

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237243.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_SRR6237243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:01:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,805,844
Mapped reads	2,508,911 / 89.42%
Unmapped reads	296,933 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,632 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	126,128 / 4.5%
Duplication rate	3.75%
Clipped reads	1,085,095 / 38.67%

2.2. ACGT Content

Number/percentage of A's	46,679,029 / 27.71%
Number/percentage of C's	30,667,913 / 18.21%
Number/percentage of T's	53,759,085 / 31.92%
Number/percentage of G's	37,325,863 / 22.16%
Number/percentage of N's	2,672 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.4841
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.11
----------------------	-------

2.5. Mismatches and indels

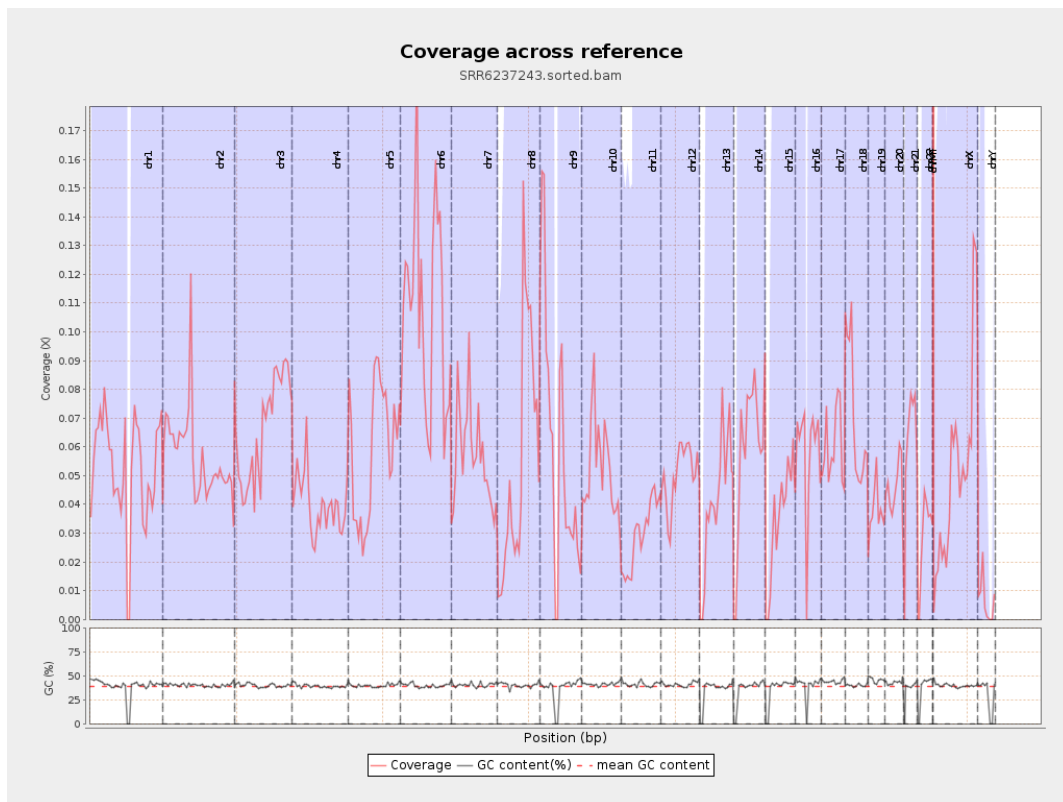
General error rate	0.81%
Mismatches	1,335,865
Insertions	13,614
Mapped reads with at least one insertion	0.54%
Deletions	41,732
Mapped reads with at least one deletion	1.65%
Homopolymer indels	46.99%

