

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 16:43:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618663.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_SRR618663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 16:43:52 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,960,773
Mapped reads	22,626,768 / 94.43%
Unmapped reads	1,334,005 / 5.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,914 / 0.29%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	4,426,767 / 18.48%
Duplication rate	17.89%
Clipped reads	2,394,523 / 9.99%

2.2. ACGT Content

Number/percentage of A's	601,154,384 / 27.22%
Number/percentage of C's	488,918,261 / 22.14%
Number/percentage of T's	611,942,921 / 27.71%
Number/percentage of G's	484,573,035 / 21.94%
Number/percentage of N's	22,000,826 / 1%
GC Percentage	44.08%

2.3. Coverage

Mean	0.7139

Standard Deviation	3.2257
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2.4. Mapping Quality

Mean Mapping Quality	49.86
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2.5. Mismatches and indels

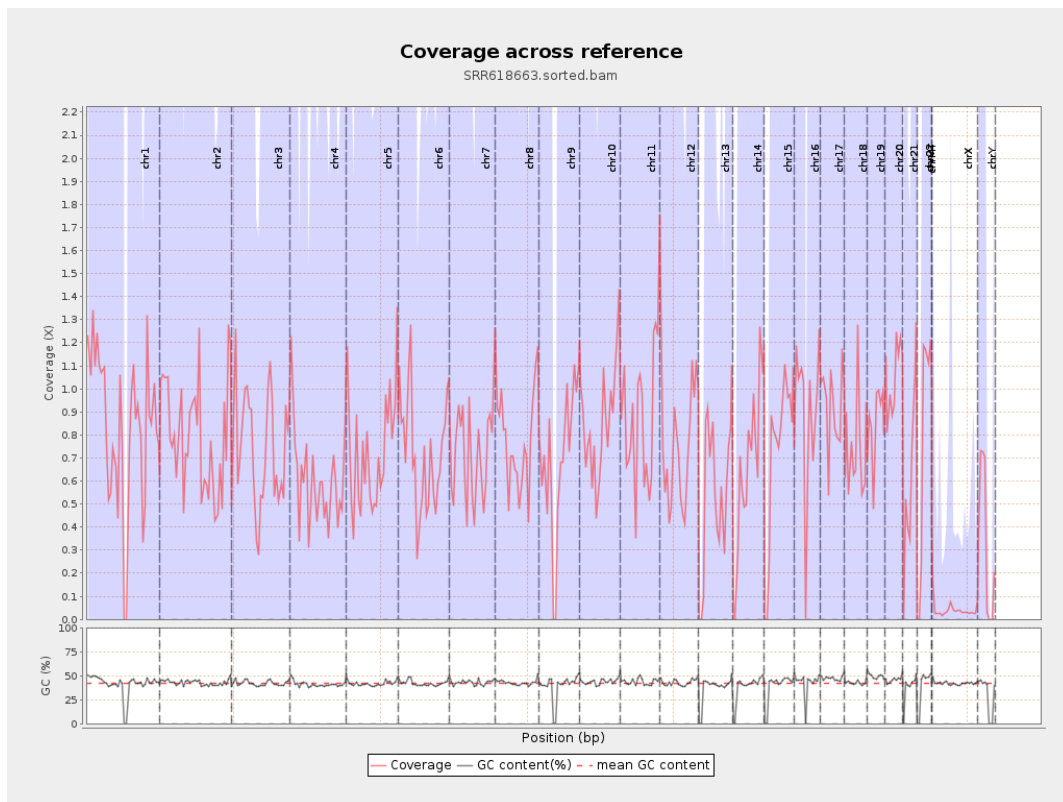
General error rate	1.97%
Mismatches	42,835,754
Insertions	412,923
Mapped reads with at least one insertion	1.79%
Deletions	1,099,338
Mapped reads with at least one deletion	4.74%
Homopolymer indels	52.84%

