

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:39:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251067.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_SRR10251067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:39:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,918,213
Mapped reads	3,695,212 / 94.31%
Unmapped reads	223,001 / 5.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,340 / 0.8%
Read min/max/mean length	30 / 80 / 80.29
Duplicated reads (estimated)	790,435 / 20.17%
Duplication rate	19%
Clipped reads	528,626 / 13.49%

2.2. ACGT Content

Number/percentage of A's	83,644,675 / 29.21%
Number/percentage of C's	57,413,497 / 20.05%
Number/percentage of T's	84,499,797 / 29.51%
Number/percentage of G's	60,820,776 / 21.24%
Number/percentage of N's	2,489 / 0%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0926

Standard Deviation	0.9135
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2.4. Mapping Quality

Mean Mapping Quality	48.05
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2.5. Mismatches and indels

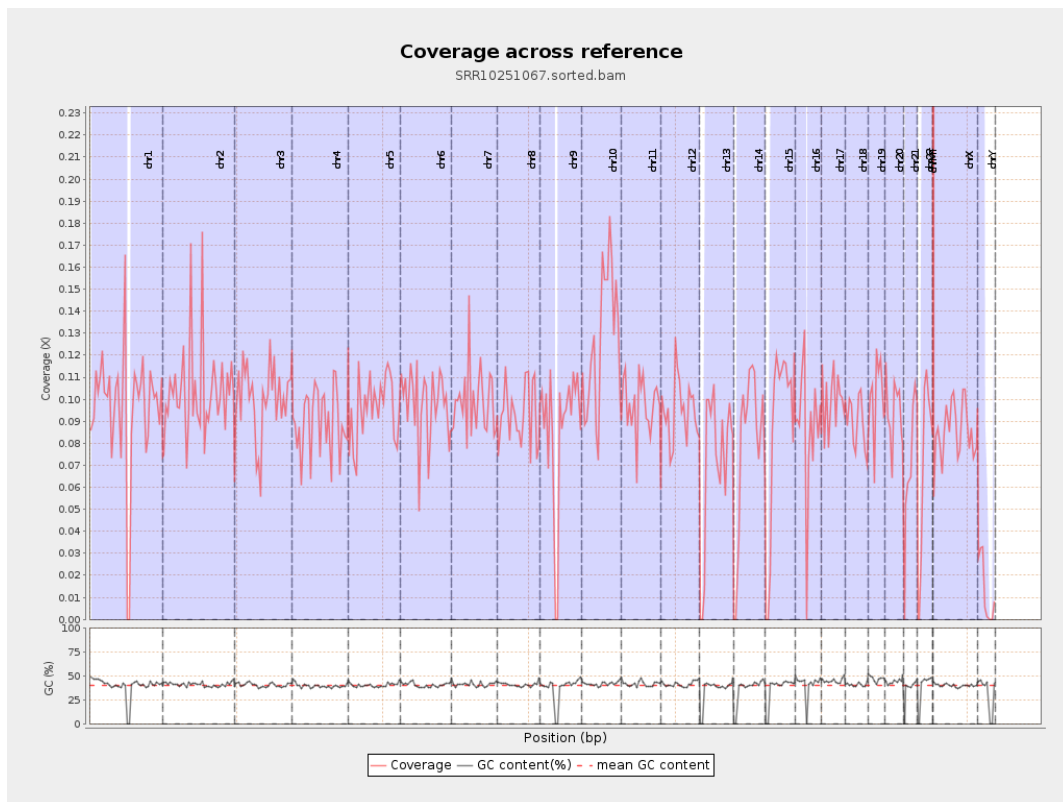
General error rate	0.61%
Mismatches	1,670,116
Insertions	36,561
Mapped reads with at least one insertion	0.97%
Deletions	107,399
Mapped reads with at least one deletion	2.86%
Homopolymer indels	45.15%

