

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:03:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004019.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_SRR6004019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:03:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,126,257
Mapped reads	1,864,726 / 87.7%
Unmapped reads	261,531 / 12.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,895 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	85,366 / 4.01%
Duplication rate	3.78%
Clipped reads	834,165 / 39.23%

2.2. ACGT Content

Number/percentage of A's	34,357,021 / 27.58%
Number/percentage of C's	23,712,205 / 19.04%
Number/percentage of T's	38,741,572 / 31.1%
Number/percentage of G's	27,726,707 / 22.26%
Number/percentage of N's	22,755 / 0.02%
GC Percentage	41.3%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3221
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2.4. Mapping Quality

Mean Mapping Quality	46.02
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2.5. Mismatches and indels

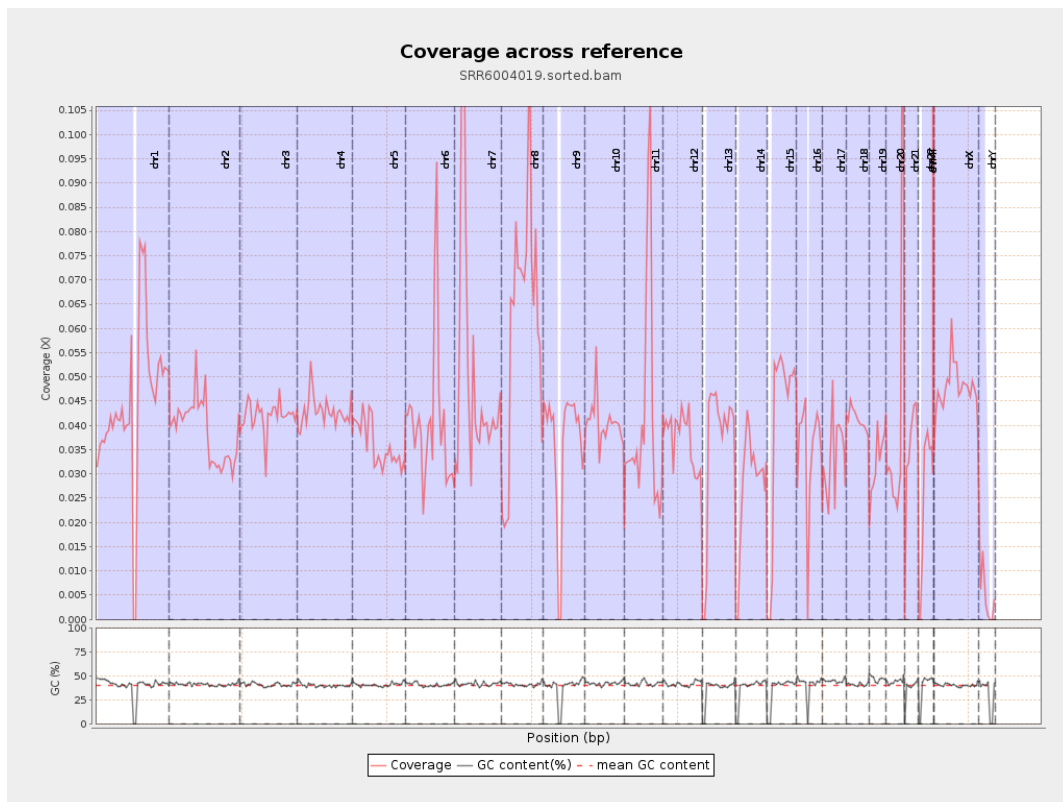
General error rate	0.88%
Mismatches	1,083,907
Insertions	8,743
Mapped reads with at least one insertion	0.47%
Deletions	29,390
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.22%