2.6. Chromosome stats

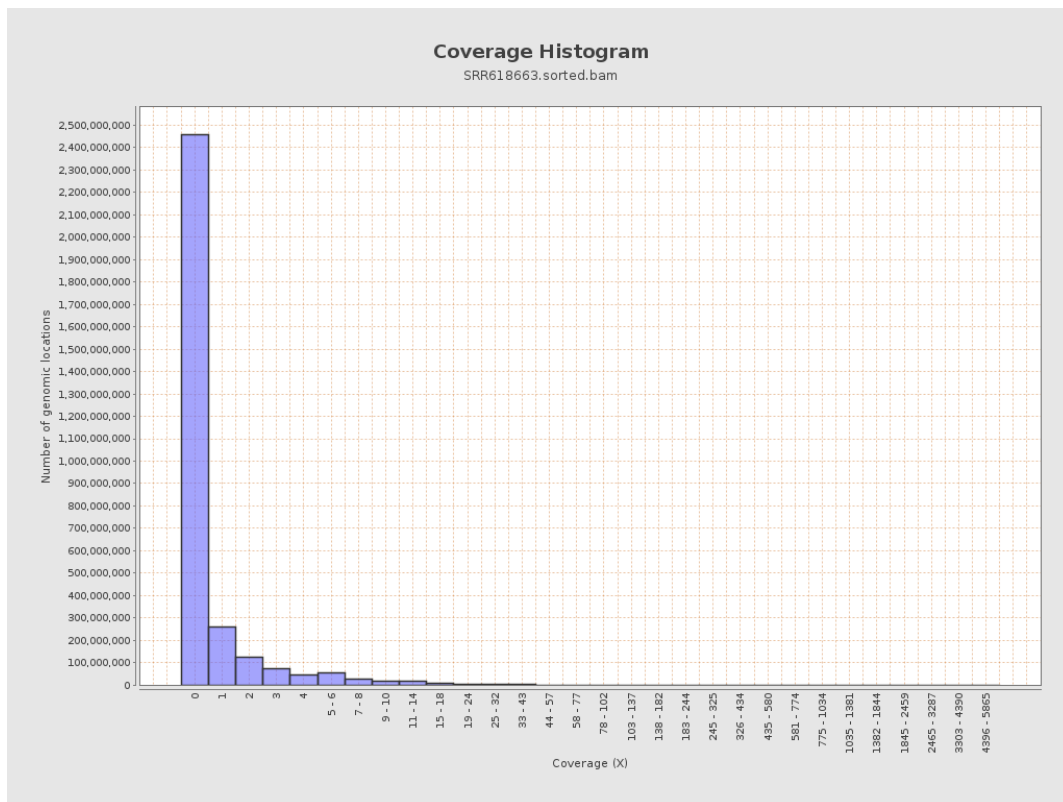
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	207287335	0.8316	3.3835
chr2	243199373	192762542	0.7926	4.5116
chr3	198022430	147809125	0.7464	2.4405
chr4	191154276	114522344	0.5991	2.5161
chr5	180915260	132369596	0.7317	2.4157
chr6	171115067	123025155	0.719	2.4796
chr7	159138663	114851932	0.7217	2.4814

chr8	146364022	112306379	0.7673	2.495
chr9	141213431	98422062	0.697	2.6888
chr10	135534747	115909664	0.8552	2.7526
chr11	135006516	116761366	0.8649	2.9924
chr12	133851895	101238970	0.7564	2.6281
chr13	115169878	61964543	0.538	2.0486
chr14	107349540	69241120	0.645	2.3632
chr15	102531392	74187447	0.7236	2.5172
chr16	90354753	80112264	0.8866	8.9848
chr17	81195210	75054143	0.9244	3.1067
chr18	78077248	58476074	0.749	2.9196
chr19	59128983	50798122	0.8591	3.3075
chr20	63025520	66001352	1.0472	3.2594
chr21	48129895	30233172	0.6282	4.0724
chr22	51304566	40261195	0.7847	3.0096
chrMT	16571	6588	0.3976	1.1871
chrX	155270560	5985100	0.0385	0.705
chrY	59373566	20548639	0.3461	3.1613

