

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:03:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237316.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_SRR6237316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237316.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:03:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,213,934
Mapped reads	2,877,382 / 89.53%
Unmapped reads	336,552 / 10.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,994 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	181,245 / 5.64%
Duplication rate	4.82%
Clipped reads	1,191,913 / 37.09%

2.2. ACGT Content

Number/percentage of A's	54,571,040 / 28.09%
Number/percentage of C's	35,264,877 / 18.15%
Number/percentage of T's	62,190,417 / 32.01%
Number/percentage of G's	42,238,290 / 21.74%
Number/percentage of N's	3,329 / 0%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0628

Standard Deviation	0.6259
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2.4. Mapping Quality

Mean Mapping Quality	44.35
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2.5. Mismatches and indels

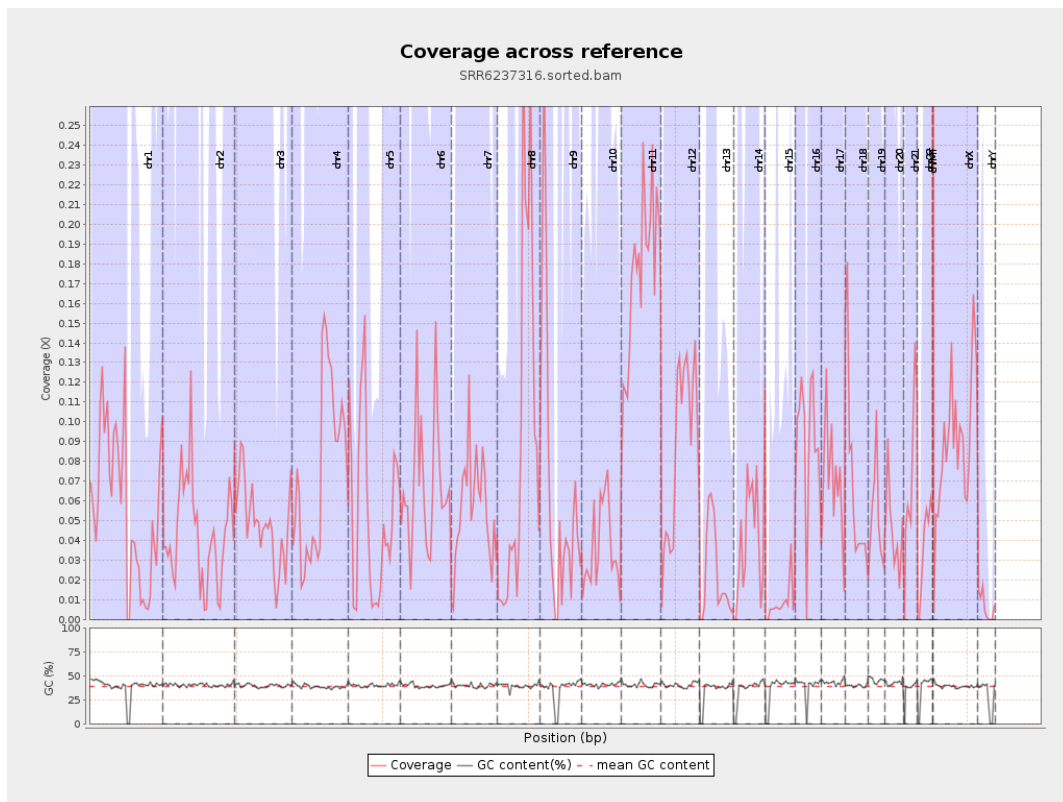
General error rate	0.8%
Mismatches	1,524,521
Insertions	14,780
Mapped reads with at least one insertion	0.51%
Deletions	49,838
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.39%

