

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:51:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237258.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_SRR6237258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:51:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,730,294
Mapped reads	2,473,798 / 90.61%
Unmapped reads	256,496 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,280 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	580,269 / 21.25%
Duplication rate	18.02%
Clipped reads	1,662,181 / 60.88%

2.2. ACGT Content

Number/percentage of A's	38,210,767 / 25.2%
Number/percentage of C's	26,764,797 / 17.65%
Number/percentage of T's	49,965,359 / 32.95%
Number/percentage of G's	36,697,530 / 24.2%
Number/percentage of N's	15,417 / 0.01%
GC Percentage	41.85%

2.3. Coverage

Mean	0.049

Standard Deviation	0.5817
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2.4. Mapping Quality

Mean Mapping Quality	44.88
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2.5. Mismatches and indels

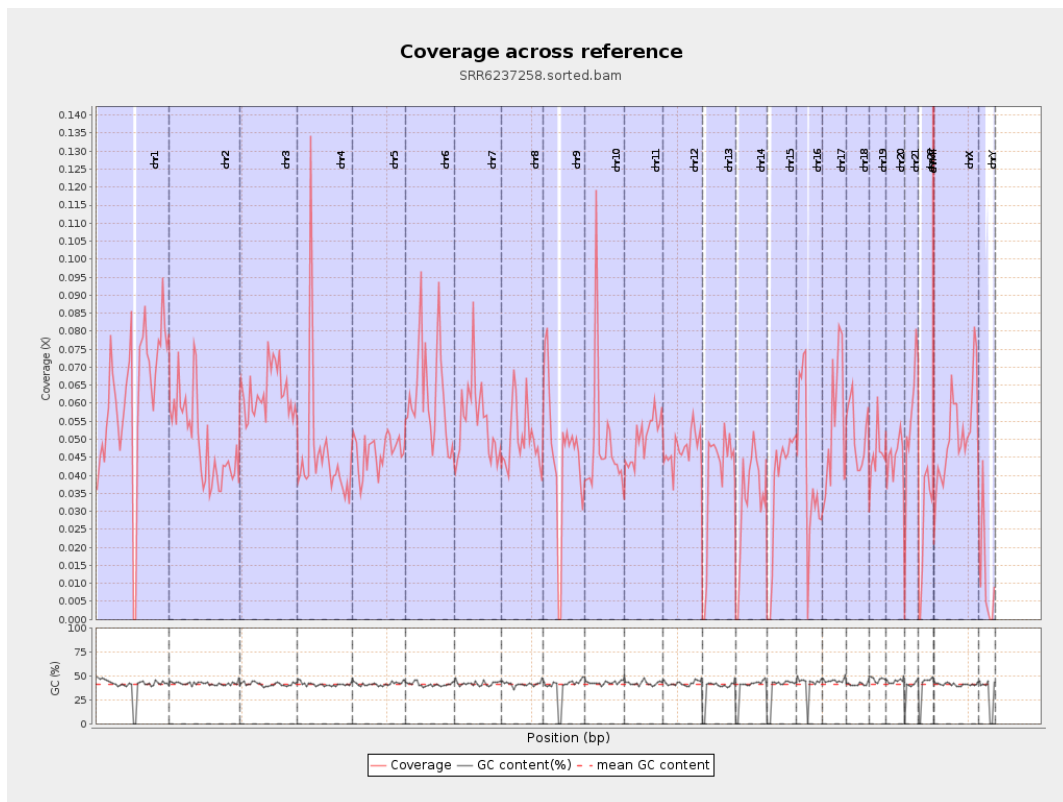
General error rate	0.7%
Mismatches	1,031,870
Insertions	11,960
Mapped reads with at least one insertion	0.48%
Deletions	46,088
Mapped reads with at least one deletion	1.84%
Homopolymer indels	42.9%

