

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 19:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618571.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_SRR618571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 19:13:58 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	79,638,923
Mapped reads	75,053,217 / 94.24%
Unmapped reads	4,585,706 / 5.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237,558 / 0.3%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	45,163,848 / 56.71%
Duplication rate	38.27%
Clipped reads	9,920,282 / 12.46%

2.2. ACGT Content

Number/percentage of A's	1,926,967,192 / 26.48%
Number/percentage of C's	1,715,360,340 / 23.58%
Number/percentage of T's	2,049,193,931 / 28.16%
Number/percentage of G's	1,584,100,098 / 21.77%
Number/percentage of N's	489,503 / 0.01%
GC Percentage	45.35%

2.3. Coverage

Mean	2.3521

Standard Deviation	48.6468
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2.4. Mapping Quality

Mean Mapping Quality	50.7
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2.5. Mismatches and indels

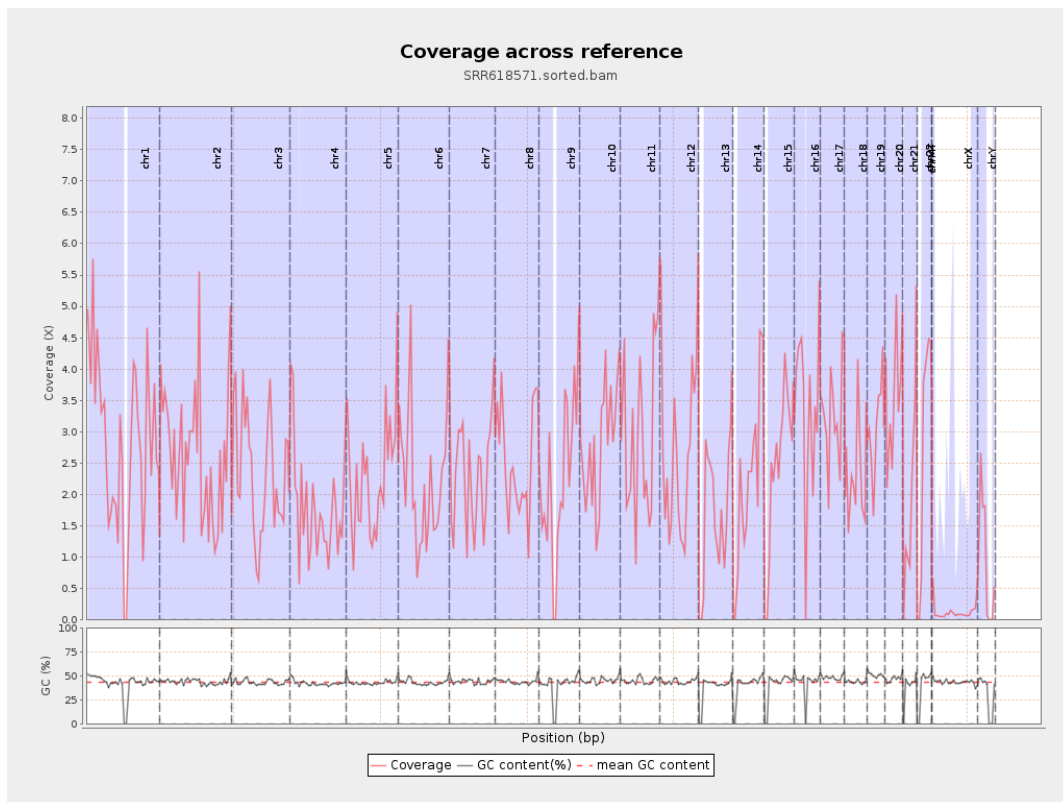
General error rate	0.96%
Mismatches	67,262,006
Insertions	1,306,243
Mapped reads with at least one insertion	1.71%
Deletions	3,445,826
Mapped reads with at least one deletion	4.48%
Homopolymer indels	51.92%

