

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251065.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_SRR10251065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:27:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,576,150
Mapped reads	3,471,860 / 97.08%
Unmapped reads	104,290 / 2.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,045 / 0.9%
Read min/max/mean length	30 / 80 / 80.32
Duplicated reads (estimated)	703,101 / 19.66%
Duplication rate	18.06%
Clipped reads	484,760 / 13.56%

2.2. ACGT Content

Number/percentage of A's	79,062,998 / 29.32%
Number/percentage of C's	53,736,640 / 19.93%
Number/percentage of T's	79,957,000 / 29.66%
Number/percentage of G's	56,843,453 / 21.08%
Number/percentage of N's	21,134 / 0.01%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0871

Standard Deviation	0.7924
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2.4. Mapping Quality

Mean Mapping Quality	48.23
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2.5. Mismatches and indels

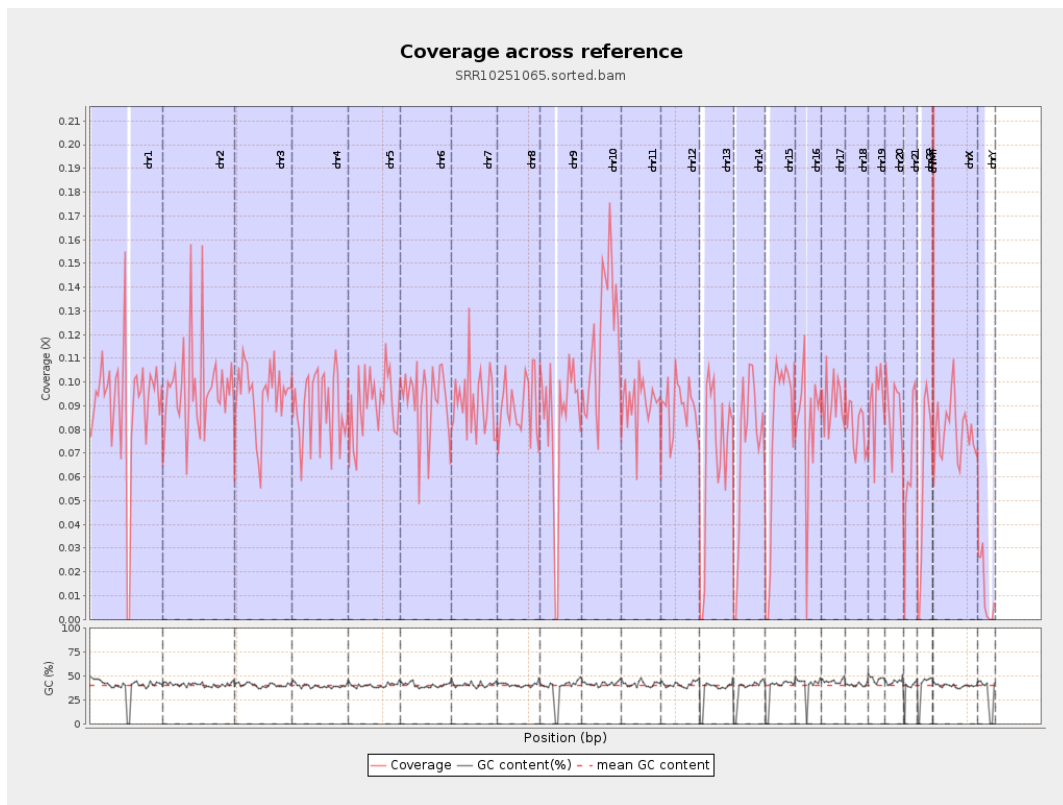
General error rate	0.59%
Mismatches	1,518,379
Insertions	33,435
Mapped reads with at least one insertion	0.95%
Deletions	93,962
Mapped reads with at least one deletion	2.66%
Homopolymer indels	45.78%

