

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:56:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240237.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_SRR6240237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:56:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,328,611
Mapped reads	2,744,709 / 82.46%
Unmapped reads	583,902 / 17.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,031 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	577,163 / 17.34%
Duplication rate	14.07%
Clipped reads	1,331,094 / 39.99%

2.2. ACGT Content

Number/percentage of A's	49,944,266 / 27.67%
Number/percentage of C's	32,817,922 / 18.18%
Number/percentage of T's	58,333,154 / 32.32%
Number/percentage of G's	39,347,729 / 21.8%
Number/percentage of N's	67,924 / 0.04%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0583

Standard Deviation	0.6603
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2.4. Mapping Quality

Mean Mapping Quality	46.85
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2.5. Mismatches and indels

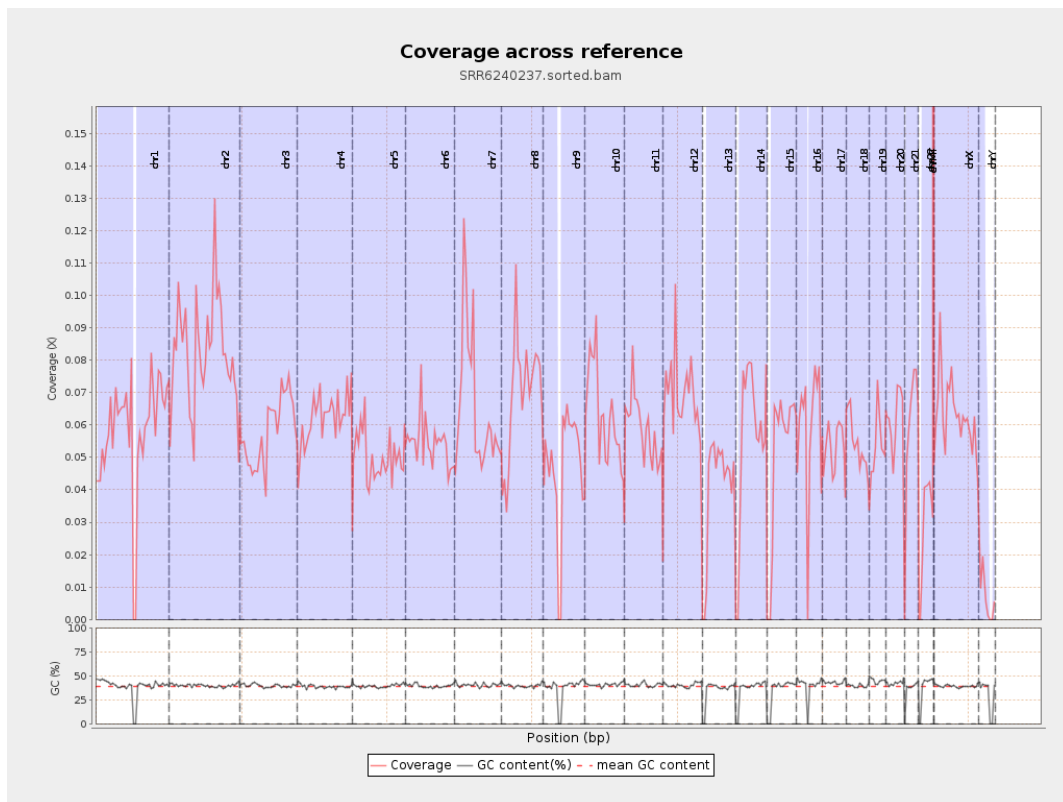
General error rate	0.89%
Mismatches	1,584,559
Insertions	13,255
Mapped reads with at least one insertion	0.48%
Deletions	50,519
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.99%