2.6. Chromosome stats

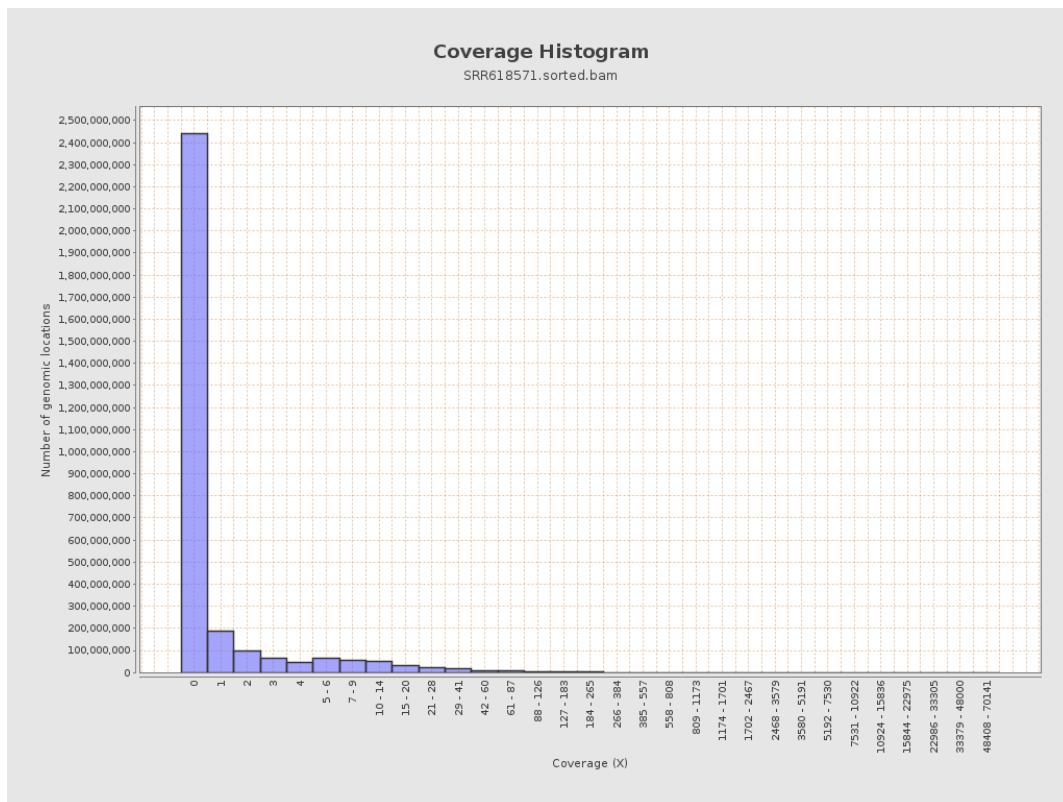
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	702943102	2.8202	51.8864
chr2	243199373	641450002	2.6375	64.3386
chr3	198022430	467441907	2.3606	59.8848
chr4	191154276	336567732	1.7607	30.0425
chr5	180915260	416864696	2.3042	51.4745
chr6	171115067	380798798	2.2254	31.1325
chr7	159138663	374909272	2.3559	46.5238

chr8	146364022	365681398	2.4984	51.4345
chr9	141213431	321058203	2.2736	36.8395
chr10	135534747	381347663	2.8137	75.2631
chr11	135006516	399335515	2.9579	46.6544
chr12	133851895	351826528	2.6285	55.3268
chr13	115169878	192728384	1.6734	40.1589
chr14	107349540	229230864	2.1354	34.1868
chr15	102531392	247692887	2.4158	39.5322
chr16	90354753	301429555	3.3361	72.2201
chr17	81195210	266332290	3.2801	39.9946
chr18	78077248	184664749	2.3652	43.2525
chr19	59128983	184306396	3.117	39.511
chr20	63025520	222444718	3.5294	54.0799
chr21	48129895	93903235	1.951	29.501
chr22	51304566	142443307	2.7764	38.5294
chrMT	16571	3986	0.2405	0.8914
chrX	155270560	17997953	0.1159	14.5742
chrY	59373566	58098793	0.9785	36.2347

