

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:40:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008702.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_SRR6008702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008702.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:40:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,122,656
Mapped reads	1,103,137 / 51.97%
Unmapped reads	1,019,519 / 48.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,569 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	74,139 / 3.49%
Duplication rate	5.26%
Clipped reads	531,173 / 25.02%

2.2. ACGT Content

Number/percentage of A's	19,595,023 / 27.12%
Number/percentage of C's	13,701,316 / 18.96%
Number/percentage of T's	22,512,902 / 31.16%
Number/percentage of G's	16,353,146 / 22.63%
Number/percentage of N's	91,490 / 0.13%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.3016
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.77
----------------------	-------

2.5. Mismatches and indels

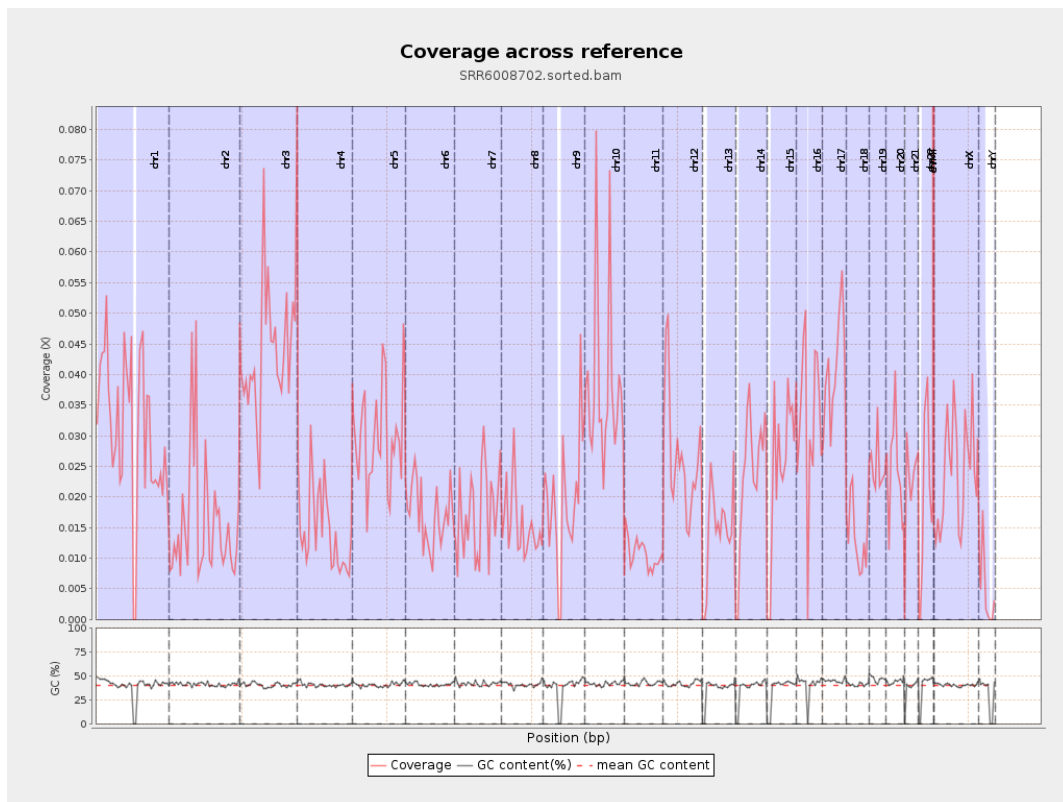
General error rate	0.89%
Mismatches	630,764
Insertions	5,670
Mapped reads with at least one insertion	0.51%
Deletions	21,152
Mapped reads with at least one deletion	1.9%
Homopolymer indels	45.52%

