

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:05:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818970.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_SRR1818970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:05:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	639,230
Mapped reads	630,105 / 98.57%
Unmapped reads	9,125 / 1.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,316 / 1.46%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	167,821 / 26.25%
Duplication rate	23.46%
Clipped reads	638,835 / 99.94%

2.2. ACGT Content

Number/percentage of A's	16,401,076 / 28.13%
Number/percentage of C's	12,584,366 / 21.58%
Number/percentage of T's	16,452,446 / 28.21%
Number/percentage of G's	12,870,918 / 22.07%
Number/percentage of N's	3,133 / 0.01%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2737
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2.4. Mapping Quality

Mean Mapping Quality	47.11
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2.5. Mismatches and indels

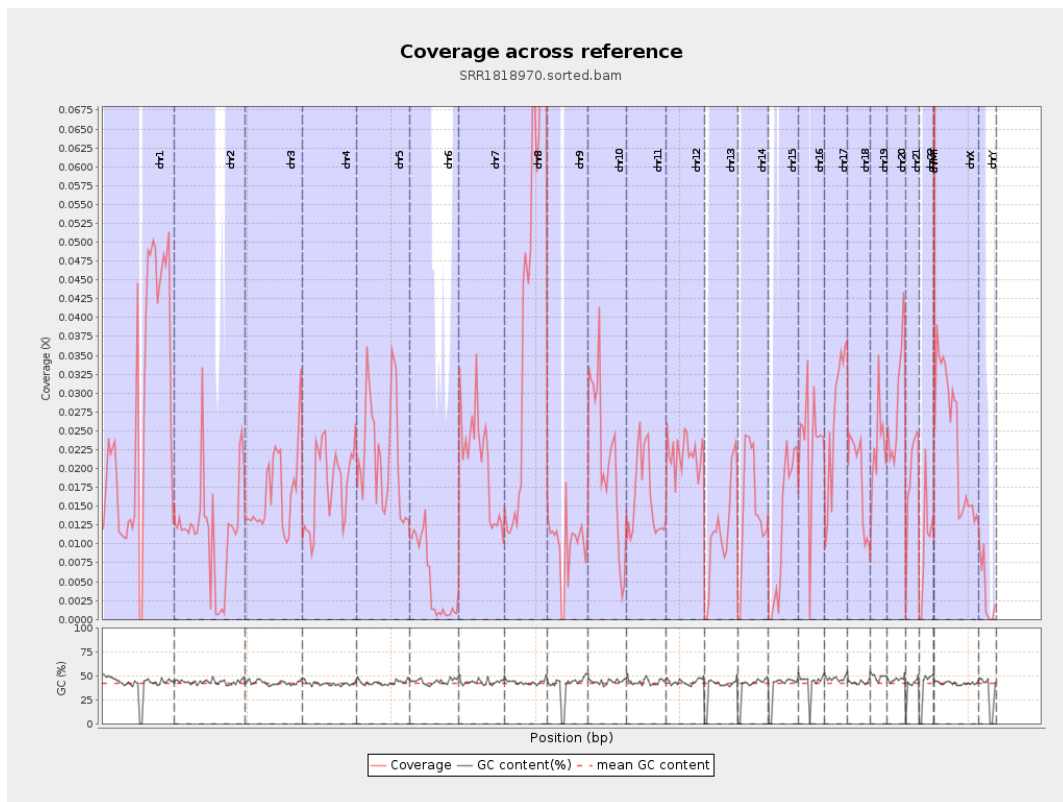
General error rate	0.64%
Mismatches	358,577
Insertions	7,633
Mapped reads with at least one insertion	1.17%
Deletions	17,828
Mapped reads with at least one deletion	2.77%
Homopolymer indels	42.51%