2.6. Chromosome stats

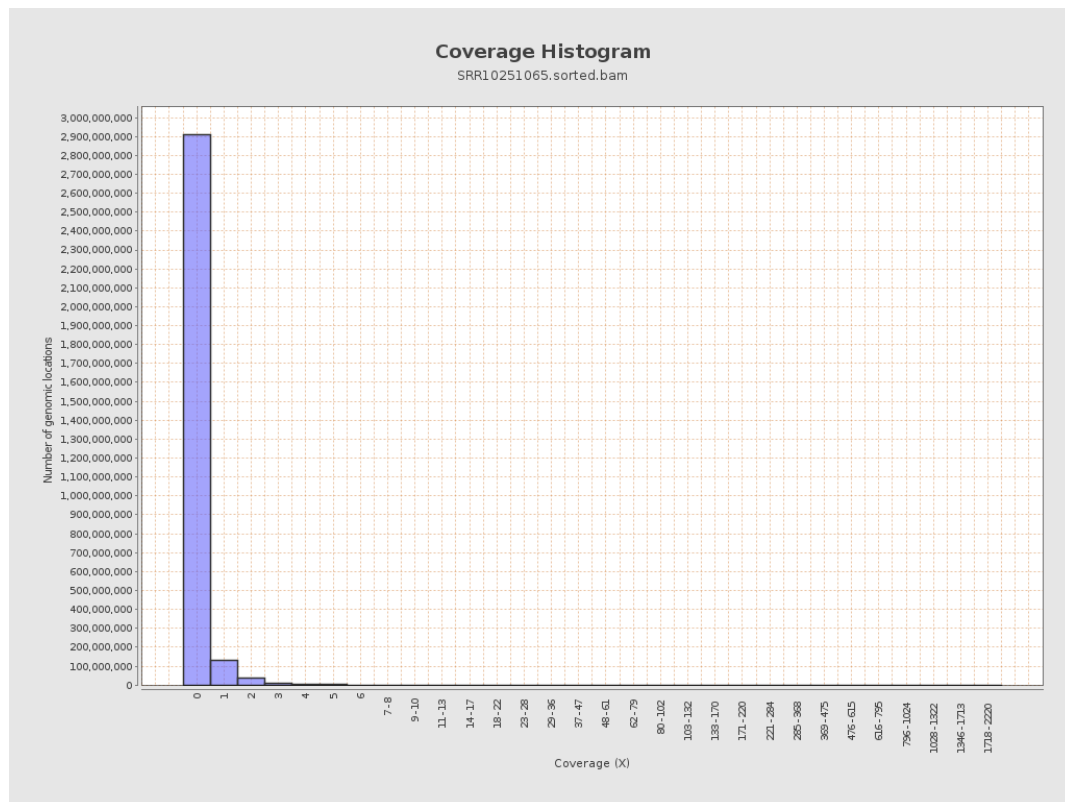
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22543246	0.0904	1.5284
chr2	243199373	23788526	0.0978	1.1375
chr3	198022430	18678077	0.0943	0.4195
chr4	191154276	17065716	0.0893	0.4586
chr5	180915260	16432580	0.0908	0.4258
chr6	171115067	15753358	0.0921	0.4902
chr7	159138663	14562925	0.0915	1.0629

chr8	146364022	13078394	0.0894	0.5626
chr9	141213431	11782091	0.0834	0.7946
chr10	135534747	16107710	0.1188	0.847
chr11	135006516	12351753	0.0915	0.5237
chr12	133851895	12109550	0.0905	0.4162
chr13	115169878	7964776	0.0692	0.3539
chr14	107349540	7820482	0.0729	0.4973
chr15	102531392	7916521	0.0772	0.3761
chr16	90354753	7383523	0.0817	0.6921
chr17	81195210	7488296	0.0922	0.4894
chr18	78077248	6369145	0.0816	0.9198
chr19	59128983	5378174	0.091	1.5183
chr20	63025520	5498916	0.0872	0.4375
chr21	48129895	3199849	0.0665	0.3811
chr22	51304566	3150813	0.0614	0.3614
chrMT	16571	325408	19.6372	10.4699
chrX	155270560	12345706	0.0795	0.4427
chrY	59373566	693980	0.0117	0.8149