2.6. Chromosome stats

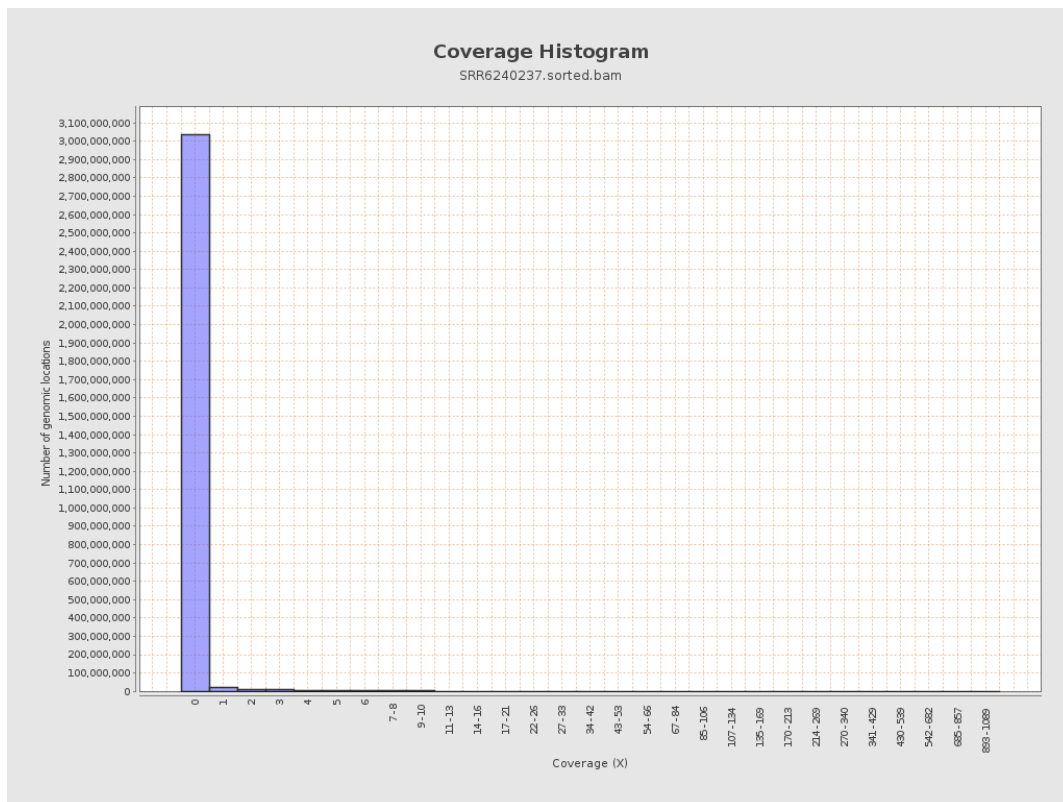
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14506039	0.0582	0.9133
chr2	243199373	20061167	0.0825	0.7897
chr3	198022430	11493677	0.058	0.558
chr4	191154276	11899935	0.0623	0.5759
chr5	180915260	9066032	0.0501	0.5164
chr6	171115067	9292480	0.0543	0.5779
chr7	159138663	10515255	0.0661	0.8692

chr8	146364022	10150261	0.0693	0.89
chr9	141213431	6688496	0.0474	0.5972
chr10	135534747	8571103	0.0632	0.6307
chr11	135006516	7870050	0.0583	0.6396
chr12	133851895	9263579	0.0692	0.6042
chr13	115169878	4636499	0.0403	0.4677
chr14	107349540	5988336	0.0558	0.5473
chr15	102531392	5235696	0.0511	0.5166
chr16	90354753	5320388	0.0589	0.5505
chr17	81195210	4239213	0.0522	0.5347
chr18	78077248	4251958	0.0545	0.827
chr19	59128983	3201976	0.0542	0.6804
chr20	63025520	3805746	0.0604	0.5686
chr21	48129895	2871468	0.0597	0.5612
chr22	51304566	1450025	0.0283	0.3578
chrMT	16571	43379	2.6178	3.5747
chrX	155270560	9741962	0.0627	0.592
chrY	59373566	434466	0.0073	0.1641

