

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 06:43:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514716.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_SRR5514716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 06:43:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	104,430,813
Mapped reads	103,041,822 / 98.67%
Unmapped reads	1,388,991 / 1.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,723,999 / 5.48%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	69,672,178 / 66.72%
Duplication rate	43.34%
Clipped reads	23,406,602 / 22.41%

2.2. ACGT Content

Number/percentage of A's	2,909,387,469 / 29.66%
Number/percentage of C's	1,994,064,040 / 20.33%
Number/percentage of T's	2,868,725,638 / 29.25%
Number/percentage of G's	2,033,754,795 / 20.73%
Number/percentage of N's	2,717,088 / 0.03%
GC Percentage	41.06%

2.3. Coverage

Mean	3.171

Standard Deviation	329.7768
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2.4. Mapping Quality

Mean Mapping Quality	49.01
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2.5. Mismatches and indels

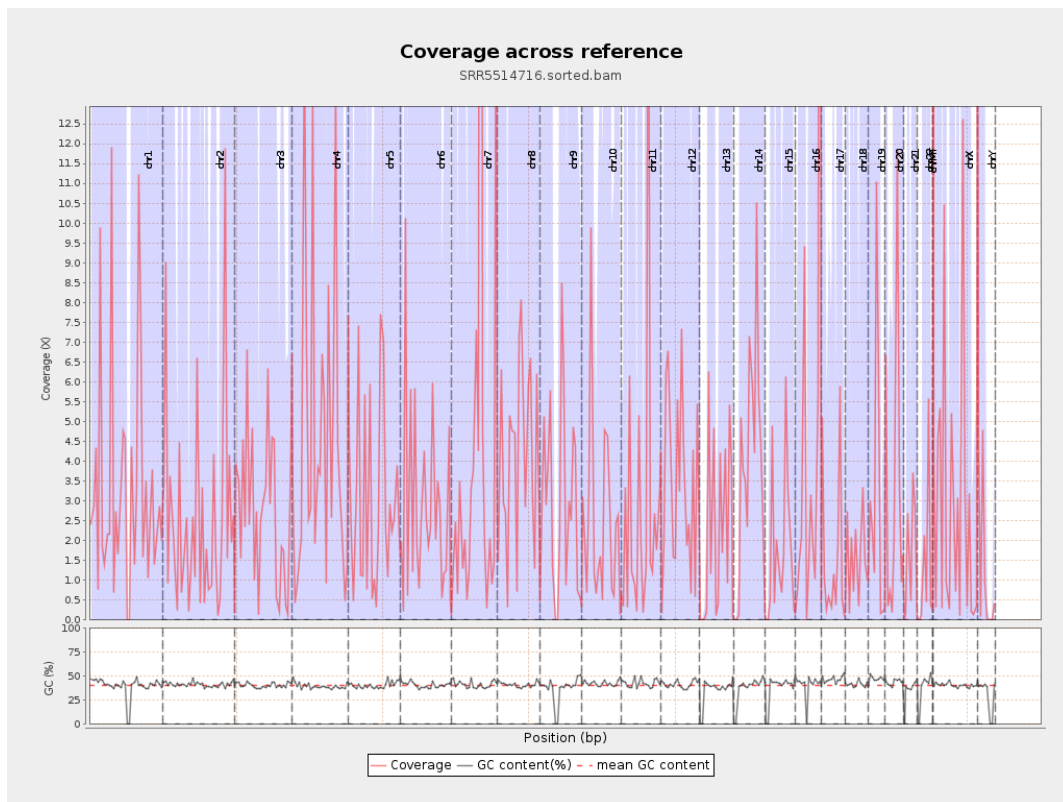
General error rate	0.66%
Mismatches	59,378,147
Insertions	3,229,712
Mapped reads with at least one insertion	2.95%
Deletions	3,240,404
Mapped reads with at least one deletion	2.95%
Homopolymer indels	38.57%

