

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 07:21:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524937.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_SRR10524937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524937.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 07:21:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	413,689
Mapped reads	385,353 / 93.15%
Unmapped reads	28,336 / 6.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,597 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	10,004 / 2.42%
Duplication rate	2.17%
Clipped reads	386,247 / 93.37%

2.2. ACGT Content

Number/percentage of A's	5,641,935 / 24.71%
Number/percentage of C's	4,427,611 / 19.39%
Number/percentage of T's	7,173,560 / 31.41%
Number/percentage of G's	5,593,808 / 24.49%
Number/percentage of N's	183 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0074

Standard Deviation	0.0995
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2.4. Mapping Quality

Mean Mapping Quality	45.41
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2.5. Mismatches and indels

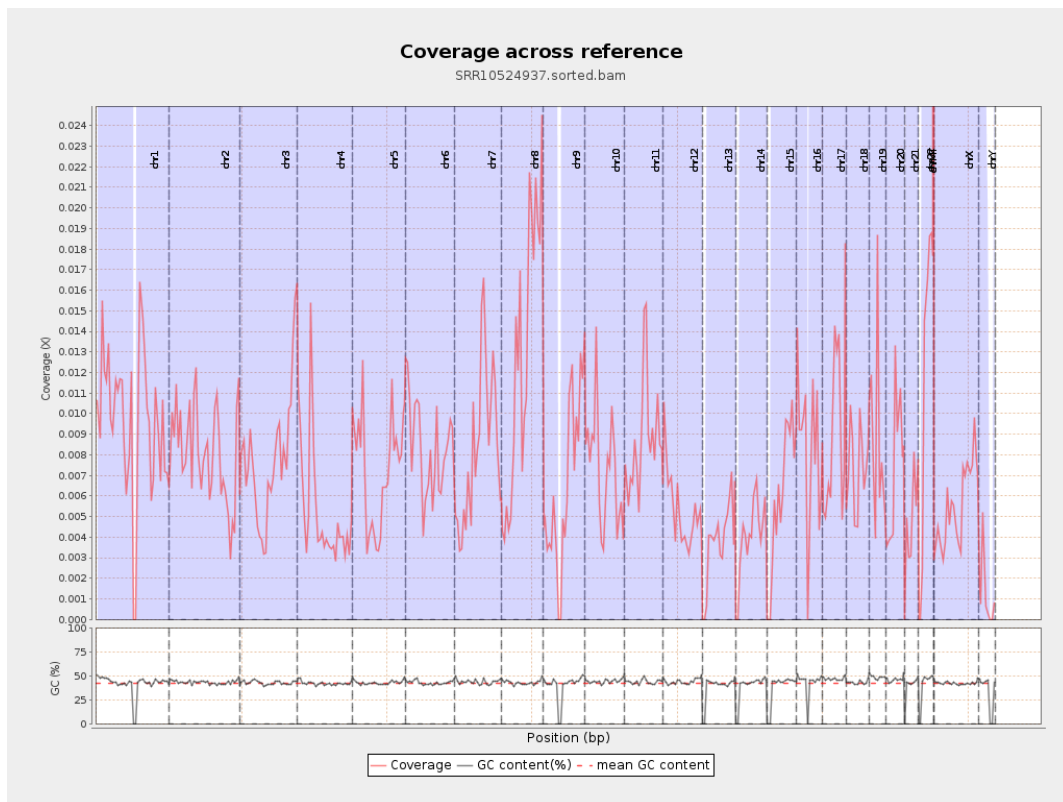
General error rate	0.5%
Mismatches	110,607
Insertions	1,563
Mapped reads with at least one insertion	0.4%
Deletions	4,187
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.81%

