

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:56:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003998.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_SRR6003998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:56:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,476,070
Mapped reads	3,104,368 / 89.31%
Unmapped reads	371,702 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,606 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	110,426 / 3.18%
Duplication rate	2.23%
Clipped reads	1,687,254 / 48.54%

2.2. ACGT Content

Number/percentage of A's	54,901,717 / 27.46%
Number/percentage of C's	38,868,110 / 19.44%
Number/percentage of T's	59,989,061 / 30%
Number/percentage of G's	46,176,236 / 23.09%
Number/percentage of N's	28,422 / 0.01%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0646

Standard Deviation	0.6029
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2.4. Mapping Quality

Mean Mapping Quality	41.53
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2.5. Mismatches and indels

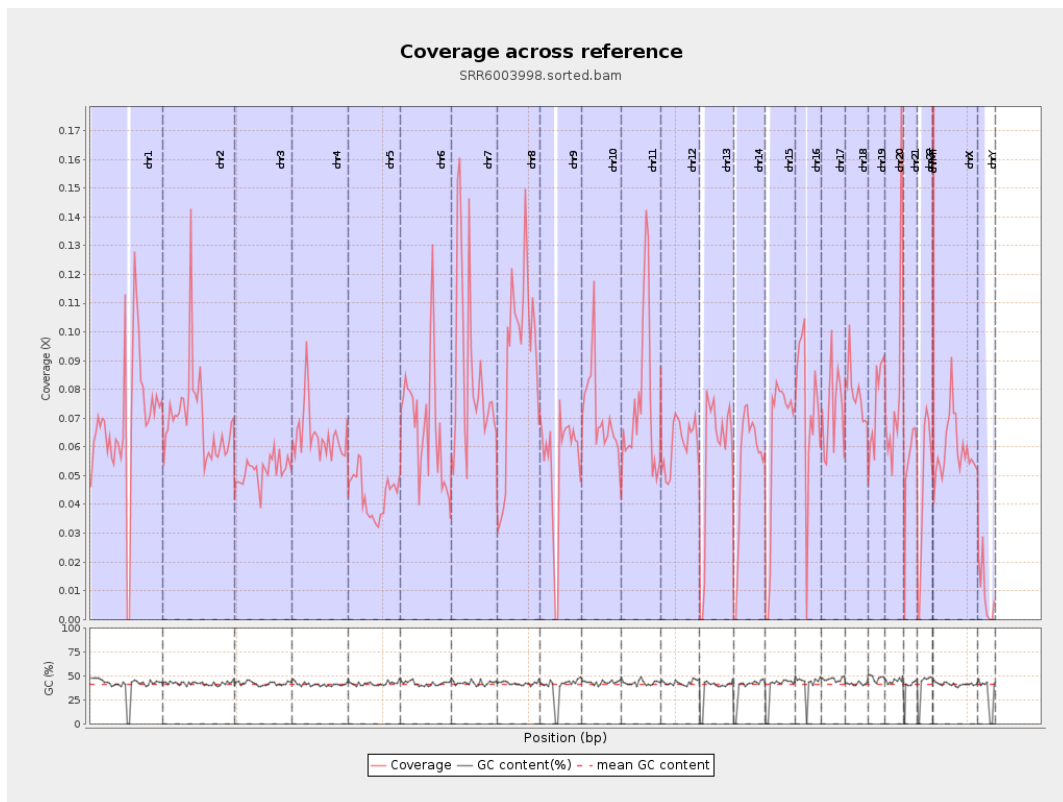
General error rate	0.88%
Mismatches	1,729,452
Insertions	17,069
Mapped reads with at least one insertion	0.54%
Deletions	49,331
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.18%

