

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:05:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237299.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_SRR6237299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:05:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,463,678
Mapped reads	1,958,252 / 79.48%
Unmapped reads	505,426 / 20.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,168 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	736,156 / 29.88%
Duplication rate	22.38%
Clipped reads	1,406,763 / 57.1%

2.2. ACGT Content

Number/percentage of A's	28,857,451 / 24.6%
Number/percentage of C's	20,537,292 / 17.51%
Number/percentage of T's	39,180,583 / 33.4%
Number/percentage of G's	28,712,014 / 24.48%
Number/percentage of N's	11,615 / 0.01%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0379

Standard Deviation	0.6639
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2.4. Mapping Quality

Mean Mapping Quality	43.1
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2.5. Mismatches and indels

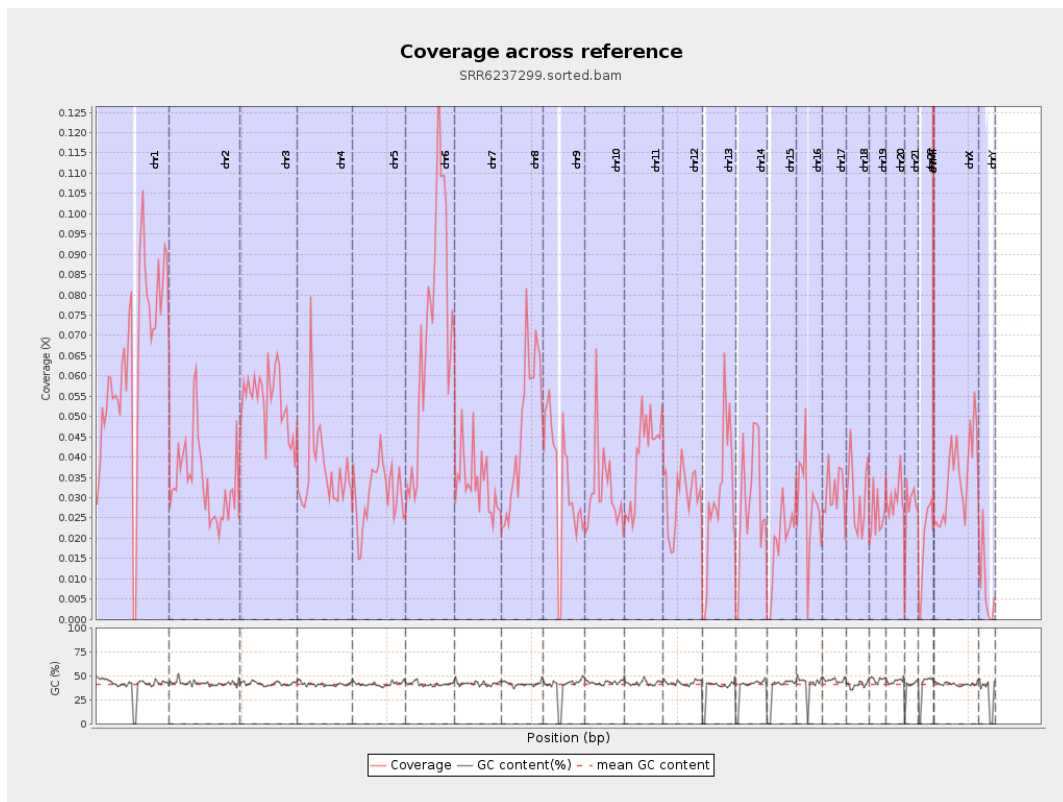
General error rate	0.73%
Mismatches	835,299
Insertions	8,885
Mapped reads with at least one insertion	0.45%
Deletions	38,728
Mapped reads with at least one deletion	1.95%
Homopolymer indels	42.57%

