

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:04:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818850.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_SRR1818850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:04:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,830,951
Mapped reads	1,805,925 / 98.63%
Unmapped reads	25,026 / 1.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,974 / 1.64%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	450,195 / 24.59%
Duplication rate	21.61%
Clipped reads	1,826,759 / 99.77%

2.2. ACGT Content

Number/percentage of A's	46,621,874 / 27.91%
Number/percentage of C's	36,819,686 / 22.04%
Number/percentage of T's	48,476,743 / 29.02%
Number/percentage of G's	35,102,203 / 21.02%
Number/percentage of N's	2,561 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.054

Standard Deviation	0.6272
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2.4. Mapping Quality

Mean Mapping Quality	49.26
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2.5. Mismatches and indels

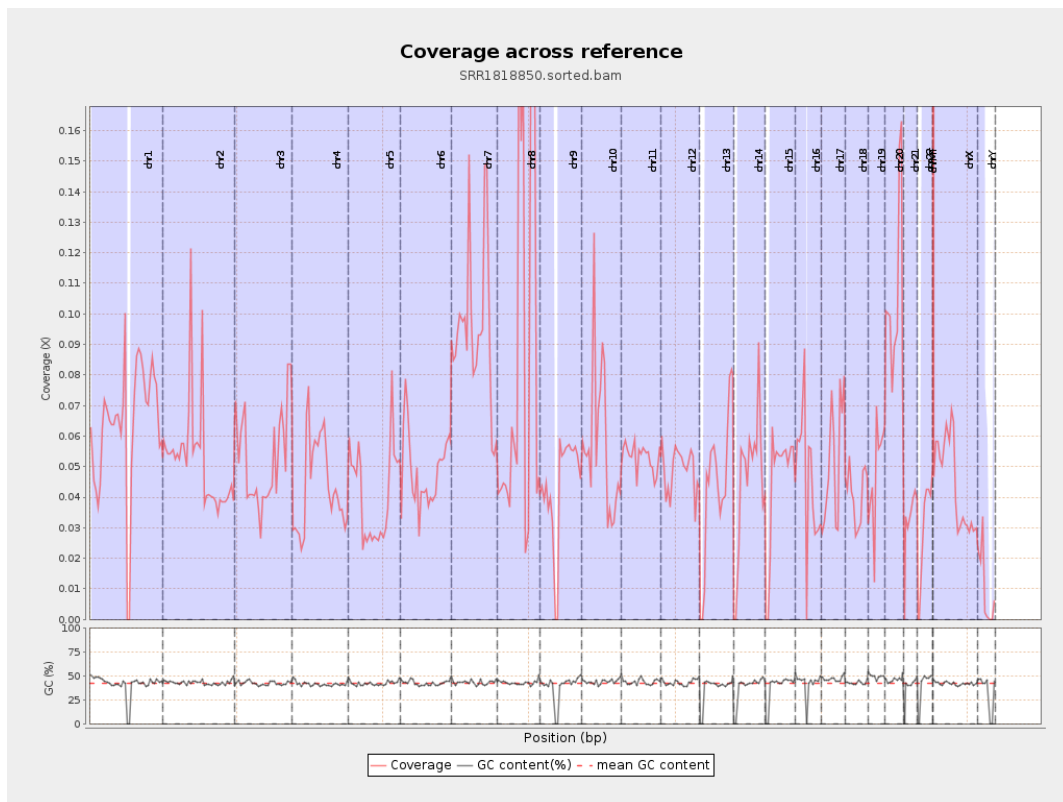
General error rate	0.64%
Mismatches	1,012,201
Insertions	24,201
Mapped reads with at least one insertion	1.3%
Deletions	55,063
Mapped reads with at least one deletion	2.98%
Homopolymer indels	41.11%

