

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:39:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240062.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_SRR6240062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:39:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,445,223
Mapped reads	2,088,971 / 85.43%
Unmapped reads	356,252 / 14.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,944 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	163,706 / 6.69%
Duplication rate	5.91%
Clipped reads	1,017,596 / 41.62%

2.2. ACGT Content

Number/percentage of A's	39,693,381 / 28.71%
Number/percentage of C's	25,857,830 / 18.7%
Number/percentage of T's	43,736,652 / 31.63%
Number/percentage of G's	28,964,730 / 20.95%
Number/percentage of N's	12,249 / 0.01%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.6675
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.59
----------------------	-------

2.5. Mismatches and indels

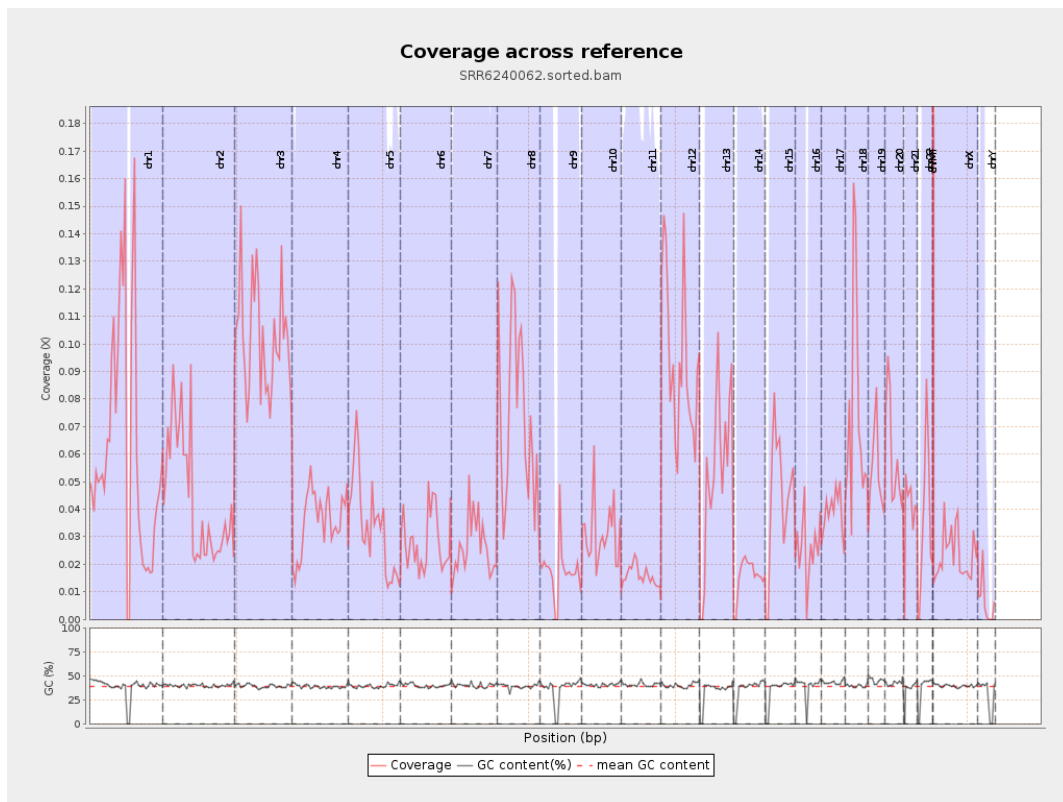
General error rate	0.94%
Mismatches	1,286,697
Insertions	10,708
Mapped reads with at least one insertion	0.51%
Deletions	53,041
Mapped reads with at least one deletion	2.5%
Homopolymer indels	44.32%

