

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084793.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_SRR3084793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:03:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,886
Mapped reads	1,568,104 / 89.41%
Unmapped reads	185,782 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,214 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	54,540 / 3.11%
Duplication rate	2.85%
Clipped reads	658,353 / 37.54%

2.2. ACGT Content

Number/percentage of A's	29,396,463 / 27.81%
Number/percentage of C's	19,957,438 / 18.88%
Number/percentage of T's	32,914,342 / 31.13%
Number/percentage of G's	23,403,127 / 22.14%
Number/percentage of N's	51,160 / 0.05%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.2744
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2.4. Mapping Quality

Mean Mapping Quality	46.91
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2.5. Mismatches and indels

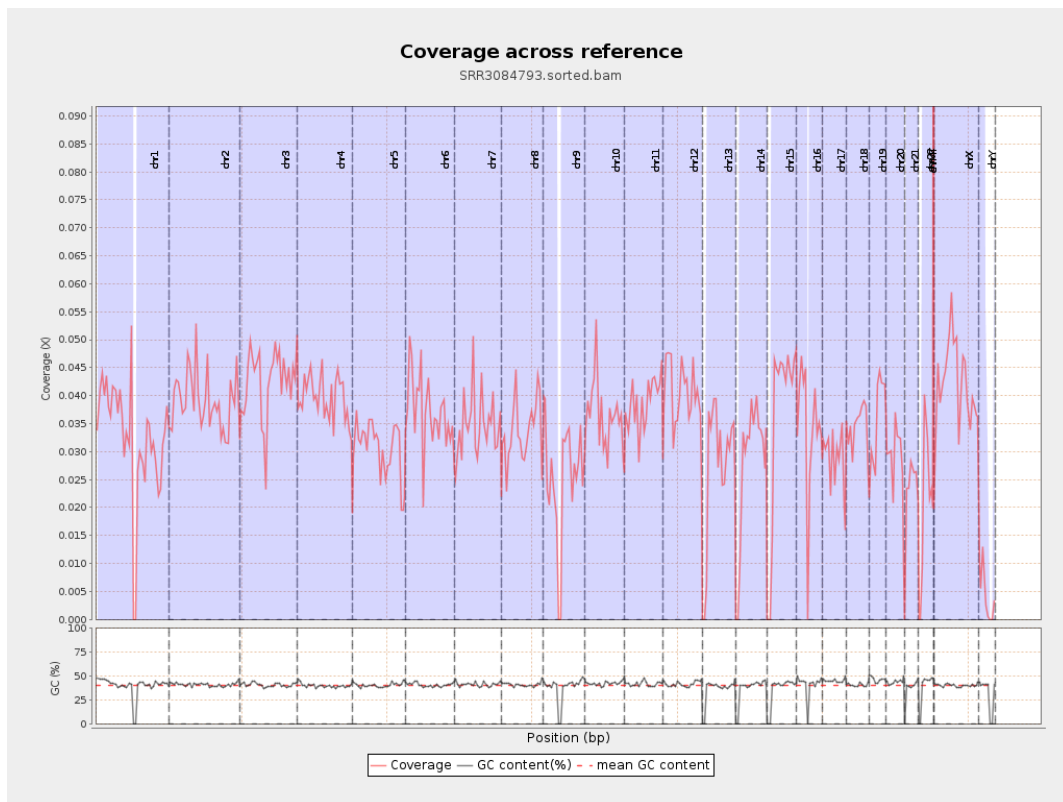
General error rate	0.87%
Mismatches	908,334
Insertions	7,987
Mapped reads with at least one insertion	0.5%
Deletions	25,414
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47%

