

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:49:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237867.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_SRR6237867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237867.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:49:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,919,747
Mapped reads	1,820,576 / 94.83%
Unmapped reads	99,171 / 5.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,870 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	48,855 / 2.54%
Duplication rate	1.69%
Clipped reads	539,501 / 28.1%

2.2. ACGT Content

Number/percentage of A's	39,239,802 / 30.18%
Number/percentage of C's	26,042,012 / 20.03%
Number/percentage of T's	38,065,938 / 29.27%
Number/percentage of G's	26,465,382 / 20.35%
Number/percentage of N's	224,292 / 0.17%
GC Percentage	40.38%

2.3. Coverage

Mean	0.042

Standard Deviation	0.5904
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2.4. Mapping Quality

Mean Mapping Quality	42.82
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2.5. Mismatches and indels

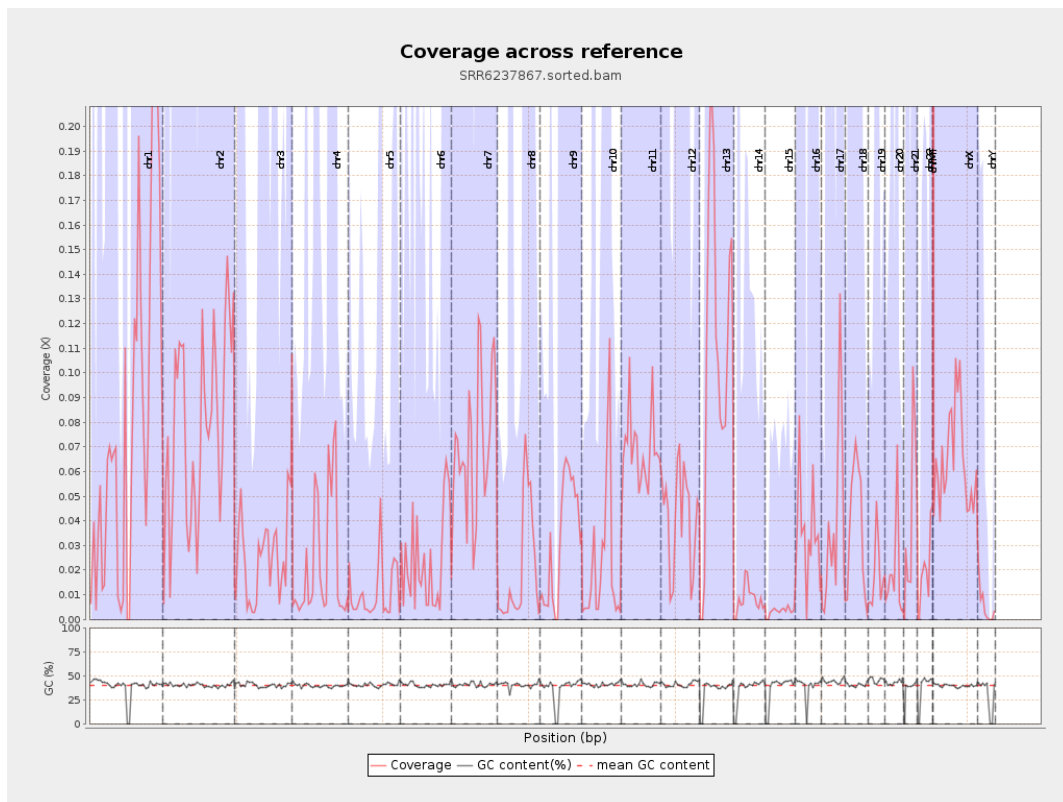
General error rate	0.88%
Mismatches	1,130,185
Insertions	8,998
Mapped reads with at least one insertion	0.49%
Deletions	34,433
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.04%

