

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:18:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237336.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_SRR6237336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:18:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,098,336
Mapped reads	2,791,099 / 90.08%
Unmapped reads	307,237 / 9.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,992 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	812,157 / 26.21%
Duplication rate	22.22%
Clipped reads	2,014,894 / 65.03%

2.2. ACGT Content

Number/percentage of A's	42,008,171 / 25.25%
Number/percentage of C's	28,194,021 / 16.95%
Number/percentage of T's	56,286,591 / 33.83%
Number/percentage of G's	39,872,564 / 23.97%
Number/percentage of N's	16,460 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0538

Standard Deviation	0.7009
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2.4. Mapping Quality

Mean Mapping Quality	42.74
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2.5. Mismatches and indels

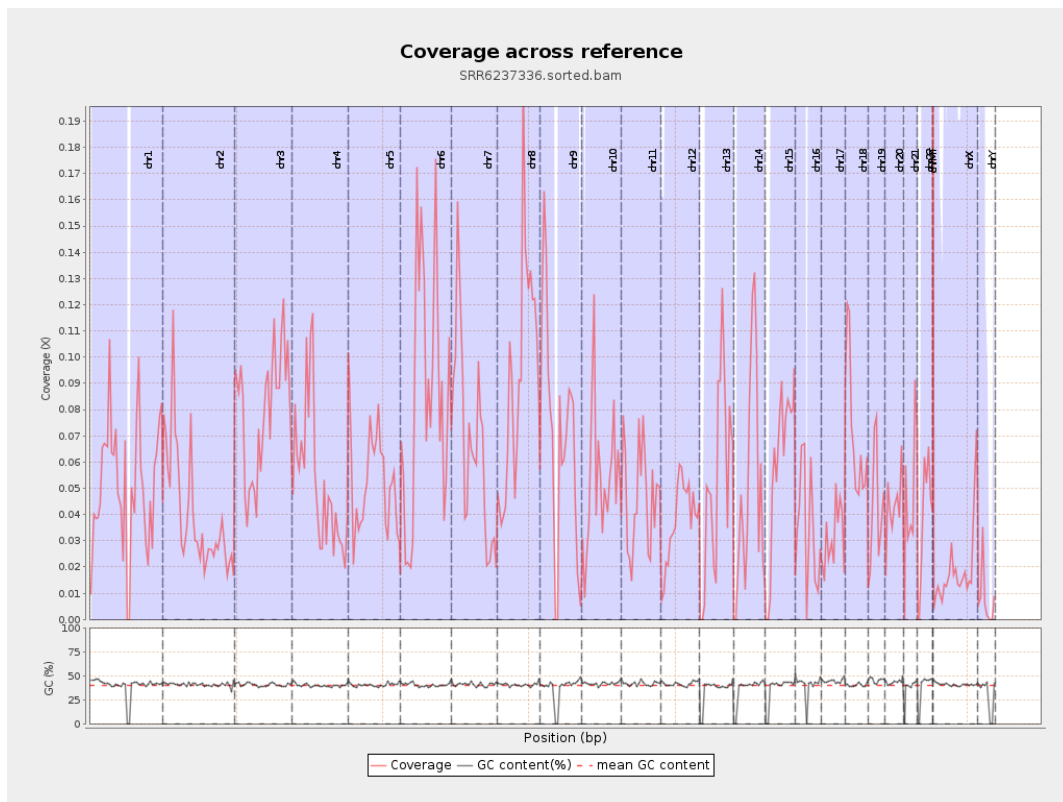
General error rate	0.66%
Mismatches	1,074,609
Insertions	11,562
Mapped reads with at least one insertion	0.41%
Deletions	55,525
Mapped reads with at least one deletion	1.97%
Homopolymer indels	41.23%

