

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:49:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240065.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_SRR6240065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:49:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,941,300
Mapped reads	1,522,147 / 78.41%
Unmapped reads	419,153 / 21.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,804 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	112,378 / 5.79%
Duplication rate	6.06%
Clipped reads	726,861 / 37.44%

2.2. ACGT Content

Number/percentage of A's	28,422,169 / 28.26%
Number/percentage of C's	18,369,290 / 18.26%
Number/percentage of T's	32,332,963 / 32.15%
Number/percentage of G's	21,437,828 / 21.32%
Number/percentage of N's	9,176 / 0.01%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3362
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2.4. Mapping Quality

Mean Mapping Quality	46.25
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2.5. Mismatches and indels

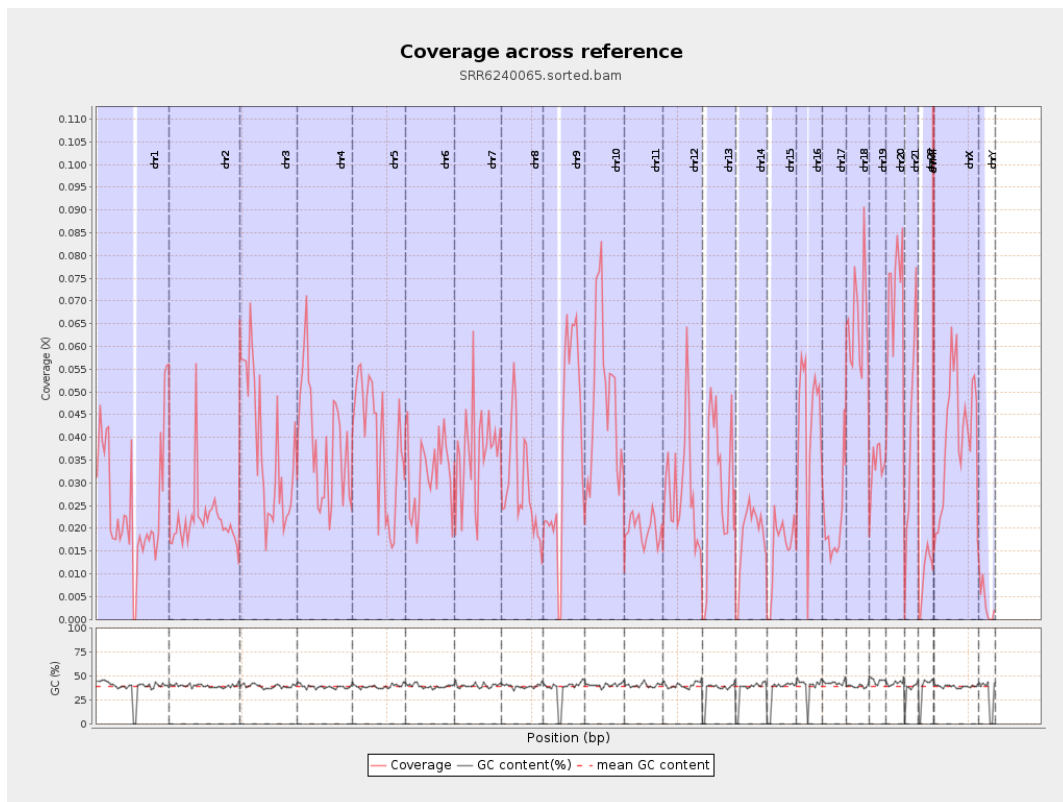
General error rate	0.81%
Mismatches	797,287
Insertions	7,212
Mapped reads with at least one insertion	0.47%
Deletions	22,776
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.86%