2.6. Chromosome stats

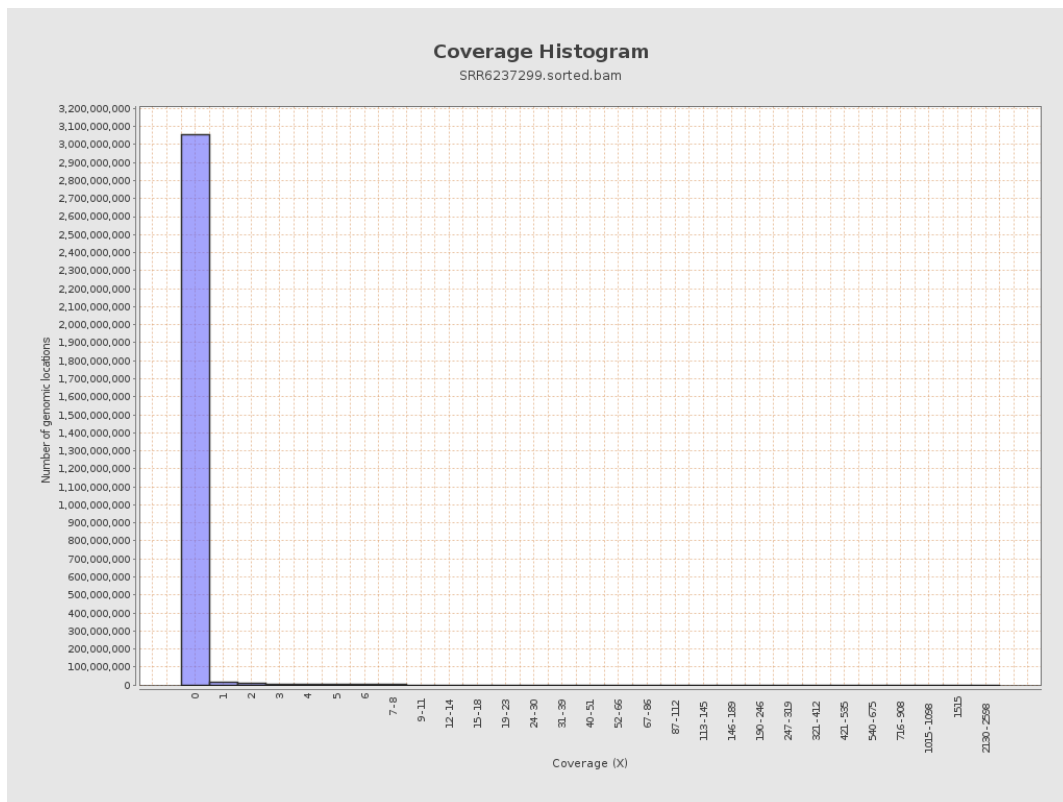
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15810173	0.0634	0.709
chr2	243199373	8231003	0.0338	1.3229
chr3	198022430	10615407	0.0536	0.5162
chr4	191154276	7003225	0.0366	0.5013
chr5	180915260	5613275	0.031	0.4261
chr6	171115067	11886685	0.0695	0.7617
chr7	159138663	5399435	0.0339	0.6046

chr8	146364022	6878992	0.047	0.6689
chr9	141213431	4729201	0.0335	0.4857
chr10	135534747	4317126	0.0319	0.5936
chr11	135006516	5423994	0.0402	0.5042
chr12	133851895	4059156	0.0303	0.4584
chr13	115169878	3385918	0.0294	0.4985
chr14	107349540	3047737	0.0284	0.4357
chr15	102531392	1918784	0.0187	0.3446
chr16	90354753	2578193	0.0285	0.4172
chr17	81195210	2513463	0.031	0.4414
chr18	78077248	2416608	0.031	1.3103
chr19	59128983	1530717	0.0259	0.4723
chr20	63025520	1880444	0.0298	0.4564
chr21	48129895	1303243	0.0271	0.4481
chr22	51304566	966595	0.0188	0.3738
chrMT	16571	23959	1.4458	3.1533
chrX	155270560	5416756	0.0349	0.4881
chrY	59373566	415789	0.007	0.3146

