

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 14:44:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618658.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_SRR618658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 14:44:28 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,523,005
Mapped reads	35,553,418 / 92.29%
Unmapped reads	2,969,587 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	117,620 / 0.31%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,301,884 / 24.15%
Duplication rate	23.4%
Clipped reads	3,754,350 / 9.75%

2.2. ACGT Content

Number/percentage of A's	951,710,963 / 27.42%
Number/percentage of C's	762,744,008 / 21.98%
Number/percentage of T's	966,985,780 / 27.86%
Number/percentage of G's	754,686,760 / 21.74%
Number/percentage of N's	34,585,051 / 1%
GC Percentage	43.72%

2.3. Coverage

Mean	1.1219

Standard Deviation	4.7479
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2.4. Mapping Quality

Mean Mapping Quality	51.41
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2.5. Mismatches and indels

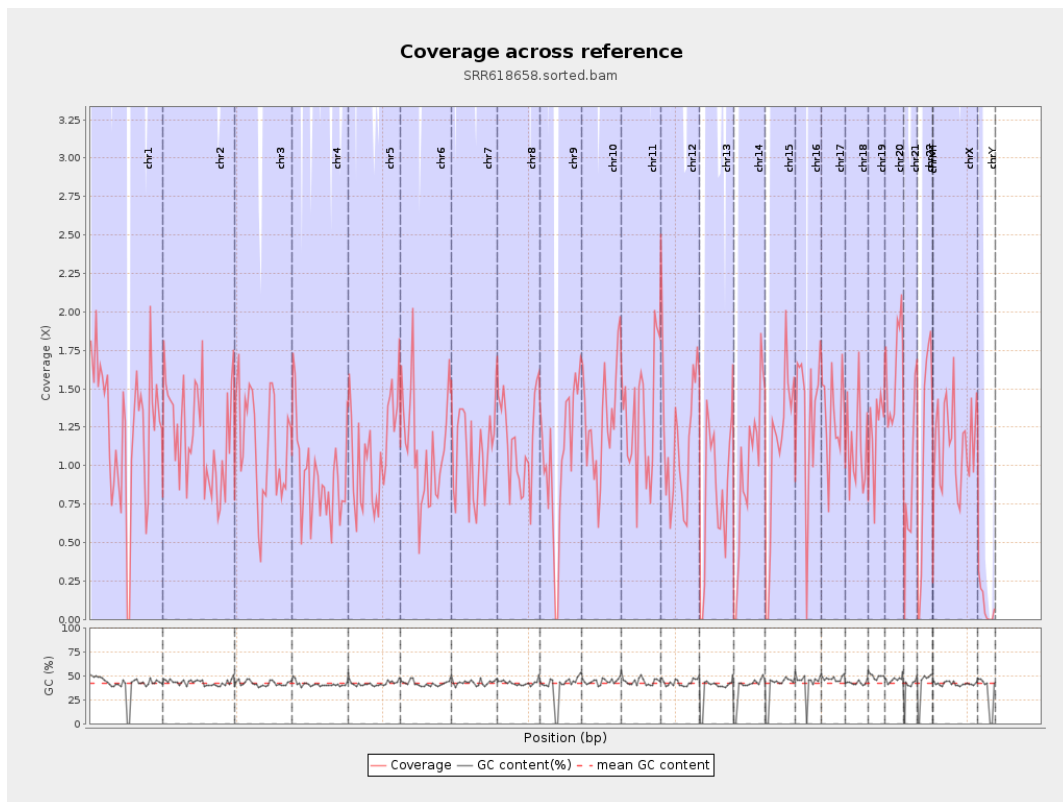
General error rate	1.95%
Mismatches	66,814,527
Insertions	653,749
Mapped reads with at least one insertion	1.81%
Deletions	1,738,717
Mapped reads with at least one deletion	4.77%
Homopolymer indels	53.03%

