

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:45:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013223.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_SRR6013223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:45:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,901,965
Mapped reads	1,711,114 / 89.97%
Unmapped reads	190,851 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,068 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	63,103 / 3.32%
Duplication rate	2.74%
Clipped reads	752,143 / 39.55%

2.2. ACGT Content

Number/percentage of A's	31,720,816 / 27.84%
Number/percentage of C's	21,019,615 / 18.45%
Number/percentage of T's	36,110,918 / 31.7%
Number/percentage of G's	25,068,256 / 22%
Number/percentage of N's	1,657 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3565
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.42
----------------------	-------

2.5. Mismatches and indels

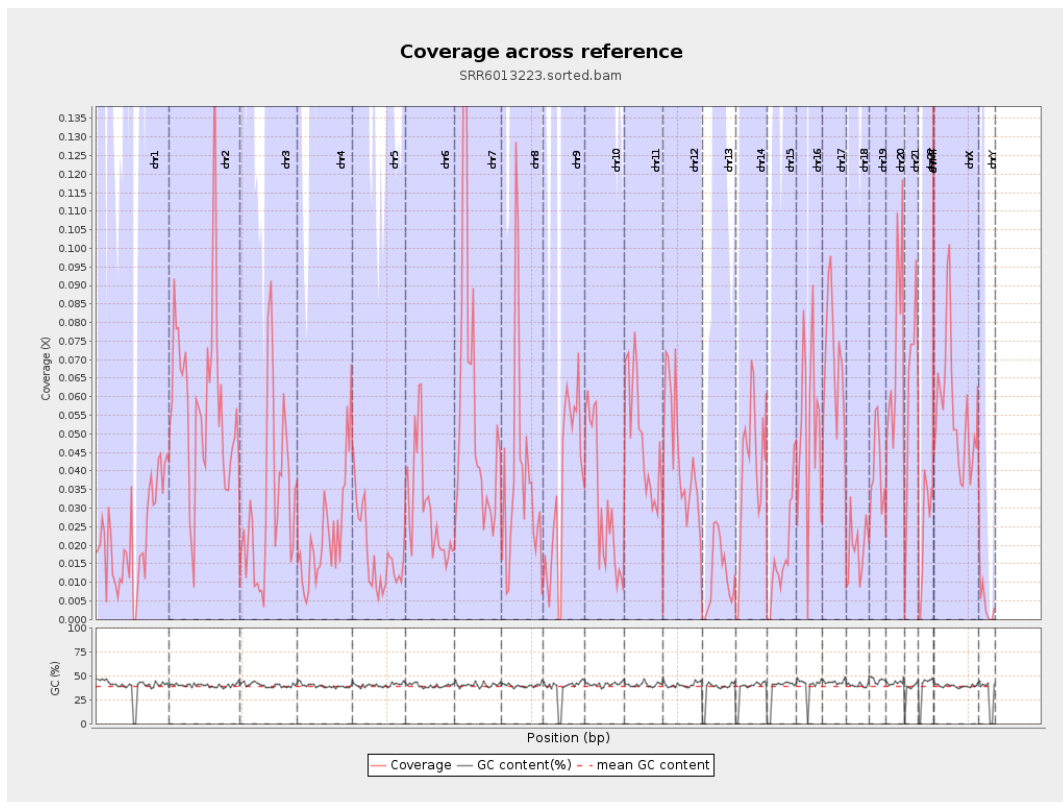
General error rate	0.75%
Mismatches	835,892
Insertions	8,319
Mapped reads with at least one insertion	0.48%
Deletions	31,354
Mapped reads with at least one deletion	1.81%
Homopolymer indels	45.94%

