

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:07:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237245.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_SRR6237245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:07:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,051,947
Mapped reads	2,846,671 / 93.27%
Unmapped reads	205,276 / 6.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,273 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	121,103 / 3.97%
Duplication rate	3.28%
Clipped reads	812,980 / 26.64%

2.2. ACGT Content

Number/percentage of A's	58,560,659 / 29.08%
Number/percentage of C's	38,924,315 / 19.33%
Number/percentage of T's	61,910,050 / 30.74%
Number/percentage of G's	41,976,461 / 20.84%
Number/percentage of N's	3,579 / 0%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0651

Standard Deviation	0.6889
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2.4. Mapping Quality

Mean Mapping Quality	44.47
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2.5. Mismatches and indels

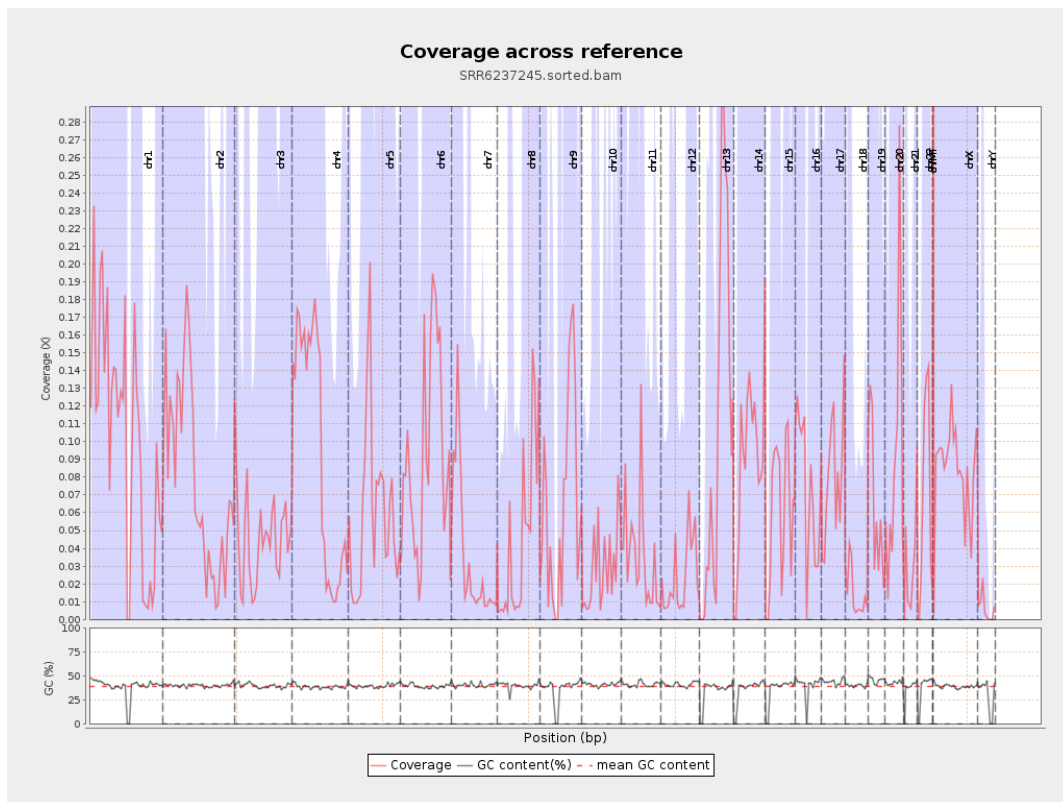
General error rate	0.76%
Mismatches	1,512,749
Insertions	15,600
Mapped reads with at least one insertion	0.54%
Deletions	52,346
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.32%

