

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:33:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708628.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_SRR1708628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708628.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:33:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,309,753
Mapped reads	2,436,875 / 73.63%
Unmapped reads	872,878 / 26.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	783 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	87,017 / 2.63%
Duplication rate	2.49%
Clipped reads	369,329 / 11.16%

2.2. ACGT Content

Number/percentage of A's	35,193,053 / 29.62%
Number/percentage of C's	22,358,871 / 18.82%
Number/percentage of T's	37,413,898 / 31.49%
Number/percentage of G's	23,829,684 / 20.06%
Number/percentage of N's	10,270 / 0.01%
GC Percentage	38.88%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3906
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2.4. Mapping Quality

Mean Mapping Quality	43.91
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2.5. Mismatches and indels

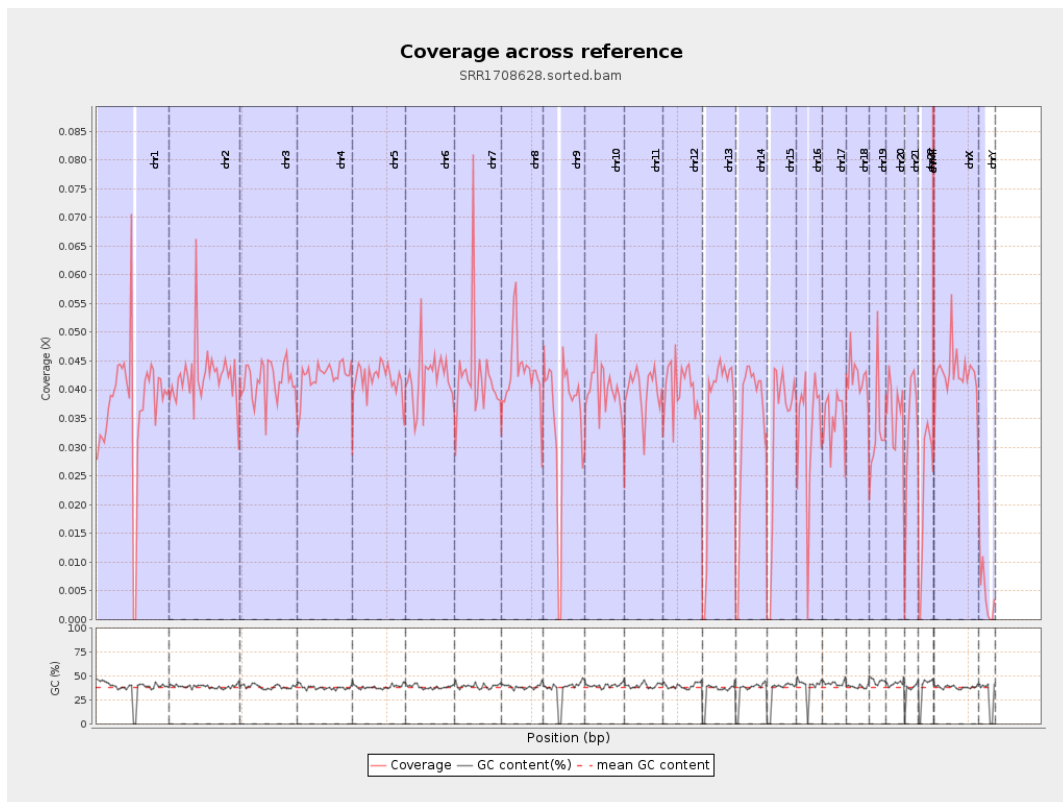
General error rate	0.64%
Mismatches	746,517
Insertions	5,524
Mapped reads with at least one insertion	0.23%
Deletions	14,251
Mapped reads with at least one deletion	0.58%
Homopolymer indels	48.41%

2.6. Chromosome stats

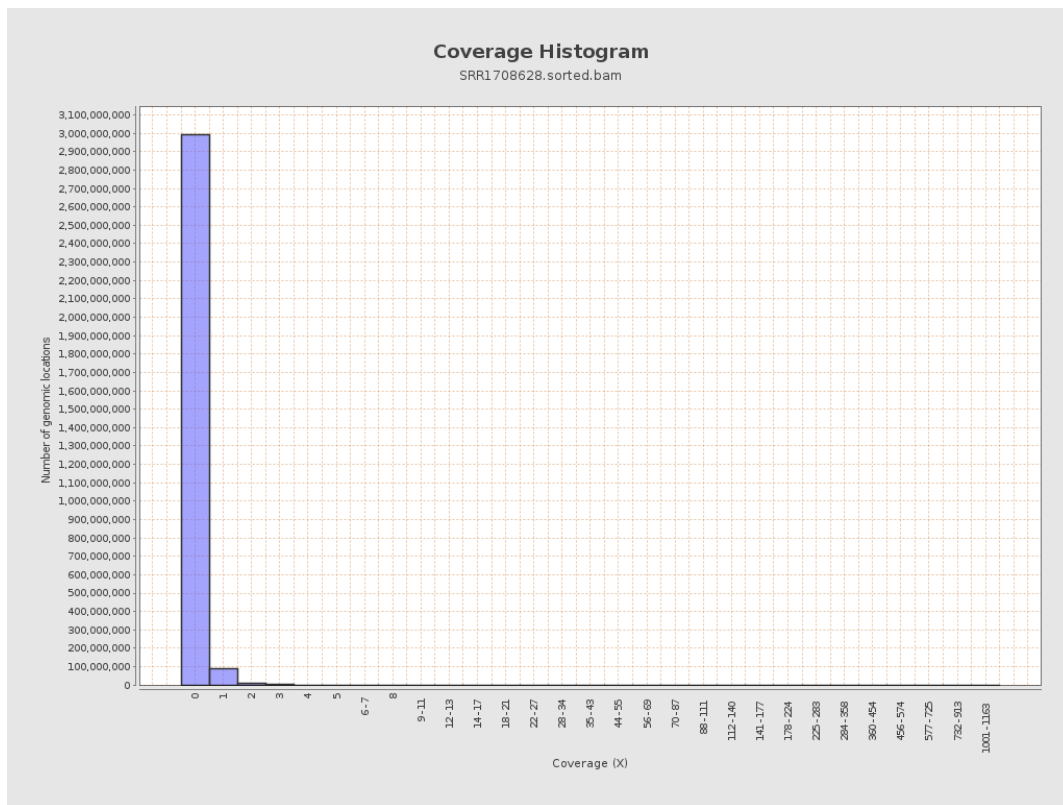
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9290379	0.0373	0.7247
chr2	243199373	10299968	0.0424	0.3823
chr3	198022430	8222337	0.0415	0.2313
chr4	191154276	8112715	0.0424	0.2355
chr5	180915260	7575891	0.0419	0.2385
chr6	171115067	7202816	0.0421	0.2989
chr7	159138663	6778350	0.0426	0.5639

chr8	146364022	6265328	0.0428	0.6787
chr9	141213431	4937887	0.035	0.3183
chr10	135534747	5428306	0.0401	0.3005
chr11	135006516	5359474	0.0397	0.3373
chr12	133851895	5354141	0.04	0.2364
chr13	115169878	4045379	0.0351	0.2129
chr14	107349540	3653222	0.034	0.2257
chr15	102531392	3319807	0.0324	0.2028
chr16	90354753	2989228	0.0331	0.224
chr17	81195210	2800729	0.0345	0.2633
chr18	78077248	3307921	0.0424	0.6382
chr19	59128983	1961820	0.0332	0.5111
chr20	63025520	2275820	0.0361	0.2284
chr21	48129895	1580816	0.0328	0.2224
chr22	51304566	1143558	0.0223	0.1668
chrMT	16571	22471	1.356	1.4255
chrX	155270560	6641145	0.0428	0.2725
chrY	59373566	258340	0.0044	0.0869