2.6. Chromosome stats

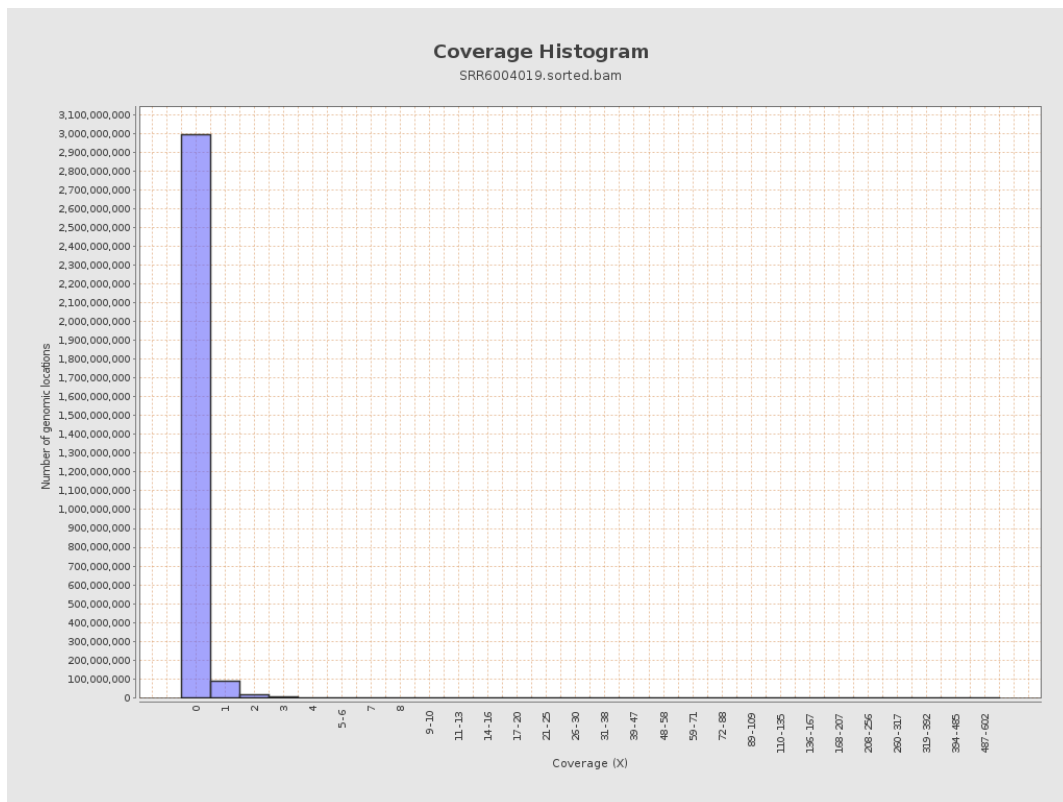
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11141213	0.0447	0.5202
chr2	243199373	9418204	0.0387	0.373
chr3	198022430	8310255	0.042	0.2373
chr4	191154276	8190830	0.0428	0.255
chr5	180915260	6489590	0.0359	0.22
chr6	171115067	6995935	0.0409	0.2536
chr7	159138663	8126380	0.0511	0.4549

chr8	146364022	8850179	0.0605	0.4197
chr9	141213431	5079147	0.036	0.2942
chr10	135534747	5509687	0.0407	0.2987
chr11	135006516	5611224	0.0416	0.2955
chr12	133851895	4956098	0.037	0.2286
chr13	115169878	4103838	0.0356	0.2266
chr14	107349540	2953252	0.0275	0.2087
chr15	102531392	4161001	0.0406	0.2372
chr16	90354753	3163982	0.035	0.2287
chr17	81195210	2752663	0.0339	0.2257
chr18	78077248	3228105	0.0413	0.5068
chr19	59128983	1937649	0.0328	0.3613
chr20	63025520	2908821	0.0462	0.2667
chr21	48129895	1655870	0.0344	0.2311
chr22	51304566	1290299	0.0251	0.1832
chrMT	16571	63825	3.8516	3.3415
chrX	155270560	7413722	0.0477	0.2739
chrY	59373566	299762	0.005	0.109