2.6. Chromosome stats

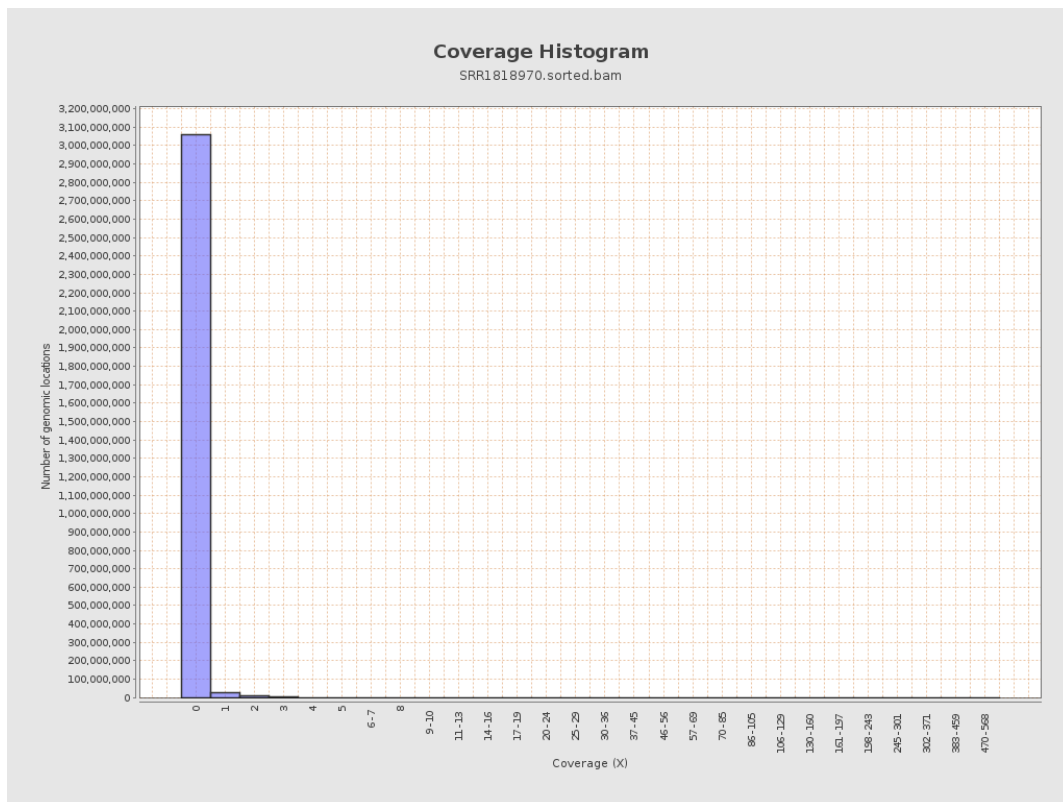
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6698544	0.0269	0.5259
chr2	243199373	2849525	0.0117	0.2861
chr3	198022430	3311117	0.0167	0.1799
chr4	191154276	3404547	0.0178	0.196
chr5	180915260	3975028	0.022	0.2092
chr6	171115067	901355	0.0053	0.1053
chr7	159138663	3330516	0.0209	0.324

chr8	146364022	5981972	0.0409	0.3038
chr9	141213431	1385712	0.0098	0.1976
chr10	135534747	2923181	0.0216	0.2982
chr11	135006516	2201027	0.0163	0.1977
chr12	133851895	2949306	0.022	0.2083
chr13	115169878	1357382	0.0118	0.1524
chr14	107349540	1587219	0.0148	0.1725
chr15	102531392	1284370	0.0125	0.1592
chr16	90354753	2080471	0.023	0.292
chr17	81195210	2139061	0.0263	0.2472
chr18	78077248	1457146	0.0187	0.2759
chr19	59128983	1362856	0.023	0.4983
chr20	63025520	1815251	0.0288	0.2493
chr21	48129895	931435	0.0194	0.2002
chr22	51304566	525041	0.0102	0.1463
chrMT	16571	17605	1.0624	1.6463
chrX	155270560	3670167	0.0236	0.2351
chrY	59373566	204747	0.0034	0.2262

