

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:50:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237312.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_SRR6237312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:50:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,040,865
Mapped reads	923,088 / 88.68%
Unmapped reads	117,777 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,059 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	25,860 / 2.48%
Duplication rate	1.94%
Clipped reads	287,274 / 27.6%

2.2. ACGT Content

Number/percentage of A's	18,845,845 / 29.17%
Number/percentage of C's	11,912,689 / 18.44%
Number/percentage of T's	20,448,004 / 31.64%
Number/percentage of G's	13,410,387 / 20.75%
Number/percentage of N's	1,026 / 0%
GC Percentage	39.19%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.2425
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2.4. Mapping Quality

Mean Mapping Quality	46.47
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2.5. Mismatches and indels

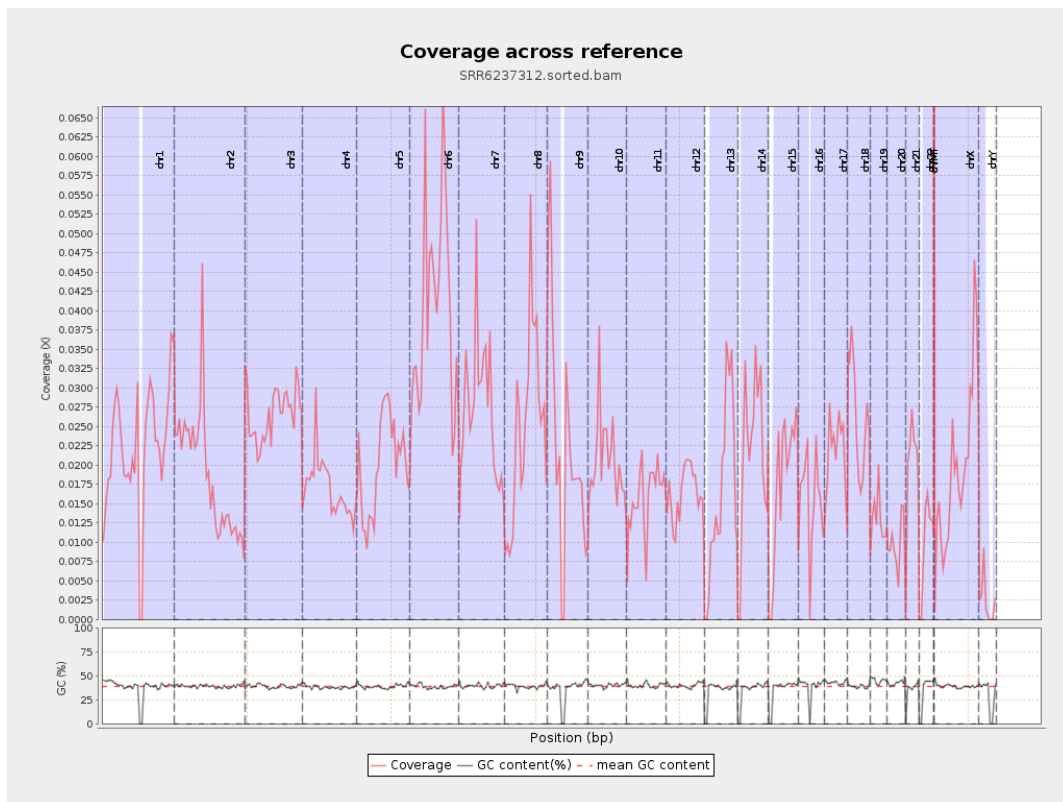
General error rate	0.87%
Mismatches	549,865
Insertions	5,735
Mapped reads with at least one insertion	0.62%
Deletions	17,405
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.84%