2.6. Chromosome stats

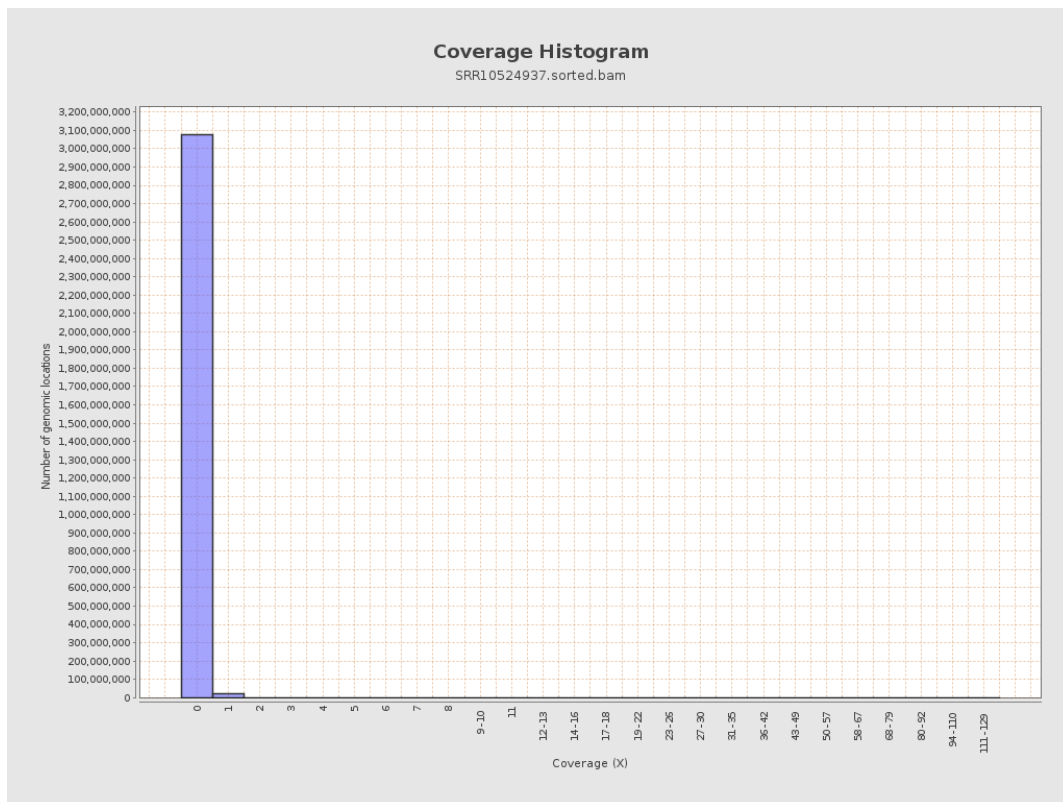
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2394802	0.0096	0.133
chr2	243199373	1971714	0.0081	0.1141
chr3	198022430	1532552	0.0077	0.0921
chr4	191154276	988728	0.0052	0.086
chr5	180915260	1304252	0.0072	0.0891
chr6	171115067	1429517	0.0084	0.0969
chr7	159138663	1329389	0.0084	0.1048

chr8	146364022	1879050	0.0128	0.1376
chr9	141213431	890800	0.0063	0.087
chr10	135534747	971659	0.0072	0.1072
chr11	135006516	1184968	0.0088	0.1009
chr12	133851895	716239	0.0054	0.077
chr13	115169878	431171	0.0037	0.0641
chr14	107349540	428742	0.004	0.0662
chr15	102531392	620727	0.0061	0.0814
chr16	90354753	728870	0.0081	0.0958
chr17	81195210	741576	0.0091	0.1013
chr18	78077248	583603	0.0075	0.1077
chr19	59128983	508492	0.0086	0.1114
chr20	63025520	462222	0.0073	0.0908
chr21	48129895	229778	0.0048	0.0807
chr22	51304566	585150	0.0114	0.1131
chrMT	16571	5725	0.3455	0.6646
chrX	155270560	856454	0.0055	0.0793
chrY	59373566	68002	0.0011	0.0587