2.6. Chromosome stats

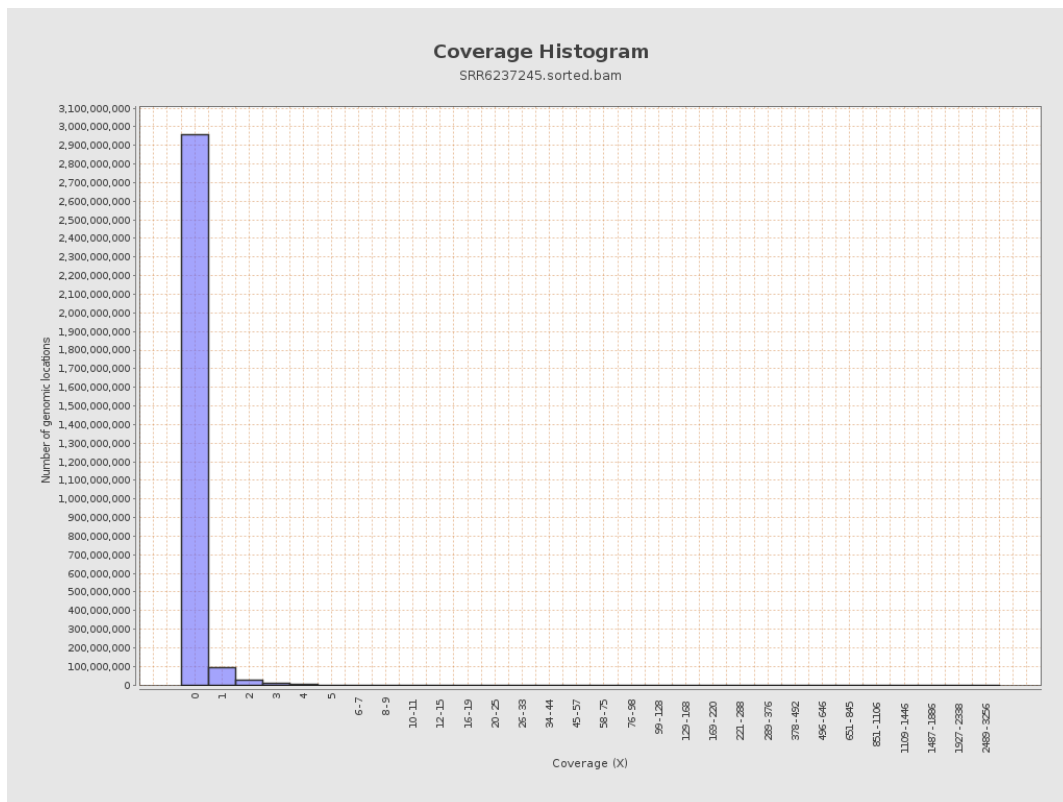
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24949558	0.1001	1.2348
chr2	243199373	18986489	0.0781	0.4944
chr3	198022430	9097575	0.0459	0.2905
chr4	191154276	18005535	0.0942	0.4325
chr5	180915260	10522382	0.0582	0.3304
chr6	171115067	15826951	0.0925	0.4216
chr7	159138663	5531074	0.0348	0.2743

chr8	146364022	6816325	0.0466	2.0241
chr9	141213431	9348321	0.0662	0.4826
chr10	135534747	3870758	0.0286	0.3637
chr11	135006516	4876265	0.0361	0.3001
chr12	133851895	3311643	0.0247	0.228
chr13	115169878	12237863	0.1063	0.4626
chr14	107349540	9406865	0.0876	0.4161
chr15	102531392	6026801	0.0588	0.3237
chr16	90354753	6609504	0.0732	0.3811
chr17	81195210	6283488	0.0774	0.4892
chr18	78077248	1173828	0.015	0.6897
chr19	59128983	3747102	0.0634	0.9932
chr20	63025520	6049426	0.096	0.443
chr21	48129895	1536280	0.0319	0.2555
chr22	51304566	3589615	0.07	0.3556
chrMT	16571	296010	17.8631	10.7582
chrX	155270560	12976571	0.0836	0.4443
chrY	59373566	386518	0.0065	0.1653