2.6. Chromosome stats

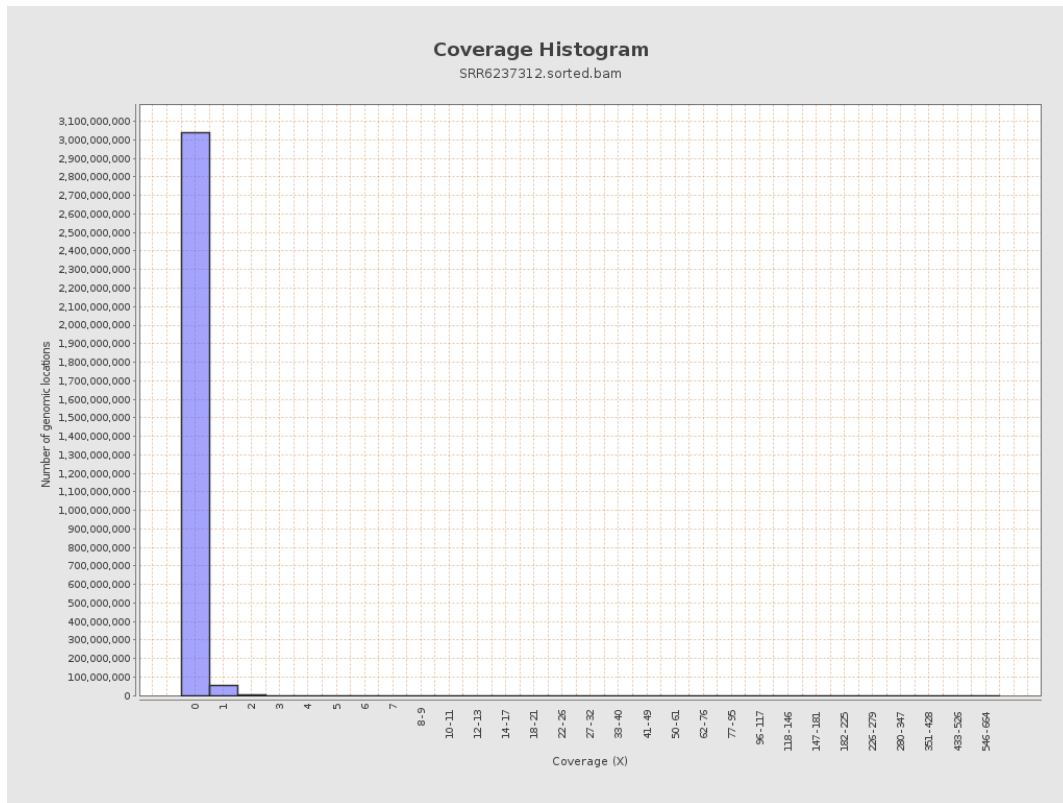
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5547409	0.0223	0.2868
chr2	243199373	4514499	0.0186	0.2495
chr3	198022430	5266546	0.0266	0.1734
chr4	191154276	3237705	0.0169	0.1518
chr5	180915260	3652047	0.0202	0.1522
chr6	171115067	6870295	0.0402	0.2939
chr7	159138663	4296045	0.027	0.3832

chr8	146364022	3691439	0.0252	0.4645
chr9	141213431	3222456	0.0228	0.2631
chr10	135534747	2786510	0.0206	0.2116
chr11	135006516	2142671	0.0159	0.193
chr12	133851895	2177779	0.0163	0.1404
chr13	115169878	1884853	0.0164	0.1355
chr14	107349540	2265650	0.0211	0.1686
chr15	102531392	1813439	0.0177	0.1416
chr16	90354753	1374545	0.0152	0.159
chr17	81195210	1757274	0.0216	0.1871
chr18	78077248	2024736	0.0259	0.4536
chr19	59128983	783388	0.0132	0.2192
chr20	63025520	622879	0.0099	0.1108
chr21	48129895	980861	0.0204	0.1669
chr22	51304566	519821	0.0101	0.1061
chrMT	16571	5429	0.3276	0.5911
chrX	155270560	3063533	0.0197	0.1644
chrY	59373566	145593	0.0025	0.0825

