

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:23:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818833.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_SRR1818833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:23:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,357,106
Mapped reads	2,249,986 / 95.46%
Unmapped reads	107,120 / 4.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,068 / 1.53%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	641,931 / 27.23%
Duplication rate	24.62%
Clipped reads	2,277,908 / 96.64%

2.2. ACGT Content

Number/percentage of A's	59,284,242 / 28.47%
Number/percentage of C's	43,624,095 / 20.95%
Number/percentage of T's	60,111,055 / 28.87%
Number/percentage of G's	45,225,324 / 21.72%
Number/percentage of N's	2,738 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0673

Standard Deviation	0.7844
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2.4. Mapping Quality

Mean Mapping Quality	49.34
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2.5. Mismatches and indels

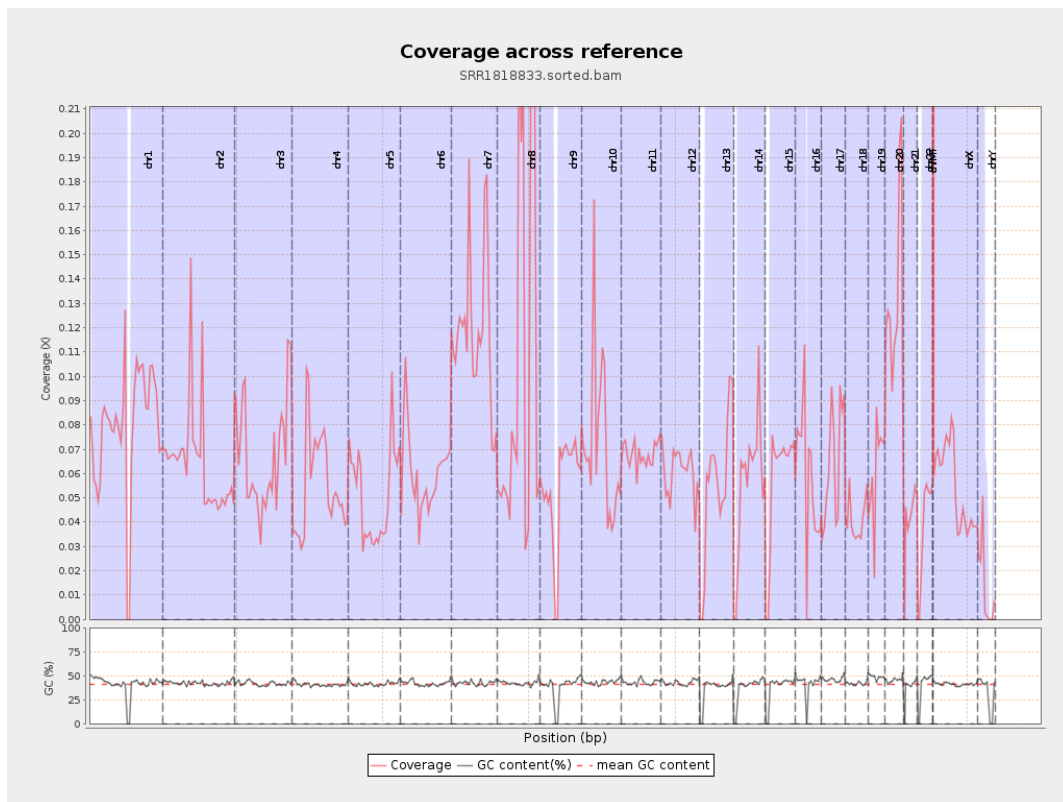
General error rate	0.63%
Mismatches	1,245,066
Insertions	28,194
Mapped reads with at least one insertion	1.21%
Deletions	66,599
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.49%