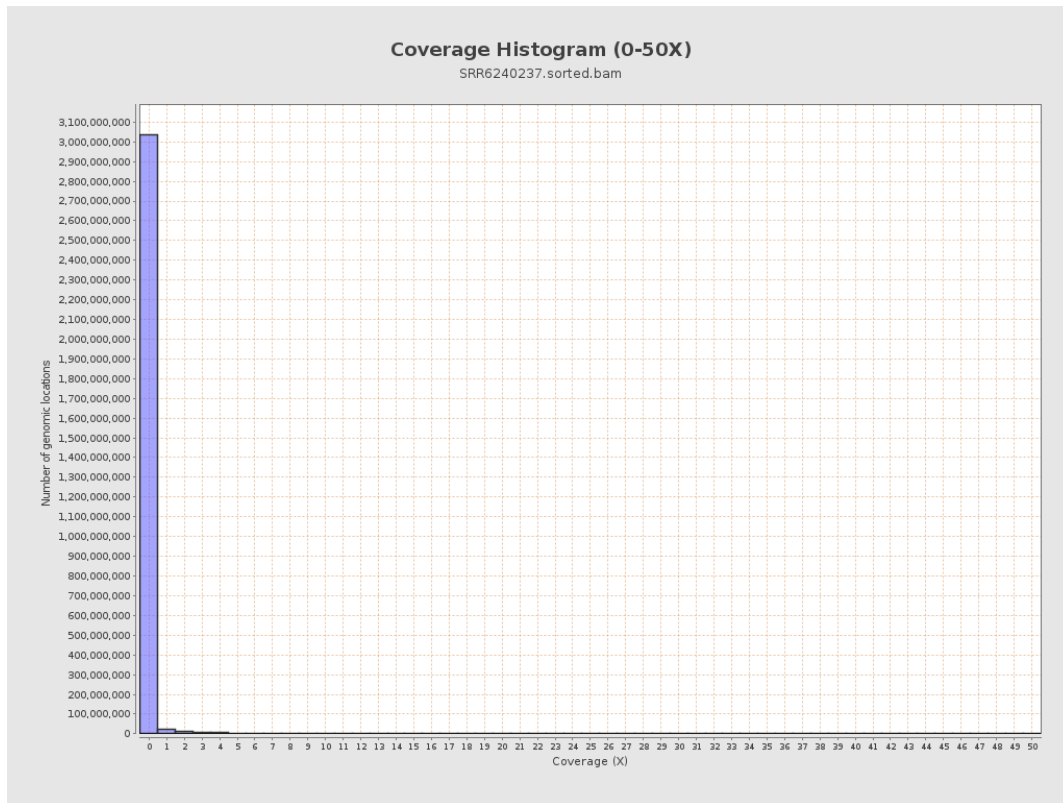
3. Results : Coverage across reference



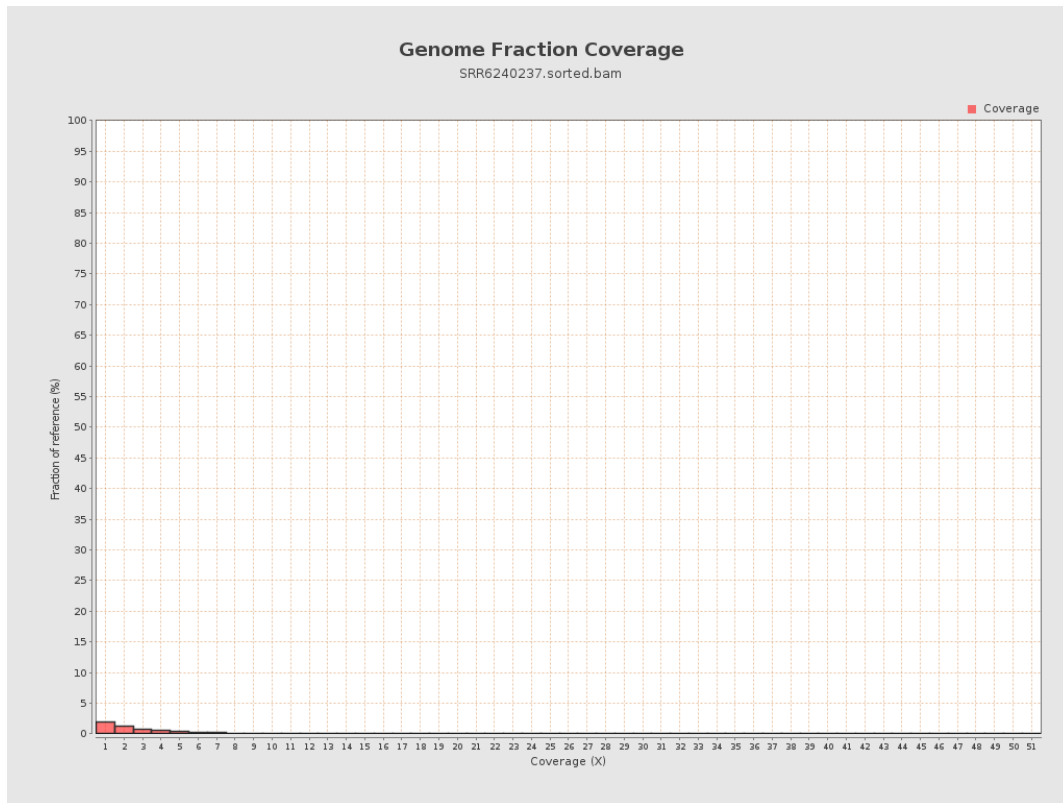
