

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:45:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818979.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_SRR1818979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818979.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:45:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,297,236
Mapped reads	2,263,881 / 98.55%
Unmapped reads	33,355 / 1.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,360 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	1,078,468 / 46.95%
Duplication rate	39.17%
Clipped reads	2,289,495 / 99.66%

2.2. ACGT Content

Number/percentage of A's	58,943,181 / 28.13%
Number/percentage of C's	43,167,689 / 20.6%
Number/percentage of T's	60,991,816 / 29.11%
Number/percentage of G's	46,435,501 / 22.16%
Number/percentage of N's	9,714 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0677

Standard Deviation	0.7812
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2.4. Mapping Quality

Mean Mapping Quality	49.3
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2.5. Mismatches and indels

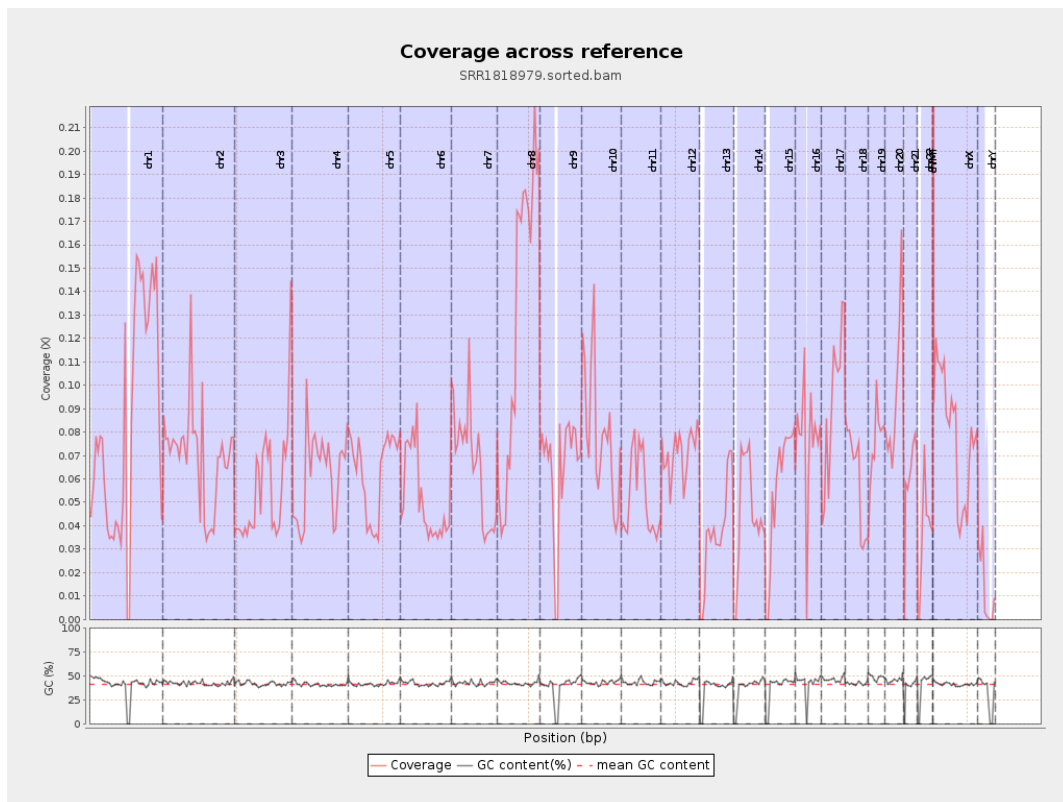
General error rate	0.64%
Mismatches	1,278,725
Insertions	29,407
Mapped reads with at least one insertion	1.26%
Deletions	67,721
Mapped reads with at least one deletion	2.92%
Homopolymer indels	43.19%