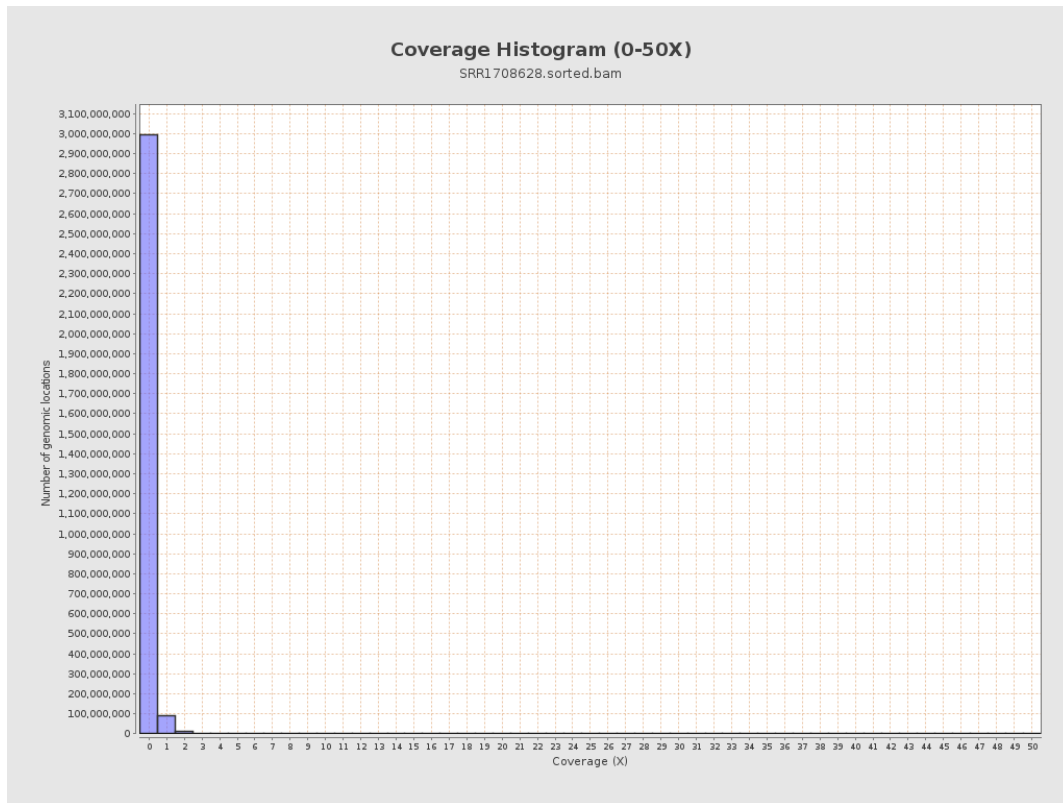
3. Results : Coverage across reference



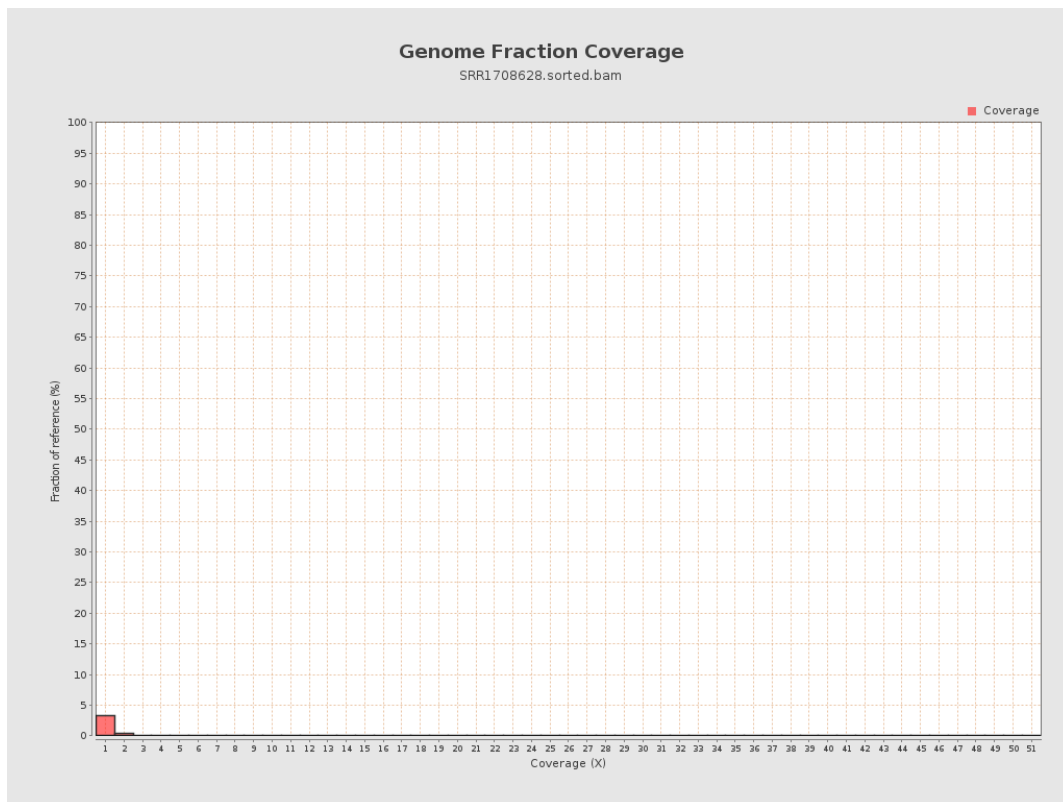
