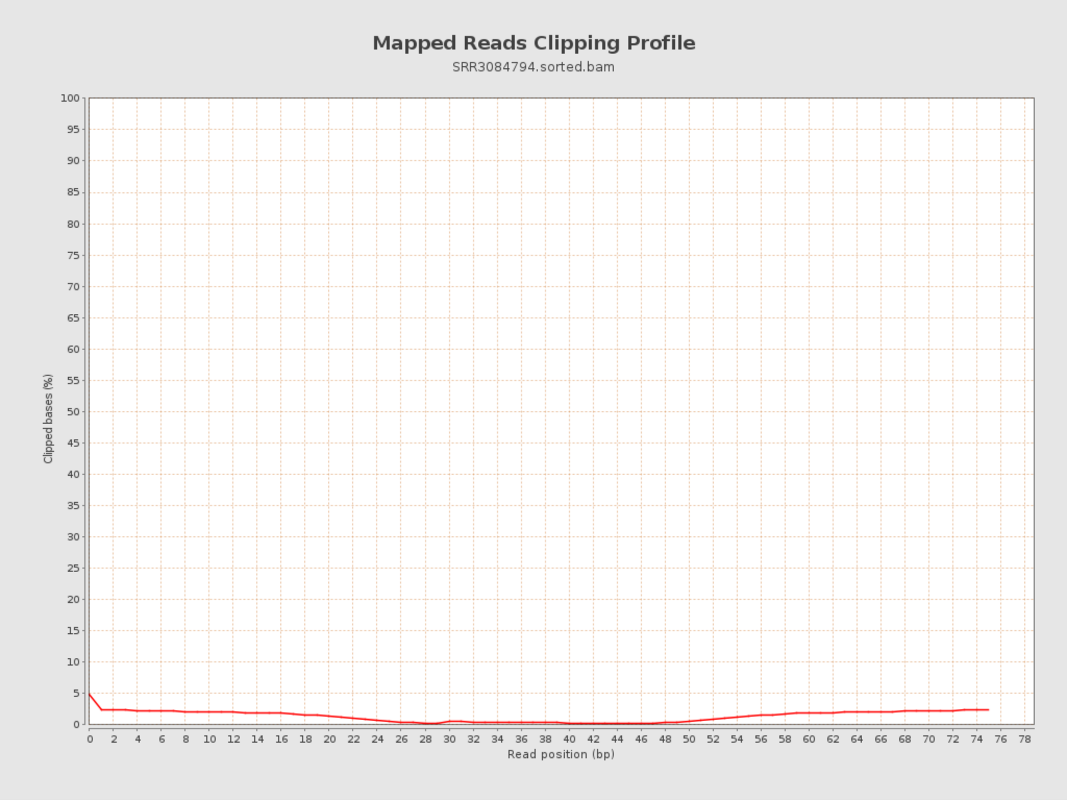
8. Results : Mapped Reads Nucleotide Content



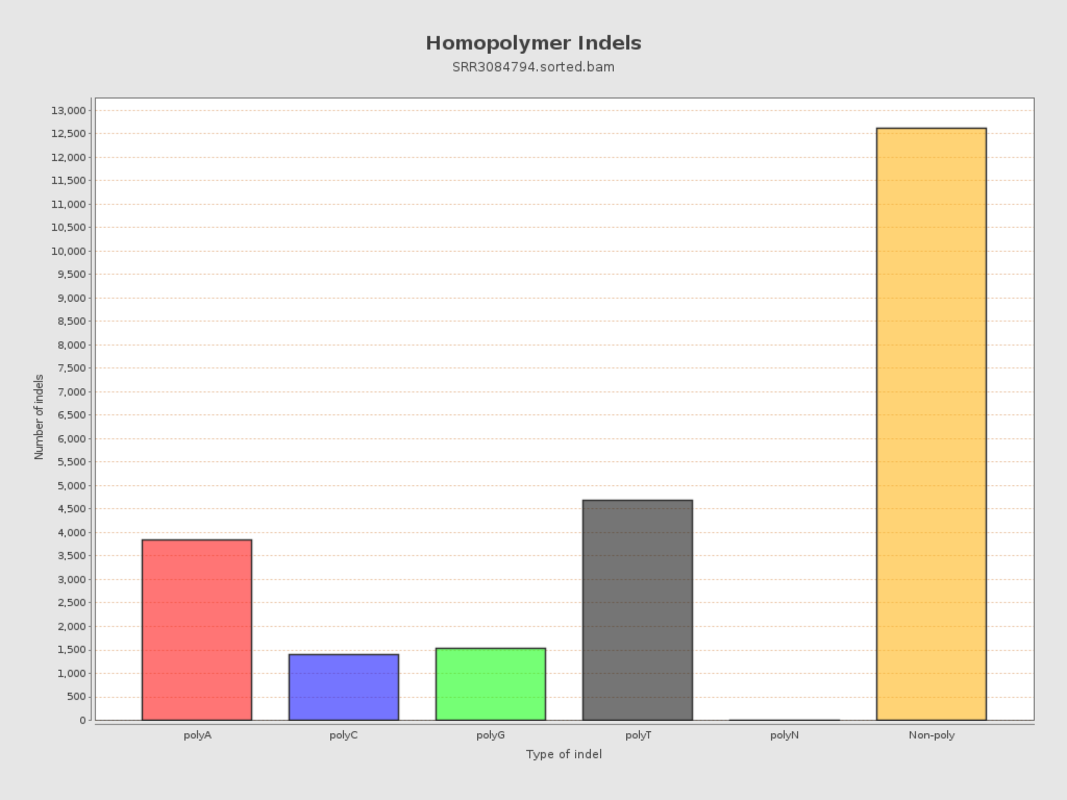