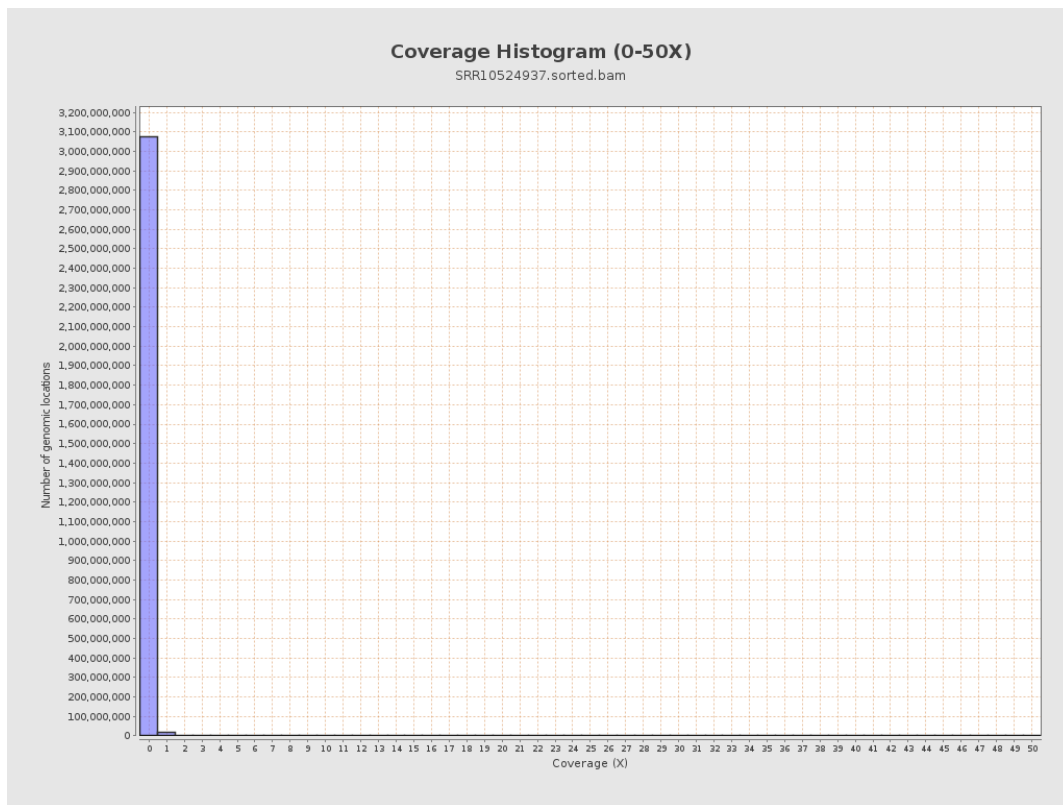
3. Results : Coverage across reference



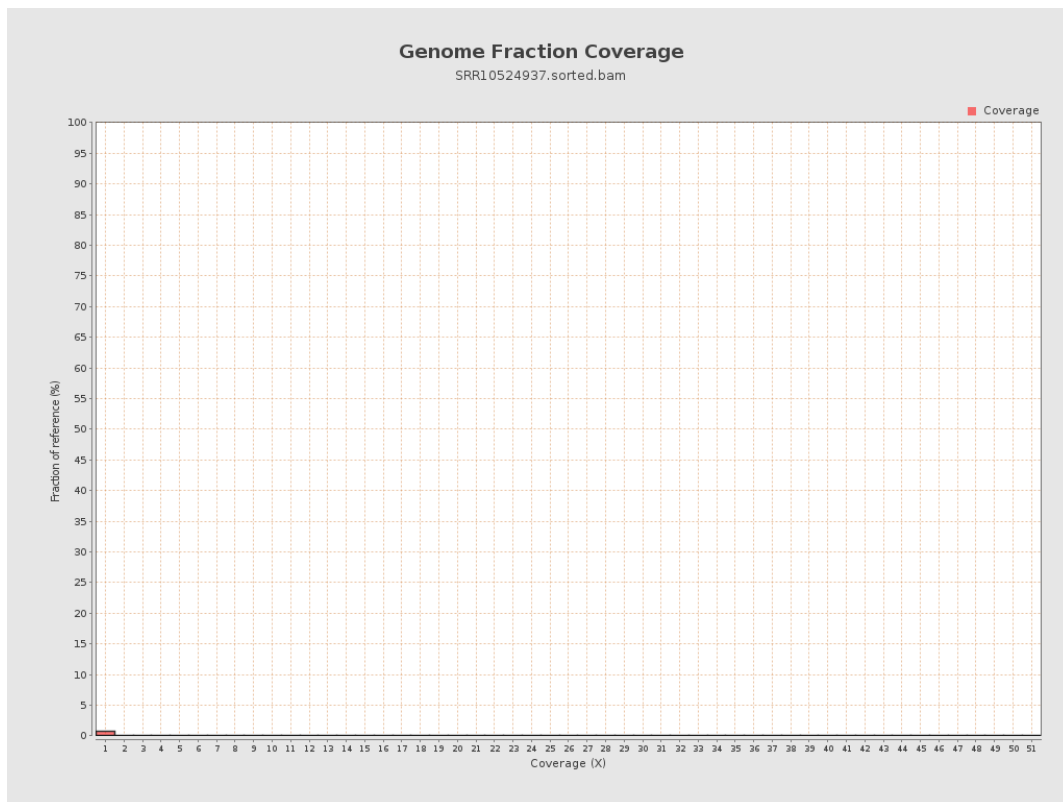