2.6. Chromosome stats

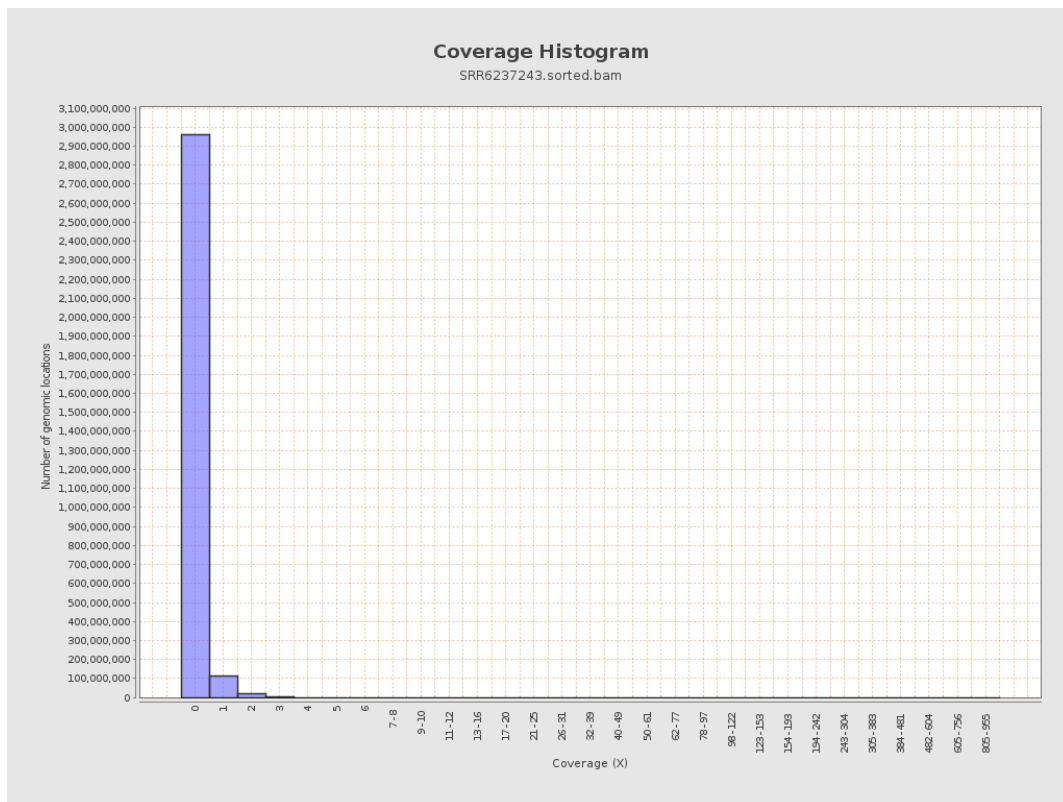
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13051669	0.0524	0.6713
chr2	243199373	13813056	0.0568	0.6476
chr3	198022430	13103951	0.0662	0.3009
chr4	191154276	7688162	0.0402	0.2949
chr5	180915260	10749071	0.0594	0.2896
chr6	171115067	18465458	0.1079	0.7497
chr7	159138663	9063907	0.057	0.5705

chr8	146364022	8133345	0.0556	0.685
chr9	141213431	8316201	0.0589	0.531
chr10	135534747	7037120	0.0519	0.4483
chr11	135006516	3987264	0.0295	0.3166
chr12	133851895	6771389	0.0506	0.2782
chr13	115169878	4780217	0.0415	0.2403
chr14	107349540	6319334	0.0589	0.3217
chr15	102531392	3532205	0.0344	0.2386
chr16	90354753	5132031	0.0568	0.3171
chr17	81195210	4973385	0.0613	0.3675
chr18	78077248	5549321	0.0711	0.9105
chr19	59128983	2269307	0.0384	0.5163
chr20	63025520	2939745	0.0466	0.2686
chr21	48129895	2953855	0.0614	0.3378
chr22	51304566	1450262	0.0283	0.1929
chrMT	16571	44886	2.7087	2.5042
chrX	155270560	7975957	0.0514	0.3072
chrY	59373566	402439	0.0068	0.1773