2.6. Chromosome stats

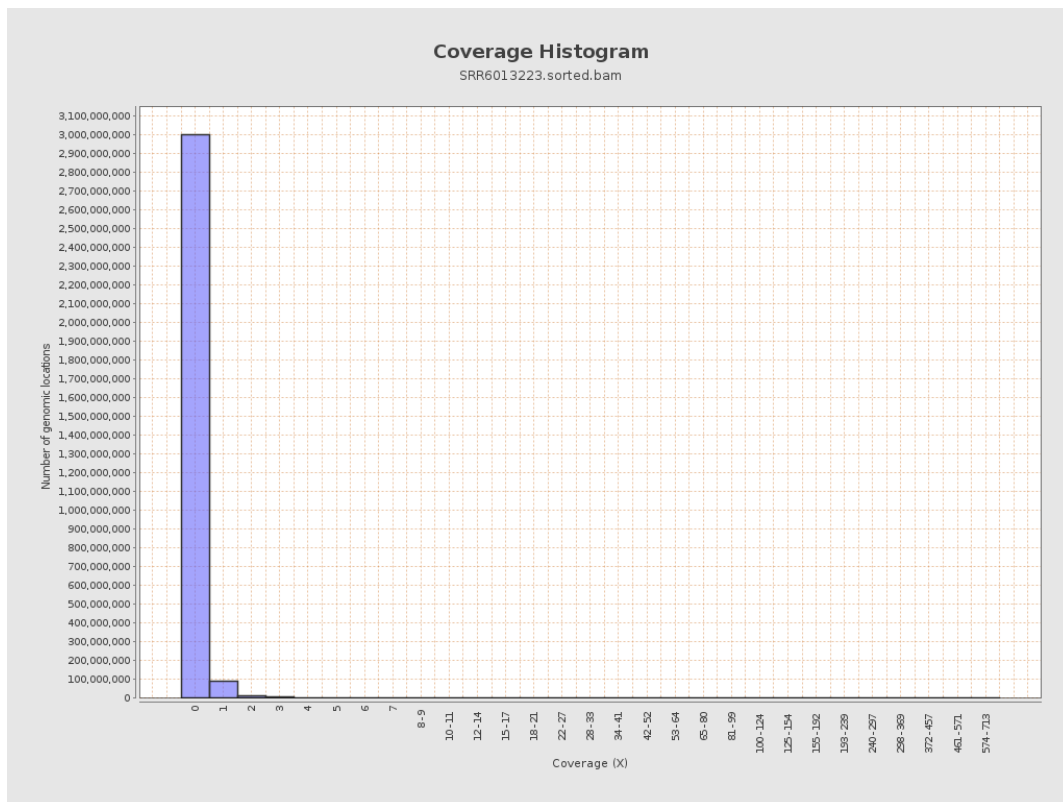
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5540798	0.0222	0.5671
chr2	243199373	14025996	0.0577	0.4142
chr3	198022430	6109971	0.0309	0.1981
chr4	191154276	4465414	0.0234	0.1806
chr5	180915260	3212601	0.0178	0.1548
chr6	171115067	5075749	0.0297	0.2744
chr7	159138663	9199392	0.0578	0.6953

chr8	146364022	5504850	0.0376	0.3924
chr9	141213431	5086304	0.036	0.3196
chr10	135534747	4237690	0.0313	0.3392
chr11	135006516	6470317	0.0479	0.3139
chr12	133851895	5837853	0.0436	0.2402
chr13	115169878	1341985	0.0117	0.1217
chr14	107349540	4234071	0.0394	0.2319
chr15	102531392	1802316	0.0176	0.1485
chr16	90354753	4626952	0.0512	0.2809
chr17	81195210	5618468	0.0692	0.438
chr18	78077248	1501695	0.0192	0.472
chr19	59128983	2403912	0.0407	0.4627
chr20	63025520	4571887	0.0725	0.3084
chr21	48129895	2934133	0.061	0.2896
chr22	51304566	1238369	0.0241	0.172
chrMT	16571	4242	0.256	0.5757
chrX	155270560	8675130	0.0559	0.3033
chrY	59373566	254359	0.0043	0.0946

