

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:29:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237587.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_SRR6237587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237587.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:29:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,088,496
Mapped reads	1,803,873 / 86.37%
Unmapped reads	284,623 / 13.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,395 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	78,240 / 3.75%
Duplication rate	3.49%
Clipped reads	896,950 / 42.95%

2.2. ACGT Content

Number/percentage of A's	32,779,679 / 27.82%
Number/percentage of C's	20,561,476 / 17.45%
Number/percentage of T's	38,402,069 / 32.6%
Number/percentage of G's	25,837,735 / 21.93%
Number/percentage of N's	226,613 / 0.19%
GC Percentage	39.39%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3495
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2.4. Mapping Quality

Mean Mapping Quality	46.55
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2.5. Mismatches and indels

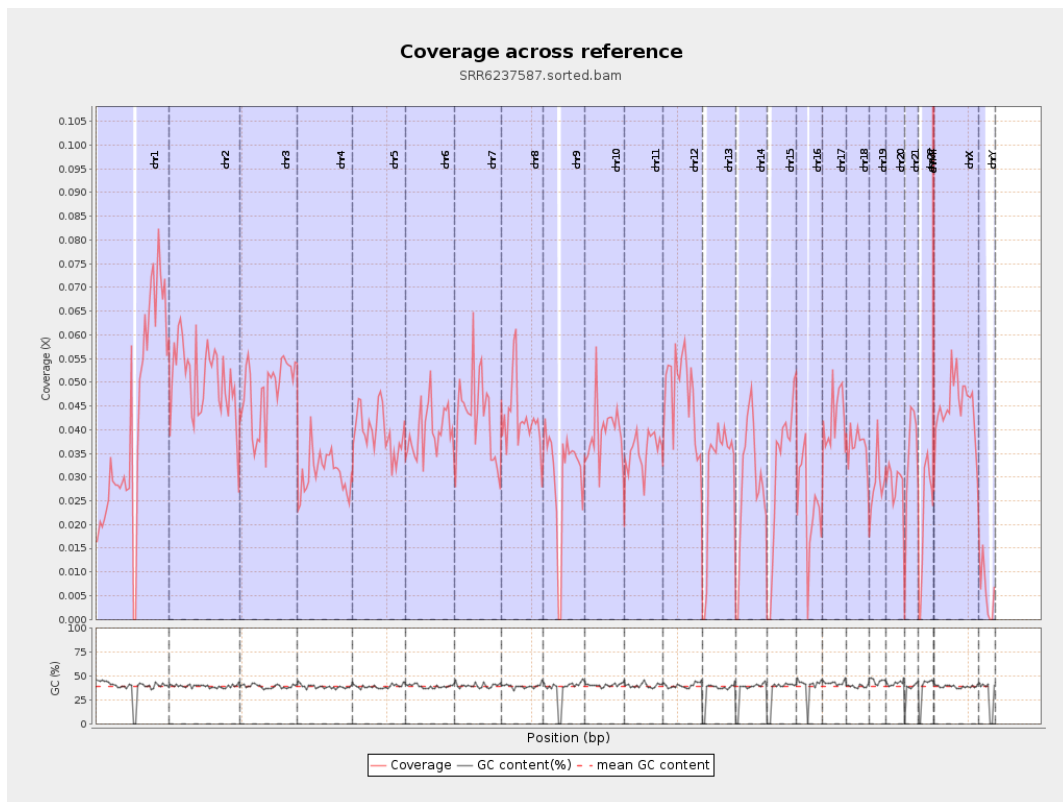
General error rate	0.92%
Mismatches	1,064,189
Insertions	9,832
Mapped reads with at least one insertion	0.54%
Deletions	43,312
Mapped reads with at least one deletion	2.37%
Homopolymer indels	46.25%