2.6. Chromosome stats

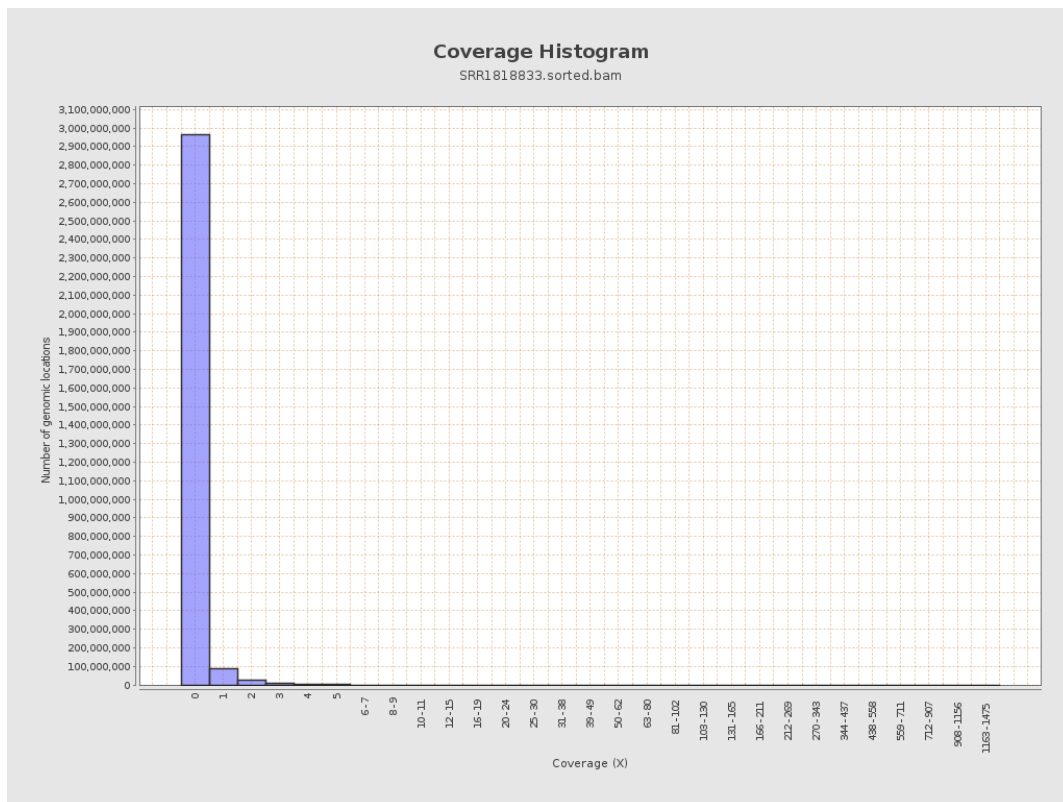
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19749311	0.0792	1.196
chr2	243199373	15703901	0.0646	1.125
chr3	198022430	13374710	0.0675	0.3801
chr4	191154276	10657006	0.0558	0.4835
chr5	180915260	9294570	0.0514	0.3466
chr6	171115067	10341386	0.0604	0.4018
chr7	159138663	18810885	0.1182	1.6625

chr8	146364022	18205758	0.1244	0.6652
chr9	141213431	7708461	0.0546	0.614
chr10	135534747	9640266	0.0711	1.0733
chr11	135006516	9156271	0.0678	0.4713
chr12	133851895	8123321	0.0607	0.362
chr13	115169878	6408281	0.0556	0.3403
chr14	107349540	6127100	0.0571	0.3934
chr15	102531392	5807196	0.0566	0.3418
chr16	90354753	5232232	0.0579	0.8059
chr17	81195210	5139179	0.0633	0.4927
chr18	78077248	3219238	0.0412	0.7495
chr19	59128983	3605939	0.061	0.9848
chr20	63025520	8567755	0.1359	0.5913
chr21	48129895	2022272	0.042	0.4072
chr22	51304566	1901140	0.0371	0.3536
chrMT	16571	314868	19.0011	12.1346
chrX	155270560	8464172	0.0545	0.407
chrY	59373566	802400	0.0135	1.0242

