

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:37:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004048.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_SRR6004048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:37:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,083,224
Mapped reads	2,658,848 / 86.24%
Unmapped reads	424,376 / 13.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,868 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	221,075 / 7.17%
Duplication rate	6.75%
Clipped reads	1,264,425 / 41.01%

2.2. ACGT Content

Number/percentage of A's	49,004,112 / 27.92%
Number/percentage of C's	32,166,871 / 18.33%
Number/percentage of T's	55,742,081 / 31.76%
Number/percentage of G's	38,443,821 / 21.91%
Number/percentage of N's	142,254 / 0.08%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.462
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2.4. Mapping Quality

Mean Mapping Quality	37.01
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2.5. Mismatches and indels

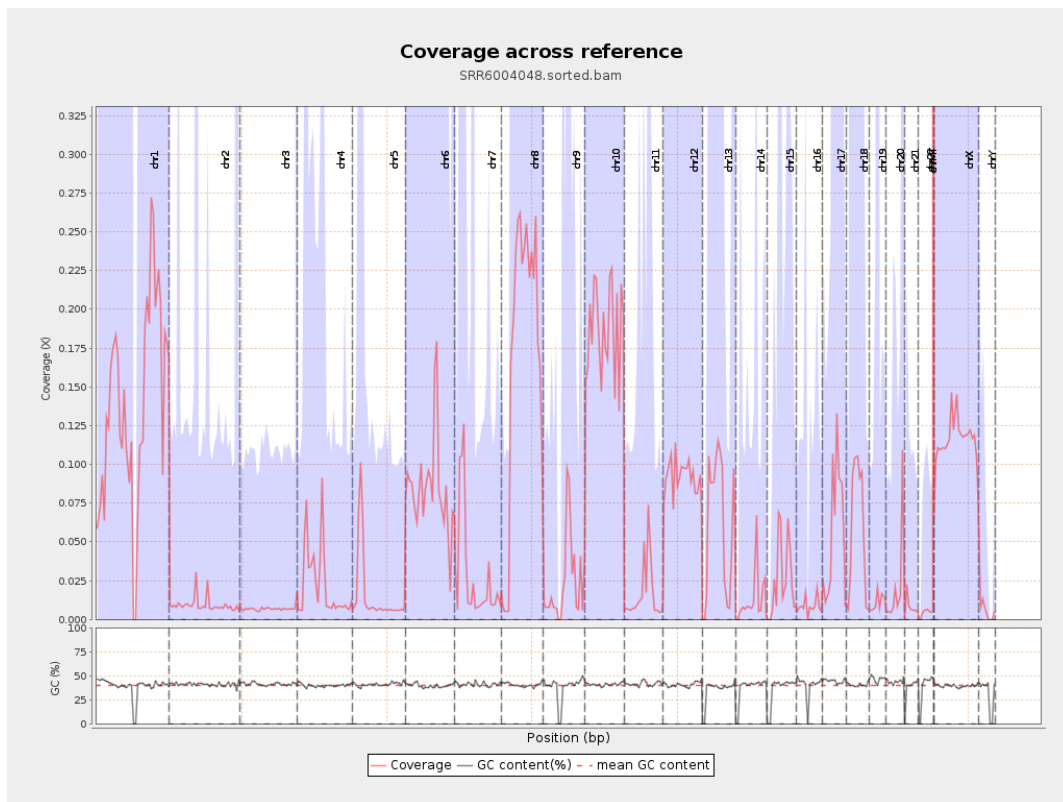
General error rate	0.86%
Mismatches	1,494,493
Insertions	11,632
Mapped reads with at least one insertion	0.43%
Deletions	47,600
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.28%

