

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:46:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240064.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_SRR6240064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,160,835
Mapped reads	2,356,498 / 74.55%
Unmapped reads	804,337 / 25.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,874 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	484,677 / 15.33%
Duplication rate	12.83%
Clipped reads	1,111,400 / 35.16%

2.2. ACGT Content

Number/percentage of A's	44,690,146 / 28.47%
Number/percentage of C's	29,482,092 / 18.78%
Number/percentage of T's	49,536,978 / 31.56%
Number/percentage of G's	33,245,052 / 21.18%
Number/percentage of N's	15,057 / 0.01%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.7191
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2.4. Mapping Quality

Mean Mapping Quality	46.56
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2.5. Mismatches and indels

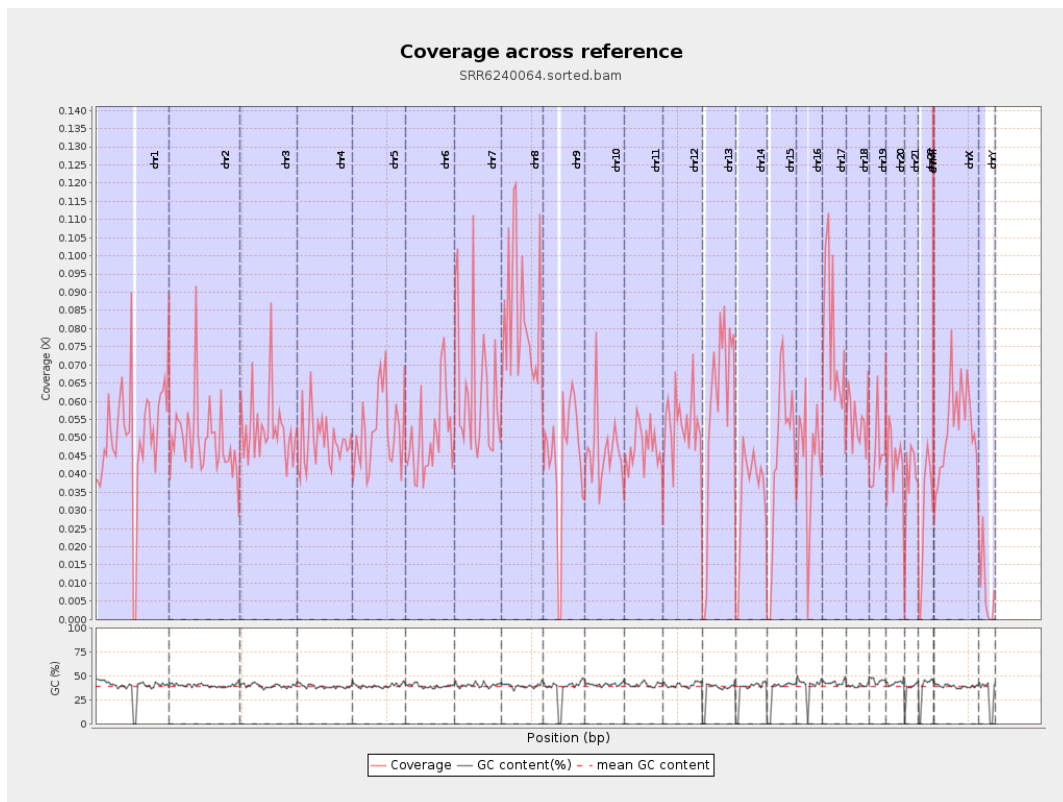
General error rate	0.82%
Mismatches	1,259,323
Insertions	12,384
Mapped reads with at least one insertion	0.52%
Deletions	35,688
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.33%