2.6. Chromosome stats

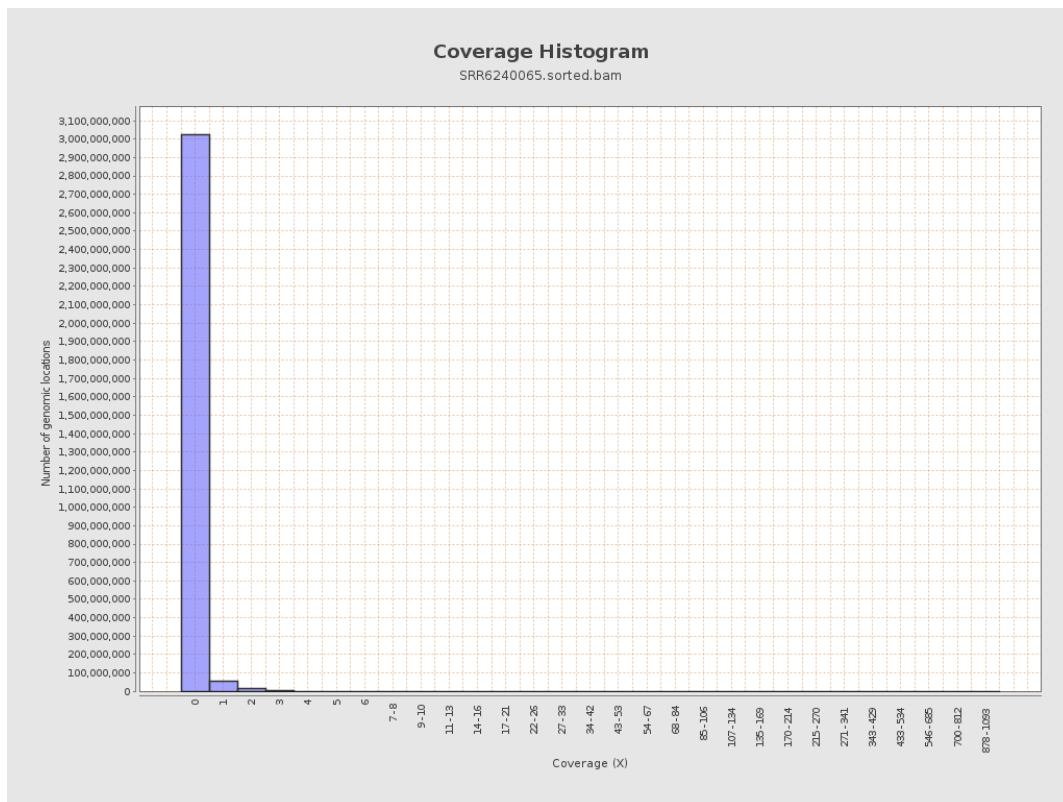
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6329712	0.0254	0.4745
chr2	243199373	5268118	0.0217	0.3478
chr3	198022430	7486252	0.0378	0.2564
chr4	191154276	7466315	0.0391	0.2665
chr5	180915260	7010241	0.0387	0.26
chr6	171115067	5524055	0.0323	0.2694
chr7	159138663	5879974	0.0369	0.3849

chr8	146364022	4180008	0.0286	0.6779
chr9	141213431	5313638	0.0376	0.3197
chr10	135534747	6438014	0.0475	0.3569
chr11	135006516	2677345	0.0198	0.2153
chr12	133851895	3835241	0.0287	0.2292
chr13	115169878	3343340	0.029	0.225
chr14	107349540	1960362	0.0183	0.1915
chr15	102531392	1606792	0.0157	0.1715
chr16	90354753	3991478	0.0442	0.2819
chr17	81195210	1739250	0.0214	0.2017
chr18	78077248	5115344	0.0655	0.4721
chr19	59128983	2005179	0.0339	0.4235
chr20	63025520	4470726	0.0709	0.3528
chr21	48129895	1978391	0.0411	0.2705
chr22	51304566	499593	0.0097	0.1232
chrMT	16571	19016	1.1475	1.5472
chrX	155270560	6261671	0.0403	0.2893
chrY	59373566	210333	0.0035	0.0856