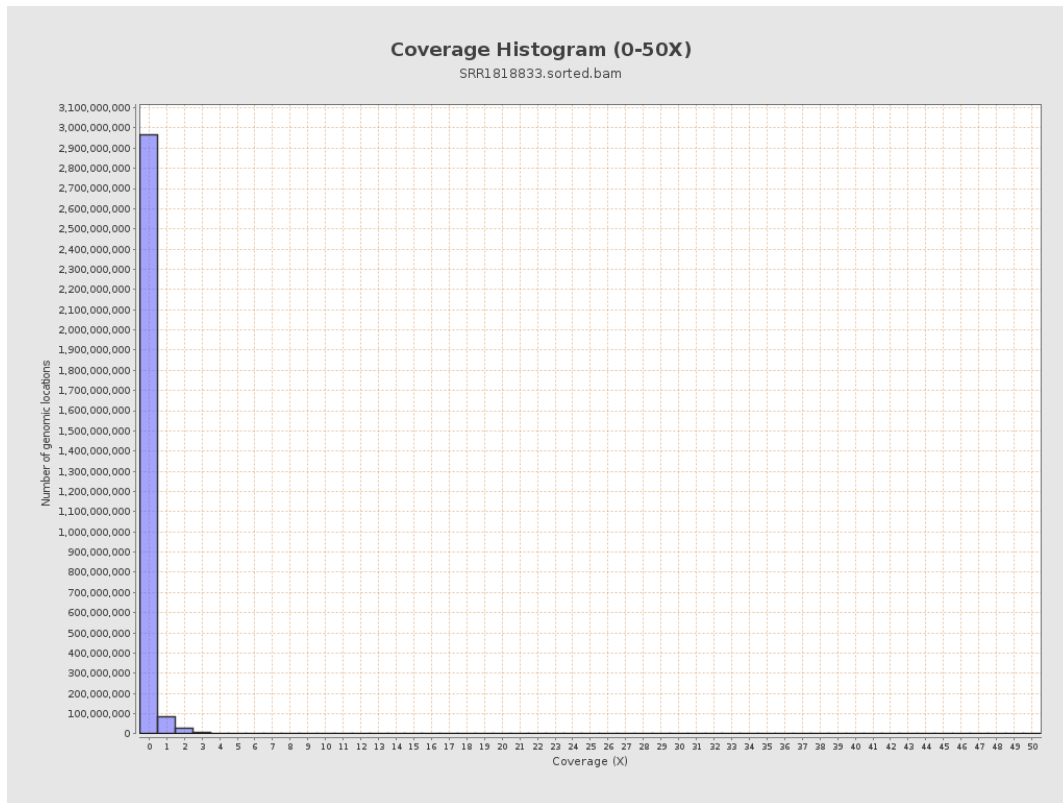
3. Results : Coverage across reference



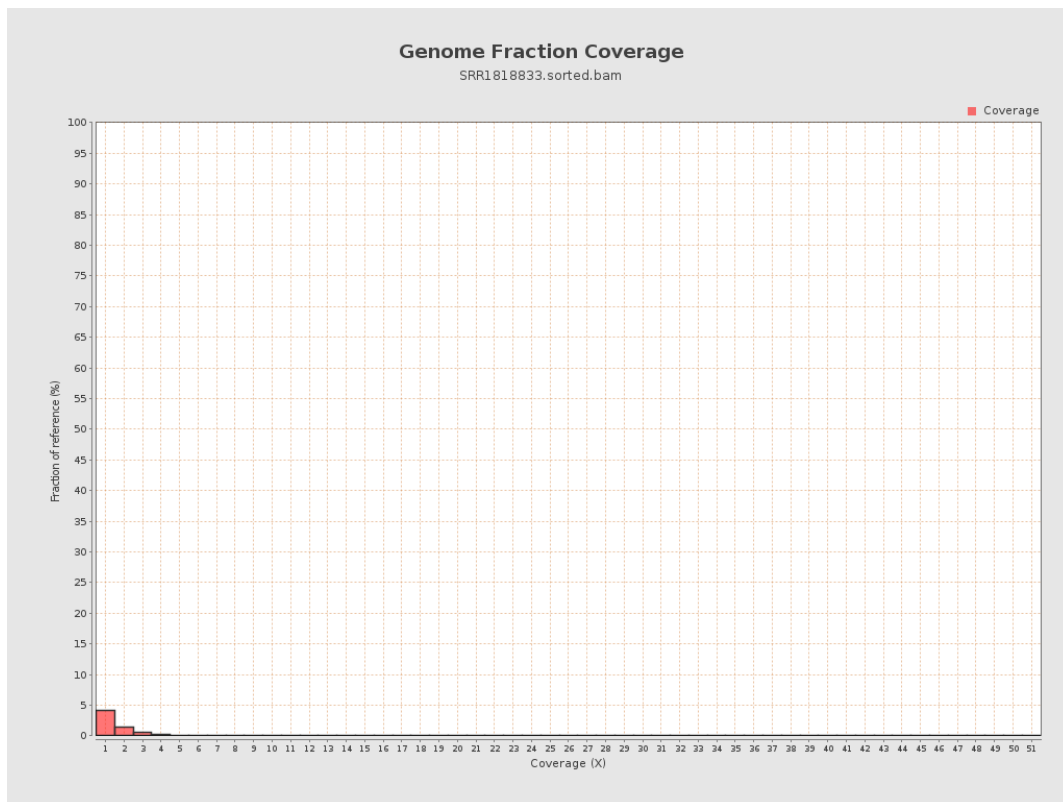