2.6. Chromosome stats

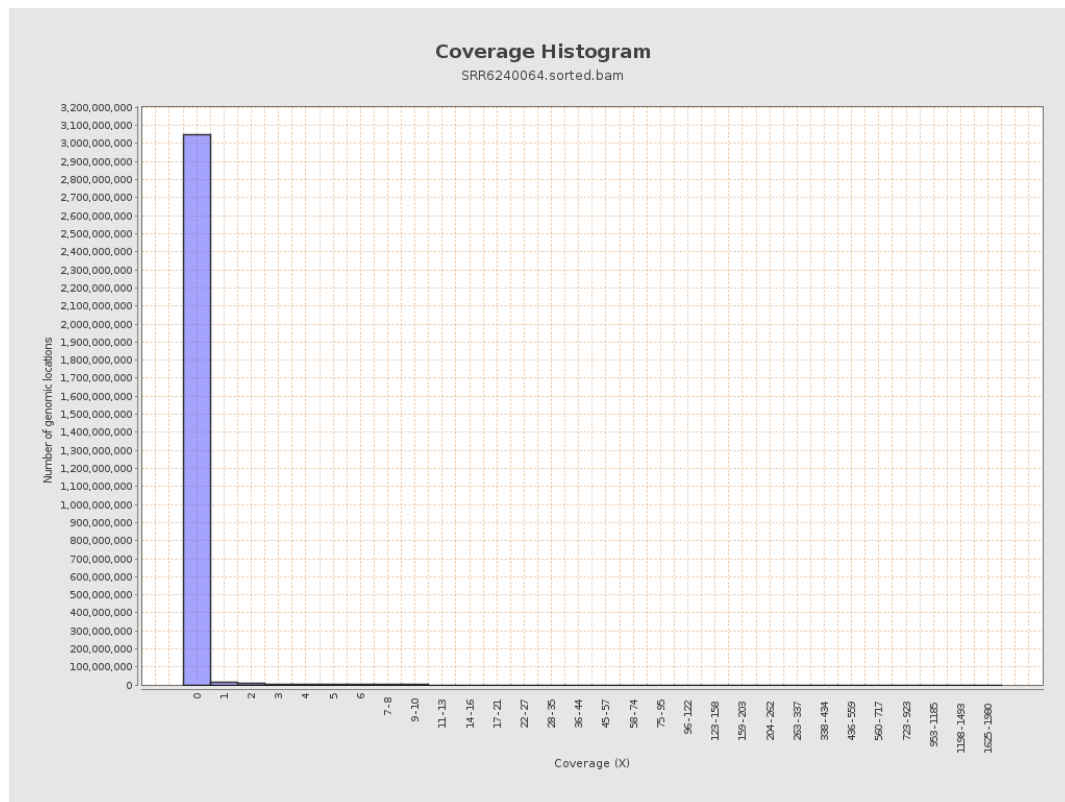
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12552766	0.0504	0.9631
chr2	243199373	12036216	0.0495	0.7039
chr3	198022430	10354547	0.0523	0.5669
chr4	191154276	9344398	0.0489	0.5675
chr5	180915260	9367788	0.0518	0.5636
chr6	171115067	8554414	0.05	0.5811
chr7	159138663	9879546	0.0621	0.9348

chr8	146364022	12005069	0.082	1.4069
chr9	141213431	6312721	0.0447	0.6286
chr10	135534747	6271298	0.0463	0.5824
chr11	135006516	6355447	0.0471	0.6943
chr12	133851895	7186587	0.0537	0.5755
chr13	115169878	6595995	0.0573	0.6037
chr14	107349540	3708912	0.0345	0.4742
chr15	102531392	4576062	0.0446	0.5167
chr16	90354753	3945375	0.0437	0.5193
chr17	81195210	6183066	0.0762	0.7452
chr18	78077248	4272667	0.0547	1.0399
chr19	59128983	2742053	0.0464	0.651
chr20	63025520	2749331	0.0436	0.5154
chr21	48129895	1832798	0.0381	0.4861
chr22	51304566	1454795	0.0284	0.3846
chrMT	16571	137725	8.3112	7.7364
chrX	155270560	8132843	0.0524	0.5924
chrY	59373566	479390	0.0081	0.2442

