

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:14:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082928.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_SRR3082928 /home/luna/Desktop/database/homo_hsa/hsa.fa SRR3082928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:14:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,154,774
Mapped reads	1,920,652 / 89.13%
Unmapped reads	234,122 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,331 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	112,727 / 5.23%
Duplication rate	4.98%
Clipped reads	877,037 / 40.7%

2.2. ACGT Content

Number/percentage of A's	34,205,732 / 26.83%
Number/percentage of C's	24,244,852 / 19.02%
Number/percentage of T's	39,718,936 / 31.16%
Number/percentage of G's	29,309,745 / 22.99%
Number/percentage of N's	6,330 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3205
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.06
----------------------	-------

2.5. Mismatches and indels

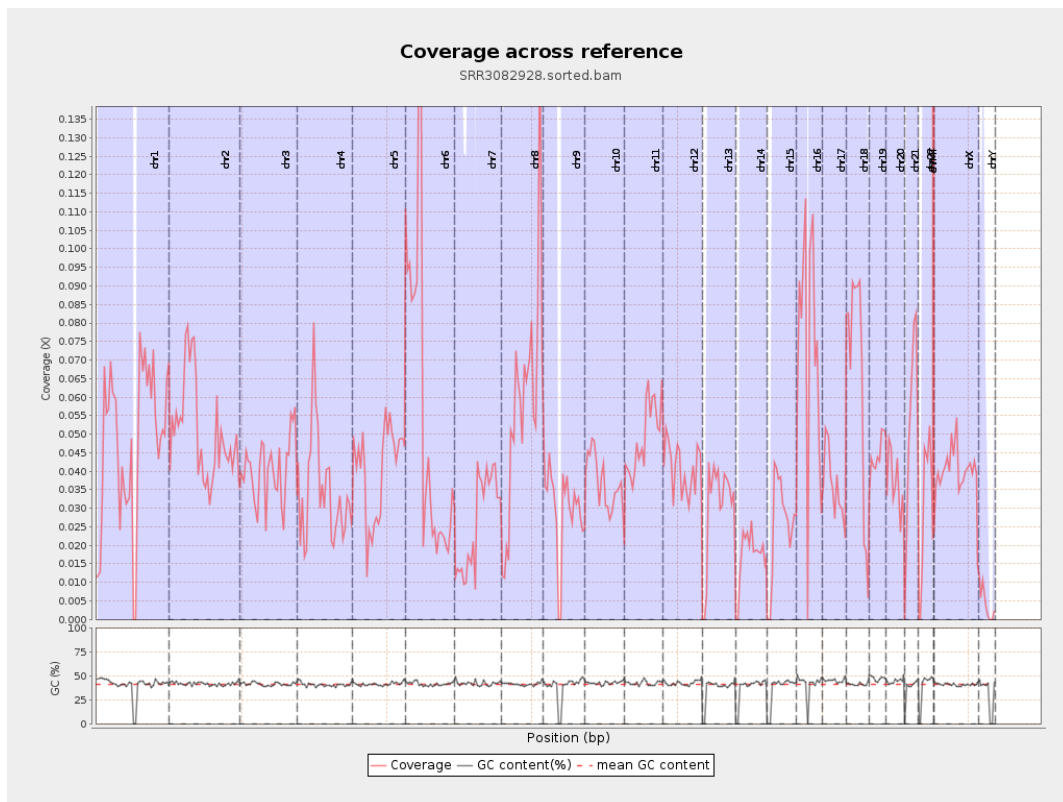
General error rate	0.75%
Mismatches	935,817
Insertions	9,937
Mapped reads with at least one insertion	0.51%
Deletions	29,804
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.36%

