

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:39:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008658.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_SRR6008658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:39:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,203,954
Mapped reads	1,682,455 / 76.34%
Unmapped reads	521,499 / 23.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,594 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	72,212 / 3.28%
Duplication rate	2.94%
Clipped reads	1,134,929 / 51.5%

2.2. ACGT Content

Number/percentage of A's	27,034,636 / 26.53%
Number/percentage of C's	17,435,493 / 17.11%
Number/percentage of T's	32,688,808 / 32.08%
Number/percentage of G's	24,732,494 / 24.27%
Number/percentage of N's	18,683 / 0.02%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3496
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.4
----------------------	------

2.5. Mismatches and indels

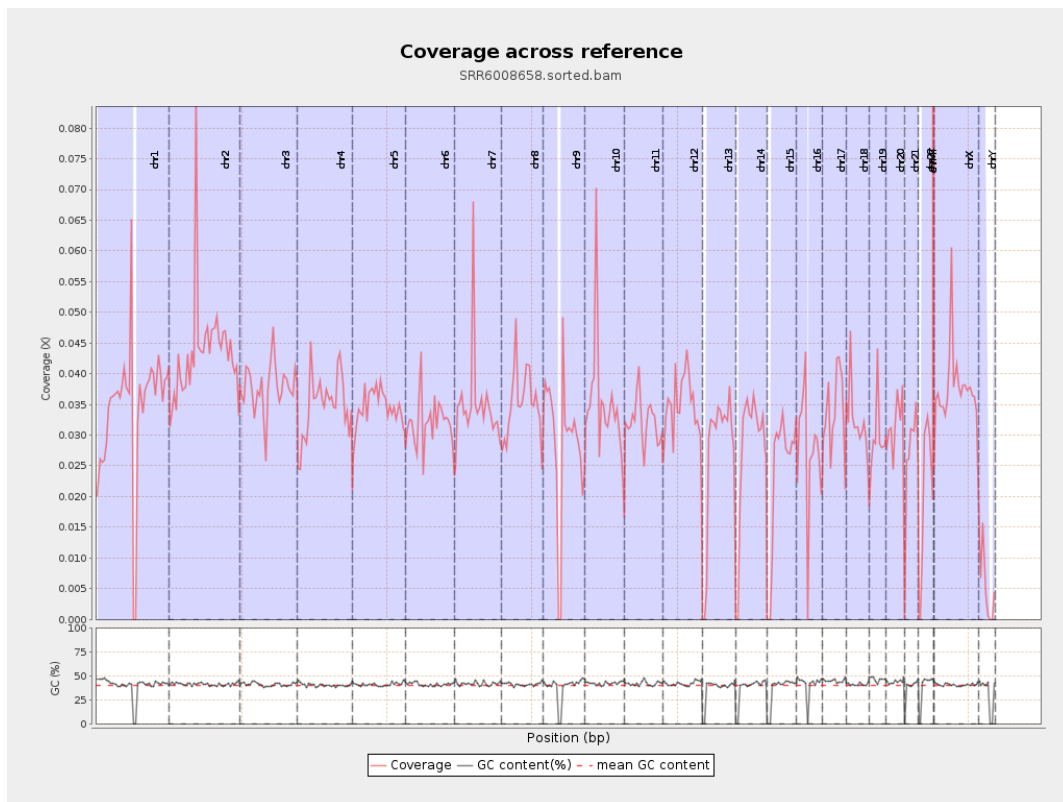
General error rate	0.84%
Mismatches	837,724
Insertions	8,568
Mapped reads with at least one insertion	0.51%
Deletions	32,706
Mapped reads with at least one deletion	1.92%
Homopolymer indels	47.34%