2.6. Chromosome stats

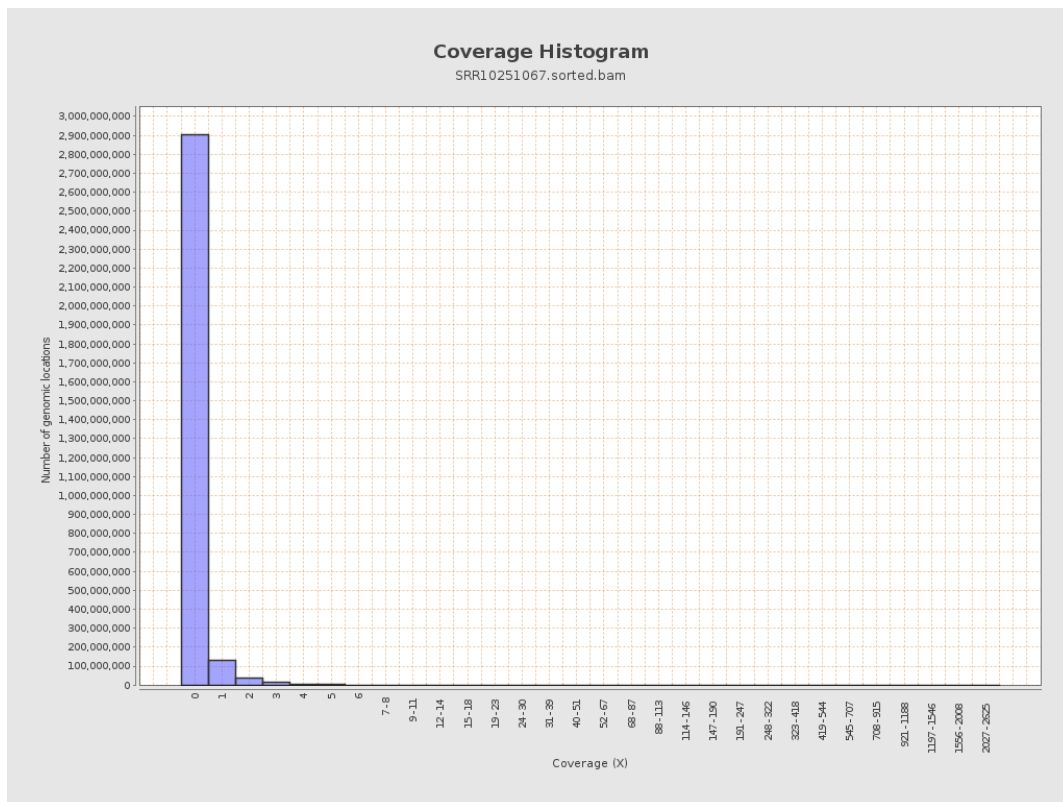
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23993655	0.0963	1.7929
chr2	243199373	25297058	0.104	1.3831
chr3	198022430	19744420	0.0997	0.4397
chr4	191154276	17091582	0.0894	0.492
chr5	180915260	17442054	0.0964	0.4571
chr6	171115067	16666638	0.0974	0.5365
chr7	159138663	15721231	0.0988	1.2395

chr8	146364022	13563231	0.0927	0.6048
chr9	141213431	12196154	0.0864	0.9401
chr10	135534747	17165316	0.1266	0.9795
chr11	135006516	13133121	0.0973	0.5596
chr12	133851895	12823828	0.0958	0.4452
chr13	115169878	8187428	0.0711	0.3683
chr14	107349540	8630189	0.0804	0.5554
chr15	102531392	8758635	0.0854	0.4075
chr16	90354753	7771043	0.086	0.8244
chr17	81195210	8118994	0.1	0.4976
chr18	78077248	6984332	0.0895	1.0207
chr19	59128983	5985954	0.1012	1.6635
chr20	63025520	5876501	0.0932	0.4523
chr21	48129895	3454738	0.0718	0.3968
chr22	51304566	3594783	0.0701	0.3984
chrMT	16571	307677	18.5672	10.8829
chrX	155270560	13297901	0.0856	0.4698
chrY	59373566	766906	0.0129	1.0068