2.6. Chromosome stats

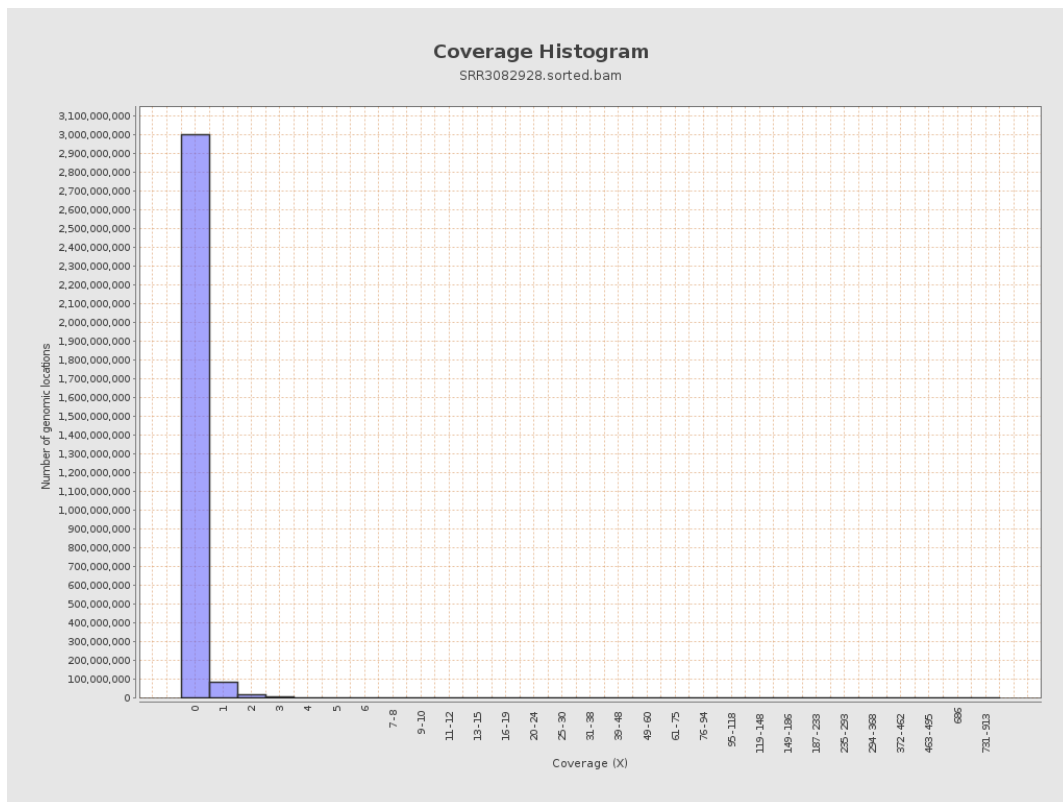
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11886016	0.0477	0.4126
chr2	243199373	12340153	0.0507	0.5387
chr3	198022430	8022819	0.0405	0.2469
chr4	191154276	6497111	0.034	0.2305
chr5	180915260	7298096	0.0403	0.2458
chr6	171115067	9395373	0.0549	0.3482
chr7	159138663	4215716	0.0265	0.2243

chr8	146364022	8547955	0.0584	0.3492
chr9	141213431	4199266	0.0297	0.2827
chr10	135534747	5049284	0.0373	0.2544
chr11	135006516	6608894	0.049	0.3362
chr12	133851895	5413328	0.0404	0.2485
chr13	115169878	3461666	0.0301	0.2217
chr14	107349540	1846023	0.0172	0.1696
chr15	102531392	2635198	0.0257	0.2035
chr16	90354753	6583994	0.0729	0.3559
chr17	81195210	2891008	0.0356	0.261
chr18	78077248	5122065	0.0656	0.5132
chr19	59128983	2630387	0.0445	0.3767
chr20	63025520	2324379	0.0369	0.2439
chr21	48129895	2475345	0.0514	0.2825
chr22	51304566	1551754	0.0302	0.2138
chrMT	16571	120352	7.2628	5.1814
chrX	155270560	6184606	0.0398	0.2601
chrY	59373566	233770	0.0039	0.0819

