

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:58:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237812.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_SRR6237812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:58:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,800,043
Mapped reads	2,270,694 / 59.75%
Unmapped reads	1,529,349 / 40.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,899 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	338,384 / 8.9%
Duplication rate	11.56%
Clipped reads	1,569,206 / 41.29%

2.2. ACGT Content

Number/percentage of A's	36,983,828 / 27.31%
Number/percentage of C's	26,912,982 / 19.87%
Number/percentage of T's	41,112,241 / 30.35%
Number/percentage of G's	30,315,220 / 22.38%
Number/percentage of N's	117,832 / 0.09%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.4663
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.53
----------------------	-------

2.5. Mismatches and indels

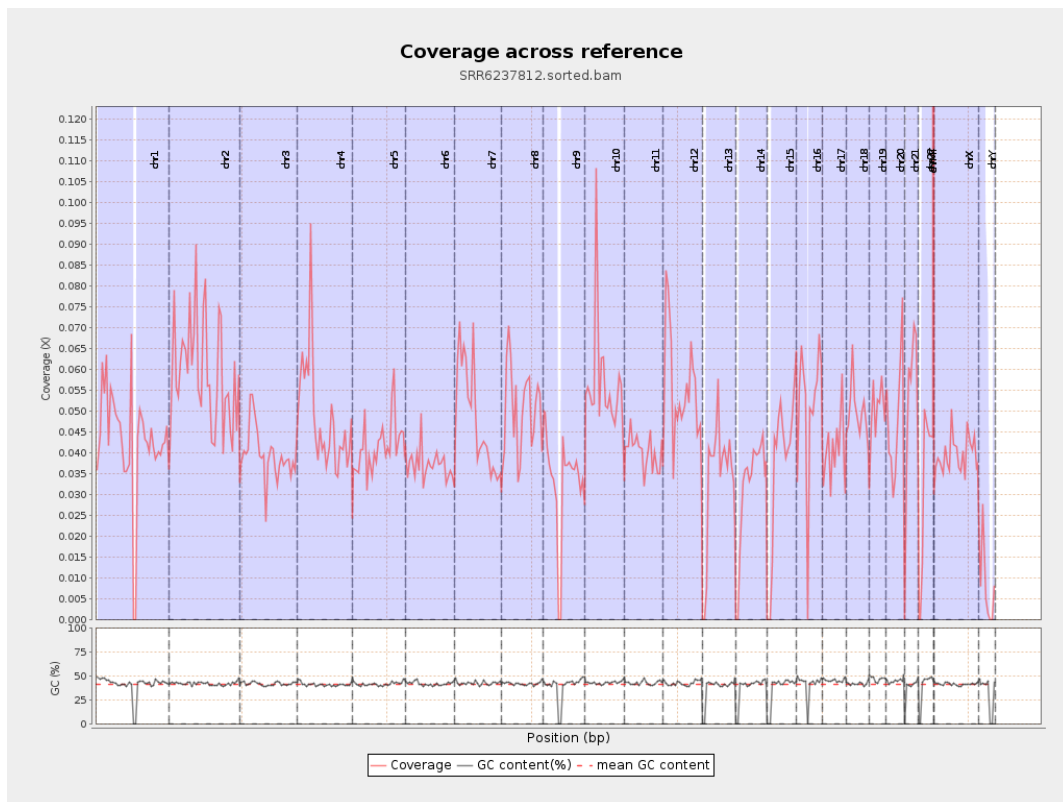
General error rate	0.92%
Mismatches	1,224,842
Insertions	10,400
Mapped reads with at least one insertion	0.45%
Deletions	34,803
Mapped reads with at least one deletion	1.51%
Homopolymer indels	45.7%

