

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 16:25:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618662.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_SRR618662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 16:25:29 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,840,088
Mapped reads	27,231,165 / 94.42%
Unmapped reads	1,608,923 / 5.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	72,756 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	5,585,631 / 19.37%
Duplication rate	18.91%
Clipped reads	2,875,050 / 9.97%

2.2. ACGT Content

Number/percentage of A's	726,923,244 / 27.37%
Number/percentage of C's	580,279,865 / 21.85%
Number/percentage of T's	740,930,735 / 27.9%
Number/percentage of G's	581,553,783 / 21.9%
Number/percentage of N's	26,411,436 / 0.99%
GC Percentage	43.74%

2.3. Coverage

Mean	0.8586

Standard Deviation	3.3592
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2.4. Mapping Quality

Mean Mapping Quality	51.36
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2.5. Mismatches and indels

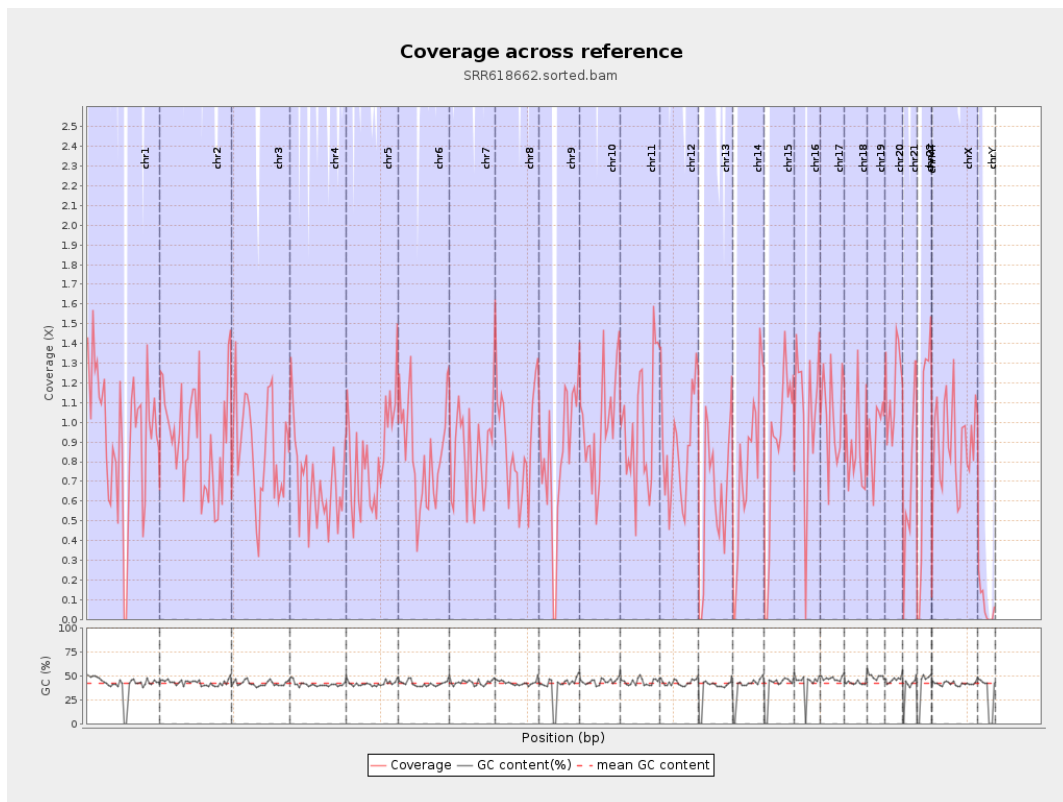
General error rate	1.97%
Mismatches	51,588,127
Insertions	486,069
Mapped reads with at least one insertion	1.76%
Deletions	1,319,656
Mapped reads with at least one deletion	4.73%
Homopolymer indels	53.29%

