

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:17:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506014.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_SRR1506014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:17:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,286,687
Mapped reads	2,993,893 / 69.84%
Unmapped reads	1,292,794 / 30.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	121 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	189,608 / 4.42%
Duplication rate	4.79%
Clipped reads	456,387 / 10.65%

2.2. ACGT Content

Number/percentage of A's	41,065,626 / 29.49%
Number/percentage of C's	28,634,005 / 20.56%
Number/percentage of T's	40,251,180 / 28.9%
Number/percentage of G's	28,849,385 / 20.71%
Number/percentage of N's	471,891 / 0.34%
GC Percentage	41.27%

2.3. Coverage

Mean	0.045

Standard Deviation	0.4494
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2.4. Mapping Quality

Mean Mapping Quality	43.74
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2.5. Mismatches and indels

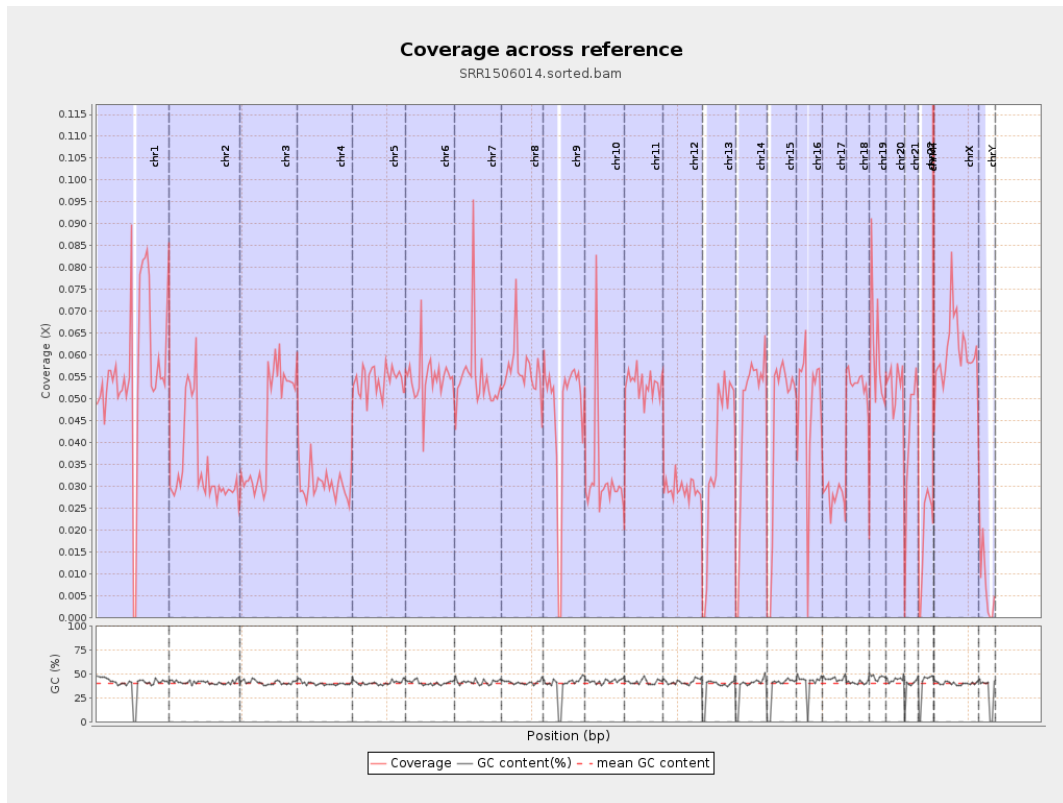
General error rate	0.82%
Mismatches	1,128,828
Insertions	6,114
Mapped reads with at least one insertion	0.2%
Deletions	20,627
Mapped reads with at least one deletion	0.69%
Homopolymer indels	45.81%

