

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:37:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234126.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_SRR6234126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:37:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,035,923
Mapped reads	4,713,626 / 93.6%
Unmapped reads	322,297 / 6.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,358 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	691,730 / 13.74%
Duplication rate	5.85%
Clipped reads	1,651,031 / 32.79%

2.2. ACGT Content

Number/percentage of A's	82,555,486 / 25.5%
Number/percentage of C's	59,442,984 / 18.36%
Number/percentage of T's	90,020,461 / 27.81%
Number/percentage of G's	91,649,309 / 28.31%
Number/percentage of N's	70,619 / 0.02%
GC Percentage	46.67%

2.3. Coverage

Mean	0.1046

Standard Deviation	48.4394
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2.4. Mapping Quality

Mean Mapping Quality	38.02
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2.5. Mismatches and indels

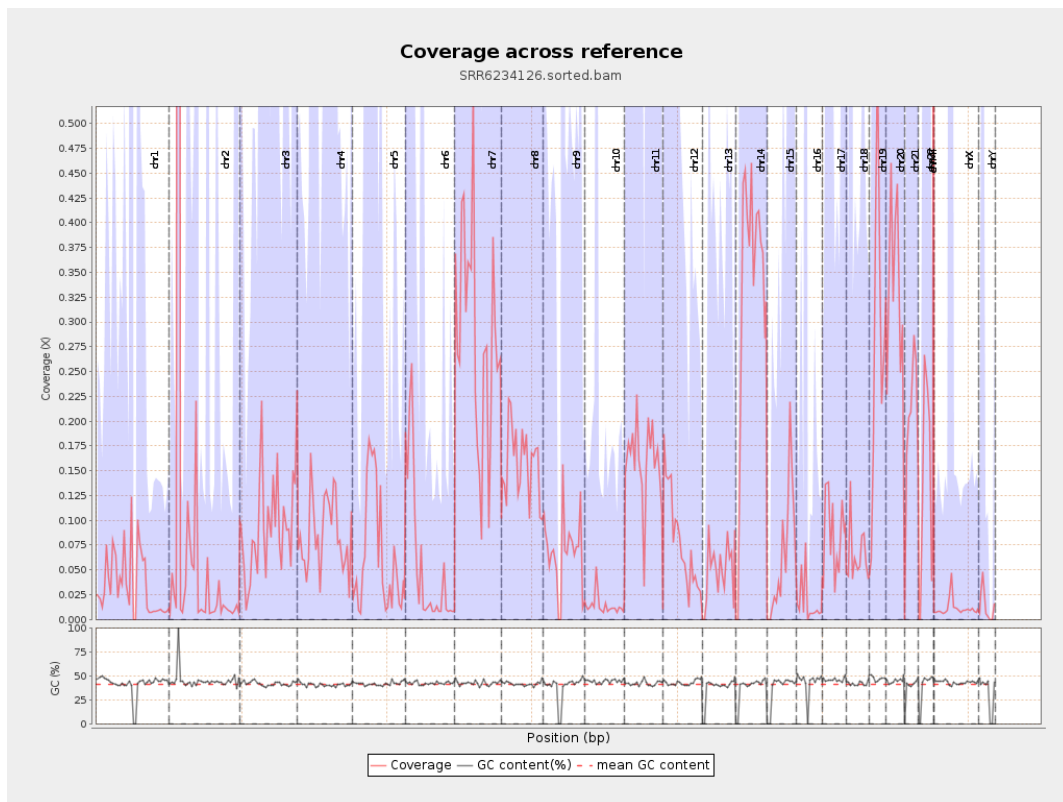
General error rate	0.69%
Mismatches	2,189,273
Insertions	23,648
Mapped reads with at least one insertion	0.5%
Deletions	68,256
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.6%

