

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 21:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618573.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_SRR618573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 21:13:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,790,613
Mapped reads	62,641,026 / 93.79%
Unmapped reads	4,149,587 / 6.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	126,425 / 0.19%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	26,106,426 / 39.09%
Duplication rate	35.13%
Clipped reads	5,899,070 / 8.83%

2.2. ACGT Content

Number/percentage of A's	1,593,174,272 / 26.05%
Number/percentage of C's	1,458,275,654 / 23.84%
Number/percentage of T's	1,587,114,718 / 25.95%
Number/percentage of G's	1,476,810,358 / 24.15%
Number/percentage of N's	366,559 / 0.01%
GC Percentage	47.99%

2.3. Coverage

Mean	1.9768

Standard Deviation	12.3557
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2.4. Mapping Quality

Mean Mapping Quality	51.68
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2.5. Mismatches and indels

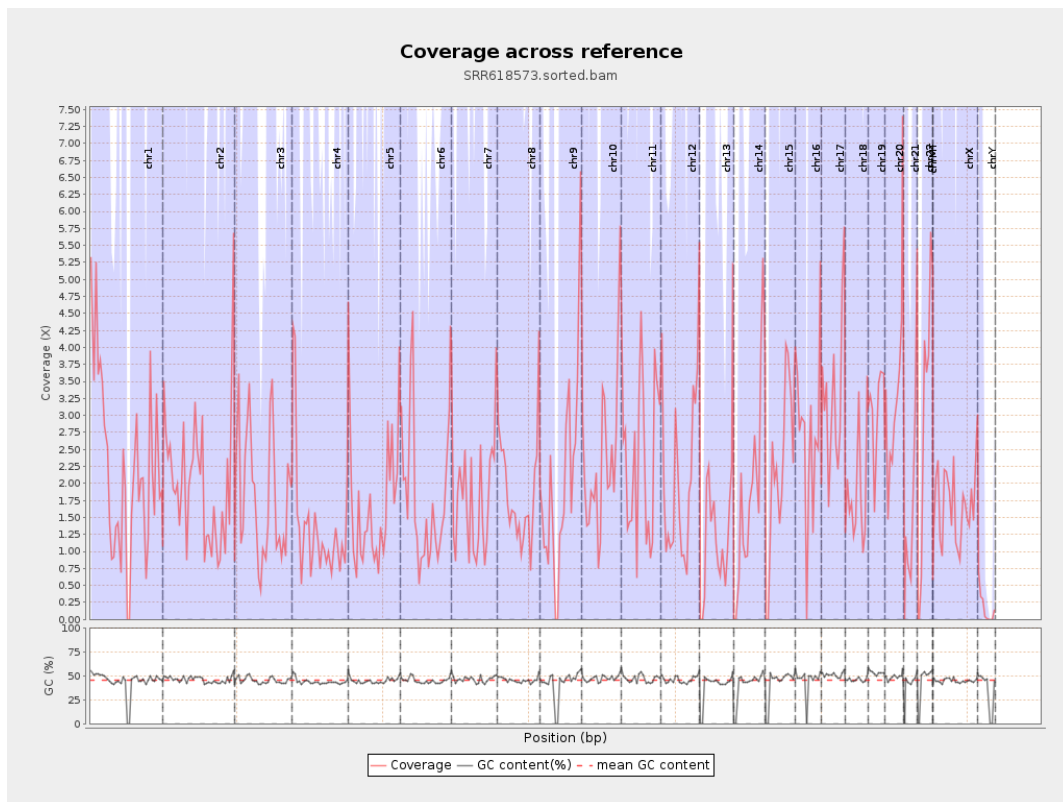
General error rate	0.92%
Mismatches	54,653,177
Insertions	947,297
Mapped reads with at least one insertion	1.49%
Deletions	2,682,577
Mapped reads with at least one deletion	4.19%
Homopolymer indels	53.7%

2.6. Chromosome stats

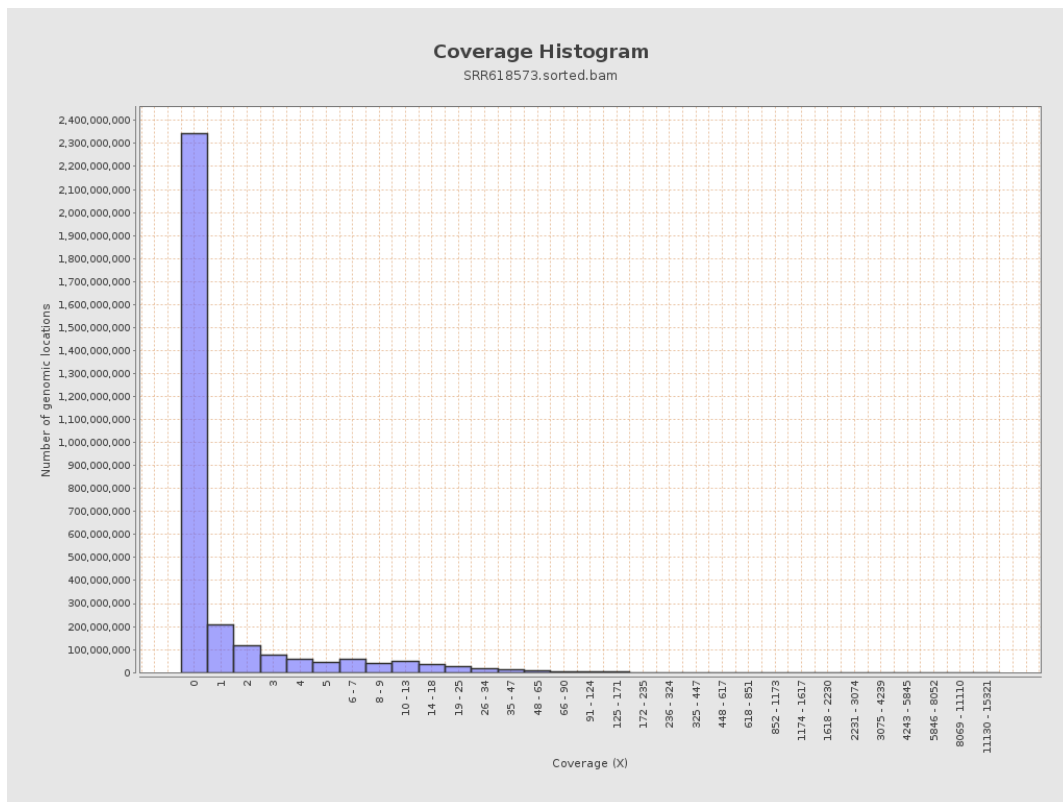
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	548975600	2.2025	12.391
chr2	243199373	486312060	1.9996	12.1151
chr3	198022430	356293188	1.7993	9.4202
chr4	191154276	256342103	1.341	9.9557
chr5	180915260	306393269	1.6936	9.6324
chr6	171115067	304173665	1.7776	8.5916
chr7	159138663	291179539	1.8297	8.5794

chr8	146364022	269258167	1.8396	14.2229
chr9	141213431	283011015	2.0041	10.3196
chr10	135534747	314984021	2.324	17.5269
chr11	135006516	321040377	2.378	12.4795
chr12	133851895	278039942	2.0772	14.7357
chr13	115169878	141078082	1.225	8.1866
chr14	107349540	198560887	1.8497	10.1003
chr15	102531392	223474451	2.1796	15.8316
chr16	90354753	246480982	2.7279	20.1108
chr17	81195210	265255664	3.2669	21.5386
chr18	78077248	140796733	1.8033	8.9343
chr19	59128983	179115078	3.0292	12.7554
chr20	63025520	201434171	3.1961	12.3828
chr21	48129895	84636771	1.7585	15.5515
chr22	51304566	149188643	2.9079	12.6318
chrMT	16571	9471	0.5715	3.0475
chrX	155270560	263514440	1.6971	10.5292
chrY	59373566	9966569	0.1679	6.6711

