

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:22:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013279.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_SRR6013279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:22:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,644,238
Mapped reads	1,352,660 / 82.27%
Unmapped reads	291,578 / 17.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,918 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	137,014 / 8.33%
Duplication rate	8.37%
Clipped reads	842,928 / 51.27%

2.2. ACGT Content

Number/percentage of A's	23,709,317 / 27.99%
Number/percentage of C's	14,897,355 / 17.59%
Number/percentage of T's	27,691,187 / 32.69%
Number/percentage of G's	18,384,833 / 21.71%
Number/percentage of N's	17,689 / 0.02%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.299
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	44.26
----------------------	-------

2.5. Mismatches and indels

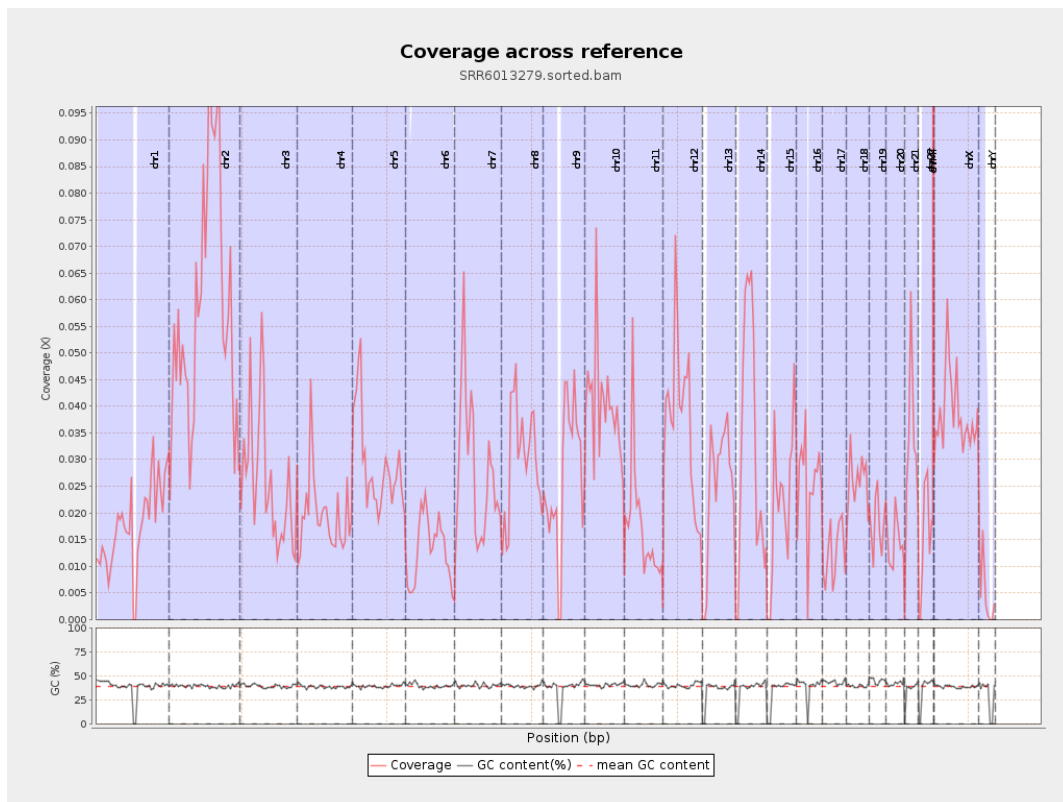
General error rate	1.01%
Mismatches	844,417
Insertions	6,483
Mapped reads with at least one insertion	0.48%
Deletions	42,396
Mapped reads with at least one deletion	3.08%
Homopolymer indels	42.16%