2.6. Chromosome stats

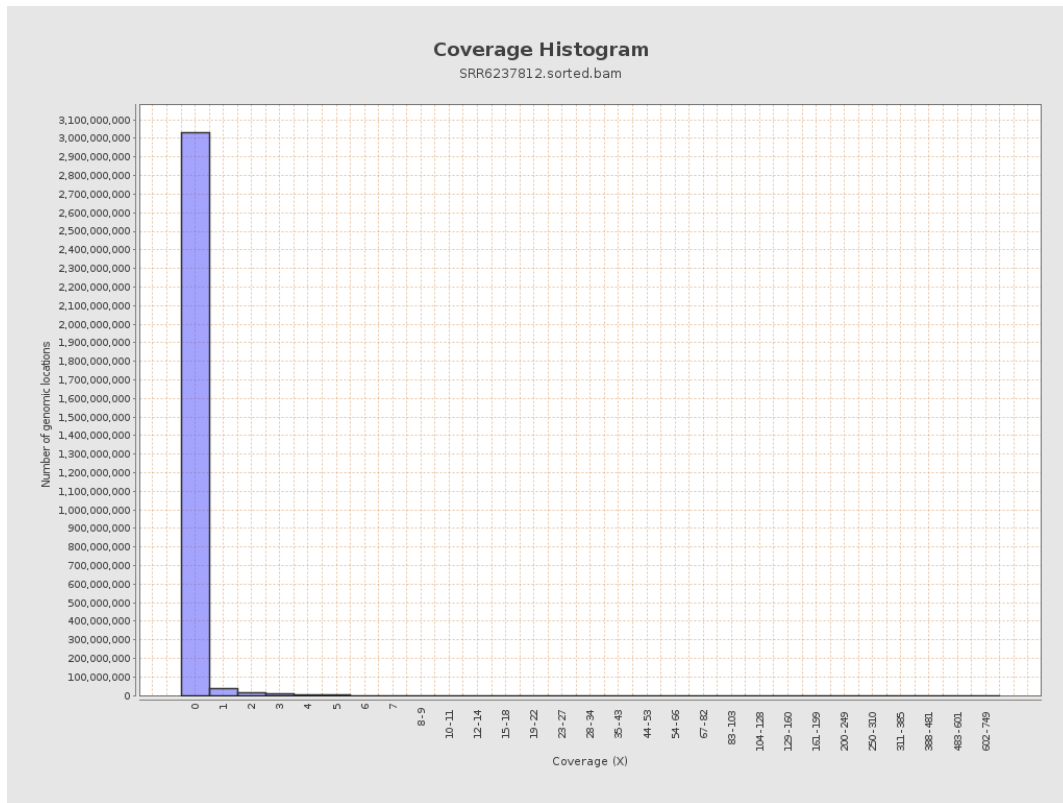
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10701940	0.0429	0.7054
chr2	243199373	14431652	0.0593	0.5639
chr3	198022430	7805061	0.0394	0.3633
chr4	191154276	9195063	0.0481	0.4221
chr5	180915260	7538573	0.0417	0.365
chr6	171115067	6335890	0.037	0.37
chr7	159138663	7680282	0.0483	0.5612

chr8	146364022	7319101	0.05	0.4705
chr9	141213431	4628365	0.0328	0.3718
chr10	135534747	7639455	0.0564	0.6148
chr11	135006516	5416731	0.0401	0.4041
chr12	133851895	7365833	0.055	0.4306
chr13	115169878	3856198	0.0335	0.3398
chr14	107349540	3367260	0.0314	0.3264
chr15	102531392	3830817	0.0374	0.3476
chr16	90354753	4631300	0.0513	0.4482
chr17	81195210	3238769	0.0399	0.39
chr18	78077248	3911146	0.0501	0.6179
chr19	59128983	2969873	0.0502	0.5479
chr20	63025520	2954473	0.0469	0.4022
chr21	48129895	2453228	0.051	0.4288
chr22	51304566	1616718	0.0315	0.3213
chrMT	16571	61186	3.6924	4.3248
chrX	155270560	6086356	0.0392	0.3679
chrY	59373566	463506	0.0078	0.2065