2.6. Chromosome stats

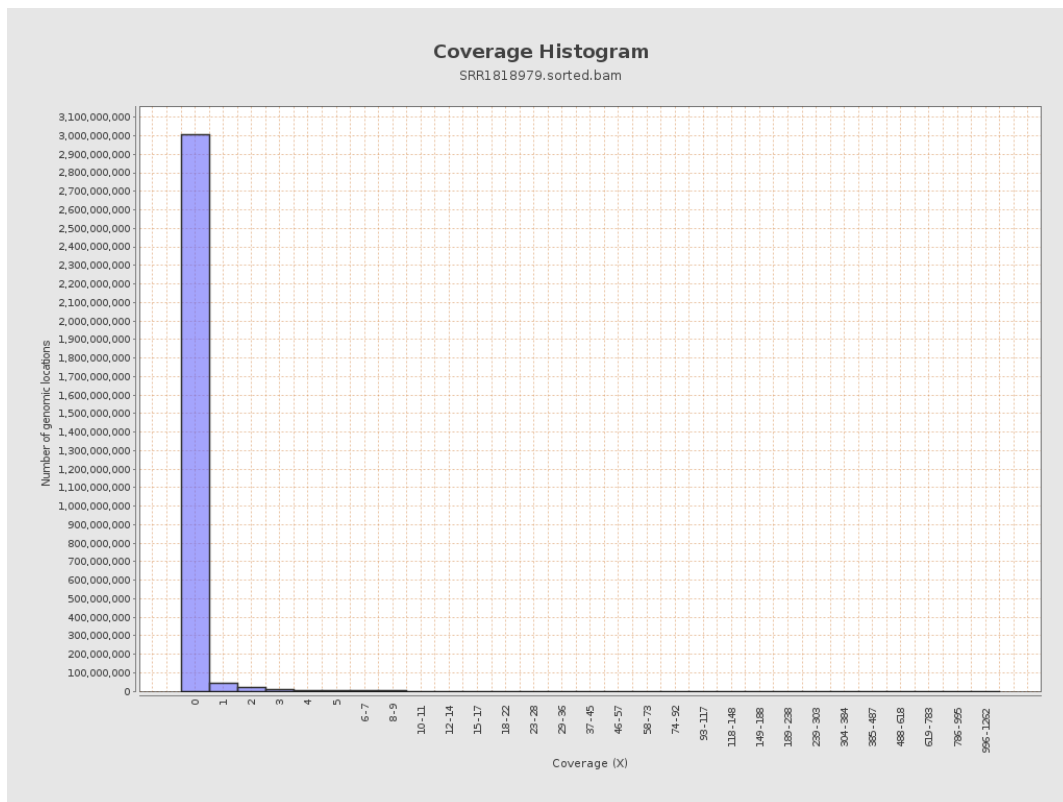
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20805122	0.0835	1.2436
chr2	243199373	17007503	0.0699	1.1005
chr3	198022430	11185557	0.0565	0.4565
chr4	191154276	11841090	0.0619	0.5626
chr5	180915260	11432063	0.0632	0.5087
chr6	171115067	8801468	0.0514	0.5037
chr7	159138663	10537335	0.0662	1.0075

chr8	146364022	19215479	0.1313	0.7872
chr9	141213431	9185000	0.065	0.7118
chr10	135534747	10538531	0.0778	0.9896
chr11	135006516	6962968	0.0516	0.5219
chr12	133851895	9583306	0.0716	0.5383
chr13	115169878	4350168	0.0378	0.3746
chr14	107349540	4946646	0.0461	0.4361
chr15	102531392	5614572	0.0548	0.4587
chr16	90354753	6831899	0.0756	0.9136
chr17	81195210	7450858	0.0918	0.6775
chr18	78077248	4698221	0.0602	0.8645
chr19	59128983	4486385	0.0759	1.2629
chr20	63025520	6214154	0.0986	0.6574
chr21	48129895	2923387	0.0607	0.5233
chr22	51304566	1832169	0.0357	0.4312
chrMT	16571	22211	1.3404	2.3166
chrX	155270560	12438954	0.0801	0.6515
chrY	59373566	769458	0.013	0.8646

