

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:29:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085126.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_SRR3085126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:29:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,045
Mapped reads	1,824,738 / 88.97%
Unmapped reads	226,307 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,561 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	63,359 / 3.09%
Duplication rate	2.7%
Clipped reads	830,522 / 40.49%

2.2. ACGT Content

Number/percentage of A's	33,917,648 / 27.87%
Number/percentage of C's	22,533,089 / 18.51%
Number/percentage of T's	38,150,918 / 31.35%
Number/percentage of G's	27,084,071 / 22.25%
Number/percentage of N's	22,262 / 0.02%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3339
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2.4. Mapping Quality

Mean Mapping Quality	45.64
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2.5. Mismatches and indels

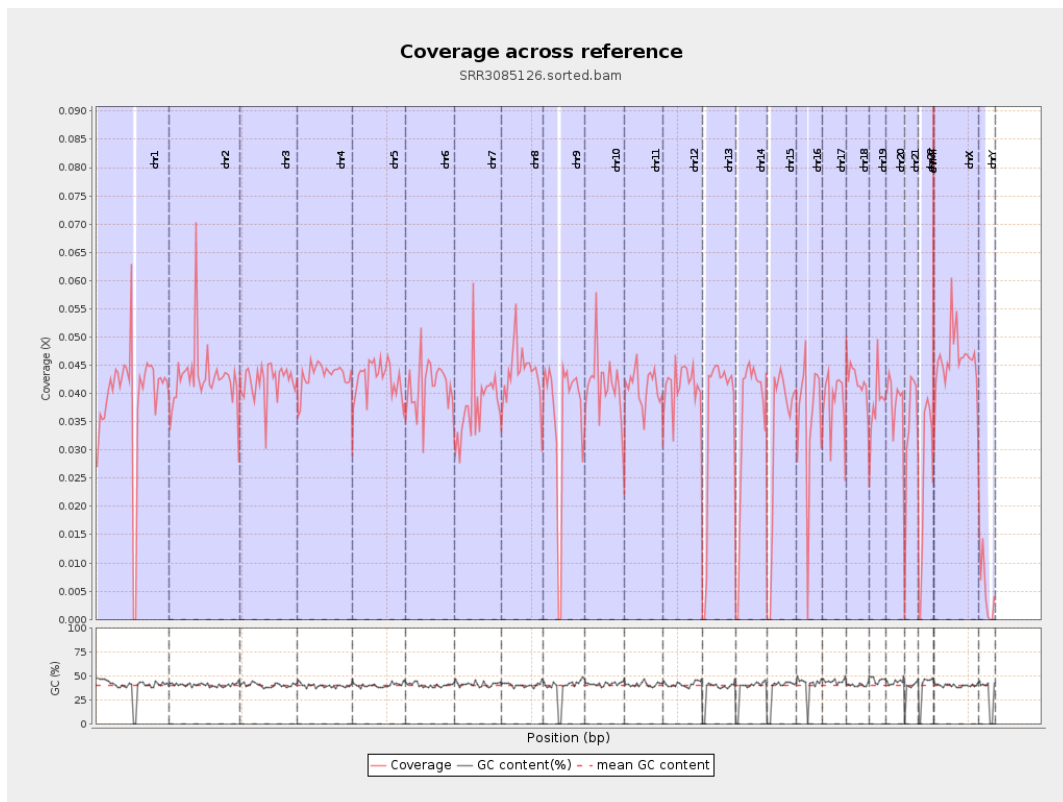
General error rate	0.9%
Mismatches	1,078,661
Insertions	9,644
Mapped reads with at least one insertion	0.52%
Deletions	27,102
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.58%