2.6. Chromosome stats

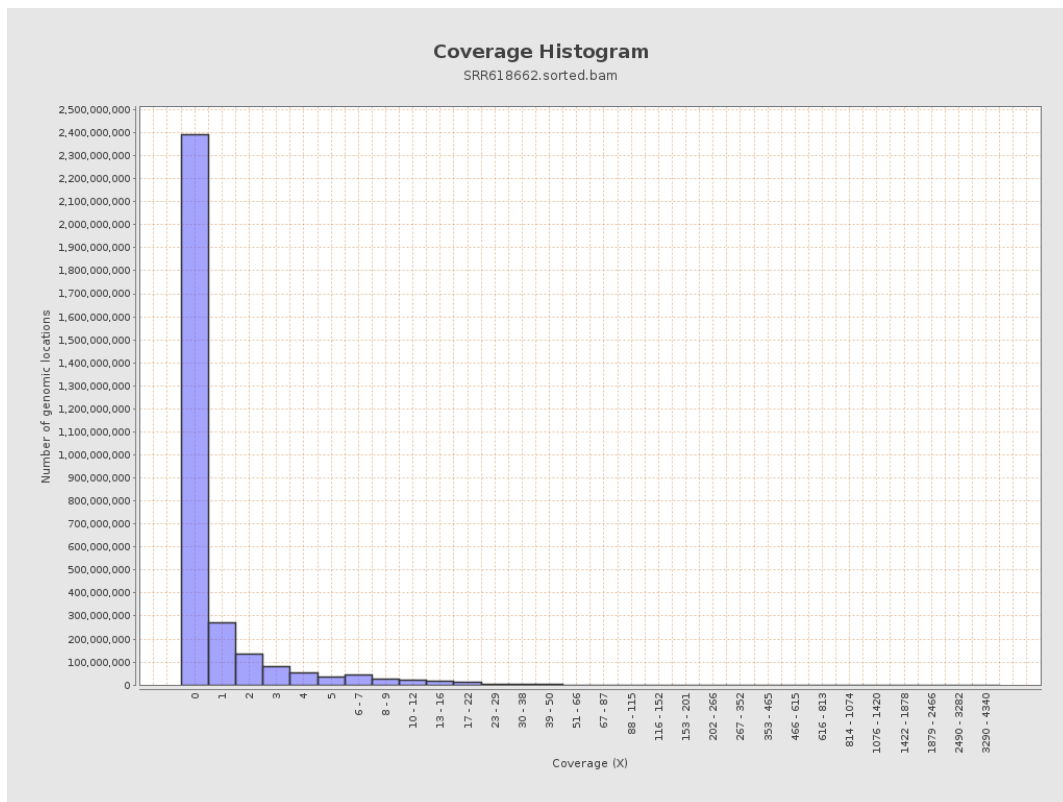
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	231596027	0.9292	3.8686
chr2	243199373	222982897	0.9169	3.9623
chr3	198022430	172119974	0.8692	2.8131
chr4	191154276	131857343	0.6898	2.8753
chr5	180915260	150760363	0.8333	2.7208
chr6	171115067	143291813	0.8374	2.8659
chr7	159138663	133705458	0.8402	2.8599

chr8	146364022	128487802	0.8779	2.8956
chr9	141213431	116241015	0.8232	3.0543
chr10	135534747	133444114	0.9846	3.1924
chr11	135006516	132711648	0.983	3.4051
chr12	133851895	116727800	0.8721	2.9869
chr13	115169878	71487968	0.6207	2.3699
chr14	107349540	82997445	0.7732	2.7865
chr15	102531392	88524129	0.8634	3.04
chr16	90354753	94035694	1.0407	6.8317
chr17	81195210	84365600	1.039	3.503
chr18	78077248	68296315	0.8747	3.2806
chr19	59128983	56003424	0.9471	3.6161
chr20	63025520	74206374	1.1774	3.6452
chr21	48129895	34716959	0.7213	4.9753
chr22	51304566	46439015	0.9052	3.5163
chrMT	16571	1853	0.1118	0.6929
chrX	155270560	138628379	0.8928	2.89
chrY	59373566	4292100	0.0723	1.9272