4. Results : Coverage Histogram



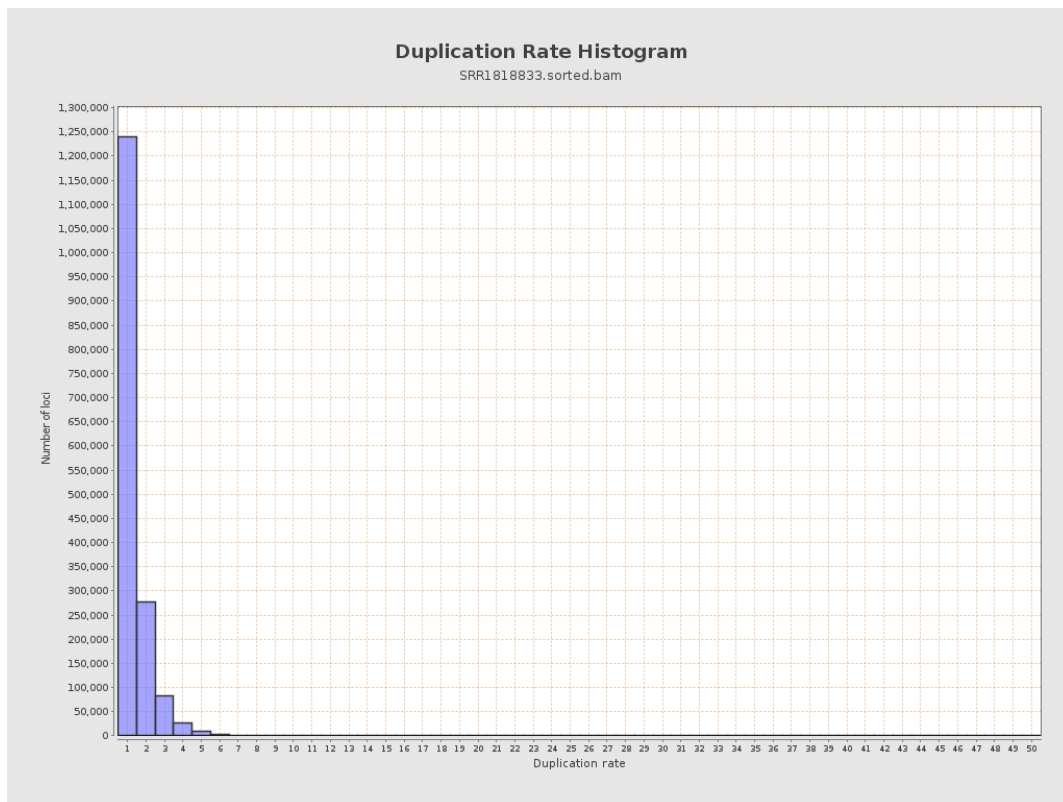
5. Results : Coverage Histogram (0-50X)