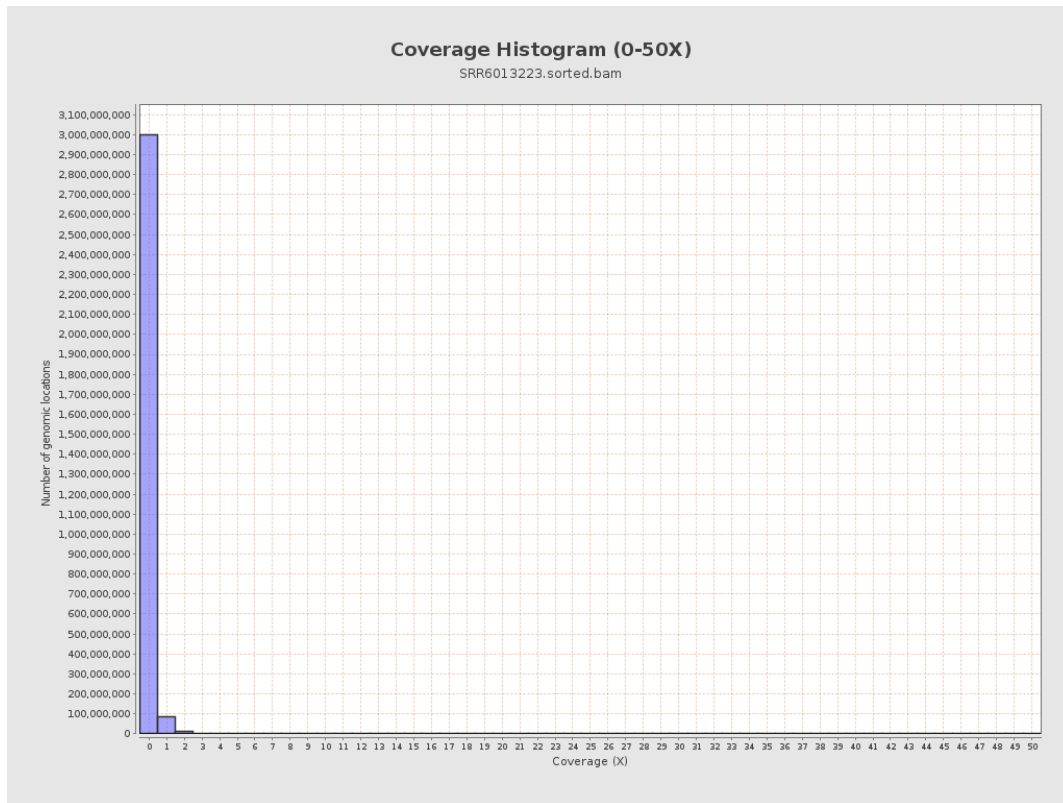
3. Results : Coverage across reference



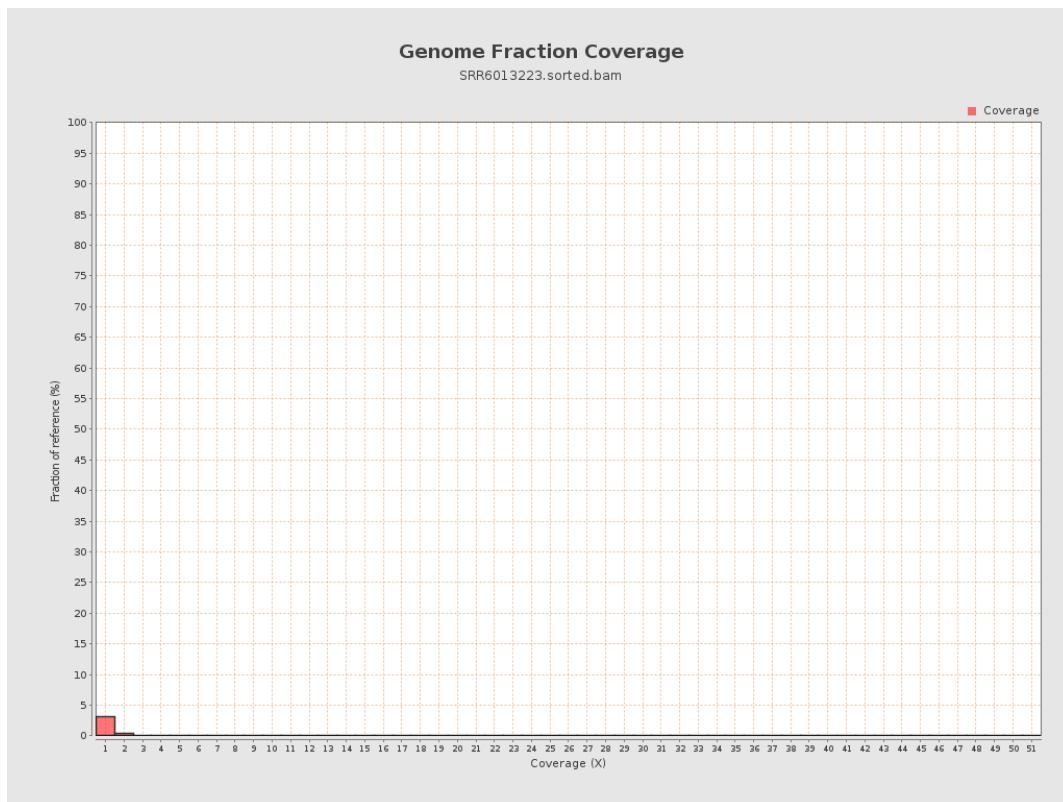