4. Results : Coverage Histogram



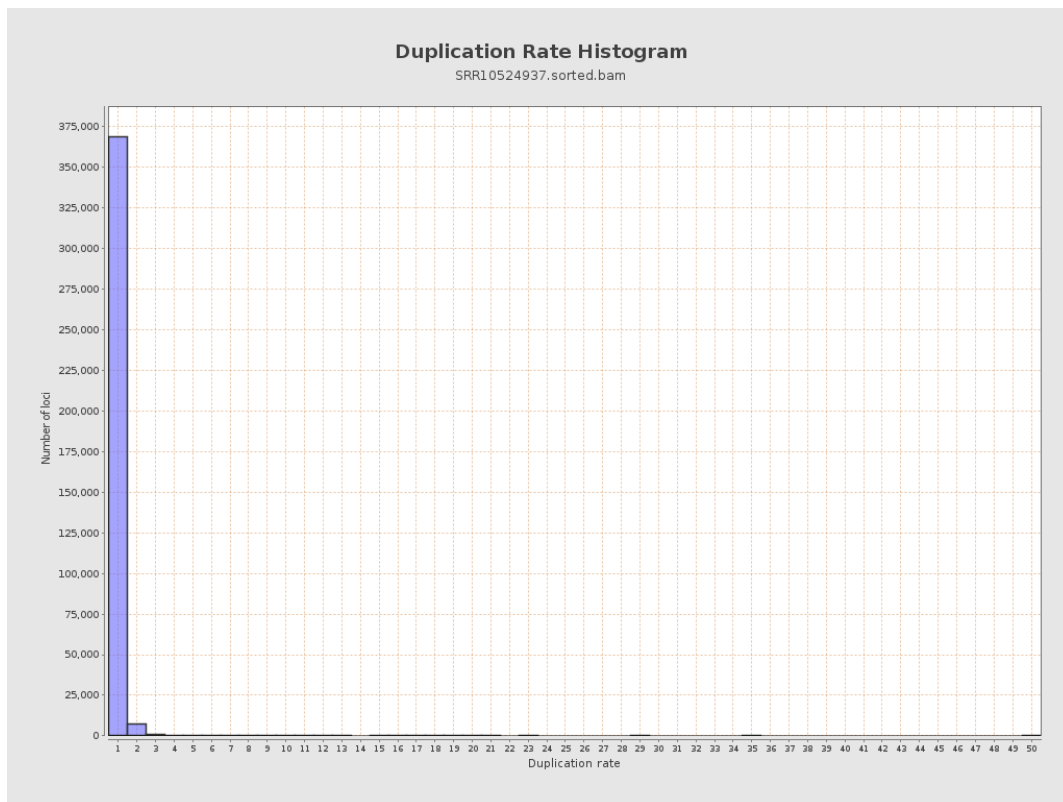
5. Results : Coverage Histogram (0-50X)



