

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004059.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_SRR6004059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:16:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,388,820
Mapped reads	2,956,951 / 87.26%
Unmapped reads	431,869 / 12.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,931 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	165,246 / 4.88%
Duplication rate	4.42%
Clipped reads	1,517,210 / 44.77%

2.2. ACGT Content

Number/percentage of A's	52,778,490 / 27.42%
Number/percentage of C's	35,174,955 / 18.27%
Number/percentage of T's	60,886,339 / 31.63%
Number/percentage of G's	43,520,348 / 22.61%
Number/percentage of N's	142,964 / 0.07%
GC Percentage	40.88%

2.3. Coverage

Mean	0.0622

Standard Deviation	0.5166
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2.4. Mapping Quality

Mean Mapping Quality	45.09
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2.5. Mismatches and indels

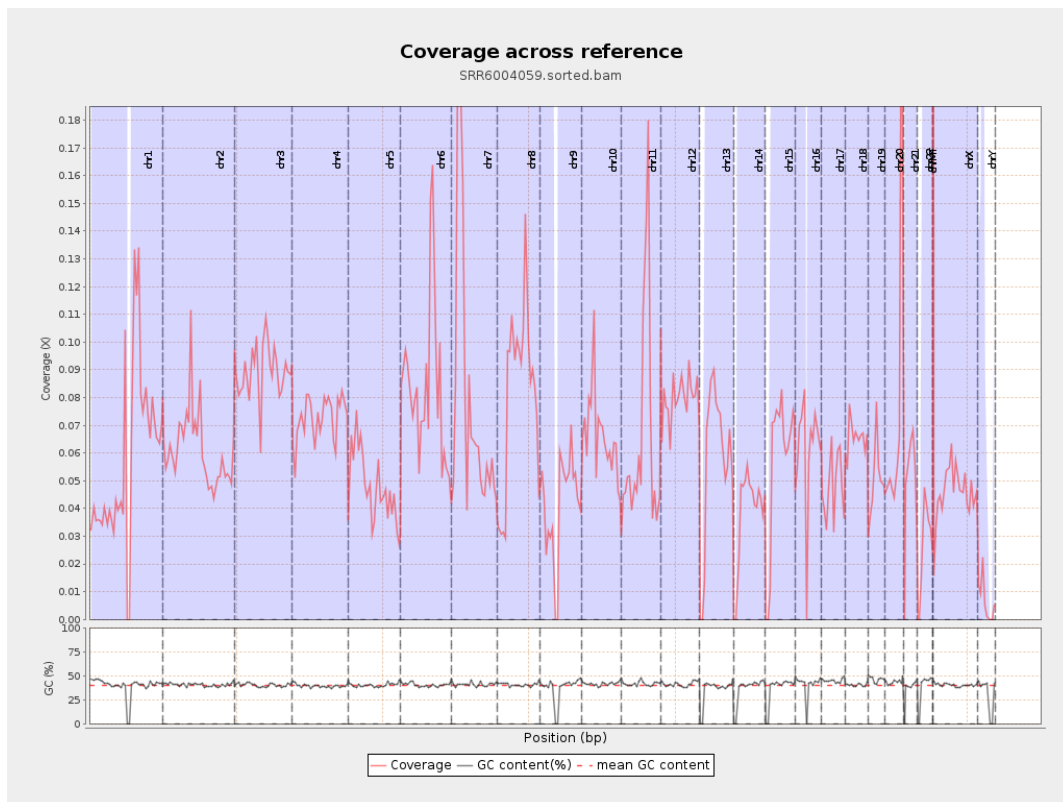
General error rate	0.9%
Mismatches	1,702,242
Insertions	13,877
Mapped reads with at least one insertion	0.47%
Deletions	59,276
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.66%