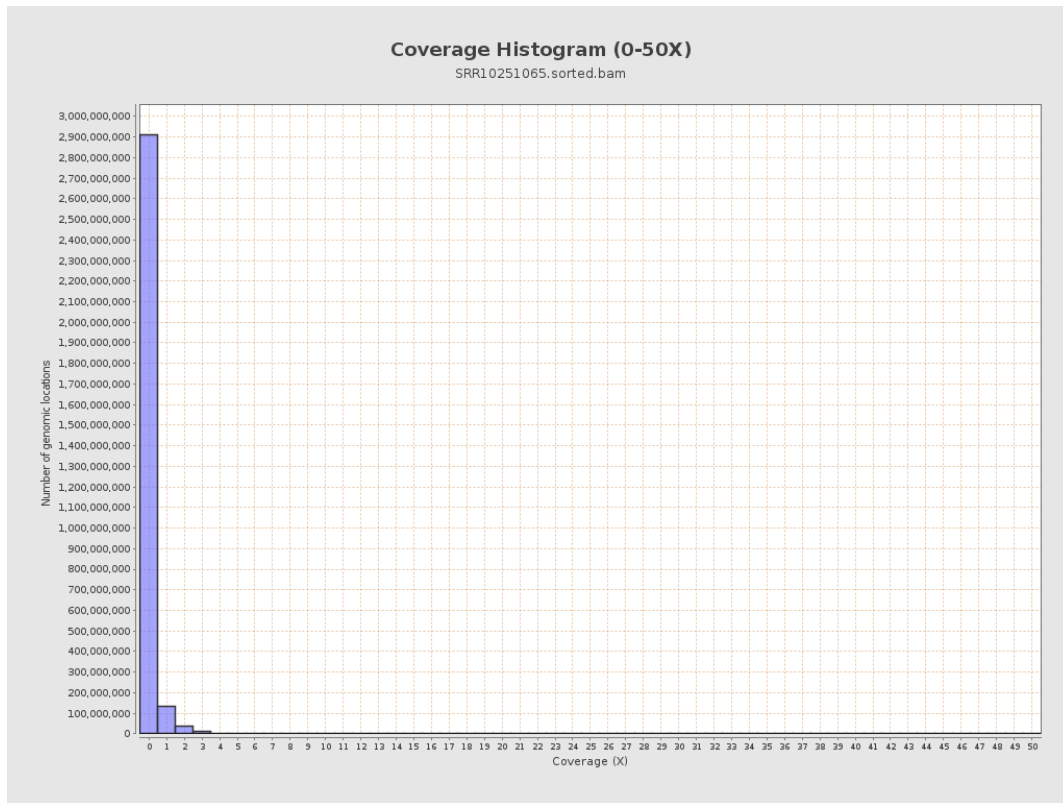
3. Results : Coverage across reference



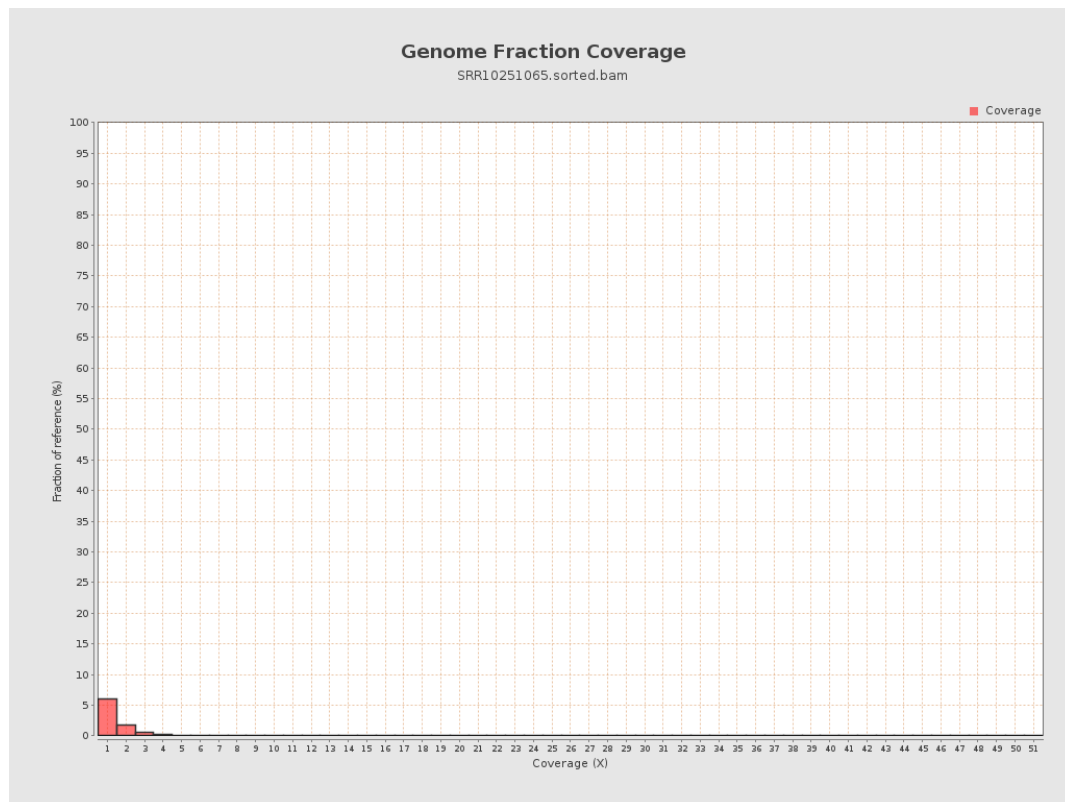