2.6. Chromosome stats

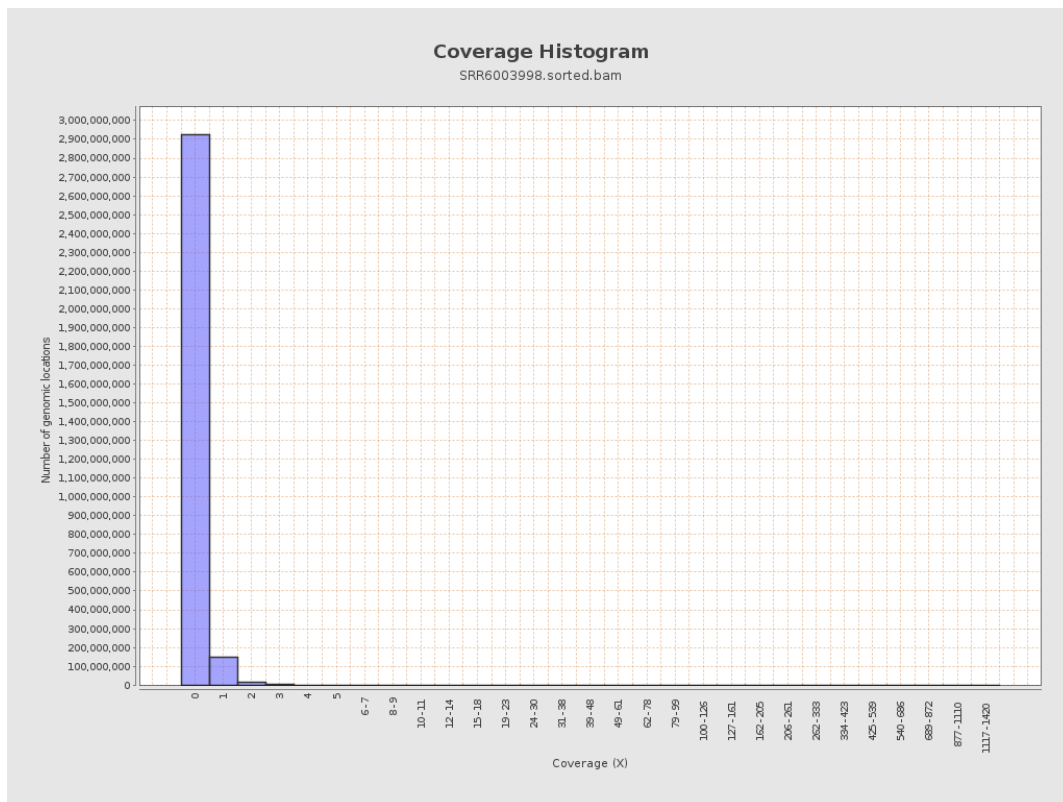
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17137202	0.0688	1.0849
chr2	243199373	16879824	0.0694	0.8531
chr3	198022430	10243176	0.0517	0.2593
chr4	191154276	12331874	0.0645	0.3203
chr5	180915260	7884969	0.0436	0.2429
chr6	171115067	11569382	0.0676	0.3796
chr7	159138663	13522245	0.085	1.0732

chr8	146364022	13190431	0.0901	0.5342
chr9	141213431	7700438	0.0545	0.5755
chr10	135534747	9661871	0.0713	0.5243
chr11	135006516	9967250	0.0738	0.5338
chr12	133851895	8199602	0.0613	0.293
chr13	115169878	6625228	0.0575	0.2713
chr14	107349540	5794165	0.054	0.3482
chr15	102531392	6262552	0.0611	0.3036
chr16	90354753	6591195	0.0729	0.3721
chr17	81195210	5892104	0.0726	0.3617
chr18	78077248	6147000	0.0787	1.1159
chr19	59128983	4431875	0.075	0.798
chr20	63025520	5260969	0.0835	0.3606
chr21	48129895	2580065	0.0536	0.3095
chr22	51304566	2386032	0.0465	0.2434
chrMT	16571	64874	3.9149	4.1056
chrX	155270560	9178904	0.0591	0.3541
chrY	59373566	541527	0.0091	0.1878