2.6. Chromosome stats

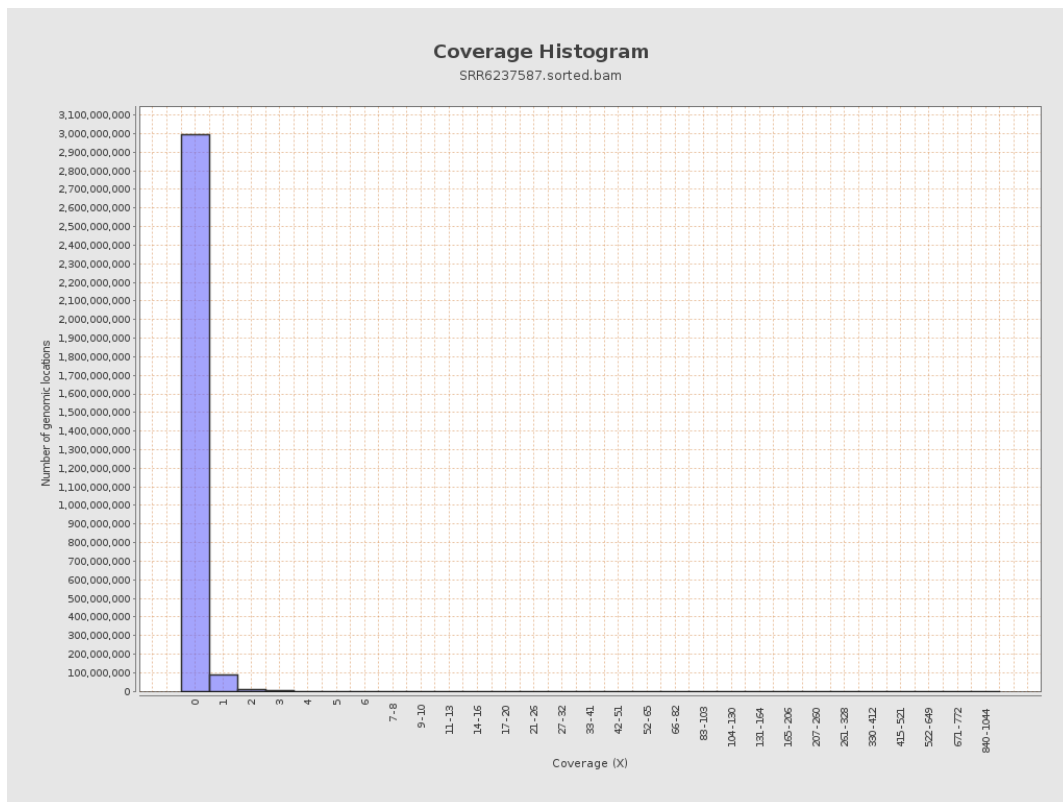
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10403204	0.0417	0.6268
chr2	243199373	12313325	0.0506	0.4161
chr3	198022430	9554999	0.0483	0.2462
chr4	191154276	5899355	0.0309	0.2113
chr5	180915260	7160747	0.0396	0.2229
chr6	171115067	6793986	0.0397	0.2532
chr7	159138663	6838937	0.043	0.4213

chr8	146364022	6185318	0.0423	0.6633
chr9	141213431	4300978	0.0305	0.2643
chr10	135534747	5350056	0.0395	0.3034
chr11	135006516	4791864	0.0355	0.2596
chr12	133851895	6338119	0.0474	0.2459
chr13	115169878	3515977	0.0305	0.1969
chr14	107349540	3129011	0.0291	0.2013
chr15	102531392	3195260	0.0312	0.1984
chr16	90354753	2204899	0.0244	0.1945
chr17	81195210	3463136	0.0427	0.2503
chr18	78077248	2868521	0.0367	0.4642
chr19	59128983	1721077	0.0291	0.4108
chr20	63025520	1811923	0.0287	0.1968
chr21	48129895	1619996	0.0337	0.2169
chr22	51304566	1106913	0.0216	0.1627
chrMT	16571	43032	2.5968	2.265
chrX	155270560	6925578	0.0446	0.2532
chrY	59373566	343125	0.0058	0.119

