

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 10:27:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618651.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_SRR618651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 10:27:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,430,591
Mapped reads	62,293,553 / 79.43%
Unmapped reads	16,137,038 / 20.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	382,520 / 0.49%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	42,025,207 / 53.58%
Duplication rate	52.58%
Clipped reads	12,022,881 / 15.33%

2.2. ACGT Content

Number/percentage of A's	1,590,007,485 / 26.77%
Number/percentage of C's	1,342,698,008 / 22.6%
Number/percentage of T's	1,888,045,941 / 31.78%
Number/percentage of G's	1,119,328,358 / 18.84%
Number/percentage of N's	374,451 / 0.01%
GC Percentage	41.45%

2.3. Coverage

Mean	1.9208

Standard Deviation	54.6225
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2.4. Mapping Quality

Mean Mapping Quality	50.45
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2.5. Mismatches and indels

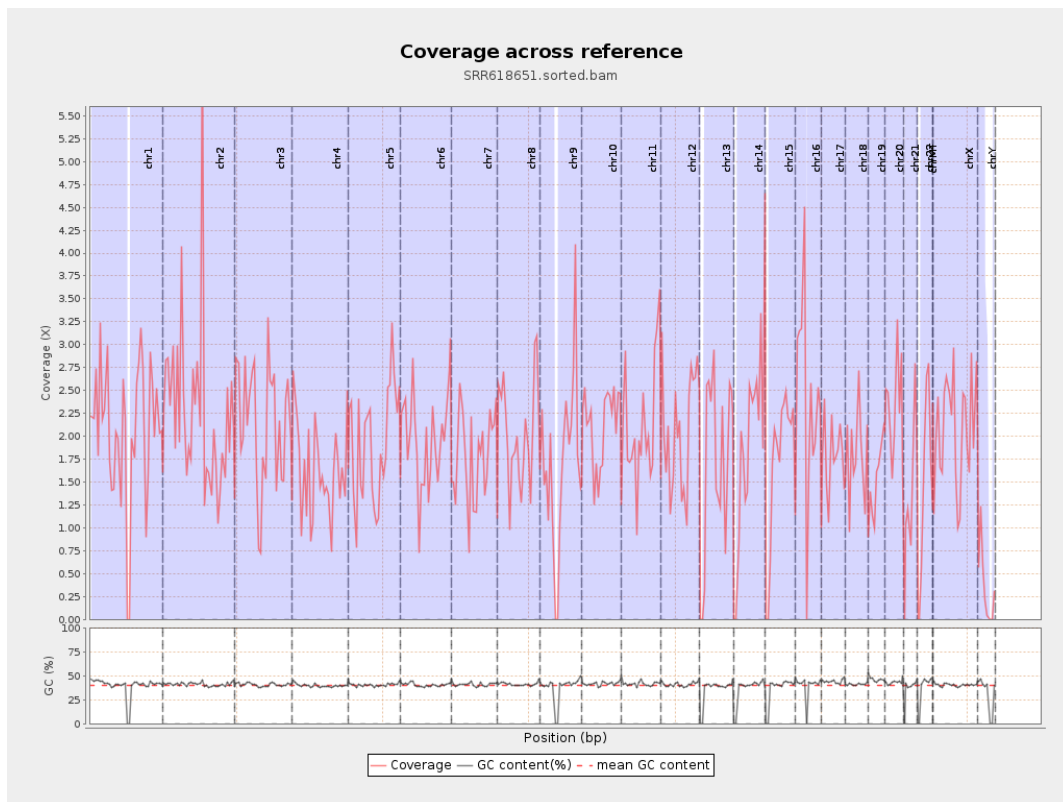
General error rate	0.96%
Mismatches	53,762,646
Insertions	1,479,187
Mapped reads with at least one insertion	2.28%
Deletions	3,130,528
Mapped reads with at least one deletion	4.85%
Homopolymer indels	46.13%