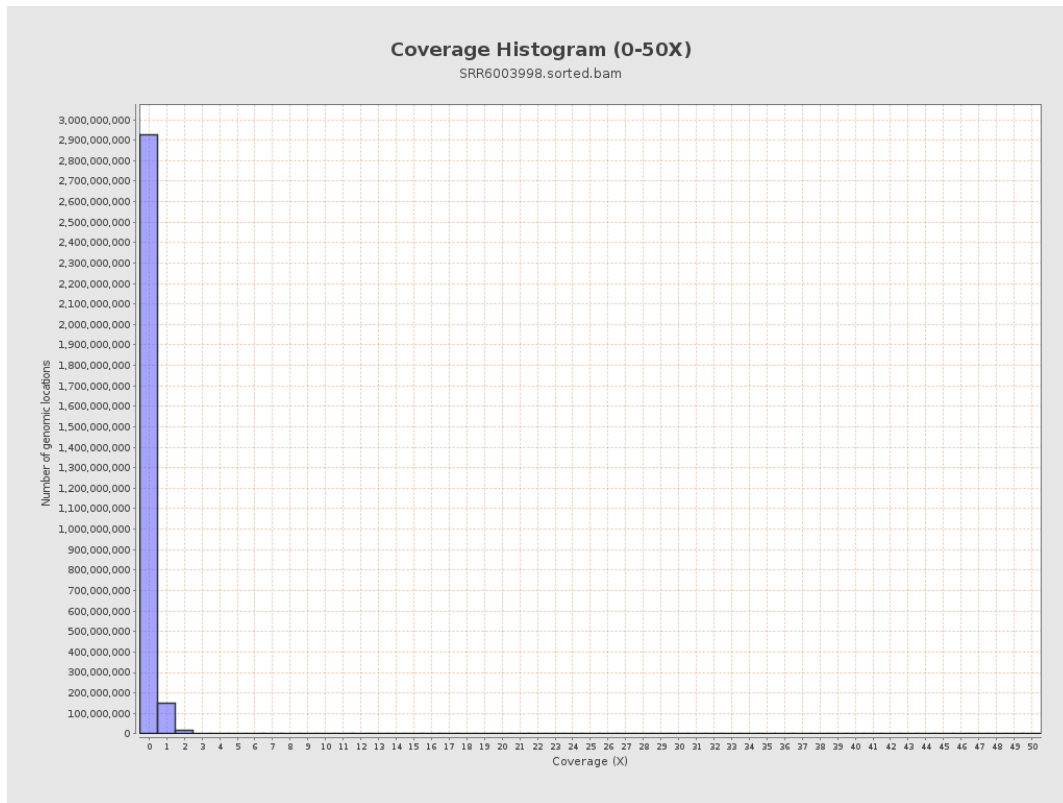
3. Results : Coverage across reference



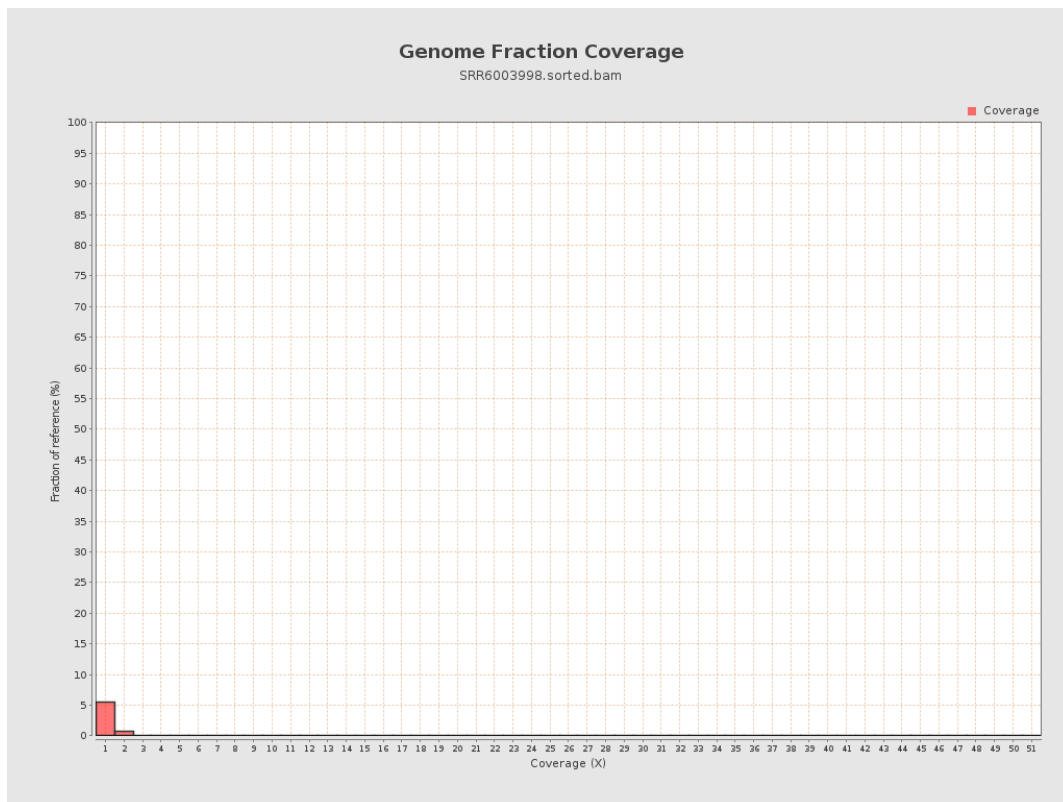
