

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 13:44:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618656.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_SRR618656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618656.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 13:44:56 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,608,431
Mapped reads	43,847,013 / 83.35%
Unmapped reads	8,761,418 / 16.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	96,031 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	20,230,430 / 38.45%
Duplication rate	32.17%
Clipped reads	5,162,446 / 9.81%

2.2. ACGT Content

Number/percentage of A's	1,107,943,809 / 26.07%
Number/percentage of C's	1,007,481,707 / 23.7%
Number/percentage of T's	1,155,399,388 / 27.18%
Number/percentage of G's	978,531,328 / 23.02%
Number/percentage of N's	872,297 / 0.02%
GC Percentage	46.73%

2.3. Coverage

Mean	1.3738

Standard Deviation	19.9868
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2.4. Mapping Quality

Mean Mapping Quality	50.1
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2.5. Mismatches and indels

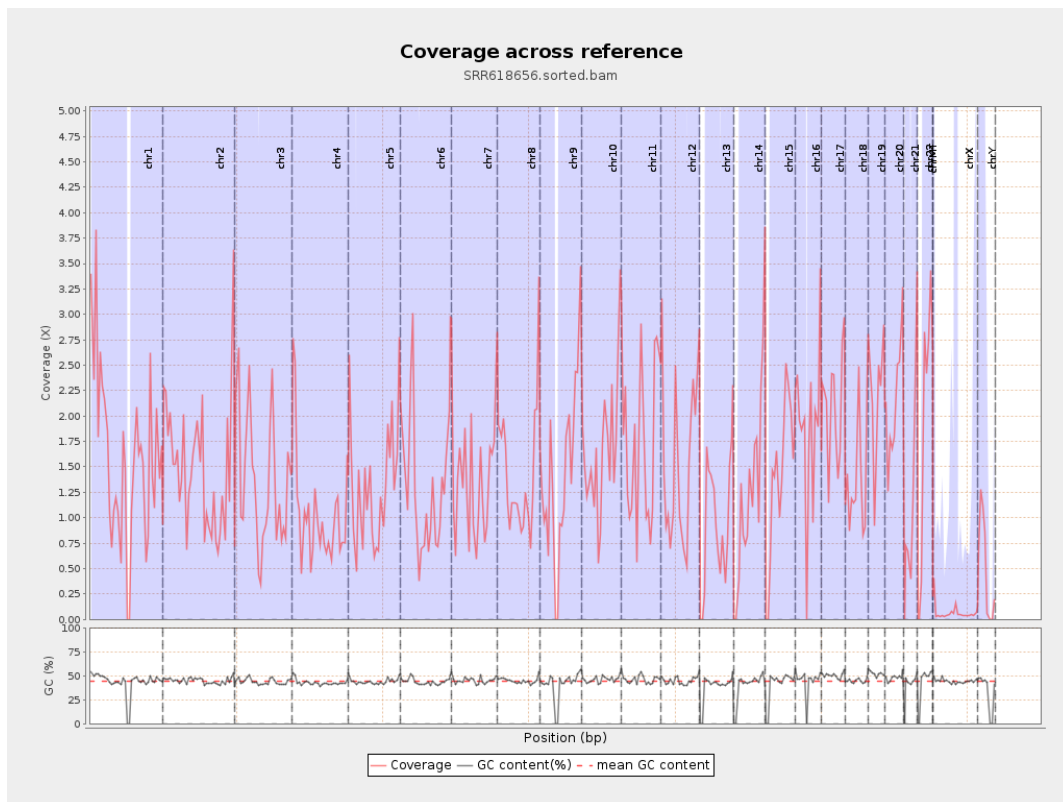
General error rate	0.85%
Mismatches	34,857,606
Insertions	677,877
Mapped reads with at least one insertion	1.52%
Deletions	1,868,309
Mapped reads with at least one deletion	4.17%
Homopolymer indels	53.48%