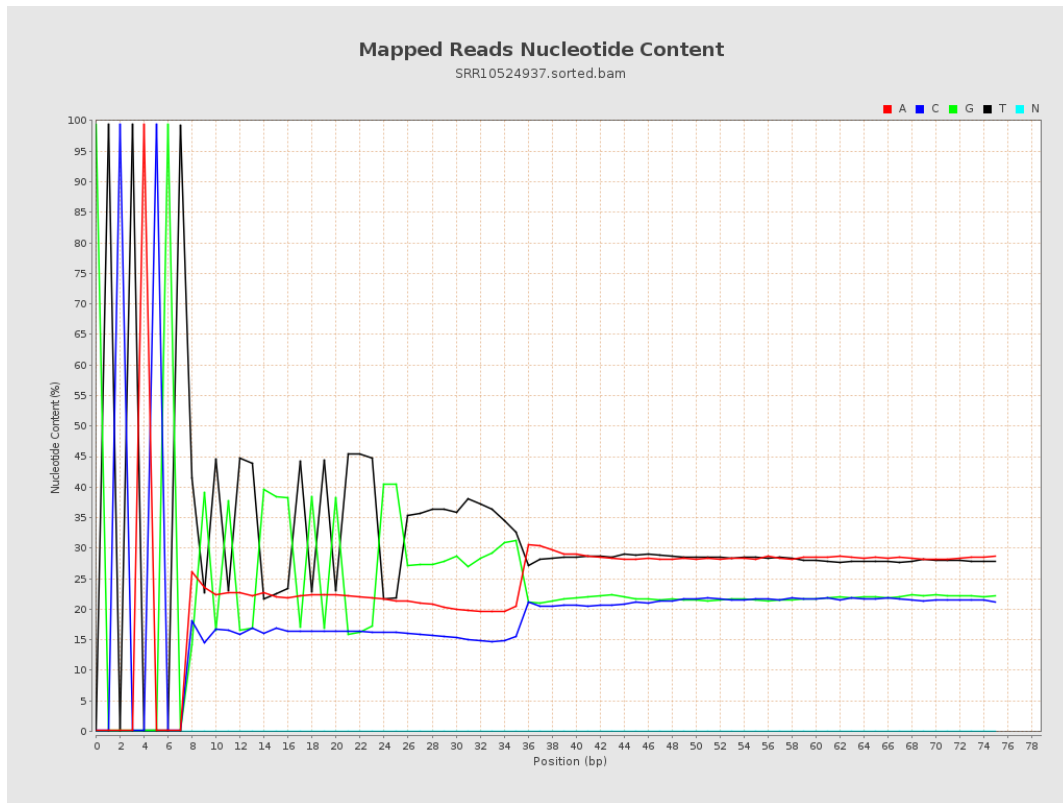
6. Results : Genome Fraction Coverage



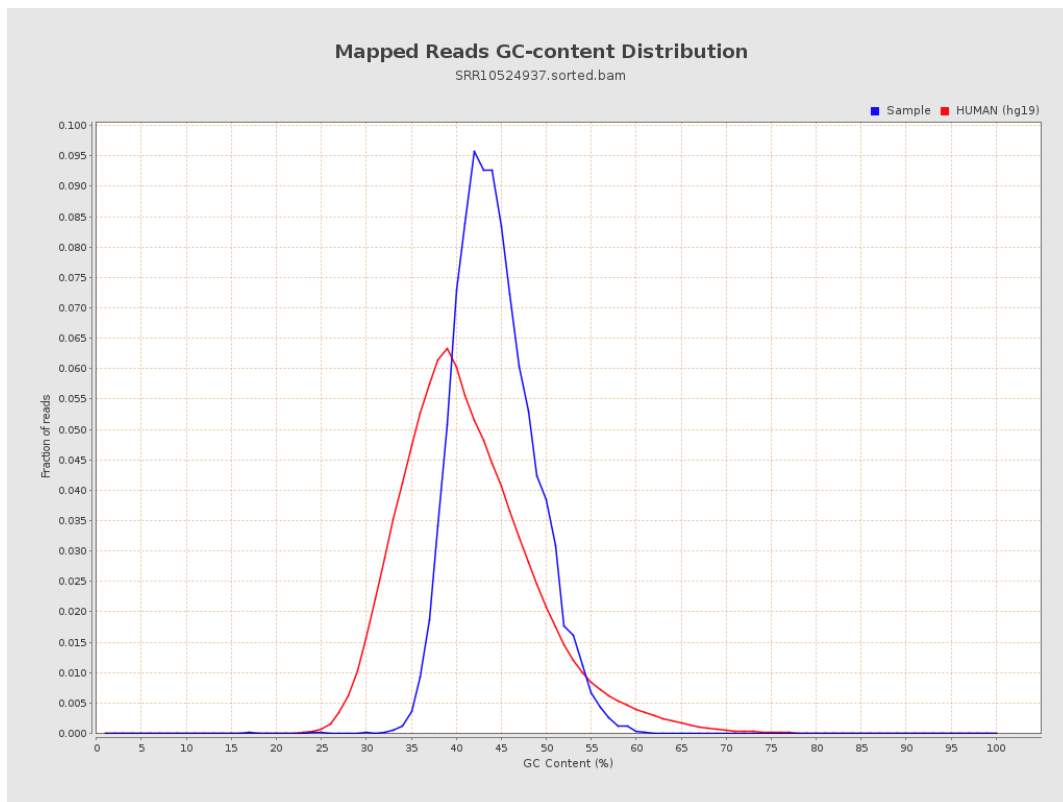