2.6. Chromosome stats

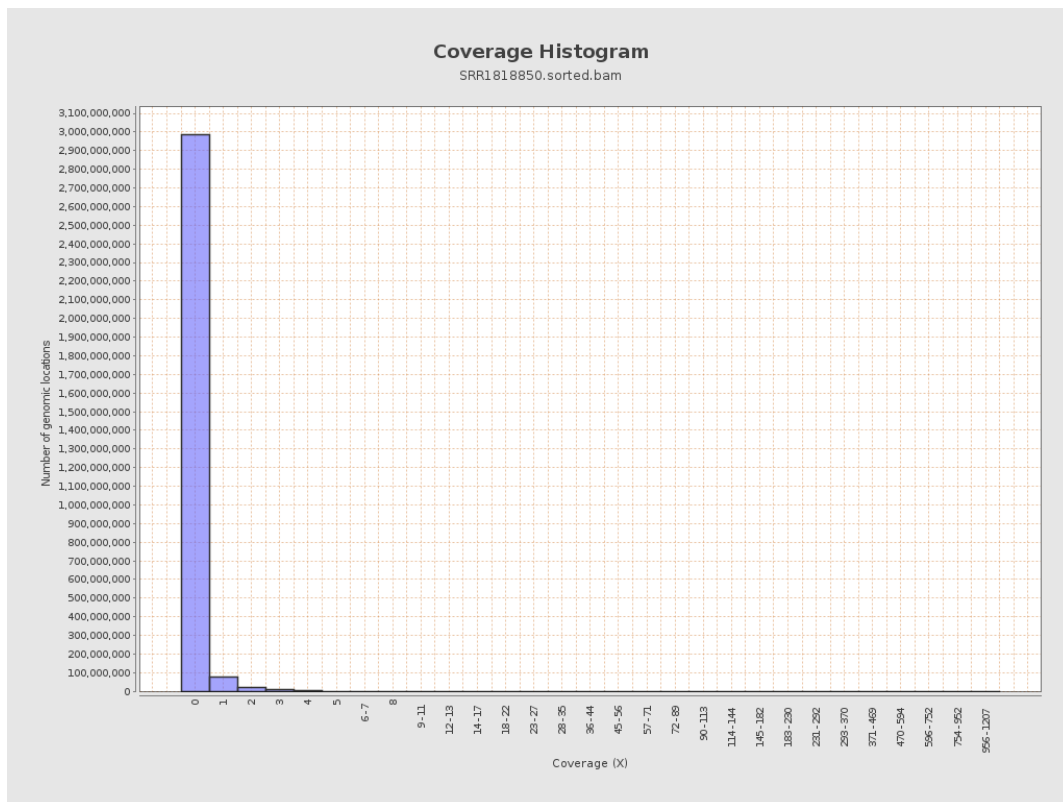
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15847687	0.0636	0.9437
chr2	243199373	12719906	0.0523	0.959
chr3	198022430	10447055	0.0528	0.3162
chr4	191154276	8486568	0.0444	0.3646
chr5	180915260	7423383	0.041	0.301
chr6	171115067	8333964	0.0487	0.333
chr7	159138663	15091787	0.0948	1.2999

chr8	146364022	14668896	0.1002	0.5588
chr9	141213431	6151837	0.0436	0.5184
chr10	135534747	7668836	0.0566	0.7916
chr11	135006516	7149669	0.053	0.3862
chr12	133851895	6573611	0.0491	0.3099
chr13	115169878	5146195	0.0447	0.2898
chr14	107349540	4987693	0.0465	0.3194
chr15	102531392	4563131	0.0445	0.2913
chr16	90354753	4131316	0.0457	0.6387
chr17	81195210	4088838	0.0504	0.4035
chr18	78077248	3209684	0.0411	0.609
chr19	59128983	2837276	0.048	0.7593
chr20	63025520	6819996	0.1082	0.4923
chr21	48129895	1586389	0.033	0.3121
chr22	51304566	1488841	0.029	0.2692
chrMT	16571	250785	15.134	9.6933
chrX	155270560	6861482	0.0442	0.3479
chrY	59373566	593371	0.01	0.7062