9. Results : Mapped Reads GC-content Distribution



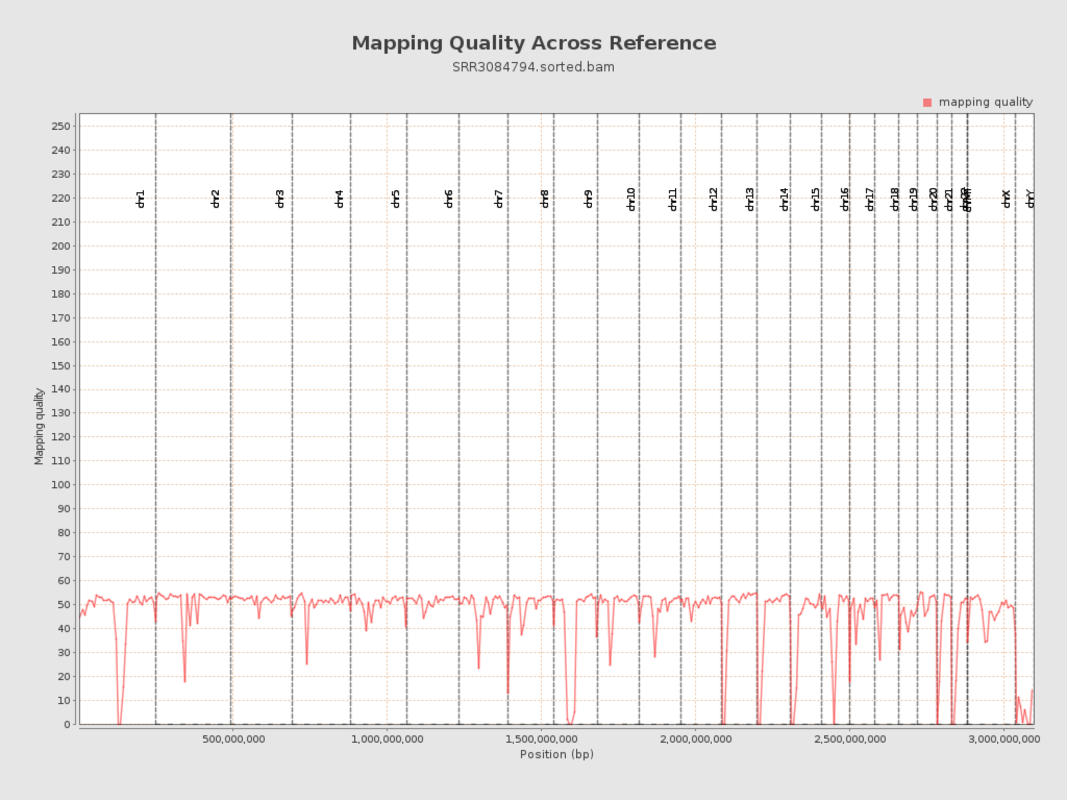
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram