

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 07:43:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163084.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_SRR1163084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 07:43:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	90,557,844
Mapped reads	89,178,100 / 98.48%
Unmapped reads	1,379,744 / 1.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	581,589 / 0.64%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	53,211,795 / 58.76%
Duplication rate	47.48%
Clipped reads	20,598,045 / 22.75%

2.2. ACGT Content

Number/percentage of A's	2,110,250,305 / 24.93%
Number/percentage of C's	2,122,543,450 / 25.08%
Number/percentage of T's	2,080,877,457 / 24.59%
Number/percentage of G's	2,149,522,484 / 25.4%
Number/percentage of N's	331,827 / 0%
GC Percentage	50.48%

2.3. Coverage

Mean	2.7343

Standard Deviation	34.6478
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2.4. Mapping Quality

Mean Mapping Quality	49.14
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2.5. Mismatches and indels

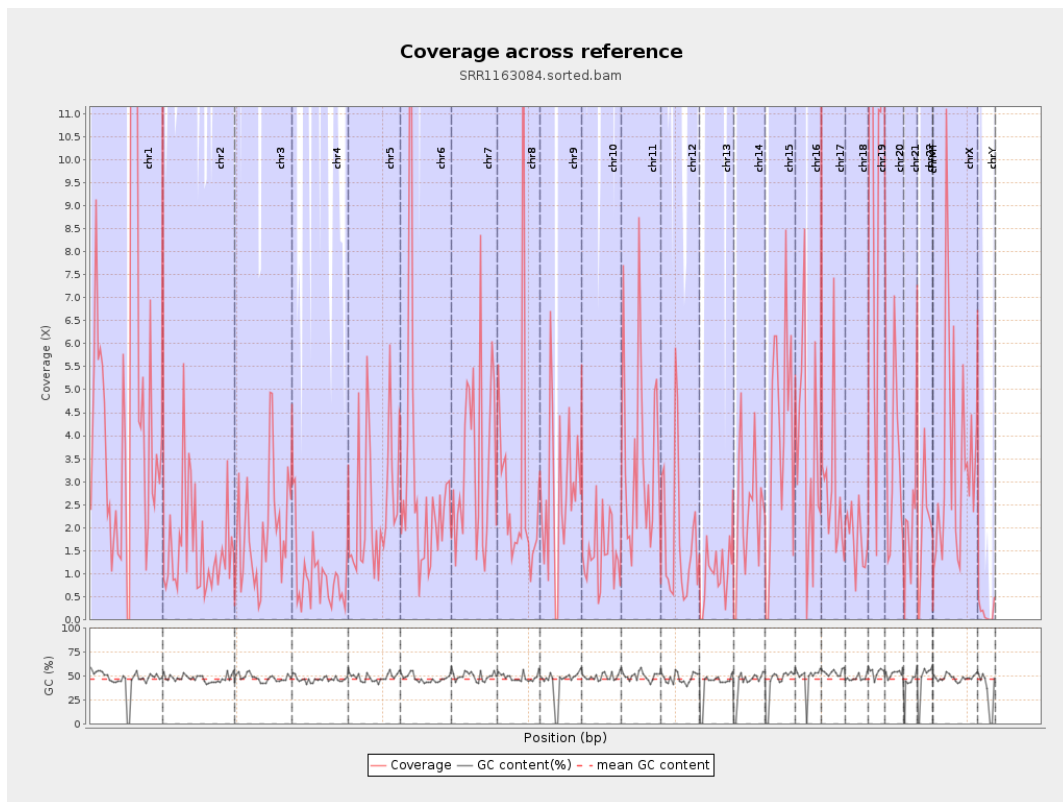
General error rate	0.38%
Mismatches	31,376,894
Insertions	556,249
Mapped reads with at least one insertion	0.62%
Deletions	496,952
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.89%

2.6. Chromosome stats

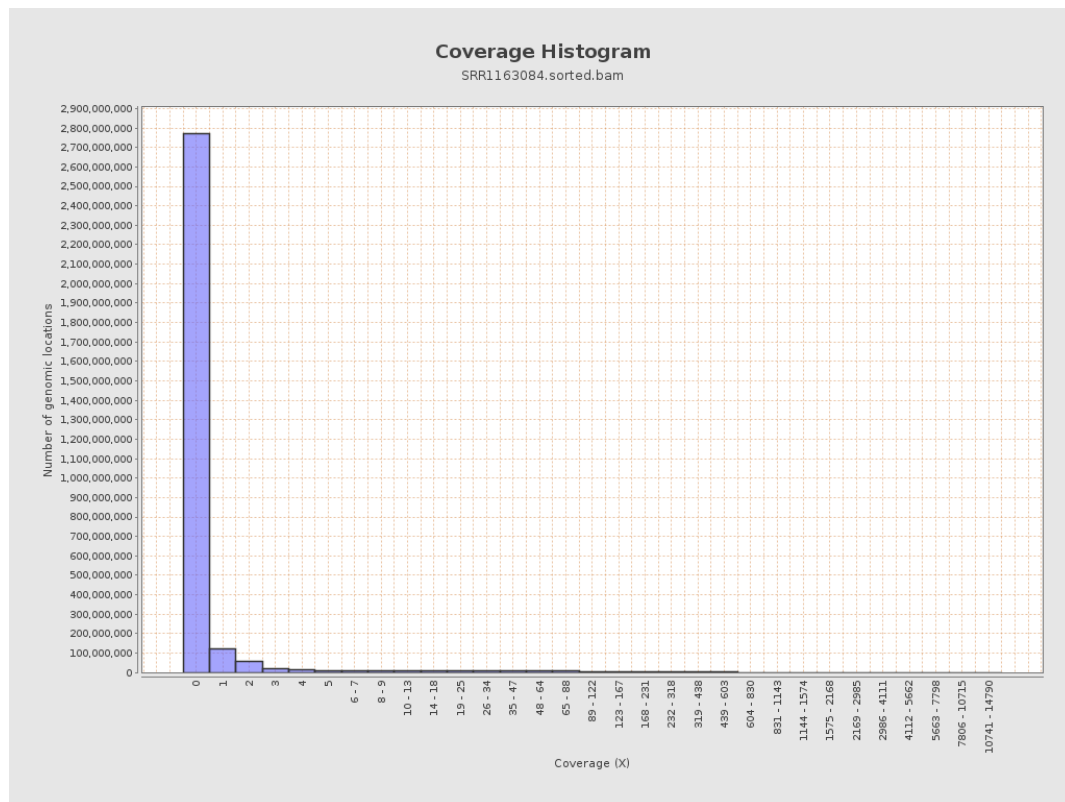
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1257663875	5.0458	50.9303
chr2	243199373	379032665	1.5585	19.7785
chr3	198022430	380903435	1.9235	23.8833
chr4	191154276	182392883	0.9542	15.0583
chr5	180915260	446558537	2.4683	36.8101
chr6	171115067	488447294	2.8545	31.4061
chr7	159138663	541936734	3.4054	42.5399

chr8	146364022	426059093	2.911	49.11
chr9	141213431	382596937	2.7094	30.0323
chr10	135534747	194462053	1.4348	16.8289
chr11	135006516	473924950	3.5104	34.6582
chr12	133851895	243258812	1.8174	23.6973
chr13	115169878	116081001	1.0079	14.5228
chr14	107349540	252874120	2.3556	26.368
chr15	102531392	398567408	3.8873	37.7509
chr16	90354753	324672351	3.5933	33.1038
chr17	81195210	230941513	2.8443	29.1363
chr18	78077248	137978065	1.7672	21.2263
chr19	59128983	635563958	10.7488	85.6674
chr20	63025520	213934099	3.3944	35.1335
chr21	48129895	115579136	2.4014	46.6452
chr22	51304566	101303618	1.9746	21.1484
chrMT	16571	3020	0.1822	0.5061
chrX	155270560	530609580	3.4173	41.0476
chrY	59373566	9240642	0.1556	7.4079

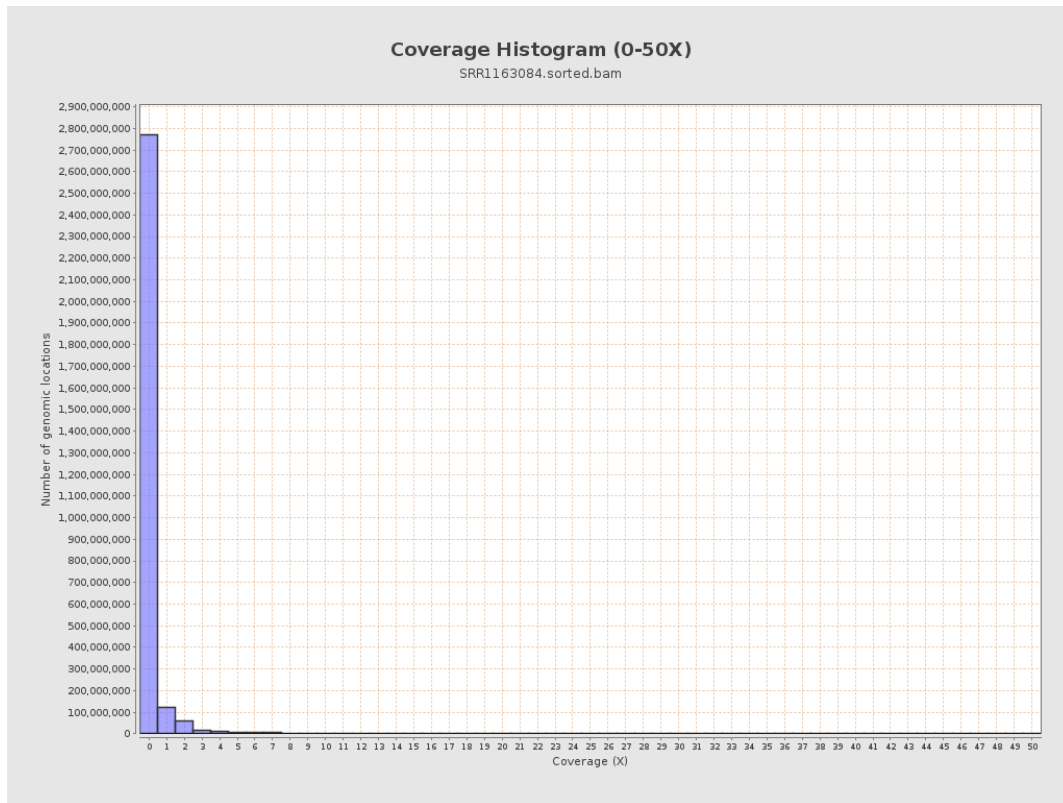
3. Results : Coverage across reference



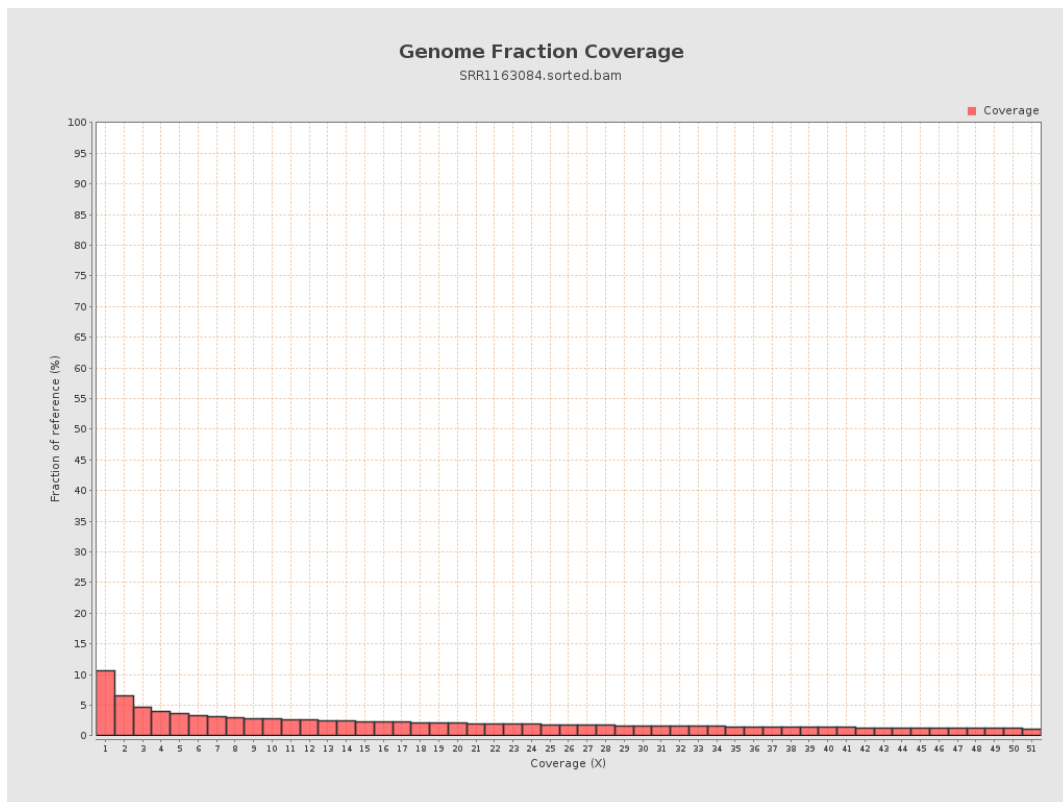
4. Results : Coverage Histogram



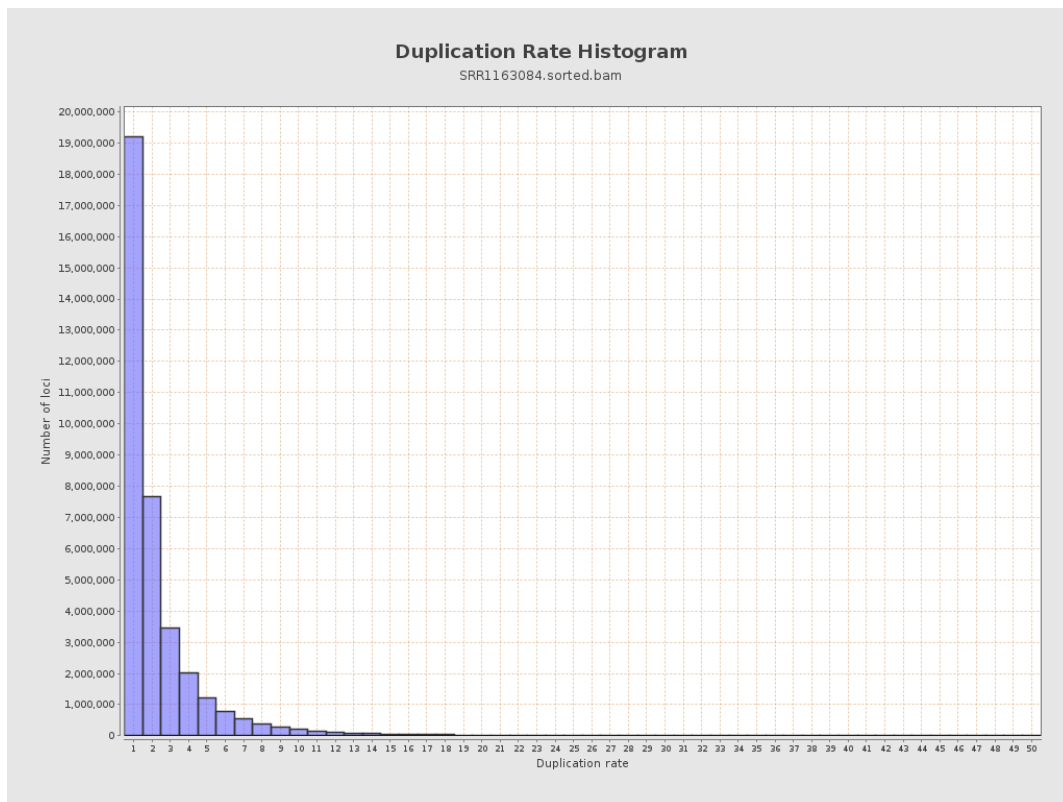
5. Results : Coverage Histogram (0-50X)