2.6. Chromosome stats

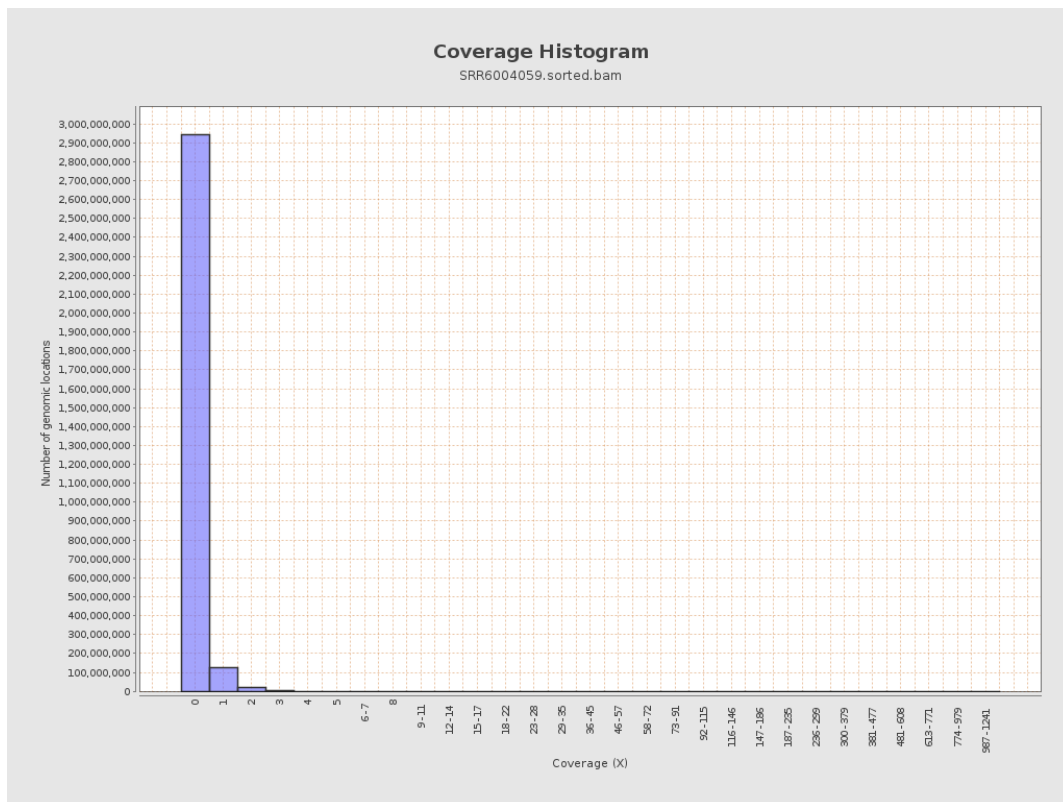
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14378942	0.0577	1.0276
chr2	243199373	14773610	0.0607	0.5776
chr3	198022430	17708589	0.0894	0.3697
chr4	191154276	13847502	0.0724	0.3349
chr5	180915260	8635993	0.0477	0.2678
chr6	171115067	14226185	0.0831	0.4245
chr7	159138663	12217307	0.0768	0.5448

chr8	146364022	11901133	0.0813	0.794
chr9	141213431	5869102	0.0416	0.403
chr10	135534747	8961387	0.0661	0.5385
chr11	135006516	8744473	0.0648	0.3915
chr12	133851895	10671485	0.0797	0.3457
chr13	115169878	6734191	0.0585	0.2889
chr14	107349540	4139807	0.0386	0.2697
chr15	102531392	5749497	0.0561	0.2887
chr16	90354753	5458065	0.0604	0.3345
chr17	81195210	3871437	0.0477	0.2846
chr18	78077248	5129646	0.0657	0.787
chr19	59128983	3032028	0.0513	0.7064
chr20	63025520	5231240	0.083	0.3782
chr21	48129895	2401771	0.0499	0.2841
chr22	51304566	1388336	0.0271	0.1933
chrMT	16571	16319	0.9848	1.3147
chrX	155270560	7113263	0.0458	0.2964
chrY	59373566	400518	0.0067	0.1398

