

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:26:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231819.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_SRR6231819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:26:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,968,866
Mapped reads	4,646,751 / 93.52%
Unmapped reads	322,115 / 6.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,765 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	433,033 / 8.71%
Duplication rate	7.29%
Clipped reads	2,538,474 / 51.09%

2.2. ACGT Content

Number/percentage of A's	77,136,835 / 26.02%
Number/percentage of C's	53,090,732 / 17.91%
Number/percentage of T's	96,266,074 / 32.48%
Number/percentage of G's	69,790,456 / 23.55%
Number/percentage of N's	111,866 / 0.04%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0958

Standard Deviation	1.1777
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2.4. Mapping Quality

Mean Mapping Quality	43.18
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2.5. Mismatches and indels

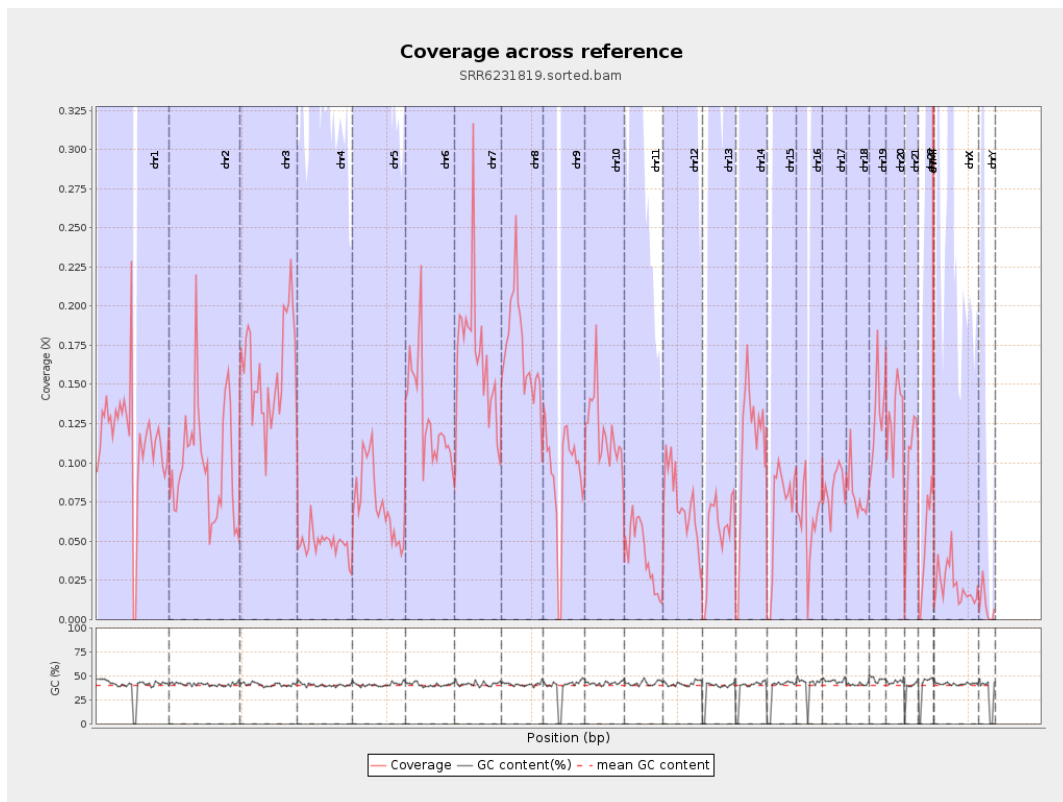
General error rate	0.61%
Mismatches	1,765,182
Insertions	17,434
Mapped reads with at least one insertion	0.37%
Deletions	60,575
Mapped reads with at least one deletion	1.29%
Homopolymer indels	44.59%