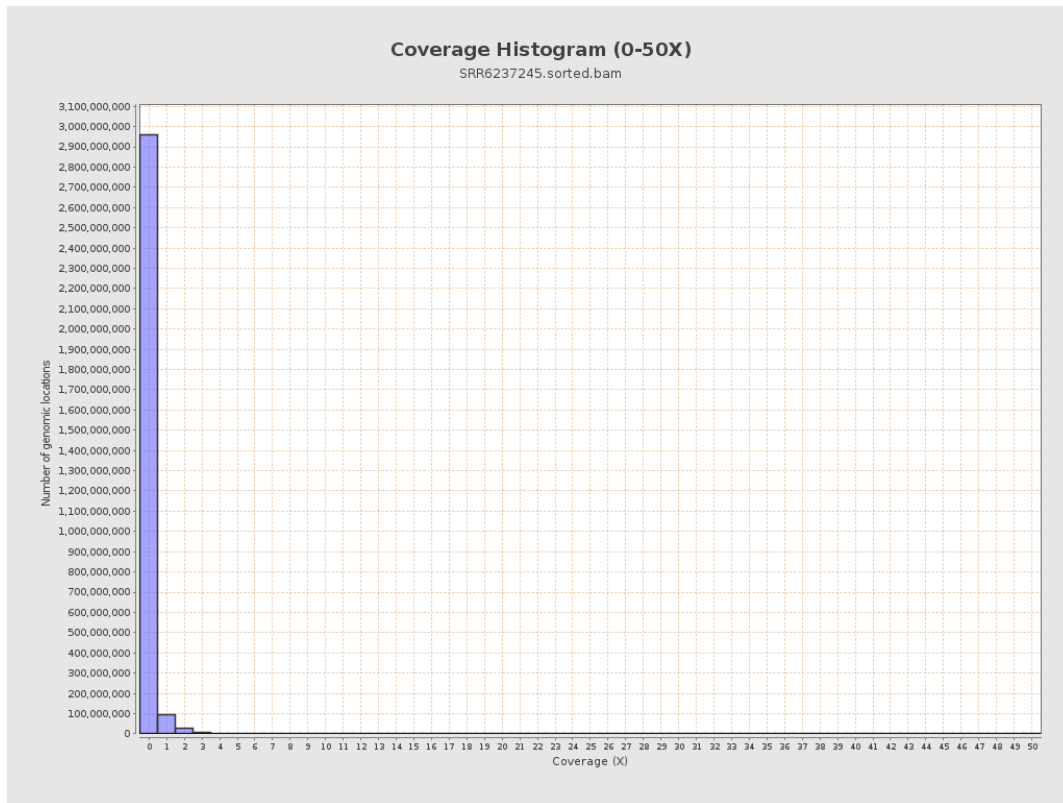
3. Results : Coverage across reference



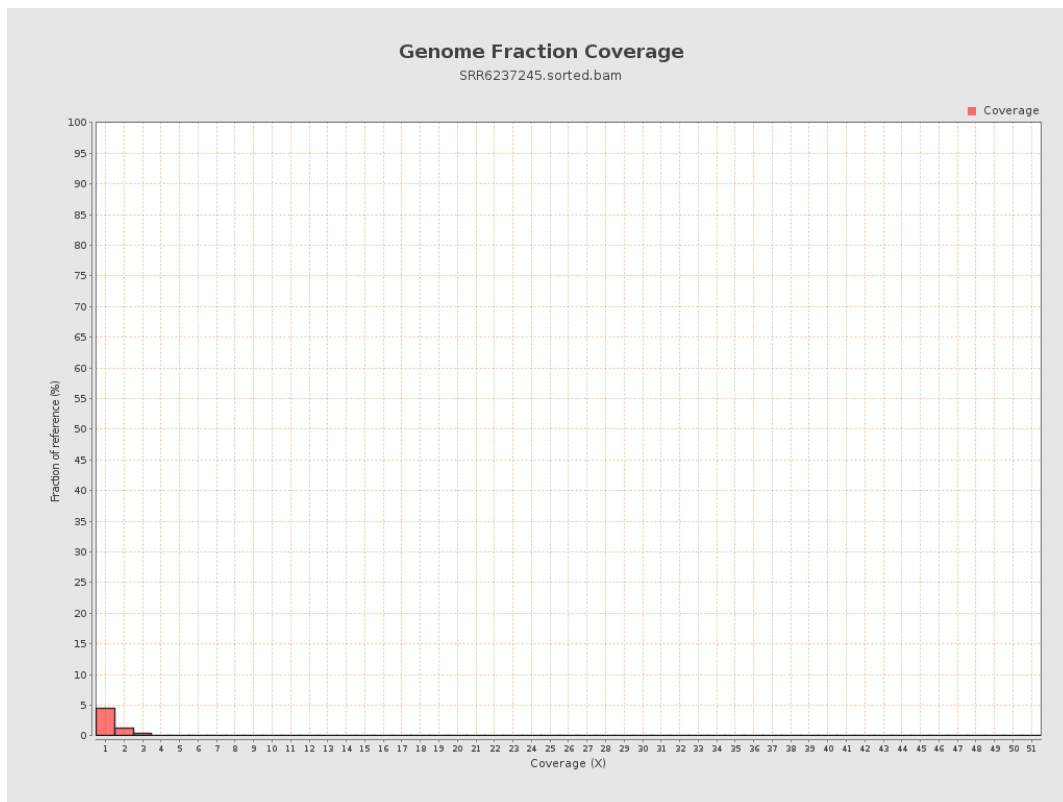
