

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:24:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818870.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_SRR1818870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:24:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,497,043
Mapped reads	2,454,565 / 98.3%
Unmapped reads	42,478 / 1.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,314 / 1.65%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	765,684 / 30.66%
Duplication rate	27.08%
Clipped reads	2,480,924 / 99.35%

2.2. ACGT Content

Number/percentage of A's	64,605,527 / 28.45%
Number/percentage of C's	50,240,173 / 22.13%
Number/percentage of T's	65,469,118 / 28.83%
Number/percentage of G's	46,730,526 / 20.58%
Number/percentage of N's	3,272 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0734

Standard Deviation	0.7883
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2.4. Mapping Quality

Mean Mapping Quality	49.44
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2.5. Mismatches and indels

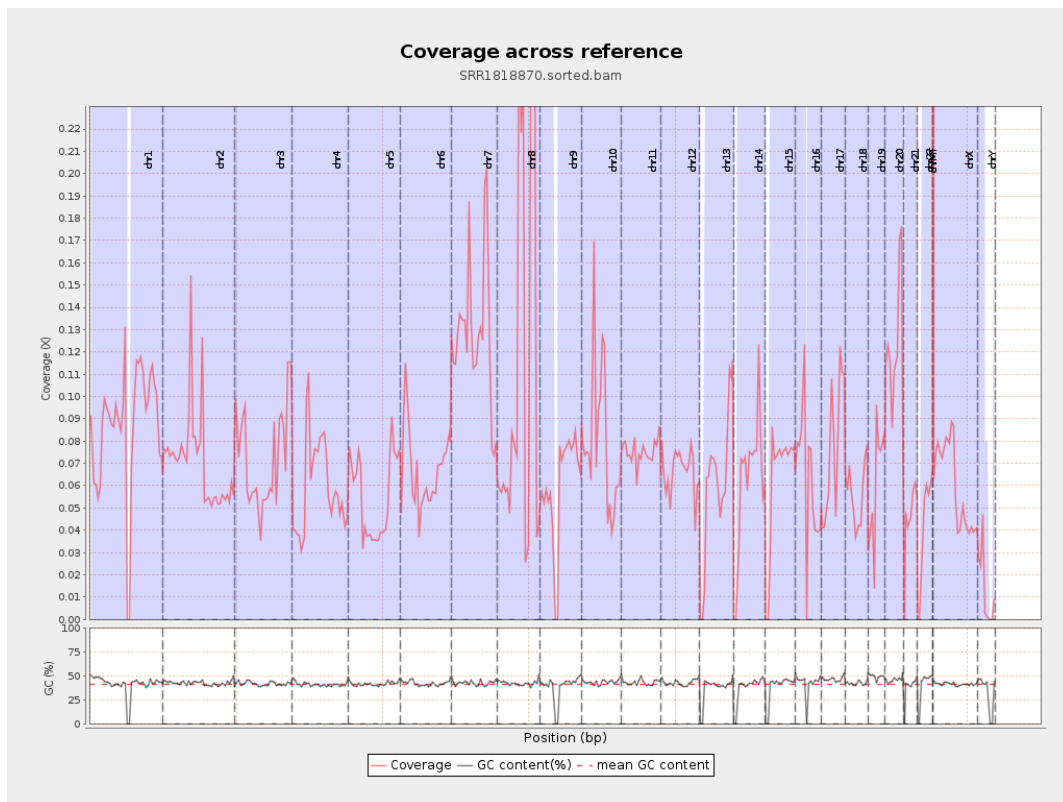
General error rate	0.64%
Mismatches	1,375,730
Insertions	29,069
Mapped reads with at least one insertion	1.14%
Deletions	73,878
Mapped reads with at least one deletion	2.93%
Homopolymer indels	42.02%