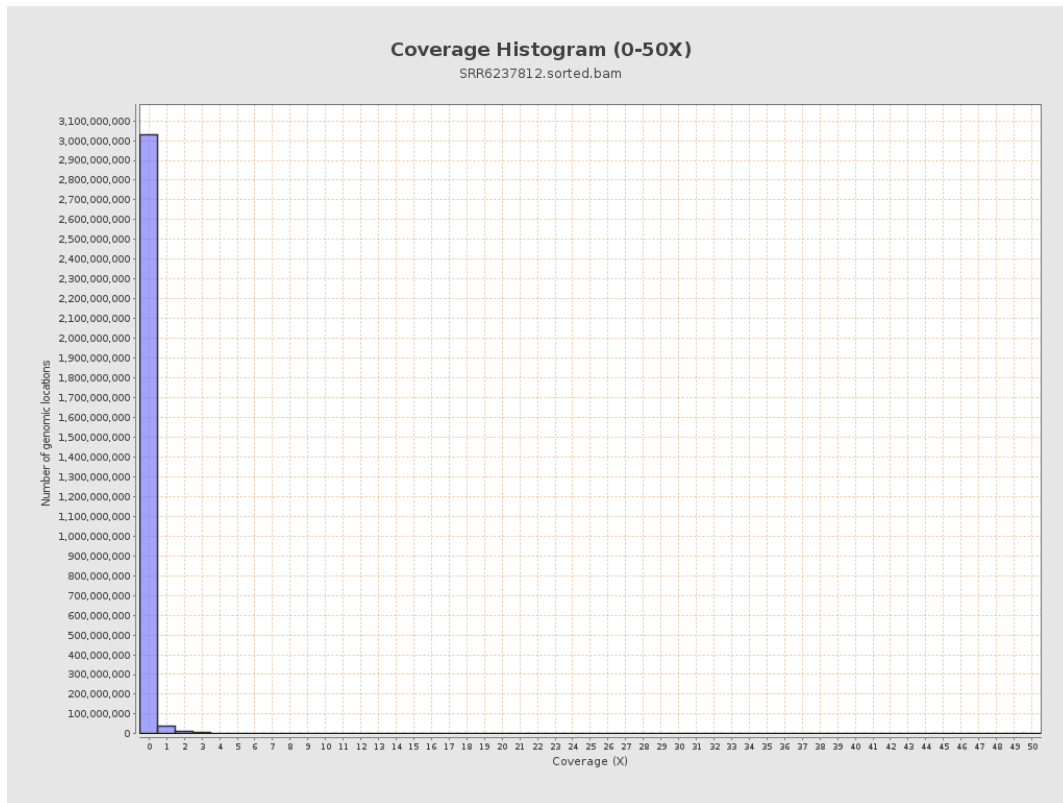
3. Results : Coverage across reference



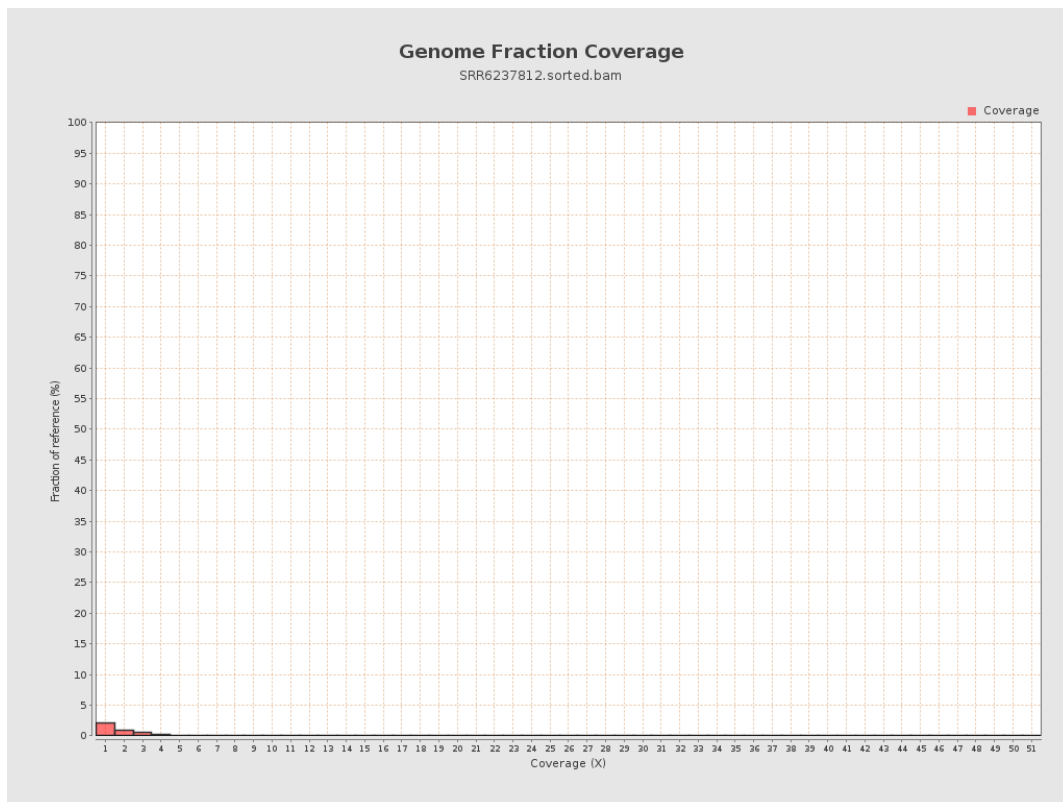