2.6. Chromosome stats

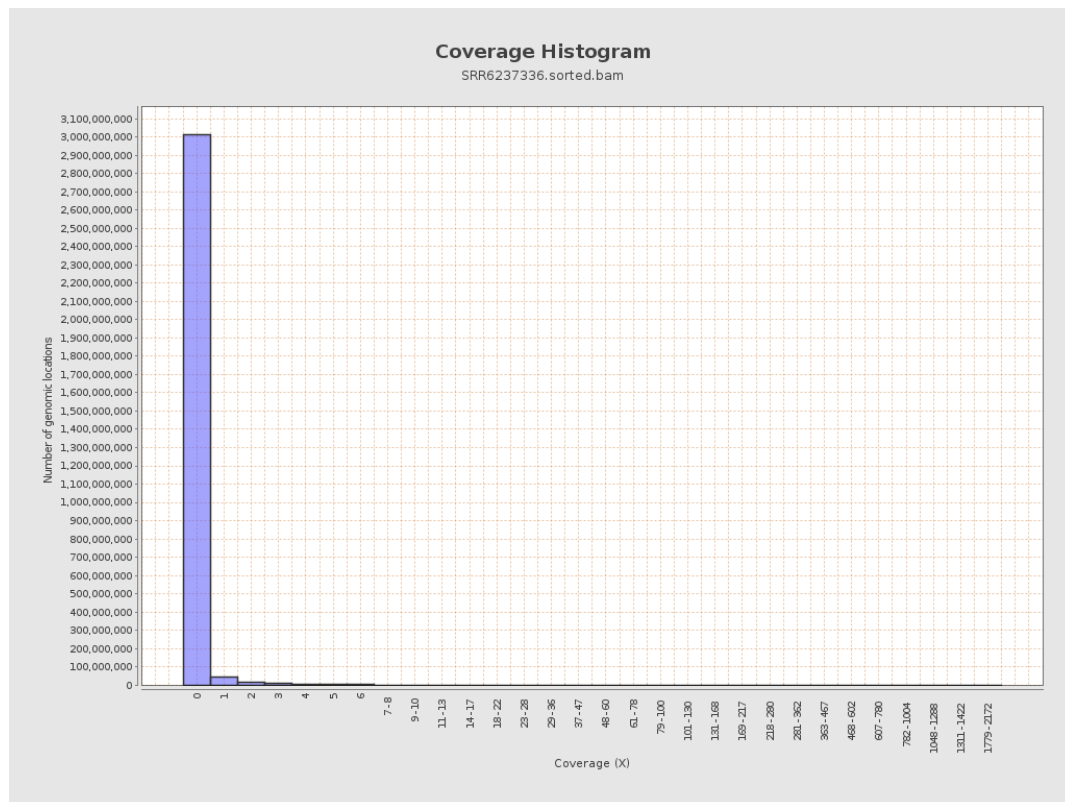
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12727561	0.0511	1.0515
chr2	243199373	9752030	0.0401	1.1642
chr3	198022430	15635583	0.079	0.5017
chr4	191154276	10121150	0.0529	0.5191
chr5	180915260	9406214	0.052	0.4093
chr6	171115067	14652701	0.0856	0.843
chr7	159138663	10588017	0.0665	0.5615

chr8	146364022	13630798	0.0931	0.9849
chr9	141213431	9874095	0.0699	0.6182
chr10	135534747	7121472	0.0525	0.7008
chr11	135006516	6221424	0.0461	0.4523
chr12	133851895	5074835	0.0379	0.3844
chr13	115169878	6033417	0.0524	0.4474
chr14	107349540	5439700	0.0507	0.4366
chr15	102531392	5904467	0.0576	0.4478
chr16	90354753	3116269	0.0345	0.3707
chr17	81195210	2576523	0.0317	0.3356
chr18	78077248	5552475	0.0711	1.3561
chr19	59128983	2566592	0.0434	0.686
chr20	63025520	2773299	0.044	0.3903
chr21	48129895	2285160	0.0475	0.4424
chr22	51304566	1989767	0.0388	0.3405
chrMT	16571	7541	0.4551	1.1005
chrX	155270560	2928792	0.0189	0.2902
chrY	59373566	494012	0.0083	0.3233