2.6. Chromosome stats

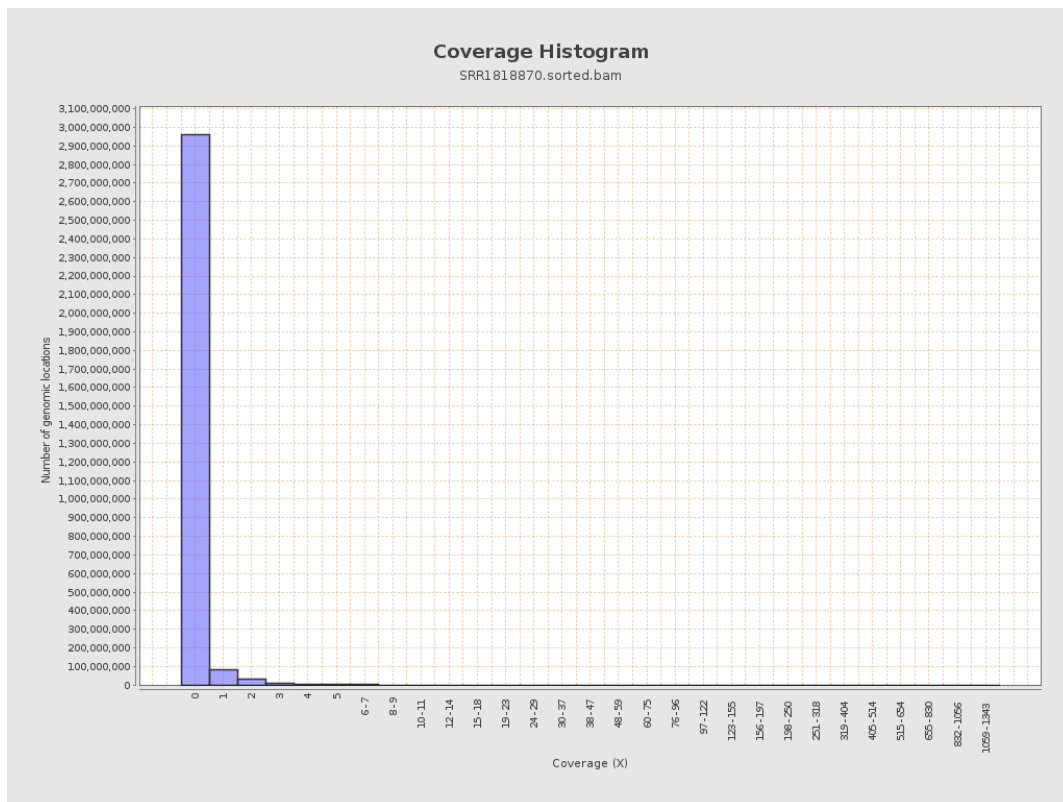
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21545579	0.0864	1.1481
chr2	243199373	17251294	0.0709	1.1321
chr3	198022430	14284406	0.0721	0.4091
chr4	191154276	11496024	0.0601	0.4875
chr5	180915260	10026059	0.0554	0.381
chr6	171115067	11506106	0.0672	0.4404
chr7	159138663	20365629	0.128	1.5802

chr8	146364022	19889255	0.1359	0.7326
chr9	141213431	8481211	0.0601	0.6749
chr10	135534747	10636251	0.0785	1.1014
chr11	135006516	10133903	0.0751	0.5084
chr12	133851895	8919994	0.0666	0.3963
chr13	115169878	7007250	0.0608	0.3712
chr14	107349540	6733270	0.0627	0.4219
chr15	102531392	6330148	0.0617	0.3782
chr16	90354753	5661174	0.0627	0.8618
chr17	81195210	6167571	0.076	0.523
chr18	78077248	4387931	0.0562	0.7563
chr19	59128983	3592916	0.0608	1.0287
chr20	63025520	7932771	0.1259	0.5842
chr21	48129895	2236103	0.0465	0.4052
chr22	51304566	2084412	0.0406	0.3515
chrMT	16571	423163	25.5364	15.1777
chrX	155270560	9300290	0.0599	0.4441
chrY	59373566	798994	0.0135	0.9688