2.6. Chromosome stats

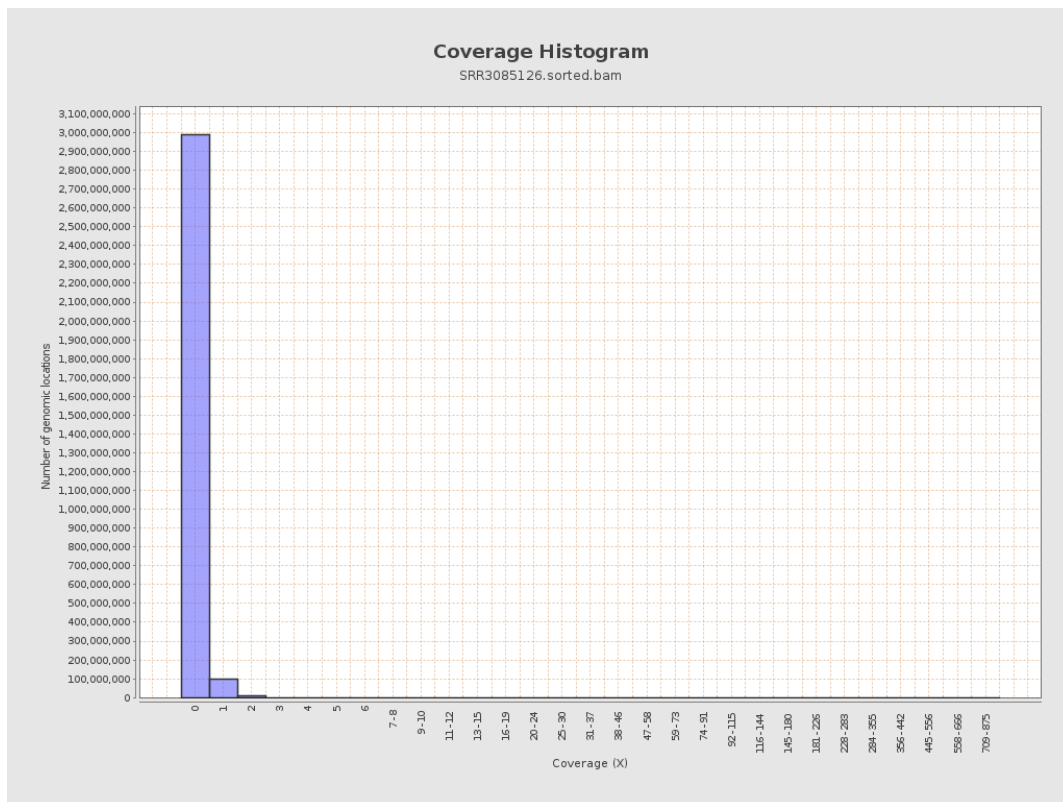
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9792363	0.0393	0.5611
chr2	243199373	10414336	0.0428	0.4066
chr3	198022430	8351531	0.0422	0.2229
chr4	191154276	8264813	0.0432	0.234
chr5	180915260	7706160	0.0426	0.2249
chr6	171115067	7039111	0.0411	0.2592
chr7	159138663	6070093	0.0381	0.4032

chr8	146364022	6371123	0.0435	0.5651
chr9	141213431	5091483	0.0361	0.2926
chr10	135534747	5641167	0.0416	0.3011
chr11	135006516	5514435	0.0408	0.2833
chr12	133851895	5532814	0.0413	0.2242
chr13	115169878	4109652	0.0357	0.207
chr14	107349540	3764133	0.0351	0.2168
chr15	102531392	3374955	0.0329	0.2049
chr16	90354753	3253268	0.036	0.2228
chr17	81195210	3119898	0.0384	0.2286
chr18	78077248	3309895	0.0424	0.4892
chr19	59128983	2273686	0.0385	0.448
chr20	63025520	2432536	0.0386	0.2177
chr21	48129895	1610495	0.0335	0.2082
chr22	51304566	1289719	0.0251	0.1716
chrMT	16571	2445	0.1475	0.4106
chrX	155270560	7120965	0.0459	0.2543
chrY	59373566	300690	0.0051	0.1078