2.6. Chromosome stats

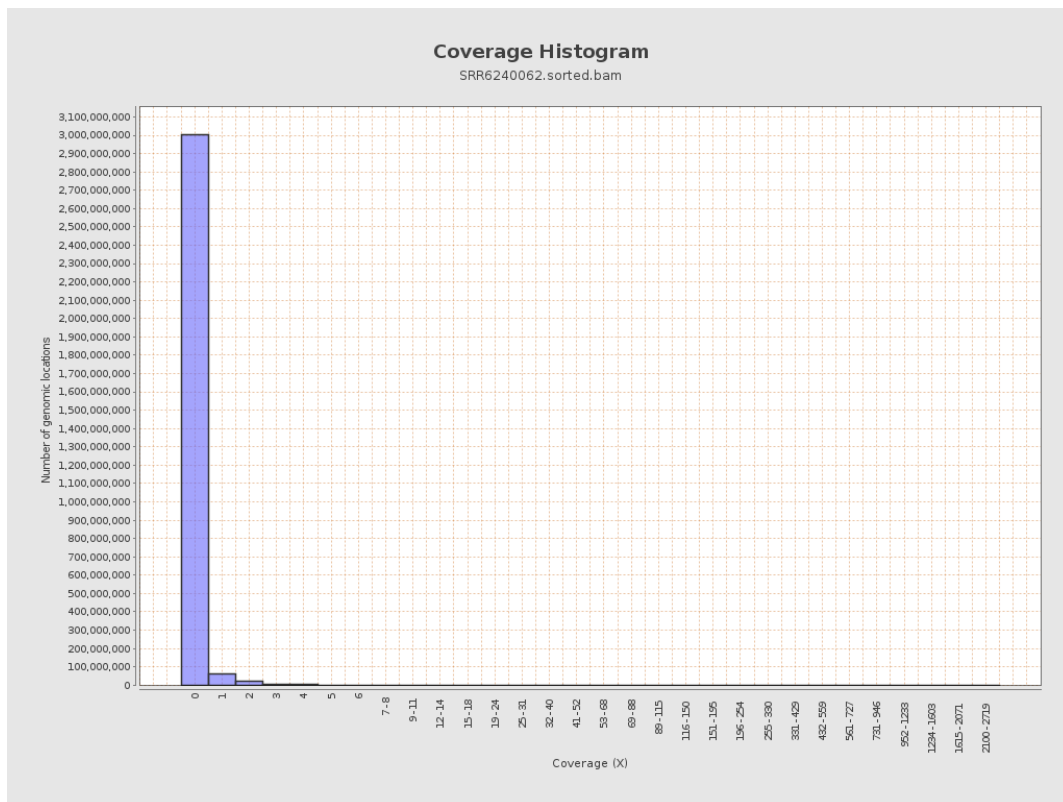
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15098997	0.0606	1.4595
chr2	243199373	10554020	0.0434	0.488
chr3	198022430	20183074	0.1019	0.4469
chr4	191154276	6889971	0.036	0.2753
chr5	180915260	6031819	0.0333	0.2711
chr6	171115067	4832513	0.0282	0.2434
chr7	159138663	4167741	0.0262	0.3711

chr8	146364022	10557048	0.0721	1.6943
chr9	141213431	2464371	0.0175	0.3819
chr10	135534747	4174626	0.0308	0.4484
chr11	135006516	2149348	0.0159	0.2384
chr12	133851895	12498623	0.0934	0.4737
chr13	115169878	6320673	0.0549	0.327
chr14	107349540	1692434	0.0158	0.2066
chr15	102531392	4526802	0.0442	0.2925
chr16	90354753	2307025	0.0255	0.2874
chr17	81195210	3200198	0.0394	0.3073
chr18	78077248	5820418	0.0745	0.9621
chr19	59128983	3239626	0.0548	0.8239
chr20	63025520	3812988	0.0605	0.3647
chr21	48129895	1894251	0.0394	0.2952
chr22	51304566	1888037	0.0368	0.2631
chrMT	16571	26451	1.5962	5.3593
chrX	155270560	3636598	0.0234	0.252
chrY	59373566	389038	0.0066	0.2549