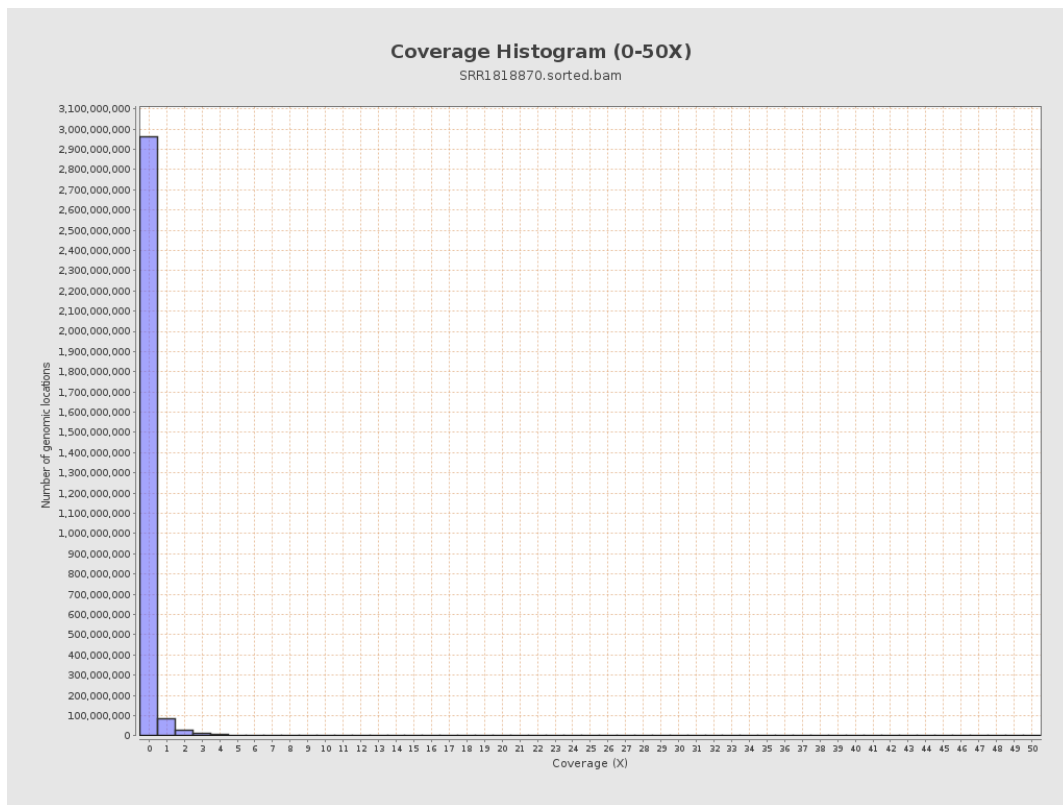
3. Results : Coverage across reference



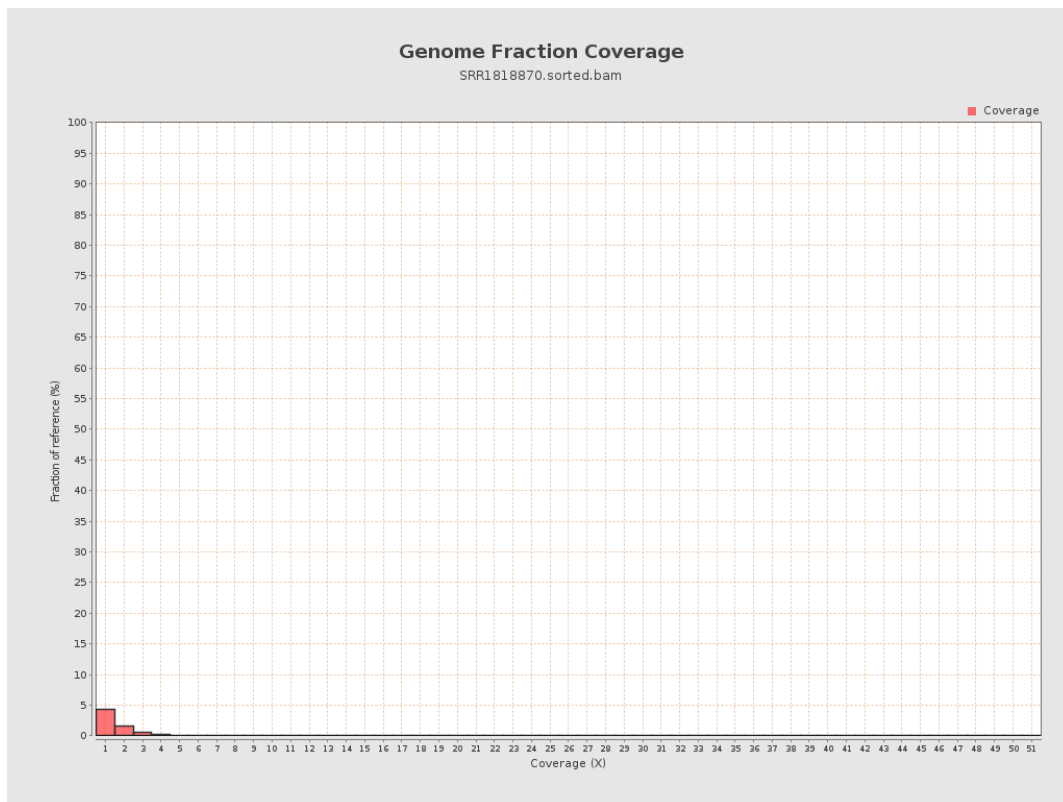