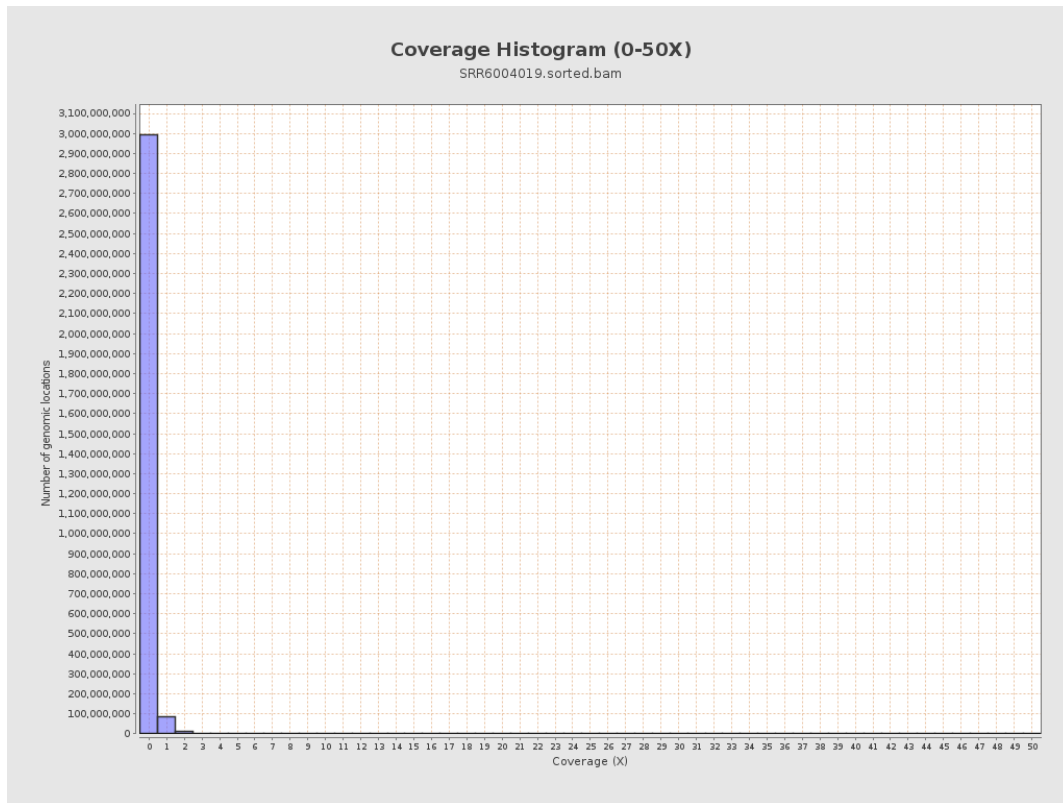
3. Results : Coverage across reference



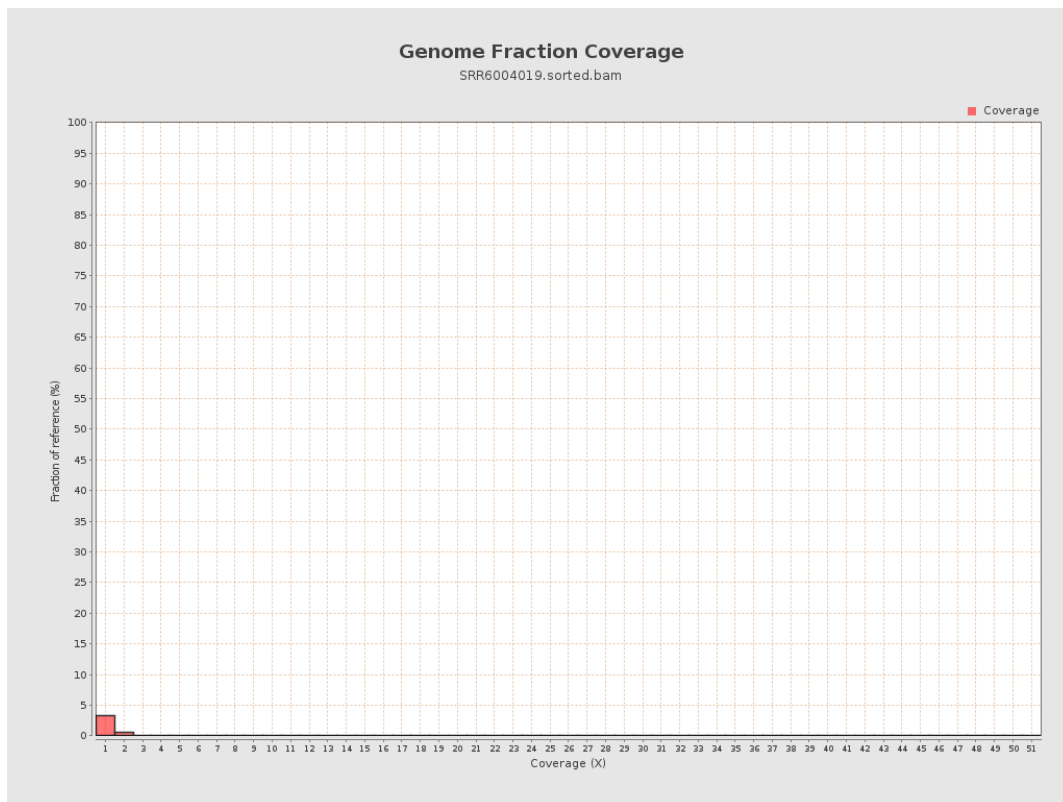
