

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:00:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013228.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_SRR6013228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:00:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,164,874
Mapped reads	1,878,908 / 86.79%
Unmapped reads	285,966 / 13.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,903 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	95,708 / 4.42%
Duplication rate	4.02%
Clipped reads	778,693 / 35.97%

2.2. ACGT Content

Number/percentage of A's	35,236,252 / 27.85%
Number/percentage of C's	23,288,452 / 18.41%
Number/percentage of T's	40,400,750 / 31.93%
Number/percentage of G's	27,565,957 / 21.79%
Number/percentage of N's	27,284 / 0.02%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.383
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2.4. Mapping Quality

Mean Mapping Quality	46.95
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2.5. Mismatches and indels

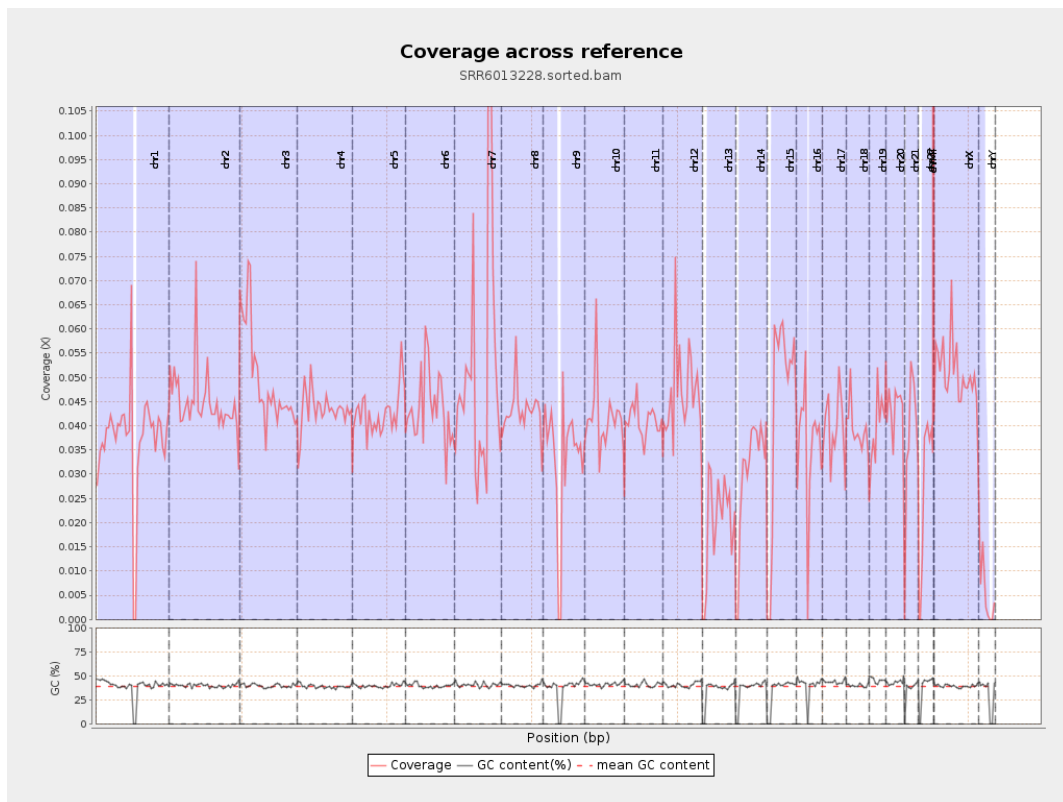
General error rate	0.82%
Mismatches	1,026,200
Insertions	9,127
Mapped reads with at least one insertion	0.48%
Deletions	30,743
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.6%