2.6. Chromosome stats

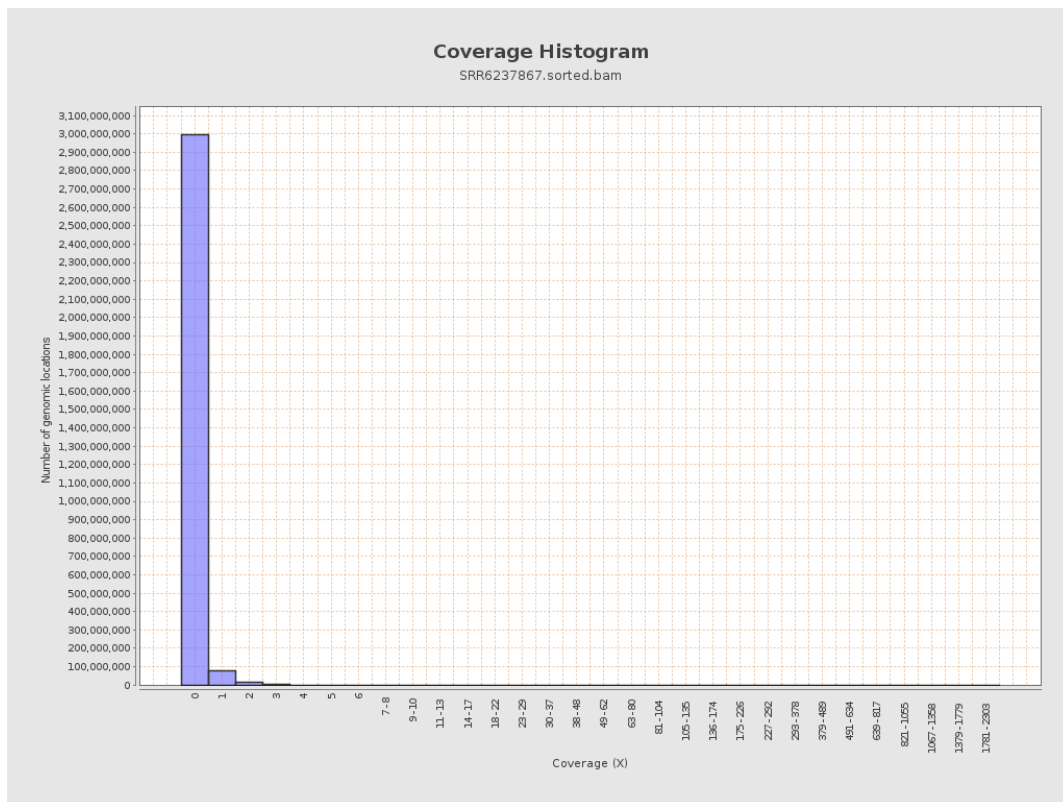
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20167840	0.0809	1.6984
chr2	243199373	19312469	0.0794	0.4222
chr3	198022430	5040485	0.0255	0.2007
chr4	191154276	4209042	0.022	0.1881
chr5	180915260	1960157	0.0108	0.1267
chr6	171115067	4080742	0.0238	0.1905
chr7	159138663	11374138	0.0715	0.6445

chr8	146364022	2929420	0.02	0.2808
chr9	141213431	4539392	0.0321	0.2845
chr10	135534747	2945302	0.0217	0.296
chr11	135006516	9331390	0.0691	0.5172
chr12	133851895	5557860	0.0415	0.2504
chr13	115169878	12477562	0.1083	0.4127
chr14	107349540	895220	0.0083	0.1537
chr15	102531392	328330	0.0032	0.065
chr16	90354753	3102115	0.0343	0.2933
chr17	81195210	3269709	0.0403	0.3134
chr18	78077248	2964188	0.038	0.6667
chr19	59128983	1102346	0.0186	0.8395
chr20	63025520	1140490	0.0181	0.1854
chr21	48129895	2109633	0.0438	0.2802
chr22	51304566	966735	0.0188	0.167
chrMT	16571	64042	3.8647	3.2024
chrX	155270560	9918896	0.0639	0.3724
chrY	59373566	311102	0.0052	0.1092