2.6. Chromosome stats

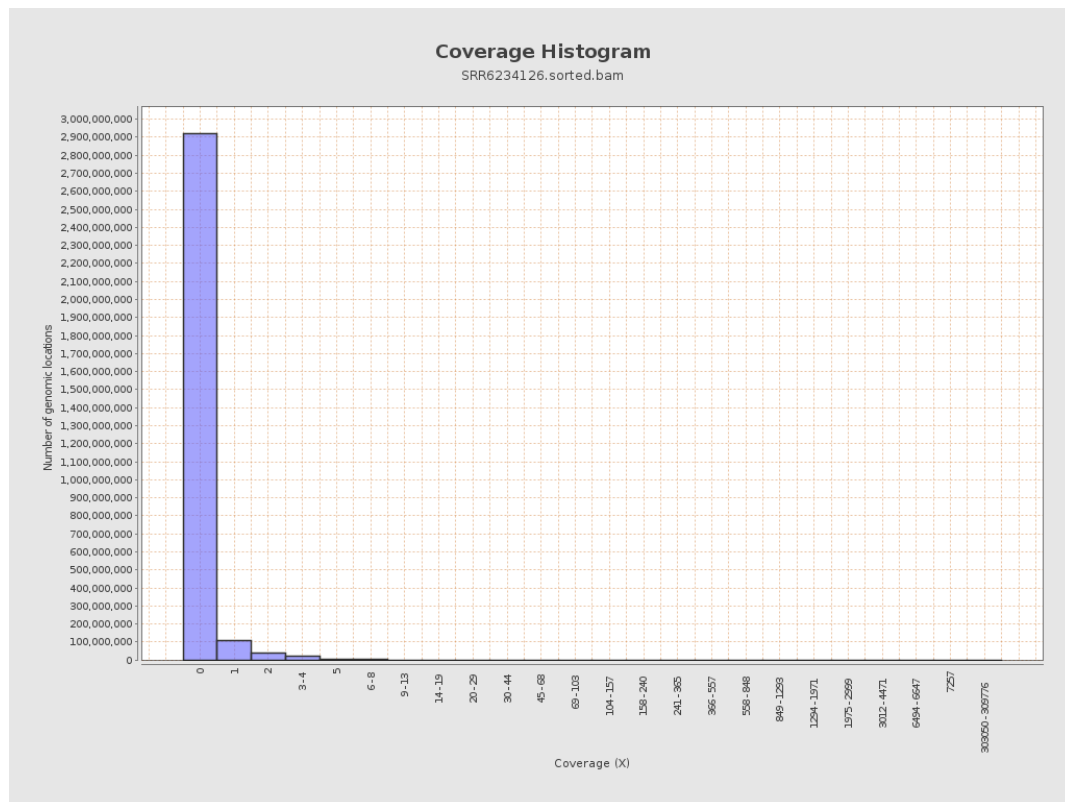
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8688061	0.0349	2.4014
chr2	243199373	31365864	0.129	172.7498
chr3	198022430	18321624	0.0925	0.4658
chr4	191154276	16280979	0.0852	0.503
chr5	180915260	11678722	0.0646	0.4702
chr6	171115067	9194724	0.0537	0.4244
chr7	159138663	44954085	0.2825	4.2142

chr8	146364022	23006041	0.1572	0.9206
chr9	141213431	9535803	0.0675	1.1532
chr10	135534747	1814549	0.0134	0.3007
chr11	135006516	20937604	0.1551	1.3138
chr12	133851895	10476853	0.0783	0.4436
chr13	115169878	5483974	0.0476	0.3276
chr14	107349540	35124504	0.3272	1.0238
chr15	102531392	6609422	0.0645	0.3946
chr16	90354753	1563288	0.0173	0.5108
chr17	81195210	6849684	0.0844	0.6917
chr18	78077248	5131222	0.0657	2.5131
chr19	59128983	16841379	0.2848	1.2584
chr20	63025520	21213718	0.3366	0.95
chr21	48129895	9484668	0.1971	0.7839
chr22	51304566	6735528	0.1313	0.5742
chrMT	16571	27730	1.6734	1.8631
chrX	155270560	1761716	0.0113	0.5229
chrY	59373566	771801	0.013	0.3462