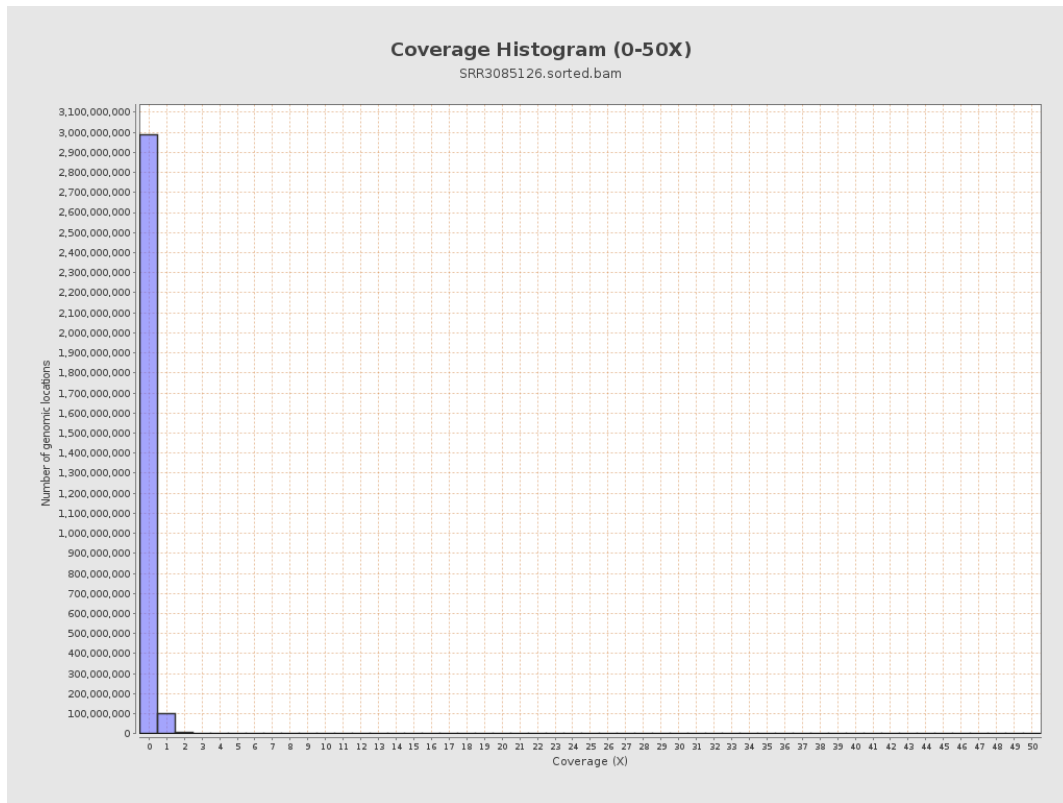
3. Results : Coverage across reference



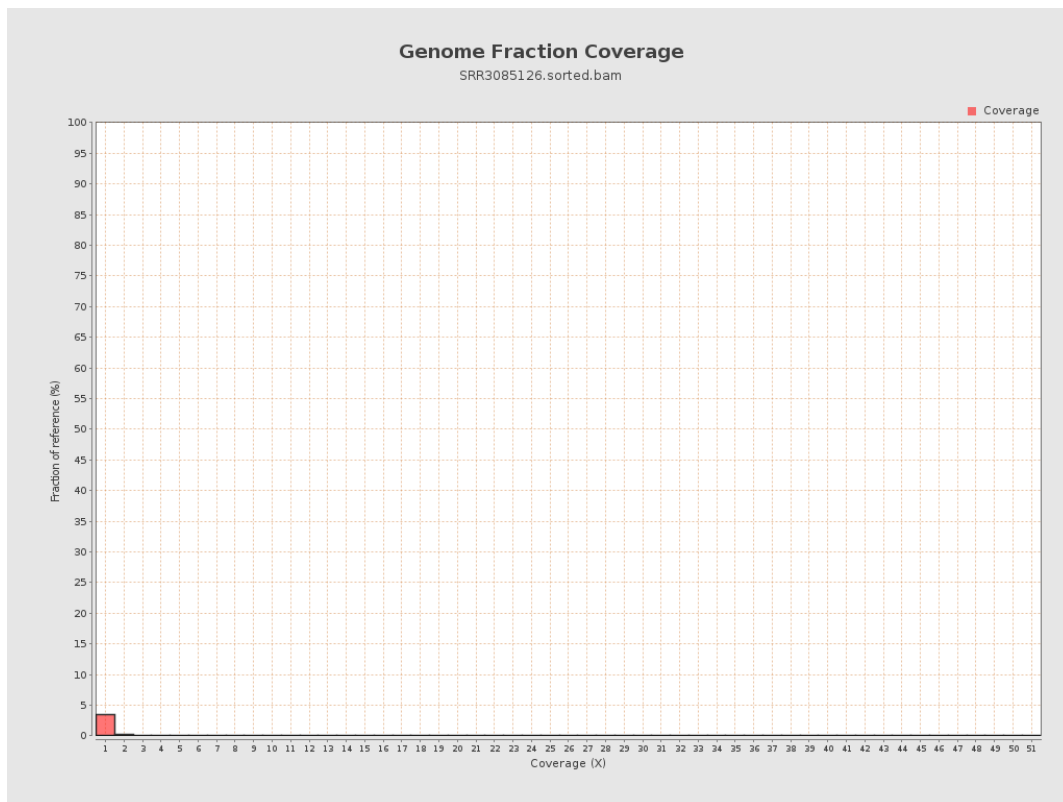