2.6. Chromosome stats

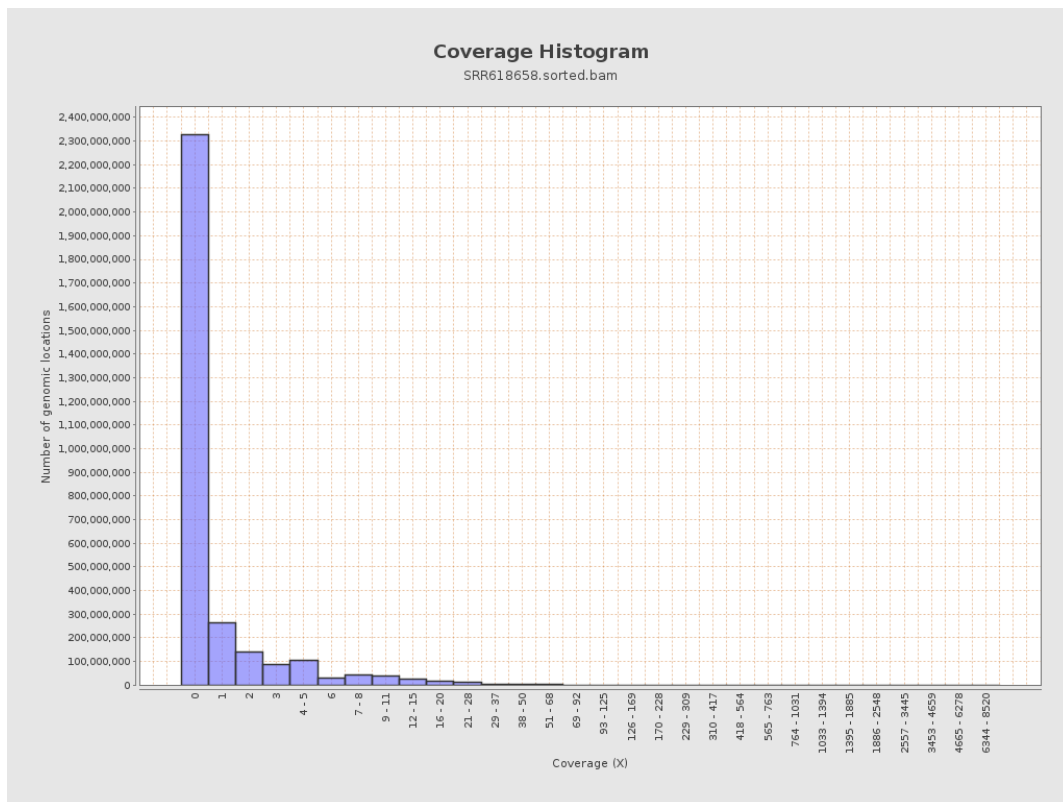
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	307729943	1.2346	4.7592
chr2	243199373	290150109	1.1931	6.462
chr3	198022430	223350073	1.1279	3.6154
chr4	191154276	177250250	0.9273	3.8438
chr5	180915260	198207694	1.0956	3.6227
chr6	171115067	189010130	1.1046	3.8027
chr7	159138663	172885556	1.0864	3.7188

chr8	146364022	168522921	1.1514	3.7523
chr9	141213431	148235546	1.0497	4.0379
chr10	135534747	173568456	1.2806	4.1614
chr11	135006516	178459183	1.3219	4.5409
chr12	133851895	156629788	1.1702	4.1111
chr13	115169878	95636837	0.8304	3.1126
chr14	107349540	104239894	0.971	3.4548
chr15	102531392	114174920	1.1136	3.902
chr16	90354753	119782328	1.3257	12.5269
chr17	81195210	107105994	1.3191	4.4339
chr18	78077248	86674202	1.1101	4.181
chr19	59128983	73081391	1.236	4.6546
chr20	63025520	102124417	1.6204	4.9879
chr21	48129895	44422686	0.923	6.254
chr22	51304566	57890091	1.1284	4.3505
chrMT	16571	3924	0.2368	0.7692
chrX	155270560	178487204	1.1495	3.7088
chrY	59373566	5518933	0.093	3.45