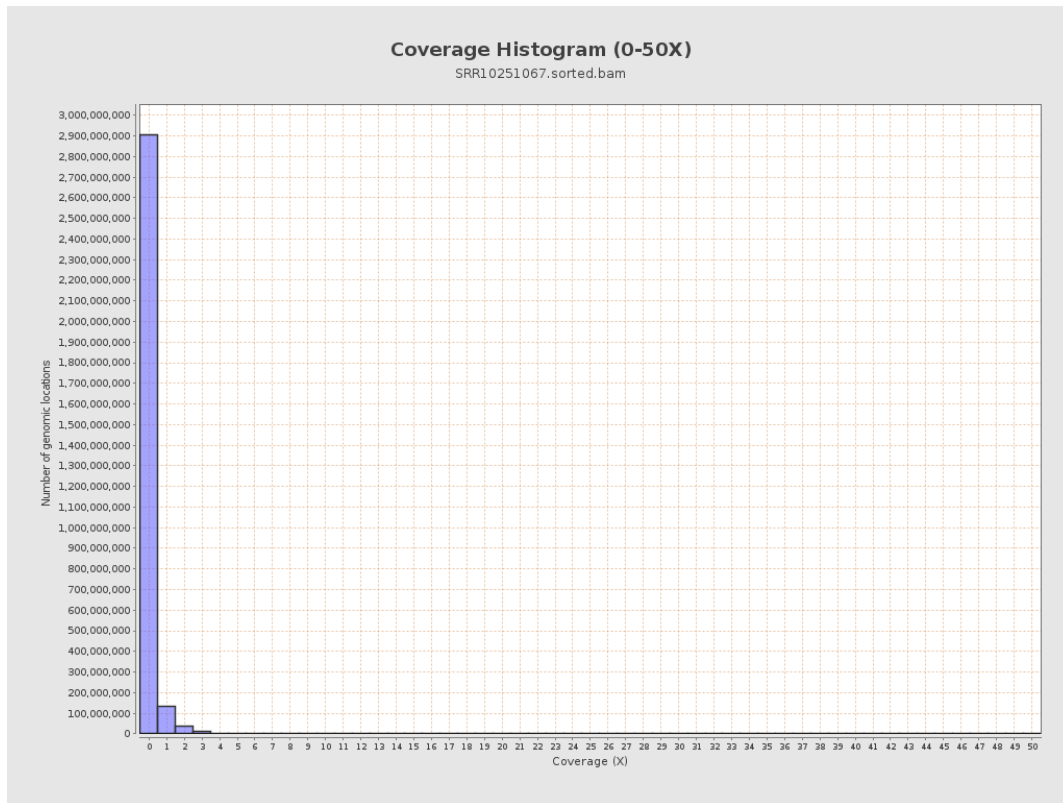
3. Results : Coverage across reference



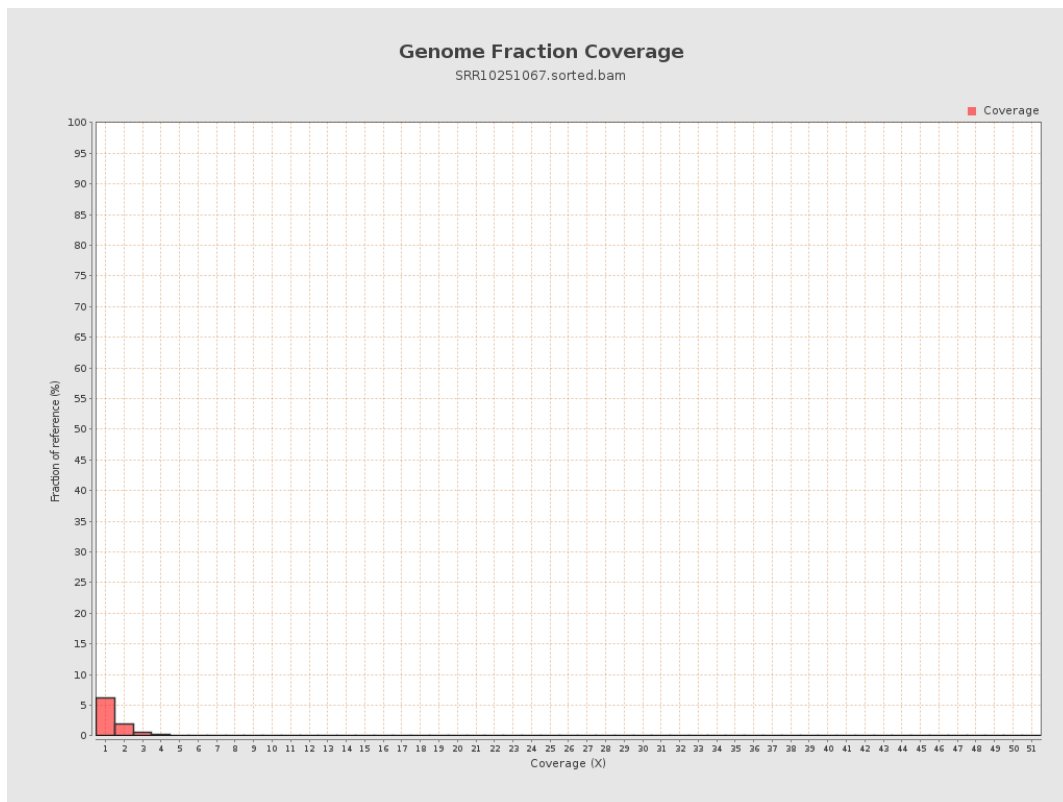