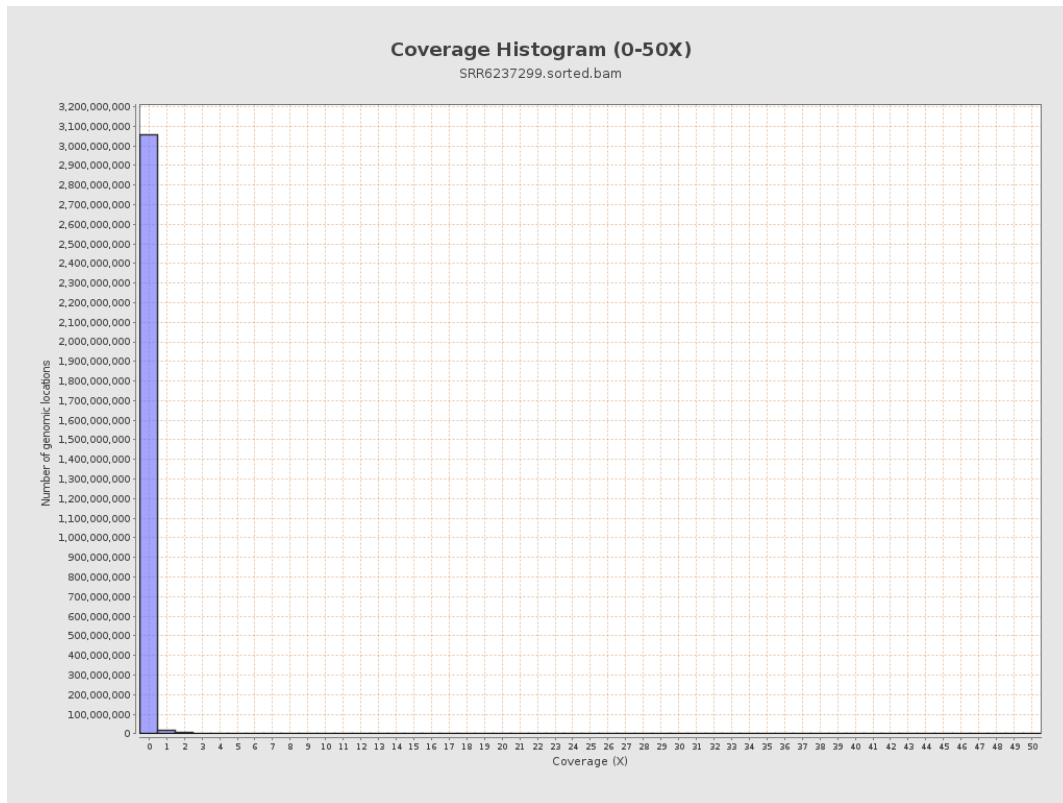
3. Results : Coverage across reference



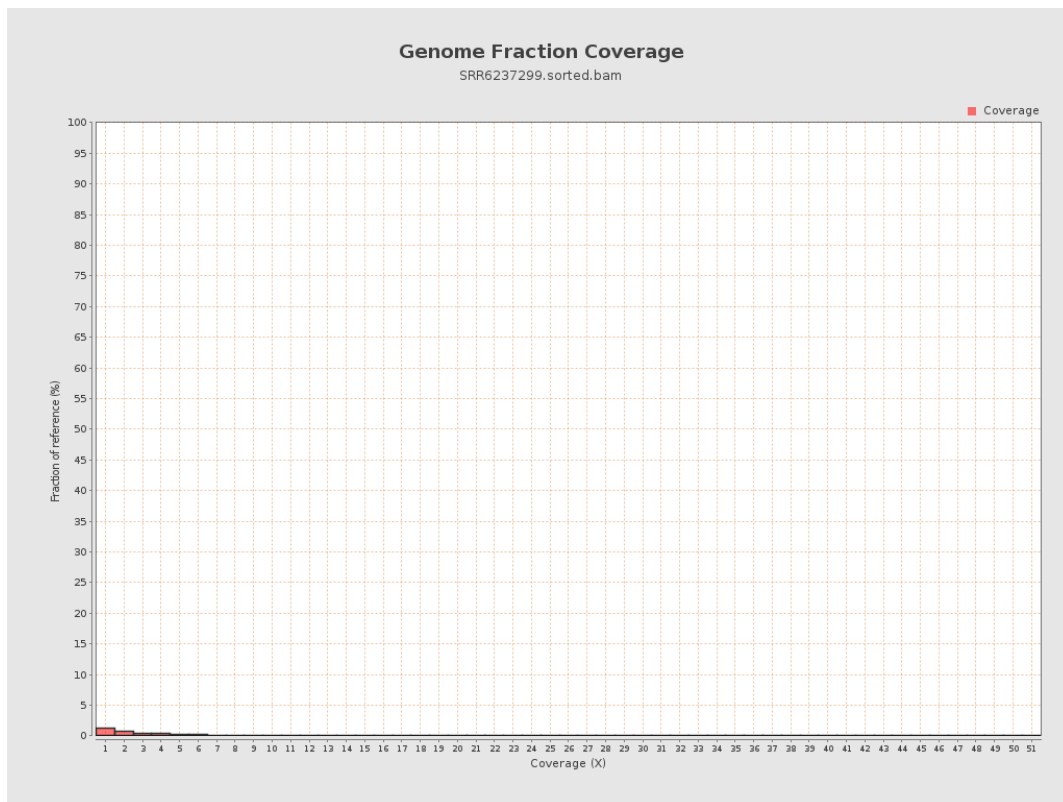