2.6. Chromosome stats

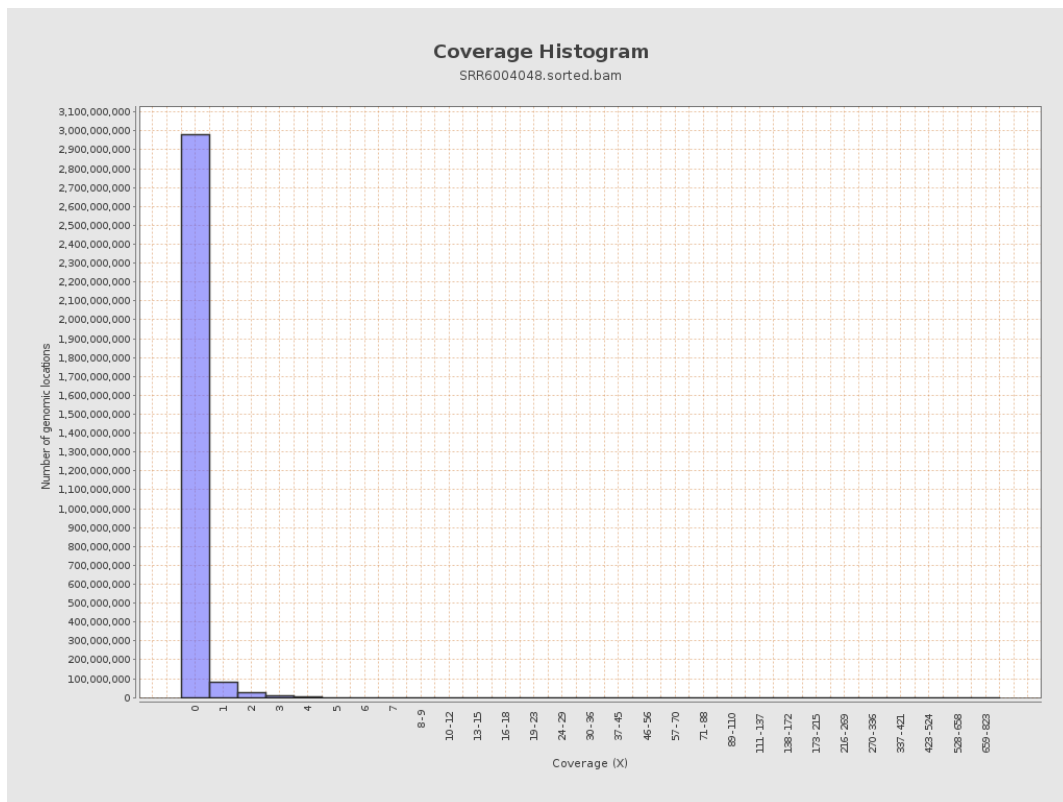
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34535587	0.1386	0.8439
chr2	243199373	2306616	0.0095	0.3653
chr3	198022430	1353316	0.0068	0.1506
chr4	191154276	4320371	0.0226	0.2077
chr5	180915260	2935623	0.0162	0.171
chr6	171115067	14474679	0.0846	0.4947
chr7	159138663	4628902	0.0291	0.2823

chr8	146364022	25128059	0.1717	0.8255
chr9	141213431	3286540	0.0233	0.24
chr10	135534747	25250962	0.1863	0.9245
chr11	135006516	2328322	0.0172	0.1933
chr12	133851895	12304706	0.0919	0.4124
chr13	115169878	7125270	0.0619	0.3397
chr14	107349540	1397635	0.013	0.1759
chr15	102531392	2745897	0.0268	0.2304
chr16	90354753	788323	0.0087	0.1484
chr17	81195210	4748074	0.0585	0.3499
chr18	78077248	4565504	0.0585	0.5209
chr19	59128983	641130	0.0108	0.482
chr20	63025520	1520968	0.0241	0.2229
chr21	48129895	406073	0.0084	0.1165
chr22	51304566	214998	0.0042	0.081
chrMT	16571	152601	9.2089	7.3442
chrX	155270560	17997833	0.1159	0.5119
chrY	59373566	420770	0.0071	0.1096