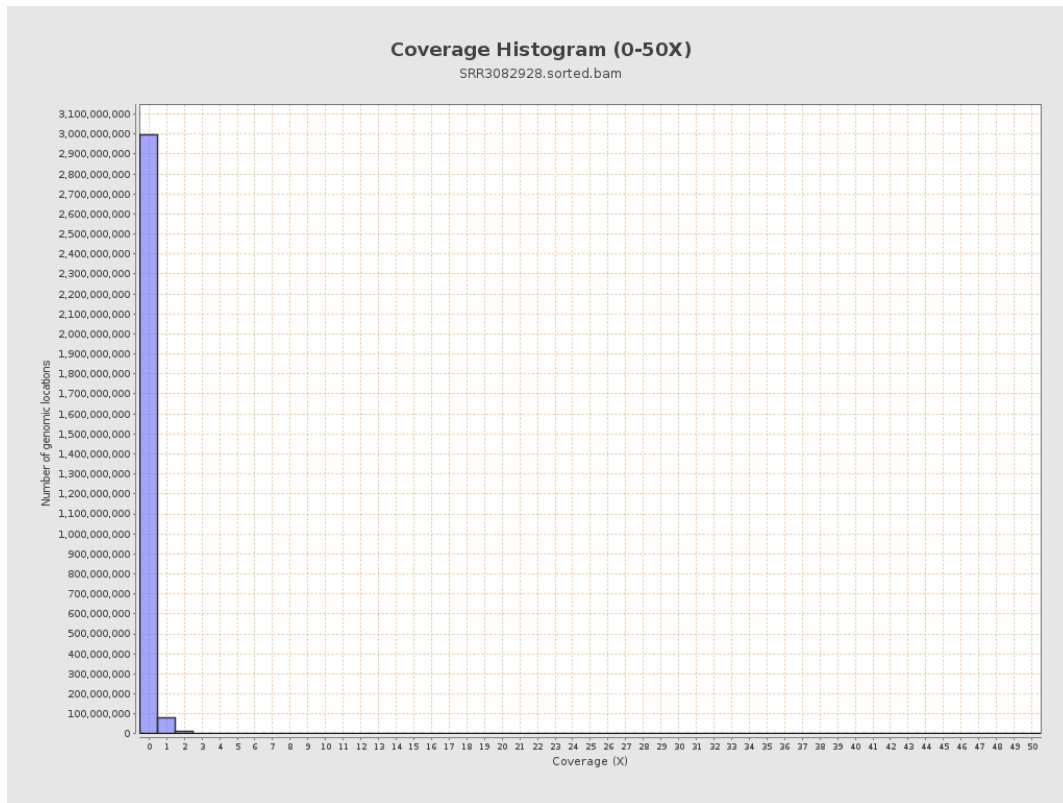
3. Results : Coverage across reference



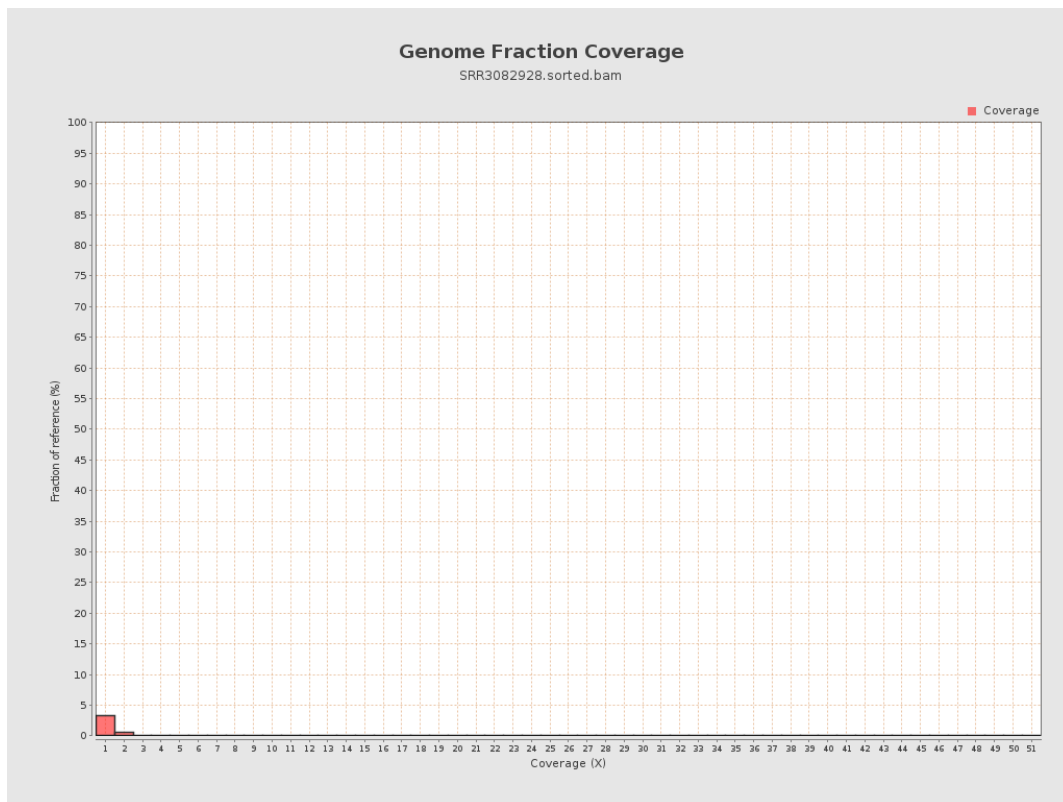
