

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:33:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237253.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_SRR6237253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:33:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,137,148
Mapped reads	2,816,851 / 89.79%
Unmapped reads	320,297 / 10.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,195 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	957,284 / 30.51%
Duplication rate	22.27%
Clipped reads	1,886,347 / 60.13%

2.2. ACGT Content

Number/percentage of A's	44,153,792 / 25.66%
Number/percentage of C's	29,570,801 / 17.18%
Number/percentage of T's	57,882,633 / 33.63%
Number/percentage of G's	40,473,711 / 23.52%
Number/percentage of N's	18,389 / 0.01%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.8608
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2.4. Mapping Quality

Mean Mapping Quality	39.45
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2.5. Mismatches and indels

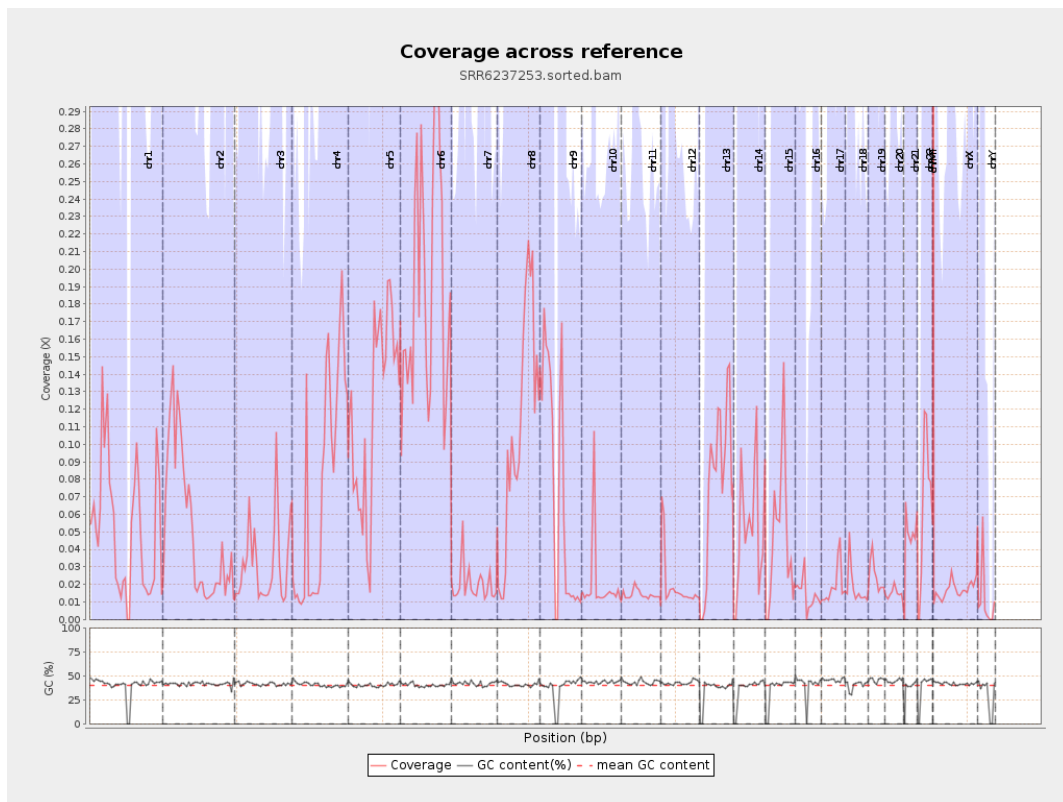
General error rate	0.66%
Mismatches	1,090,428
Insertions	15,002
Mapped reads with at least one insertion	0.53%
Deletions	52,899
Mapped reads with at least one deletion	1.85%
Homopolymer indels	41.31%