4. Results : Coverage Histogram



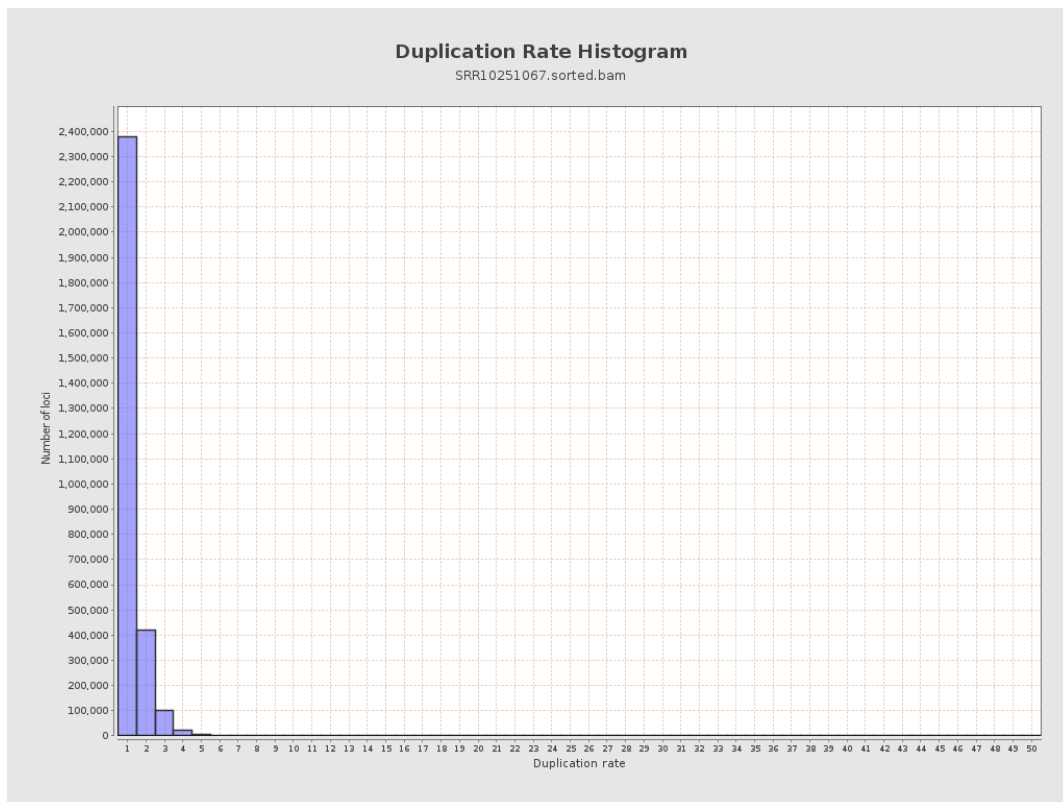
5. Results : Coverage Histogram (0-50X)