2.6. Chromosome stats

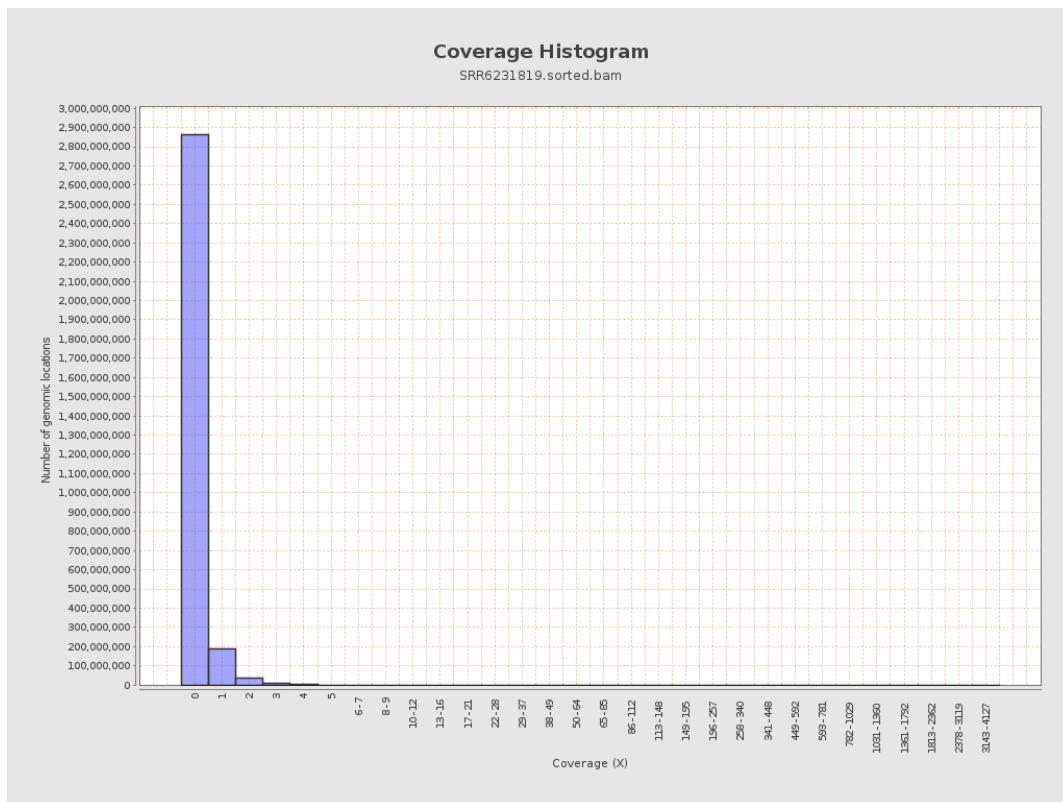
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28471199	0.1142	2.9412
chr2	243199373	23935672	0.0984	1.0528
chr3	198022430	31607053	0.1596	0.4837
chr4	191154276	9191854	0.0481	0.3117
chr5	180915260	13429271	0.0742	0.3625
chr6	171115067	22243424	0.13	0.817
chr7	159138663	26672226	0.1676	2.2629

chr8	146364022	25000332	0.1708	1.123
chr9	141213431	12999802	0.0921	0.7199
chr10	135534747	16290511	0.1202	0.9528
chr11	135006516	5493034	0.0407	0.5124
chr12	133851895	9899044	0.074	0.371
chr13	115169878	6337807	0.055	0.2929
chr14	107349540	11788498	0.1098	0.4433
chr15	102531392	7186609	0.0701	0.3454
chr16	90354753	5707673	0.0632	0.4171
chr17	81195210	6796403	0.0837	0.3995
chr18	78077248	6221036	0.0797	1.4542
chr19	59128983	7807856	0.132	1.4481
chr20	63025520	8067026	0.128	0.4688
chr21	48129895	4729827	0.0983	0.4038
chr22	51304566	2484287	0.0484	0.2601
chrMT	16571	236374	14.2643	8.6331
chrX	155270560	3396194	0.0219	0.327
chrY	59373566	510623	0.0086	0.1898