4. Results : Coverage Histogram



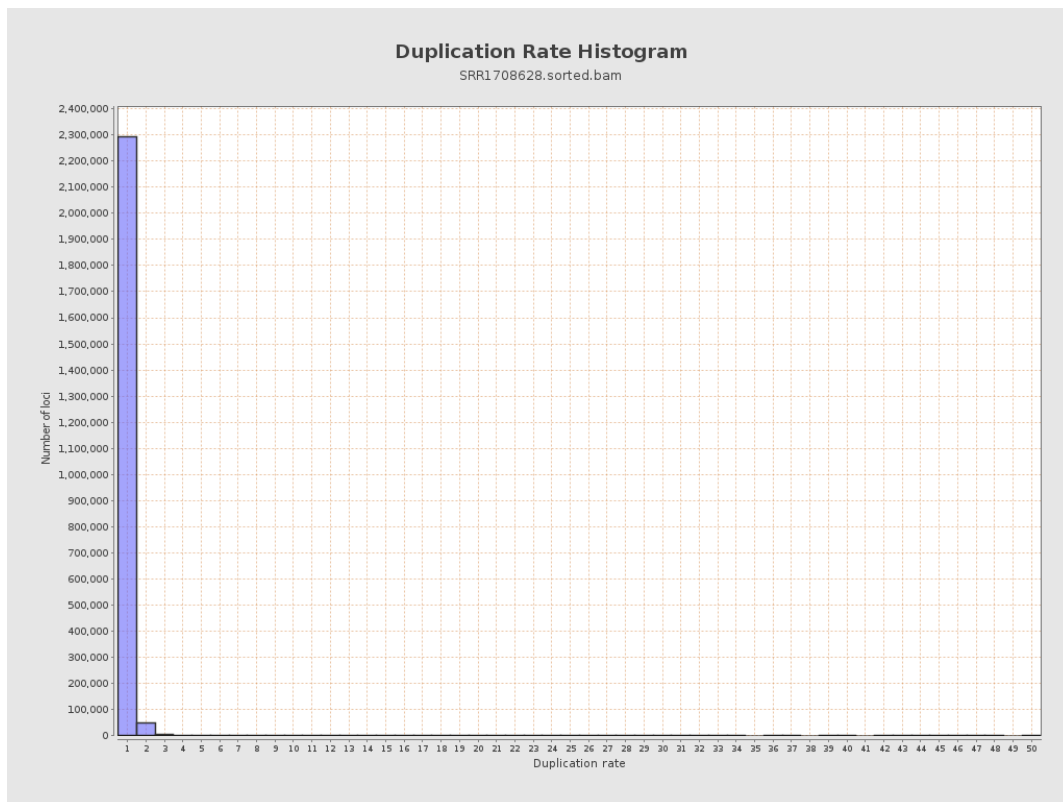
5. Results : Coverage Histogram (0-50X)