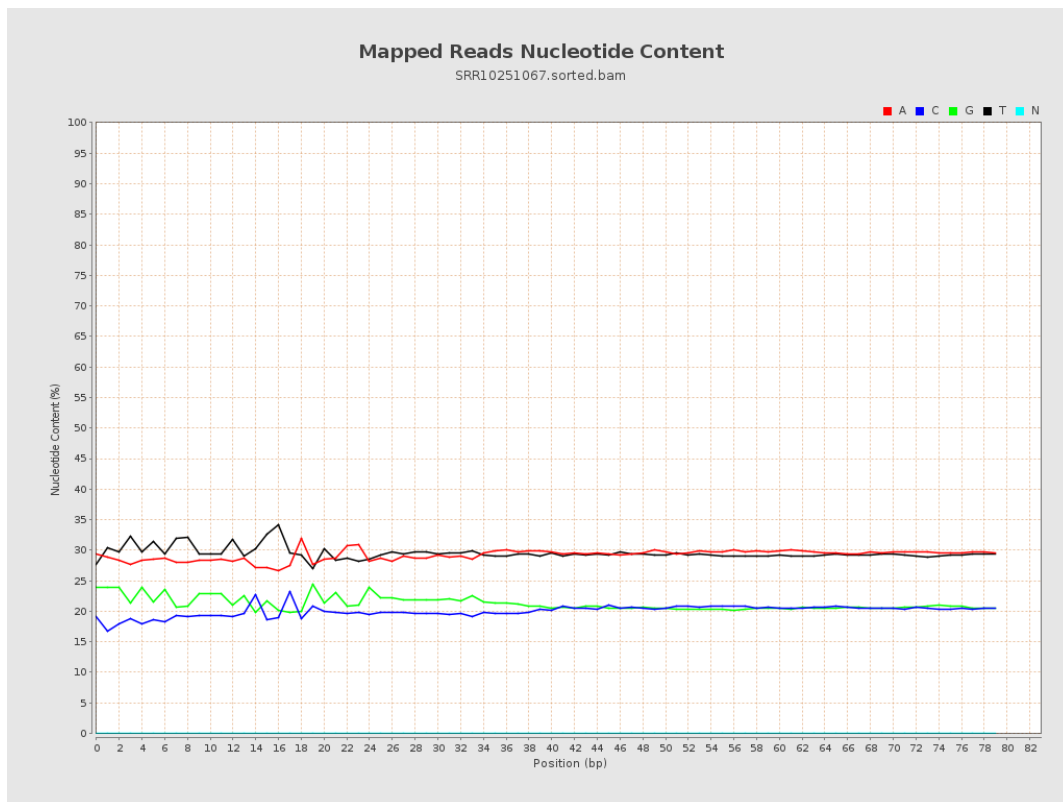
6. Results : Genome Fraction Coverage



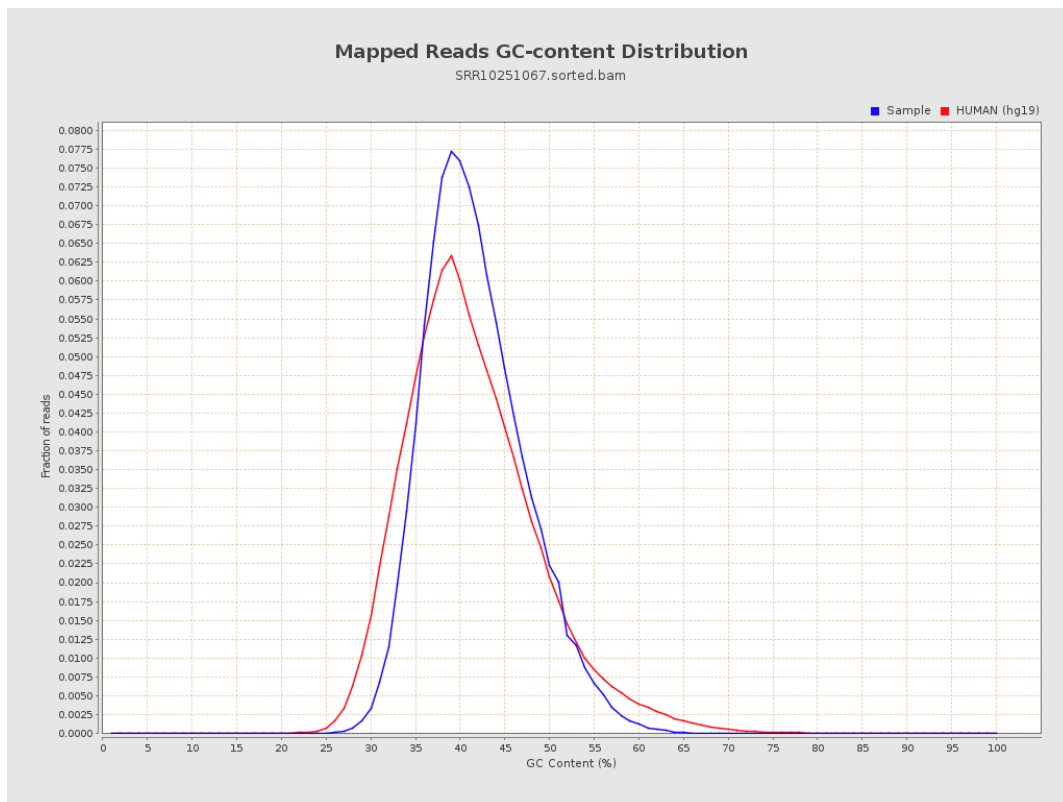