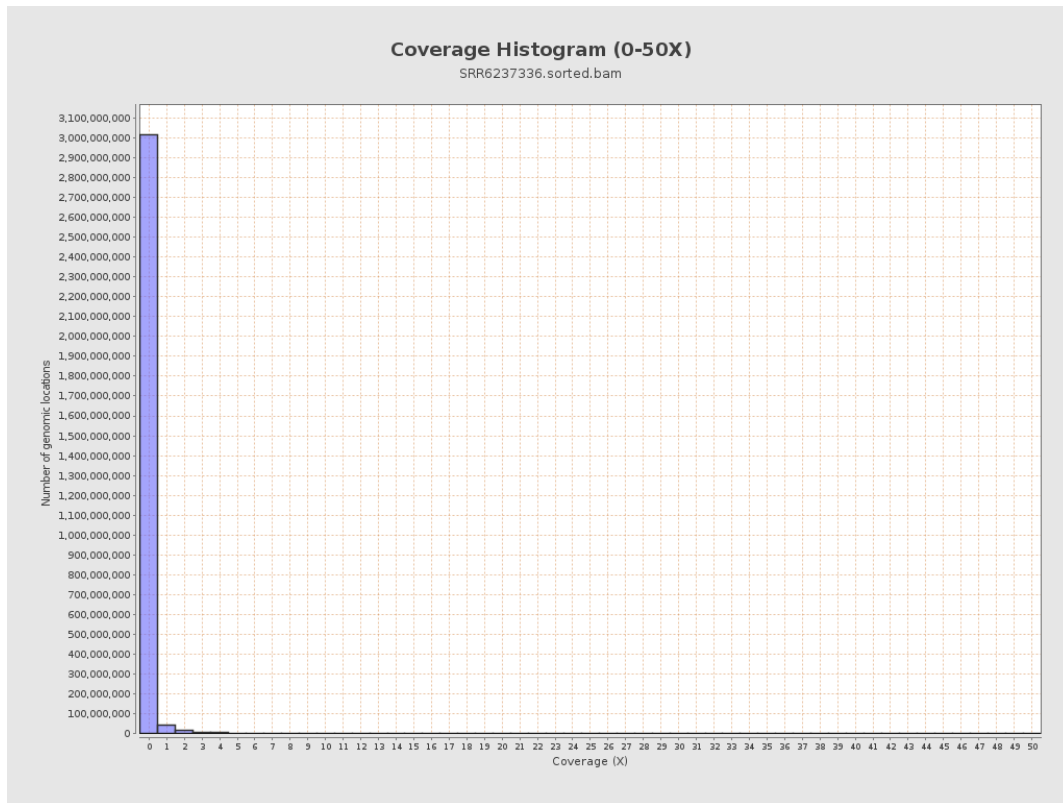
3. Results : Coverage across reference



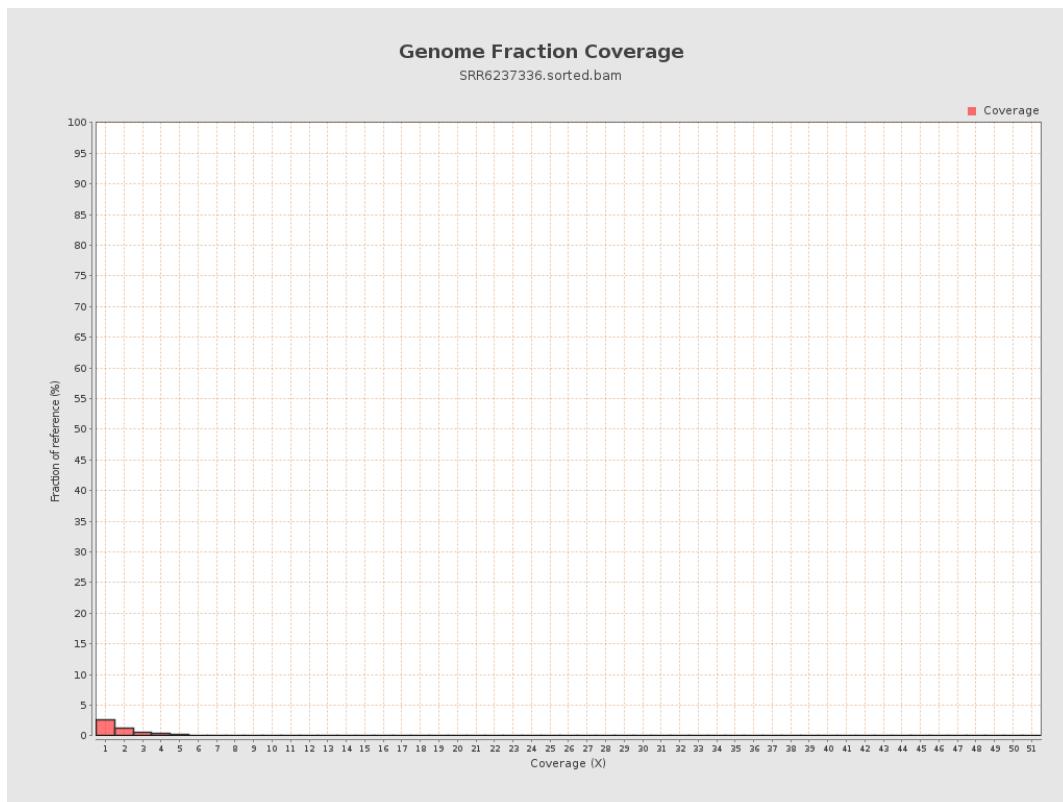