2.6. Chromosome stats

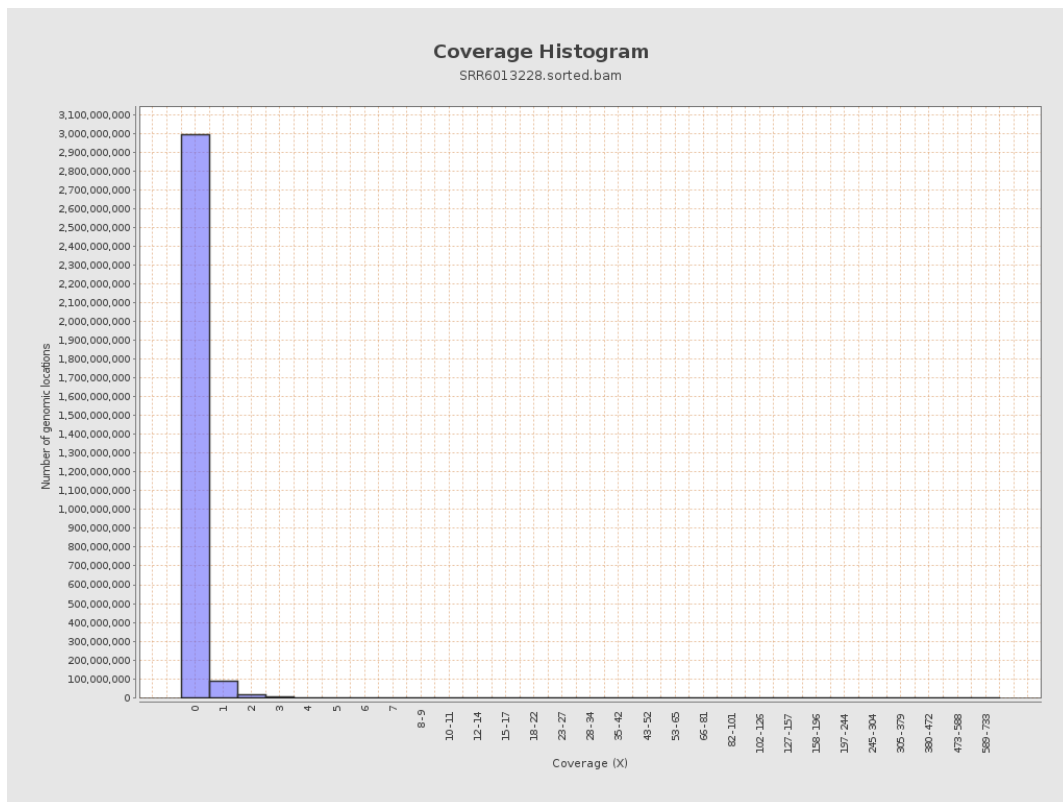
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9261315	0.0372	0.6607
chr2	243199373	10958968	0.0451	0.4485
chr3	198022430	9795593	0.0495	0.259
chr4	191154276	8273509	0.0433	0.2541
chr5	180915260	7743921	0.0428	0.2439
chr6	171115067	7425526	0.0434	0.2938
chr7	159138663	8528364	0.0536	0.6074

chr8	146364022	6295089	0.043	0.3957
chr9	141213431	4708539	0.0333	0.3591
chr10	135534747	5648833	0.0417	0.373
chr11	135006516	5518560	0.0409	0.3074
chr12	133851895	6303866	0.0471	0.2593
chr13	115169878	2271425	0.0197	0.1636
chr14	107349540	3226288	0.0301	0.2204
chr15	102531392	4626990	0.0451	0.249
chr16	90354753	3247374	0.0359	0.2602
chr17	81195210	3161437	0.0389	0.259
chr18	78077248	3091268	0.0396	0.7202
chr19	59128983	2369463	0.0401	0.5028
chr20	63025520	2702390	0.0429	0.2437
chr21	48129895	1797682	0.0374	0.2382
chr22	51304566	1366886	0.0266	0.1867
chrMT	16571	42778	2.5815	2.1499
chrX	155270560	7885240	0.0508	0.2921
chrY	59373566	320855	0.0054	0.1343