2.6. Chromosome stats

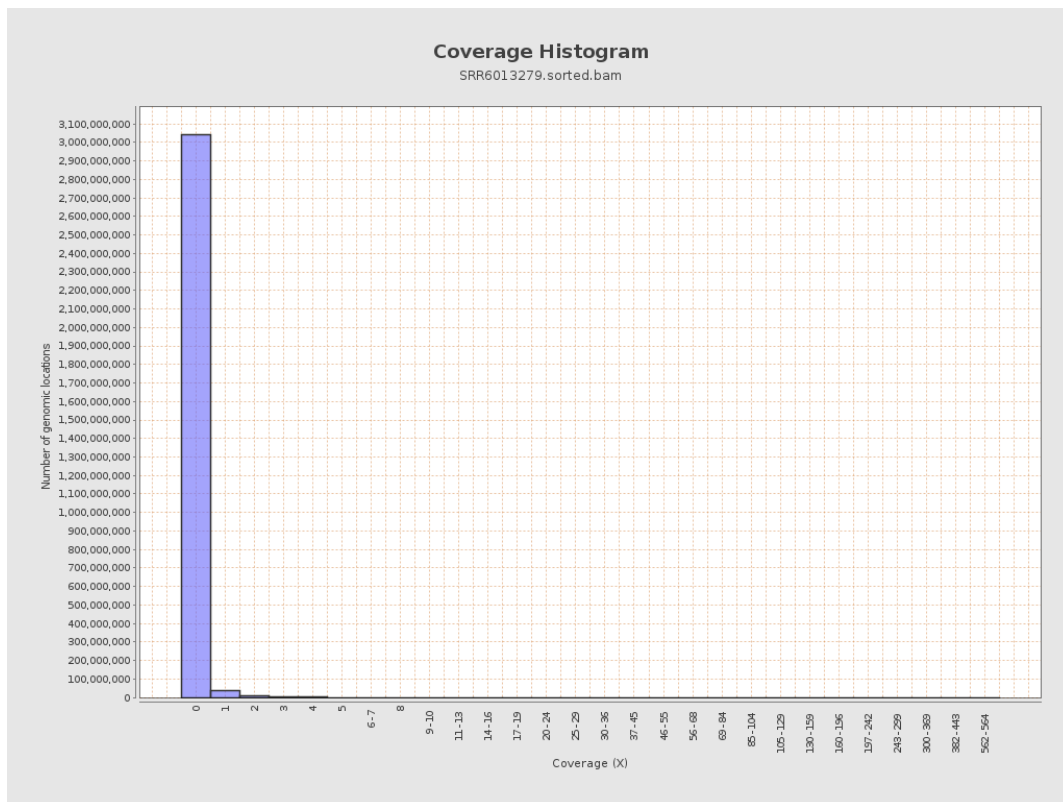
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4397968	0.0176	0.3622
chr2	243199373	14281207	0.0587	0.4688
chr3	198022430	5133174	0.0259	0.2261
chr4	191154276	3695094	0.0193	0.2284
chr5	180915260	5212777	0.0288	0.2406
chr6	171115067	2230084	0.013	0.183
chr7	159138663	4481350	0.0282	0.3209

chr8	146364022	4337736	0.0296	0.364
chr9	141213431	3773046	0.0267	0.2779
chr10	135534747	5436029	0.0401	0.4356
chr11	135006516	2335502	0.0173	0.2077
chr12	133851895	4946624	0.037	0.274
chr13	115169878	2814368	0.0244	0.2218
chr14	107349540	3505595	0.0327	0.2623
chr15	102531392	2284932	0.0223	0.2043
chr16	90354753	2323058	0.0257	0.2366
chr17	81195210	1003779	0.0124	0.1581
chr18	78077248	2042686	0.0262	0.42
chr19	59128983	1068331	0.0181	0.3349
chr20	63025520	905508	0.0144	0.1675
chr21	48129895	1515634	0.0315	0.2696
chr22	51304566	761175	0.0148	0.1652
chrMT	16571	9468	0.5714	0.9617
chrX	155270560	5999157	0.0386	0.2841
chrY	59373566	279932	0.0047	0.1649