4. Results : Coverage Histogram



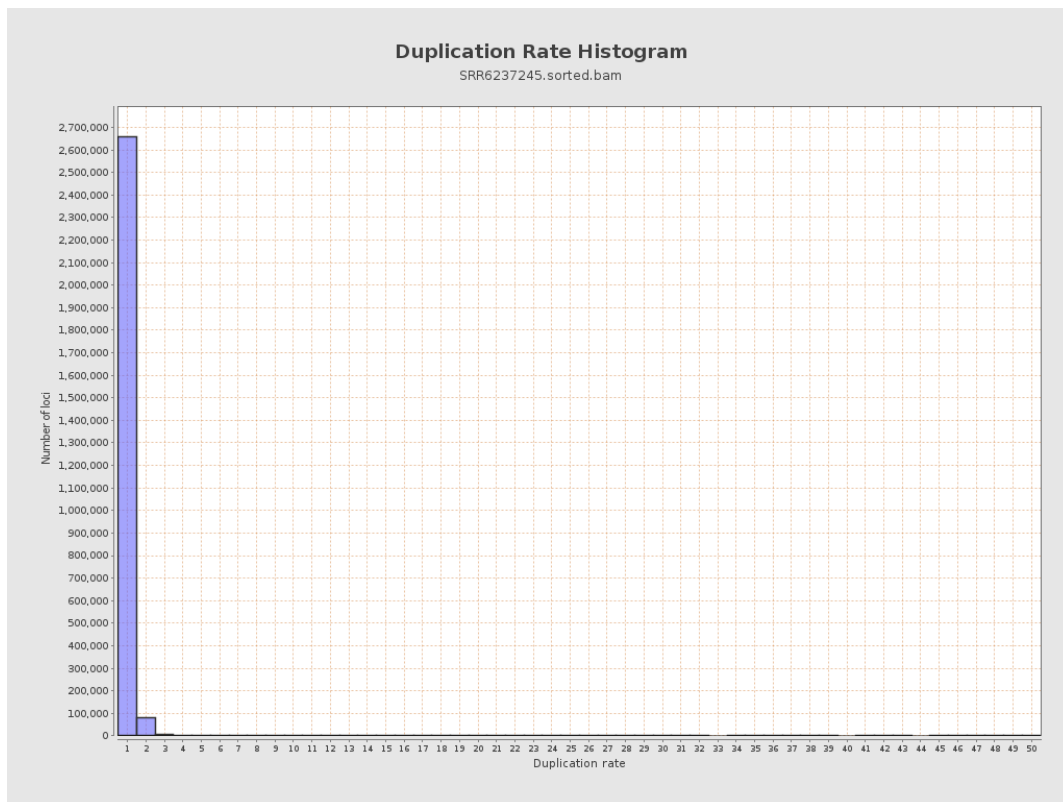
5. Results : Coverage Histogram (0-50X)