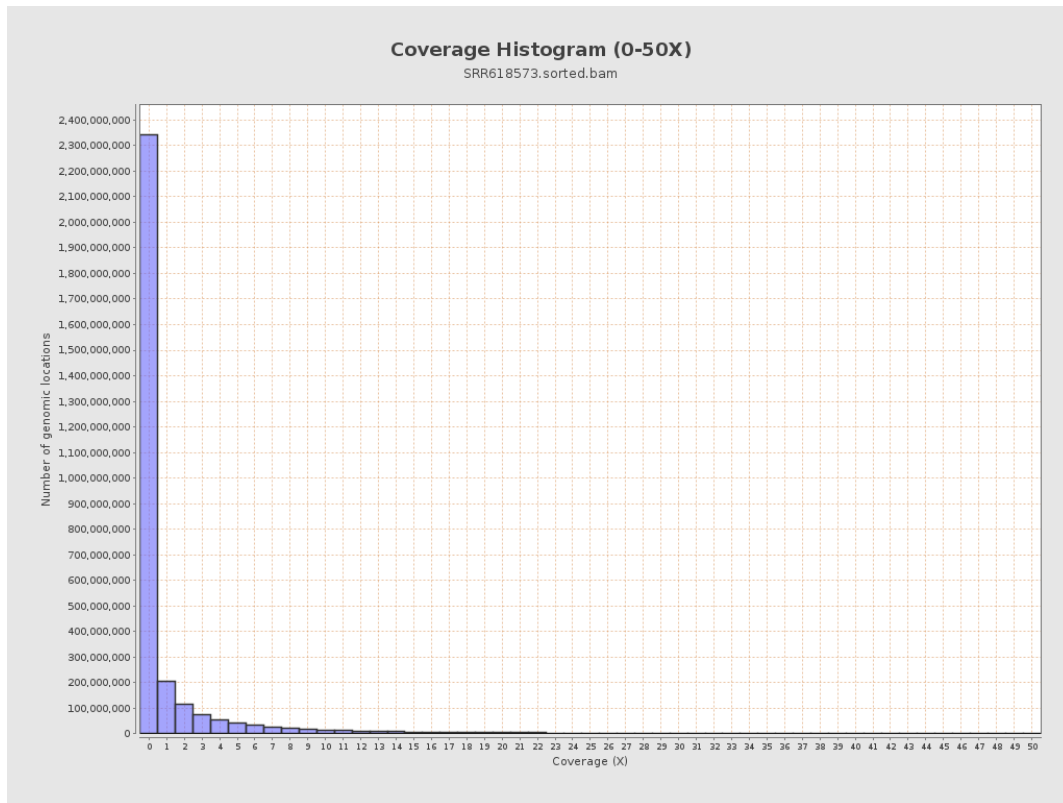
3. Results : Coverage across reference



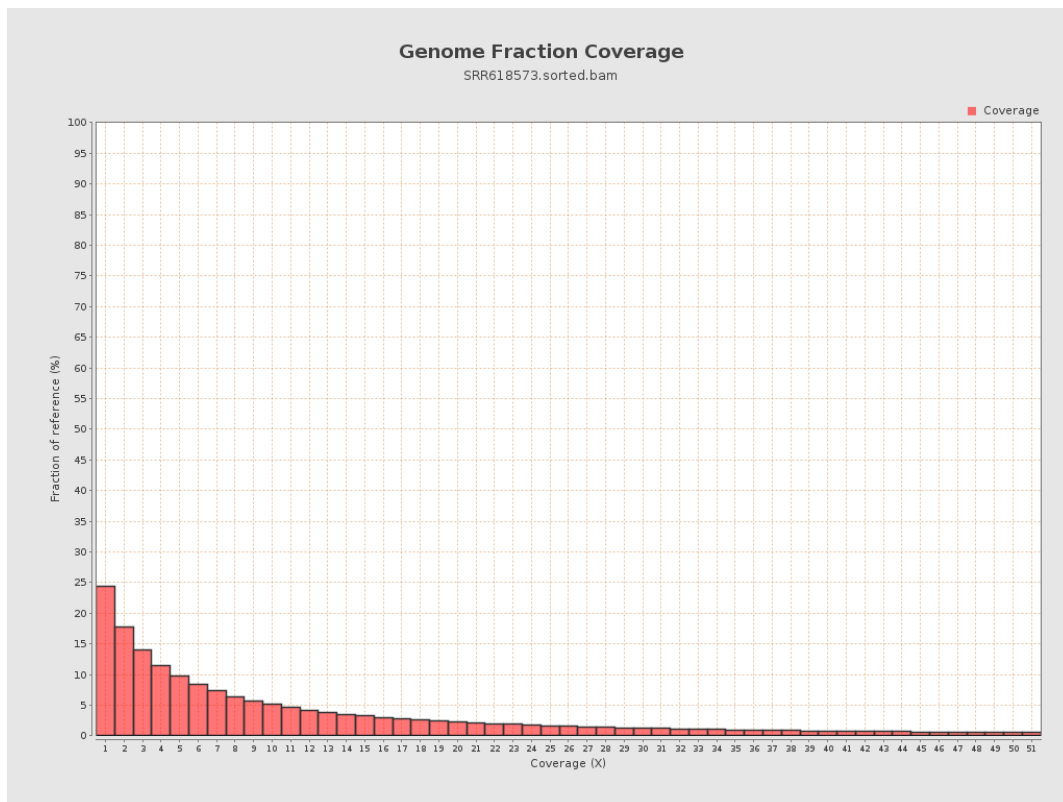