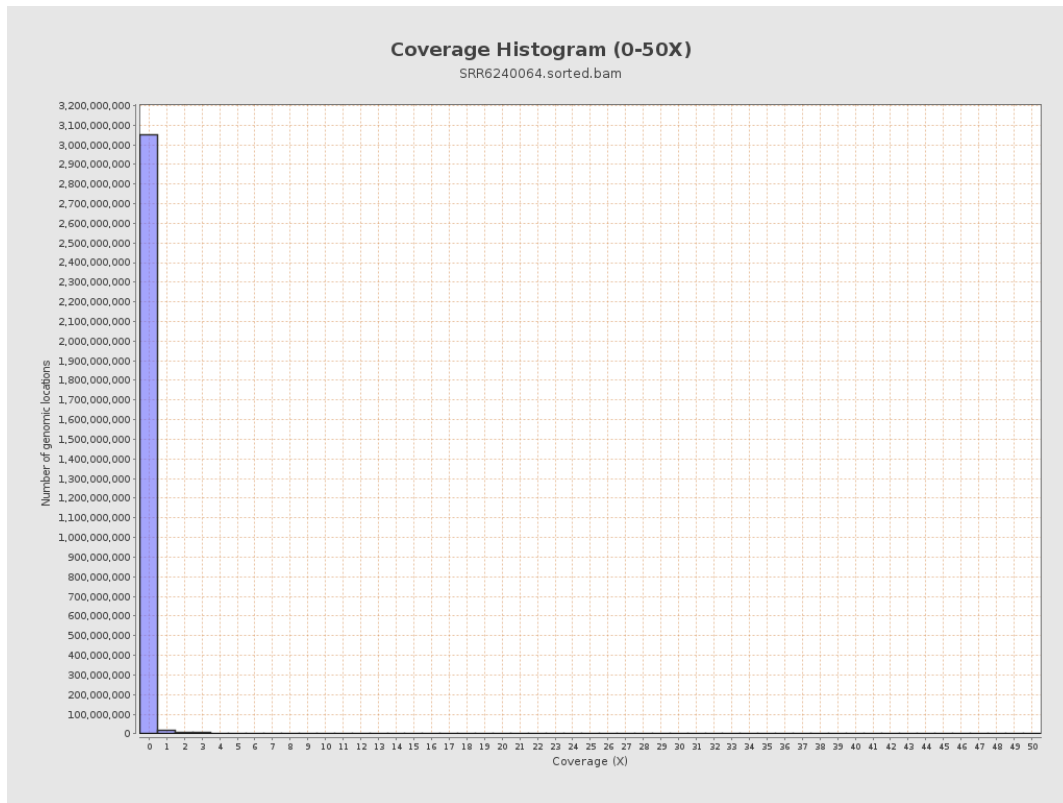
3. Results : Coverage across reference



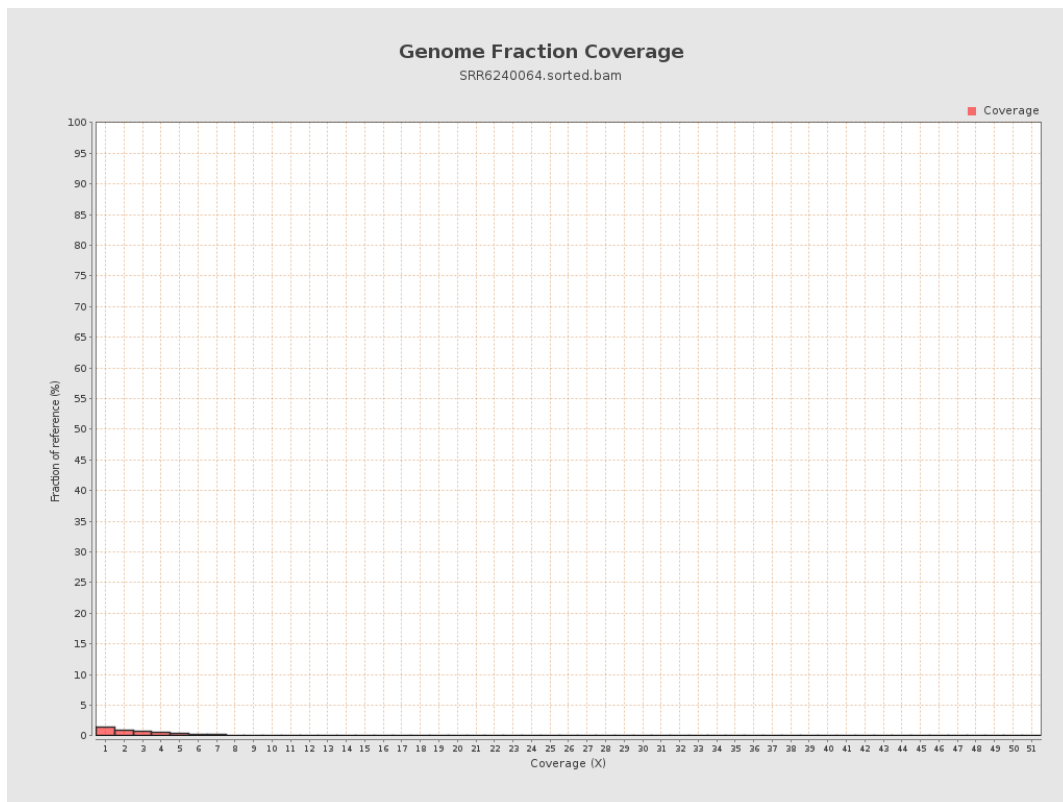