2.6. Chromosome stats

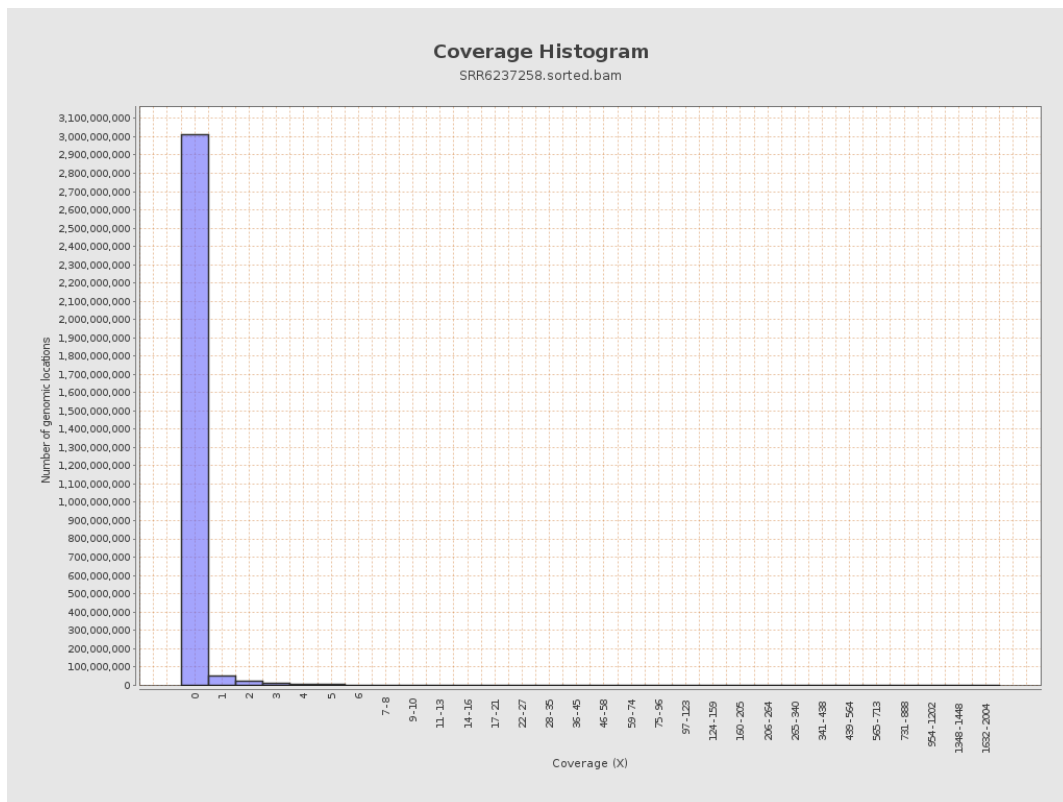
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15336865	0.0615	0.7415
chr2	243199373	11972795	0.0492	1.0239
chr3	198022430	12464429	0.0629	0.4046
chr4	191154276	8617721	0.0451	0.5342
chr5	180915260	8369525	0.0463	0.3525
chr6	171115067	10564386	0.0617	0.5252
chr7	159138663	8812140	0.0554	0.6104

chr8	146364022	7280053	0.0497	0.9315
chr9	141213431	6444857	0.0456	0.406
chr10	135534747	6516585	0.0481	0.6967
chr11	135006516	6758513	0.0501	0.4428
chr12	133851895	6361003	0.0475	0.366
chr13	115169878	4507946	0.0391	0.3459
chr14	107349540	3496954	0.0326	0.3082
chr15	102531392	3805884	0.0371	0.338
chr16	90354753	3848156	0.0426	0.3719
chr17	81195210	4340369	0.0535	0.421
chr18	78077248	4048590	0.0519	0.7392
chr19	59128983	2736196	0.0463	0.5321
chr20	63025520	2836375	0.045	0.3827
chr21	48129895	2669853	0.0555	0.4621
chr22	51304566	1350835	0.0263	0.2566
chrMT	16571	11642	0.7026	1.4745
chrX	155270560	7978097	0.0514	0.3933
chrY	59373566	605763	0.0102	0.4087