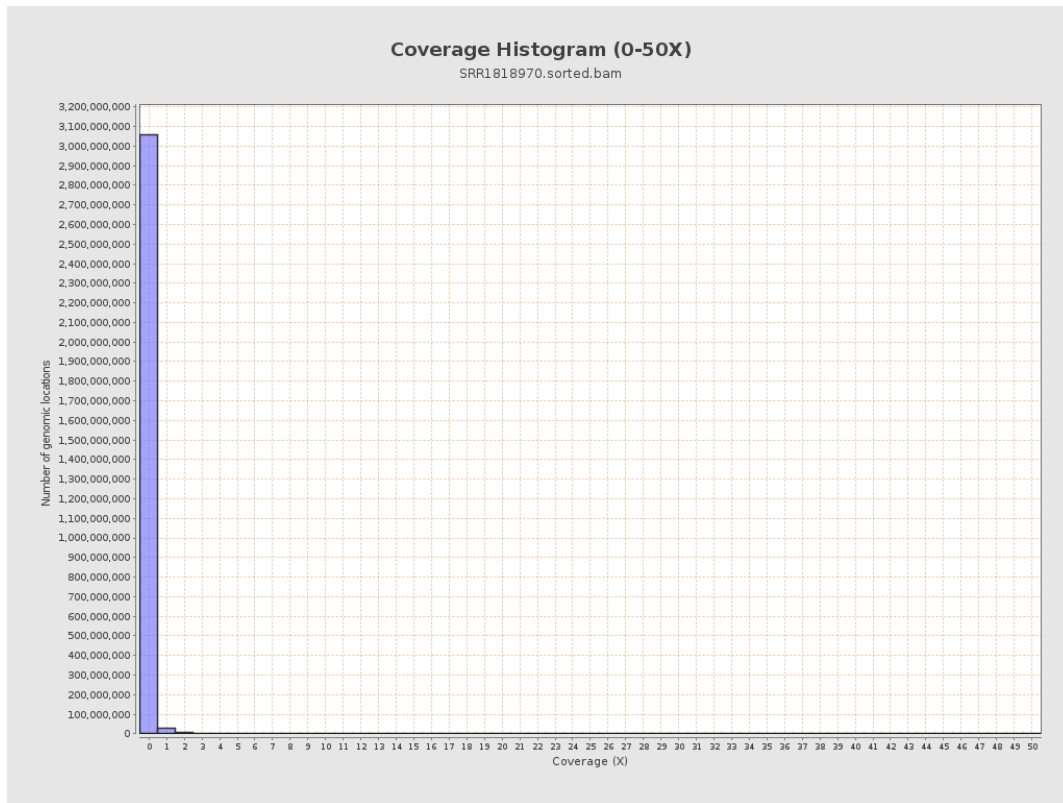
3. Results : Coverage across reference



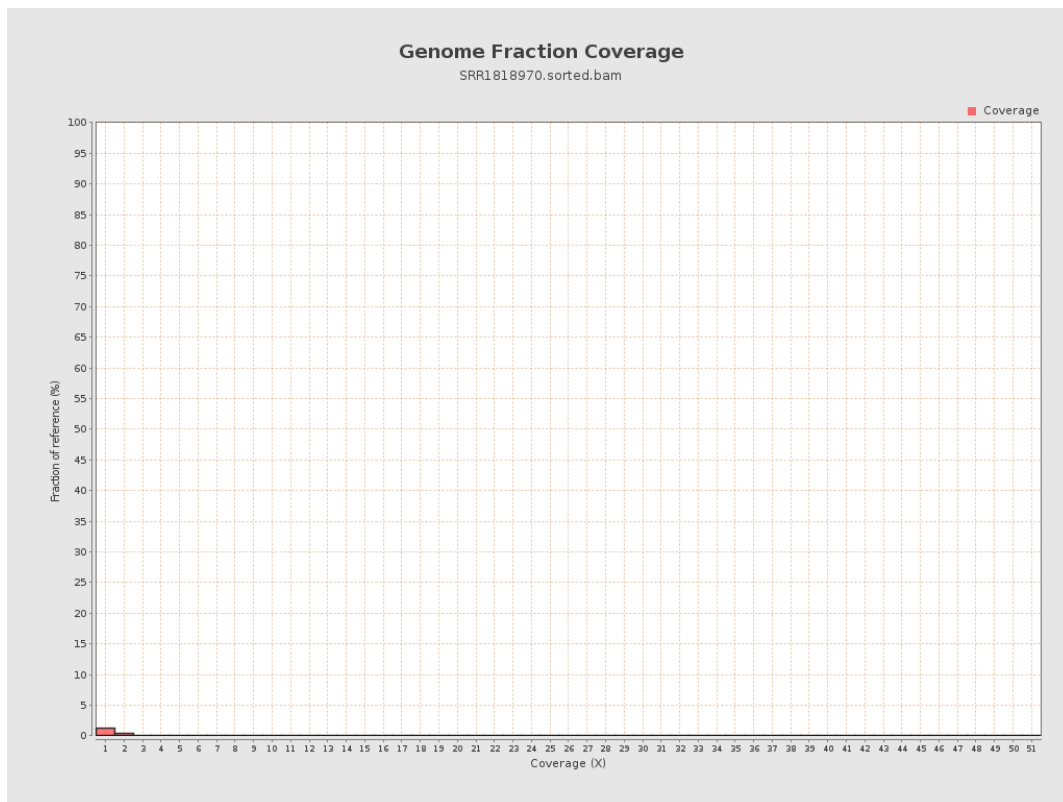