4. Results : Coverage Histogram



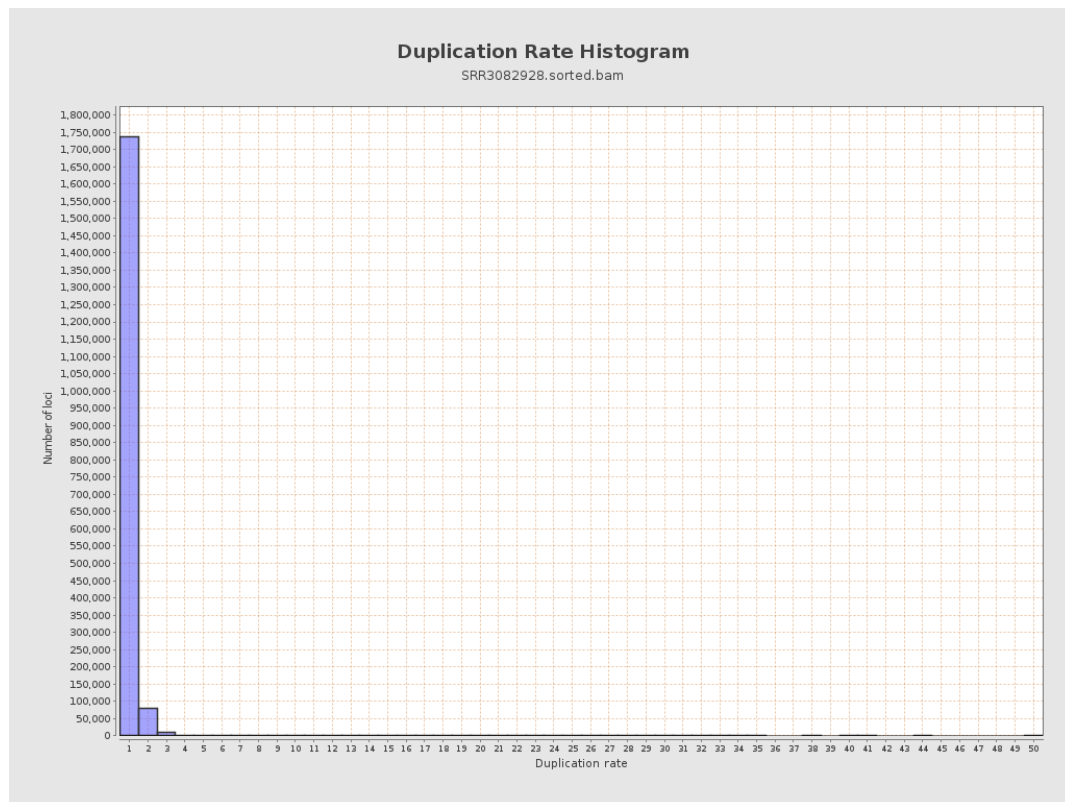
5. Results : Coverage Histogram (0-50X)