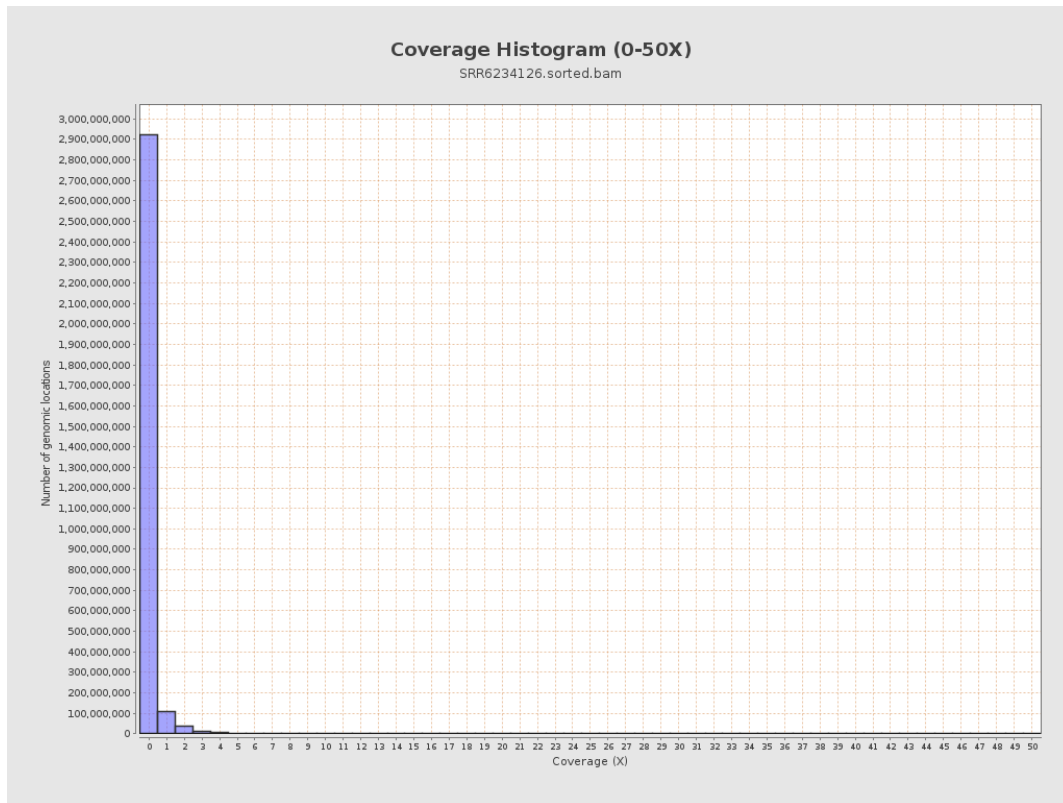
3. Results : Coverage across reference



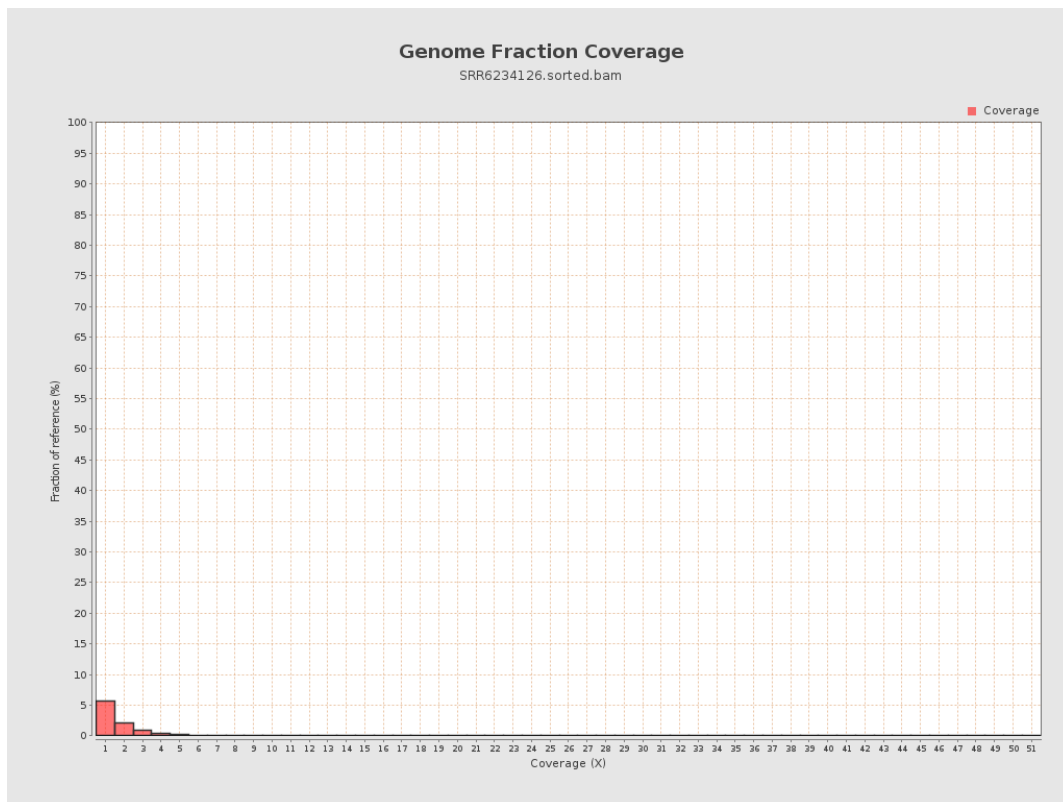