2.6. Chromosome stats

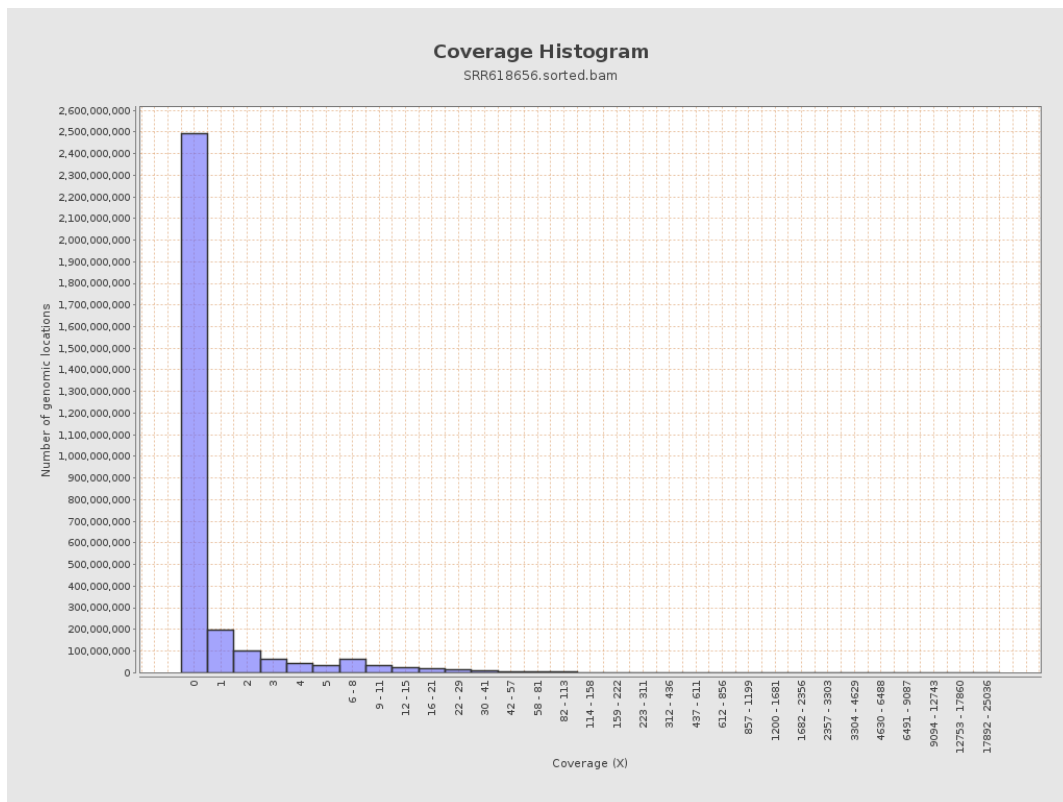
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	393947115	1.5805	19.8578
chr2	243199373	360403665	1.4819	25.3743
chr3	198022430	267988873	1.3533	26.2084
chr4	191154276	195751282	1.024	14.7426
chr5	180915260	241362450	1.3341	20.4305
chr6	171115067	222151162	1.2983	16.9742
chr7	159138663	218225221	1.3713	22.7693

chr8	146364022	208726644	1.4261	20.3158
chr9	141213431	201050021	1.4237	20.3356
chr10	135534747	221892992	1.6372	20.0619
chr11	135006516	233133102	1.7268	19.6062
chr12	133851895	207028723	1.5467	28.3513
chr13	115169878	108061208	0.9383	16.4075
chr14	107349540	128935946	1.2011	17.0381
chr15	102531392	142912984	1.3938	13.1661
chr16	90354753	170884324	1.8913	18.0424
chr17	81195210	168218577	2.0718	21.5545
chr18	78077248	104826374	1.3426	15.7923
chr19	59128983	127579372	2.1576	17.7329
chr20	63025520	134720872	2.1376	19.9518
chr21	48129895	57640932	1.1976	25.9352
chr22	51304566	96587552	1.8826	15.8064
chrMT	16571	3661	0.2209	1.1652
chrX	155270560	10159541	0.0654	5.804
chrY	59373566	30729186	0.5176	6.9144