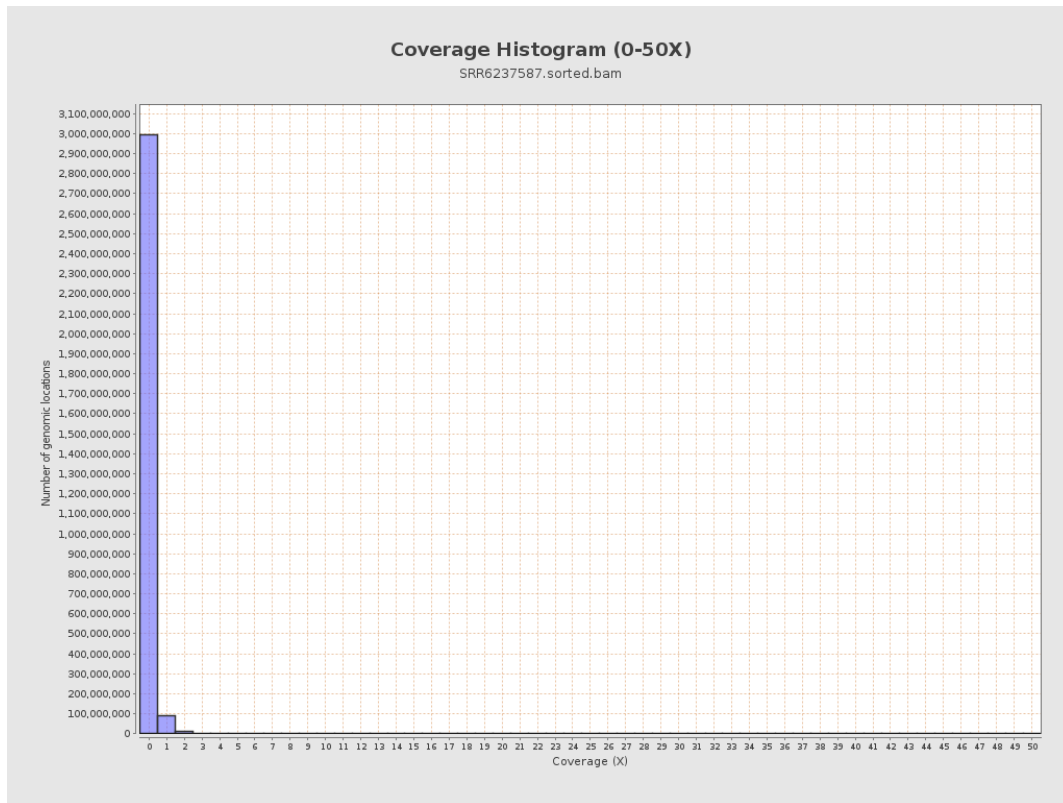
3. Results : Coverage across reference



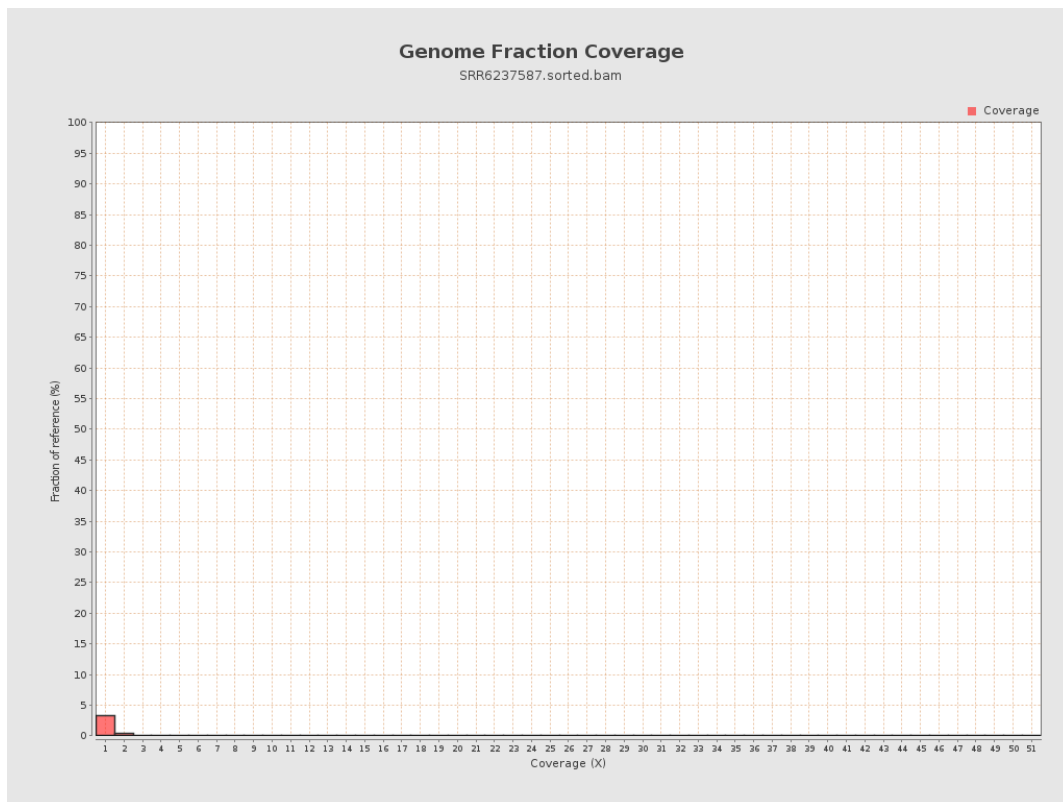