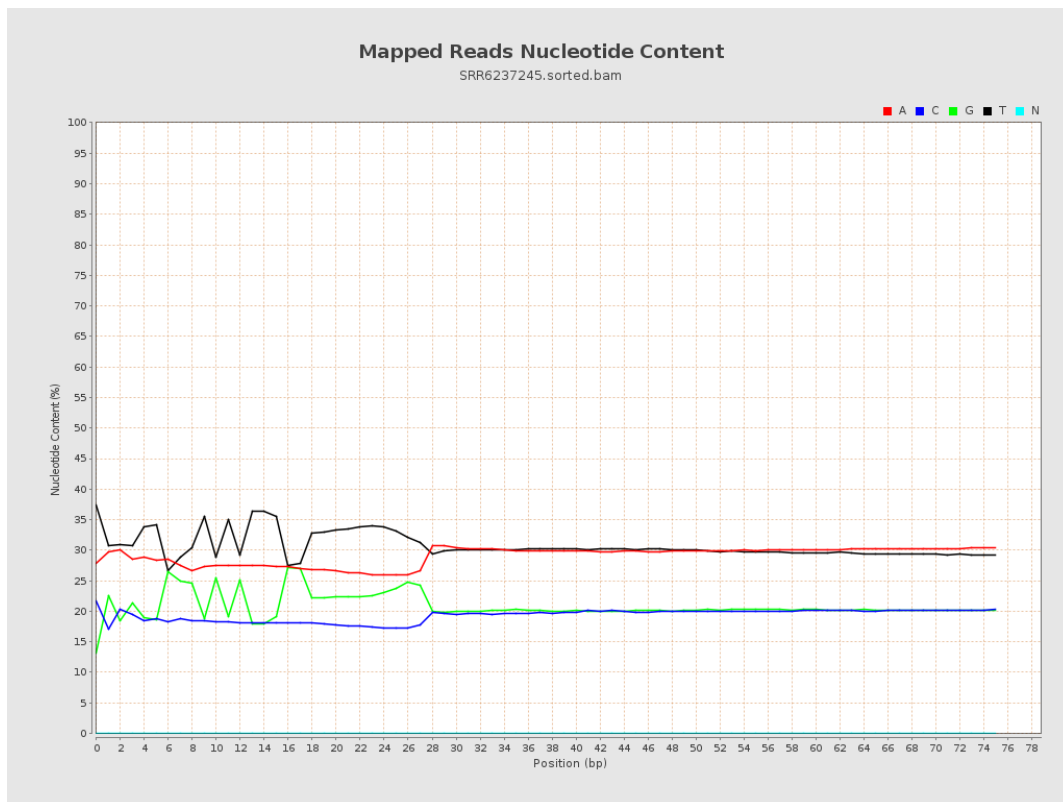
6. Results : Genome Fraction Coverage



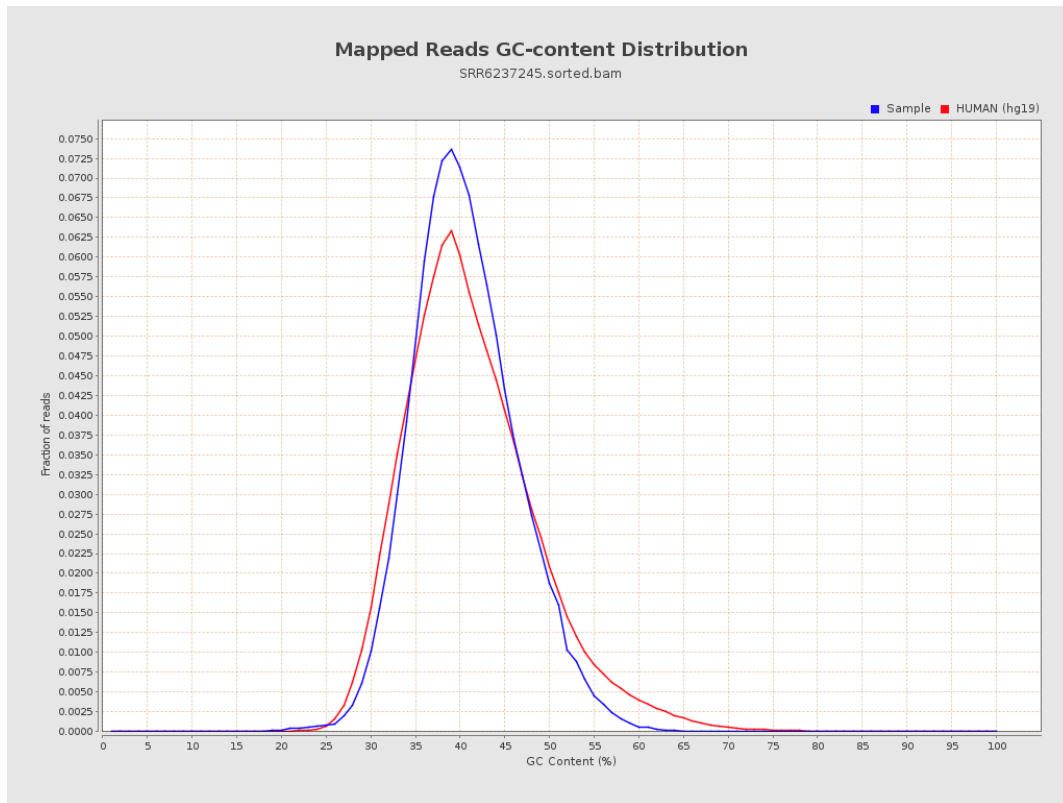