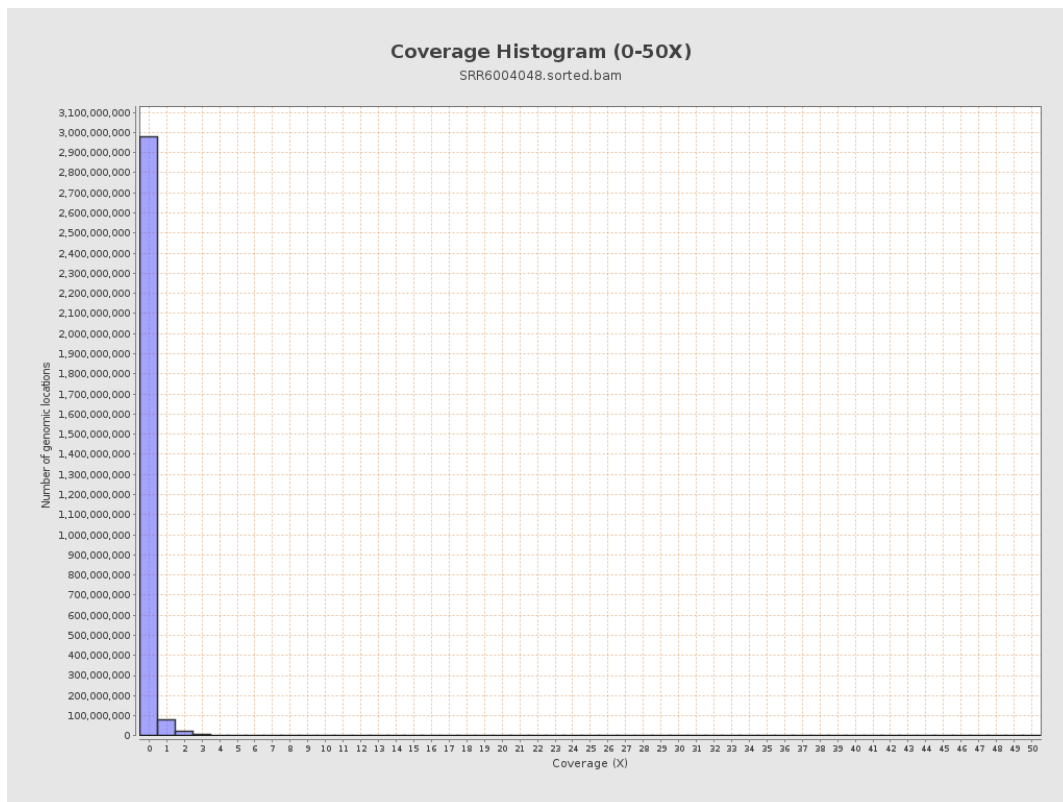
3. Results : Coverage across reference



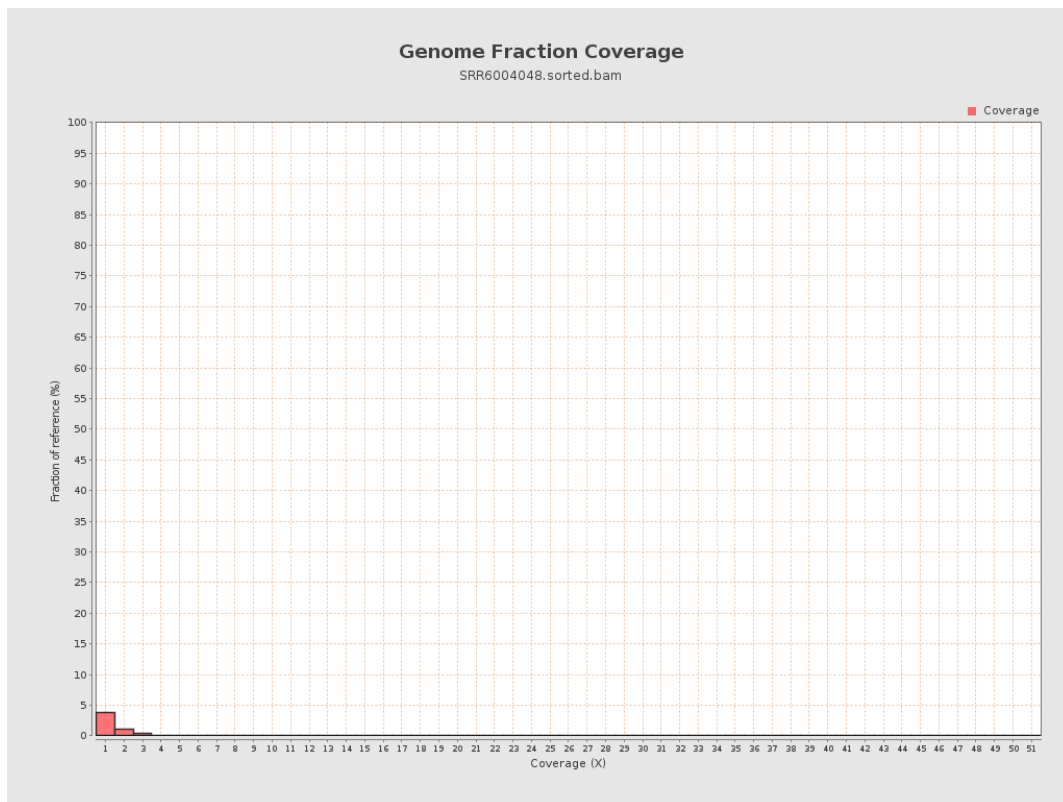