4. Results : Coverage Histogram



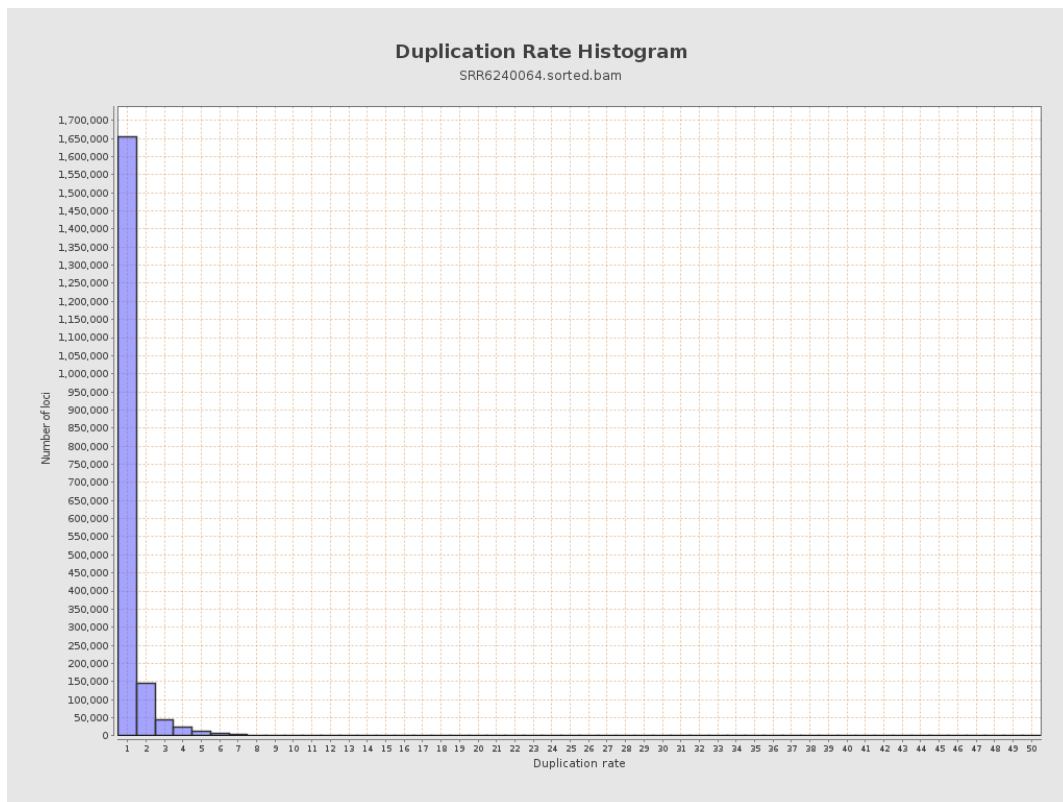
5. Results : Coverage Histogram (0-50X)