2.6. Chromosome stats

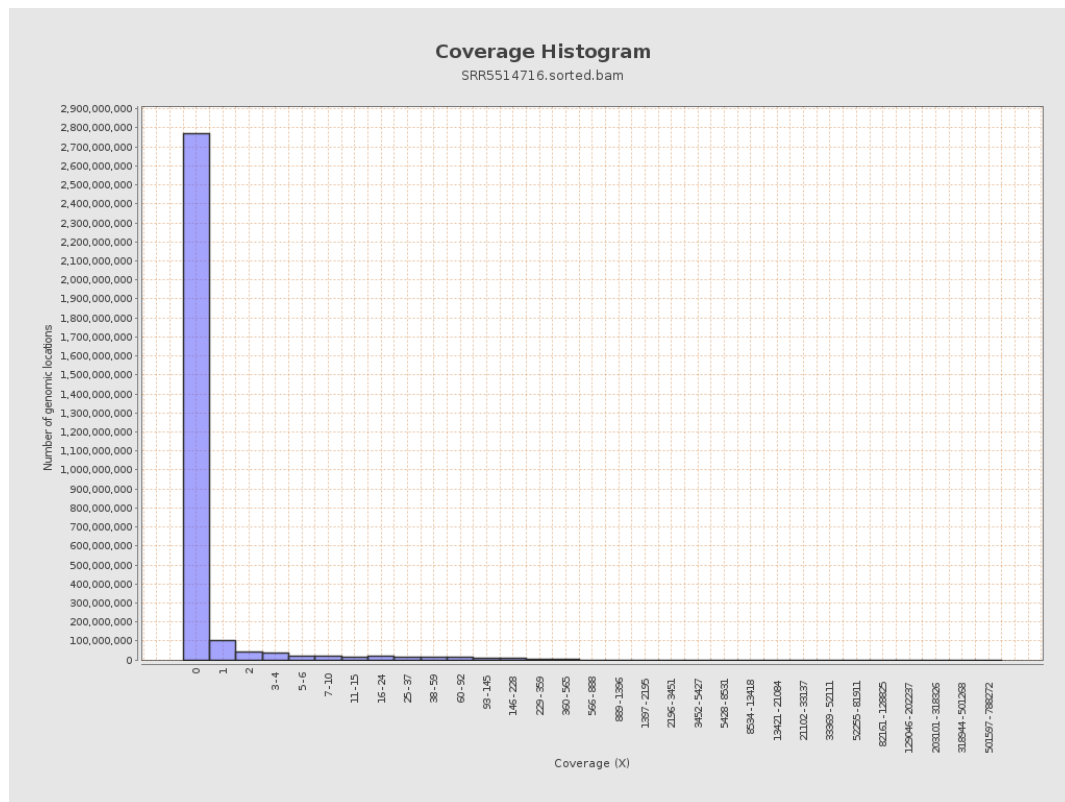
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	823744172	3.3049	57.7947
chr2	243199373	604483790	2.4855	57.1552
chr3	198022430	552029772	2.7877	27.379
chr4	191154276	870150844	4.5521	36.0363
chr5	180915260	537362933	2.9702	27.6306
chr6	171115067	491802301	2.8741	47.3807
chr7	159138663	946241087	5.946	995.4163

chr8	146364022	607668565	4.1518	36.2819
chr9	141213431	431335591	3.0545	28.2351
chr10	135534747	329080518	2.428	50.1328
chr11	135006516	400066993	2.9633	34.5976
chr12	133851895	458938336	3.4287	30.6249
chr13	115169878	257553731	2.2363	24.5242
chr14	107349540	426497718	3.973	34.7831
chr15	102531392	179111100	1.7469	48.9792
chr16	90354753	556566855	6.1598	1,378.9169
chr17	81195210	130390931	1.6059	21.1923
chr18	78077248	122460943	1.5685	17.6919
chr19	59128983	188454303	3.1872	145.0756
chr20	63025520	194225966	3.0817	36.8915
chr21	48129895	76590811	1.5913	15.7875
chr22	51304566	66972609	1.3054	49.1617
chrMT	16571	5510884	332.5619	167.8114
chrX	155270560	487956252	3.1426	61.9171
chrY	59373566	71107323	1.1976	137.8056