4. Results : Coverage Histogram



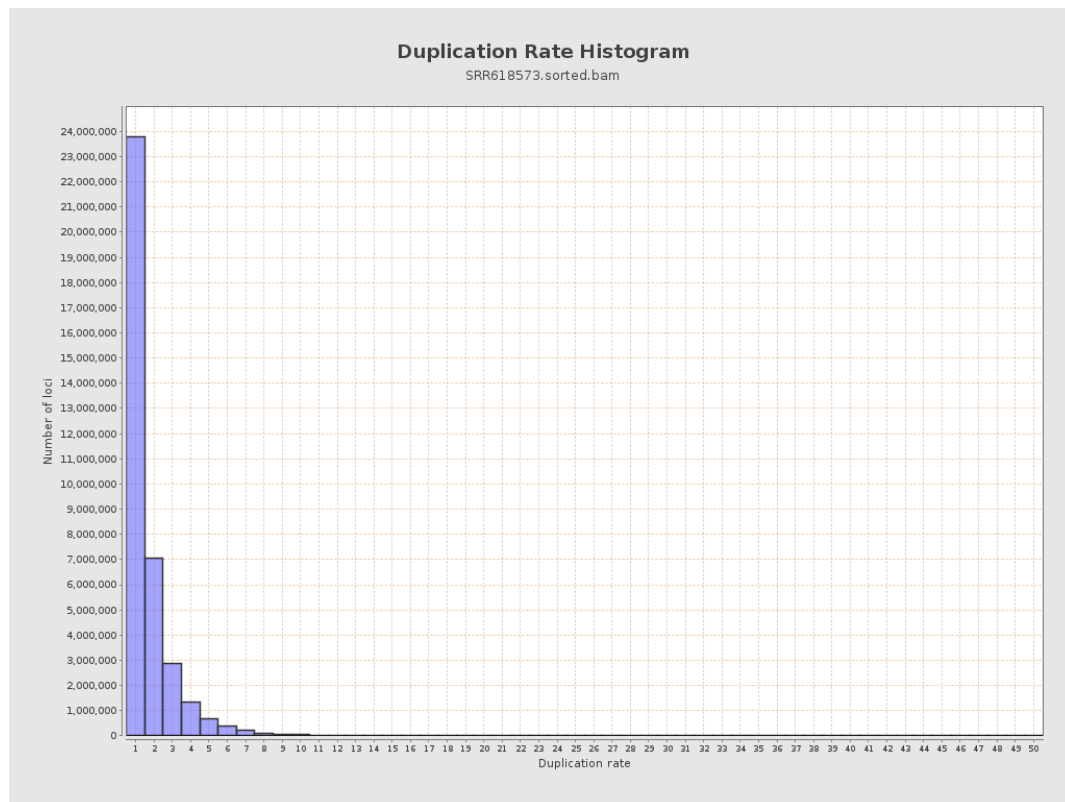
5. Results : Coverage Histogram (0-50X)