4. Results : Coverage Histogram



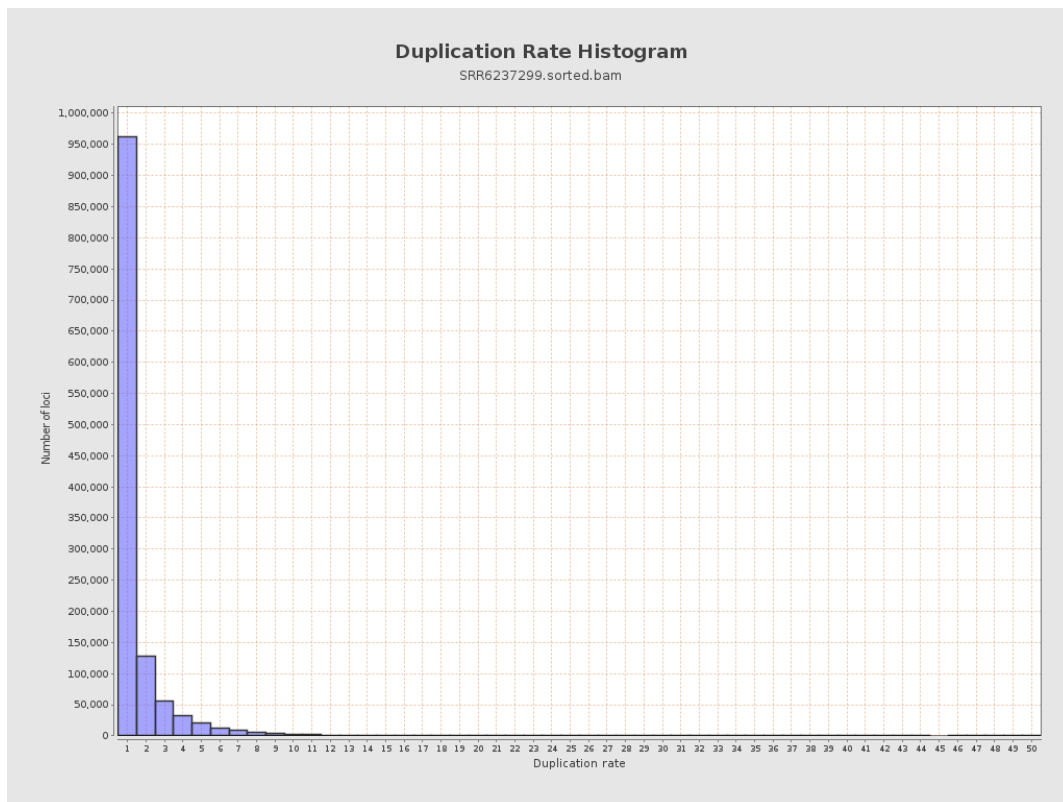
5. Results : Coverage Histogram (0-50X)