2.6. Chromosome stats

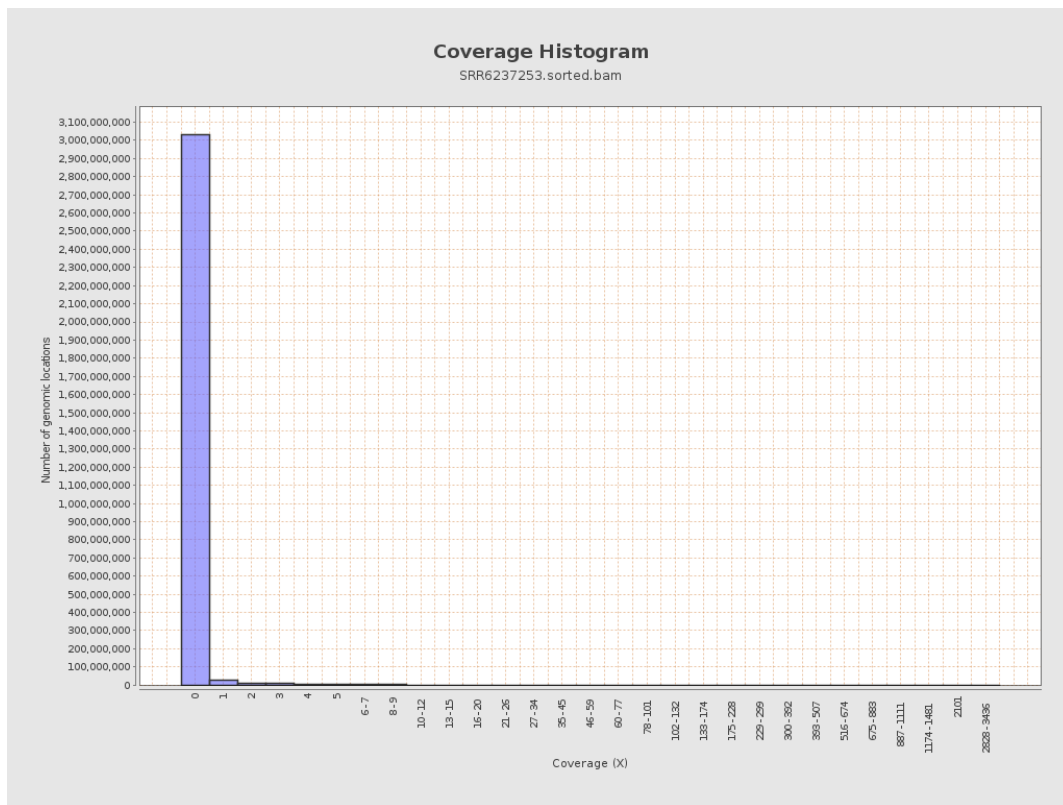
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12600884	0.0506	0.5257
chr2	243199373	12374217	0.0509	1.7711
chr3	198022430	6133946	0.031	0.3839
chr4	191154276	14461324	0.0757	0.8986
chr5	180915260	22128407	0.1223	0.7693
chr6	171115067	32800782	0.1917	1.21
chr7	159138663	3121672	0.0196	0.38

chr8	146364022	16030170	0.1095	0.796
chr9	141213431	10251010	0.0726	0.7264
chr10	135534747	2610644	0.0193	1.0417
chr11	135006516	1905688	0.0141	0.298
chr12	133851895	2624551	0.0196	0.3618
chr13	115169878	9012391	0.0783	0.6663
chr14	107349540	5466016	0.0509	0.5208
chr15	102531392	4872690	0.0475	0.5027
chr16	90354753	1252389	0.0139	0.4108
chr17	81195210	1597325	0.0197	0.339
chr18	78077248	1443239	0.0185	2.0255
chr19	59128983	1473649	0.0249	0.4014
chr20	63025520	937681	0.0149	0.331
chr21	48129895	2284833	0.0475	0.6775
chr22	51304566	3371405	0.0657	0.5583
chrMT	16571	31257	1.8862	3.0152
chrX	155270560	2717062	0.0175	0.3053
chrY	59373566	690375	0.0116	0.6787