4. Results : Coverage Histogram



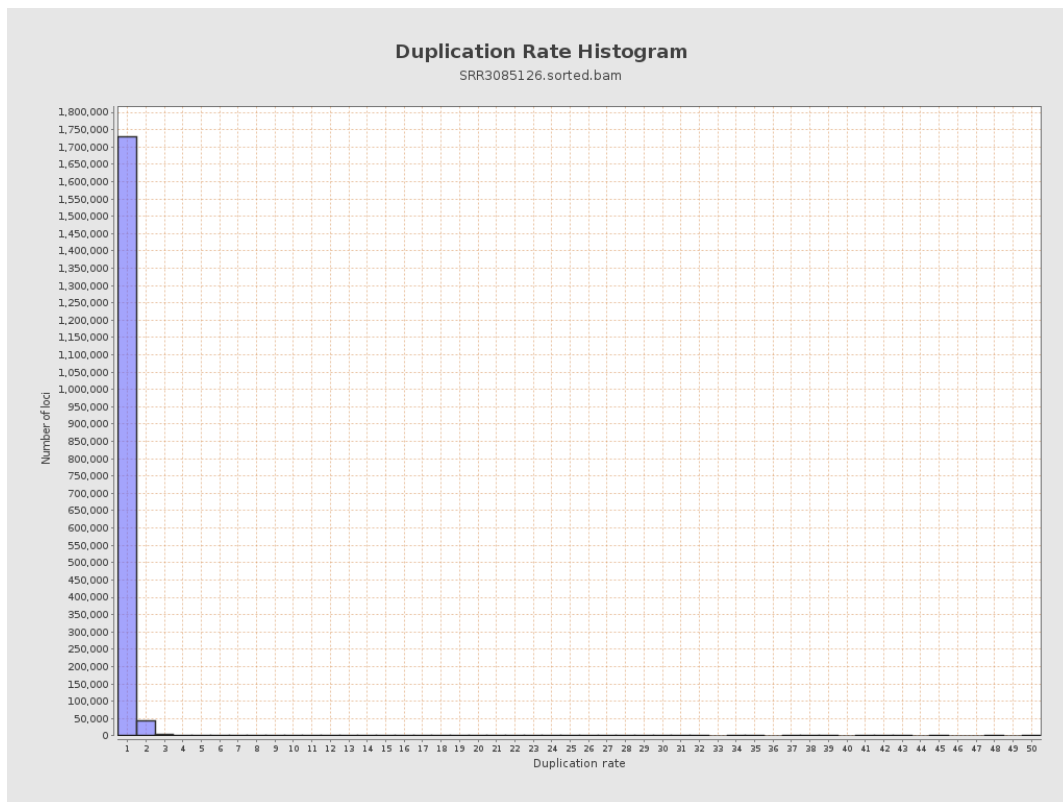
5. Results : Coverage Histogram (0-50X)