2.6. Chromosome stats

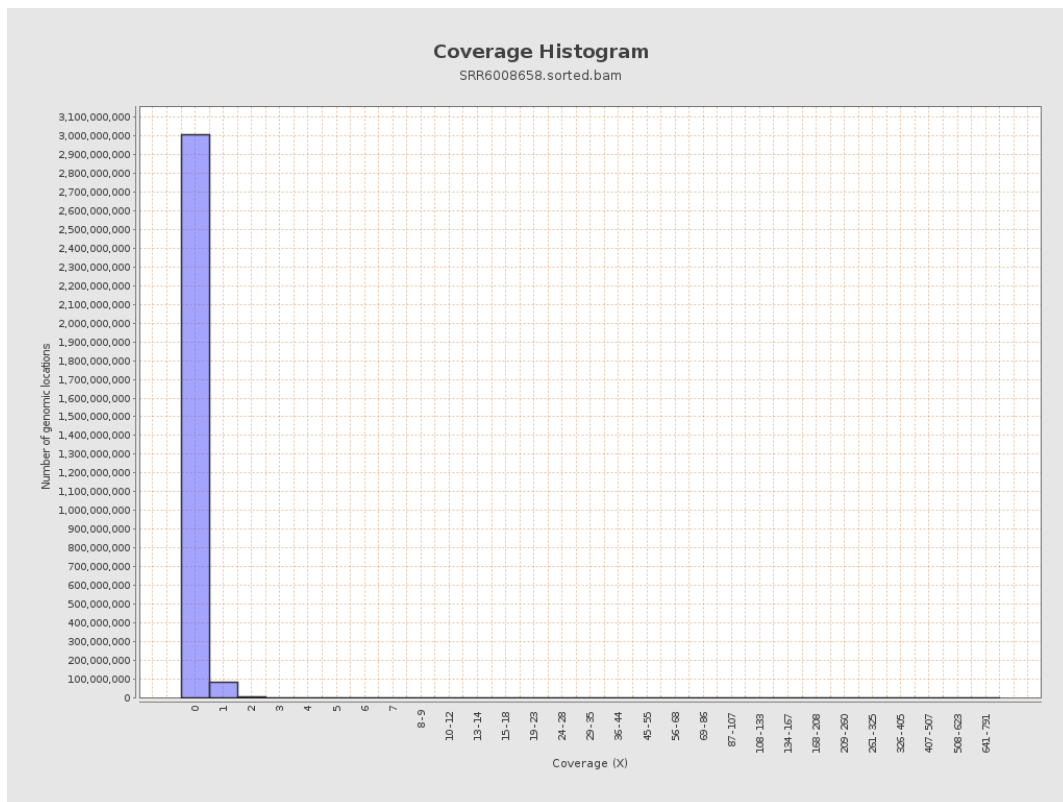
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8546211	0.0343	0.5838
chr2	243199373	10589135	0.0435	0.4418
chr3	198022430	7491208	0.0378	0.2173
chr4	191154276	6645290	0.0348	0.2192
chr5	180915260	6243615	0.0345	0.2072
chr6	171115067	5475645	0.032	0.2591
chr7	159138663	5591932	0.0351	0.5083

chr8	146364022	5120756	0.035	0.3677
chr9	141213431	4060162	0.0288	0.4013
chr10	135534747	4749495	0.035	0.3553
chr11	135006516	4303084	0.0319	0.3362
chr12	133851895	4667000	0.0349	0.2169
chr13	115169878	3084053	0.0268	0.1795
chr14	107349540	2972401	0.0277	0.2302
chr15	102531392	2443751	0.0238	0.1788
chr16	90354753	2488456	0.0275	0.2293
chr17	81195210	2720720	0.0335	0.2536
chr18	78077248	2535291	0.0325	0.6593
chr19	59128983	1755597	0.0297	0.4191
chr20	63025520	1973730	0.0313	0.2087
chr21	48129895	1280517	0.0266	0.202
chr22	51304566	1029746	0.0201	0.1534
chrMT	16571	57230	3.4536	2.6529
chrX	155270560	5827848	0.0375	0.276
chrY	59373566	310187	0.0052	0.1121