4. Results : Coverage Histogram



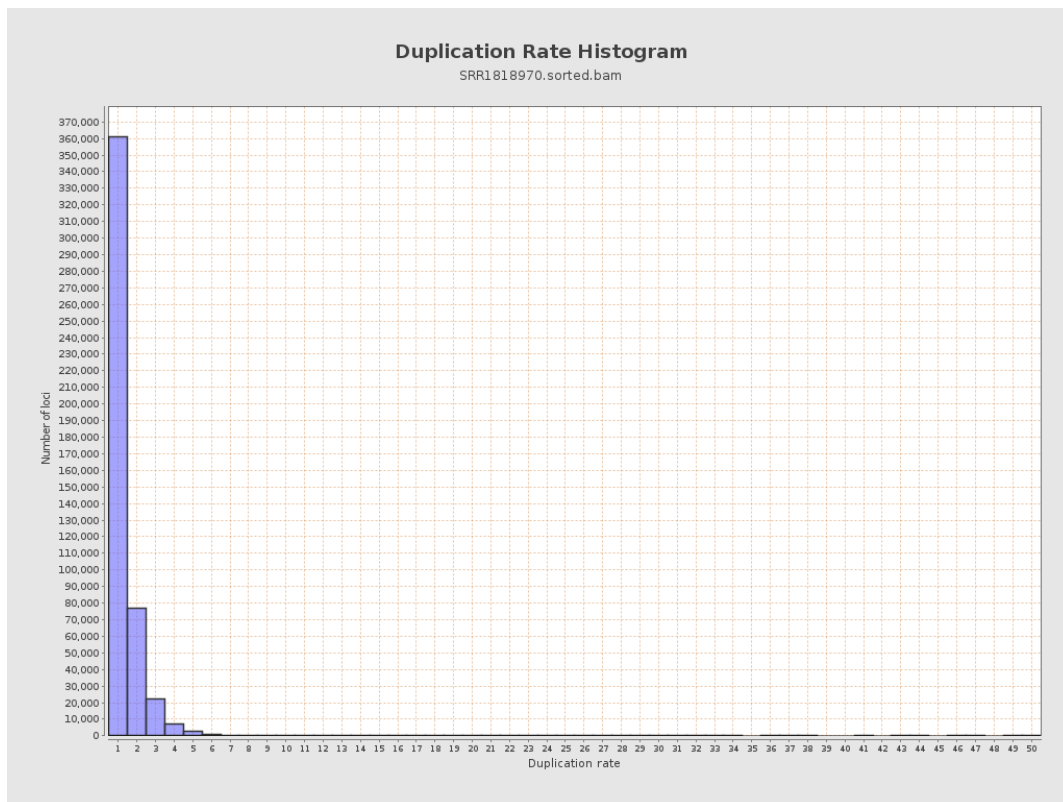
5. Results : Coverage Histogram (0-50X)