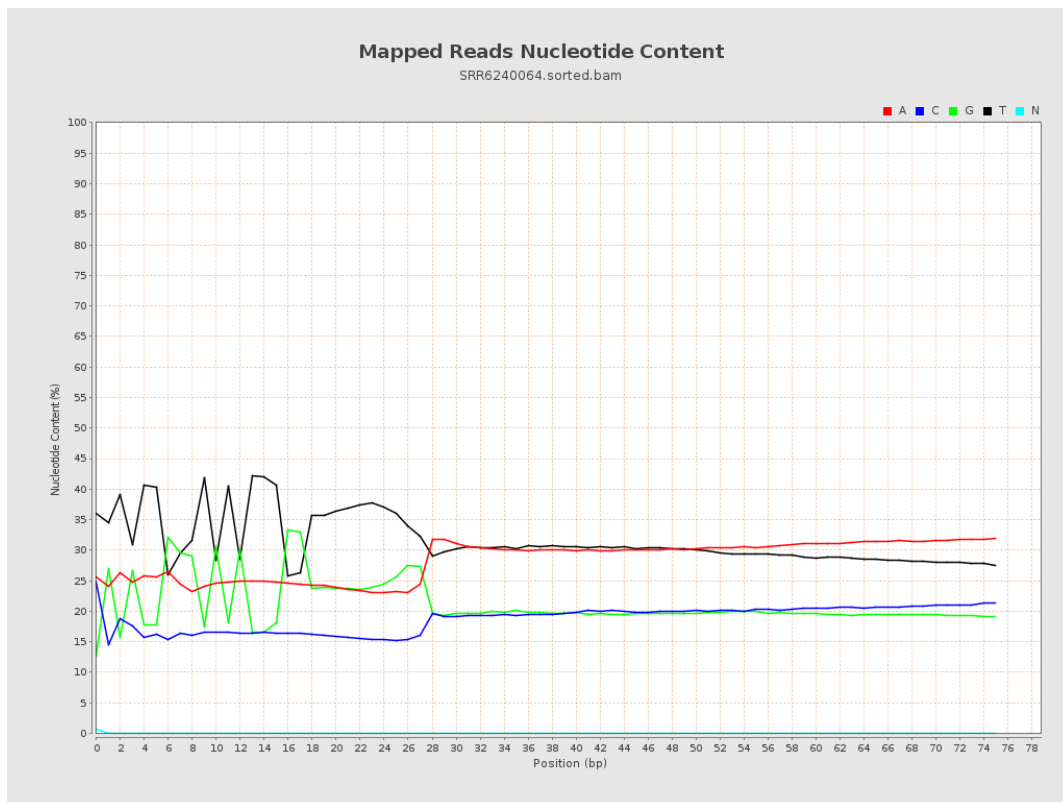
6. Results : Genome Fraction Coverage



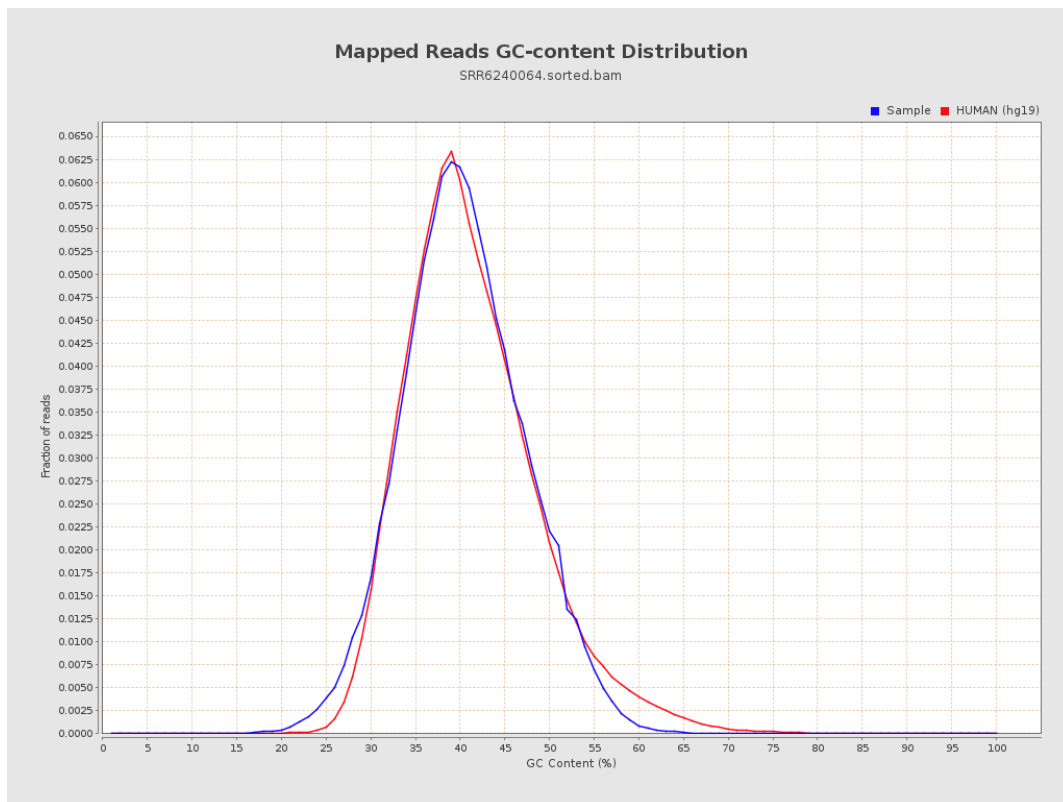