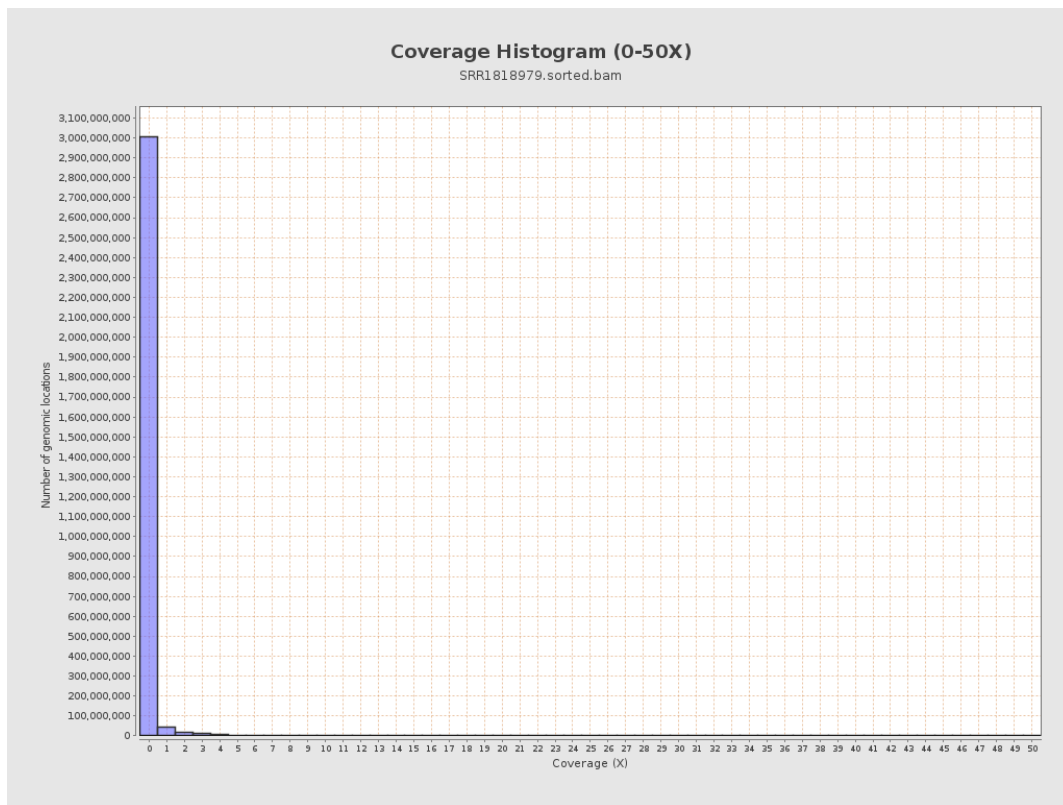
3. Results : Coverage across reference



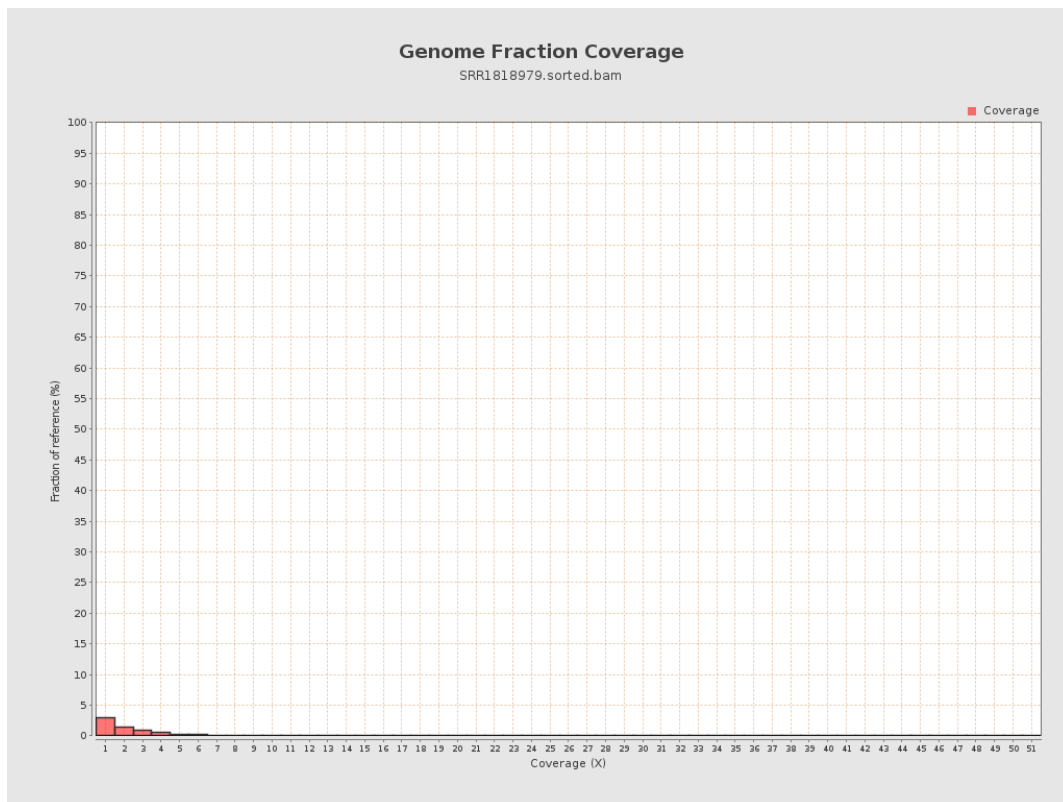