4. Results : Coverage Histogram



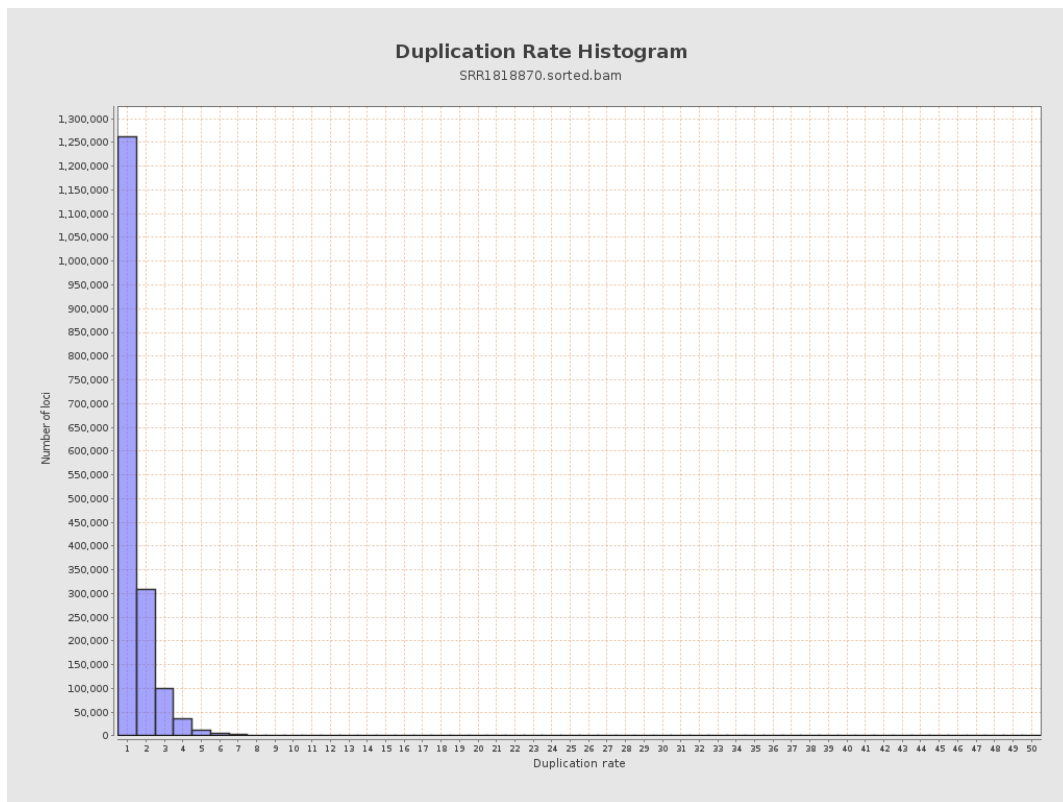
5. Results : Coverage Histogram (0-50X)