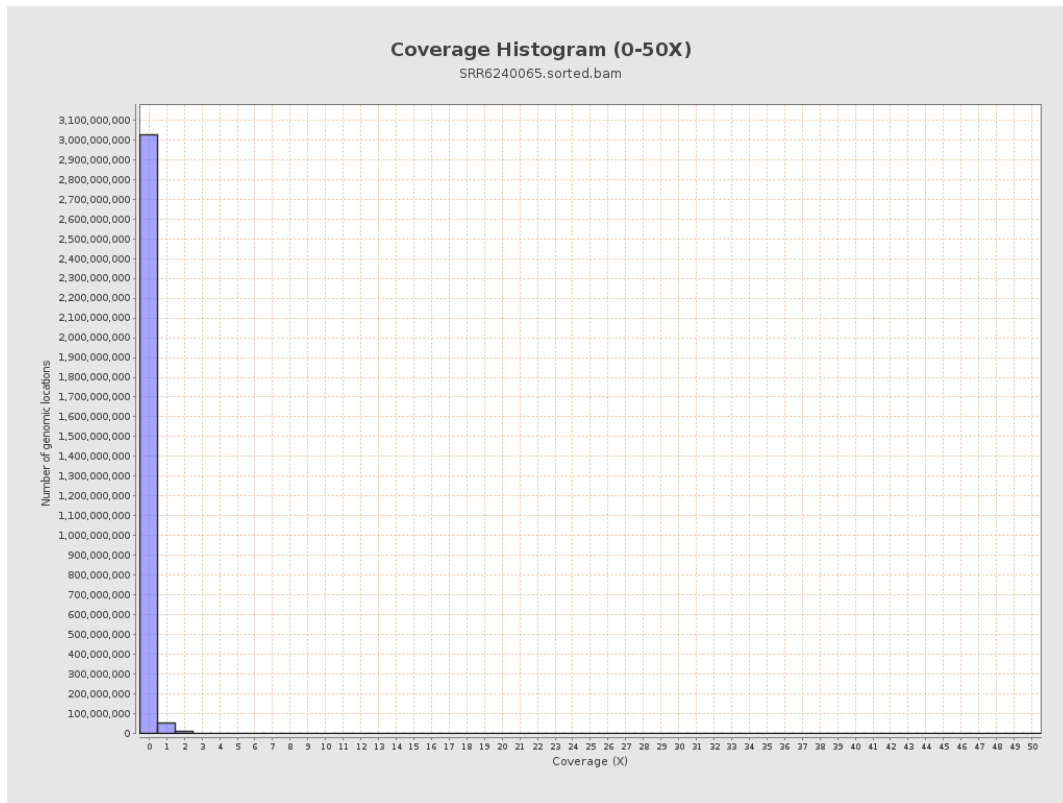
3. Results : Coverage across reference



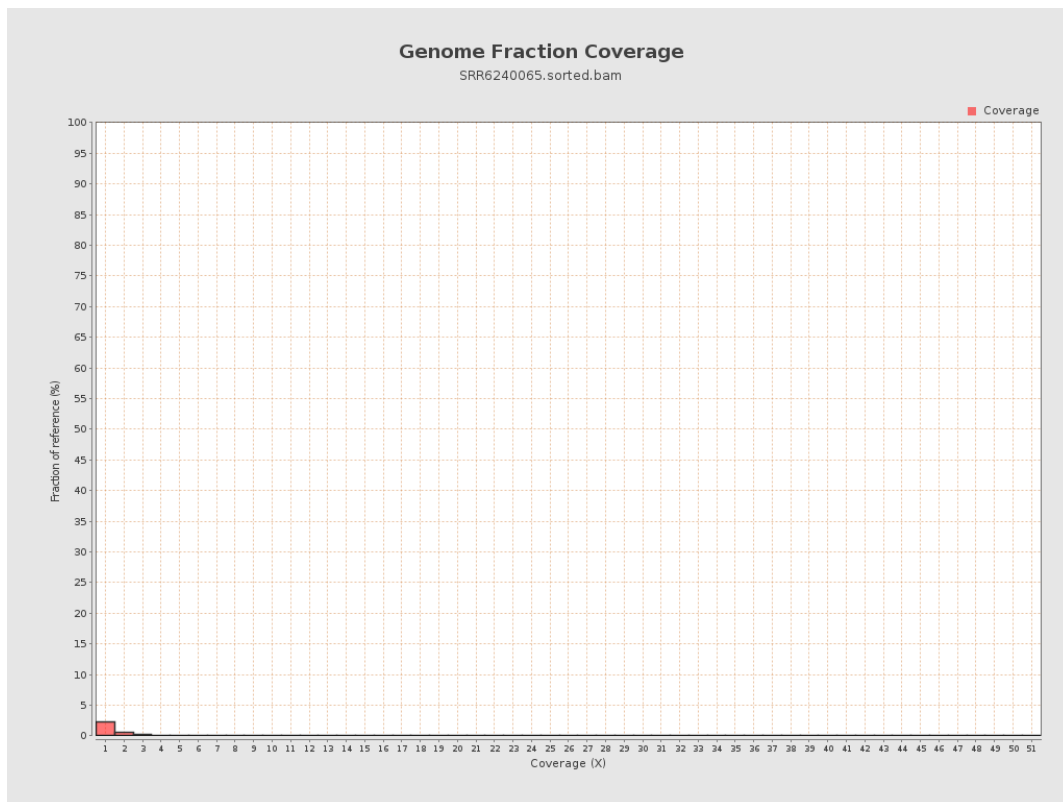
