

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237262.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_SRR6237262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:06:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,793,260
Mapped reads	3,367,318 / 88.77%
Unmapped reads	425,942 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,596 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	858,999 / 22.65%
Duplication rate	18.2%
Clipped reads	1,923,171 / 50.7%

2.2. ACGT Content

Number/percentage of A's	57,487,342 / 26.8%
Number/percentage of C's	37,296,328 / 17.39%
Number/percentage of T's	71,253,340 / 33.22%
Number/percentage of G's	48,433,340 / 22.58%
Number/percentage of N's	24,435 / 0.01%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0693

Standard Deviation	0.9815
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2.4. Mapping Quality

Mean Mapping Quality	45.77
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2.5. Mismatches and indels

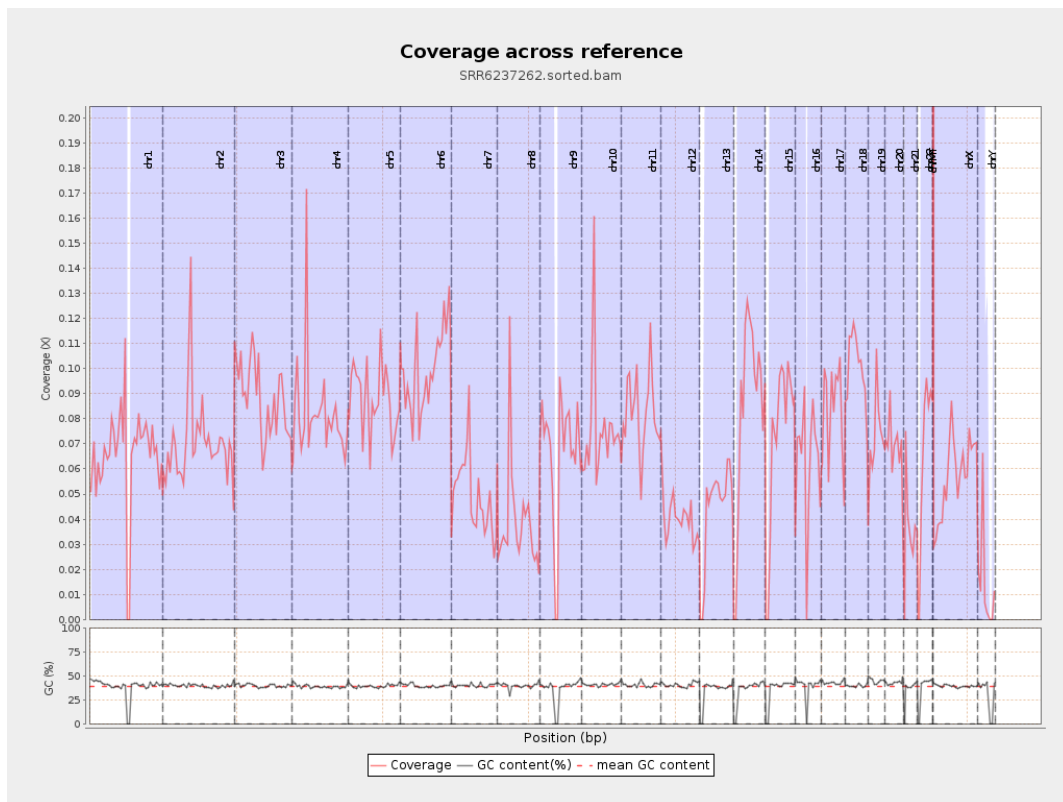
General error rate	0.64%
Mismatches	1,332,745
Insertions	17,729
Mapped reads with at least one insertion	0.52%
Deletions	60,077
Mapped reads with at least one deletion	1.76%
Homopolymer indels	43.09%

