

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:57:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238074.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_SRR6238074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:57:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,606,572
Mapped reads	1,283,901 / 79.92%
Unmapped reads	322,671 / 20.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,627 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	175,138 / 10.9%
Duplication rate	10.05%
Clipped reads	614,091 / 38.22%

2.2. ACGT Content

Number/percentage of A's	22,723,380 / 26.93%
Number/percentage of C's	15,946,987 / 18.9%
Number/percentage of T's	26,448,741 / 31.34%
Number/percentage of G's	19,255,099 / 22.82%
Number/percentage of N's	11,553 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.3497
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.14
----------------------	-------

2.5. Mismatches and indels

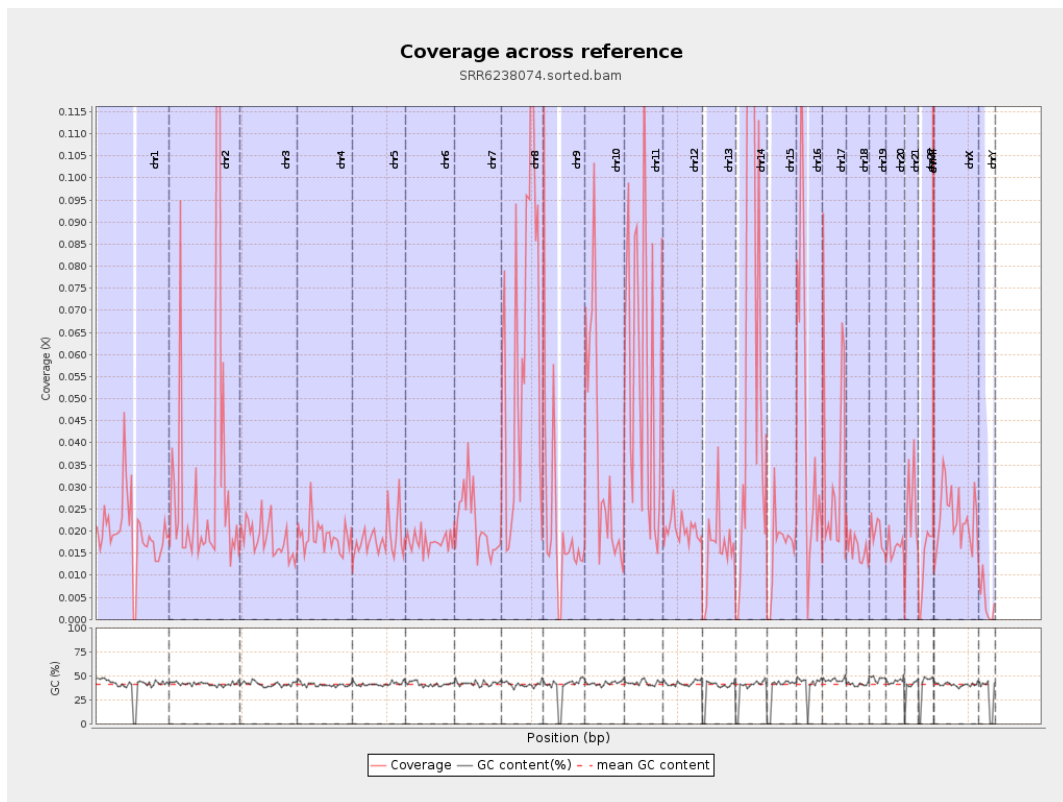
General error rate	0.8%
Mismatches	660,746
Insertions	5,712
Mapped reads with at least one insertion	0.44%
Deletions	22,234
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.99%