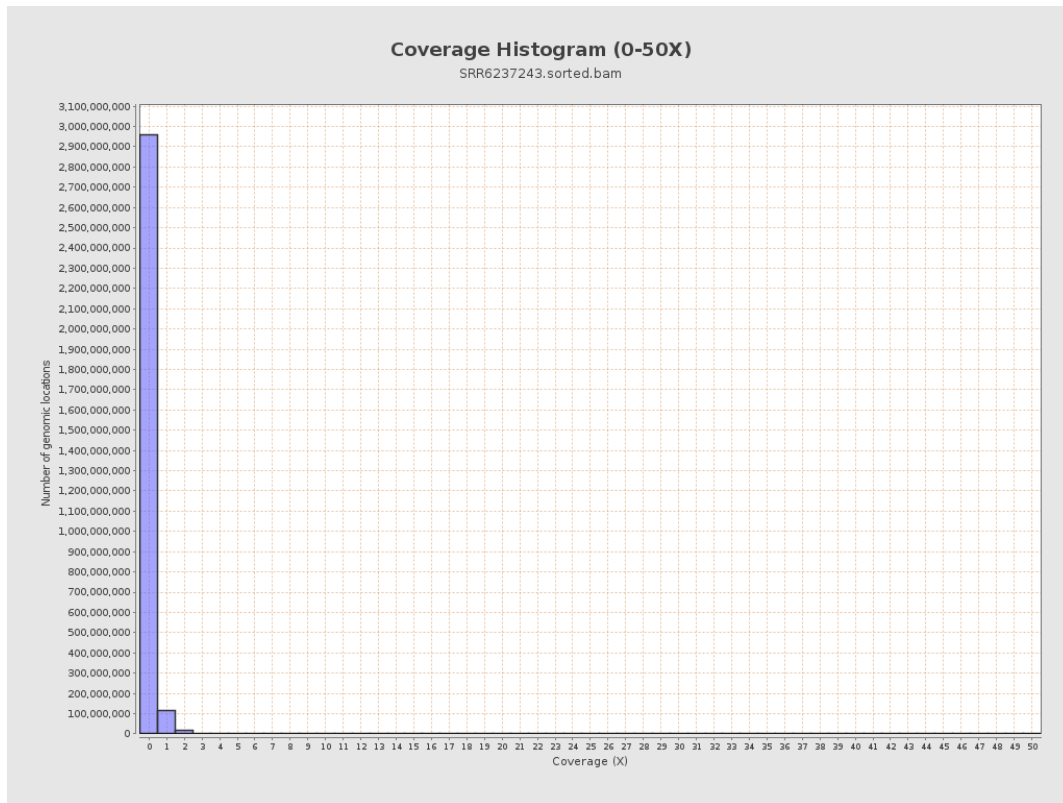
3. Results : Coverage across reference



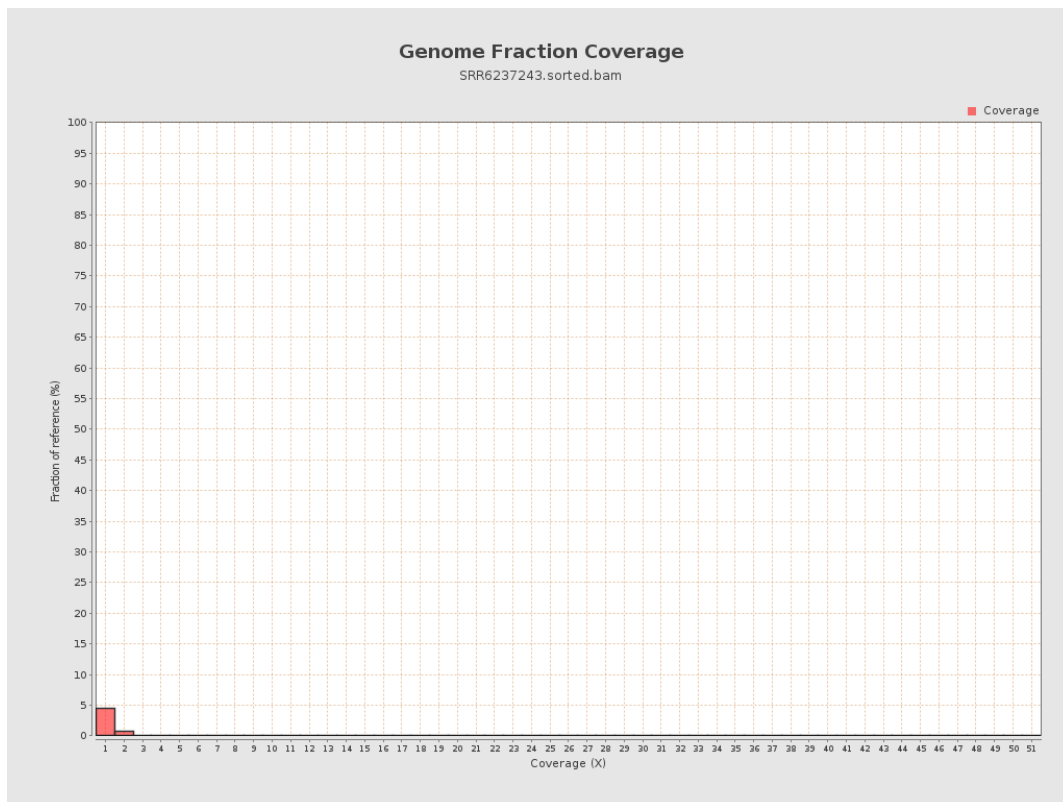