2.6. Chromosome stats

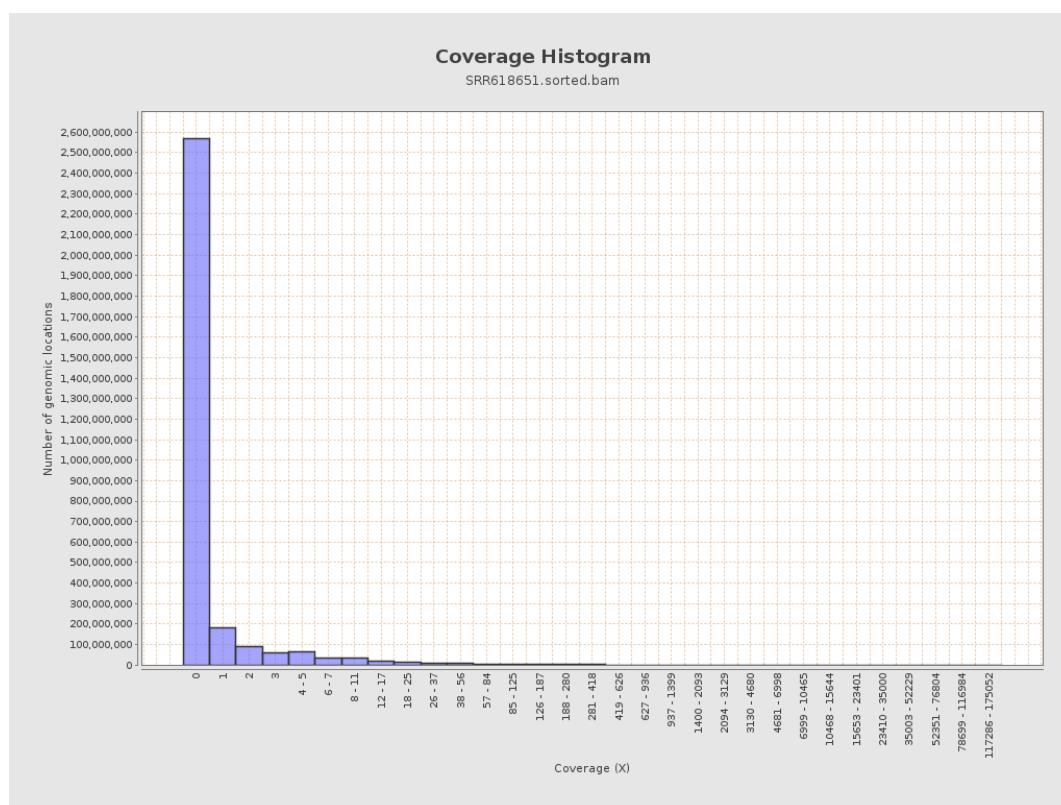
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	513122457	2.0587	49.2549
chr2	243199373	554079053	2.2783	123.6769
chr3	198022430	421057222	2.1263	48.9059
chr4	191154276	313504160	1.6401	38.9475
chr5	180915260	348489486	1.9263	37.1414
chr6	171115067	336108536	1.9642	32.8761
chr7	159138663	282685005	1.7763	33.2194

chr8	146364022	296342539	2.0247	36.9769
chr9	141213431	240551067	1.7035	35.1072
chr10	135534747	286157213	2.1113	40.2214
chr11	135006516	286309825	2.1207	37.7932
chr12	133851895	278656169	2.0818	39.5008
chr13	115169878	194642715	1.69	36.9875
chr14	107349540	196190712	1.8276	33.3645
chr15	102531392	174638170	1.7033	33.5305
chr16	90354753	212151145	2.348	124.6185
chr17	81195210	146684084	1.8066	31.6549
chr18	78077248	138219965	1.7703	32.35
chr19	59128983	90554540	1.5315	27.1053
chr20	63025520	147347211	2.3379	36.1027
chr21	48129895	67309130	1.3985	34.2965
chr22	51304566	77532544	1.5112	41.9726
chrMT	16571	39289	2.3709	7.6307
chrX	155270560	322361992	2.0761	35.3841
chrY	59373566	21375284	0.36	44.3886