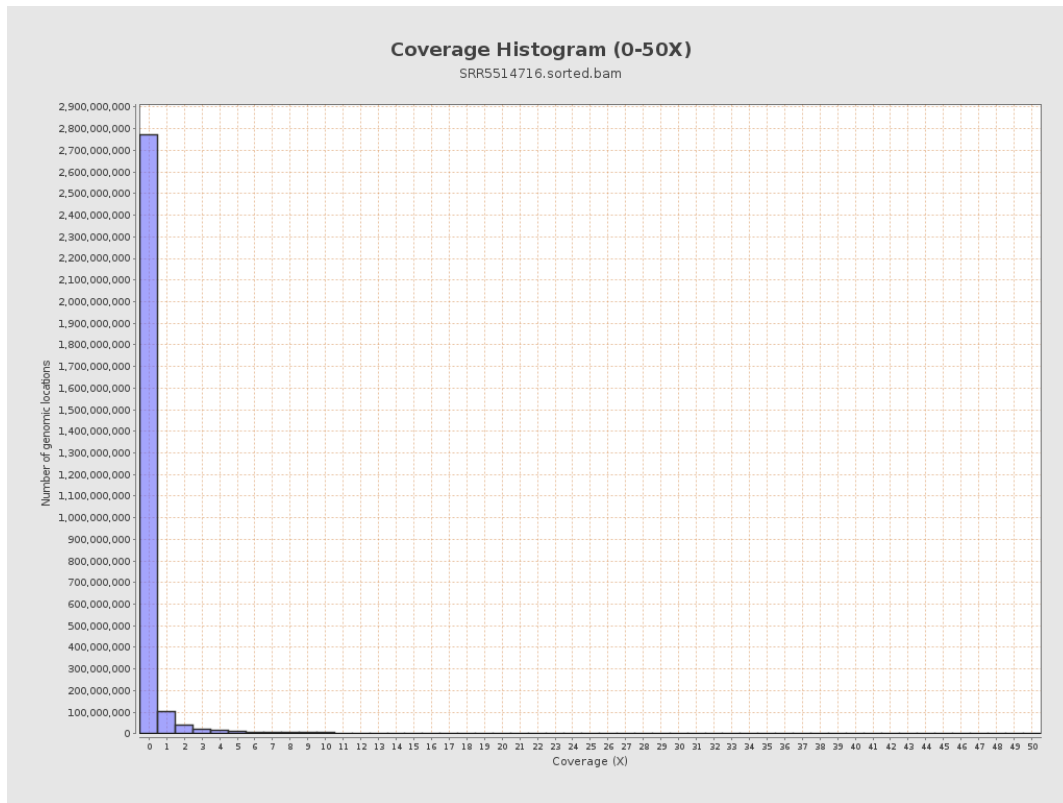
3. Results : Coverage across reference



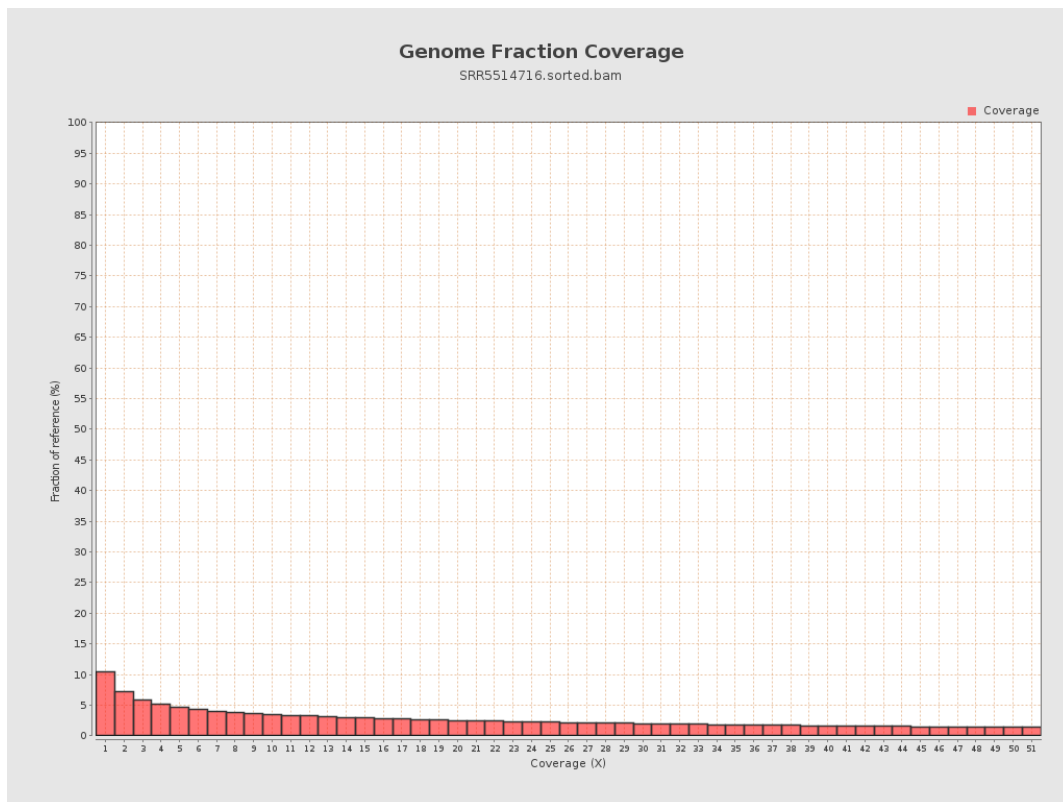