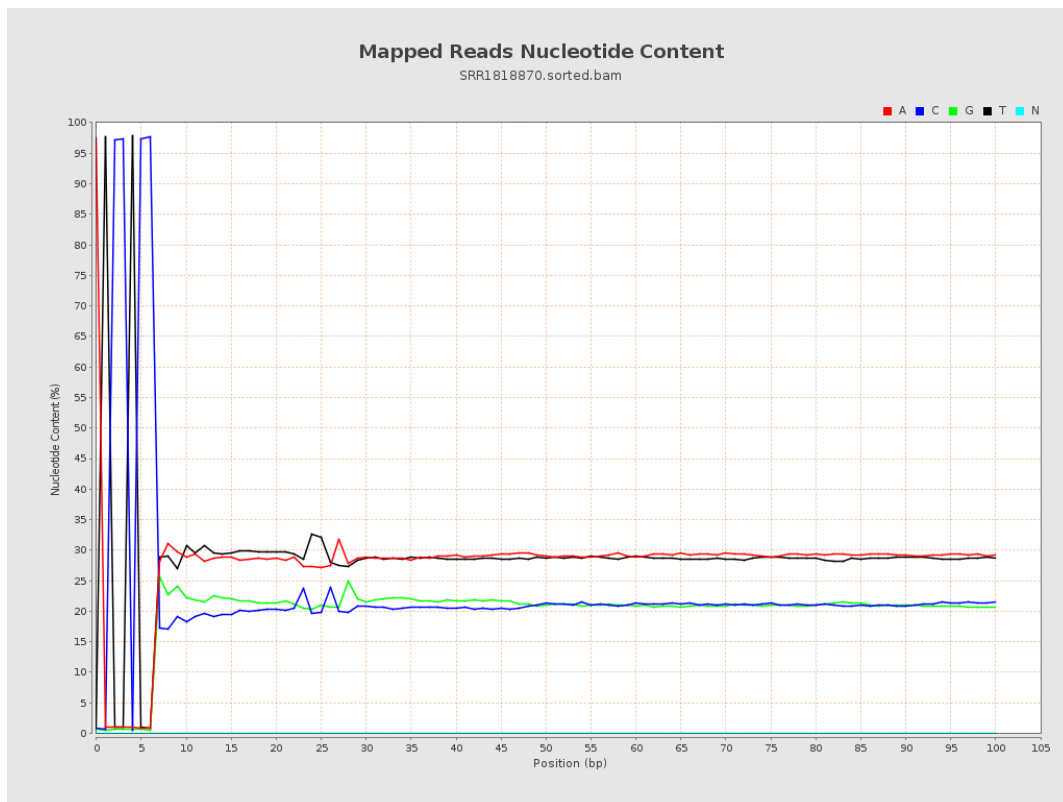
6. Results : Genome Fraction Coverage



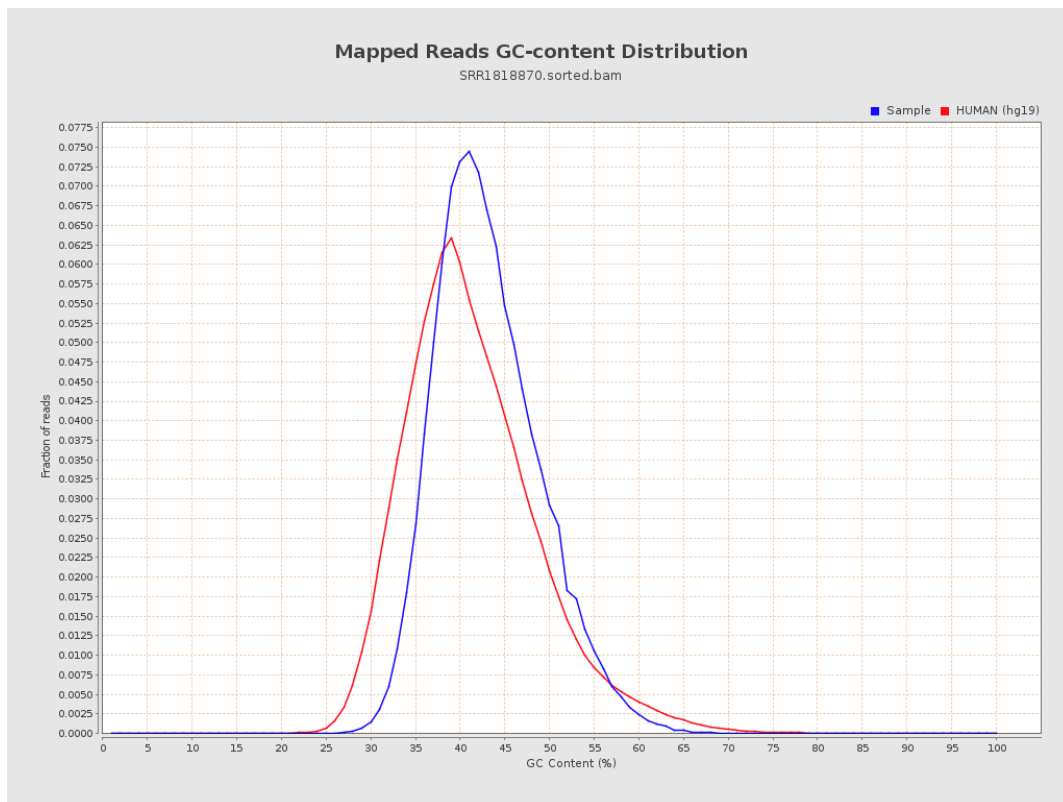