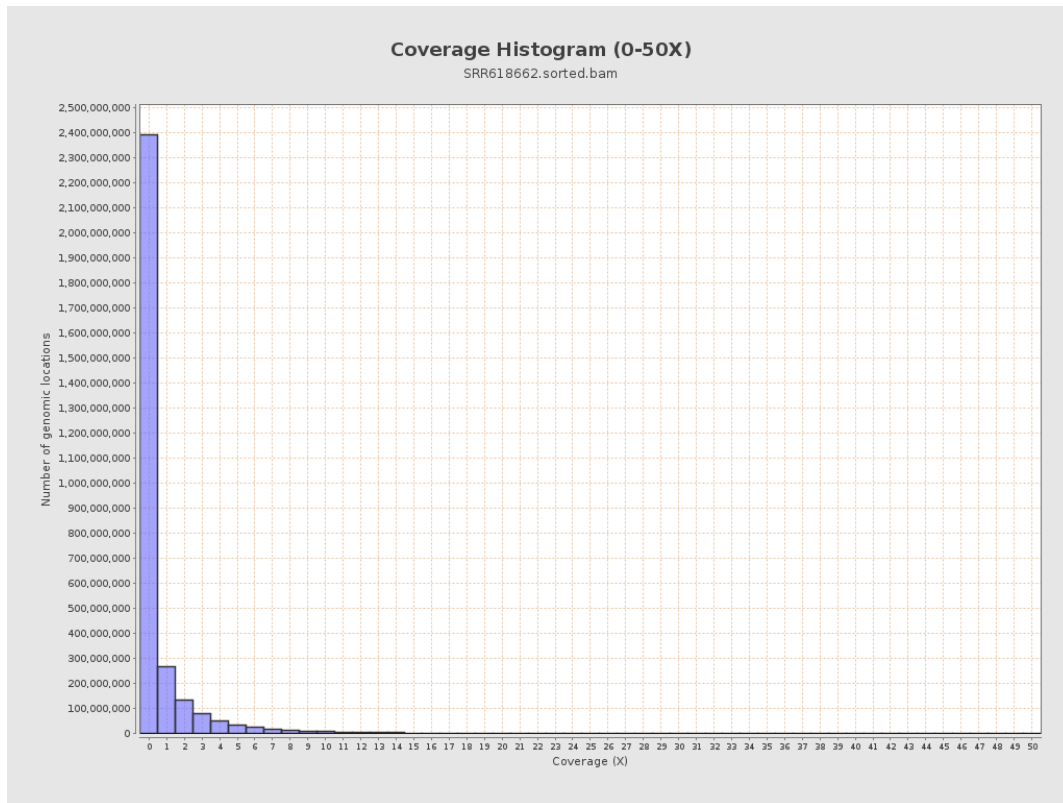
3. Results : Coverage across reference



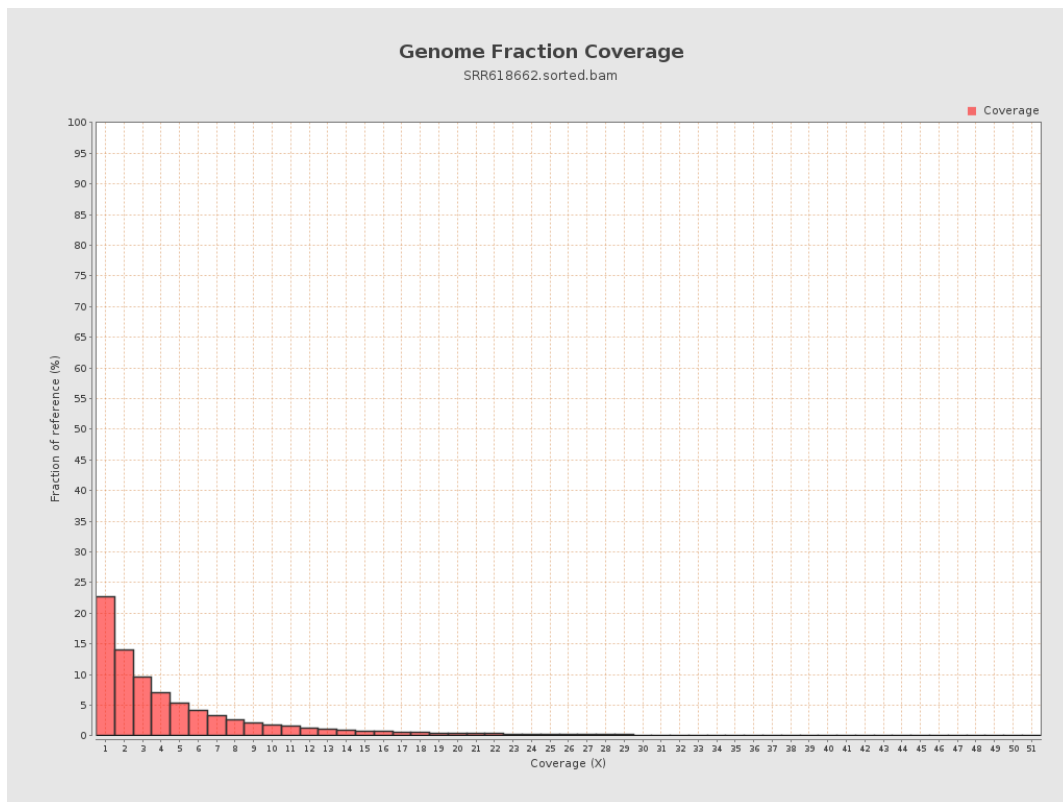