4. Results : Coverage Histogram



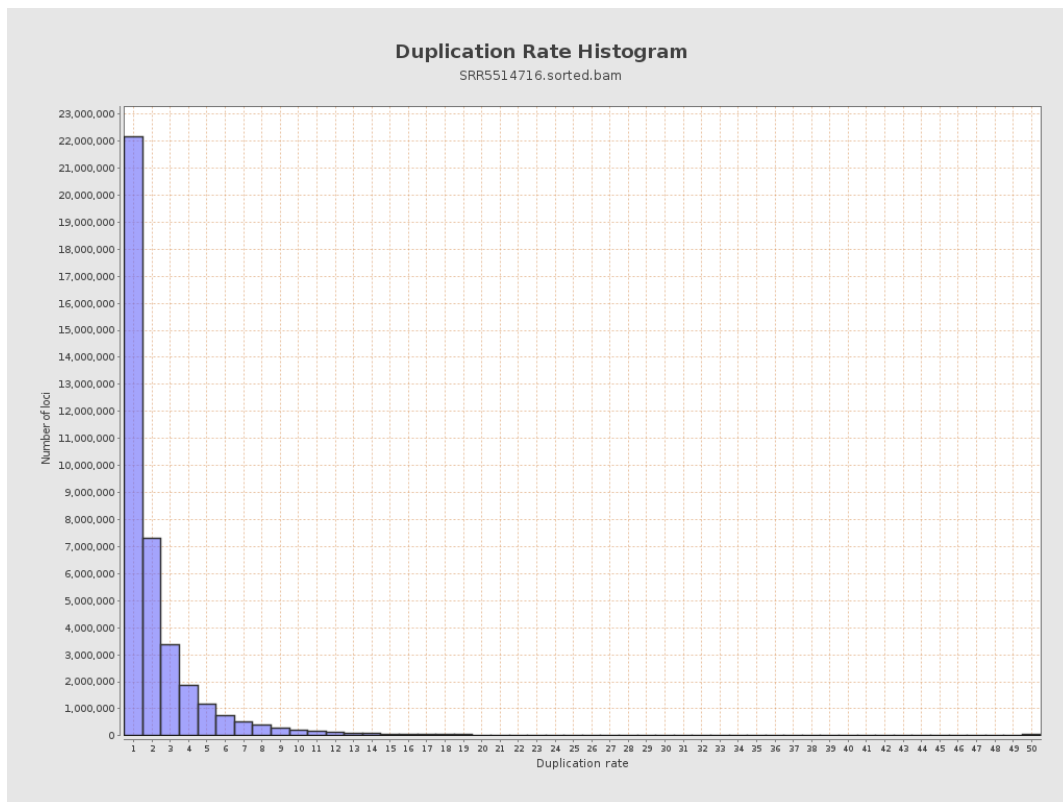
5. Results : Coverage Histogram (0-50X)