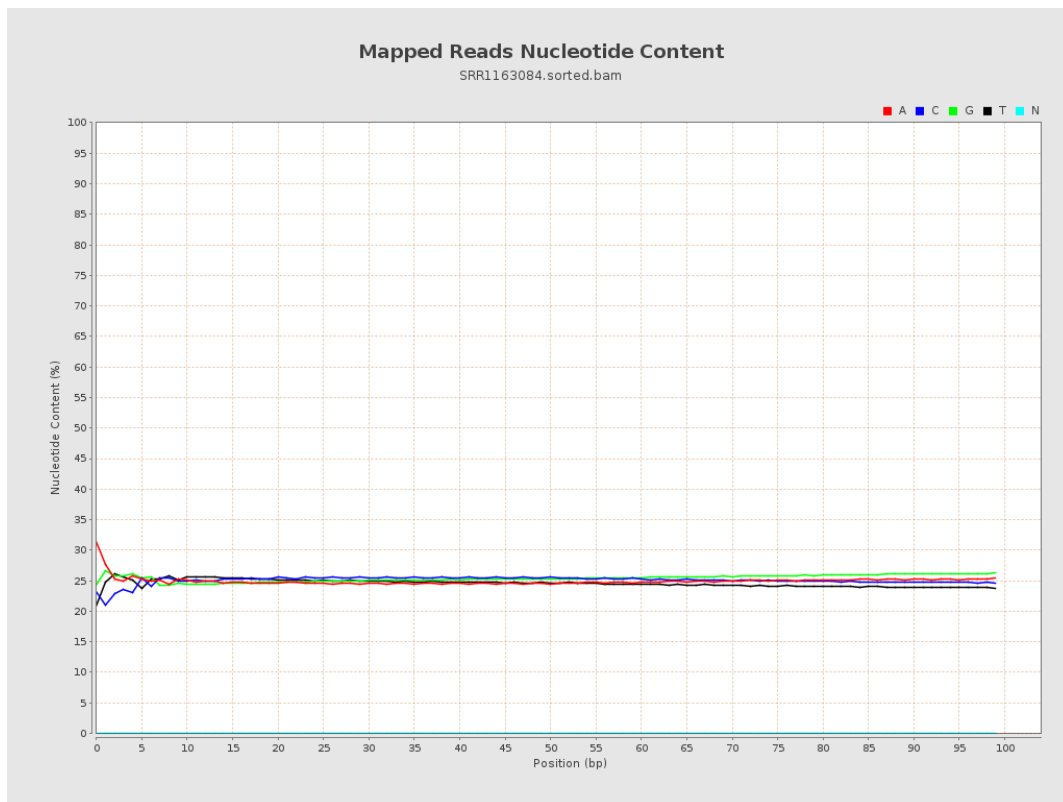
6. Results : Genome Fraction Coverage



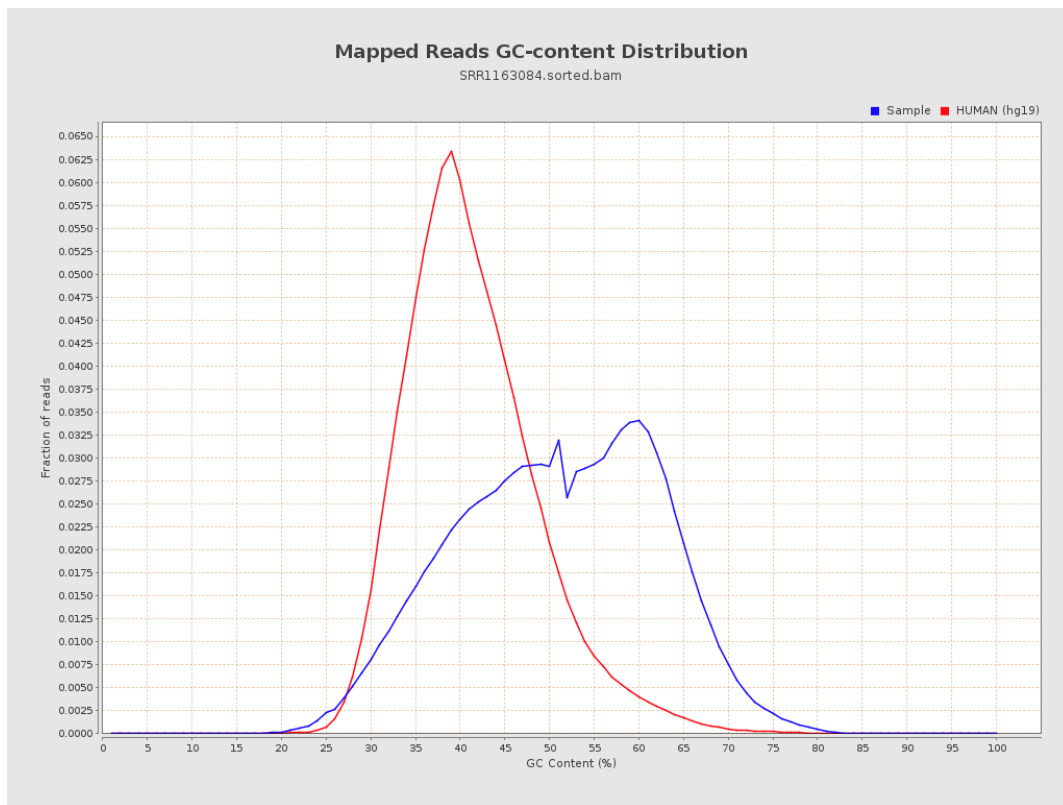