2.6. Chromosome stats

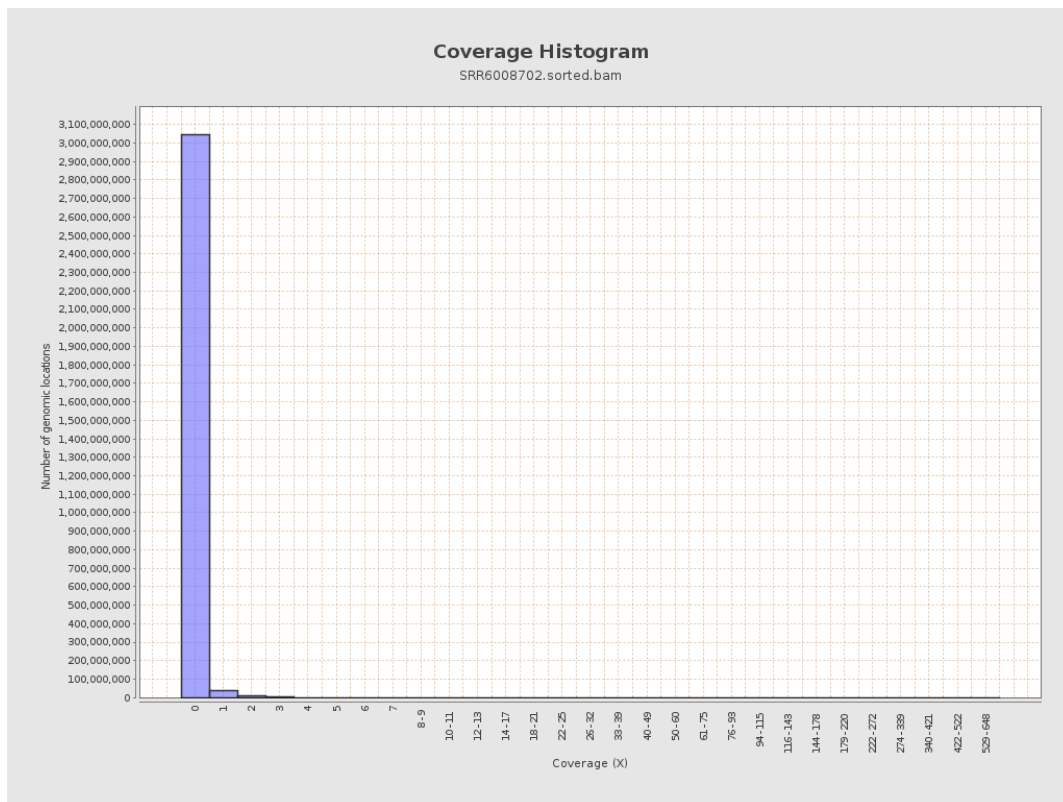
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7679165	0.0308	0.5556
chr2	243199373	3845917	0.0158	0.3003
chr3	198022430	8673157	0.0438	0.2798
chr4	191154276	2764105	0.0145	0.1704
chr5	180915260	5405825	0.0299	0.2255
chr6	171115067	2926186	0.0171	0.1861
chr7	159138663	2747236	0.0173	0.2001

chr8	146364022	2240308	0.0153	0.4175
chr9	141213431	2689071	0.019	0.2524
chr10	135534747	5158778	0.0381	0.4908
chr11	135006516	1430421	0.0106	0.1581
chr12	133851895	3512181	0.0262	0.2269
chr13	115169878	1645606	0.0143	0.1527
chr14	107349540	2578181	0.024	0.2375
chr15	102531392	2580368	0.0252	0.2047
chr16	90354753	2997718	0.0332	0.2857
chr17	81195210	3304270	0.0407	0.2695
chr18	78077248	1056151	0.0135	0.3893
chr19	59128983	1477234	0.025	0.38
chr20	63025520	1531696	0.0243	0.2077
chr21	48129895	1096449	0.0228	0.2351
chr22	51304566	971147	0.0189	0.1756
chrMT	16571	17469	1.0542	1.424
chrX	155270560	3708269	0.0239	0.2098
chrY	59373566	254932	0.0043	0.1784