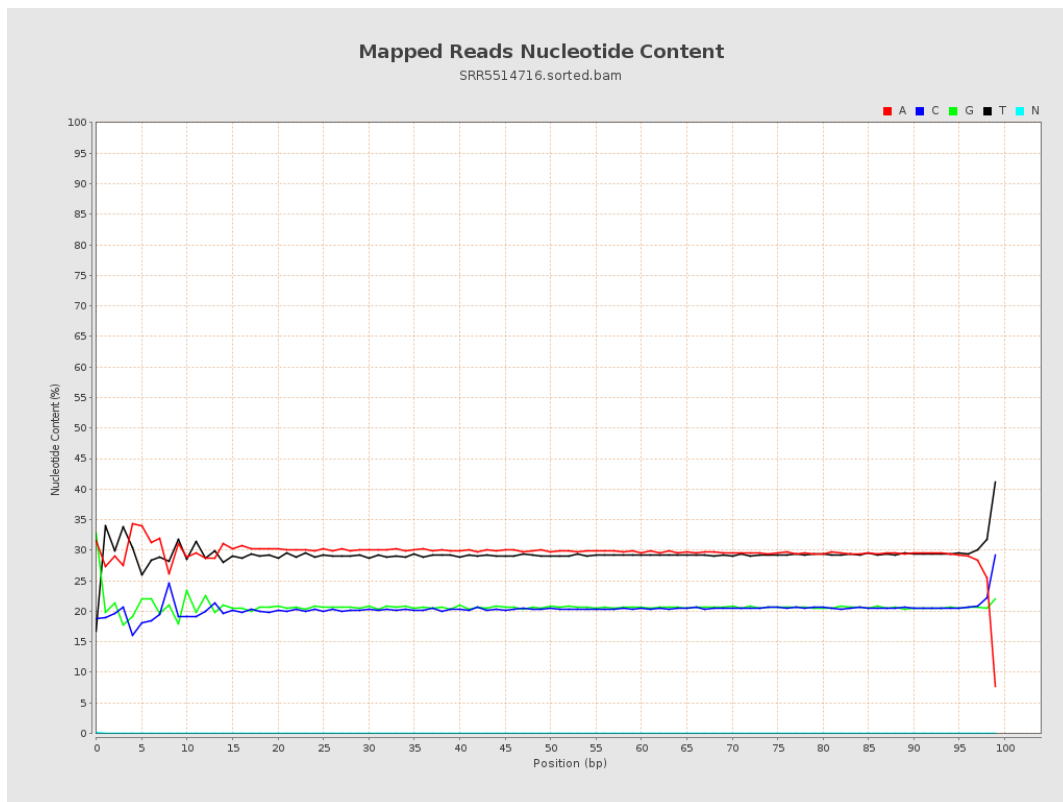
6. Results : Genome Fraction Coverage



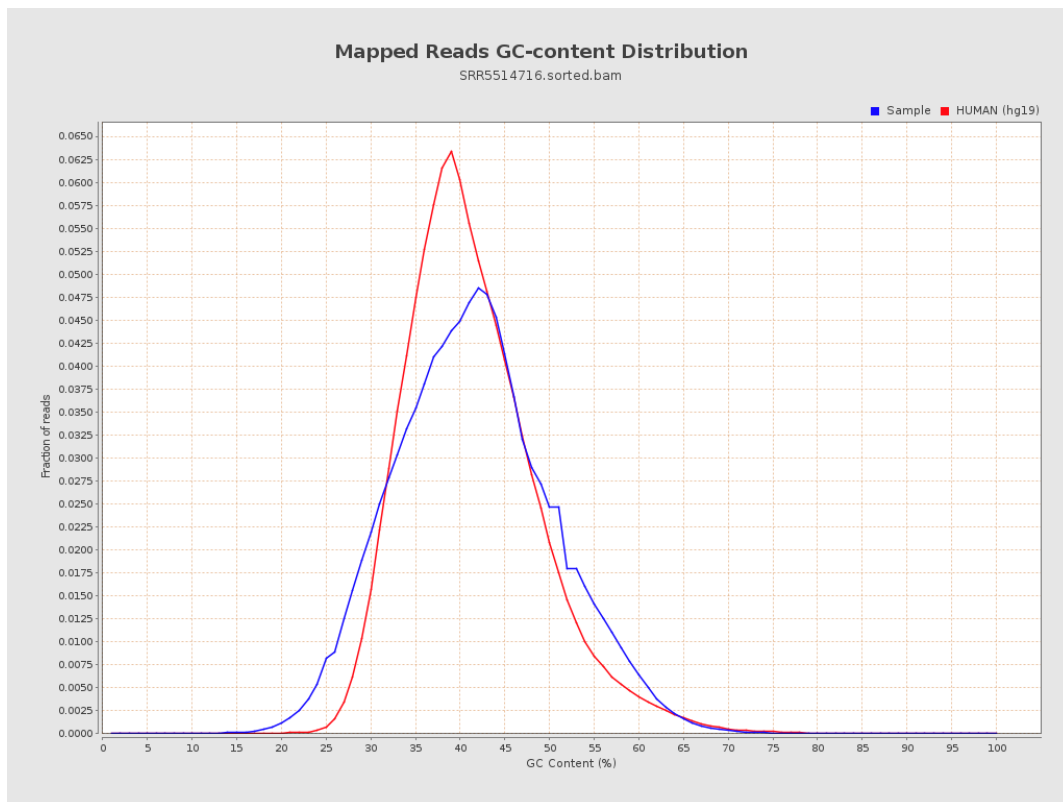