7. Results : Duplication Rate Histogram



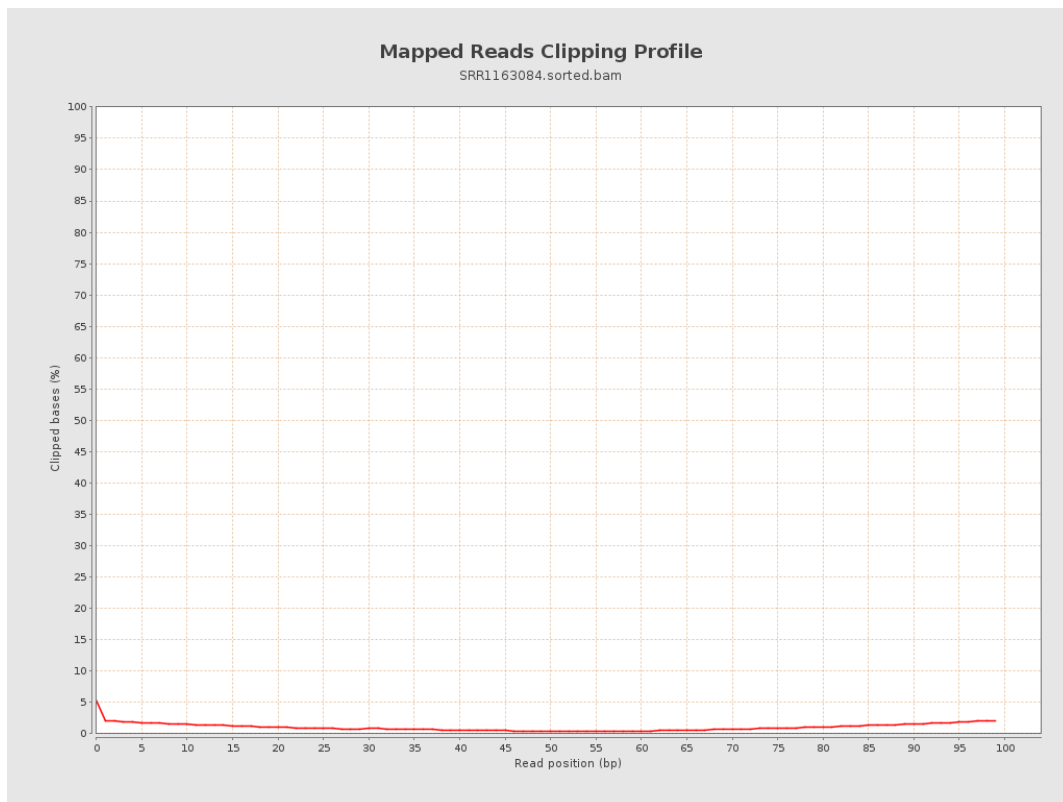
8. Results : Mapped Reads Nucleotide Content