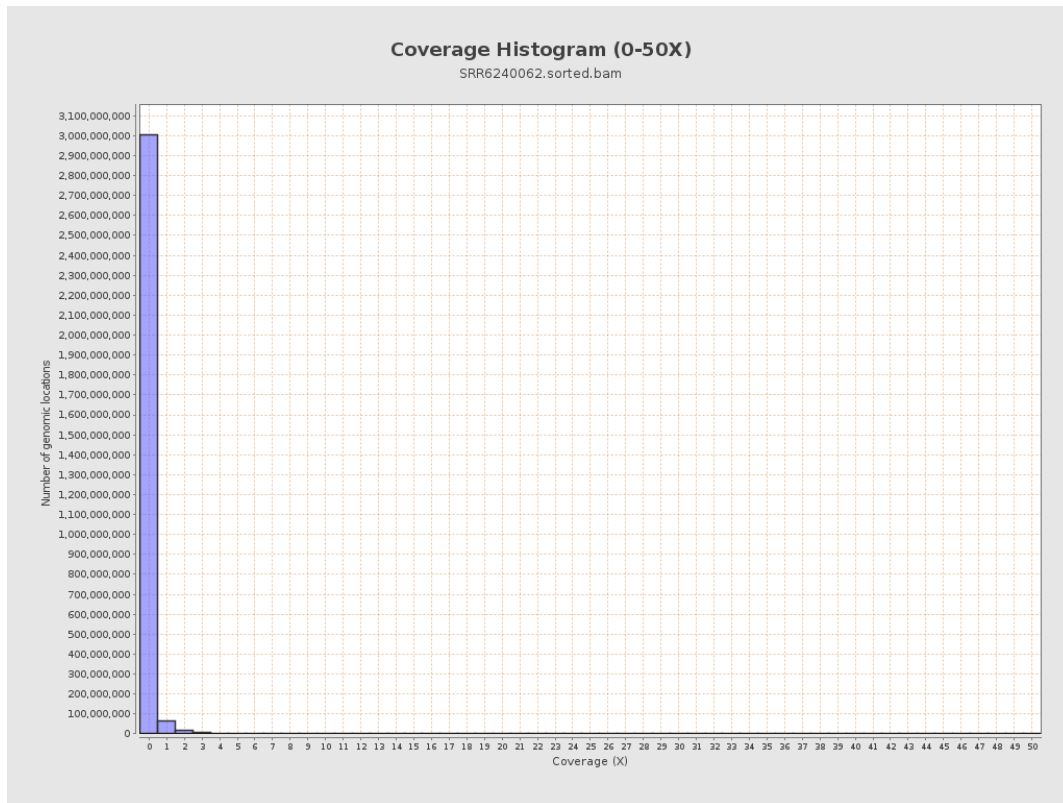
3. Results : Coverage across reference



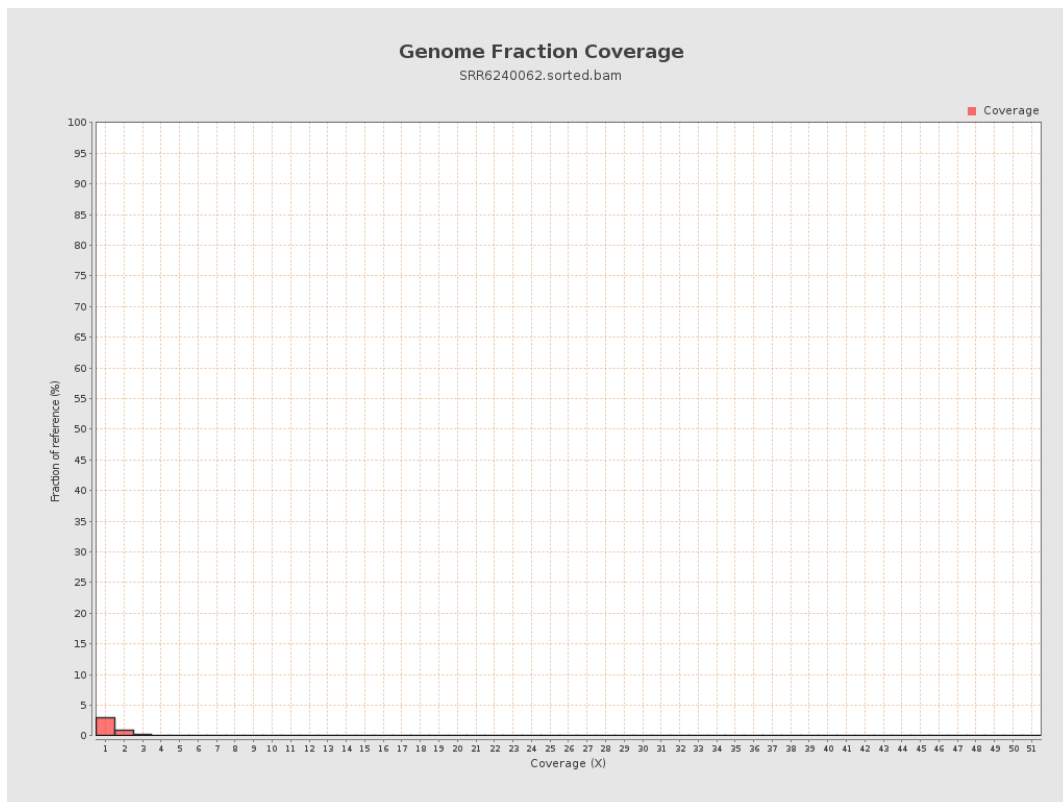