2.6. Chromosome stats

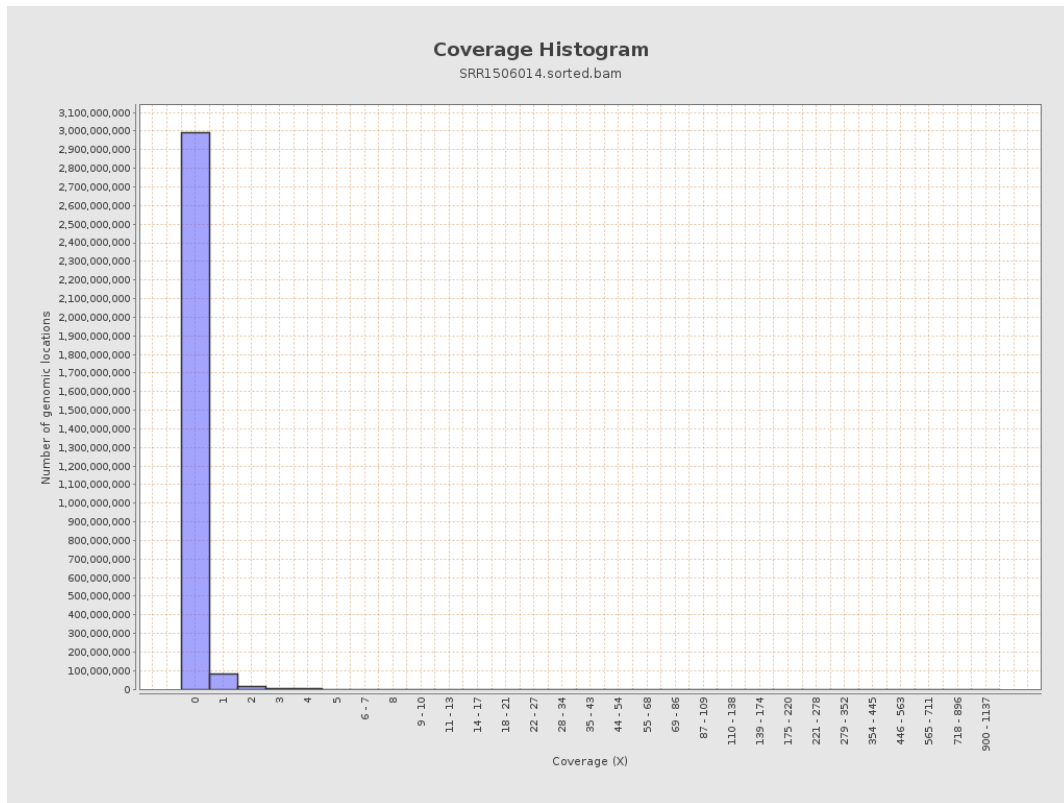
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13916889	0.0558	0.8791
chr2	243199373	8402215	0.0345	0.3572
chr3	198022430	8575952	0.0433	0.2667
chr4	191154276	5794394	0.0303	0.2282
chr5	180915260	9798935	0.0542	0.2991
chr6	171115067	9354632	0.0547	0.3664
chr7	159138663	8754734	0.055	0.6418

chr8	146364022	8238250	0.0563	0.4857
chr9	141213431	6538400	0.0463	0.3553
chr10	135534747	4332209	0.032	0.4539
chr11	135006516	7117066	0.0527	0.3647
chr12	133851895	3925673	0.0293	0.2332
chr13	115169878	4318347	0.0375	0.2455
chr14	107349540	4963408	0.0462	0.7186
chr15	102531392	4511595	0.044	0.2659
chr16	90354753	4397504	0.0487	0.3236
chr17	81195210	2232362	0.0275	0.2357
chr18	78077248	4185691	0.0536	0.5357
chr19	59128983	3512319	0.0594	0.648
chr20	63025520	3319479	0.0527	0.3081
chr21	48129895	2017048	0.0419	0.2838
chr22	51304566	969728	0.0189	0.1715
chrMT	16571	229946	13.8764	8.7281
chrX	155270560	9451118	0.0609	0.3499
chrY	59373566	442689	0.0075	0.134