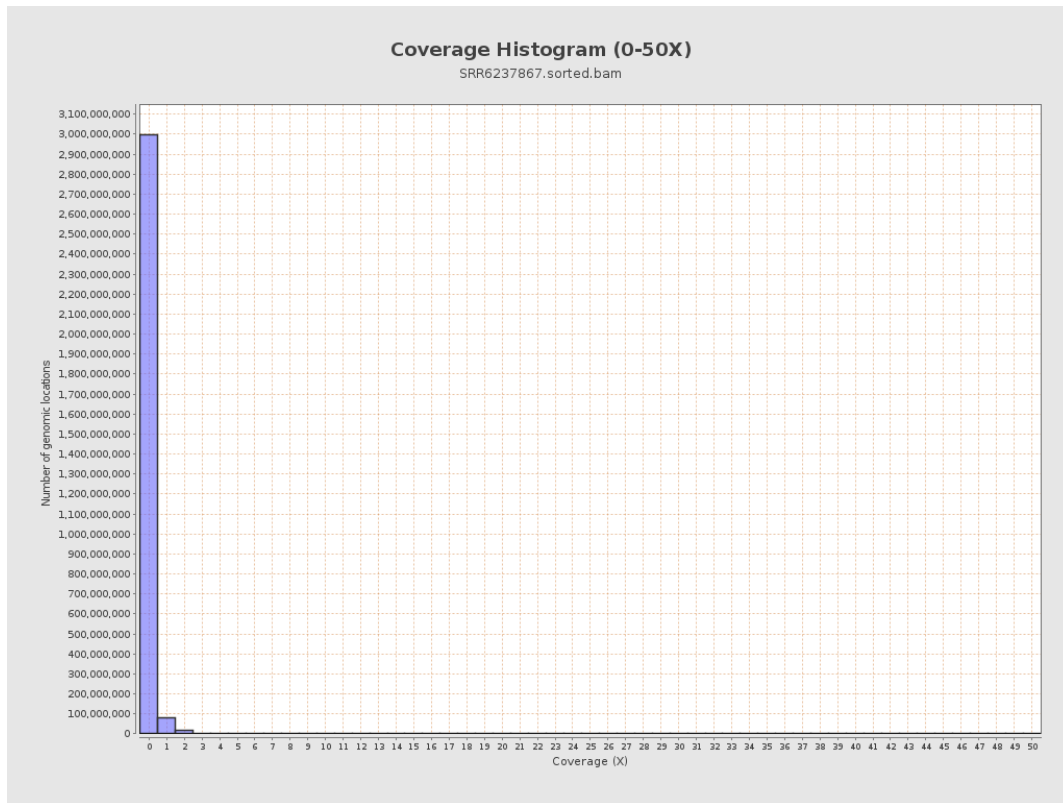
3. Results : Coverage across reference



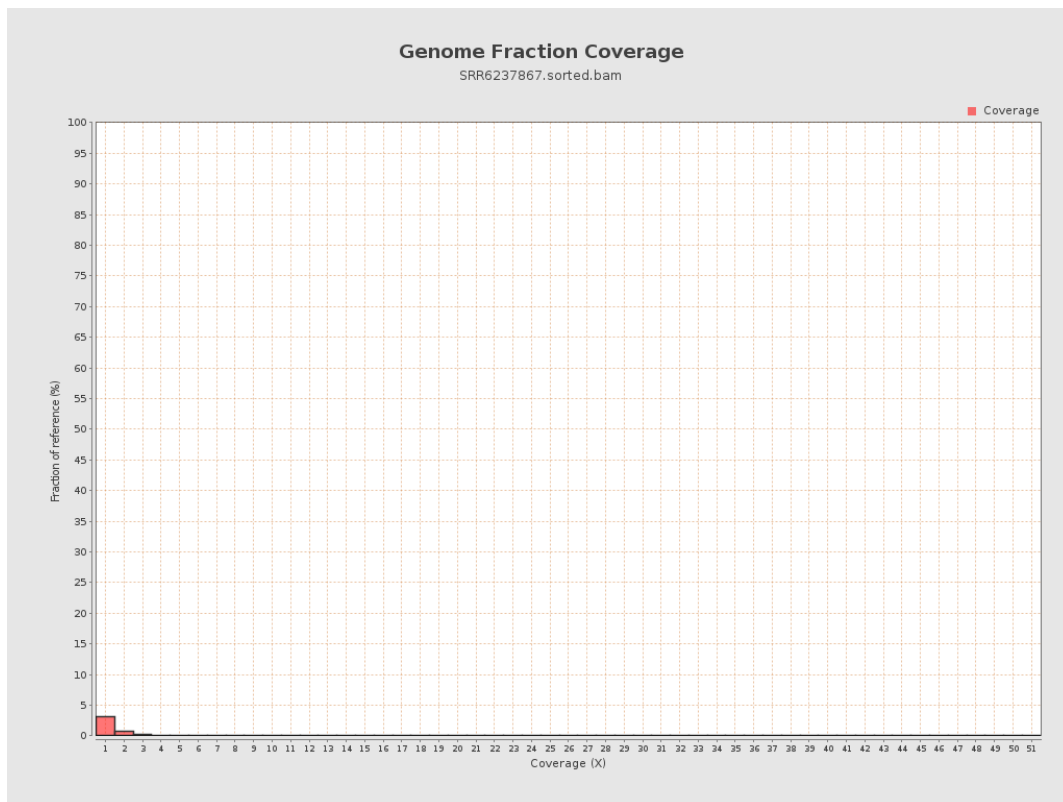