4. Results : Coverage Histogram



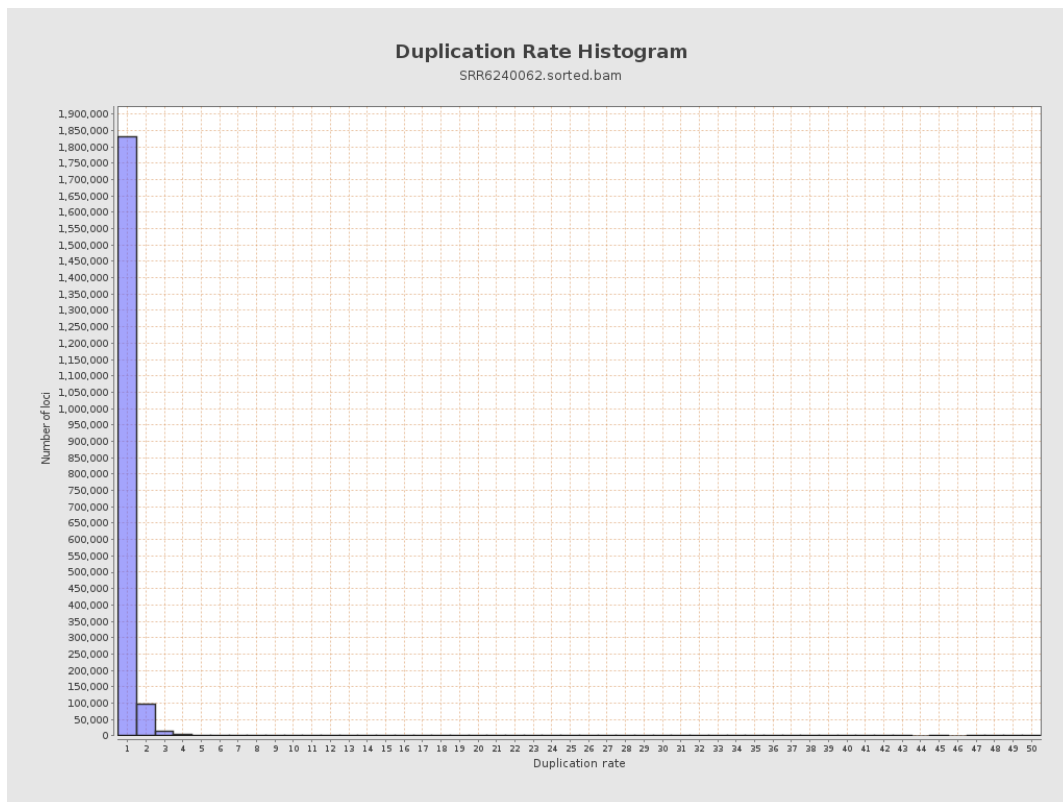
5. Results : Coverage Histogram (0-50X)