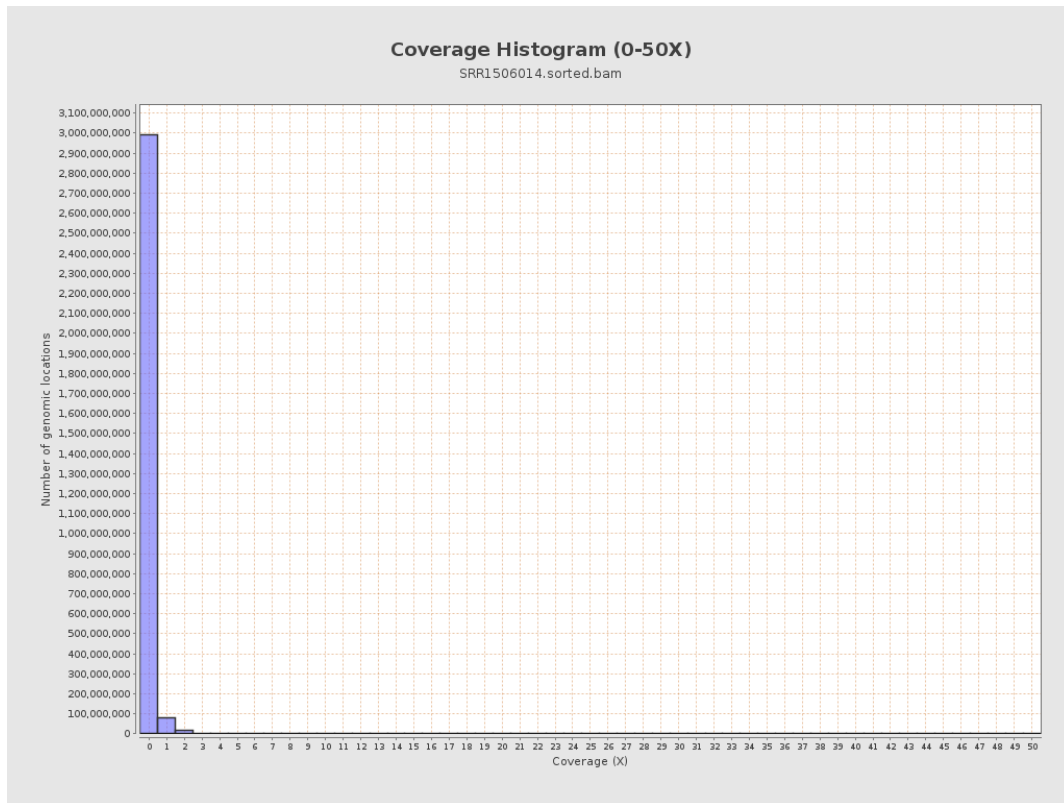
3. Results : Coverage across reference



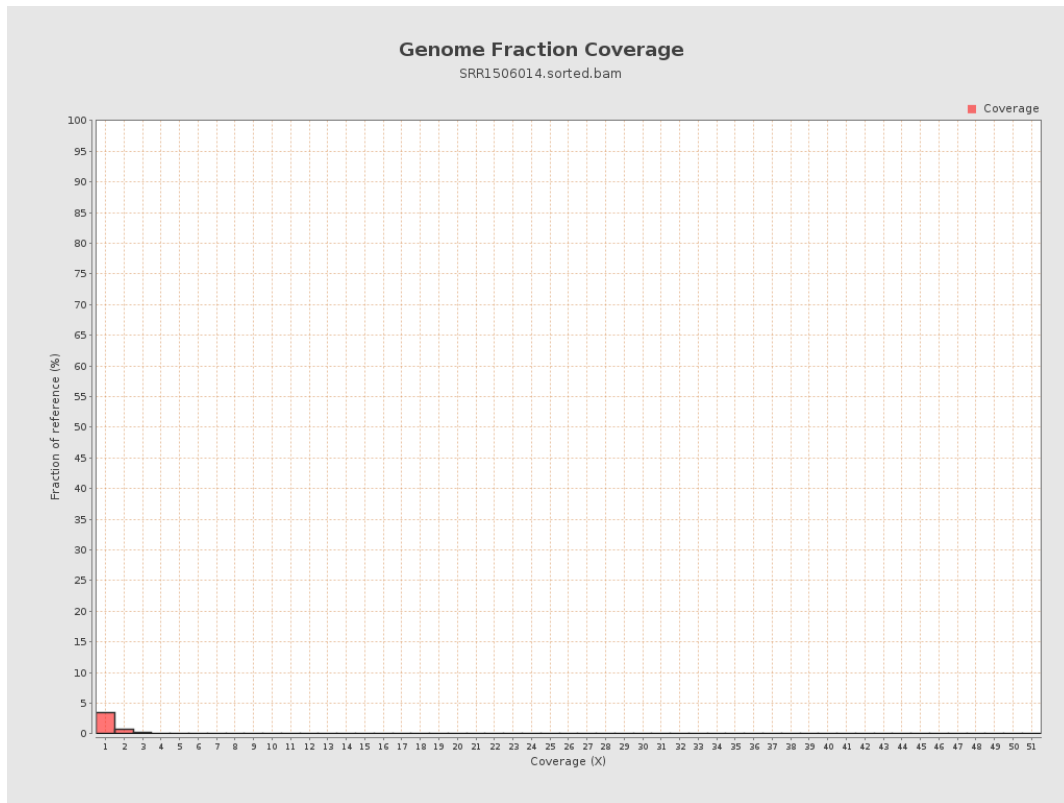