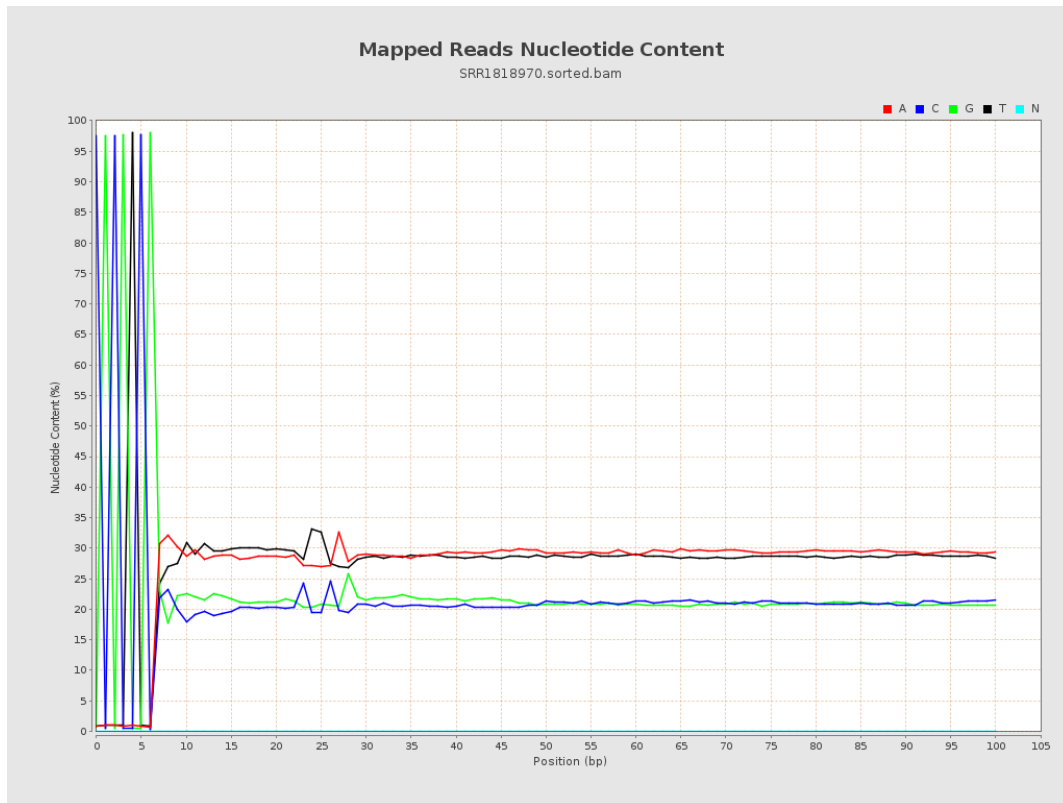
6. Results : Genome Fraction Coverage



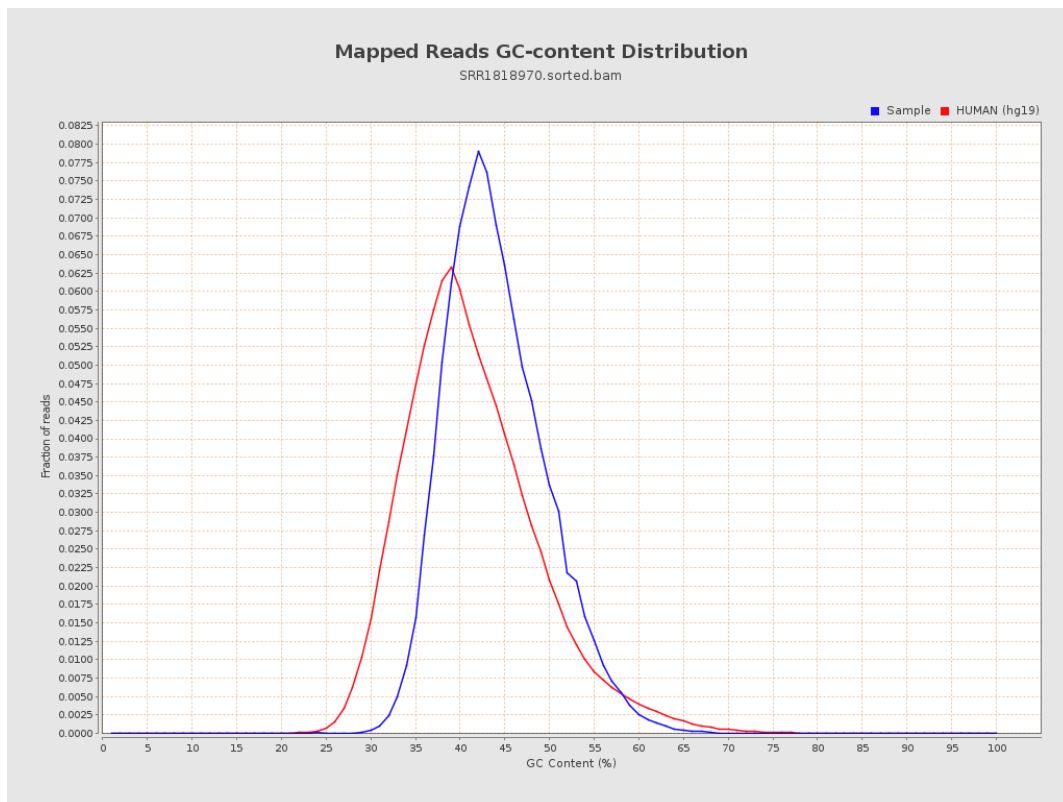