4. Results : Coverage Histogram



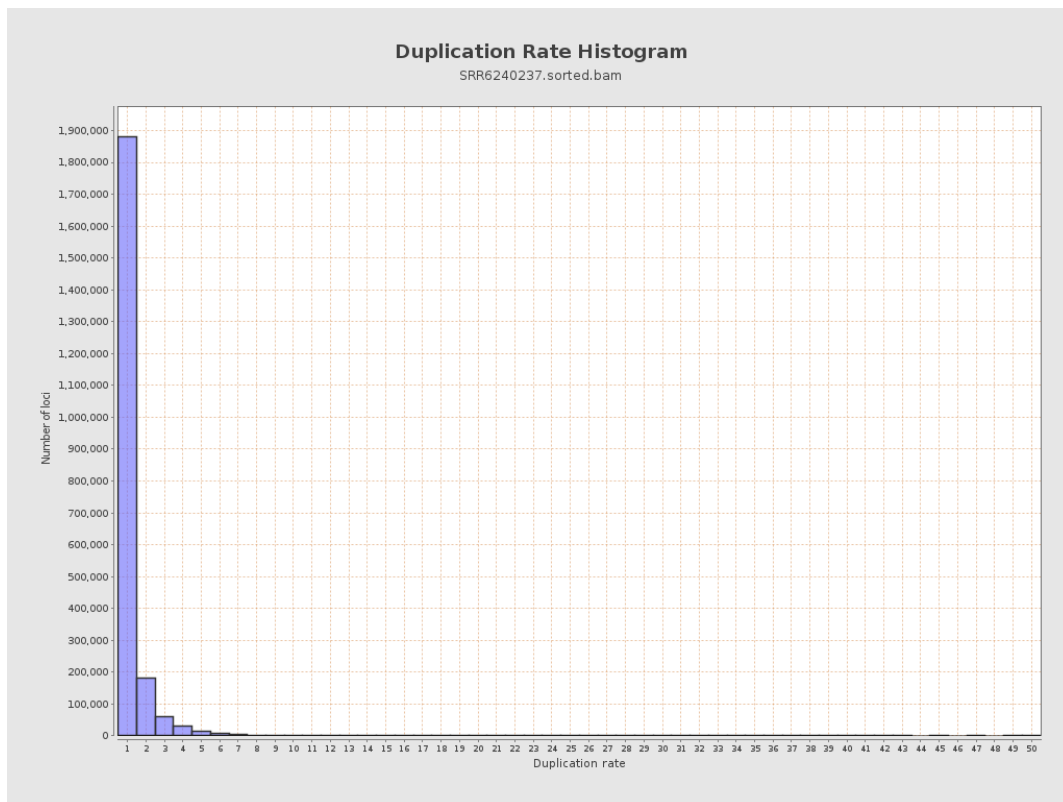
5. Results : Coverage Histogram (0-50X)