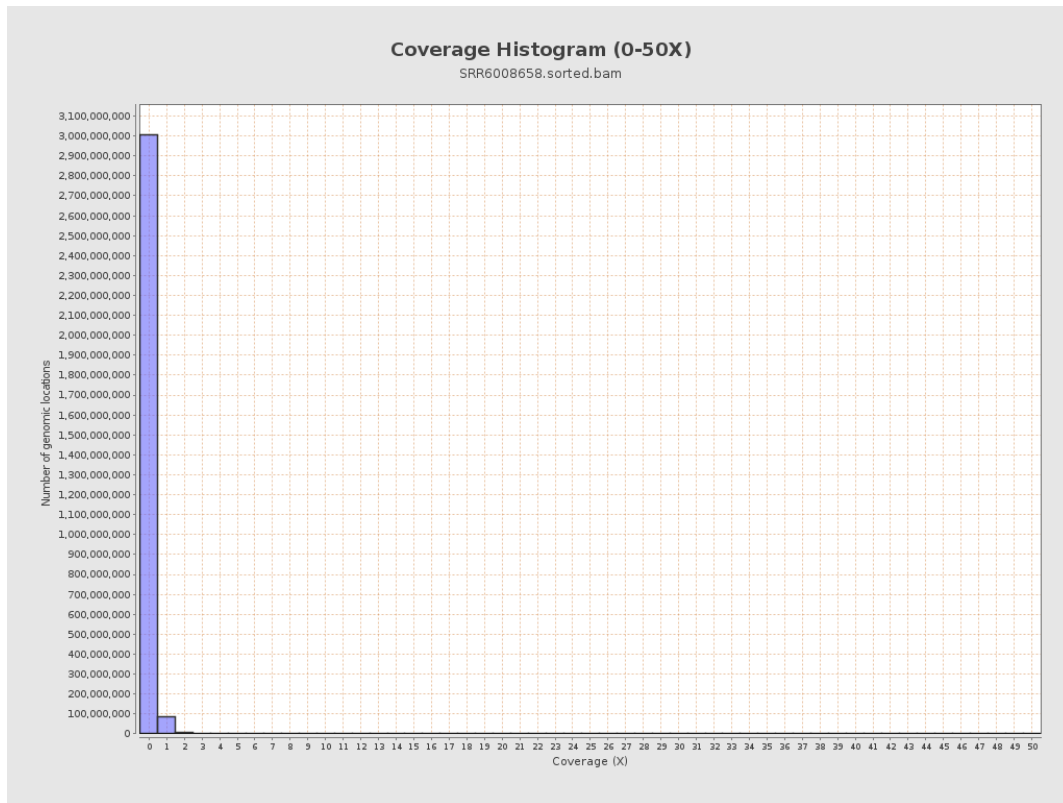
3. Results : Coverage across reference



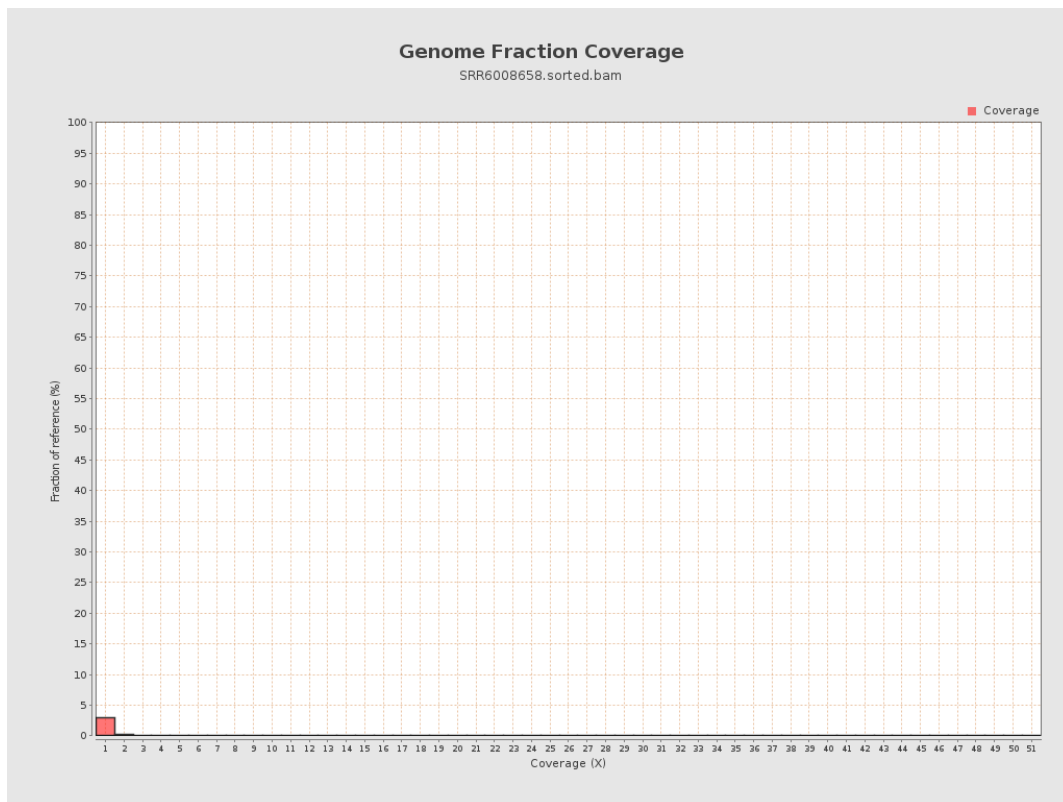