2.6. Chromosome stats

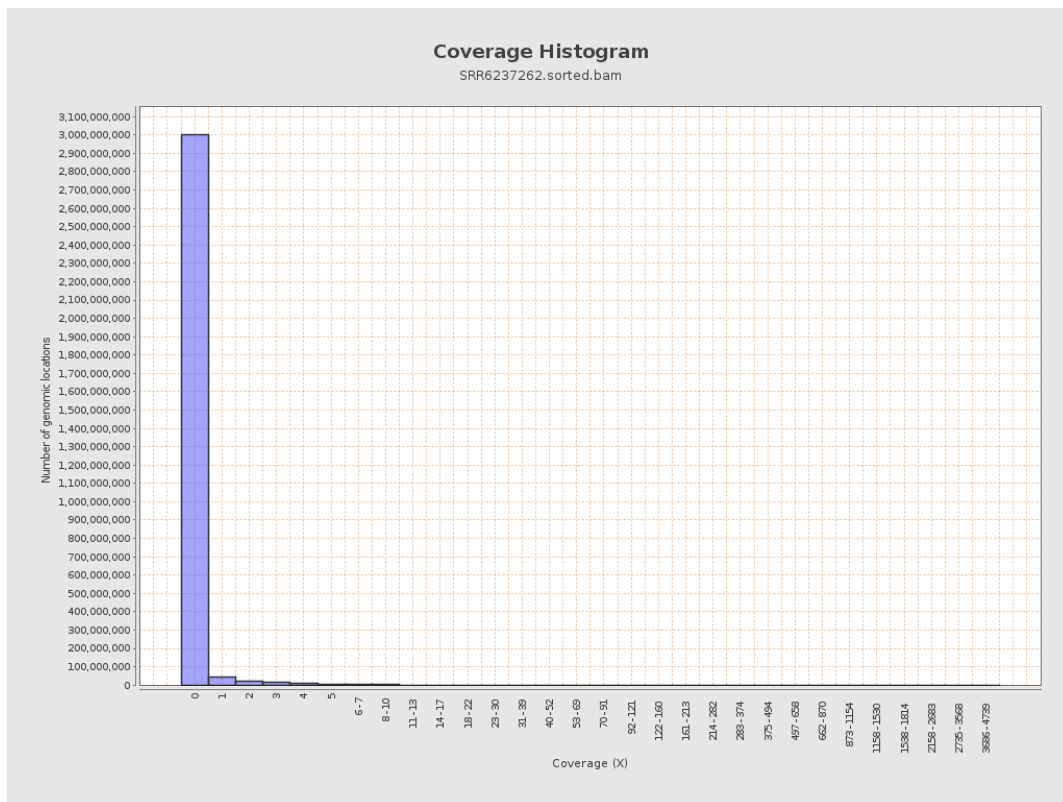
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16228766	0.0651	1.1909
chr2	243199373	17150069	0.0705	1.0907
chr3	198022430	17497218	0.0884	0.561
chr4	191154276	15756289	0.0824	0.7286
chr5	180915260	15883765	0.0878	0.5602
chr6	171115067	17044486	0.0996	0.6958
chr7	159138663	7776145	0.0489	0.6407

chr8	146364022	5618850	0.0384	2.8462
chr9	141213431	9356808	0.0663	0.7322
chr10	135534747	10108585	0.0746	0.938
chr11	135006516	11182080	0.0828	0.7107
chr12	133851895	5351577	0.04	0.3945
chr13	115169878	5118881	0.0444	0.4051
chr14	107349540	9228546	0.086	0.5736
chr15	102531392	7334665	0.0715	0.503
chr16	90354753	5585211	0.0618	0.5369
chr17	81195210	6826985	0.0841	0.6341
chr18	78077248	7929393	0.1016	1.6172
chr19	59128983	4370203	0.0739	0.9493
chr20	63025520	4370633	0.0693	0.5279
chr21	48129895	1800419	0.0374	0.5208
chr22	51304566	3297301	0.0643	0.4649
chrMT	16571	71543	4.3174	4.3577
chrX	155270560	8857695	0.057	0.4986
chrY	59373566	855746	0.0144	0.6196