4. Results : Coverage Histogram



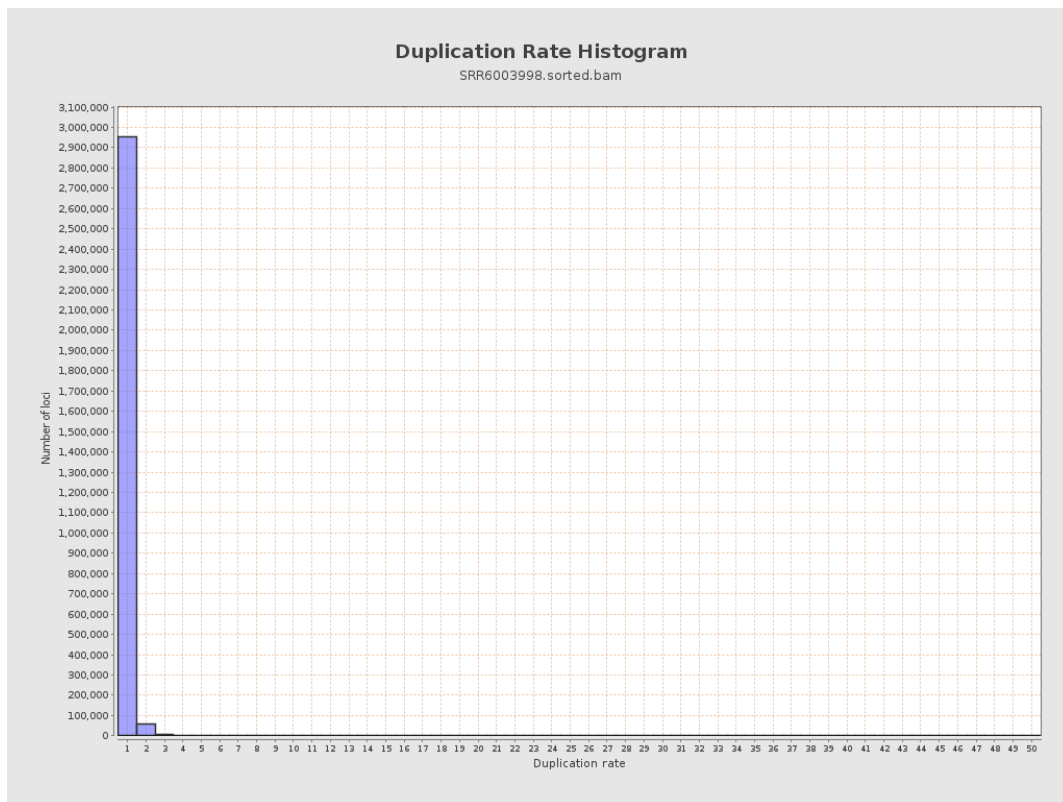
5. Results : Coverage Histogram (0-50X)