7. Results : Duplication Rate Histogram



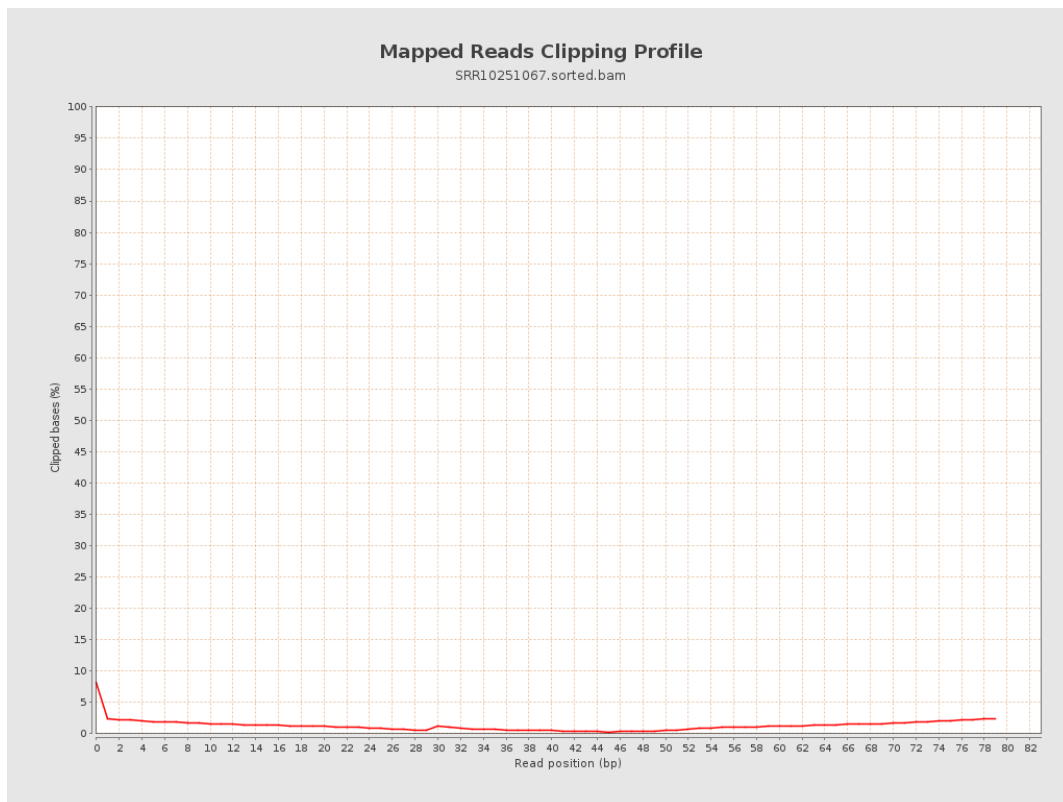
8. Results : Mapped Reads Nucleotide Content