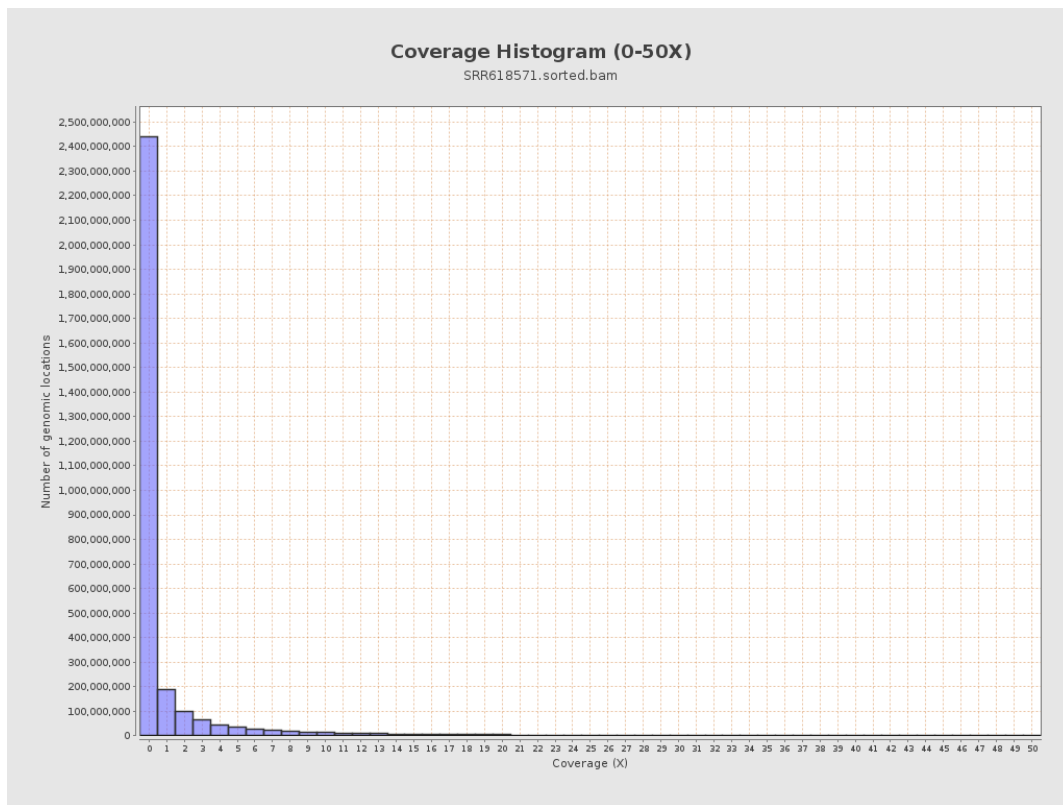
3. Results : Coverage across reference



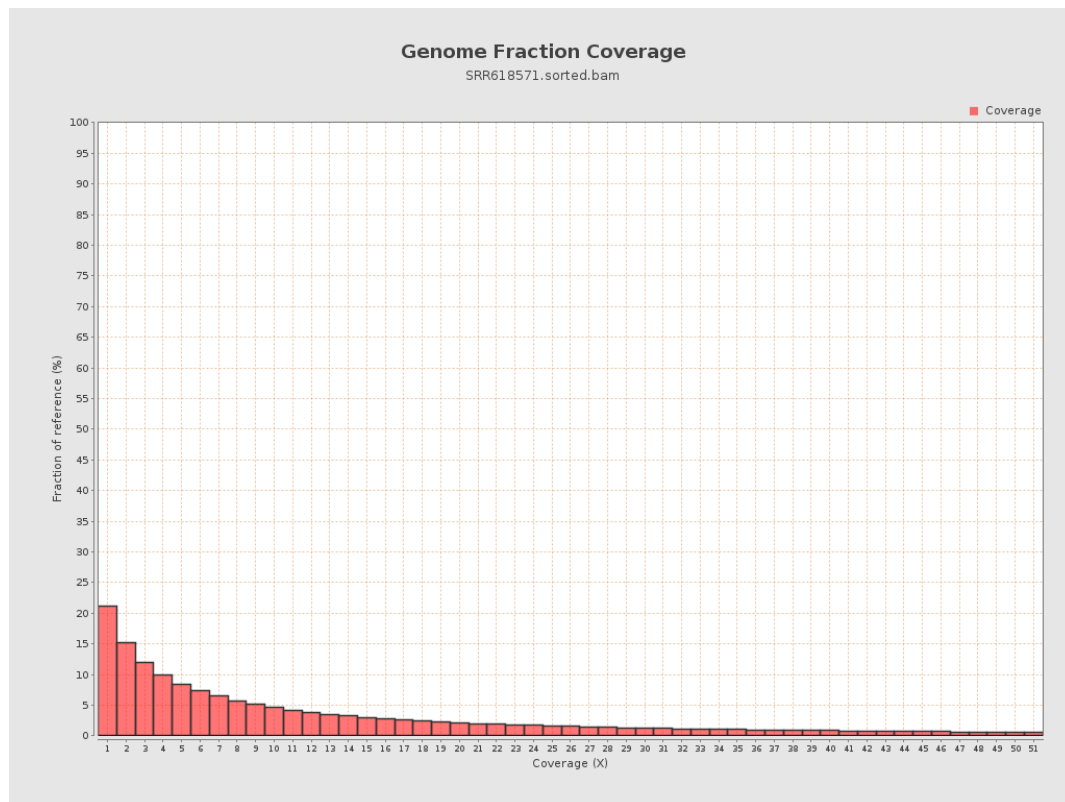