4. Results : Coverage Histogram



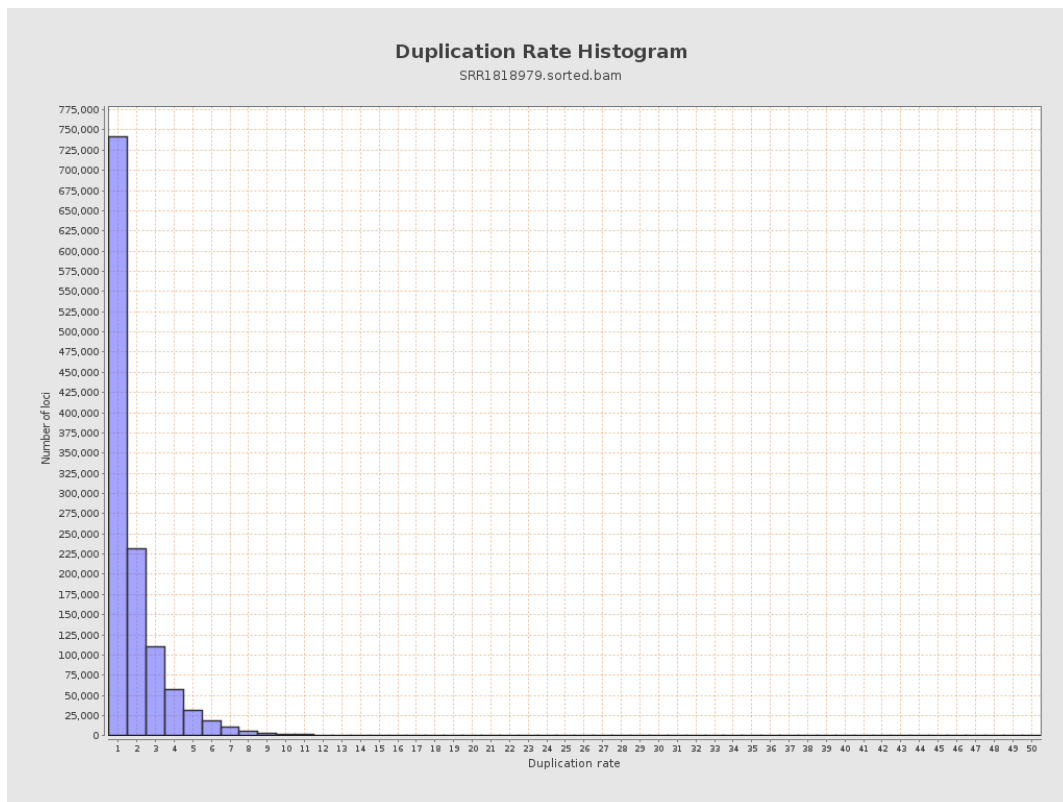
5. Results : Coverage Histogram (0-50X)