4. Results : Coverage Histogram



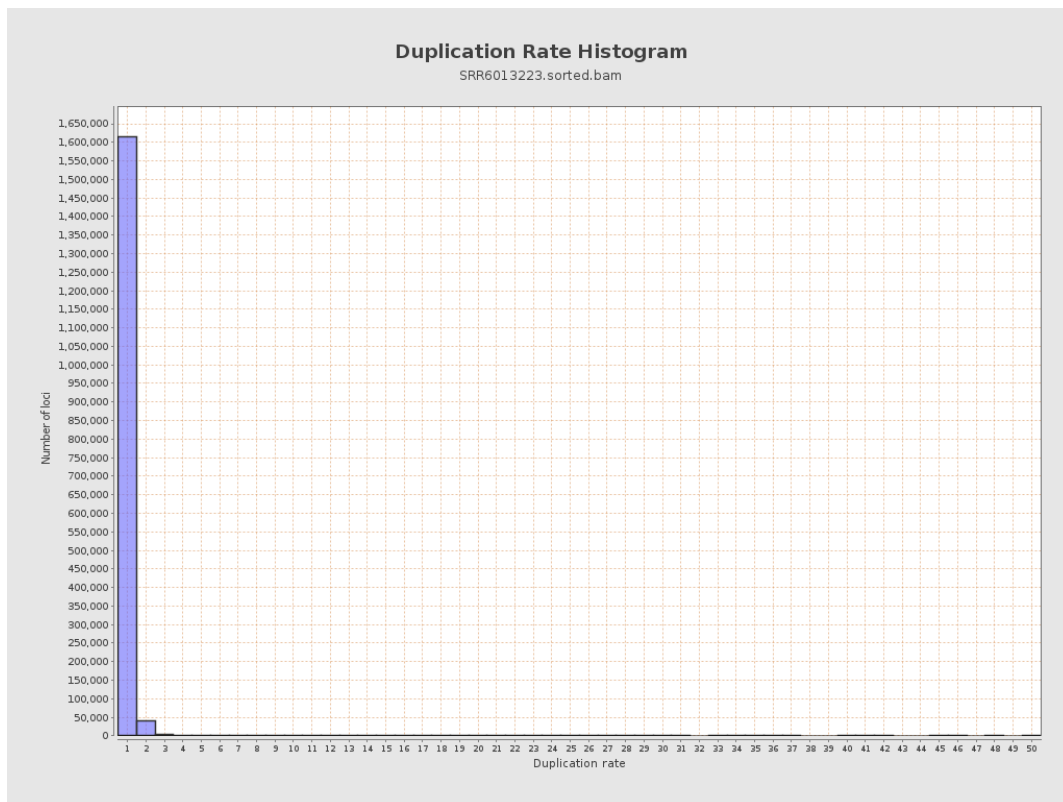
5. Results : Coverage Histogram (0-50X)