4. Results : Coverage Histogram



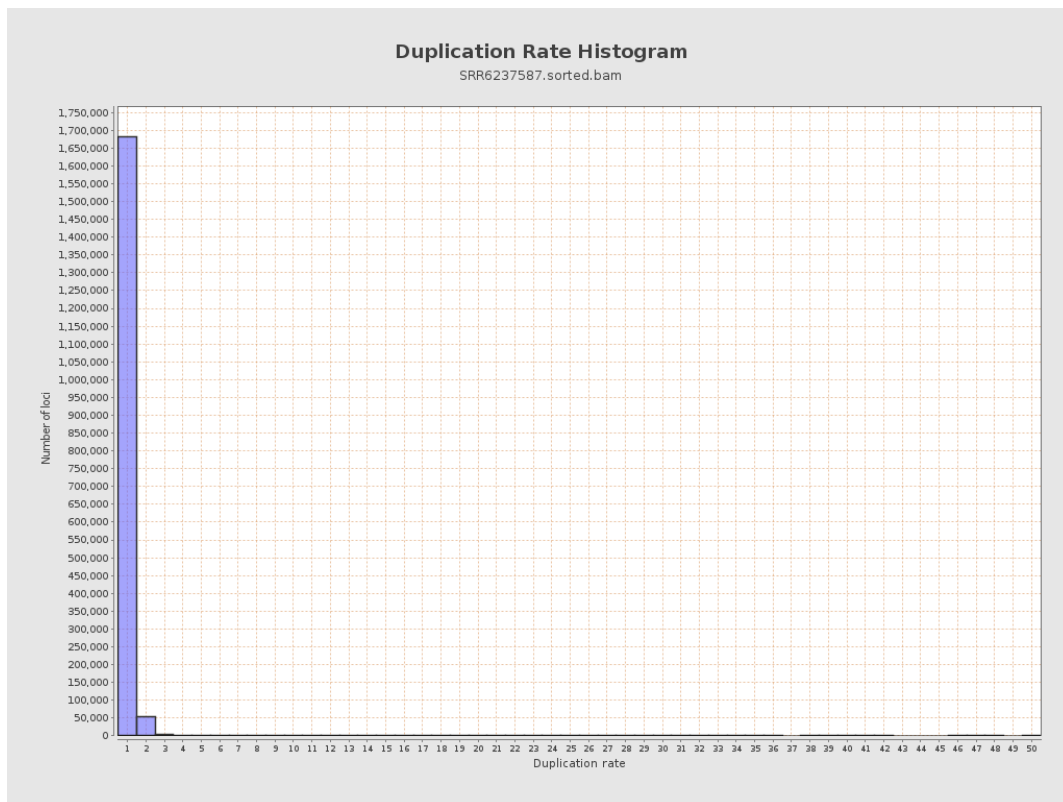
5. Results : Coverage Histogram (0-50X)