7. Results : Duplication Rate Histogram



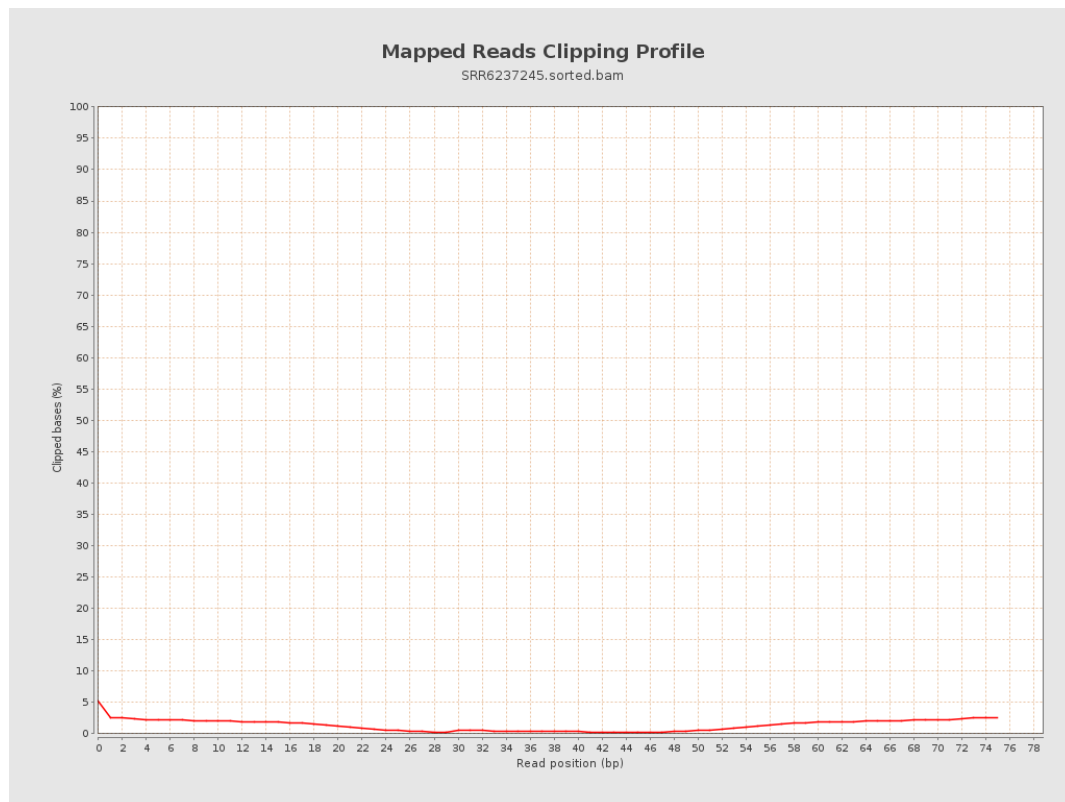
8. Results : Mapped Reads Nucleotide Content