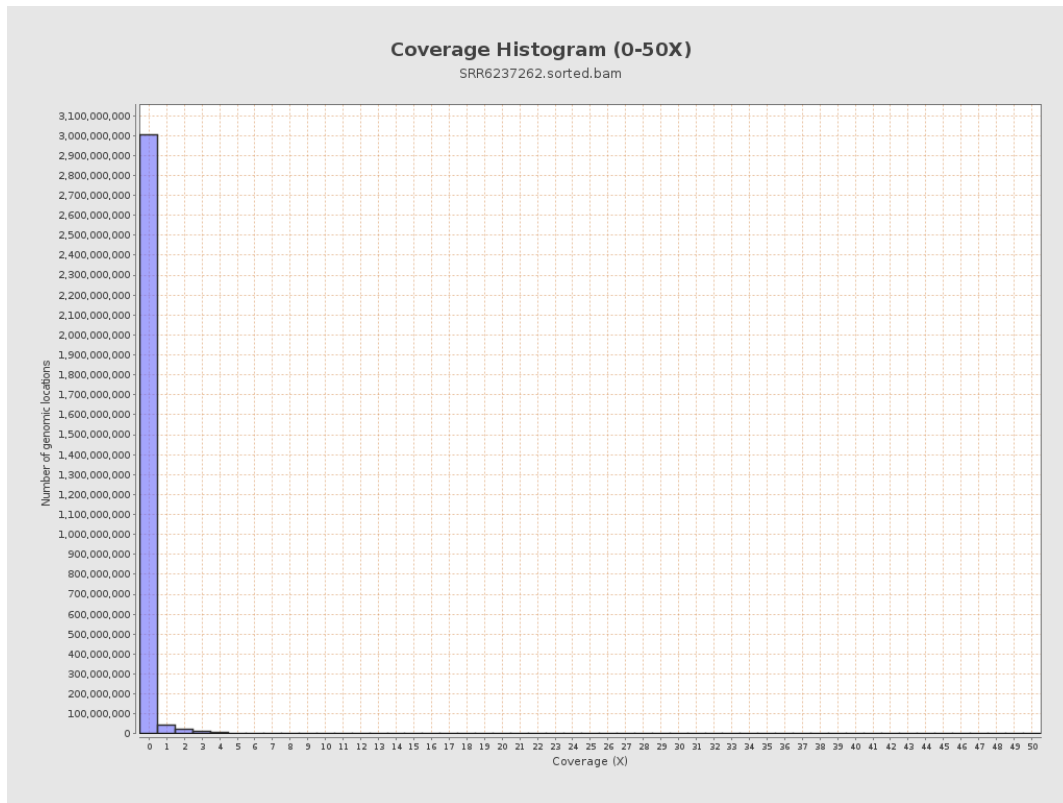
3. Results : Coverage across reference



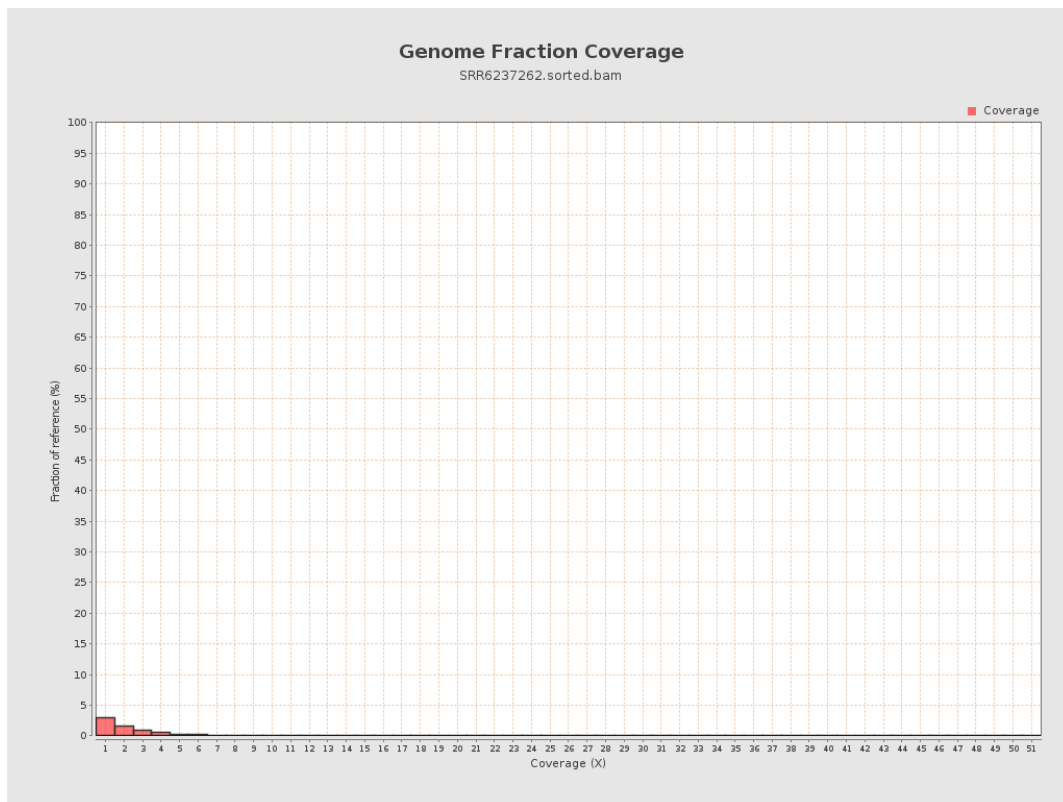