4. Results : Coverage Histogram



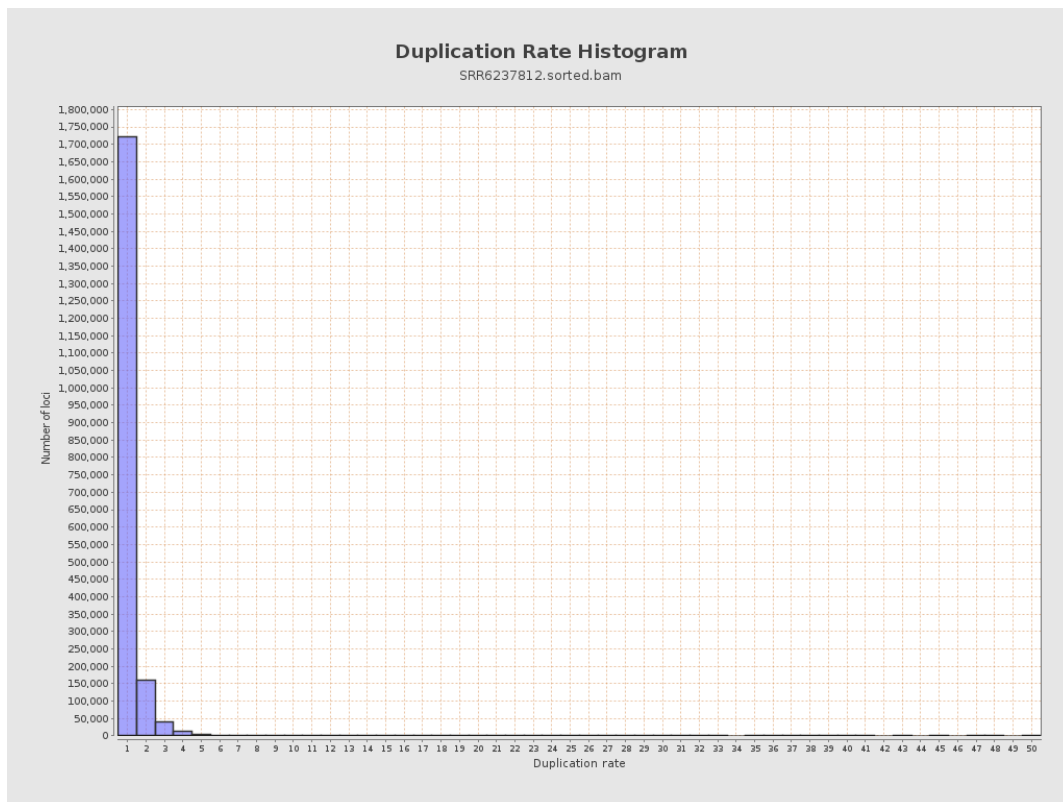
5. Results : Coverage Histogram (0-50X)