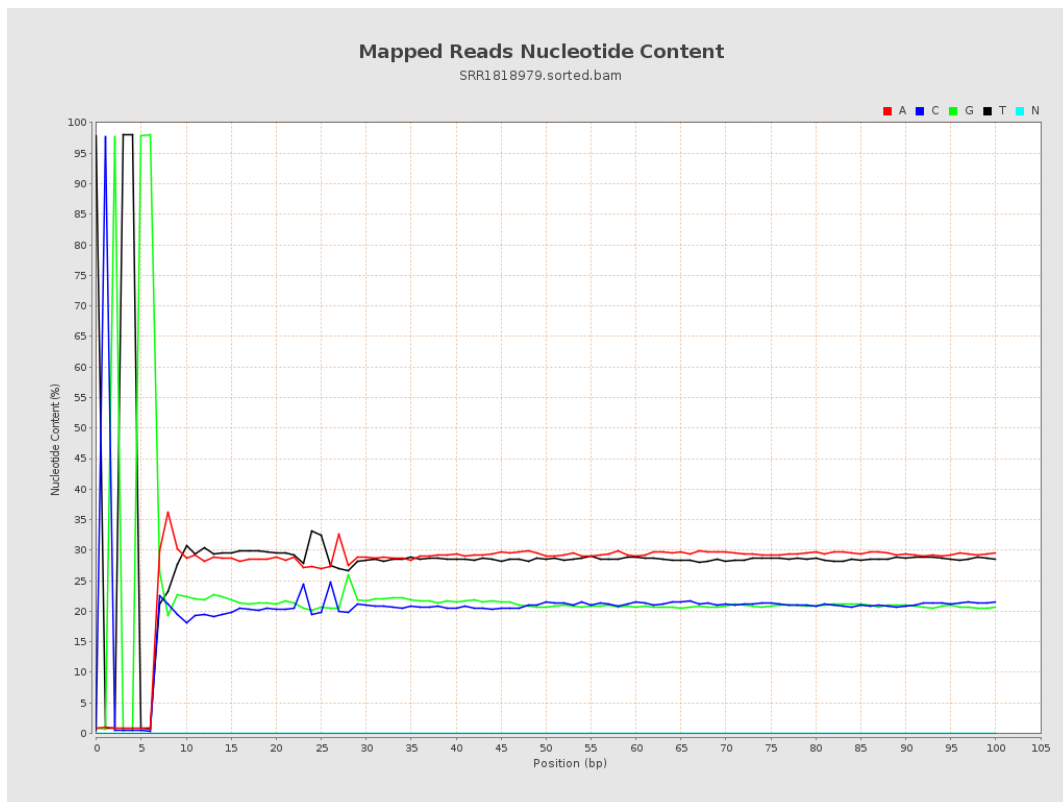
6. Results : Genome Fraction Coverage



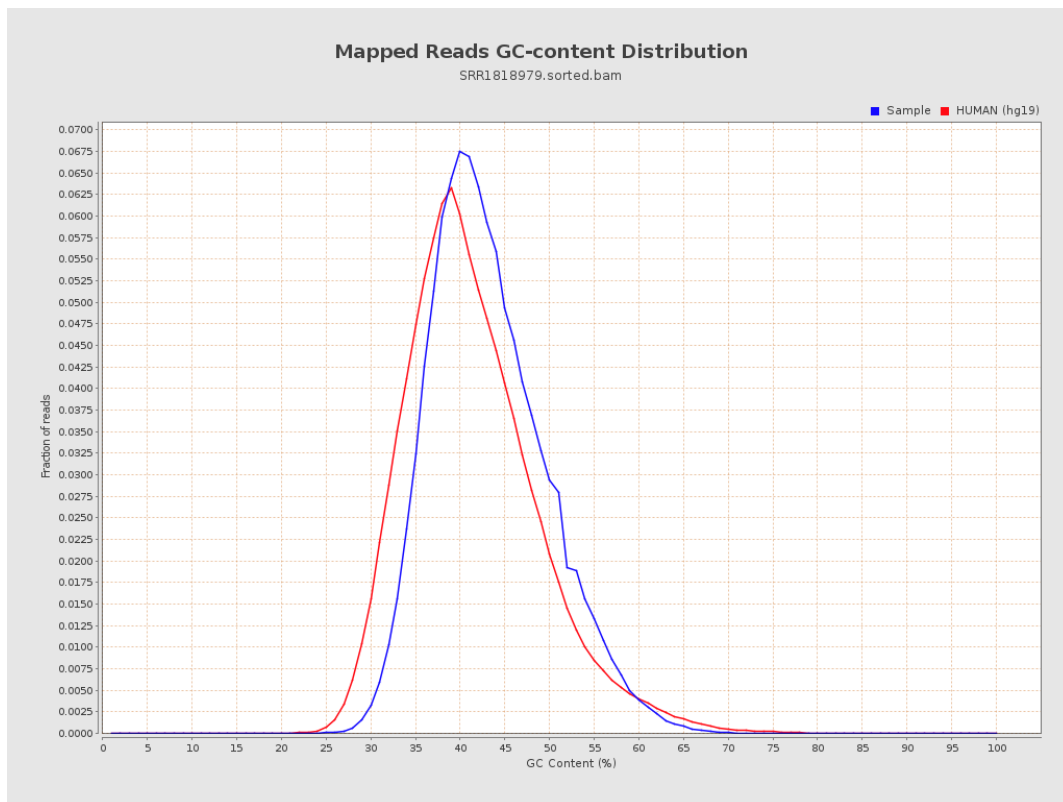