2.6. Chromosome stats

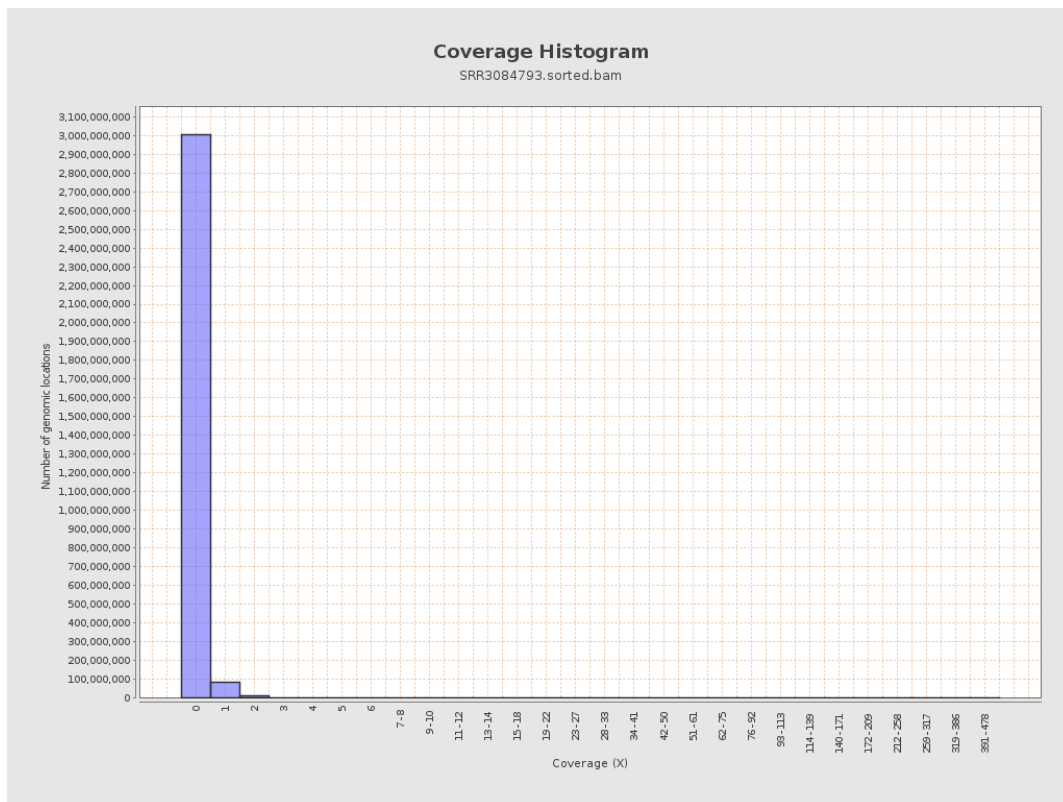
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8097383	0.0325	0.4285
chr2	243199373	9548981	0.0393	0.3156
chr3	198022430	8395778	0.0424	0.2268
chr4	191154276	7566748	0.0396	0.2275
chr5	180915260	5513508	0.0305	0.1934
chr6	171115067	6314121	0.0369	0.2375
chr7	159138663	5563074	0.035	0.3375

chr8	146364022	4926873	0.0337	0.3519
chr9	141213431	3517128	0.0249	0.2292
chr10	135534747	4961216	0.0366	0.2839
chr11	135006516	5214355	0.0386	0.2404
chr12	133851895	5400534	0.0403	0.2239
chr13	115169878	3134344	0.0272	0.1829
chr14	107349540	2979017	0.0278	0.1927
chr15	102531392	3732862	0.0364	0.2152
chr16	90354753	3101921	0.0343	0.2165
chr17	81195210	2298281	0.0283	0.2024
chr18	78077248	2704606	0.0346	0.4287
chr19	59128983	2110156	0.0357	0.3553
chr20	63025520	1817655	0.0288	0.1936
chr21	48129895	1091546	0.0227	0.1747
chr22	51304566	1022084	0.0199	0.155
chrMT	16571	4301	0.2595	0.5355
chrX	155270560	6503344	0.0419	0.249
chrY	59373566	244154	0.0041	0.104