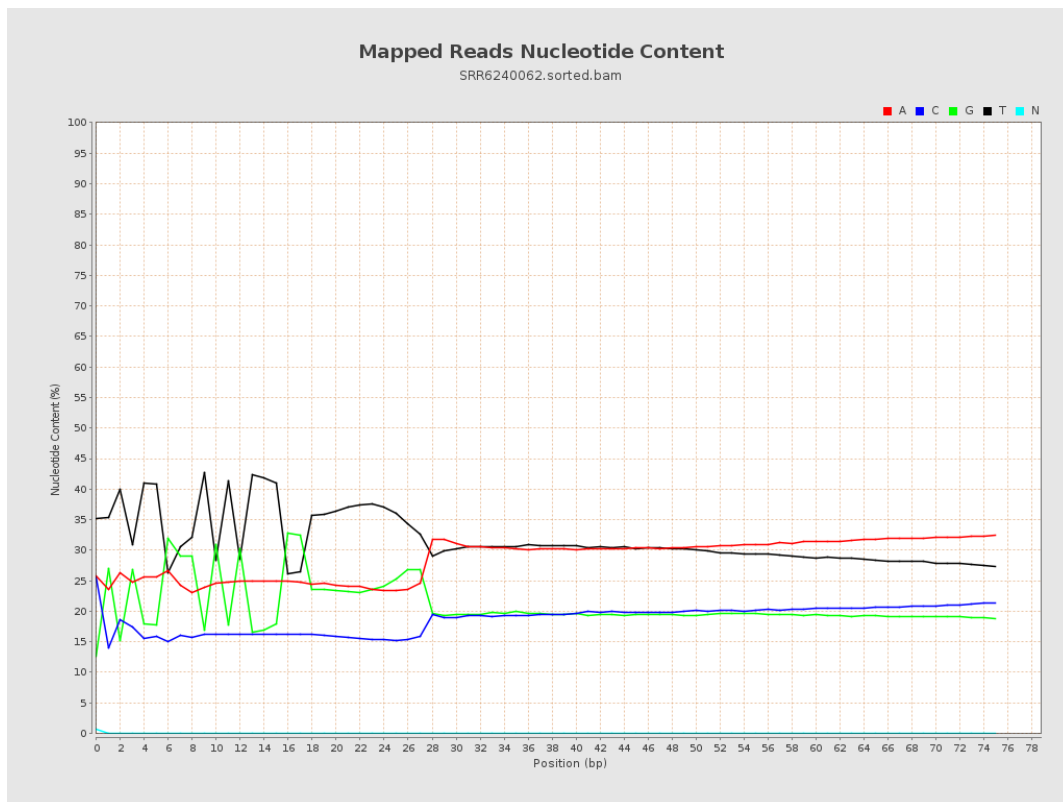
6. Results : Genome Fraction Coverage



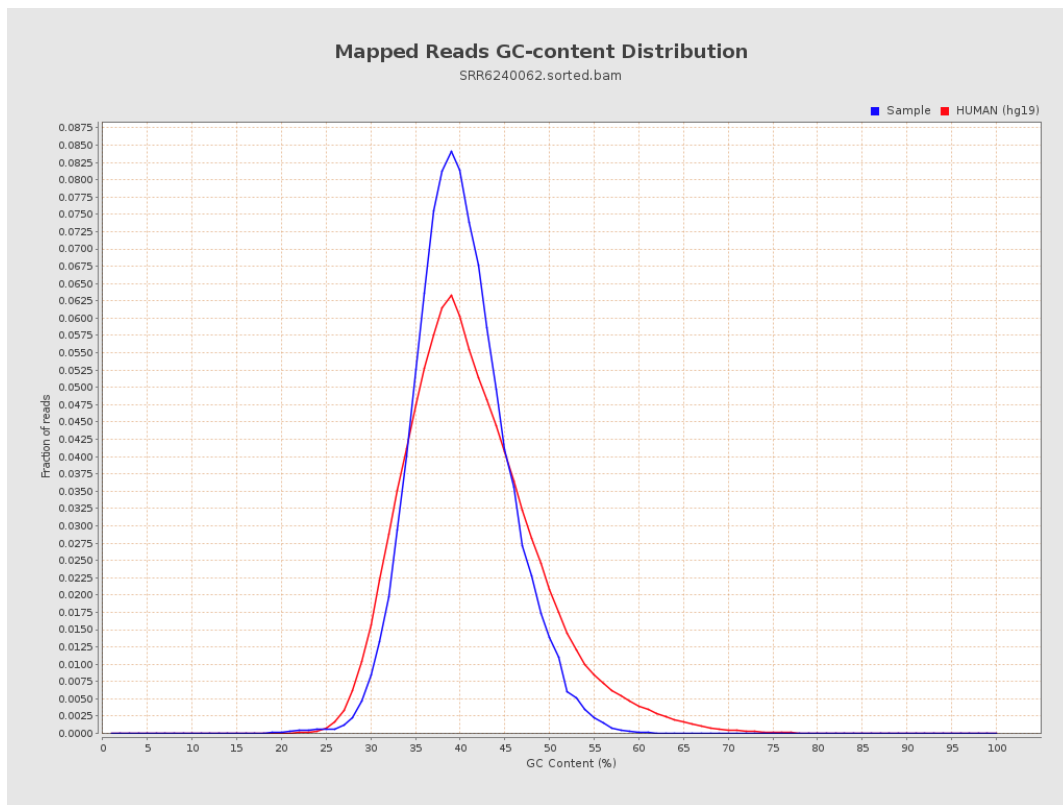