7. Results : Duplication Rate Histogram



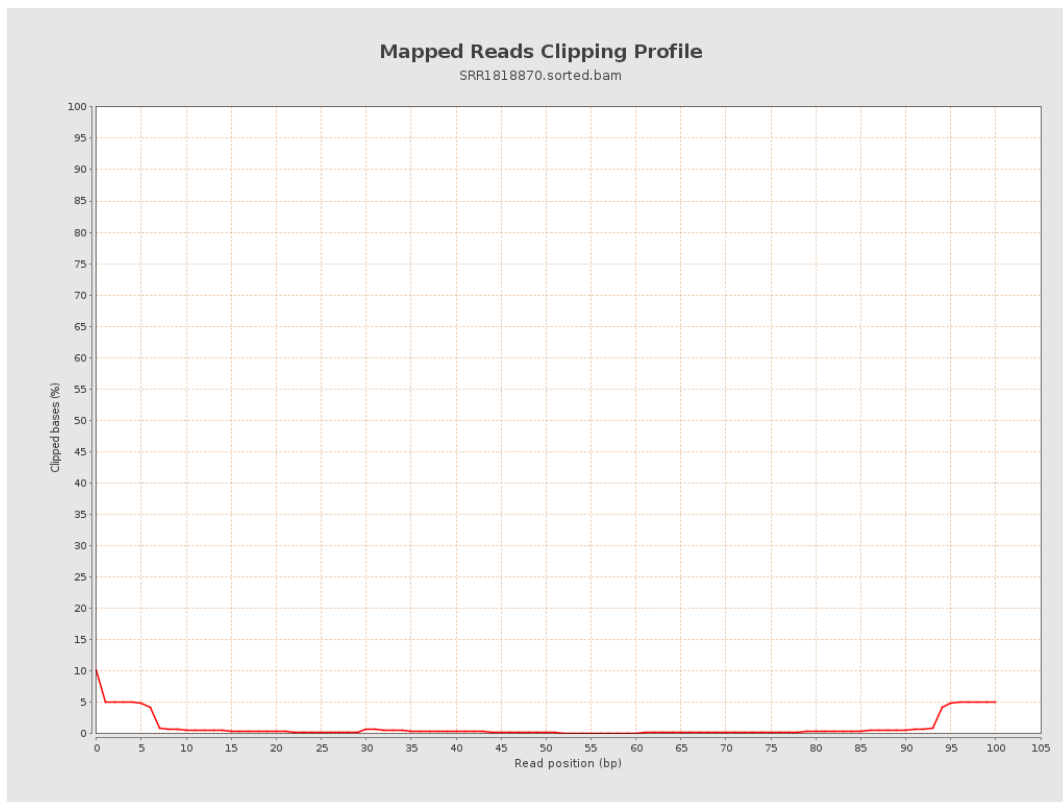
8. Results : Mapped Reads Nucleotide Content