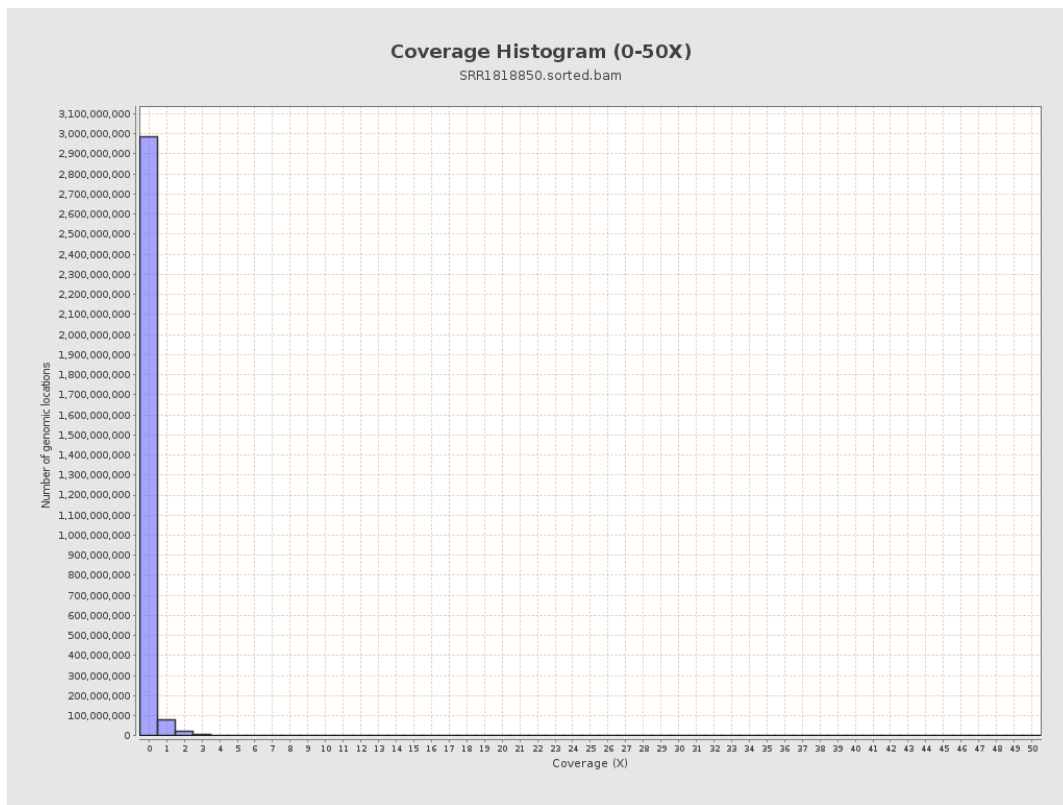
3. Results : Coverage across reference



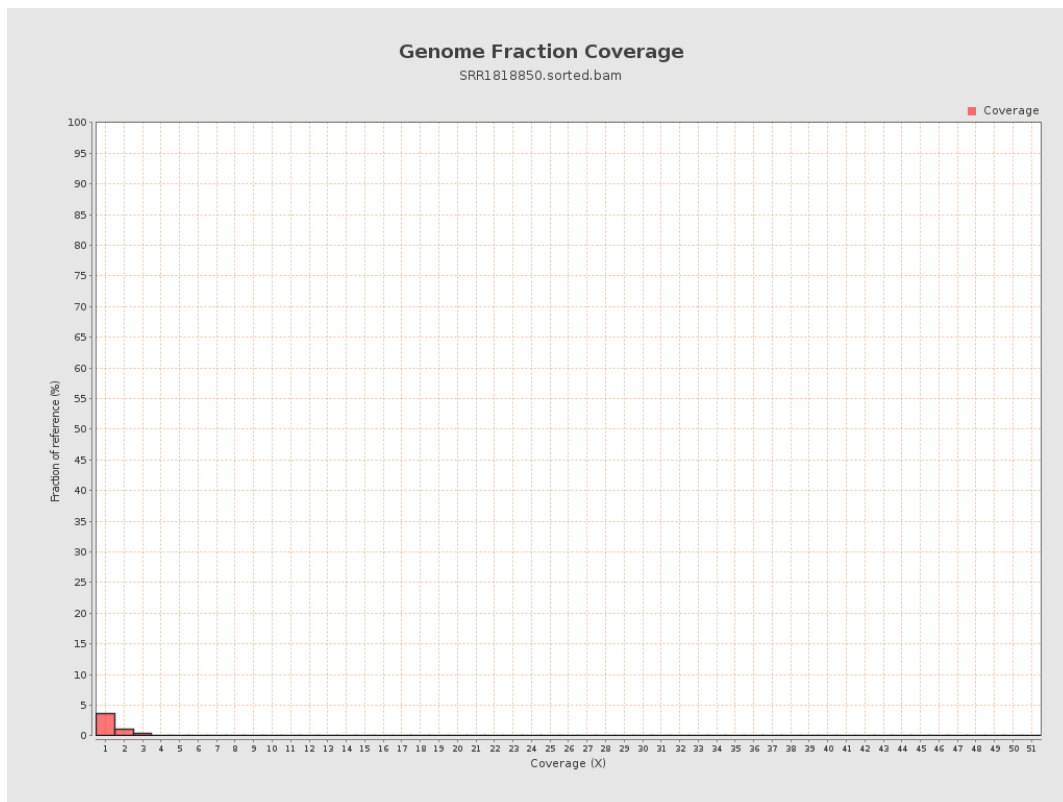