4. Results : Coverage Histogram



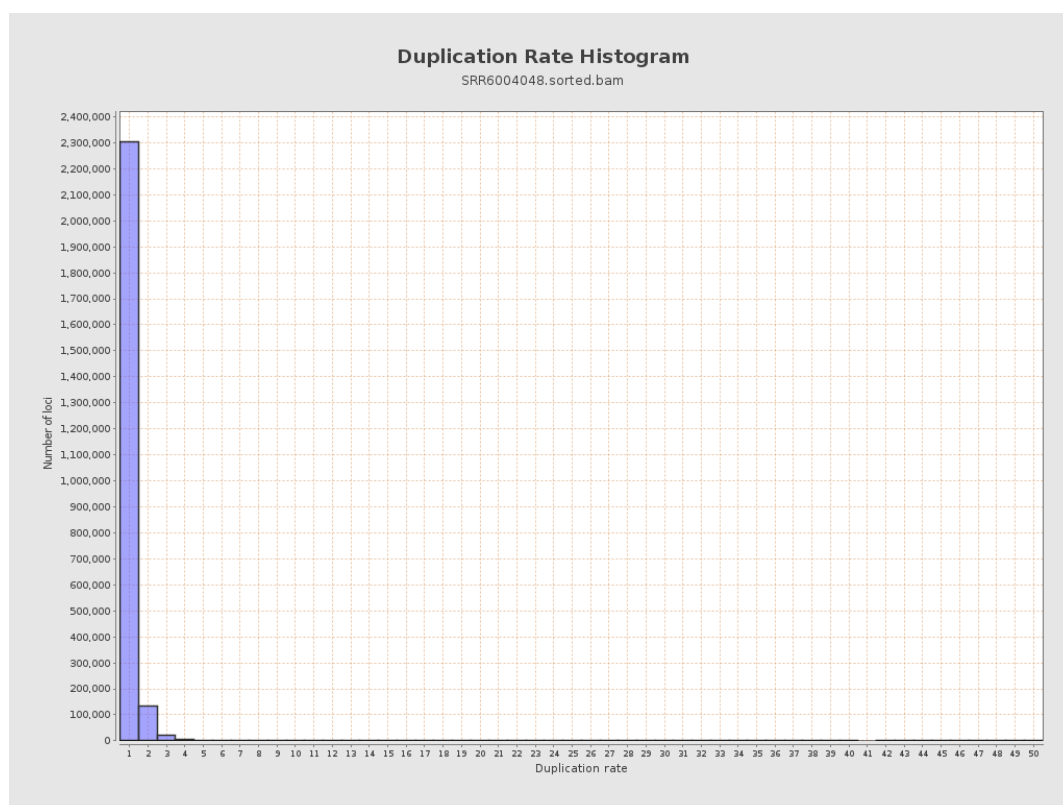
5. Results : Coverage Histogram (0-50X)