4. Results : Coverage Histogram



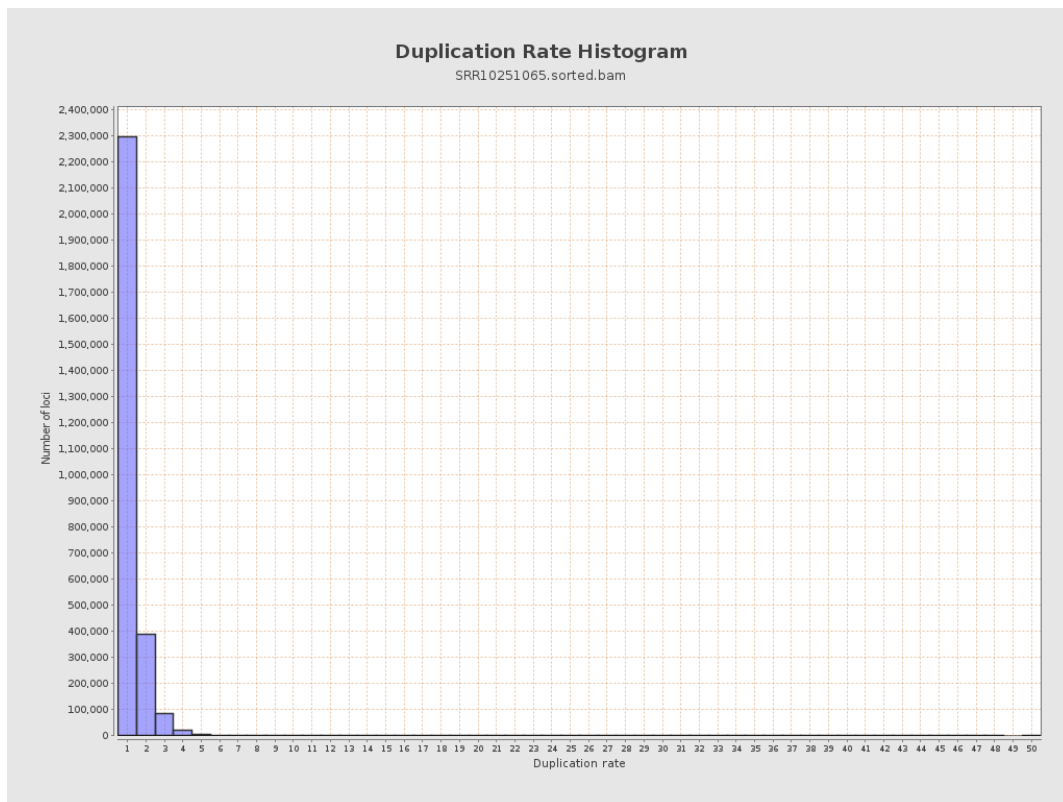
5. Results : Coverage Histogram (0-50X)