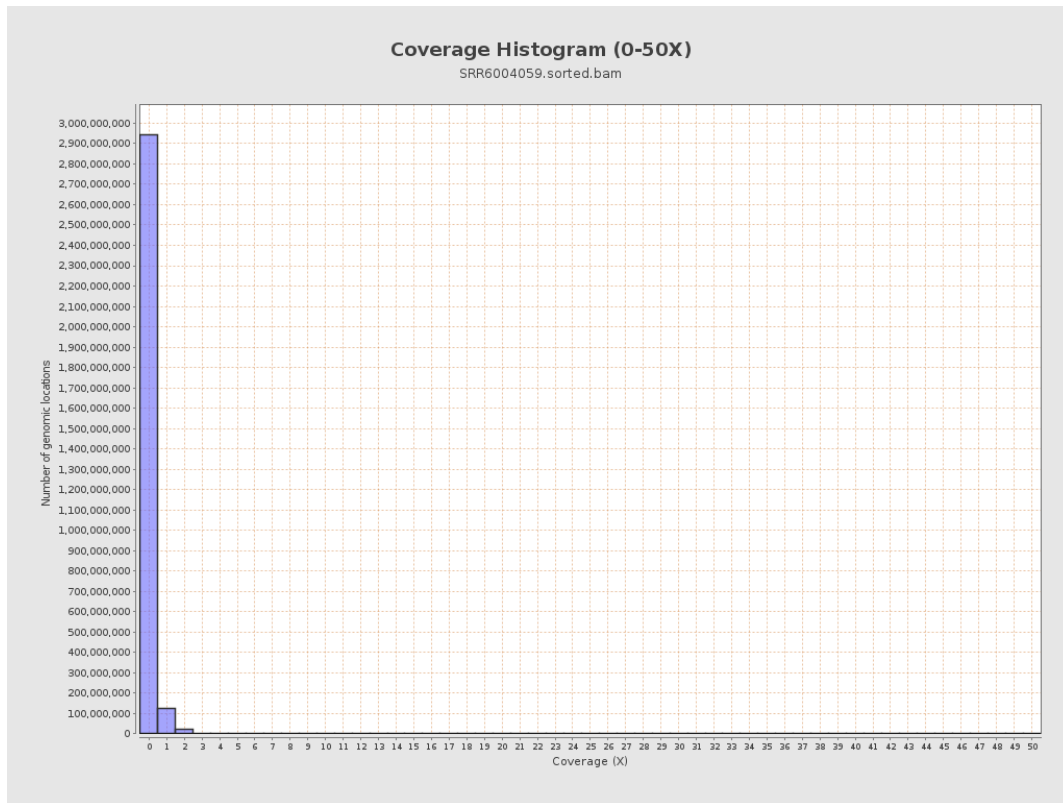
3. Results : Coverage across reference



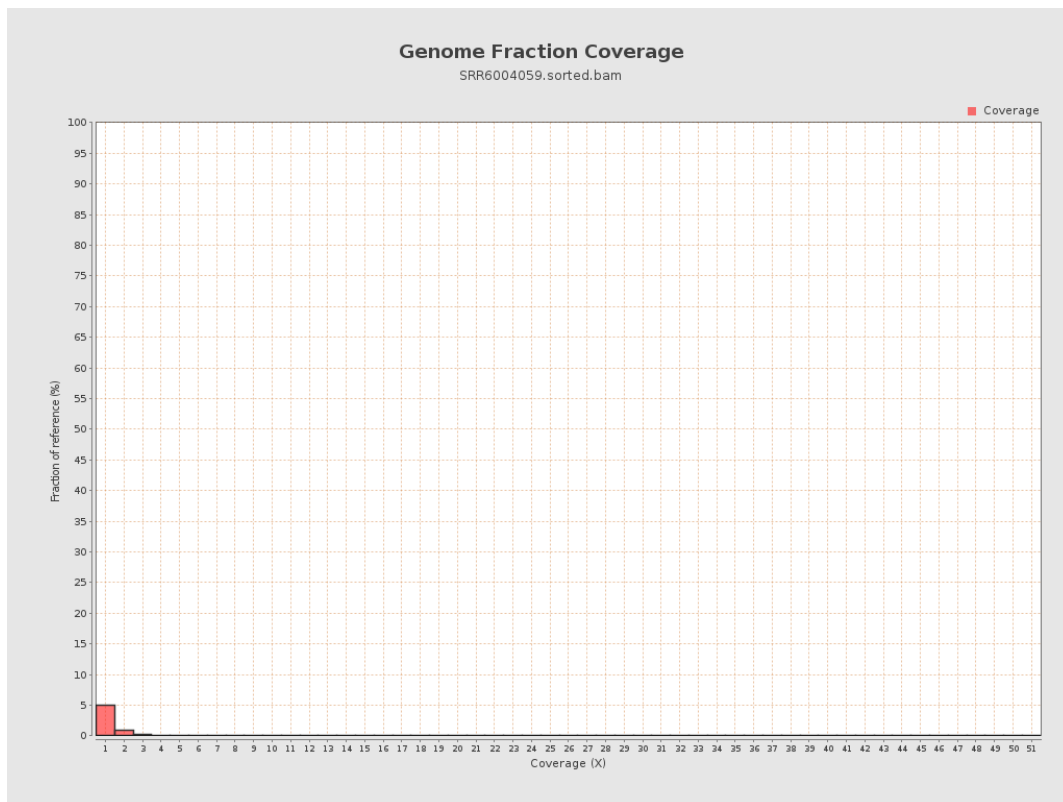