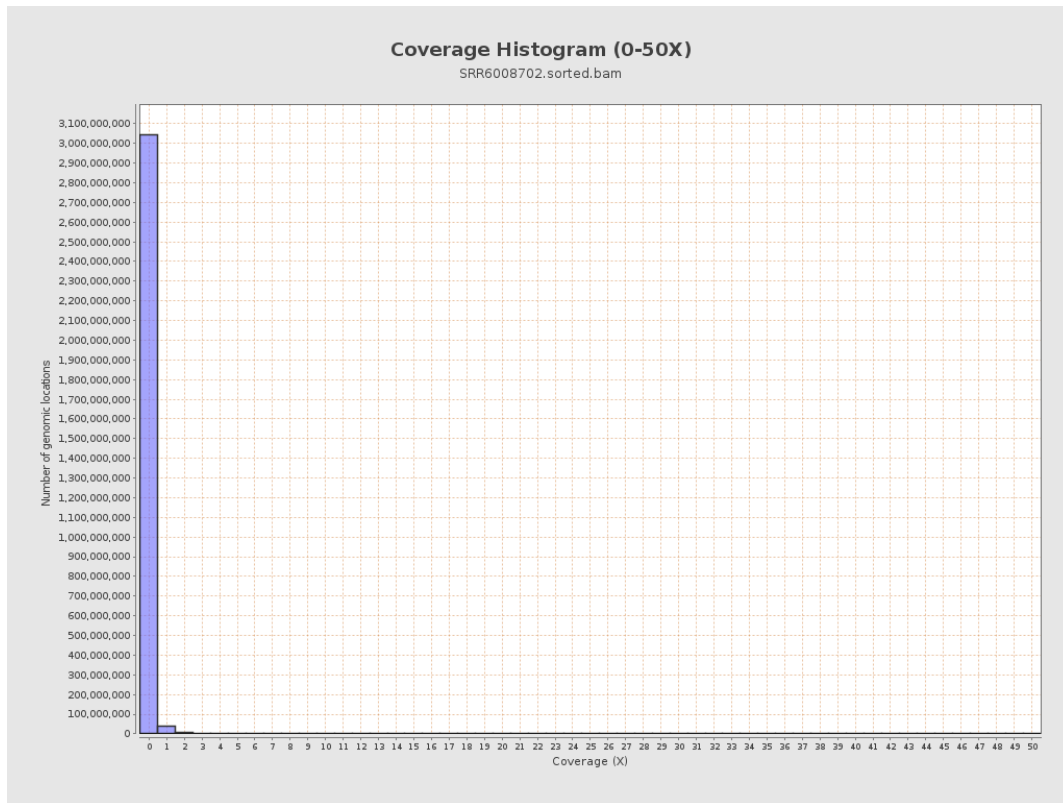
3. Results : Coverage across reference



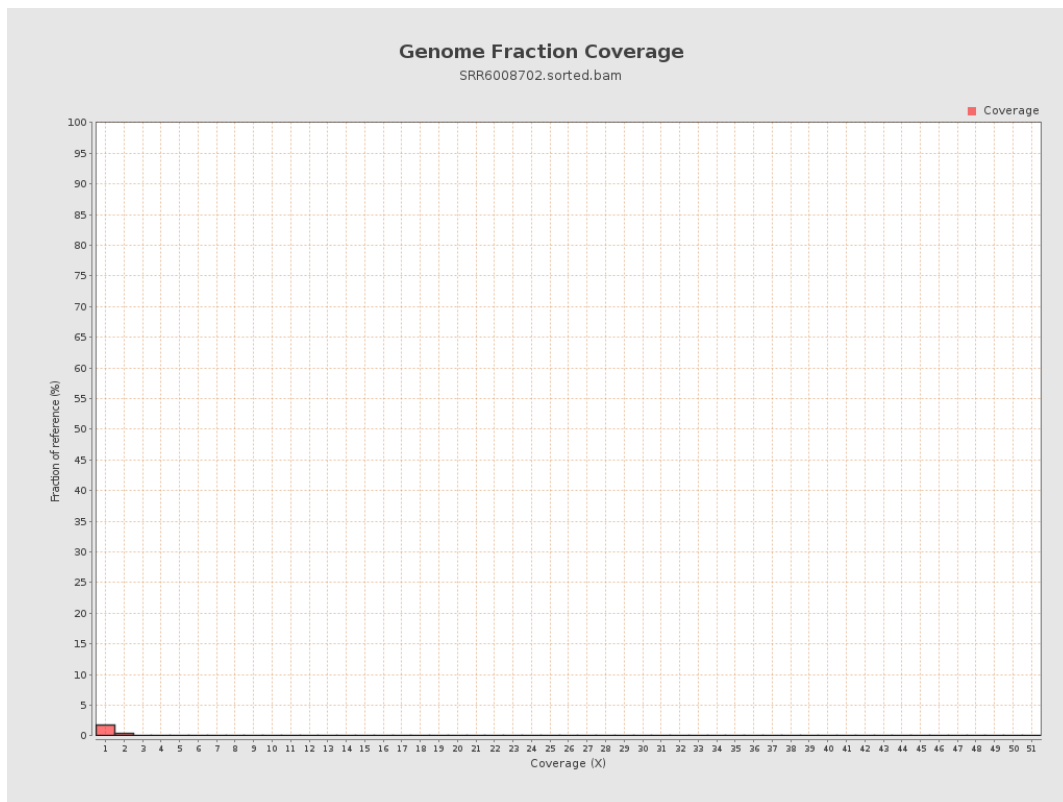