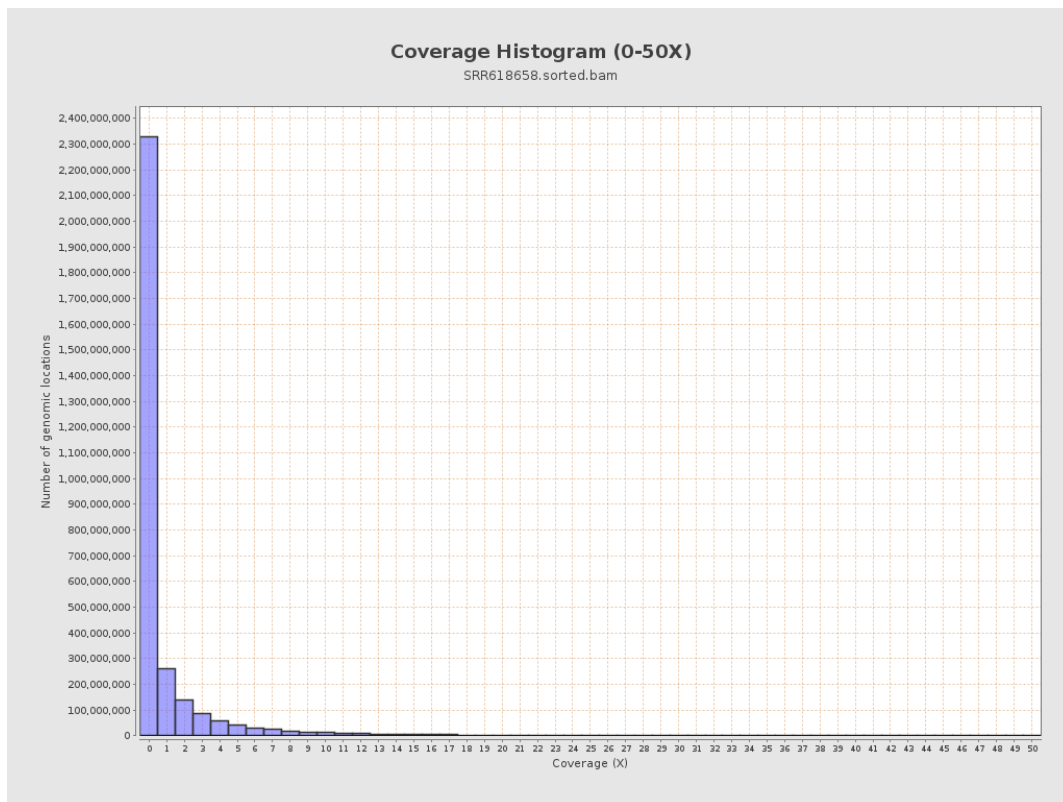
3. Results : Coverage across reference



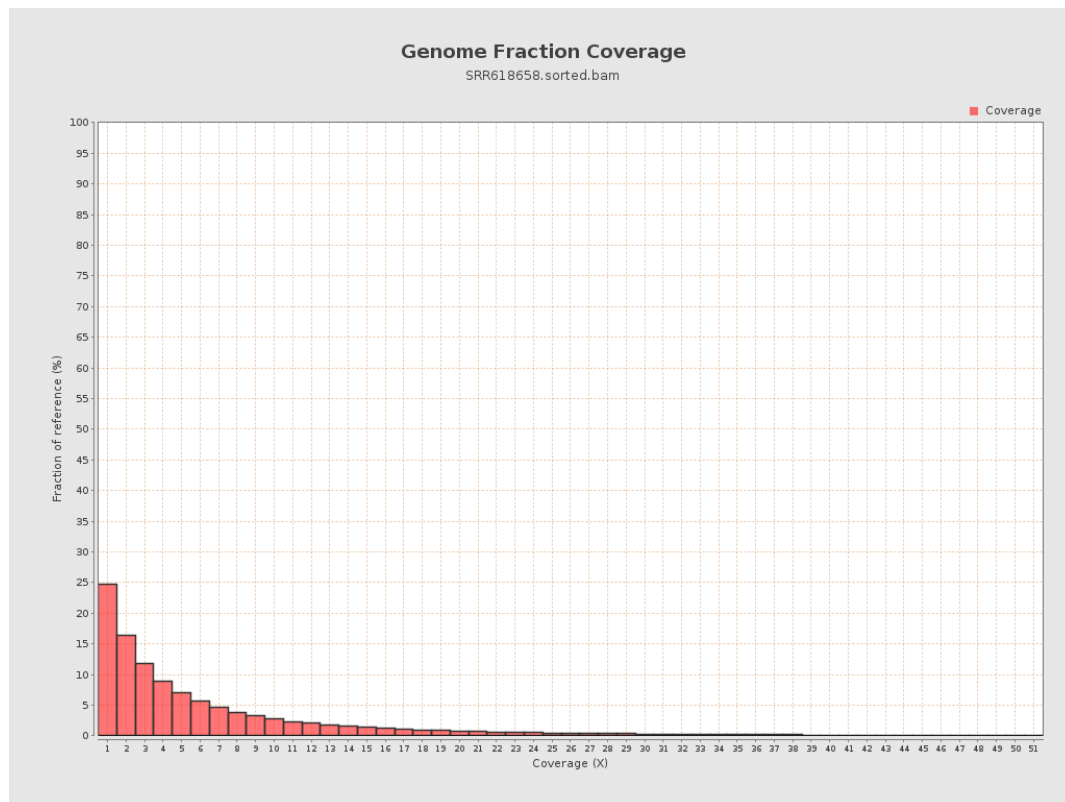