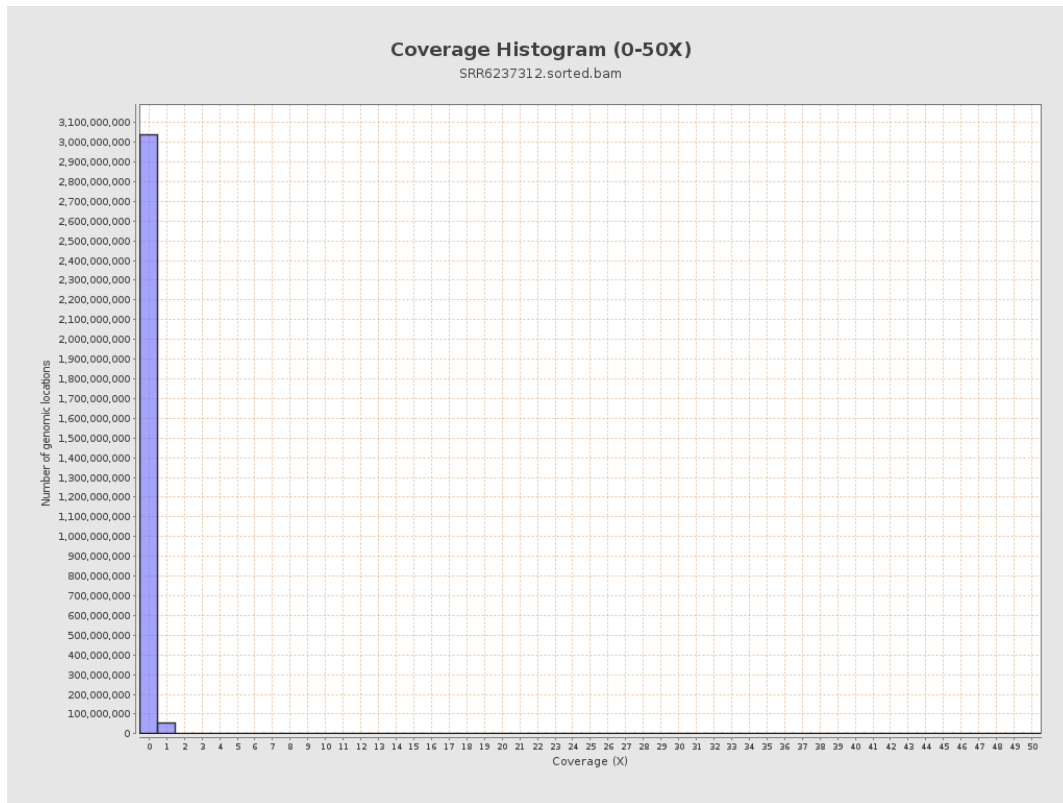
3. Results : Coverage across reference



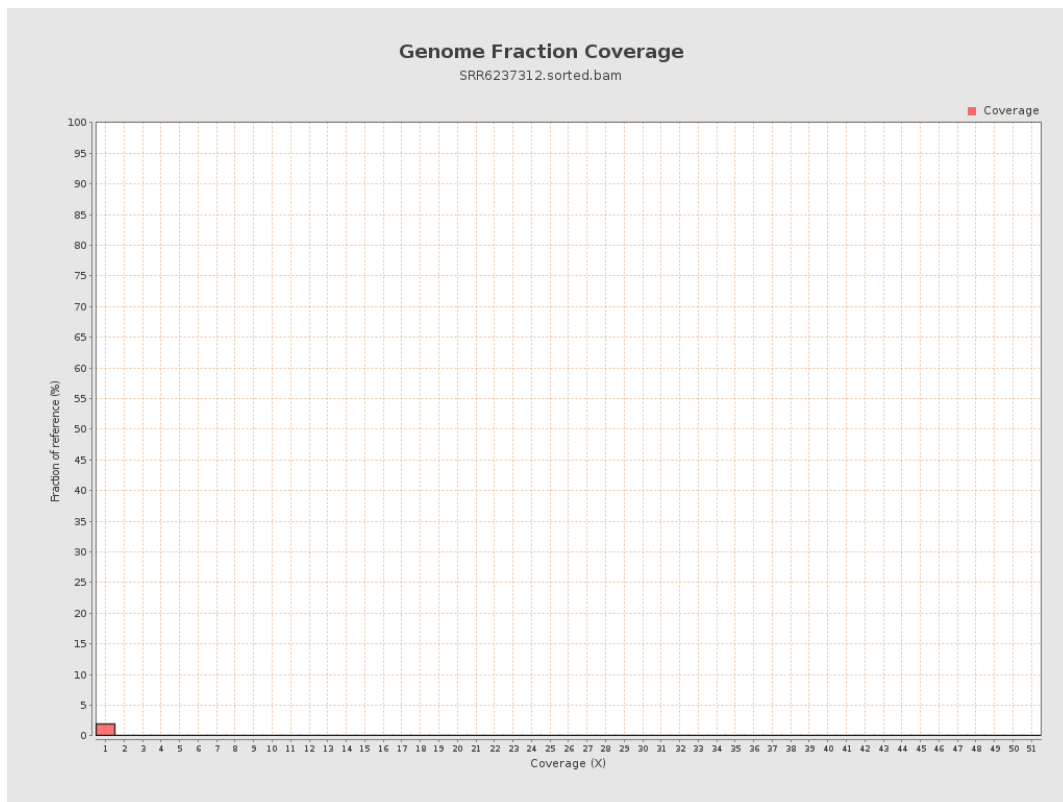