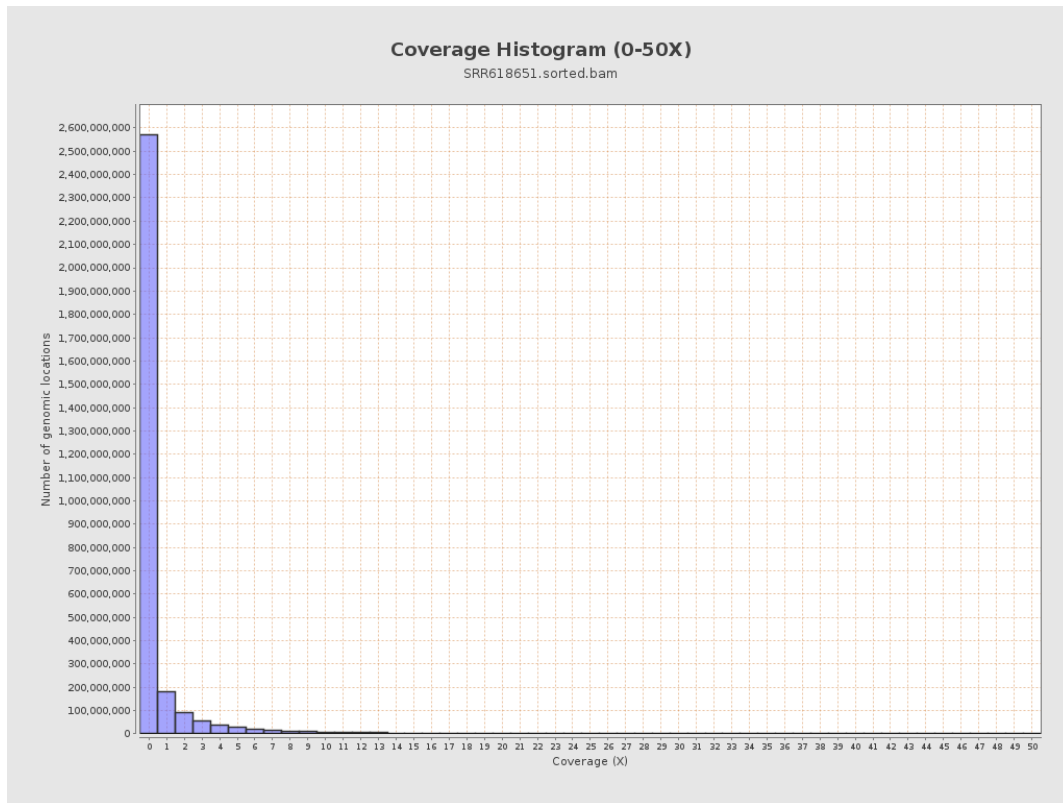
3. Results : Coverage across reference



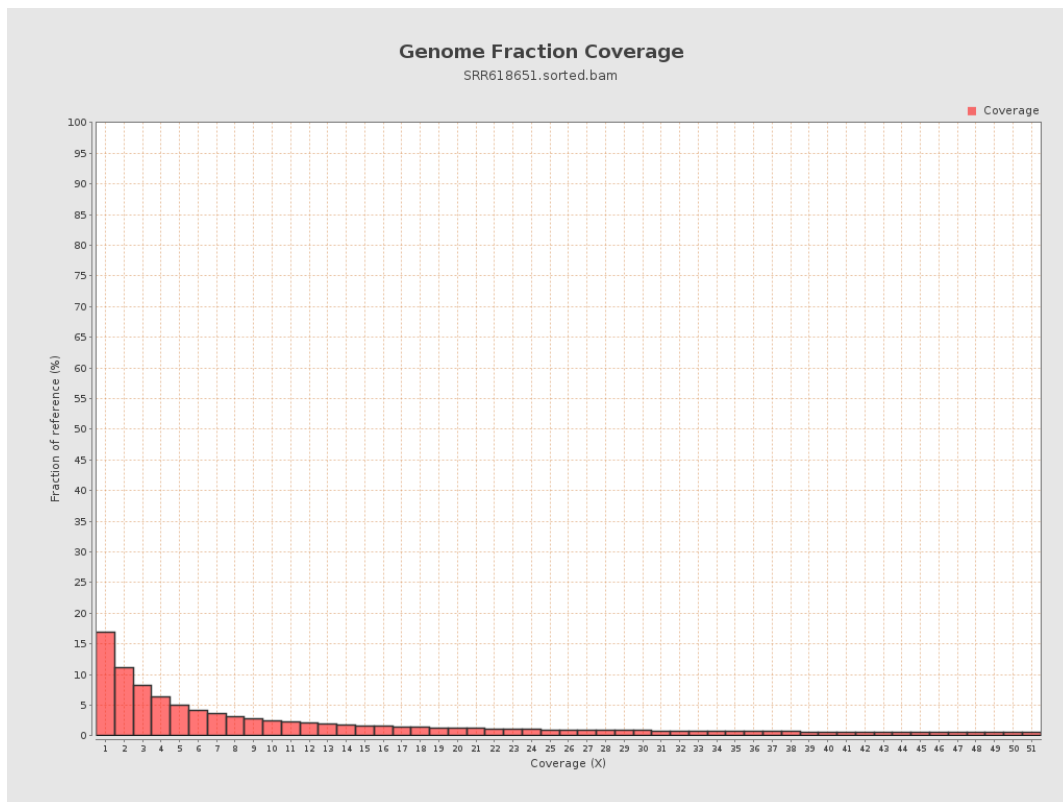