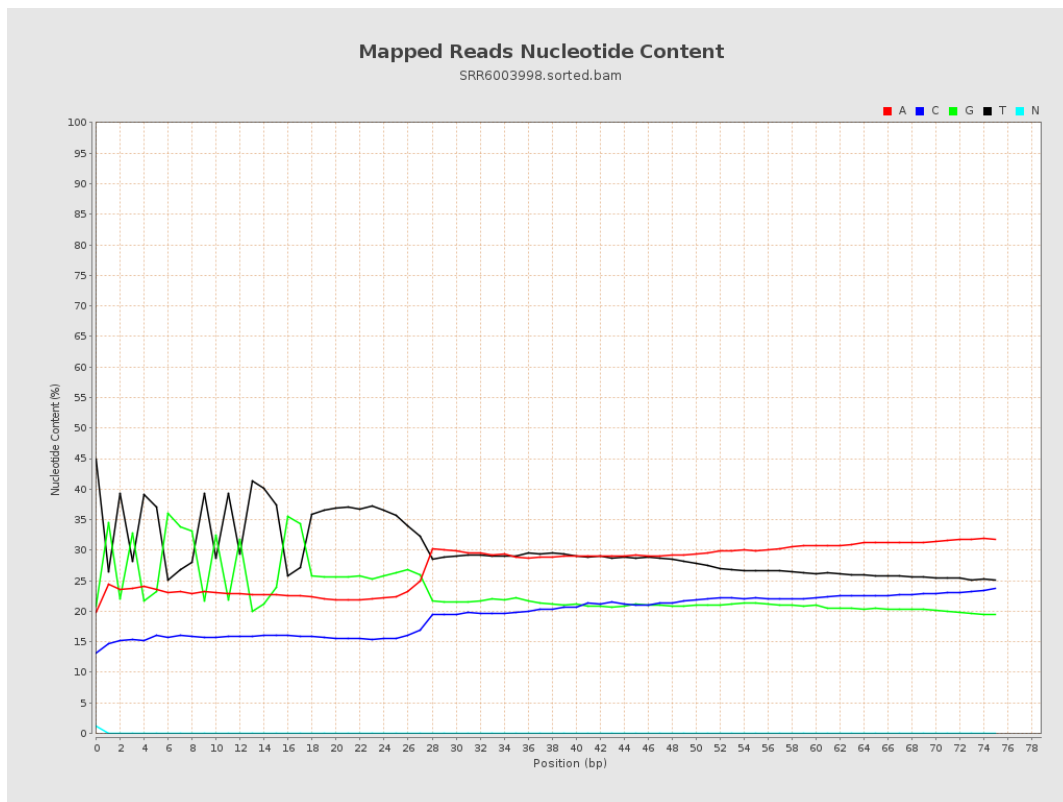
6. Results : Genome Fraction Coverage



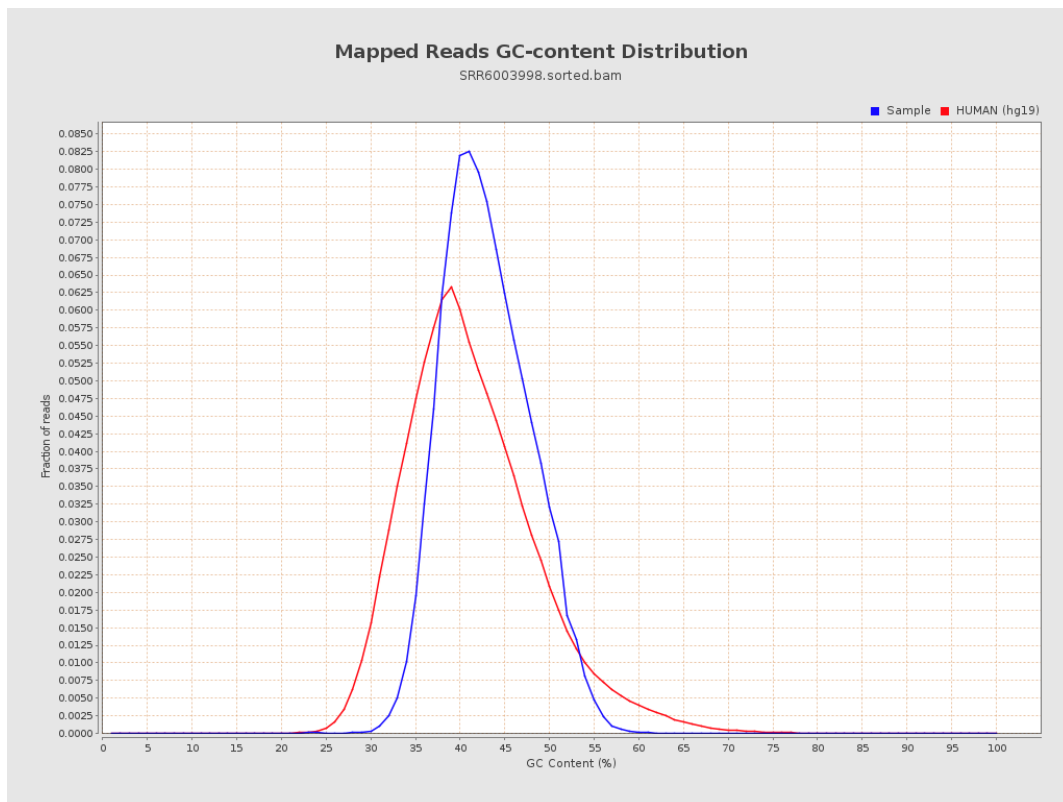