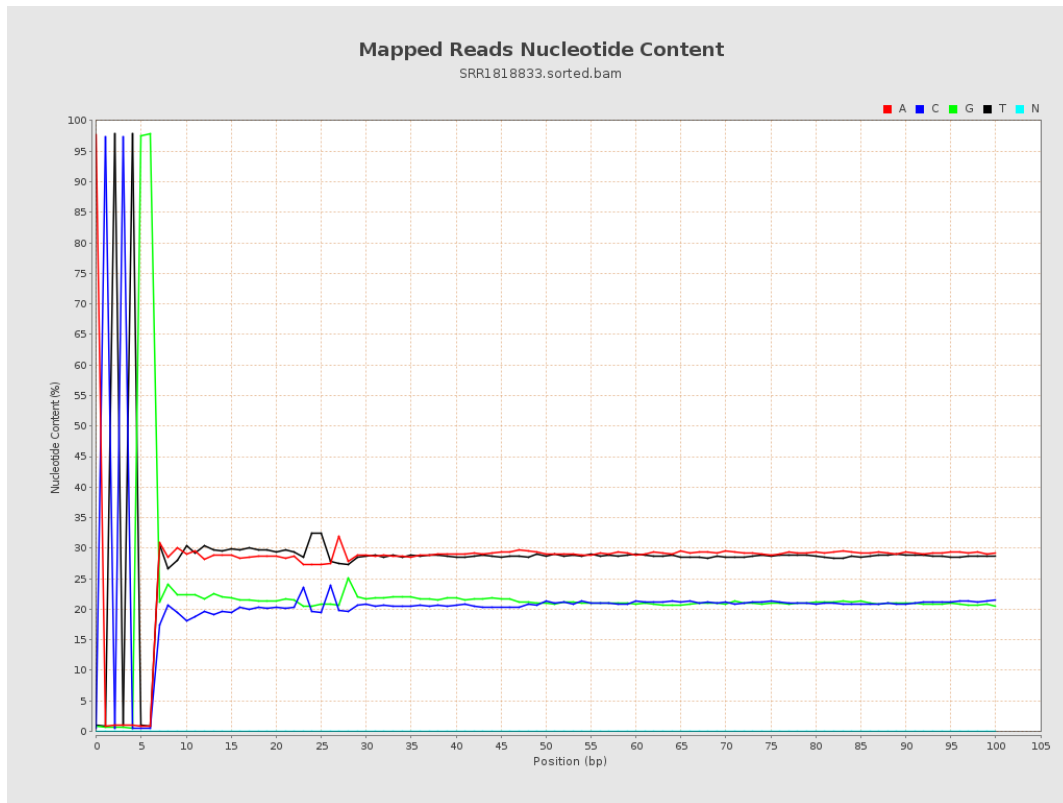
6. Results : Genome Fraction Coverage



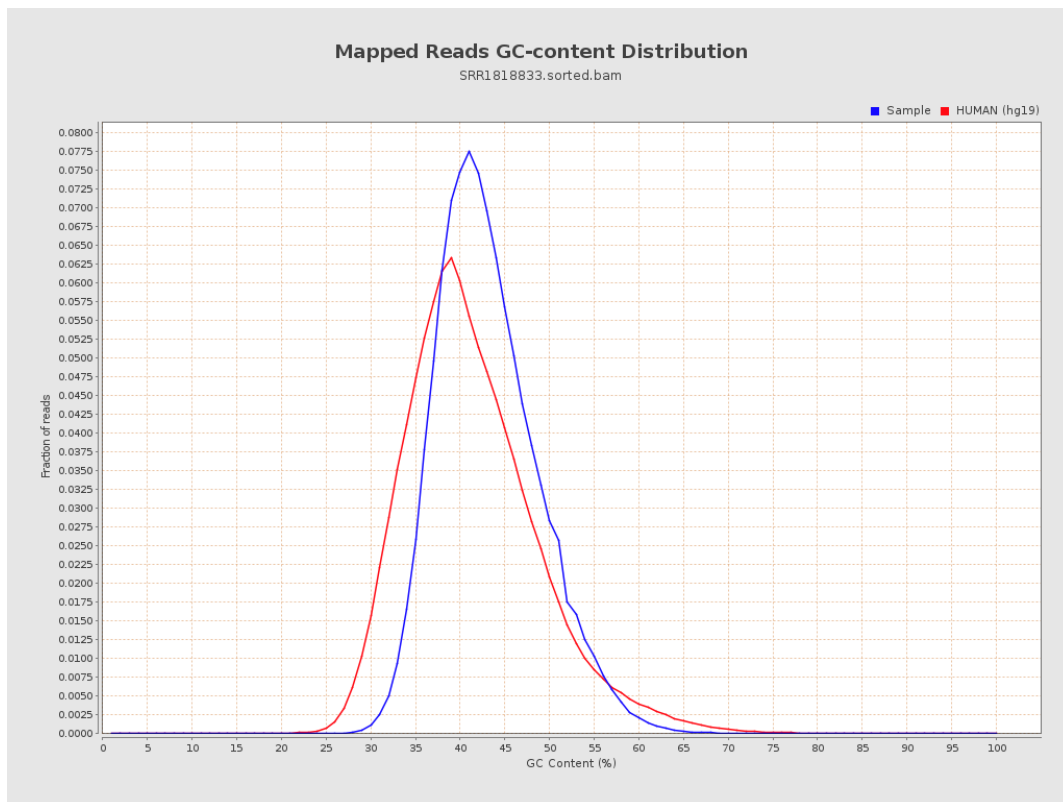