4. Results : Coverage Histogram



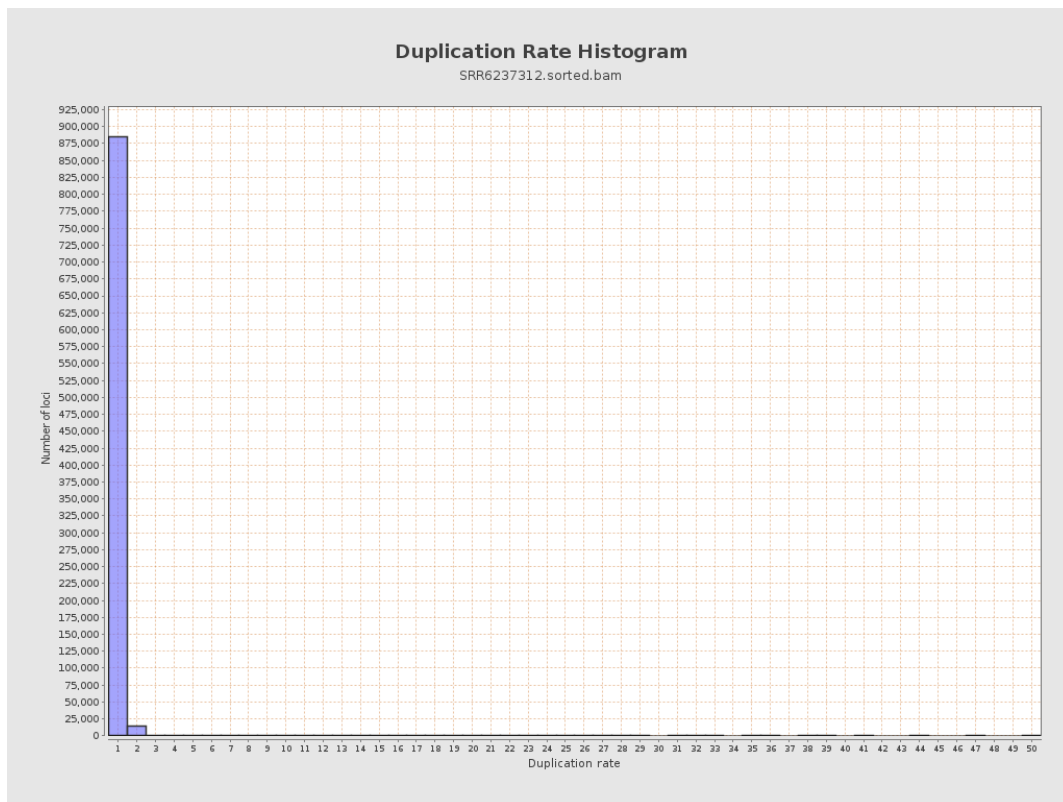
5. Results : Coverage Histogram (0-50X)