7. Results : Duplication Rate Histogram



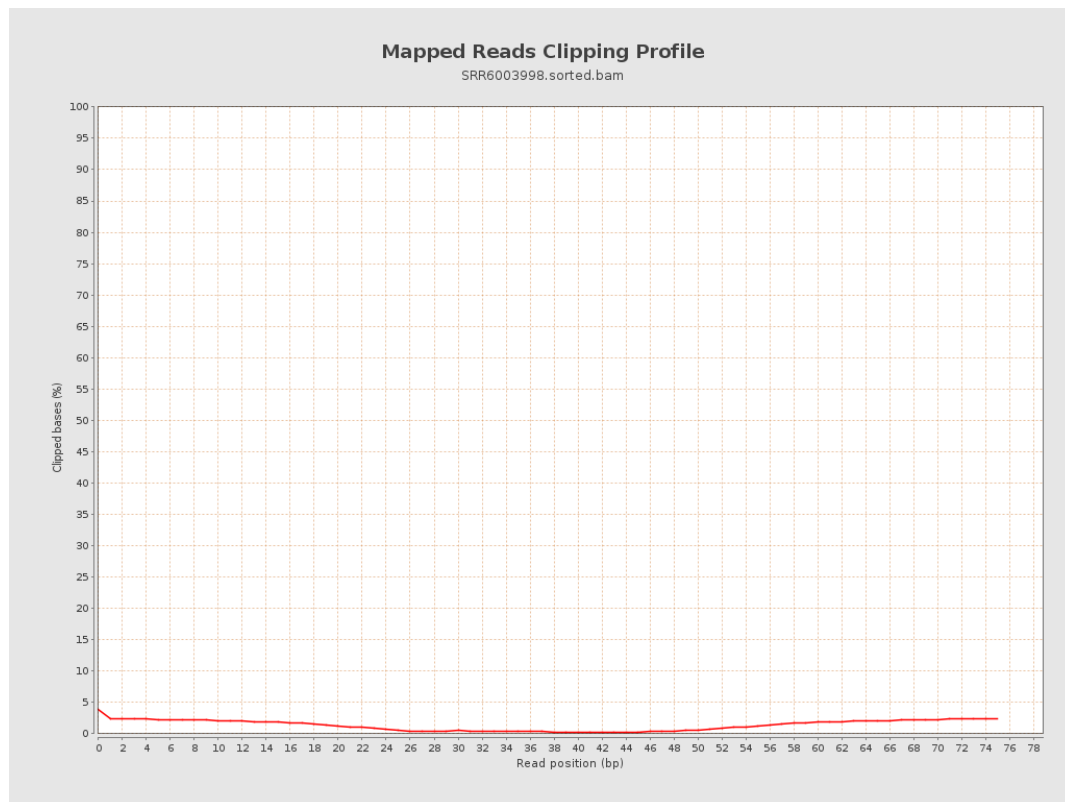
8. Results : Mapped Reads Nucleotide Content