4. Results : Coverage Histogram



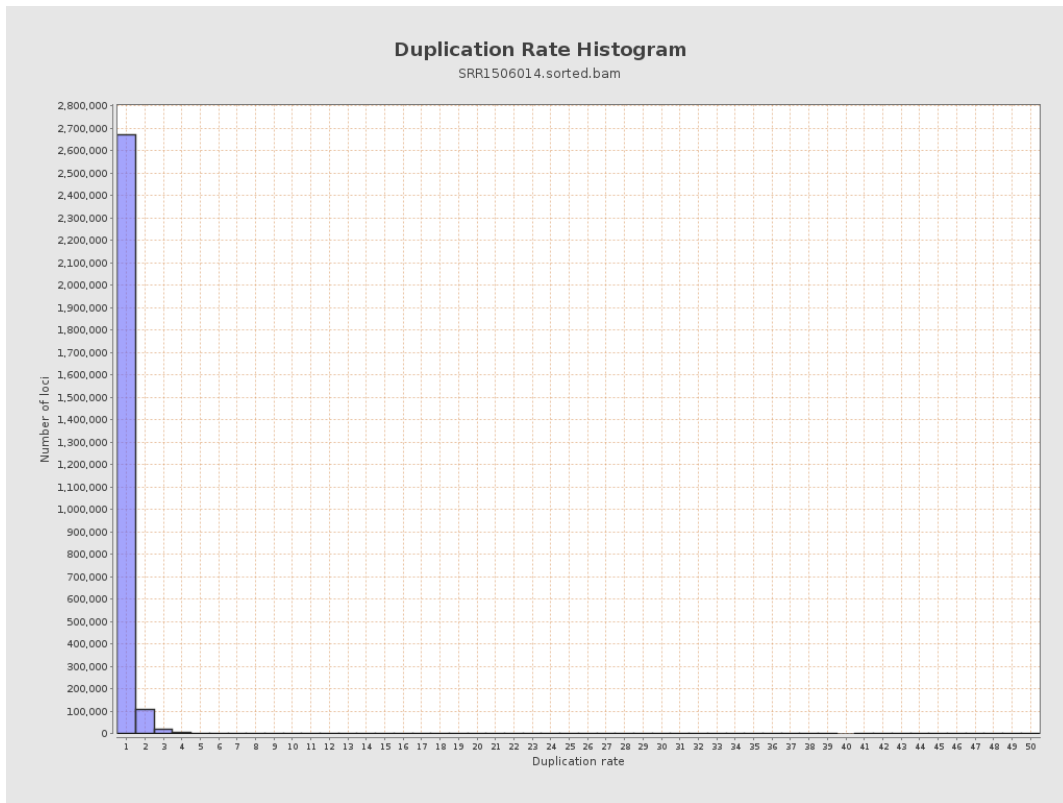
5. Results : Coverage Histogram (0-50X)