4. Results : Coverage Histogram



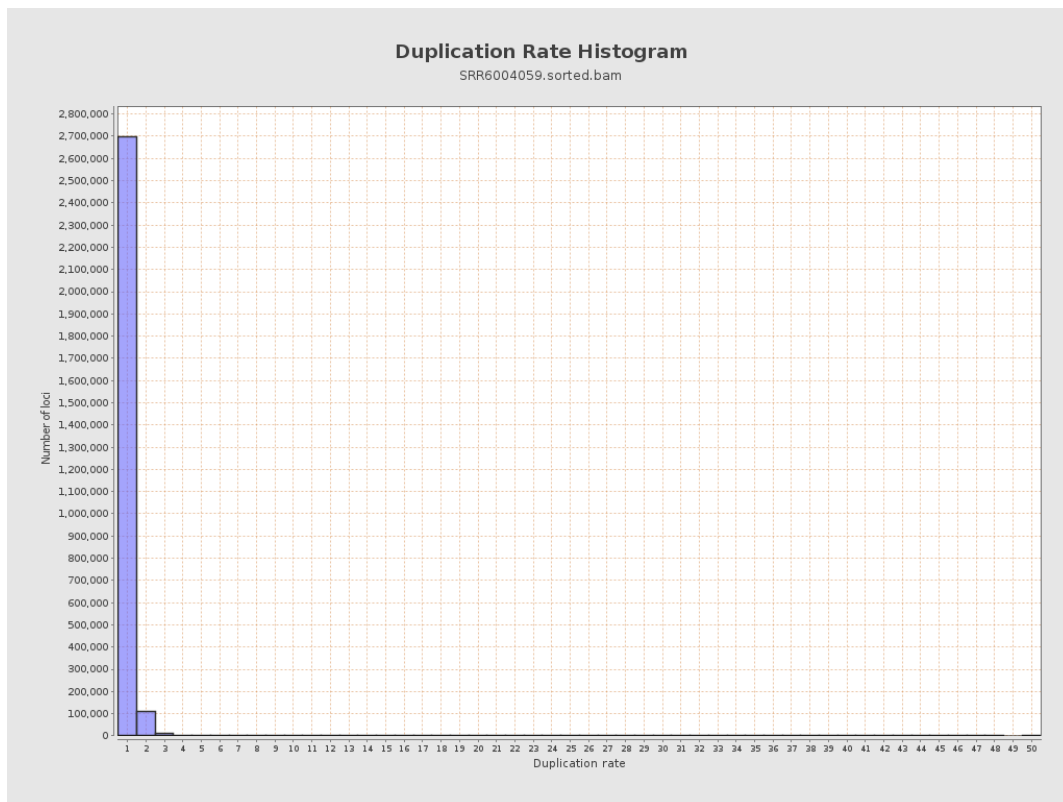
5. Results : Coverage Histogram (0-50X)