4. Results : Coverage Histogram



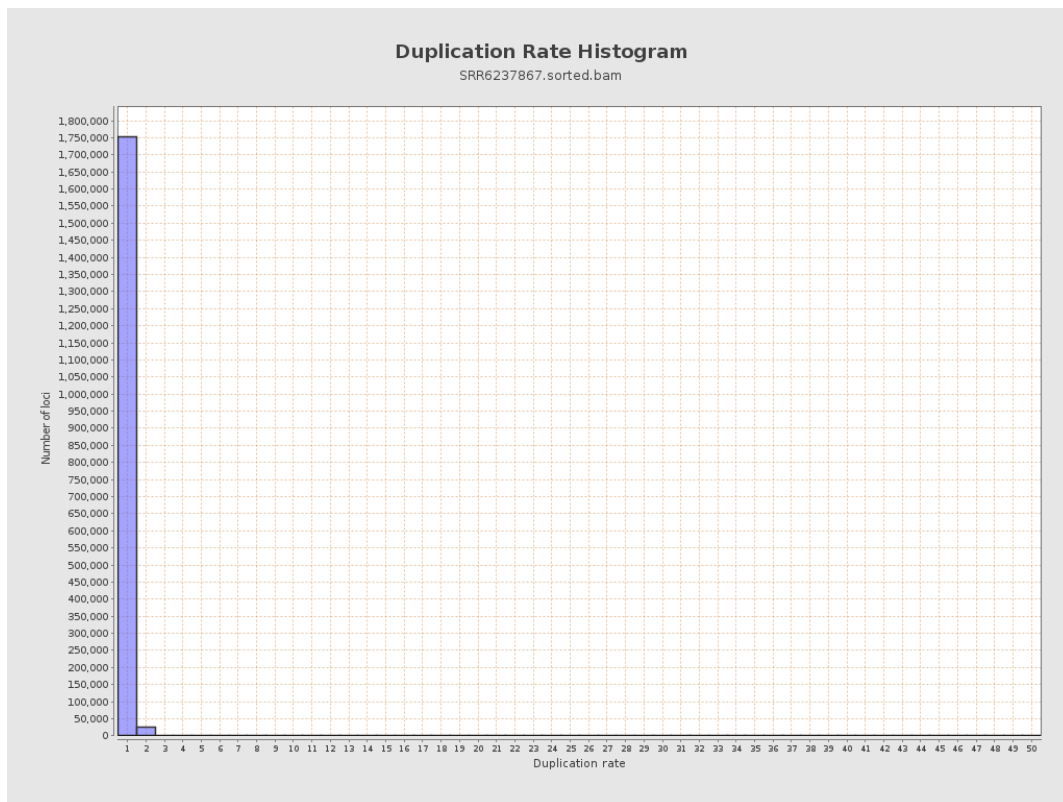
5. Results : Coverage Histogram (0-50X)