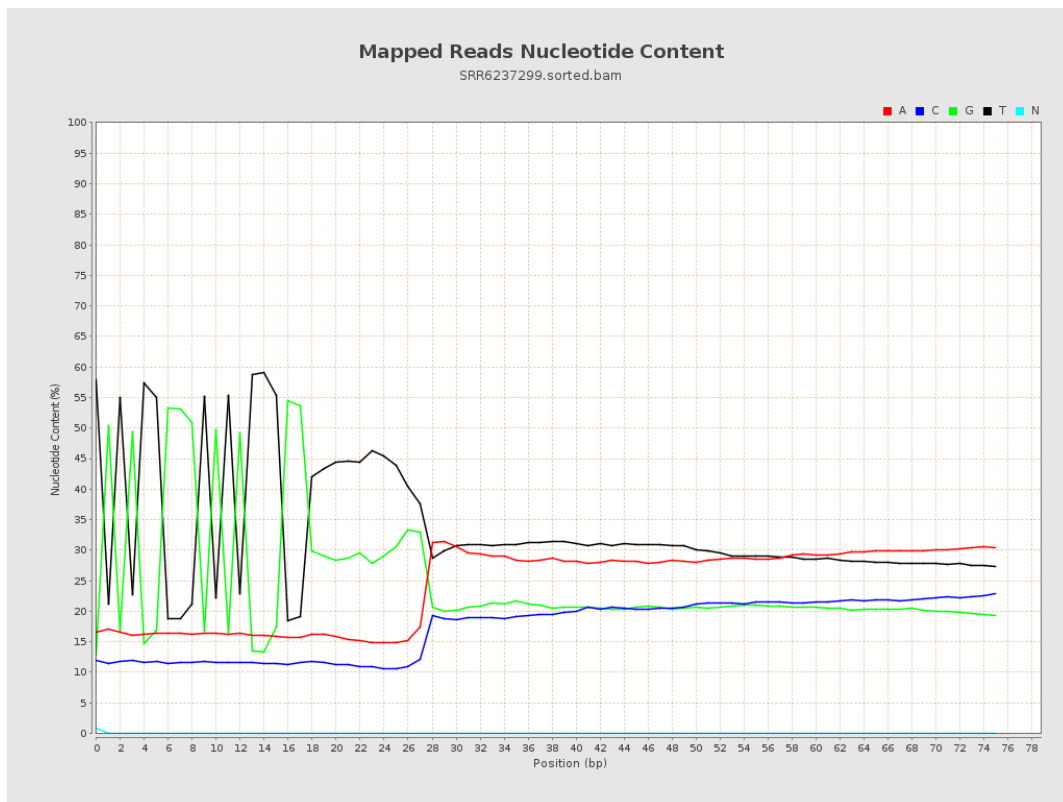
6. Results : Genome Fraction Coverage



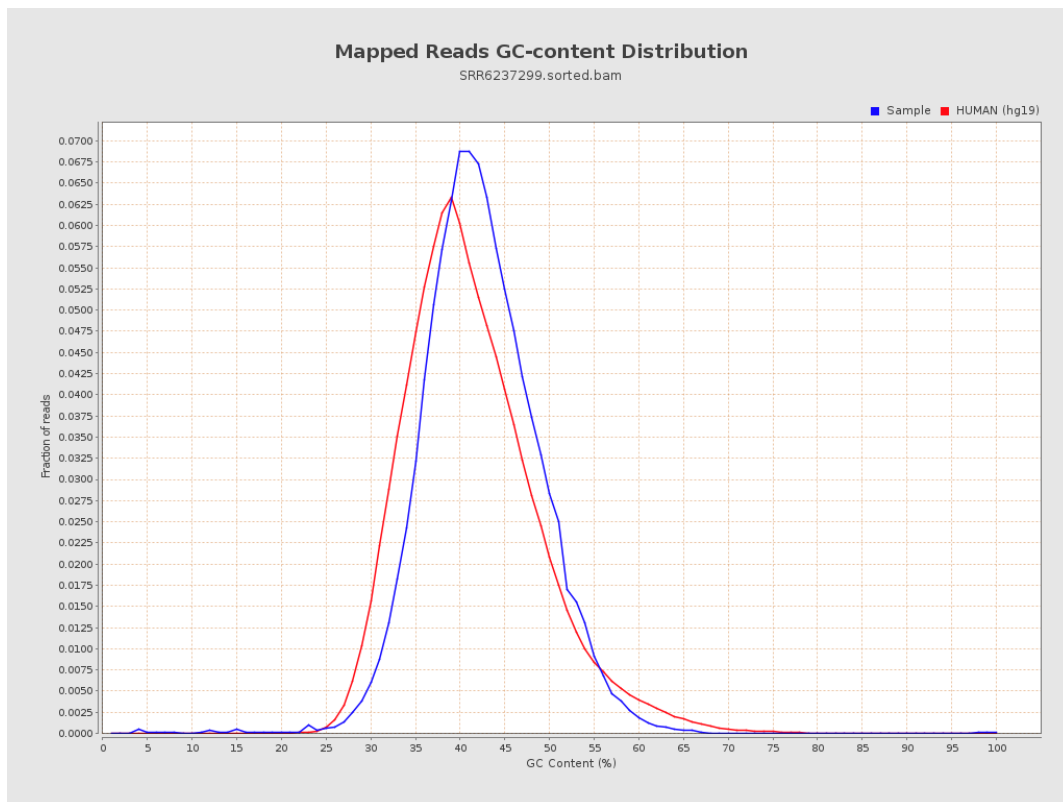