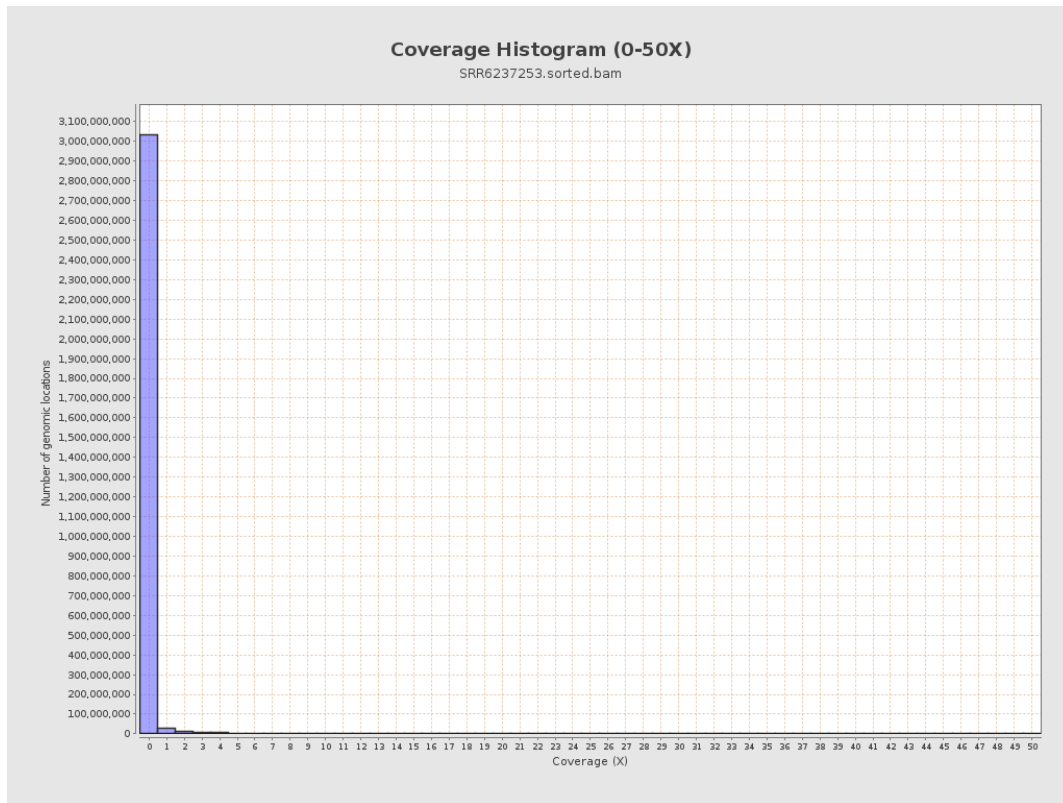
3. Results : Coverage across reference



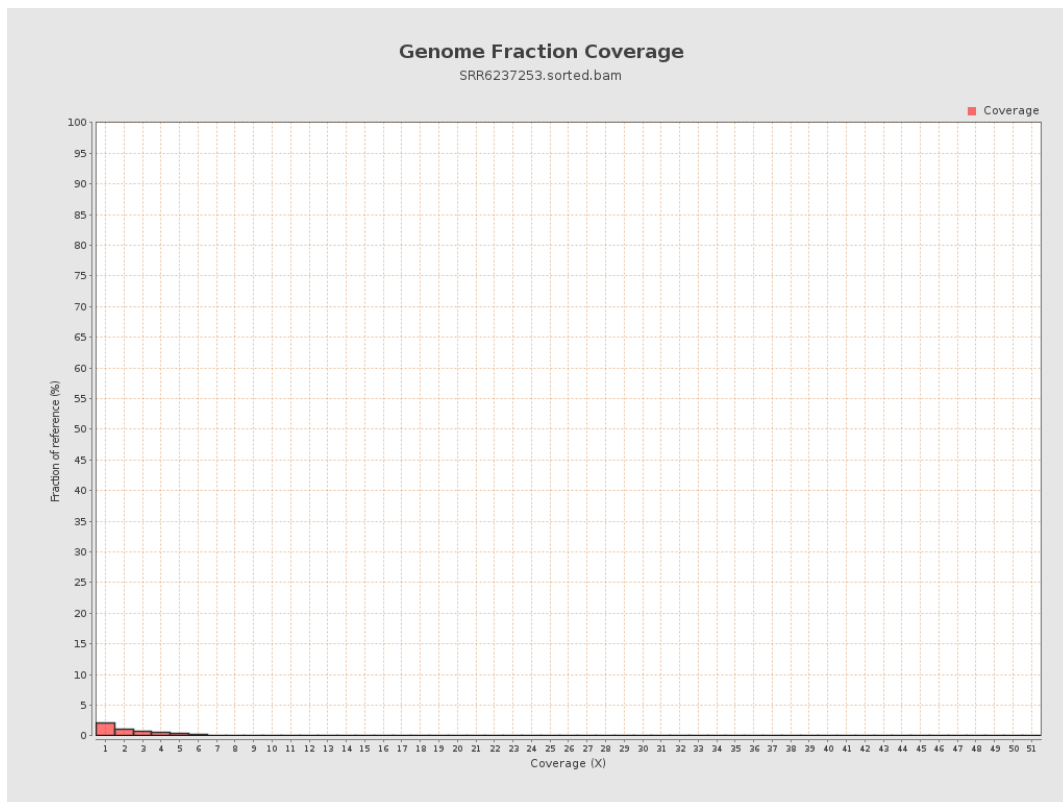