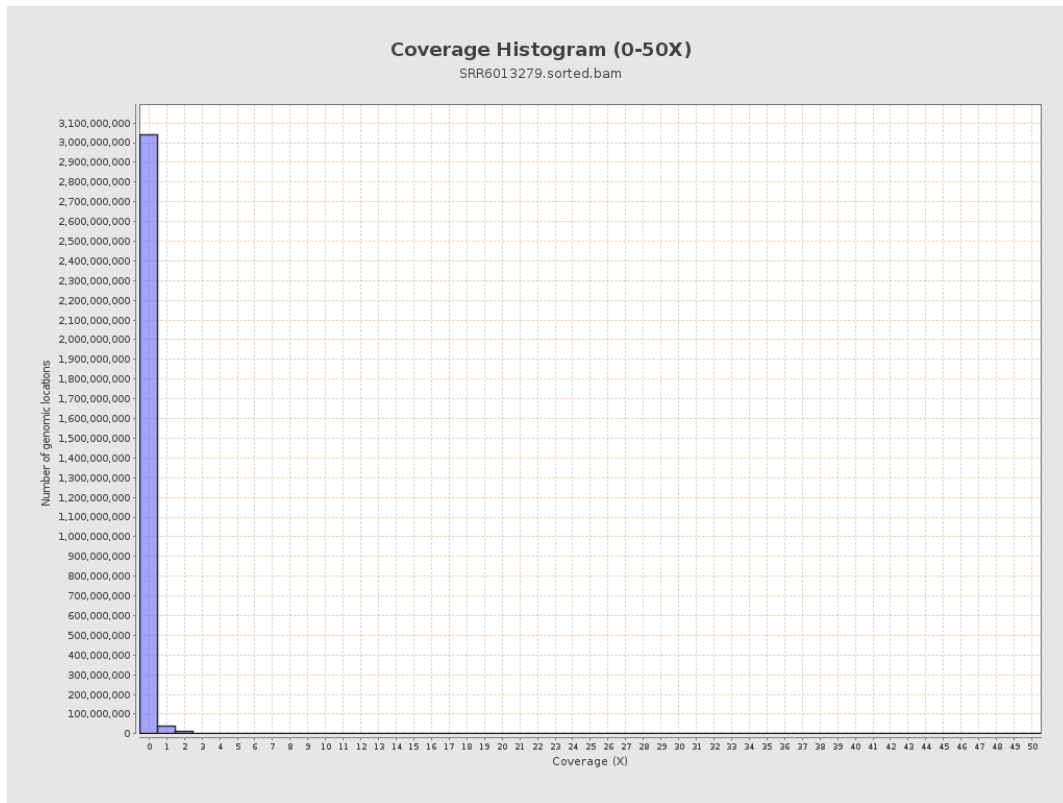
3. Results : Coverage across reference



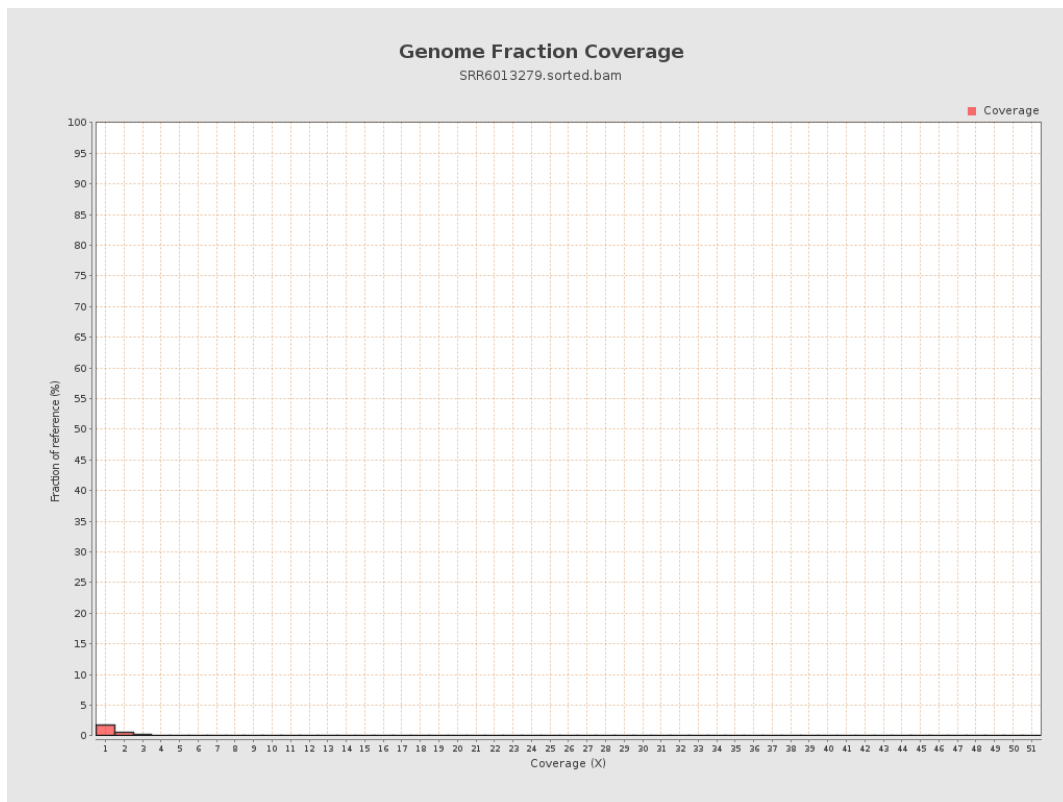