4. Results : Coverage Histogram



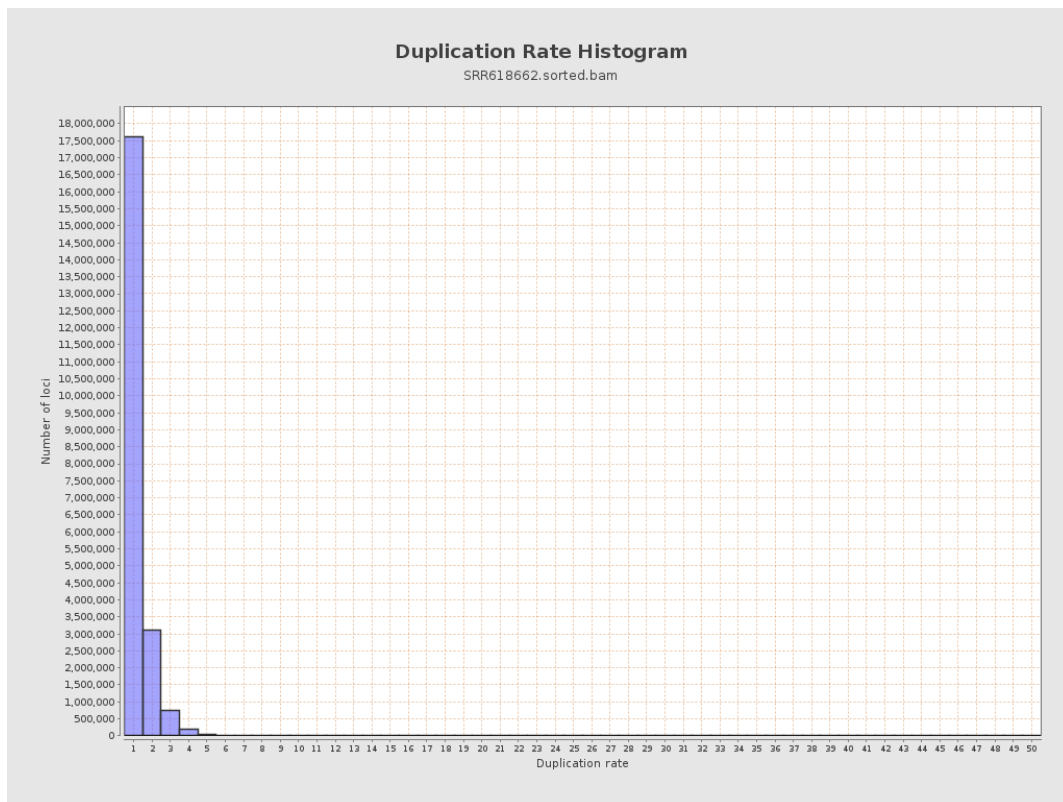
5. Results : Coverage Histogram (0-50X)