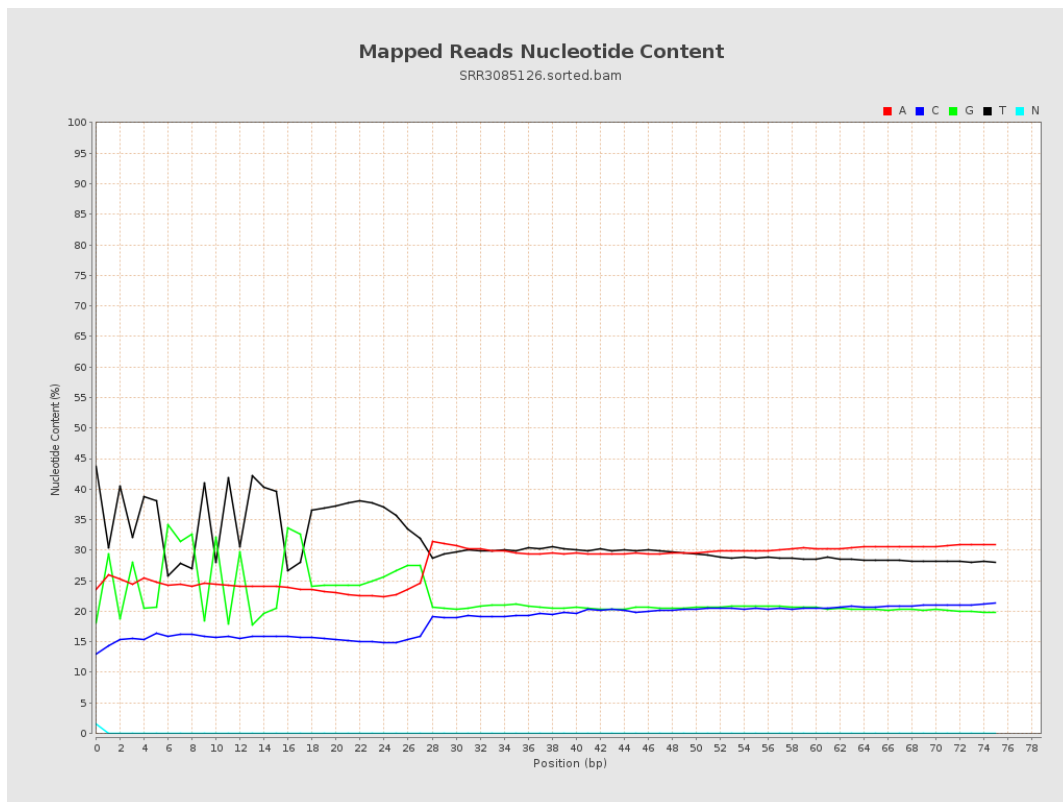
6. Results : Genome Fraction Coverage



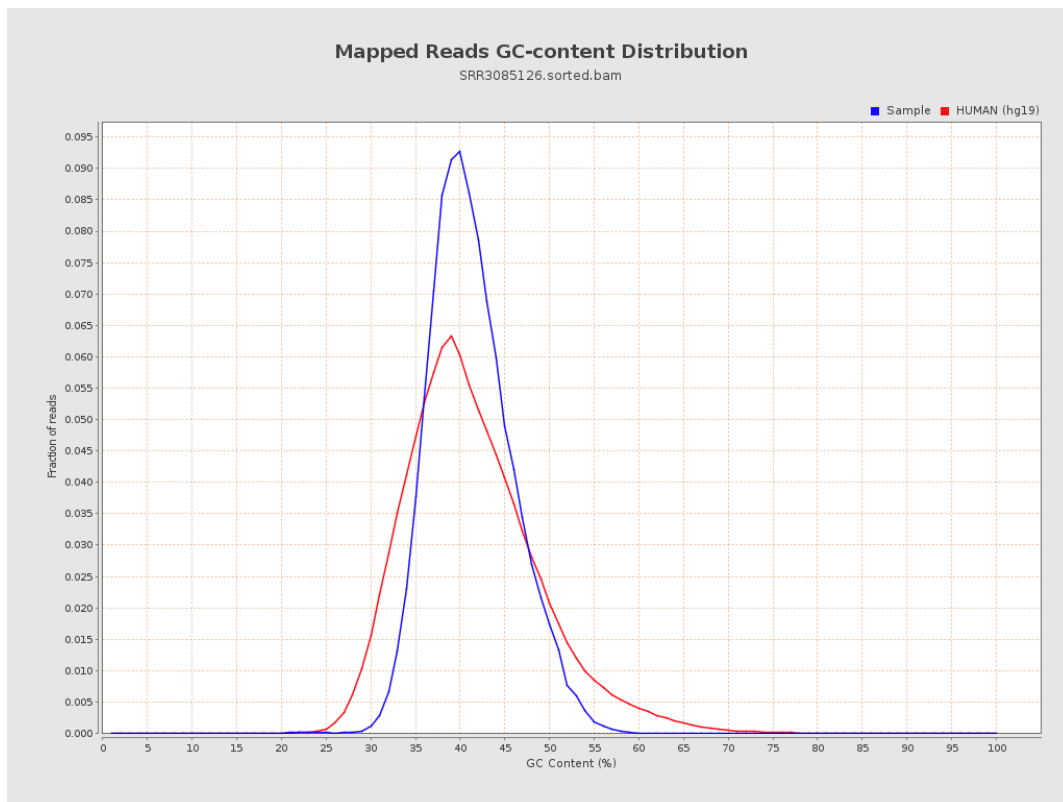