7. Results : Duplication Rate Histogram



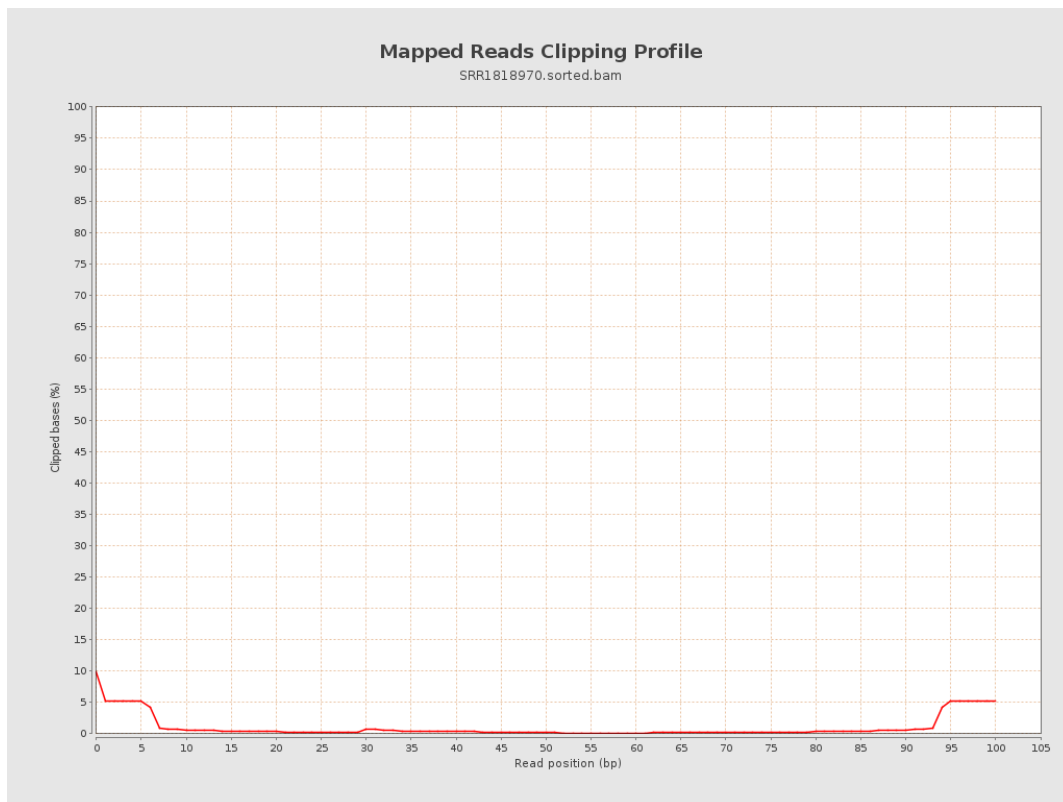
8. Results : Mapped Reads Nucleotide Content