4. Results : Coverage Histogram



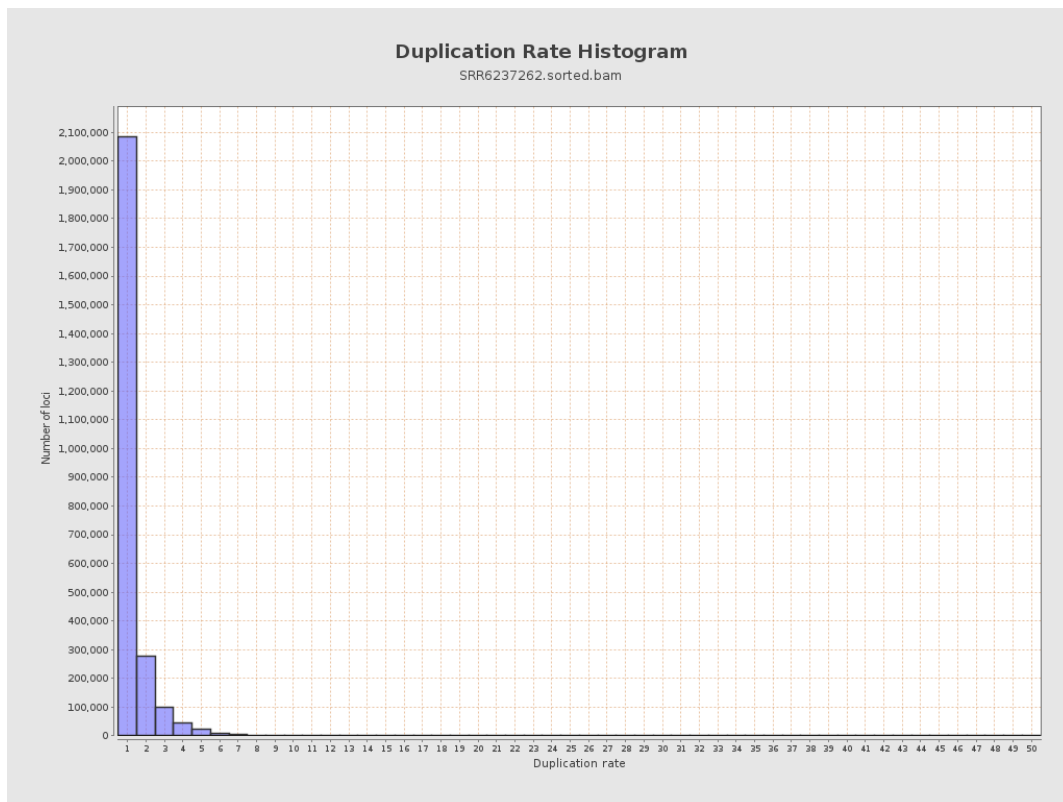
5. Results : Coverage Histogram (0-50X)