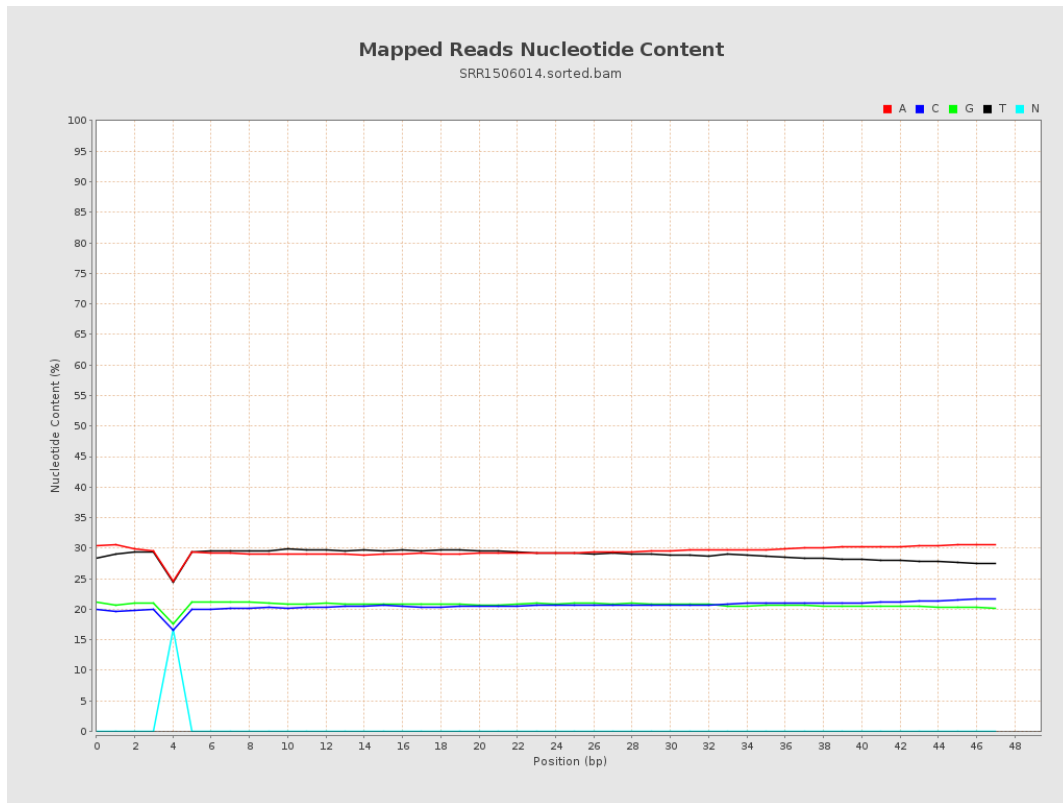
6. Results : Genome Fraction Coverage



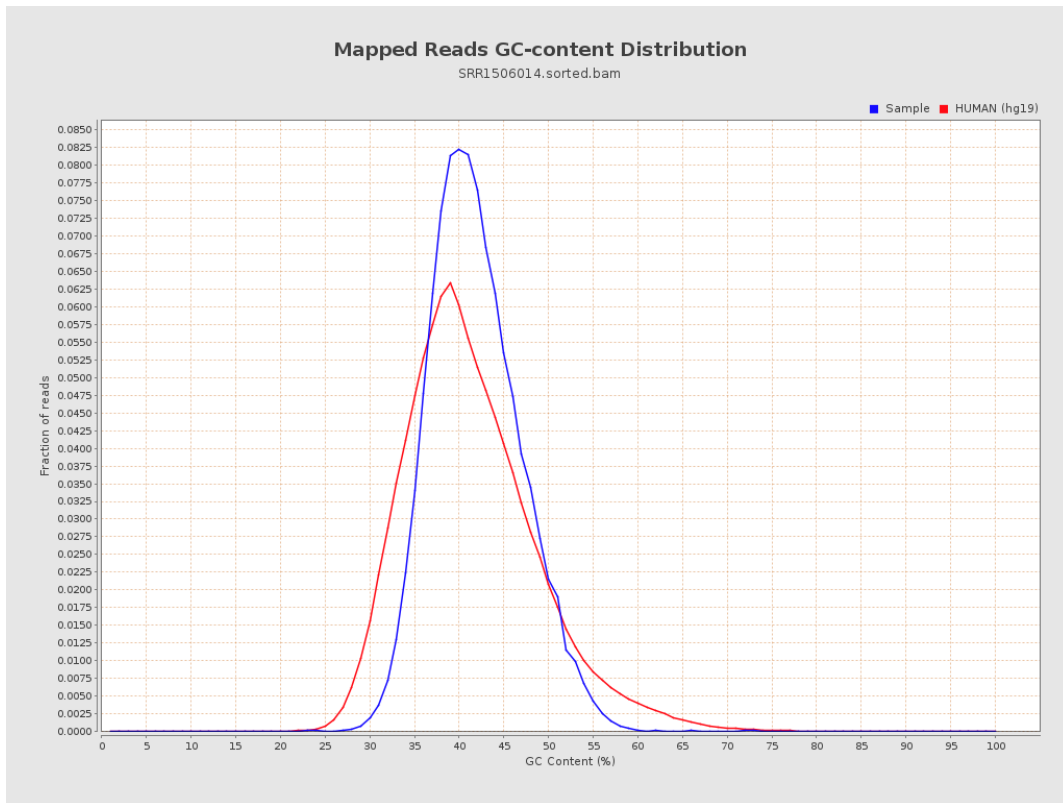