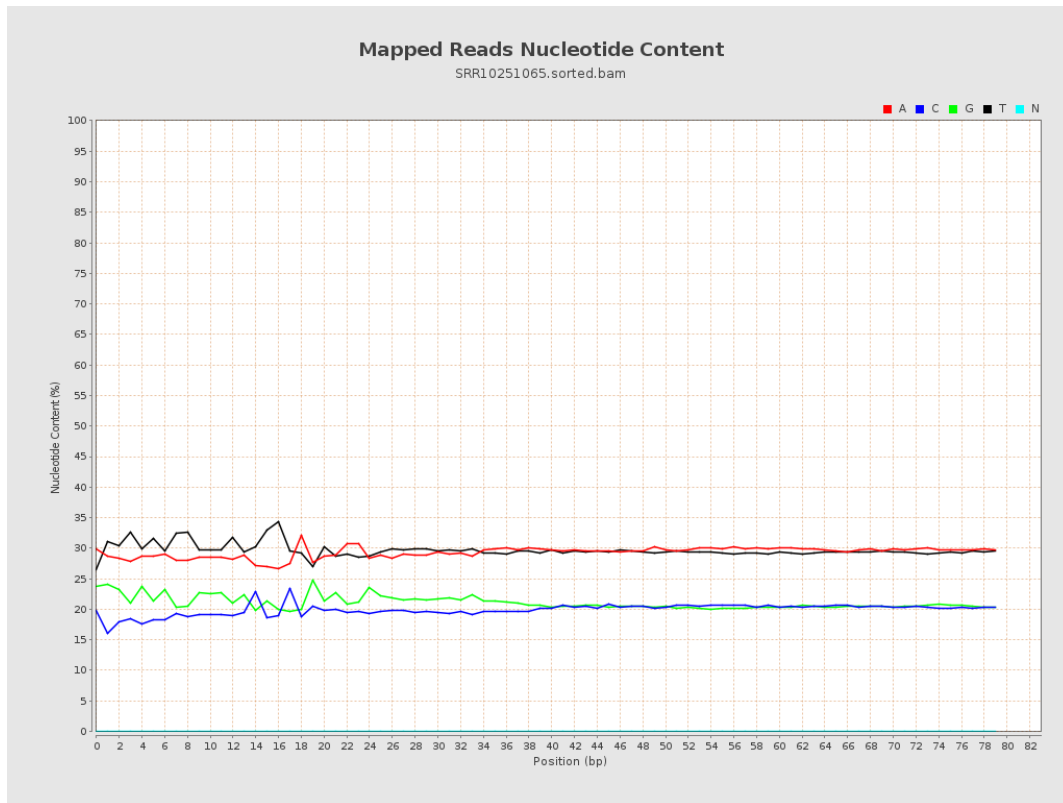
6. Results : Genome Fraction Coverage



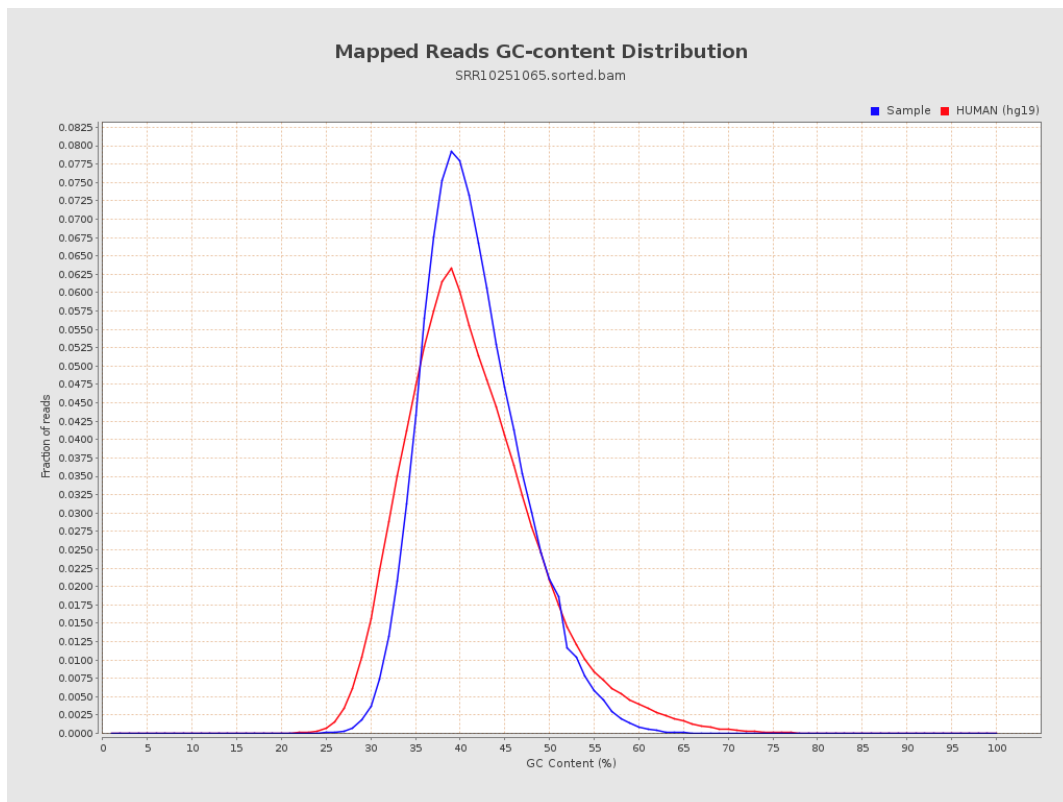