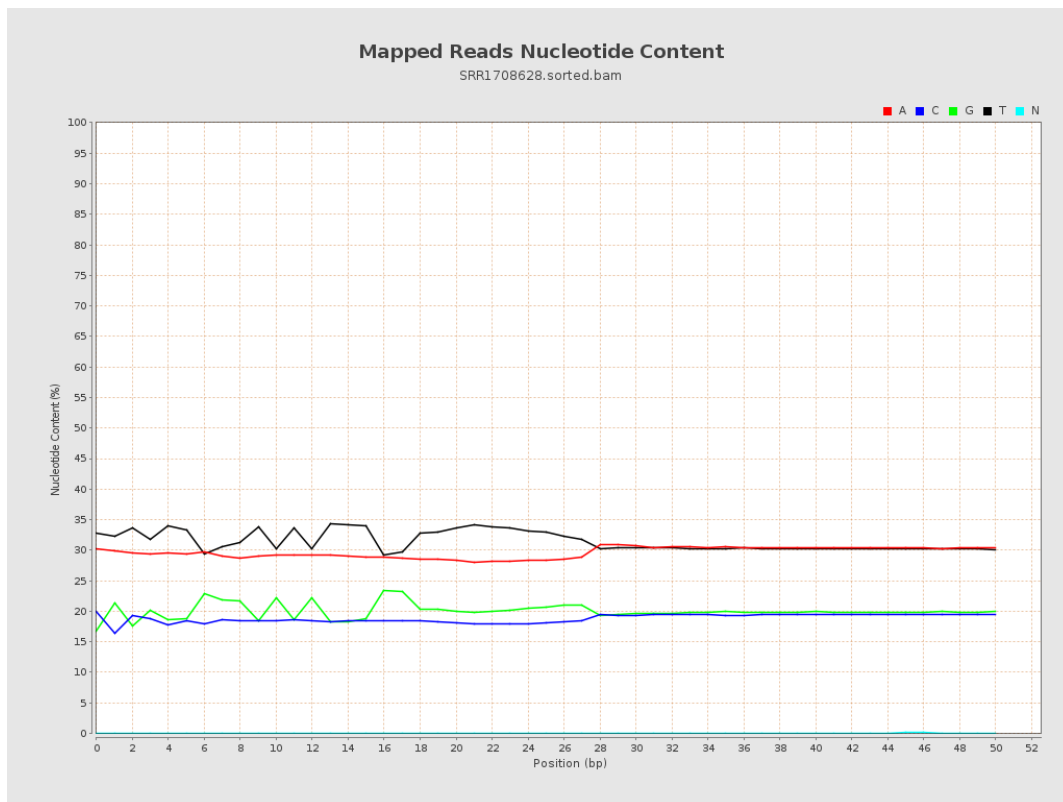
6. Results : Genome Fraction Coverage



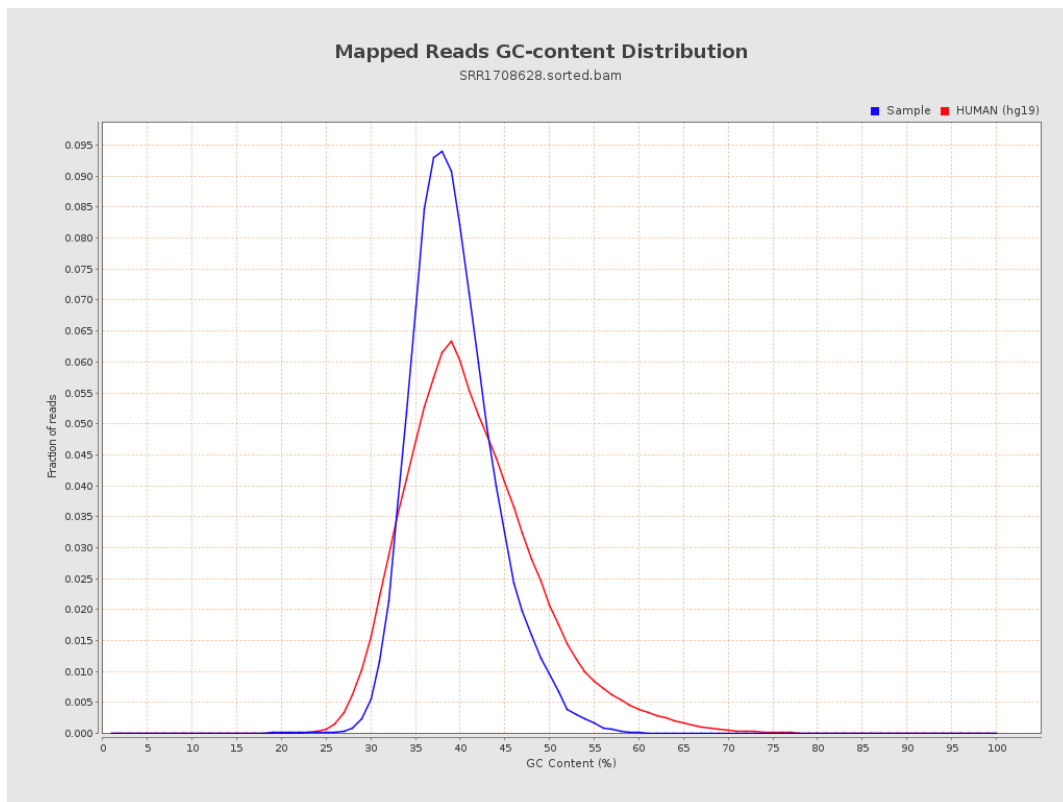