4. Results : Coverage Histogram



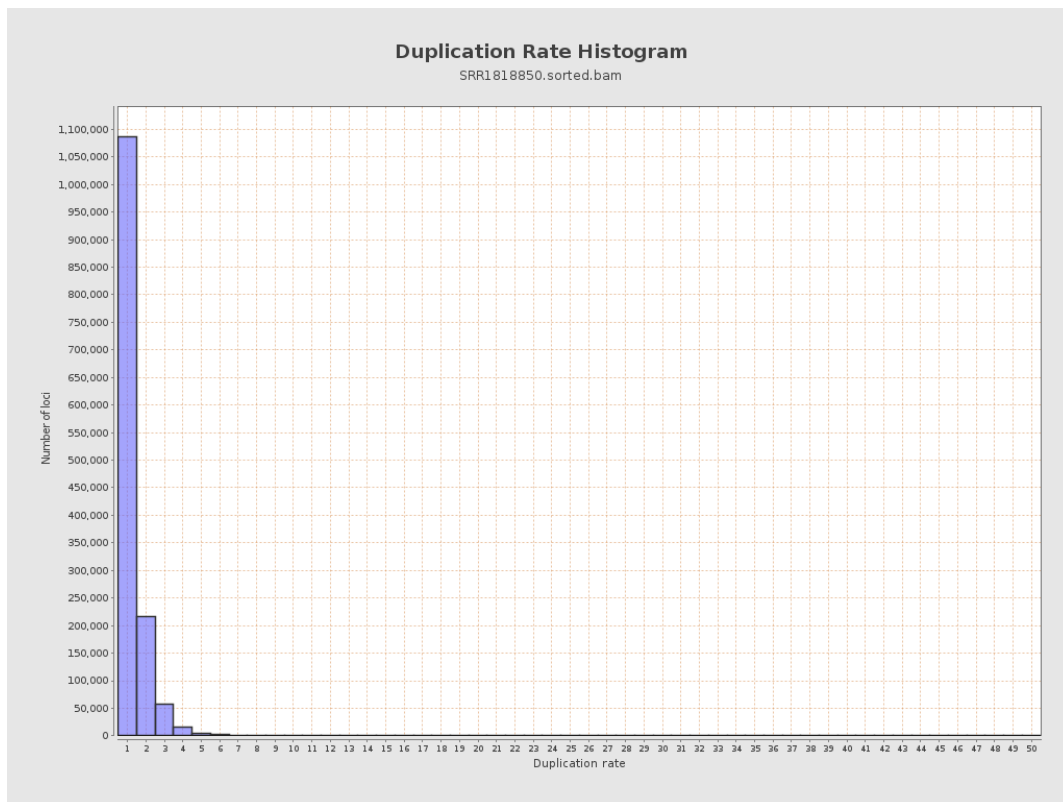
5. Results : Coverage Histogram (0-50X)