2.6. Chromosome stats

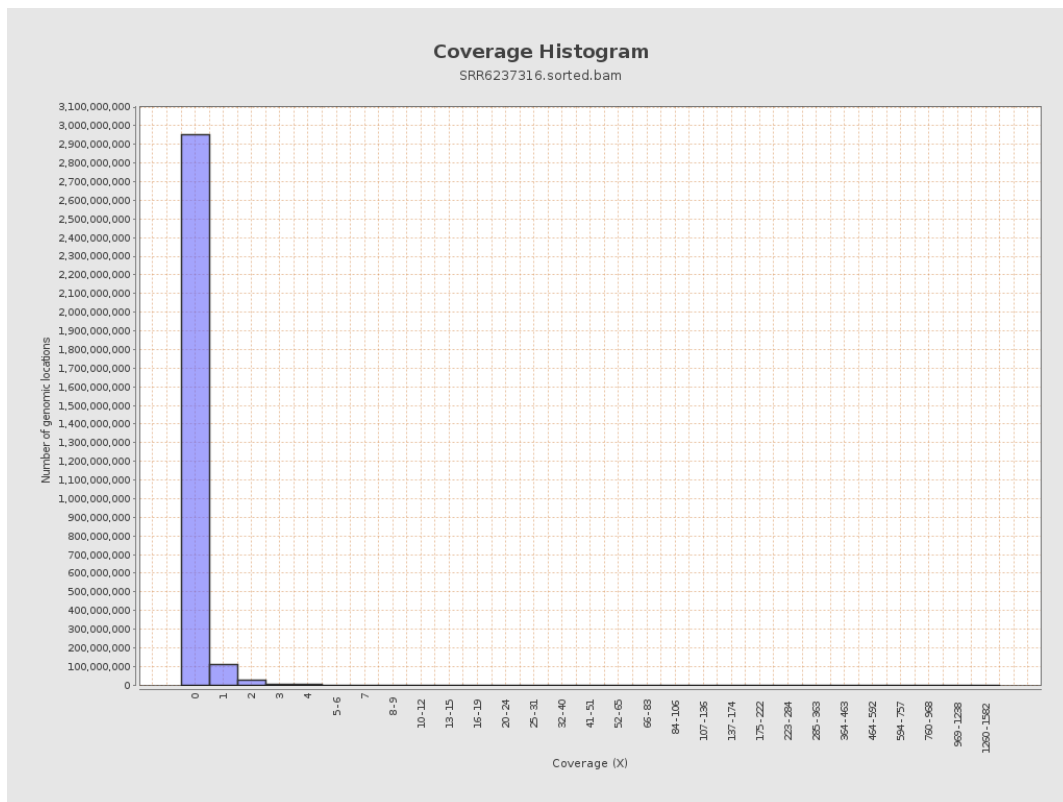
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14391145	0.0577	1.0459
chr2	243199373	10557913	0.0434	0.6246
chr3	198022430	9767340	0.0493	0.2829
chr4	191154276	14428754	0.0755	0.3667
chr5	180915260	10007006	0.0553	0.3091
chr6	171115067	11516406	0.0673	0.743
chr7	159138663	8805619	0.0553	0.9454

chr8	146364022	13084961	0.0894	0.802
chr9	141213431	9229280	0.0654	0.4571
chr10	135534747	4904824	0.0362	0.3724
chr11	135006516	23588620	0.1747	1.2111
chr12	133851895	11650208	0.087	0.3794
chr13	115169878	2608185	0.0226	0.1925
chr14	107349540	4132173	0.0385	0.2602
chr15	102531392	816521	0.008	0.1447
chr16	90354753	8002612	0.0886	0.3933
chr17	81195210	5810545	0.0716	0.6691
chr18	78077248	5306918	0.068	0.5834
chr19	59128983	3122971	0.0528	0.8609
chr20	63025520	2851107	0.0452	0.2807
chr21	48129895	3566531	0.0741	0.3705
chr22	51304566	1893936	0.0369	0.237
chrMT	16571	103874	6.2684	4.7664
chrX	155270560	13820829	0.089	0.4809
chrY	59373566	380649	0.0064	0.1264