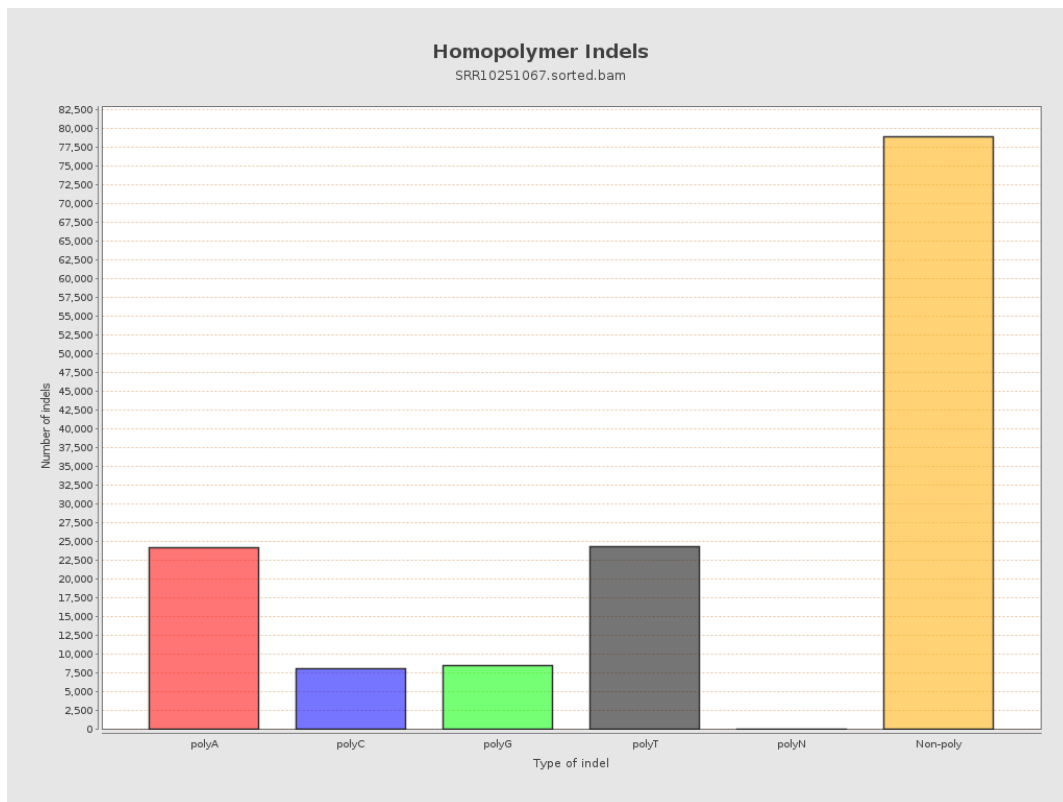
9. Results : Mapped Reads GC-content Distribution



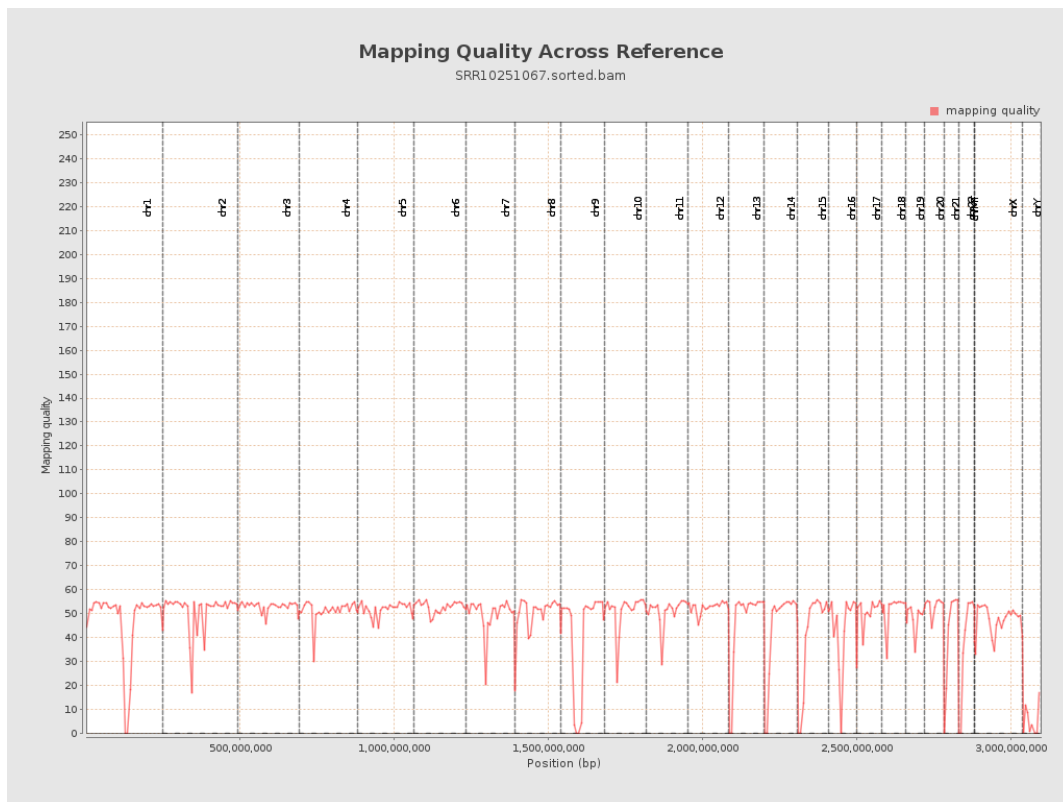
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