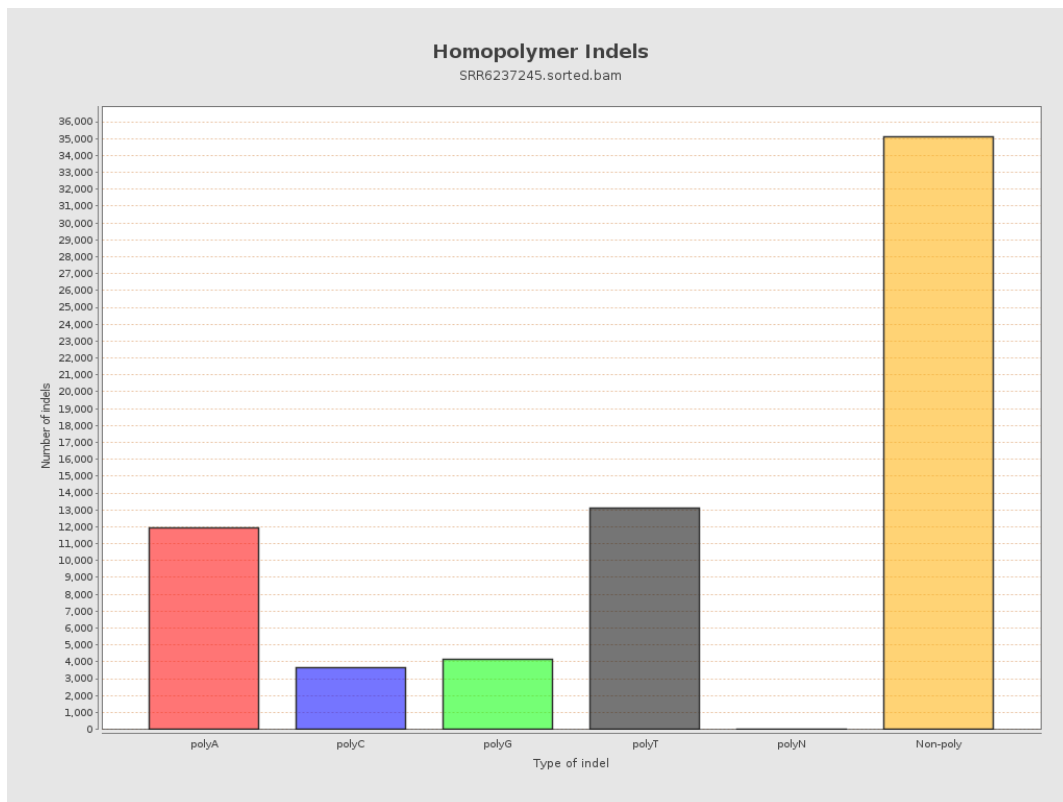
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