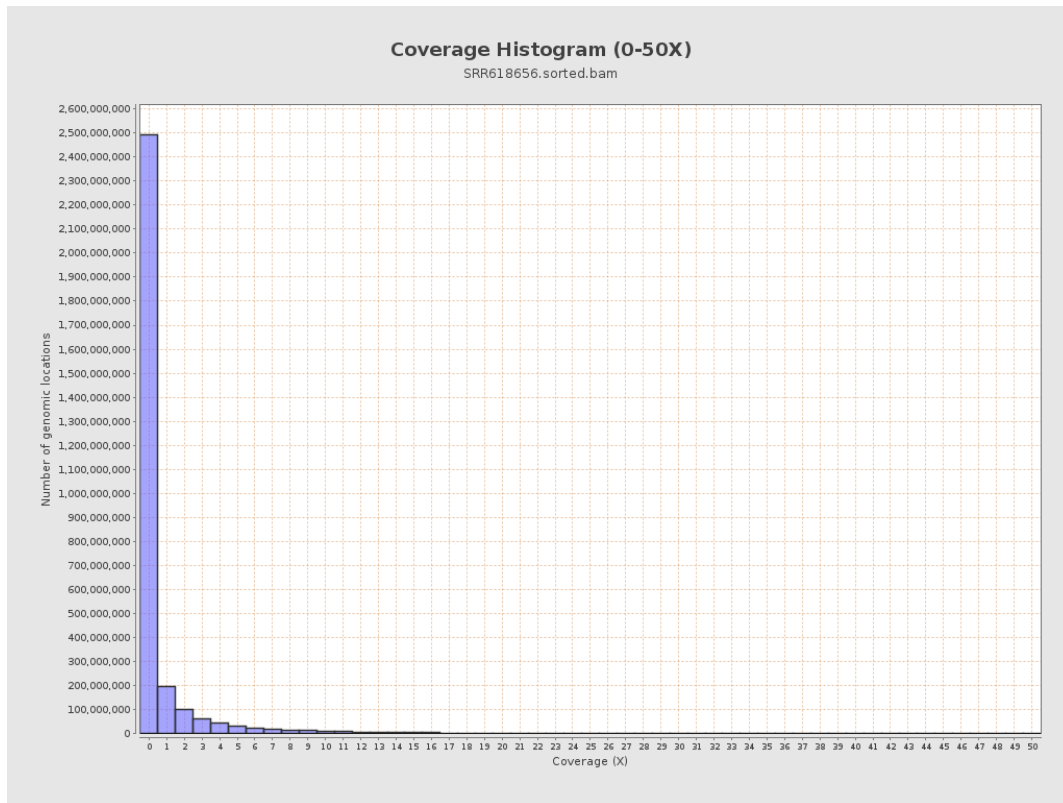
3. Results : Coverage across reference



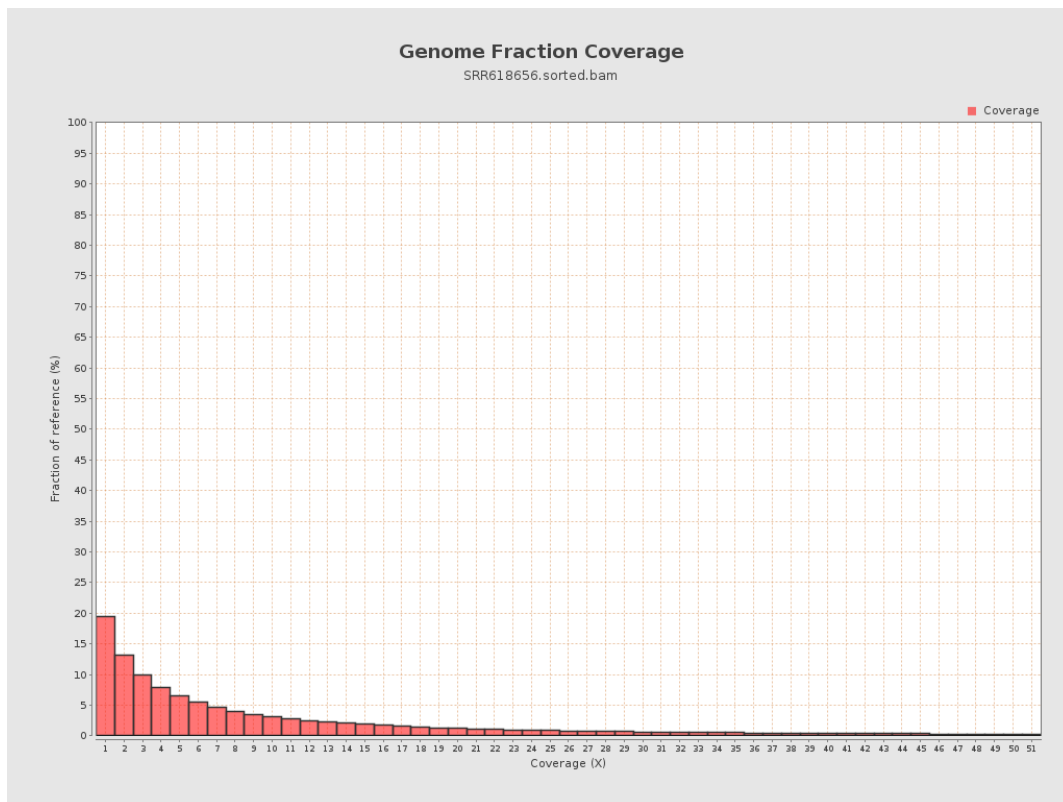