4. Results : Coverage Histogram



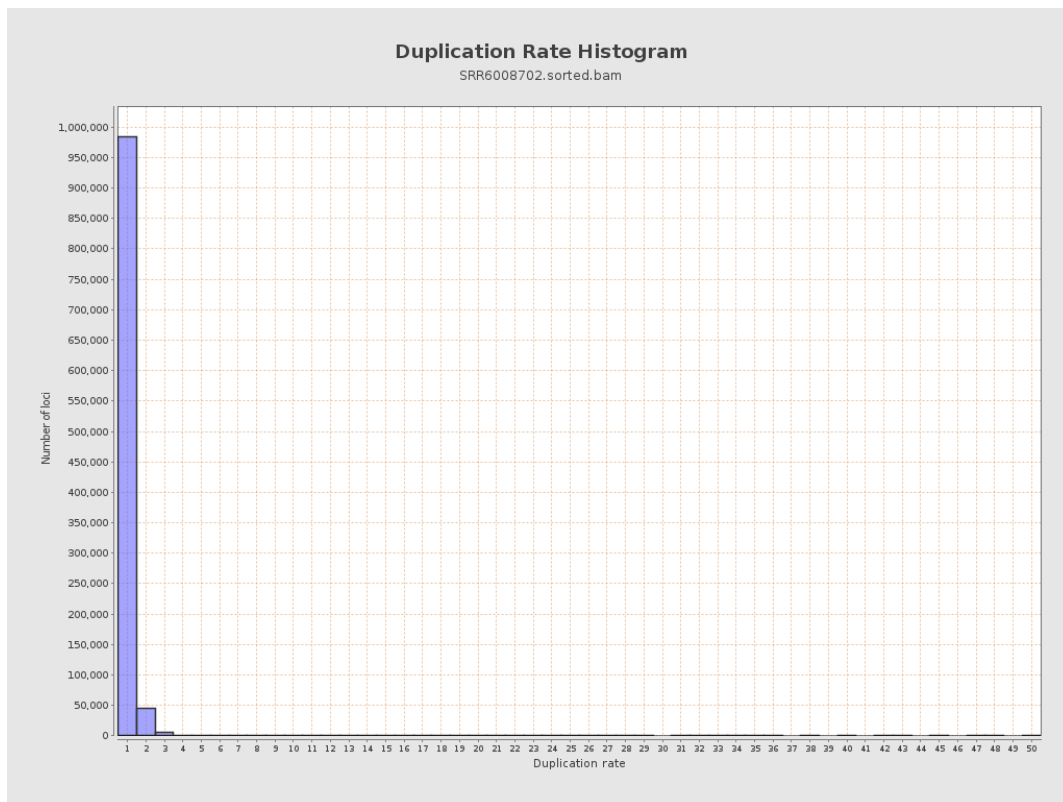
5. Results : Coverage Histogram (0-50X)