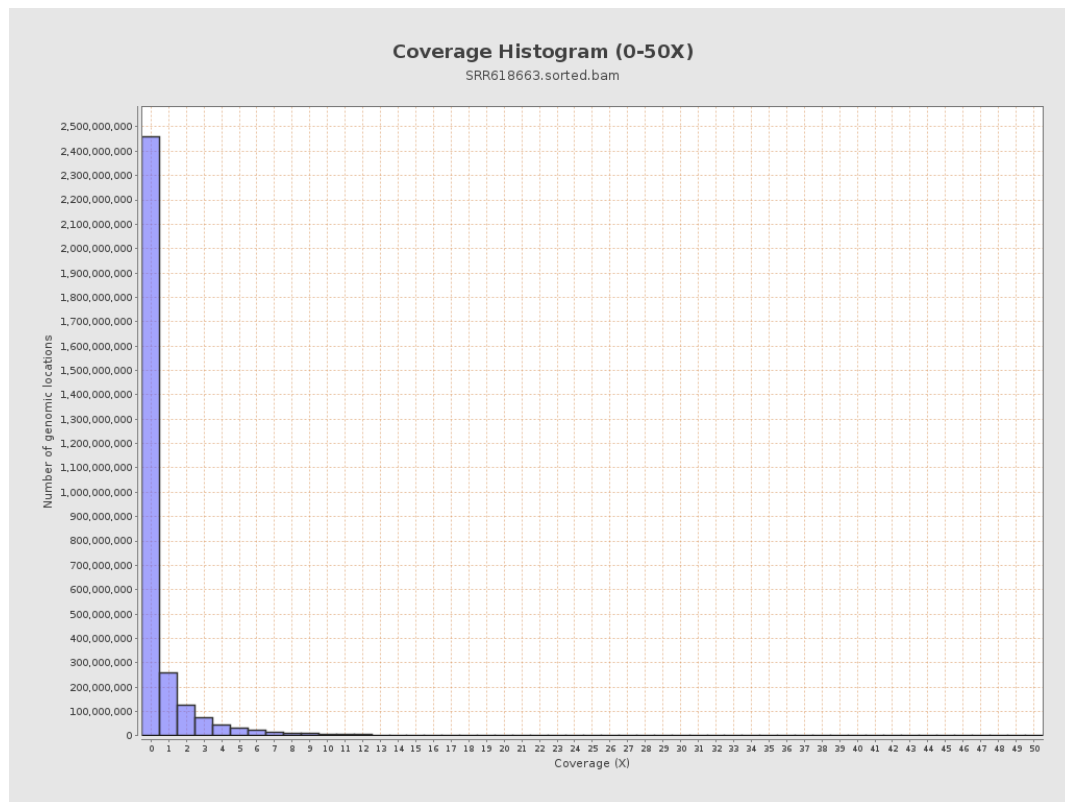
3. Results : Coverage across reference



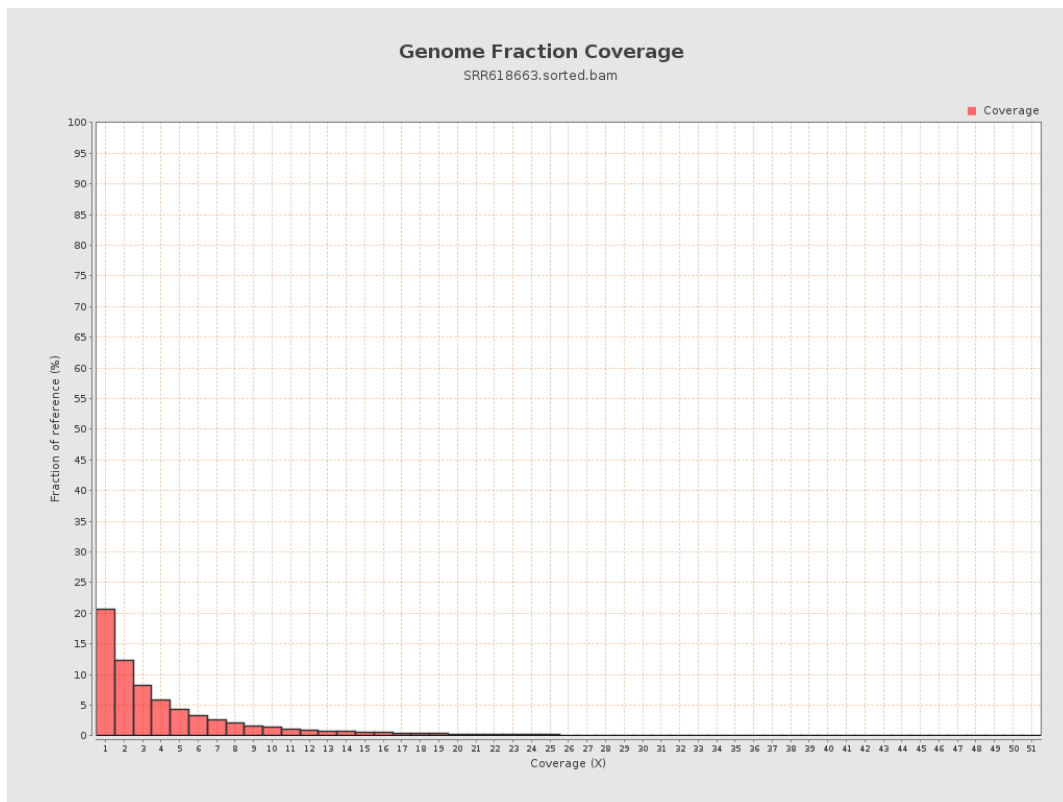