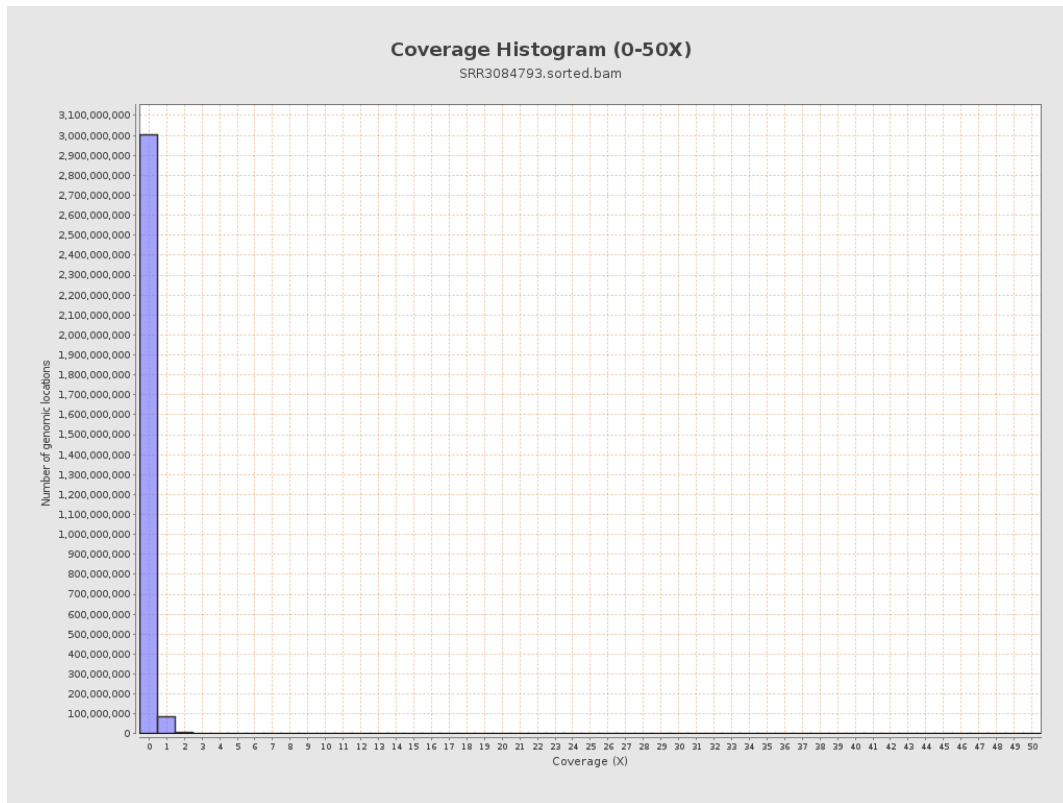
3. Results : Coverage across reference



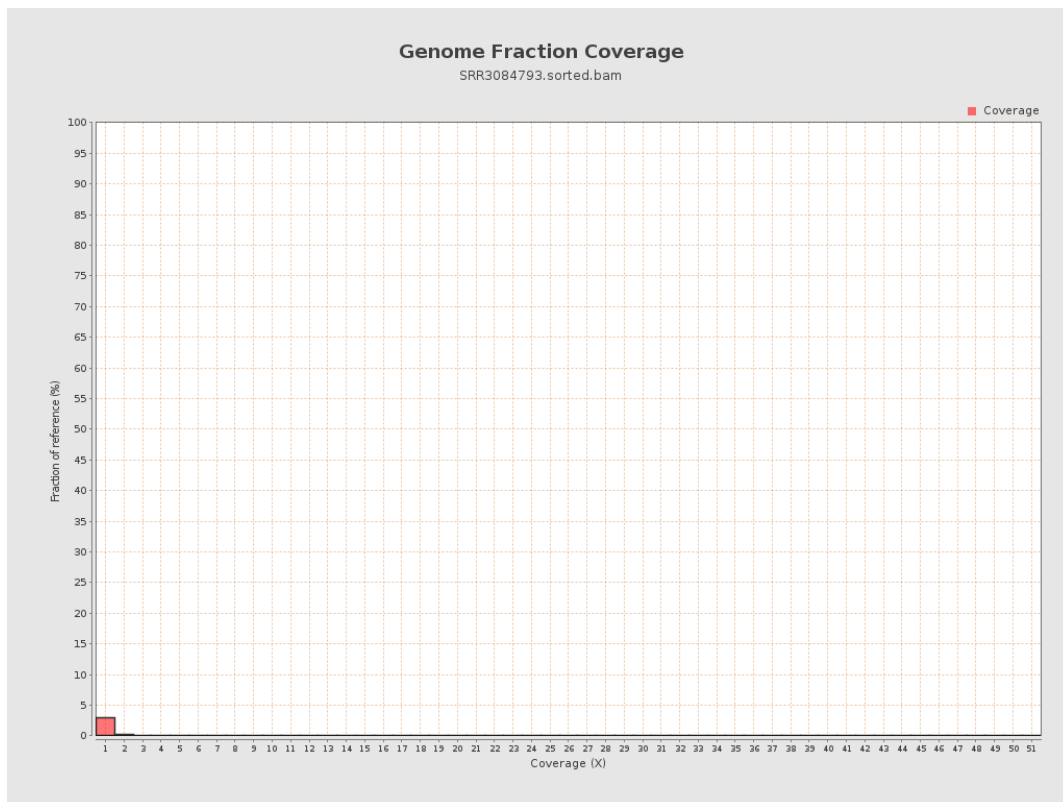