4. Results : Coverage Histogram



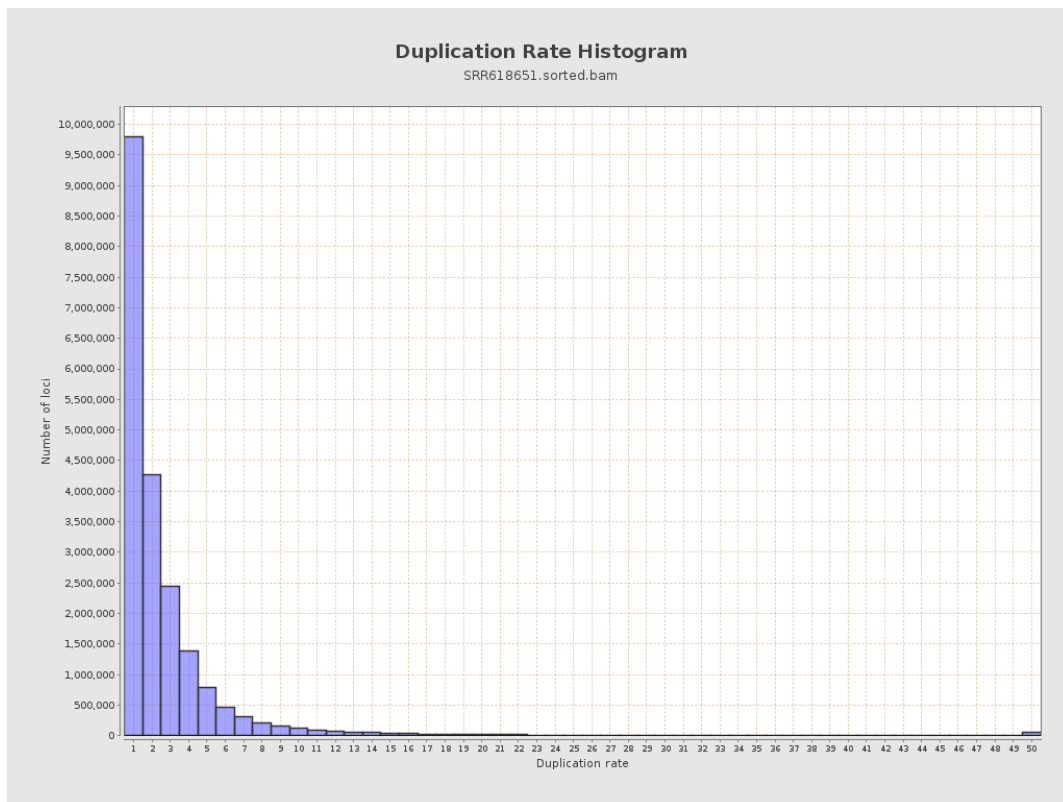
5. Results : Coverage Histogram (0-50X)