7. Results : Duplication Rate Histogram



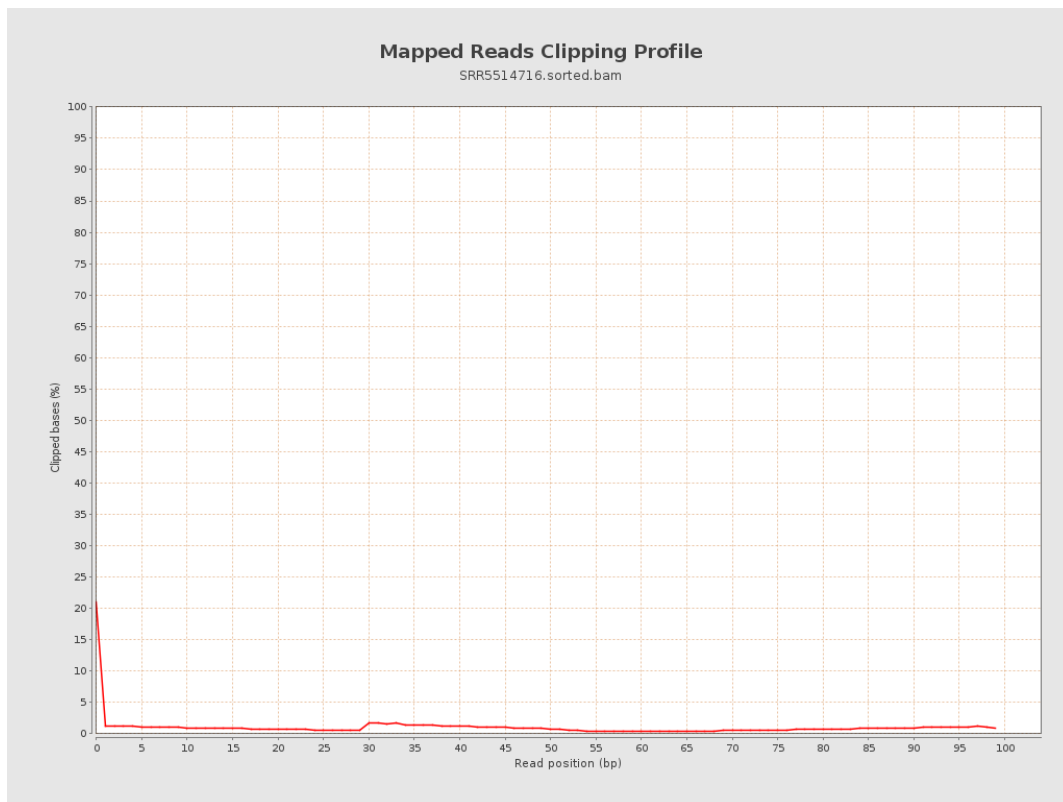
8. Results : Mapped Reads Nucleotide Content