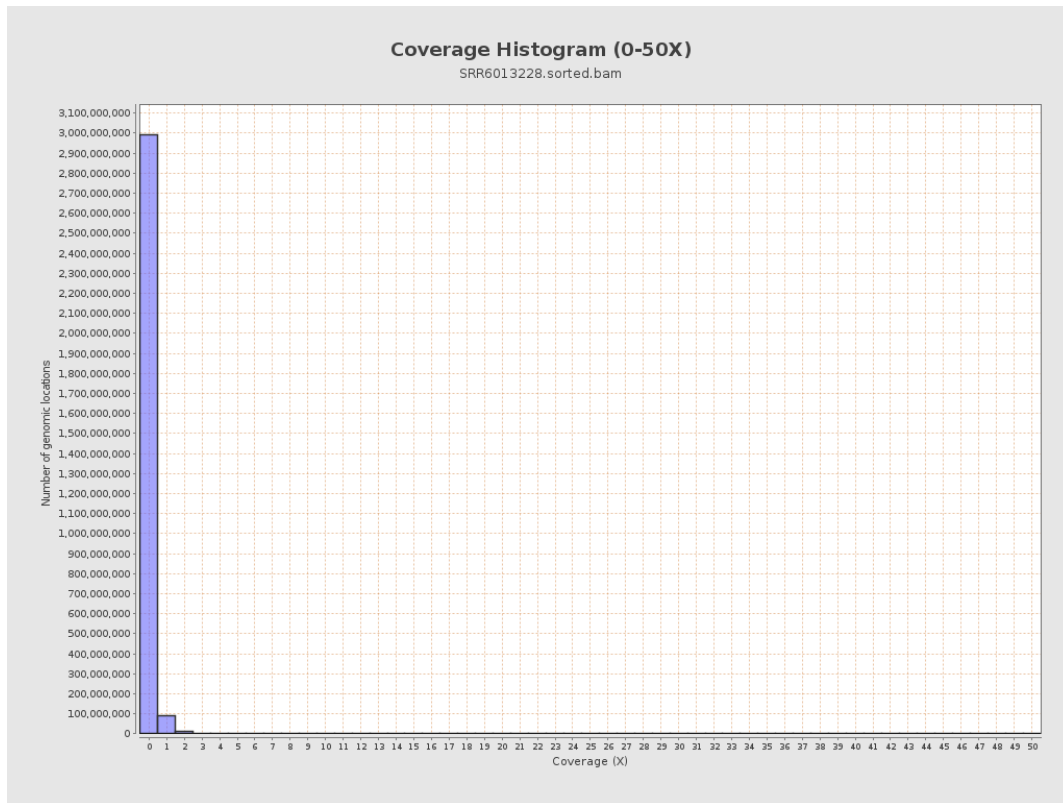
3. Results : Coverage across reference



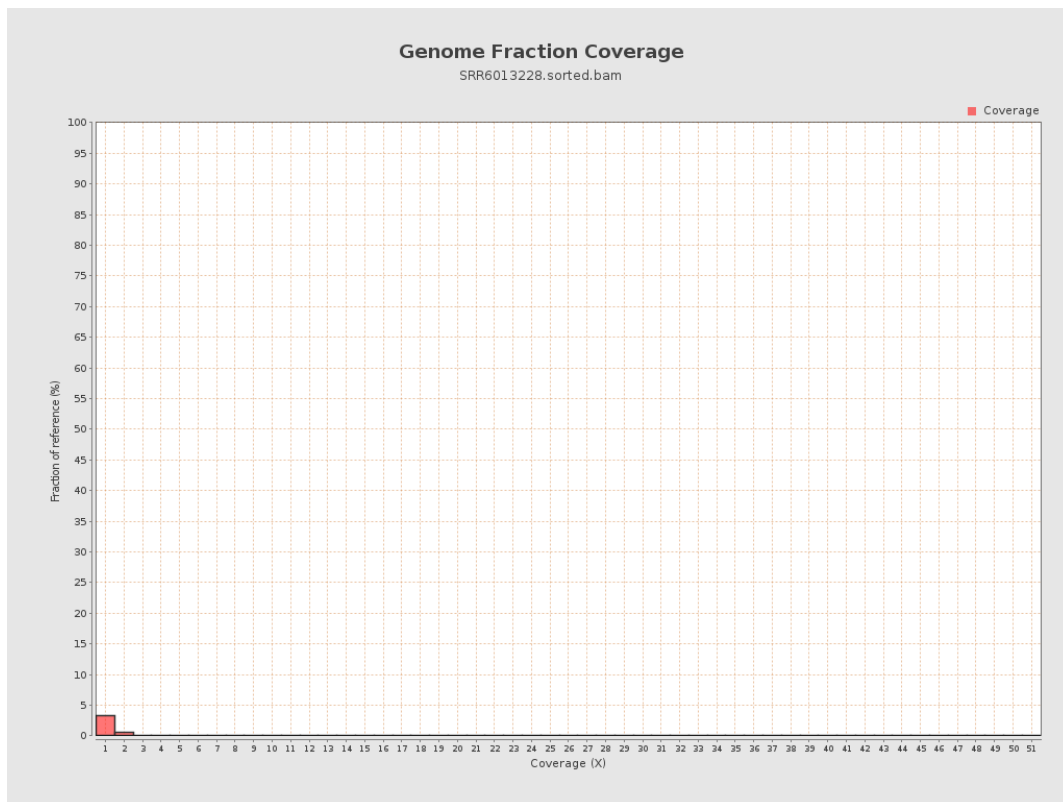