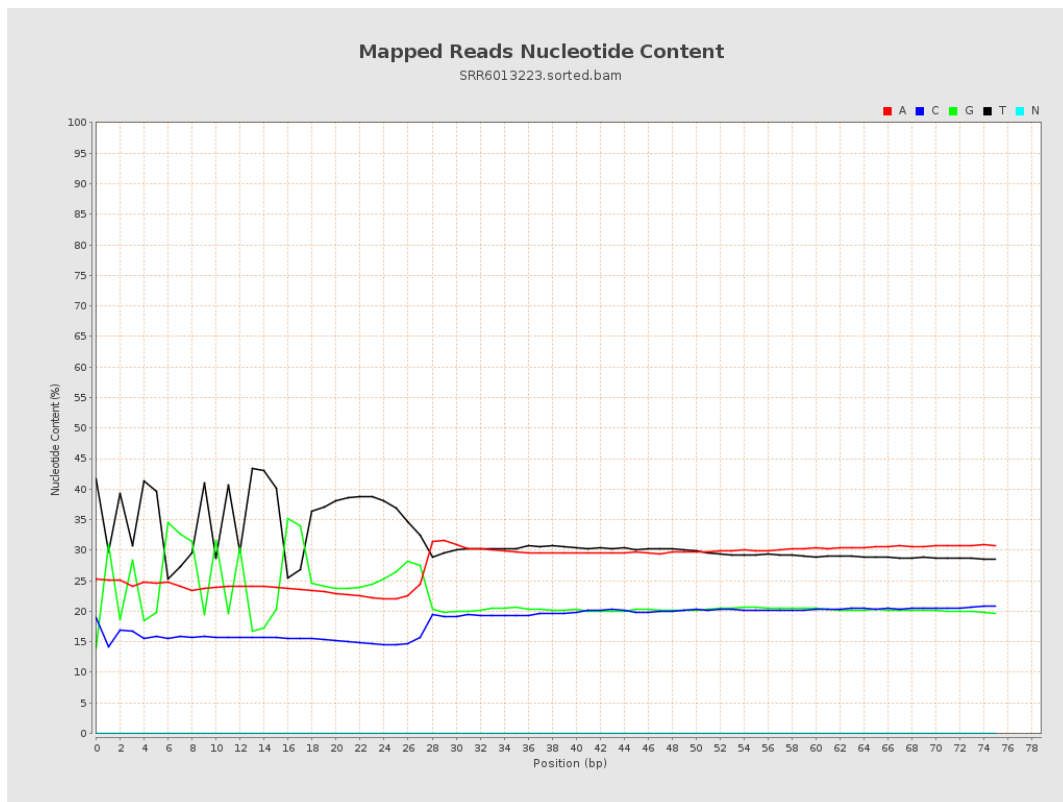
6. Results : Genome Fraction Coverage



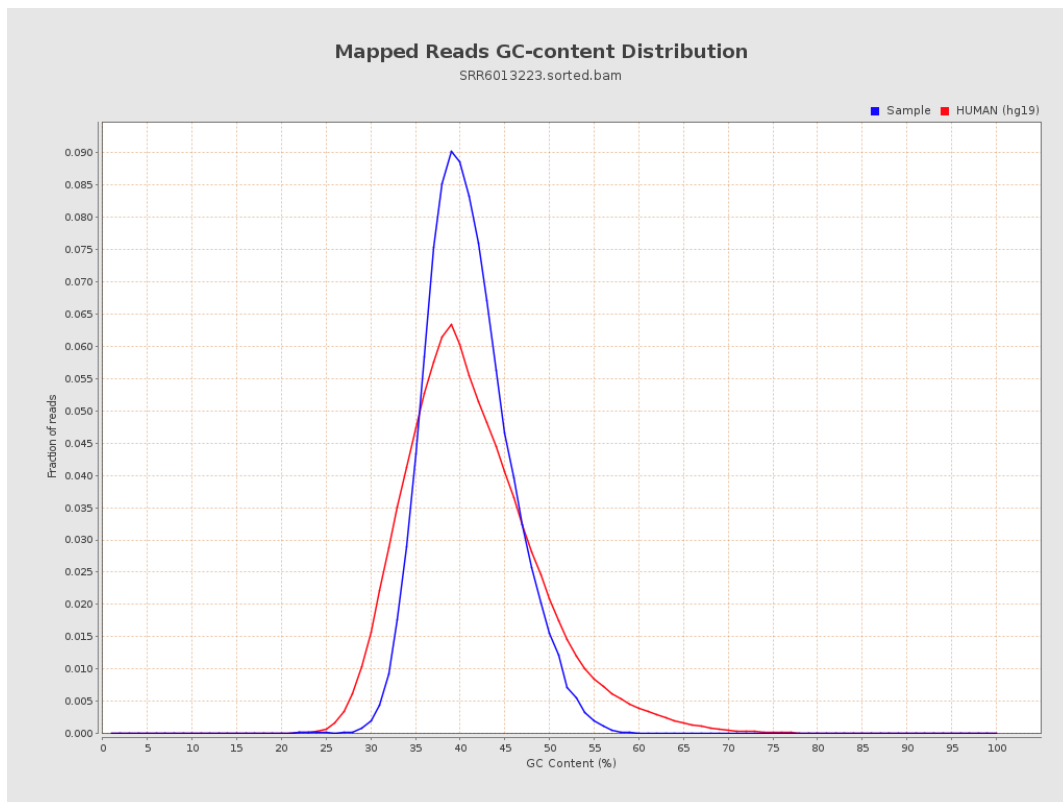