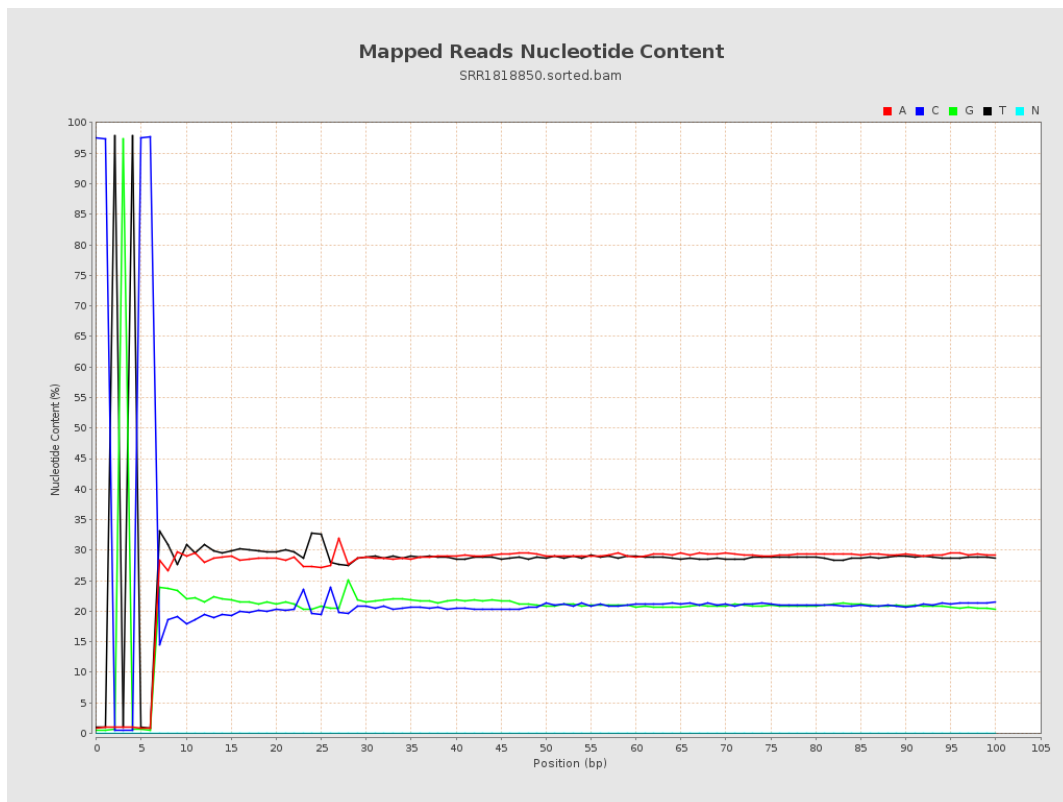
6. Results : Genome Fraction Coverage



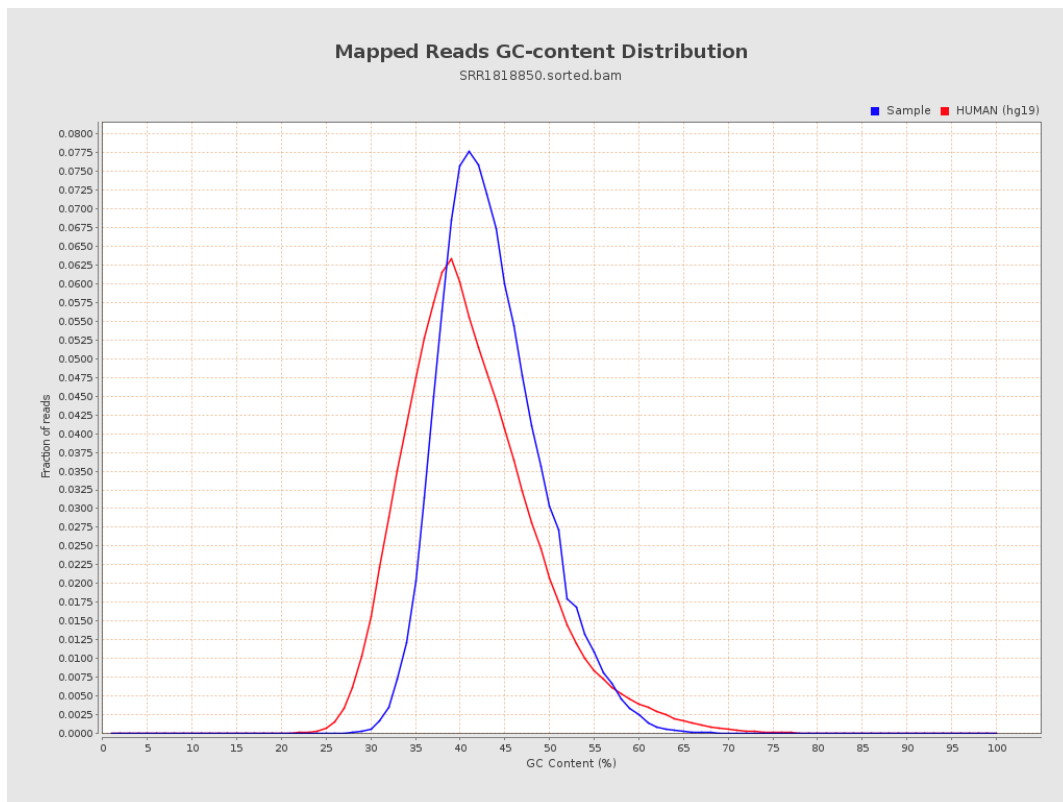