4. Results : Coverage Histogram



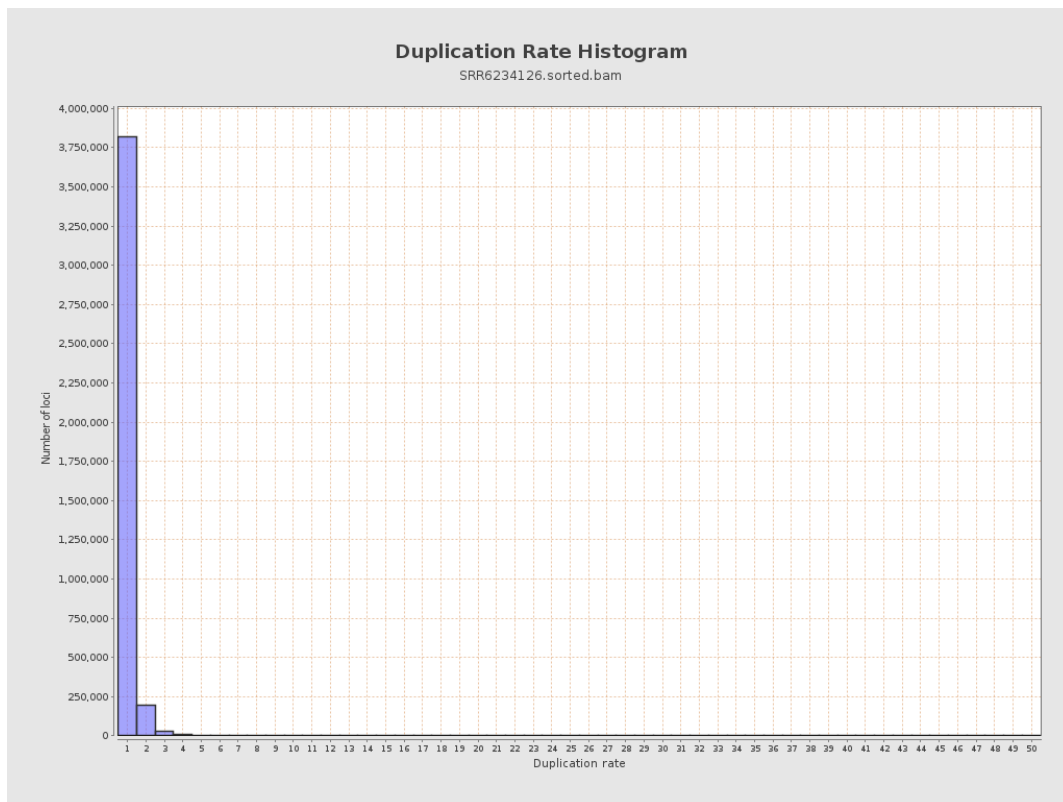
5. Results : Coverage Histogram (0-50X)