4. Results : Coverage Histogram



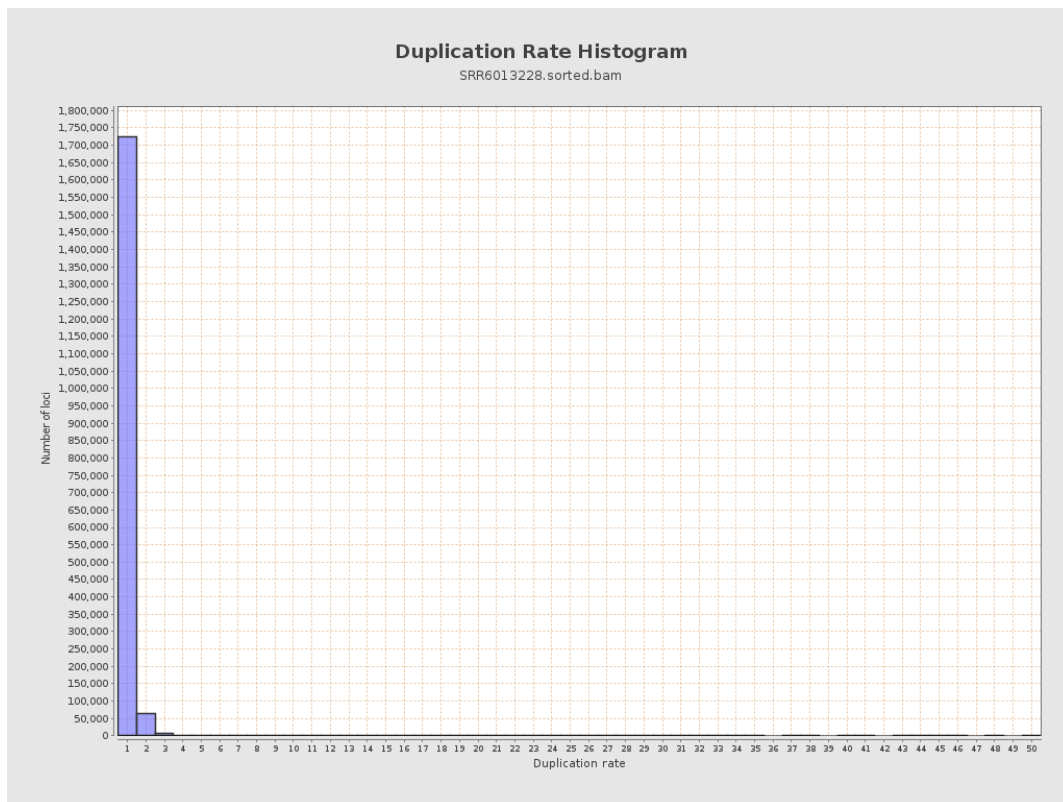
5. Results : Coverage Histogram (0-50X)