2.6. Chromosome stats

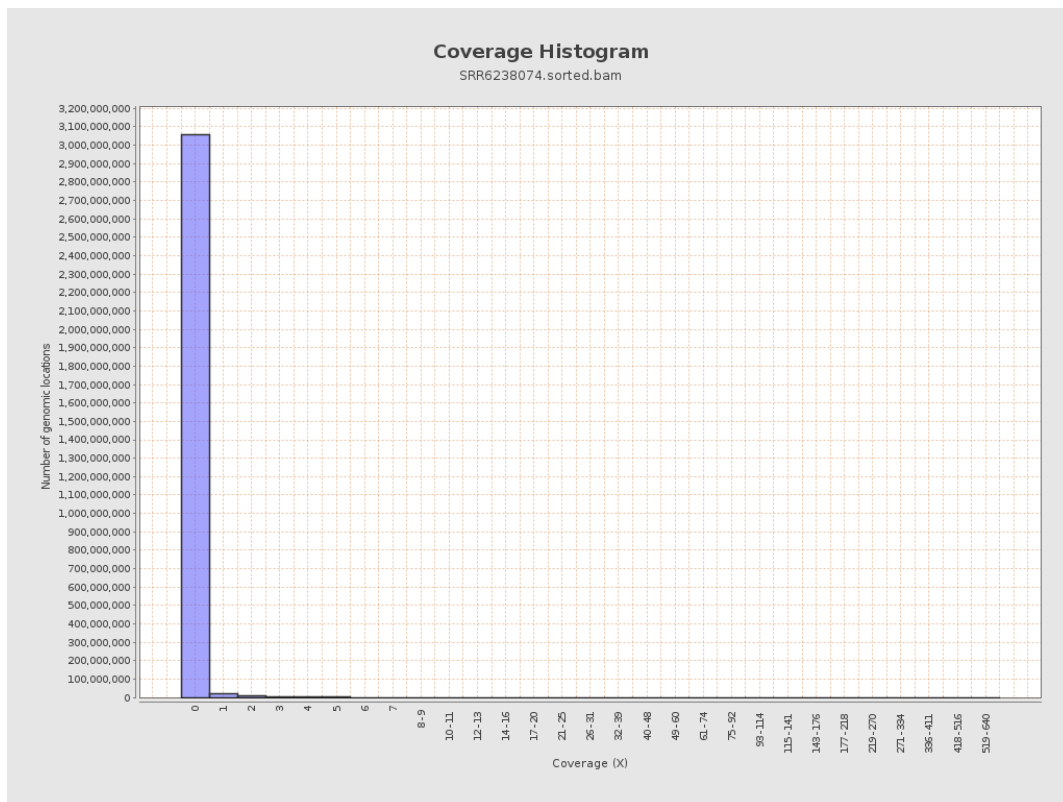
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4878500	0.0196	0.3914
chr2	243199373	8212166	0.0338	0.3916
chr3	198022430	3582735	0.0181	0.2417
chr4	191154276	3613534	0.0189	0.2484
chr5	180915260	3298583	0.0182	0.2459
chr6	171115067	3023566	0.0177	0.2514
chr7	159138663	3430520	0.0216	0.3044

chr8	146364022	9195200	0.0628	0.5673
chr9	141213431	2593643	0.0184	0.2545
chr10	135534747	4992599	0.0368	0.3916
chr11	135006516	7790521	0.0577	0.6287
chr12	133851895	2738047	0.0205	0.2623
chr13	115169878	1821760	0.0158	0.2306
chr14	107349540	7446724	0.0694	0.5029
chr15	102531392	1670878	0.0163	0.2332
chr16	90354753	4110488	0.0455	0.4012
chr17	81195210	2904933	0.0358	0.3955
chr18	78077248	1254364	0.0161	0.2979
chr19	59128983	1138750	0.0193	0.2989
chr20	63025520	1041346	0.0165	0.2354
chr21	48129895	1143371	0.0238	0.2897
chr22	51304566	657814	0.0128	0.1937
chrMT	16571	87366	5.2722	4.8355
chrX	155270560	3570881	0.023	0.2955
chrY	59373566	226215	0.0038	0.1099