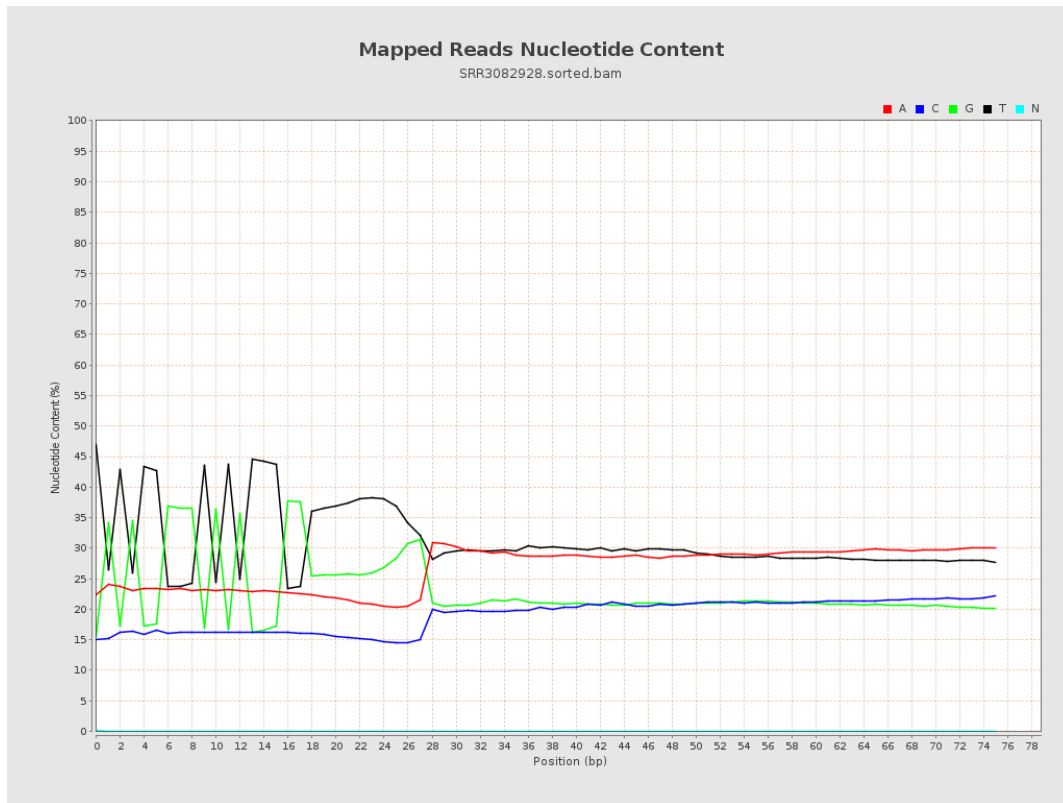
6. Results : Genome Fraction Coverage



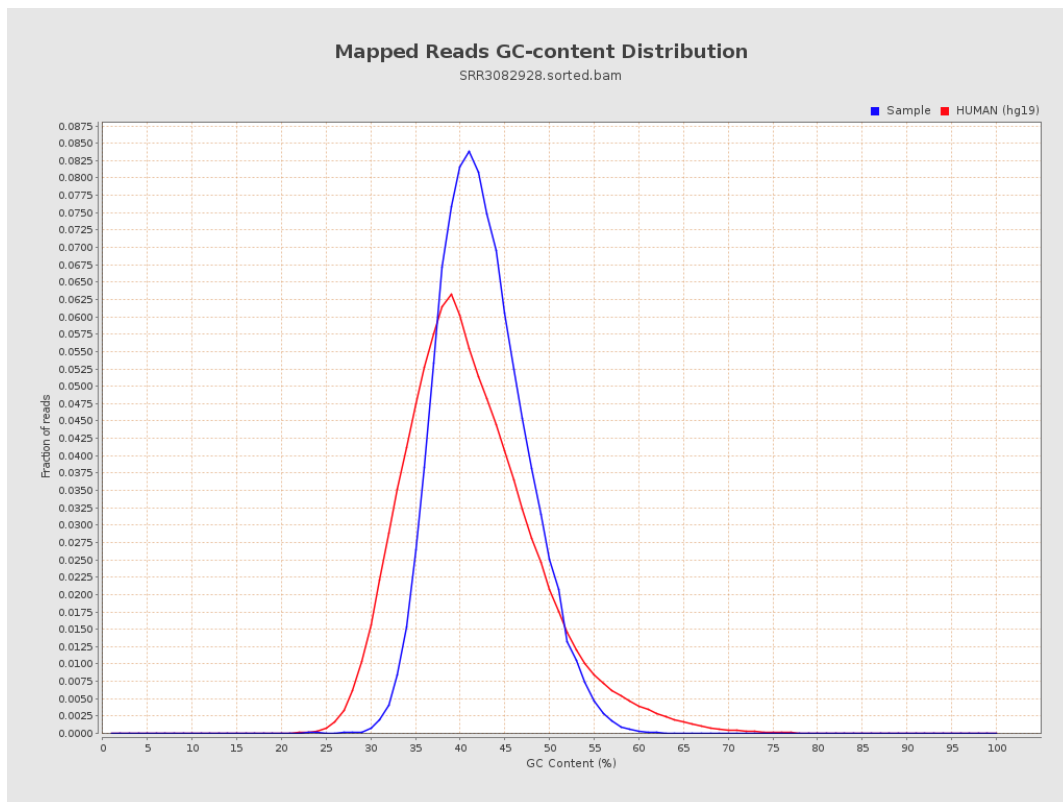