4. Results : Coverage Histogram



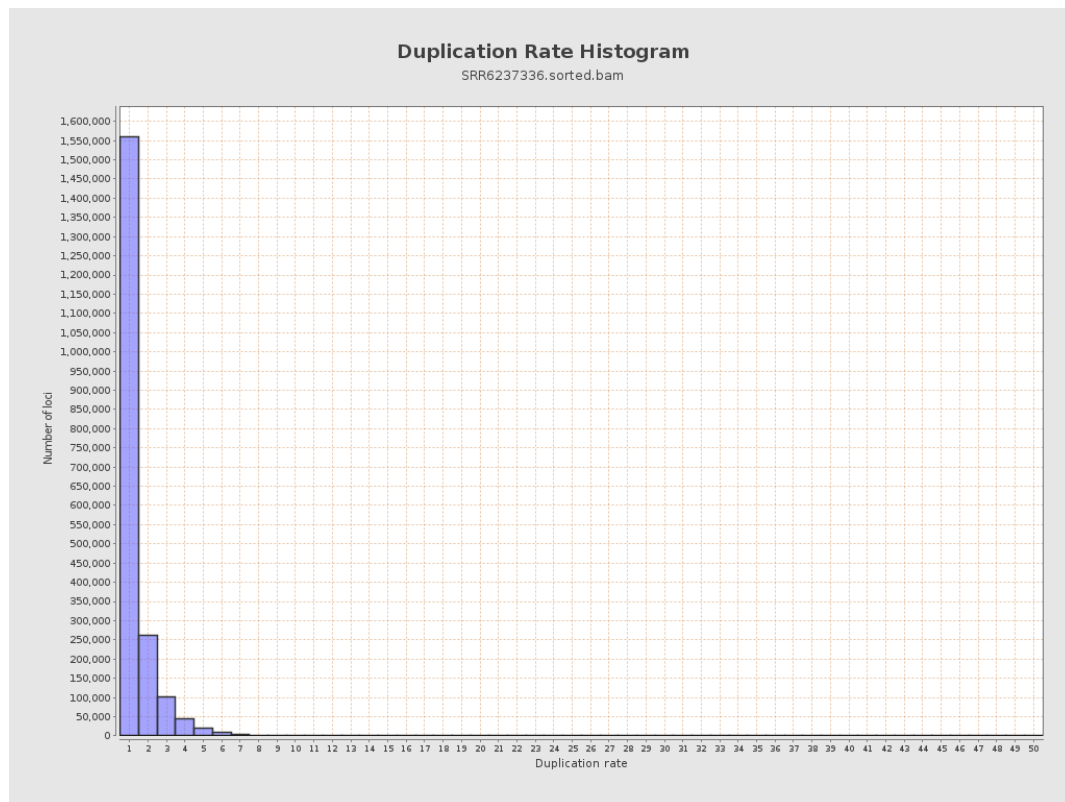
5. Results : Coverage Histogram (0-50X)