4. Results : Coverage Histogram



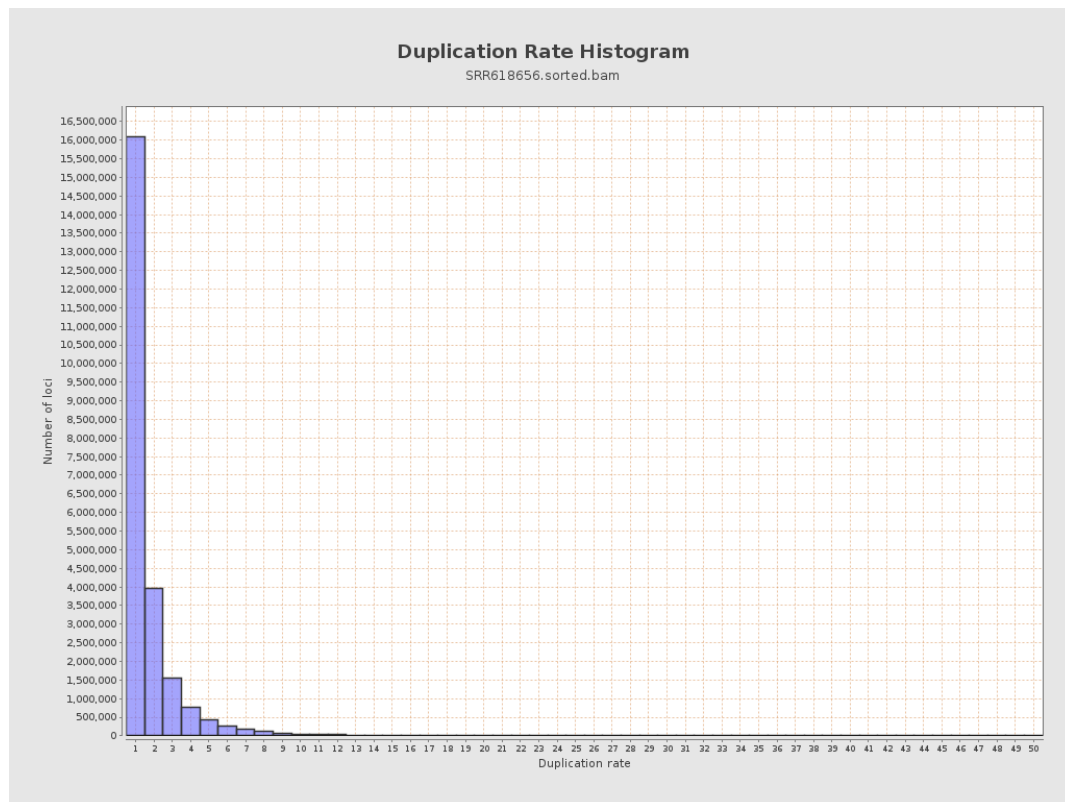
5. Results : Coverage Histogram (0-50X)