7. Results : Duplication Rate Histogram



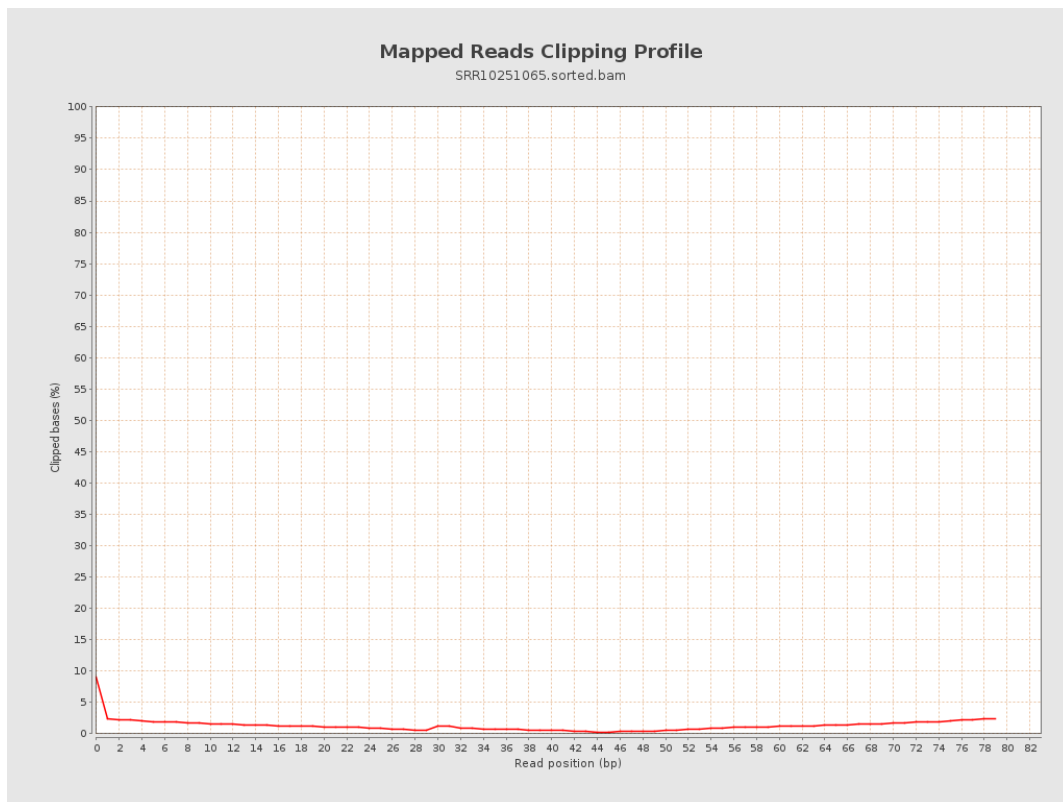
8. Results : Mapped Reads Nucleotide Content