7. Results : Duplication Rate Histogram



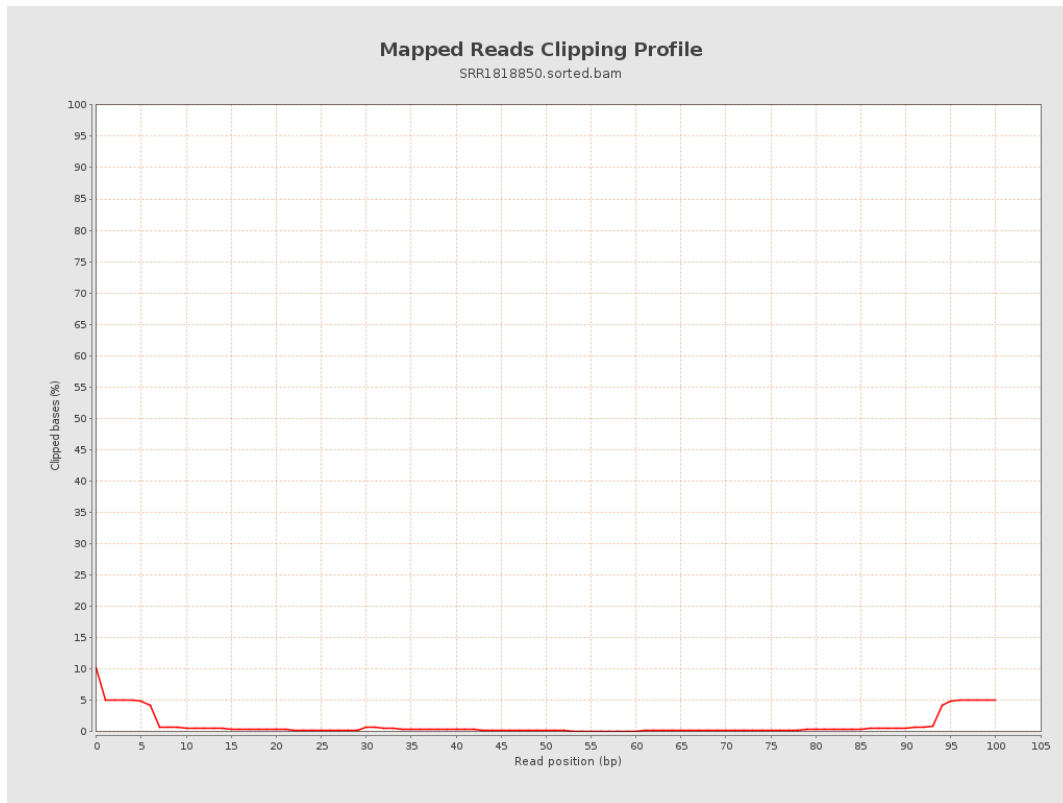
8. Results : Mapped Reads Nucleotide Content