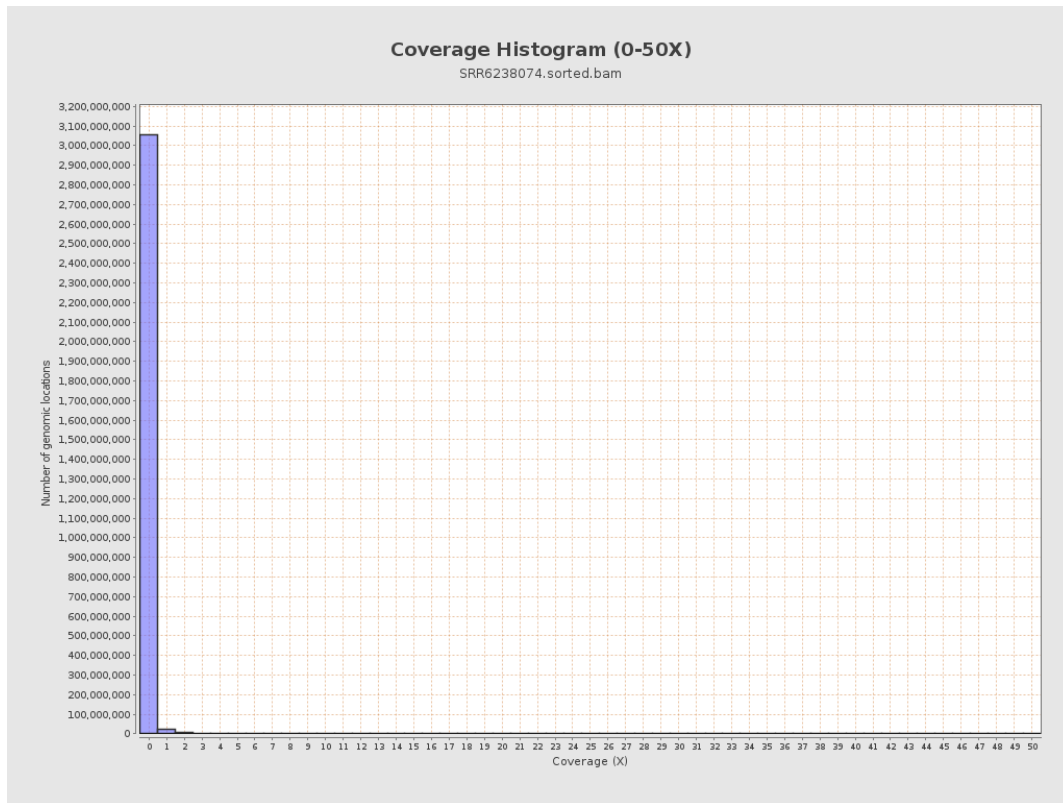
3. Results : Coverage across reference



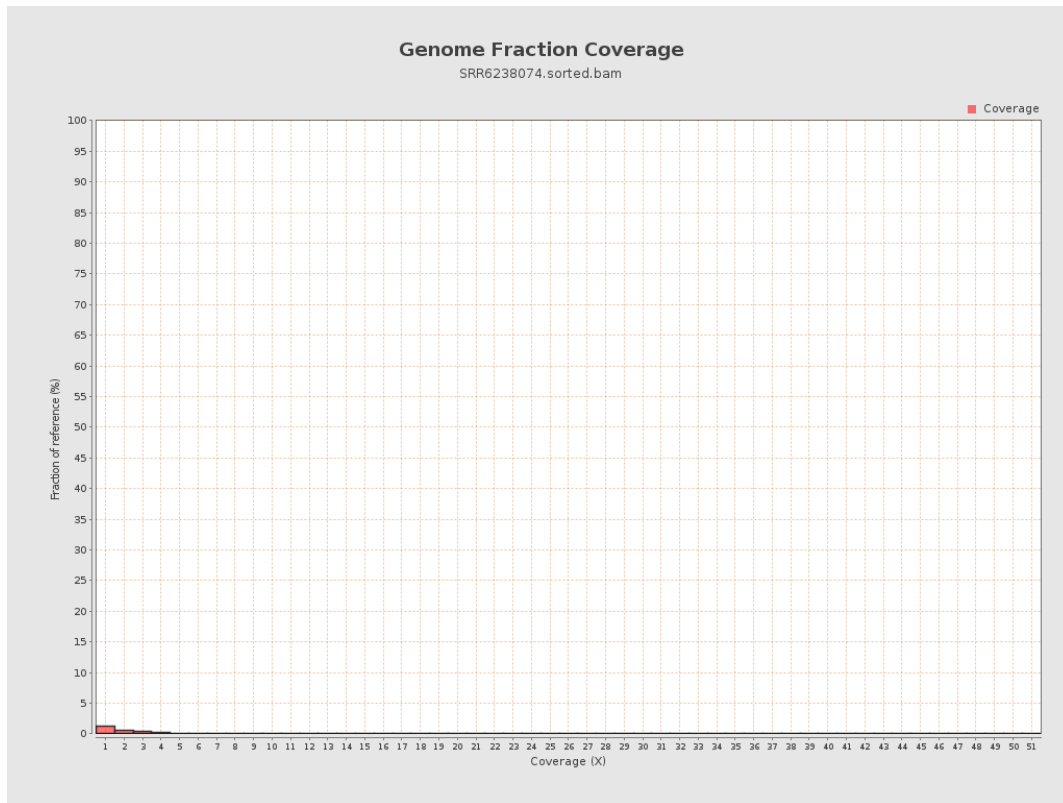