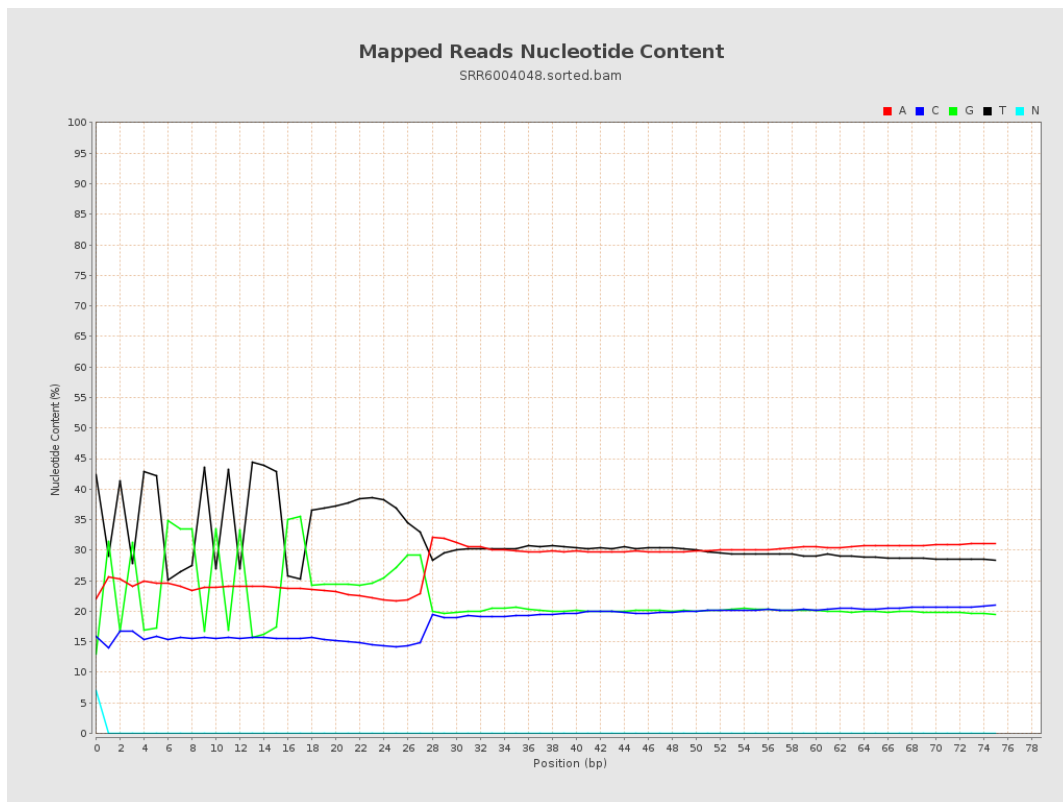
6. Results : Genome Fraction Coverage



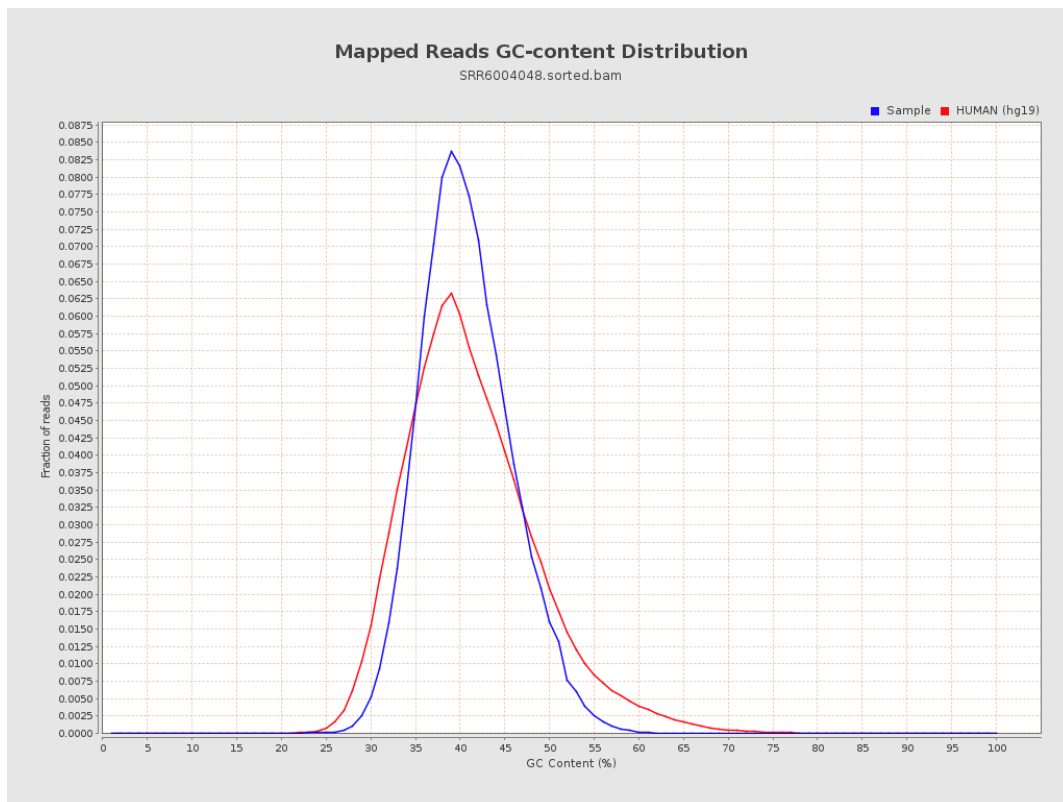