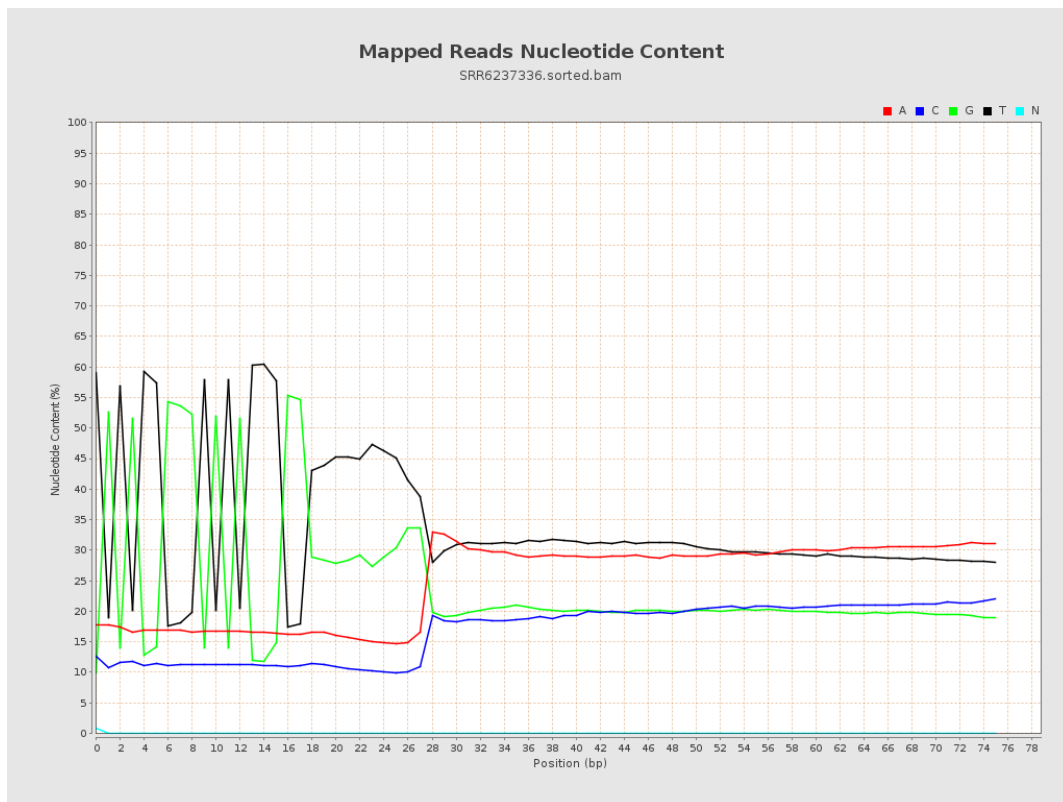
6. Results : Genome Fraction Coverage



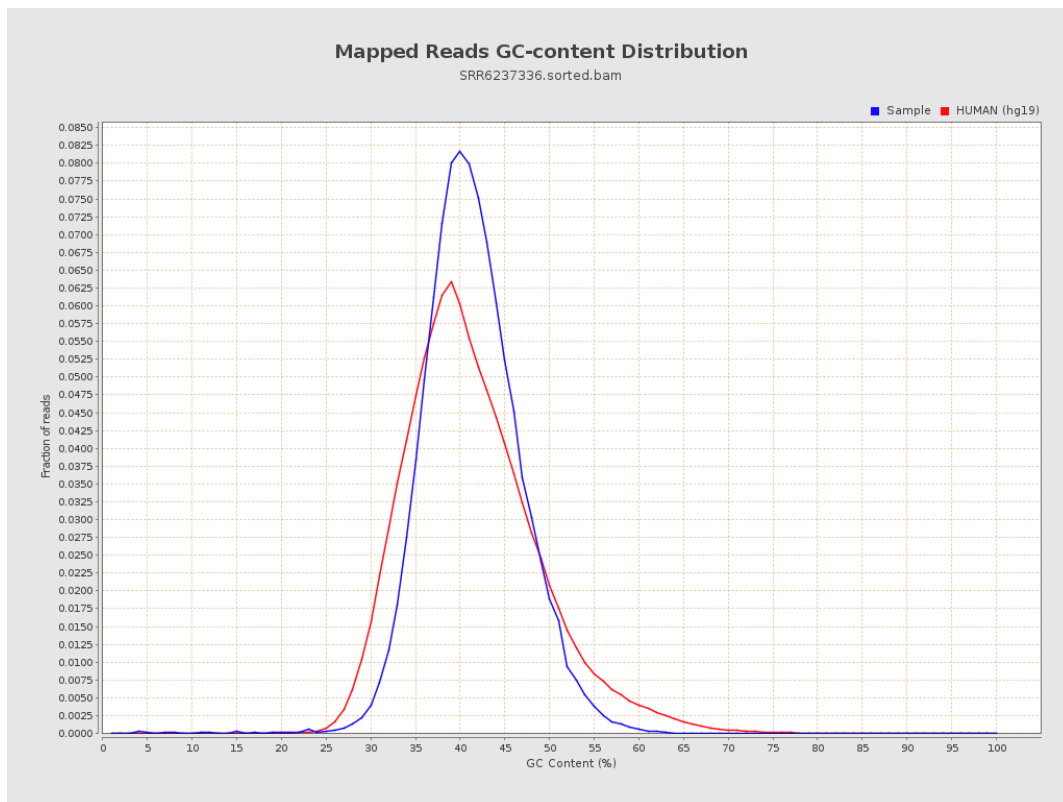