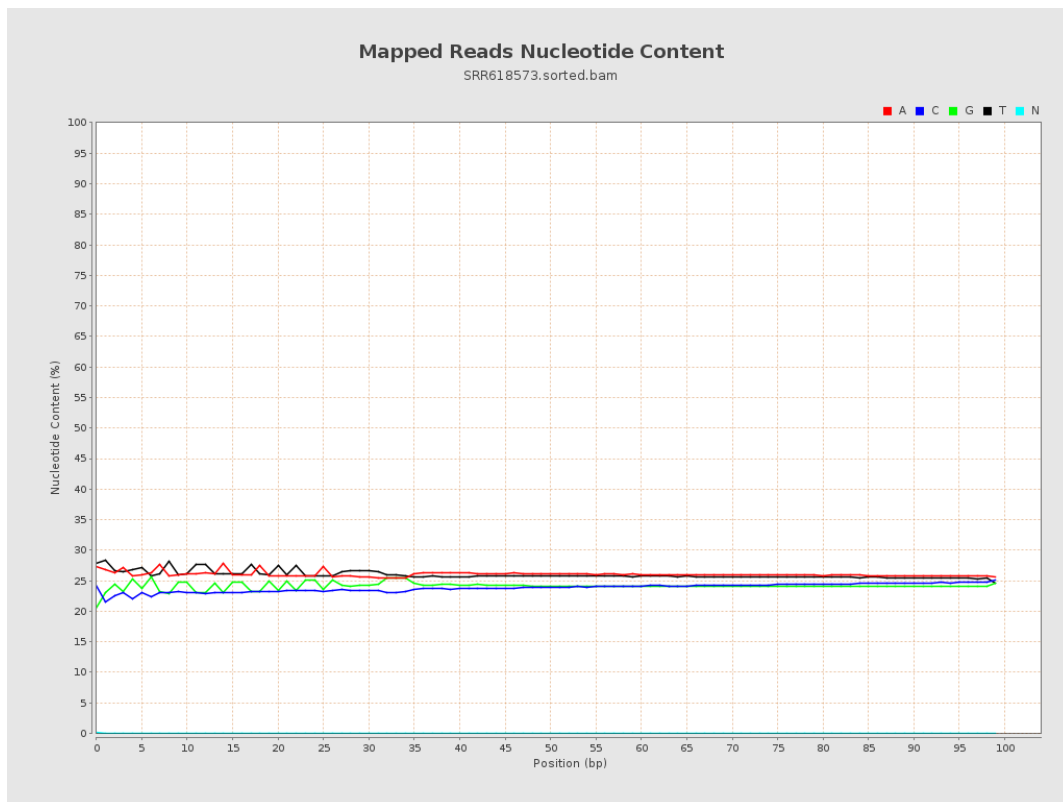
6. Results : Genome Fraction Coverage



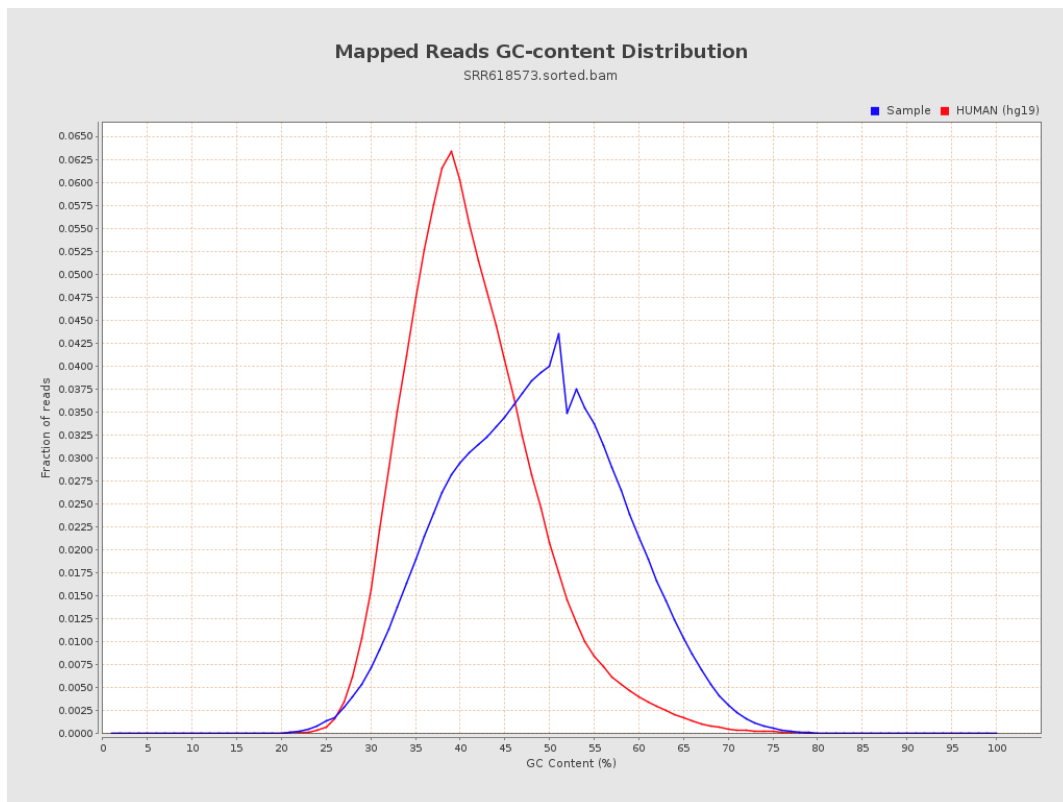