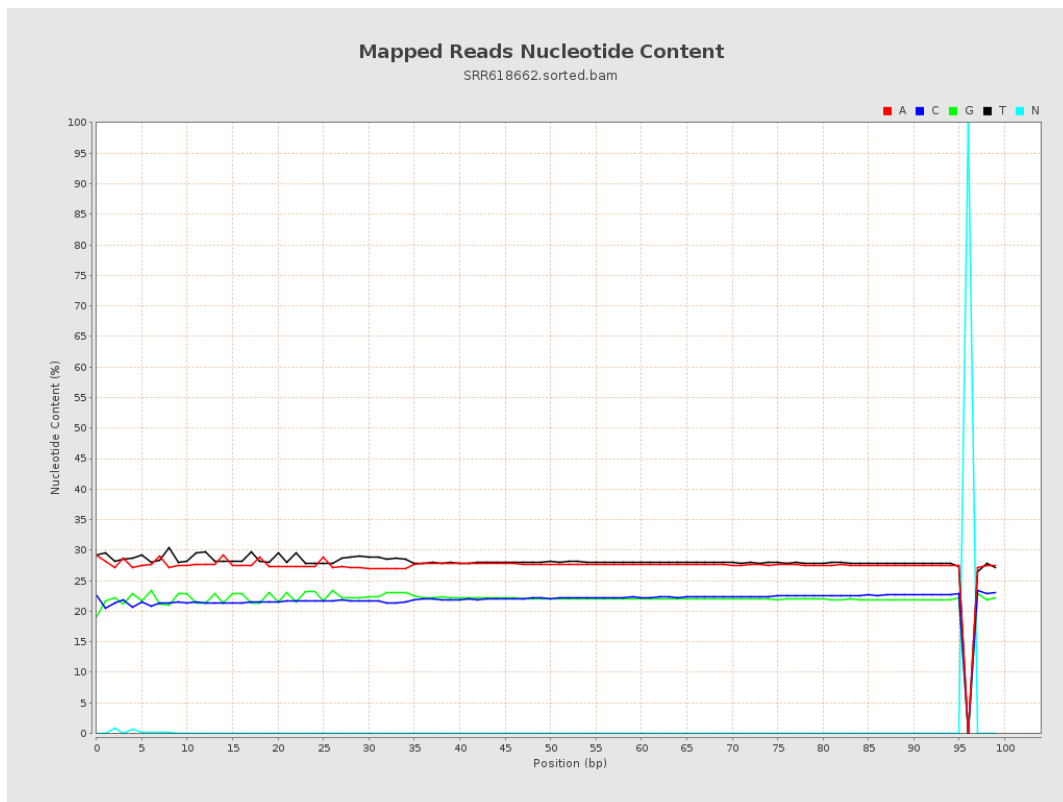
6. Results : Genome Fraction Coverage



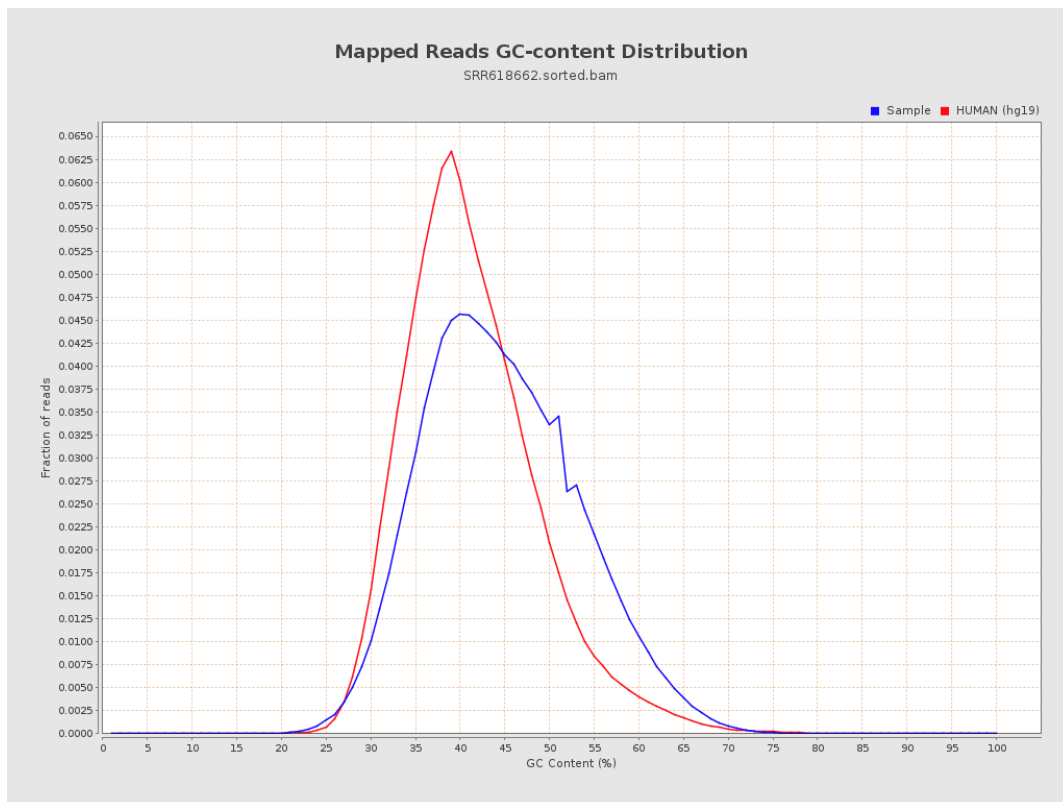