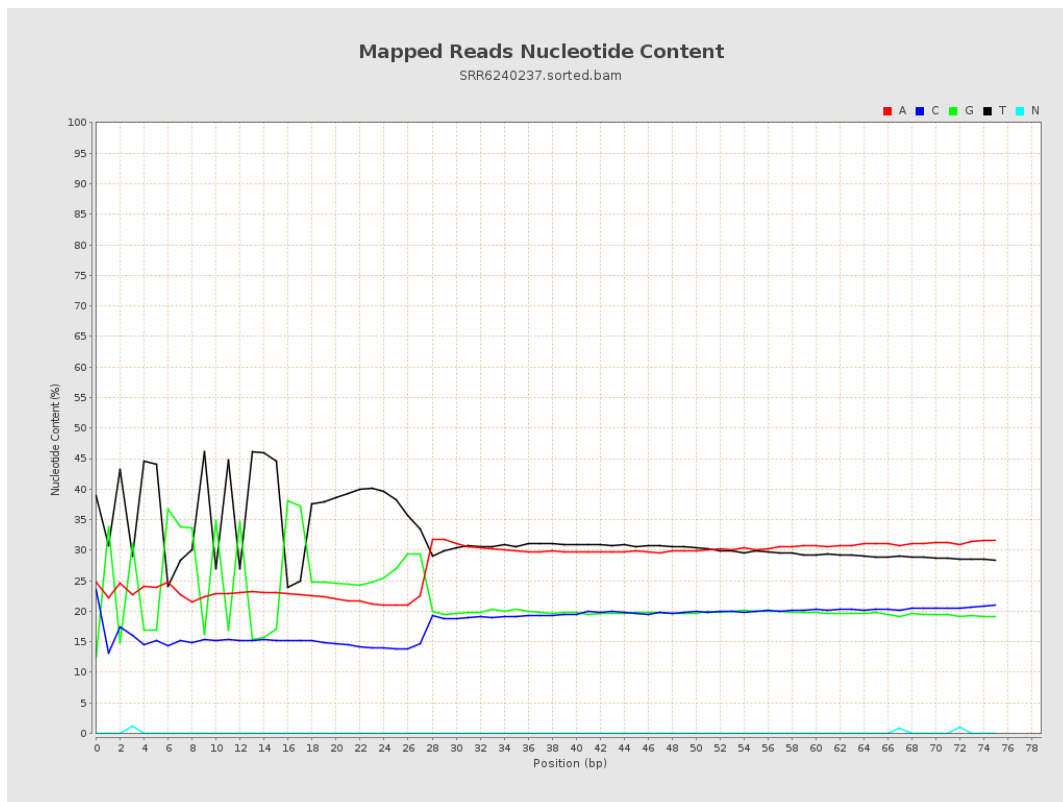
6. Results : Genome Fraction Coverage



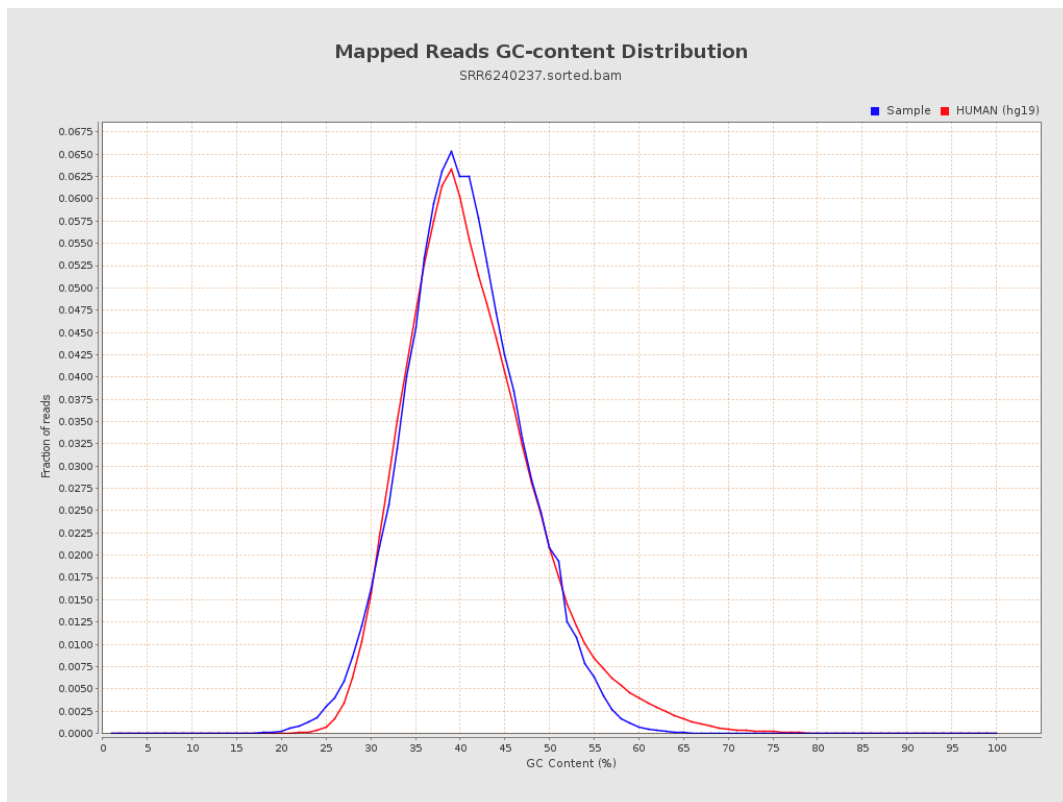