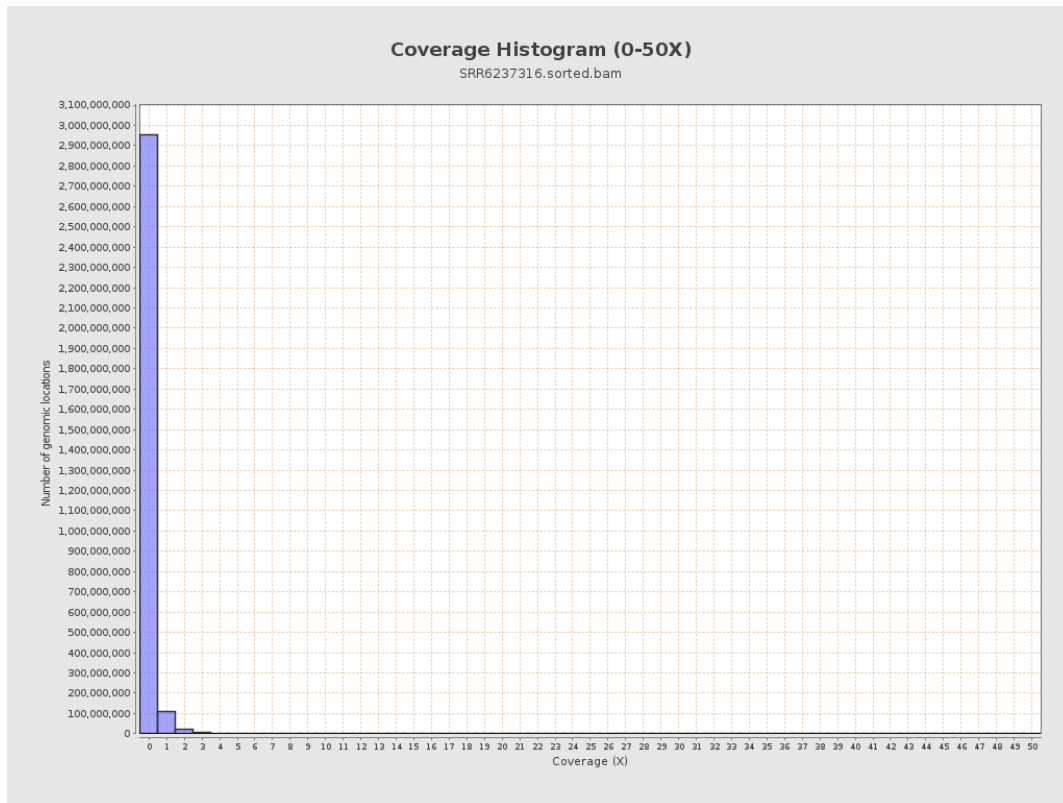
3. Results : Coverage across reference



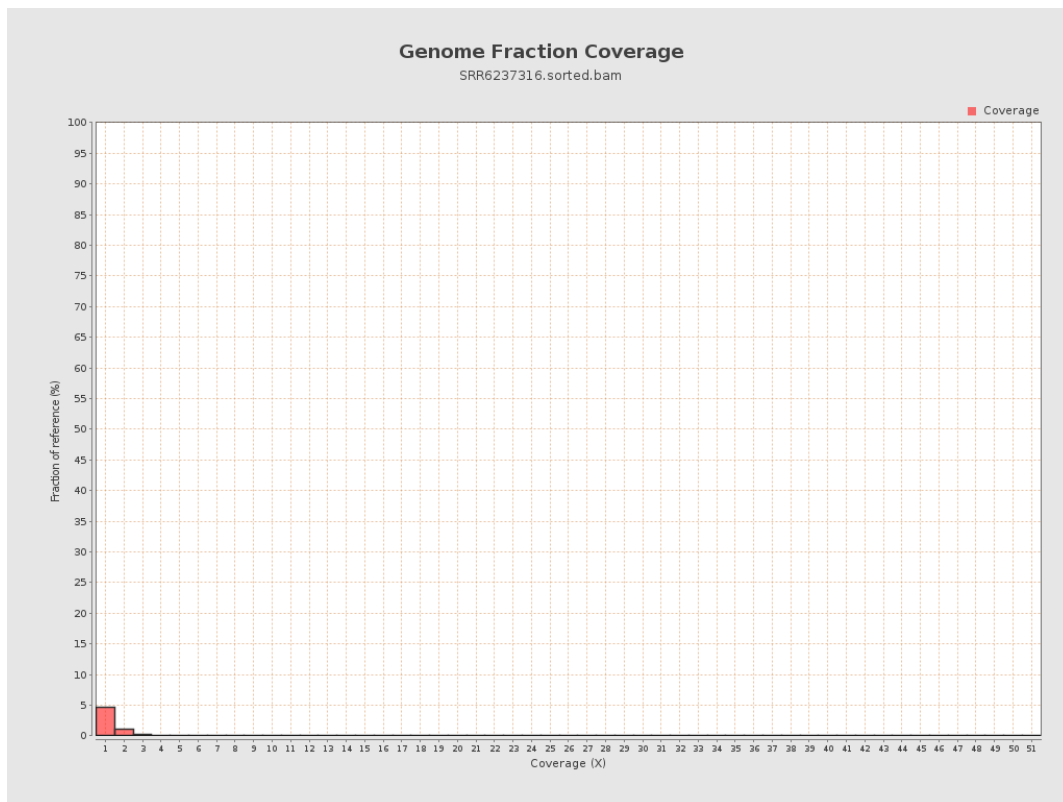