7. Results : Duplication Rate Histogram



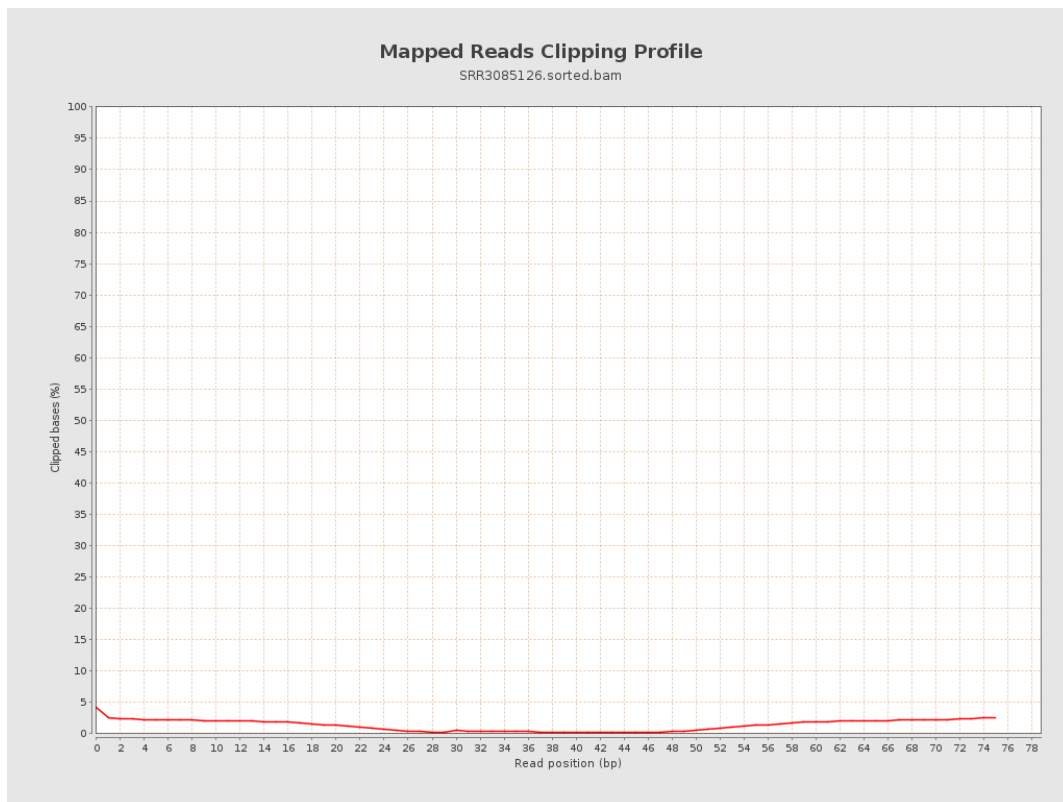
8. Results : Mapped Reads Nucleotide Content