7. Results : Duplication Rate Histogram



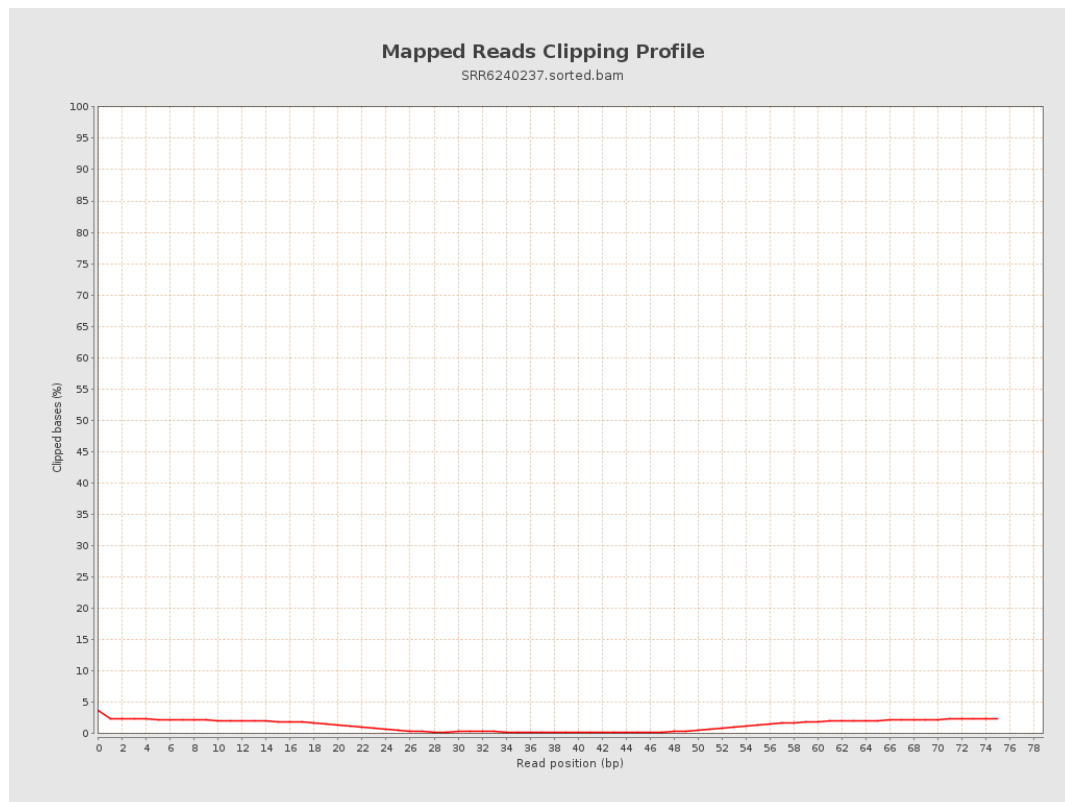
8. Results : Mapped Reads Nucleotide Content