4. Results : Coverage Histogram



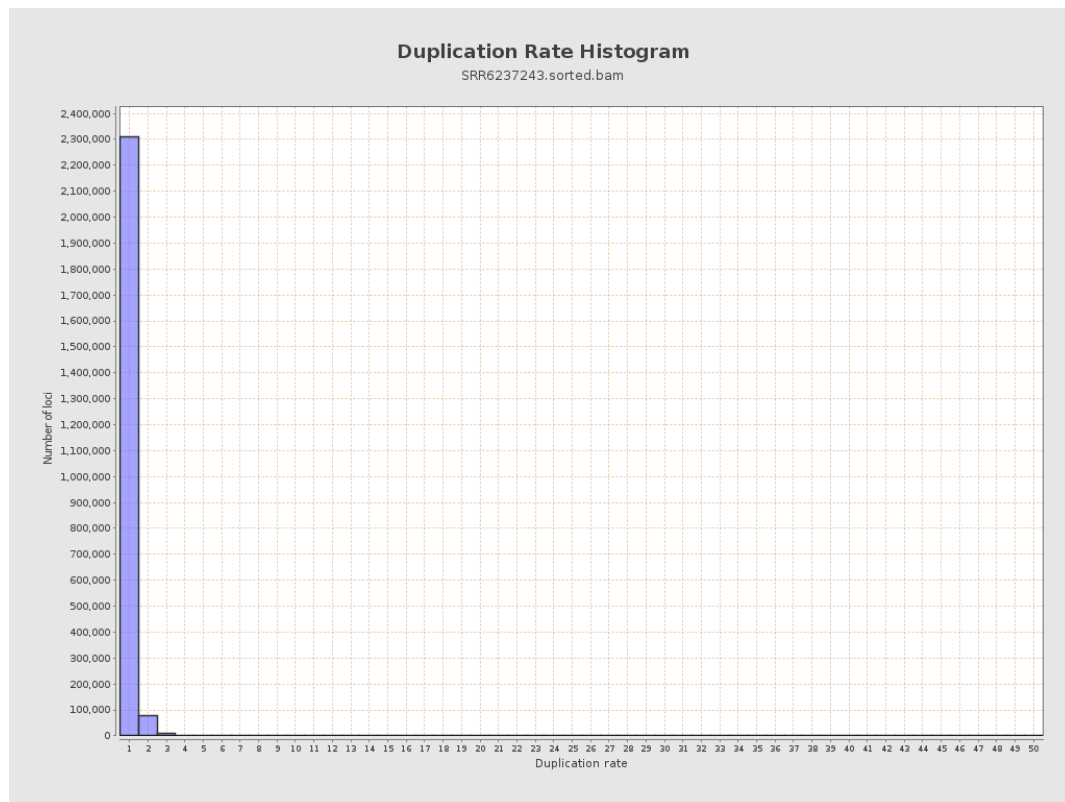
5. Results : Coverage Histogram (0-50X)