4. Results : Coverage Histogram



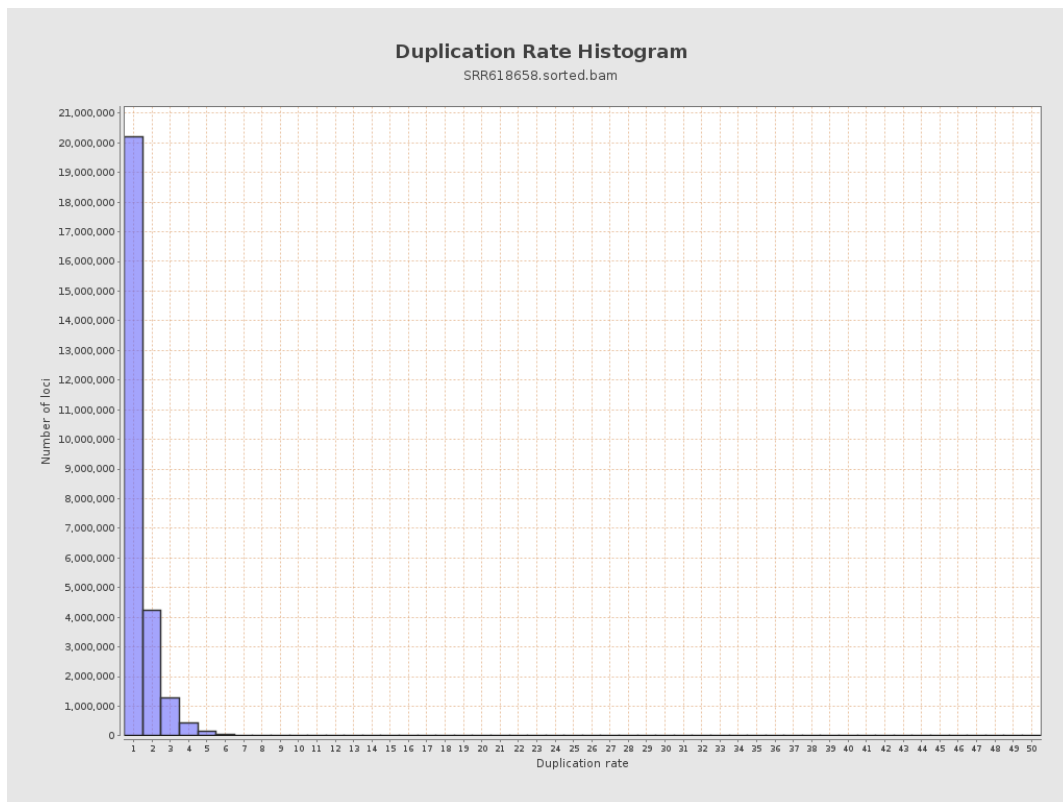
5. Results : Coverage Histogram (0-50X)