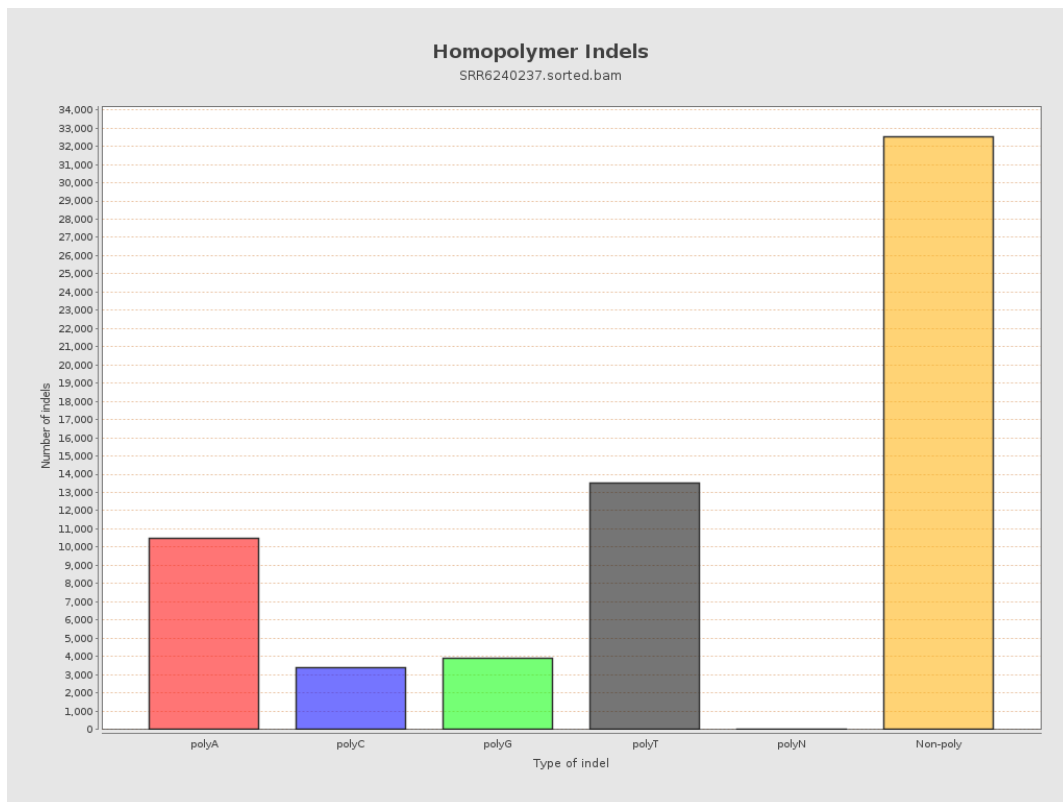
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