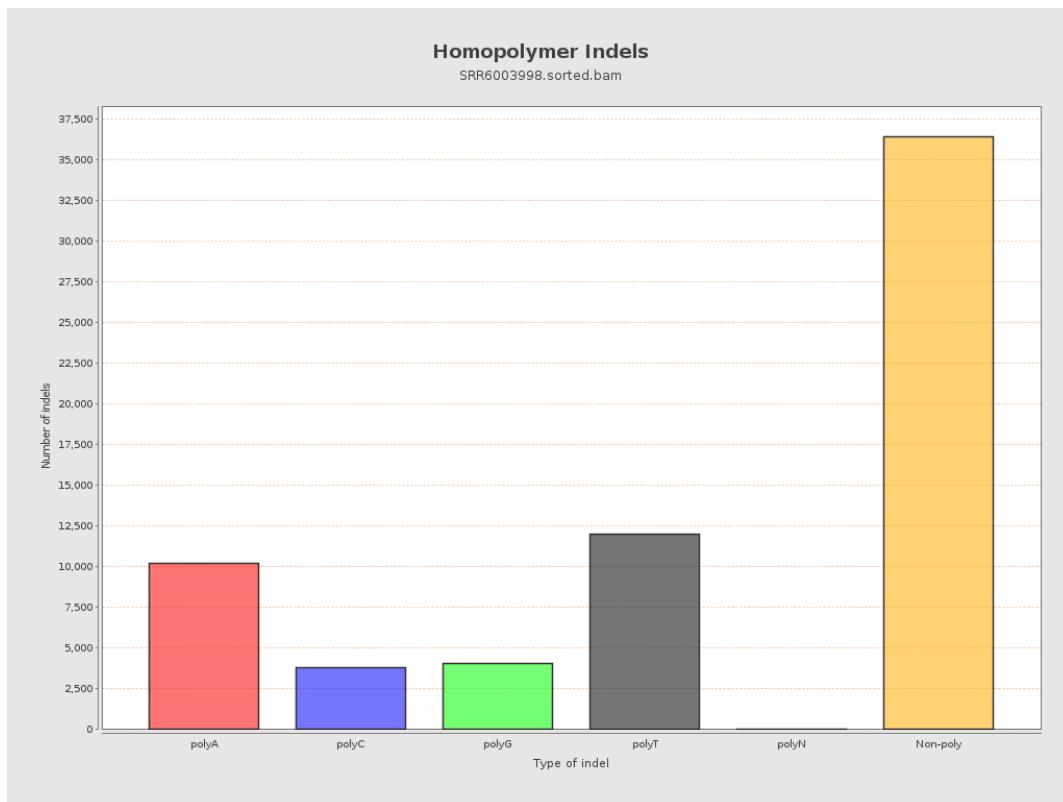
9. Results : Mapped Reads GC-content Distribution



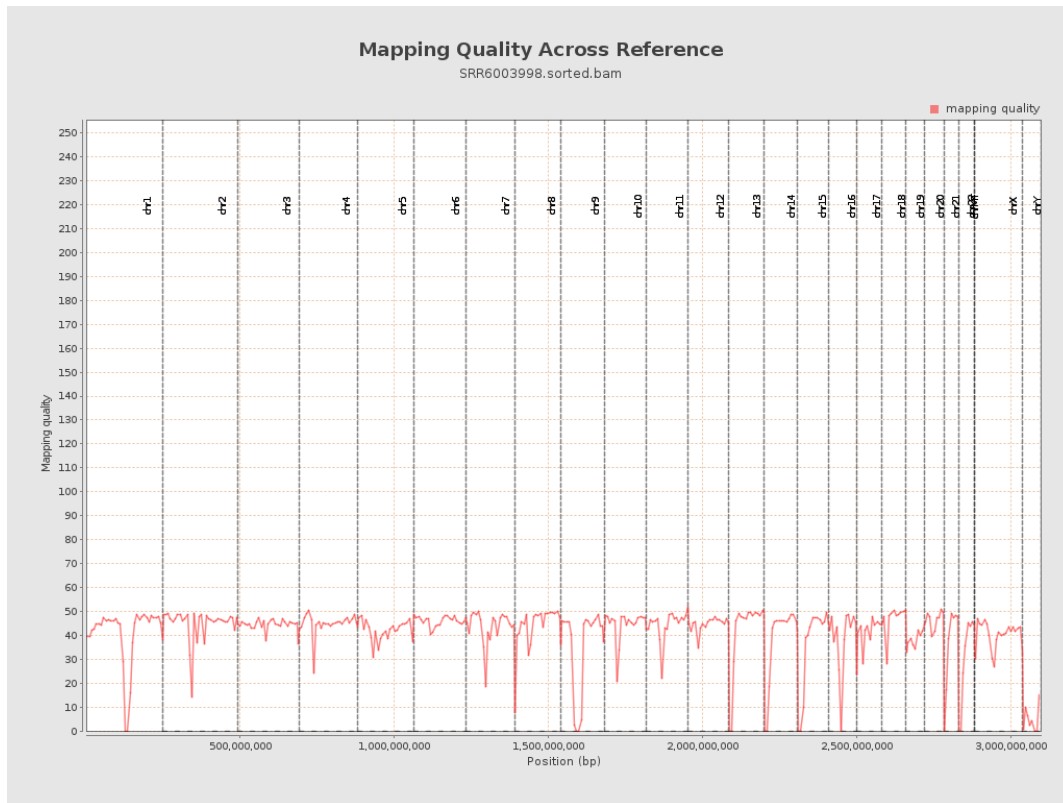
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