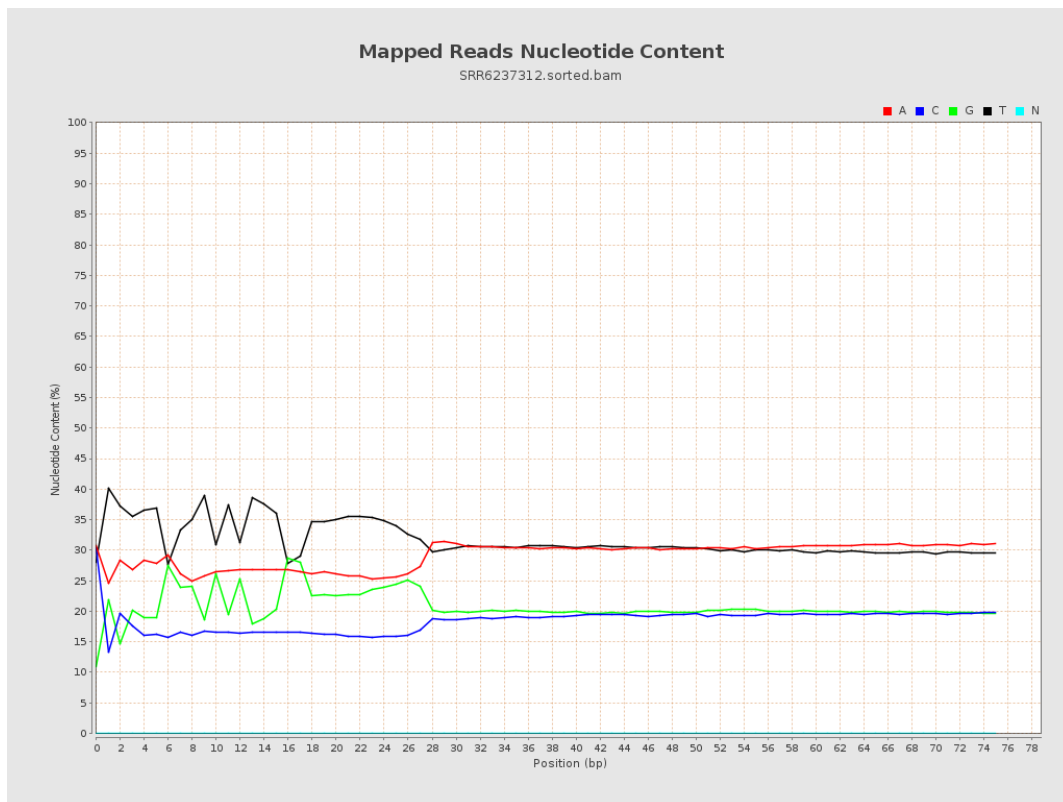
6. Results : Genome Fraction Coverage



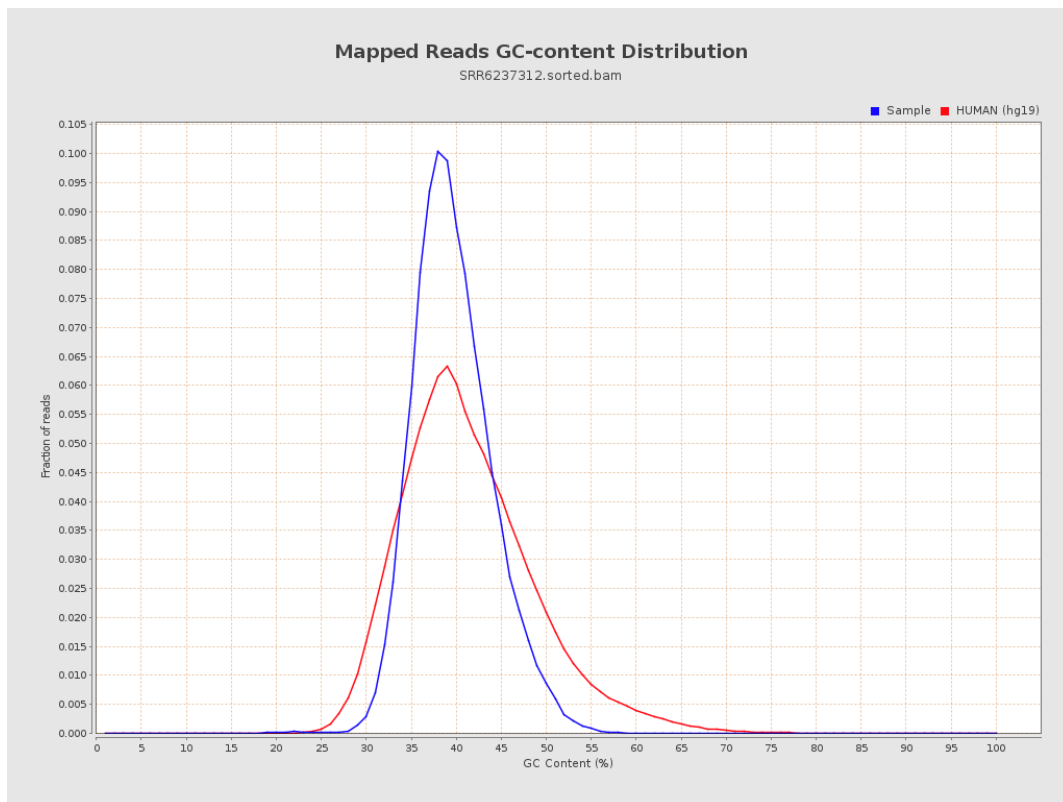