4. Results : Coverage Histogram



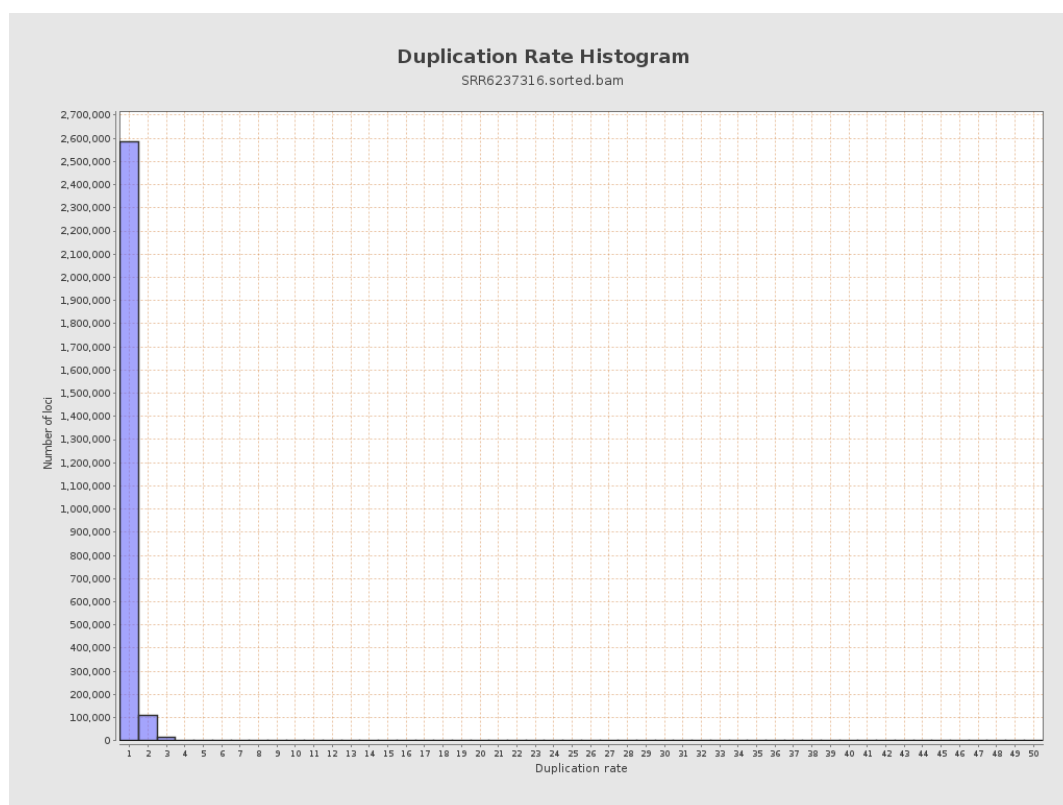
5. Results : Coverage Histogram (0-50X)