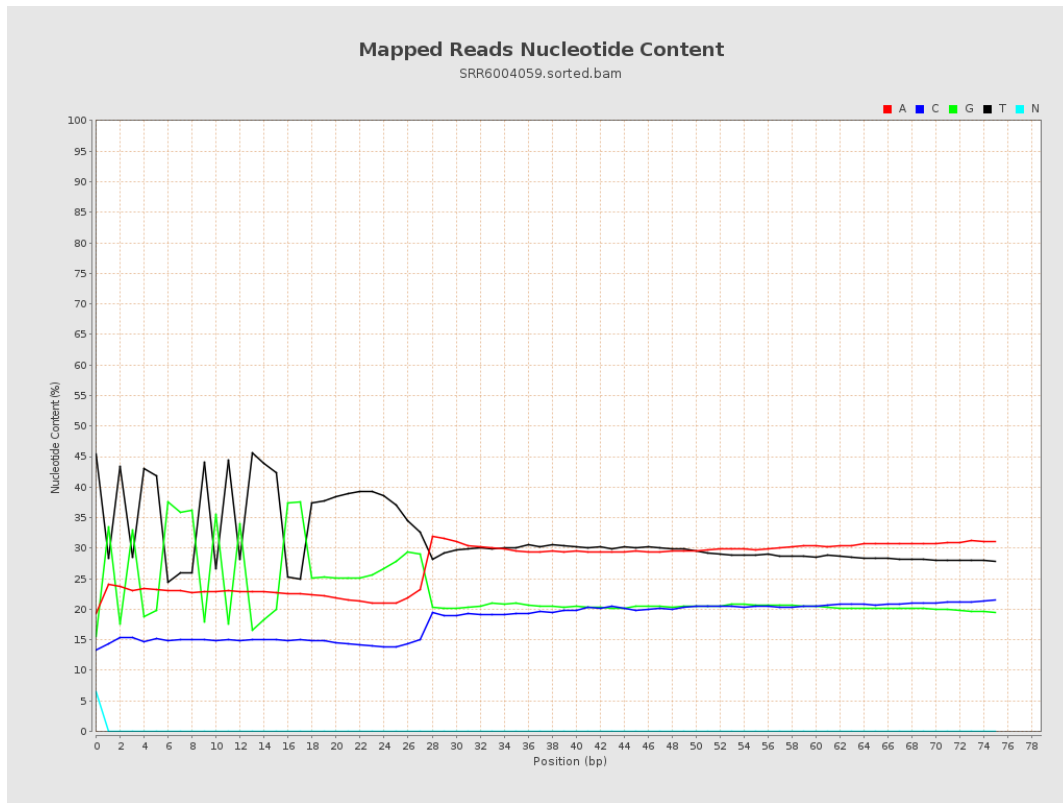
6. Results : Genome Fraction Coverage



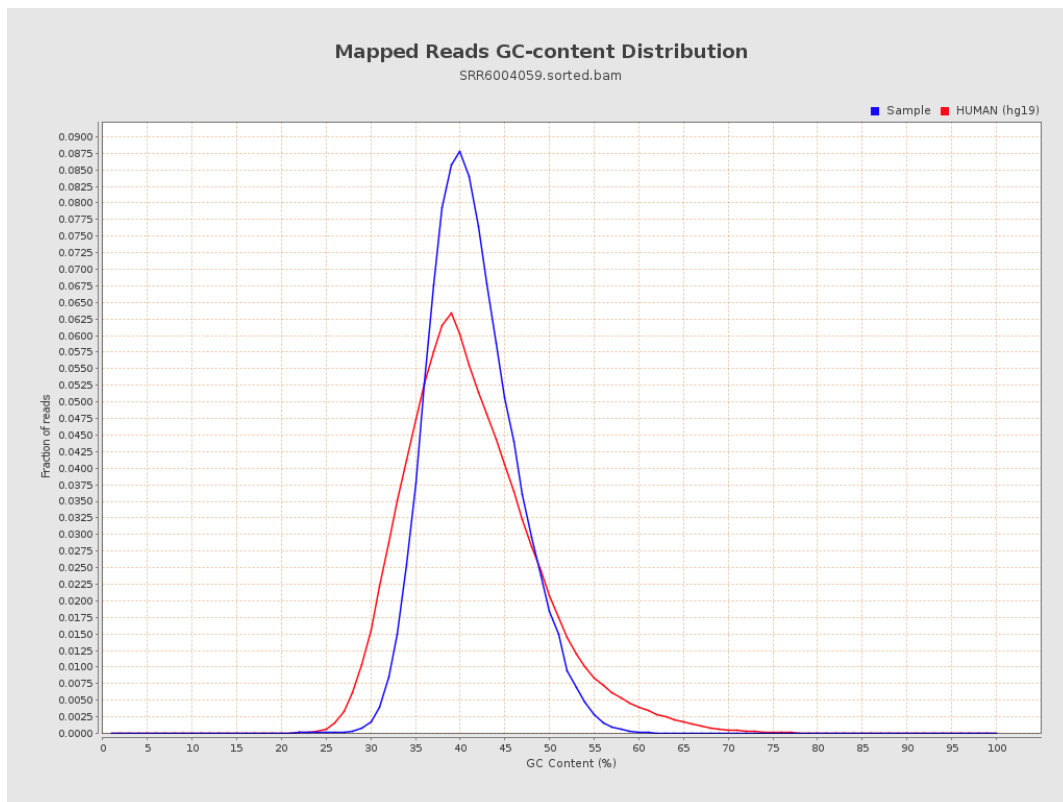