7. Results : Duplication Rate Histogram



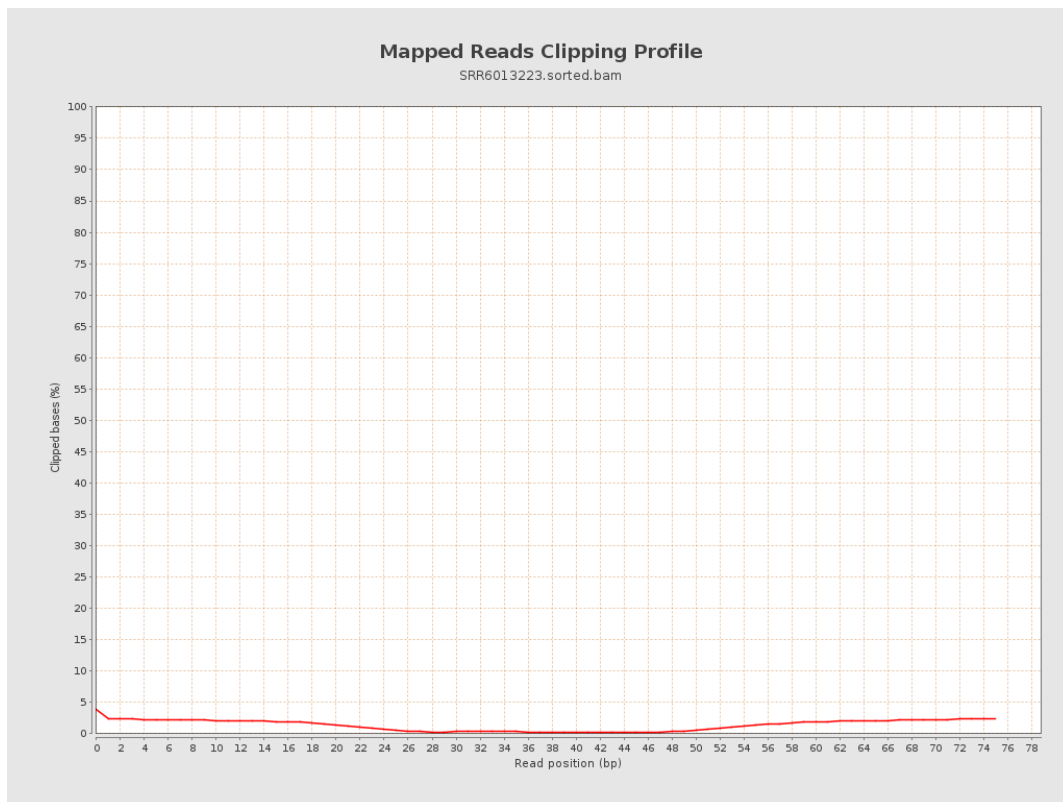
8. Results : Mapped Reads Nucleotide Content