4. Results : Coverage Histogram



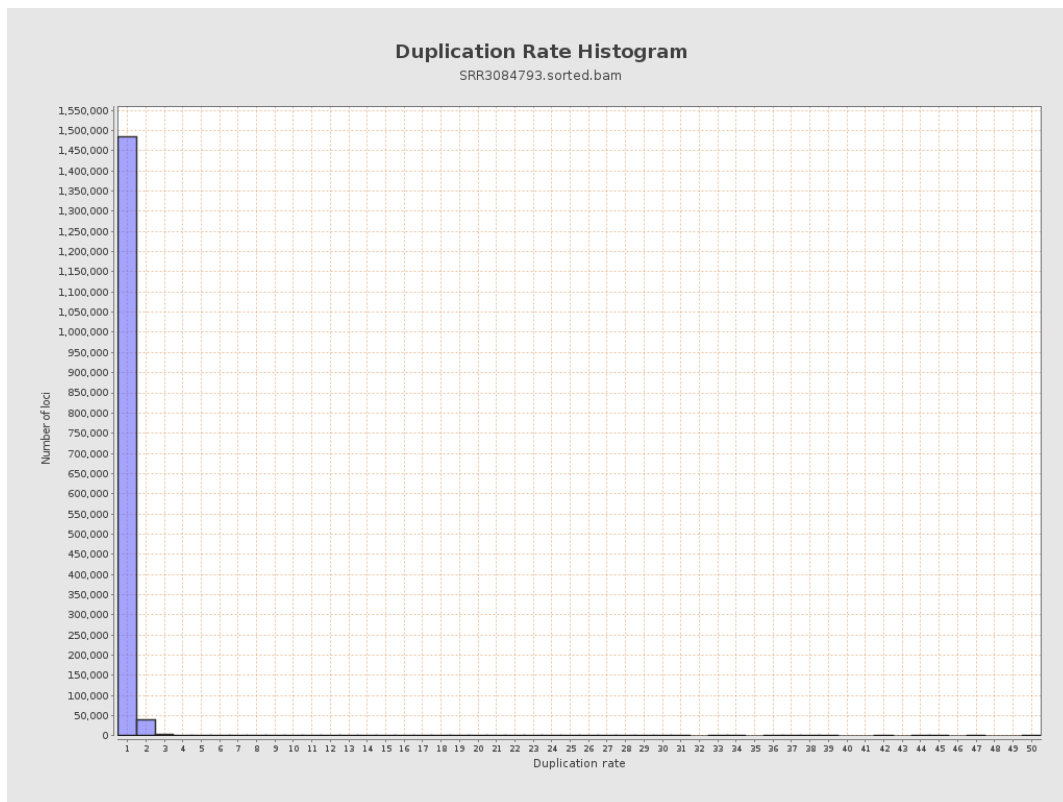
5. Results : Coverage Histogram (0-50X)