7. Results : Duplication Rate Histogram



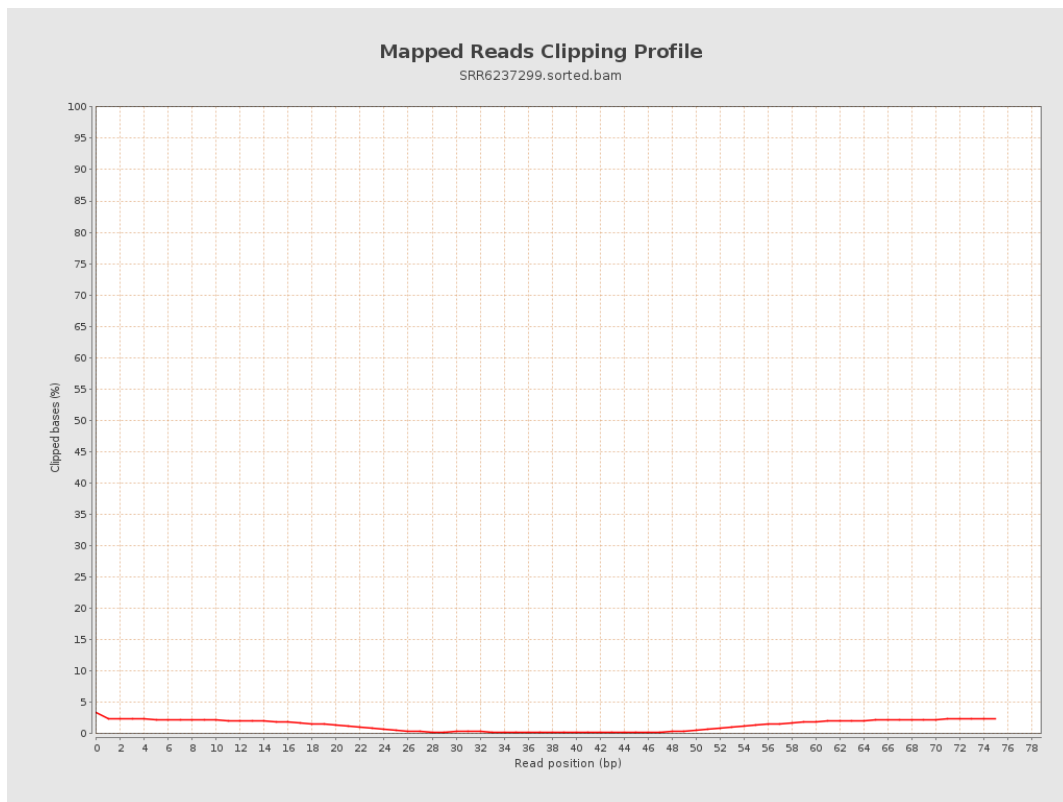
8. Results : Mapped Reads Nucleotide Content