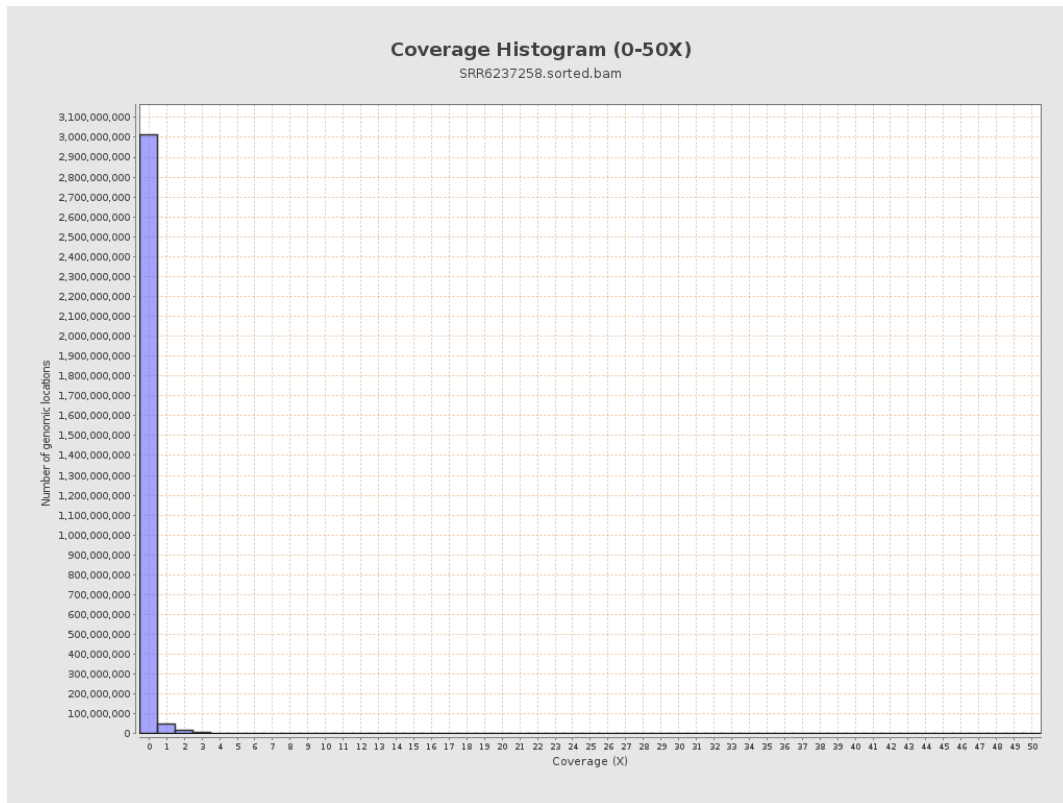
3. Results : Coverage across reference



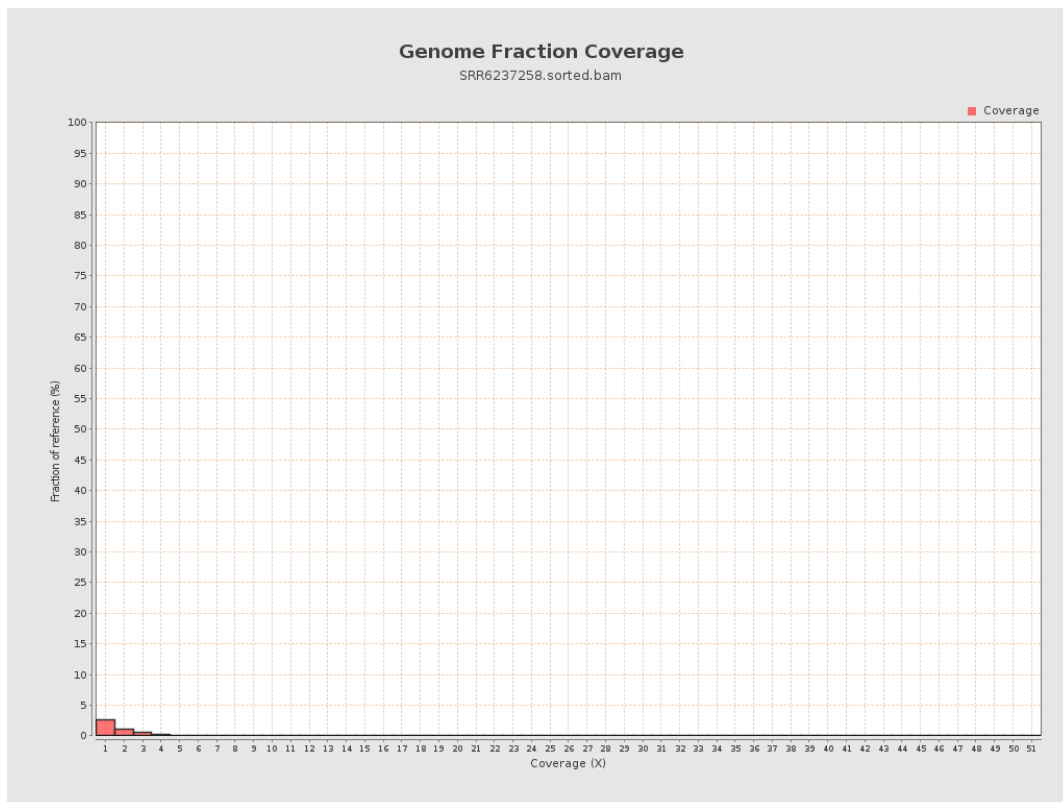