4. Results : Coverage Histogram



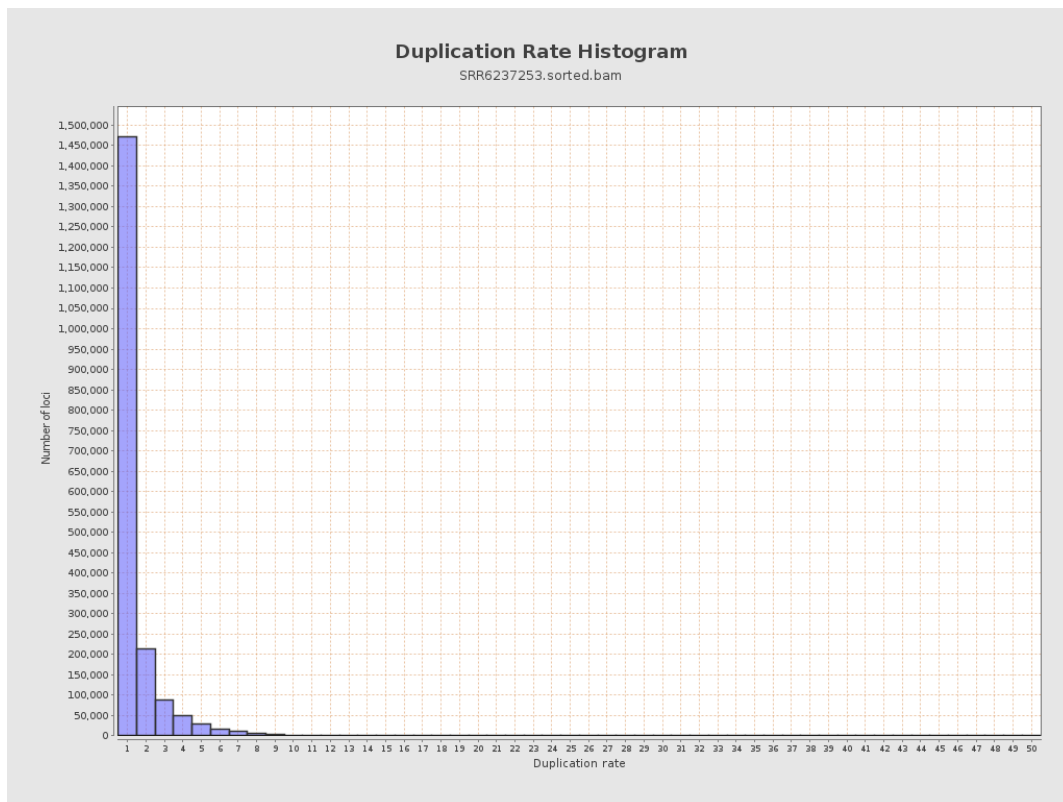
5. Results : Coverage Histogram (0-50X)