4. Results : Coverage Histogram



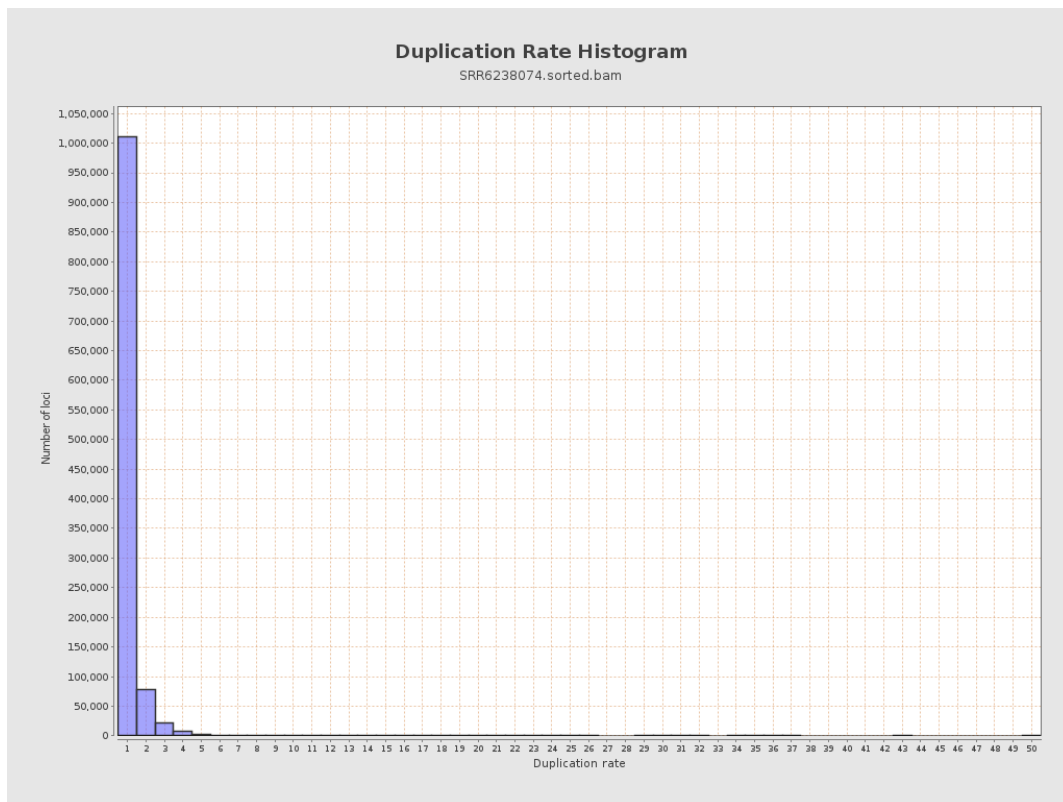
5. Results : Coverage Histogram (0-50X)