4. Results : Coverage Histogram



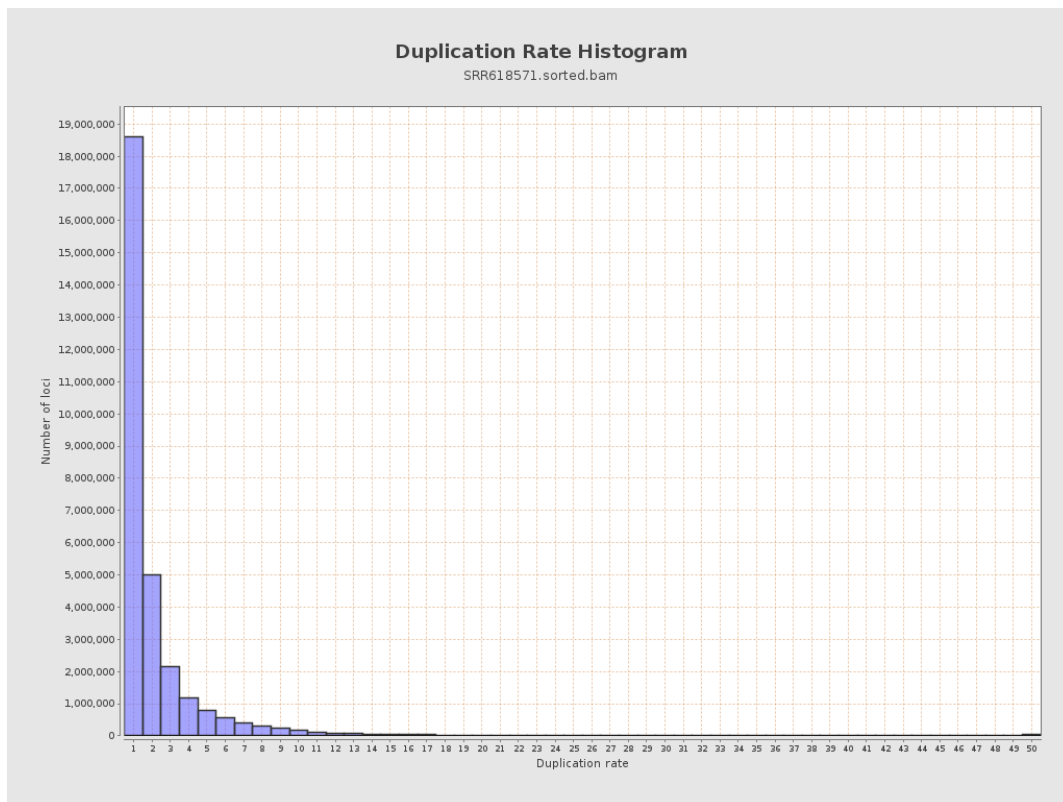
5. Results : Coverage Histogram (0-50X)