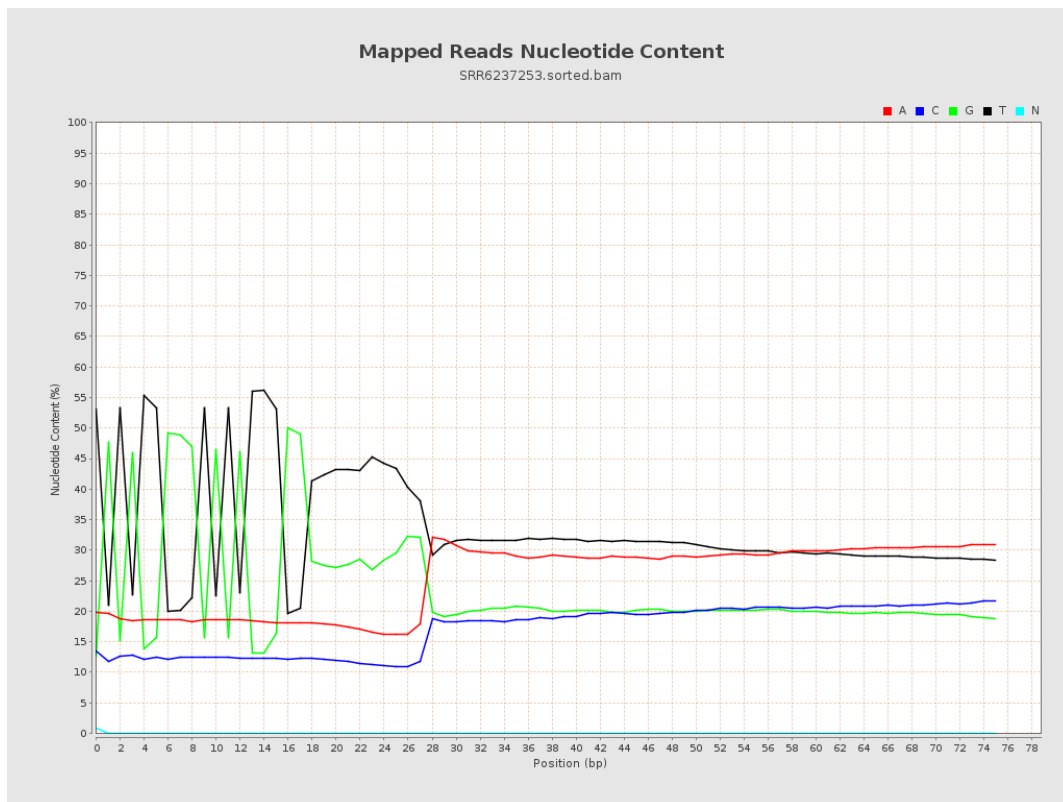
6. Results : Genome Fraction Coverage



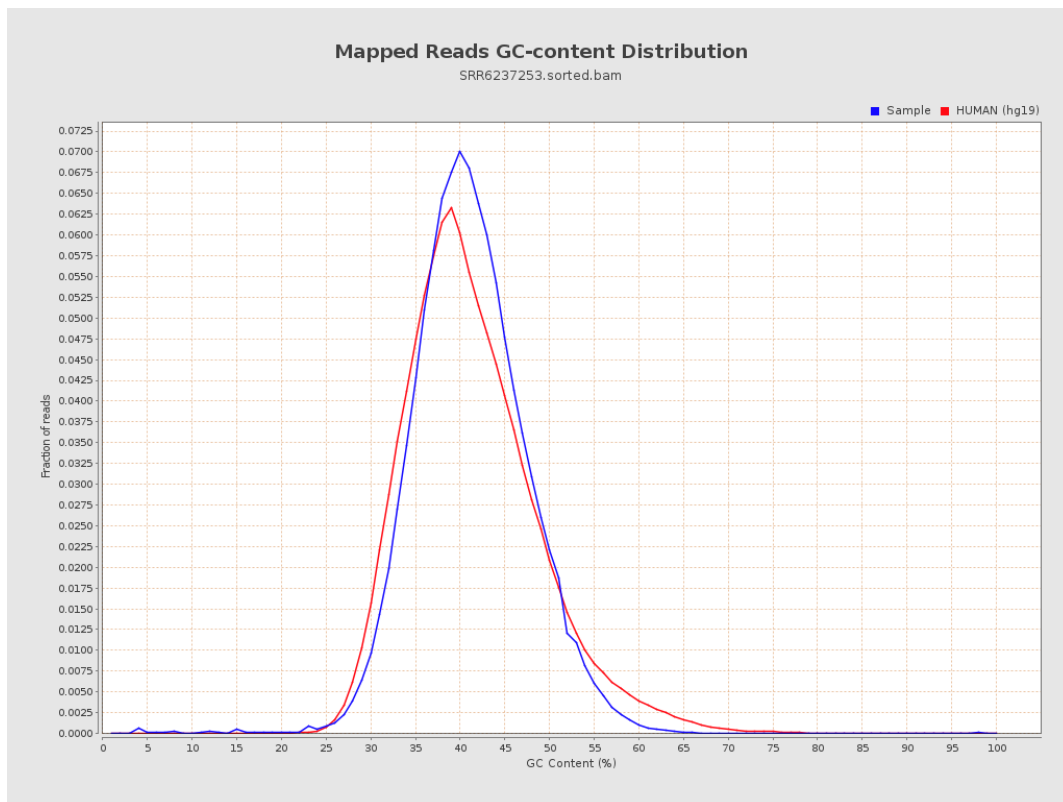