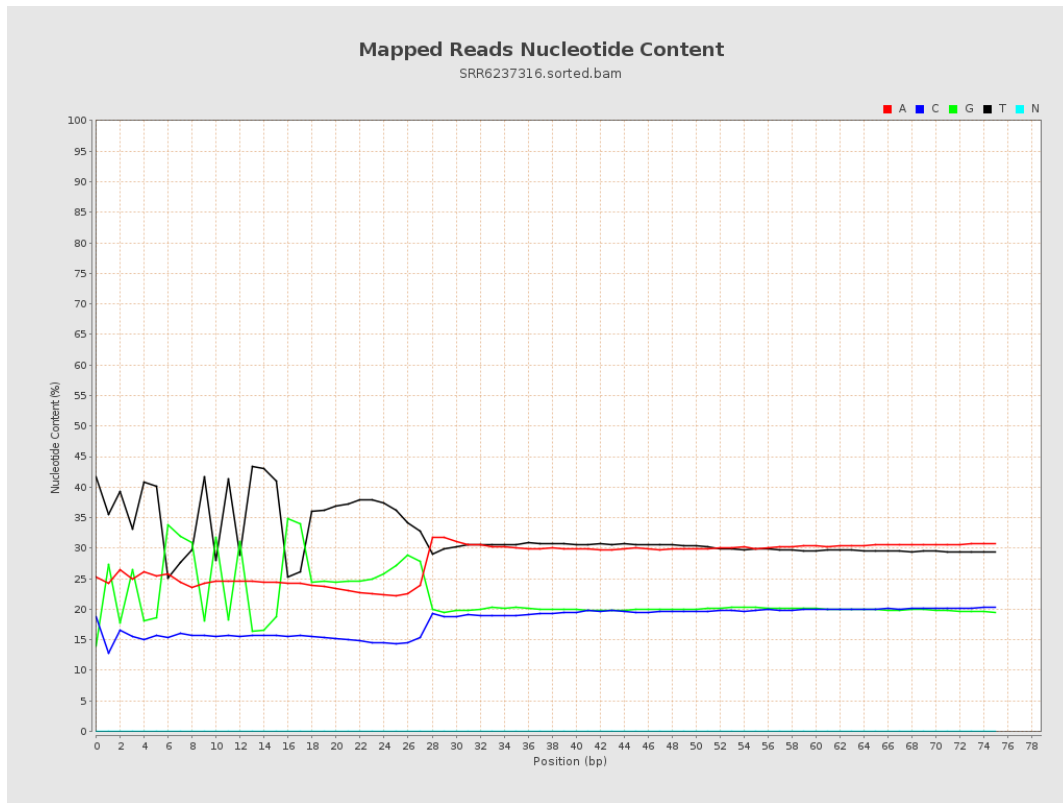
6. Results : Genome Fraction Coverage



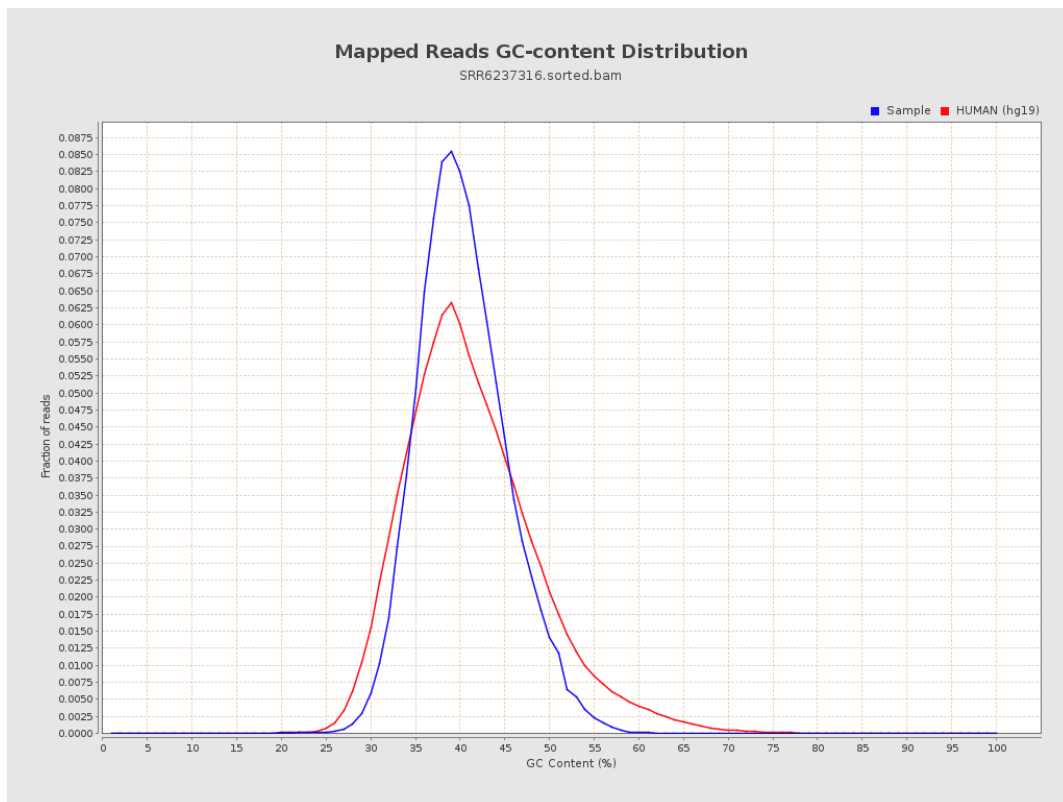