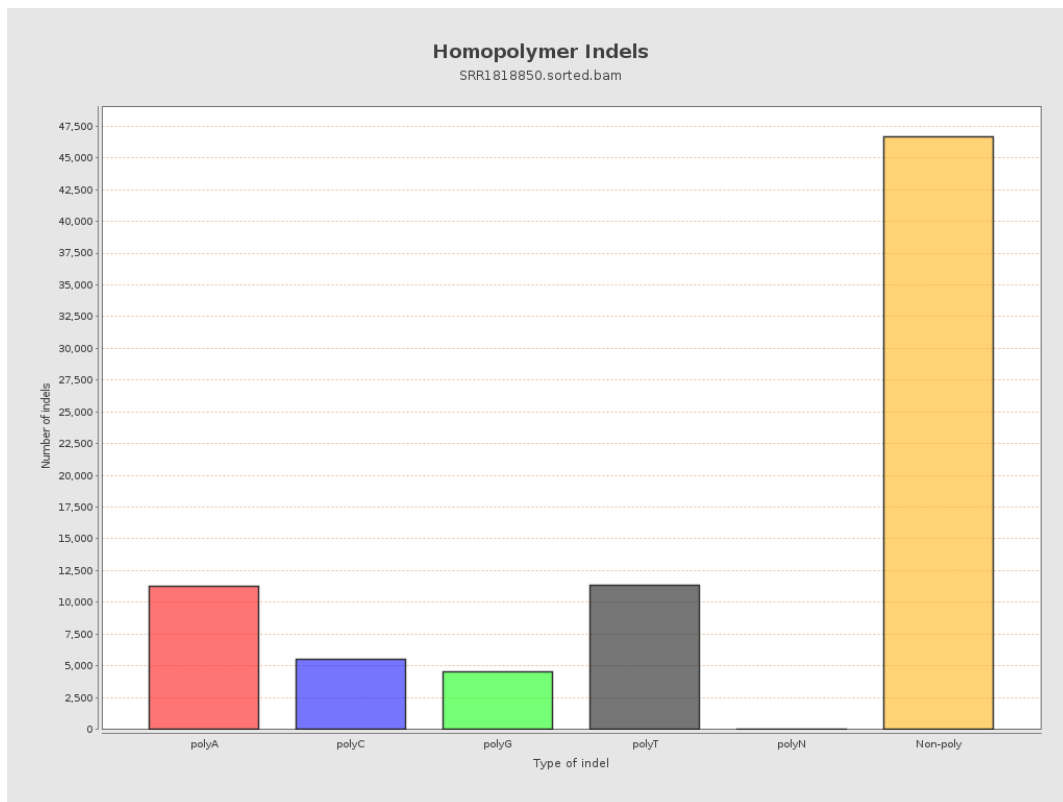
9. Results : Mapped Reads GC-content Distribution



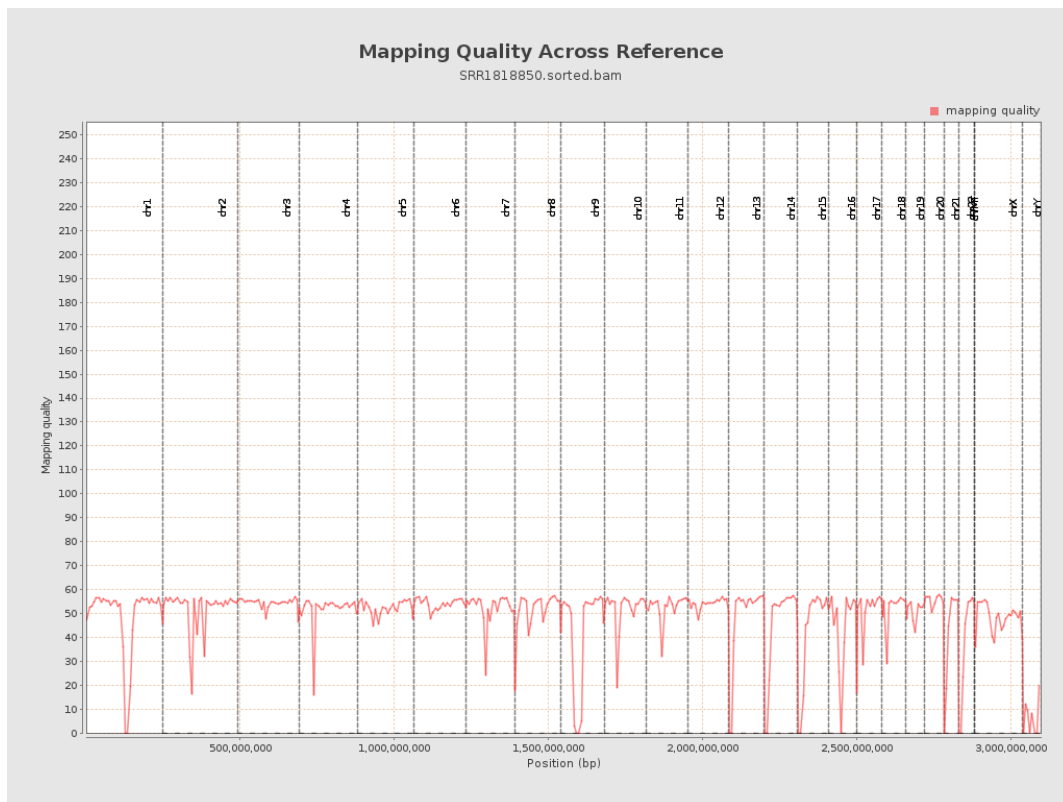
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