4. Results : Coverage Histogram



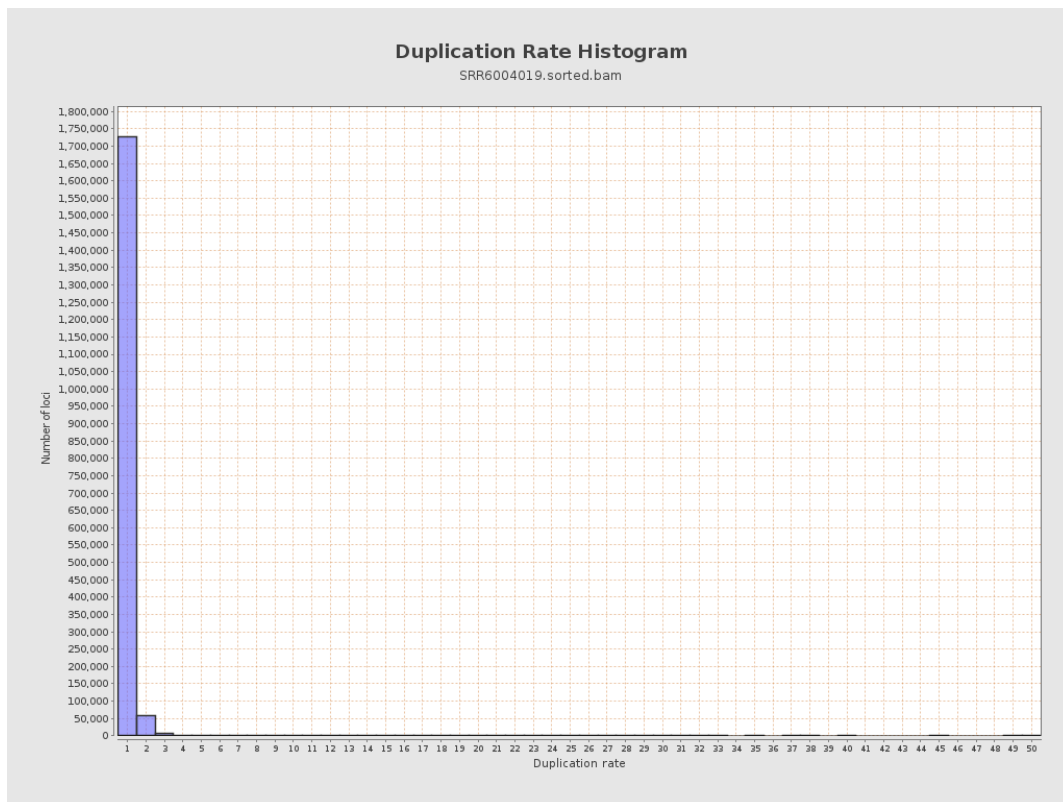
5. Results : Coverage Histogram (0-50X)