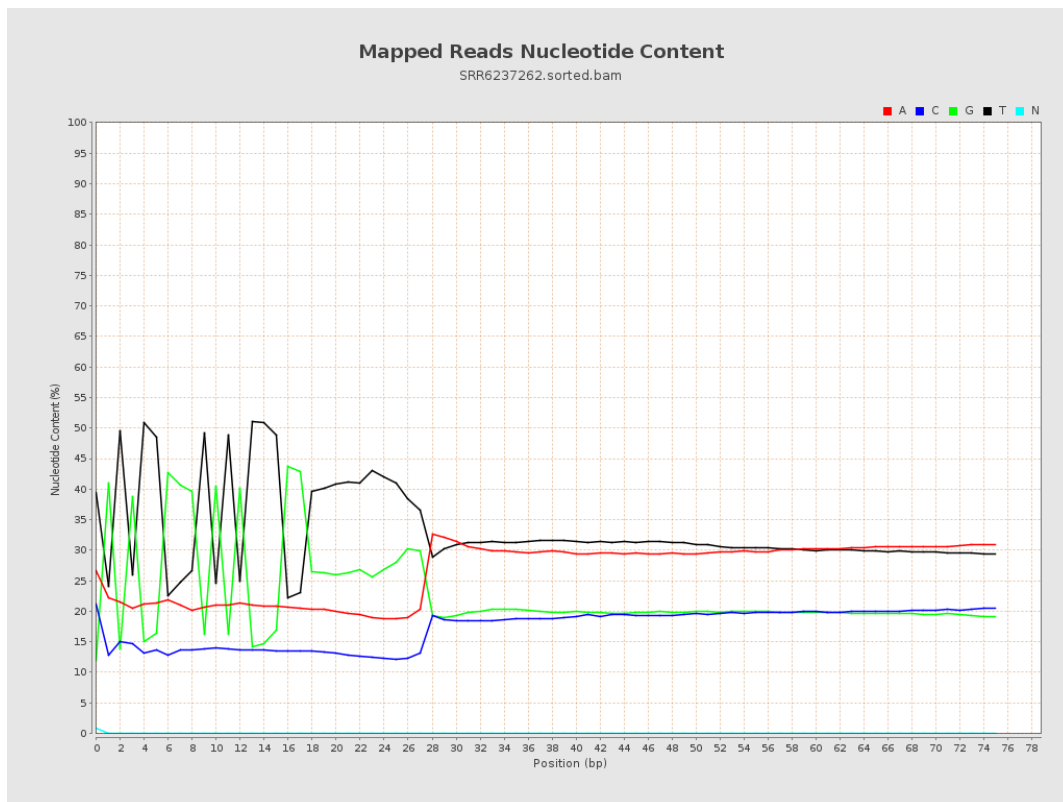
6. Results : Genome Fraction Coverage



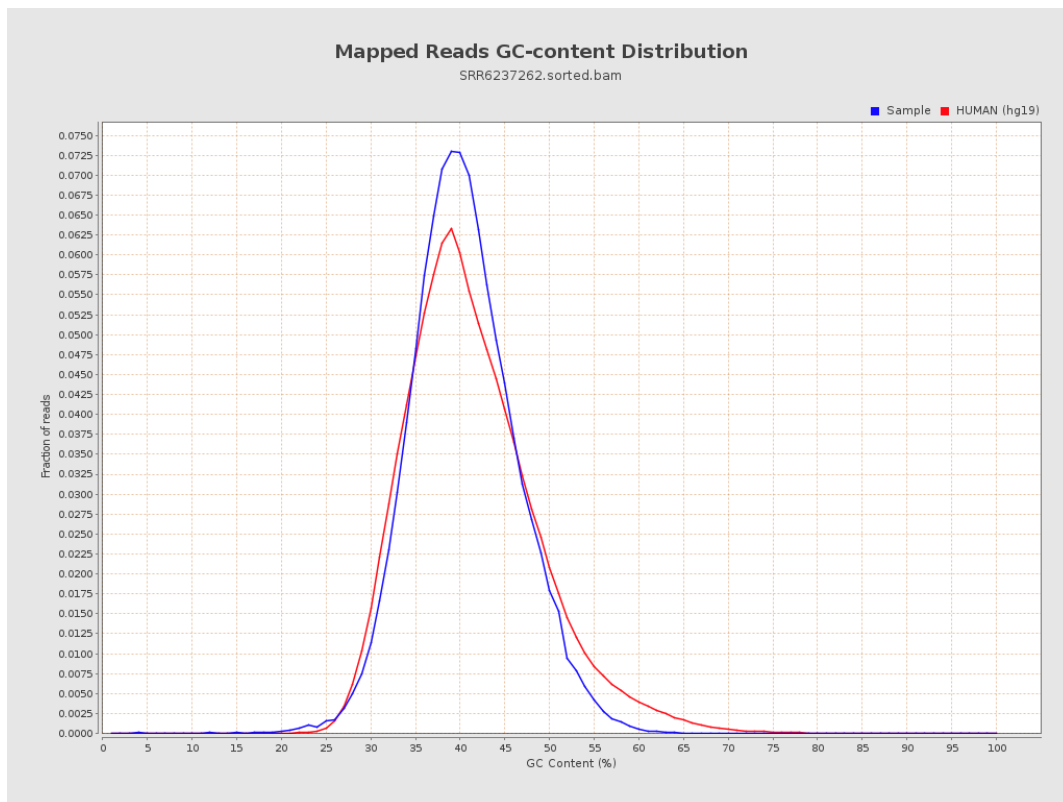