7. Results : Duplication Rate Histogram



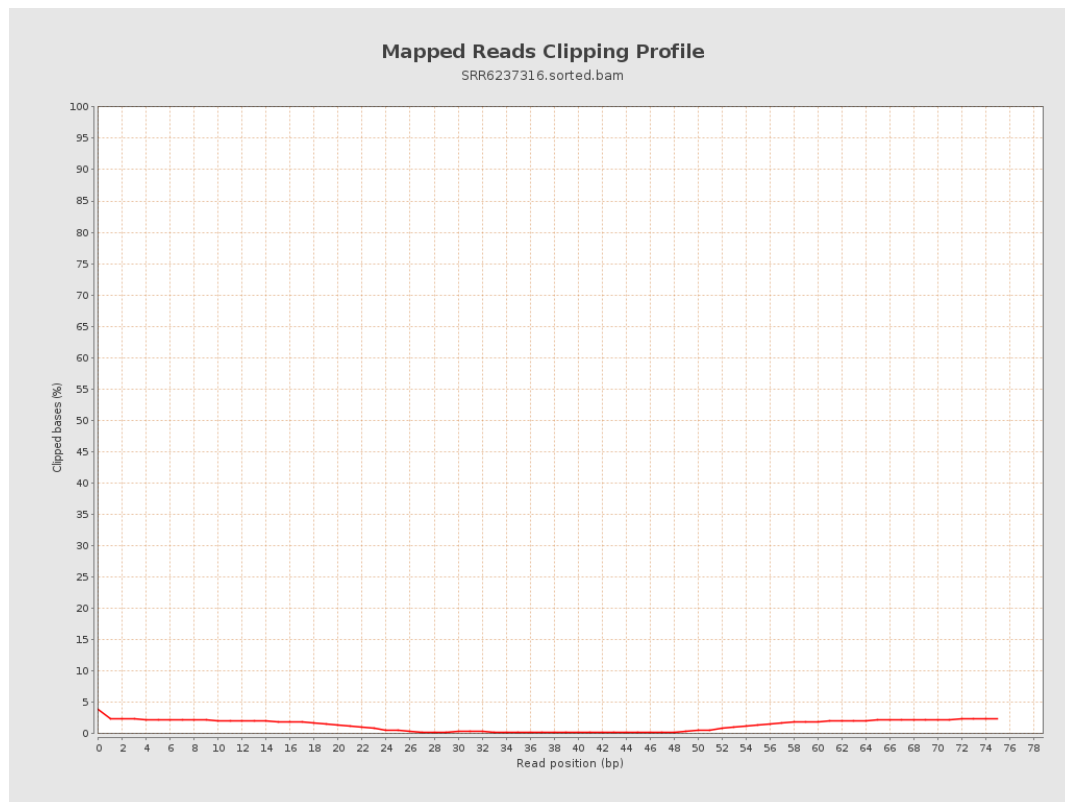
8. Results : Mapped Reads Nucleotide Content