7. Results : Duplication Rate Histogram



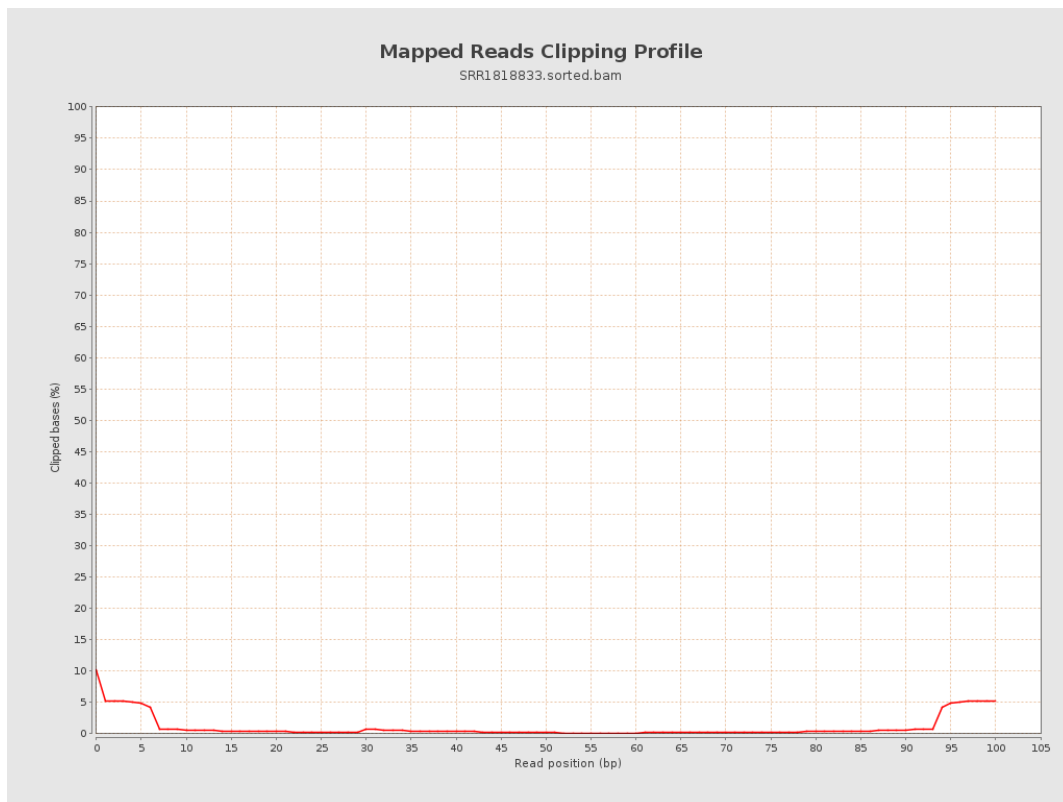
8. Results : Mapped Reads Nucleotide Content