4. Results : Coverage Histogram



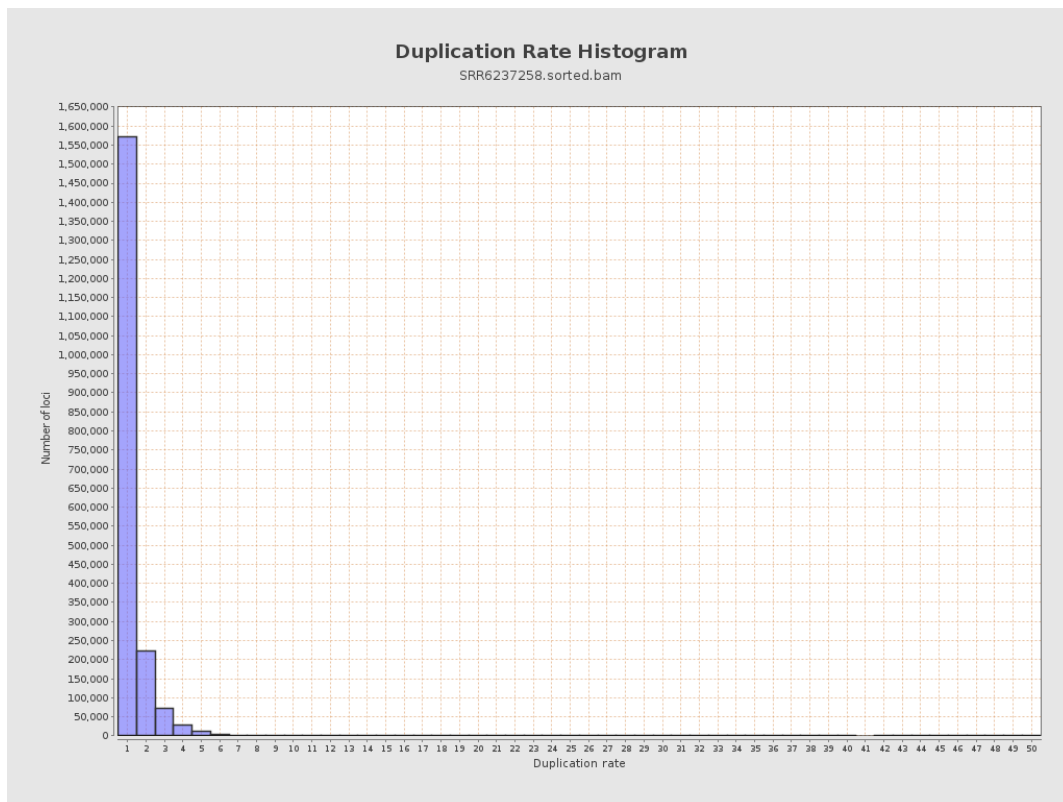
5. Results : Coverage Histogram (0-50X)