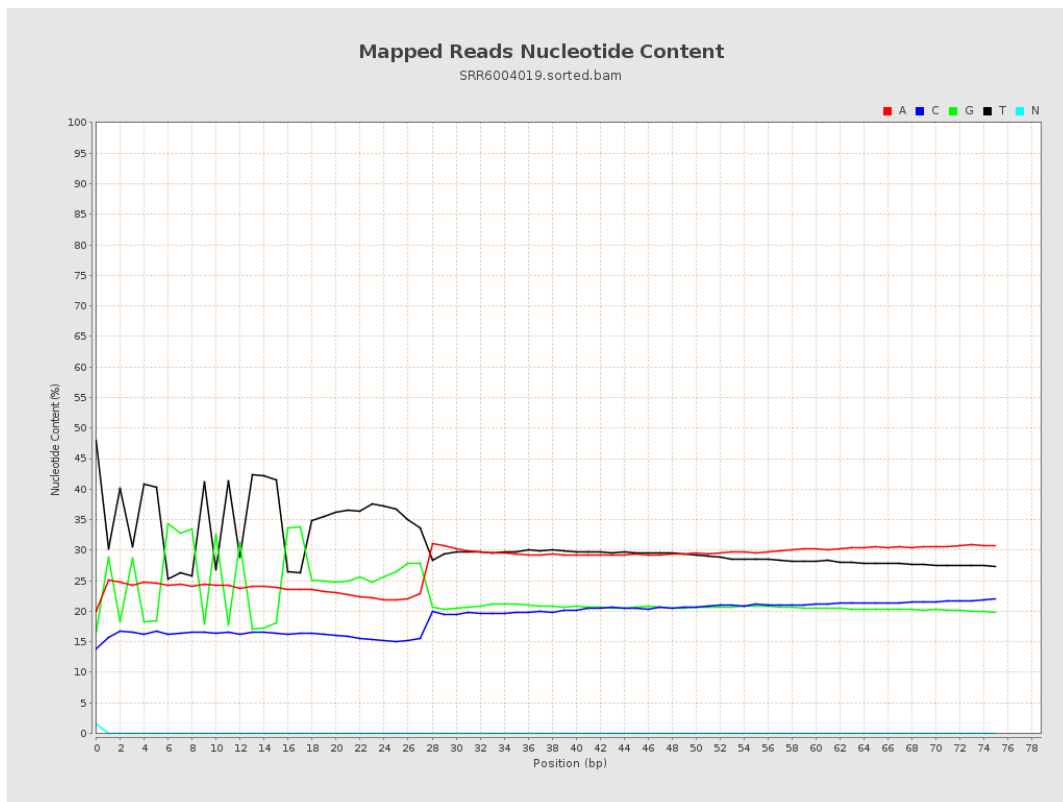
6. Results : Genome Fraction Coverage



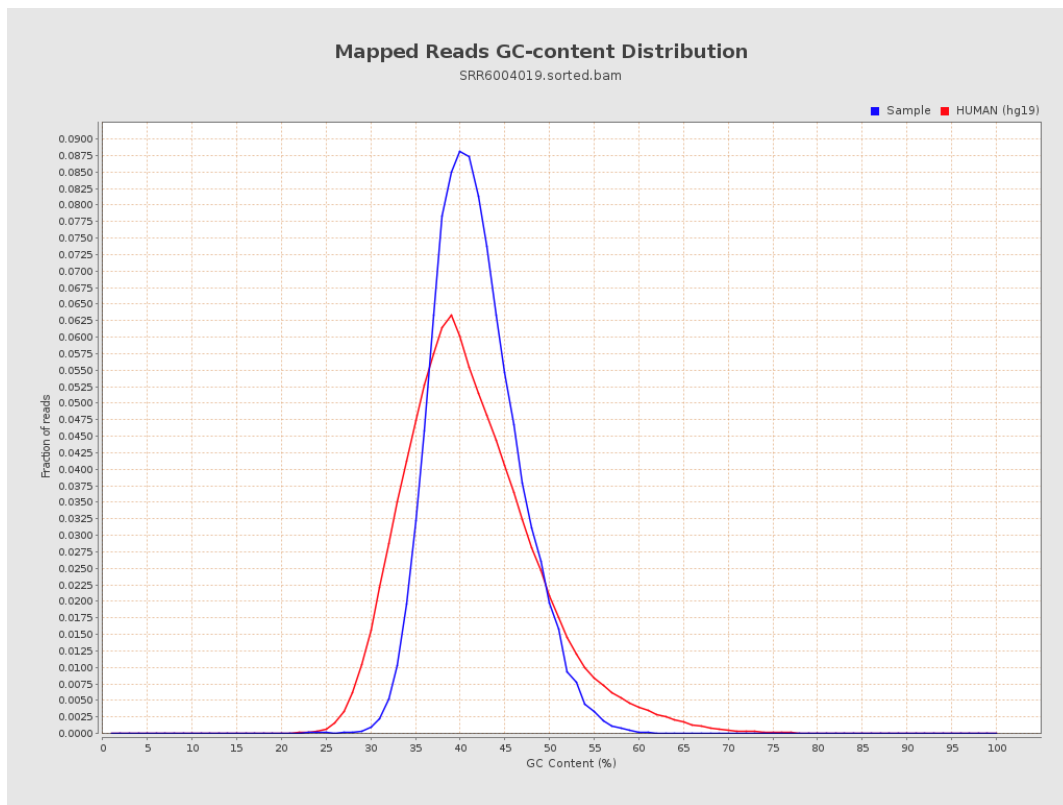