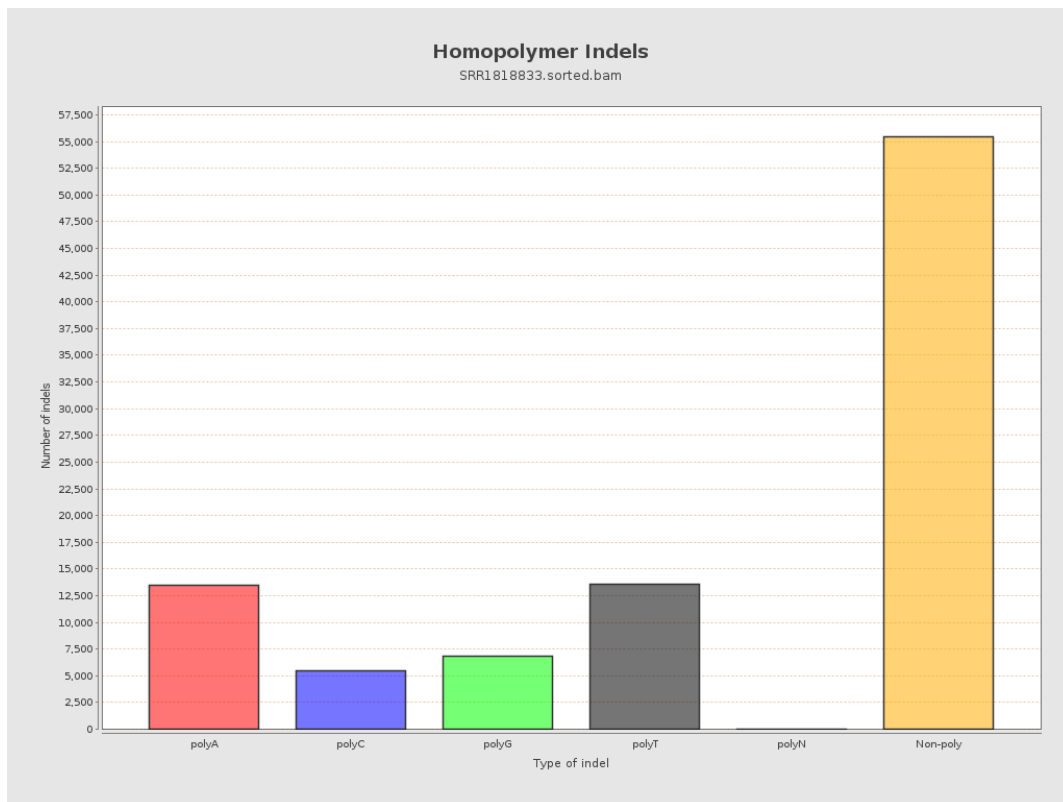
9. Results : Mapped Reads GC-content Distribution



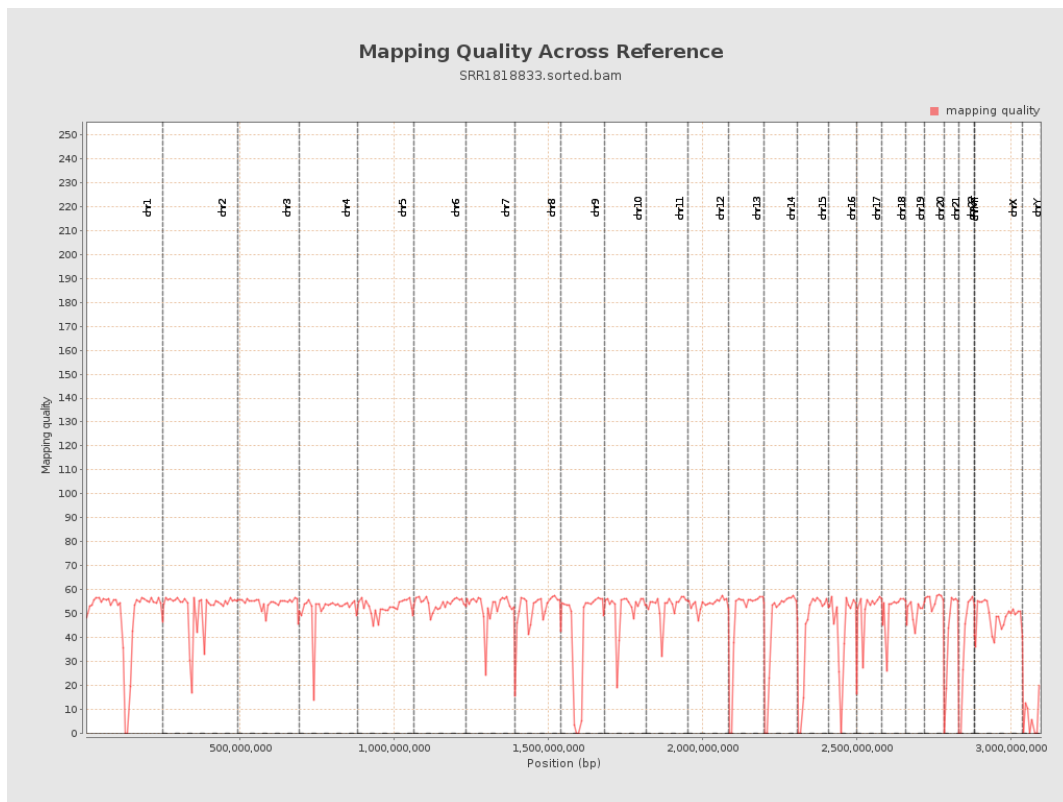
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