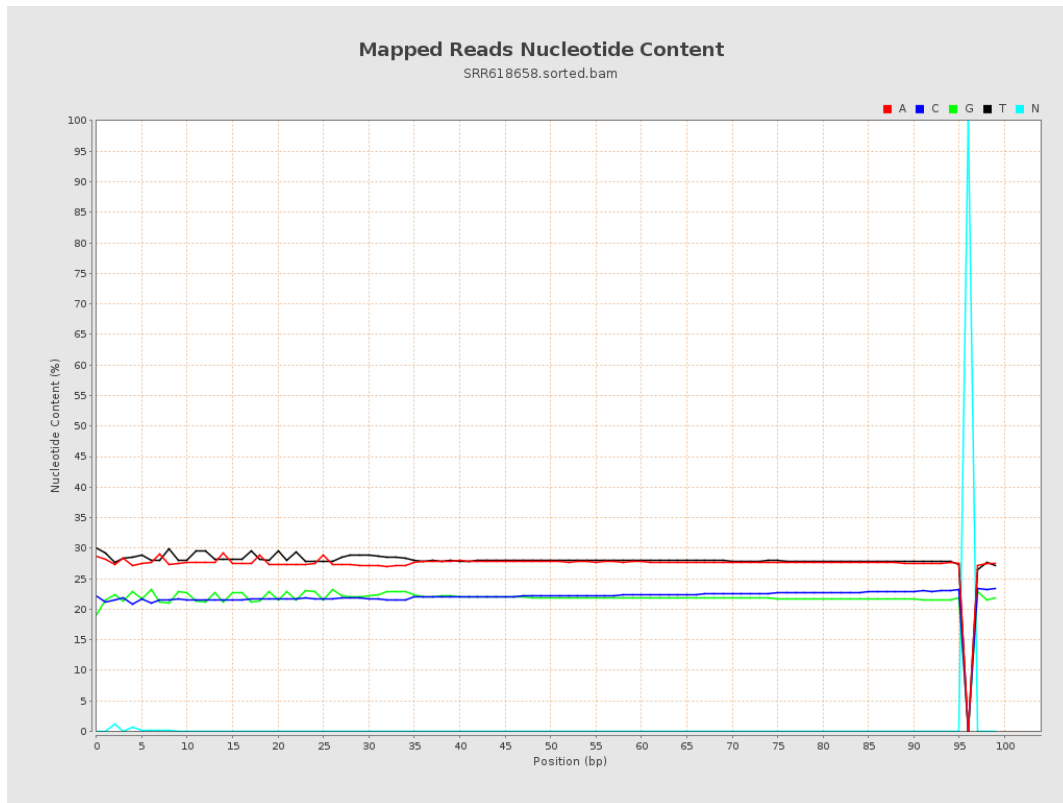
6. Results : Genome Fraction Coverage



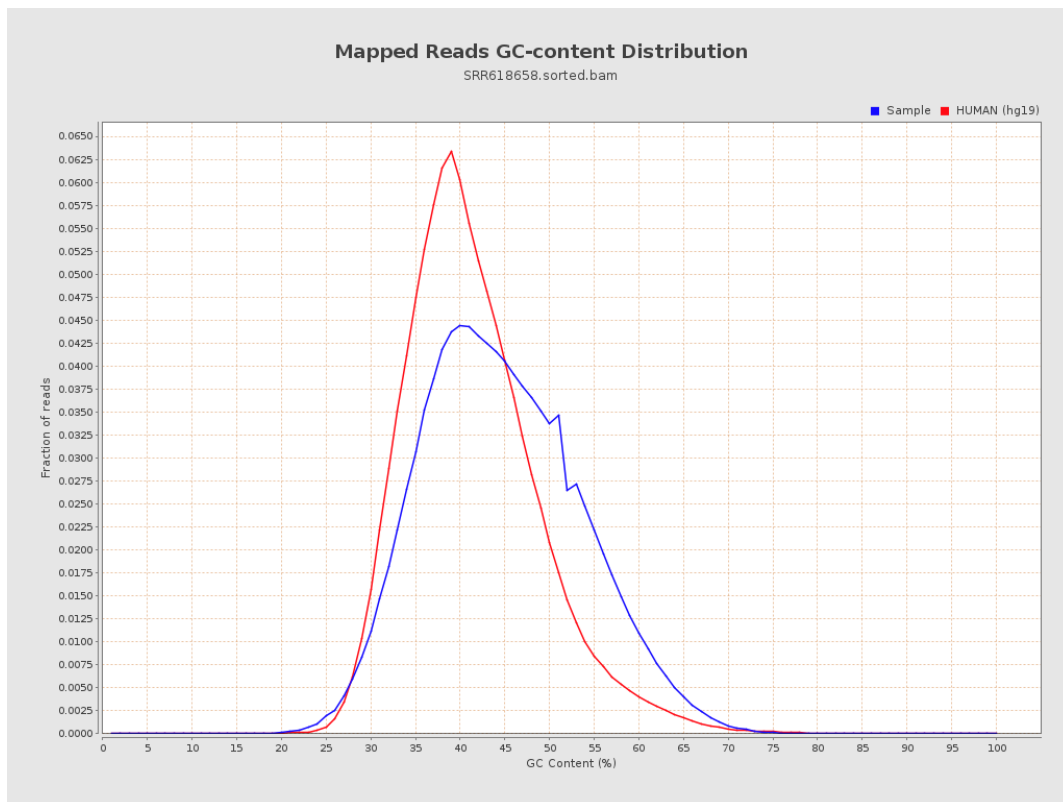