4. Results : Coverage Histogram



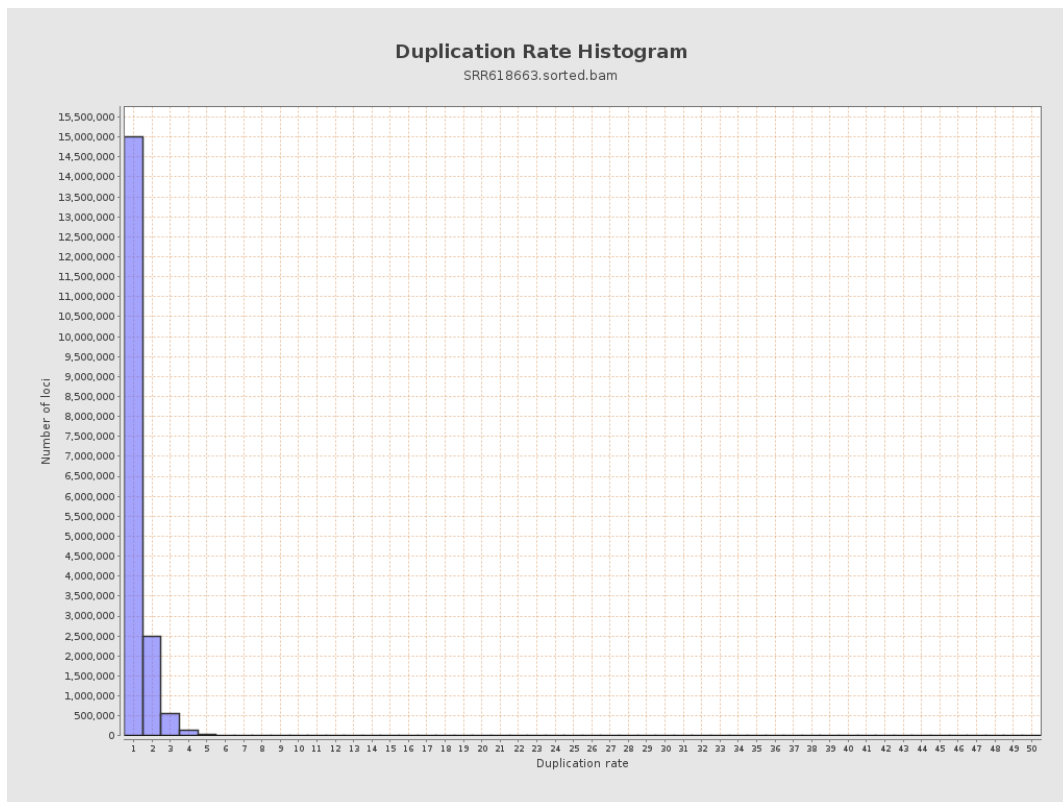
5. Results : Coverage Histogram (0-50X)