7. Results : Duplication Rate Histogram



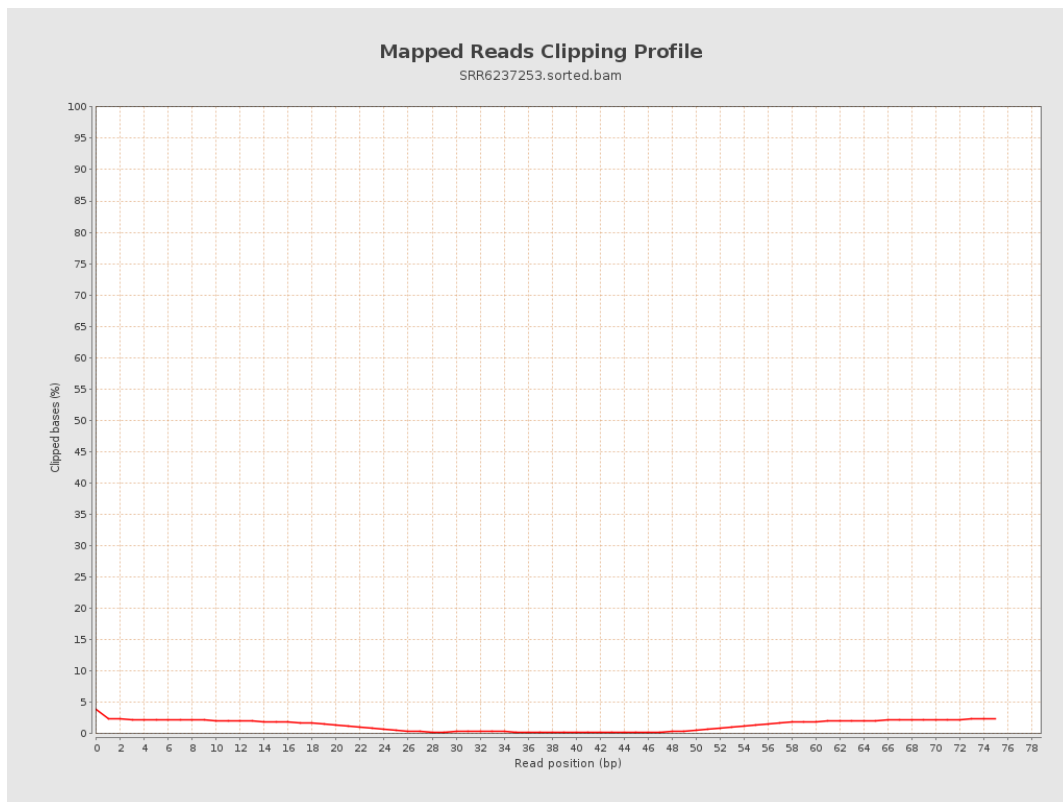
8. Results : Mapped Reads Nucleotide Content