7. Results : Duplication Rate Histogram



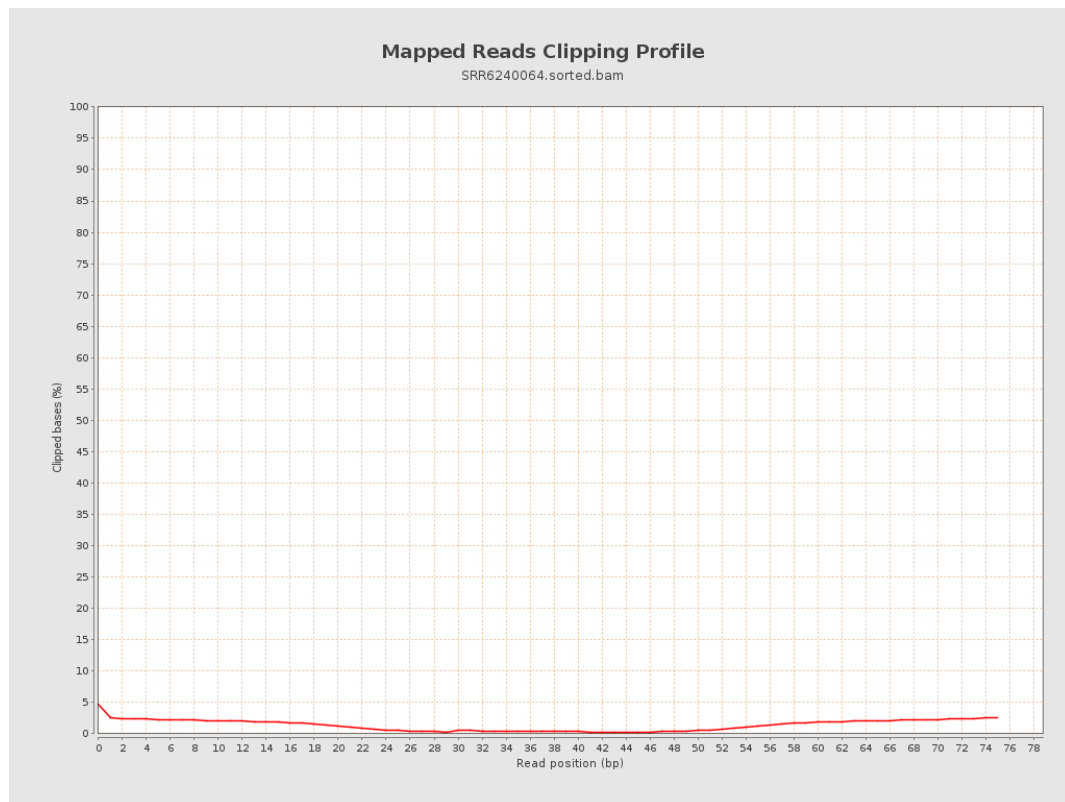
8. Results : Mapped Reads Nucleotide Content