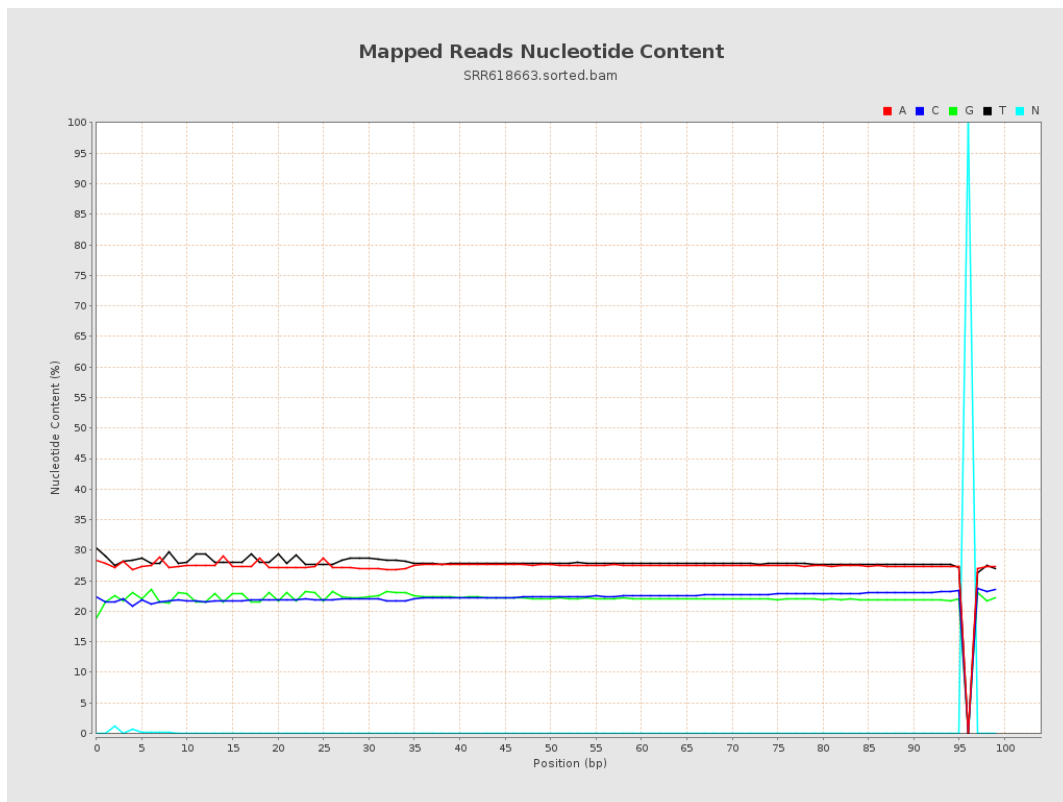
6. Results : Genome Fraction Coverage



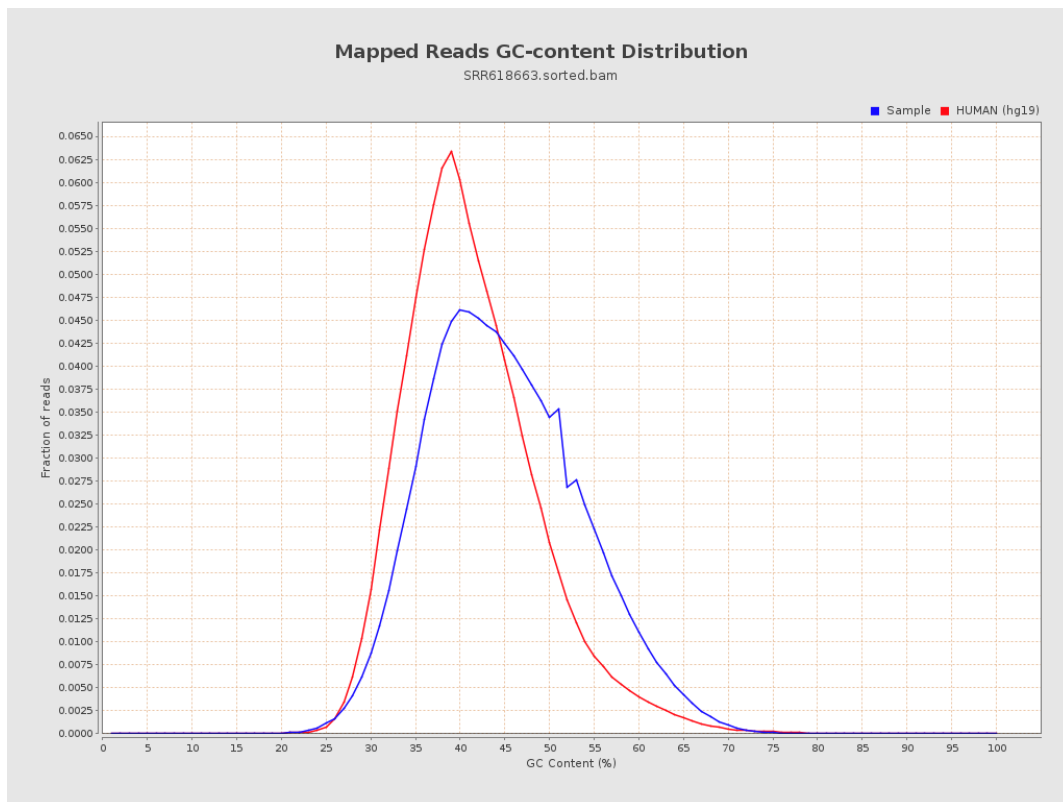