7. Results : Duplication Rate Histogram



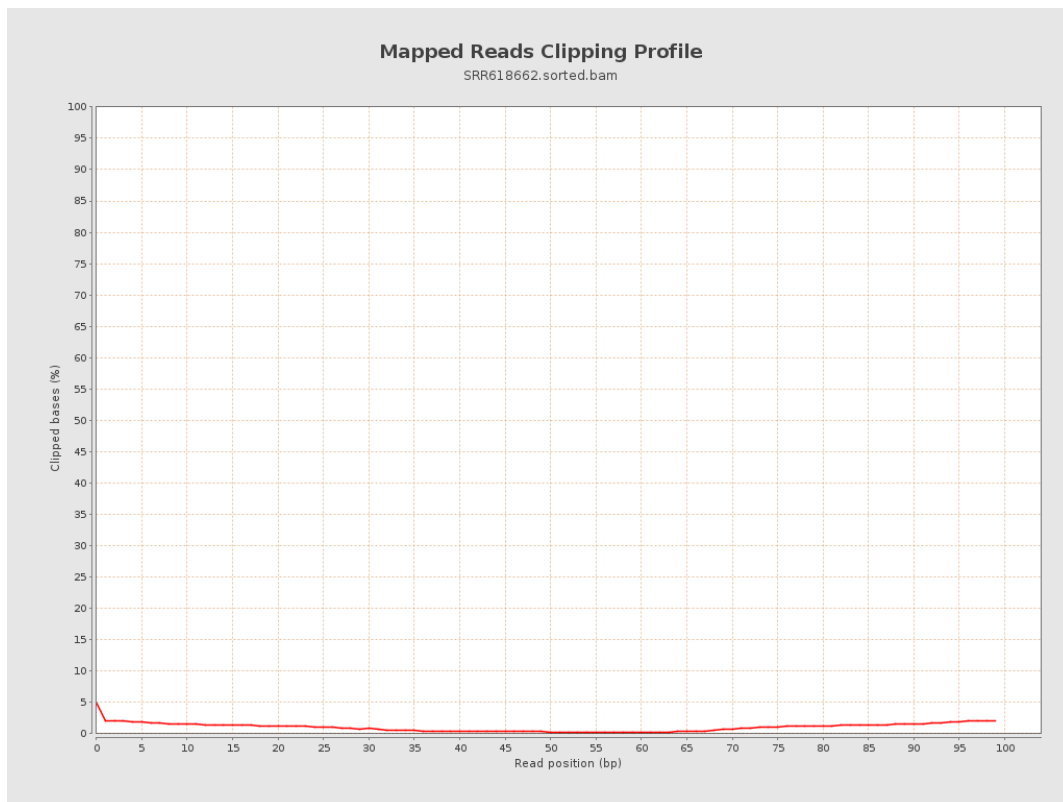
8. Results : Mapped Reads Nucleotide Content