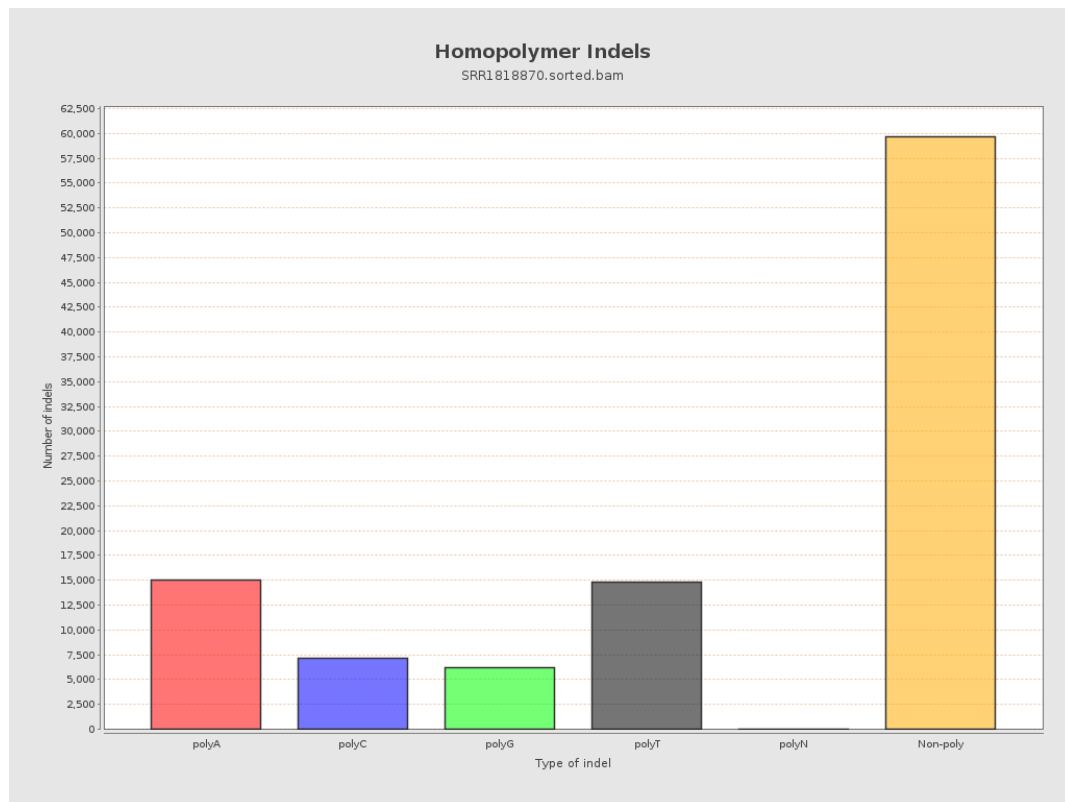
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