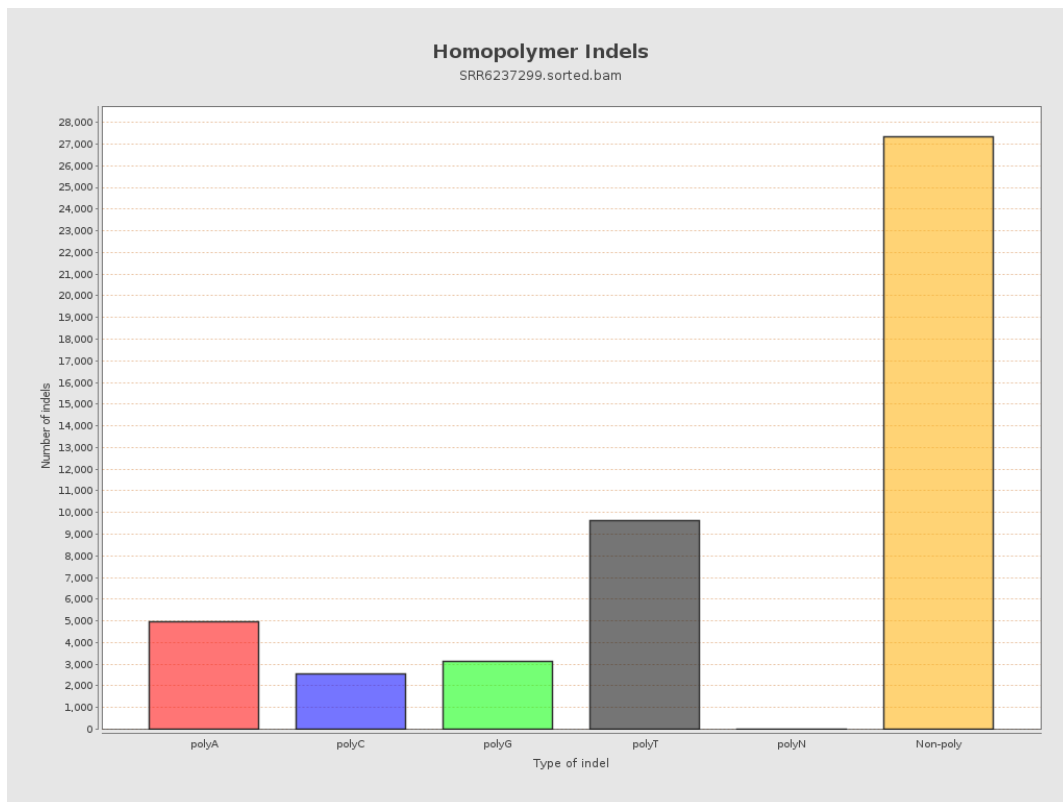
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