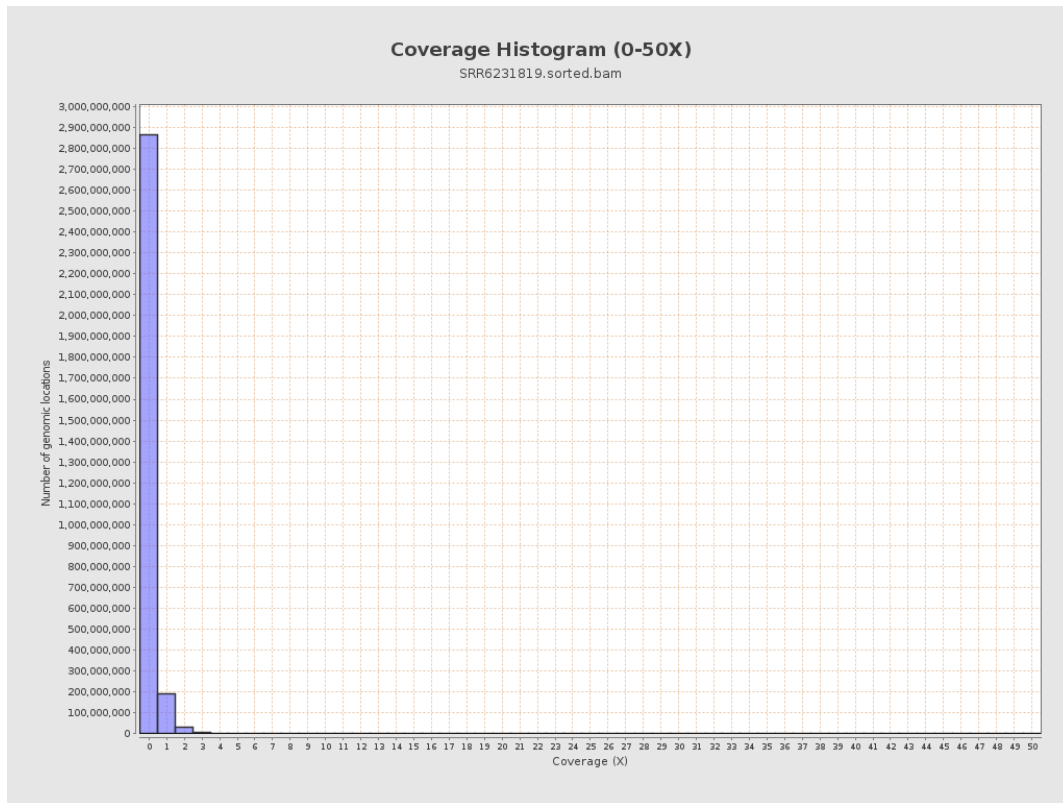
3. Results : Coverage across reference



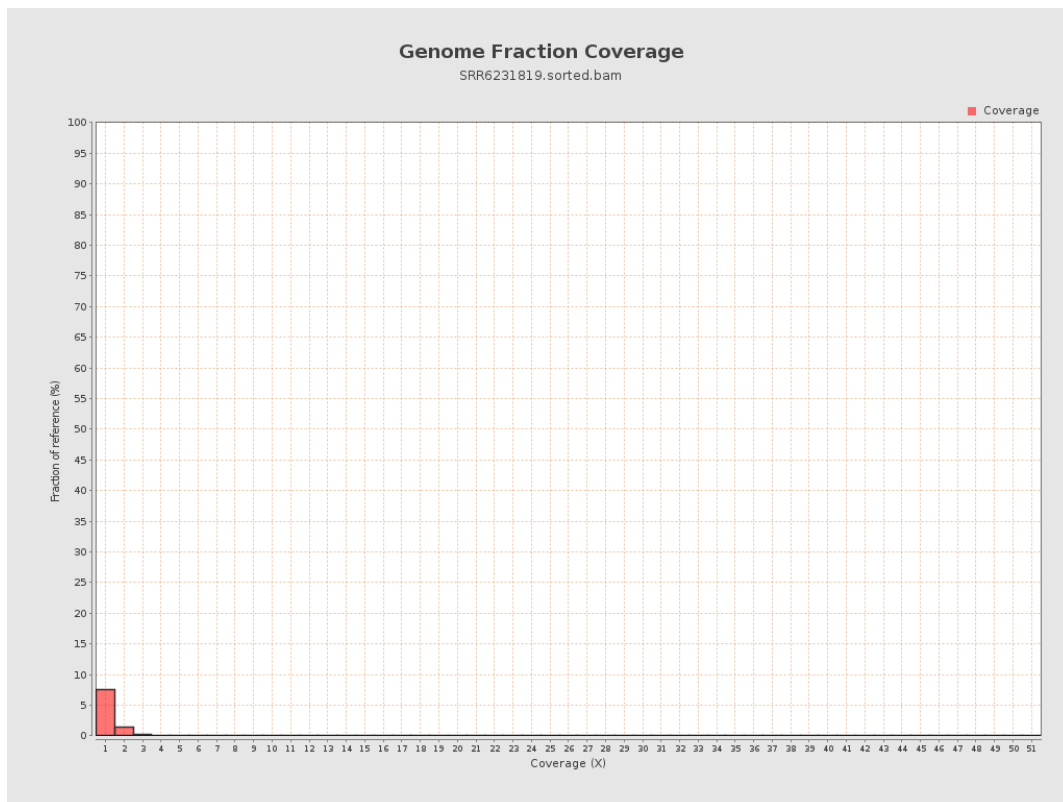