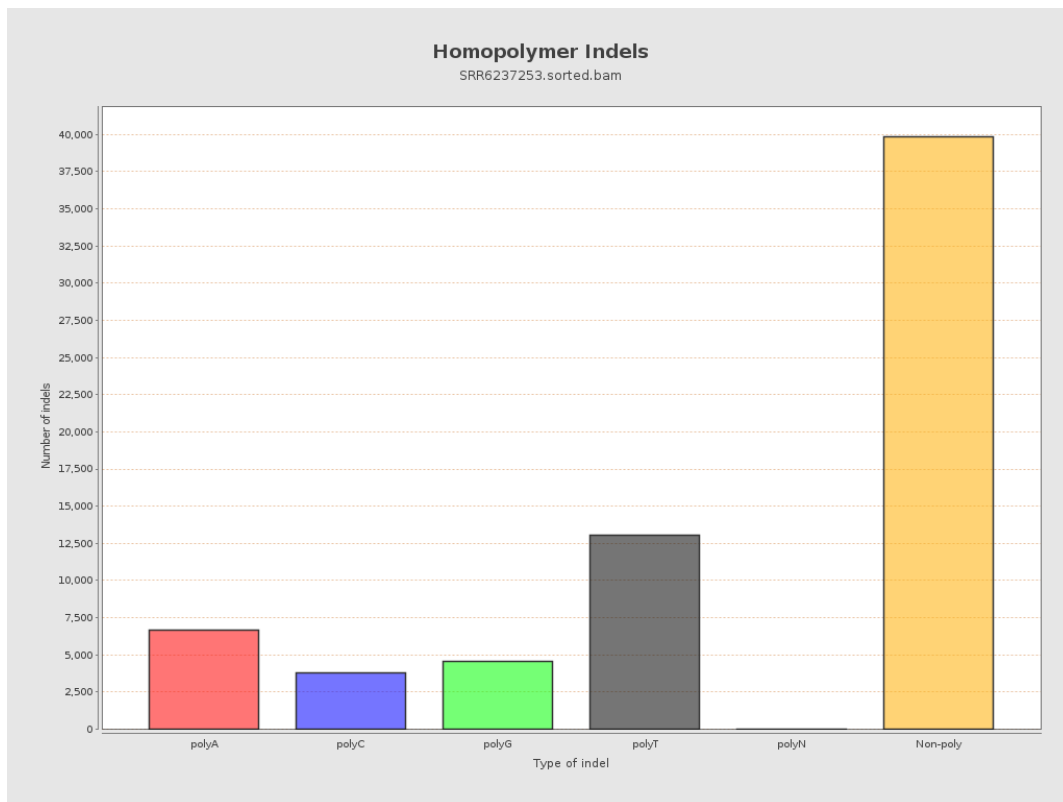
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