7. Results : Duplication Rate Histogram



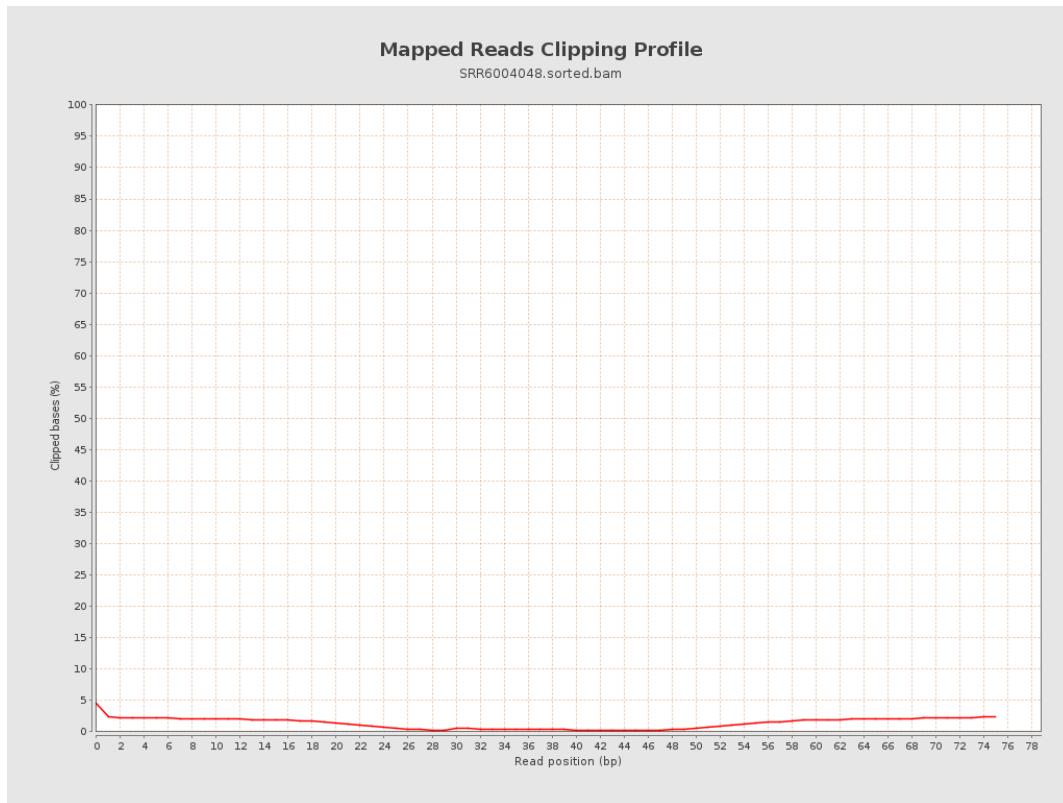
8. Results : Mapped Reads Nucleotide Content