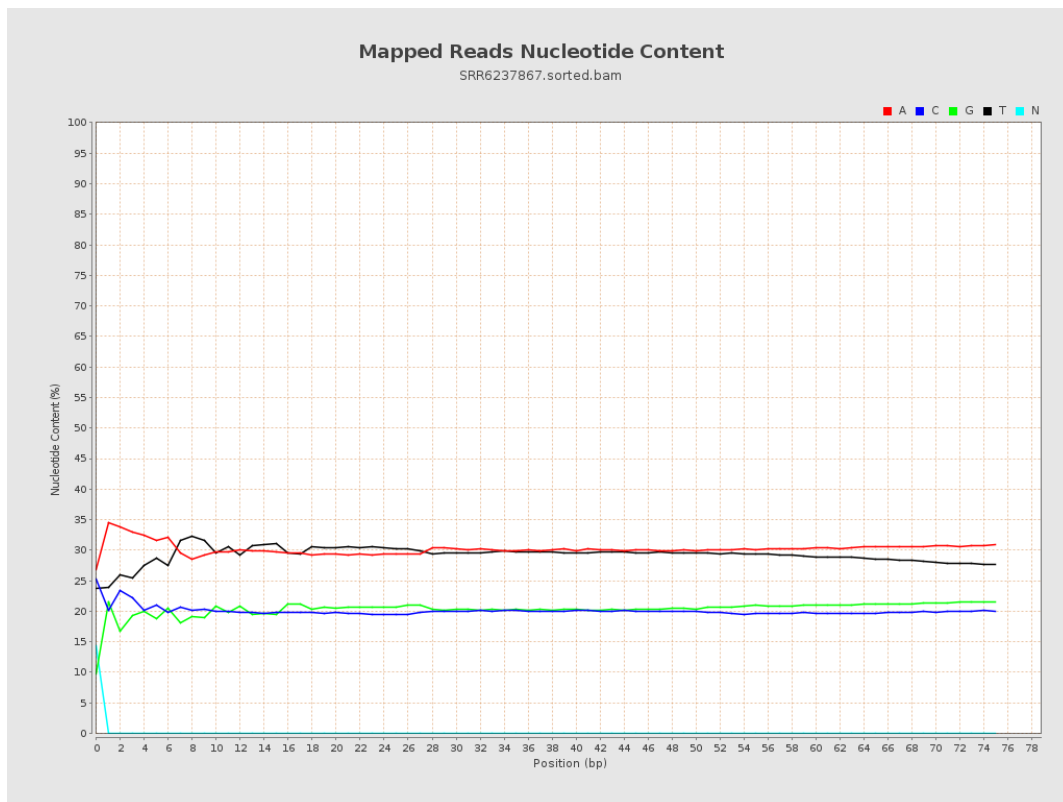
6. Results : Genome Fraction Coverage



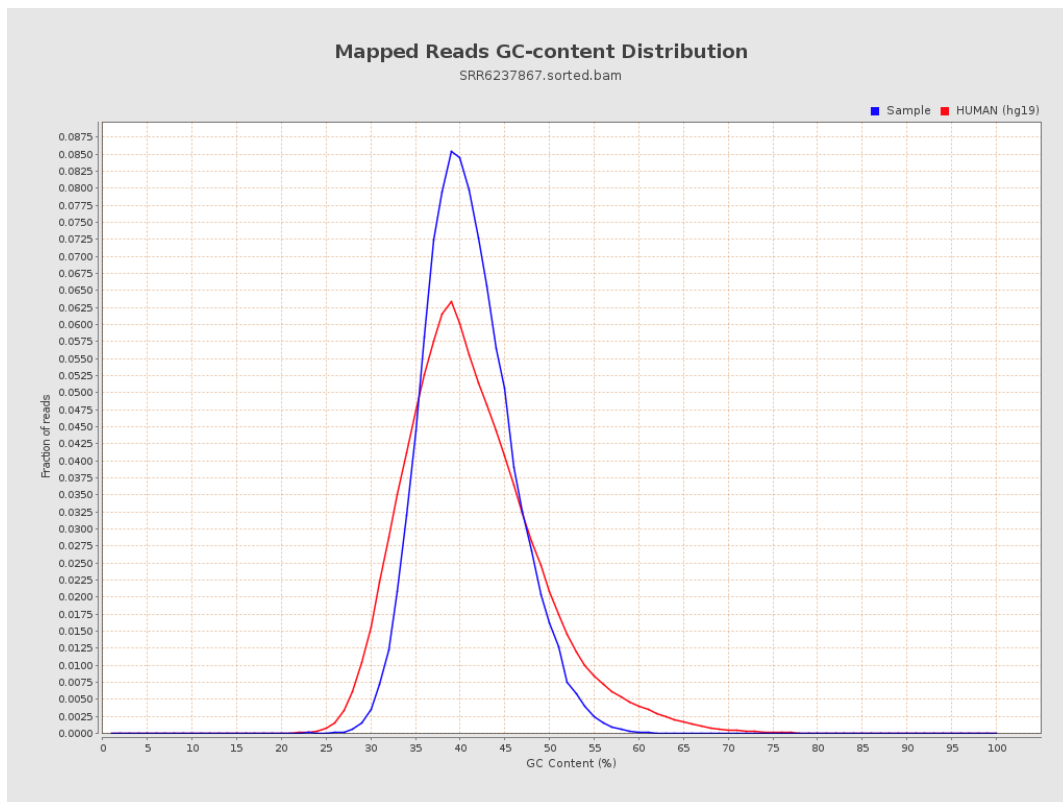