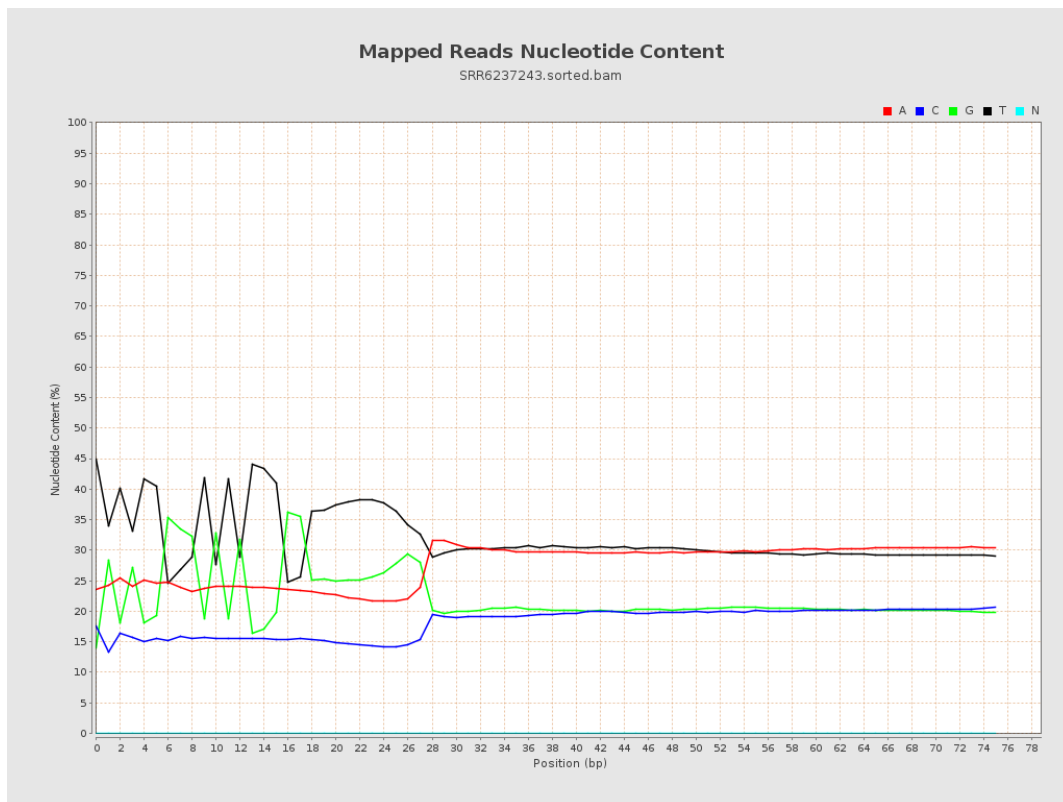
6. Results : Genome Fraction Coverage



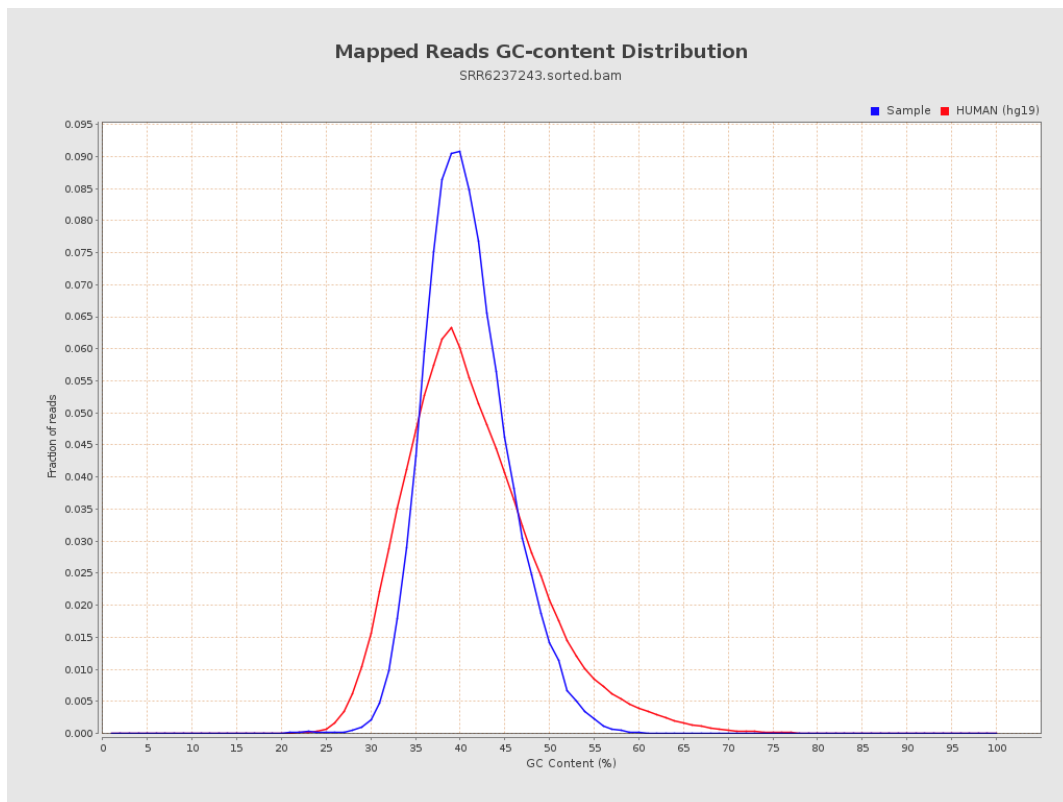