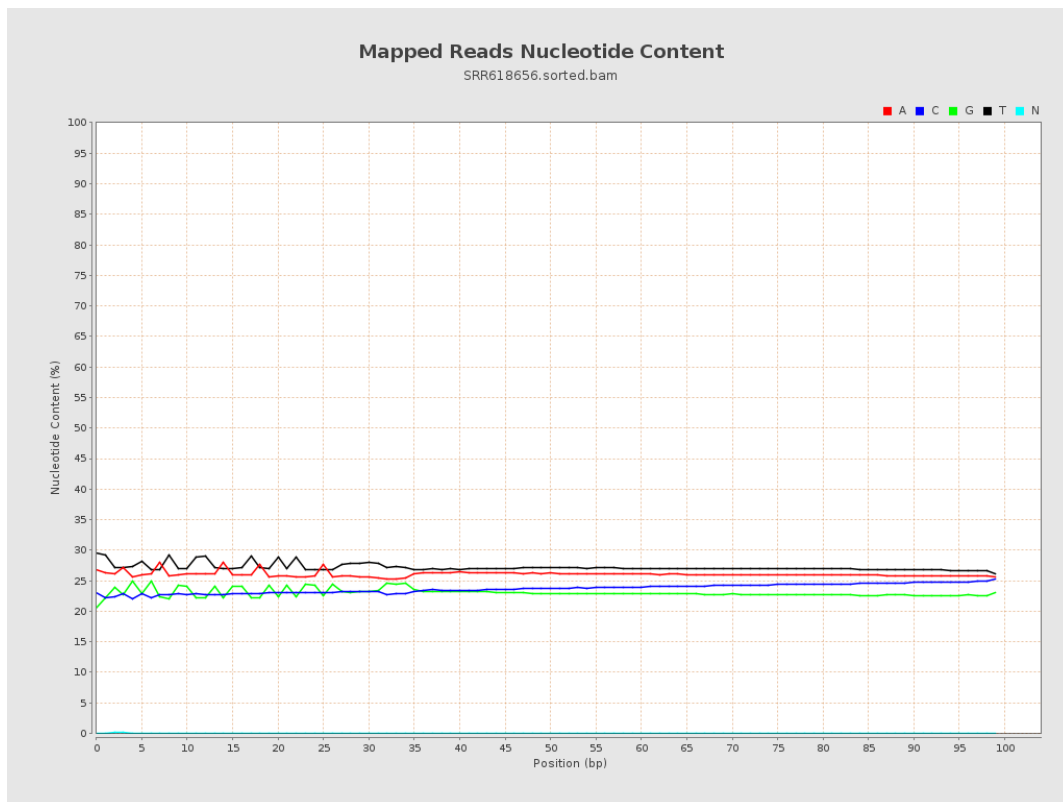
6. Results : Genome Fraction Coverage



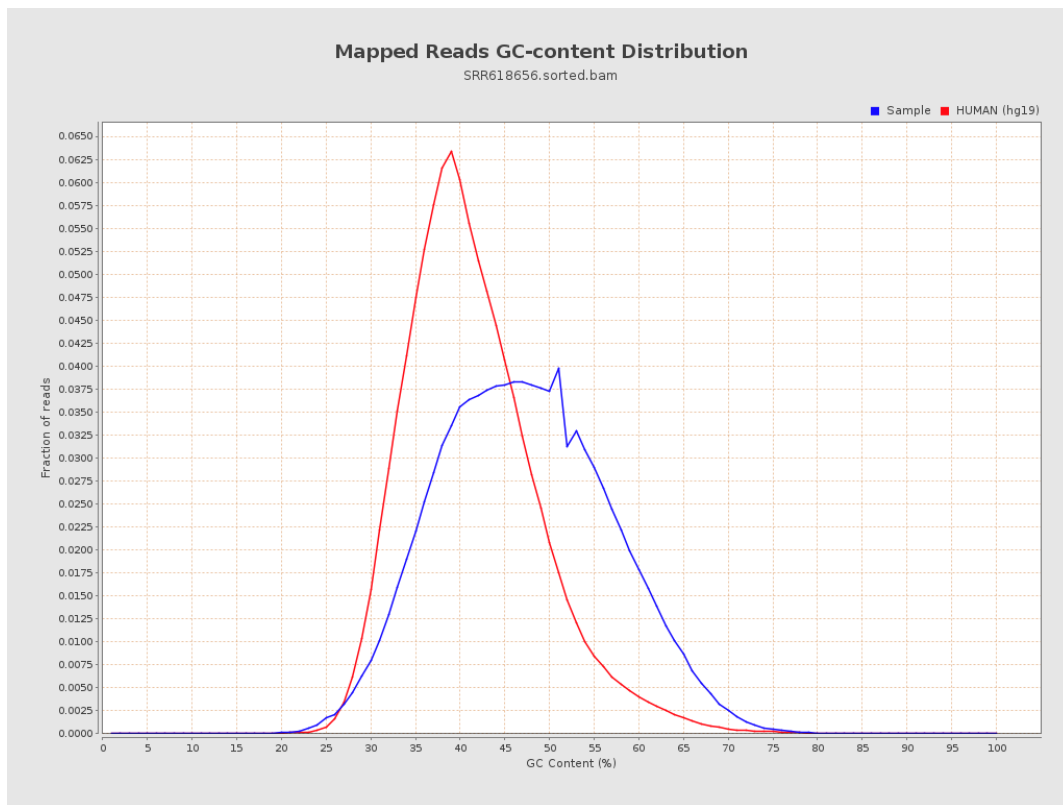