7. Results : Duplication Rate Histogram



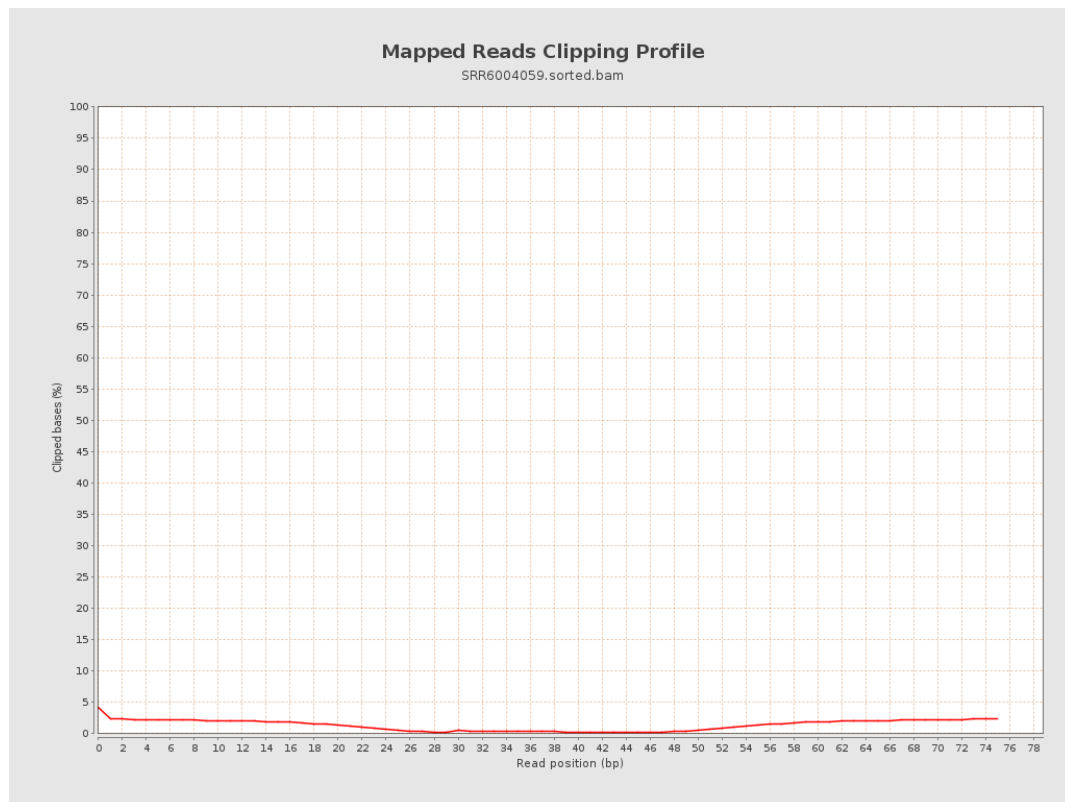
8. Results : Mapped Reads Nucleotide Content