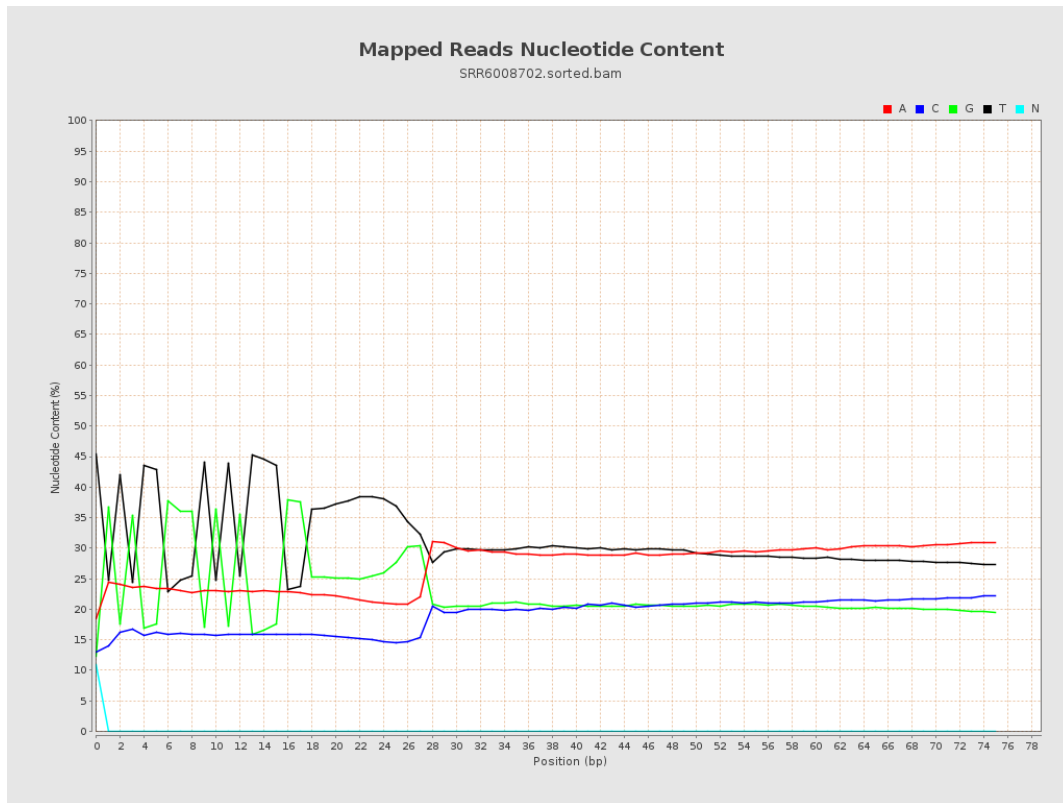
6. Results : Genome Fraction Coverage



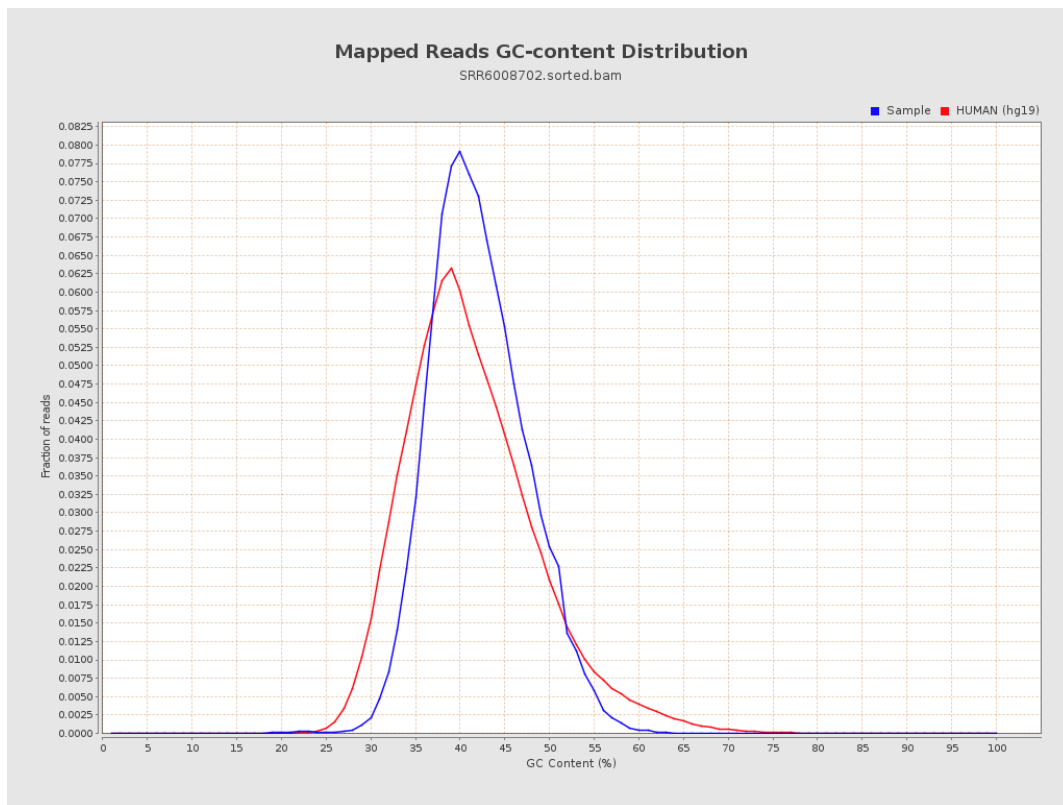