7. Results : Duplication Rate Histogram



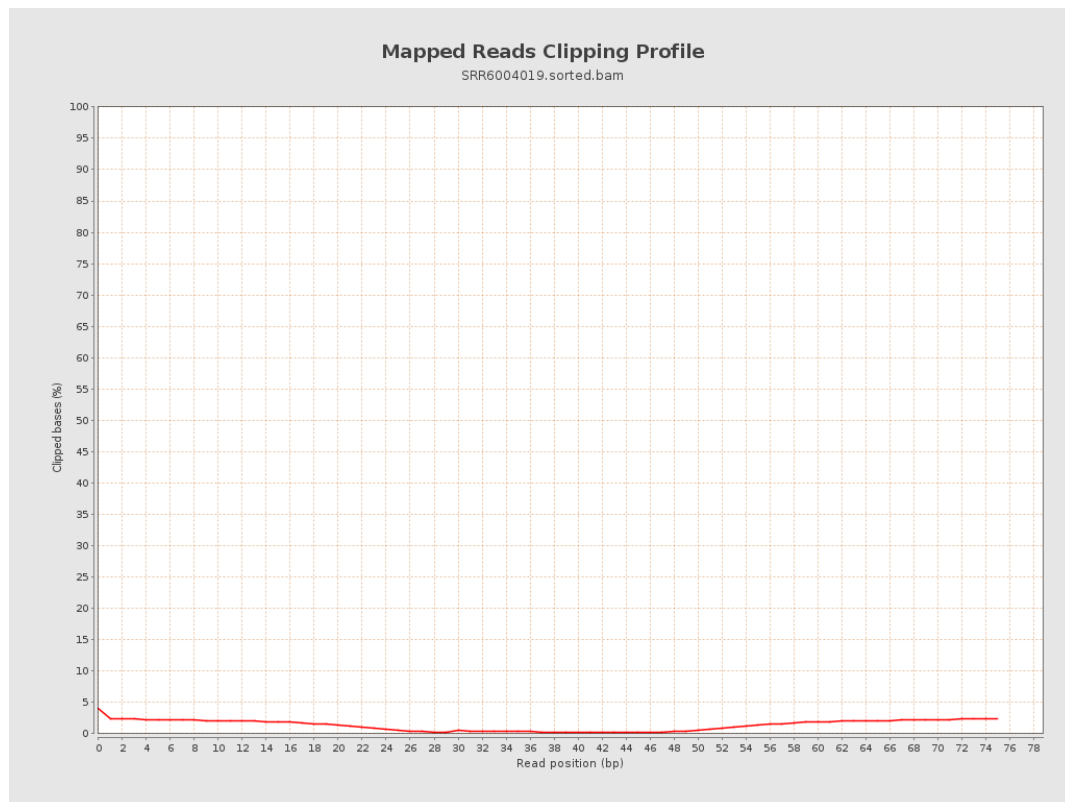
8. Results : Mapped Reads Nucleotide Content