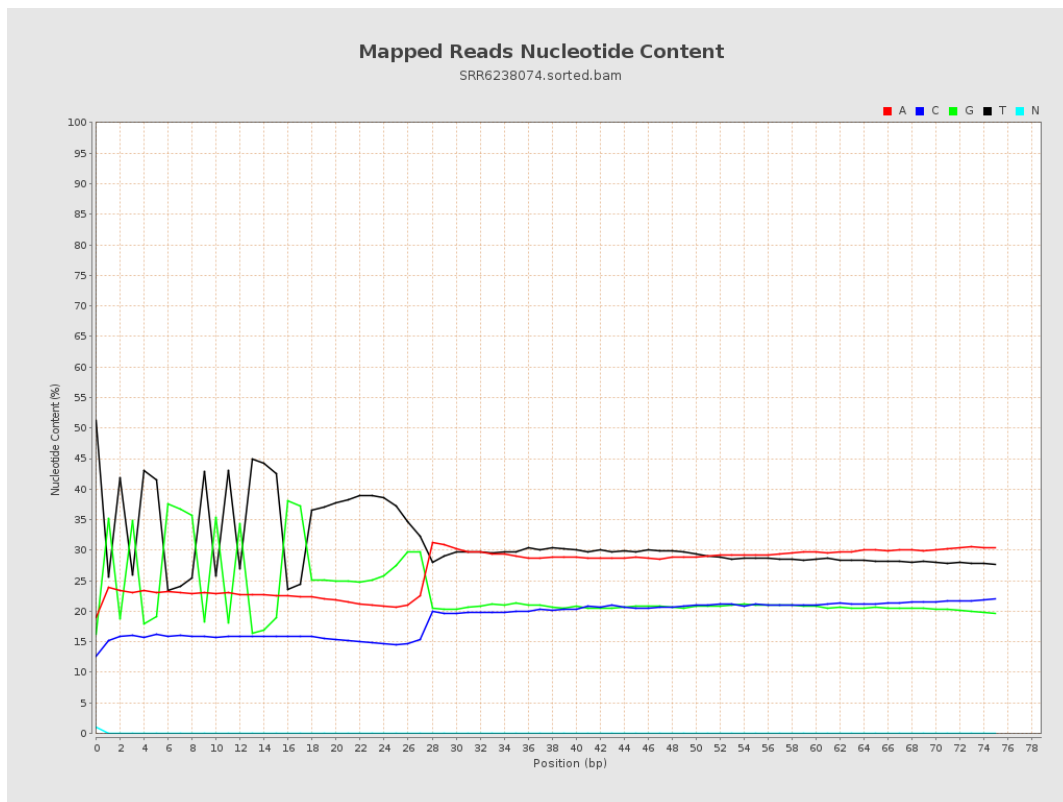
6. Results : Genome Fraction Coverage



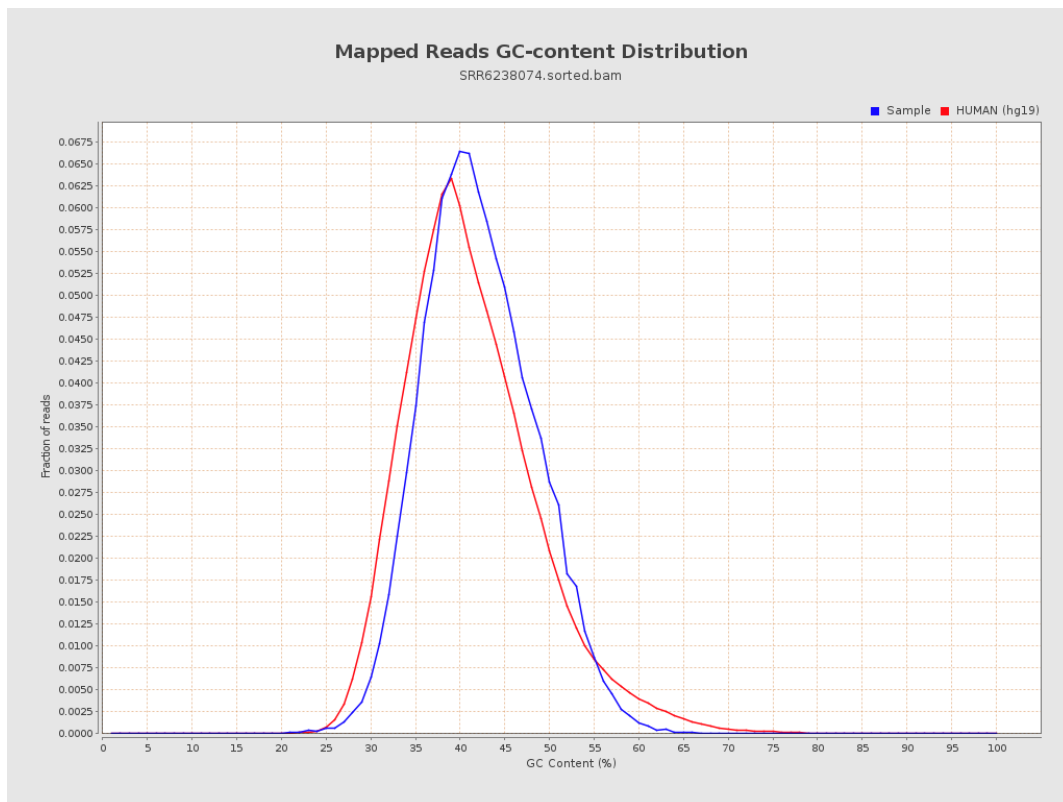