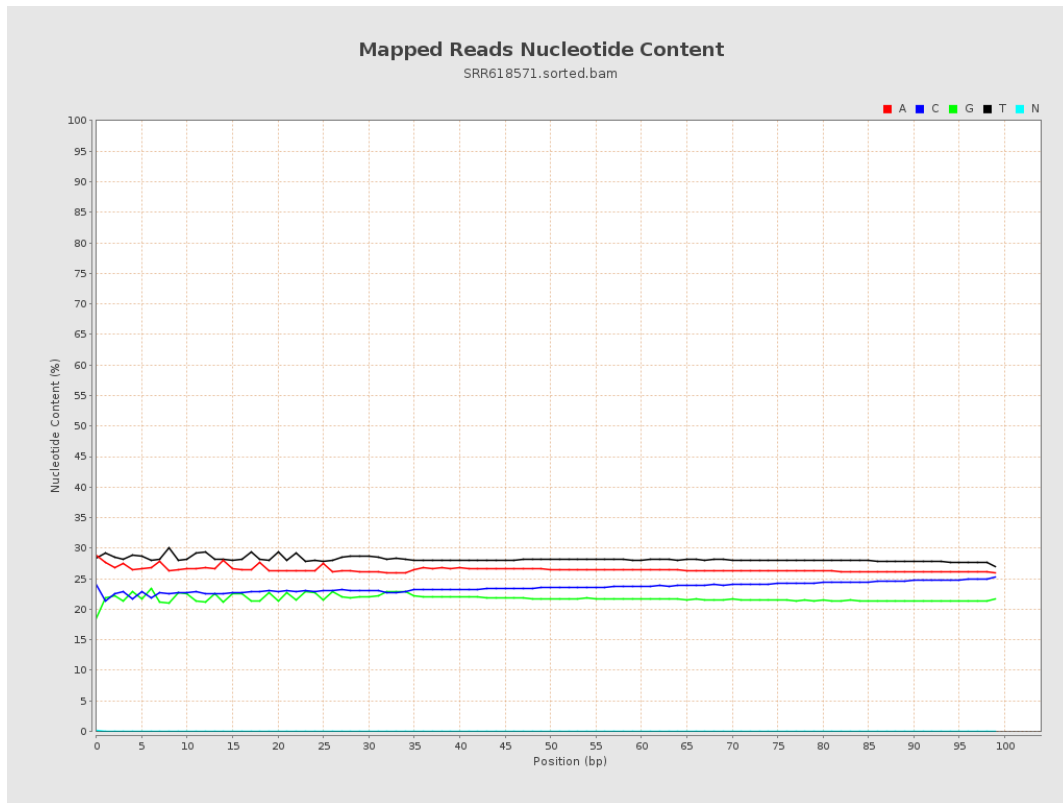
6. Results : Genome Fraction Coverage



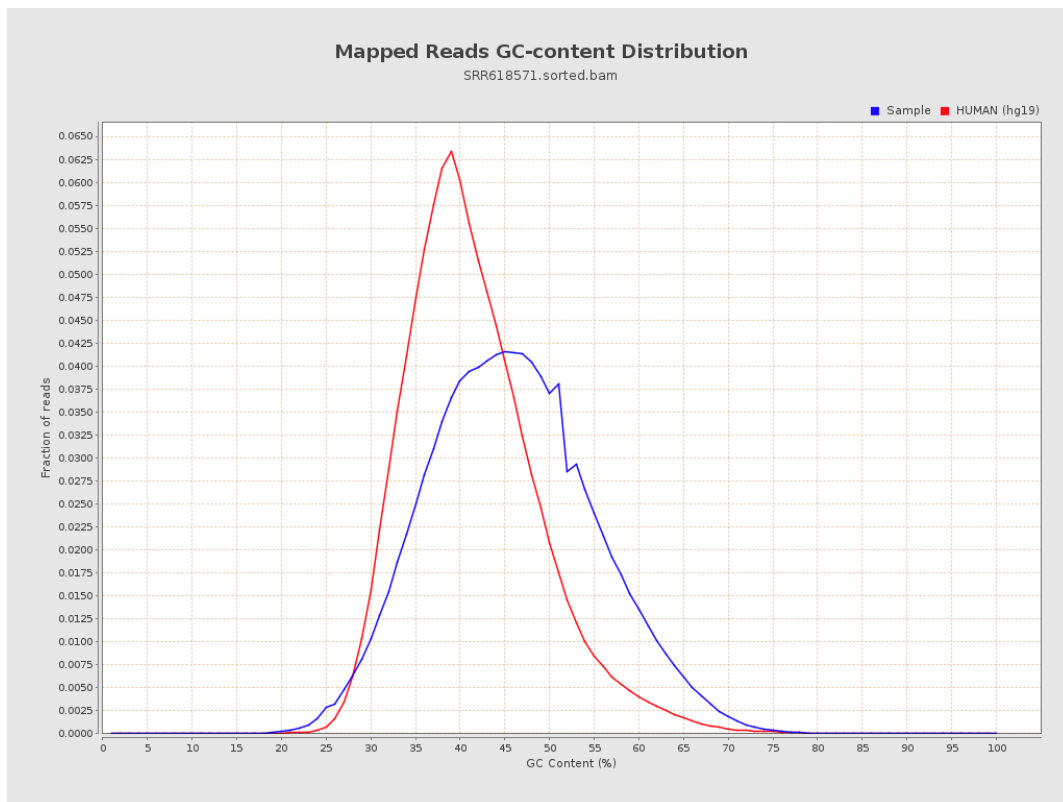