7. Results : Duplication Rate Histogram



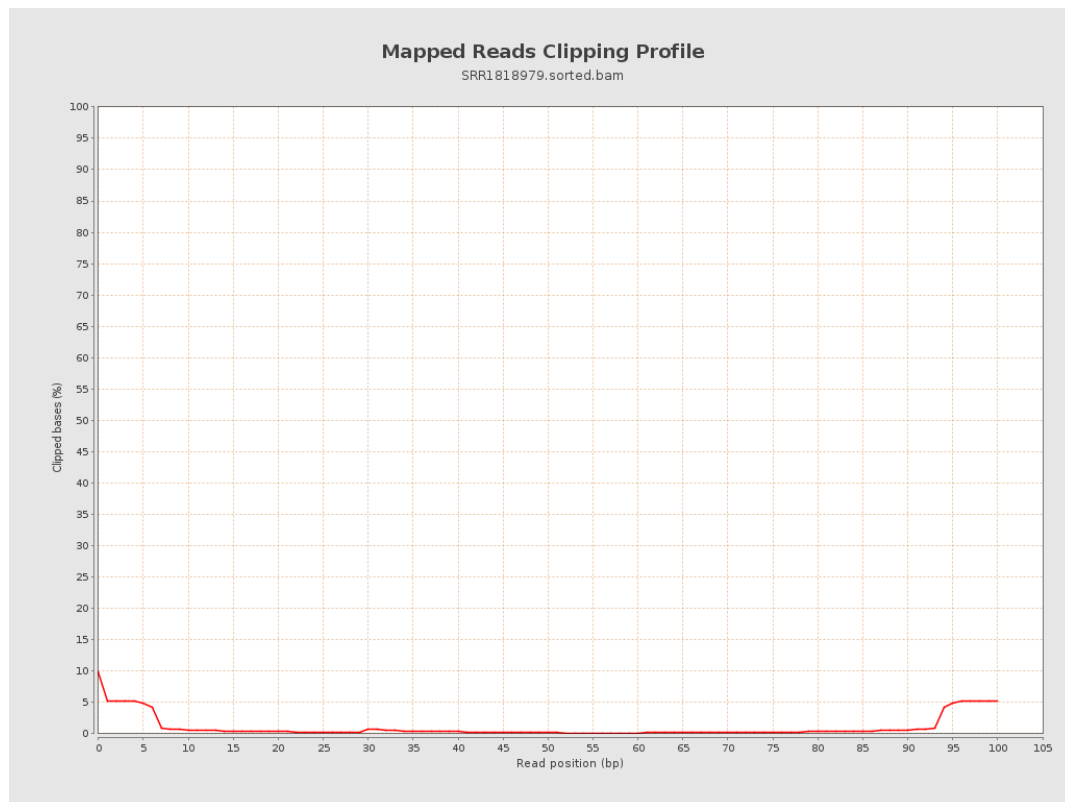
8. Results : Mapped Reads Nucleotide Content