7. Results : Duplication Rate Histogram



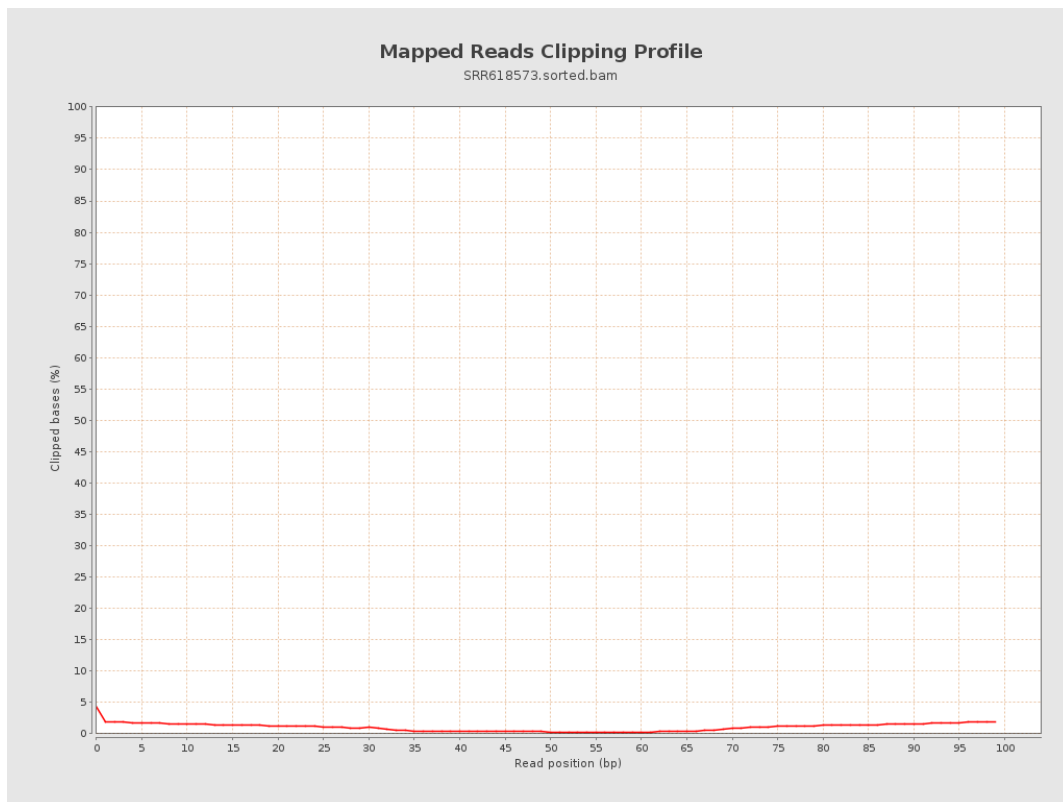
8. Results : Mapped Reads Nucleotide Content