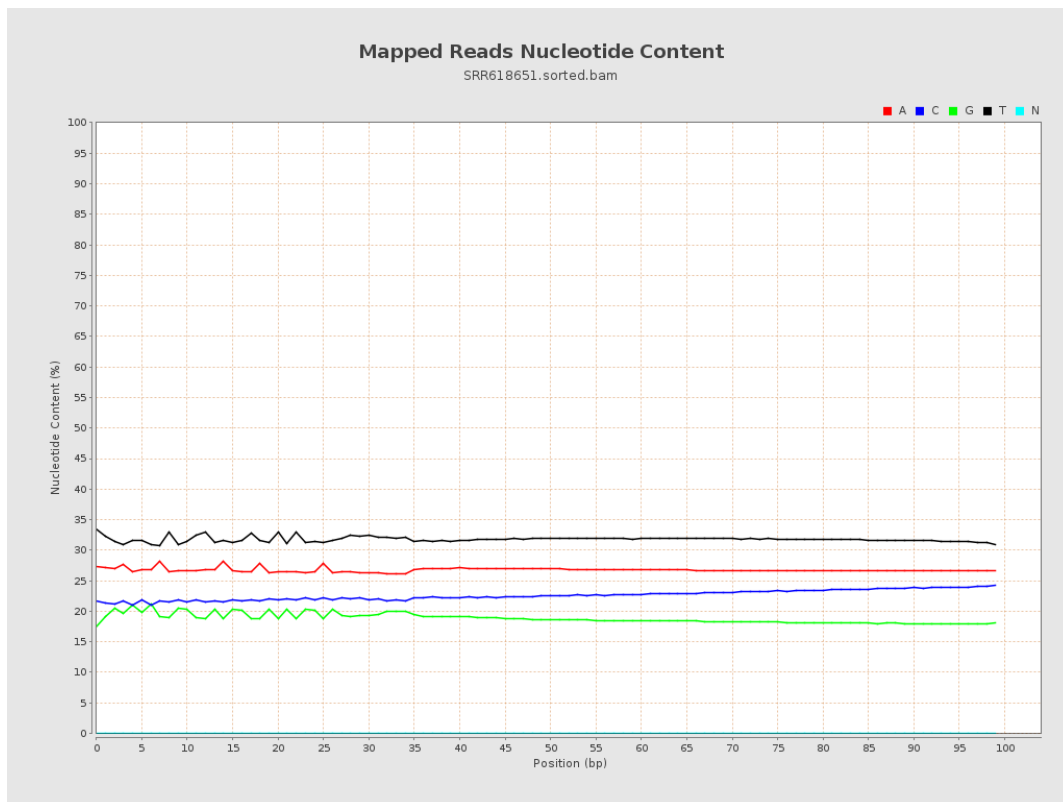
6. Results : Genome Fraction Coverage



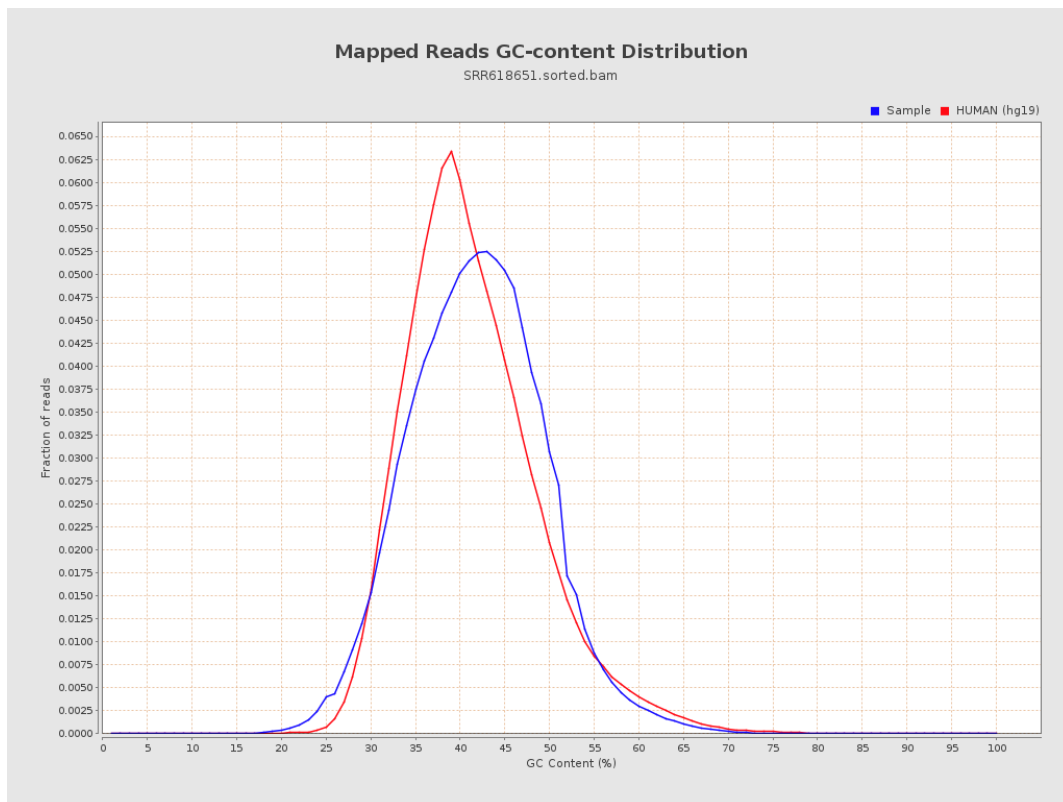