7. Results : Duplication Rate Histogram



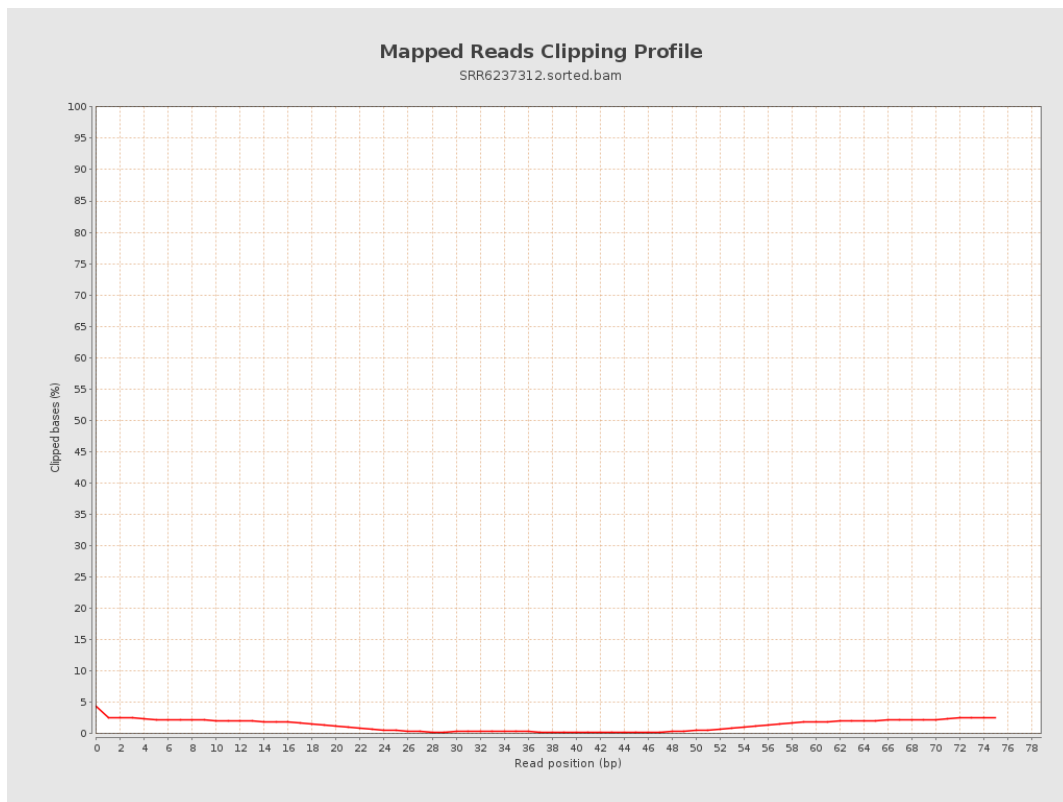
8. Results : Mapped Reads Nucleotide Content