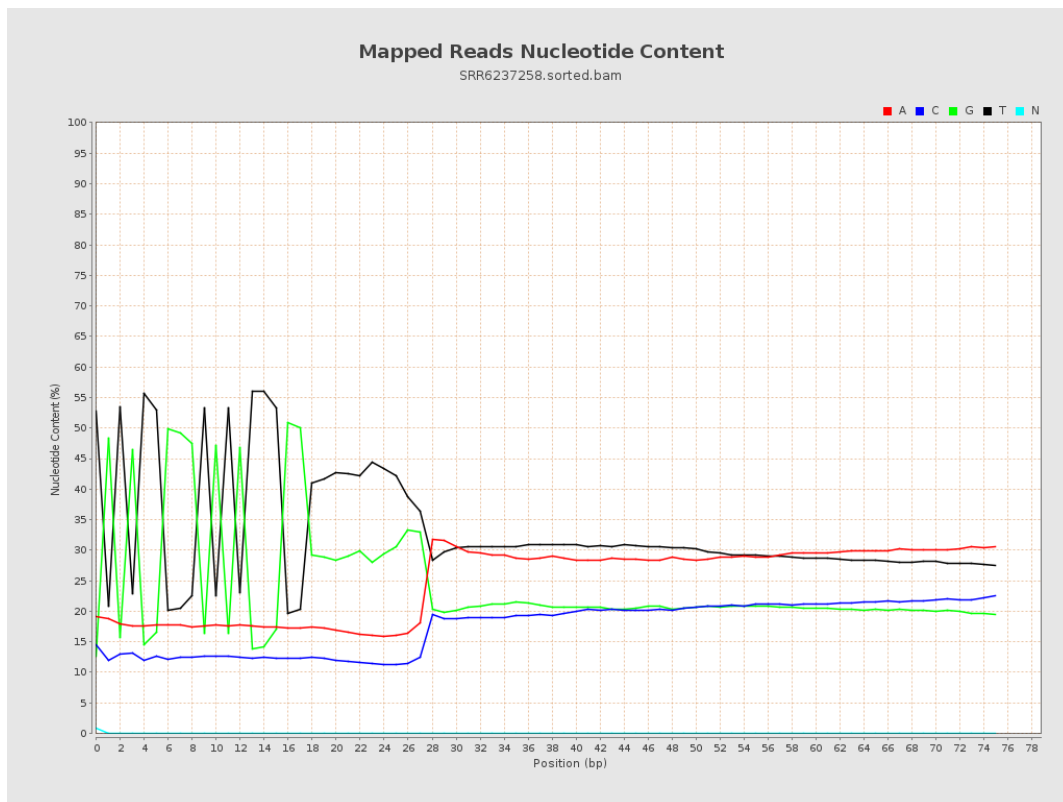
6. Results : Genome Fraction Coverage



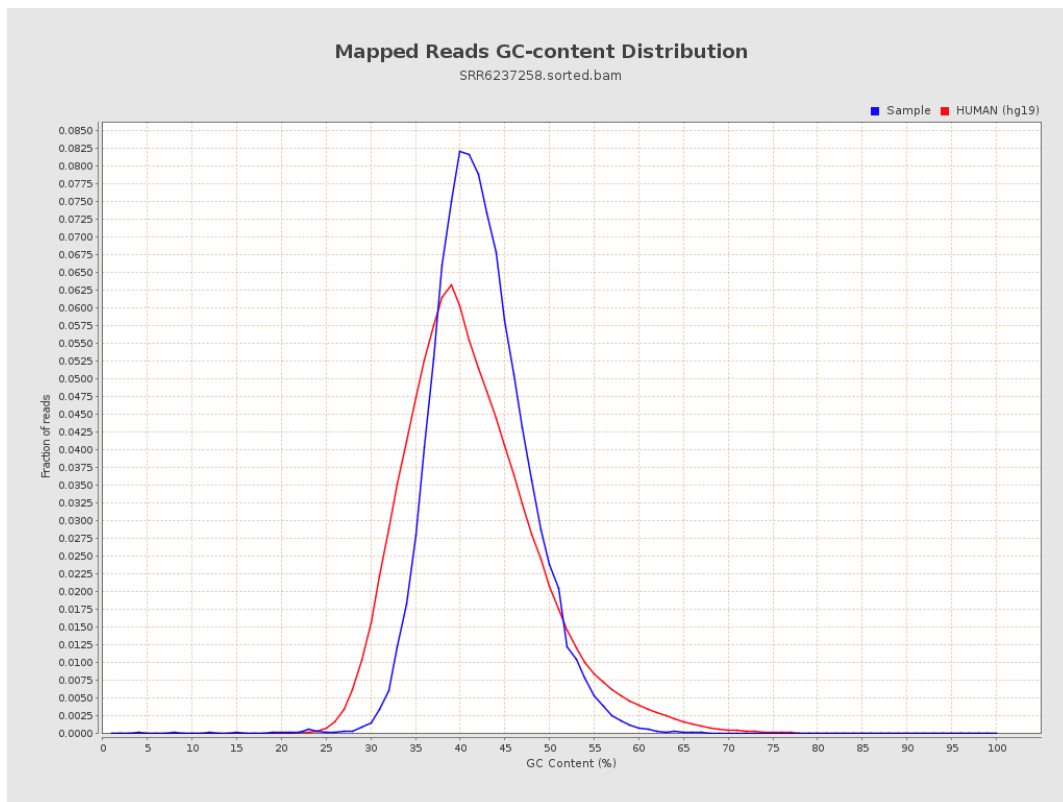