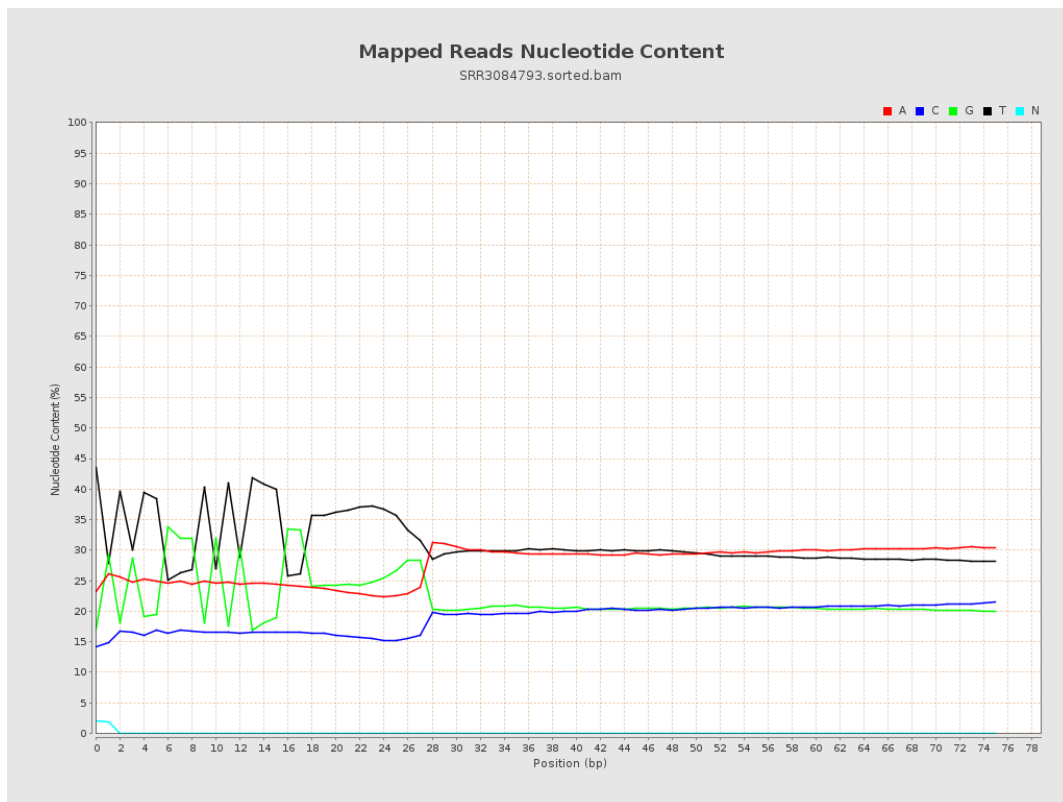
6. Results : Genome Fraction Coverage



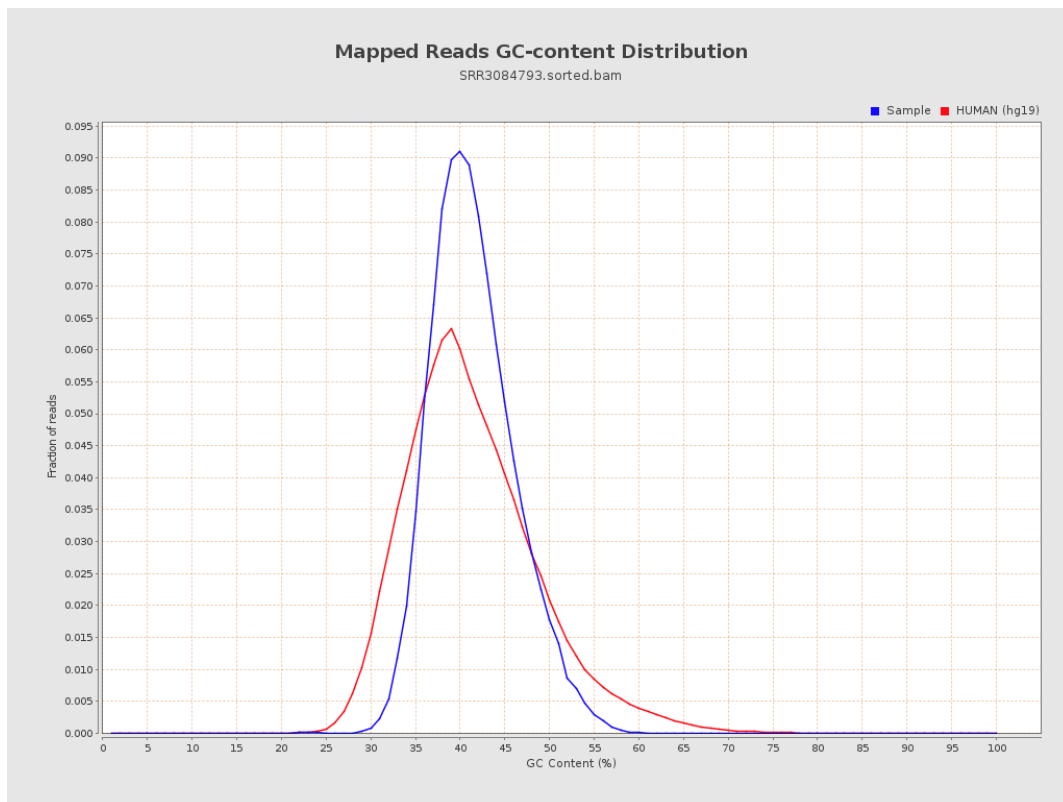