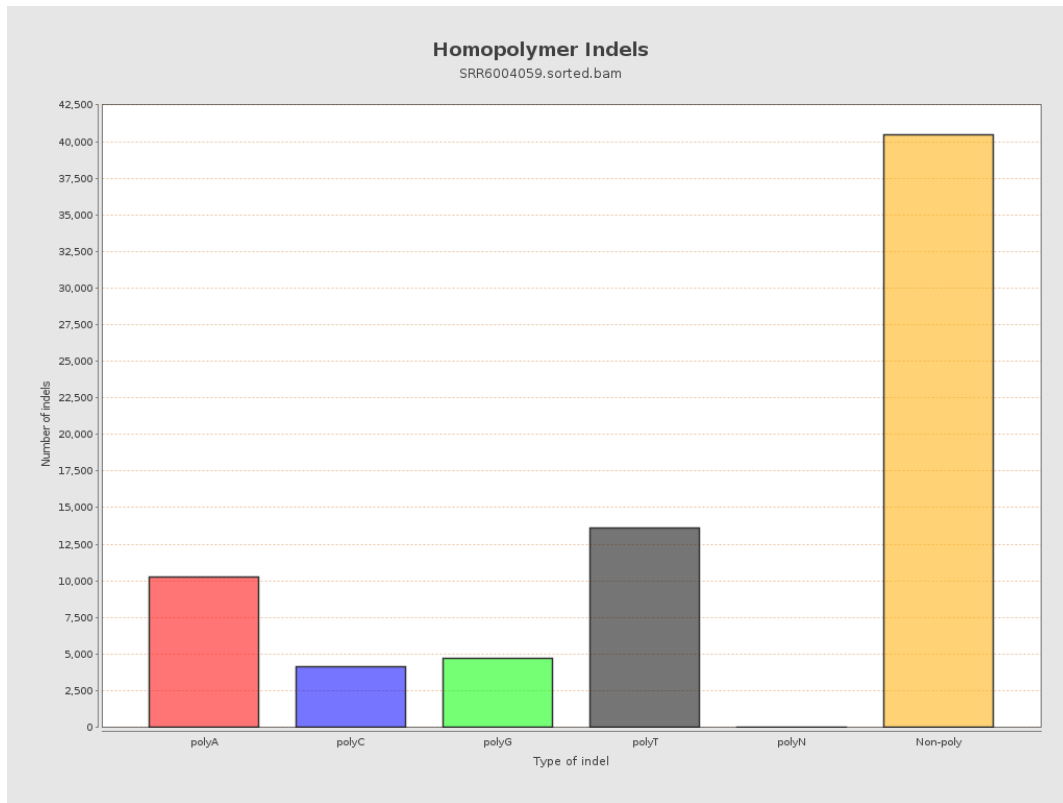
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