4. Results : Coverage Histogram



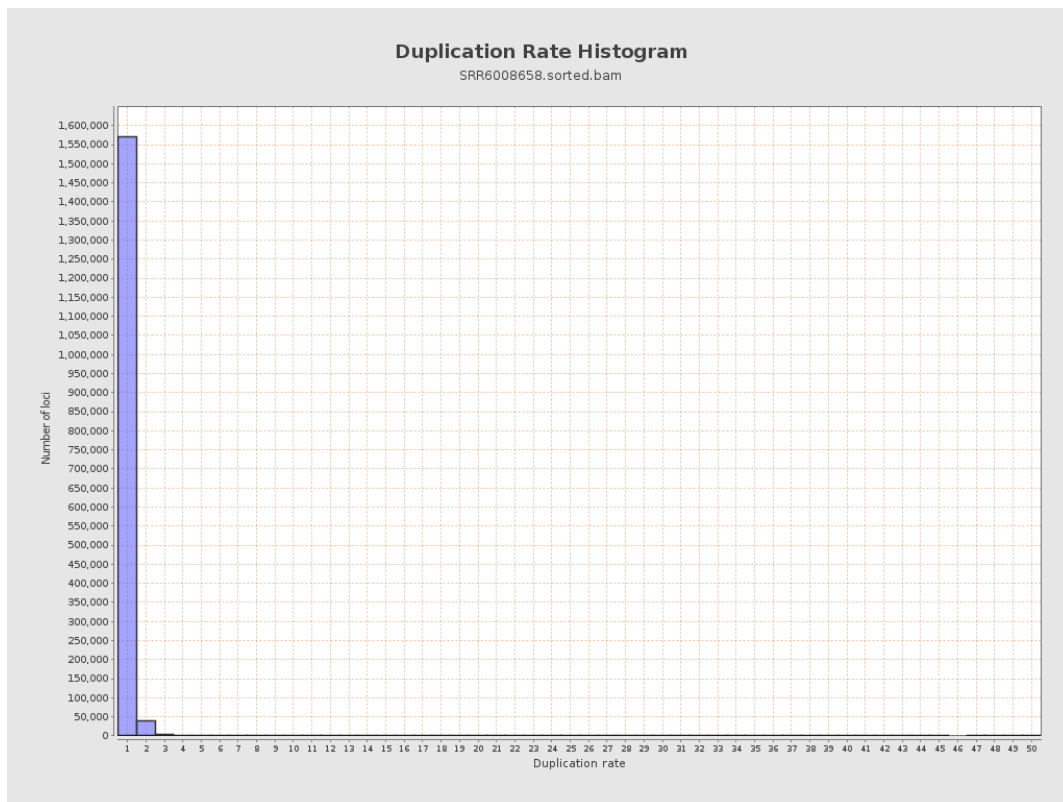
5. Results : Coverage Histogram (0-50X)