7. Results : Duplication Rate Histogram



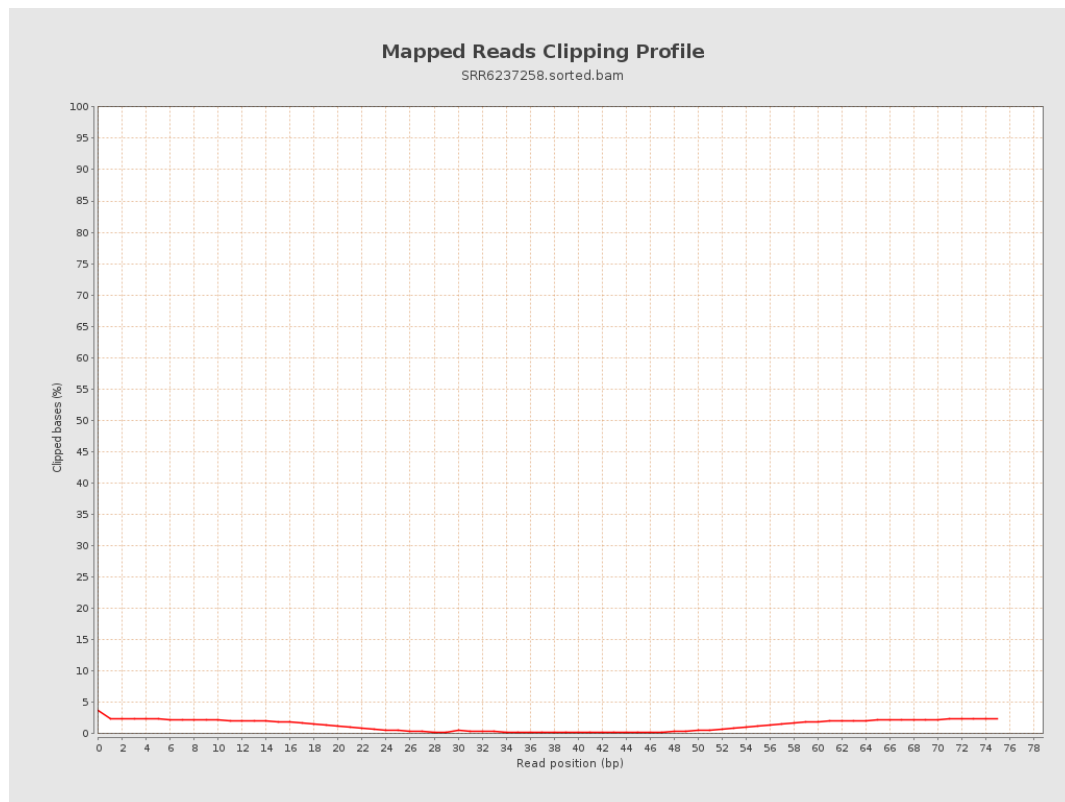
8. Results : Mapped Reads Nucleotide Content