7. Results : Duplication Rate Histogram



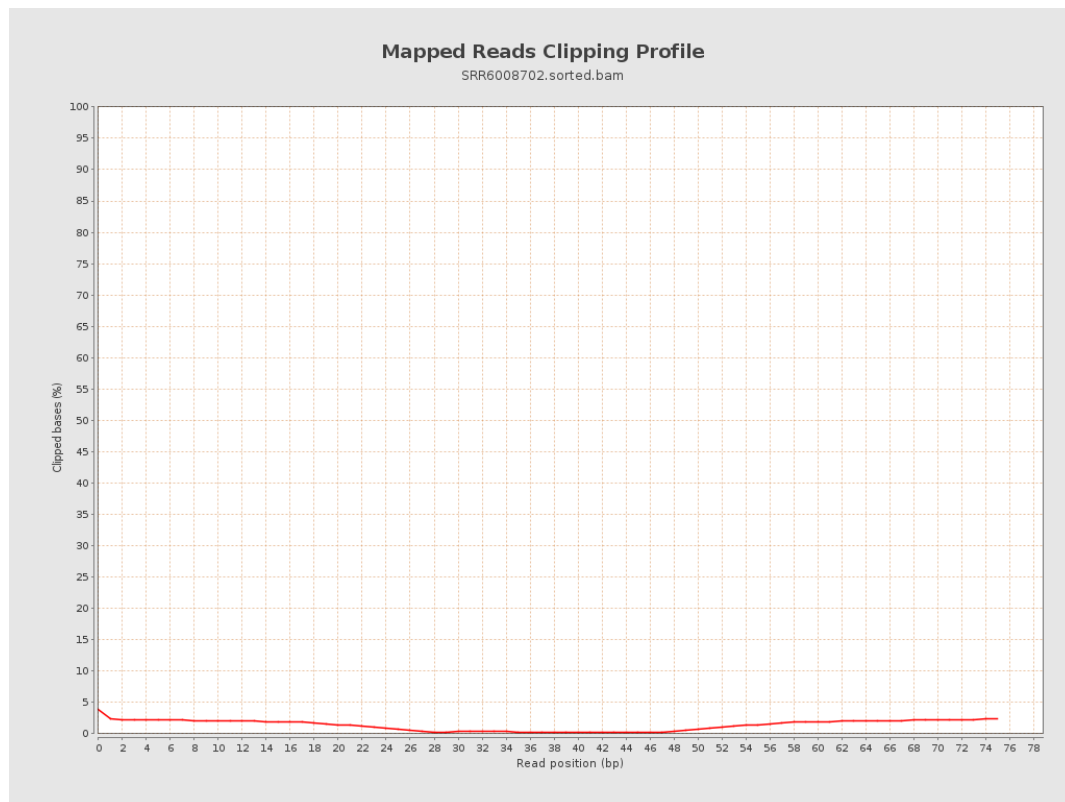
8. Results : Mapped Reads Nucleotide Content