7. Results : Duplication Rate Histogram



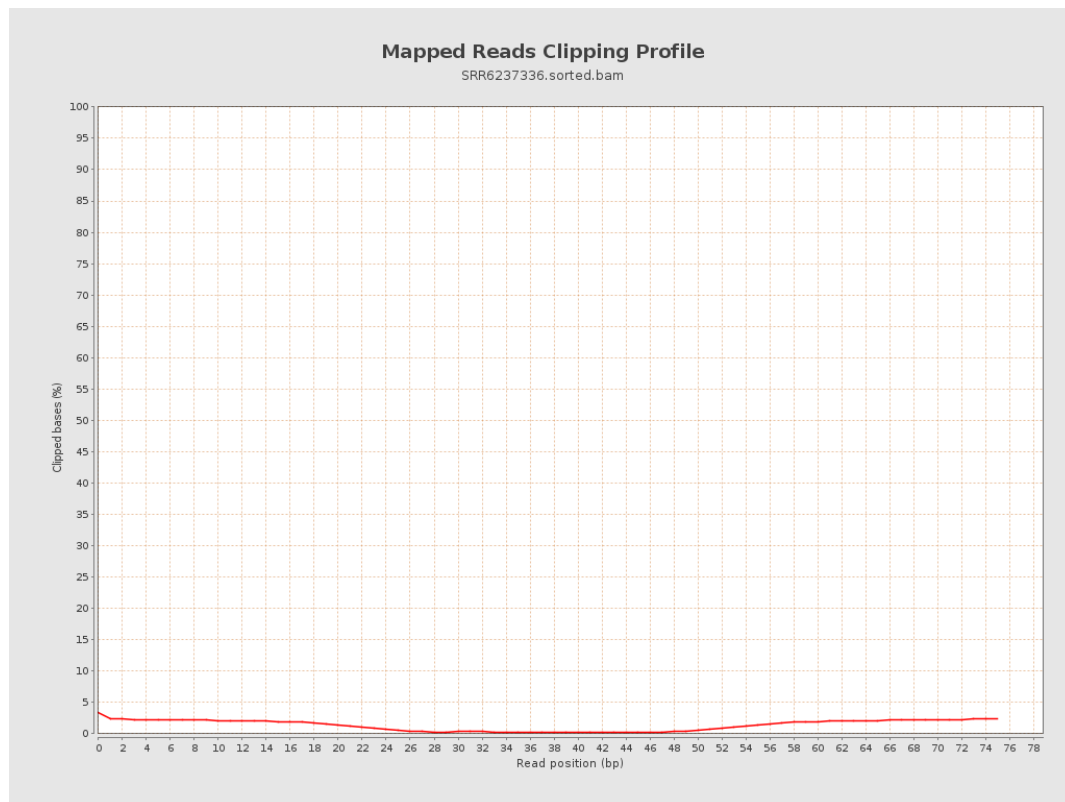
8. Results : Mapped Reads Nucleotide Content