7. Results : Duplication Rate Histogram



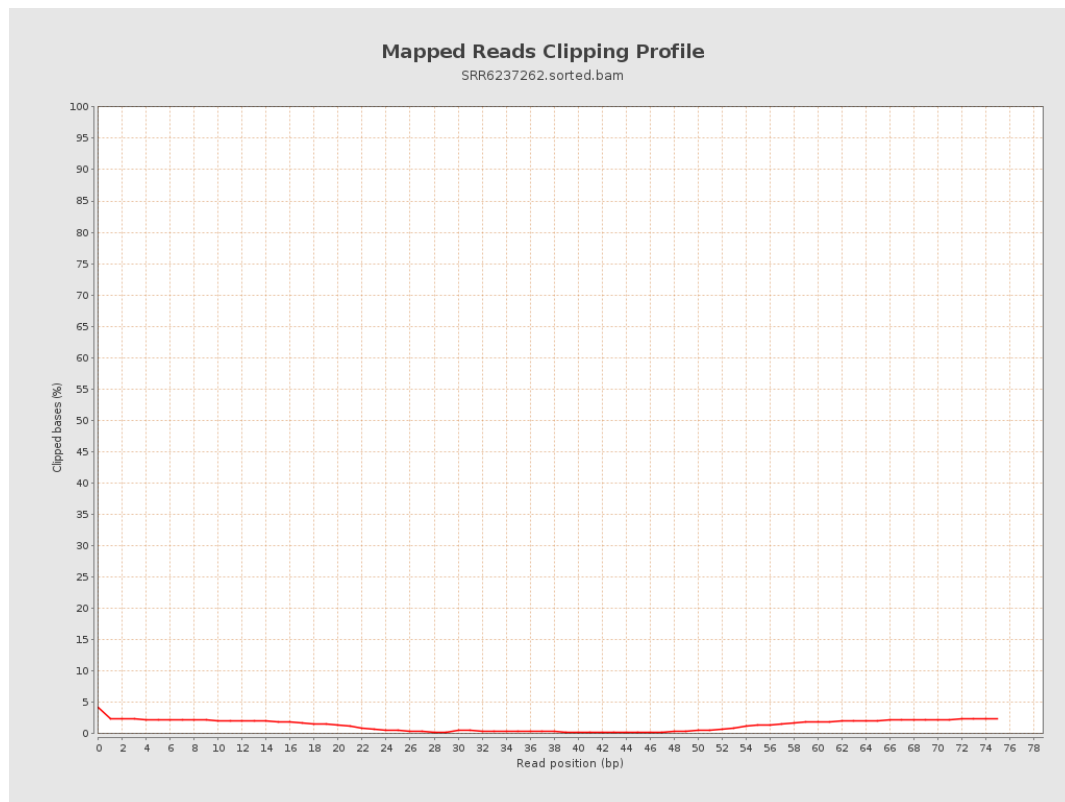
8. Results : Mapped Reads Nucleotide Content