7. Results : Duplication Rate Histogram



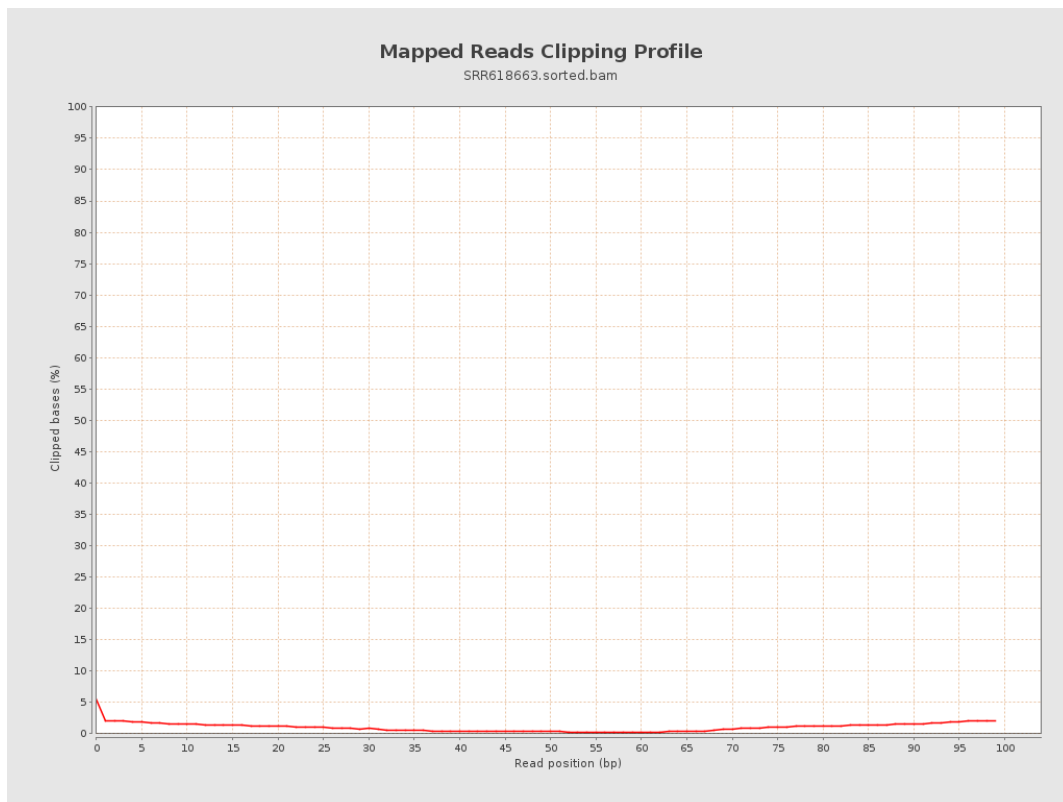
8. Results : Mapped Reads Nucleotide Content