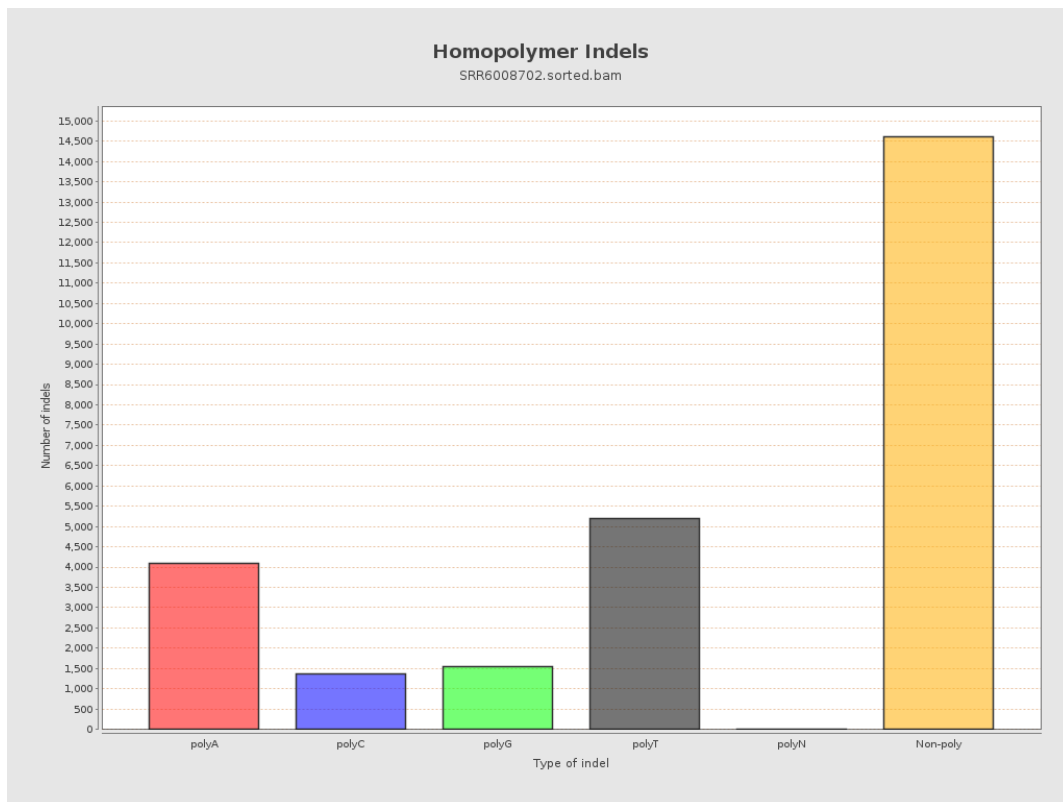
9. Results : Mapped Reads GC-content Distribution



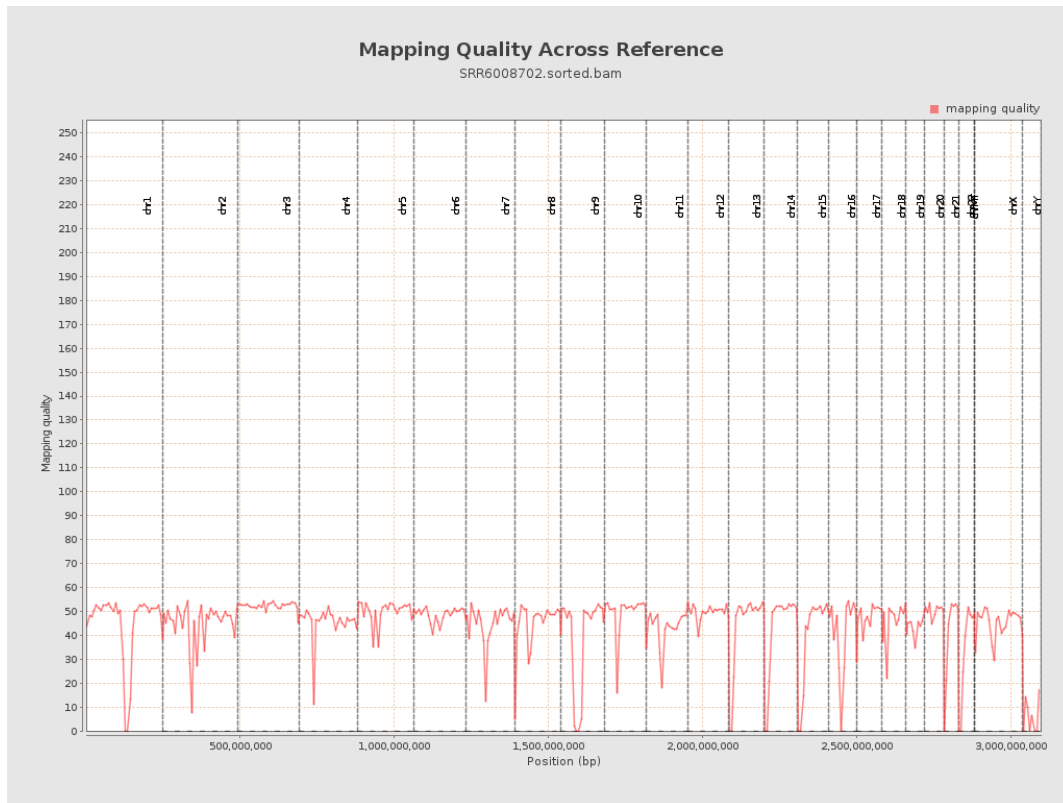
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