4. Results : Coverage Histogram



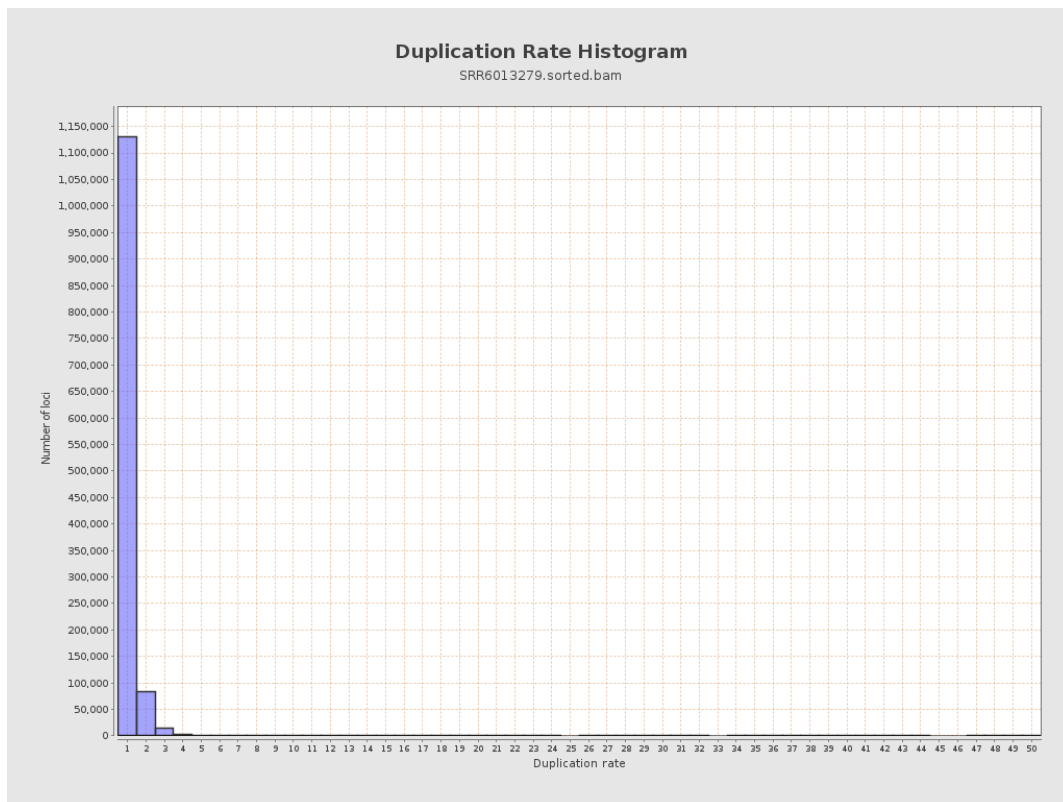
5. Results : Coverage Histogram (0-50X)