7. Results : Duplication Rate Histogram



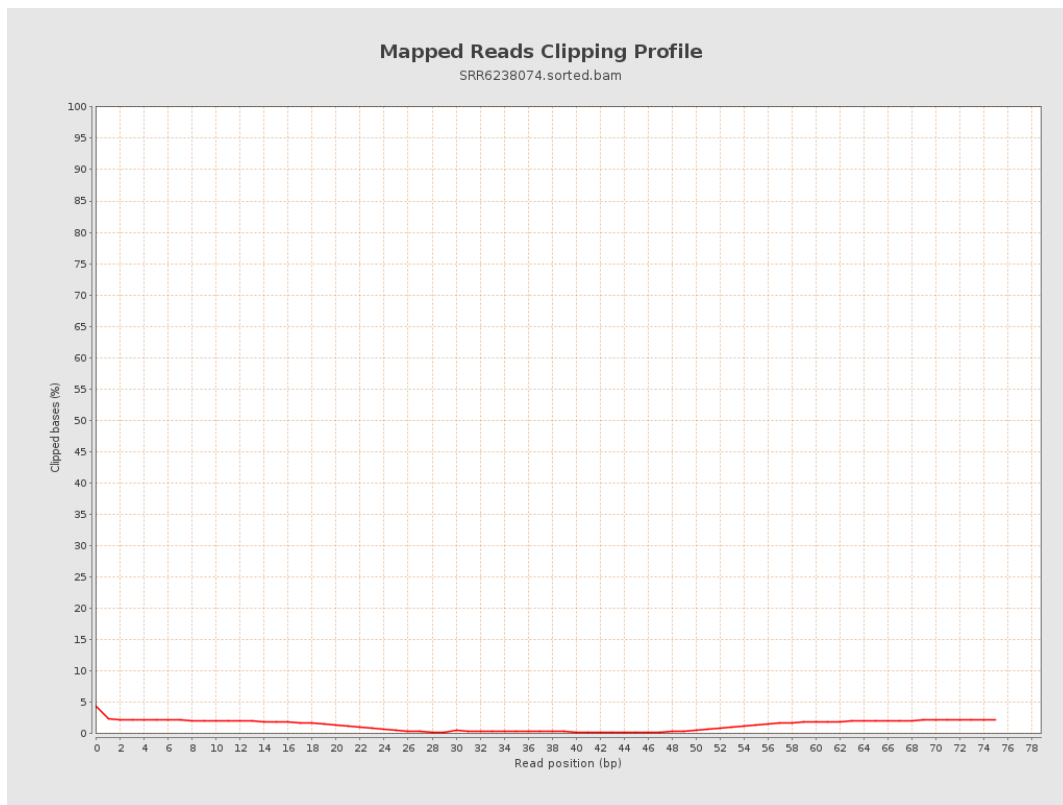
8. Results : Mapped Reads Nucleotide Content