7. Results : Duplication Rate Histogram



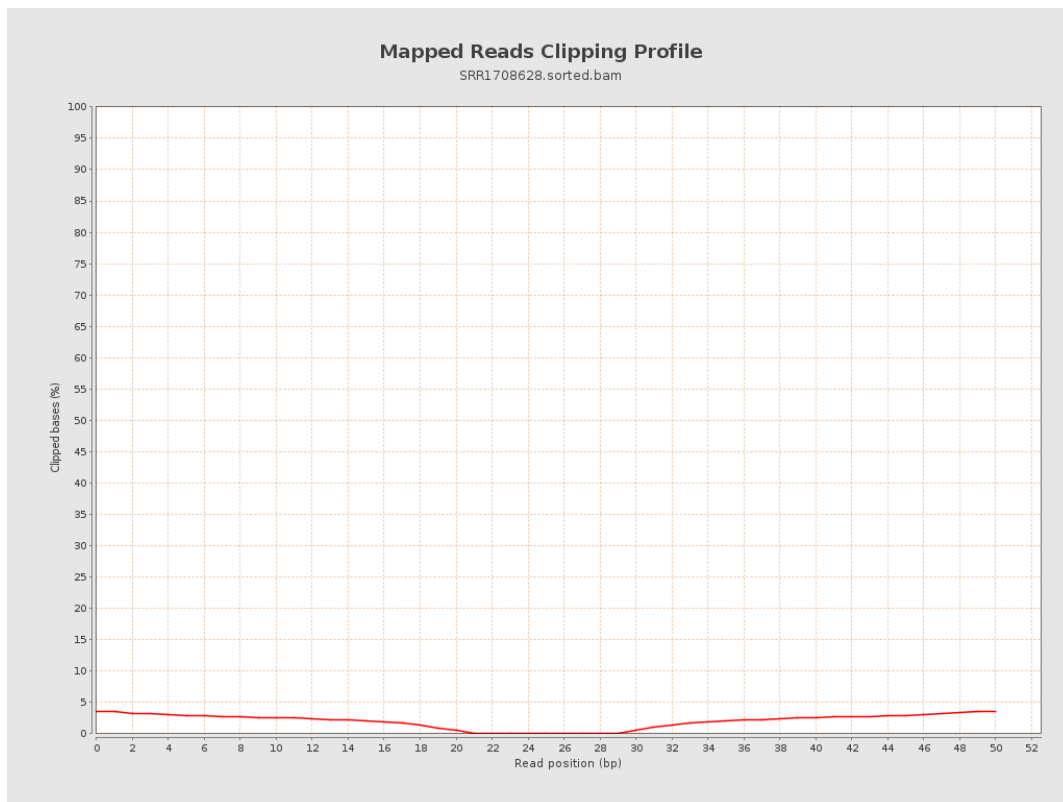
8. Results : Mapped Reads Nucleotide Content