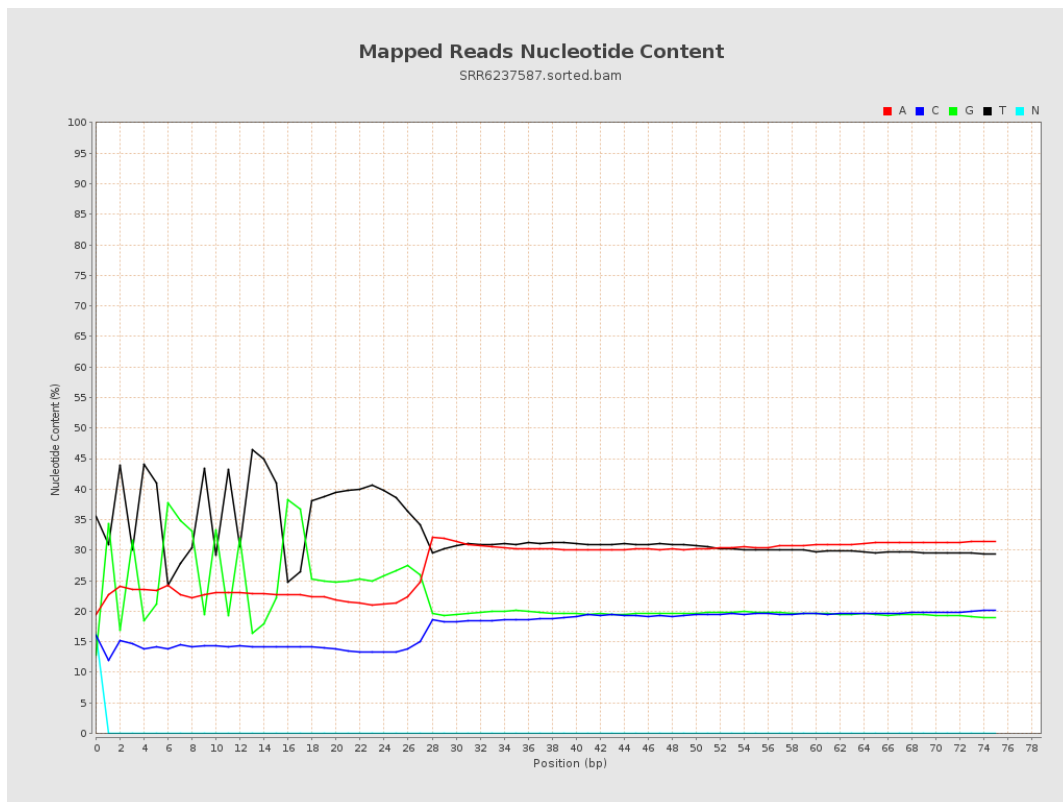
6. Results : Genome Fraction Coverage



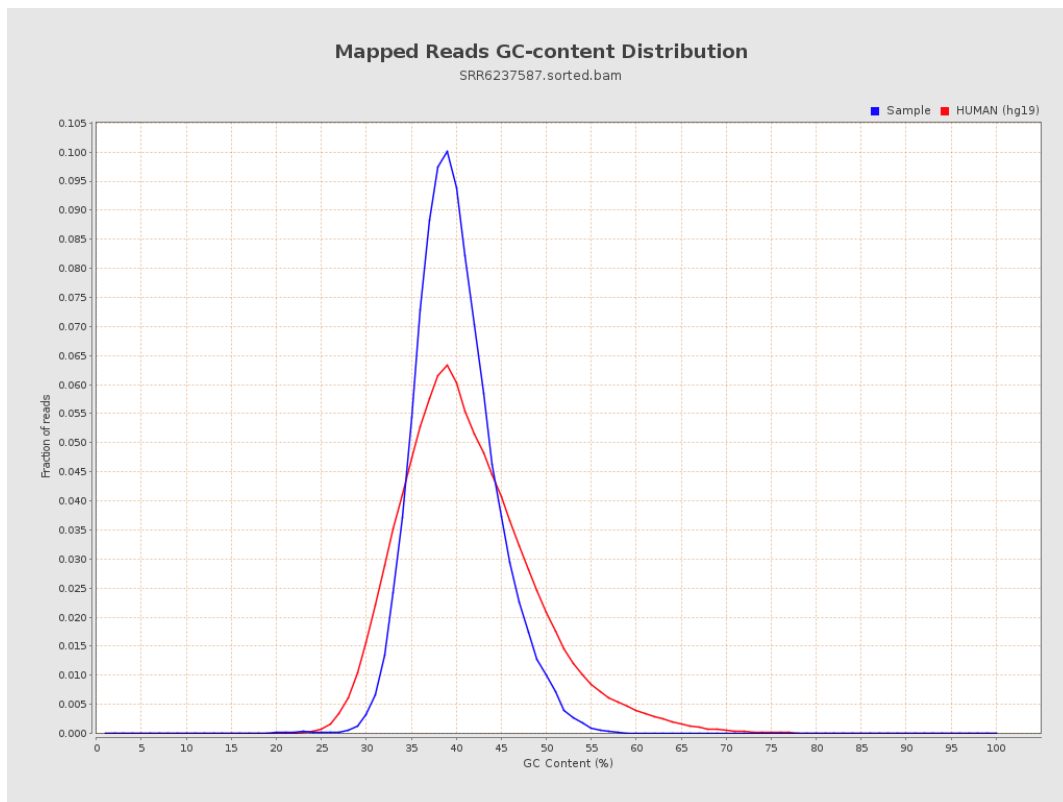