7. Results : Duplication Rate Histogram



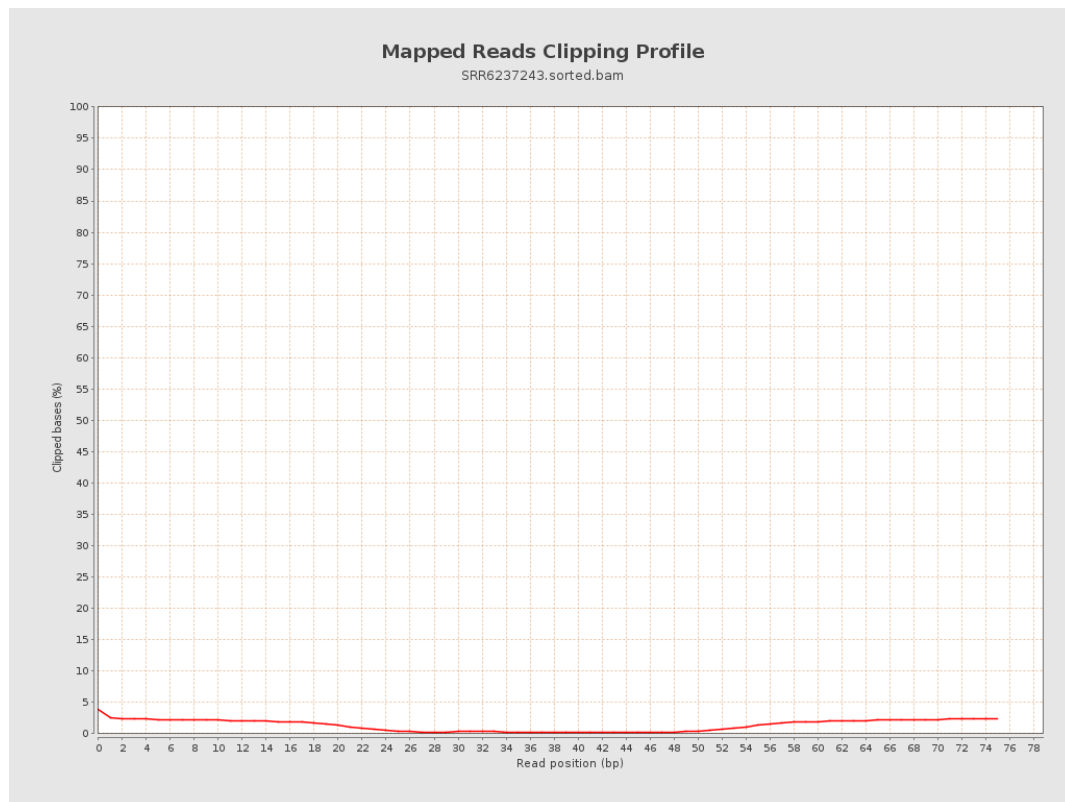
8. Results : Mapped Reads Nucleotide Content