7. Results : Duplication Rate Histogram



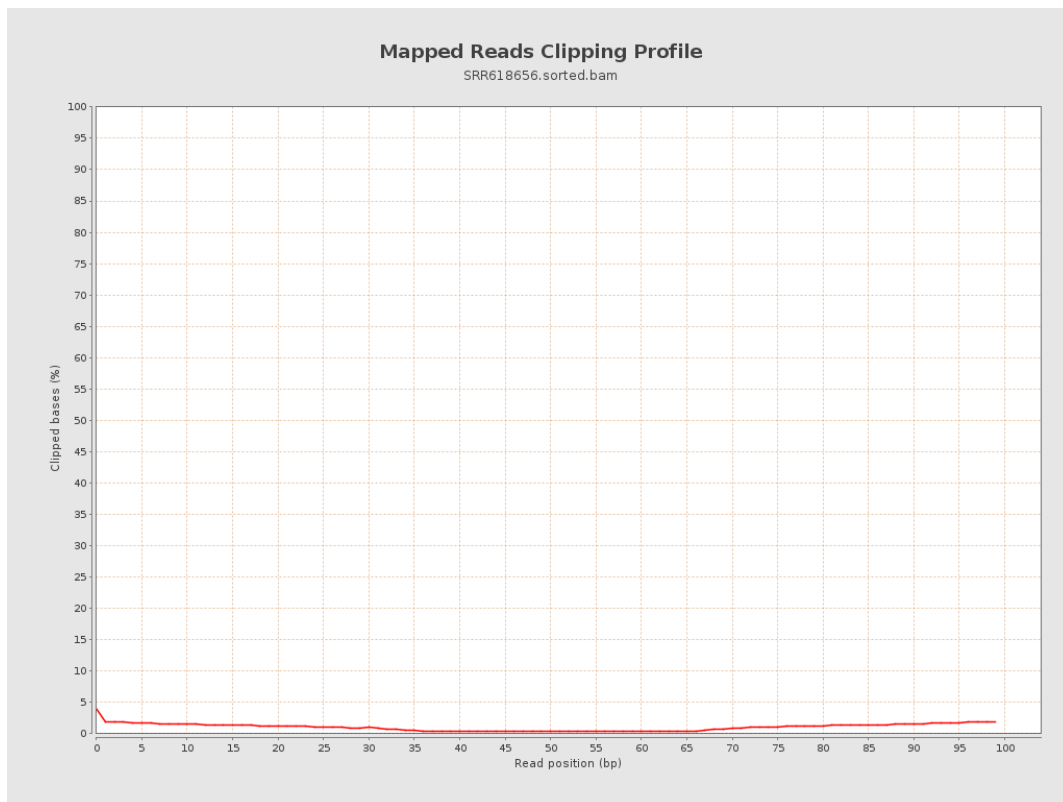
8. Results : Mapped Reads Nucleotide Content