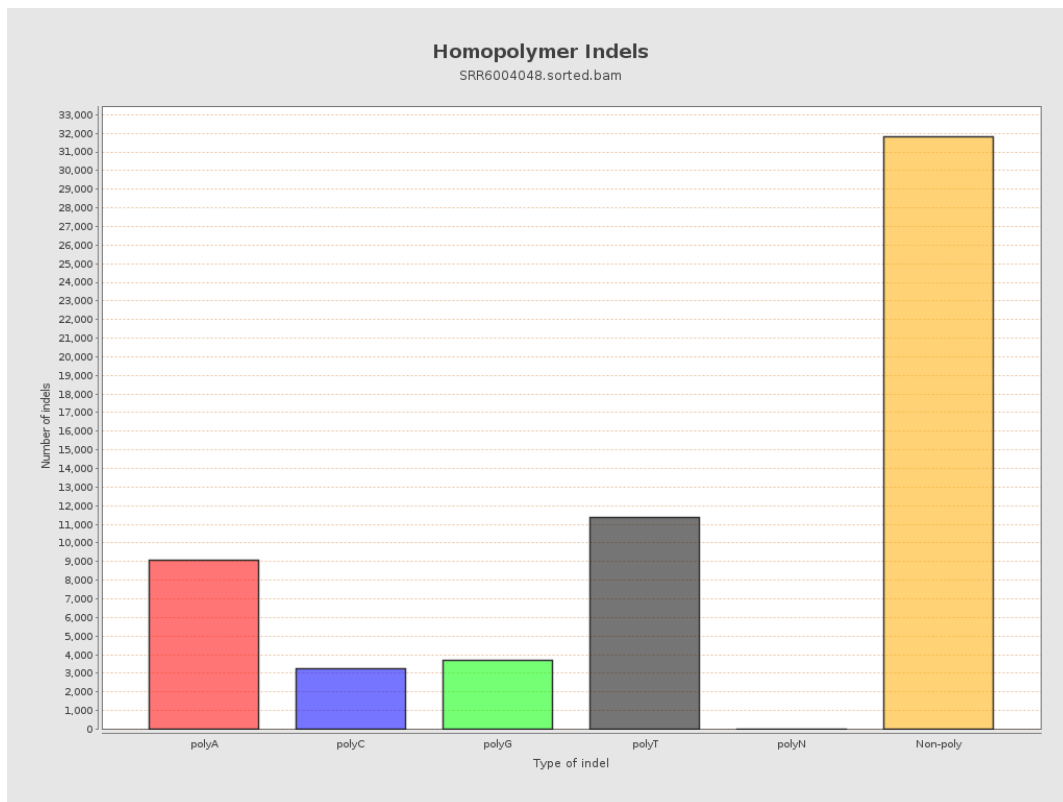
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