7. Results : Duplication Rate Histogram



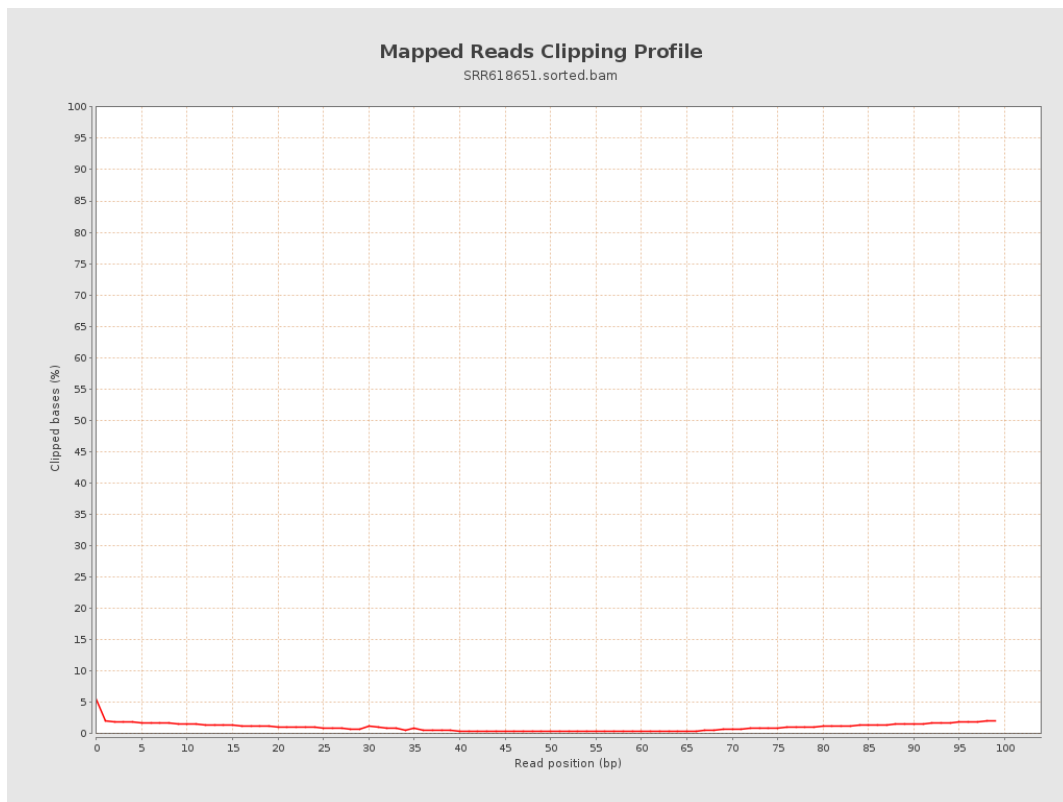
8. Results : Mapped Reads Nucleotide Content