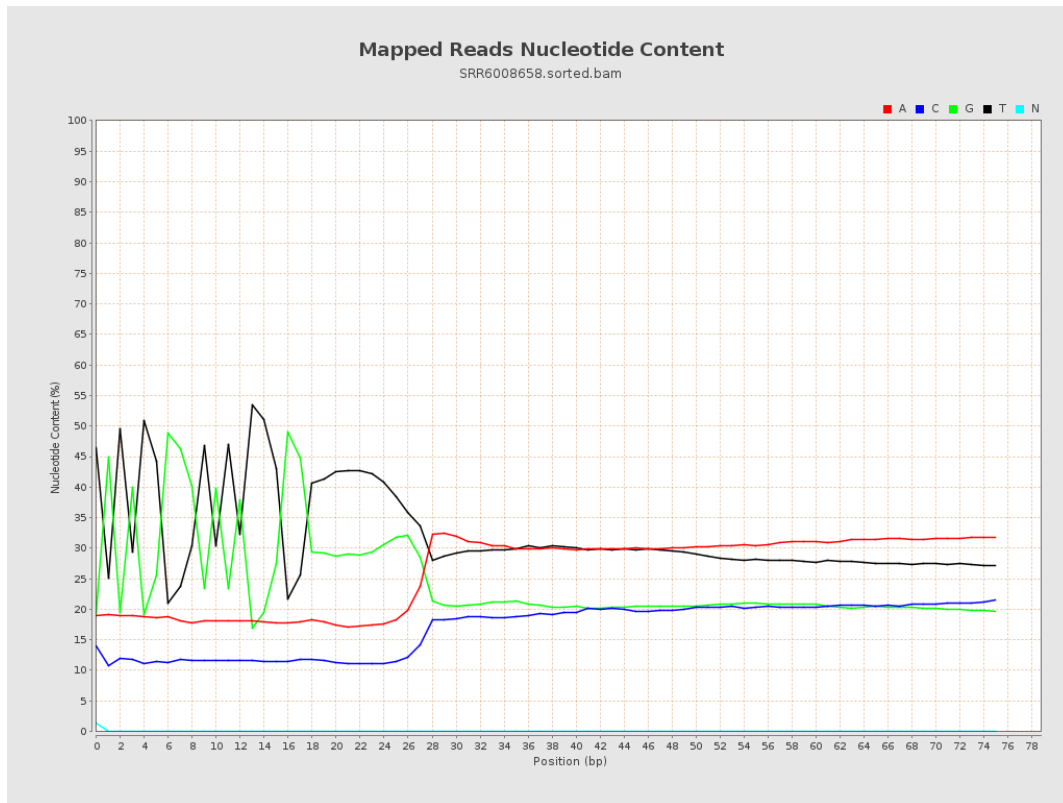
6. Results : Genome Fraction Coverage



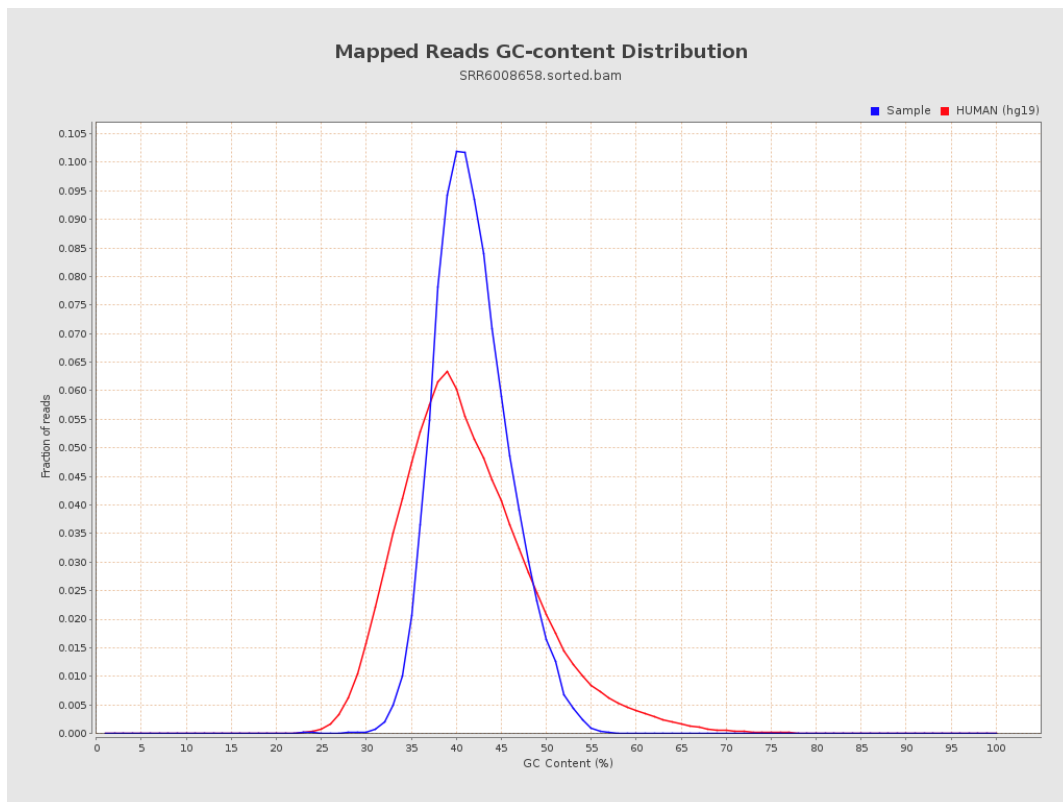