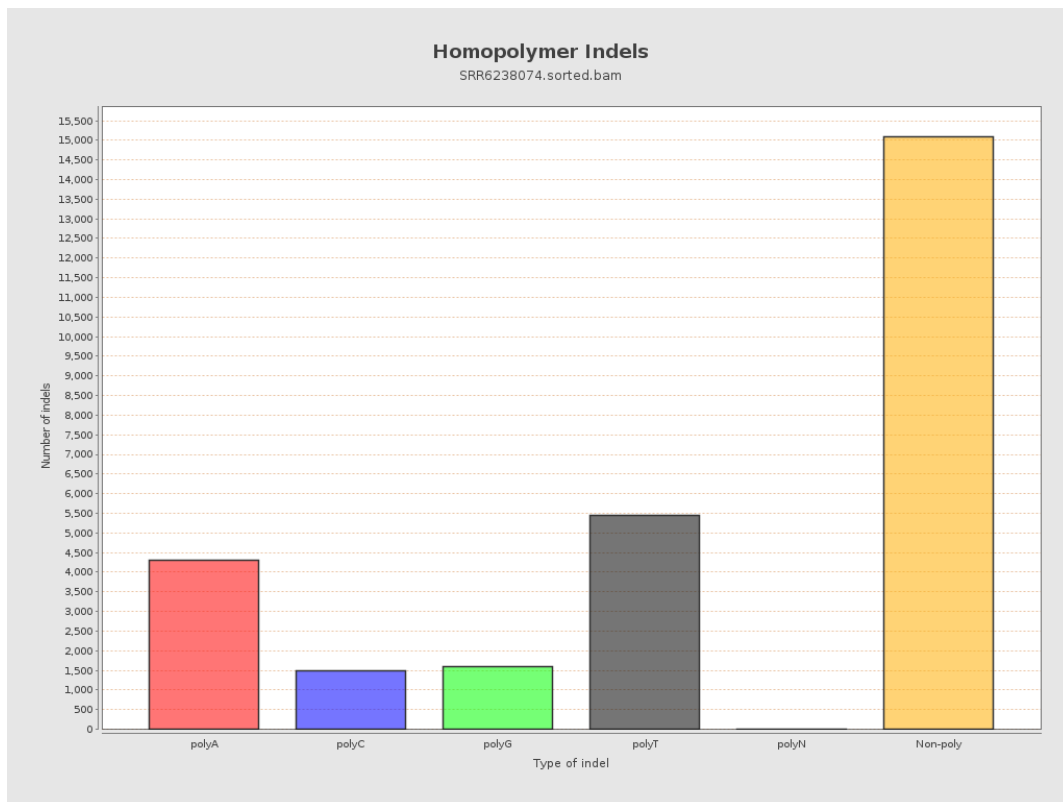
9. Results : Mapped Reads GC-content Distribution



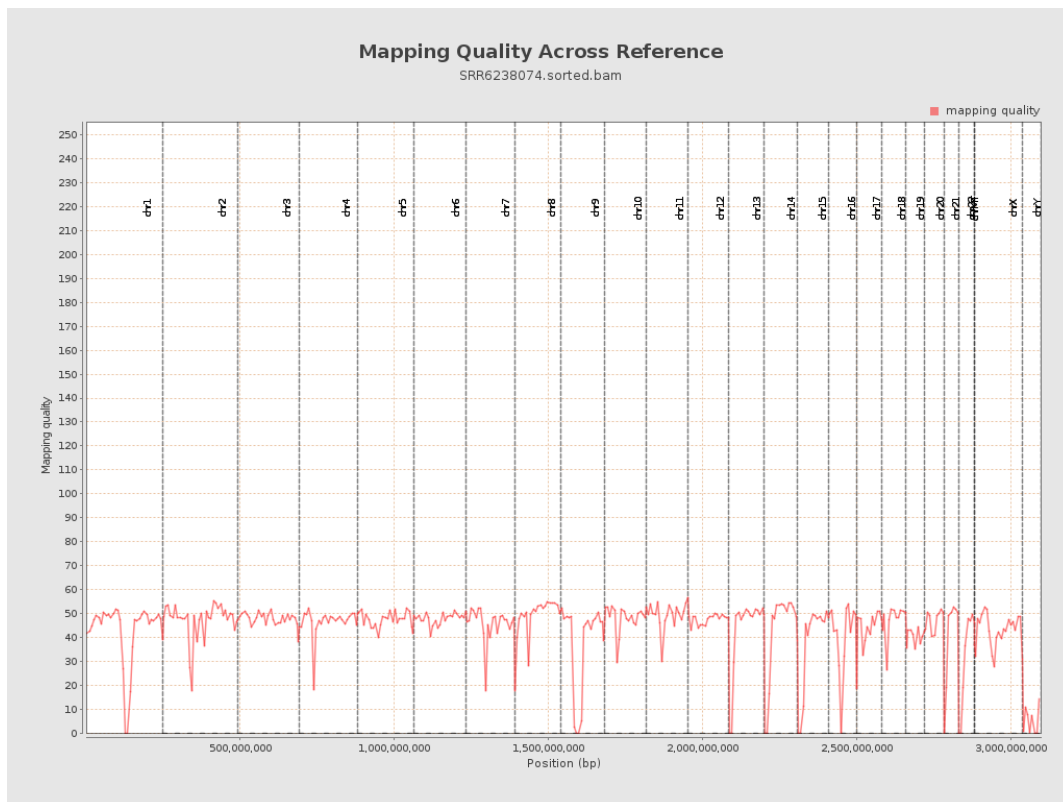
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