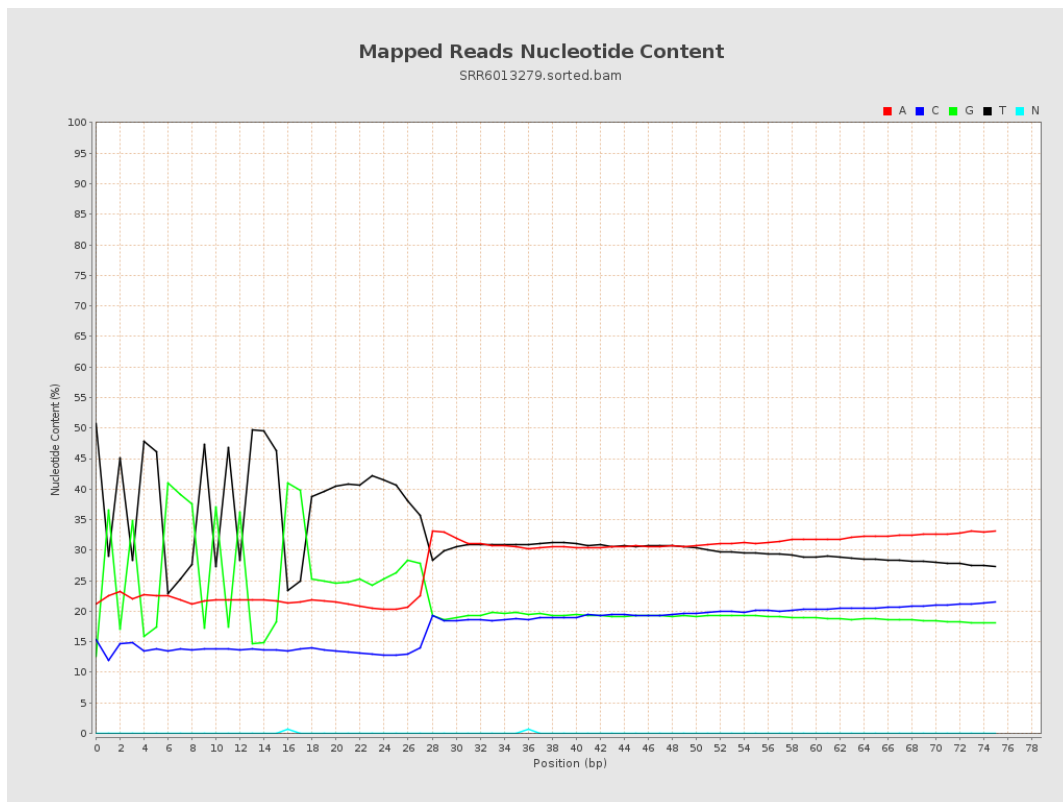
6. Results : Genome Fraction Coverage



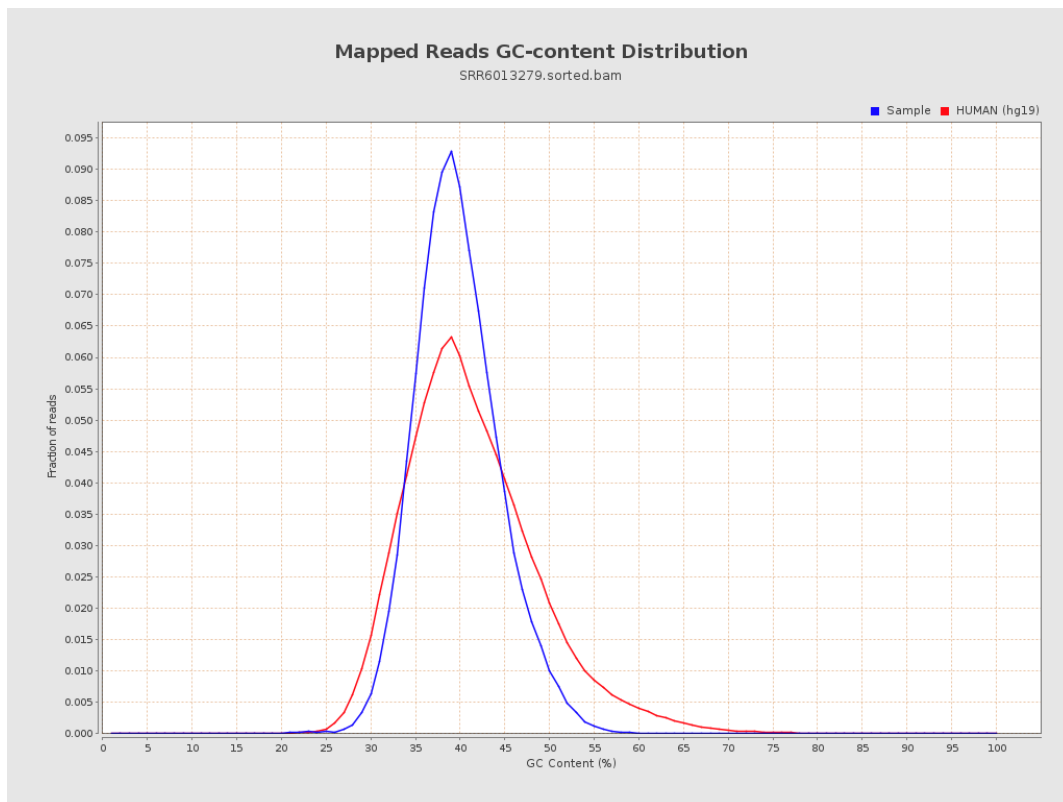