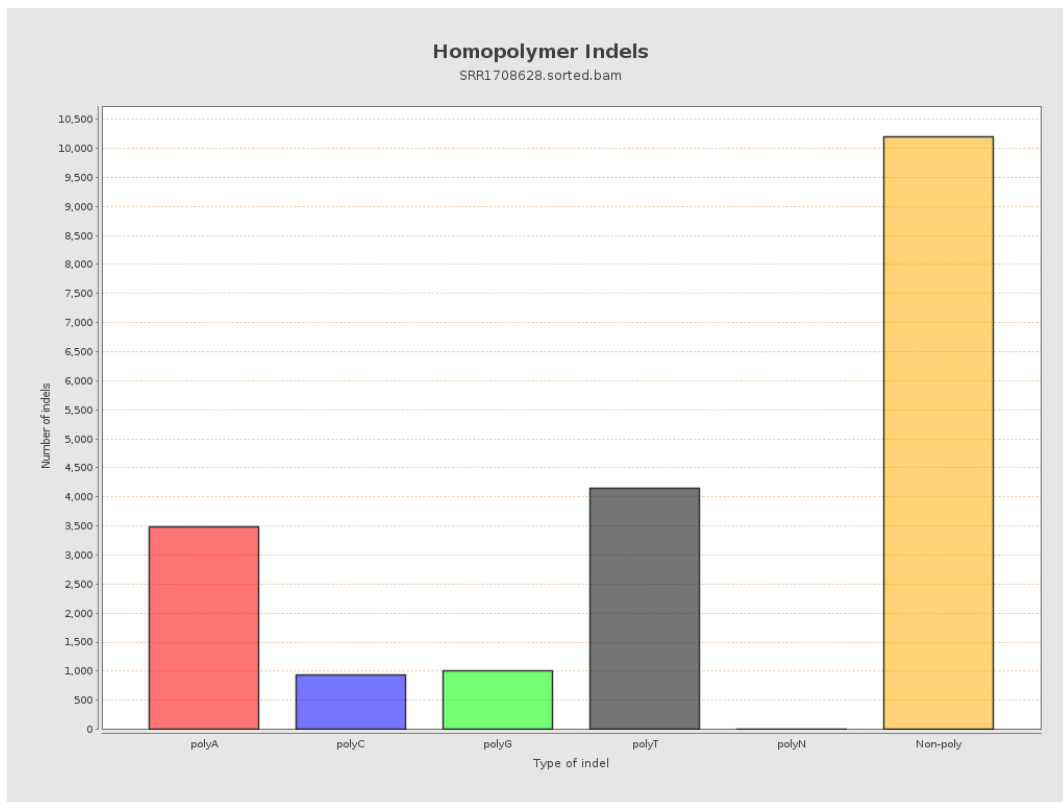
9. Results : Mapped Reads GC-content Distribution



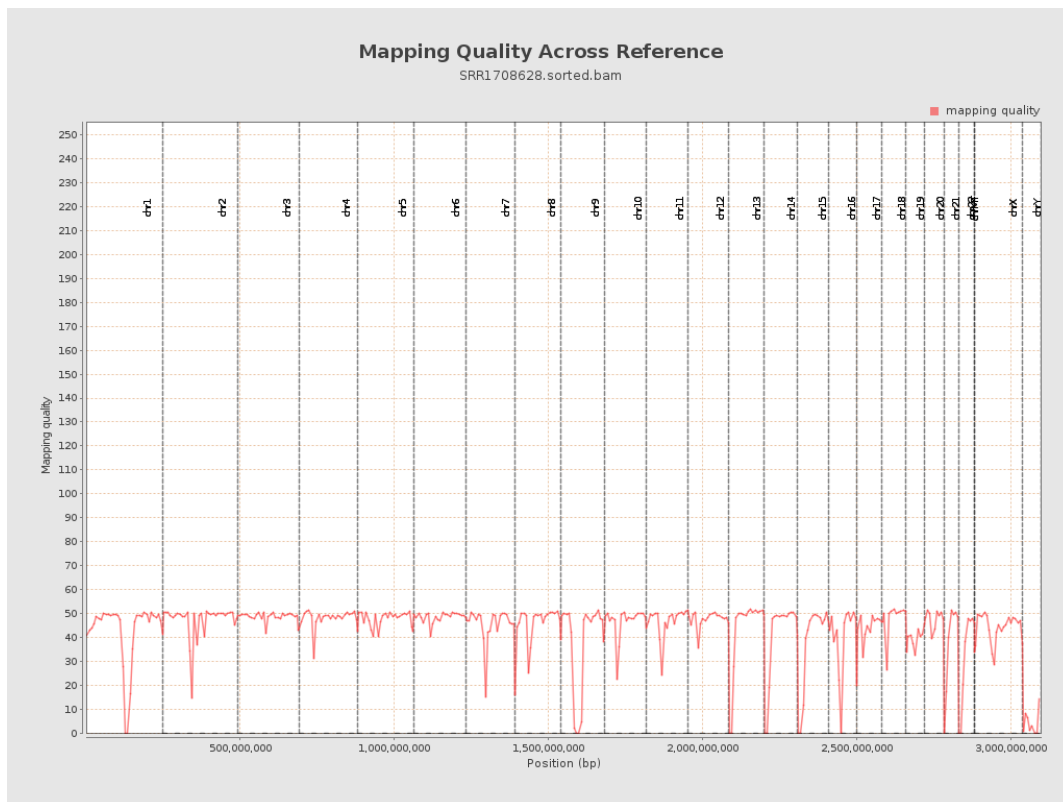
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