4. Results : Coverage Histogram



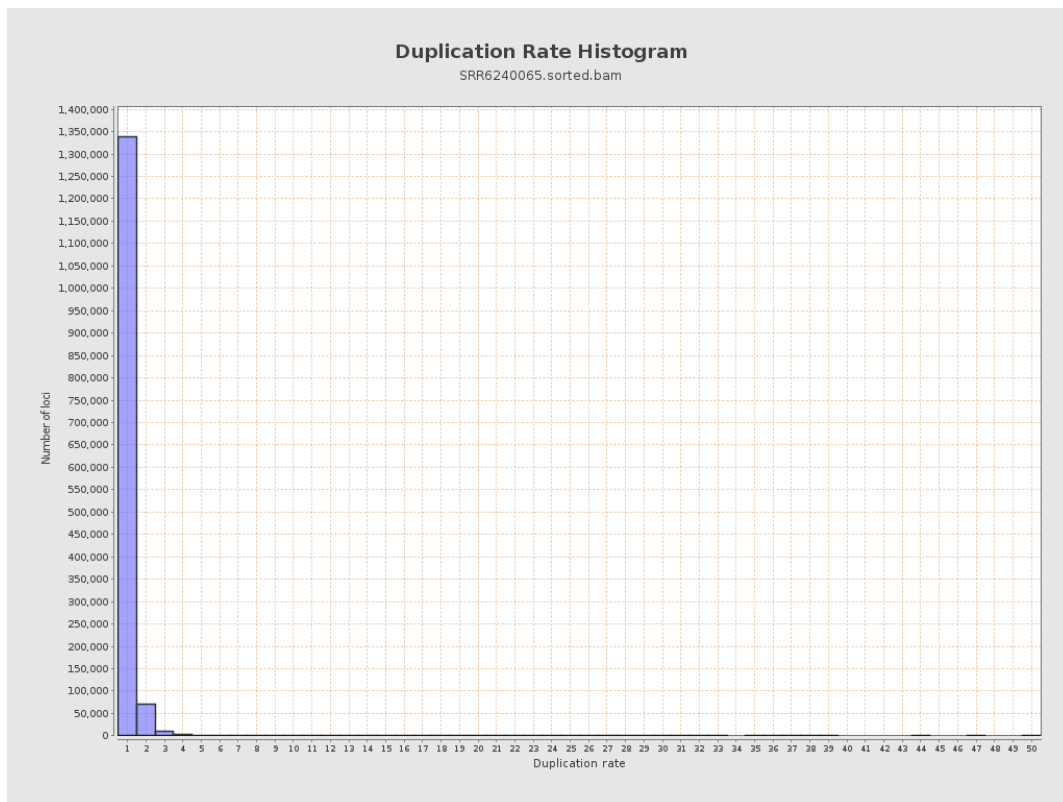
5. Results : Coverage Histogram (0-50X)