4. Results : Coverage Histogram



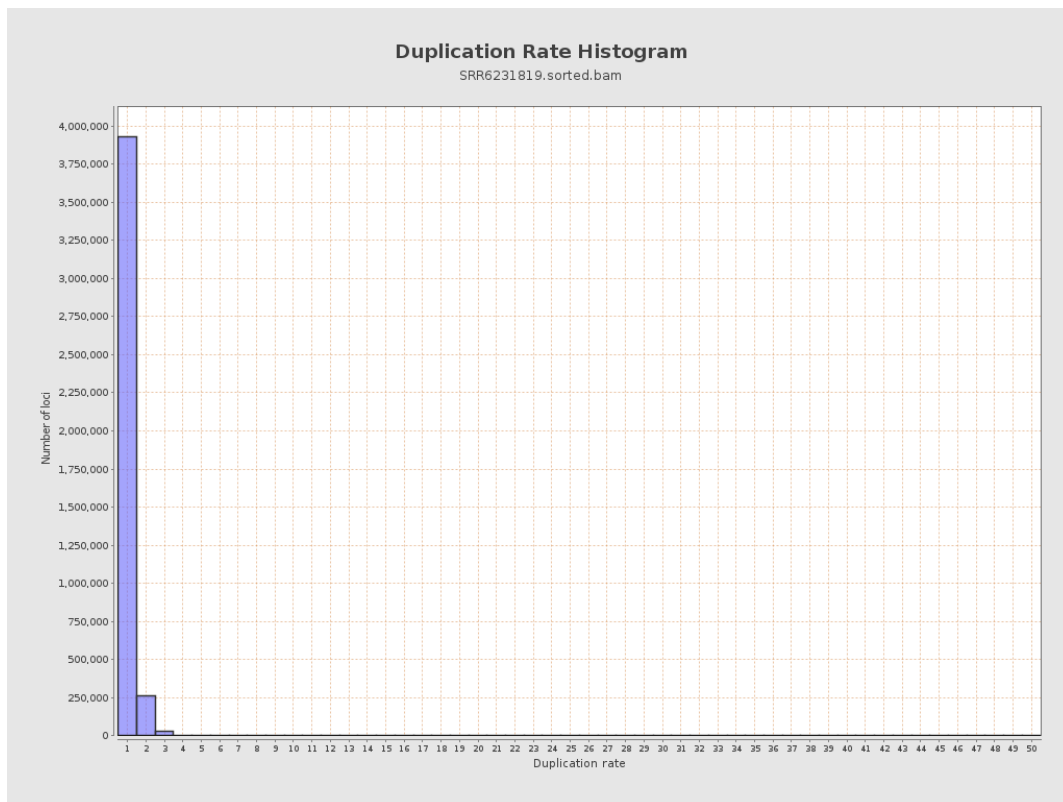
5. Results : Coverage Histogram (0-50X)