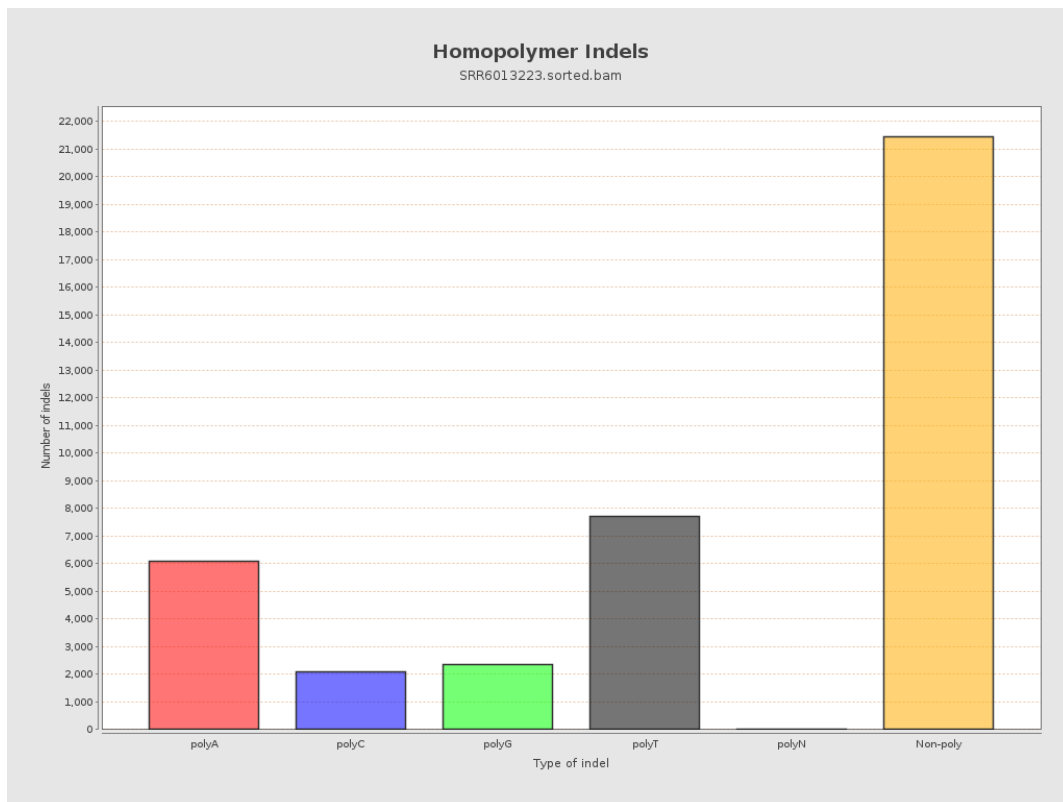
9. Results : Mapped Reads GC-content Distribution



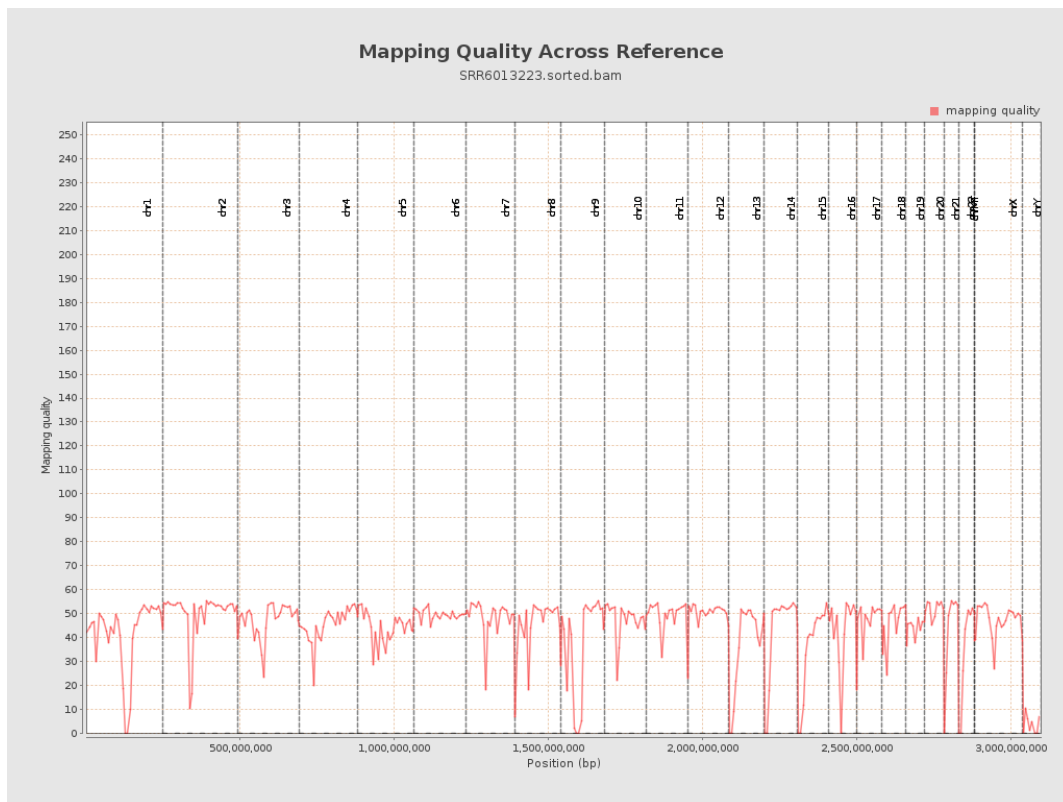
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