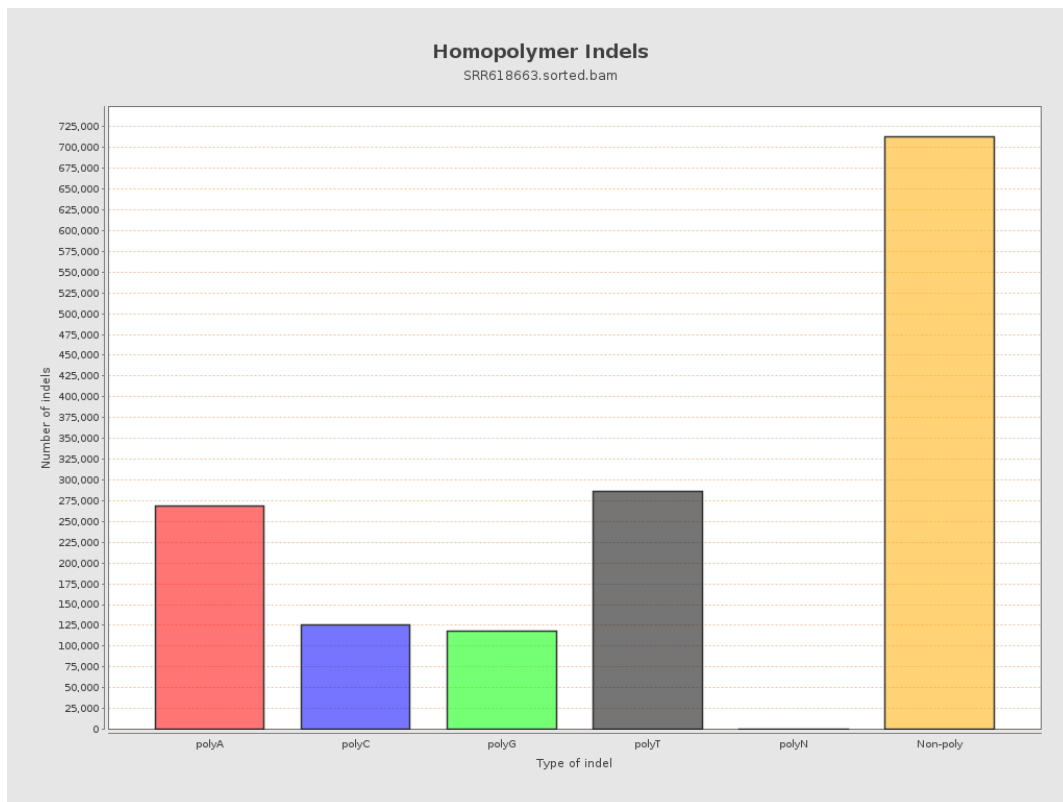
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