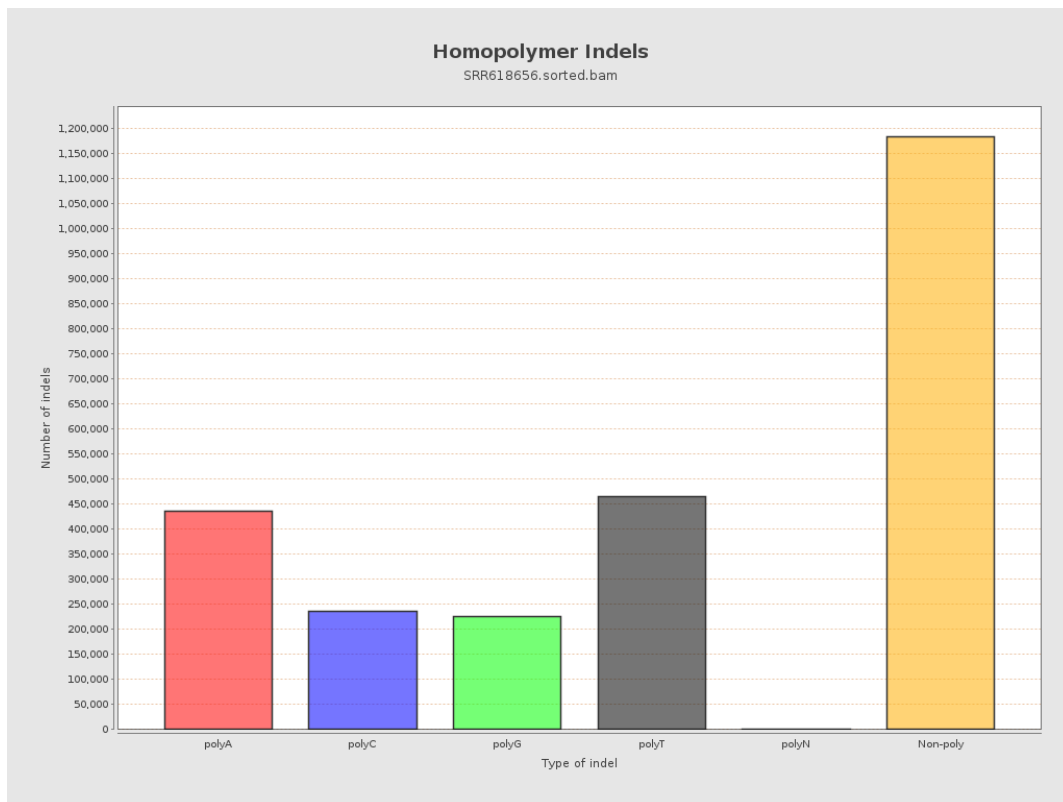
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