7. Results : Duplication Rate Histogram



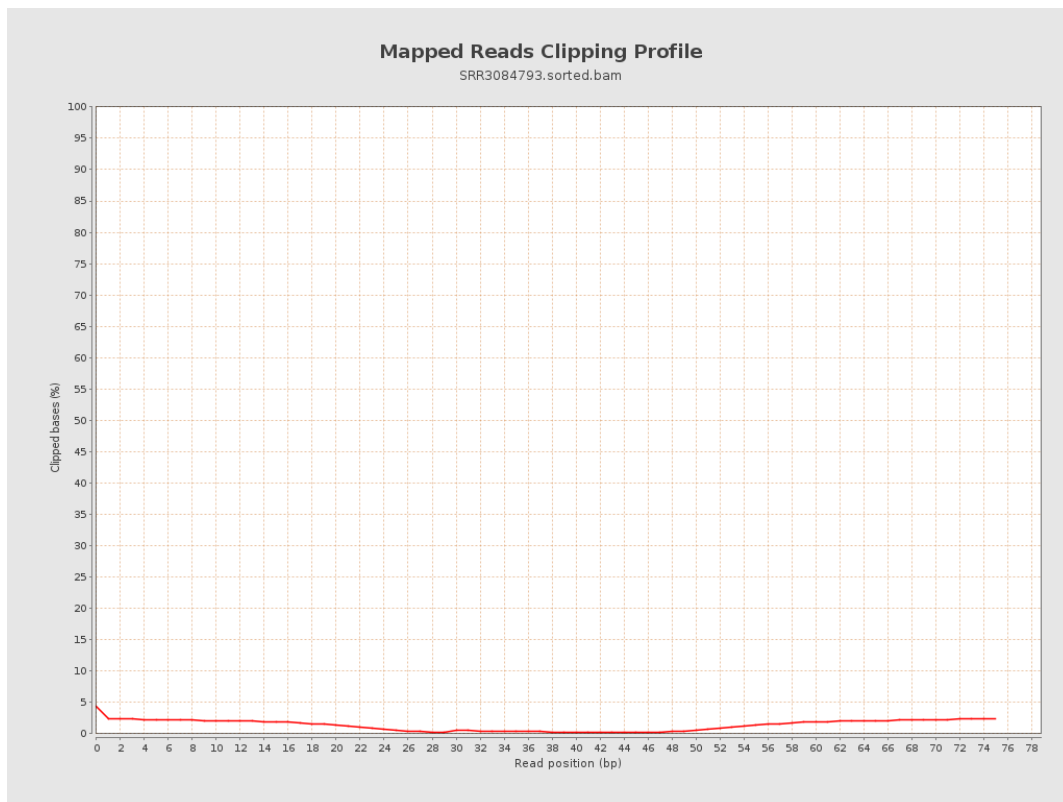
8. Results : Mapped Reads Nucleotide Content