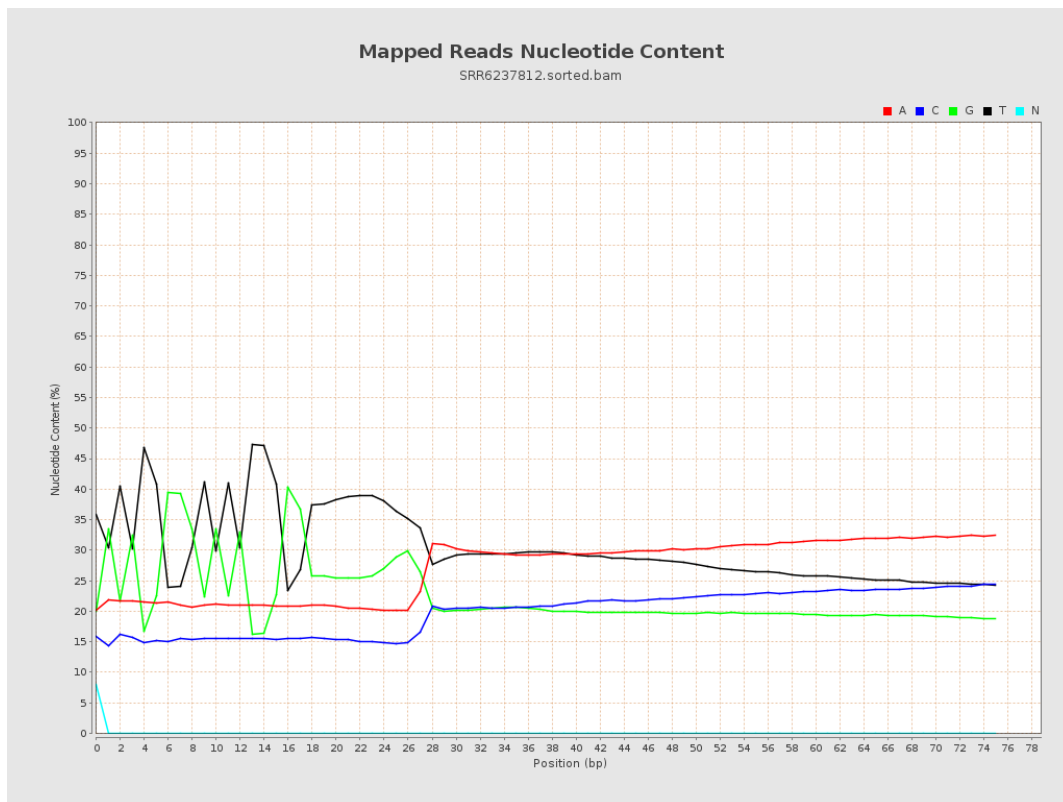
6. Results : Genome Fraction Coverage



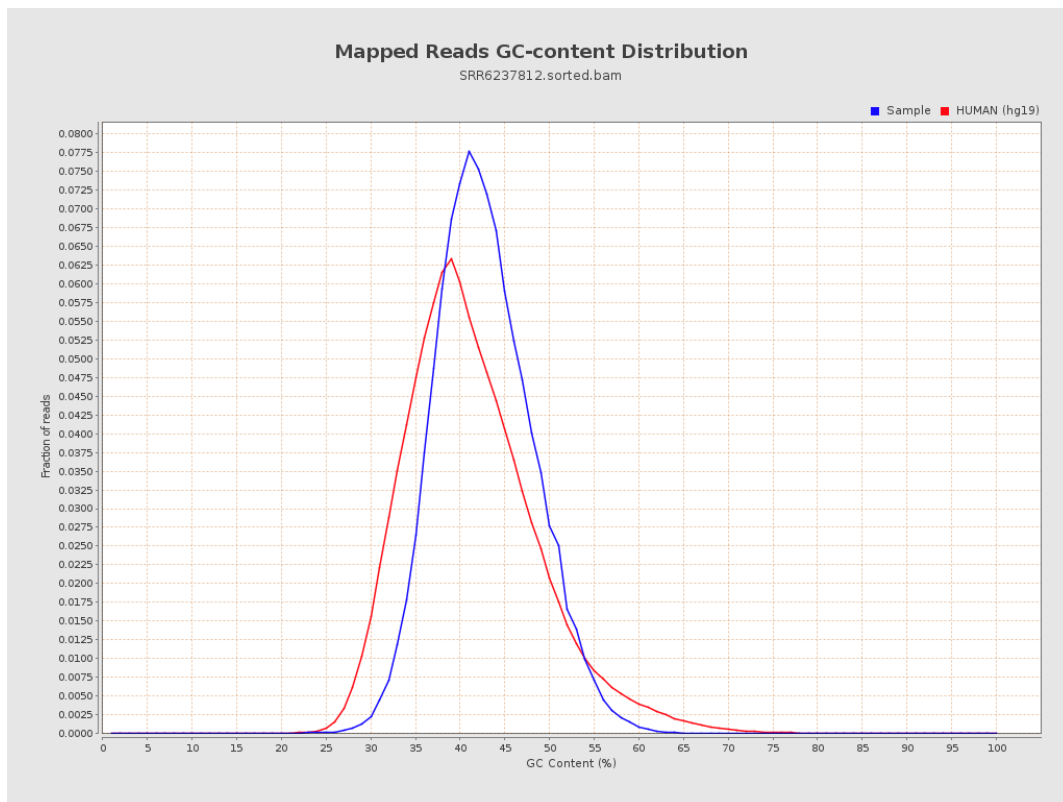