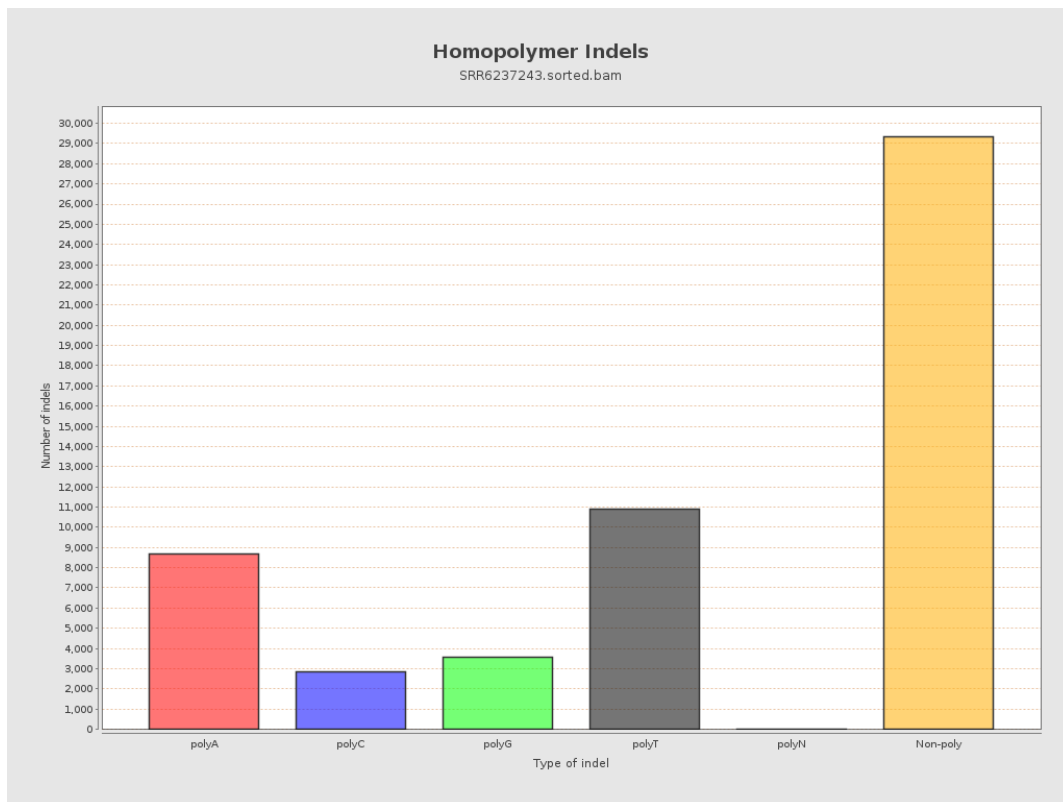
9. Results : Mapped Reads GC-content Distribution



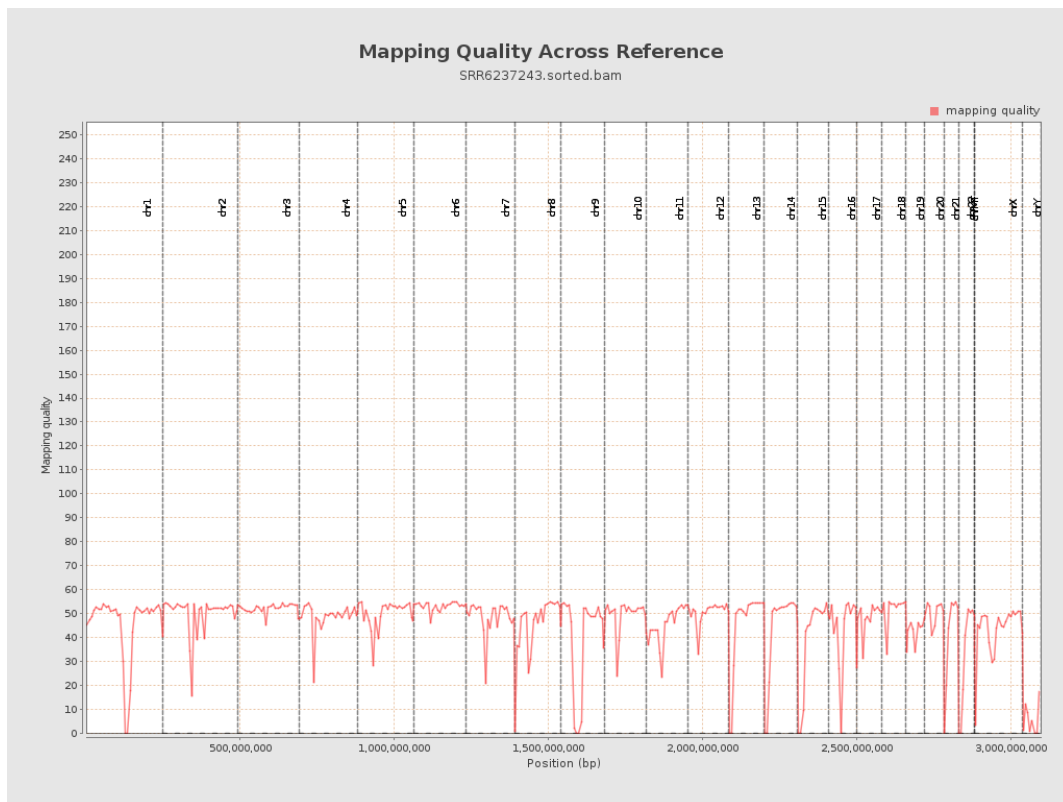
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