7. Results : Duplication Rate Histogram



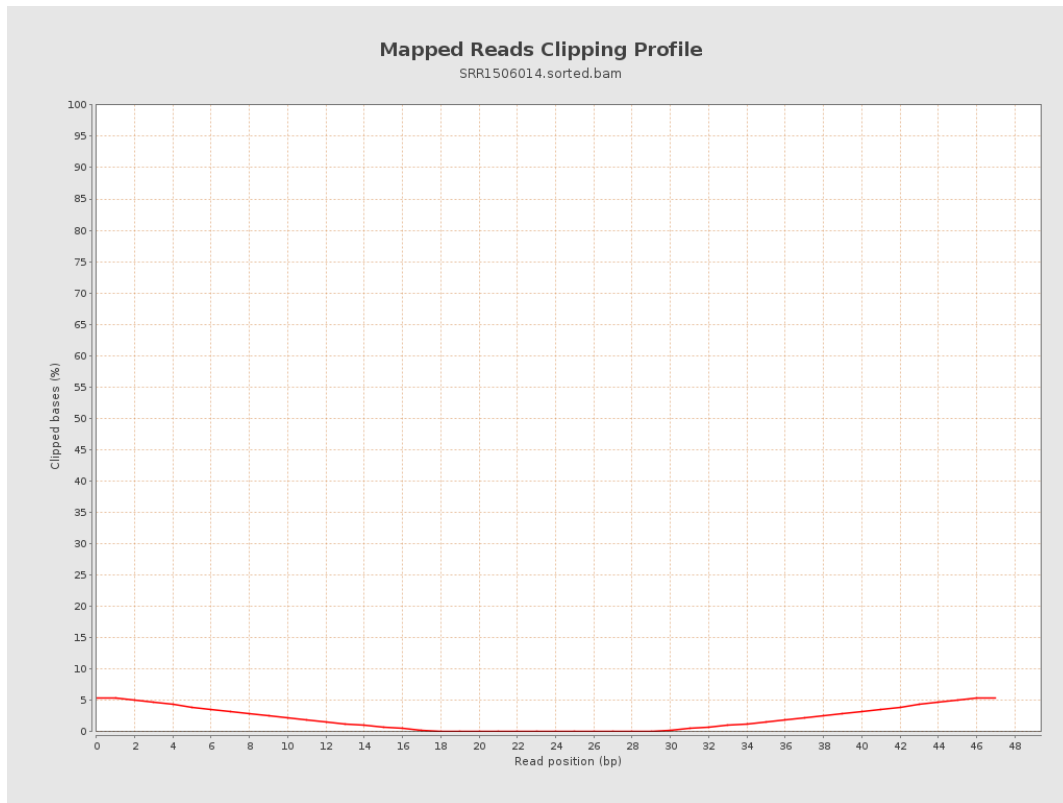
8. Results : Mapped Reads Nucleotide Content