7. Results : Duplication Rate Histogram



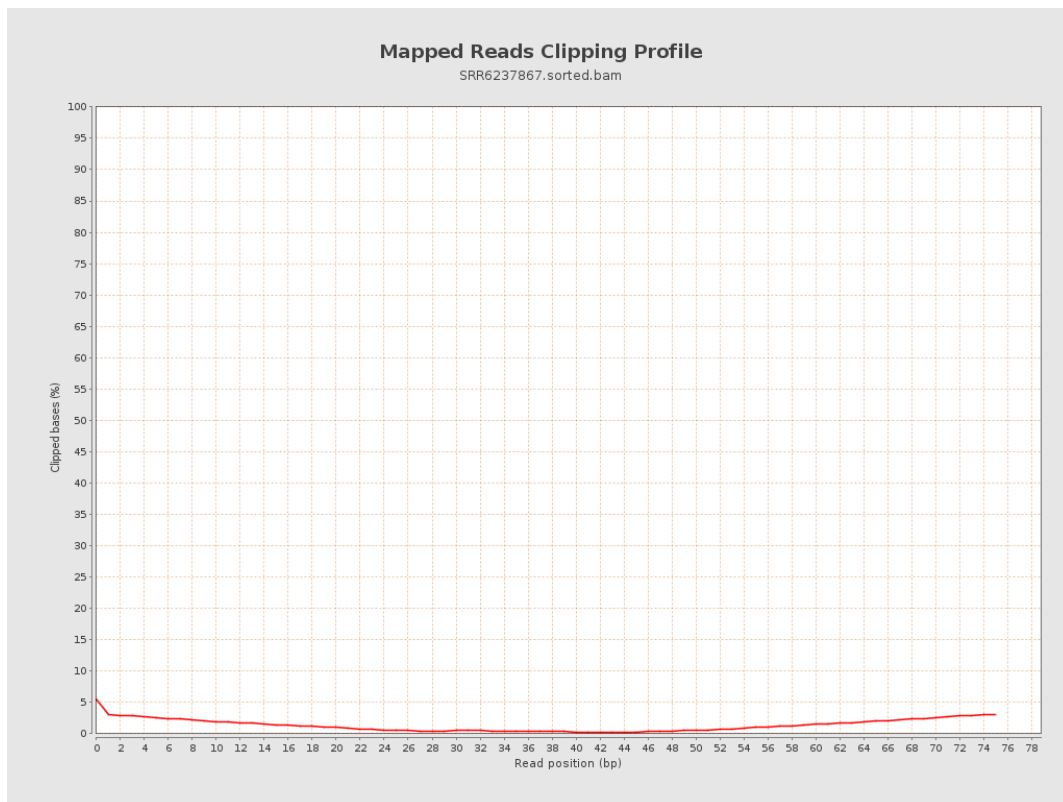
8. Results : Mapped Reads Nucleotide Content