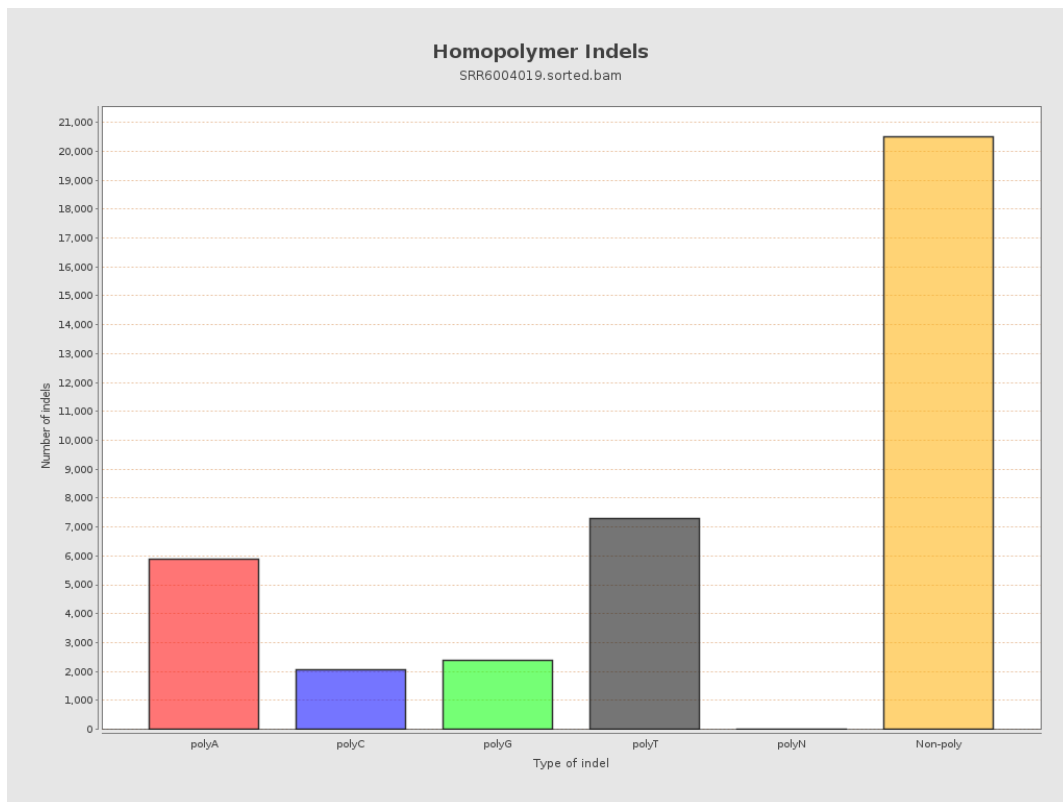
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