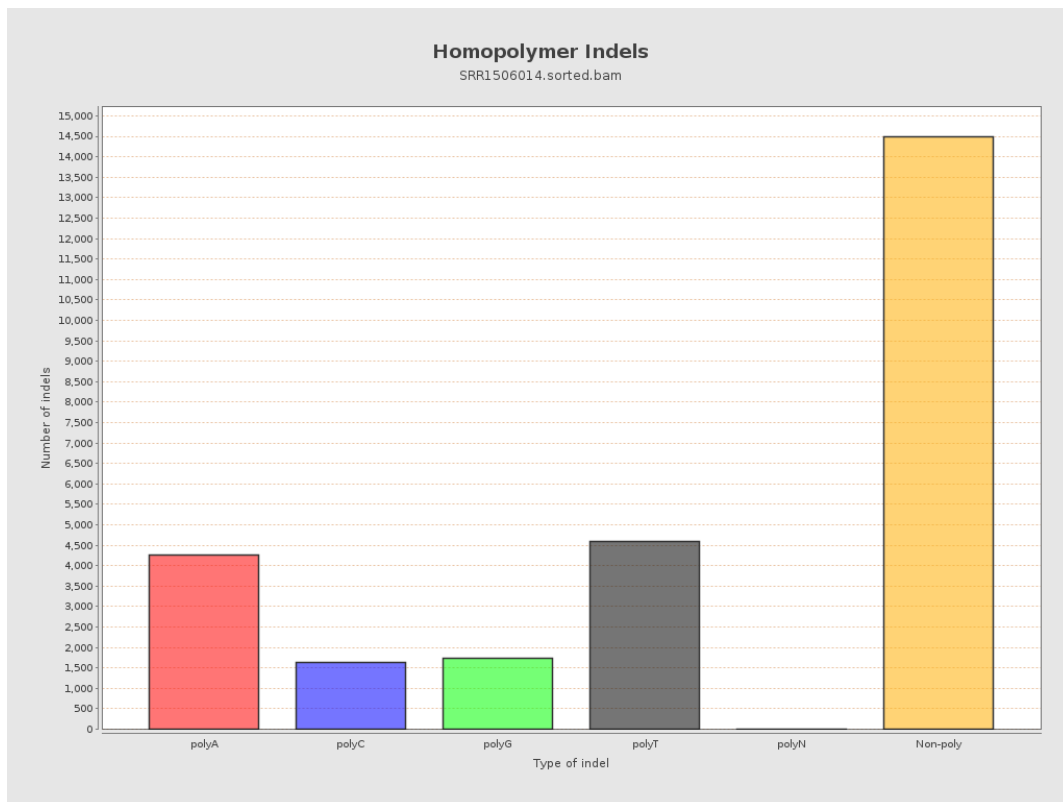
9. Results : Mapped Reads GC-content Distribution



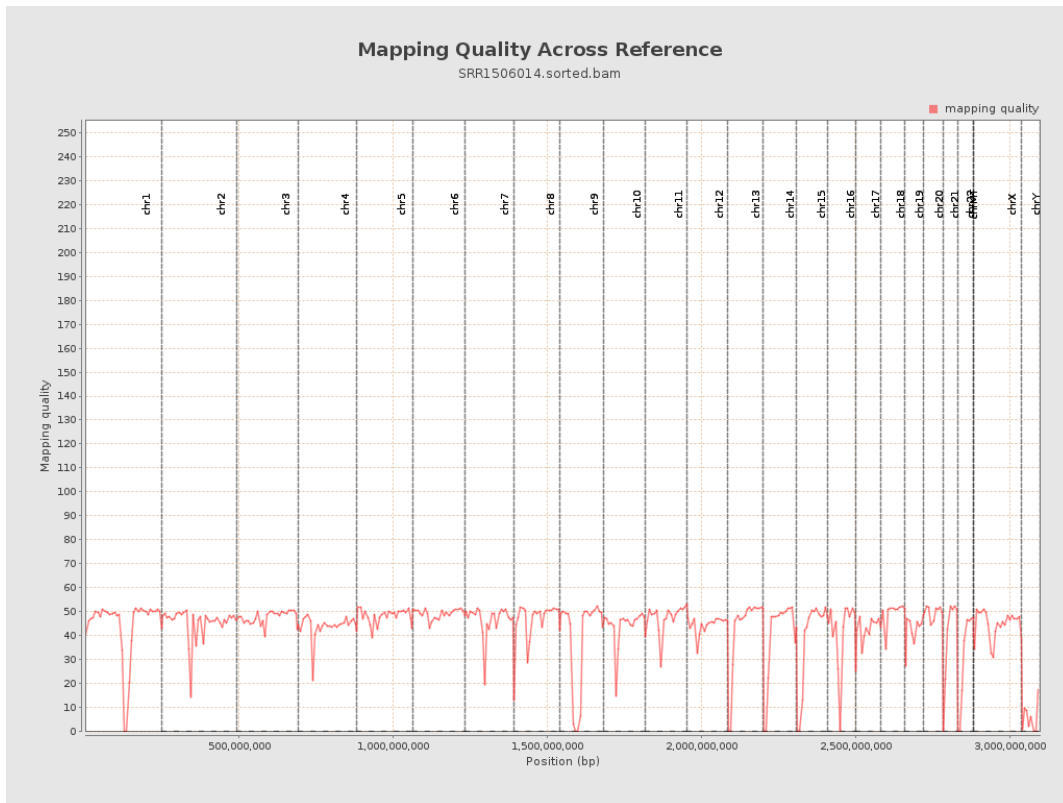
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