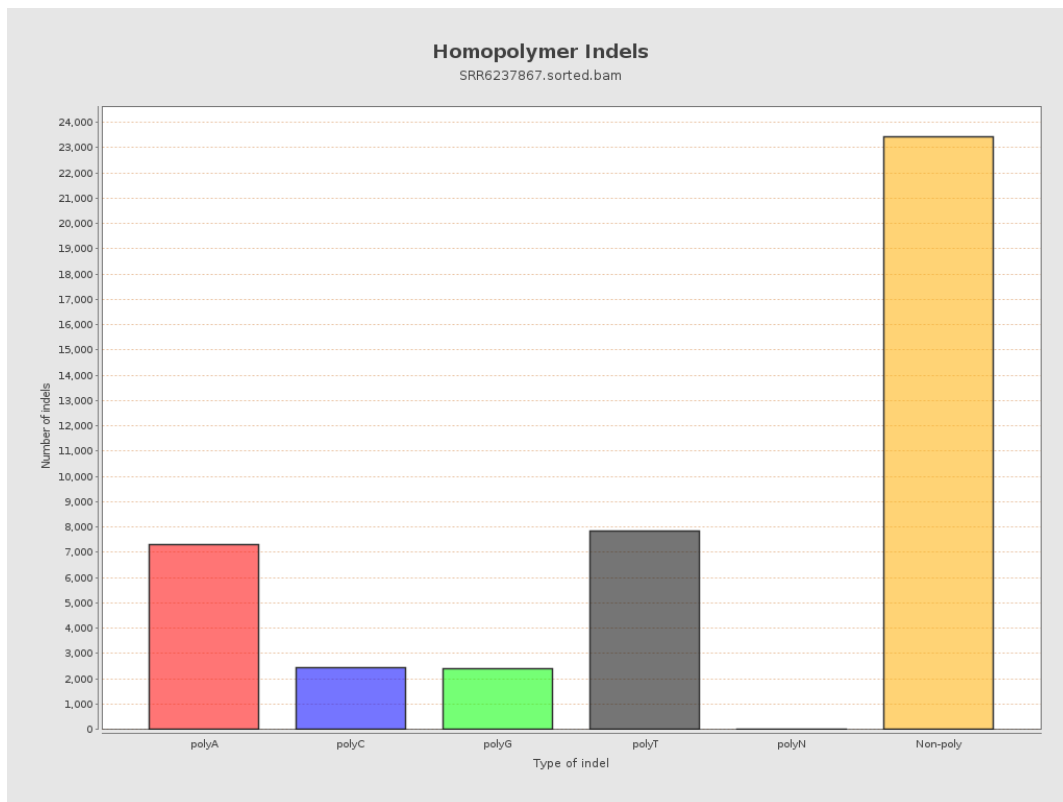
9. Results : Mapped Reads GC-content Distribution



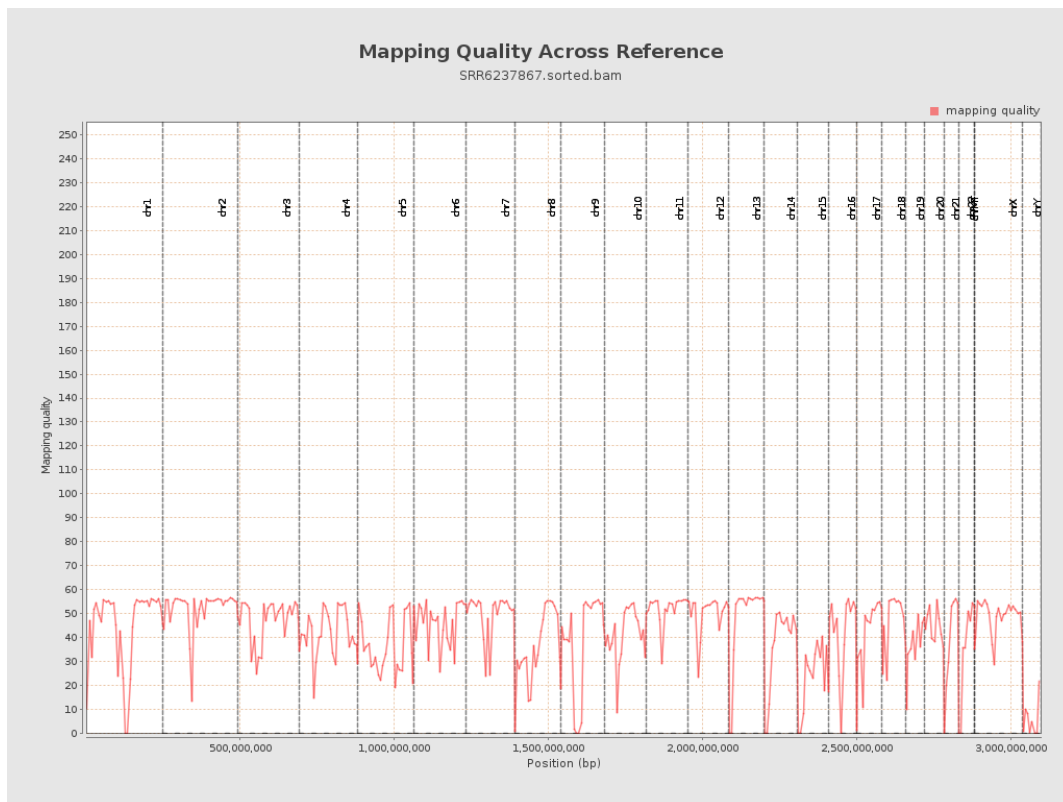
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