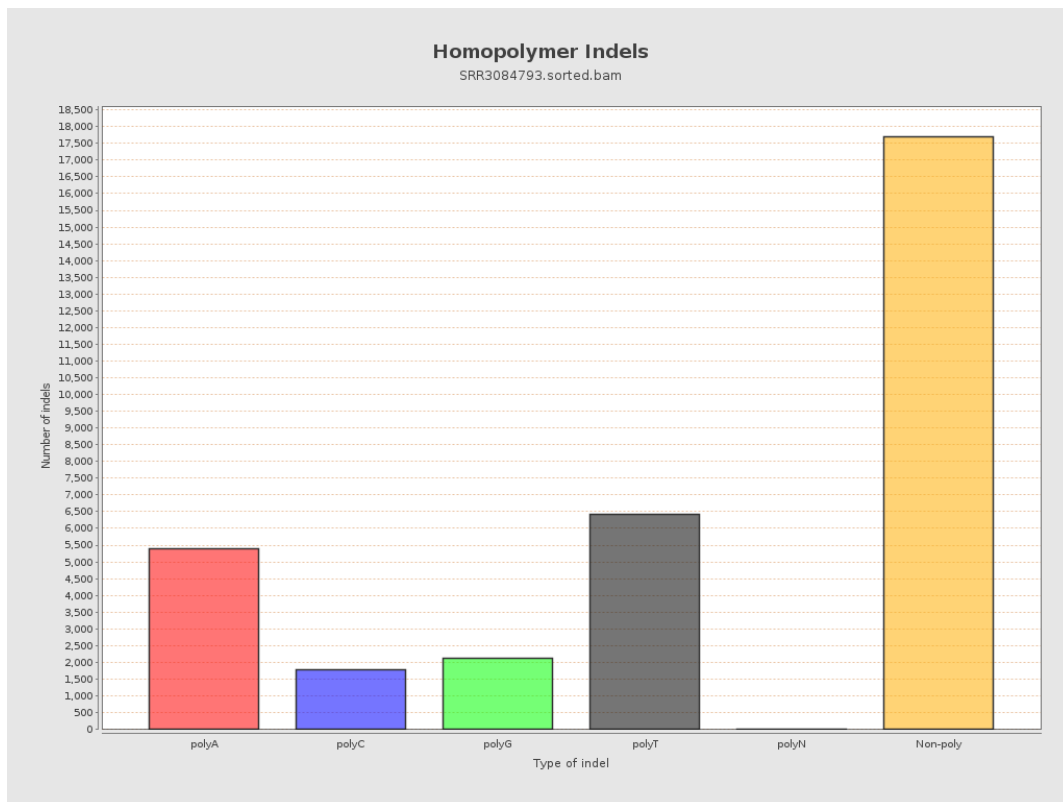
9. Results : Mapped Reads GC-content Distribution



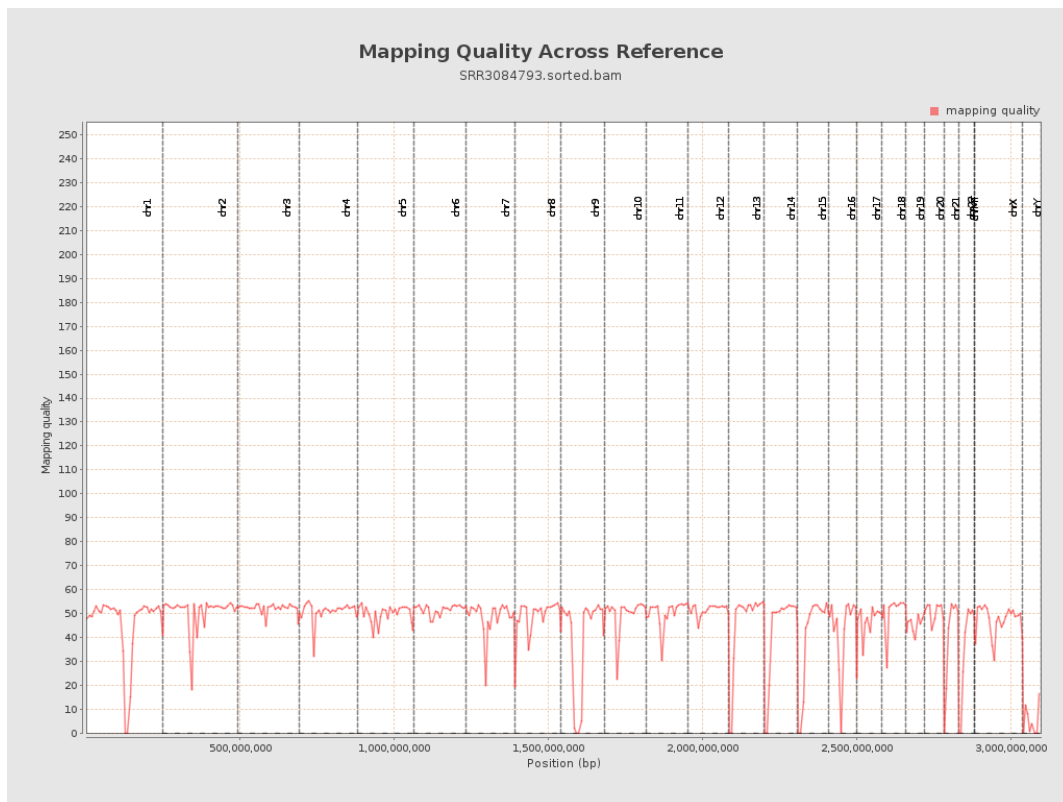
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