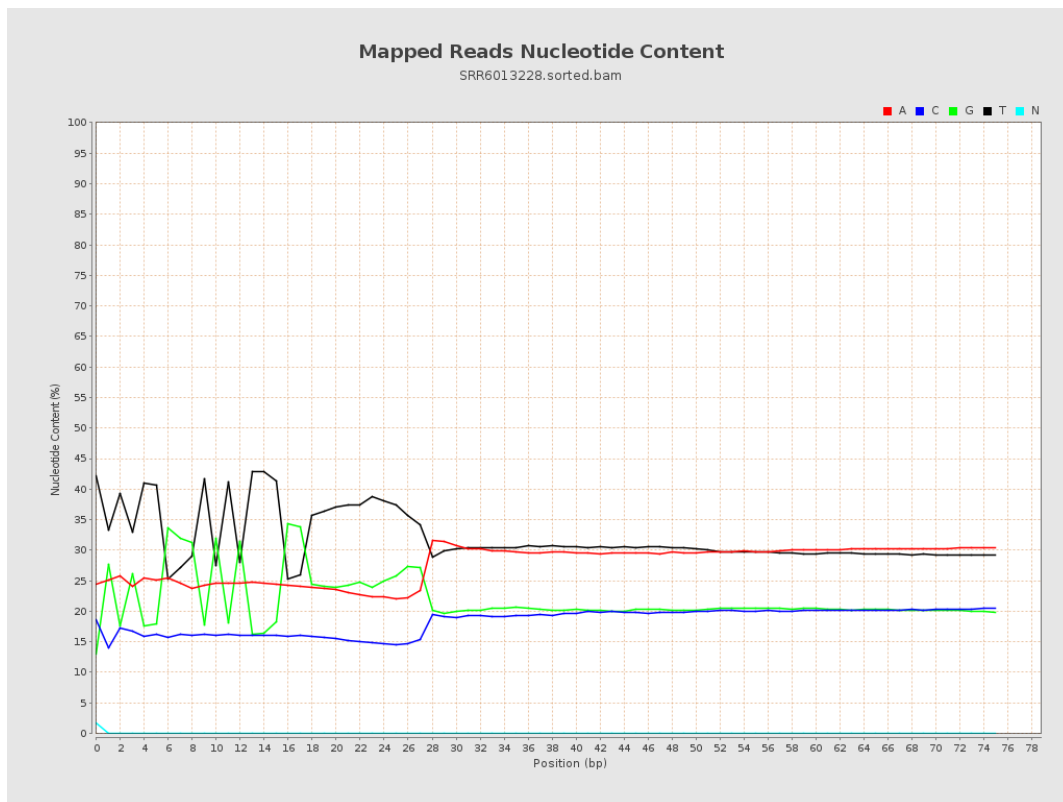
6. Results : Genome Fraction Coverage



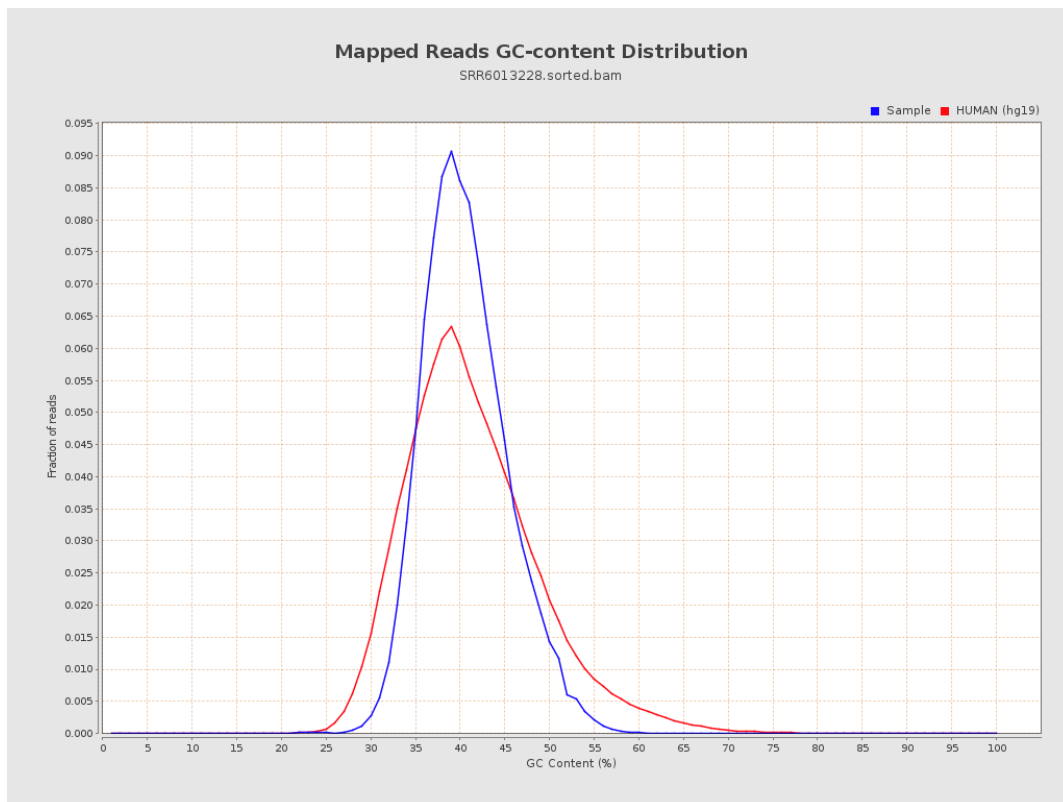