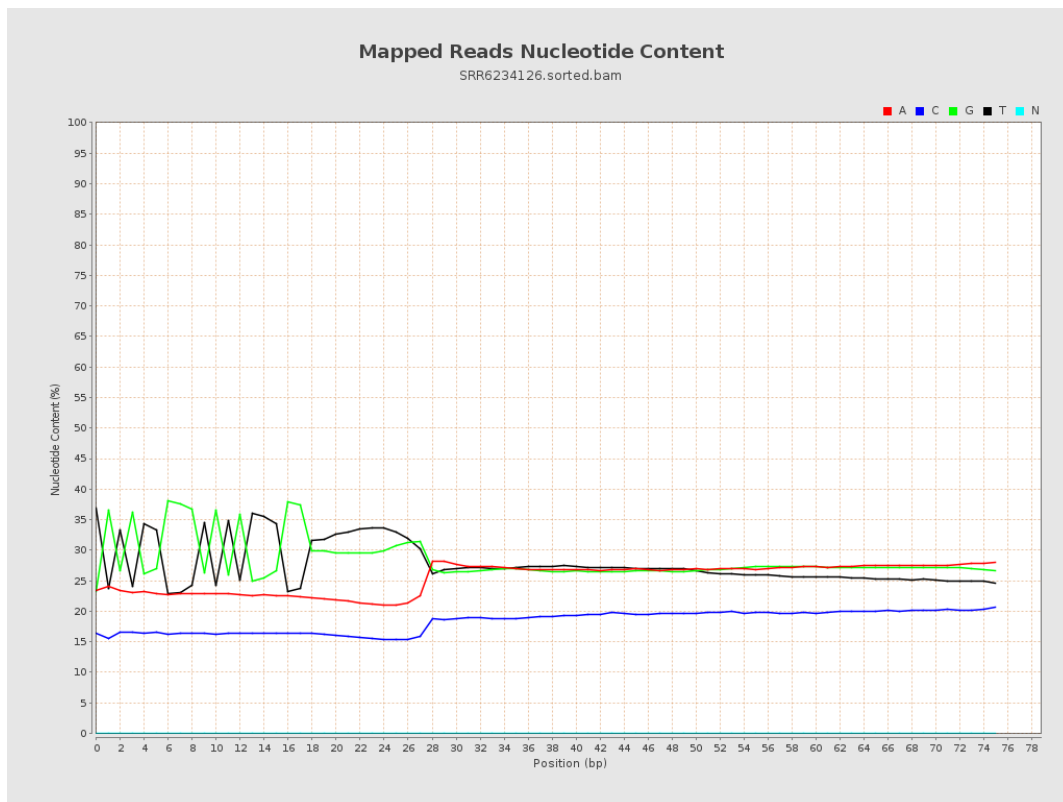
6. Results : Genome Fraction Coverage



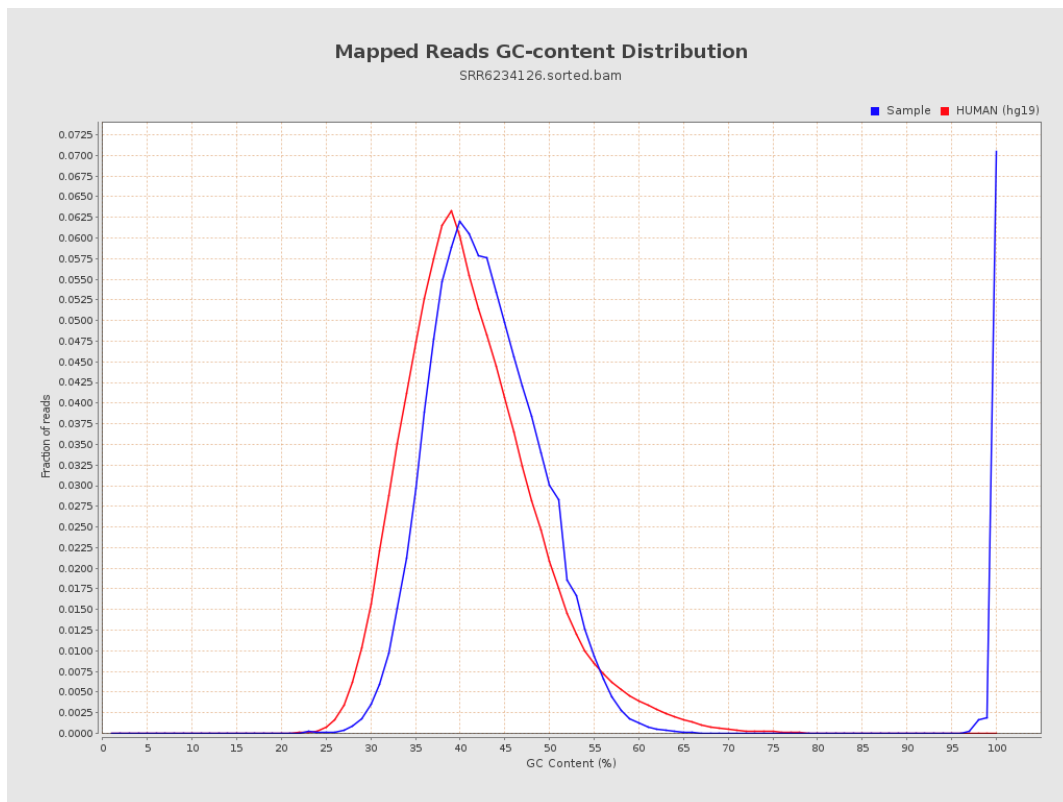