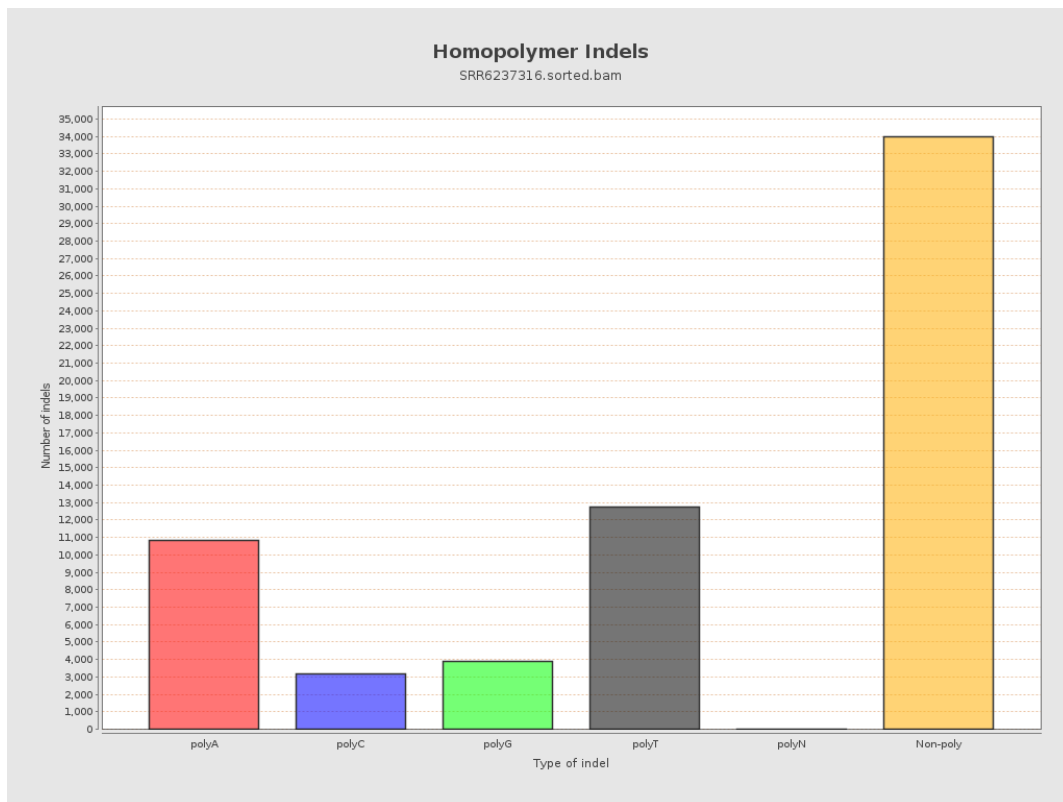
9. Results : Mapped Reads GC-content Distribution



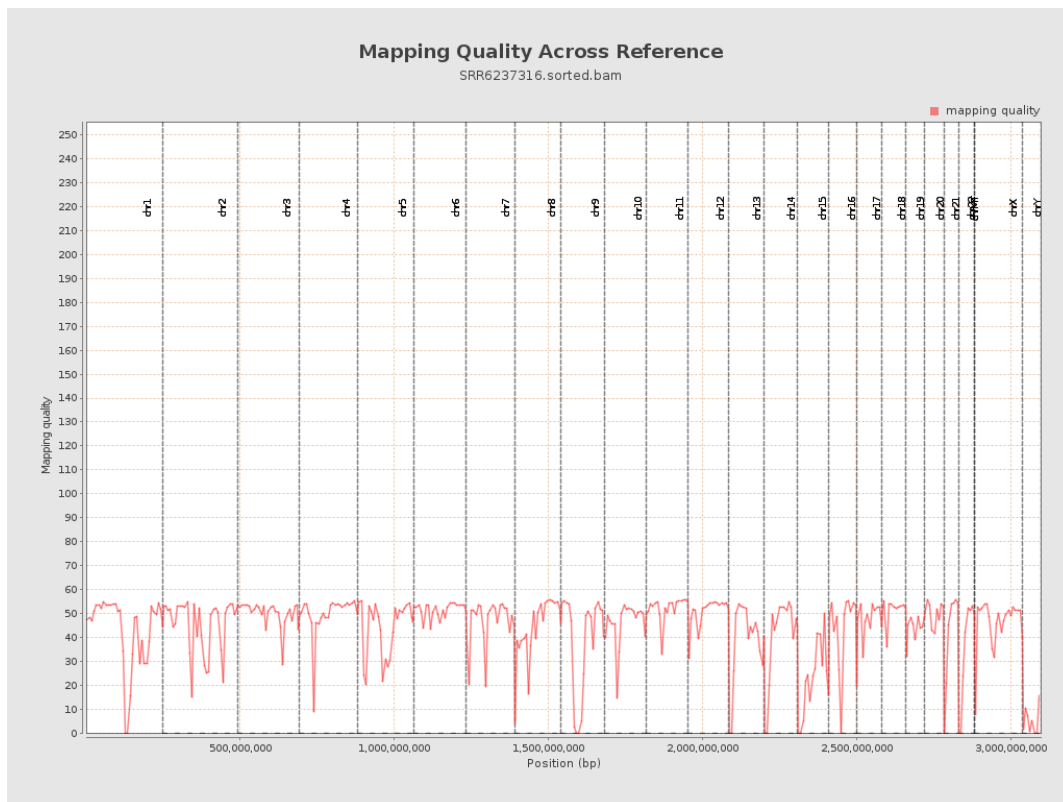
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