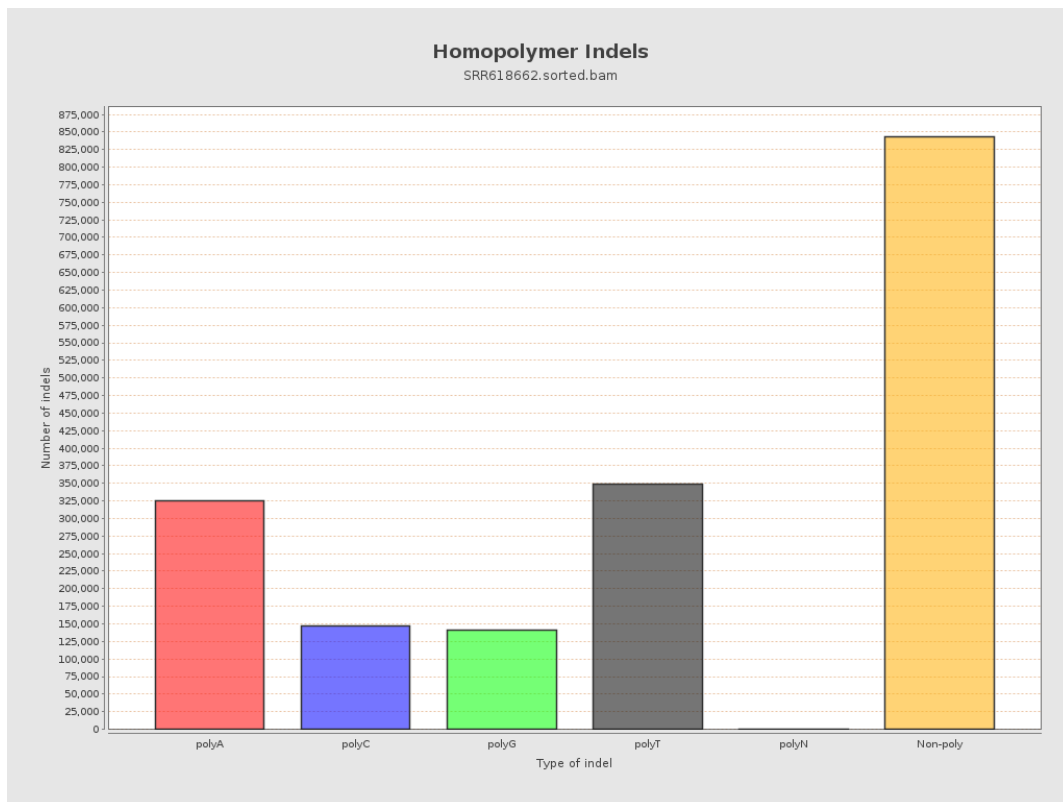
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