7. Results : Duplication Rate Histogram



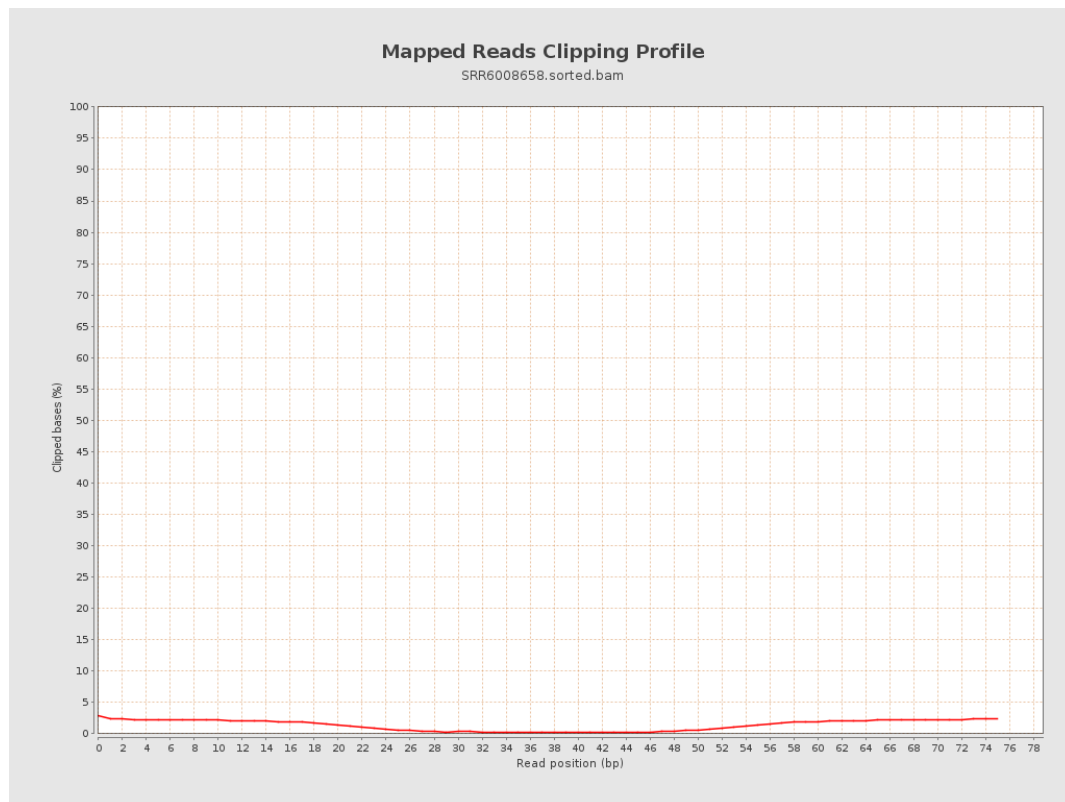
8. Results : Mapped Reads Nucleotide Content