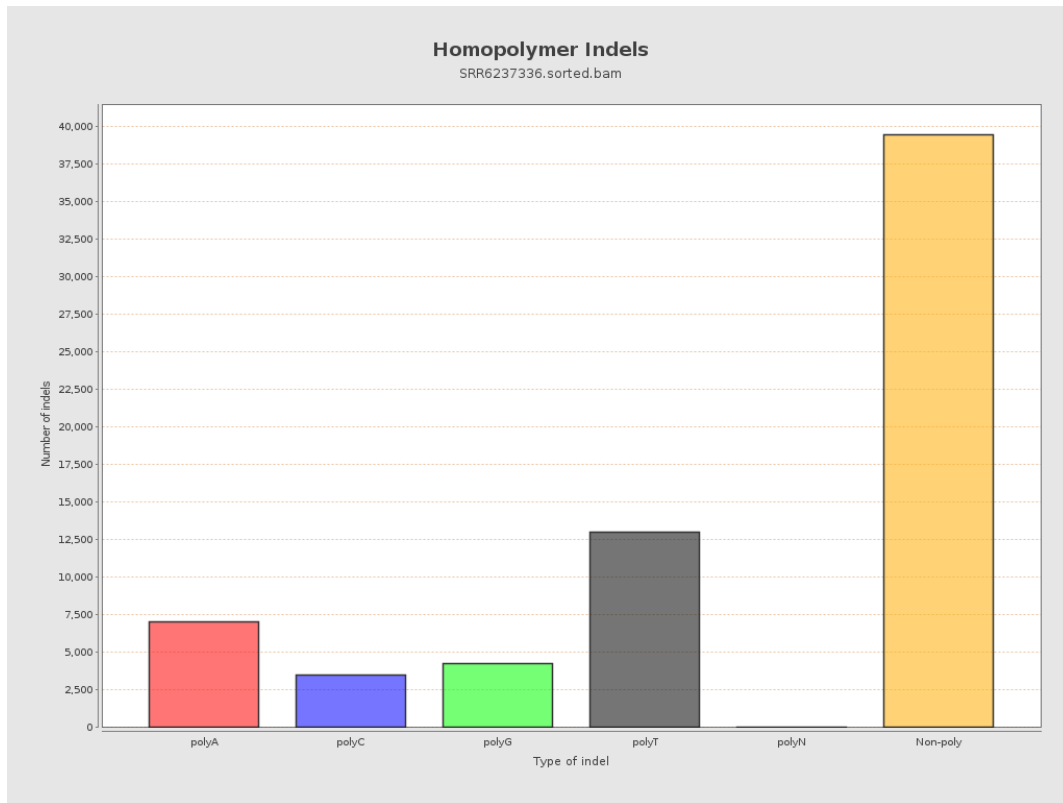
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