7. Results : Duplication Rate Histogram



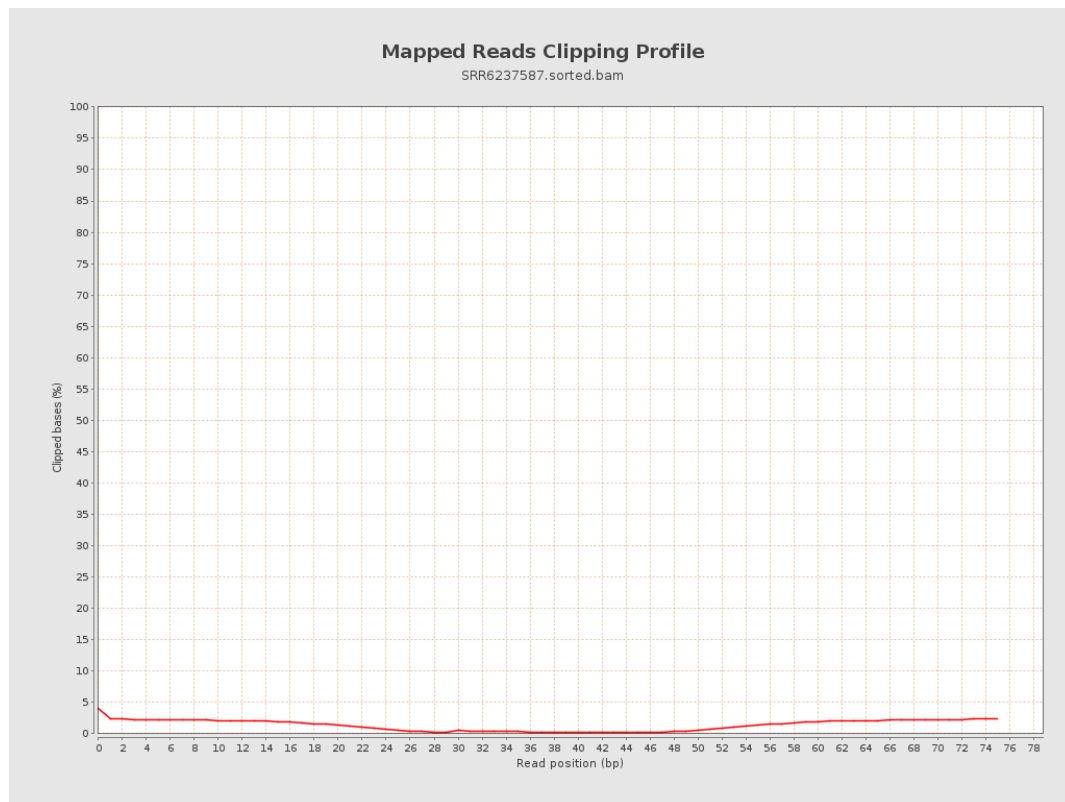
8. Results : Mapped Reads Nucleotide Content