7. Results : Duplication Rate Histogram



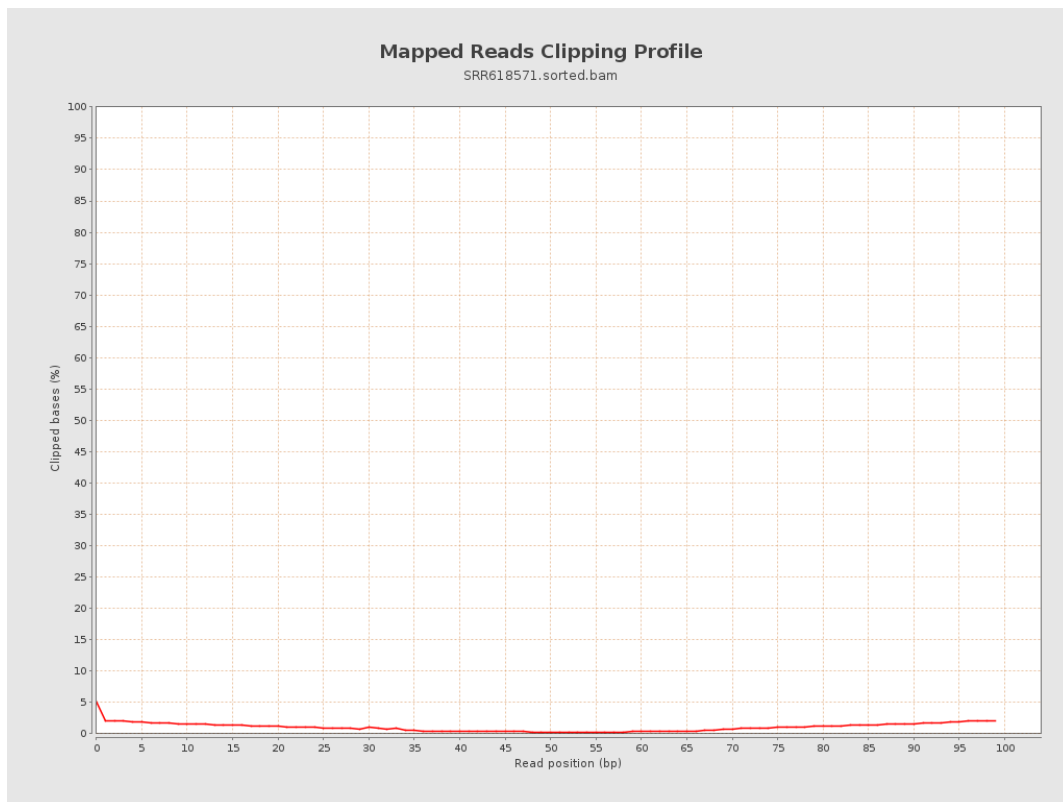
8. Results : Mapped Reads Nucleotide Content