7. Results : Duplication Rate Histogram



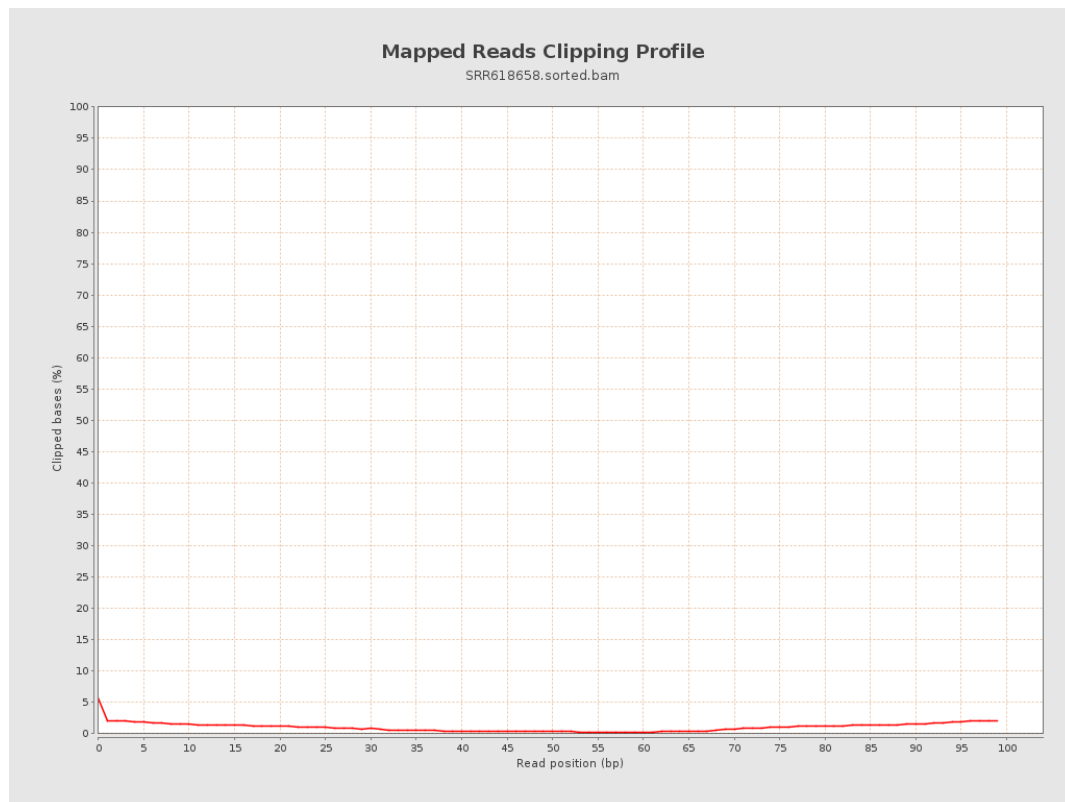
8. Results : Mapped Reads Nucleotide Content