7. Results : Duplication Rate Histogram



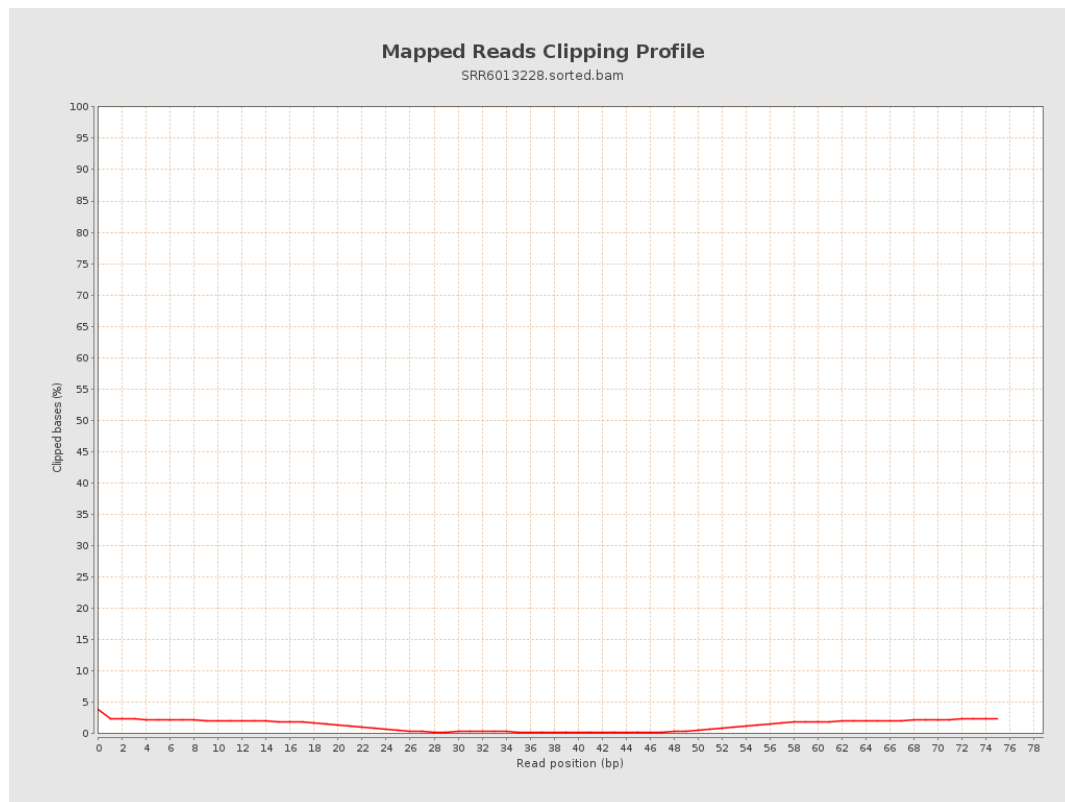
8. Results : Mapped Reads Nucleotide Content