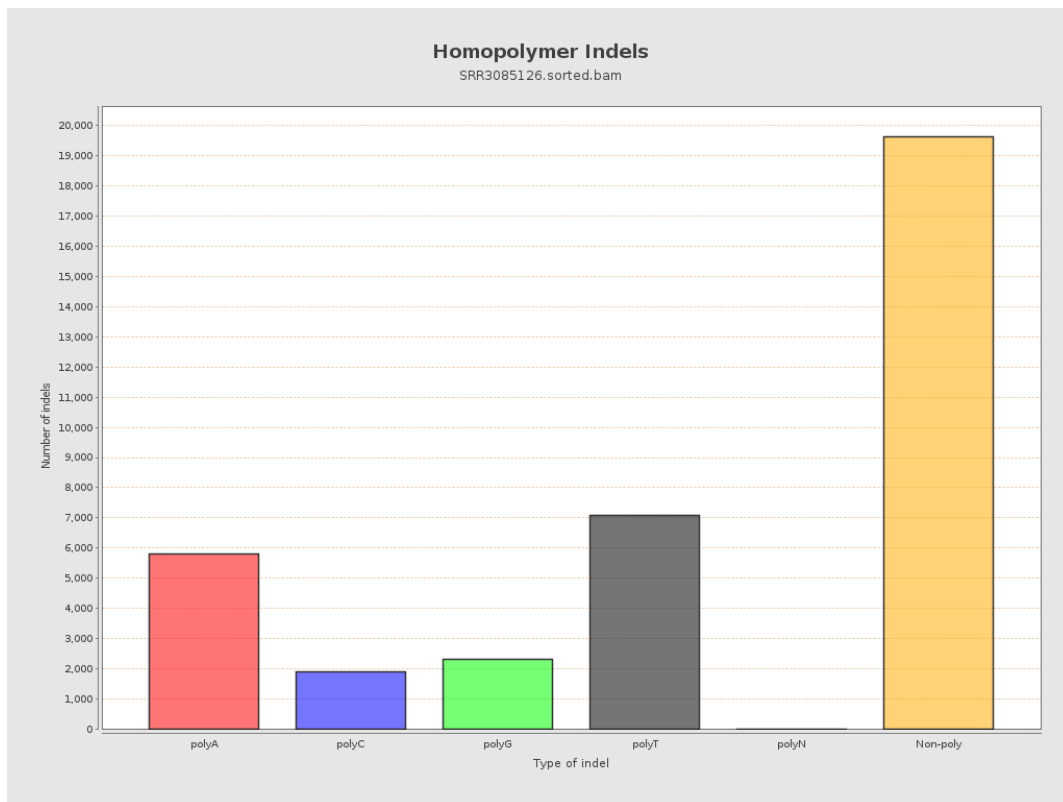
9. Results : Mapped Reads GC-content Distribution



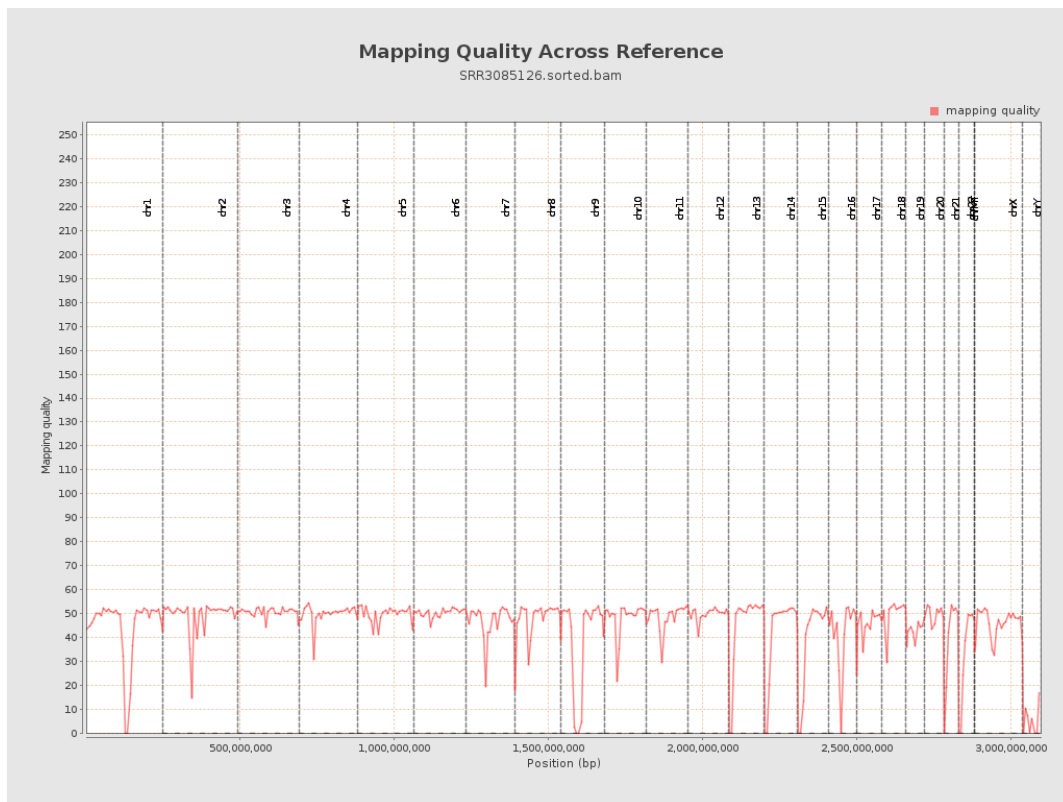
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