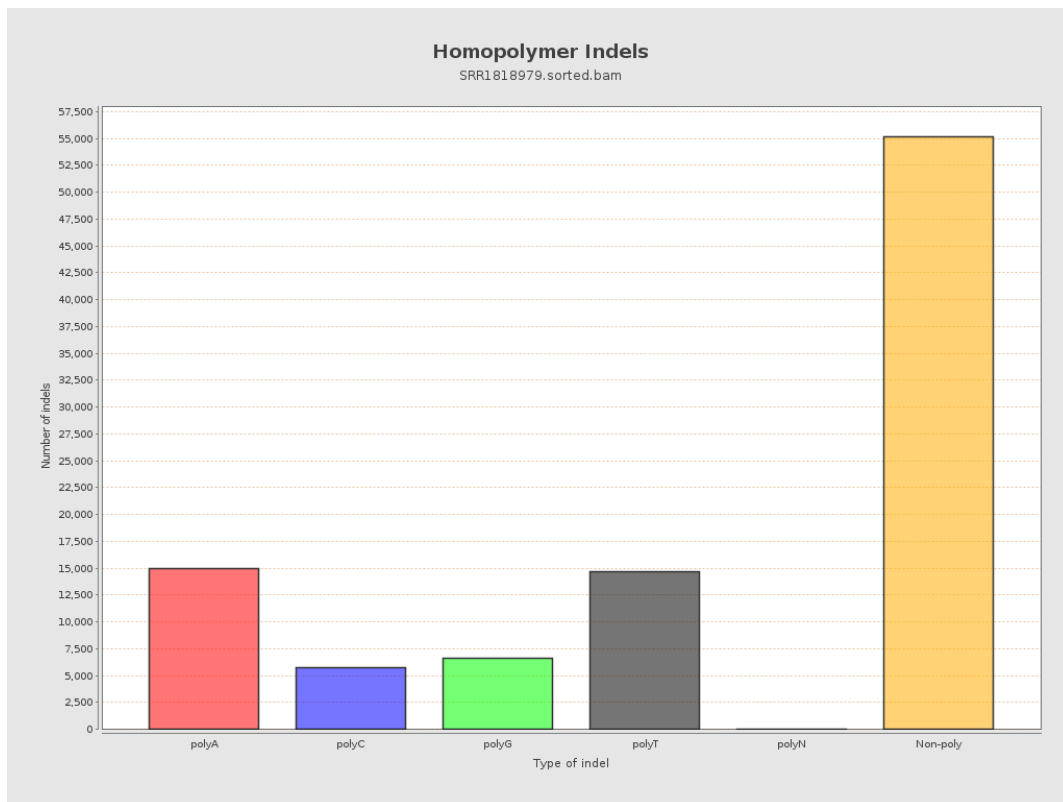
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