7. Results : Duplication Rate Histogram



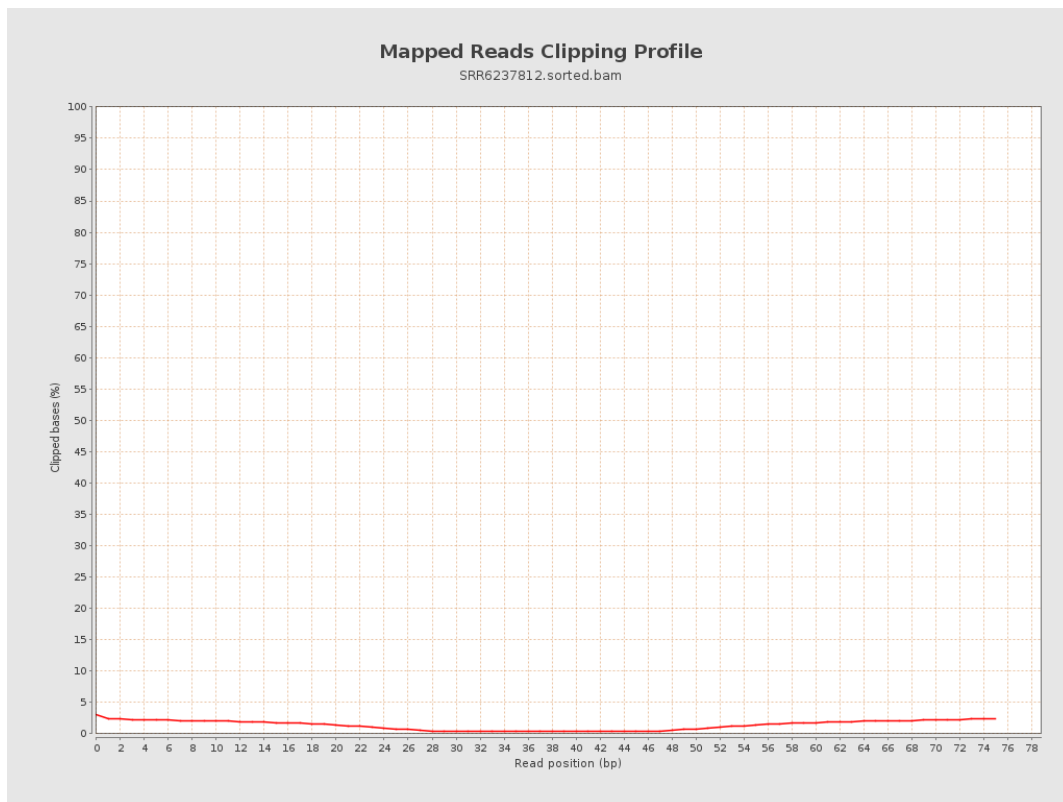
8. Results : Mapped Reads Nucleotide Content