7. Results : Duplication Rate Histogram



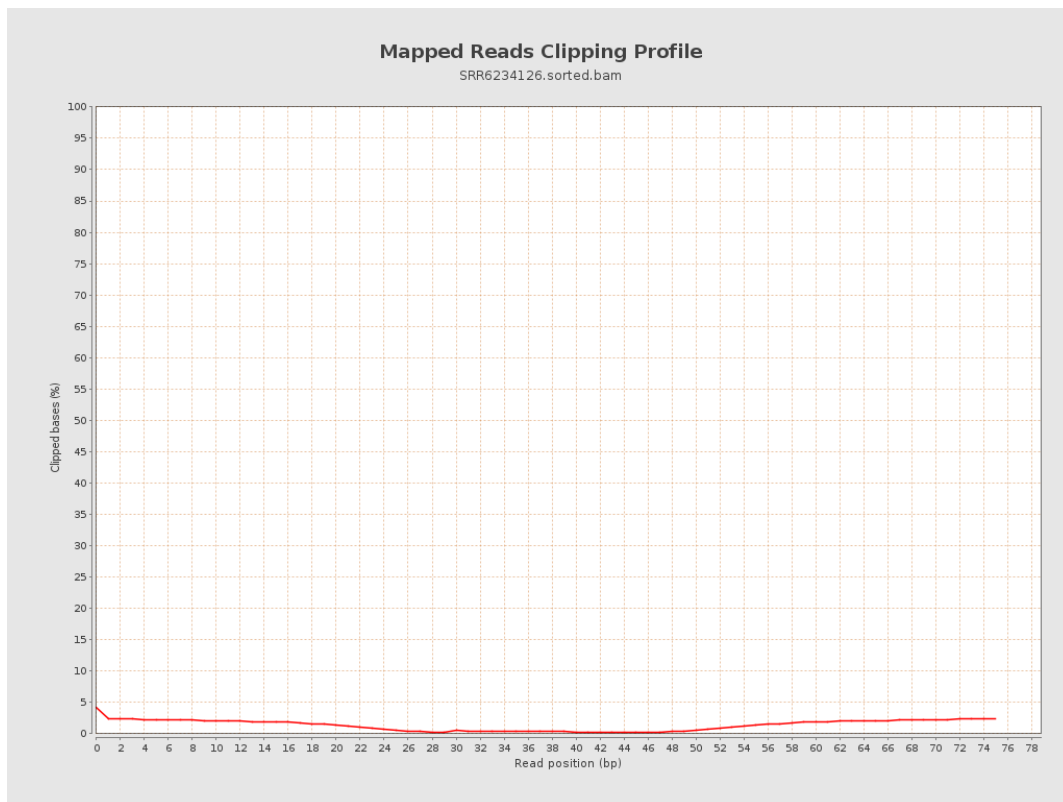
8. Results : Mapped Reads Nucleotide Content