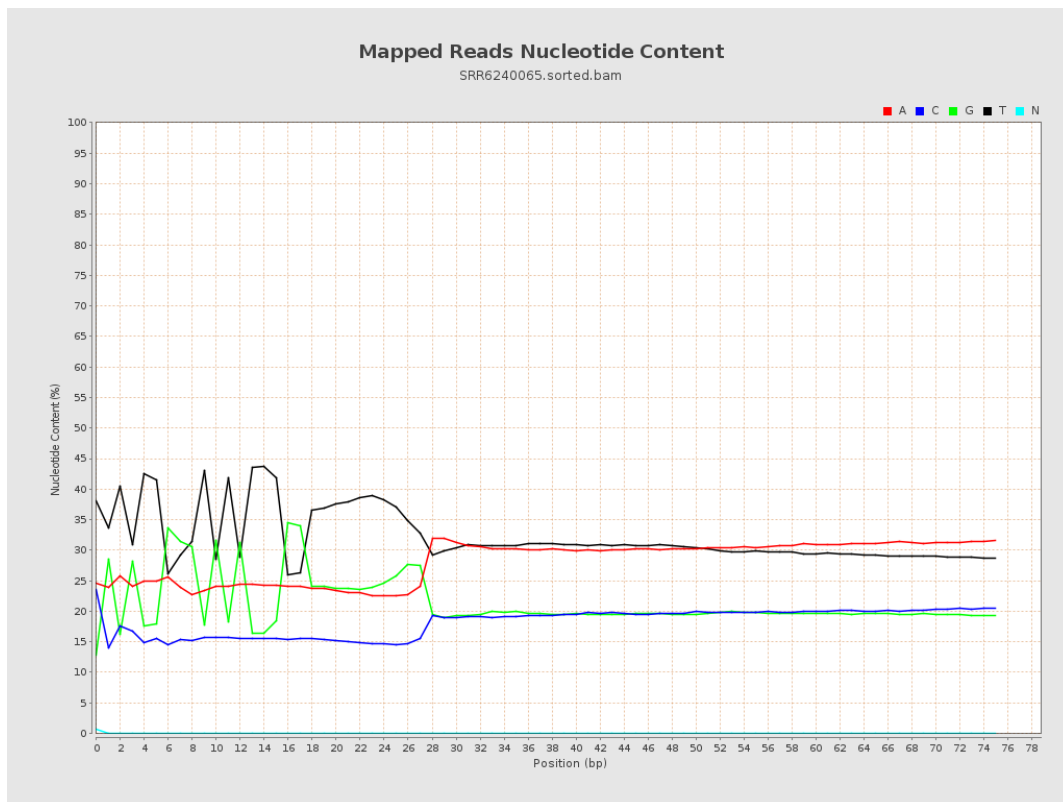
6. Results : Genome Fraction Coverage



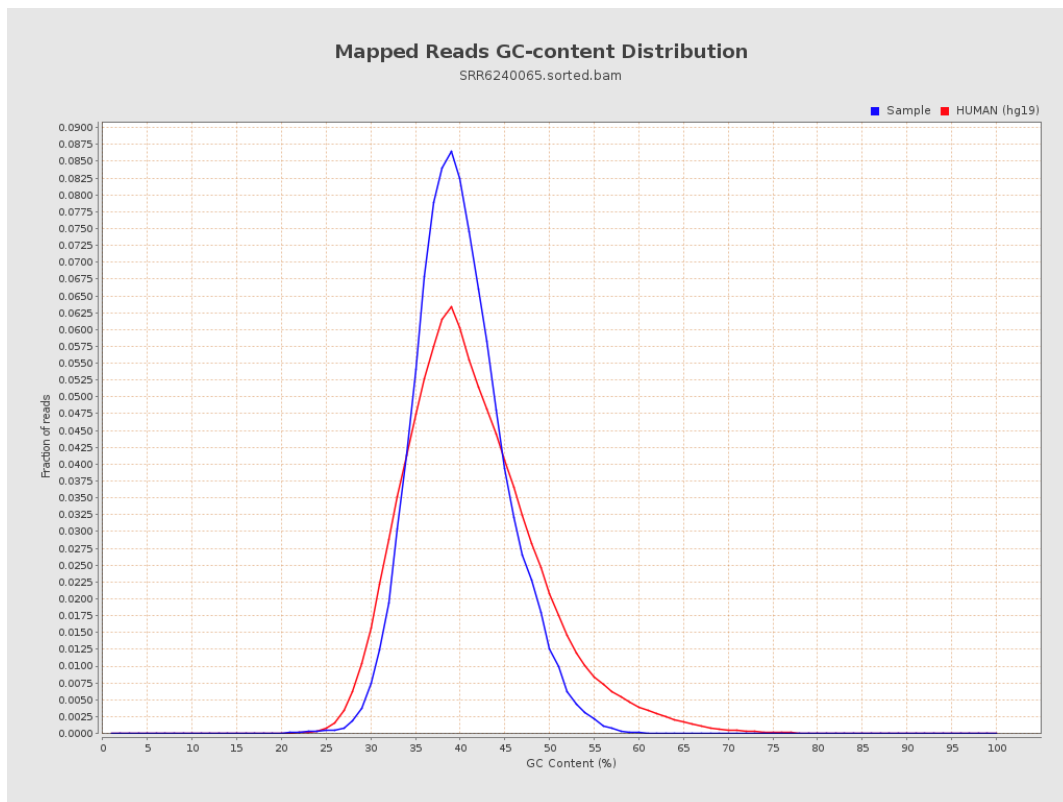