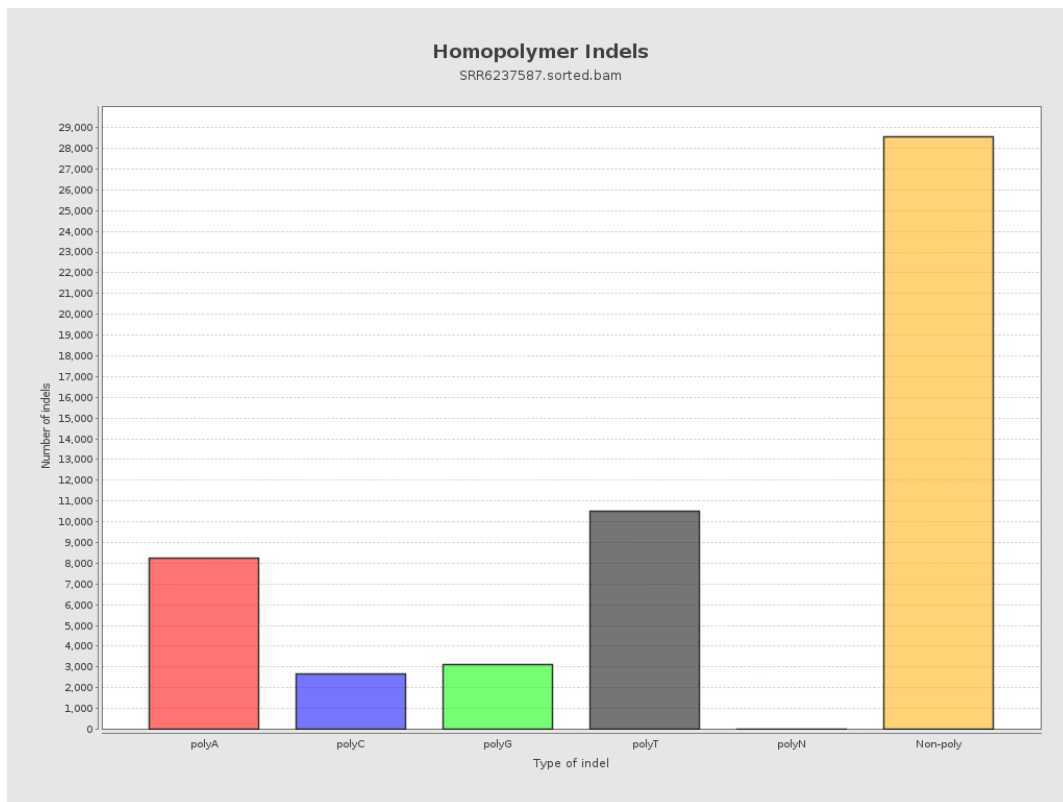
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