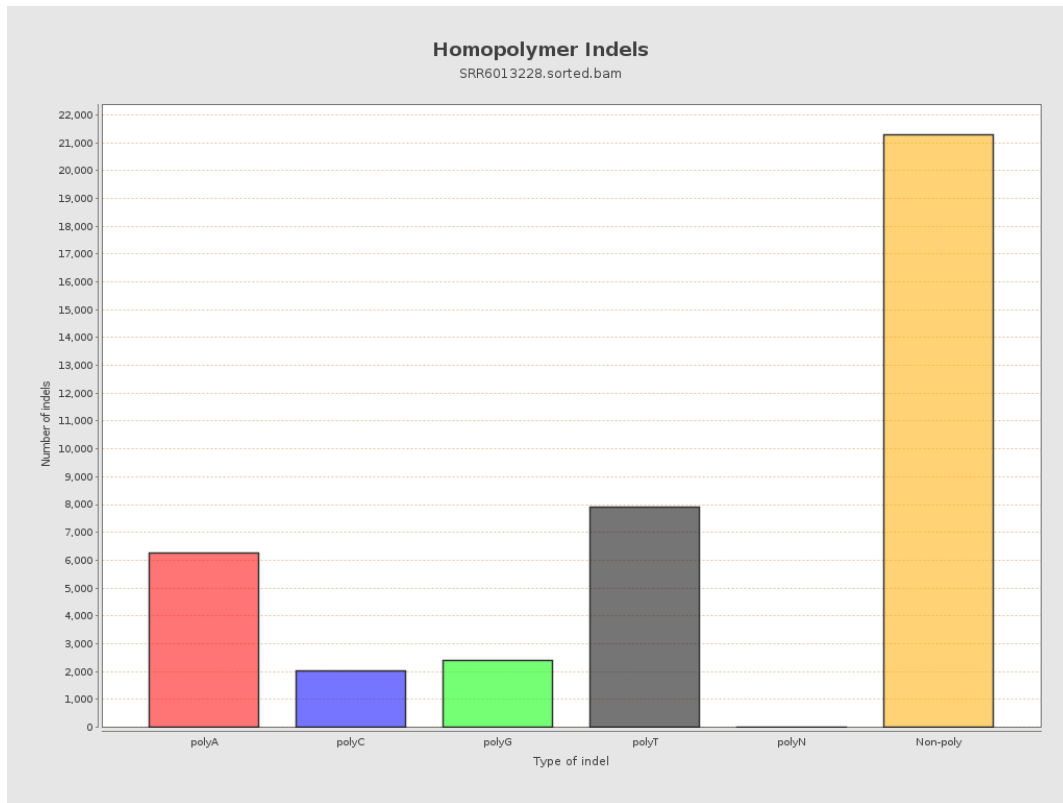
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