7. Results : Duplication Rate Histogram



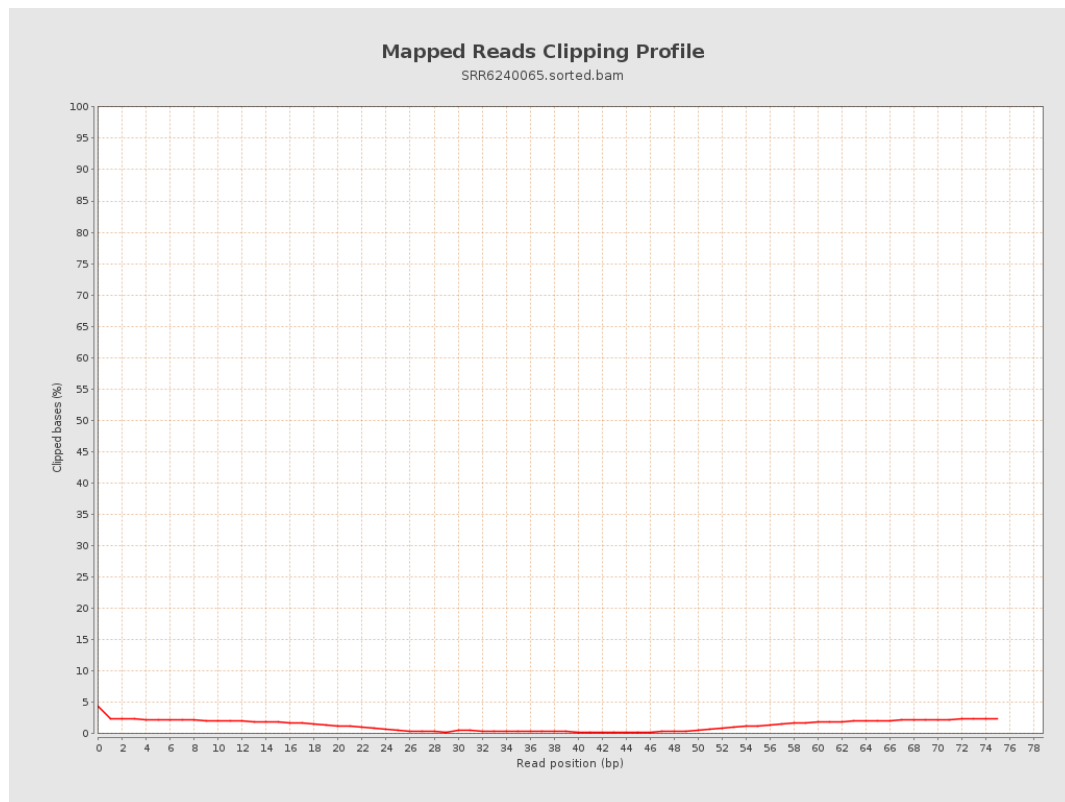
8. Results : Mapped Reads Nucleotide Content