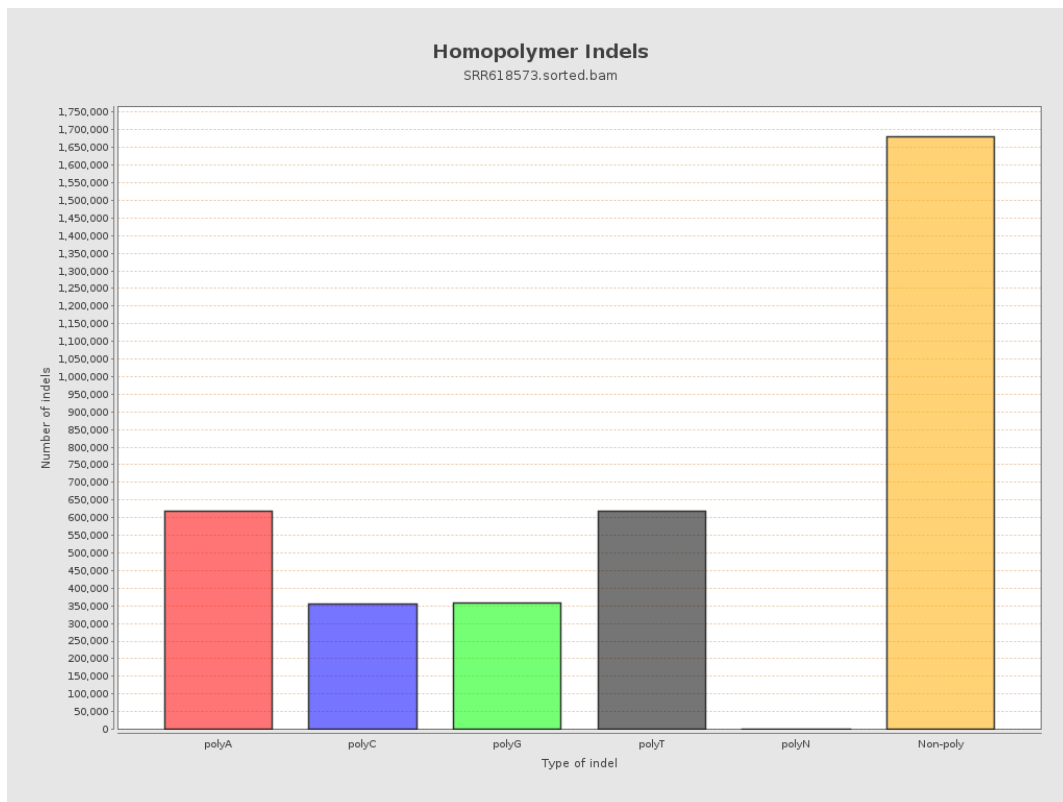
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