7. Results : Duplication Rate Histogram



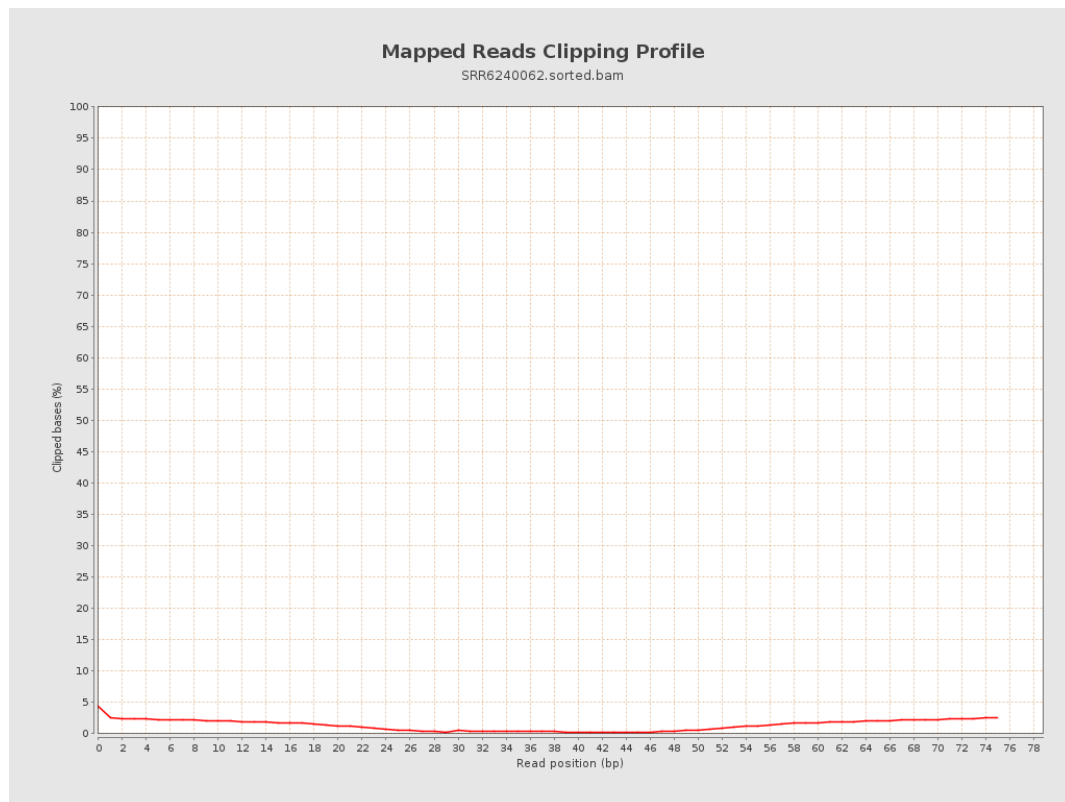
8. Results : Mapped Reads Nucleotide Content