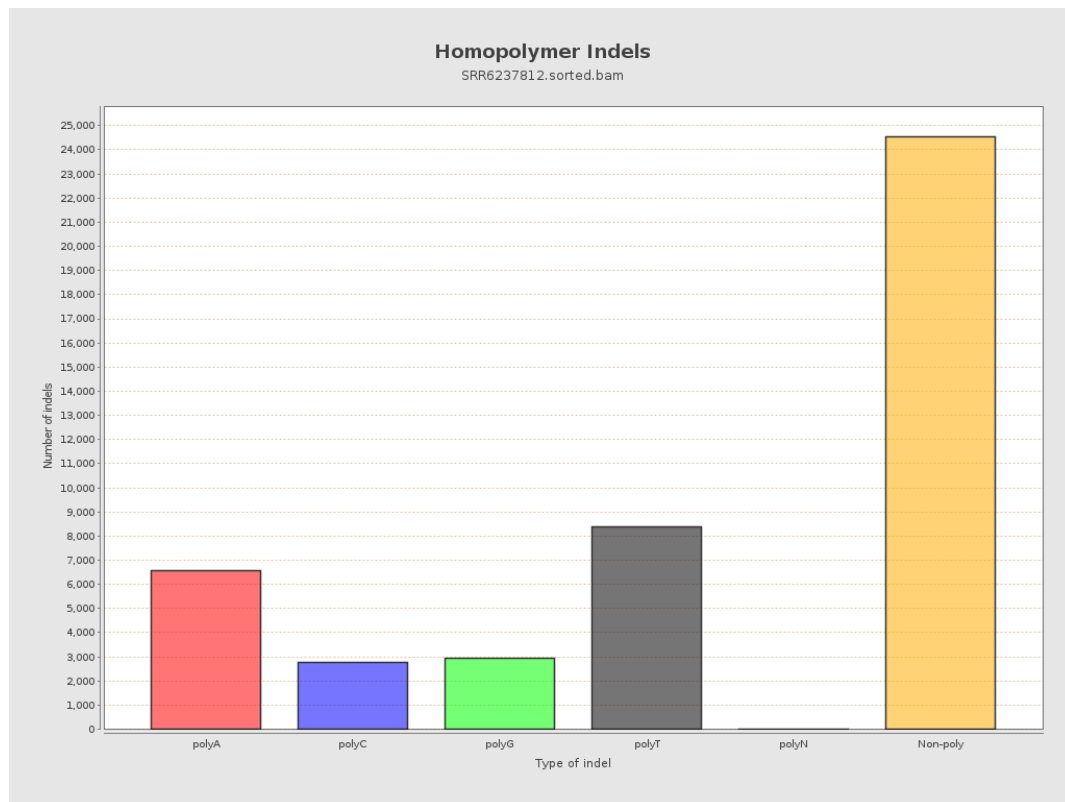
9. Results : Mapped Reads GC-content Distribution



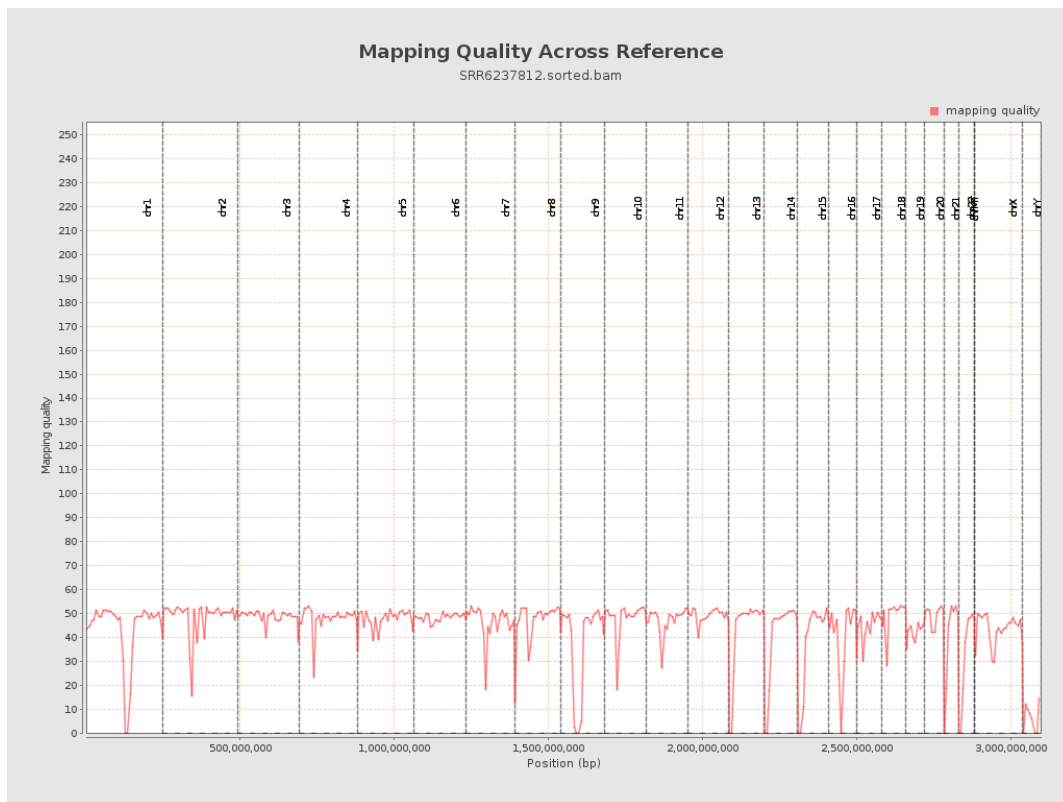
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