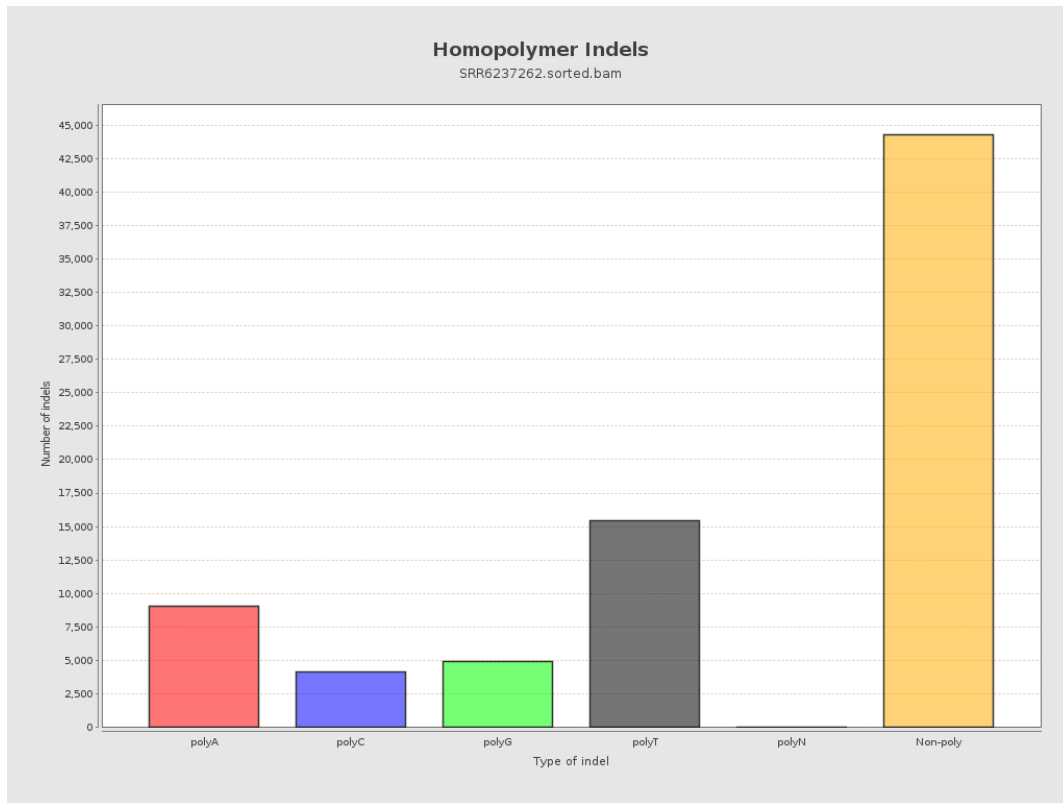
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