7. Results : Duplication Rate Histogram



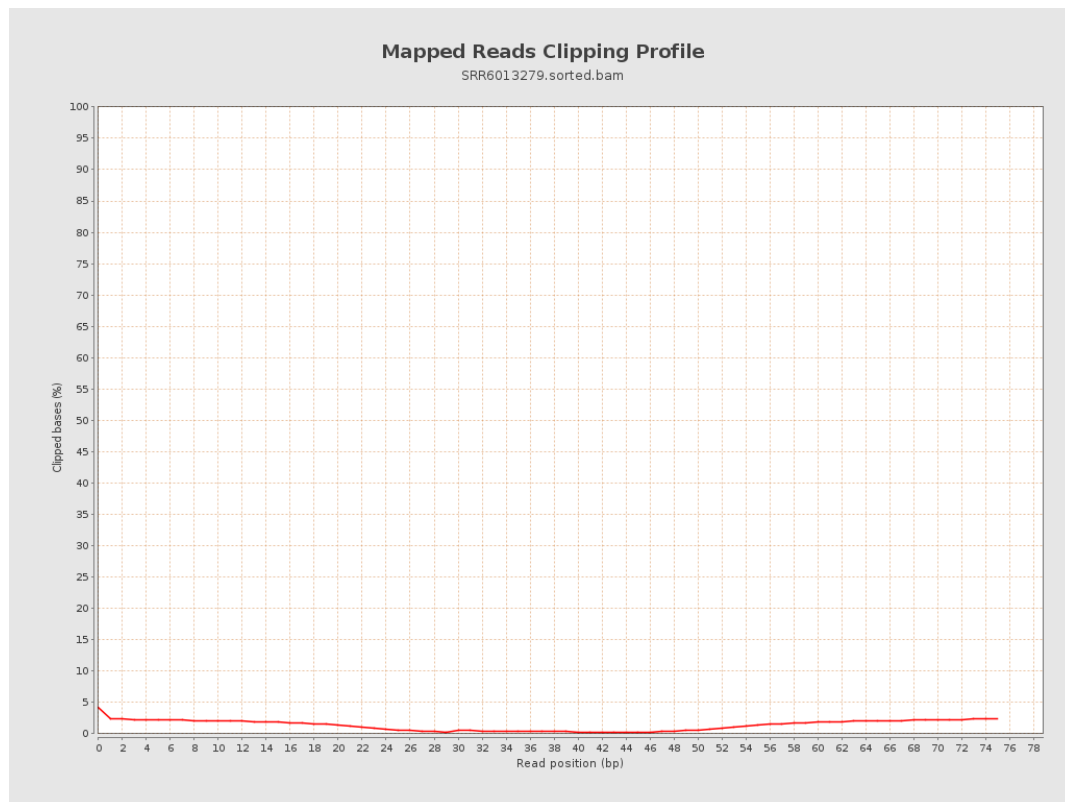
8. Results : Mapped Reads Nucleotide Content