7. Results : Duplication Rate Histogram



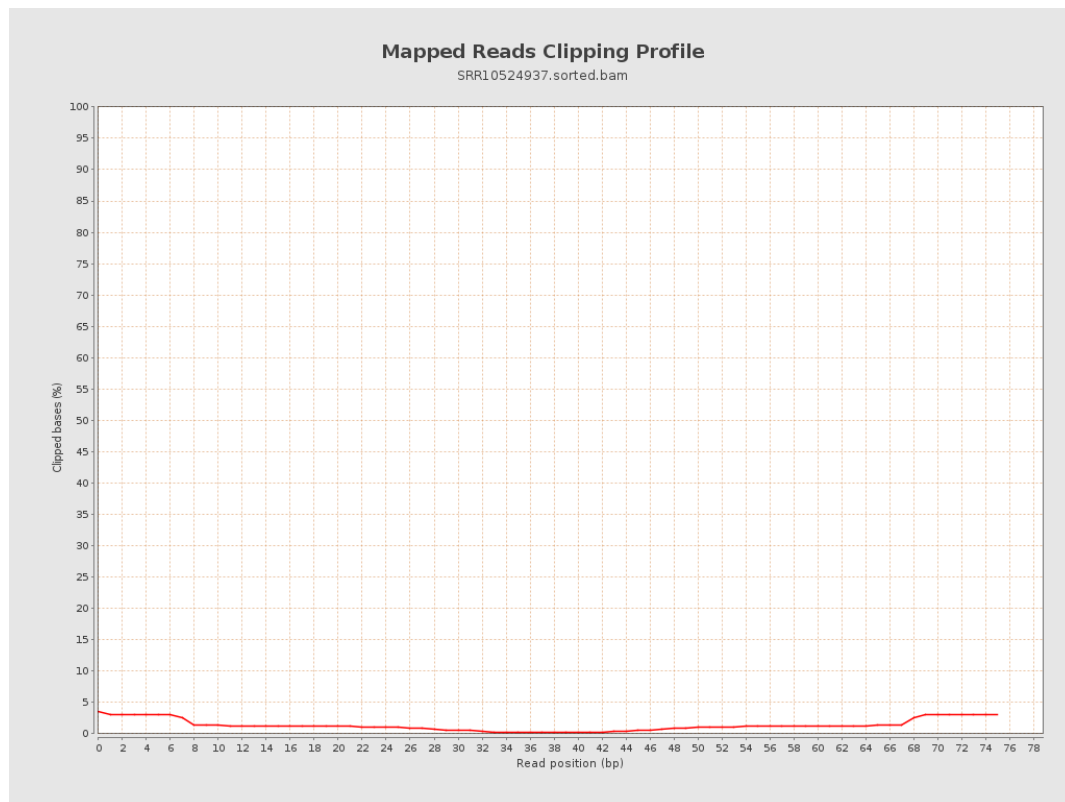
8. Results : Mapped Reads Nucleotide Content