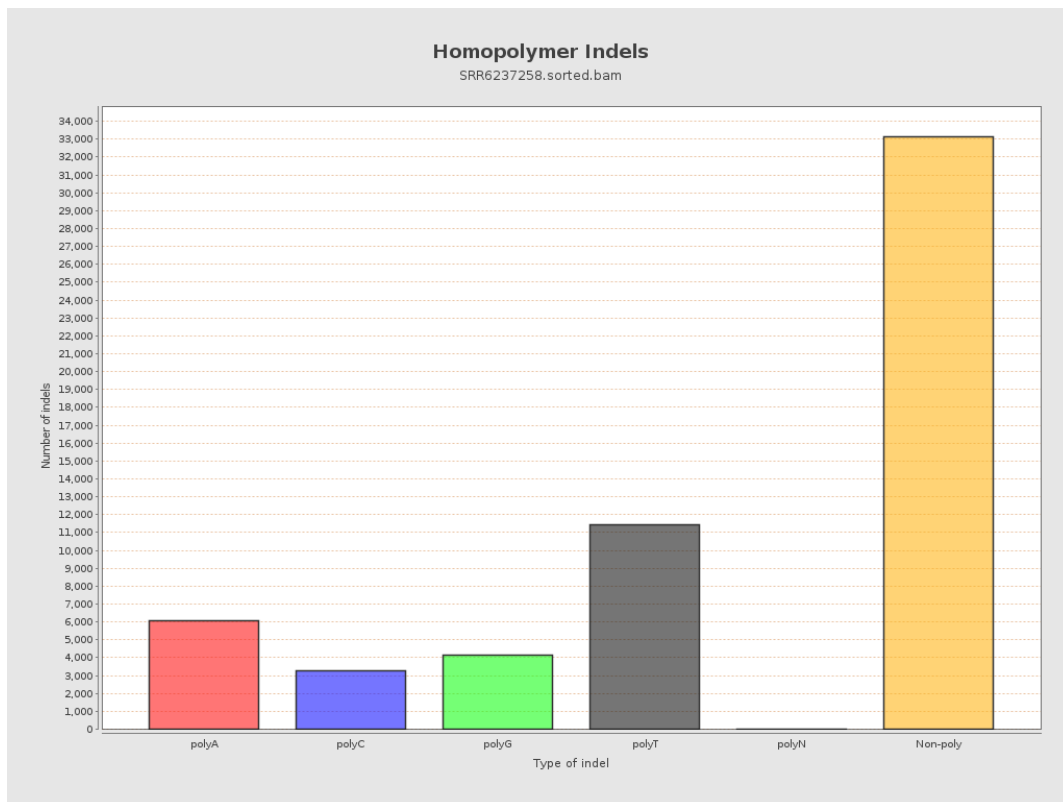
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