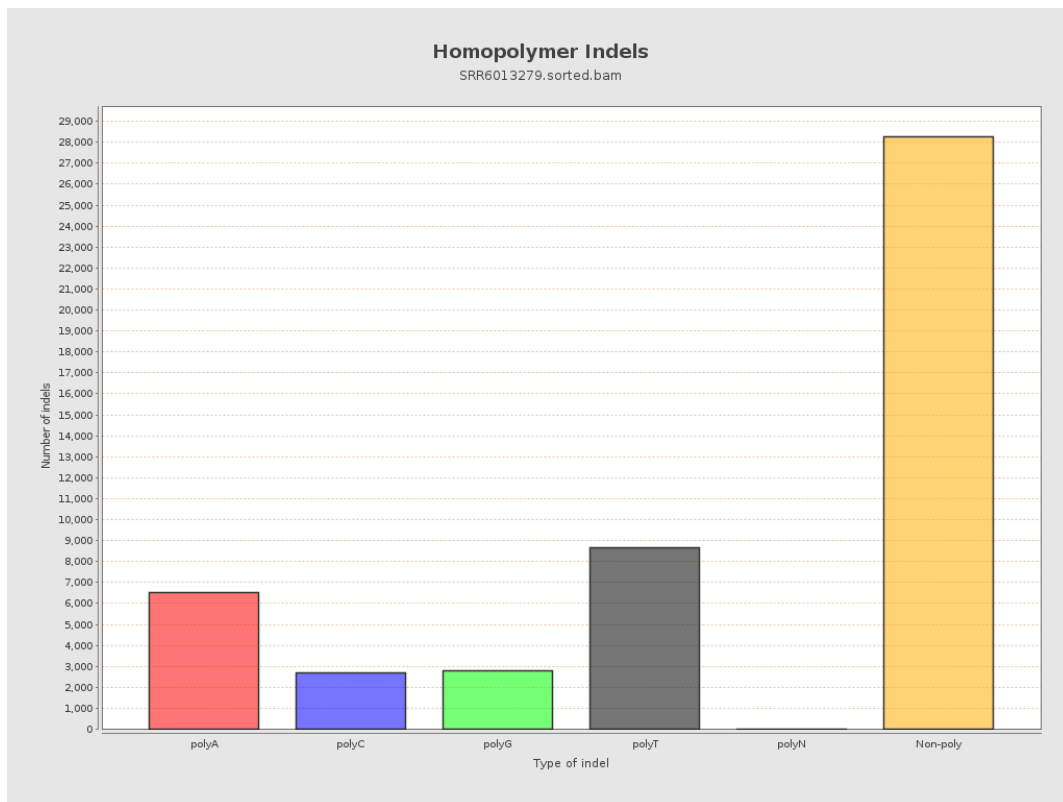
9. Results : Mapped Reads GC-content Distribution



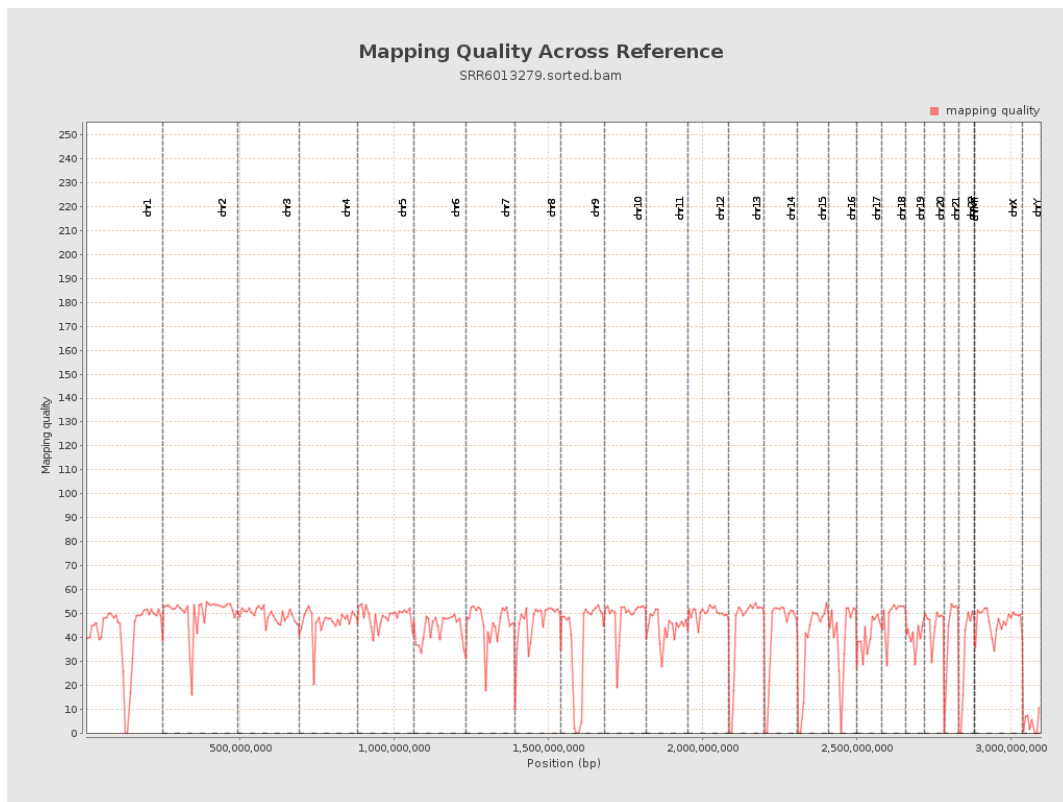
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