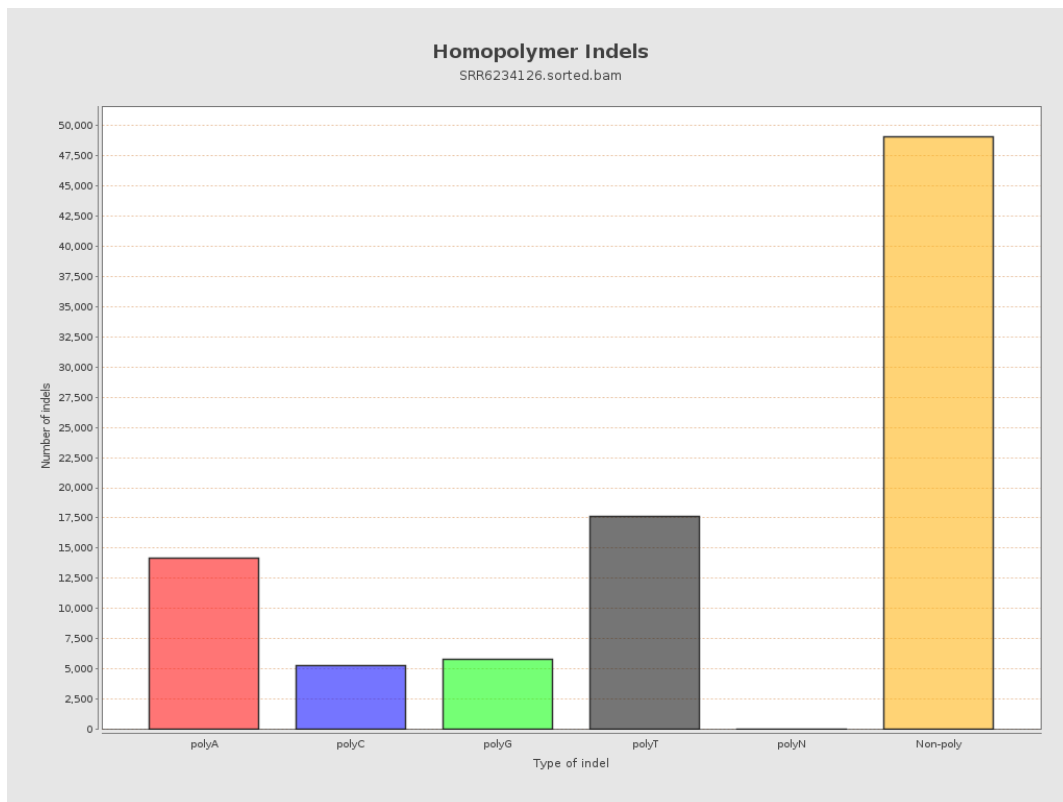
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