7. Results : Duplication Rate Histogram



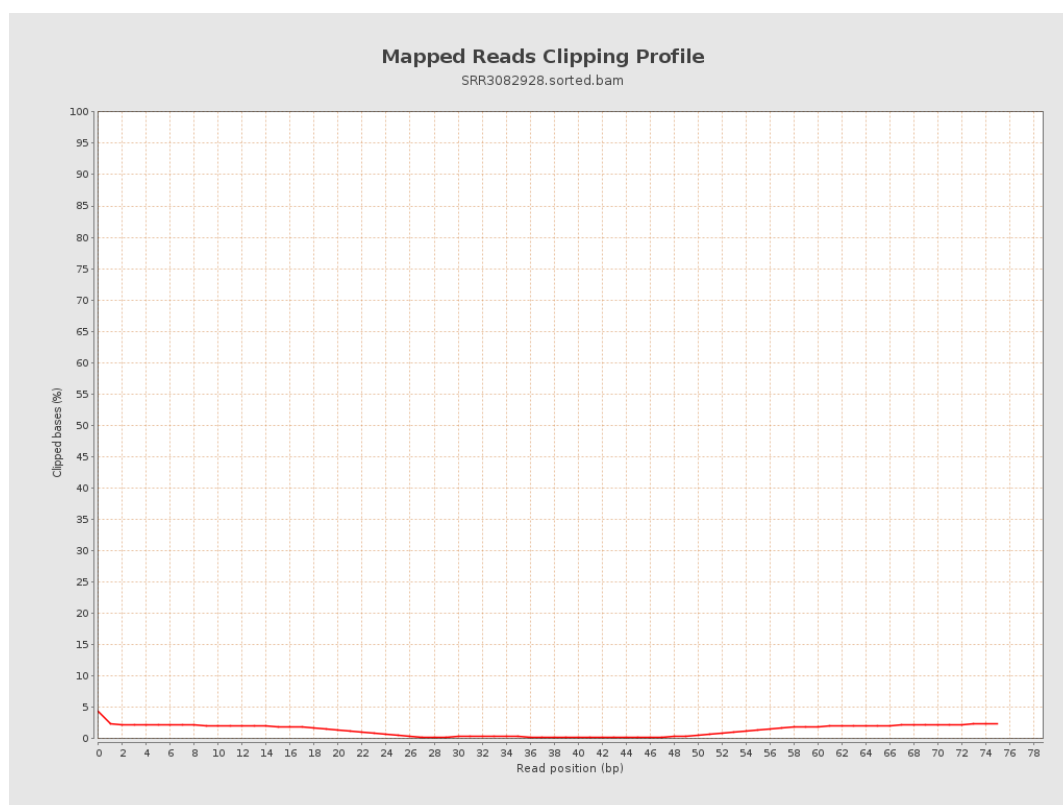
8. Results : Mapped Reads Nucleotide Content