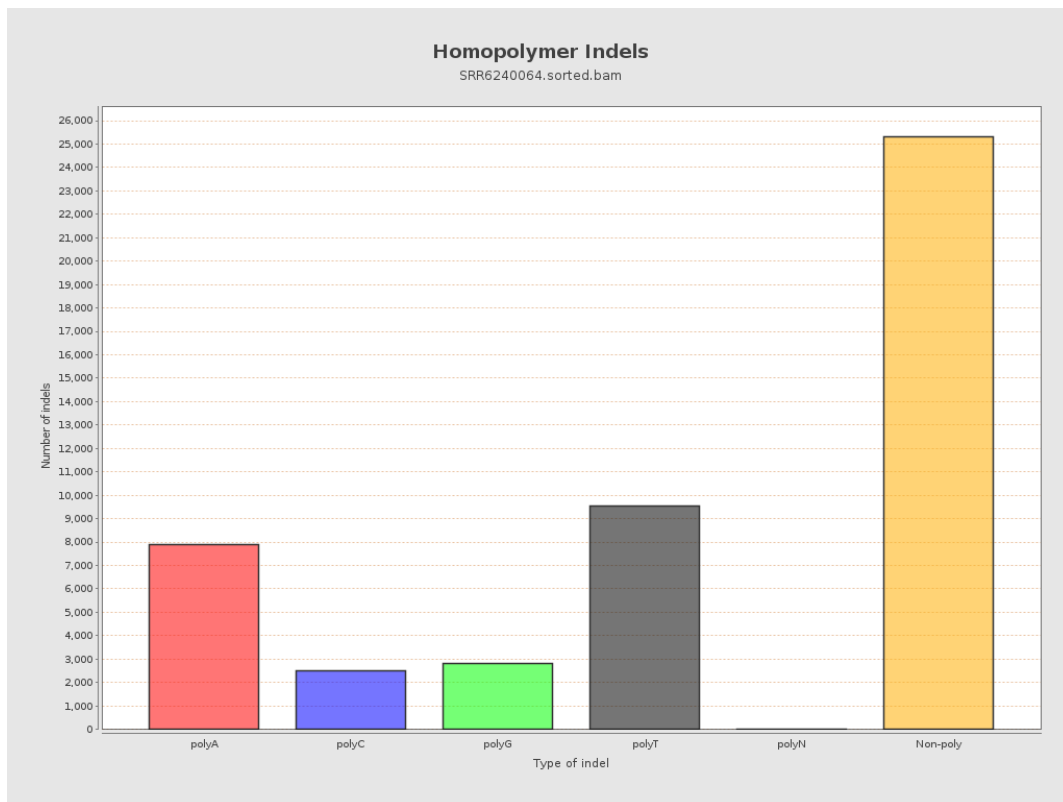
9. Results : Mapped Reads GC-content Distribution



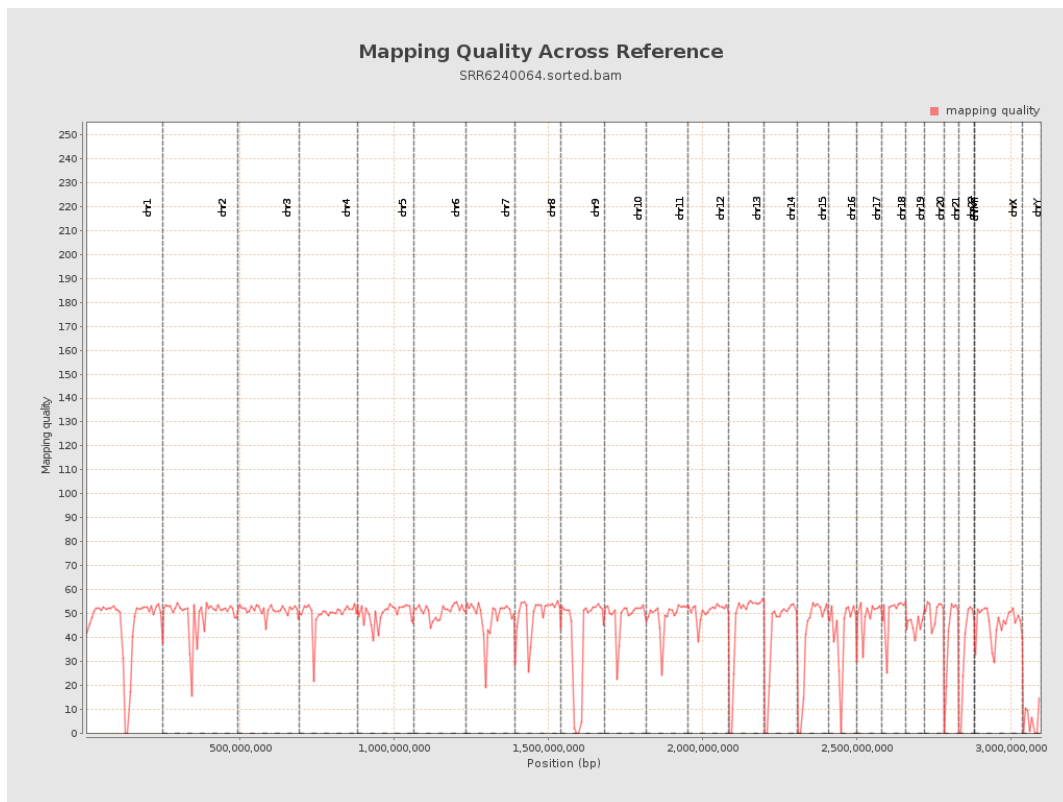
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