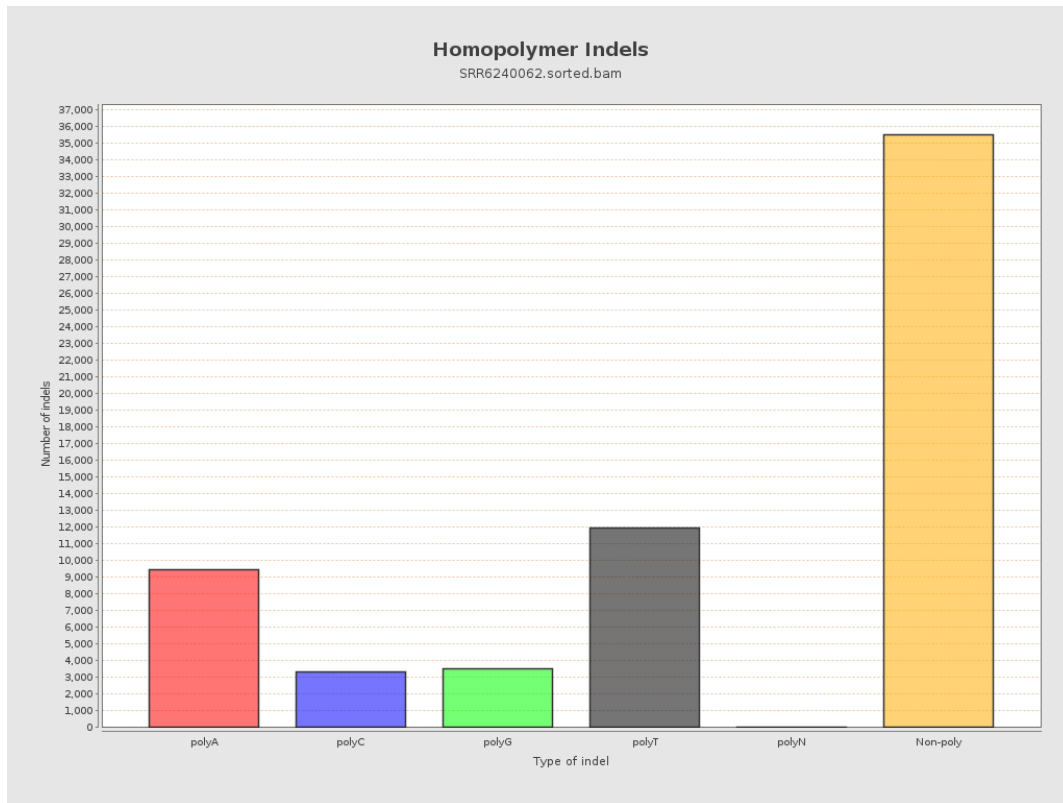
9. Results : Mapped Reads GC-content Distribution



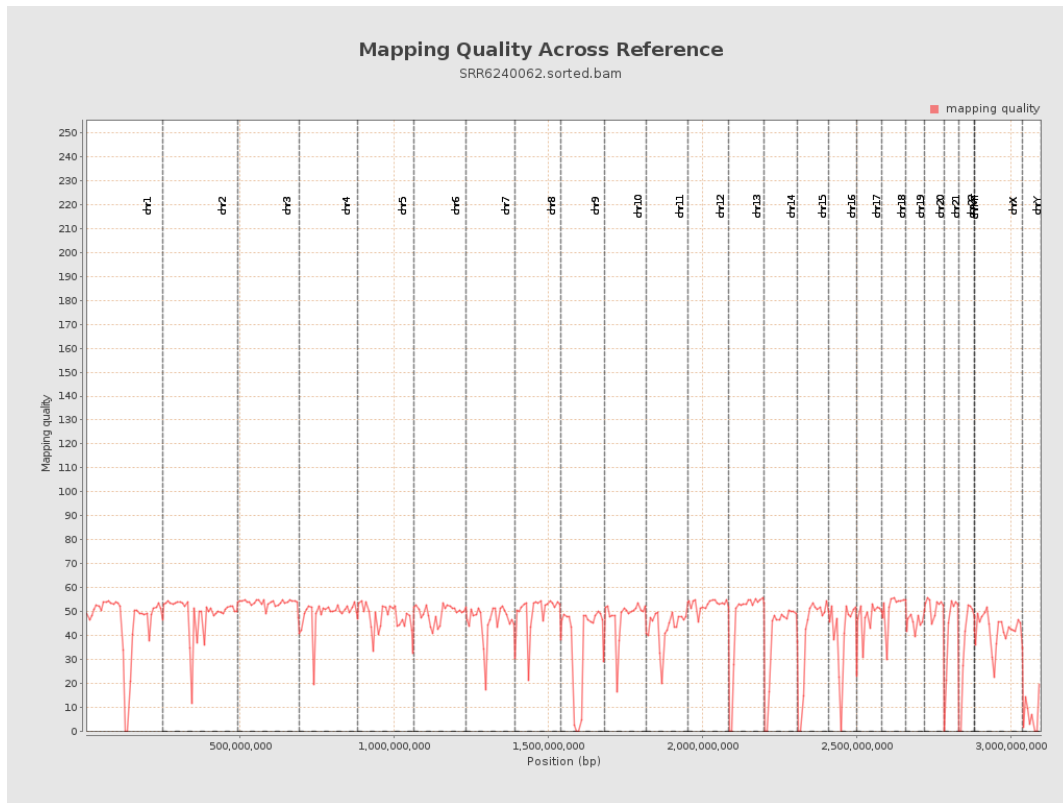
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