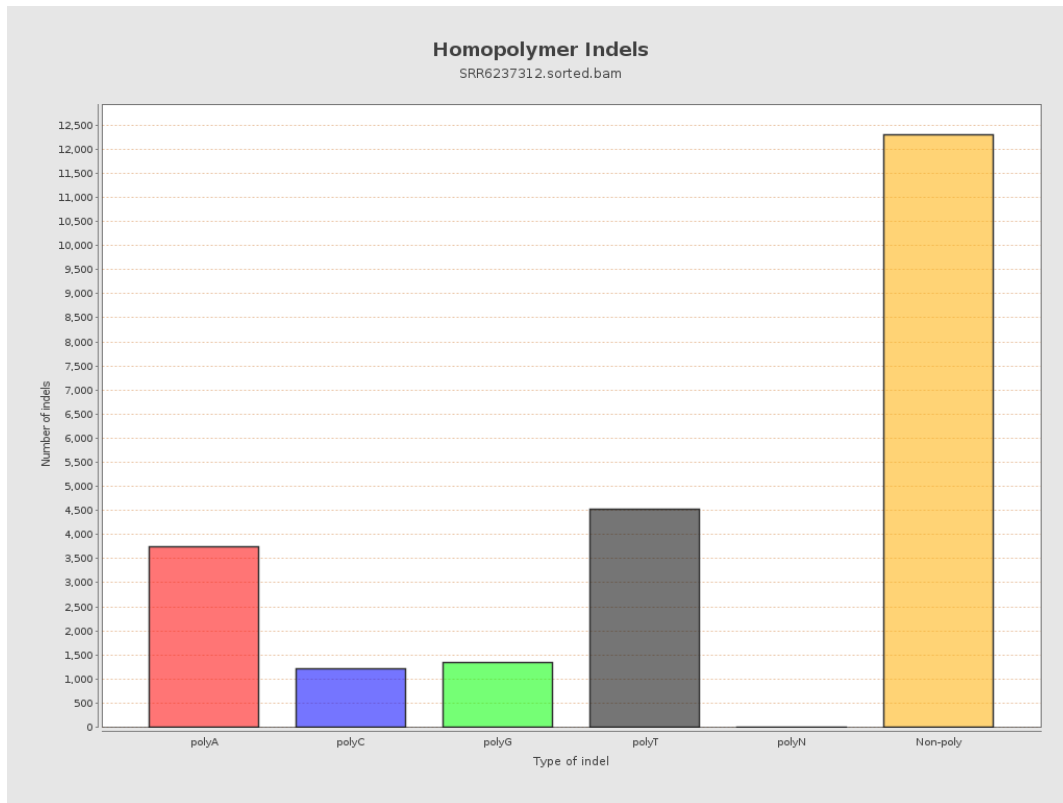
9. Results : Mapped Reads GC-content Distribution



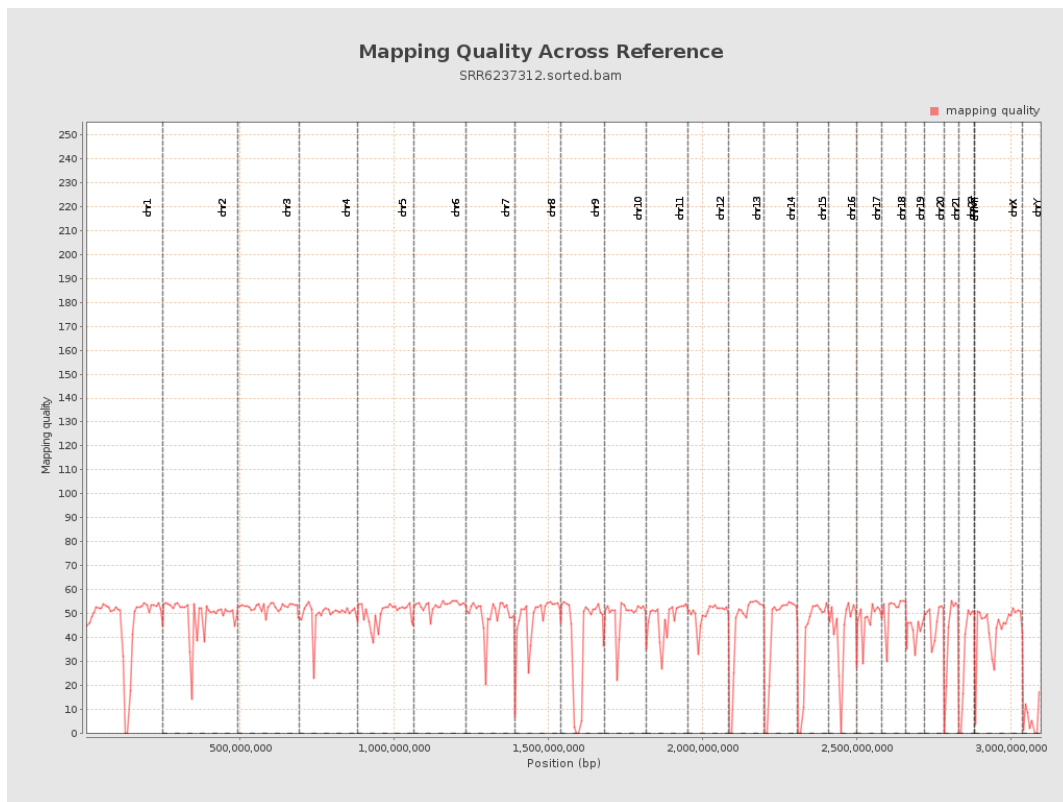
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