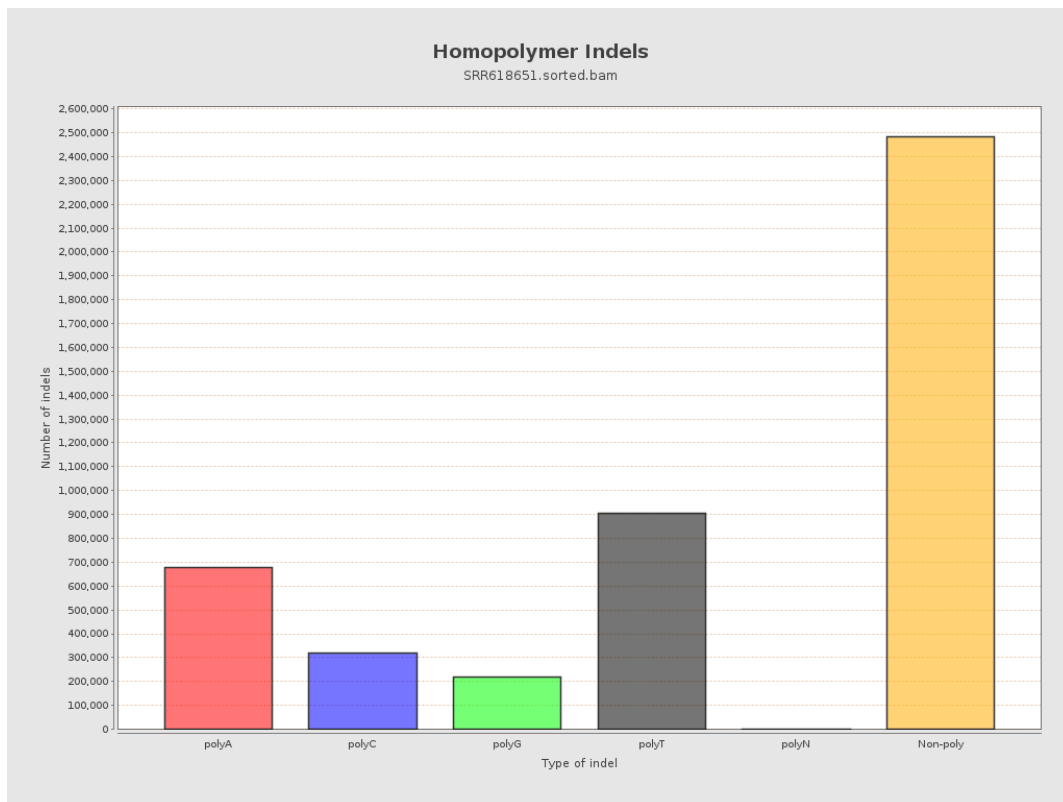
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