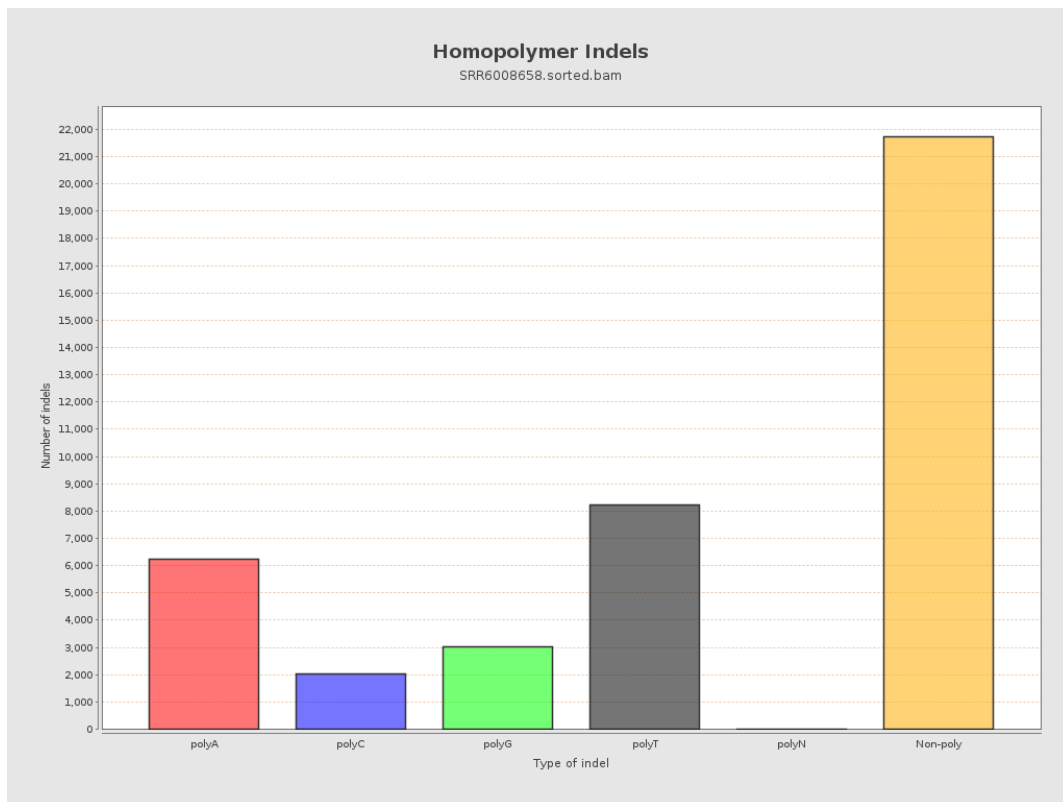
9. Results : Mapped Reads GC-content Distribution



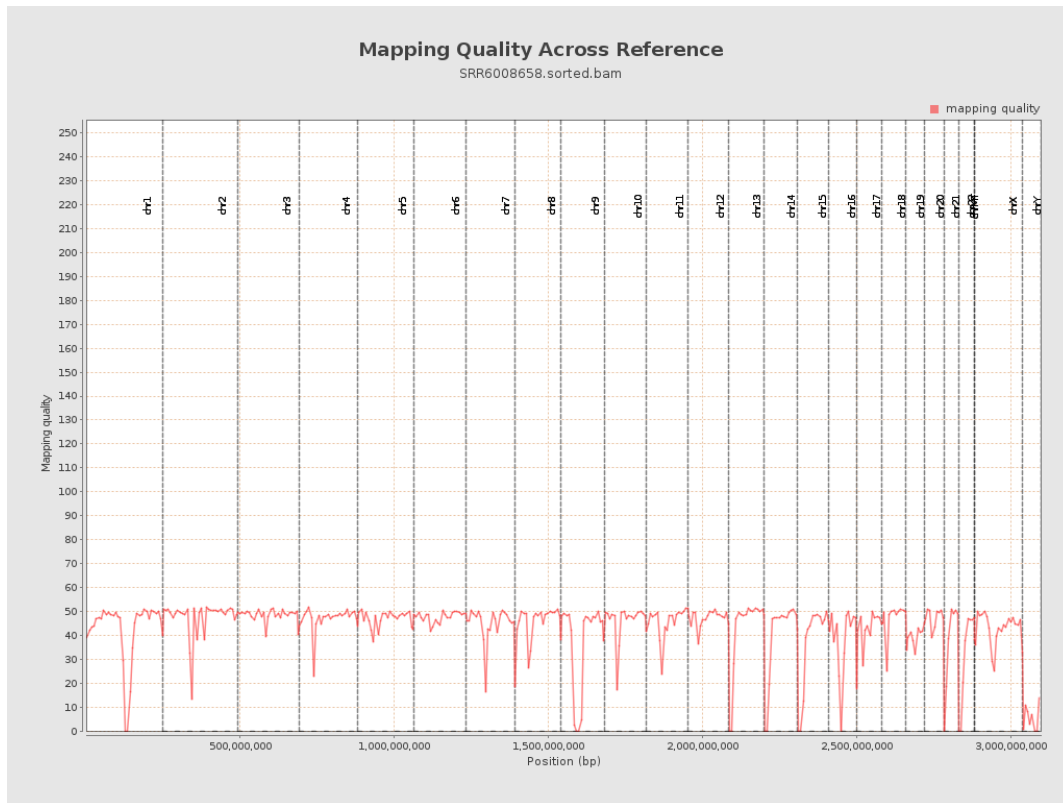
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