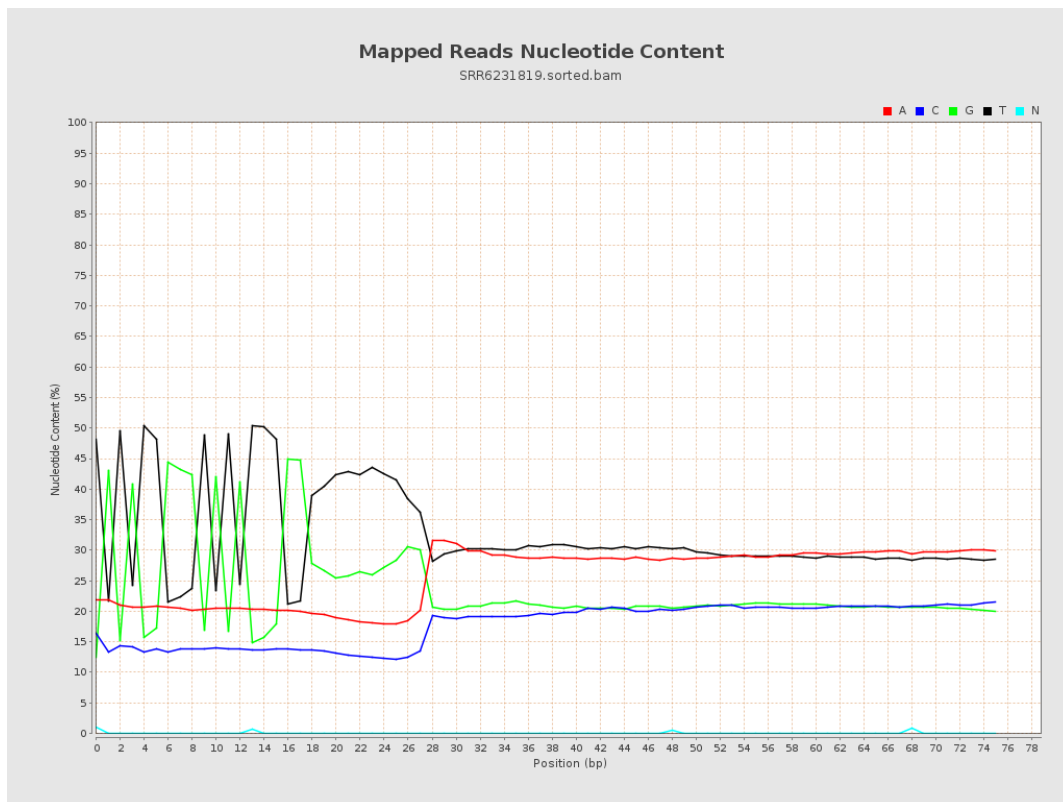
6. Results : Genome Fraction Coverage



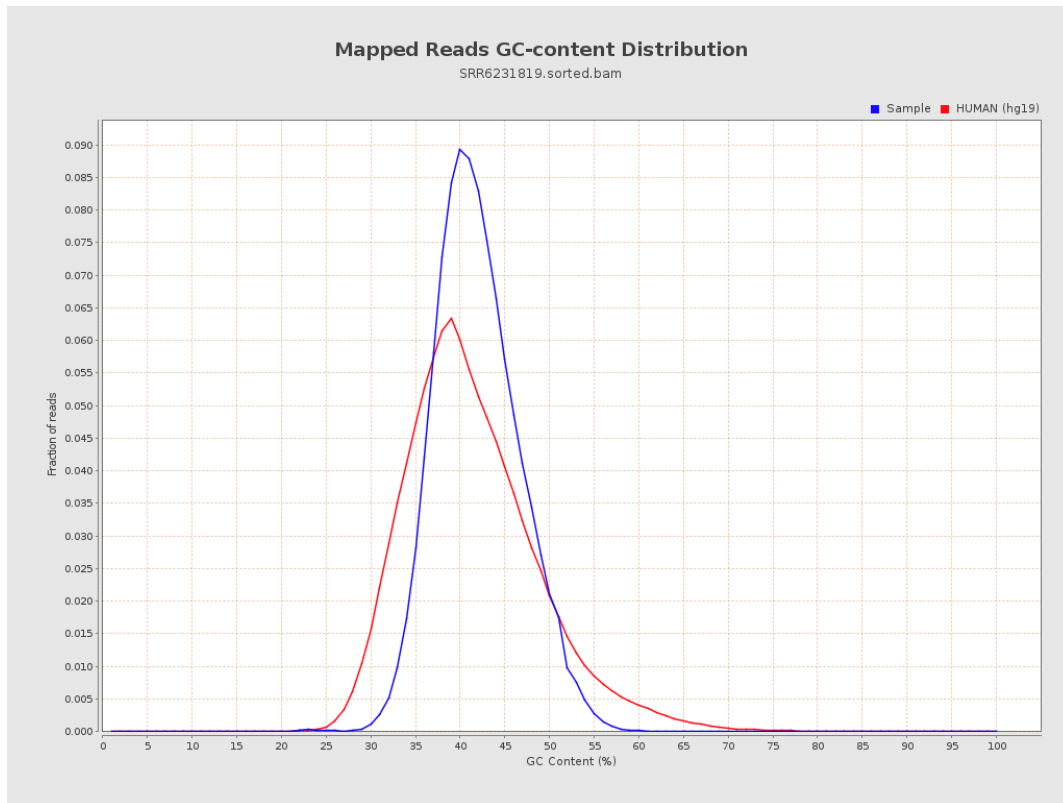