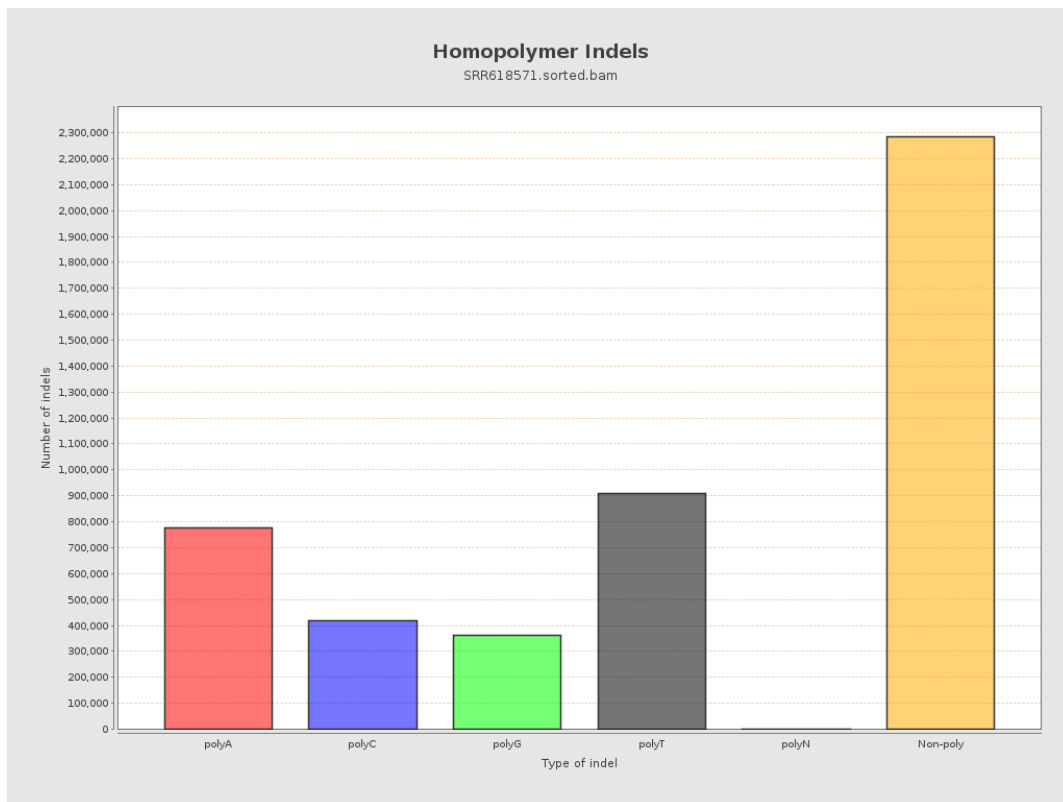
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