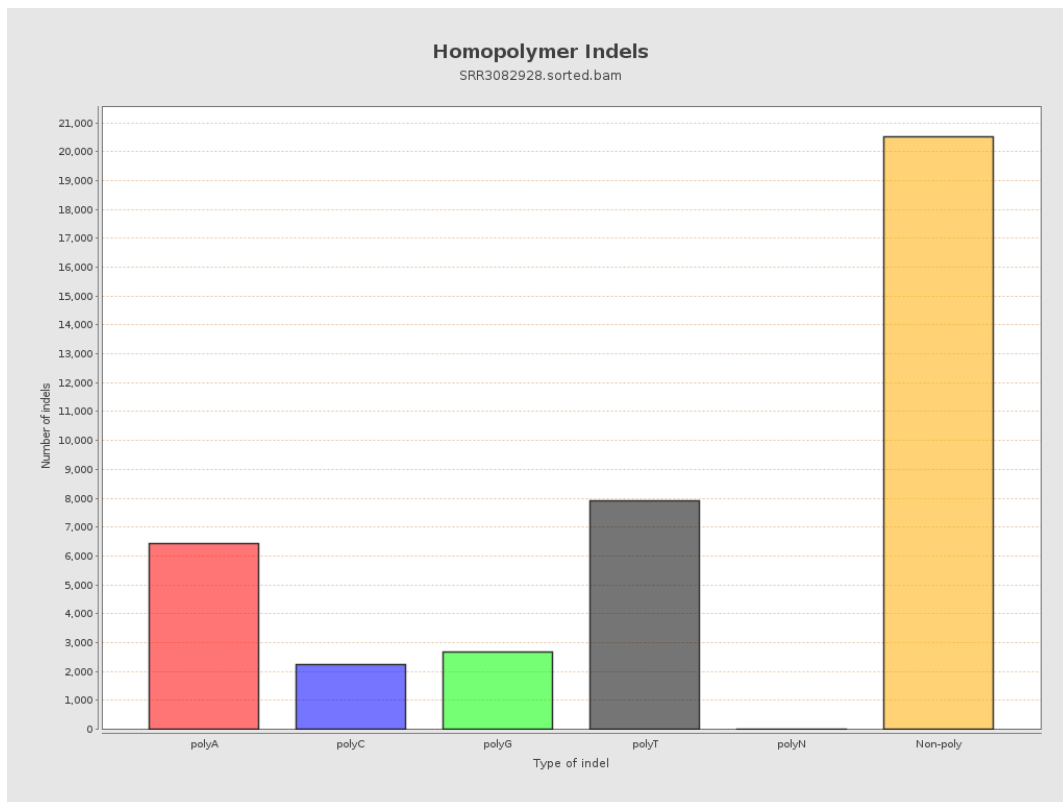
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