7. Results : Duplication Rate Histogram



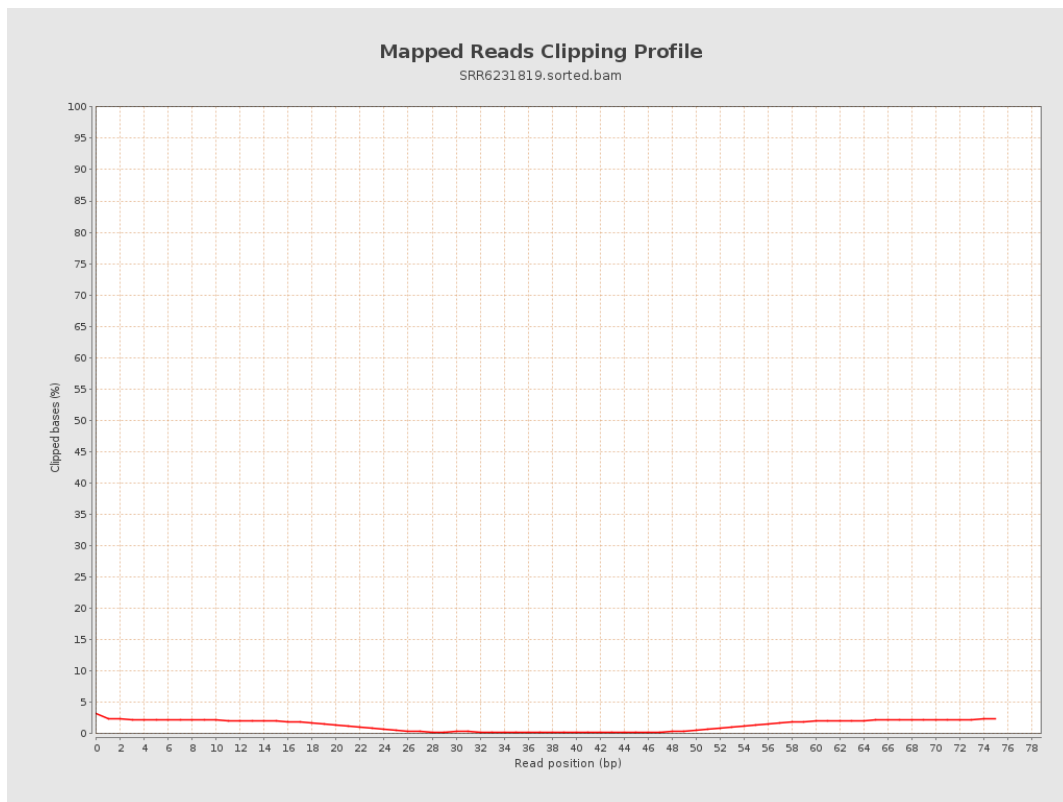
8. Results : Mapped Reads Nucleotide Content