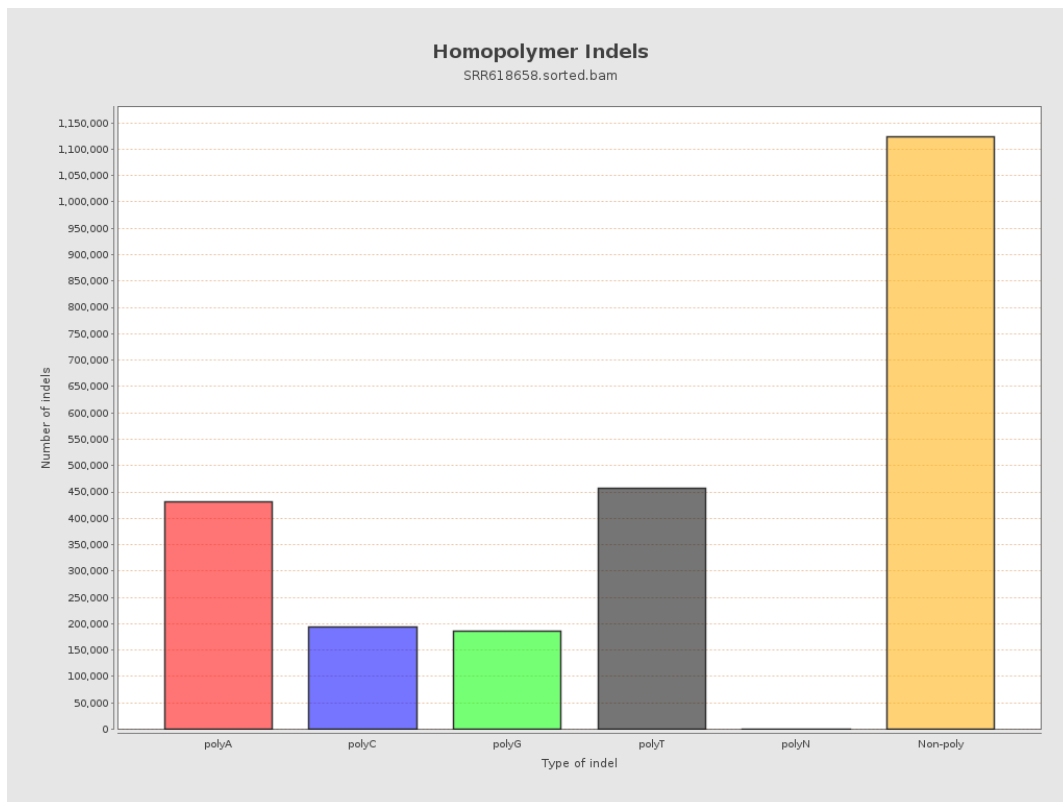
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