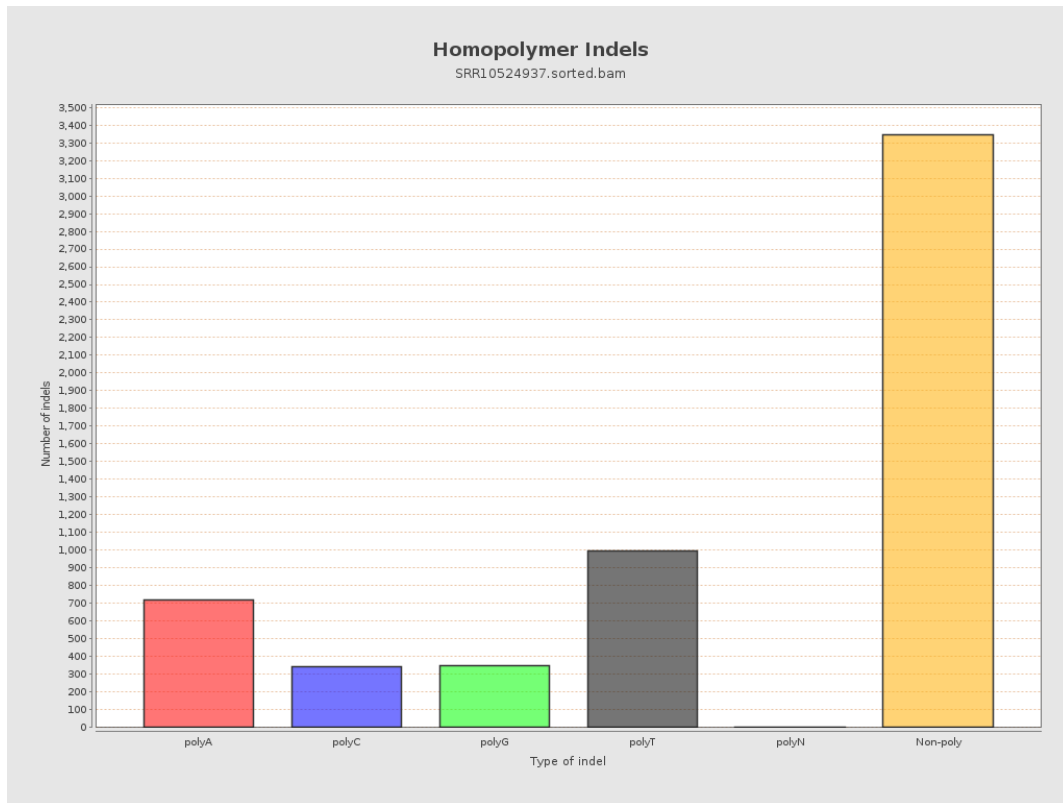
9. Results : Mapped Reads GC-content Distribution



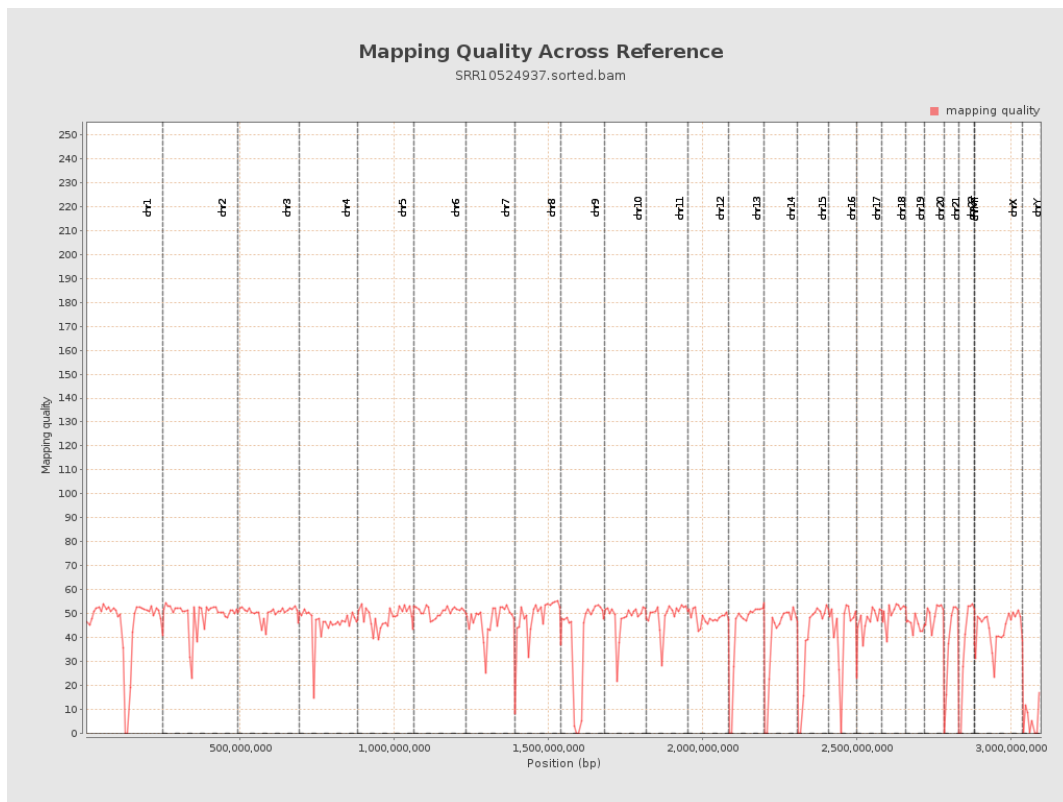
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