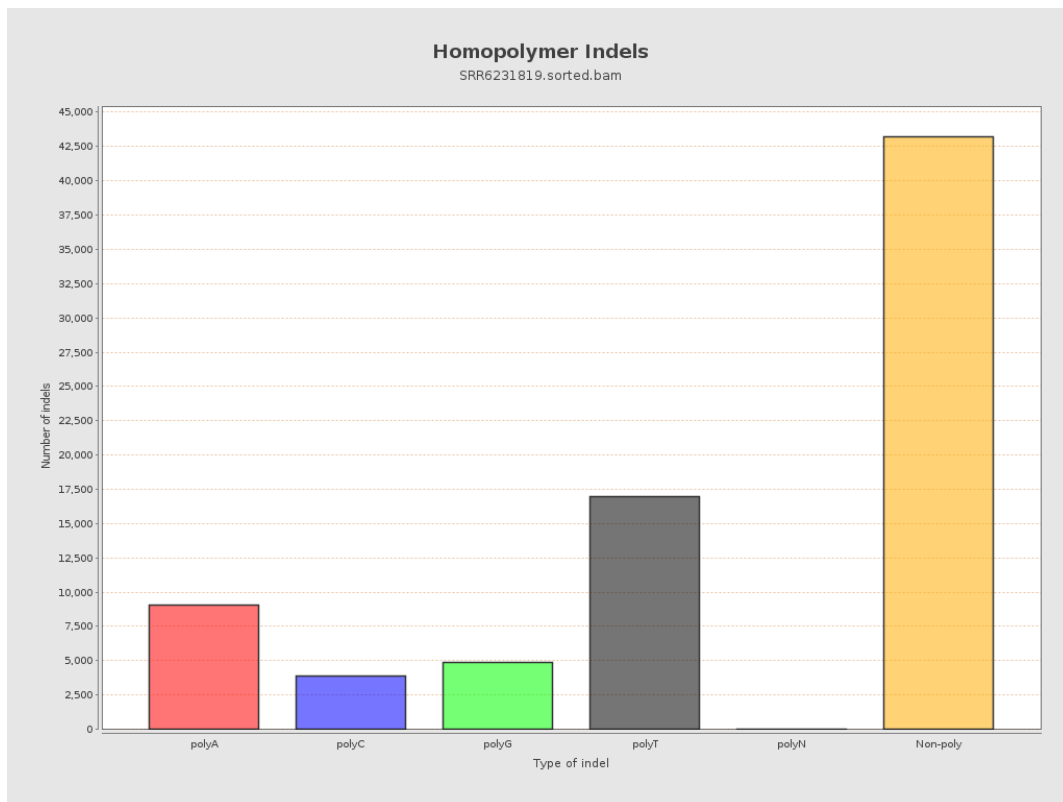
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