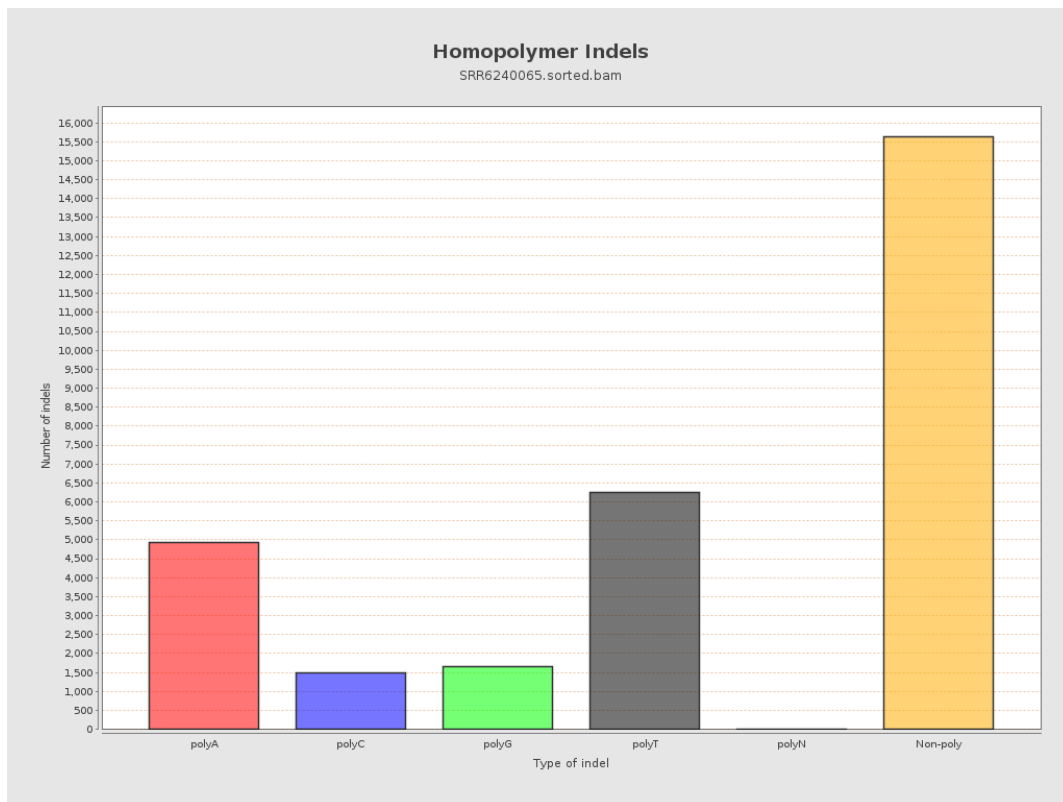
9. Results : Mapped Reads GC-content Distribution



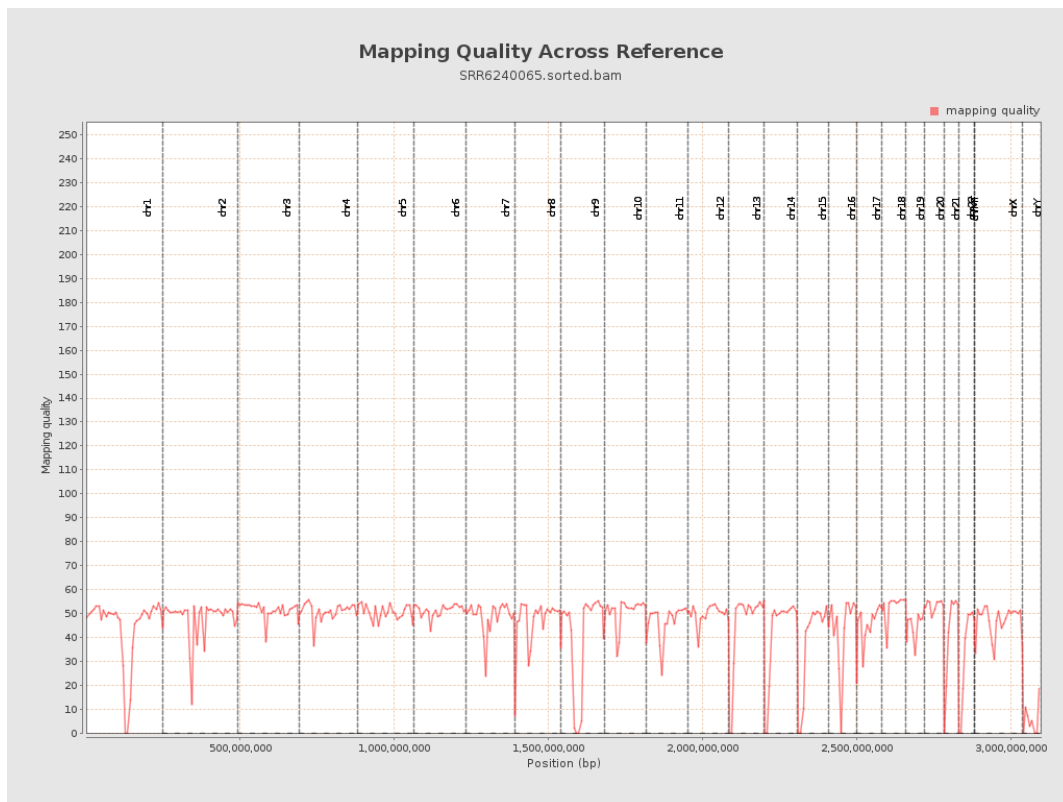
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