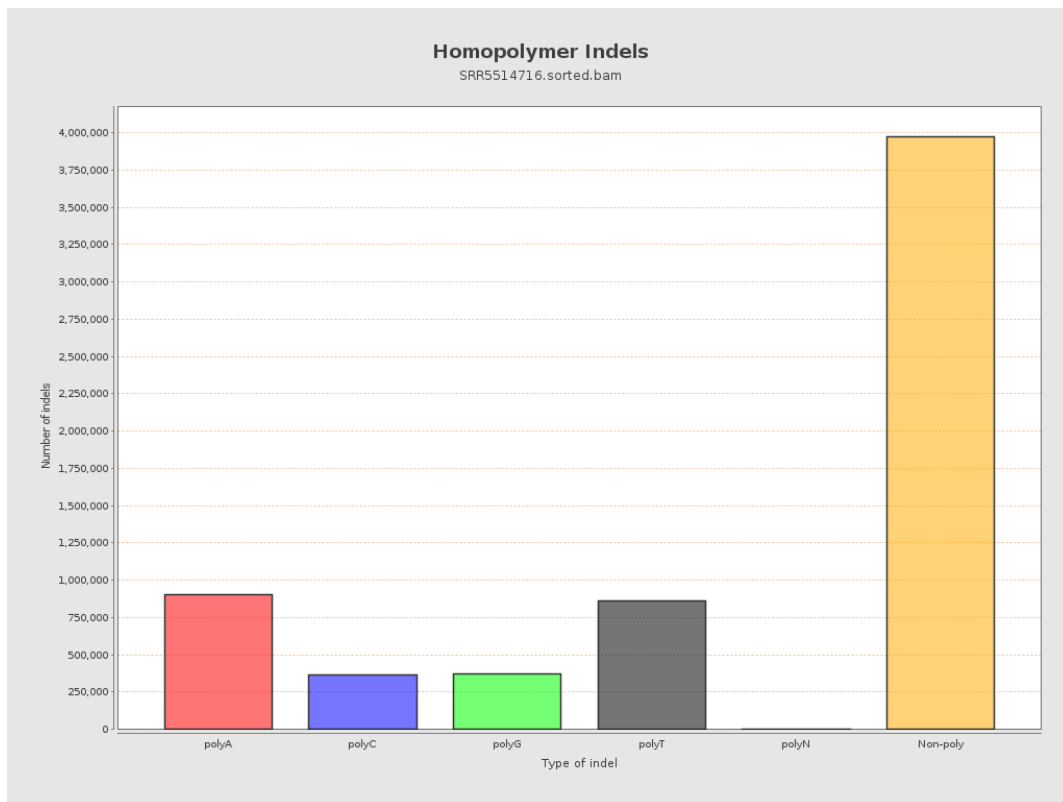
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