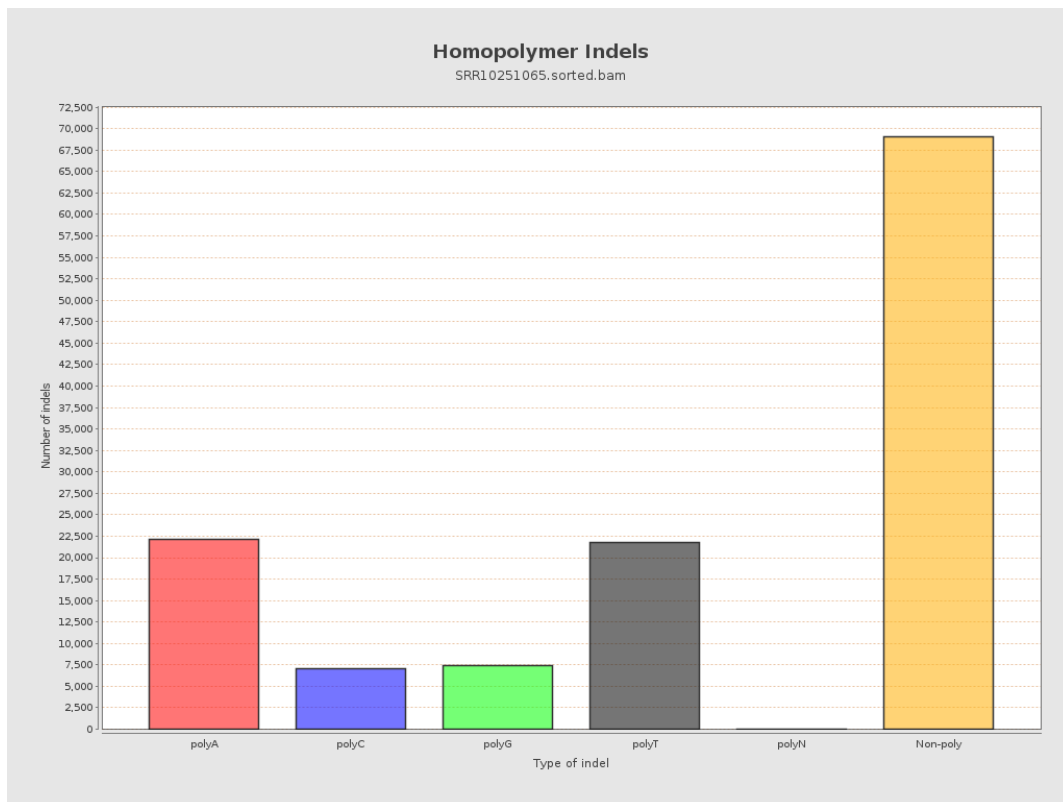
9. Results : Mapped Reads GC-content Distribution



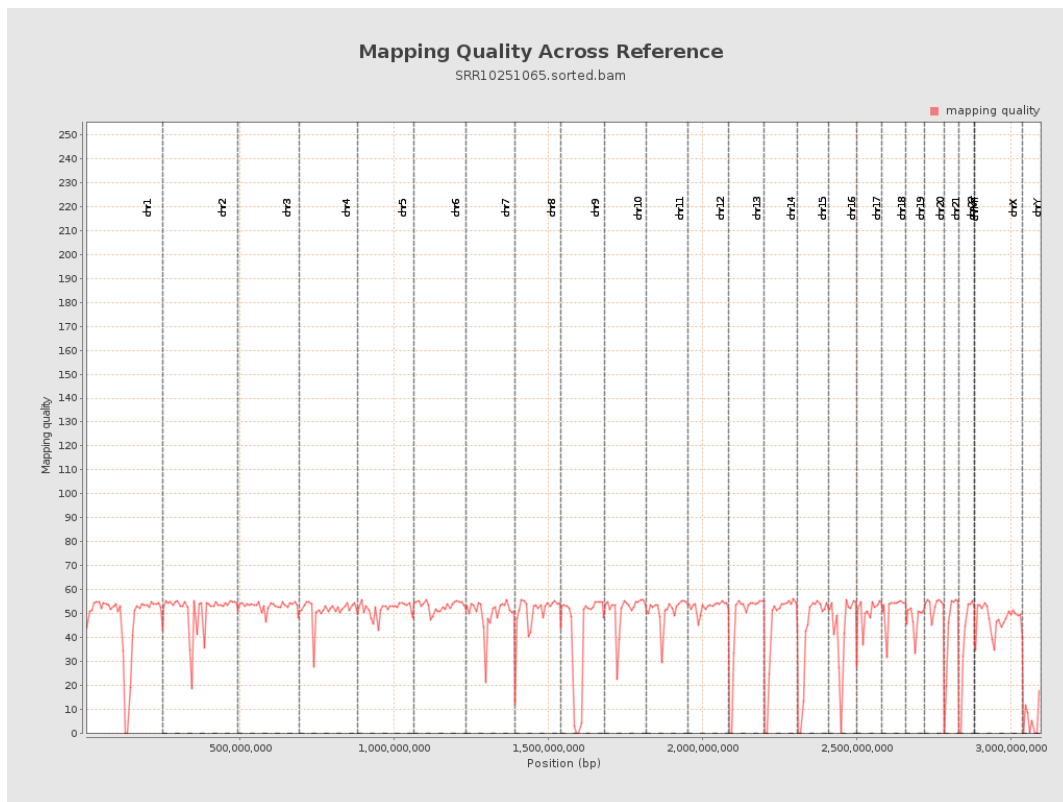
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