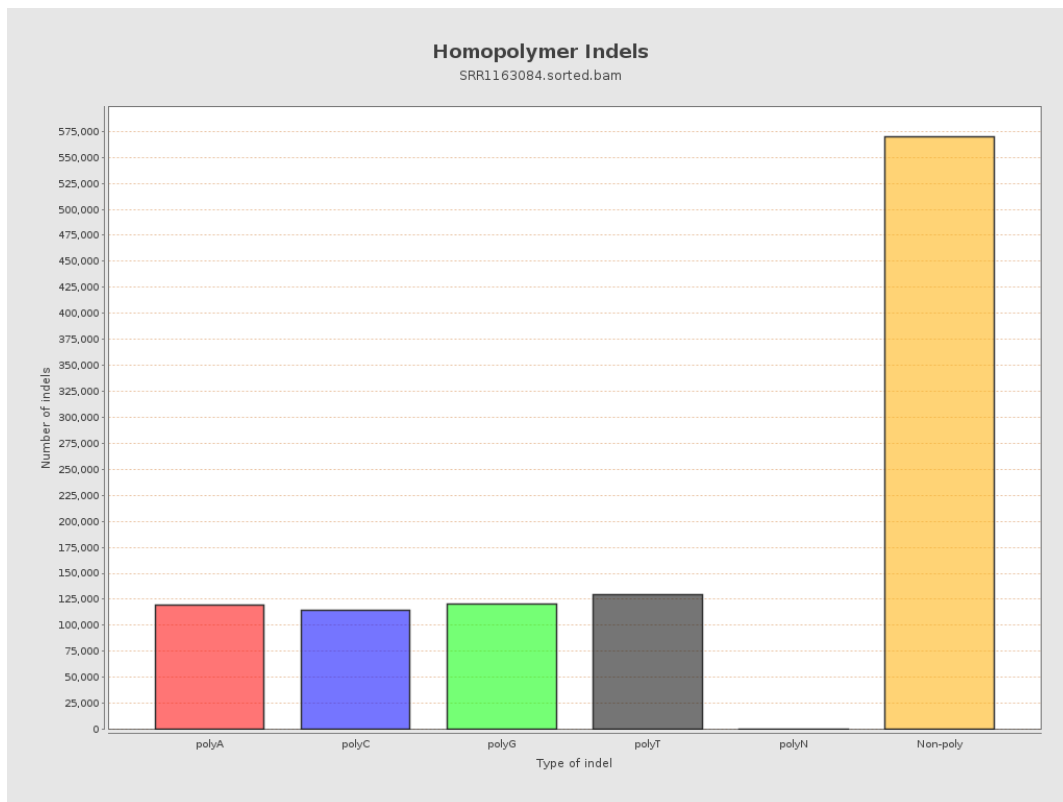
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