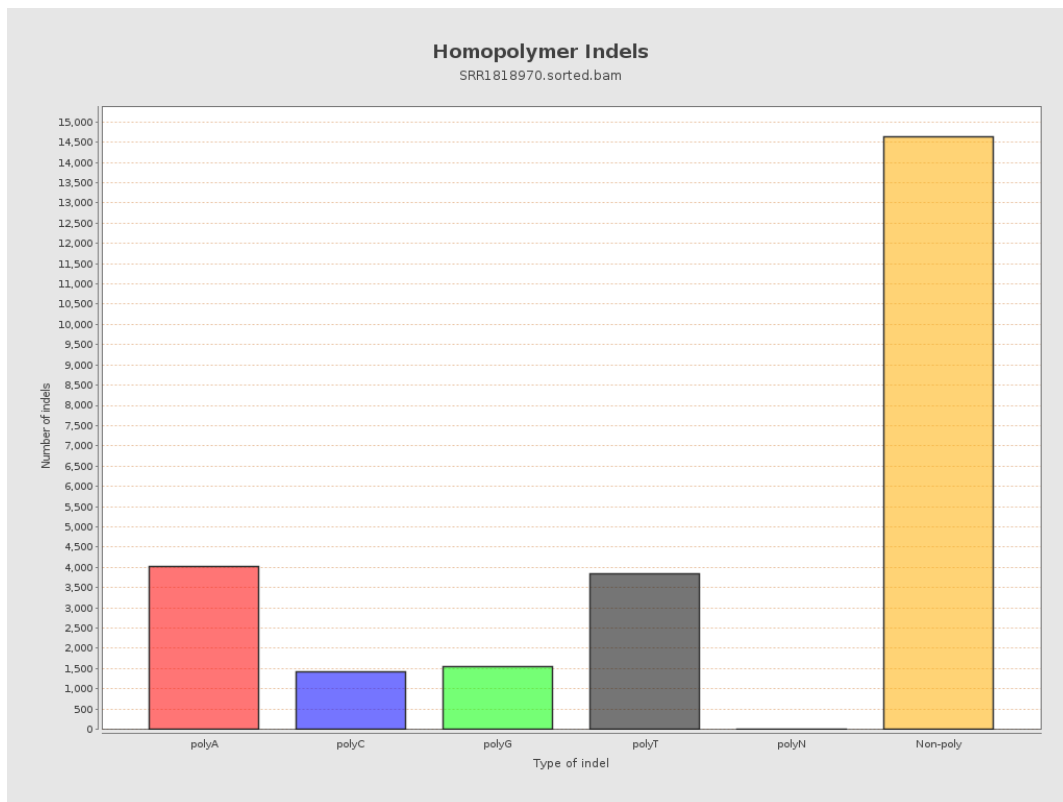
9. Results : Mapped Reads GC-content Distribution



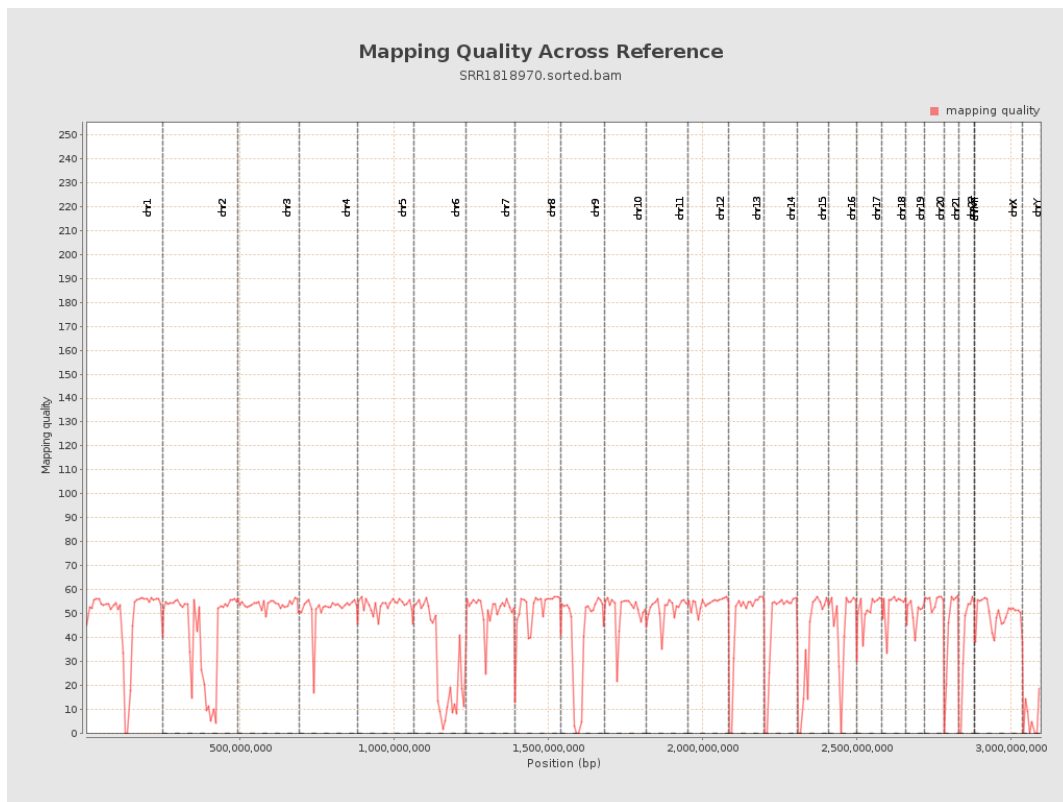
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

